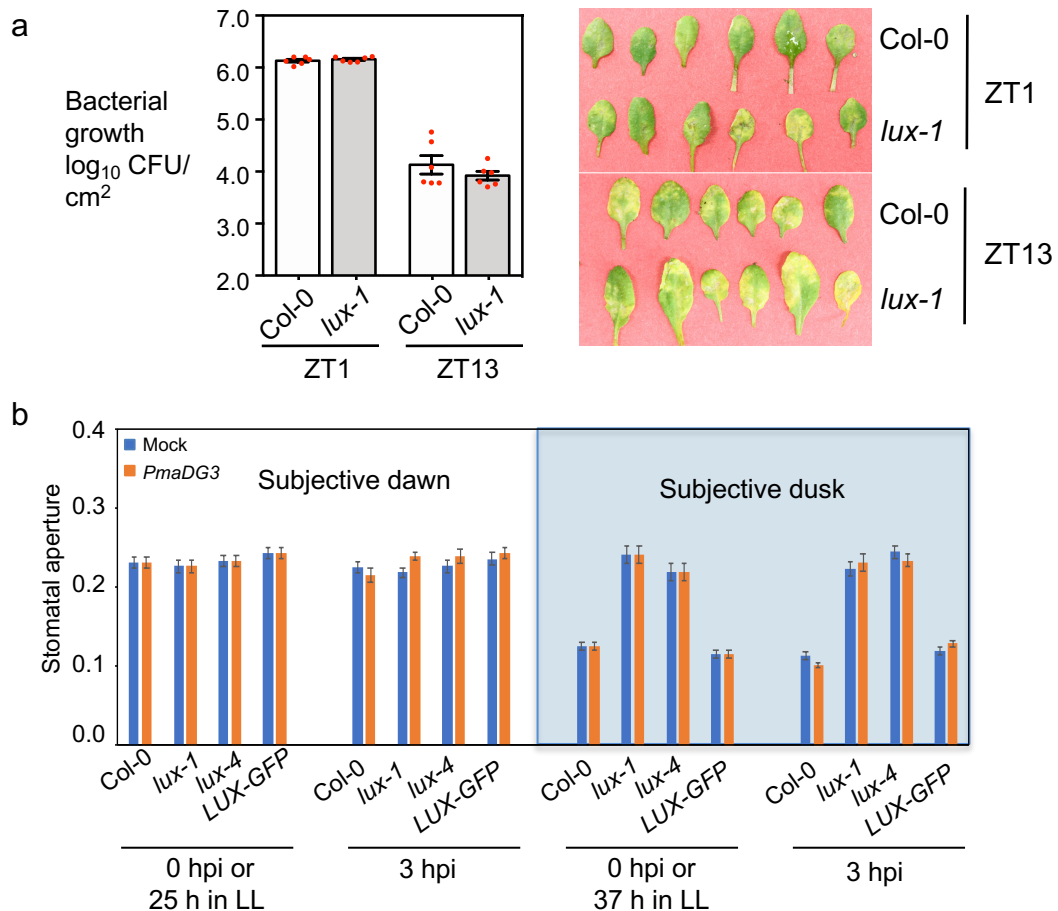
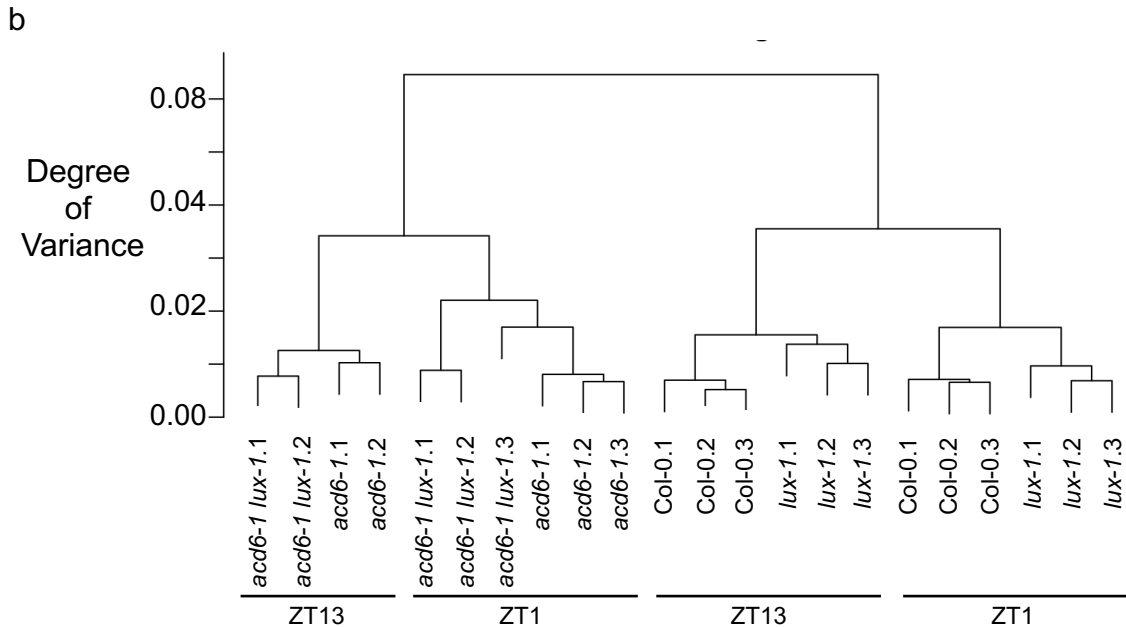
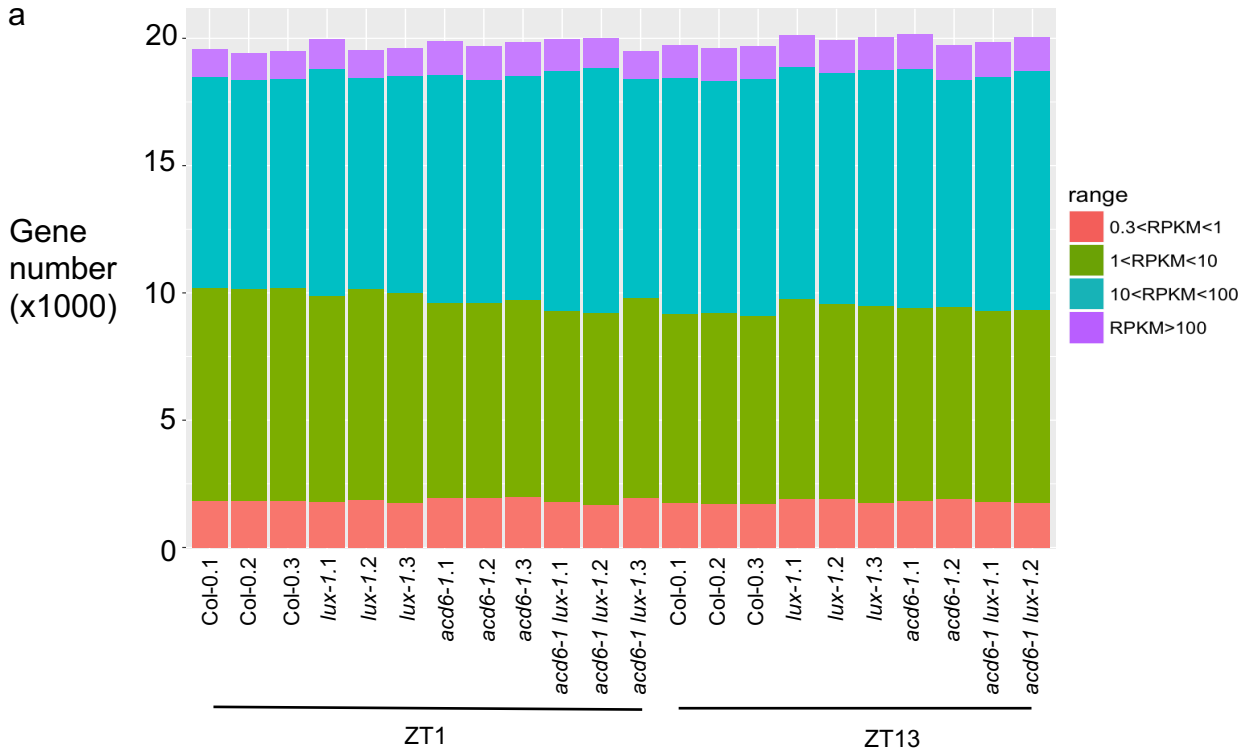


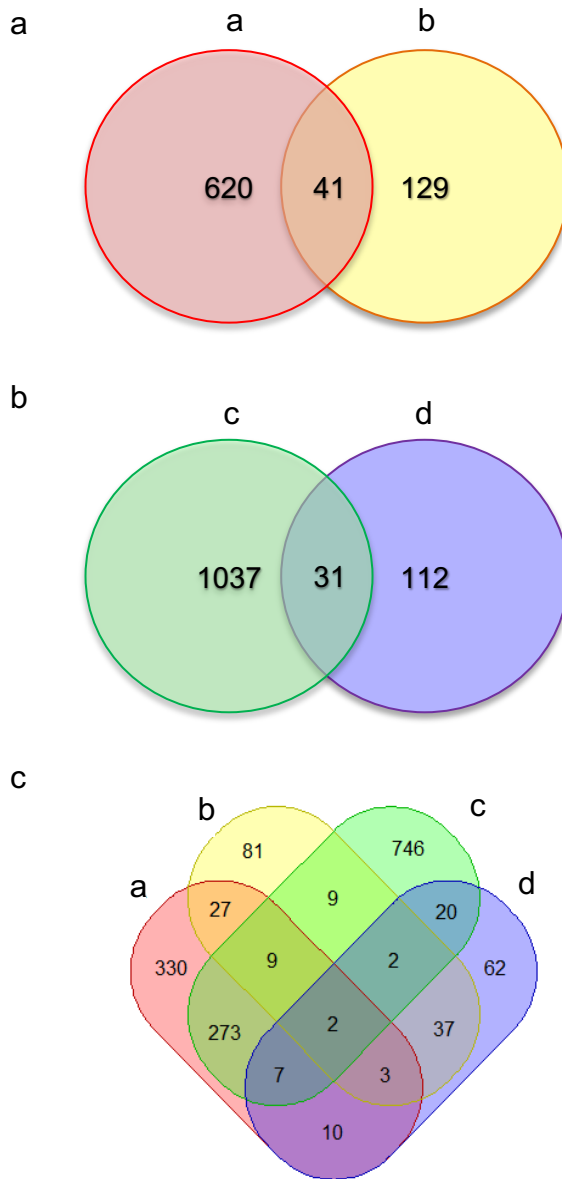
Supplementary Figure 1. Expression of *LUX* is induced by *P. syringae* infection. Total RNA was extracted from 25-d old plants at the indicated hour post infiltration with *P. syringae* strains. Statistical analysis was performed by One-way ANOVA with post-hoc Tukey HSD test. Asterisks indicate significant difference in *LUX* expression between the infected and mock-treated samples at the same time point (n=2; P<0.05). These experiments were repeated two times and similar results were obtained.



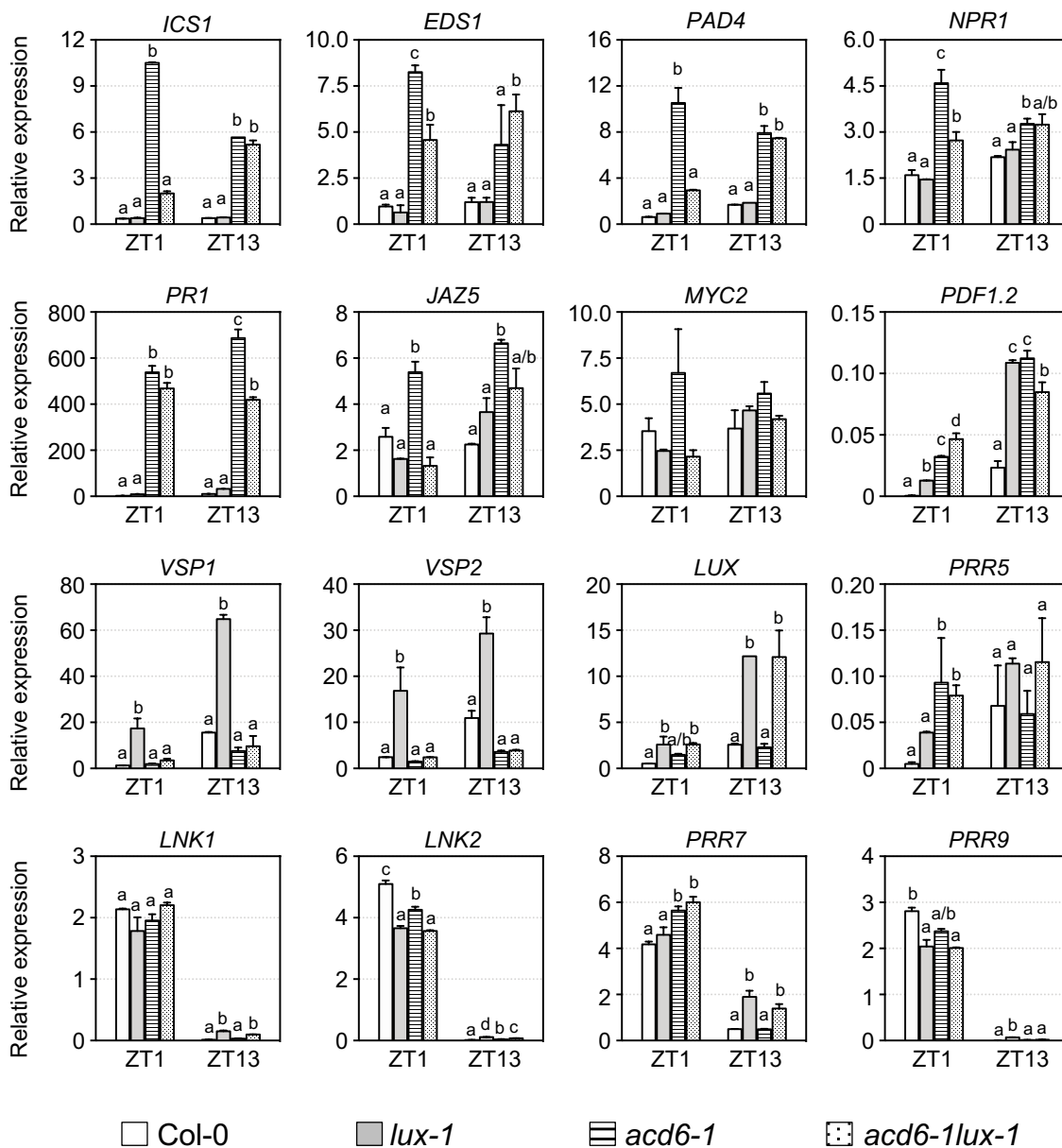
Supplementary Figure 2. *lux*-conferred *P. syringae* susceptibility is influenced by light and stomata. **a** Bacterial growth (left) and pictures (right) of infected leaves. Plants grown in LD with a light intensity of $180 \mu\text{mol m}^{-2} \text{s}^{-1}$ and spray-infected with *PmaDG3* ($\text{OD} = 0.01$) 1 or 13 h after transfer to LL ($n = 6$). **b** Stomatal aperture measurement ($n = 80$). LD ($180 \mu\text{mol m}^{-2} \text{s}^{-1}$ light intensity) entrained 25-day old plants were transferred to LL ($10 \mu\text{mol m}^{-2} \text{s}^{-1}$ light intensity) for one day. The fifth to seventh leaves of each genotype taken at LL25 or LL37 were incubated with *PmaDG3* ($\text{OD}_{600} = 0.1$) or sterile water for 0, 1, or 3 hpi followed by immediate processing for stomata imaging. The stomatal aperture was determined by the ratio between the width and the length of a stoma. Data are presented as mean \pm SEM. Statistical analysis was performed with One-way ANOVA post-hoc Tukey HSD test. These experiments were repeated two times and similar results were obtained.



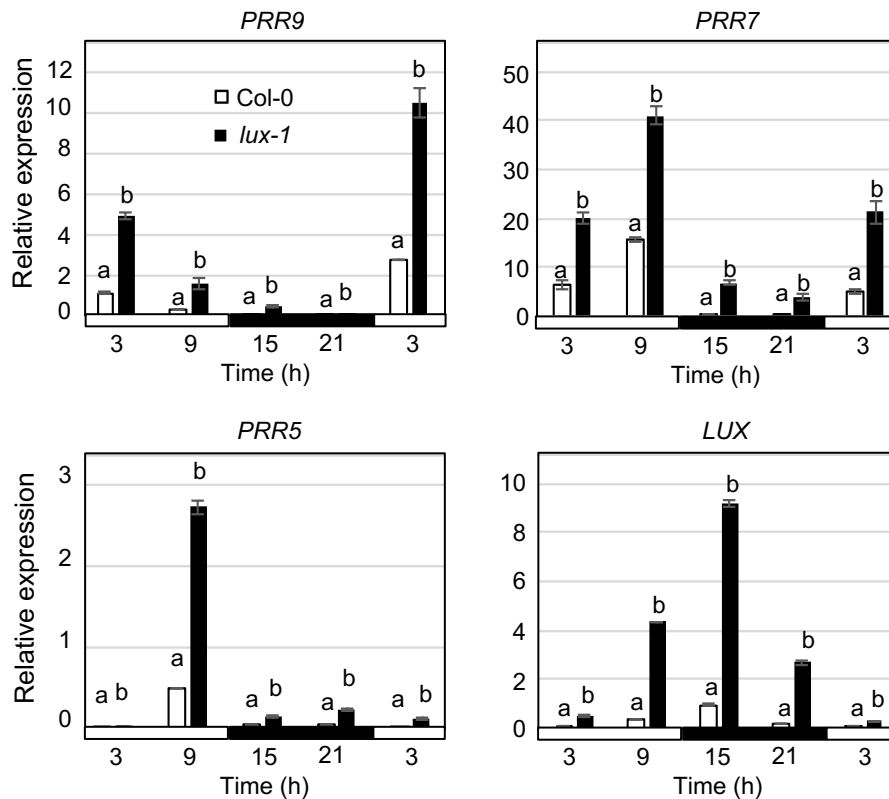
Supplementary Figure 3. Global gene expression analysis of RNA-seq data. a Number of genes expressed in each sample. The relative expression value RPKM of higher than 0.3 was used as a cutoff to define expressed genes. **b** Cluster dendrogram analysis shows global gene expression profiles in biological replicates.



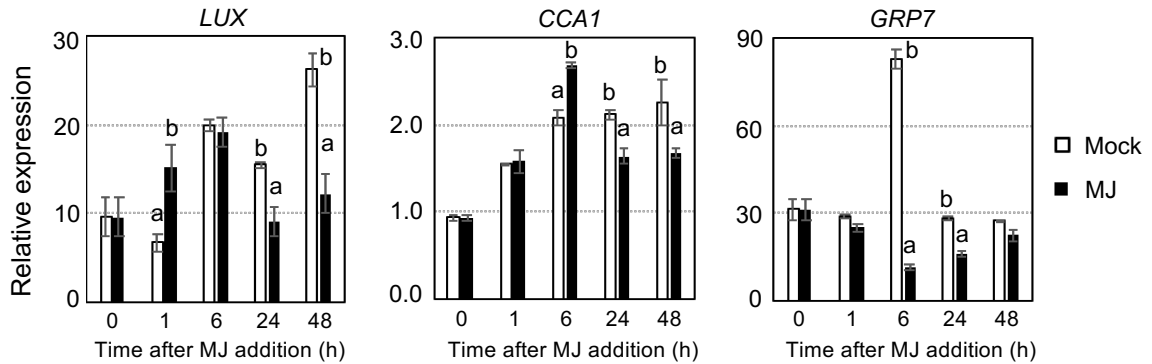
Supplementary Figure 4. Venn diagrams show the number of genes affected by *lux-1*. The comparison groups are: (a) Col-0 vs. *lux-1* at ZT1; (b) Col-0 vs. *lux-1* at ZT13; (c) *acd6-1* vs. *acd6-1lux-1* at ZT1; and (d) *acd6-1* vs. *acd6-1lux-1* at ZT13. **a** Genes affected by *lux-1* under non-defense conditions (the Col-0 background; a & b). **b** Genes affected by *lux-1* under defense conditions (the *acd6-1* background; c & d). **c** Genes affected by *lux-1* in all four comparison groups.



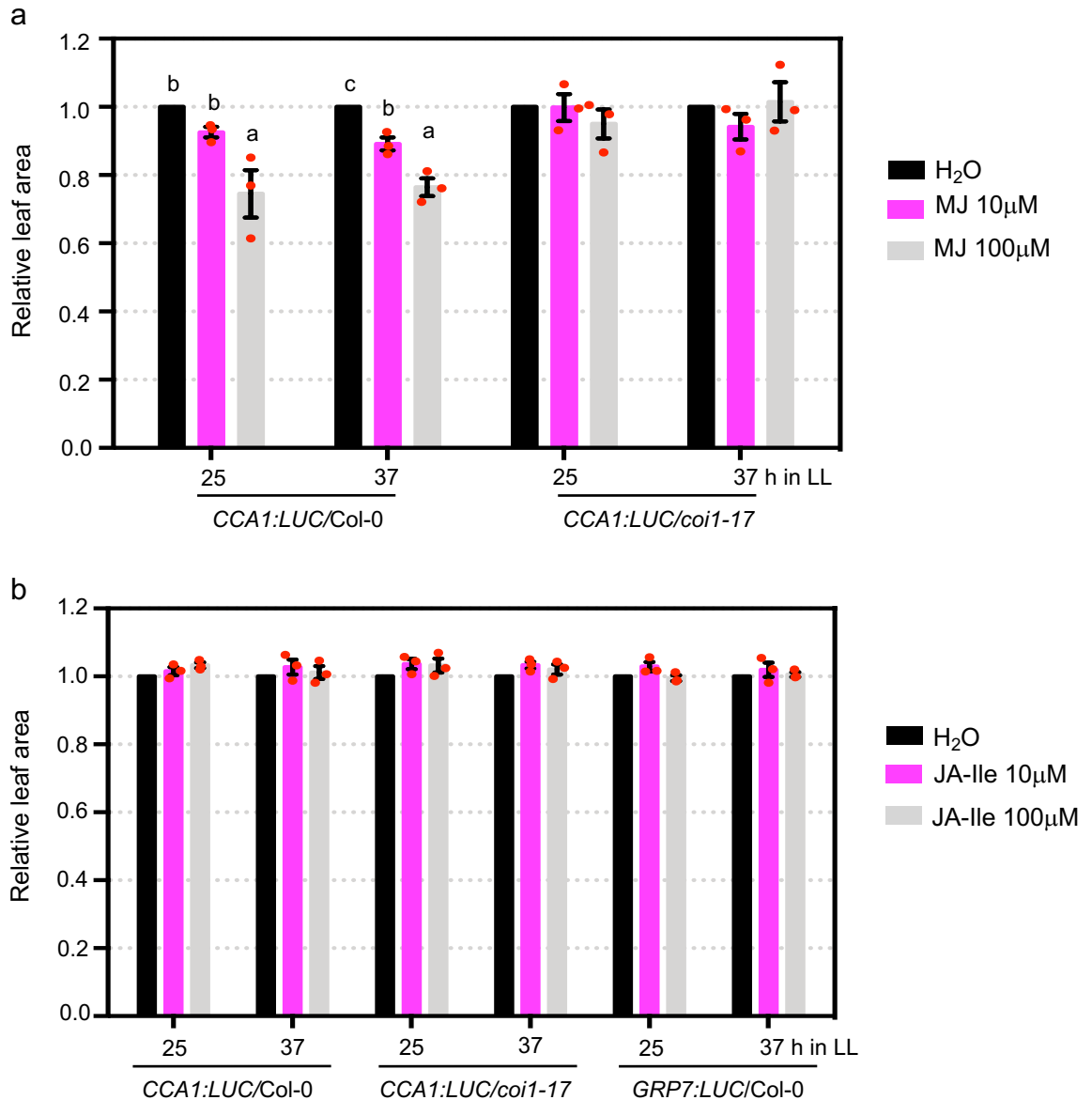
Supplementary Figure 5. Quantification of gene expression by qRT-PCR in Col-0, *acd6-1*, *lux-1*, and *acd6-1lux-1*. 25-d old plants of each genotype grown in LD were collected at ZT1 or ZT13 for RNA extraction followed by qRT-PCR analysis. Data are presented as mean ($n=2$) \pm SD. Statistical analysis was done by One-way ANOVA with post-hoc Tukey HSD test. Different letters indicate significant difference among the samples at the same time point ($P<0.05$). These experiments were repeated two times and similar results were obtained.



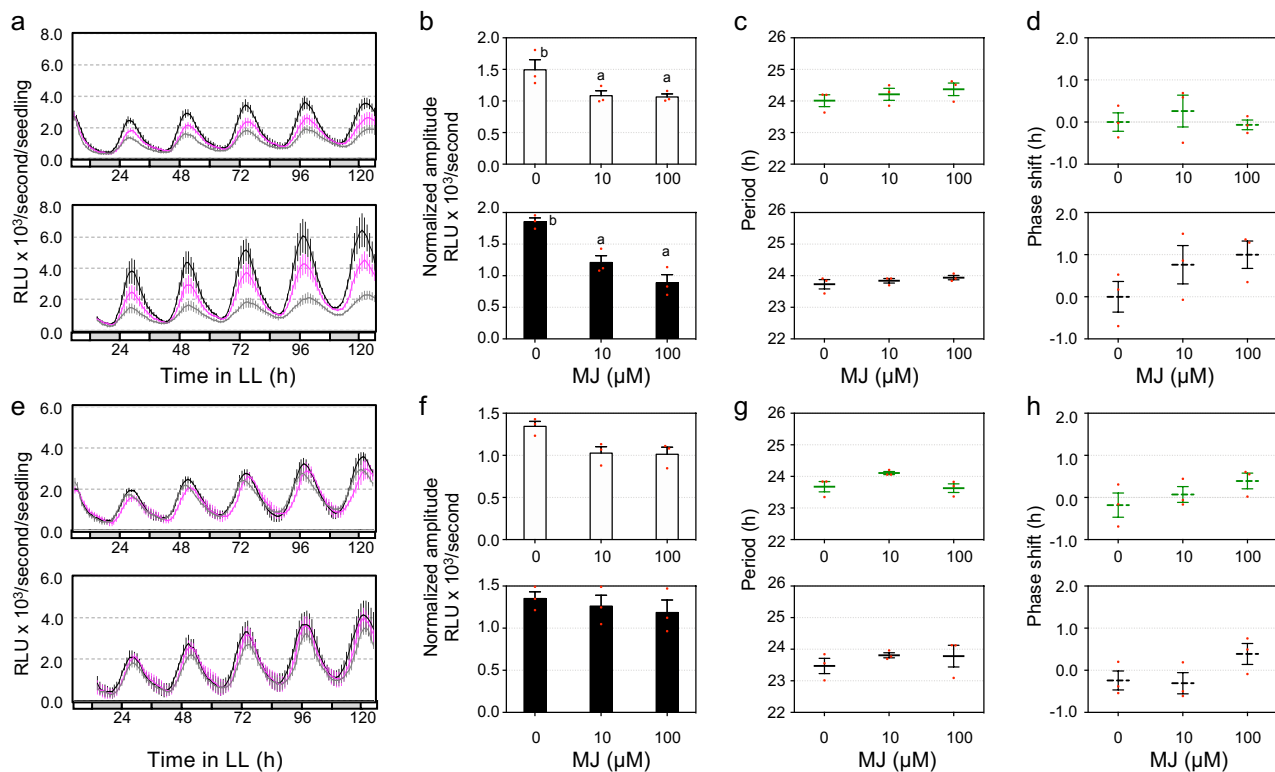
Supplementary Figure 6. Rhythmic clock gene expression in Col-0 and *lux-1* in LD. 25-d old plants of each genotype grown in LD were collected at the indicated time for RNA extraction followed by qRT-PCR analysis. Data are presented as mean (n=2) \pm SD. Statistical analysis was done by One-way ANOVA with post-hoc Tukey HSD test. Different letters indicate significant difference among the samples at the same time point (P<0.05). Light and dark bars beneath the graphs indicate day and night, respectively, in the light-dark (LD) cycle. These experiments were repeated two times and similar results were obtained.



Supplementary Figure 7. MJ treatment suppresses clock gene expression in seedlings. 6-d-old seedlings grown in LD were transferred to sterile water in a 24-well plate and kept in LL for 1 d. The seedlings were treated at 25 h after the onset of LL with 100 μ M MJ and were harvested at the indicated times post treatment for RNA extraction followed by qRT-PCR analysis. Data are presented as mean \pm SD (n=2). Statistical analysis was done by One-way ANOVA with post-hoc Tukey HSD test. Different letters indicate significant difference among the samples at the same time point (P<0.05). These experiments were repeated two times and similar results were obtained.



Supplementary Figure 8. Seedling growth inhibition by MJ treatment. a Relative seedling leaf area with MJ treatment. **b** Relative seedling leaf area with JA-Ile treatment. Seedlings used in the luciferase assay were photographed at the end of luminescence recording. The area of each seedling was measured with ImageJ. The average leaf area of mock-treated samples of each genotype was set to 1 and used to calculate the relative leaf area of seedlings of the same genotype that were chemically treated at the same time. Data represent mean (\pm SEM) of three independent experiments ($n=8$ or 12 for each experiment). Statistical analysis was performed by One-way ANOVA post-hoc Tukey HSD test. Different letters indicate significant difference among the samples treated at the same time point, 25 h or 37 h after LL ($P<0.05$).



Supplementary Figure 9. MJ treatment affects clock activity. Five-day old seedlings entrained in LD were transferred to LL for 1 d and were treated with MJ. Luminescence was recorded at 1-h intervals for five days and analyzed for amplitude, period, and phase with the R package *MetaCycle*. **a-d** Expression of *CCA1:LUC* in *Col-0* treated with MJ 25 h (top) or 37 h (bottom) after onset of LL. **e-h** Expression of *CCA1:LUC* in *coi-17* treated with MJ 25 (top) or 37 (bottom) h after onset of LL. **a** and **e** Luminescence traces. RLU: Relative luminescence units. The color indicates MJ concentration, black for 0, magenta for 10 μM, and gray for 100 μM. **b** and **f** Normalized amplitude. The amplitude of the reporter was normalized to the relative leaf area shown in Supplementary Figure 8. **c** and **g** Period. **d** and **h** Phase shift. Data represent mean (± SEM) of three independent experiments (n=8 or 12 for each experiment). Statistical analysis was performed by One-way ANOVA post-hoc Tukey HSD test. Different letters indicate significant difference among the samples (P<0.05).

Supplementary Table 1. ChIP analysis of selected LBS motifs of LUX-affected genes. The positions of LBS motifs within the 1500 bp-promoter region, relative to the transcription start site, of selected LUX-affected genes were predicted via bioinformatics analysis and were indicated in parentheses []. ChIP experiments were conducted with the LBS motifs highlighted in color. Magenta indicates a detection of LUX binding to the motif and blue for no LUX binding in our experiments. Black indicates that motifs need to be tested.

AGI	Name	sense (GATTCG)	anti-sense (CGAATC)	sense (GATACG)	anti-sense (CGTATC)
AT1G17380	JAZ5	□	□	[927]	[856]
AT1G30135	JAZ8	□	[957, 625]	[507]	□
AT1G32640	MYC2	□	[1475]	□	□
AT1G74710	ICS1	□	[393]	□	[607]
AT2G14610	PR1	[977]	□	[455, 223]	□
AT2G34600	JAZ7	[607]	[1550]	□	□
AT2G38470	WRKY33	□	□	[713]	□
AT3G48090	EDS1	□	[936]	□	□
AT3G52430	PAD4	[110]	□	□	[1068]
AT5G20480	EFR	[612]	□	[819]	□
AT1G22770	GI	□	[1074]	□	□
AT2G46790	PRR9	□	[172]	□	□
AT3G46640	LUX	□	[367]	□	□
AT3G54500	LNK2	□	□	[74]	□
AT5G02810	PRR7	[1020]	□	[1127]	[595]
AT5G15840	CO	[723, 47]	[360]	[311]	[1234]
AT5G60100	PRR3	□	[646]	□	[950]
AT5G62430	CDF1	□	□	□	[30]
AT5G64170	LNK1	[492]	[701, 500]	□	□

Supplementary Table 2. Primers used in this report. Position of LBS motif indicates the location of each LBS site relative to the transcription start site of the gene.

Genotyping primers			
	Primer names	Primer sequence (5' > 3')	
<i>acd6-1</i>	acd6 d*TMboII	GCCATTTACATGGGCAATTGCAGTG ATCACGCCAAAGA	
	acd6_dCAPSfor	CTTCATTTTTCTGCTTTTTGACATCTT G	
<i>lux-1</i>	lux-1 NalIII dCaps-F	TTCCGGCGACGGAGATAGGGTTTCTG CAT	
	lux-1 dCaps-R	ACCACGTAGCGACGAGAGCGT	
qRT-PCR primers			
<i>LUX</i>	LUX-qPCR-f	AACACCTGTTCCACAGAGC	
	LUX-qPCR-r	TCCAACATTACCGCTGCTACCG	
<i>ICS1</i>	SID2-qPCR-f	GCTTGGCTAGCACAGTTACAGC	
	SID2-qPCR-r	CACTGCAGACACCTAATTGAGTCC	
<i>EDS1</i>	EDS1-qPCR-f	GCTCAATGACCTTGGAGTGAGC	
	EDS1-qPCR-r	TCTTCCTCTAATGCAGCTTGAACG	
<i>PAD4</i>	PAD4-qPCR-f	AGATACGCGAGCACAACGCAAG	
	PAD4-qPCR-r	TTCTCGCCTCATCCAACCACTC	
<i>NPR1</i>	NPR1-qPCR-f	AACGATTCTTCCCGCGCTGTTC	
	NPR1-qPCR-r	TTCTCCGCAAGCCAGTTGAGTC	
<i>PRR5</i>	PRR5-qPCR-f	AGCTTTCACACGGTACGTTCAC	
	PRR5-qPCR-r	TTGGAGGCGGTTTCAGATGTATTG	
<i>PRR7</i>	PRR7-qPCR-f	AAGCGGAAGTGGAAGTGGTAGC	
	PRR7-qPCR-r	TCCGGCTTTGGTATCGTACCTTC	
<i>PR1</i>	PR1-qPCR-f	ACACGTGCAATGGAGTTTGTGG	
	PR1-qPCR-r	TTGGCACATCCGAGTCTCACTG	
<i>JAZ5</i>	JAZ5-qPCR-f	TTCCAAAGGCGAACCCTCTACC	
	JAZ5-qPCR-r	TCCTGGCTGTGATTCCTGAGG	

<i>PDF1.2</i>	PDF1.2-qPCR-f	CTTGTTCTCTTTGCTGCTTTTCGAC	
	PDF1.2-qPCR-r	TTGGCTCCTTCAAGGTTAATGCAC	
<i>VSP1</i>	VSP1-qPCR-f	TCGAGAATCTCAAGGCTGTTGGTG	
	VSP1-qPCR-r	TCAACTTCGATCCGTTTGGCTTG	
<i>VSP2</i>	VSP2-qPCR-f	GGACTTGCCCTAAAGAACGACACC	
	VSP2-qPCR-r	GTCGGTCTTCTCTGTTCCGTATCC	
<i>LNK1</i>	LNK1-qPCR-f	GGATGTGGACAACATGCTTAGGAG	
	LNK1-qPCR-r	TTTGGCTGGGCAGAAGAGAACC	
<i>LNK2</i>	LNK2-qPCR-f	GCAGAATTCGCAGTTCTTTATCGG	
	LNK2-qPCR-r	CCGTGTTCCCATATCCAAC TTTGC	
<i>MYC2</i>	MYC2-qPCR-f	AACCACGTCGAAGCAGAGAGAC	
	MYC2-qPCR-r	TTGGTACAACCGCTCGTAACGC	
Primers used for ChIP assays			Position of LBS motif
<i>PRR3</i>	PRR3-chip-f1	GTGGTAGAGAATGCGCTCGT	950
	PRR3-chip-r1	GCCTTCTTCTGTGCCGCTAT	
<i>PRR7</i>	PRR7-chip-f1	GTTCTGAGGCAGAGTTGGT	1020, 1127
	PRR7-chip-r1	TGTTCTGAGCTCGACCGTA	
<i>PRR7</i>	PRR7-chip-f2	GTAGATAGCCACGACGACGG	595
	PRR7-chip-r2	TGCGTTTCTAAGTCTACCCCT	
<i>PRR9</i>	PRR9-chip-f	CCTGCGAAGCAGAGGACCACC	172
	PRR9-chip-r	AGCGGGCCTTCACTGAGCTG	
<i>GI</i>	GI-chip-f1	AGCCCATCACATCACATGGT	1074
	GI-chip-r1	GGACGTTGATCACTCGCAA	
<i>CDF1</i>	CDF1-chip-f1	AGAGGCCACATAAACTTGTGGT	30
	CDF1-chip-r1	TCTGACTCTGTGTCTCTTTTCC	
<i>CDF1-5'</i>	CDF1-5'-f	TGA CCA AGA TGC AGG TGA GT	
	CDF1-5'-r	ACC AAA AAG GTC TCT GCC ACA	

<i>CDF1-3'</i>	CDF1-3'-f	TCA TTG TCT TGC ATC AGA ACC A	
	CDF1-3'-r	CCA TGC TGT TGC ATC TTG GAC	
<i>LUX</i>	LUX-chip-f	TCCAACGGTGGAAAGATCACATTGC	367
	LUX-chip-r	GTTCGGCCAGCTGGAGAGTG	
<i>CO</i>	CO-chip-f1	CTCATGTGGACTCCAAAATGCC	723
	CO-chip-r1	ATGAGAATCATATCGGAAAAGTGAC	
<i>CO</i>	CO-chip-f2	ACAGTAATCACAAGGTTTCAGGA	311, 360
	CO-chip-r2	CCATGGTGTTCAGGCAAAT	
<i>LNK1</i>	LNK1-chip-f1	CCTTGATTGTTTCGGGCTTGC	492, 500
	LNK1-chip-r1	GGGAGCGATGAGAGATGGAA	
<i>LNK1-3'</i>	LNK1-3'-f	ATA CAA TCT CTT CTA TCT GCT GAG T	
	LNK1-3'-r	GCC GAA CGA AAT AAG CTC ACC	
<i>LNK1-5'</i>	LNK1-5'-f	TCT CCA CAA ACT CAG GAG TAC AA	
	LNK1-5'-r	GTT GGG AAA AAG CGA CGT GA	
<i>LNK2</i>	LNK2-chip-f1	ACCACAGCCAGGGAAAGTCA	74
	LNK2-chip-f2	CAAACGAGTGGCTGAGAGAGA	
<i>LNK2-3'</i>	LNK2-3'-f	AGC TGA GCA AAA GAT AAC TGG GA	
	LNK2-3'-r	AAA TCT GGC TGA GGA AGC CC	
<i>LNK2-5'</i>	LNK2-5'-f	AAA AAT TGT TGA ATT GGT GGG AAA A	
	LNK2-5'-r	CCT TTC GTT CAT CAA AGT CCA CA	
<i>ICS1</i>	SID2-chip-f1	CGAGAACTTGTAATGCGTTTGC	607
	SID2-chip-r1	GATACGGAAGCGTTTGCAC	
<i>PR1</i>	PR1-chip-f1	TTCAGCCATAGGCAAGAGTGA	455
	PR1-chip-r1	ATCGTATCGGACAGTTTGGC	
<i>PR1</i>	PR1-chip-f2	CAAAACAACCTGAATGACATGAAACA	223
	PR1-chip-r2	TGCAATTGTCCAAATGAATAGAAGT	
<i>EDS1</i>	EDS1-chip-f1	ACCGTTCATTACACGAAGACA	936

	EDS1-chip-r1	GGGGAAATTTCTACGAAAAGCCA	
<i>EDS1-5'</i>	EDS1-5'-f	GAG CTG GCC ATT TTC TGT ATC C	
	EDS1-5'-r	TCA GCT CCT TCT TCA AGA CAT C	
<i>EDS1-3'</i>	EDS1-3'-f	TGA GTC TCC AAT AGC CAA AGA GT	
	EDS1-3'-r	ACC CCA TCA TGA GAC CAT TTC AA	
<i>PAD4</i>	PAD4-chip-f1	CGAGCTGTATTATTAAGGTGGAAGA	1068
	PAD4-chip-r1	TTTGCTCTAACATGCTTCTTTTCA	
<i>PAD4</i>	PAD4-chip-f2	AAACTCTTACCAAAGTTTCTGCAT	110
	PAD4-chip-r2	AGAAGAAAATGCGAATCAAAGCA	
<i>EFR</i>	EFR-chip-f1	TTGCAGAAGCAAATCTATCTGAACT	819
	EFR-chip-r1	CGTCGACGAAGGAGAAAAACAAT	
<i>EFR</i>	EFR-chip-f2	TCACAGTGACAACACTTCCCAA	612
	EFR-chip-r2	GGAAGCCCATCGATTCTTGC	
<i>GRX480</i>	GRX480-chip-f1	AGGAACCAAATTA AAAACGTGCAG	181
	GRX480-chip-r1	AGCTATGGGTGATGGTGCTG	
<i>WRKY33</i>	WRKY33-chip-f1	GGGTCAATTTGTAGCCTATCTCTA	713
	WRKY33-chip-r1	AAATCCATGTGCGGCTGTTT	
<i>JAZ5</i>	JAZ5-chip-f1	TACTGTTGCTAGTGCGTCGT	927
	JAZ5-chip-r1	TCTCCGATACGATCCGACAG	
<i>JAZ5-3'</i>	JAZ5-3'-f	TCC ATT TTA CGC GCA ATC CAC	
	JAZ5-3'-r	TCA GAT TTC TCC GGC GCT TG	
<i>JAZ5-5'</i>	JAZ5-5'-f	AAC CCG AGA CTA GCT ACA GCA	
	JAZ5-5'-r	AAT CAA TCT CCA TCT CCA ACT GTG	
<i>JAZ7</i>	JAZ7-chip-f1	GGCGAAAATGTGTGGGTTCAACG	607
	JAZ7-chip-r1	GTAACGTCCTGCCAAACCCGTCC	
<i>JAZ7</i>	JAZ7-chip-f2	TGGCATTTCACCGTGGATT	1550
	JAZ7-chip-r2	TGGTCGTCGCGTGATTTAGT	

<i>JAZ8</i>	JAZ8-chip-f1	TCATCAATCCCGTTTAACTCACA	957
	JAZ8-chip-r1	GTCTGACCATTTCGCATTACGC	
<i>JAZ8</i>	JAZ8-chip-f2	TGGAACGTTACTTTCGGCTC	507, 625
	JAZ8-chip-r2	TGTGATCCATTGCTCACGCA	
<i>MYC2</i>	MYC2-chip-f2	GAATAACTCGAATTGGTCACATACA	1772
	MYC2-chip-r2	GGACATTAGTCGGGATTCGGG	
<i>MYC2</i>	MYC2-chip-f3	GTTTTCTAGTGGCGTCACCCCCAAAG	1475
	MYC2-chip-r3	CCAAACCATTGTCTGGTGGTTGTGAG	