



Figure S10. Association of SNP markers with adult maize leaf cuticular conductance (g_s) across a genomic region on chromosome 7. Scatter plot of association results from a mixed linear model analysis of g_s conducted across all four environments (AllEnv) and linkage disequilibrium (LD) estimates (r^2) for a genomic region that contains the peak SNP. 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 23,984,279 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.