

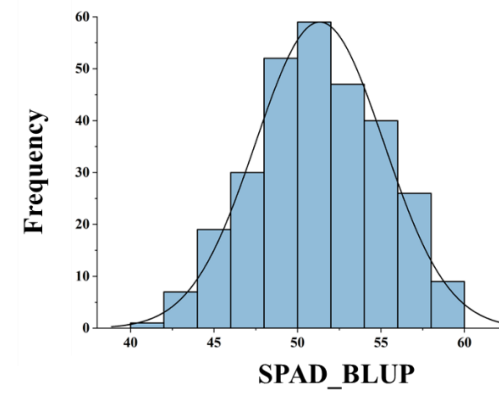
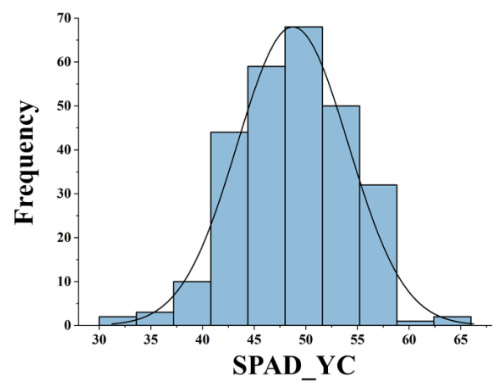
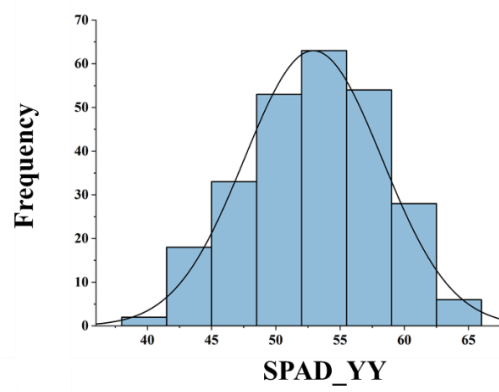
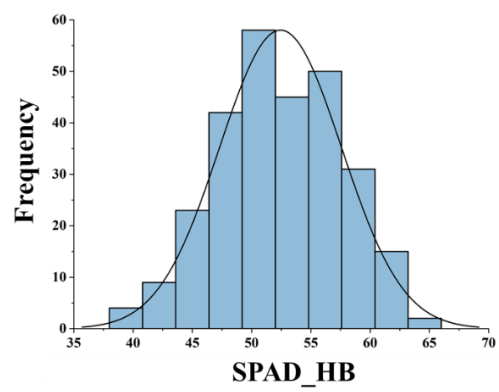


Figure S1. Normal distribution of CC (SPAD value) in different environments.

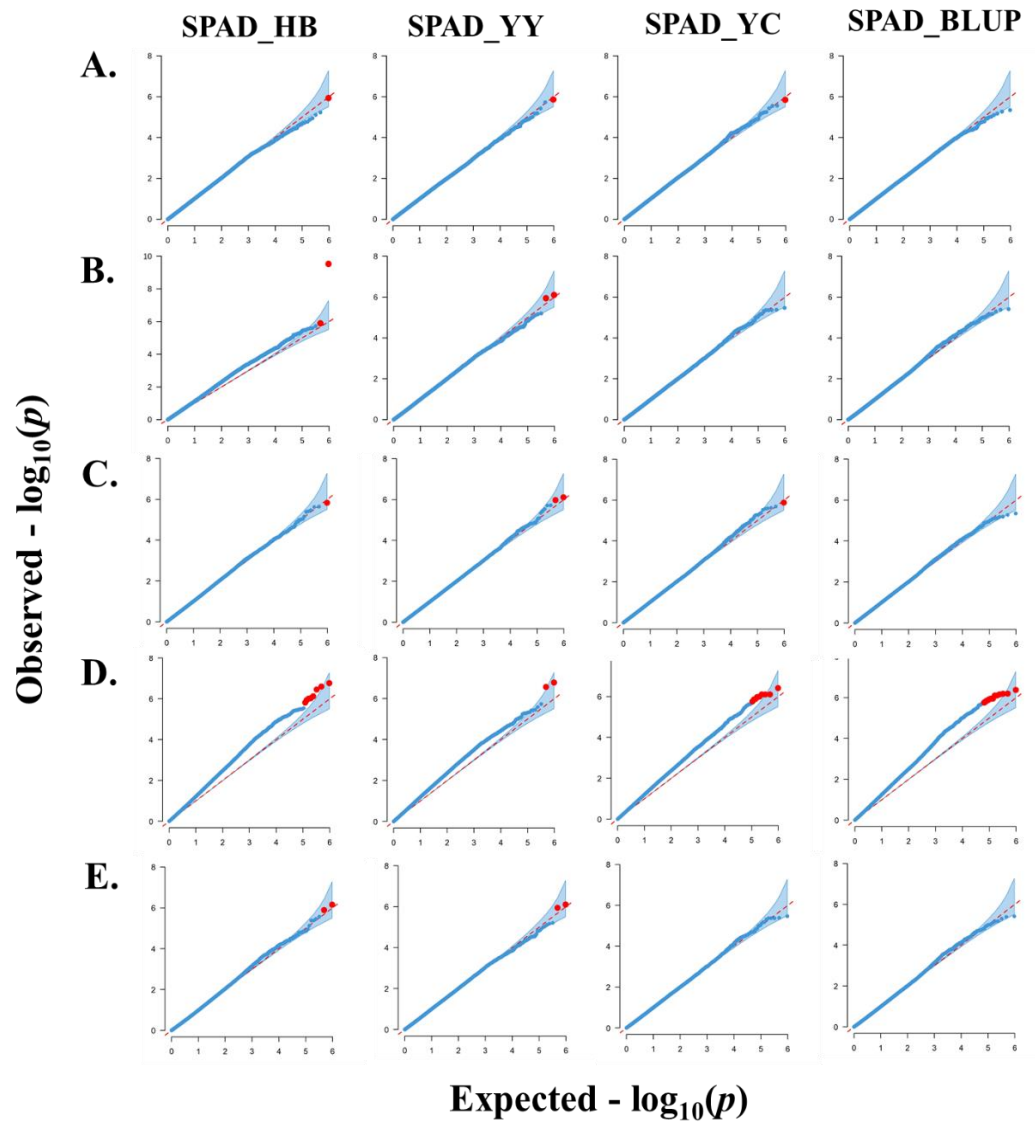


Figure S2. QQ plots of the chlorophyll content (CC) for five models in different environments. (A-E) represent the five models of MLM, BLINK, MLMM, SUPER, and FarmCPU, respectively.

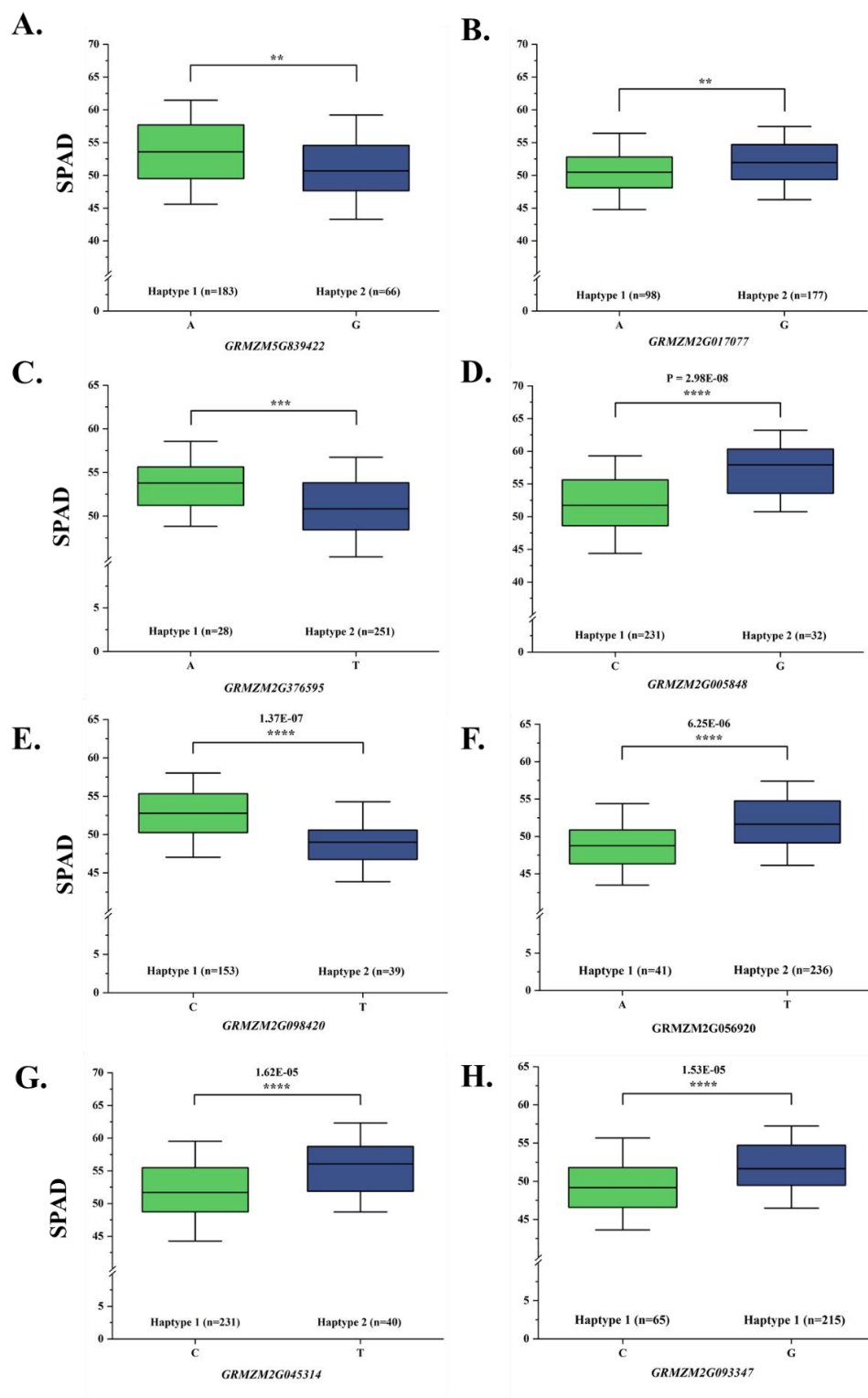


Figure S3. Differences in the chlorophyll content (CC) associated with key candidate genes. (A) *GRMZM5G839422*. (B) *GRMZM2G017077*. (C) *GRMZM2G376595*. (D) *GRMZM2G005848*. (E) *GRMZM2G098420*. (F) *GRMZM2G056920*. (G) *GRMZM2G045314*. (H) *GRMZM2G093347*. *: $p < 0.05$, **: $p < 0.01$, ***: $p < 0.001$, ****: $p < 0.0001$. Whisker range: standard deviation (SD), the coefficient is 1.5 to set the parameters of the box plot.

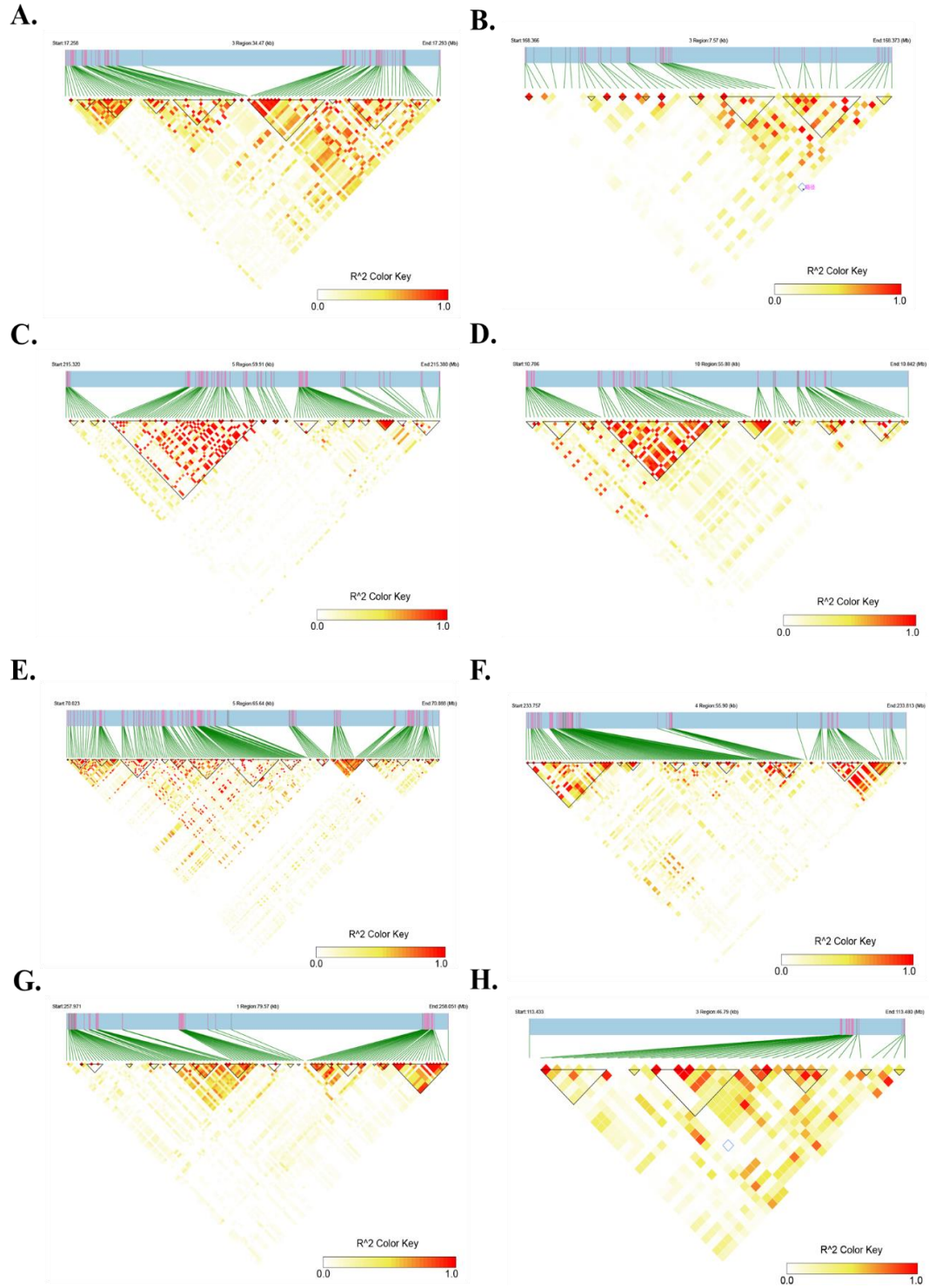
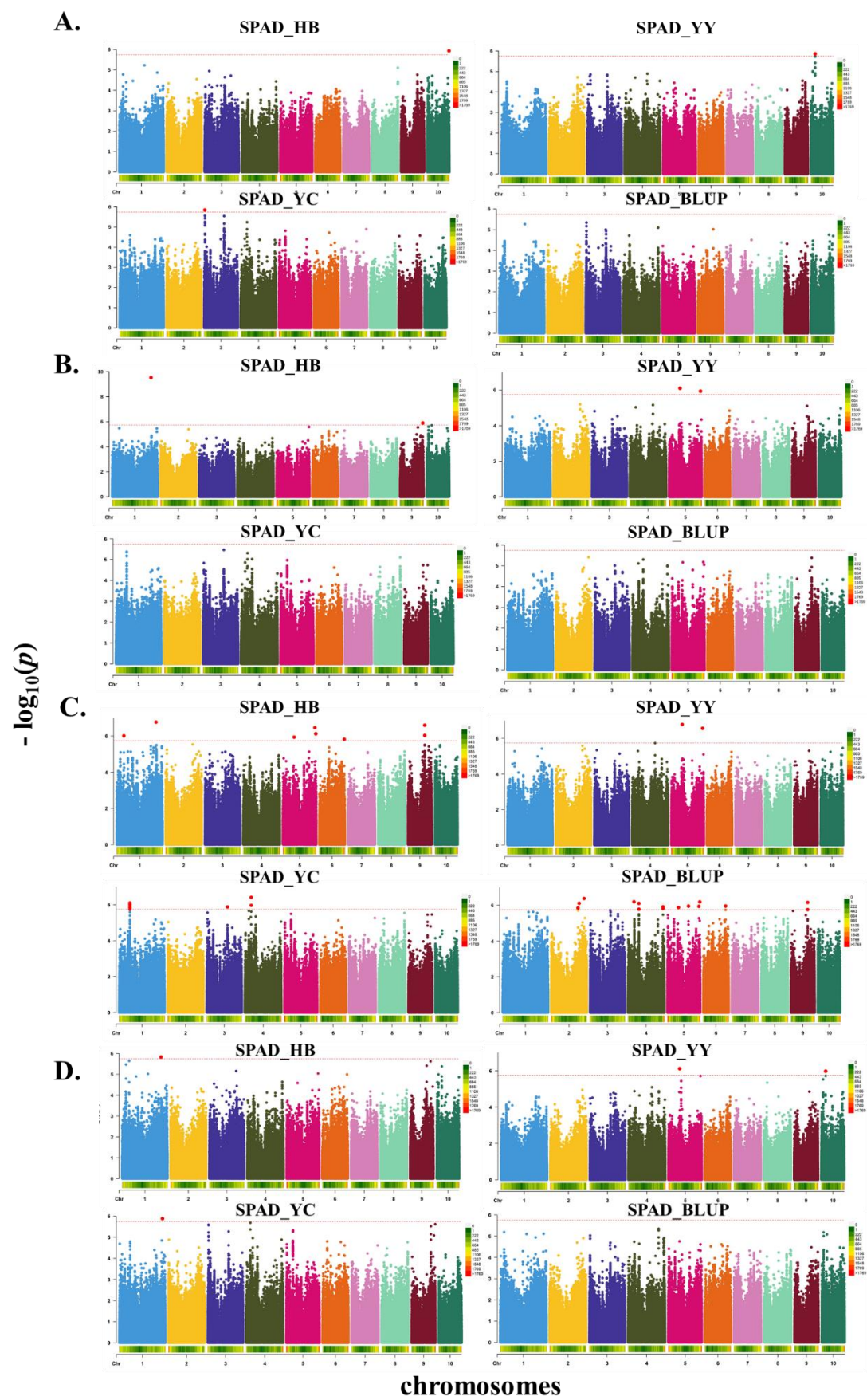


Figure S4. R^2 values for all SNPs in the QTL of the significant QTN. (A) *GRMZM5G839422*. (B) *GRMZM2G017077*. (C) *GRMZM2G376595*. (D) *GRMZM2G005848*. (E) *GRMZM2G098420*. (F) *GRMZM2G056920*. (G) *GRMZM2G045314*. (H) *GRMZM2G093347*.



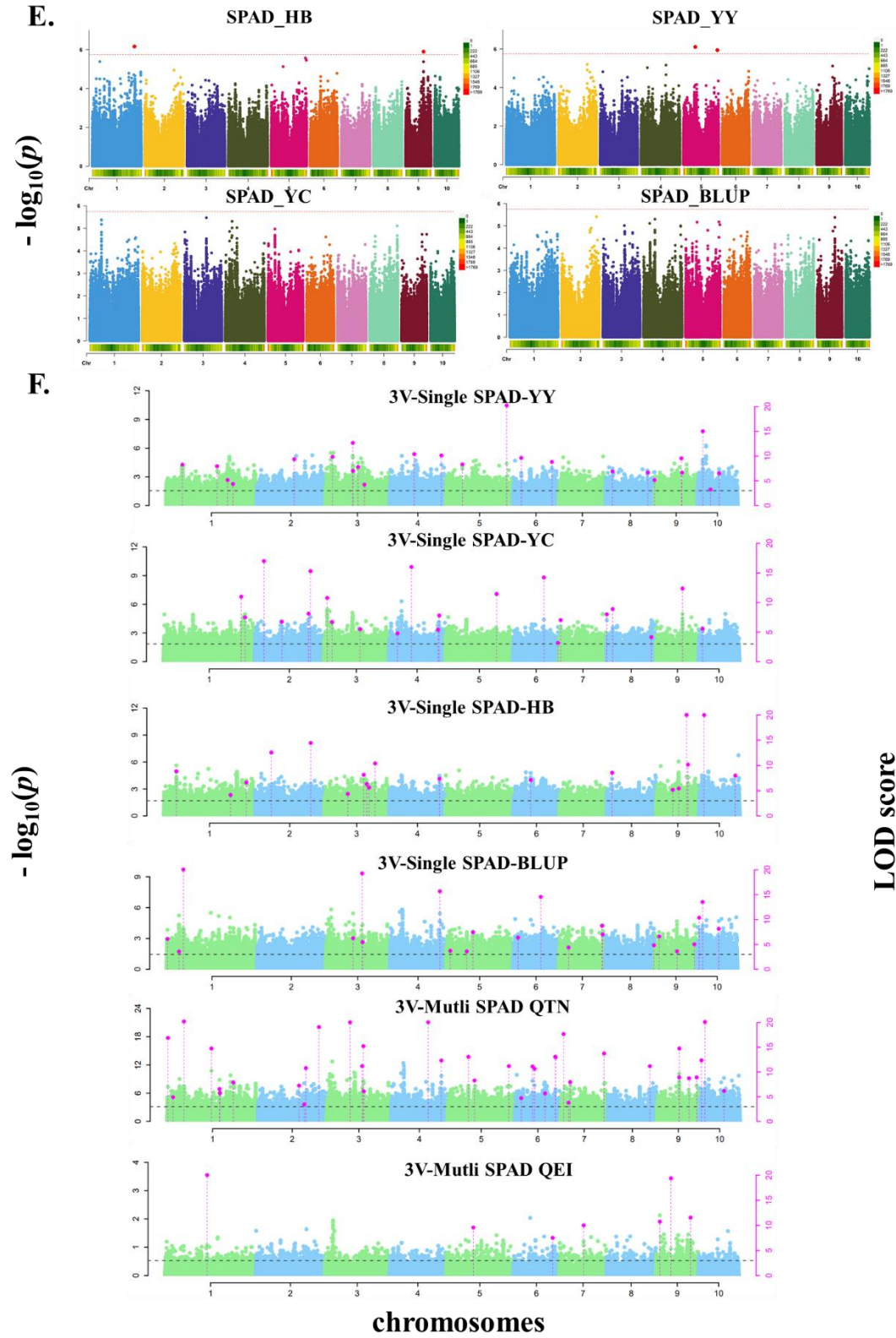


Figure S5. Manhattan plots of the CC for six models in different environments or involving different methods. (A-F) represent the six models of MLM, BLINK, SUPER, MLMM, FarmCPU and 3VmrMLM, respectively.