**S1 Table. Identification of ALP2 candidate genes by sequencing.**  A. Annotation of high scoring mutations from fast isogenic mapping identified two candidate genes (Hartwig et al. 2012). Score indicates Shore quality score ranged from 1 (low) to 40 (high). Protein position indicates amino acid number in translated coding sequence. B. Allele frequency at the two candidate mutations reveals high frequency of the mutant allele in DNA from bulked mutant plants.