



Figure 5. Motifs and transcription factors associated with cell-preferential gene expression. A) Four clusters were selected for analysis. DNA-binding motifs enriched in mesophyll clusters 15 and 6, or bundle sheath clusters 3 and 7. **B)** Heatmap illustrating Pearson's correlation coefficient (PCC) values for bundle sheath-preferential photosynthesis genes in clusters 7 and 3 and candidate transcriptional regulators. DNA-binding One Zinc Finger 2 (DOF2), GRMZM2G009406; MADS-domain protein 1 (MADS1), GRMZM2G171365; DNA-binding One Zinc Finger 21 (DOF21), GRMZM2G162749; Dwarf Plant 8 (D8), GRMZM2G144744; NLP-transcription factor 13 (NLP13), GRMZM2G053298; BBR/BCP-transcription factor 4 (BBR4), GRMZM2G118690; BBR/BCP-transcription factor 3 (BBR3), GRMZM2G164735. **C)** Line plots of diel transcript abundance for candidate regulators of bundle sheath-preferential photosynthesis genes. x-axis shows time and y-axis Z-score. White and black bars in the x-axis denote light and dark periods, respectively. M and BS represent mesophyll and bundle sheath cells. MADS-domain protein 1 (MADS1), GRMZM2G171365; DNA-binding One Zinc Finger 21 (DOF21), GRMZM2G162749; DNA-binding One Zinc Finger 2 (DOF2), GRMZM2G009406; BBR/BCP-transcription factor 3 (BBR3), GRMZM2G164735; BBR/BCP-transcription factor 4 (BBR4), GRMZM2G118690. **D)** Black dots denote the individual data points and white diamonds represent the mean. The middle line in the boxplot denotes the median, the box shows the interquartile ranges and the whiskers denote maximum and minimums. p-values were obtained from a two-sided, pairwise t-tests. n=6 for $pNADMEa$, $pRBCS$ and $pRBCS+MADS1$, n=5 for $pNADPMEb$ and $pPEPCK$, n=4 for $pNADMEa+DOF2$ and $pPEPCK+MADS1$ and n=3 for $pNADMEb+DOF1$.