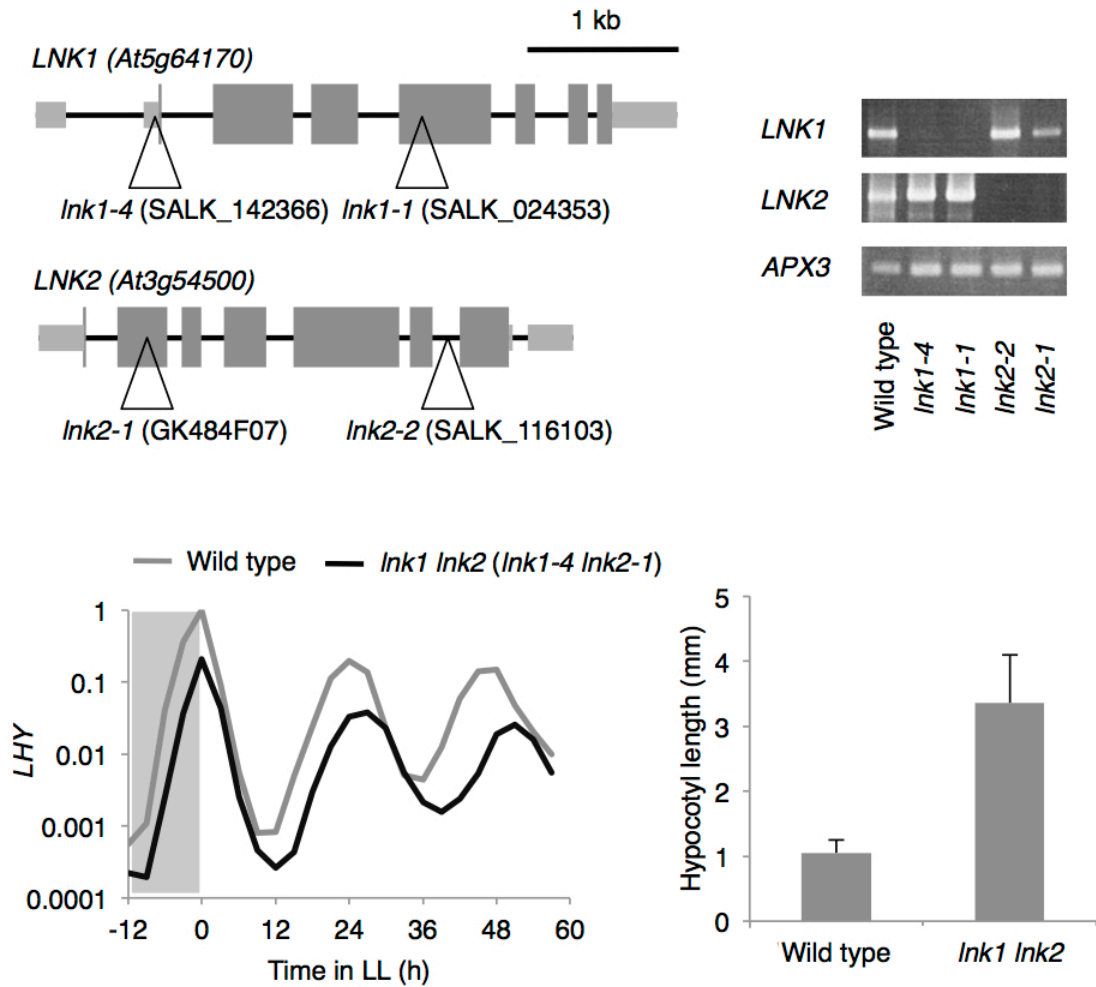


Supplemental Figure 1. *PRR5* and *CCA1* promoter activities in *Arabidopsis* mesophyll protoplasts.

Bioluminescence of the mesophyll protoplasts transfected with *CCA1pro:LUC* (blue) and *PRR5pro:LUC* (red) plasmid. Error bars are SD of three biological replicates.



Supplemental Figure 2. The *Ink1 Ink2* mutants used in this study.

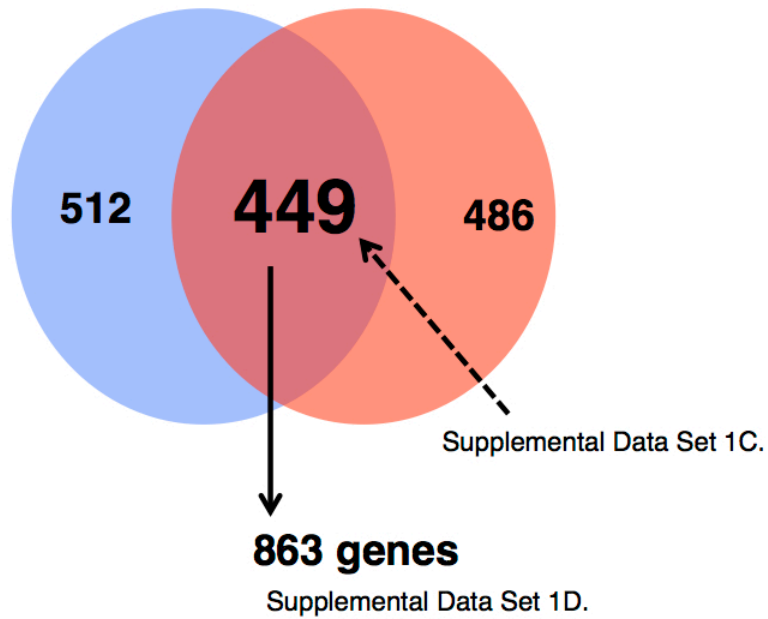
Schematic drawing of T-DNA insertions for *Ink1* and *Ink2* (upper left). Dark gray areas indicate exons of coding region, and right grays are un-translated regions. *LNK1* and *LNK2* expression in *Ink1* and *Ink2* T-DNA insertion lines (upper right). Full length of coding regions for *LNK1* and *LNK2*, and part of *APX3* coding region were amplified. *LHY* expression of the *Ink1 Ink2* double mutants (*Ink1-4 Ink2-1*) (lower left). Estimated period length in Wild-Type and *Ink1 Ink2* are 23.41 and 24.93, respectively. Hypocotyl length of *Ink1 Ink2* grown under 6 days of 12 h white light (70-80 $\mu\text{mol s}^{-1} \text{m}^{-2}$) / 12 h dark (n=15, error bars are SD) (lower right).

**CCA1-bound loci
determined by
IonPGM
(FDR $q < 10^{-20}$)**

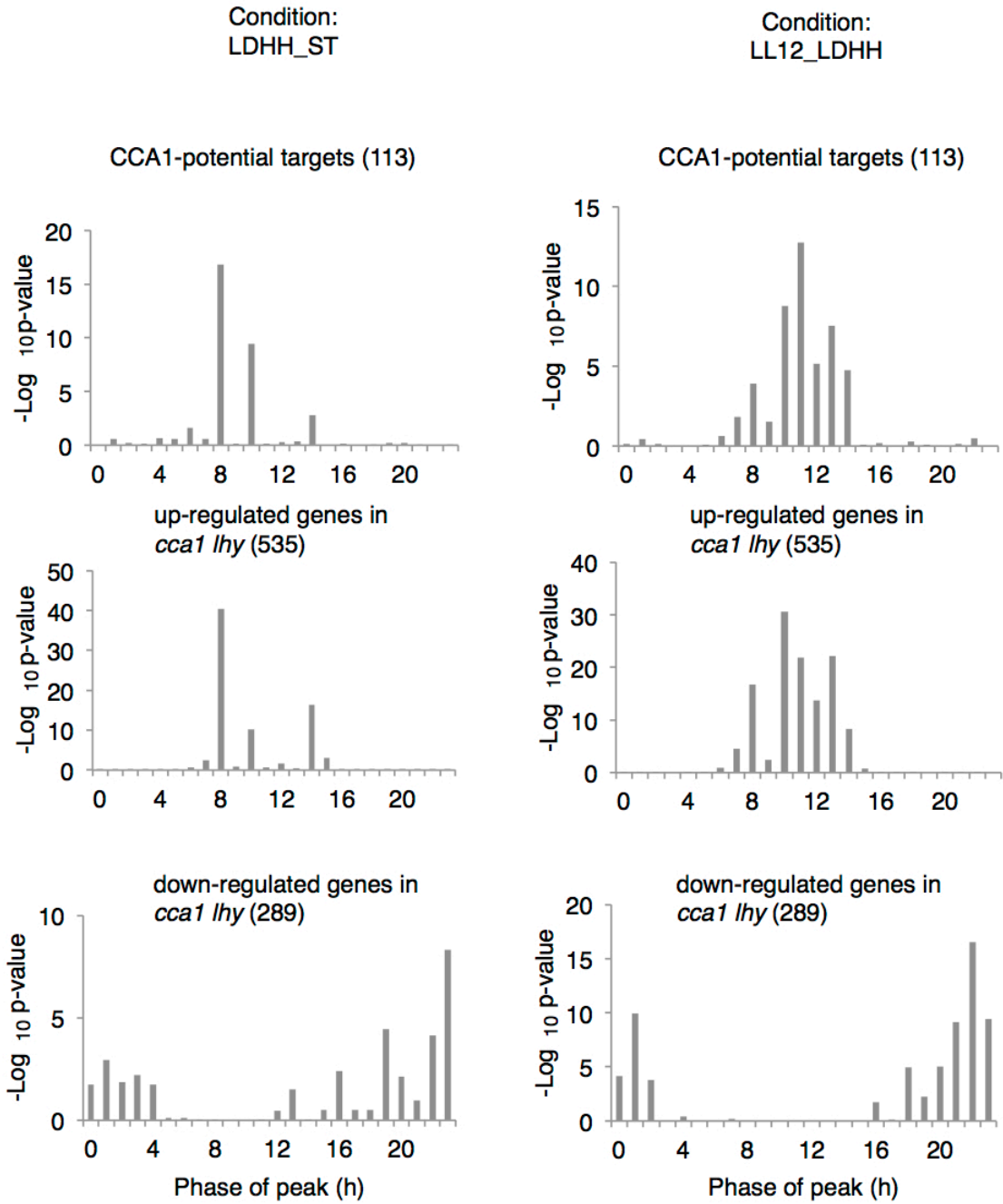
Supplemental Data Set 1A.

**CCA1-bound loci
determined by Illumina
GAII(FDR $q < 10^{-20}$)**

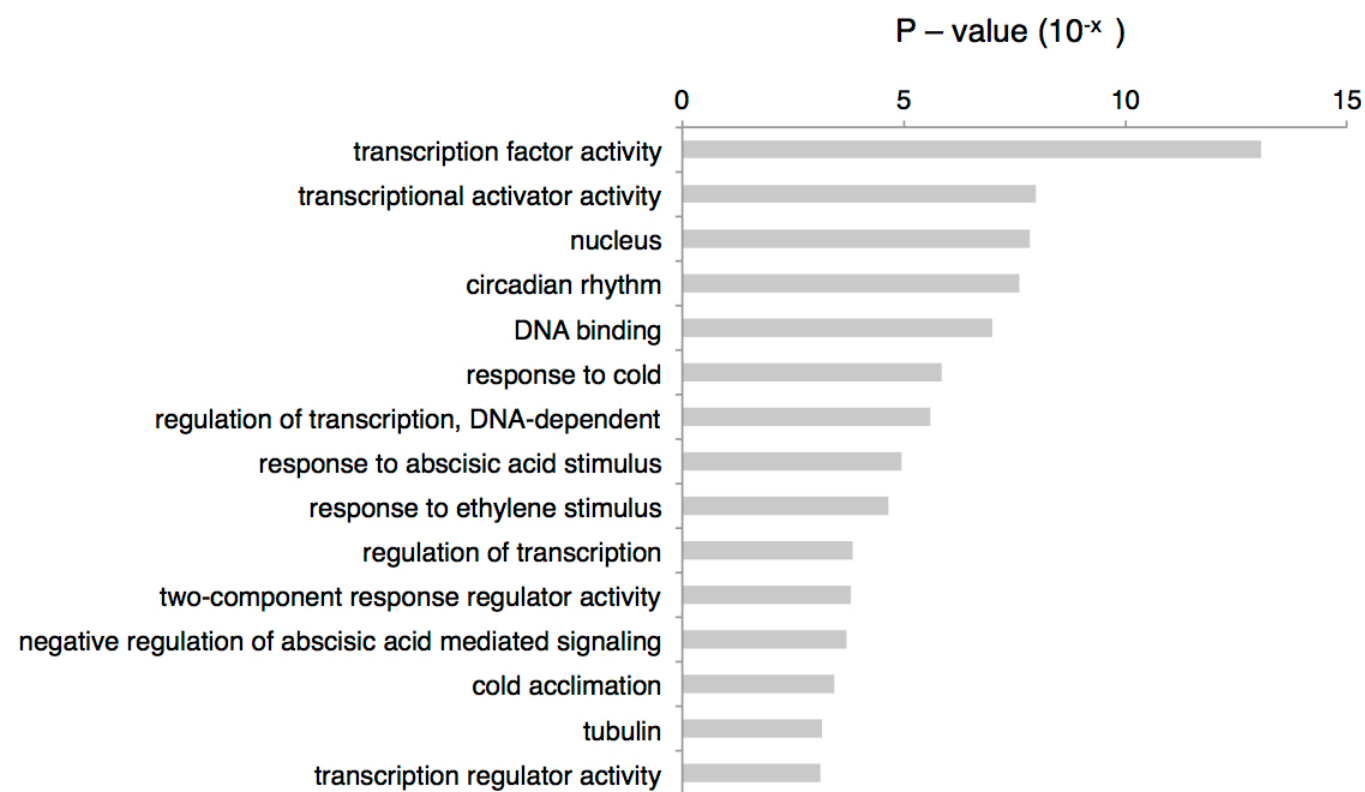
Supplemental Data Set 1B.



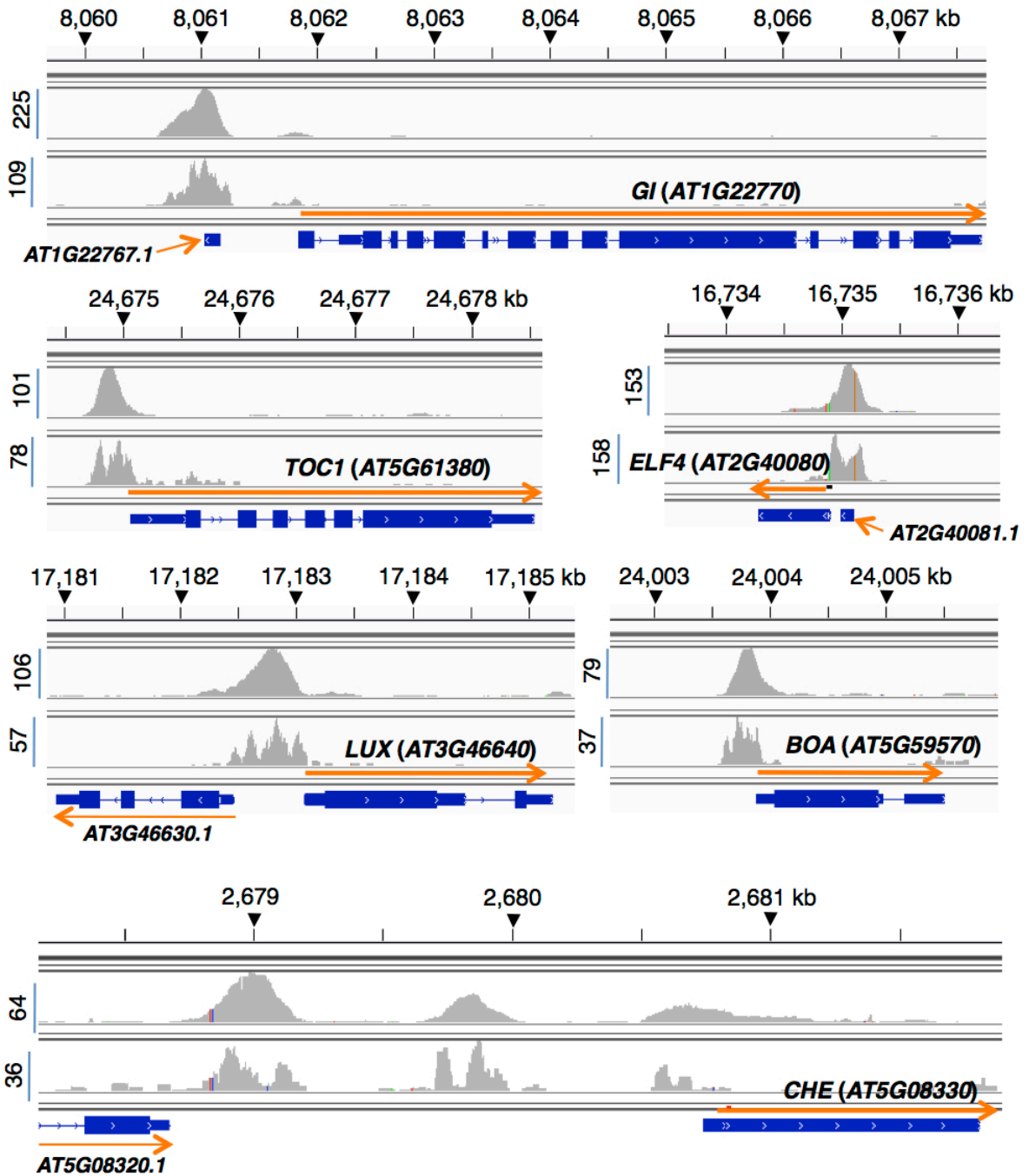
Supplemental Figure 3. Overlap between CCA1-binding loci determined by IonPGM and Illumina GA II.



Supplemental Figure 4. Peak-phase enrichment in the sets of 113 CCA1-potential target genes, 535 up-regulated genes in *cca1 lhy*, and 289 down-regulated genes in *cca1 lhy*. Phase of peaks were determined by a web tool, Phaser (<http://phaser.mocklerlab.org/>), for 3 gene sets. Similar results were obtained under other LL condition (LL23_LDHH) and LD condition (LDHH_SM).

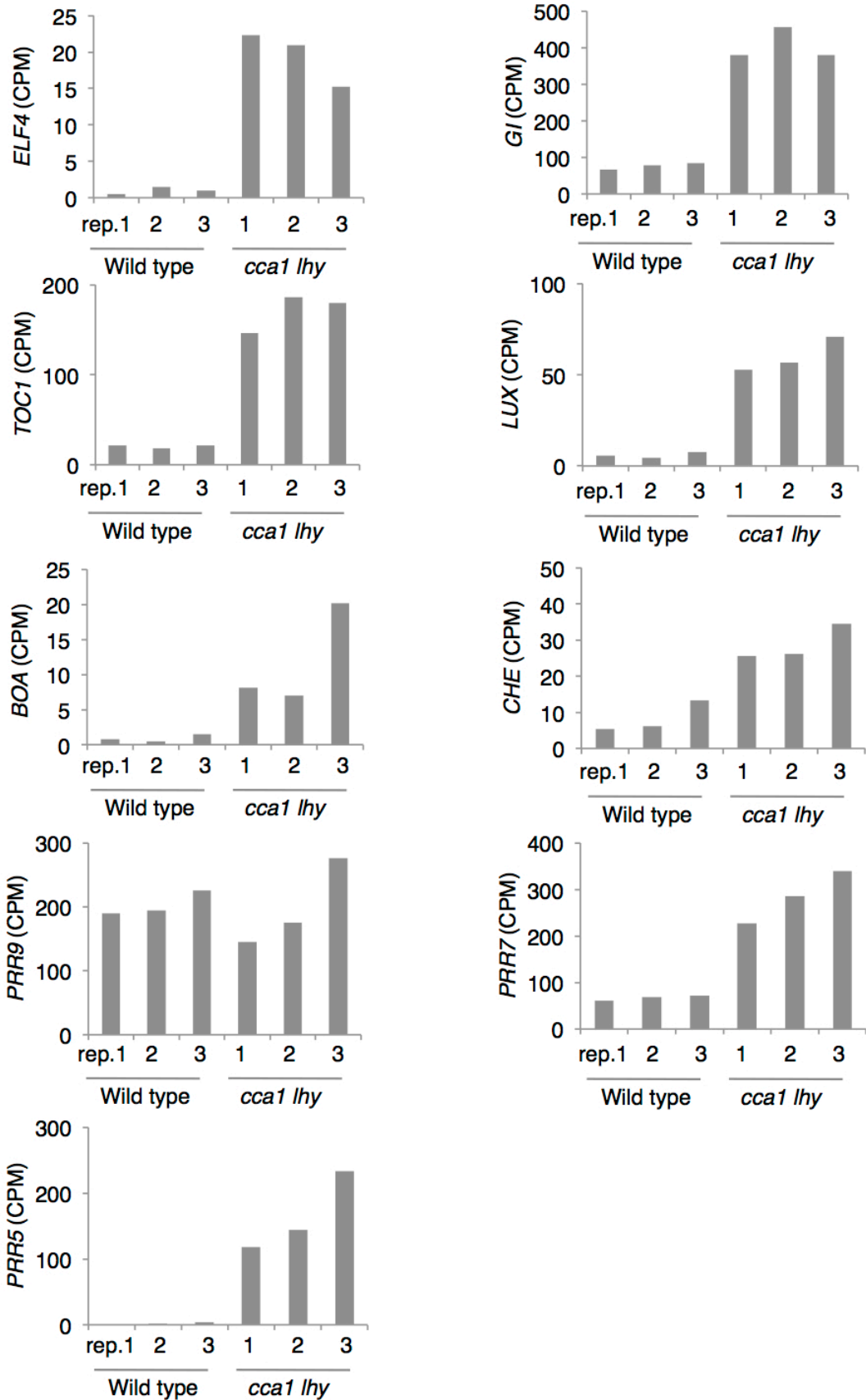


Supplemental Figure 5. eGO analysis for CCA1-bound genes.



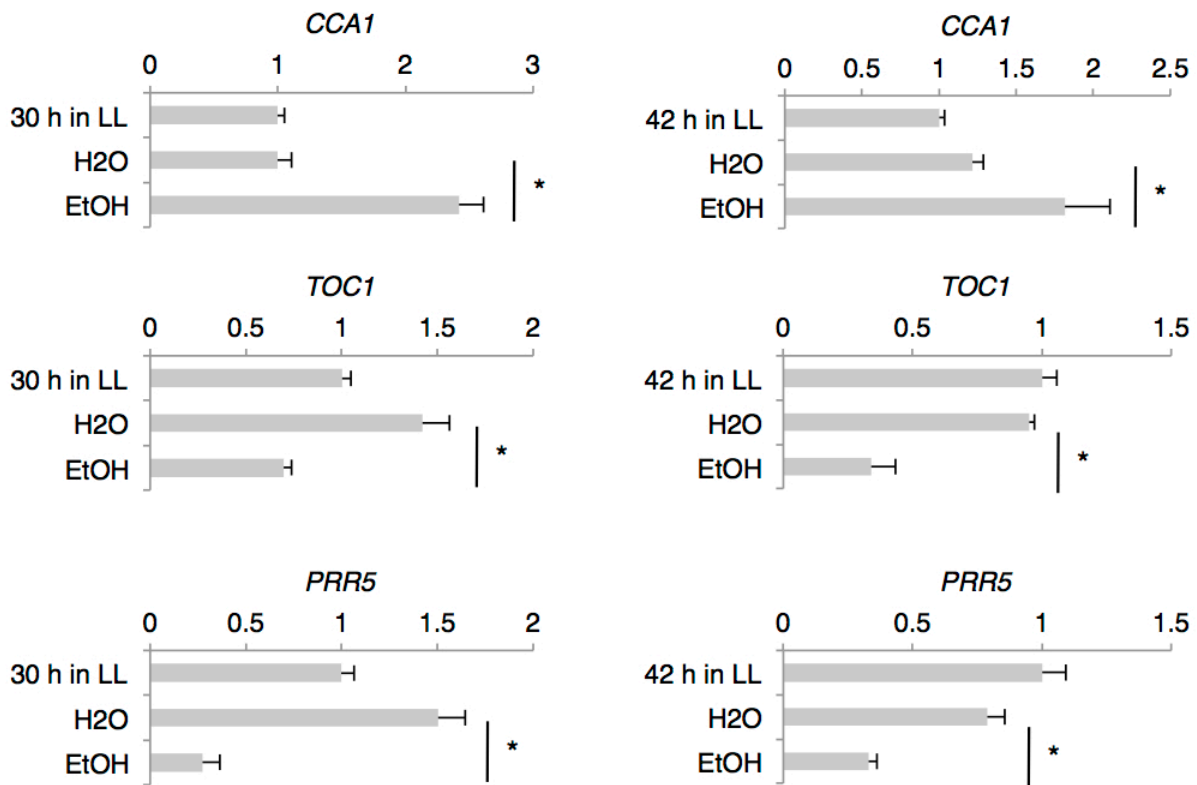
Supplemental Figure 6. CCA1-binding profile around clock-associated genes.

Upper and lower panels are mapping profile determined by IonPGM and GA II, respectively. Vertical bars indicate read counts. Horizontal numbers show base pairs.



Supplemental Figure 7. Expression of clock-associated genes in *cca1 lhy* at ZT1.

These genes are also bound by CCA1. Except for *PRR9*, these genes expression are up-regulated in *cca1 lhy* (FDR $q < 0.01$). CPM means counts per million.



Supplemental Figure 8. Expression of *CCA1*, *TOC1*, and *PRR5* upon ethanol induction in *Alc:CCA1*.

Error bars indicate the SE of four biological replicates. Asterisks indicates a significant change between samples treated with ethanol (EtOH) and H₂O (Student's t test; P < 0.05).

Supplemental Table 1. Primers used in this study.

name	sequence (5'-sequence-3')	purpose	plasmid	E.coli/Agro selection	Plant selection	Target gene or locus
gCCA1comp_F	CACCGTCTTCTACCCCTCATGCATGG	CCA1pro:CCA1 cloning on pENTR/D-TOPO	pENTR/D-CCA1pro:CCA1	Km		CCA1 (At2g46830), genomic
gCCA1comp_R	TGTGGAAGCTTGAGTTTCCAAC	CCA1pro:CCA1 cloning on pENTR/D-TOPO	pENTR/D-CCA1pro:CCA1	Km		CCA1 (At2g46830), genomic
M13 F	GTAACACGACGGCCAGT	sequencing pENTR/D-CCA1pro:CCA1				
M13 R	CAGGAACAGCTATGAC	sequencing pENTR/D-CCA1pro:CCA1				
CCA1pro300F	TGATTACGCCAAGCTTAAAGTTTGAGGTTAAAG	sequencing pENTR/D-CCA1pro:CCA1				
CCA1_sygF	GGTGGACTGAGGAAGAAC	sequencing pENTR/D-CCA1pro:CCA1				
CCA1_compli_1.5F	CTTGTTGTCTTACCGATTG	sequencing pENTR/D-CCA1pro:CCA1				
CCA1_compli_2.0F	GAAGATCGACAACAATCAAAGC	sequencing pENTR/D-CCA1pro:CCA1				
CCA1_compli_2.5F	GTTGCAGCTGCTAGTGCTTG	sequencing pENTR/D-CCA1pro:CCA1				
APX3proF	CTCGTGTGCCGTTTTTTG	ChIP-qPCR	pBA-CCA1pro:CCA1-FLAG	Spec	Basta	APX3 (At4g35000), upstream
APX3proR	GTCAAGGATGTGTGTGAAG	ChIP-qPCR				APX3 (At4g35000), upstream
PRR5_regionA_F	GCAGACATTAGCCATTTATG	ChIP-qPCR				PRR5 (At5g24470), regionA
PRR5_regionA_R	GGCCTAACCTACACTGAACATGC	ChIP-qPCR				PRR5 (At5g24470), regionA
PRR5_regionB_F	CTCTGACAGTGACAGCTAC	ChIP-qPCR				PRR5 (At5g24470), regionB
PRR5_regionB_R	GAGTAGGGACAAAGGGTGATG	ChIP-qPCR				PRR5 (At5g24470), regionB
PRR5_regionC_F	GCTGATGTGGCAAACGTGG	ChIP-qPCR				PRR5 (At5g24470), regionC
PRR5_regionC_R	GAGAGATAAATGAGAAGAGAGC	ChIP-qPCR				PRR5 (At5g24470), regionC
PRR5_ods_F	GCCGCTTAAACCAATTCGG	ChIP-qPCR				PRR5 (At5g24470), coding sequence
PRR5_ods_R	CGAATTGGCCTTTGATTCGTG	ChIP-qPCR				PRR5 (At5g24470), coding sequence
IPP2sygF	GAGACGTCTCATGTTTGAGGATG	RT-qPCR				IPP2 (At3g02780)
IPP2sygR	GGAGAAGCAACTCATACTTCGAG	RT-qPCR				IPP2 (At3g02780)
PRR5sygF	CTTCATCCTTCTAGTGCC	RT-qPCR				PRR5 (At5g24470)
PRR5sygR	GTCGTTTCTTCTGGAGC	RT-qPCR				PRR5 (At5g24470)
PRR7sygF	CTGCACCTCGTTATATCGTACTG	RT-qPCR				PRR7 (At5g02810)
PRR7sygR	GGCATGATCACCTCTGTAG	RT-qPCR				PRR7 (At5g02810)
PRR9sygF	CCAATGAGGAAAACGAG	RT-qPCR				PRR9 (At2g46790)
PRR9sygR	GCACCACTTCCTTGATCTG	RT-qPCR				PRR9 (At2g46790)
CCA1sygF	GGTGGACTGAGGAAGAAC	RT-qPCR				CCA1 (At2g46830)
CCA1sygR	GGAGAAAAATTTCTGAGCGTGAC	RT-qPCR				CCA1 (At2g46830)
TOC1sygF	CTCTCGTTTCAGAGTGTCTTATC	RT-qPCR				TOC1 (At5g61380)
TOC1sygR	CACAGGGATTCTGCGAAG	RT-qPCR				TOC1 (At5g61380)
LHYsygF	CGCGGTTCAAGATGTTCC	RT-qPCR				LHY (At1g01060)
LHYsygR	GAACATGAAGTCTTGAGATACC	RT-qPCR				LHY (At1g01060)
APX3sygF	CTCCGTTCTCTCATCGC	RT-PCR				APX3 (At4g35000)
APX3sygR	CAGAGATCGAGAGCCGATC	RT-PCR				APX3 (At4g35000)
LNK1_topF	CACCATGTGGCACTTGTACATTCATGAG	RT-PCR				LNK1 (At5g64170)
LNK1_topR(+ter)	TTAATTGTTGTCACTTGTTACAACCTTC	RT-PCR				LNK1 (At5g64170)
LNK2_F	CACCATGTTTGTGGAAAGCTTGAAGTTCACAAC	RT-PCR				LNK2 (At3g54500)
LNK2_R	CAATTTCCTTTTCTTCTGGGATG	RT-PCR				LNK2 (At3g54500)
CCA1_XbaI_F	GACTCTAGAATGGAGACAAATTCGTGGAG	CCA1 cloning on pBS-FLAG	pBS-35Spro:CCA1-FLAG	Amp		CCA1 (At2g46830)
CCA1_BamHI_R	CGGGGATCCTTTGTGGAAAGCTTGAAGTTCACAAC	CCA1 cloning on pBS-FLAG	pBS-35Spro:CCA1-FLAG	Amp		CCA1 (At2g46830)
LHY_BamHI_F	ATCGGATCCTATGGATACTAATACATCTGGAGAAGAATTATTAG	LHY cloning on pBS-FLAG	pBS-35Spro:LHY-FLAG	Amp		LHY (At1g01060)
LHY_NcoI_R	GATCCATGGATGTAGAAGCTTCTCCTTCC	LHY cloning on pBS-FLAG	pBS-35Spro:LHY-FLAG	Amp		LHY (At1g01060)
LNK1_topF	CACCATGTGGCACTTGTACATTCATGAG	LNK1 cloning on pENTR/D-TOPO	pENTR/D-LNK1+ter	Km		LNK1 (At5g64170)
LNK1_topR(+ter)	TTAATTGTTGTCACTTGTTACAACCTTC	LNK1 cloning on pENTR/D-TOPO	pENTR/D-LNK1+ter	Km		LNK1 (At5g64170)
PRR5pro_0_F	ACGCCAAGCTAAGCTCTCTGACAGTGACAGCTACC	PRR5pro (1) cloning on pSP-luc+	pSP-PRR5pro (1):LUC	Amp		PRR5 (At5g24470), upstream
PRR5pro_1.4_R	GAAGGGTCTTGGGATCACAACACAACACTTAGCTTTG	PRR5pro (1) cloning on pSP-luc+	pSP-PRR5pro (1):LUC	Amp	Hyg	PRR5 (At5g24470), upstream
PRR5pro_0_F	ACGCCAAGCTAAGCTCTCTGACAGTGACAGCTACC	PRR5pro (2) cloning on pSP-luc+	pSP-PRR5pro (2):LUC	Amp		PRR5 (At5g24470), upstream
PRR5pro_0.7_R	GAAGGGTCTTGGGATCCTTTGGGATAATACCAAAACCC	PRR5pro (2) cloning on pSP-luc+	pSP-PRR5pro (2):LUC	Amp	Hyg	PRR5 (At5g24470), upstream
PRR5pro_0.4_F	ACGCCAAGCTAAGCTTCCAAAAGTCACGAGTGGG	PRR5pro (3) cloning on pSP-luc+	pSP-PRR5pro (3):LUC	Amp		PRR5 (At5g24470), upstream
PRR5pro_1.0_R	GAAGGGTCTTGGGATCCTTCAATACGCCAAATAACCTTC	PRR5pro (3) cloning on pSP-luc+	pSP-PRR5pro (3):LUC	Amp	Hyg	PRR5 (At5g24470), upstream
PRR5pro_0.7_F	ACGCCAAGCTAAGCTTCCAAAAGTCACGAGTGGG	PRR5pro (4) cloning on pSP-luc+	pSP-PRR5pro (4):LUC	Amp		PRR5 (At5g24470), upstream
PRR5pro_1.4_R	GAAGGGTCTTGGGATCACAACACAACACTTAGCTTTG	PRR5pro (4) cloning on pSP-luc+	pSP-PRR5pro (4):LUC	Amp	Hyg	PRR5 (At5g24470), upstream
PRR5pro_1.0_F	ACGCCAAGCTAAGCTTCCAAAAGTCACGAGTGGG	PRR5pro (5) cloning on pSP-luc+	pSP-PRR5pro (5):LUC	Amp		PRR5 (At5g24470), upstream
PRR5pro_1.4_R	GAAGGGTCTTGGGATCACAACACAACACTTAGCTTTG	PRR5pro (5) cloning on pSP-luc+	pSP-PRR5pro (5):LUC	Amp	Hyg	PRR5 (At5g24470), upstream
PRR7pro_F	CTTAAAGCTTGAATGGCCCATATGTAAGC	PRR7 cloning on pSP-luc+	pSP-PRR7pro:LUC	Amp		PRR7 (At5g02810), upstream
PRR7pro_R	TTAAGGCATGGTACACCAACTCTGCTTCG	PRR7 cloning on pSP-luc+	pSP-PRR7pro:LUC	Amp		PRR7 (At5g02810), upstream
PRR9pro_F	TGATTACGCCAAGCTTCCGCGCCACTAACGAAATTTG	PRR9 cloning on pSP-luc+	pSP-PRR9pro:LUC	Amp		PRR9 (At2g46790), upstream
PRR9pro_R	TTGGCGTCTTCCATGGCCCATAGACTCAGACC	PRR9 cloning on pSP-luc+	pSP-PRR9pro:LUC	Amp		PRR9 (At2g46790), upstream