



Figure S8. Association of SNP markers with adult maize leaf cuticular conductance (g_s) across a genomic region on chromosome 1. Scatter plot of association results from a mixed linear model analysis of g_s conducted in Maricopa (MA) and linkage disequilibrium (LD) estimates (r^2) for a genomic region that contains genes encoding a CYCLASE-ASSOCIATED PROTEIN1 (CAP, *Zm00001d033830*), two SEC14-like proteins [SEC14 (3836), *Zm00001d033836*; SEC14 (3837), *Zm00001d033837*], and a homolog of ECERIFERUM7 (CER7, *Zm00001d033842*). The $-\log_{10} P$ -values of tested single-nucleotide polymorphisms (SNPs) are represented by vertical lines. Blue vertical lines are SNPs that are statistically significant at a false discovery rate (FDR) of 10%. The r^2 values of each SNP relative to the peak SNP (indicated by a solid orange triangle) at 275,318,146 bp (B73 RefGen_v4) are indicated by triangles. Open orange triangles represent SNPs with $r^2 > 0.1$ relative to the peak SNP. The least significant SNP at a genome-wide FDR of 10% is indicated by a dashed horizontal orange line. The black dashed vertical line indicates the genomic positions of the CAP, two SEC14-like proteins, and a CER7 homolog.