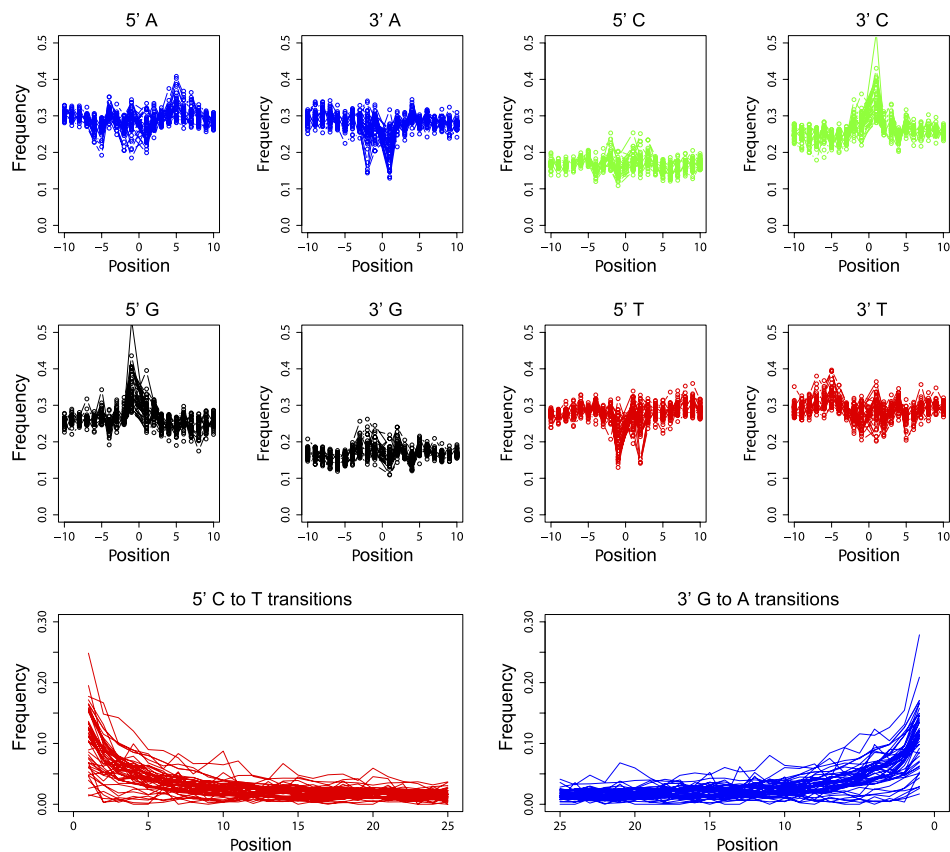
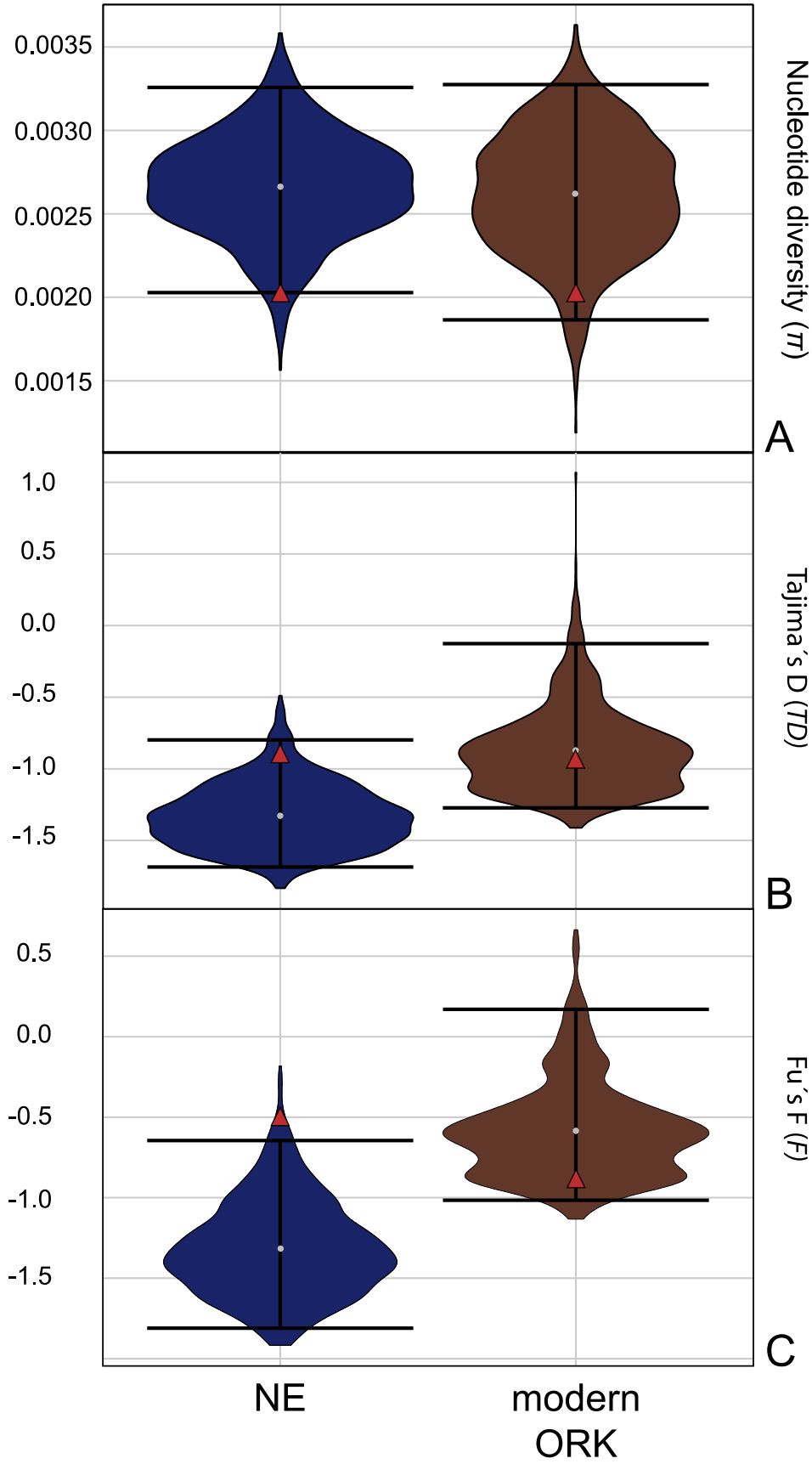


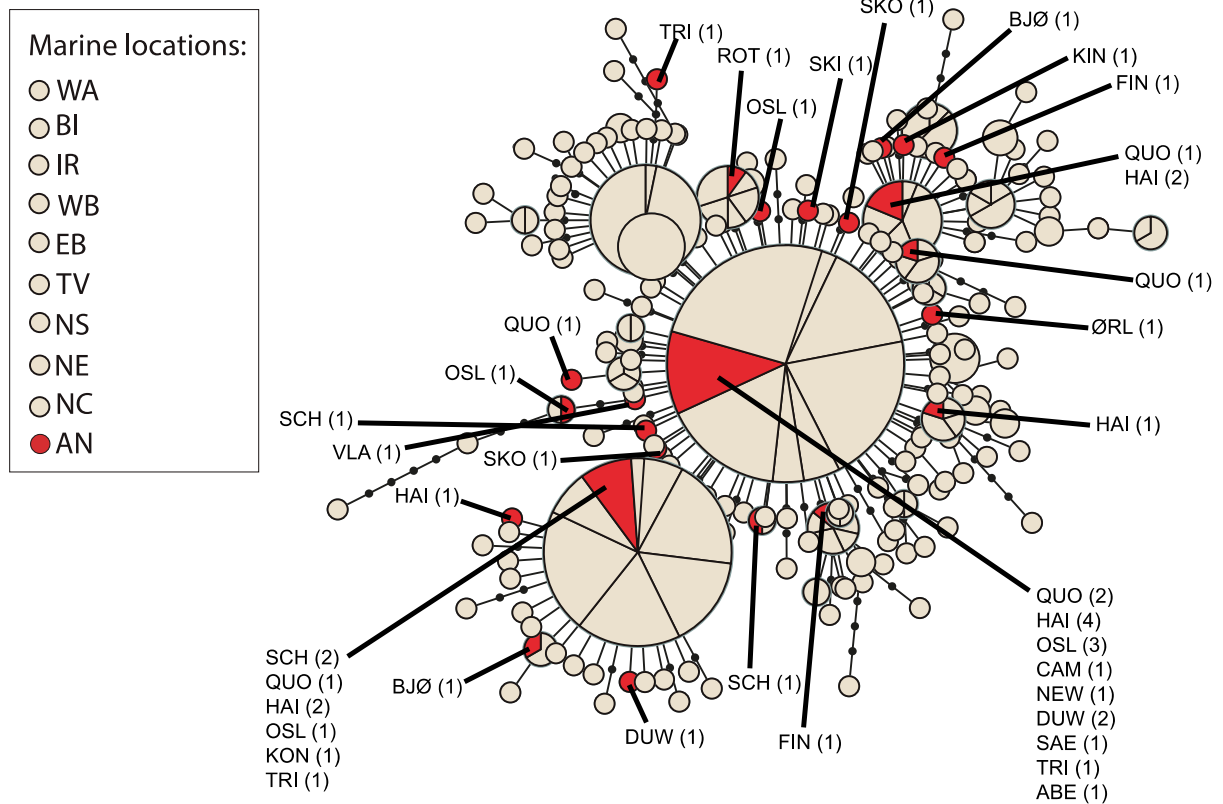
Supplementary Material



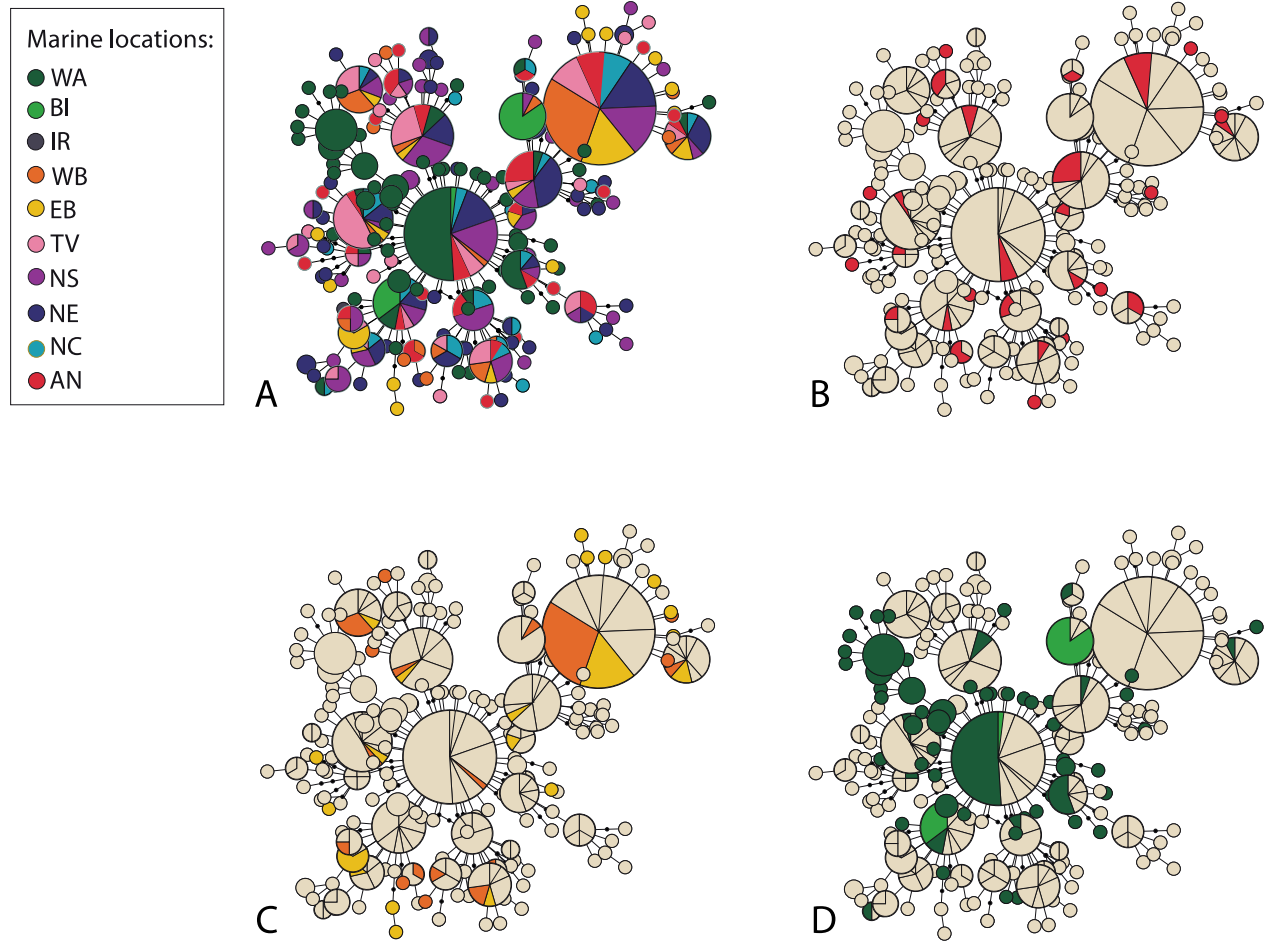
Supplementary Figure S1. aDNA damage patterns of read data from Atlantic cod ancient samples (see archaeological dates in Supplementary Table S1) obtained using MapDamage v.2.0.9 (Jónsson et al., 2013).



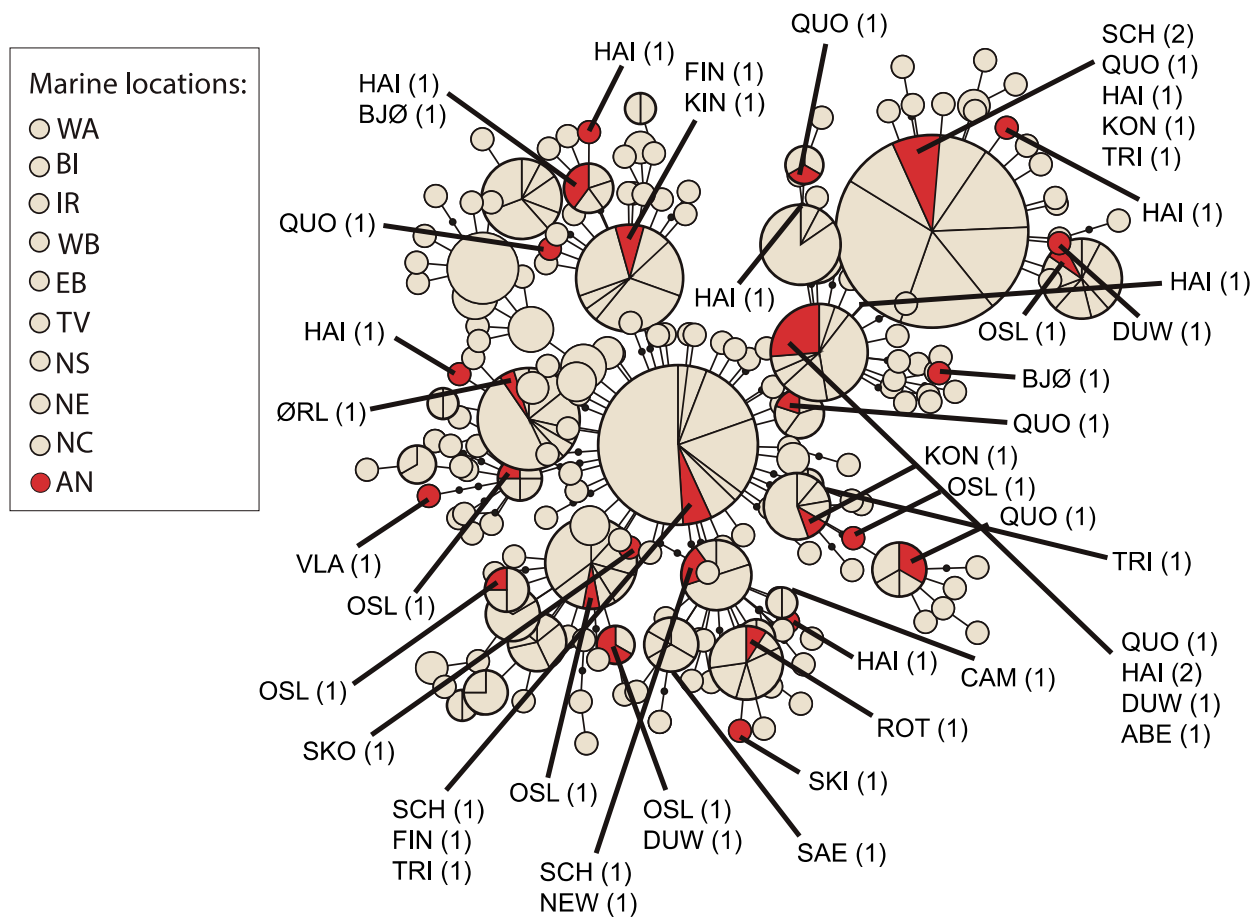
Supplementary Figure S2. Violin plot representing the data distribution of our temporal comparisons after 1000 bootstrap replicates without replacement. Black line represents the 95% confidence interval of data distribution. Gray circle represents the mean value of the data. Red triangle represents the observation of the ancient populations Quoygrew (QUO) and Haithabu (HAI), in comparison to their specific temporal pair (see Materials and Methods section). Location North East Arctic (NE) = dark blue. Location modern Orkney = brown. **(A)** Nucleotide diversity (π) statistic (95% CI: NE = 0.00203 to 0.00326; modern Orkney = 0.00186 to 0.00327), **(B)** Tajima's D (TD) statistic (95% CI: NE = -1.686 to -0.798; modern Orkney = -1.273 to -0.126) and **(C)** Fu's F (F) statistic (95% CI: NE = -1.811 to -0.645; modern Orkney = -1.016 to 0.170).



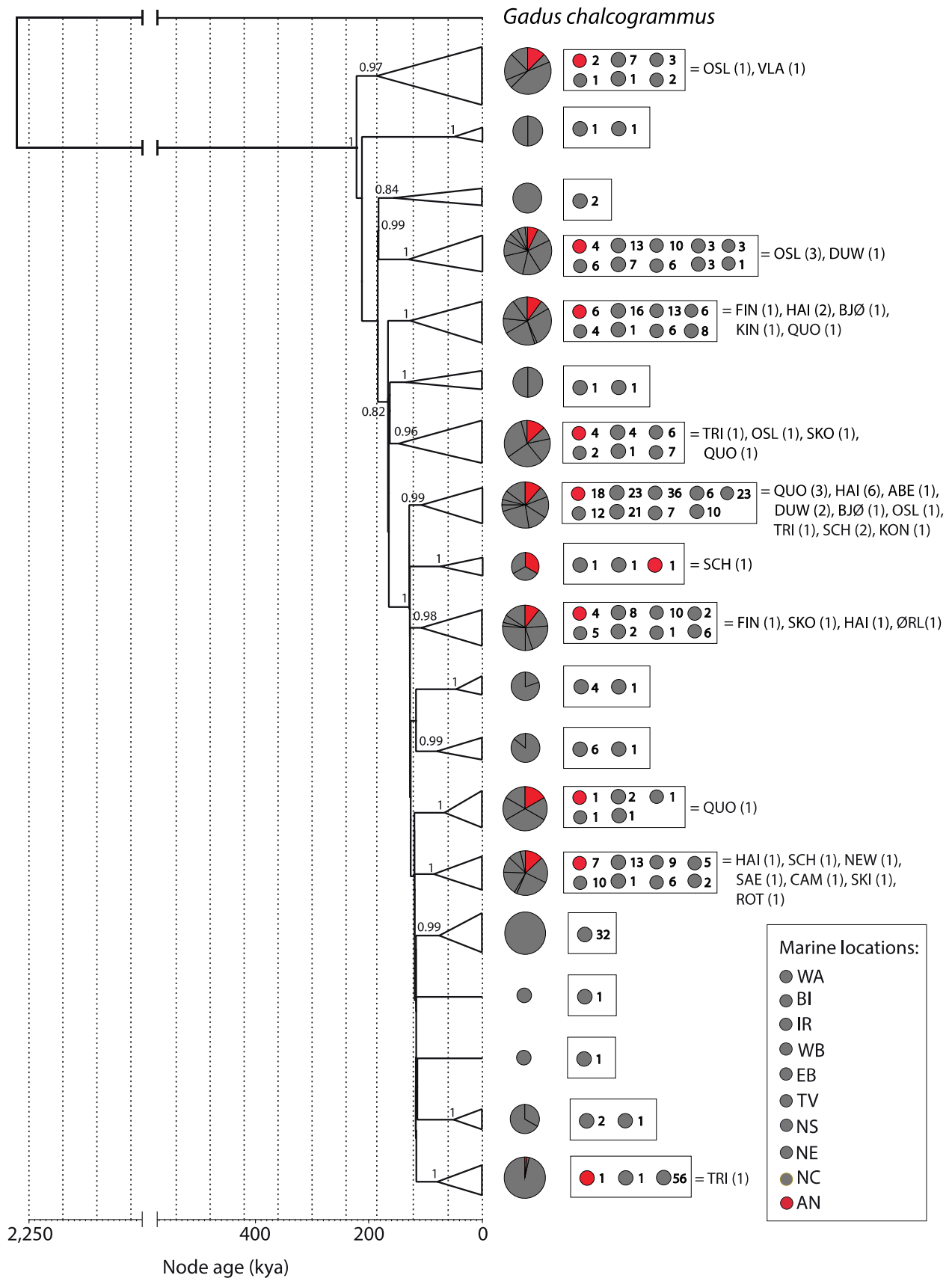
Supplementary Figure S3. Star-like haplotype genealogy based on complete mitogenomes of 545 samples of Atlantic cod. Only transversions (336) are depicted in this genealogy. Haplotype genealogy highlighting ancient specimens and their original sampling site (in red; see Figure 1; Supplementary Table S1). Ancient specimens are not consistently constrained to a specific mitogenomic cluster according to geographic location. Ancient specimens (as a single group) = AN, Sævarhelleren = SAE, Ørland Kampflybase = ØRL, Bjørkum = BJØ, Haithabu = HAI, Quoygrew = QUO, Schleswig Schild = SCH, Oslo Mindets Tomt = OSL, Bristol Dundas Wharf = DUW, Skonsvika = SKO, King's Lynn Raynham House = KIN, Kongshavn = KON, London Trig Lane = TRI, Vlaardingen Gat in de Markt = VLA, Bristol Finzel's Reach = FIN, Rotterdam, Hoogstraat 13-26 = ROT, Aberdeen = ABE, Cambridge Grand Arcade = CAM, Skriðuklaustur = SKI, Newport Ship = NEW.



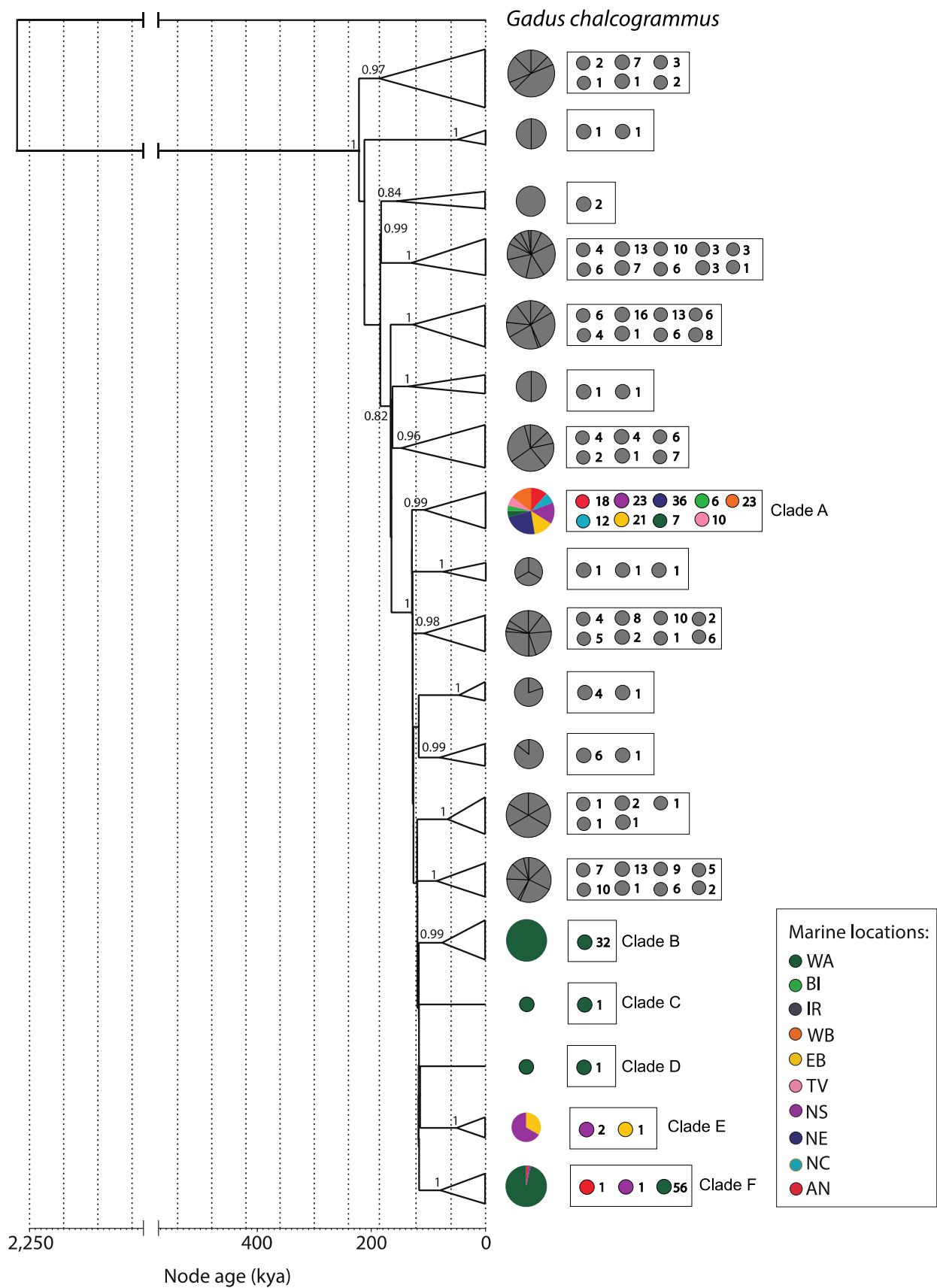
Supplementary Figure S4. Star-like haplotype genealogy based on the CytB gene fragment (positions 14343-15484) of 545 samples of Atlantic cod. Only 312 substitutions (transitions or transversions) are represented in this genealogy. **(A)** Haplotype genealogy colored by location. **(B)** Haplotype genealogy highlighting ancient specimens as a single group (in red; see Figure 1, Supplementary Table S1; for specific distribution of sampling sites of ancient samples see Supplementary Figure S5). **(C)** Haplotype genealogy highlighting samples from the western (orange) and eastern (yellow) Baltic. **(D)** Haplotype genealogy highlighting western Atlantic (green) and Baffin Island (light green) specimens. Circle size is proportional to haplotype frequency. Black dots indicate intermediate haplotypes not found among the specimens and black lines connecting black circles correspond to mutation steps between haplotypes.



Supplementary Figure S5. Star-like haplotype genealogy based on the CytB gene fragment (positions 14343-15484) of 545 samples of Atlantic cod. Only 312 substitutions (transitions or transversions) are represented in this genealogy. Haplotype genealogy highlighting ancient specimens and their original sampling site (in red; see Figure 1; Supplementary Table S1). Ancient specimens are not consistently constrained to a specific mitogenomic cluster according to geographic location. Ancient specimens (as a single group) = AN, Sævarhelleren = SAE, Ørland Kampflybase = ØRL, Bjørkum = BJØ, Haithabu = HAI, Quoygrew = QUO, Schleswig Schild = SCH, Oslo Mindets Tomt = OSL, Bristol Dundas Wharf = DUW, Skonsvika = SKO, King's Lynn Raynham House = KIN, Kongshavn = KON, London Trig Lane = TRI, Vlaardingen Gat in de Markt = VLA, Bristol Finzel's Reach = FIN, Rotterdam, Hoogstraat 13-26 = ROT, Aberdeen = ABE, Cambridge Grand Arcade = CAM, Skriðuklaustur = SKI, Newport Ship = NEW. If a pie chart containing a specific sampling site is behind another pie chart, the closest position to the location of the sample is indicated.



Supplementary Figure S6. Time calibrated collapsed Bayesian phylogeny of full mitogenomes from 525 Atlantic cod specimens highlighting the distribution of all ancient samples (in red) according to their sampling site. In each clade that includes an ancient sample, the name(s) of the corresponding sampling site(s) of the specimen is indicated. Numbers in parenthesis after the name of the sampling site indicate the number of ancient specimens present in each clade. Ancient specimens are not consistently constrained to a specific mitogenomic cluster according to geographic location. Ancient specimens (as a single group) = AN, Sævarhelleren = SAE, Ørland Kampflybase = ØRL, Bjørkum = BJØ, Haithabu = HAI, Quoygrew = QUO, Schleswig Schild = SCH, Oslo Mindets Tomt = OSL, Bristol Dundas Wharf = DUW, Skonsvika = SKO, King's Lynn Raynham House = KIN, Kongshavn = KON, London Trig Lane = TRI, Vlaardingen Gat in de Markt = VLA, Bristol Finzel's Reach = FIN, Rotterdam, Hoogstraat 13-26 = ROT, Aberdeen = ABE, Cambridge Grand Arcade = CAM, Skriðuklaustur = SKI, Newport Ship = NEW.



Supplementary Figure S7. Time calibrated collapsed Bayesian phylogeny of 525 Atlantic cod specimens highlighting the clades excluded in data sets III, IV and V for the different Skyline analyses. Clades in full color represent the 6 clades (A-F) that were excluded in various combinations. Clade A (156 individuals) includes most Baltic Sea samples. Clades B-F represent the clades including most western Atlantic samples (95 individuals). First, clade A-F (Baltic Sea and western Atlantic) were excluded in data set III. Second, clade A (Baltic Sea) was excluded in data set IV. Third, clades B-F (western Atlantic) were excluded in data set V. Pie charts represent the marine locations distributed in each clade. Numbers beside pie charts indicate the number of individuals from each marine region distributed in each clade.