

Supplementary Figure 4. Genic or non-genic TASs for each dissected QTL region and the proportion of genic SNPs among all tested in the region for Leaf Length and Days to Anthesis (DTA). Genic region is defined as from the transcription start site to the end of 3' UTR. With the merged data set, the probability of a TAS being genic or non-genic is significantly independent of whether more genic or non-genic SNPs in the target region are tested ($P < 0.05$) for all five traits. Each row represents a single QTL region for the indicated traits. Genic and non-genic TASs are equally likely to be identified for QTLs with large or small effects, which are sorted in descending order within each trait.

