



Appendix S5. Heat map of expression differences for the 249 genes that were identified as having a significant genotype by treatment interaction ($P_{\text{FDR}} \leq 0.05$ for the comparison of IT to SW). The value of each cell represents the \log_2 fold-change in gene expression before and after cold acclimation (counts per million reads). Yellow-red color represents genes that are more highly expressed after cold acclimation, while black-purple color represents genes that are more highly expressed before cold acclimation. Plot was generated using the heatmap.2 function in the R package plots (Warnes et al., 2019).