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10 (A)

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16 **Table S2.** Population summary statistics from *Stacks* for (A) the single SNP per marker data only including variant
17 sites and (B) from microhaplotype data including all variant and fixed RAD loci. The percentage polymorphic
18 represents the proportion of nucleotides that are variant for the population within all RAD loci, including those RAD
19 loci that have no polymorphisms present. The number of individuals is a fractional number due to missing data at
20 some loci.

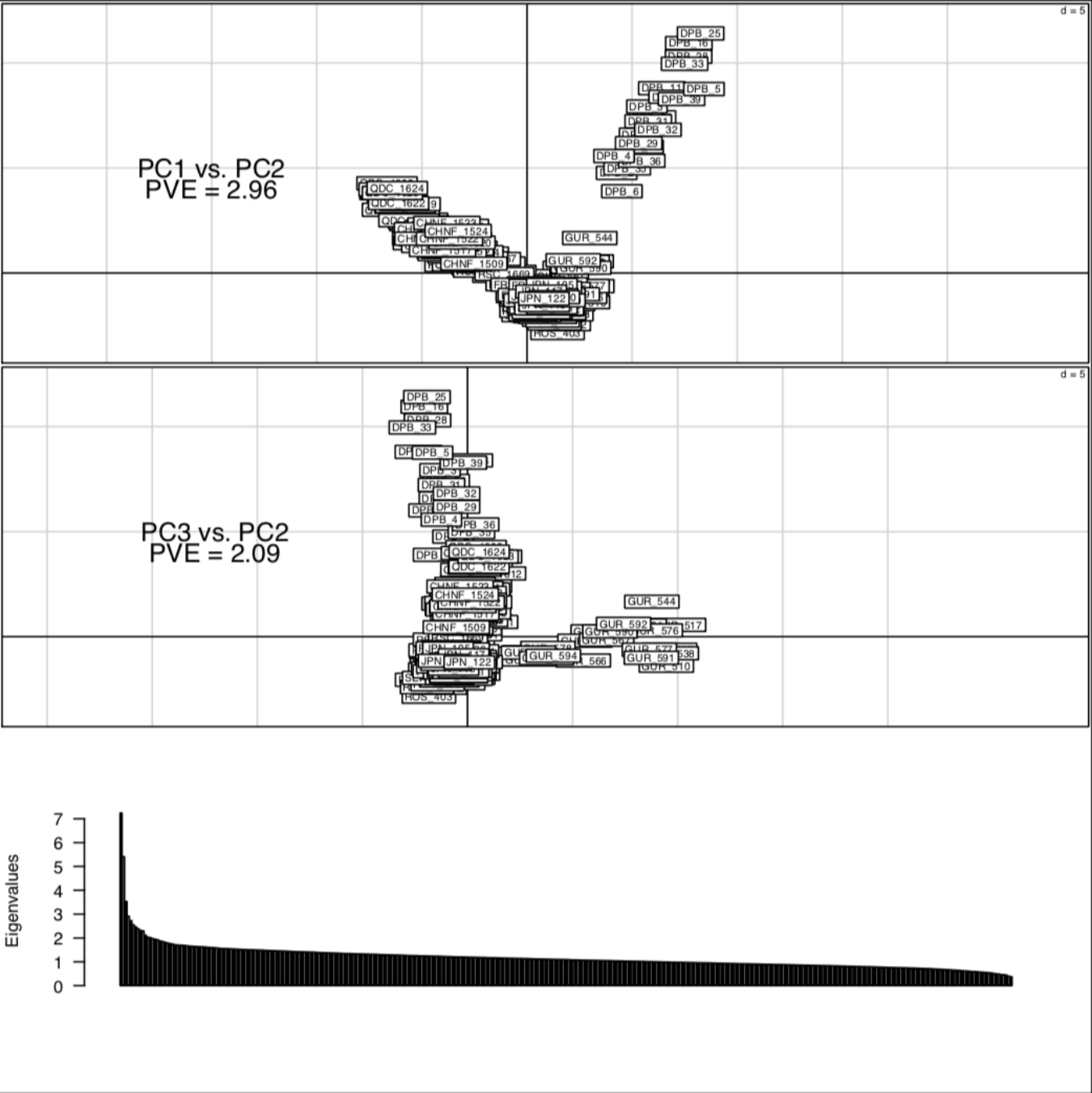
21 (A)

Pop ID	Num. Indiv.	Obs. Het.	Std. Err.	Obs. Hom.	Std. Err.	Fis	StdErr	95% C.I.
PIP	23.1	0.07553	0.00084	0.92447	0.00084	0.072	0.016	0.041-0.103
PEN	32.5	0.07680	0.00082	0.92320	0.00082	0.086	0.021	0.045-0.127
DPB	18.9	0.08179	0.00107	0.91821	0.00107	0.031	0.012	0.008-0.053
ROS	21.5	0.07834	0.00089	0.92166	0.00089	0.064	0.013	0.038-0.09
PENF	22.7	0.07745	0.00084	0.92255	0.00084	0.074	0.012	0.05-0.098
SER	21.6	0.07735	0.00085	0.92265	0.00085	0.060	0.013	0.035-0.085
HIS	36.5	0.07720	0.00081	0.92280	0.00081	0.082	0.020	0.043-0.122
GUR	20.7	0.07918	0.00094	0.92082	0.00094	0.052	0.013	0.028-0.077
RSC	21.7	0.07732	0.00086	0.92268	0.00086	0.070	0.012	0.047-0.093
QDC	22.7	0.07847	0.00092	0.92153	0.00092	0.055	0.013	0.03-0.08
CHN	22.8	0.07531	0.00083	0.92469	0.00083	0.073	0.012	0.05-0.096
CHNF	22.6	0.07588	0.00085	0.92412	0.00085	0.073	0.013	0.048-0.098
FRA	21.8	0.07828	0.00084	0.92172	0.00084	0.079	0.011	0.057-0.101
FRAF	22.7	0.07866	0.00084	0.92134	0.00084	0.080	0.012	0.057-0.103
JPN	12.2	0.07931	0.00093	0.92069	0.00093	0.053	0.008	0.038-0.068

22 (B)

Pop ID	Num. Indiv.	Polymorphic Sites	Percent Polymorphic Loci
PIP	23.9	10951	0.28
PEN	33.6	12445	0.32
DPB	19.3	7244	0.19
ROS	22.1	10041	0.26
PENF	23.2	11056	0.29
SER	22.0	10702	0.28
HIS	37.4	12894	0.33
GUR	21.1	8623	0.22
RSC	22.0	10398	0.27
QDC	23.1	9174	0.24
CHN	23.1	10684	0.28
CHNF	23.1	10711	0.28
FRA	22.1	11134	0.29
FRAF	23.2	11291	0.29
JPN	12.5	8442	0.22

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26 **Figure S1.** Principal Components Analysis (PCA) of all samples using a single SNP per locus with all loci.
27 Sample IDs are plotted along PC 1 and 2 (A) or PC3 and 2 (B).
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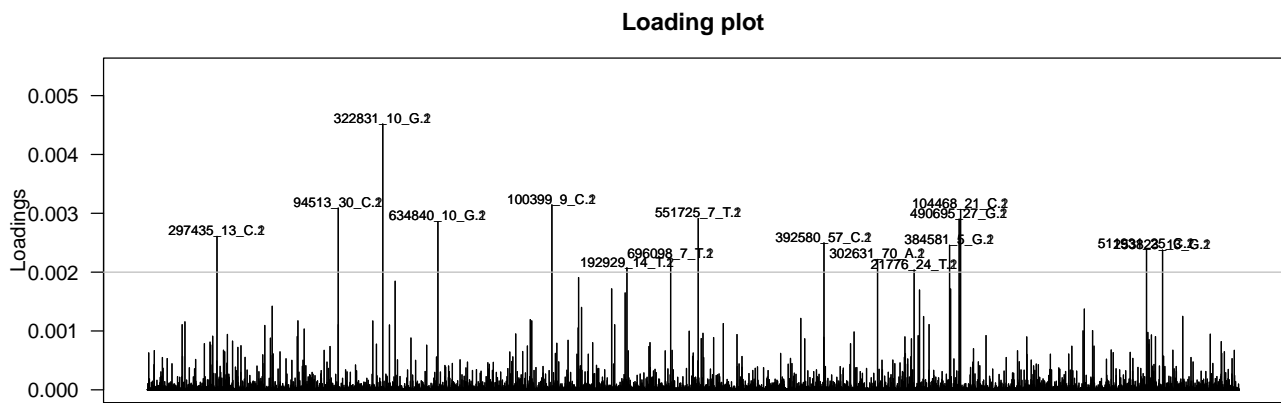


Figure S2. Discriminant Analysis of Principal Components (DAPC) marker loading values indicates that a small number of markers contributes the most to the DAPC differentiation. The 16 markers with loadings greater than 0.002 (grey line) are named.

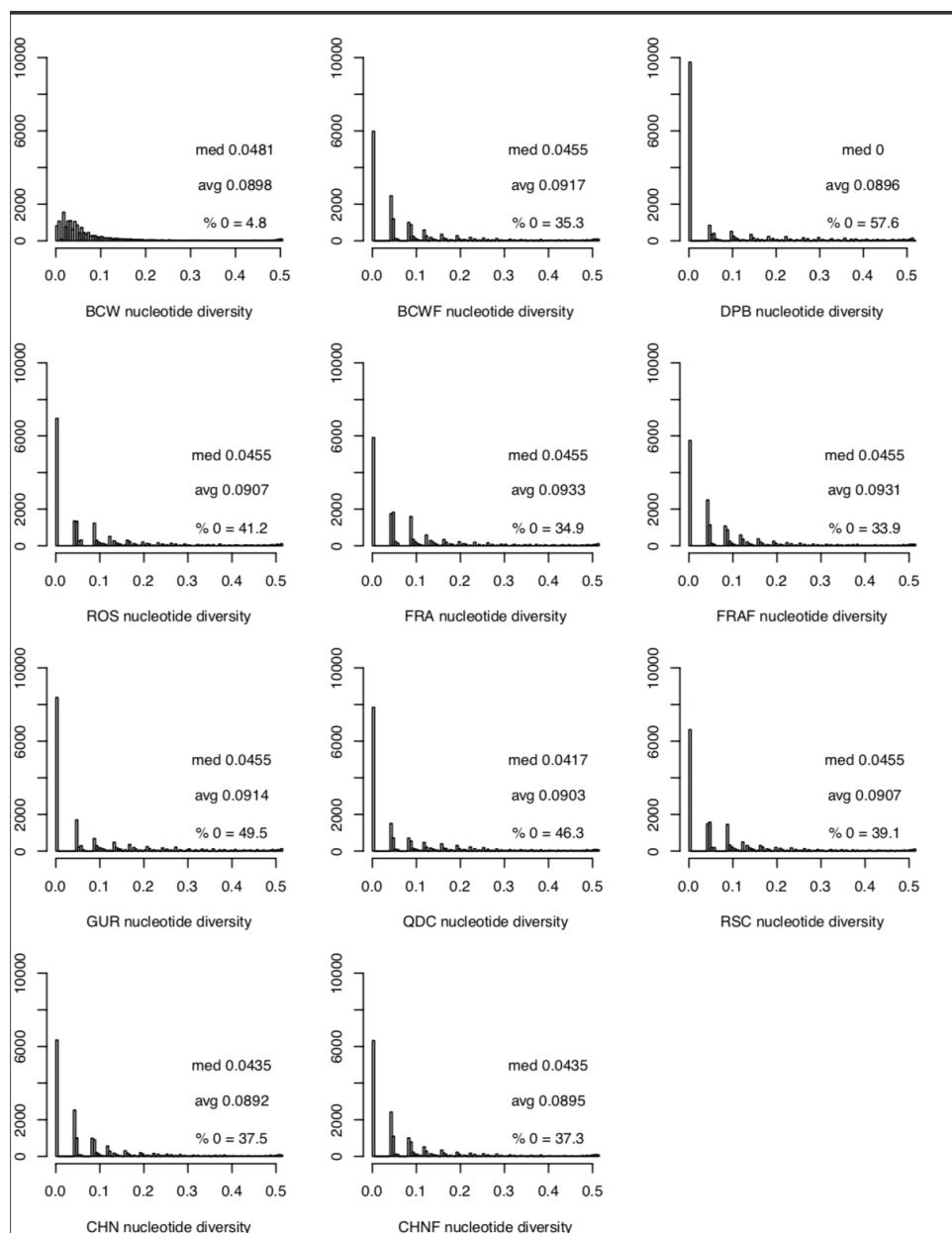
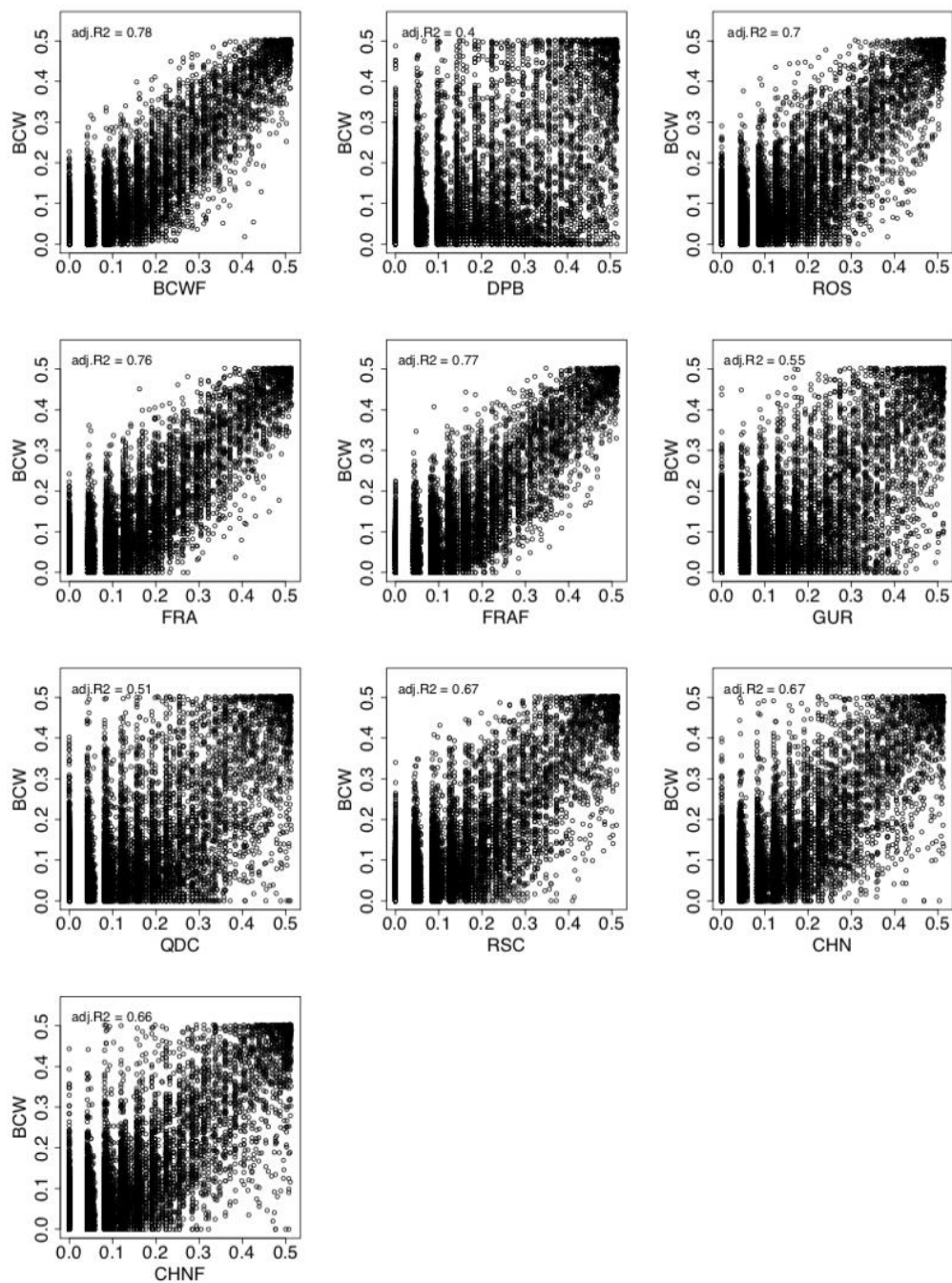


Figure S3. Per population distribution of nucleotide diversity (π), shown as frequencies of specific bins of nucleotide diversity as calculated by vcftools (--site-pi). Values are shown per population for the median, average, and percentage of markers with a zero value.

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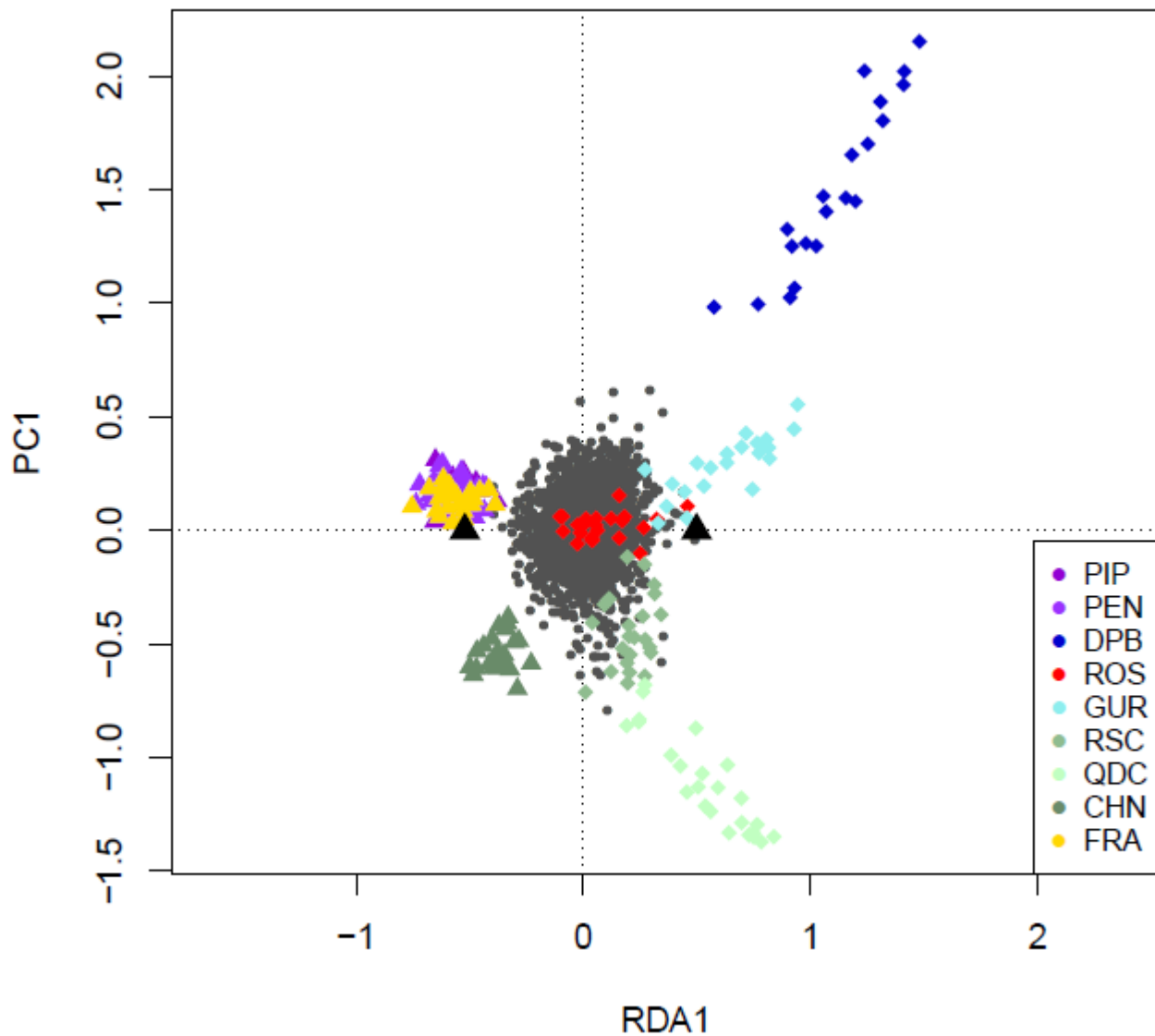
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Figure S4. Nucleotide diversity (π) for each marker (dot) correlated between each population with the BC wild population. Correlated populations with BC wild samples, such as France (FRAF) show high correlation coefficients ($R^2 = 0.77$), whereas the hatchery-farmed populations that are more divergent have in general lower correlation, such as GUR ($R^2 = 0.55$), QDC ($R^2 = 0.51$), and DPB ($R^2 = 0.4$). Not all hatchery-farm populations have such low correlation, and are typically more similar to local wild populations, such as ROS and RSC ($R^2 = 0.7$ and 0.67 , respectively).



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51 **Figure S5.** Comparison between Redundancy Analysis (RDA) and PCA in differentiating populations. RDA1
 52 differentiated hatchery/hatchery-farmed samples (coloured triangles) from naturalized/wild samples (coloured
 53 diamonds). PC1 broadly separated the Chinese samples (negative PC1) from the BC samples, as well as separating
 54 out the DPB samples (positive PC1). The tight clustering of naturalized samples along PC1 and RDA1 contrasts that
 55 observed in the farmed samples, particularly for QDC, DPB, and GUR, which also display high genetic
 56 differentiation from other populations. The grey circles are individual loci. The black triangles indicate the average
 57 position along RDA1 of the two groupings, farms or wild.

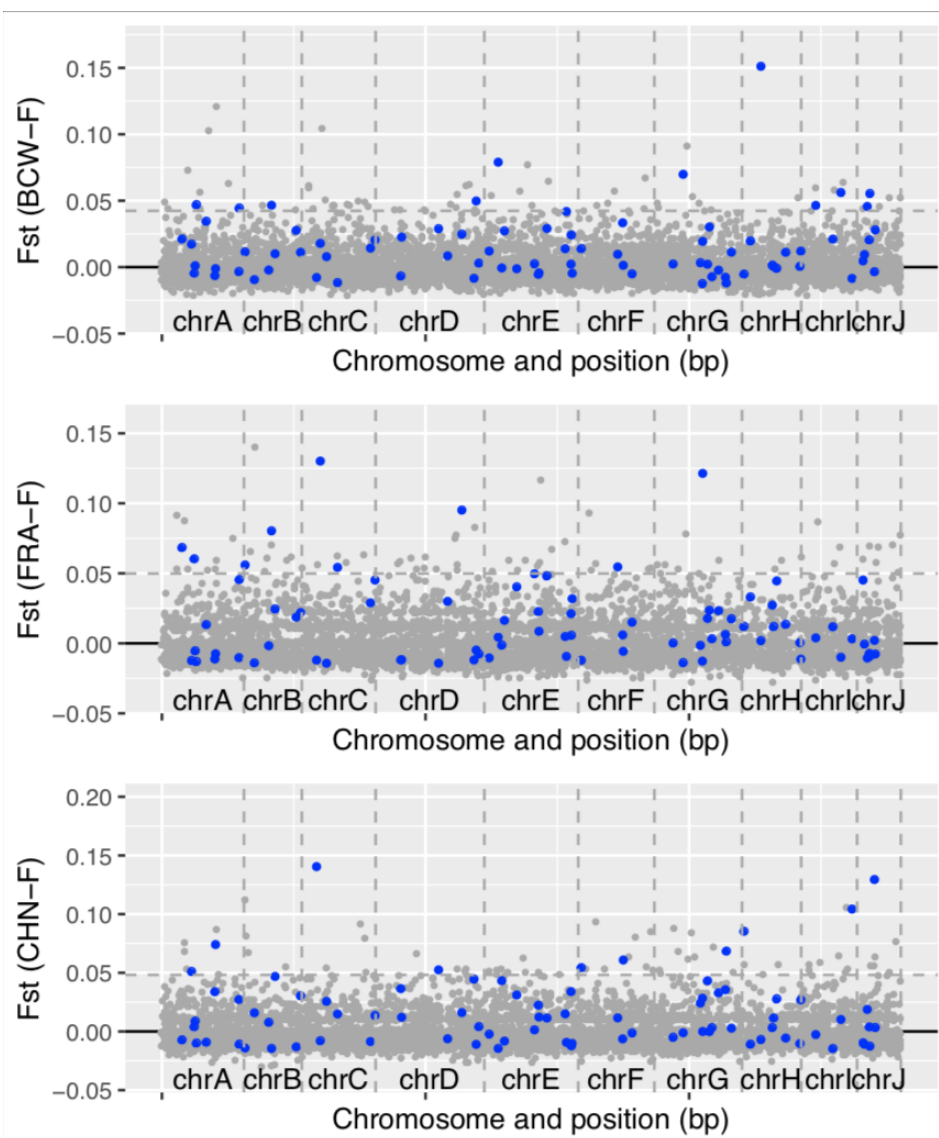
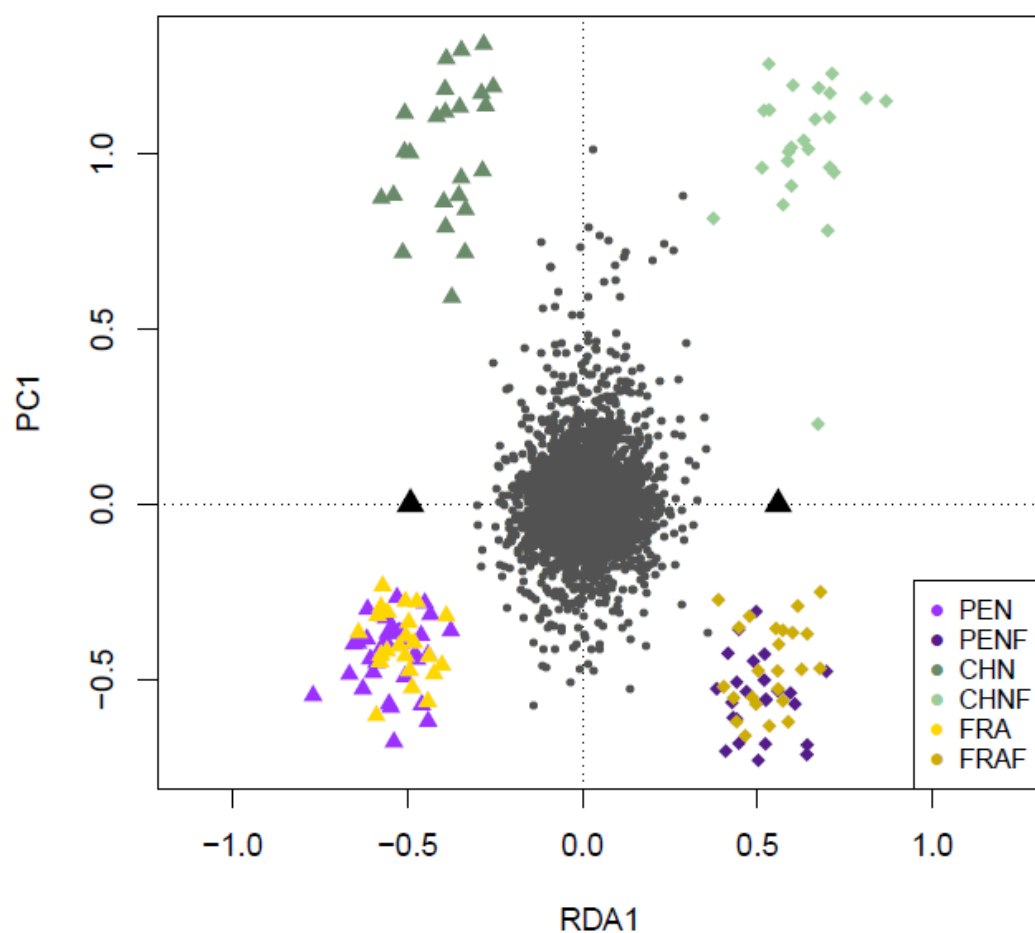
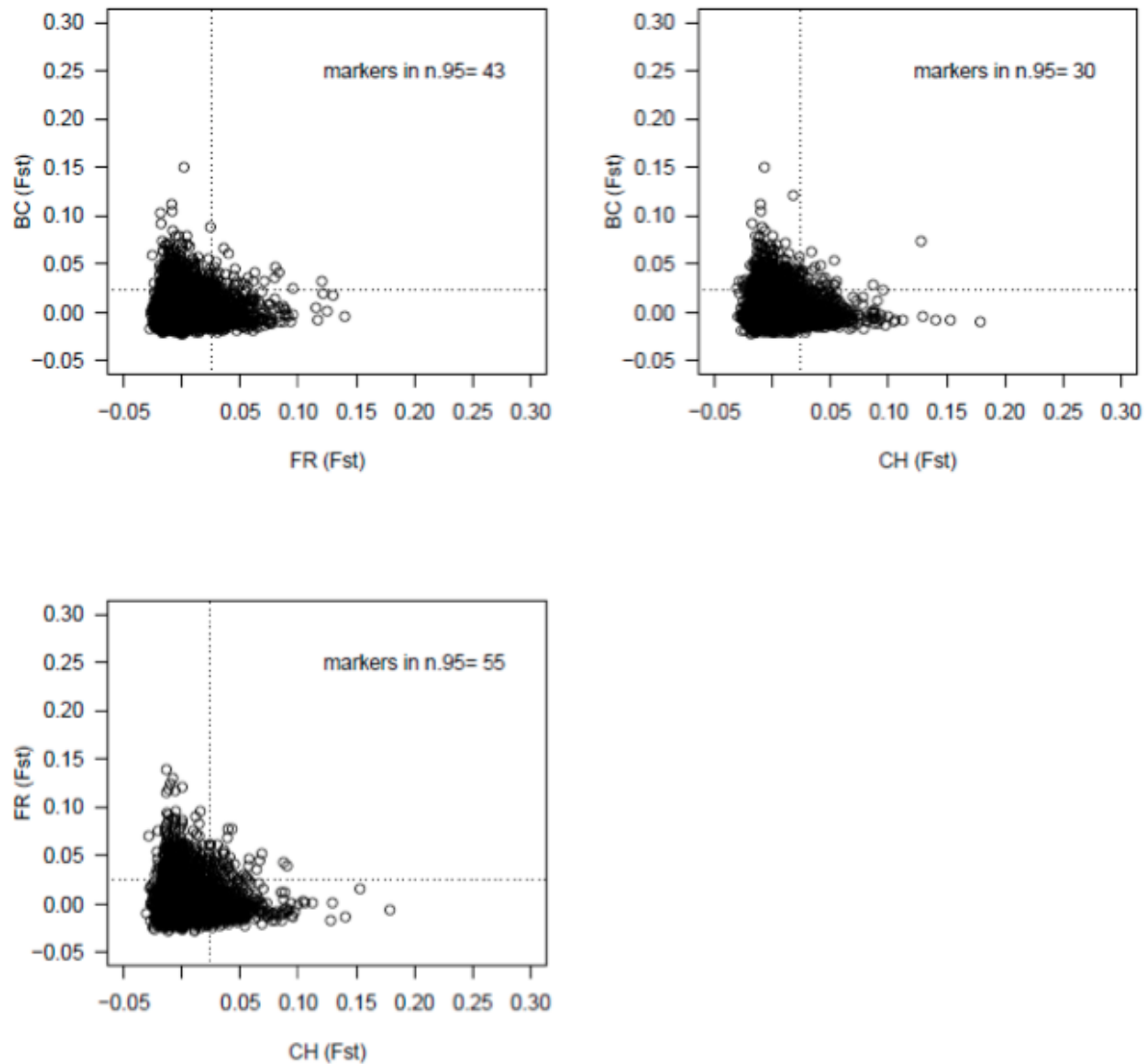


Figure S6. Outliers identified between naturalized/wild oysters moved onto a farm and naturalized populations (NAT-F vs. NAT) using RDA analysis (significant outliers shown by blue dots). The RDA was calculated using all NAT-F vs. NAT, whereas in plots, the F_{ST} is calculated per contrast (see Table 2).



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63 **Figure S7.** Comparison between Redundancy Analysis (RDA) and PCA in differentiating populations. RDA1
64 differentiated naturalized/wild oysters moved to farms (coloured diamonds) from naturalized/wild populations
65 (coloured triangles), and PC1 differentiates the Chinese oysters from the oysters from France and Canada (PEN).
66 The grey circles are individual loci. The black triangles indicate the average position along RDA1 of the two
67 groupings, naturalized/wild oysters grown on farms or naturalized/wild oysters.



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Figure S8. Per locus F_{ST} values compared between different countries to detect signatures of parallel selection from being moved onto a farm. Genetic differentiation (F_{ST}) was calculated between oysters moved from naturalized populations into farms and compared per marker between sets of two contrasts each (e.g. F_{ST} for FRA vs. FRAF compared to F_{ST} for CHN vs. CHNF). The 95th percentile of F_{ST} values are shown along each axis for each comparison, and the number of shared markers in both comparisons is shown on the graph (markers in n.95). Often high F_{ST} markers were specific to one population, suggesting non-parallel selection from transplantation and growth on a farm.