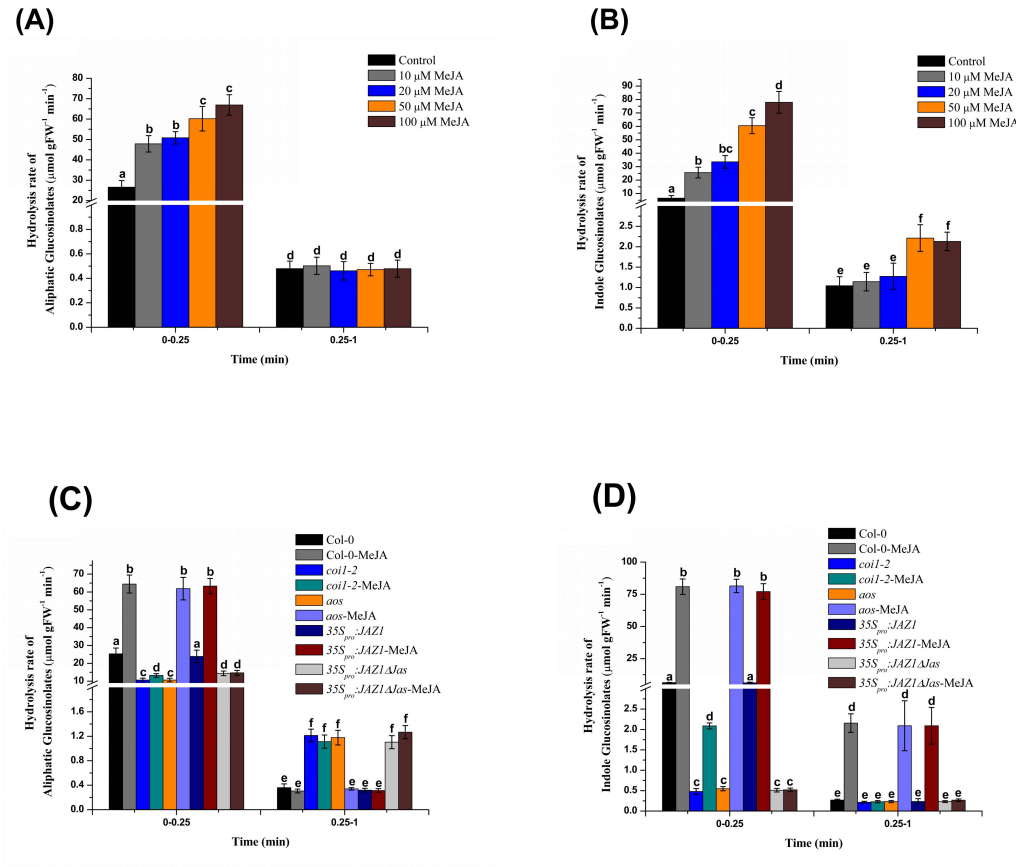
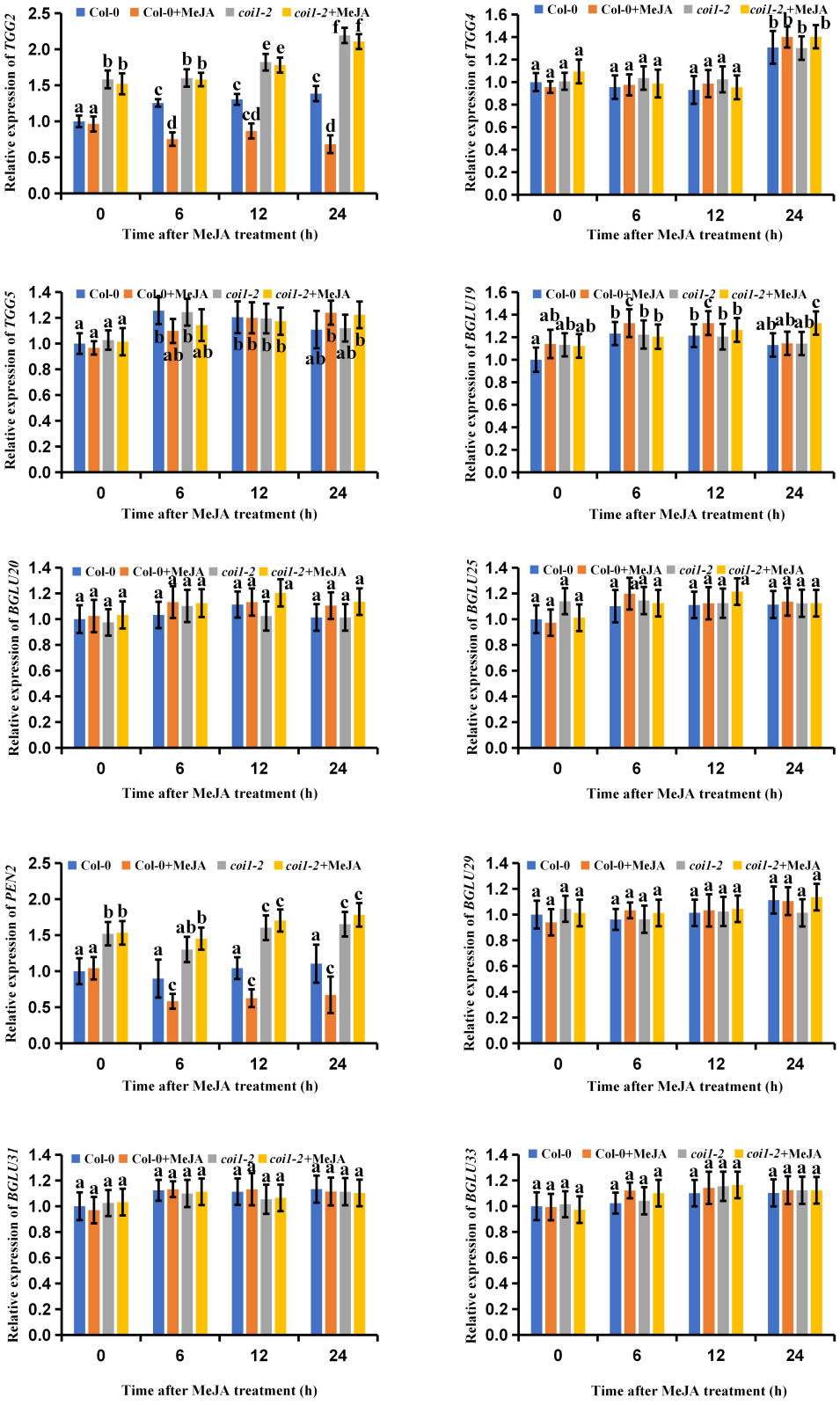


Supplemental Figure S1. The JA signal positively regulates the hydrolysis rate of glucosinolates.

(A) and (B) Hydrolysis rate of aliphatic glucosinolates (A) and indole glucosinolates (B) at different times after different concentrations of MeJA pretreatment for 72 h.

(C) and (D) Hydrolysis rate of aliphatic glucosinolates (C) and indole glucosinolates (D) at different times of 21-old-day seedlings of different genetic materials of JA synthesis and signal molecules after 100 μM of MeJA pretreatment for 72 h.

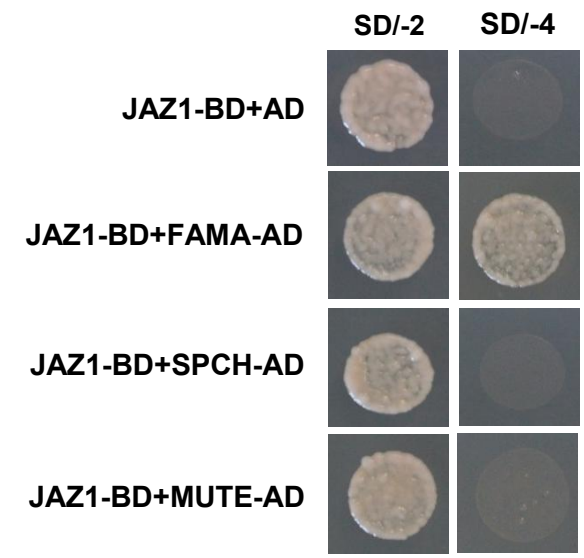
A-D, seedlings of 21-day-old plants were crushed in water to allow a breakdown of glucosinolates by myrosinase. Myrosinase activity was stopped by heat inactivation at the indicated time points and the remaining glucosinolates were extracted. For details on calculating the hydrolysis rate of glucosinolate, see the method section. Values are means ± SEM of eight independently grown plants. The experiments were repeated at least three times with similar results. Different letters represent significant differences ($P < 0.05$, Student's *t*-test).



Supplemental Figure S2. Expression levels of JA-unaffected and -downregulated myrosinase genes.

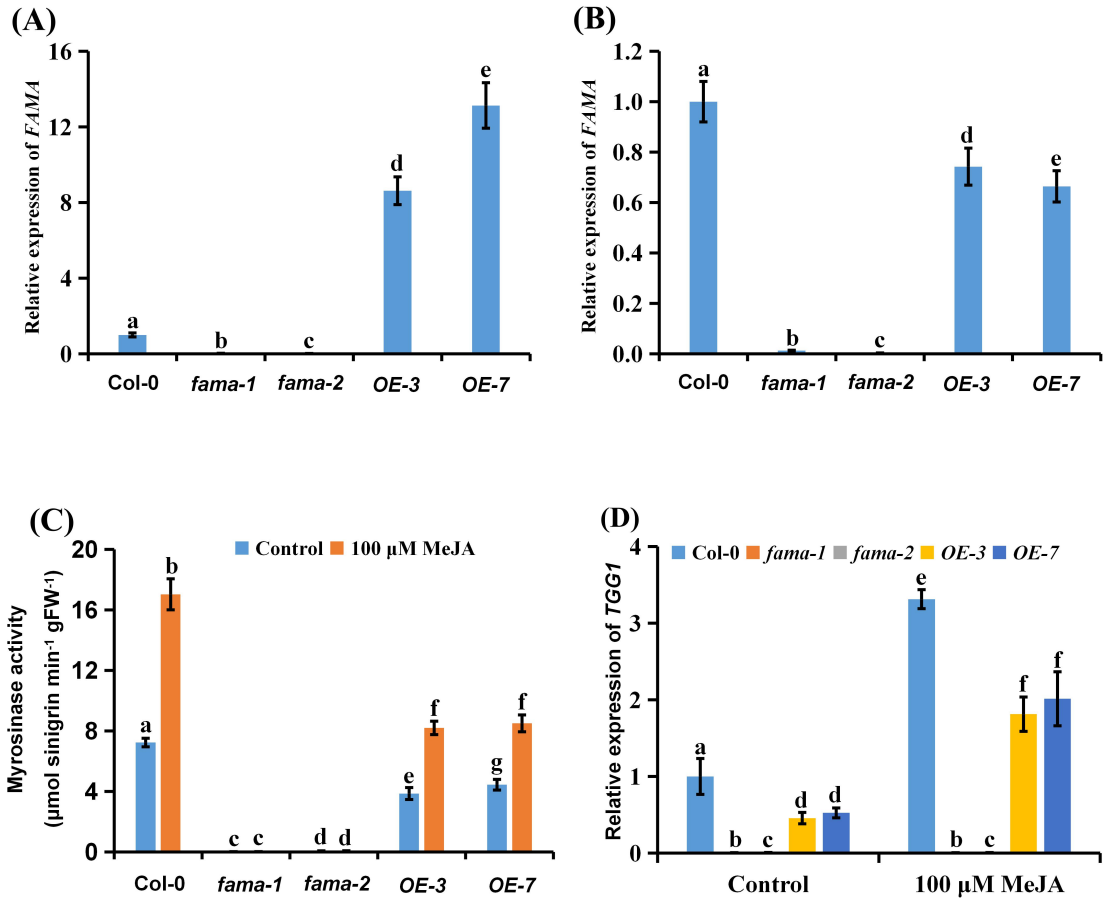
Expression levels of *TGG2*, *TGG4*, *TGG5*, *BGLU19*, *BGLU20*, *BGLU25*, *PEN2*, *BGLU29*, *BGLU31*, and *BGLU33* of 21-day-old seedlings of wild-type (Col-0) and

coi1-2 were treated with 100 μM of MeJA for the indicated time periods. The treated plants were harvested for total RNA extraction and RT-qPCR assays. Means ± SEM are relative values obtained from three technical replicates. Different letters represent significant differences ($P < 0.05$, Student's *t*-test).



Supplemental Figure S3. JAZ1 did not interact with MUTE or SPCH.

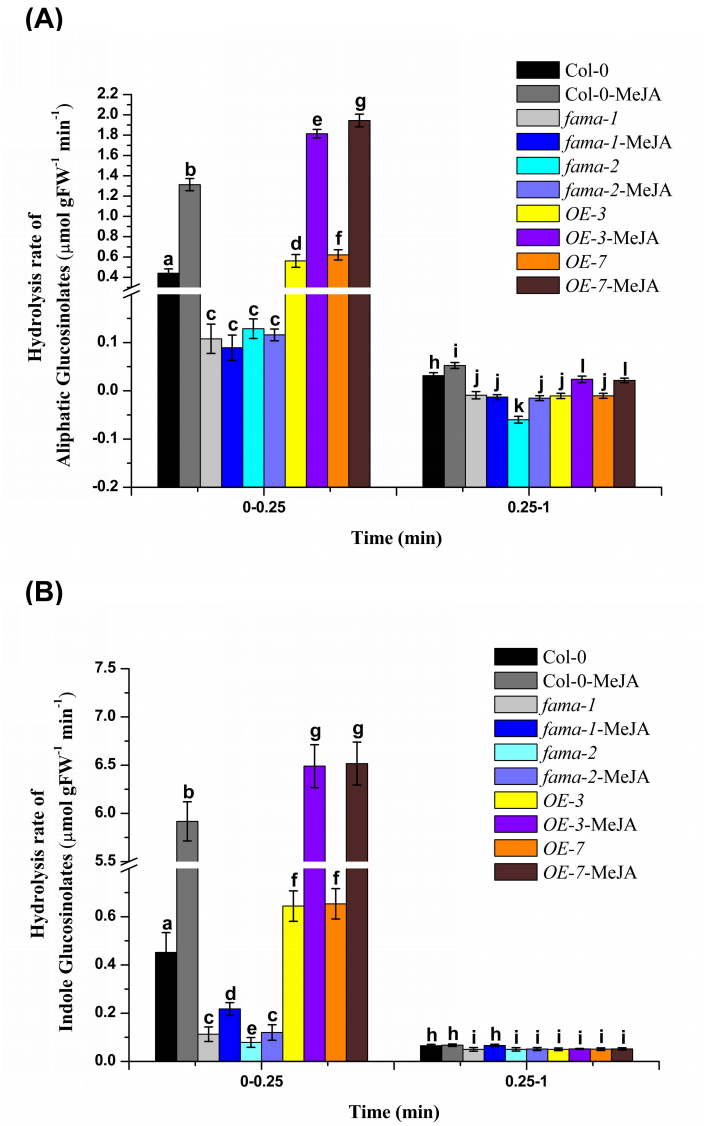
Yeast cells cotransformed with pGADT7-FAMA, or pGADT7-MUTE, or pGADT7-SPCH, or pGADT7-AP2 (preys) and pGBKT7-JAZ1-12 (bait) were grown on yeast synthetic dropout lacking Leu and Trp (SD/-2) as transformation control or on selective media lacking Ade, His, Leu, and Trp (SD/-4) to test protein interactions.



Supplemental Figure S4. The phenotypes of 21-day-old *FAMA* mutants and overexpression plants in JA-regulated myrosinase activity.

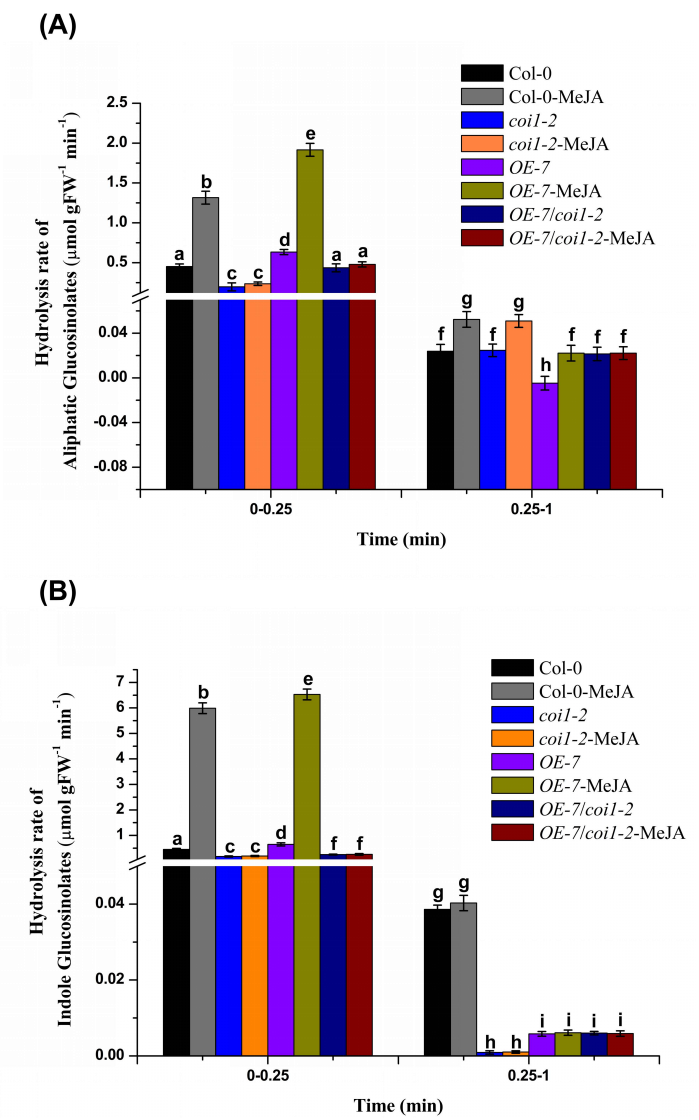
(A) and (B) The expression levels of *FAMA* of five-day-old seedlings of indicated genotypes (A) and *FAMA* of 21-day-old seedlings of indicated genotypes. Plants of different growth stages were harvested for total RNA extraction and RT-qPCR assays. Means ± SEM are relative values obtained from three technical replicates; different letters represent significant differences ($P < 0.05$, Student's *t*-test).

(C) and (D) Myrosinase activity (C) and expression levels of *TGG1* (D) of 21-day-old seedlings of the indicated genotypes after treating with 100 μM of MeJA for 24 h. Values are means ± SEM of 8 to 16 plants. The experiments were repeated at least three times with similar results. Different letters represent significant differences ($P < 0.05$, Student's *t*-test).



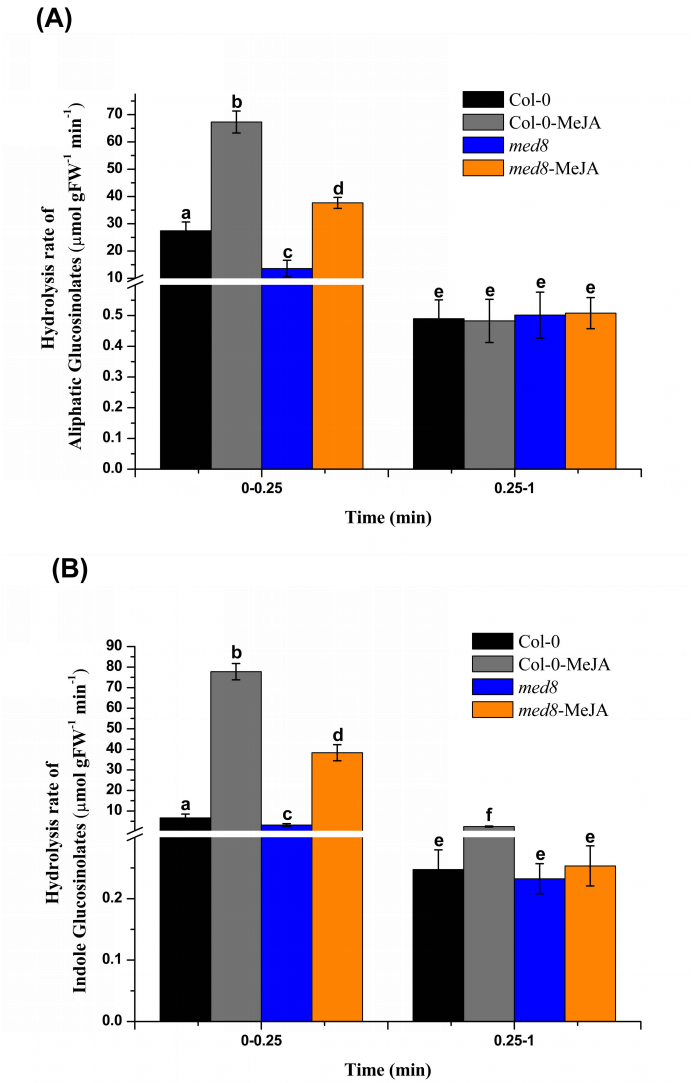
Supplemental Figure S5. FAMA positively regulates the hydrolysis rate of glucosinolates.

(A) and (B) Hydrolysis rate of aliphatic glucosinolates (A) and indole glucosinolates (B) at different times of five-old-day seedlings of indicated genetic plants after 100 μM of MeJA pretreatment for 72 h. Seedlings of five-day-old plants were crushed in water to allow a breakdown of glucosinolates by myrosinase. Myrosinase activity was stopped by heat inactivation at the indicated time points and the remaining glucosinolates were extracted. For details on calculating the hydrolysis rate of glucosinolate, see the method section. Values are means ± SEM of eight independently grown plants. The experiments were repeated at least three times with similar results. Different letters represent significant differences ($P < 0.05$, Student's *t*-test).



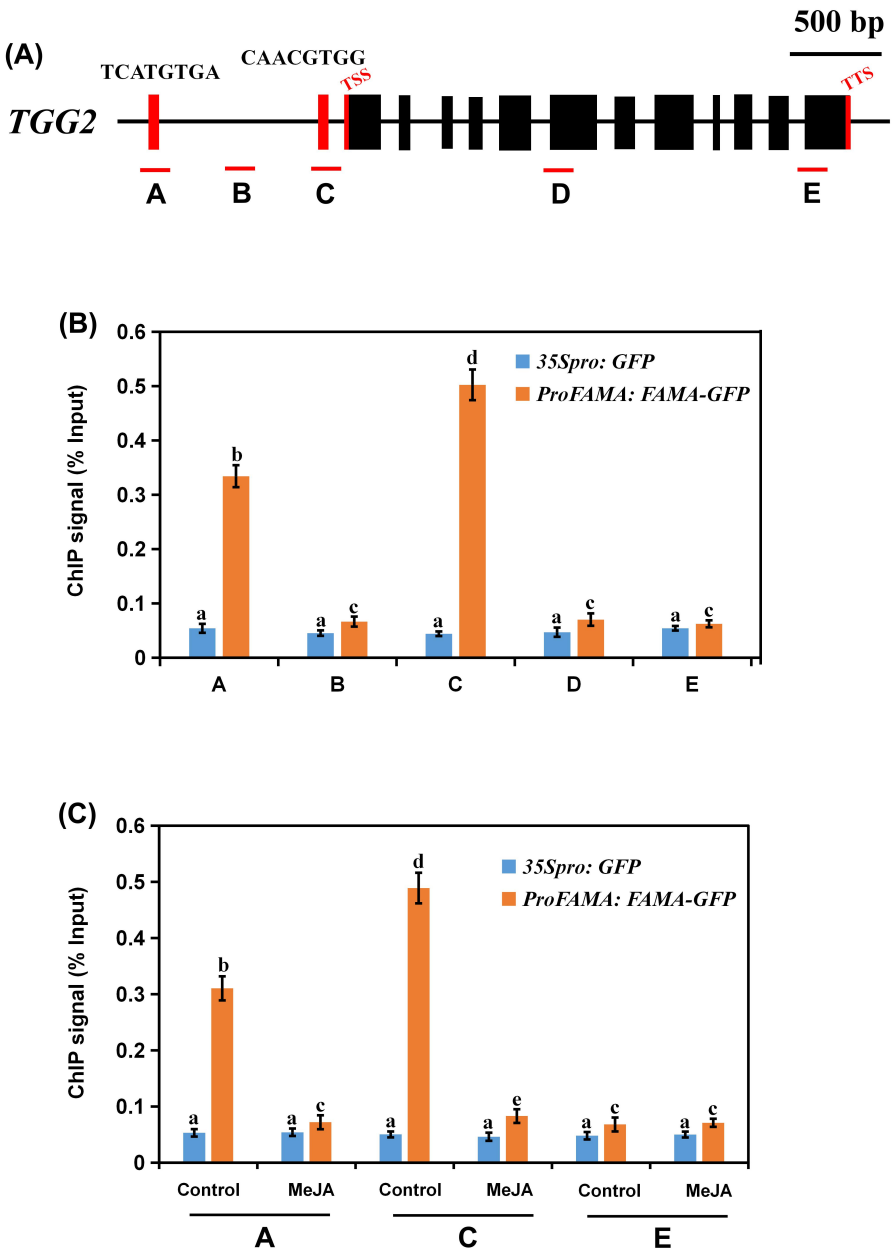
Supplemental Figure S6. Transgenic expression of *FAMA* rescues the reduced hydrolysis rate of glucosinolates of *coi1-2* mutant.

(A) and (B) Hydrolysis rate of aliphatic glucosinolates (A) and indole glucosinolates (B) at different times of five-old-day seedlings of indicated genetic plants after 100 μM of MeJA pretreatment for 72 h. Seedlings of five-day-old plants were crushed in water to allow a breakdown of glucosinolates by myrosinase. Myrosinase activity was stopped by heat inactivation at the indicated time points and the remaining glucosinolates were extracted. For details on calculating the hydrolysis rate of glucosinolate, see the method section. Values are means ± SEM of eight independently grown plants. The experiments were repeated at least three times with similar results. Different letters represent significant differences ($P < 0.05$, Student's *t*-test).



Supplemental Figure S7. MED8 positively regulates the hydrolysis rate of glucosinolates.

(A) and (B) Hydrolysis rate of aliphatic glucosinolates (A) and indole glucosinolates (B) at different times of 21-old-day seedlings of indicated genetic plants after 100 μM of MeJA pretreatment for 72 h. Seedlings of 21-day-old plants were crushed in water to allow a breakdown of glucosinolates by myrosinase. Myrosinase activity was stopped by heat inactivation at the indicated time points and the remaining glucosinolates were extracted. For details on calculating the hydrolysis rate of glucosinolate, see the method section. Values are means ± SEM of eight independently grown plants. The experiments were repeated at least three times with similar results. Different letters represent significant differences ($P < 0.05$, Student's *t*-test).



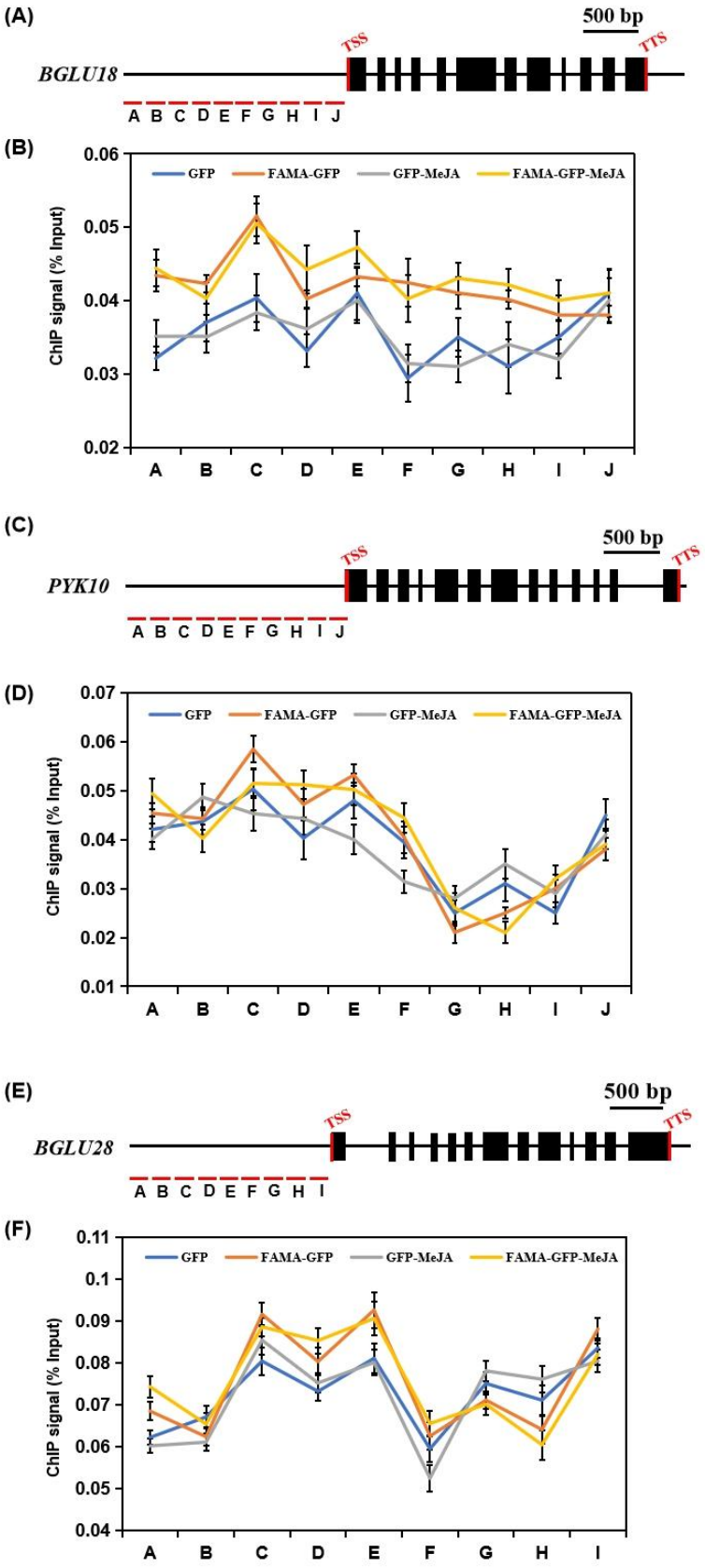
Supplemental Figure S8. JA repressed the occupation of FAMA on the G-box like region in the promoter of *TGG2*.

(A) Schematic diagram of *TGG2* indicating the amplicons and probe used for the ChIP-qPCR assay. Positions of the transcription start site (TSS) and transcription termination site (TTS) are indicated with thin red bars.

(B) ChIP-qPCR assays showing that FAMA associates with the *TGG2* locus. The chromatin of transgenic plants expressing *ProFAMA: FAMA-GFP* or *35S$_{pro}$: GFP* was immunoprecipitated with an anti-GFP antibody, and *35Spro: GFP* plants served as control. Immunoprecipitated chromatin was analyzed by RT-qPCR using primers

corresponding to the amplicons represented by the schematic diagram of *TGG2* (A). ChIP signal was displayed as the percentage of total input DNA. Means ± SEM are relative values obtained from three technical replicates; different letters represent significant differences ($P < 0.05$, Student's *t*-test).

(C) Dynamic recruitment of FAMA to the *TGG2* locus. ChIP assays were performed as in (B), except that *ProFAMA: FAMA-GFP* and $35S_{pro}$*: GFP* plants were treated with 100 μM of MeJA for 30 min before cross-linking. Means ± SEM are relative values obtained from three technical replicates; different letters represent significant differences ($P < 0.05$, Student's *t*-test).



Supplemental Figure S9. FAMA did not bind the promoters of *BGLU18*, *PYK10*, or *BGLU28*.

(A) Schematic diagram of *BGLU18* indicating the amplicons and probe used for the

ChIP-qPCR assay. Positions of the transcription start site (TSS) and transcription termination site (TTS) are indicated with thin red bars.

(B) ChIP-qPCR assays showing that FAMA does not associate with the *BGLU18* locus. *ProFAMA: FAMA-GFP* and $35S_{pro}$*: GFP* plants were first treated with 100 μM of MeJA for 30 min, and then the chromatins of the treated plants were immunoprecipitated with an anti-GFP antibody, and $35S_{pro}$*: GFP* plants served as control. Immunoprecipitated chromatin was analyzed by RT-qPCR using primers corresponding to the amplicons represented by the schematic diagram of *BGLU18* (A). ChIP signal was displayed as the percentage of total input DNA. Means ± SEM are relative values obtained from three technical replicates.

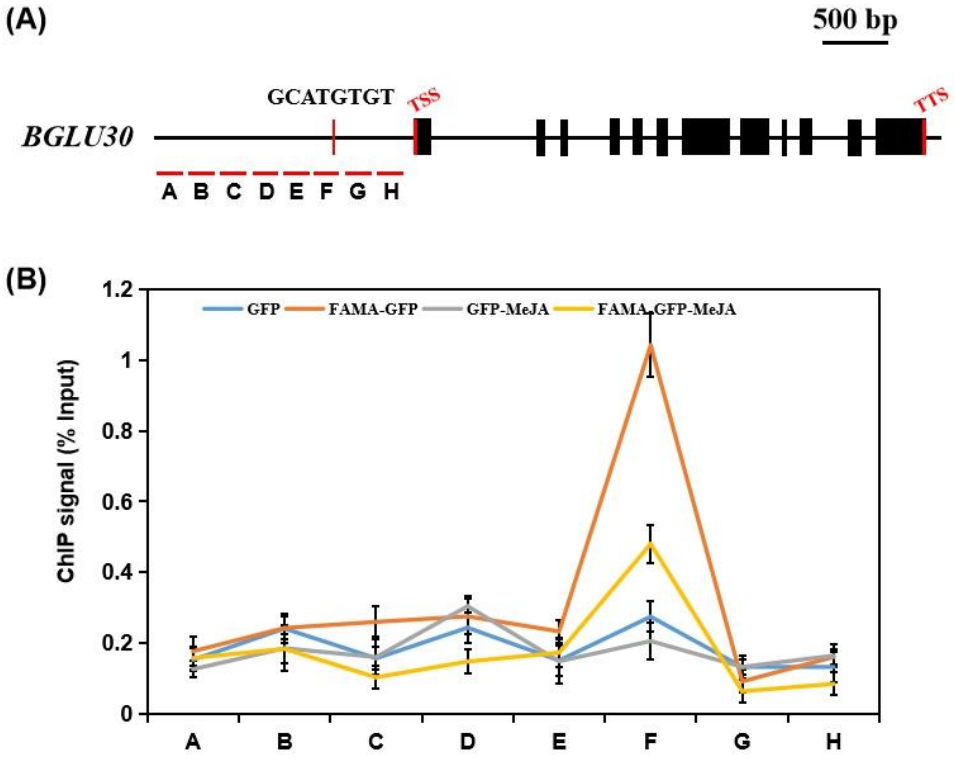
(C) Schematic diagram of *PYK10* indicating the amplicons and probe used for the ChIP-qPCR assay. Positions of the transcription start site (TSS) and transcription termination site (TTS) are indicated with thin red bars.

(D) ChIP-qPCR assays showing that FAMA does not associate with the *PYK10* locus. *ProFAMA: FAMA-GFP* and $35S_{pro}$*: GFP* plants were first treated with 100 μM of MeJA for 30 min, and then the chromatins of the treated plants were immunoprecipitated with an anti-GFP antibody, and $35S_{pro}$*: GFP* plants served as control. Immunoprecipitated chromatin was analyzed by RT-qPCR using primers corresponding to the amplicons represented by the schematic diagram of *PYK10* (A). ChIP signal was displayed as the percentage of total input DNA. Means ± SEM are relative values obtained from three technical replicates.

(E) Schematic diagram of *BGLU28* indicating the amplicons and probe used for the ChIP-qPCR assay. Positions of the transcription start site (TSS) and transcription termination site (TTS) are indicated with thin red bars.

(F) ChIP-qPCR assays showing that FAMA does not associate with the *BGLU28* locus. *ProFAMA: FAMA-GFP* and $35S_{pro}$*: GFP* plants were first treated with 100 μM of MeJA for 30 min, and then the chromatins of the treated plants were immunoprecipitated with an anti-GFP antibody, and $35S_{pro}$*: GFP* plants served as control. Immunoprecipitated chromatin was analyzed by RT-qPCR using primers corresponding to the amplicons represented by the schematic diagram of *BGLU28*

(A). ChIP signal was displayed as the percentage of total input DNA. Means ± SEM are relative values obtained from three technical replicates.



Supplemental Figure S10. FAMA bound the promoters of *BGLU30*.

(A) Schematic diagram of *BGLU30* indicating the amplicons and probe used for the ChIP-qPCR assay. Positions of the transcription start site (TSS) and transcription termination site (TTS) are indicated with thin red bars.

(B) ChIP-qPCR assays showing that FAMA associates with the *BGLU30* locus. *ProFAMA: FAMA-GFP* and *35S$_{pro}$: GFP* plants were first treated with 100 μM of MeJA for 30 min, and then the chromatins of the treated plants were immunoprecipitated with an anti-GFP antibody, and *35S$_{pro}$: GFP* plants served as control. Immunoprecipitated chromatin was analyzed by RT-qPCR using primers corresponding to the amplicons represented by the schematic diagram of *BGLU30* (A). ChIP signal was displayed as the percentage of total input DNA. Means ± SEM are relative values obtained from three technical replicates.

278 **Supplemental Table S1.** Primers used in this study.

Primer name	Sequence (5'-3')	Purpose
TGG1-RT-F	CGTTGATGTTTACAGGACGAAA	Gene expression
TGG1-RT-R	CAGTTGCATCTTTGCTCTCTTG	
TGG2-RT-F	TGGCAGAAAGATCTAGACGTGA	
TGG2-RT-R	TTCCTTTTGGAAGGATTCTTGA	
TGG4-RT-F	TCCCCAAACTTTAGAAGACGAA	
TGG4-RT-R	GTTGCAAGAGAGAAAGGCTGAT	
TGG5-RT-F	ACGCTGAGCTTCTATTCCAAAG	
TGG5-RT-R	CCAGAATCTCCTCCAAGTTCAC	
BGLU18-RT-F	GGGACACAAGATCACAACAGAA	
BGLU18-RT-R	CCACTCAAAGTTGTCCATCAAA	
BGLU19-RT-F	CTGTGGGACATCTACACCAAGA	
BGLU19-RT-R	CCATCAGTGTTCAGCTTTTTCA	
BGLU20-RT-F	GTTTTTCACTGGGACACTCCTC	
BGLU20-RT-R	TGATCCAATGCTTCACTTTGTC	
PYK10-RT-F	ATACGCAAATCCGGAAATTATG	
PYK10-RT-R	TTATGATCAGCGGTACCAACAG	
BGLU21-RT-F	CTCAATCGCATGGTCAAGAATA	
BGLU21-RT-R	ATCGATGAGCTCGTGGTAGAAT	
BGLU22-RT-F	CTCAATCGCATGGTCAAGAATA	
BGLU22-RT-R	CAGGTCGTGGTAGAATTTCACA	
BGLU24-RT-F	ACTTTGAGTGGCAAGATGGTTT	
BGLU24-RT-R	CTCATGACGTGTGAGGTTGTTT	
BGLU25-RT-F	TCAAAGTCCAATGTGGTTTGAG	
BGLU25-RT-R	CCTGAGGGTAATCTCCATGTGT	
PEN2-RT-F	TCGCTTTTCGTGAAGAGTATCA	
PEN2-RT-R	TCCACTCTGATCCTCCTTGTTT	
BGLU27-RT-F	CTTGGCCTAGGATTTTTCCTCT	
BGLU27-RT-R	GCGAGAGGTGTTATTCCGTTAG	
BGLU28-RT-F	TTCCCGATAATTTTGTTTTTGG	
BGLU28-RT-R	GGTTCTTTCTGGAAAAGTGTGG	
BGLU29-RT-F	AAATCGCAGTAACCACGAAACT	
BGLU29-RT-R	AGAACTCTTCGCAAACCTTCTG	
BGLU30-RT-F	TACCCAGTGGAAAGCTAAAGGA	
BGLU30-RT-R	ATGATAGAGCGTCATCGAAGGT	
BGLU31-RT-F	GGGTCGATGTTCTAAATGGGTA	
BGLU31-RT-R	TTTCCTGAACTCTTCAACAGCA	
BGLU32-RT-F	AATGGATCAGTGACACGTGAAG	

BGLU32-RT-R	ATCCAACAATGACCATGTGAAA	
BGLU33-RT-F	CAAATTCTTGCTCATCTTGCTG	
BGLU33-RT-R	ACGTCTTCACTCGAATTTGGAT	
FAMA-RT-F	GGTGAAGAGCAAGAGGAAGAGA	
FAMA-RT-R	AGCCAGGCATGAGAGATCTAAG	
ACT7-RT-F	CCATTCAGGCCGTTCTTTC	
ACT7-RT-R	CGTTCTGCGGTAGTGGTGA	
pGADT7-FAMA-NdeI-F	GGAATTCcatatgATGGATAAAGATTACTCGGCAC	Y2H
pGADT7-FAMA-BamHI-R	CGCggatccTCAAGTAAACACAATATTTCCC	
pGADT7-FAMA head-NdeI-F	GGAATTCcatatgATGGATAAAGATTACTCGGCAC	
pGADT7-FAMA head-BamHI-R	CGCggatccCCACTTCTTCGCTGGTCTTGC	
pGADT7-FAMA tail-NdeI-F	GGAATTCcatatgATGGCAAGACCAGCGAAGAAGTG	
pGADT7-FAMA tail-BamHI-R	CGCggatccTCAAGTAAACACAATATTTCCC	
pGADT7-MUTE-NdeI-F	GGAATTCcatatgATGTCTCACATCGCTGTTGAA	
pGADT7-MUTE-BamHI-R	CGCggatccTTAATTGGTAGAGACGATCAC	
pGADT7-SPCH-NdeI-F	GGAATTCcatatgATGCAGGAGATAATACCGGAT	
pGADT7-SPCH-BamHI-R	CGCggatccCTAGCAGAATGTTTGCTGAAT	
pGBKT7-JAZI-EcoRI-F	TCgaattcATGTCGAGTTCTATGGAAT	
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pGBKT7-JAZ2-SalI-R	CTTgtcgacgCCGTGAACTGAGCCAAGCTGGGTTA	
pGBKT7-JAZ3-EcoRI-F	TCgaattcATGGAGAGAGATTTTCTCGGG	
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pGBKT7-JAZ5-EcoRI-F	GCgaattcATGTCGTCGAGCAATGAAAATGCTAAGGCA	

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pGBKT7-JAZ6-SalI-R	CTTgtcgacgAAGCTTGAGTTCAAGGTTTTTGGA	
pGBKT7-JAZ7-EcoRI-F	gaattcATGATCATCATCATCAAAAACTGC	
pGBKT7-JAZ7-SalI-R	CTTgtcgacgTCGGTAACGGTGGTAAGGGGA	
pGBKT7-JAZ8-EcoRI-F	GGgaattcATGAAGCTACAGCAAAATTGTGACTTGGA	
pGBKT7-JAZ8-PstI-R	AAActgcaggTCGTCGTGAATGGTACGGTGAAGTA	
pGBKT7-JAZ9-EcoRI-F	gaattcATGGAAAGAGATTTTCTGGGTTTG	
pGBKT7-JAZ9-SalI-R	CTTgtcgacgTGTAGGAGAAGTAGAAGAGTAATT	
pGBKT7-JAZI0-EcoRI-F	GCgaattcATGTCGAAAGCTACCATAGAACTCGA	
pGBKT7-JAZI0-SalI-R	CTTgtcgacgGGCCGATGTCGGATAGTAAGGA	
pGBKT7-JAZII-EcoRI-F	GCgaattcATGGCTGAGGTAAACGGAGATTT	
pGBKT7-JAZII-SalI-R	CTTgtcgacgTGTCACAATGGGGCTGGTTTCA	
pGBKT7-JAZI2-EcoRI-F	GGgaattcATGACTAAGGTGAAAGATGAGCCA	
pGBKT7-JAZI2-SalI-R	CTTgtcgacgAGCAGTTGGAAATTCCTCCTT	
pGBKT7-JAZI Jas-EcoRI-F	TCgaattcATGCTTAGCCAAGAATCAAAC	
pGBKT7-JAZI Jas-SalI-R	TTAgtcgacTATTTCAGCTGCTAAACCG	
pGBKT7-JAZI NT-EcoRI-F	TCgaattcATGTCGAGTTCTATGGAAT	
pGBKT7-JAZI NT-SalI-R	TTAgtcgacGGTGCAGTTTGAGACTCTGG	
pGBKT7-JAZI ZIM-EcoRI-F	TCgaattcATGAGAGTCTCAAACTGCACC	
pGBKT7-JAZI ZIM-SalI-R	TTAgtcgacGCTATTAGCGGTGCCTTTGC	
ChIP-TGG1-A-F	GGCTCGTGATGAATGGCAAAC	ChIP-PCR
ChIP-TGG1-A-R	CATATTAGAAATATGATCAAG	
ChIP-TGG1-B-F	GGACAAGAAATCTATTTTTTG	
ChIP-TGG1-B-R	GTTTTCAAATAGGTTCTTCTC	
ChIP-TGG1-C-F	CACATTAAAATGATCAATTG	

ChIP-TGG1-C-R	GAATCCCGTGGGATTGCTTAC	
ChIP-TGG1-D-F	GGTTTGTCGCTTGCATGGTTG	
ChIP-TGG1-D-R	GAGATTACTATGAATATATAG	
ChIP-TGG1-E-F	CTTTATTTTCTCAGTTCAATG	
ChIP-TGG1-E-R	CTCAGTGACATATATTAAAGG	
ChIP-TGG1-F-F	GATGCATGAAATATCCAATCC	
ChIP-TGG1-F-R	CAATACATATGGTAGAAAAAG	
ChIP-TGG2-A-F	TTGAAACGATTAAAAAGTGC	
ChIP-TGG2-A-R	CACCGCTGACATCACATATC	
ChIP-TGG2-B-F	CCAATCCAACCCAAATTGAC	
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ChIP-TGG2-C-F	GCTTGAGATAAAGAAATTTTC	
ChIP-TGG2-C-R	GGGTTCACGTACACGTACTC	
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ChIP-TGG2-D-R	CAGGTCCAATCTTCCCTCCT	
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ChIP-TGG2-E-R	CCCCATCCCATGGCATAATG	
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ChIP-BGLU18-A-R	GTTACAAAGGCAATCTAGTC	
ChIP-BGLU18-B-F	TAAAAATGAAGGTGAGTTTTTG	
ChIP-BGLU18-B-R	CTAAACCAAAAAAGCTGATC	
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ChIP-BGLU18-C-R	CTTATTGGCTTTCGTATTGCG	
ChIP-BGLU18-D-F	TGTTATAGTGCTTTTGCAATT	
ChIP-BGLU18-D-R	CTCTATTTCTCTACCACGAAA	
ChIP-BGLU18-E-F	TTTTGTTGAAAGCCAATGAC	
ChIP-BGLU18-E-R	ATCTTAATTTATTATATTATT	
ChIP-BGLU18-F-F	AACATAGATAAGTTTTTTTTTA	
ChIP-BGLU18-F-R	CAATACGTAAATATATGAATG	
ChIP-BGLU18-G-F	AGTTTTTGATTAAATGTAAAT	
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ChIP-BGLU18-J-F	TAATGTACTAAGTAGTGACTA	
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ChIP-PYK10-B-F	TACACAAACAGCCTTTCTTTC	

ChIP-PYK10-B-R	CCAAAACGTGTACATCCGCTC	
ChIP-PYK10-C-F	TGTGGGTGCGAGTTCCACATC	
ChIP-PYK10-C-R	TGCAGTGGCGAGTCCAAAAAC	
ChIP-PYK10-D-F	ACGAAGTGTACCAACAACTTG	
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ChIP-PYK10-E-F	ATTTGGTCCCCAACAGTCGAAA	
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ChIP-PYK10-G-F	ATTGGGAAATATGCTCTAAGA	
ChIP-PYK10-G-R	GTATAATACTATCTCGTGTTT	
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ChIP-PYK10-I-R	TATTGTTTCTTTACCTTTTTA	
ChIP-PYK10-J-F	TACAACCTATAACGTCAATAT	
ChIP-PYK10-J-R	TTTTACATATCGAAGACGTTC	
ChIP-BGLU28-A-F	GGCTCTGAATTTTTTTATTTTC	
ChIP-BGLU28-A-R	GTTTGATACAAATTCTGCTTG	
ChIP-BGLU28-B-F	TTTTCTTGTGTATCAAACAAA	
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ChIP-BGLU28-C-R	GTCTTTGGATCAGATTCAGG	
ChIP-BGLU28-D-F	TTATGCACGGTTTGATGTAAA	
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ChIP-BGLU28-E-F	ATTCTCTTAATCAAAATGATT	
ChIP-BGLU28-E-R	TAGCCCATTAAGATAATGTTC	
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ChIP-BGLU28-F-R	GTATGATTTACAAGCAGGCG	
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ChIP-BGLU28-H-F	TTCCTTGTGGAATCGGAATTG	
ChIP-BGLU28-H-R	ATTACAATCCAAACCCTTTTTG	
ChIP-BGLU28-I-F	GACACACACTTATTTCTATAG	
ChIP-BGLU28-I-R	TAACTTAATTAACATTAAAC	
ChIP-BGLU30-A-F	AAATTAATTCAACGTTTAGTG	
ChIP-BGLU30-A-R	TTAATCGAGTATTATTAGCTC	
ChIP-BGLU30-B-F	AAAGATATTTTTTGACTTTC	
ChIP-BGLU30-B-R	TTTAGTAAATTATACATTTC	
ChIP-BGLU30-C-F	AGGGAGGGACAAGACAAAAAA	

ChIP-BGLU30-C-R	GAGTGCAGATTTTGTATGGAAG	
ChIP-BGLU30-D-F	AGTAAAAAGAAATTATGTATTG	
ChIP-BGLU30-D-R	CAATACTACCCTCTGTTAAATT	
ChIP-BGLU30-E-F	GATTCTAGAAACCTAAGAATA	
ChIP-BGLU30-E-R	ACTAAATTTATTTTTATTTTAT	
ChIP-BGLU30-F-F	AATAGTATAATTAAATATGTA	
ChIP-BGLU30-F-R	GATTTTAATTGCTTAGAAACA	
ChIP-BGLU30-G-F	TTATCAAAACTTCATTGCCC	
ChIP-BGLU30-G-R	ATTTGTGTGTAAAGTAATGTT	
ChIP-BGLU30-H-F	ATATGATTATATATACATATG	
ChIP-BGLU30-H-R	CATAAGATTTCTTTCCAAGG	
FAMA-nLuc-BamHI-F	CGGggtaccATGGATAAAGATTACTCGGCAC	Firefly luciferase complementation imaging assay
FAMA-nLuc-SalI-R	ACGCgtcgacTCAAGTAAACACAATATTTCCC	
cLuc-JAZI-BamHI-F	CGGggtaccATGTCGAGTTCTATGGAATG	
cLuc-JAZI-PstI-R	AActgcagTCATATTTCAGCTGCTAAAC	
cLuc-JAZ9-BamHI-F	CGGggtaccATGGAAAGAGATTTTCTGGG	
cLuc-JAZ9-PstI-R	AActgcagTTATGTAGGAGAAGTAGAAG	
TGGIPro-LUC-HindIII-F	CCCaagcttAGAAGGATAGAATTATGTTTTG	
TGGIPro-LUC-PstI-R	TAActgcagGGTTTATTAGTAGTGTGTATG	
pMAL-C2X-FAMA-BamHI-F	CGggatccATGGATAAAGATTACTCGGC	Protein purification
pMAL-C2X-FAMA-PstI-R	GCctgcagTCAAGTAAACACAATATTTC	
pET32a-JAZI-SalI-F	GCgtcgacATGTCGAGTTCTATGGAATG	
pET32a-JAZI-XhoI-R	CCGctcgagTCATATTTCAGCTGCTAAAC	

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