



Figure 4-figure supplement 1: Local Manhattan plots for (a) flower color, (b) saponin content, and (c) mildew infection. Candidate genes are shown in the color legend. LD heat maps are placed at the Bottom. The colors of the heat map represent the pairwise correlation between individual SNPs. SNPs with significant P-values and SNPs on candidate genes were used to create the heatmap for the saponin content. Gene models and names are given on top of the heatmap. Haplotype blocks were identified using the Gabriel method in LDBlockShow software (Dong et al. 2020).