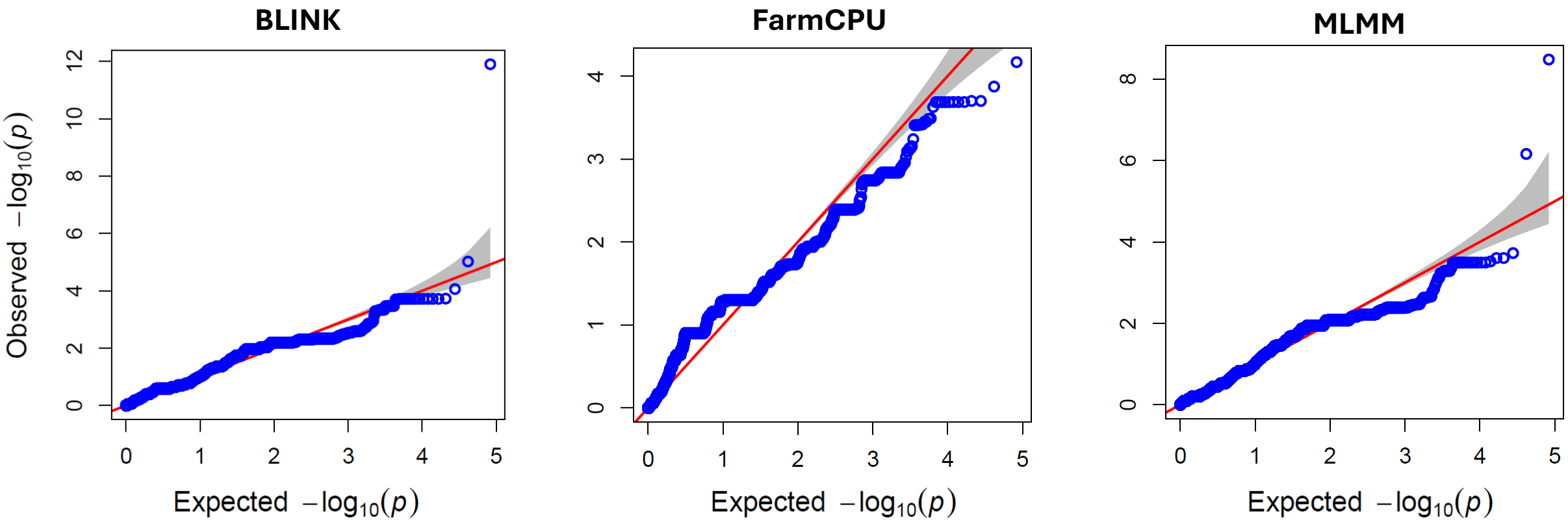
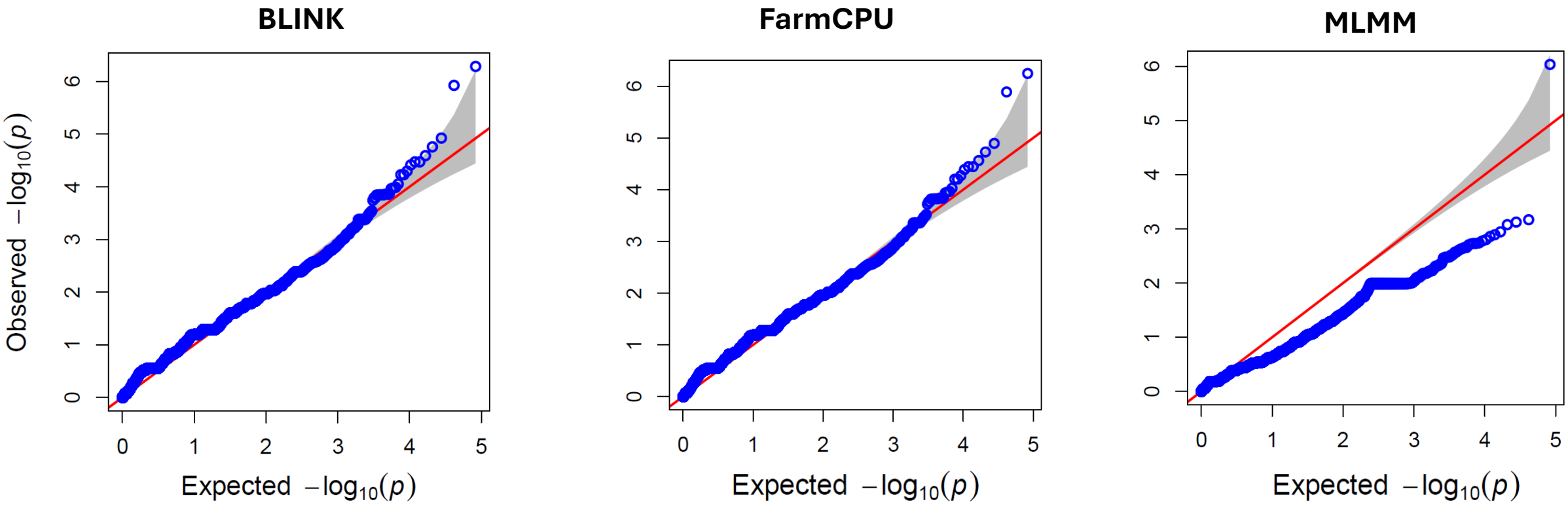
Supplementary data 2 - Quantile–quantile plots from GWAS analyses of disease-response traits using MLMM, BLINK and FarmCPU models.

QQ plots for TSWV mean symptoms showed that the three GWAS models adequately controlled the overall distribution of association signals, with most markers following the expected distribution. However, clear differences were observed in the upper tail. MLMM and BLINK showed a marked deviation from the expected line, indicating the presence of strong marker–trait associations for TSWV symptom severity. This deviation was strongest in BLINK, which produced the highest observed $-\log_{10}(p)$ values, followed by MLMM. In contrast, FarmCPU showed a more conservative distribution, with weaker tail deviation and lower maximum significance values. For TSWV mean DAS-ELISA values, MLMM showed a conservative distribution, with most markers below the expected line, although one clear upper-tail deviation suggested a strong association signal. By contrast, BLINK and FarmCPU closely followed the expected distribution across most of the plot and displayed a moderate upward deviation in the upper tail. Overall, these results suggest stronger and more consistent association signals for TSWV symptom severity than for viral accumulation measured by DAS-ELISA, although both traits showed evidence of relevant marker–trait associations.

QQ-plots for TSWV mean symptoms for the three GWAS models tested.

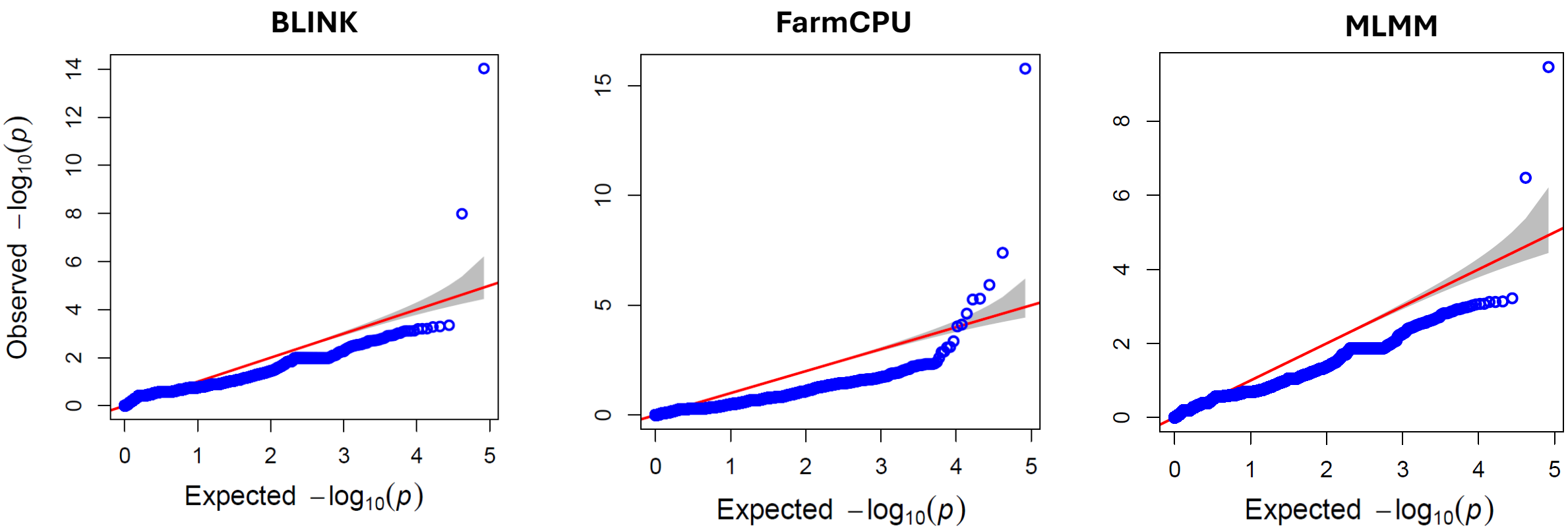


QQ-plots for TSWV mean DAS-ELISA values for the three GWAS models tested.

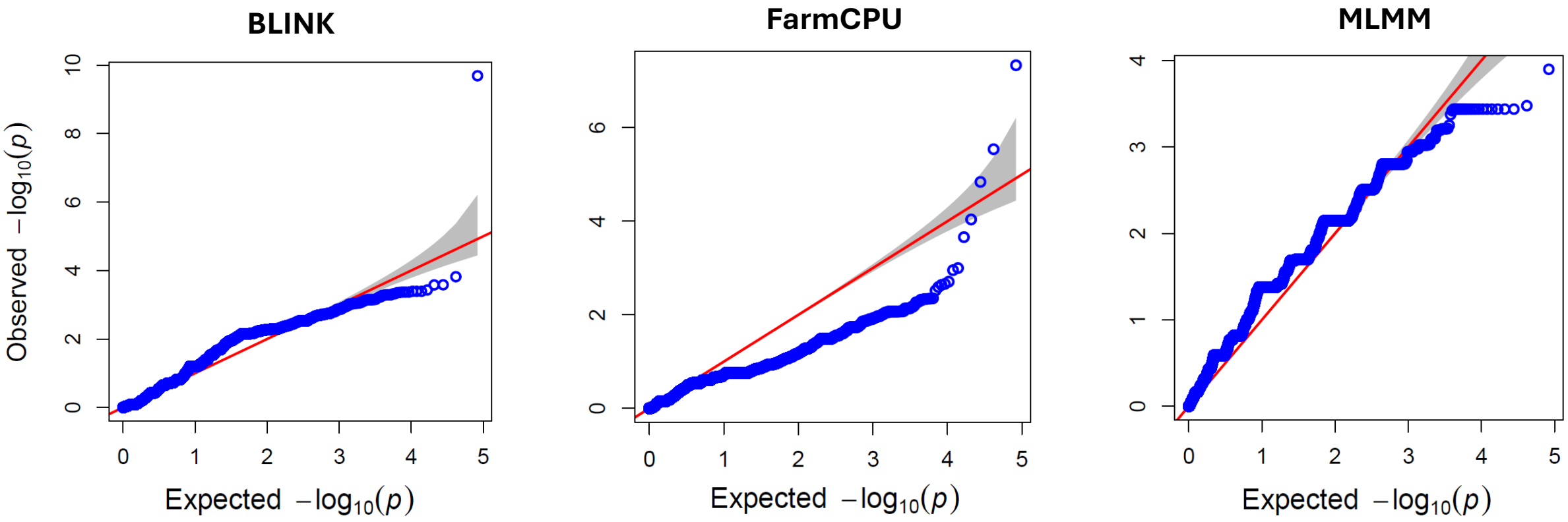


QQ plots for ToMV mean symptoms showed that the three GWAS models adequately controlled the overall distribution of association signals, with most markers following or remaining below the expected distribution. However, a clear upper-tail deviation was observed in all models, indicating the presence of strong marker–trait associations for ToMV symptom severity. This deviation was strongest in FarmCPU and BLINK, which produced the highest observed $-\log_{10}(p)$ values, followed by MLMM. For ToMV mean DAS-ELISA values, MLMM showed a more conservative distribution, with limited deviation from the expected line. In contrast, BLINK and FarmCPU displayed clearer upper-tail deviations, suggesting stronger association signals for viral accumulation. Overall, these results indicate that ToMV symptom severity generated stronger and more consistent association signals than DAS-ELISA values, although both traits showed evidence of relevant marker–trait associations.

QQ-plots for ToMV mean symptoms for the three GWAS models tested.



QQ-plots for ToMV mean symptoms for the three GWAS models tested.



QQ plots for FOL mean symptoms showed no strong association signals across the three GWAS models, indicating adequate control of population structure and relatedness. MLMM displayed slightly stronger association signals than BLINK and FarmCPU, with higher observed $-\log_{10}(p)$ values in the upper tail. In contrast, BLINK and FarmCPU showed nearly identical and more conservative distributions, with most markers remaining below the expected significance line. Overall, these results suggest the absence of major-effect loci for FOL symptom severity.

QQ-plots for FOL mean symptoms for the three GWAS models tested.