

**Figure S1 Pearson correlation among the branch angles.** The lower panel displays a bivariate scatter plot with the best fitting lines. Pearson correlation coefficients between the traits are presented on the upper panel. \*, \*\*, and \*\*\* represent significant at 0.05, 0.01, and 0.001, respectively. Histograms are also showed on the middle of panel. BBA: basal branch angle; MBA: middle branch angle; TBA: top branch angle; BAI: branch angle index

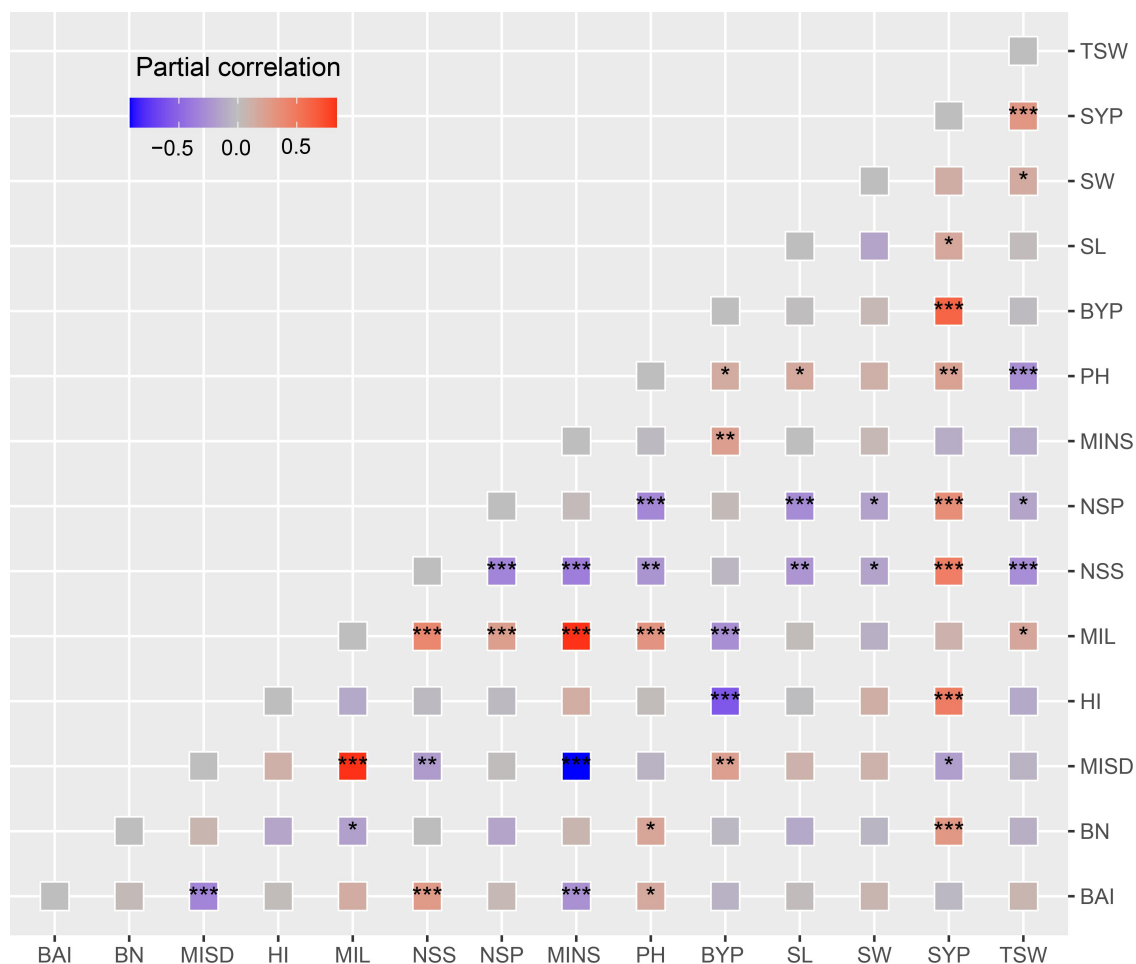
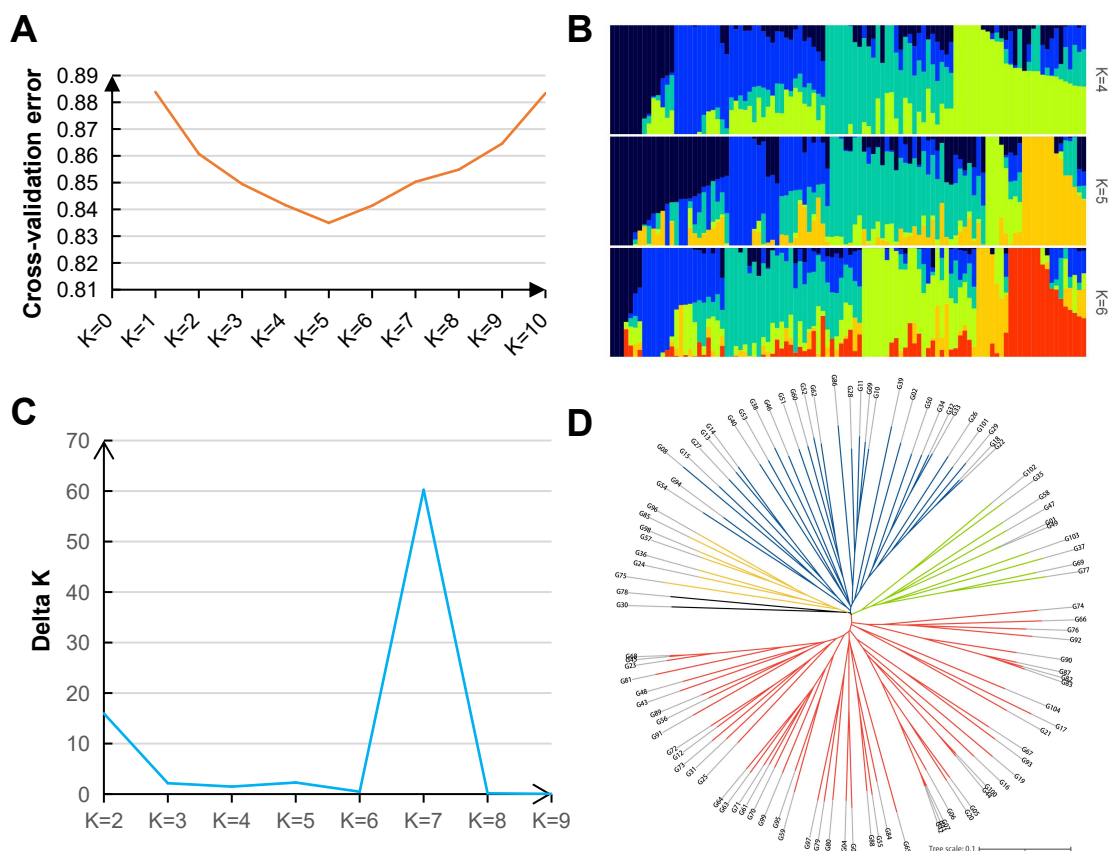
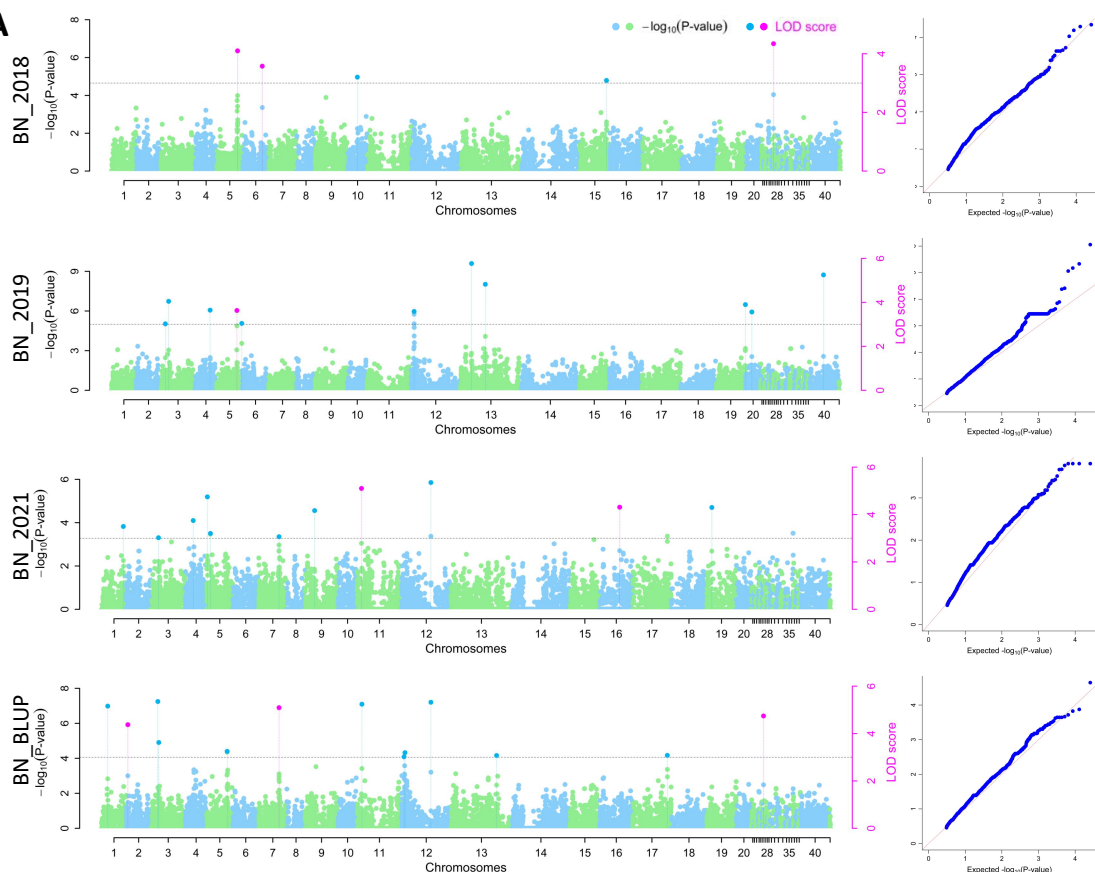
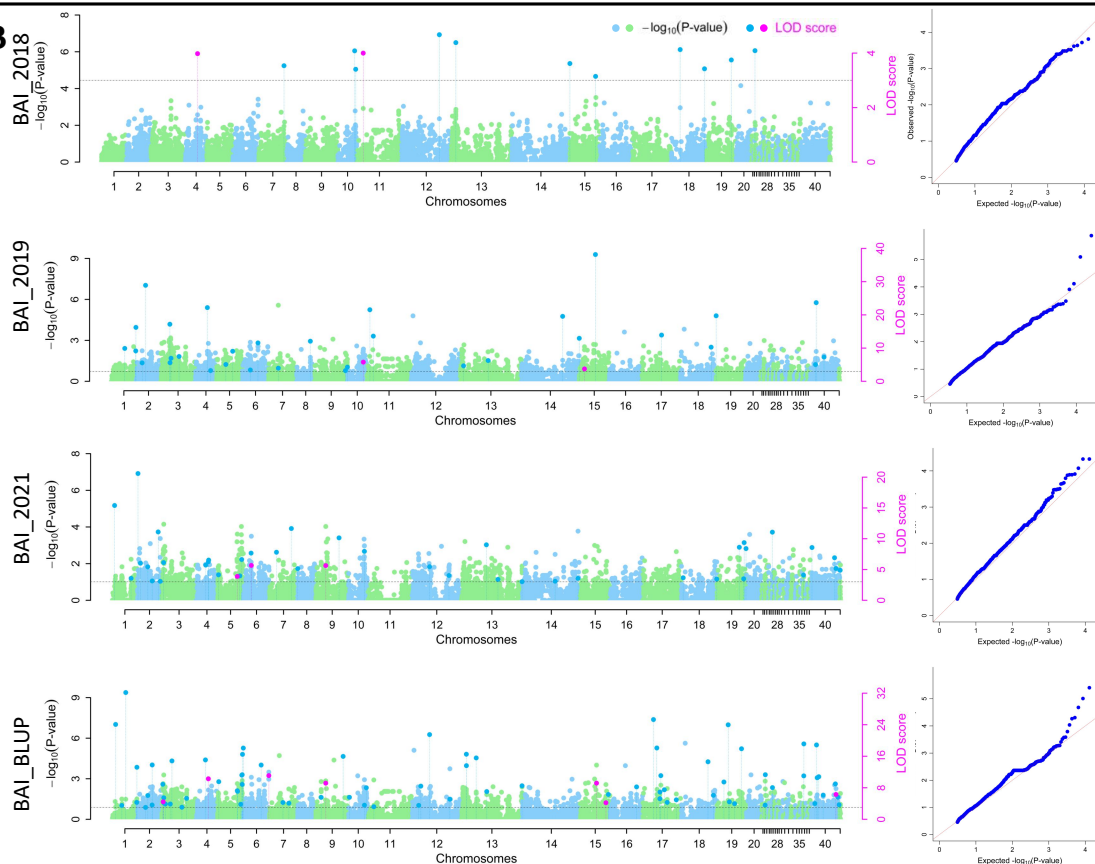


Figure S2 Partial correlation among the agronomic traits. Red and blue indicate positive and negative correlation, respectively. \*, \*\*, and \*\*\* represent significant at 0.05, 0.01, and 0.001, respectively. BAI, branch angle index; BN, numbers of primary valid branch; BYP, biomass yield per plant; HI, harvest index; MIL, main inflorescence length; MINS, number of effective siliques on main inflorescence; MISD, silique density of the main inflorescence; NSP, number of siliques per plant; NSS, number of seeds per silique; PH, plant height; SL, silique length; SW, silique width; SYP, seed yield per plant; TSW, thousand-seed weight.

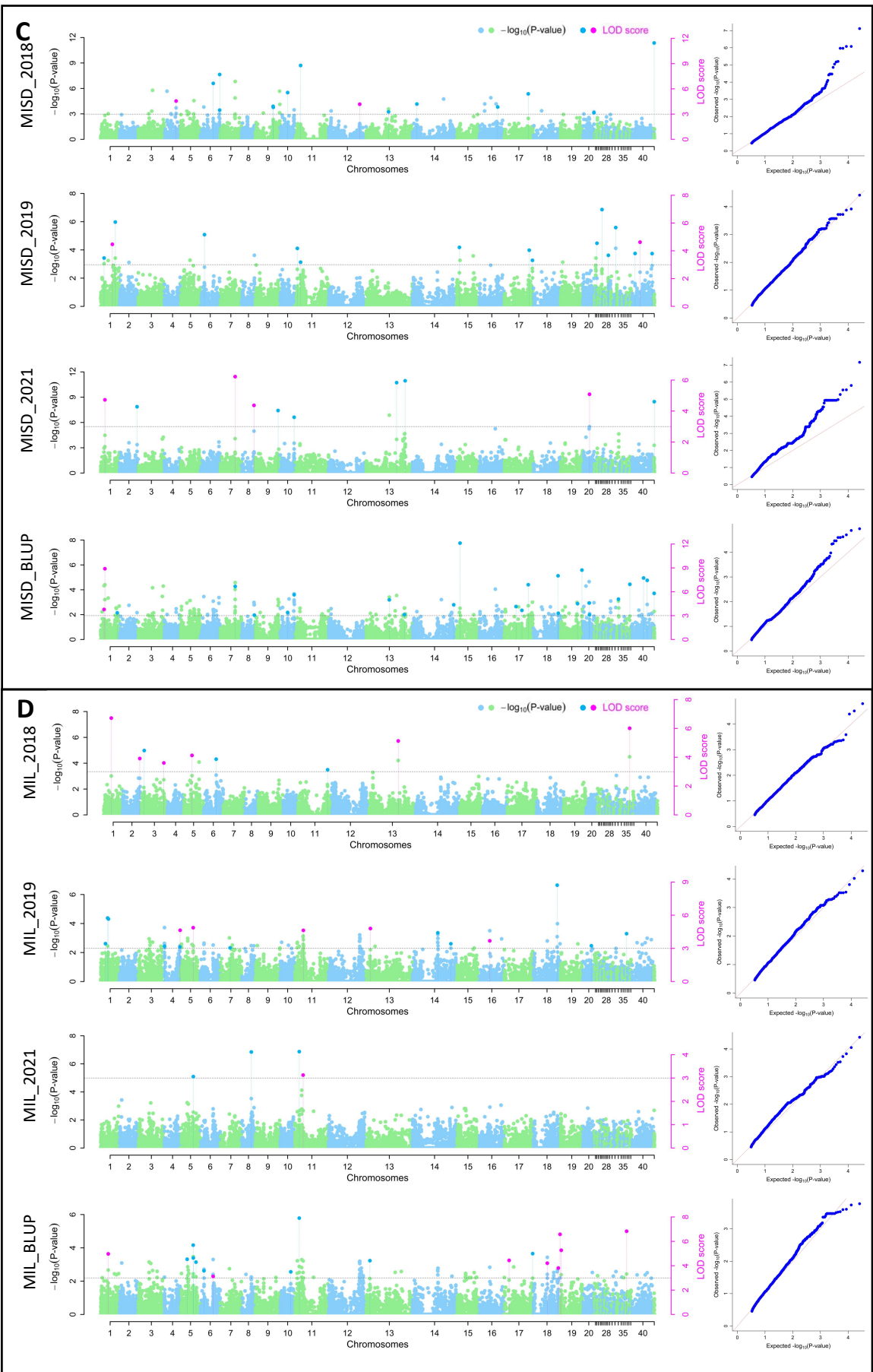


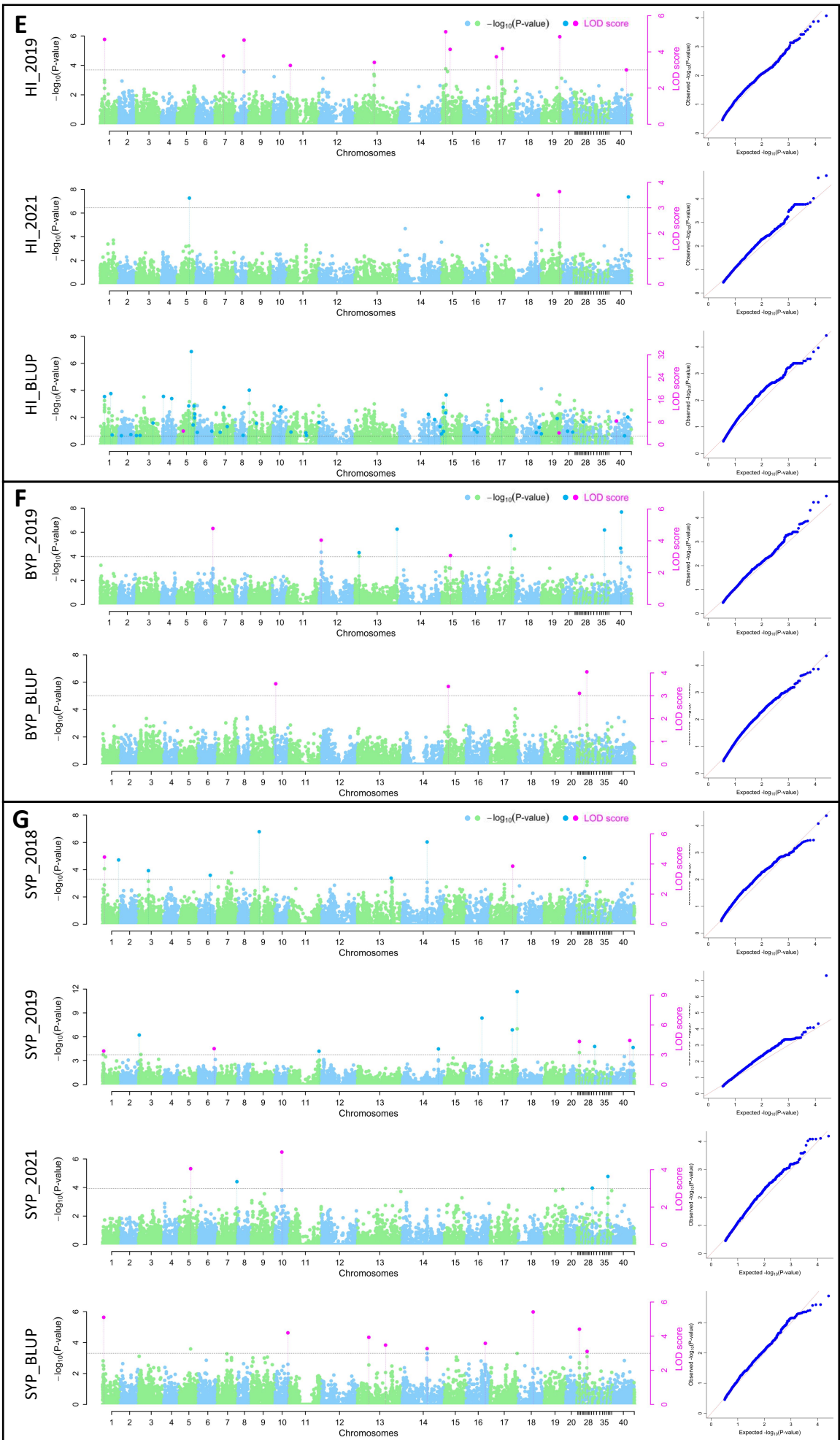
**Figure S3 Population structure variation and phylogeny tree in rapeseed.**

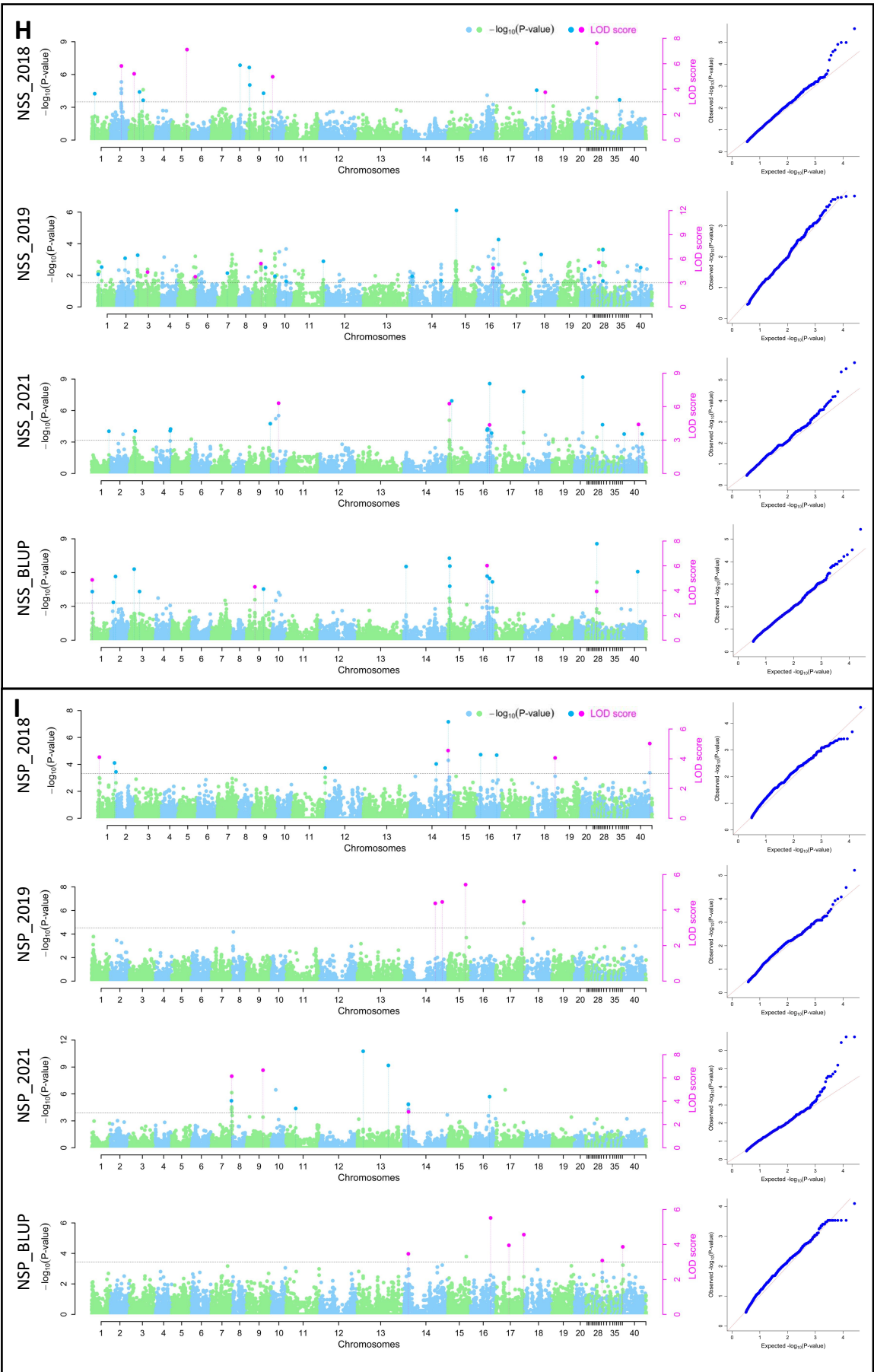
(A) The change of cross-validation error detected by ADMIXTURE from K=1 to 10. When K = 5, the cross-validation error is the lowest. (B) Population structure of 104 rapeseed lines detected by ADMIXTURE. (C) Population structure determined by STRUCTURE. The 104 rapeseed lines could be assigned to 7 groups. (D) Phylogenetic tree of 104 inbred lines. Different colors indicate different groups.

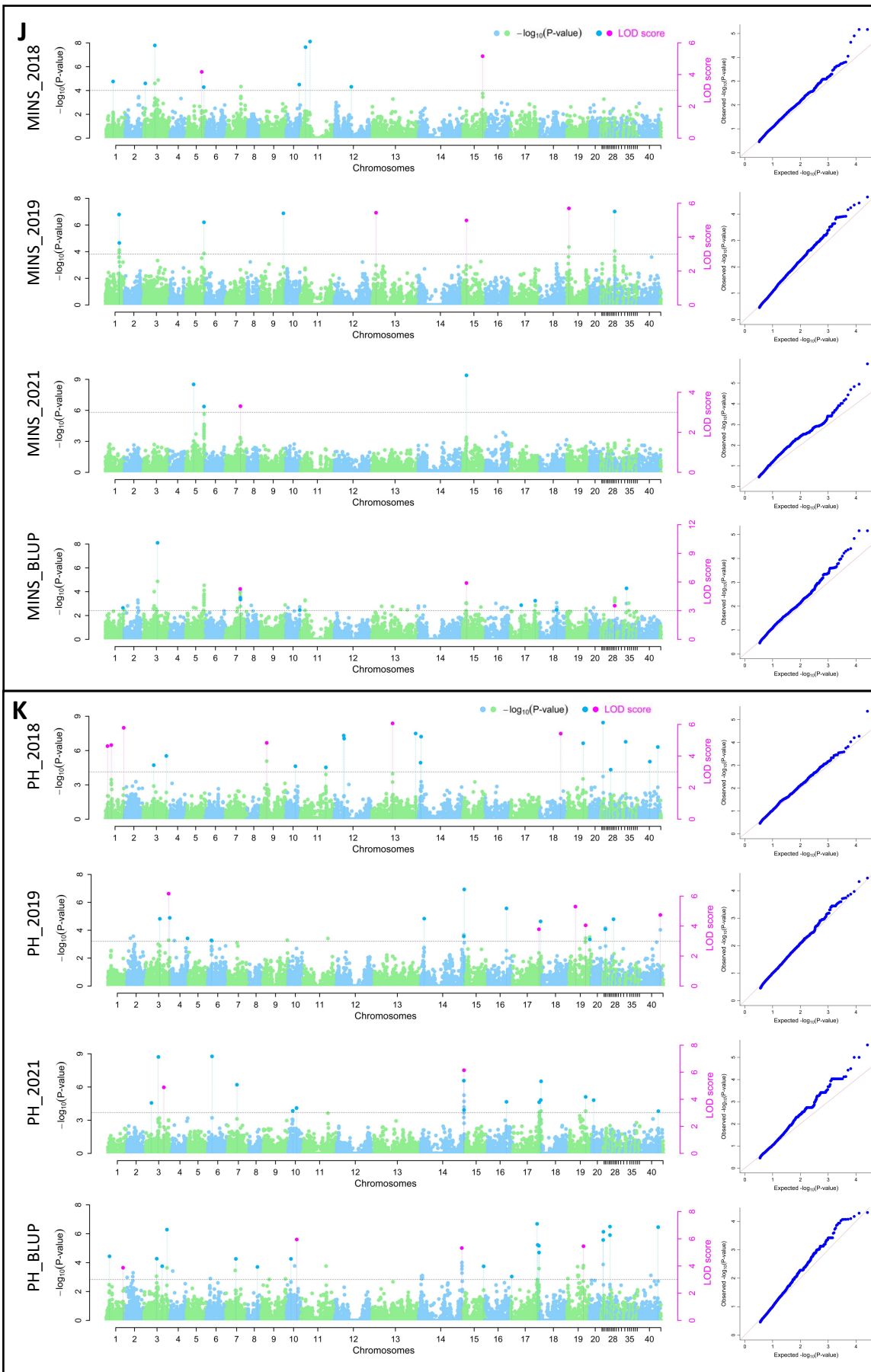
**A****B**



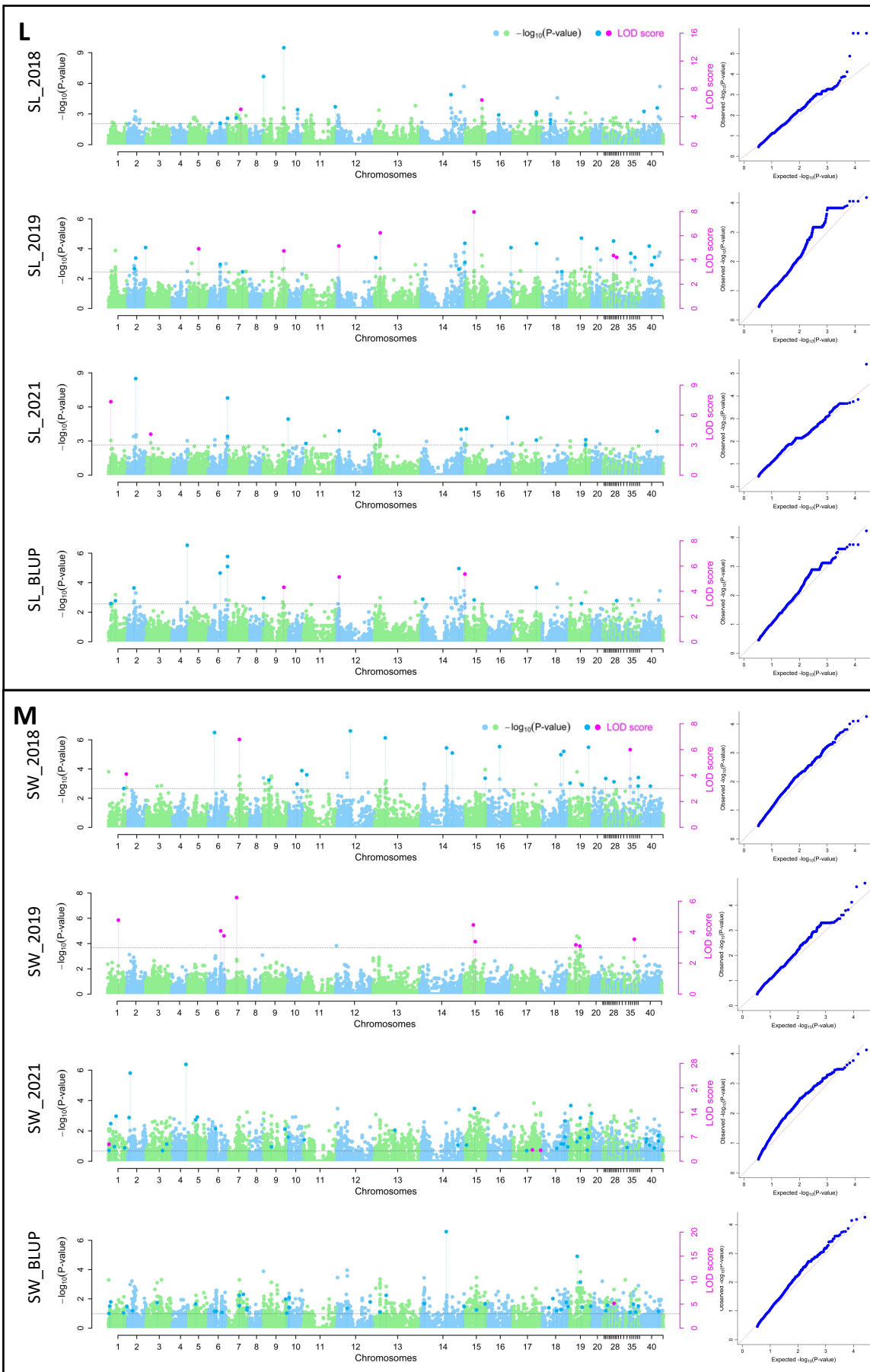


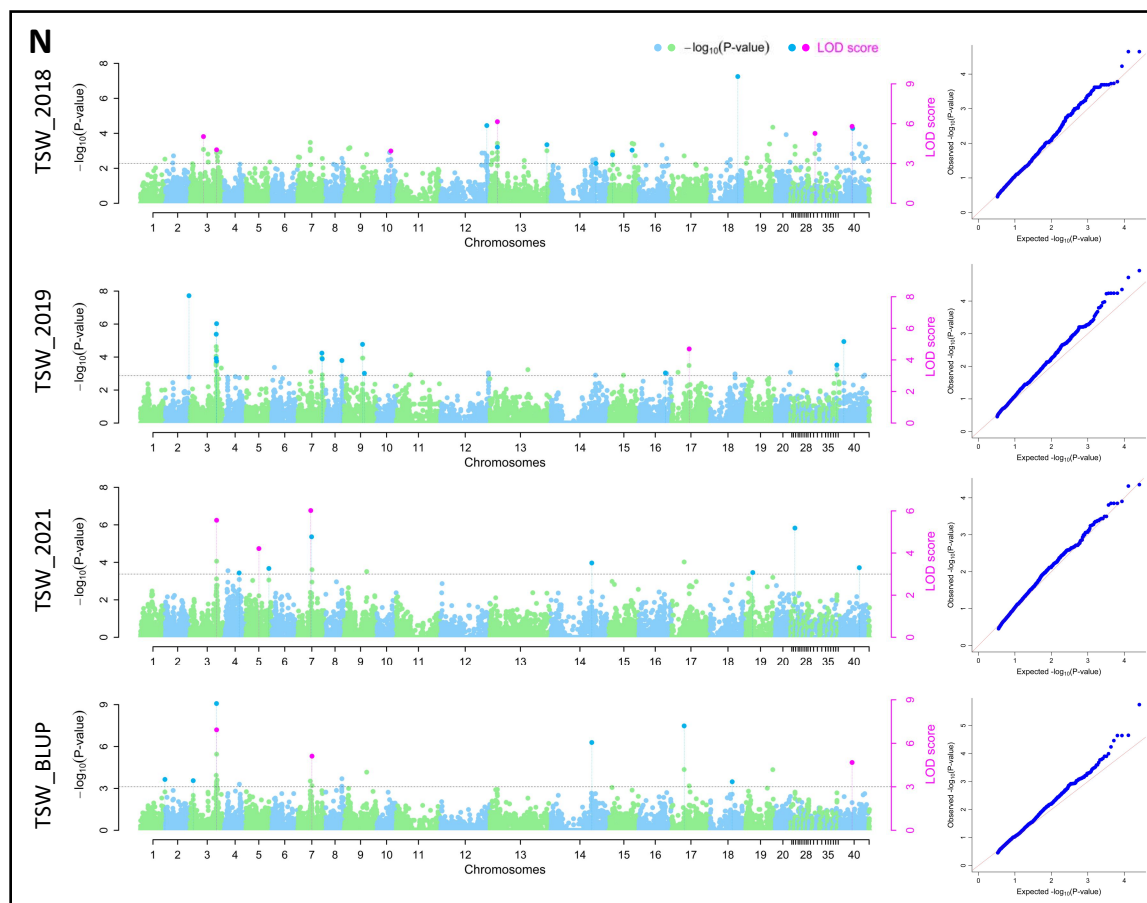






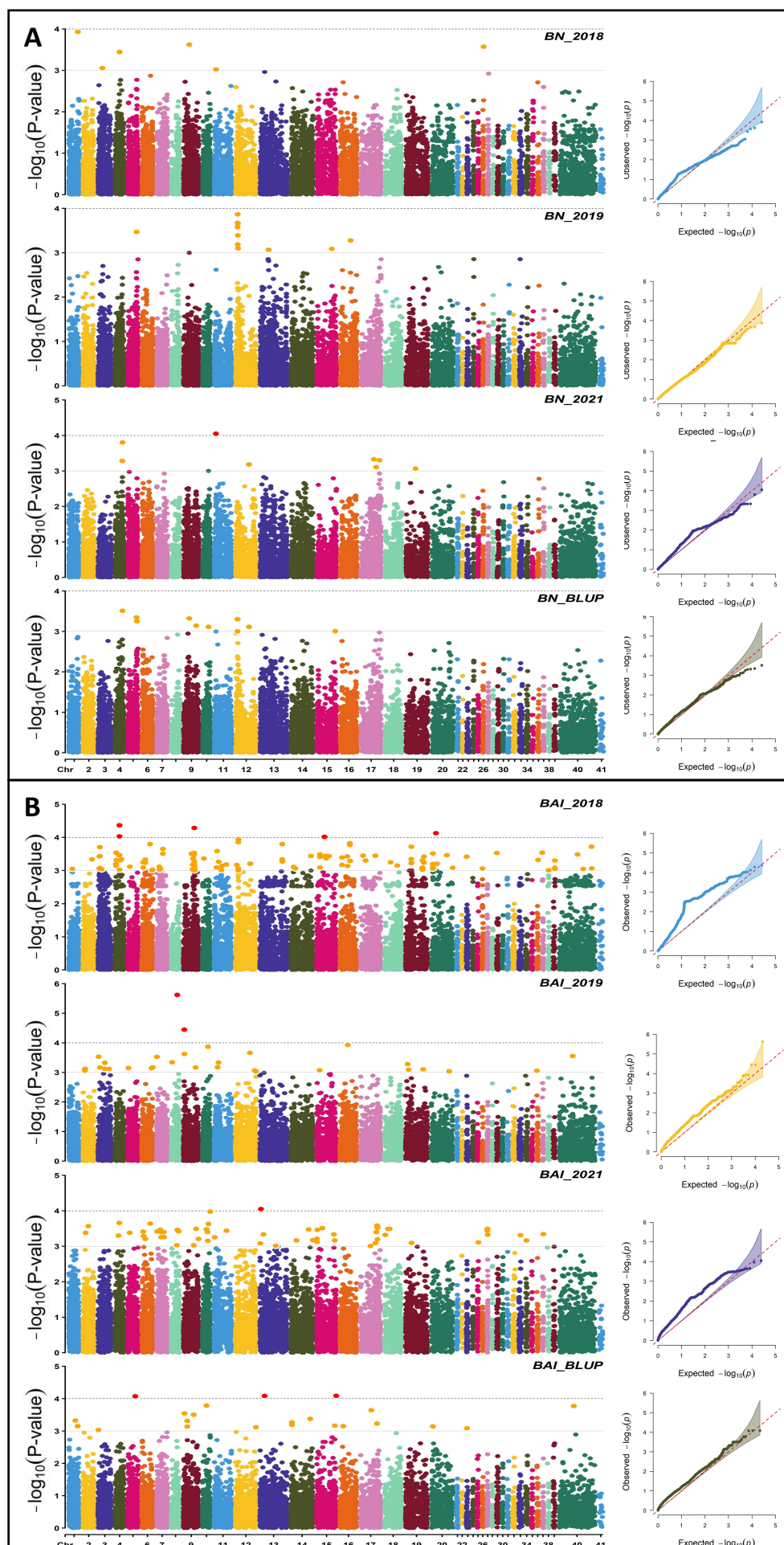


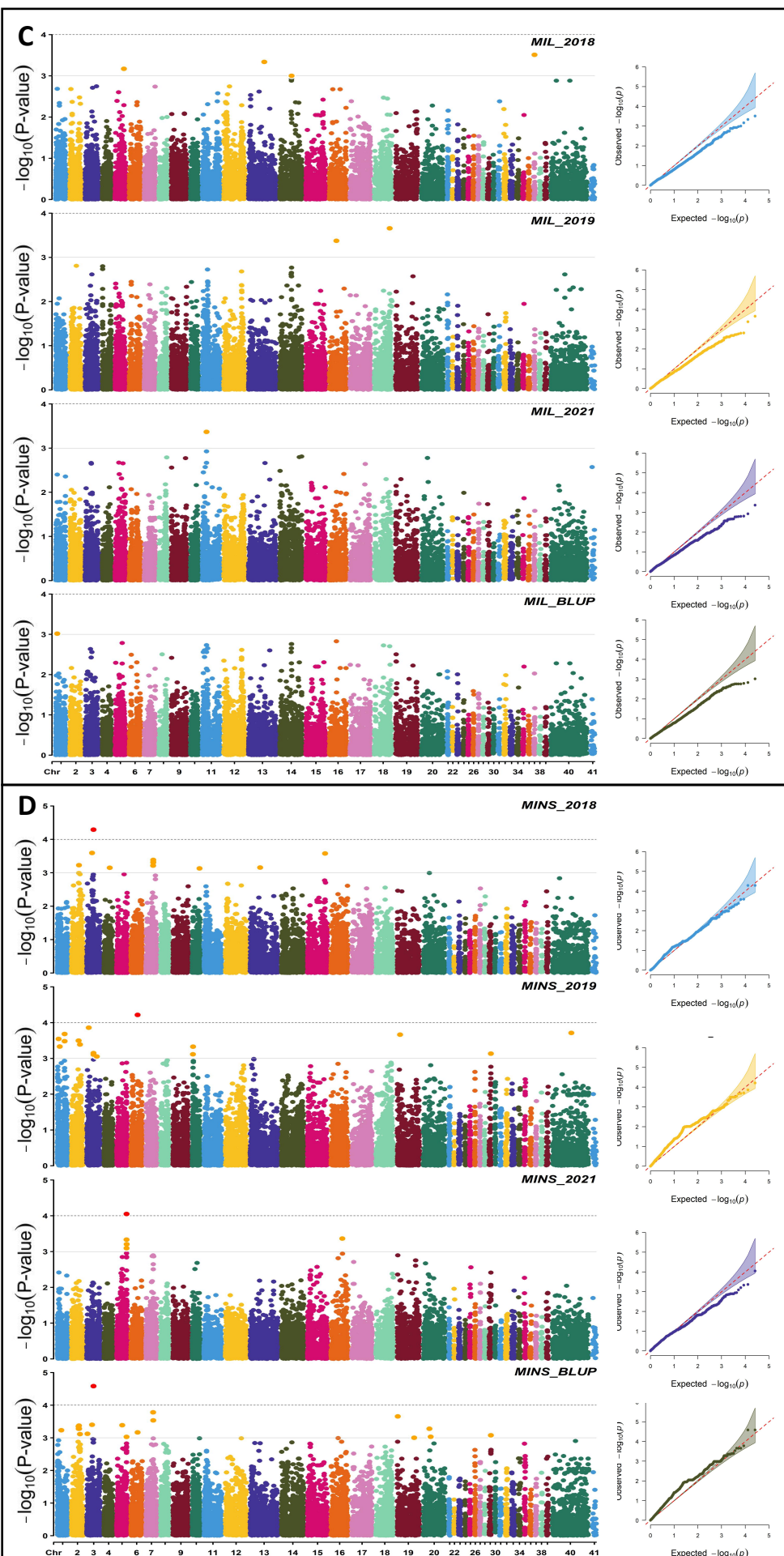


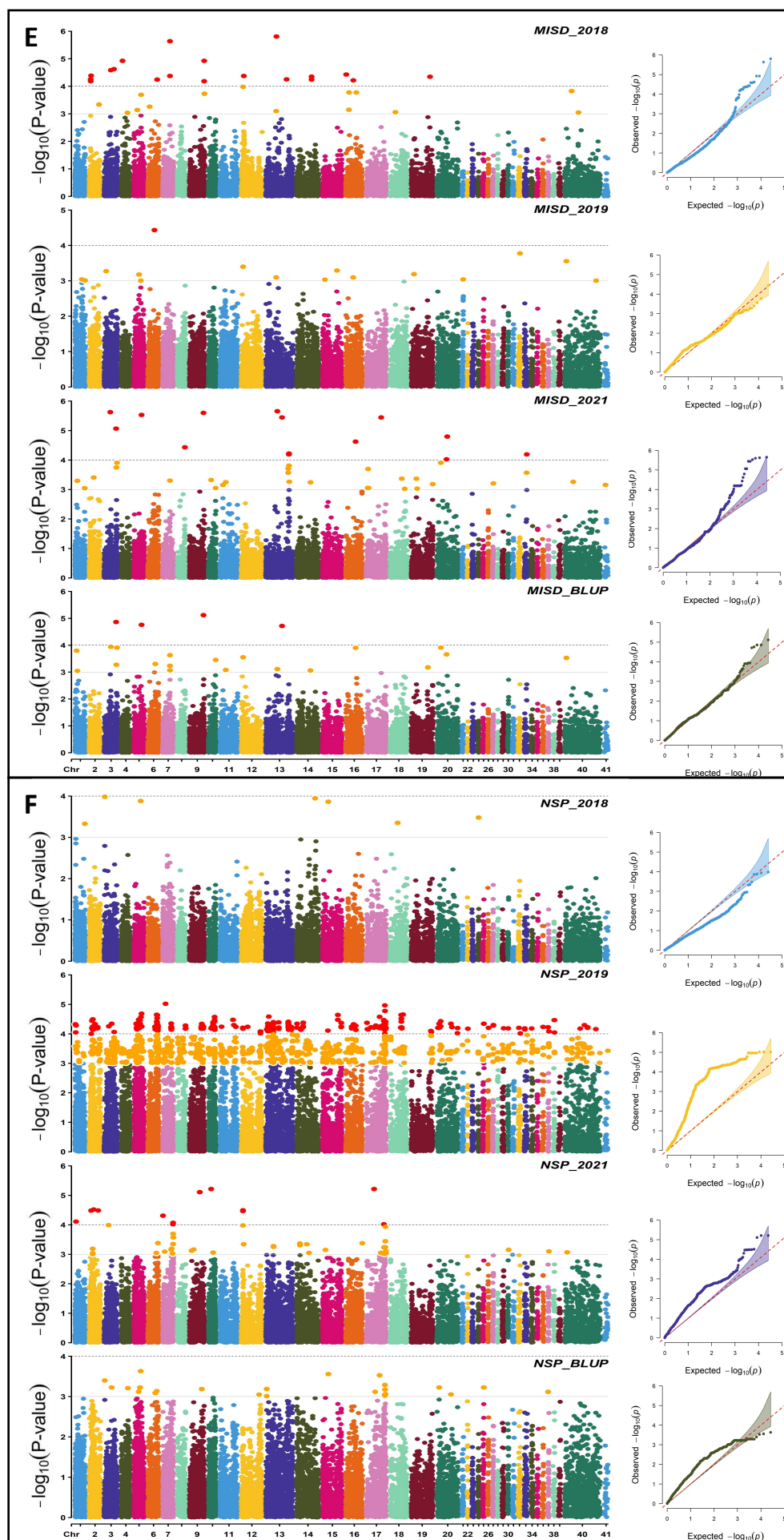


**Figure S4** Manhattan plots and quantile-quantile plots of estimated  $-\log_{10}(P\text{-value})$  for the test traits using mrMLM. Chromosome numbers from 1-41 are ranked as the order A01-10, C01-09, Ann\_random, A01\_random-A10\_random, C01\_random-C09\_random, Cnn\_random, and Unn\_random, respectively. The pink dot represents the locus detected by different algorithms, and blue dot is detected by only one algorithm.

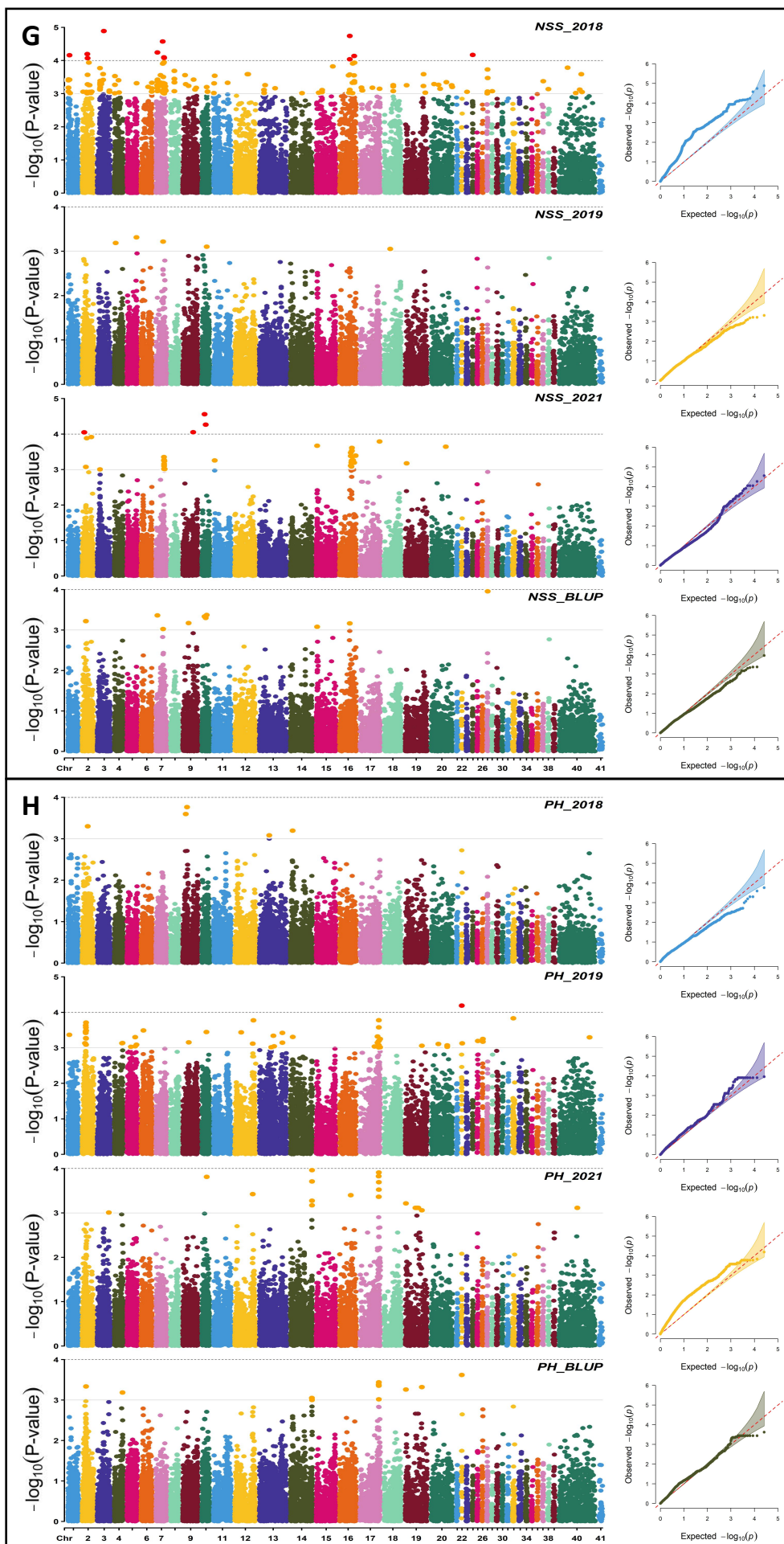


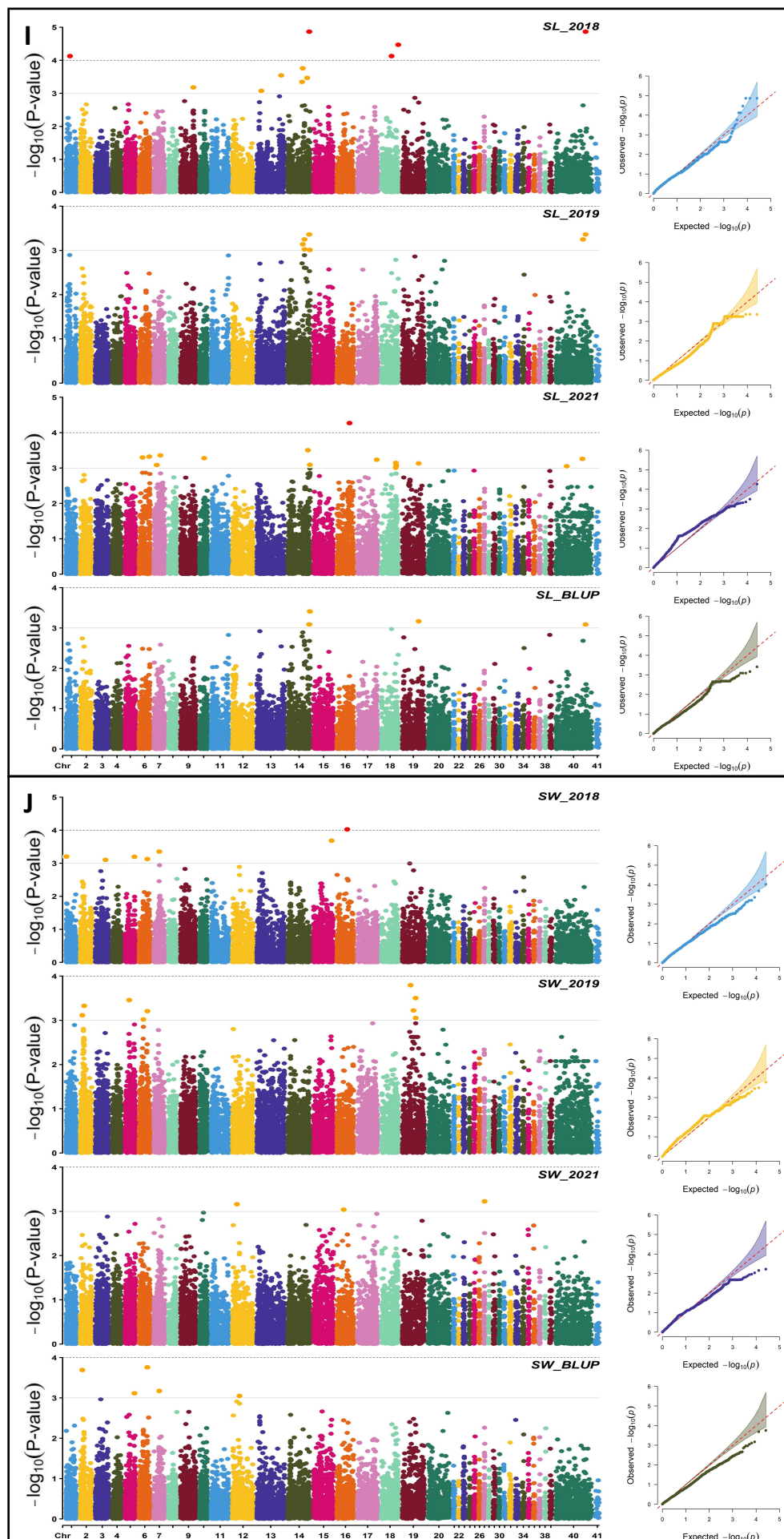




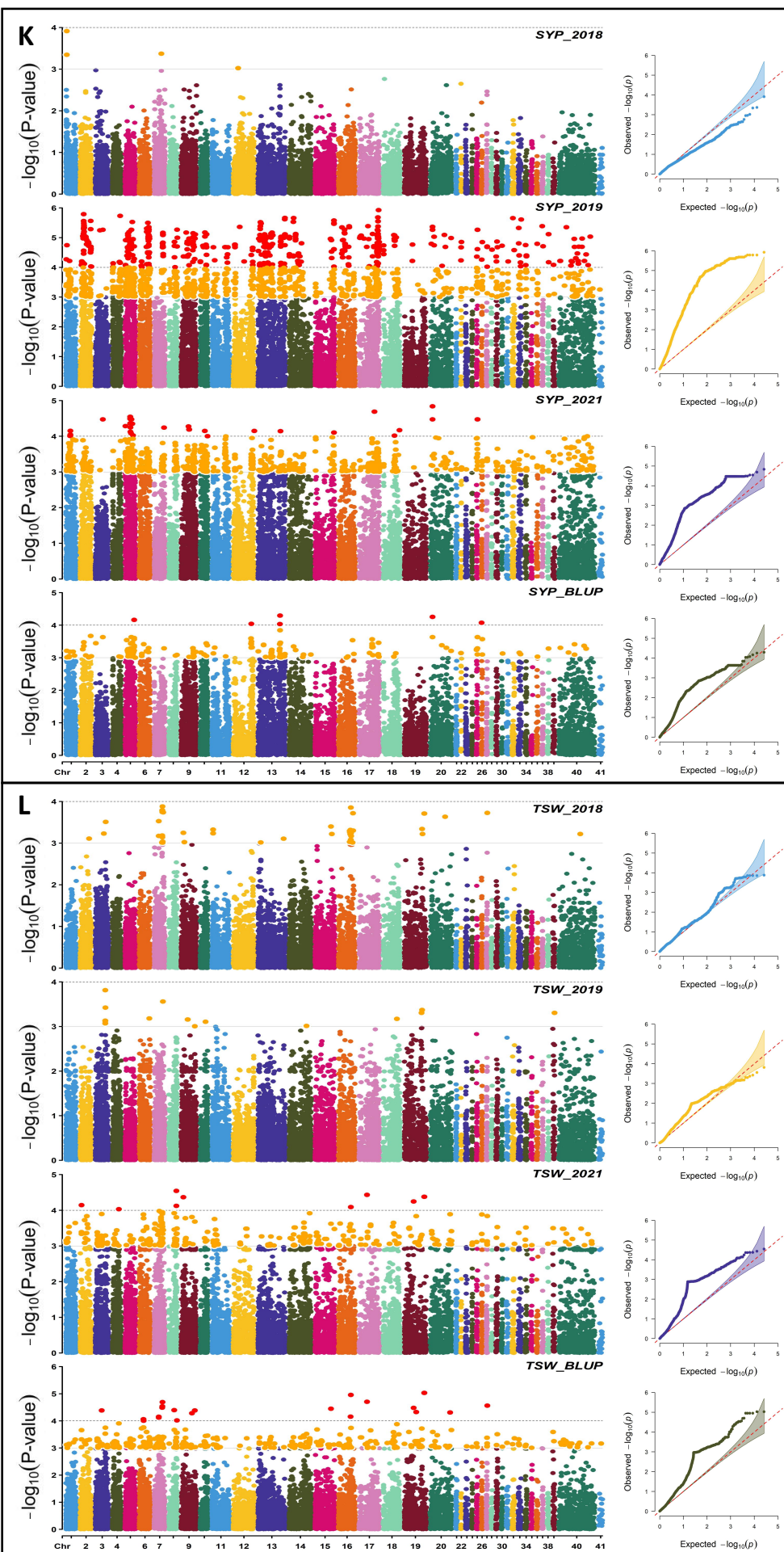




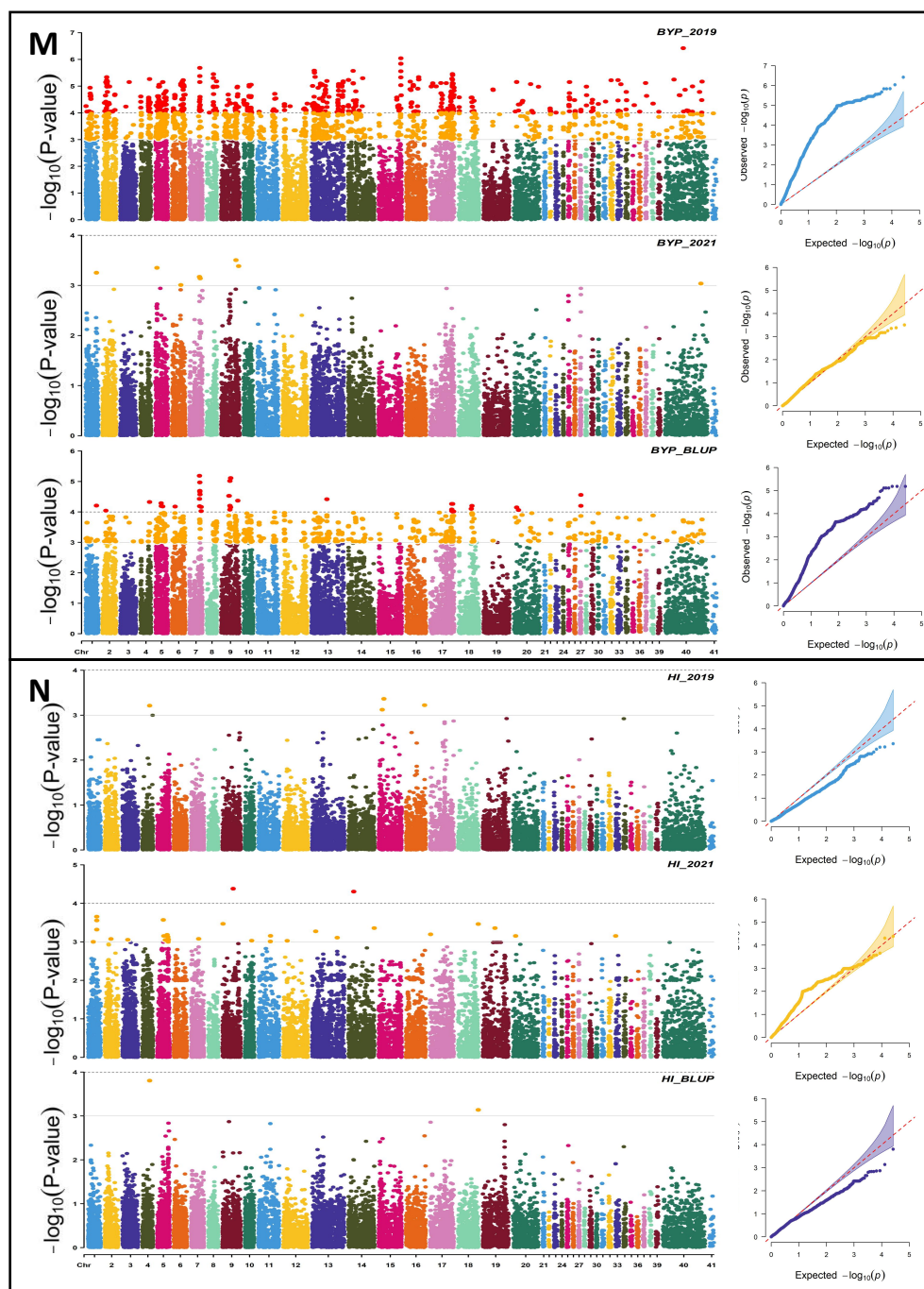












**Figure S5 Manhattan plots and quantile-quantile plots of estimated  $-\log_{10}(\text{p-value})$  for the test traits using TASSEL 5.0.**

