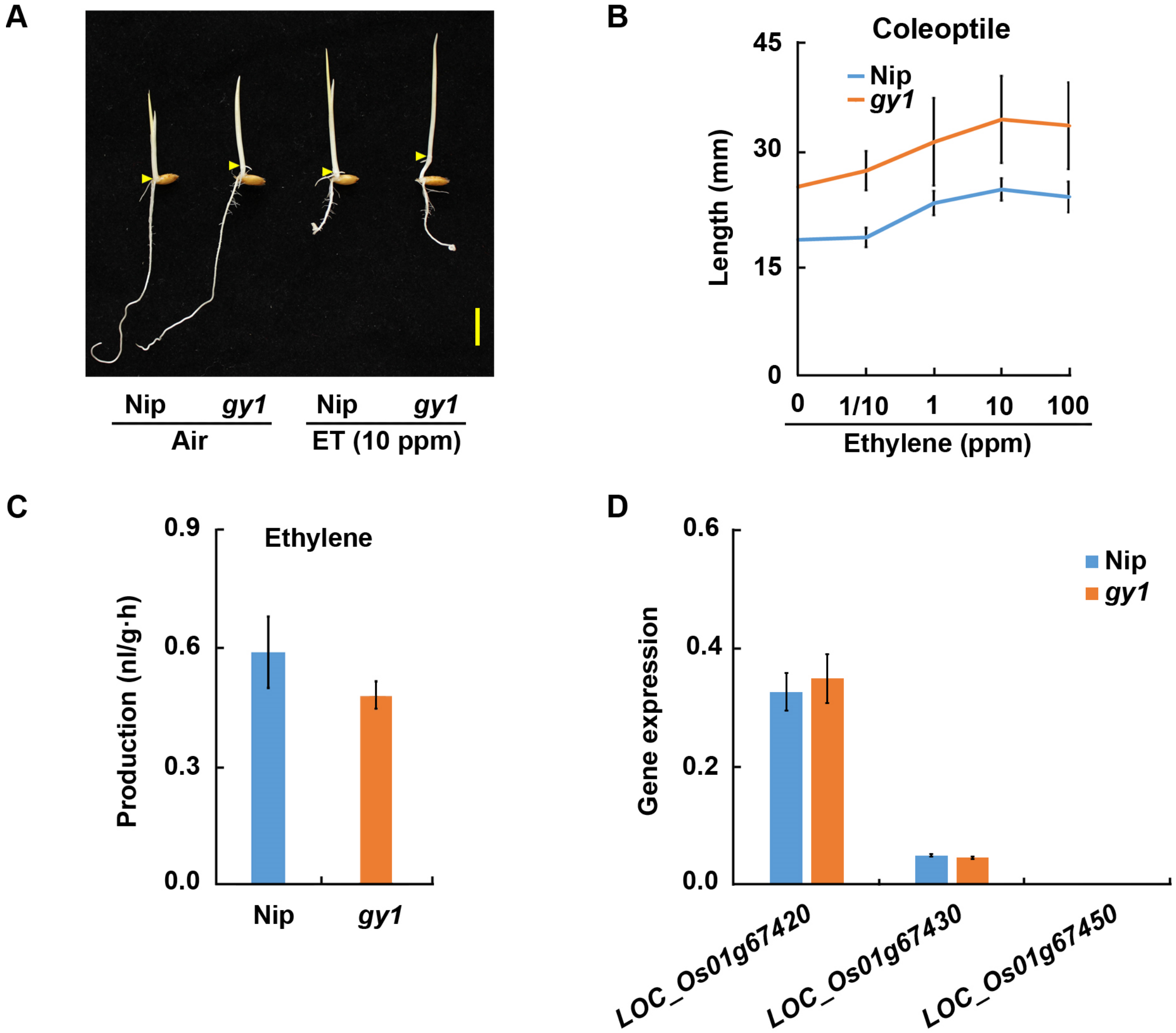


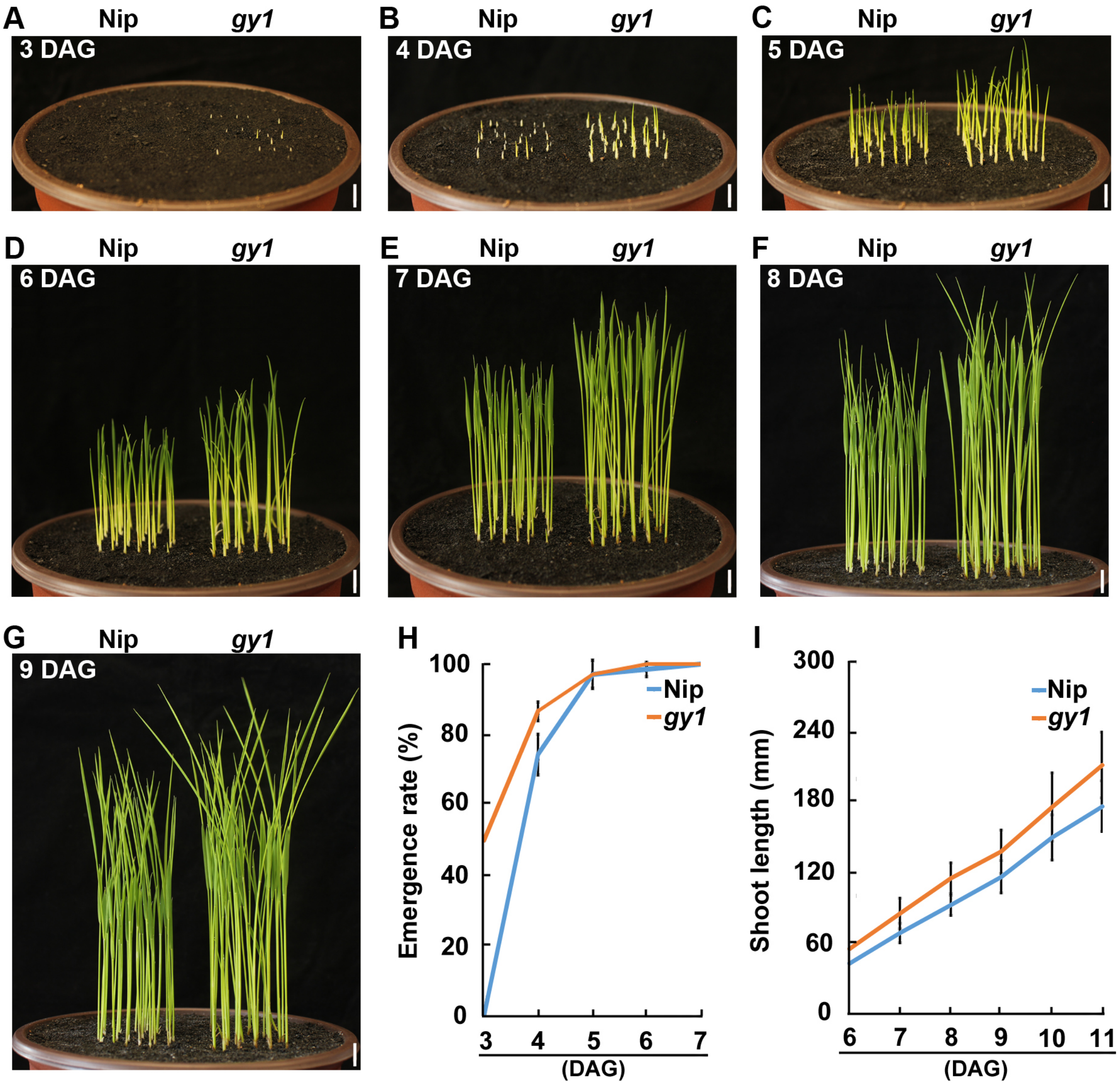
Supplemental Figure 1. Ethylene Response and Ethylene Production of *gy1*.

(A) Etiolated seedlings from Nip and *gy1* with or without 10 ppm ethylene (ET) treatment grown for three days after germination in darkness. Arrows indicate positions of the coleoptilar nodes between mesocotyl and coleoptile. Bar = 10 mm.

(B) Ethylene dose-response curves for coleoptile length from Nip and *gy1* under 0, 1/10, 1, 10 and 100 ppm ethylene treatment. The values are means ± SD of 20 to 30 seedlings per sample.

(C) Ethylene production in Nip and *gy1* etiolated seedlings. The values are means ± SD of three biological replicates (independent pools of tissue) per sample. There is no significant difference between them.

(D) The expression of three genes (*LOC_Os01g67420*, *LOC_Os01g67430* and *LOC_Os01g67450*) located in the fine mapped region. The values are means ± SD of three biological replicates (independent pools of tissue) per sample.



Supplemental Figure 2. Emergence Rate of *gy1* Compared to the Nip Control.

(A) Seedlings of Nip and *gy1* sown at a depth of 2 cm in soil and grown for three days after germination (DAG) with a photoperiod of 14 h light/10 h dark. Bar = 10 mm.

(B) Seedlings of Nip and *gy1* sown at a depth of 2 cm grown for 4 DAG with a photoperiod of 14 h light/10 h dark. Bar = 10 mm.

(C) Seedlings of Nip and *gy1* sown at a depth of 2 cm grown for 5 DAG with a photoperiod of 14 h light/10 h dark. Bar = 10 mm.

(D) Seedlings of Nip and *gy1* sown at a depth of 2 cm grown for 6 DAG with a photoperiod of 14 h light/10 h dark. Bar = 10 mm.

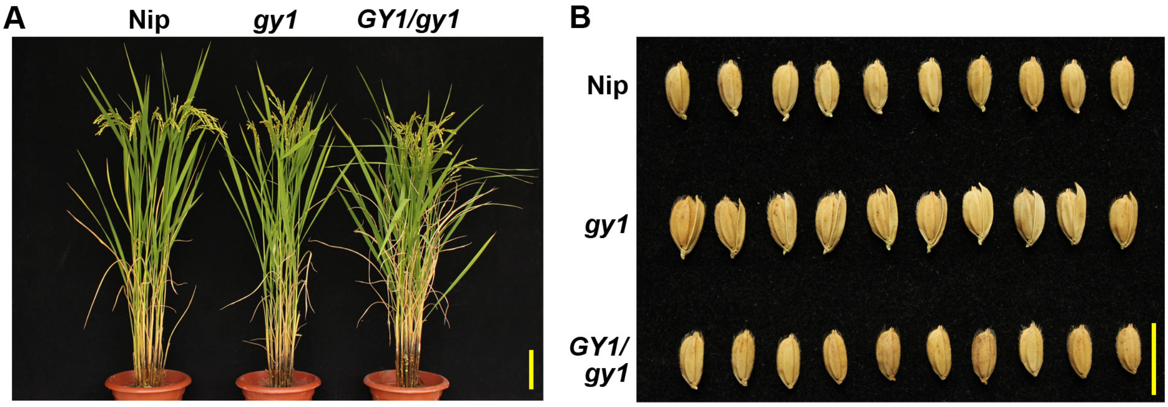
(E) Seedlings of Nip and *gy1* sown at a depth of 2 cm grown for 7 DAG with a photoperiod of 14 h light/10 h dark. Bar = 10 mm.

(F) Seedlings of Nip and *gy1* sown at a depth of 2 cm grown for 8 DAG with a photoperiod of 14 h light/10 h dark. Bar = 10 mm.

(G) Seedlings of Nip and *gy1* sown at a depth of 2 cm grown for 9 DAG with a photoperiod of 14 h light/10 h dark. Bar = 10 mm.

(H) Emergence rate of Nip and *gy1* sown at a depth of 2 cm grown for 3 to 7 DAG with a photoperiod of 14 h light/10 h dark. The values are means ± SD of three biological replicates (independent pools of tissue) per sample.

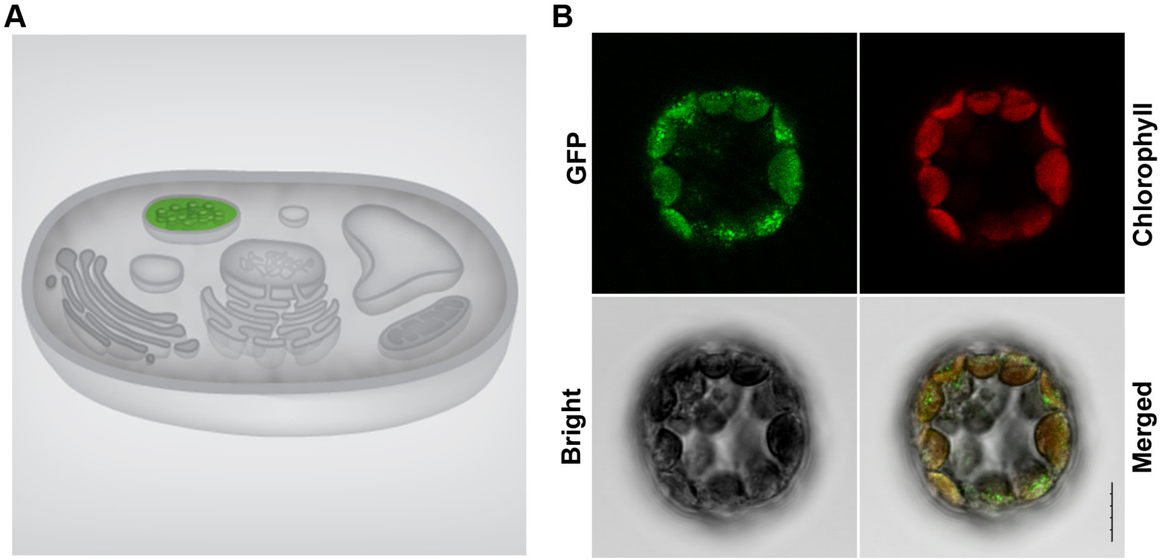
(I) Shoot length of Nip and *gy1* sown at a depth of 2 cm grown for 6 to 11 DAG with a photoperiod of 14 h light/10 h dark. The measurement started from the day when most Nip and *gy1* had emerged from soil. The values are means ± SD of 20 to 30 seedlings per sample.



Supplemental Figure 3. Phenotype of *gy1* and *GY1*-complemental Plants at Maturity.

(A) Adult plants of Nip, *gy1* and the *GY1*-complemented line of *gy1* after grain-filling time in the field. As the panicle shape showed, the complemented line of *gy1* had similar filled grain rate as Nip, while the filled grain rate of *gy1* was much lower. Bar = 10 cm.

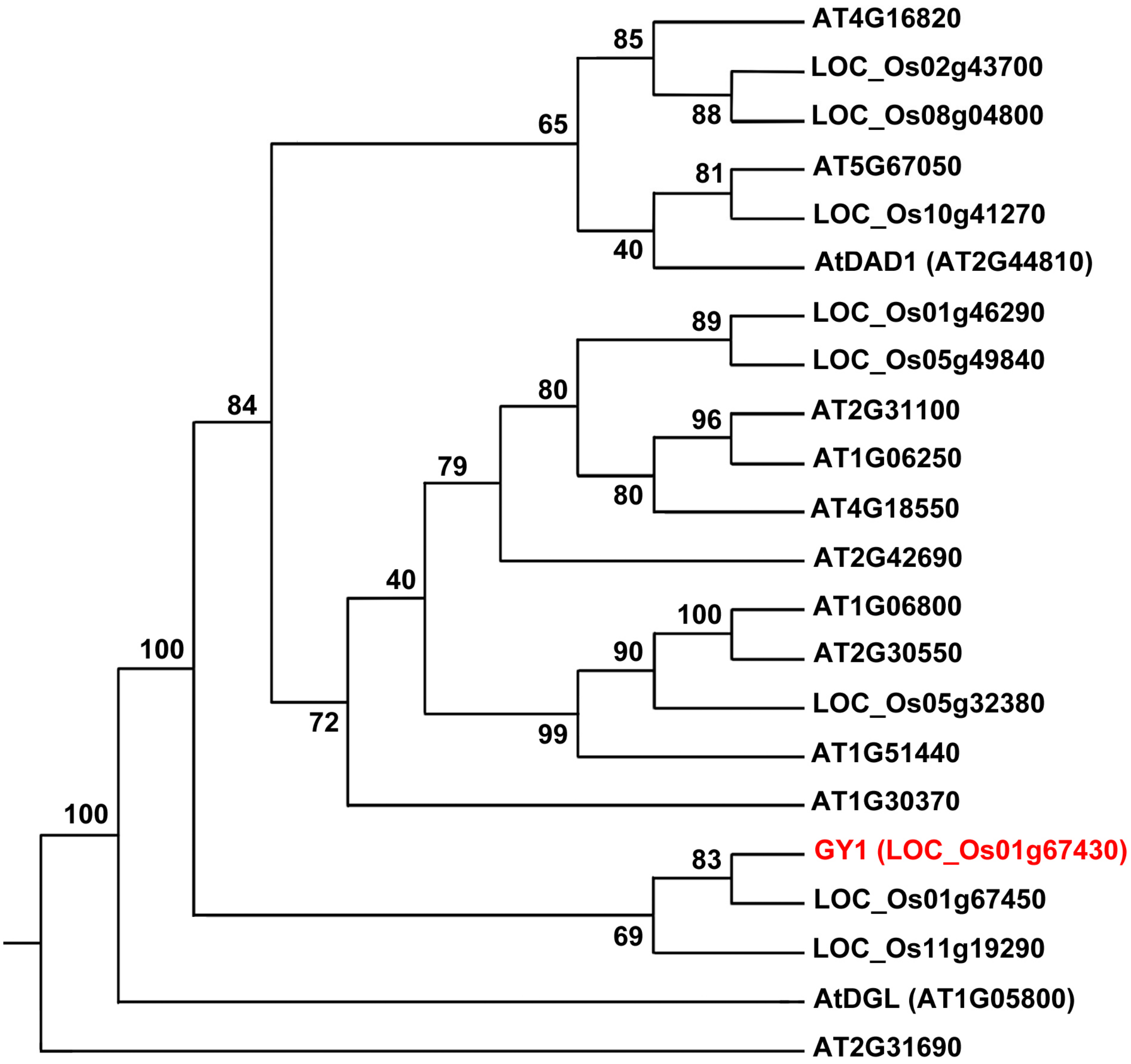
(B) Seeds of Nip, *gy1* and the *GY1*-complemented line of *gy1* after harvest. The extra glume phenotype of *gy1* was completely complemented by *GY1*. Bar = 10 mm.



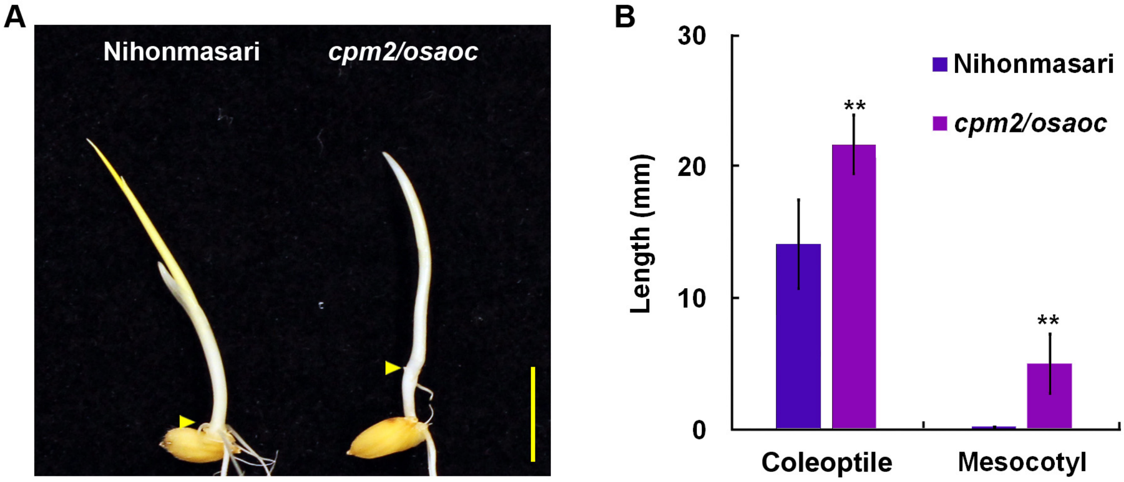
Supplemental Figure 4. GY1 Subcellular Localization in Arabidopsis protoplasts.

(A) GY1 is predicted to localize to the chloroplast, as indicated in green by LocTree3.

(B) GY1 is localized in chloroplasts of Arabidopsis protoplasts as revealed by the merged green fluorescence of GY1-GFP fusion protein and the red autofluorescence of chlorophyll. Bar = 7.5 μM.



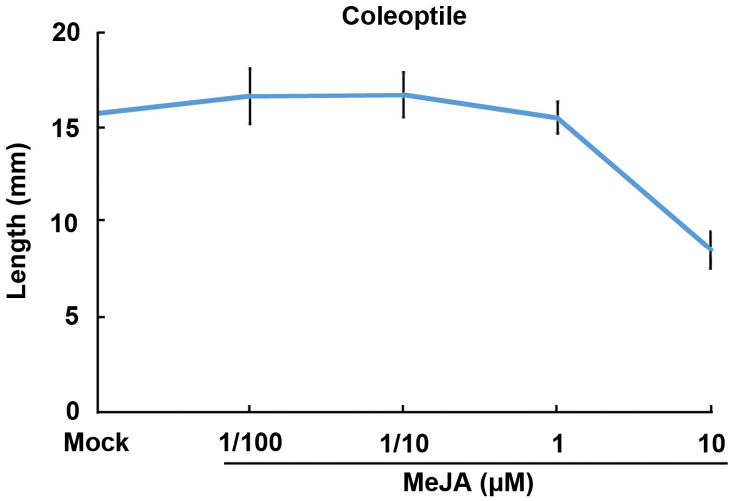
Supplemental Figure 5. Phylogenetic Analysis of GY1 and its Homologues. GY1 (red) is clustered with AtDGL in Arabidopsis. The tree was constructed by Phylip v3.69 with 1000 bootstrap replicates, and the bootstrap value was showed in the branch.



Supplemental Figure 6. Phenotype Analysis of Another JA Biosynthesis Mutant.

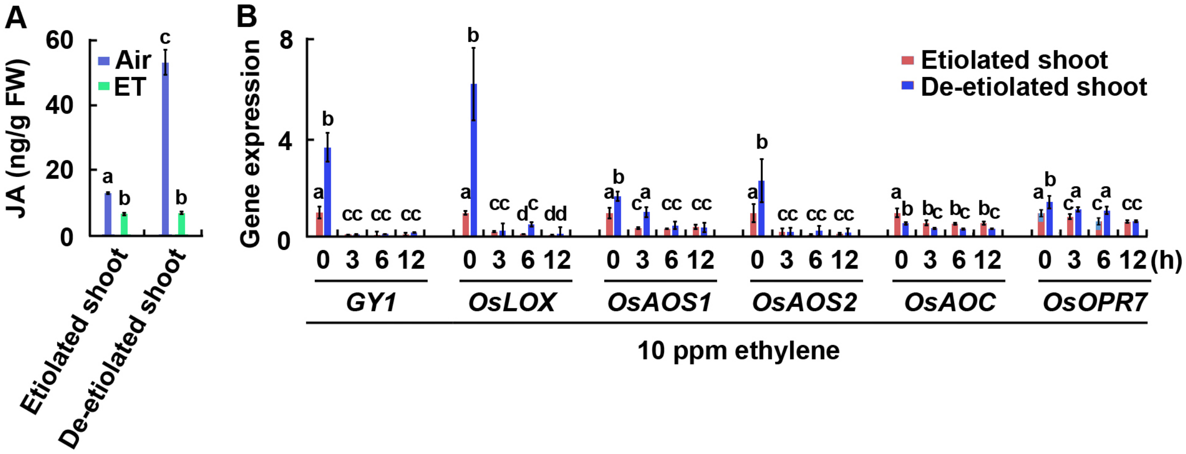
(A) Phenotype of etiolated seedlings from Nihonmasari (wild type of *cpm2/osaoc*) and *cpm2/osaoc* (a JA biosynthesis mutant) grown for three days after germination in dark. Arrowheads indicate the coleoptilar nodes between the mesocotyl and coleoptile. Bar = 10 mm.

(B) Coleoptile and mesocotyl length of etiolated seedlings from (A). The values are means ± SD of 20 to 30 seedlings per sample. The asterisks indicate significant difference compared to Nihonmasari (**, $p < 0.01$, Student’s t-test).



Supplemental Figure 7. MeJA Dose-response Curve for Coleoptile Length of Etiolated Seedlings.

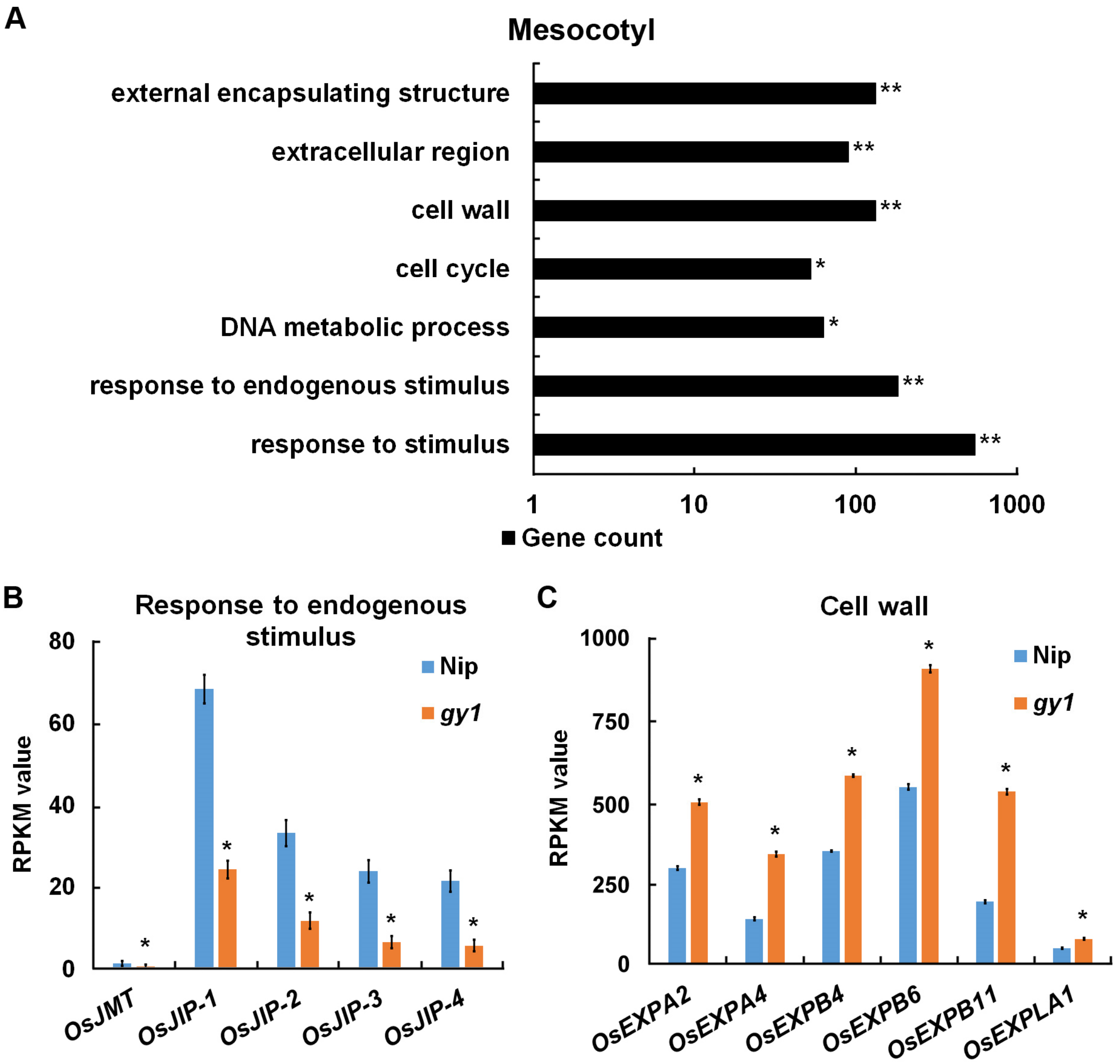
MeJA dose-response curve for coleoptile length of etiolated seedlings from Nip grown for three days after germination in dark. The values are means ± SD of 20 to 30 seedlings per sample. MeJA treatments at concentrations of less than or equal to 1 μM showed no significant effects on coleoptile length.



Supplemental Figure 8. Ethylene Inhibits JA biosynthesis and *GY1* Expression in shoots of de-etiolated seedlings.

(A) JA content in shoots of de-etiolated seedlings. De-etiolated seedling was produced by exposing etiolated seedling to light for 1 hour. ET indicates treatment with 10 ppm ethylene for 8 h. The values are means ± SD of three biological replicates (independent pools of tissue) per sample. Different letters above each column indicate significant difference between the compared pairs ($p < 0.05$, LSD and S-N-K test).

(B) The expression of *GY1*, *OsLOX*, *OsAOS1*, *OsAOS2*, *OsAOC* and *OsOPR7* in shoots of Nip de-etiolated seedlings after 10 ppm ethylene treatment for 8 h. De-etiolated seedling was produced by exposing etiolated seedling to light for 1 hour. The quantitation was performed by qPCR relative to *OsActin2* expression. Each gene expression level at ‘0 h’ treatment was set to 1 and other values were compared with it. The values are means ± SD of three biological replicates (independent pools of tissue) per sample. Different letters above each column indicate significant difference between the compared pairs ($p < 0.05$, LSD and S-N-K test).

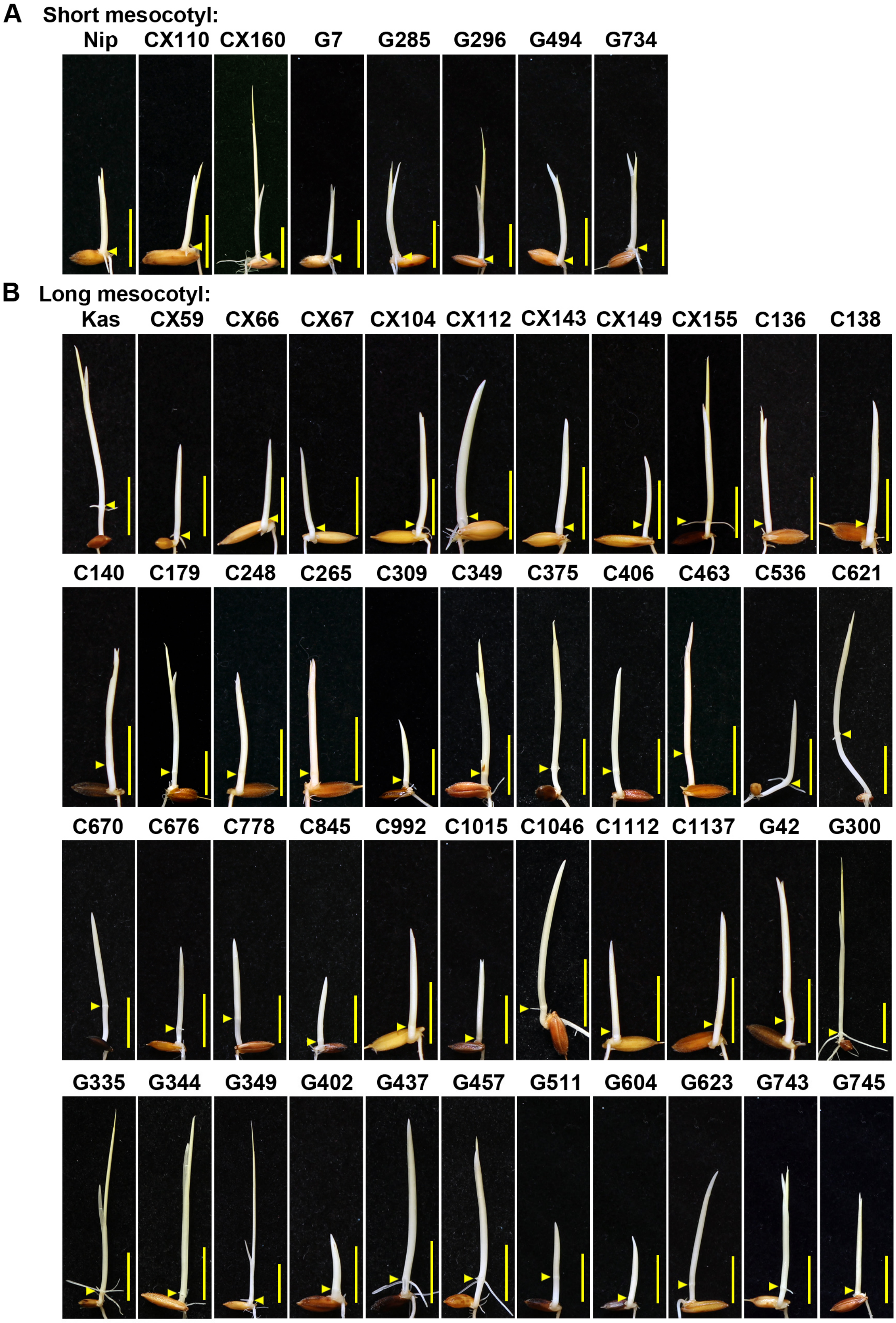


Supplemental Figure 9. Identification of Differentially Expressed Genes and GO Enrichment Analysis.

(A) GO enrichment terms for the shared 2623 DEGs (differentially expressed genes in *gy1* compared to Nip in the mesocotyls of etiolated seedlings) in mesocotyls.

(B) Expression of DEGs in the GO term 'response to endogenous stimulus'. JA biosynthesis-related genes *OsJMT*, and JA-induced gene *OsJIP-1*, *OsJIP-2*, *OsJIP-3* and *OsJIP-4* are significantly down-regulated in *gy1* compared to Nip.

(C) Expression of DEGs in the GO term 'cell wall'. The expression of *OsEXPA2*, *OsEXPA4*, *OsEXPB4*, *OsEXPB6*, *OsEXPB11* and *OsEXPLA1* (*expansin-like A1*) are significantly up-regulated in *gy1* compared to Nip.



Supplemental Figure 10. Phenotype of Etiolated Seedlings from Different Rice Accessions.

(A) Etiolated seedlings from 8 rice varieties with short mesocotyls grown for three days after germination in darkness. Arrowheads indicate the coleoptilar nodes. Bar = 10 mm.

(B) Etiolated seedlings from 44 rice varieties with long mesocotyl grown for three days after germination in darkness. Arrowheads indicate the coleoptilar nodes between coleoptile and mesocotyl. Bar = 10 mm.

Supplemental Table 1. Dominant/Recessive Analysis of Mutant Phenotype.

Cross	F1		F2 segregation			
	−	+	−	+	Expected ratio	χ^2
gy1 × Nip	42	0	68	21	3:1	0.76

+: the gy1 mutant phenotype. −: Nip phenotype. Critical value (0.05, 1) = 3.84.

Supplemental Table 2. Agronomic Traits of Field-Grown Nip and *gy1* in 2012 and 2014.

Plant	In 2012			In 2014		
	Nip	*gy1*		Nip	*gy1*	
Total plant height (cm)	88+/−4	83+/−3	**	93+/−3	88+/−3	**
Tiller number	11+/−3	9+/−3	*	13+/−3	11+/−3	*
Panicle length (cm)	19+/−1	18+/−1		19+/−1	19+/−1	**
Grain number per plant	991+/−319	697+/−265	**	1,044+/−230	727+/−204	**
Grain number per spike	88+/−12	75+/−11	**	82+/−9	65+/−6	**
Filled grains per plant	827+/−324	191+/−126	**	873+/−225	287+/−105	**
Filled grain rate (%)	82+/−14	26+/−9	**	84+/−12	40+/−10	**
Filled grain weight (g)	18+/−7	4+/−3	**	19+/−5	7+/−3	**
1000 grain weight (g)	21+/−1	21+/−1		22+/−1	23+/−1	

The values are means +/− SD of 25 plants per sample. SPSS 18.0 one-way ANOVA (LSD and S-N-K) was used in the statistical analysis. The asterisks indicate significant difference compared to the corresponding controls (*, P<0.05; **, P<0.01).

Supplemental Table 3. Allelic Variation of GY1 in Rice Accessions.

Species	Subgroup	Total	*GY1* 376 bp			
			G	T (%)	C	A
Indica	Aus/boro	189	151	38 (20.1)	0	0
	Indica	1,564	1,511	53 (3.4)	0	0
Intermediate type	Intermediate type	84	75	9 (10.7)	0	0
Japonica	Aromatic (basmati/sandri type)	55	24	31 (57.4)	0	0
	Japonica	66	63	3 (4.5)	0	0
	Temperate japonica	49	44	5 (10.2)	0	0
	Tropical japonica	76	74	2 (2.6)	0	0

The nucleotide at 376 bp of GY1 is G for Nip. The percentage represents its ratio in each subgroup.

Supplemental Table 4. The Mesocotyl and Coleoptile Length in Different Genotypes of *GY1* in Etiolated Seedlings of Different Varieties.

Name	376 bp	Mesocotyl Phenotype	Mesocotyl length (mm)	Coleoptile length (mm)	Variety	Subgroup
Nip	G	short	0.0	13.3+/−1.3	NIPPONBARE	Japonica
CX110	G	short	0.0	14.4+/−1.5	UP15	Aromatic
CX160	G	short	0.0	18.6+/−1.7	W1263	Indica
G7	G	short	0.0	15.5+/−1.7	BASMATI 1	Aromatic
G285	G	short	0.0	20.4+/−3.3	RAYADA	Aus/boro
G296	G	short	0.0	17.4+/−1.9	KOTTEYARAN	Indica
G494	G	short	0.0	19.9+/−2.9	O. SATIVA	Indica
G734	G	short	0.0	20.6+/−2.5	RAJHUSAI (ACR 12)	Indica
Kas	T	long	6.0+/−2.8	23.9+/−1.9	KASALATH	Indica
CX59	T	long	1.3+/−0.6	15.2+/−1.5	MILAGROSA	Japonica
CX66	T	long	0.8+/−0.6	14.1+/−1.8	TAROM MOLAII	Intermediate
CX67	T	long	1.0+/−0.6	14.4+/−1.9	BINAM	Japonica
CX104	T	long	1.2+/−0.8	20.6+/−1.9	SADRI RICE 1	Aromatic
CX112	T	long	1.3+/−0.7	19.7+/−1.6	GINGA	Aromatic
CX143	T	long	1.4+/−0.6	15.0+/−2.1	KHASAR	Aromatic
CX149	T	long	2.4+/−1.0	12.1+/−1.9	KARNAL LOCAL	Aromatic
CX155	T	long	2.7+/−1.3	23.2+/−1.4	MADHUKAR	Indica
C136	T	long	1.7+/−0.5	16.6+/−2.1	AUS 278	Aus/boro
C138	T	long	1.7+/−1.0	19.6+/−1.4	AUS 295	Aus/boro
C140	T	long	3.4+/−1.3	17.1+/−3.1	AUS 301	Aus/boro
C179	T	long	2.9+/−1.1	23.2+/−2.1	BONGEZA	Aus/boro
C248	T	long	2.8+/−0.7	15.7+/−1.5	DJ 47	Aus/boro
C265	T	long	1.6+/−0.6	18.3+/−1.6	DV 86	Aus/boro
C309	T	long	1.8+/−0.5	13.6+/−1.7	HERATH BANDA	Aus/boro
C349	T	long	2.0+/−0.8	17.4+/−2.0	JHUL DIGA	Aus/boro
C375	T	long	4.6+/−2.4	23.3+/−3.5	KARIA	Aus/boro
C406	T	long	3.3+/−1.2	18.9+/−2.9	KORTIK KAIKA	Aus/boro
C463	T	long	4.6+/−2.1	19.5+/−3.0	MALCHI	Aus/boro
C536	T	long	7.3+/−2.4	14.7+/−2.3	P 335	Aus/boro
C621	T	long	14.1+/−2.1	23.0+/−3.4	SIDALI	Aus/boro
C670	T	long	8.3+/−3.2	18.6+/−3.1	UCP 122	Aus/boro
C676	T	long	3.5+/−1.1	15.6+/−2.3	UPRH 58	Aus/boro
C778	T	long	6.0+/−1.9	16.7+/−2.2	BENA JHUPI	Aus/boro
C845	T	long	1.9+/−0.5	13.6+/−1.7	KARUTHA SEENATI	Aus/boro
C992	T	long	2.0+/−1.3	16.5+/−3.1	BAMLA SUFFAID 320	Aus/boro
C1015	T	long	2.2+/−1.1	16.8+/−2.6	CIPPI	Aus/boro
C1046	T	long	3.4+/−2.0	22.4+/−5.9	HIJOL DIGA	Aus/boro
C1112	T	long	2.2+/−0.4	13.4+/−2.1	MOTIA	Aus/boro

The values are means +/− SD of 20 to 30 seedlings per sample.

Supplemental Table 4. The Mesocotyl and Coleoptile Length in Different Genotypes of *GY1* in Etiolated Seedlings of Different Varieties (continued).

Name	376 bp	Mesocotyl Phenotype	Mesocotyl length (mm)	Coleoptile length (mm)	Variety	Subgroup
C1137	T	long	3.2+/−1.1	17.2+/−1.6	PANDRI PAREWA	Aus/boro
G42	T	long	3.8+/−1.4	22.4+/−2.4	KHARSU 80	Aus/boro
G300	T	long	2.4+/−0.9	30.0+/−3.8	PERUNEL	Indica
G335	T	long	2.8+/−3.8	22.4+/−4.2	BADUIE	Indica
G344	T	long	1.7+/−0.5	28.3+/−2.3	BENGALY MORIMO	Indica
G349	T	long	1.1+/−0.7	15.7+/−1.5	BK 26	Indica
G402	T	long	1.6+/−0.6	9.9+/−1.6	GALWAKA HANDERAN	Indica
G437	T	long	2.4+/−1.0	26.5+/−2.3	KALU ILANKALAYAN	Indica
G457	T	long	5.8+/−2.0	23.0+/−2.8	LALKA (LAL DHAN)	Indica
G511	T	long	6.8+/−2.6	11.8+/−1.7	RACE PERUMAL	Indica
G604	T	long	1.4+/−0.6	13.4+/−2.2	POKKALI	Indica
G623	T	long	3.9+/−1.3	23.7+/−3.7	498-2A BR 8	Indica
G743	T	long	2.5+/−0.9	24.2+/−2.8	URAIBOOL	Indica
G745	T	long	0.4+/−0.6	21.1+/−1.8	XITTO	Indica

The values are means +/− SD of 20 to 30 seedlings per sample.

Supplemental Table 5. Primers Used for Gene Expression Analysis and Vector Construction.

Genes or Constructs	Locus	Forward primers (5’→3’)	Reverse primers (5’→3’)
qRT-PCR			
GY1	LOC_Os01g67430	gatacagatgggcggcttggt	tgtcgaagaggattagtggtctgtta
	LOC_Os01g67420	gcggaactgagactcctgaaga	agctggcactgcatctggtt
	LOC_Os01g67450	cacgacctcggatcctacgt	tgcgtccttcgactgccatt
OsLOX	LOC_Os02g10120	aggcatttgctagtgtgtttgagt	catccgtccgcatgacatactg
OsAOS1	LOC_Os03g55800	ctcgctcaagaaggccacct	cgtacaagctgattgatcacaccata
OsAOS2	LOC_Os03g12500	gtgctcgtcggaaggctgtt	cgattgacggcggaggttga
OsAOC	LOC_Os03g32314	ctgcctcaacaacttcaccaact	cgcacatgccgcaattaacac
OsOPR7	LOC_Os08g35740	gggcggctcttcatatcaaacc	cgacttaggctgtccgaggaa
OsEXPA2	LOC_Os01g60770	gcggccagttctgatcgagta	gcagcctcagaatagccaaagc
OsEXPA4	LOC_Os05g39990	ccgtctccgacacccacatat	tggacgaagtccagagaaggaa
OsEXPB4	LOC_Os10g40730	cccaacacattctaccgctcct	acagaccgaccacacaatccc
OsEXPB6	LOC_Os10g40700	aatttgcgtgggattgaggtgt	tgggtagtacagtgacagtggg
OsEXPB11	LOC_Os02g44108	tgcagtgcagagttgcggtaa	cagagaccgtggagggaagaac
OsEXPLA1	LOC_Os03g04020	acacgcacgagtggaagtagaa	tgccgagggattaggaggact
OsActin2	LOC_Os10g36650	ttatggttgggatgggaca	agcacggcttgaatagcg
Region a	LOC_Os01g67430	cttgagagtctctgcccatgtatcta	atattacactcttctgtacgctctgc
Region b	LOC_Os01g67430	gcagagcgtacagaagagtgtaat	catcatcaatggctaaagctaagca
Region c	LOC_Os01g67430	gatacagatgggcggcttggt	tgtcgaagaggattagtggtctgtta
Vectors			
pC-*GY1*		cccccgggaccggcgacttcattgcacacgaac	cctgcagggttggcgctccggctagcag
p*GY1*-OX		cgggatccatgacgctcccgaggcaatg	gctctagagattagccgtcttgacagtggtgg
p*GY1*:*LUC*		ggggacaagtttgtacaaaaaagcaggcttcaccggcgacttcattgcacacgaac	ggggaccactttgtacaagaaagctgggtttgccgccgcgctgctcgtgcca
pBI-*GY1*-*GFP*		ggatccatgacgctcccgaggcaatg	aagcttgattagcccgagcgtctgca
p*OsEIL2*-OX		ggggtaccatgatgggagcagcggtgac	gctctagatcagtagaaccagttggatccg

Supplemental Table 6. Oligonucleotides Used for EMSA.

Oligonucleotides	Orientation (5’→3’)
Probe a	gtctctgcccatgtatctagatgcctcgggaatgtagtggcagagc
Probe b	gtgtaatataatgtatgtatgtgtgtgtgtacaggtccaattaaatcatgaaagcaaagggaaaatggggggacatgtatgtgt

Supplemental Table 7. dCAPS Primers Used for *gy1* Allelic Mutant Analysis.

Allele	Forward primers (5’→3’)	Reverse primers (5’→3’)
gy1	tgctggaggaggtcgggatg	acgagacgagcacgtagcgc
Kasalath	gtgcggggattgggagggga	tgacctcgtaccctgcgc