Supplementary Figure 2. GWAS for five quantitative traits with one million merged SNPs from the RNA-seq and HapMap data sets to identify TASs. (A) Three leaf architecture traits; and (B) Two flowering-time traits. Dark-colored dots indicate TASs with the highest association values for each of 164 QTL regions. TASs in three genes implicated for three traits are illustrated as examples to show TAS locations in (C), (D), and (E). Blue and green arrows indicate implicated and nearby genes, respectively. Red dots indicate TASs for tagged genes. DTA, days to anthesis; DTS, days to silking.