

Figure S1. Comparison of previously reported dark- or heat- responsive genes with the dataset in this study.

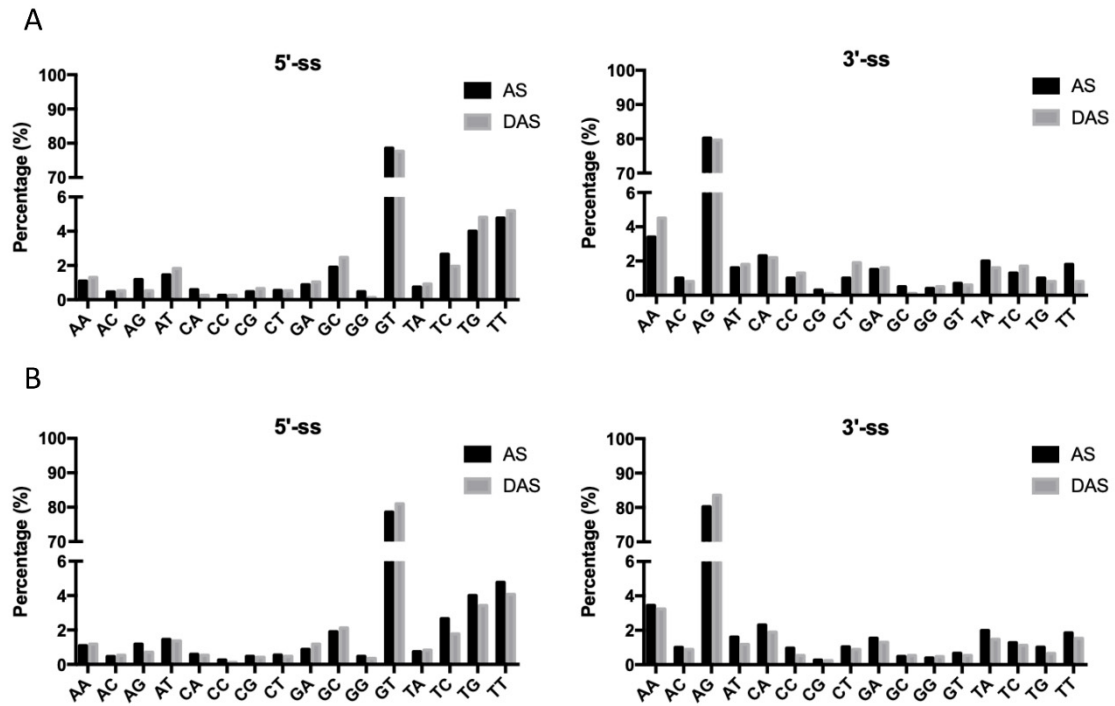
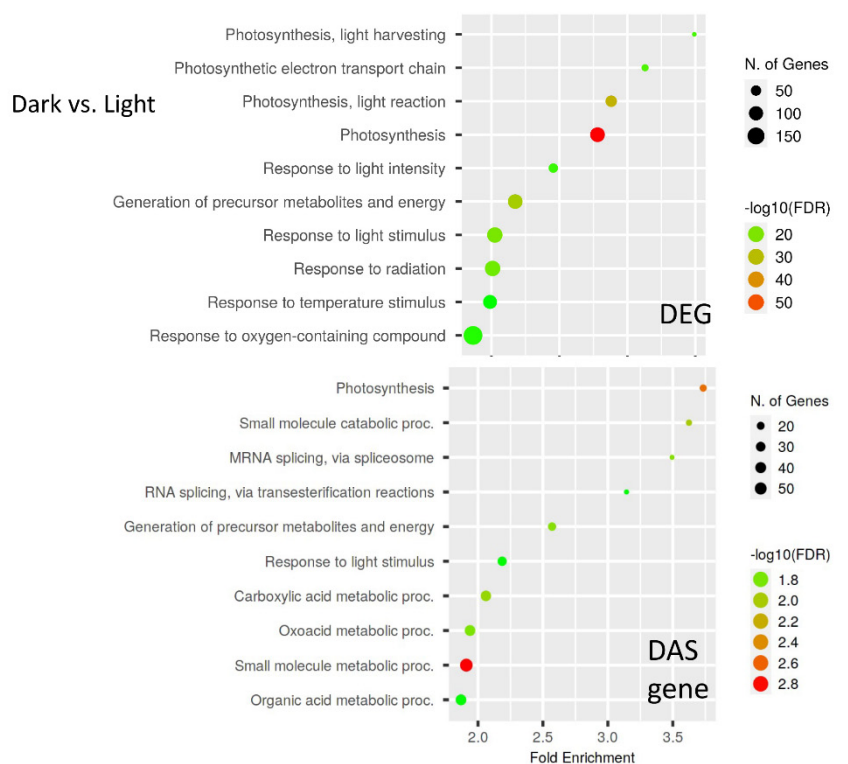


Figure S2. Analysis of the splice sites (ss) between total AS events and DAS events regulated by dark (A) and heat (B) treatments.



Heat vs. Dark

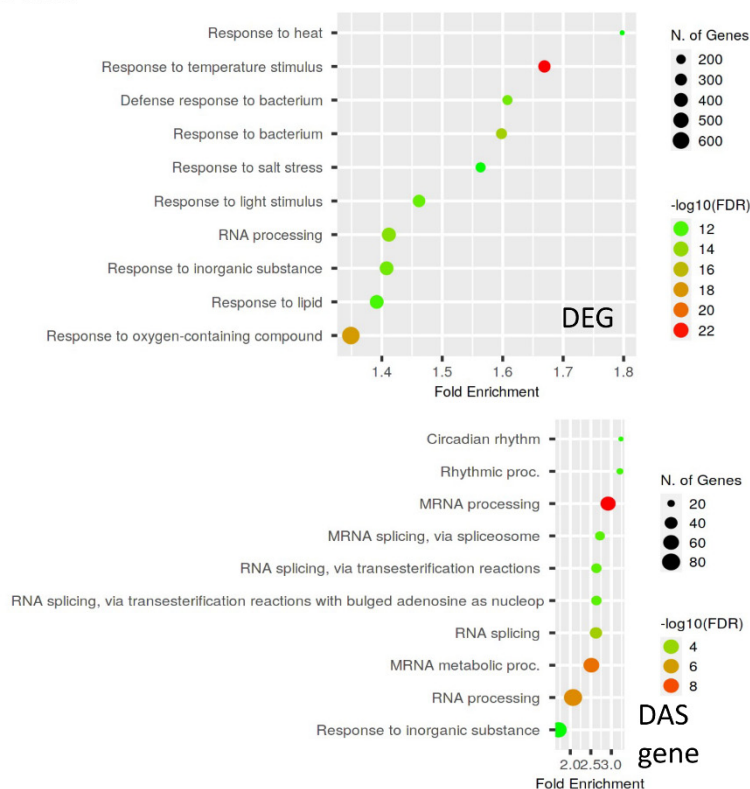


Figure S3. GO analysis of dark- or heat- regulated DEGs and DAS genes. Biological processes were sorted by fold enrichment and top ten pathways are shown.

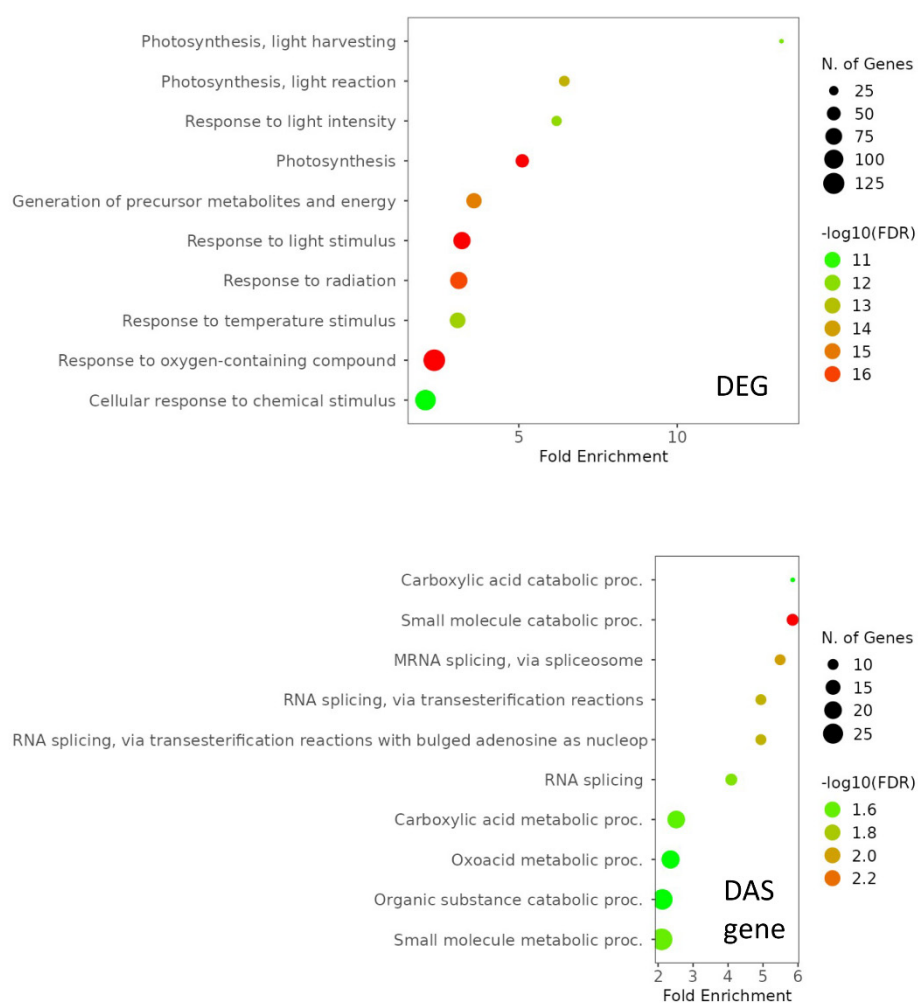


Figure S4. GO analysis of DEGs and DAS genes that were co-regulated by dark and heat treatments. Biological processes were sorted by fold enrichment and top ten pathways are shown.

AS5

ACACTGTGCTGCTTCATTCGTACGATGACGTACGTGAGAGACTCCACGAGCAGTAGTCAGACGACGAGCCCATCGCACCGCTTCCCGTG
GTGCGATCATAGCGGTGCAGATGTTGAGATGAAGCGGCATGAGCCACCAATATGTGGTACTCATCATGGCACGCAGCTTTCATTTATGC
TGCGCTCGTATGTTGTGGAATTTGAGAGCGGATACCATTTACACAGGAAACATCTATGACCATGATTACGCCAAGCTCAGATTACCCCTCAC
TAAAGGTACTAGTCCTGCAGGTTTAAACGAATTCGCCCTTCACCATGAGTAGCCGATGGAATCGTACGATCTACGTGGGATTTGCCTGG
AGATATTCGCAAGTGTGAGGTTGAAGATCTCTTCTACAAGTATGGACCAATTGTGGACATTGATTGAAGATTCCACCGAGACCTCCTGG
TTATGCCTTTGTCGAGTTTGAAGATCCTCGTGATGCAGACGATGCAATTTATGGACGTGATGGTTATGATTTTGATGGGTGTCGACTTCG
GGTTAGTAAACGCATGATGAAAGCTAGCTTAATTTCTGTAATTTCTTGTAAGGTGTTATCTTTGTGTGATGTTTTAGGTTGAGATTGC
ACATGGTGGTCGTAGATTTTACCATCAGTTGATAGGTACAGCAGCAGCTACAGTGCAGCCGTGCACCTTCAAGACGCTCTGACTACC
GCGTGCTTGTGACCGGATTACCGCTTCTGCTTCGTGGCAGGACCTTAAGGATCACATGCGCAAAGCTGGAGATGTCTGCTTCTTGAA
GTTTTCCCTGACCGTAAAGGCATGTCTGGGGTTGTGGATTATAGCAACTATGATGATATGAAGTACGCAATAAGGAAACTTGATGCCAC
TGAATTCGAAATGCTTCTCTAGTGCTTATATACGGGTGAGGGAATATGAGTCGAGGAGTGTGAGTCGAAGCCCAGATGATTCTAAAA
GCTATAGAAGCAGGAGTCGGAGCCGTGGTCCAAGCTGTAGCTATAGTAGCAAGAGCAGGAGTGTGTACCTGCTAGATCCATTTCCCC
GCGTTCACGGCCCTTAGTCGTTCTCGCTCGCTATACAGCTCTGTCTCAAGGTCCCAATCAAGATCAAAATCAAGATCAAGATCAAGATC
GAATTCCTCAGTTTACCTGTGATATCTGGTTGAAAGGGCGAATTCGCGGCCGCTAAATCAATCGCCCTATAGAATGCCC

AS6

GGGCATCTATAGGGCGATTGATTTAGCGGCCGCGAATTCGCCCTTCACCATGAGTAGCCGATGGAATCGTACGATCTACGTTGGGAATT
TGCTGGAGATATTCGCAAGTGTGAGGTTGAAGATCTCTTCTACAAGTTTGAATTTCTCTCTCGATAAAATGAATTCATT
TGACTTGTGGGTTTCATAAATTTGCAATTCCTGCTTCTGCTGAGACAATTTAAATCGACTCTTATGTATATTGTTTCAGTATGGACCAATTG
TGGACATTGATTGAAGATTCACCGAGACCTCCTGGTTATGCCTTGTGCGAGTTTGAAGATCCTCGTGATGCAGACGATGCAATTTATG
GACGTGATGGTTATGATTTGATGGGTGTCGACTTCGGGTTGAGATTGCACATGGTGGTCTGATGATTTTCAACATCAGTTGATAGGTAC
AGCAGCAGCTACAGTGCAGCCGTGCACCTTCAAGACGCTCTGACTACCGCGTGCTTGTGACCGGATTACCGCTTCTGCTTCGTGGCA
GGACCTTAAGGATCACATCCGCAAAGCTGGAGATGTCTGCTTCTGAAGTTTTCCCTGACCGTAAAGGCATGTCTGGGGTTGTGGATT
ATAGCAACTATGATGATATGAAGTACGCAATAAGGAACTTGATGCCACTGAATTCGAAATGCTTCTCTAGTGCTTATATACGGGTGA
GGGAATATGAGTCGAGGAGTGTGAGTCGAAGCCCAGATGATTCTAAAAGCTATAGAAGCAGGAGTCGGAGCCGTGGTCCAAGCTGTA
GCTATAGTAGCAAGAGCAGGAGTGTGTACCTGCTAGATCCATTTCCCCGCGTTCACGGCCCTTAGTCGTTCTCGCTCGCTATACAGCT
CTGTCTCAAGGTCCCAATCAAGATCAAAATCAAGATCAAGATCAAGATCGAATTCCTCAGTTTACCTGTGATATCTGGTTGAAAGGGCG
AATTCGTTTAACTGTCAGGACTAGTACCTTTATTGAGGGTTAATTCGAGCTTGGCGTATCATGGCATAGCTGTTTCTGTGTGAAATTGT
ATCCGCTCACATTTCCCCAACTACGGCCGGAGCAAAAAGTAAGCTGGGGGCTATGAGGGCTACCATATGGTGGGCTCTGCCCTTCA
CTCGAACCTACTGCCCCGCTAAGATCGCACCCCCGAGACGAGTGCGATTGGGGTC

Figure S5. Sequences of *SR30* isoforms identified by Sanger sequencing. Shaded sequences indicate those correspond to the sequences of *SR30*. Underlined sequences indicate the retained intron sequence.