



Figure S6. Genome-wide association study (GWAS) of adult maize leaf cuticular conductance (g_c) conducted in locations (Maricopa, MA; and San Diego, SD) and across all four environments (AllEnv). The $-\log_{10} P$ -value of each SNP tested in a mixed linear model analysis of g_c is plotted as a point against its physical position (B73 RefGen_v4) for the 10 chromosomes of maize. The least significant single-nucleotide polymorphism (SNP) at a genome-wide false discovery rate of 10% is indicated by a dashed horizontal black line.