

Figure 2 figure supplement 1. Minimal cross-entropy values assuming 1 to 5 ancestral populations (K=1 to K=5) obtained with the program sNMF, which estimates admixture coefficients based on genotype data.

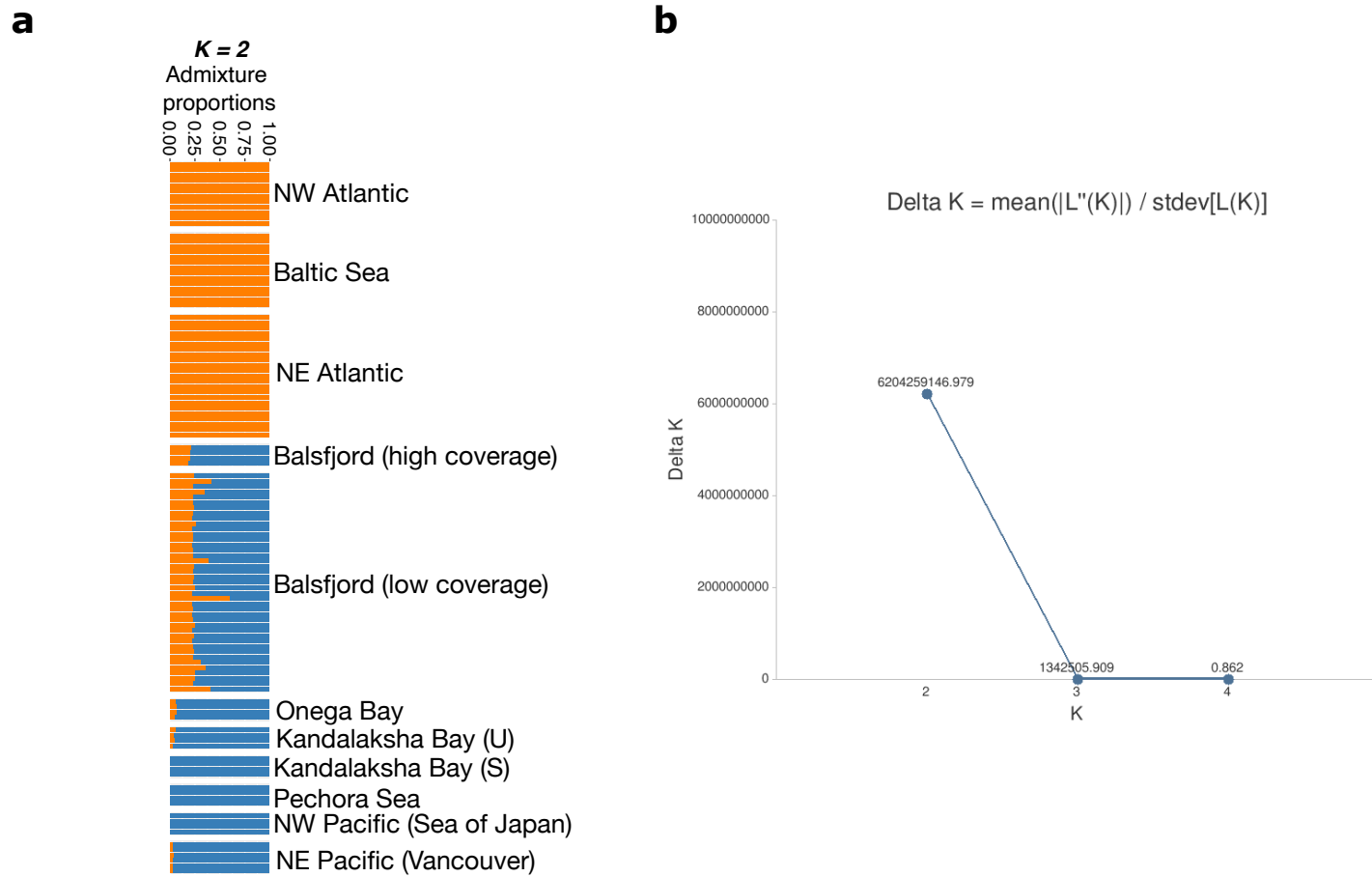


Figure 2 figure supplement 2. Admixture analysis of Atlantic, Pacific, and Balsfjord individuals sequenced to high and low depth. A total of 120 samples and 1 464 528 LD-pruned SNP markers were included in the admixture analysis performed with the program NGSadmix (Skotte et al., 2013). *a*) Bar plot representing individual admixture proportions assuming $K = 2$, which is the most likely number of clusters in the dataset according to the Evanno method based on 10 replicates per K value tested (from 1 to 5). In the bar plot, each horizontal bar corresponds to an individual and individuals from the same location are grouped in the same block. The size of each color division per individual bar represents the proportion of an individual's genome that likely originated from the ancestral populations (K) identified, or clusters. For $K = 2$, the Atlantic cluster is indicated in orange, and the Pacific cluster in blue. *b*) Plot representing the Delta K value for K from 2 to 4 calculated with CLUMPAK (Kopelman et al., 2015).

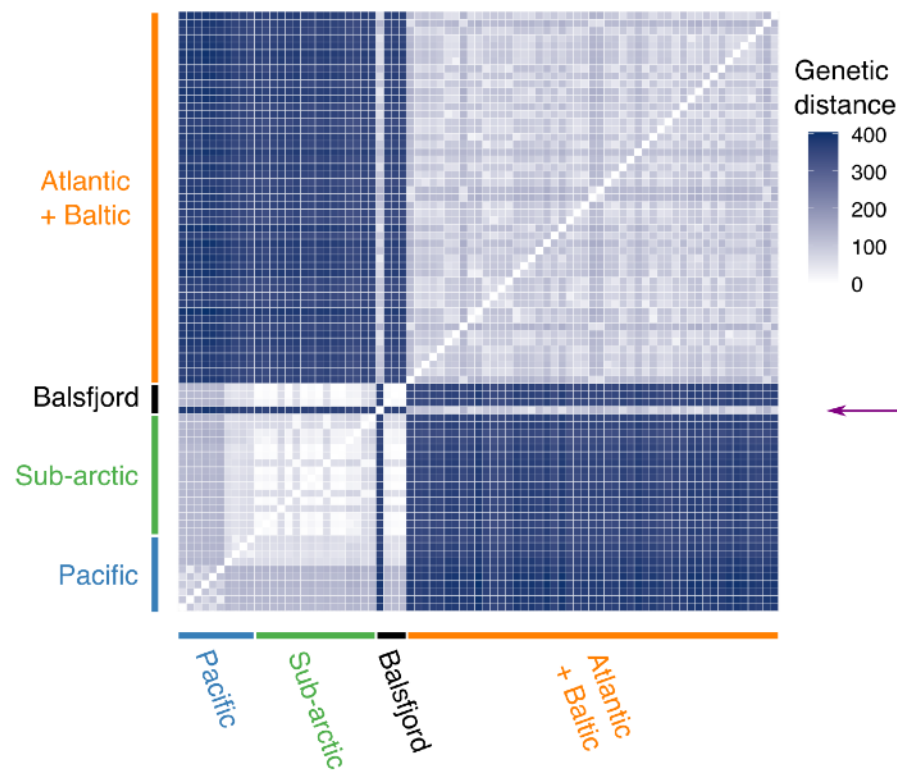
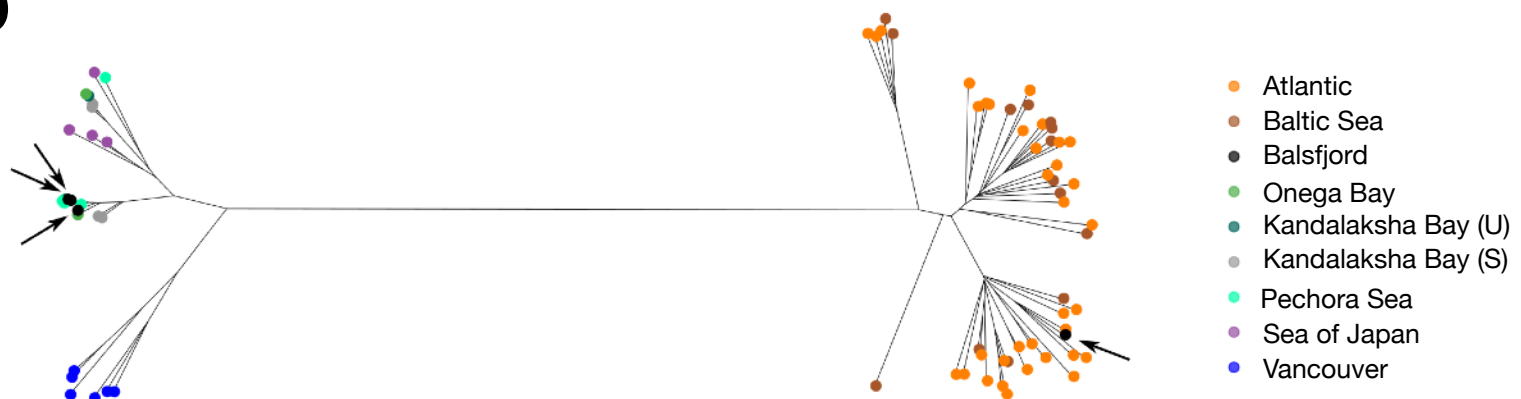
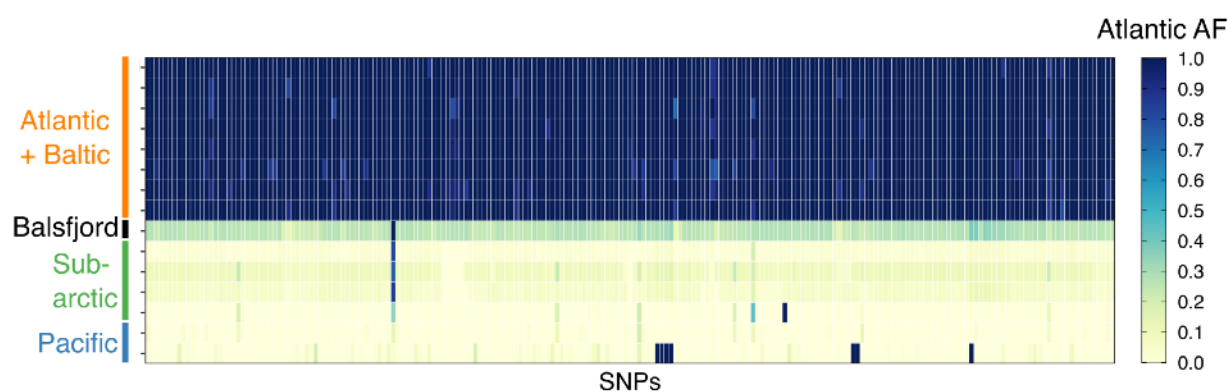
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Figure 2 figure supplement 3. Atlantic mitochondrial introgression in Balsfjord herring. *a)* Pairwise genetic distance among 79 individuals based on 1,382 SNPs in the mtDNA. The genetic distance corresponds to the effective number of nucleotide differences (counts) between pairs. Low to high genetic distance is represented in gray shades from white to black, respectively. Individuals from the various geographic groups are denoted with a colored bar on the left, in orange for Atlantic-Baltic, black for Balsfjord, green for Subarctic, and blue for Pacific. The arrow on the right points to the Balsfjord individual with an Atlantic mtDNA type. *b)* Distance-based unrooted neighbor-joining tree based on individual mtDNA sequences. Besides the broad distinction between the Atlantic and the Pacific herring species, the Pacific herring is subdivided into a NE Pacific (Vancouver) lineage and NW Pacific + European lineage. Three of the four Balsfjord sequences cluster with NW Pacific sequences, and the fourth clusters with Atlantic. The four Balsfjord sequences are denoted with arrows. Sample label colors indicate region of origin. *c)* Heatmap plot showing the pool allele frequency (AF) of 213 SNPs in 15 populations. Cell colors indicate the frequency of the Atlantic mtDNA allele. Same as in (*b*), pool samples from the various geographic groups are denoted with a color bar on the left. Notice that in the Balsfjord pool the Atlantic allele frequency is around 27%.

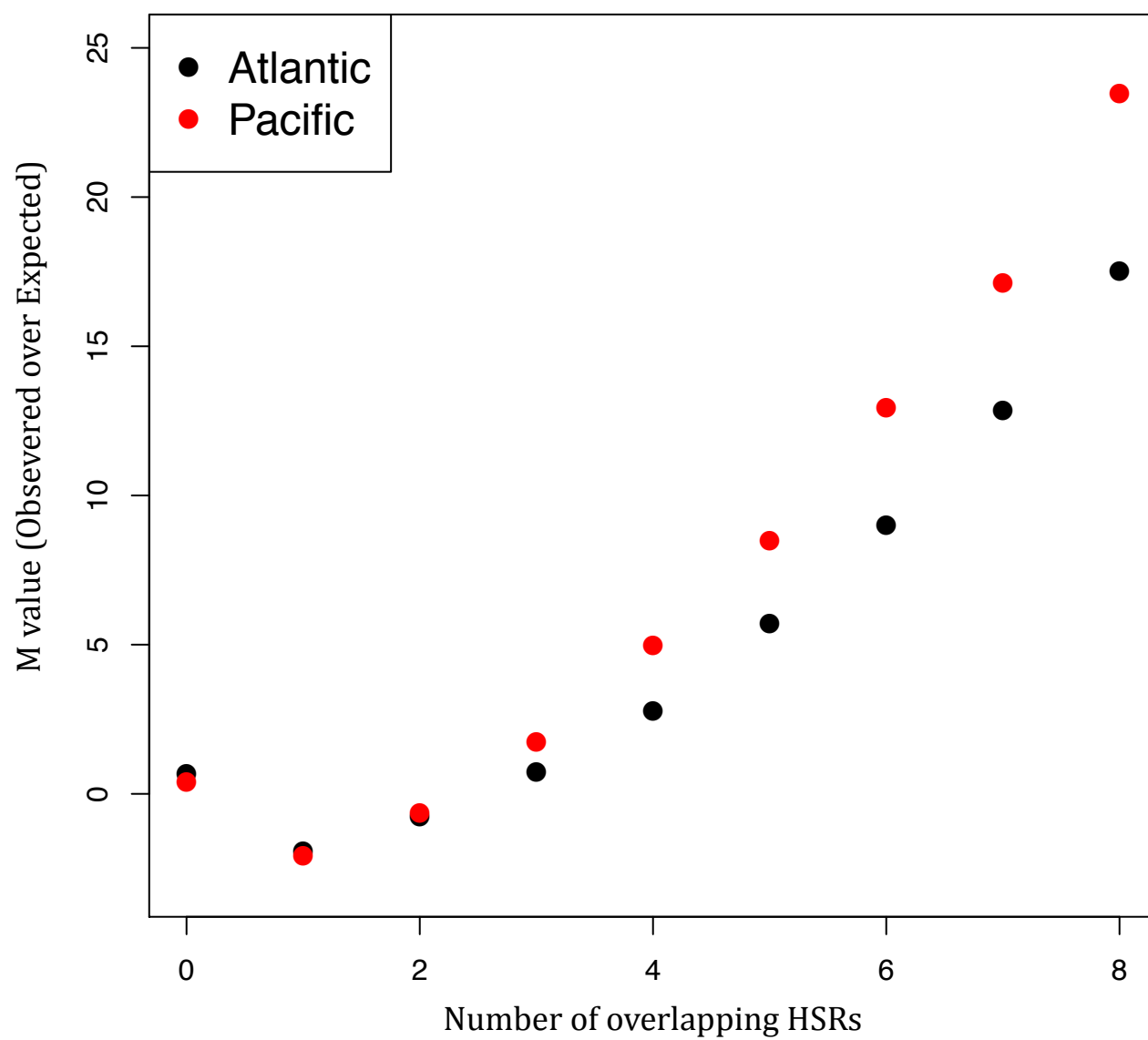


Figure 3 figure supplement 1. M-values (i.e., $\log_2(\text{Observed}/\text{Expected})$) for different counts of HSRs among the 8 haploid genomes from Balsfjord individuals for regions of Atlantic and Pacific origin, respectively.

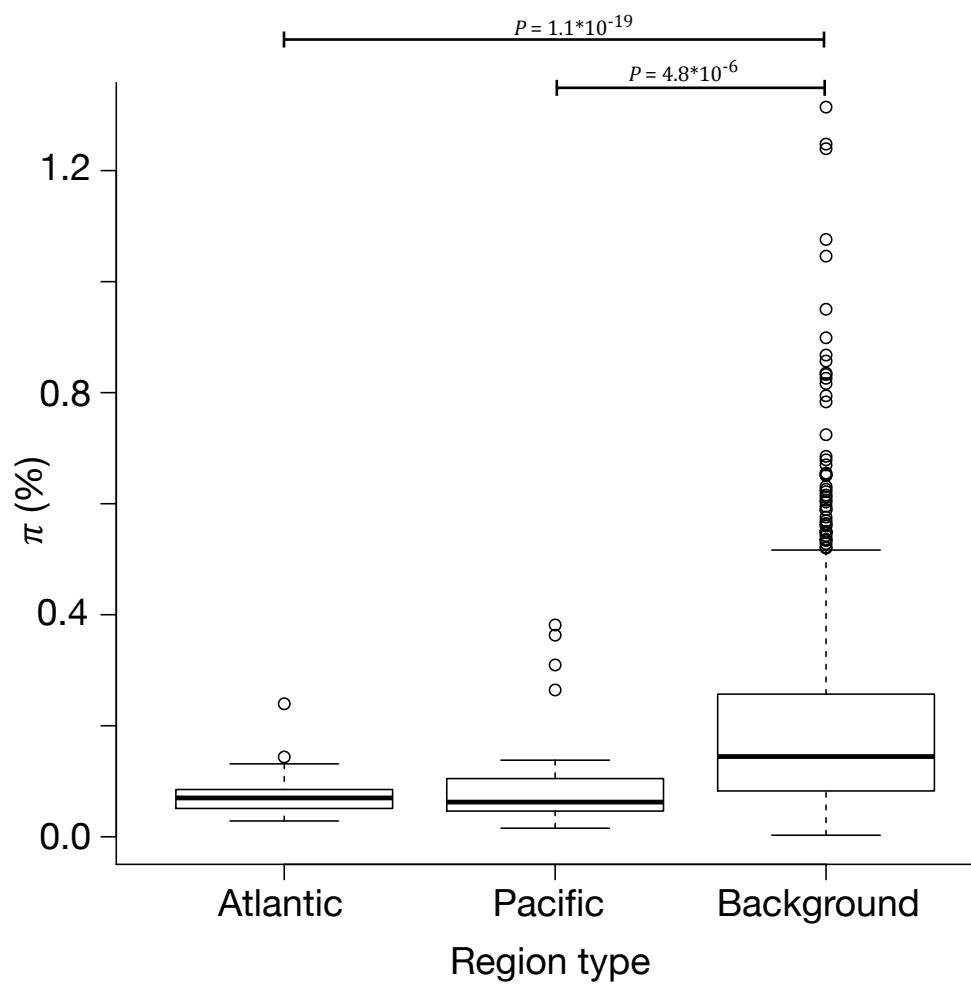
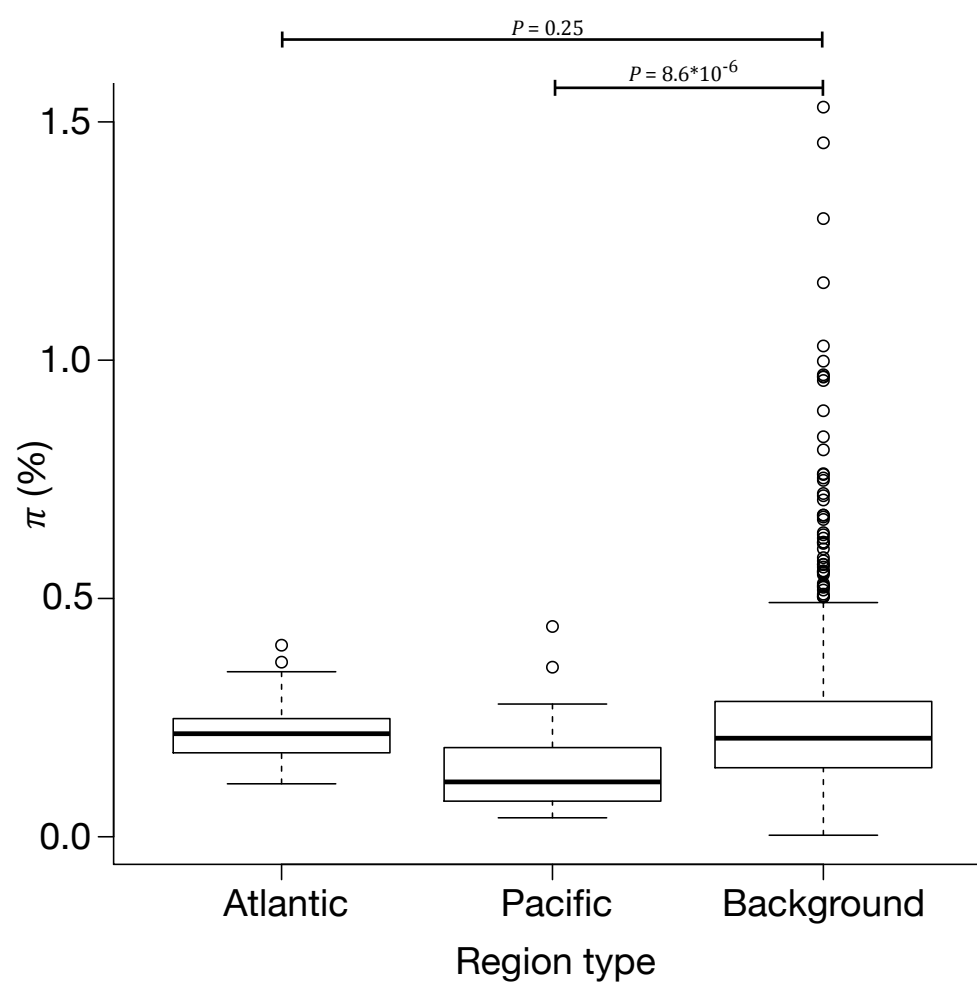
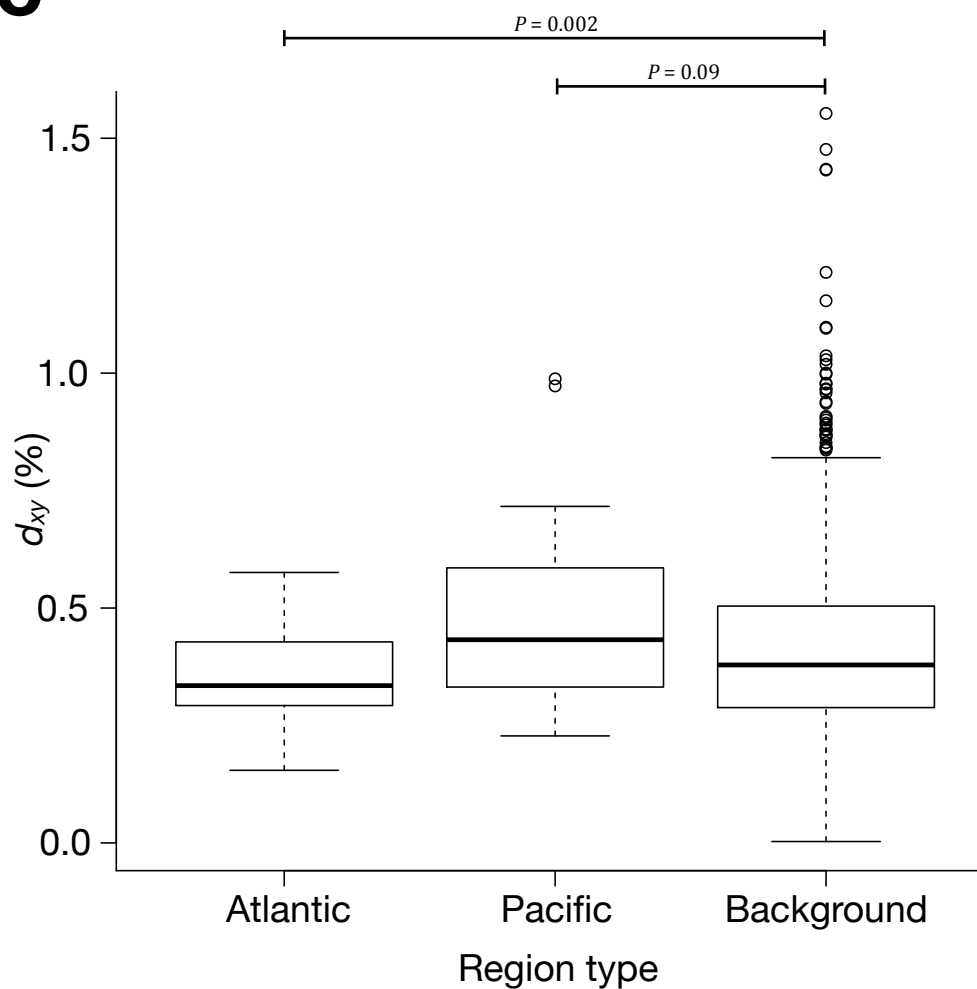
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Figure 7 figure supplement 2. Diversity summary statistics of Atlantic and Pacific herring in regions with 8x-recurring HSRs detected in Balsfjord populations. a) Nucleotide diversity (π) in Atlantic and Baltic samples of Atlantic herring. b) Nucleotide diversity (π) in European and Northwest Pacific samples of Pacific herring. c) d_{xy} between those Atlantic herring and Pacific herring samples. The labels on the x-axis indicate the type of recurring HSR.

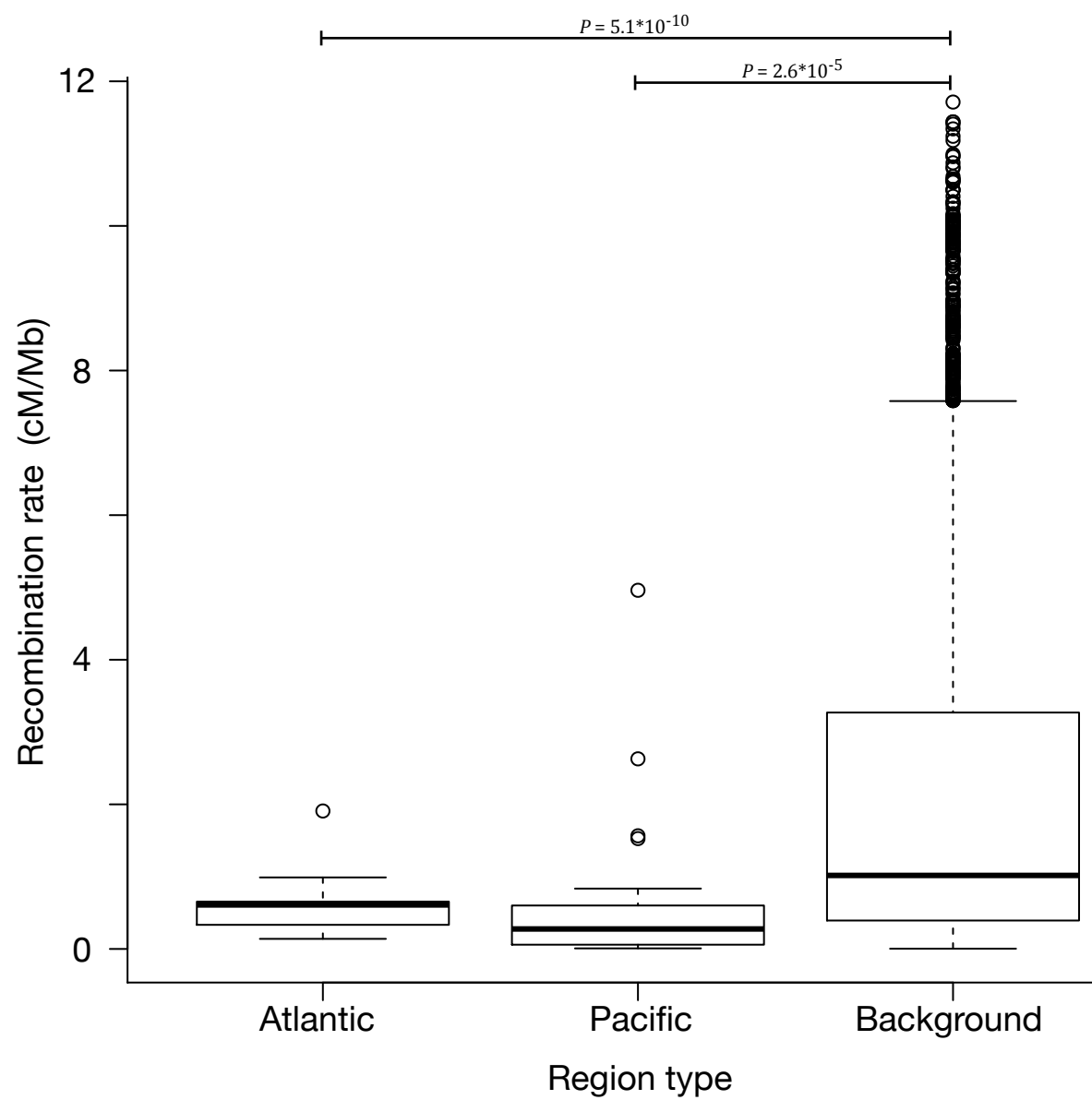


Figure 7 figure supplement 3. Recombination rate in regions of 8x-recurring HSRs.

Recombination rate across introgressed and background regions, respectively. The labels on the x-axis indicate the type of recurring HSR.