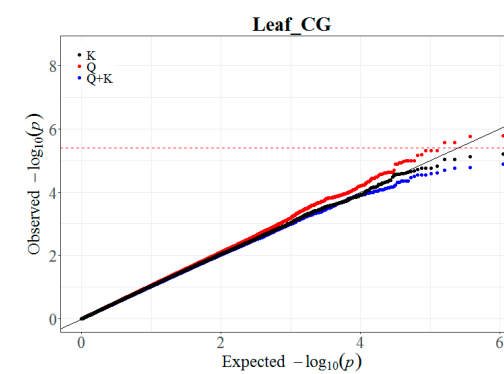
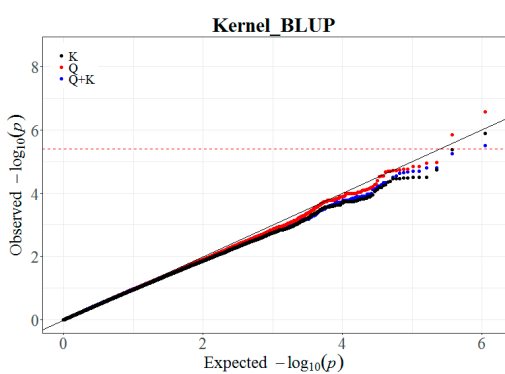
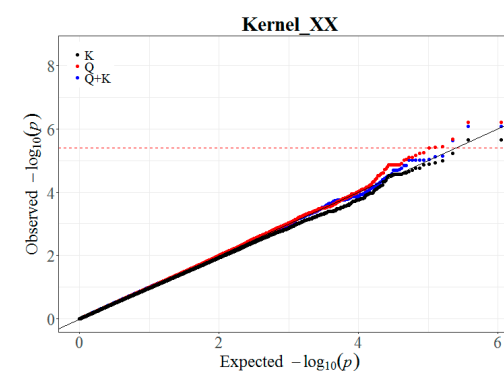
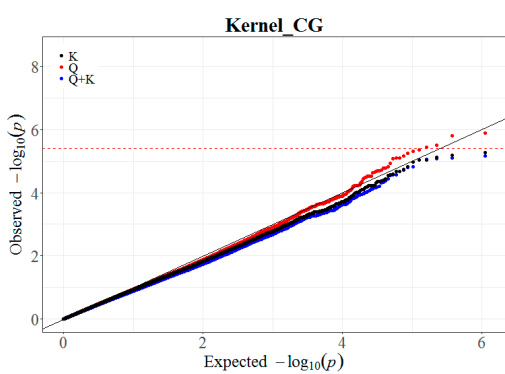
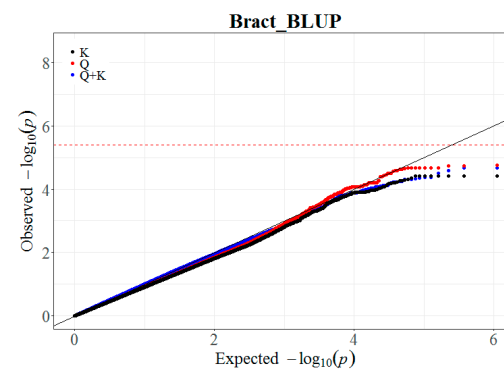
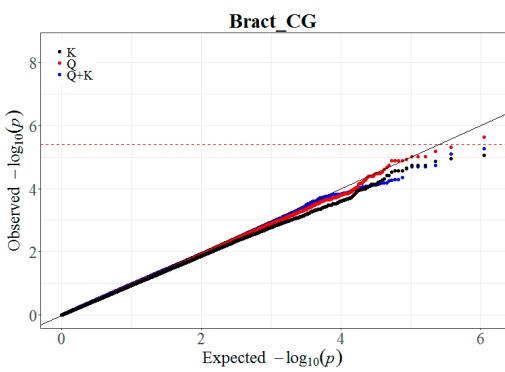
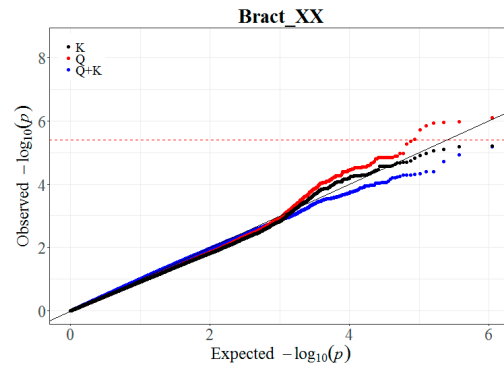
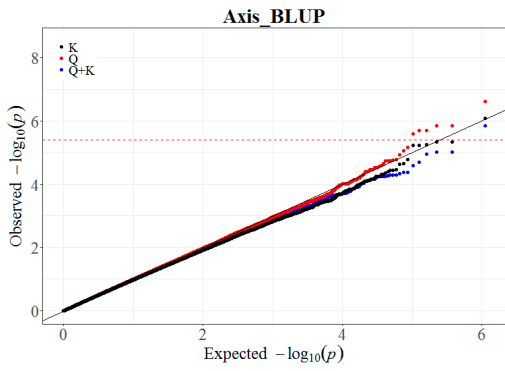
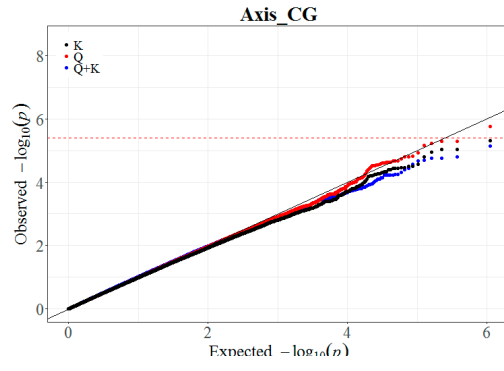
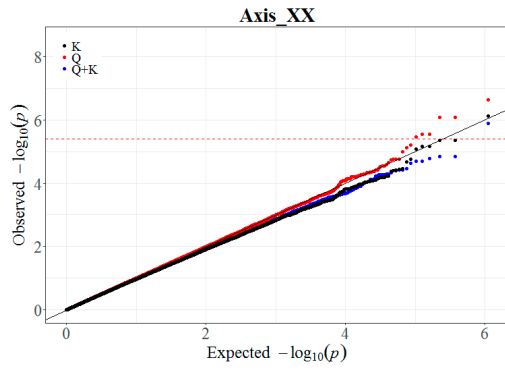
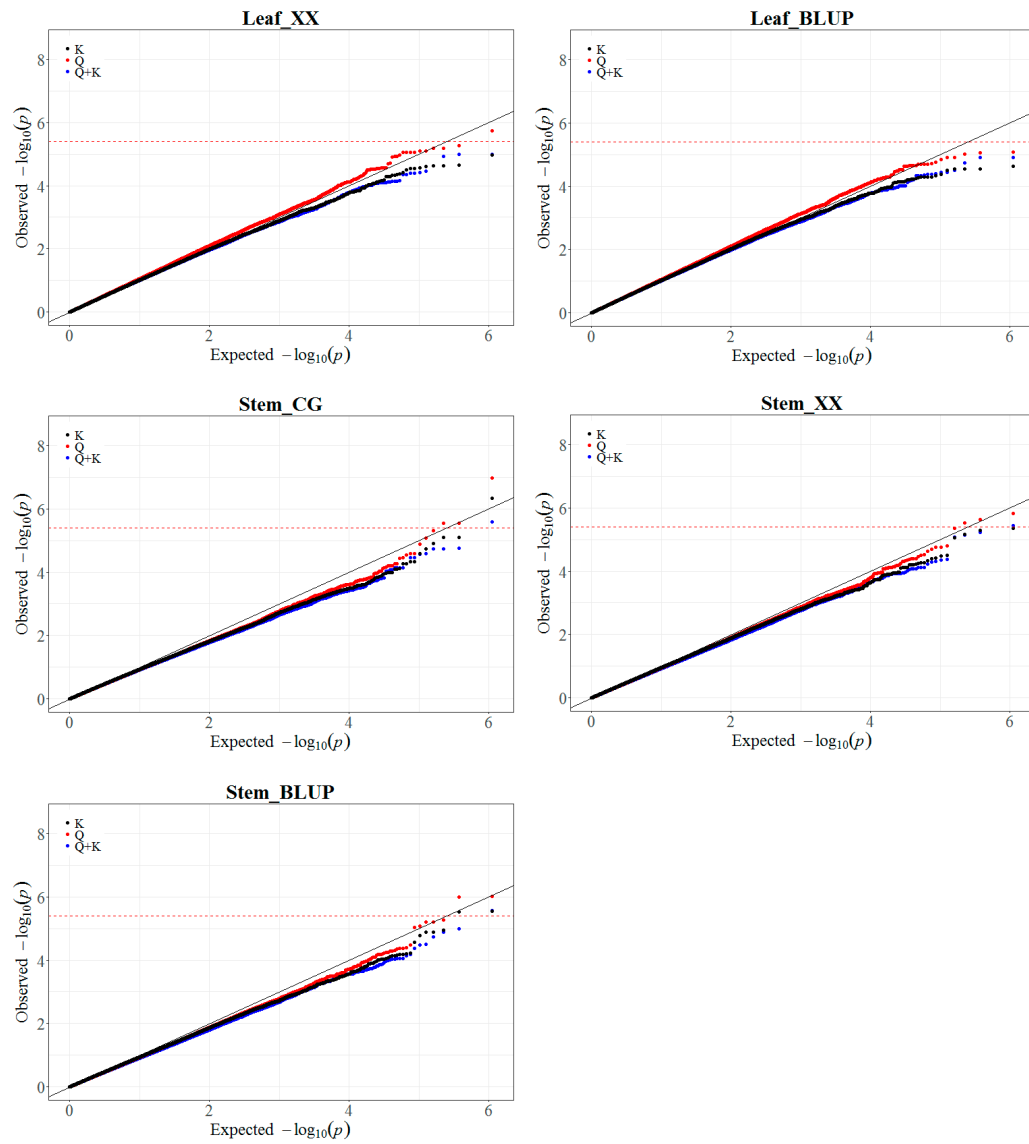
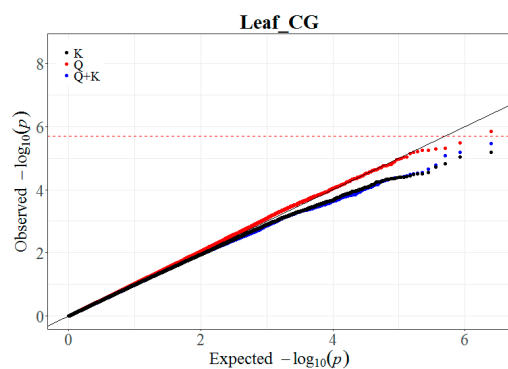
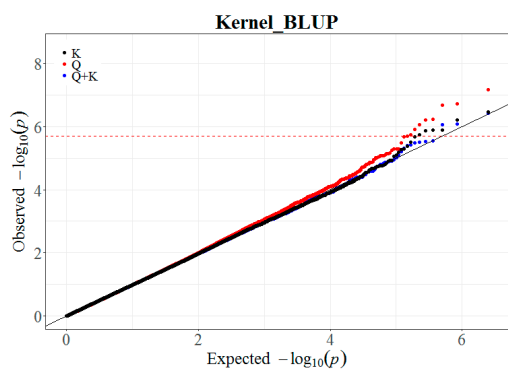
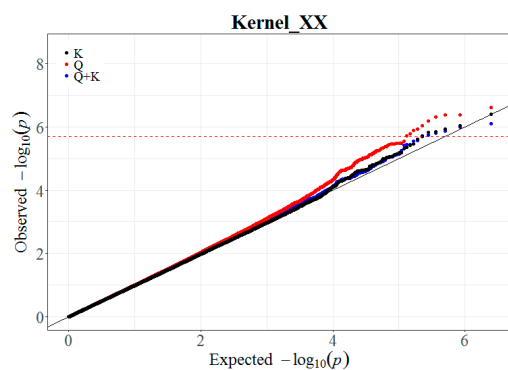
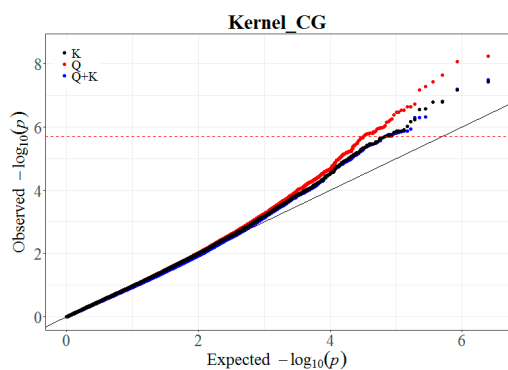
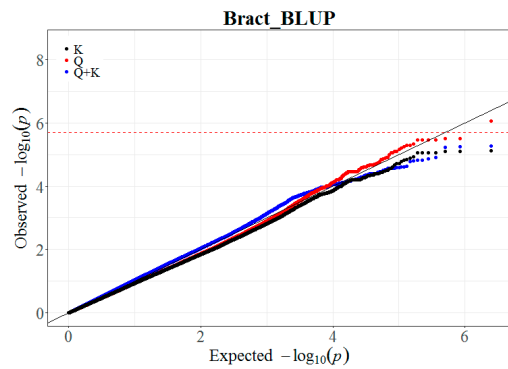
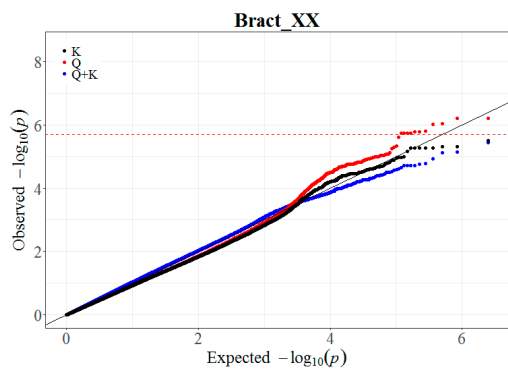
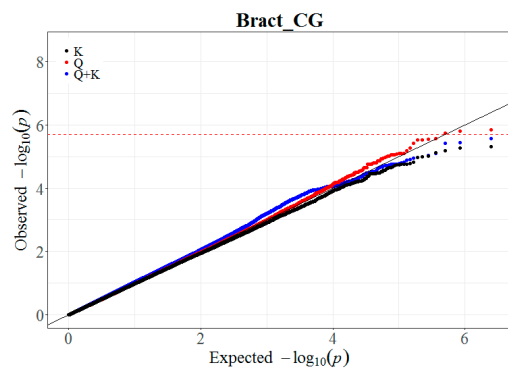
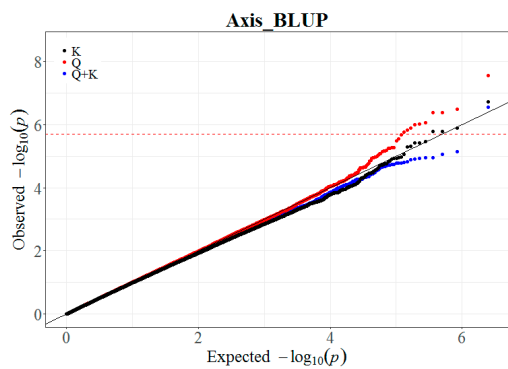
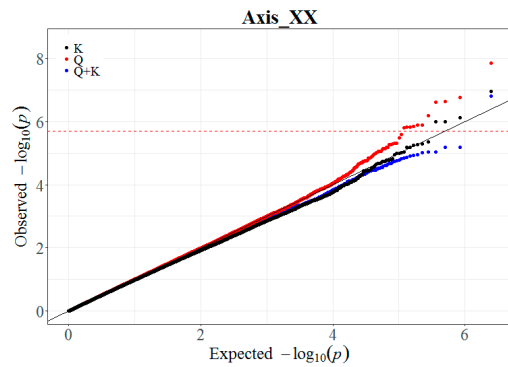
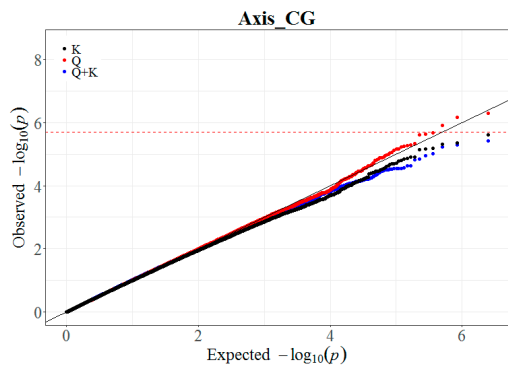


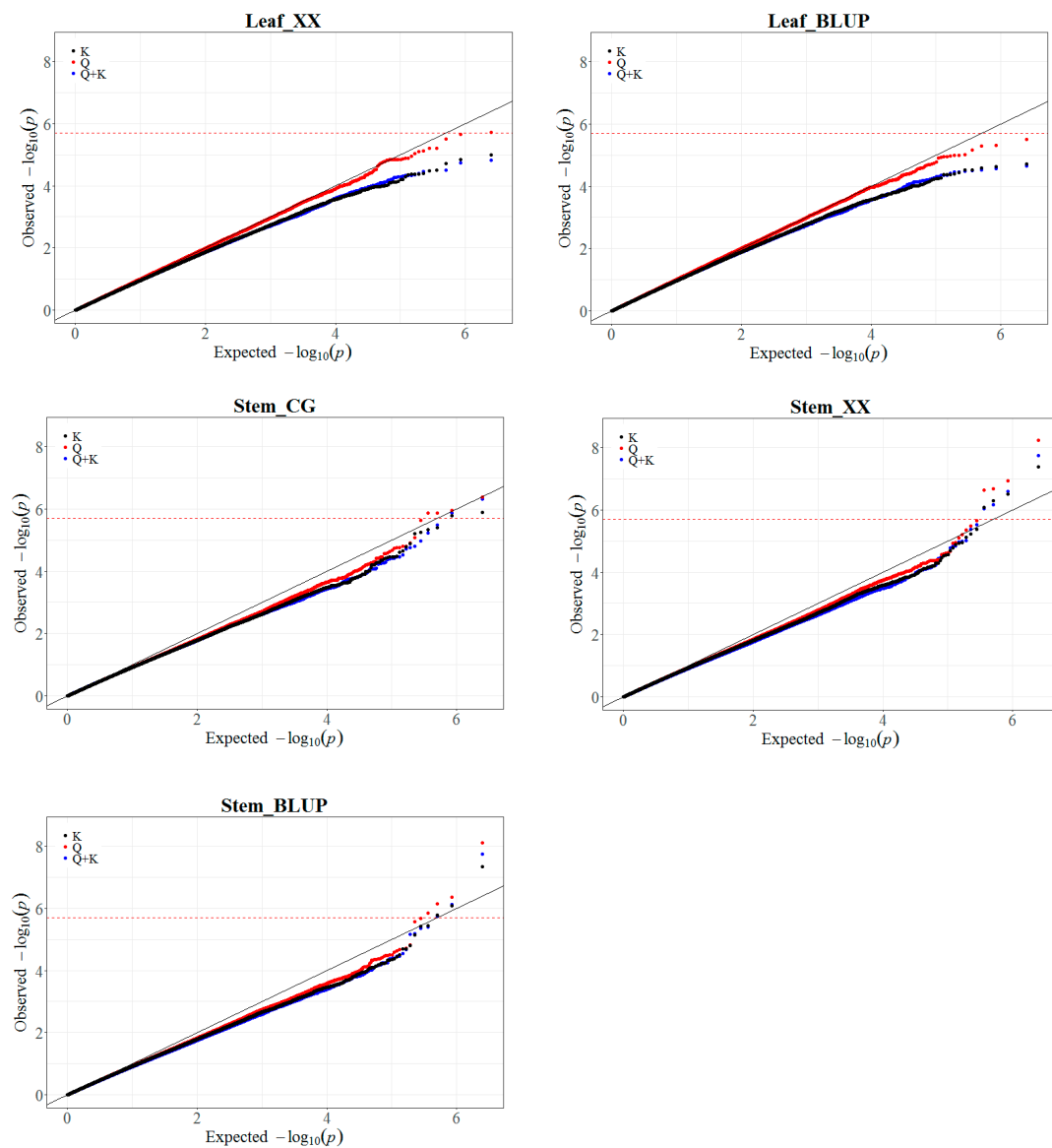
**Figure S1.** Comparison of Manhattan plots resulting from GWAS, based on 0.55 M SNPs, using Q model and 5PCs + K model for mercury content in maize axis, stem, bract, leaf, and kernel at BLUP environments.



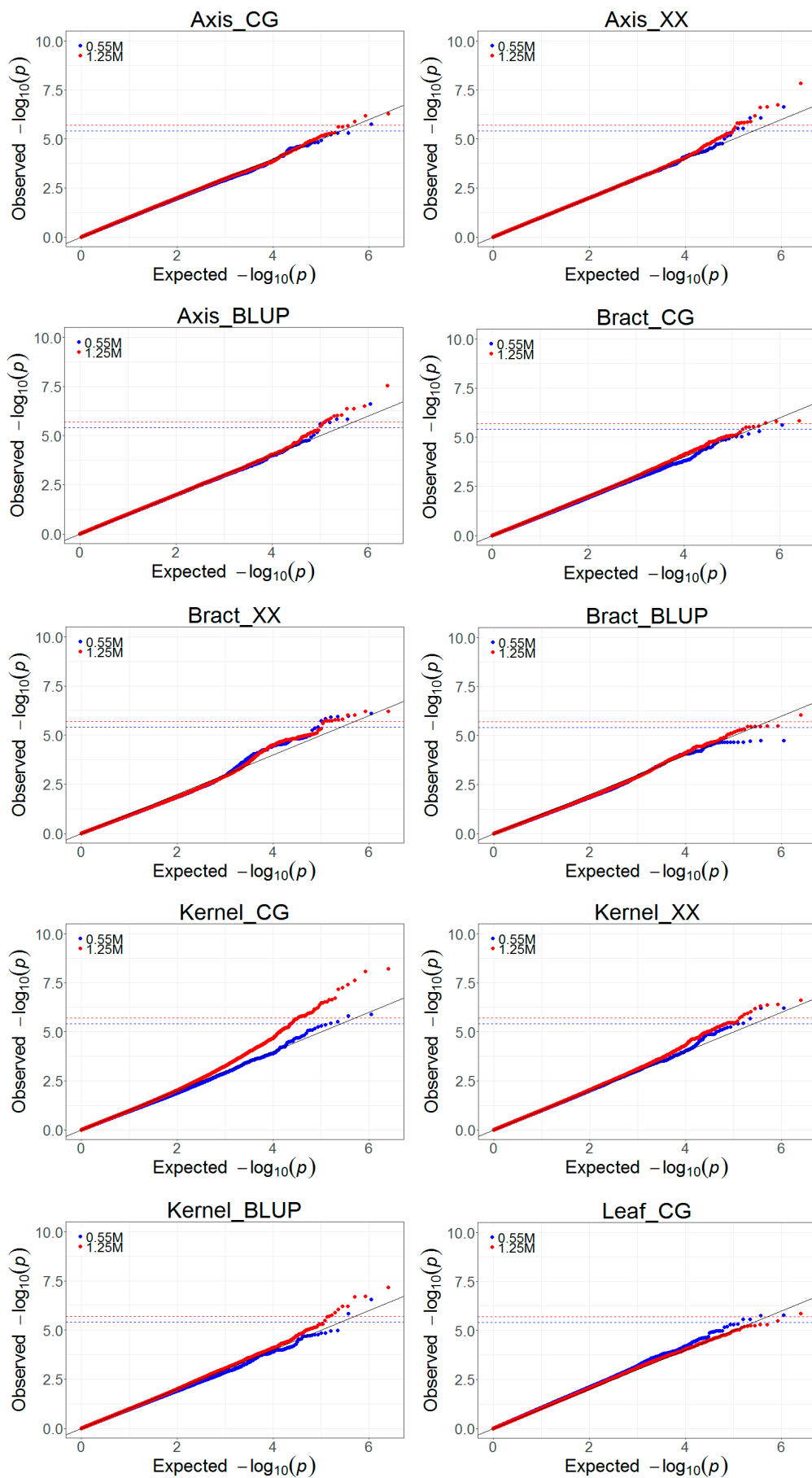


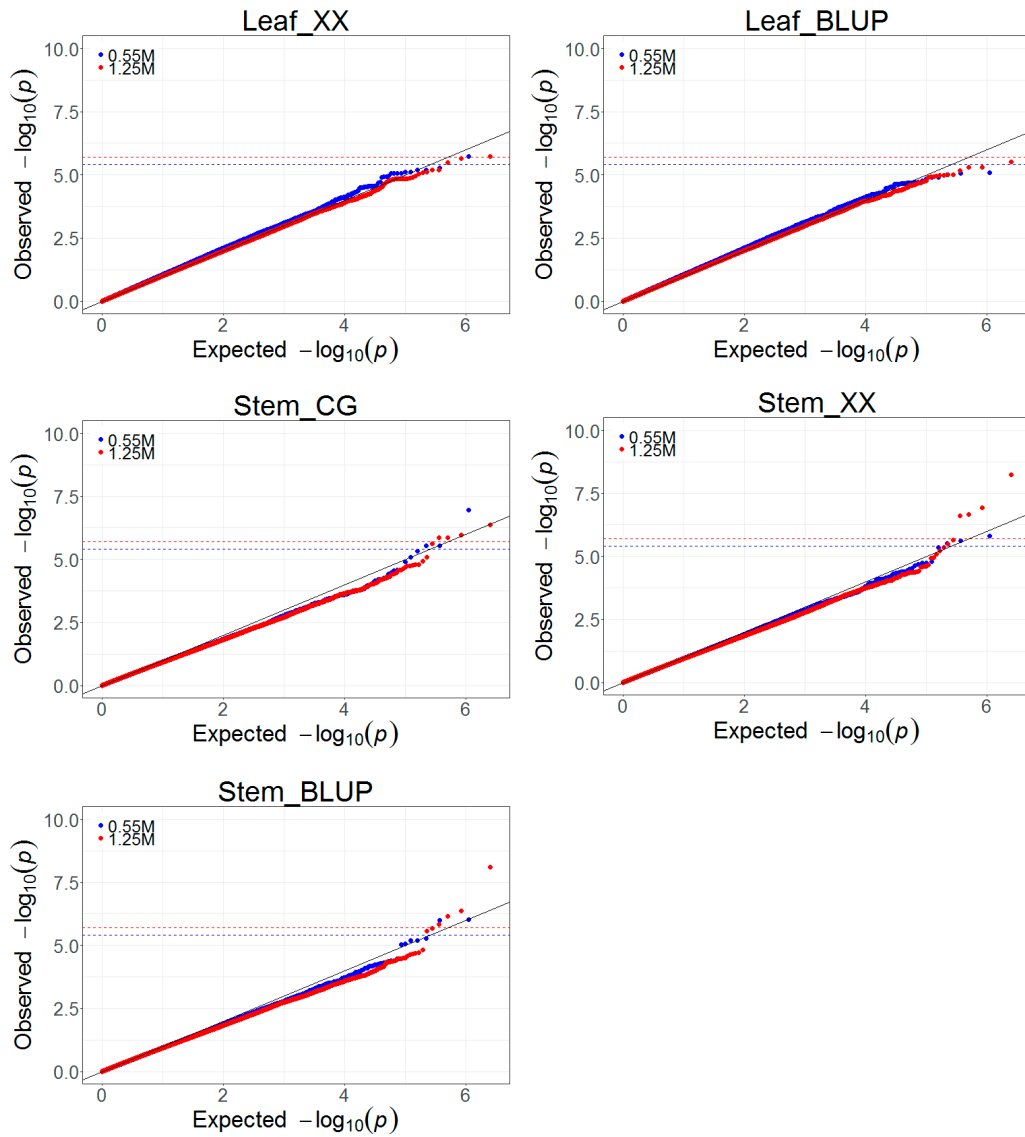
**Figure S2.** Comparison of quantile–quantile (QQ) plots resulting from GWAS, based on 0.55 M SNPs, using three models (Q, K, and Q + K) for mercury content in maize axis, stem, bract, leaf, and kernel in three environments.



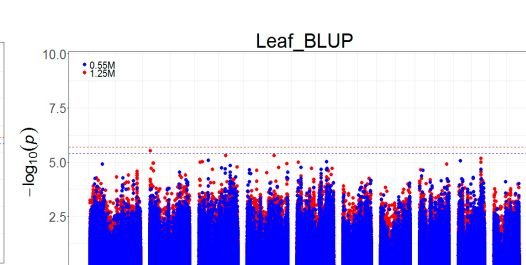
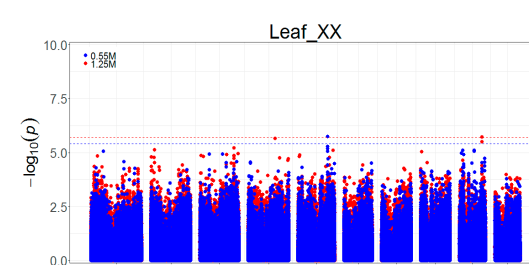
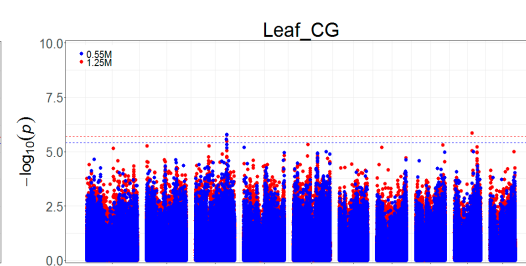
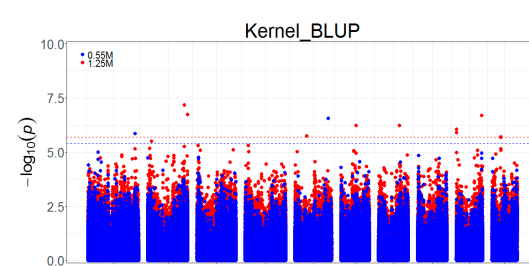
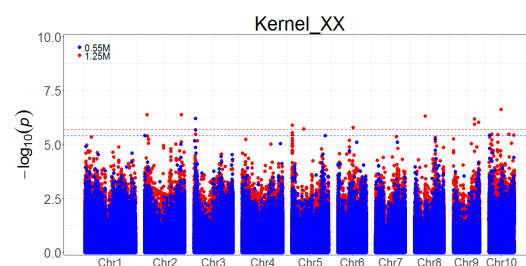
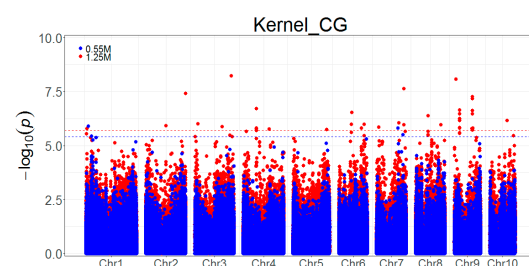
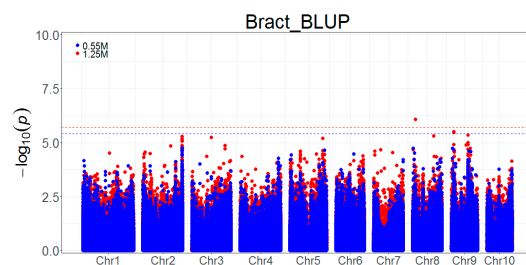
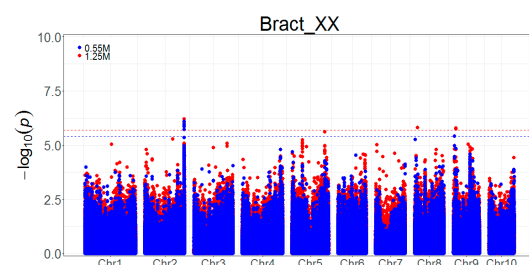
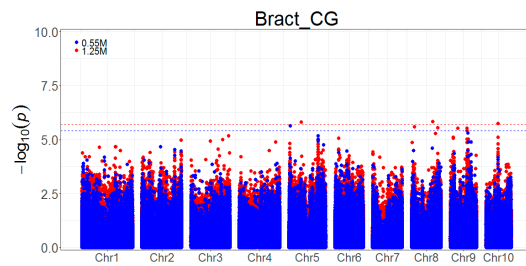
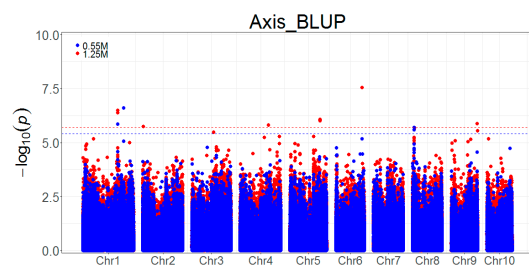
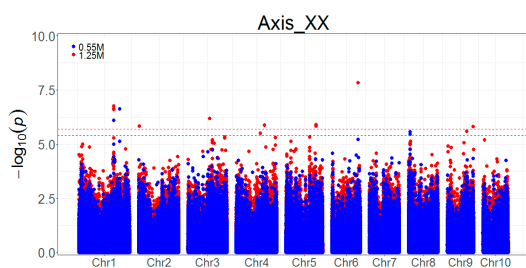
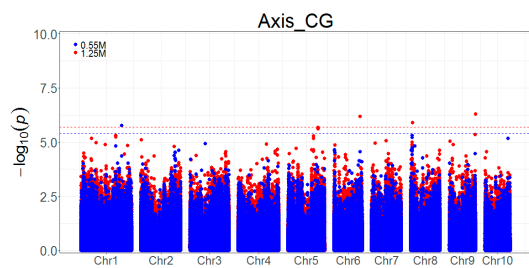


**Figure S3.** Comparison of quantile–quantile (QQ) plots resulting from GWAS, based on 1.25 M SNPs, using three models (Q, K, and Q + K) for mercury content in maize axis, stem, bract, leaf, and kernel in three environments.

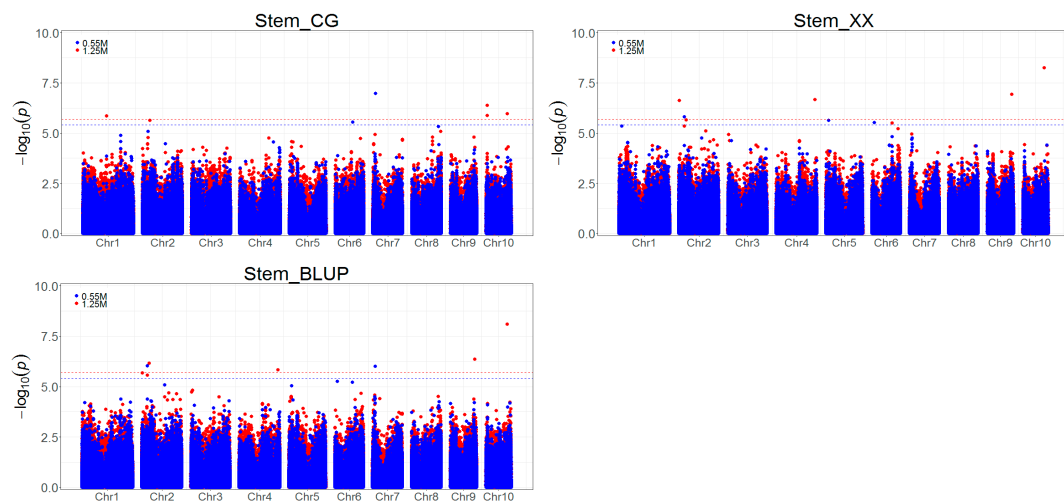




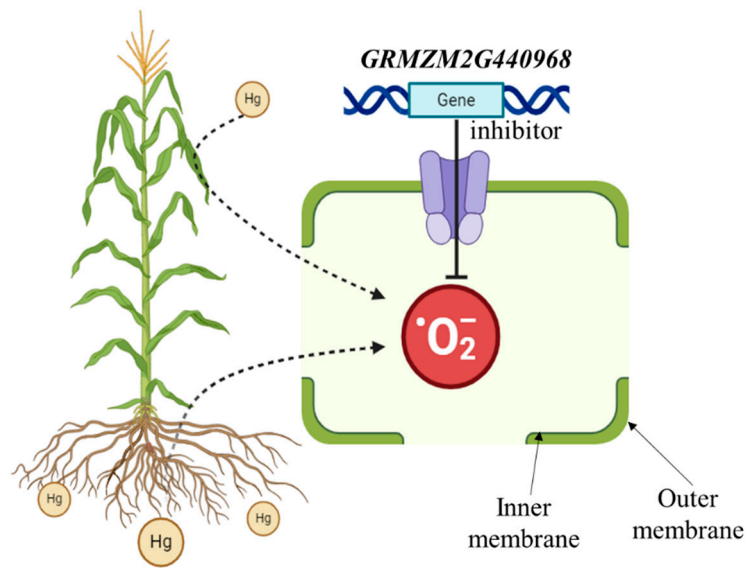
**Figure S4.** Comparison of quantile–quantile (QQ) plots resulting from GWAS, based on 0.55 M SNPs and 1.25 M SNPs, using Q model for mercury content in maize axis, stem, bract, leaf, and kernel in three environments.







**Figure S5.** Comparison of Manhattan plots resulting from GWAS, based on 0.55 M SNPs and 1.25 M SNPs, using Q model for mercury content in maize axis, stem, bract, leaf, and kernel in three environments.



**Figure S6.** Schematic representation of GRMZM2G440968 modulating cysteine protease in response to oxidative stress.