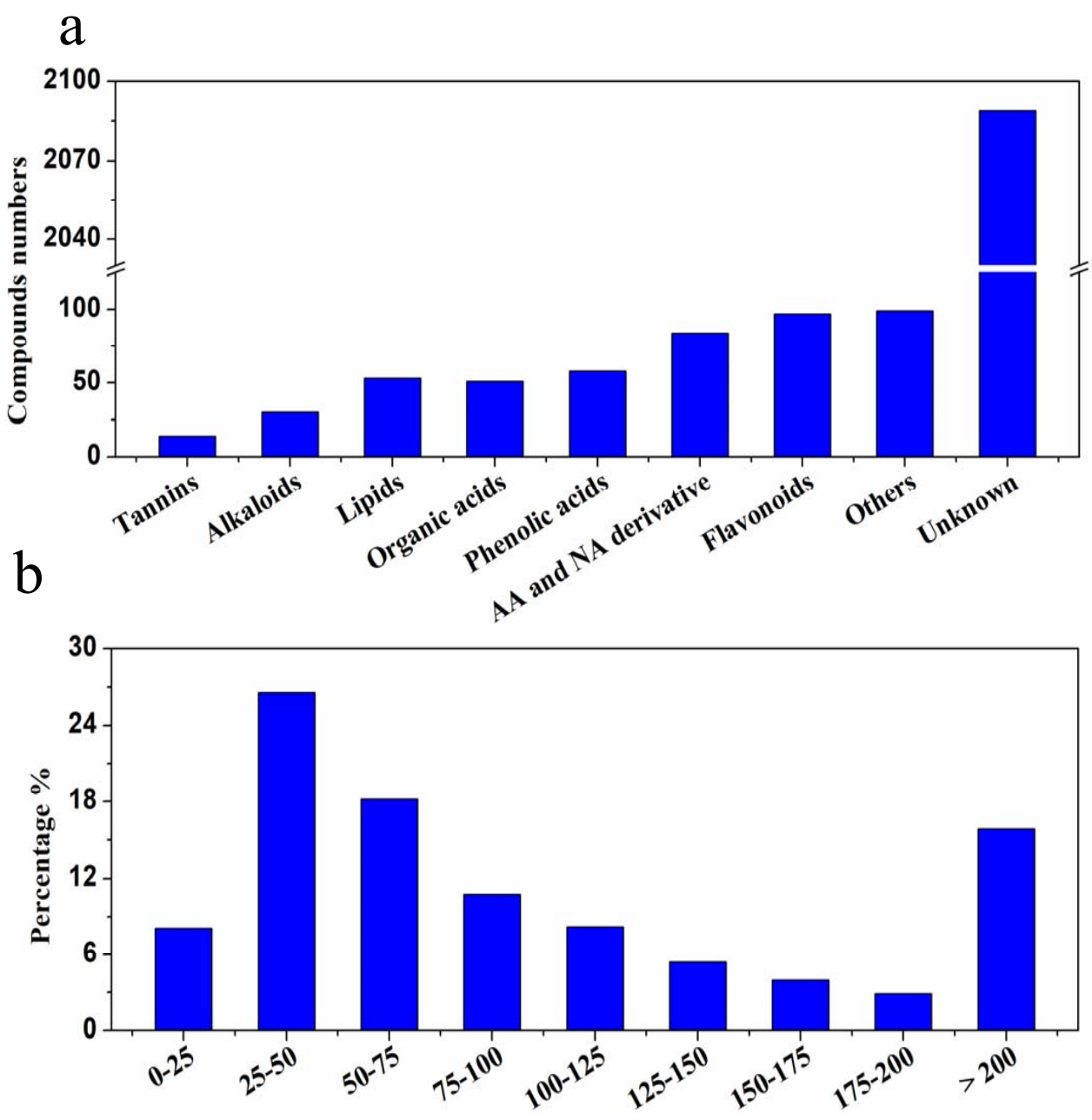
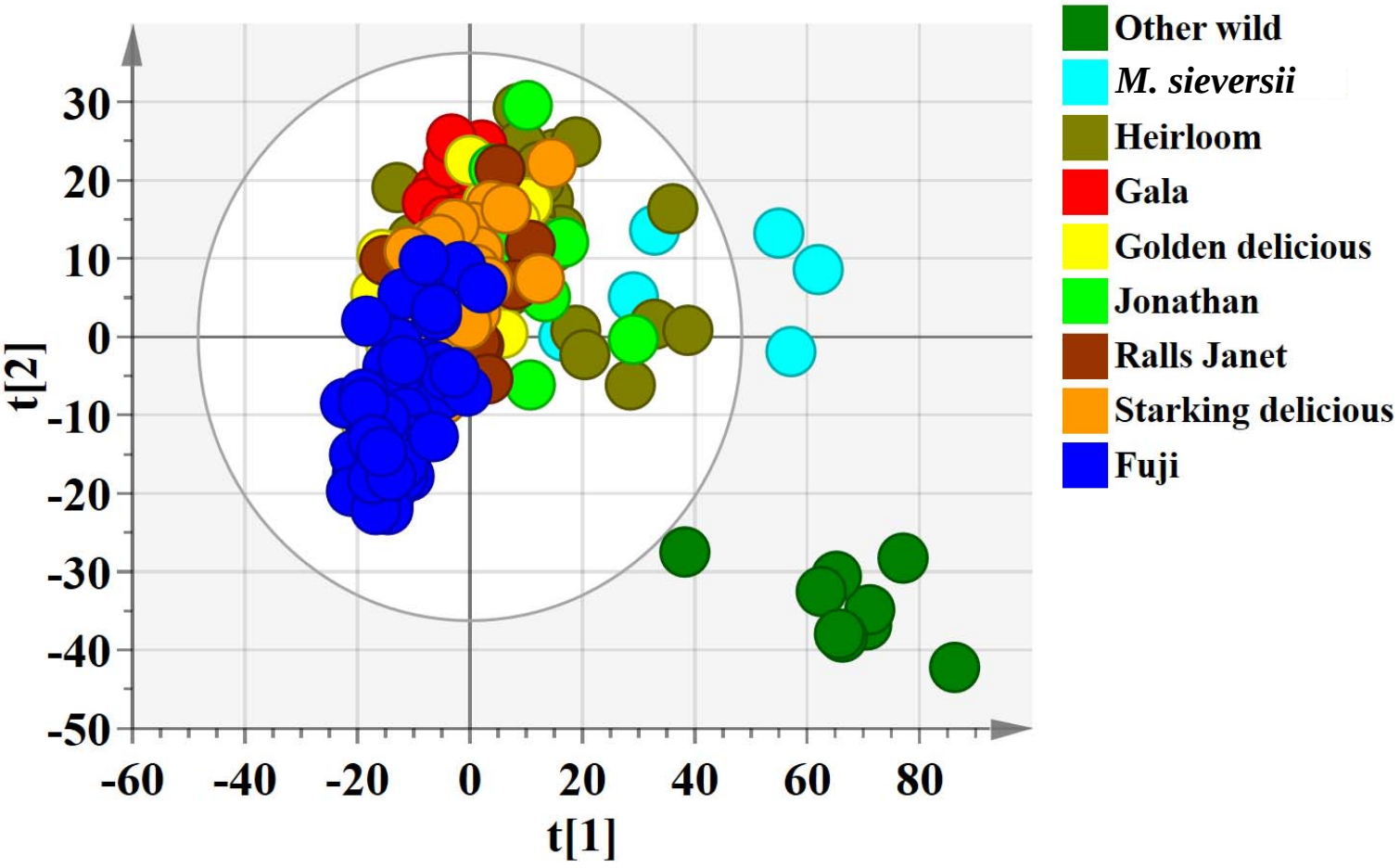
Additional file 1: Fig. S1. Classification (a) and coefficient of variation (b) values for all metabolites detected in apple flesh. Coefficients of variations of each metabolite were independently calculated as follows: s/m, where ‘s’ and ‘m’ represent the standard deviation and mean of each metabolite in all accessions, respectively. Fig. S2. PCA analysis of all metabolite contents detected in other wild, *M. sieversii*, heirloom, and six apple cultivar groups. t[1] and t[2] represent the first and second principal component. R2x[1] and R2x[2] indicate the proportion of variance explained by t[1] and t[2], respectively. The colored dots indicate different apple accessions and the ellipses indicate the 95% confidence interval for each data set. Fig. S3. Fruit weight, total tannin content and titratable acid content in apple accessions among *M. sieversii* group, low-weight (≤ 90) domesticated group, and high-weight (≥ 300) domesticated group. ‘*’ indicates $p \leq 0.05$ by *t*-test. Fig. S4. Manhattan plots of procyanidin C1, procyanidin B4, arecatannin B1, cinnamtannin D1 and procyanidin A2 contents by GWAS. Co-mapped regions of the soluble tannins were identified on Chr 16. Fig. S5. Differences between amino acid sequences of *MdMyb9* and MD15G1051400 were marked by highlighting. Fig. S6. Whole-genome screen for selective sweeps during apple domestication and improvement. The horizontal gray dotted lines indicate genome-wide thresholds that were estimated based on the top 5% of Fst values. Fig. S7. Manhattan plots of LPE 18:1 and LPE 18:1 (2n isomer) contents by GWAS. Co-mapped regions of LPE contents were identified on Chr 12.

Additional file 1: Fig. S1



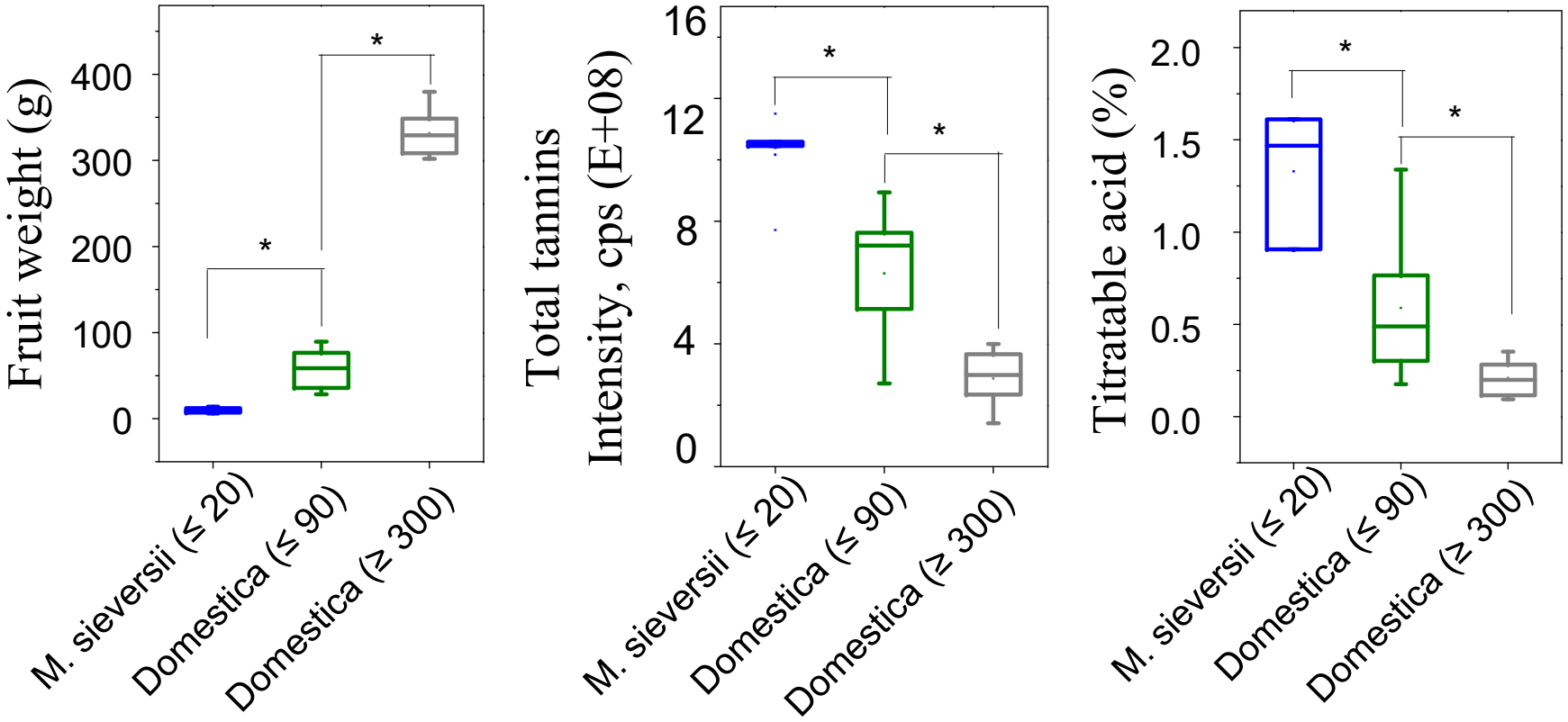
Additional file 1: Fig. S2



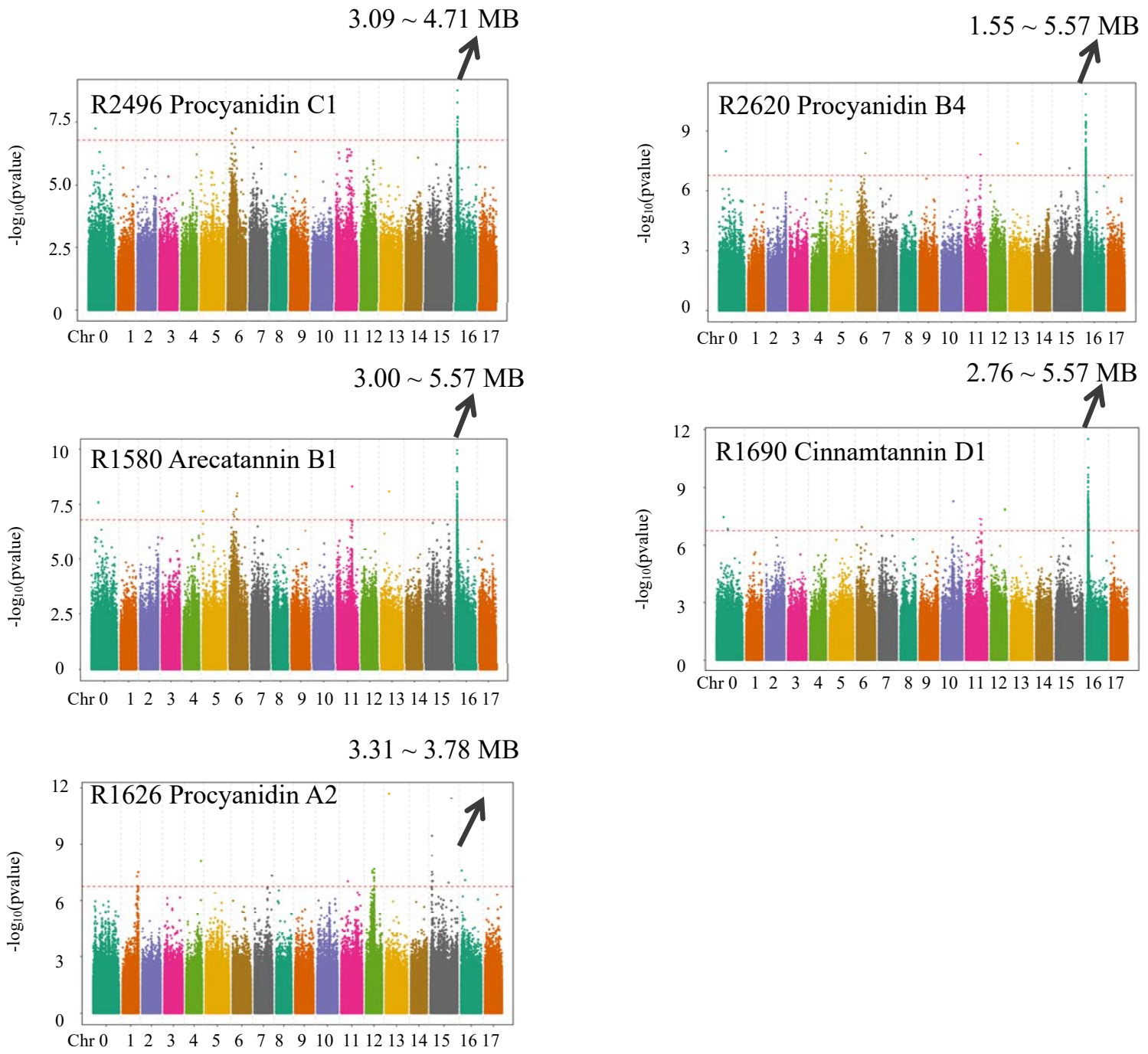
R2x[1] = 0.177 R2x[2] = 0.090

Ellipse: Hotelling's T2 (95%)

Additional file 1: Fig. S3

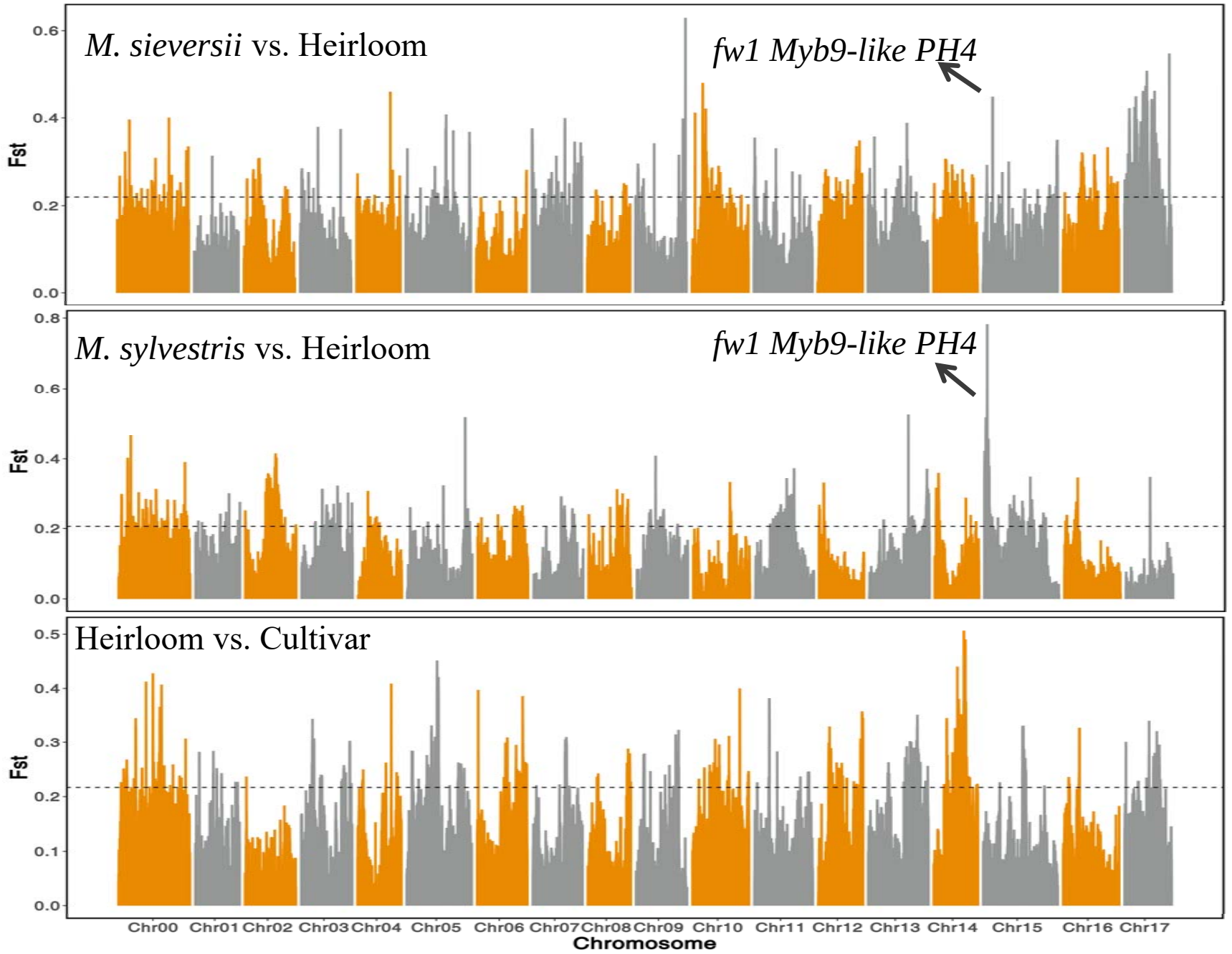


Additional file 1: Fig. S4

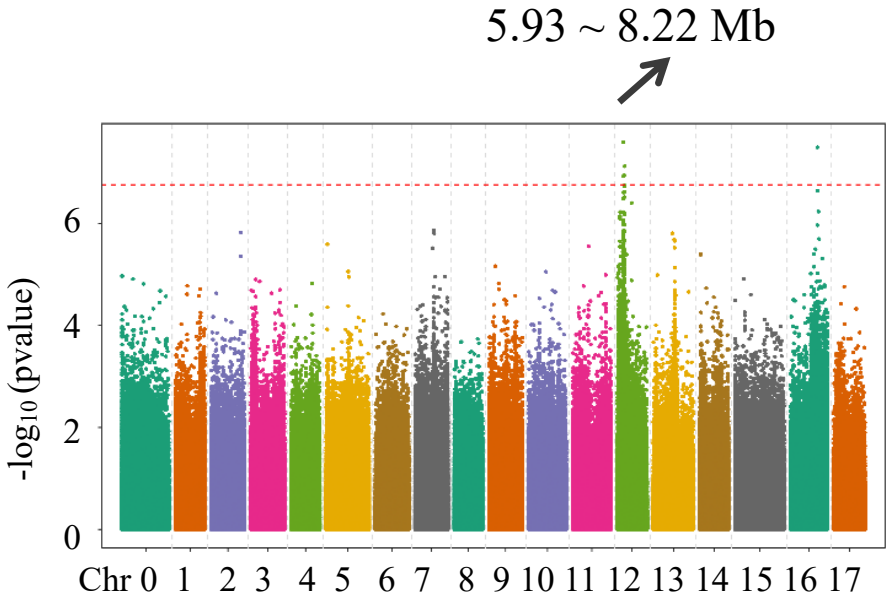


Additional file 1: Fig. S5

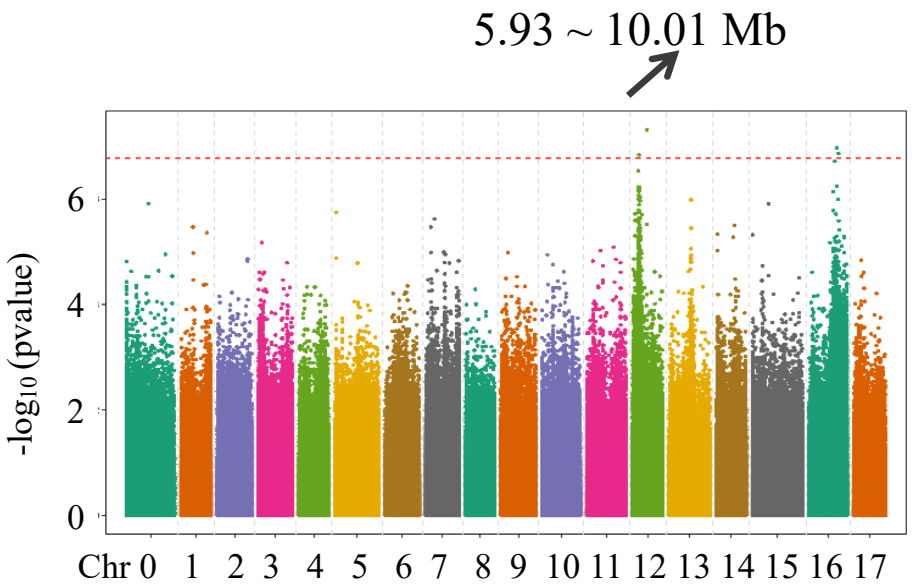
Additional file 1: Fig. S6



Additional file 1: Fig. S7



R2201 LPE 18:1



R1571 LPE 18:1 (2n isomer)