



Supplemental Fig. S5 WGCNA of samples in the deacclimation experiment. A) Module-trait relationships; B) ME visualization across all timepoints in the experiment. Input genes are all genes after low count filtering. Error bars are not shown due to minimum variance among replicates. The Module-trait relationships were computed using Pearson method. The first line and second line of cells represent correlation coefficient and correlation p-value, respectively.