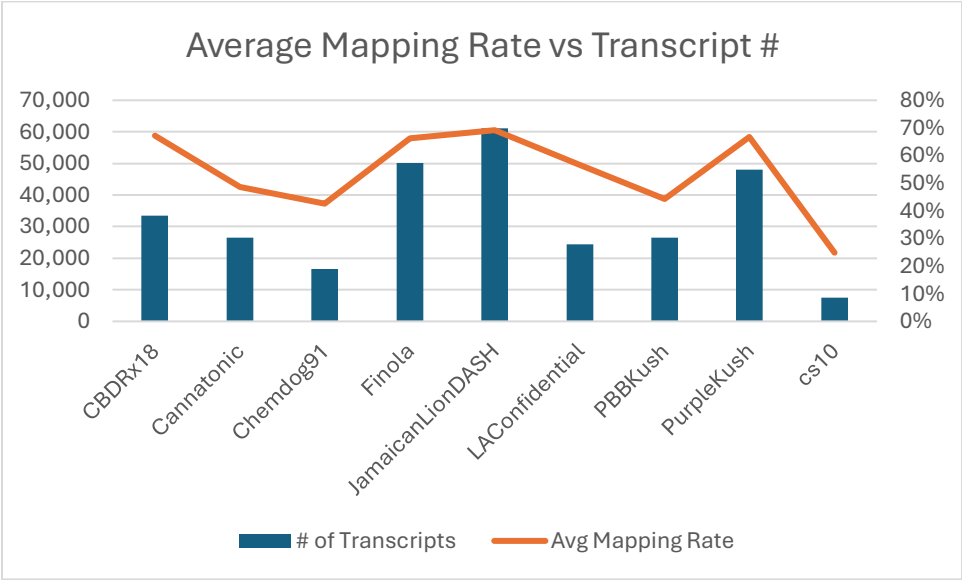
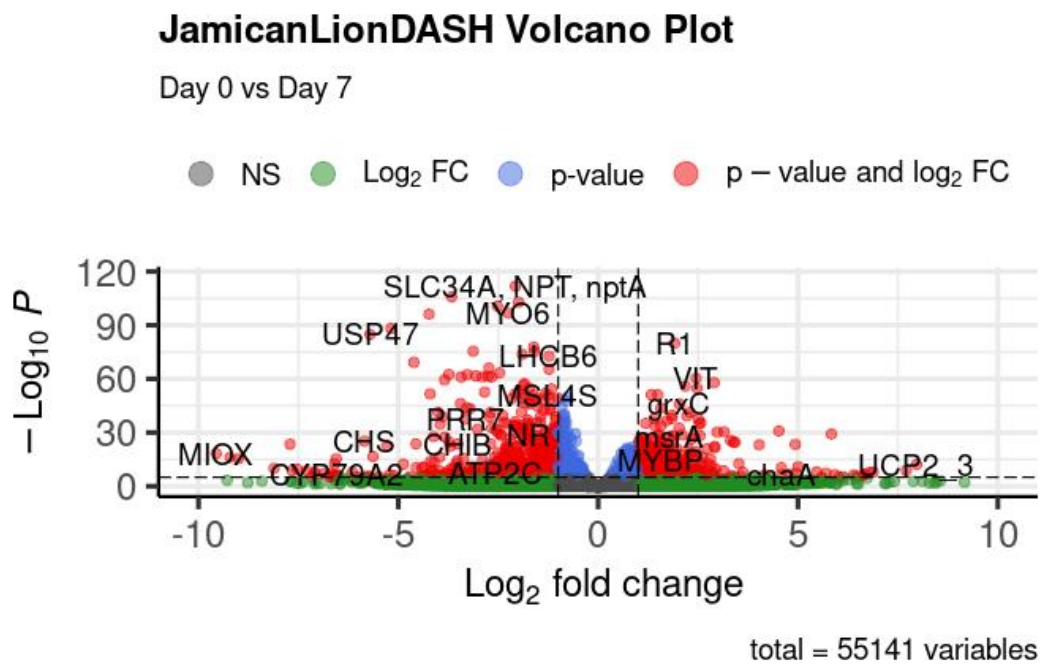


Supplementary Figures & Tables



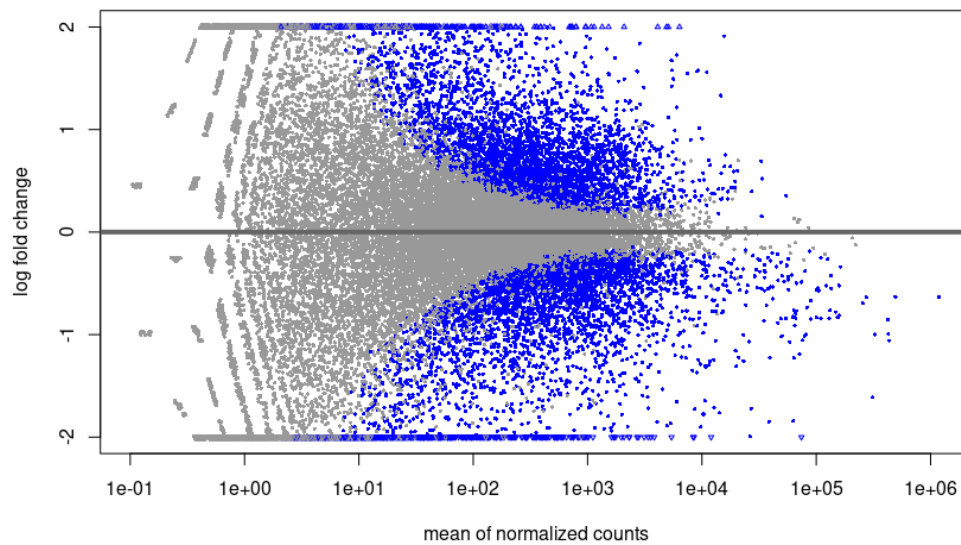
Supplemental Figure 1. The Average Mapping Rate for 9 different transcriptome references. The Y-axis on the left is the number of transcripts defined within the reference. The y-axis on the right is the mapping rate percent. The x-axis is the different models. As can be seen the mapping rate is inconsistently associated with transcript definition and mapping rate.



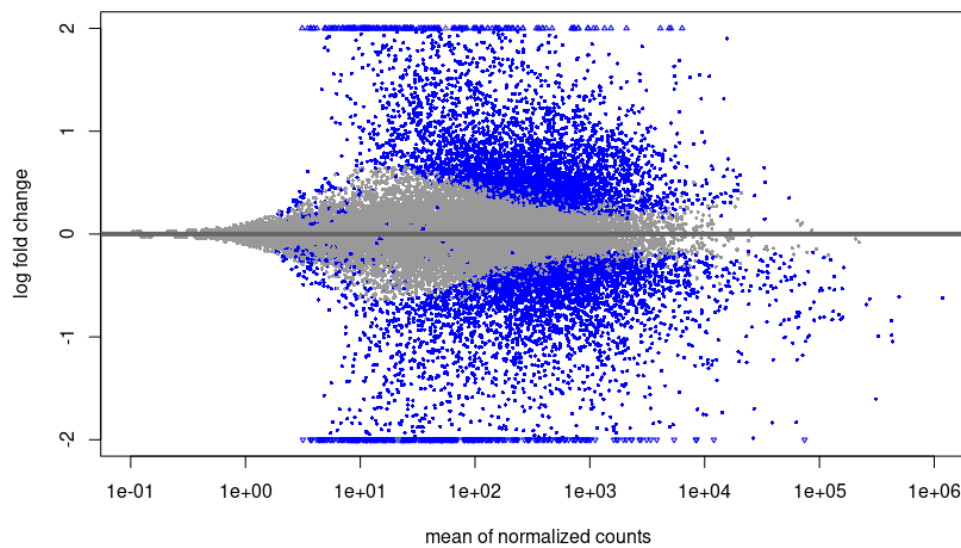
Supplemental Figure 2: Alternative Volcano Plot for DESeq

Table 1: DEGs related to circadian rhythm and photoperiodic flowering control. “Basemean” indicates the average normalized expression level of a gene across all samples. “Log2 Fold Change” indicates the log2 of a given fold change value. “padj” indicates the adjusted p-value (confidence level) for the given fold change. The “NCBI” column indicates the XM accession which can be used to locate the gene on NCBI. “Gene Name” indicates the common nomenclature for the given accession.

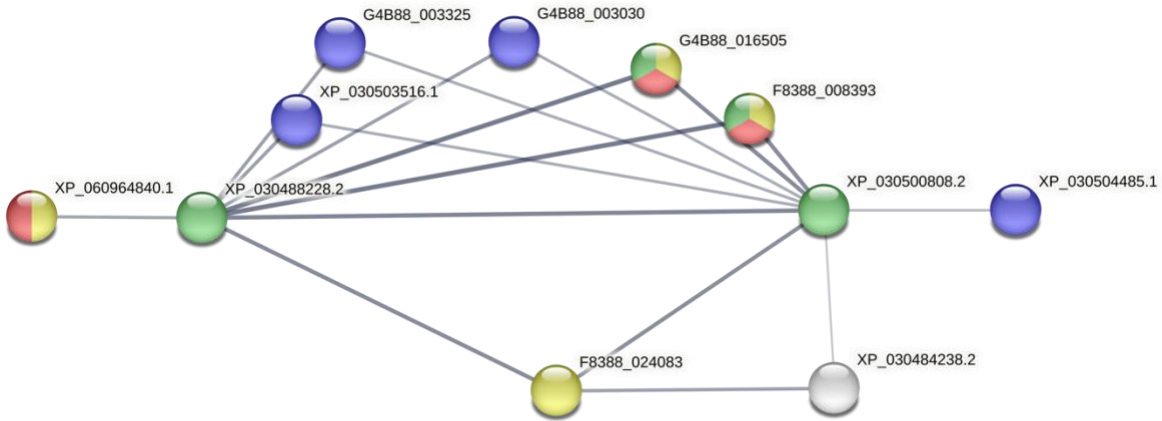
baseMean	log2Fold Change	padj	NCBI	Gene Name
287.41	-4.21	1.78E-49	XM_030628378.2	CsCOL10
18.83	-3.89	1.48E-02	XM_030636935.2	TFL1, Terminal Flower 1, similar to FT
540.04	-3.45	3.21E-44	XM_030628378.2	CsCOL10
116.65	-3.33	1.20E-35	XM_030632368.2	PRR37
2786.19	-2.72	5.75E-37	XM_061106171.1	Late Elongated Hypocotyl
88.58	-2.38	2.83E-12	XM_030648625.2	WNK4
161.40	-2.11	6.40E-14	XM_030648625.2	WNK4
11.16	-2.07	3.89E-02	XM_061102789.1	WNK11
2.53	-1.78	5.00E-01	XM_061110596.1	PIF3
830.15	-1.16	2.41E-09	XM_030635543.2	CsCOL7
50.21	-1.12	2.88E-03	XM_061108435.1	TOE1, Related to AP2
3356.89	-0.94	8.09E-15	XM_030654807.2	CsCOL4
3759.25	-0.92	3.04E-23	XM_030635543.2	CsCOL7
100.02	-0.90	6.55E-04	XM_061105389.1	HY5
1161.29	-0.53	7.96E-05	XM_030627201.2	PIF5
595.84	-0.45	2.57E-03	XM_030647656.2	WNK9
2564.81	-0.45	1.19E-06	XM_030624505.2	ELF3
10848.38	-0.44	4.78E-04	XM_030644948.2	APRR3
3311.31	-0.14	3.08E-01	XM_030640020.2	CsCOL6
3333.12	-0.14	3.82E-01	XM_030651223.2	CsCOL1
1798.10	0.12	7.28E-01	XM_030643599.2	CsCOL5 (16)
1691.35	0.28	1.32E-02	XM_030642410.2	PIF1
1050.72	1.02	2.09E-23	XM_030630649.2	ELF3
129.11	4.52	2.72E-29	XM_061112247.1 , XM_030629748.2	Truncated CAL
57.75	9.17	2.92E-02	XM_061107305.1	DICER1
1526.23	13.89	6.44E-39	XM_030623885.2	Vernalization 3
2086.30	14.34	1.20E-41	XM_030637236.2	FT-like
4899.33	15.57	2.60E-49	XM_030624853.2	HD3A



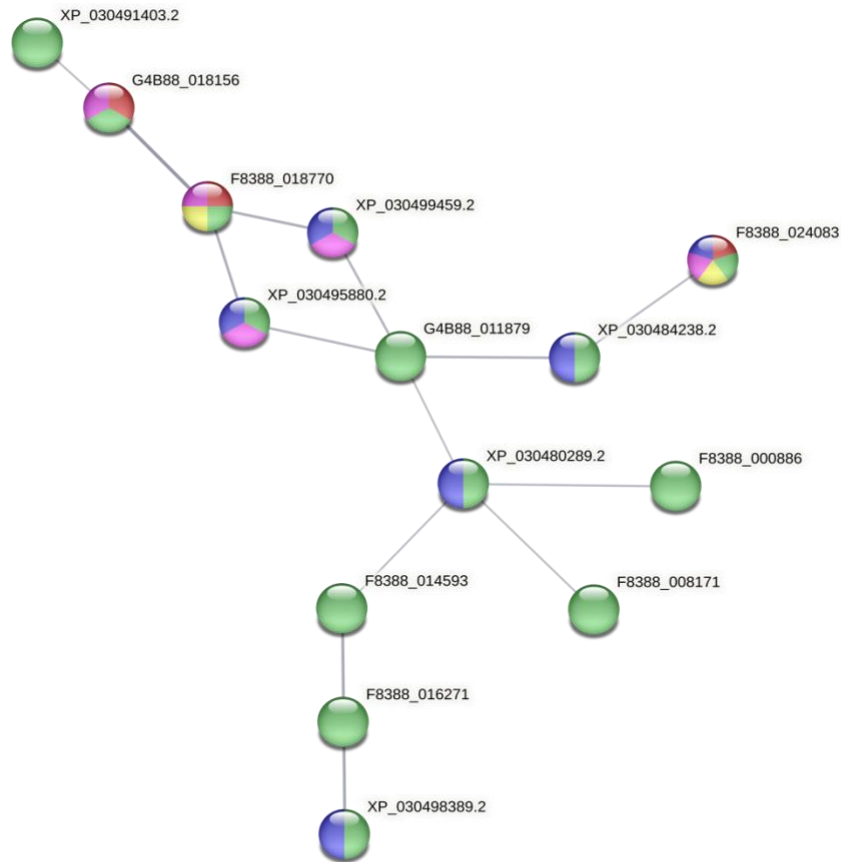
Supplemental Figure 3: Not using shrinkage.



Supplemental Figure 4. Using shrinkage.



Supplemental Figure 5: This prediction of functional relationship also displays phytochrome and photoreceptor-related genes in red, circadian rhythm genes/ PRR genes in green, WNK genes in blue, and light-responsive genes in gold. The white dot indicates CsCOL10, which was highly differentially expressed upon the SD transition in leaves. The data suggests that there is a high likelihood that a B-box domain containing gene integrates signals from the PRR genes, which connects to the CO signaling cascade via CsCOL10. Also, two PAS-domain genes are implicated in the integration of signals from PRR genes, colorized in green, gold and red.

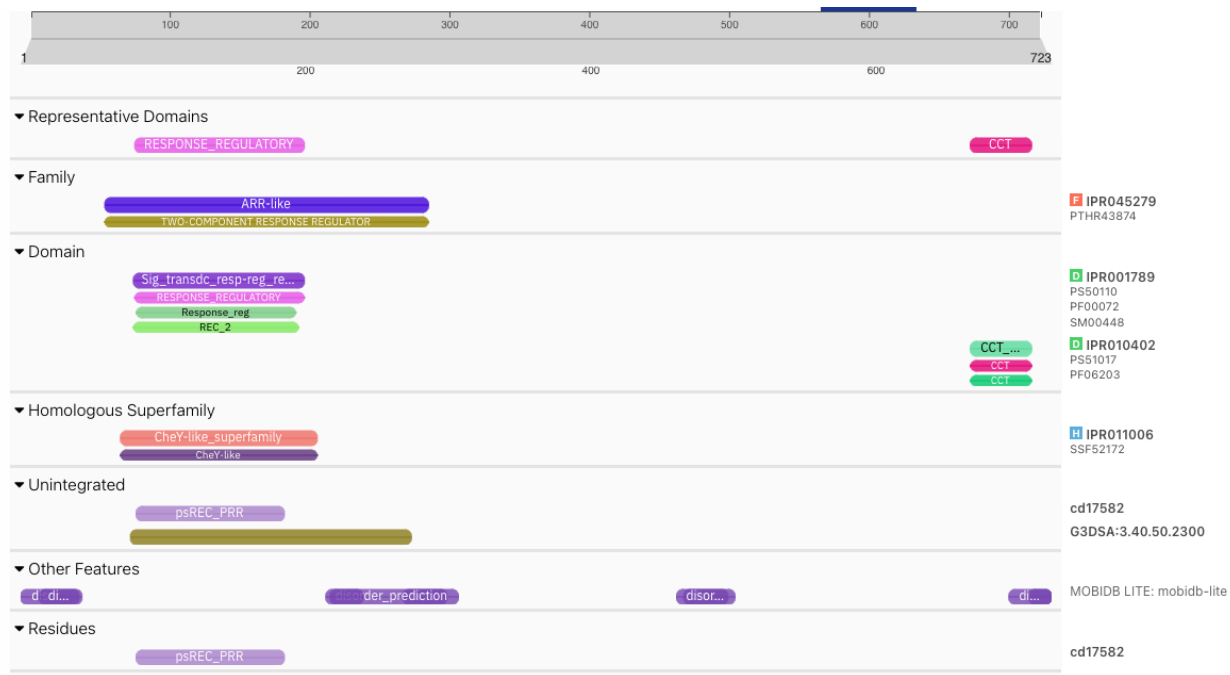


Supplemental Figure 6: In this physical interaction network (Figure 4), phytochrome regulates HY5, which in turn regulates two CO genes, which induce a signaling cascade related to circadian rhythms, which includes CsCOL10 and the putative B-box domain protein indicated in

the PRR37 functional analysis.

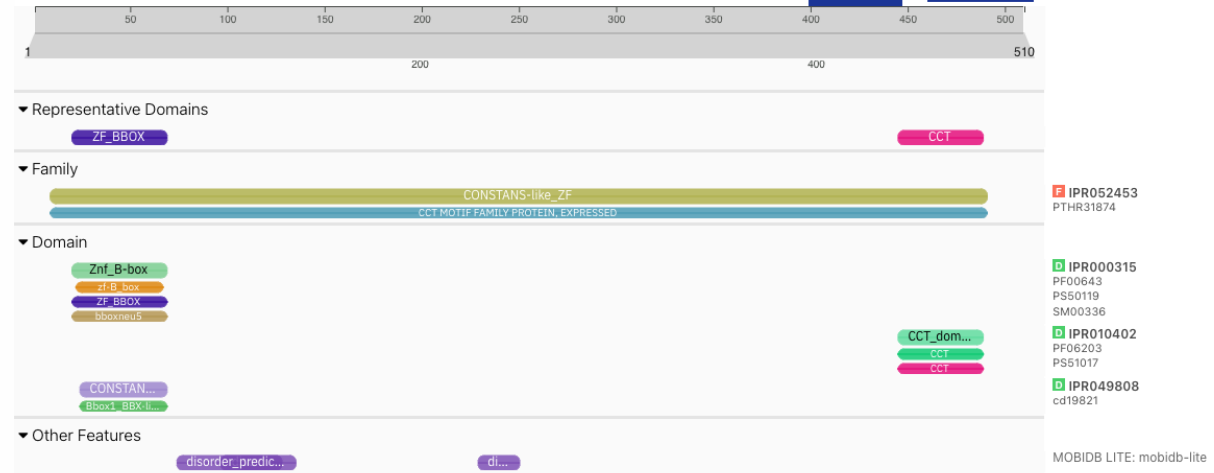


Supplemental Figure 7: Interpro CsPRR37 Domains

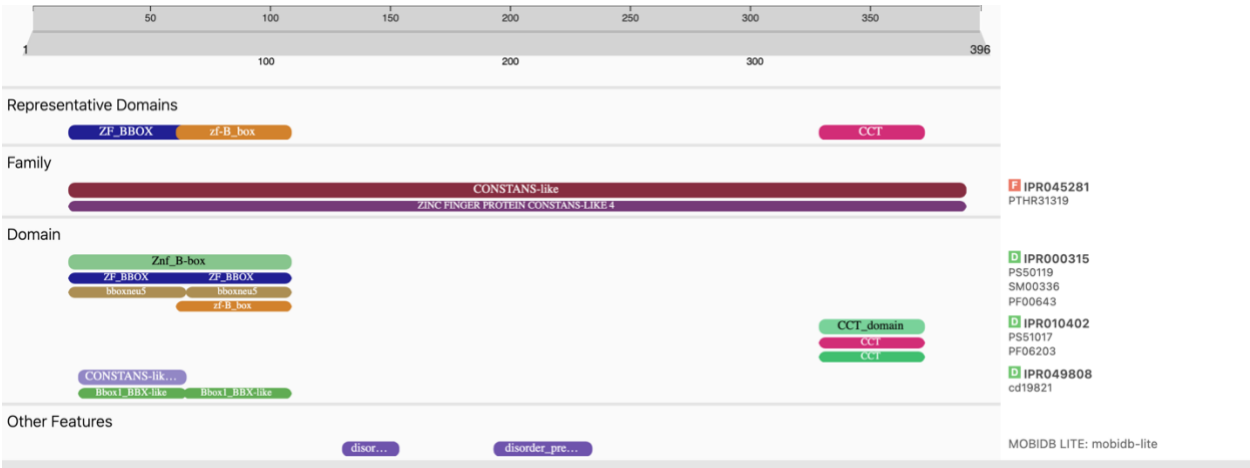


Supplemental Figure 8: Interpro CsAPRR3 Domains

Entry matches to this protein



Supplemental Figure 9: Interpro CsCOL5 Domains



Supplemental Figure 10: Interpro CsCOL10 Domains