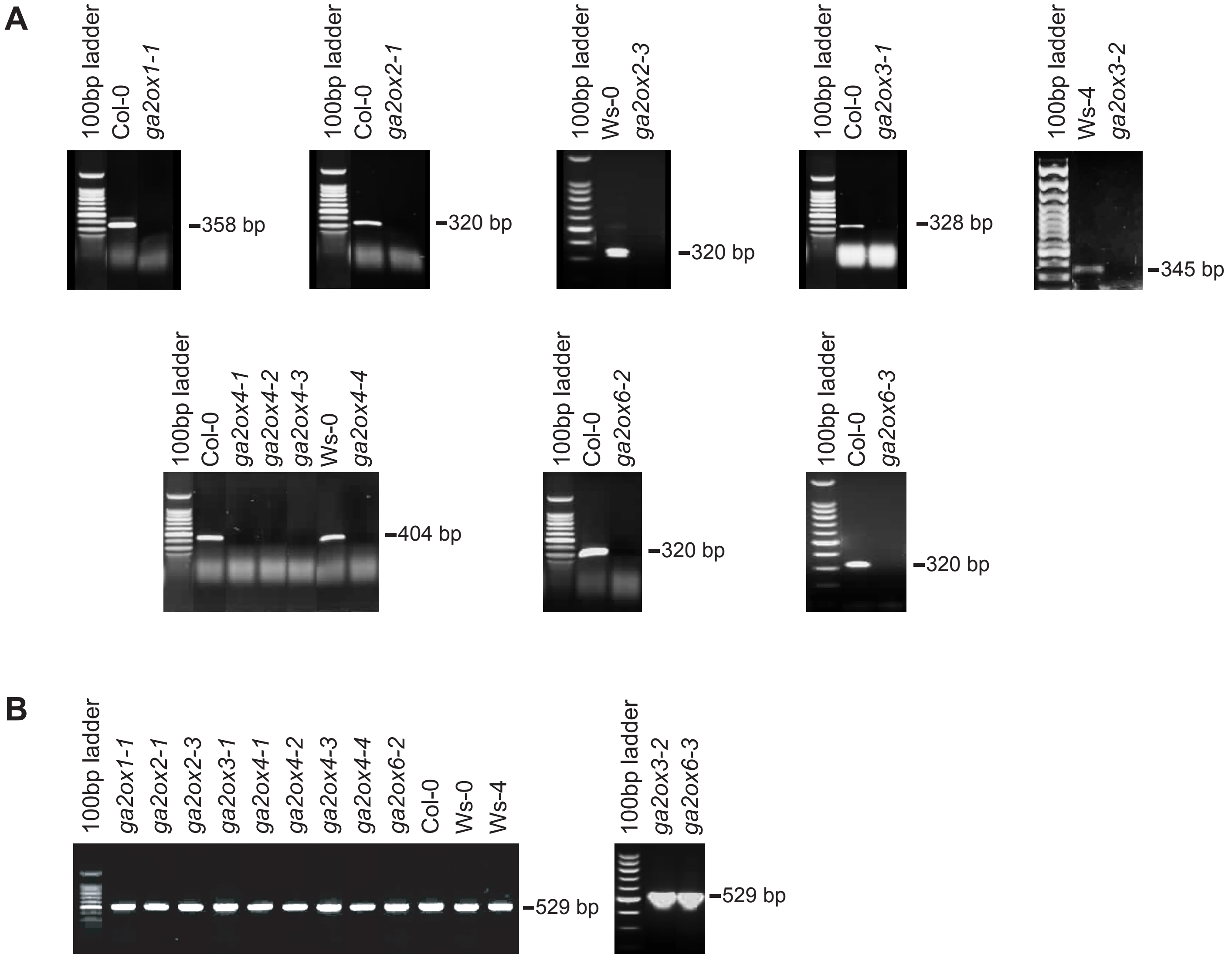
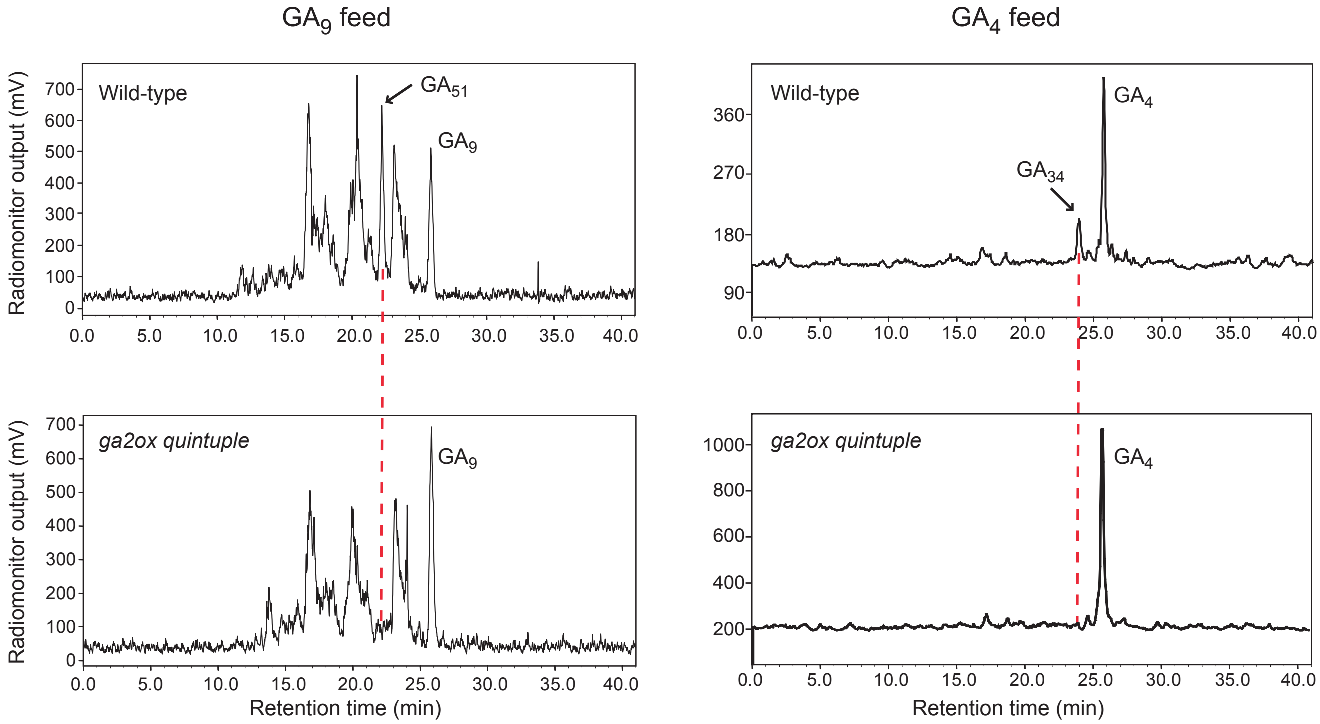
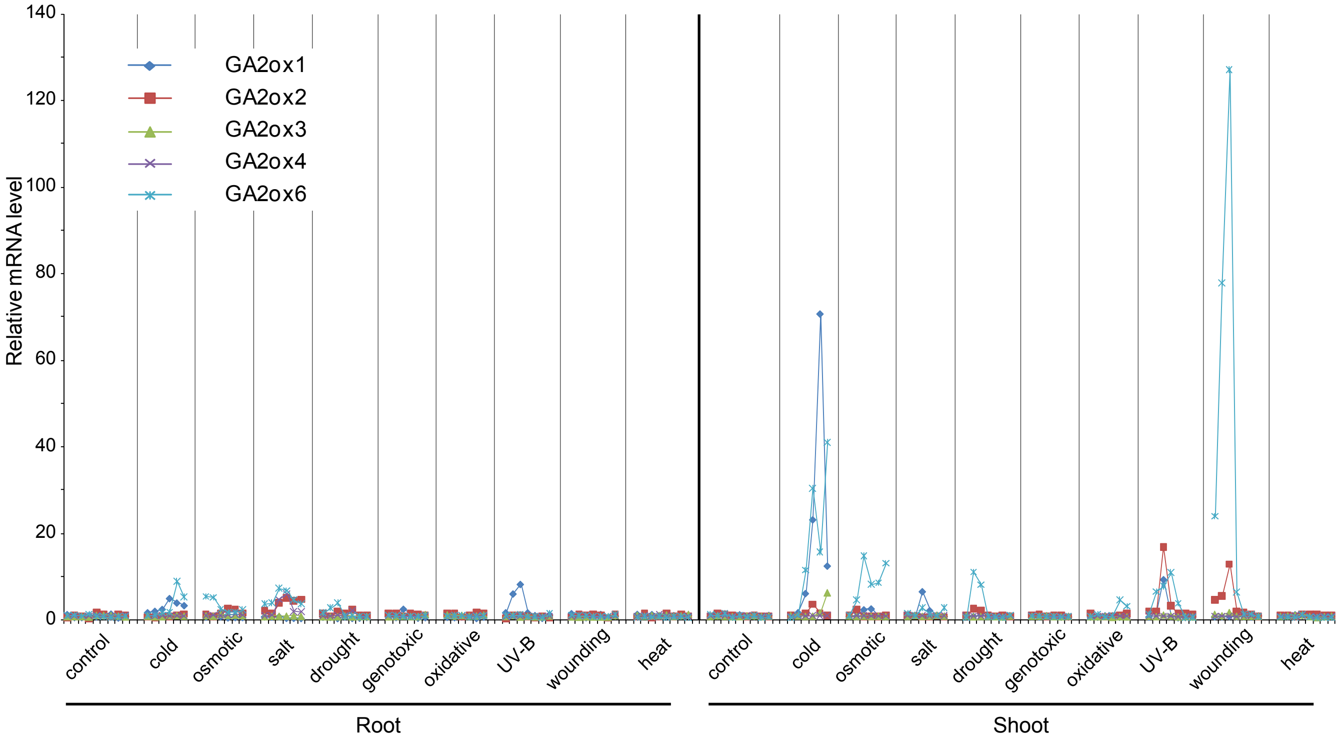


Supplemental Figure 1 online. RT-PCR to Confirm Null Status of Insertion Alleles Used in this Study. Total RNA was isolated from 7 day old seedlings of homozygous lines; RNA extraction, DNase treatment and reverse transcription were carried out as described previously (Griffiths et al., 2006). The resulting cDNA was used in PCR reactions wiith the gene-specific primers listed in Supplemental Table 11 online. (A) PCR reactions with individual alleles and their corresponding wild type lines. (B) PCR using Actin2 (At3g18780) primers to demonstrate presence of cDNA in all samples. bp, base pairs.



Supplemental Figure 2 online. Metabolism of [17-^{14}C]GA$_9$ and [17-^{14}C]GA$_4$ by Wild-Type and the *ga2ox quintuple* Mutant.



Supplemental Figure 3 online. Expression of C_{19}-*GA2ox* Genes in Response to Abiotic Stress. Microarray data were extracted from the AtGenExpress compendium (Kilian et al., 2007). Expression levels were normalized to the per-gene average across the control samples for root and shoot separately. Each treatment block represents a time series up to 24 h after start of treatment. See http://www.weigelworld.org/resources/microarray/AtGenExpress for a detailed description of samples.

Reference

Kilian, J., Whitehead, D., Horak, J., Wanke, D., Weinl, S., Batistic, O., D'Angelo, C., Bornberg-Bauer, E., Kudla, J., and Harter, K. (2007). The AtGenExpress global stress expression data set: protocols, evaluation and model data analysis of UV-B light, drought and cold stress responses. Plant Journal 50, 347-363.

SUPPLEMENTAL TABLES ONLINE

Supplemental Table 1 online. Characterisation of Insertion Lines.

Gene	Line	Background	Insertion detected[a]	mRNA absent	Allele name
GA2ox1	WiscDsLox_333C08	Col-0	yes (exon 2)	yes[b]	*ga2ox1-1*
	SALK_020228	Col-0	yes (3’ UTR)	no	
	SALK_001079	Col-0	no	-	
	FLAG_299A02	Ws-4	yes (5’ UTR)	no	
GA2ox2	SALK_051749	Col-0	yes (exon 2)	yes[b]	*ga2ox2-1*
	Wisc_2ox2	Ws-0	yes (exon1)	yes[b]	*ga2ox2-3*
	GABI-KAT_541C06	Col-0	no	-	
GA2ox3	SALK_042818	Col-0	yes (intron 2)	yes[b,c]	*ga2ox3-1*
	FLAG_088C02	Ws-4	yes (exon 1)	yes[b]	*ga2ox3-2*
	SALK_002824	Col-0	yes (5’ UTR)	no	
	Wisc_2ox3	Ws-0	yes (5’ UTR)	no	
GA2ox4	SALK_036923	Col-0	yes (exon 2)	yes[b]	*ga2ox4-1*
	SALK_142382	Col-0	yes (exon 2)	yes[b]	*ga2ox4-2*
	GABI-KAT_171B04	Col-0	yes (exon 2)	yes[b]	*ga2ox4-3*
	Wisc_2ox4	Ws-0	yes (intron 1)	yes[b]	*ga2ox4-4*
	SALK_040658	Col-0	yes (intron 1)	no	
	SALK_112150	Col-0	yes (intron 1)	no	
	SALK_036921	Col-0	no	-	
GA2ox6	SLAT_SM_3_1859	Col-0	yes (intron 1)	yes[b,c]	*ga2ox6-2*
	Wisc_2ox6	Col-0	yes (intron 1)	yes[b]	*ga2ox6-3*
	SALK_044189	Col-0	yes (5’ UTR)	no	
	SLAT_SM_3_42130	Col-0	no	-	
	SALK_059724	Col-0	yes (intron 1)	no	
	SALK_059851	Col-0	no	-	
	GABI-KAT_119G12	Col-0	yes (intron 1)	no	
	GABI-KAT 390B07	Col-0	yes (intron 1)	no	

[a], The structural element in which the insertion is located is indicated between parenthesis; [b], see Supplemental Figure 1 online; [c], see Supplemental Table 2 online; -, not determined.

Supplemental Table 2 online. Mean Ct Values and LSDs of Gene Expression Studies Shown in Figure 4A, B (GA-responsive genes) and of *GA2ox3* and *GA2ox6*.

Sample	*At2g45210*	*At2g21220*	*At1g23205*	*SCL3*	*At5g45460*
Wild type	25.8 ± 0.1	24.9 ± 0.0	22.1 ± 0.1	23.6 ± 0.0	25.7 ± 0.0
Wild type +GA	24.5 ± 0.0 **	23.1 ± 0.1 **	21.6 ± 0.1 **	24.6 ± 0.0 **	26.0 ± 0.0 **
ga2ox quintuple	25.3 ± 0.1 **	24.3 ± 0.1 **	21.5 ± 0.1 **	24.1 ± 0.0 **	26.0 ± 0.0 **
ga2ox quintuple +GA	24.5 ± 0.1 **	23.0 ± 0.1 **	21.7 ± 0.0 *	24.6 ± 0.1 **	26.1 ± 0.1 **
LSD(5%/1%) (df)	0.34/0.50 (8)	0.29/0.42 (8)	0.26/0.38 (8)	0.11/0.16 (8)	0.15/0.21 (8)
n	3	3	3	3	3

Sample	*GA20ox1*	*GA3ox1*	*GA2ox8*	*GID1b*
Wild type	24.9 ± 0.1	24.8 ± 0.1	28.9 ± 0.1	26.2 ± 0.0
Wild type +GA	25.6 ± 0.1 **	25.6 ± 0.1 **	27.4 ± 0.1 **	27.4 ± 0.1 **
ga2ox quintuple	25.4 ± 0.0 **	25.3 ± 0.1 *	28.2 ± 0.0 **	26.5 ± 0.2
ga2ox quintuple +GA	25.8 ± 0.1 **	25.8 ± 0.1 **	27.3 ± 0.1 **	27.4 ± 0.2 **
LSD(5%/1%) (df)	0.34/0.50 (8)	0.33/0.49 (8)	0.27/0.40 (8)	0.47/0.69 (8)
n	3	3	3	3

Sample	*GA2ox3*	*GA2ox6*
Wild type	31.4 ± 0.4	27.4 ± 0.1
Wild type +GA	31.4 ± 0.1	28.0 ± 0.1
ga2ox quintuple	-	-
ga2ox quintuple +GA	-	-
LSD(5%/1%) (df)	n.a.	n.a.
n	3	3

See Methods for details on statistical analysis. The measurements are the mean reference-genes-corrected threshold-cycle (Ct) values ± SE. *, significantly different from the untreated wild type (P<0.05); **, significantly different from the untreated wild type (P<0.01); df, degrees of freedom; LSD, least significant difference; n.a., not applicable;-, not detected.

Supplemental Table 3 online. Mean Ct Values and LSDs of Gene Expression Studies Shown in Figure 4C.

Sample	*GA2ox1*	*GA2ox2*	*GA2ox3*	*GA2ox4*	*GA2ox6*	*GA2ox7*	*GA2ox8*
Col 0 h	31.9 ± 0.4	30.6 ± 0.1	35.0 ± 0.6	31.8 ± 0.1	28.8 ± 0.1	32.0 ± 0.2	29.4 ± 0.1
Col 3 h mock	31.6 ± 0.1	30.5 ± 0.0	35.9 ± 0.3	31.9 ± 0.1	28.2 ± 0.0	31.0 ± 0.2	29.4 ± 0.0
Col 3 h GA	29.8 ± 0.0 **	27.9 ± 0.0 **	37.5 ± 1.5	29.6 ± 0.1 **	27.6 ± 0.1 **	30.6 ± 0.3	28.8 ± 0.1 **
LSD(5%/1%) (df)	0.67/0.93 (12)	0.30/0.43 (12)	2.60/3.64 (12)	0.42/0.59 (12)	0.37/0.52 (12)	0.84/1.18 (12)	0.29/0.41 (12)
N	3	3	3	3	3	3	3

See Methods for details on statistical analysis. The measurements are the mean reference-genes-corrected threshold cycle (Ct) values ± SE.

**, significantly different from the 0 h and 3 h mock controls ($P<0.01$); df, degrees of freedom; LSD, least significant difference.

Supplemental Table 4 online. Germination Characteristics of Wild-type and ga2ox quintuple Seeds as Shown in Figure 5A.

	Dark	+cold	+light pulse	+cold +light pulse
Wild type	0.2 ± 0.2 (-6.32)[a]	0.7 ± 0.2 (-4.91)	77.2 ± 3.5 (1.24)	99.6 ± 0.2 (5.61)
ga2ox quintuple	8.8 ± 1.0 (-2.34) **	22.1 ± 1.0 (-1.26) **	70.6 ± 1.8 (0.88)	99.9 ± 0.1 (6.34)
LSD(5%/1%) (df)	1.167/1.608 [a] (16) (for all comparisons)			
n	3	3	3	3

See Methods for details on statistical analysis. The measurements are the mean germination% ± SE. **, significantly different from the wild type with the same treatment ($P<0.01$); [a], Logit-transformed values (shown in parentheses) were used for statistical analysis (see Methods), and the LSDs correspond to these values; df, degrees of freedom; LSD, least significant difference.

Supplemental Table 5 online. Germination Characteristics of Wild-type and *ga2ox quintuple* Seeds after FR and PAC Treatment.

	-PAC	+PAC
Wild type +FR	0.0 ± 0.0	0.0 ± 0.0
ga2ox quintuple +FR	14.8 ± 1.3 **	0.0 ± 0.0
t-test t (df)	11.73 (2)	n.a.
n	3	3

See Methods for details on statistical analysis. The measurements are the mean germination% ± SE. **, significantly different from the wild type with the same treatment (P<0.01); df, degrees of freedom; FR, far-red light; LSD, least significant difference; n.a., not applicable; PAC, paclobutrazol.

Supplemental Table 6 online. Flowering Time under Short Day Conditions as Shown in Figure 5B, Including Single Mutants.

	Number of leaves at flowering
Wild-type Col-0	66.1 ± 0.6
35S::GA20ox1	57.3 ± 0.7 **
ga2ox quintuple	58.7 ± 1.3 **
ga2ox2 ga2ox4 ga2ox6	58.5 ± 0.6 **
ga2ox2 ga2ox4	57.9 ± 0.7 **
ga2ox4 ga2ox6	59.5 ± 0.6 **
ga2ox2 ga2ox6	63.6 ± 0.7 **
ga2ox2	64.3 ± 0.6 *
ga2ox4	61.6 ± 0.7 **
ga2ox6	65.1 ± 0.7
LSD(5%/1%) (df)	1.90/2.50 (443)
n	15-40

Wild-type Col-0	68.0 ± 1.8
ga2ox1-1	69.2 ± 1.5
ga2ox2-1	65.0 ± 0.8
ga2ox3-1	67.0 ± 1.9
ga2ox4-1	62.8 ± 1.9 **
ga2ox4-2	62.6 ± 1.0 **
ga2ox4-3	61.1 ± 1.0 **
ga2ox6-2	67.1 ± 1.2
Wild-type Ws-0	39.7 ± 0.7
ga2ox2-3	38.5 ± 0.7
ga2ox4-4	34.4 ± 0.7 **
ga2ox6-3	41.1 ± 0.4

Wild-type Ws-4	38.9 ± 0.5
ga2ox3-2	40.3 ± 0.9
LSD(5%/1%) (df)	3.36/4.44 (202)
n	10

See Methods for details on design and statistical analysis. The two sections of the table represent separate experiments. The measurements are the means ± SE. *, significantly different from the corresponding wild type ($P<0.05$); **, significantly different from the corresponding wild type ($P<0.01$); df, degrees of freedom; LSD, least significant difference.

Supplemental Table 7 online. Silique Phenotype as Shown in Figure 5C and D.

	Silique length (mm)	Number of seeds per silique
Wild type	14.5 ± 0.6	54.6 ± 4.0
Wild type + GA	10.4 ± 0.4 **	21.9 ± 2.9 **
ga2ox quintuple	10.0 ± 0.6 **	17.5 ± 3.4 **
ga2ox quintuple + GA	10.4 ± 0.4 **	19.0 ± 2.6 **
LSD(5%/1%) (df)	1.42/1.90 (46)	9.52/12.70 (47)
n	36-55	36-55

See Methods for details on design and statistical analysis. The measurements are the means ± SE. **, significantly different from the wild type ($P<0.01$); df, degrees of freedom; LSD, least significant difference.

Supplemental Table 8 online. Parthenocarpic Growth of *GA2ox* Mutants as Shown in Figure 6E.

	Carpel length (mm)
Wild-type Col-0	5.1 ± 0.1
Wild-type Col-0 + GA	11.5 ± 0.1 **
ga2ox quintuple	10.2 ± 0.1 **
ga2ox2	8.0 ± 0.2 **
ga2ox1 ga2ox3	5.1 ± 0.1
ga2ox4 ga2ox6	5.0 ± 0.1
LSD(5%/1%) (df)	0. 48/0.64 (31)
Wild-type Ws-0	5.6 ± 0.1
ga2ox2-3	7.3 ± 0.1 **
LSD(5%/1%) (df)	0.43/0.59 (21)

See Methods for details on design and statistical analysis. The two sections of the table represent separate experiments. The measurements are the means ± SE. **, significantly different from the wild type (P<0.01); df, degrees of freedom; LSD, least significant difference.

Supplemental Table 9 online. Phenotype of the *ga2ox* Mutants under Low-GA Conditions, Including as Shown in Figure 7B, C and D.

	Flowering time (days)			
PAC (uM):	0	1	5	25
Wild type	18.7 ± 0.2 (2.93)[a]	19.0 ± 0.2 (2.94)	20.1 ± 0.4 (2.99)	21.0 ± 0.5 (3.04)
ga2ox quintuple	17.4 ± 0.1 (2.86) *	17.2 ± 0.1 (2.85) **	17.9 ± 0.2 (2.89) **	17.8 ± 0.2 (2.88) **
LSD(5%/1%) (df)	0.056/0.079 [a] (10) (for comparisons within a PAC treatment)			
n	18	18	18	18

	Total plant height (cm)			
PAC (uM):	0	1	5	25
Wild type	52.2 ± 0.7	26.3 ± 0.9	10.2 ± 0.5	6.8 ± 0.5
ga2ox quintuple	57.8 ± 0.7 **	44.0 ± 0.6 **	27.5 ± 0.9 **	14.0 ± 1.1 **
LSD(5%/1%) (df)	2.42/3.52 (8) (for comparisons within a PAC treatment)			
n	18	18	18	18

	No. of flowers / inflorescence internodes			
PAC (uM):	0	1	5	25
Wild type	55.4 ± 1.5	52.5 ± 1.0	40.9 ± 1.0	36.0 ± 1.0
ga2ox quintuple	63.2 ± 1.5 **	61.6 ± 1.4 **	57.3 ± 1.6 **	45.8 ± 0.8 **
LSD(5%/1%) (df)	4.93/7.18 (8) (for comparisons within a PAC treatment)			
n	18	18	18	18

	Rosette radius (mm)			
PAC (uM):	0	1	5	25
Wild type	58.5 ± 0.9	51.9 ± 1.0	48.8 ± 0.9	38.3 ± 1.0
ga2ox quintuple	59.0 ± 0.8	56.2 ± 0.6 *	54.9 ± 0.6 **	46.9 ± 0.9 **
LSD(5%/1%) (df)	3.44/4.89 (10) (for comparisons within a PAC treatment)			
n	18	18	18	18

	No. of vegetative internodes			
PAC (uM):	0	1	5	25
Wild type	2.61 ± 0.12	2.50 ± 0.12	1.89 ± 0.18	1.28 ± 0.21
ga2ox quintuple	2.67 ± 0.11	2.83 ± 0.09	2.61 ± 0.12 *	2.28 ± 0.11 **
LSD(5%/1%) (df)	0.594/0.864 (8) (for comparisons within a PAC treatment)			
n	18	18	18	18

	Length of vegetative internodes (cm)			
PAC (uM):	0	1	5	25
Wild type	3.45 ± 0.19 (1.86)[b]	1.96 ± 0.13 (1.40)	0.76 ± 0.05 (0.87)	0.45 ± 0.07 (0.67)
ga2ox quintuple	3.43 ± 0.12 (1.85)	2.60 ± 0.12 (1.61) **	1.49 ± 0.06 (1.22) **	0.79 ± 0.10 (0.89) **
LSD(5%/1%) (df)	0.064/0.094 [b] (8) (for comparisons within a PAC treatment)			
n	18	18	18	18

See Methods for details on statistical analysis. The measurements are the means ± SE. *, significantly different from *ga20ox1-3* (P<0.05); **, significantly different from *ga20ox1-3* (P<0.01); [a], Log-transformed values (shown in parentheses) were used for statistical analysis (see Methods), and the LSDs correspond to these values; [b], Square-root-transformed values (shown in parentheses) were used for statistical analysis (see Methods), and the LSDs correspond to these values; df, degrees of freedom; LSD, least significant difference.

Supplemental Table 10 online. Suppression of the *ga20ox1-3* Phenotype by *ga2ox2-1* as Shown in Figure 7E.

	Total plant height (cm)	Length of vegetative stem (cm)	Length of inflorescence stem (cm)
Wild type	61.4 ± 3.6 **	15.7 ± 1.7 **	45.8 ± 1.9 **
ga2ox2-1	60.1 ± 2.5 **	13.2 ± 0.6 **	46.9 ± 2.6 **
ga20ox1-3	26.7 ± 1.9	4.8 ± 0.5	22.1 ± 1.4
ga20ox1-3 ga2ox2-1	41.2 ± 1.5 *	6.7 ± 0.5	34.3 ± 1.0 *
LSD(5%/1%) (df)	11.54/17.56 (7)	3.50/5.33 (7)	11.49/18.02 (7)
n	3-7	3-7	3-7

See Methods for details on statistical analysis. The measurements are the means ± SE. *, significantly different from *ga20ox1-3* ($P<0.05$); **, significantly different from *ga20ox1-3* ($P<0.01$); df, degrees of freedom; LSD, least significant difference.

Supplemental Table 11 online. Primers Used for Genotyping, Real-time Quantitative RT-PCR and Preparation of Standard Curves.

GENOTYPING

Primer	Sequence	Used for
GA2ox1 gF GA2ox1 gR	TCTTCCGGTTCGATATCTCCCA TGACCAAAACACGGACTCGAT	Genotyping *ga2ox1-1* (wild-type allele: 1350bp)
GA2ox2 gF GA2ox2 gR	CTGCGAGGAGTTCGGGTTCTT TTTTTGTCGACCCTCCACACC	Genotyping *ga2ox2-1* (wild-type allele: 1100bp)
GA2ox2 gF GA2ox2 gR	see above see above	Genotyping *ga2ox2-3* (wild-type allele: 1100bp)
GA2ox3 gF1 GA2ox3 gR1	TTGAAAATTTGTCCTTTAACCCCA TCCGGATGTGAAAACTGAAATCAA	Genotyping *ga2ox3-1* (wild-type allele: 1150bp)
GA2ox3 gF2 GA2ox3 gR2	CCACTCGAATTCAAATCCGCATA TAACCCCTGTTTCTCGCCGTT	Genotyping *ga2ox3-2* (wild-type allele: 1100bp)
GA2ox4 gF1 GA2ox4 gR1	TGACAGCTCGGCAGTGAATTG TGGGGTATCACATTTCACCTCAA	Genotyping *ga2ox4-1* (wild-type allele: 1100bp)
GA2ox4 gF1 GA2ox4 gR1	see above see above	Genotyping *ga2ox4-2* (wild-type allele: 1100bp)
GA2ox4 gF1 GA2ox4 gR1	see above see above	Genotyping *ga2ox4-3* (wild-type allele: 1100bp)
GA2ox4 gF2 GA2ox4 gR2	TTCGCTCTCAGCTCTCCTTCA GTCACTATCGACGGAGCTGATTA	Genotyping *ga2ox4-4* (wild-type allele: 1150bp)
GA2ox6 gF1 GA2ox6 gR1	TTGTCAACCGTATGGAAACCG CAACCAAGAACCAACGATTGC	Genotyping *ga2ox6-2* (wild-type allele: 950bp)
GA2ox6 gF1 GA2ox6 gR1	see above see above	Genotyping *ga2ox6-3* (wild-type allele: 950bp)
WiscDs-Lox p745	AACGTCCGCAATGTGTTATTAAGTTGTC	Genotyping *ga2ox1-1* (mutant allele, with GA2ox1 gF: 1300bp)
SALK LBa1	TGGTTCACGTAGTGGGCCATCG	Genotyping *ga2ox2-1* (mutant allele, with GA2ox2 gR: 600bp), *ga2ox3-1* (mutant

		allele, with GA2ox3 gR1: 850bp), *ga2ox4-1* (mutant allele, with GA2ox4 gR1: 1100bp), *ga2ox4-2* (mutant allele, with GA2ox4 gF1: 650bp)
JL-202	CATTTTATAATAACGCTGCGGACATACTAC	Genotyping *ga2ox2-3* (mutant allele, with GA2ox2 gR: 1200bp), *ga2ox4-4* (mutant allele, with GA2ox4 gF2: 350bp), *ga2ox6-3* (mutant allele, with GA2ox6 gF1: 750bp)
GABI_LBo8409	ATATTGACCATCATACTCATTGC	Genotyping *ga2ox4-3* (mutant allele, with GA2ox4 gF1: 300bp)
FLAG_LB4	CGTGTGCCAGGTGCCCACGGAATAGT	Genotyping *ga2ox3-2* (mutant allele, with GA2ox3 gR2: 550bp),
SLAT 3' dspm1	CTTATTTCAGTAAGAGTGTGGGGTTTTGG	Genotyping *ga2ox6-2* (mutant allele, with GA2ox6 gR1: 400bp)
RT-PCR TESTING NULL STATUS OF INSERTION ALLELES		
Primer	Sequence	Used for
GA2ox1 KOF	TGACCAAAACACGGACTCGAT	RT-PCR of ga2ox1 mutants. Wild type allele 358 bp.
GA2ox1 KOR	CGGAGCGATTCTCTGAGTCAA	
GA2ox2 KOF	GAGAAGATGGTGAAGGTGGGG	RT-PCR of ga2ox2 mutants. Wild type allele 320 bp.
GA2ox2 KOR	AGCCAATCATCTTGCTCAGGG	
GA2ox3 KOF1	GGAAGAGACTCCGGTCAAGGA	RT-PCR of ga2ox3-1 mutant. Wild type allele 328 bp.
GA2ox3 KOR1	GCAATCATCTTGCTTTGGCAC	
GA2ox3 KOF2	ACCGACTCAGATGCCAAAACC	RT-PCR of ga2ox3-2 mutant. Wild type allele 345 bp.
GA2ox3 KOF2	TTTGCTCGACATTCTCTTCATCTC	
GA2ox4 KOF	TTCGCTCTCAGCTCTCCTTCA	RT-PCR of ga2ox4 mutants.

GA2ox4 KOR	CCCGTTCGTCATCACCTGTAA	Wild type allele 404 bp.
GA2ox6 KOF	TTACGGATGCAAGAACATCGG	RT-PCR of ga2ox6 mutants. Wild type size 320 bp.
GA2ox6 KOR	TTTGACCAACGCCACTTAACG	
Actin-F2	TCGTACAACCGGTATTGTGCTG	RT-PCR of Actin-2. Expected product size 529 bp.
Actin-R2	TGGTGCAAGTGCTGTGATTTCT	
AMPLIFICATION OF TEMPLATES FOR STANDARD CURVES		
Primer	Sequence	Used for
GA2ox1 scF	CAAGGAAATATATCAATGGCGG	*GA2ox1* cDNA fragment
GA2ox1 scR	AAAAGATGGGAGCGATGTTGA	
GA2ox2 scF	CCTTCTTCTTCCTCAACCTTTGC	*GA2ox2* cDNA fragment
GA2ox2 scR	TCCAAAACACTATCCATTTCCTTC	
GA2ox3 scF	ATGGTAATTGTGTTACAGCCAGCC	*GA2ox3* cDNA fragment
GA2ox3 scR	CAAACATTGGATAGAGAAAATGGAGG	
GA2ox4 scF	ATGGTGAAAGGGTCCCAGAA	*GA2ox4* cDNA fragment
GA2ox4 scR	CTAGTCCTTACATGTACGAAACATGTCT	
GA2ox6 scF	ATGGTTTTGCCATCTTCAACAC	*GA2ox6* cDNA fragment
GA2ox6 scR	CTATAAAGTCTTGAAAAACTCGAGACGA	
REAL-TIME QUANTITATIVE RT-PCR		
Primer	Sequence	Used for
GA2ox1 qF	TGAGGACGAGAGGTTGTACGA	*GA2ox1* quantification
GA2ox1 qR	TCCTTTCGAATTGTTGAAGCC	
GA2ox2 qF	CCGGTTCTCACTTCCCATT	*GA2ox2* quantification
GA2ox2 qR	GCTTCCGGATCGGCTAG	
GA2ox3 qF	AGGAGAAGCTGAGCCGTTT	*GA2ox3* quantification
GA2ox3 qR	TTCTCCGGGTAATGGTTCAT	
GA2ox4 qF	GGCTCCAAGTGTCCAATTCA	*GA2ox4* quantification
GA2ox4 qR	TCCTACATTGACGCAGAAAGC	
GA2ox6 qF	GGGACAGAAGTCTAGCGAAGTG	*GA2ox6* quantification
GA2ox6 qR	TCGCTACGAACGTCTCTGATC	
GA2ox7 qF	AGTAATGGAGTGTACCAAAGCG	*GA2ox7* quantification

GA2ox7 qR	GAAAGCTATTGACATCCTCTCG	
GA2ox8 qF	GTGTGAGAAATACATGTTATCTAAGGATG	*GA2ox8* quantification
GA2ox8 qR	TACACCTCCGATGGTTTGG	
At1g23205 qF	TGACCGTCCATTCTCAATCAG	*At1g23205* quantification
At1g23205 qR	TTGCAGCTAGTACGGATGAAATC	
At2g21220 qF	AGAGCTTGCTTCAACAGGCAG	*At2g21220* quantification
At2g21220 qR	CCACTCCCTCATCCGATCAT	
At2g45210 qF	AACGTTCAGGATACAACCGG	*At2g45210* quantification
At2g45210 qR	AATGGTCTCATCAGCATGCA	
At5g45460 qF	GATGAGTTCCGCTCCTTATGG	*At5g45460* quantification
At5g45460 qR	TGACTATGCTGCGGATCCA	
SCL3 qF	GGAGAGGCCTTAGCCGTTAG	*SCL3* quantification
SCL3 qR	GGCCAAGAAGGTATGCAATTG	