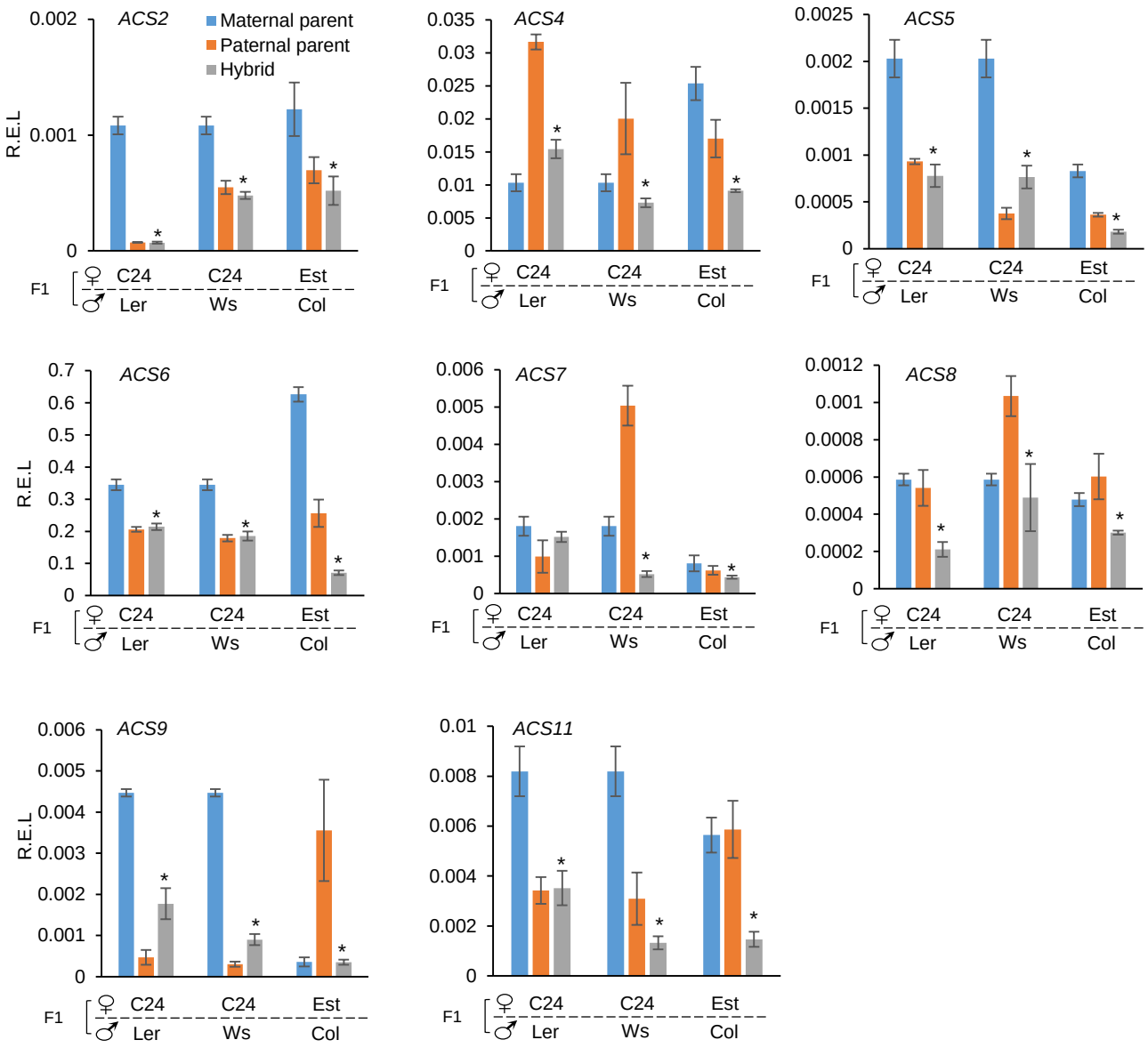

Fig. S1. Downregulation of *ACS* genes in hybrids of various *Arabidopsis* ecotypes. Relative expression levels (R.E.L.) of *ACS* genes at ZT0 in hybrids of various *Arabidopsis* ecotypes (C24, L*er*, Ws, Est, and Col). Asterisks indicate down-regulation in the hybrids at statistical significance levels of $P < 0.05$, compared with MPV.

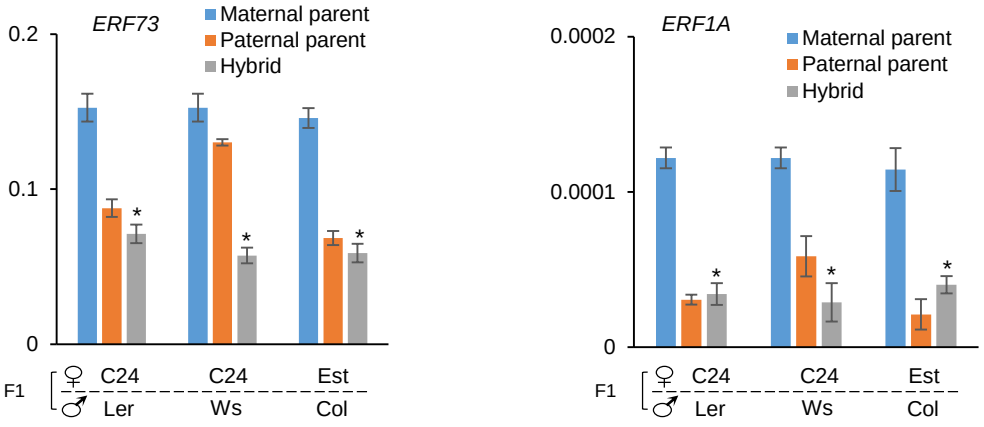

Fig. S2. Downregulation of *ERF73 and ERF1A* in hybrids of various *Arabidopsis* ecotypes. Relative expression levels (R.E.L.) of *ACS* genes at ZT0 in hybrids of various *Arabidopsis* ecotypes (C24, L*er*, Ws, Est, and Col). Asterisks indicate down-regulation in the hybrids at statistical significance levels of $P < 0.05$, compared with MPV.

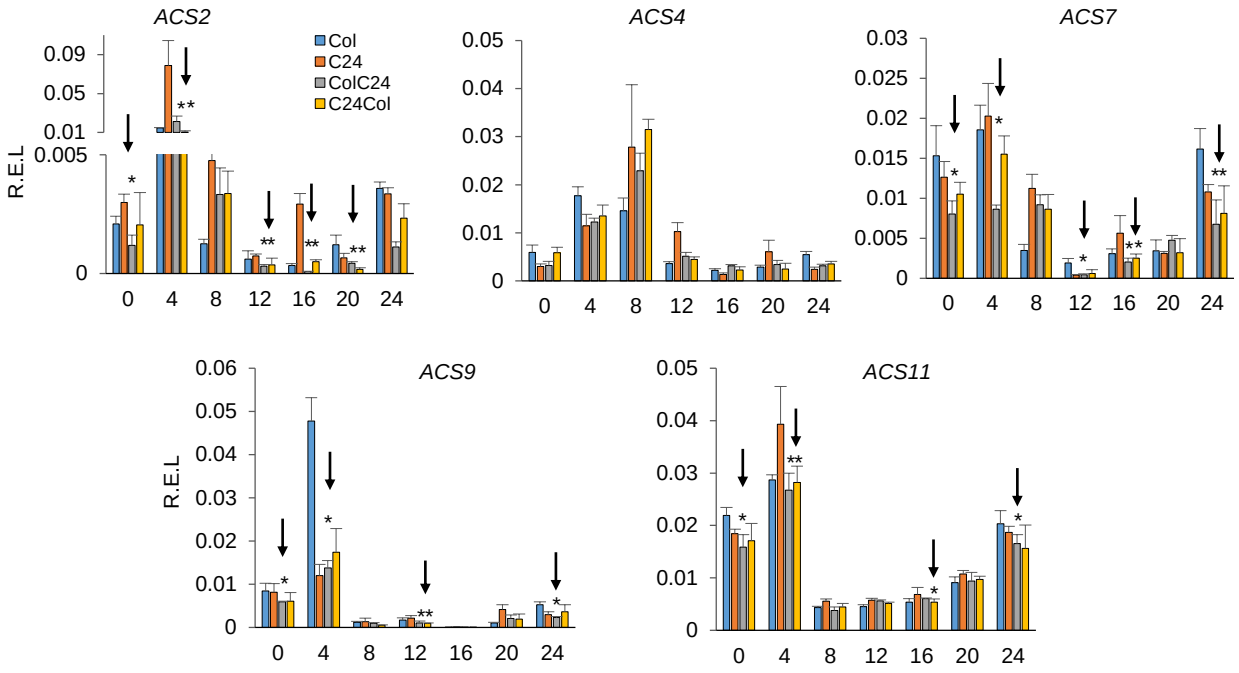

Fig. S3. Downregulation of *ACS* genes at different time points in hybrid. Relative expression levels (R.E.L.) of *ACS* genes every 4h in a 24h period (ZT0 = dawn) in the reciprocal F1 hybrids (ColXC24 and C24XCol) and the parents (Col and C24). Asterisks indicate down-regulation (arrows) in the hybrids at statistical significance levels of $P < 0.05$, compared with MPV.

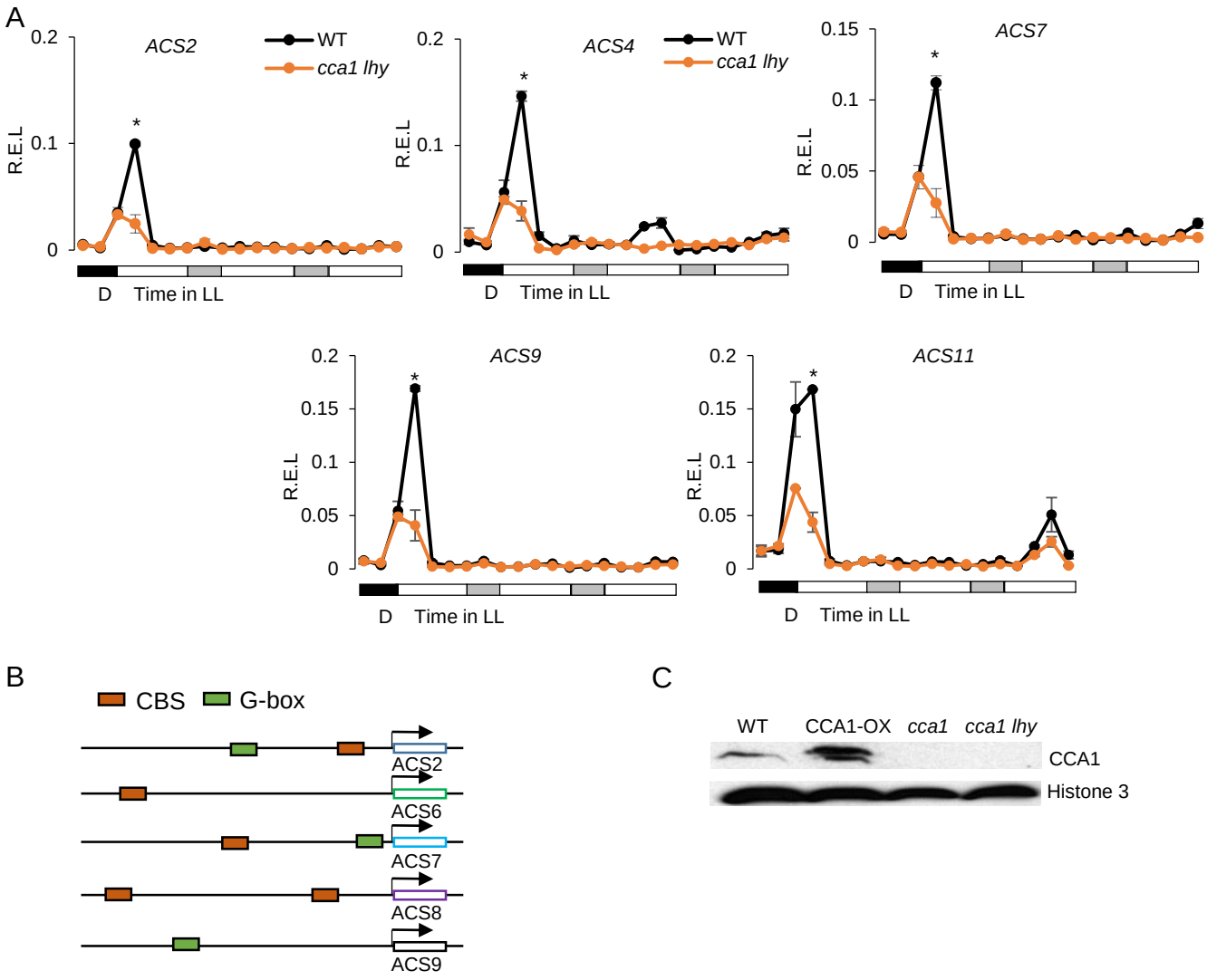

Fig. S4. Indirect roles of CCA1 on expression regulation of *ACS* genes.(*A*) Relative expression levels of *ACS2*, *ACS4*, *ACS7*, *ACS9* and *ACS11* in WT (Ws) and *cca1 lhy* mutant every 4h under a diurnal cycle (24h) followed by constant light (LL) (48h) conditions. Black, white, and grey boxes indicate dark, light, and subjective night, respectively. Asterisks indicate down-regulation in *cca1 lhy* mutant at statistical significance levels of $P < 0.05$, compared with wild type. (*B*) Distribution of CCA1-binding site (CBS) and G-box (PIF-binding motif) elements in promoters of *ACS2*, *ACS6*, *ACS7*, *ACS8* and *ACS9*. (*C*) Western blot confirmed specific binding activity of anti-CCA1 antibodies to CCA1 protein.

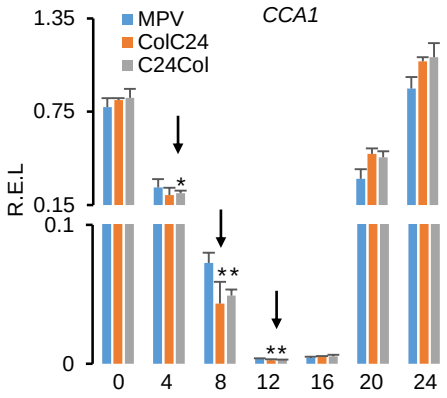

Fig. S5. Relative expression levels (R.E.L.) of *CCA1* every 4h in a 24h period (ZT0 = dawn) in the reciprocal F1 hybrids (ColXC24 and C24XCol) compared with MPV. Asterisks indicate down-regulation (arrows) in the hybrids at statistical significance levels of $P < 0.05$, compared with MPV.

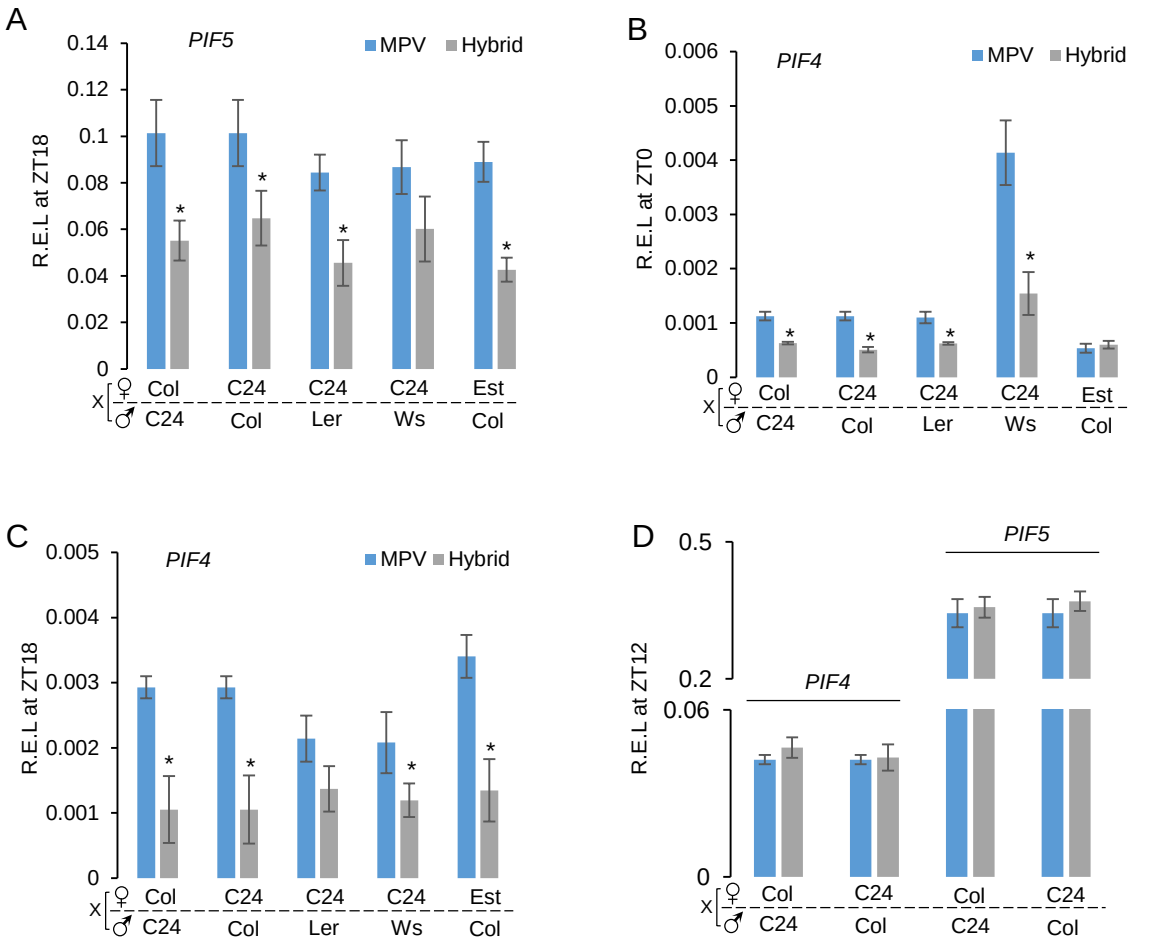

Fig. S6. *PIFs* were repressed in hybrids of various *Arabidopsis* ecotypes. (*A*) Relative expression levels to the mid-parent level of *PIF5* at ZT18 in hybrids of various *Arabidopsis* ecotypes. Asterisks indicate down-regulation in the hybrids at statistical significance levels of P < 0.05, compared with MPV. (*B-C*) Relative expression levels to the mid-parent level of *PIF4* at ZT0 (*B*) and ZT18 (C) in hybrids of various *Arabidopsis* ecotypes. Asterisks indicate down-regulation in the hybrids at statistical significance levels of *P* < 0.05, compared with MPV. (*D*) Relative expression levels to the mid-parent level of *PIF4* and *PIF5* at ZT12 in hybrids of Col-0 and C24.

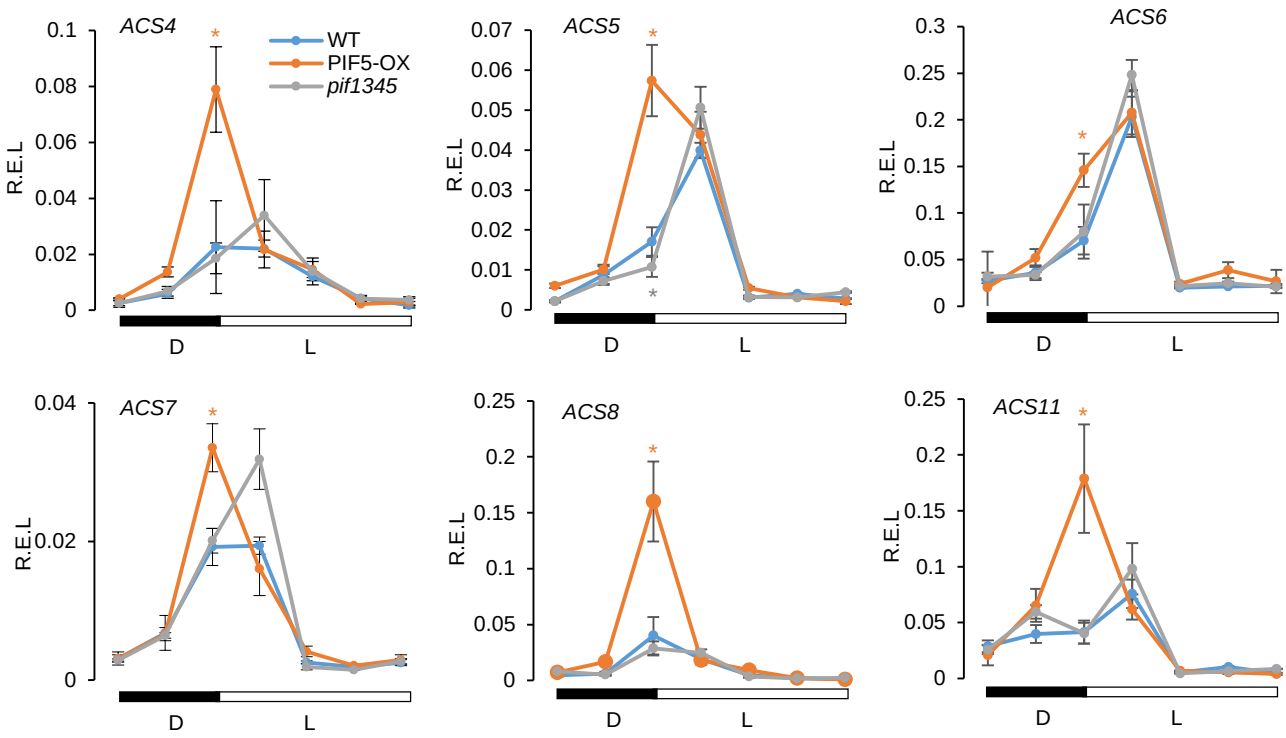

Fig. S7. *ACS* genes were regulated by *PIFs*. Relative expression levels of *ACS4*, *ACS5*, *ACS6*, *ACS7*, *ACS8* and *ACS11* in WT (Col-0), PIF5-OX and *pif1345* mutant in diurnal conditions (dark, D and light, L). Asterisks in orange and grey respectively indicate upregulation in PIF5-OX and downregulation in *pif1345* at statistical significance levels of $P < 0.05$, compared with WT.

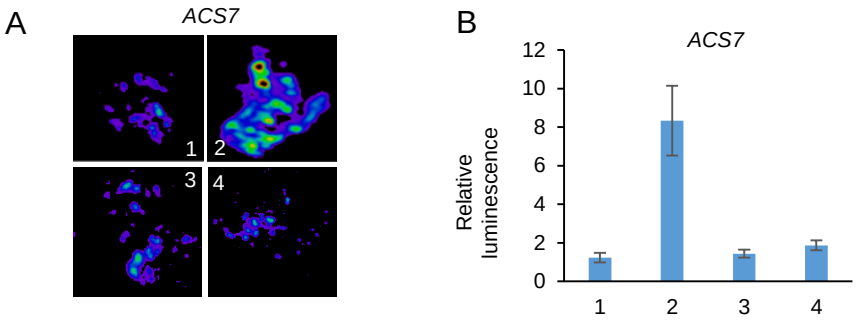

Fig. S8. *ACS* genes were directly activated by PIF5. (*A*) Transient expression assays showed that PIF5 directly activated expression of ACS7 as in Fig. 2*F*. (*B*) Relative luminescence intensity (*Y*-axis) for each comparison in (*A*).

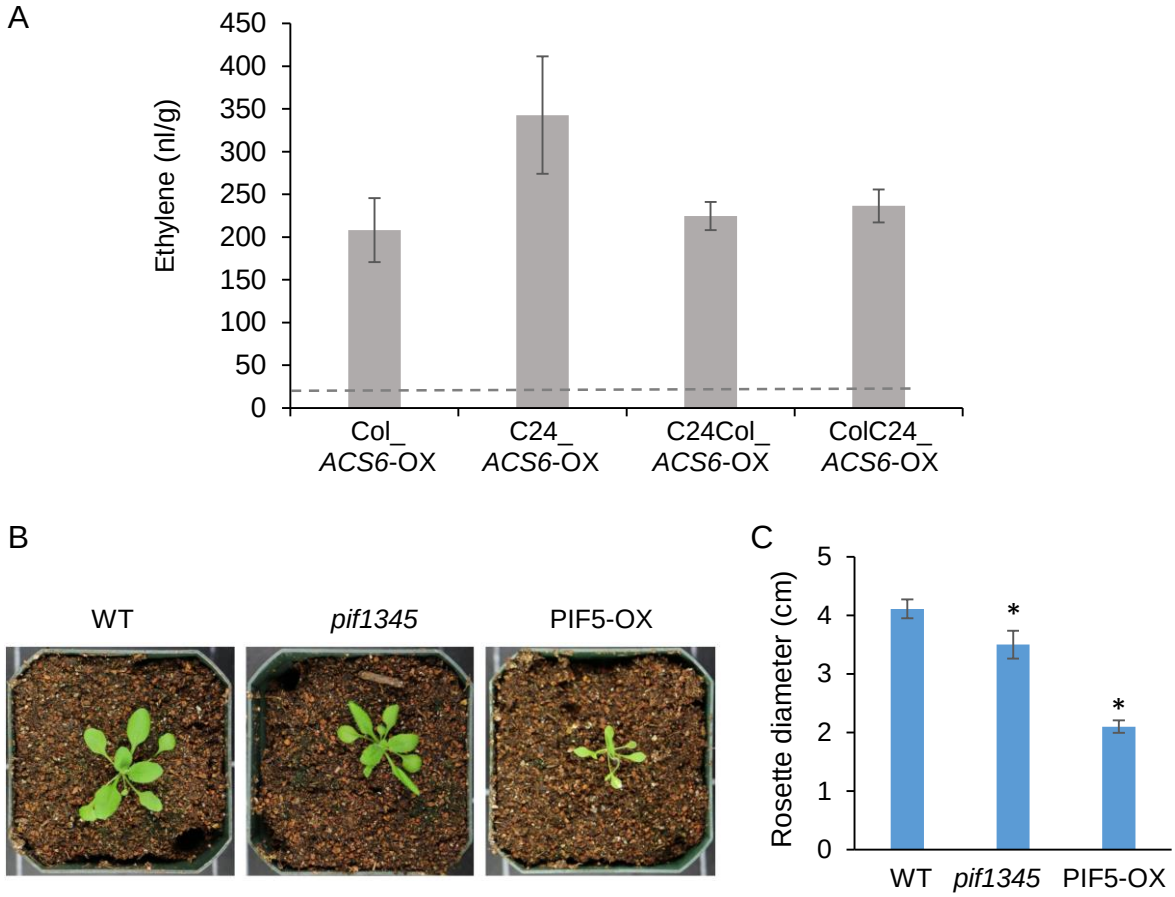

Fig. S9. Ethylene production in ACS6-OX lines and plant growth reduction in *PIF* lines. (*A*) Ethylene production in the transgenic plants that over-expressed *ACS6*^{DDD} in Col_*ACS6*-OX, C24_*ACS6*-OX, F1 hybrid (ColXC24_*ACS6*-OX), and reciprocal hybrid (C24XCOL_*ACS6*-OX) lines. A dashed line indicates an average level of ethylene in the wild-type plant. (B) Representative seedling images of the wild type (WT), *pif1345* mutant, and PIF5-OX line at 21 days after sowing. (*C*) Quantitative analysis of rosette diameter of the plants in (*A*). Asterisks indicate a statistical significant level ($P < 0.05$) compared with WT.

Table S1 Primers used in this study.

Name	Primer sequence	Usage
ACS2F	ATTTGCGTGGATGGATTTGAGACA	RT-qPCR
ACS2R	AACGGAAGGAAGAGCCAGGAGACA	
ACS4F	CCGGGTTGGTTTAGAGTTTGTTTC	
ACS4R	TTCGCTTTTACTCTTTTGGCATCT	
ACS5F	TAAATGGAGAACCGGAGCAGAGAT	
ACS5R	CAAGTGGGTTAGATGGATTCGTGA	
ACS6F	CCGATGGCTGCAACAACTATGATG	
ACS6R	AGGCGAATGAGGCGAGAAGAAGC	
ACS7F	TATGCTGGCTTCTATGTTGTCG	
ACS7R	AATAGCCCTGCGTTCCCTTTCA	
ACS8F	TTGCGAATTTGAGCGAAGAGACAT	
ACS8R	AGCCGGAAAACCCAATTAGAGACT	
ACS9F	ACATACCTCGACGAAAACCAGAAA	
ACS9R	GTCAACCCAACAGAACAAACCA	
ACS11F	CCTGGTTGGTTTAGAGTTTGTTTC	
ACS11R	GGAGACCCATTTGTTGATAAGAGA	
ERF1aF	TTTGTTGAATTTTCCGTTGAGAGT	
ERF1aR	TCGTTAGAAGAAGAAAAAGAAGAT	
ERF73F	AATAATCCGGACACGCTTCTG	
ERF73R	CGTTGTTGGCTTCTTCACTATCAT	
PIF4F	TTGGGCGTGGAACTTGGACT	
PIF4R	CTGGGTTTGGGTTTGTTCTCTATG	
PIF5F	GTTTCCCGGGGTACAATCATCTCC	
PIF5R	GCTGGTTGTTGTTGCACGGTCTG	
ACS2pF	CTCGAGATCAACTTATTATTTATTGGC	Promoter cloning
ACS2pR	TCTAGATTGCTGTGTCAATTCTCACTT	
ACS6pF	CTCGAGAACATCAGTCTGATAAAAAA	
ACS6pR	GGATCCTTTTTGTTTCTTCTTTAATA	
ACS7pF	CTCGAGGTACATGAAAAGTGGTAAAAGTAT	
ACS7pR	GGATCCTTTTTTCTTAGAGCTTCGAACCTGA	
ACS8pF	CTCGAGATATCAAACTAAACATACACAC	
ACS8pR	GGATCCTTTCTTAATTAGCTCTAGAGAT	
ACS9pF	CTCGAGCTAATAGTGACAAGTGAACCT	
ACS9pR	GGATCCTTTTTGATATAAAAATCAAAAAG	
CCA1-CDSF	CTCGAGATGGAGACAAATTCGTCTGGA	CDS cloning
CCA1-CDSR	TCTAGATCATGTGGAAGCTTGAGTTTC	
PIF5CDSF	TACCGCTCGAGATGGAACAAGTGTTTGCTGATTG	
PIF5CDSR	CGCGGATCCTCAGCCTATTTTACCCATATGAA	
UBQ10ChipF	TCCAGGACAAGGAGGTATTCCTCCG	ChIP-qPCR for CCA1
UBQ10ChipR	CCACCAAAGTTTTACATGAAACGAA	
TOC1EEF	TTTTATGGCCTGCACTTTTTATTG	
TOC1EER	GGTGGGACTTGGGATATTTTAGG	
ACS2CBSF	TGCTAGCAAAACACAACCATCT	
ACS2CBSR	TGAAAAGTAACAAGCGAACCAA	
ACS6CBSF	TTGGTCAAAGTGAAGGCTTCAAAA	
ACS6CBSR	TGATAGTGGCAGACATTGGAC	
ACS7CBSF	TCATACTTAATTAGAGACGAA	
ACS7CBSR	GGCTATCCATTTACACTTTATT	
ACS8CBSF	TACATTAAGACGGTCCAAAGAG	
ACS8CBSR	CTAACAAAAACTATATCGGCAACA	
ACS2GF	AGGAGGATTTGAGTTTTTGACATT	ChIP-qPCR for PIF5
ACS2GR	GTTGGTGGGTTTGGACTCTTT	
ACS7GF	GGTCACGTCTGCTATATATACTC	
ACS7GR	CTTAGAGCTTCGAACCTGACACGT	
ACS9GF	CAAGGCCCATTTATTATGGGCT	
ACS9GR	AACTGAATAACAACAGATTCTA	
PP2AF	CTGGCGTGTGCGTTATATGGTT	
PP2AR	CAACAAACATGGACTTCCAAGTACCA	