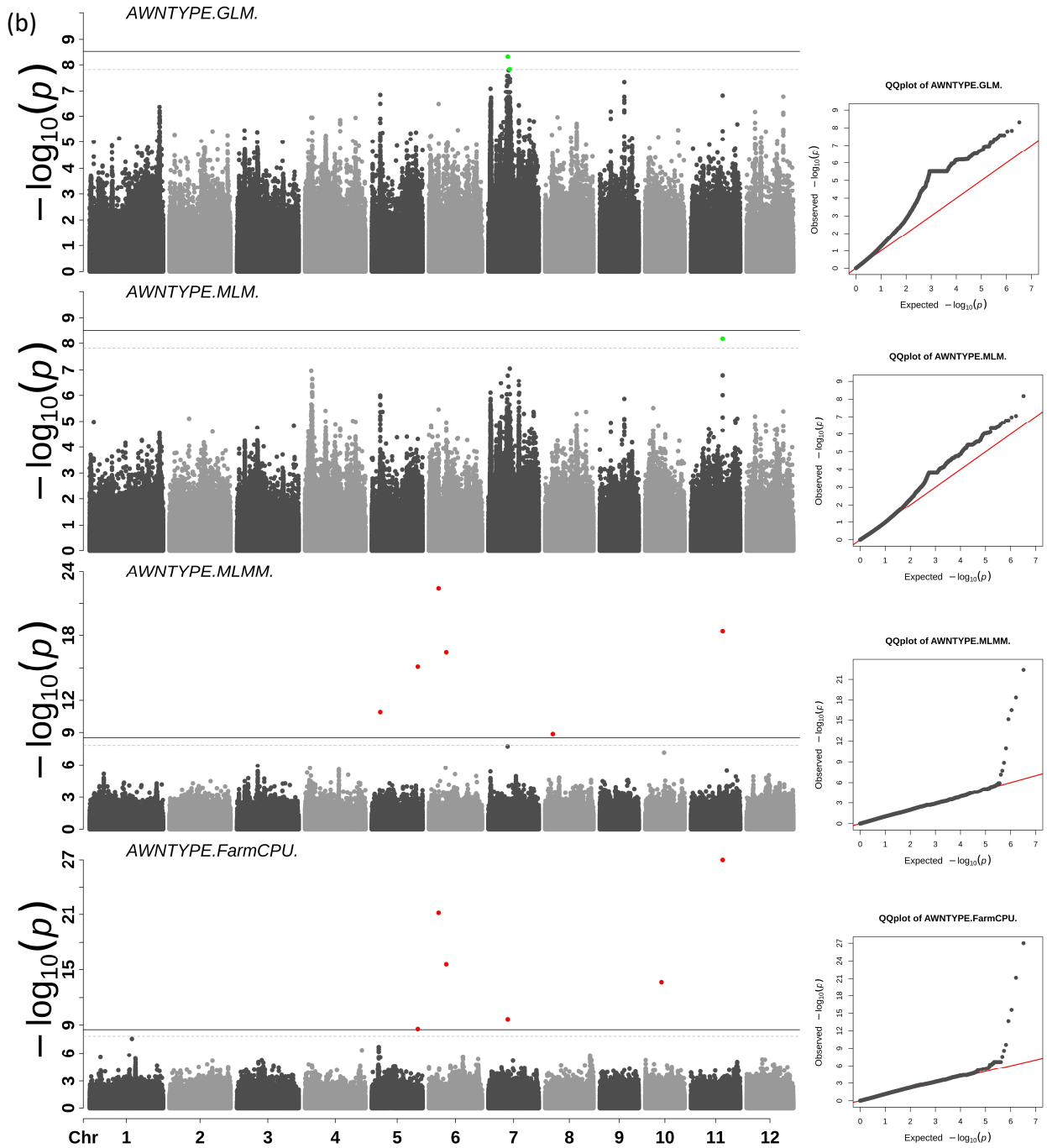
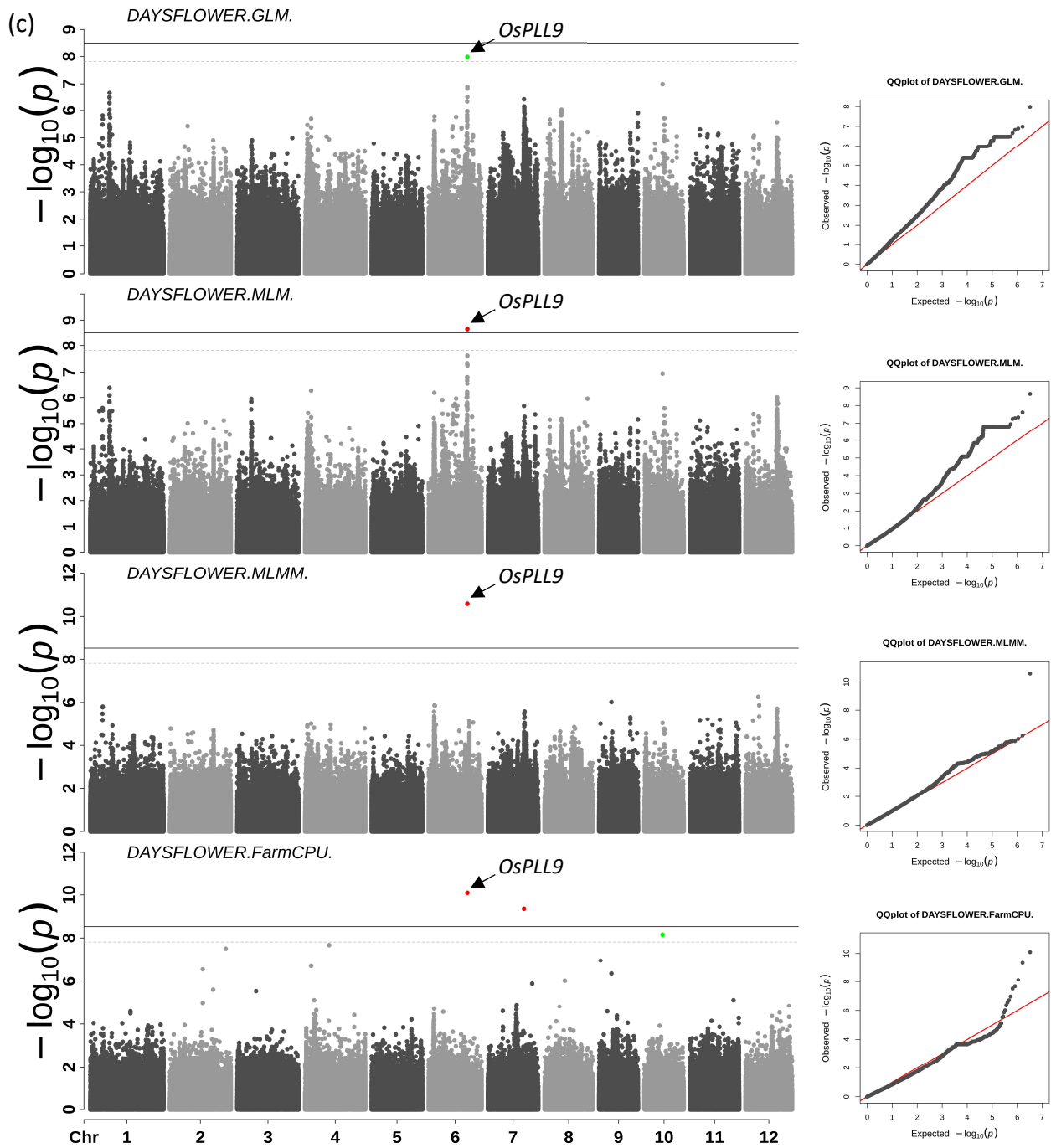


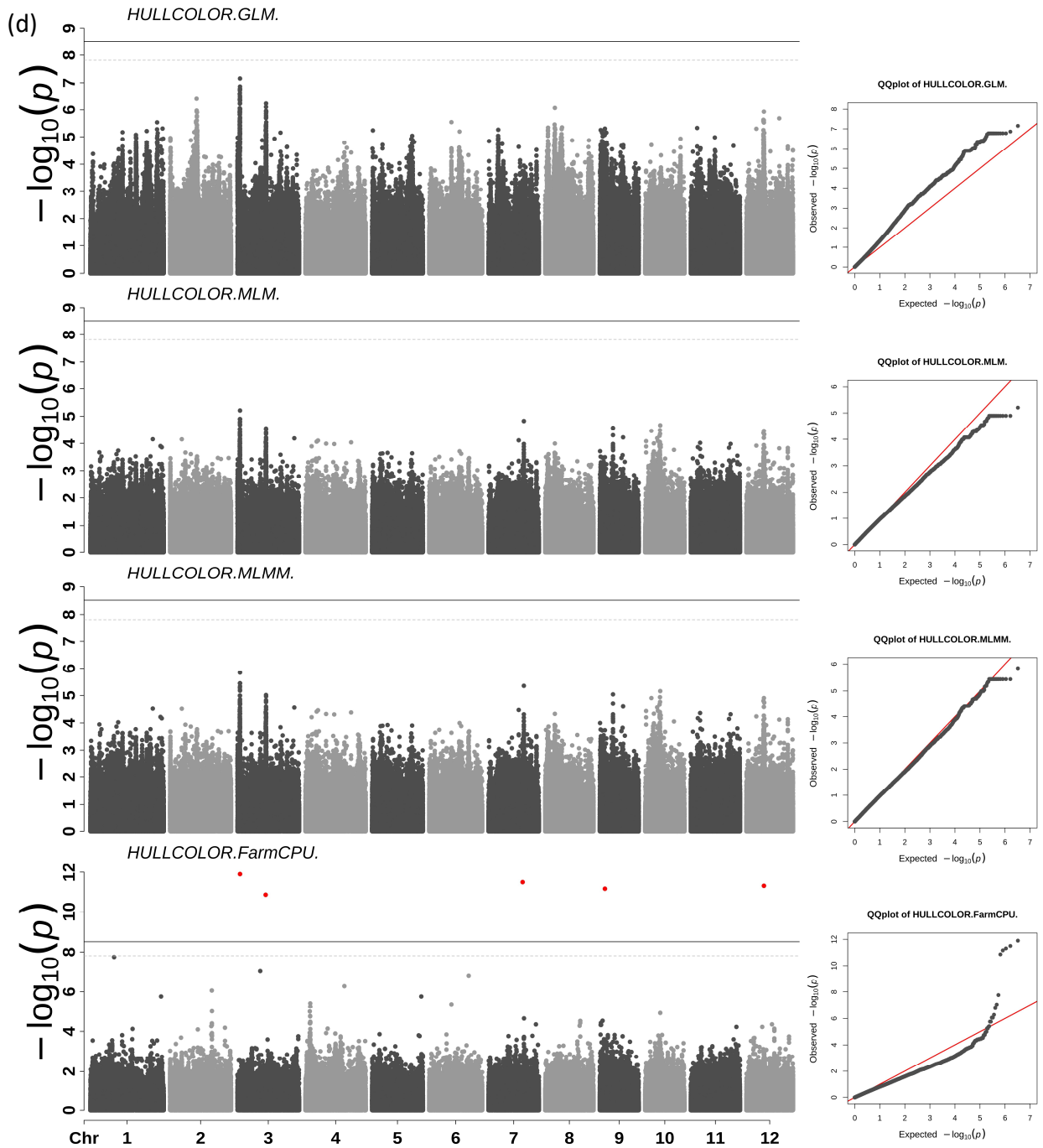
Supplementary Figure 3 (a) Genome-wide association analysis for AMYLOSE with GLM, MLM, MLMM, and FarmCPU methods (left). Quantile-quantile plot of each model (right). Red arrows indicate published genes. The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 7.81$. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 8.51$.



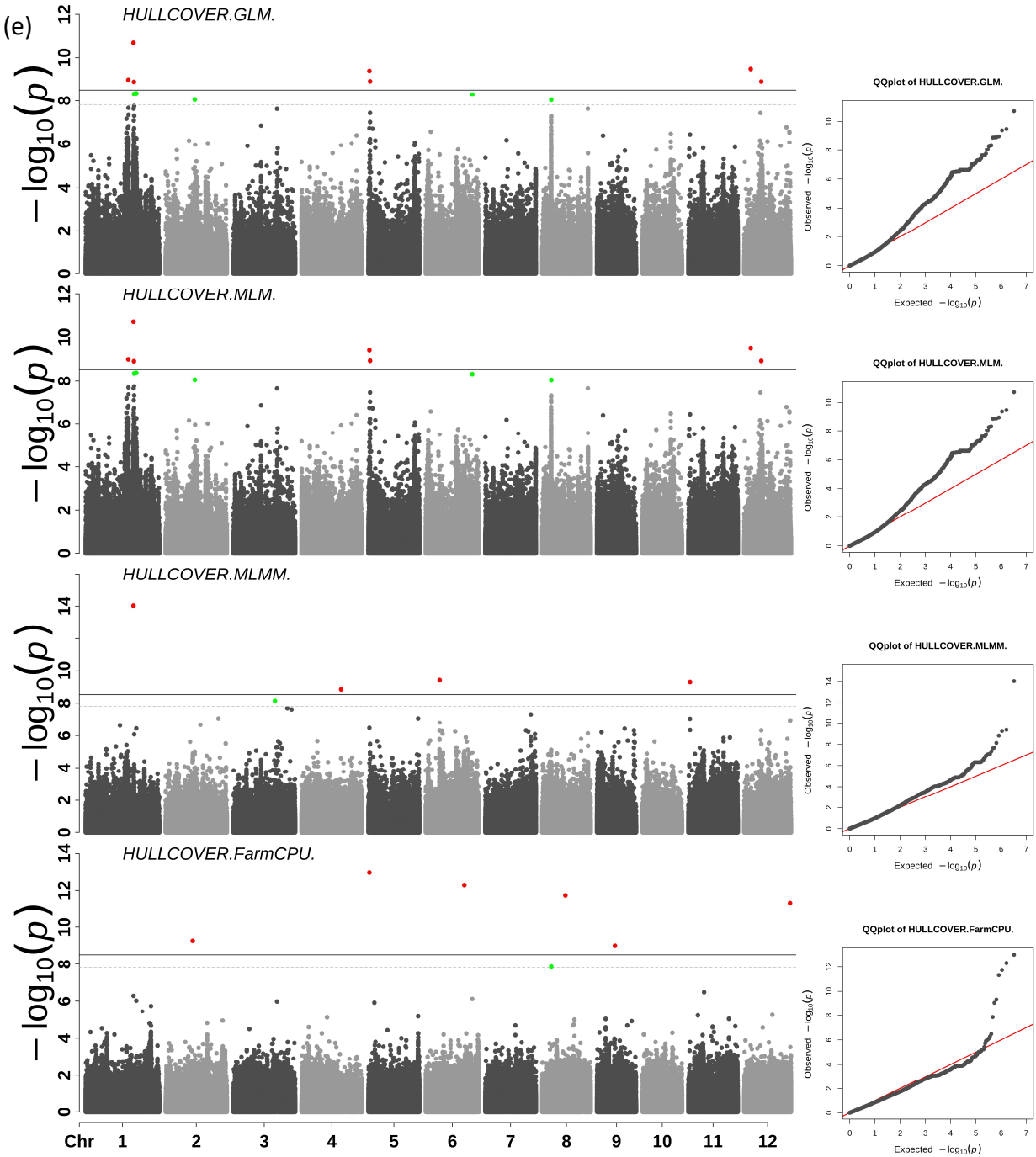
Supplementary Figure 3 (b) Genome-wide association analysis for AWNTYPE with GLM, MLM, MLMM, and FarmCPU methods (left). Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 7.81$. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 8.51$.



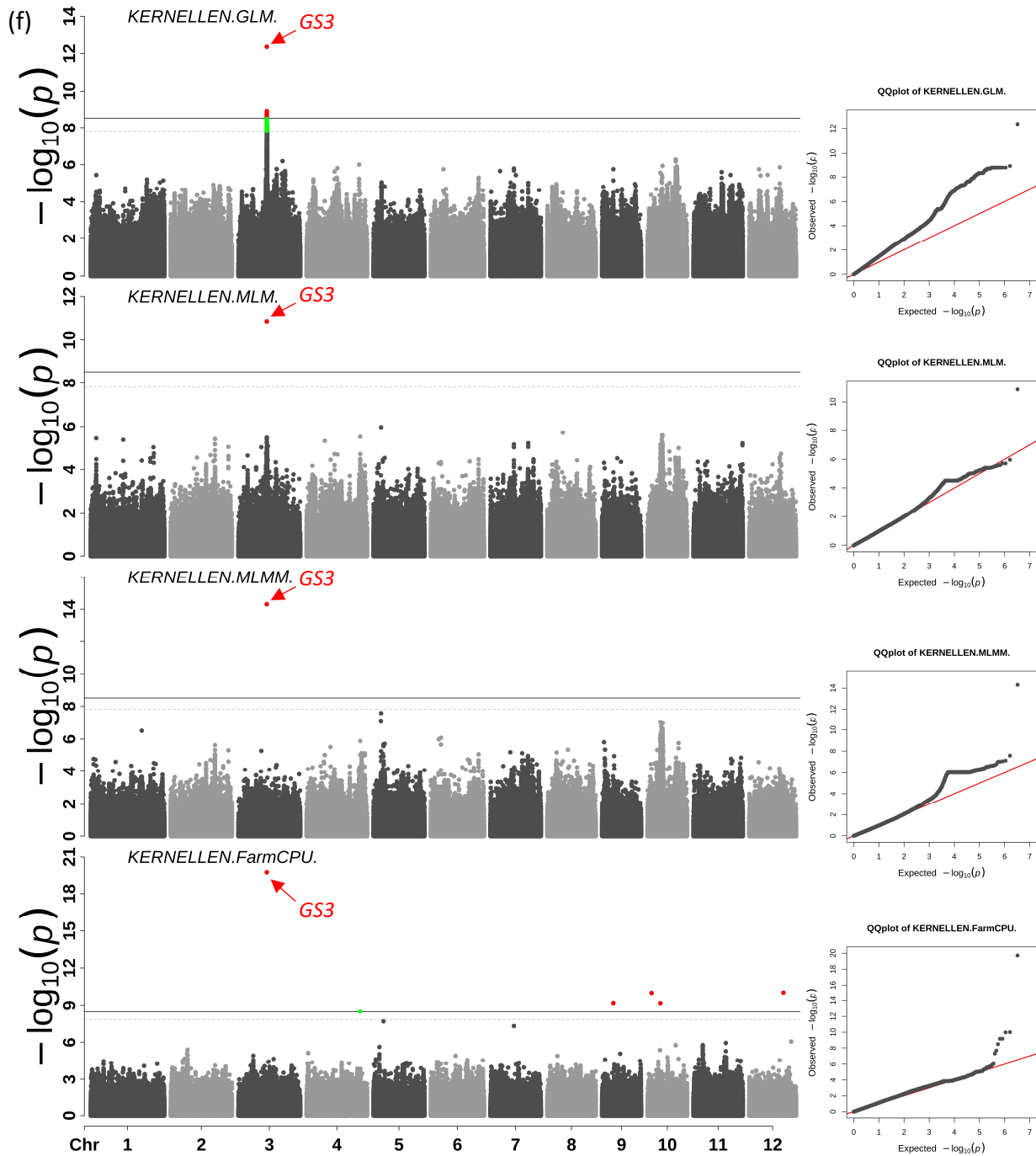
Supplementary Figure 3 (c) Genome-wide association analysis for DAYSFLOWER with GLM, MLM, MLMM, and FarmCPU methods (left). Quantile-quantile plot of each model (right). Black arrow indicates candidate gene. The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 7.81$. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 8.51$.



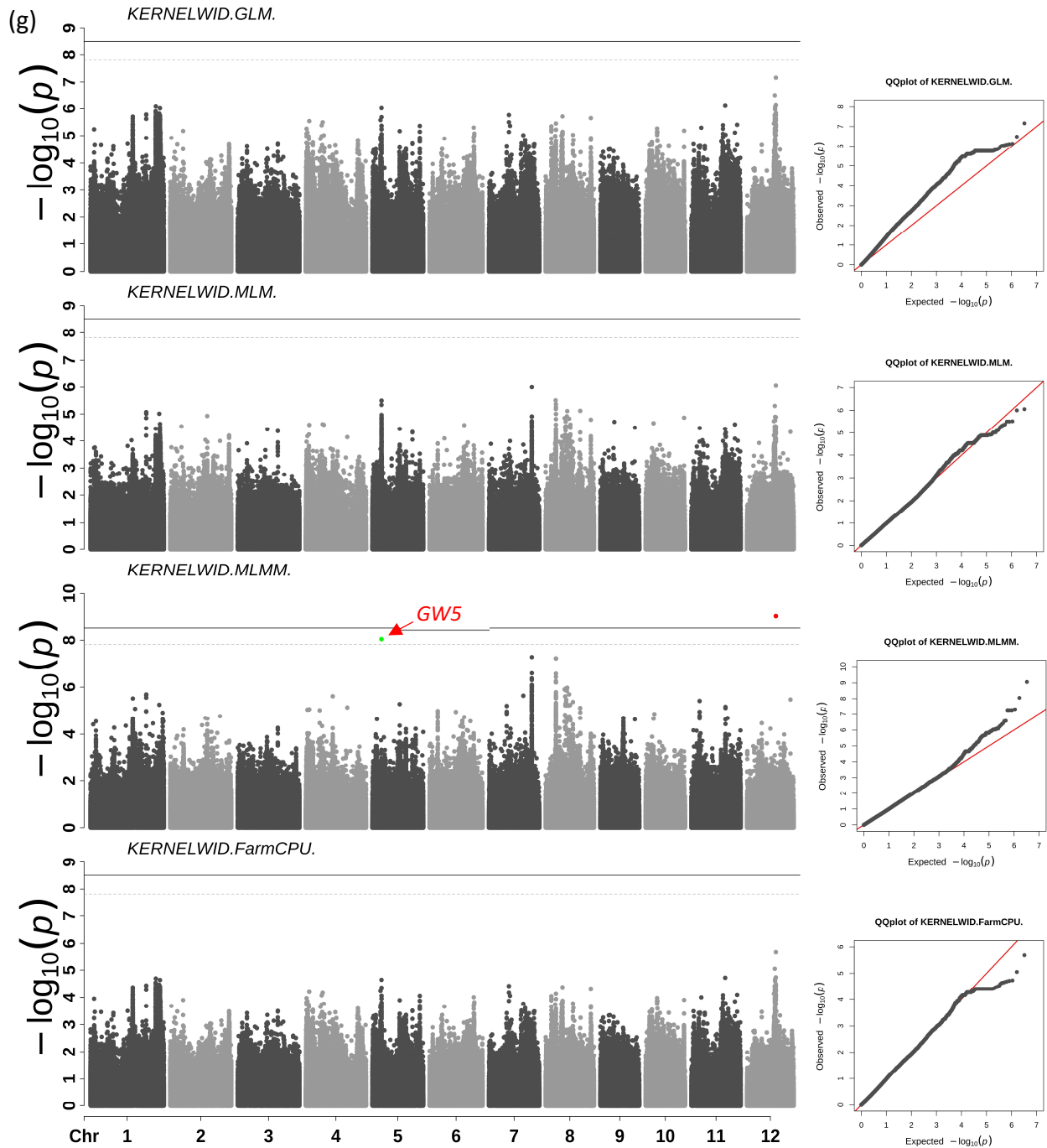
Supplementary Figure 3 (d) Genome-wide association analysis for HULLCOLOR with GLM, MLM, MLMM, and FarmCPU methods (left). Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 7.81$. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 8.51$.



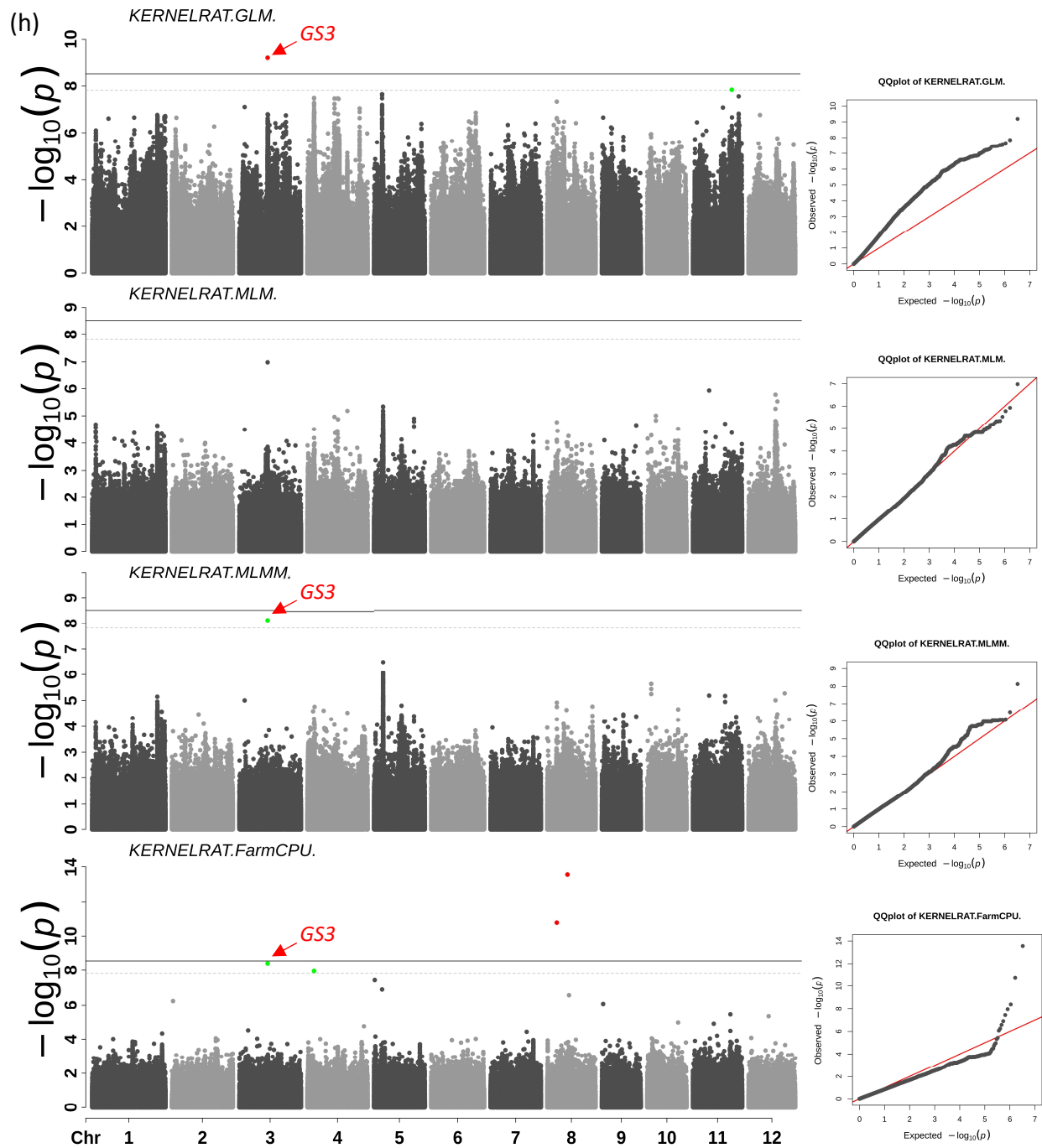
Supplementary Figure 3 (e) Genome-wide association analysis for HULLCOVER with GLM, MLM, MLMM, and FarmCPU methods (left). Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 7.81$. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 8.51$.



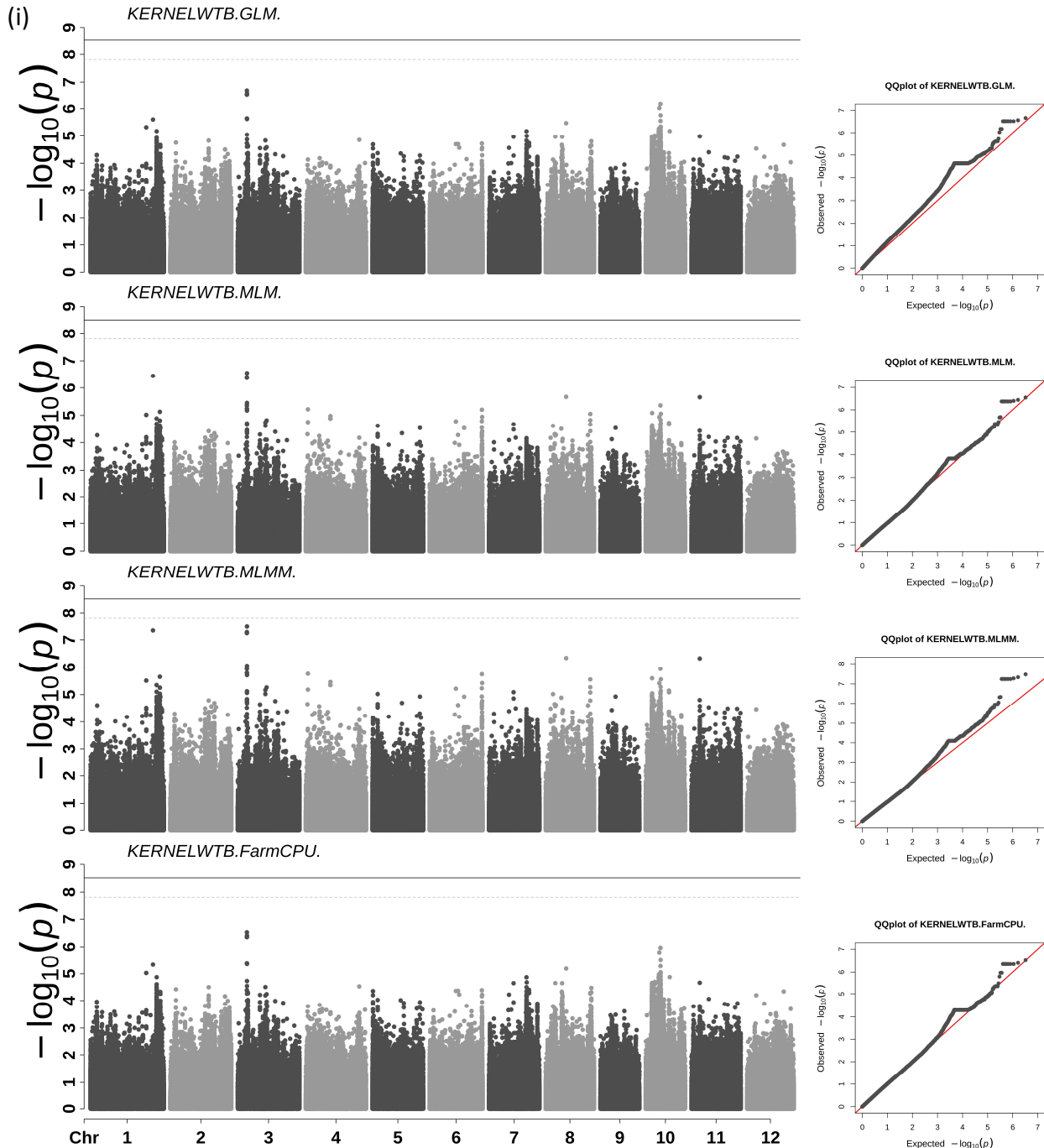
Supplementary Figure 3 (f) Genome-wide association analysis for KERNELLEN with GLM, MLM, MLMM, and FarmCPU methods (left). Quantile-quantile plot of each model (right). Red arrow indicates published gene. The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 7.81$. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 8.51$.



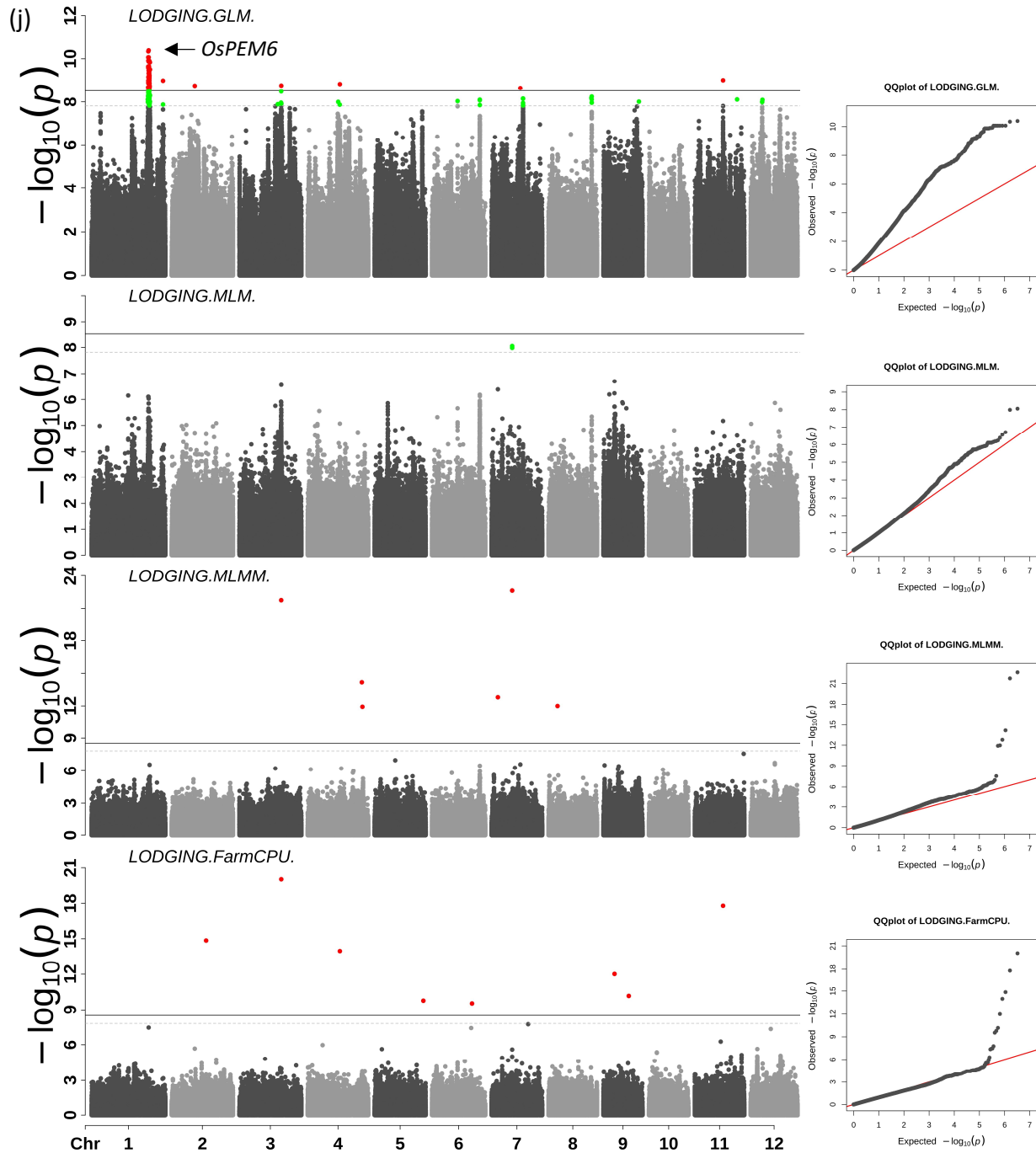
Supplementary Figure 3 (g) Genome-wide association analysis for KERNELWID with GLM, MLM, MLMM, and FarmCPU methods (left). Quantile-quantile plot of each model (right). Red arrow indicates published gene. The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 7.81$. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 8.51$.



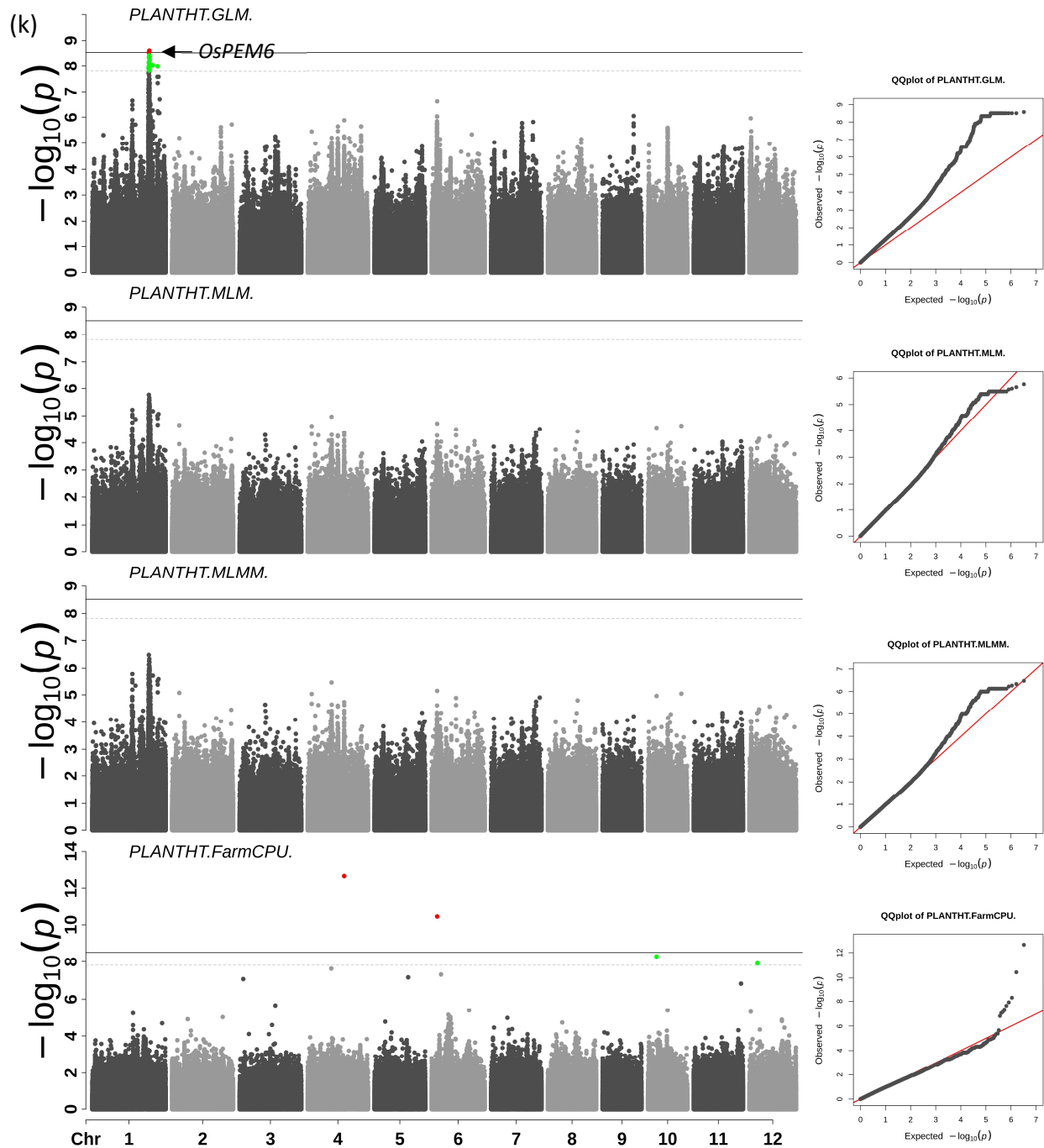
Supplementary Figure 3 (h) Genome-wide association analysis for KERNELRAT with GLM, MLM, MLMM, and FarmCPU methods (left). Quantile-quantile plot of each model (right). Red arrow indicates published gene. The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 7.81$. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 8.51$.



Supplementary Figure 3 (i) Genome-wide association analysis for KERNELWTB with GLM, MLM, MLMM, and FarmCPU methods (left). Quantile-quantile plot of each model (right). The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 7.81$. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 8.51$.



Supplementary Figure 3 (j) Genome-wide association analysis for LODGING with GLM, MLM, MLMM, and FarmCPU methods (left). Quantile-quantile plot of each model (right). Black arrow indicates candidate gene. The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 7.81$. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 8.51$.



Supplementary Figure 3 (k) Genome-wide association analysis for PLANTHT with GLM, MLM, MLMM, and FarmCPU methods (left). Quantile-quantile plot of each model (right). Black arrow indicates candidate gene. The horizontal dot grey line and green dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 7.81$. The horizontal solid grey line and red dots indicate the Bonferroni-corrected significance thresholds and SNPs at $-\log_{10}(P) = 8.51$.