

Figure S1. Scatter plots and LD decay against physical distance among co-chromosomes.

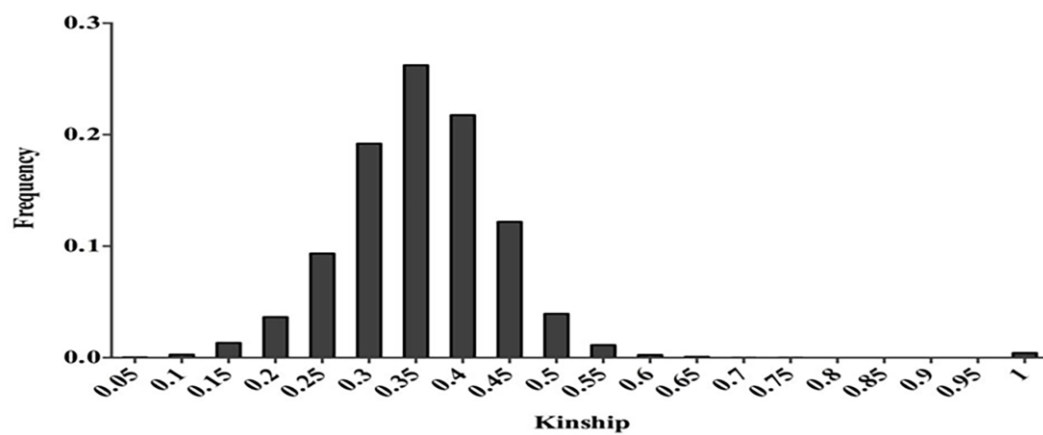


Figure S2. Distributions of pairwise relative kinship estimates between mini core collections.

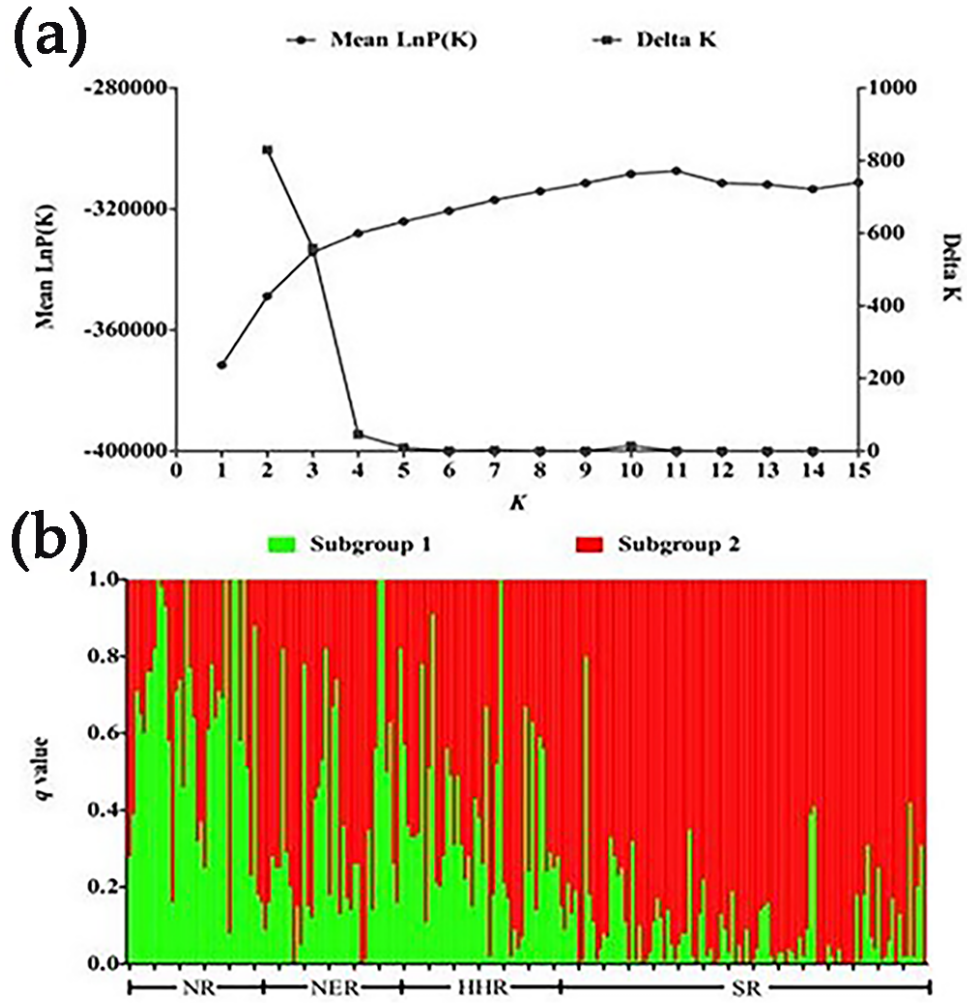


Figure S3. Population structure of soybean mini core collection.

Note: Figure (a) shows the LnP(D) and Delta K value when K from 1 to 15. Figure (b) shows the q value of 224 germplasm belonged to two subgroups. The subgroup 1 shows in green and subgroup 2 shows in red. The digits on the horizontal coordinate represent the geographical origin of soybean, and the vertical coordinate of each subgroup indicates the q value for each individual. NR: the northern soybean ecological region; NER: the northeast soybean ecological region; HHR: the Huanghuai region; SR: the southern soybean ecoregion [25].

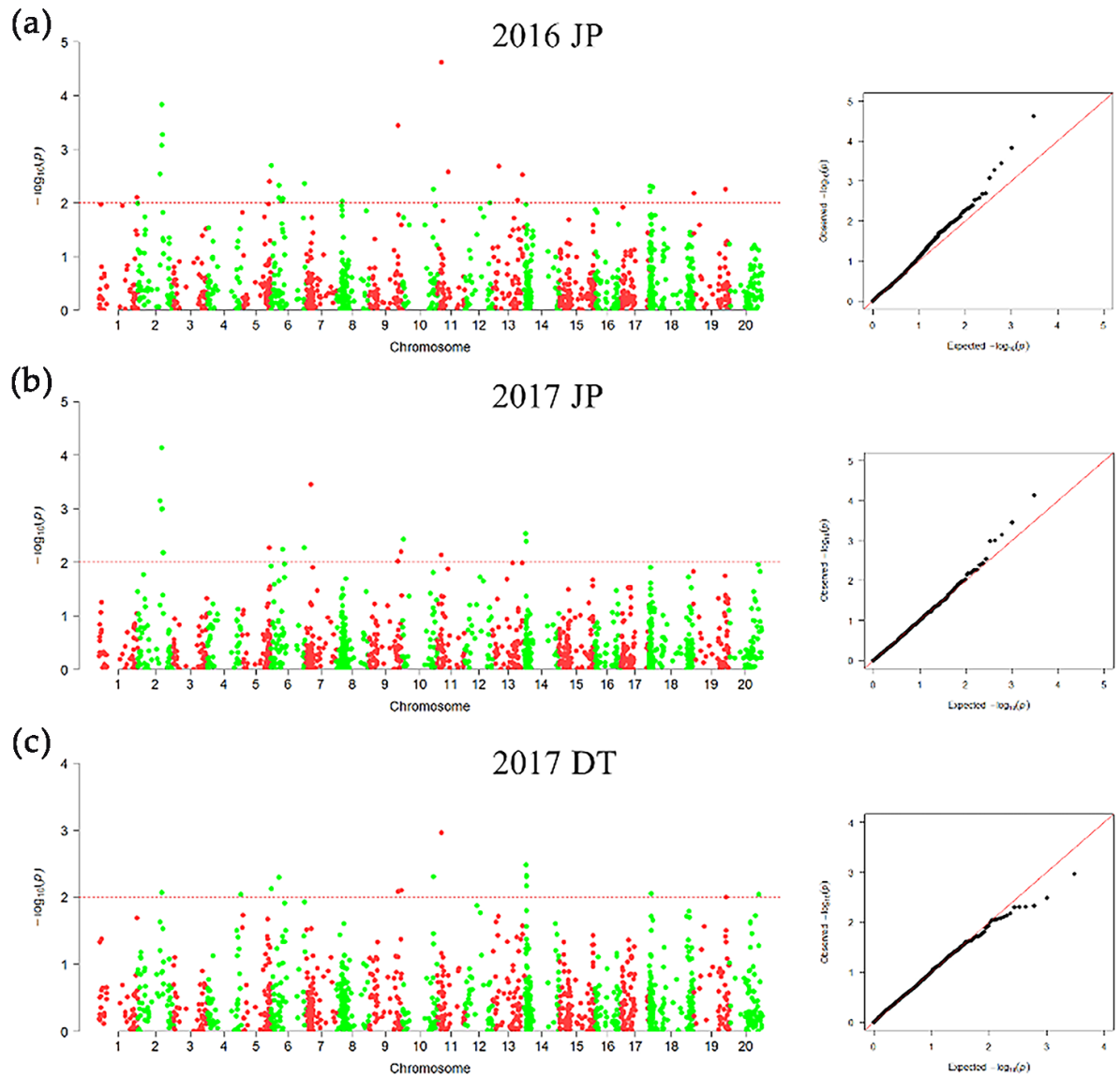


Figure S4. (a-c) Manhattan plots and Q-Q plots of GWAS for PH in 2016JP, 2017JP, and 2017DT, respectively. The horizontal red line indicates the genome-wide significance threshold ($-\log_{10}(p) \geq 2$).

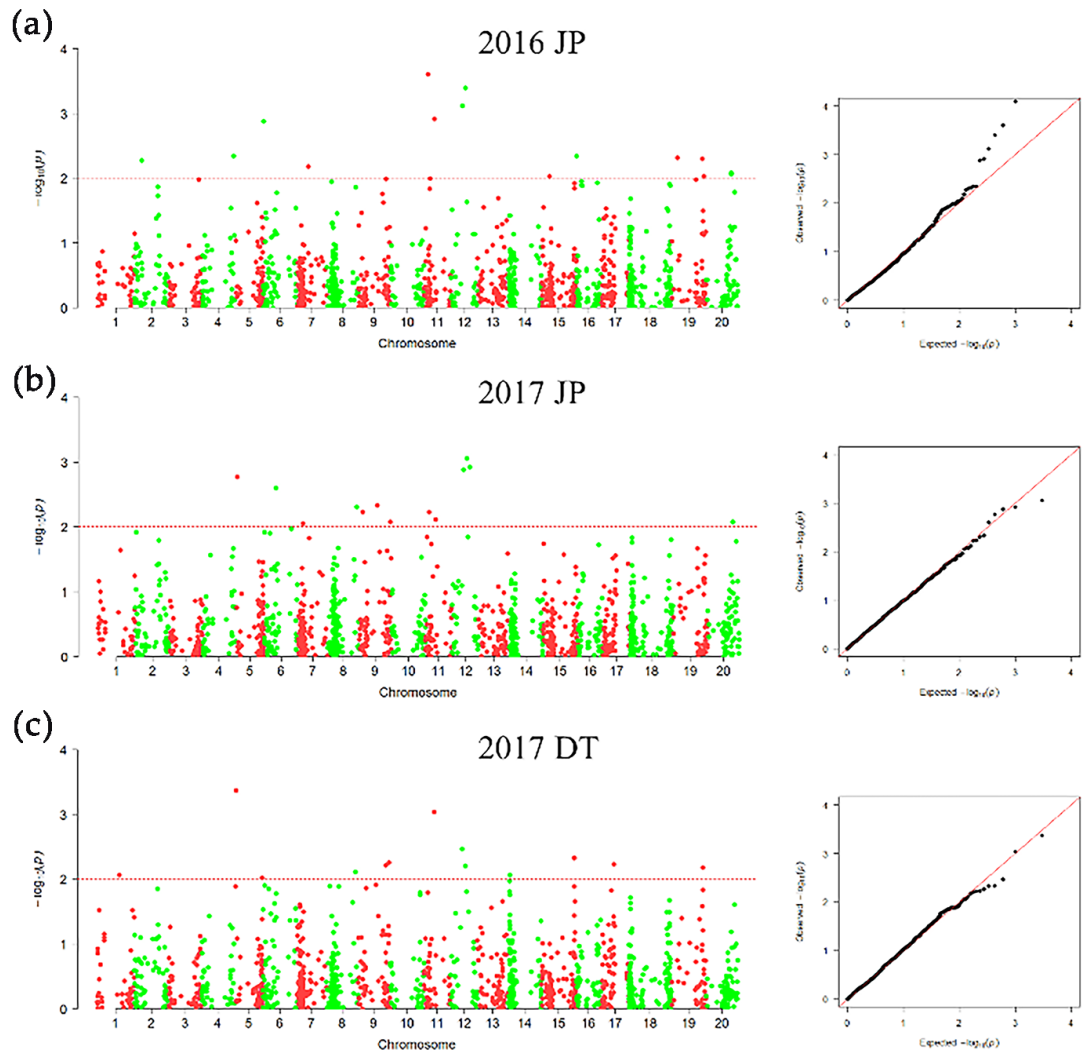


Figure S5. (a–c) Manhattan plots and Q-Q plots of GWAS for NN in 2016JP, 2017JP, and 2017DT, respectively. The horizontal red line indicates the genome-wide significance threshold ($-\log_{10}(p) \geq 2$).

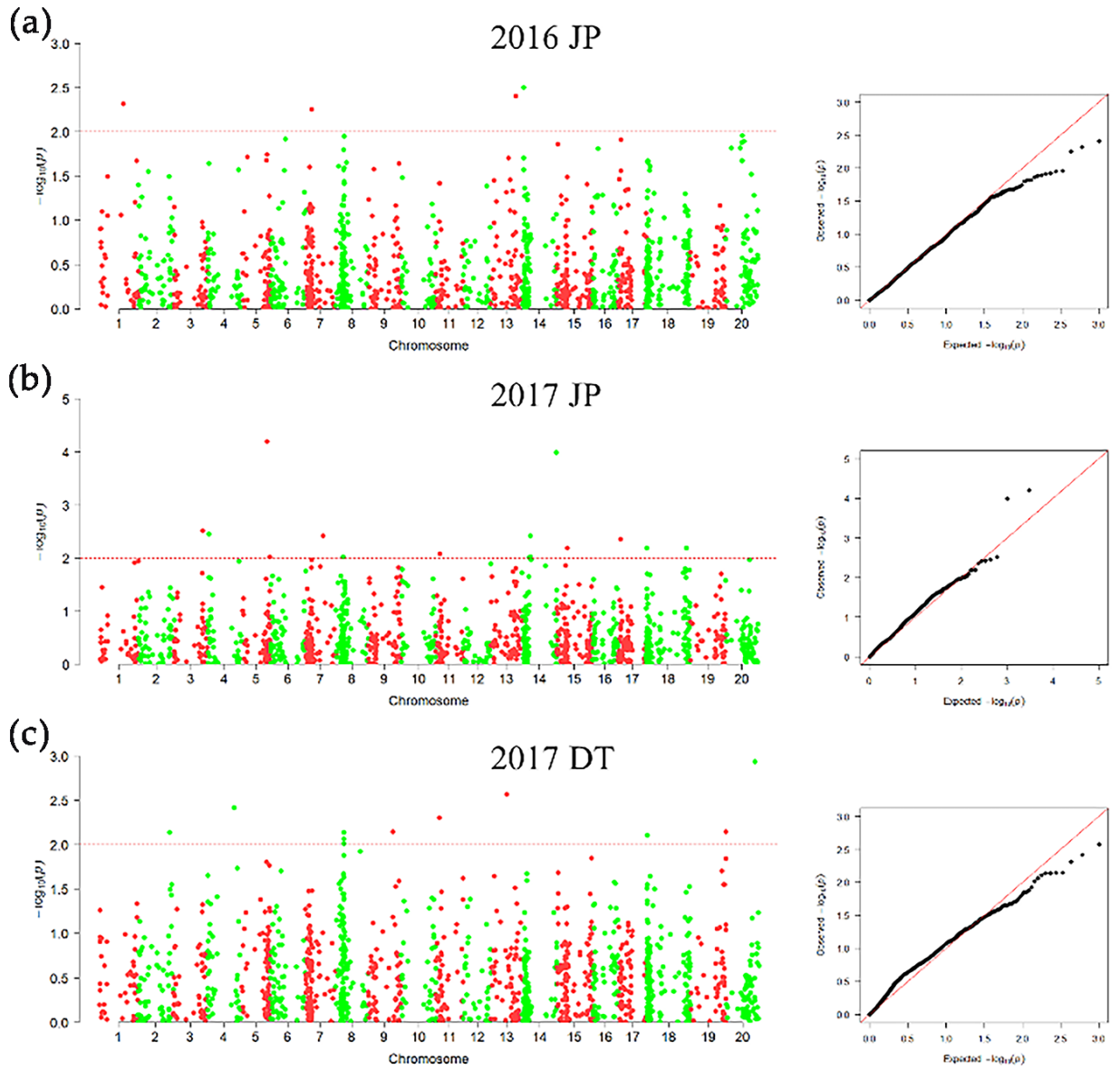


Figure S6. (a-c) Manhattan plots and Q-Q plots of GWAS for BN in 2016JP, 2017JP, and 2017DT, respectively. The horizontal red line indicates the genome-wide significance threshold ($-\log_{10}(p) \geq 2$).

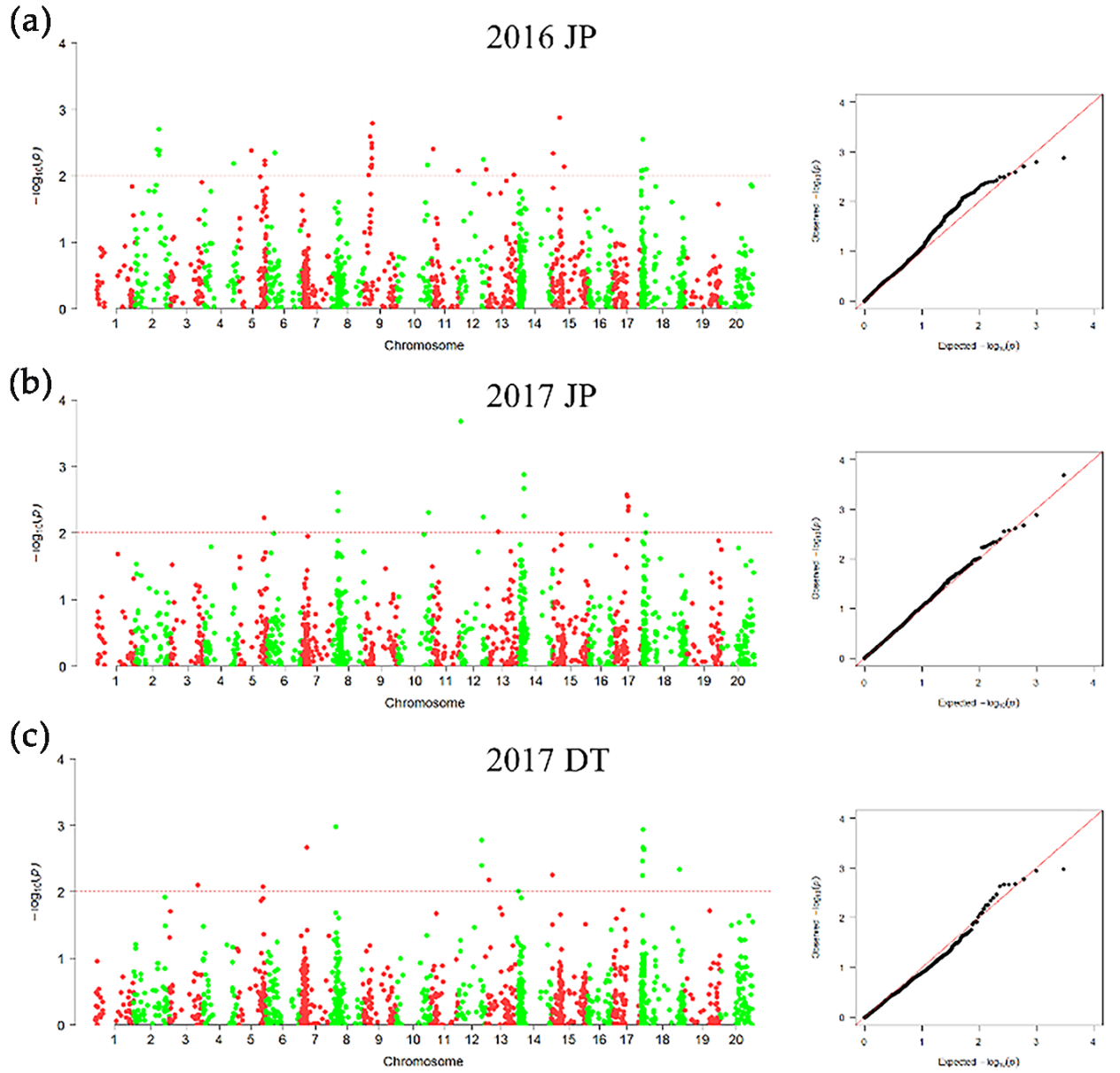


Figure S7. (a–c) Manhattan plots and Q-Q plots of GWAS for DI in 2016JP, 2017JP, and 2017DT, respectively. The horizontal red line indicates the genome-wide significance threshold ($-\log_{10}(p) \geq 2$).