

Supplemental Figures

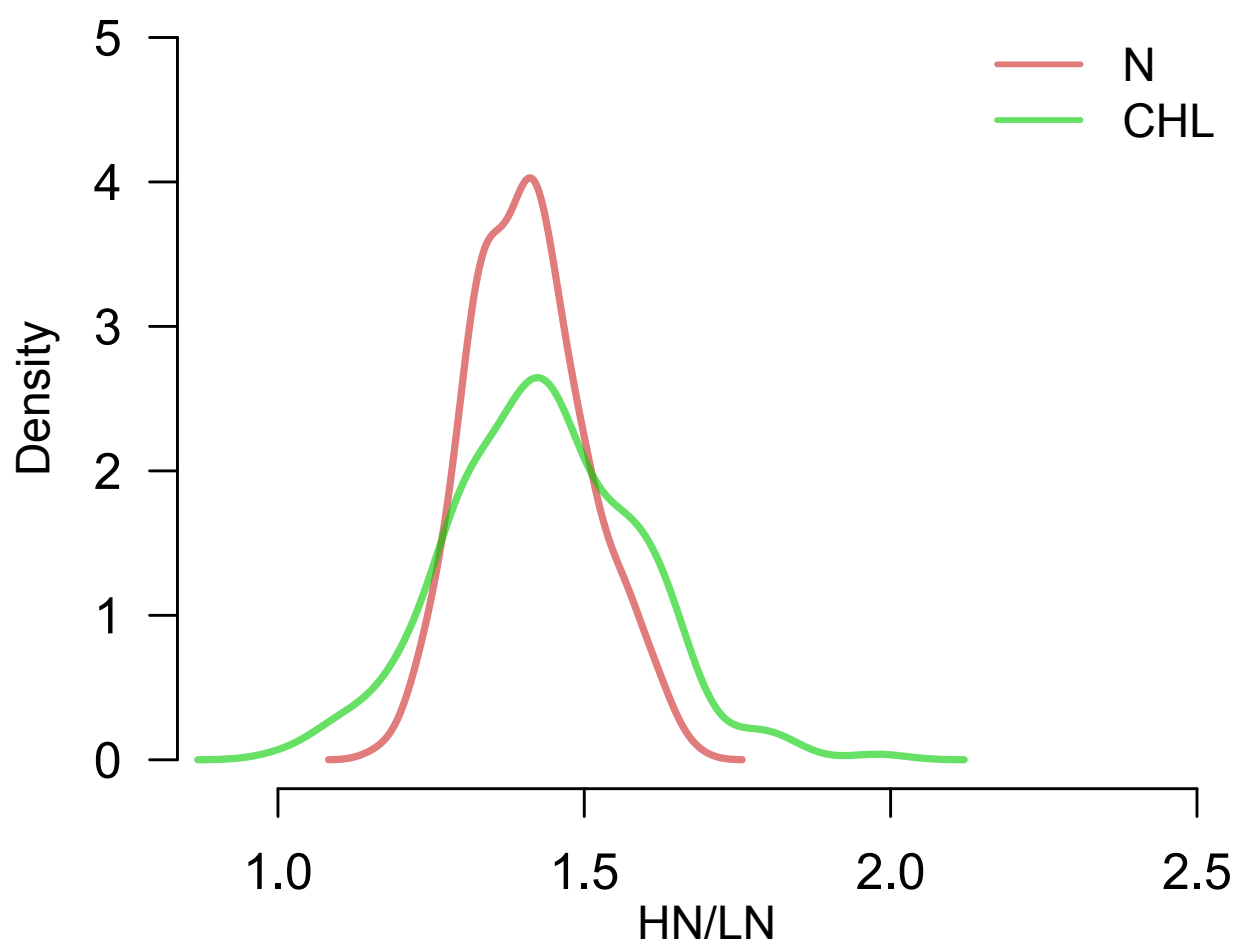


Figure S1 Density plots of leaf nitrogen (N) and chlorophyll (CHL) contents under high (HN) and low N (LN) conditions.

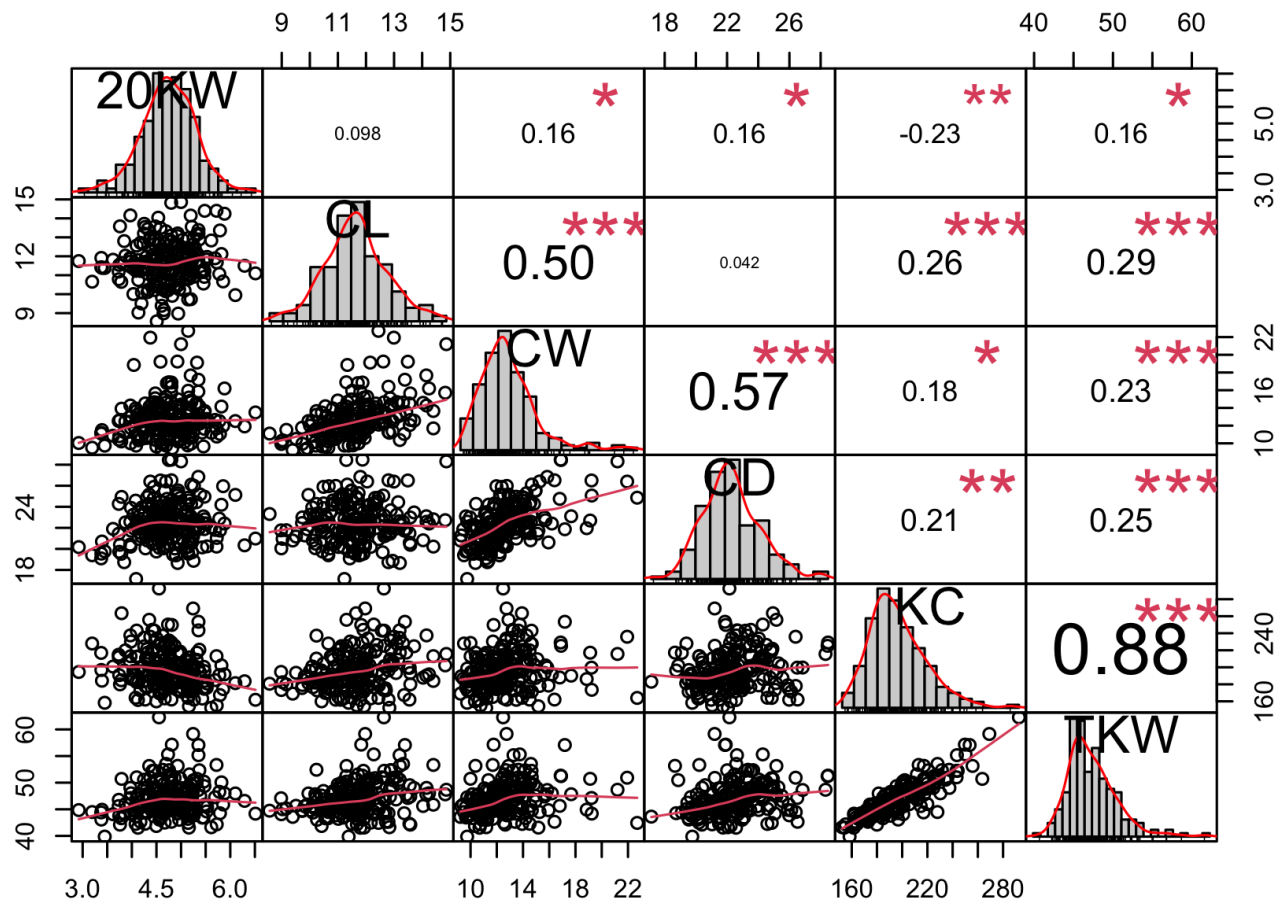


Figure S2 Correlation between yield-related traits under HN condition. The diagonal boxes are the histograms with density curves of different traits. Above the diagonal are correlation coefficients with significance levels. Below the diagonal are scatter plots with fitted regression curves. Red asterisks indicate significant correlations at the * $P = 0.05$, ** $P = 0.01$, and *** $P = 0.001$ levels.

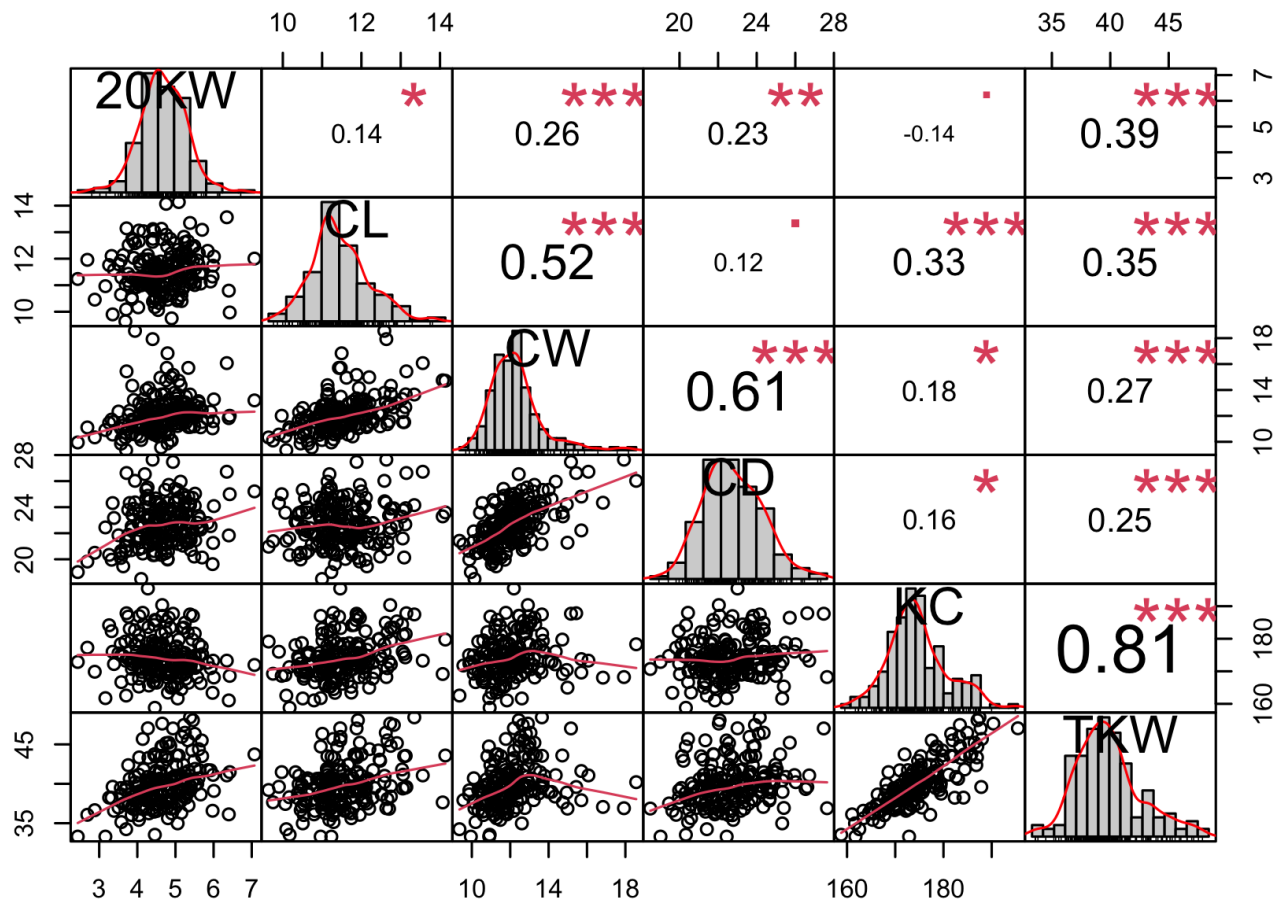


Figure S3 Correlation between yield-related traits under LN condition. The diagonal boxes are the histograms with density curves of different traits. Above the diagonal are correlation coefficients with significance levels. Below the diagonal are scatter plots with fitted regression curves. Red asterisks indicate significant correlations at the * $P = 0.05$, ** $P = 0.01$, and *** $P = 0.001$ levels.

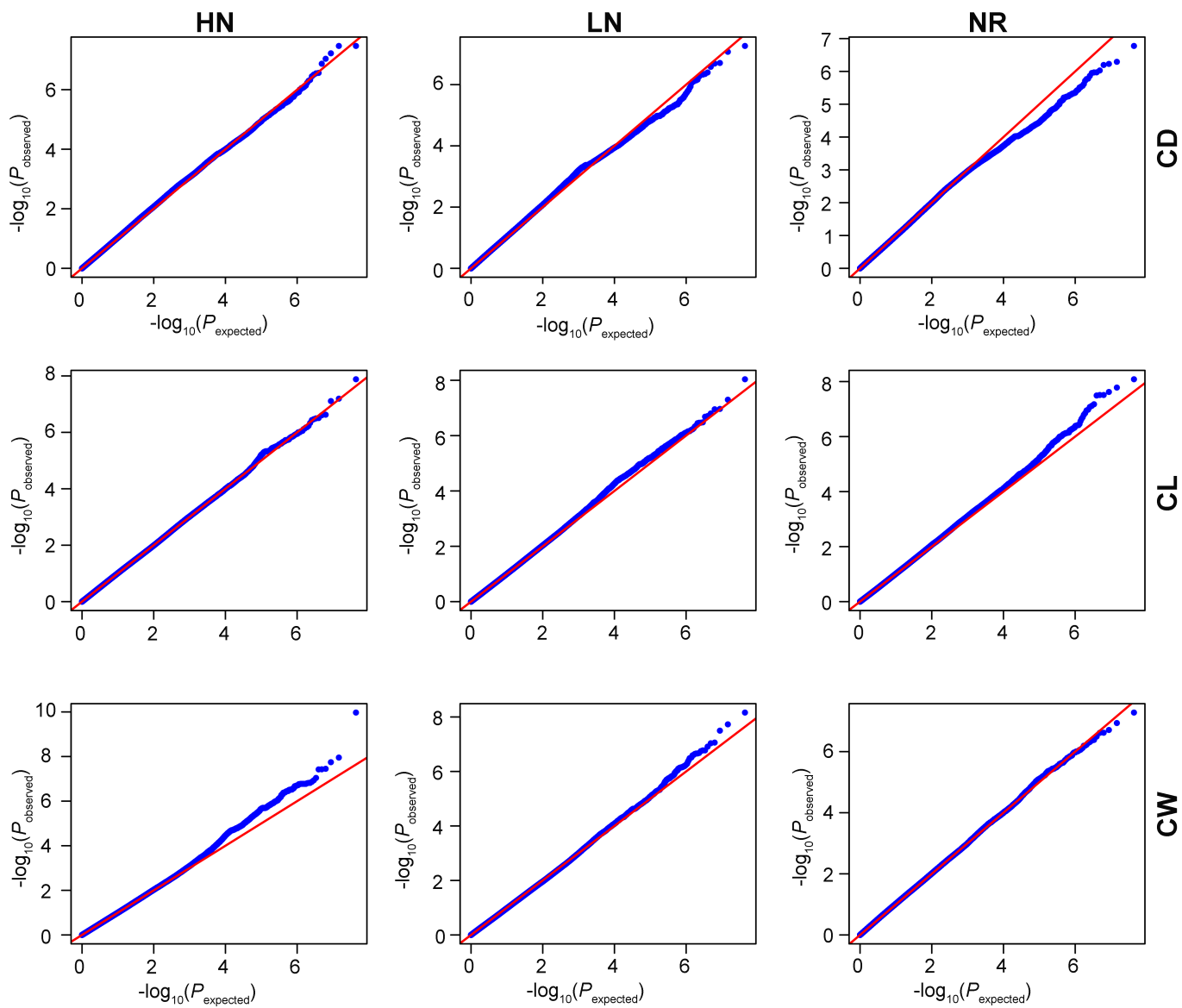


Figure S4 Quantile-quantile (Q-Q) plots for cob-related traits. Red diagonal line indicates the expected values and the blue dots represent the observations.

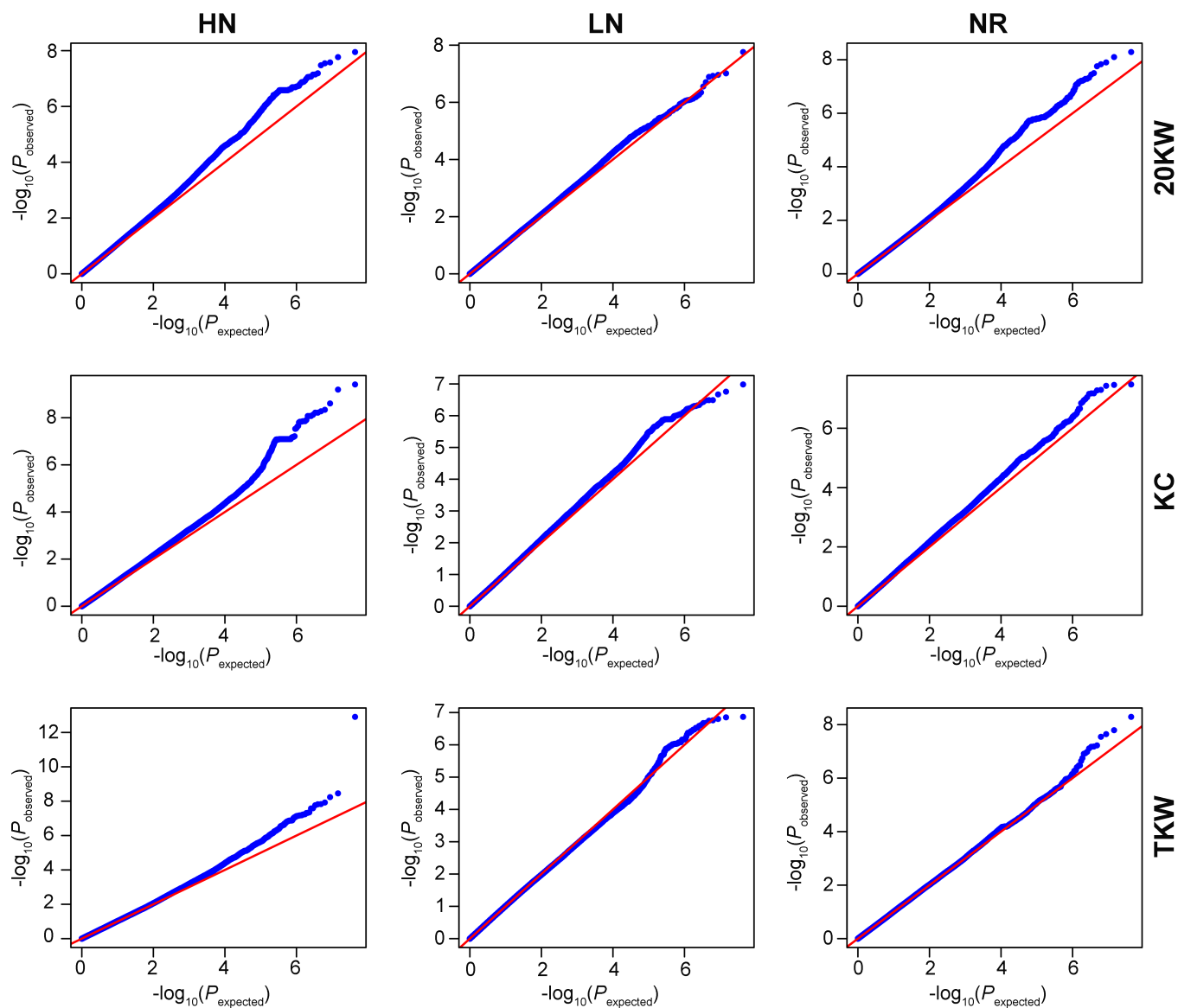


Figure S5 Quantile-quantile (Q-Q) plots for kernel-related traits. Red diagonal line indicates the expected values and the blue dots represent the observations.

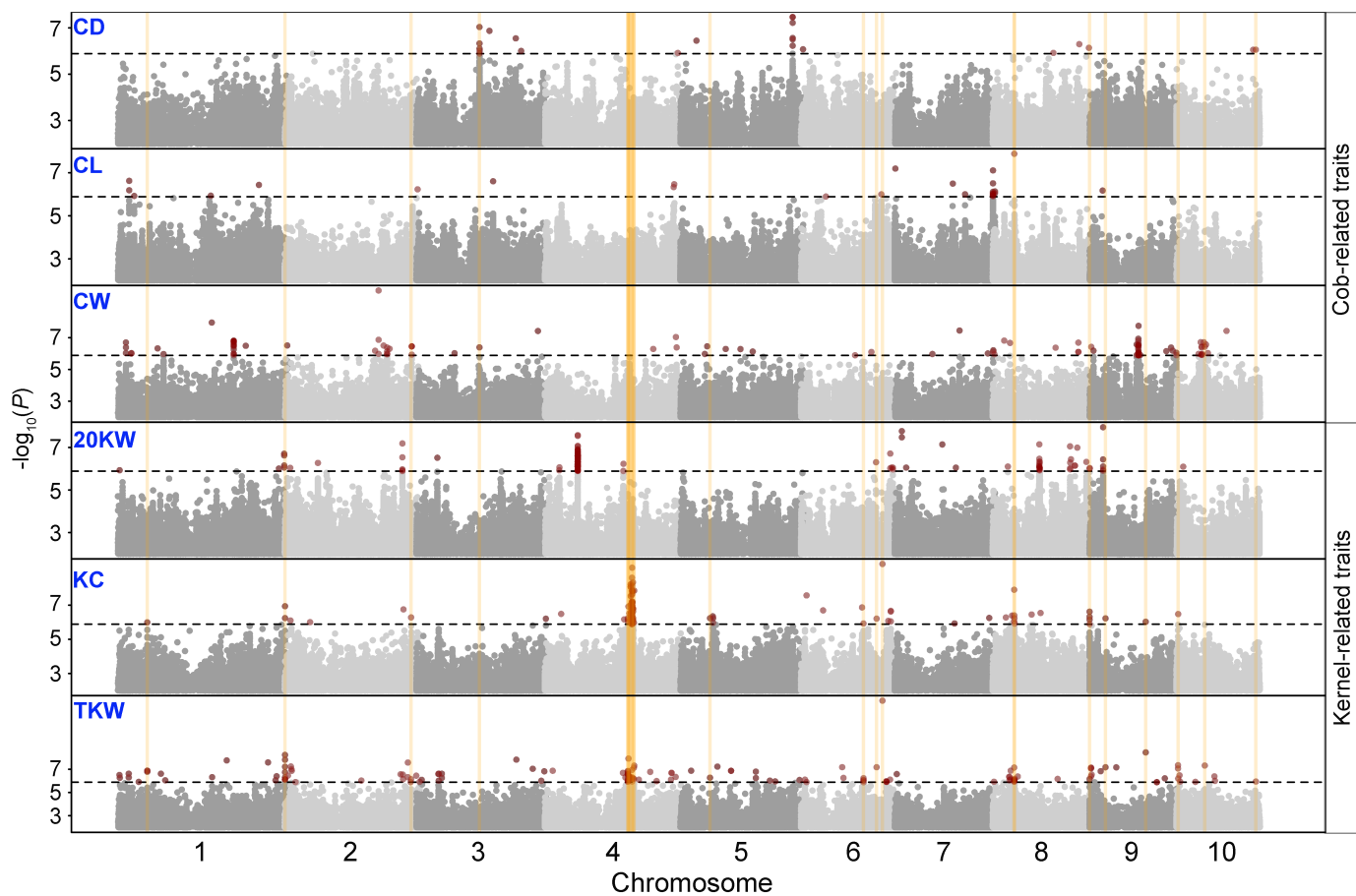


Figure S6 Stacking Manhattan plot of cob- and kernel-related traits under HN conditions. The black horizontal dashed line indicates the GWAS threshold. Each red dot above the threshold represents the SNP significantly associated with a trait. The vertical orange lines indicate the overlapped trait-associated loci (TALs).

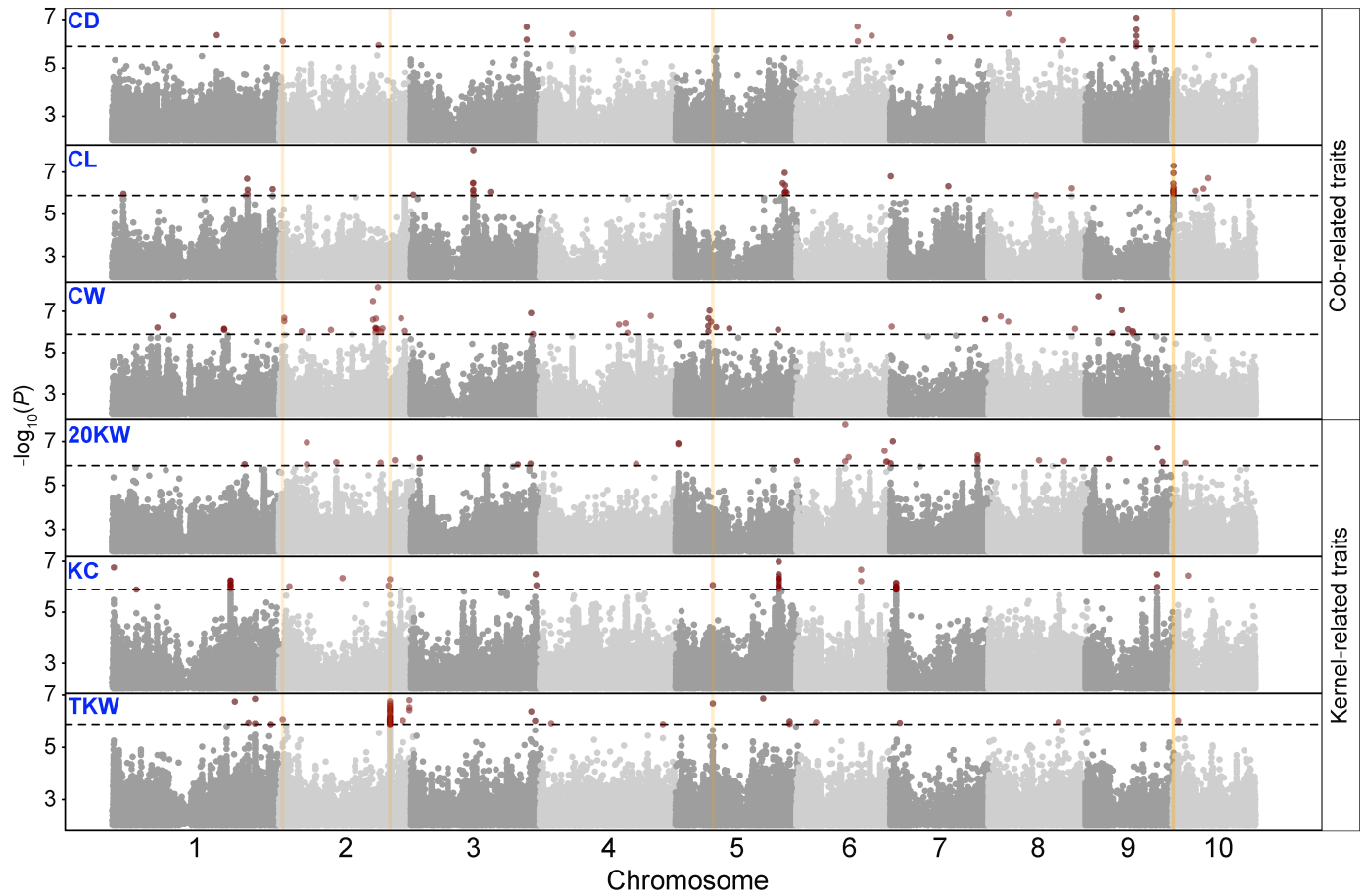


Figure S7 Stacking Manhattan plot of cob- and kernel-related traits under LN conditions. The red horizontal dashed line indicates the GWAS threshold. Each red dot above the threshold represents the SNP significantly associated with a trait. The vertical orange lines indicate the overlapped trait-associated loci (TALs).

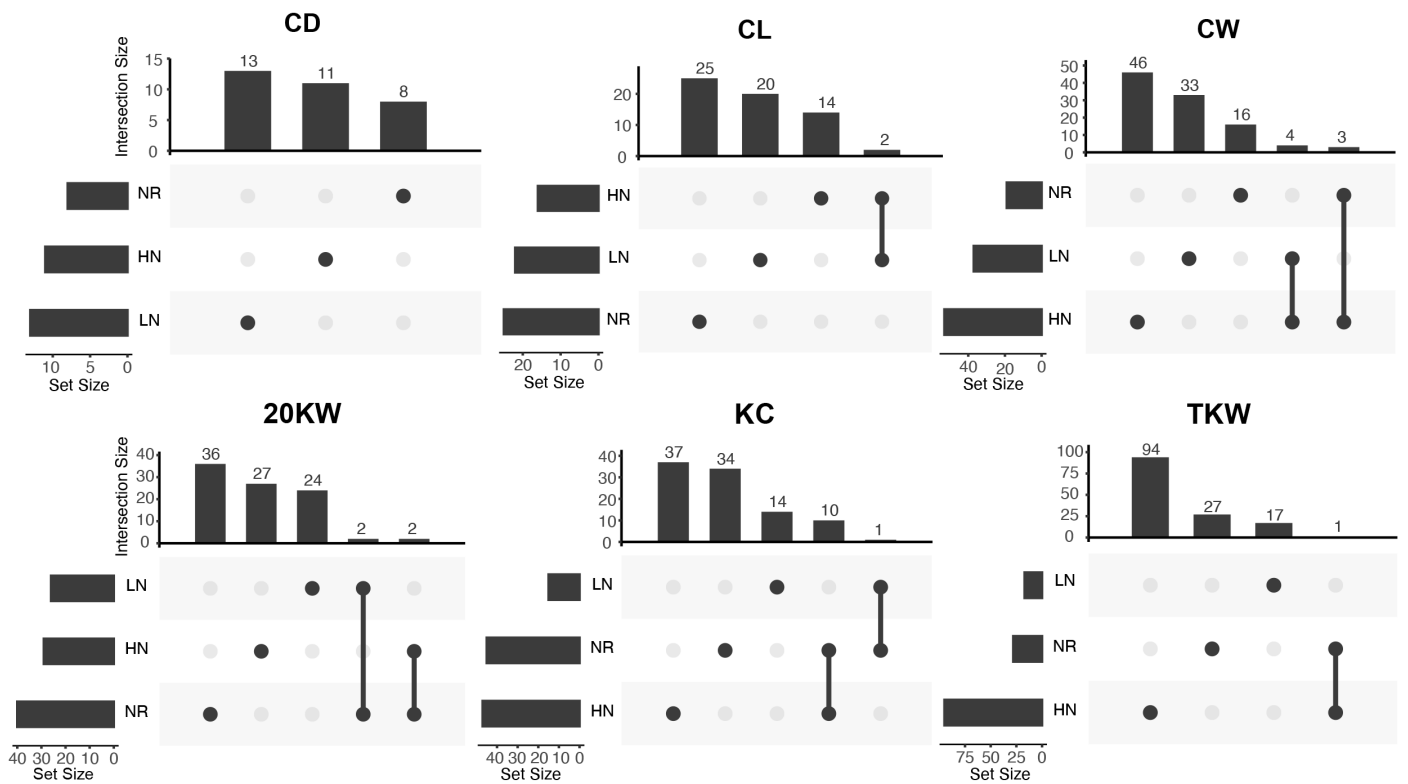


Figure S8 Overlapping results of trait-associated loci (TALs) for each trait under three different N conditions. Numbers on top of the barplots indicate the number of unique (only dots) and shared (dots and lines) TALs.

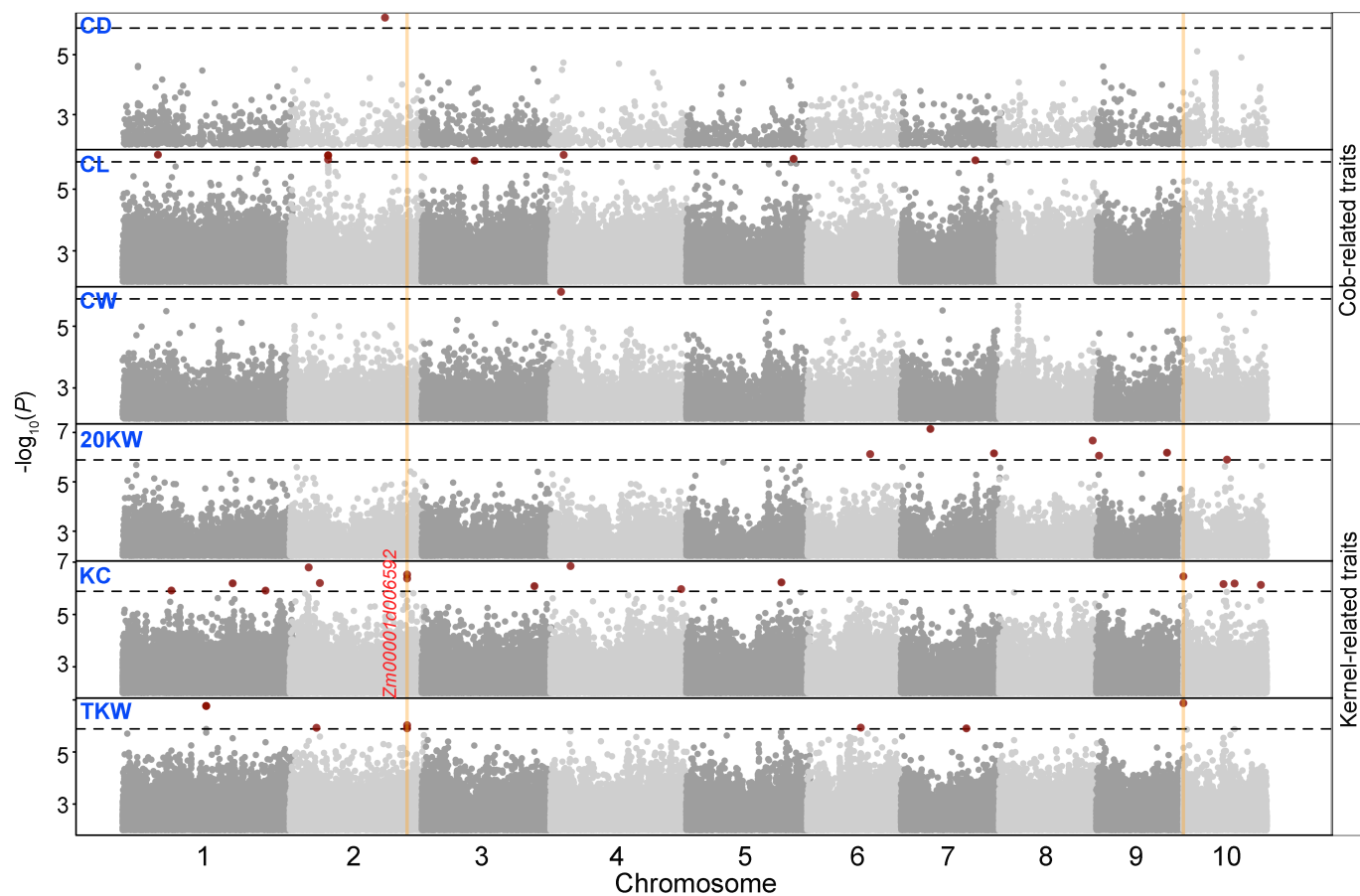


Figure S9 Stacking manhattan plot for genotype-by-nitrogen ($G \times N$) interaction of the cob- and kernel-related traits. The black horizontal dashed line indicates the GWAS threshold. Each red dot above the threshold represents the SNP significantly associated with a trait. The vertical orange lines indicate the overlapped trait-associated loci (TALs) for $G \times N$.