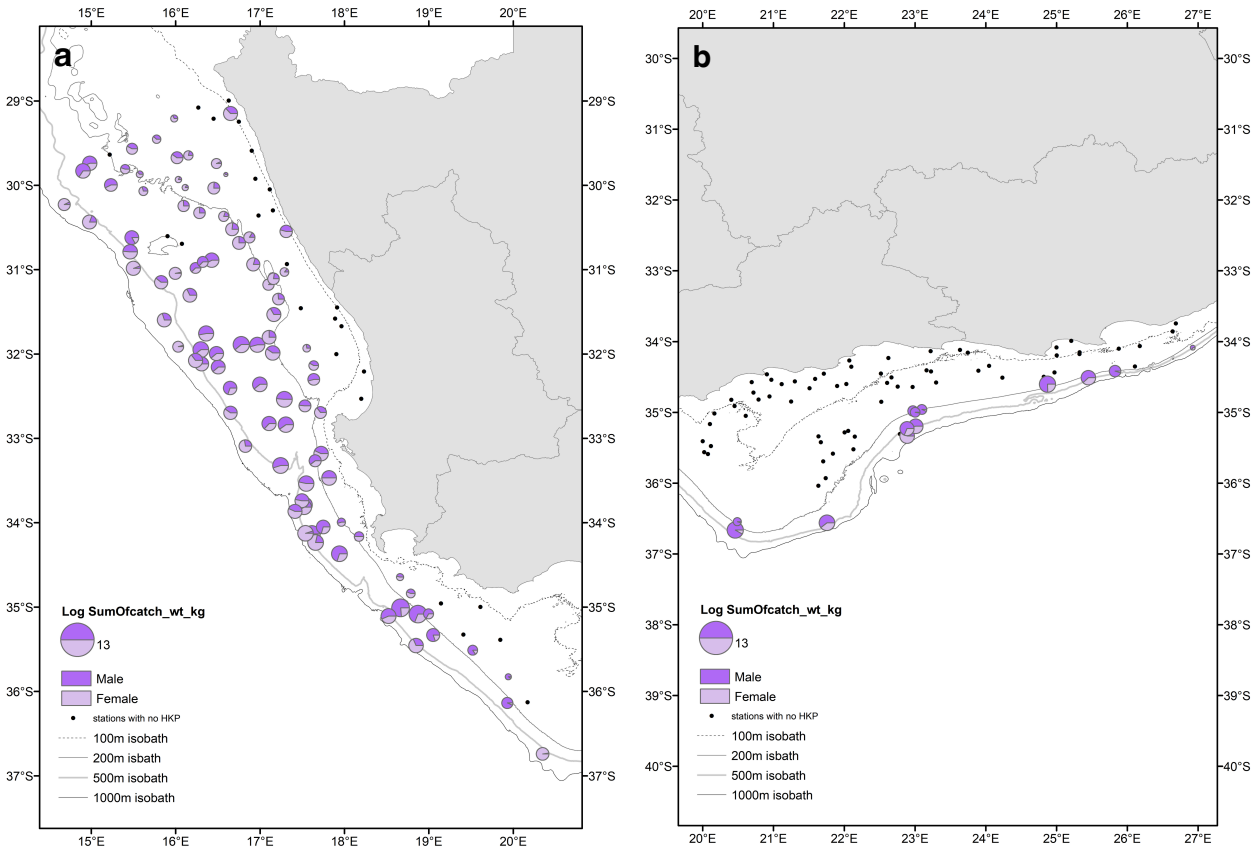
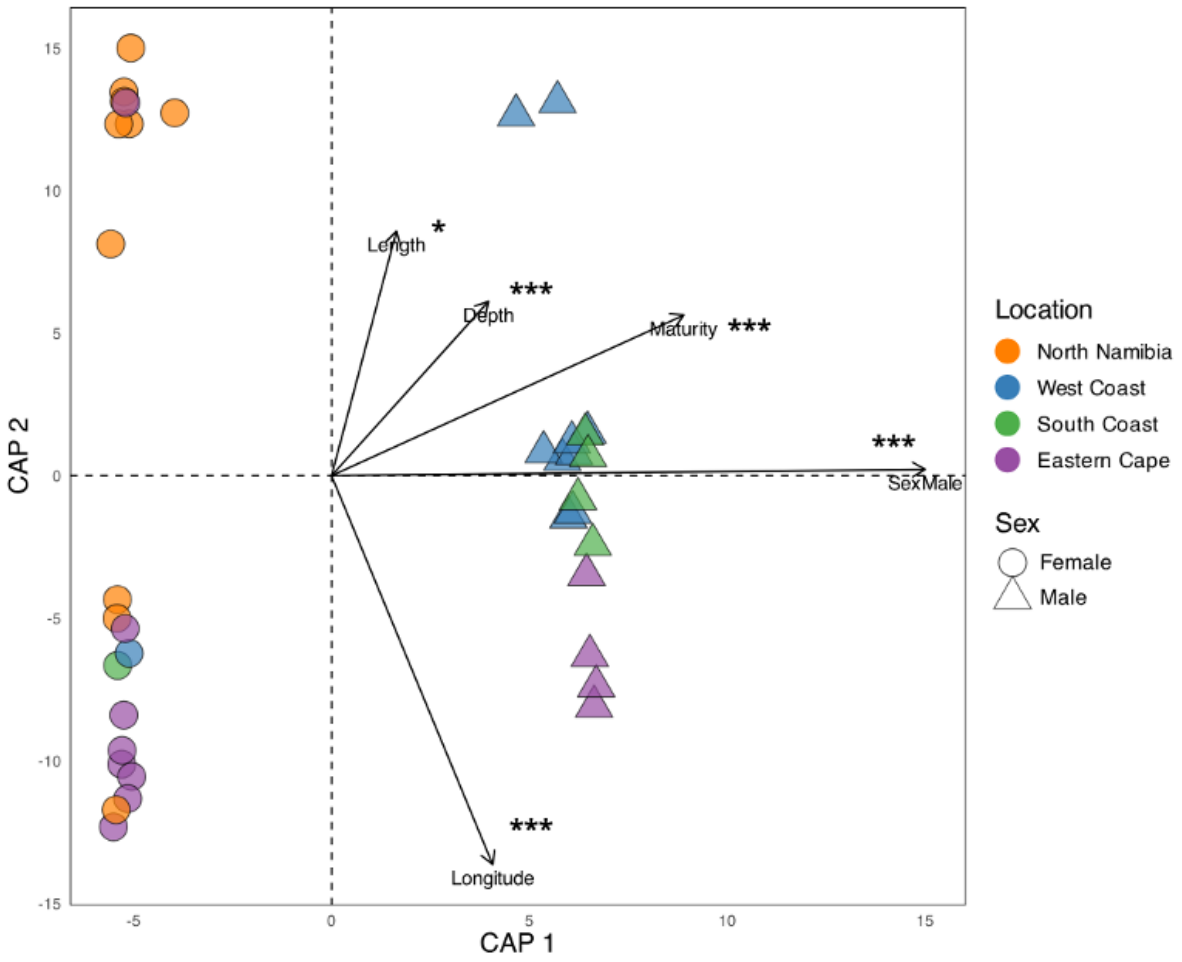
Supplementary data



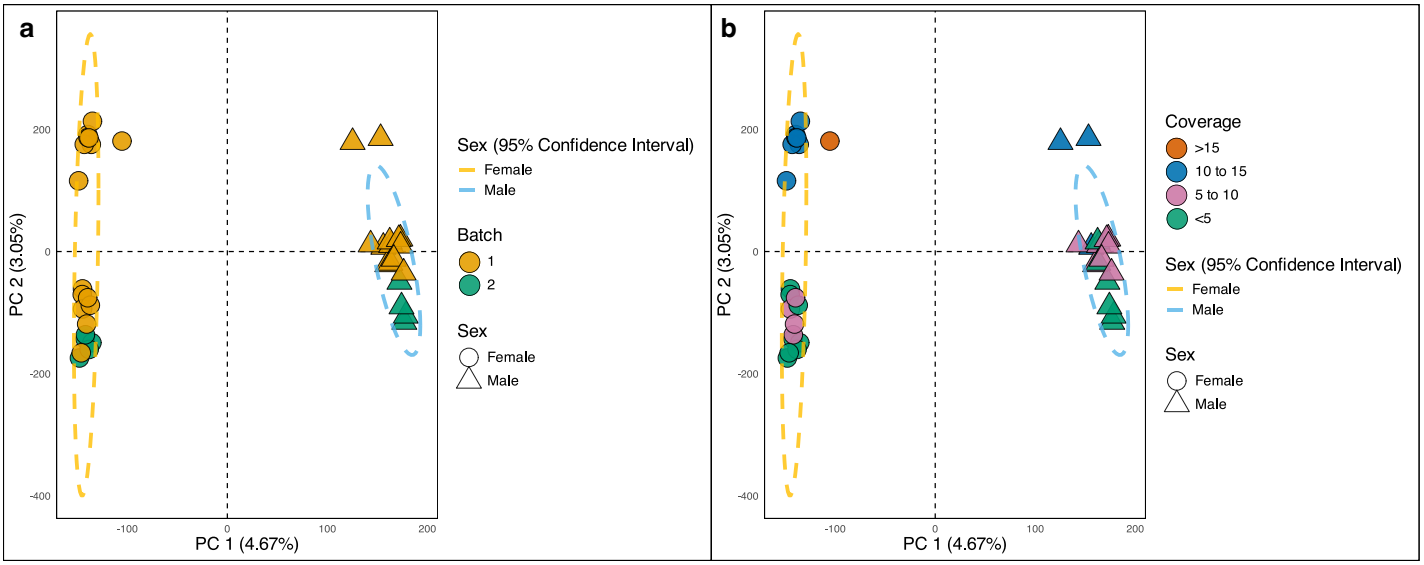
Supplementary Figure 1: Spatial distribution of *Merluccius paradoxus* along the South African coastline based on fishery-independent demersal research surveys conducted on **(a)** the West Coast in February 2022 and the South Coast in April 2021 by the Fisheries branch of the Department of Forestry, Fisheries, and the Environment, South Africa. The proportion of males are shown in dark purple, and females in light purple. Black circles represent sampling stations where *M. paradoxus* was absent. Circle size represents the log-transformed total catch (kg), while line weight and style denote different depth intervals (isobaths).

Supplementary Table 1: Summary of *Merluccius paradoxus* samples sequenced for this study. The table includes the sample sites, the number of samples per region (N), the number of samples collected per location (n), geographic coordinates (decimal degrees), depth (meters), and the month and year of sample collection.

Region	**Sites**	***N***	***n***	**Latitude**	**Longitude**	**Depth (m)**	**Month**	**Year**
North Namibia	NN1	10	3	-18.99	11.33	592	March	2021
	NN2		3	-18.69	11.40	413	March	2021
	NN3		4	-18.32	11.78	411	March	2021
West Coast	WC1	10	3	-34.60	18.33	390	Oct	2021
	WC2		3	-34.23	17.66	413	Feb	2022
	WC3		4	-32.70	16.65	489	Feb	2022
South Coast	SC1	5	1	-36.74	20.35	646	Feb	2022
	SC2		4	-35.33	22.89	638	April	2021
Eastern Cape	EC1	12	5	-34.42	25.83	240	April	2021
	EC2		4	-34.09	26.93	471	April	2021
	EC3		3	-34.51	25.45	365	April	2021



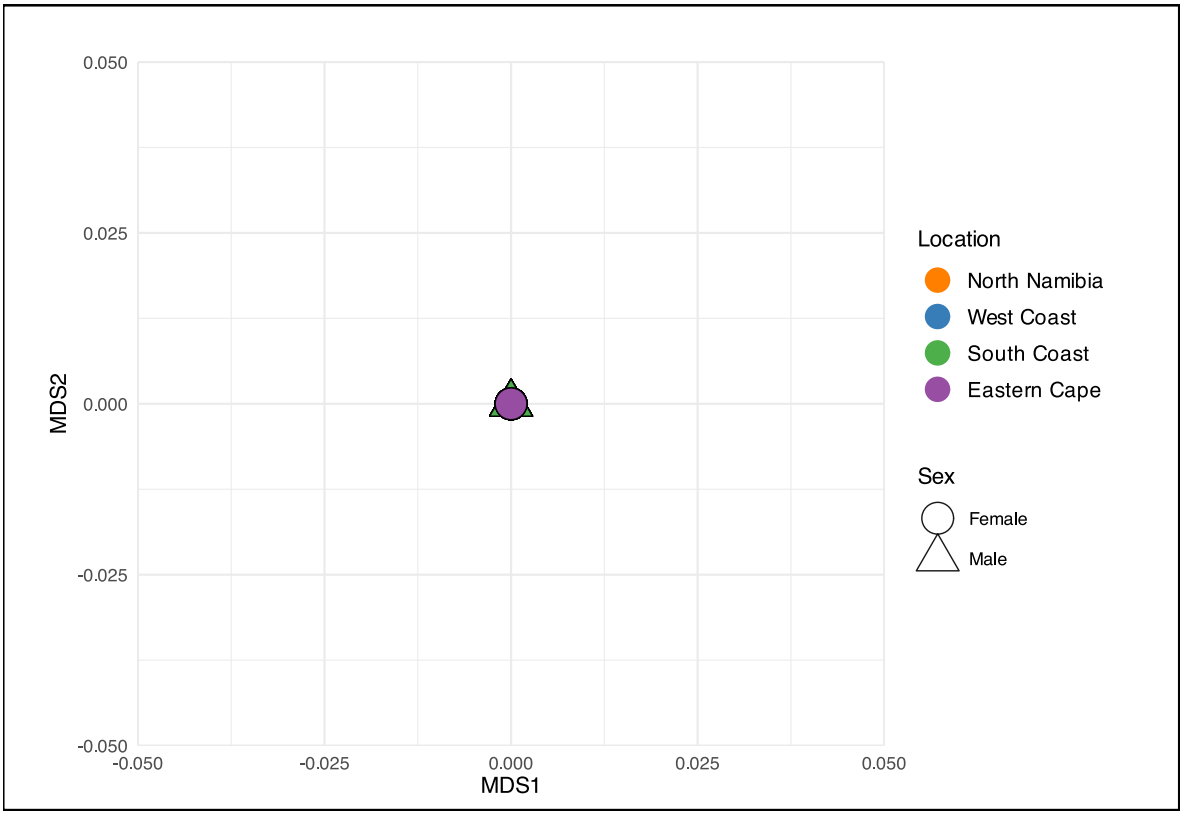
Supplementary Figure 2: Distance-based redundancy analysis (dbRDA) of 2,347,710 SNP data from 37 *Merluccius paradoxus* samples along the southern African coastline. Individuals are coloured by region, with sex indicated by point shape (circles represent females, and triangles represent males). Arrows represent predictor variables included in the model, with arrow length indicating the strength of their contribution to genetic differentiation. Significance levels for predictor variables are denoted as follows: $p < 0.001$ (***), $p < 0.01$ (**), $p < 0.05$ (*) and $p > 0.05$ (blank).



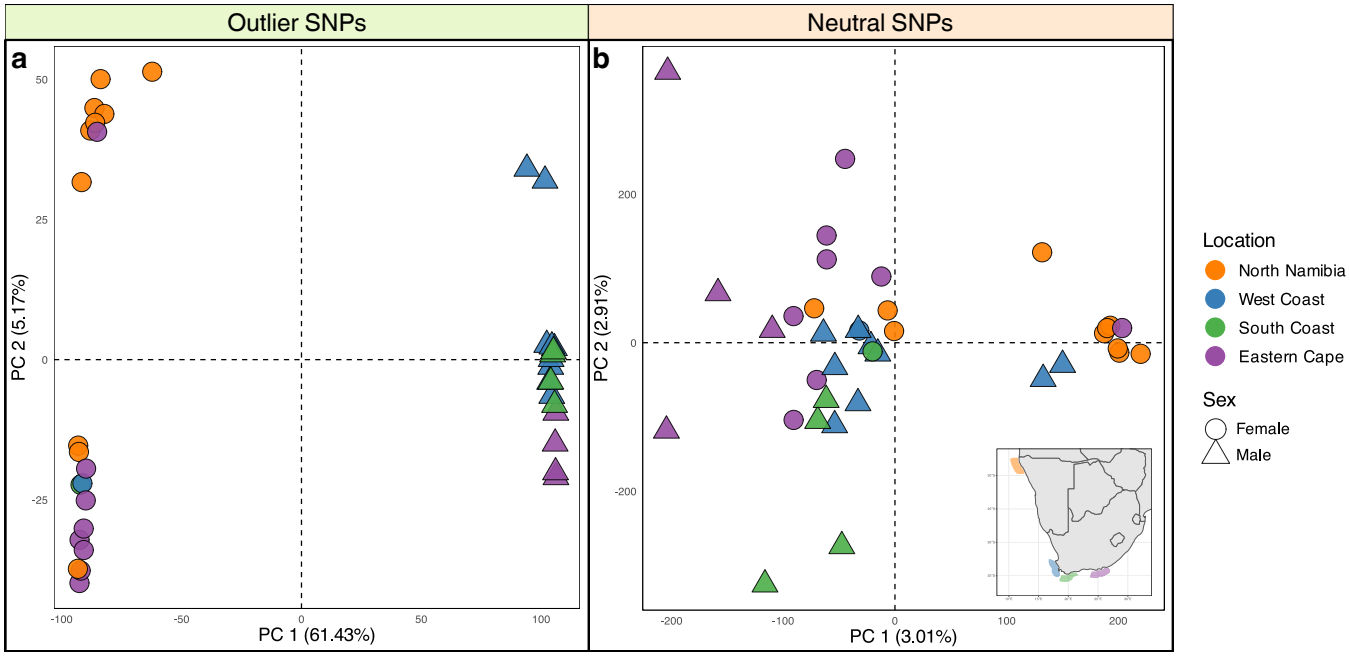
Supplementary Figure 3: Principal component analysis (PCAs) of 2,347,710 SNP data for all 37 *M. paradoxus* samples from the southern African coastline. Each plot displays the first and second principal components. Individuals are coloured by sequencing batch **(a)** and sequencing coverage **(b)** respectively with sex denoted by point shape: circles represent females, and triangles represent males. A 95% confidence interval ellipse is drawn around male and female clusters to indicate group dispersion.

Supplementary Table 2: Summary of distance-based redundancy analysis (dbRDA) results for the reduced model examining the effects of depth, length, longitude, maturity, and sex on genetic variation in *Merluccius paradoxus*. Genetic variation is based on 2,347,710 SNPs from 37 individuals sampled along the southern African coastline. Significance levels for predictor variables are denoted as follows: $p < 0.001$ (***), $p < 0.01$ (**), $p < 0.05$ (*) and $p > 0.05$ (blank).

Variable	**Df**	**Variance**	**F-value**	**p-value**
Depth	1	2740.6	9.553	0.001 ***
Length	1	1335.4	4.655	0.01 **
Longitude	1	6390.0	22.275	0.001 ***
Maturity	1	9653.7	33.652	0.001 ***
Sex	1	10027.7	34.955	0.001 ***



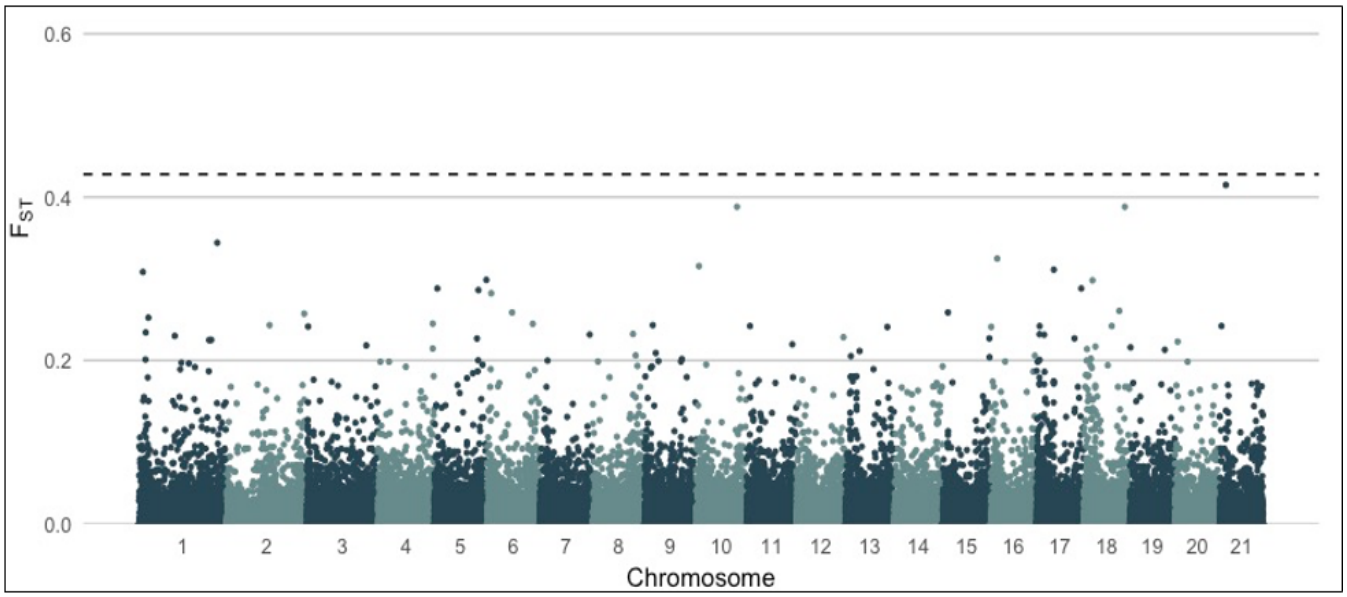
Supplementary Figure 4: Multidimensional scaling (MDS) plot based on Identity-by-Missingness (IBM) analysis using the filtered SNP dataset (2,347,710 SNPs) for 37 *M. paradoxus* samples. Individuals are coloured by region, with sex indicated by point shape (circles represent females, and triangles represent males).



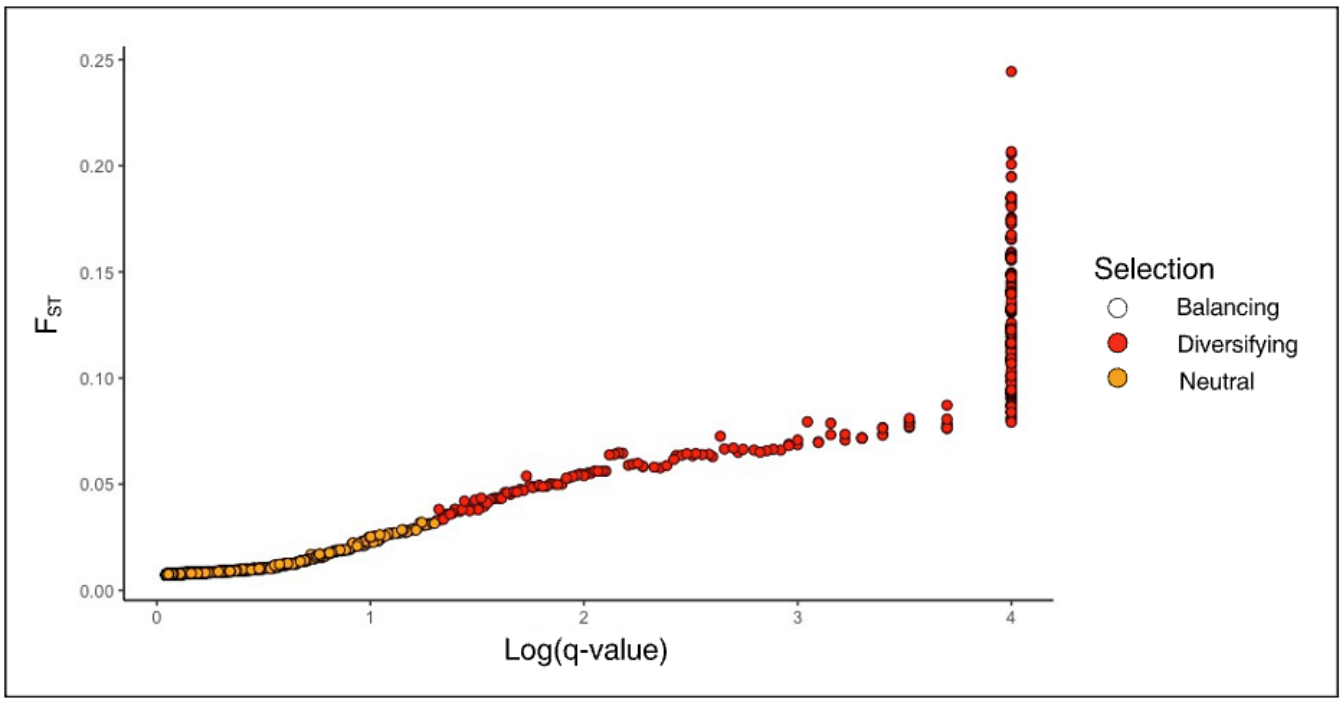
Supplementary Figure 5: Principal component analyses (PCAs) of **(a)** outlier (53,522 SNPs) and **(b)** neutral (2,294,188 SNPs) datasets for all 37 *Merluccius paradoxus* samples from the southern African coastline. Each plot displays the first and second principal components. Individuals are coloured by region, with sex denoted by point shape: circles represent females, and triangles represent males.

Supplementary Table 3: Global weighted pairwise Weir and Cockerham F_{ST} estimates for *Merluccius paradoxus* based on 2,347,710 SNPs, calculated between four sampling locations along the southern African coastline. Significance levels are indicated as follows: * p < 0.05; ** p < 0.01; *** p < 0.001

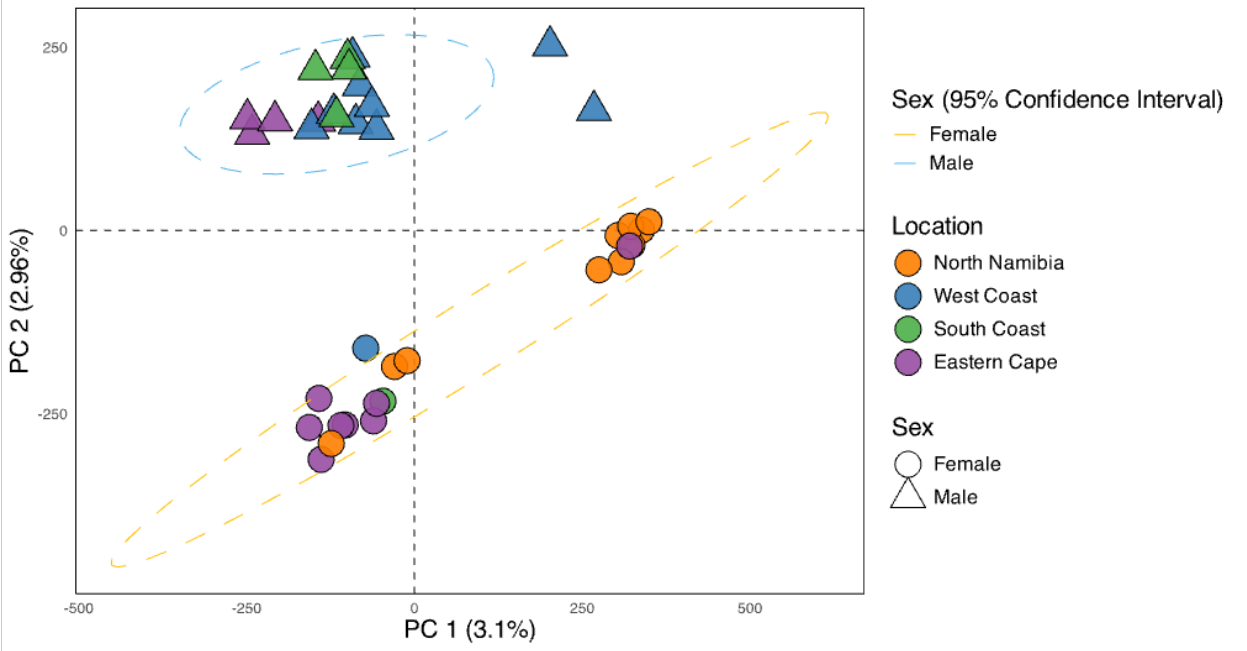
	North Namibia	*West Coast*	*South Coast*
North Namibia	-	-	-
West Coast	0.005 ***	-	-
South Coast	0.004 ***	-0.004 ***	-
Eastern Cape	0.001 ***	0.002 ***	-0.002 ***



Supplementary Figure 6: Genome-wide pairwise Weir and Cockerham F_{ST} estimates between West Edge (n = 10) and East Edge (n = 8) female *Merluccius paradoxus* individuals, based on 2,347,710 SNPs. The grey dashed line indicates the 99th percentile threshold for F_{ST} values observed in male-female comparisons across the genome.



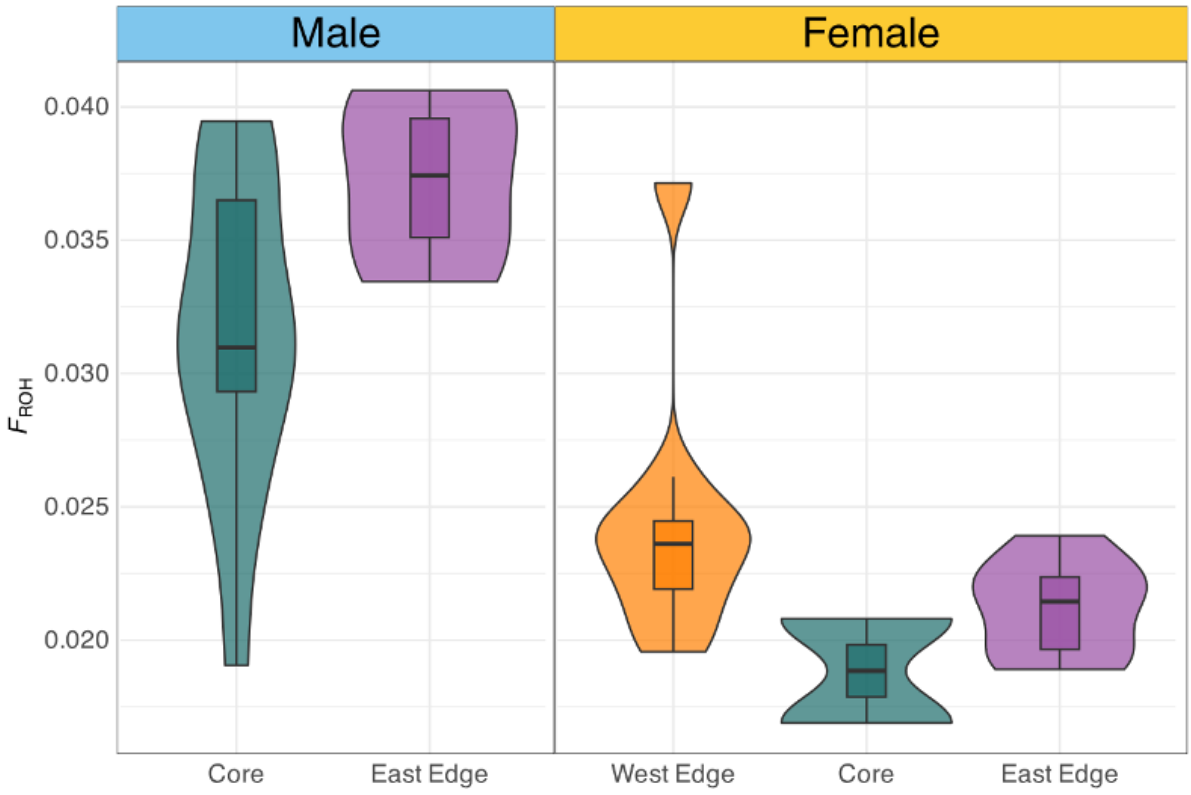
Supplementary Figure 7: BayeScan results for 58, 100 SNPs found on Chromosome 2 in *Merluccius paradoxus*. The plot shows the relationship between F_{ST} and log-transformed q-values where each point represents a SNP. SNPs are coloured according to the type of selection they are under namely, balancing selection (white; $q < 0.05$, $a < 0$), diversifying selection (red; $q < 0.05$, $a > 0$), and neutral SNPs (orange; $q > 0.05$).



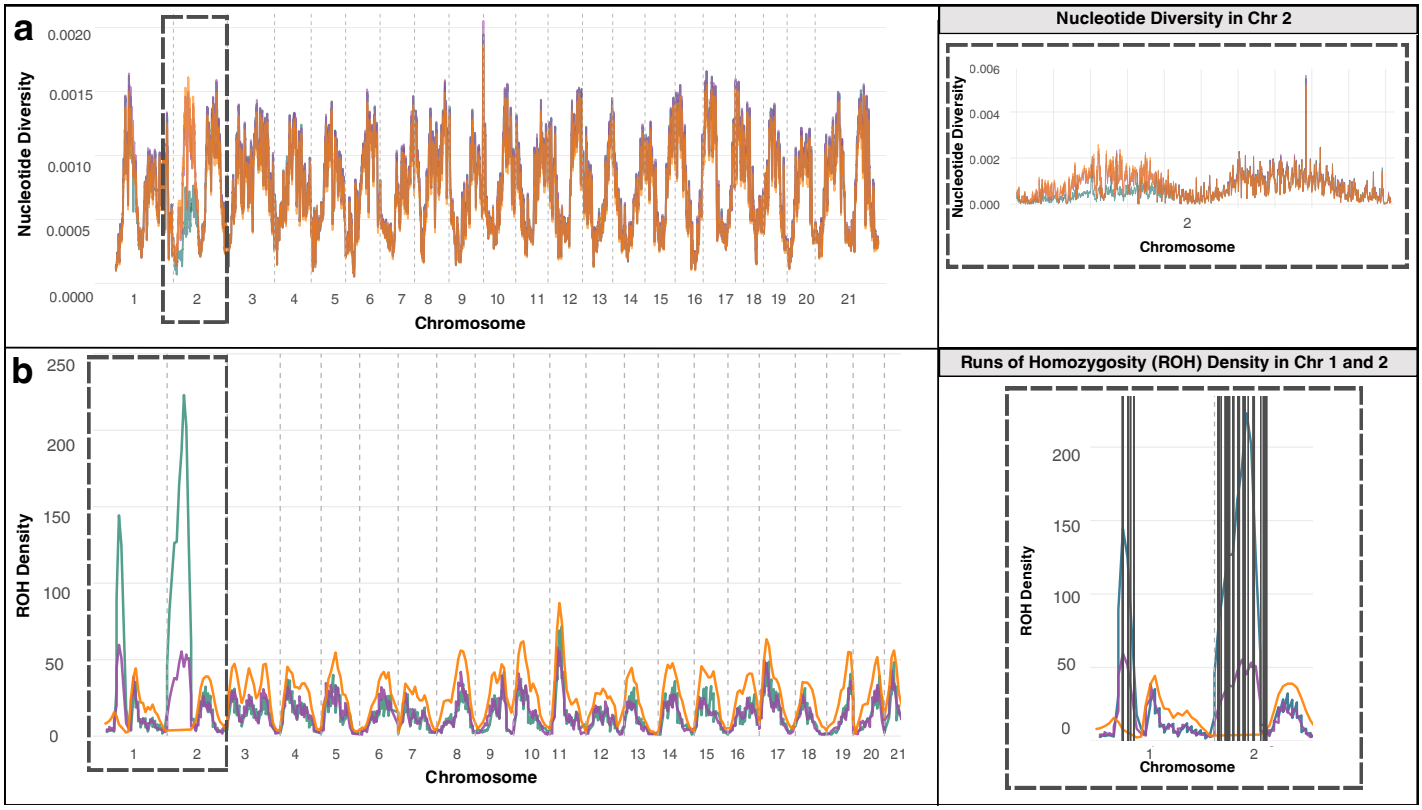
Supplementary Figure 8: Principal component analysis (PCAs) of 1,173,439 SNPs that were retained after filtering for linkage disequilibrium (r^2 > 0.2) for all 37 *Merluccius paradoxus* samples. Each plot displays the first and second principal components. Individuals are coloured by region, with sex denoted by point shape: circles represent females, and triangles represent males. A 95% confidence interval ellipse is drawn around male and female clusters to indicate group dispersion.

Supplementary Table S4: Average measures of genomic diversity for each location and sex, based on 2,347,710 SNPs: n – number of individuals; $\boldsymbol{\pi}$ – nucleotide diversity (per site); D –Tajima's D (50kb windows); H_o –observed heterozygosity (per site); H_e –expected heterozygosity (per site); F_{IS} – inbreeding coefficient (per individual); F_{ROH} – genomic inbreeding coefficient. Standard error values are reported in brackets next to each mean.

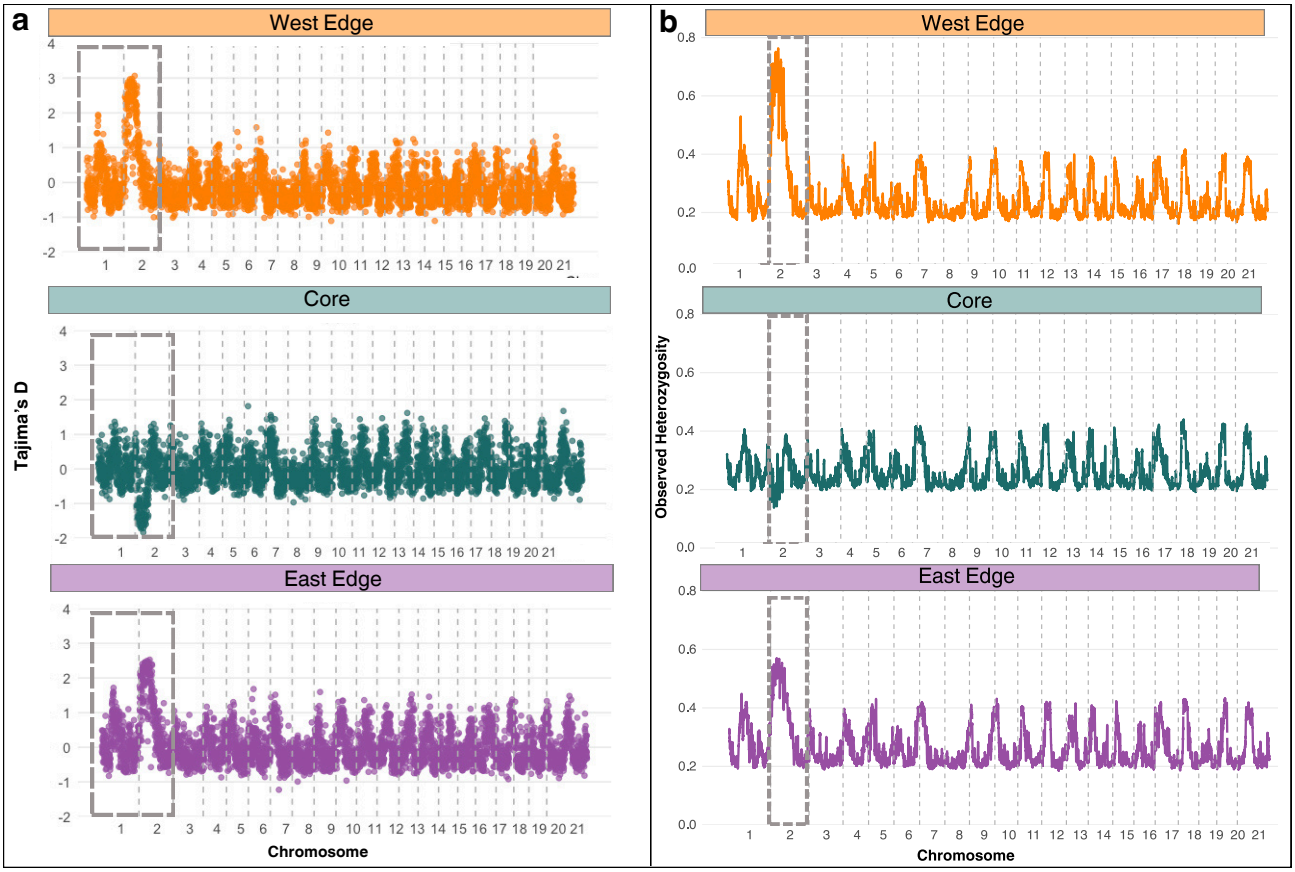
		n	$\boldsymbol{\pi}$	D	H_O	H_E	F_{IS}	F_{ROH}
Location	West Edge	10	0.219 (± 0.001)	-0.116 (± 0.005)	0.227 (± 1 x 10^{-4})	0.208 (± 1 x 10^{-4})	-0.003 (± 0.026)	0.024 (± 0.001)
	Core	15	0.226 (± 0.001)	-0.014 (± 0.004)	0.241 (± 1 x 10^{-4})	0.218 (± 9.8 x 10^{-5})	-0.062 (± 0.016)	0.030 (± 0.002)
	East Edge	12	0.231 (± 0.001)	0.016 (± 0.005)	0.241 (± 1 x 10^{-4})	0.221 (± 1 x 10^{-4})	-0.065 (± 0.012)	0.027 (± 0.002)
Sex	Male	17	0.224 (± 0.001)	0.073 (± 0.004)	0.239 (± 1 x 10^{-4})	0.218 (± 9.8 x 10^{-5})	-0.053 (± 0.013)	0.033 (± 0.001)
	Female	20	0.225 (± 0.001)	0.148 (± 0.006)	0.236 (± 1 x 10^{-4})	0.219 (± 9.8 x 10^{-5})	-0.042 (± 0.017)	0.023 (± 0.001)



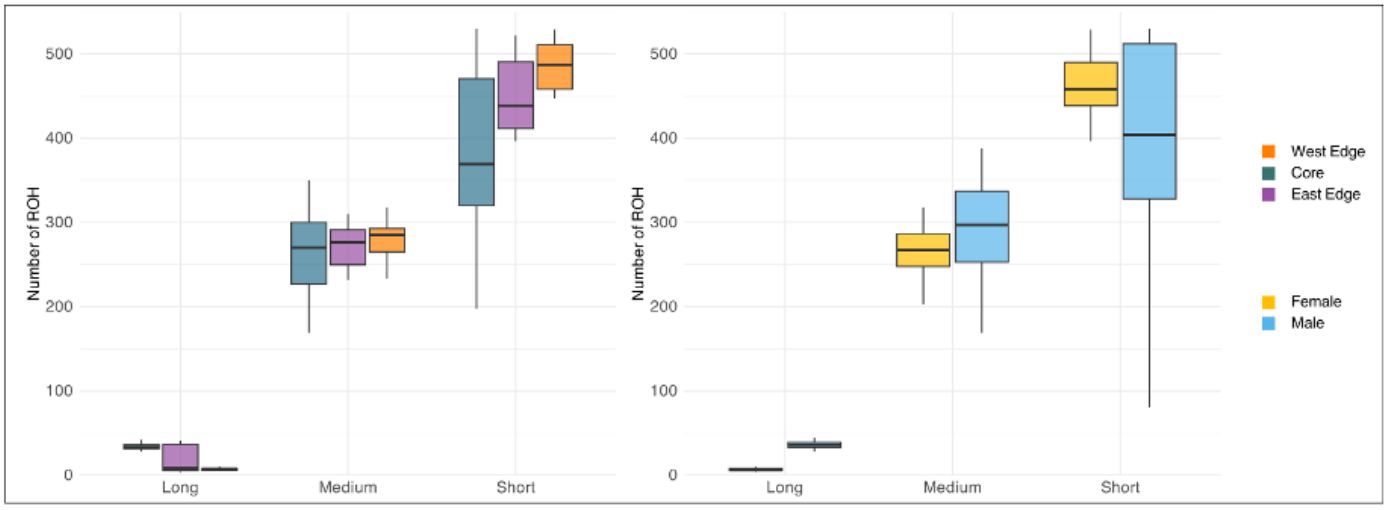
Supplementary Figure 9: Genomic inbreeding coefficient (F_{ROH}) for males and females across sampling locations, based on 2,347,710 SNPs. Violin plots show the distribution of F_{ROH} within each sex-population group with embedded boxplots representing the data spread. The bold line within each box indicates the median, while the upper and lower box edges correspond to the interquartile range.



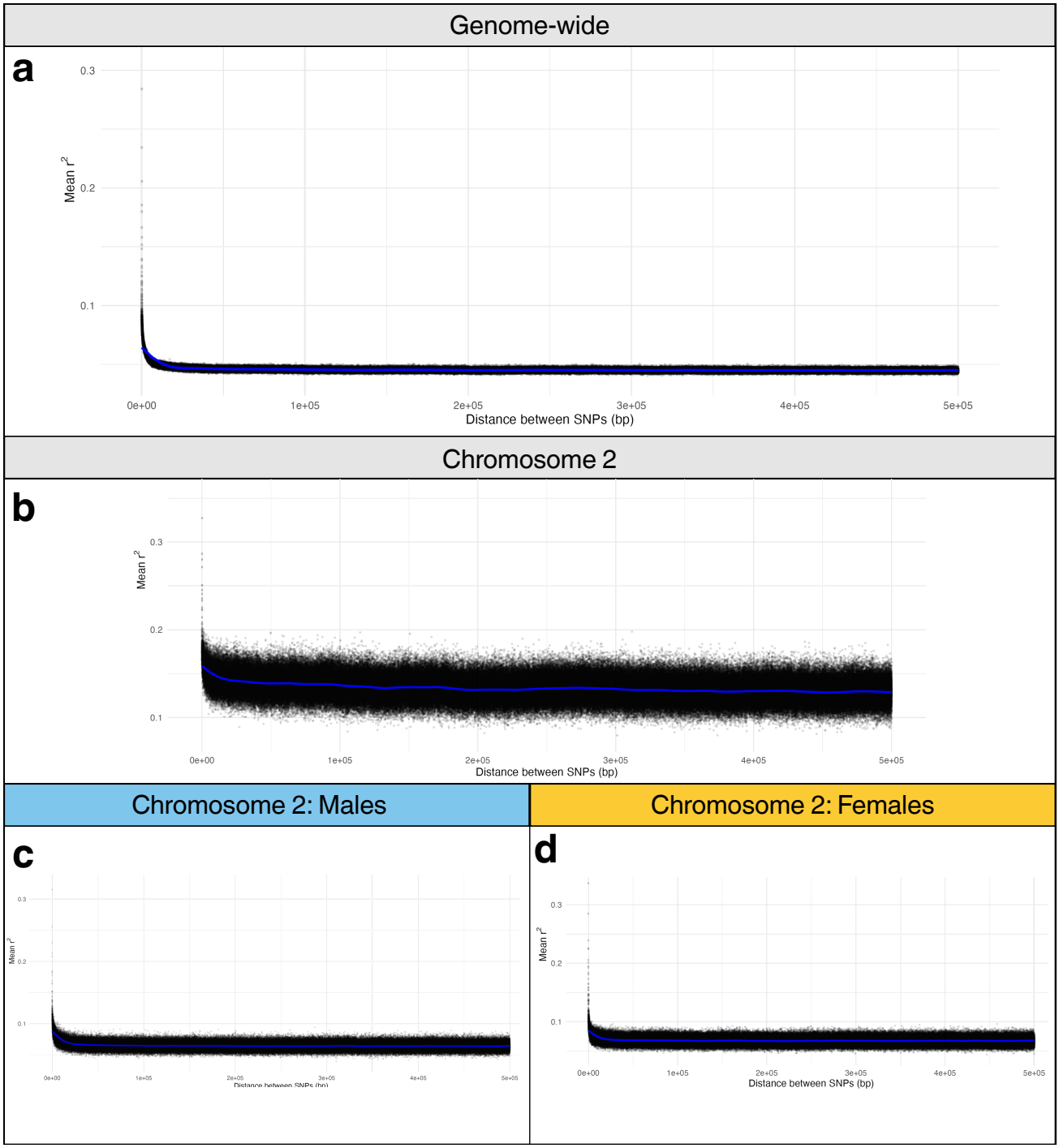
Supplementary Figure 10: Genome-wide nucleotide diversity **(π; a)** and Runs of Homozygosity (ROH) density **(b)** for the individuals collected from the West Edge (orange; originally Namibia), Core (turquoise; originally West and South Coast), and East Edge (purple; originally Eastern Cape) of the *Merluccius paradoxus* distribution, based on 2,347,710 SNPs. Chromosomes are separated by grey dashed lines on the x-axis. The right of each panel shows a zoomed-in view of chromosomes of interest, highlighting sex-specific genomic patterns. Nucleotide diversity **(π; a)** was calculated in 50kb windows, and ROH density **(b)** was calculated in 2Mb bins along the genome.



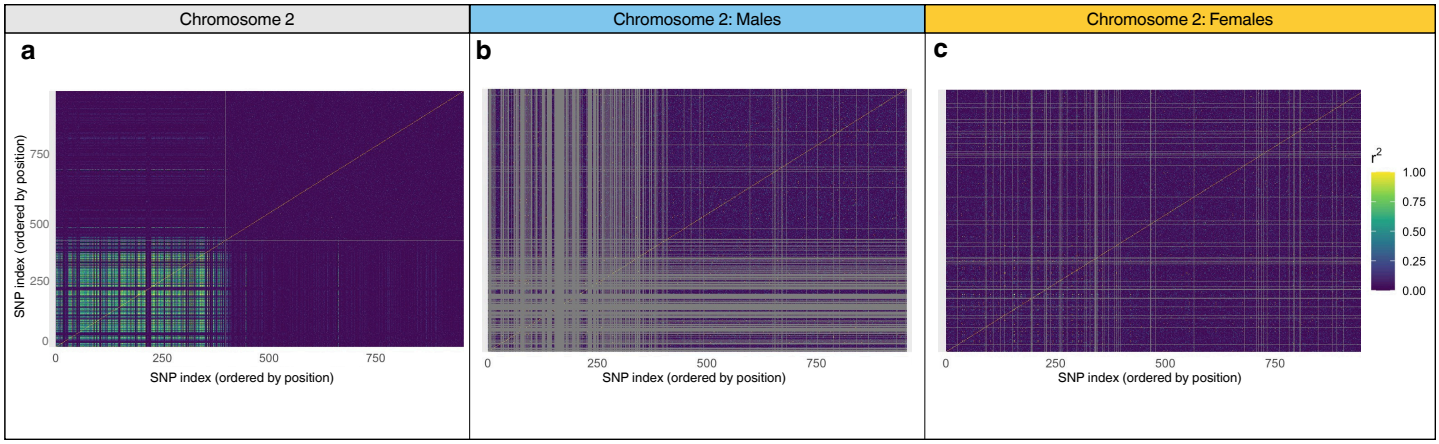
Supplementary Figure 11: Genome-wide Tajima's D **(a)** and observed heterozygosity **(**H_o; **b)** for *Merluccius paradoxus,* based on 2,347,710 SNPs for each sampling location. Chromosomes are separated by grey dashed lines on the x-axis, with regions of interest highlighted by grey dashed boxes. Panel A shows Tajima's D in 150kb windows for the West Edge (orange; originally Namibia), Core (turquoise; originally West and South Coast), and East Edge (purple; originally Eastern Cape) of the distribution. Right panels show observed heterozygosity (per SNP, 50kb windows) for windows for the West Edge (orange; originally Namibia), Core (turquoise; originally West and South Coast), and East Edge (purple; originally Eastern Cape) of the distribution.



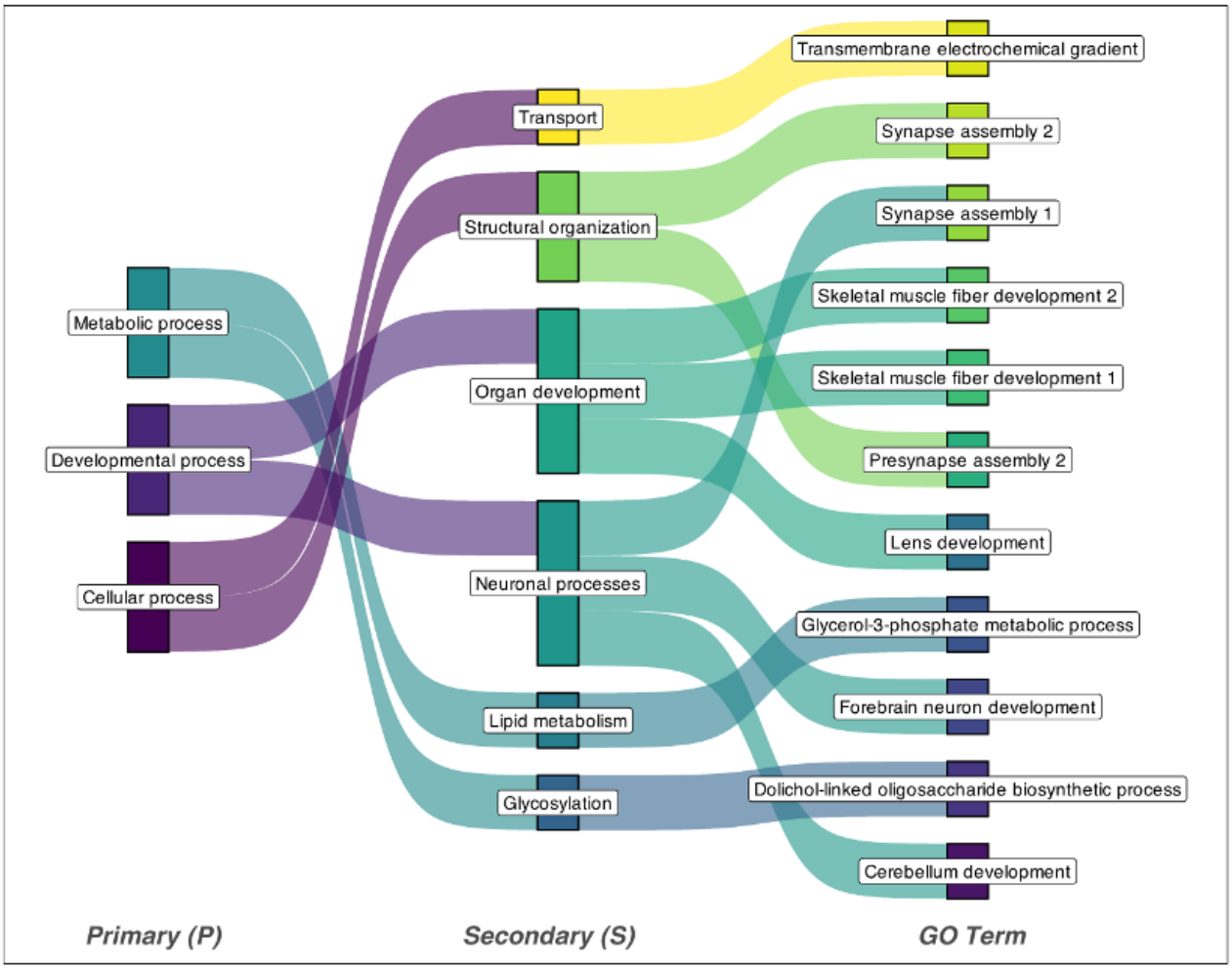
Supplementary Figure 12: The number of Runs of Homozygosity (ROH) within three length categories (short, medium, and long) across sexes and sampling locations, based on 2,347,710 SNPs. Box plots represent the distribution of ROH counts within each category: short ROH (< 20 kb), medium ROH (20 – 100 kb), and long (> 100 kb). The bold line within each box indicates the median, while the upper and lower box edges correspond to the interquartile range.



Supplementary Figure 13: Linkage disequilibrium (LD) decay across the genome **(a)** and on Chromosome 2 for all individuals **(b)**, for males **(c)**, and for females **(d)** in *Merluccius paradoxus*. LD was measured as mean pairwise r^2 and plotted as a function of distance (bp) between SNPs within a 500kb window.



Supplementary Figure 14: Linkage disequilibrium (LD) heatmaps showing mean pairwise r^2 values between SNPs on Chromosome 2 in *Merluccius paradoxus.* Heatmaps are shown for **(a)** all individuals, **(b)** males, and **(c)** and females. Colour indicates the strength of LD, with green representing higher r^2 values and purple representing lower r^2 values.



Supplementary Figure 15: Sankey plot summarizing significantly enriched GO terms from the gene ontology (GO) enrichment analysis for genomic regions with high-F_{ST} between males and females on Chromosomes 1 and 2. The pot displays GO terms and their classification into primary and secondary functional groups.