

Genome-wide association analysis reveals the gene loci of yield traits under drought stress at rice reproductive stage

**Figure S1.** Histogram of the phenotypic frequency distribution of yield trait in 305 rice accessions.

**Figure S2.** Distribution of single nucleotide polymorphisms (SNPs) and nucleotide diversity across the rice Nipponbare genome in the rice association panel.

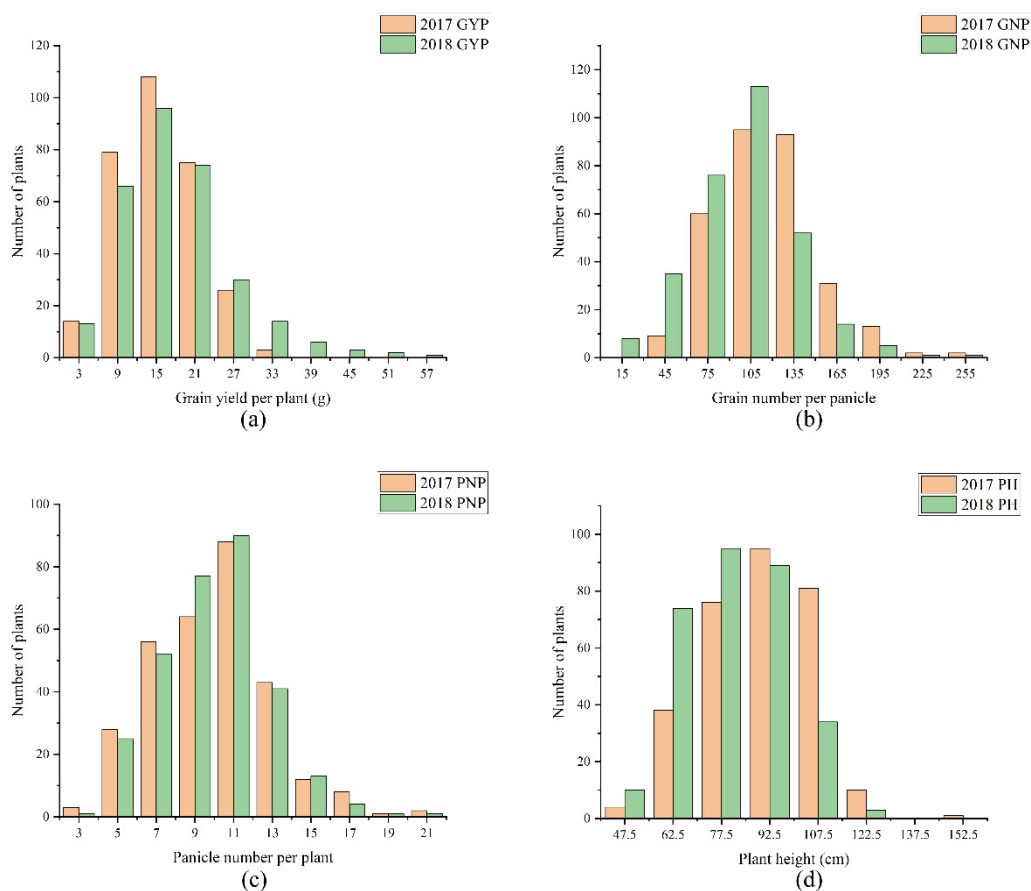


Figure S1. Histogram of the phenotypic frequency distribution of yield trait in 305 rice accessions. (a) Grain yield per plant; (b) Grain number per panicle; (c) Panicle number per plant; (d) Plant height.

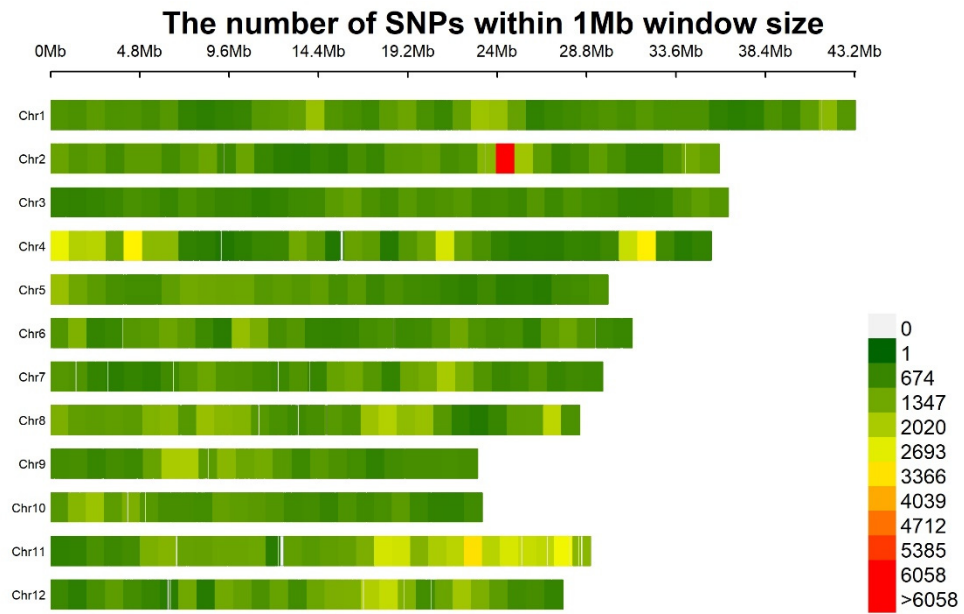


Figure S2. Distribution of single nucleotide polymorphisms (SNPs) and nucleotide diversity across the rice Nipponbare genome in the rice association panel.