

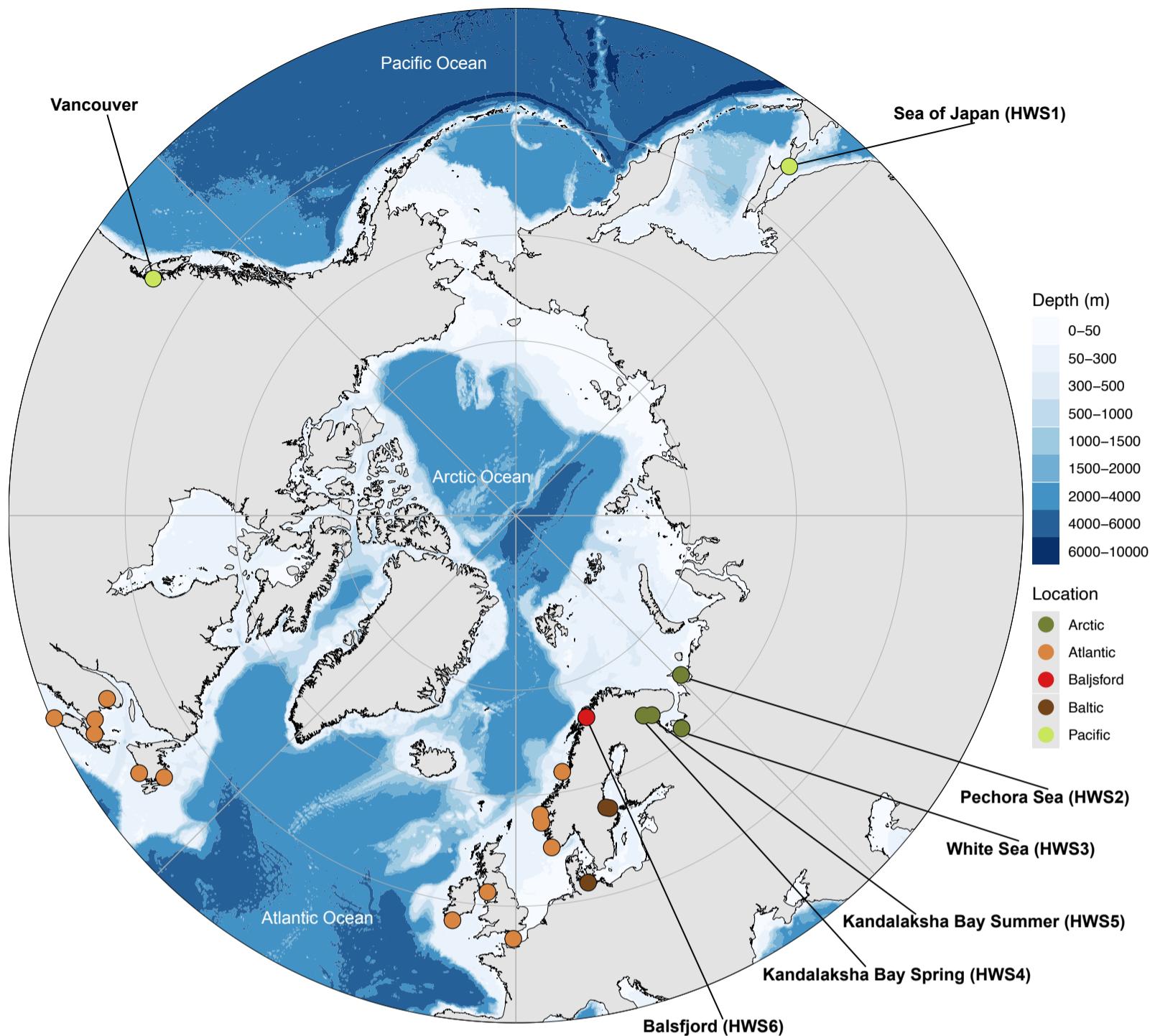
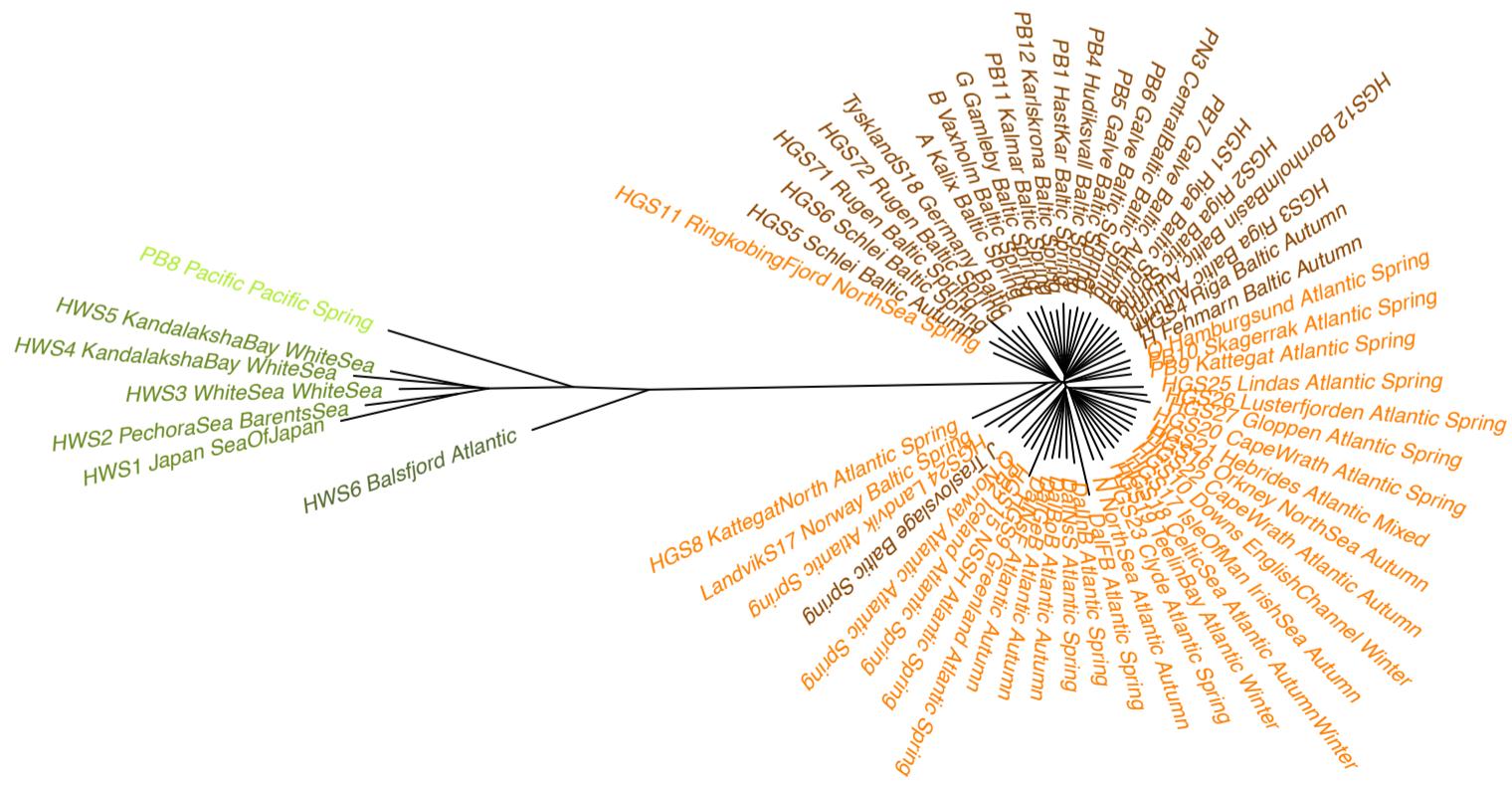
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Figure 1. Sample locations and genetic distances among Pacific herring in the Arctic and sub-Arctic. a) Location of samples from Balsfjord, the White sea, Sea of Japan and Vancouver. For locations of Atlantic and Baltic samples, see Han et al (2020) b) Neighbor-joining tree based on allele frequency distances from 10^5 randomly selected markers.

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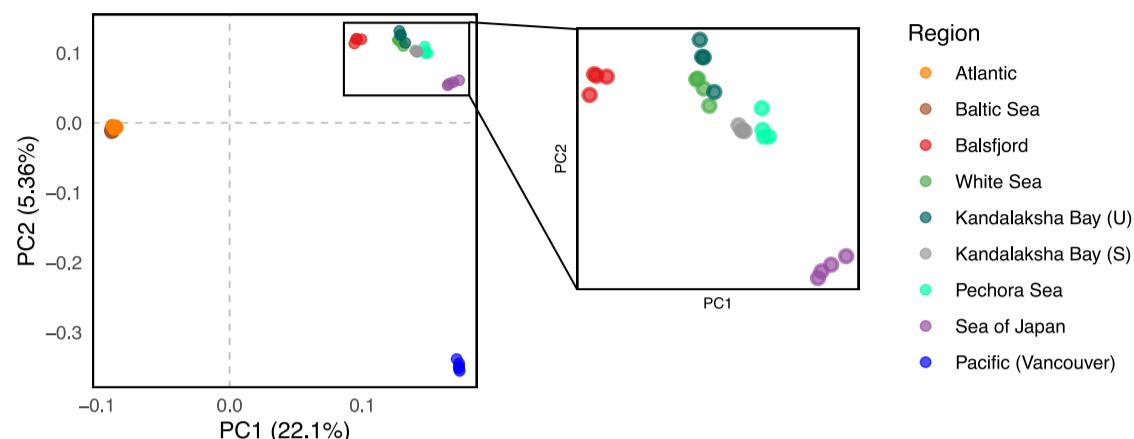
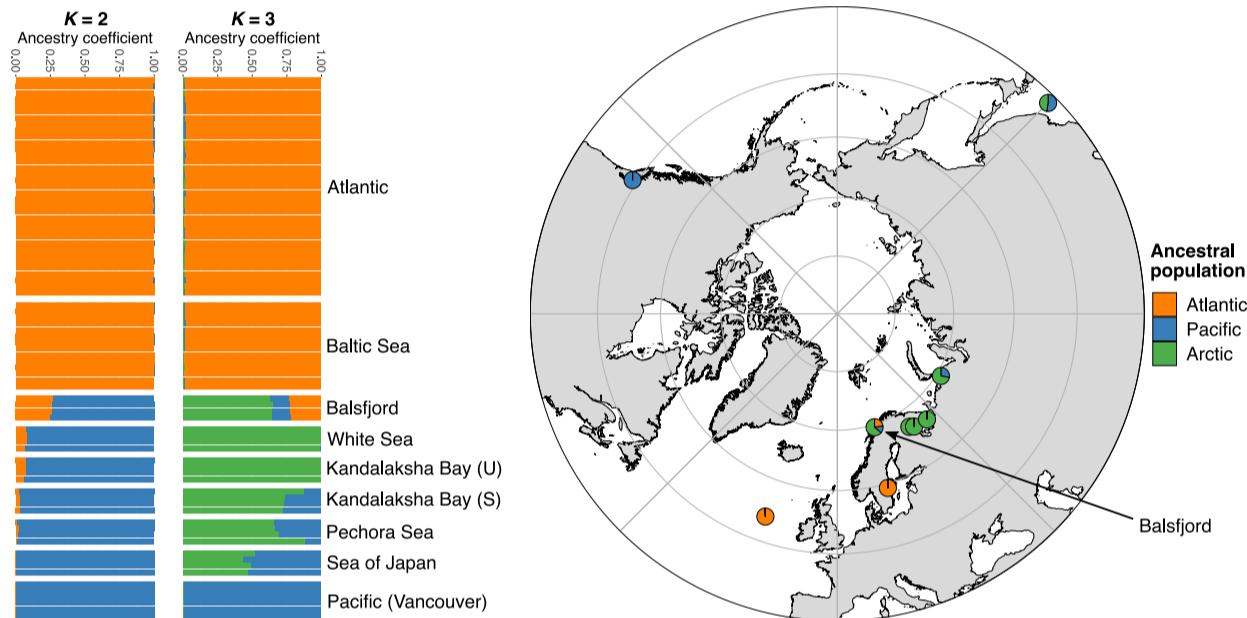
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Figure 2. Population structure and admixture of Atlantic and Pacific herring in the Arctic and sub-Arctic. *a)* PCA plot based on 2.9 million SNPs. Inset, zoom-in to the Balsfjord, Arctic and Sea of Japan samples. In the Kandalaksha Bay samples, "U" indicates summer- and "S" indicates spring-collected individuals. *b)* Graphical representation of ancestry coefficients estimated with the program sNMF. Individual ancestry coefficients for K=2 and K=3 are shown as bar plots (left), and average ancestry coefficients per location for K=3 are shown as pie charts on a map (right), both to illustrate the extent of admixture at the contact zone in Balsfjord, where Atlantic and Pacific herring have hybridized. In the bar plots, each row corresponds to an individual, and the size of each color division represents the proportion of an individual's genome that likely originated from different ancestral populations (K), or clusters. For K=3, the Atlantic cluster is indicated in orange, the Pacific cluster in blue, and the Arctic cluster in green.

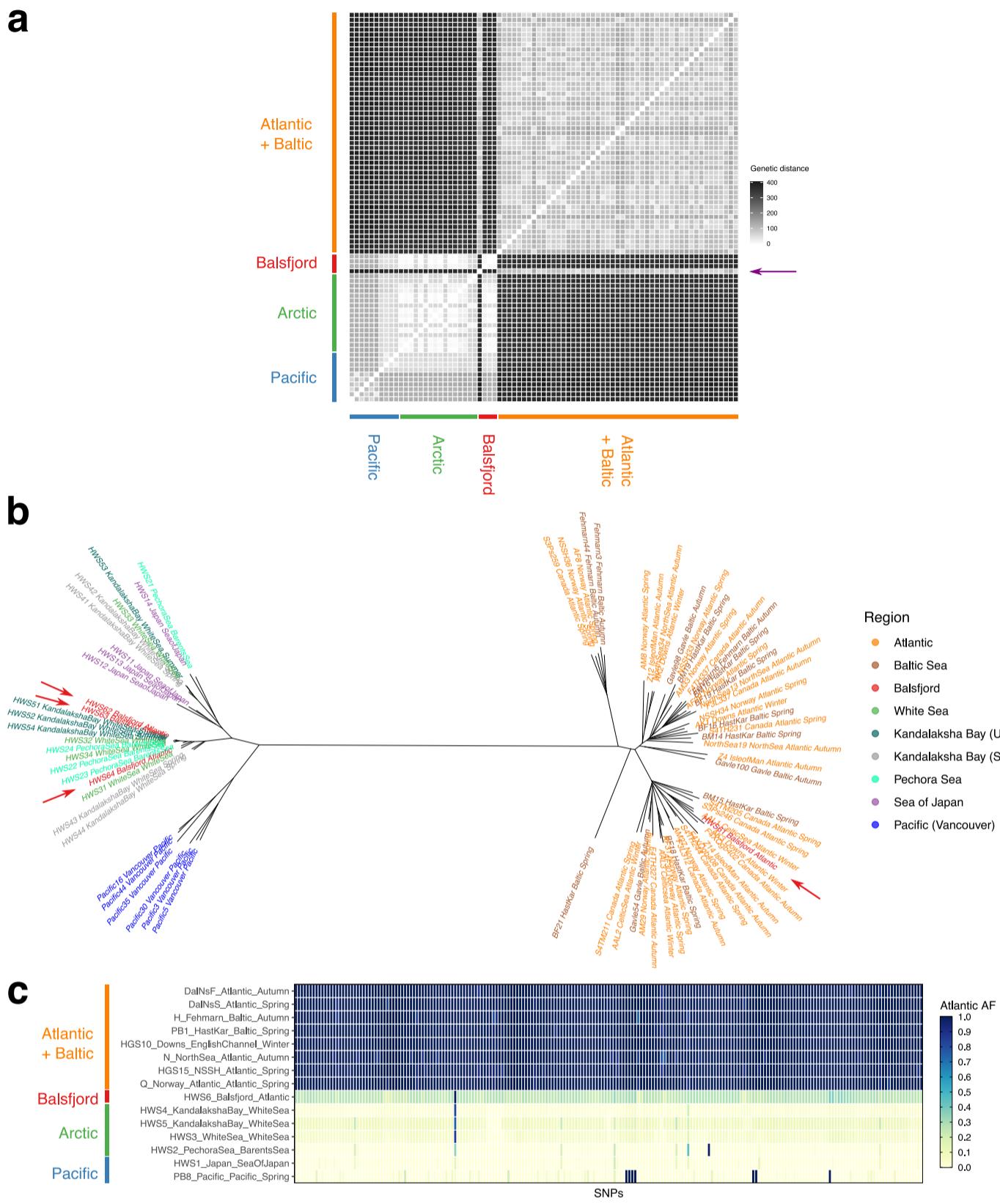


Figure 3. Atlantic mitochondrial introgression in Balsfjord herring detected from individual and Pool-seq data. *a)* Pairwise genetic distance among 79 individuals based on 1382 SNPs. The genetic distance corresponds to the effective number of nucleotide differences (counts) between pairs. Low to high 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, red for Balsfjord, green for Artic, and blue for Pacific. The purple arrow on the right points to the Balsfjord individual with Atlantic mitochondrial alleles. *b)* Distance-based unrooted-NJ tree representing the genetic structure among individuals. Two main groups are observed, the Atlantic and the Pacific. Notably, three of the four Balsfjord individuals cluster with the Pacific group, and the other one cluster with the Atlantic group. The four Balsfjord samples are denoted with a red arrow. 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 mitochondrial allele in color shades from navy blue (high AF) to light yellow (low AF). 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 average Atlantic allele frequency is 27%.

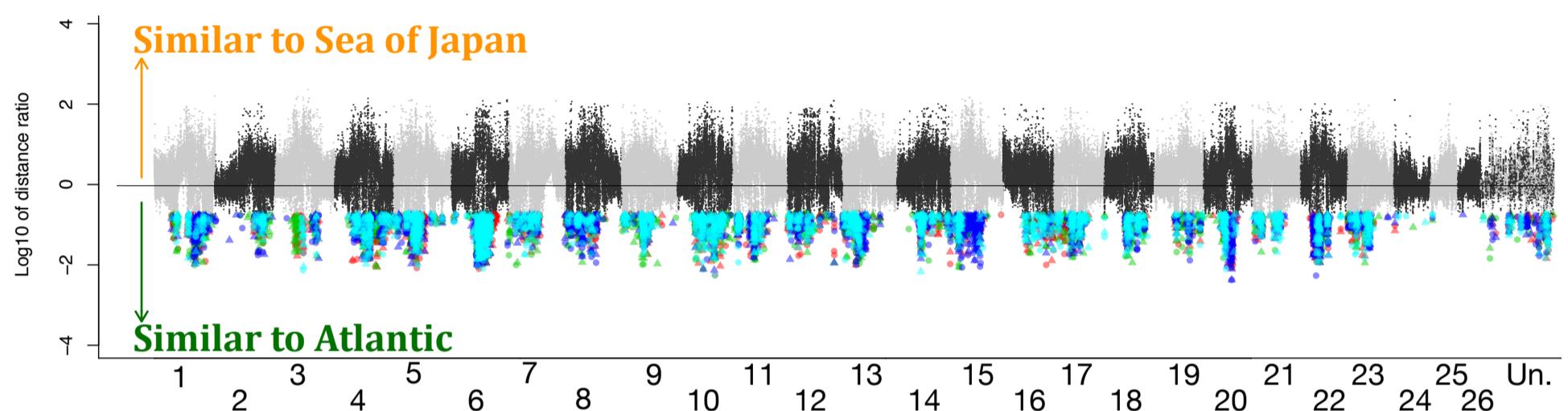
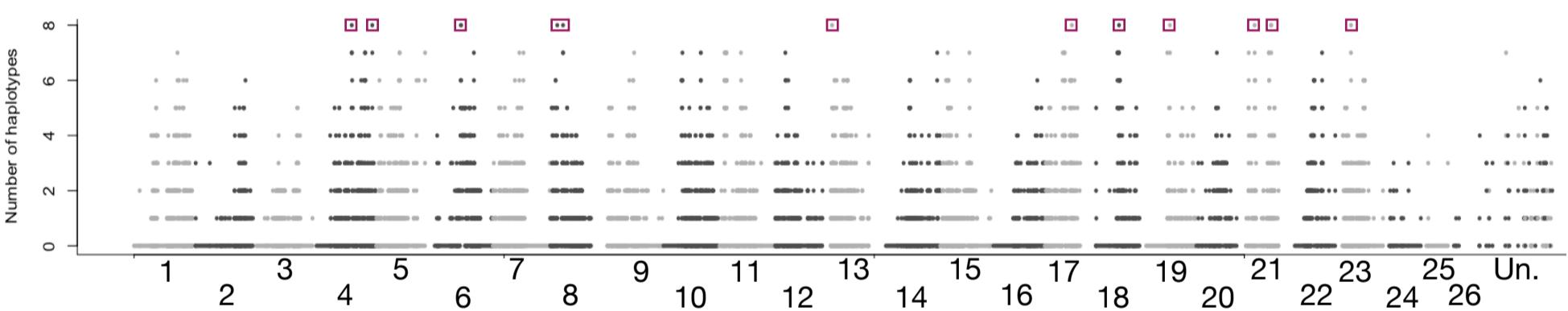
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Figure 4. Location of Atlantic introgressions in Balsfjord herring. *a)* locations of detected introgressions, based on 20 kb windows. The different symbols each represent one of the eight sequenced haplotypes from Balsfjord individuals. *b)* Pile-up of the detected introgression regions in the eight haplotypes. The regions where all haplotypes carry an introgression (purple rectangles) are listed in Supplementary Table S2.

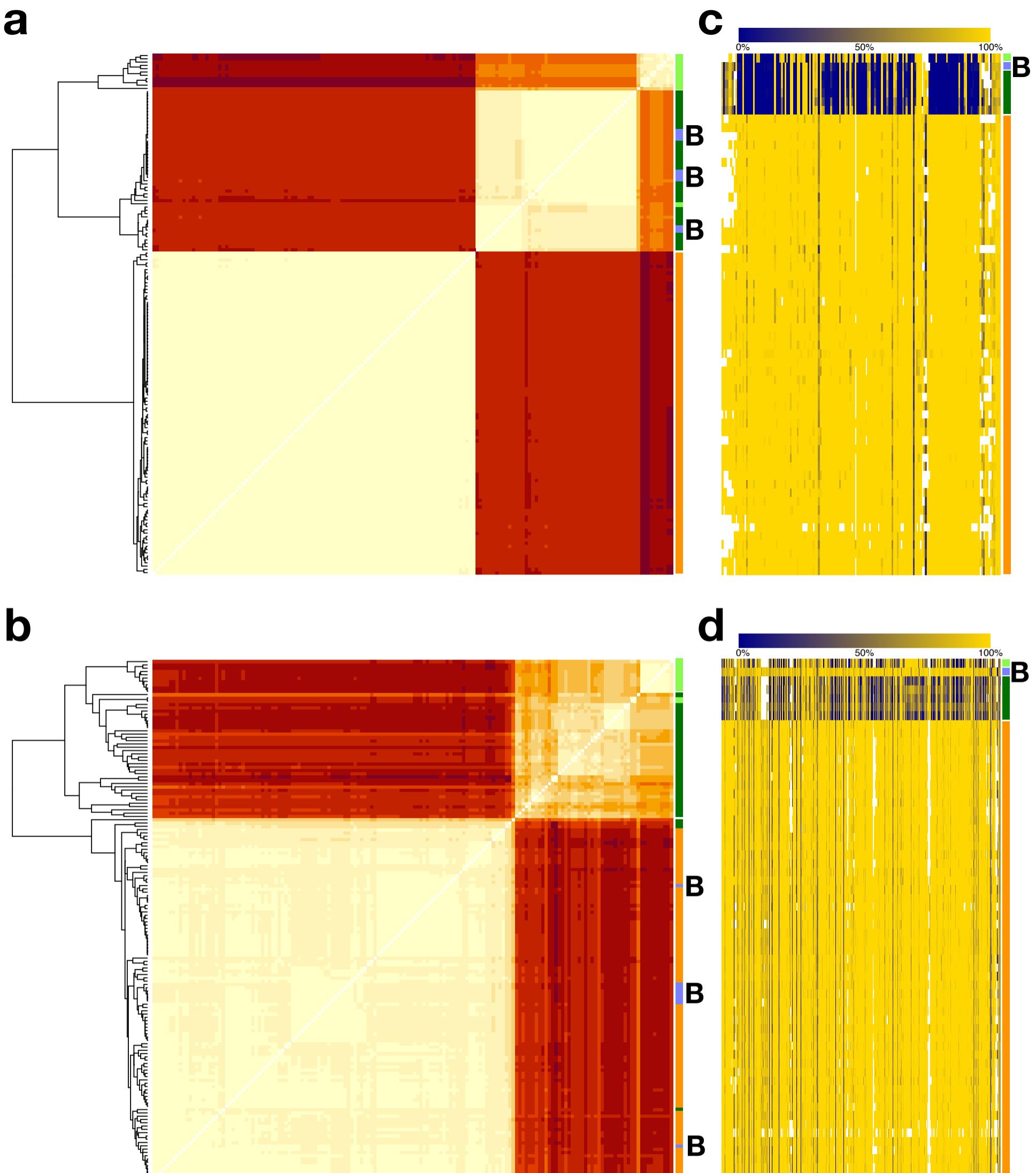


Figure 5. Neighboring regions on Chr 4 with different origins for Balsfjord haplotypes. Panels *a* and *b* show heatmaps based on hamming distances between individual haplotypes. The bars on the side indicate samples from Vancouver (light green), Sea of Japan and White Sea (dark green) and Atlantic (orange), respectively. The purple rectangles, and capital **B**, indicate the location of Balsfjord herring haplotypes. *a)* Chr4:18.30-18.32 Mb. *b)* Chr4:19.04-19.06 Mb. Panels *c* and *d* show heatmaps that indicate reference allele frequencies in pooled samples. *c)* Chr4:18.30-18.32 Mb. *d)* Chr4:19.02-19.08 Mb.

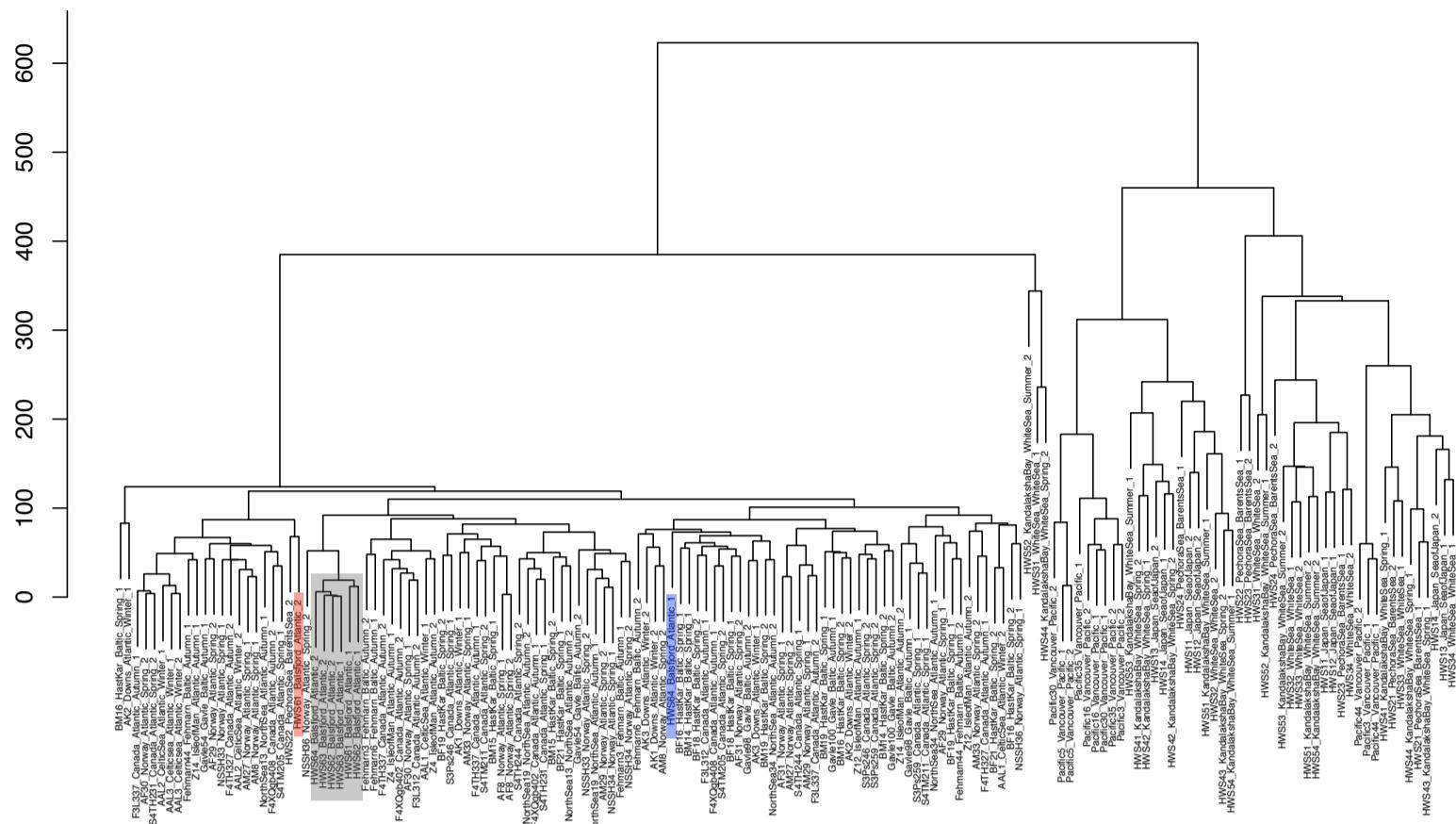
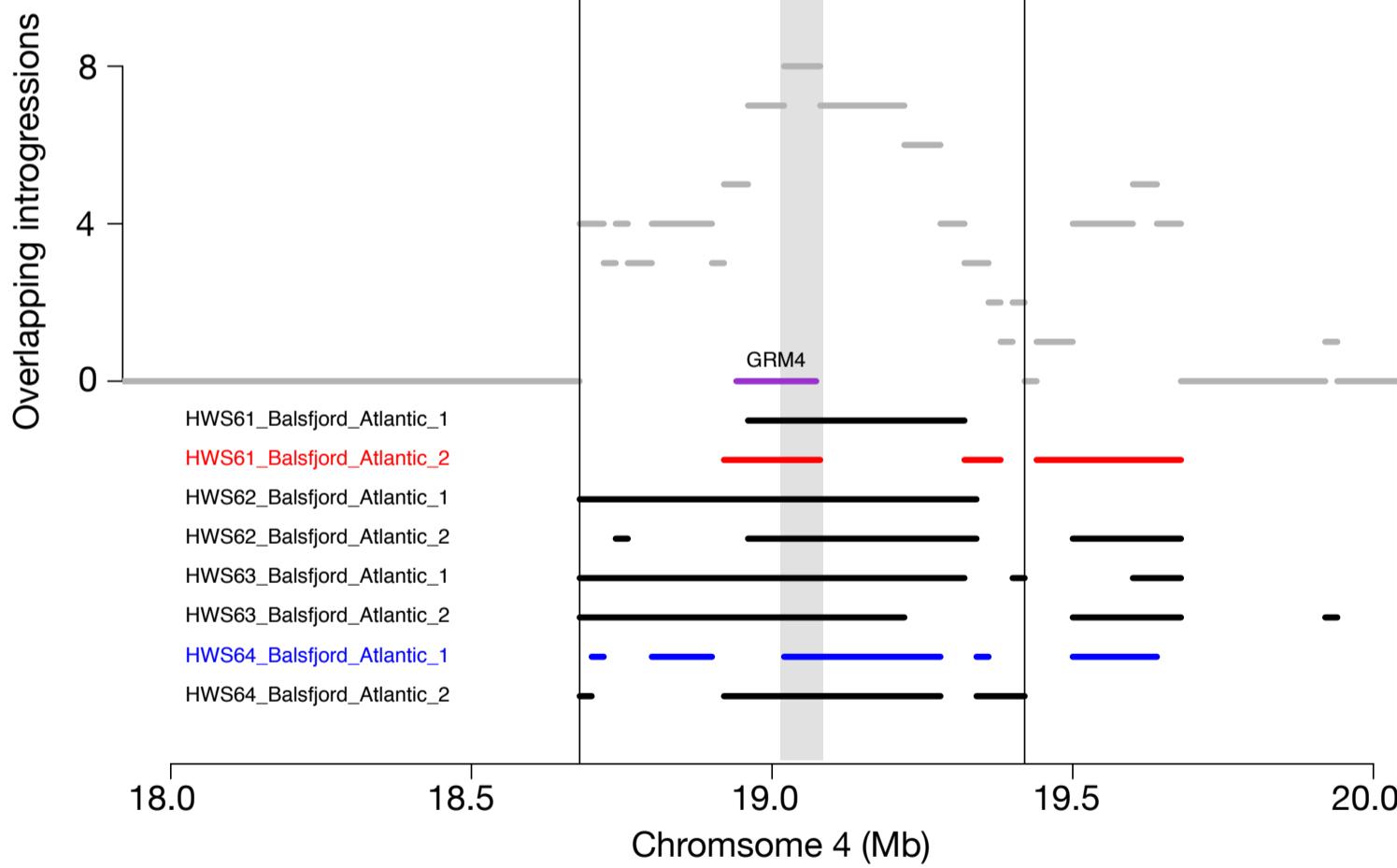
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Figure 6. Overlapping introgressions on Chr 4: 19.0-19.1 Mb are derived from three different Atlantic haplotypes. a) A hierarchical clustering dendrogram based on edit distance between haplotypes. The shaded rectangles indicate separate haplotypes introgressed into Balsfjord herring. **b)** Schematic view of the introgressed haplotypes, and the resulting ingestion coverage.

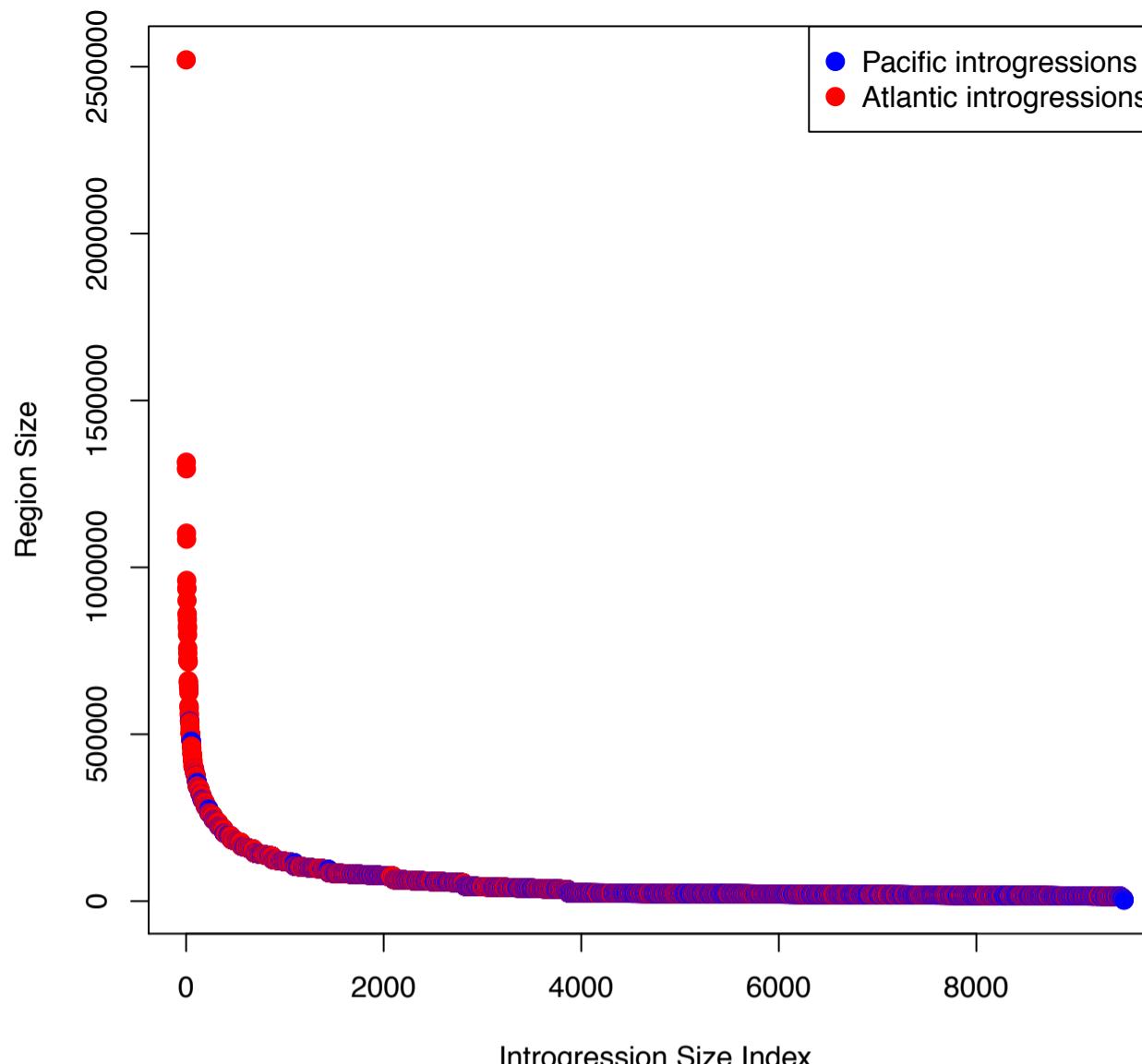
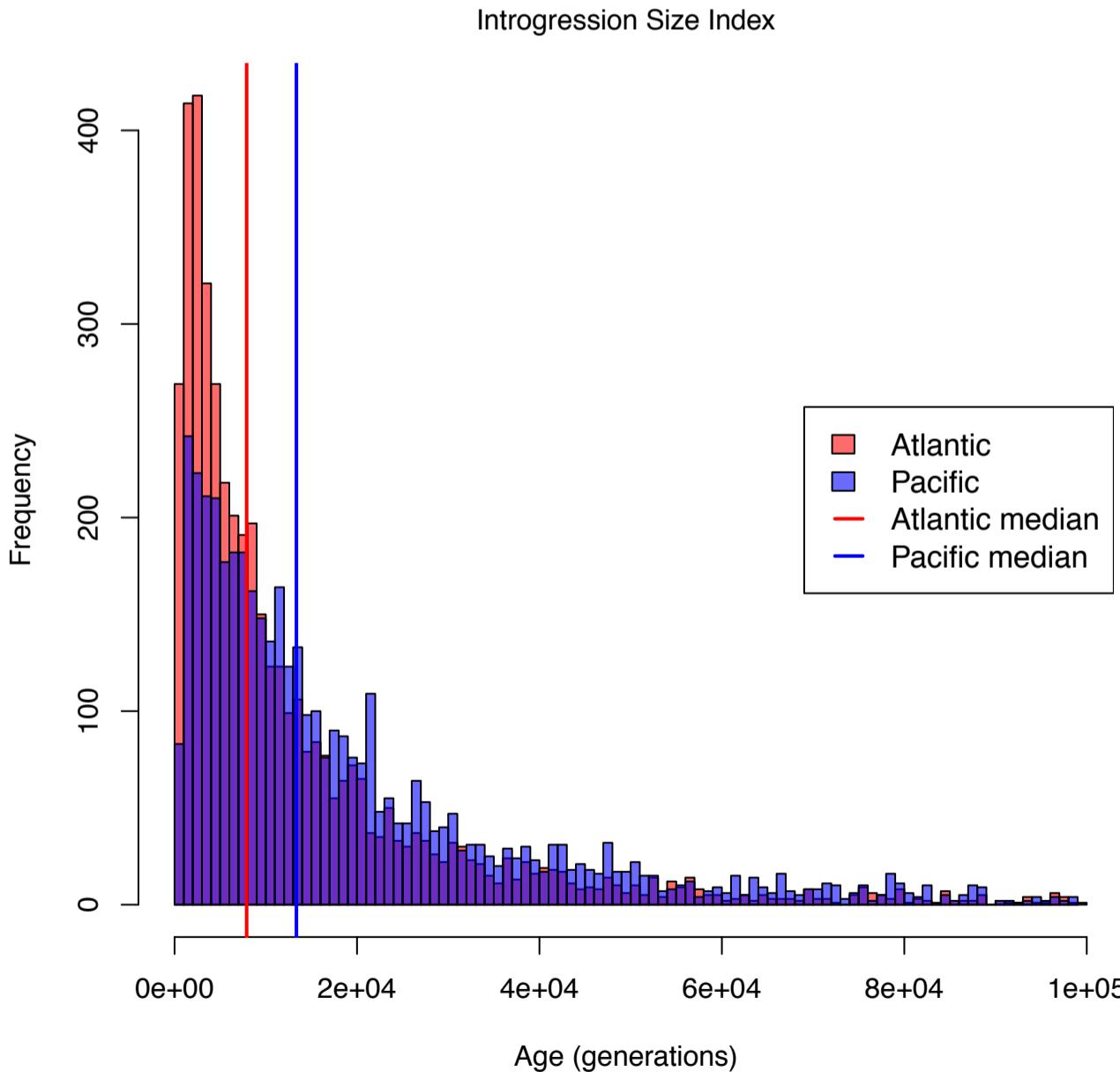
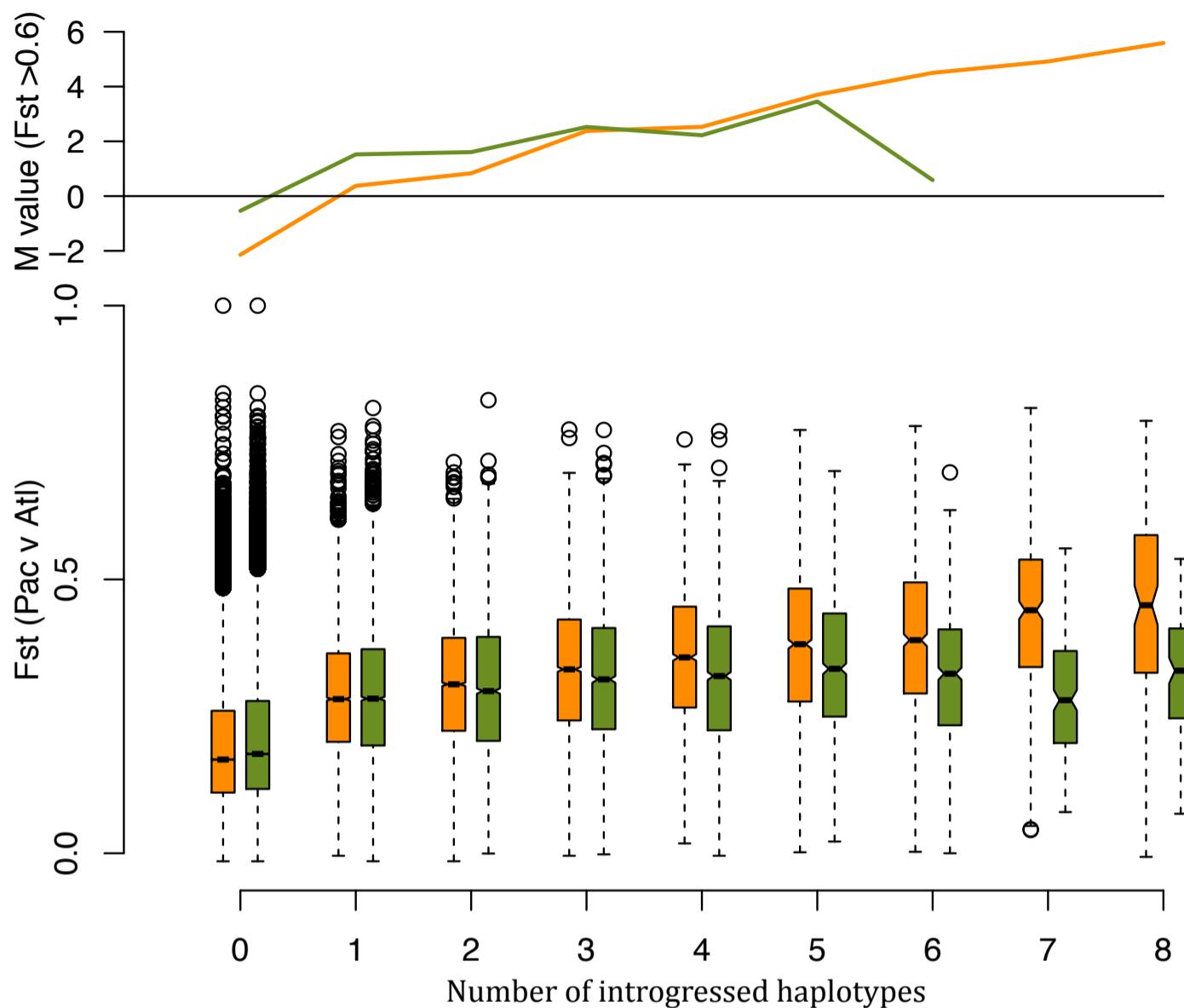
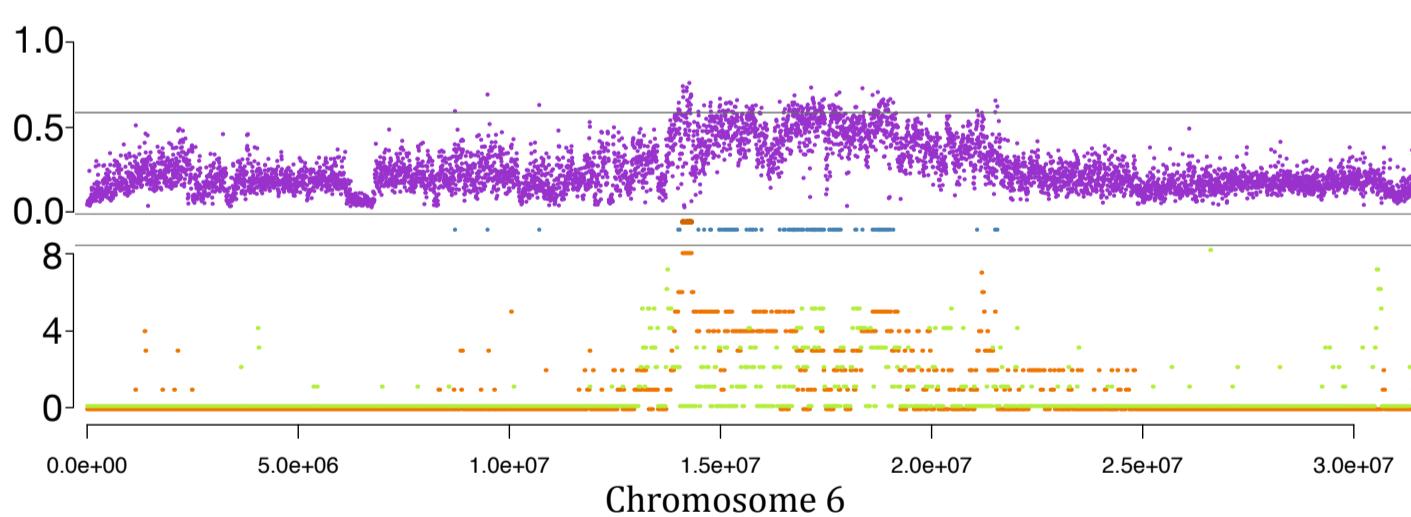
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Figure 7. Size ranking and age distribution of Atlantic and Pacific introgression regions. *a)* The detected introgressions have been ordered with respect to size, from largest to smallest. The *p*-value refers to the rank of Atlantic- and Pacific introgression regions, respectively, in this ordering. *a)* Distribution of the estimated ages of introgressions, up to 10^5 generations ago. There are 248 Pacific and 136 Atlantic regions excluded from view. Medians are calculated from all loci, including the outlier with estimated ages above 10^5 generations.

a**b****Figure 8. Correlation between Atlantic introgressions and inter-species F_{ST} . a)**

Boxplots showing the F_{ST} distribution for regions binned by the number of introgressed haplotypes. Atlantic introgressions are shown in orange, Pacific ones in green. M-values are based on comparing against the genomic average abundance of 5 kb blocks with $F_{ST} > 0.6$. b) Introgression coverage (bottom track: Atlantic in orange, Pacific in green) and inter-species F_{ST} (top track: the grey line is the high F_{ST} threshold of 0.6) and their overlap (mid track: blue for only high F_{ST} , orange for high and 8 Atlantic introgressions) shown across Chr 6, as an example of their co-variation. See supplementary Figure S2 for all chromosomes.