Supplementary Material

Environmental DNA complements scientific trawling in surveys of marine fish biodiversity.

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Methods S1: Calculation of the phylogenetic trees

For Actinopterygii, we used the molecular phylogenetic trees of Rabosky et al. (2018) as a backbone tree including 204 species known to occur in the Bay of Biscay. For taxa detected at the genus level, we arbitrarily selected one representative species if the genus forms a clade (i.e., a monophyletic group) in which all species diverged over the same amount of time from their common ancestor and thus have the same phylogenetic distances, as in Rozanski et al. (2022). We further re-grafted 21 species on the backbone tree that were initially absent, based on their taxonomic affinities and a list of taxonomic constraints, using the phylogenetic classification of bony fishes (Betancur *et al.*, 2017). We randomly sampled the time between two speciation events, defining the branch length for the 21 missing taxa from an exponential distribution based on a Yule model parameter of speciation estimated by maximum likelihood from the molecular tree of the 204 species (Nee *et al.*, 1994). The Yule model accounted for the incomplete and small fraction of species present in our tree in comparison to the known extent of species diversity in Actinopterygii. Here, we used a sampling fraction of 204/36149 = 0.0056, as 36,149 species were officially recognized (Fricke *et al.*, 2022). To account for the phylogenetic uncertainty introduced by re-grafting the species, we generated 100 trees including the 225 Actynopterygii species.

For the Elasmobranchii, we extracted 100 trees from the posterior distribution of the molecular phylogenies published by Stein et al. (2018) and selected the 28 species present in the area. Finally, we built a single set of 100 trees grouping both Actinopterygii and Elasmobranchii taxa, with a total of 253 species, considering an estimated divergence time between the two clades between 421 and 468 Ma (Benton *et al.*, 2015; Stein *et al.*, 2018). To account for the phylogenetic uncertainties in the downstream analyses, we computed the phylogenetic diversity indices for each of the 100 trees and reported averages (and standard deviations). To build this distribution of trees including both Actinopterygii and Elasmobranchii taxa we used the ape (Paradis and Schliep 2019) and phytools (Revell, 2012) R packages.

Table S1: Corrections on taxa detected by both the trawling and the eDNA metabarcoding sampling methods. To perform taxa aggregation and analyses based on fish clades, we retrieved the taxonomic classification from the online databases Barcode of Life Data System (BOLD; Ratnasingham and Herbert 2007) and World Register of Marine Species (WoRMS; Horton *et al.*, 2022).

Taxa detected	Merged into
A., A. fallax	*Alosa fallax*
Anguilla	*Anguilla anguilla*
A., A. silus, A. sphyranea	*Argentina*
A., A. imperialis, A. laterna	*Arnoglossus*
B., B. capriscus	*Balistes capriscus*
B. B. belone	*Belone*
B., B. splendens	*Beryx splendens*
B. B. boops	*Boops boops*
C., C. aper	*Capros aper*
C., C macrophthalma	*Cepola*
C., C. cuculus, C. cuculus, C. obscurus	*Chelidonichthys*
C., C. ramada	*Chelon*
C., C. caelorhincus	*Coelorinchus*
C., C. conger	*Conger conger*
C., C. linearis	*Crystallogobius linearis*
E., E. encrasicolus	*Engraulis*
E., E. spinax	*Etmopterus*
E., E. gurnardus	*Eutrigla gurnardus*
G., G. argenteus	*Gadiculus*
G., G. melastomus	*Galeus*
G., G. semisquamatus	*Gymnammodytes*
H., H. dactylopterus	*Helicolenus dactylopterus*
L., L. boscii, L. whiffiagonis	*Lepidorhombus*
L., L. circularis, L. fullonica, L. naevus	*Leucoraja*
L., L. budegassa, L. piscatorius	*Lophius*
M., M. muelleri	*Maurolicus*
M., M. merluccius	*Merluccius*
M., M. poutassou	*Micromesistius poutassou*
M., M. mola	*Mola mola*
M., M. molva, M. macrophtalma	*Molva*
M., M. surmuletus	*Mullus surmuletus*
N., N. elongatus, N. kroyeri	*Notoscopelus*
P., P. acarne, P. bogaraveo, P. erythrinus	*Pagellus*
P. P. lascaris	*Pegusa*
P., P. fluviatilis	*Perca*
P., P. blennoides	*Phycis*
P., P. lozanoi, P. minutus, P. norvegicus	*Pomatoschistus*
R., R. brachyura, R. clavata, R. microocellata, R. montagui, R. undulata	*Raja*
S. S. sarda	*Sarda sarda*
S., S. pilchardus	*Sardina pilchardus*
S., S. colias	*Scomber colias*
S., S. canicula, S. stellaris	*Scyliorhinus*
S., S. koefoedi	*Searsia koefoedi*
S. S. senegalensis, S. solea	*Solea*
S., S. cantharus	*Spondyliosoma cantharus*
S., S. boa	*Stomias*
T., T. thynnus	*Thunnus*
T., T. draco	*Trachinus draco*
T., T. mediterraneus, T. picturatus, T. trachurus	*Trachurus*
T., T. esmarkii, T. minutus	*Trisopterus*
U., U. canariensis	*Umbrina*
X., X. copei	*Xenodermichthys*
Z., Z. faber	*Zeus faber*

Table S2: Species traits used to calculate functional diversity. We chose nine traits associated with several functions (habitat, feeding, reproduction and mobility) performed by fish in the ecosystem: maximum length (cm), average depth and depth range (m), trophic level, position in the water column (environment), body shape, reproduction mode (Repro; D: dioecism, A: protandry, G: protogyny, H: hermaphroditism), fertilization mode (Fert; E: external, I: internal, B: brood pouch), and parental care (Y: yes, N: no).

	Max length (cm)	**Average depth (m)**	**Depth range (m)**	**Trophic level**	**Environment**	**Body shape**	**Repro**	**Fert**	**Parental care**
Alosa fallax	60	205	390	4	pelagic	fusiform	D	E	N
Ammodytes marinus	25	80	140	3.3	demersal	elongated	D	E	N
Anguilla anguilla	122	350	700	3.6	demersal	eel-like	D	E	N
Aphanopus carbo	151	1250	2100	4.5	bathypelagic	eel-like	D	E	N
Aphia minuta	7.9	48.5	97	3.1	pelagic	elongated	D	E	
Argentina silus	70	790	1300	3.3	bathypelagic	elongated	D	E	N
Argentina sphyraena	35	375	650	3.5	bathydemersal	elongated	D	E	N
Argyrosomus regius	230	157.5	285	4.3	demersal	fusiform	D	E	
Arnoglossus imperialis	25	185	330	3.8	demersal	flat	D	E	N
Arnoglossus laterna	25	105	190	3.6	demersal	flat	D	E	N
Arnoglossus rueppelii	15	491	812	4	demersal	flat	D	E	N
Arnoglossus thori	18	157.5	285	3.3	demersal	flat	D	E	N
Atherina presbyter	20	10	20	3.7	pelagic	elongated	D	E	N
Balistes capriscus	60	50	100	4.1	reef-associated	short/deep	D	E	Y
Belone belone	104	10	20	4.2	pelagic	elongated	D	E	N
Belone svetovidovi	41.8	10	20	4	pelagic	elongated	D	E	N
Beryx splendens	70	662.5	1275	4.3	demersal	fusiform	D	E	
Boops boops	40	175	350	2.8	demersal	fusiform	G	E	N
Borostomias antarcticus	30	1465	2330	3.6	bathydemersal	elongated	D	E	
Buglossidium luteum	16.4	227.5	445	3.3	demersal	flat	D	E	N
Callionymus lyra	30.5	217.5	425	3.3	demersal	elongated	D	E	N
Callionymus maculatus	16.5	347.5	605	3.3	demersal	elongated	D	E	N
Capros aper	30	370	660	3.1	demersal	short/deep	D	E	N
Cepola macrophthalma	80	207.5	385	3.1	demersal	elongated	D	E	N
Ceratoscopelus maderensis	8.1	765.5	1429	3.3	bathypelagic	elongated	D	E	
Chelidonichthys cuculus	70	207.5	385	3.8	demersal	fusiform	D	E	N
Chelidonichthys lastoviza	40	80	140	3.5	demersal	fusiform	D	E	N
Chelidonichthys lucerna	75.1	169	298	4	demersal	elongated	D	E	N
Chelidonichthys obscurus	50.5	95	150	3.7	demersal	fusiform	D	E	N
Chelon auratus	59	15	10	2.8	pelagic	fusiform	D	E	N
Chelon labrosus	75	7.5	15	2.6	demersal	elongated	D	E	N
Chelon ramada	70	15	10	2.3	pelagic	fusiform	D	E	N
Chimaera monstrosa	150	720	1360	3.5	bathydemersal	elongated	D	I	N
Coelorinchus caelorhincus	48	787.5	1395	3.5	demersal	elongated			
Coelorinchus caudani	36	1090	640	3.5	bathydemersal	elongated			
Coelorinchus labiatus	50	1340	1760	4	bathydemersal	elongated			
Conger conger	300	585.5	1171	4.3	demersal	eel-like	D	E	
Crystallogobius linearis	4.7	200.5	399	3.4	demersal	elongated	D	E	Y
Cyclothone microdon	7.6	2750.5	5101	3	bathypelagic	elongated	A		
Dasyatis pastinaca	69.5	102.5	195	4.1	demersal	ray-like	D	I	Y
Dasyatis tortonesei	80	150	100	4	demersal	ray-like	D	I	
Dicentrarchus labrax	103	55	90	3.5	demersal	fusiform	D	E	N
Dicentrarchus punctatus	70	55	90	3.9	pelagic	fusiform	D	E	N
Dicologlossa cuneata	30	235	450	3.3	demersal	short/deep	D	E	N
Dipturus intermedius	230	750.5	1499	4.1	demersal	ray-like	D	I	N

	Max length (cm)	**Average depth (m)**	**Depth range (m)**	**Trophic level**	**Environment**	**Body shape**	**Repro**	**Fert**	**Parental care**
Echiichthys vipera	15	75	150	4.4	demersal	elongated	D	E	N
Enchelyopus cimbrius	41	335	630	3.5	demersal	elongated	D	E	N
Engraulis encrasicolus	20	200	400	3.1	pelagic	elongated	D	E	N
Etmopterus princeps	94	1256.5	1913	4.2	bathydemersal	elongated	D	I	
Etmopterus pusillus	50	560	1120	4.2	bathydemersal	elongated	D	I	Y
Etmopterus spinax	60	1280	2420	4.1	bathydemersal	elongated	D	I	Y
Eutrigla gurnardus	60	175	330	3.9	demersal	elongated	D	E	N
Gadiculus argenteus	15.3	550	900	3.6	pelagic	fusiform	D	E	N
Gadiculus thori	15	550	900	3.5	pelagic	fusiform	D	E	N
Gaidropsarus macrophthalmus	25	340	380	3.5	demersal	elongated	D	E	N
Galeus atlanticus	45	540	200	4	bathydemersal	elongated	D	I	
Galeus melastomus	75	964	1818	4.2	demersal	elongated	D	I	N
Galeus murinus	63	837.5	725	4	bathydemersal	elongated	D	I	
Gymnammodytes cicerelus	17	60	120	3.4	demersal	eel-like	D	E	N
Gymnammodytes semisquamatus	30	65	110	2.7	demersal	elongated	D	E	
Helicolenus dactylopterus	50	575	1050	3.5	bathydemersal	fusiform	D	I	N
Hexanchus griseus	482	1250.5	2499	4.5	bathydemersal	elongated	D	I	Y
Hippocampus hippocampus	15	15	30	3.2	demersal	other	D	B	Y
Lamna nasus	350	680	1360	4.6	pelagic	fusiform	D	I	
Lampanyctus crocodilus	30	600	1200	3.2	bathypelagic	elongated	D	E	N
Lampanyctus festivus	13.8	546	1012	3.2	bathypelagic	elongated			
Lampanyctus intricarius	20	395	710	3.4	bathypelagic	elongated			
Lampanyctus macdonaldi	16	762	1404	3.1	bathypelagic	elongated			
Lampanyctus photonotus	8.5	570	1060	3.2	bathypelagic	elongated			
Lampanyctus pusillus	4.3	445	810	3.4	bathypelagic	elongated			
Lepidorhombus boscii	40	403.5	793	3.7	demersal	flat	D	E	N
Lepidorhombus whiffiagonis	60	400	600	4.3	bathydemersal	flat	D	E	N
Lepidotrigla dieuzeidei	20	328	536	3.7	demersal	fusiform	D	E	N
Lesueurigobius friesii	13	70	120	3.4	demersal	fusiform	D	E	
Leucoraja circularis	120	405	790	3.5	demersal	ray-like	D	I	N
Leucoraja fullonica	120	315	570	3.5	bathydemersal	ray-like	D	I	N
Leucoraja naevus	81	456	888	4.2	demersal	ray-like	D	I	N
Lithognathus mormyrus	55	75	150	3.4	demersal	fusiform	A	E	N
Lophius budegassa	100	541.5	943	4.4	bathydemersal	short/deep	D	E	N
Lophius piscatorius	200	510	980	4.5	bathydemersal	short/deep	D	E	N
Macroramphosus scolopax	20	312.5	575	3.5	demersal	short/deep	D	E	N
Malacocephalus laevis	60	600	800	3.8	bathydemersal	elongated			
Maurolicus amethystinopunctatus	5	765	670	3.1	pelagic	fusiform			
Maurolicus muelleri	8	897.5	1253	3	bathypelagic	elongated	D		
Melanostigma atlanticum	15	1126.5	1453	3	bathypelagic	elongated	D	E	N
Merlangius merlangus	91.5	105	190	4.4	demersal	fusiform	D	E	N
Merluccius merluccius	140	552.5	1045	4.4	demersal	elongated	D	E	N
Merluccius senegalensis	81	407.5	785	4.5	demersal	elongated	D	E	N
Microchirus variegatus	35	210	380	3.3	demersal	flat	D	E	N
Micromesistius poutassou	55.5	1575	2850	4.1	bathypelagic	elongated	D	E	N
Microstomus kitt	65	105	190	3.2	demersal	short/deep	D	E	N
Mola mola	333	255	450	3.3	pelagic	short/deep	D	E	N
Molva dypterygia	155	575	850	4.5	demersal	elongated	D	E	N
Molva macrophthalma	108	515	970	4.5	demersal	elongated	D	E	N
Molva molva	200	550	900	4.4	demersal	elongated	D	E	N
Mora moro	80	1475	2050	3.8	bathypelagic	fusiform	D	E	N
Mullus surmuletus	40	207	404	3.5	demersal	fusiform	D	E	
Mustelus asterias	140	175	350	3.6	demersal	elongated	D	I	
Myctophum punctatum	11	500	1000	3.4	bathypelagic	fusiform	D	E	
Myliobatis aquila	183	150.5	299	3.6	demersal	ray-like	D	I	
Nezumia aequalis	36	1260	2120	3.3	demersal	elongated	D	E	N
Notoscopelus bolini	10.2	650	1300	3.1	pelagic	fusiform			
Notoscopelus caudispinosus	14	180	360	3.2	bathypelagic	fusiform			
Notoscopelus kroeyeri	14.3	500	1000	3.2	pelagic	fusiform			

	Max length (cm)	Average depth (m)	Depth range (m)	Trophic level	Environment	Body shape	Repro	Fert	Parental care
Pagellus acarne	36	270	460	3.8	demersal	fusiform	A	E	N
Pagellus bogaraveo	70	425	550	4.2	demersal	fusiform	A	E	N
Pagellus erythrinus	60	160	280	3.5	demersal	fusiform	G	E	N
Parablennius pilicornis	12.7	12.5	25	3.2	demersal	fusiform	D	E	
Pegusa lascaris	40	177.5	345	3.3	demersal	short/deep	D	E	N
Phycis blennoides	110	605	1190	3.7	demersal	fusiform	D	E	N
Polymetme thaeocoryla	21.6	806	1187	3.6	demersal	fusiform			
Pomatoschistus lozanoi	8	75	10	3.1	demersal	fusiform	D	E	
Pomatoschistus marmoratus	8	45	50	3.4	demersal	fusiform	D	E	
Pomatoschistus microps	9	6	12	3.3	demersal	elongated	D	E	
Pomatoschistus minutus	11	102	196	3.2	demersal	elongated	D	E	Y
Pomatoschistus norvegicus	8	171.5	307	3.3	demersal	fusiform	D	E	
Pomatoschistus pictus	6	28	54	3.1	demersal	fusiform	D	E	
Prionace glauca	400	500.5	999	4.4	pelagic	fusiform	D	I	
Raja asterias	75	172.5	341	3.8	demersal	ray-like	D	I	N
Raja brachyura	120	195	370	3.8	demersal	ray-like	D	I	N
Raja clavata	105	512.5	1015	3.8	demersal	ray-like	D	I	N
Raja microocellata	87	60	80	3.9	demersal	ray-like	D	I	N
Raja miraletus	63	239.5	445	3.7	demersal	other	D	I	N
Raja montagui	83.5	269	522	3.9	demersal	ray-like	D	I	N
Raja undulata	100	125	150	3.5	demersal	ray-like	D	I	N
Rhynchoconger flavus	150	104.5	157	4.2	demersal	eel-like	D	E	
Sarda sarda	91.4	140	120	4.5	pelagic	fusiform	D	E	N
Sardina pilchardus	27.5	55	90	3.1	pelagic	fusiform	D	E	N
Sarpa salpa	51	37.5	65	2	demersal	fusiform	A	E	N
Scomber colias	55	500	1000	3.9	pelagic	fusiform	D	E	N
Scomber scombrus	60	500	1000	3.6	pelagic	fusiform	D	E	N
Scomberesox saurus	50	15	30	3.9	pelagic	elongated	D	E	
Scophthalmus maximus	100	45	50	4.4	demersal	short/deep	D	E	
Scophthalmus rhombus	75	27.5	45	4.4	demersal	short/deep	D	E	N
Scorpaena scrofa	50	260	480	4.3	demersal	fusiform	D	E	N
Scyliorhinus canicula	100	395	770	3.8	demersal	elongated	D	I	N
Scyliorhinus stellaris	170	200.5	399	4	reef-associated	elongated	D	I	N
Searsia koefoedi	15	975	1050	3.4	bathypelagic	elongated			
Serranus cabrilla	40	252.5	495	3.4	demersal	fusiform	H	E	
Solea senegalensis	60	38.5	53	3.3	demersal	short/deep	D	E	N
Solea solea	70	75	150	3.2	demersal	flat	D	E	N
Spondyliosoma cantharus	60	152.5	295	3.3	demersal	fusiform	G	E	
Sprattus sprattus	16	80	140	3	pelagic	fusiform	D	E	N
Squalus acanthias	160	730	1460	4.4	demersal	elongated	D	I	Y
Syngnathus acus	50	55	110	3.3	demersal	eel-like	D	B	Y
Thunnus alalunga	140	300	600	4.3	pelagic	fusiform	D	E	N
Thunnus albacares	239	125.5	249	4.4	pelagic	fusiform	D	E	N
Thunnus obesus	250	750	1500	4.5	pelagic	fusiform	D	E	N
Thunnus thynnus	458	492.5	985	4.5	pelagic	fusiform	D	E	N
Torpedo marmorata	100	186	368	4.5	reef-associated	ray-like	D	I	
Trachinus draco	53	75.5	149	4.2	demersal	elongated	D	E	N
Trachurus mediterraneus	60	250	500	3.8	pelagic	fusiform	D	E	N
Trachurus picturatus	60	337.5	65	3.3	demersal	fusiform	D	E	N
Trachurus trachurus	70	525	1050	3.7	pelagic	fusiform	D	E	N
Trachyscorpia cristulata	50	615	970	4.2	demersal	fusiform	D	E	N
Trigla lyra	60	425	550	3.7	bathydemersal	fusiform	D	E	N
Trisopterus esmarkii	35	175	250	3.2	demersal	fusiform	D	E	N
Trisopterus luscus	46	65	70	3.7	demersal	fusiform	D	E	N
Trisopterus minutus	40	220.5	439	3.7	demersal	fusiform	D	E	N
Umbrina cirrosa	73	50	100	3.4	demersal	fusiform	D	E	N
Umbrina ronchus	100	110	180	3.4	demersal	fusiform	D	E	N
Xenodermichthys copei	31	1375	2550	3.2	bathypelagic	elongated	D	E	
Zeus faber	90	202.5	395	4.5	demersal	short/deep	D	E	N

Table S3: Summary of the statistical tests comparing the average SES values of the different alpha diversity metric obtained with eDNA metabarcoding and trawling for the 15 sites in the Bay of Biscay. We reported the values of the non-parametric Wilcoxon's test and the parametric Student's test that were considered using paired data. Bold p.values highlight significant differences in average for the corresponding biodiversity indices.

Test	**Index**	**Statistic**	**p.value**	**Av.ses.eDNA**	**Sd.ses.eDNA**	**Av.ses.Trawl**	**Sd.ses.Trawl**
Wilcoxon	SR	120	**7e-04**	42.2	6.5049	18.4667	3.9255
Wilcoxon	PD.ses	113	**0.0012**	0.9586	0.8045	-0.3311	1.0915
Wilcoxon	VPD.ses	67	0.7197	-0.0733	0.8221	-0.0844	1.1666
Wilcoxon	MPD.ses	83	0.2078	0.1039	0.8018	-0.1958	0.9373
Wilcoxon	FD.ses	89	0.107	-1.6985	0.8805	-2.3093	0.9097
Wilcoxon	FEve.ses	102	**0.0151**	0.3816	0.9979	-0.8636	1.655
Wilcoxon	FDiv.ses	87	0.1354	0.4207	0.9307	-0.1561	0.9461
T.test	SR	12.8628	**0**	42.2	6.5049	18.4667	3.9255
T.test	PD.ses	4.1793	**9e-04**	0.9586	0.8045	-0.3311	1.0915
T.test	VPD.ses	0.0261	0.9796	-0.0733	0.8221	-0.0844	1.1666
T.test	MPD.ses	0.8921	0.3874	0.1039	0.8018	-0.1958	0.9373
T.test	FD.ses	1.718	0.1078	-1.6985	0.8805	-2.3093	0.9097
T.test	FEve.ses	2.8602	**0.0126**	0.3816	0.9979	-0.8636	1.655
T.test	FDiv.ses	1.6548	0.1202	0.4207	0.9307	-0.1561	0.9461

Table S4: Results of the model selection (based on the Akaike information criterion, AIC) performed to select the optimized interspecific allometric scaled abundance coefficient (*b*) maximizing the fit of the generalized linear model (GLM) between the number of eDNA reads and the allometric scaled abundance per species for each sample replicate (filter). GLM was fitted using a negative binomial distribution error with a log link function. A second series of models was run to maximize the fit of a linear model (LM) between the relative number of eDNA reads per taxa per filter and the allometric scaled abundance per species for each sample replicate (filter). Response.var: indicates the response variable, "Nb. reads" indicates that the response variable is the number of eDNA reads, "Relat nb. reads" indicates that the response variables was the relative number of reads that were modelled with a LM. best.b: the best inter-specific allometric scaling coefficient retained when optimizing the fit of the model. nb.taxa: the number of taxa used to fit the relationship. Res

Response.var	**Station**	**Filter**	**AIC**	**R^2**	**Intercept**	**Slope**	**P.value**	**nb.taxa**	**best.b**
Nb. reads	1	1	198.958	0.043	8.556	0.012	0.554	10	1
Nb. reads	1	2	149.595	0.172	8.352	-0.014	0.105	8	0.6
Nb. reads	2	1	345.652	0.132	10.953	-0.014	0.027	15	1
Nb. reads	2	2	315.085	0.097	10.549	-0.01	0.114	14	1
Nb. reads	3	1	278.336	0.563	9.171	0.001	0.002	13	0
Nb. reads	3	2	283.53	0.228	9.546	0.001	0.131	13	0
Nb. reads	4	1	273.383	0.366	11.116	-0.147	0	12	0.88
Nb. reads	4	2	296.78	0.265	10.876	-0.119	0.01	13	1
Nb. reads	5	1	226.299	0.191	9.487	-0.027	0.013	11	0.47
Nb. reads	5	2	216.723	0.124	10.095	-0.014	0.08	10	0
Nb. reads	6	1	295.604	0.031	9.699	-0.01	0.328	14	1
Nb. reads	6	2	348.91	0.078	9.004	0.001	0.278	17	0
Nb. reads	7	1	339.614	0.009	11.298	-0.021	0.666	14	0.96
Nb. reads	7	2	311.82	0.032	9.818	0.002	0.469	14	0
Nb. reads	8	1	158.213	0.061	9.728	0.038	0.53	7	1
Nb. reads	8	2	170.818	0.006	9.261	0.001	0.834	8	0
Nb. reads	9	1	372.126	0.347	8.743	0.09	0.001	18	1
Nb. reads	9	2	330.302	0.495	9.217	0.069	0.001	15	1
Nb. reads	10	1	334.615	0.002	9.415	-0.007	0.845	16	1
Nb. reads	10	2	397.664	0.029	9.966	-0.021	0.412	18	1
Nb. reads	11	1	228.914	0.019	10.719	-0.034	0.596	10	1
Nb. reads	11	2	266.825	0.016	10.658	-0.04	0.562	12	1
Nb. reads	12	1	178.061	0.07	10.289	-0.091	0.352	8	1
Nb. reads	12	2	175.759	0.015	9.795	-0.033	0.706	8	1
Nb. reads	13	1	301.95	0.089	10.463	0	0.304	13	0

Nb. reads	13	2	230.931	0.158	10.236	0	0.215	10	0
Nb. reads	14	1	207.24	0.249	9.932	-0.051	0.002	10	0.71
Nb. reads	14	2	247.334	0.046	10.372	-0.031	0.378	11	1
Nb. reads	15	1	167.499	0.317	8.877	0.105	0.083	8	1
Nb. reads	15	2	164.88	0.176	8.6	0.108	0.194	8	1
Relat nb. reads	1	1	-45.692	0.081	0.015	0	0.426	10	111
Relat nb. reads	1	2	-51.274	0.075	0.006	0	0.51	8	56
Relat nb. reads	2	1	-33.748	0.055	0.059	0	0.383	16	111
Relat nb. reads	2	2	-19.163	0.033	0.067	0	0.516	15	111
Relat nb. reads	3	1	-59.238	0.903	0.013	0	0	14	11
Relat nb. reads	3	2	-51.028	0.717	0.016	0	0	14	11
Relat nb. reads	4	1	-53.874	0.856	0.026	0	0	13	11
Relat nb. reads	4	2	-32.981	0.11	0.046	0	0.247	14	11
Relat nb. reads	5	1	-26.746	0.069	0.049	0	0.434	11	11
Relat nb. reads	5	2	-22.521	0.065	0.052	0	0.477	10	11
Relat nb. reads	6	1	-43.075	0.547	0.028	0	0.002	15	11
Relat nb. reads	6	2	-67.856	0.889	0.011	0	0	18	11
Relat nb. reads	7	1	-25.615	0.005	0.065	-0.001	0.798	15	111
Relat nb. reads	7	2	-42.267	0.396	0.028	0	0.012	15	11
Relat nb. reads	8	1	-33.45	0.954	0.027	0	0	8	111
Relat nb. reads	8	2	-47.989	0.972	0.014	0	0	9	11
Relat nb. reads	9	1	-59.026	0.627	0.012	0.003	0	19	111
Relat nb. reads	9	2	-53.882	0.737	0.006	0.003	0	16	111
Relat nb. reads	10	1	-57.984	0.204	0.017	0	0.069	17	24
Relat nb. reads	10	2	-63.287	0.104	0.025	0	0.178	19	19
Relat nb. reads	11	1	-16.489	0.151	0.043	0	0.237	11	11
Relat nb. reads	11	2	-21.005	0.02	0.044	0	0.641	13	11
Relat nb. reads	12	1	-16.488	0.03	0.043	0	0.656	9	111
Relat nb. reads	12	2	-26.187	0.331	0.031	0.001	0.105	9	97
Relat nb. reads	13	1	-35.415	0.278	0.04	0	0.053	14	11
Relat nb. reads	13	2	-31.125	0.623	0.04	0	0.004	11	11
Relat nb. reads	14	1	-12.576	0.042	0.069	-0.002	0.546	11	111
Relat nb. reads	14	2	-19.351	0.013	0.06	-0.001	0.725	12	111
Relat nb. reads	15	1	-22.203	0.015	0.031	0.002	0.753	9	111
Relat nb. reads	15	2	-17.59	0.01	0.045	0	0.799	9	11

Table S5: Summary of the statistical tests comparing the average SES values of the different alpha diversity metric obtained with eDNA metabarcoding and trawl for the 15 sites in the Bay of Biscay, after removing 10 abundant (and ubiquitous) species showing multiple successive occurrences. We reported the values of the non-parametric Wilcoxon's test and the parametric Student's test that were considered using paired data. Bold p.values highlight significant differences in average for the corresponding biodiversity indices.

Test	**Index**	**Statistic**	**p.value**	**Mean.ses.eDNA**	**Sd.ses.eDNA**	**Mean.ses.Trawl**	**Sd.ses.Trawl**
Wilcoxon	SR	120	**7e-04**	30.4	6.3336	12.6667	3.5389
Wilcoxon	PD.ses	94	0.0554	0.5671	2.4176	-1.152	2.228
Wilcoxon	VPD.ses	76	0.3894	0.8084	0.9837	0.5283	1.6217
Wilcoxon	MPD.ses	86	0.1514	0.9215	1.9693	-0.0218	1.5719
Wilcoxon	FD.ses	78	0.3303	-2.6589	1.708	-4.1184	3.7229
Wilcoxon	FEve.ses	70	0.5995	-1.678	3.8221	-1.9781	2.1225
Wilcoxon	FDiv.ses	101	**0.0181**	0.2993	1.1759	-1.0055	1.2715
T.test	SR	10.011	**0**	30.4	6.3336	12.6667	3.5389
T.test	PD.ses	2.2856	**0.0384**	0.5671	2.4176	-1.152	2.228
T.test	VPD.ses	0.5144	0.615	0.8084	0.9837	0.5283	1.6217
T.test	MPD.ses	1.625	0.1265	0.9215	1.9693	-0.0218	1.5719
T.test	FD.ses	1.2968	0.2157	-2.6589	1.708	-4.1184	3.7229
T.test	FEve.ses	0.3337	0.7435	-1.678	3.8221	-1.9781	2.1225
T.test	FDiv.ses	2.848	**0.0129**	0.2993	1.1759	-1.0055	1.2715

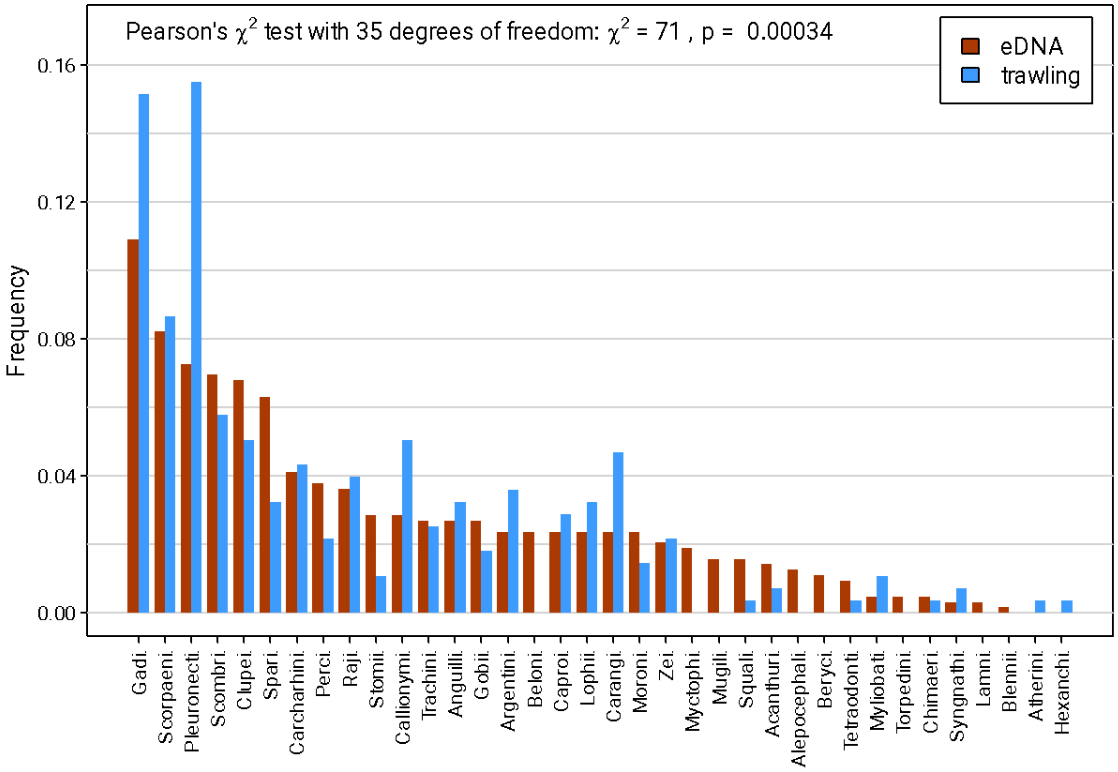


Figure S1: Detection frequencies of the fishes by order and by sampling method. One occurrence corresponds to one taxon of each order detected in one site.

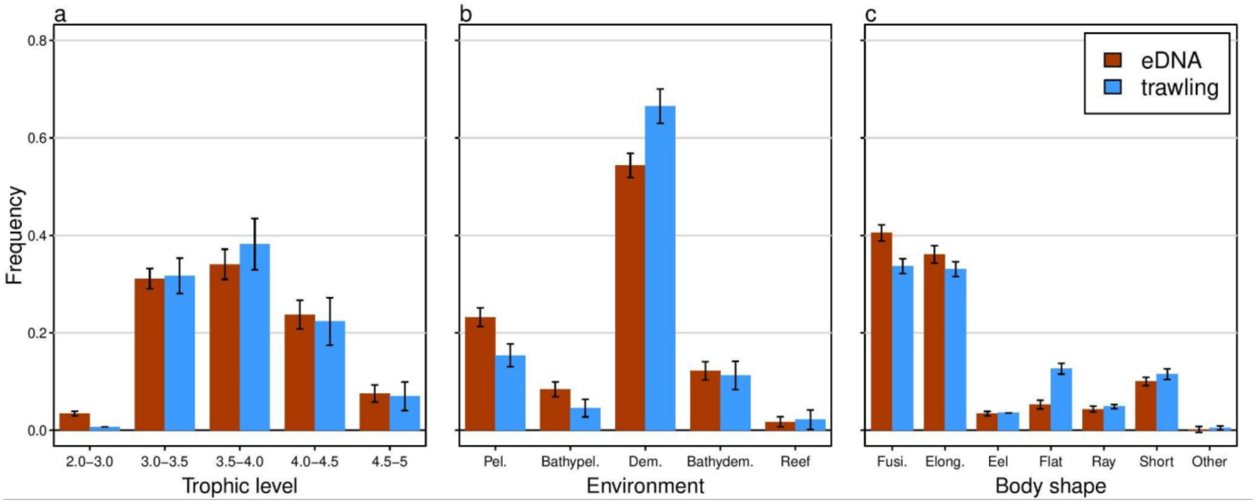


Figure S2: Detection frequencies of the fishes with the eDNA metabarcoding and trawling sampling methods, for different (a) trophic levels, (b) environments (PEL: pelagic; Bathypel: bathypelagic; Dem: demersal; Bathydem: bathydemersal) and (c) body shapes (Fusi: fusiforme; Elong: elongated). Error bars indicate the standard deviation, as uncertainty in the traits could exist for taxa detected at the genus level.

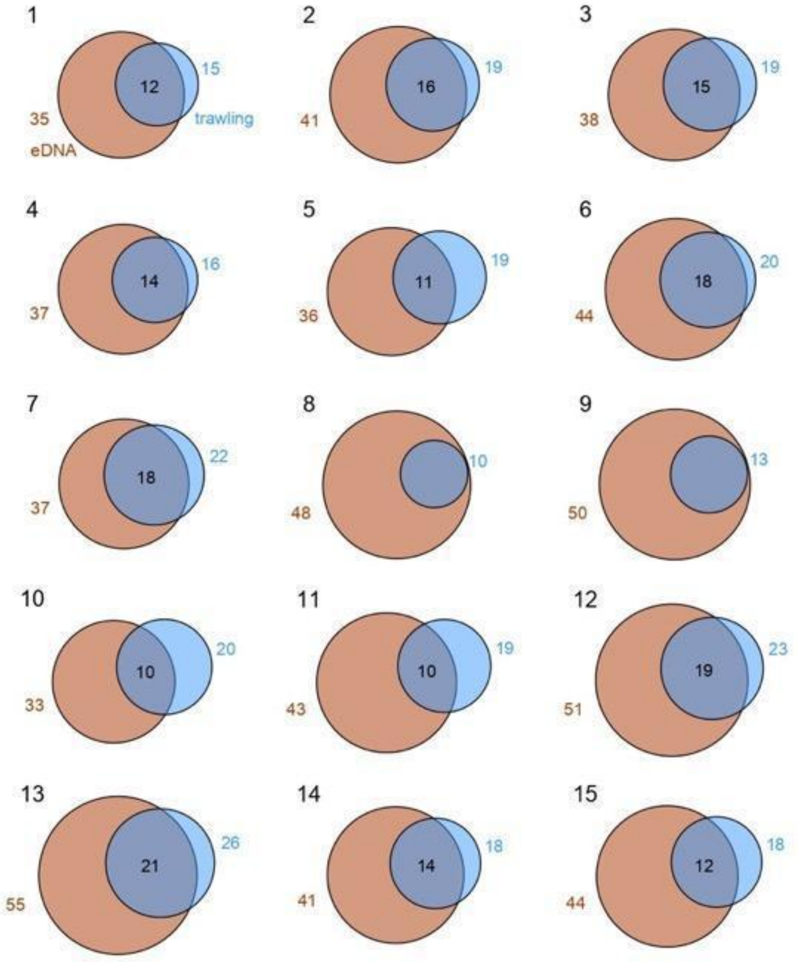


Figure S3: Venn diagrams of the number of detected taxa at each site, between eDNA metabarcoding (after pooling the species list of the two filter replicates per site) and trawling sampling methods. The red circles represent the number of taxa detected by eDNA, whereas the blue circles represent the number of taxa detected by trawling. The intersection between circles shows the taxa detected by both sampling methods.

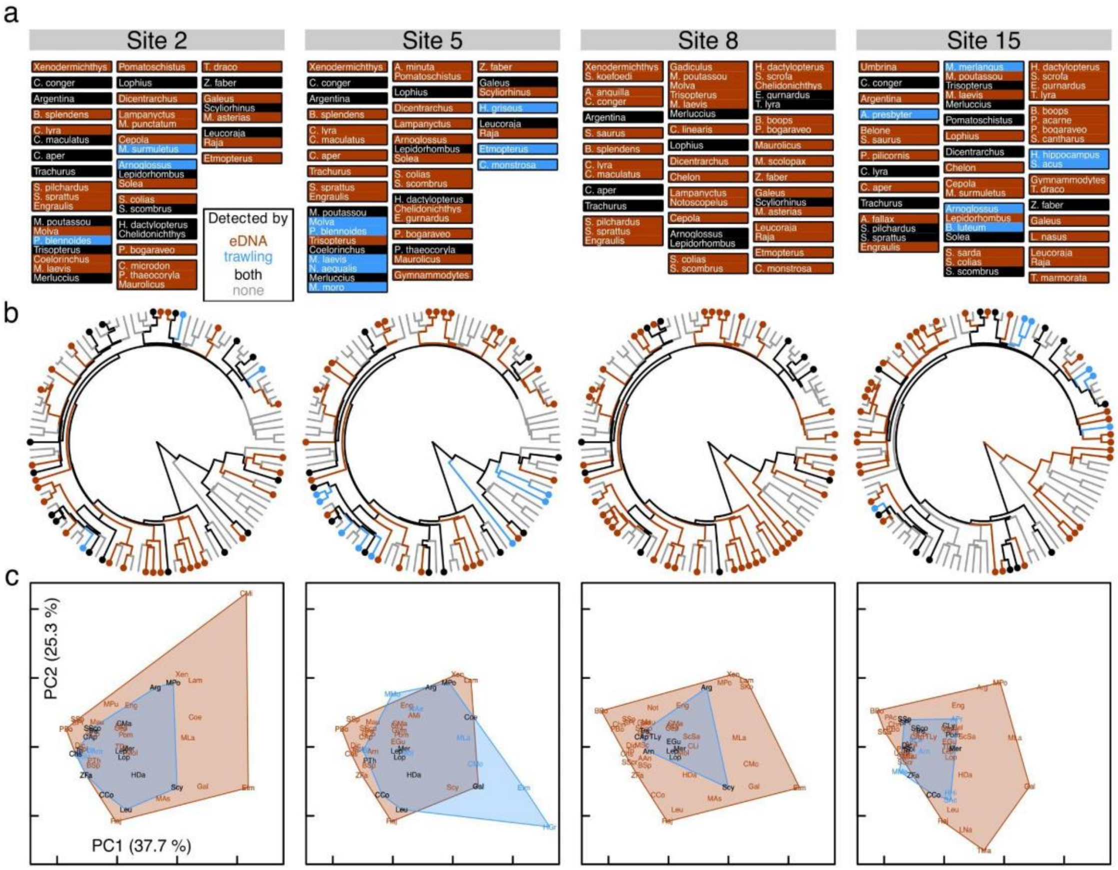


Figure S4: (a) Taxonomic composition, (b) phylogenetic tree and (c) functional space of four selected sampling sites, presented to illustrate the identified diversity patterns. We chose to represent site 2 (offshore, high phylogenetic richness), site 5 (offshore, high functional richness detected with trawling, some rare species detected), site 8 (closer to the coast, high taxonomic diversity, with all the taxa detected by trawling nested in the list of taxa detected by eDNA metabarcoding) and site 15 (coastal, low functional diversity).

Additional text associated with Figure S4

The focus on site-specific phylogenetic trees and functional space made it possible to categorize the sites. Sites 2 and 15 displayed the same patterns for the three diversity components. They were characterized by relatively high species richness for both sampling methods. Considering phylogenetic diversity, the detected taxa were dispersed on the phylogenetic tree for both methods. In terms of functional diversity, the eDNA metabarcoding functional space included almost the whole functional space of trawling, which was also the case for most other sites (except sites 5 and 10; see Supp. Mat. Fig. S4). These sites were characterized by a high richness for all diversity components with eDNA metabarcoding (Table 1). Moreover, all taxa detected by trawling were also detected by eDNA metabarcoding for both sites 8 and 9 (Supp. Mat. Fig. S4). This was probably due to the low species richness (SR) in trawling, leading to a very restricted functional space (3.23) and a low phylogenetic richness (PD = 1710 Ma). Finally, site 5 was dominated by trawling in terms of functional space (the bluntnose sixgill shark *Hexanchus griseus,* only detected in this site by trawling, enlarged the space), but the relatively low SES.PD indicated a high level of phylogenetic clustering of species detected by trawling. Even with a larger functional space, we measured a slightly lower FD with trawling (5.44) than with eDNA (5.61).

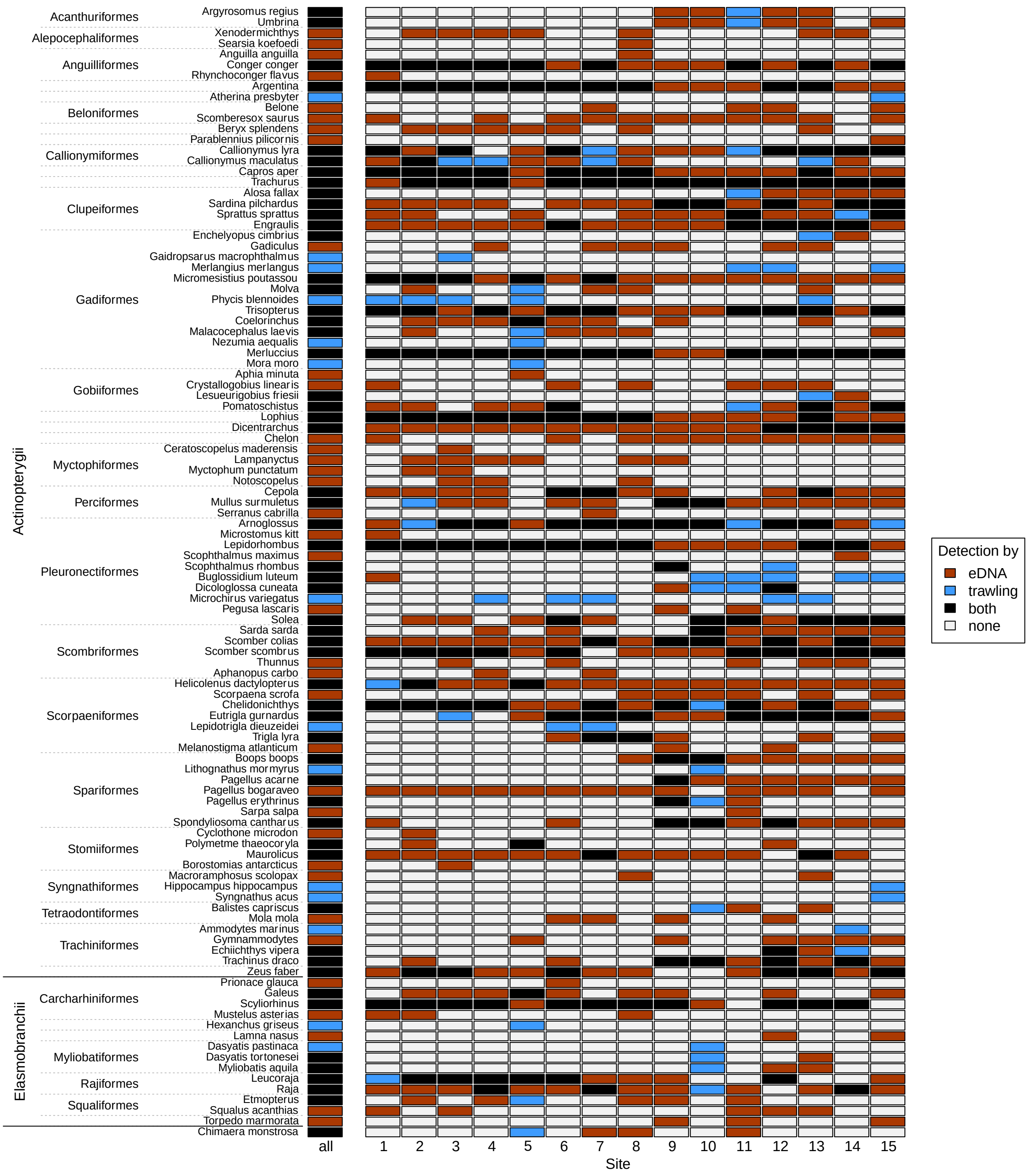


Figure S5: Community matrix of the detected taxa in the individual sampling sites. Taxa are indicated with their class and order. Colours indicate if taxa were not detected (white) or were detected by eDNA metabarcoding (red), trawling (blue), or both (black).

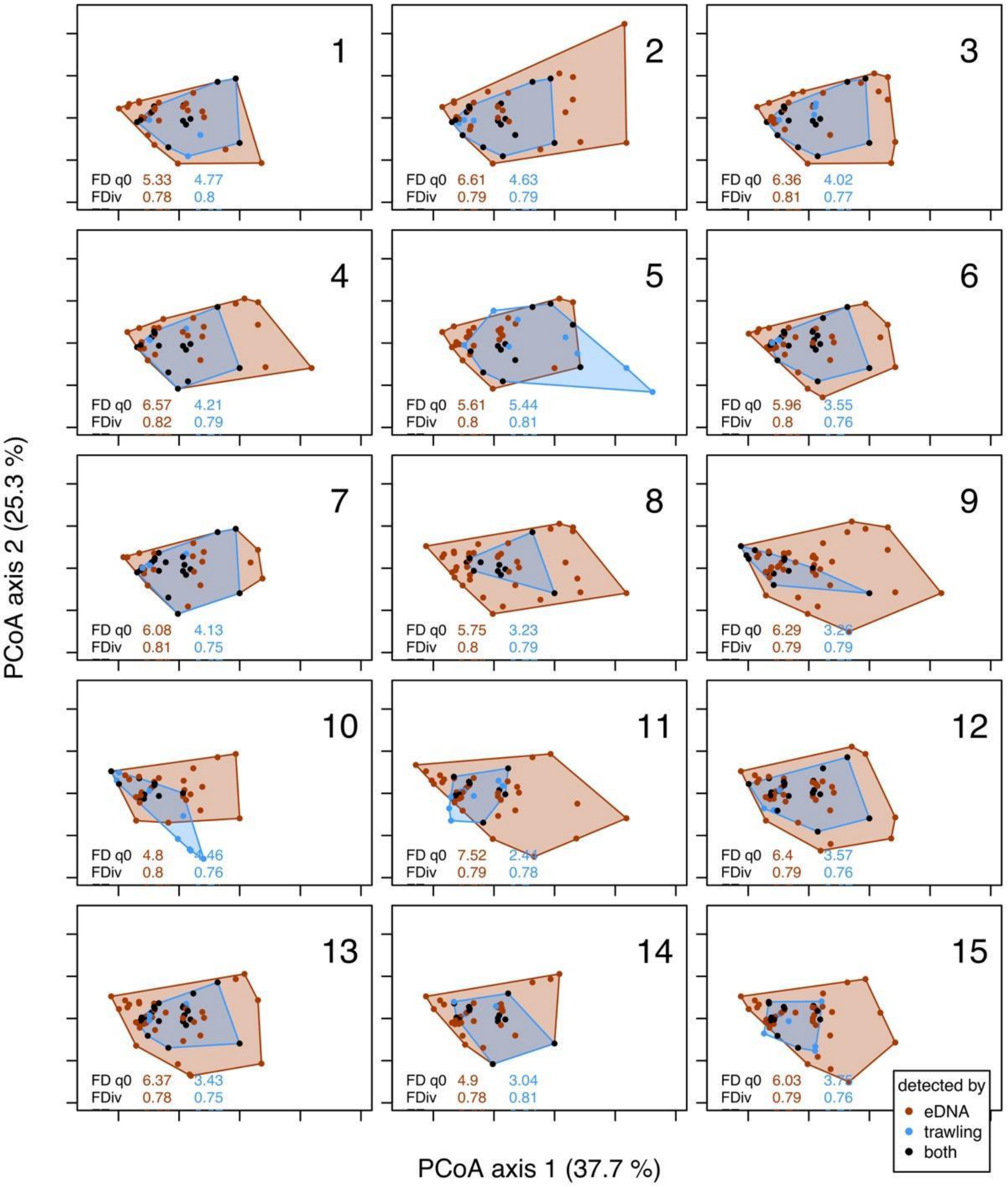


Figure S6: Functional space (first two axes of a principal coordinates analysis, PCoA) calculated for each sampling site and each sampling method (eDNA metabarcoding and trawling). The associated functional measures of richness (FD), regularity (FEve) and divergence (FDiv) are shown.

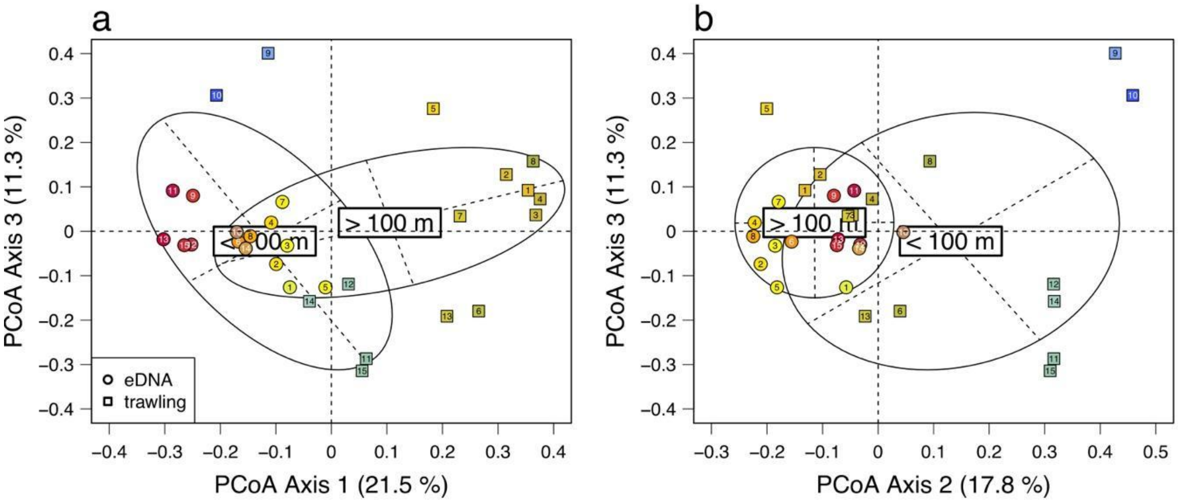


Figure S7: Principal coordinates analysis (PCoA) of the species composition detected with eDNA metabarcoding (circles) and trawl hauls (squares). The ellipses of dispersion of the points are based on a water depth criterion. The colours of the symbols correspond to their positions in the PCoA space, where points with similar colours have a similar species composition. (a) Relationship between axes 1 and 3; (b) relationship between axes 2 and 3.

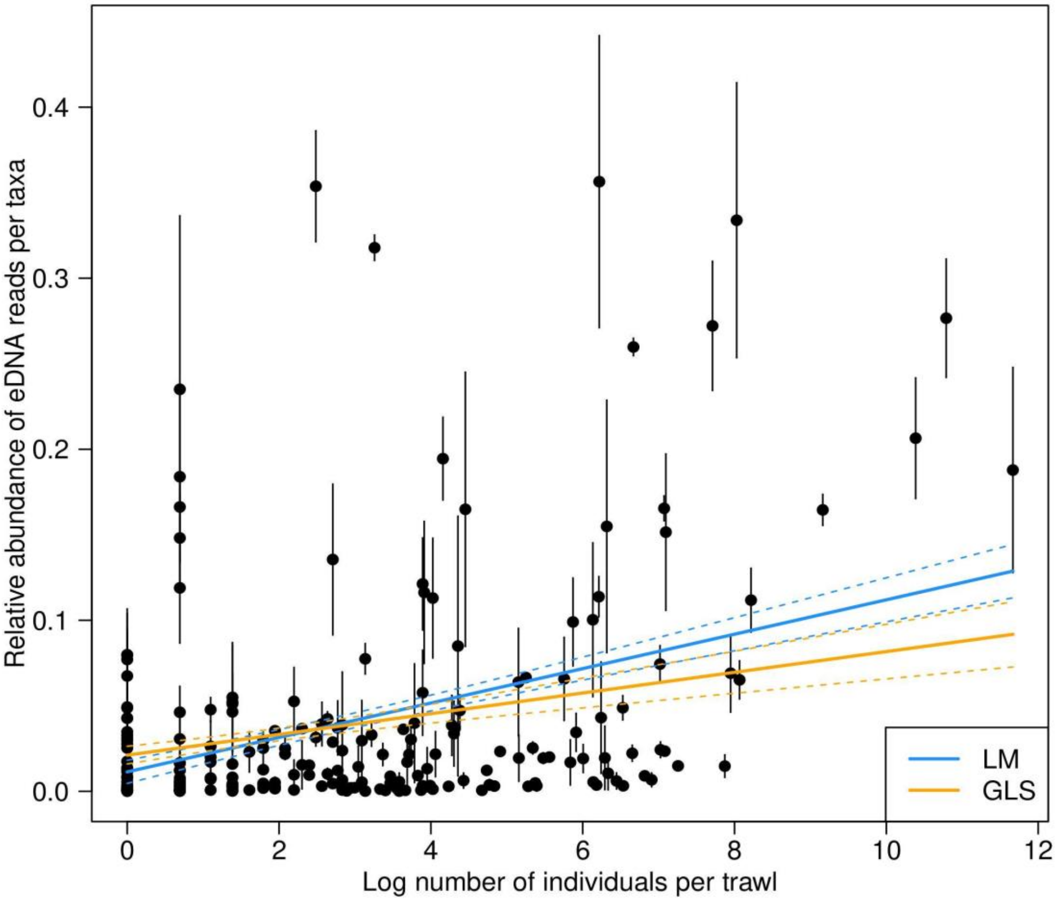


Figure S8: Relationship between the average relative number of eDNA reads between the two filter replicates per site and the $\log_{10}$ number of individuals sampled by trawling, inferred from a linear model (LM, intercept 0.0114, slope 0.0101, $p = 2.10\text{-}8$, $R^2 = 0.14$) and a generalized least square model (GLS) accounting for the heterogeneity in the model residuals using an exponential variance structure (intercept 0.021, slope 0.006, $p = 0.002$, R^2 Cox Snell = 0.23, exponential residuals variance parameter = 0.11). A lower Akaike information criterion (AIC) value of the GLS model (GLS AIC = -603.5, LM AIC = -571.3) indicates that accounting for the increase in variance of the residuals significantly improves the model fit compared with the LM model. Each point corresponds to a single site and fish. Error bars represent the difference between the two filter replicates at a given site. Solid lines correspond to the fit of the LM (blue) and the GLS model (orange), while dashed lines correspond to the standard error of the fitted models.

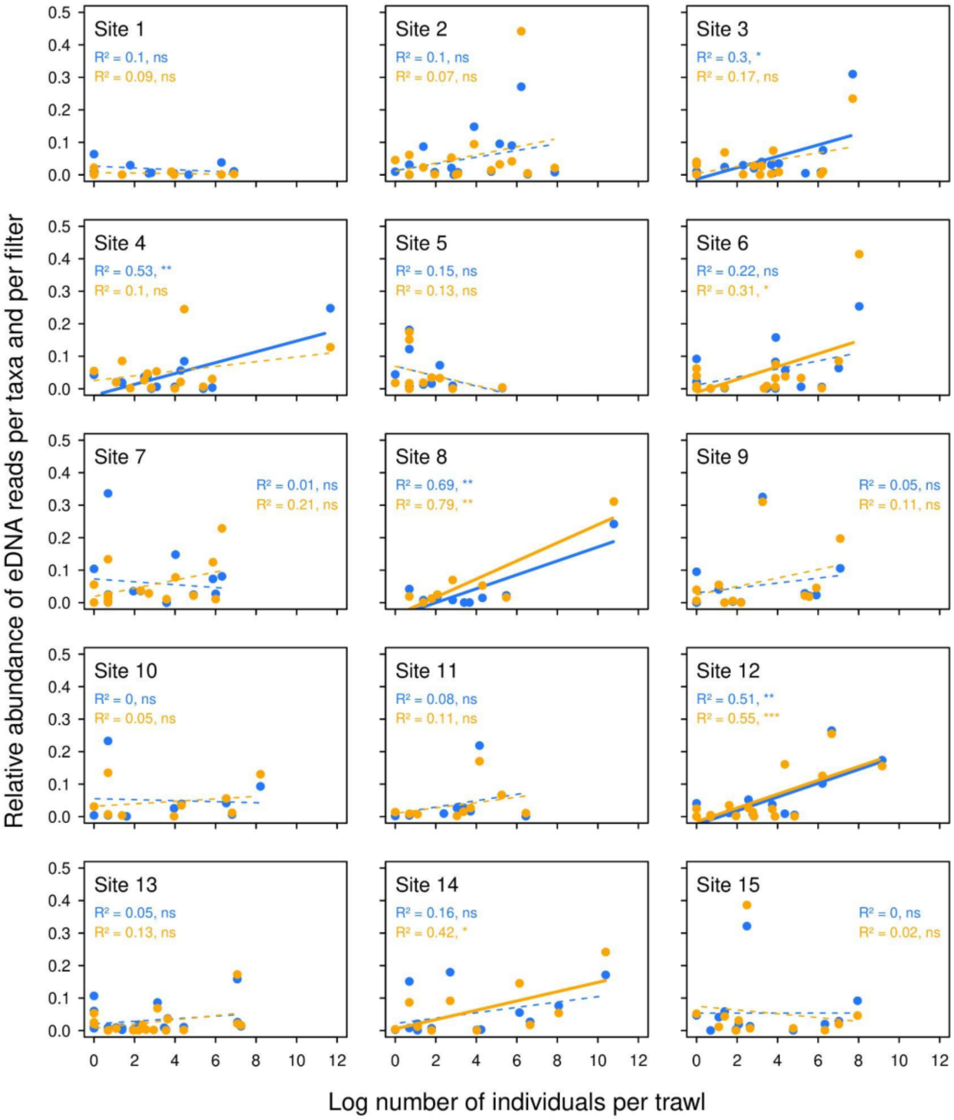
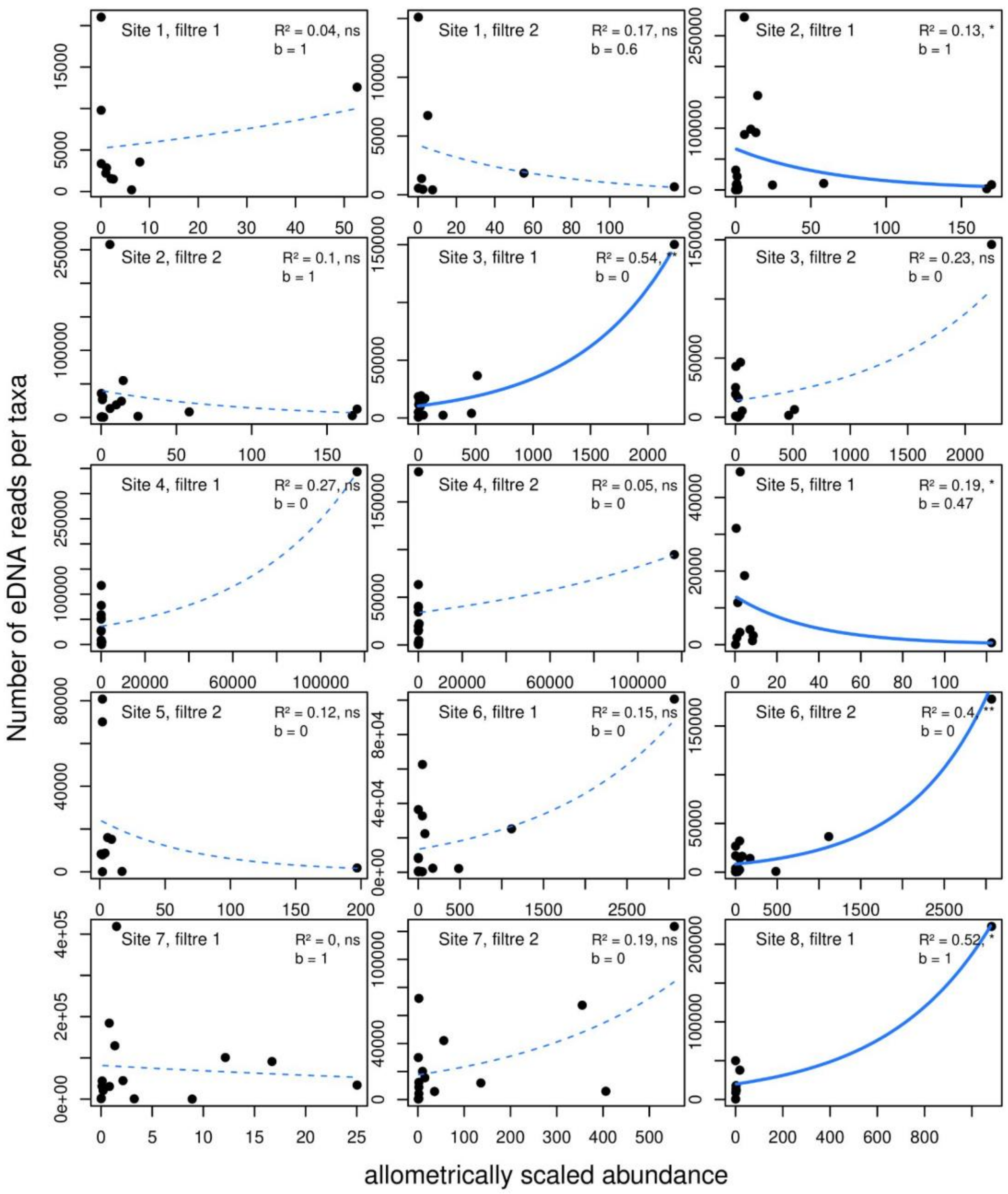


Figure S9: Relative abundance of eDNA reads per taxa per filter replicate compared with the $\log_{10}$ number of individuals per taxa sampled by trawling for the 15 sites. Blue and orange points correspond to the two eDNA filter replicates processed at each site. Each point corresponds to a fish detected by both methods. Solid lines indicate a significant fit of the linear model (LM), while dashed lines indicate a non-significant trend only of the LM. Asterisks indicate the degree of significance of the slope of the LM, with *** ($p < 0.001$), ** ($0.001 < p < 0.01$), * ($0.01 < p < 0.05$), and ns ($p > 0.05$).


Number of eDNA reads per taxa
allometrically scaled abundance
Site 1, filtre 1
R² = 0.04, ns
b = 1
Site 1, filtre 2
R² = 0.17, ns
b = 0.6
Site 2, filtre 1
R² = 0.13, *
b = 1
Site 2, filtre 2
R² = 0.1, ns
b = 1
Site 3, filtre 1
R² = 0.54, **
b = 0
Site 3, filtre 2
R² = 0.23, ns
b = 0
Site 4, filtre 1
R² = 0.27, ns
b = 0
Site 4, filtre 2
R² = 0.05, ns
b = 0
Site 5, filtre 1
R² = 0.19, *
b = 0.47
Site 5, filtre 2
R² = 0.12, ns
b = 0
Site 6, filtre 1
R² = 0.15, ns
b = 0
Site 6, filtre 2
R² = 0.4, **
b = 0
Site 7, filtre 1
R² = 0, ns
b = 1
Site 7, filtre 2
R² = 0.19, ns
b = 0
Site 8, filtre 1
R² = 0.52, *
b = 1

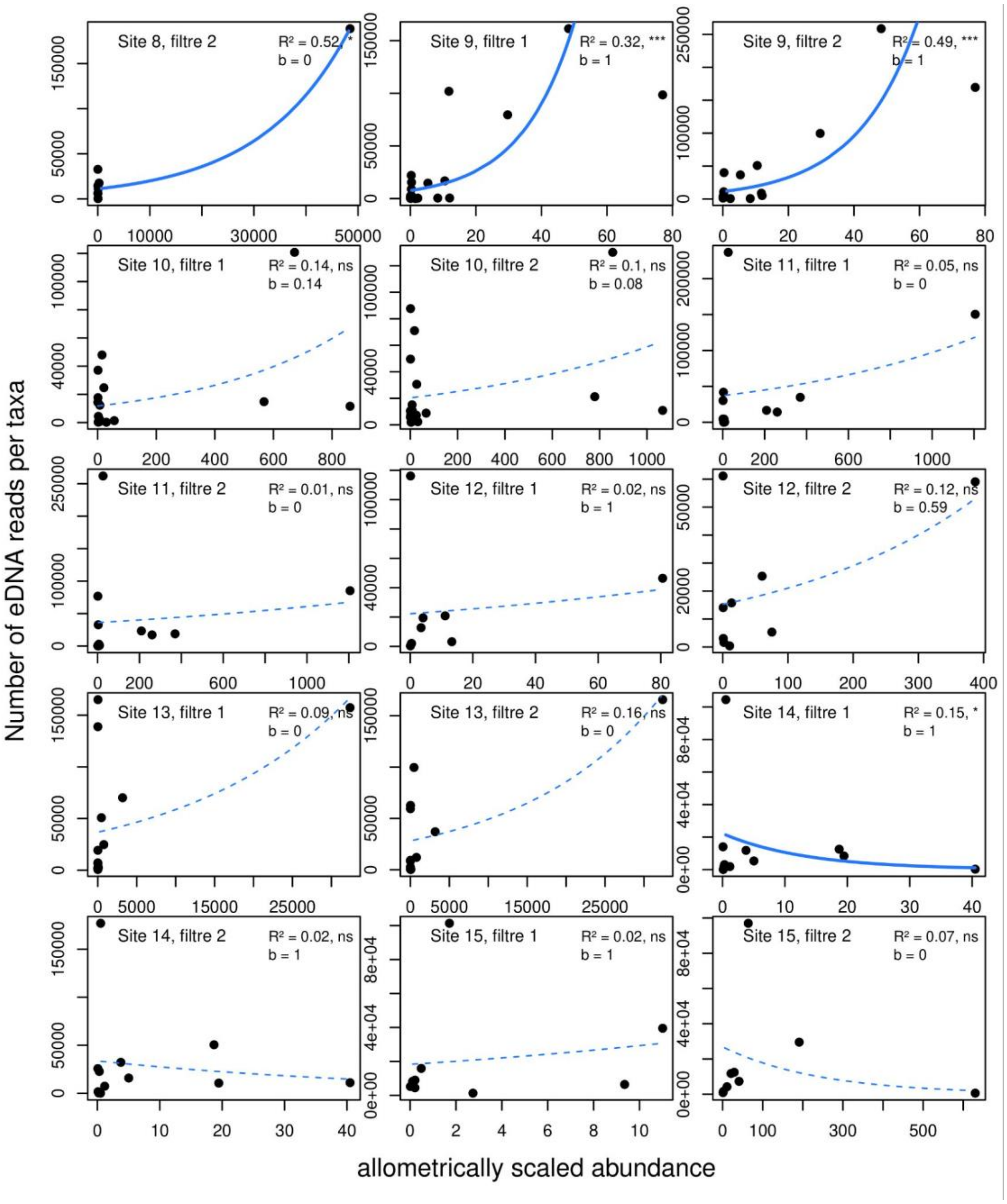
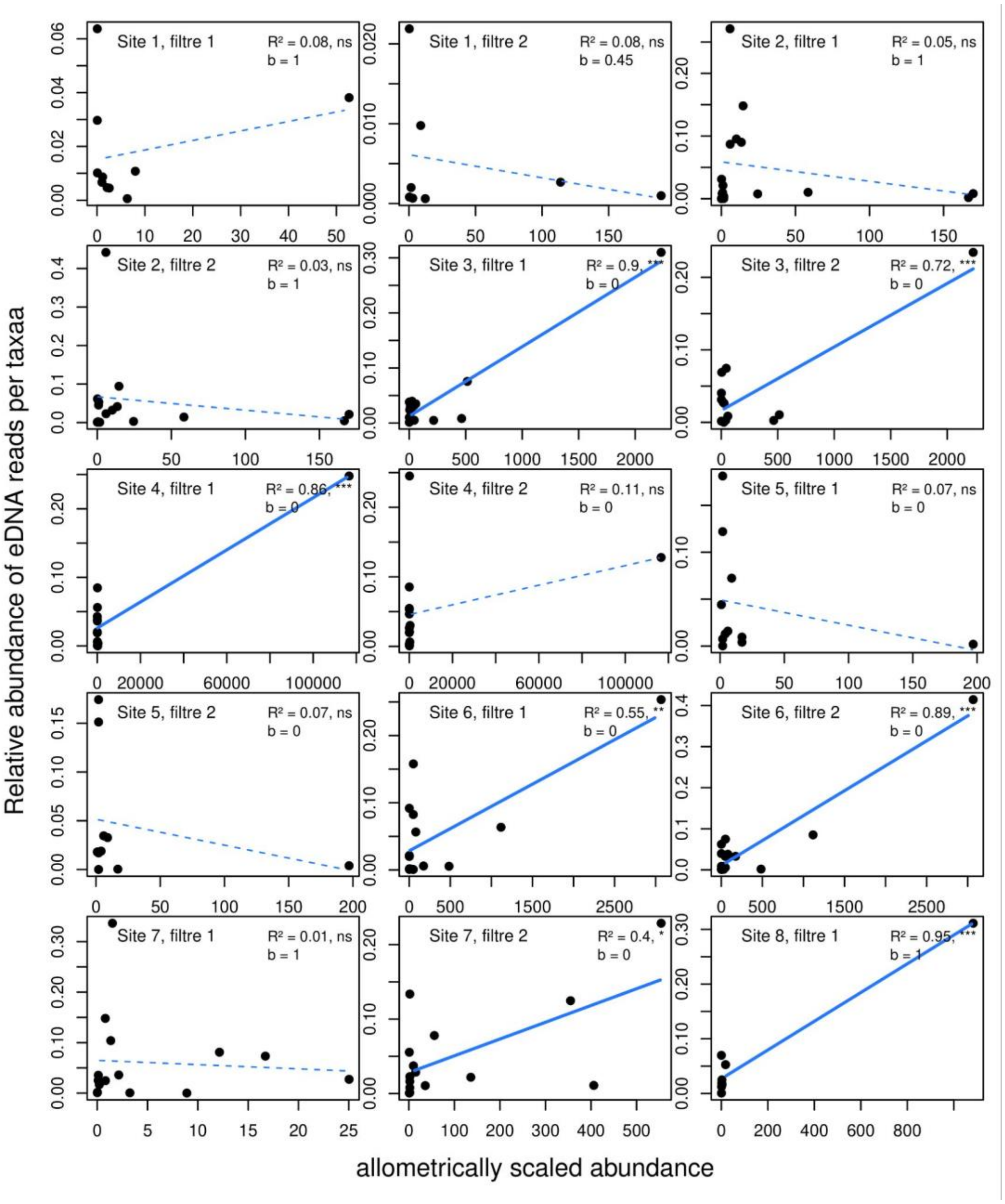


Figure S10: Relationships between the number of eDNA reads per species per filter replicate and the best allometric scaled abundance coefficient (b) estimated from the species abundance and mass from the closest trawl. The relationships come from a generalized linear model (GLM) with a negative binomial distribution error and a log link function. Continuous lines indicate a significant fit of the GLM model, while dashed lines indicate a non-significant trend only of the GLM. Asterisks indicate the degree of significance of the slope of the GLM, with *** ($p < 0.001$), ** ($0.001 < p < 0.01$), * ($0.01 < p < 0.05$), and ns ($p > 0.05$).


Relative abundance of eDNA reads per taxaa
allometrically scaled abundance
Site 1, filtre 1
R² = 0.08, ns
b = 1
Site 1, filtre 2
R² = 0.08, ns
b = 0.45
Site 2, filtre 1
R² = 0.05, ns
b = 1
Site 2, filtre 2
R² = 0.03, ns
b = 1
Site 3, filtre 1
R² = 0.9, ***
b = 0
Site 3, filtre 2
R² = 0.72, ***
b = 0
Site 4, filtre 1
R² = 0.86, ***
b = 0
Site 4, filtre 2
R² = 0.11, ns
b = 0
Site 5, filtre 1
R² = 0.07, ns
b = 0
Site 5, filtre 2
R² = 0.07, ns
b = 0
Site 6, filtre 1
R² = 0.55, **
b = 0
Site 6, filtre 2
R² = 0.89, ***
b = 0
Site 7, filtre 1
R² = 0.01, ns
b = 1
Site 7, filtre 2
R² = 0.4, *
b = 0
Site 8, filtre 1
R² = 0.95, ***
b = 1
0 10 20 30 40 50
0 50 100 150
0 50 100 150
0 50 100 150
0 500 1000 1500 2000
0 500 1000 1500 2000
0 20000 60000 100000
0 20000 60000 100000
0 50 100 150 200
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0 100 200 300 400 500
0 200 400 600 800

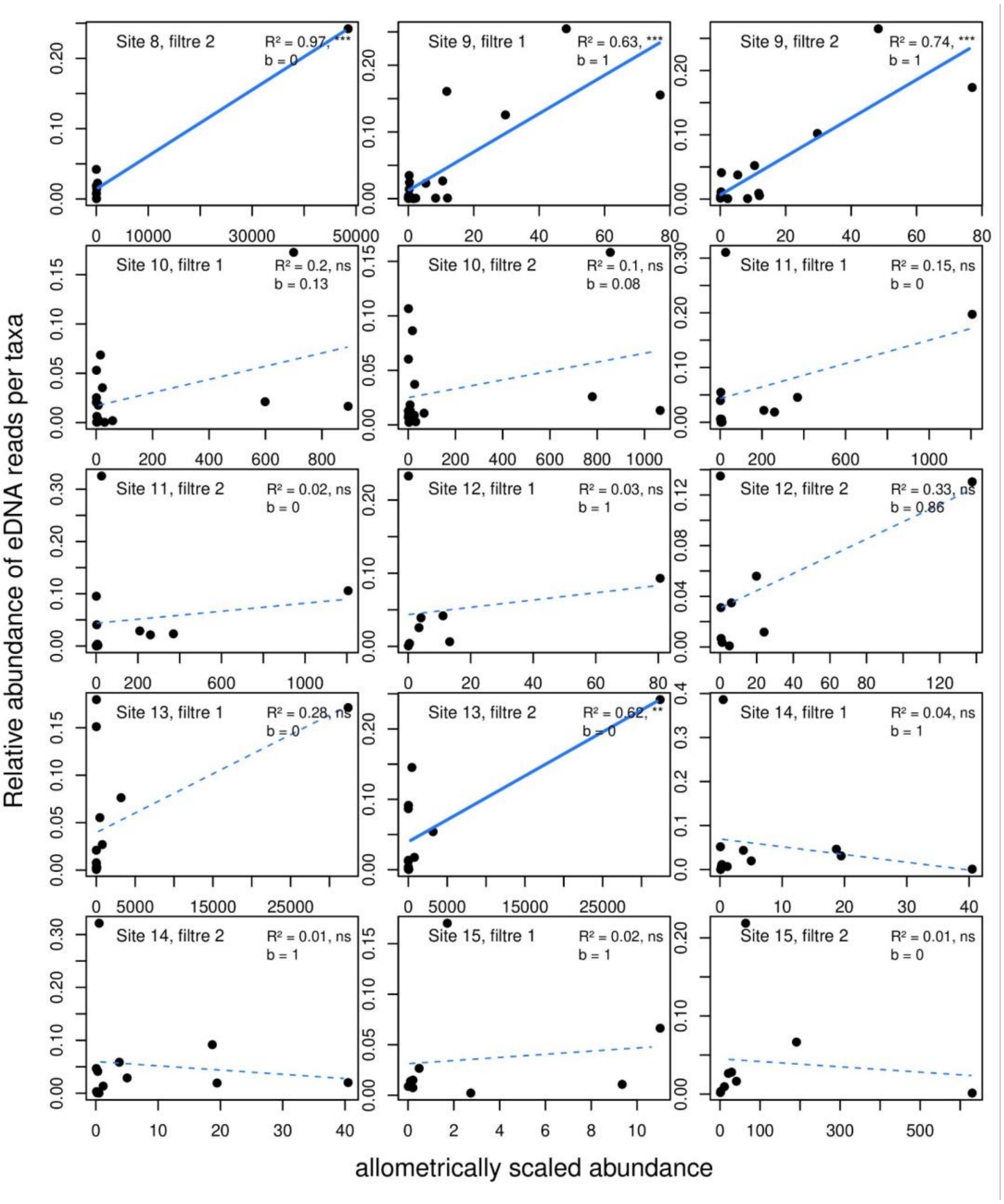

Figure S11: Relationships between the relative number/abundance of eDNA reads per species per filter replicate and the best allometric scaled abundance coefficient (*b*) estimated from the species abundance and mass from the closest trawl. The relationships come from a linear model (LM) with a Gaussian distribution error. Continuous lines indicate a significant fit of the LM model, while dashed lines indicate a non-significant trend only of the LM. Asterisks indicate the degree of significance of the slope of the LM, with *** ($p < 0.001$), ** ($0.001 < p < 0.01$), * ($0.01 < p < 0.05$), and ns ($p > 0.05$).

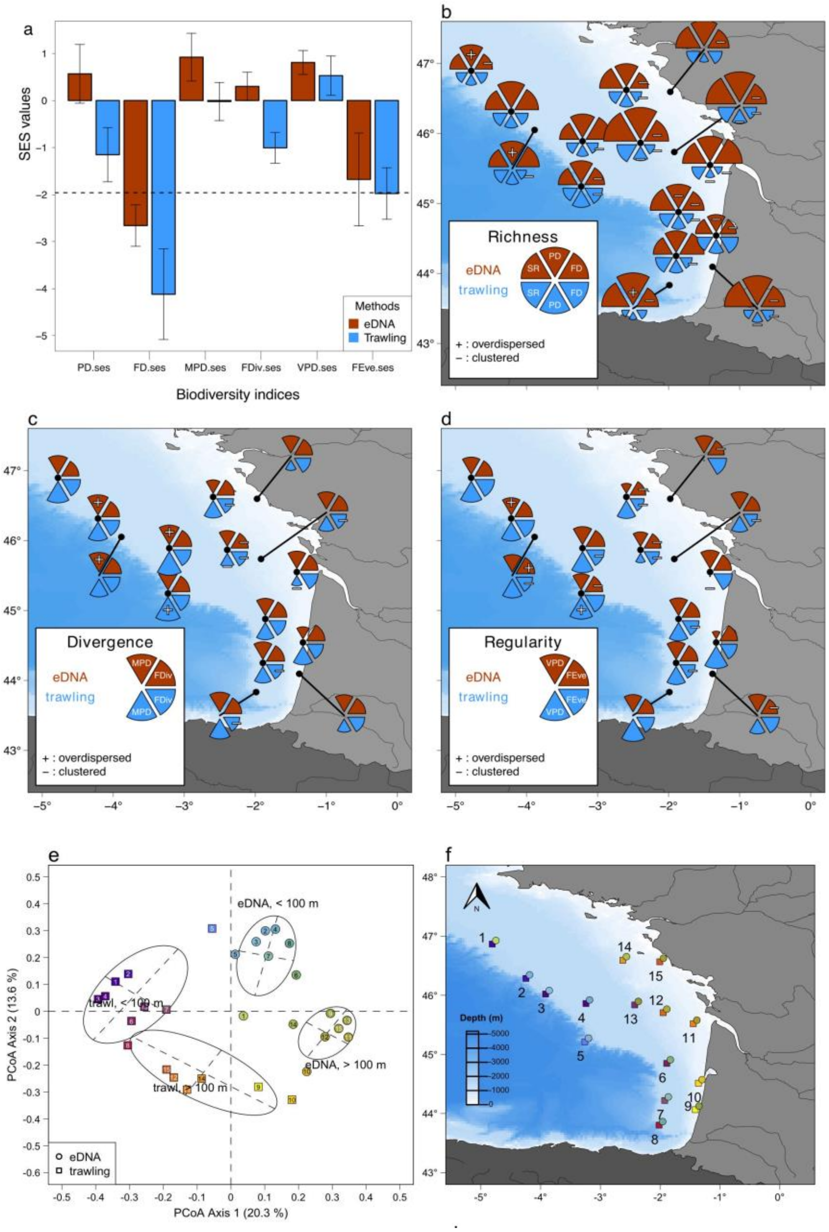

Figure S12: Sensitivity analysis results (removal of species which could have suffered from contamination, see list below). Comparison of average standard effect sizes (SES) for phylogenetic and functional indices including richness, divergence and regularity facets (a) associated with the two sampling methods (eDNA vs trawling). Colour bars show the average value over the 15 sites and error bars represent the standard error. The dashed horizontal line indicates a threshold of significant clustering (-1.96) for the SES of the indices. Spatial distribution of the αdiversity indices of (b) richness, (c) divergence and (d) regularity separated by site and by sampling method for the three biodiversity components, recalculated for the sensitivity analysis. The radius of each circle slice is proportional to the value of the index. For functional and phylogenetic diversity, indices significantly different from the null model (based on the standardized effect size, SES) are indicated with − for overdispersion and + for clustering. Panel (e) represents the first two axes of a principal coordinates analysis of the species composition sampled by eDNA metabarcoding (circles) and by bottom trawl hauls (squares), based on the Jaccard dissimilarity distance. Ellipses display the dispersion of the sampling sites according to depth and sampling method. Panel (f) shows geographical positions of the corresponding sites, with 7 shallow sites (< 100m) and 8 deep sites (> 100m). The colour of each point corresponds to its position in the PCoA space: points with similar colours share a similar species composition. List of removed species: *Capros aper, Conger conger, Trachurus sp., Engraulis sp., Argentina sp., Dicentrarchus sp., Sardina pilchardus., Lophius sp., Pagellus bogaraveo, Micromesistius poutassou, Lepidorhombus sp*.

References for the Supplementary Material

Benton, M., Donoghue, P., Vinther, J., Asher, R., Friedman, M. & Near, T. (2015). Constraints on the timescale of animal evolutionary history. *Palaeontologia Electronica,* 18.1.1FC; 1-106.

Betancur-R, R., Wiley, E.O., Arratia, G., Acero, A., Bailly, N., Miya, M., et al. (2017). Phylogenetic classification of bony fishes. *BMC Evolutionary Biology*, 17, 162.

Fricke, R., Eschmeyer, W.N. & der Laan, R.V. (2022). Eschmeyer's catalog of fishes: genera, species, references. Available at: https://researcharchive.calacademy.org/research/ichthyology/catalog/fishcatmain.asp

Horton, T., Kroh, A., Ahyong, S., Bailly, N., Bieler, R., Boyko, C.B., et al. (2022). World Register of Marine Species (WoRMS).

Nee, S., May, R.M. & Harvey, P.H. (1994). The reconstructed evolutionary process. Philosophical Transactions of the Royal Society of London. *Series B: Biological Sciences*, 344, 305–311.

Paradis E. & Schliep K. (2019). ape 5.0: an environment for modern phylogenetics and evolutionary analyses in R. *Bioinformatics* 35, 526-528.

Rabosky, D.L., Chang, J., Title, P.O., Cowman, P.F., Sallan, L., Friedman, M., et al. (2018). An inverse latitudinal gradient in speciation rate for marine fishes. Nature, 559, 392–395.

Ratnasingham, S. & Herbert, P.D.N. (2007). bold: The Barcode of Life Data System. Molecular Ecology Notes, 7, 355–364.

Revell, L. J. (2012). phytools: An R package for phylogenetic comparative biology (and other things). *Methods in Ecology and Evolution*, 3, 217-223.

Rozanski, R., Trenkel, V.M., Lorance, P., Valentini, A., Dejean, T., Pellissier, L., et al. (2022). Disentangling the components of coastal fish biodiversity in southern Brittany by applying an environmental DNA approach. *Environmental DNA*, 4, 920–939.

Stein, R.W., Mull, C.G., Kuhn, T.S., Aschliman, N.C., Davidson, L.N.K., Joy, J.B., et al. (2018). Global priorities for conserving the evolutionary history of sharks, rays and chimaeras. *Nature Ecology & Evolution*, 2, 288–298.