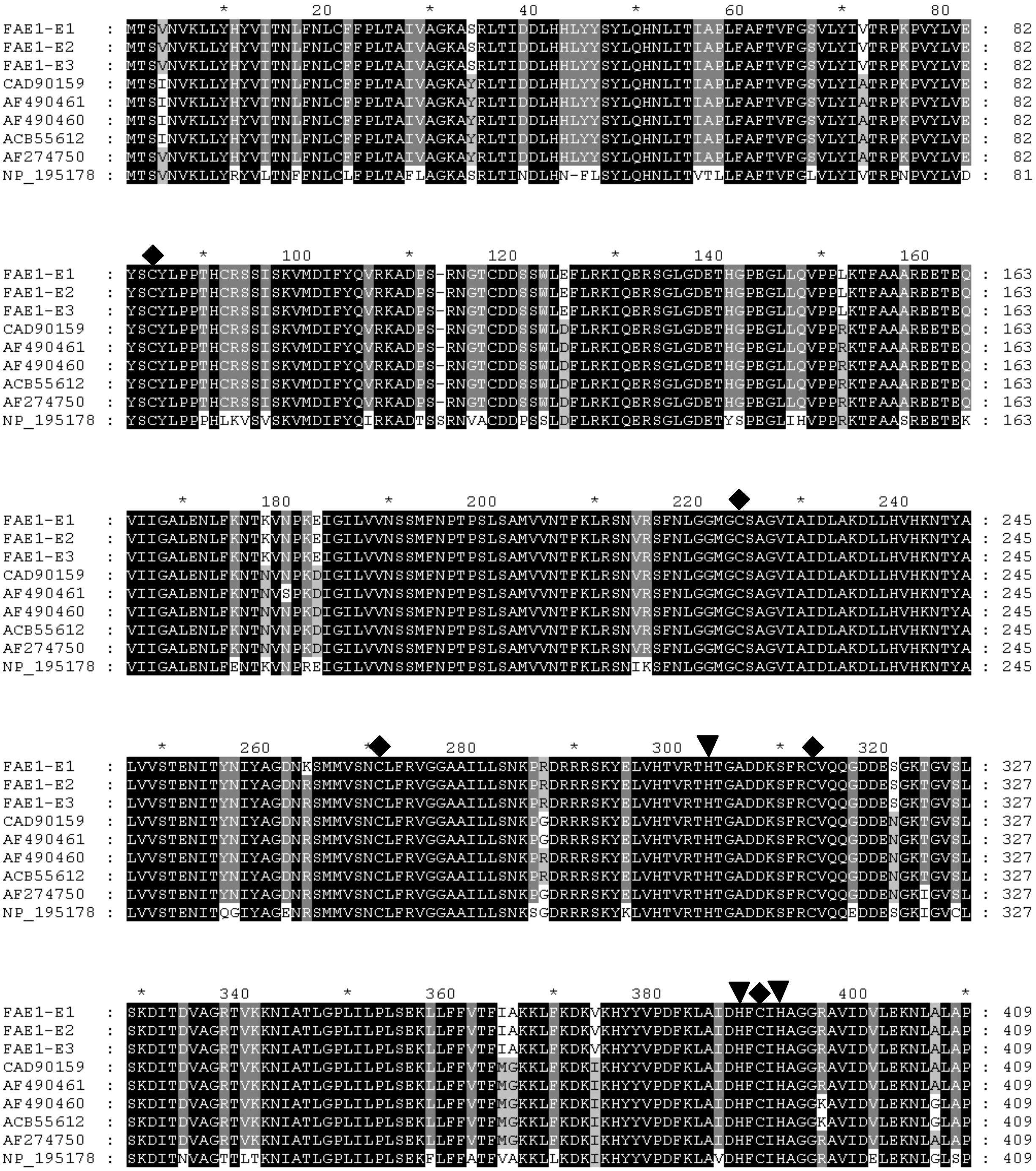
Supplemental Data. Zeng and Cheng (2014). Plant Cell 10.1105/tpc.114.126631



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FAE1-E2   : MTSVNVKLLYHYVITNLFNLCFFPLTAIVAGKASRLTIDDLHHLYYSYLQHNLITIAPLFAFTVFGSVLYIVTRPKPVYLVE :  82
FAE1-E3   : MTSVNVKLLYHYVITNLFNLCFFPLTAIVAGKASRLTIDDLHHLYYSYLQHNLITIAPLFAFTVFGSVLYIVTRPKPVYLVE :  82
CAD90159  : MTSINVKLLYHYVITNLFNLCFFPLTAIVAGKAYRLTIDDLHHLYYSYLQHNLITIAPLFAFTVFGSVLYIATRPKPVYLVE :  82
AF490461  : MTSINVKLLYHYVITNLFNLCFFPLTAIVAGKAYRLTIDDLHHLYYSYLQHNLITIAPLFAFTVFGSVLYIATRPKPVYLVE :  82
AF490460  : MTSINVKLLYHYVITNLFNLCFFPLTAIVAGKAYRLTIDDLHHLYYSYLQHNLITIAPLFAFTVFGSVLYIATRPKPVYLVE :  82
ACB55612  : MTSINVKLLYHYVITNLFNLCFFPLTAIVAGKAYRLTIDDLHHLYYSYLQHNLITIAPLFAFTVFGSVLYIATRPKPVYLVE :  82
AF274750  : MTSVNVKLLYHYVITNLFNLCFFPLTAIVAGKAYRLTIDDLHHLYYSYLQHNLITIAPLFAFTVFGSVLYIATRPKPVYLVE :  82
NP_195178 : MTSVNVKLLYRYVLTNFFNLCLFPLTAFLAGKASRLTINDLHN-FLSYLQHNLITVTLLFAFTVFGLVLYIVTRPNPVYLVD :  81

                   *       100         *       120         *       140         *       160
FAE1-E1   : YSCYLPPTHCRSSISKVMDIFYQVRKADPS-RNGTCDDSSWLEFLRKIQERSGLGDETHGPEGLLQVPPLKTFAAAREETEQ : 163
FAE1-E2   : YSCYLPPTHCRSSISKVMDIFYQVRKADPS-RNGTCDDSSWLEFLRKIQERSGLGDETHGPEGLLQVPPLKTFAAAREETEQ : 163
FAE1-E3   : YSCYLPPTHCRSSISKVMDIFYQVRKADPS-RNGTCDDSSWLEFLRKIQERSGLGDETHGPEGLLQVPPLKTFAAAREETEQ : 163
CAD90159  : YSCYLPPTHCRSSISKVMDIFYQVRKADPS-RNGTCDDSSWLDFLRKIQERSGLGDETHGPEGLLQVPPRKTFAAAREETEQ : 163
AF490461  : YSCYLPPTHCRSSISKVMDIFYQVRKADPS-RNGTCDDSSWLDFLRKIQERSGLGDETHGPEGLLQVPPRKTFAAAREETEQ : 163
AF490460  : YSCYLPPTHCRSSISKVMDIFYQVRKADPS-RNGTCDDSSWLDFLRKIQERSGLGDETHGPEGLLQVPPRKTFAAAREETEQ : 163
ACB55612  : YSCYLPPTHCRSSISKVMDIFYQVRKADPS-RNGTCDDSSWLDFLRKIQERSGLGDETHGPEGLLQVPPRKTFAAAREETEQ : 163
AF274750  : YSCYLPPTHCRSSISKVMDIFYQVRKADPS-RNGTCDDSSWLDFLRKIQERSGLGDETHGPEGLLQVPPRKTFAAAREETEQ : 163
NP_195178 : YSCYLPPPHLKVSVSKVMDIFYQIRKADTSSRNVACDDPSSLDFLRKIQERSGLGDETYSPEGLIHVPPRKTFAASREETEK : 163

                  *       180         *       200         *       220         *       240
FAE1-E1   : VIIGALENLFKNTKVNPKEIGILVVNSSMFNPTPSLSAMVVNTFKLRSNVRSFNLGGMGCSAGVIAIDLAKDLLHVHKNTYA : 245
FAE1-E2   : VIIGALENLFKNTKVNPKEIGILVVNSSMFNPTPSLSAMVVNTFKLRSNVRSFNLGGMGCSAGVIAIDLAKDLLHVHKNTYA : 245
FAE1-E3   : VIIGALENLFKNTKVNPKEIGILVVNSSMFNPTPSLSAMVVNTFKLRSNVRSFNLGGMGCSAGVIAIDLAKDLLHVHKNTYA : 245
CAD90159  : VIIGALENLFKNTNVNPKDIGILVVNSSMFNPTPSLSAMVVNTFKLRSNVRSFNLGGMGCSAGVIAIDLAKDLLHVHKNTYA : 245
AF490461  : VIIGALENLFKNTNVSPKDIGILVVNSSMFNPTPSLSAMVVNTFKLRSNVRSFNLGGMGCSAGVIAIDLAKDLLHVHKNTYA : 245
AF490460  : VIIGALENLFKNTNVNPKDIGILVVNSSMFNPTPSLSAMVVNTFKLRSNVRSFNLGGMGCSAGVIAIDLAKDLLHVHKNTYA : 245
ACB55612  : VIIGALENLFKNTNVNPKDIGILVVNSSMFNPTPSLSAMVVNTFKLRSNVRSFNLGGMGCSAGVIAIDLAKDLLHVHKNTYA : 245
AF274750  : VIIGALENLFKNTNVNPKDIGILVVNSSMFNPTPSLSAMVVNTFKLRSNVRSFNLGGMGCSAGVIAIDLAKDLLHVHKNTYA : 245
NP_195178 : VIIGALENLFENTKVNPREIGILVVNSSMFNPTPSLSAMVVNTFKLRSNIKSFNLGGMGCSAGVIAIDLAKDLLHVHKNTYA : 245

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FAE1-E1   : LVVSTENITYNIYAGDNKSMMVSNCLFRVGGAAILLSNKPRDRRRSKYELVHTVRTHTGADDKSFRCVQQGDDESGKTGVSL : 327
FAE1-E2   : LVVSTENITYNIYAGDNRSMMVSNCLFRVGGAAILLSNKPRDRRRSKYELVHTVRTHTGADDKSFRCVQQGDDESGKTGVSL : 327
FAE1-E3   : LVVSTENITYNIYAGDNRSMMVSNCLFRVGGAAILLSNKPRDRRRSKYELVHTVRTHTGADDKSFRCVQQGDDESGKTGVSL : 327
CAD90159  : LVVSTENITYNIYAGDNRSMMVSNCLFRVGGAAILLSNKPGDRRRSKYELVHTVRTHTGADDKSFRCVQQGDDENGKTGVSL : 327
AF490461  : LVVSTENITYNIYAGDNRSMMVSNCLFRVGGAAILLSNKPGDRRRSKYELVHTVRTHTGADDKSFRCVQQGDDENGKTGVSL : 327
AF490460  : LVVSTENITYNIYAGDNRSMMVSNCLFRVGGAAILLSNKPRDRRRSKYELVHTVRTHTGADDKSFRCVQQGDDENGKTGVSL : 327
ACB55612  : LVVSTENITYNIYAGDNRSMMVSNCLFRVGGAAILLSNKPRDRRRSKYELVHTVRTHTGADDKSFRCVQQGDDENGKTGVSL : 327
AF274750  : LVVSTENITYNIYAGDNRSMMVSNCLFRVGGAAILLSNKPGDRRRSKYELVHTVRTHTGADDKSFRCVQQGDDENGKIGVSL : 327
NP_195178 : LVVSTENITQGIYAGENRSMMVSNCLFRVGGAAILLSNKSGDRRRSKYKLVHTVRTHTGADDKSFRCVQQEDDESGKIGVCL : 327

              *       340         *       360         *       380         *       400        *
FAE1-E1   : SKDITDVAGRTVKKNIATLGPLILPLSEKLLFFVTFIAKKLFKDKVKHYYVPDFKLAIDHFCIHAGGRAVIDVLEKNLALAP : 409
FAE1-E2   : SKDITDVAGRTVKKNIATLGPLILPLSEKLLFFVTFIAKKLFKDKVKHYYVPDFKLAIDHFCIHAGGRAVIDVLEKNLALAP : 409
FAE1-E3   : SKDITDVAGRTVKKNIATLGPLILPLSEKLLFFVTFIAKKLFKDKVKHYYVPDFKLAIDHFCIHAGGRAVIDVLEKNLALAP : 409
CAD90159  : SKDITDVAGRTVKKNIATLGPLILPLSEKLLFFVTFMGKKLFKDKIKHYYVPDFKLAIDHFCIHAGGRAVIDVLEKNLALAP : 409
AF490461  : SKDITDVAGRTVKKNIATLGPLILPLSEKLLFFVTFMGKKLFKDKIKHYYVPDFKLAIDHFCIHAGGRAVIDVLEKNLALAP : 409
AF490460  : SKDITDVAGRTVKKNIATLGPLILPLSEKLLFFVTFMGKKLFKDKIKHYYVPDFKLAIDHFCIHAGGKAVIDVLEKNLGLAP : 409
ACB55612  : SKDITDVAGRTVKKNIATLGPLILPLSEKLLFFVTFMGKKLFKDKIKHYYVPDFKLAIDHFCIHAGGKAVIDVLEKNLGLAP : 409
AF274750  : SKDITDVAGRTVKKNIATLGPLILPLSEKLLFFVTFMGKKLFKDKIKHYYVPDFKLAIDHFCIHAGGRAVIDVLEKNLALAP : 409
NP_195178 : SKDITNVAGTTLTKNIATLGPLILPLSEKFLFFATFVAKKLLKDKIKHYYVPDFKLAVDHFCIHAGGRAVIDELEKNLGLSP : 409
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                   420▼        *       440         *       460◆        *       480         *
FAE1-E1   : IDVEASRSTLHRFGNTSSSSIWYELAYIEAKGRMKKGNKVWQIALGSGFKCNSAVWVALSNVKASTNSPWEHCIDRYPVQID : 491
FAE1-E2   : IDVEASRSTLHRFGNTSSSSIWYELAYIEAKGRMKKGNKVWQIALGSGFKCNSAVWVALSNVKASTNSPWEHCIDRYPVQID : 491
FAE1-E3   : IDVEASRSTLHRFGNTSSSSIWYELAYIEAKGRMKKGNKVWQIALGSGFKCNSAVWVALSNVKASTNSPWEHCIDRYPVQID : 491
CAD90159  : IDVEASRSTLHRFGNTSSSSIWYELAYIEAKGRMKKGNKVWQIALGSGFKCNSAVWVALNNVKASTNSPWEHCIDRYPVKID : 491
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ACB55612  : IDVEASRSTLHRFGNTSSSSIWYELAYIEAKGRMKKGNKVWQIALGSGFKCNSAVWVALNNVKASTNSPWEHCIDRYPVKID : 491
AF274750  : IDVEASRSTLHRFGNTSSSSIWYELAYIEAKGRMKKGNKVWQIALGSGFKCNSAVWVALNNVKASTNSPWEHCIDRYPVKID : 491
NP_195178 : IDVEASRSTLHRFGNTSSSSIWYELAYIEAKGRMKKGNKAWQIALGSGFKCNSAVWVALRNVKASANSPWQHCIDRYPVKID : 491


                 500
FAE1-E1   : SDSAKSETRVQNGRS : 506
FAE1-E2   : SDSAKSETRVQNGRS : 506
FAE1-E3   : SDSAKSETRVQNGRS : 506
CAD90159  : SDSGKSETRVQNGRS : 506
AF490461  : SDSGKSETRVQNGRS : 506
AF490460  : SDSGKSETRAQNGRS : 506
ACB55612  : SDSGKSETRVQNGRS : 506
AF274750  : SDSGKSETRVQNGRS : 506
NP_195178 : SDLSKSKTHVQNGRS : 506
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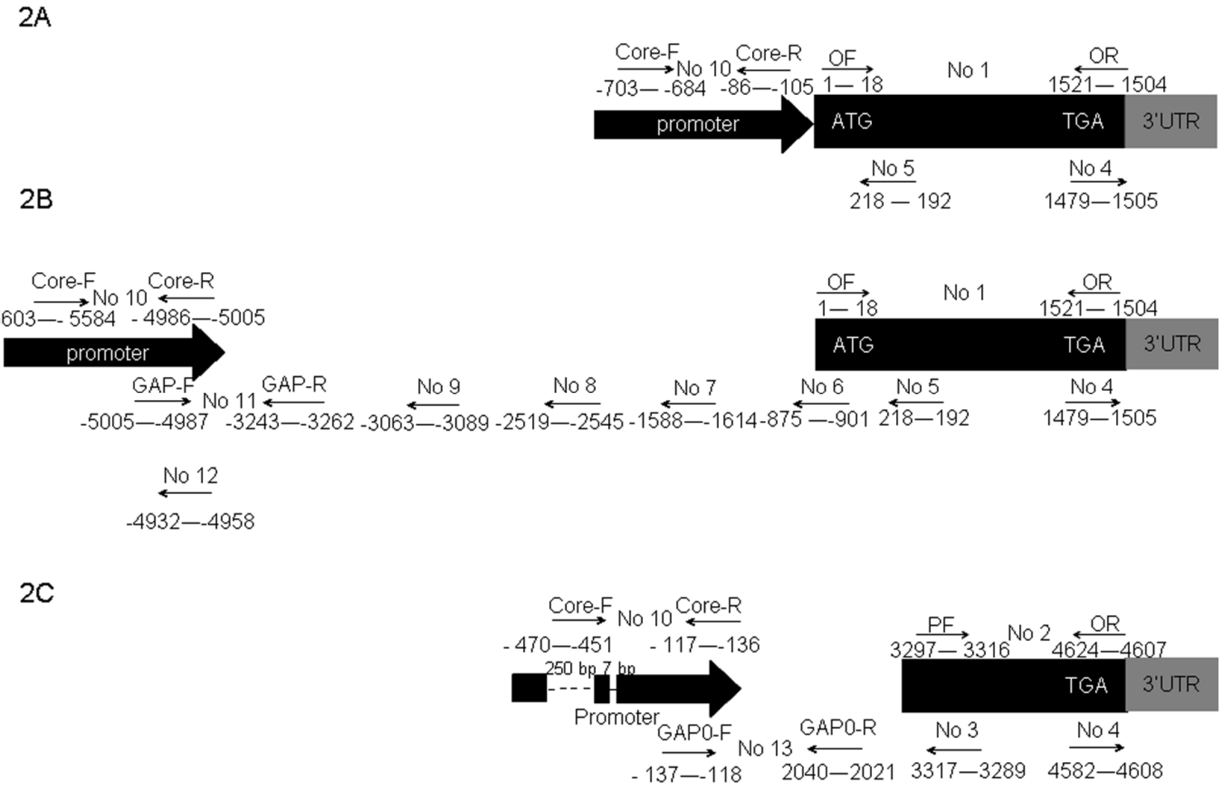
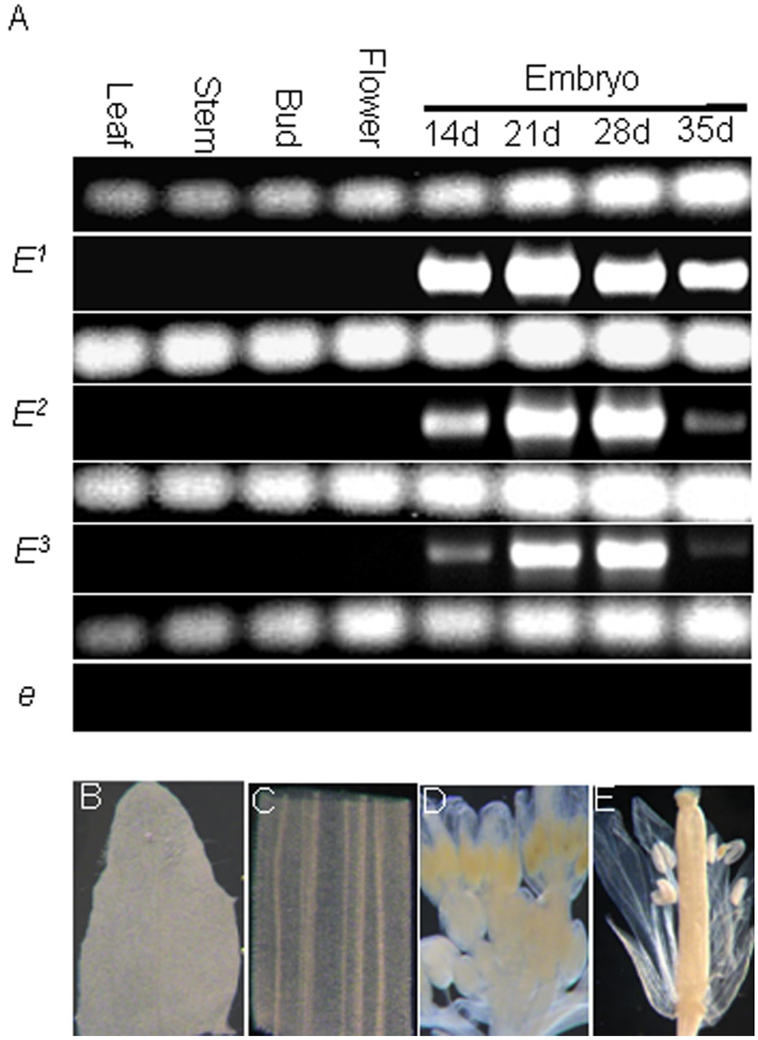
Supplemental Figure 1. Alignment of amino acid sequences encoded by the *FAE1* alleles *E*^{1}, *E*^{2} and *E*^{3} of yellow mustard, CAD90159 of *B. juncea*, AF490461 of *B. rapa*, AF490460 of *B.oleracea*, ACB55612 and AF274750 of *B. napus* and NP_195178 of *Arabidopsis*.

The amino acid sequence alignment was carried out using the ClustalW program (http://www.ebi.ac.uk/Tools/msa/clustalw2/). Conserved cysteine and histidine residues are indicated by a diamond and a triangle, respectively.



Supplemental Figure 2. Schematic diagram showing the position of each primer used for cloning of the *FAE1* alleles *E*^{1}, *E*^{2}, *E*^{3} and *e*.

(**A)** Primers used for cloning the *FAE1* allele *E*^{1}. (**B)** Primers used for cloning the *FAE1* allele *E*^{2} and *E*^{3}. **C.** Primers used for cloning the *FAE1* allele *e*. Arrows indicated the direction of the primers. The number under each arrow indicates its nucleotide position. The “A” of translation start codon ATG represents the first nucleotide.



Supplemental Figure 3. Expression pattern of the *FAE1* alleles E^1, E^2 and E^3.
(**A)** The *FAE1* alleles E^1, E^2 and E^3 were expressed in 14-35d old embryos, but not in the vegetative tissues of leaf, stem, bud and flower as revealed by RT-PCR. The *FAE1* allele *e* was not expressed in the embryo or vegetative tissues. Actin (FG576123) was used as an internal control. (**B-E)** GUS activity was not detected in leaf (**B**), stem (**C**), bud (**D**) or flower (**E**) of transgenic *Arabidopsis* plants containing the construct pBI101 Pro^{E1}-GUS with the promoter of the *FAE1* allele E^1.

TATTACGATATATGTTATATCGTATATTCTATGCACTCGATAATATTAACTTTCCTATT
GTTTAGCTAGAGATAAGTATAGTTTCCTATTTATCGACAGAAAGGTTTATACTAAAC
CGTCATAGAACTTGTATATAATGCAAAGTTAGCATAACTTAATAAACAAGTCAGTTT
GATATCTTATTCTACATGGTATCAGAGCTGAGATCTCTTTGATTCTCTTGCTTAAAAT
PBS
CGAGTTCTTGTTCAAAGTTTGAACAAATTGTCTATCGTCGGTGACGATGTCTGTCGA
AAGTTCTGAAGTTAAGAACACACCCGAGAAGAGTACGAGAGATGTATCGTCTCTTC
CATCCCCGTACATCTTGTATGGTTCCGATAATCCCGGAGCCATGATTACTCCAGTC
ATGTTGAACGGAGAGAACTACAATCAATGGGCTAACGAGATGCTTAATGCGCTTCA
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CAAATCAAAGCACAGCTGGCAGCCTGTCGACAGGAAGGTCAAAGTGTGCTTGAAT
ACTATGGgAAAGTTGTGCACTCATTGGGAAGAACTCGACGTCTATCGACCTCTGCC
AATGTGTACGTGgTgGGGGCTGCTAAAGATATCAGAAAGGAAAGAGACGATGACAA
GGTCCACCAGTTCATAaTGGGTCTTGATGACTCACGGTTTGGGAGTCTTTGTACGT
CTCTAATCGGCATGGATCCCCTGCCATCGATCGGAGAAGTCTACTCCAAGGTAGTT
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AGAGATCGTGTGACAATTTGTTCACACTGTGGACGTCGAGGTCATGATAAGAAGGA
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GGCAGAGGCCAAGTAGCAGCAGCACACGCCACCAGCTCCAACCTTTCTGCCTTTC
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ACACAGTTGACGCATCTTCTGACCAATCACTGTGGCATCAGCGTTTAGGGCATCCT
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CCTCCAGTTCTGGTGGACTTGATCGATAGGGGGAGCTTGGCTGGTGTTACCCCTA
CAACTGATTCACCCGTTAACACAGCCAGTGGCAGTGAGAATTTATCACCTTTAGCC
GACGAGAGTGATGATATTGATGAAGAAGTYACAACAGGAGCAGCTGATTTAACAGA
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TGAAGGACAACATACGTGGGATATTTGTGATCTTCCTCTCAACAAAACTGCGCTTG
GAAGCCAATGGGTCTATAAAATCAAATATAATACTGACGGTACTATTAGACGTCATA
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GACTACTTGGGAAAATGTTTTTCTATGAAGGATCTTGGCAAACTCAAGTATTTTCTA
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CAAGTATCGGAGGCTCGTAGGTCGTCTGCTCTATCTTGTTCACACCAGACCTGAGT
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TGGGATGCAGCTCAACGAGTTGTGCgGGTTTTTAAAAGGCTCACCTGGACAAGGC

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TCGCCTATCAGTTGGAAAACGAAGAAGCAGGACACAGTATCTCACTCTTCCGCAGA
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CAGCAATTTACATCGCCACTAACCCTGTCTTCCATGAACGTACTAAACATGTTGAAA
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TACGAACAAATGAGCAGATTGCGGACATTCTGACAAAGGCATTGGGACGAGCTCA
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GGGGAGTATTACGATATATGTTATATCGTATATTCTATGCACTCGATAATATTAACTT
PPT
TCCTATTGTTTAGCTAGAGATAAGTATAGTTTCCTATTTATCGACAGAAAGGTTTATA
CTAAACCGTCATAGAACTTGTATATAATGCAAAGTTAGCATAACTTAATAAACAAGT
CAGTTTGATATCTTATTCTACA

Supplemental Figure 4. DNA sequence of the retrotransposable element Sal-*T1* inserted in the 5' UTR of the *FAE1* alleles *E*^{2} and *E*^{3}.

The long terminal repeats (LTR) was highlighted in red. The motifs representing the primer binding site (PBS) and polypurine tract (PPT) are underlined, and highlighted in green and pink, respectively. Sequence annotation of the transposable element Sal-*T1* was predicted using GenScan at GeniusNet (http://genome.dkfz-heidelberg.de/cgi-in/GENSCAN/genscan.cgi). The start codon (ATG) and stop codon (TGA) are in red type. The open reading frame is highlighted in grey.

MSVESSEVKNTPEKSTRDVSSLPSPYILYGSDNPGAMITPVMLNGENYNQWANEMLN
ALQAKRKVCFINETLKKPATDDPDYDNWVAVNSMIIGWIRASIDPKIKASVTFVSEASLL
WTDLKQRFSVGNKVRIHQIKAQLAACRQEGQSVLEYYGKVVHSLGRTRRLSTSANVY
VVGAAKDIRKERDDDKVHQFIMGLDDSRFGSLCTSLIGMDPLPSIGEVYSKVVQEEQR
LSTFTKQRTAARDFTPDQWKVLTQLIQEKSGSDKLSGPFLEDSDWNRLHTATCLWVR
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VGIDVWDNSMVDEIVALEGQHTWDICDLPLNKTALGSQWVYKIKYNTDGTIRRHKSRV
VVMGNKQVEGEDYNETFAPVVKMTTVRMFLRLVAANQWEVFQMDVNNAFLHGDLDE
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FSYTRKGIQLHVLIYVDDLLISGNDRHMVQRFKDYLGKCFSMKDLGKLKYFLGIEVSRG
PEGIFLSQRNICRLRKKLTGMQLNELCGFLKGSPGQGIMLSSSTDLSLTIYCDSDWSSC
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FDIKQVSTRFFCDSKAAIYIATNPVFHERTKHVENDCHAVRDAVRDGLIILHHIRTNEQIA
DILTKALGRAQFTTLLSKLGVCDLHAPT

Supplemental Figure 5. The 959 amino acids of the deduced protein of the retrotransposable element Sal-*T1* predicted using GenScan at GeniusNet (http://genome.dkfz-heidelberg.de/cgi-in/GENSCAN/genscan.cgi).

The putative locations of gag integrase, reverse transcriptase and RNase H are highlighted in green, yellow, and red, respectively.

GAGCACCCTCATCGCTGGTGCTTAGGGGATTGCTTAACCTAATTTTGTGTTTAAAAT
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TCGGTGTTTGTCGTCGACGACATGGTCGATGAtTGTCTTCCTCACTGTGGGTCTCAT
CGTGGGCGGTGGACCGGTAAATCGTTGTTGCCTTTCCGCGAATCTGAAGGTAAAG
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CACCTTTTGGAAGGTGTATTTTGTTTCTTTTGTGTCAAGGTCATGTCATGTATTTTG
GAGTCACTTGGAGTCACTTGGAGTCAGTTGGAGTCATGTGTTTTGATCAATTGTGT
CACGGACTGTCCTTGGAGTCCCTTCTCCTTATGTAATTTGYAATCTAATTTTGTTTG
TAATATTGTGTCACGGATTTAGTTGTTATGTATGTTTGATGTACTATAAATTATTATC
AACTTCTCTTCTCTTTTCTCATCAATAGCAAAGCCAAATCATATCCTCTCTTCTCTCA
CCATTACCAAACCGAAATCATCTCTTCTCTTTTATCCATCTCCAAGATTCAAATAAAA
AAAAGTATGTCTTCTTCTTCTGAAAATACTTTTGAAGATTTATTTGATGATGCATTTG
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CTAAGTTGCTTAACCCAAATAAATTATTAAATACTATTAATTTTTAATTAAGCAaCCCA
TAATGGGtTGTTAGGATGAGGGTGCTC

Supplemental Figure 6. The sequence of the DNA transposon Sal-*PIF* inserted in the coding region of the *FAE1* allele *e*.

Sequence annotation of DNA transposon Sal-*PIF* was predicted using GenScan at GeniusNet (http://genome.dkfz-heidelberg.de/cgi-in/GENSCAN/genscan.cgi). ORF1: highlighted in grey; ORF2: highlighted in light blue. The start codon (ATG) and stop codon (TAA, TGA) are underlined. The terminal inverted repeats (TIRs) are highlighted in red.

7A

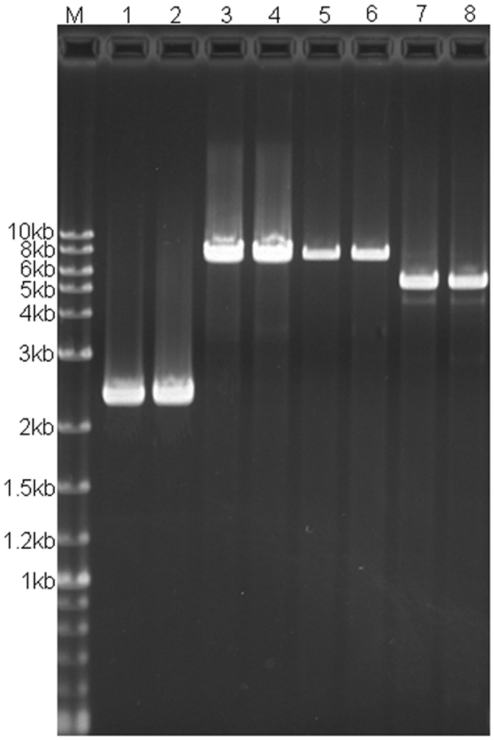
MTLTQKKQNTPSKRRIKVKRSKRRSFTRPIRGHRRPTIIELLLRRCERHHRAPPSPLFA
ERQQRFTGPPPTMRPTVRKTIIDHVVDDKHRDRMTGRRLRRRAT

7B

MSSSSENTFEDLFDDAFDQYFDQTFEKFTMGHQEEPRKXKKKRAYIERNREEGHIRL
WISLSPLQKCTAAIRVLAYGCAGDMVDEYLRLGETTTRLCVENFVEGVINLFGDEYLRR
PTPTDLQRLLDVGEYRGFPGMIGSIDCMHWEWKNCPTAWKGQYSRGSGKPTIVLEAV
ASYDLWIWHAFFGPPGTLNDINVLDRSPVFDDIIHGQAPPVTFSVNGRQYHMAYYLTD
GIYPKWATFIQSIRLPQVPKAVLFAQRQEAVRKDVERAFGVLQARFAIVKNPALFWDKV
KIGKIMRACIILHNMVVEDERDGYTQYDVSEFVQGEENRSSHVDLDFDRDIPSNIANTM
DARTRIRDKPMHQQLKHDLVEHIWHKFGGDEDNN

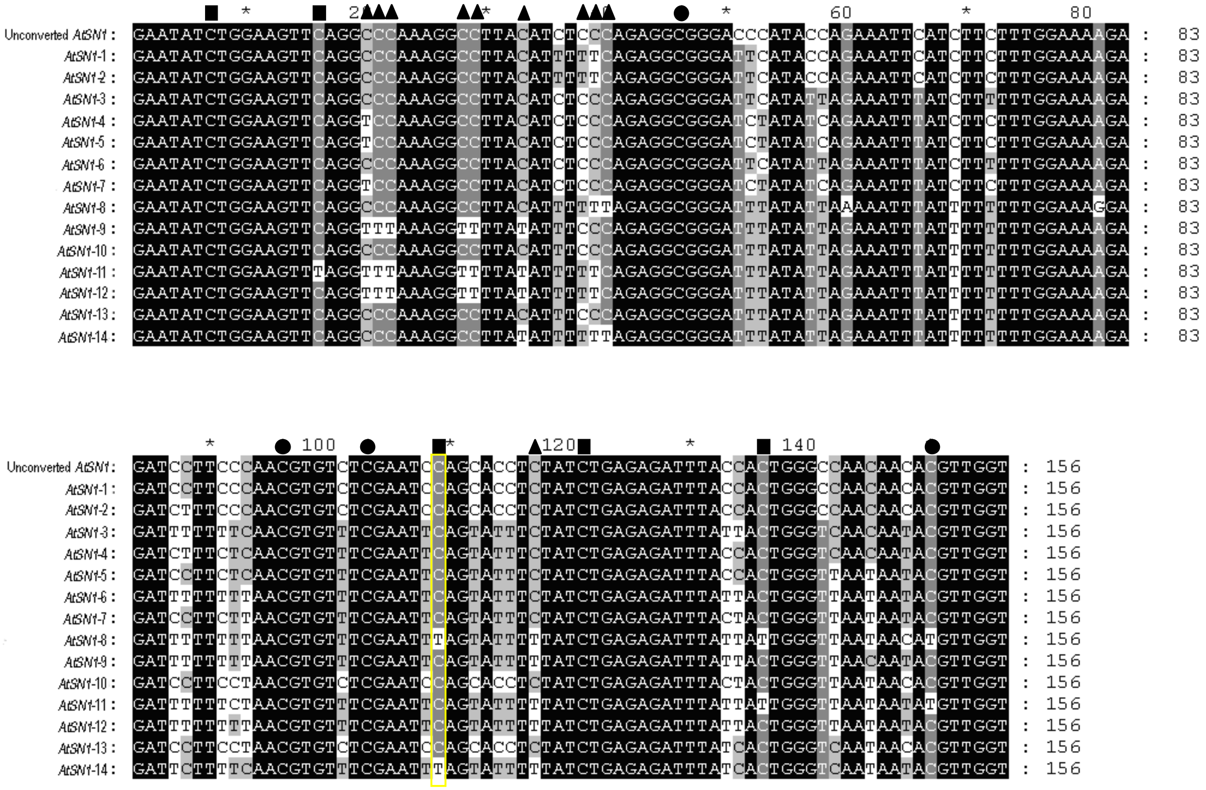
Supplemental Figure 7. Deduced amino acid sequences of the DNA transposon Sal-*PIF* predicted using GenScan at GeniusNet (http://genome.dkfz-heidelberg.de/cgi-in/GENSCAN/genscan.cgi).

(**A)** The 103 amino acids of the deduced protein of ORF1. (**B)** The 383 amino acids of the deduced protein of ORF2.



Supplemental Figure 8. PCR amplification of the entire *FAE1* alleles E^1, E^2, E^3 and *e* using the primer pair WF/WR No 14 (Supplemental Table 1 online).

M: 1 kb DNA ladder; Lanes 1 and 2: 2524 bp fragment of E^1; Lanes 3 and 4: 7424 bp fragment of E^2; Lanes 5 and 6: 7424 bp fragment of E^3; Lane 7 and 8: 5369 bp of *e*.



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          AtSN1-4 : GAATATCTGGAAGTTCAGGTCCAAAGGCCTTACATCTCCCAGAGGCGGGATCTATATCAGAAATTTATCTTCTTTGGAAAAGA  :  83
          AtSN1-5 : GAATATCTGGAAGTTCAGGTCCAAAGGCCTTACATCTCCCAGAGGCGGGATCTATATCAGAAATTTATCTTCTTTGGAAAAGA  :  83
          AtSN1-6 : GAATATCTGGAAGTTCAGGCCCAAAGGCCTTACATCTCCCAGAGGCGGGATTCATATTAGAAATTTATCTTTTTTGGAAAAGA  :  83
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          AtSN1-8 : GAATATCTGGAAGTTCAGGCCCAAAGGCCTTACATTTTTTAGAGGCGGGATTTATATTAAAAATTTATTTTTTTTGGAAAGGA  :  83
          AtSN1-9 : GAATATCTGGAAGTTCAGGTTTAAAGGTTTTATATTTCCCAGAGGCGGGATTTATATTAGAAATTTATTTTTTTTGGAAAAGA  :  83
         AtSN1-10 : GAATATCTGGAAGTTCAGGCCCAAAGGCCTTACATTTCCCAGAGGCGGGATTTATATTAGAAATTTATTTTTTTTGGAAAAGA  :  83
         AtSN1-11 : GAATATCTGGAAGTTTAGGTTTAAAGGTTTTATATTTTTCAGAGGCGGGATTTATATTAGAAATTTATTTTTTTTGGAAAAGA  :  83
         AtSN1-12 : GAATATCTGGAAGTTCAGGTTTAAAGGTTTTATATTTTTCAGAGGCGGGATTTATATTAGAAATTTATTTTTTTTGGAAAAGA  :  83
         AtSN1-13 : GAATATCTGGAAGTTCAGGCCCAAAGGCCTTACATTTCCCAGAGGCGGGATTTATATTAGAAATTTATTTTTTTTGGAAAAGA  :  83
         AtSN1-14 : GAATATCTGGAAGTTCAGGCCCAAAGGCCTTATATTTTTTAGAGGCGGGATTTATATTAGAAATTTATTTTTTTTGGAAAAGA  :  83

Unconverted AtSN1 : GATCCTTCCCAACGTGTCTCGAATCCAGCACCTCTATCTGAGAGATTTACCACTGGGCCAACAACACGTTGGT : 156
          AtSN1-1 : GATCCTTCCCAACGTGTCTCGAATCCAGCACCTCTATCTGAGAGATTTACCACTGGGCCAACAACACGTTGGT : 156
          AtSN1-2 : GATCTTTCCCAACGTGTCTCGAATCCAGCACCTCTATCTGAGAGATTTACCACTGGGCCAACAACACGTTGGT : 156
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         AtSN1-10 : GATCCTTCCTAACGTGTCTCGAATCCAGCACCTCTATCTGAGAGATTTACTACTGGGTTAATAACACGTTGGT : 156
         AtSN1-11 : GATTTTTTCTAACGTGTTTCGAATTCAGTATTTTTATCTGAGAGATTTATTATTGGGTTAATAATATGTTGGT : 156
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         AtSN1-13 : GATCCTTCCTAACGTGTCTCGAATCCAGCACCTCTATCTGAGAGATTTATCACTGGGTCAATAACACGTTGGT : 156
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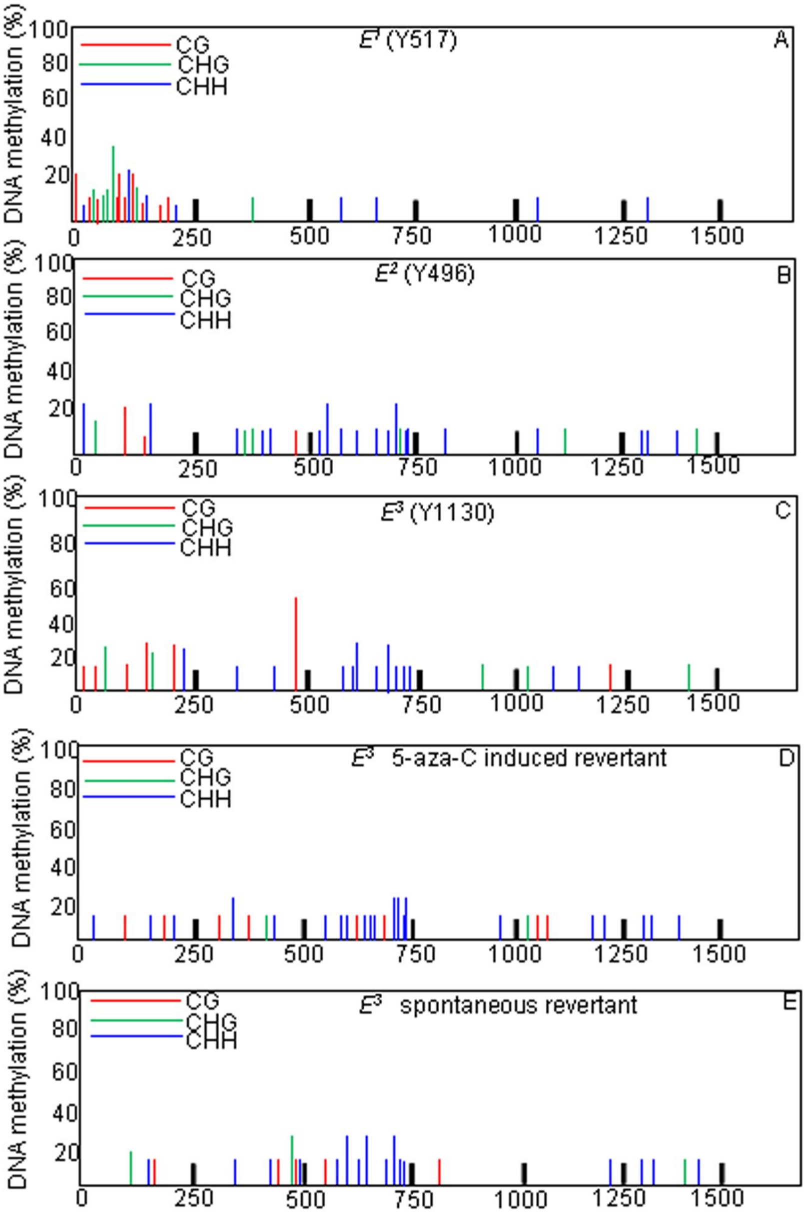
Supplemental Figure 9. DNA methylation in the internal region between the long terminal repeats of *AtSN1* (positive control).

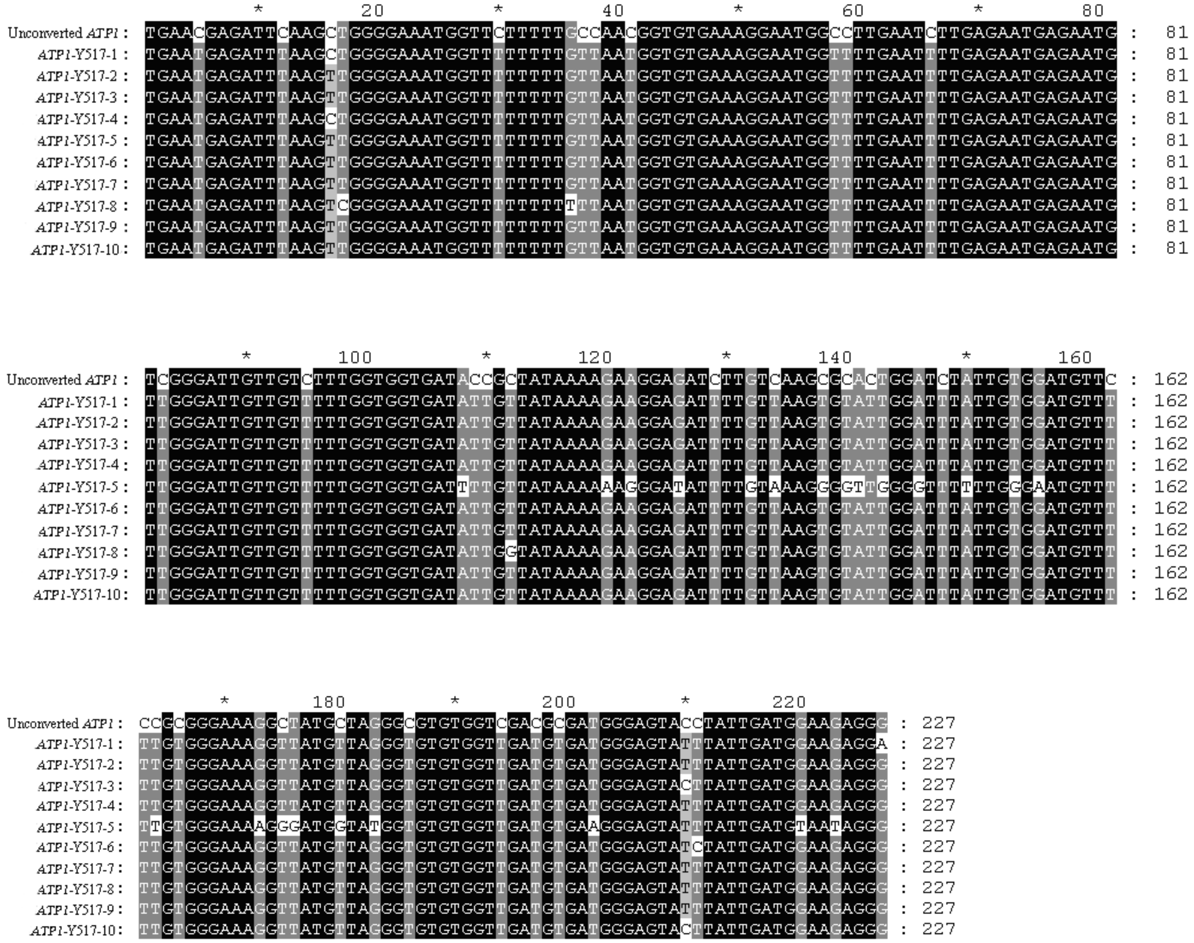
The known eighteen methylated cytosines as reported by Kuhlmann and Mette (2012), and one additional methylated cytosine (highlighted as yellow) were detected in the internal region between the long terminal repeats of *AtSN1* (positive control). Circle: CG; Rectangle: CHG; Triangle: CHH.



Supplemental Figure 10. DNA methylation in the coding regions of the *FAE1* alleles *E*^{1}, *E*^{2} and *E*^{3}.

DNA methylation was not detected in the 1515 bp coding region (nucleotides 1-1515) of *E*^{1} in Y517 (**A**), *E*^{2} in Y496 (**B**) and *E*^{3} in Y1130 (**C**), *E*^{3} in 5-azaC induced revertants of Y1130 (**D**) and *E*^{3} in spontaneous revertant of Y1130 (**E**).

11A



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ATP1-Y517-1 :	TGAATGAGATTTAAGCTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG	: 81
ATP1-Y517-2 :	TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG	: 81
ATP1-Y517-3 :	TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG	: 81
ATP1-Y517-4 :	TGAATGAGATTTAAGCTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG	: 81
ATP1-Y517-5 :	TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG	: 81
ATP1-Y517-6 :	TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG	: 81
ATP1-Y517-7 :	TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG	: 81
ATP1-Y517-8 :	TGAATGAGATTTAAGTCGGGGAAATGGTTTTTTTTTTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG	: 81
ATP1-Y517-9 :	TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG	: 81
ATP1-Y517-10 :	TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG	: 81

	* 100 * 120 * 140 * 160	
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	* 180 * 200 * 220	
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ATP1-Y517-1 :	TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATTTATTGATGGAAGAGGA	: 227
ATP1-Y517-2 :	TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATTTATTGATGGAAGAGGG	: 227
ATP1-Y517-3 :	TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTACTTATTGATGGAAGAGGG	: 227
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ATP1-Y517-8 :	TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATTTATTGATGGAAGAGGG	: 227
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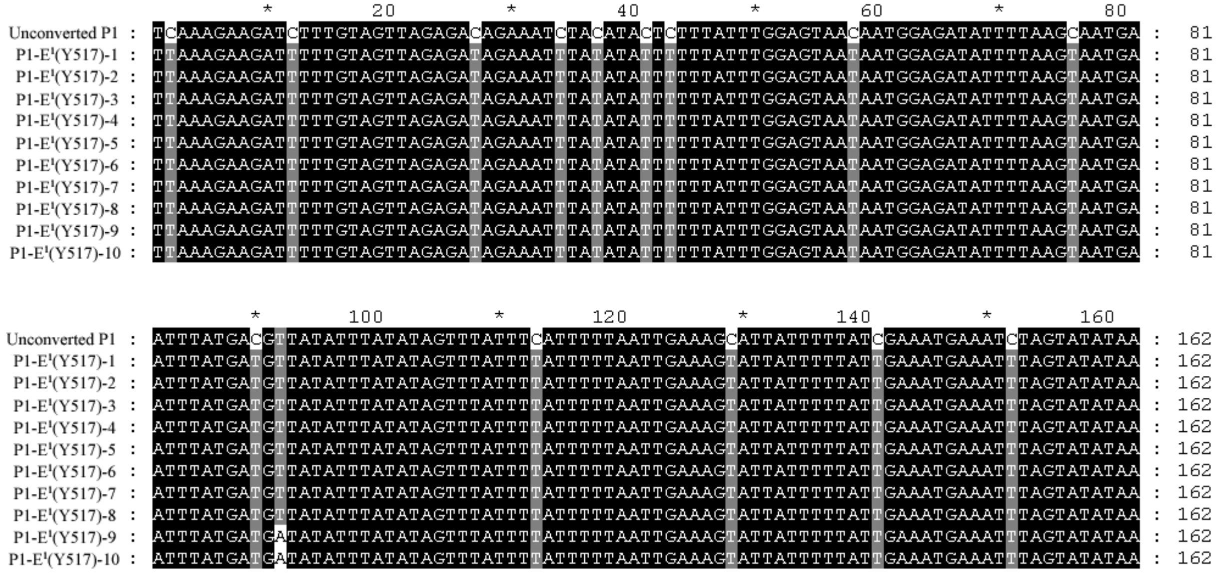
11B



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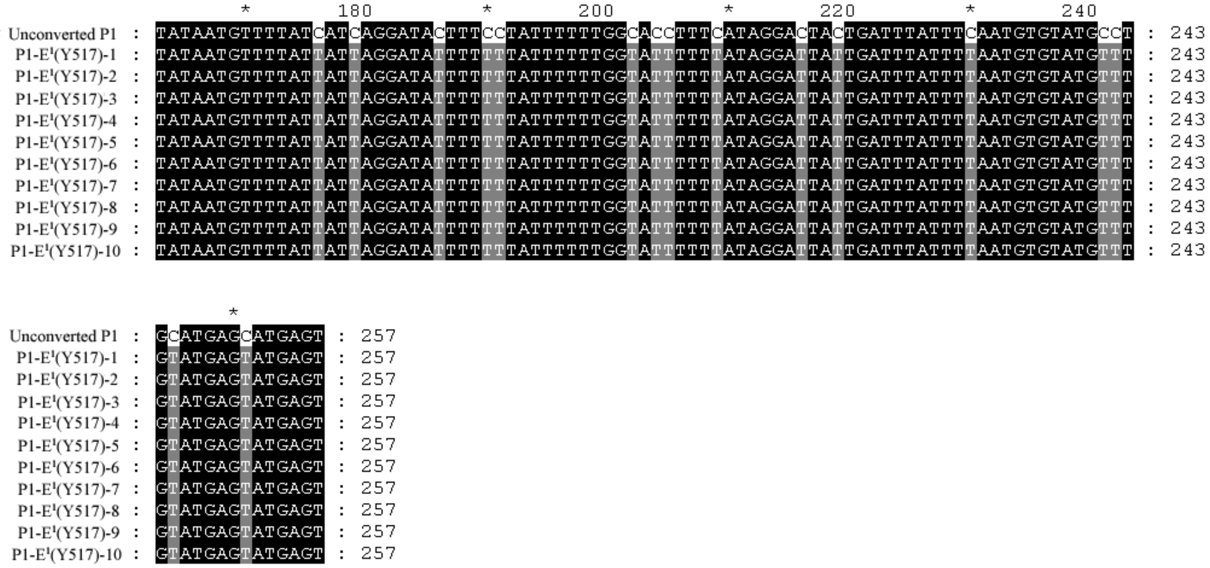
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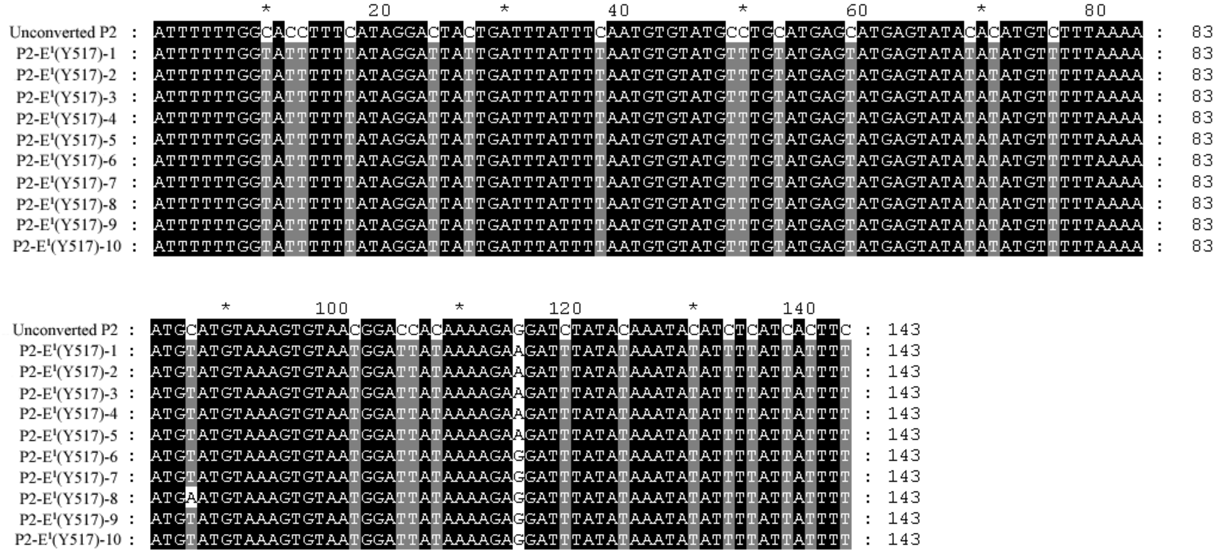
11C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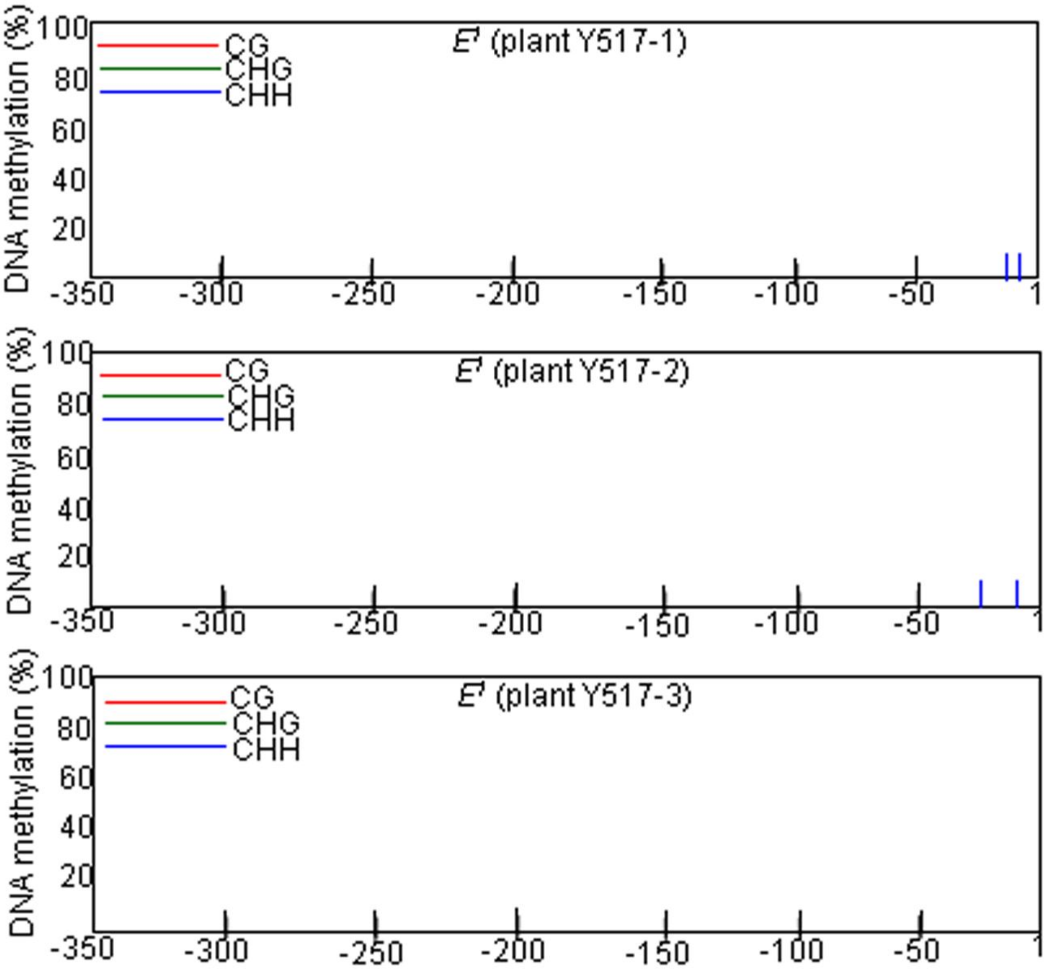
P2-E^{I}(Y517)-5 : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA : 83
P2-E^{I}(Y517)-6 : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA : 83
P2-E^{I}(Y517)-7 : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA : 83
P2-E^{I}(Y517)-8 : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA : 83
P2-E^{I}(Y517)-9 : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA : 83
P2-E^{I}(Y517)-10 : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA : 83
* 100 * 120 * 140
Unconverted P2 : ATGCATGTAAAGTGTAACGGACCACAAAAGAGGATCTATACAAATACATCTCATCACTTC : 143
P2-E^{I}(Y517)-1 : ATGTATGTAAAGTGTAATGGATTATAAAAGAAGATTTATATAAATATATTTTATTATTTT : 143
P2-E^{I}(Y517)-2 : ATGTATGTAAAGTGTAATGGATTATAAAAGAAGATTTATATAAATATATTTTATTATTTT : 143
P2-E^{I}(Y517)-3 : ATGTATGTAAAGTGTAATGGATTATAAAAGAAGATTTATATAAATATATTTTATTATTTT : 143
P2-E^{I}(Y517)-4 : ATGTATGTAAAGTGTAATGGATTATAAAAGAAGATTTATATAAATATATTTTATTATTTT : 143
P2-E^{I}(Y517)-5 : ATGTATGTAAAGTGTAATGGATTATAAAAGAAGATTTATATAAATATATTTTATTATTTT : 143
P2-E^{I}(Y517)-6 : ATGTATGTAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143
P2-E^{I}(Y517)-7 : ATGTATGTAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143
P2-E^{I}(Y517)-8 : ATGAATGTAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143
P2-E^{I}(Y517)-9 : ATGTATGTAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143
P2-E^{I}(Y517)-10 : ATGTATGTAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143

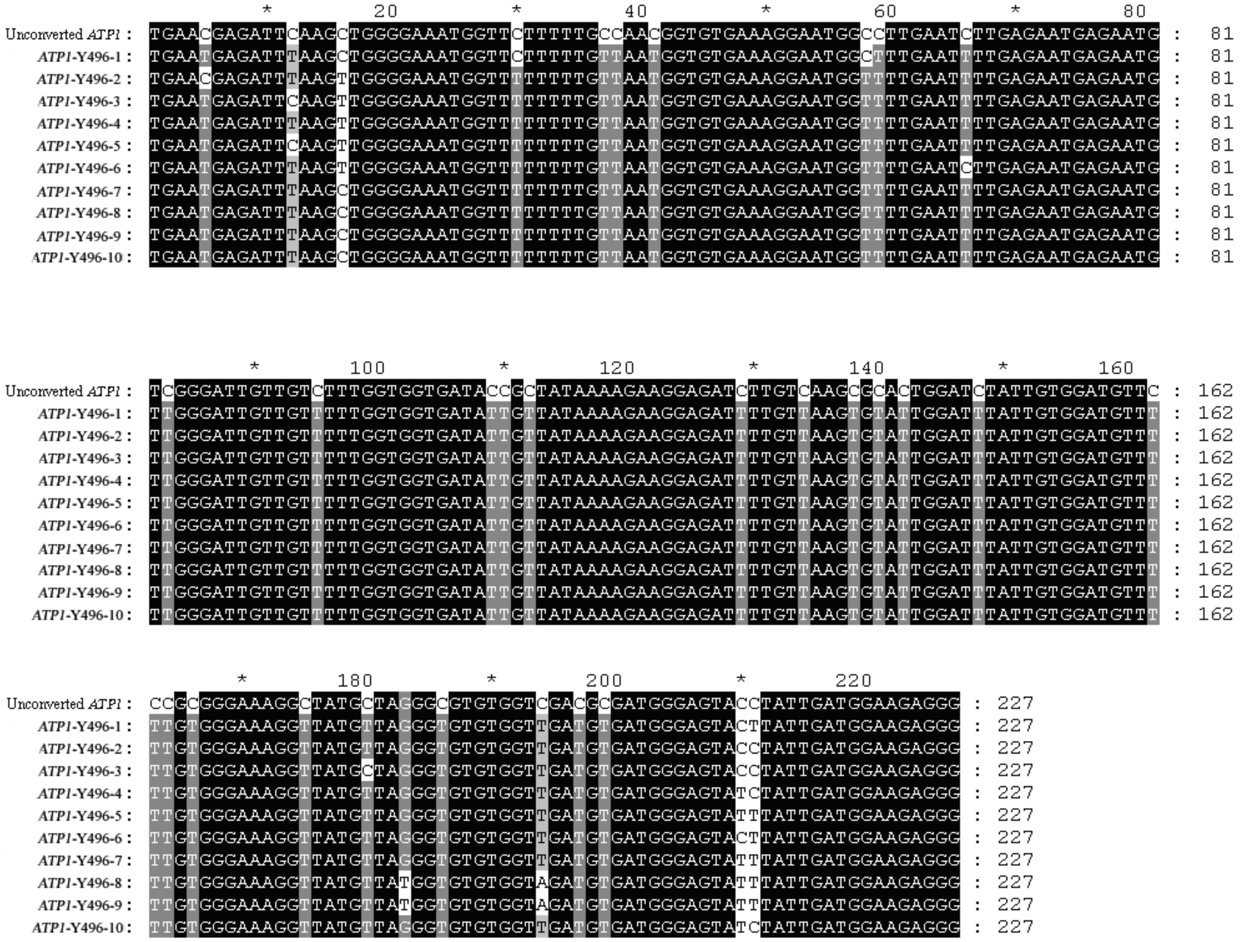
11D



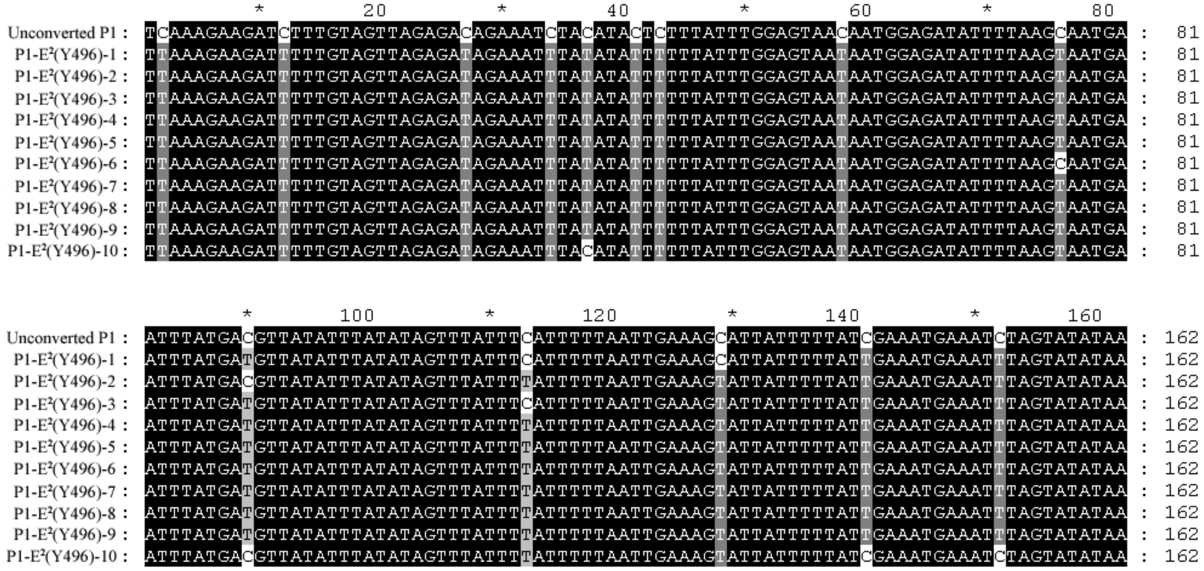
Supplemental Figure 11. Bisulfite sequence alignment of *ATP1* (control gene) and the *FAE1* allele E^1 in line Y517.

(**A)** The control gene *ATP1* had 100% conversion of C to T in the 10 clones analyzed. (**B)** DNA methylation was not detected in the promoter region (nucleotides -335 to -79) of E^1. (**C)** DNA methylation was not observed in the partial promoter region (nucleotides -143 to 1) of E^1. Unconverted genomic sequence is shown on the top. P1: The promoter region (nucleotides -335 to -79) was amplified using primer pair No 30. P2: The promoter region (nucleotides -143 to 1) was amplified using primer pair No 28. (**D)** DNA methylation was not detected in the promoter region (-335 to 1) of the *FAE1* allele E^1 in the three plants Y517-1, -2 and -3. Ten clones were analyzed for each bisulfite experiment.

12A


Unconverted *ATP1*
ATP1-Y496-1
ATP1-Y496-2
ATP1-Y496-3
ATP1-Y496-4
ATP1-Y496-5
ATP1-Y496-6
ATP1-Y496-7
ATP1-Y496-8
ATP1-Y496-9
ATP1-Y496-10
81
162
227

12B


Unconverted P1
P1-E²(Y496)-1
P1-E²(Y496)-2
P1-E²(Y496)-3
P1-E²(Y496)-4
P1-E²(Y496)-5
P1-E²(Y496)-6
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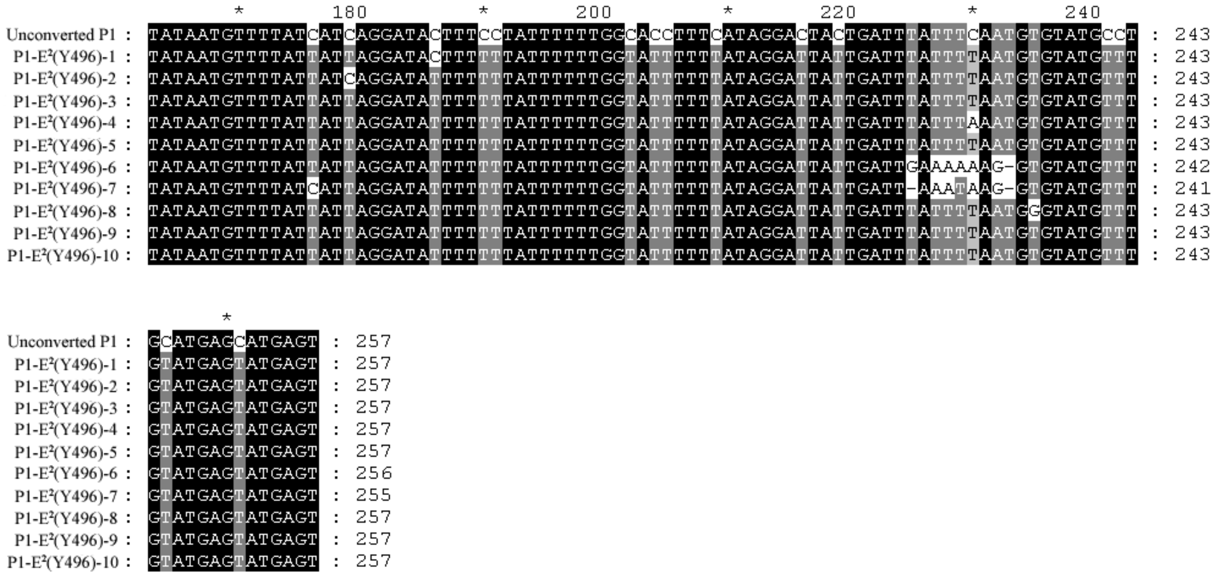
P1-E²(Y496)-9
P1-E²(Y496)-10
81
162



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Unconverted P1 : TATAATGTTTTATCATCAGGATACTTTCCTATTTTTTGGCACCTTTCATAGGACTACTGATTTATTTCAATGTGTATGCCT : 243
P1-E2(Y496)-1  : TATAATGTTTTATTATTAGGATACTTTTTTATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTT : 243
P1-E2(Y496)-2  : TATAATGTTTTATTATCAGGATATTTTTTTATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTT : 243
P1-E2(Y496)-3  : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTT : 243
P1-E2(Y496)-4  : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTAAATGTGTATGTTT : 243
P1-E2(Y496)-5  : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTT : 243
P1-E2(Y496)-6  : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTTGGTATTTTTTATAGGATTATTGATTGAAAAAAG-GTGTATGTTT : 242
P1-E2(Y496)-7  : TATAATGTTTTATCATTAGGATATTTTTTTATTTTTTGGTATTTTTTATAGGATTATTGATT-AAATAAG-GTGTATGTTT : 241
P1-E2(Y496)-8  : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGGGTATGTTT : 243
P1-E2(Y496)-9  : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTT : 243
P1-E2(Y496)-10 : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTT : 243

                         *
Unconverted P1 : GCATGAGCATGAGT : 257
P1-E2(Y496)-1  : GTATGAGTATGAGT : 257
P1-E2(Y496)-2  : GTATGAGTATGAGT : 257
P1-E2(Y496)-3  : GTATGAGTATGAGT : 257
P1-E2(Y496)-4  : GTATGAGTATGAGT : 257
P1-E2(Y496)-5  : GTATGAGTATGAGT : 257
P1-E2(Y496)-6  : GTATGAGTATGAGT : 256
P1-E2(Y496)-7  : GTATGAGTATGAGT : 255
P1-E2(Y496)-8  : GTATGAGTATGAGT : 257
P1-E2(Y496)-9  : GTATGAGTATGAGT : 257
P1-E2(Y496)-10 : GTATGAGTATGAGT : 257
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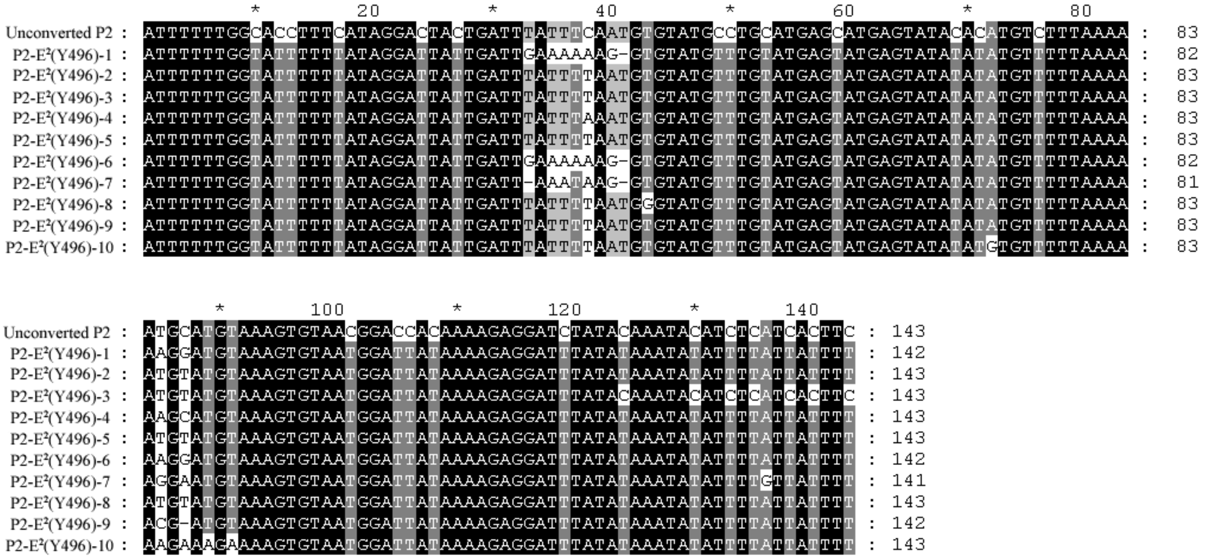
12C



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                          *        20         *        40         *        60         *        80
Unconverted P2  : ATTTTTTGGCACCTTTCATAGGACTACTGATTTATTTCAATGTGTATGCCTGCATGAGCATGAGTATACACATGTCTTTAAAA  :  83
P2-E2(Y496)-1   : ATTTTTTGGTATTTTTTATAGGATTATTGATTGAAAAAAG-GTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA  :  82
P2-E2(Y496)-2   : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA  :  83
P2-E2(Y496)-3   : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA  :  83
P2-E2(Y496)-4   : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTAAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA  :  83
P2-E2(Y496)-5   : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA  :  83
P2-E2(Y496)-6   : ATTTTTTGGTATTTTTTATAGGATTATTGATTGAAAAAAG-GTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA  :  82
P2-E2(Y496)-7   : ATTTTTTGGTATTTTTTATAGGATTATTGATT-AAATAAG-GTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA  :  81
P2-E2(Y496)-8   : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGGGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA  :  83
P2-E2(Y496)-9   : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA  :  83
P2-E2(Y496)-10  : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATGTGTTTTTAAAA  :  83

                        *        100         *        120         *        140
Unconverted P2  : ATGCATGTAAAGTGTAACGGACCACAAAAGAGGATCTATACAAATACATCTCATCACTTC : 143
P2-E2(Y496)-1   : AAGGATGTAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 142
P2-E2(Y496)-2   : ATGTATGTAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143
P2-E2(Y496)-3   : ATGTATGTAAAGTGTAATGGATTATAAAAGAGGATTTATACAAATACATCTCATCACTTC : 143
P2-E2(Y496)-4   : AAGCATGTAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143
P2-E2(Y496)-5   : ATGTATGTAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143
P2-E2(Y496)-6   : AAGGATGTAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 142
P2-E2(Y496)-7   : AGGAATGTAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTGTTATTTT : 141
P2-E2(Y496)-8   : ATGTATGTAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143
P2-E2(Y496)-9   : ACG-ATGTAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 142
P2-E2(Y496)-10  : AAGAAAGAAAAGTGTAATGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143
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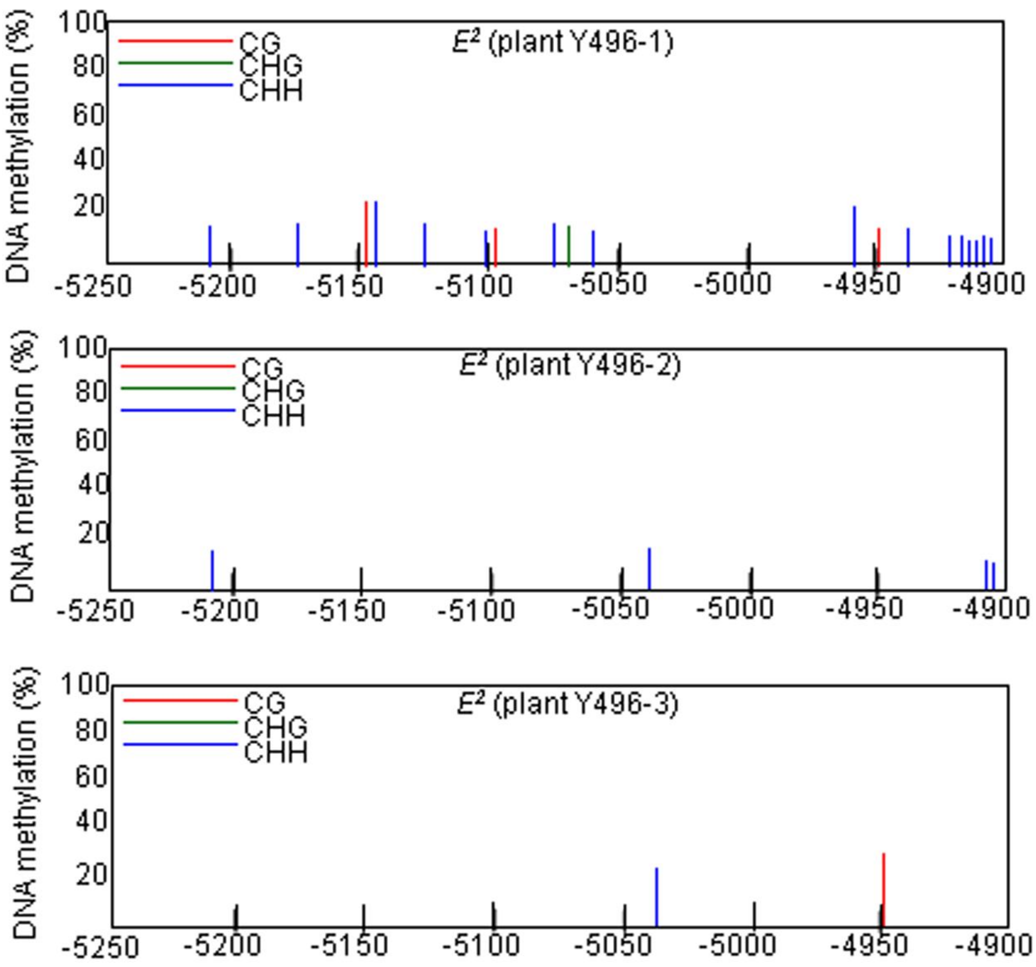
12D

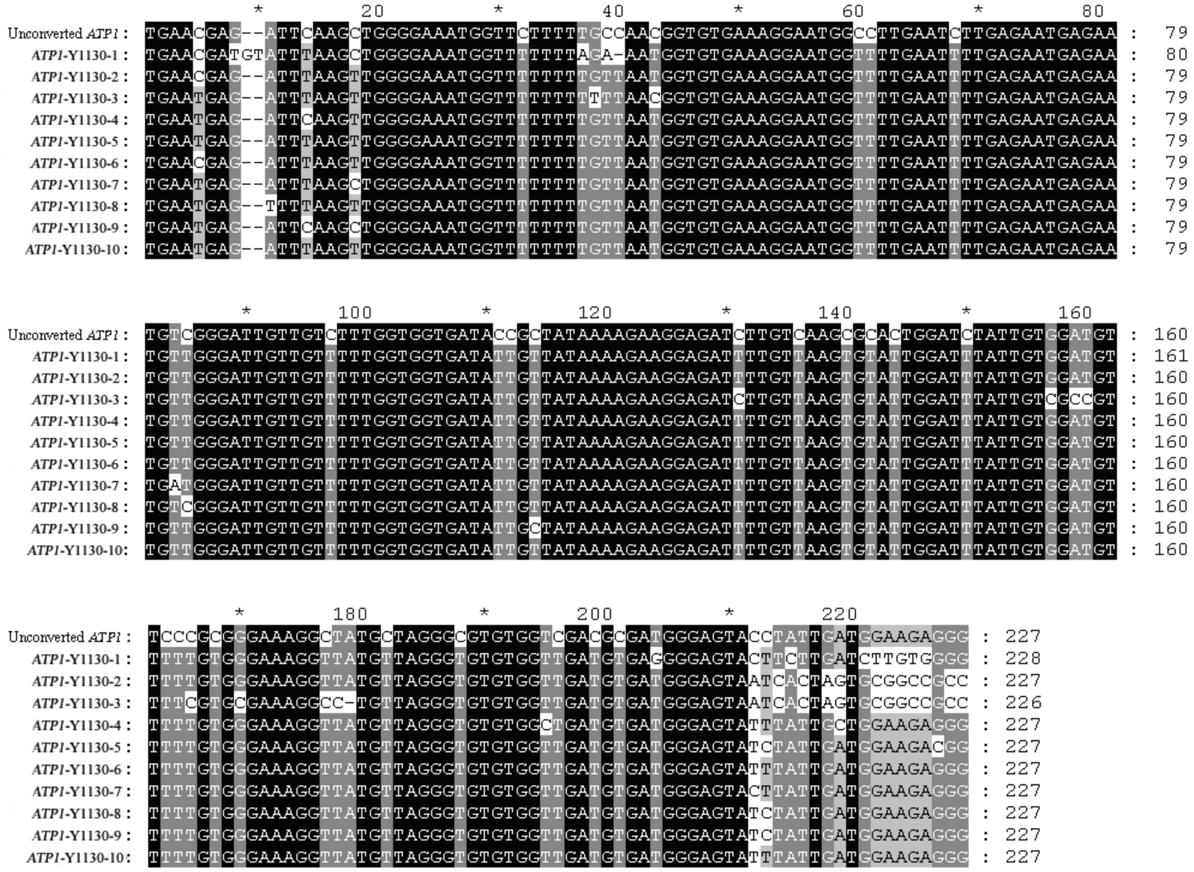


Supplemental Figure 12. Bisulfite sequence alignment of *ATP1* (control gene) and the *FAE1* allele *E*^{2} in line Y496.

(**A**) The control gene *ATP1* had 97% conversion of C to T in the 10 clones analyzed. (**B)** DNA methylation was not detected in the promoter region (nucleotides -5234 to -4978) of *E*^{2}. (**C)** DNA methylation was not observed in the promoter region (nucleotides -5042 to -4900) of *E*^{2}. Unconverted genomic sequence is shown on the top. P1: The promoter region (nucleotides -5234 to -4978) was amplified using primer pair No 30. P2: The promoter region (nucleotides -5042 to -4900) was amplified using primer pair No 29. (**D)** DNA methylation was not detected in the promoter region (-5234 to -4900) of the *FAE1* allele *E*^{2} in the three plants Y496-1, -2 and -3. Ten clones were analyzed for each bisulfite treatment.

Supplemental Data. Zeng and Cheng (2014). Plant Cell 10.1105/tpc.114.126631

13A



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                          *        20         *        40         *        60         *        80
Unconverted ATP1 : TGAACGAG--ATTCAAGCTGGGGAAATGGTTCTTTTTGCCAACGGTGTGAAAGGAATGGCCTTGAATCTTGAGAATGAGAA :  79
     ATP1-Y1130-1 : TGAACGATGTATTTAAGCTGGGGAAATGGTTTTTTTACA-AATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAA :  80
     ATP1-Y1130-2 : TGAACGAG--ATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAA :  79
     ATP1-Y1130-3 : TGAATGAG--ATTTAAGTTGGGGAAATGGTTTTTTTTTTTAACGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAA :  79
     ATP1-Y1130-4 : TGAATGAG--ATTCAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAA :  79
     ATP1-Y1130-5 : TGAATGAG--ATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAA :  79
     ATP1-Y1130-6 : TGAACGAG--ATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAA :  79
     ATP1-Y1130-7 : TGAATGAG--ATTTAAGCTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAA :  79
     ATP1-Y1130-8 : TGAATGAG--TTTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAA :  79
     ATP1-Y1130-9 : TGAATGAG--ATTCAAGCTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAA :  79
    ATP1-Y1130-10 : TGAATGAG--ATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAA :  79

                         *       100         *       120         *       140         *       160
Unconverted ATP1 : TGTCGGGATTGTTGTCTTTGGTGGTGATACCGCTATAAAAGAAGGAGATCTTGTCAAGCGCACTGGATCTATTGTGGATGT : 160
     ATP1-Y1130-1 : TGTTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGT : 161
     ATP1-Y1130-2 : TGTTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGT : 160
     ATP1-Y1130-3 : TGTTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATCTTGTTAAGTGTATTGGATTTATTGTCGCCGT : 160
     ATP1-Y1130-4 : TGTTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGT : 160
     ATP1-Y1130-5 : TGTTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGT : 160
     ATP1-Y1130-6 : TGTTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGT : 160
     ATP1-Y1130-7 : TGATGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGT : 160
     ATP1-Y1130-8 : TGTCGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGT : 160
     ATP1-Y1130-9 : TGTTGGGATTGTTGTTTTTGGTGGTGATATTGCTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGT : 160
    ATP1-Y1130-10 : TGTTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGT : 160

                         *       180         *       200         *       220
Unconverted ATP1 : TCCCGCGGGAAAGGCTATGCTAGGGCGTGTGGTCGACGCGATGGGAGTACCTATTGATGGAAGAGGG : 227
     ATP1-Y1130-1 : TTTTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGAGGGGAGTACTTCTTGATCTTGTGGGG : 228
     ATP1-Y1130-2 : TTTTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTAATCACTAGTGCGGCCGCC : 227
     ATP1-Y1130-3 : TTTCGTGCGAAAGGCC-TGTTAGGGTGTGTGGTTGATGTGATGGGAGTAATCACTAGTGCGGCCGCC : 226
     ATP1-Y1130-4 : TTTTGTGGGAAAGGTTATGTTAGGGTGTGTGGCTGATGTGATGGGAGTATTTATTGCTGGAAGAGGG : 227
     ATP1-Y1130-5 : TTTTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATCTATTGATGGAAGACGG : 227
     ATP1-Y1130-6 : TTTTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATTTATTGATGGAAGAGGG : 227
     ATP1-Y1130-7 : TTTTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTACTTATTGATGGAAGAGGG : 227
     ATP1-Y1130-8 : TTTTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATCTATTGATGGAAGAGGG : 227
     ATP1-Y1130-9 : TTTTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATCTATTGATGGAAGAGGG : 227
    ATP1-Y1130-10 : TTTTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATTTATTGATGGAAGAGGG : 227
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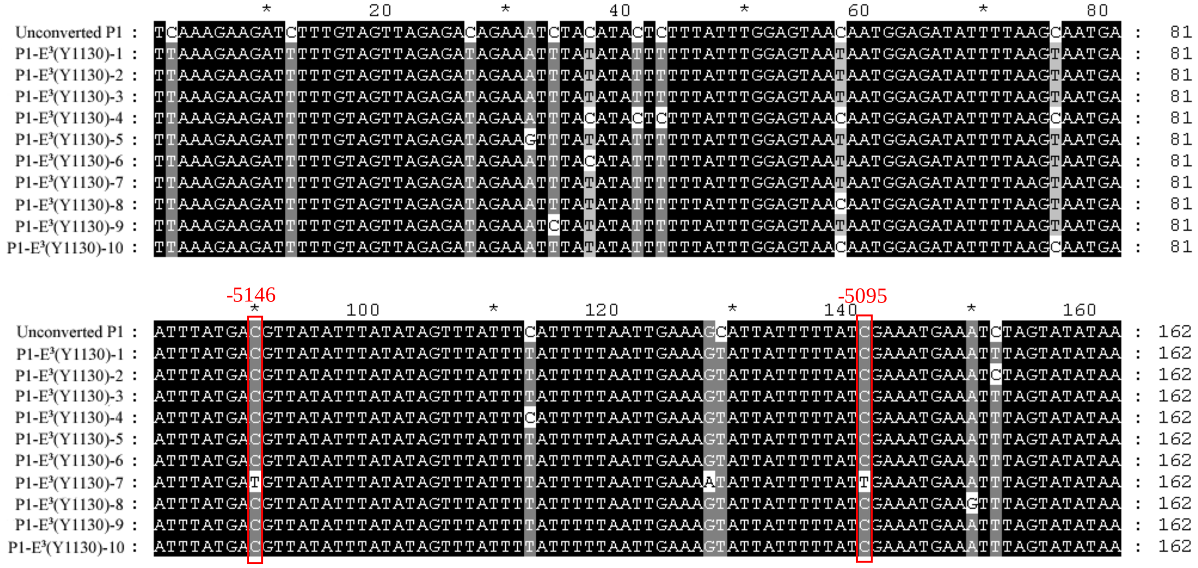
13B



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                           *        20         *        40         *        60         *        80
 Unconverted P1 : TCAAAGAAGATCTTTGTAGTTAGAGACAGAAATCTACATACTCTTTATTTGGAGTAACAATGGAGATATTTTAAGCAATGA :  81
 P1-E3(Y1130)-1 : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
 P1-E3(Y1130)-2 : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
 P1-E3(Y1130)-3 : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
 P1-E3(Y1130)-4 : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTACATACTCTTTATTTGGAGTAACAATGGAGATATTTTAAGCAATGA :  81
 P1-E3(Y1130)-5 : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAGTTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
 P1-E3(Y1130)-6 : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTACATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
 P1-E3(Y1130)-7 : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
 P1-E3(Y1130)-8 : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAACAATGGAGATATTTTAAGTAATGA :  81
 P1-E3(Y1130)-9 : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATCTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-E3(Y1130)-10 : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAACAATGGAGATATTTTAAGCAATGA :  81

                       -5146                                                  -5095
                         *       100         *       120         *       140         *       160
 Unconverted P1 : ATTTATGACGTTATATTTATATAGTTTATTTCATTTTTAATTGAAAGCATTATTTTTATCGAAATGAAATCTAGTATATAA : 162
 P1-E3(Y1130)-1 : ATTTATGACGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATCGAAATGAAATTTAGTATATAA : 162
 P1-E3(Y1130)-2 : ATTTATGACGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATCGAAATGAAATCTAGTATATAA : 162
 P1-E3(Y1130)-3 : ATTTATGACGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATCGAAATGAAATTTAGTATATAA : 162
 P1-E3(Y1130)-4 : ATTTATGACGTTATATTTATATAGTTTATTTCATTTTTAATTGAAAGTATTATTTTTATCGAAATGAAATTTAGTATATAA : 162
 P1-E3(Y1130)-5 : ATTTATGACGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATCGAAATGAAATTTAGTATATAA : 162
 P1-E3(Y1130)-6 : ATTTATGACGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATCGAAATGAAATTTAGTATATAA : 162
 P1-E3(Y1130)-7 : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAATATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
 P1-E3(Y1130)-8 : ATTTATGACGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATCGAAATGAAGTTTAGTATATAA : 162
 P1-E3(Y1130)-9 : ATTTATGACGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATCGAAATGAAATTTAGTATATAA : 162
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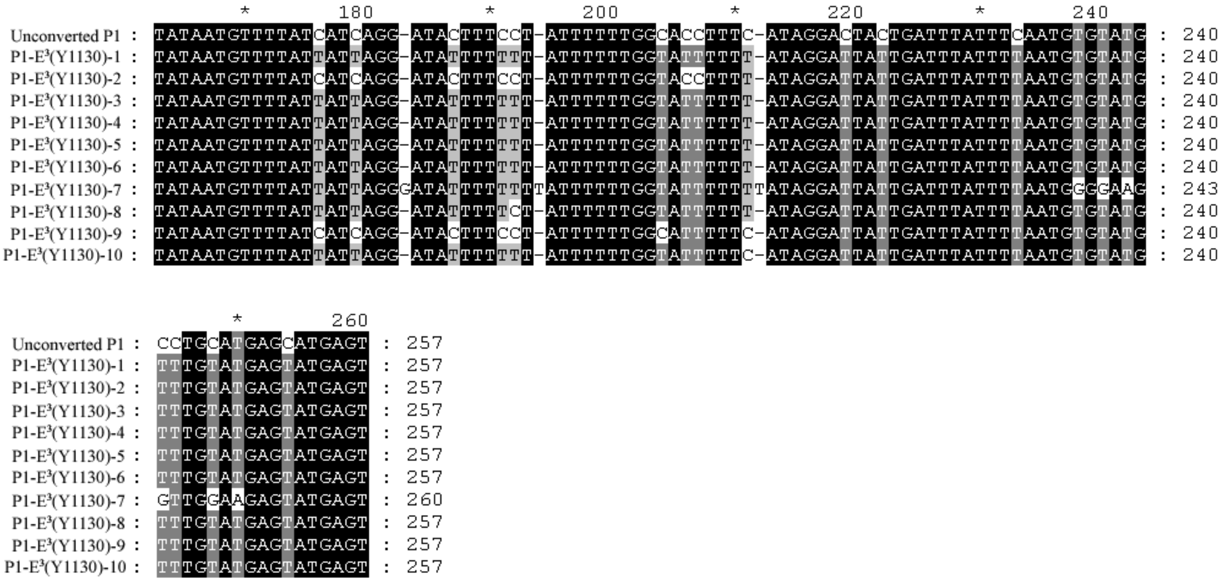

Unconverted P1
P1-E³(Y1130)-1
P1-E³(Y1130)-2
P1-E³(Y1130)-3
P1-E³(Y1130)-4
P1-E³(Y1130)-5
P1-E³(Y1130)-6
P1-E³(Y1130)-7
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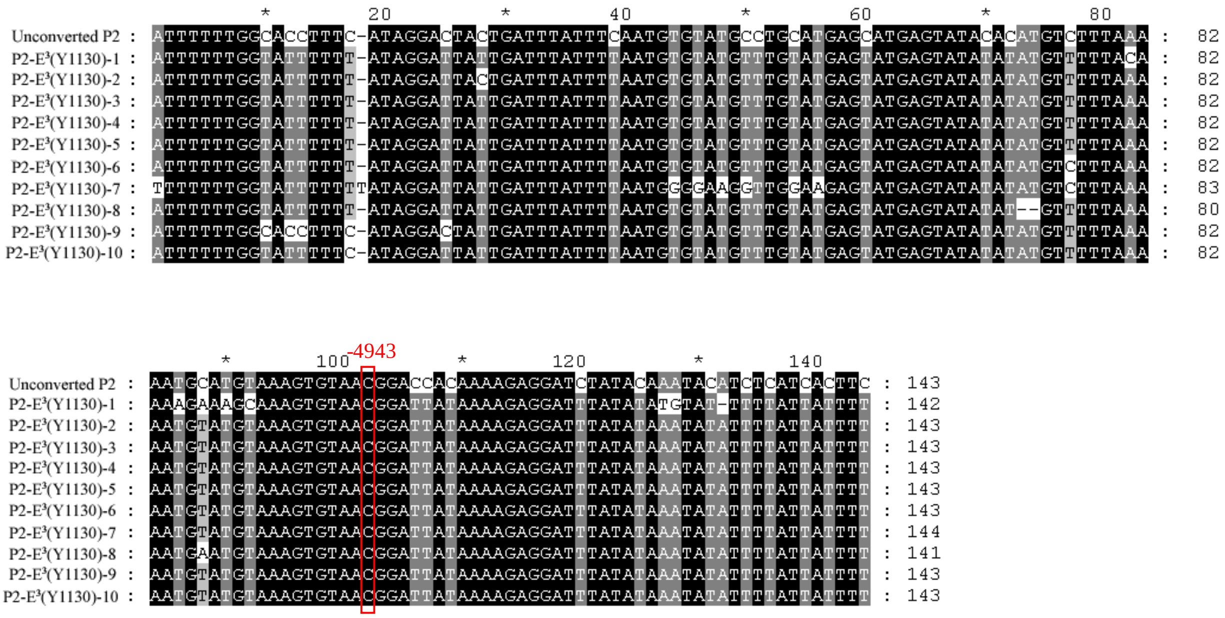
P1-E³(Y1130)-10
180
200
220
240
260

13C



Unconverted P2
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P2-E³(Y1130)-3
P2-E³(Y1130)-4
P2-E³(Y1130)-5
P2-E³(Y1130)-6
P2-E³(Y1130)-7
P2-E³(Y1130)-8
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P2-E³(Y1130)-10
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60
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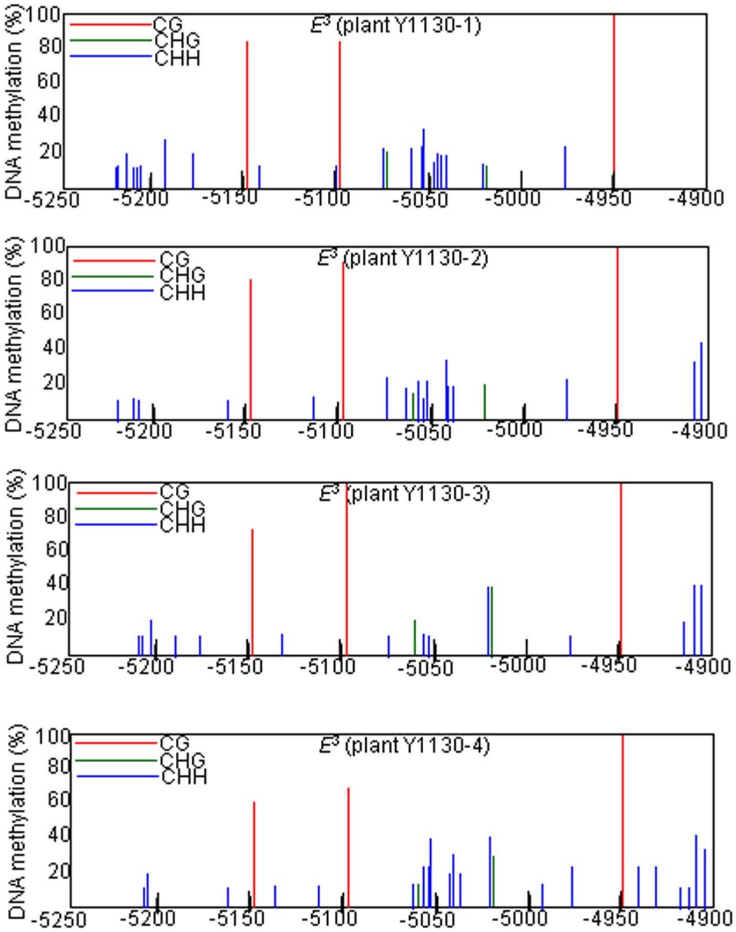
100
-4943
120
140

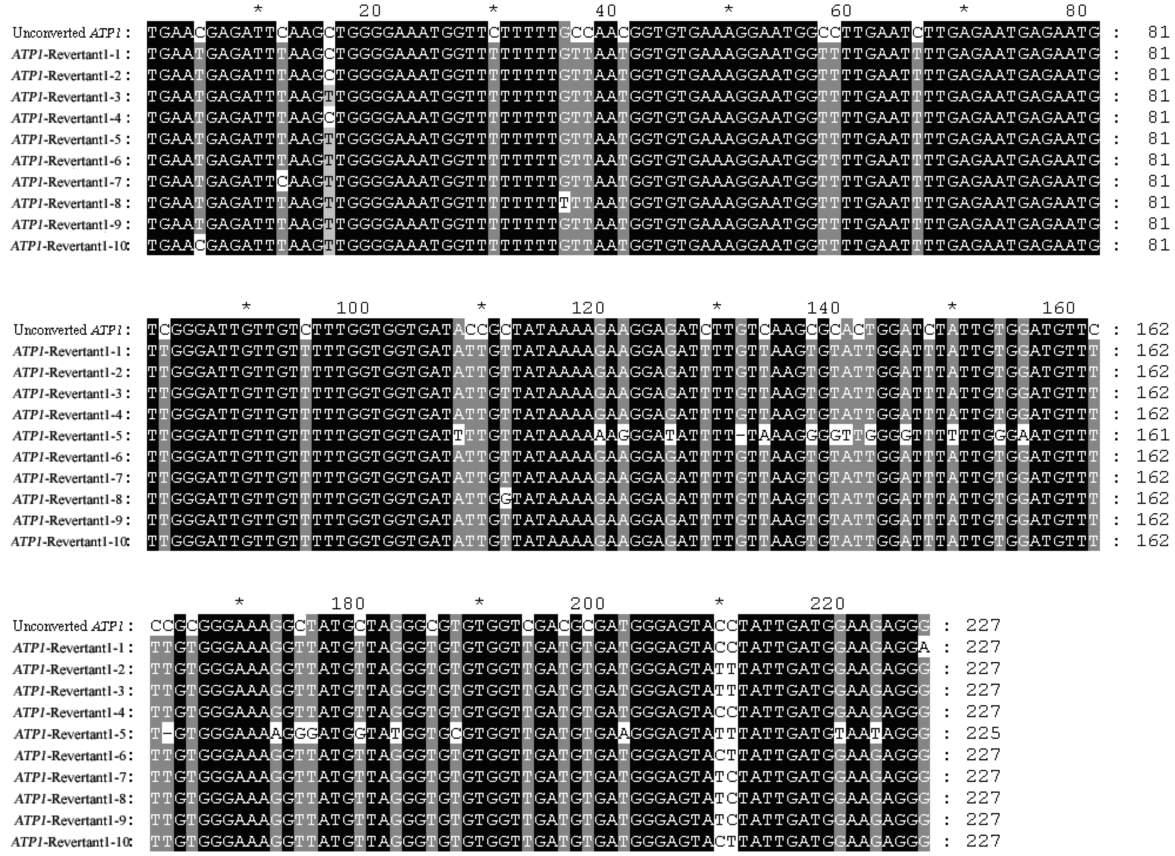
13D



Supplemental Figure 13. Bisulfite sequence alignment of *ATP1* (control gene) and the *FAE1* allele E^3 in line Y1130.

(**A)** The control gene *ATP1* in Y1130 had 100% conversion of C to T in the bisulfite treatment. (**B)** Methylation occurred at positions -5146 and -5095. (**C)** Methylation occurred at position -4943. Unconverted genomic sequence is shown on the top. P1: The promoter region (nucleotides -5234 to -4978) was amplified using primer pair No 30. P2: The promoter region (nucleotides -5042 to -4900) was amplified using primer pair No 29. (**D)** DNA methylation was detected at positions -5146, -5095 and -4943 in the promoter region (-5234 to -4900) of the *FAE1* allele E^3 in the four plants Y1130-1, -2, -3 and -4. Ten clones were analyzed for each bisulfite experiment.

14A



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ATP1-Revertant1-1    : TGAATGAGATTTAAGCTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant1-2    : TGAATGAGATTTAAGCTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant1-3    : TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant1-4    : TGAATGAGATTTAAGCTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant1-5    : TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant1-6    : TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant1-7    : TGAATGAGATTCAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant1-8    : TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTTTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant1-9    : TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant1-10   : TGAACGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81

                               *       100         *       120         *       140         *       160
Unconverted ATP1     : TCGGGATTGTTGTCTTTGGTGGTGATACCGCTATAAAAGAAGGAGATCTTGTCAAGCGCACTGGATCTATTGTGGATGTTC : 162
ATP1-Revertant1-1    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant1-2    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant1-3    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant1-4    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant1-5    : TTGGGATTGTTGTTTTTGGTGGTGATTTTGTTATAAAAAAGGGATATTTT-TAAAGGGGTTGGGGTTTTTTGGGAATGTTT : 161
ATP1-Revertant1-6    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant1-7    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant1-8    : TTGGGATTGTTGTTTTTGGTGGTGATATTGGTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant1-9    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant1-10   : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162

                              *       180         *       200         *       220
Unconverted ATP1     : CCGCGGGAAAGGCTATGCTAGGGCGTGTGGTCGACGCGATGGGAGTACCTATTGATGGAAGAGGG : 227
ATP1-Revertant1-1    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTACCTATTGATGGAAGAGGA : 227
ATP1-Revertant1-2    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATTTATTGATGGAAGAGGG : 227
ATP1-Revertant1-3    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATTTATTGATGGAAGAGGG : 227
ATP1-Revertant1-4    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTACCTATTGATGGAAGAGGG : 227
ATP1-Revertant1-5    : T-GTGGGAAAAGGGATGGTATGGTGCGTGGTTGATGTGAAGGGAGTATTTATTGATGTAATAGGG : 225
ATP1-Revertant1-6    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTACTTATTGATGGAAGAGGG : 227
ATP1-Revertant1-7    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATCTATTGATGGAAGAGGG : 227
ATP1-Revertant1-8    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATCTATTGATGGAAGAGGG : 227
ATP1-Revertant1-9    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATCTATTGATGGAAGAGGG : 227
ATP1-Revertant1-10   : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTACTTATTGATGGAAGAGGG : 227
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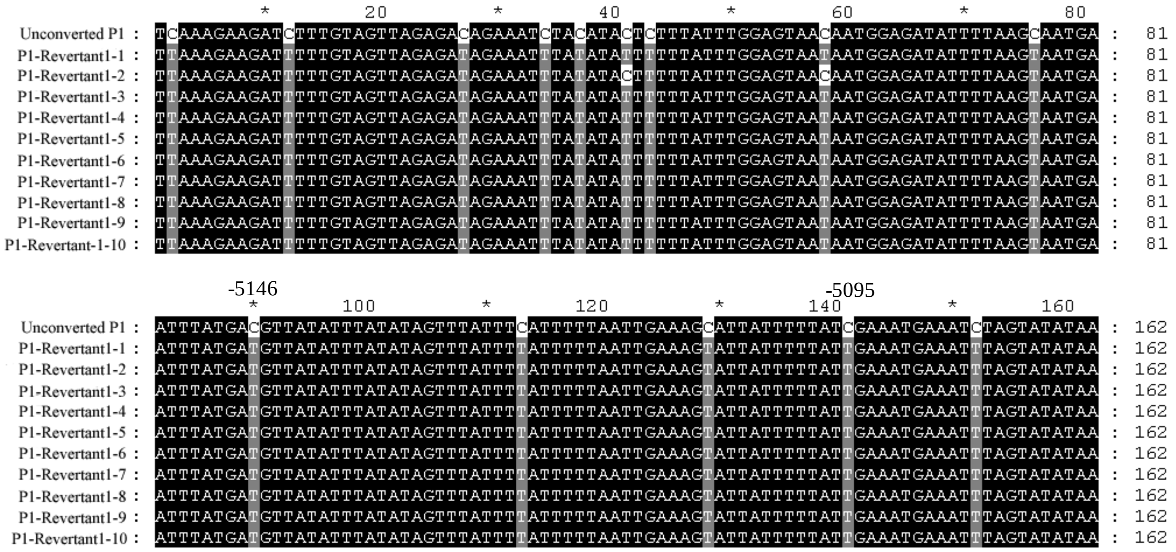
14B



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Unconverted P1       : TCAAAGAAGATCTTTGTAGTTAGAGACAGAAATCTACATACTCTTTATTTGGAGTAACAATGGAGATATTTTAAGCAATGA :  81
P1-Revertant1-1      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant1-2      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATACTTTTTATTTGGAGTAACAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant1-3      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant1-4      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant1-5      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant1-6      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant1-7      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant1-8      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant1-9      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant-1-10    : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81

                             -5146                                               -5095
                               *       100         *       120         *       140         *       160
Unconverted P1       : ATTTATGACGTTATATTTATATAGTTTATTTCATTTTTAATTGAAAGCATTATTTTTATCGAAATGAAATCTAGTATATAA : 162
P1-Revertant1-1      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant1-2      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant1-3      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant1-4      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant1-5      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant1-6      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant1-7      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant1-8      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant1-9      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant1-10     : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
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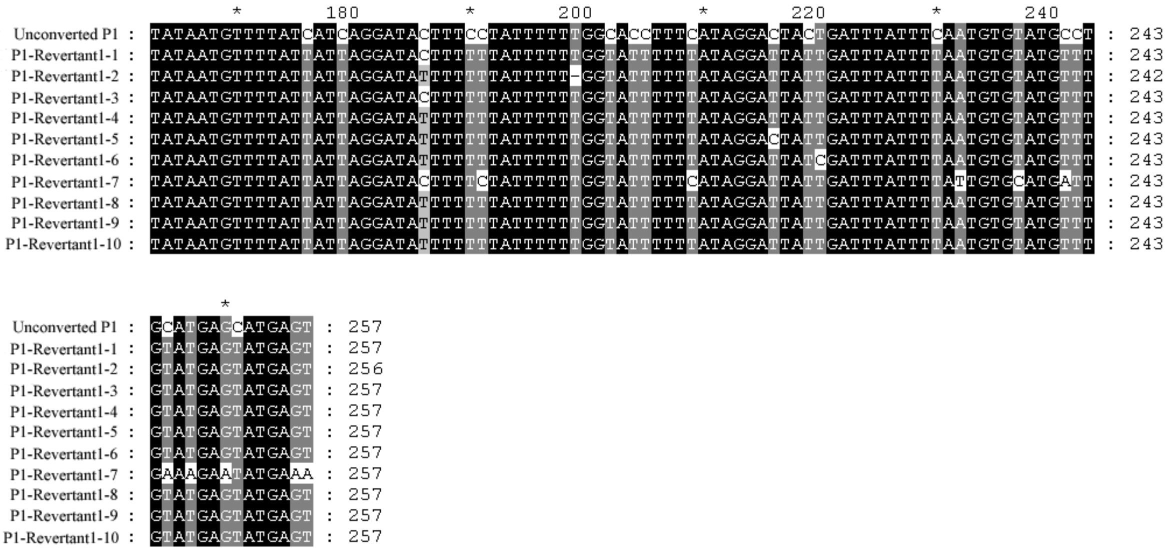

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P1-Revertant1-1   : TATAATGTTTTATTATTAGGATACTTTTTTATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTT : 243
P1-Revertant1-2   : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTT-GGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTT : 242
P1-Revertant1-3   : TATAATGTTTTATTATTAGGATACTTTTTTATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTT : 243
P1-Revertant1-4   : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTT : 243
P1-Revertant1-5   : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTTTGGTATTTTTTATAGGACTATTGATTTATTTTAATGTGTATGTTT : 243
P1-Revertant1-6   : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTTTGGTATTTTTTATAGGATTATCGATTTATTTTAATGTGTATGTTT : 243
P1-Revertant1-7   : TATAATGTTTTATTATTAGGATACTTTTCTATTTTTTGGTATTTTTCATAGGATTATTGATTTATTTTATTGTGCATGATT : 243
P1-Revertant1-8   : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTT : 243
P1-Revertant1-9   : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTT : 243
P1-Revertant1-10  : TATAATGTTTTATTATTAGGATATTTTTTTATTTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTT : 243

                          *
Unconverted P1    : GCATGAGCATGAGT : 257
P1-Revertant1-1   : GTATGAGTATGAGT : 257
P1-Revertant1-2   : GTATGAGTATGAGT : 256
P1-Revertant1-3   : GTATGAGTATGAGT : 257
P1-Revertant1-4   : GTATGAGTATGAGT : 257
P1-Revertant1-5   : GTATGAGTATGAGT : 257
P1-Revertant1-6   : GTATGAGTATGAGT : 257
P1-Revertant1-7   : GAAAGAATATGAAA : 257
P1-Revertant1-8   : GTATGAGTATGAGT : 257
P1-Revertant1-9   : GTATGAGTATGAGT : 257
P1-Revertant1-10  : GTATGAGTATGAGT : 257
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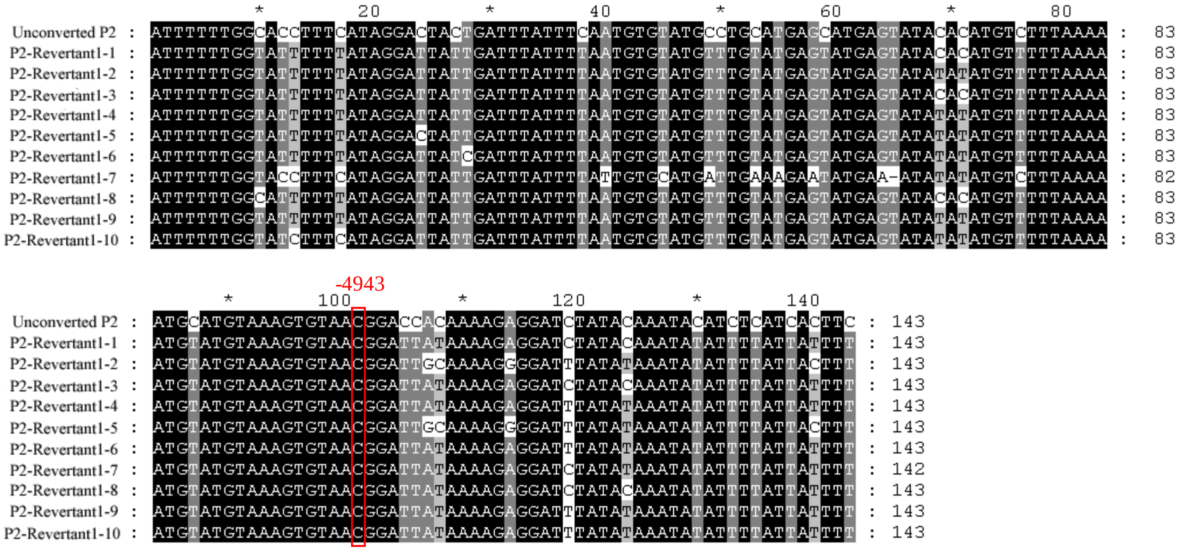
14C



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Unconverted P2    : ATTTTTTGGCACCTTTCATAGGACTACTGATTTATTTCAATGTGTATGCCTGCATGAGCATGAGTATACACATGTCTTTAAAA :  83
P2-Revertant1-1   : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATACACATGTTTTTAAAA :  83
P2-Revertant1-2   : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA :  83
P2-Revertant1-3   : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATACACATGTTTTTAAAA :  83
P2-Revertant1-4   : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA :  83
P2-Revertant1-5   : ATTTTTTGGTATTTTTTATAGGACTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA :  83
P2-Revertant1-6   : ATTTTTTGGTATTTTTTATAGGATTATCGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA :  83
P2-Revertant1-7   : ATTTTTTGGTACCTTTCATAGGATTATTGATTTATTTTATTGTGCATGATTGAAAGAATATGAA-ATATATATGTCTTTAAAA :  82
P2-Revertant1-8   : ATTTTTTGGCATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATACACATGTTTTTAAAA :  83
P2-Revertant1-9   : ATTTTTTGGTATTTTTTATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA :  83
P2-Revertant1-10  : ATTTTTTGGTATCTTTCATAGGATTATTGATTTATTTTAATGTGTATGTTTGTATGAGTATGAGTATATATATGTTTTTAAAA :  83

                                   -4943
                          *       100         *       120         *       140
Unconverted P2    : ATGCATGTAAAGTGTAACGGACCACAAAAGAGGATCTATACAAATACATCTCATCACTTC : 143
P2-Revertant1-1   : ATGTATGTAAAGTGTAACGGATTATAAAAGAGGATCTATACAAATATATTTTATTATTTT : 143
P2-Revertant1-2   : ATGTATGTAAAGTGTAACGGATTGCAAAAGGGGATTTATATAAATATATTTTATTACTTT : 143
P2-Revertant1-3   : ATGTATGTAAAGTGTAACGGATTATAAAAGAGGATCTATACAAATATATTTTATTATTTT : 143
P2-Revertant1-4   : ATGTATGTAAAGTGTAACGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143
P2-Revertant1-5   : ATGTATGTAAAGTGTAACGGATTGCAAAAGGGGATTTATATAAATATATTTTATTACTTT : 143
P2-Revertant1-6   : ATGTATGTAAAGTGTAACGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143
P2-Revertant1-7   : ATGTATGTAAAGTGTAACGGATTATAAAAGAGGATCTATATAAATATATTTTATTATTTT : 142
P2-Revertant1-8   : ATGTATGTAAAGTGTAACGGATTATAAAAGAGGATCTATACAAATATATTTTATTATTTT : 143
P2-Revertant1-9   : ATGTATGTAAAGTGTAACGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143
P2-Revertant1-10  : ATGTATGTAAAGTGTAACGGATTATAAAAGAGGATTTATATAAATATATTTTATTATTTT : 143
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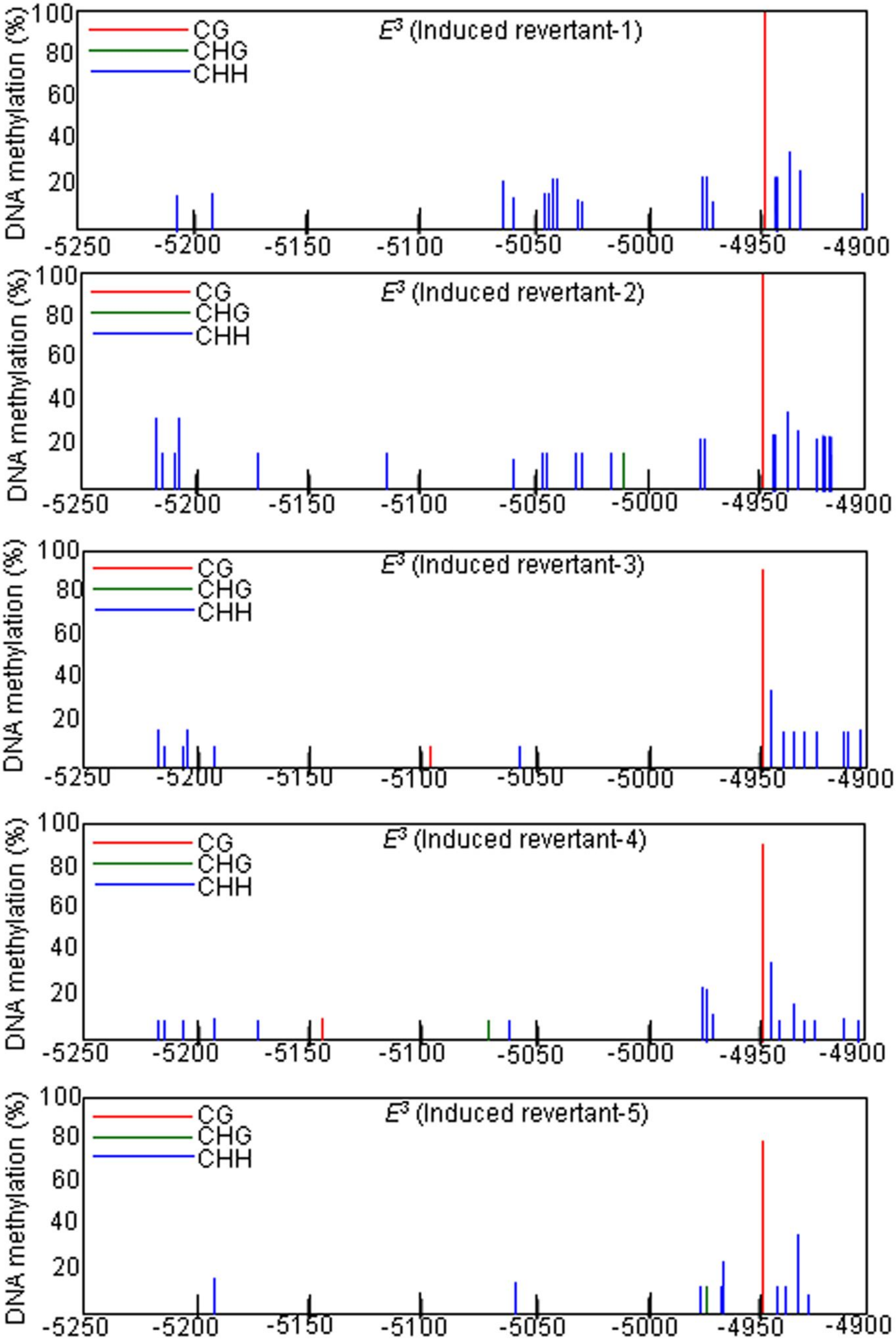
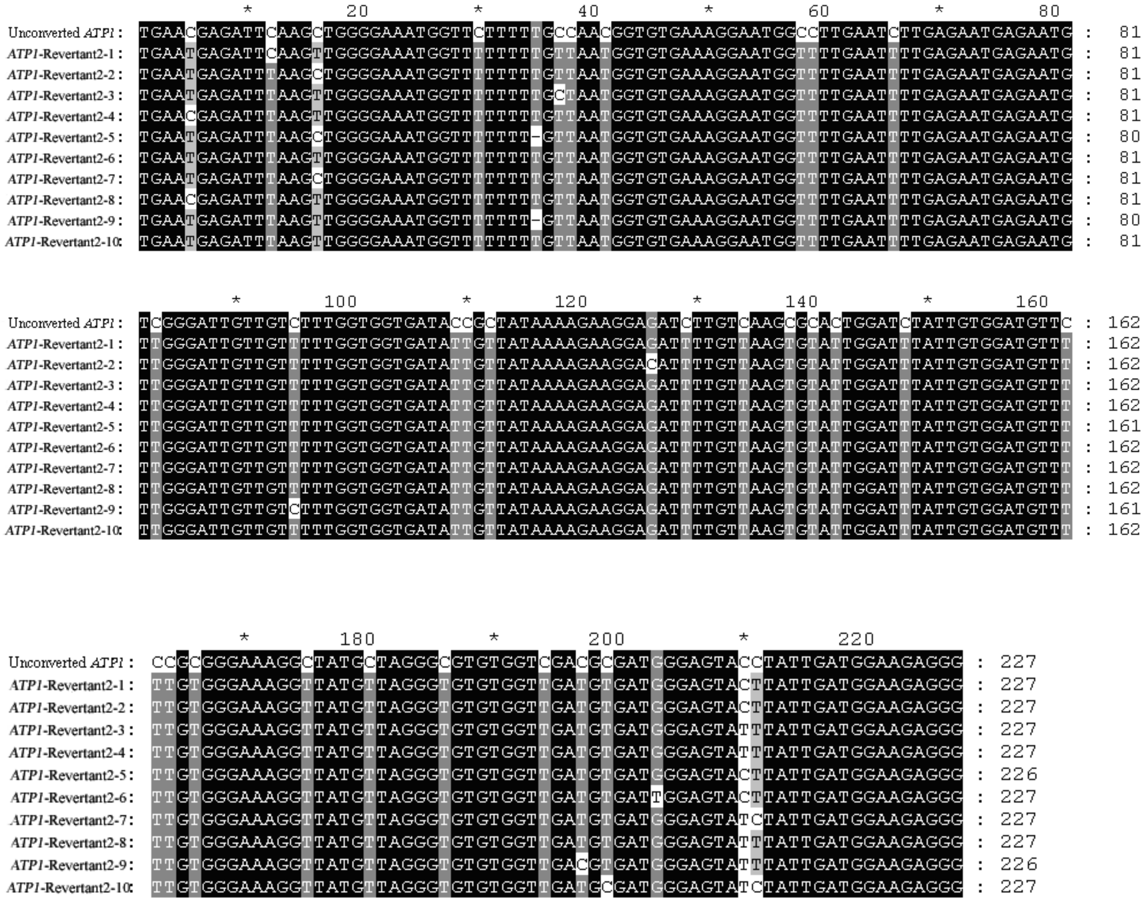
14D


DNA methylation (%)
100
80
60
40
20
CG
CHG
CHH
E^3 (Induced revertant-1)
-5250
-5200
-5150
-5100
-5050
-5000
-4950
-4900
DNA methylation (%)
100
80
60
40
20
CG
CHG
CHH
E^3 (Induced revertant-2)
-5250
-5200
-5150
-5100
-5050
-5000
-4950
-4900
DNA methylation (%)
100
80
60
40
20
CG
CHG
CHH
E^3 (Induced revertant-3)
-5250
-5200
-5150
-5100
-5050
-5000
-4950
-4900
DNA methylation (%)
100
80
60
40
20
CG
CHG
CHH
E^3 (Induced revertant-4)
-5250
-5200
-5150
-5100
-5050
-5000
-4950
-4900
DNA methylation (%)
100
80
60
40
20
CG
CHG
CHH
E^3 (Induced revertant-5)
-5250
-5200
-5150
-5100
-5050
-5000
-4950
-4900

Supplemental Figure 14. Bisulfite sequence alignment of *ATP1* (control gene) and the *FAE1* allele E^3 in the 5-azaC induced revertants of Y1130.

(**A)** The control gene *ATP1* had 97% conversion of C to T in the bisulfite treatment. (**B)** Methylation was not detected at positions -5146 and -5095. (**C)** Methylation was detected at position -4943. Unconverted genomic sequence is shown on the top. P1: The promoter region (nucleotides -5234 to -4978) was amplified using primer pair No 30. P2: The promoter region (nucleotides -5042 to -4900) was amplified using primer pair No 29. Revertant 1: 5-azaC induced revertant of Y1130. **(D)** DNA methylation was detected at position -4943 in the promoter region (nucleotides -5234 to -4900) of *FAE1* allele E^3 in 5-azaC induced revertant-1, -2, -3, -4 and -5. Ten clones were analyzed for each bisulfite experiment.

15A



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Unconverted ATP1     : TGAACGAGATTCAAGCTGGGGAAATGGTTCTTTTTGCCAACGGTGTGAAAGGAATGGCCTTGAATCTTGAGAATGAGAATG :  81
ATP1-Revertant2-1    : TGAATGAGATTCAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant2-2    : TGAATGAGATTTAAGCTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant2-3    : TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGCTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant2-4    : TGAACGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant2-5    : TGAATGAGATTTAAGCTGGGGAAATGGTTTTTTT-GTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  80
ATP1-Revertant2-6    : TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant2-7    : TGAATGAGATTTAAGCTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant2-8    : TGAACGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81
ATP1-Revertant2-9    : TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTT-GTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  80
ATP1-Revertant2-10   : TGAATGAGATTTAAGTTGGGGAAATGGTTTTTTTTGTTAATGGTGTGAAAGGAATGGTTTTGAATTTTGAGAATGAGAATG :  81

                               *       100         *       120         *       140         *       160
Unconverted ATP1     : TCGGGATTGTTGTCTTTGGTGGTGATACCGCTATAAAAGAAGGAGATCTTGTCAAGCGCACTGGATCTATTGTGGATGTTC : 162
ATP1-Revertant2-1    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant2-2    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGACATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant2-3    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant2-4    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant2-5    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 161
ATP1-Revertant2-6    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant2-7    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant2-8    : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162
ATP1-Revertant2-9    : TTGGGATTGTTGTCTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 161
ATP1-Revertant2-10   : TTGGGATTGTTGTTTTTGGTGGTGATATTGTTATAAAAGAAGGAGATTTTGTTAAGTGTATTGGATTTATTGTGGATGTTT : 162

                              *       180         *       200         *       220
Unconverted ATP1     : CCGCGGGAAAGGCTATGCTAGGGCGTGTGGTCGACGCGATGGGAGTACCTATTGATGGAAGAGGG : 227
ATP1-Revertant2-1    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTACTTATTGATGGAAGAGGG : 227
ATP1-Revertant2-2    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTACTTATTGATGGAAGAGGG : 227
ATP1-Revertant2-3    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATTTATTGATGGAAGAGGG : 227
ATP1-Revertant2-4    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATTTATTGATGGAAGAGGG : 227
ATP1-Revertant2-5    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTACTTATTGATGGAAGAGGG : 226
ATP1-Revertant2-6    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATTGGAGTACTTATTGATGGAAGAGGG : 227
ATP1-Revertant2-7    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATCTATTGATGGAAGAGGG : 227
ATP1-Revertant2-8    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGTGATGGGAGTATTTATTGATGGAAGAGGG : 227
ATP1-Revertant2-9    : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGACGTGATGGGAGTATTTATTGATGGAAGAGGG : 226
ATP1-Revertant2-10   : TTGTGGGAAAGGTTATGTTAGGGTGTGTGGTTGATGCGATGGGAGTATCTATTGATGGAAGAGGG : 227
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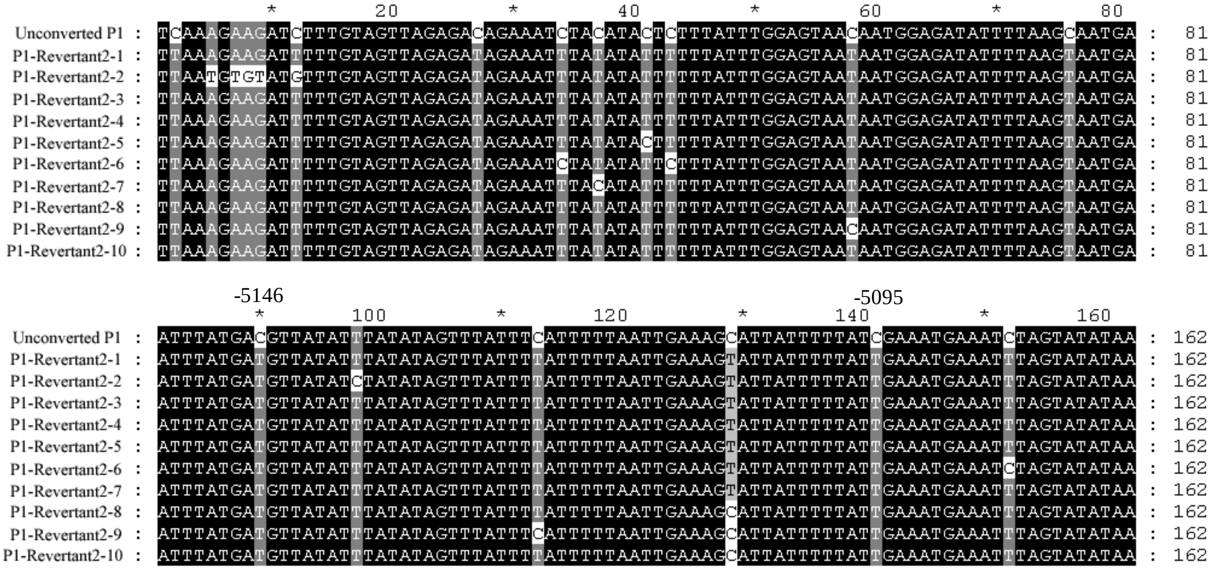
15B



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                                 *        20         *        40         *        60         *        80
Unconverted P1       : TCAAAGAAGATCTTTGTAGTTAGAGACAGAAATCTACATACTCTTTATTTGGAGTAACAATGGAGATATTTTAAGCAATGA :  81
P1-Revertant2-1      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant2-2      : TTAATGTGTATGTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant2-3      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant2-4      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant2-5      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATACTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant2-6      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATCTATATATTCTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant2-7      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTACATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant2-8      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant2-9      : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAACAATGGAGATATTTTAAGTAATGA :  81
P1-Revertant2-10     : TTAAAGAAGATTTTTGTAGTTAGAGATAGAAATTTATATATTTTTTATTTGGAGTAATAATGGAGATATTTTAAGTAATGA :  81

                            -5146                                        -5095
                               *       100         *       120         *       140         *       160
Unconverted P1       : ATTTATGACGTTATATTTATATAGTTTATTTCATTTTTAATTGAAAGCATTATTTTTATCGAAATGAAATCTAGTATATAA : 162
P1-Revertant2-1      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant2-2      : ATTTATGATGTTATATCTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant2-3      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant2-4      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant2-5      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant2-6      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATCTAGTATATAA : 162
P1-Revertant2-7      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGTATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant2-8      : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGCATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant2-9      : ATTTATGATGTTATATTTATATAGTTTATTTCATTTTTAATTGAAAGCATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
P1-Revertant2-10     : ATTTATGATGTTATATTTATATAGTTTATTTTATTTTTAATTGAAAGCATTATTTTTATTGAAATGAAATTTAGTATATAA : 162
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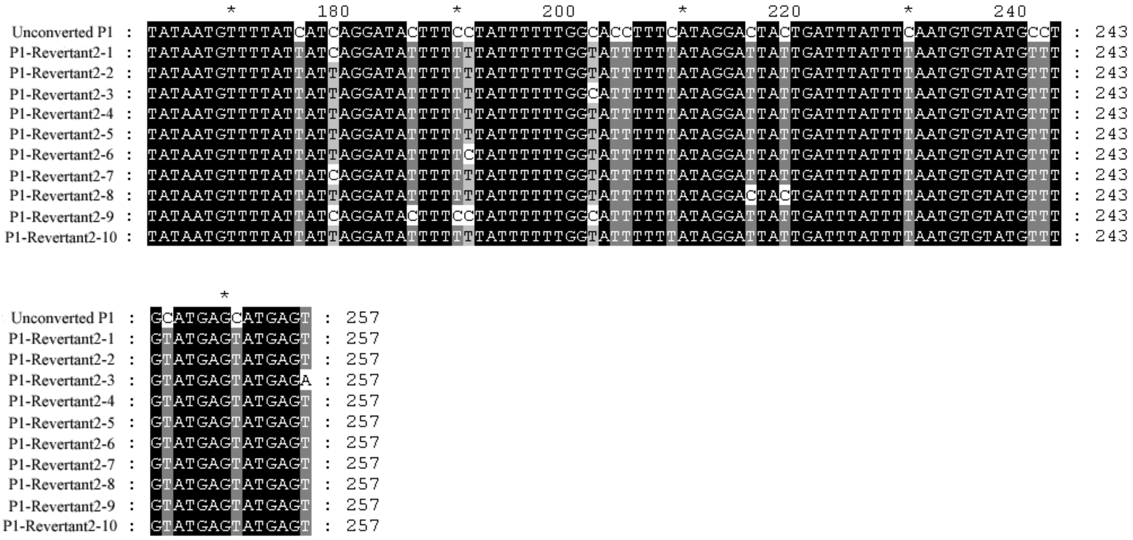
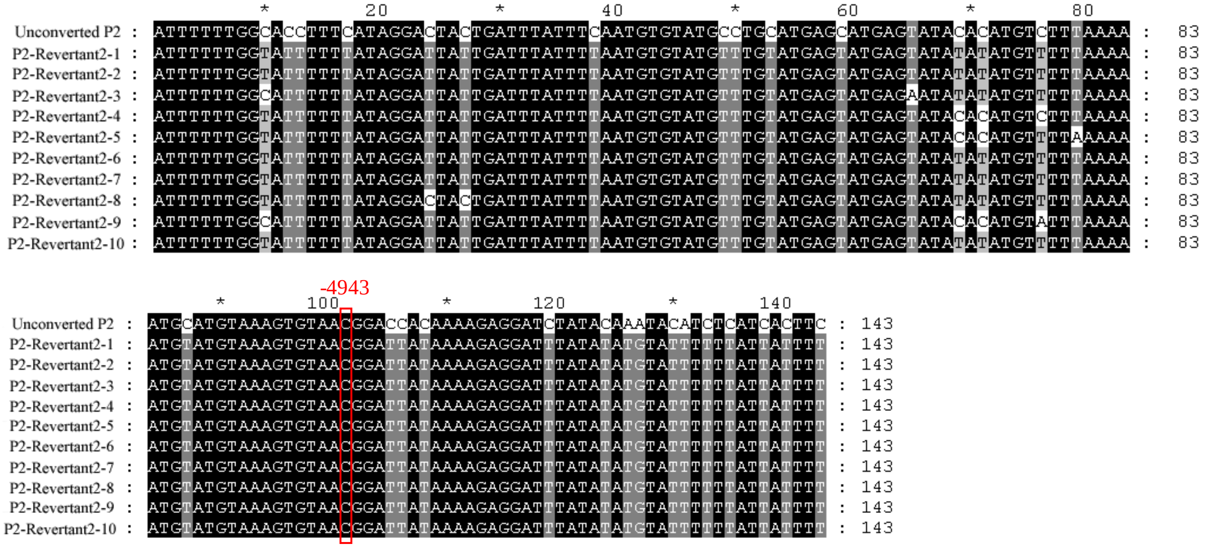


15C



Supplemental Figure 15. Bisulfite sequence alignment of *ATP1* (control gene) and the *FAE1* allele *E*^{3} in the spontaneous revertant Y1130-16.

(**A)** The control gene *ATP1* had 100% complete conversion of C to T in the bisulfite treatment. (**B)** Methylation was not detected at positions -5146 and -5095. (**C)** Methylation was detected at position -4943. Unconverted genomic sequence is shown on the top. P1: The promoter region (nucleotides -5234 to -4978) amplified using primer pair No 30. P2: The promoter region (nucleotides -5042 to -4900) amplified using primer pair No 29. Revertant 2: Spontaneous revertant Y1130-16. Ten clones were analyzed for each bisulfite experiment.

Supplemental Table 1 Primer pairs used in this study

No	Primer name	Sequence (5'-3')	Purpose
1	OF	ATGACGTCCGTTAACGTA	To clone the entire coding region of E^{1}, E^{2}, E^{3}
	OR	TTAGGACCGACCGTTTTG	
2	PF	TCGGTTCGGTTCTCTACATC	To clone the partial coding region of allele *e*
	OR	TTAGGACCGACCGTTTTG	
3	ZUP1-GSP-1*	GAAGGTAGCATGAGTACTCAACGAGGT	To clone the remaining coding region of *e* by PCR walking
	ZUP1-GSP-2**	GATGTAGAGAACCGAACCGAAGACGGT	
4	DOWN-GSP-1*	TGGAGGCATCAAGATCAACGTTACATA	To clone the 3' downstream sequences from the translation stop coding site for E^{1}, E^{2}, E^{3} and *e*
	DOWN-GSP-2**	TTCAGCTAAGTCAGAGACTCGTGTCCA	
5	HUP1-GSP-1*	TGATAGGCTGAACCGACAGAGACTCTG	To clone the 5' upstream sequence of E^{1}, E^{2}, E^{3}
	HUP1-GSP-2**	ACCGACAGAGACTCTGACTAATTATGG	
6	MUP1-GSP-1*	ACGTCTATCGACCTCTGCCAATGTGTA	Primer pairs 6-9: to clone further 5' upstream sequence of E^{2} and E^{3}
	MUP1-GSP-2**	CGATGACAAGGTCCACCAGTTCATAAT	
7	MUP2-GSP-1*	AATCTTGTCTCCATACCACCTTGTTCG	
	MUP2-GSP-2**	GTTCTATATGTGCCATCCTTGAACTGC	
8	MUP3-GSP-1*	TCACACCATCTCTGTTCCTCAGTCCTC	
	MUP3-GSP-2**	CGTCTTCGGTCCAAGGTAACACACTCT	
9	MUP4-GSP-1*	TGCTTGGAGACTCGCCTATCAGTTGGA	
	MUP4-GSP-2**	CAGGACACAGTATCTCACTCTTCCGCA	
10	CORE-F	GCCTATCATTGCTAAGTACA	To clone the 703 bp putative promoter sequences of E^{2}, E^{3} and *e*
	CORE-R	CTCATGCAGGCATACACATT	
11	GAP-F	CAATGTGTATGCCTGCATGA	To clone the DNA fragment between the promoter and 5' flanking sequence of E^{2} and E^{3}
	GAP-R	TTGAAGGACAACATACGTGG	

12	MUP5-GSP-1* MUP5-GSP-2**	ATCCTCTTTTGTGGTCCGTTACACTTT TTTTGTGGTCCGTTACACTTTACATGC	To clone further promoter sequences of E^2 and E^3
13	GAP0-F GAP0-R	CGACACACACACAGAGCA CACGGATGGCTGCAGTACAC	To clone the DNA fragment between the promoter and 5’ flanking sequence of *e*
14	WF WR	GCCTATCATTGCTAAGTAGA TACTAGAACACCACTGCATT	To clone the entire gene sequences of E^1, E^2, E^3 and *e*
15	YF YR	GAGCAATGACGTCCGTTA GGACCGACCGTTTTG	To amplify the coding regions of E^1 and E^2 for yeast expression
16	ProF ProR	CGTAAGCTTCCTATCATTGCTAAGTAGAA AGCTCTAGACTCATGCAGGCATACACATT	To clone the 5’ upstream sequence from the translation start site for E^1
17	FP1 FP2	CGTAAGCTTTCTTCTTGAACTACCTTGGA AGCTCTAGATGCTCTGTGTGTGTGTCG	To clone the 5’ upstream sequence from the translation start site for E^2 and E^3
18	OF RTR	ATGACGTCCGTTAACGTA AAGACTTGTCGTCAGCTCCA	RT-PCR
19	FAE1F1 FAE1R1	AGACGGTCCAAGTACGAGCTAGTTC TGCCGCTCTCATCATCTCCTT	Quantatitive Real-time PCR
20	ActinF ActinR	ACGAGCTACCTGACGGACAAG GAGCGACGGCTGGAAGAGTA	RT-PCR, Quantatitive Real-time PCR
21	ATP1-F ATP1-R	TGAAYGAGATTYAAGYTGGGGAAATGGT CCCTCTTCCATCAATARRTACTCCCA	To amplify the *ATP1* gene as bisulfite control
22	BSPCF1 BSPCR1	YGTTYGTTAAYGTAAAGTTTTTTT TCCTCAAAAACTCAAACCAAAAC	To study DNA methylation of the coding region of position 1 to 200 of E^1 E^2 and E^3
23	BSPCF2 BSPCR2	TTTTTATCGTTTTCGGTTCGG CTACAACCCATACCACCAAAA	To study DNA methylation of the coding region of position 181 to 651 of E^1, E^2 and E^3
24	BSPCF3 BSPCR3	TTTTGGTTTGAGTTTTTGAGG CAACAAATCCTTAACCAAATCA	To study DNA methylation of the coding region of position 361 to 711 of E^1, E^2 and E^3
25	BSPCF4	TGATTTGGTTAAGGATTTGTTG	To study DNA methylation of the coding region of position 689 to 1143

	BSPCR4	AAATAATCAATAACAAATTTA	of E^1, E^2 and E^3
26	BSPCF5 BSPCR5	TTTAAATTTGTTATTGATTATTTTTGT CATTACTTAAAACCACCCAA	To study DNA methylation of the coding region of position 1141 to 1411 of E^1, E^2 and E^3
27	BSPCF6 BSPCR6	GTTAGGGTTTAAGTGTAATAG CCGACCGTTTTAAACACGAATC	To study DNA methylation of the coding region of position 1365 to 1515 of E^1, E^2 and E^3
28	BSP1F BSP1R	ATTTTTTGGTATTTTTTATAGGATTAT AATAAACCRTAAAACTTTTCC	To study DNA methylation of the promoter region of position -143 to 56 of E^1
29	BSP1F BSP2R	ATTTTTTGGTATTTTTTATAGGATTAT AATTTCCTATTTATCRACAAAAAA	To analyze DNA methylation of the promoter region of position-5042 to -4843 of E^2 and E^3
30	BSP2F BSP3R	TAAAGAAGATTTTTGTAGTTAGAGATAGA ACTCATACTCATACAAACATACACA	To study DNA methylation of the promoter region of position -335 to -79 and position -5234 to -4978 of E^2 and E^3
31	OF GR	ATGACGTCCGTTAACGTA AAGGTGCCAGAACACTGCTC	To produce marker specific for *e*
32	MF MR	CAATGTGTATGCCTGCATGA CGAGTATCGAGCTATGTCTG	To generate marker specific for E^2
33	AtSN1F AtSN1R	AGTGGTGGTTGTATAAGTTTAG TAAACATAAAAAAAAATTCCTTT	To amplify the *AtSN1* (positive control for bisulfite sequencing)

*: *FAE1* gene-specific primer for the primary PCR. The adapter primer for the primary PCR is AP1 (5'-GTAATACGACTCACTATAGGGC -3') (Siebert et al., 1995).

**: *FAE1* gene-specific primer for the nested (secondary) PCR. The adapter primer for the nested PCR is AP2 (5'-ACTATAGGGCACGCGTGGT -3') (Siebert et al., 1995).