Supplementary Material

1 Methods

1.1 Genetic analysis

1.1.1 Molecular dataset

Individual samples were collected from different areas in the Mediterranean Sea obtained from commercial fishery catches in the framework of FishPopTrace project (FishPopTrace Project) and detailed in Nielsen et al., 2012. Muscle tissue samples were collected and stored in RNA later (Qiagen) at –80°C. RNA extraction cDNA libraries were constructed and sequenced using the 454 sequencing of the transcriptome platform (Roche 454 GS FLX sequencer). Reads were clustered, assembled into contigs and mined for SNPs. 1,536 putative SNPs were selected and included on an Illumina Golden Gate array for simultaneous validation and genotyping (Helyar et al., 2012, Milano et al. 2011). After assessment of the simultaneous validation and genotyping, 426 SNPs proved polymorphic with reliable genotyping across the assessed *S. solea* population samples (Nielsen et al., 2012).

1.1.2 Assessment of missing data and data filtering

Preparation and processing of SNP data can produce misleading artefacts which can generate erroneous patterns or considered hints of population structure and adaptive processes. In this scenario, stresses the importance of creating a rigorous and documented filtering process to minimize or remove errors. In particular, filtering SNP data is crucial to remove genotyping errors and prevent wrong interpretations of standing-out signals. However, the filtering procedure is contingent on the analysis and type of data, and the development of a standardized method is not always feasible.

In our study, we applied several filtering methods to understand how to handle missing data. Specially, we tried to respond to the following questions. How different amounts of missing data affect the data? Which filtering approach is more suitable to obtain reliable data avoiding loss of information? Removing all variables or samples with missing data, imputing missing data, filtering for different thresholds of missing data or combining the last two methods are some ways to account for missing data. Among those, filtering for different values of acceptable missing data seems the more flexible method, despite the arbitrary choice of filtering thresholds.

In our study, the percentage of missing data in the original data set was 7.56%. Among the geographical samples, GSA10_2000, GSA10_2003 and GSA18e_2000 were particularly affected by missing data. We assessed the amount of missing data at two different levels: individuals and SNPs. We applied two main filtering methods defined as fixed and sequential filtering approaches. Through the fixed filtering approach, we applied different coupled thresholds of allowed missing data per loci and individuals on the original data set. Whereas the sequential methods used the same thresholds having as input of each step the data set obtained from the previous filtering stage. We tried also this second method due to the high level of missing data in the data set to minimize the effect of tight thresholds and retain as many loci and individuals as possible. For this same reason we started filtering from loci since samples sizes were uneven and the three above-

mentioned populations were particularly affected by missing genotypes. The thresholds were chosen based on previous studies and trials and resumed in Table 1.1. The thresholds employed were the following:

- for loci: 20, 18, 16, 14, 12 and 10%
- for individuals: 40, 36, 32, 28, 24 and 20%

Max % di MD allowed – loci	Max % di MD allowed - individuals	Number of individuals	Number of loci
100	100	410	426
20	40	410	420
18	36	398	420
16	32	378	420
14	28	347	404
12	24	368	394
10	20	352	380

Supplementary Table 1.1. Details of number of loci and individuals identified applying different thresholds of missing data (MD) and data filtering approaches.

The final data set should represent the real population genetic differentiation, preserving a reasonable number of individuals for each of the 13 geographical sampling sites without being affected by the filtering approach. Since most of the metrics used in populations genetics (i.e., F_{ST}) are contingent on the allele frequency, we decided to use MAF (minor allele frequency) as a metric to choose the final data set. For this purpose, we investigated MAF distribution of different filtering steps for the entire data set (populations pooled) and for each separate geographical sample. We used the Kolmogorov-Smirnov test to determine statistically significant differences in MAF distributions at each filtering step with respect to the original distribution ($\alpha = 0.05$). Moreover, we inspected the data set without the three populations most affected by missing data. We assessed the results of the filtering steps for this data set through Principal Component Analysis (PCA). We then excluded monomorphic SNPs from the final data set prior to the analysis.

1.1.3 Heterozygosity, *FSI* and Hardy-Weinberg equilibrium

We used *Genepop* program (R version 4.7.5) to compute the observed and expected heterozygosity, estimate Fis and test for Hardy-Weinberg equilibrium. We used *genedivFis* function to calculate the observed and expected heterozygosity and F_{IS} values per sample. Then, we obtained a global estimate of Fis (argument **pairs=FALSE**) with *Fst* function. We used *test_HW* function to test three alternative hypotheses: probability test (exact test), heterozygote deficiency and excess (score test). We used the complete enumeration method since the individuals were less than 1000 and the distinct alleles less than 5 in the data set. Then, we used the same function to test each sample (multi-locus versions). Finally, the function also returned a global result for all SNPs and all samples.

1.1.4 F-statistics (*FST*)

As input file we used the *genind* object, which we transformed a *gtype* object by using *genind2gtypes* function. We used the *overallTest* function to calculate global F_{ST} and the *pairwiseTest* function to calculate the pairwiseF_{ST}. For both functions we set **stats = "fst"** and **nrep = 10,000**, and we then applied Benjamini and Yekutieli p-values correction. We considered significant pairwise comparisons with p-value lower than $\alpha = 0.05$.

1.1.5 Discriminant Analysis of Principal Components (DAPC)

Discriminant Analysis of Principal Components (DAPC) is a method to identify genetic clusters and describe the relationships between them. This method relies on the computation of new variables as linear combinations of the alleles. These new variables, referred to as discriminant functions, reflect the genetic variation among individuals and groups of individuals minimising the variation within clusters. However, DAPC needs the definition of prior groups, and this requirement is often difficult to meet. Alternatively, the method allows to infer the groups by clustering algorithm such as *k*-means. This multivariate approach combines PCA, *k*-means clustering and Discriminant Analysis (DA) to group individuals into a pre-determined number of clusters that better describes the data. First, data are transformed by PCA to reduce the number of variables, then *k*-means clustering with increasing number of K is performed. Finally, relationships between the different clusters are described by DA. This latter method leads to the identification of discriminant functions, which are variables that optimize the variance between groups while minimizing the variance within them. Moreover, it allows to identify probability memberships of individuals to each group, that can be interpreted as proximity to the clusters.

The first step relies on the *find.clusters* function. This function performs *k*-means clustering algorithm over a range of k to identify clusters while maximising the variation between them. We ran *find.clusters* function on the genind object for k from 1 to 20, setting 25 starting points for each run (**n.start**) and 10 iterations for each k (**n.iter**). First, the function transforms the data using PCA, at this step we retained 400 PCs in the interactive mode looking at the cumulative distribution of variance. Indeed, k-means algorithm benefits from retaining all the variance, thus reducing the number of PCs at this step is only useful in terms of computation. Then, we used the Bayesian Information Criterion (BIC) to compare clustering solutions obtained. Secondly, *dapc* function was run to provide transformation of the data by PCA prior to the discriminant analysis (DA). Given the optimal number of clusters identified by k-means, we ran the *dapc* function for the range of k from 2 to 6. We retained 170 PCs and two discriminant functions since the k values were

lower than 10. In the second step we performed the DAPC analysis with prior knowledge of the subgroups. Using prior populations, it is possible to assess the quality of the discrimination by looking at the re-assignment of each individual to its group of origin.

We used the 13 geographical sampling locations as **grp** argument in the *dapc* function. Moreover, when prior groups are defined you can use the α-score criterion or the cross-validation procedure to find the best number of PCs to retain. We ran the cross-validation method starting with a low number of replicates (**n.rep=30**). From those results, we chose a smaller range of PCs, and we repeated the cross-validation with higher repetitions (**n.rep=1,000**). The number of PCs with the lowest error was 125. So, we ran the DAPC with this optimal number of PCs and, having a number of k greater than 10, we retained 5 discriminant functions. Here we performed a DAPC analysis with prior knowledge of the population samples on all datasets integrating the clusters information of the probability memberships of individuals from *find.cluster* to the results obtained with prior knowledge in one graph.

1.1.6 Outlier detection methods

Here, we explained detailed methodologies for some outlier detection methods. Among methods, we used the method implemented in *pcadapt* R package. First, a Principal Component Analysis (PCA) is used to identify the number of principal components *K*. Then, each SNP is regressed by the K principal components. The results are reported as a vector of z -scores between each SNP, and the first K components obtained with the linear regression. Based on this vector, the outliers are then identified using Mahalanobis distance that calculates the distance between the covariance matrix of the z -scores and the vector of the z -score means. Finally, Mahalanobis distances are transformed in p-values based on the correlations between SNPs and the K principal components. To run the Bayescan program we set: 50,000 burn-in period, 100,000 number of iterations, 20 pilot runs and thinning interval size set to 50. For the FDIST approach we set 50,000 simulations, 100 demes with all geographical samples assigned to only one group and expected heterozygosity ranging from 0 to 0.5.

1.1.7 STRUCTURE

The software was run assuming admixture, correlated allele frequency and testing the scenarios with locality information (LOCPRIOR). We ran the analysis for K from 1 to 10 with 20 iterations, burn-in period at 20,000 and run length at 100,000. Alpha value was kept as default ($\alpha = 1$). Mean L(K) method was employed to visualize the mean likelihood values of different K partitions and identify the optimal K. R package pophelper (Francis, 2017) was utilized to align and merge the multiple runs for each K, as well as to visualize the posterior membership probability of each individual to clusters from 1 to 10.

1.2 Otolith analysis

For otolith analysis we used the data produced by FishPopTrace project (https://fishpoptrace.jrc.ec.europa.eu/) as described below. Biological descriptive data for each sampling site (Site ID) are listed in Table 1.2. including the total fish length and the weight ratio, the remaining information is described in Table 1. Both the right and left otolith of the same individuals were extracted, cleaned, and photographed in the project. In our study only images of left otoliths were used for morphometrics analysis. For otolith shape analysis we used ImageJ-Fiji (https://imagej.net/software/fiji/) to automatically detect the otolith outline and calculate the shape

indices (SIs) based on otolith morphometric parameters (area, perimeter, length, and width). The images were converted to silhouettes and EFDs extracted using the program SHAPE and the *Momocs* R package. All the analysis on Elliptical Fourier descriptors were performed using *Momocs* R package. We used *import_jpg* function to import otolith outlines from otolith images. Starting from closed outlines, we then created the Out object with *Out* function. This object is a list of closed outlines, for each outline there are a list matrix of coordinates and a factor specifying the sampling sites. After outlines inspection, we decided to normalize the outlines aligning the shapes using as control points two landmarks chosen on each shape (*def_ldk* function). The shapes were then centered on the origin with *coo_center* function, scaled by the centroid size with *coo_scale* function and aligned with a full generalized Procruster alignment using *fgProcruster* function.

Site ID	Number of individuals (N)	Total fish length (mm, mean ± SD)	Weight ratio (g, mean ± SD)
GSA7_2009	30	359.47 ± 40.50	437.28 ± 179.38
GSA9_2009	39	278.38 ± 21.03	199.29 ± 59.06
GSA17_2009	44	281.91 ± 26.01	200.33 ± 55.03
GSA22_2009	47	291.36 ± 35.52	214.60 ± 96.99
GSA24_2009	30	251.83 ± 23.69	147.14 ± 38.24

Supplementary Table 1.2. Details otolith data of the total fish length and the weight ratio for each geographical site reporting the mean and the standard deviation.

1.3 Environmental analysis

Monthly mean value of physical and biochemistry environmental variables were downloaded at a resolution of 12 km^2 from E.U. Copernicus Marine Service Information (https://marine.copernicus.eu/). We selected the following variables considering their availability over the analysis period from 2000 to 2010. Meridional component of the currents (northward) (curM, m/s), zonal component of the currents (eastward) (curZ, m/s), salinity (sal, psu) and potential temperature (temp, °C) data were extracted from Mediterranean Sea Physical Reanalysis (https://doi.org/10.25423/MEDSEA_REANALYSIS_PHYS_006_004) on a grid with 1/16° x 1/16° horizontal resolution (approximatively 6 km) and 72 vertical levels of thickness. Chlorophyll (chl, milligram m^{-3}), dissolved oxygen (dox, millimol m^{-3}), nitrate (NO_3-) (nit, millimol m^{-3}), CO_2 (ocean pCO_2 expresses as carbon dioxide partial pressure) (pco, Pa), pH (ph, PH), phosphate (PO_4) (pho, millimol m^{-3}), phytoplankton carbon biomass (phyto, mol m^{-3}), net primary production (tendency of mole concentration of particulate organic matter expressed as carbon in sea water due to net primary production) (ppn, mol m^{-3} s^{-1}) were extracted from Mediterranean Sea

Biogeochemical Reanalysis (https://doi.org/10.25423/MEDSEA_REANALYSIS_BIO_006_008) on a grid with 1/16° x 1/16° horizontal resolution (approximatively 6 km) and 72 vertical levels of thickness. For those variables in each macro-area, we calculated average, range, minimum and maximum values according to the variables features. In order to account for differences between bottom and surface, we selected both bottom and the weighted average value in the water column (Wclm). Also, daily mean values of turbidity (Diffuse Attenuation Coefficient at 490nm (Kd_490)) (turb, m^{-1}) were downloaded from E.U. Copernicus Marine Service Information (https://doi.org/10.48670/moi-00299) at a resolution of 1 km_2. In addition, monthly mean values of total precipitation (mm) as proxy of freshwater input were extracted from CRU-TS 4.03 (Harris et al., 2014) and downloaded from WorldClim 2.1 at a resolution of 441 km_2. We selected 17 environmental variables reported in Table 1.2 based on their influence in common sole distribution.

Supplementary Table 1.2. Summary of 17 environmental variables.

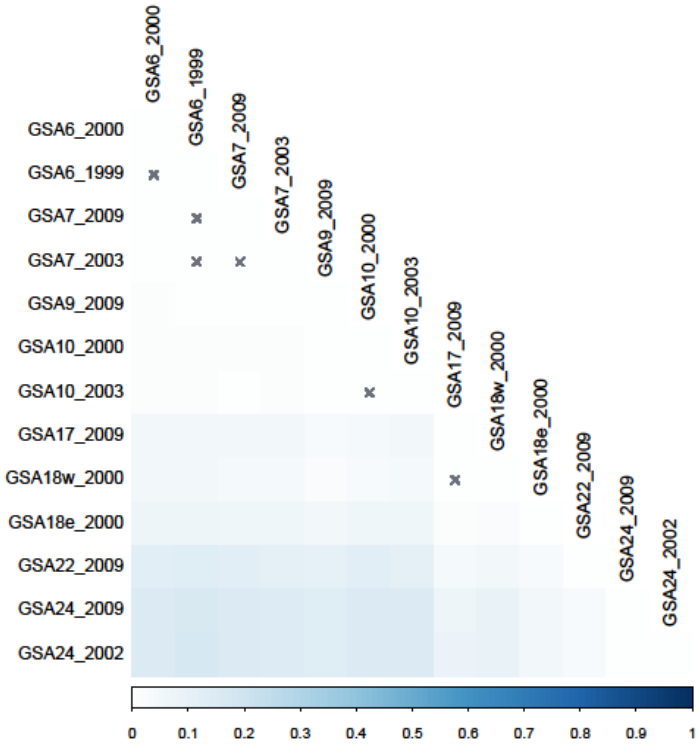
Environmental variables
curM_Wclm_mean
curZ_Wclm_mean
sal_bottom_mean
sal_bottom_range
temp_bottom_mean
temp_bottom_range
mean_turb
mean_prec
min_prec
chl_Wclm_mean
dox_Wclm_mean
nit_Wclm_mean
pco_Wclm_mean
ph_Wclm_mean
pho_Wclm_mean
phyto_Wclm_mean
ppn_Wclm_mean

From the *pcnm* function in *VEGAN* R package we obtained 5 dbMEMs eigenvectors. According to the scales of the pattern showed by dbMEMs represented in Figure 3.3, dbMEM1 and dbMEM2 were arbitrarily defined as broad scale variables, and dbMEM3, dbMEM4 and dbMEM5 as fine-scale variable. Visual inspection of dbMEM1 suggested a broad scale west-to-east gradient. These eigenvectors were used as spatial variables in the RDA analysis. Before the application of the RDA analysis, we calculated the VIFs using *vif.cca* function in *vegan* R package (Oksanen et al., 2022), resulting in these values for each variable: dbMEM1 (30.78), dbMEM2 (8.05), dbMEM3 (16.16), dbMEM4 (8.52), dbMEM5 (3.45), curM_Wclm_mean (1.67), sal_bottom_mean (54.28),

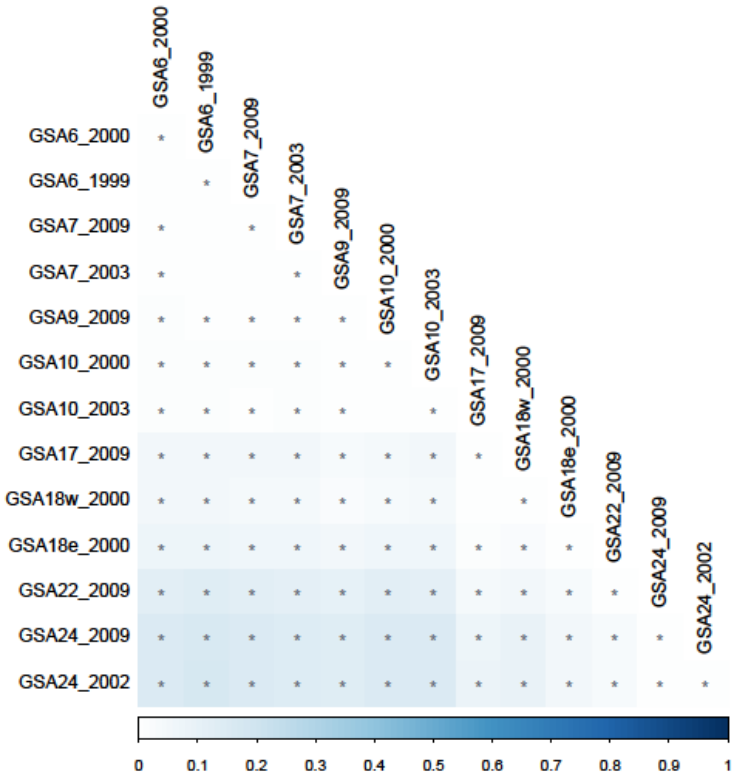
temp_bottom_range (7.65), pco_Wclm_mean (NA). Following Bocard et al, 2018 we decided to not remove variables with high VIFs before the application of a procedure of selection of variables (ordistep).

2 Results

2.1 Genetic analysis



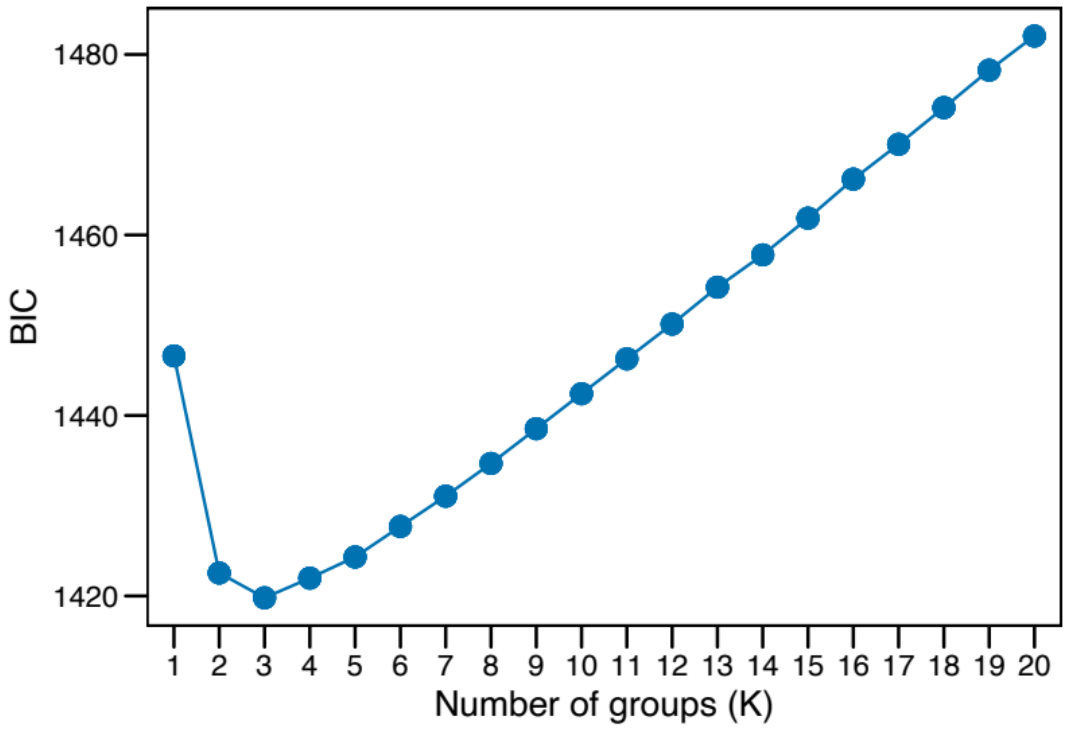
A



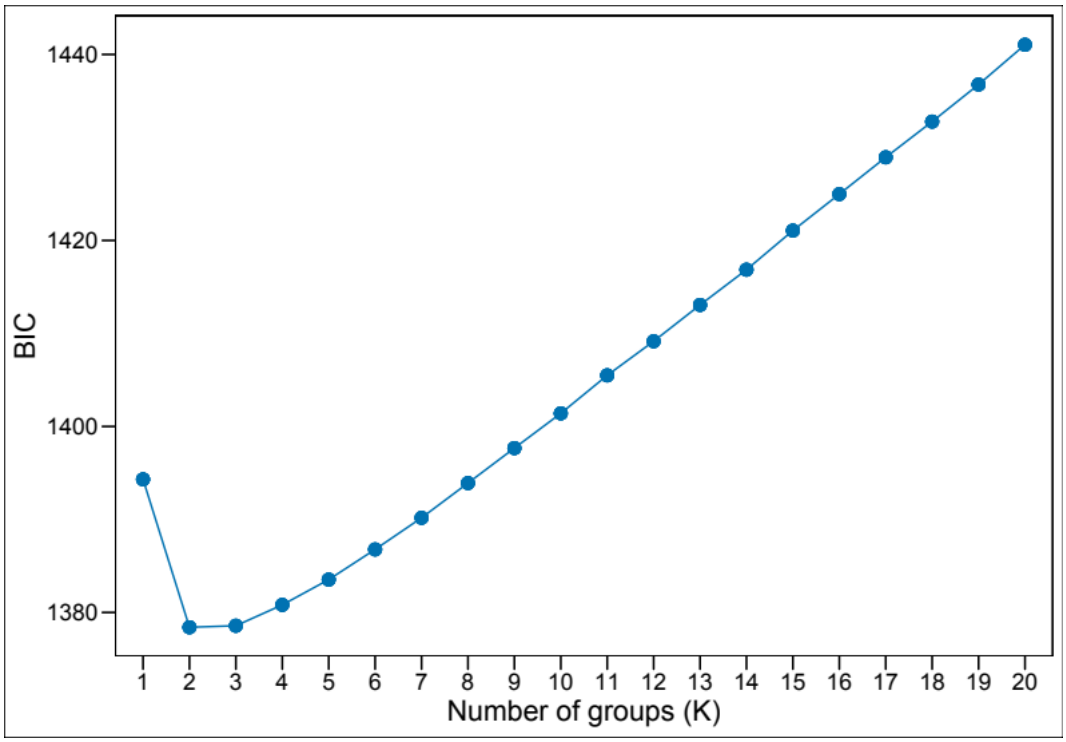
B

Supplementary Figure 1.1. Matrix of pairwise Fst values among Mediterranean population samples of *Solea solea* after Benjamini–Yekutieli correction for strataG indicating non-significant comparison (A) and significant comparison (B) for ($\alpha = 0.05$). Code of population samples are given in Table 1.

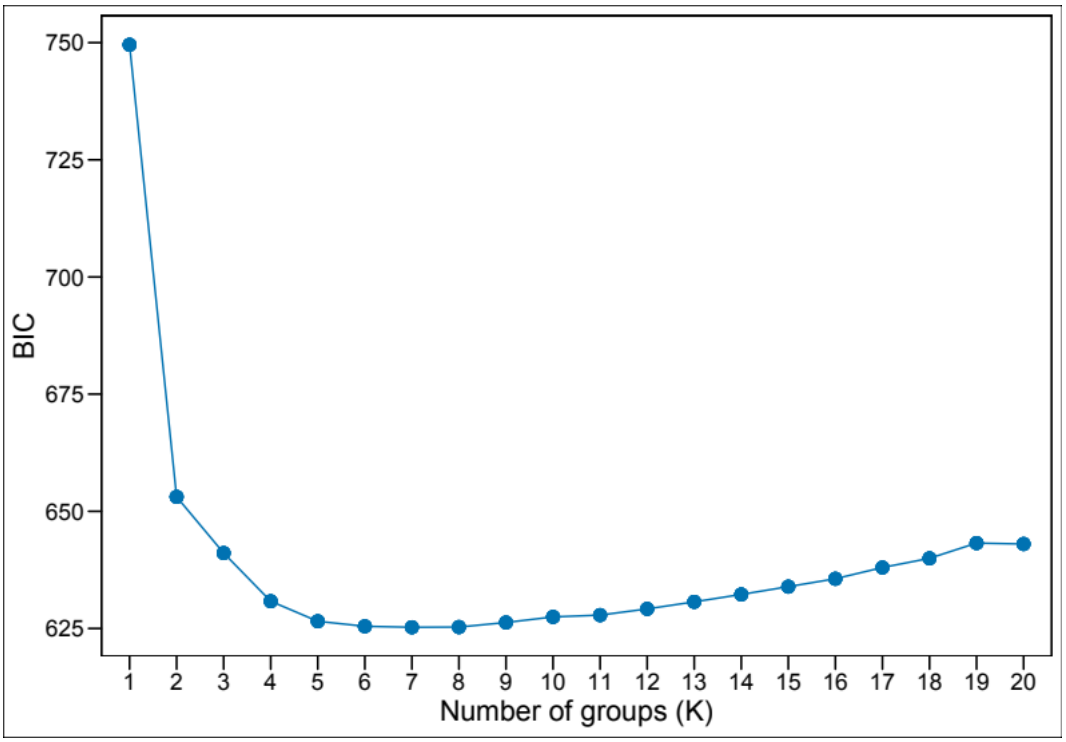
A


1480
1460
1440
1420
BIC
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Number of groups (K)

B

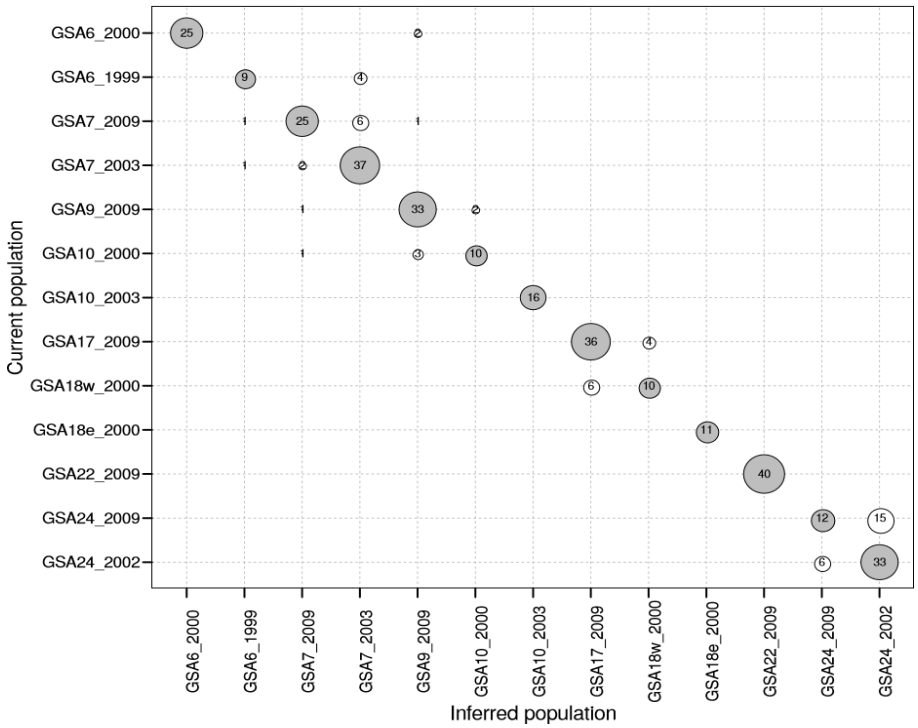

1440
1420
1400
1380
BIC
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Number of groups (K)

C

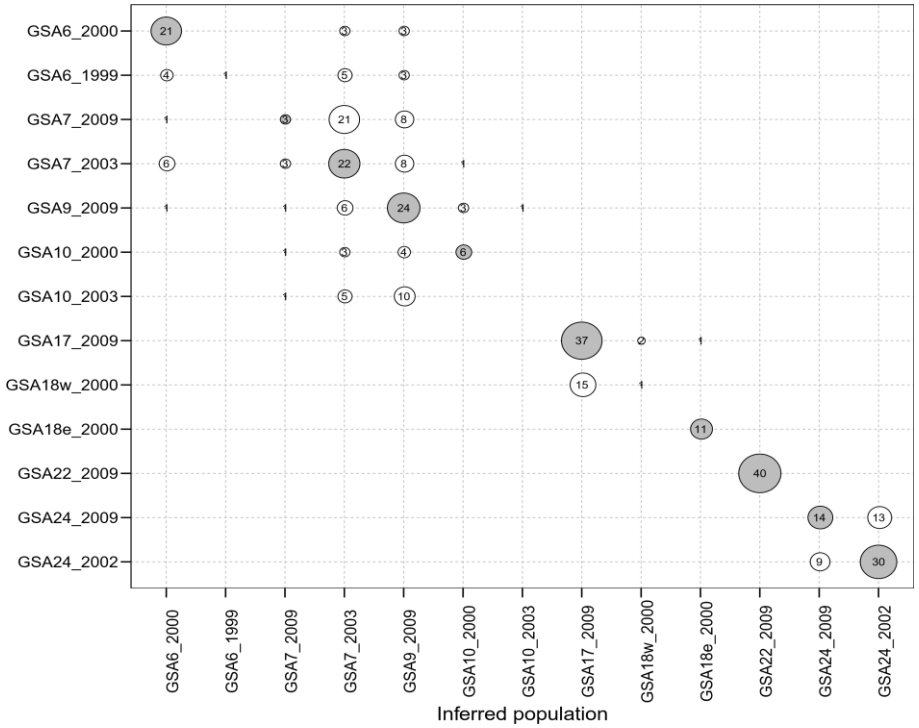


Supplementary Figure 1.2. Bayesian Information Criterion (BIC) summary statistics resulted by DAPC analysis for whole (A), neutral (B) and outlier (C) dataset. BIC values are plotted as a function of k. The BIC value that changed the curve indicates the optimal number of clusters.

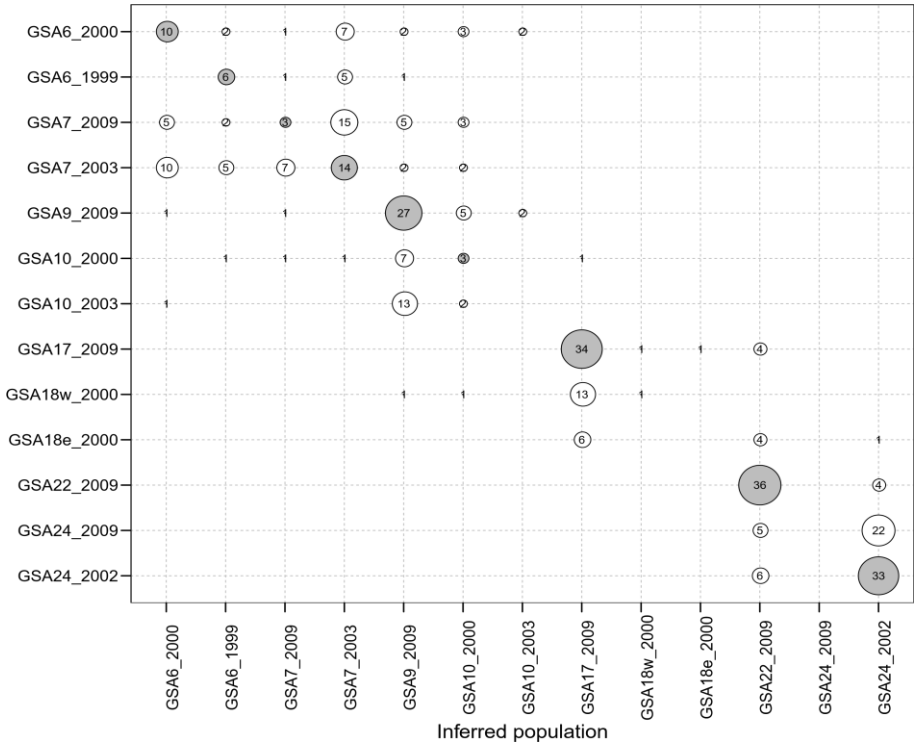
A


Current population
GSA6_2000
GSA6_1999
GSA7_2009
GSA7_2003
GSA9_2009
GSA10_2000
GSA10_2003
GSA17_2009
GSA18w_2000
GSA18e_2000
GSA22_2009
GSA24_2009
GSA24_2002
Inferred population

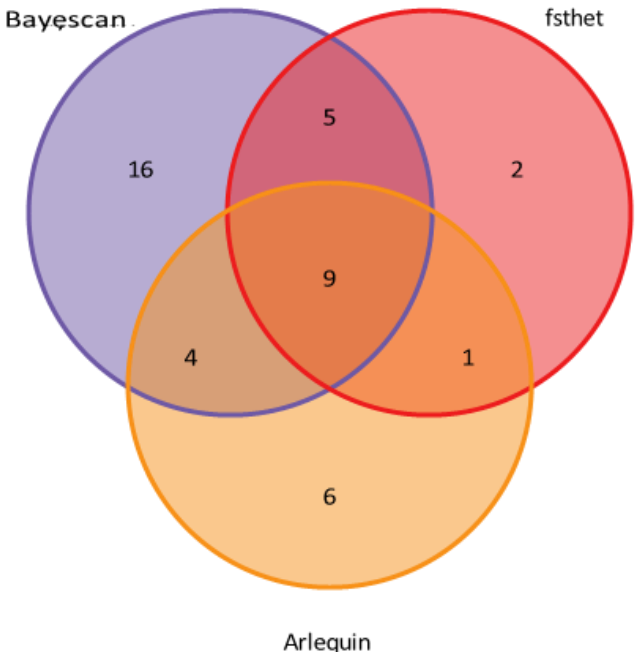
B


GSA6_2000
GSA6_1999
GSA7_2009
GSA7_2003
GSA9_2009
GSA10_2000
GSA10_2003
GSA17_2009
GSA18w_2000
GSA18e_2000
GSA22_2009
GSA24_2009
GSA24_2002
Inferred population

C



Supplementary Figure 1.3. Comparison of individual assignment between inferred groups and actual samples corresponding to sampling sites resulted by DAPC analysis for whole (A), neutral (B) and outlier (C) dataset.



Supplementary Figure 1.4. Venn diagram summarizing the comparison of SNPs identified by Bayescan, fsthet, Arlequin in the outlier detection analysis.

Supplementary Table 1.3. Full list of loci analysed in this study, with categories of variants identified as neutral (337 SNP loci) or outlier (43 SNP loci), as well as SNPs identified by at least one GEA method (148 SNP loci). Further details are provided with respect to SNPs identified by *Samβada*, *LFMM* and *Bayenv* associated with the environmental variables (curM_Wclm_mean, temp_bottom_range, sal_bottom_mean and pco_Wclm_mean).

SNPs name	**Neutral**	**Outlier**	**GEA methods**	***Samβada***	***LFMM***	***Bayenv***
SNP1001	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1002	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1004	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP1008	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1010	TRUE	FALSE	TRUE	TRUE	TRUE	FALSE
SNP1012	FALSE	TRUE	TRUE	TRUE	FALSE	FALSE
SNP1014	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1017	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1018	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1022	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1023	FALSE	TRUE	TRUE	FALSE	TRUE	TRUE
SNP1025	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1029	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1030	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
SNP1031	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP1033	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1035	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP1038	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP104	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1040	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1046	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1047	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1049	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1052	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1054	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1058	FALSE	TRUE	TRUE	TRUE	FALSE	FALSE
SNP106	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP1060	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP1062	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE

SNPs name	**Neutral**	**Outlier**	**GEA methods**	***Samβada***	***LFMM***	***Bayenv***
SNP1063	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1067	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1068	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1070	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1074	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1077	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1079	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1084	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1089	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1091	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1094	FALSE	TRUE	TRUE	FALSE	TRUE	FALSE
SNP1105	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1110	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1111	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1113	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1114	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1118	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1120	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1125	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1127	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1128	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1129	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1133	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1137	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1139	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1146	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1147	TRUE	FALSE	TRUE	TRUE	TRUE	FALSE
SNP1154	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
SNP1156	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1159	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP116	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1160	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1163	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1166	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE

SNPs name	**Neutral**	**Outlier**	**GEA methods**	***Samβada***	***LFMM***	***Bayenv***
SNP1169	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1182	TRUE	FALSE	TRUE	FALSE	FALSE	TRUE
SNP1183	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1184	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1190	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1191	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP1193	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1199	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP120	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1200	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP1202	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1203	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1205	FALSE	TRUE	TRUE	FALSE	TRUE	FALSE
SNP1206	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1208	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1213	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1214	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1220	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1231	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1232	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1234	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1235	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1236	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1238	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1240	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1246	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1250	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP1251	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP1259	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1260	FALSE	TRUE	TRUE	TRUE	TRUE	FALSE
SNP1261	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1262	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1264	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1268	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE

SNPs name	**Neutral**	**Outlier**	**GEA methods**	***Samβada***	***LFMM***	***Bayenv***
SNP1269	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP127	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1282	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1283	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1284	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1286	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1293	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP1294	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP1301	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1302	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1305	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1307	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1308	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP131	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1310	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1314	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1317	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1319	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP1320	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP1328	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP1333	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1335	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1337	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP134	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1340	FALSE	TRUE	TRUE	TRUE	TRUE	FALSE
SNP1343	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1346	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1347	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1349	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP135	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1353	FALSE	TRUE	TRUE	TRUE	FALSE	FALSE
SNP1354	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
SNP1355	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP1359	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE

SNPs name	**Neutral**	**Outlier**	**GEA methods**	***Samβada***	***LFMM***	***Bayenv***
SNP1370	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1373	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1376	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1379	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1380	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1388	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1400	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP1402	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP1407	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1408	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1411	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1416	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1417	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1427	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1432	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1436	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1439	FALSE	TRUE	TRUE	FALSE	TRUE	FALSE
SNP1445	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1451	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1455	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1456	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1466	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP147	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1479	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1484	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1489	FALSE	TRUE	TRUE	TRUE	FALSE	FALSE
SNP1491	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1492	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1493	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1496	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP1501	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP1502	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1512	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1515	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE

SNPs name	**Neutral**	**Outlier**	**GEA methods**	***Samβada***	***LFMM***	***Bayenv***
SNP1516	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1519	TRUE	FALSE	TRUE	TRUE	TRUE	FALSE
SNP1531	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP1536	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP1546	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1554	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP158	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP164	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP167	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP170	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP182	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP184	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP188	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP191	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP192	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP199	TRUE	FALSE	TRUE	FALSE	TRUE	TRUE
SNP2	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP200	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP201	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP206	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP220	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP225	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP228	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP232	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP235	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP246	FALSE	TRUE	TRUE	FALSE	TRUE	FALSE
SNP25	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP250	FALSE	TRUE	TRUE	FALSE	TRUE	FALSE
SNP256	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP267	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP275	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP276	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP278	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP284	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE

SNPs name	**Neutral**	**Outlier**	**GEA methods**	***Samβada***	***LFMM***	***Bayenv***
SNP35	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP350	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP355	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP357	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP36	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP360	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP37	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP376	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP383	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP386	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP388	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP391	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP392	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP393	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP394	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP395	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP396	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP398	FALSE	TRUE	TRUE	TRUE	TRUE	FALSE
SNP399	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP410	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP411	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP418	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP42	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP422	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP424	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP431	TRUE	FALSE	TRUE	FALSE	TRUE	TRUE
SNP432	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP435	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP44	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP450	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP451	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP452	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP455	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP461	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE

SNPs name	**Neutral**	**Outlier**	**GEA methods**	***Samβada***	***LFMM***	***Bayenv***
SNP463	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP464	FALSE	TRUE	TRUE	FALSE	TRUE	TRUE
SNP465	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP466	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP469	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP476	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP488	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP490	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP497	FALSE	TRUE	TRUE	FALSE	TRUE	FALSE
SNP503	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP504	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP516	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP520	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP528	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP530	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP533	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP543	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP550	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP563	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP567	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP569	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP573	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP577	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP58	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP590	FALSE	TRUE	TRUE	TRUE	FALSE	FALSE
SNP597	TRUE	FALSE	TRUE	FALSE	TRUE	TRUE
SNP599	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP60	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP600	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP601	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP605	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP609	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP614	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP626	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE

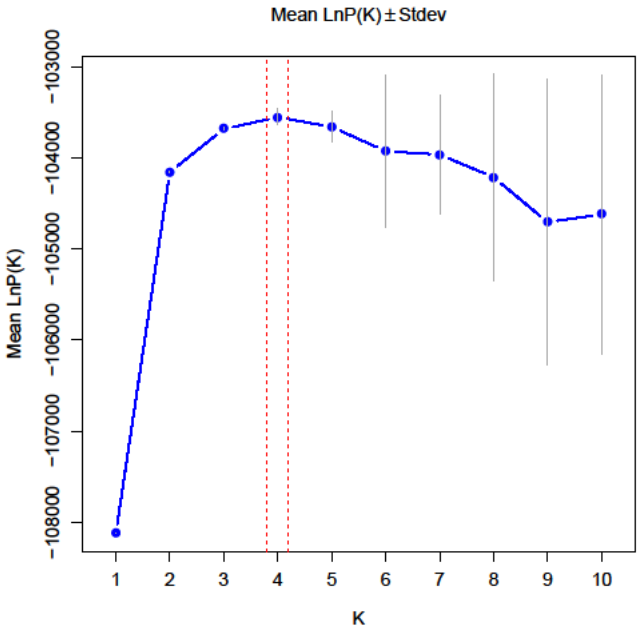
SNPs name	**Neutral**	**Outlier**	**GEA methods**	***Samβada***	***LFMM***	***Bayenv***
SNP633	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP637	TRUE	FALSE	TRUE	TRUE	TRUE	FALSE
SNP638	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP640	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP642	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP645	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP647	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP652	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP664	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP666	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP674	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP708	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP709	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP726	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP73	FALSE	TRUE	TRUE	FALSE	TRUE	FALSE
SNP737	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP739	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP747	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP749	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP750	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP752	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP757	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP766	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP767	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP768	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP769	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP771	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP773	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP776	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP779	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP780	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP781	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP782	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP788	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE

SNPs name	**Neutral**	**Outlier**	**GEA methods**	***Samβada***	***LFMM***	***Bayenv***
SNP789	TRUE	FALSE	TRUE	TRUE	TRUE	FALSE
SNP790	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP80	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP800	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP803	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP809	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP810	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP811	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP812	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP813	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP814	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP815	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP817	TRUE	FALSE	TRUE	FALSE	FALSE	TRUE
SNP821	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP826	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP831	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP834	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP835	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP840	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP844	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP845	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP848	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP851	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP853	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP854	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP855	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP861	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP864	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP871	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP875	TRUE	FALSE	TRUE	TRUE	TRUE	FALSE
SNP877	FALSE	TRUE	TRUE	TRUE	TRUE	TRUE
SNP879	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP88	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP883	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE

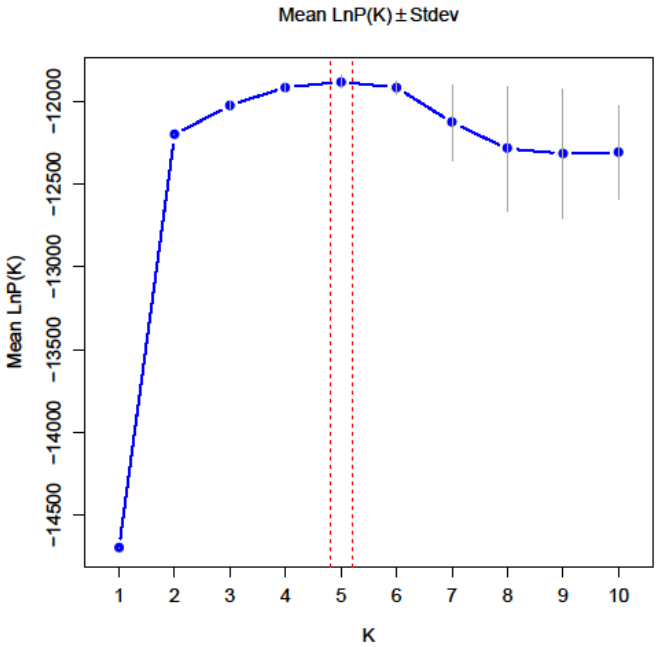
SNPs name	**Neutral**	**Outlier**	**GEA methods**	***Samβada***	***LFMM***	***Bayenv***
SNP884	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP885	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP890	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP891	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP898	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP899	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP90	FALSE	TRUE	TRUE	TRUE	FALSE	FALSE
SNP914	TRUE	FALSE	TRUE	TRUE	TRUE	TRUE
SNP915	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP919	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP920	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP923	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP928	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP930	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP933	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP935	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP943	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP944	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP945	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP946	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP948	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP949	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP951	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP953	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP955	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP956	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP961	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP962	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP963	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP965	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP968	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP970	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP971	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP972	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE

SNPs name	**Neutral**	**Outlier**	**GEA methods**	***Samβada***	***LFMM***	***Bayenv***
SNP973	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP975	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP977	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP986	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP987	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP988	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP989	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE
SNP990	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP992	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP995	TRUE	FALSE	TRUE	FALSE	TRUE	FALSE
SNP996	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE

A

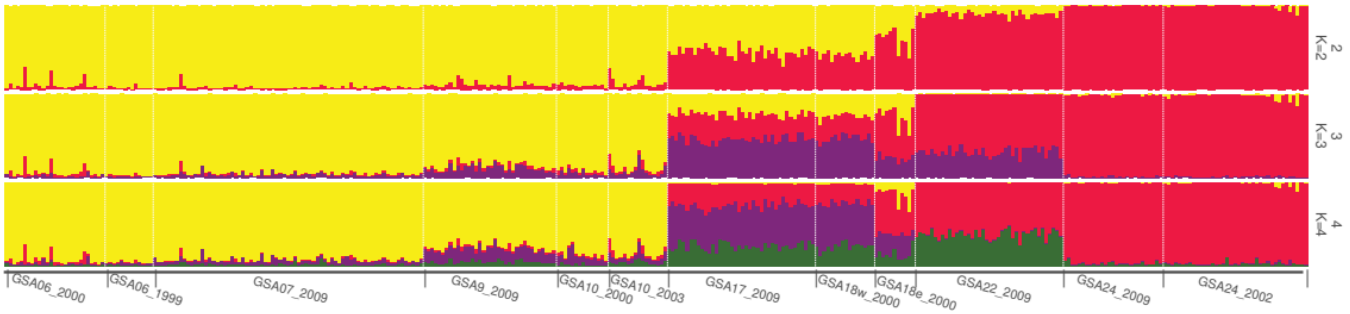


B

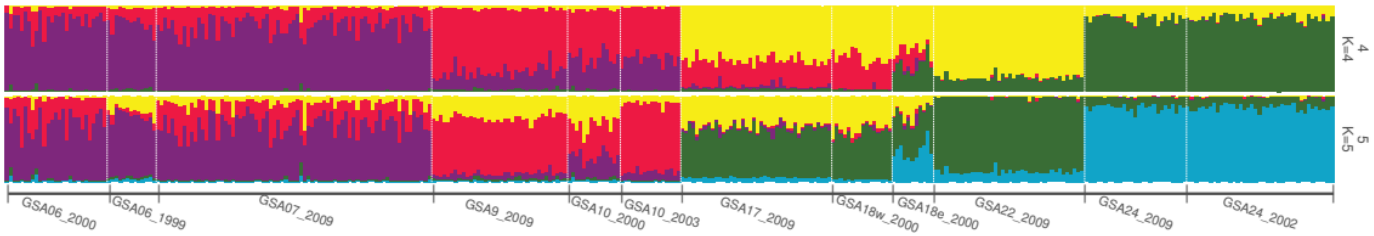


Supplementary Figure 1.5. The mean L(K) over 20 iterations for each K for neutral (A) and outlier (B) SNPs datasets. The highest mean L(K) value corresponds to the optimal K, and it is shown in red dashed lines.

A



B



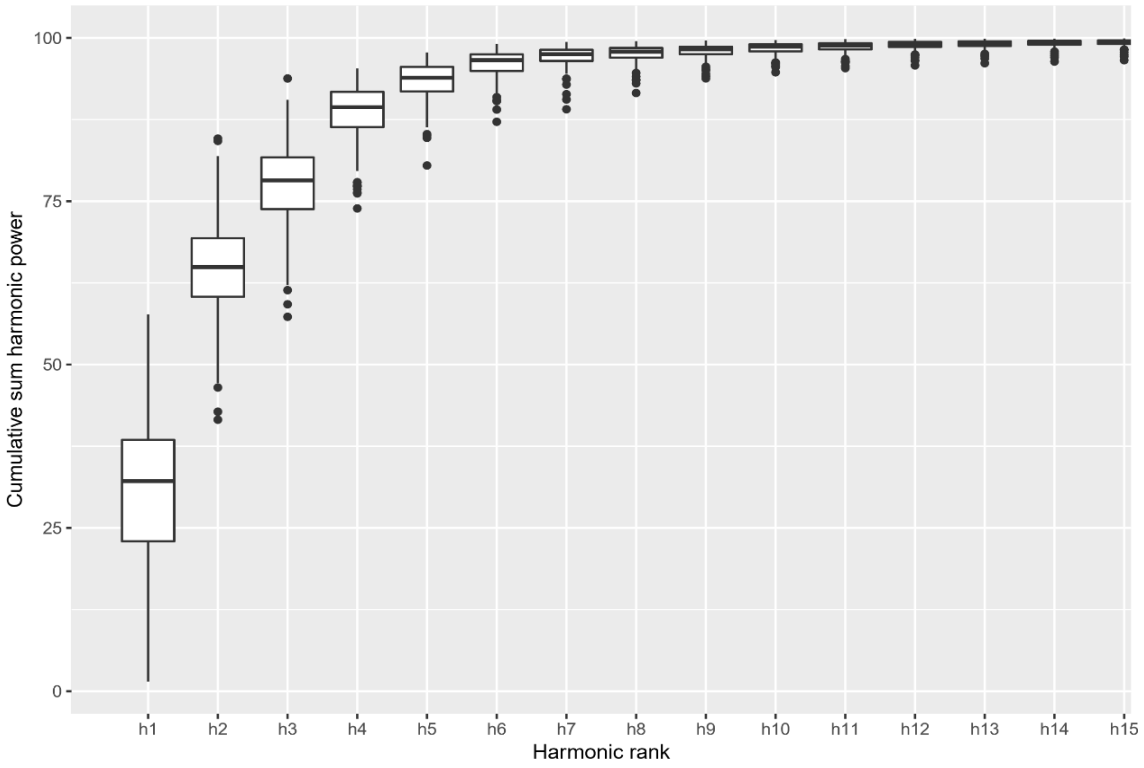
Supplementary Figure 1.6. Graphical representation of the Bayesian clustering analysis of STRUCTURE for neutral (A) and outlier (B) SNPs datasets.

2.2 Otolith analysis

Supplementary Table 2.1. Results of PERMANOVA analysis using otolith shape: shape indices (SIs), elliptical Fourier descriptors (EFDs).

	Pairwise comparison	F model	p-adjusted	Significance
SIs	GSA7 2009 vs GSA9 2009	23.6415	0.0025	*
	GSA7 2009 vs GSA17 2009	15.0566	0.0025	*
	GSA7 2009 vs GSA22 2009	13.7214	0.0025	*
	GSA7 2009 vs GSA24 2009	31.4544	0.0025	*
	GSA9 2009 vs GSA17 2009	2.084	0.1277	
	GSA9 2009 vs GSA22 2009	3.9083	0.01	*
	GSA9 2009 vs GSA24 2009	5.9418	0.004	*
	GSA17 2009 vs GSA22 2009	0.4822	0.6593	
	GSA17 2009 vs GSA24 2009	4.0592	0.0125	
	GSA22 2009 vs GSA24 2009	5.0402	0.005	*
EFDs	GSA7 2009 vs GSA9 2009	1.5526	0.0012	*
	GSA7 2009 vs GSA17 2009	1.9799	0.0012	*
	GSA7 2009 vs GSA22 2009	2.6622	0.0012	*
	GSA7 2009 vs GSA24 2009	1.7576	0.0012	*
	GSA9 2009 vs GSA17 2009	1.5848	0.0033	*
	GSA9 2009 vs GSA22 2009	2.3969	0.0012	*

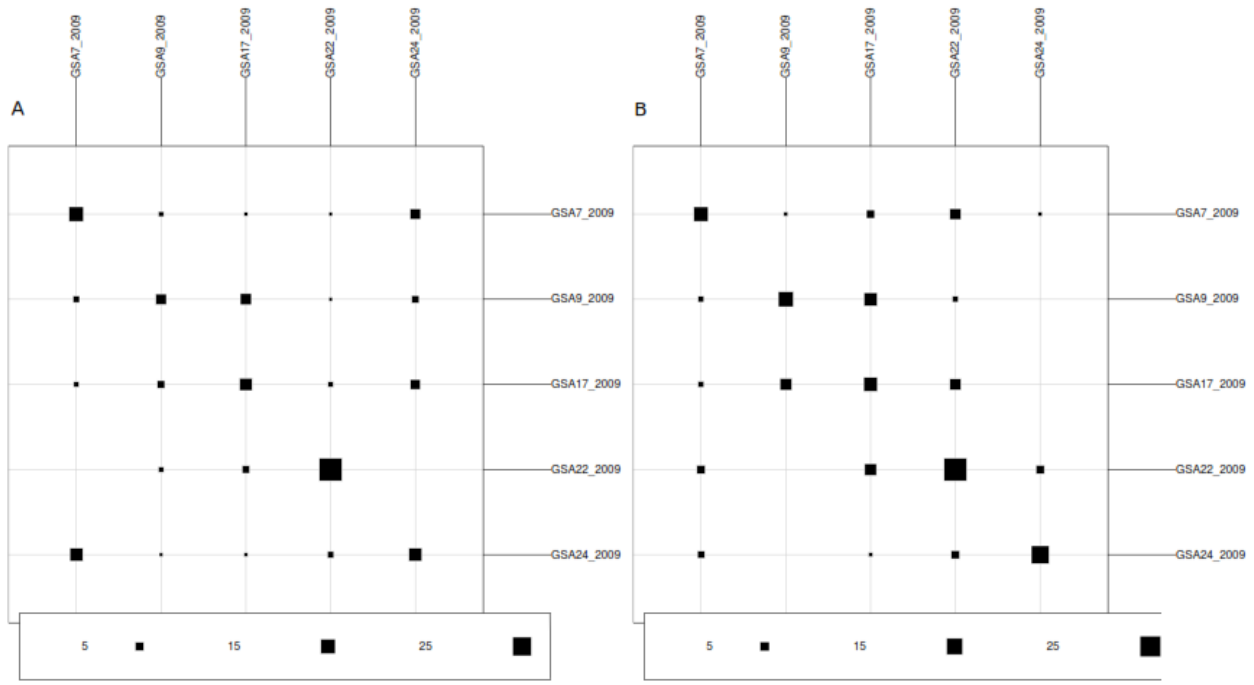
	GSA9 2009 vs GSA24 2009	1.3777	0.007	*
	GSA17 2009 vs GSA22 2009	3.4781	0.0012	*
	GSA17 2009 vs GSA24 2009	2.0571	0.0012	*
	GSA22 2009 vs GSA24 2009	2.383	0.0012	*



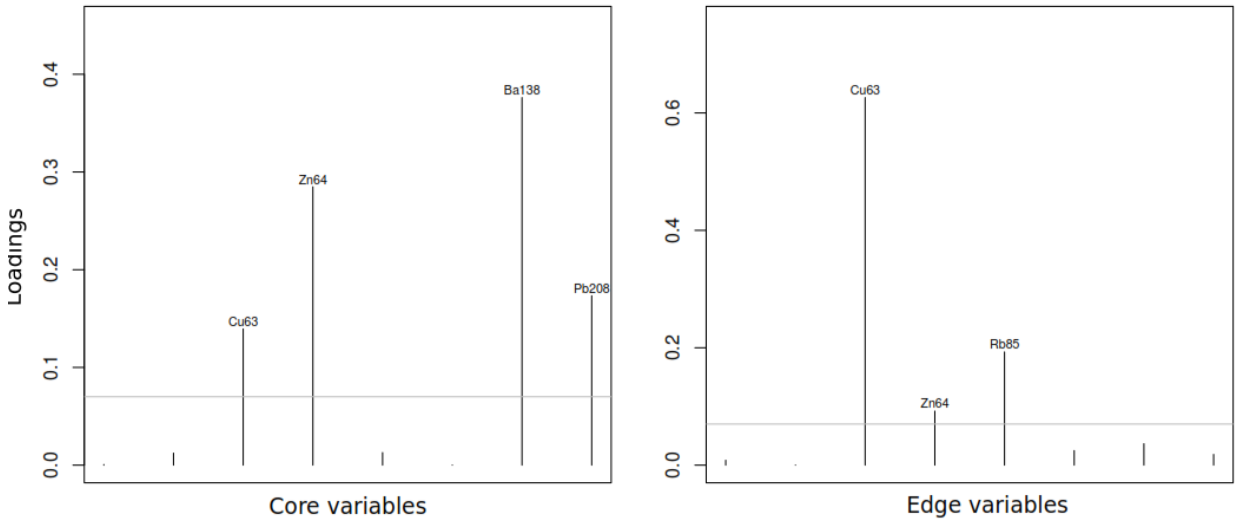
Supplementary Figure 2.1. Cumulative Fourier power in relation to the number of harmonics describing the otolith shape. Each harmonic rank is composed of 3 harmonics.

Supplementary Table 2.2. Cross-validation classification matrix from CAP analysis using otolith shape: shape indices (SIs), elliptical Fourier descriptors (EFDs) and both (SIs + EFDs).

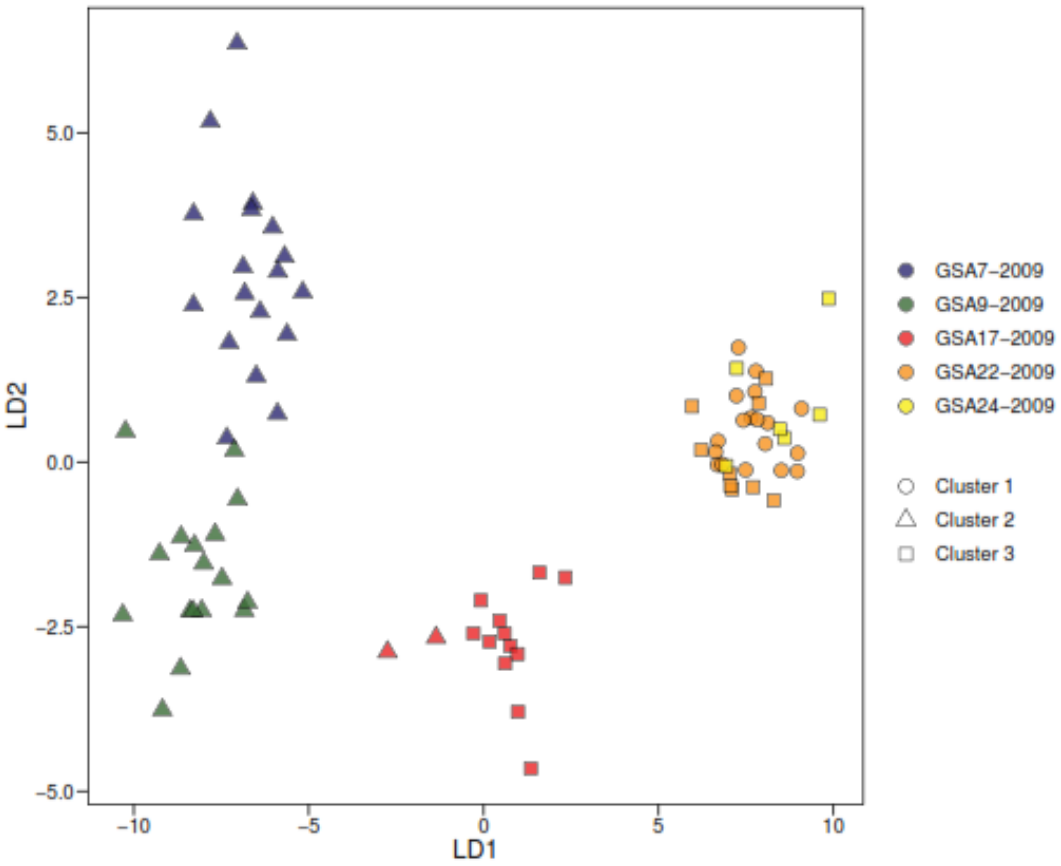
Original sites		Predicted sites					Total	%correct
		GSA7_2009	GSA9_2009	GSA17_2009	GSA22_2009	GSA24_2009		
SIs	GSA7_2009	21	0	0	7	0	28	75
	GSA9_2009	2	13	11	11	1	38	34.21
	GSA17_2009	1	12	4	19	6	42	9.52
	GSA22_2009	6	10	4	18	7	45	40
	GSA24_2009	0	6	4	6	13	28	44.83
	Total							37.91
EFDs	GSA7_2009	20	4	5	0	1	28	66.67
	GSA9_2009	3	17	8	7	4	38	43.59
	GSA17_2009	3	12	29	0	0	42	65.91
	GSA22_2009	2	0	1	44	0	45	93.62
	GSA24_2009	2	4	3	0	20	28	68.97
	Total							68.78
SIs + EFDs	GSA7_2009	22	0	2	3	0	28	82.14
	GSA9_2009	2	18	11	4	3	38	47.37
	GSA17_2009	2	9	31	0	0	42	73.81
	GSA22_2009	0	2	0	42	1	45	93.33
	GSA24_2009	0	3	5	2	18	28	64.29
	Total							72.93



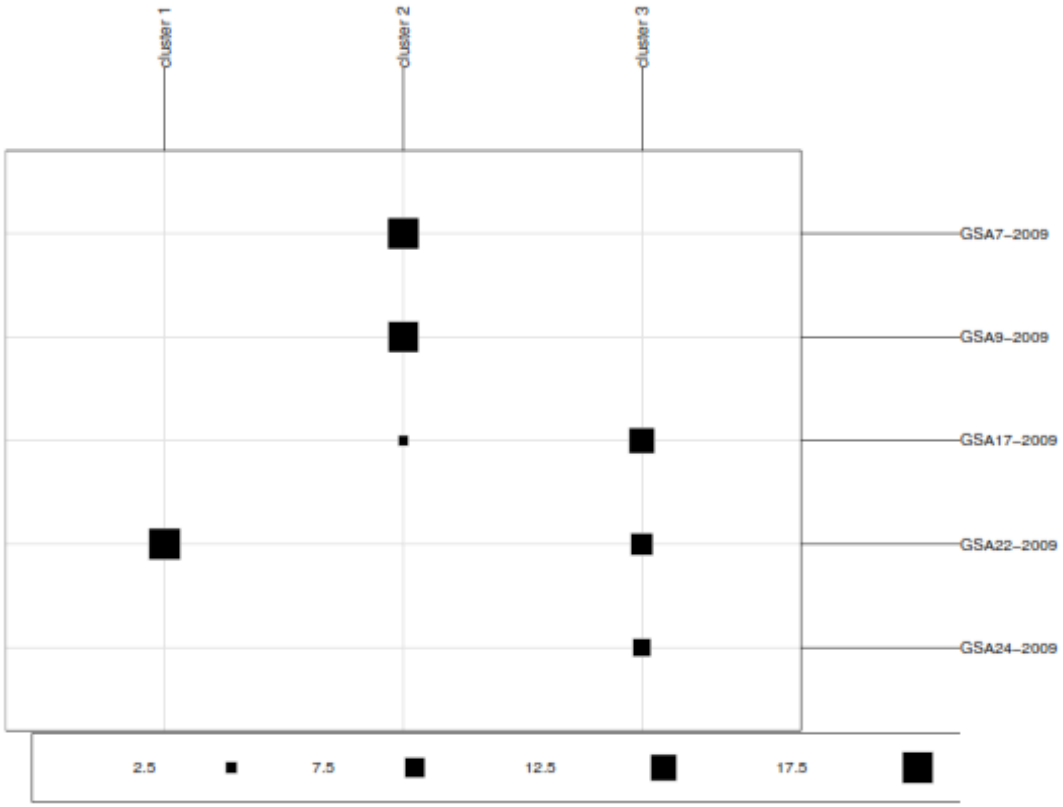
Supplementary Figure 2.2. Membership counts plot showing the number of corrected assignments to the group of origin for core (A) and edge (B) data respectively. Rows correspond to actual groups, while columns correspond to inferred groups.



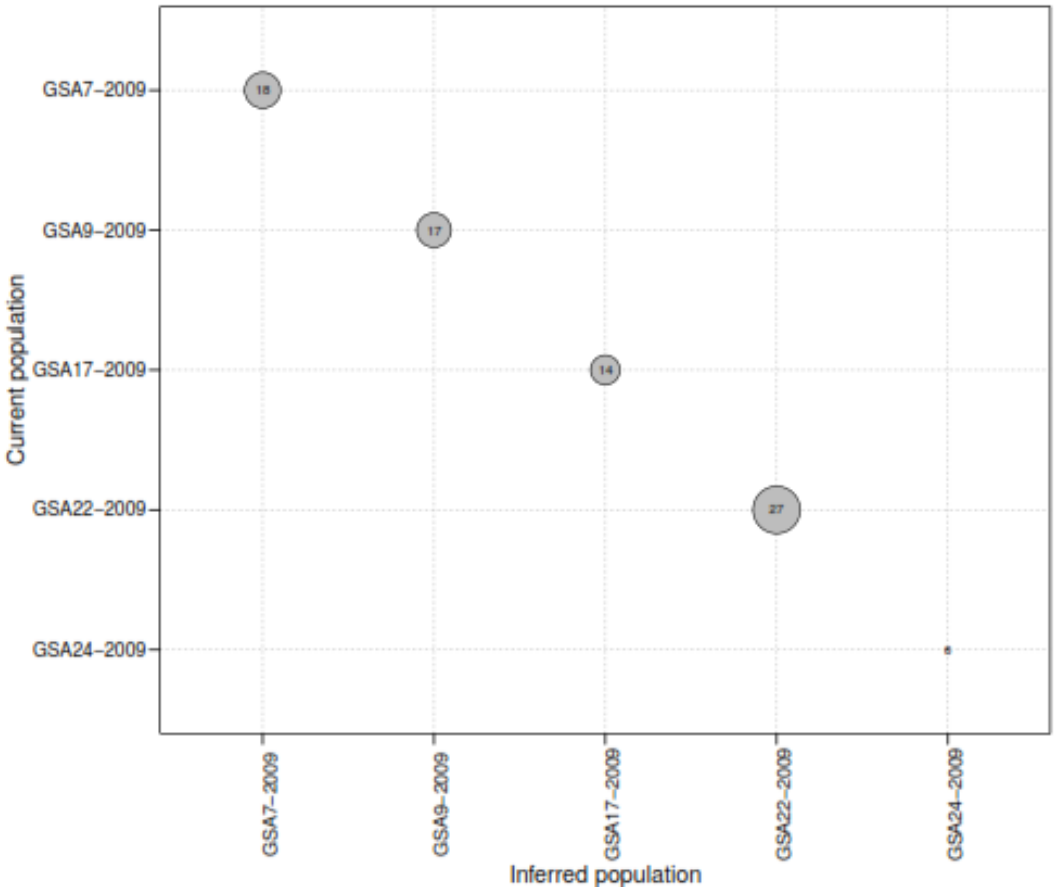
Supplementary Figure 2.3. Loadings of elements (^{63}Cu, ^{64}Zn, ^{85}Rb, ^{138}Ba, ^{208}Pb) for the first and second DAPC components for core and edge data. The plot shows the weight of each variable (loadings) in a given analysis.



Supplementary Figure 2.4. Discriminant Analysis of Principal Components (DAPC) plots of the 5 population samples of *Solea solea* included in the combined dataset (380 SNPs, shape indexes, elemental composition for both core and edge available for 82 individuals). Geographical population samples are colour coded according to sampling site, with Site ID reported as in Table 1. The subdivision of individuals according to identified clusters is shown assigning to data points different geometric shapes.

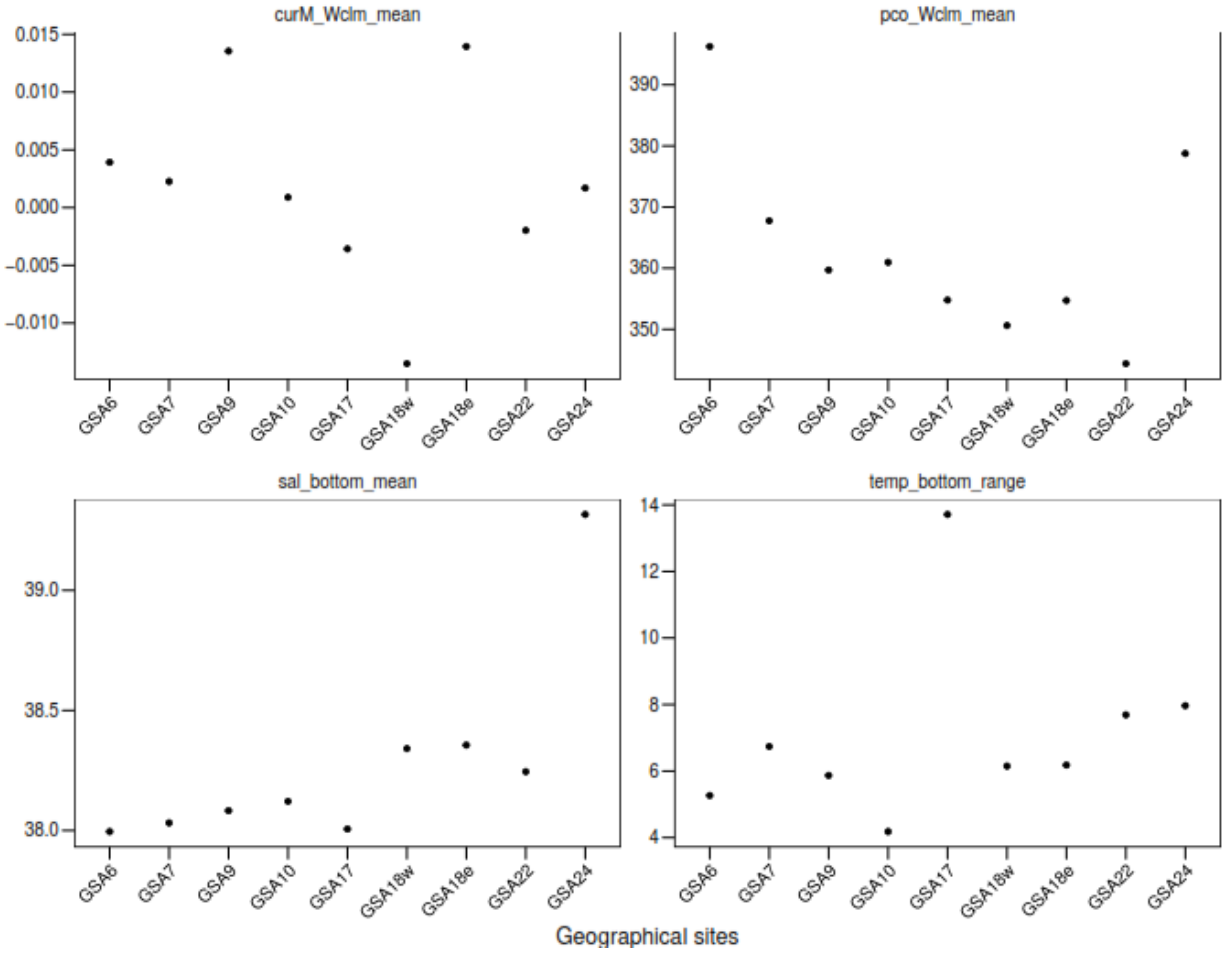


Supplementary Figure 2.5. Membership counts plot showing the number of corrected assignments to the group of origin for combined dataset (380 SNPs, shape indexes, elemental composition for both core and edge available for 82 individuals). Rows correspond to actual groups, while columns correspond to cluster groups.

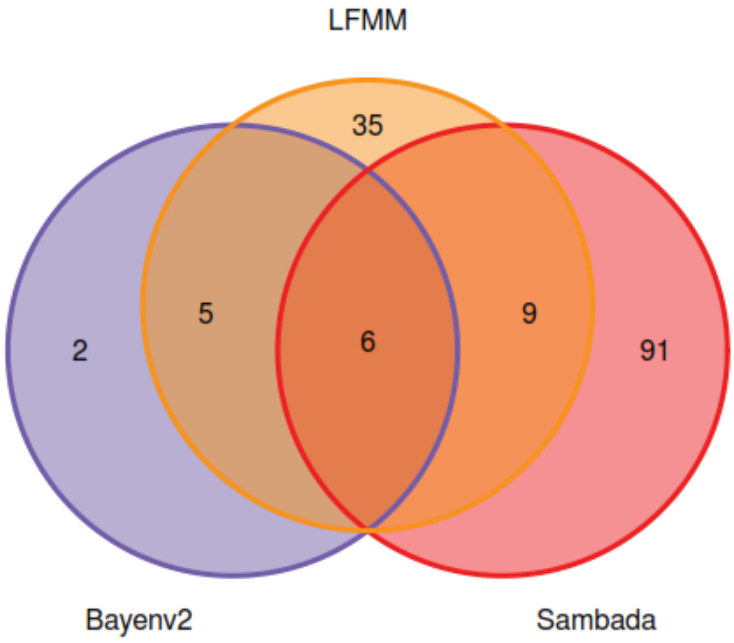


Supplementary Figure 2.6. Comparison of individual assignment between inferred groups and actual samples corresponding to sampling sites resulted by DAPC analysis for combined dataset.

2.3 Environmental analysis

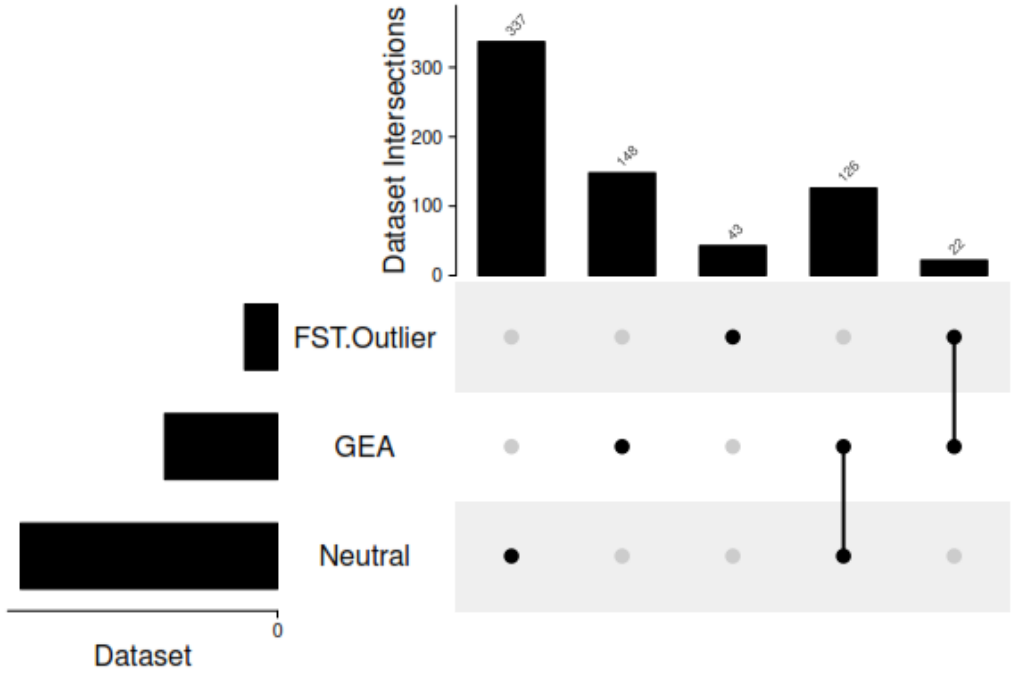


Supplementary Figure 3.1. Plot represents the environmental values with their corresponding measures used in this study for macro-area reported as the corresponding GSA: the mean meridional component of the currents (northward) (curM, m/s) using the weighted average value in the water column (Wclm) (curM_Wclm_mean), the range of potential temperature (temp, °C°) at the bottom (temp_bottom_range), the mean salinity (sal, psu) at the bottom (sal_bottom_mean) and the mean CO_2 (ocean pCO_2 expresses as carbon dioxide partial pressure) (pco, Pa) (pco_Wclm_mean).



Supplementary Figure 3.2. Venn diagram of candidate SNPs identified by *Samβada*, *LFMM* and *Bayenv* associated with curM_Wclm_mean, temp_bottom_range, sal_bottom_mean and pco_Wclm_mean.

Supplementary Figure 3.3. Maps showing 5 dbMEMs eigenvectors used as spatial variables with positive and negative eigenvalues represented by black and white squares, respectively.

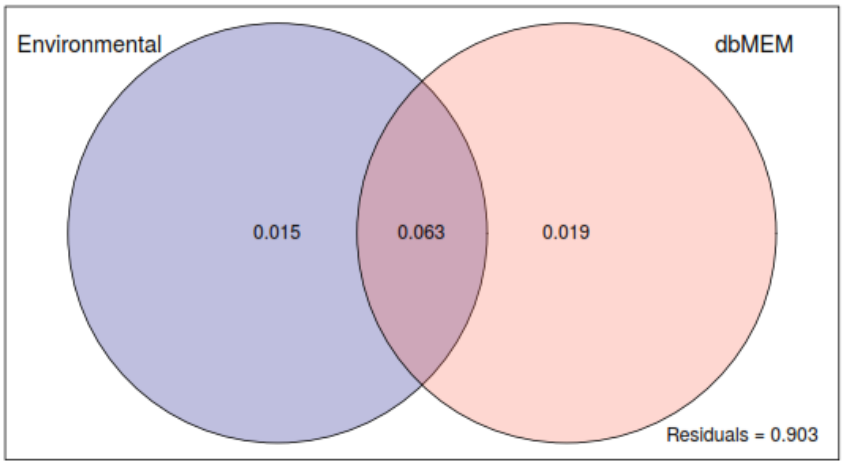


Supplementary Figure 3.4. UpSet diagram: matrix layout for all intersections of the three datasets (Neutral, Outlier and GEA) sorted by their number of SNPs. Dark circles in the matrix indicate the datasets that are part of the intersection. Vertical bars show the size of the intersection. The first three vertical bars indicate the single dataset. The total number of loci included in each dataset is displayed by the horizontal bars on the left. The intersection and the graph are provided using the ComplexHeatmap package (Gu, 2022).

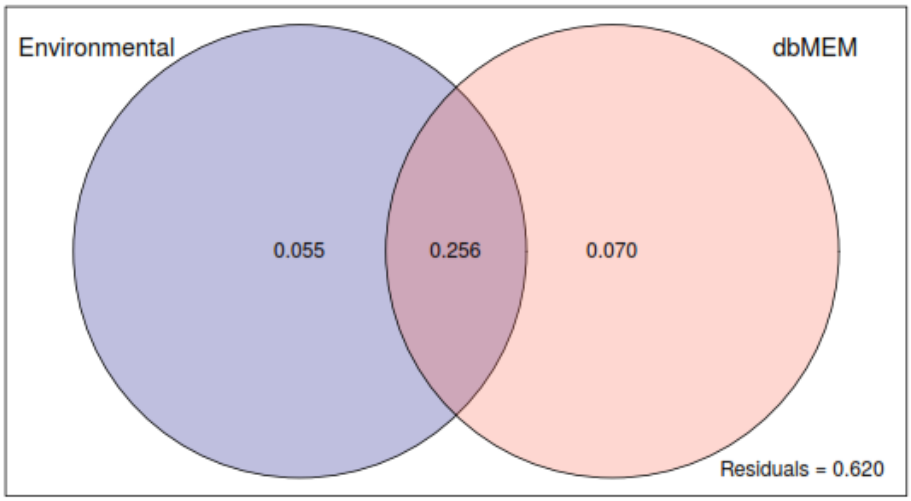
Supplementary Table 3.1. Details of 16 out of 19 markers that are in common with the outlier dataset identified by Diopere et al. (2018) in Atlantic population samples. The table provides the details of these 16 loci identified in our study as neutral (12 SNP loci) or outlier (4 SNP loci), SNPs identified by Samβada, LFMM and Bayenv associated with which environmental variables (curM Wclm mean, temp bottom range, sal bottom mean and pco Wclm mean), and SNPs identified by at least one GEA methods (6 SNP loci).

SNPs name	**Neutral**	**Outlier**	**GEA methods**	**Samβada**	***LFMM***	***Bayenv***
SNP1129	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP116	TRUE	FALSE	TRUE	TRUE (sal_bottom_mean)	FALSE	FALSE
SNP1199	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1200	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP1347	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP1353	FALSE	TRUE	TRUE	TRUE (pco_Wclm_mean)	FALSE	FALSE
SNP1354	FALSE	TRUE	TRUE	TRUE (sal_bottom_mean)	TRUE (sal_bottom_mean, pco_Wclm_mean)	TRUE (pco_Wclm_mean)
SNP1432	TRUE	FALSE	TRUE	TRUE (temp_bottom_range, sal_bottom_mean)	FALSE	FALSE
SNP1466	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP200	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP228	FALSE	TRUE	FALSE	FALSE	FALSE	FALSE
SNP573	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP609	TRUE	FALSE	TRUE	FALSE	TRUE (sal_bottom_mean)	FALSE
SNP737	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE
SNP789	TRUE	FALSE	TRUE	TRUE (sal_bottom_mean)	TRUE (sal_bottom_mean)	FALSE
SNP933	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE

2.4 Redundancy analysis



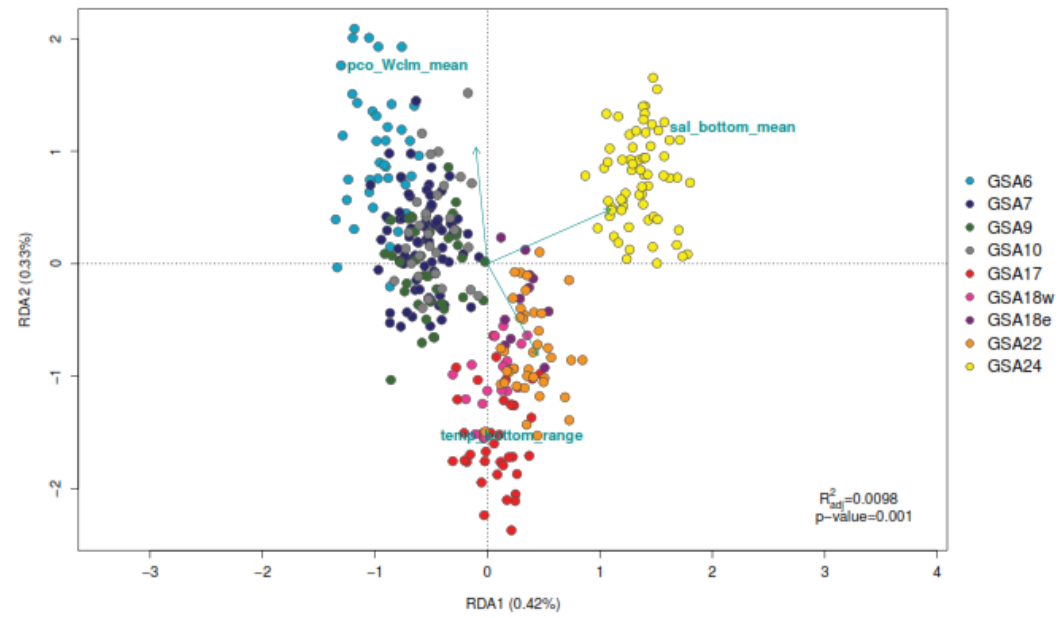
Supplementary Figure 3.5. Results from variation partitioning analysis on neutral SNPs expressed by the adjusted coefficient of determination (R^2_{adj}). Venn's diagram shows the independent and shared variance explained by environmental and spatial variables.



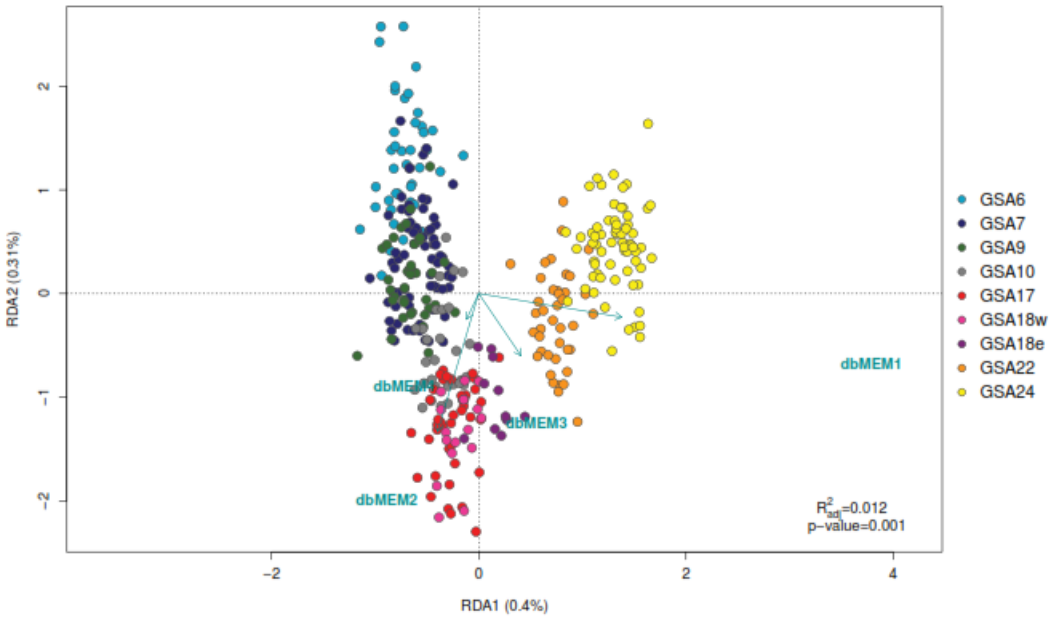
Supplementary Figure 3.6. Results from variation partitioning analysis on outlier SNPs expressed by the adjusted coefficient of determination (R^2_{adj}) Venn's diagram shows the independent and shared variance explained by environmental and spatial variables.

Partial RDA performed with environmental variables as condition, confirmed that most of the genetic variation both for neutral and outlier structure was explained by spatial variables (Supplementary Figure 3.7, 3.8, Supplementary Table 3.2).

A

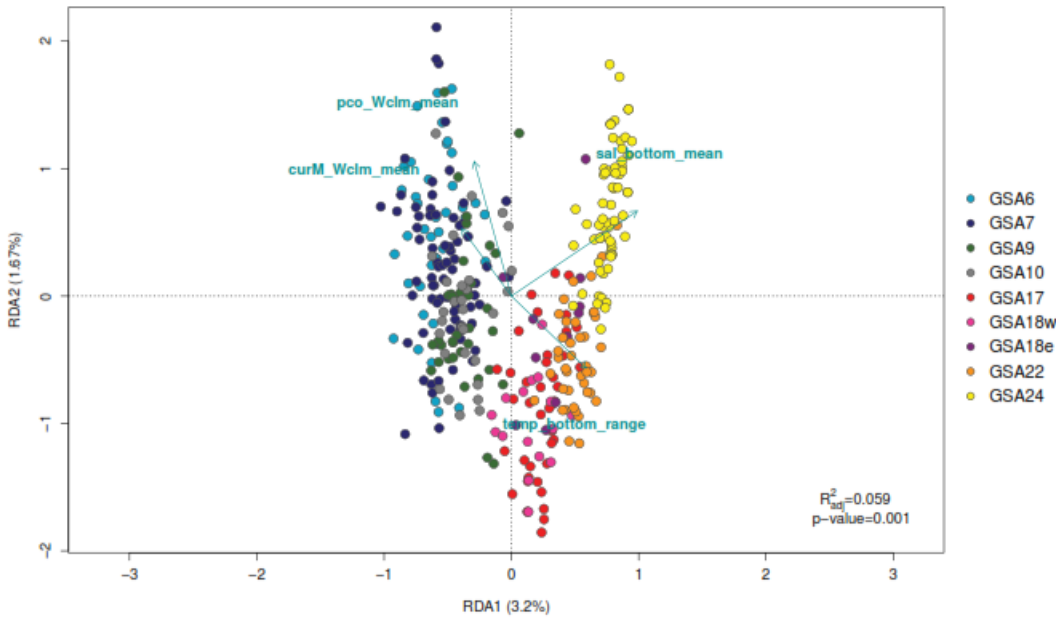


B

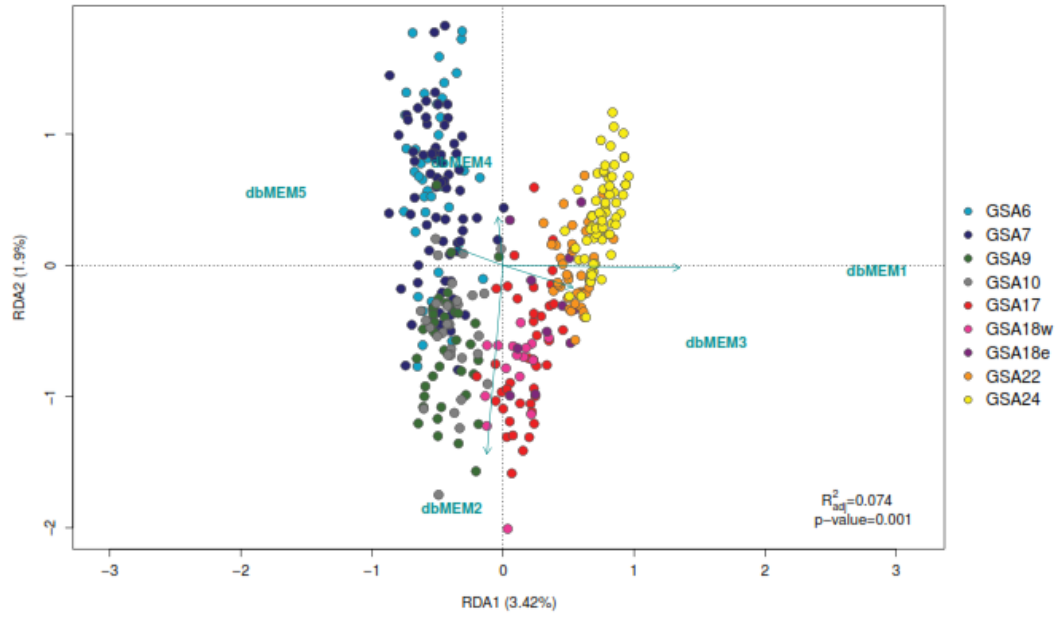


Supplementary Figure 3.7. Partial redundancy analysis (RDA) on environmental (A) and spatial (B) variables performed on neutral SNPs. Environmental and spatial variables are shown with arrows.

A



B



Supplementary Figure 3.8. Partial redundancy analysis (RDA) on environmental (A) and spatial (B) variables performed on outlier SNPs. Environmental and spatial variables are shown with arrows.

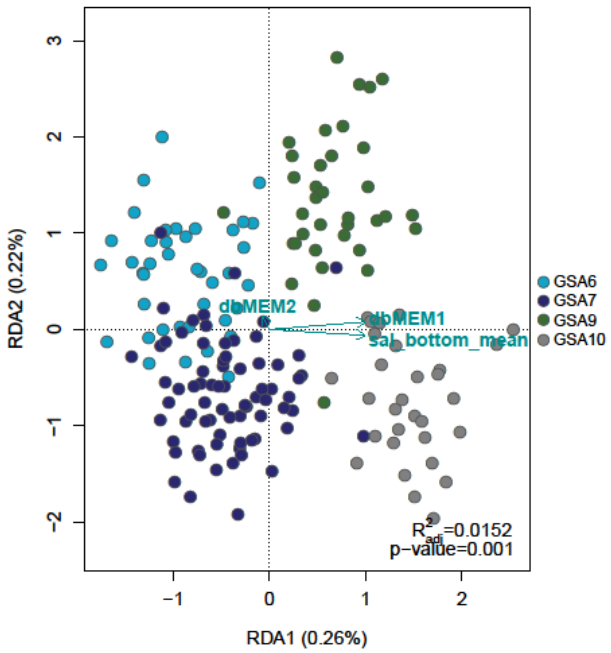
Supplementary Table 3.2. Results from RDA and partial RDA for each response variables divided in neutral and outlier SNPs.

		Selected variables (*ordistep* function)			
SNPs	Analysis	Environmental	Spatial	p	R^2_{adj}
Neutral	RDA			0.0010	0.0152
		sal_Wclm_mean*			
		temp_bottom_range***			
		pco_Wclm_mean*			
			dbMEM1*		
			dbMEM2***		
			dbMEM3**		
	partial RDA			0.0010	0.0098
		pho_Wclm_mean***			
		temp_bottom_range***			
		dox_Wclm_mean***			
	partial RDA			0.0010	0.0120
			dbMEM1***		
			dbMEM2***		
			dbMEM3***		
			dbMEM4***		
Outlier	RDA			0.0010	0.0850
		sal_Wclm_mean**			
		temp_bottom_range***			
		pco_Wclm_mean***			
			dbMEM1*		
			dbMEM2**		
			dbMEM3***		
			dbMEM4***		
	partial RDA			0.0010	0.0590
		sal_Wclm_mean***			
		temp_bottom_range***			
		pco_Wclm_mean***			
		curM_Wclm_mean***			
	partial RDA			0.0010	0.0740
			dbMEM1***		

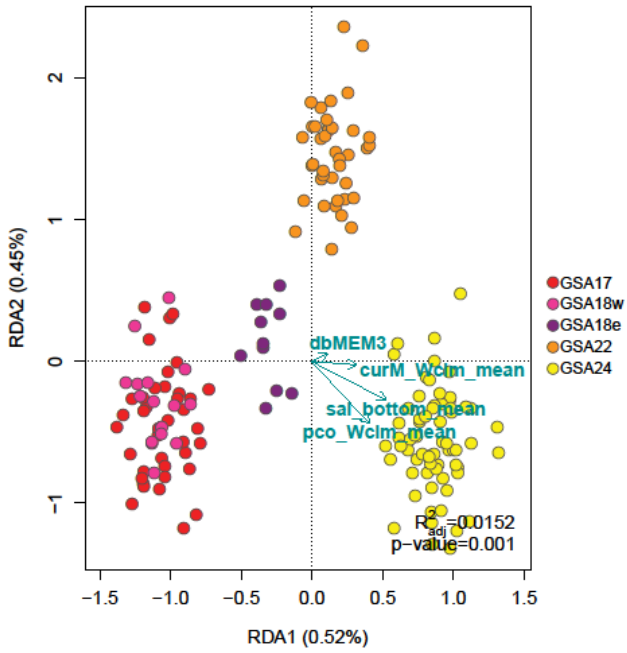
		Selected variables (*ordistep* function)			
			dbMEM2***		
			dbMEM3***		
			dbMEM4***		
			dbMEM5***		

Significant explanatory variables are indicated with the following symbols:
$p < 0.05$
* $p < 0.01$
** $p = 0.001$

A



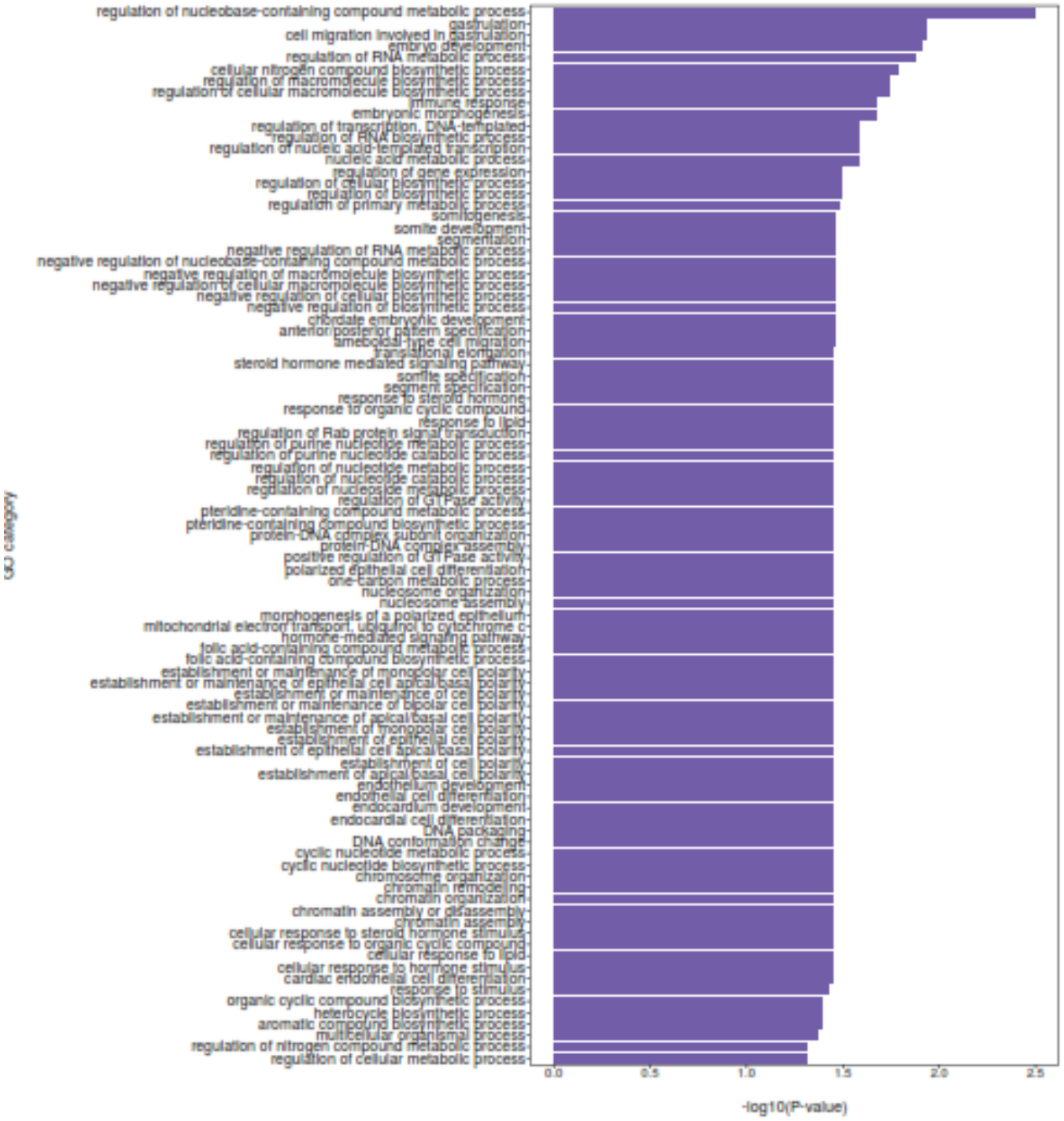
B



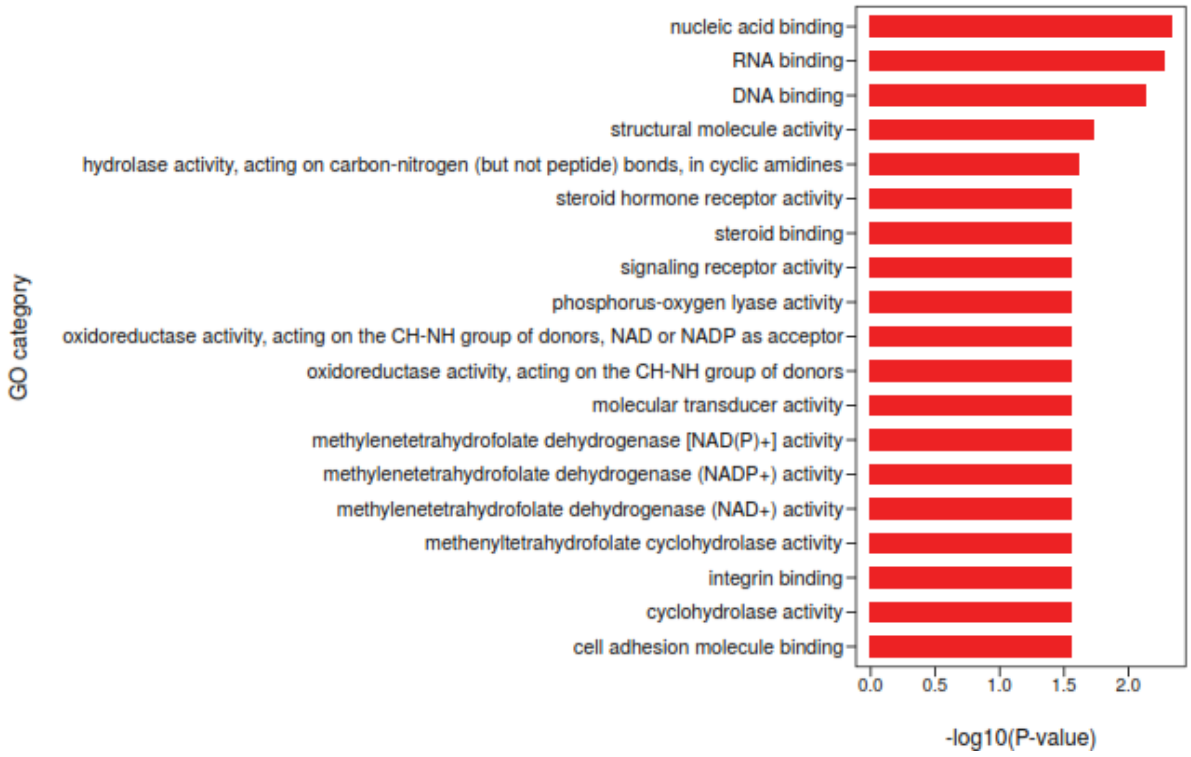
Supplementary Figure 3.9. Redundancy analysis (RDA) performed on western (A) and eastern (B) Mediterranean SNPs cluster datasets from population samples of *Solea solea* following the forward and backward selection of variables using *ordistep* function. Spatial (dbMEMs) and environmental variables found as significant predictors are shown with arrows.

The results of variation partitioning based on western SNPs cluster indicated that spatial variables (0.6%) explained approximately the same individual fraction of variance as the environmental variables (0.4%) and as the shared variance (0.6%). In contrast, the environmental variables explained more of the individual fraction of variance in the eastern SNPs cluster (6.4%), whereas spatial variables explained 1.1% that was the same individual fraction of variance as the shared variance (1.6%). The results of variation partitioning based on otolith dataset indicated that the spatial variables explained more of the individual fraction of variance (17.0%), whereas environmental variables explained 2.1%. Shared variance (1.0%) resulted in the lowest amount of explained variance.

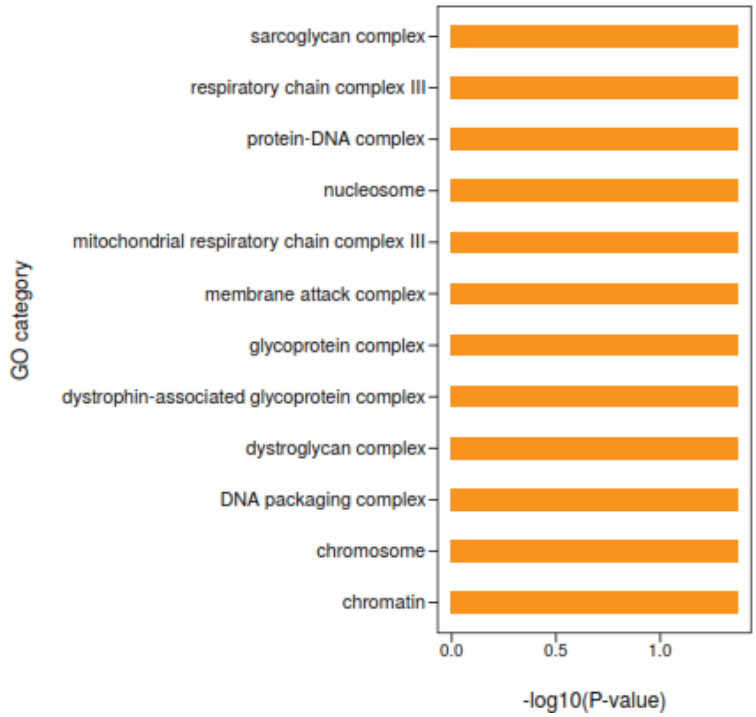
2.5 Gene Ontology



Supplementary Figure 4.1. GO terms enriched in the biological process aspect. Names of GO terms founded significantly enriched ($p < 0.05$) are reported along the vertical axes.



Supplementary Figure 4.2. GO terms enriched in the molecular function aspect. Names of GO terms founded significantly enriched ($p < 0.05$) are reported along the vertical axes.



Supplementary Figure 4.3. GO terms enriched in the cellular component aspect. Names of GO terms founded significantly enriched ($p < 0.05$) are reported along the vertical axes.

Supplementary Table 4.1. SNPs associated with GO terms significantly enriched ($p < 0.05$) in at least one of the three aspects of Gene Ontology, biological processes (BP), molecular functions (MF), cellular components (CC). These 22 markers are all included in the outlier dataset, with 12 (*) of them also included in the environmental dataset.

SNPs	Gene symbol	Gene description	Aspects
SNP1012*	sgcb	sarcoglycan, beta (dystrophinassociated glycoprotein)	CC
SNP1023*	LOC104962262	titinlike	CC, MF, BP
SNP206	LOC119503422	cytochrome bc1 complex subunit 7	CC, BP
SNP398*	c7a	complement component 7a	CC, BP
SNP1293	fn1a	fibroectin 1a	MF, BP
SNP1531	Erbeta		MF, BP
SNP943	mthfd2	Methenyltetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	MF, BP
SNP250*	ybx1	Y box binding protein 1	MF, BP
SNP1058*	ampd1	adenosine monophosphate deaminase 1 (isoform M)	MF, BP
SNP528	znf106a	zinc finger protein 106	MF
SNP530	znf106a	zinc finger protein 106	MF
SNP569	cirbpa	cold inducible RNA binding protein a	MF, BP
SNP90*	fxr1	fragile X mental retardation, autosomal homolog 1	MF, BP
SNP1353*	LOC111650759	keratin, type I cytoskeletal 13-like	MF, BP
SNP1354*	LOC111650759	keratin, type I cytoskeletal 13-like	MF, BP
SNP73*	LOC103378706	60S acidic ribosomal protein P2-like	MF, BP
SNP854	cd74	CD74 molecule, major histocompatibility complex, class II invariant chain a	BP
SNP1439*	ldha	lactate dehydrogenase A4	BP
SNP398*	selenop	complement component 7a	BP
SNP464*	LOC118300284	heat shock protein, alphacrystallinrelated, b11	BP
SNP877*	selenop	selenoprotein P	BP
SNP228	LOC103362009	troponin C, skeletal musclelike	BP
SNP476	tcap	titincap (telethonin)	BP

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