



Figure S12. Heatmap of average \log_2 transformed transcript abundance (counts per million; cpm) for the 24 candidate genes declared to be expressed in epidermal cells of expanding adult leaf 8 of maize inbred B73. A logarithmic scale was used due to the large range of cpm values across genes, and a constant with a value of 1 was added to all cpm values ($\text{cpm} + 1$) to prevent the generation of negative values after \log_2 transformation. Candidate genes are grouped by the five genomic regions associated with g_c , which is indicated by the peak SNP of each genomic region.