

Applying genotypic principal component scores as latent phenotypes in genome-wide and epistatic analyses of soybean agronomic traits.

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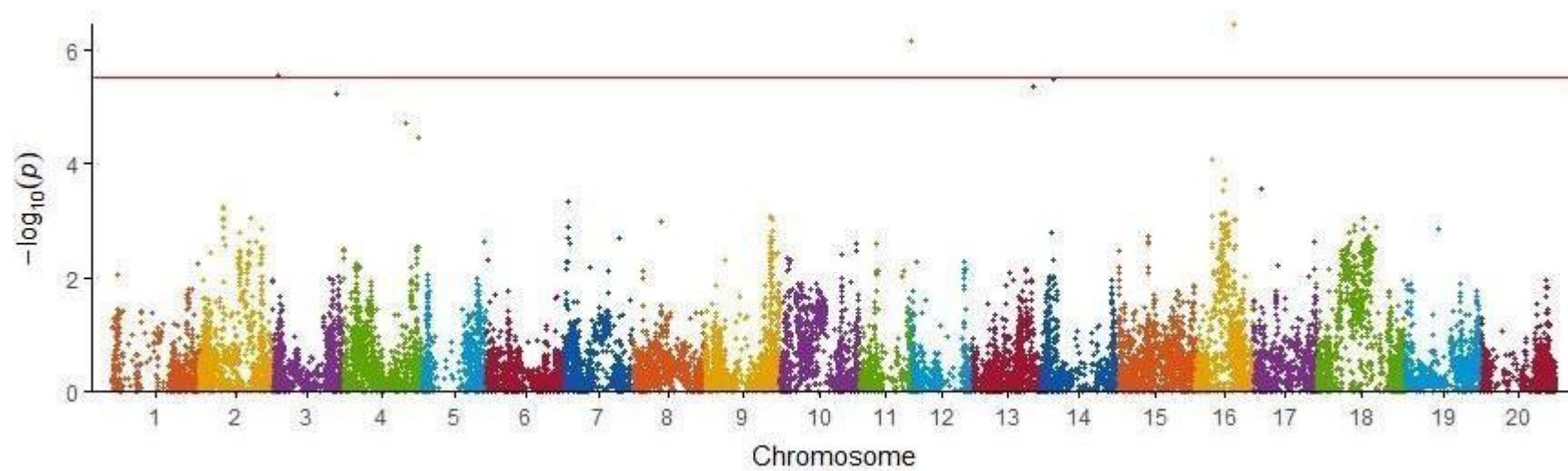
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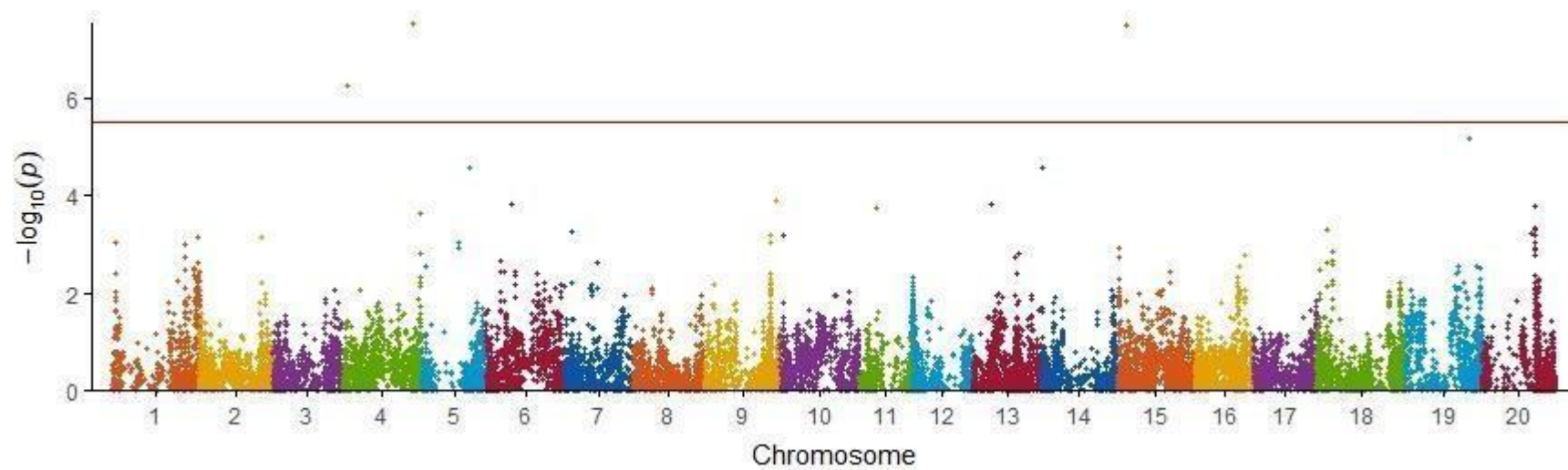
Elroy Cober, elroy.cober@agr.gc.ca

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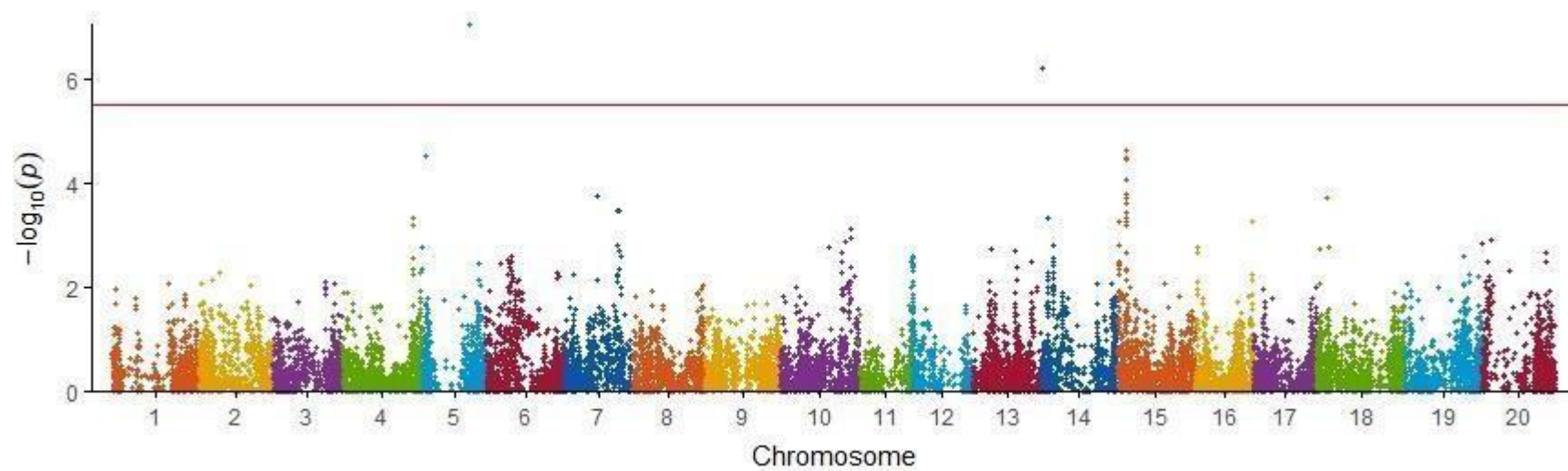
a Gapit, FarmCPU, Maturity PC2



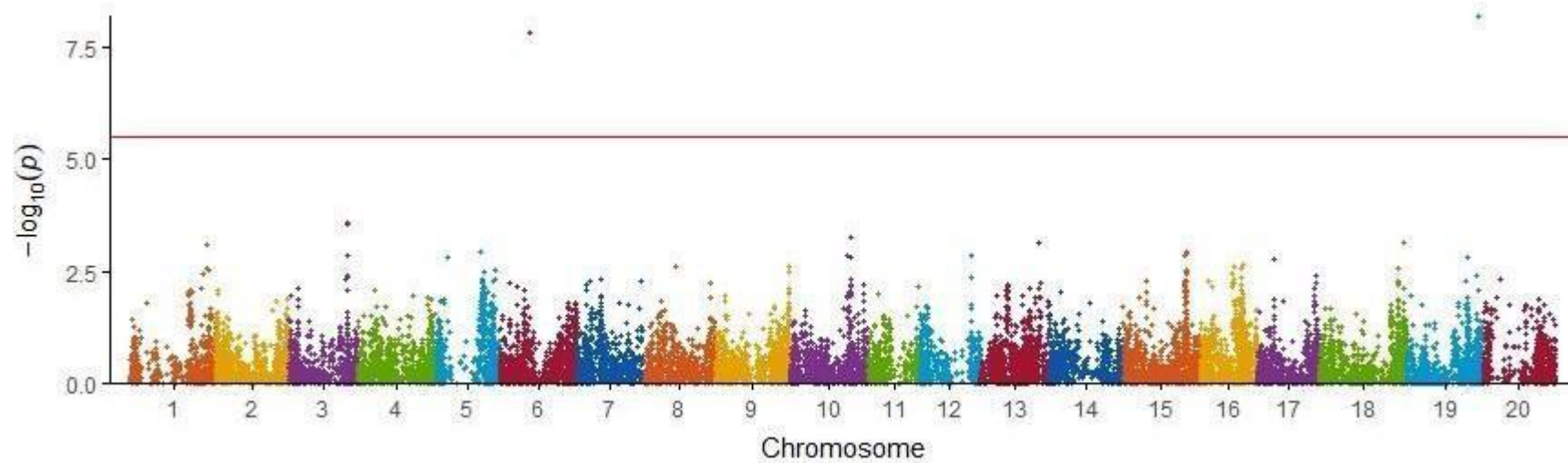
b Gapit, FarmCPU, Oil PC1



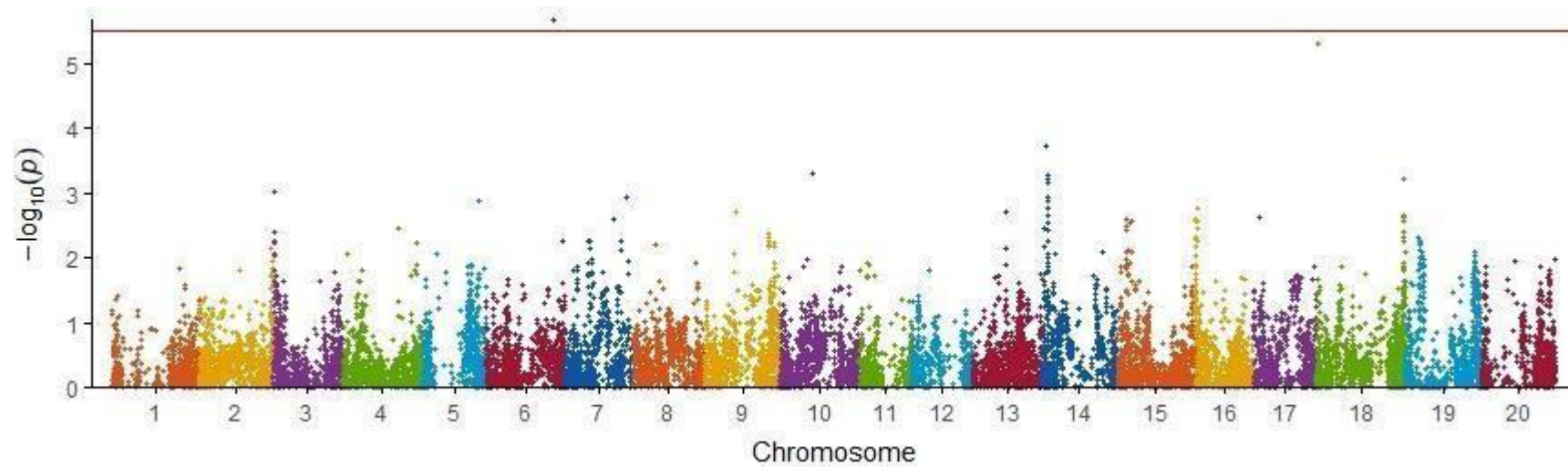
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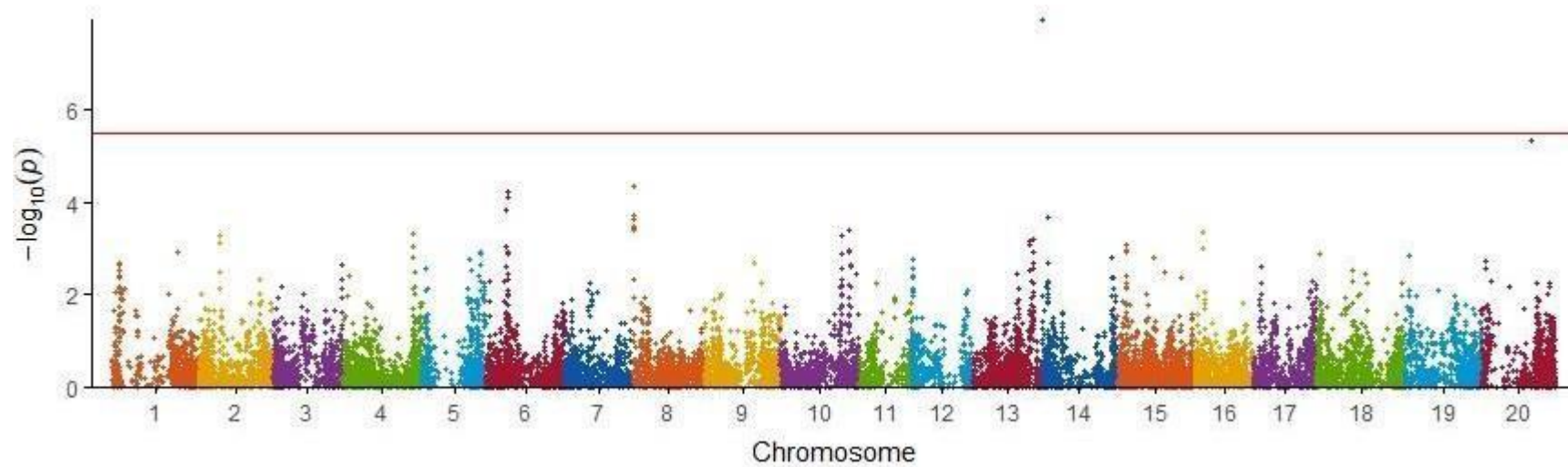
d Gapit, MLMM, Plant Height PC1



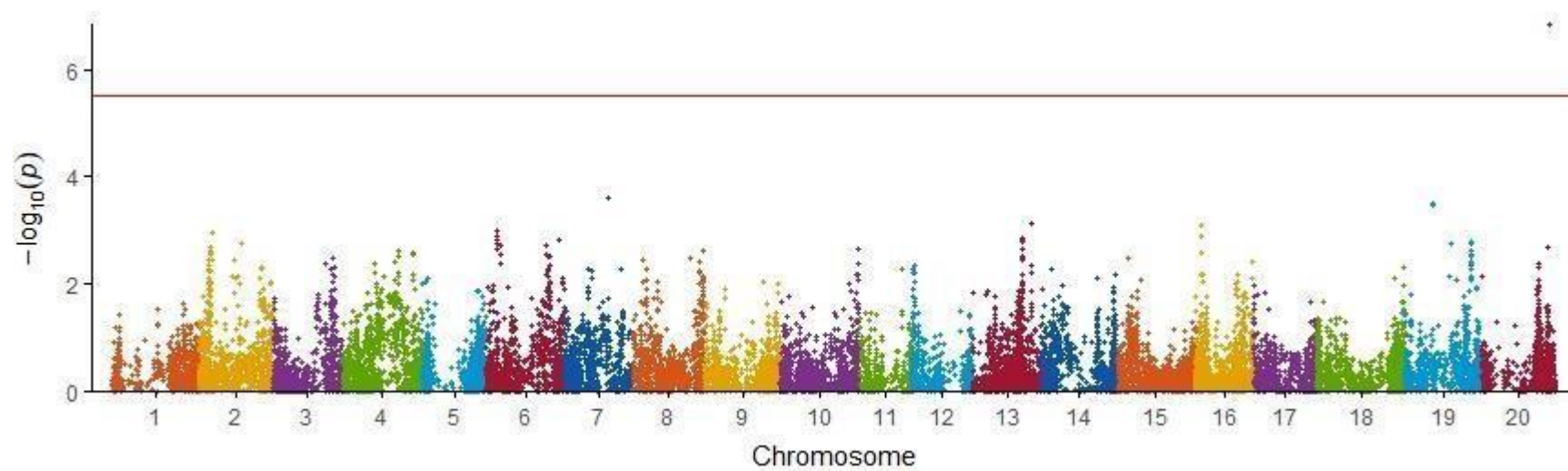
e Gapit, MLMM, Plant Height PC4



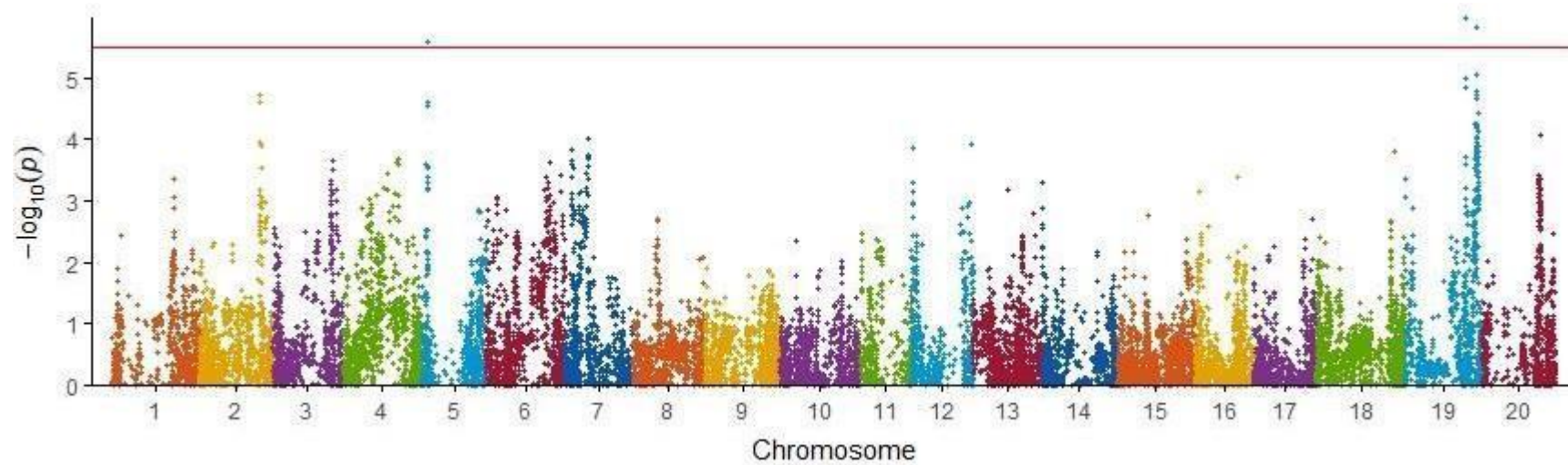
f Gapit, MLMM, Protein PC1



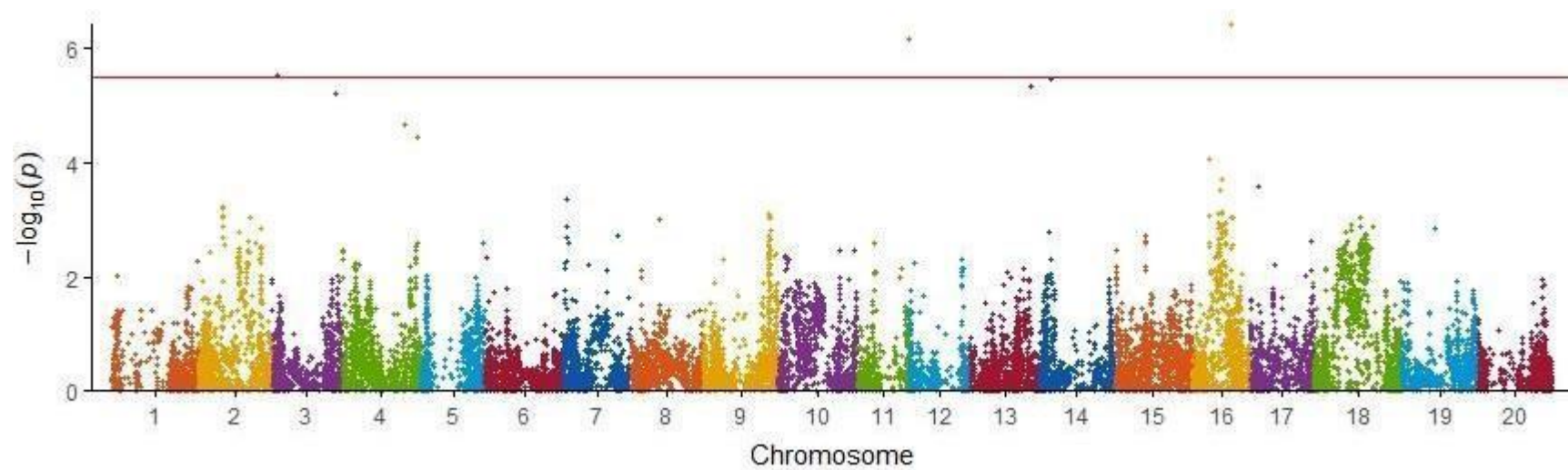
g Gapit, MLMM, Seed Weight PC1



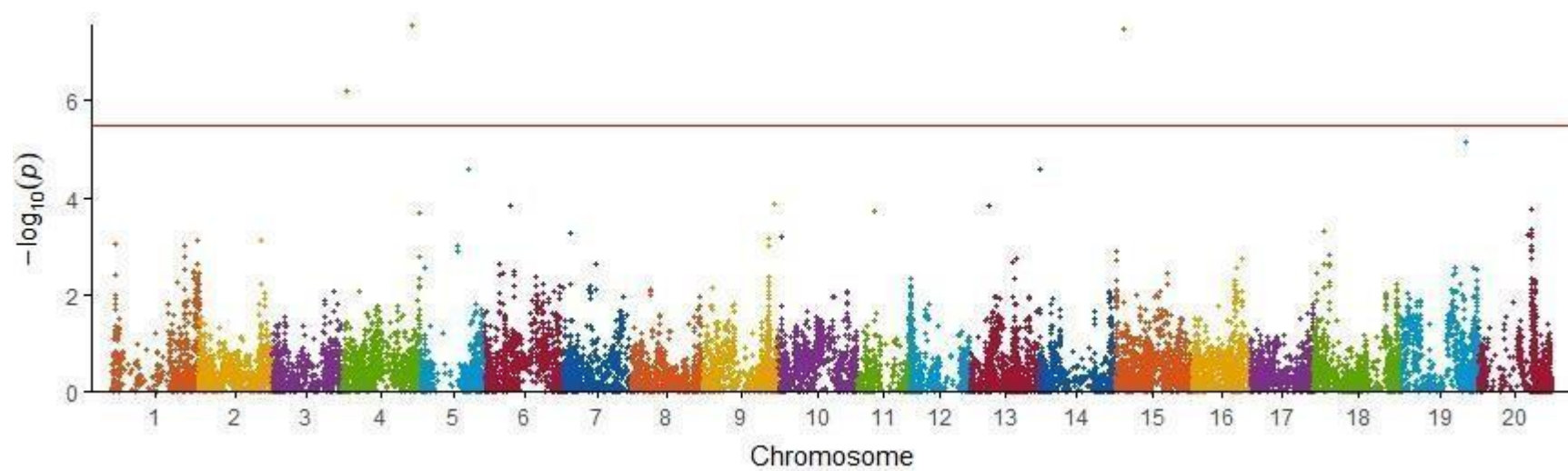
h rMVP, FamCPU, Maturity PC1



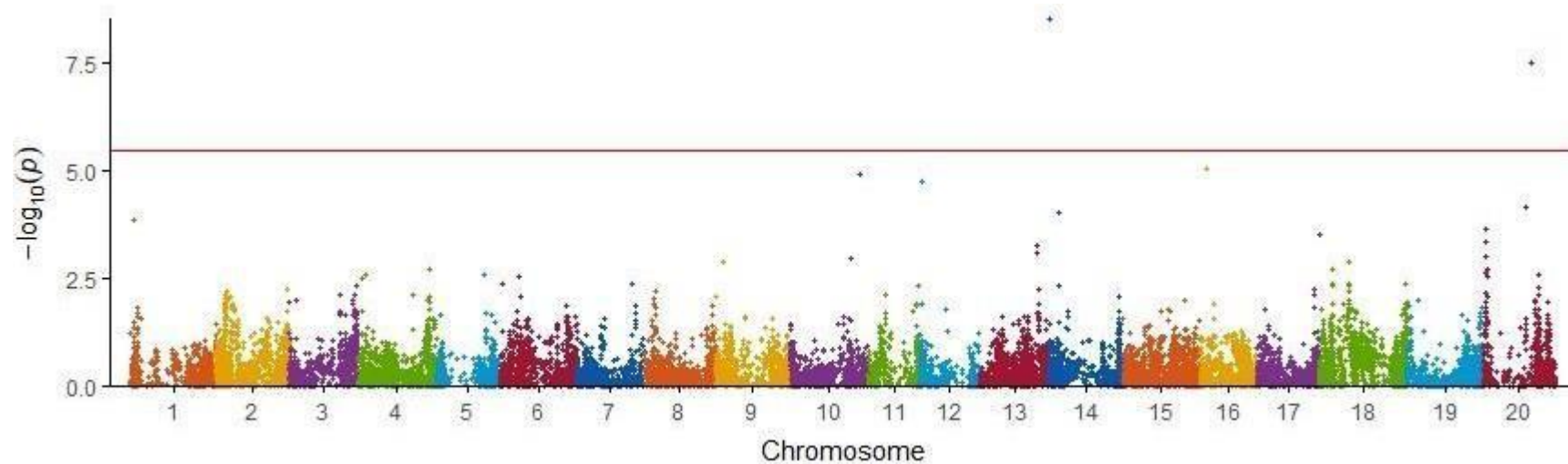
i rMVP, FamCPU, Maturity PC2



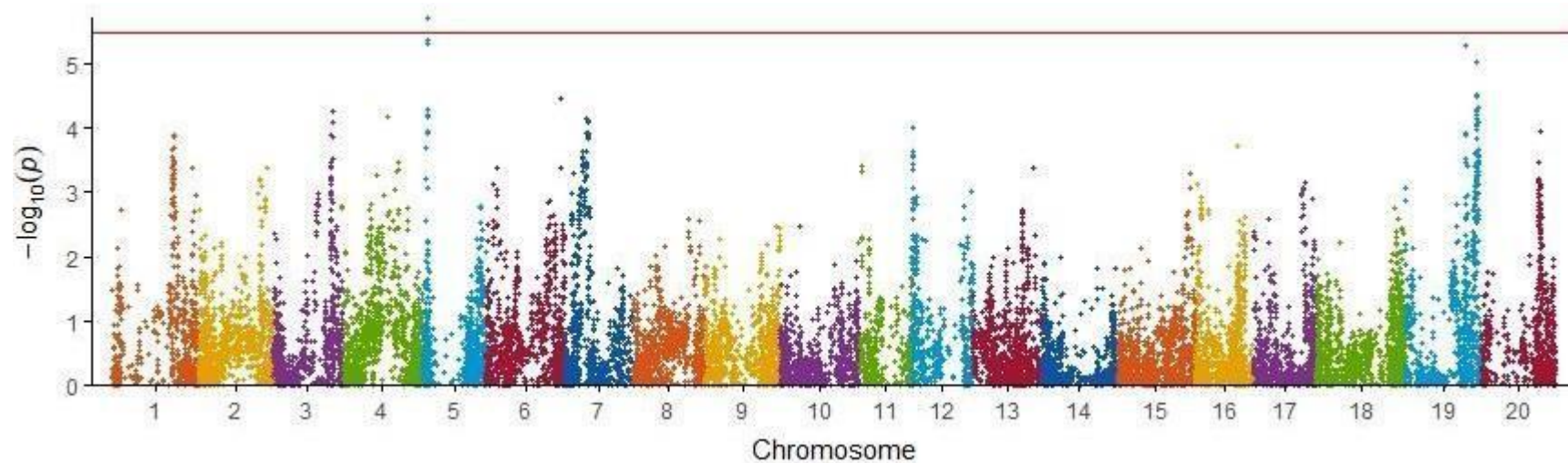
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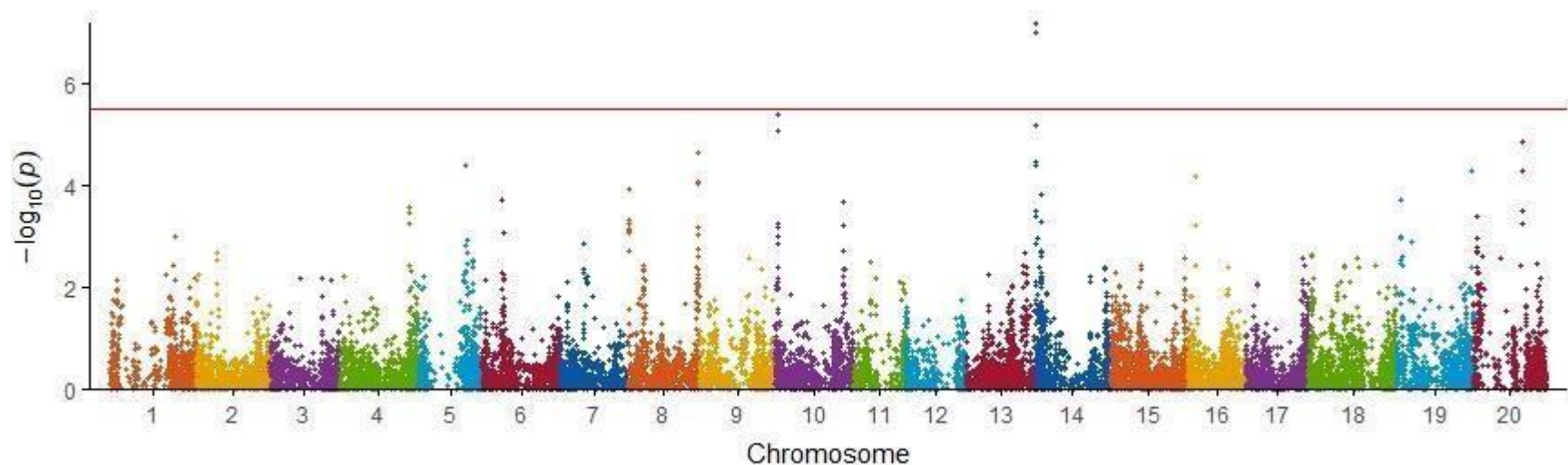
k rMVP, FamCPU, Protein PC1



l rMVP, FamCPU, Yield PC1



m rMVP, MLM, Protein PC1



Supplementary Fig. S2 Manhattan Plots of results from GWAS of gPCs of agronomic traits in soybean. The red line represents a significance threshold of $-\log_{10}(p)=5.5$, each dot represents one association, dots above the significance threshold are considered significant MTAs. Each panel represents a different R package, method and trait combination: a) Gapit, FarmCPU, Maturity PC2, b) Gapit, FarmCPU, Oil PC1, c) Gapit, MLMM, Oil PC1, d) Gapit, MLMM, Plant Height PC1, e) Gapit, MLMM, Plant Height PC4, f) Gapit, MLMM, Protein PC1, g) Gapit, MLMM, Seed Weight PC1, h) rMVP, FarmCPU, Maturity PC1, i) rMVP, FarmCPU, Maturity PC2, j) rMVP, FarmCPU, Oil PC1, k) rMVP, FarmCPU, Protein PC1, l) rMVP, FarmCPU, Yield PC1, m) rMVP, MLM, Protein PC1. Manhattan plots were generated using the fastman package in R