



x-axis: number of annotated genes per bin/IL

y-axis: -log(p value) of regression of bin identity and phenotype

A: -log(p value) of regression of bin identity and phenotype

B: Bin names

C: IL structure and p-values for difference of IL from cv. M82

Supplemental Figure 15: Bin mapping result legend. For each trait, bin and IL mapping results are visualized (Supplemental Figures 16–47 online). Below each graph is an IL map, the color of the ILs indicating the direction and significance of the QTL. Above this map is a graph, the height of the columns indicating the significance of the bin from the bin mapping results. Bin columns are colored based on their significance values. The y-axis indicates -log₁₀(p-value). For both the IL map and bin mapping results graph, the size of bins and ILs is proportional to the number of annotated genes that they harbor.