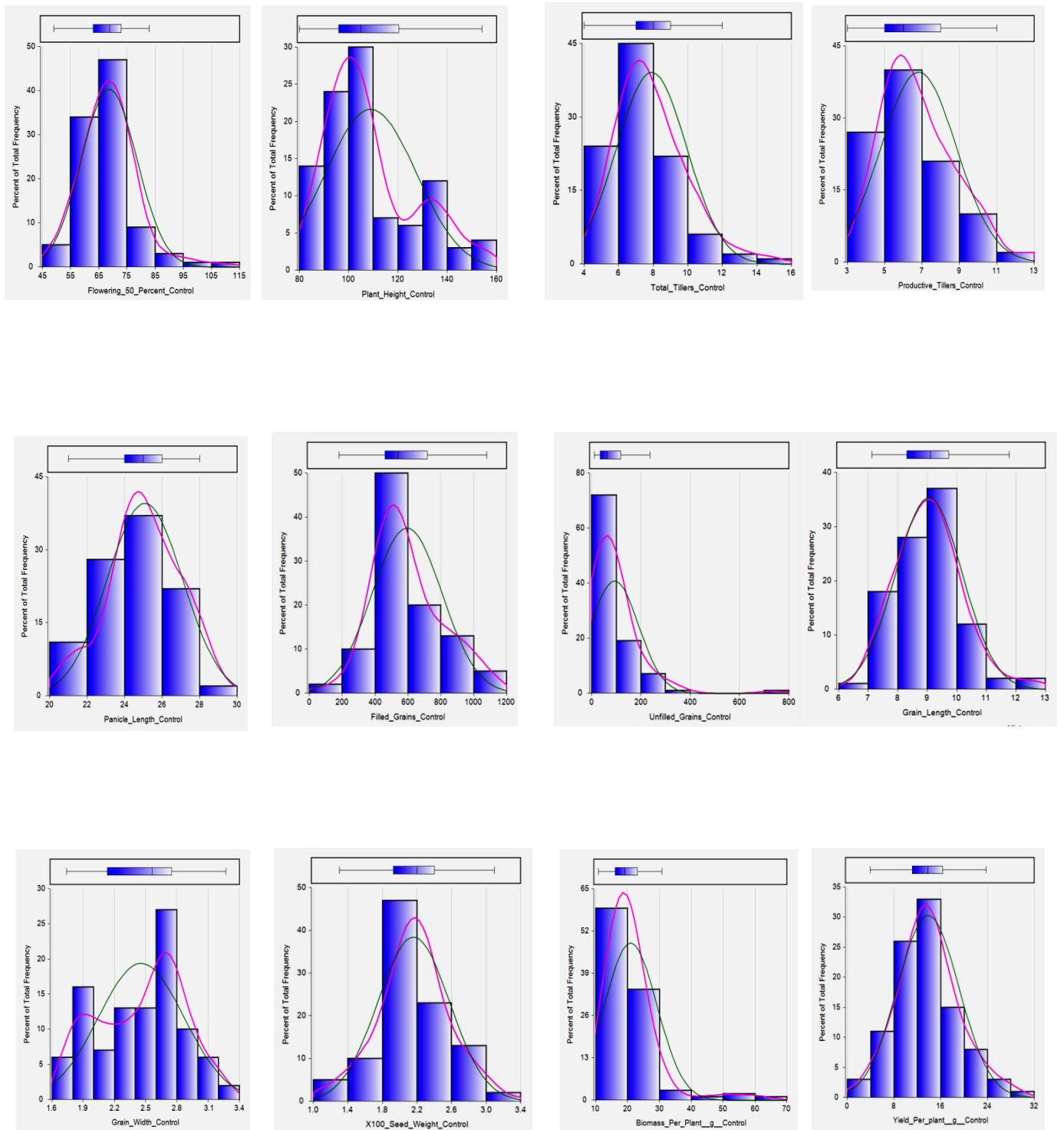
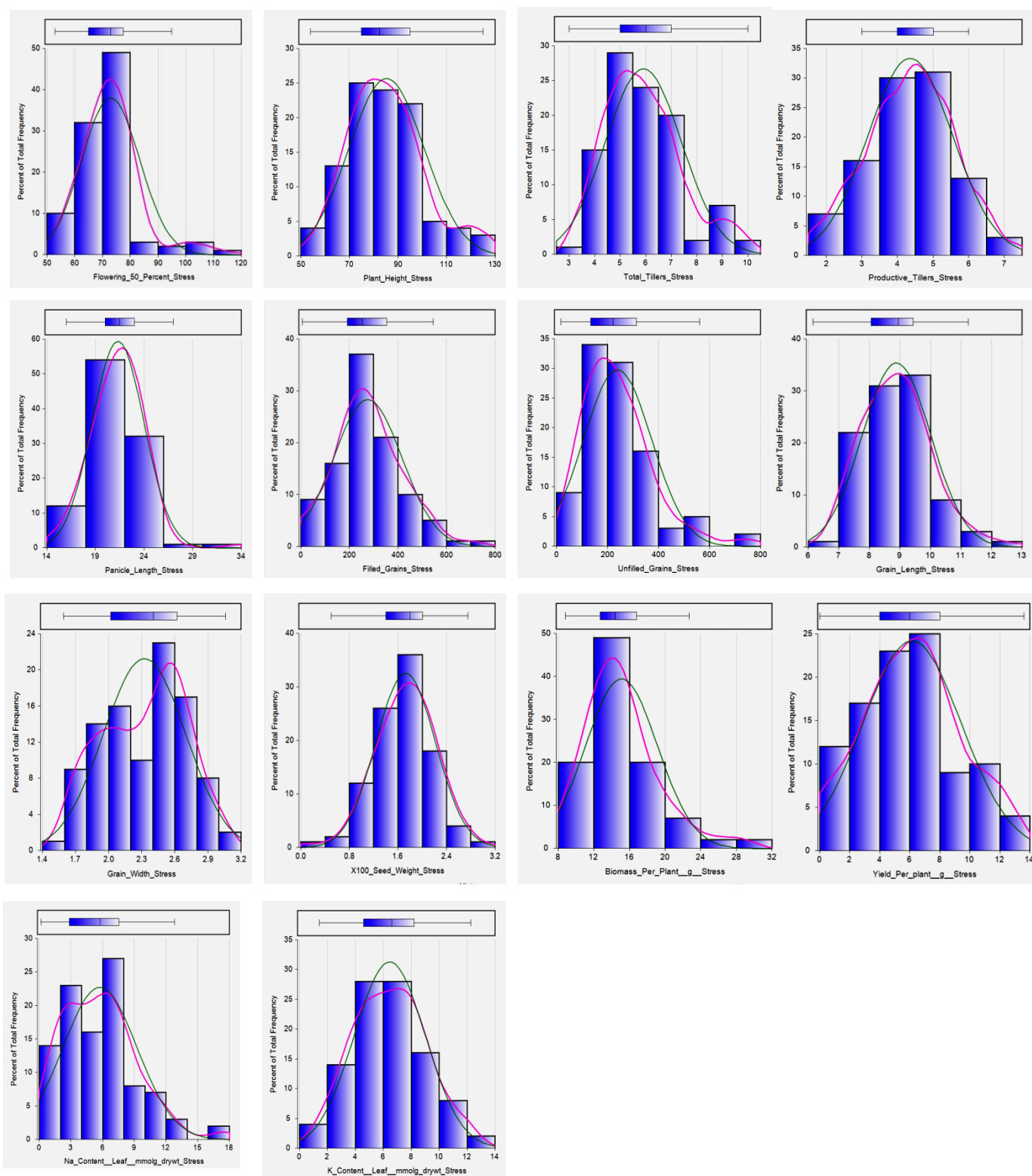


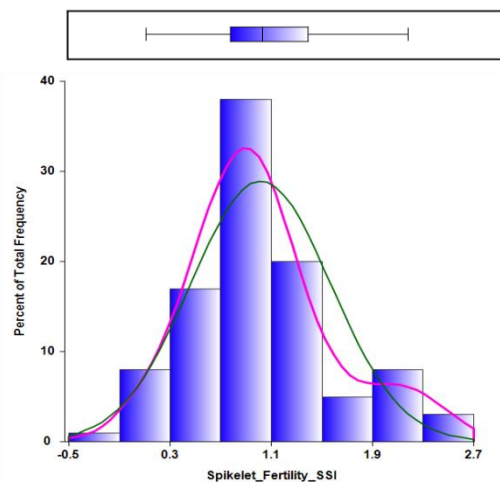
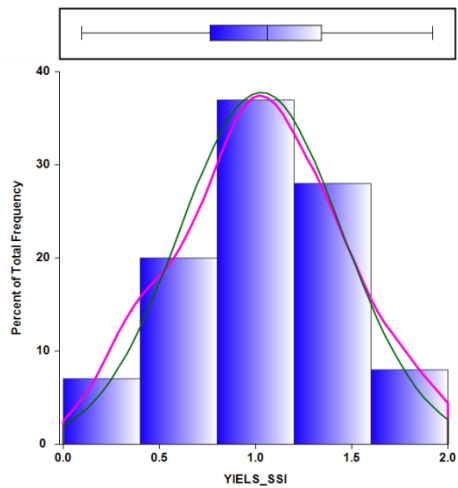
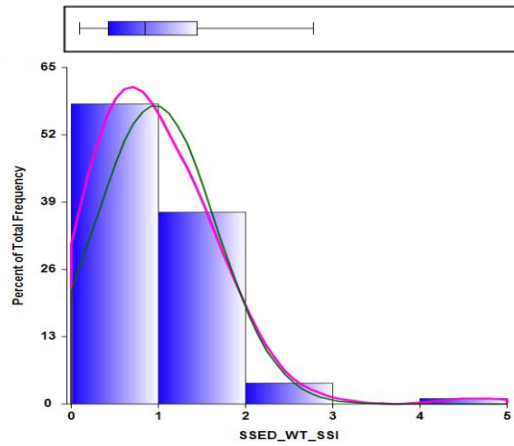
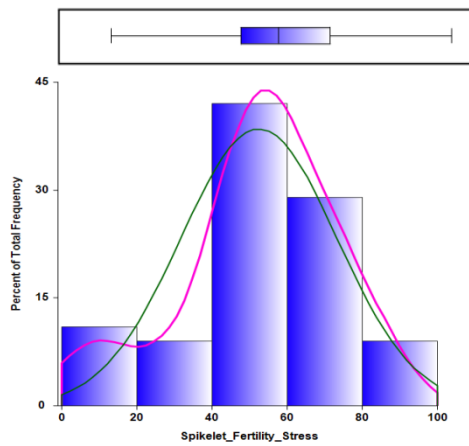
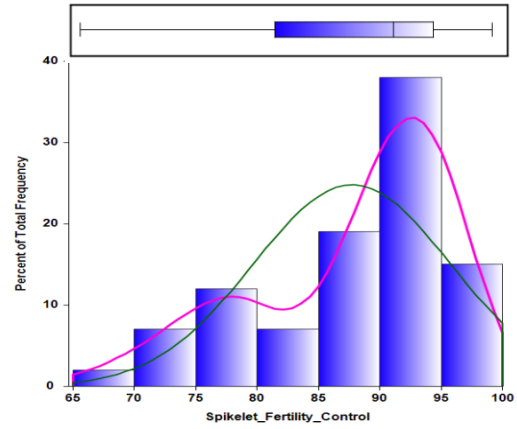
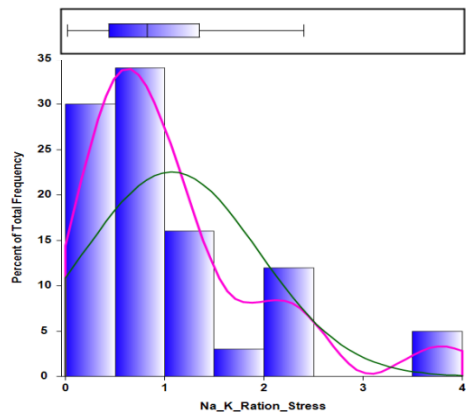
Supplementary Figure S1. The kinship association among current association panel based on EMMA algorithm implemented in GAPIT. The kinship values varies from 0 to 1 as shown in the color key and histogram.



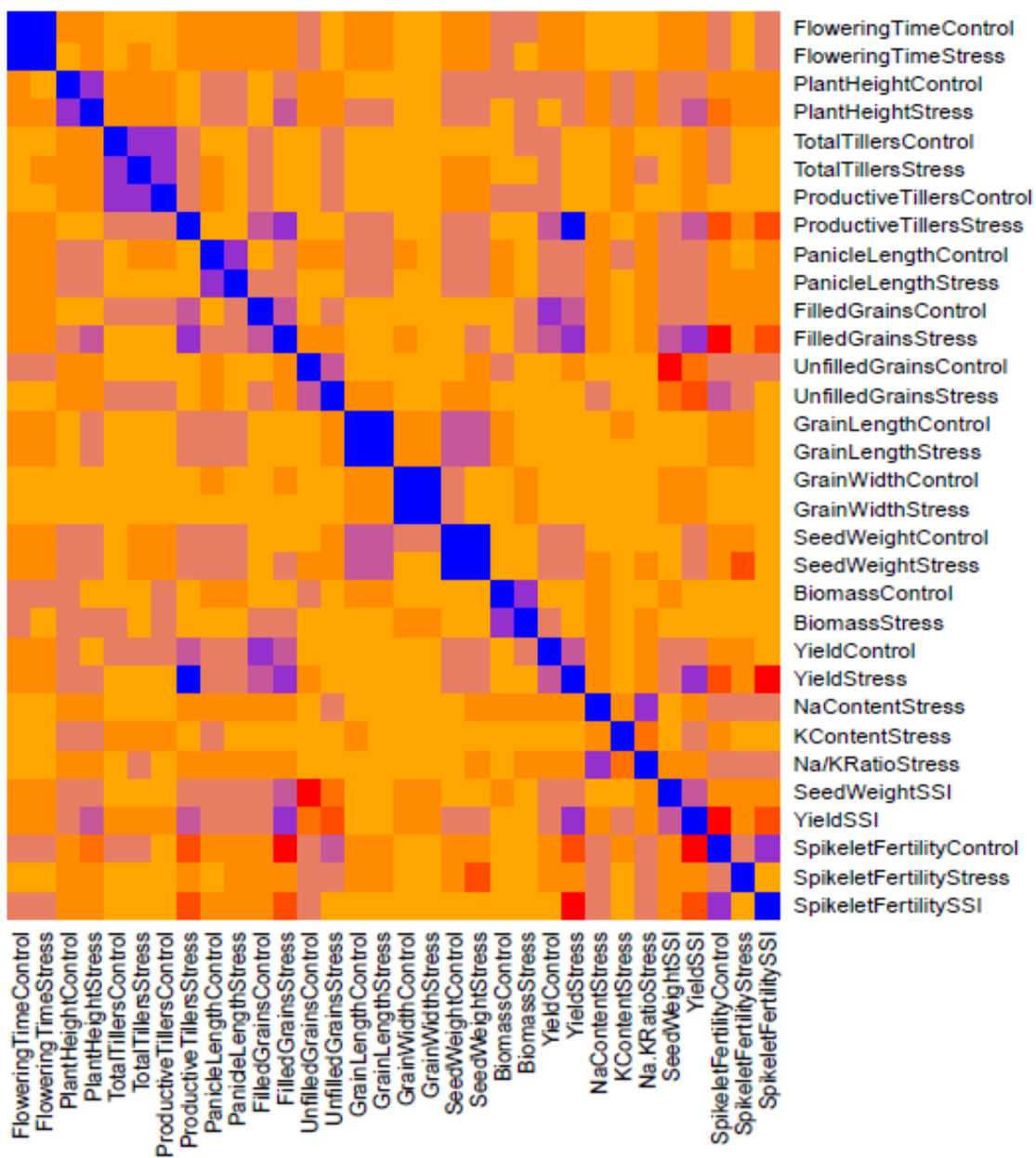
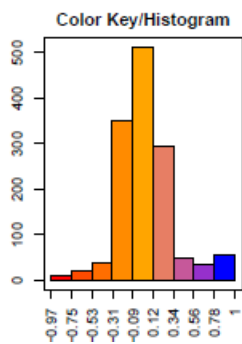
Supplementary Figure S2a. A histogram with box plot showing the distribution of 12 traits phenotyped for germplasm set used in the study under control condition.



Supplementary Figure S2b. A histogram with box plot showing the distribution of 14 traits phenotyped for germplasm set used in the study under salinity stress condition.



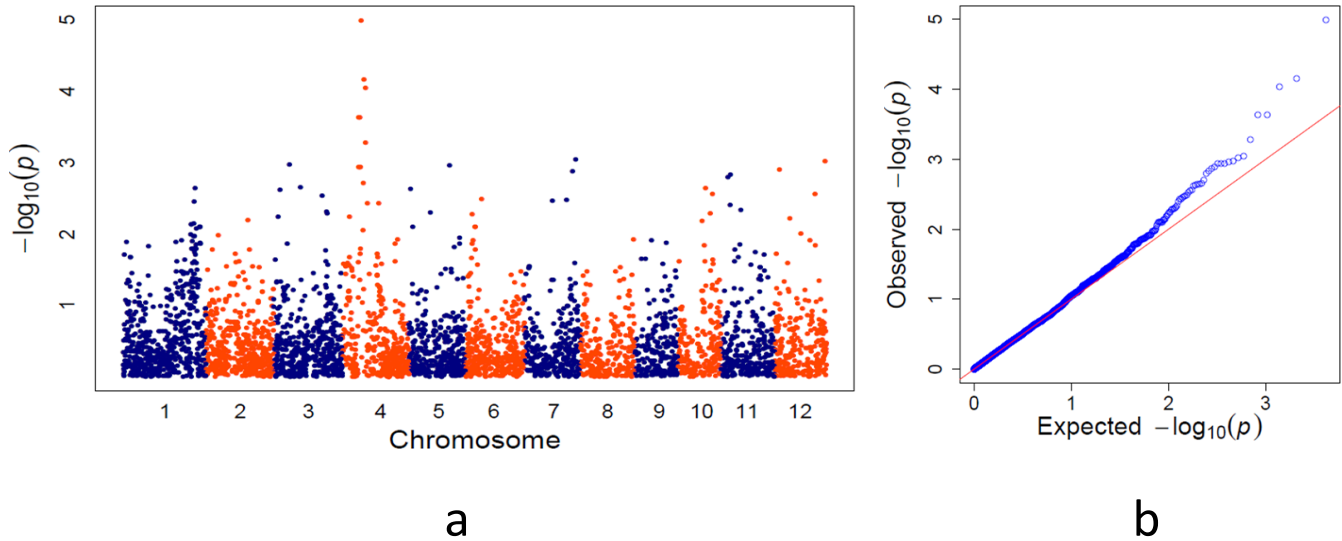
Supplementary Figure S2c. A histogram with box plot showing the distribution of derived traits.



Supplementary Figure S3. The Pearson correlation coefficients computed for all the traits measured under control and stress, and susceptibility indices of yield related traits.

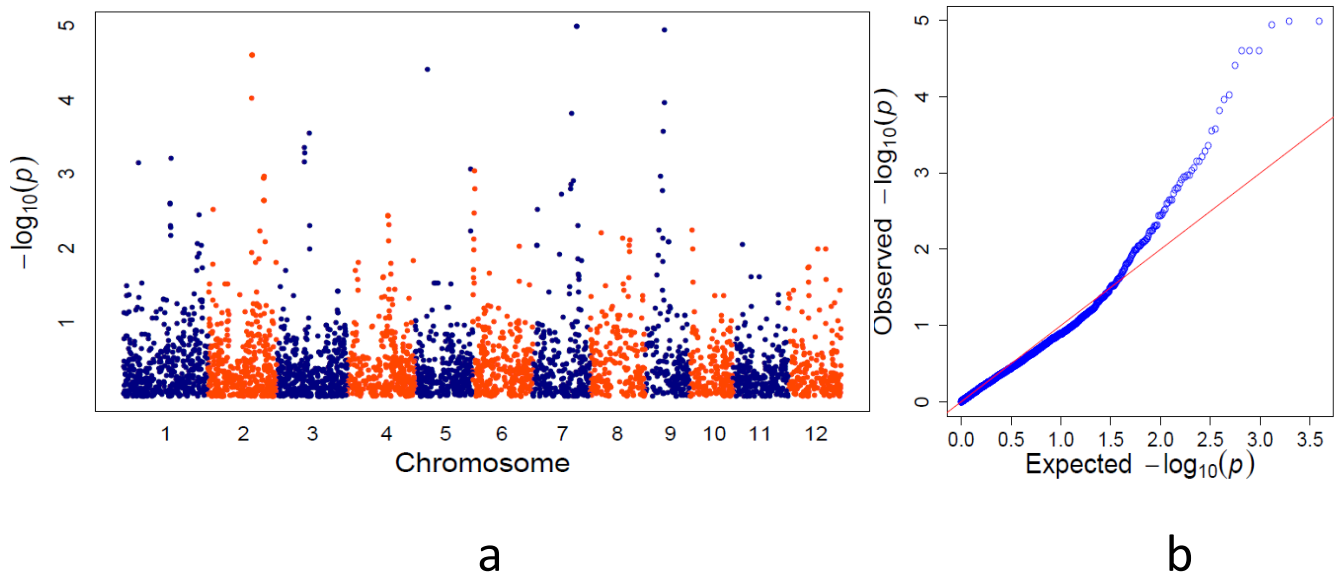
Supplementary Figure S4 to S12. The p -value of the SNPs and Quantile-Quantile plot of p -values for traits showed significant association. (a) Manhattan plot showing the P -values along the genome from the mixed linear model. (b) Q - Q plot showing the expected null distribution of p -values, assuming no associations, represented as a red line and distribution of p -values observed using the CMLM model represented as a blue line.

CMLM for plant height under control



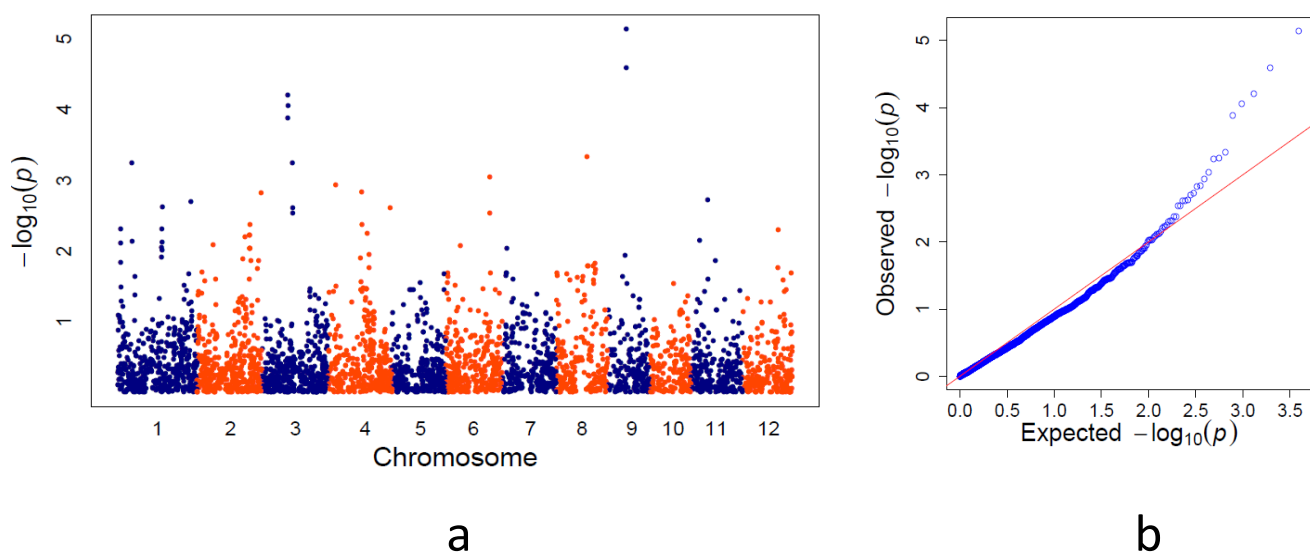
Supplementary Figure S4. Manhattan plot (a) and corresponding quantile-quantile plots (b) of p -values analyzed using mixed model for plant height.

CMLM for spikelet fertility under control



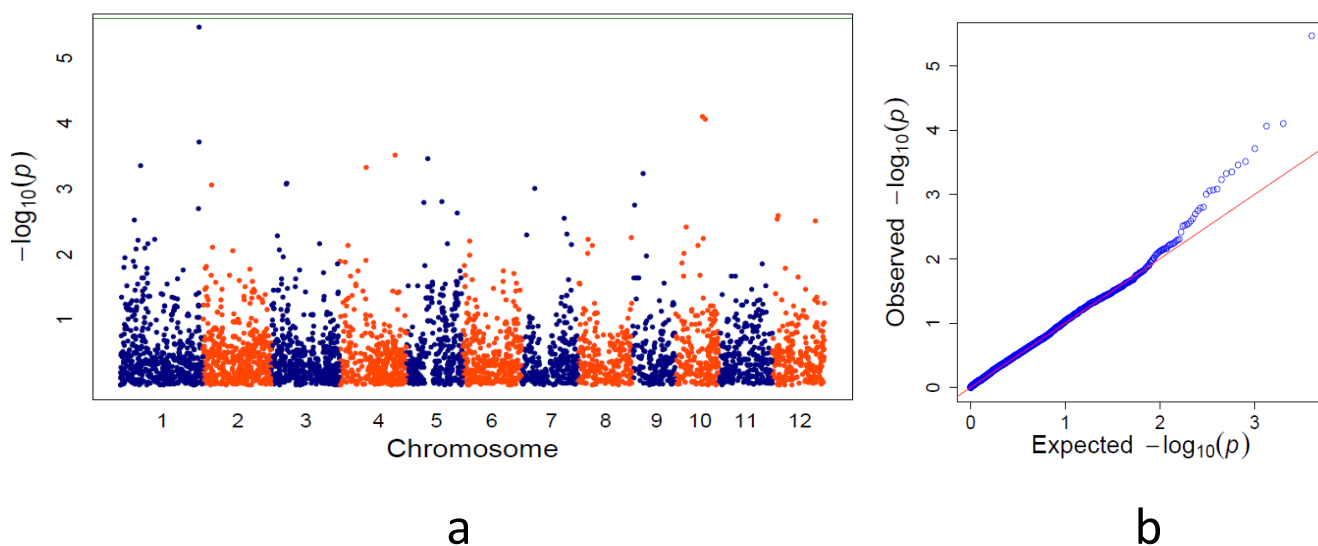
Supplementary Figure S5. Manhattan plot (a) and corresponding quantile-quantile plots (b) of p -values analyzed using mixed model for spikelet fertility under control.

CMLM for unfilled grains under control



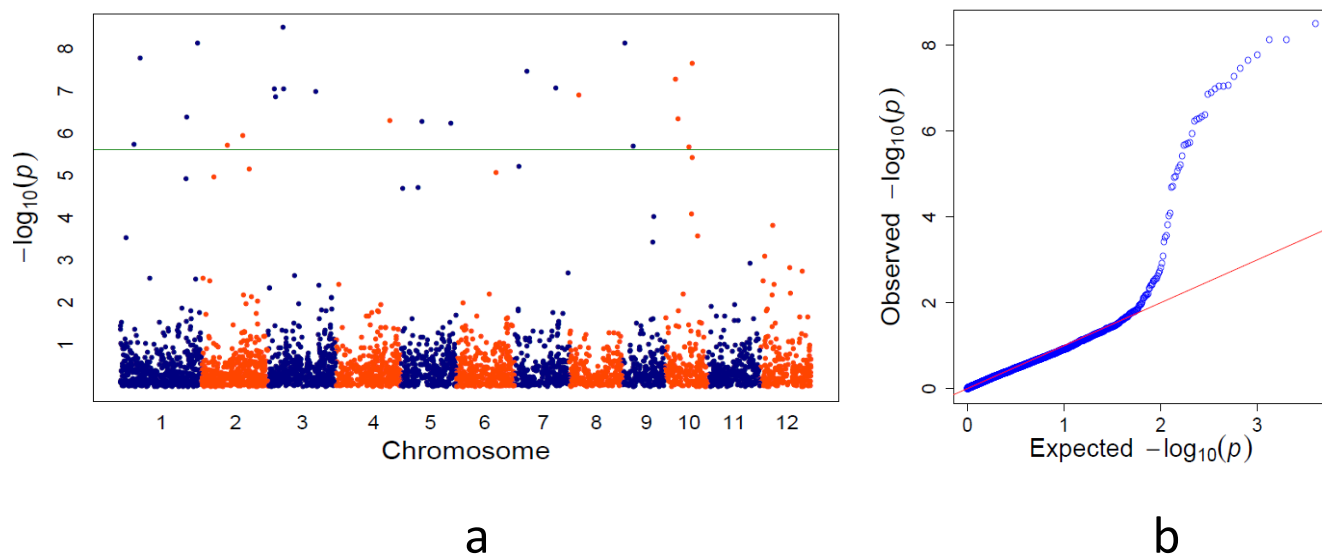
Supplementary Figure S6. Manhattan plot (a) and corresponding quantile-quantile plots (b) of p -values analyzed using mixed model for unfilled grains under control.

CMLM for Na^+ content under stress



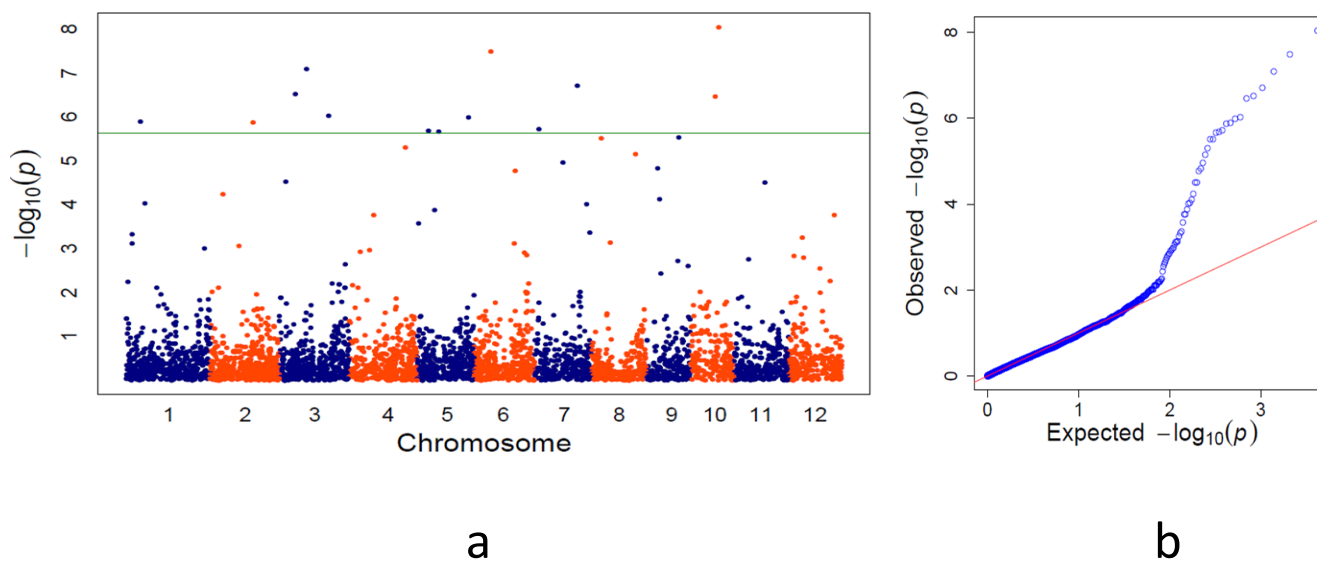
Supplementary Figure S7. Manhattan plot (a) and corresponding quantile-quantile plots (b) of p -values analyzed using mixed model for Na^+ content under stress.

CMLM for spikelet fertility under stress



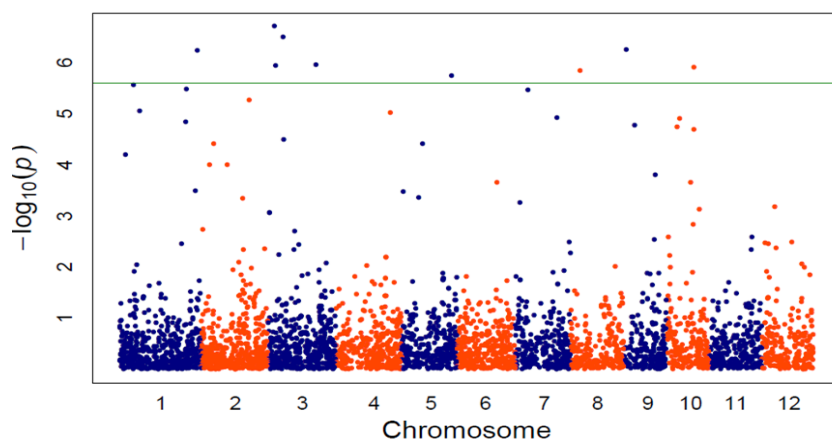
Supplementary Figure S8. Manhattan plot (a) and corresponding quantile-quantile plots (b) of p -values analyzed using mixed model for spikelet fertility under stress.

CMLM for spikelet fertility SSI

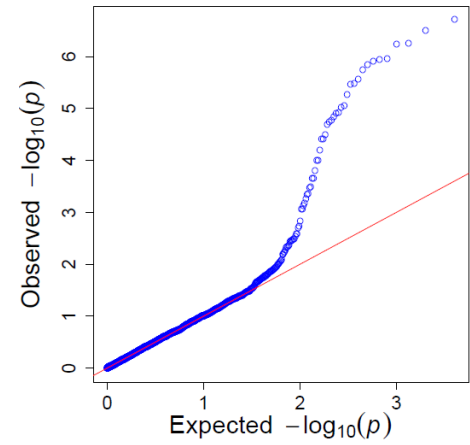


Supplementary Figure S9. Manhattan plot (a) and corresponding quantile-quantile plots (b) of p -values analyzed using mixed model for spikelet fertility SSI.

CMLM for filled grains under stress



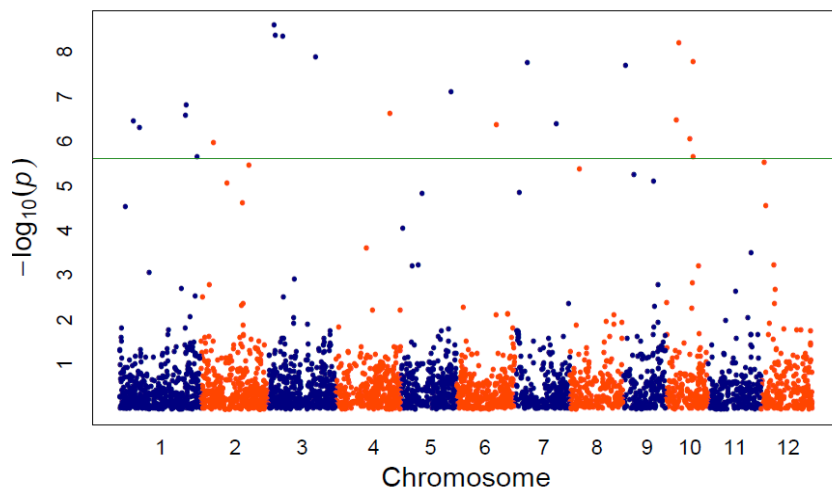
a



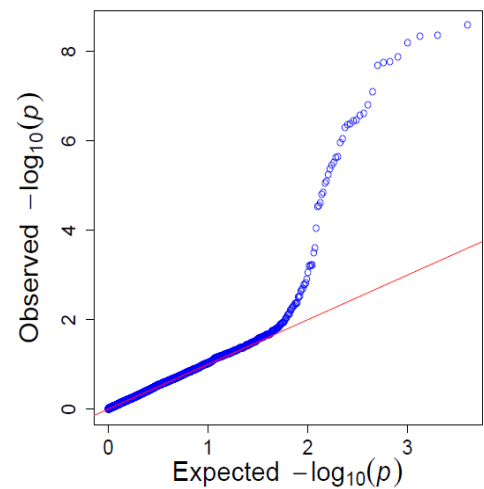
b

Supplementary Figure S10. Manhattan plot (a) and corresponding quantile-quantile plots (b) of p -values analyzed using mixed model for filled grains under stress.

CMLM for productive tillers under stress



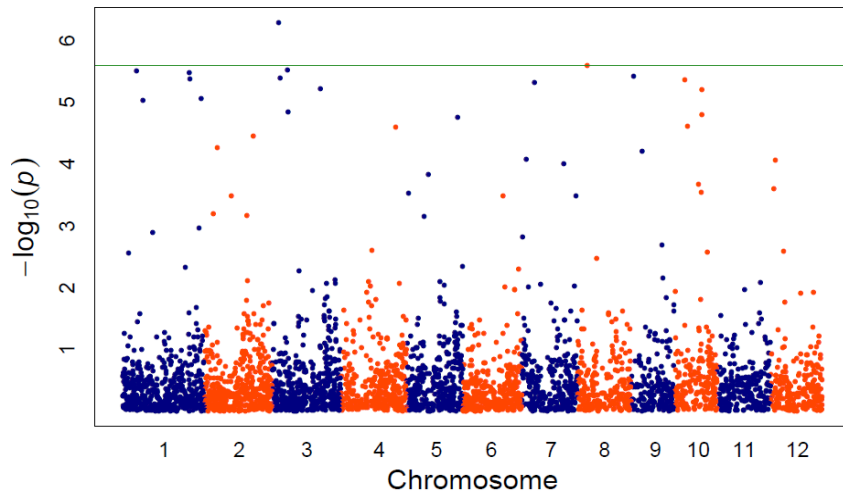
a



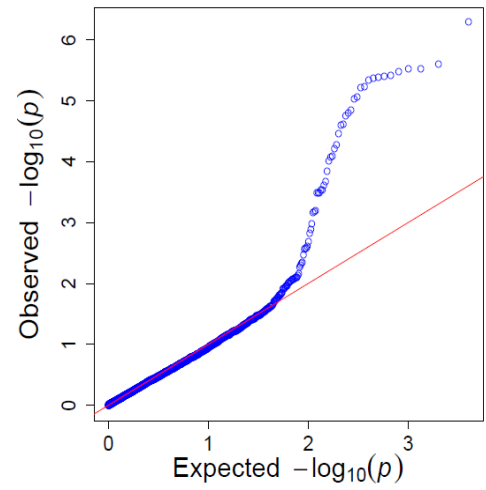
b

Supplementary Figure S11. Manhattan plot (a) and corresponding quantile-quantile plots (b) of p -values analyzed using mixed model for productive tillers under stress.

CMLM for yield/plant under stress



a



b

Supplementary Figure S12. Manhattan plot (a) and corresponding quantile-quantile plots (b) of p -values analyzed using mixed model for yield/plant under stress.