Supplemental Figures

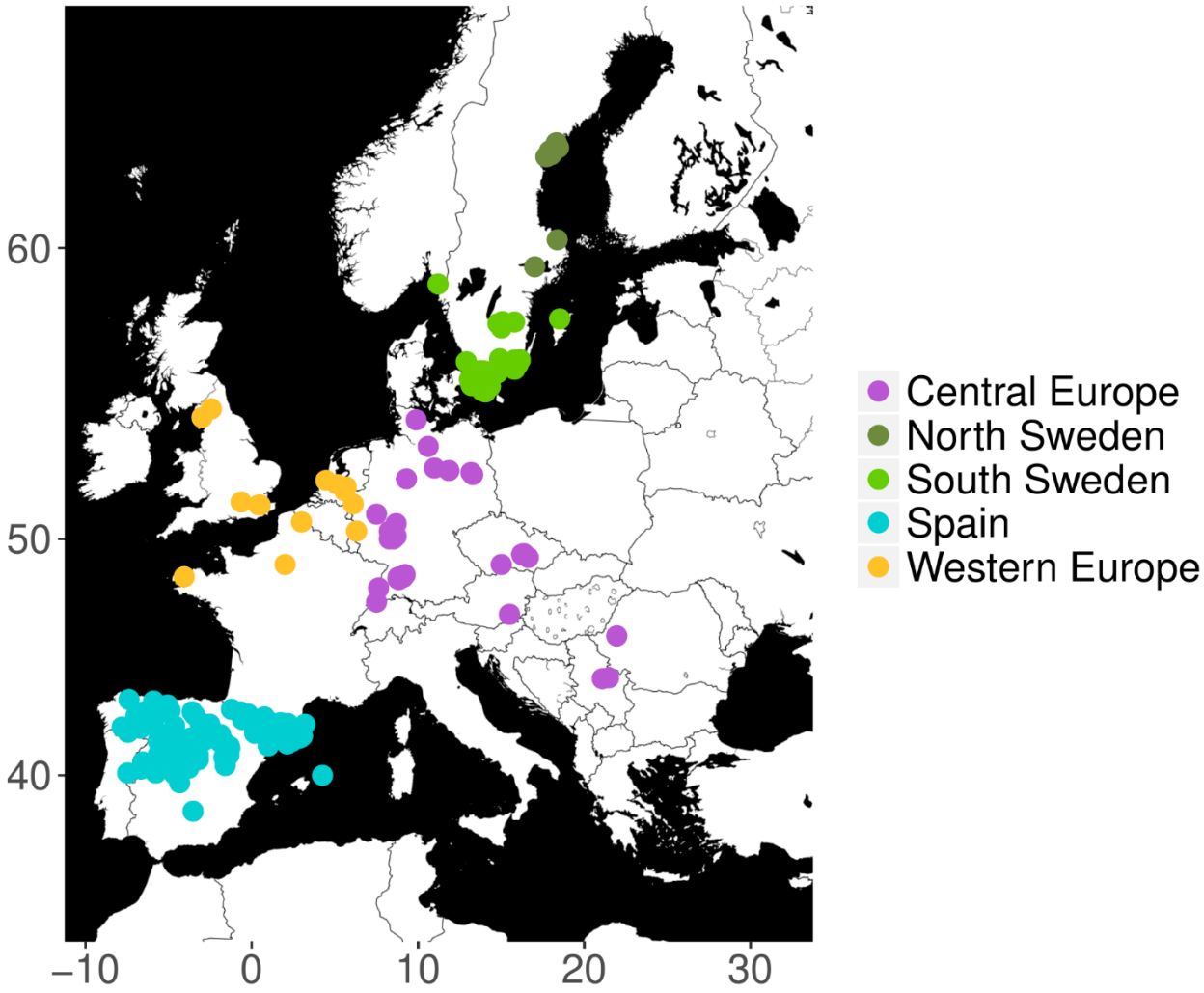


Figure S 1: Map of all accessions used in the study. Accessions are colored by assigned region of origin.

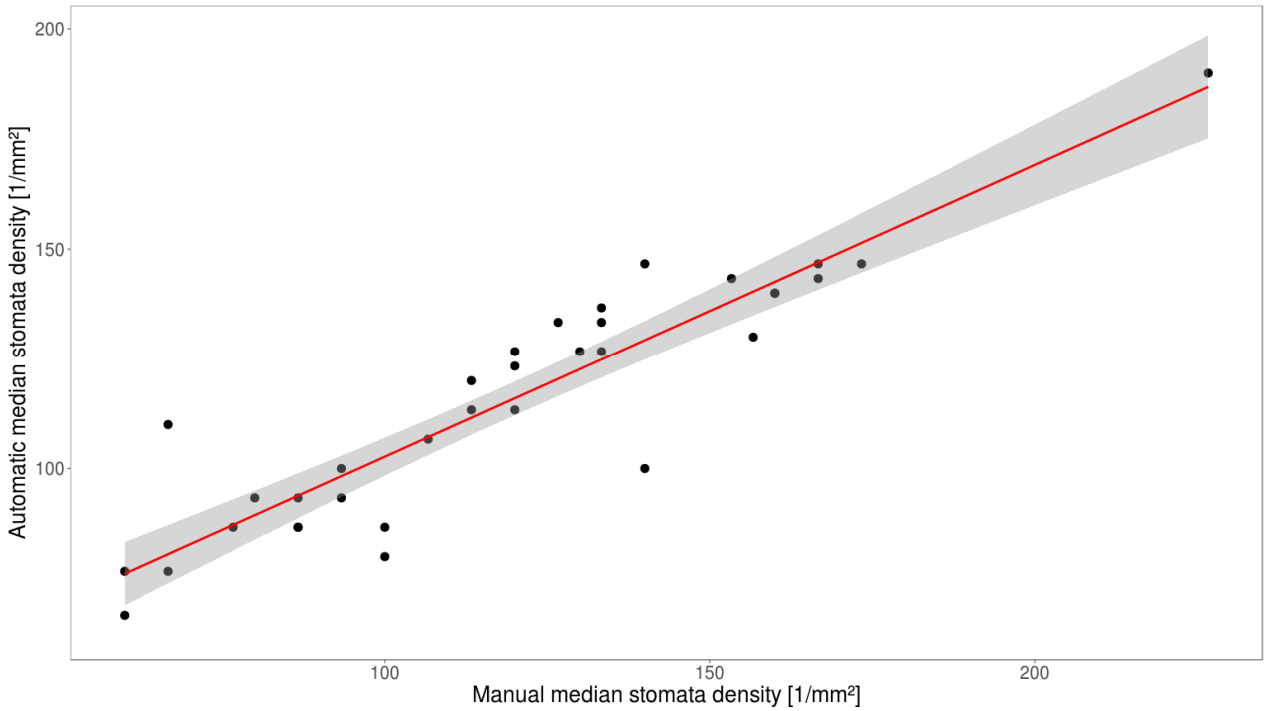


Figure S 2: Correlation plot of manual and automatic stomata counts in a pre-experiment. Each point represents one leaf. The red line represents a linear model fit of the data and the gray shadows indicate the error of the fit.

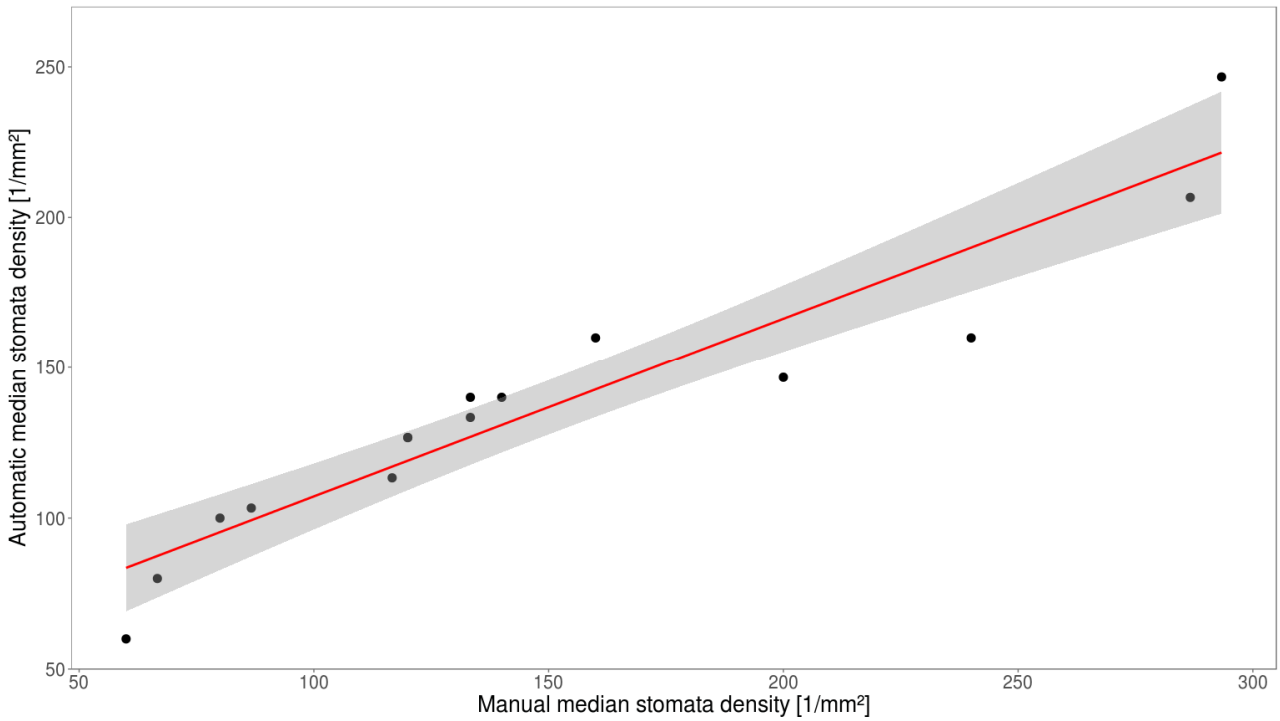


Figure S 3: Correlation plot of manual and automatic stomata counts in the main experiment. Each point represents one leaf. The red line represents a linear model fit of the data and the gray shadows indicate the error of the fit.

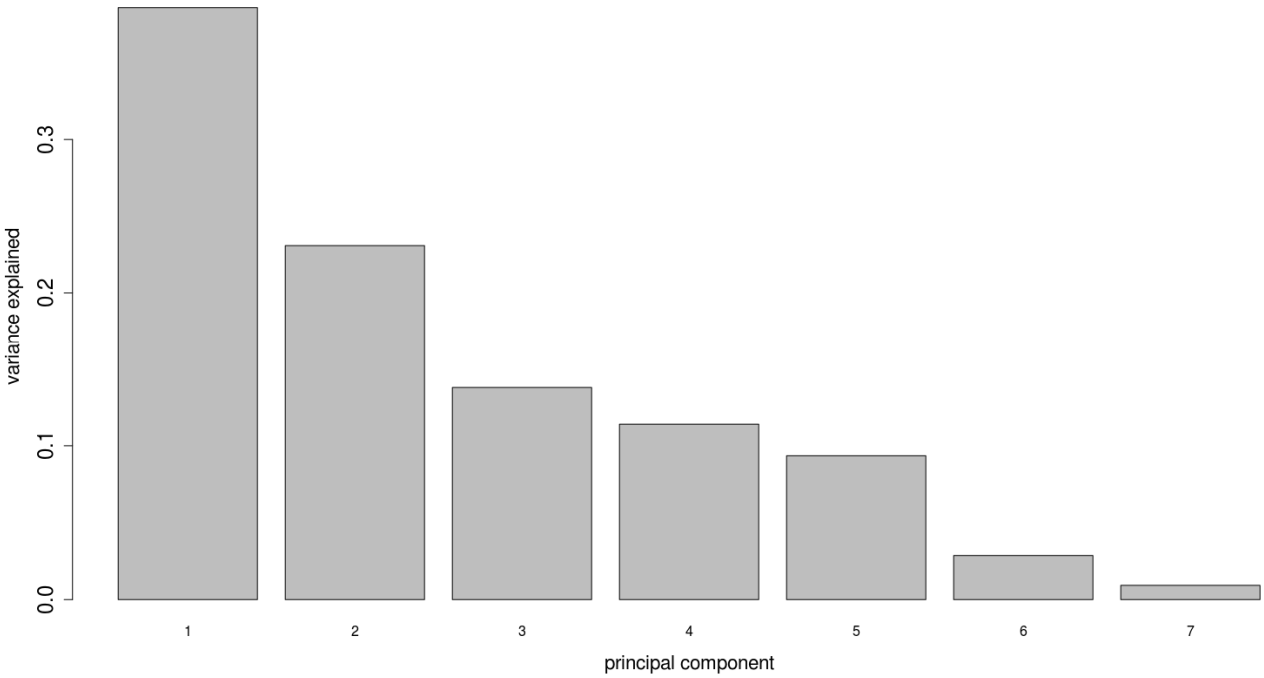


Figure S 4: Barplot of amount of variance explained by each climatic principal component.

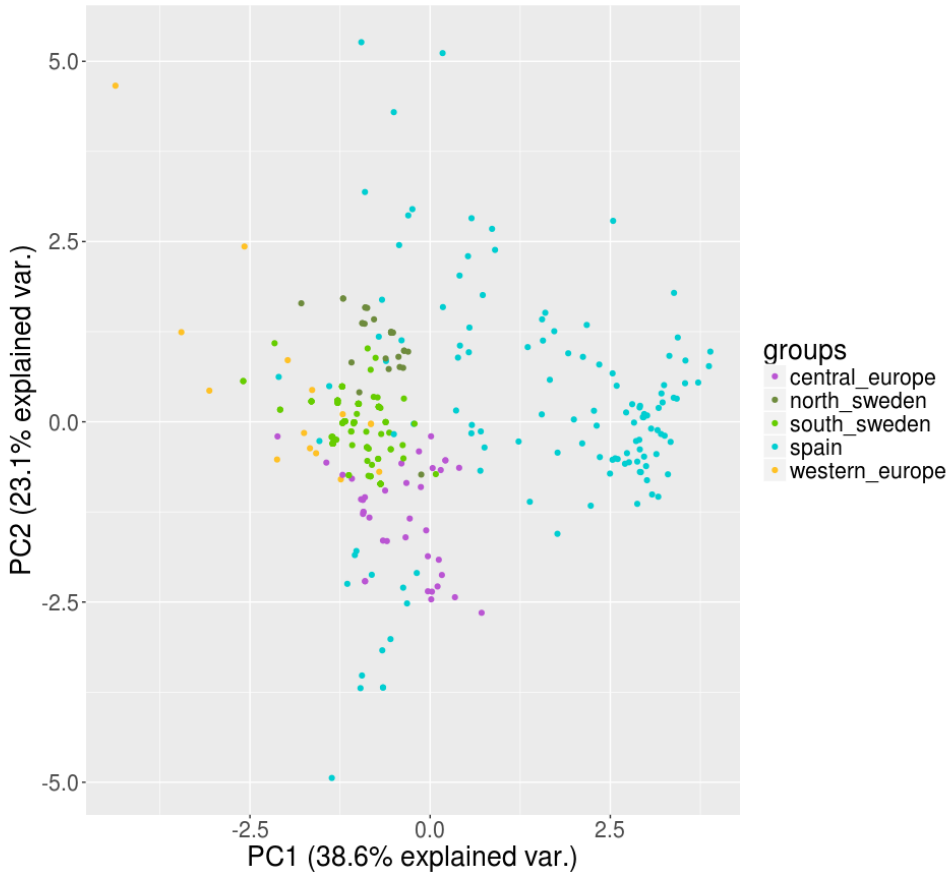


Figure S 5: Plot of first two climatic principal components. Each point is one accession and accessions are colored by region of origin.

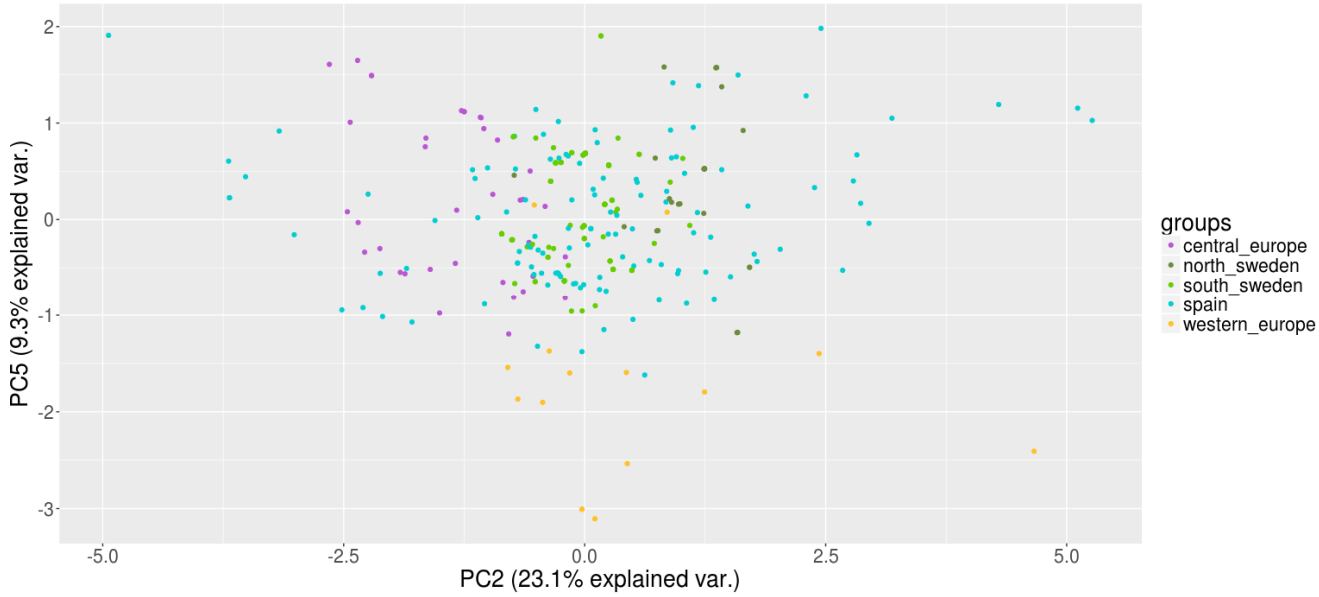


Figure S 6: Plot of climatic principal components two and five, which significantly correlate with stomatal patterns. Each point is one accession and accessions are colored by region of origin.

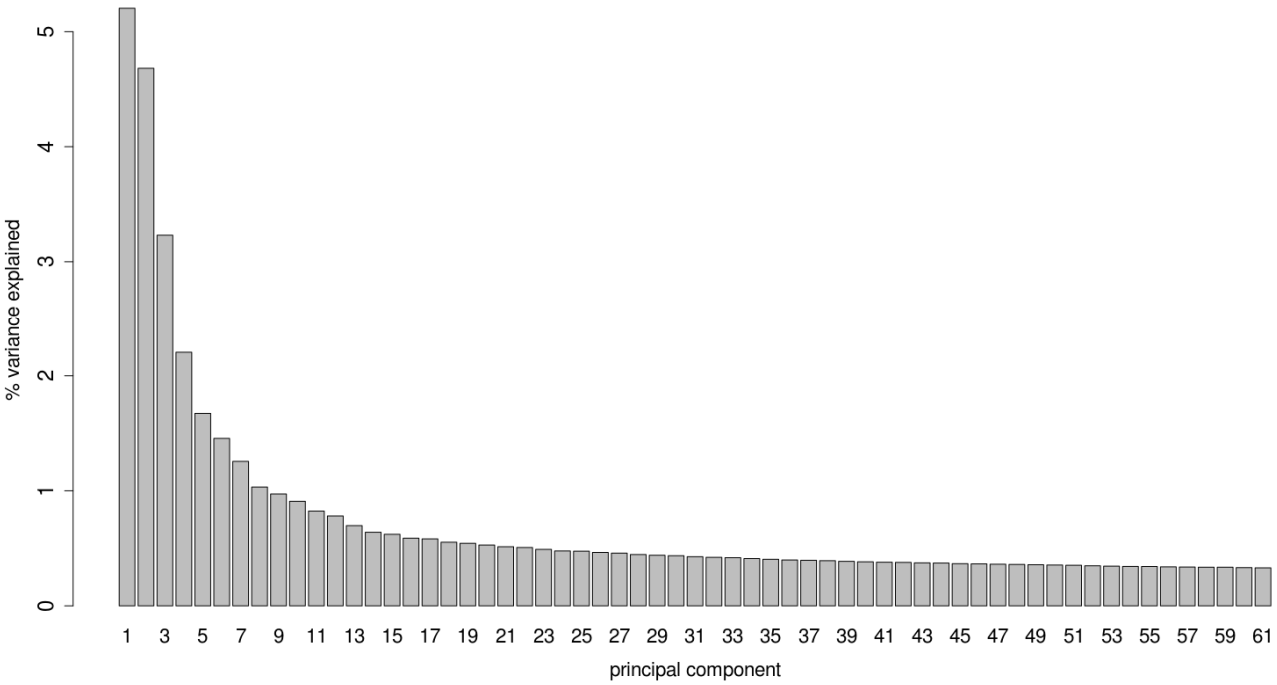


Figure S 7: Barplot of amount of variance explained by each genetic principal component.

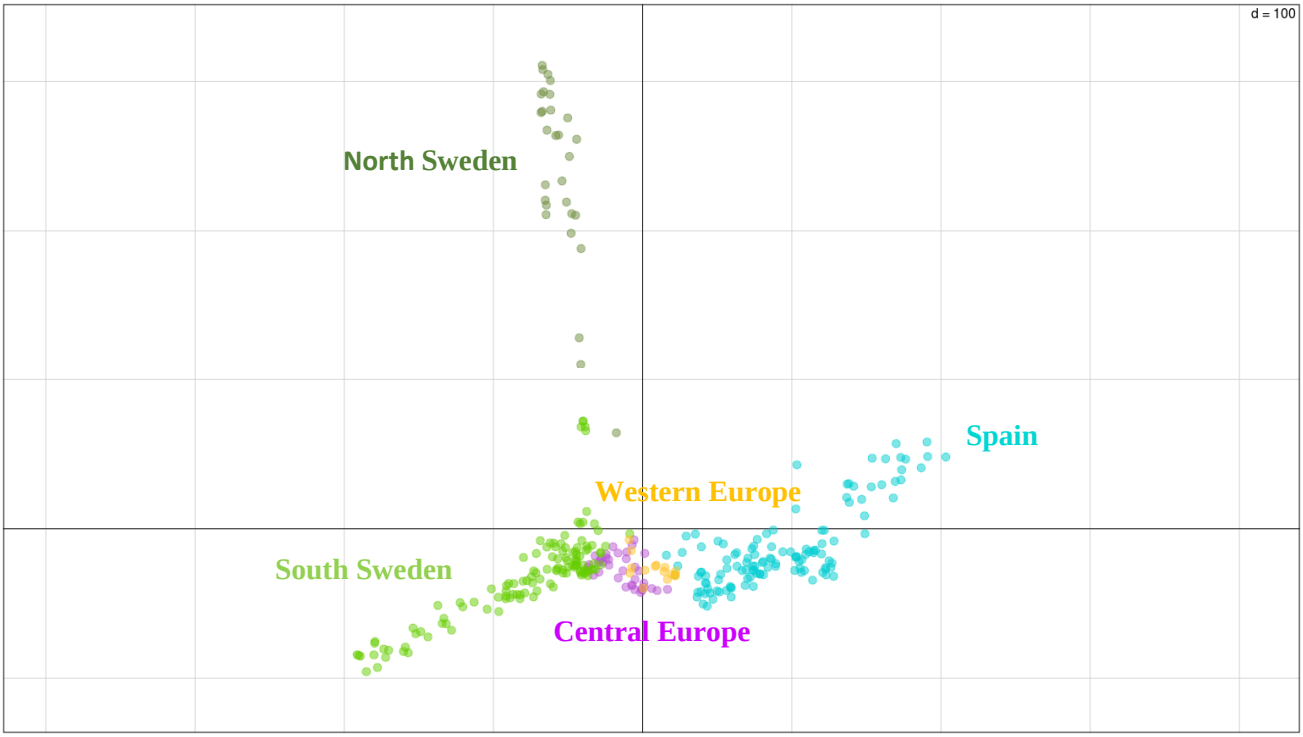


Figure S 8: Plot of first two genetic principal components. Each point is one accession and accessions are colored by region of origin.

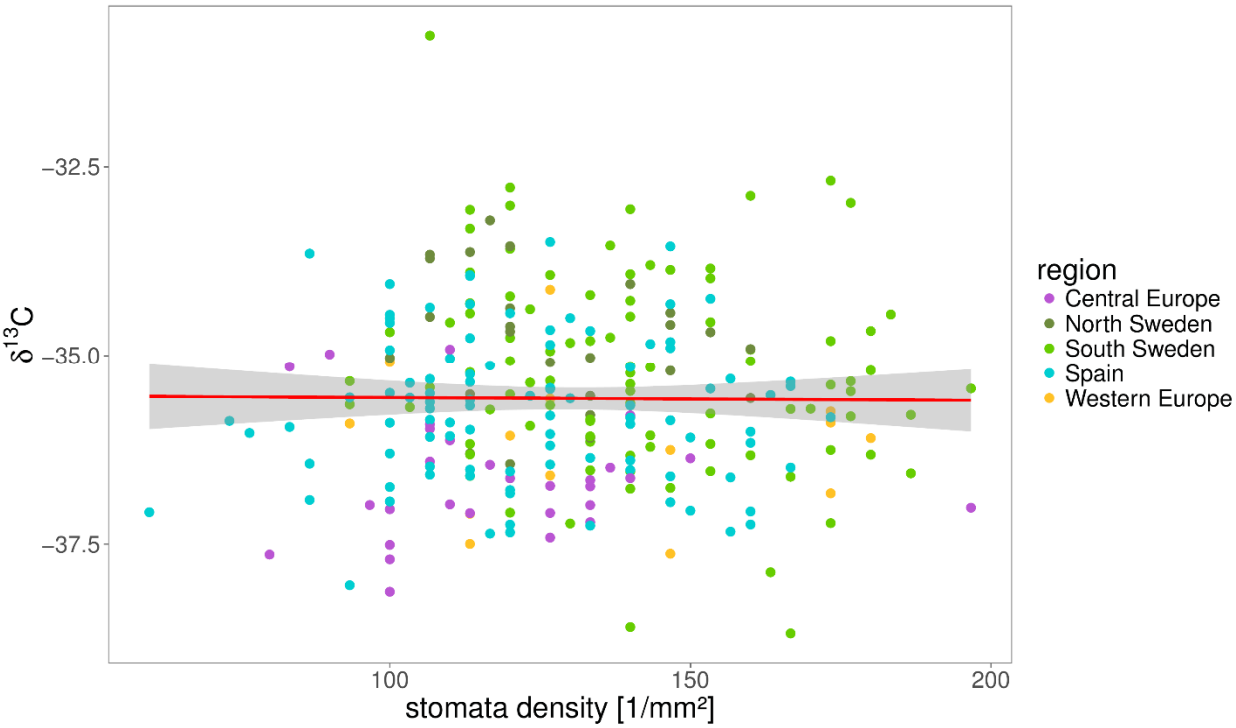


Figure S 9: Correlation plot of $\delta^{13}C$ and stomata density. Each point represents one individual. Accessions are colored by region of origin. The red line represents a linear model fit of the data and the gray shadows indicate the error of the fit.

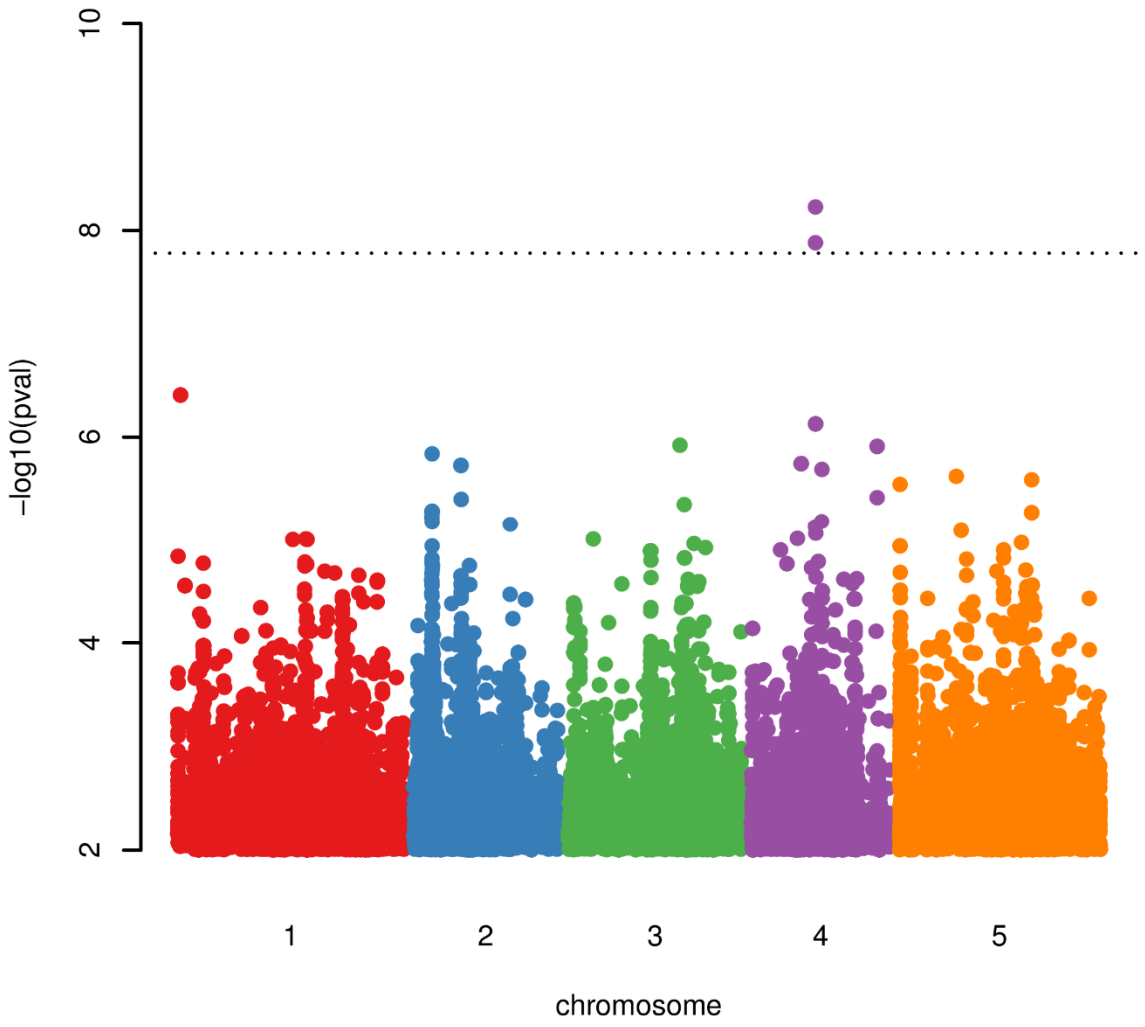


Figure S 10: Manhattan plot of GWAS for mean stomata size with 330 accessions. Each point represents the association p-value of one polymorphism. The dotted horizontal line indicates the Bonferroni significance threshold at type I error rate alpha=0.05. Minor allele count is five.

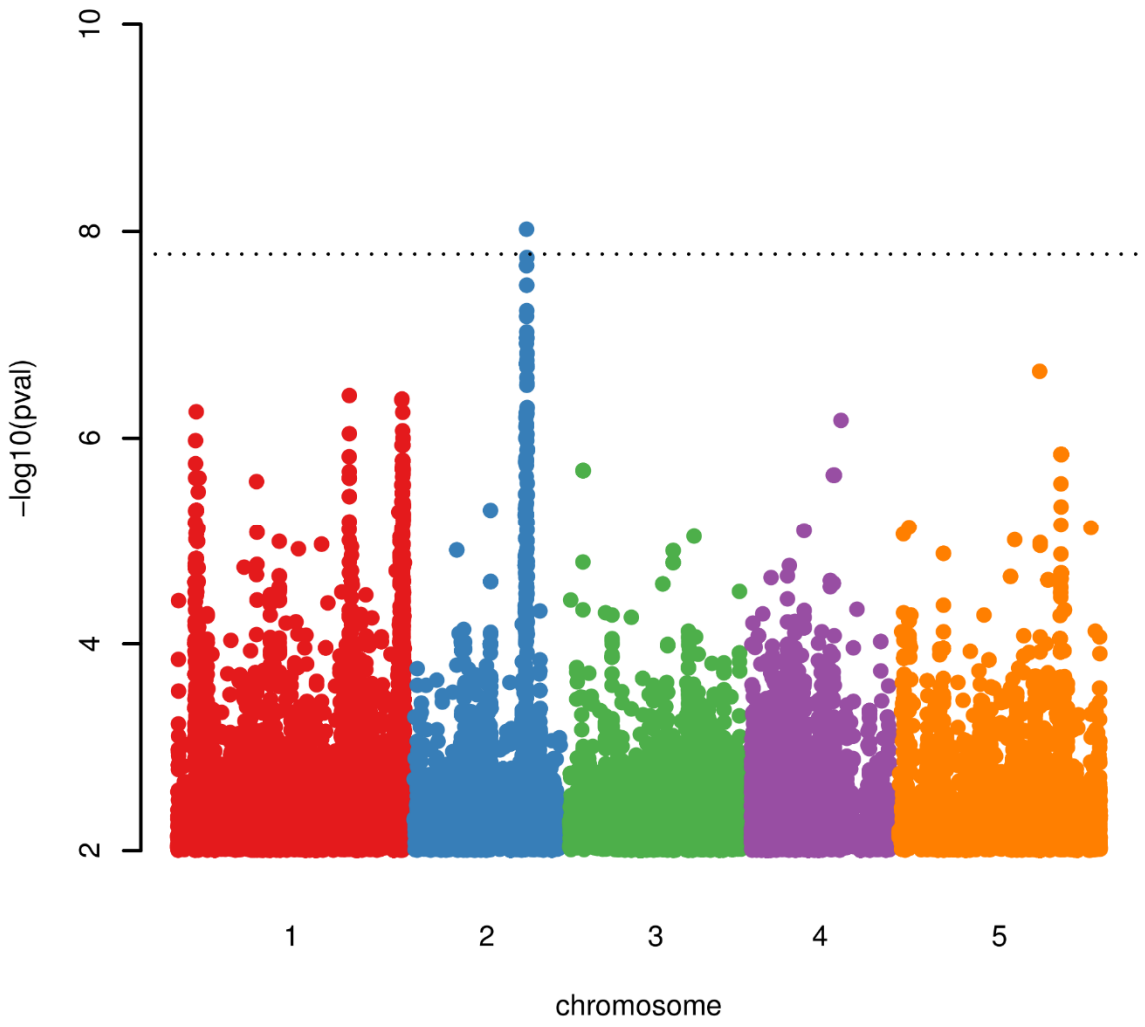


Figure S 11: Manhattan plot of GWAS for $\delta^{13}C$ with 310 accessions. Each point represents the association p-value of one polymorphism. The dotted horizontal line indicates the Bonferroni significance threshold at type I error rate alpha=0.05. Minor allele count is five.

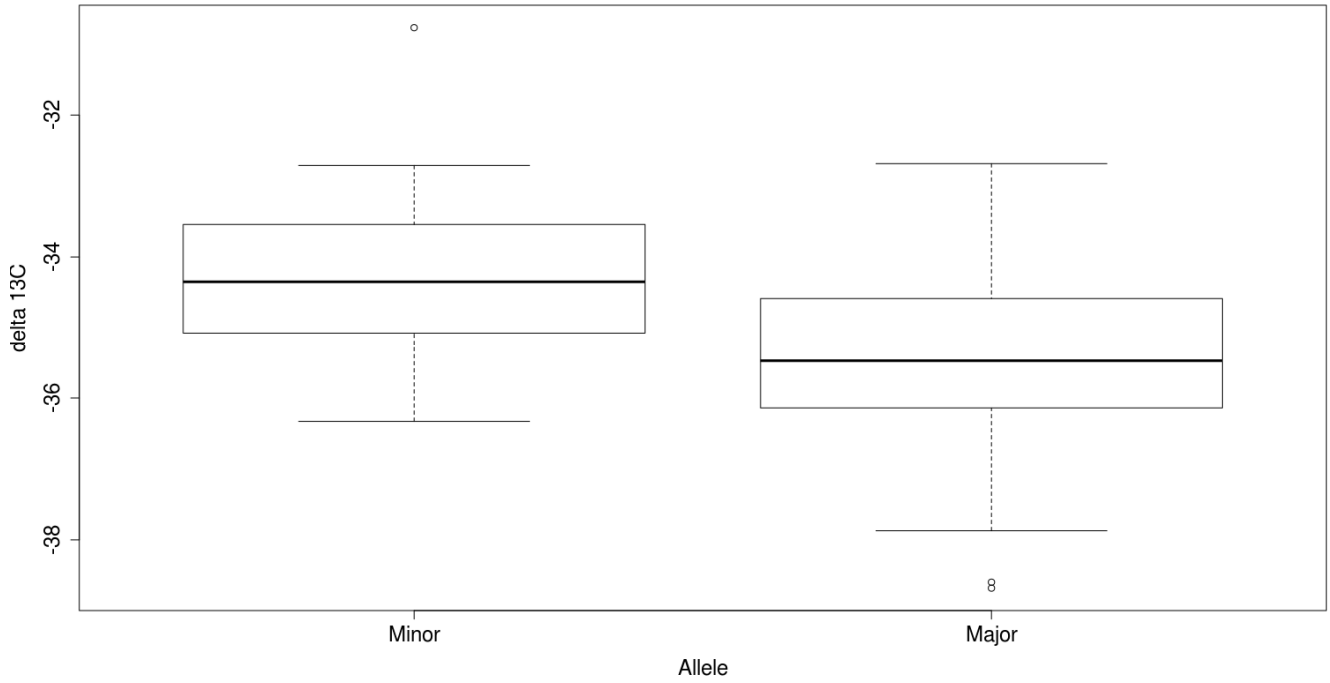


Figure S 12: Boxplot of $\delta^{13}C$ in Southern Swedish accession carrying either the major or minor allele of the QTL on chromosome 2. Two-sided Wilcoxon-Rank-Sum-Test: W = 1868, p-value = 6.569e-05.

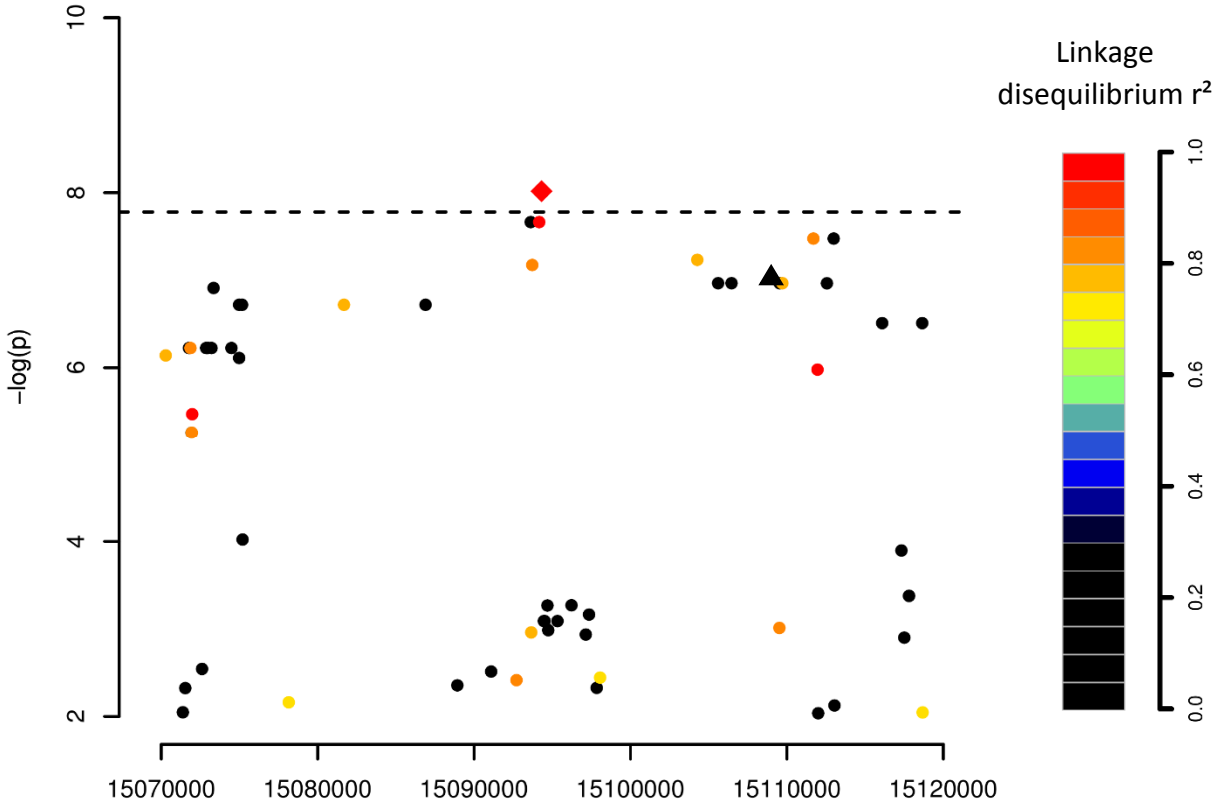


Figure S 13: Local Manhattan plot around QTL on Chr2 for $\delta^{13}C$ with 310 accessions. Points are colored by their level of Linkage Disequilibrium (LD) with the focal SNP (red diamond) in an ascending scale from yellow to red. Black points are not in LD with the focal SNP. A non-synonymous SNP in a candidate gene (AT2G35970.1) is marked by a black triangle.

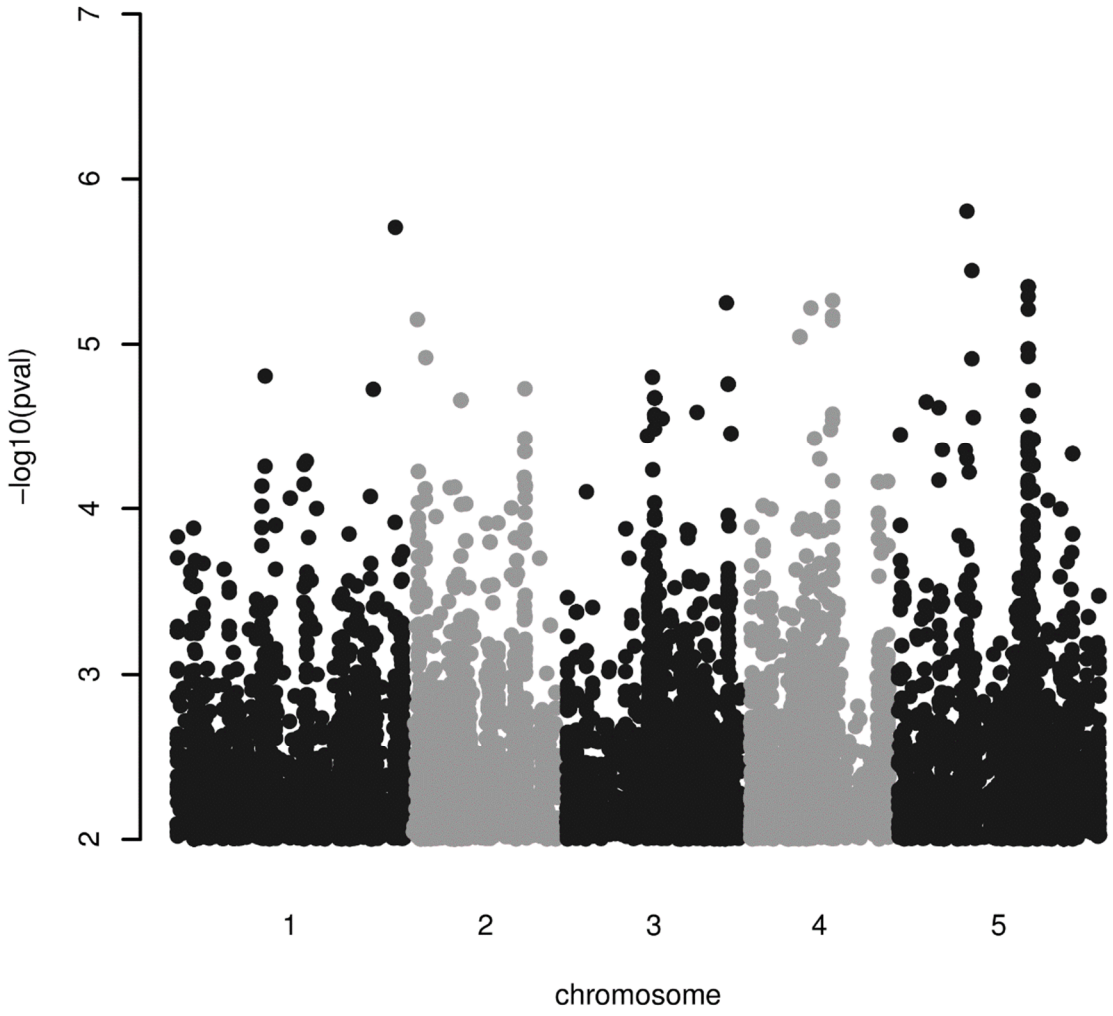


Figure S 14: Manhattan plots of MTMM GWAS testing for SNPs increasing the correlation between stomata size and $\delta^{13}C$. Each point represents the association p-value of one SNP.

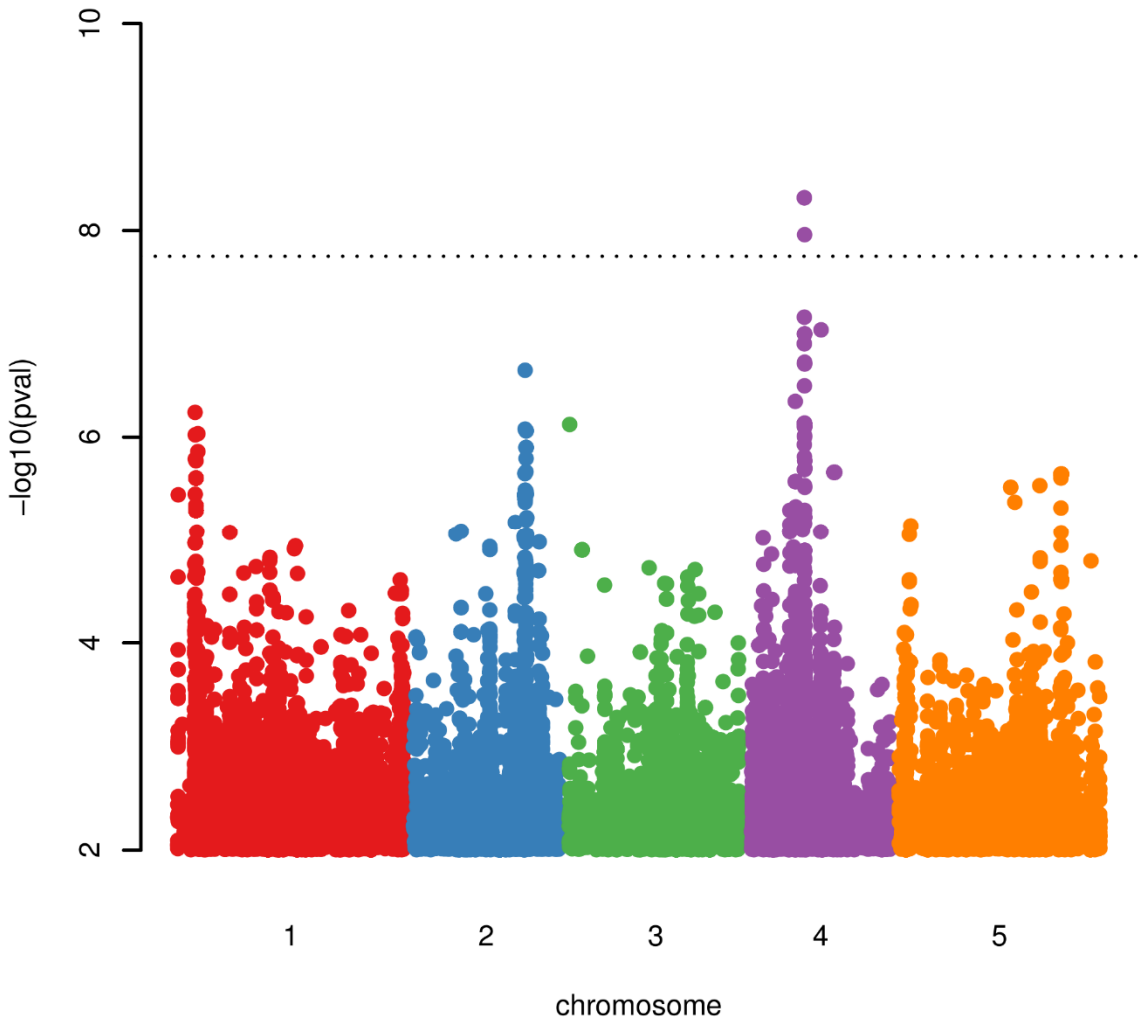


Figure S 15: Manhattan plot of GWAS for $\delta^{13}C$ with the 261 accessions used in MTMM analysis. Each point represents the association p-value of one polymorphism. The dotted horizontal line indicates the Bonferroni significance threshold at type I error rate alpha=0.05. Minor allele count is five.

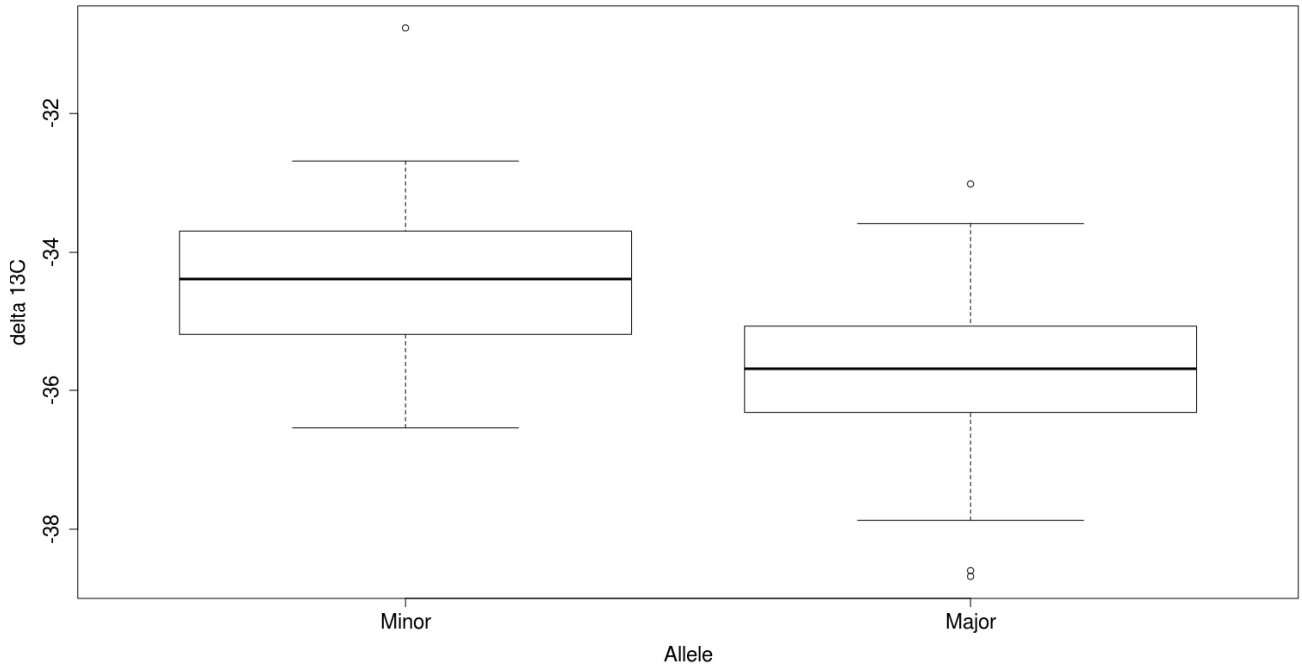


Figure S 16: Boxplot of $\delta^{13}C$ in Southern Swedish accession carrying either the major or minor allele of the QTL on Chr 4. Two-sided Wilcoxon-Rank-Sum-Test: W = 1707, p-value = 1.15e-06.

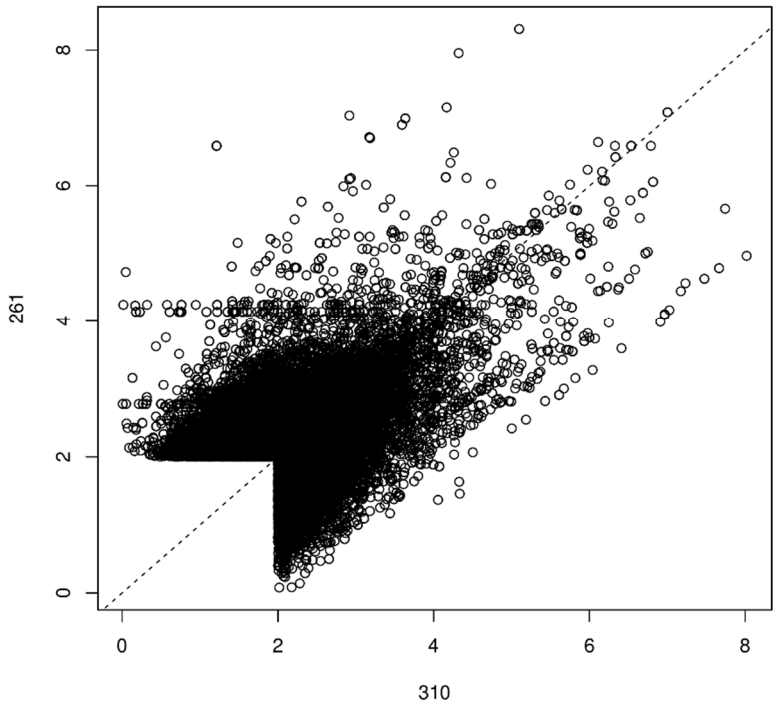


Figure S 17: Correlation plot of the two GWAS datasets with 310 and 261 lines. Each point represents the p-value of one SNP in both datasets. Pearson's moment correlation: r=0.87, p<<0.0001.

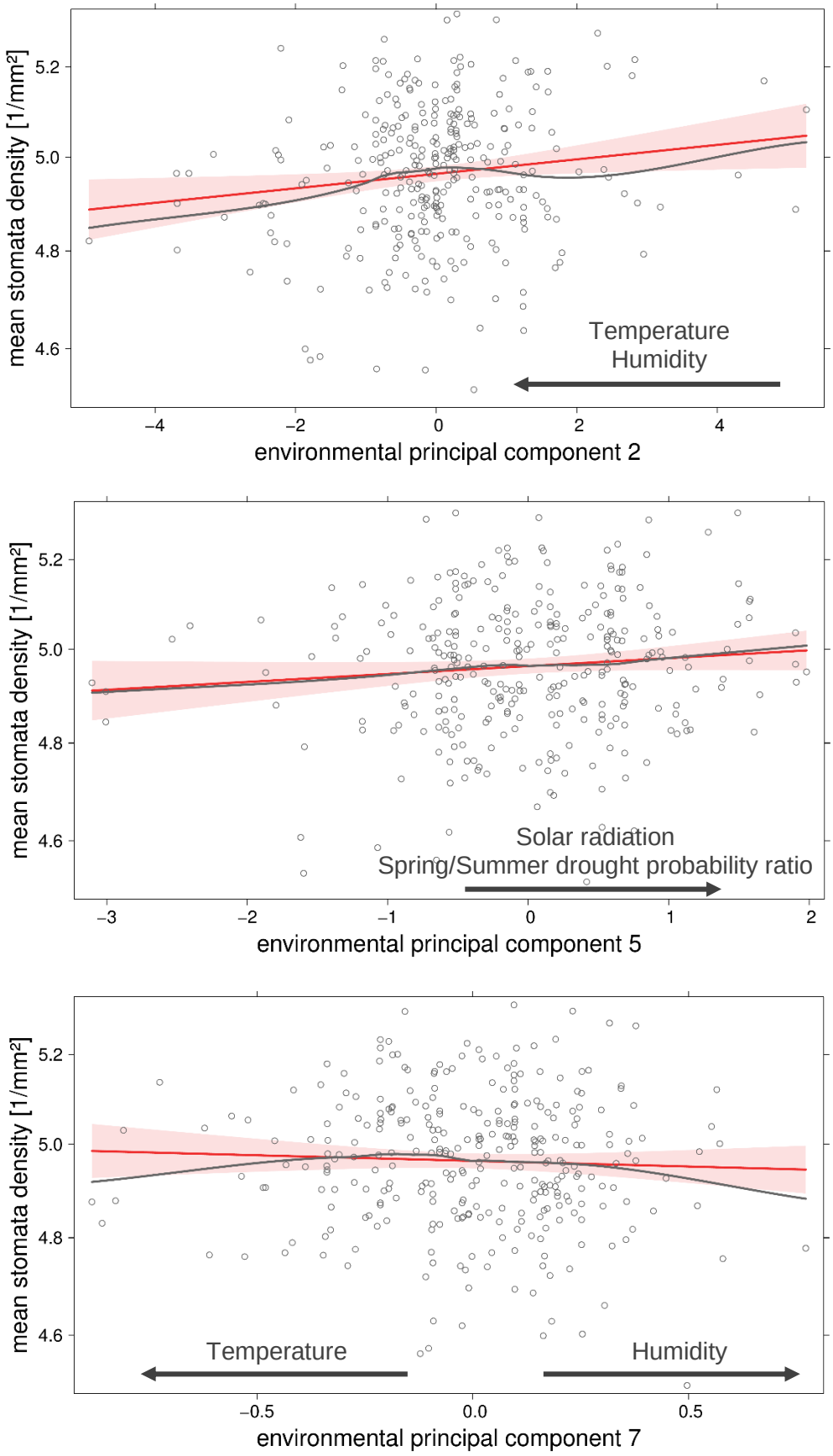
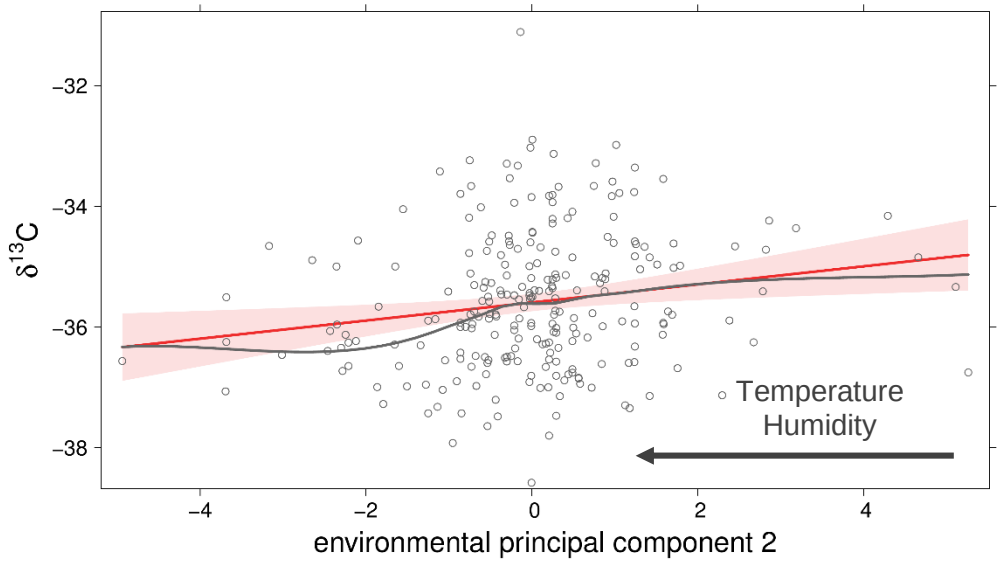
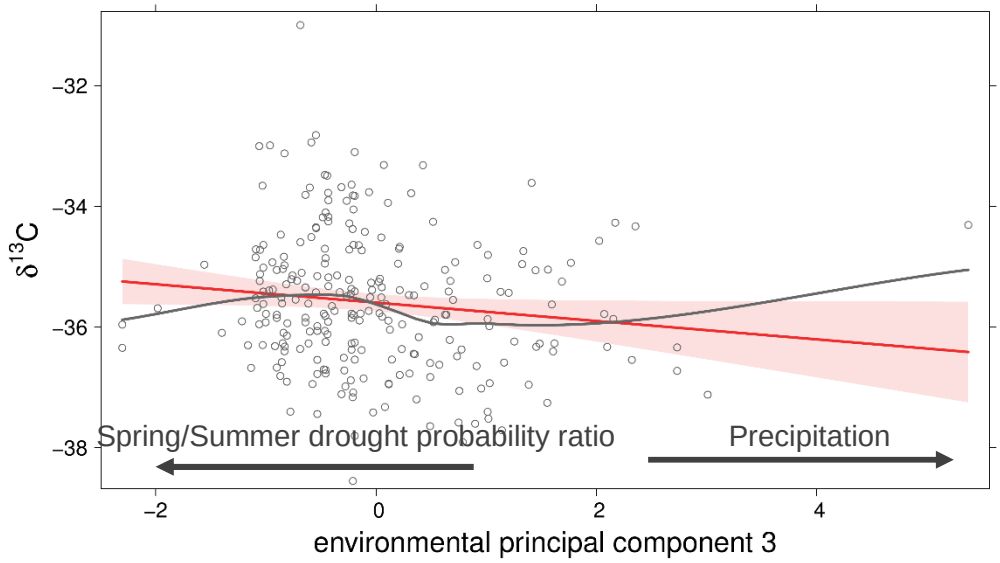


Figure S 18: Correlation between stomata density and climatic principal components (PCs) was tested for each phenotype using a generalized linear model including genetic population

structure. Plots are effect plots based on the model (see methods), showing the correlation between stomata density and two PCs. Black arrows indicate correlation with the climatic variables showing the strongest loadings for the respective principal component. Plots show the linear fit (red solid line) and the smoothed fit of partial residuals (grey) of the specific predictor. Grey dots are partial residuals. The red shade shows the error of the linear fit. All three principal components shown here are significant predictors of the respective response variable ($p<0.05$).


δ13C
−32
−34
−36
−38
−4
−2
0
2
4
Temperature
Humidity
environmental principal component 2


δ13C
−32
−34
−36
−38
Spring/Summer drought probability ratio
Precipitation
−2
0
2
4
environmental principal component 3

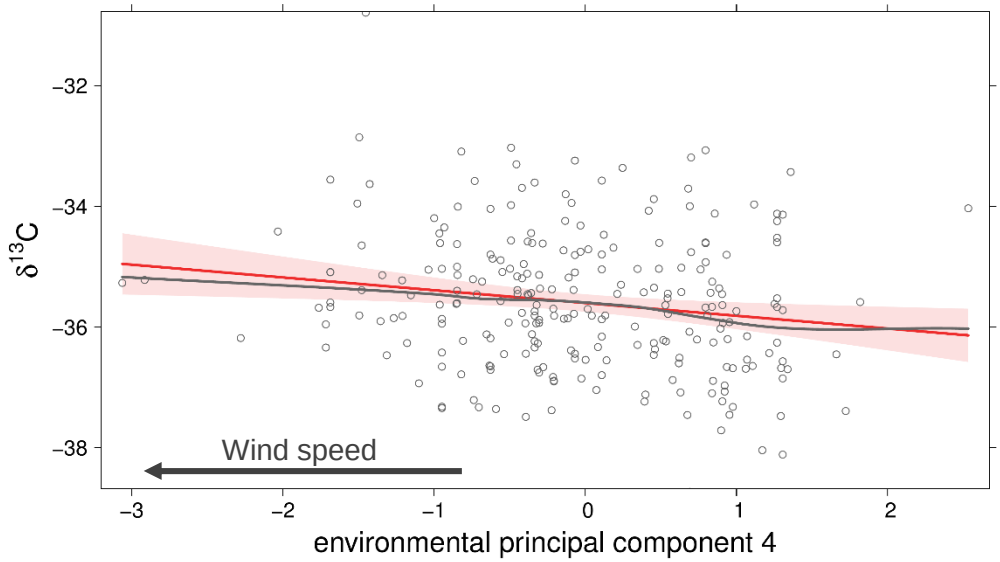

δ13C
−32
−34
−36
−38
Wind speed
−3
−2
−1
0
1
2
environmental principal component 4

Figure S 19: Correlation between stomata patterns and climatic principal components (PCs) was tested for each phenotype using a generalized linear model excluding genetic population structure. Plots are effect plots based on the model (see methods), showing the correlation between stomata size and two PCs. Black arrows indicate correlation with the climatic variables showing the strongest loadings for the respective principal component Plots show the linear fit (red solid line) and the smoothed fit of partial residuals (grey) of the specific predictor. Grey dots are partial residuals. The red shade shows the error of the linear fit. All three principal components shown here are significant predictors of the respective response variable ($p<0.05$).

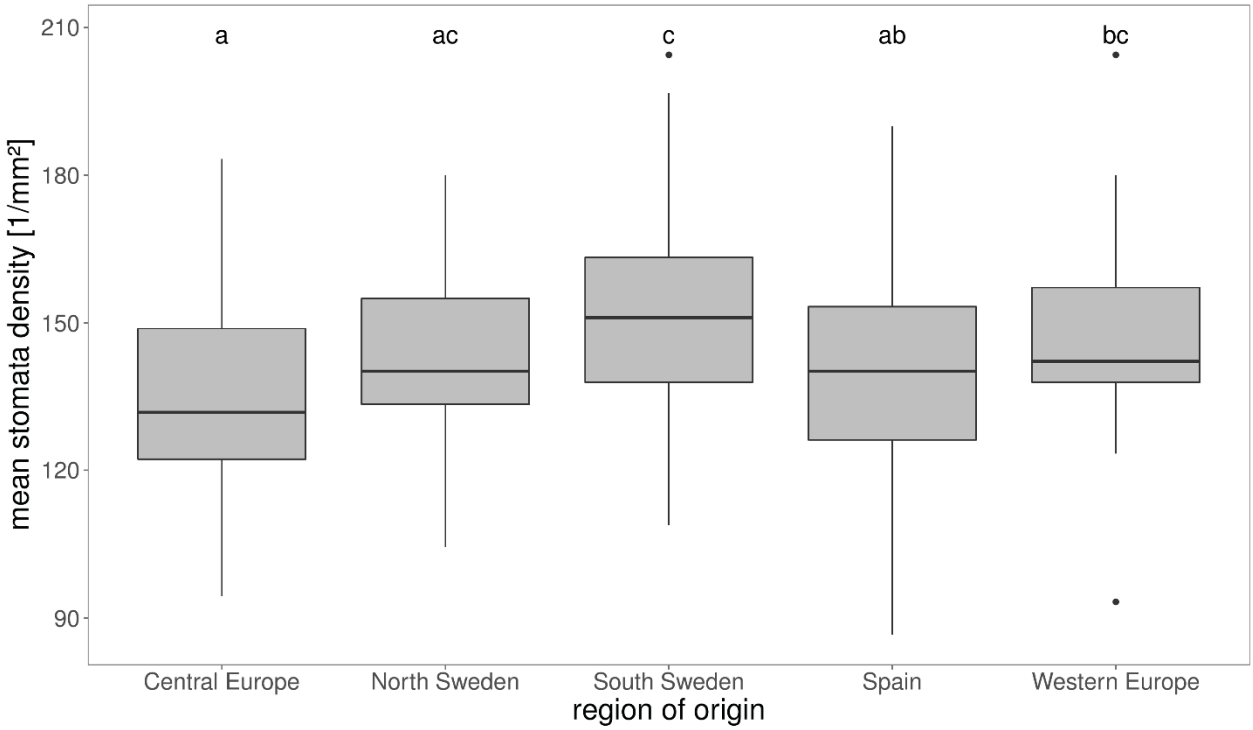


Figure S 20: Boxplot of mean stomata density per accession grouped by region of origin. Significance of differentiation was tested using a generalized linear model followed by a post-hoc test. Significance is indicated by letters on top: Groups that do not share a common letter are significantly different.