

Figure S1. The proposed brassinosteroid pathway and measured intermediates from *na2-1* and wild-type plants.

Brassinosteroid intermediates in ng/g fresh weight from 28d old wild-type and *na2-1* plants are presented in black and red text, respectively. The early C-22 oxidation pathway is highlighted in purple, the late C-6 oxidation pathway is highlighted in green, and the early C-6 oxidation pathway is highlighted in blue. Data are means of two independent experiments of 10 plants each. n.d., not detected. Proposed brassinosteroid pathway modified from Nakamura et al., 2009; Ohnishi et al., 2012; Verhoef et al., 2013; Chung and Choe, 2013.

- Chung Y, Choe S (2013) The regulation of brassinosteroid biosynthesis in Arabidopsis. Crit Rev Plant Sci 32: 396–410
- Nakamura A, Fujioka S, Takatsuto S, Tsujimoto M, Kitano H, Yoshida S, Asami T, Nakano T (2009) Involvement of C-22-hydroxylated brassinosteroids in auxininduced lamina joint bending in rice. Plant Cell Physiol 50: 1627–1635
- Ohnishi T, Godza B, Watanabe B, Fujioka S, Hategan L, Ide K, Shibata K, Yokota T, Szekeres M, Mizutani M (2012) CYP90A1/CPD, a brassinosteroid biosynthetic cytochrome P450 of Arabidopsis, catalyzes C-3 oxidation. J Biol Chem 287: 31551–31560
- Verhoef N, Yokota T, Shibata K, De Boer GJ, Gerats T, Vandenbussche M, Koes R, Souer E (2013) Brassinosteroid biosynthesis and signalling in *Petunia hybrida*. J Exp Bot 64: 2435–2448



Figure S2. Phylogenetic tree of presumed Δ^{24} -sterol reductases from 36 taxa.

Presented is a maximum likelihood, Bayesian MCMC, phylogenetic consensus tree of conceptually-translated protein sequences derived from the genes encoding likely Δ^{24} -sterol reductases identified within plant whole genome assemblies in Phytozome. All genes annotated as similar to GRMZM2G057000 with an alignment score greater than 1500 and sequence similarity greater than 50% were included in the analysis. Scale bar indicates the number of amino acid changes per orthologous site. Posterior probabilities

for selected nodes are indicated. The Arabidopsis *DWF1*, maize *na2*, and the gene encoded by the maize paralog of *na2* are indicated by bold text.

	1	100
Zm		RLKORNEKKDGLVCTARKPWIAV
Zm	Zm*MADPLVRARPKRKKVLADYLVRLRWIPALFVALPISALIYLSVFLVNTWSAMKSEKRRQKEHQENVVK	RLK <mark>ERDPKR</mark> DGLVCTAR <mark>K</mark> PWVVV
SD	50MADVHEPLYKRKRKKVLVDYLVDFRWILVIFVVLPISSLIYFNIFLGDMMSAM(SEKKROKOHDENVOKVVK	
Si	51 MADVHEPLWRRKRKKVLVDYLVOFRVTLVTFVVLPTSSLTYFNTYLGDMWSAMSSEKKROKOHDENVOKVKK	RLKORNPKKDGLVCTARKPWIAV
Si	Sj*MADLHEPLVRRKRKKVLVDYLVKFRWILVIFVVLPISALIYFNIYLGDMWSAMKSEKKRQKQHDENVQKVVK	RLK <mark>QRNPKK</mark> DGLVCTARKPWIAV
0s	05MADLQEPLWRPKRKKVLVDYLVKFRWILVIFVVLPISALIYFNIYLCDVWSAMKSEKRRQKEHDDNVKVK	
Gm	ALMSDLQIPLVIPLC-KKKIWVDIVKKRWIJIIIIIVVPSAIFYELIIGDWWSESSFERRUREDERWKWIK CmWSDLFADI-DDI-BOK-RKKVVVYEVOERWIJVIFVVIPISETIYEIIVIGDV856WSYKKRKKEDERWKVKK	
Gm	GM*MSDLEAPL-RPKRKKVWVDYFVOFRWTLVIFVVLPISFTIYFLTYLGDVRSEMKSYKTROKEHDENVKKVTK	RLKORNPSKDGLVCTARKPWIAV
Me	MeMSDLEAPL-RPKRKKYLVDYLVKFRWILVIFWLPISFTFYELIYLGDVKSGMKSYKQRQKEHEENVQKVVK	RLK <mark>QRNPSK</mark> DGLVCTARKPWVAV
Sm	5m MSDLEKPI-RPRKARSWVDWAVQFRWIIVILVVLPOSFTFYSLDVLRSOWSASKSYKKROKEHDANVAKVIK	
Sm" Pn	3///*MDQQKRGEEKRAREKKAPSIADELUQERWIVIPMLEPLSELEIQLVKWEPAIWILLIGEPSEESJIKAADKEWKK PrWGCIOKDI-PDKKRTWVWAYOERWIIVIIWIPAIKSEDTYAWKEPGWGAEKSEKROKEROKENOKKWIX	
Pp	Pp*MSDLRKPL-RPKKARSWOWAVKLRWILVIFWLPVSVSFAICARSRELWSAWKSEKKRQKEHDENVEKVIK	RLK <mark>SRDPAH</mark> DGLVCTAR <mark>R</mark> PWVVV
-	101 Kna2-3	200
∠m Zm ²	2m GMRNVDYKKARHFEDDLSSERNILEIDKERMVARVEPLVMNGQIIRAICLMMLALAVVAELDDLIVGGIIRGYGIEG 7m GMRNVDYKARHFEDDLSALDNILETDAEPMADVEDLVSMAOTIKAICDMMLSLAVADELDDLIVGGIITGYGIEG	SSHLYGLFSDTVVAMEVVLADGR
sb	5b GNRNVDYKRAR FEVDLSSFRNILEIDKERMAKVEPLVNMGOITRAICPUNLALAVVAELDDLTVGGLINGYGIEG	SSHLYGLFSDTVVAMEVVLADGR
sb;	<i>sb</i> *RRLQACQTFSVDLSAFRNILEIDTERMYAKYEPLVSMGQITKATCPMNLSLAVAPEFDDLTVGGLINSYGISG	GSHIYGLFTDTVVAMEVVLADGQ
51	57 GMRNVDYKRARHFEVDLSAFRNILEIDKERMVAKVEPLVNMGQITRATCPMILALAVVAELDDLTVGGLINGVGIEG	SSHLYGLFSDTVVAMEIVLADGR
05	37 GNRNVDYKRARHEVDLSAFRITLEIDKERNVARVEPVNMGQTIRATCPMNLALAVVAEDDDIVGGLINGYGIG 05 GNRNVDYKRARHEVDLSAFRITIETDRENVARVEPVNMGQTIRATCPMNLALAVVAEDDDIVGGITNGYGIG	SSHLYGLFSDTVVAMEVVLADGR
Αt	AT GMRNVDYKRARHFEVDLGEFRNILEINKEKMTARVEPLVNMGQISRATVPMNLSLAVVAELDDLTVGGLINGYGIEG	SSHIYGLFADTVEAYEIVLAGGE
Gm	Gm CMRNVDYKRAR FEVDLSAFRNVLEIDKERMIARVEPLVNMCQISRVTVPMNLSLAVVAELDDLTVGGLINGYGTEG	SSHKYGLFADTVVAYEIILADGT
GM ^o Me		SSHKYGLFADTVVAYEIILADGT
Sm	5m GNRNVDYKRAR FEVDLSPFGQILDIDTKNMIARVEPLVNMGQISRATVPLGVSLAVVAELDDLTVGGLINGYGIEG	SSHIYGLFSDTVVAYEIILADGR
Sm	<i>sm</i> *ALRNAEHKRGARYEVDLGELRNVVWIDRRRLLIKCEPMVTMSQLSAATLPEGVAPEVLPELDDLTIGGVINGYGIEG	SSHIYGLFAETCSAFELVLADGR
Pp	Pp GNRNVDYKRARHFEVDLNDFNQVLEIDRENTIARCEPLVNMGQITRMTVPMGLSLAVVAELDDLTVGGITRQGIEG	SSHIYGLFADTCVAYEIILADGR
Pp.	201 $Rna2-2$	300
Zm	ZM VVRATKONEYSOLF-YGIPWSQGTLEFLVSAEIKLIPIKEYMKLTYTOVKGGLKEIAQAYAOSEAPROGDPAKV	PDFVEGMVYTESEGVMMIGVYAS
Zm	Z#* VVRATNONEHSOLF-YGMPWSQCTICLVSAEIRLVRVKEYMRLTYTPVRGTLKEIAEAVADSLFLPAKV	PDFVEGMVYSSSEGVMMTGVYAS
SD	50 WRATKIDNEYSDLF-YGIPUSOCTLCFLVSAEIIKUJPLIKEVIKLTYTEVKOSLKEIAOANAOSFAPROGDPAKV 547 WPATNIDNEYSDLFLWIAMVQDPUDWADCSSDDOAUSCOCTHEANTYTENPOTIKETAAAASSAVQDPCODAX	PDFVEGMVYTESEGVMMTIGVYAS
Si	30 WIAA HONE BOLF LWRAIWY FRIUWER CPSROUARS CONTRAINT WKST NET ACTIVE STORES	PDFVEGNVYTESEGVMMTGVYAS
Si	<i>si</i> *vvratkoneysolf-ygipwsqgtlgflvsaeiklipikeymkltyipvkgnukeiaqayadsfaprogdpakv	PDFVEGMVYNESEGVMMTGVYAS
05	05 VVRATKONEYSOLF-YGTPWSQGTLGFLVSAETIKLTPTIKEYMRLTYTPVKGSUKEIAQGYCDSFAPROGPPAK	PDFVEGMVYTENEGVMMTGVYAS
Gm		PDEVEGNVYNPTEGVMMVGTYAS
Gm	GM* LVRATKONEYTOLY-YAIPWSQCTLGLLVAAETKLIPVKEYMKLAYKPVVGTLQDLAOANCOSFAPROGOODNEEKV	PDFVEGMIYTPTEGVMMIGRYAS
Me	Me VVRATKDNEYSDLF-YAIP//SOGTLGLLVSAETKLTPVOEYMKVTYKPVVGNLKELAQAYIDSFAPRDLDODNPAKV	PDFVEGMIYSRTEGVMMTGRYAS
Sm	5m LVRATADNEHKELF-VAIPASOCTLIGLLVAAEIKLIPVKEVKVIVIPVROSLRDLAOAVIDSEOPAGDOBADKV	PDFVEAMIYNRNEGVMMTGRYAS
PD		PDFVEGIVISGSTAVITIGRYAS
Pp*	PP*LVRVIADNEFSDLY-YAIP/SQCTLGLLVAAEIKLIEVGPYMRLTYSPARCNLQELADAYNDTYIPRDGDQDNPEKV	PDFVESMVYSESEAVCMSGRYAG
7		
2m 7m ²	2m Keeakk Konkinc vgwerwerydhau al kroefveyipi Refyhrhits Lyweaklipfedd wrrhugw 2m Kofartk (Scritn Vgwerkeneydhaftai Froffvyrhrits Lyweaklipfedd wrrhugwerker)	
sb	sb KEEAKKKGNKINCVGWWFKPWFYQHAQTALKRGEFVEYIPTREYYHRHTRCLYWEGKLILPFGDQ WFRFLLGW	MPPKVSLLKATQGEAIRNYYHD
sb;	Sb*EEEAKKKGNRINRVGWWFKPWFYQYAETALKRGEFVEYIPTREYYHRHTRSLYWEGKLIIPFCDQEWFRFLIGW	LMPPKISLLKITQGEAIRNYYHD
57	57 KEEAKKKGNKINCVGWWFKPWFYQHAOIALKRGEFVEYIPTREYYHRHTRCLYWEGKLILPFGOOR MFRFLLGW	
05	05 KEEAKKKGNKINCVGWWFKPWFYOHAOTALKKGEFVEYIPTREYYHRHTRCLYWEGKLILPFGOOFWFRFLLGW	MPPKVSLLKATQGESIRNYYHD
At	At KEEAKKKGNKINNYGWWFKPWFYQHAQTALKKGQFVEYIPTREYYHRHTRCLYWEGKLILPFSDQFWFRYLLGW	LMPPKVSLLKATQGEAIRNYYHD
Gm	Gm KEEAKKKGNKINSYGWWFKPWFYQHAOTALKKGEFYEYIPTREYYHRHTRCLYWEGKLILPFADOCWFRYLFGW	MPPKVSLLKATQGDAIRNYYHE
Gm" Me	G//* REEARN KONNINS YGWWFRWHYDHAU AL NA GEFVEYIPI RETYHRHIRD TWEGRULLPFADD WIRTUHGW Ma KEFAKO KONKINS YGWWFRWHYDHAU AN KGEFVEYIPI RETYHRHIRD TWEGRULLPFADD WIRTUHGW	
Sm	Sm REEAKQRGNKTNEQGWWFKPWFYQHAQTALDKGEFVEYIPTREYYHRHTRCLYWEGKLTLPFADQFWFRWLMGW	AMPPKVSFLKATQGDAIRNYYHE
Sm	Sm#REEAARKGNVTNDFGWMMKPWFHTHAQSALERGTFVEYVPVRSYYHRHTRSLYWEGGLTVPMGNHPLFRULTGW	MPPKVSULKUTQUDGIRKYYIQ
Pp	Pp KDEAKRKGNKINCQGWWYKWFYQHAQEALIRGEFVEYIPTRDYYHRHTRCLYWEGKLILPFADQEMERYLFG D#%YEGKINCQGWEKUHYQHAQEALIRGEFVEYIPTRDYYHRHTRCLYWEGKLILPFADQEMERYLFG	
rρ		500
Zm	Zm NHVIQDMLVPLYKVGDALEFVHREMEVYPLWLCPHRLYKLPVKTMVYPEPGFEHQHRQGDTSYAQMFTDVGVYYAPG	AMLRGEEENGAEAVHRLEQWLIE
Zm ⁿ		
sb	Sb*NHVTODVLVPLHKVSDALEFAHRELEVYPVWLCPHRLYKLPVKTMVHPEPGFEOHRRKGDTSYAOMETDVGFYYAPA	SMLRGEEENGAEAVHRLEOWLTR
si	57 NHVIQDMLVPLYKVGDALEFVHREMEVYPLWLCPHRLYKLPVKTMVYPEPGFEHQHRQGDTSYAQMFTDVGVYYAPA	AVLRGEEFNGAEAVHRLEQWLIE
Si	57*NHVIQOMLVPLYKVGDALEFVHREMEVYPLWLCPHRLYKLPVKTMVYPEPGFEHOHROGDTSYAQMFTDVCVYAPA	AMLRGEEFNGAEAVHRLEOWLIE
$\frac{0}{4t}$	05 NHVIQUMLYHLYNVGDALEN YNRHENEVYPLWLCPHRLYRLPVNIMVIPEPGFEHHNRGGDTEDAGWYDVGYMYAPG 4t hYvDDMLVPLYNVGDALEWYHRENEVYPLWLCPHRLFROPTRGOTVDEPGFEYENRGGDTEDAGWYTDVGYWYAPG	
Gm	Gm MHVIQDMLVPLYKVGDALEwVHREMEVYPIWLCPHKLFKLPVKIMIYPEPGFELHRRQGDTQTAQMYTDVGVYYAPG	PVLRGEVFDGAEAVRKMENWLIE
Gm	GM*MHVIQDMLVPLYKVGEALEWYHRENEVYPIWLCPHKLFKLPVKTMIYPEPGFELHRRCGDTOTAQMYTDVGVYYAPG	PVFRGEVFDGAEAVRKMENWLIE
Me Sm		
Sm	5mt*RHACODMLVPNHKLAACLEFCHENFETYPLWLCPHRLFKTEMGTMLDCEPGFSSNKOPGDTDYAOMMTDVGIWGVPG	PVLRCEVWDGVQATKNMEKWLRD
Pp	Pp RHVIQDMLVPSYKVGYALEFSDREFEVYPIWLCPHRLFKHPMRTQINPEPGFEYAGRPGDTPYAQMYTDVGVYYTPR	CVFKGEEFDGVAAVKKMEAWMIE
Pp	PP*SO1 SO1 SO1	CMFQGEEFDGIAAVKKMEAMMIE
Zm	Zm NHSYOPOYAYSEUNEKDEWRMEDASHYEHCROKYGAYGTEMSVYYKSKKGRIXTEKEVOEAEAAILEPAYADEEA	
Zm	Zm [#] NHGYQAQYAVSELSGKDFWRMFDASHYHHCRRKYGAVGTFMSAHYKSKKGKKTQEEVLQAEAEAADADVVDAVTS	
Sb	SD NHSVOROVAVSELNEKOFWRMEDASHYEHORHKYGAVGTENSVYYKSKKGRKTEKEVQEAEAAILEPAYADEA	
su" Si	57 NHSYOPOYAVSELNEKDEWRMEDASHYEHORIKAKI SAVGSENSAHYKSKKKGRKTEKEVOEAEAATI EPAYADEA	
51	S7*NHSYOPQYAVSELNEKDEWRMEDASHYEHORRKYGAVGTEMSVYYKSKKGRKTEKEVQEAEAAILEPAYADEA	
05	OS NHSYOPOYAVSELNEKDEWRMEDASHYEHCROKYGAVGTEMSVYYKSKKGRKTEKEVQEAEAAILEPAYADEA	
AT Gm	A C NIGEOROTAVSELUEKSEWKRENGELYEEUKKKYKATGIENSVYYKSKKGRITEKEVREAEQAHLETAYAEAD GM NIGEOROYAVSELSEKNEWRMEDAGLYEHTRRKYGAVGTEMSVYYKSKKGRITEKEVOFAFOAHLETAVAEVDOPVD	
	ATREVDQFVD	
Gm	Gm*NHGFQPQYAVSELSEKNFWRMFDAGLYEHTRRKYGAVGTFMSVYYKSKKGRKTEKEVQEAEQAHLETAYAEADQPVD	
Gm ^a Me	GM [#] NHGFQPQYAVSELSEKNFWRMFDAGLYEHTRRKYGAVGTFMSVYYKSKKGRKTEKEVQEAEQAHLETAYAEADQPVD MeNHGFQPQYAVSELTEKNFWRMFDAGLYEOCRRRYGAVGTFMSVYYKSKKGRKTEKEVQEAEQAHLETAYAEGV	
Gm ⁴ Me Sm	Gm ^a NHGFQPQYAVSELSEKNFWRMFDAGLYEHTRRKYGAVGTFMSVYYKSKKGRKTEKEVQEAEQAHLETAYAEADQPVD Me NHGFQPQYAVSELTEKNFWRMFDAGLYEQCRRRYGAVGTFMSVYYKSKKGRKTEKEVQEAEQAHLETAYAEGV Sm NHGFQPQYAVTELNEHDFWRMFDATLYNACREKYRAVGTFMSVYYKCKKGRKTEQEVQEEQKVHDNGYKDLERPLD sm SpSYCI X MEVGOSCEFENGHEDSI MAADANYXADE ALLENDYYKCKKGRKTEQEVQEEQKVHDNGYKDLERPLD	A
Gm [®] Me Sm Sm [®] PD	Gm ^a NIGFOPQYAVSELSEXNFWRMEDAGLYEHTRRYCAVGTFMSVYYKSKKGRKTEKEVQEAEQAHLETAYAEADQPVD MeNHGFOPQYAVSELTEXNFWRMEDAGLYEQCRRYCAVGTFMSVYKSKKGRKTEKEVQEAEQAHLETAYAEQV 5m/NHGFOPQYAVSELIBKNFWRMEDAGLYEQCRRYCAVGTFMSVYYKCKKGRKTEQEVKQEEQKVHDNGYKDLERPLD 5m ^a SRSYQCLYAEVEQSEGEFWQMFDPSLYNAVRNKYGAESAFMSVYYKESNCKKGSKHGKKD PD/NHCFOPQYAVSELINBRDFWRMEDPTLYPQCROXYKAVGTEMSVYYKCKKGRKTEKEVAEEEAKVTBSAYADVEKPF	A

Figure S3. Multiple sequence alignment of *Zea mays* NA2 protein sequence with orthologous sequences.

Red amino acids indicate the SNP induced amino acid changes and are denoted above the sequence in *na2-1*, Q to *; *na2-2*, G to R; *na2-3*, E to K; and *na2-4*, G to *. Black background indicates identity conservation of \geq 90%, grey indicates conservation of \geq 50%, and white indicates conservation of \leq 50%. Dashed lines indicate gaps in the alignment. *Zm, Zea mays* (GRMZM2G057000); *Zm**, *Zea mays* (GRMZM2G455658); *Sb*, *Sorghum bicolor* (Sobic.010G277300); *Sb**, *Sorghum bicolor* (Sobic.004G355600); *Si*, *Setaria italic* (Si006158m); *Si**, *Setaria italic* (Si034967m); *Os*, *Oryza sativa* (LOC_Os10g25780); *At*, *Arabidopsis thaliana* (AT3G19820); *Gm*, *Glycine max* (Glyma12g03210); *Gm**, *Glycine max* (Glyma11g103500); *Me*, *Manihot esculenta* (cassava4.1_004670m.g); *Sm*, *Selaginella moellendorfii* (139528); *Sm**, *Selaginella moellendorfii* (144134); *Pp*, *Physcomitrella patens* (Phpat.007G004200); *Pp**, *Physcomitrella patens* (Phpat.011G104600).



Figure S4. RNA expression levels of maize or sorghum genes from qTeller dataset.

RNA expression FPKM values from previously published RNA-seq experiments for (A) GRMZM2G057000 (*na2*), (B) GRMZM2G455658, (C) Sb10g031090 (Sobic.010G277300), and (D) Sb04g038200 (Sobic.004G355600). Data are taken from the from qTeller database. Figures can be regenerated using the following links:

GRMZM2G057000:

http://qteller.com/qteller3/bar_chart.php?name=GRMZM2G057000&info=

GRMZM2G455658:

http://qteller.com/qteller3/bar_chart.php?name=GRMZM2G455658&info=

Sb10g031090 (Sobic.010G277300):

http://qteller.com/sorghum/bar_chart.php?name=Sb10g031090&info=

Sb04g038200 (Sobic.004G355600):

http://qteller.com/sorghum/bar_chart.php?name=Sb04g038200&info=



Figure S5. Internode lengths of *na2-1*, *d5*, and wild-type siblings with and without GA₃ application.

(A) Internode lengths in centimeters measured at maturity under mock conditions. (B) Internode lengths in centimeters measured at maturity treated with GA₃. 1 mL GA₃ application was applied to the leaf whorl at a concentration of 866 μ M every third day, starting 25 d after sowing. (A-B) Errors bars represent ± standard deviation.

Site	Ear #	Mother	Father	WT	mut	TOT	χ² <i>p</i> -val
WL2011	CN833	+/na1-1	na2-1/na2-1	31	0	31	2.58E-08
WL2011	CN1393	+/ <i>na</i> 2-3	na1-1/na1-1	15	0	15	0.0001
WL2011	CN1394	+/ <i>na</i> 2-3	na1-1/na1-1	18	0	18	2.21E-05
WL2011	CN1395	+/ <i>na</i> 2-3	na1-1/na1-1	17	0	17	3.74E-05
WL2011	CN841	+/ <i>na</i> 2-7	na1-1/na1-1	32	0	32	1.54E-08
GH2011	MA45	+/ <i>na</i> 2-506D	na2-1/na2-1	40	31	71	0.2854
GH2011	MA46	+/na2-506D	na2-1/na2-1	33	28	61	0.5221
WL2011	CN857	+/na2-1	na2-518C/na2-518C	16	15	31	0.8575
WL2011	CN828	+/ <i>na</i> 2-7	na2-506D/na2-506D	18	14	32	0.4795
WL2011	CN939	+/ <i>na</i> 2-7	na2-518C/na2-518C	9	8	17	0.8084
WL2011	CN745	+/ <i>na</i> 2-7	na2-1/na2-1	17	15	32	0.7327
WL2010	CN560	+/ <i>na</i> 2-7	na2-1/na2-1	13	2	15	0.0045
WL2010	CN561	+/ <i>na</i> 2-7	na2-1/na2-1	6	8	14	0.5930
WL2010	CN578	+/ <i>na</i> 2-7	na2-1/na2-1	8	9	17	0.8084
GH2010	CN673	+/ <i>na2-2</i>	na2-7/na2-7	19	16	35	0.6121
GH2010	CN674	+/ <i>na</i> 2-2	na2-7/na2-7	16	15	31	0.8575
GH2010	CN646	+/ <i>na</i> 2-3	na2-7/na2-7	15	13	28	0.7055
GH2010	CN648	+/ <i>na</i> 2-3	na2-7/na2-7	19	15	34	0.4927
GH2011	MA37	+/na2-4	na2-506D/na2-506D	4	2	6	0.4142
GH2011	MA38	+/na2-4	na2-506D/na2-506D	14	11	25	0.5485
GH2011	MA160	+/na2-4	na2-506D/na2-506D	28	26	54	0.7855
WL2011	CN1384	+/na2-1	na2-6/na2-6	13	11	24	0.6831

 Table SI. Segregation ratios of crosses.

	+/na2-1	na2-1/na2-1	+/na2-2	na2-2/na2-2
SI abaxial ^a	15.7 ±1.2	16.9 ±1.7	17.4 ±1.6	18.7 ±2.2
SD abaxial ^b	158.5 ±29.4	166.2 ±15.5	181.4 ±24.7	192.8 ±20.2
SI adaxial ^a	10.5 ±0.7	12.1 ±1.7	12.1 ±2.3	11.8 ±1.1
SD adaxial ^b	110.4 ±14.2	121.8 ±17.4	115.4 ±20.7	109.1 ±10.4
RS adaxial/abaxial ^c	0.696	0.733	0.636	0.566

Table SII. Stomatal indices and densities of *na2-1*, *na2-2*, and wild-type plants.

^aSI, stomatal index, ^bSD, stomatal density, and ^cRS, ratio of stomata, were measured at the widest portion of leaf 5 of 30 d old plants.

Data is presented as means with standard deviation of 6 biological replicates.

Allele	Source	Stock Name	Genetic Background
na2-1	Maize COOP	4407D d*-N2374	Unknown
na2-2	Maize TILLING	PB03NM417	B73
na2-3	Maize TILLING	04INW22CW04351	W22
na2-4	Maize TILLING	04IAB73PS020G1	B73
na2-5	Identified in Mu-tagging	na2- <i>Mu</i> 13 (<i>Mu</i> #8)	Unknown
na2-6	Maize TILLING	04CAB73SH0365	B73
na2-7	Maize COOP	4405B d*-N1074C	Unknown
na2-506D	Maize COOP	506D	Unknown
na2-518C	Maize COOP	518C	Hi27
na1-1	Maize COOP	310G	Unknown
d5	Carolina Bio Sup Co	177110	Unknown
d1	Maize COOP	302A d1-6016	Unknown

Table SIII. Source of maize genetic stocks.

Table SIV. Primers used in this study.

Primer Name	Primer sequence- 5' to 3'		
Genomic			
ZmDWF1988FOR	GTGTCAACTGGTAGGATAATAGCCCA		
ZmDWF1440FOR	GTGTGCATATTCTCAAGGCTGTGG		
ZmDWF1163FOR	CAGATAACAATGTGCTTCCTTCAGC		
ZmDWF1163REV	GCTGAAGGAAGCACATTGTTATCTG		
ZmDWF121FOR	AACGACCACGAGCTTTTAGGC		
ZmDWF1_+144FOR	CTTCAACATCTTCCTGGGCGAC		
ZmDWF1_+144REV	GTCGCCCAGGAAGATGTTGAAG		
ZmDWF1_+675FOR	CACTGGGGTTCCTTGTCTCTGCG		
ZmDWF1_+675REV	CGCAGAGACAAGGAACCCCAGTG		
ZmDWF1_+1168FOR	GCTATCAGGAACTACTACCACGACAACC		
ZmDWF1_+1168REV	GGTTGTCGTGGTAGTAGTTCCTGATAGC		
ZmDWF1_+1243FOR	TACAATGGCTGGCTGGTGCT		
ZmDWF1_+1243REV	AGCACCAGCCAGCCATTGTA		
ZmDWF1_+1850REV	TGGATGTAGTGTGTGTCTGTCTCAAG		
ZmDWF1_na2-1DC	GTAGTACACGCCCACGTCCGTGAACAGC		
MuExt22D	CCAACGCCAWSGCCTCYATTTC		
Mulnt19	GCCTCYATTTCGTCGAATC		
qRT-PCR			
ZmDWF1qRT_FOR2	GAGCAGTGGCTGATCGAGAAC		
ZmDWF1qRT_REV2	AACATGCGCCAGAAGTCCTT		
ZmMOLqRT_FOR2	CTGTGTCCTCCGTGCTCCAT		
ZmMOLqRT_REV2	AGGACTCCCGCATCTCCATA		

Table SV. Two i	ndependent experiments	showing BR interme	ediates in wild-type
and <i>na2-1</i> plant	S.		

	Exp. 1		E>	кр. 2
Compound ^a	+/na2-1	na2-1/na2-1	+/na2-1	na2-1/na2-1
24-methylenecholesterol	2040	14000	1860	11100
campesterol	25400	190	17900	143
campestanol	555	6.10	329	1.13
6-oxocampestanol	12.5	0.35	11.6	0.64
6-deoxocathasterone	0.19	n.d. ^b	0.23	n.d. ^b
6-deoxoteasterone	0.02	n.d. ^b	0.05	n.d. ^b
3-dehydro-6-deoxoteasterone	0.55	n.d. ^b	0.27	n.d. ^b
6-deoxotyphasterol	3.09	n.d. ^b	2.32	n.d. ^b
6-deoxocastasterone	7.71	n.d. ^b	5.84	n.d. ^b
cathasterone	n.d. ^b	n.d. ^b	n.d. ^b	n.d. ^b
teasterone	n.d. ^b	n.d. ^b	n.d. ^b	n.d. ^b
3-dehydroteasterone	n.d. ^b	n.d. ^b	n.d. ^b	n.d. ^b
typhasterol	0.03	n.d. ^b	0.04	n.d. ^b
castasterone	0.58	n.d. ^b	0.43	n.d. ^b
brassinolide	n.d. ^b	n.d. ^b	n.d. ^b	n.d. ^b

^a ng/g fresh weight from 28 DAG plants.

^b n.d., not detected.