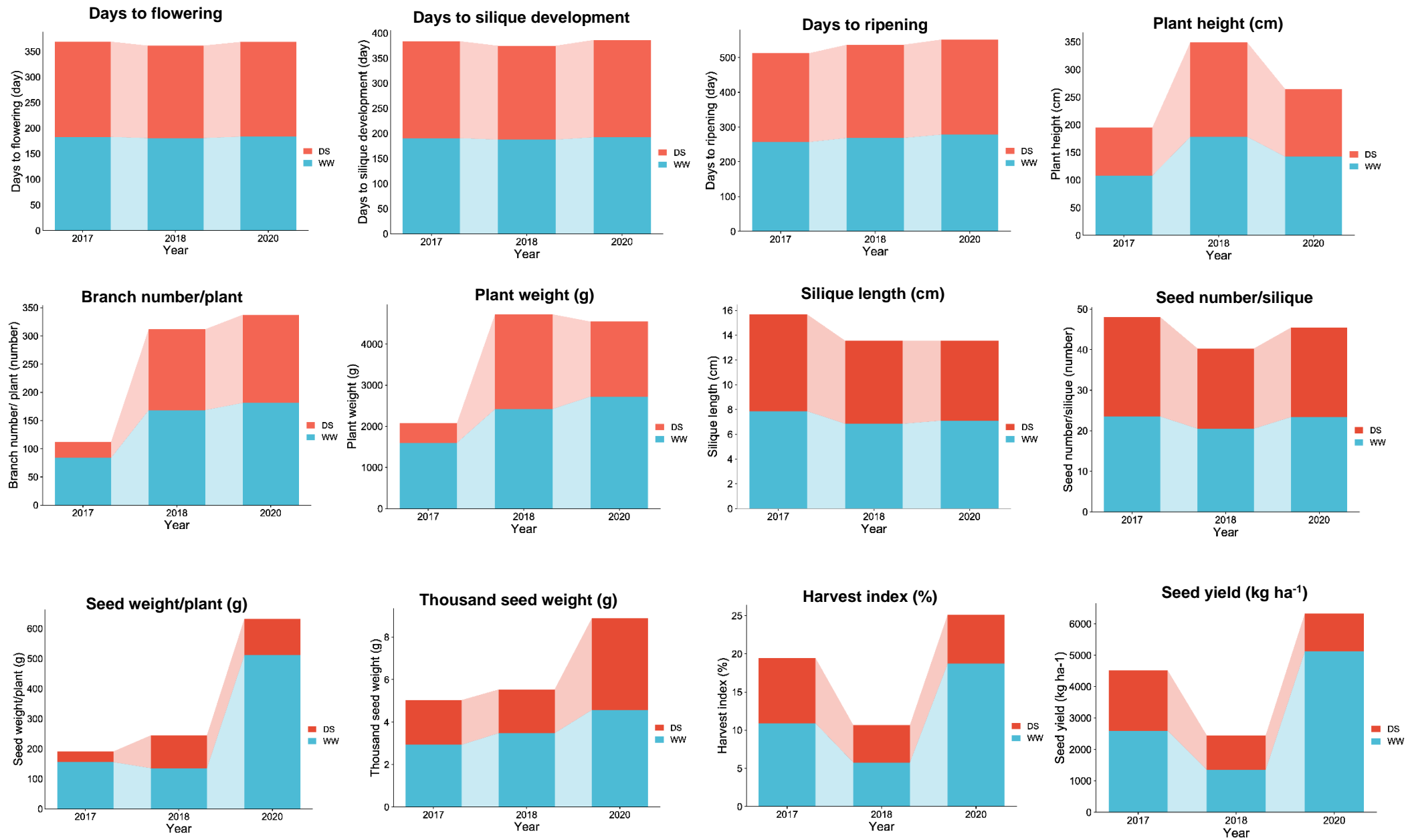
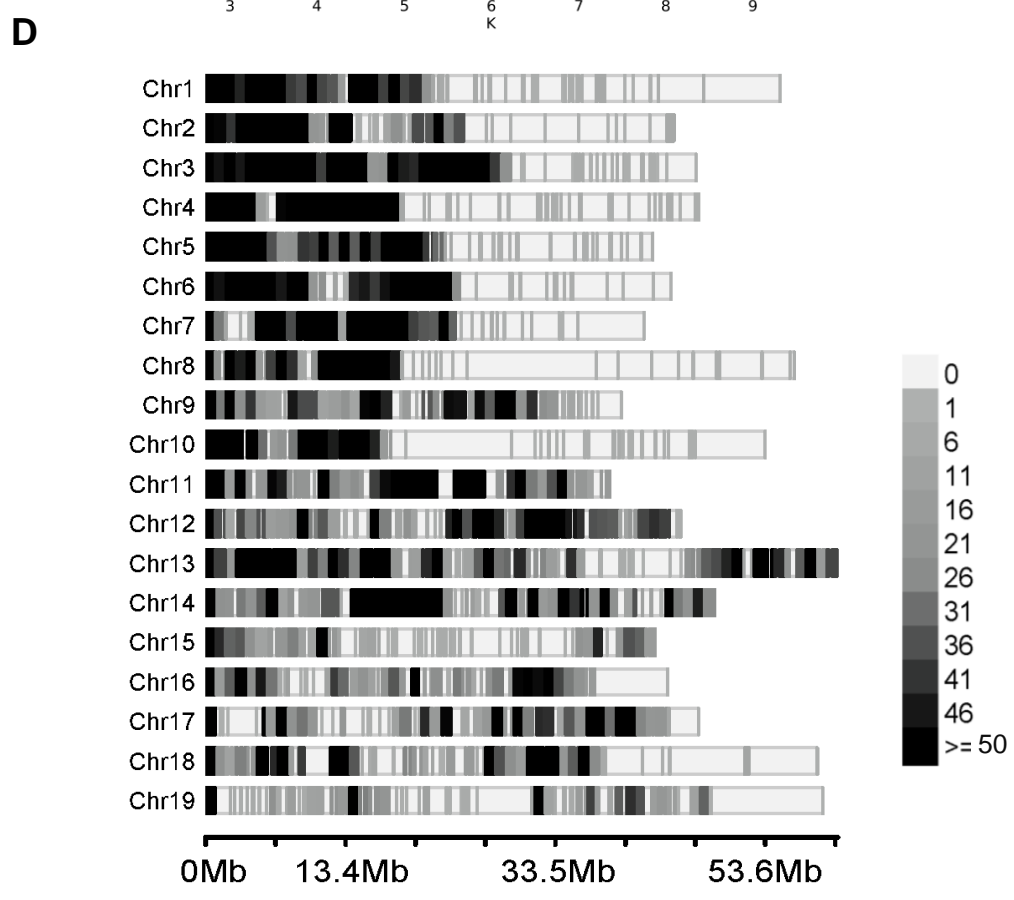
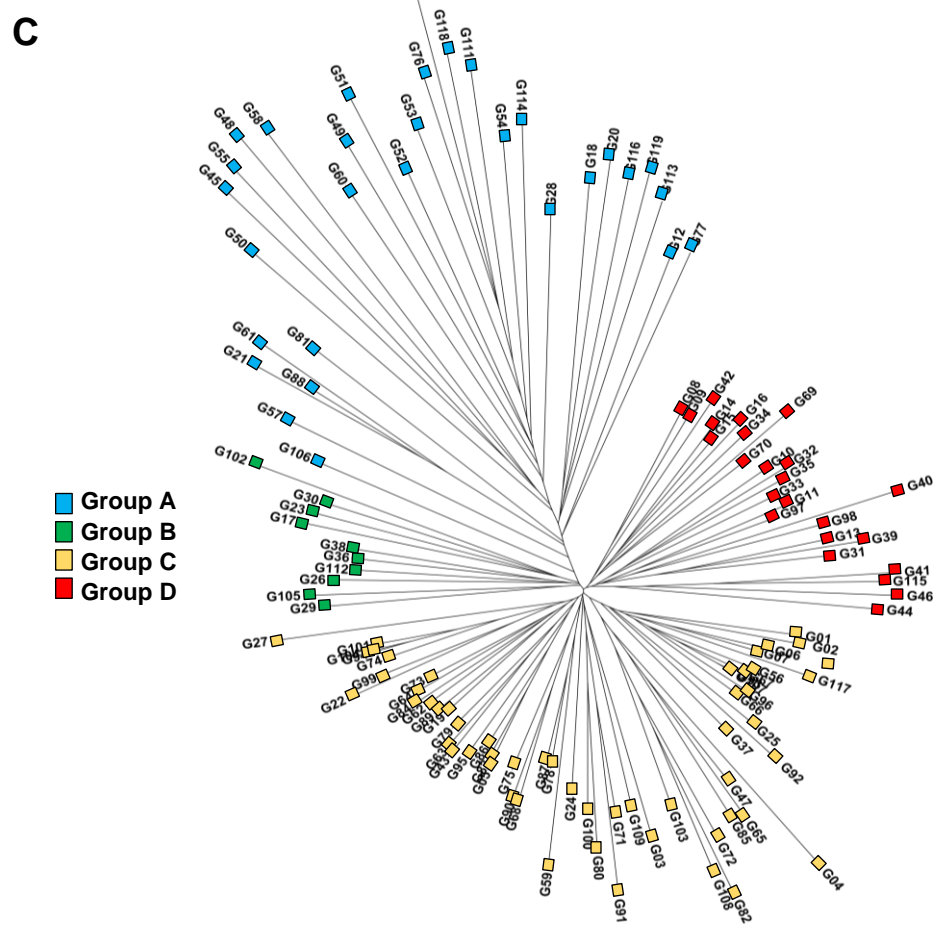
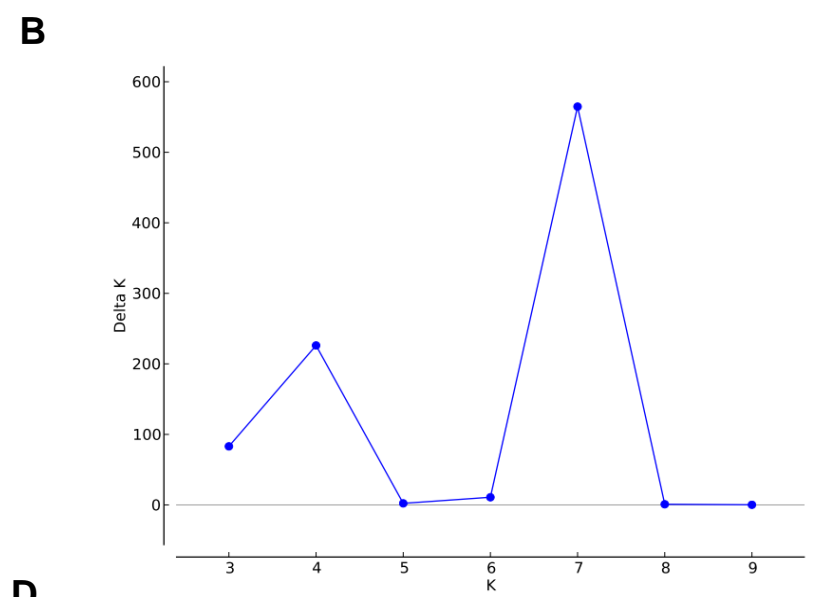
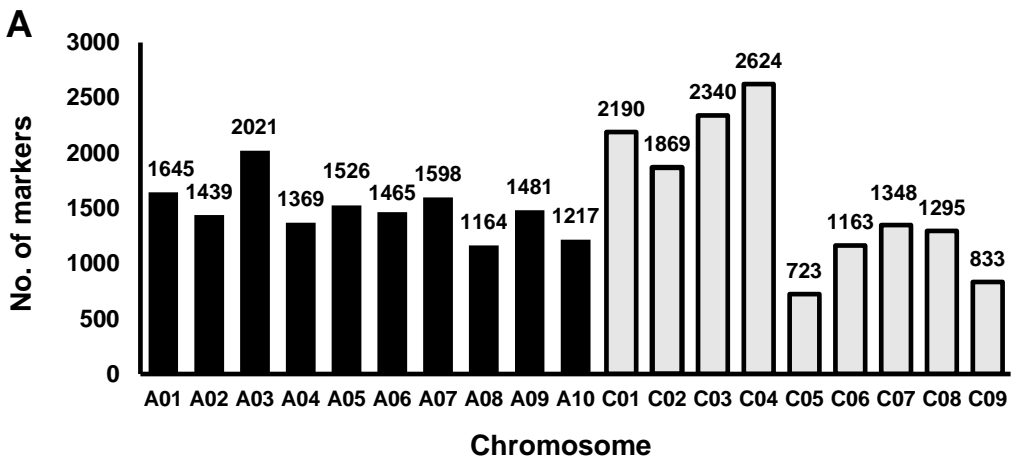
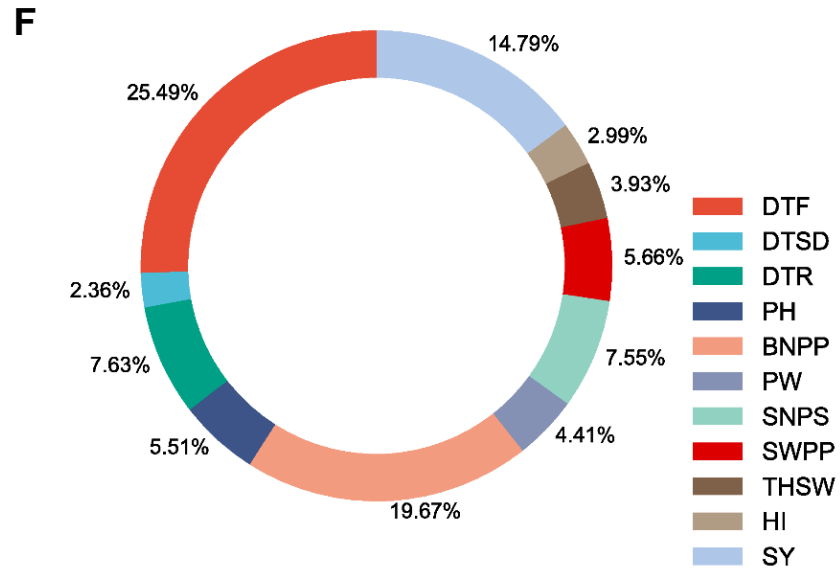
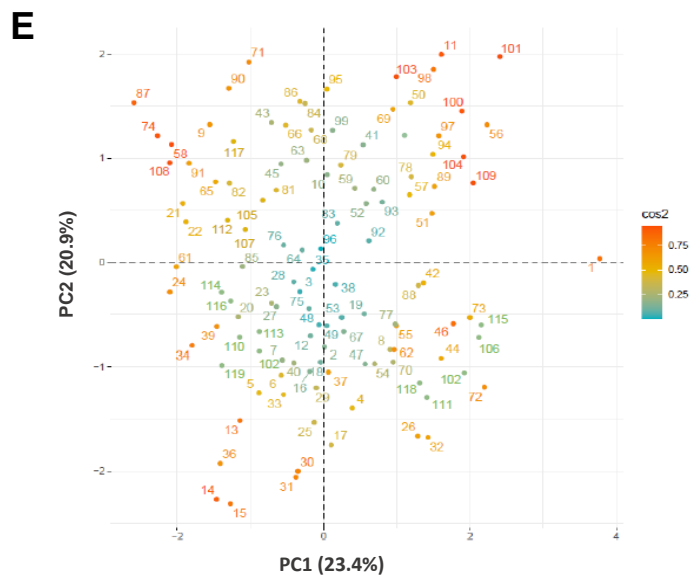


Supplementary Figure S1 Seasonal minimum, maximum and mean temperature, seasonal mean values of air relative humidity, and seasonal mean precipitation during the rapeseed (*Brassica napus*) growing season across three years (2017, 2018, and 2020).

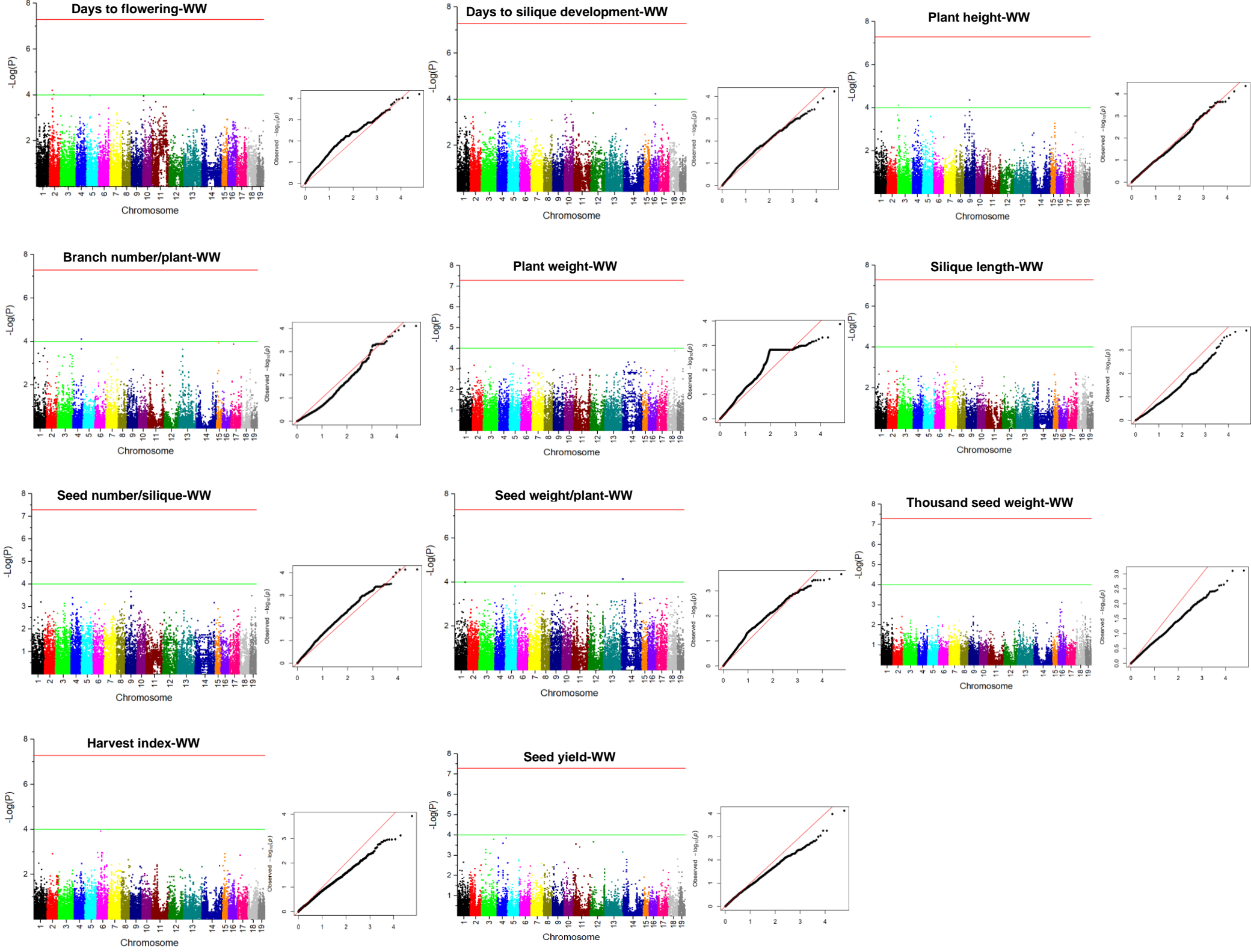


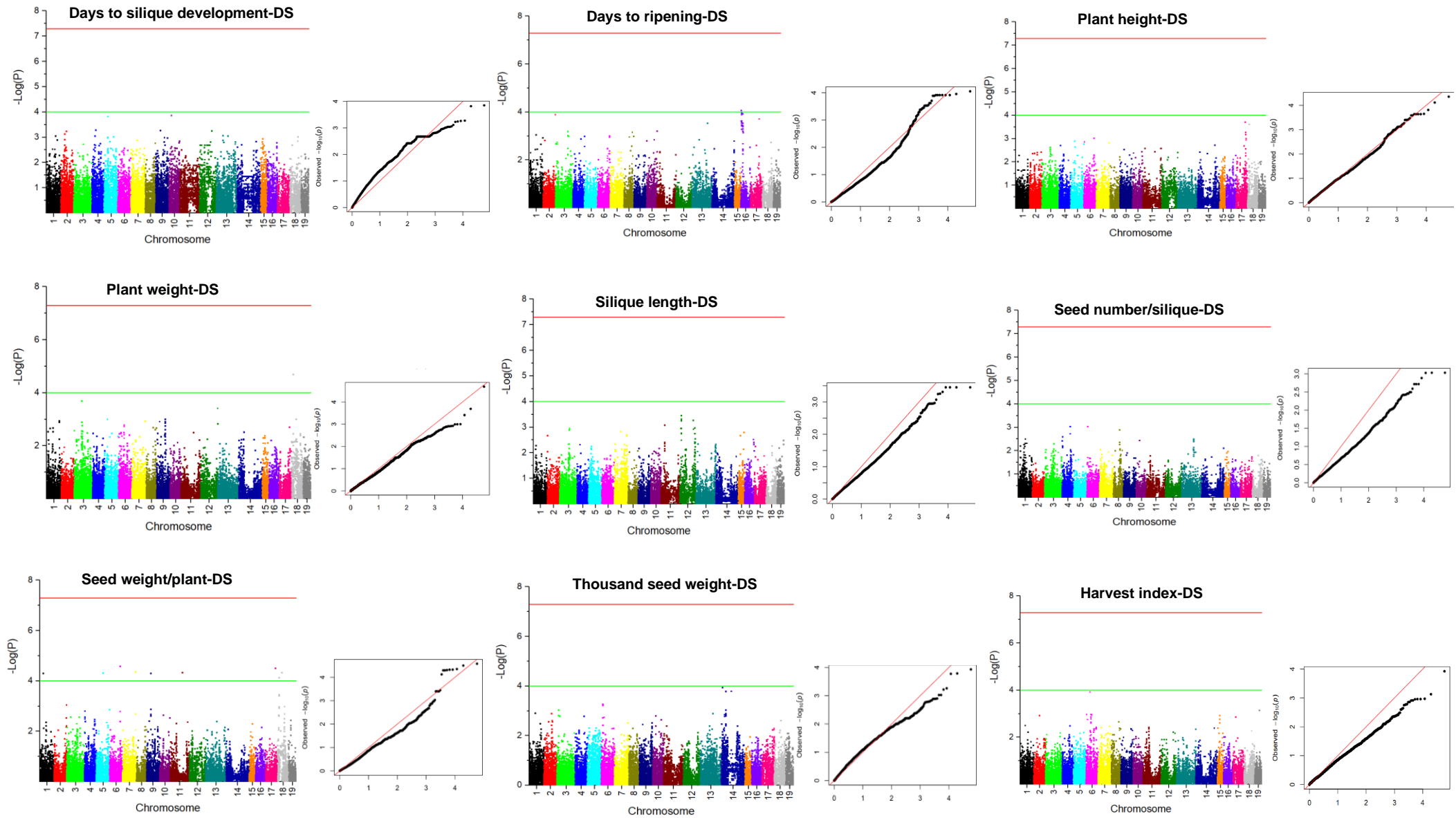
Supplementary Figure S2 Effects of drought stress on agronomic and yield related traits in rapeseed (*Brassica napus*) across three years (2017, 2018, and 2020). Vertical axes represent proportions. Blue and red column represent well-watered and drought stress conditions, respectively.



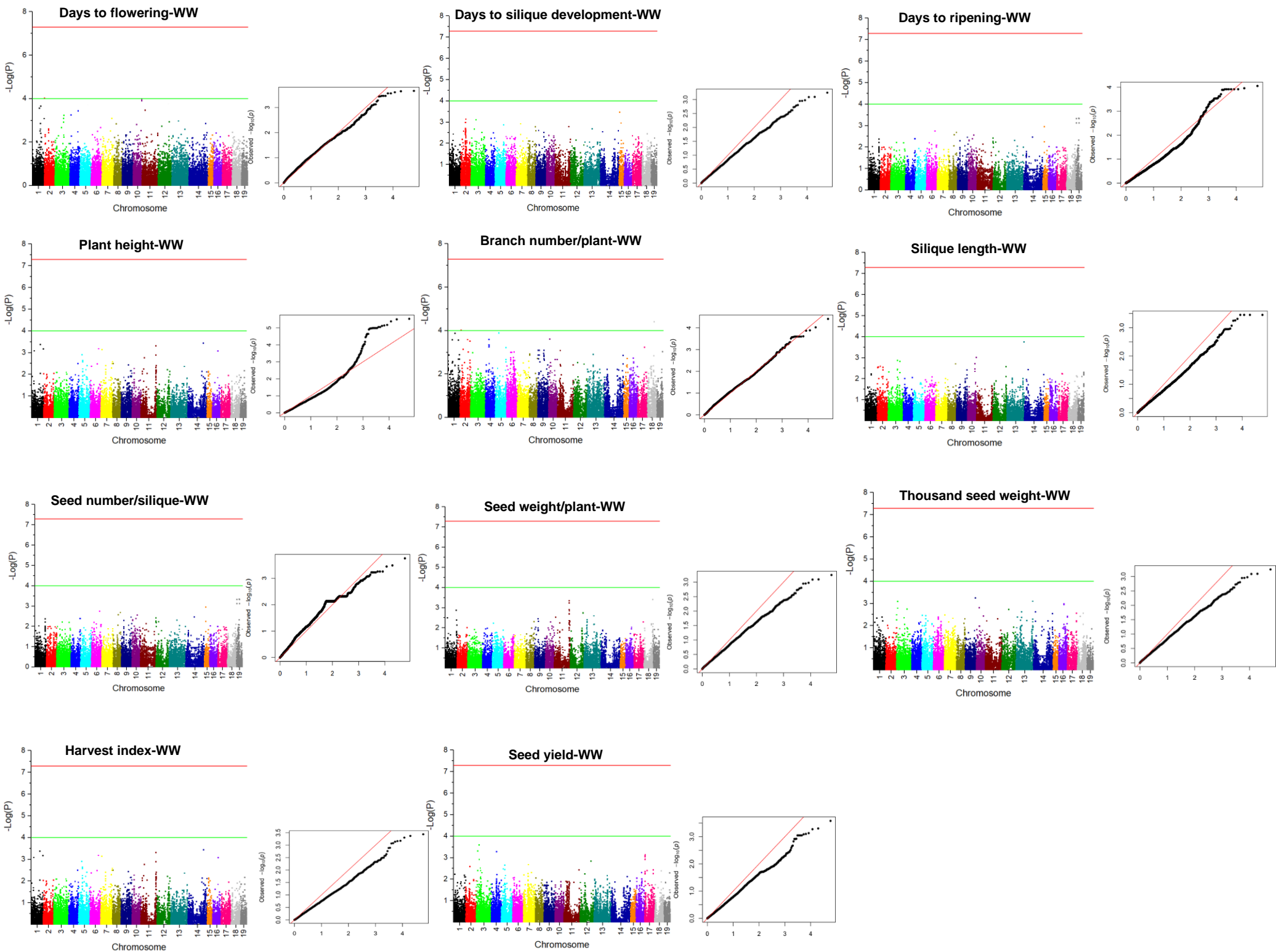


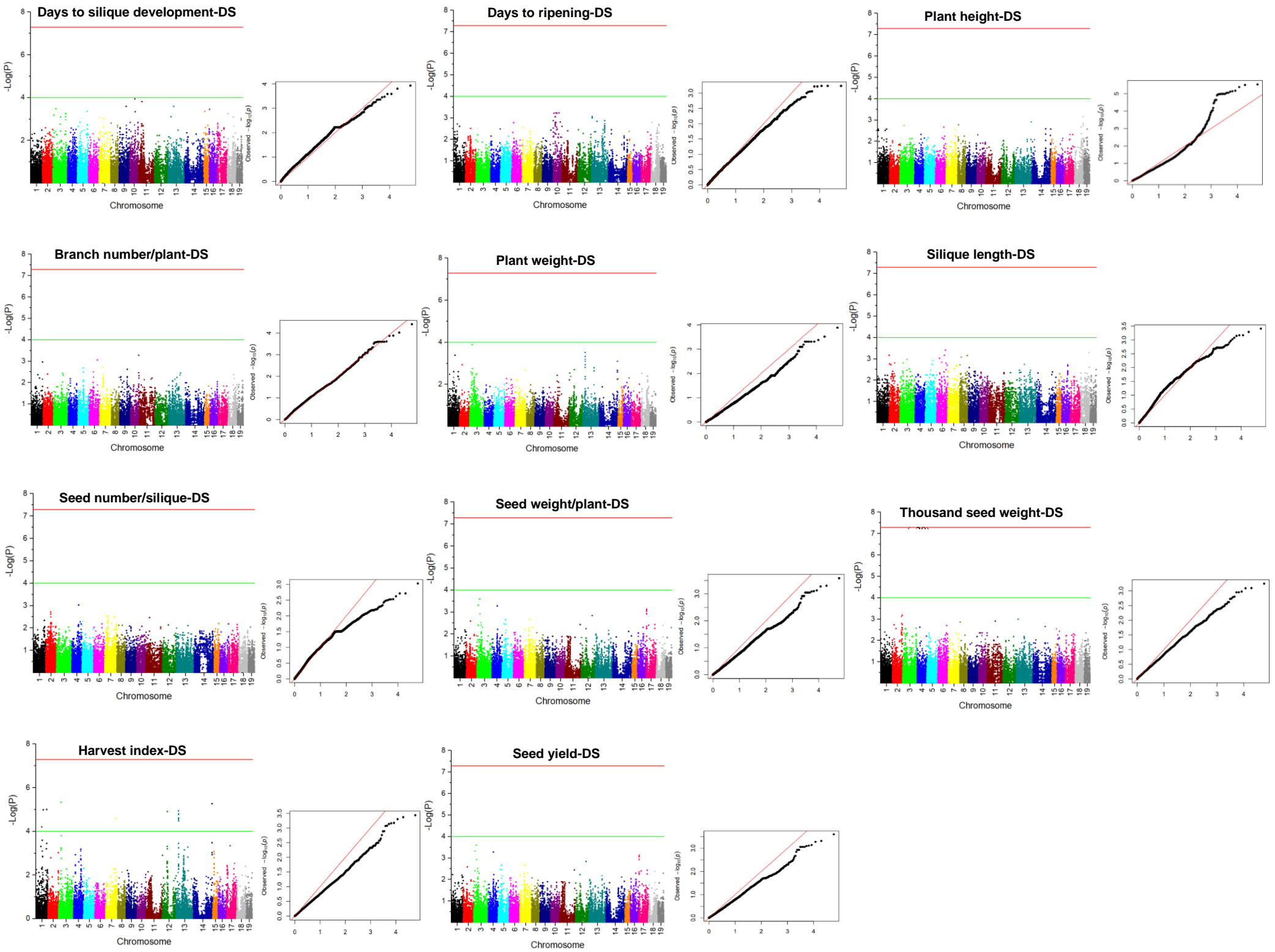
Supplementary Figure S3 (A) Distribution of 29,310 SNP markers across different chromosomes of rapeseed (*Brassica napus* L.). (B) Delta K values for different numbers of populations assumed (K) in the STRUCTURE analysis. (C) Neighbor-joining (NJ) cluster analysis of 119 rapeseed varieties inferred from 29,310 SNPs. G01-G119 stand for code of the rapeseed varieties. (D) Heatmap for distribution of 29,310 SNPs within 1 Mb window size in the rapeseed. The horizontal axis shows the chromosome length (Mb). (E) PCA plots of first two components of 29,310 SNPs in 119 rapeseed varieties. (F) *B. napus* single nucleotide polymorphism (SNP)-trait association chart under two watering regimes (well-watered and drought stress conditions) across three years (2017, 2018, and 2020). DTF, DTSD, DTR, PH, BNPP, PW, SNPS, SWPP, THSW, HI, and SY were the abbreviations of days to flowering, days to silique development, days to ripening, plant height, branch number/plant, plant weight, seed number/silique, seed weight/plant, thousand seed weight, harvest index, and seed yield.



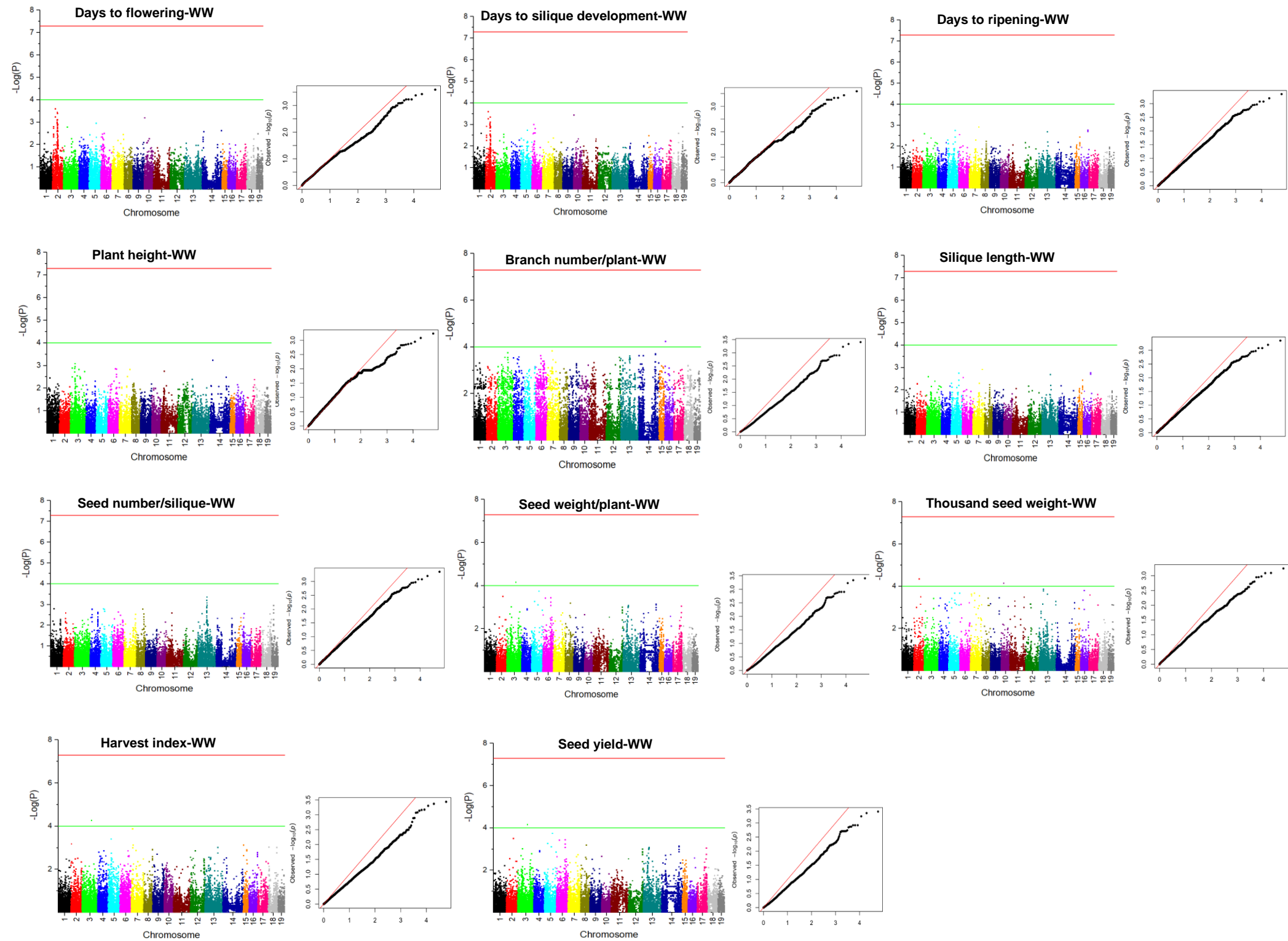


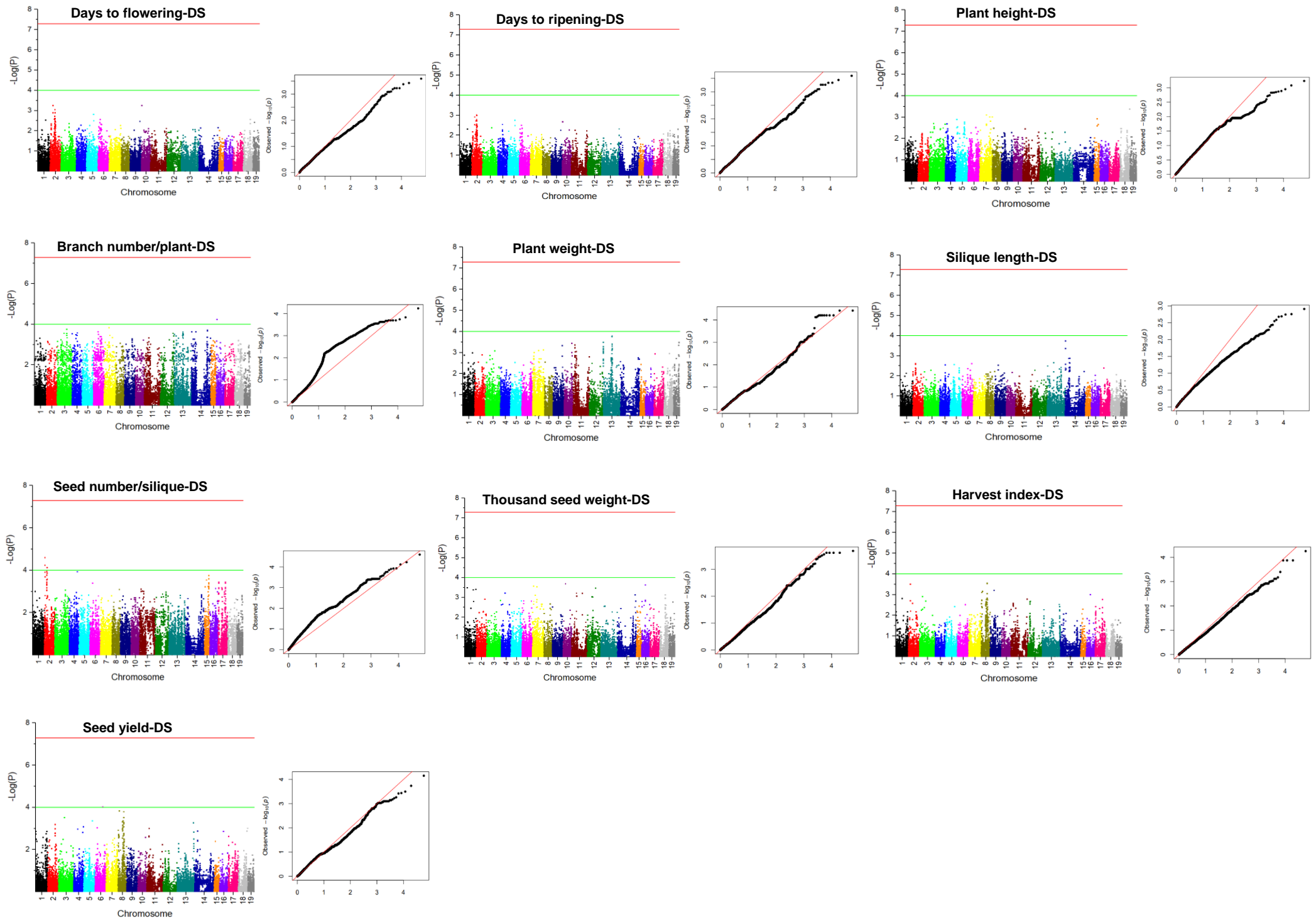
Supplementary Figure S4 Genome-wide association-mapping results for agronomic and yield related traits in rapeseed (*Brassica napus*) using single-trait analysis in all accessions grown in season 2017. Manhattan plot and corresponding quantile-quantile (QQ) plot displaying the GWAS result of agronomic and yield related traits in 19 chromosomes at well-watered (WW) and drought stress (DS) conditions. In the QQ plot, the x-axis displayed the expected $-\log_{10} p$ -value and y-axis represented the observed $-\log_{10} p$ -value.



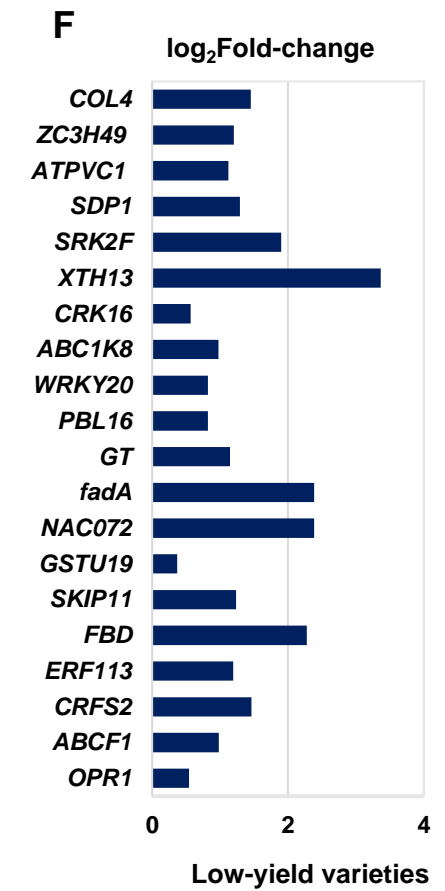
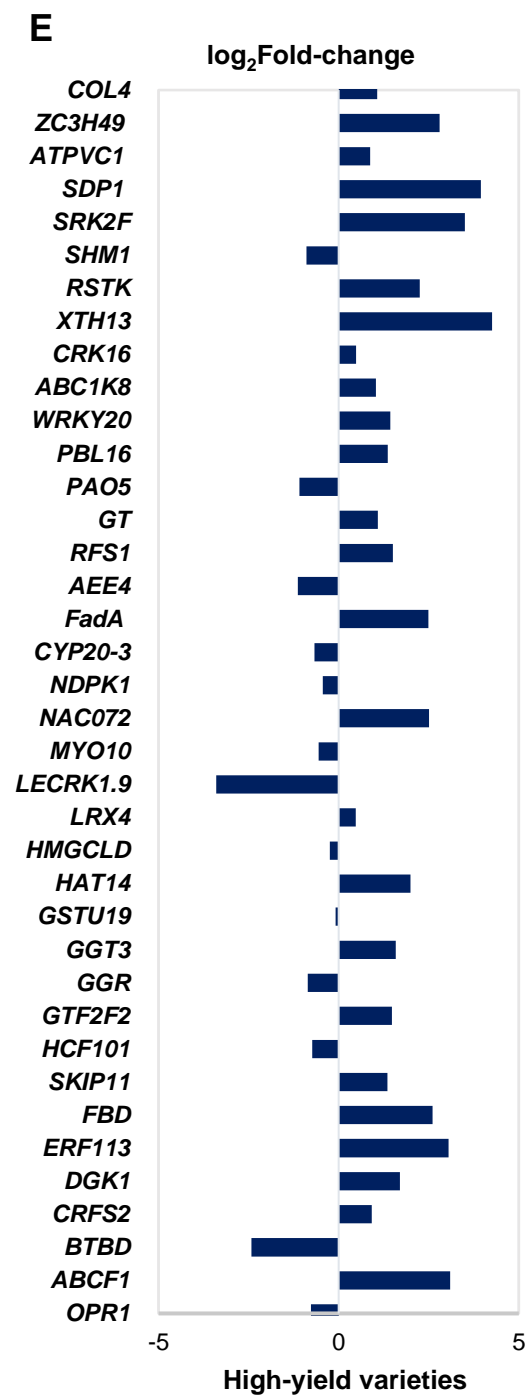
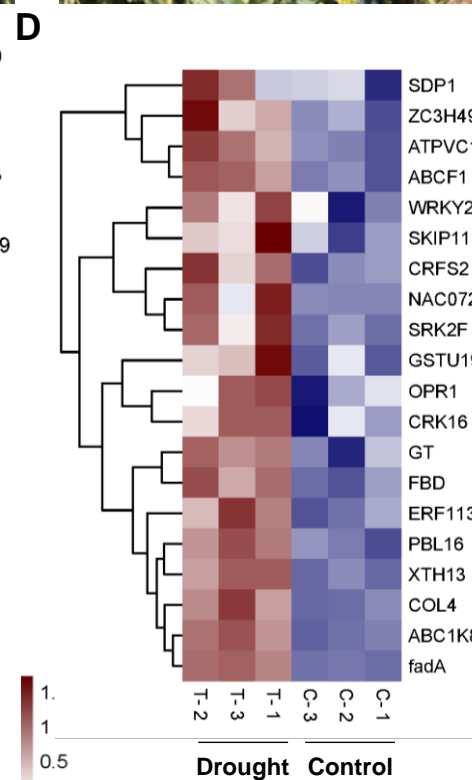
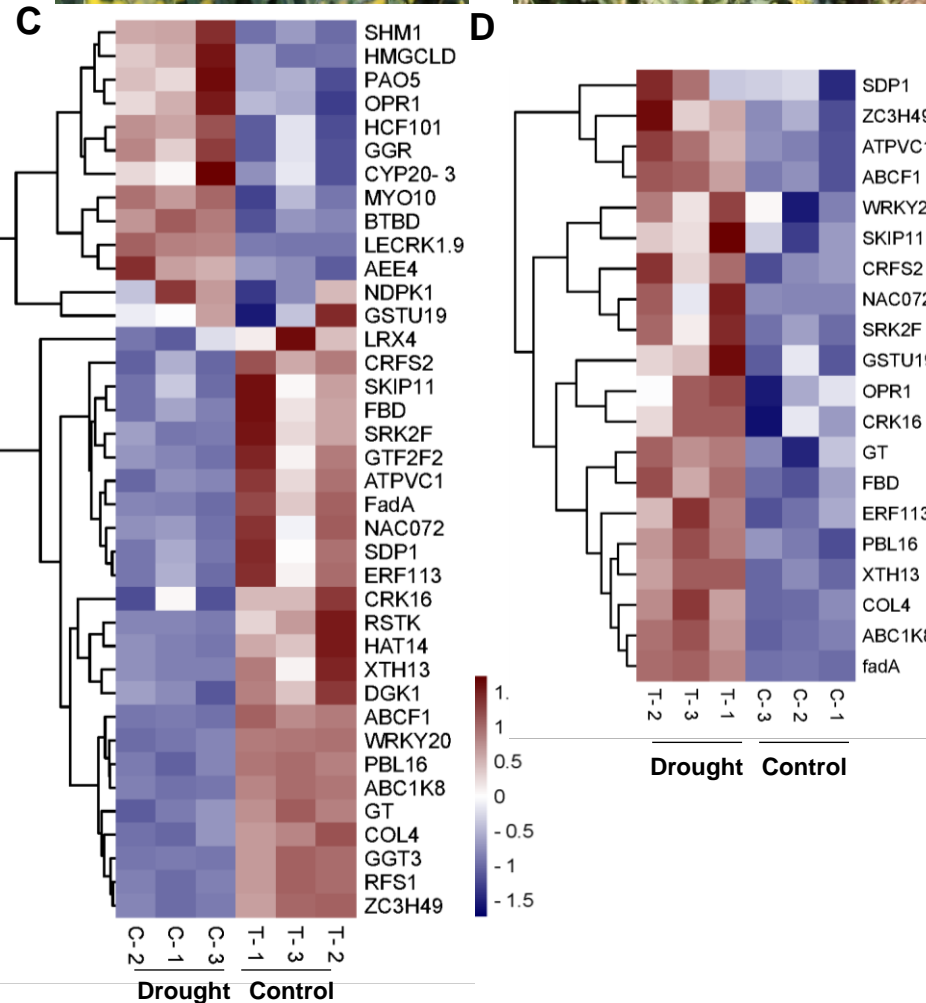
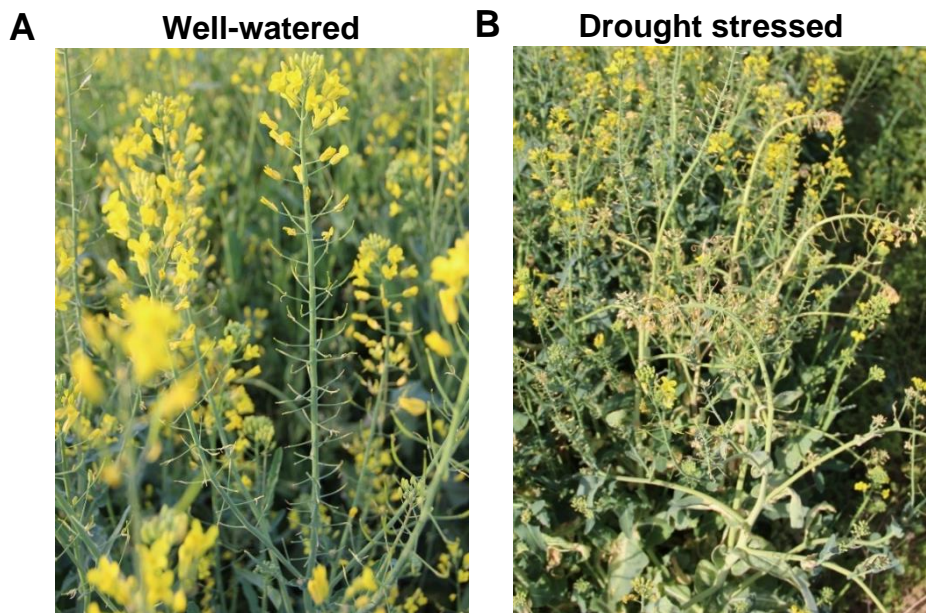


Supplementary Figure S5 Genome-wide association-mapping results for agronomic and yield related traits in rapeseed (*Brassica napus*) using single-trait analysis in all accessions grown in season 2018. Manhattan plot and corresponding quantile-quantile (QQ) plot displaying the GWAS result of agronomic and yield related traits in 19 chromosomes at well-watered (WW) and drought stress (DS) conditions. In the QQ plot, the x-axis displayed the expected $-\log_{10} p$ -value and y-axis represented the observed $-\log_{10} p$ -value.





Supplementary Figure S6 Genome-wide association-mapping results for agronomic and yield related traits in rapeseed (*Brassica napus*) using single-trait analysis in all accessions grown in season 2020. Manhattan plot and corresponding quantile-quantile (QQ) plot displaying the GWAS result of agronomic and yield related traits in 19 chromosomes at well-watered (WW) and drought stress (DS) conditions. In the QQ plot, the x-axis displayed the expected $-\log_{10} p$ -value and y-axis represented the observed $-\log_{10} p$ -value.



Supplementary Figure S7 Transcriptomic analysis of high and low-yield rapeseed varieties under drought stress. (A and B) Responses of the rapeseed plant to drought stress at flowering stage. (A) Rapeseed plant phenotypes under well-watered condition. (B) Rapeseed plant phenotypes at 3 weeks after stress. (C and D) Heatmap of drought-induced genes in high and low-yield varieties under drought stress. (C) Thirty-eight drought-induced genes in high-yield varieties. (D) Twenty drought-induced genes in the low-yield varieties. (E) Bar plot of upregulated and downregulated of key drought-induced genes in high-yield varieties. (F) Bar plot of upregulated and downregulated of key drought-induced genes in low-yield varieties.