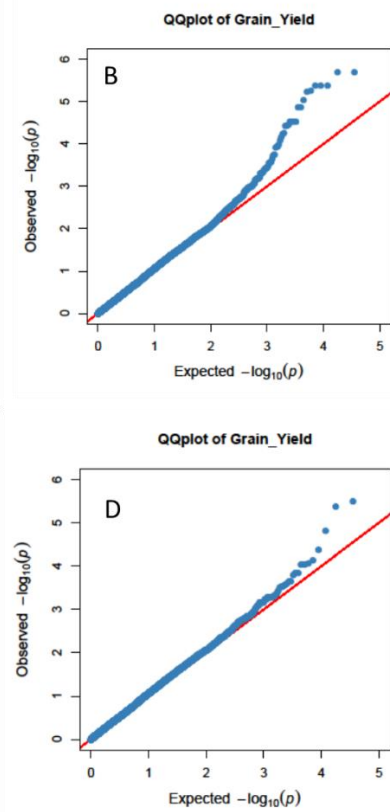
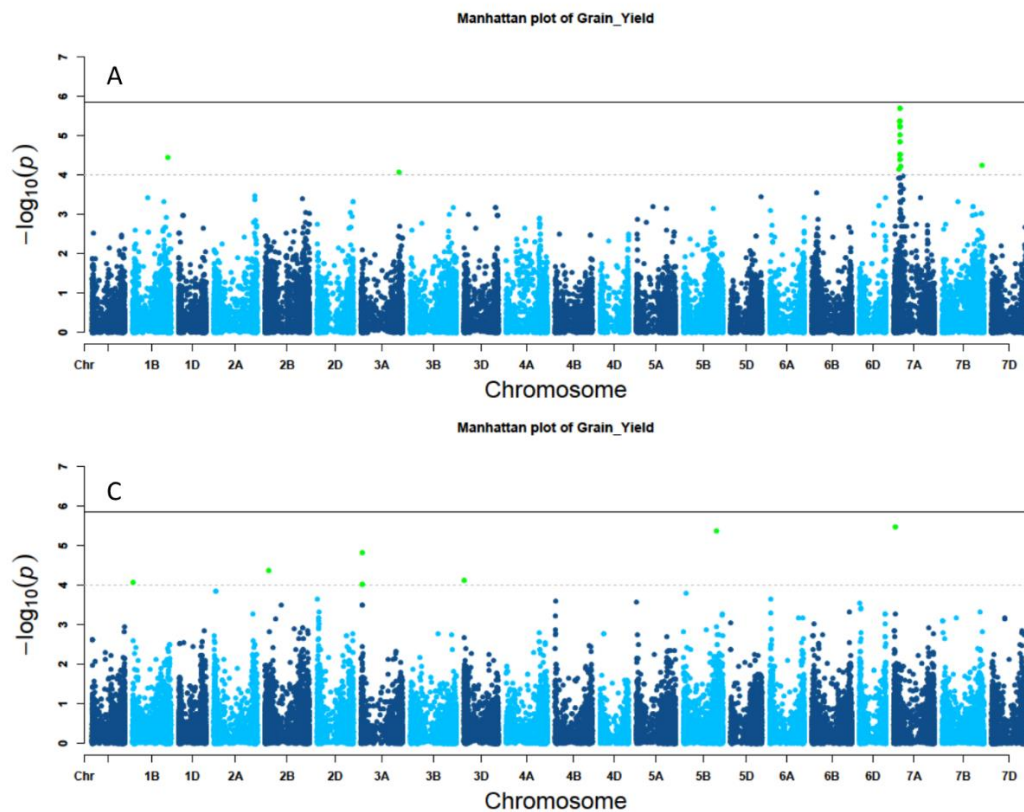


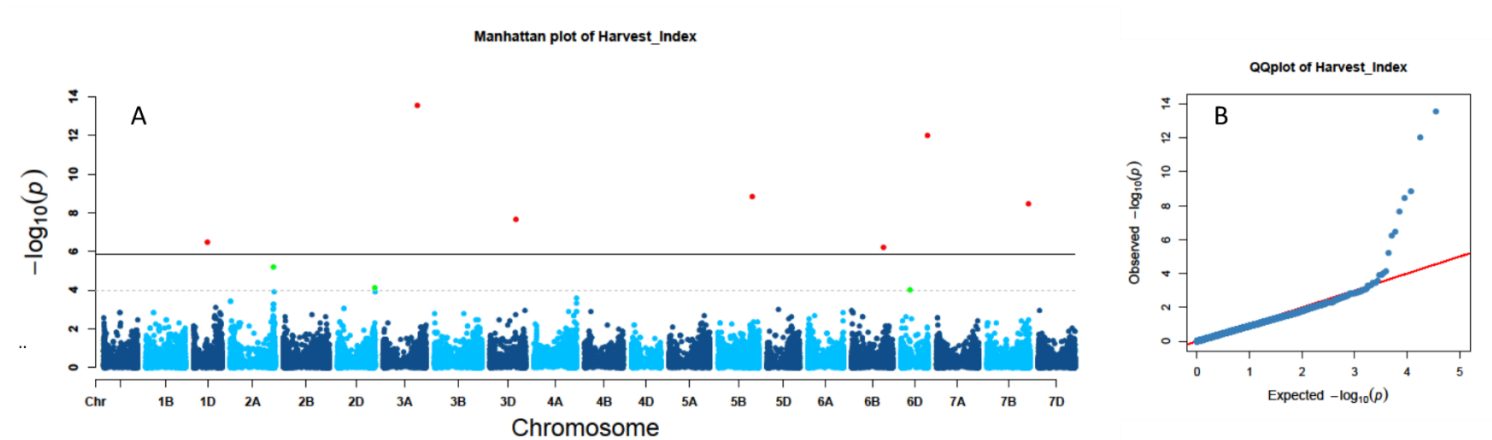
**Figure S4.** Manhattan and quantile-quantile plots for 11 traits in 123 synthetic hexaploid wheat germplasm based on best linear unbiased prediction values.

(A) Manhattan plot in 2016 (B) quantile-quantile (Q-Q) plots in 2016 (C) Manhattan plot in 2017 (D) Q-Q plot in 2017



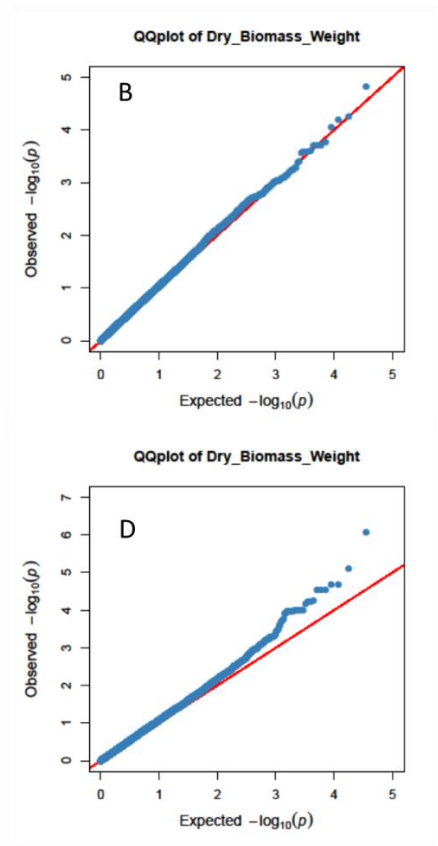
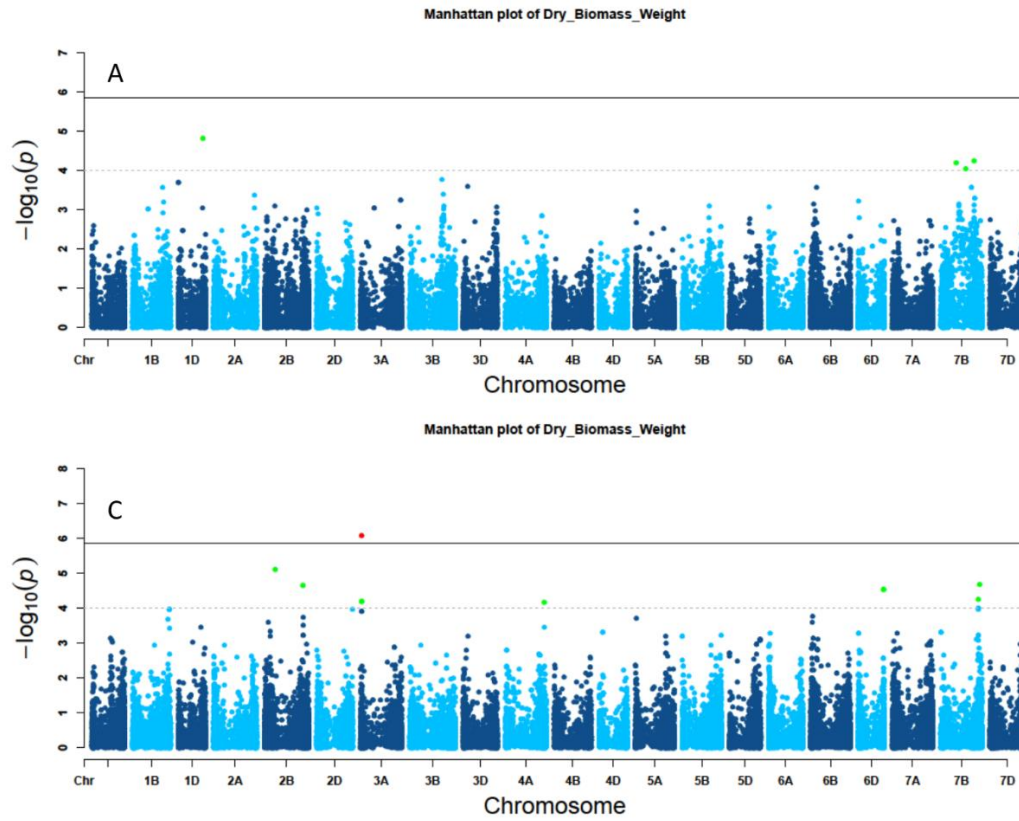
## Grain yield (GY)

(A) Manhattan plot in 2016. (B) quantile-quantile (Q-Q) plots in 2016. (C) Manhattan plot in 2017. (D) Q-Q plot in 2017. The solid black line showed the expected value at Bonferroni correction at 5% level of significance [ $-\log_{10}(P) = 5.85$ ] and dotted black line showed the expected value with a uniform suggestive genome wide significance threshold [ $-\log_{10}(P) = 4.00$ ].



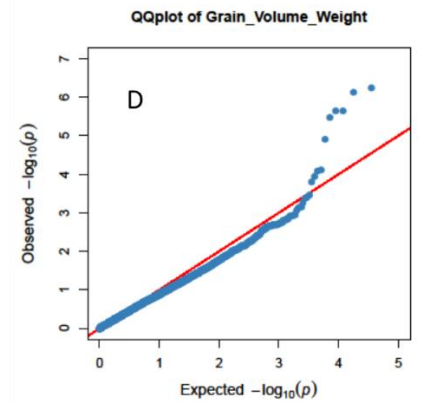
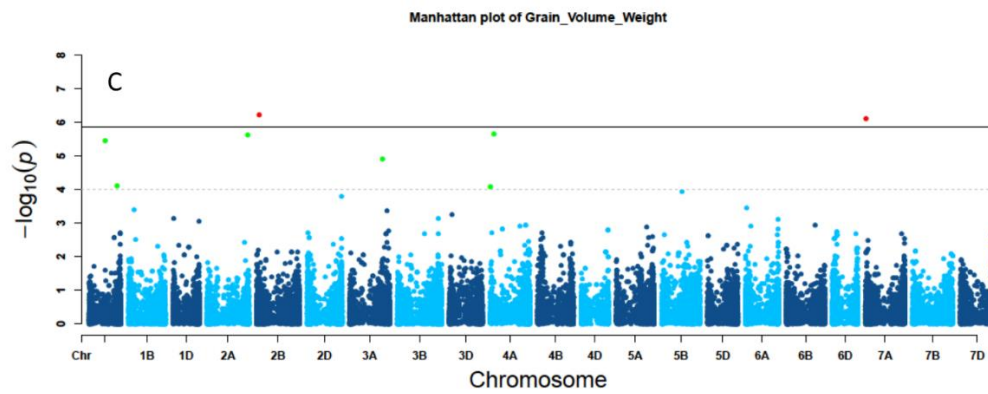
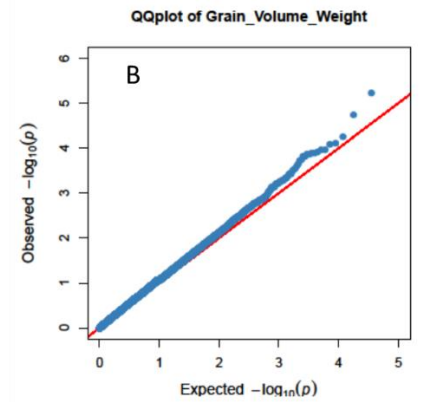
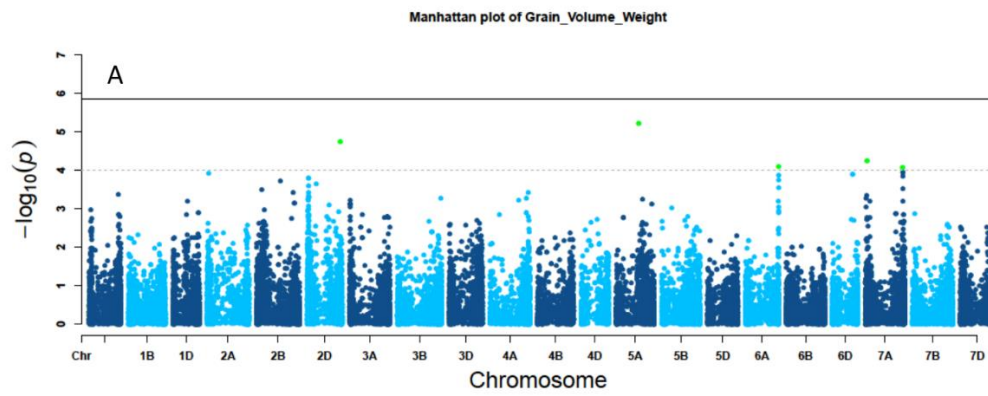
### Harvest index (HI)

(A) Manhattan plot in 2016. (B) quantile-quantile (Q-Q) plots in 2016. The solid black line showed the expected value at Bonferroni correction at 5% level of significance [ $-\log_{10}(P) = 5.85$ ] and dotted black line showed the expected value with a uniform suggestive genome wide significance threshold [ $-\log_{10}(P) = 4.00$ ].



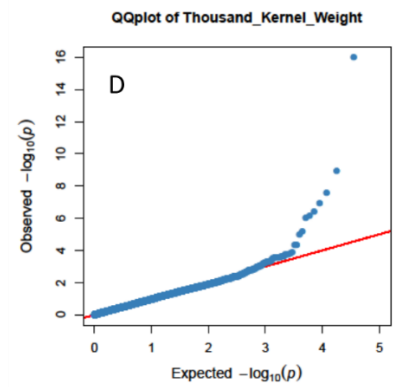
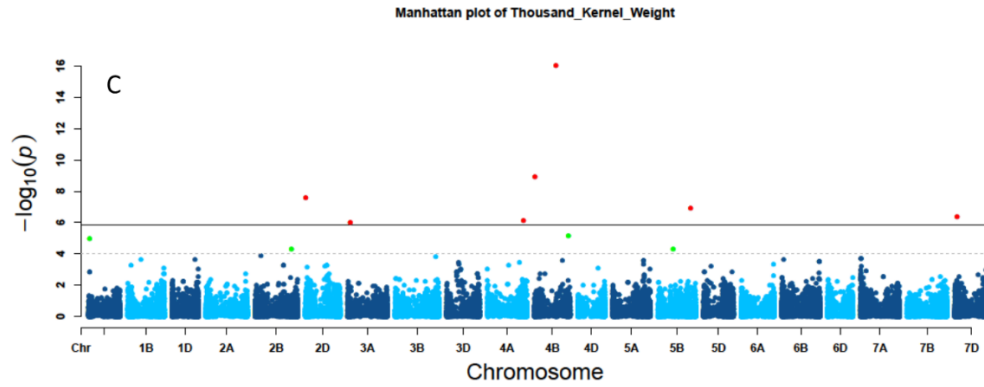
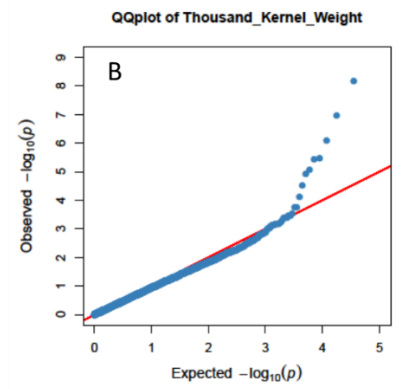
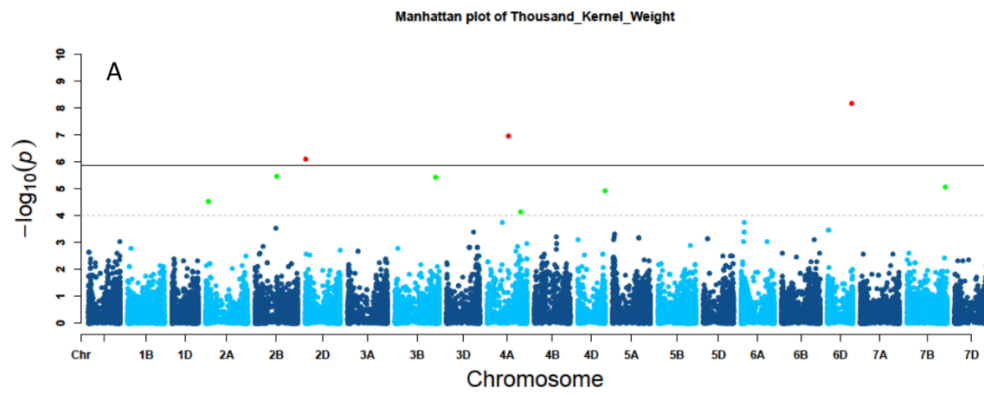
### Dry biomass weight (BMWT)

(A) Manhattan plot in 2016. (B) quantile-quantile (Q-Q) plots in 2016. (C) Manhattan plot in 2017. (D) Q-Q plot in 2017. The solid black line showed the expected value at Bonferroni correction at 5% level of significance [ $-\log_{10}(P) = 5.85$ ] and dotted black line showed the expected value with a uniform suggestive genome wide significance threshold [ $-\log_{10}(P) = 4.00$ ].



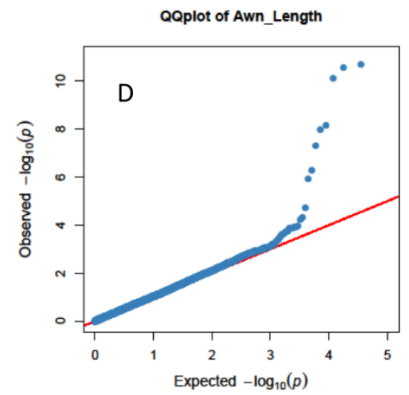
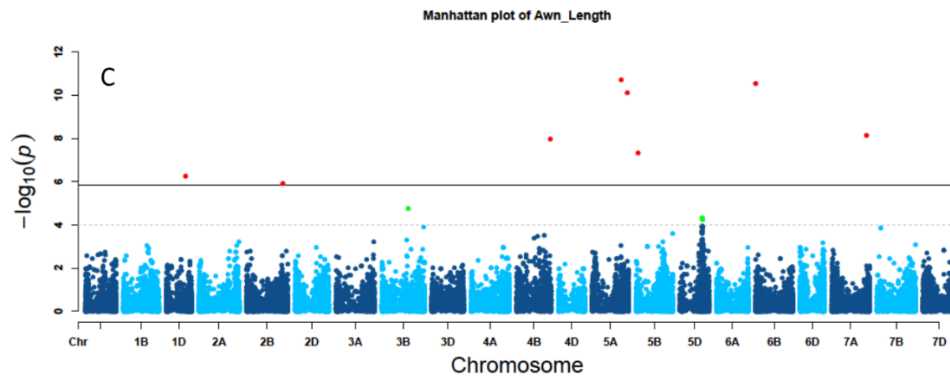
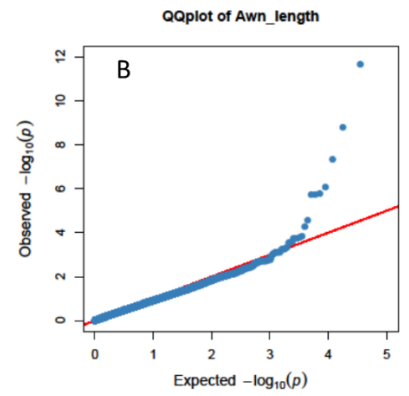
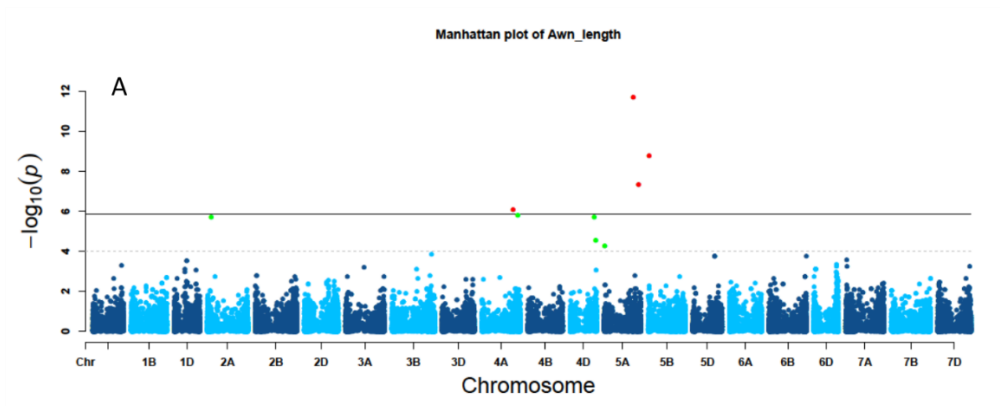
### Grain volume weight (GVWT)

(A) Manhattan plot in 2016. (B) quantile-quantile (Q-Q) plots in 2016. (C) Manhattan plot in 2017. (D) Q-Q plot in 2017. The solid black line showed the expected value at Bonferroni correction at 5% level of significance [ $-\log_{10}(P) = 5.85$ ] and dotted black line showed the expected value with a uniform suggestive genome wide significance threshold [ $-\log_{10}(P) = 4.00$ ].



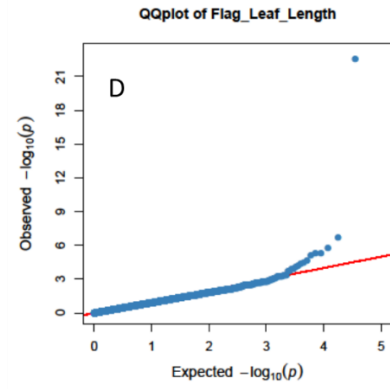
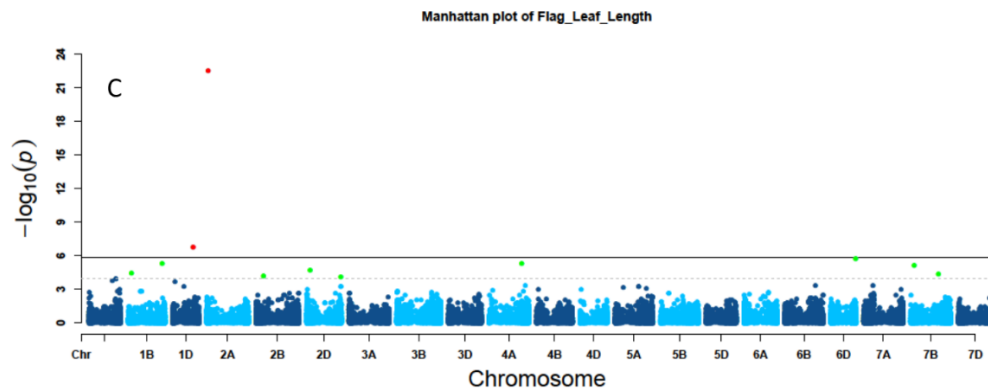
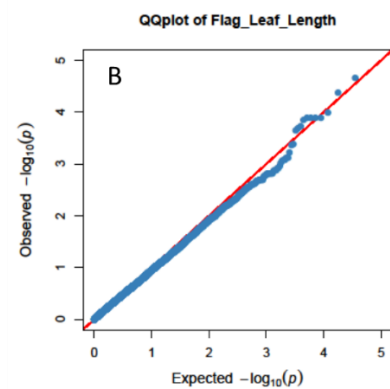
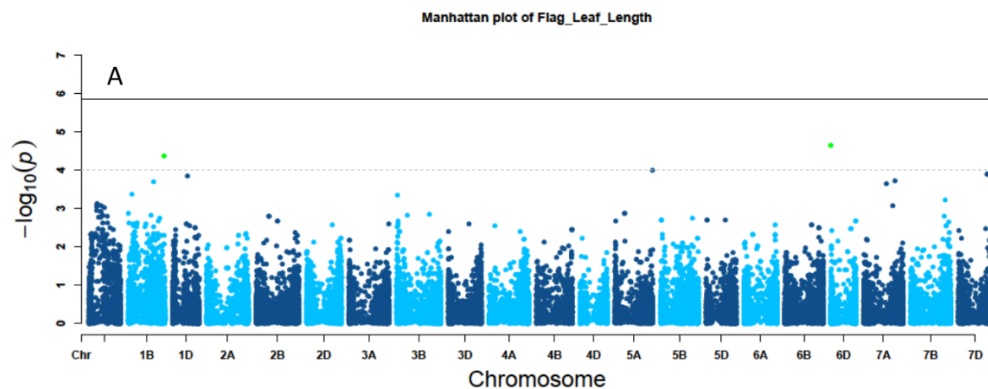
## Thousand kernel weight (TKW)

(A) Manhattan plot in 2016. (B) quantile-quantile (Q-Q) plots in 2016. (C) Manhattan plot in 2017. (D) Q-Q plot in 2017. The solid black line showed the expected value at Bonferroni correction at 5% level of significance [ $-\log_{10}(P) = 5.85$ ] and dotted black line showed the expected value with a uniform suggestive genome wide significance threshold [ $-\log_{10}(P) = 4.00$ ].



### Awn length (AWNLN)

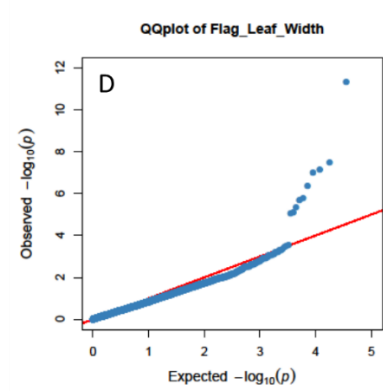
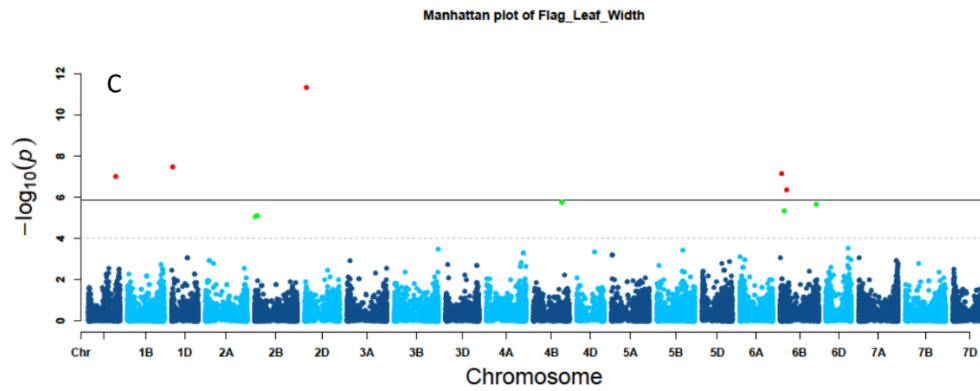
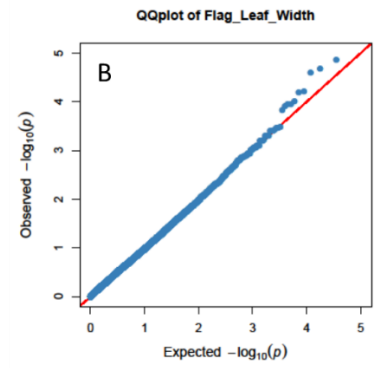
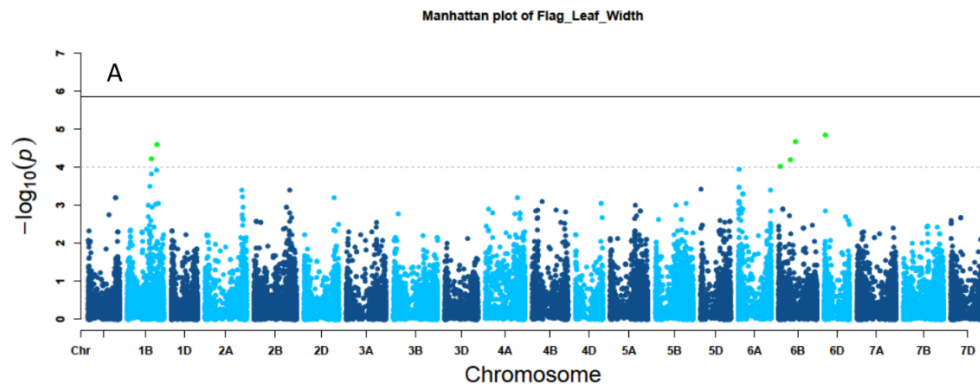
(A) Manhattan plot in 2016. (B) quantile-quantile (Q-Q) plots in 2016. (C) Manhattan plot in 2017. (D) Q-Q plot in 2017. The solid black line showed the expected value at Bonferroni correction at 5% level of significance [ $-\log_{10}(P) = 5.85$ ] and dotted black line showed the expected value with a uniform suggestive genome wide significance threshold [ $-\log_{10}(P) = 4.00$ ].



## Flag leaf length (FLLN)

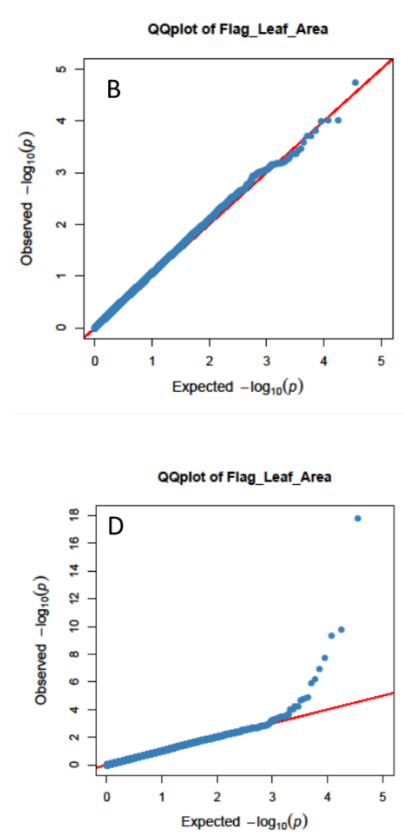
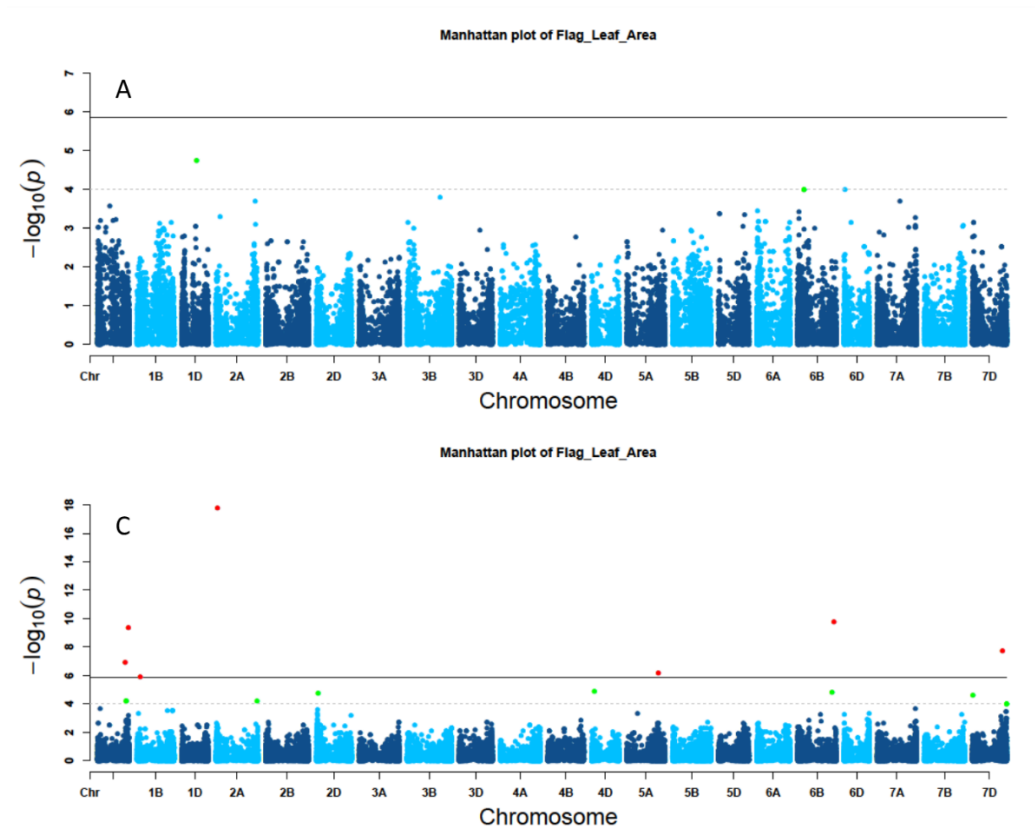
(A) Manhattan plot in 2016. (B) quantile-quantile (Q-Q) plots in 2016. (C) Manhattan plot in 2017. (D) Q-Q plot in 2017. The solid black line showed the expected value at Bonferroni correction at 5% level of significance [ $-\log_{10}(P) = 5.85$ ] and dotted black line showed the expected value with a uniform suggestive genome wide significance threshold [ $-\log_{10}(P) = 4.00$ ].





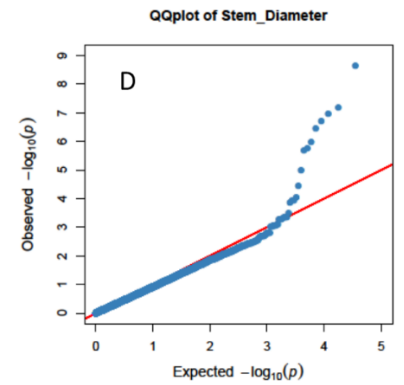
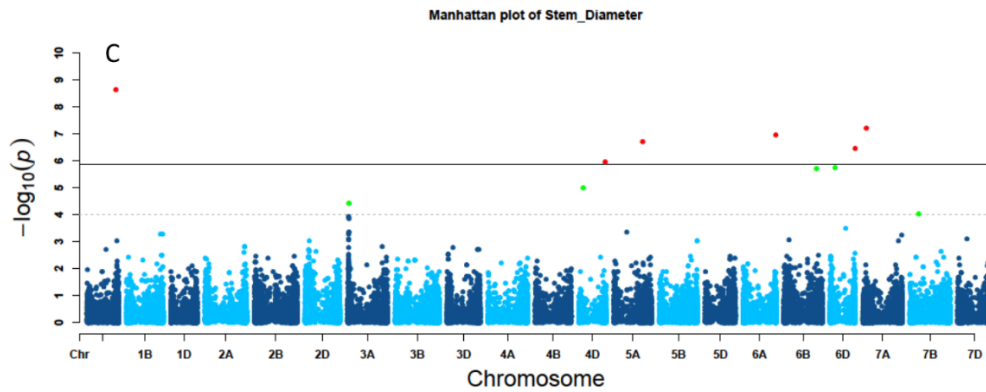
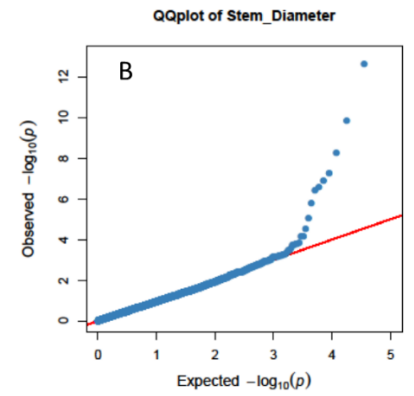
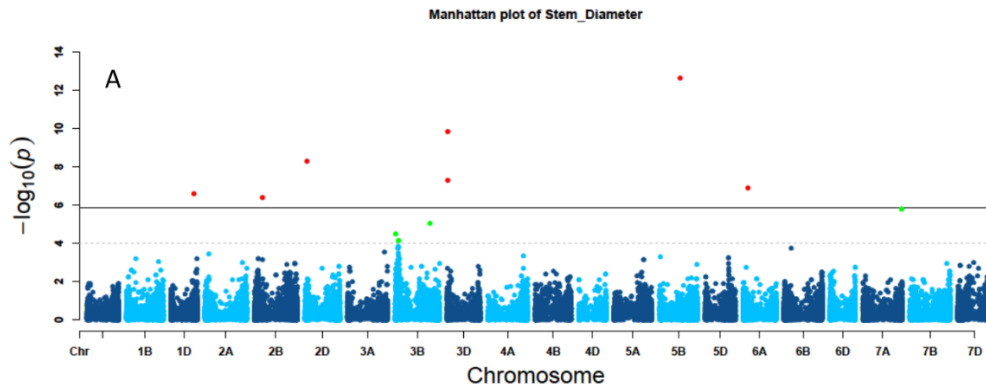
## Flag leaf width (FLW)

(A) Manhattan plot in 2016. (B) quantile-quantile (Q-Q) plots in 2016. (C) Manhattan plot in 2017. (D) Q-Q plot in 2017. The solid black line showed the expected value at Bonferroni correction at 5% level of significance [ $-\log_{10}(P) = 5.85$ ] and dotted black line showed the expected value with a uniform suggestive genome wide significance threshold [ $-\log_{10}(P) = 4.00$ ].



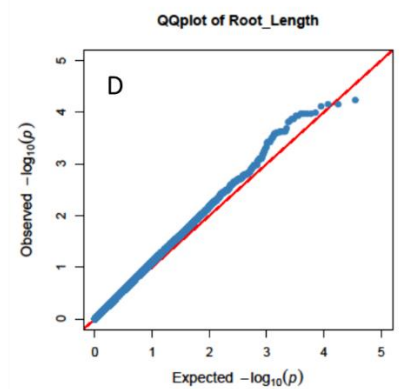
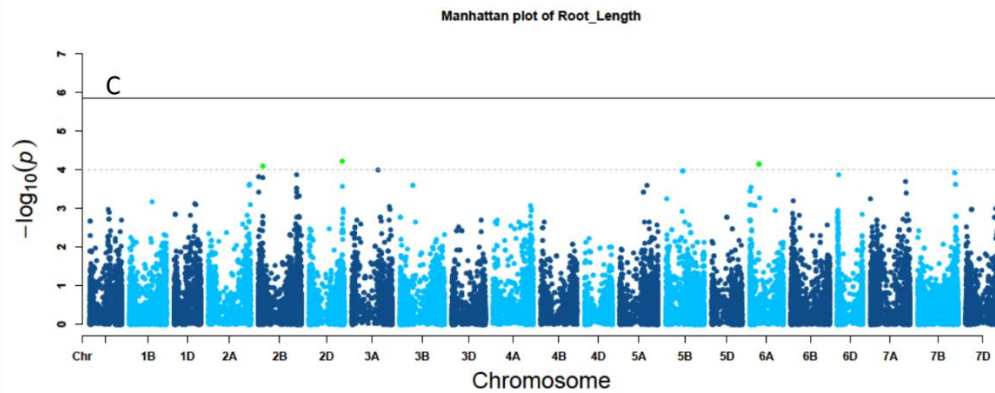
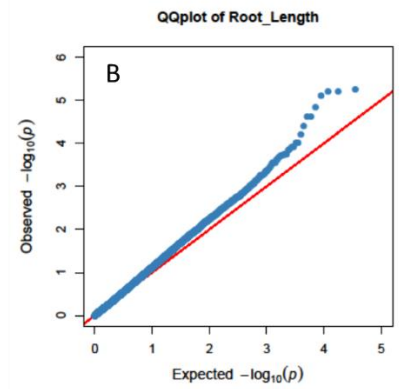
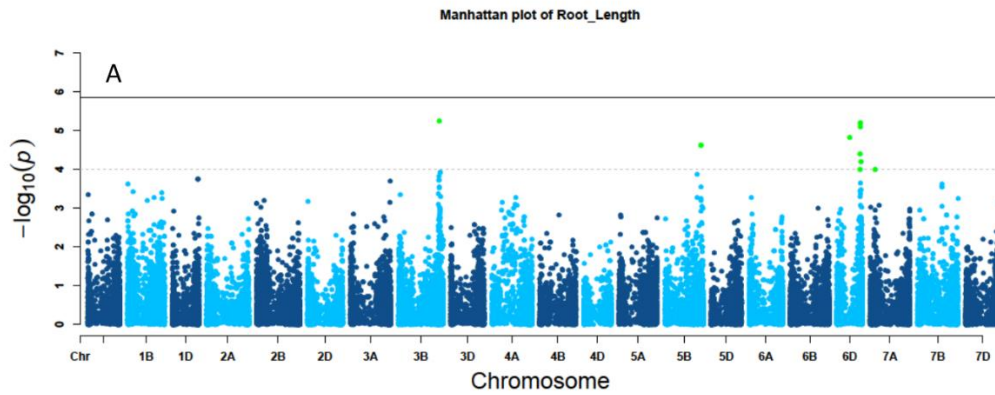
### Flag leaf area (FLA)

(A) Manhattan plot in 2016. (B) quantile-quantile (Q-Q) plots in 2016. (C) Manhattan plot in 2017. (D) Q-Q plot in 2017. The solid black line showed the expected value at Bonferroni correction at 5% level of significance [ $-\log_{10}(P) = 5.85$ ] and dotted black line showed the expected value with a uniform suggestive genome wide significance threshold [ $-\log_{10}(P) = 4.00$ ].



### Stem diameter (STMDIA)

(A) Manhattan plot in 2016. (B) quantile-quantile (Q-Q) plots in 2016. (C) Manhattan plot in 2017. (D) Q-Q plot in 2017. The solid black line showed the expected value at Bonferroni correction at 5% level of significance [ $-\log_{10}(P) = 5.85$ ] and dotted black line showed the expected value with a uniform suggestive genome wide significance threshold [ $-\log_{10}(P) = 4.00$ ].



## Root length (RTLN)

(A) Manhattan plot in 2016. (B) quantile-quantile (Q-Q) plots in 2016. (C) Manhattan plot in 2017. (D) Q-Q plot in 2017. The solid black line showed the expected value at Bonferroni correction at 5% level of significance [ $-\log_{10}(P) = 5.85$ ] and dotted black line showed the expected value with a uniform suggestive genome wide significance threshold [ $-\log_{10}(P) = 4.00$ ].