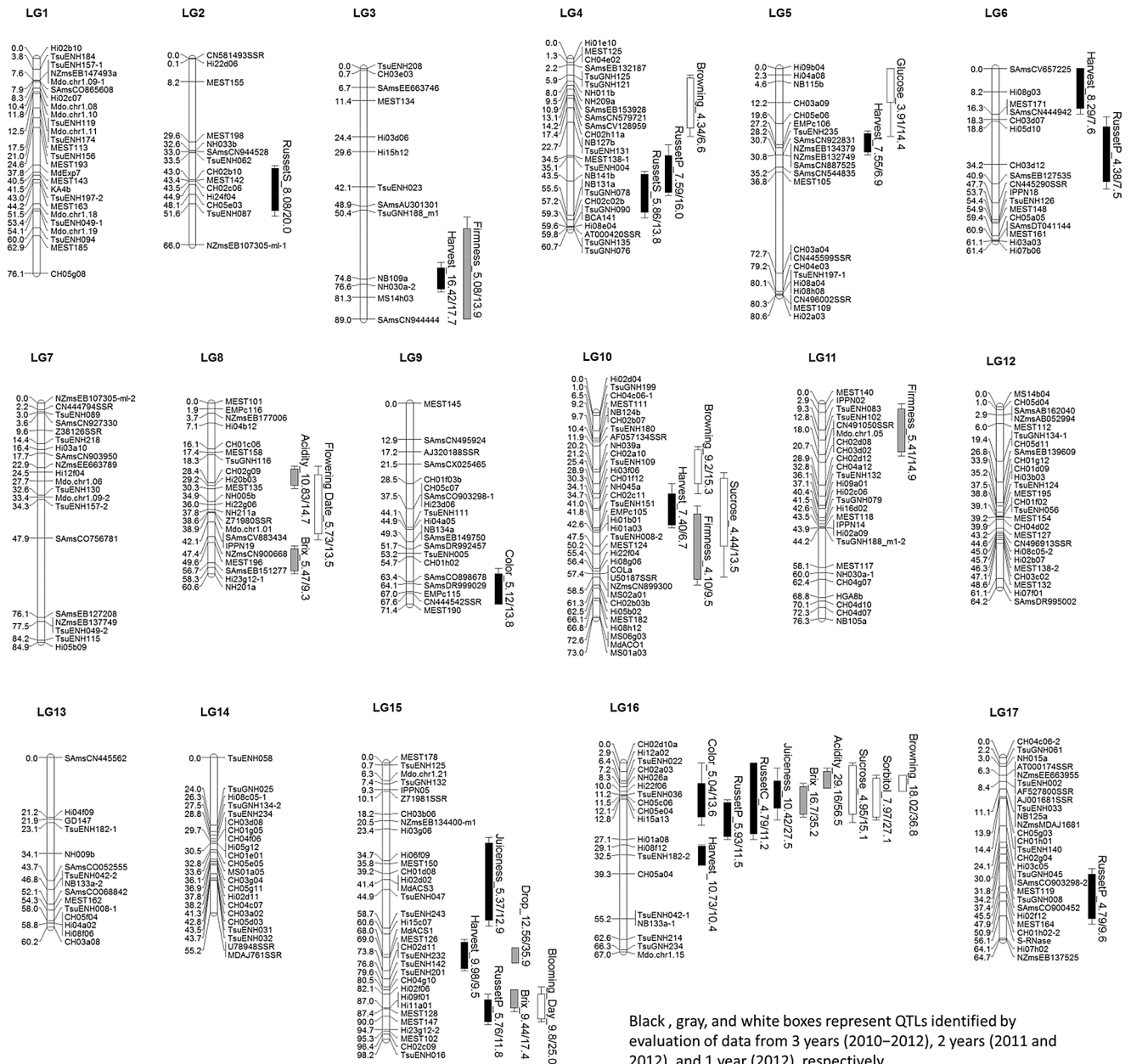


**Supplemental Fig. 1.** Distribution of the phenotypes in the 'Orin' × 'Akane' F<sub>1</sub> seedlings. Frequency is shown on the vertical axis. White and black arrows indicate the mean values for 'Orin' and 'Akane', respectively. The average, SD, and distribution type (D) are shown in each histogram. The skin color of 'Orin' (green) could not be indicated in the histogram, because the color score only considered three categories of red (pale red, normal red, and vivid red).



**Supplemental Fig. 2.** The integrated genetic linkage map for 'Orin' and 'Akane', and overview of the significant QTLs detected in the integrated map. Numbering and orientation of the LGs follows that in the apple reference map (Liebhard *et al.* 2003a). The significant QTLs are shown to the side of each LG, with boxes and range lines indicating 1-LOD and 1.5-LOD support intervals. LOD and the proportion of the phenotypic variance explained are presented after the QTL name as LOD/proportion (%). The following traits are represented by abbreviations: russet on the calyx side (RussetC), russet on the pedicel side (RussetP), depth of skin color (Color), preharvest fruit drop (Drop), and juice browning (Browning).

Black, gray, and white boxes represent QTLs identified by evaluation of data from 3 years (2010–2012), 2 years (2011 and 2012), and 1 year (2012), respectively.