

Supplementary to

A diverse panel of 755 bread wheat accessions harbors untapped genetic diversity in landraces and reveals novel genetic regions conferring powdery mildew resistance

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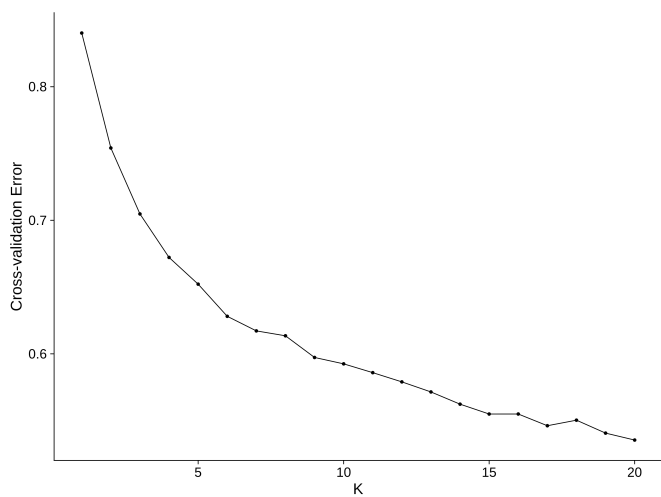


Figure S1. Cross-validation error of Admixture kinship analysis for K=2 to K=20 for 29,965 SNPs.

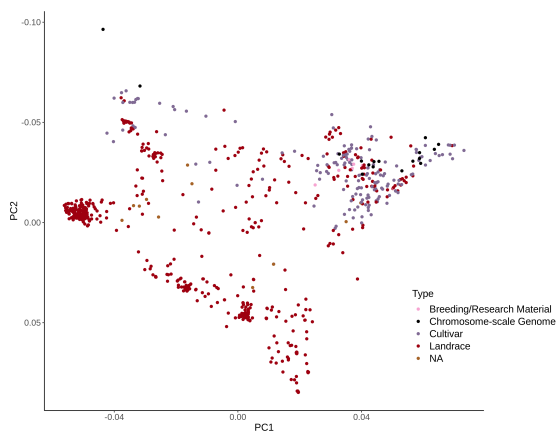
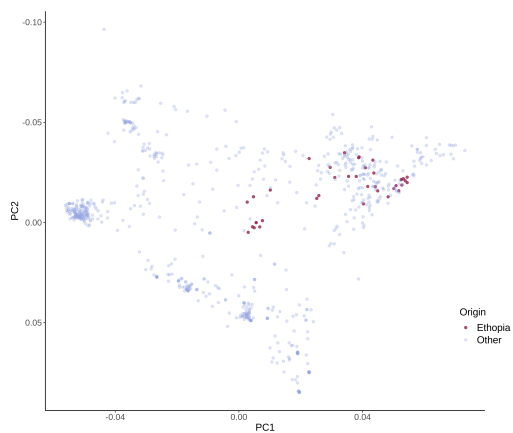
a**b**

Figure S2. PCAs from 27,337 SNPs of the LandracePLUS panel including high-quality sequenced genomes with PC1 = 8.4% and PC2 = 5.1%

a Types of wheat accessions are highlighted in different colors. **b** Ethiopian landraces are highlighted by color in comparison to accessions of another origin

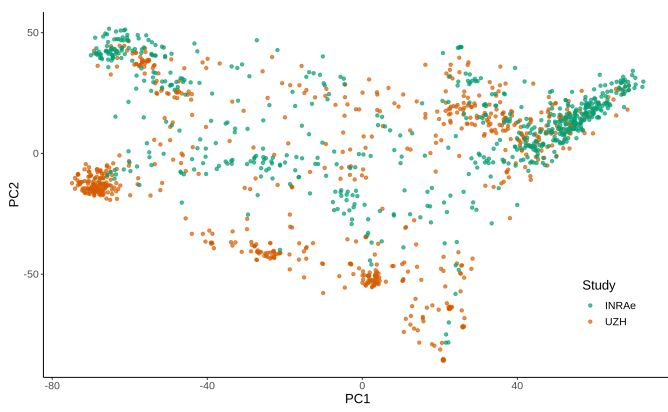
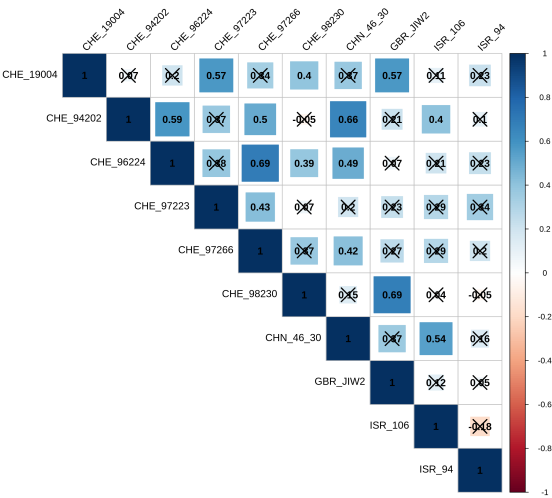


Figure S3. Genetic diversity of the LandracePLUS panel compared to 632 landraces from an INRAe study that represent the original pool of worldwide hexaploid diversity (Balfourier et al. 2019).

PCA from the filtered 29,965 polymorphic SNPs that were present in SNP arrays of both studies. PC1 = 8.9%, PC2 = 4.0%. Accessions from the LandracePLUS panel are shown in orange, while INRAe landraces are colored in green.

a



b

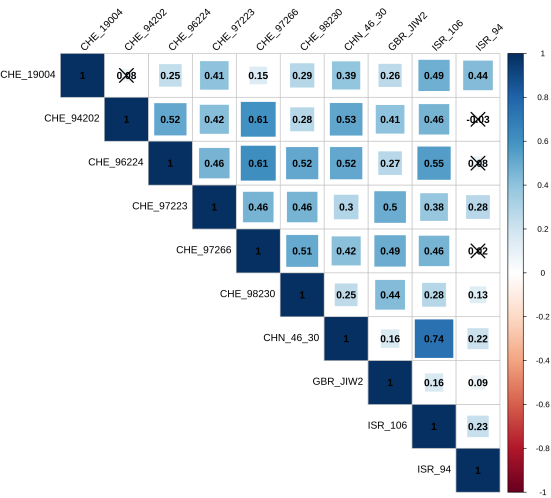


Figure S4. Correlation matrix showing Pearson correlation of virulence between the ten isolates used for phenotyping.
a Correlation coefficients based on phenotypic variation of the differential lines. **b** Correlation coefficients based on phenotypic variation in the LandracePLUS panel. Correlation coefficients with corresponding p-values below the significance 0.05 are crossed out.

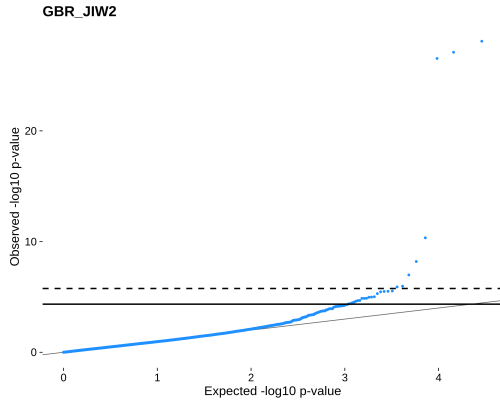
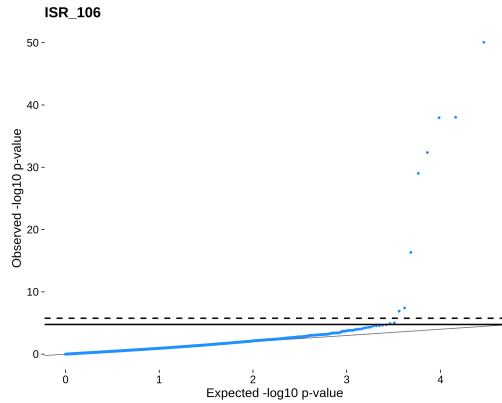
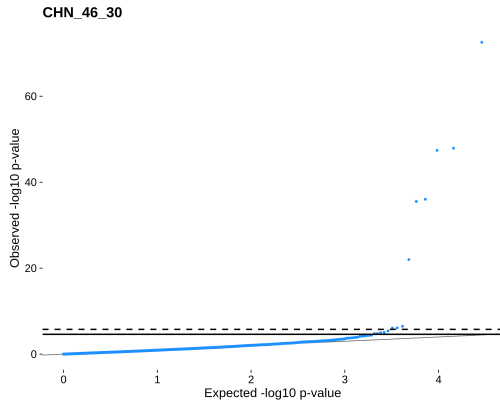
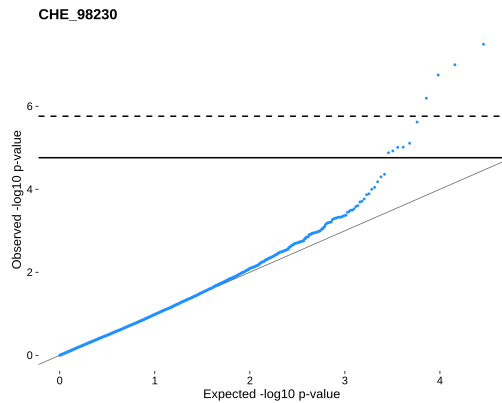
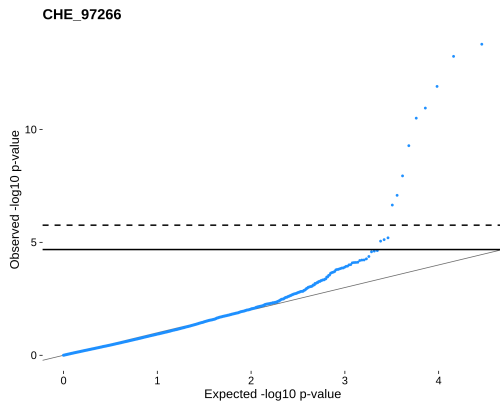
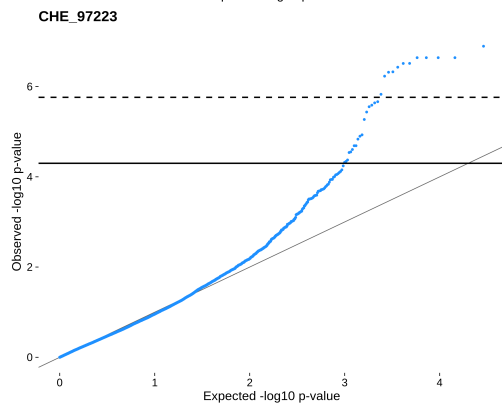
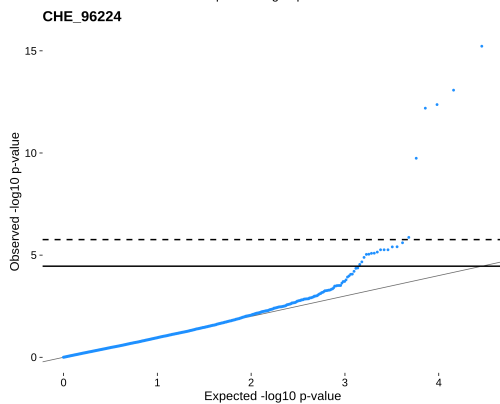
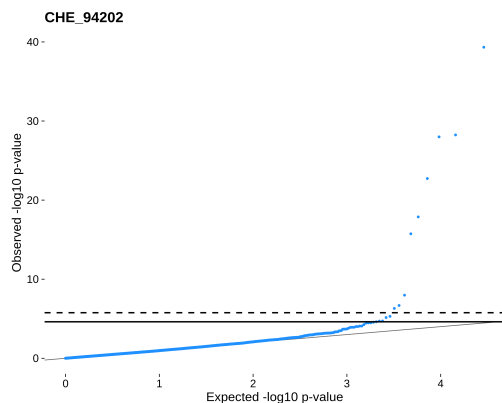
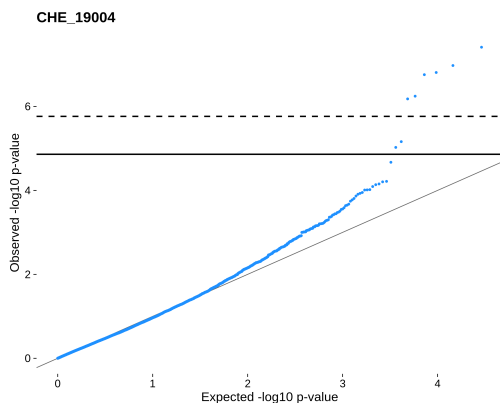


Figure S5. QQ Plots for GWAS with nine powdery mildew isolates and the LandracePLUS panel. Isolate names are depicted in the top-left corner. Solid lines represent the threshold for False discovery rate (FDR) and dashed lines for Bonferroni correction.

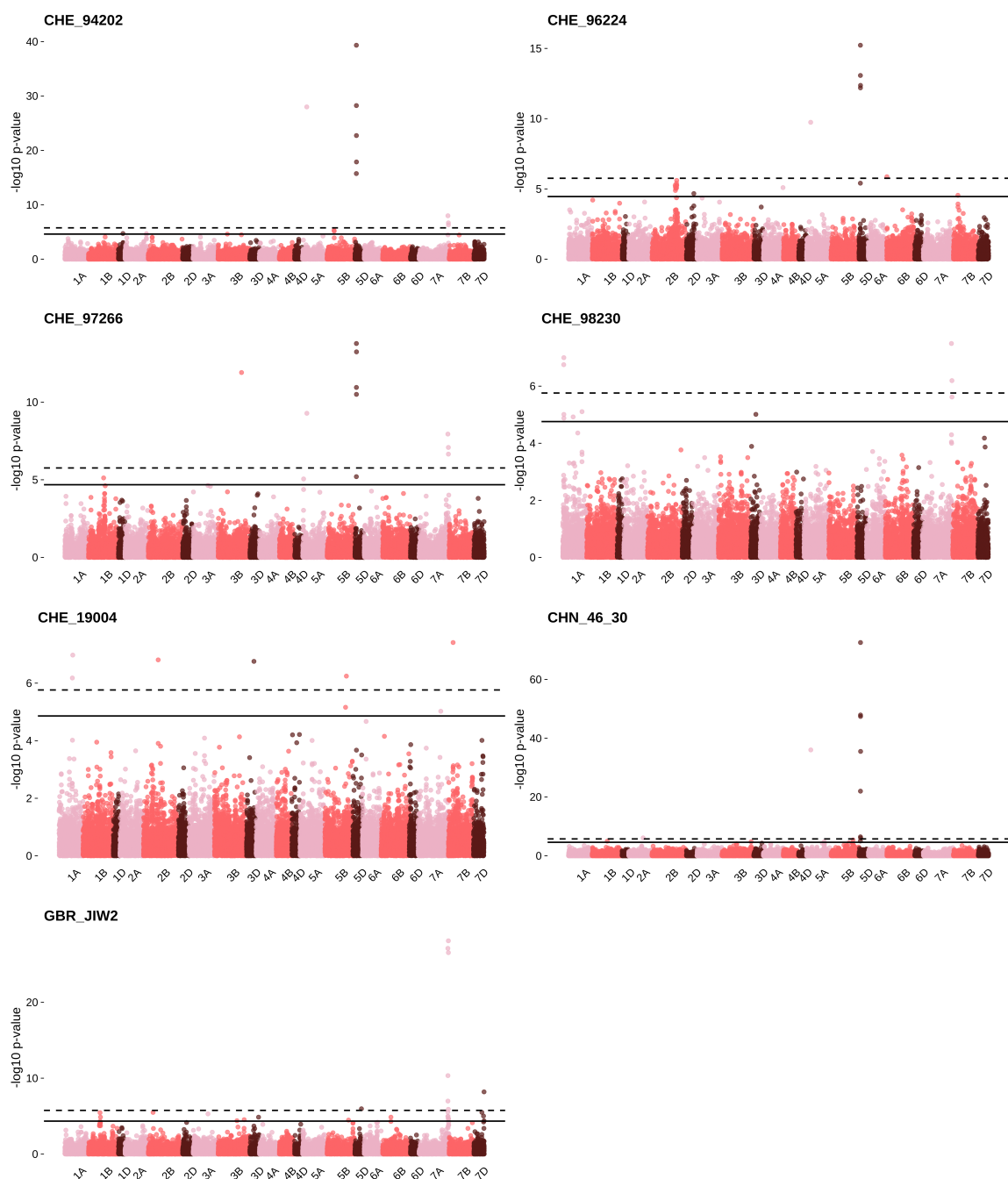


Figure S6. Manhattan Plots for GWAS with the seven powdery mildew isolates and the LandracePLUS panel that showed a good fit in the QQ plots for the univariate linear mixed model.

Isolate names are depicted in the top-left corner. Solid lines represent the threshold for False discovery rate (FDR) and dashed lines for Bonferroni correction.

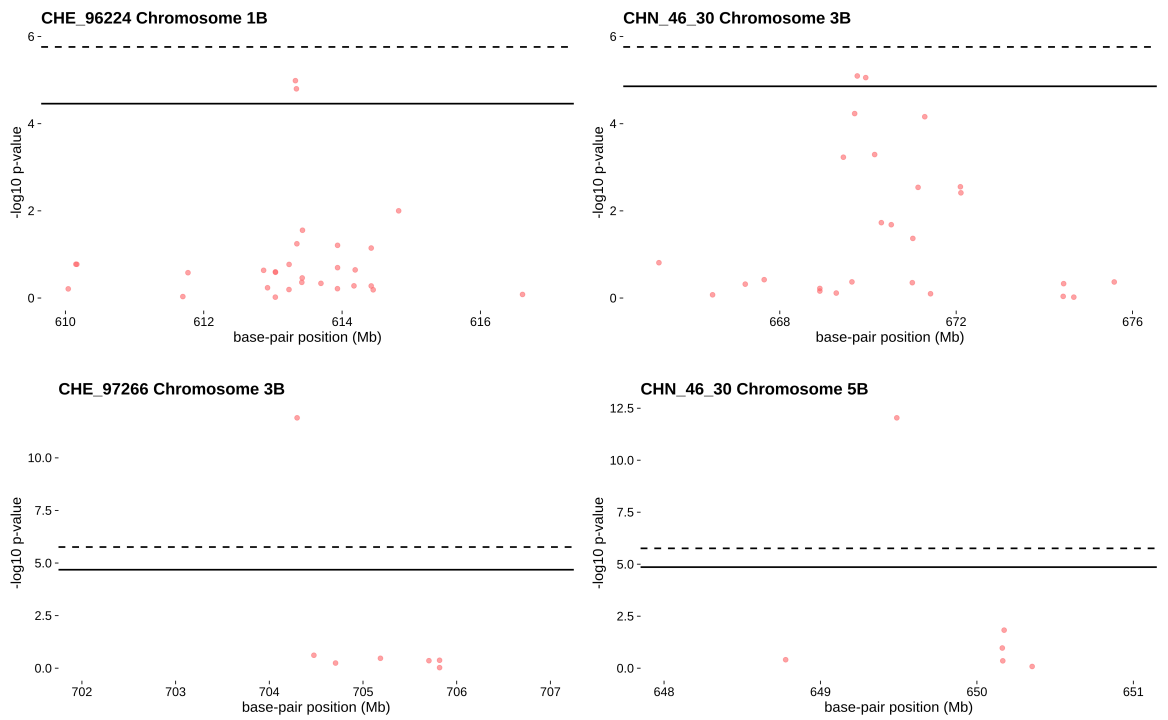


Figure S7. Manhattan Plots for GWAS of the LandracePLUS panel using a *Pm2* covariate and the isolates that contain *AvrPm2*. Isolate and chromosomes are depicted in the top-left corner. Solid lines represent the threshold for False discovery rate (FDR) and dashed lines for Bonferroni correction.

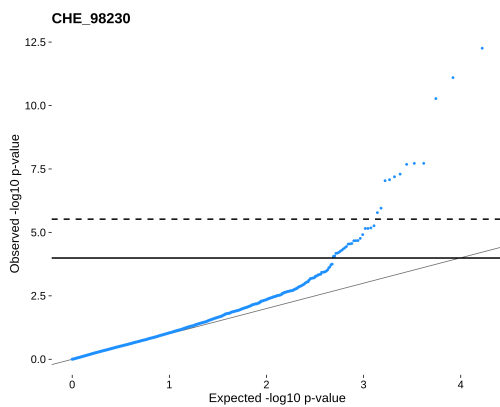


Figure S8. QQ Plot for GWAS with powdery mildew isolate CHE_98230 and landraces from Pakistan and Iran. Isolate names are depicted in the top-left corner. Solid lines represent the threshold for False discovery rate (FDR) and dashed lines for Bonferroni correction.

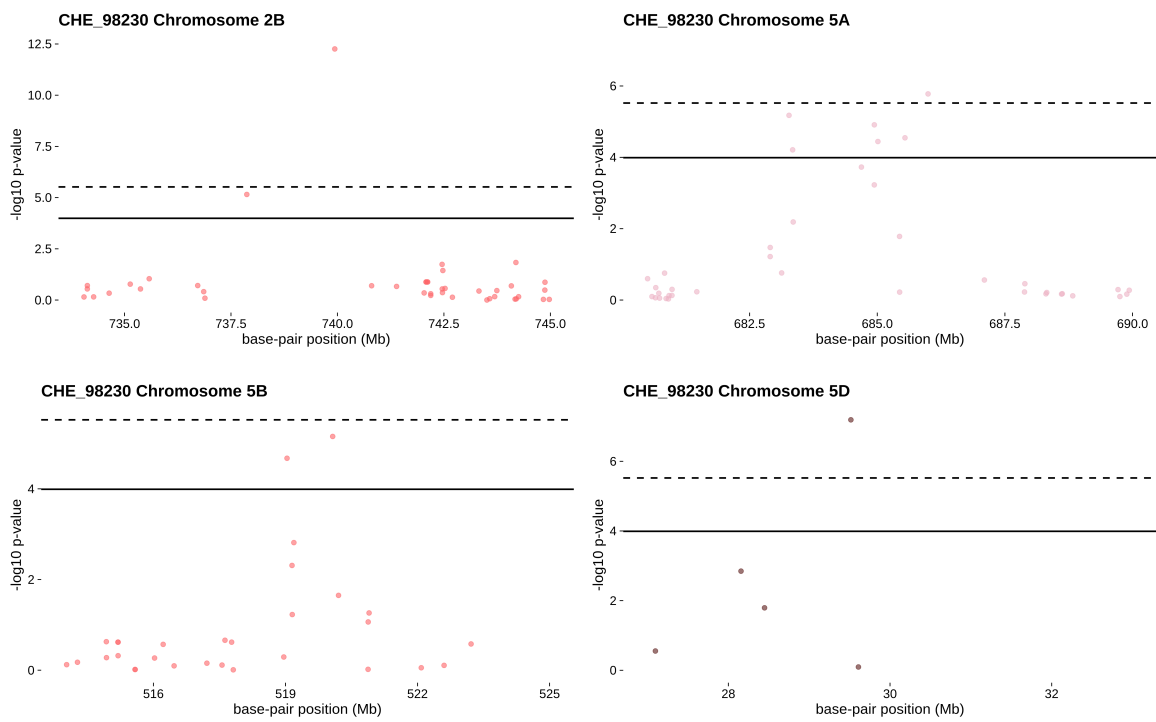


Figure S9. Manhattan Plots of CHE_98230 resistance-associated loci of accessions from Pakistan and Iran. Isolate and chromosomes are depicted in the top-left corner. Solid lines represent the threshold for False discovery rate (FDR) and dashed lines for Bonferroni correction.

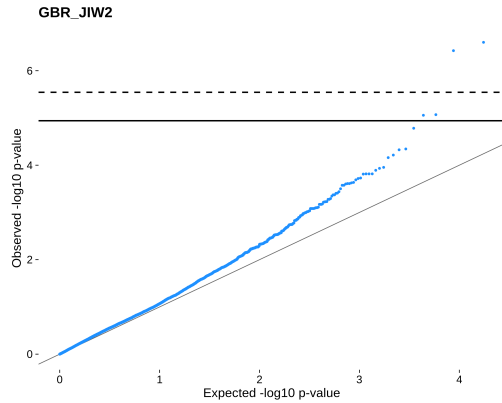
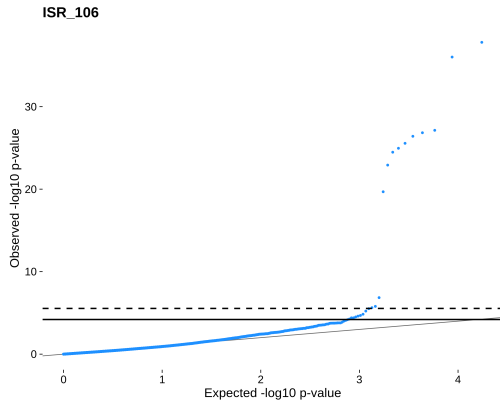
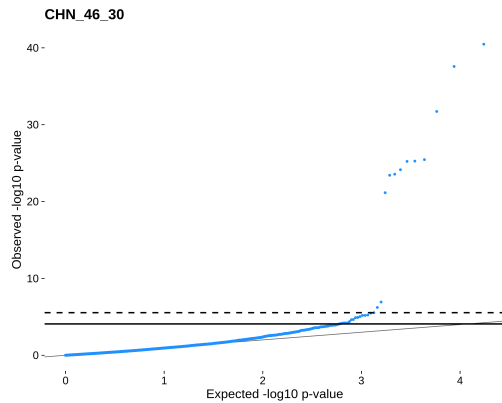
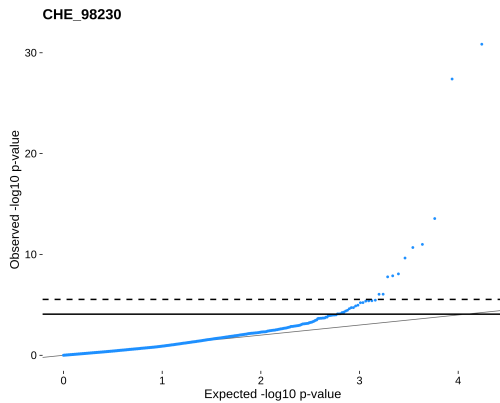
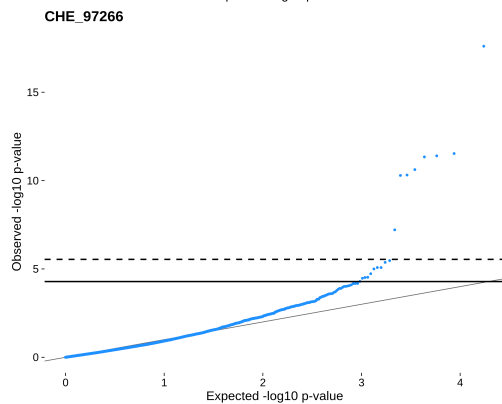
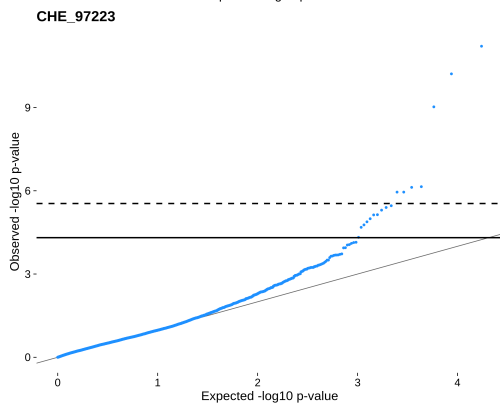
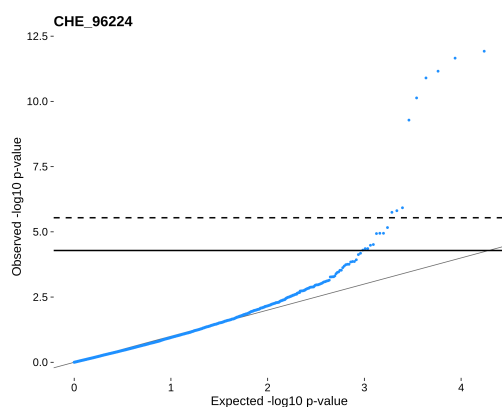
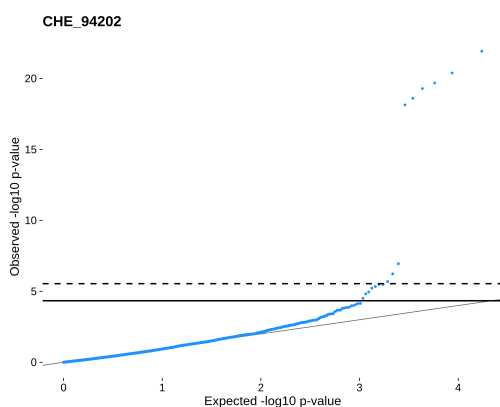
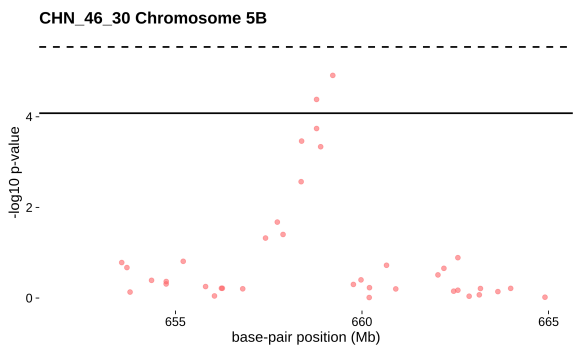
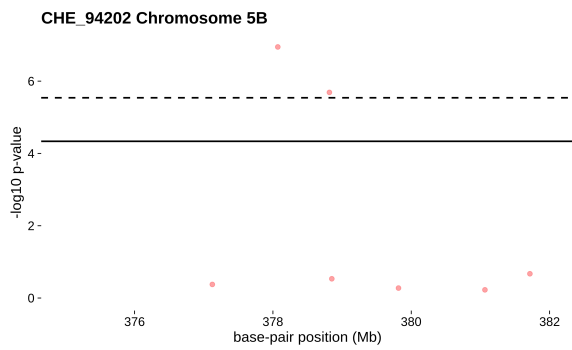
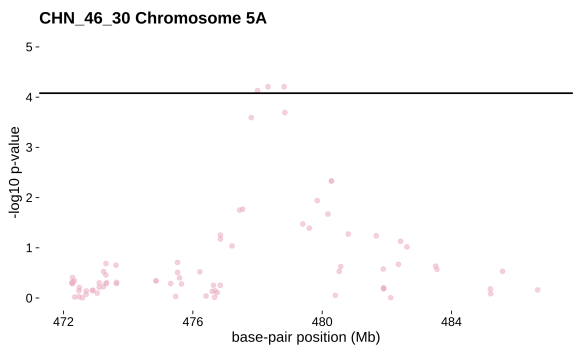
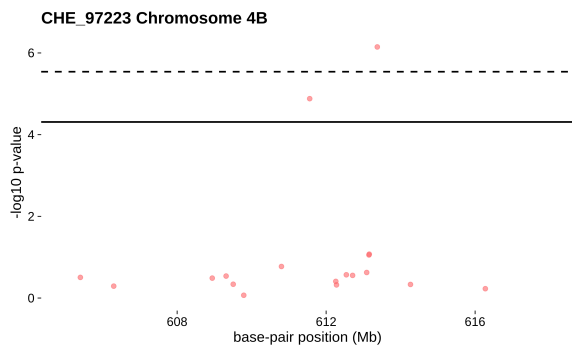
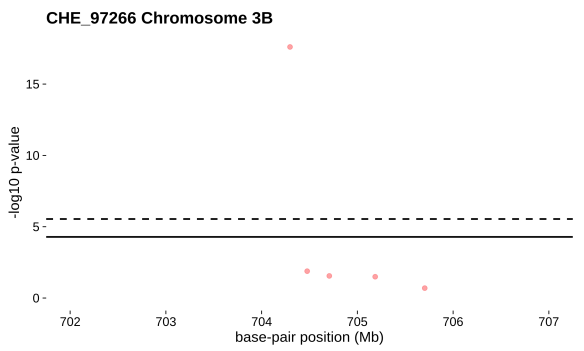
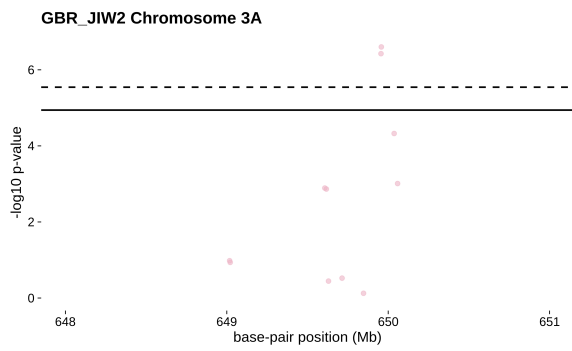
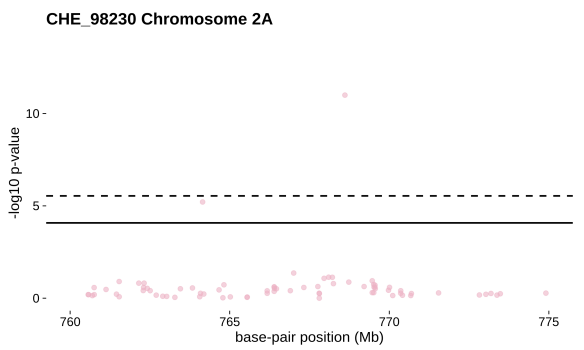
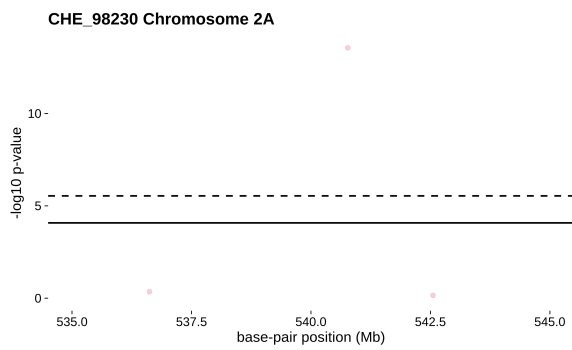
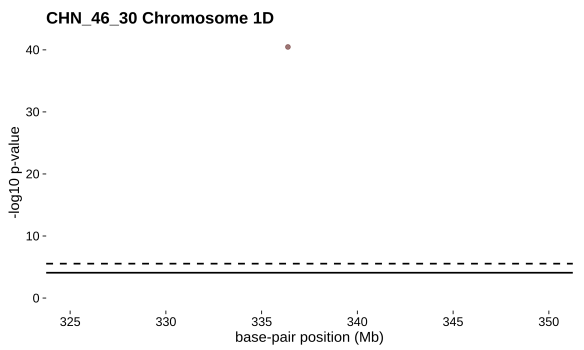
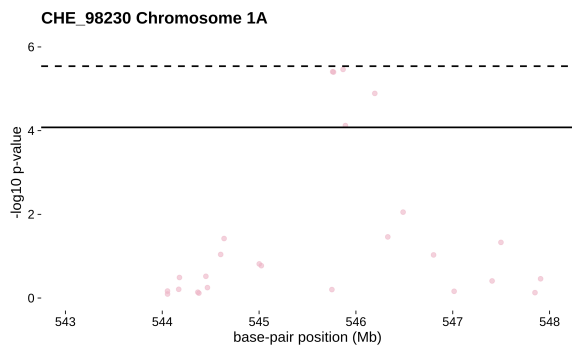


Figure S10. QQ Plots for GWAS with eight powdery mildew isolates and landraces from Turkey. Isolate names are depicted in the top-left corner. Solid lines represent the threshold for False discovery rate (FDR) and dashed lines for Bonferroni correction.



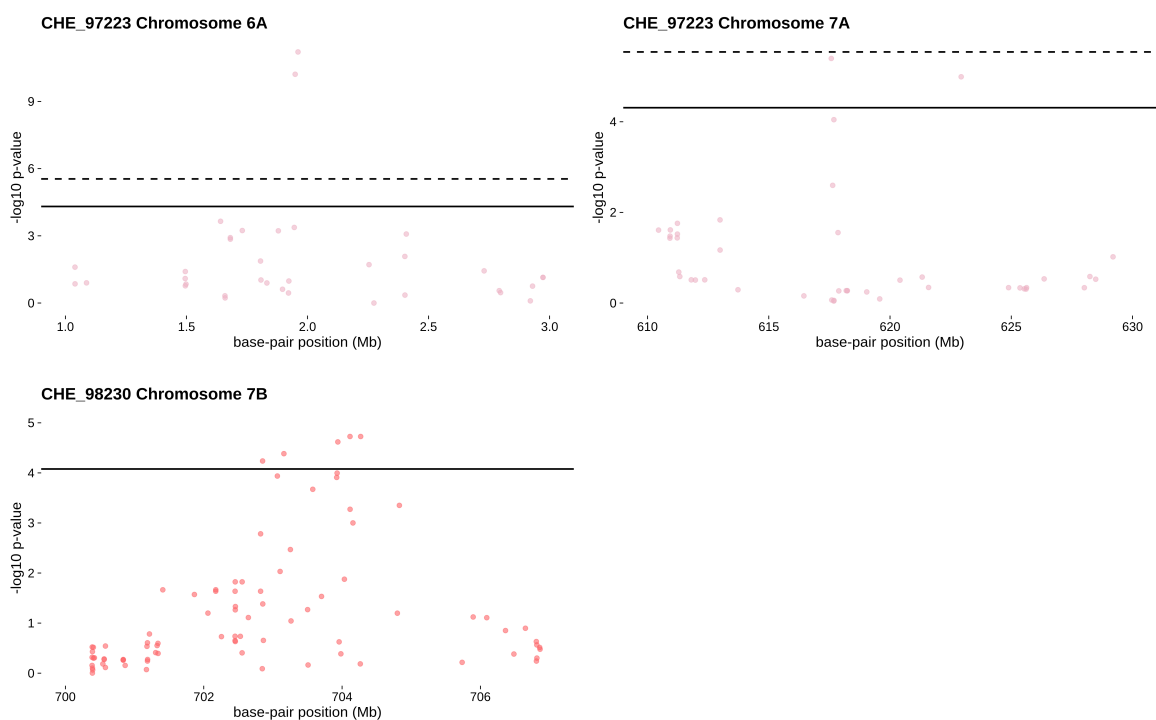


Figure S11. Manhattan Plots of resistance-associated loci of Turkish accessions. Isolates and chromosomes are depicted in the top-left corner. Solid lines represent the threshold for False discovery rate (FDR) and dashed lines for Bonferroni correction. Associations that occurred for several isolates are represented by one isolate only.

References

Balfourier F et al. (2019) Worldwide phylogeography and history of wheat genetic diversity. *Sci Adv* 5.