



Figure S1 Genome-wide association study of tannin presence in a small association panel. Manhattan plots for GWAS using a (A,B) general linear model (GLM) and (C,D) compressed mixed linear model (MLM [K]) with 265,487 SNPs and 142 accessions. The horizontal line indicates the Bonferroni significance threshold at a 5% nominal family-wise error rate. The *Tannin1* locus is identified with Mb resolution but the *Tannin1* gene (red bar) is not precisely identified with either model. Other flavonoid-related genes are indicated by the blue bars, while all other annotated genes in the detailed view are indicated in green.