

Supplemental Figures for Myers et al., Improving the health benefits of snap bean: Genome wide association studies of total phenolic content

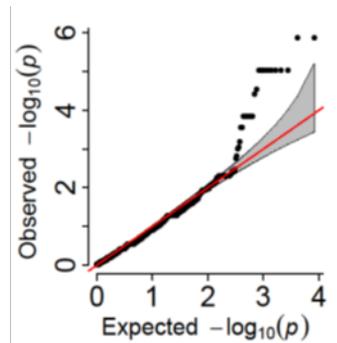
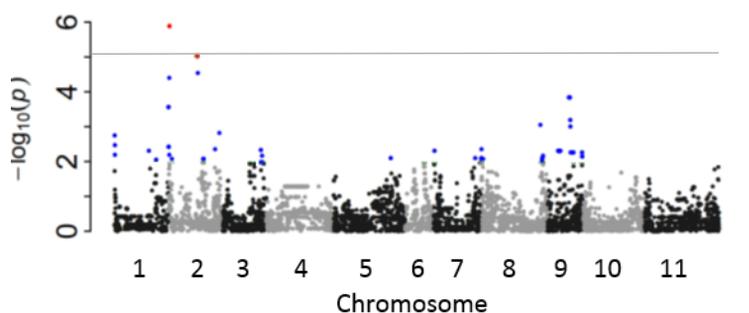


Figure S1. Manhattan and QQ plots for the CIE color parameter L* of pods from a genome wide association mapping study of the Bean CAP snap bean diversity panel. Output from GAPIT using EMMA model with one PCA. Horizontal line represents the Bonferroni cut-off ($\alpha = 0.05$).

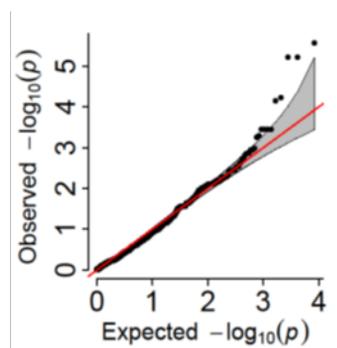
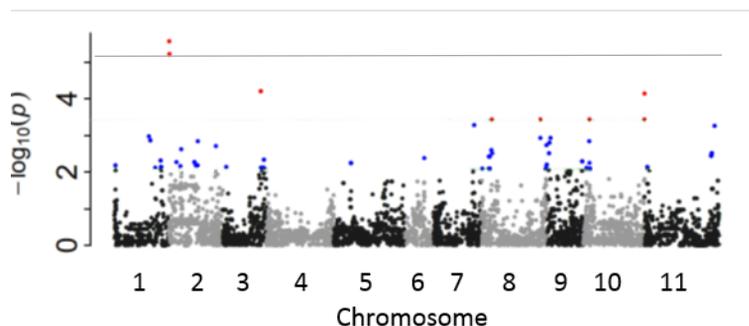


Figure S2. Manhattan and QQ plots for CIE color parameter a* of pods from a genome wide association mapping study of the Bean CAP snap bean diversity panel. Output from GAPIT using EMMA model with one PCA. Horizontal line represents the Bonferroni cut-off ($\alpha = 0.05$).

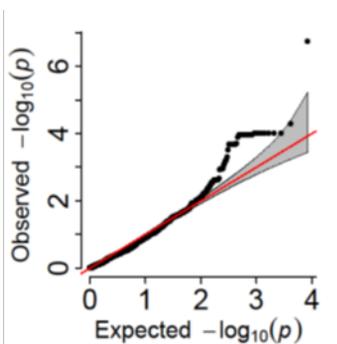
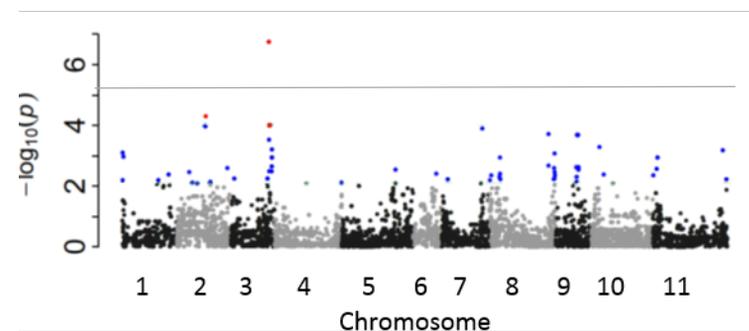


Figure S3. Manhattan and QQ plots for b* of pods from a genome wide association mapping study of the Bean CAP snap bean diversity panel. Output from GAPIT using EMMA model with one PCA. Horizontal line represents the Bonferroni cut-off ($\alpha = 0.05$).

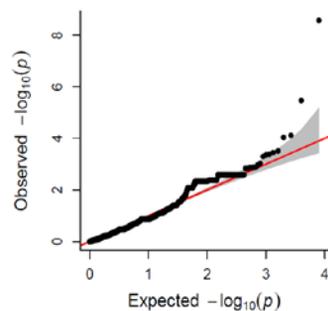
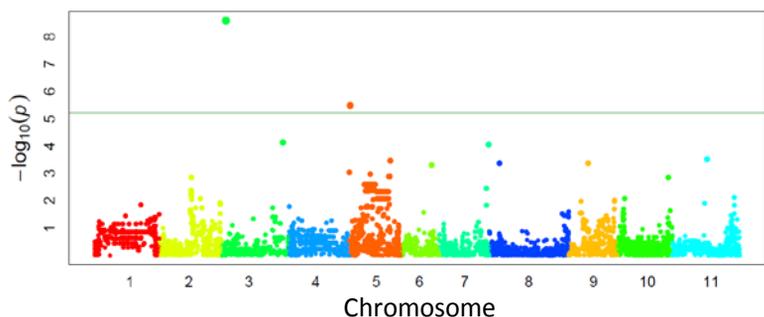


Figure S4. Manhattan and QQ plots for the CIE color parameter b^* of pods from a genome wide association mapping study of the Bean CAP snap bean diversity panel. Output from FarmCPU with one PCA. Horizontal line represents the Bonferroni cut-off ($\alpha = 0.05$).

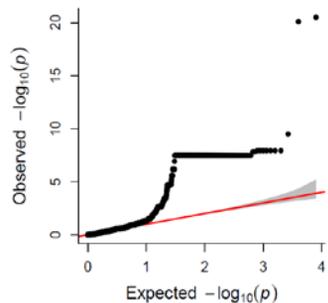
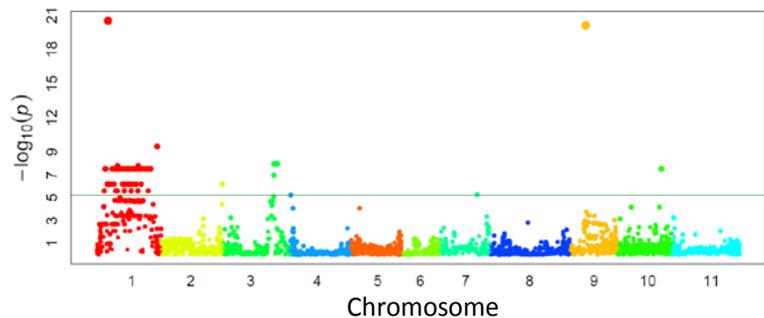


Figure S5. Manhattan and QQ plots for flower color from a genome wide association study of the Bean CAP snap bean diversity panel. Output from FarmCPU with one PCA. Horizontal line represents the Bonferroni cut-off ($\alpha = 0.05$).

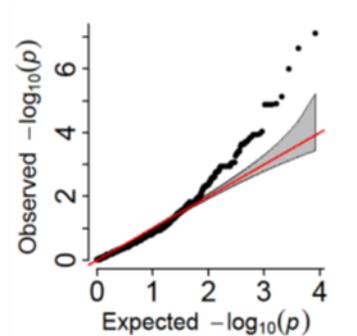
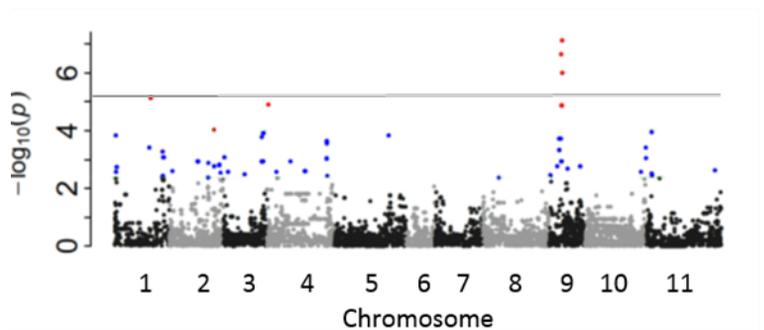


Figure S6. Manhattan and QQ plots for flower color from a genome wide association study of the Bean CAP snap bean diversity panel. Output from GAPIT using EMMA model with one PCA. Horizontal line represents the Bonferroni cut-off ($\alpha = 0.05$).