Figure S1 The principal components analysis using genotyping data from 5,800 SNPs. (A) The proportion of variance explained by each of the 20 principal components. (B) The population structure displayed by PC1 and PC2. (C) The population structure displayed by PC1 and PC3. (D) The population structure displayed by PC2 and PC3.
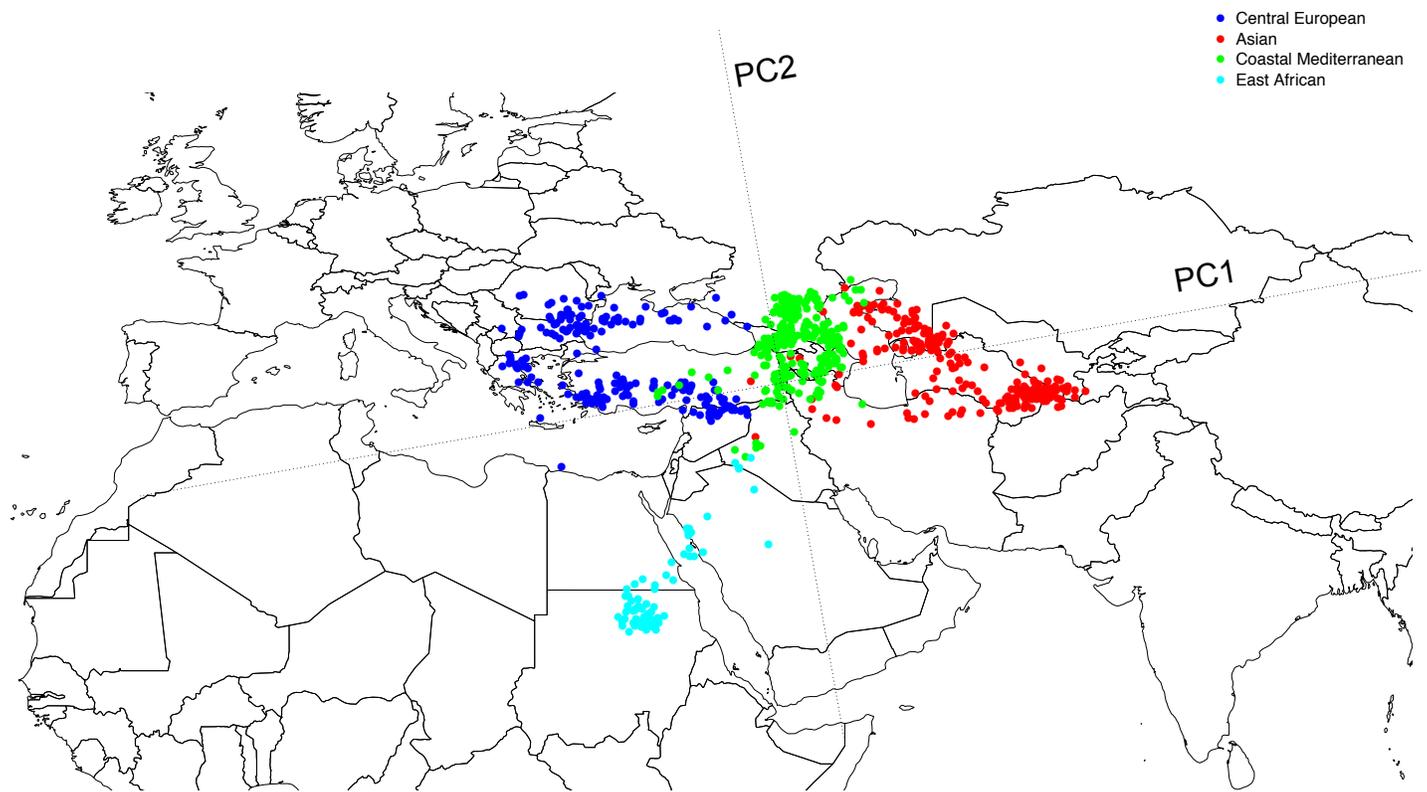
Figure S2 Relationship of barley landrace accessions based on principal components. PC1 and PC2 are depicted relative to a map of the landrace distribution in Africa and Eurasia.
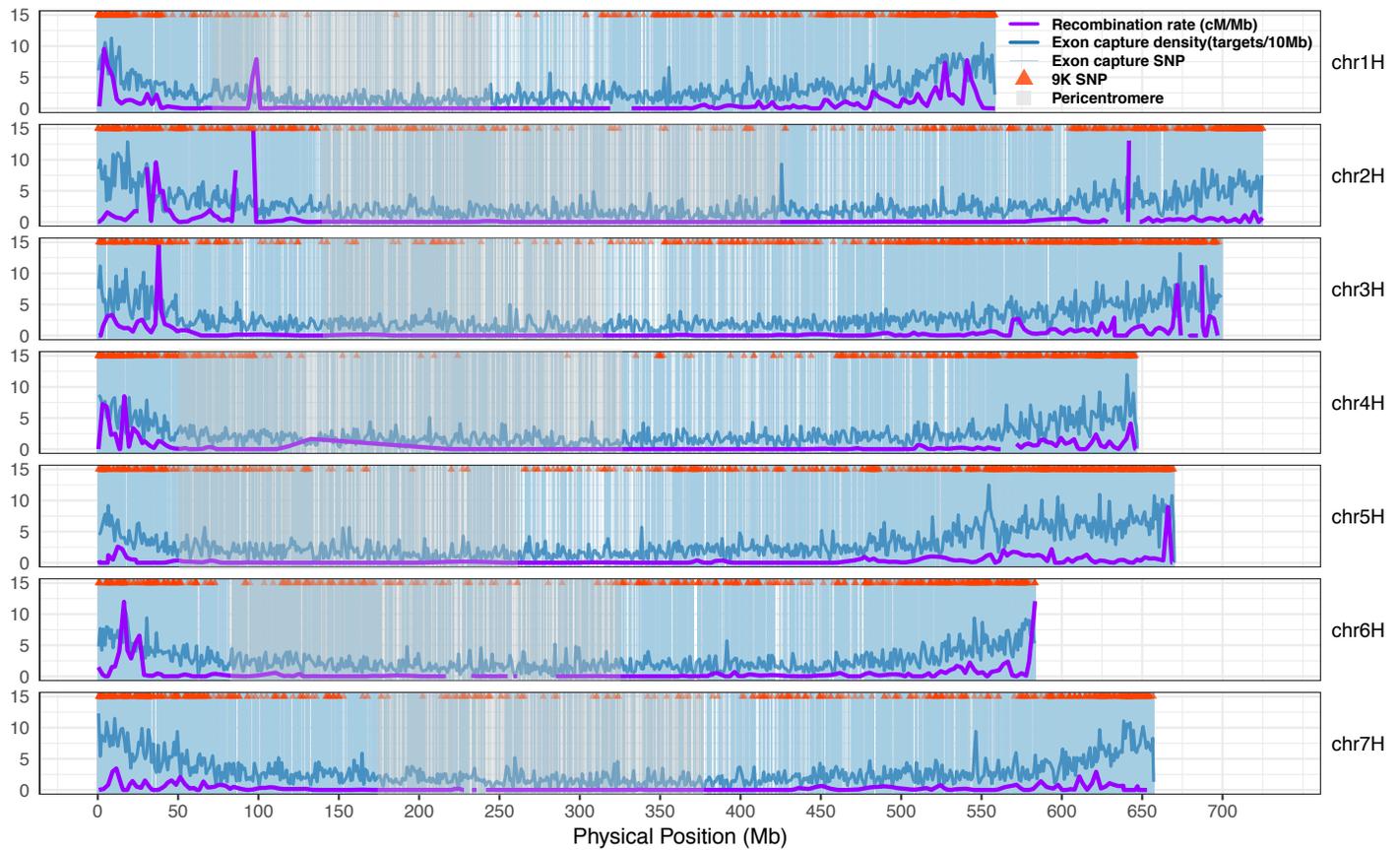
Figure S3 Exome capture target density (dark blue line), crossover rate in cM/Mb (purple line), the genomic distribution of SNPs identified in 62 barley landraces (vertical light blue lines), and 9K iSelect SNPs (red triangles) for seven chromosomes. Crossover rates were calculated using 9K SNPs. SNP genetic positions are based on the genetic map of Muñoz-Amatriaín et al. (2011).
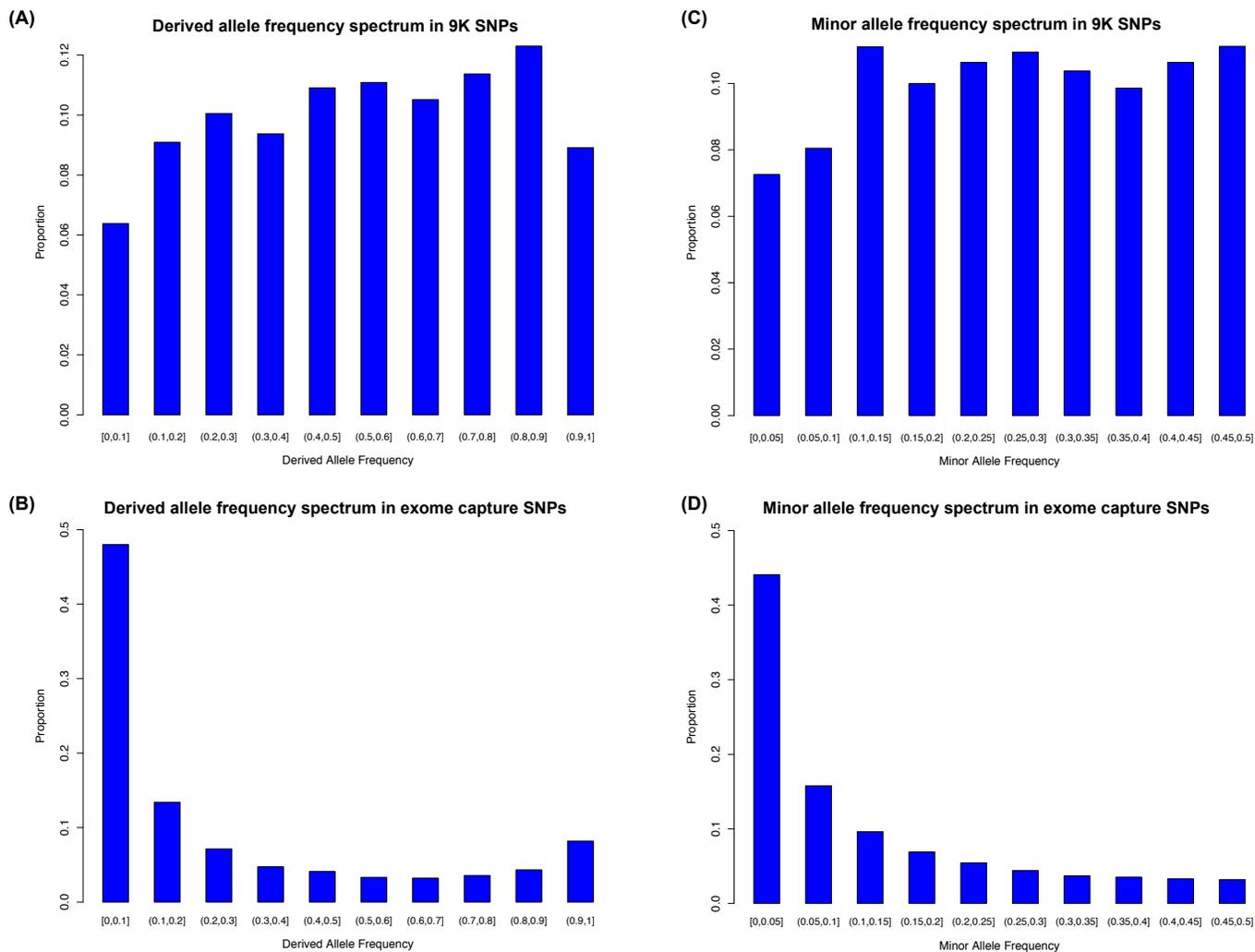
Figure S4 The derived site frequency spectrum (SNPs with inferred ancestral state) for (A) 2,806 SNPs from the 9K iSelect genotyped in the 784 landraces and (B) 340,260 SNPs with exome capture resequencing data in 62 landraces. The ancestral state was inferred based on majority state from *H. murinum spp. glaucum* resequencing mapped to the Morex assembly. For all SNPs, the minor allele frequency for (C) 5,800 SNPs from the 9K iSelect and (D) 482,714 SNPs from exome capture resequencing.
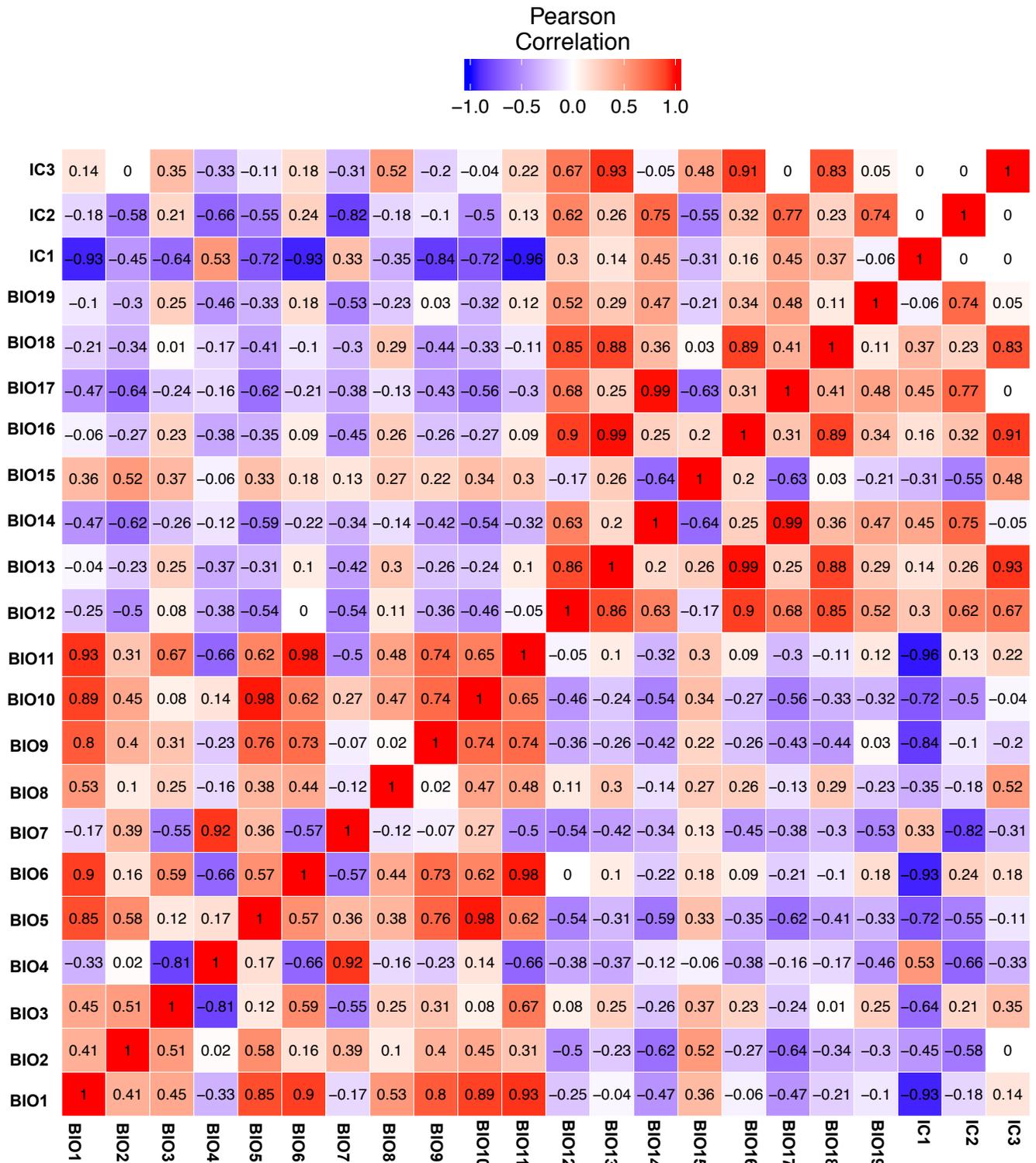
Figure S5 A heat map of the Pearson pairwise correlation coefficient for 22 environmental variables.

**The distribution of the pairwise genetic distance from 784 barley landraces**
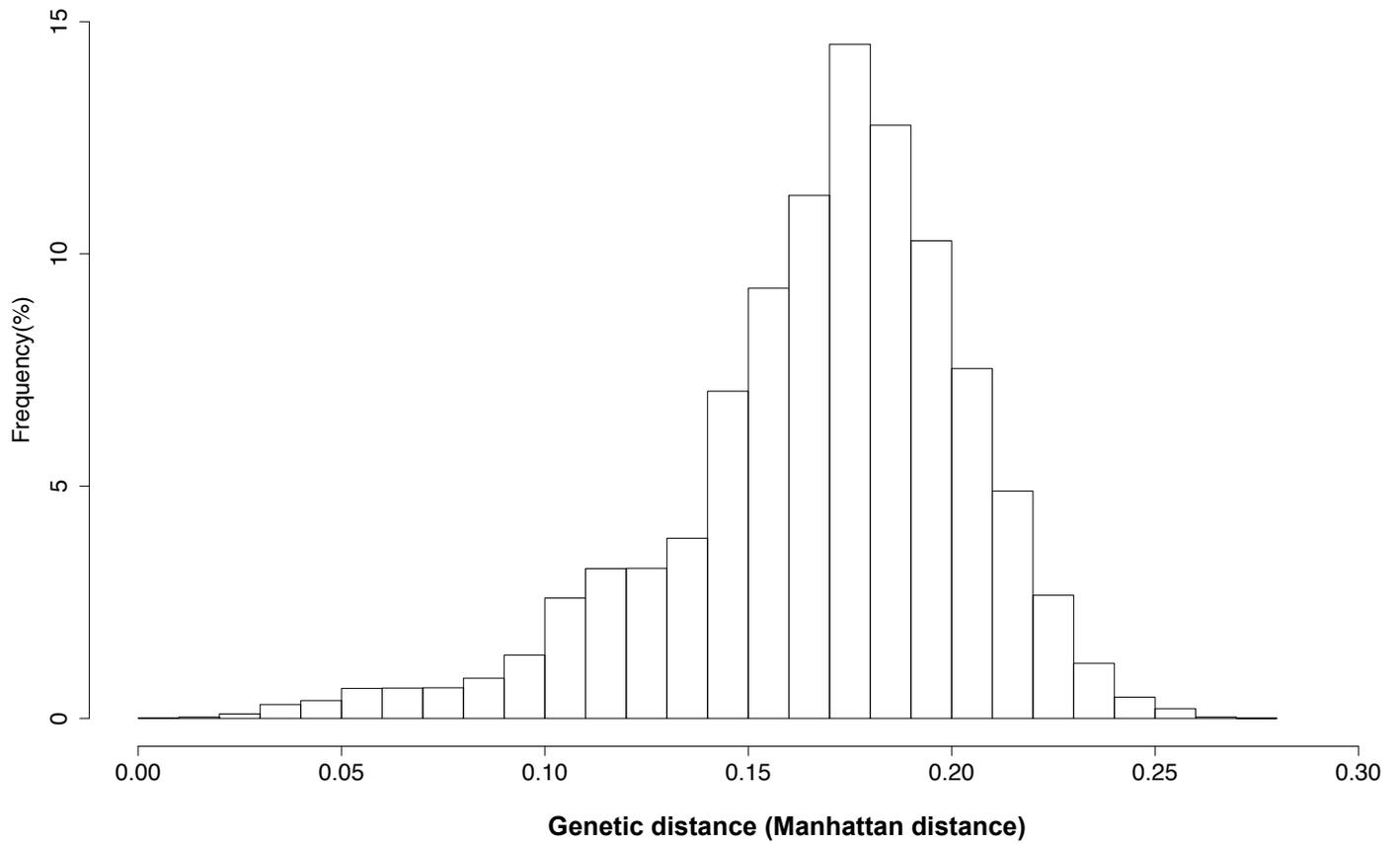
Figure S6 The distribution of pairwise genetic distance (Manhattan distance) from 784 barley landraces.
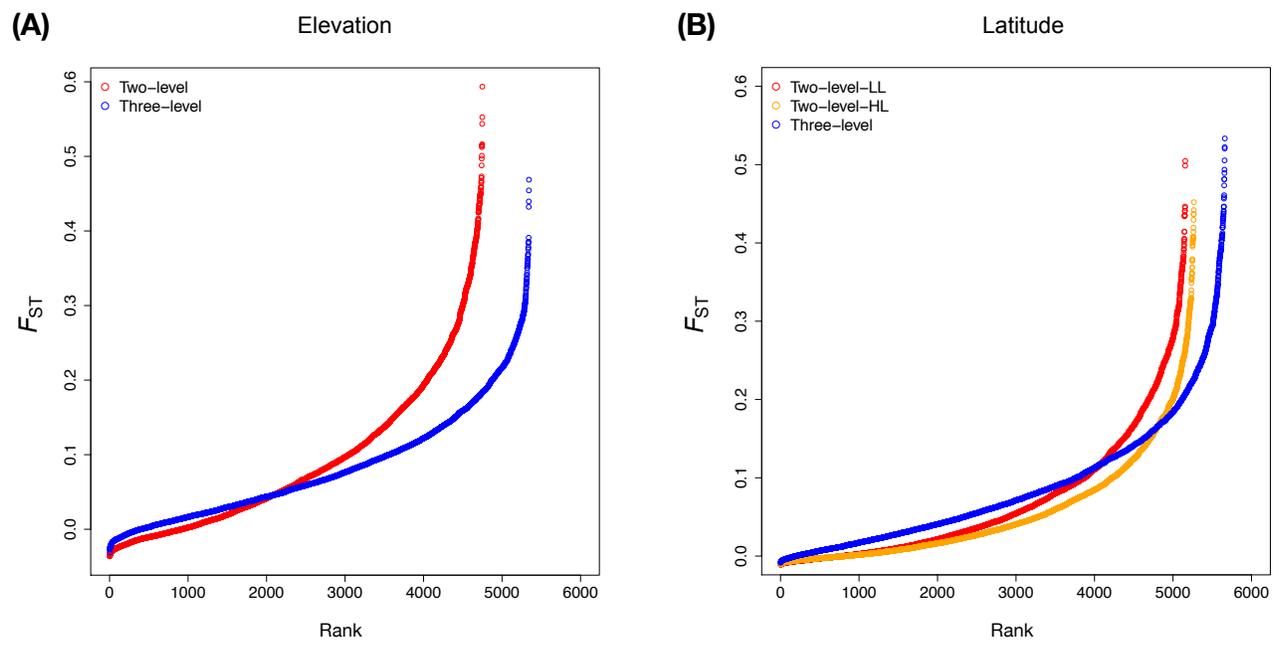
**Figure S7** The distribution of ranked F_{ST} from two- and three-level comparisons of elevation and latitude.
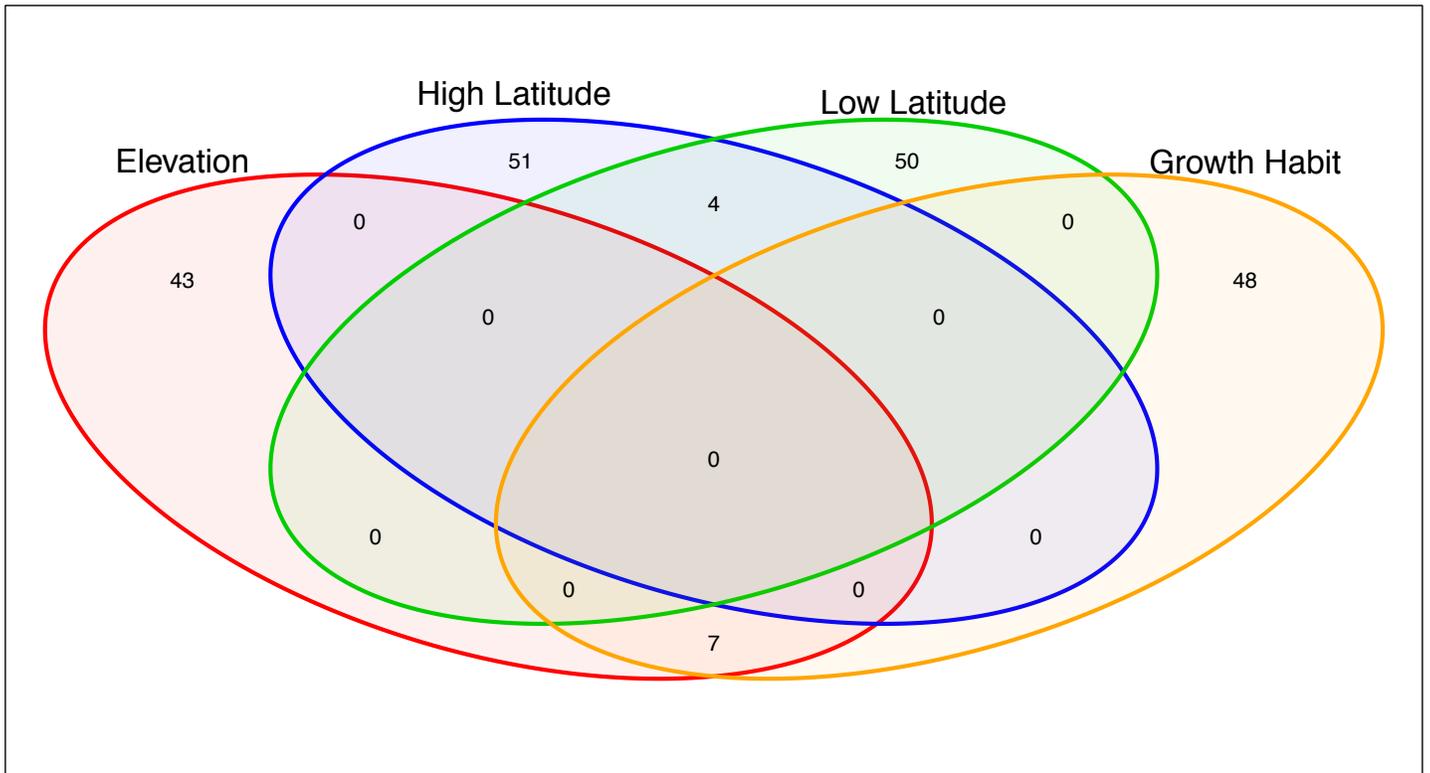
Figure S8 Venn diagram of F_{ST} outliers from the comparisons of elevation, high and low latitude, and growth habit.
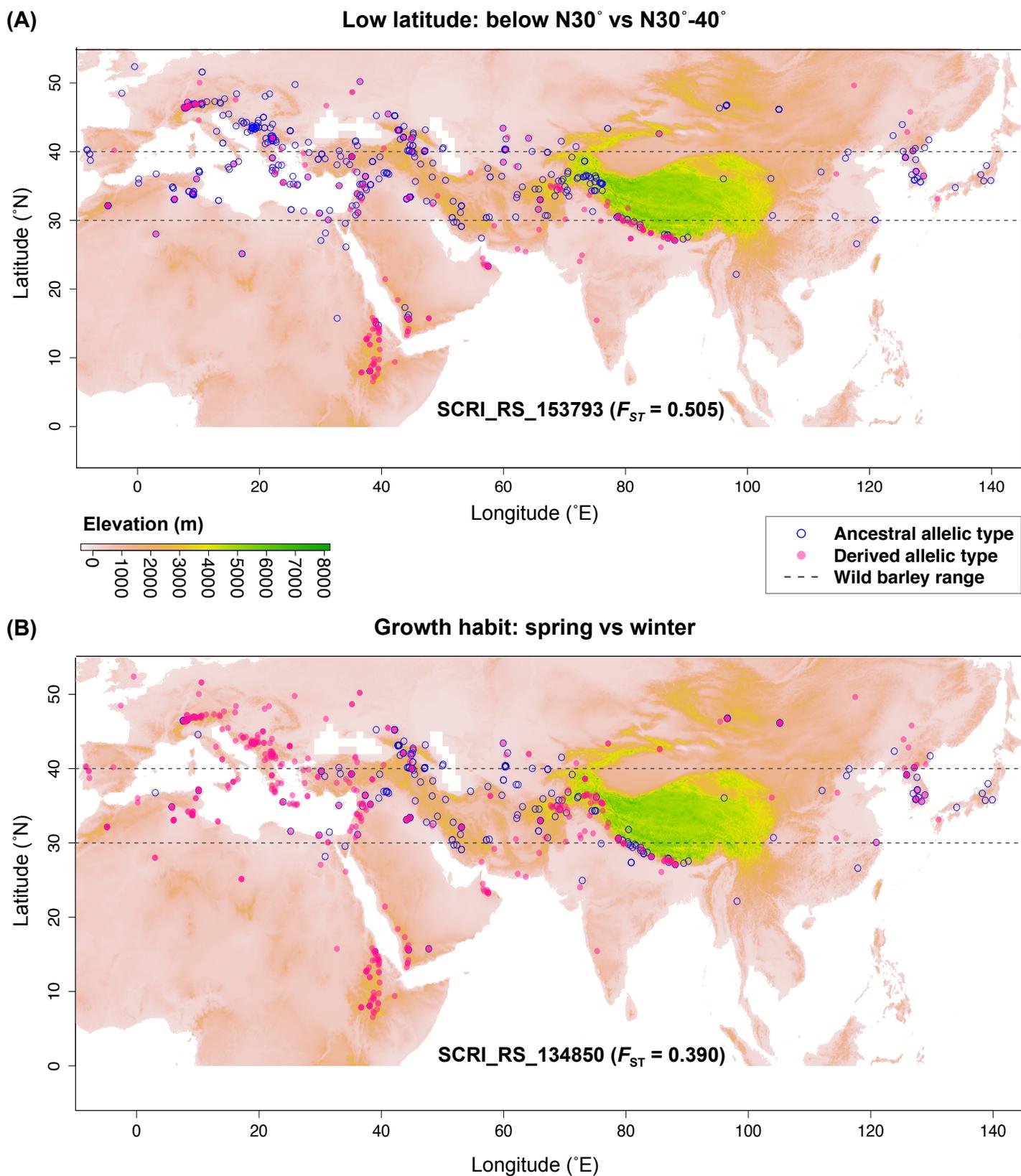
Figure S9 The geographic distribution of SNPs with high F_{ST}. (A) The geographic distribution of allelic types for 9K SNP SCRI_RS_153793 with the highest $F_{ST} = 0.505$. The F_{ST} was from the low latitude (LL) comparison. (B) The geographic distribution of allelic types for 9K SCRI_RS_134850 with the highest $F_{ST} = 0.390$. The F_{ST} was from the growth habit (GH) comparison. The color bar indicates the elevation in meters. The filled pink circles indicate the derived allele, while the blue open circles indicate the ancestral allele.
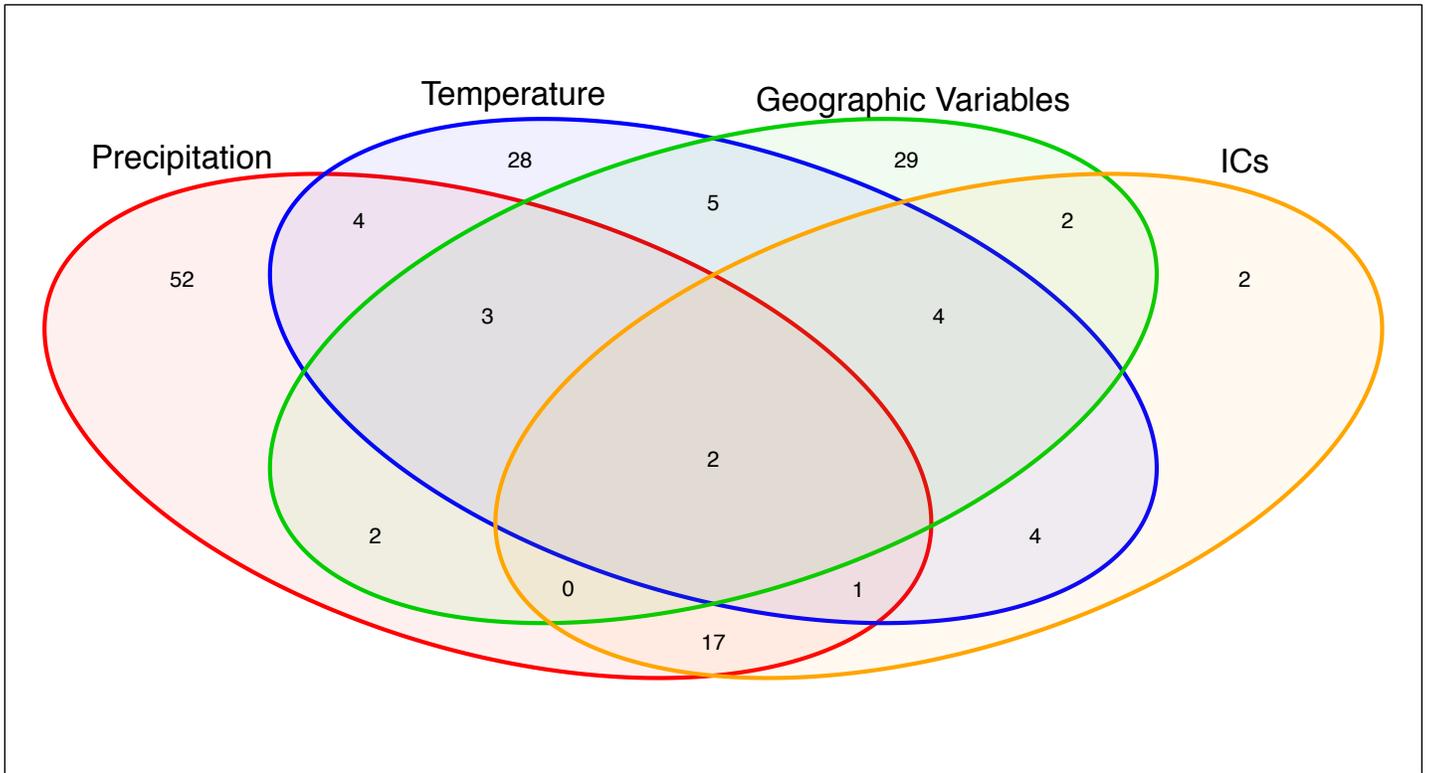
Figure S10 Venn diagram of candidate SNPs that are significantly associated with three categories of environmental variables: precipitation, temperature, and geographic factors.
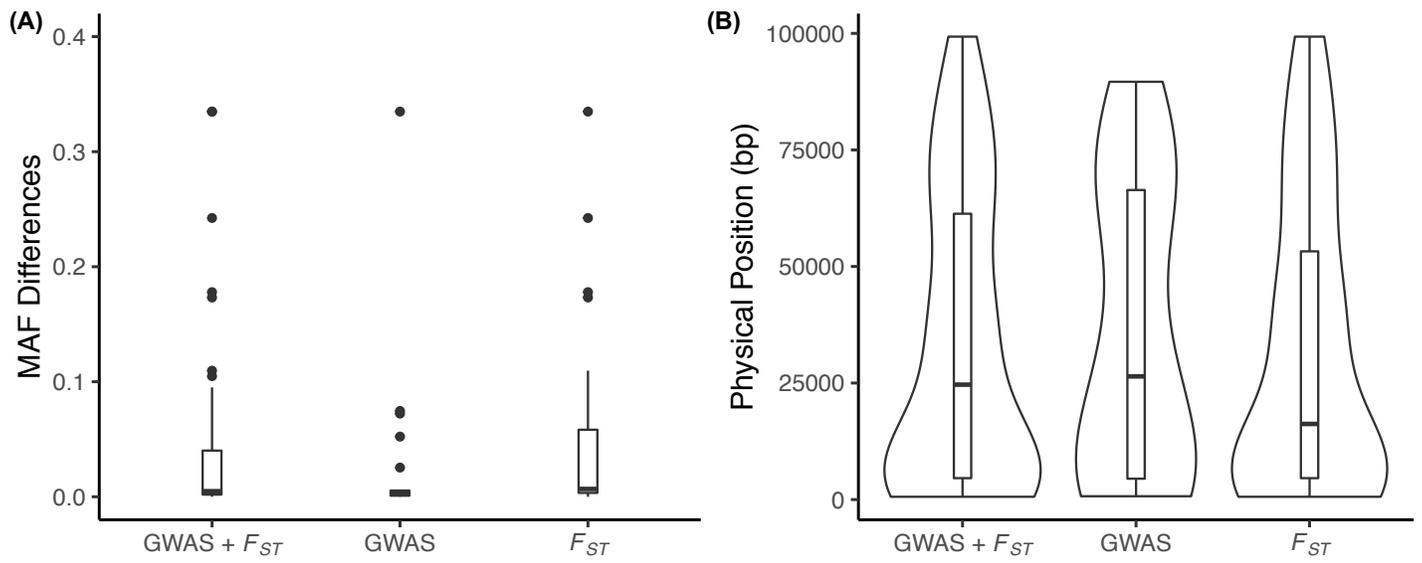
Figure S11 The difference between the replaced SNPs and queried SNPs not in the exome capture data. (A) Shows the minor allele frequency (MAF) and (B) the physical distance.
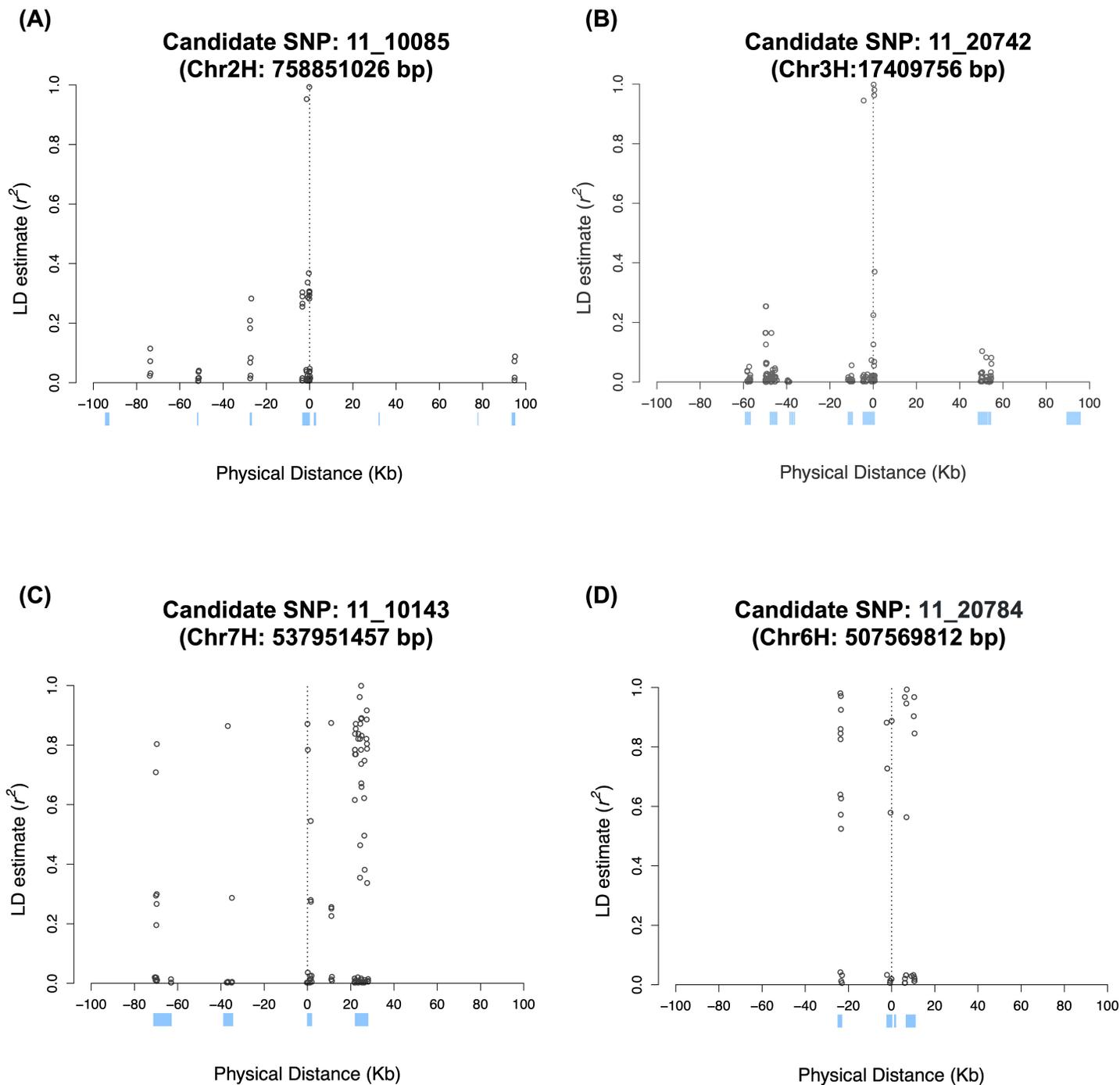
Figure S12 The linkage disequilibrium (LD) decay plot for 200 Kb windows around the significant SNPs associated with environmental variables. The blue bars underneath the x-axis are the annotated genes in the 200 Kb windows. The vertical dashed lines are candidate SNP locations. The negative signs on the x-axis refer to positions downstream of the candidate SNP.

(A)

11_10380 (chr3H : 142551916 bp)

WCI16

Physical Distance (Kb)

LD estimate (r^2)

(B)

WCI/HORVU3Hr1G030150

0   1356

21	41	119		460	523	655
C/T	A/G	G/C		A/G	T/C	T/C

Red: Nonsynonymous SNP

Blue: Significant associated SNP

☐ : LD with significant associated SNP (r^2>0.4)
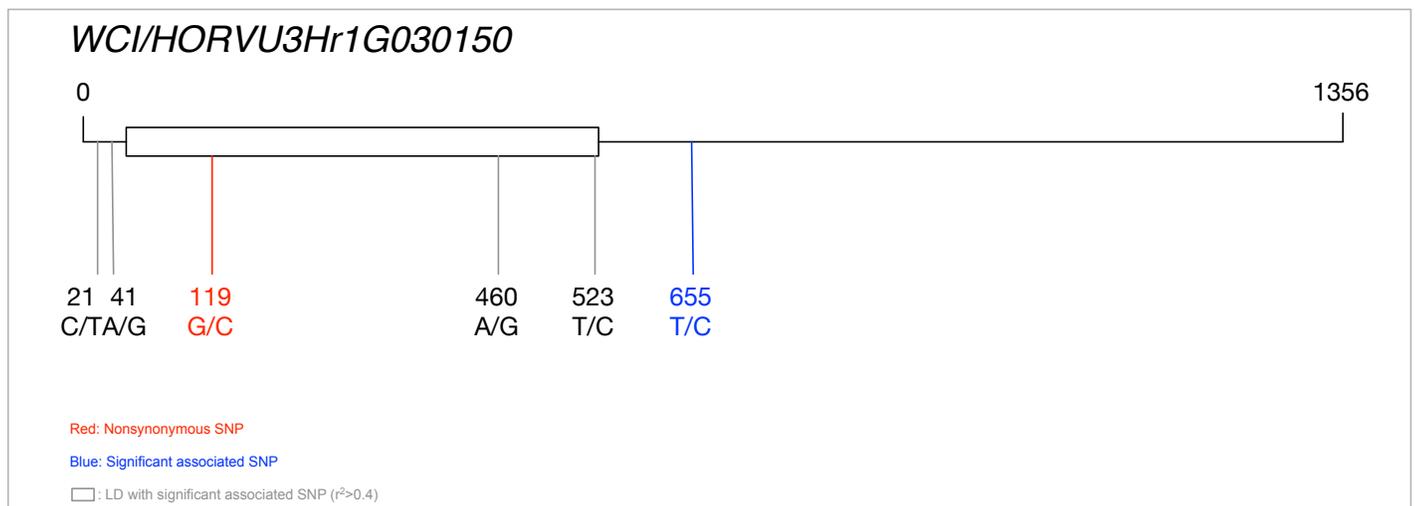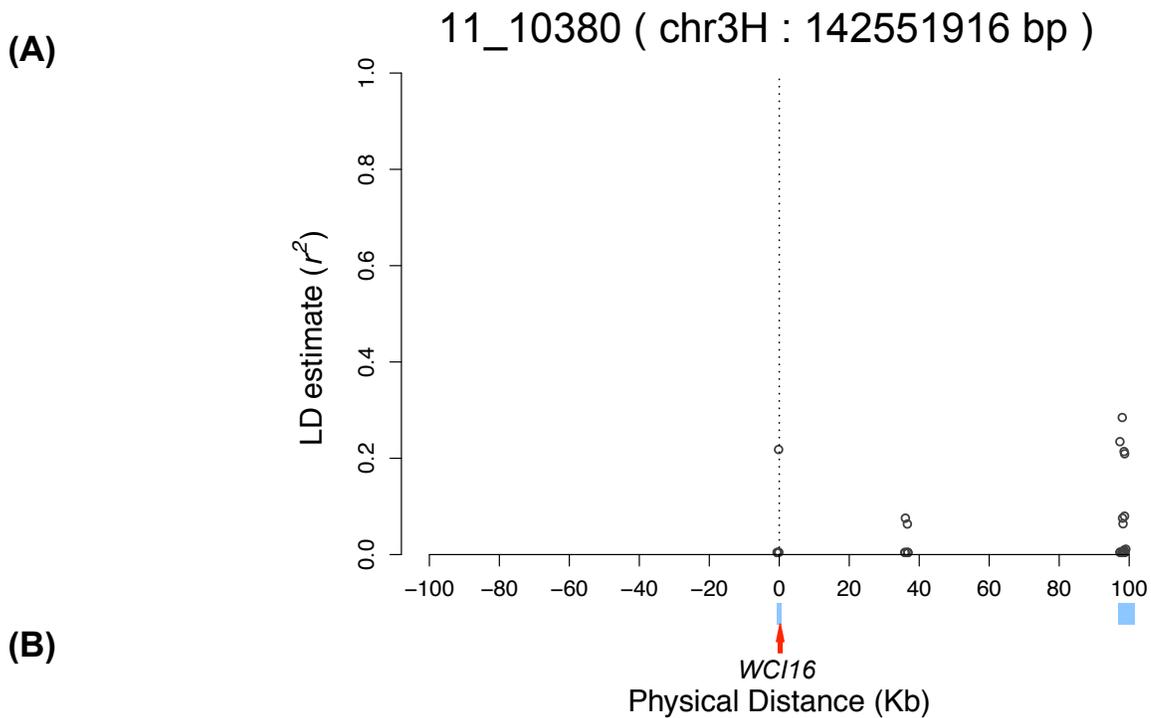
(C)

| Sites	21	41	119	460	523	655	General				Subsets			
Physical position	1282	1302	1380	1721	1784	1916					L_Latitude Elevation		H_Latitude Elevation	
Consensus	C	A	G	G	T	T	Elevation		Latitude					
Ancestral	.	.	.	-	.	.	L	H	L	H	L	H	L	H
Hap1	.	.	.	.	.	.	21	2	16	7	14	2	7	-
Hap2	.	.	.	.	.	C	13	-	5	8	5	-	8	-
Hap3	.	.	.	A	.	C	1	-	1	-	1	-	-	-
Hap4	.	.	.	A	.	.	31	2	21	12	19	2	12	-
Hap5	.	.	C	.	.	.	1	-	1	-	1	-	-	-
Hap6	.	.	C	A	.	.	1	-	1	-	1	-	-	-
Hap7	.	G	.	A	.	.	1	-	1	-	1	-	-	-
Hap8	T	.	.	.	C	.	1	-	1	-	1	-	-	-

Figure S13 (A) The linkage disequilibrium (LD) analysis of the candidate SNP 11_10380 which is significantly associated with BIO6 ("min temperature of the coldest month") and BIO11 ("mean temperature of the coldest quarter"). The blue bars indicate genes in the 200 Kb window surrounding 11_10380 and the red arrow indicates the *WCI 16* (cold tolerance related gene) that is hit by 11_10380. (B) The gene structure of *WCI 16* and the functional annotation of SNPs in this gene. (C) Haplotype structure of *WCI 16* based on the SNPs in this gene. L: low; H: high.

Figure S14 (A) The linkage disequilibrium (LD) analysis of the candidate SNP SCRI_RS_235243 which is significantly associated with BIO14 ("precipitation of the driest months"). The blue bars indicate genes in the 200 Kb window surrounding SCRI_RS_235243 and the red arrow indicates the drought tolerance related gene (DHAR) that is hit by SCRI_RS_235243. (B) The gene structure of DHAR and the functional annotation of SNPs in this gene. (C) Haplotype structure of DHAR based on the SNPs in this gene. L: low; H: high.