**C:\Users\YZ\Desktop\G3\circRNA大文章\提交\Supplementary\Fig.S1.tifFigure legends**

**Figure S1.** The distribution of identified circRNAs per scaffold.

C:\Users\YZ\Desktop\G3\circRNA大文章\提交\Supplementary\Fig.S2.tif**Figure S2.** circRNA expression analysis in each sample of Las\_SL, Las\_ML, and Las\_WL treatment groups, was performed to compare treatments. Las\_SL, 340±2 μmol·m–2·s–1 (high light intensity); Las\_ML, 175±2 μmol·m–2·s–1 (medium light intensity); Las\_WL, 60±2 μmol·m–2·s–1 (low light intensity). **(A)** The overall expression of circRNAs in each sample of Las\_SL, Las\_ML, and Las\_WL treatment groups. Abscissa, sample name; ordinate, log10 (srpbm), srpbm, the normalized expression of circRNA, which can be directly used for later analysis. The box plot of each region illustrates five statistics (top to bottom: maximum, upper quartile, median, lower quartile, and minimum values). **(B)** Expression density map of circRNAs in each sample of Las\_SL, Las\_ML, and Las\_WL treatment groups. Abscissa, log10 (FPKM); ordinate, gene density. **(C–E)** Heat maps of expression patterns of the differentially expressed circRNAs in pairwise comparisons **(C)** Las\_SL vs. Las\_ML, **(D)** Las\_SL vs. Las\_WL, **(E)** Las\_WL vs. Las\_ML in lettuce. Abscissa, the sample; ordinate, the differentially expressed gene screened. Different colors indicate different gene expression levels. The color code indicating the Z-value (z = (x - µ)/σ, where x is the sample data, σ is the data standard deviation, and μ is the sample mean.) is provided on the right (blue to white to red indicate the expression from low to high).

C:\Users\YZ\Desktop\G3\circRNA大文章\提交\Supplementary\Fig.S3.tif**Figure S3.** Cyclization analysis validating circRNA presence in lettuce. **(A–C)** Agarose gel electrophoresis confirming the expected PCR product size. **(D–J)** Detailed analysis of circRNA cyclization and Sanger sequence verification using divergent primers. The red and blue sequences presented on top indicate the 5’- and 3’-termini of linear mRNA, respectively, proposed to produce circRNA. The linker sequence and cyclization of the circRNA are shown in the middle of each panel. The Sanger sequencing data are shown at the bottom of the panel and were obtained using divergent primers to amplify the junction of circRNA reverse-splicing. The reverse-splice point from head to tail is indicated by scissors. The sequence of the reverse-splicing sites is indicated in blue and red.

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**Figure S4.** Pairwise GO and KEGG enrichment analysis of differentially expressed circRNA-hosting genes. **(A–C)** Histograms of GO enrichment analysis of differentially expressed circRNA-hosting genes in pairwise comparisons. GO terms include biological processes, molecular functions, and cellular components. GO annotation is shown on the x-axis, and the number of genes is shown on the y-axis. **(D–F)** Scatter plots of the GO enrichment analysis of differentially expressed circRNA-hosting genes in pairwise comparisons. Abscissa, Rich factor. Rich factor indicates the ratio of the number of differential GO genes to the total number of GO genes (Rich factor = S gene number/B gene number). The larger the Rich factor, the greater the GO enrichment. Ordinate, GO\_Term (the GO function comment). In the scatter plot, the dot size represents the number of genes with a significant difference in the S gene number matched to a single GO. The dot color represents the p-value of the enrichment analysis, i.e., the significance of enrichment; p ≤ 0.05 represents significant enrichment. **(G–I)** Scatter plots ofKEGG enrichment analysis of differentially expressed circRNA-hosting genes in pairwise comparisons. Abscissa, Rich factor. Rich factor indicates the ratio of the number of differential KEGG genes (S gene number) to the total number of KEGG genes (B gene number). The larger the Rich factor, the greater the KEGG enrichment. Ordinate, pathway term (the KEGG metabolic pathway). In the scatter plot, the dot size represents the number of genes with a significant difference in S gene number matching a single KEGG. The dot color represents the p-value of the enrichment analysis, i.e., the significance of enrichment; p ≤ 0.05 represents significant enrichment.