Figure S1

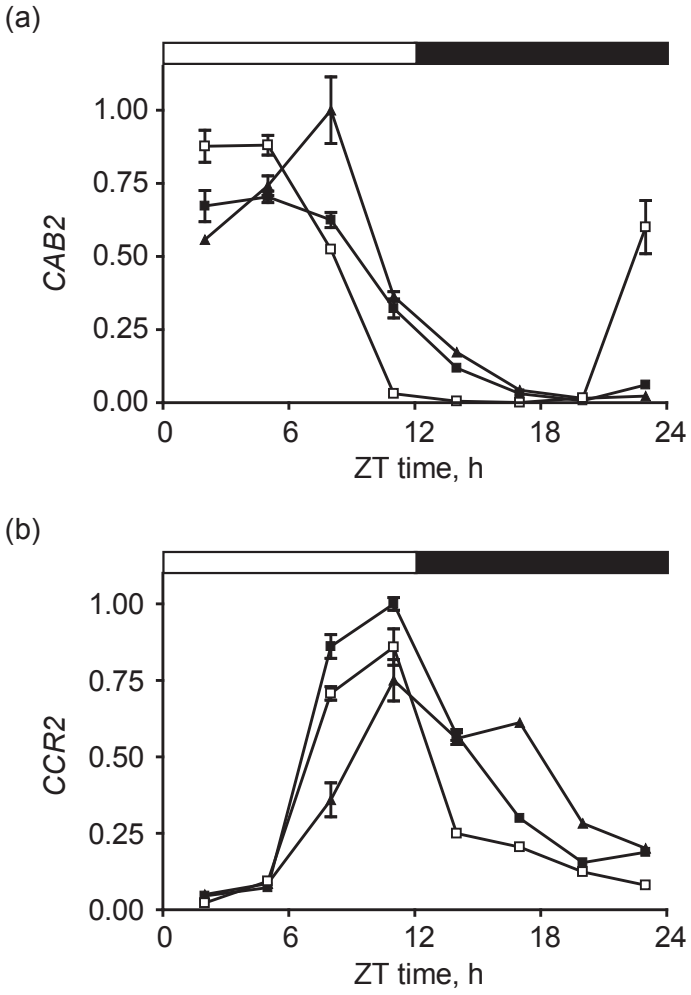

(a)
1.00
0.75
0.50
0.25
0.00
CAB2
0
6
12
18
24
ZT time, h
(b)
1.00
0.75
0.50
0.25
0.00
CCR2
0
6
12
18
24
ZT time, h

Figure S2

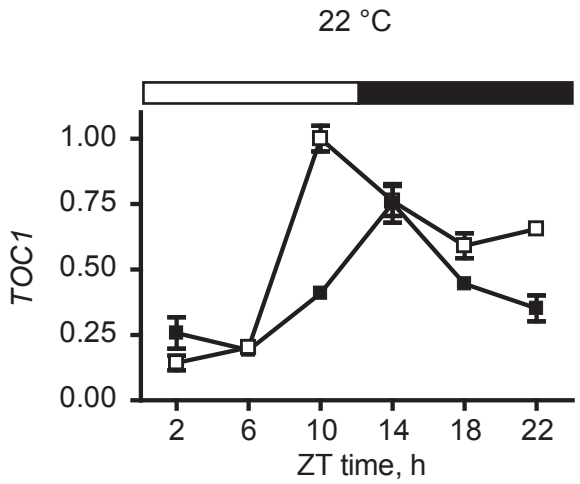
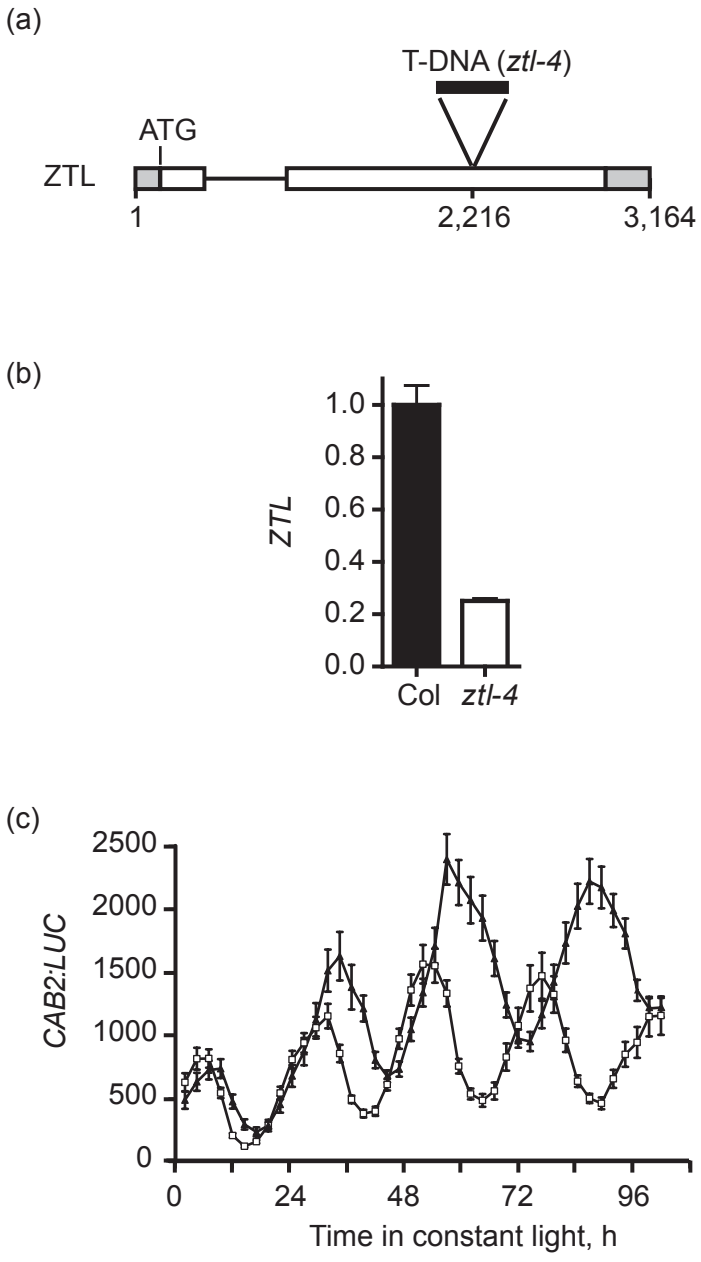


Figure S3


(a)
T-DNA (*ztl-4*)
ATG
ZTL
1
2,216
3,164
(b)
ZTL
1.0
0.8
0.6
0.4
0.2
0.0
Col
ztl-4
(c)
CAB2:LUC
2500
2000
1500
1000
500
0
0
24
48
72
96
Time in constant light, h

Supplementary Material

Figure S1. Expression of *CAB2* and *CCR2* in light:dark cycles.

CAB2 (a) and *CCR2* (b) transcript abundance in one week-old seedlings of wt (open squares), *axr6-3* (filled squares), and *ztl-4* (filled triangles) grown in diurnal conditions. White and black bars above the graphs indicate times of light and dark, respectively. Data are the average of two independent replicates and error bars represent the range. Gene expression was determined by real-time PCR and expression of *IPP2* (see "Experimental Procedures") was used as a normalization control. The expression level for each experimental gene was calculated using the formula $2^{(C_T\textit{IPP2} - C_T\text{experimental})}$, where C_T is the average threshold cycle for three technical replicates. The expression value for each gene was normalized to the highest value for each experiment.

Figure S2. *TOC1* expression in *axr6-3* and wt TMG lines.

TOC1 transcript abundance in one week-old seedlings of wt (open squares) and *axr6-3* (filled squares) TMG grown in diurnal conditions at 22°C. Black and white bars above graphs indicate times of dark and light, respectively. Data are the average of two independent replicates and error bars represent ± SEM. Gene expression was determined by real-time PCR and expression of *IPP2* (see "Experimental Procedures") was used as a normalization control. The expression level for each experimental gene was calculated using the formula $2^{(C_T\textit{IPP2} - C_T\text{experimental})}$, where C_T is the average threshold cycle for three technical replicates. The expression value for each gene was normalized to the highest value for each experiment.

Figure S3. Characterization of *ztl-4*.

(a) Diagram of the T-DNA insertion in *ZTL* (SALK_35701), which corresponds to *ztl-4*. The insert is at base pair 2,216 interrupting the portion of the gene encoding the second kelch repeat. Filled regions correspond to UTRs and open regions represent coding sequence. (b) Average expression (± SEM) of *ZTL* in wt (black bar) and *ztl-4* (white bar), as determined by real-time PCR. Values represent the average of six individual time points taken every 4 hours between 25-45 h in constant light. The expression level of *ZTL* was calculated using the formula $2^{(C_T IPP2 - C_T ZTL)}$, where C_T is the average threshold cycle for three technical replicates and *IPP2* (see "Experimental Procedures") was the normalization control. (c) Trace of *CAB2:LUC* expression in *ztl-4* (filled triangles) and wt (open squares) seedlings entrained in light:dark cycles for one week then transferred to constant light. Error bars represent ± SEM where n = 16.