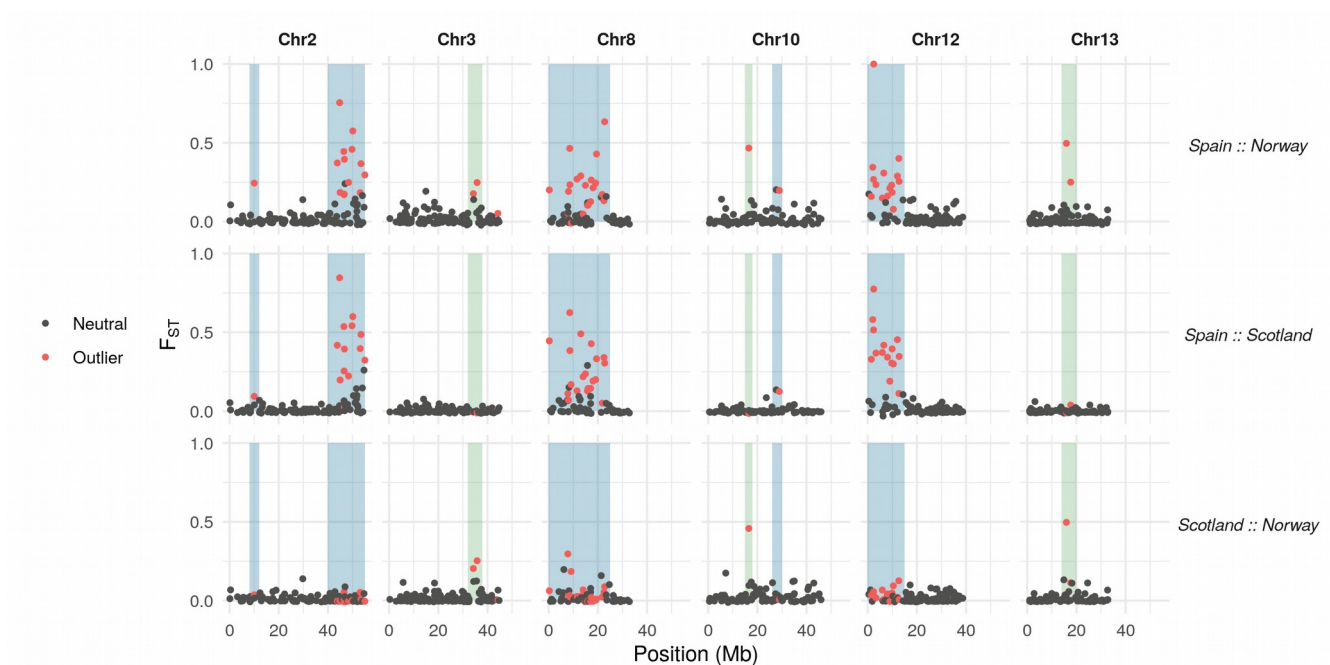
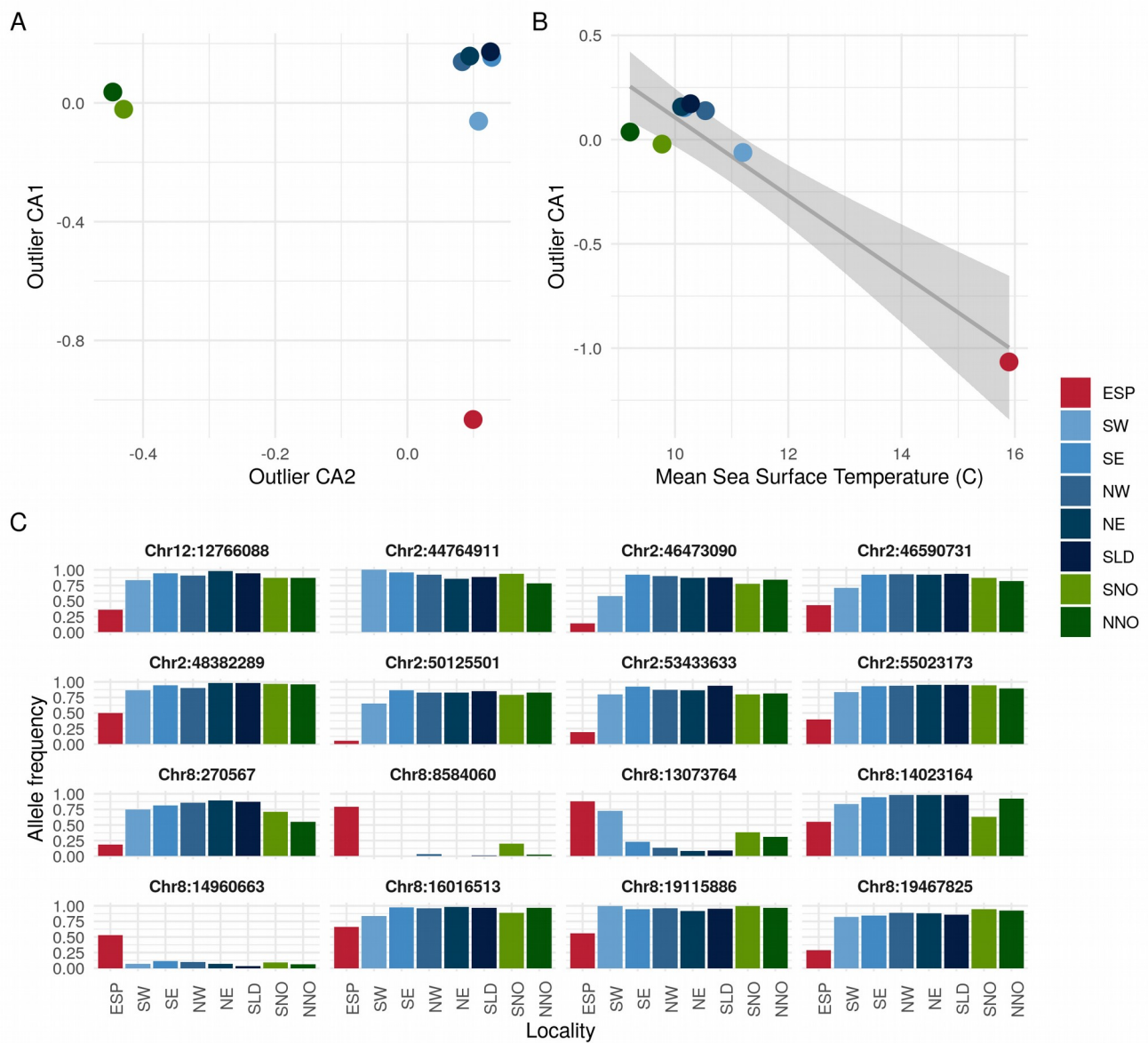


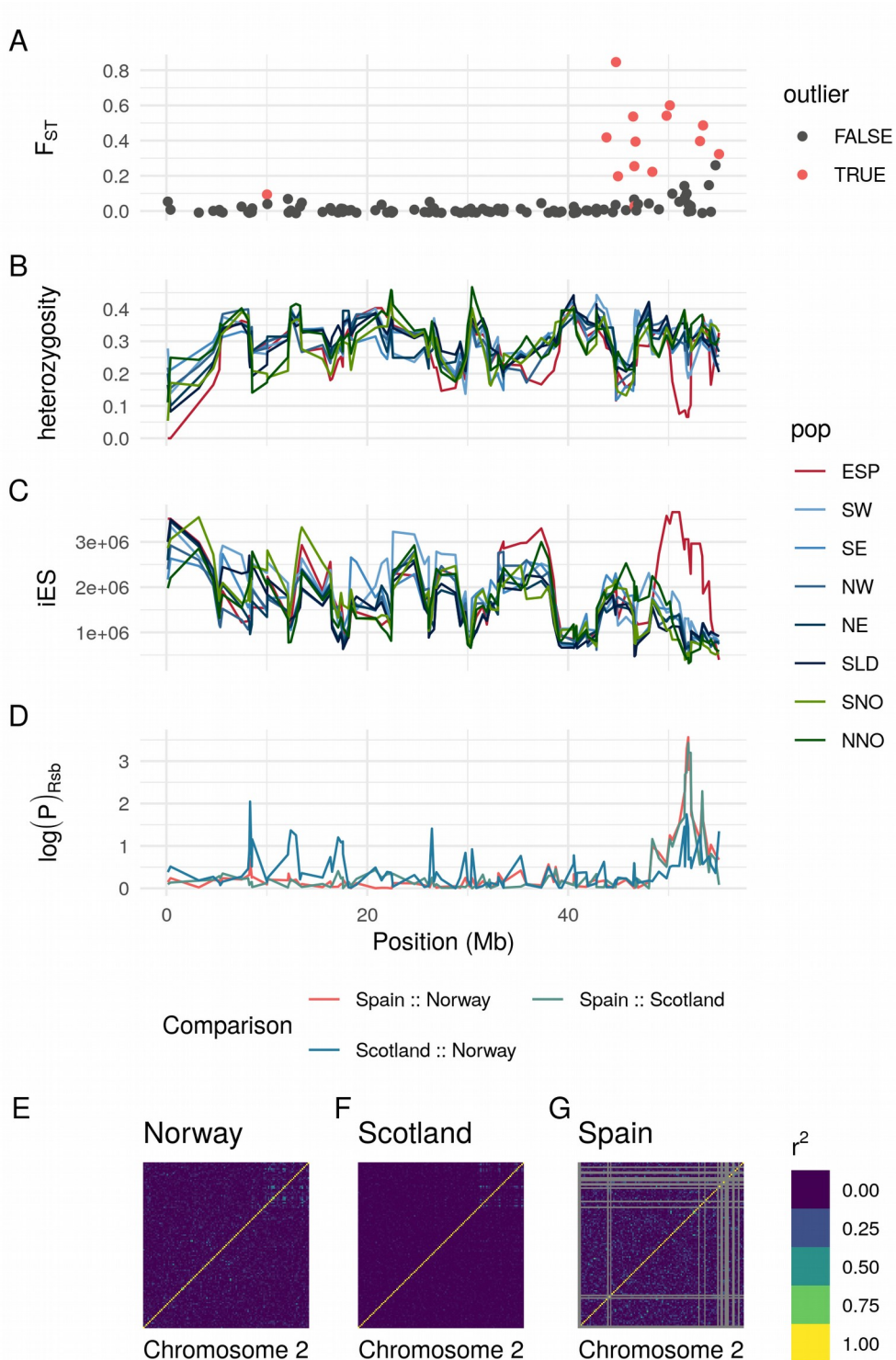
1 **Supplemental Figures:**
2



3 **Supplemental Figure 1:** Comparison of regional pairwise F_{ST} at selected chromosomes. Regions
4 highlighted in blue indicate chromosomal regions that differentiate Spain from Scotland and Norway.
5 Regions highlighted in green indicate chromosomal regions that differentiate Norway from Scotland
6 and Spain.



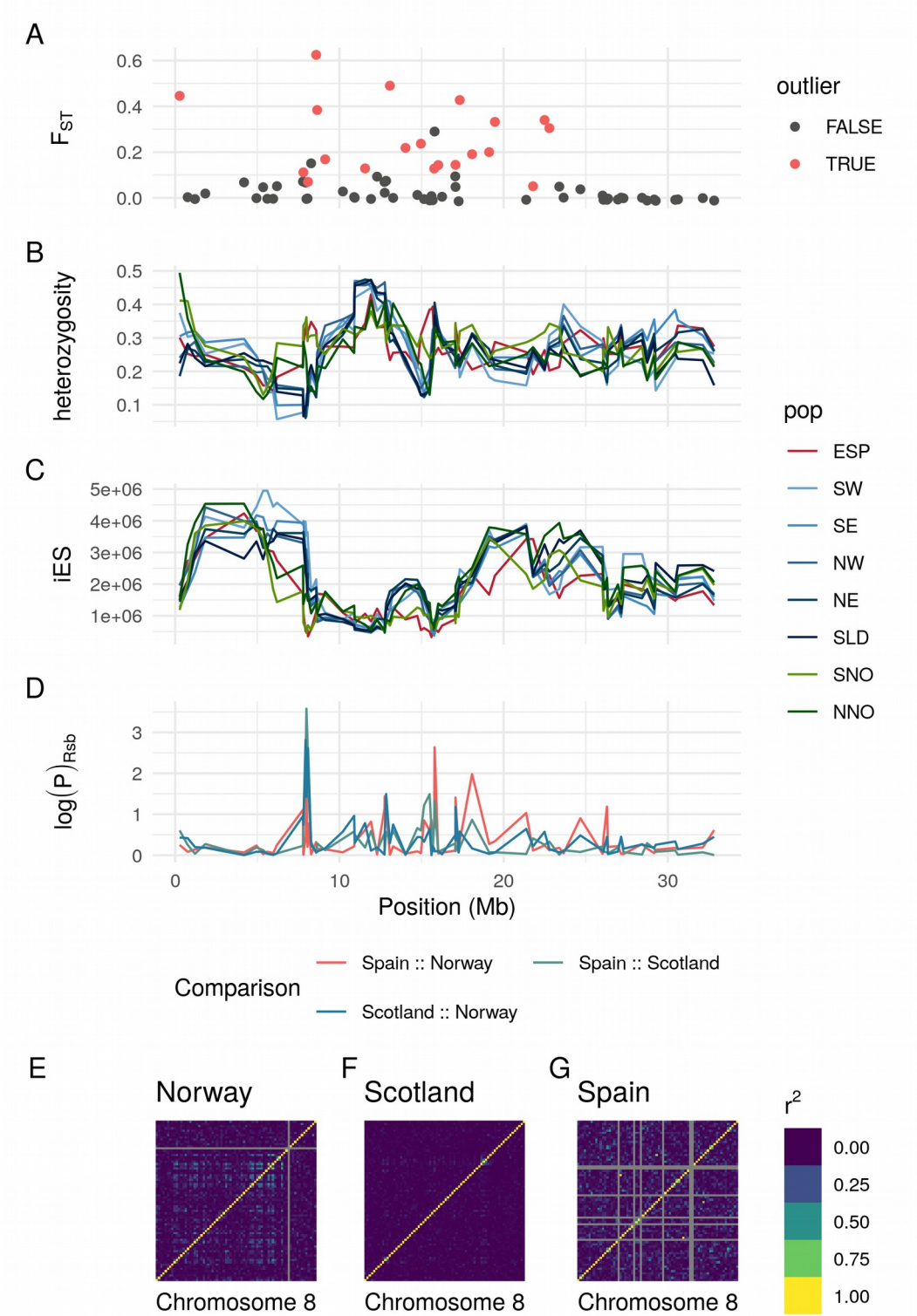
8 **Supplemental Figure 2:** A) Plot of first two principal axes of correspondence analysis (CA), a
9 population-level PCA analogue, for outlier loci; B) CA Component 1 plotted against mean sea surface
10 temperature; C) Allele frequencies for SNPs with highest loadings in CA component 1. Locality
11 abbreviations: NNO: North Norway, SNO: South Norway, SLD: Shetland Islands, NE: Northeast
12 Scotland, SE: Southeast Scotland, NW: Northwest Scotland, SW: Southwest Scotland, ESP: Spain
13



14 **Supplemental Figure 3:** Signatures of selection at chromosome 2. A) Pairwise F_{ST} (Scotland/Spain)
 15 plotted against genomic position for *Pecten maximus* chromosome 2; B) smoothed expected
 16 heterozygosity plotted against genomic position for each locality; C) iES, a statistic that measures the
 17 average length in base pairs of shared haplotypes (where larger values indicate larger regions of
 18 extended homozygosity, an indicator of a selective sweep) plotted against genomic position for
 19 chromosome 2; D) log of the P-value for test of statistical significance of R_{sb} , the log-ratio of iES for
 20 pairs of populations, plotted against genomic position for chromosome 2; E-F) Heatmap of pairwise
 21 linkage disequilibrium (r^2) for all loci on chromosome 2 for (E) Norwegian localities (F) Scottish

- 22 localities and (G) Spain; Locality abbrevaitions: NNO: North Norway, SNO: South Norway, SLD:
23 Shetland Islands, NE: Northeast Scotland, SE: Southeast Scotland, NW: Northwest Scotland, SW:
24 Southwest Scotland, ESP: Spain

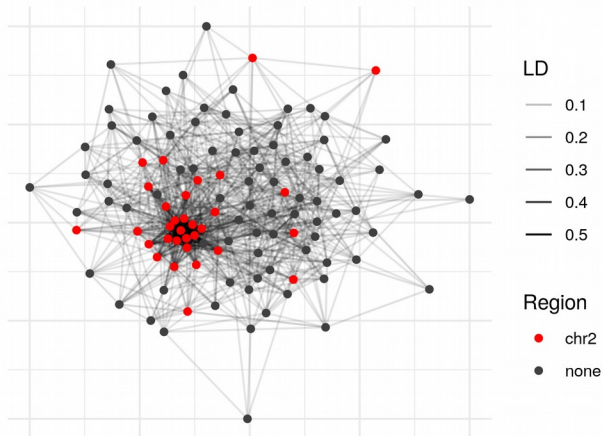
25
26



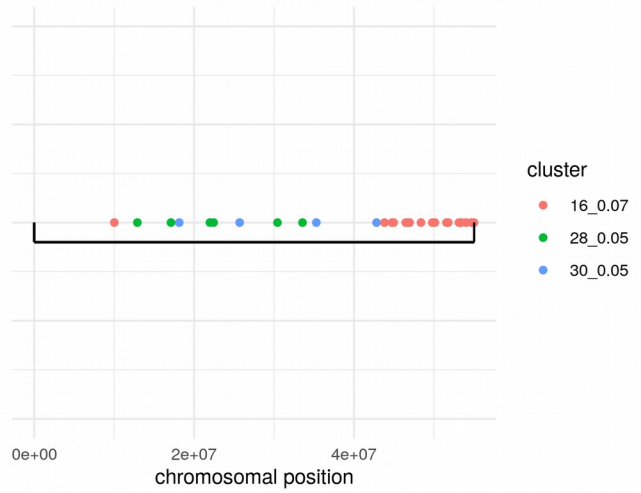
27 **Supplemental Figure 4:** Signatures of selection at *Pecten maximus* chromosome 8. A) Pairwise F_{ST}
28 (Scotland/Spain) plotted against genomic position for chromosome 8; B) smoothed expected
29 heterozygosity plotted against genomic position for each locality; C) iES, a statistic that measures the
30 average length in base pairs of shared haplotypes (where larger values indicate larger regions of
31 extended homozygosity, an indicator of a selective sweep) plotted against genomic position for
32 chromosome 8; D) log of the P-value for test of statistical significance of R_{sb} , the log-ratio of iES for
33 pairs of populations, plotted against genomic position for chromosome 8; E-F) Heatmap of pairwise

34 linkage disequilibrium (r^2) for all loci on chromosome 8 for (E) Norwegian localities (F) Scottish
35 localities and (G) Spain; Locality abbreviations: NNO: North Norway, SNO: South Norway, SLD:
36 Shetland Islands, NE: Northeast Scotland, SE: Southeast Scotland, NW: Northwest Scotland, SW:
37 Southwest Scotland, ESP: Spain

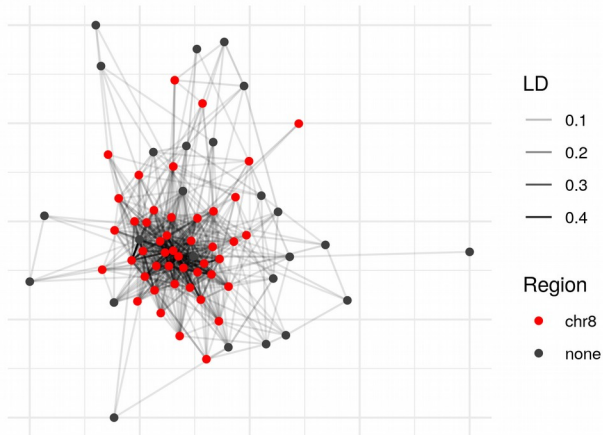
a Chrom 2



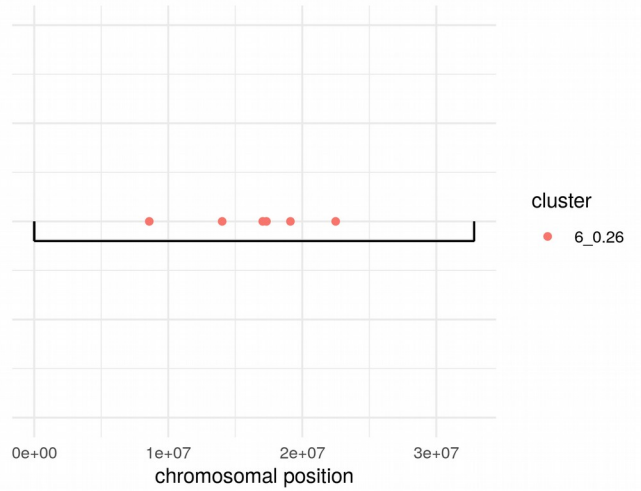
b



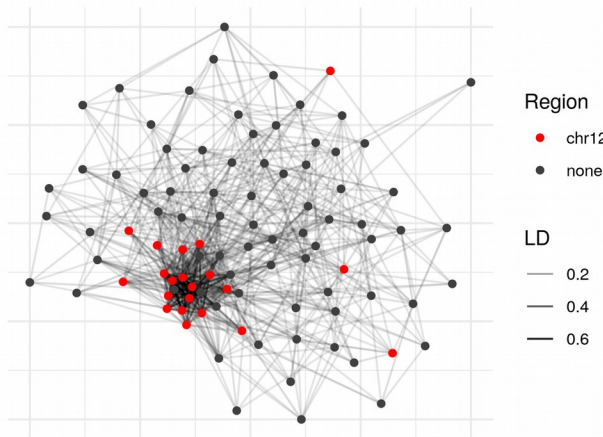
c Chrom 8



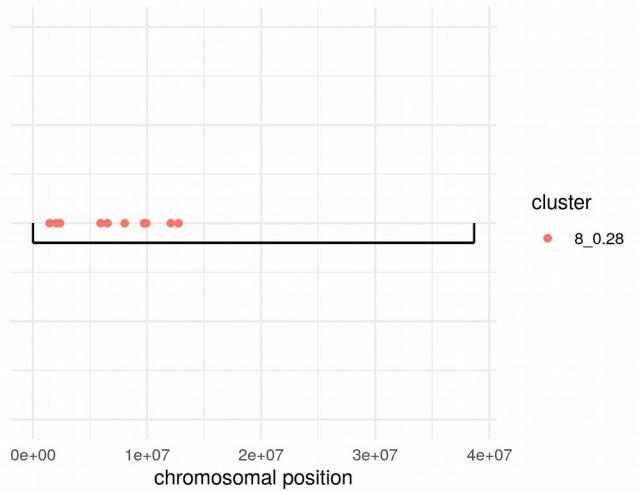
d



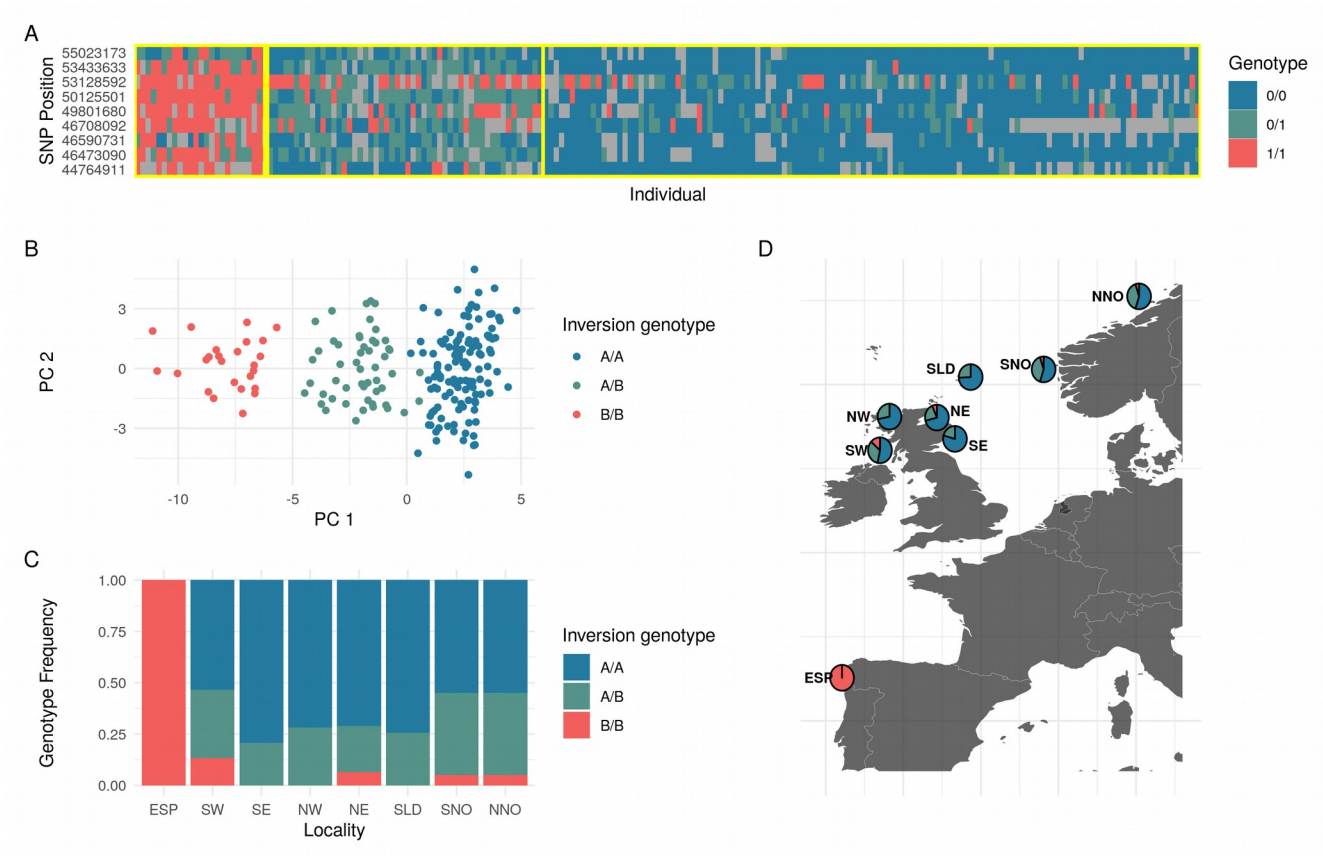
e Chrom 12



f



39 **Supplemental Figure 5:** Results of linkage disequilibrium network analysis (LDna) for chromosome 2
40 (top row), chromosome 8 (center row), and chromosome 12 (bottom row). The left column shows the
41 network of linkage disequilibrium relationships between loci on the chromosome, with nodes
42 representing loci and edges representing r^2 values, with darker lines indicating higher r^2 . Loci present
43 in observed regions of elevated LD (chr2:44727153-55023173, chr8:5964894-23386594,
44 chr12:2052968-12083837) are colored in red. The right column shows the chromosomal position of
45 single outlier clusters (SOCs) of loci with elevated LD relationships identified with *LDna* R package.
46



48 **Supplemental Figure 6:** Population frequencies of inversion genotypes on chromosome 2. A)

49 Genotype heatmap of all individuals (x axis) at SNPs contained within the putative inversion on

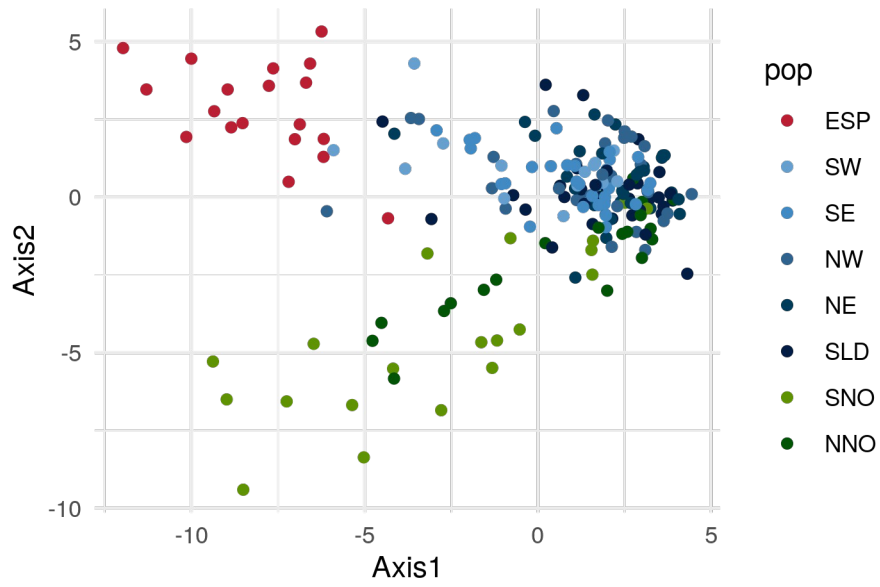
50 chromosome 12 (y axis). Colors represent SNP genotypes (blue = homozygote, green = heterozygote,

51 red = alternate homozygote) and yellow boxes indicate genotype clusters in panel B. B) Local PCA of

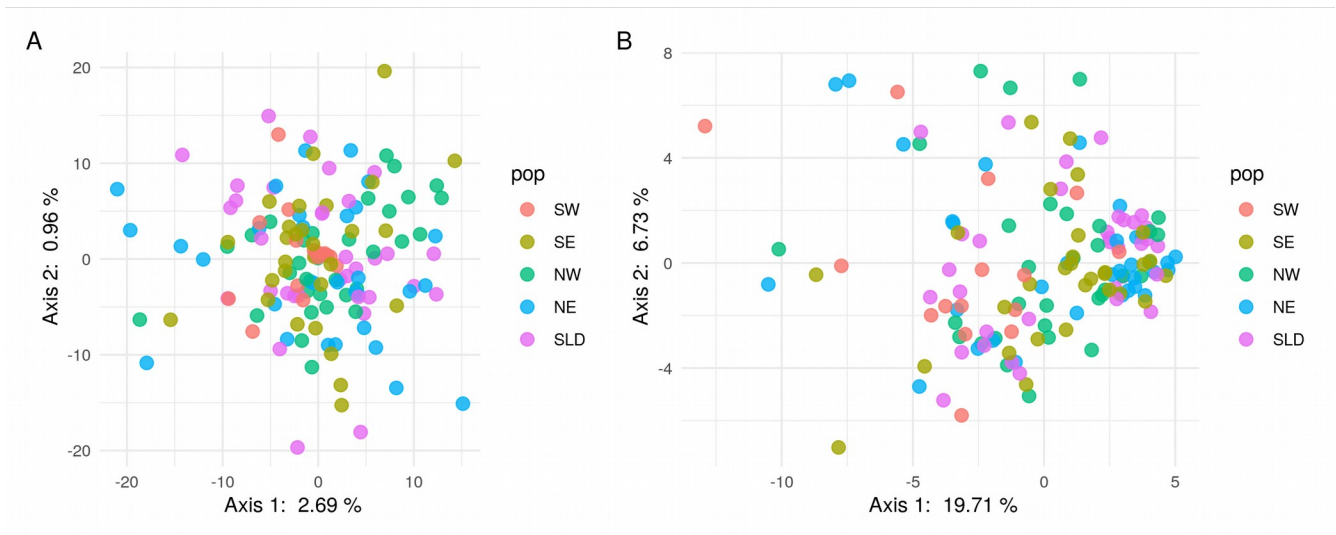
52 putative inversion on chromosome 12 showing clusters of inversion genotypes. C) Population

53 frequencies of inversion genotypes. D) Sample map with inversion genotype frequencies.

54



Supplemental Figure 7: Local PCA of putative inversion on chromosome 8. Locality abbreviations: NNO: North Norway, SNO: South Norway, SLD: Shetland Islands, NE: Northeast Scotland, SE: Southeast Scotland, NW: Northwest Scotland, SW: Southwest Scotland, ESP: Spain



73 **Supplemental Figure 8.** PCA of Scottish localities only for neutral (A) and outlier (B) datasets.
 74 Locality abbreviations: SLD: Shetland Islands, NE: Northeast Scotland, SE: Southeast Scotland, NW:
 75 Northwest Scotland, SW: Southwest Scotland