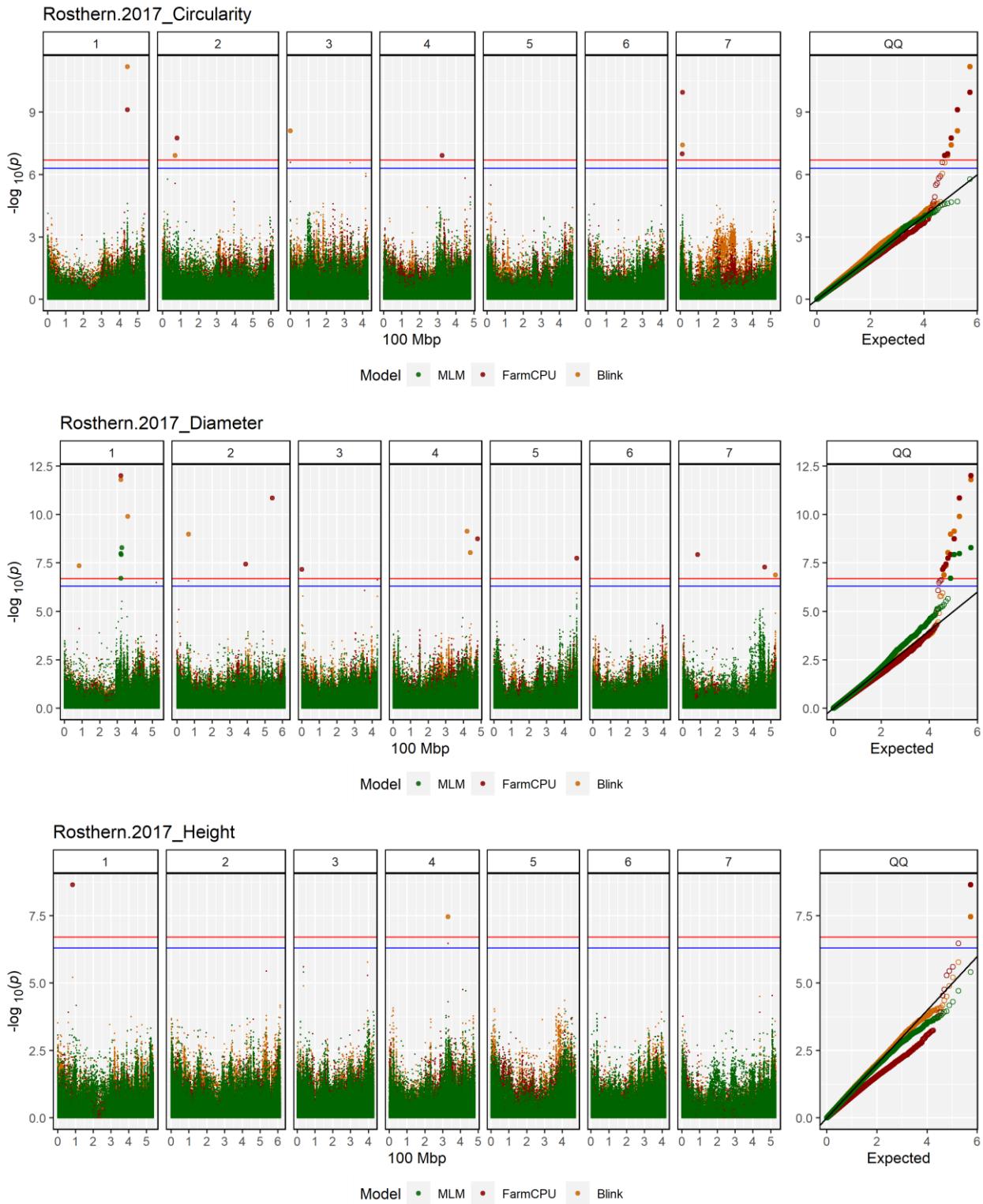


Appendix E

Manhattan plots from GWAS without covariates



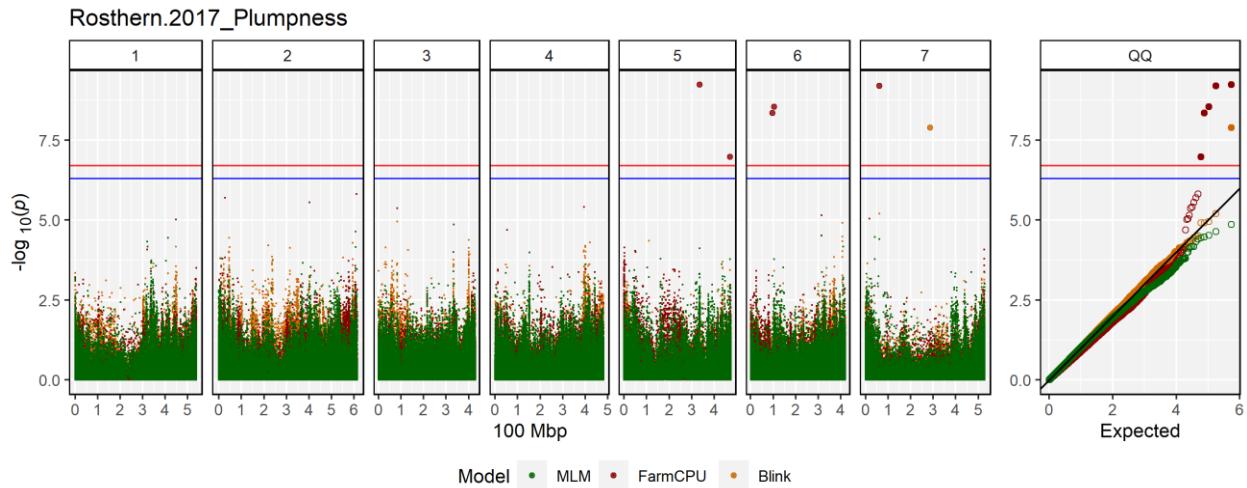
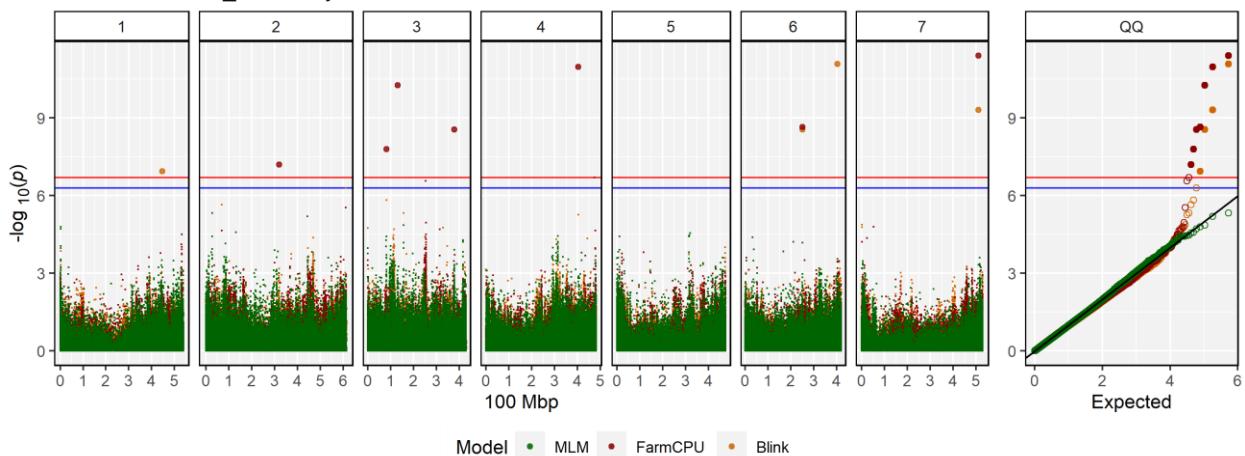
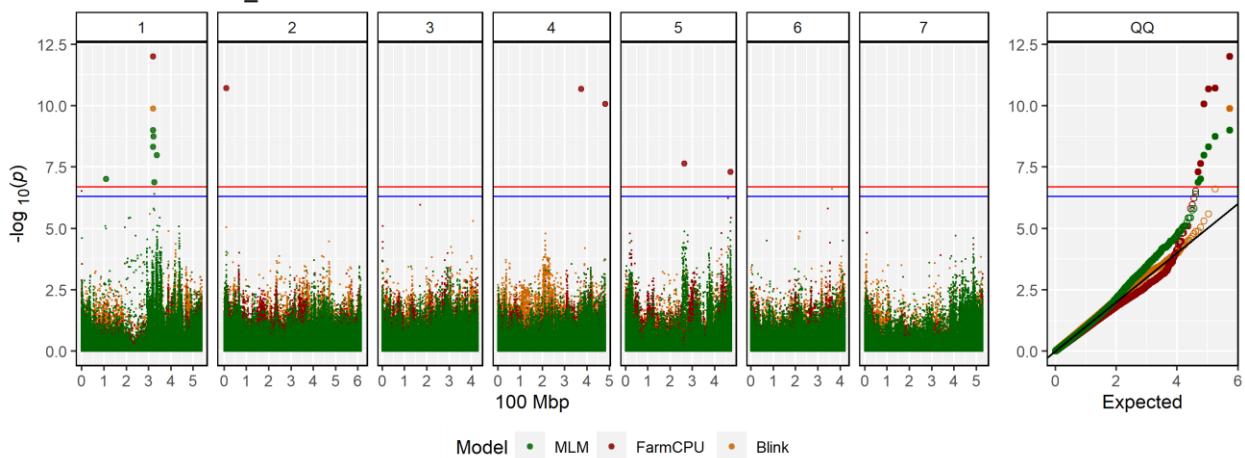


Figure E.1.1 Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using diameter, circularity, height, and plumpness of 324 genotypes grown in the field in Rosthern 2017. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold $[-\log_{10}(P) > 6.7]$ and the red line across all chromosomes indicates a suggested threshold $[-\log_{10}(P) > 6.3]$. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

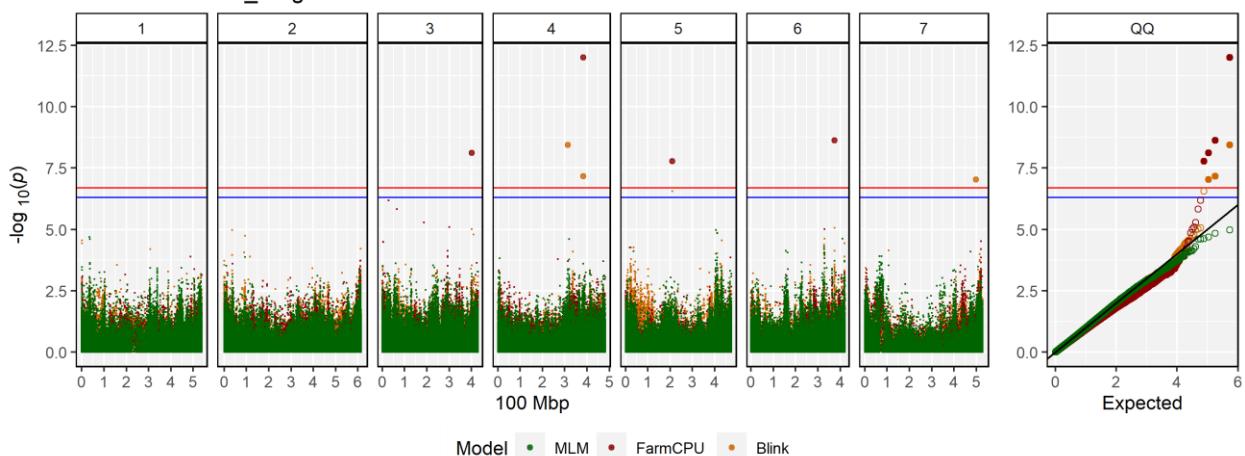
Sutherland.2017_Circularity



Sutherland.2017_Diameter



Sutherland.2017_Height



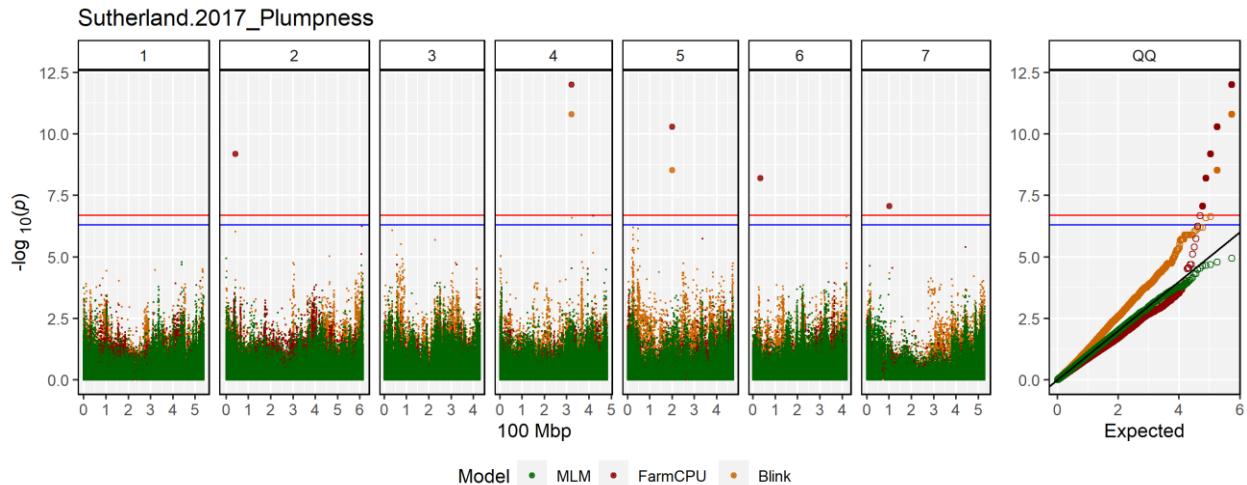
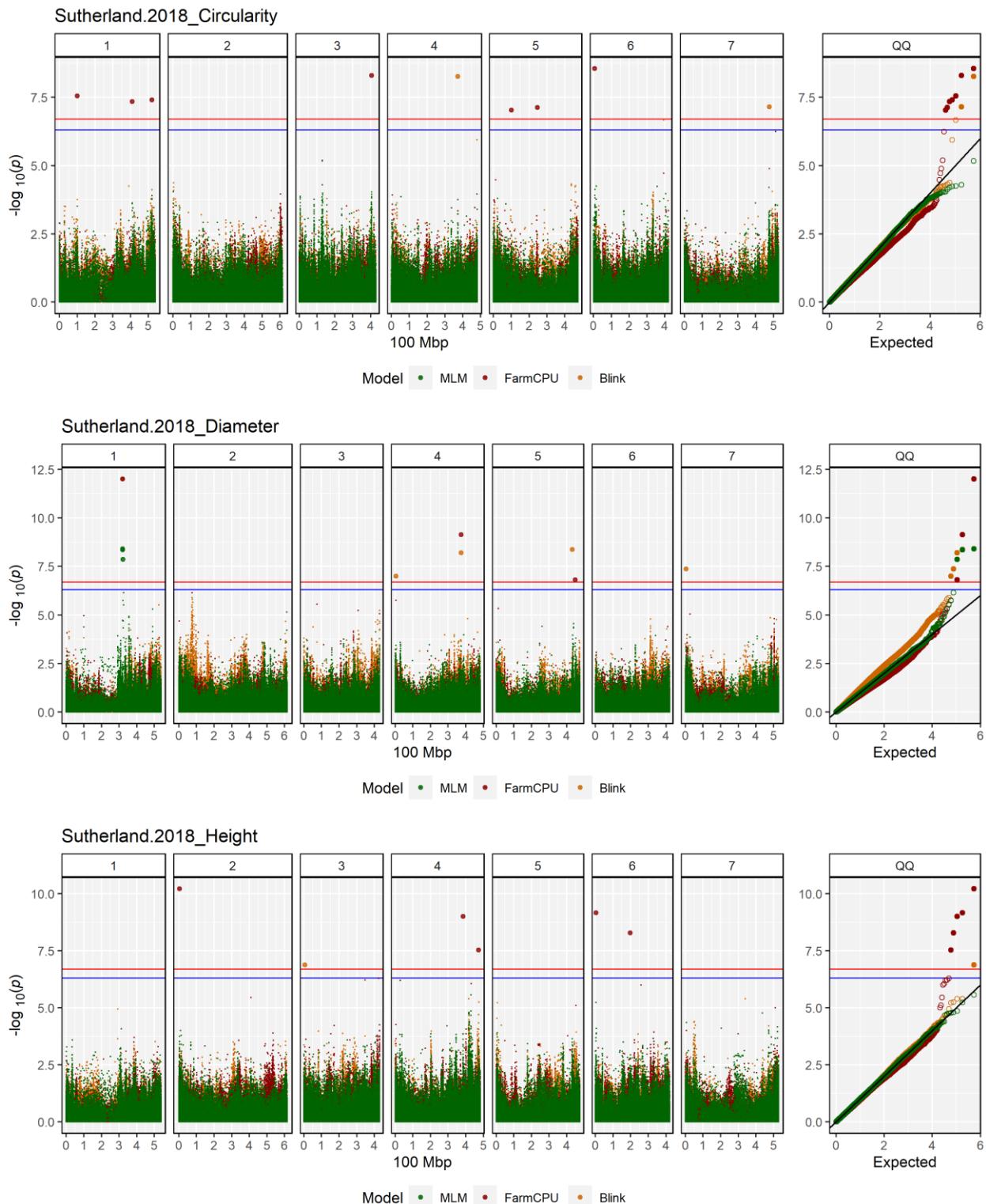


Figure E.1.2 Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using diameter, circularity, height, and plumpness of 324 genotypes grown in the field in Sutherland 2017. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold $[-\log_{10}(P) > 6.7]$ and the red line across all chromosomes indicates a suggested threshold $[-\log_{10}(P) > 6.3]$. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



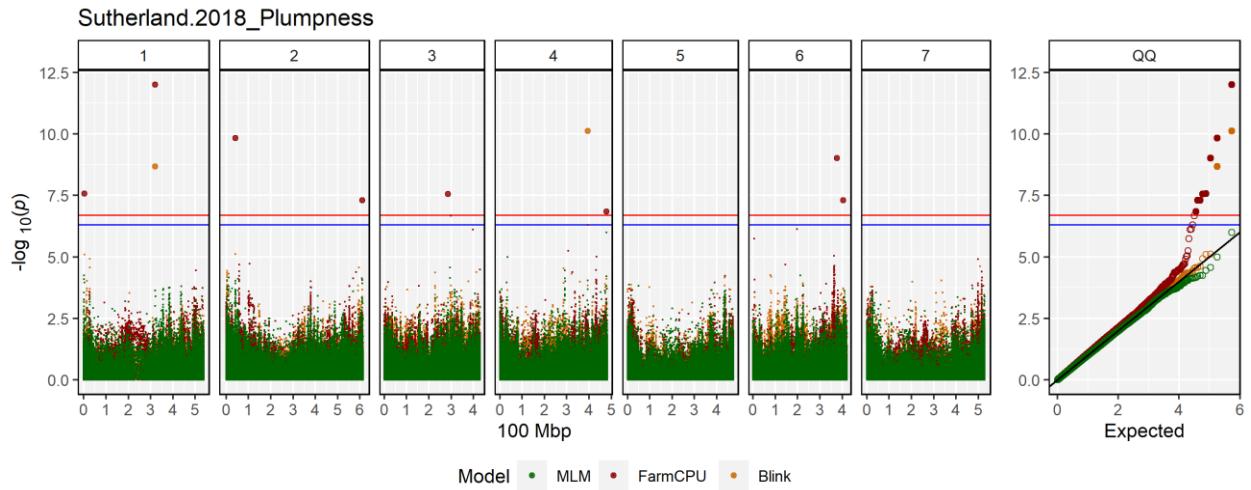
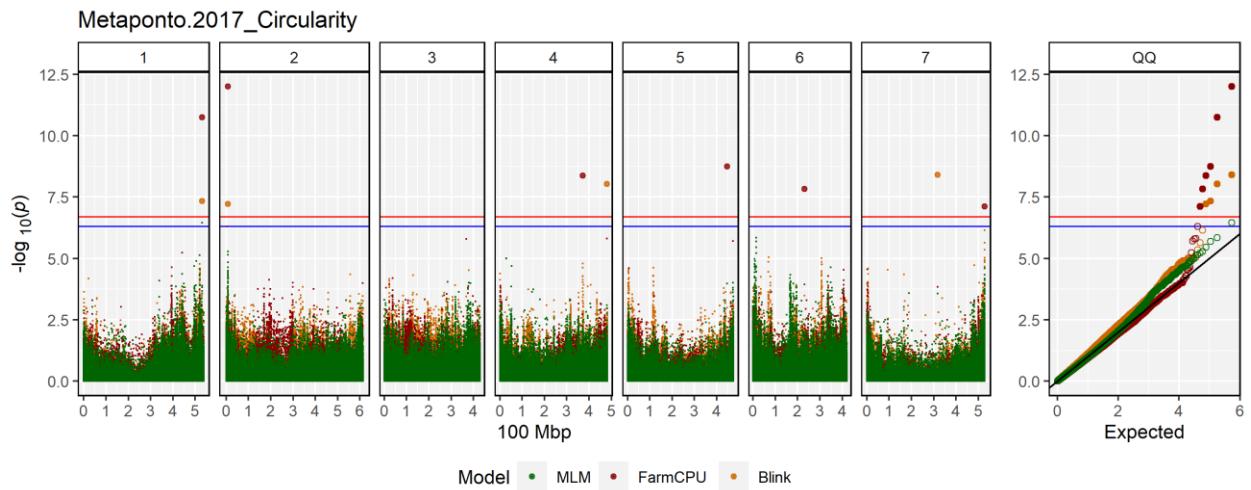


Figure E.1.3 Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using diameter, circularity, height, and plumpness of 324 genotypes grown in the field in Sutherland 2018. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



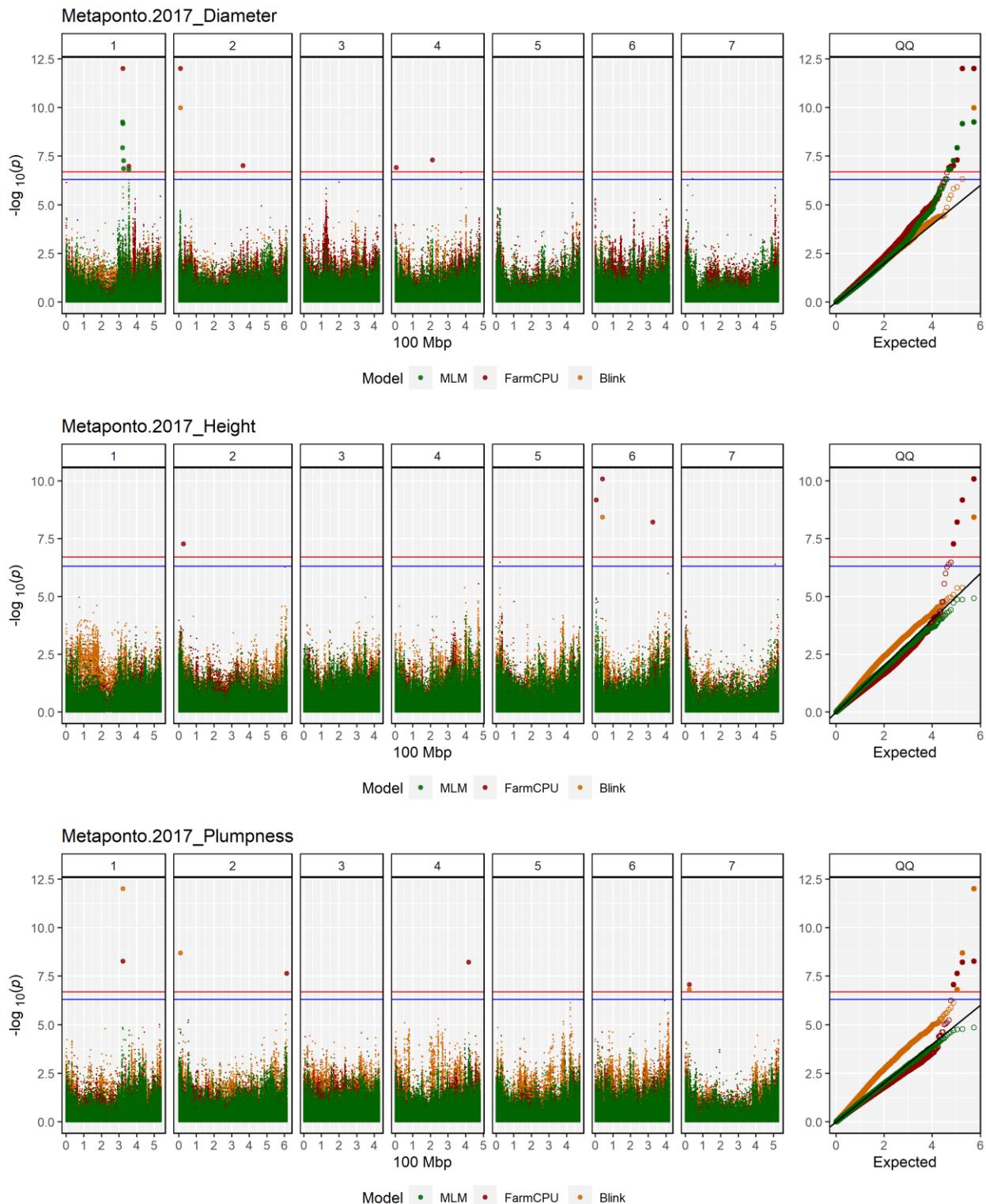
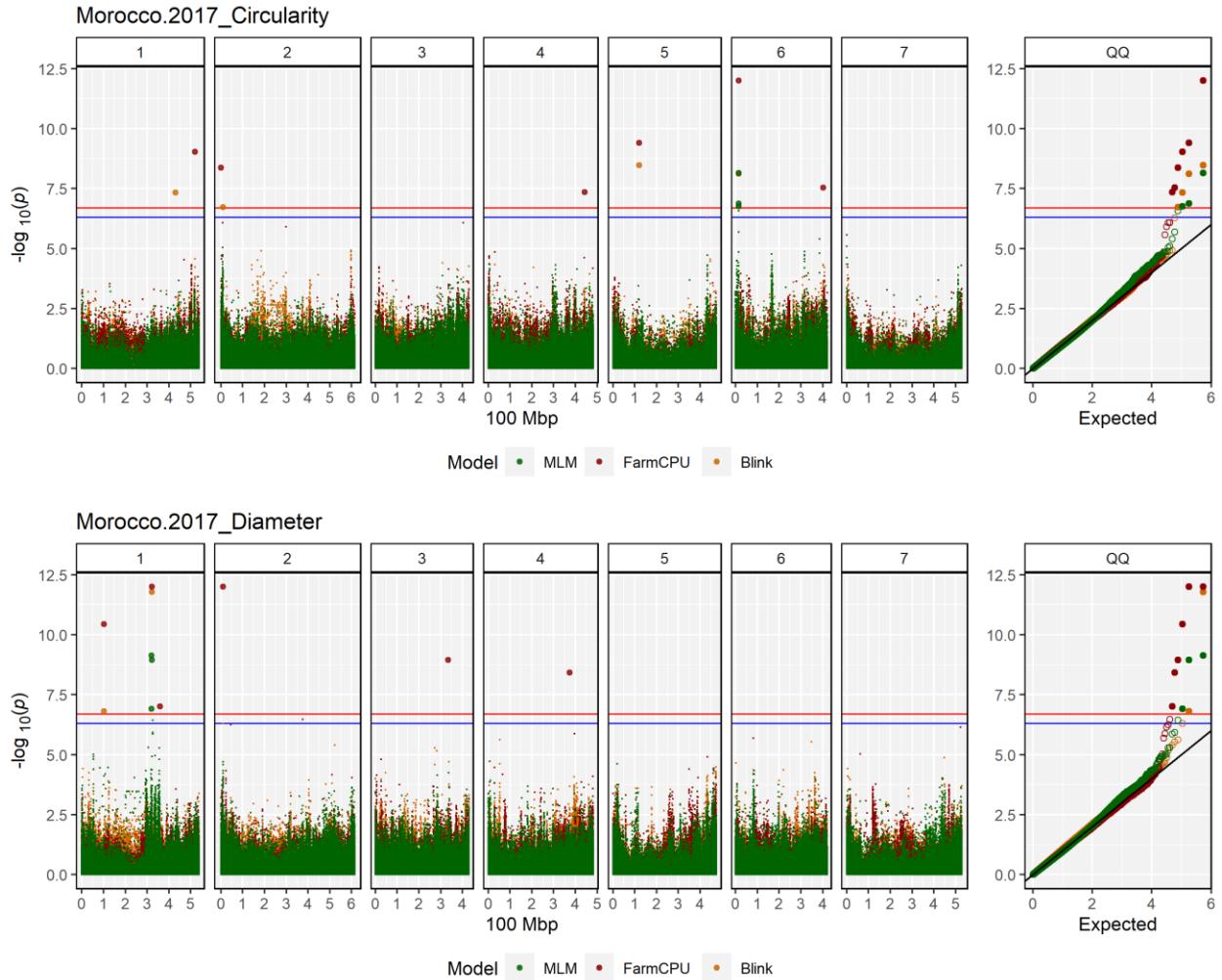


Figure E.1.4 Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using diameter, circularity, height, and plumpness of 324 genotypes grown in the field in Metaponto 2017. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-

values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



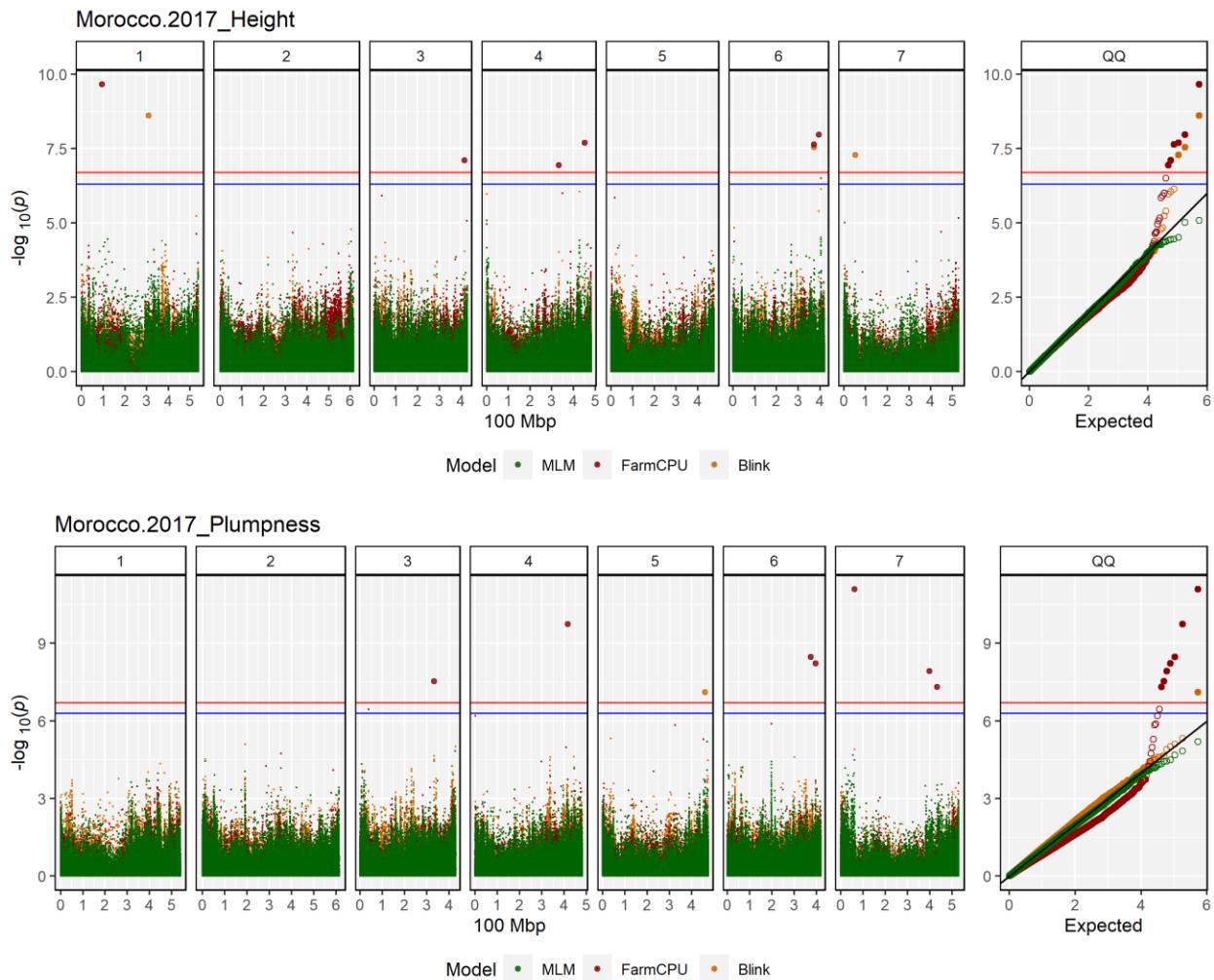
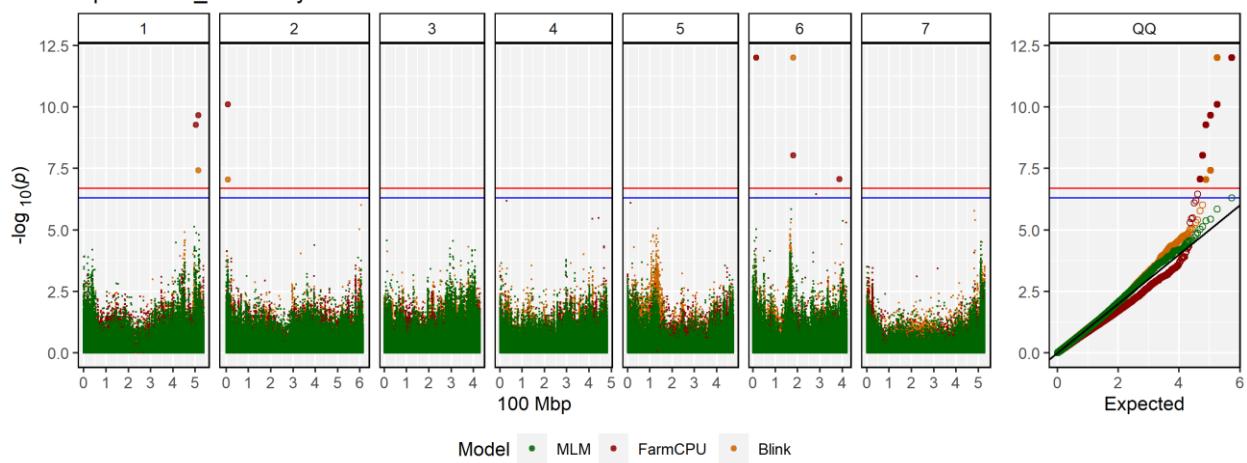
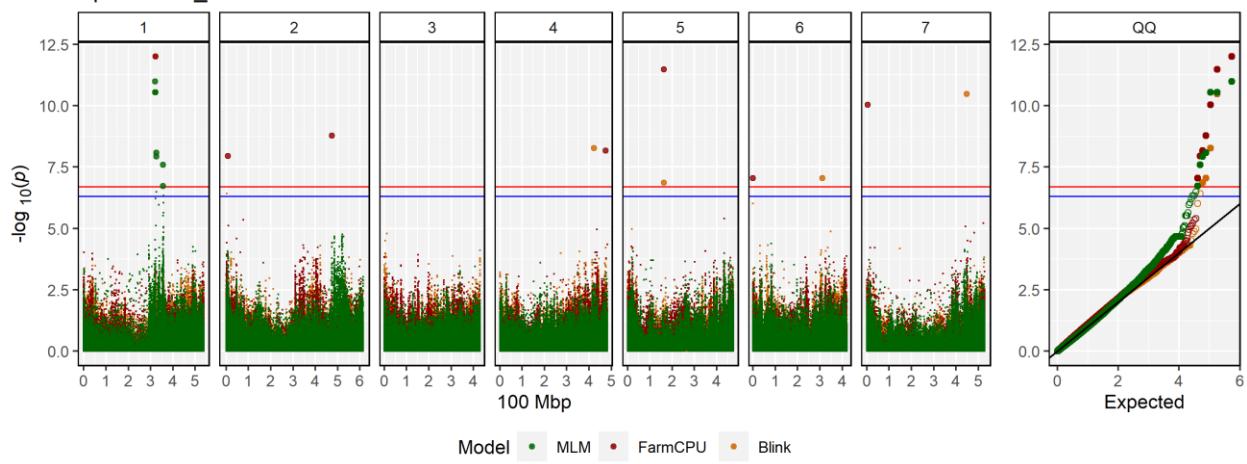


Figure E.1.5 Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using diameter, circularity, height, and plumpness of 324 genotypes grown in the field in Morocco 2017. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

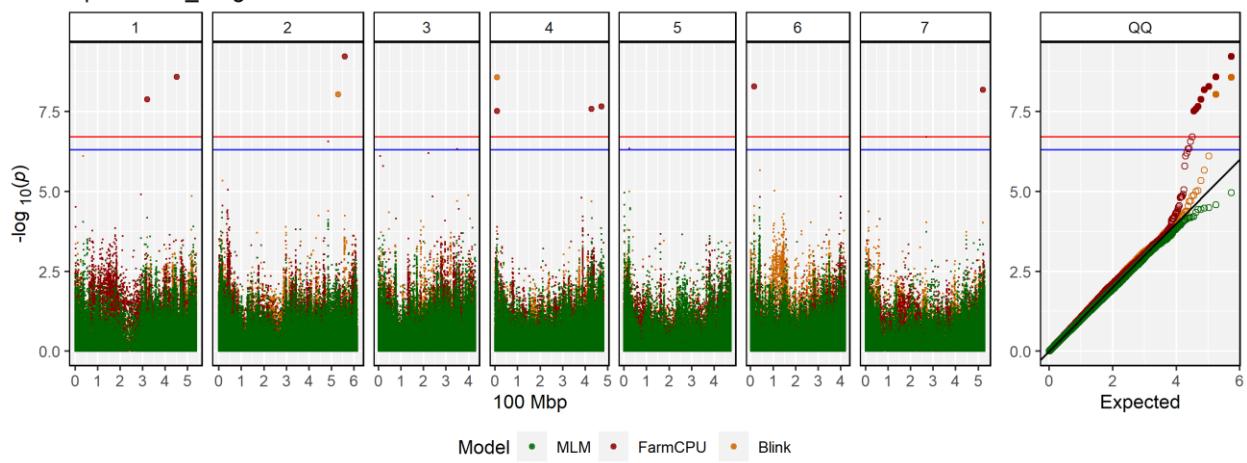
Spain.2017_Circularity



Spain.2017_Diameter



Spain.2017_Height



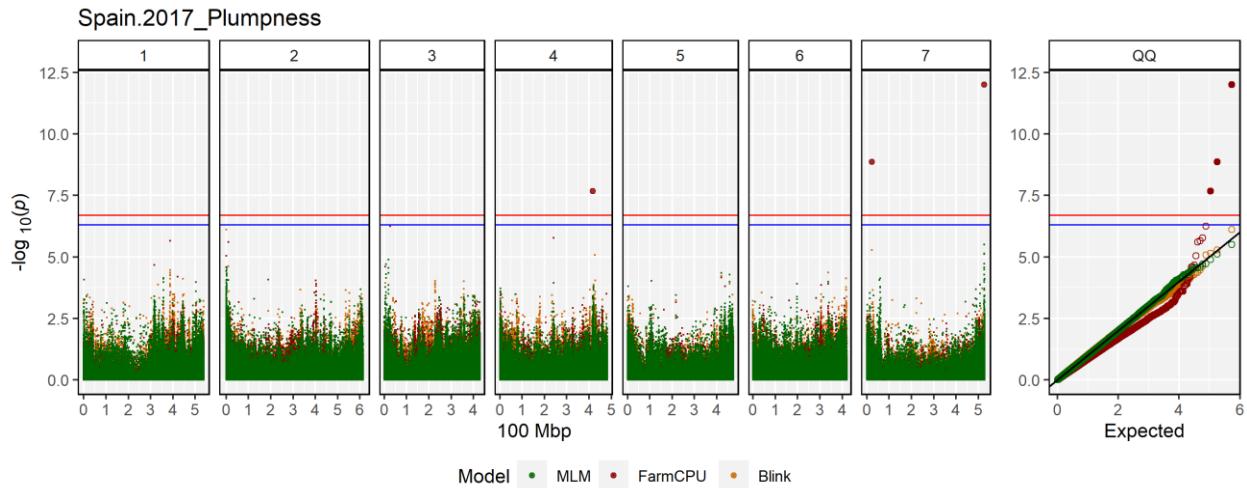
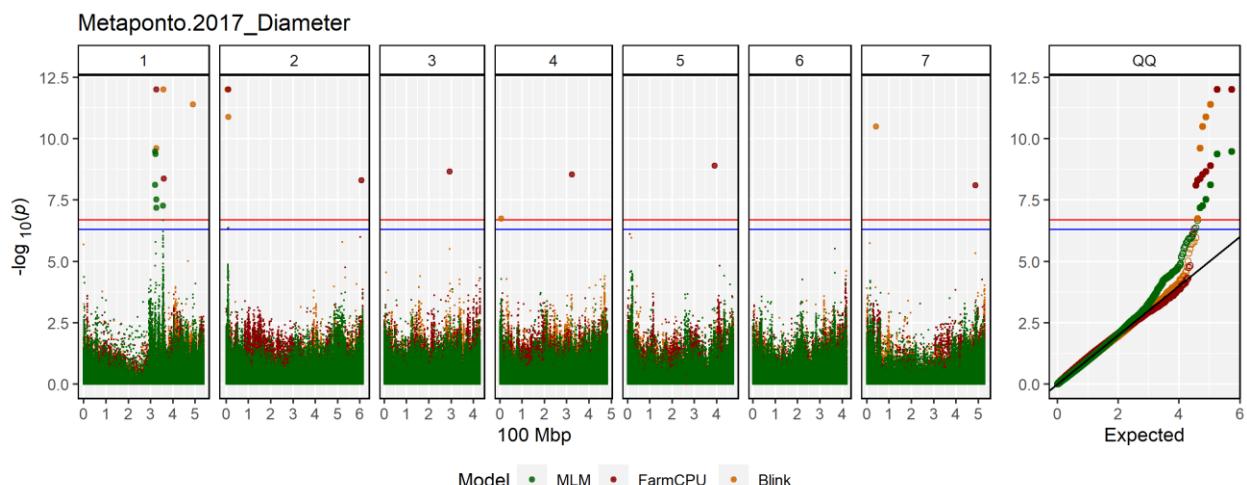


Figure E.1.6 Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using diameter, circularity, height, and plumpness of 324 genotypes grown in the field in Spain 2017. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold $[-\log_{10}(P) > 6.7]$ and the red line across all chromosomes indicates a suggested threshold $[-\log_{10}(P) > 6.3]$. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

Appendix F

Manhattan plots from GWAS with circularity as covariate



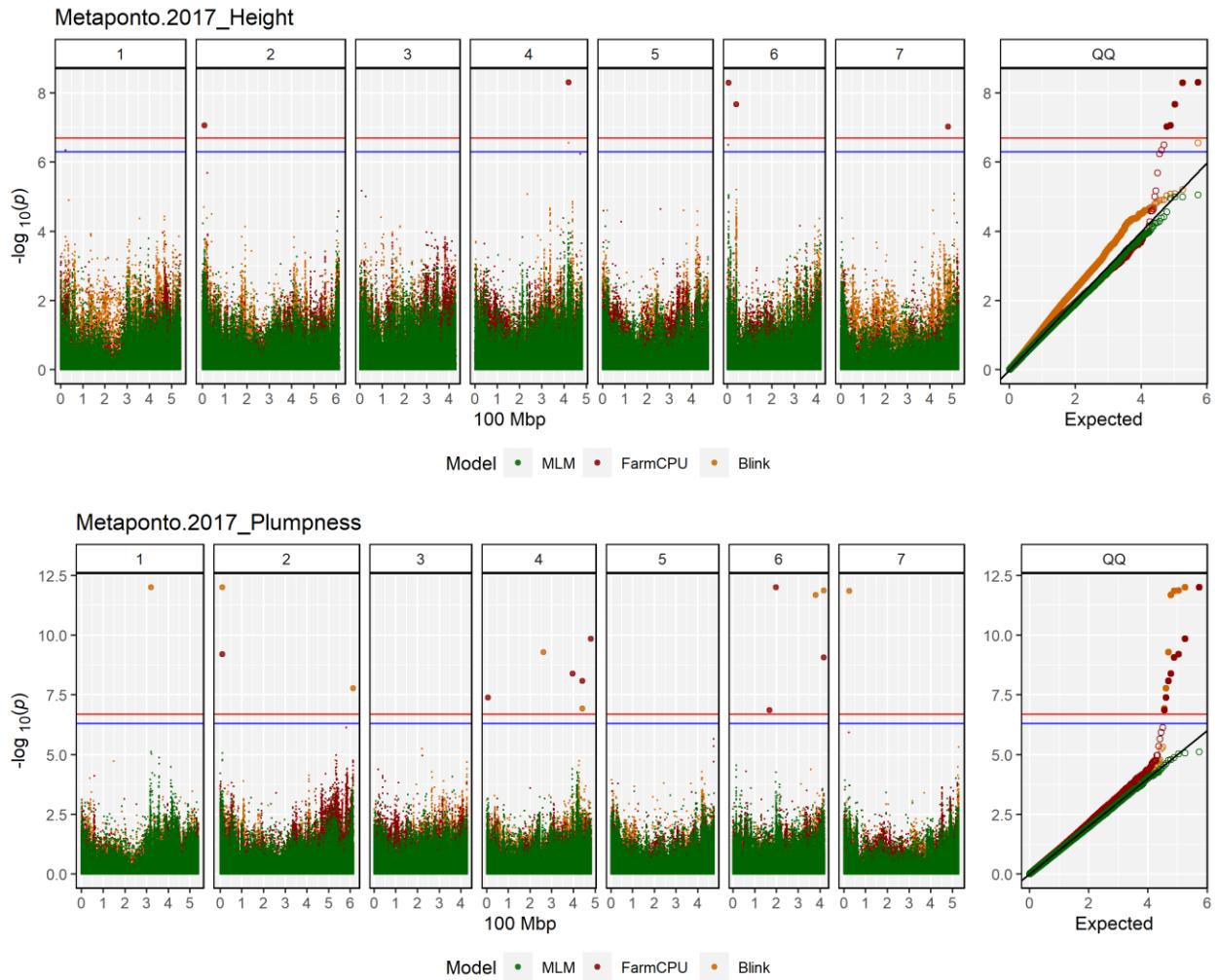


Figure F.1 Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using diameter, height, and plumpness of 324 genotypes grown in the field in Metaponto 2017 with circularity used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P)>6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P)>6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

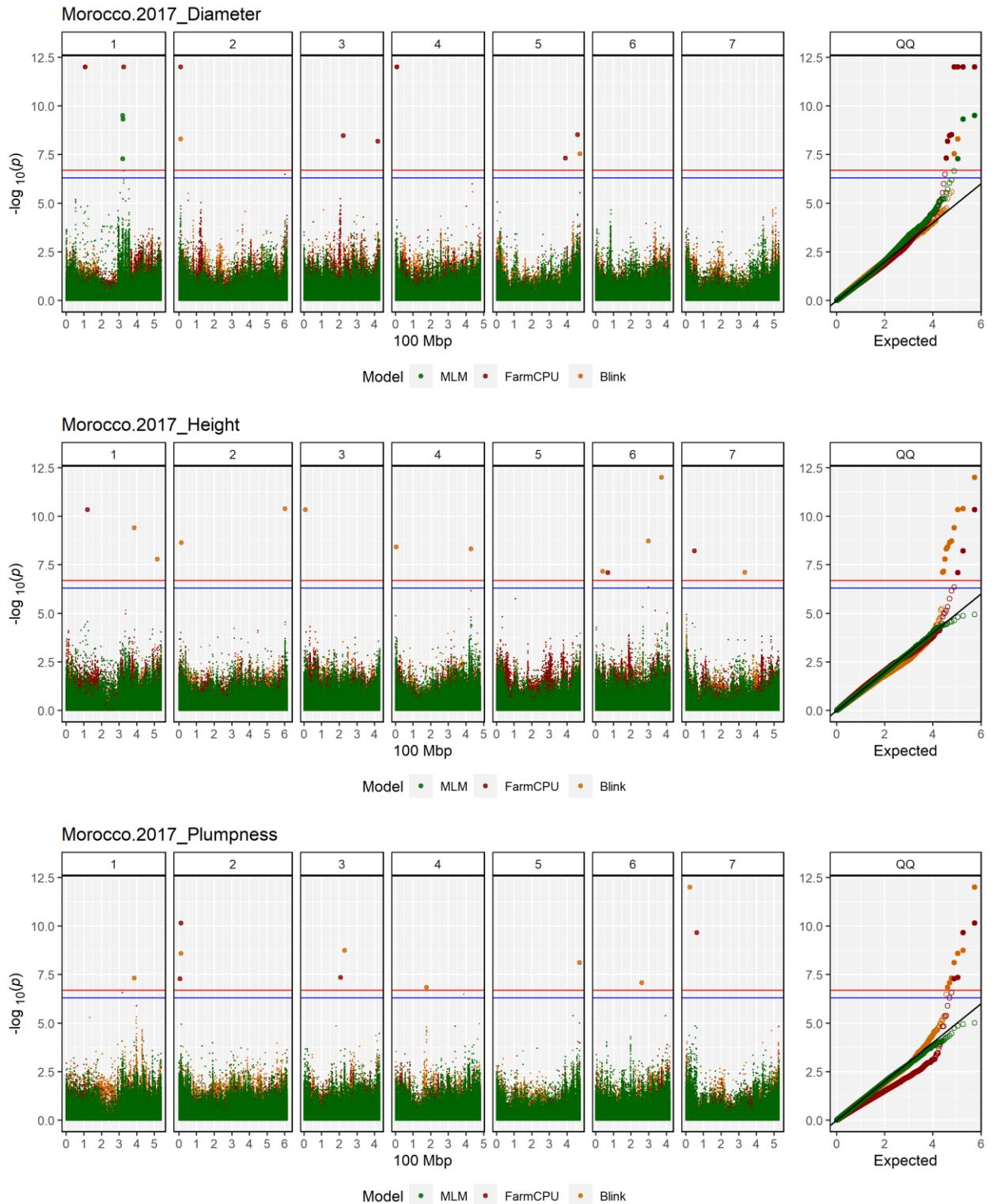
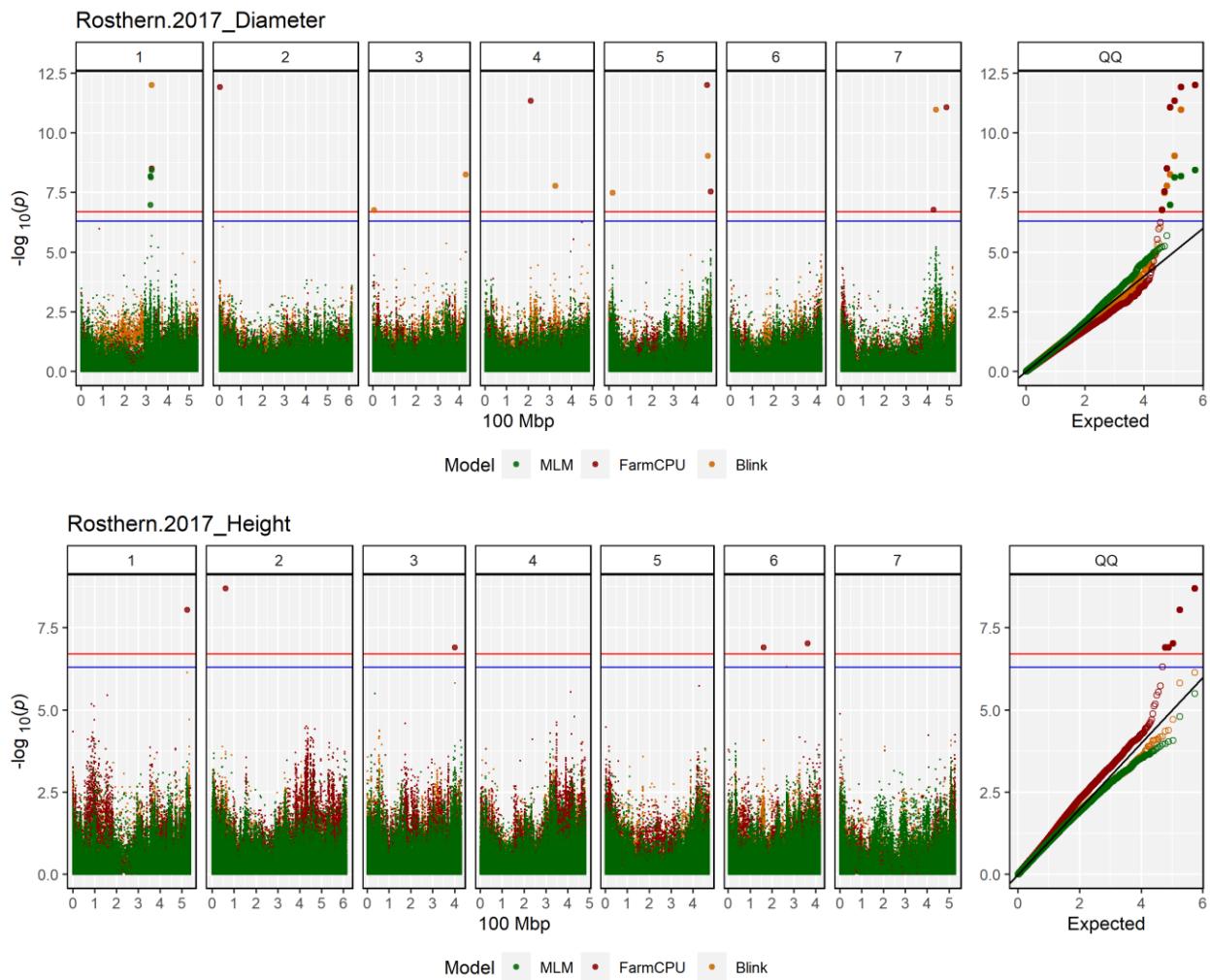


Figure F.2. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using diameter, height, and plumpness of 324 genotypes grown in the field in Morocco 2017 with circularity used as a covariate. The x axis represents lentil chromosomes, and the Y

axis is -log₁₀ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log₁₀(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log₁₀(P)>6.3]. The x axis on the Q-Q plots is the expected -log₁₀ of p-values and the y axis is the observed -log₁₀ of p-values.



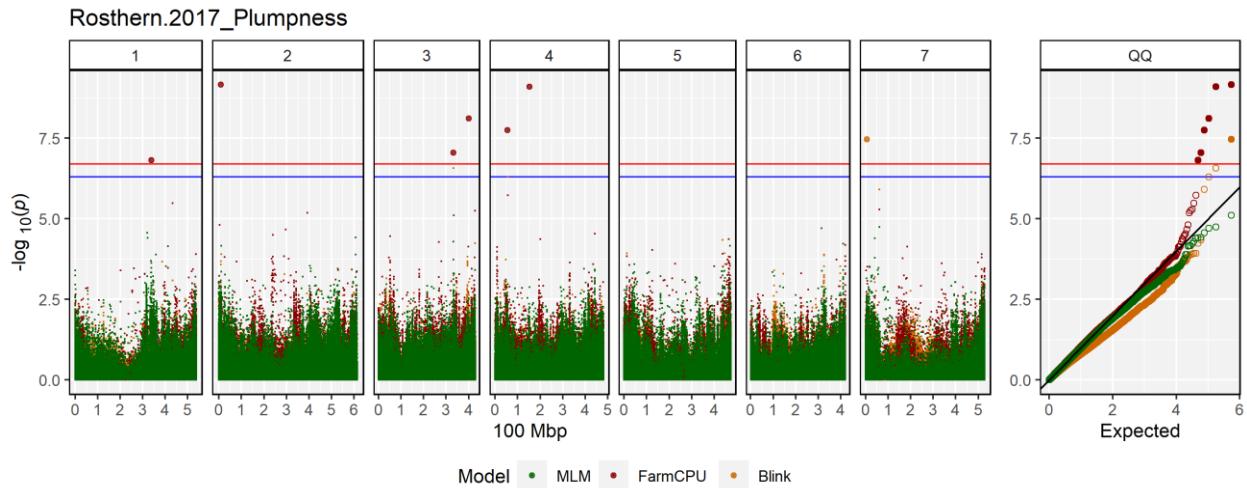
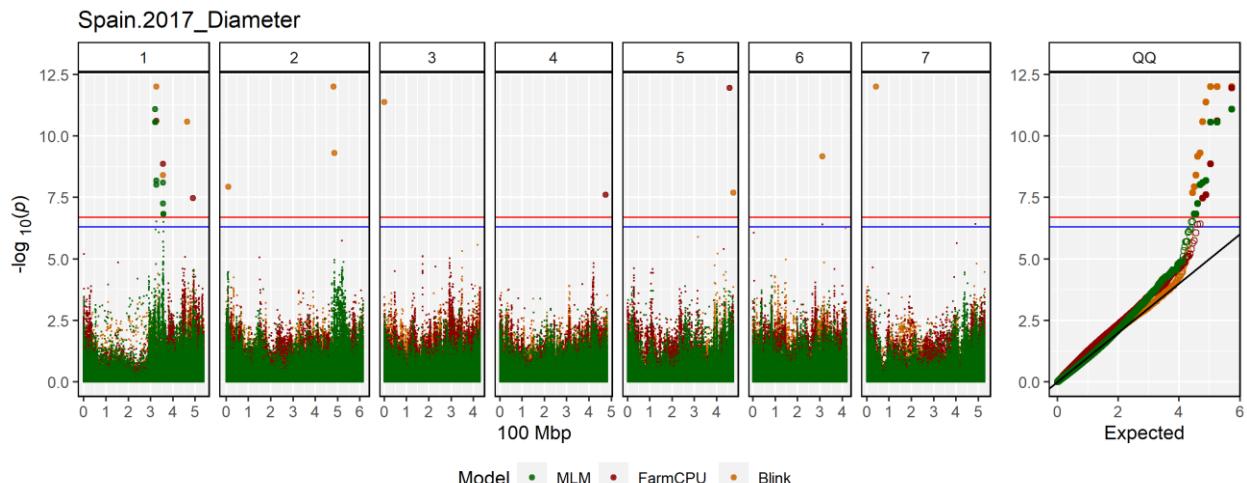


Figure F.3. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using diameter, height, and plumpness of 324 genotypes grown in the field in Rosthern 2017 with circularity used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P)>6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P)>6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



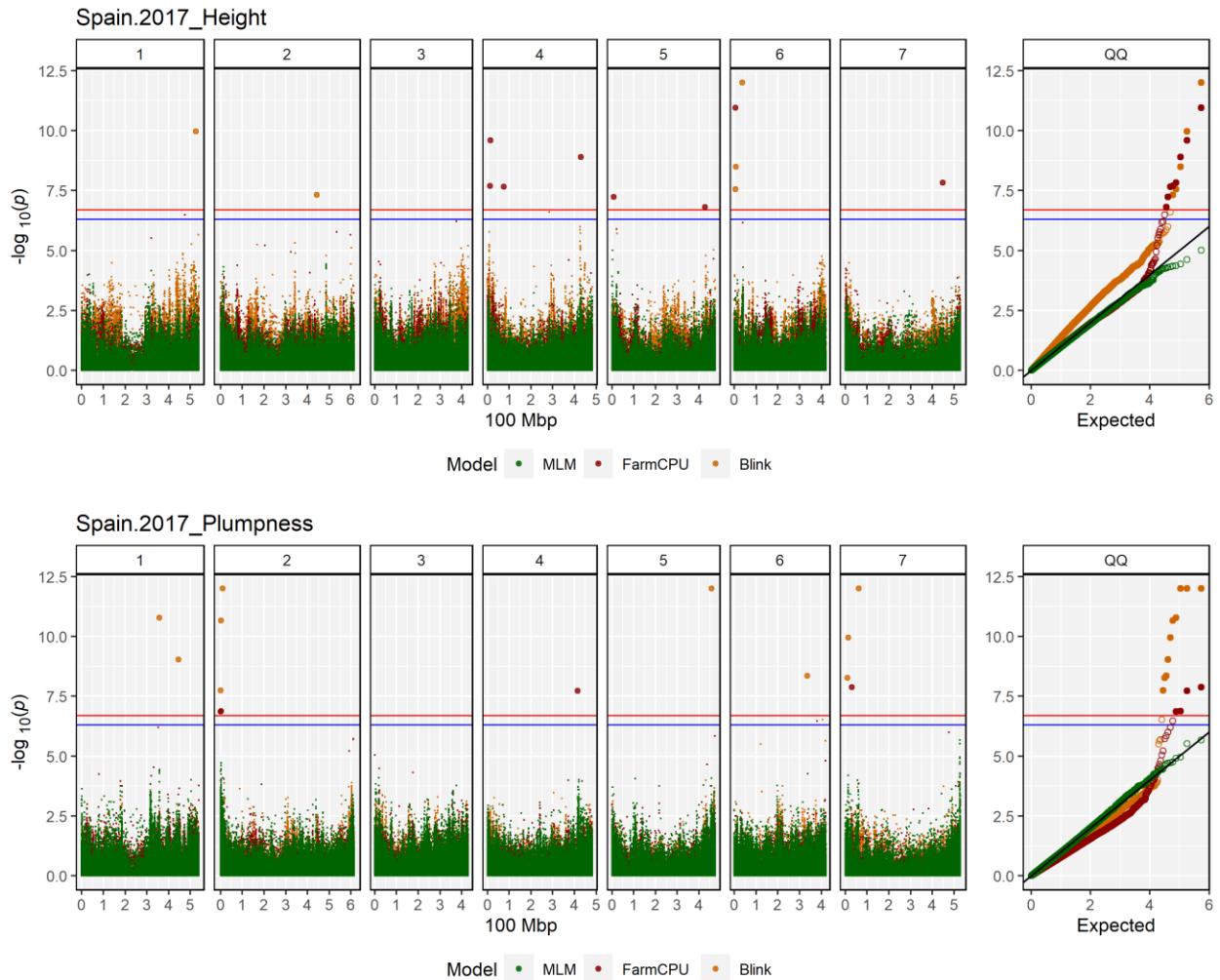


Figure F.4. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using diameter, height, and plumpness of 324 genotypes grown in the field in Spain 2017 with circularity used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

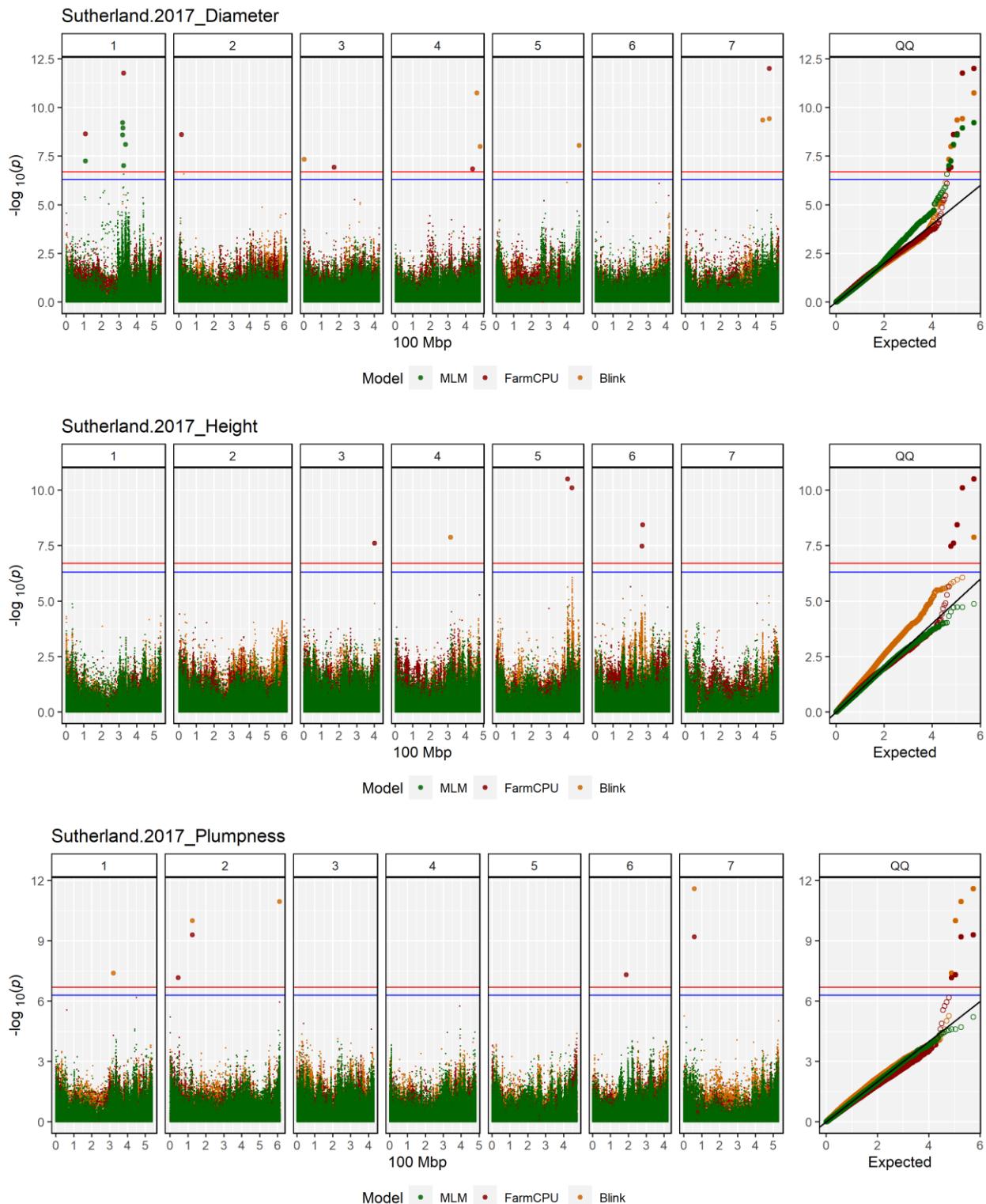
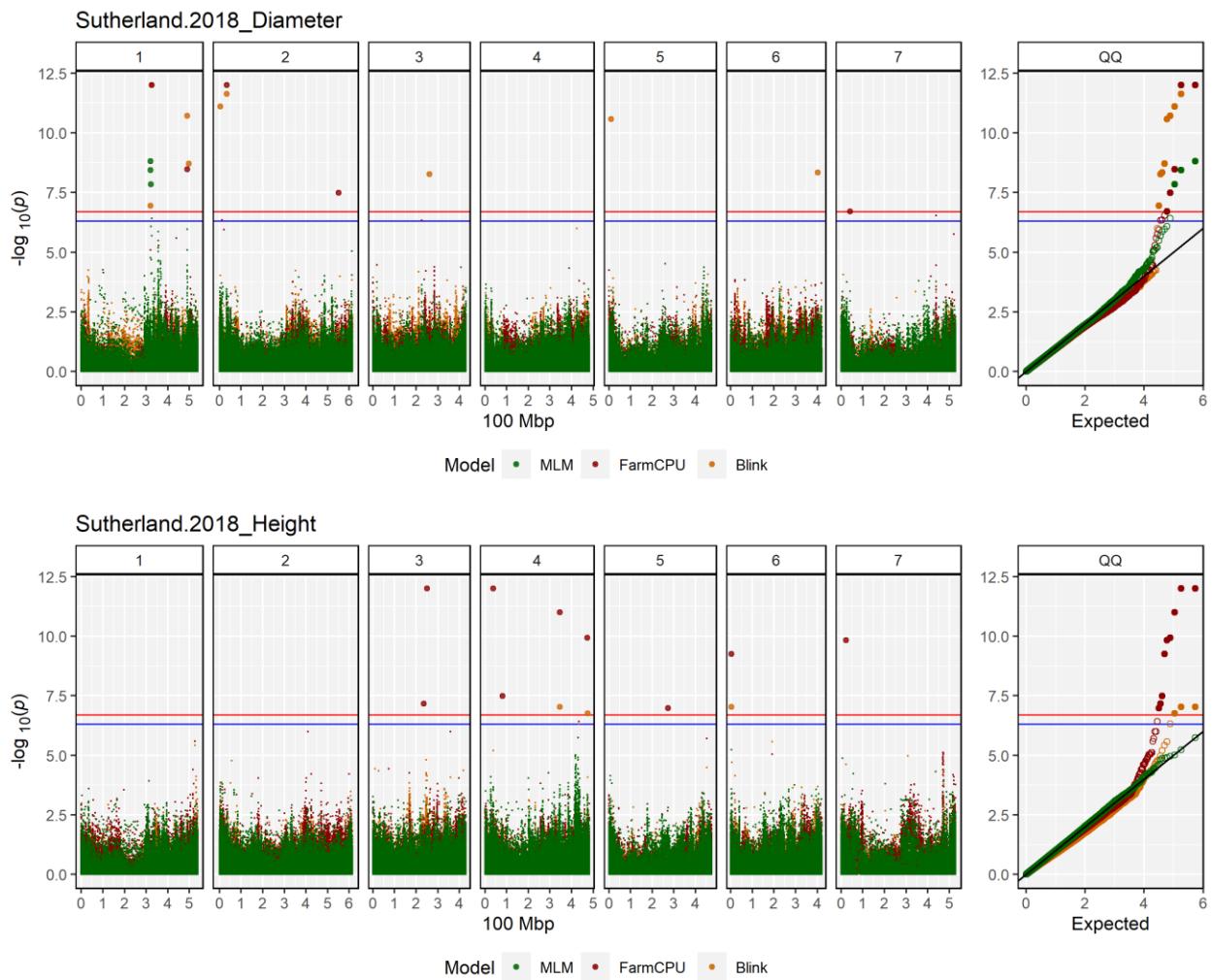


Figure F.5. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using diameter, height, and plumpness of 324 genotypes grown in the field in Sutherland 2017 with circularity used as a covariate. The x axis represents lentil chromosomes, and the Y

axis is -log₁₀ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log₁₀(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log₁₀(P)>6.3]. The x axis on the Q-Q plots is the expected -log₁₀ of p-values and the y axis is the observed -log₁₀ of p-values.



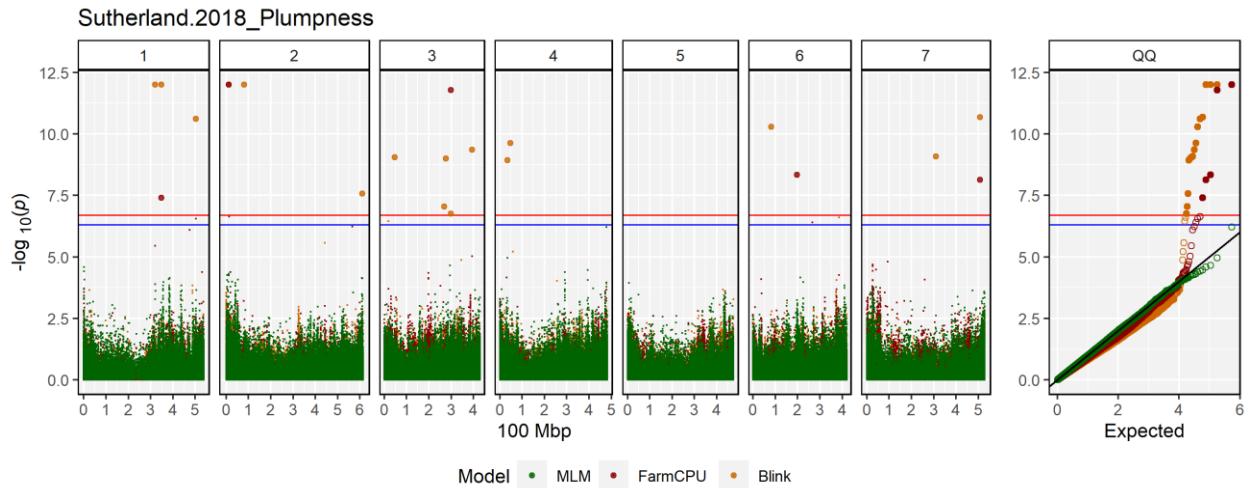
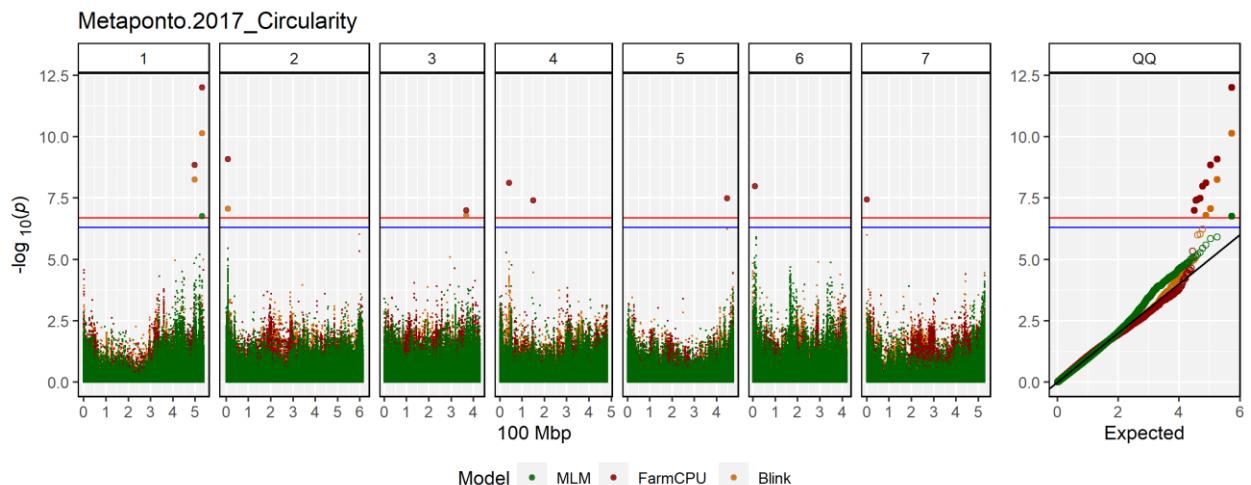


Figure F.6. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using diameter, height, and plumpness of 324 genotypes grown in the field in Sutherland 2018 with circularity used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

Appendix G

Manhattan plots with diameter as covariate



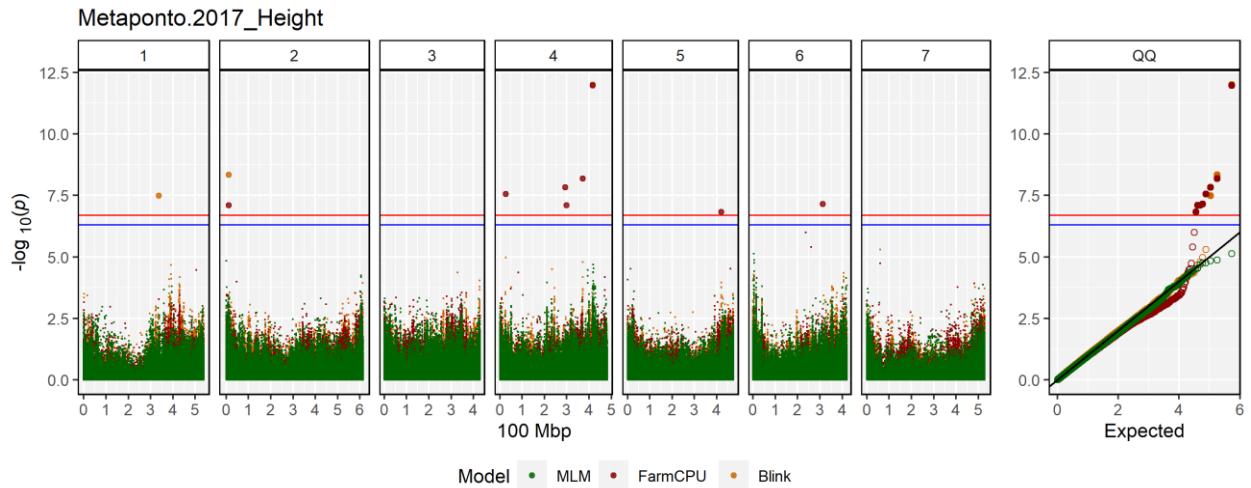
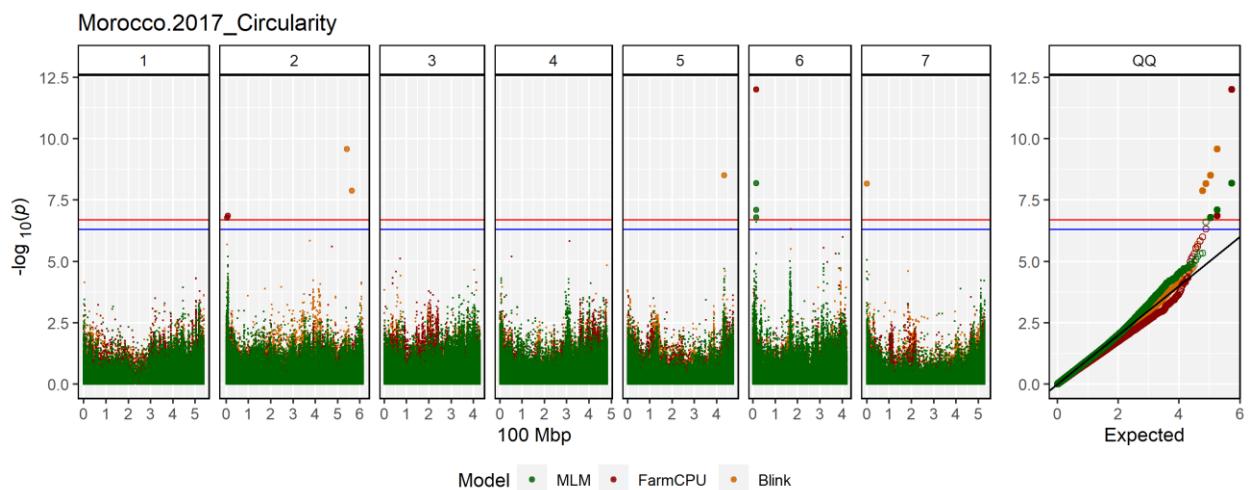


Figure G.1. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity and height of 324 genotypes grown in the field in Metaponto 2017 with diameter used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



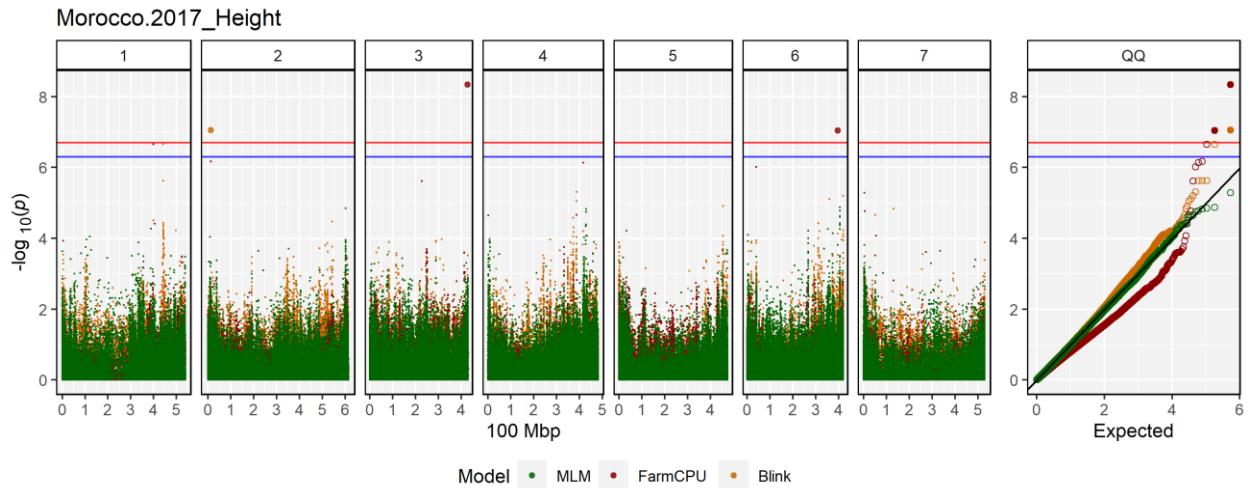


Figure G.2. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity and height of 324 genotypes grown in the field in Morocco 2017 with diameter used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

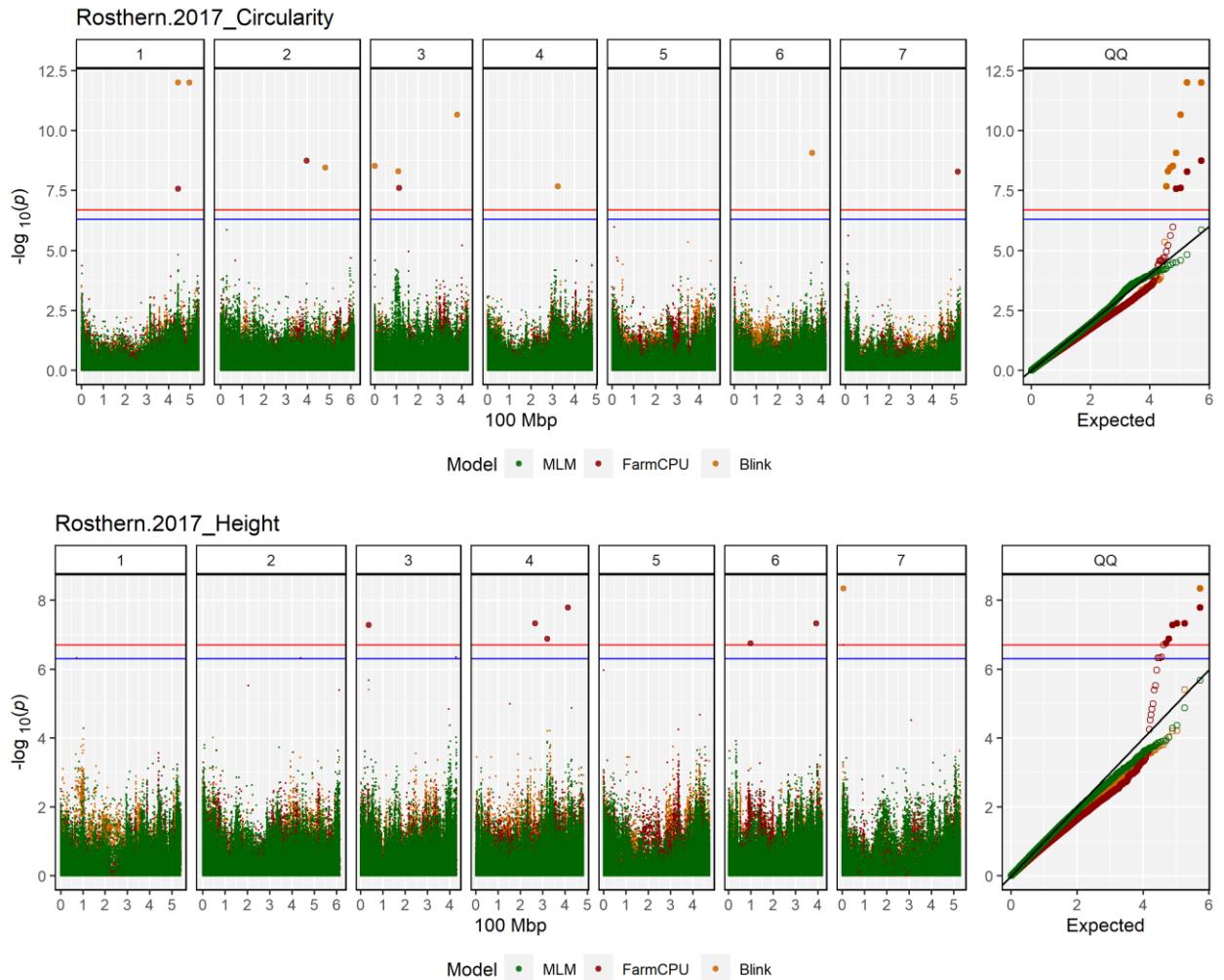


Figure G.3. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity and height of 324 genotypes grown in the field in Rosthern 2017 with diameter used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold $[-\log_{10}(P) > 6.7]$ and the red line across all chromosomes indicates a suggested threshold $[-\log_{10}(P) > 6.3]$. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

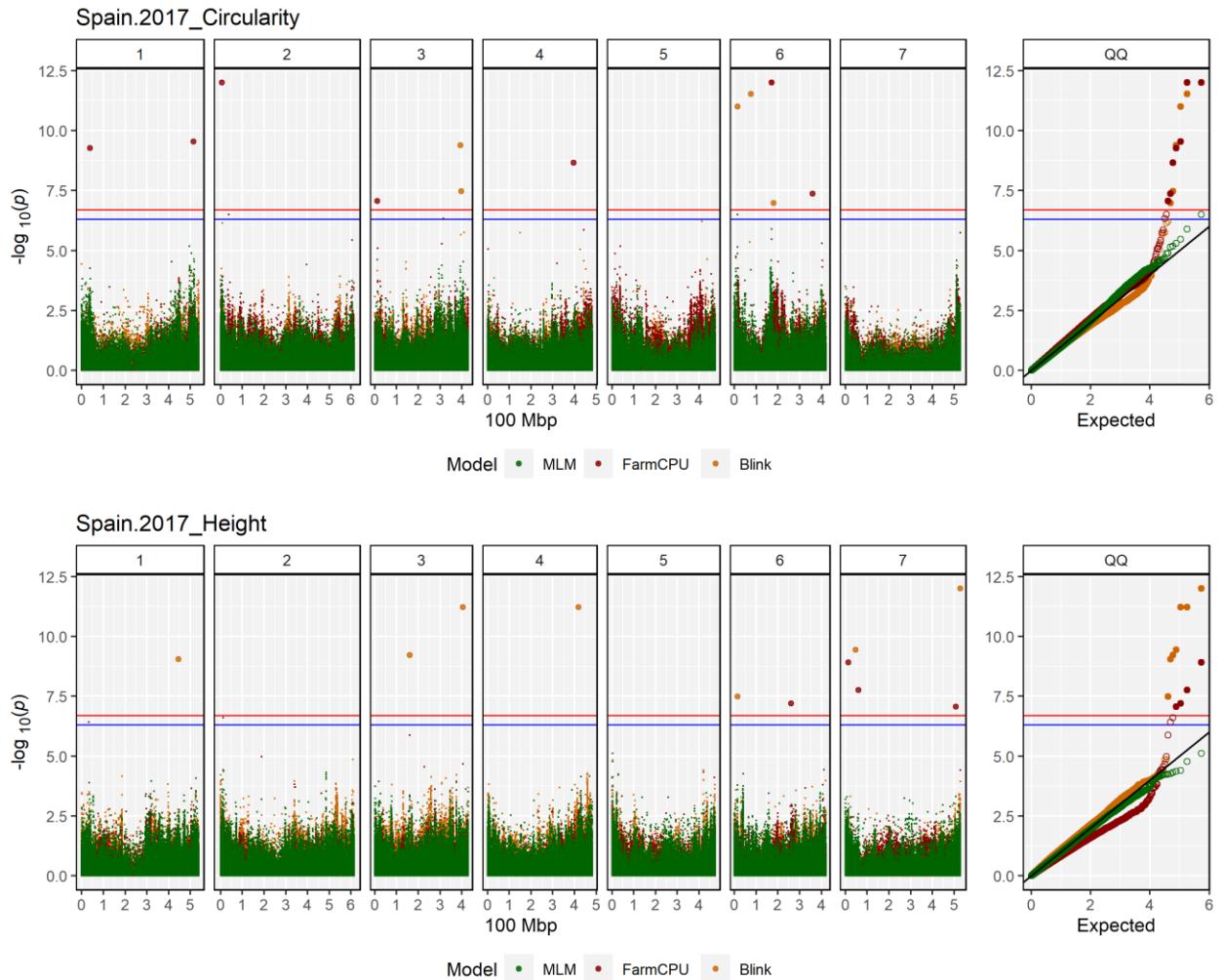


Figure G.4. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity and height of 324 genotypes grown in the field in Spain 2017 with diameter used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

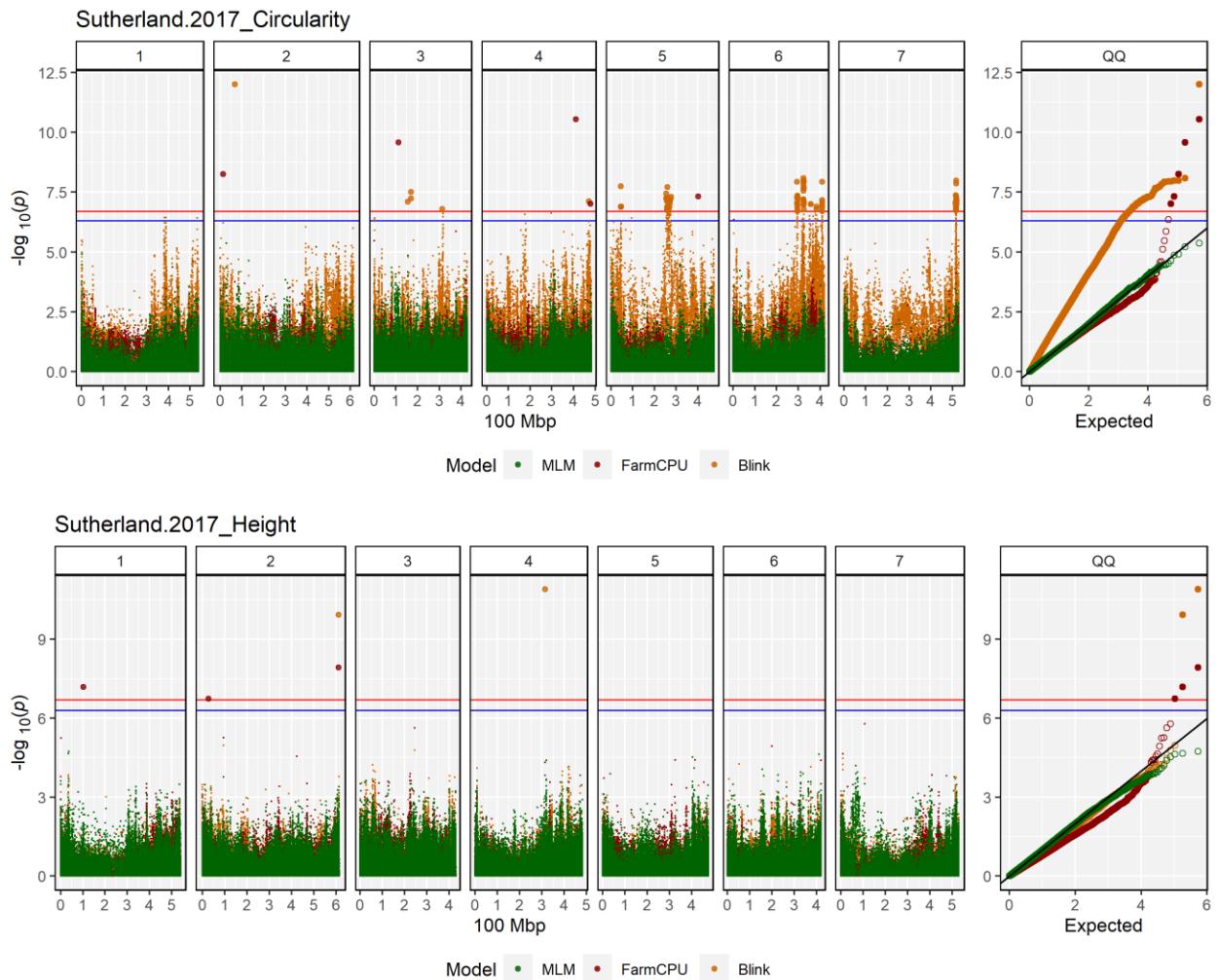


Figure G.5. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity and height of 324 genotypes grown in the field in Sutherland 2017 with diameter used as a covariate. The x axis represents lentil chromosomes, and the Y axis is -log10 of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log10(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log10(P)>6.3]. The x axis on the Q-Q plots is the expected -log10 of p-values and the y axis is the observed -log10 of p-values.

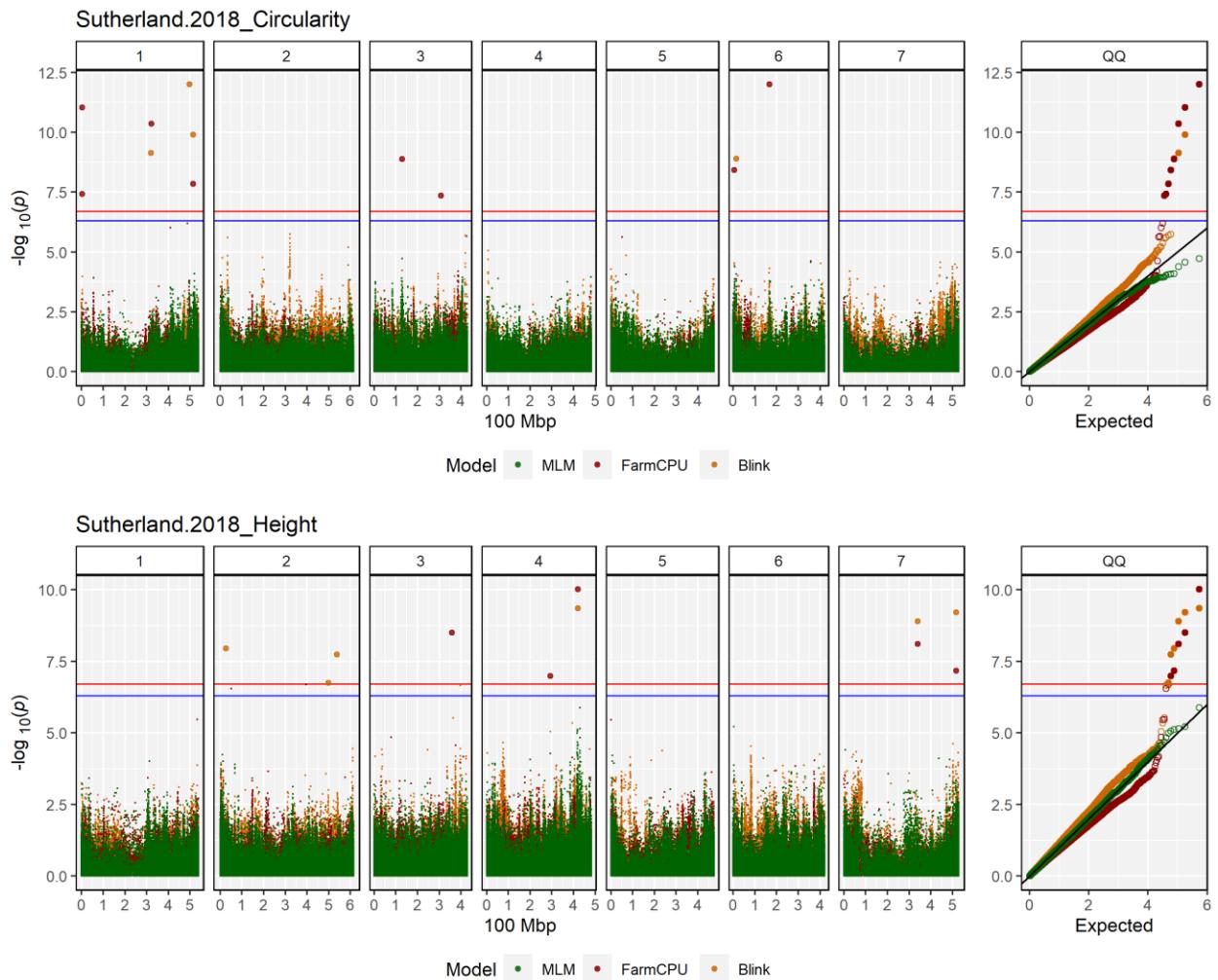


Figure G.6. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity and height of 324 genotypes grown in the field in Sutherland 2017 with diameter used as a covariate. The x axis represents lentil chromosomes, and the Y axis is -log₁₀ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log₁₀(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log₁₀(P)>6.3]. The x axis on the Q-Q plots is the expected -log₁₀ of p-values and the y axis is the observed -log₁₀ of p-values.

Appendix H

Manhattan plots from GWAS with height as covariate

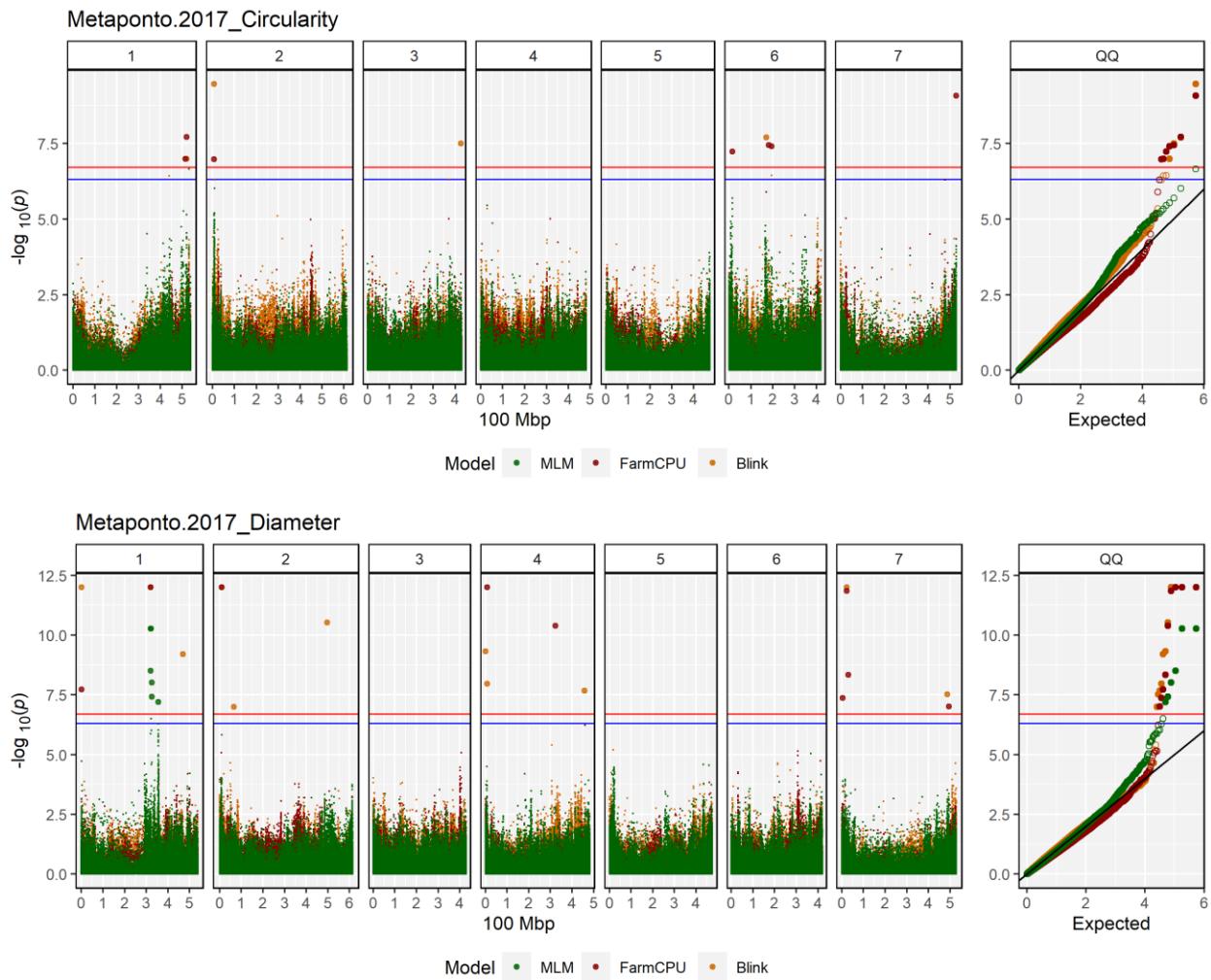


Figure H.1. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity and diameter of 324 genotypes grown in the field in Metaponto 2017 with height used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold $[-\log_{10}(P)>6.7]$ and the red line across all chromosomes indicates a suggested threshold $[-\log_{10}(P)>6.3]$. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

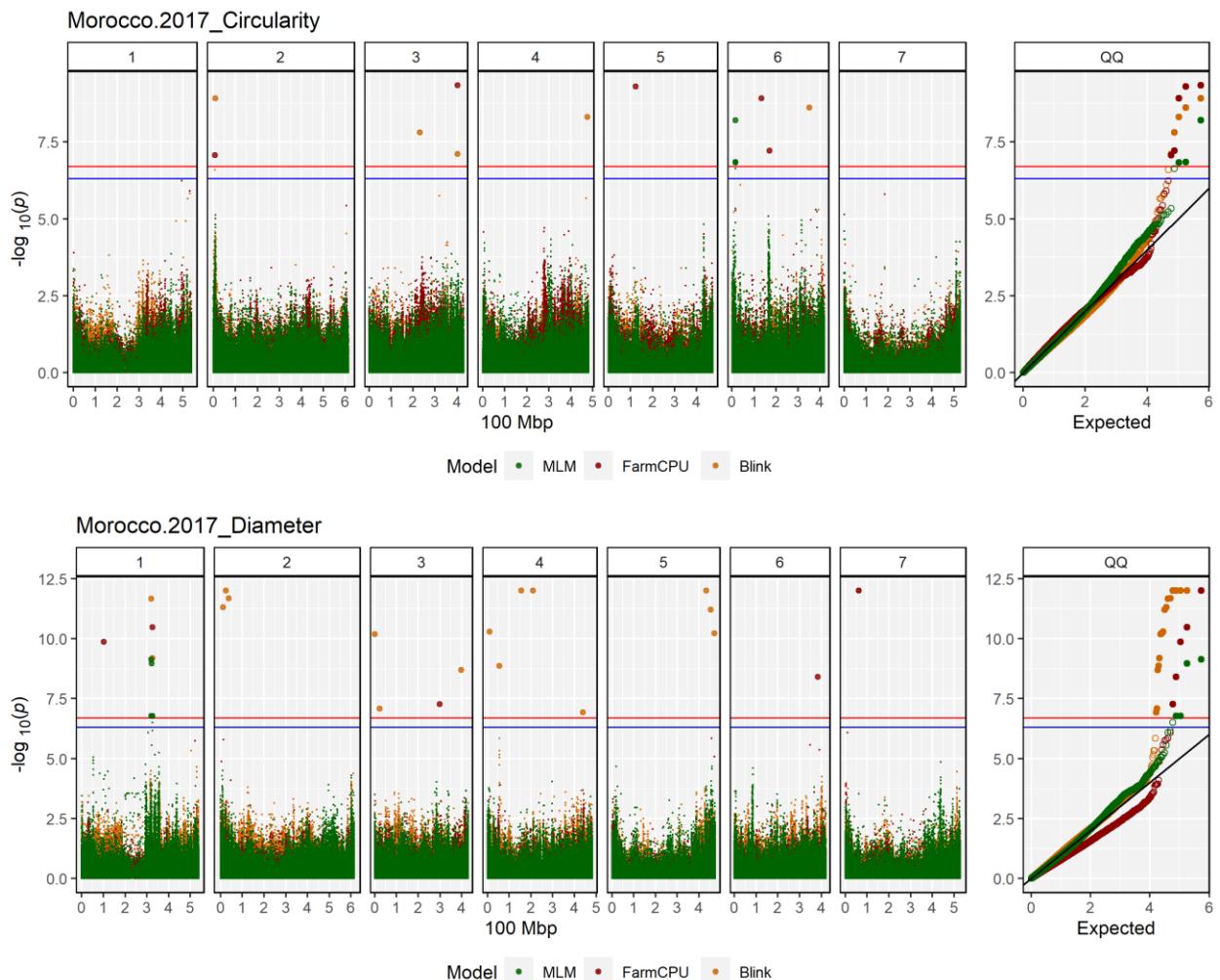


Figure H.2. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity and diameter of 324 genotypes grown in the field in Morocco 2017 with height used as a covariate. The x axis represents lentil chromosomes, and the Y axis is -log10 of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log10(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log10(P)>6.3]. The x axis on the Q-Q plots is the expected -log10 of p-values and the y axis is the observed -log10 of p-values.

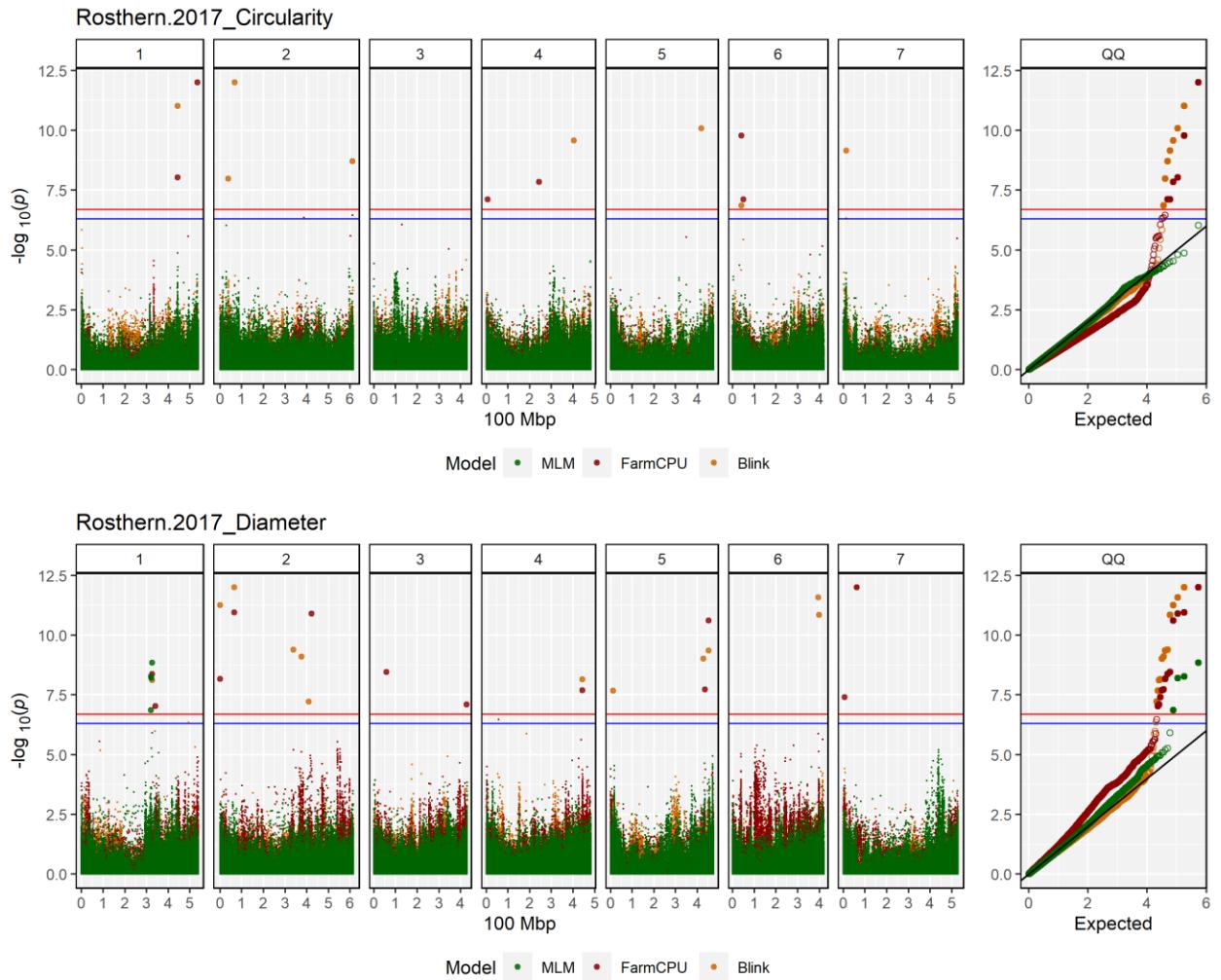


Figure H.3. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity and diameter of 324 genotypes grown in the field in Rostthern 2017 with height used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

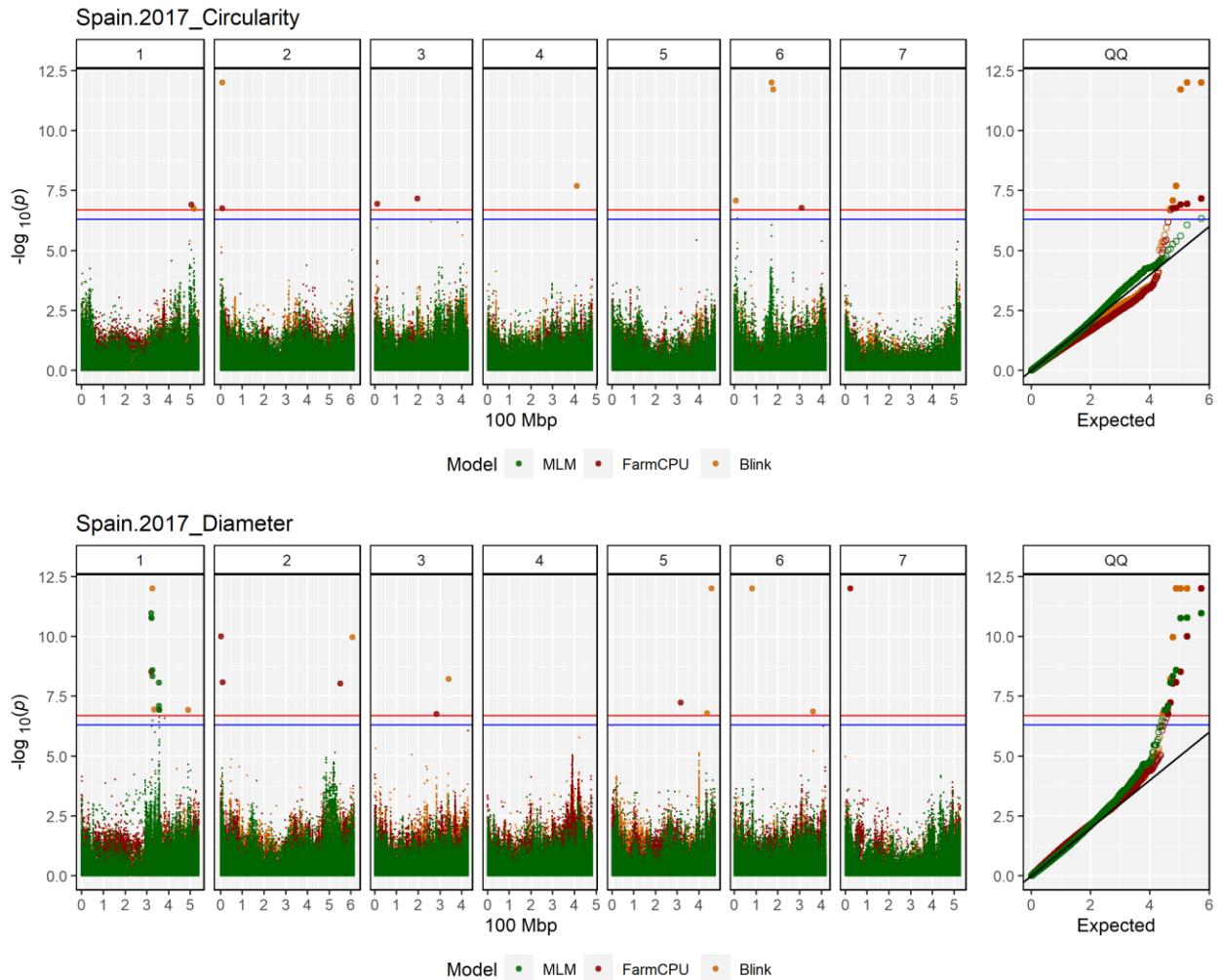


Figure H.4. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity and diameter of 324 genotypes grown in the field in Spain 2017 with height used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

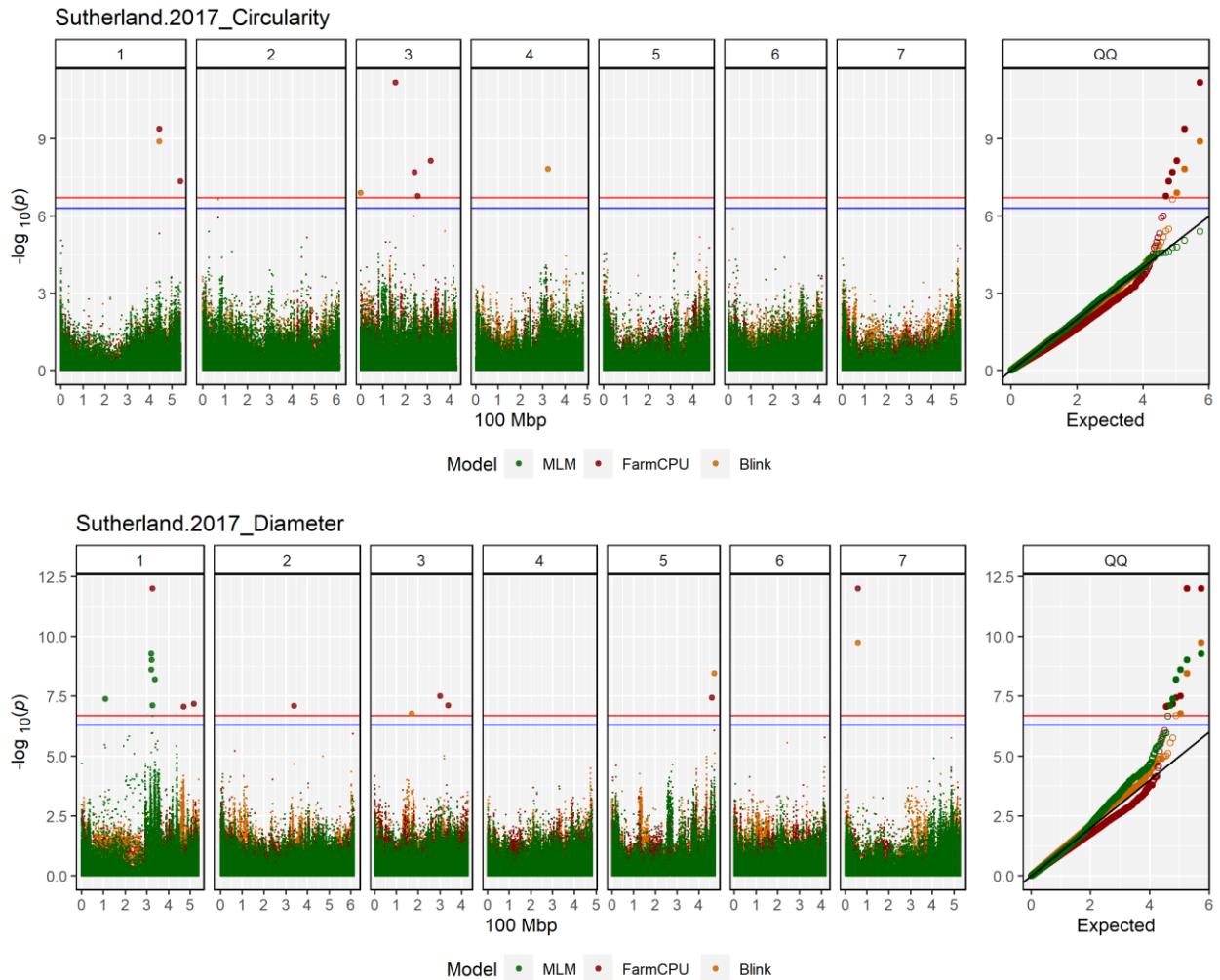


Figure H.5. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity and diameter of 324 genotypes grown in the field in Sutherland 2017 with height used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

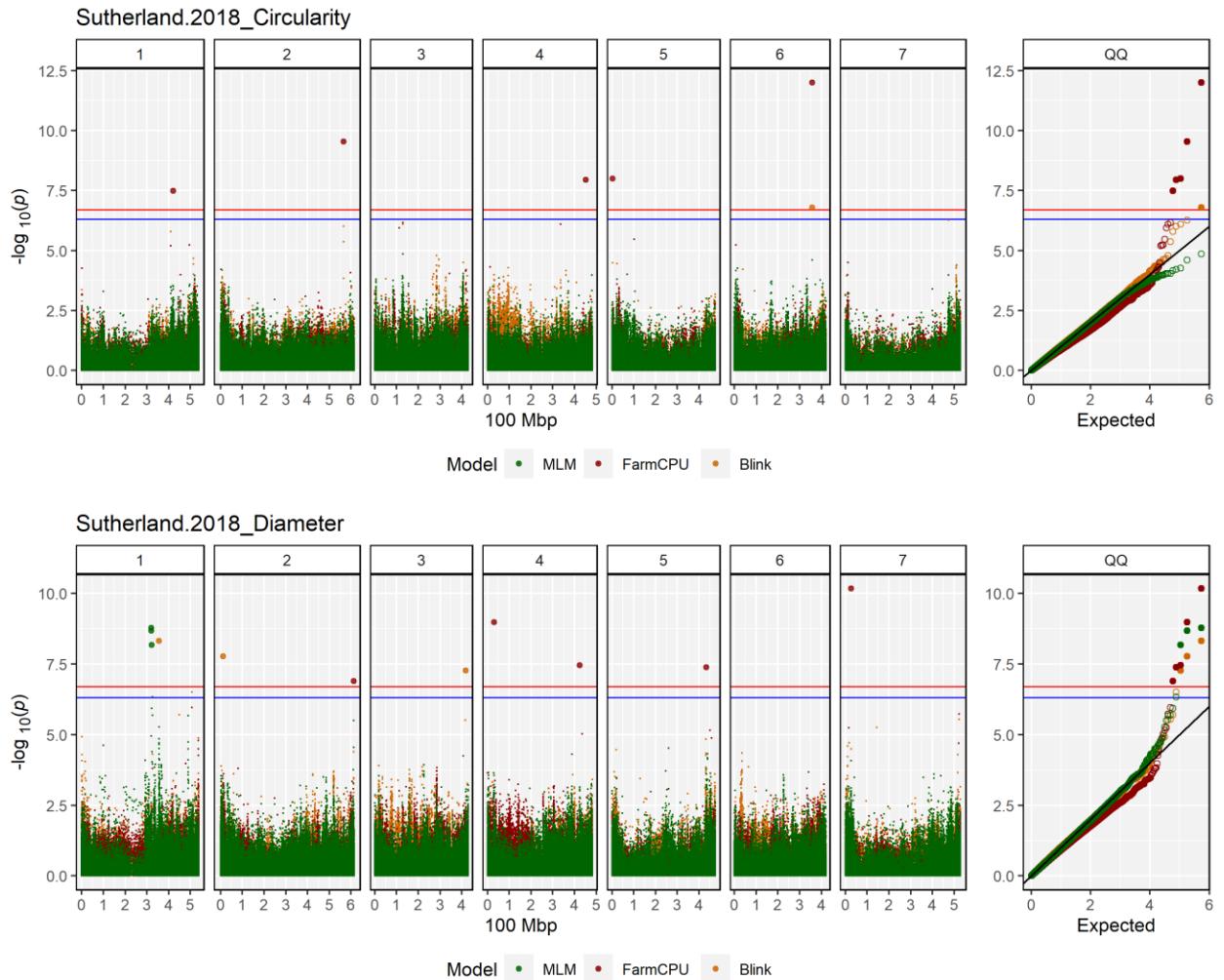
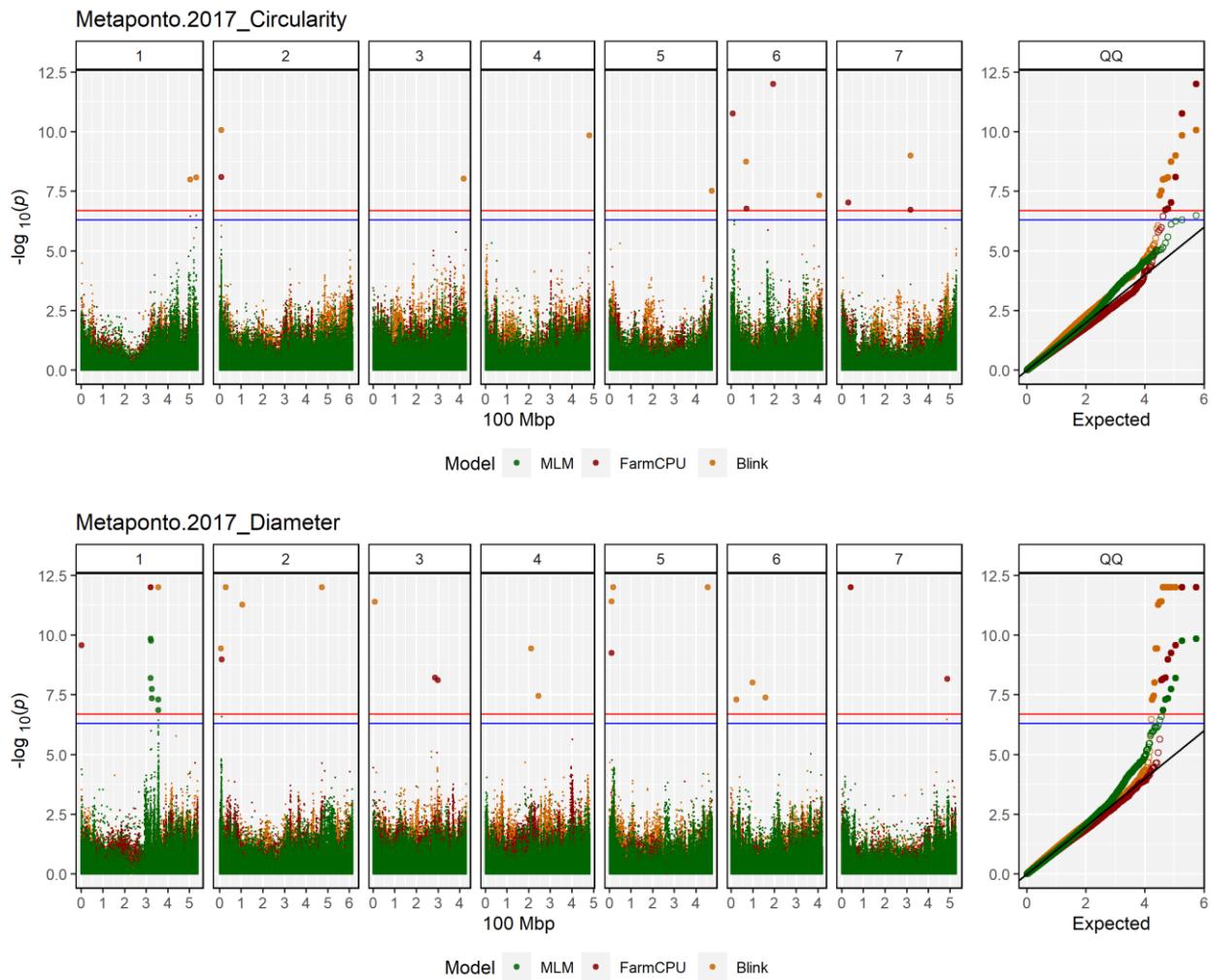


Figure H.6. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity and diameter of 324 genotypes grown in the field in Sutherland 2018 with height used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

Appendix I

Manhattan plots from GWAS with days to flowering as covariate



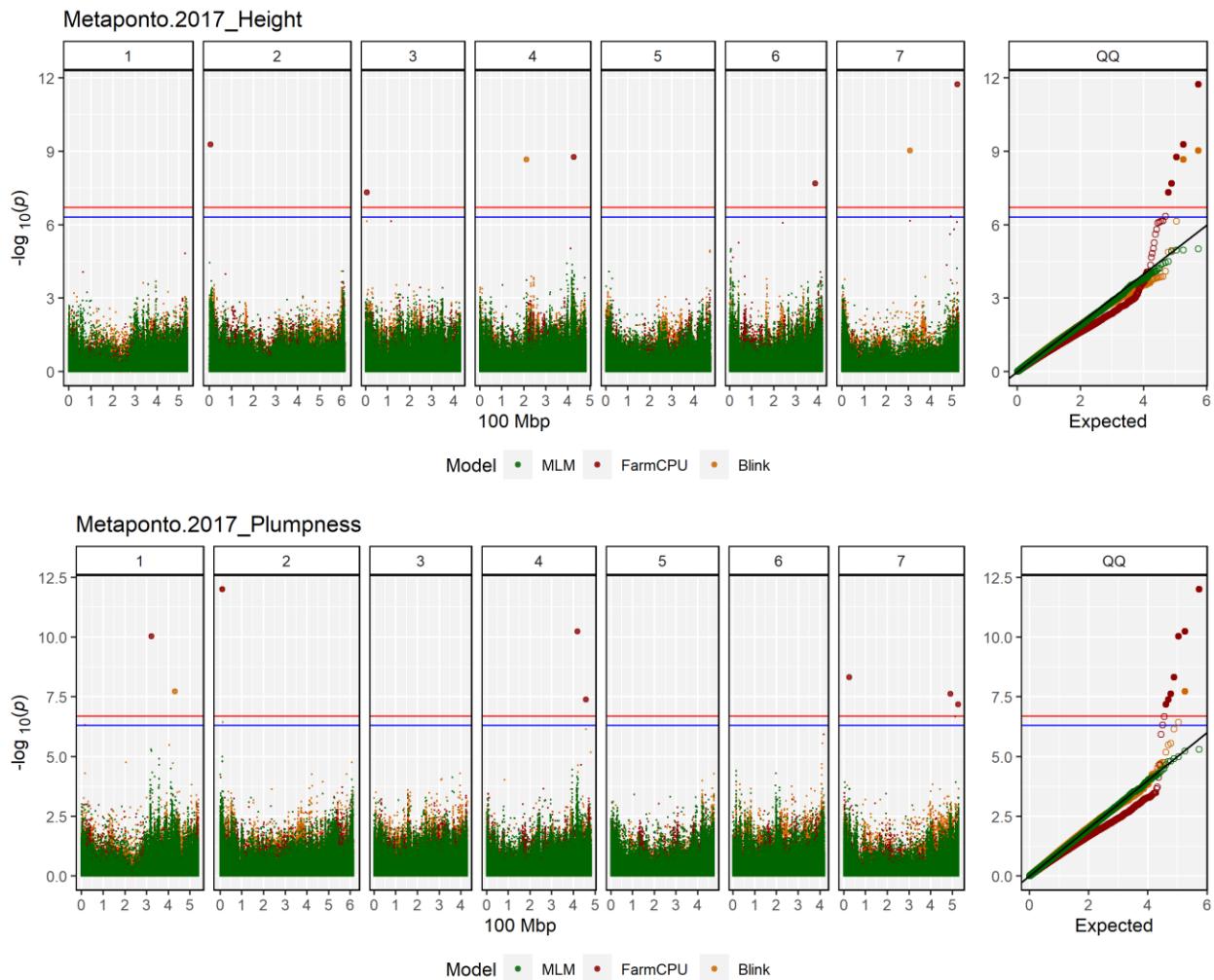
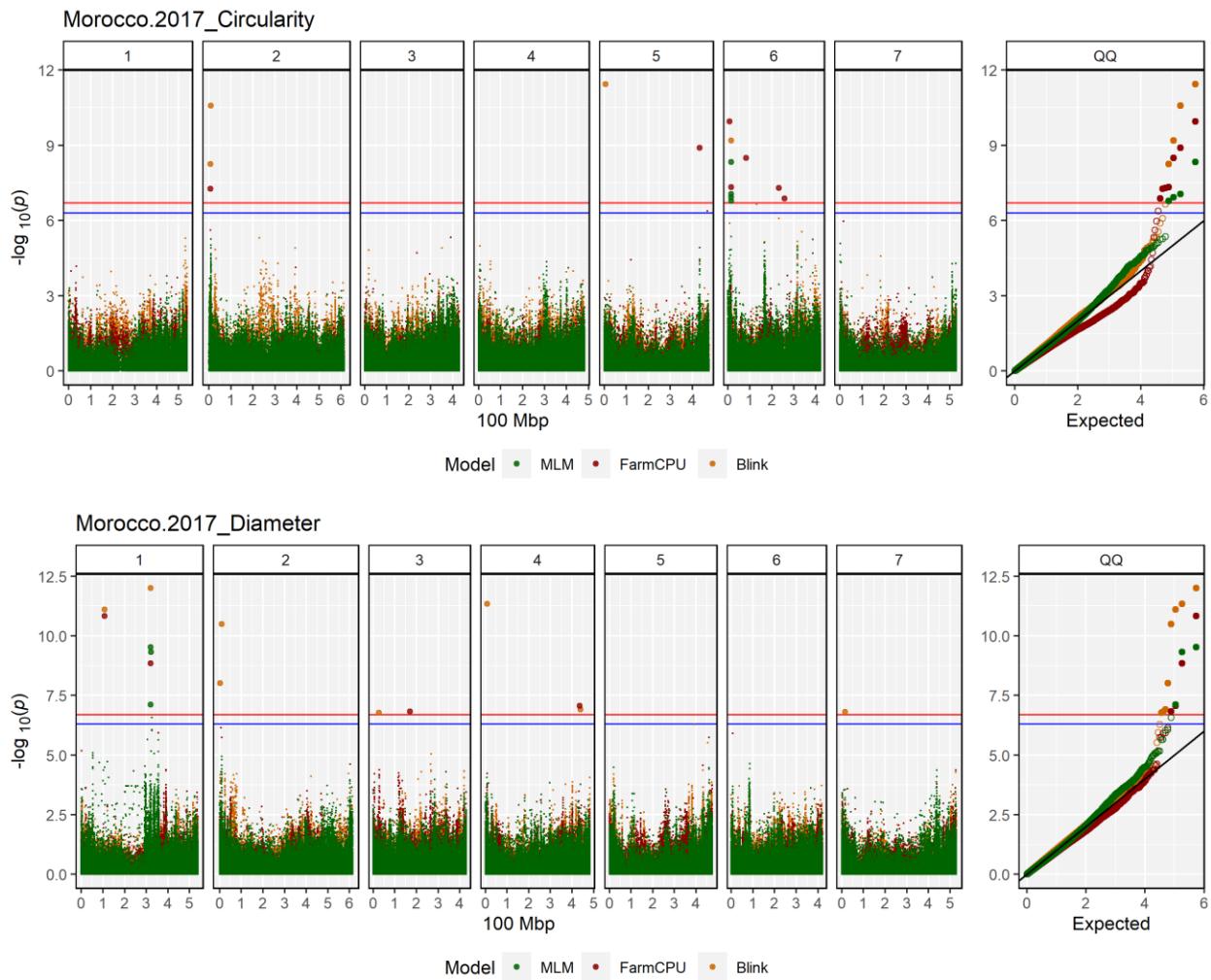


Figure I.1. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Metaponto 2017 with days to flowering used as covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



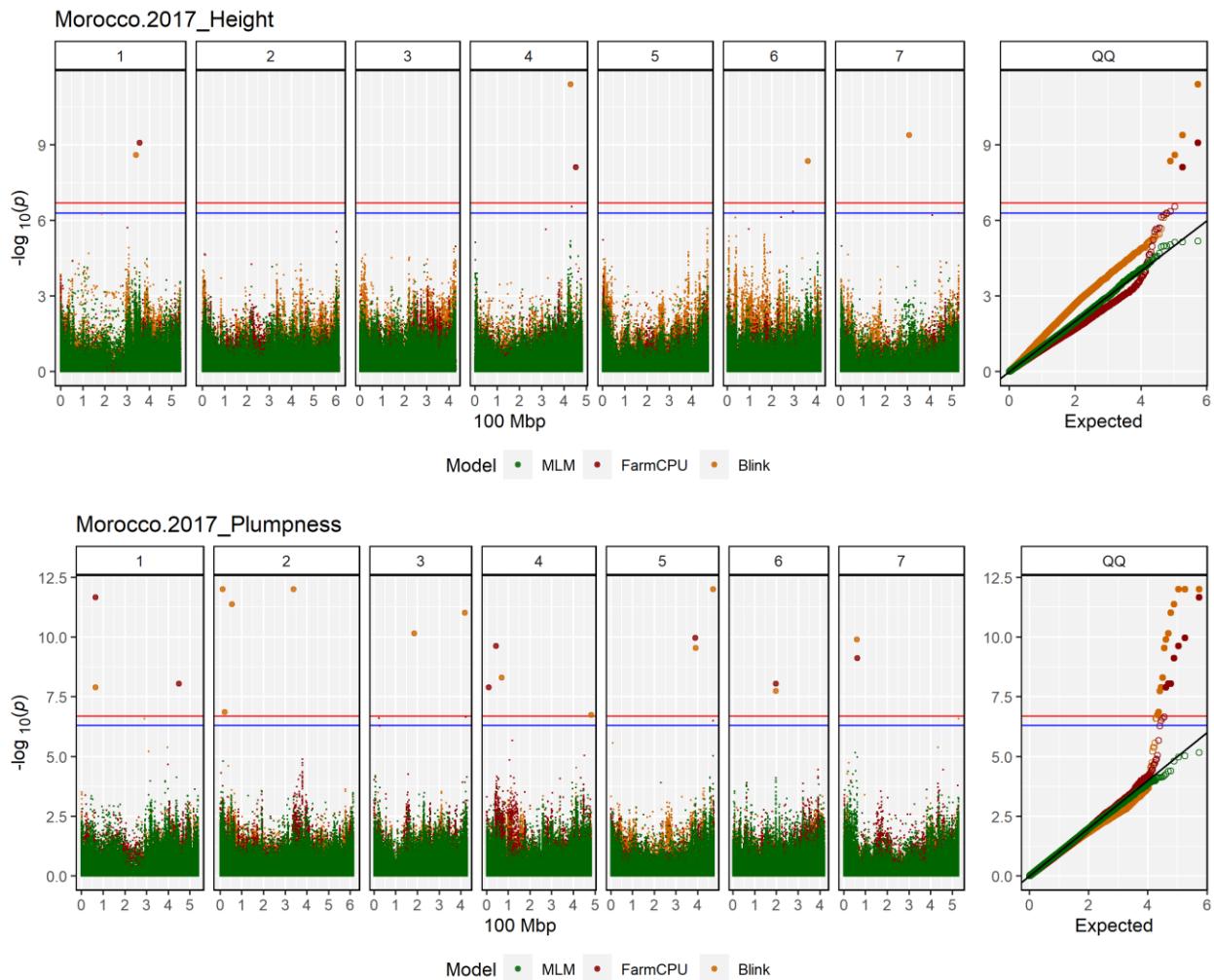
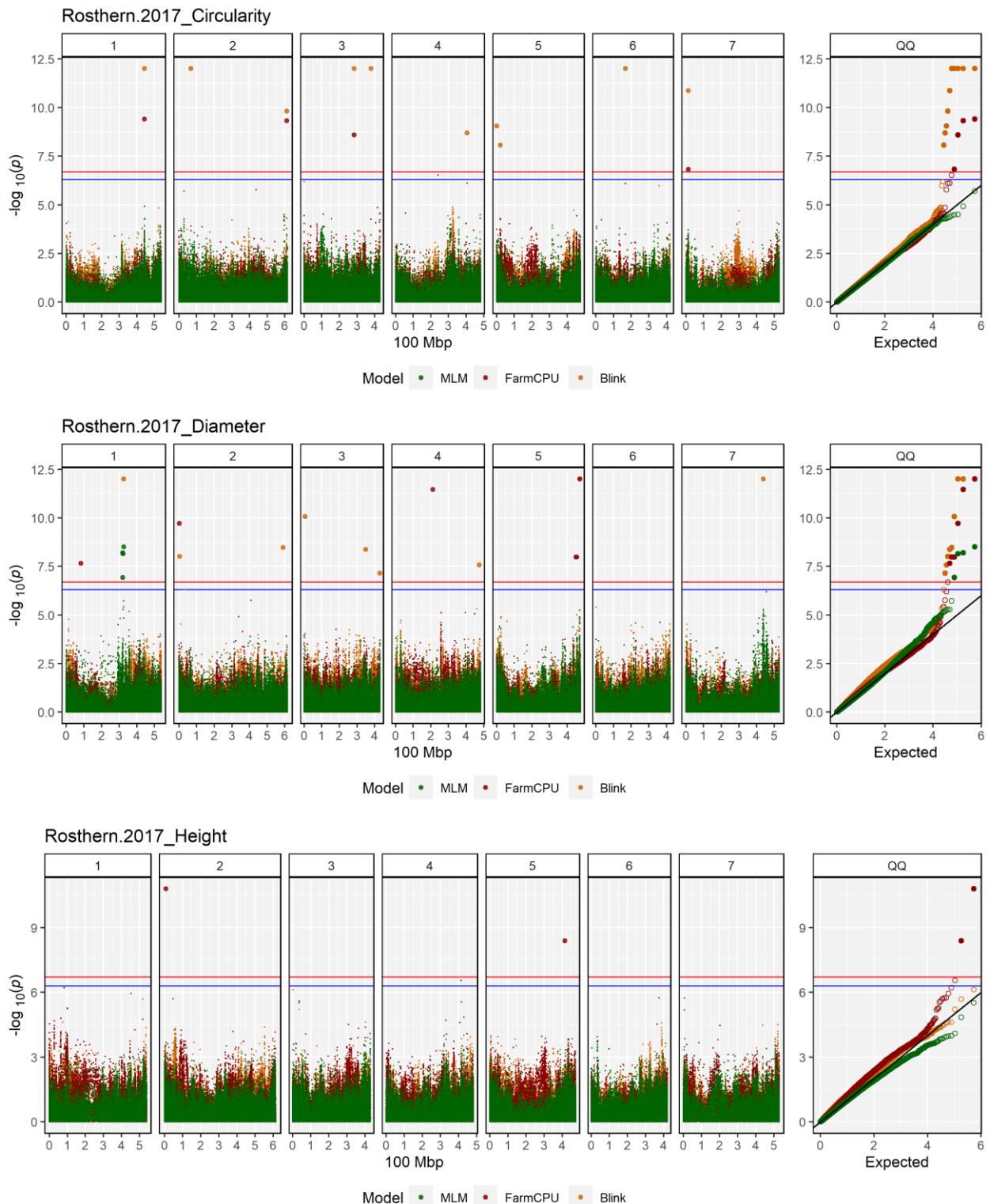


Figure I.2. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Morocco 2017 with days to flowering used as a covariate. The x axis represents lentil chromosomes, and the Y axis is -log₁₀ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log₁₀(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log₁₀(P)>6.3]. The x axis on the Q-Q plots is the expected -log₁₀ of p-values and the y axis is the observed -log₁₀ of p-values.



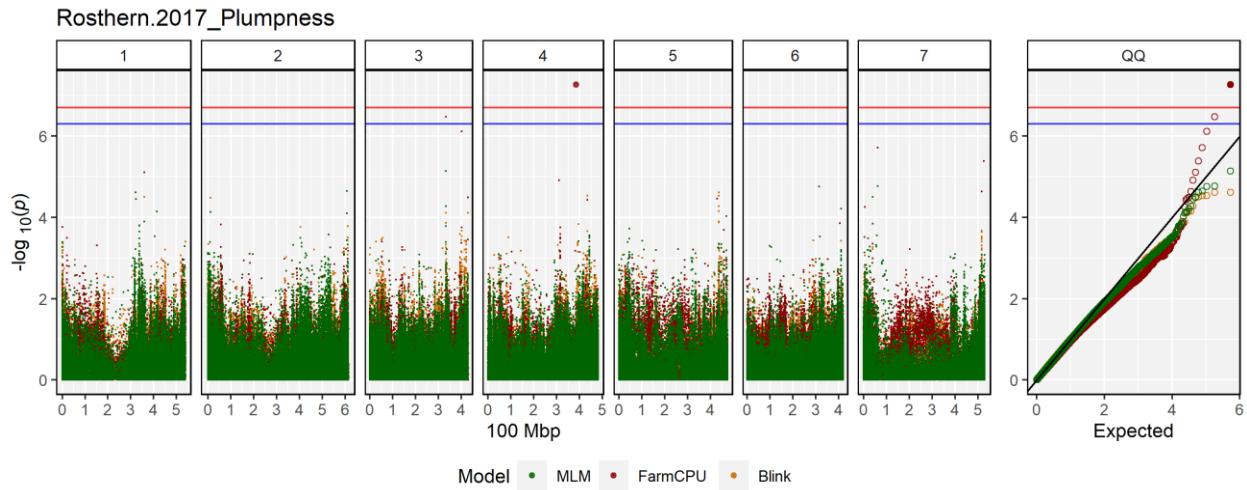
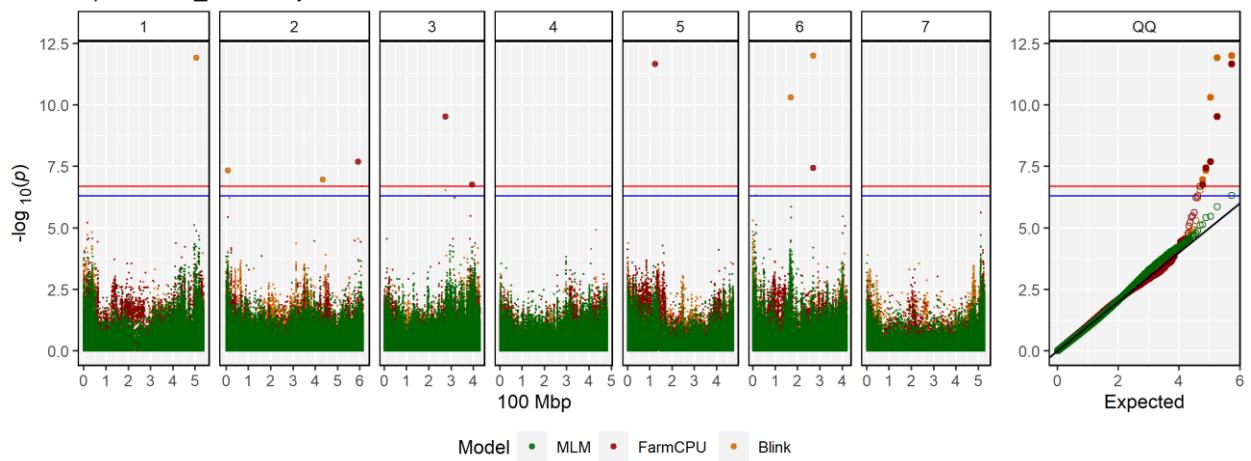
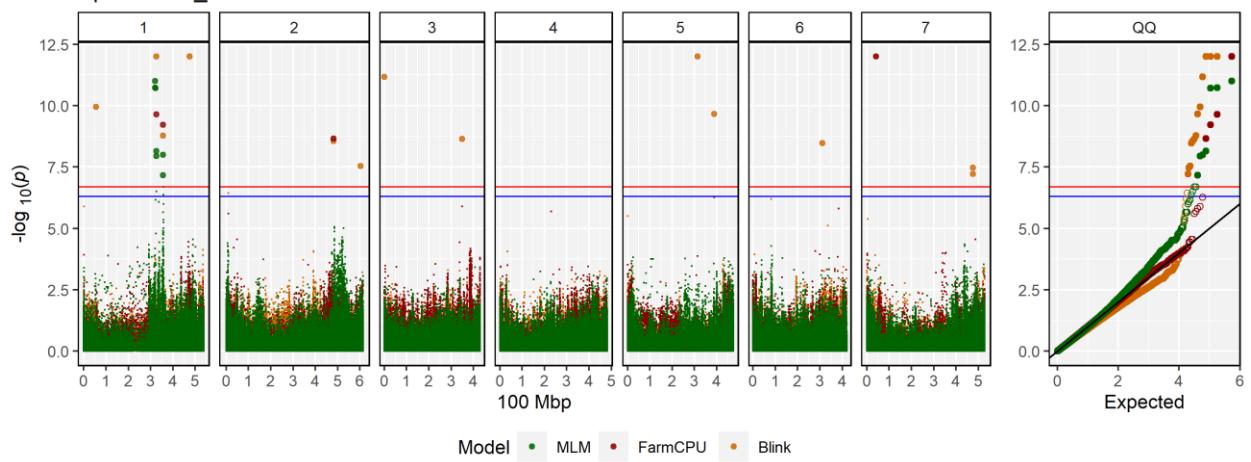


Figure I.3. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Rosthern 2017 with days to flowering used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

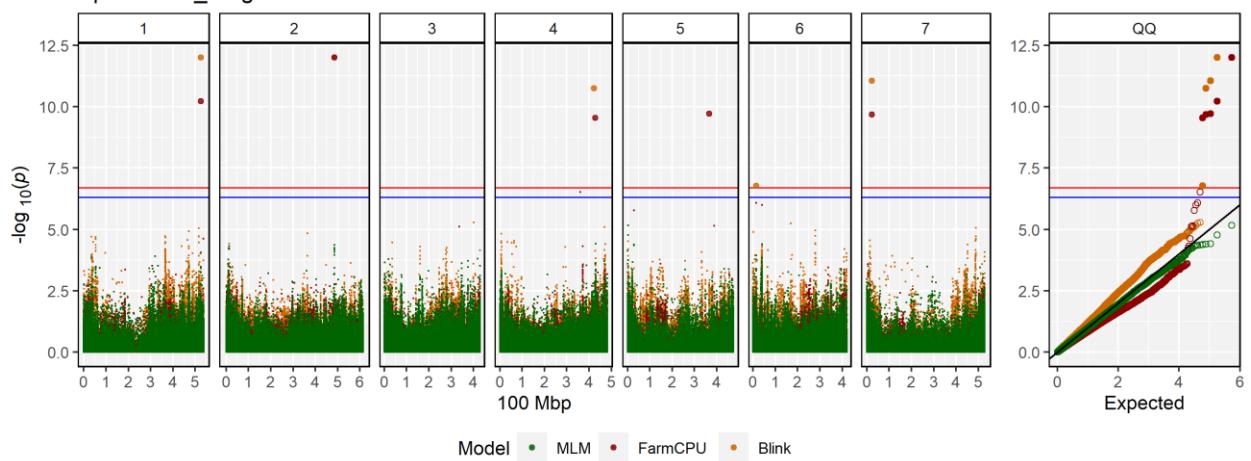
Spain.2017_Circularity



Spain.2017_Diameter



Spain.2017_Height



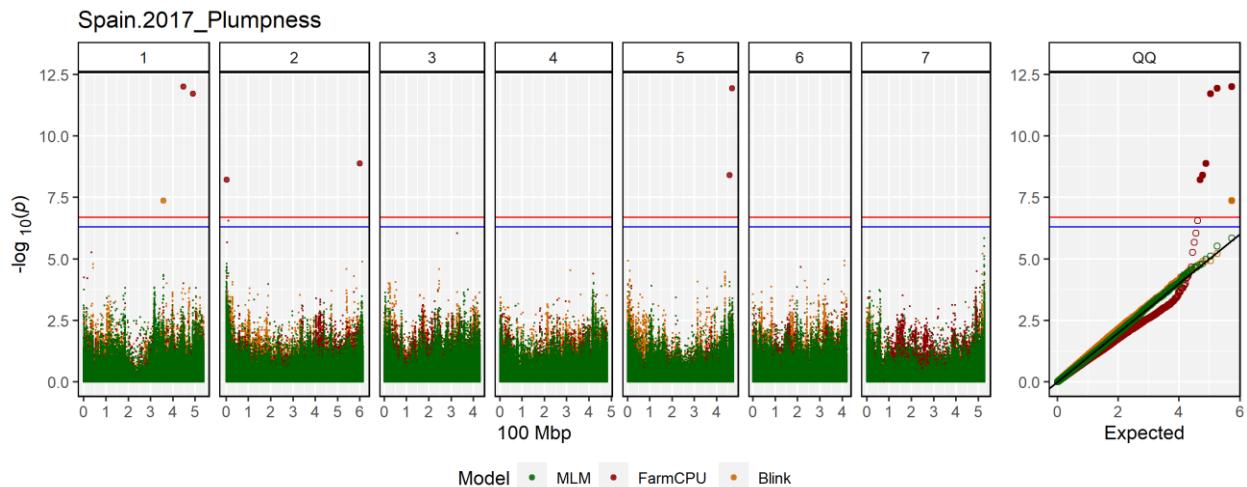
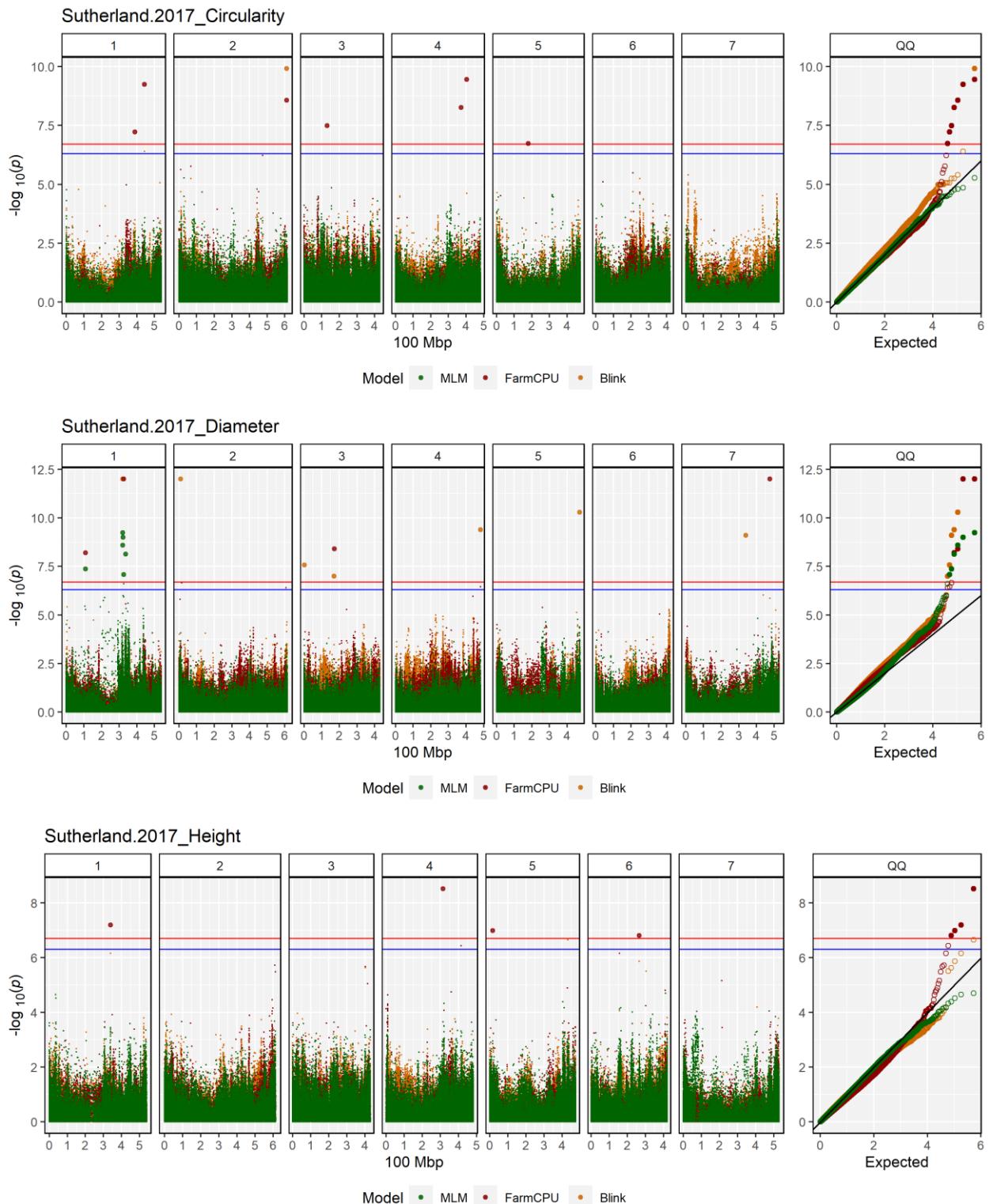


Figure I.4. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Spain 2017 using days to flowering as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



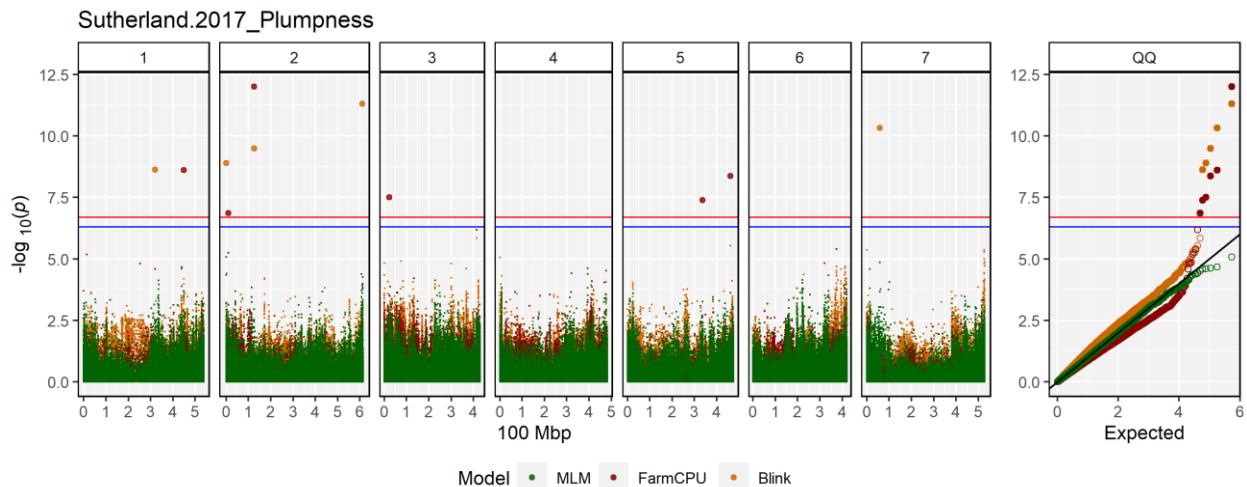
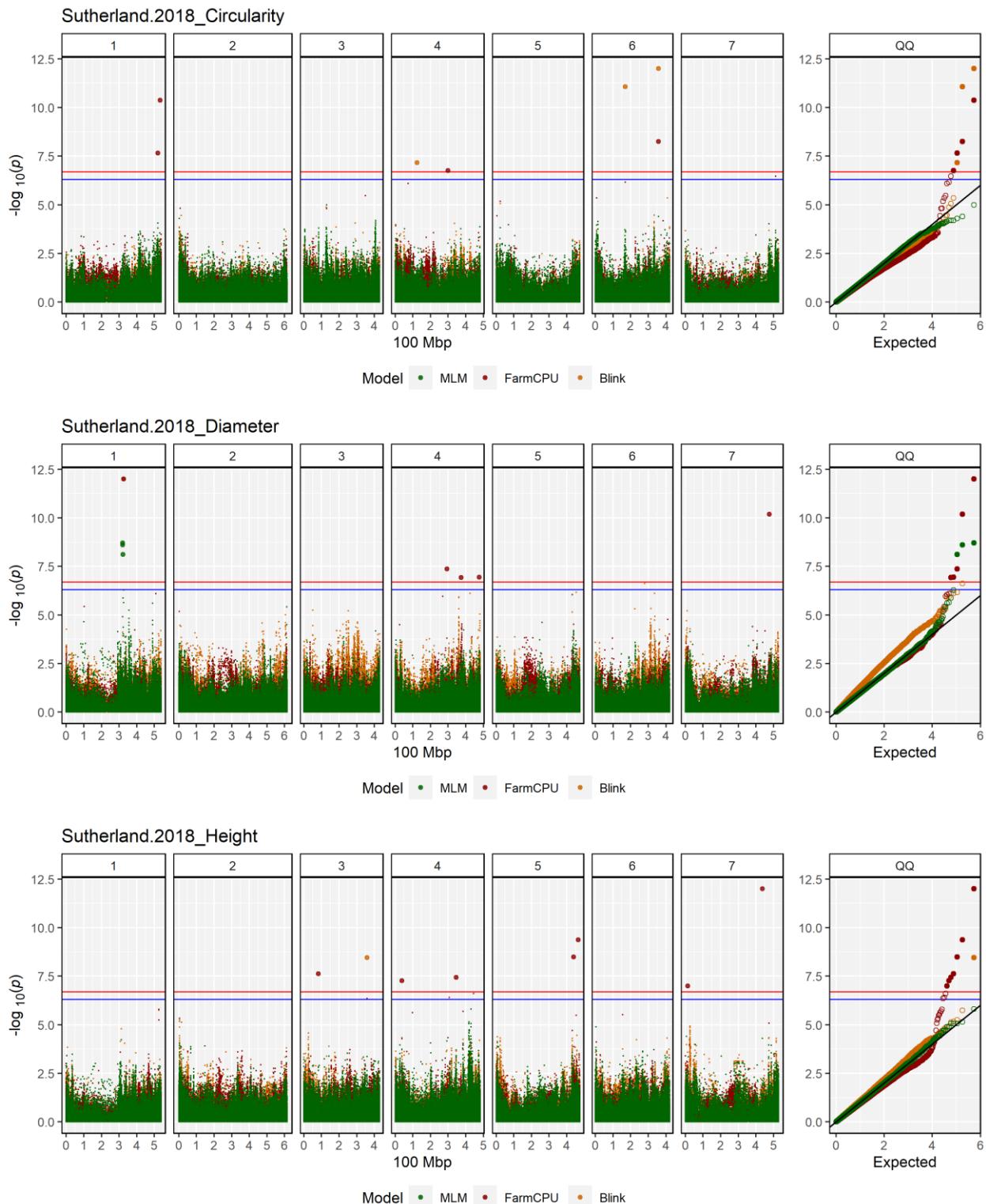


Figure I.5. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Sutherland 2017 with days to flowering used as covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



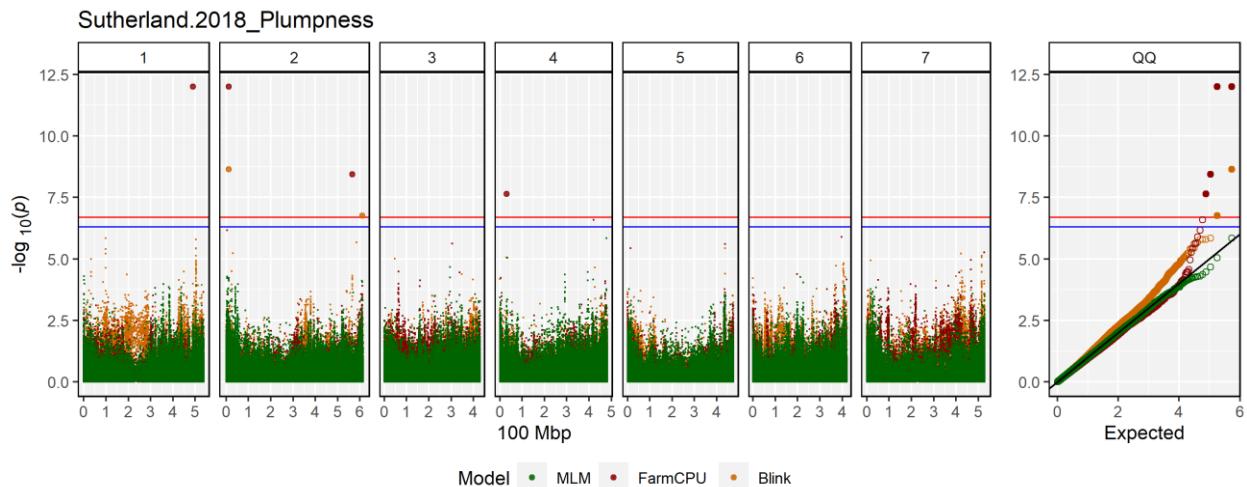
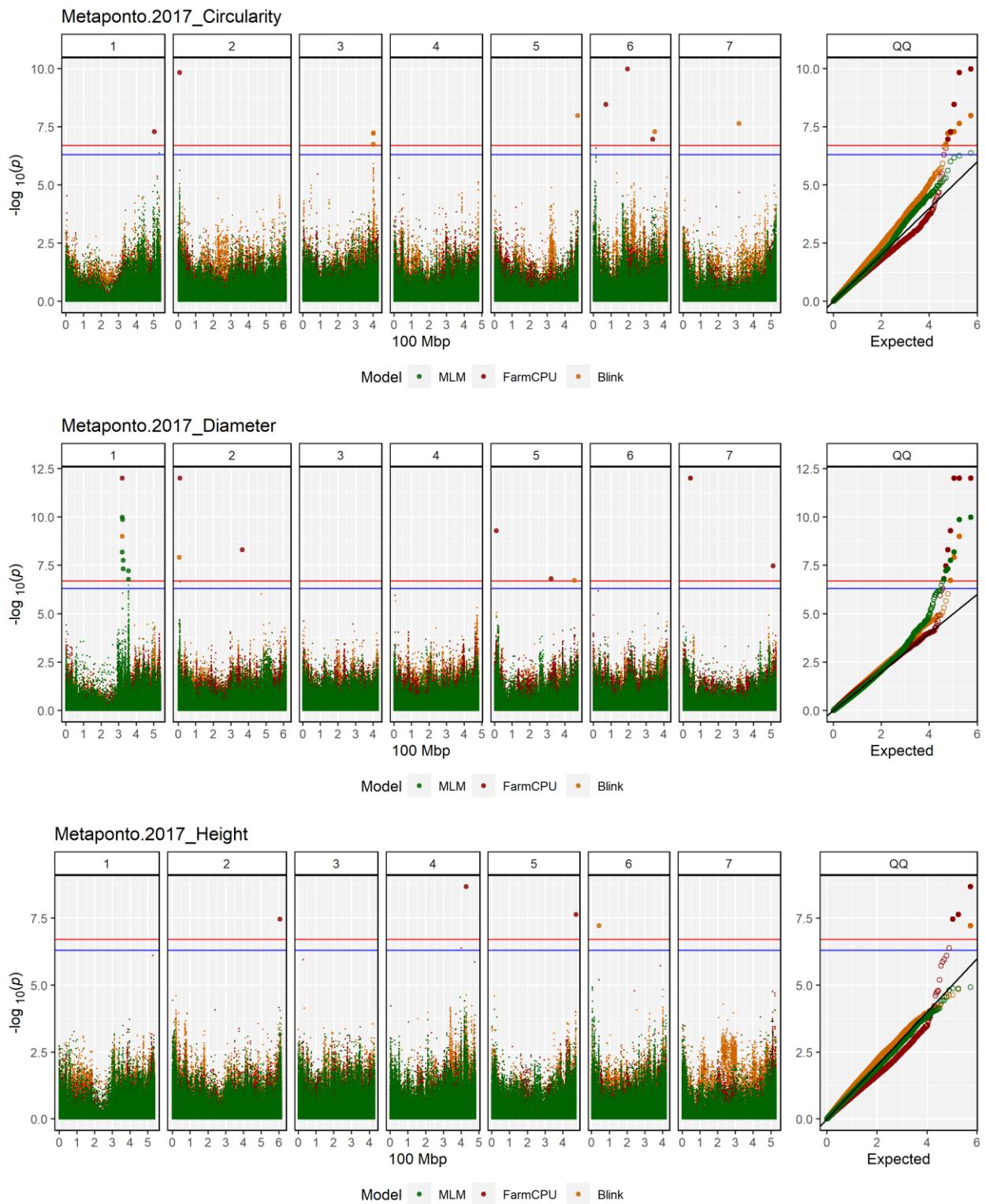


Figure I.6. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Sutherland 2018 with days to flowering used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.

Appendix J

Manhattan plots from GWAS with days to swollen pods as covariate



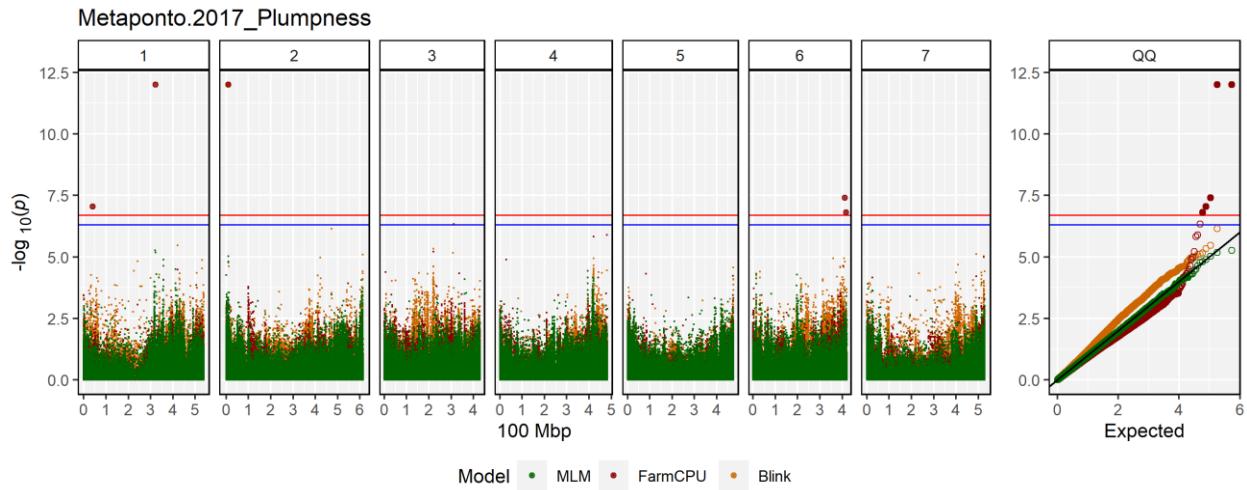
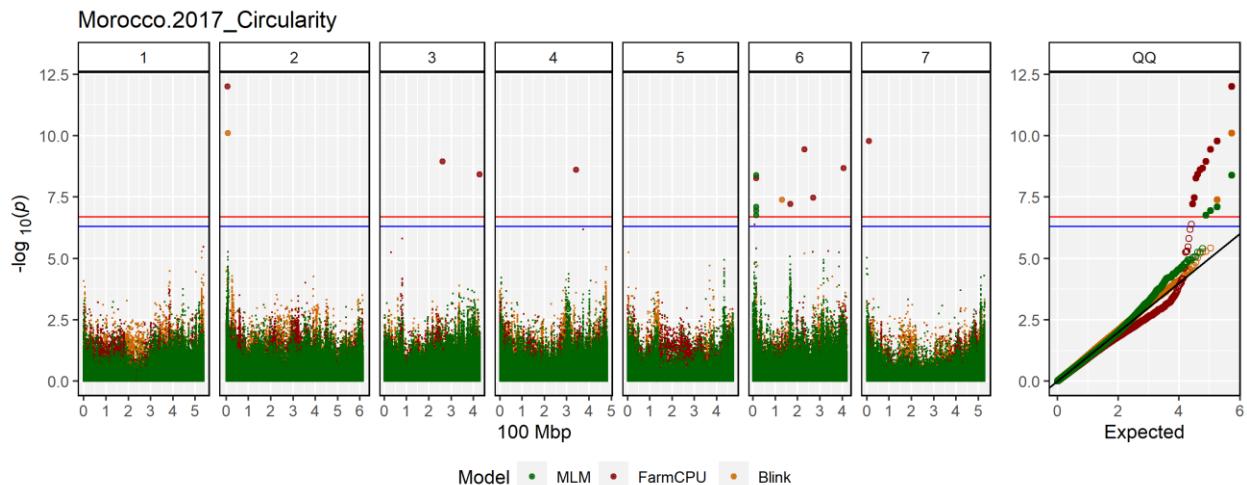
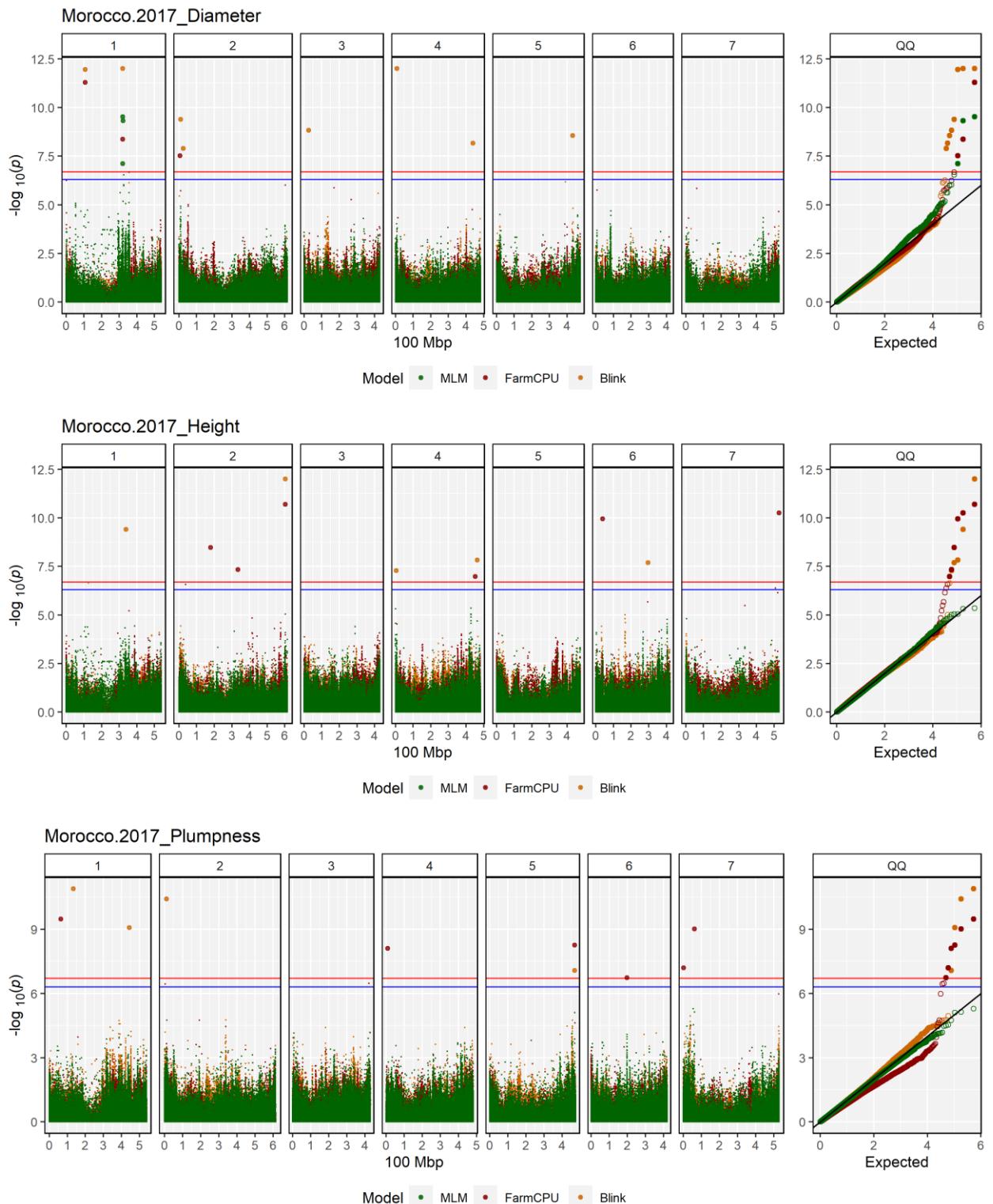


Figure J.1. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Metaponto 2017 with days to swollen pods used as covariate. The x axis represents lentil chromosomes, and the Y axis is -log₁₀ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log₁₀(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log₁₀(P)>6.3]. The x axis on the Q-Q plots is the expected -log₁₀ of p-values and the y axis is the observed -log₁₀ of p-values.





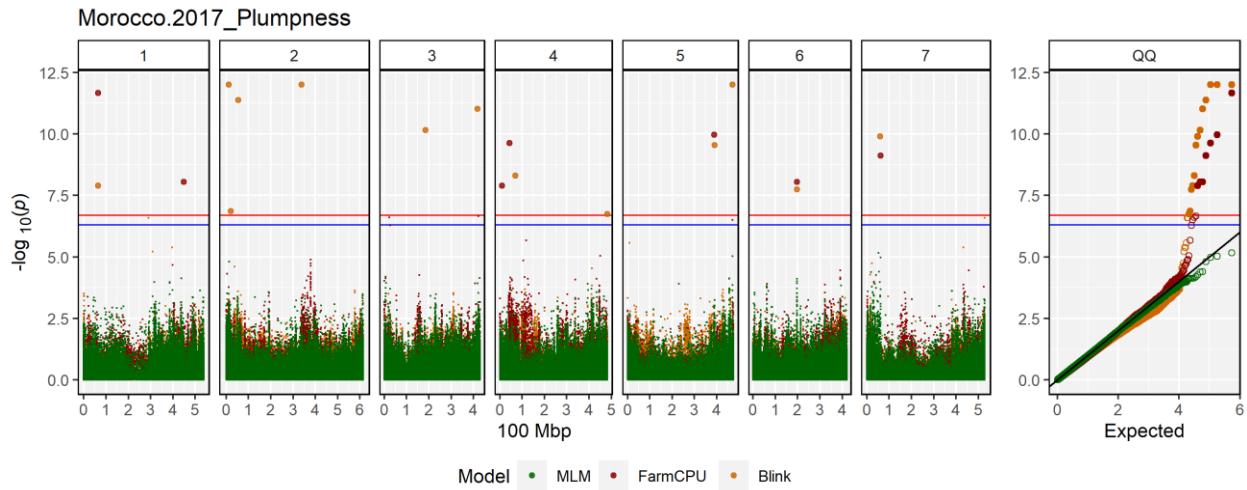
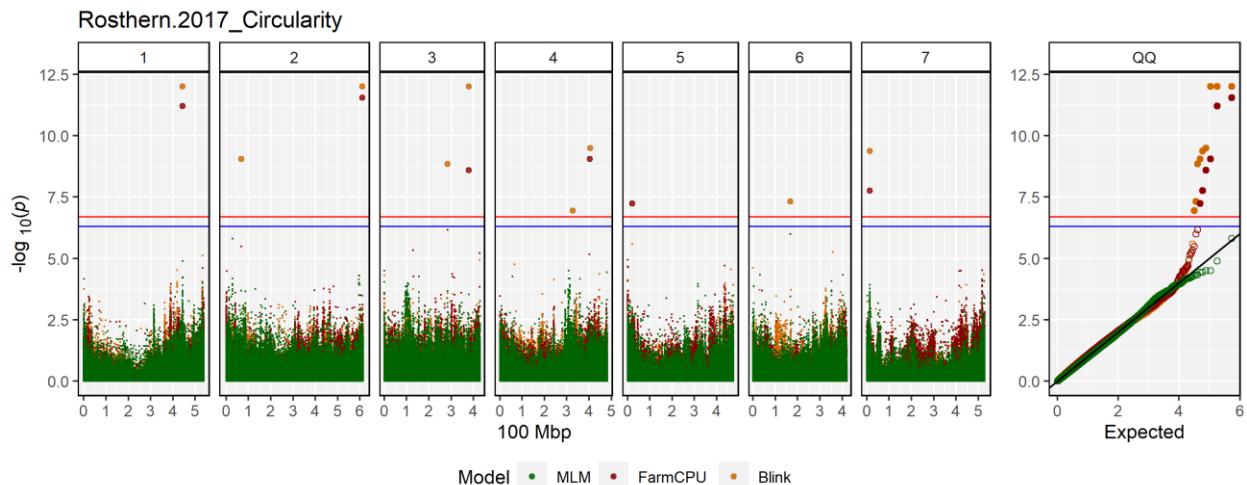


Figure J.2. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Morocco 2017 with days to swollen pods used as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



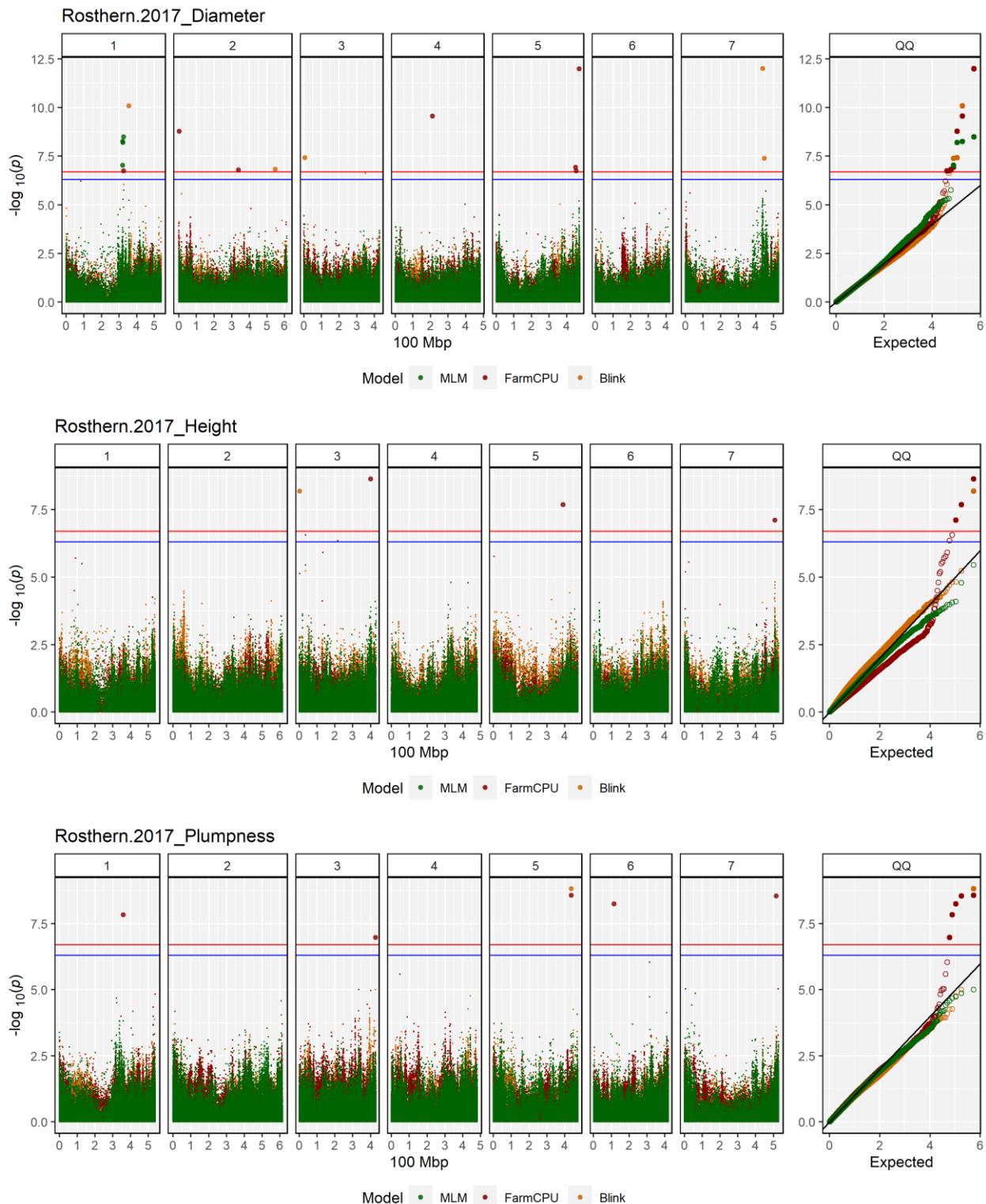
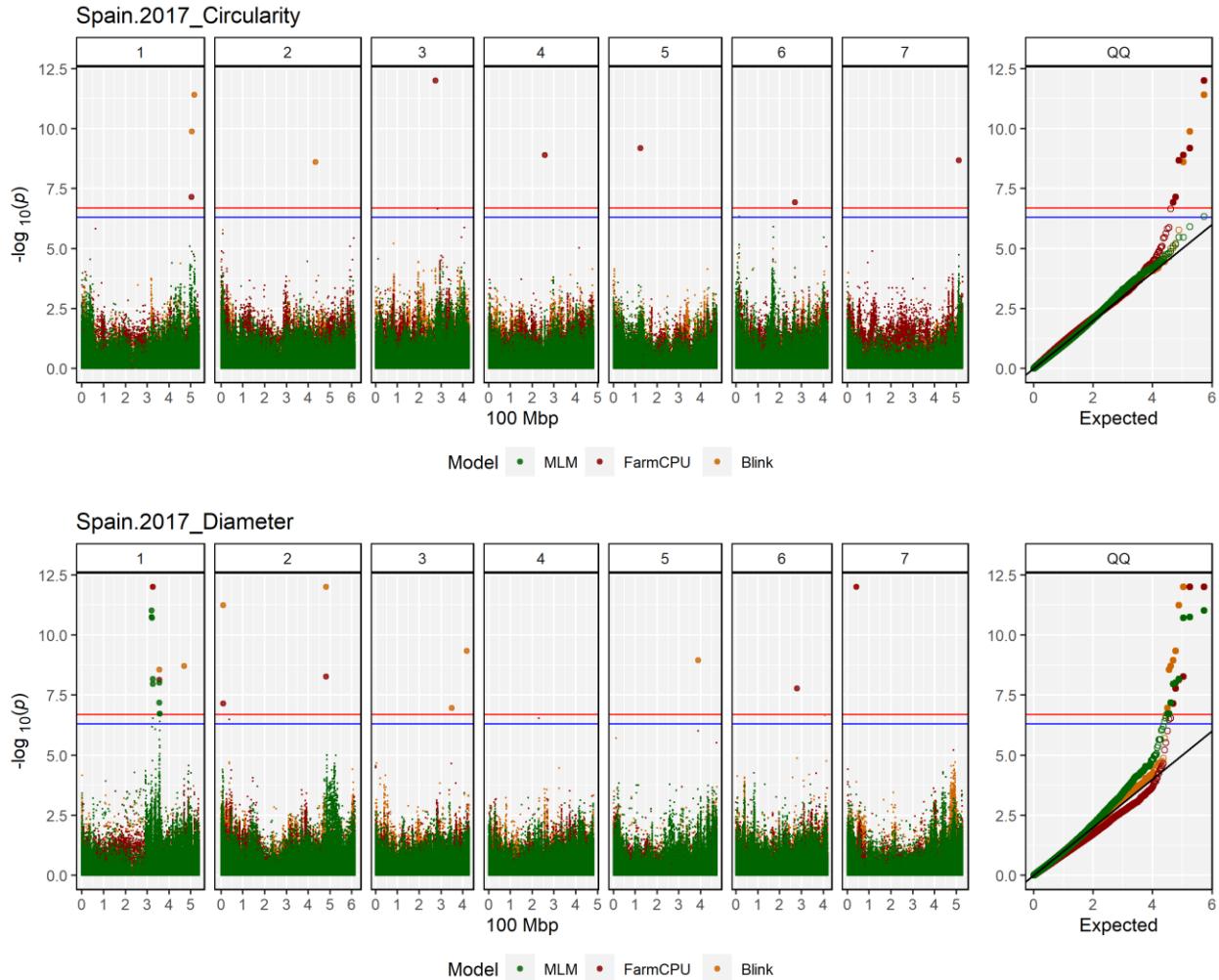


Figure J.3. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Rostthern 2017 with days to swollen pods used as a covariate. The x axis represents lentil

chromosomes, and the Y axis is -log₁₀ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log₁₀(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log₁₀(P)>6.3]. The x axis on the Q-Q plots is the expected -log₁₀ of p-values and the y axis is the observed -log₁₀ of p-values.



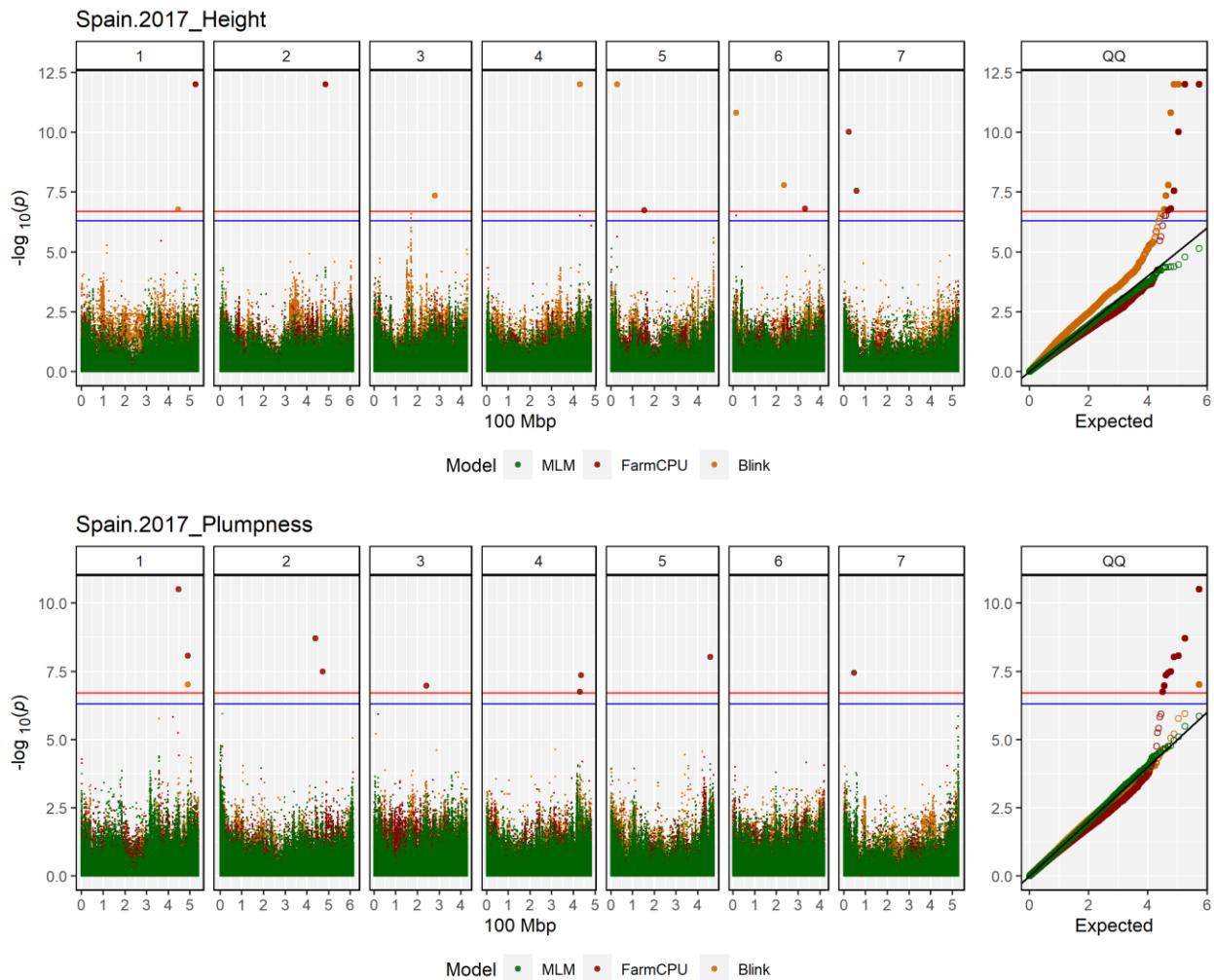
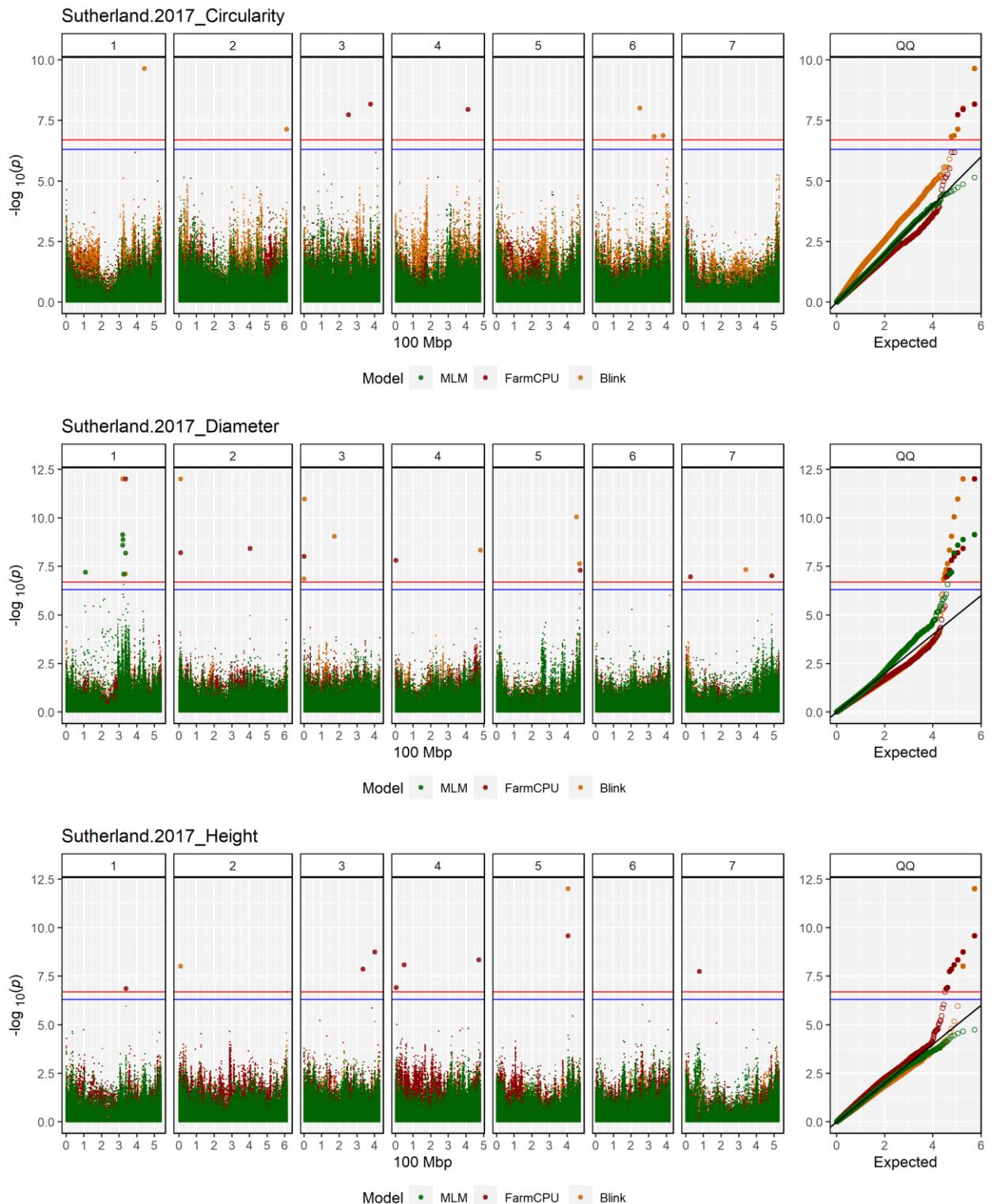


Figure J.4. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Spain 2017 using days to swollen pods as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



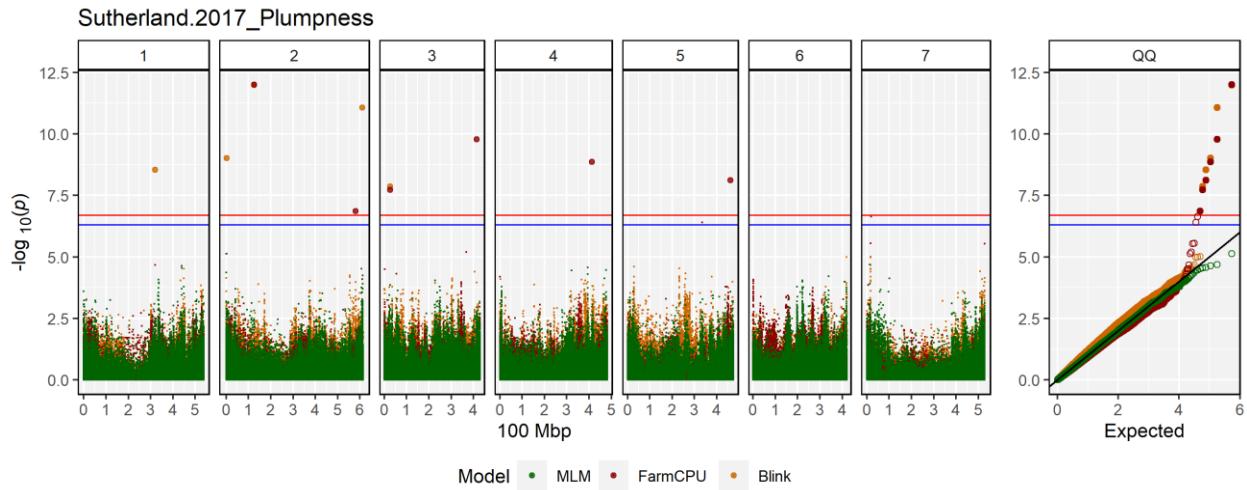
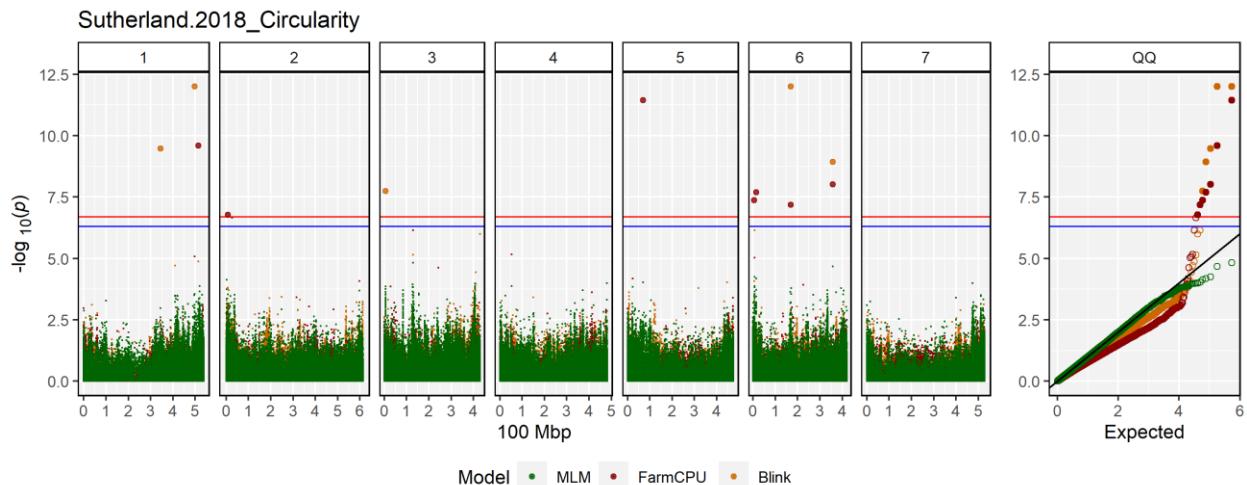


Figure J.5. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Sutherland 2017 with days to swollen pods used as covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



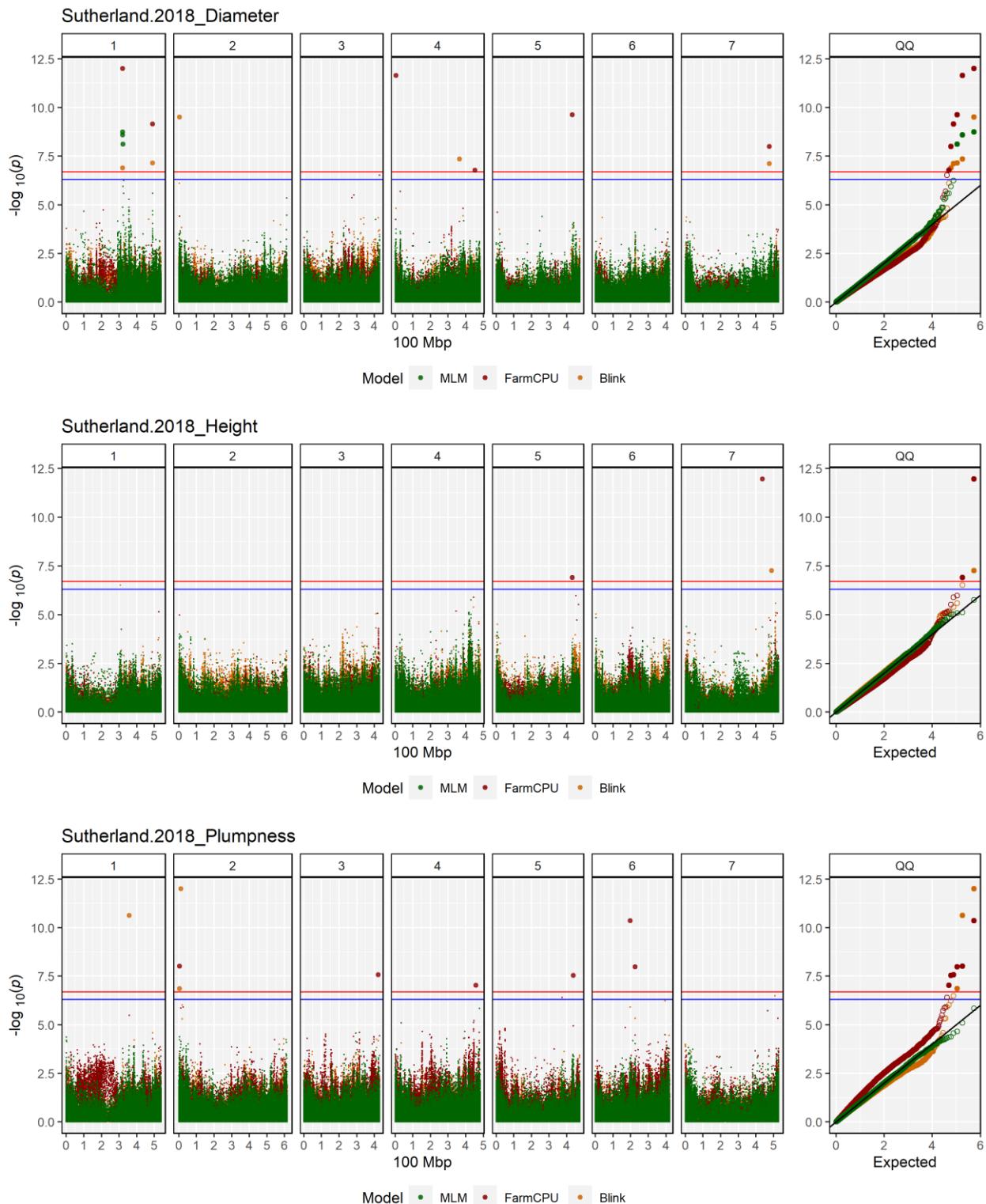
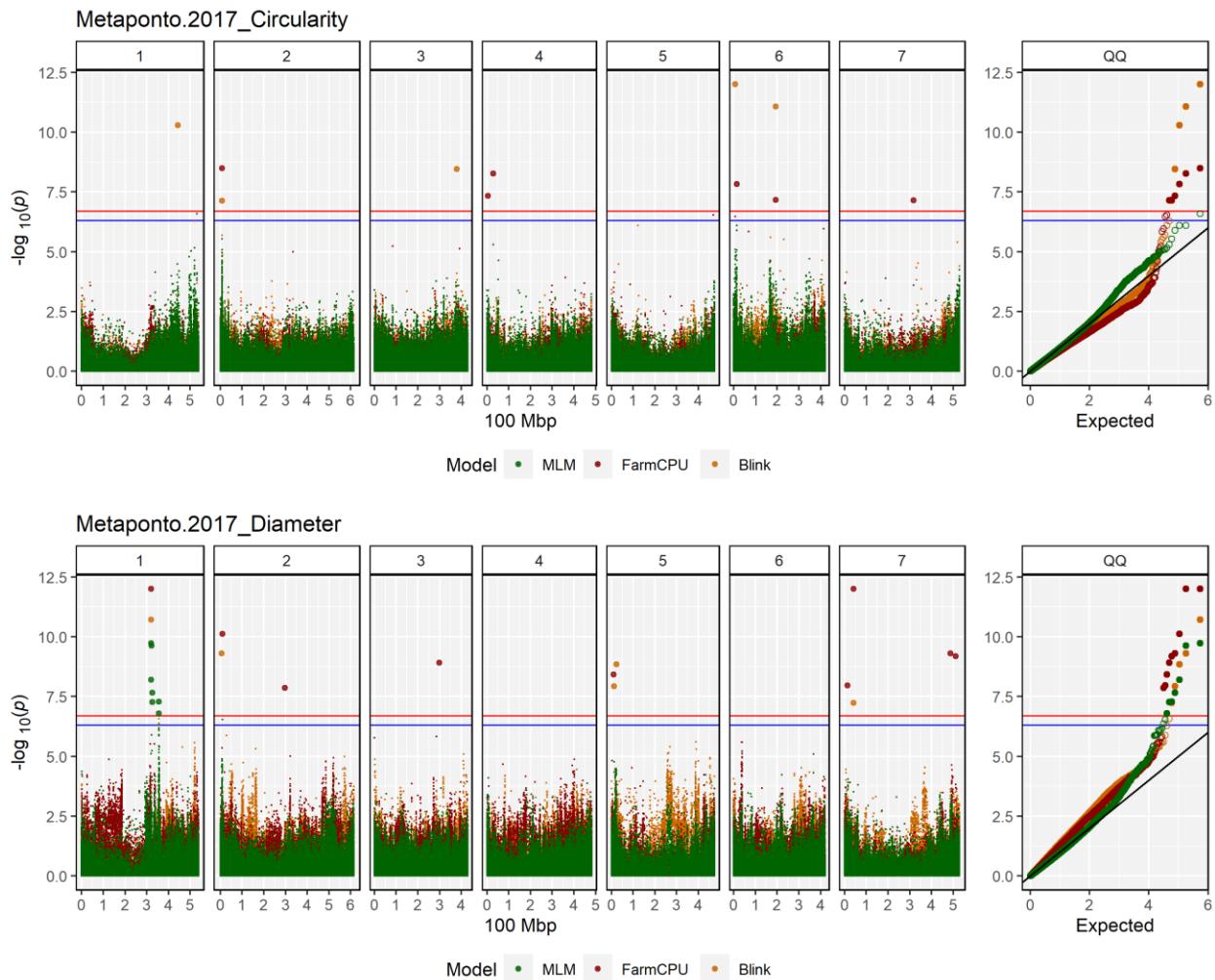


Figure J.6. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Sutherland 2018 with days to swollen pods used as a covariate. The x axis represents lentil

chromosomes, and the Y axis is -log₁₀ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log₁₀(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log₁₀(P)>6.3]. The x axis on the Q-Q plots is the expected -log₁₀ of p-values and the y axis is the observed -log₁₀ of p-values.

Appendix K

Manhattan plots from GWAS with thermal flowering time as covariate



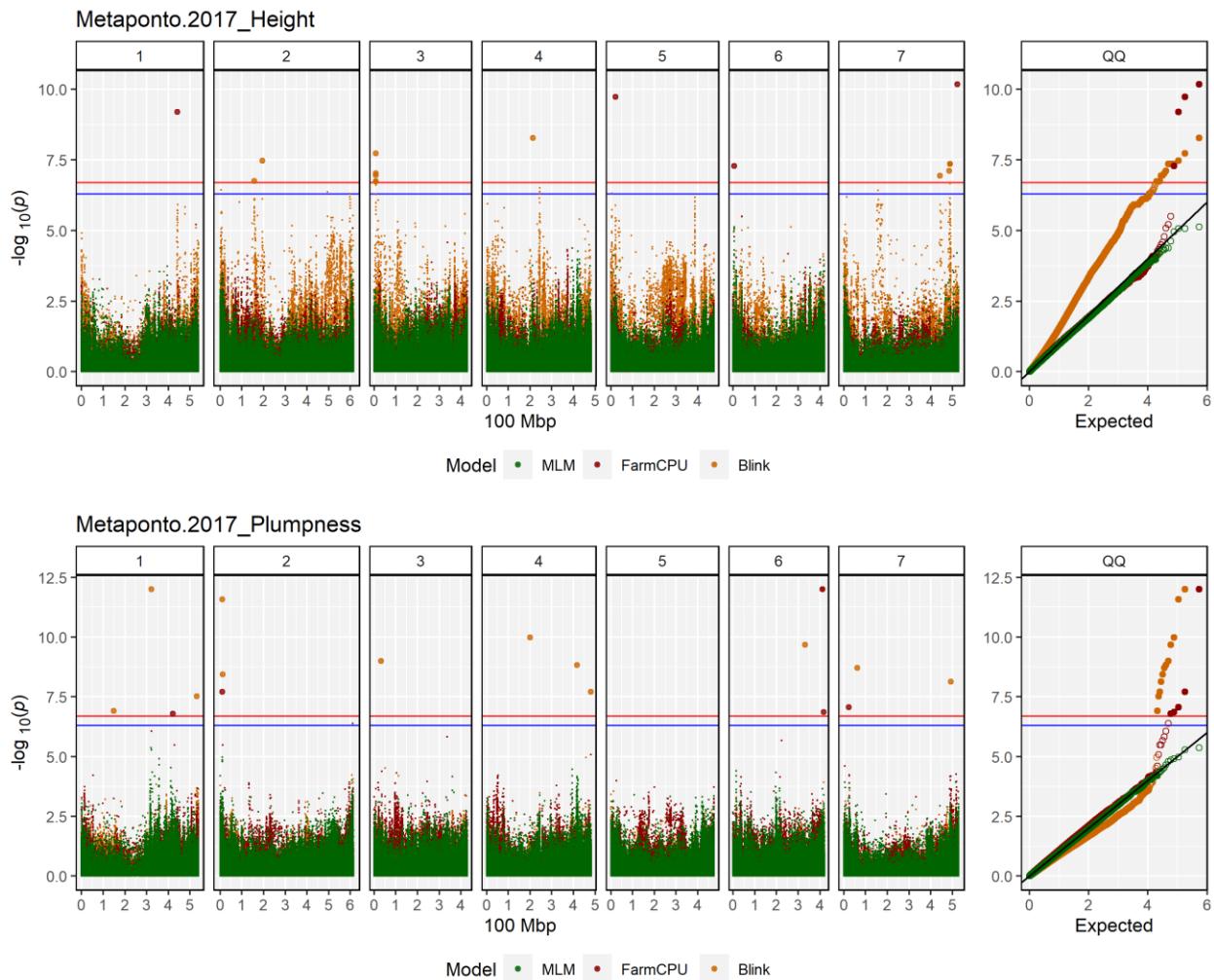
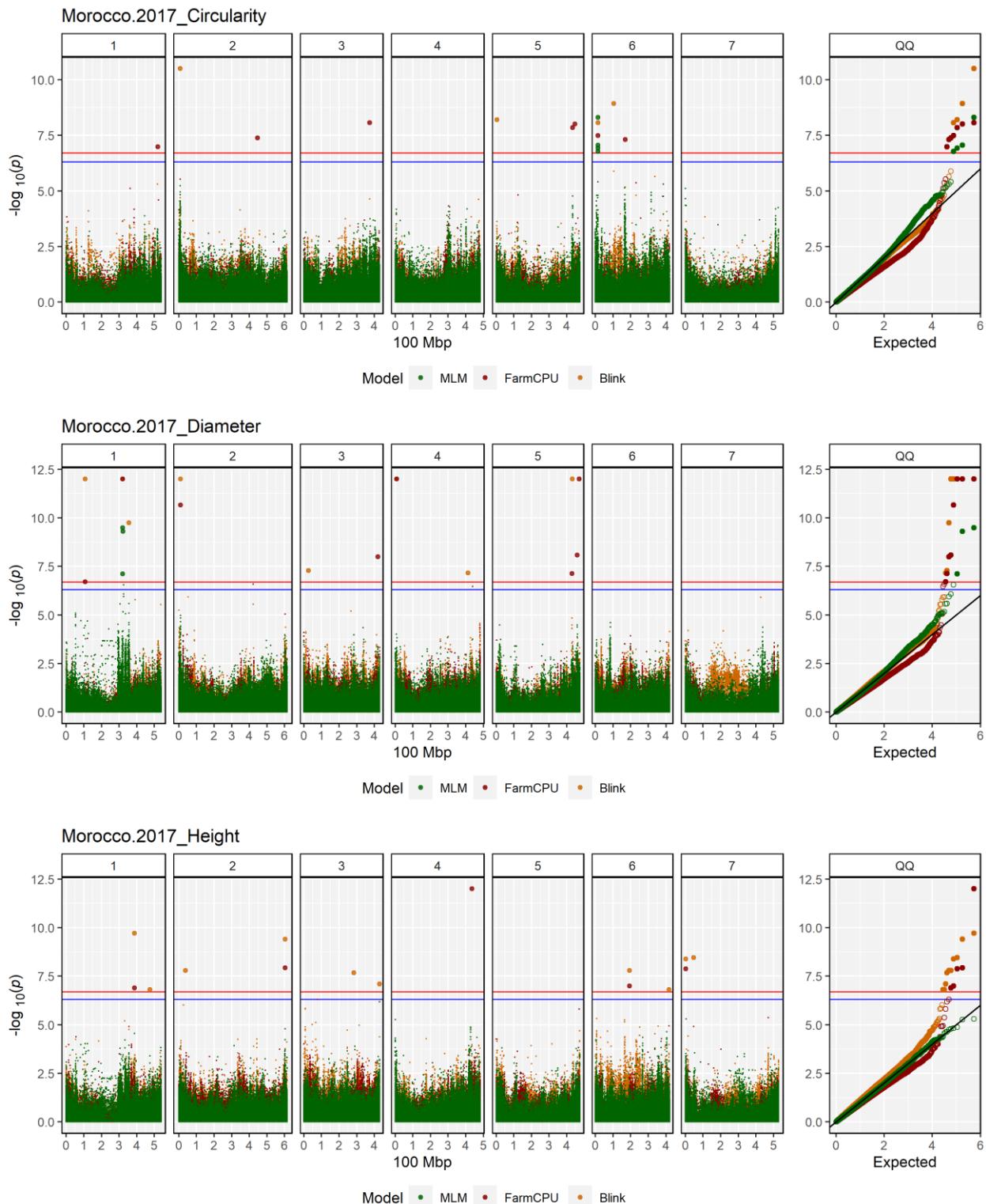


Figure K.1. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Metaponto 2017 with thermal flowering time used as covariate. The x axis represents lentil chromosomes, and the Y axis is -log₁₀ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log₁₀(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log₁₀(P)>6.3]. The x axis on the Q-Q plots is the expected -log₁₀ of p-values and the y axis is the observed -log₁₀ of p-values.



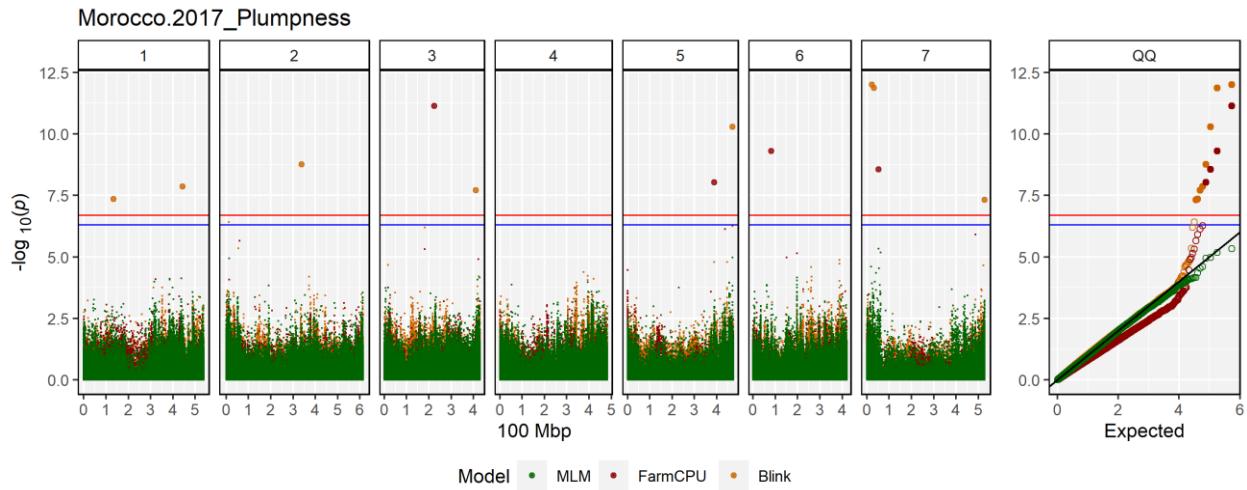
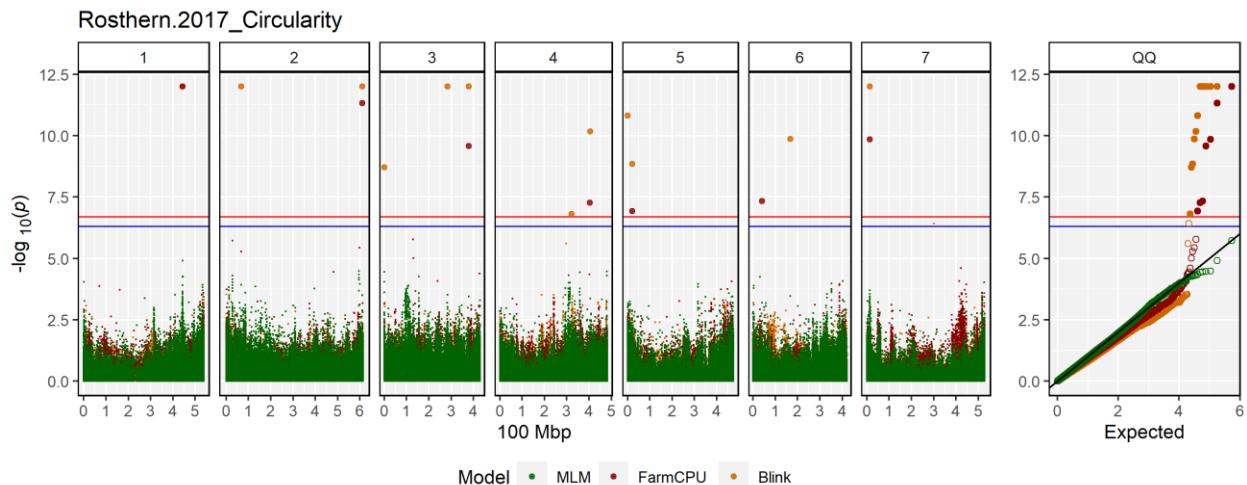


Figure K.2. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Morocco 2017 with thermal flowering time used as a covariate. The x axis represents lentil chromosomes, and the Y axis is -log10 of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log10(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log10(P)>6.3]. The x axis on the Q-Q plots is the expected -log10 of p-values and the y axis is the observed -log10 of p-values.



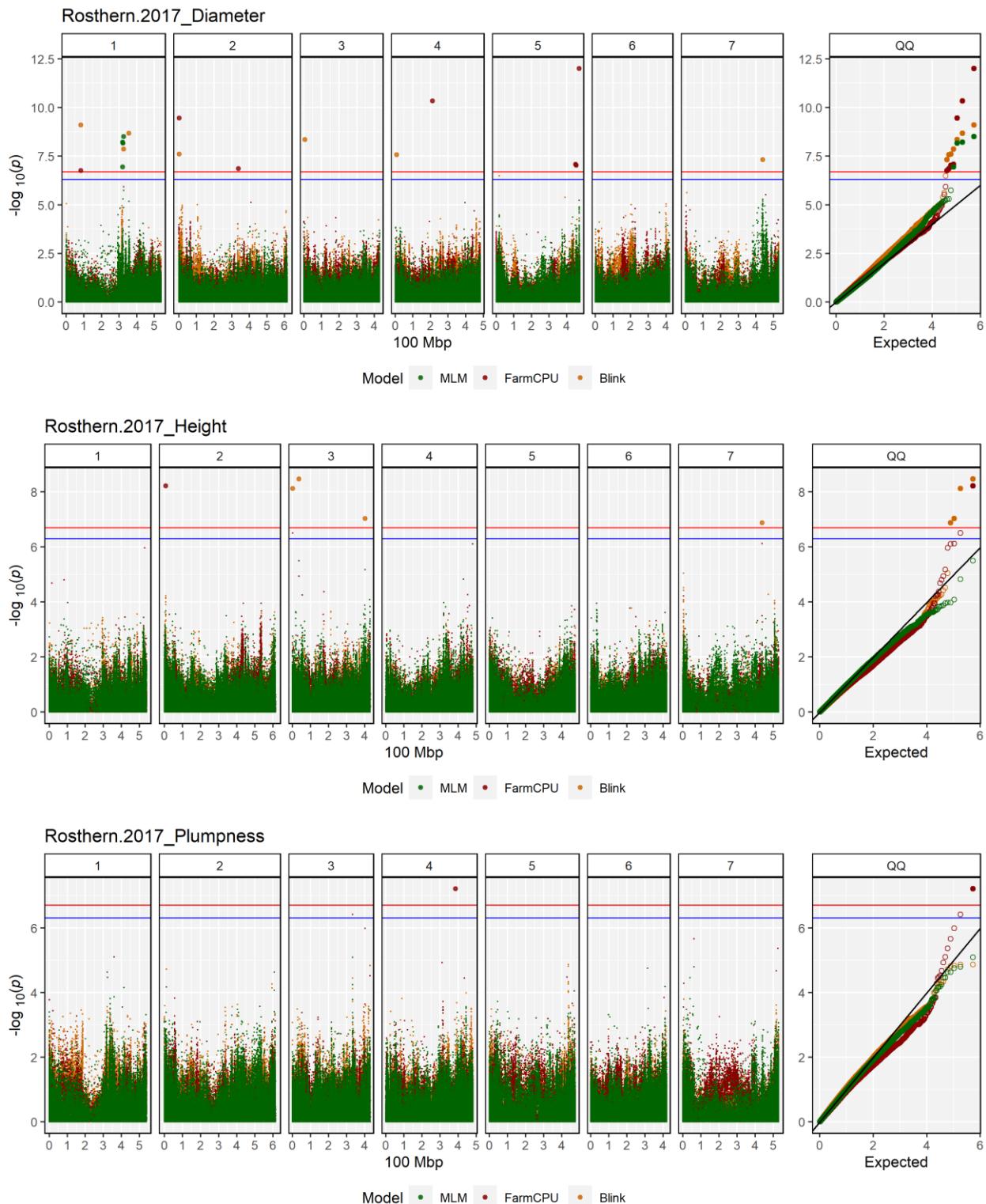
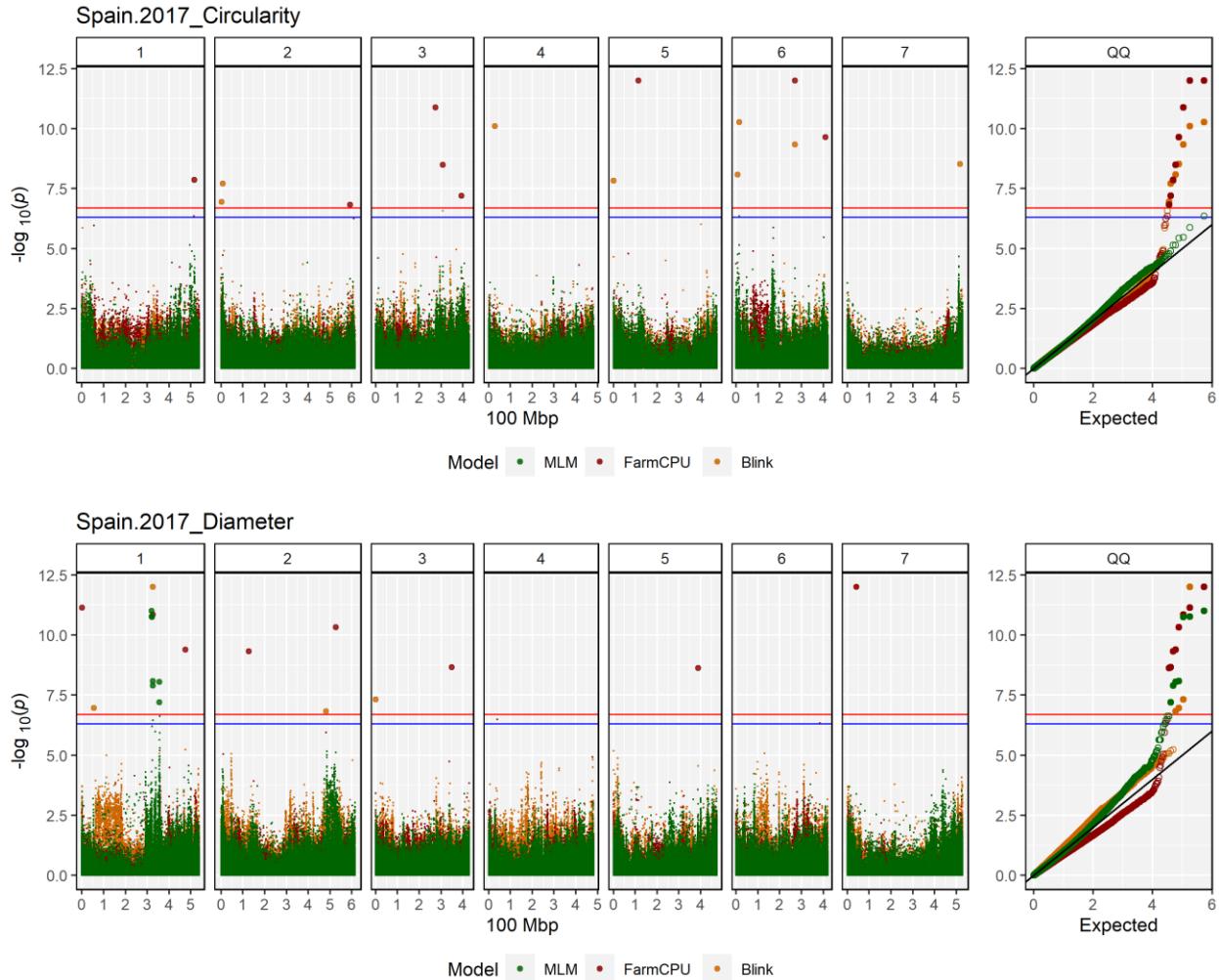


Figure K.3. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Rostthern 2017 with thermal flowering time used as a covariate. The x axis represents lentil

chromosomes, and the Y axis is -log₁₀ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log₁₀(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log₁₀(P)>6.3]. The x axis on the Q-Q plots is the expected -log₁₀ of p-values and the y axis is the observed -log₁₀ of p-values.



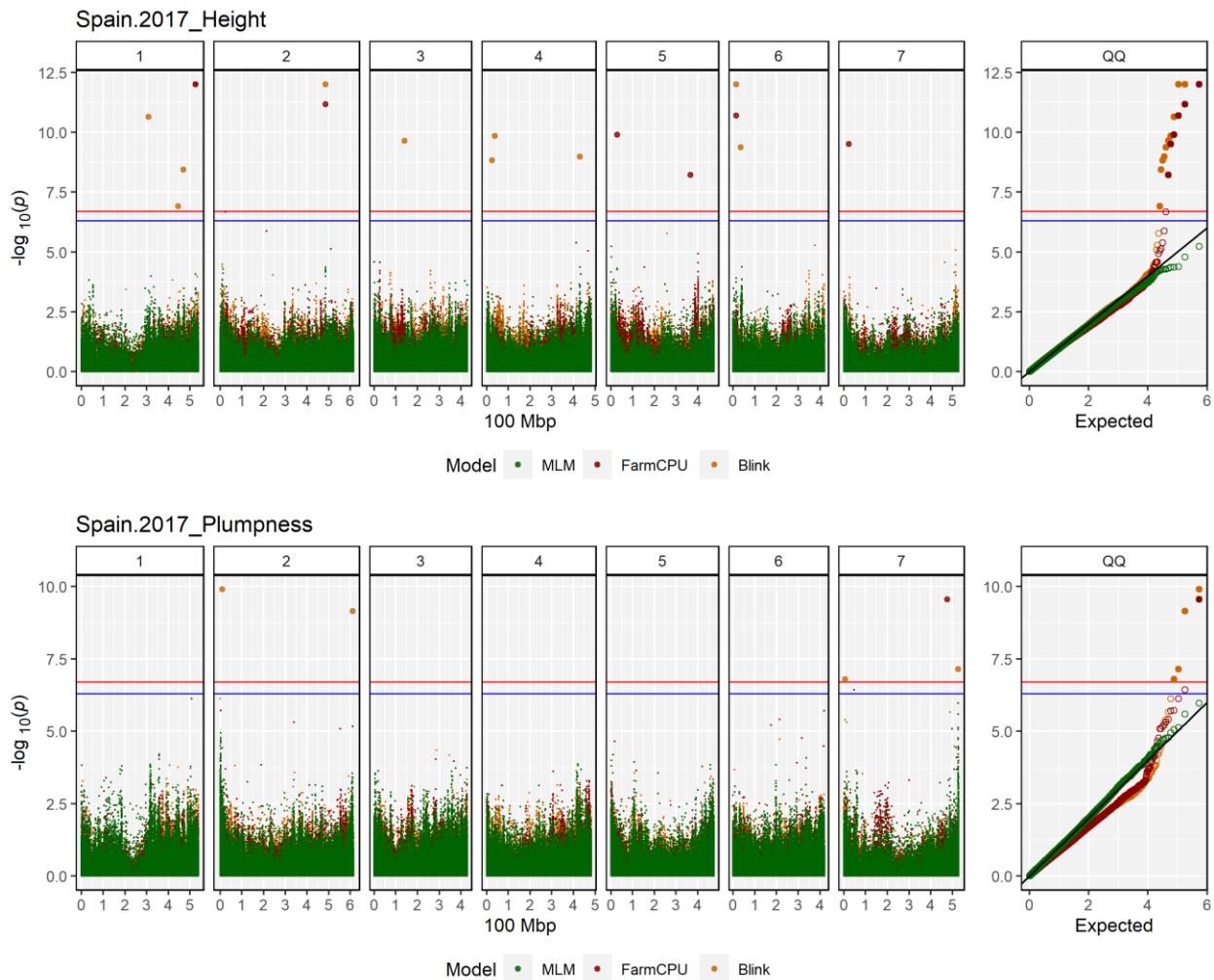
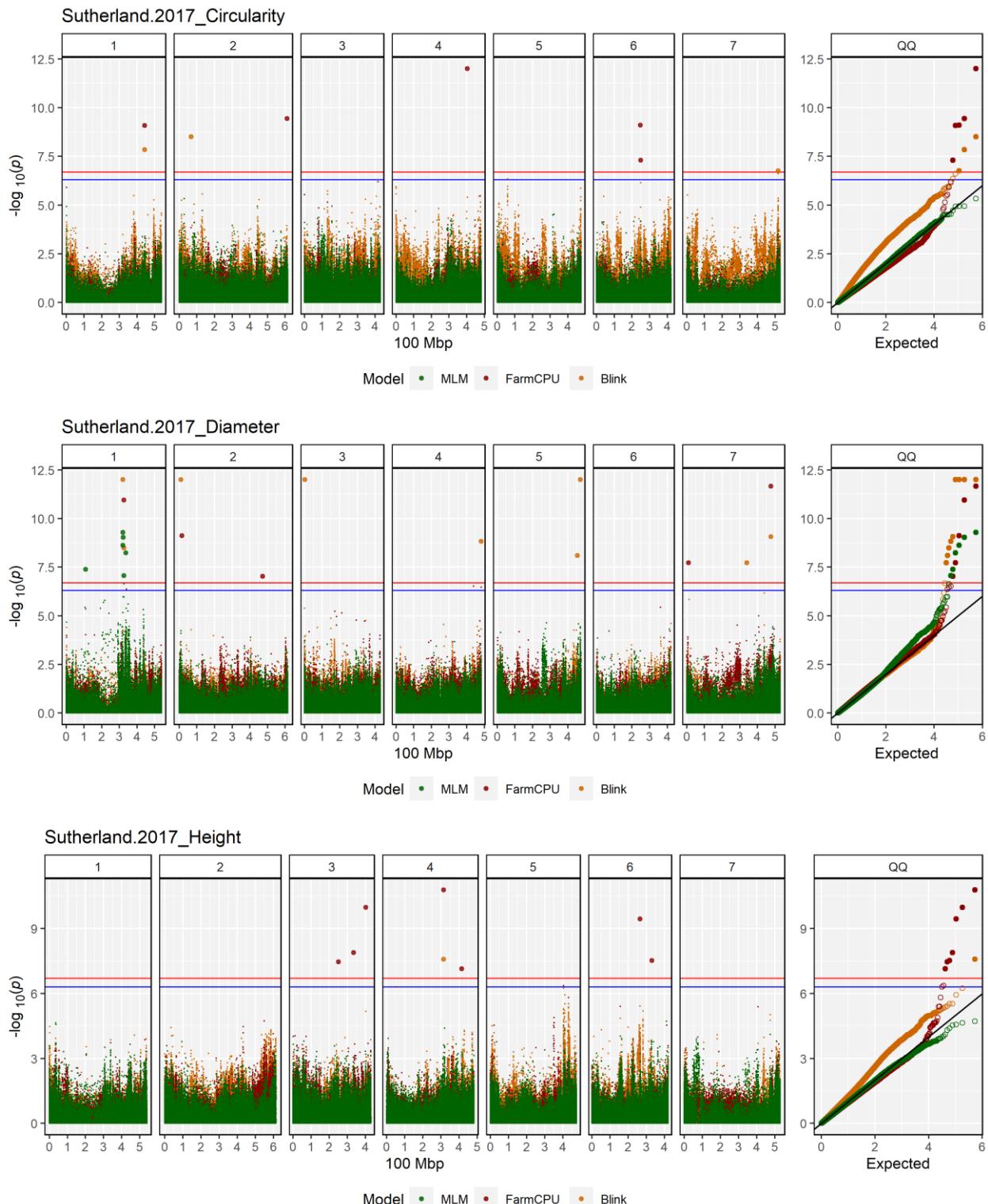


Figure K.4. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Spain 2017 using thermal flowering time as a covariate. The x axis represents lentil chromosomes, and the Y axis is -log₁₀ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log₁₀(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log₁₀(P)>6.3]. The x axis on the Q-Q plots is the expected -log₁₀ of p-values and the y axis is the observed -log₁₀ of p-values.



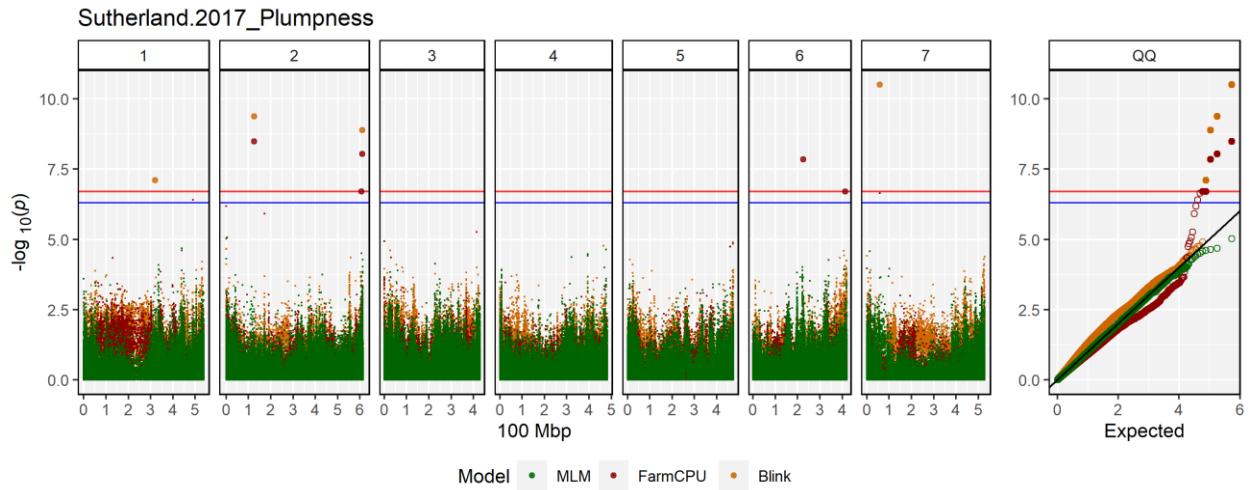
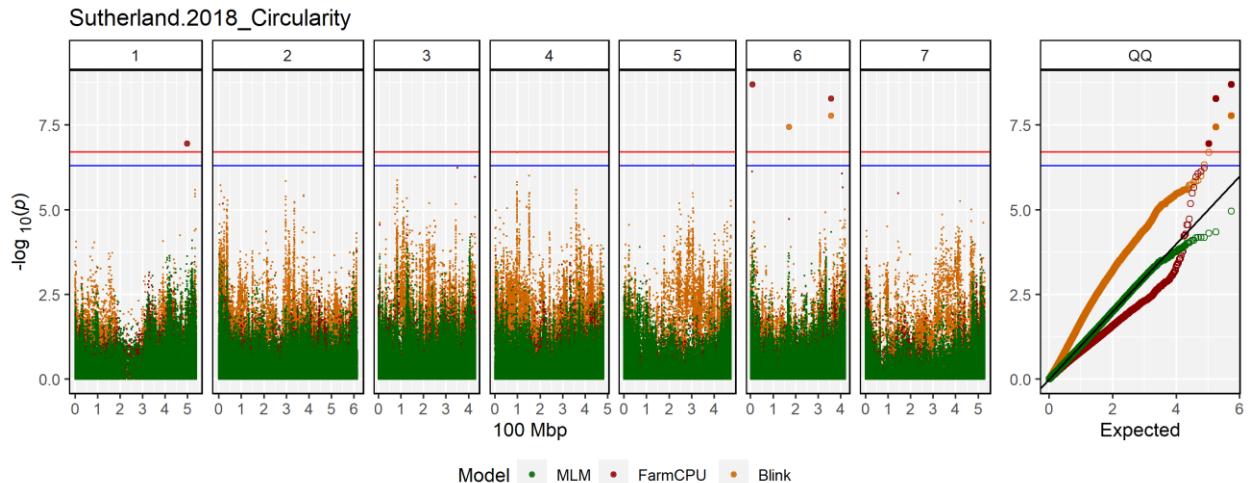


Figure K.5. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Sutherland 2017 with thermal flowering time used as covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



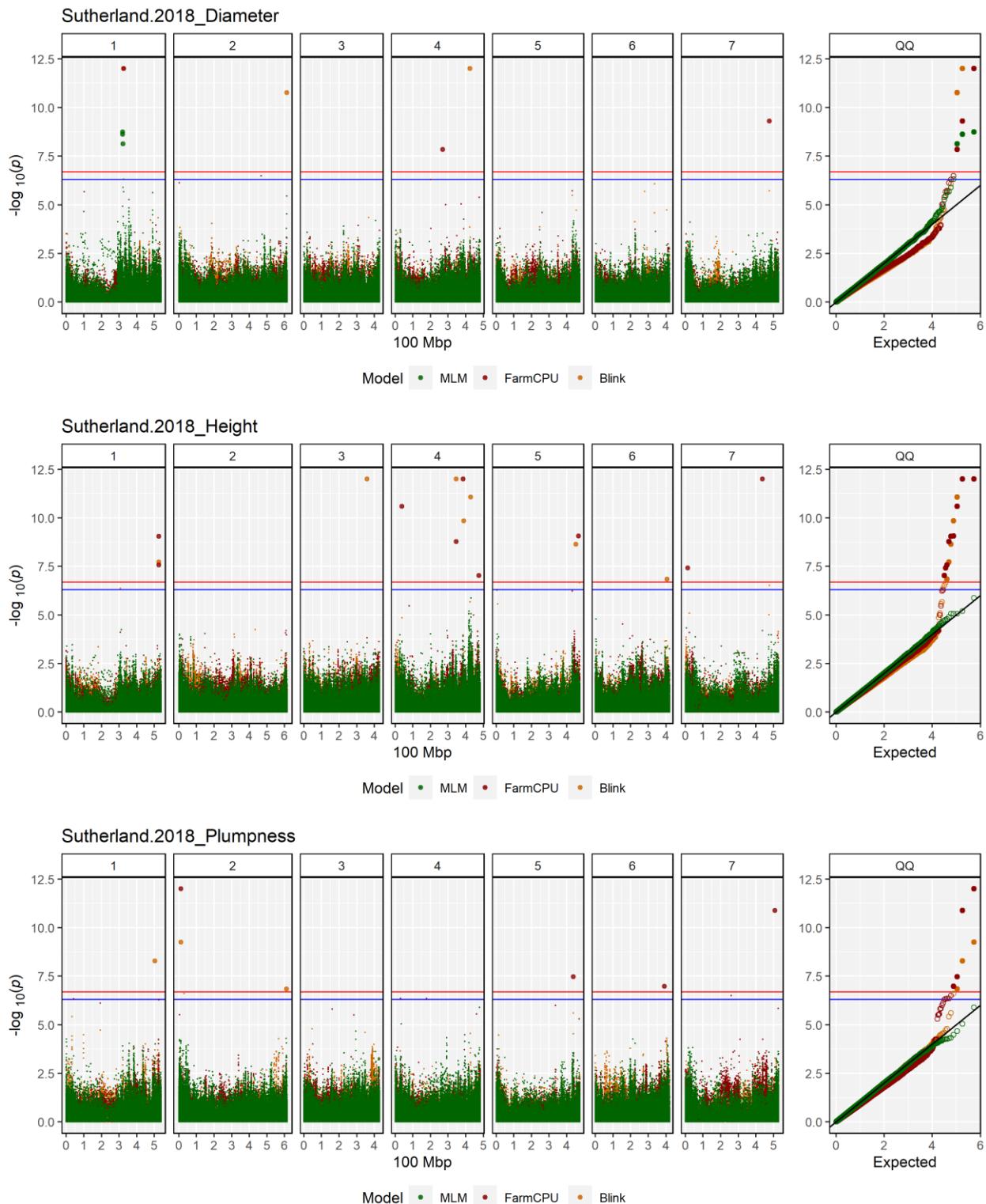
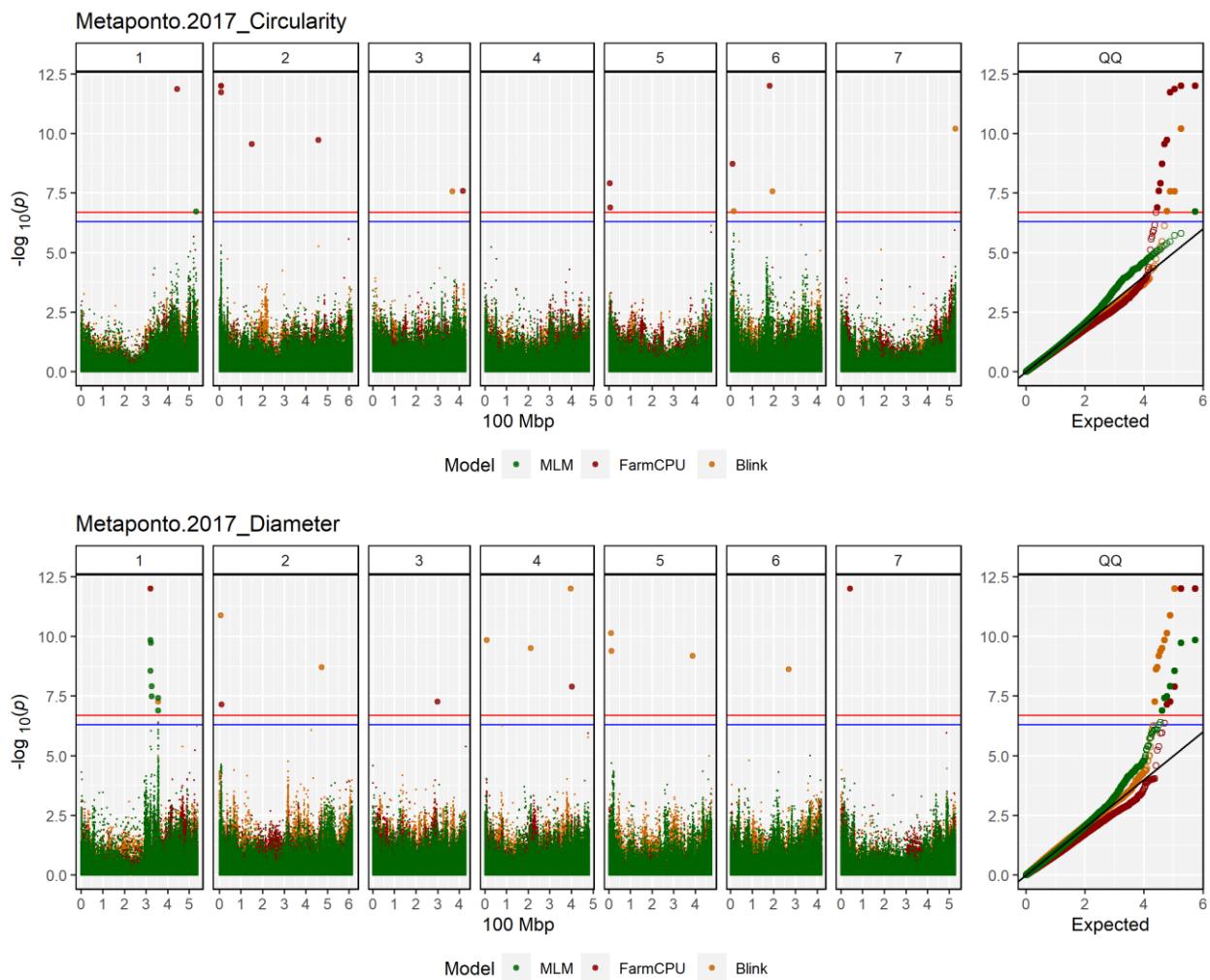


Figure K.6. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Sutherland 2018 with thermal flowering time used as a covariate. The x axis represents lentil

chromosomes, and the Y axis is -log10 of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected -log10 of p-values and the y axis is the observed -log10 of p-values.

Appendix L

Manhattan plots from GWAS with thermal reproductive time as covariate



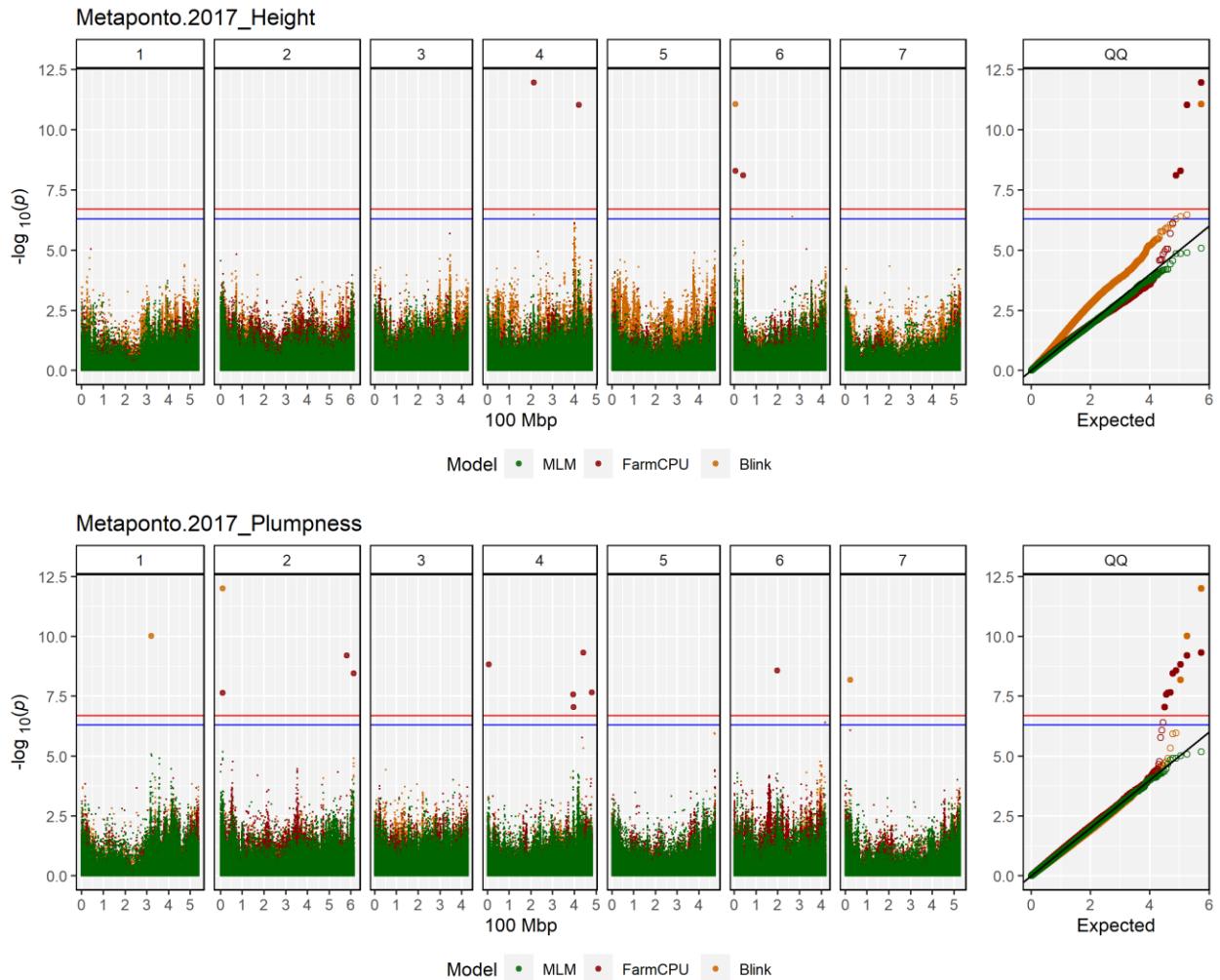
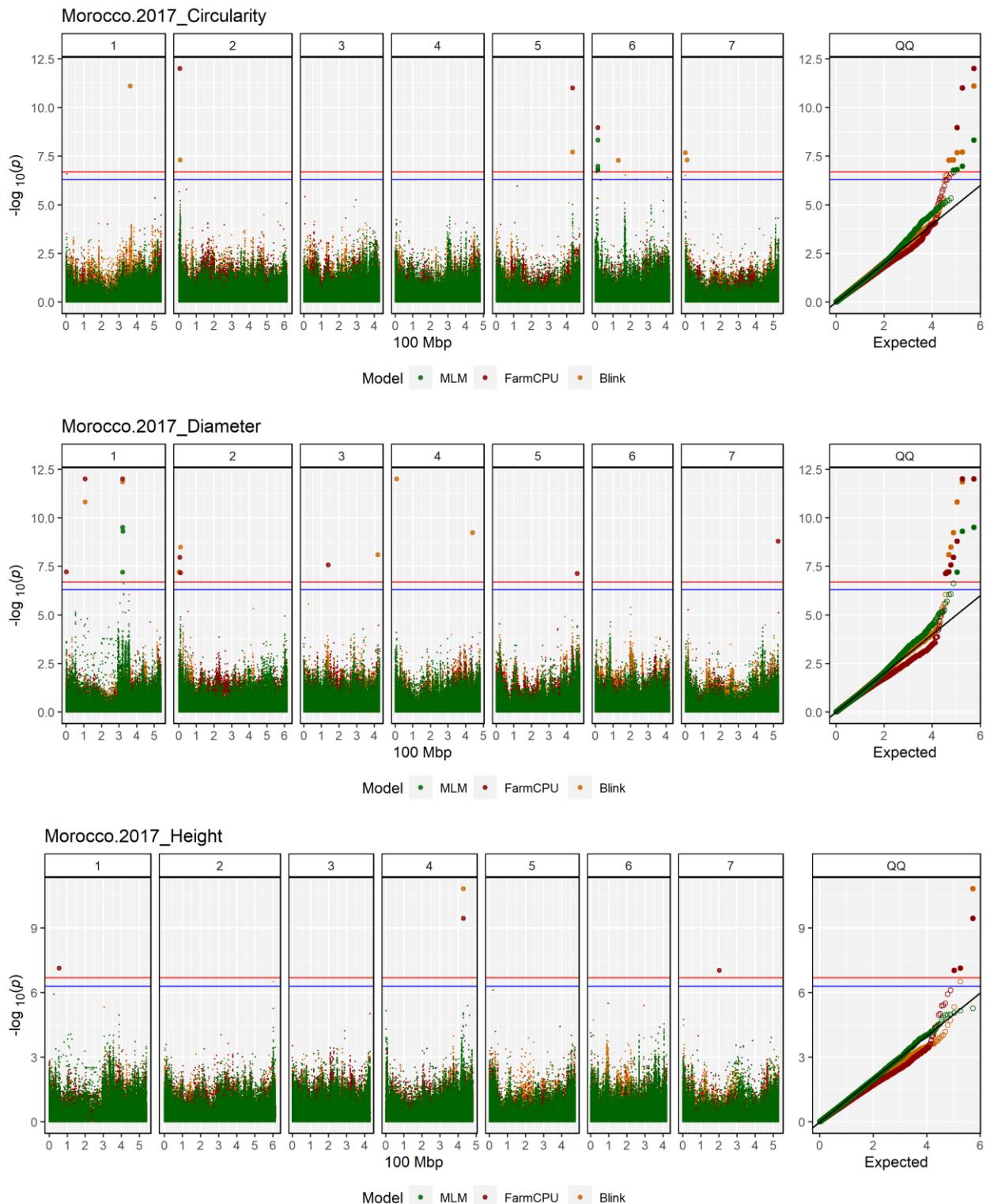


Figure L.1. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Metaponto 2017 with thermal reproductive time used as covariate. The x axis represents lentil chromosomes, and the Y axis is -log₁₀ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log₁₀(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log₁₀(P)>6.3]. The x axis on the Q-Q plots is the expected -log₁₀ of p-values and the y axis is the observed -log₁₀ of p-values.



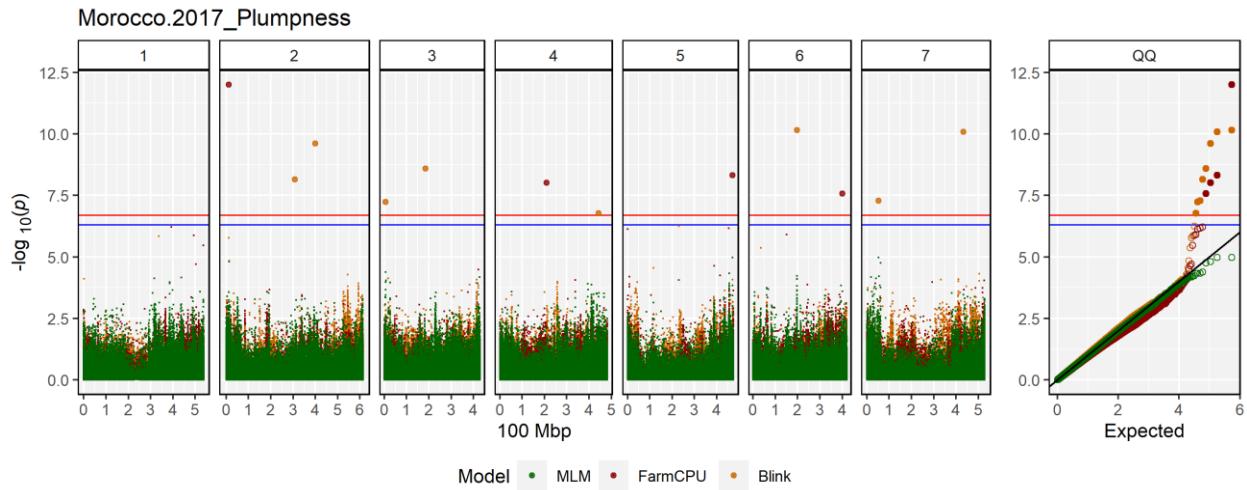
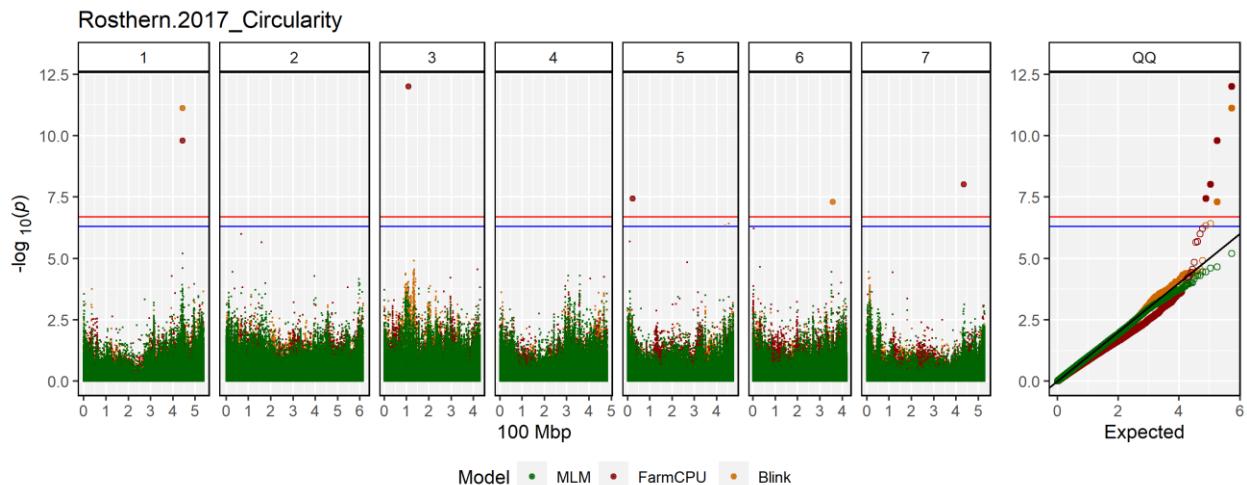


Figure L.2. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Morocco 2017 with thermal reproductive time used as a covariate. The x axis represents lentil chromosomes, and the Y axis is -log₁₀ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log₁₀(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log₁₀(P)>6.3]. The x axis on the Q-Q plots is the expected -log₁₀ of p-values and the y axis is the observed -log₁₀ of p-values.



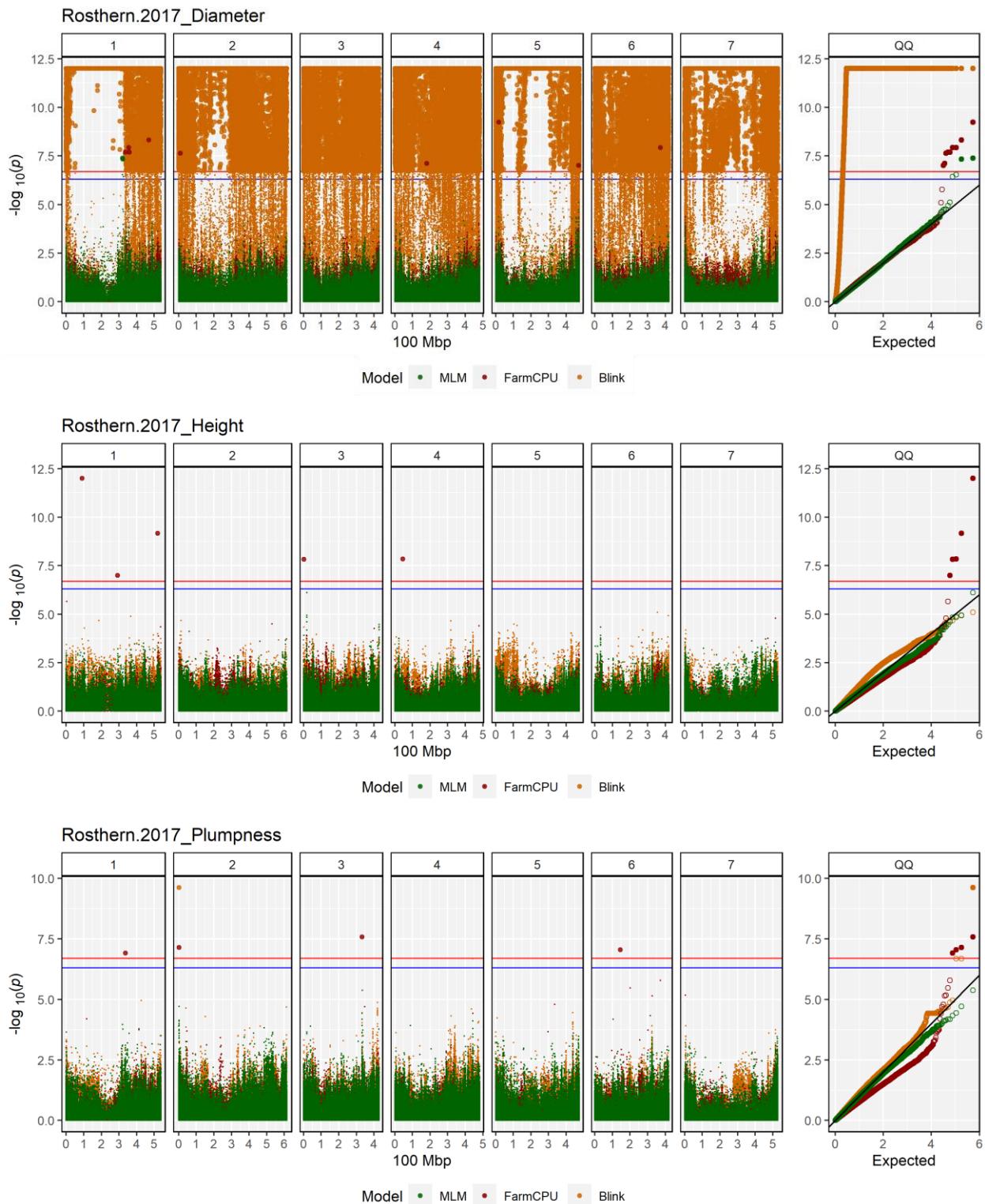
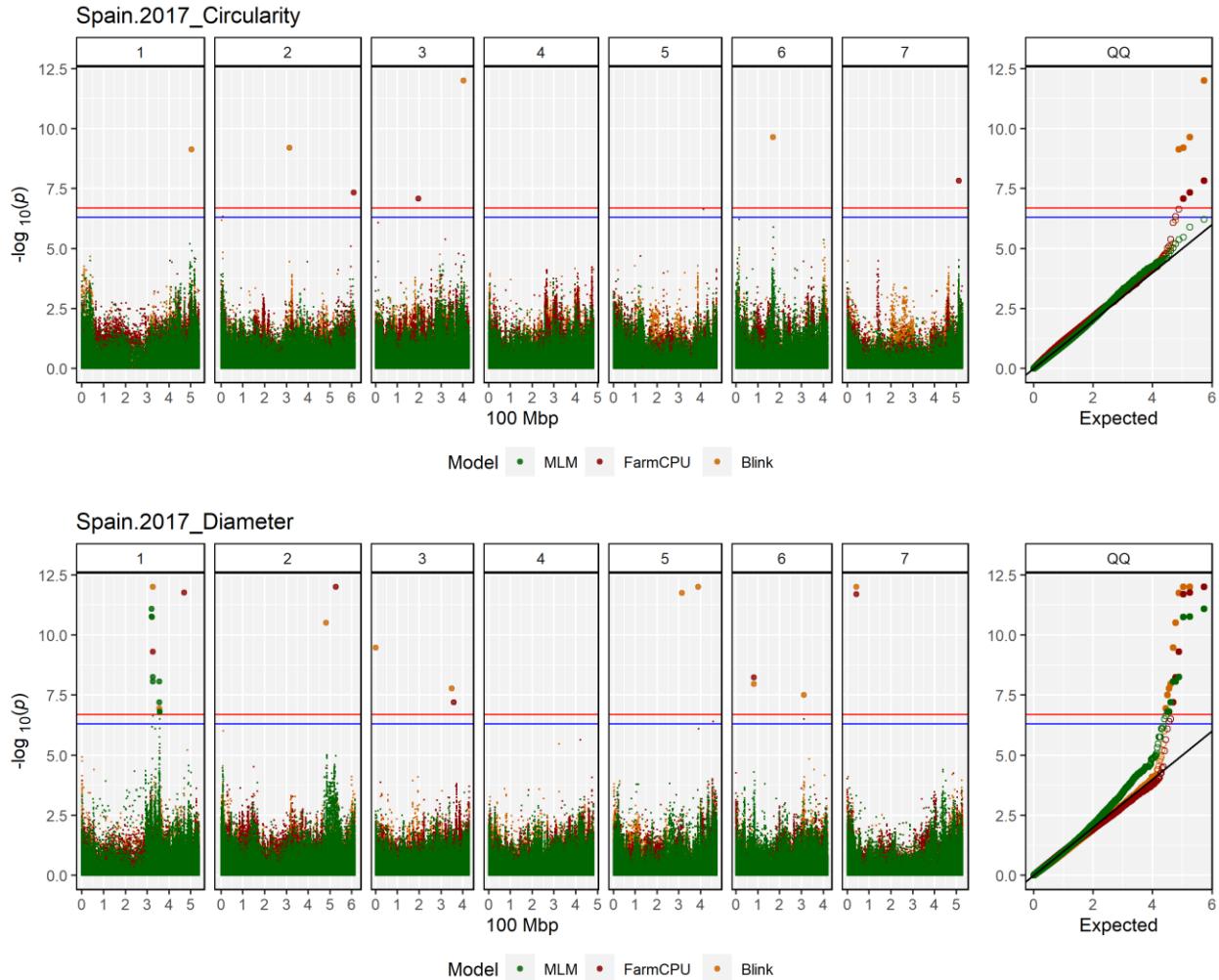


Figure L.3. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Rostthern 2017 with thermal reproductive time used as a covariate. The x axis represents lentil

chromosomes, and the Y axis is -log₁₀ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [-log₁₀(P)>6.7] and the red line across all chromosomes indicates a suggested threshold [-log₁₀(P)>6.3]. The x axis on the Q-Q plots is the expected -log₁₀ of p-values and the y axis is the observed -log₁₀ of p-values.



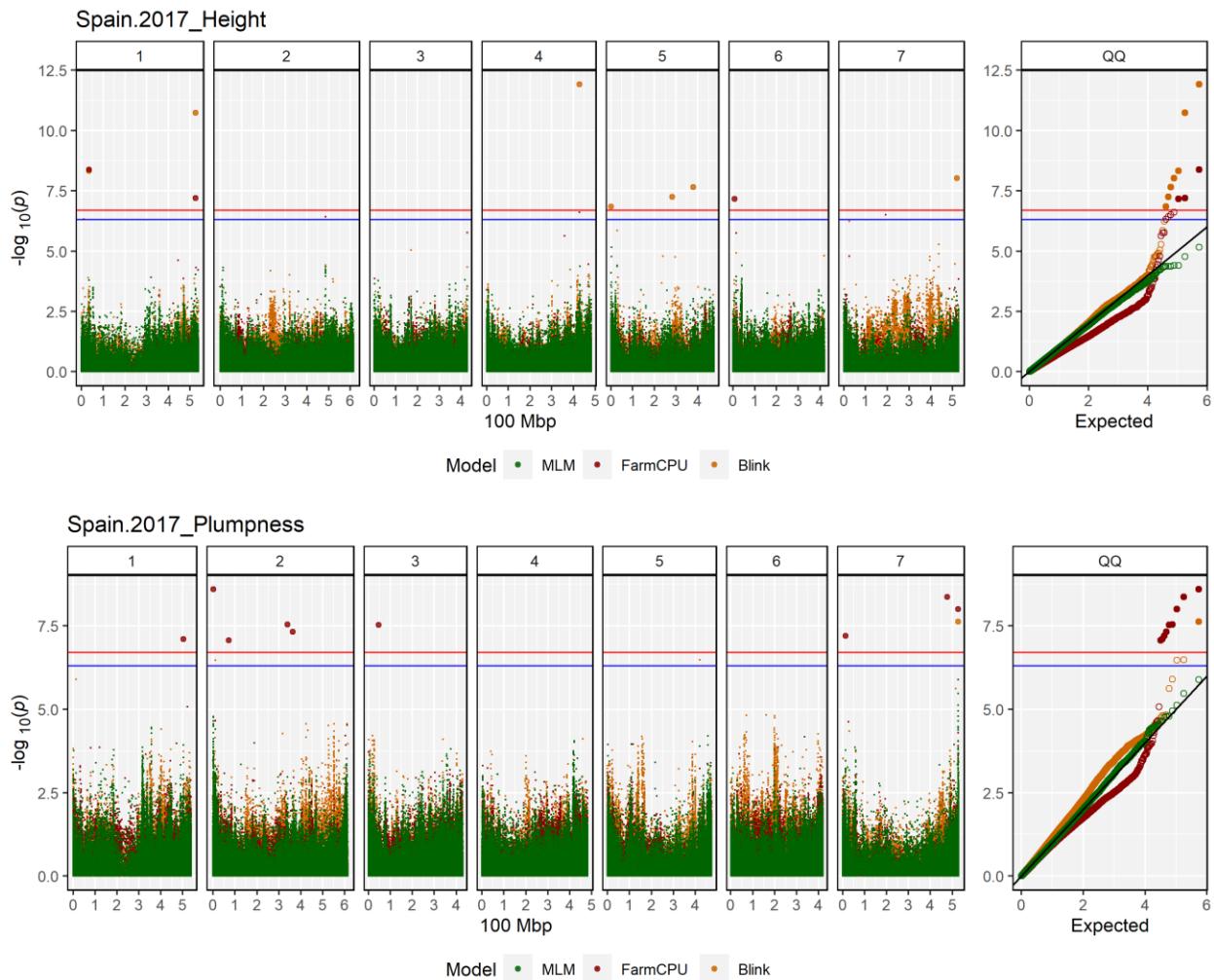
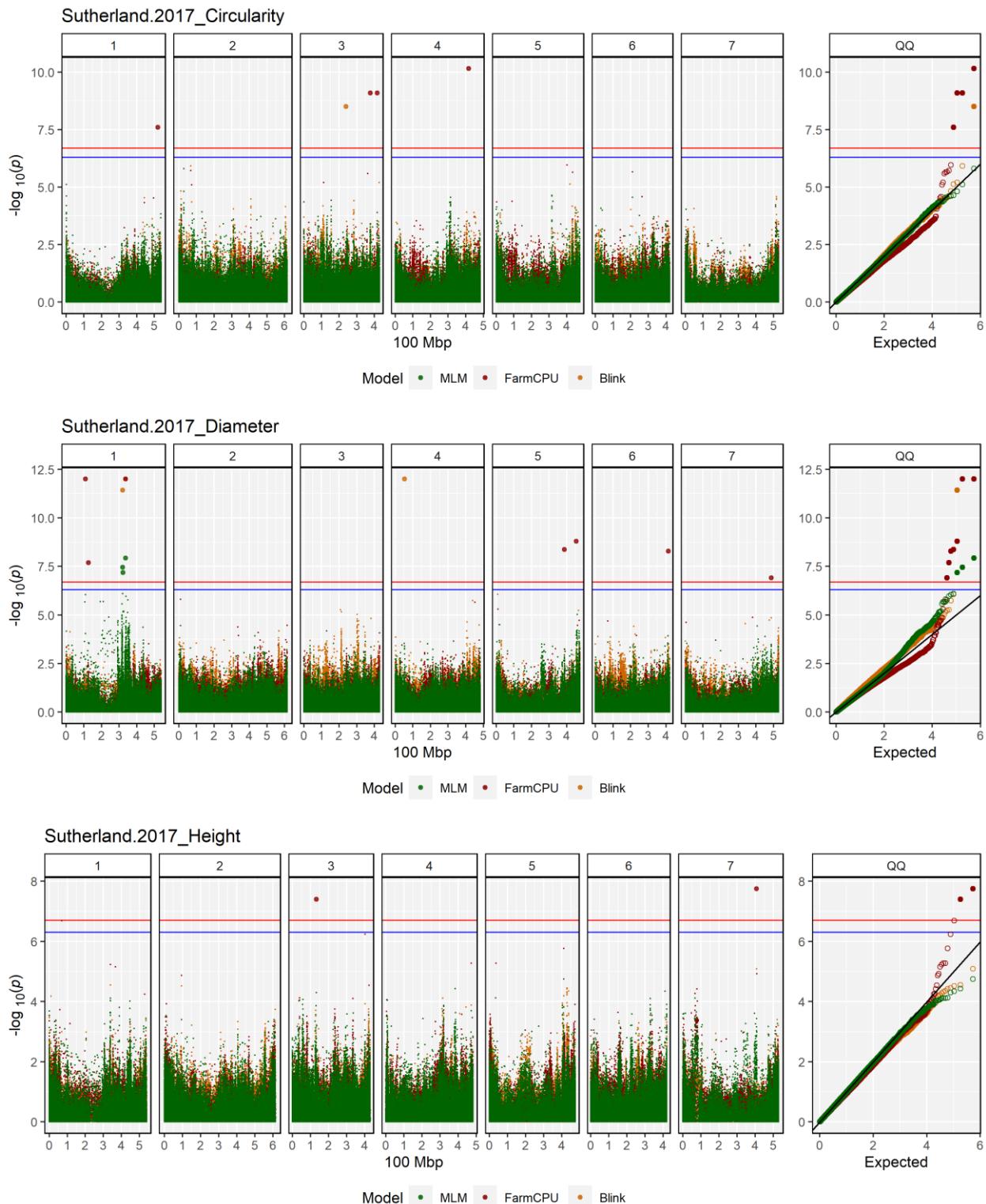


Figure L.4. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Spain 2017 using thermal reproductive time as a covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



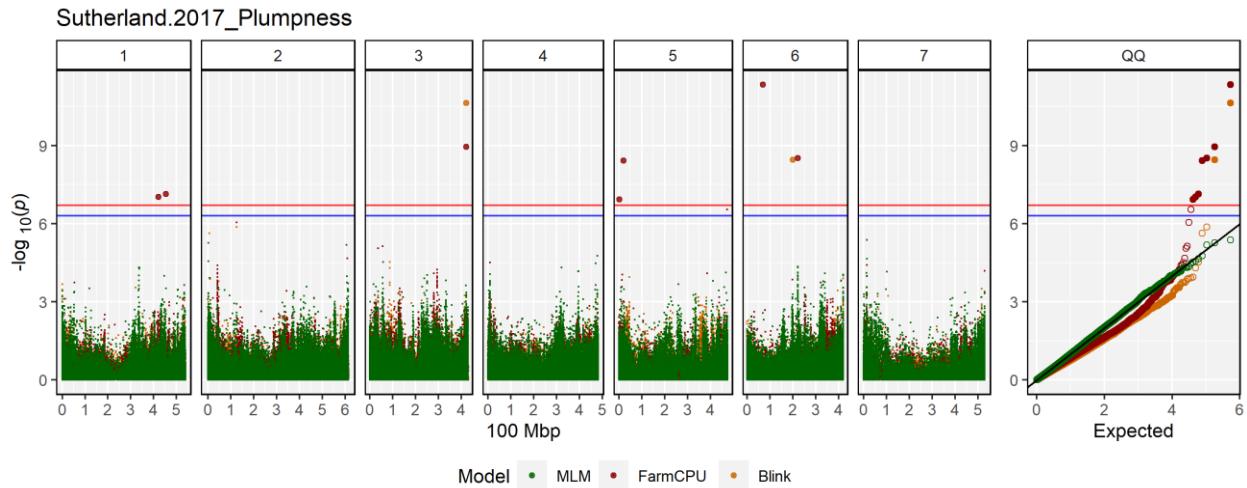
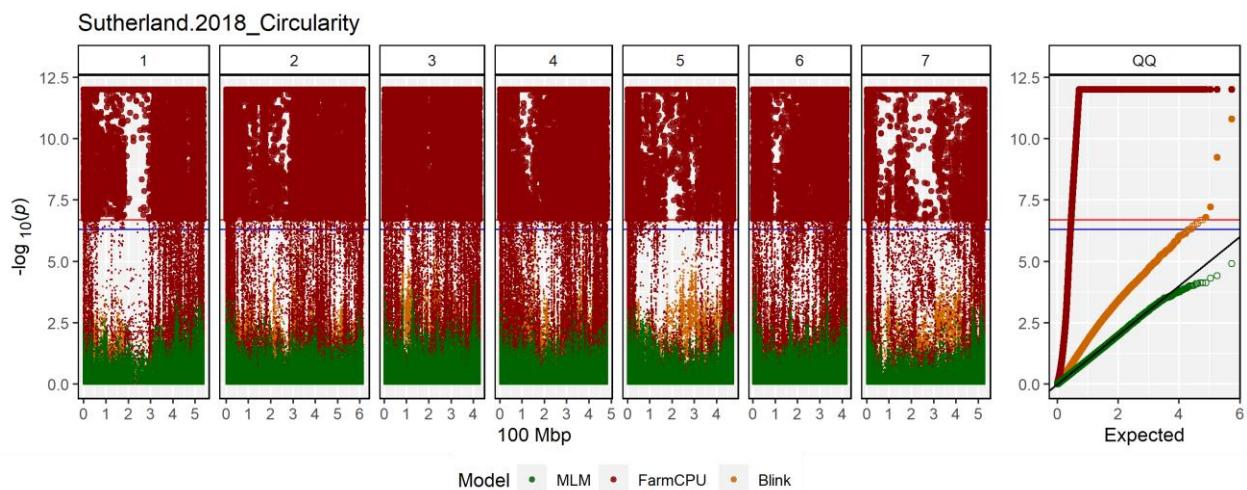


Figure L.5. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Sutherland 2017 with thermal reproductive time used as covariate. The x axis represents lentil chromosomes, and the Y axis is $-\log_{10}$ of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected $-\log_{10}$ of p-values and the y axis is the observed $-\log_{10}$ of p-values.



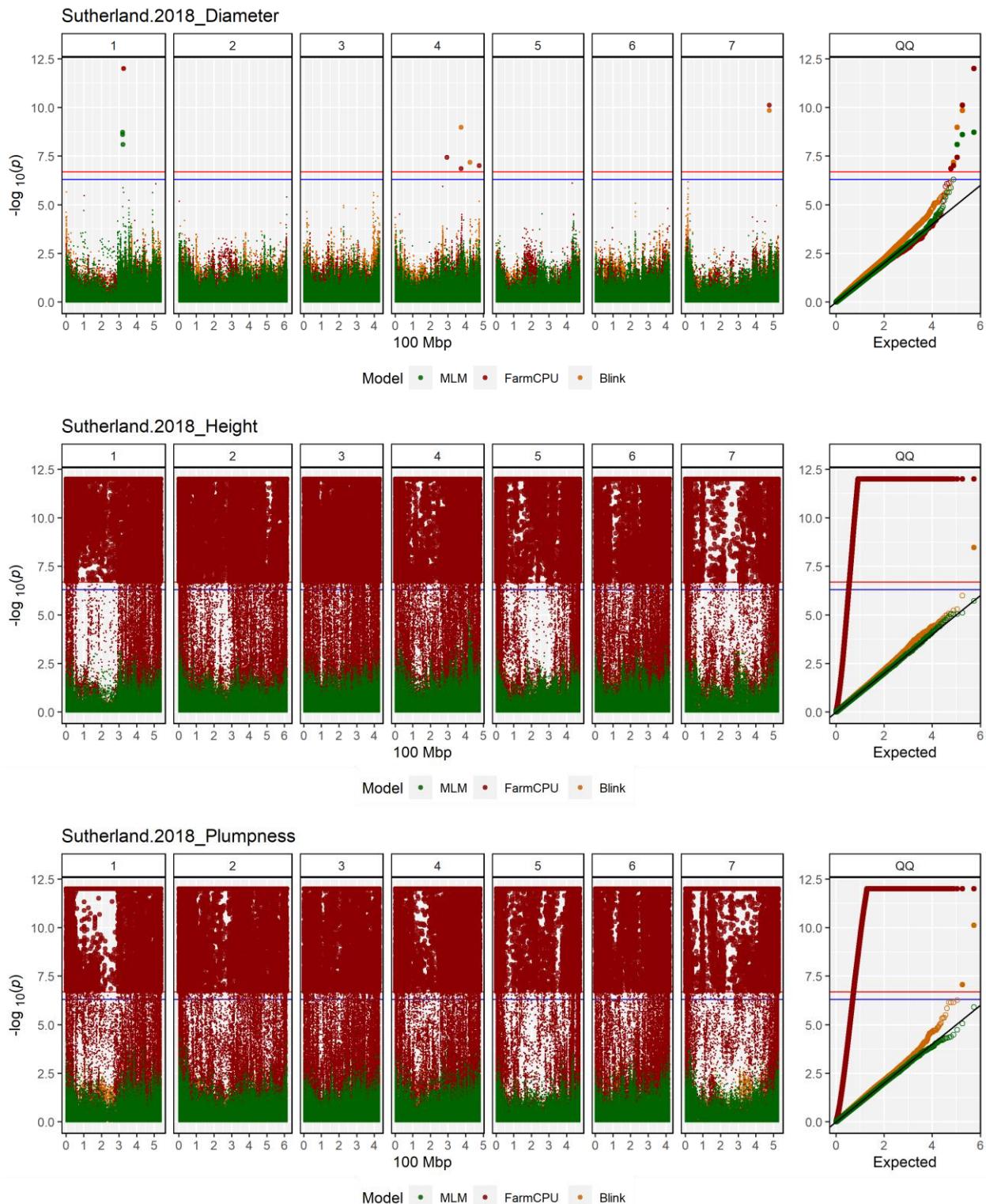


Figure L.6. Manhattan plots (left) and quantile-quantile (Q-Q) plots (right) from association studies using circularity, diameter, height, and plumpness of 324 genotypes grown in the field in Sutherland 2018 with thermal reproductive time used as a covariate. The x axis represents lentil

chromosomes, and the Y axis is -log10 of the p-values. Adjacent chromosomes are separated by boxes with the chromosome number. The blue line across all chromosomes indicates a significance threshold [$-\log_{10}(P) > 6.7$] and the red line across all chromosomes indicates a suggested threshold [$-\log_{10}(P) > 6.3$]. The x axis on the Q-Q plots is the expected -log10 of p-values and the y axis is the observed -log10 of p-values.

Appendix M

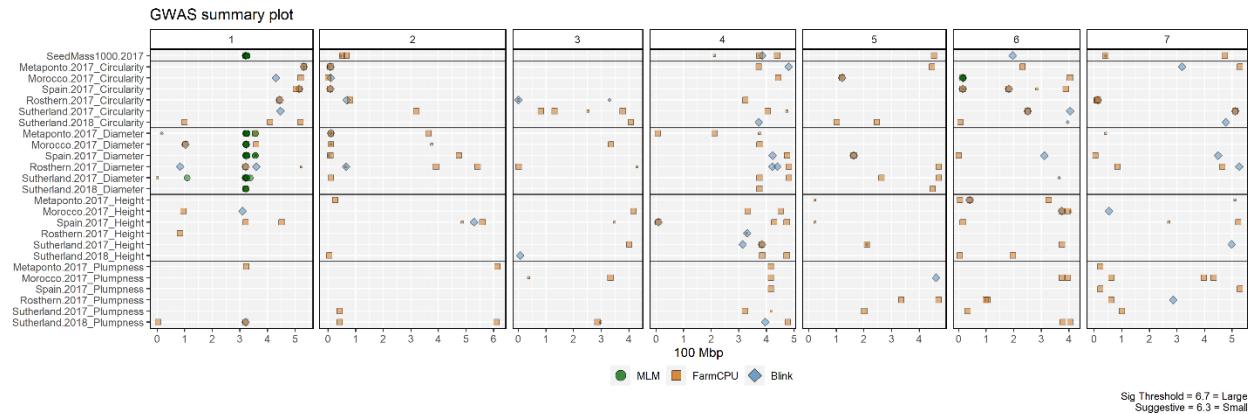


Figure M.1. Summary plots of significant GWAS results of diameter, circularity, height, plumpness and seed mass of 324 genotypes grown in the field in Metaponto 2017, Morocco 2017, Spain 2017, Rostthern 2017, Sutherland 2017 and Sutherland 2018. The x axis represents lentil chromosomes, and the Y axis is -log10 of the p-values. Boxes in the Y axis separate the traits evaluated. Adjacent chromosomes are separated by boxes with the chromosome number. The shapes within the plot show markers detected above a significance threshold [$-\log_{10}(P) > 6.7$] for larger shapes and a significance threshold [$-\log_{10}(P) > 6.3$] for smaller shapes.