## Candidate loci involved in domestication and improvement detected by a

## published 90k wheat SNP array

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## **Supporting information**

**Supplementary Figure 1.** Population structure of three populations in the K=3 model. Each accession was depicted by a vertical line segmented into 3 colored sections: blue, red and green for population W, L and M respectively. The length of each section was proportional to the estimated membership coefficient (Q) of the accession to each cluster.

**Supplementary Figure 2.** GWAS of the phenotype of tiller number (T) by Anderson– Darling test. Red and blue line indicated the Bonferroni corrected threshold of  $(-\log 10(P)=6.35, a = 0.01)$  and  $(-\log 10(P)=5.65, a = 0.05)$  respectively.

**Supplementary Figure 3.** GWAS of the phenotype of spike length (SL) by Anderson–Darling test. Red and blue line indicated the Bonferroni corrected threshold of  $(-\log 10(P)=6.35, a = 0.01)$  and  $(-\log 10(P)=5.65, a = 0.05)$  respectively.

**Supplementary Figure 4.** GWAS of the phenotype of spikelet number per spike (SLN) by Anderson–Darling test. Red and blue line indicated the Bonferroni corrected threshold of  $(-\log 10(P)=6.35, a = 0.01)$  and  $(-\log 10(P)=5.65, a = 0.05)$  respectively.

**Supplementary Figure 5.** GWAS of the phenotype of grain number (GN) by Anderson–Darling test. Red and blue line indicated the Bonferroni corrected threshold of  $(-\log 10(P)=6.35, a = 0.01)$  and  $(-\log 10(P)=5.65, a = 0.05)$  respectively.

**Supplementary Figure 6.** GWAS of the phenotype of thousand grain weight (TGW) by Anderson–Darling test. Red and blue line indicated the Bonferroni corrected threshold of  $(-\log 10(P)=6.35, a = 0.01)$  and  $(-\log 10(P)=5.65, a = 0.05)$  respectively.

**Supplementary Figure 7.** GWAS of the phenotype of yield (Y) by Anderson–Darling test. Red and blue line indicated the Bonferroni corrected threshold of  $(-\log_{10}(P)=6.35, a=0.01)$  and  $(-\log_{10}(P)=5.65, a=0.05)$  respectively.

**Supplementary Figure 8.** GWAS of the phenotype of plant height (Ph) by Anderson– Darling test. Red and blue line indicated the Bonferroni corrected threshold of  $(-\log_{10}(P)=6.35, a=0.01)$  and  $(-\log_{10}(P)=5.65, a=0.05)$  respectively.

**Supplementary Figure 9.** GWAS of the phenotype of heading time (Ht) by Anderson–Darling test. Red and blue line indicated the Bonferroni corrected threshold of  $(-\log 10(P)=6.35, a = 0.01)$  and  $(-\log 10(P)=5.65, a = 0.05)$  respectively.

**Supplementary Figure 10.** GWAS of the phenotype of mature time (Mt) by Anderson–Darling test. Red and blue line indicated the Bonferroni corrected threshold of  $(-\log 10(P)=6.35, a = 0.01)$  and  $(-\log 10(P)=5.65, a = 0.05)$  respectively.

**Supplementary Figure 11.** GWAS of the phenotype of resistance to powdery mildew (PM) by Anderson–Darling test. Red and blue line indicated the Bonferroni corrected threshold of  $(-\log_{10}(P)=6.35, a=0.01)$  and  $(-\log_{10}(P)=5.65, a=0.05)$  respectively.

**Supplementary Figure 12**. Selection map of wheat during domestication and improvement. Red, green and purple lines denote candidates subjected to selection during domestication, improvement and both processes, respectively. Centromeric regions are indicated by black dots in accordance with Cavanagh et al.<sup>25</sup> Detailed information on the mapped loci is provided in Supplementary dataset 1 to 4.

## **Supplementary Figures**



Supplementary Figure 1. Population structure of three populations in the K=3 model. Each accession was depicted by a vertical line segmented into 3 colored sections: blue, red and green for population W, L and M respectively. The length of each section was proportional to the estimated membership coefficient (Q) of the accession to each cluster.



Supplementary Figure 2. GWAS of the phenotype of tiller number (T) by Anderson–Darling test. Red and blue line indicated the Bonferroni corrected threshold of  $(-\log 10(P)=6.35, a = 0.01)$  and  $(-\log 10(P)=5.65, a = 0.05)$  respectively.



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