

Supplementary Figure 3. Diagram of the target QTL region in the two-stage genome scan.

(A) The distribution of genetic distance between two adjacent QTLs across five quantitative traits. Over 90% of adjacent QTLs had genetic distance larger than 10 cM. (B) Target region defined by three tagging SNPs to the left and right of the QTL n . On average, 7,319 SNPs were scanned in the second stage in each target region for TASs. The control of polygenic background effects during the scan is achieved by fitting all other QTLs (*e.g.*, m and k) located 10 cM away from the target region. (C) Detailed view of a TAS (red dot) within the target region. Both P -value and Q -value (adjusted for multiple testing) are indicated.

