

Figure S1. Map of the 21 sampling localities of the ‘main dataset’, named by their locality code and represented with ICES fisheries statistical areas. See detailed information corresponding to each locality code in Table S1.

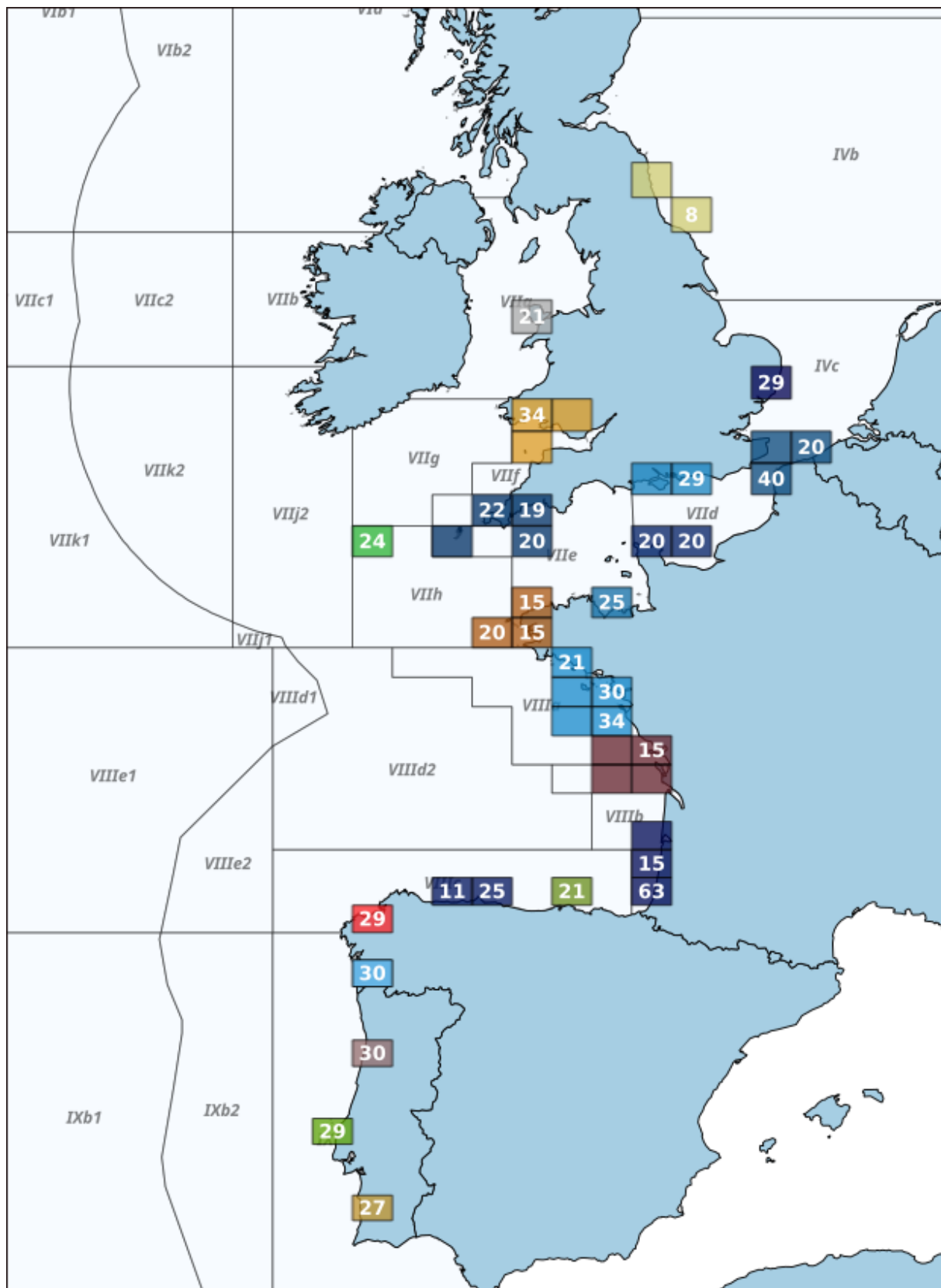


Figure S2. Map of the 31 sampling localities of the ‘refined dataset’, containing 761 individuals with a minimal number of 8 individuals per ICES rectangle. Empty rectangles represent samples from the main dataset that we excluded for the spatially refined analysis due to limited sample size.

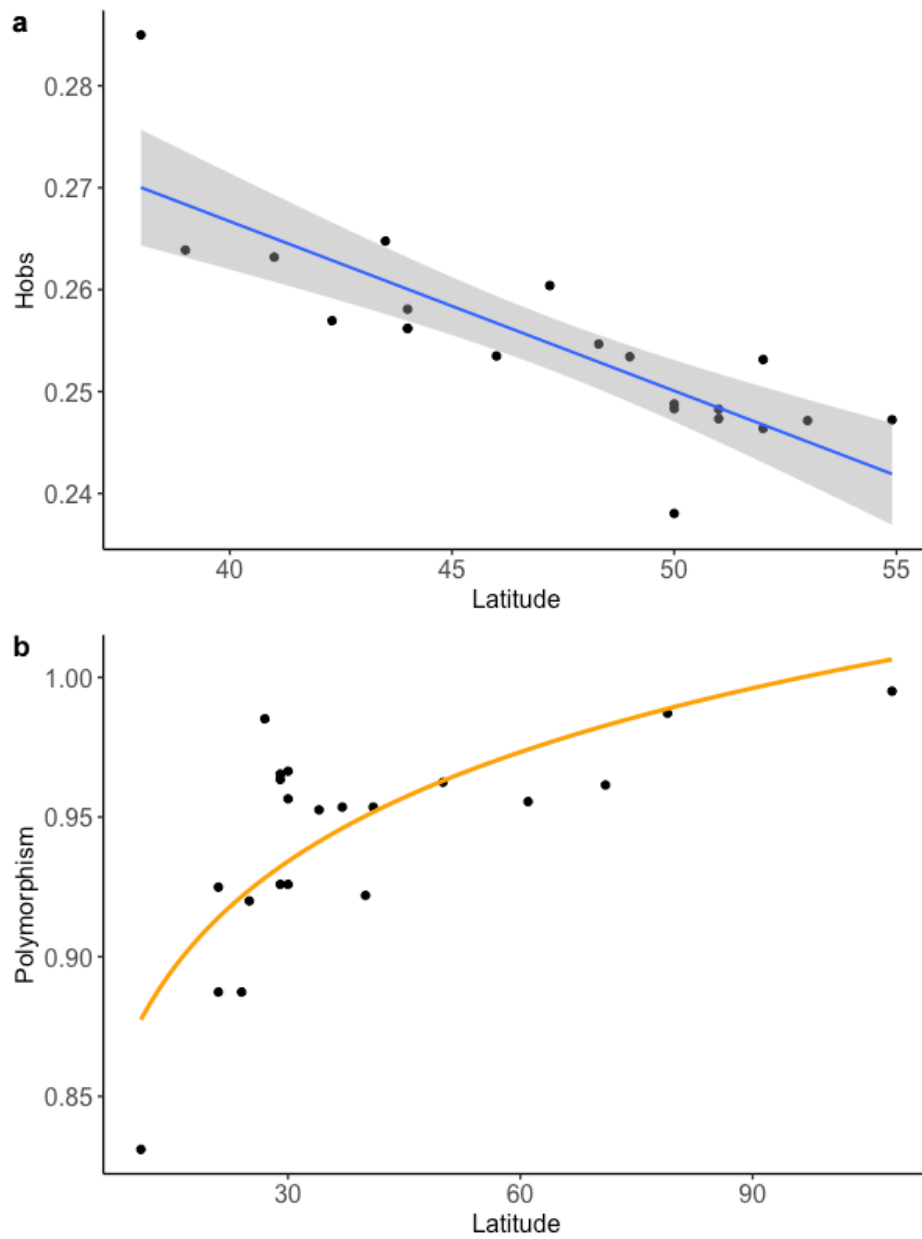


Figure S3. a: Observed sample heterozygosity (Hobs) as a function of latitude for the 21 localities of the main dataset. The blue line represents the fitted linear model (slope $p < 0.001$, $r^2 = 0.66$, grey shade 0.95 confidence interval). **b:** Relationship between SNP polymorphism rate per locality and the number of specimens (N) in each locality, fitted by a logistic model (orange line: Polymorphism = $0.05644 \ln(N) + 0.74216$, $p < 0.001$ for each coefficient).

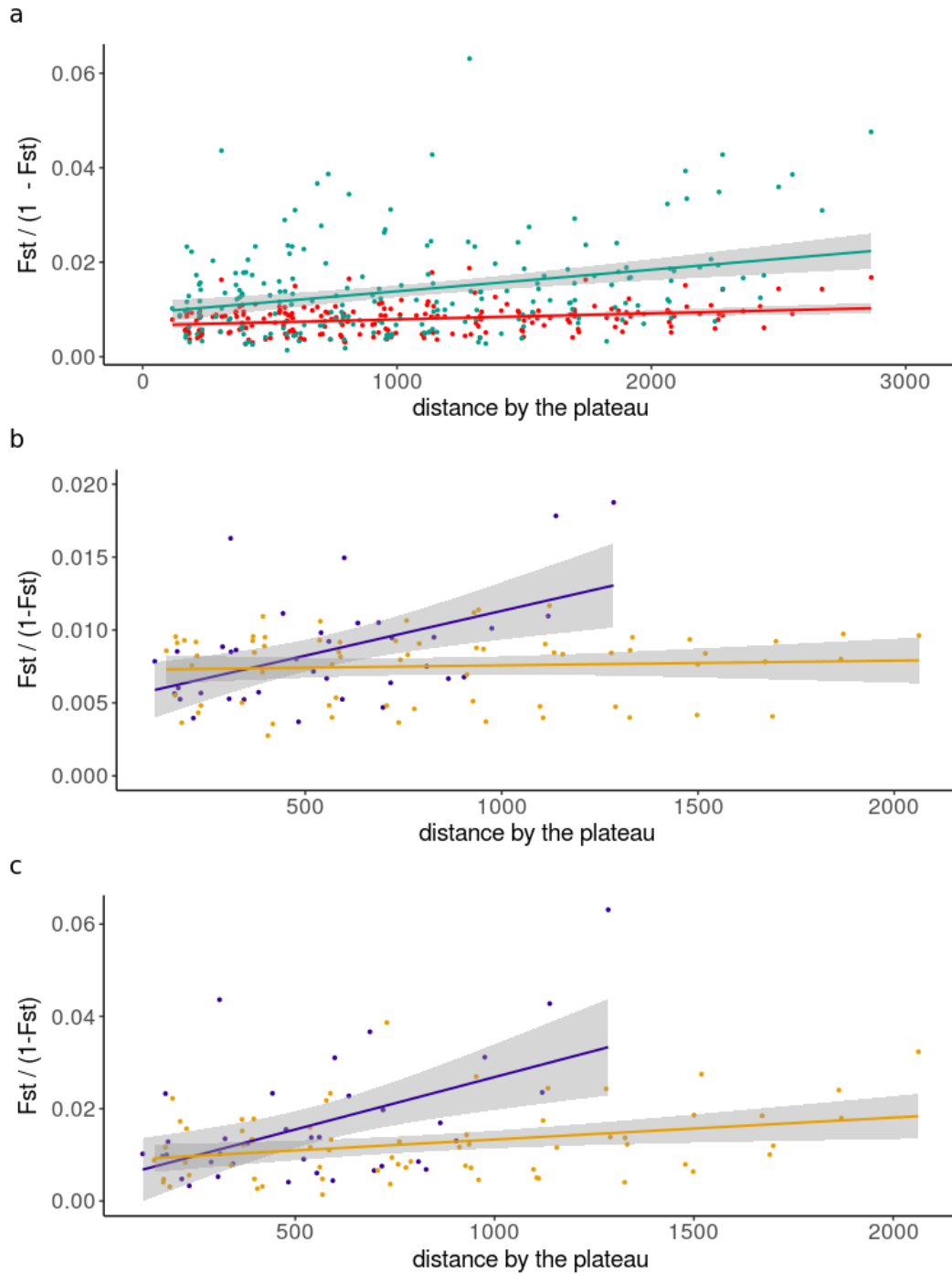


Figure S4. Pairwise genetic differentiation represented as $F_{st} / (1 - F_{st})$ as a function of the distance between the localities (main dataset of 21 localities). **a:** Positive relationships between pairwise genetic and geographic distances illustrated for neutral SNPs (red line, slope $p < 0.001$, $r^2 = 0.074$) and outlier SNPs that were detected at the within-Atlantic scale with Lositan (green line, slope $p < 0.001$, $r^2 = 0.089$). **b:** Relationships between pairwise genetic and geographic distances illustrated for neutral SNPs separately for localities south to GONB (gold line, not significant) and north to GONB (purple line, slope $p < 0.001$, $r^2 = 0.236$). **c:** Same as b but for outlier SNPs that were detected at the within-Atlantic scale with Lositan. South to GONB (gold line, slope $p < 0.001$, $r^2 = 0.083$), north to GONB (purple line, slope $p < 0.001$, $r^2 = 0.245$).

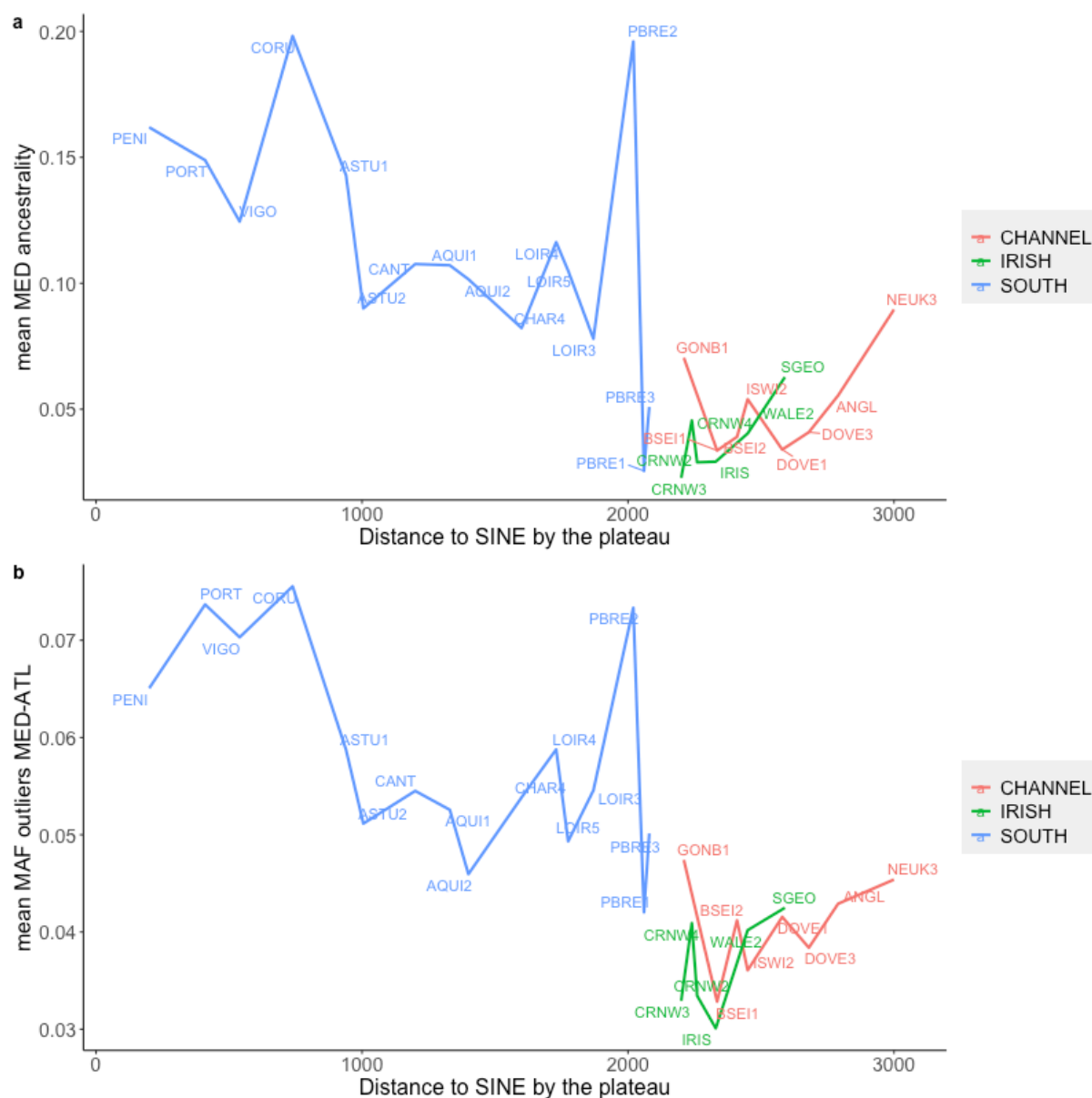


Figure S5. a: Geographic pattern of mean MED ancestry proportions along the northeast ATL coastlines, from south (the locality SINE was not represented) to north (NEUK), using the 'refined dataset' of 31 localities. **b:** Geographic pattern of mean MAF along the northeast ATL coastlines. Blue line: localities from southern Portugal to PBRE; green line: localities from CRNW to SGEO in the Irish Sea (Celtic Sea-Irish Sea branch); red line: localities from GONB to NEUK in the North Sea (Channel-North Sea branch).

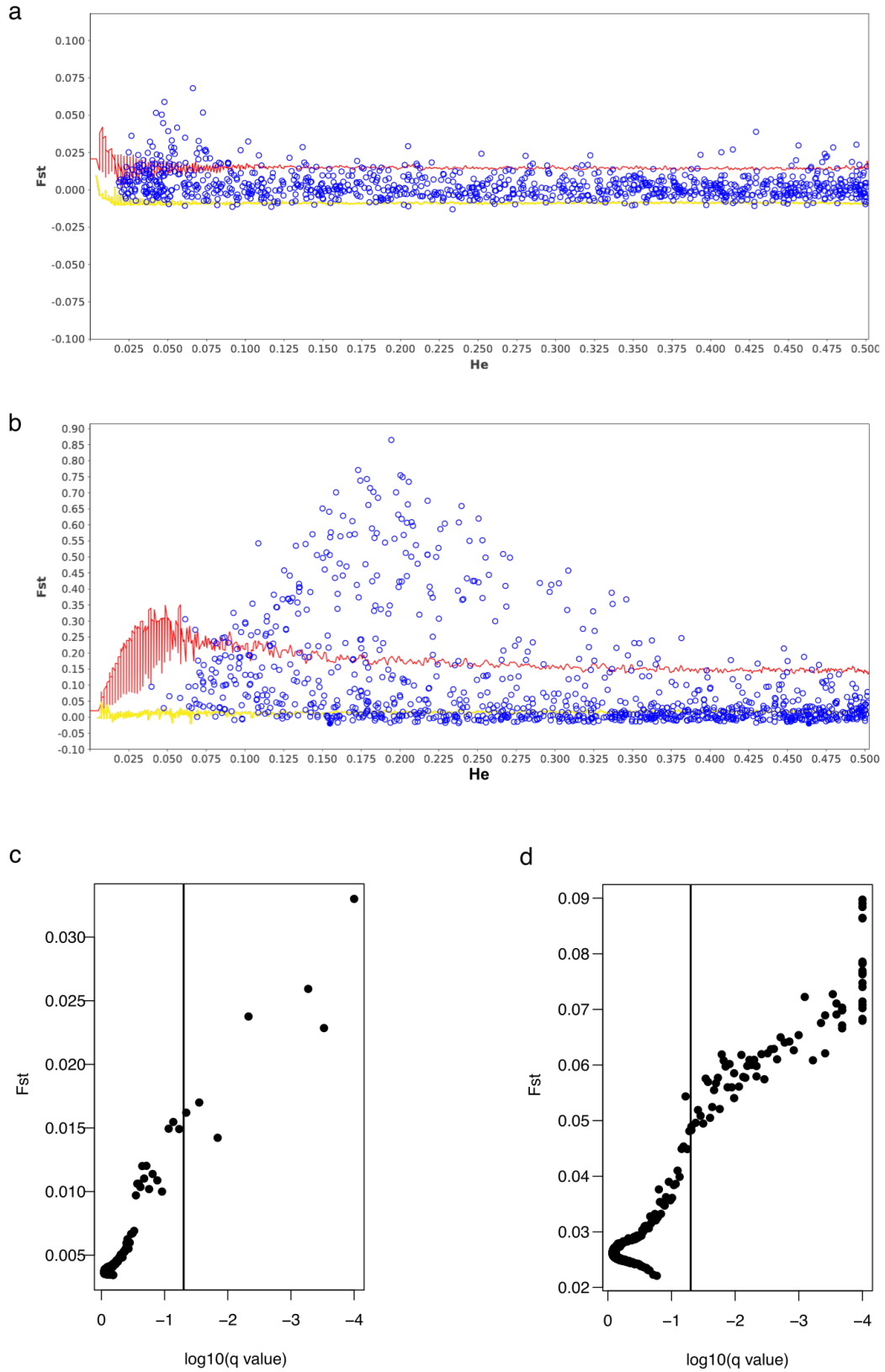


Figure S6. Outlier loci detection by LOSITAN within the Atlantic (a), and between ATL and MED lineages (b). Loci below and above the red line were classified as neutral and outlier loci, respectively. Outlier loci detection by BAYESCAN within the Atlantic (c), and between ATL and MED lineages (d). Loci left and right to the q -value threshold were classified as neutral and outlier loci, respectively.

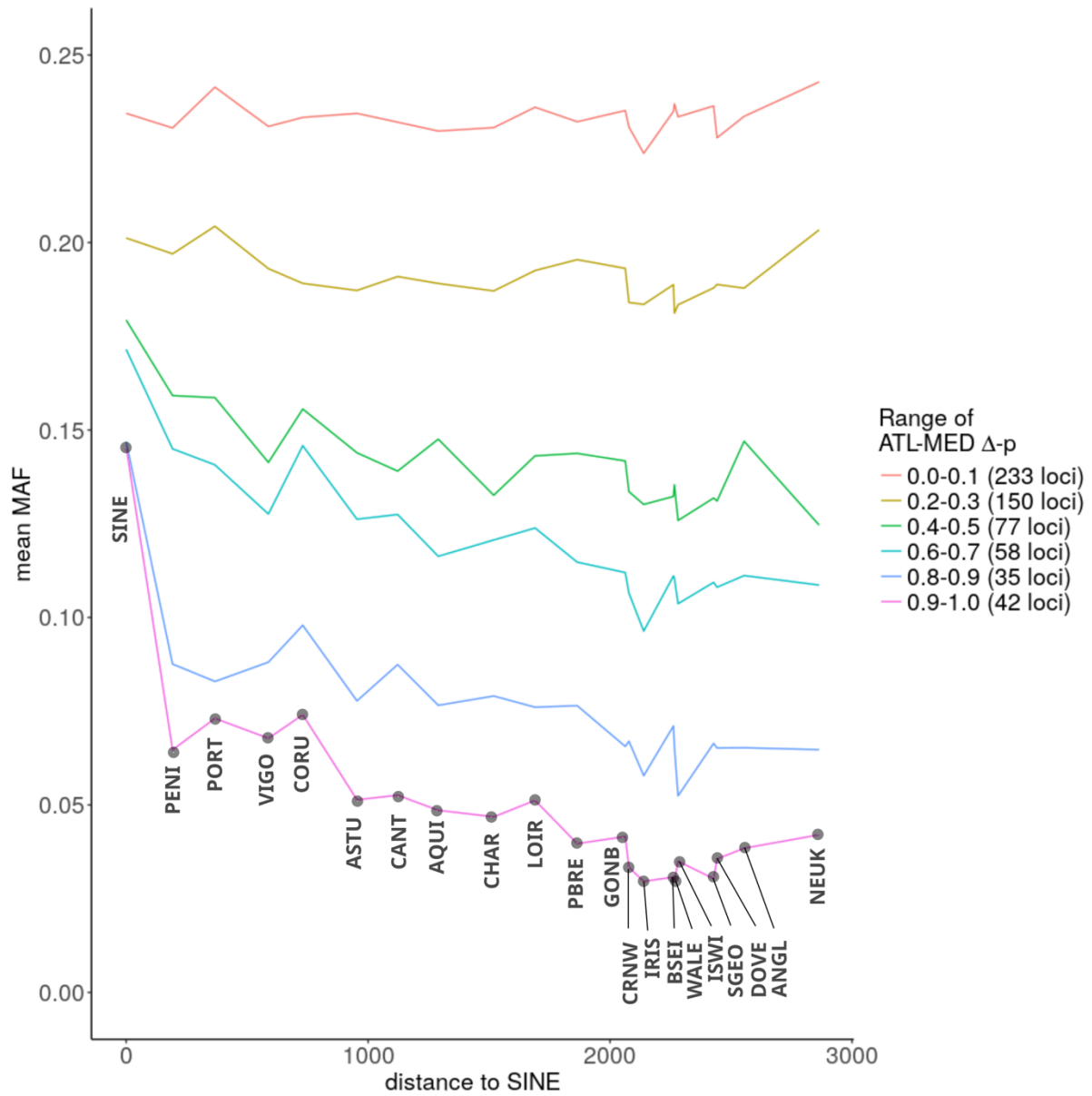


Figure S7. Geographic pattern of mean MAF for different subsets of loci, defined according to their allele frequency differences between ATL and MED lineages (ATL-MED Δp), as a function of the distance to SINE (km). The analysis is based on the main dataset.

Regions	Localities	Codes	ICES rectangles	Dates	Ng	Na
North Sea	North-East UK	NEUK	37E9, 38E9, 37E8	Win-Sum 2015	11	11
	East Anglia	ANGL	33F1	Sum 2014	30	29
Channel	Dover-Boulogne	DOVE	30F1, 31F1,31F2	Win-Sum 2014, Win 2015	61	61
	Seine Bay	BSEI	28E8, 28E9	Win 2014	40	40
	Normand-breton Gulf	GONB	26E7	Sum 2014	25	25
	Isle of Wight	ISWI	30E8, 30E9	Sum 2014	30	30
	English Cornwall	CRNW	28E3, 28E5, 29E4, 29E5	Win-Sum 2014	72	71
Irish Sea	St George's Channel	SGEO	35E5	Sum 2013	22	21
	Wales	WALE	31E5, 32E5, 32E6	Sum 2013, Win-Sum 2014	42	41
Celtic Sea	South-Ireland	IRIS	28E1	Win 2014	25	24
	Britain's cap	PBRE	25E4, 25E5, 26E5	Win-Sum 2014	56	50
North Biscay	Loire Estuary	LOIR	22E6, 22E7, 23E6, 23E7,24E6	Sum 2012, Sum 2013, Win-Sum 2014, Win 2015	111	108
	Charentes	CHAR	20E7, 20E8, 21E7, 21E8	Sum 2013, Sum 2014, Win 2015	34	34
South Biscay	Aquitaine	AQUI	16E8, 17E8, 18E8	Sum 2013, Win-Sum 2014	81	79
	Cantabria	CANT	16E6	Sum 2014	21	21
	Asturias	ASTU	16E3, 16E4	Win 2014, Win 2015	39	37
Portugal	A Coruña	CORU	15E1	Win 2014	30	29
	Vigo-Pontevedra	VIGO	13E1	Win 2014	30	30
	Porto	PORT	10E1	Win 2015	30	30
	Peniche	PENI	7E0	Win 2015	29	29
	Sine	SINE	4E1	Win 2015	27	27
Total	21 localities		44 rectangles		846	827

Table S1. Regions, localities and codes, ICES rectangles (statistical squares for international management of fisheries), dates (season and year) of specimen collection. Ng: no. of specimens genotyped; Na: no. of specimens kept after quality filtering. Win: winter season (from Dec 1st of previous year to May 31st of the year); Sum: summer (from Jun 1st to Nov 30th of the year).

Region	Pool	N	H _{obs}	H _{exp}	F _{IS}	DAF	Polym.
North sea	ANGL	29	0.2464	0.2868	0.1409	0.8265	0.9259
	NEUK	11	0.2472	0.2952	0.1626	0.8200	0.8310
Channel	BSEI	40	0.2488	0.2881	0.1365	0.8255	0.9219
	CRNW	71	0.2483	0.2850	0.1287	0.8279	0.9615
	DOVE	61	0.2473	0.2835	0.1276	0.8290	0.9555
	GONB	25	0.2534	0.2932	0.1356	0.8216	0.9200
	ISWI	30	0.2483	0.2866	0.1337	0.8267	0.9259
Irish sea	SGEO	21	0.2472	0.2895	0.1464	0.8244	0.8874
	WALE	41	0.2531	0.2905	0.1286	0.8237	0.9536
Celtic sea	IRIS	24	0.2380	0.2785	0.1454	0.8328	0.8874
	PBRE	50	0.2547	0.2929	0.1307	0.8218	0.9625
North Biscay	CHAR	34	0.2535	0.2904	0.1270	0.8238	0.9526
	LOIR	108	0.2604	0.2958	0.1196	0.8195	0.9951
South Biscay	AQUI	79	0.2581	0.2929	0.1190	0.8218	0.9872
	ASTU	37	0.2562	0.2936	0.1274	0.8212	0.9536
	CANT	21	0.2562	0.2945	0.1301	0.8205	0.9249
Portugal	CORU	29	0.2648	0.3026	0.1251	0.8141	0.9654
	VIGO	30	0.2569	0.2944	0.1271	0.8206	0.9565
	PENI	29	0.2639	0.3036	0.1309	0.8134	0.9634
	PORT	30	0.2632	0.3033	0.1322	0.8136	0.9664
	SINE	27	0.2850	0.3175	0.1024	0.8021	0.9852

Table S2. Summary of genetic variation at the 1012 retained loci, as grouped in the main dataset (21 localities from 7 regions). N: Number of genotyped individuals kept after filtering; H_{obs}: mean observed heterozygosity; H_{exp}: mean expected heterozygosity; F_{IS} index: (H_{exp}-H_{obs})/H_{exp}; DAF: mean frequency of major alleles; Polym.: proportion of polymorphic SNPs in each locality.

<i>p-val / Fst</i>	North Sea	Channel	Irish Sea	Celtic Sea	North Biscay	South Biscay	Portugal
North Sea		0.0021	0.0057	0.0046	0.0031	0.0032	0.0029
Channel	0.6877		0.0017	0.0017	0.0014	0.0014	0.0013
Irish Sea	0.0004	0.7758		0.0040	0.0026	0.0026	0.0024
Celtic Sea	0.0412	0.6915	0.0434		0.0025	0.0023	0.0022
North Biscay	0.0982	0.8728	0.1930	0.1442		0.0017	0.0019
South Biscay	0.1122	0.8856	0.2084	0.2691	0.5497		0.0015
Portugal	0.5577	0.9976	0.7341	0.7107	0.7696	0.9486	

Table S3. Pairwise FST values at the 1012 retained loci (upper triangle), for each pair among the 7 Atlantic regions. Bold black numbers indicate significantly FST values ($p < 0.05$). Significance of Fst values (empirical p -values) are given in lower triangle. Pale grey values indicate not significant values.