

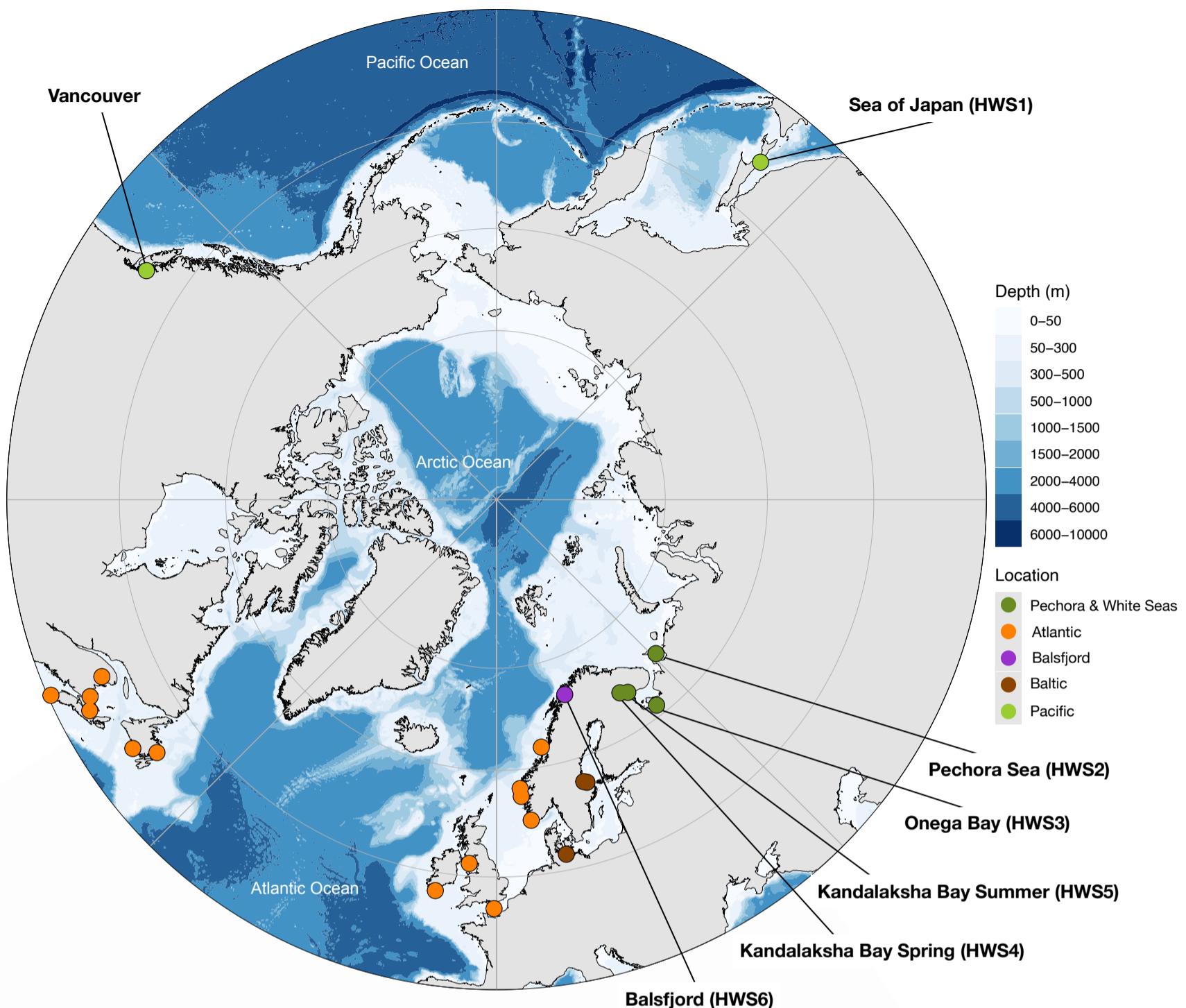
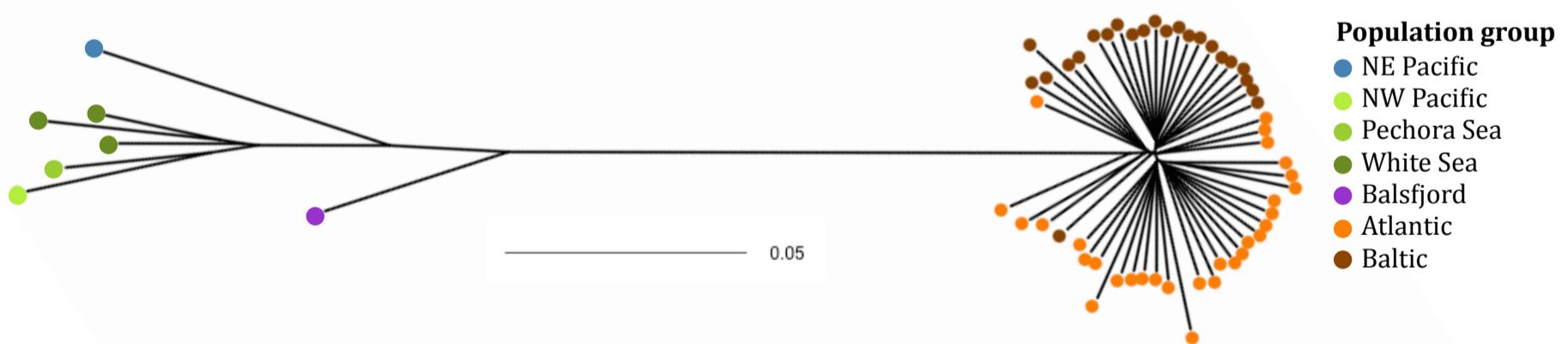
a**b**

Figure 1. Sample locations and genetic distances among Pacific and Atlantic herring populations from different oceans and sea areas. *a)* Location of samples of Pacific herring from Balsfjord, European Russia (Pechora and White Seas), and from the NW Pacific (Sea of Japan) and NE Pacific (Vancouver) (Supplementary File 1). For detailed information on locations of Atlantic and Baltic herring samples, see Han et al. (2020). The base map was created using ggOceanMaps (<https://mikkovihtakari.github.io/ggOceanMaps/>), using data from the National Centers for Environmental Information (<https://www.ngdc.noaa.gov/mgg/global/relief/ETOPO1/docs/ETOPO1.pdf>). *b)* Neighbor-joining tree based on allele frequency distances from 10^5 randomly selected SNPs in poolseq data from 60 populations of Pacific and Atlantic herring. The scale represents average frequency difference per SNP.

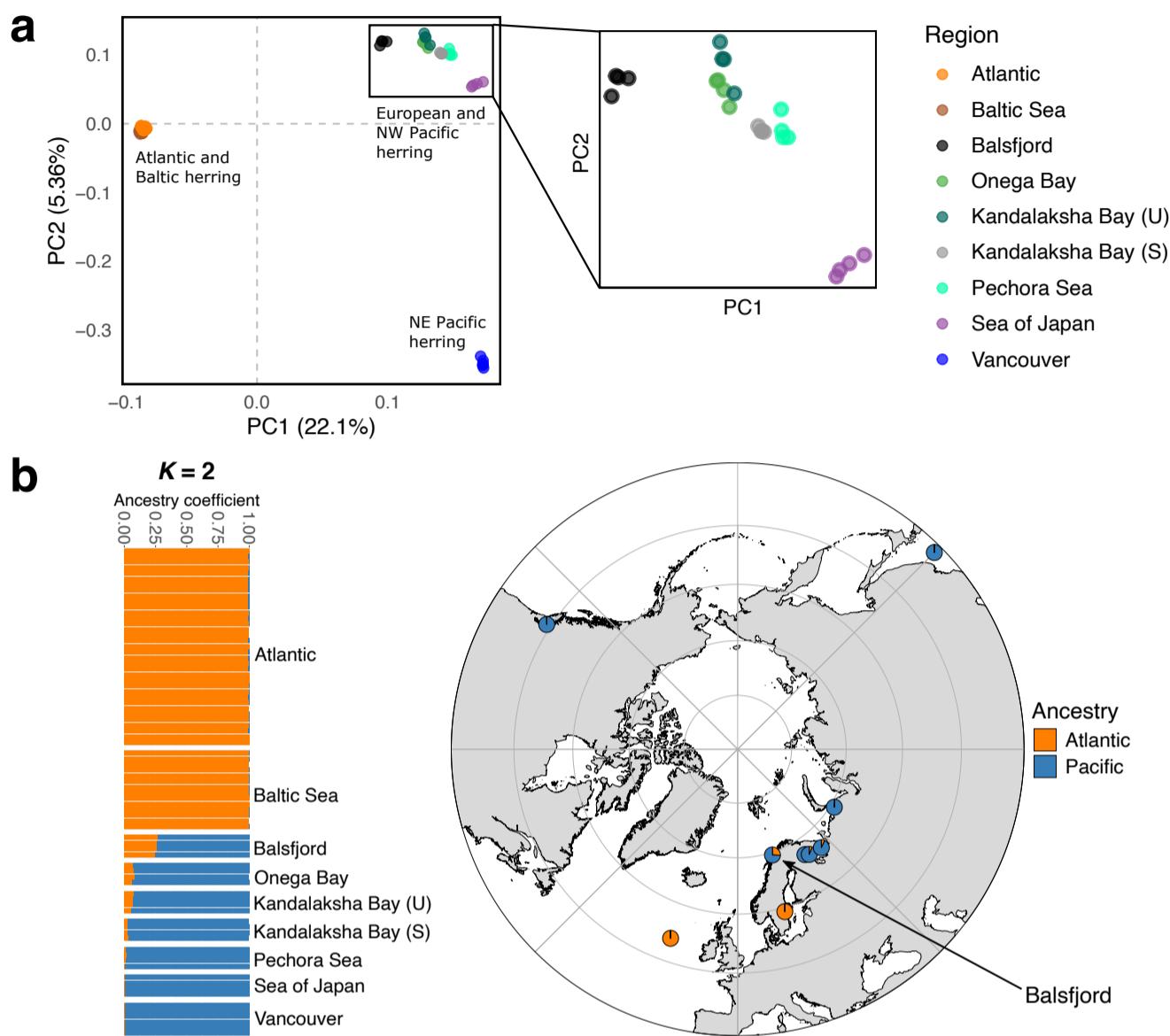


Figure 2. Population structure and admixture of Atlantic and Pacific herring. *a)* PCA plot based on 2.9 million SNPs, from data on 79 individually sequenced fish. Inset, zoom-in to the Balsfjord, White Sea, Pechora Sea, and NW Pacific (Sea of Japan) samples. In the Kandalaksha Bay samples, "U" and "S" indicate summer- and spring-spawning populations, respectively. *b)* Graphical representation of ancestry coefficients estimated with the program sNMF (Frichot et al., 2014). Individual ancestry coefficients for $K=2$ are shown as bar plots (left), and average ancestry coefficients per location are shown as pie charts on a map (right), both to illustrate the extent of admixture at the contact zone in Balsfjord. 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 Pacific and Atlantic herring.

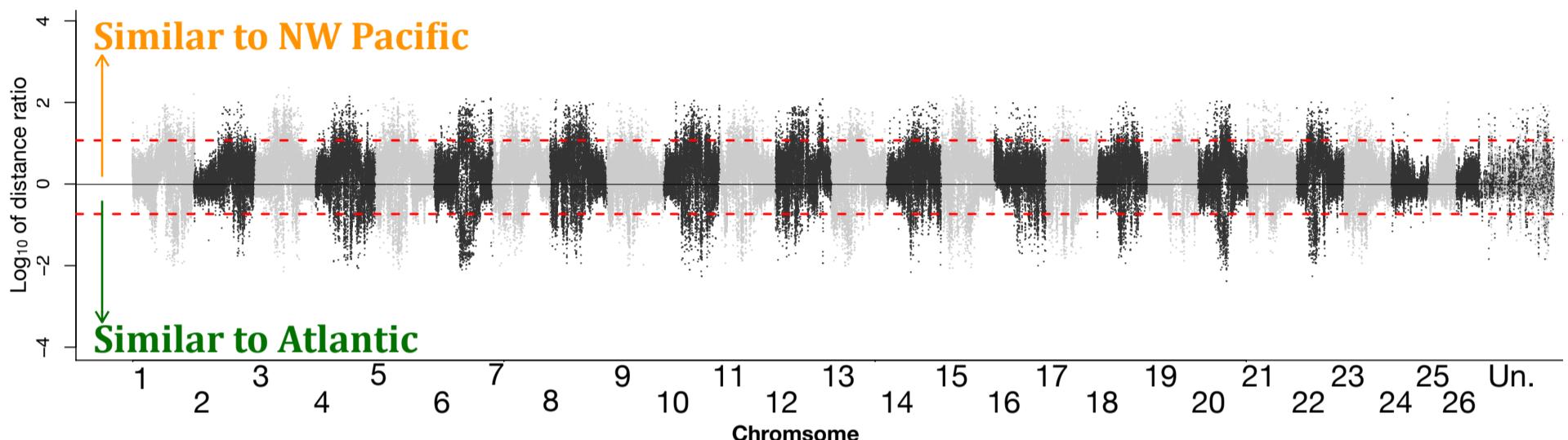
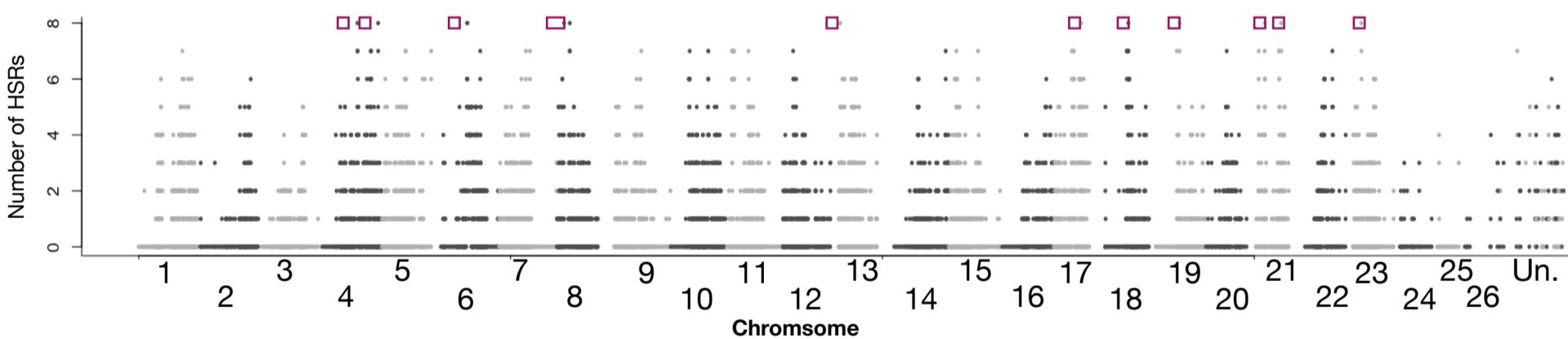
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Figure 3. Genomic regions showing introgression in Balsfjord herring. *a)* Locations of introgressed regions (HSRs) and their origin, based on 20 kb windows. The dashed red lines represent the cut-offs for definition of Pacific and Atlantic HSRs, respectively. *b)* Summary of the location and frequency of Atlantic HSRs in the eight haplotypes from four individually sequenced Balsfjord herring. The 13 regions in which all eight haplotypes were deduced to originate from Atlantic herring are highlighted (boxes). Unassigned scaffolds are collected under the “Un.” label.

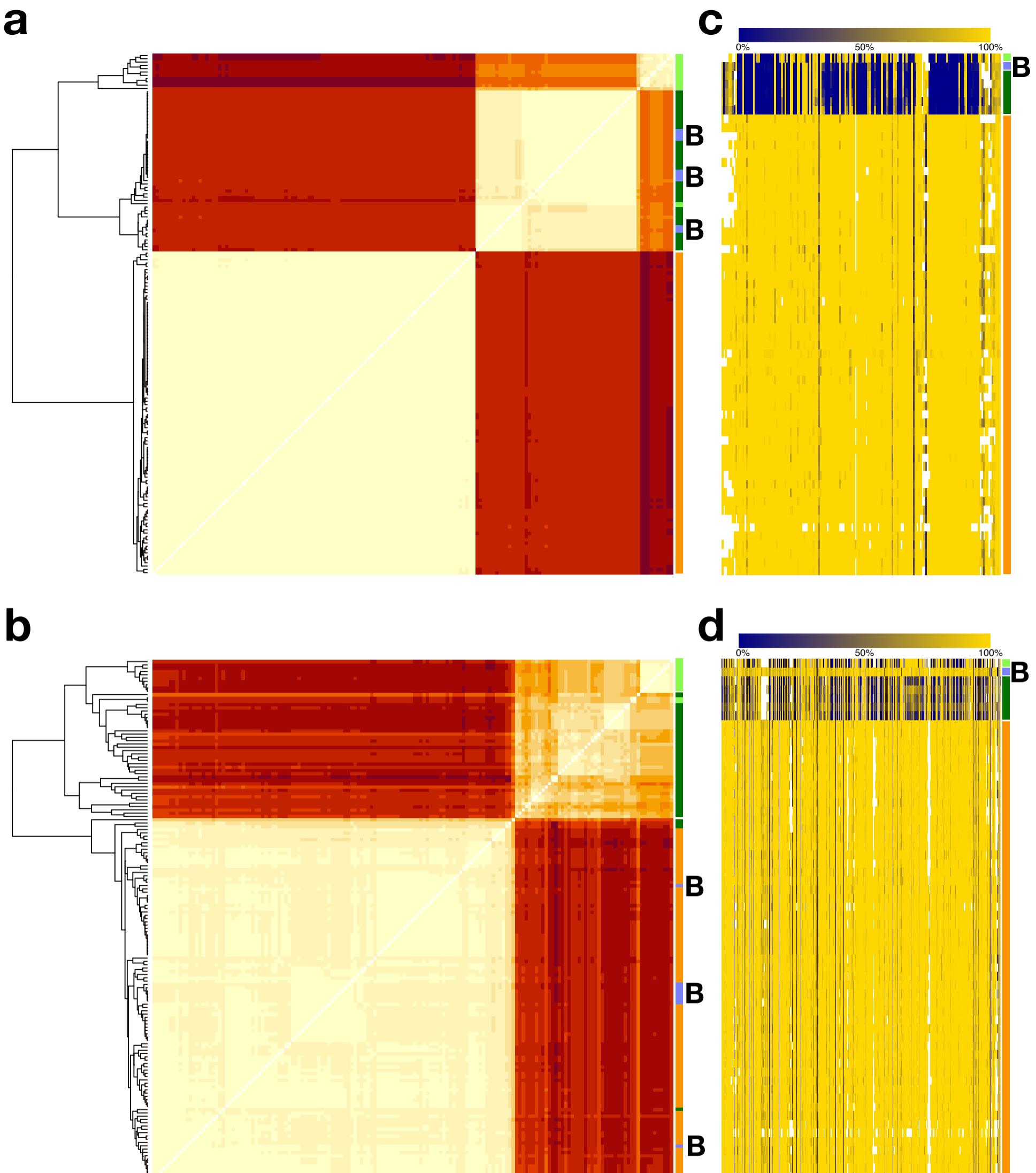


Figure 4. Two neighboring regions on chromosome 4 with different origins among Balsfjord haplotypes. In both these instances, all eight Balsfjord haplotypes are derived from one species. Panels *a* and *b* show heatmaps based on Hamming (or Edit) distances between individual haplotypes. *a)* Chr4:18.30-18.32 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. The purple rectangles, and capital **B** indicate Balsfjord herring haplotypes, the bars on the side indicate Northeast Pacific (light green), Northwest Pacific and White Sea (dark green) and Atlantic (orange), respectively.

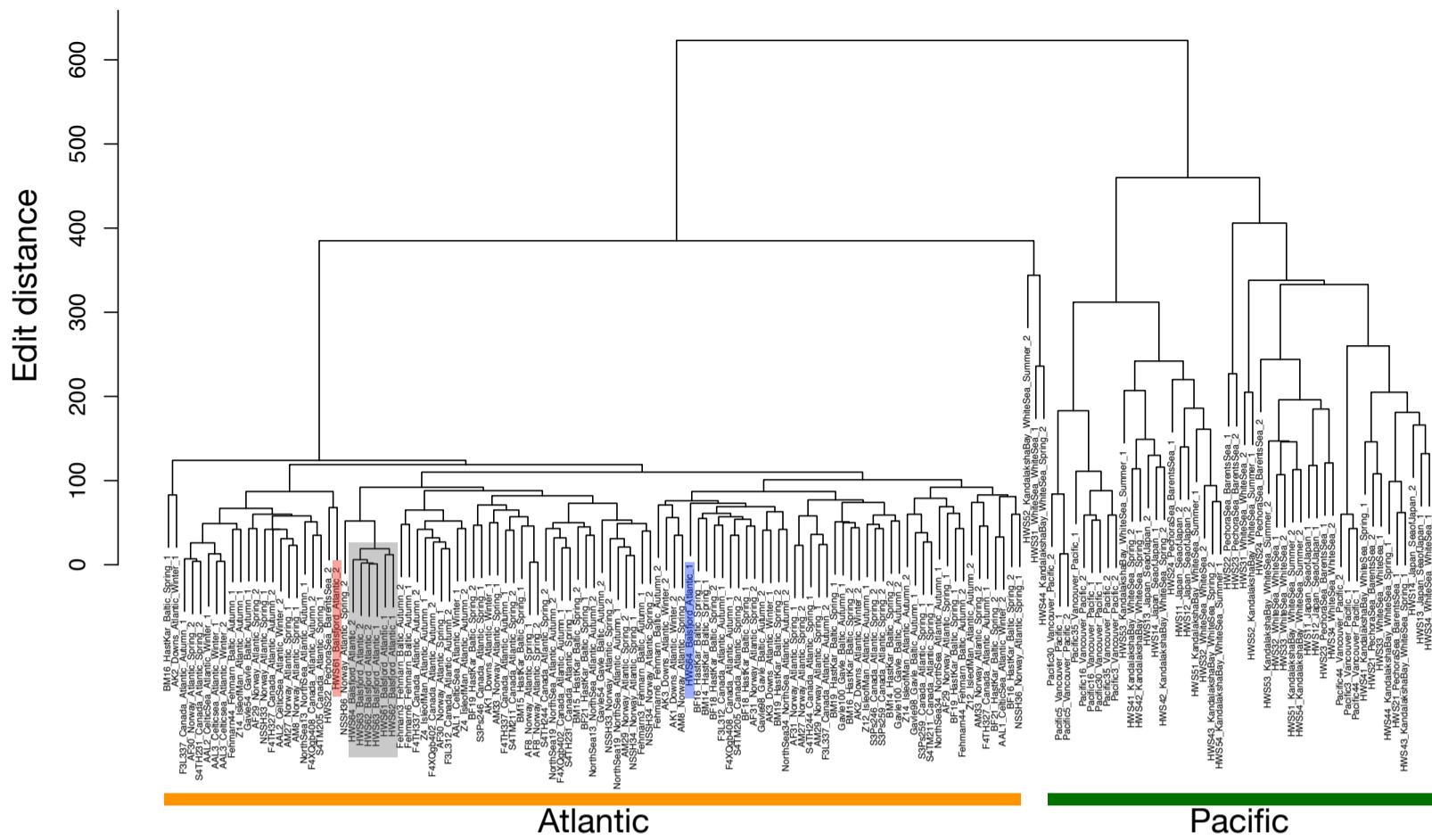
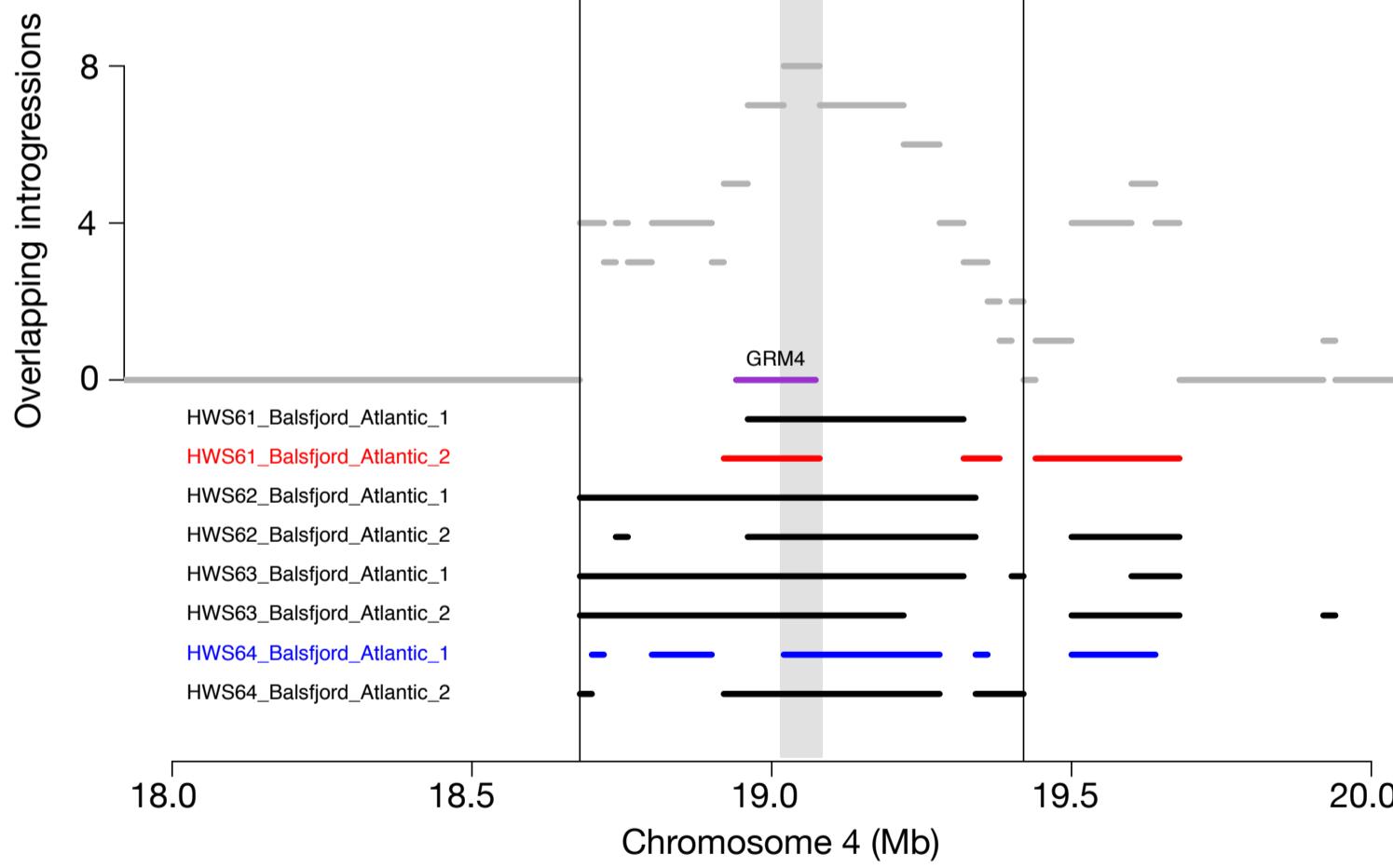
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Figure 5. Eight overlapping HSRs on chromosome 4:19.0-19.1 Mb are derived from three different Atlantic haplotypes. a) A hierarchical clustering dendrogram based on edit distances between haplotypes. The shaded rectangles indicate separate Atlantic haplotypes introgressed into Balsfjord herring. **b)** Schematic view of the introgressed haplotypes, and the resulting introgression coverage. The location of the *GRM4* gene is indicated.

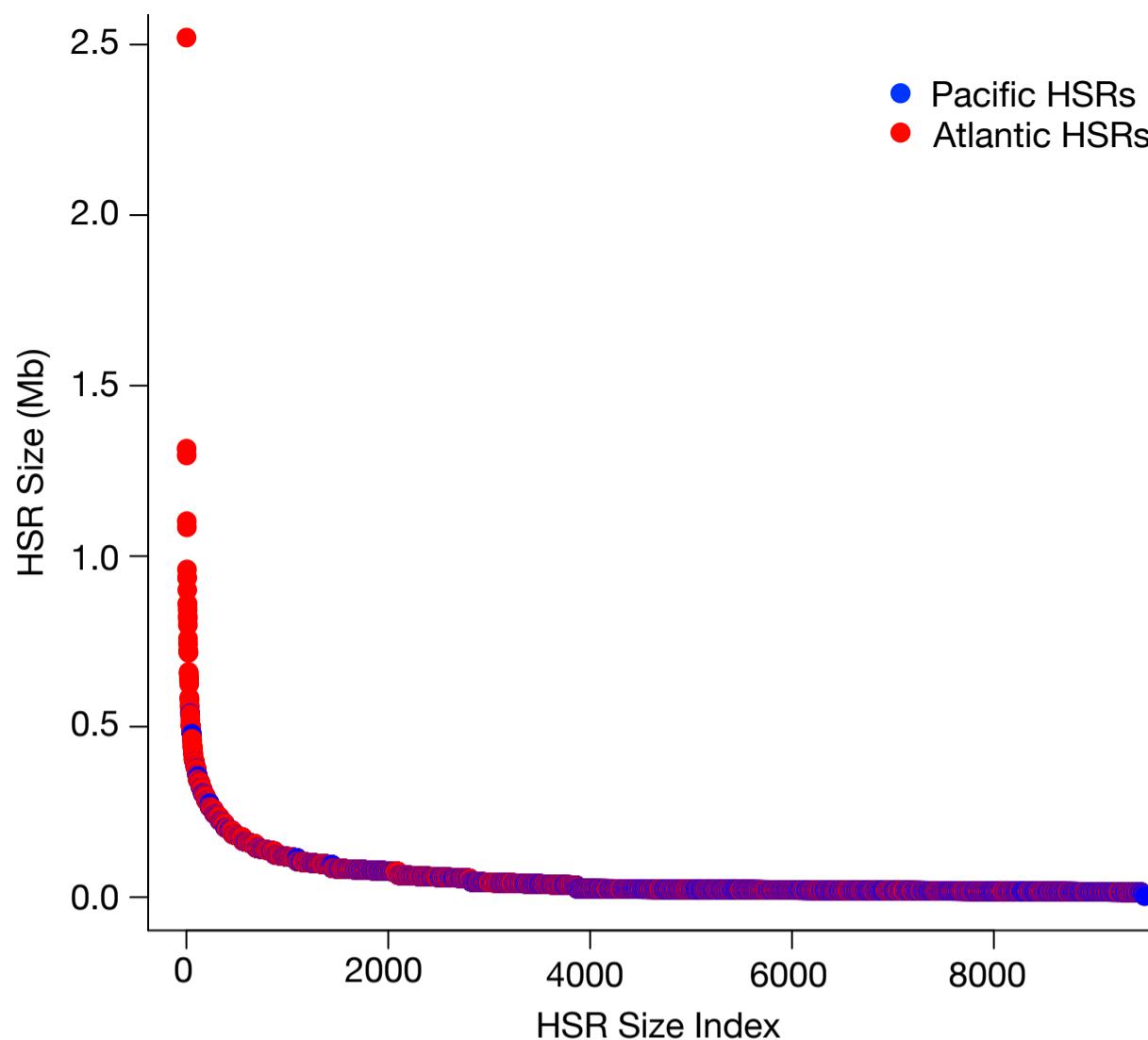
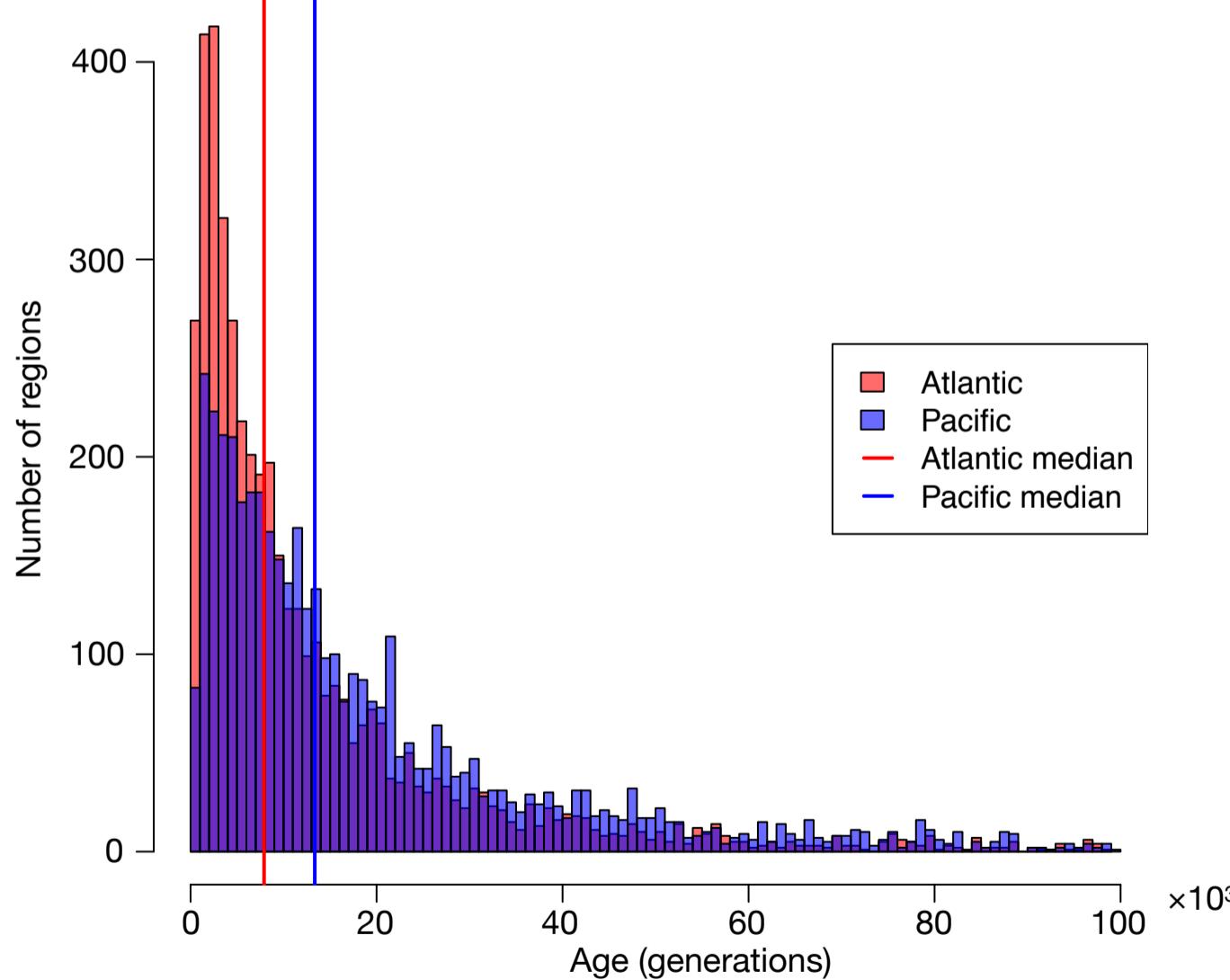
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Figure 6. Size ranking and estimated age distribution of Atlantic and Pacific HSRs in Balsfjord herring.

a) The detected HSRs have been ordered with respect to size, from largest to smallest. Color coding, by origin, demonstrates the on-average larger size of Atlantic HSRs **b)** Distribution of the estimated time since introgression, up to 10^5 generations ago. There are 248 Pacific and 136 Atlantic regions with age estimates outside of this range. Medians (indicated by vertical lines) are calculated from all loci, including the outliers with estimated ages above 10^5 generations.

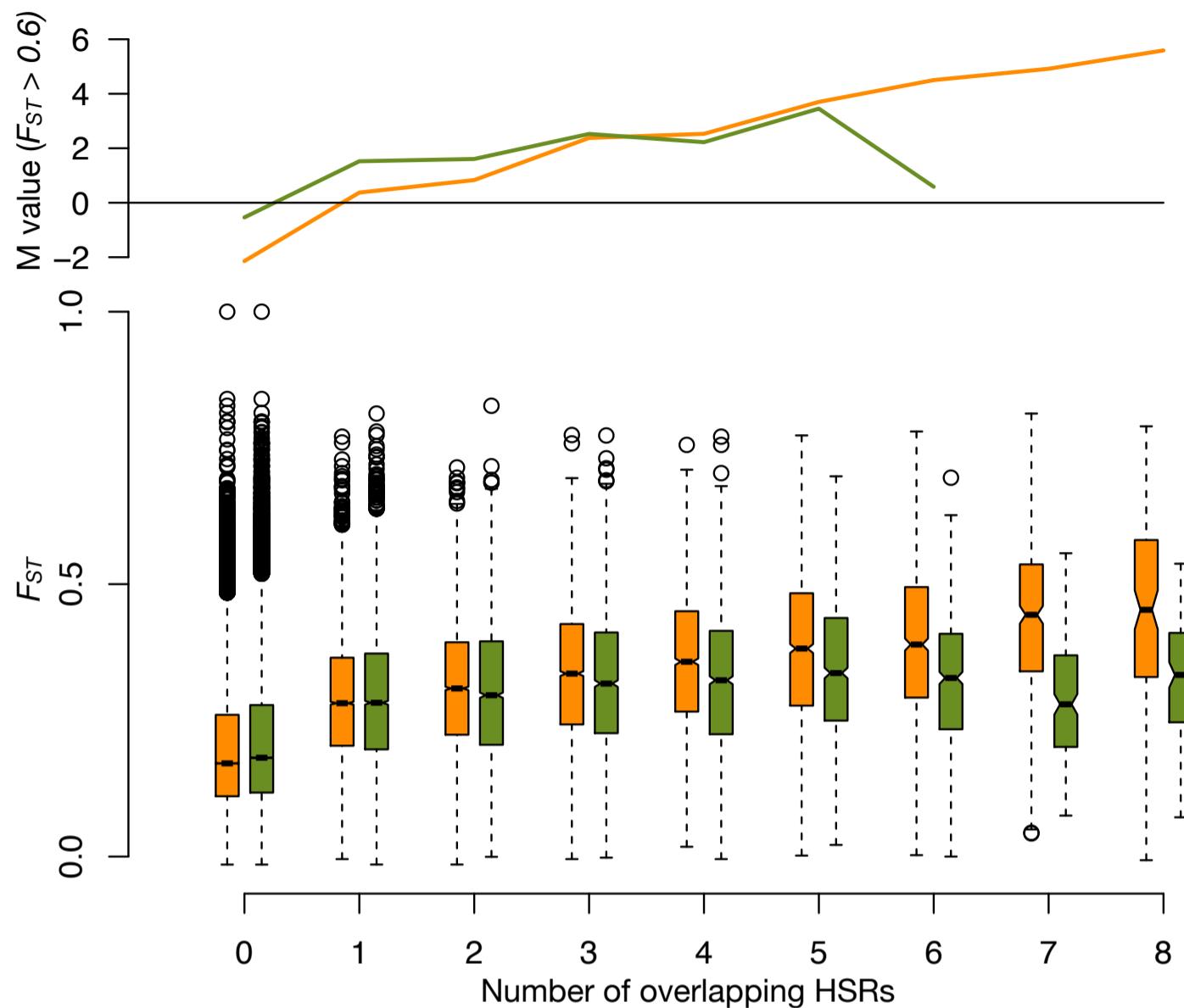
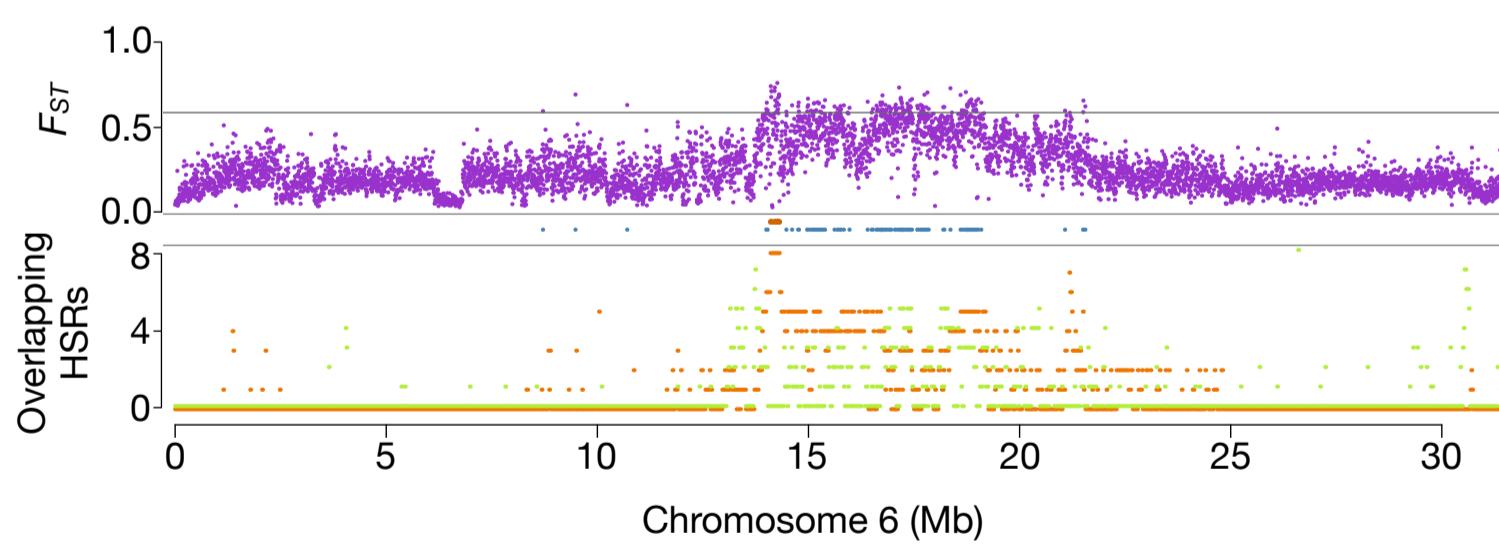
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Figure 7. Correlation between HSRs in Balsfjord herring and estimated F_{ST} between Atlantic and Pacific herring. *a)* Boxplots showing the F_{ST} distribution for regions binned by the number of recurring HSRs. Atlantic HSRs are shown in orange, Pacific ones in green. M-values are based on comparing F_{ST} values within introgressed regions against the genomic average abundance of 5 kb blocks with $F_{ST} > 0.6$. *b)* HSR 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 bars indicate high F_{ST} (>0.6) regions, orange bars indicate regions that have both high F_{ST} and 8 Atlantic HSRs) shown across chromosome 6, as an example of their co-variation. See Figure 7 figure supplement 1 for all chromosomes.