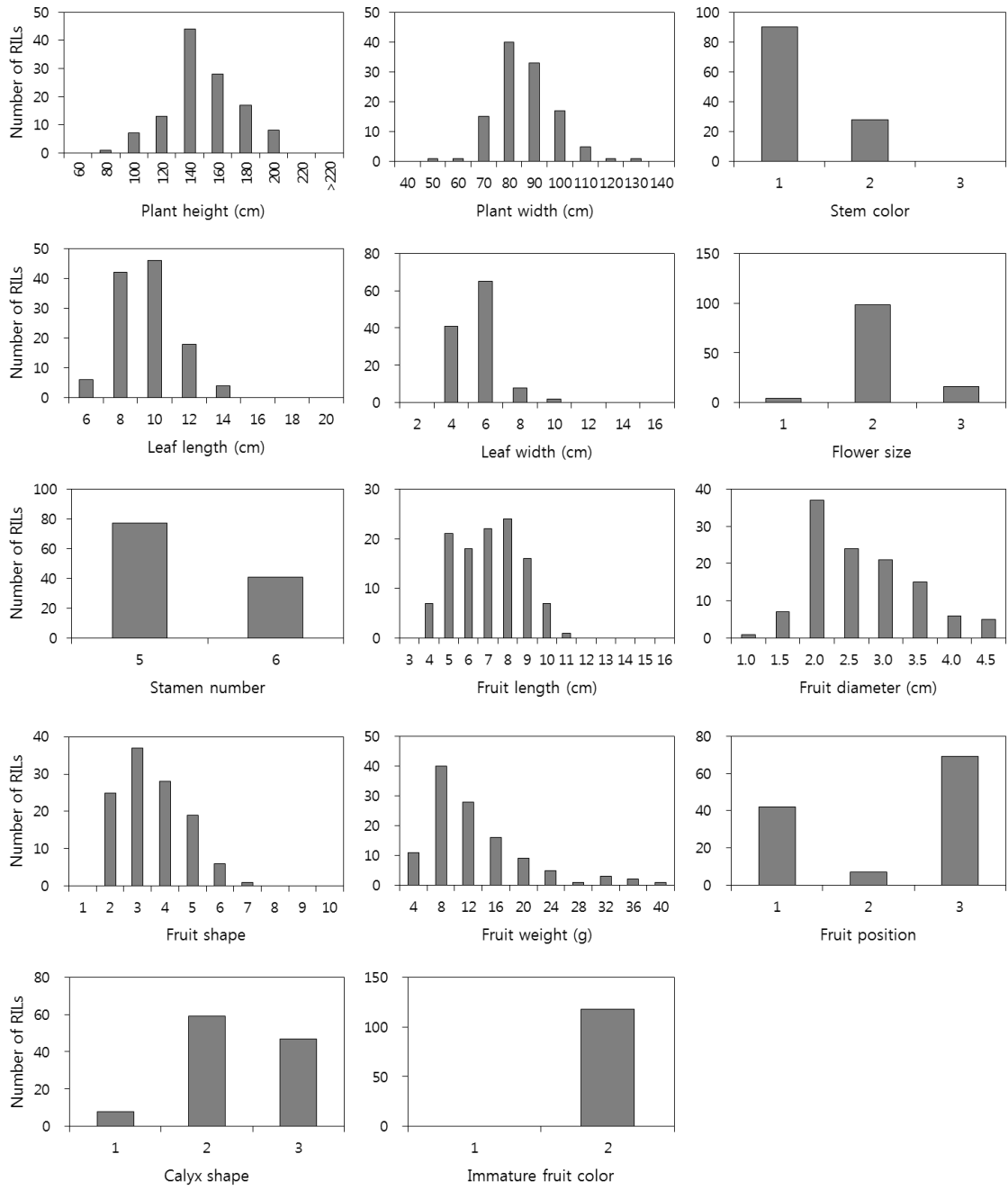
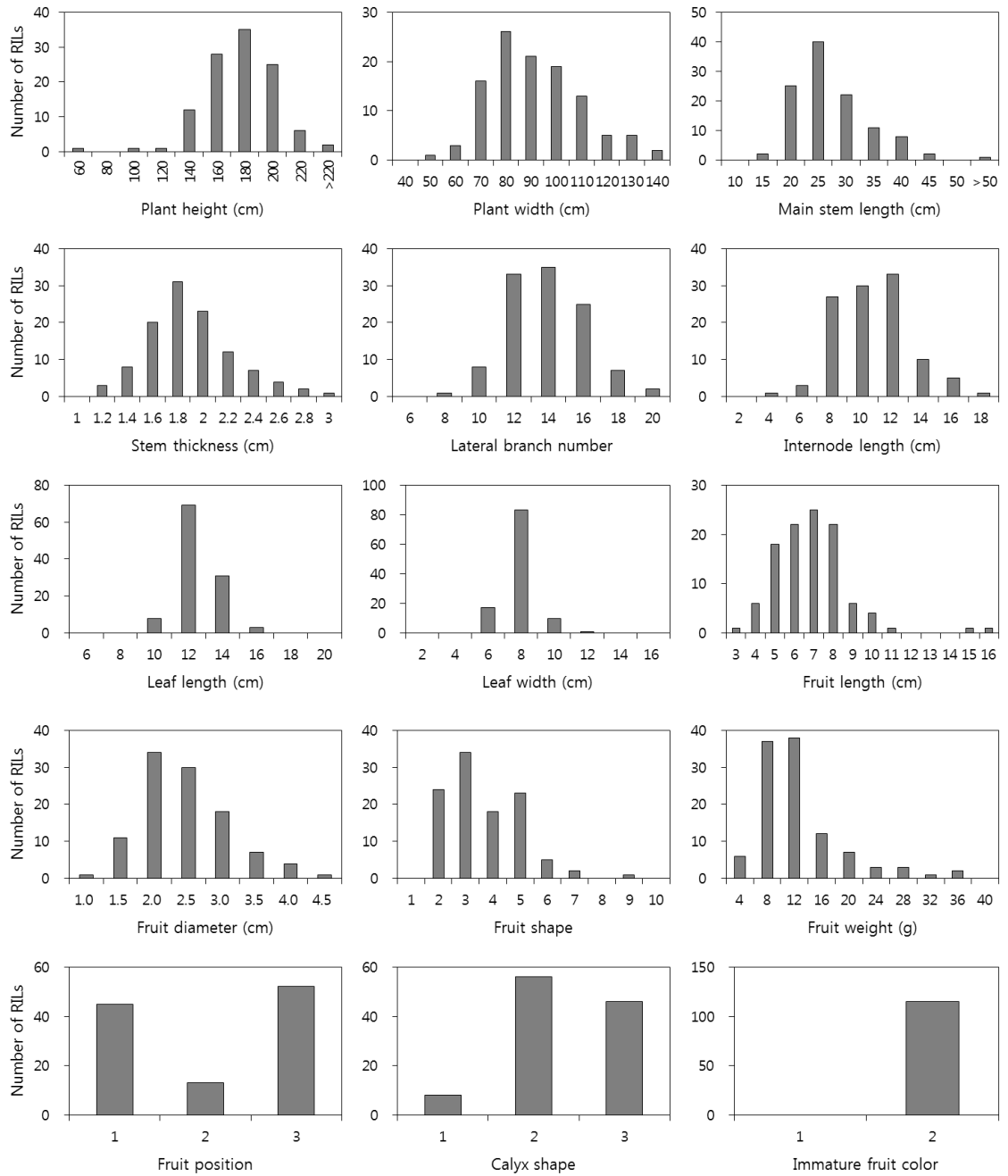


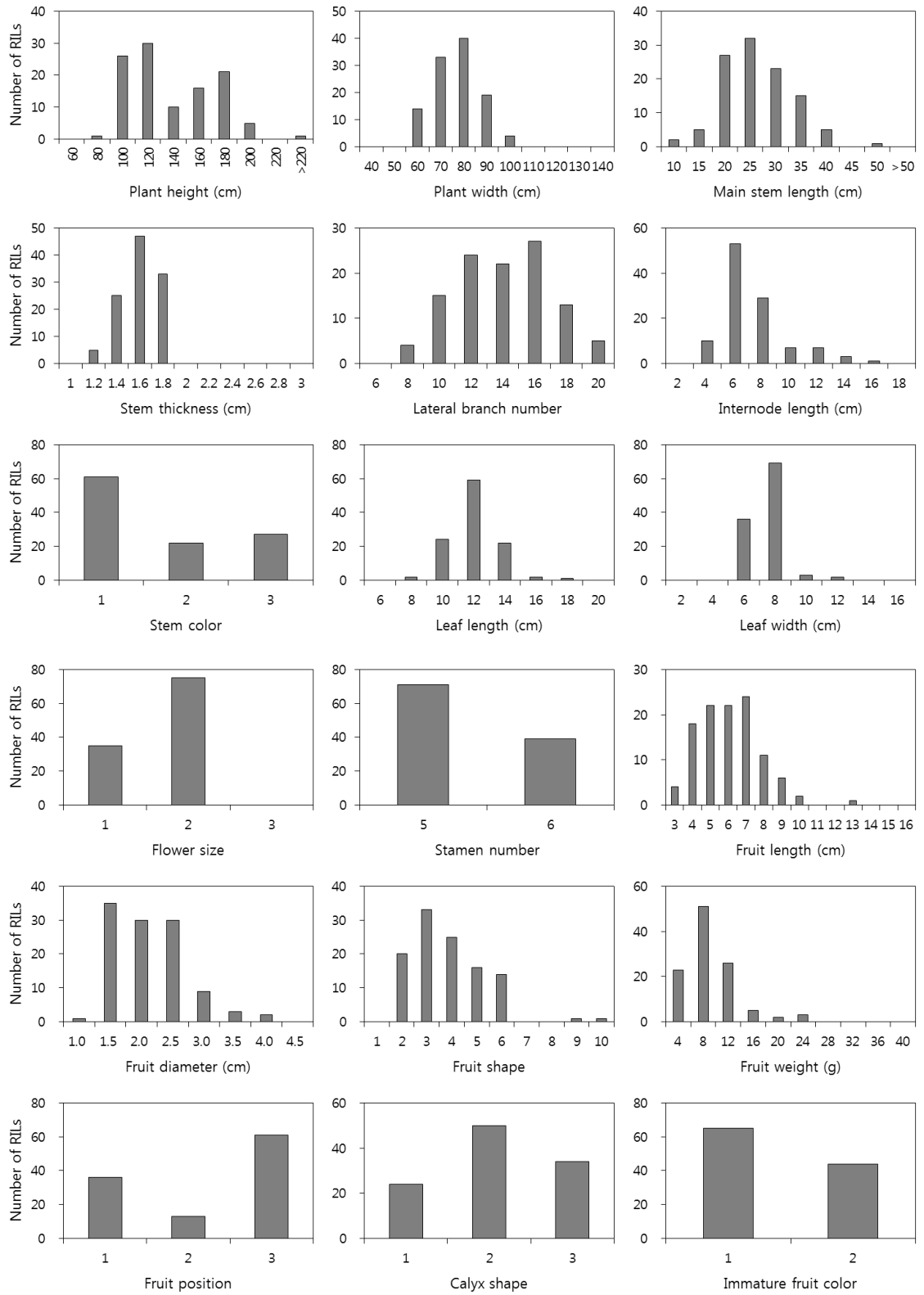
A

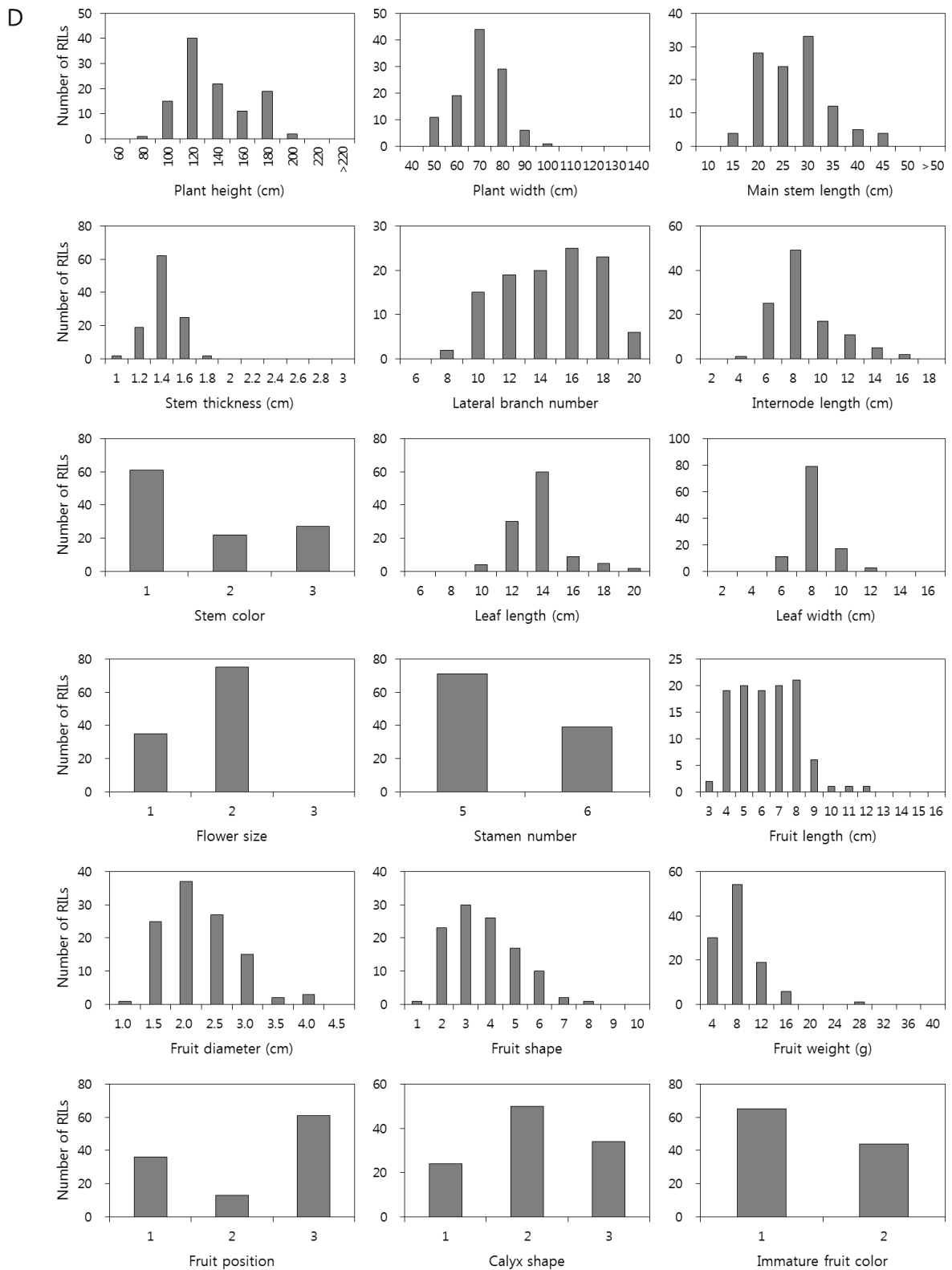


B

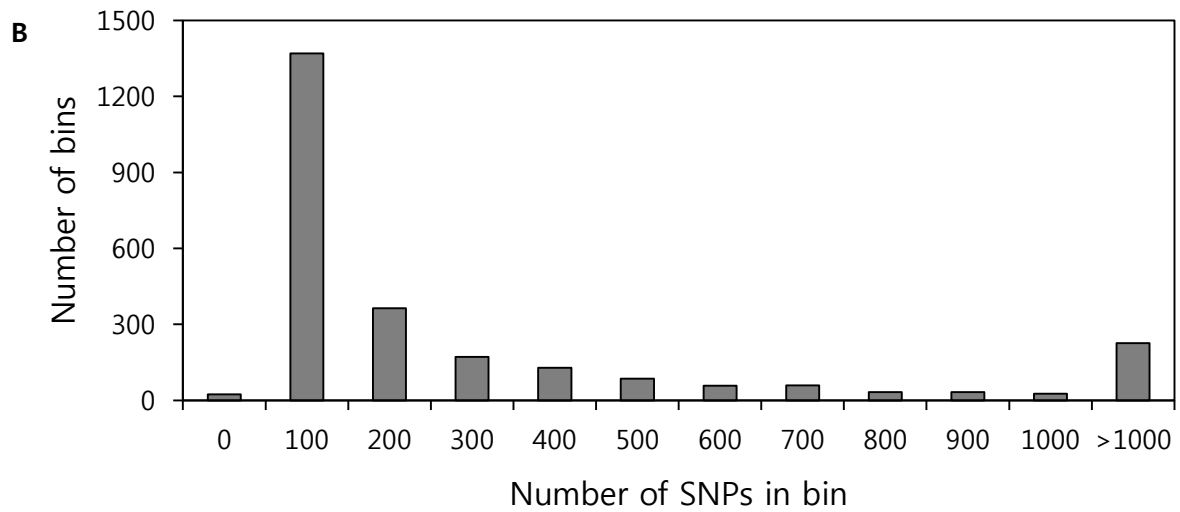
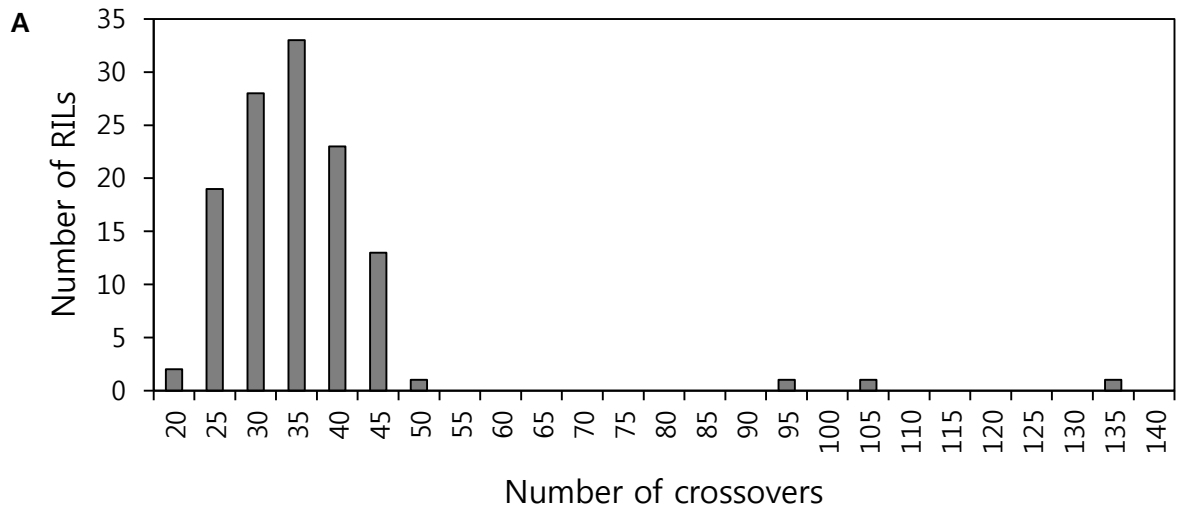


C

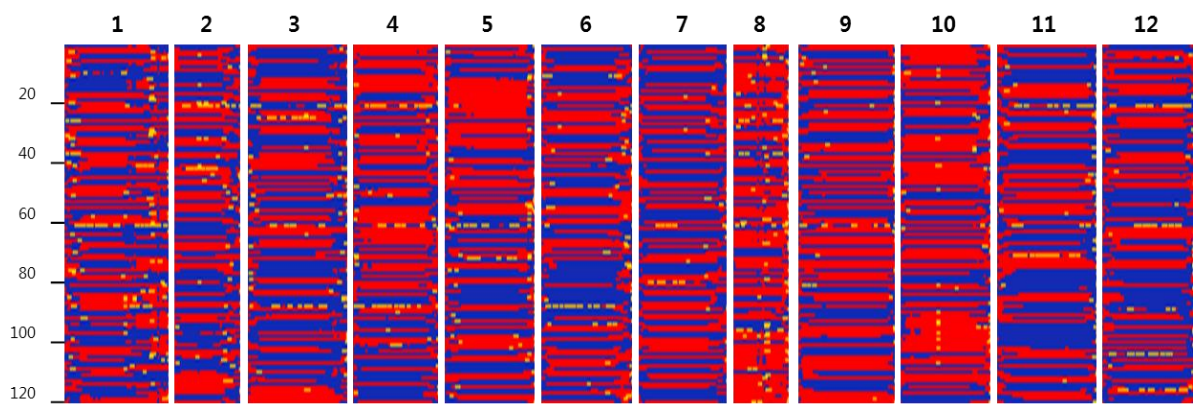




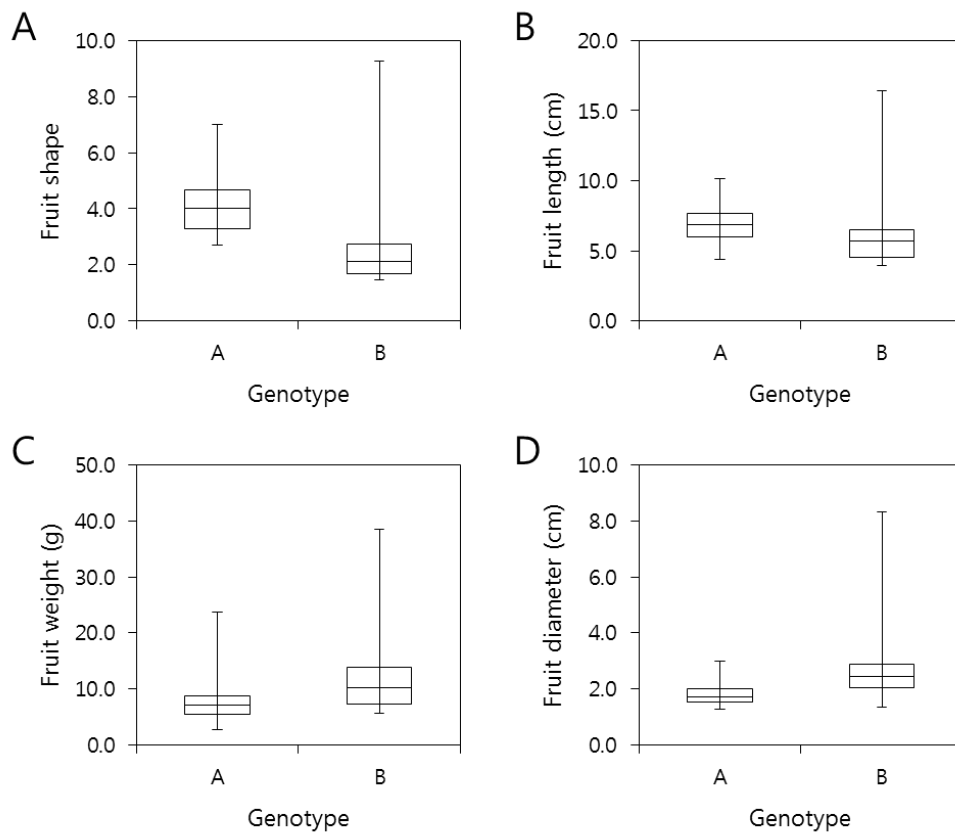
**Figure S1.** Phenotypic variation of RILs. (A), (B), (C), and (D) show the phenotypic variation of RILs grown in environment 2011, 2012a, 2012b, and 2014, respectively. Stem color, flower size, fruit position, calyx shape, and immature fruit color were described by grade instead of exact values.



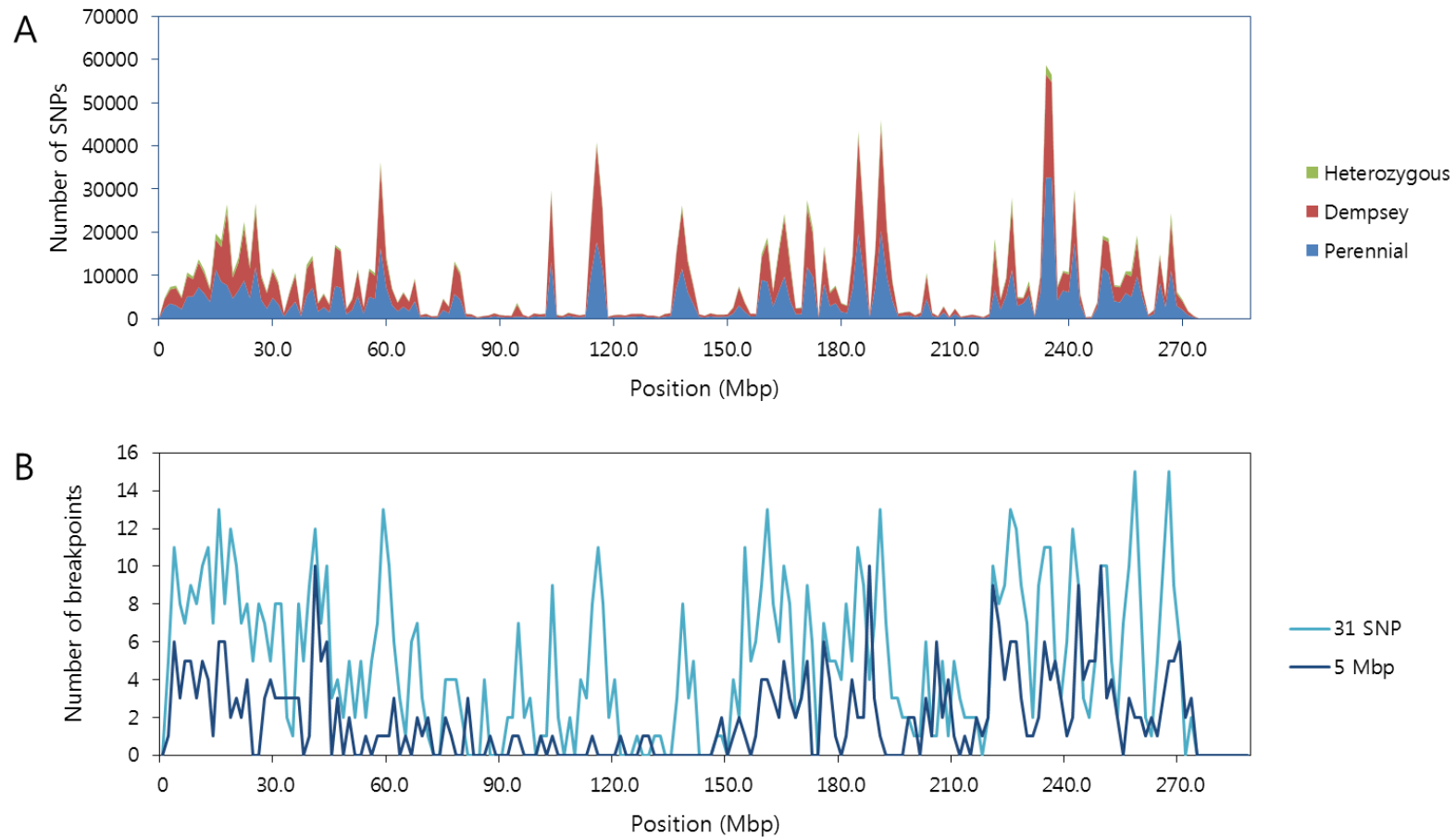
**Figure S2.** The number of crossovers and SNPs in the bin map. (A) Number of crossovers in RILs. A total of 3,983 crossovers were identified in 120 RILs and each RIL has 16 to 133 crossovers. (B) Number of SNPs in each bin. An average 556 SNPs were included in each bin and more than half of the bins contained fewer than 100 SNPs.



**Figure S3.** Recombination bin map from 120 RILs. A total of 2,712 bin markers spanned 2.7 Gbp of the genetic map. Red, 'Perennial' genotype; blue, 'Dempsey' genotype; yellow, heterozygous.



**Figure S4.** Box plots of the phenotypic distribution in RILs. Box plots show the distributions of phenotypic value for fruit shape (A), fruit length (B), fruit weight (C), and fruit diameter (D). The RILs with ‘Perennial’ and ‘Dempsey’ genotype (genotype A and B, respectively) were divided based on the bin markers linked to QTLs on chromosome 3. Genotype of PD3-bin128 linked to *FS-3.1* (A), PD3-bin115 linked to *FL-3.1* (B), PD3-bin145 linked to *FW-3* (C), and PD3-bin140 linked to *FD-3.2* (D).



**Figure S5.** Distribution of SNPs in chromosome 1. (A) Distribution of SNPs with ‘Perennial’ (blue), ‘Dempsey’ (red), and heterozygous genotype (green). (B) Number of identified recombination breakpoints when the window length was set at 31 SNPs (light blue) or 5 Mbp (dark blue).