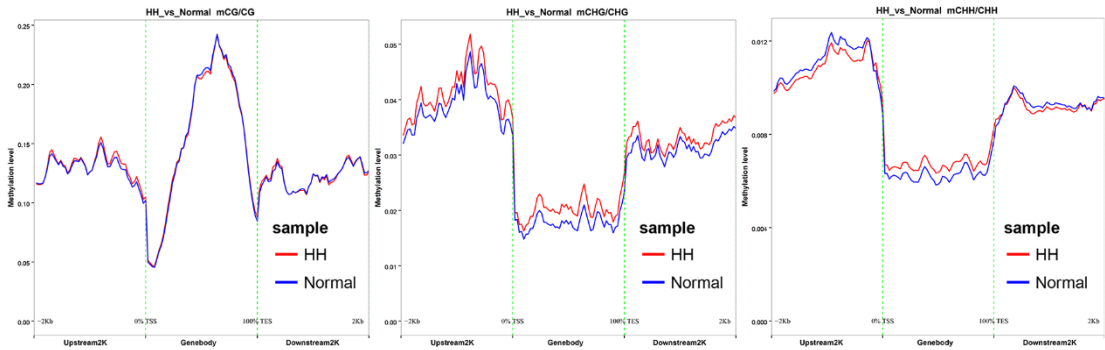


1

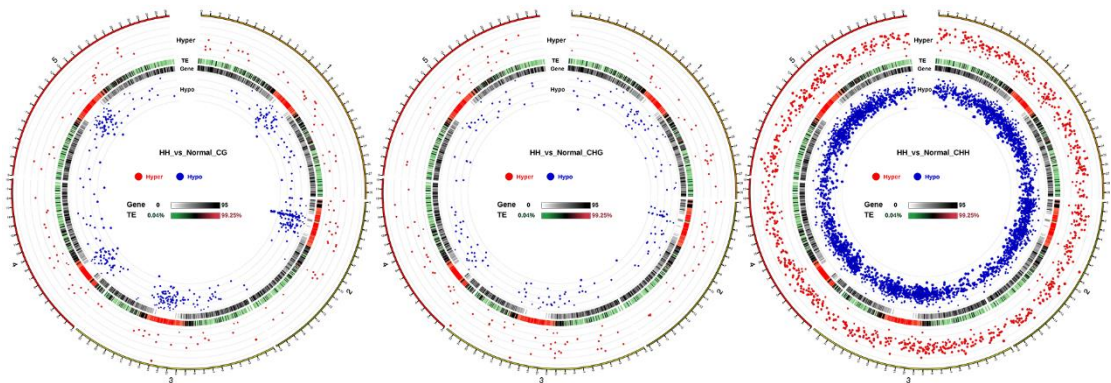
Supplemental Materials

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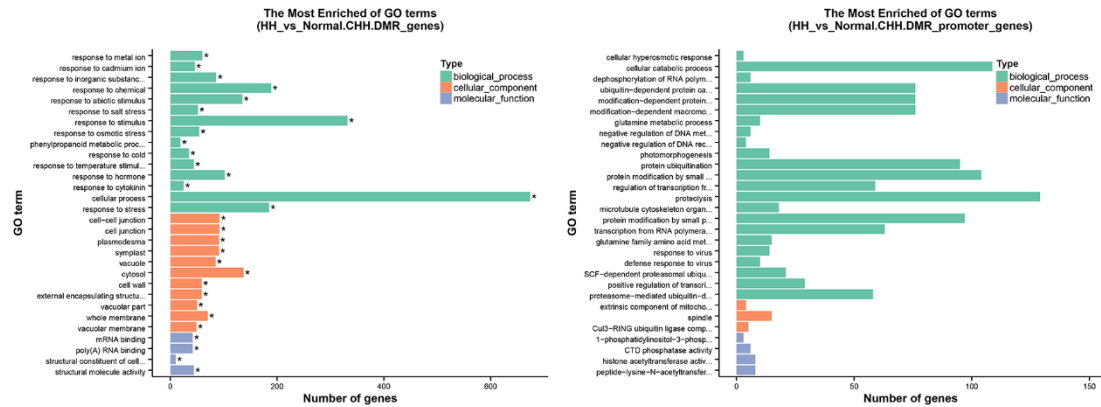


3 **Supplemental Figure S1.** ML of different genic regions in the context of CG, CHG
4 and CHH. The X-axis represents different gene elements, and the Y-axis represents the
5 ML.

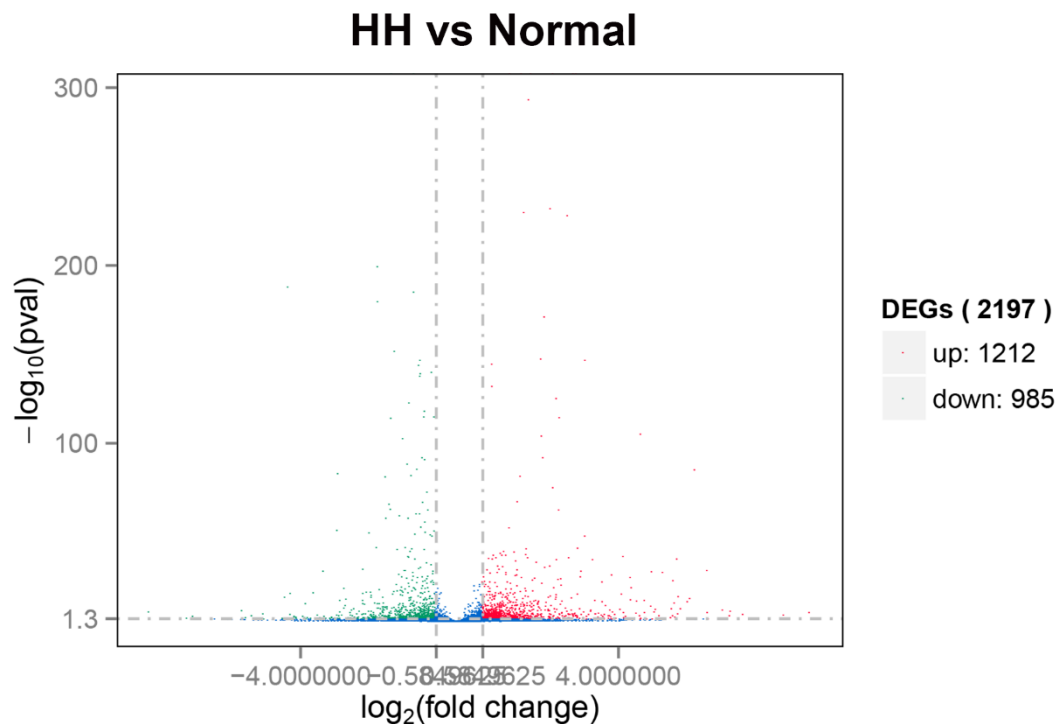
6



7 **Supplemental Figure S2.** Circular plots of DMRs. Track order: hyper-DMR; density
8 of TEs; gene density of each chromosome; hypo-DMR. The higher the density of the
9 dot, the more significant the difference in DMR.



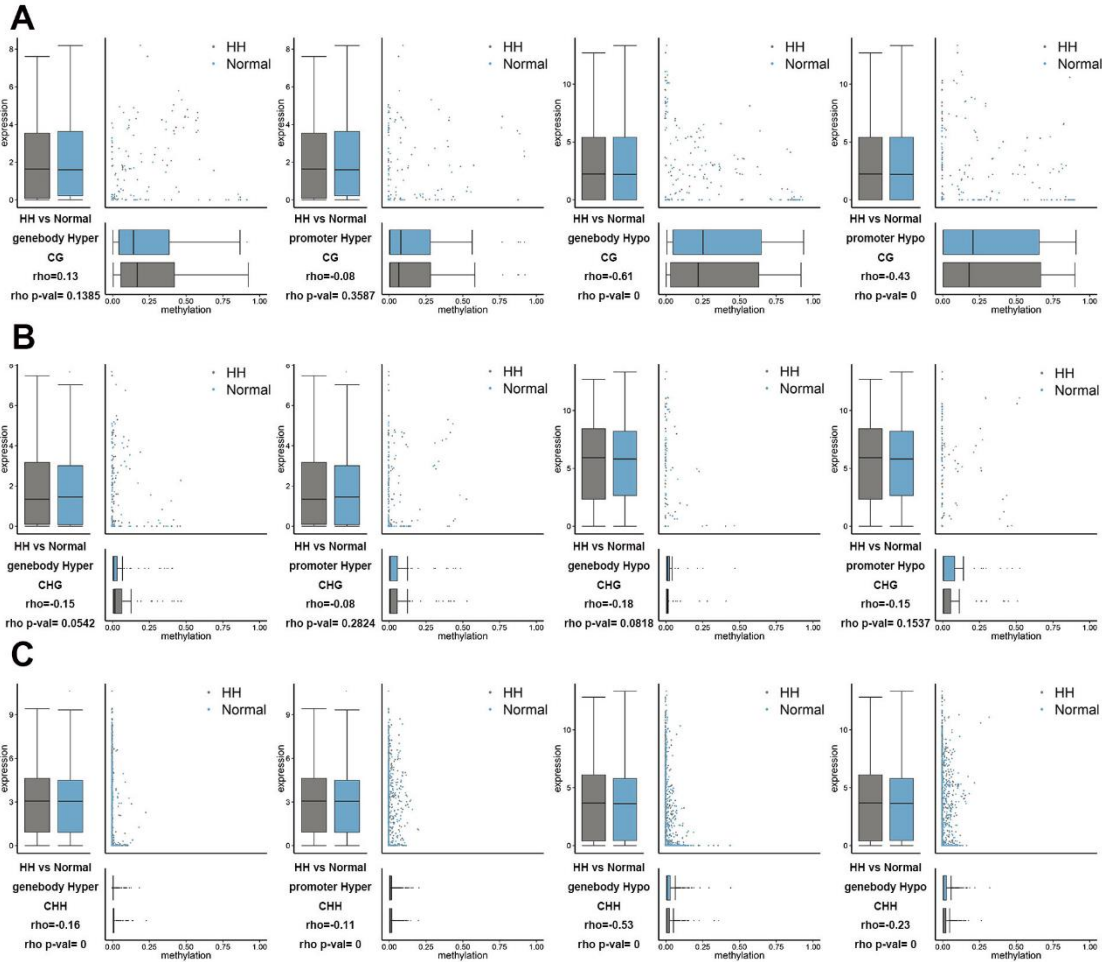
Supplemental Figure S3. The most enriched GO terms of genes with CHH DMRs (C) and genes whose promoters have DMRs (D) in normal and hyperhydric seedlings. (* represents statistical significance at the $P \leq 0.05$ level).



Supplemental Figure S4. Differentially expressed genes (DEGs) between HH and normal. Each dot represents one gene. The red dots represent up-regulated genes and the green dots represent down-regulated genes. The blue dots represent genes without

18 differential expression. The X-axis is the \log_2 value of fold change and the Y-axis is the
 19 \log_{10} value of the P-value.

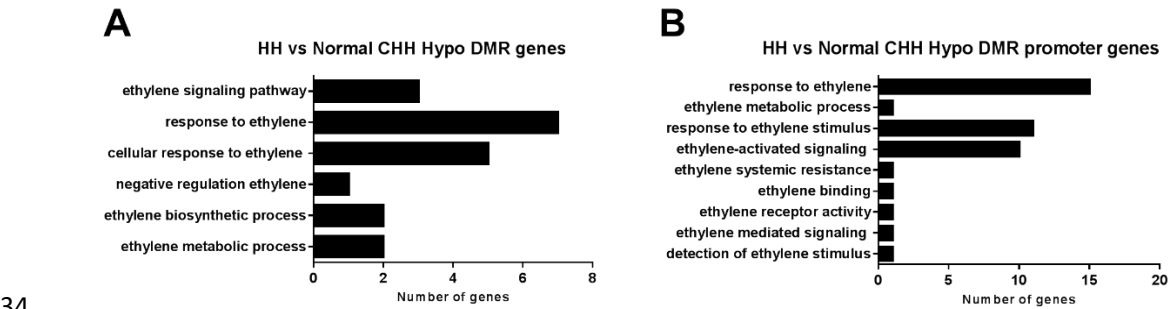
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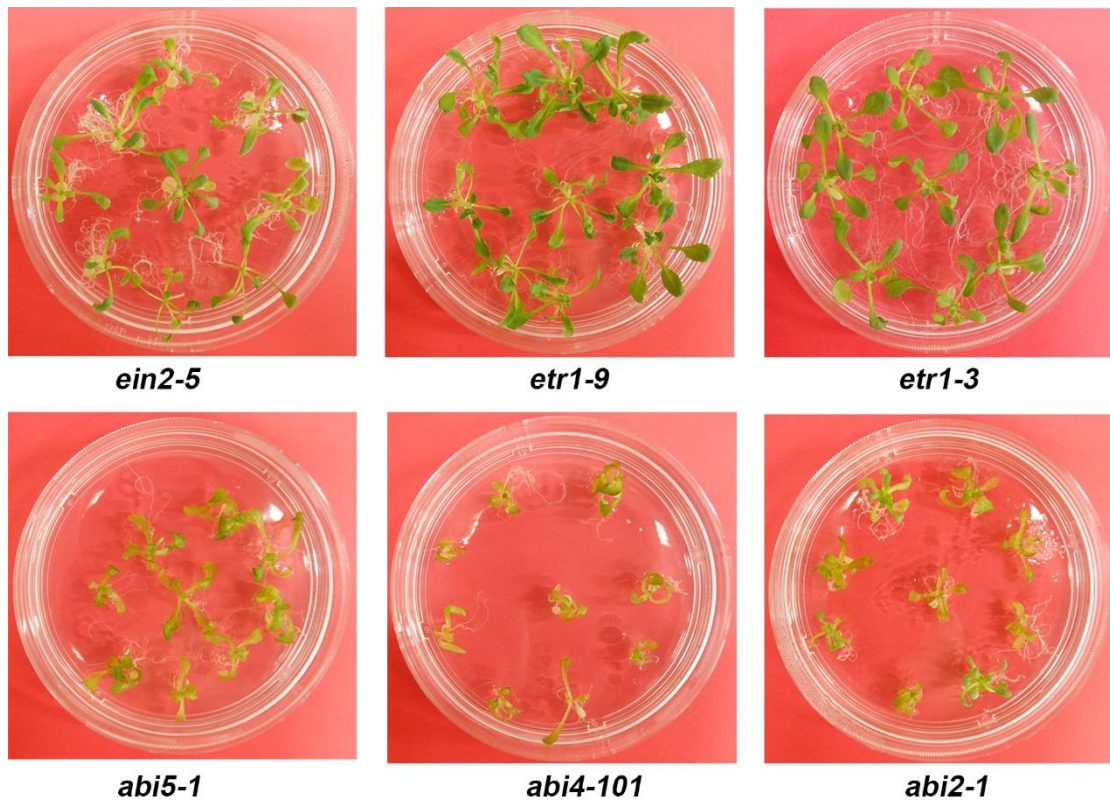
21

22 **Supplemental Figure S5.** Scatter and box plots of correlated DMR methylation and
 23 RNA expression affecting genes involved in HH. Scatter and box plots of correlated
 24 DMRs and RNA expression in CG (A), CHG (B) and CHH (C) contexts. Top left
 25 picture: box diagram of DMR-related gene expression levels. Top right picture:
 26 Comparison of the ML and expression level of DMR-related genes; the horizontal
 27 coordinates represent the gene ML, and the ordinate represents the gene expression

28 level. Bottom left legend: promoter/gene body hyper/hypo represents the ML of the
 29 promoter/gene body region in the hyper/hypo-DMR, rho represents the correlation
 30 coefficient between the gene ML and expression level in the scatter plot, and rho.p-val
 31 represents the correlation P-value. Bottom right picture: Comparison of the ML of the
 32 DMR-related genes in the form of a box diagram. The black colour represents
 33 hyperhydric seedlings, and the blue colour represents normal seedlings.

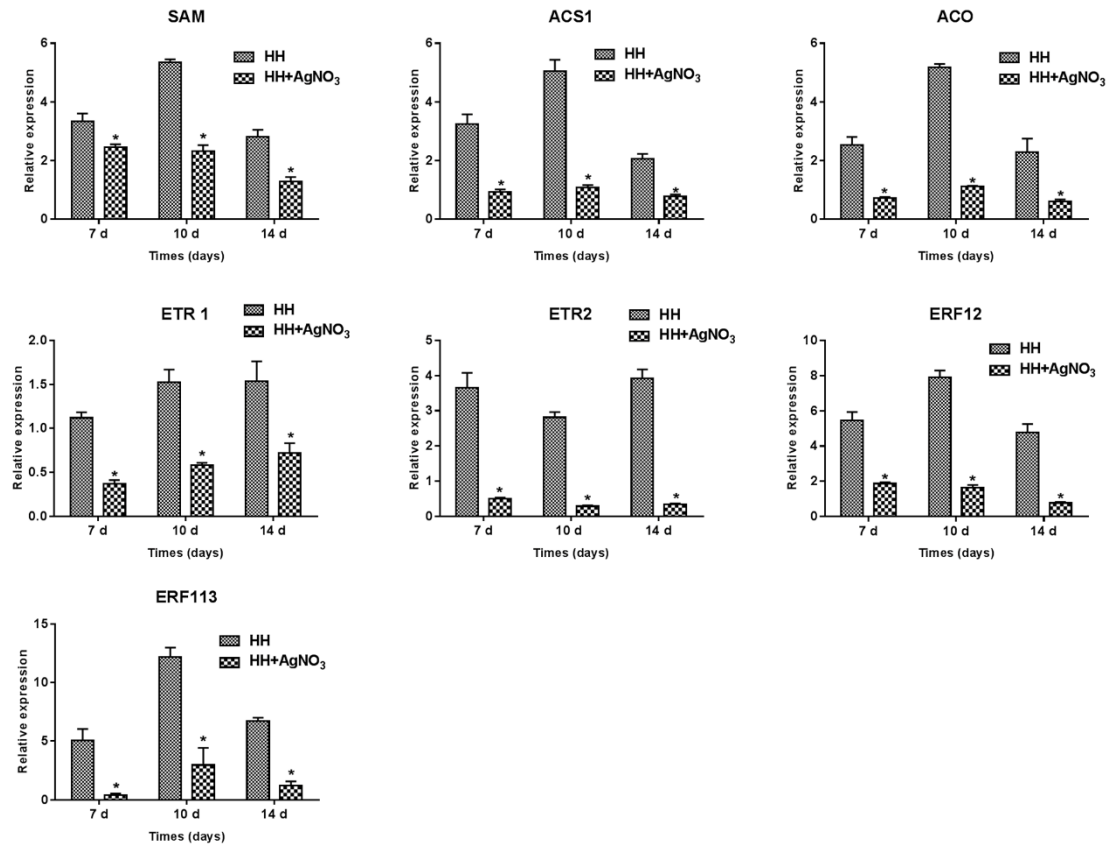


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 35 **Supplemental Figure S6.** Gene ontology (GO) analysis of ethylene-related CHH hypo
 36 DMR (A) and DMR promoter (B) genes between HH and normal.



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41 **Supplemental Figure S7.** Development of HH in *Arabidopsis* mutants.



Supplemental Figure S8. Expression of genes associated with ethylene biosynthesis and signal transduction. *SAM*, *ACS1* and *ACO* are genes related to ethylene biosynthesis; *ETR1* and *ETR2* are ethylene receptor genes; and *ERF12* and *ERF113* are ethylene response genes. The expression levels of genes in whole seedlings were quantified by qRT-PCR and normalized against the expression level of *actin*. The data are the means \pm SEs, and the values are presented as fold changes in expression (hyperhydric seedlings cultured in Gelrite or Gelrite supplemented with AgNO₃ versus normal seedlings in normal culture media). Statistical significance was calculated by Student's t-test, '*' indicates a significant difference at the $P < 0.05$ level.

53 **Supplemental Table S1.** Data description of BS-Seq reads for the three *Arabidopsis*
54 samples with three replicates.

Sample	Raw Resds/	Clean reads/	BS conversion	Mapping	Duplication
	Raw bases(G)	Clean_bases(G)	rate (%)	rate (%)	rate (%)
Normal 1	32486404/8.12	32417623/7.91	99.635	77.89	2.57
Normal 2	34917325/8.73	34157825/8.29	99.686	75.23	3.43
Normal 3	29215929/7.30	29159617/7.11	99.655	79.94	3.48
HH 1	28981333/7.25	27905322/6.69	99.462	66.67	5.07
HH 2	36679885/9.17	35438899/8.57	99.677	74.77	3.38
HH 3	36460895/9.12	35266713/8.54	99.650	72.30	3.60

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57 **Supplemental Table S2.** Percentage of methylation levels of normal and HH.

Sample	C (Mb)	mC %	CG (Mb)	mCG %	CHG (Mb)	mCHG %	CHH (Mb)	mCHH %
Normal 1	902.5	10.8%	128.0	30.35%	131.9	17.24%	642.6	6.05%
Normal 2	869.3	10.79%	131.5	29.96%	132.6	17.66%	605.2	6.02%
Normal 3	762.3	10.7%	111.3	27.99%	111.6	16.78%	539.3	6.42%
HH 1	581.7	9.06%	94.1	24.41%	90.0	15.42%	397.7	5.08%
HH 2	909.1	10.13%	133.4	30.49%	134.9	17.57%	640.7	5.04%
HH3	871.2	10.54%	130.5	29.93%	131.5	17.4%	609.1	5.73%

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60 **Supplemental Table S3.** Ethylene-related CHH hypo genes between HH and normal.

Gene_id	Gene name	Methylation difference	Region	Description
HH vs Normal CHH Hypo DMR genes				
AT1G05010	ACO4	-0.0588	exon	ethylene-forming enzyme
AT1G02500	SAM1	-0.02	exon	S-adenosylmethionine synthetase
AT5G03730	CTR1	-0.035	exon	Protein kinase superfamily protein
AT1G05850	CTL1	-0.033	3'UTR, exon	Chitinase family protein
AT5G04950	NAS1	-0.029	exon	nicotianamine synthase 1
AT3G15730	PLDALPHA1	-0.025	Exon, 3'UTR	phospholipase D alpha 1
AT4G19690	IRT1	-0.021	exon	iron-regulated transporter 1
AT2G05520	GRP3	-0.059	Exon, 3'UTR	Glycine rich protein
AT1G49950	TRB1	-0.08	Exon, 3'UTR	telomere repeat binding factor 1
HH vs Normal CHH Hypo DMR promoter genes				
AT1G66340	ETR1	-0.074	promoter	Signal transduction response regulator
AT3G61510	ACS1	-0.03	promoter	1-aminocyclopropane-1- carboxylate synthase 1
AT1G56160	ATMYB72	-0.034	promoter	Myb domain protein 72
AT1G22190	RAP2-13	-0.102	promoter	AP2/ERF domain
AT2G40220	ABI4	-0.086	promoter	AP2/ERF domain;

AT1G06160	ERF094	-0.089	promoter	ethylene response factor
AT3G15010	UBA2C	-0.024	promoter	RNA-binding (RRM/RBD/RNP motifs) family protein
AT1G46768	RAP2-1	-0.087	promoter	AP2/ERF domain
AT5G42190	SKP1B	-0.058	promoter	E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 family protein
AT5G44210	ERF9	-0.054	promoter	ethylene response factor
AT2G21150	XCT	-0.049	promoter	XAP5 family protein
AT1G28160	ERF087	-0.074	promoter	ethylene response factor
AT5G02320	MYB3R5	-0.073	promoter	myb domain protein 3r-5
AT5G24520	TTG1	-0.043	promoter	Transducin/WD40 repeat-like superfamily protein
AT4G05100	AtMYB74	-0.092	promoter	myb domain protein 74
AT1G05690	BT3	-0.072	promoter	BTB and TAZ domain protein 3

62 **Supplemental Table S4.** Primer sequences used for bisulphite sequencing analysis.

Gene name	Gene ID	Forward primer (5'→3')	Reverse primer (5'→3')
ACS1	AT3G61510	TAGGGTATTTATYGAGGGATTG	AATATTAACACRTAAAACAACCCAC
ETR1	AT1G66340	TTGGAAATTTATAAAATTTAATATAGTAAA	CTATAAAAAATAATACAAATCRATAAATT

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65 **Supplemental Table S5.** Primer sequences used for real-time PCR analysis.

Gene name	Gene ID	Forward primer (5'→3')	Reverse primer (5'→3')
SAM	AT3G17390	GGATCTGAAGAGAGGAGGTAA	GACTTGAGTGGCTTGACTAC
ACS1	AT3G61510	TGAGTGACAAACATGGAGAAG	GGCGAGACCCATTTGAATAA
ACO	AT2G19590	CTTATGAGAGGGCTGAGAGA	GTTCTTGGATGGCGGTATAG
ETR1	AT1G66340	GCTAGACGAGAAGCAGAAAC	GAGTAAGGAAGAGAGTGCAATAA
ETR2	AT3G23150	CTGGATTTCGATTGCCTTACC	CCTCATGGCCACTTCATAAC
ERF12	AT1G21910	CAAAGGAGTGAGGATGAGAAG	GCTTCAGCTGTTGAGTAAGA
ERF113	AT5G13330	GTAAATGGGCGGCAGAAA	AGCTCGGTCATAGGCTAAA
ACTIN	AT3G18780	GGTAACATTGTGCTCAGTGGTGG	AACGACCTTAATCTTCATGCTGC