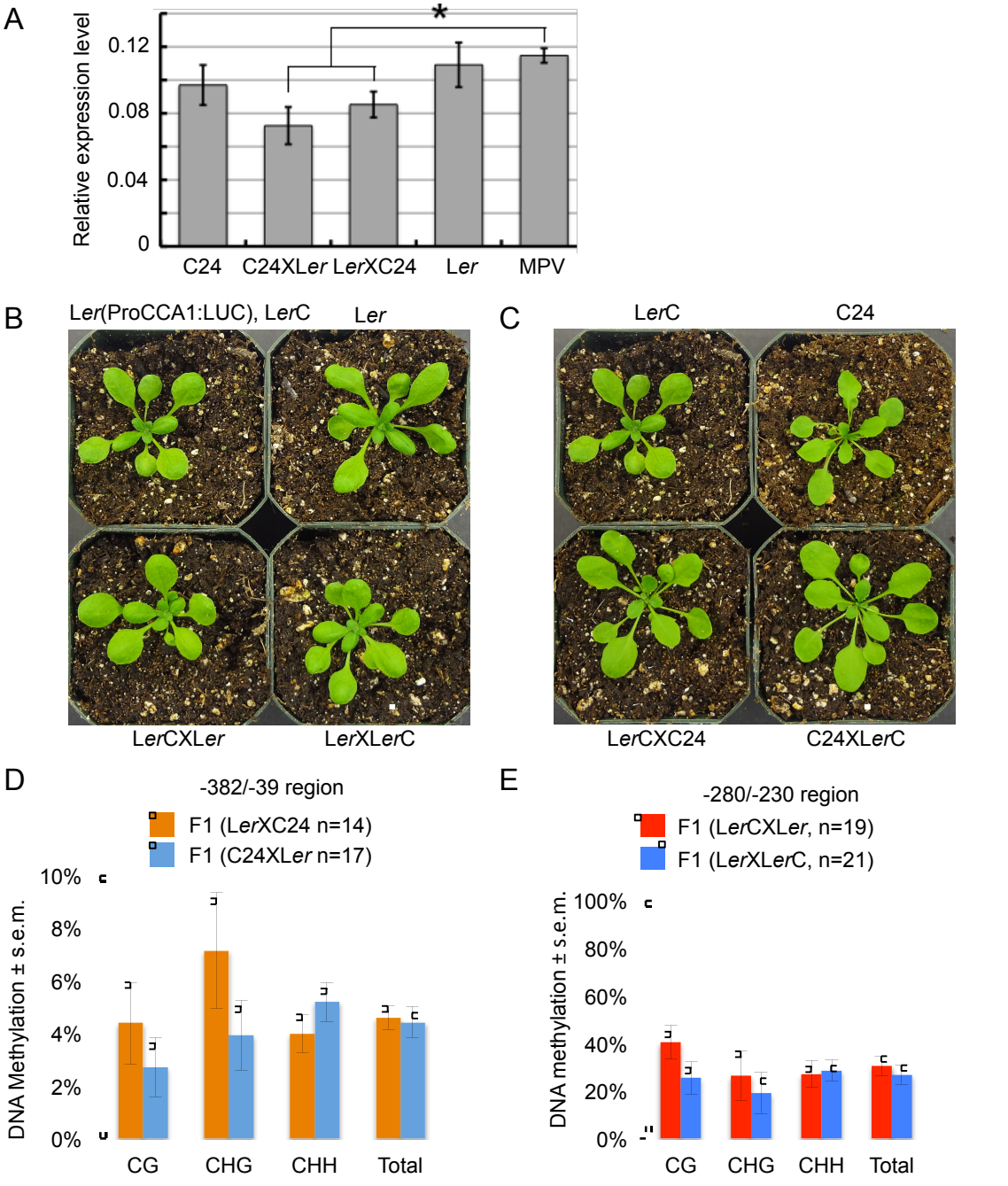


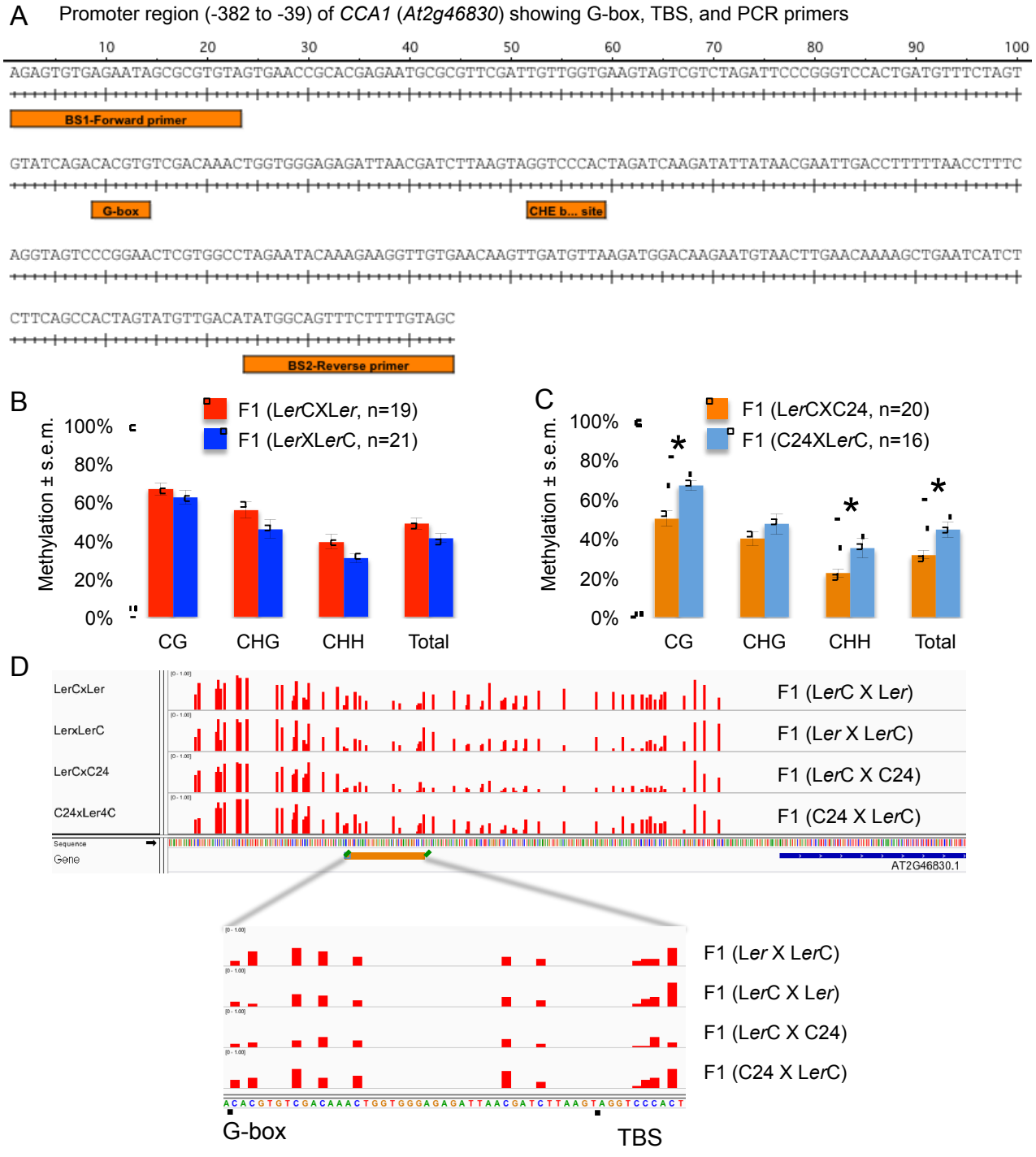
Supplemental Figure 1. *CCA1* expression, plant size, and bisulfite sequencing analyses of DNA methylation in reciprocal hybrids.

(A) Relative expression levels of endogenous *CCA1* (relative to *ACT7*) were lower in C24XL*er* than in L*er*XC24 crosses at ZT6 (dawn = ZT0) (n = 3, mean ± s.e.m., Student's t-test). MPV: mid-parent value.

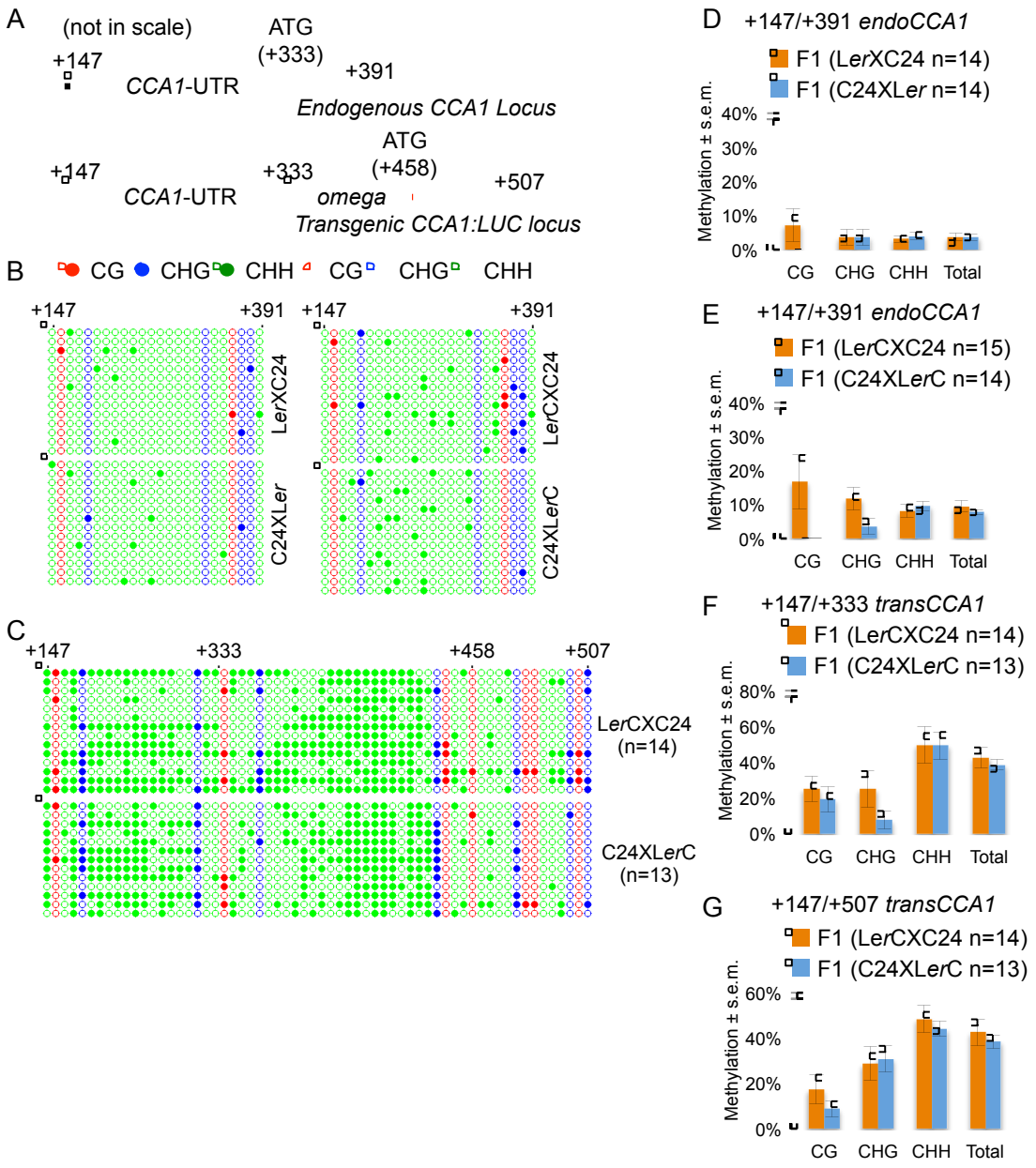
(B-C) Photos of seedling plants in L*er*(*ProCCA1:LUC*) or L*er*C, L*er*, L*er*CXL*er*, and L*er*XL*er*C **(B)** and C24, L*er*C, L*er*CXC24, and C24XL*er*C **(C)**. Scale bar = 20 mm.

(D) CG, CHG, and CHH methylation changes (± s.e.m.) in the endogenous *CCA1* promoter region (from -382 to -39) of L*er*XC24 (F1) and C24XL*er* (F1). (n = number of clones sequenced in each replicate).

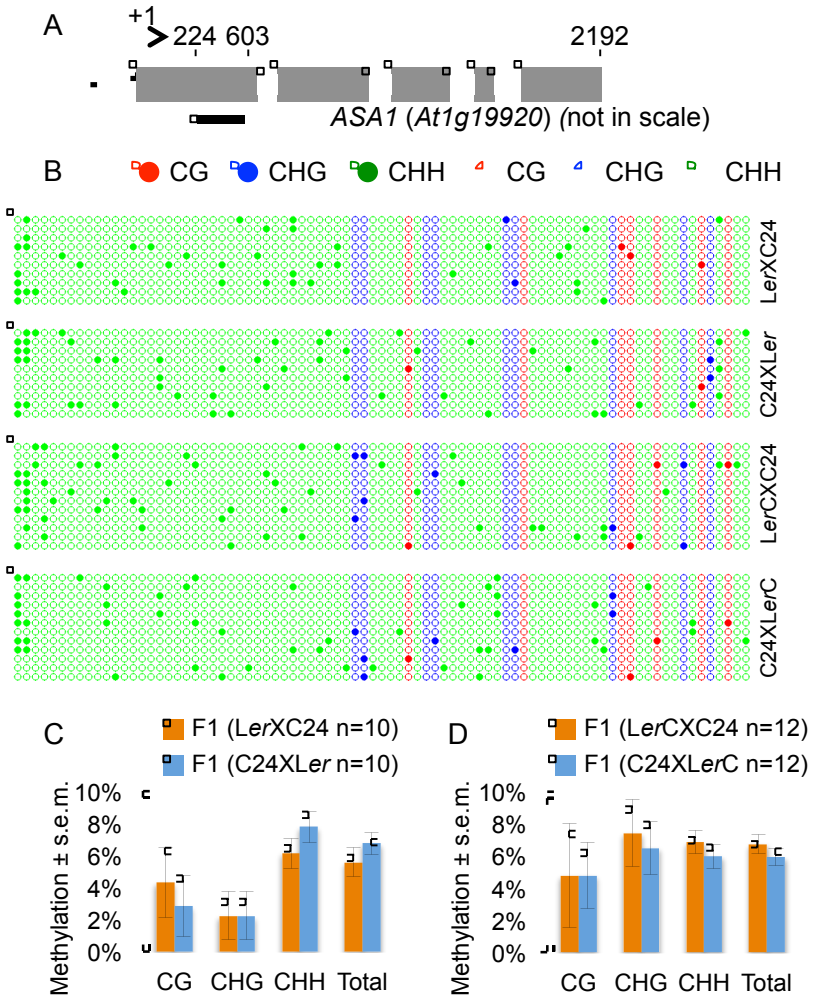
(E) CG, CHG, and CHH methylation changes (± s.e.m.) in the *CCA1:LUC* promoter region (from -280 to -230) of L*er*CXL*er* (F1) and L*er*XL*er*C (F1). (n = number of clones sequenced in each replicate).



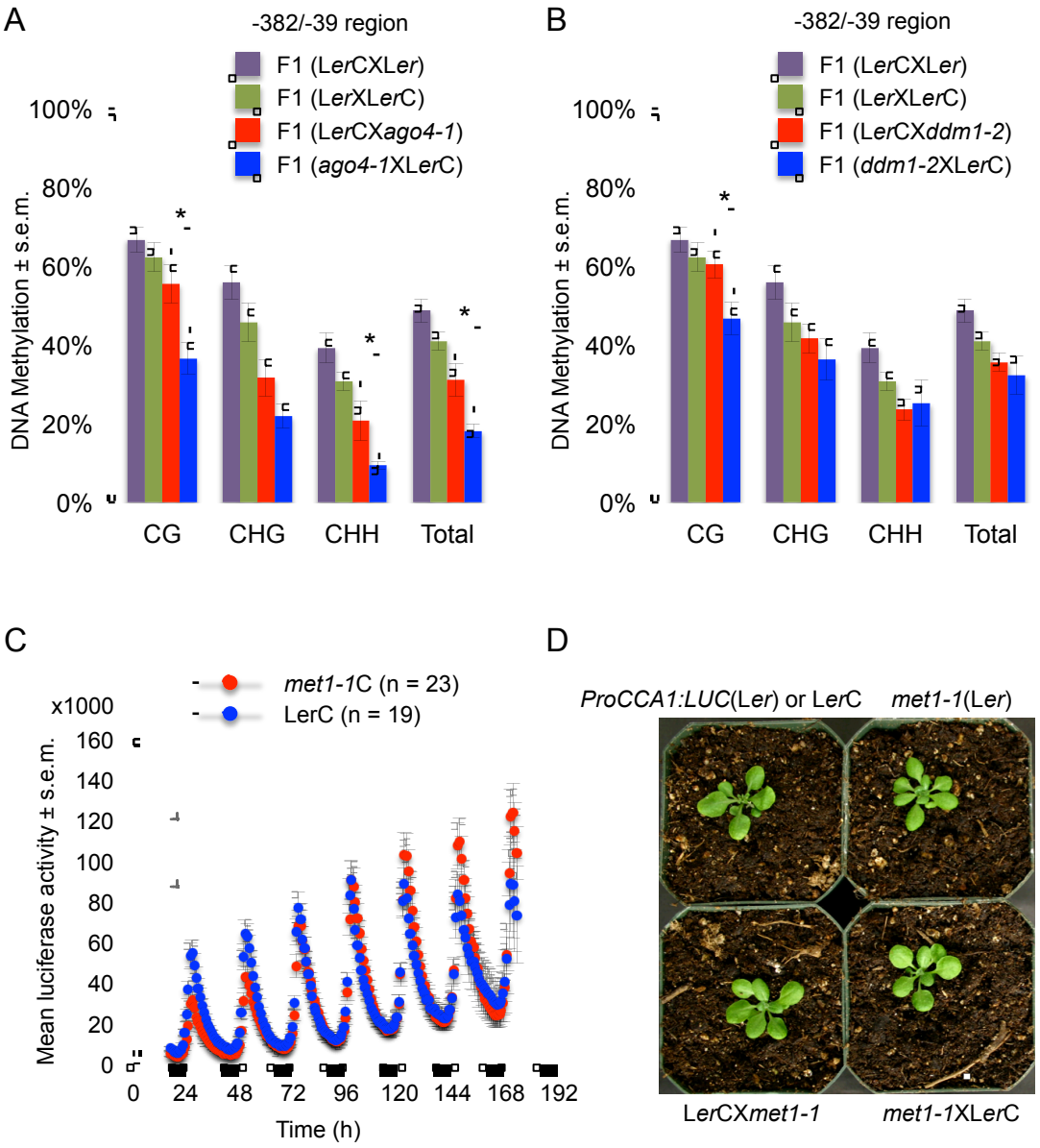
Supplemental Figure 2. Bisulfite sequencing analysis of DNA methylation in reciprocal hybrids.
(A) Promoter region (-382 to -39) of *CCA1* (*At2g46830*) showing G-box, TBS, and PCR primer sites.
(B-C) CG, CHG, and CHH methylation changes in L*er*C X L*er* and L*er X Ler*C **(B)** and in L*er*C X C24 and C24 X L*er*C **(C)**. (n = number of clones sequenced in each replicate). Asterisk denotes statistical significance at P < 0.05 (Student's t-test).
(D) Methylation profile in the regions containing G-box and CHE, a Class I TCP protein, -binding site (TBS).



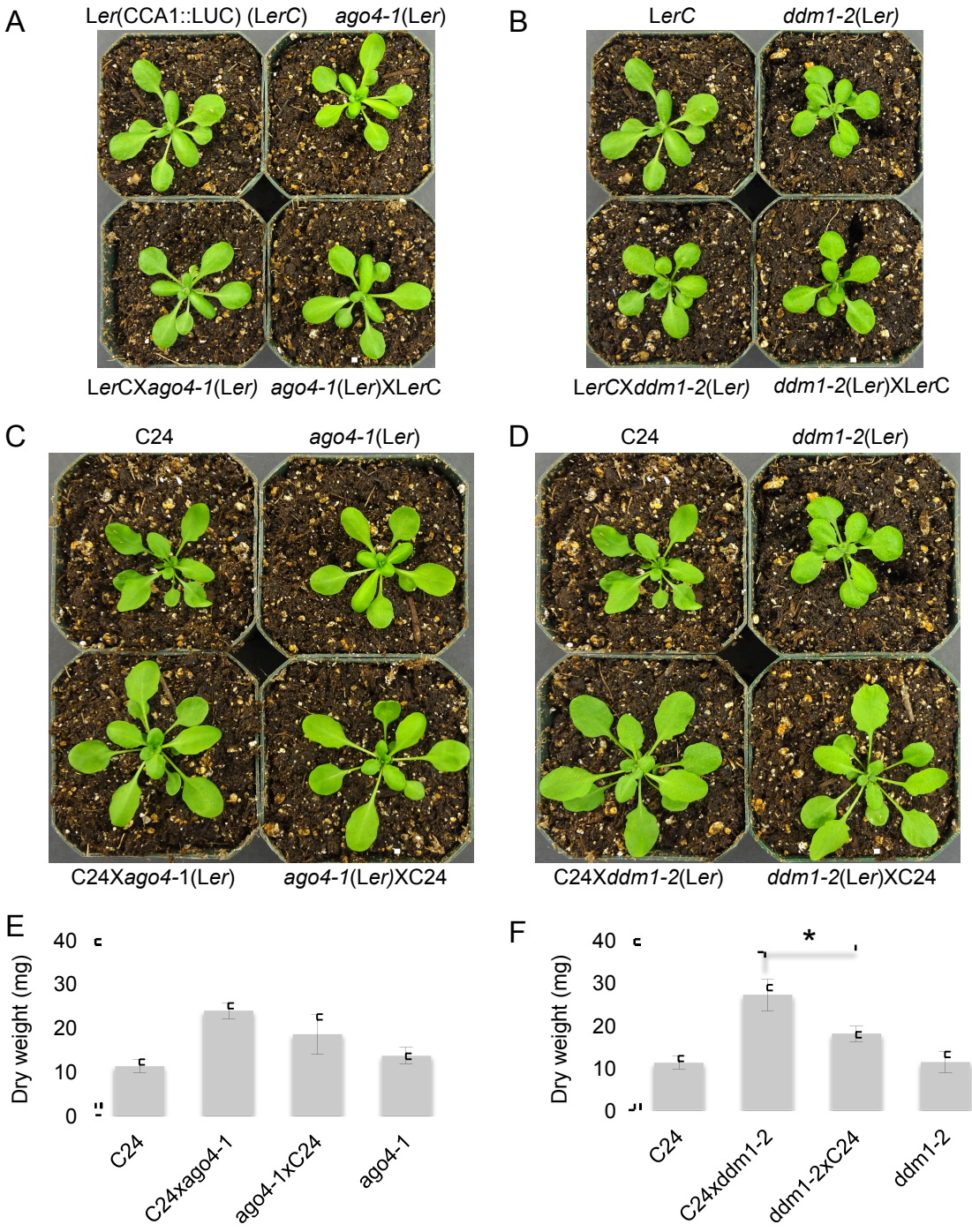
Supplemental Figure 3. Bisulfite sequencing analysis of DNA methylation at the 5'UTR of *CCA1*.
(A) Schematic diagram of the endogenous *CCA1* locus and transgene *CCA1:LUC* locus targeted for bisulfite sequencing PCR. The 5' leader of the tobacco mosaic virus (omega) in the transgenic *CCA1:LUC* is indicated. Black and red lines indicate CCA1 and LUC coding regions, respectively.
(B-C) Dot-plot analysis of CG, CHG, and CHH methylation in the indicated hybrids. A total of 10-15 individual targets were sequenced and analyzed. Red, blue, and green circles indicate CG, CHG, and CHH methylation (filled) or no methylation (open).
(D) Percentage of methylation changes (± s.e.m.) of the endogenous *CCA1* UTR region between reciprocal hybrids of L*er*XC24 (orange) and C24XL*er* (pale blue). n = number of clones sequenced.
(E-F) Percentage of methylation levels (± s.e.m.) of the endogenous *CCA1* UTR region (E) and the same region in the transgene *CCA1:LUC* locus (F) between reciprocal hybrids of L*er*CXC24 (orange) and C24XL*er*C (pale blue). n = number of clones sequenced.
(G) Percentage of methylation levels (± s.e.m.) of the CCA1-UTR and the 5' leader (omega) of tobacco mosaic virus in the transgene *CCA1:LUC* locus in L*er*CXC24 reciprocal hybrids. n = number of clones sequenced.



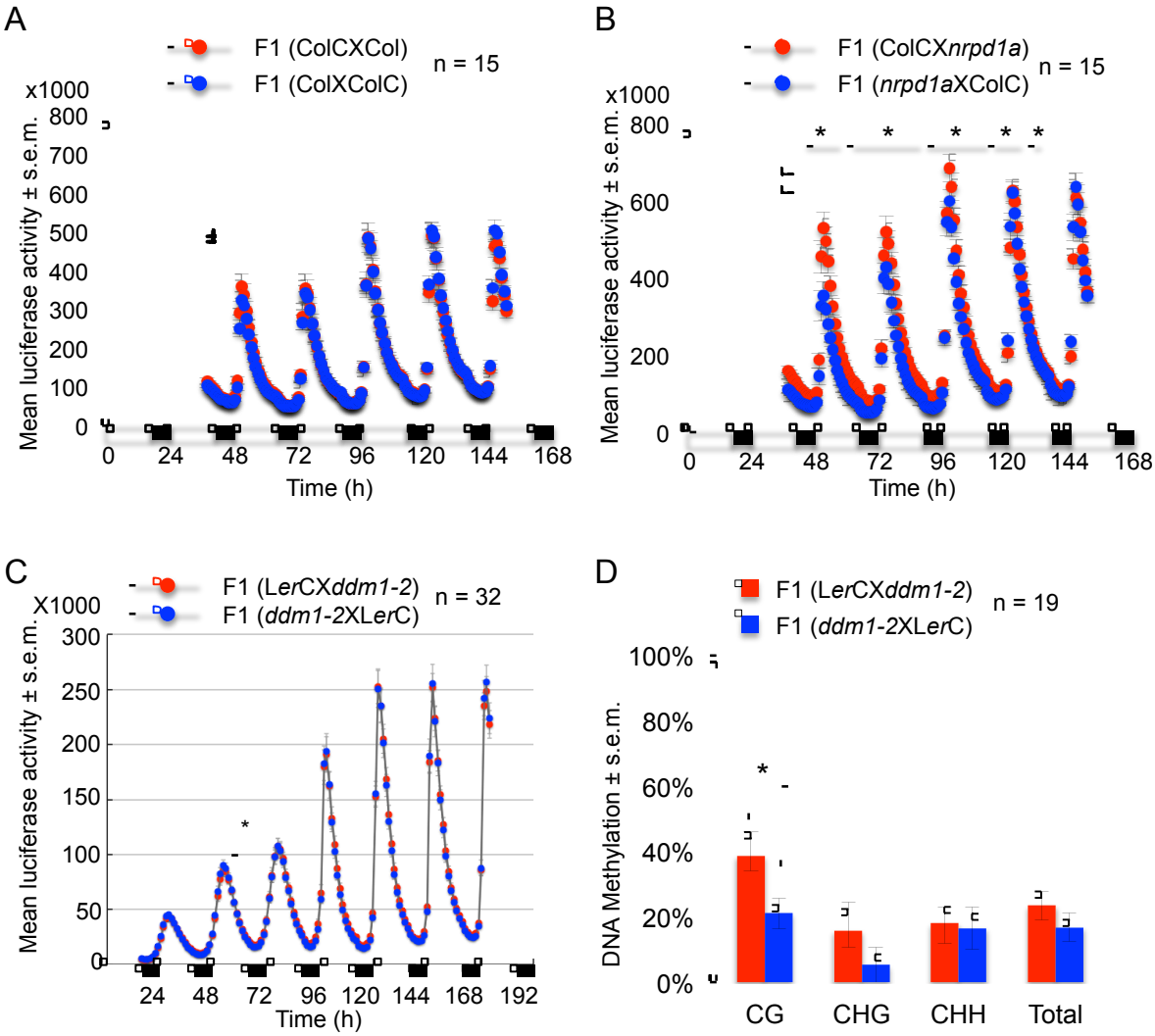
Supplemental Figure 4. Bisulfite sequencing analysis of DNA methylation at *ASA1*.
(A) Schematic diagram of the *ASA1* locus and the targeted region (224-603; black bar) used as the positive control of the bisulfite chemical reaction in bisulfite sequencing.
(B) Dot-plot analysis of CG, CHG, and CHH methylation in the indicated hybrids. A total of 10-12 individual targets were sequenced and analyzed. Red, blue, and green circles indicate CG, CHG, and CHH methylation (filled) or no methylation (open).
(C) Percentage of methylation changes (± s.e.m.) of the *ASA1* locus between reciprocal hybrids of L*er*XC24 (orange) and C24XL*er* (pale blue). (n = number of clones sequenced).
(D) Percentage of methylation changes (± s.e.m.) of the *ASA1* locus between reciprocal hybrids of L*er*CXC24 (orange) and C24XL*er*C (pale blue). (n = number of clones sequenced).



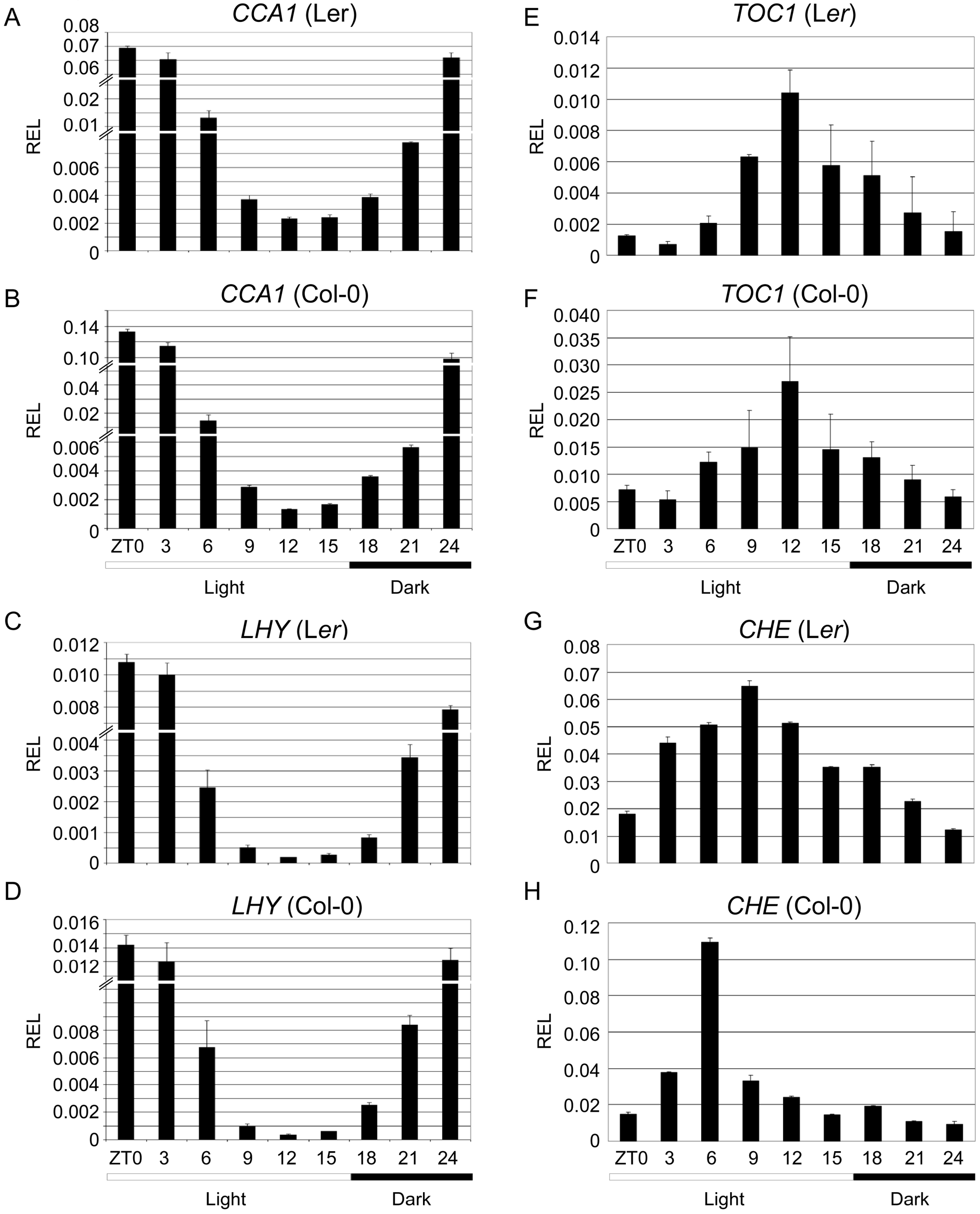
Supplemental Figure 5. Changes in DNA methylation and circadian gene expression.
(A) CG, CHG, and CHH methylation in the promoter region (from -382 to -39) of L*er*C X L*er*, L*er* X L*er*C, L*er*C X *ago4-1* (F1), and *ago4-1* X L*er*C (F1). Asterisks indicate statistical significance ($P < 0.05$, Student's t-test).
(B) CG, CHG, and CHH methylation in the promoter region (from -382 to -39) of L*er*C X L*er*, L*er* X L*er*C, L*er*C X *ddm1-2* (F1), and *ddm1-2* X L*er*C (F1). The asterisk indicates statistical significance ($P < 0.05$).
(C) Mean values (± s.e.m.) of bioluminescence counts (in thousands, Y-axis) for *proCCA1:LUC* expression in seedlings of the wild-type (L*er*C) (blue) and the *met1-1* homozygous mutant (*met1-1*C) (red).
(D) Photos of typical seedling plants in L*er*(*ProCCA1:LUC*) or L*er*C, *met1-1*(L*er*), L*er*CX*met1-1* (F1), and *met1-1*XL*er*C (F1). Scale bar = 20 mm.



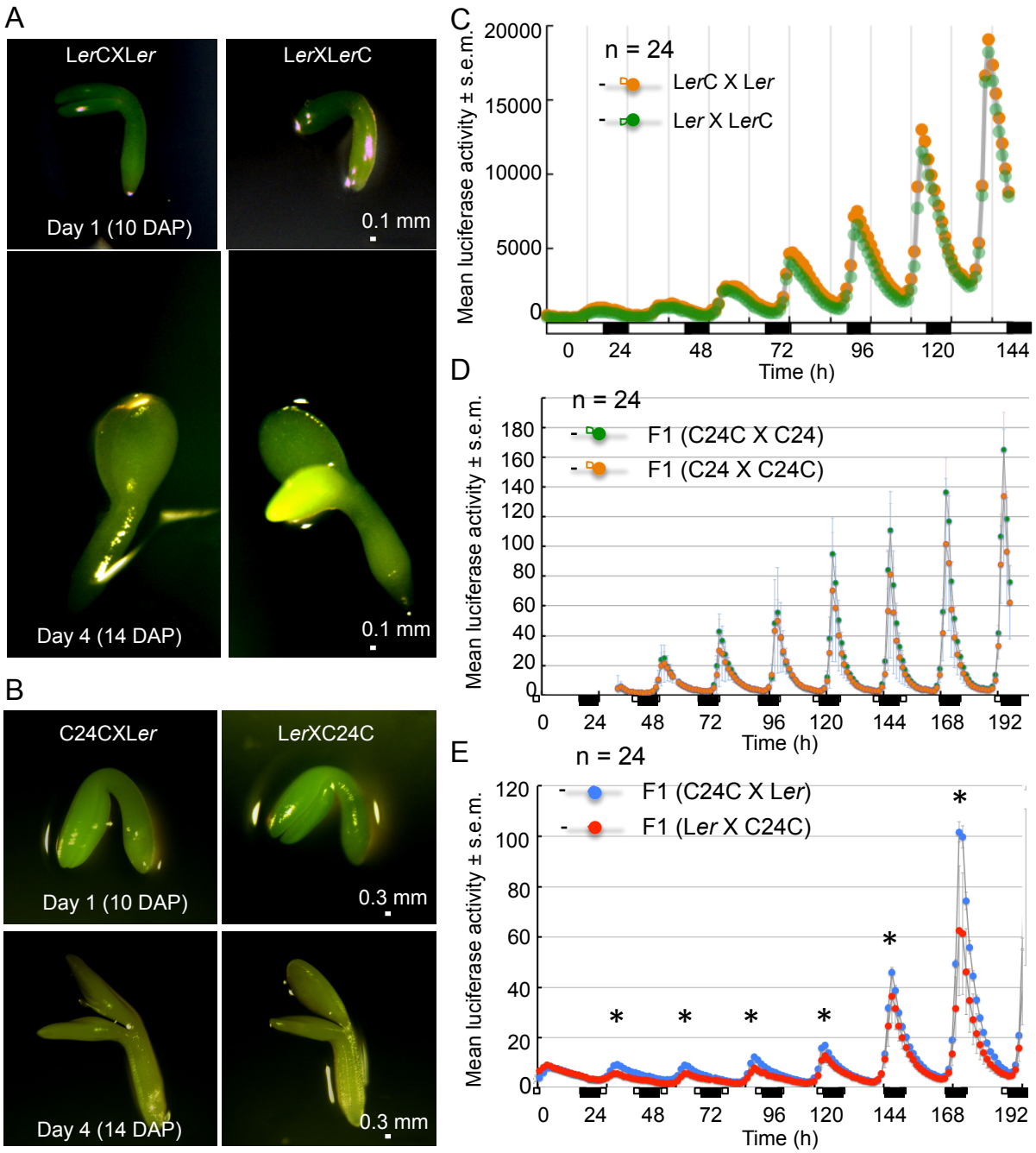
Supplemental Figure 6. Biomass analysis in reciprocal hybrids and their parents.
(A) Photos of typical seedling plants in L*er*C, *ago4-1*(L*er*), L*er*C X *ago4-1* (F1), and *ago4-1* X L*er*C (F1).
(B) Photos of typical seedling plants in L*er*C, *ddm1-2*(L*er*), L*er*C X *ddm1-2* (F1), and *ddm1-2* X L*er*C (F1). Scale bar = 20 mm.
(C-D) Photos of seedling plants in C24, *ago4-1*(L*er*), C24X*ago4-1*, and *ago4-1*XC24 **(C)** and C24, *ddm1-2*(L*er*), C24X*ddm1-2*, and *ddm1-2*XC24 **(D)**. Scale bar = 20 mm.
(E-F) Dry weight (mg) of the aboveground plants in C24, *ago4-1*(L*er*), C24X*ago4-1*, and *ago4-1*XC24 **(E)** and in C24, *ddm1-2*(L*er*), C24X*ddm1-2*, and *ddm1-2*XC24 **(F)**. (n=5, mean ± s.e.m., asterisk indicates statistical significance level of 0.05, Student's t-test).



Supplemental Figure 7. Analyses of *CCA1* expression and DNA methylation in reciprocal hybrids.
(A-B) Mean values (± standard errors, S. E.) of bioluminescence counts (in thousands, Y-axis) in seedlings of the reciprocal hybrids ColCXCol (red) and ColXColC (blue) **(A)** and in ColCX*nrpd1a* and *nrpd1a*XColC **(B)**. Col was used because *nrpd1a* is in the Col background.
(C) Mean values (± standard errors, s.e.m.) of bioluminescence counts (in thousands, Y-axis) in the seedlings of reciprocal F1 crosses between L*er*CX*ddm1-2* (red) and *ddm1-2*XL*er*C (blue).
(D) Percentage of methylation changes in the GTBS region between reciprocal F1 crosses of L*er*CX*ddm1-2* (red) and *ddm1-2*XL*er*C (blue). The asterisk indicates statistical significance ($P < 0.05$, n = number of clones sequenced in each replicate, Student's t-test).



Supplemental Figure 8. Diurnal expression of clock regulators in developing siliques in *A. thaliana* (Col-0 and L*er*).
(A) Diurnal expression of *CCA1* in L*er* (Zeitgeber 0, ZT0 = dawn for all data)
(B) Diurnal expression of *CCA1* in Col-0.
(C) Diurnal expression of *LHY* in L*er*.
(D) Diurnal expression *LHY* in Col-0.
(E) Diurnal expression of *TOC1* in siliques (L*er*)
(F) Diurnal expression of *TOC1* in Col-0.
(G) Diurnal expression of *CHE* in L*er*.
(H) Diurnal expression of *CHE* in Col-0.
R.E.L.: relative expression levels of qRT-PCR results from three replications (mean ± s.e.m.). The scales in Y-axis are broken in **(A-D)** because of wide ranges in expression values.



Supplemental Figure 9. Parent-of-origin effects of *ProCCA1:LUC* expression in embryos of reciprocal hybrids.
(A-B) Embryos of L*er*XL*er*C (left panel) and L*er*CXL*er* (right panel) **(A)** and C24CXL*er* (left panel) and L*er*XC24C (right panel) **(B)** were dissected 10 days after pollination (DAP) and cultured in the medium for one day (day 1, upper panel) or four days (day 4, lower panel), when the embryos were subjected to bioluminescence assays. The scales are 0.1 mm **(A)** and 0.3 mm **(B)**.
(C) Mean values (± s.e.m.) of bioluminescence counts (Y-axis) in cultured embryos of L*er*XL*er*C (red) and L*er*CXL*er* (blue) reciprocal hybrids.
(D) Bioluminescence counts (Y-axis) in cultured embryos of the reciprocal hybrids C24(proCCA1:LUC) or C24CXC24 (green) and C24XC24C (orange).
(E) Mean values (± s.e.m.) of bioluminescence counts (Y-axis) in cultured embryos of the reciprocal hybrids C24CXL*er* (blue) and L*er*XC24C (red). Asterisks indicate statistical significance ($P < 0.05$, Student's t-test).