

Supplemental Figure S1. Venn diagrams of differentially expressed non-flowering genes (top) and flowering genes (bottom) indicating the overlaps under long day (LD), shift (Sh) and short day (SD) in different genotypes.



Supplemental Figure S2. Numbers of differentially expressed non-flowering genes at time points T1, T3 and T5 in different genotypes under long day (LD), shift (Sh) and short day (SD). Black squares and lines indicate upregulated genes, gray squares and lines indicate downregulated genes.



Supplemental Figure S3. Numbers of differentially expressed flowering genes at time points T1, T3 and T5 in different genotypes under long day (LD), shift (Sh) and short day (SD). Black squares and lines indicate upregulated genes, gray squares and lines indicate downregulated genes.



Supplemental Figure S4. Expression of *GmTOE1b* and soybean homologs of *AP3* and *PI* in Clark and the *E1* NIL under long day (LD) or short day (SD) by qRT-PCR. SD: 10-hour light (6:45–16:45), LD: 16-hour light (6:45–22:45). Time points T1–T6 represent 6:30, 10:30, 14:30, 18:30, 22:30 and 2:30. Error bars indicate standard deviation.



Supplemental Figure S5. Tissue-specific expression of *GmTOE1b* and *AP3* and *PI* homologs in Williams 82 grown under short day (10-hour light, 6:45–16:45) at 28°C by qRT-PCR. Hypocotyl, unifoliate, 1st trifoliate, 2nd trifoliate, 3rd trifoliate, stem, flower bud, pod and seed were sampled at 30 days after sowing at 13:00. Error bars indicate standard deviation.



Supplemental Figure S6. Expression of soybean homologs of the circadian clock genes measured by RNA sequencing in Clark at three time points (T1: 6:30, T3: 14:30, T5: 22:30) under short day (SD: 10-hour light, 6:45–16:45) or long day (LD: 16-hour light, 6:45–22:45) three weeks after germination. FPKM values are displayed on the y-axes.

COL1a COL1b COL2a COL2b	A T G T T G G A T G G A G A - A G C A A C A A T G G G C A C G T G G G G T G G C A T G T G C G A C A C G T G C C G T T C A T G T T G G A G G G C C A - A G C A A C A A C G C C C A C G T G G C C G C G C A T G T G C G A C A C G T G C C G C T C A T G T T G A A G G A A G G C A C C A A C A A C G T G G T G G C C A C A C C T G G T C A C A T G T C C G C G C C G C G C A C A C G T G C C G C G C G C A C A C G T G C C G C G C G C A C A C G T G C C G C G C G C A C A C G T G C C G C G C G C A C A C G T G C C G C G C G C G C A C A C G T G C C G C G C G C G C G C A C A C G T G C C G C G C G C G C G C A C A C G T G C C G C G C G C G C A C A C G T G C C G C G C G C C C C C C C G C G	59 59 74 80
COL1a COL1b COL2a COL2b	G G C C C C T C C T C C G T C T C T G C C G C G	136 136 154 160
COL1a COL1b COL2a COL2b	TGACGTGGCACGAGCGCGTGTGGGGTGTGCGAGCCTGCGAGCGCCCTGCGGCCTTCCTCCTGCAAGGCTGAC TCACGTGGCACGAGCGCGTGTGGGTGTGCGAGGCGTGCGAGCGCCCCGGCGGCGTTCCTCCTGCAAGGCCGAC GTGTGGCCTCAAGACACGAGCGTGTGTGGGGTGTGCGAAGCGTGTGAACGTGCTCCCGCAGCGTTTCTATGCAAAGCCGAC GTGTGGCCTCGAGACACAAAGCGTGTGTGGGGTGTGCGAAAGCGTGTGCGCGCGC	210 210 234 240
COL1a COL1b COL2a COL2b	GCCGCCTCCCTCTGCGCCTCCTGCGACGCGACATCCACGGCGCCAACCCCCTCGGCAGCCGCCACCACCGTGTCCCCAT GCCGCCTCCCTCTGCGCCTCCTGCGACGCCGACATCCACGCCGCCAACCCCCCACCGCGCCACCACCACCGCGT GCAGCTTCTCTTTGTTCTTCCTGTGATGCTGACATTCACTCAGCAAACCCTCTCGCTAGCCGCCACCACCGCGTGGCCAC GCAGCTTCTCTTTGTTCTTCCTGTGATGCTGACATTCACTCAGCAAACCCTCTCGCTAGCCGCCACCACGACCGTGTCCCAT	290 290 314 320
COL1a COL1b COL2a COL2b	C C T C C C C A T C G C C G C C G G C C C G G C A A C A A C A A C A A C A C	325 322 385 398
COL1a COL1b COL2a COL2b	ACGA CAACGT CGA CGAT G CT G A CT T G G A C G A C G A T G A C G A A A G C G CT T CAT G G C T T G C T A C C C T A C G A C G A C G A C G A C G T G C T G A C G T T G A C G A C G A A G A G A G A C C G CT T CAT G G C A A G C G G A G G A G A G G A G A G A G	393 390 462 474
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COL1a COL1b COL2a COL2b	A CT CT CA T CA G CA C CA A C A TT T C G G T GT T GT T GT CT CA CAA GA GT T AT G CT G G G GA CA GT GT T GT	606 618 651 666
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COL1a COL1b COL2a COL2b	T GTTT C <mark>A</mark> GTTT CAT CAAT GGAT <mark>AT</mark> T GGT GTT GTAC OT GAAT CA <mark>C C GAT G</mark> AG <mark>G GAT G</mark> T CT CAAT <mark>T G G</mark> C AT <mark>A</mark> CAA GAA C C C <u>T GTTT C A GTTT CAT CAAT GGAT ATT GGT GTT GTAC OT GAAT CAC CAAT GAG GGAT GT CT CAAT T G C CAT A CAA GAC OC C</u> T GTTT C GGTTT CAT C GAT GGAT GTT GGT GTT GTAC T C GAAT CAAT C	766 778 811 826
COL1a COL1b COL2a COL2b	C <mark>CA A</mark> A G G G A C A A <mark>T I</mark> G A C C T A T I T <mark>T C T G G A</mark> C C T C C <mark>O</mark> A T I C <mark>A G G</mark> T G C C T T C <mark>C</mark> C A T T <mark>T T C T C</mark> C A A T G G A C A G <mark>G</mark> G A G G C <mark>C</mark> A G A C <mark>C A A</mark> A G G G A C A A T T G A C C T A T T T T T C T G G A C C T C C A A T T C A G G T G C C T T C T C T C T A C A T G G A C A G G G A G G C C C A A T A G G G A C A A C T G A C C T A T T T T T C T G G A C C C C C A T T T C C C C A T T T T T	846 858 885 900
COL1a COL1b COL2a COL2b	GT CCT A A G <mark>G</mark> T A <mark>C</mark> A G G G A G A A A A G A G A G A G A G A	926 938 965 980
COL1a COL1b COL2a COL2b	G A CT A G A C C <mark>C</mark> C G <mark>T</mark> A T A A A <mark>A</mark> G G T C G <mark>A</mark> T T T G C <mark>C</mark> A A G A G A A C A <mark>G</mark> A T G T A G A A G A T C A G A T C A G A T C A G A T C A G A T C A G A C A A G A C A C A C A C A C A C	1006 1018 1049 1060
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Supplemental Figure S7. Alignment of *GmCOL1a*, *GmCOL1b*, *GmCOL2a* and *GmCOL2b* cDNA sequences. The regions highlighted in red and yellow are the target regions of *COL1*-RNAi and *COL2*-RNAi, respectively. Sequences were retrieved from Phytozome. Dashes represent alignment indels. Black and gray shades indicate nucleotide positions shared by four and three *GmCOL* genes, respectively.