Supplementary Figure 1. The kinship plot of 406 accessions from RDP1.
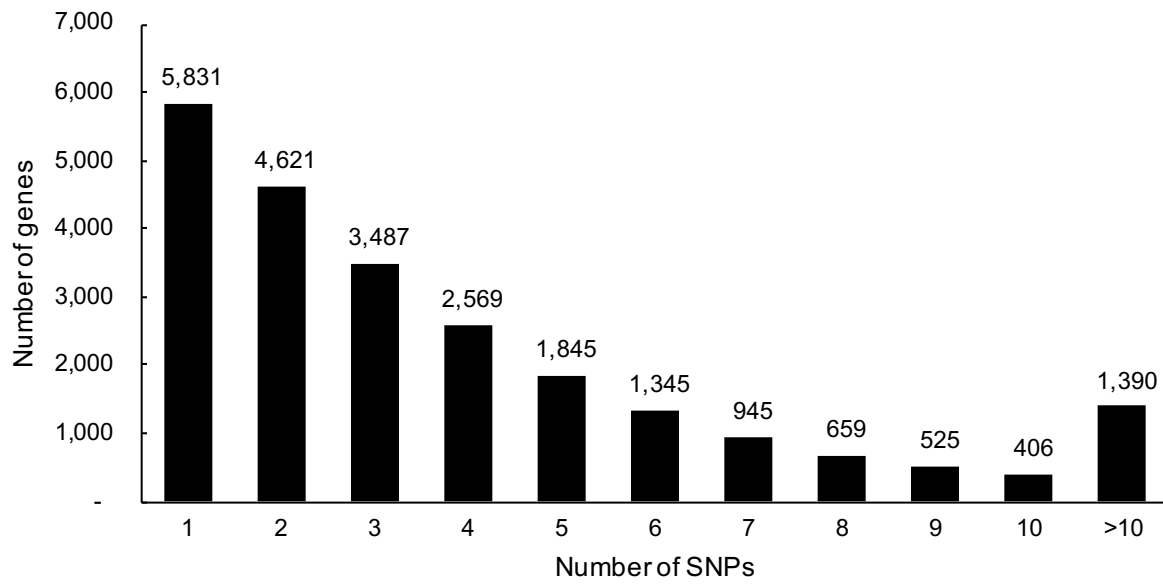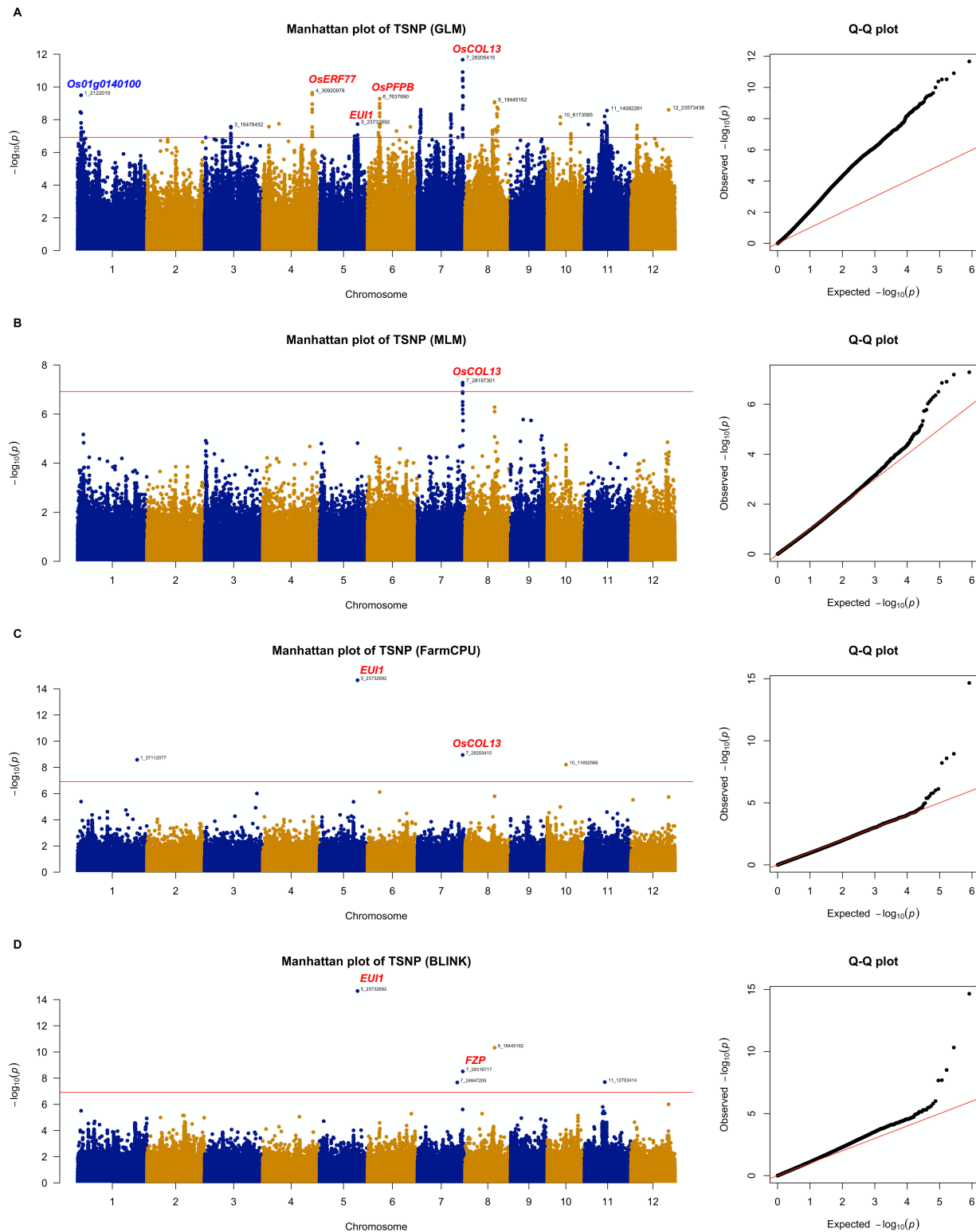
**Supplementary Figure 2.** The distribution of SNP number in genes.

Supplementary Figure 3. Genome-wide association analysis for total spikelets number per panicle (TSNP) with general linear model (GLM), mixed linear models (MLM), Fixed and random model Circulating Probability Unification (FarmCPU), and Bayesian-information and Linkage-disequilibrium Iteratively Nested Keyway (BLINK) methods (left). Quantile-quantile plot of each model (right). Red texts indicate reported genes, blue texts indicate candidate genes. The horizontal solid red line indicates the Bonferroni-corrected significance threshold -log$_{10}$(P) = 6.91.
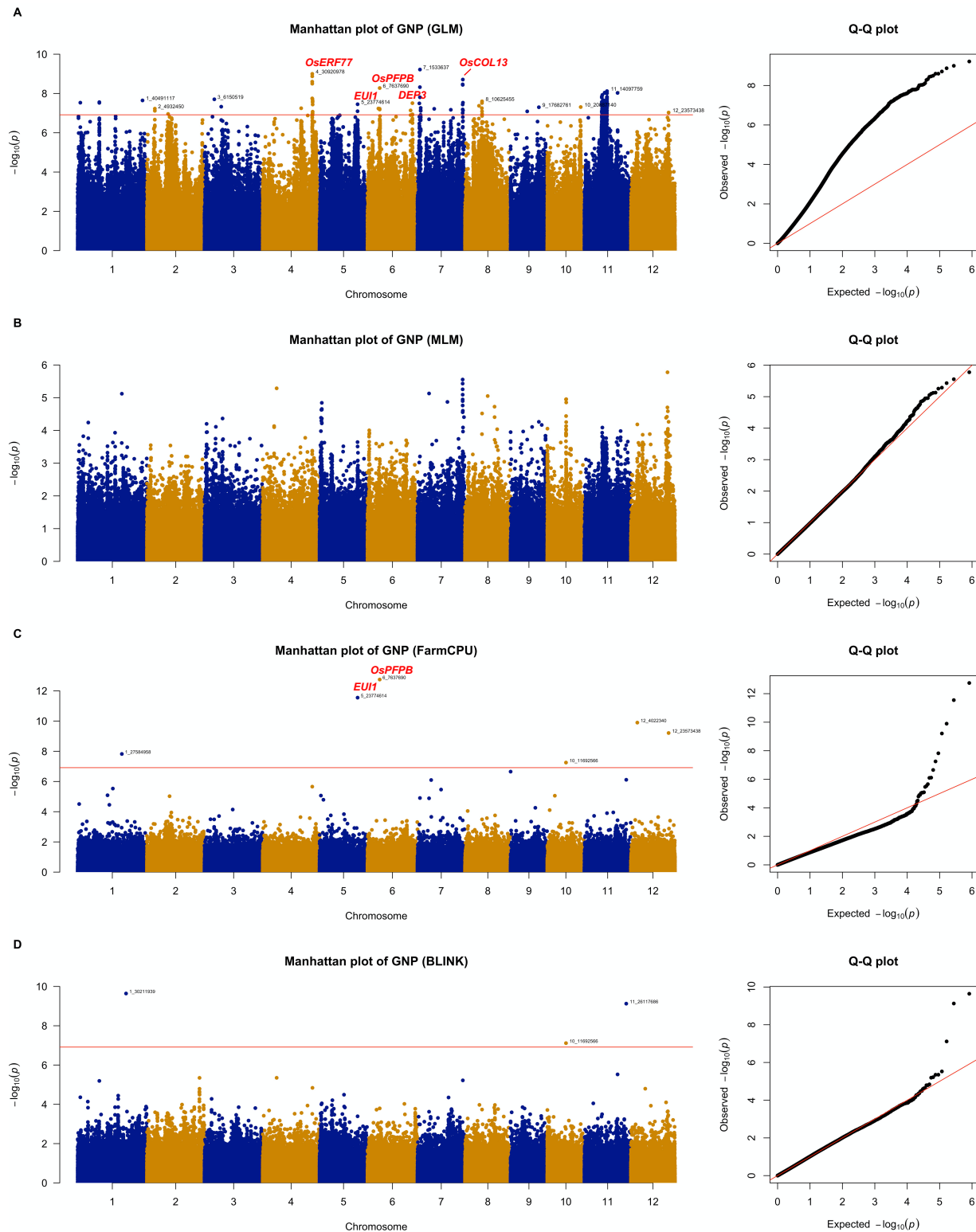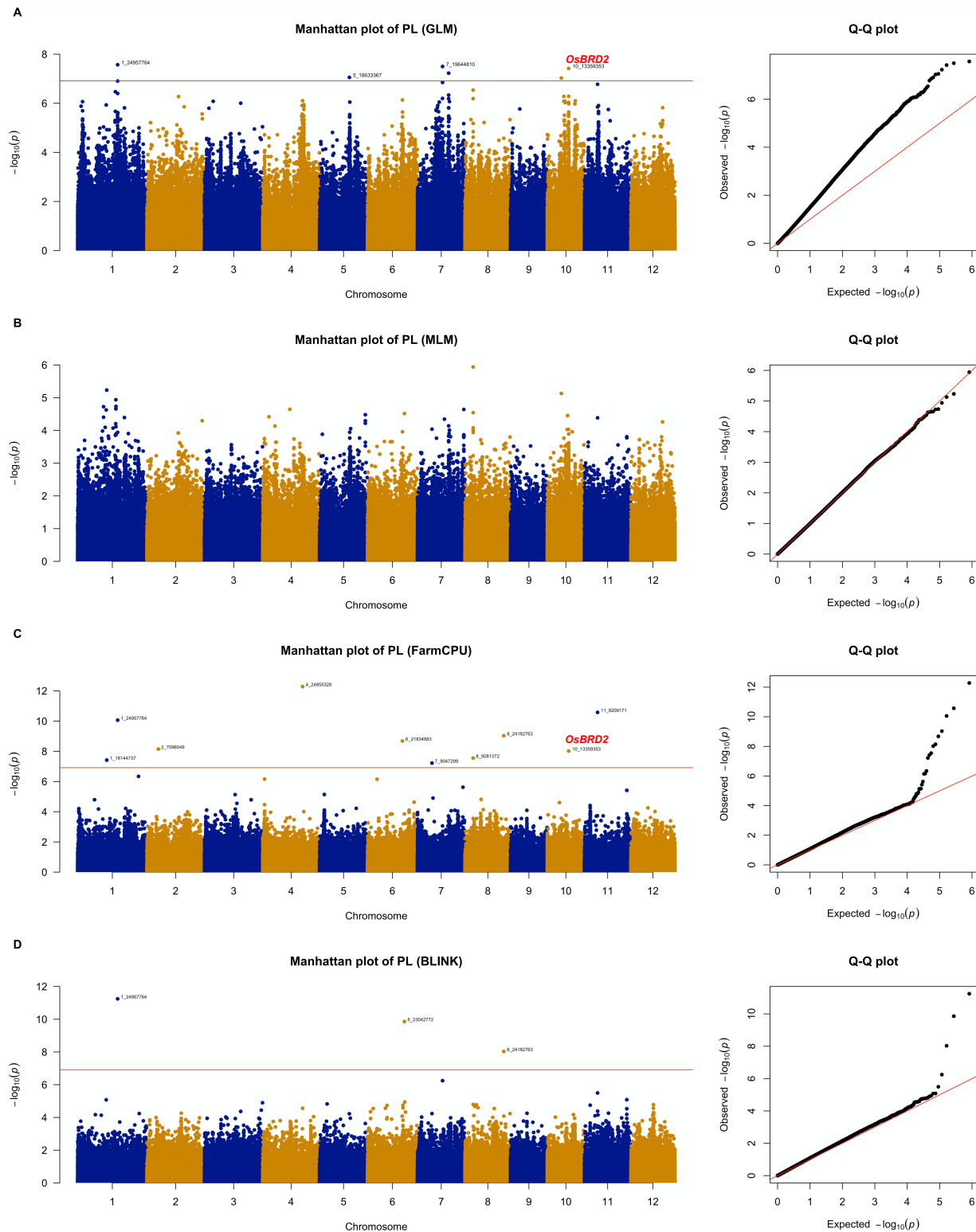
Supplementary Figure 4. Genome-wide association analysis for grain number per panicle (GNP) with general linear model (GLM), mixed linear models (MLM), Fixed and random model Circulating Probability Unification (FarmCPU), and Bayesian-information and Linkage-disequilibrium Iteratively Nested Keyway (BLINK) methods (left). Red texts indicate reported genes. The horizontal solid red line indicates the Bonferroni-corrected significance threshold -log$_{10}$(P) = 6.91.
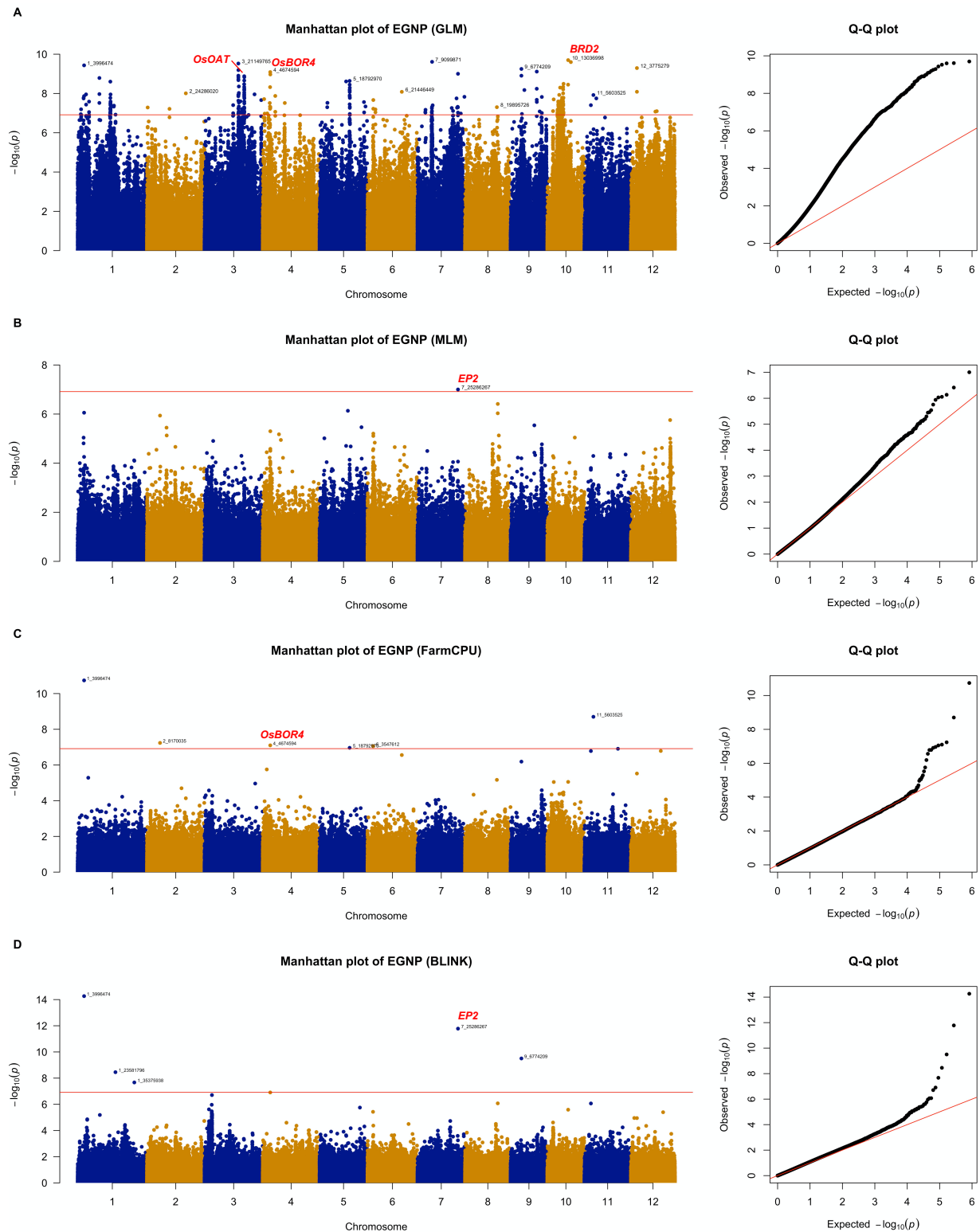
Supplementary Figure 5. Genome-wide association analysis for EGNP with general linear model (GLM), mixed linear models (MLM), Fixed and random model Circulating Probability Unification (FarmCPU), and Bayesian-information and Linkage-disequilibrium Iteratively Nested Keyway (BLINK) methods (left). Quantile-quantile plot of each model (right). Red texts indicate reported genes. The horizontal solid red line indicates the Bonferroni-corrected significance threshold -$\log_{10}$(P) = 6.91.
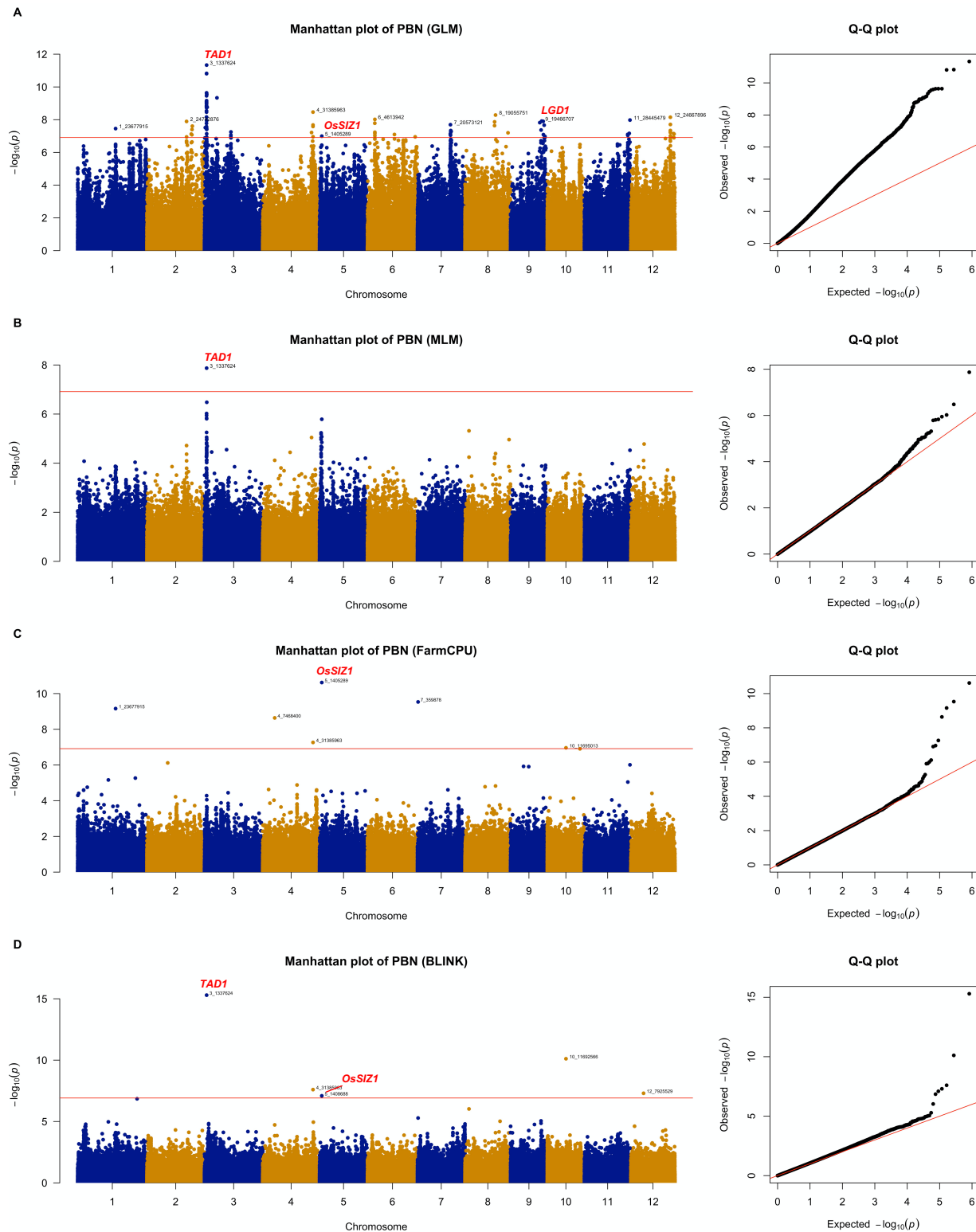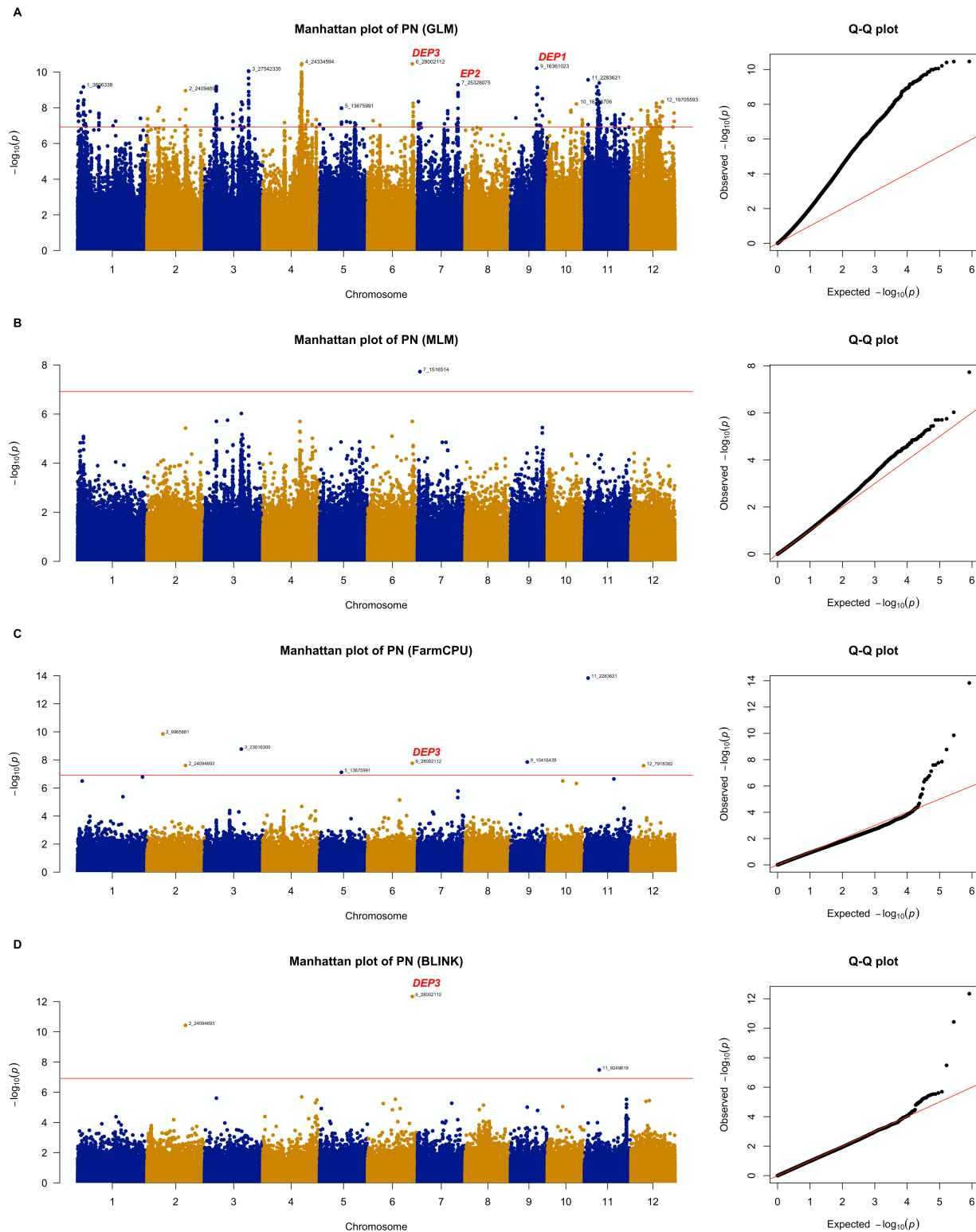
Supplementary Figure 6. Genome-wide association analysis for PBN with general linear model (GLM), mixed linear models (MLM), Fixed and random model Circulating Probability Unification (FarmCPU), and Bayesian-information and Linkage-disequilibrium Iteratively Nested Keyway (BLINK) methods (left). Quantile-quantile plot of each model (right). Red texts indicate reported genes. The horizontal solid red line indicates the Bonferroni-corrected significance threshold -log$_{10}$(P) = 6.91.

Supplementary Figure 7. Genome-wide association analysis for PL with general linear model (GLM), mixed linear models (MLM), Fixed and random model Circulating Probability Unification (FarmCPU), and Bayesian-information and Linkage-disequilibrium Iteratively Nested Keyway (BLINK) methods (left). Quantile-quantile plot of each model (right). Red texts indicate reported genes. The horizontal solid red line indicates the Bonferroni-corrected significance threshold $-\log_{10}(P) = 6.91$.

Supplementary Figure 8. Genome-wide association analysis for PN with general linear model (GLM), mixed linear models (MLM), Fixed and random model Circulating Probability Unification (FarmCPU), and Bayesian-information and Linkage-disequilibrium Iteratively Nested Keyway (BLINK) methods (left). Quantile-quantile plot of each model (right). Red texts indicate reported genes. The horizontal solid red line indicates the Bonferroni-corrected significance threshold -log$_{10}$(P) = 6.91.
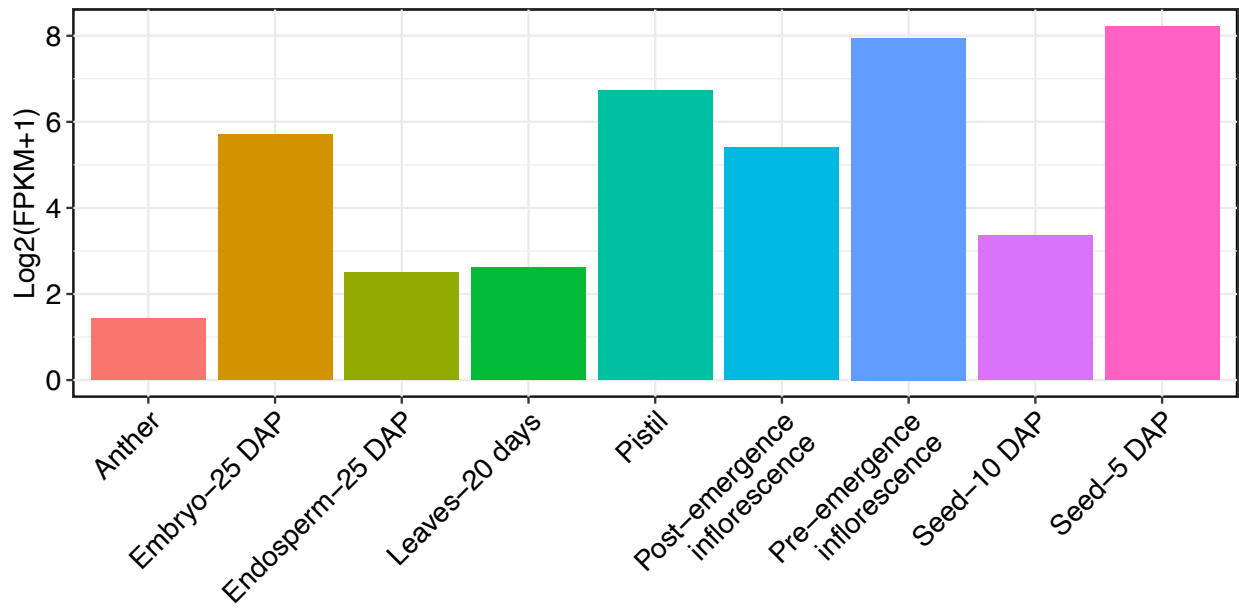
Supplementary Figure 9. Expression pattern of *Os01g0140100* in different tissues. Anther: Anther; Embryo-25 DAP: Embryo 25 Days After Pollination; Endosperm-25 DAP: Endosperm 25 Days After Pollination; Leaves-20 days: 20 Day Leaves; Pistil: Pistil; Pre-emergence inflorescence: Early Inflorescence; Post-emergence inflorescence: Emerging Inflorescence; Seed-5 DAP: Seed 5 Days After Pollination; Seed-10 DAP: Seed 10 Days After Pollination.