



**Figure 2. Maize mesophyll and bundle sheath transcriptomes over a diel time-course.** A) Mesophyll and bundle sheath transcriptomes were collected over 24-hours. White and black bars denote light and dark periods respectively. B) Transcriptome sequencing parameters. C) Principal Component Analysis of mesophyll and bundle sheath transcriptomes. Principal Component (PC) 1 and PC2 explain 45% and 27% of data variance, respectively. D) Number of differentially expressed genes (DEGs) between mesophyll and bundle sheath cells at each time-point: up-regulated in mesophyll [ $\log_2(M/BS) > 0$ ] or bundle sheath [ $\log_2(M/BS) < 0$ ] (DESeq2 differential expression testing with multiple test corrected  $p$ -adj  $< 0.01$ ). M and BS represent mesophyll and bundle sheath cells, respectively.