Supplemental Tables and Figures

Table S1. Transcript specific primers used for transcript accumulation analyses (sqRT-PCR and qRT-PCR) throughout this study.

Reference Number	Target	Direction	Primer Sequence (5'→3')
AJ236020	*Ph18S*	Forward	TTAGCAGGCTGAGGTCTCGT
		Reverse	AGCGGATGTTGCTTTTAGGA
JQ031717	*PhAAE*	Forward	GTACAGTCACAGAGGAGC
		Reverse	CGGGAGTCGTTATTTCGC
JQ031717	*PhAAE*	Forward	ATGGTGCCCAAAGCATGT
		Reverse	GAGCTGGCAATCAAGGAATC
L10115	*PhFBP1*	Forward	TGCGCCAACTTGAGATAGCA
		Reverse	TGCTGAAACACTTCGCCAATT
EU751616	*PhCM1*	Forward	CCCTGATGAGCACCCATTC
		Reverse	ACTGCATGGGTGGCAACAC
AY705976	*PhPAL1*	Forward	GCTAGGCGGTGAGACGCTAA
		Reverse	CTCGGACAGCTGCACTGTCA
CO805160	*PhPAL2*	Forward	ACTGGCAGGCCTAATTCCAA
		Reverse	GCGAAACGCTTCTTCAGCAT
AY611496	*PhBPBT*	Forward	AGTGATGCACCCGGTCTTGT
		Reverse	CAATTCTCGGCACCACACTG
AY233465/ AY233466	*PhBSMT*	Forward	TTTTCAGTGGAGTGCCTGGTT
		Reverse	GGCACCTGAGATAGCCACATG
HM447144	*PhC4H1*	Forward	AGCAGGTGTAACAAACTGCAA
		Reverse	AAACTGGGACAGGGATAGGA
HM447145	*PhC4H2*	Forward	AACTTGTCCAAACAAAAATGGA
		Reverse	TGGCAATTTAAAACGTTTGCT
AY705977	*PhIGS1*	Forward	GCCTATGTCATGCCATTGAA
		Reverse	TGCTTTAATTGTGTAGGCTGC
HM447143	*PhMYB4*	Forward	AACAATTTCTTTTGCTGCTGGAA
		Reverse	TTCATCGTCCTTGATTTGTTCAA
DQ243784	*PhPAAS*	Forward	TCCTTGTAGTTCTAGTACTGCTGGAA
		Reverse	TCAACAGCAGTTGTTGAAGTAGTTC
DQ767969	*PhCFAT*	Forward	AGGCAACTCGCAATGGAAGT
		Reverse	AGGCGCTGAAACACTCCAAT
FJ657663	*PhKAT1*	Forward	GCCCCACCATTCACATTAAC
		Reverse	GCCCCACCATTCACATTAAC
AY705977	*PhODO1*	Forward	TGCTTCAACCATGTCGAATTG
		Reverse	TCCGTGCCTGTTCTCTACGTT

Figure S1. A schematic of the *PhAAE* cloning strategy. SMART-RACE cloning kit (Clontech, Mountain View, CA) was used according to the manufacturer's specifications. In brief: a 5' cDNA library (universal adapter linked to the guanine cap, UA) and a 3' cDNA library (universal adapter linked to the poly-adenylated tail, UA) were generated from total RNA isolated from MD petal tissue. *PhAAE* specific primers (GSP-F and GSP-R) were designed from the EST sequence information available for *PhAAE*. The 'north' section of the PhAAE transcript was amplified and cloned out of the 5' library, and the 'south' section was amplified and cloned out of the 3' library. From these sections primers were designed outside of the coding sequence (CDS) and the entire *PhAAE* CDS was amplified and cloned into a pGEM®-T Easy vector (Promega, Madison, WI) from a general cDNA population produced from MD petal tissue. The CDS construct was sequenced extensively (UF ICBR sequencing core, Gainesville, FL).

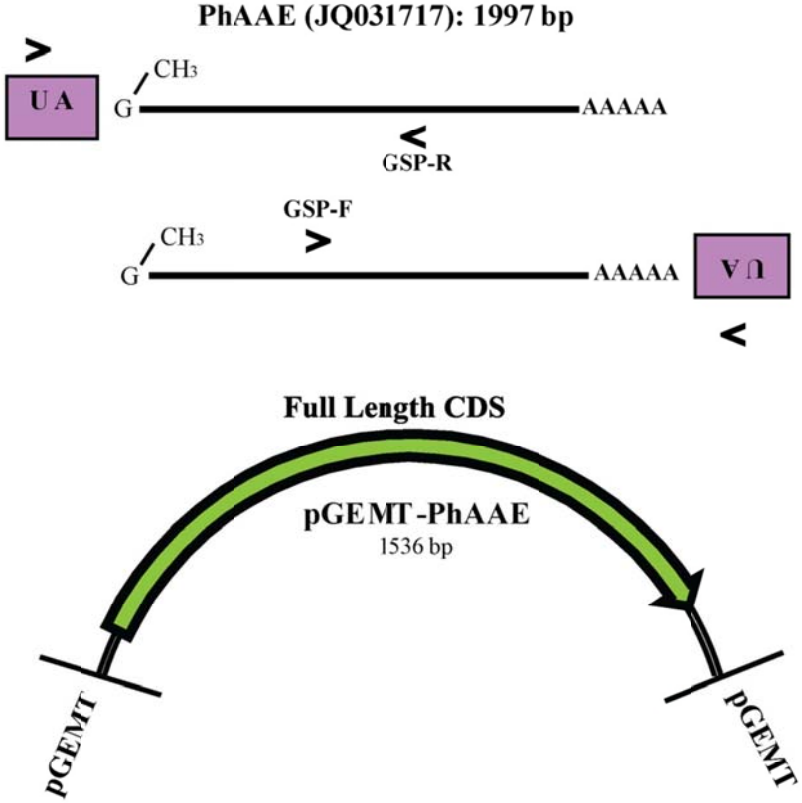
Figure S2. A comparative *PhAAE* transcript accumulation analysis with MD and 44568 (sqRT-PCR). Floral developmental analysis used MD and ethylene-insensitive 44568 flowers from 11 sequential stages collected on one day at 16:00 h (A). Ethylene treatment (two uL L^{-1}) analysis used excised MD (B) and 44568 (C) whole flowers treated for 0, 1, 2, 4, and 8 h. Total RNA was isolated, purified, and quantified. 50 ng of total RNA for each sample was used for sqRT-PCR reactions. Transcript specific primers for *PhAAE* were used with 27 cycles of amplification. *Ph18S* was used as a loading control with 18 cycles of amplification.

Figure S3. PhAAE recombinant protein expression in *E. coli* BL21/(DE3) cells. A 10% SDS-PAGE gel image of proteins from a standard protein ladder (1), cell fractions representing a non-induced culture harboring pET32-PhAAE (2), an induced (1 mM IPTG at 37^0C for 18 H) culture harboring pET32-PhAAE (3), soluble fraction of the induced culture (4), insoluble pellet fraction from induced culture (5), and soluble fraction after inclusion body isolation and His-Bind® resin purification (6). Prediction models estimate the TRX-PhAAE fusion protein to be approximately 78 kilo Daltons (KDa).

Figure S4. Schematic representation of the full-length *PhAAE* transcript model as shown in Vector NTI Advance™ 11. Depicted are the 5' and 3' untranslated regions (UTR), the coding sequence (CDS), the RNAi induction sequence region used for generating the *ir-PhAAE* plants, the highly conserved AMP-binding site (IPR020845), and the AMP-dependent synthase/ligase domain (IPR000873).

Figure S5. Comparative sqRT-PCR transcript accumulation analysis. MD and *ir-PhAAE* T_0 flowers were developmentally staged and collected at 16:00 H, total RNA was isolated, purified, and quantified. 50 ng of total RNA for each sample was used for sqRT-PCR reactions. Transcript specific primers for *PhAAE* were used with 24 cycles of amplification. *Ph18S* was used as a loading control with 15 cycles of amplification. All *ir-PhAAE* T_0 individuals are a result of an independent transformation event.

Figure S6. FVBP emission analysis of representative plants from MD, *ir-PhMYB4*, *ir-PhAAE*, and resulting progeny from crossing *ir-PhMYB4* and *ir-PhAAE*. Developmentally staged flowers (stage 8) were used to collect FVBP emission at 18:00 h (mean ± se; n = 3). Four major FVBP compounds were identified and quantified with all measurements ng/g fresh weight/hour. Figure S1.

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          F  P  T  N  K  I  T  K  P  R  T  K  H  I  S  A  V  Q  S  P  P  S  T  T  K  W  N  L  E  S  W  K  T  K  P  A  F  Q  L  P
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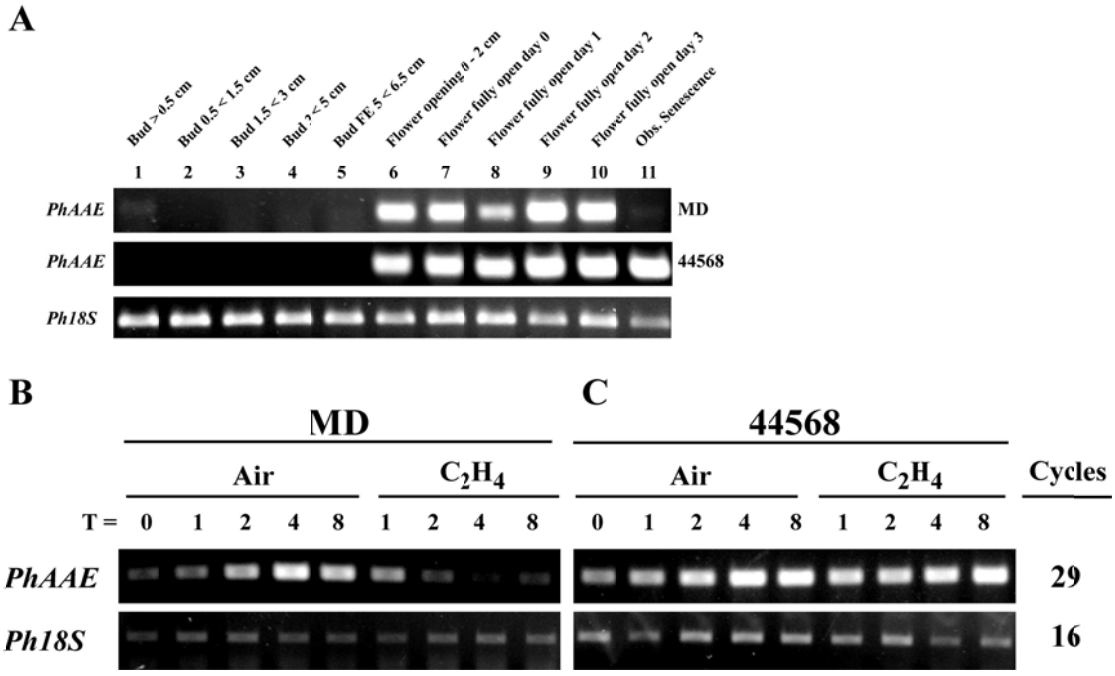
Figure S2.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Bud 0.5 < 1.5 cm
Bud 1.5 < 3 cm
Bud ? < 5 cm
Bud FE 5 < 6.5 cm
Flower opening 0 - 2 cm
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Flower fully open day 1
Flower fully open day 2
Flower fully open day 3
Obs. Senescence
1 2 3 4 5 6 7 8 9 10 11
PhAAE
MD
PhAAE
44568
Ph18S
B
MD
C
44568
Air
C2H4
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C2H4
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Ph18S
16

Figure S3.

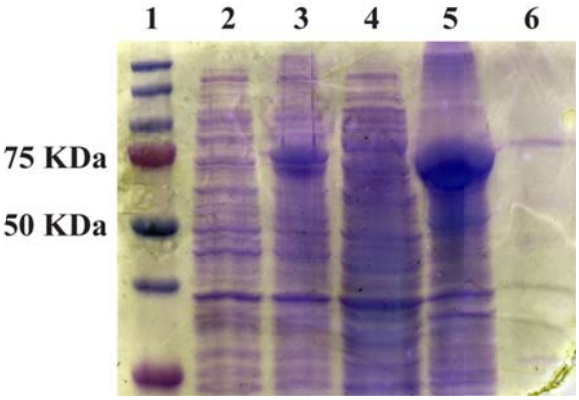
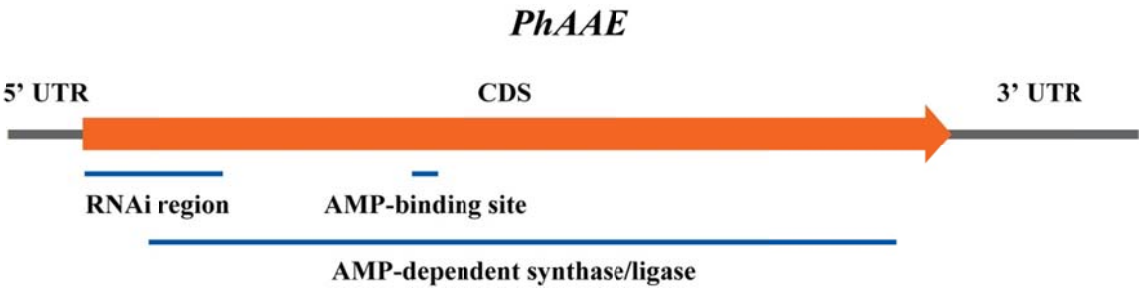


Figure S4.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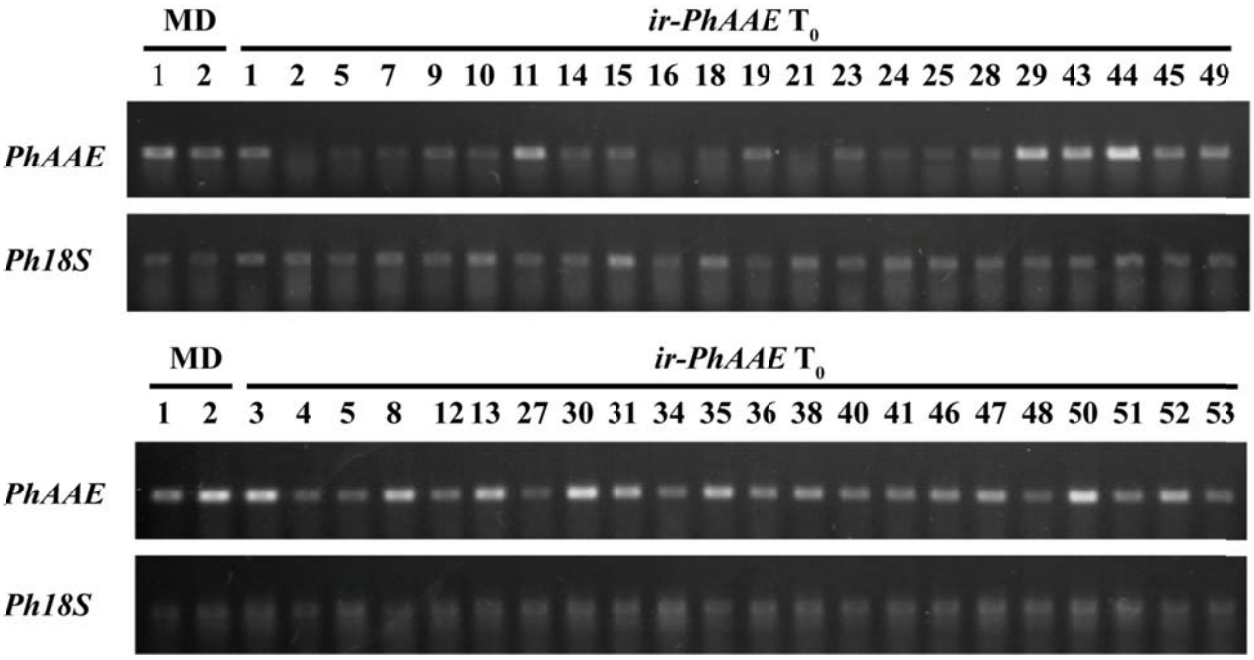
CDS
3' UTR
RNAi region
AMP-binding site
AMP-dependent synthase/ligase

Figure S5.


MD
ir-PhAAE T0
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PhAAE
Ph18S
MD
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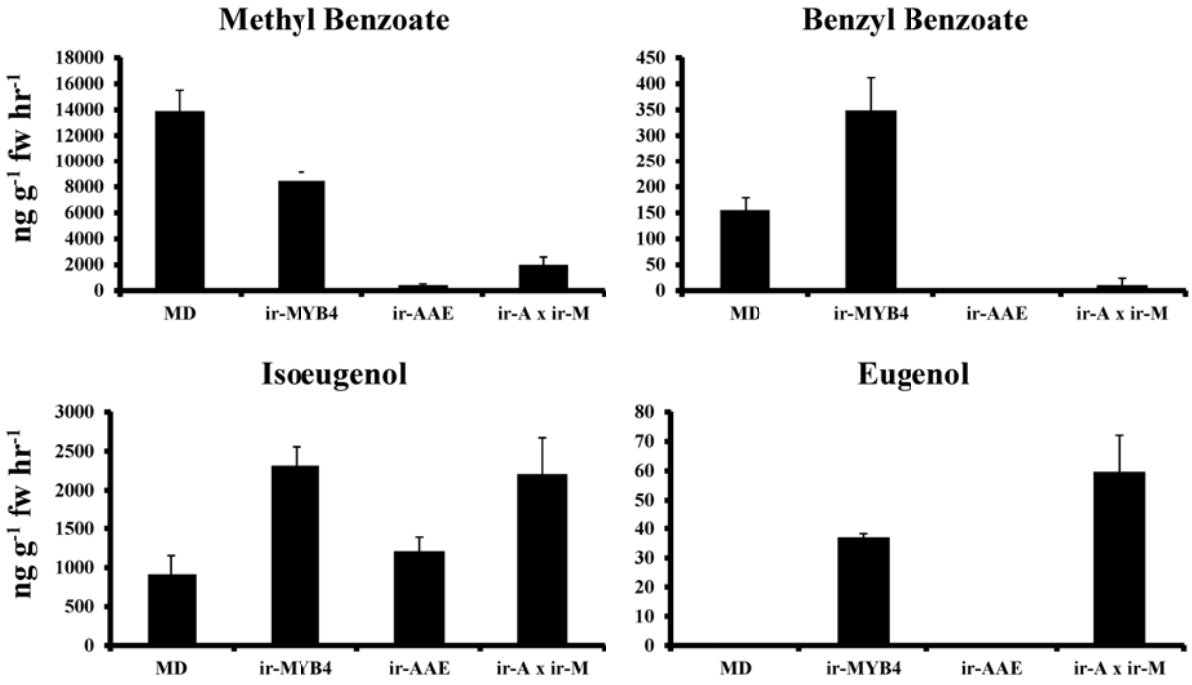
PhAAE
Ph18S

Figure S6.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16000
14000
12000
10000
8000
6000
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2000
0
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ir-AAE
ir-A x ir-M
Benzyl Benzoate
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400
350
300
250
200
150
100
50
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ir-AAE
ir-A x ir-M
Isoeugenol
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3000
2500
2000
1500
1000
500
0
MD
ir-MYB4
ir-AAE
ir-A x ir-M
Eugenol
80
70
60
50
40
30
20
10
0
MD
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ir-A x ir-M