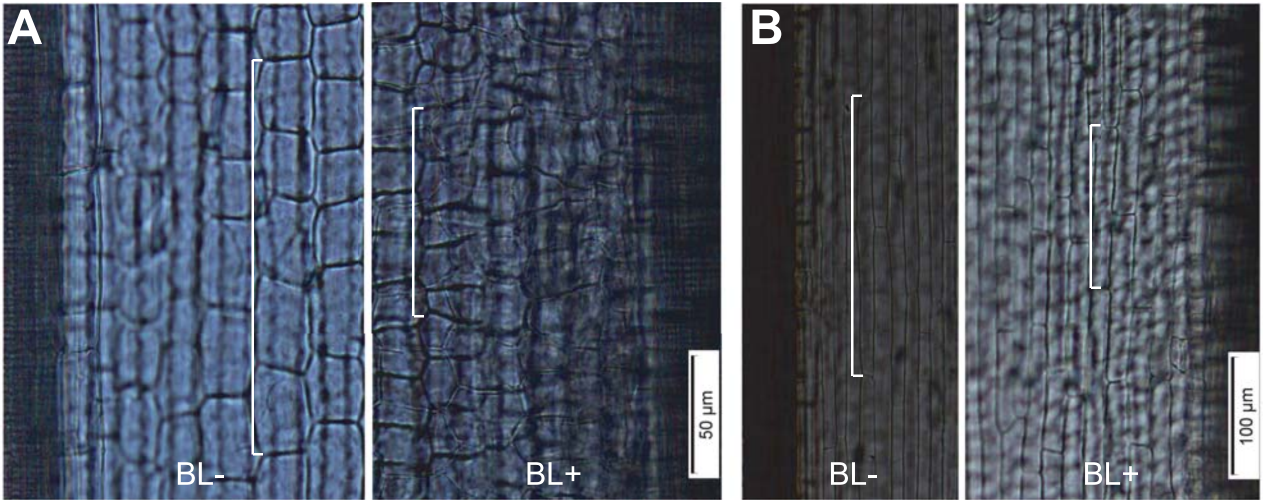
Supplemental Data. Tong et al. (2014). Plant Cell 10.1105/tpc.114.132092

Supplemental Figure 1

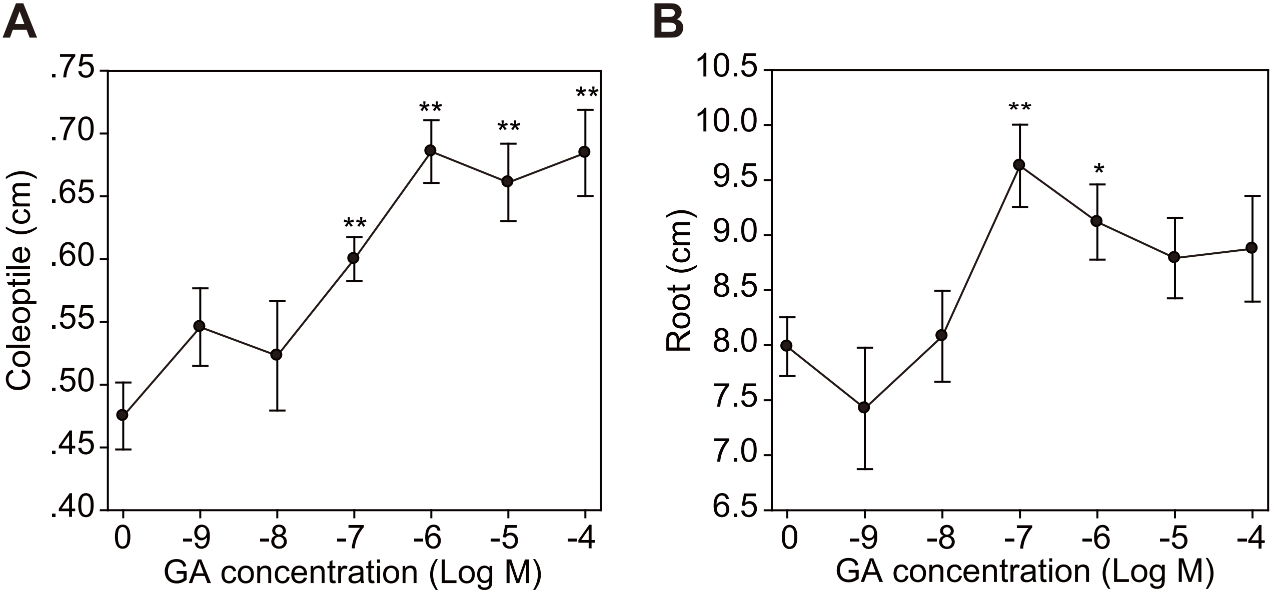


Supplemental Figure 1. Exogenous BR inhibits cell elongation in the leaf sheath. Longitudinally hand-cut slices of the second leaf sheath were used for microscopy observation.

(A) Mesophyll cell. Five cells were bracketed for comparison.

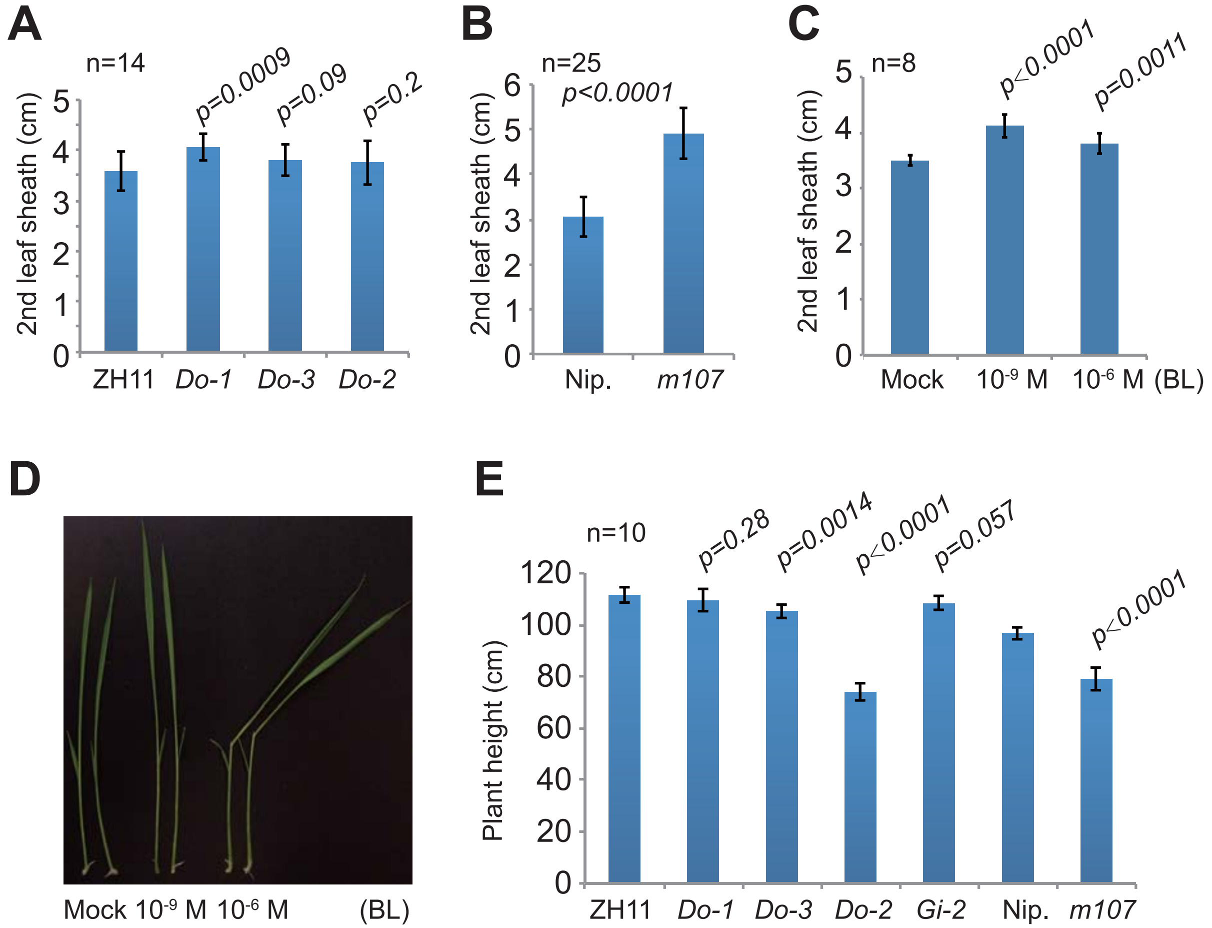
(B) Epidermal cell. One cell was bracketed for comparison.

Supplemental Figure 2



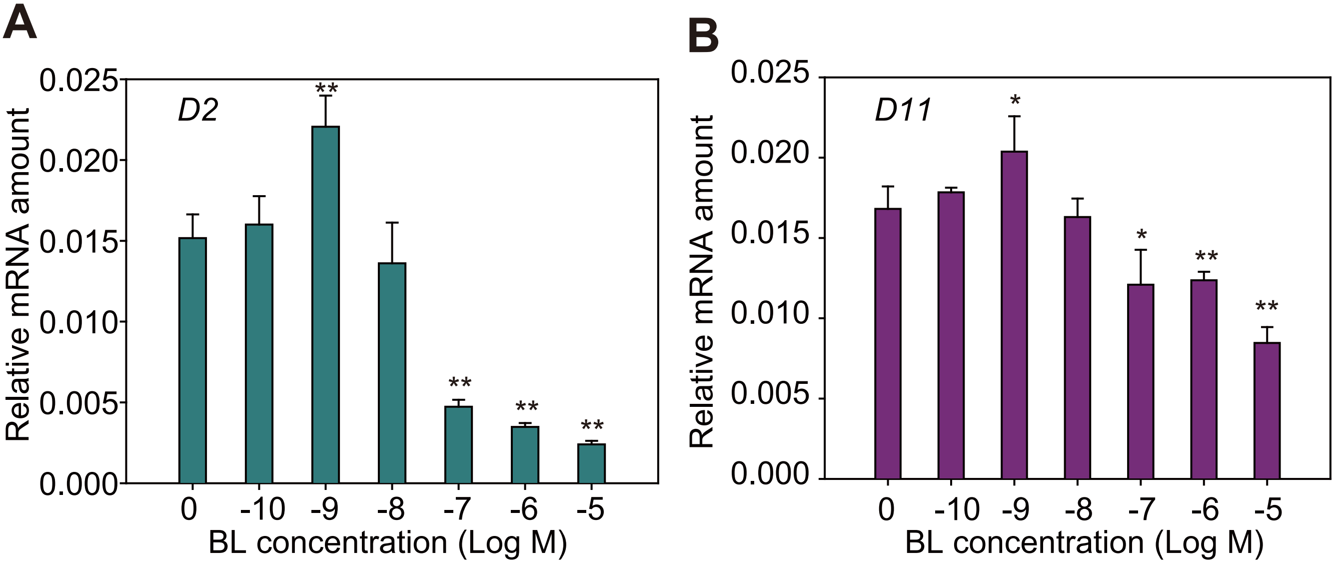
Supplemental Figure 2. GA affects wild-type plant growth.
(A) Coleoptile elongation in response to GA.
(B) Root response to GA.
Bars indicate SD (n=15). * and ** indicate $P<0.05$ and $P<0.01$, respectively in Student's *t*-test analysis.

Supplemental Figure 3



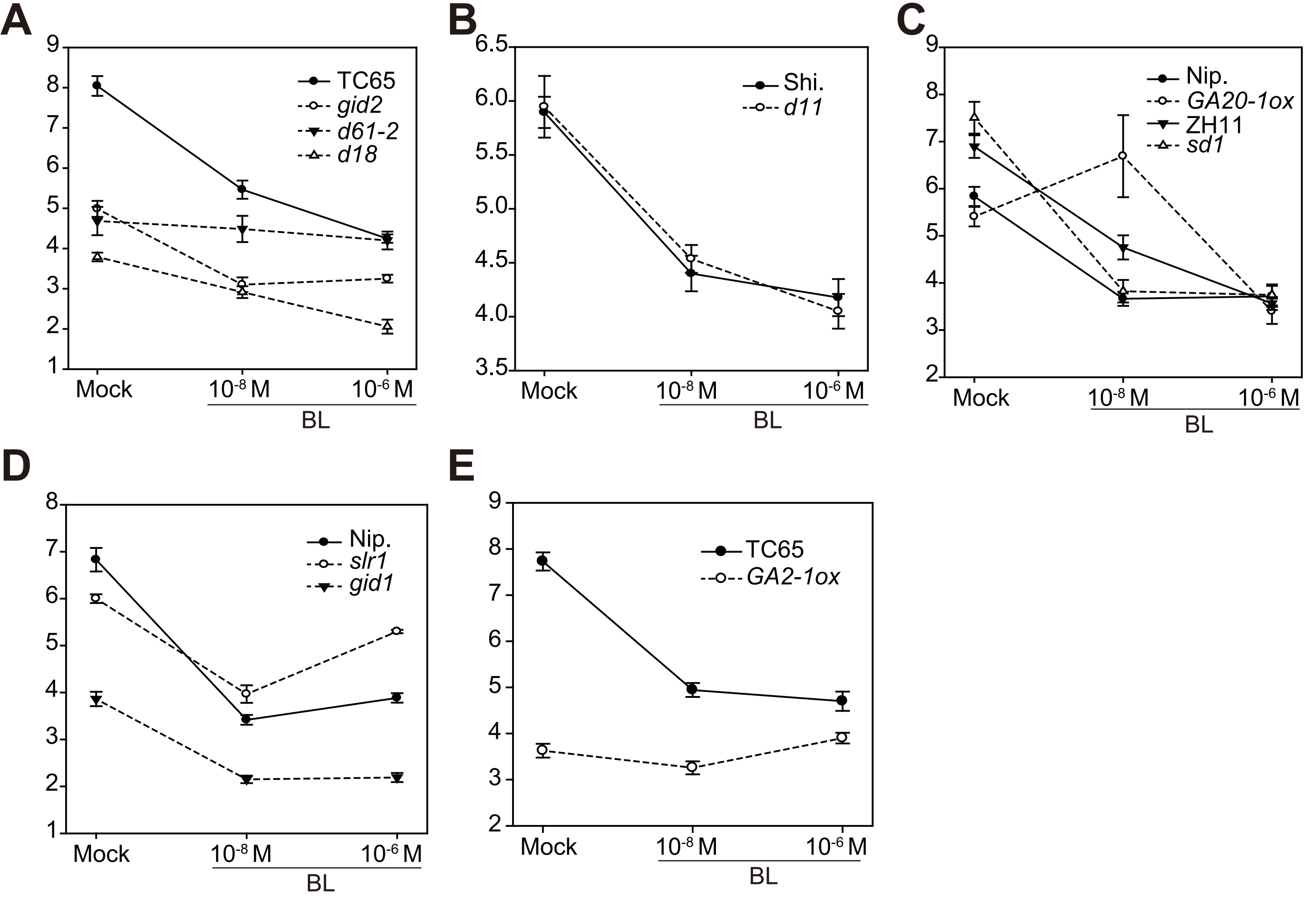
Supplemental Figure 3. Comparison of plant height of BR-related plants. The second leaf sheath length of enhanced BR-signaling plants (A), BR-accumulated plants (B), and short-term (two-day) BL-treated plants (C and D) at the seedling stage or plant height at the reproductive stage (E). P values were calculated using Student's *t*-test compared to their respective wild types or control. Bars indicate SD. Sample size was indicated on each panel.

Supplemental Figure 4



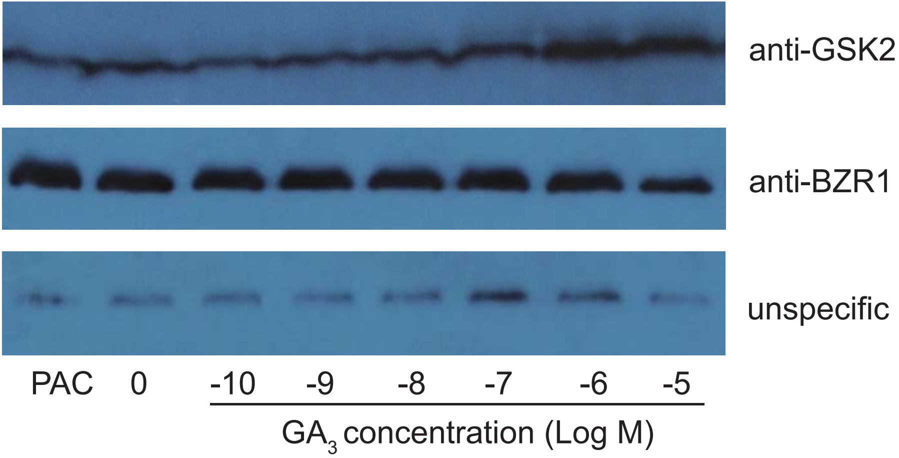
Supplemental Figure 4. Expression of *D2* and *D11* in response to various BR concentrations in shoot. $^{*}P<0.05$ and $^{**}P<0.01$ in *t*-test analysis. Bars indicate SD (n=3).

Supplemental Figure 5



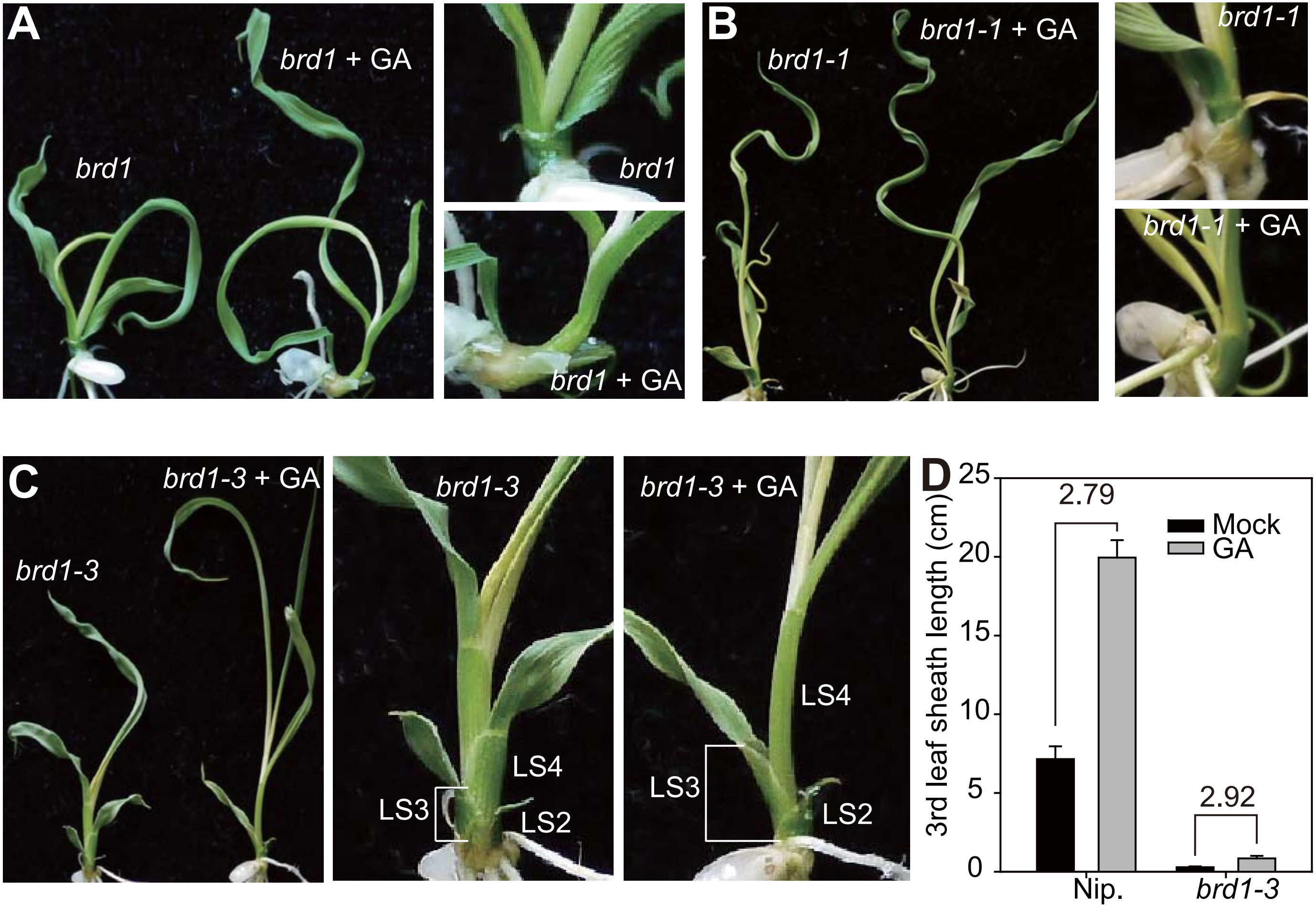
Supplemental Figure 5. Root response to BR in GA related mutant plants.
Plants were grouped by different backgrounds or independent experiments. Bars indicate SD (n=8 for *gid2*, *slr1,* and *gid1*; n=15 for others).

Supplemental Figure 6



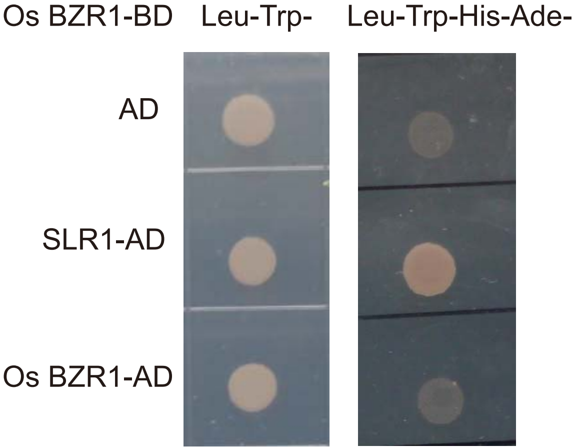
Supplemental Figure 6. The effect of GA and PAC application on GSK2 and BZR1 protein level. One-week-old seedlings were treated with 10^{-5} M PAC or indicated concentrations of GA$_3$ and grew for two days. A unspecific band blotting with BZR1 antibody was used as internal reference.

Supplemental Figure 7



Supplemental Figure 7. Response of *brd1* alleles to GA treatment.
(A) and (B) Response of the most severe alleles (A, *brd1*, identified by Mori et al., 2002; B, *brd1-1*, identified by Hong et al., 2002) to GA treatment. The enlarged images in the right panel show no visible leaf sheath was developed in either of the mutants.
(C) and (D) Response of *brd1-3*, the relatively weak allele, to GA treatment. Both leaf sheath and leaf blade of *brd1-3* have obviously elongated in response to GA (C). Statistical data for the third leaf sheath were shown in (D). Bars indicate SD (n=5).

Supplemental Figure 8



Supplemental Figure 8. SLR1 interacts with Os BZR1 in yeast.

Co-transformation of Os *BZR1-BD* and *SLR1-AD* can activate reporter gene expression in yeast two-hybrid analysis.

Supplemental Table 1. Information of the mutants and the transgenic plants used in this study. References were provided for the materials reported previously. Shi., Shiokari; Nip., Nipponbare; TC65, Taichang65; ZH11, Zhonghua11.

Classification	Name	Wild type	Information	Reference
BR-deficient	*d2-2*	Shi.	*ebisu dwarf*	Hong et al., 2003
	d11-2	Shi.	*dwarf11*	Tanabe et al., 2005
	brd1	Nip.	*brassinosteroid-deficient dwarf1*, strong allele	Mori et al., 2002
	brd1-1	Nip.	*brd1* strong allele	Hong et al., 2002
	brd1-3	Nip.	*brd1* relatively slightly weaker allele	Hong et al., 2002
BR-accumulated	*m107*	Nip.	T-DNA insertion mutant with BR biosynthetic gene *D11* activated	Wan et al., 2009
Decreased BR-signaling	*d61-1*	TC65	*dwarf61, bri1,* weak allele	Yamamuro et al., 2000
	d61-2	TC65	*d61* relatively strong allele	Yamamuro et al., 2000
	Go-2	ZH11	*GSK2*-overexpression plant	Tong et al., 2012
	dlt	ZH11	*dwarf and low-tillering*	Tong et al., 2009
Enhanced BR-signaling	*Gi-2*	ZH11	*GSK2-RNAi* plant	Tong et al., 2012
	Do-1	ZH11	*DLT*-overexpression plant, weak line	Tong et al., 2012
	Do-2	ZH11	*Do* relatively strong line	Tong et al., 2012
	Do-3	ZH11	*Do* mild line	Tong et al., 2012
GA-deficient	*d18-Id18*^{h}	Shi.	*dwarf18* with defective *GA3ox-2*	Itoh et al., 2001
	d35	Shi.	*dwarf35* with defective *KO2*, *ko2-2*	Itoh et al., 2004
	sd1	ZH11	*semi-dwarf1* with 7-bp deletion at 546-552 of *GA20ox-2*	Newly identified
	GA2-1ox	TC65	*GA2ox-1*-overexpression plant	Newly developed
GA-accumulated	*eui1-4*	ZH11	*elongated uppermost internode*	Luo et al., 2006
	GA20-1ox	Nip.	*GA20ox-1*-overexpression plant	Newly developed
Decreased GA-signaling	*gid1*	Nip.	*gibberellin insensitive dwarf1* with point mutation cDNA G(587) to T in *GID1*	Newly identified
	gid2	TC65	*gibberllin insensitive dwarf2*	Sasaki et al., 2003
Enhanced GA-signaling	*slr1*	Nip.	*slender* with cDNA T(1101) deletion in *SLR1*	Newly identified

Supplemental Table 2. Quantification of GA_1 in wild type and *Do* plants. Means ± SD of three replicates are shown (ng/g F.W.).

Analyte	GA_1
Wild type	0.30±0.02
Do-1	0.33±0.02
Do-3	0.32±0.02
Do-2	0.31±0.01

Supplemental Table 3. Quantification of GAs in wild type, *m107*, and short-term BL-treated plants. Wild-type plants were treated with10^{-6} M BL for two days. Means ± SD of three replicates are shown (ng/g F.W.).

Analyte	GA1	GA8	GA19	GA20	GA29	GA44	GA53
Wild type	1.26±0.06	0.44±0.03	11.65±0.18	0.83±0.06	0.16±0.03	0.60±0.17	0.74±0.01
m107	7.20±0.18	3.14±0.19	5.97±0.19	0.19±0.03	0.07±0.01	0.58±0.19	0.75±0.01
BL	2.88±0.13	1.39±0.13	4.93±0.25	0.17±0.03	0.09±0.01	0.27±0.05	0.53±0.02

Supplemental Table 4. Quantification of CS in wild type and *m107*. Means ± SD of three replicates are shown (ng/g F.W.).

Analyte	CS
Wild type	0.34±0.01
m107	0.94±0.04

Supplemental Table 5. Quantification of GAs in wild type and long-term BL-treated plants. Means ± SD of three replicates are shown (ng/g F.W.).

Analyte	GA1	GA8	GA19	GA20	GA29	GA44	GA53
Mock	0.30±0.02	0.47±0.02	15.41±1.80	1.06±0.06	0.24±0.03	5.43±0.21	2.34±0.17
10^{-6} M BL	0.14±0.01	0.16±0.00	8.62±0.75	0.47±0.05	0.14±0.04	3.29±0.27	1.34±0.05
10^{-5} M BL	0.12±0.01	0.20±0.02	8.51±0.67	0.57±0.03	0.17±0.01	2.04±0.19	1.39±0.03

Supplemental Table 6. Primers used for qRT-PCR and ChIP-qPCR analysis.

Name	**Forward (5’-3’)**	**Reverse (5’-3’)**
For qRT-PCR:		
GA20ox-1	GCCACTACAGGGCCGACAT	TGGTTGCAGGTGACGATGAT
GA20ox-2	CCAATTTTGGACCCTACCGC	GAGAGAAGCCCAACCCAACC
GA3ox-2	TCCTCCTTCTTCTCCAAGCTCAT	GAAACTCCTCCATCACGTCACA
GA2ox-1	TGACGATGATGACAGCGACAA	CCATAGGCATCGTCTGCAATT
GA2ox-3	TGGTGGCCAACAGCCTAAAG	TGGTGCAATCCTCTGTGCTAAC
D2	AGCTGCCTGGCACTAGGCTCTACAGATCAC	ATGTTGTCGGAGATGAGCTCGTCGGTGAGC
D11	TTGGGTCATGGCATGGCAAGAGCAAGGA	TTGTTGCTGGAGCCAGCATTCCTCCTCT
ACTIN1	TGCTATGTACGTCGCCATCCAG	AATGAGTAACCACGCTCCGTCA
For ChIP-qPCR:		
D2 P1	TCTCCTCAATCTCCCCTCTTT	CGAGTTCTAACCCACTTCGTG
D2 P2	TAGGGACGAGTATGCGAACG	ACCGGTCACCACCACCATAC
D2 P3	CGTCTCTACTCCCCCACTTG	GAGGAGAGCAGAGCAGAGGA
GA20ox-2 P1	CGTATACCATGCGGTTATCG	CGTTTTAGGTGGGGTTACCA
GA20ox-2 P2	CATGTGCCTGTATGGTGCAT	TGACAGGGAAATGGTTCCTC
GA20ox-2 P3	AAAAGGAAGAGCTCGCTGTG	CGTGGAAAACTAAACCTCTGG
GA20ox-2 P4	CAAGAAAGCCCGAGTCAATC	GTGCATTTCTTCCGGTGAAT
GA3ox-2 P1	CCCAATGCATCCTCTCTCTC	CATCATCATCCATCCATCCA
GA3ox-2 P2	CGAATGAAATTCGACGTGTATG	AACAGTAGCGTCCTCCGTTG
GA3ox-2 P3	CCTCTCCCTTGTACTTGTCCAG	TGGCAGAAAGCCAGTAACAA
GA2ox-3 P1	ATACGTTCGCCGATCTCATC	CAGTAGCTCACACGCACGAT
GA2ox-3 P2	CTTGATTACTATTTTCTCCATCGAA	GCATGAGTAATTAGCAATAGAATGGA
GA2ox-3 P3	CCCGTACCATACTCGACCAA	CATGGCTGCATAGGTGCATA
GA2ox-3 (3’-UTR)	TGGTGGCCAACAGCCTAAAG	TGGTGCAATCCTCTGTGCTAAC
DLT (codon region)	CCTGGCGTTCGAGTTCCA	TGGCGAGGACGCAGTTCA
ACTIN1 (intron)	TGGCATCTCTCAGCACATTC	GGCAAGCAACATTGTAAGCA

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