

Tab. S1. Primers for RT-qPCR

ID	Gene	Primer sequences
GRMZM2G060702	ACT	Forward: CAAACAGCCTCCCTGAGAATG Reverse: TGGACATCCTCTGCAGTAACAAA
GRMZM2G118637	UBQ	Forward: GTGAGTCGTGACTGAGCTGGTT Reverse: ATATGCGGTCGCACGATAGTT
GRMZM2G157727	PHYA1	Forward: GCAAGAGTGGTATCTGGTGGT Reverse: CATCAAGGGTTGTTTGTGCT
GRMZM2G181028	PHYA2	Forward: AGAGCAGATGAGGCAGGTTTC Reverse: GACTTACAGCAGACACCACCA
GRMZM2G124532	PHYB1	Forward: GGAGGCTGTGTGTGGAATG Reverse: CTGTGTGTGACCGAAACCAA
GRMZM2G092174	PHYB2	Forward: GAGAATGGCTGGGTAGAAA Reverse: GCAAACCTGAAGATGAAAAGC
GRMZM2G057935	PHYC1	Forward: TGGCTGCTACTGAAACATCG Reverse: CCAAATCTATCCGCACTACACA
GRMZM2G129889	PHYC2	Forward: CAAACGAGATGGTCCGCTTA Reverse: TCAACAGAATCAGCAACAACAA
GRMZM2G001457	PHOT1	Forward: CCTCAAGTTCATTGGGATGC Reverse: CATTGGACGAAGAGCAGTATC
GRMZM2G032351	PHOT2	Forward: ACGGCAAGGTCATCAAGTTC Reverse: AACTGGCATCTCGTTTGG
GRMZM2G049549	CRY2	Forward: TAGTGCGGTTGGCTTTACAA Reverse: TTACGGTTACATACATCACATACCTC

Tab. S2. Raw results of ANOVA

Ion leakage (Tab. 1)

Model term	df1	df2	F	p
Conditions	2	805	461.651	<0.001
Time	3	805	318.903	<0.001
Line	4	805	86.243	<0.001
Conditions:Time	6	805	84.242	<0.001
Conditions:Line	8	805	14.065	<0.001
Time:Line	12	805	3.805	<0.001
Conditions:Time:Line	24	805	6.482	<0.001

Leaf Area (Fig. 2A)

Model term	df1	df2	F	p
Conditions	1	375	40.384	<0.001
Line	4	375	106.130	<0.001
Conditions:Line	4	375	4.032	0.003

Shoot length (Fig. 2B)

Model term	df1	df2	F	p
Conditions	1	375	2184.998	<0.001
Line	4	375	296.268	<0.001
Conditions:Line	4	375	13.117	<0.001

Mesocotyl length (Fig. 2C)

Model term	df1	df2	F	p
Conditions	1	375	1385.902	<0.001
Line	4	375	84.759	<0.001
Conditions:Line	4	375	5.989	<0.001

FvFm (Fig. 3A)

Model term	df1	df2	F	p
Conditions	1	430	1766.147	<0.001
Line	4	430	17.494	<0.001
Conditions:Line	4	430	15.337	<0.001

Yield (Fig. 3B)

Model term	df1	df2	F	p
Conditions	1	430	821.072	<0.001
Line	4	430	4.481	0.001
Conditions:Line	4	430	12.591	<0.001

Chlorophyll (Fig. 4A)

Model term	df1	df2	F	p
Conditions	1	160	216.272	<0.001
Line	4	160	15.526	<0.001
Conditions:Line	4	160	1.714	0.149

Anthocyanin (Fig. 4B)

Model term	df1	df2	F	p
Conditions	1	160	251.964	<0.001
Line	4	160	28.559	<0.001
Conditions:Line	4	160	11.483	<0.001

Carotenoid (Fig. 4C)

Model term	df1	df2	F	p
Conditions	1	160	8.618	0.003
Line	4	160	13.706	<0.001
Conditions:Line	4	160	6.251	<0.001

Photosynthesis vs sowing depth vs soil temperature (Fig. 6 and Fig. S1, S2, S3)

Fv/Fm

model term	df1	df2	F	p.value
Conditions	1	649	6298.212	<0.001
Sowing	1	649	0.097	0.7555927
Temp	2	649	565.549	<0.001
Line	4	649	293.430	<0.001
Conditions:Sowing	1	649	2.305	0.1289300
Conditions:Temp	2	649	480.701	<0.001
Conditions:Line	4	649	194.774	<0.001
Sowing:Temp	2	649	2.682	0.0684223
Sowing:Line	4	649	9.463	<0.001
Temp:Line	8	649	17.019	<0.001
Conditions:Sowing:Temp	2	649	3.822	0.0218931
Conditions:Sowing:Line	4	649	4.812	0.0007023
Conditions:Temp:Line	8	649	15.665	<0.001
Sowing:Temp:Line	8	649	1.389	0.1954248
Conditions:Sowing:Temp:Line	8	649	0.447	0.8931585

Y

model term	df1	df2	F	p.value
Conditions	1	649	9914.979	<0.001
Sowing	1	649	40.494	<0.001
Temp	2	649	331.926	<0.001
Line	4	649	61.896	<0.001
Conditions:Sowing	1	649	34.107	<0.001
Conditions:Temp	2	649	333.614	<0.001
Conditions:Line	4	649	108.690	<0.001
Sowing:Temp	2	649	0.875	0.4167915
Sowing:Line	4	649	9.436	<0.001
Temp:Line	8	649	3.604	0.0003394
Conditions:Sowing:Temp	2	649	1.021	0.3602939
Conditions:Sowing:Line	4	649	10.293	<0.001
Conditions:Temp:Line	8	649	9.365	<0.001
Sowing:Temp:Line	8	649	1.697	0.0935286
Conditions:Sowing:Temp:Line	8	649	2.513	0.0099484

Photosensitivity (Fig. 7)

Model term	df1	df2	F	p
Conditions	1	955	3843.148	<0.001
Line	4	955	1038.822	<0.001
Light	3	955	214.044	<0.001
Conditions:Line	4	955	341.182	<0.001
Conditions:Light	3	955	317.700	<0.001
Line:Light	12	955	6.903	<0.001
Conditions:Line:Light	12	955	13.866	<0.001

Gibberellin effect (Fig. 9)

model term	df1	df2	F	p.value
Conditions	1	138	195.518	<0.001
Line	4	138	937.150	<0.001
Conditions:Line	4	138	13.741	<0.001

FvFm extended set of lines (Fig. S5)

Model term	df1	df2	F	p
Conditions	1	763	3964.066	<0.001
Line	20	763	10.662	<0.001
Conditions:Line	20	763	11.560	<0.001

Yield extended set of lines (Fig. S6)

Model term	df1	df2	F	p.value
Conditions	1	763	6637.318	<0.001
Line	20	763	6.460	<0.001
Conditions:Line	20	763	5.122	<0.001

Tab. S3. Sequence variants of genes potentially involved in gibberellin signaling in three maize inbred lines. Genes were assigned to the gibberellin signaling pathway following Reactome (<http://plantreactome.gramene.org/>). Genomes of inbred lines S160, S50676, and S68911 were re-sequenced to 30-fold coverage and compared with the reference B73 genome. SNP and indel variants were evaluated for importance with the use of Snpshift software (<http://snpeff.sourceforge.net/SnpSift.html>). Only variants of high importance are shown.

Gene name	Reference sequence	Modified sequence	S68911	S50676	S160	Description
AC194970.5_FG002 bZR7 - BZR-transcription factor 7	indel CGG	indel CGGG frameshift_variant	0/0	0/0	1/1	AT1G75080.1 (BZR1) Brassinosteroid signalling positive regulator (BZR1) family protein Encodes a positive regulator of the brassinosteroid (BR) signalling pathway that mediates both downstream BR responses and negative feedback regulation of BR biosynthesis. There is evidence for phosphorylation-dependent nucleocytoplasmic shuttling of BZR1. GSK3-like kinases (including BIN2), 14-3-3 proteins, and the phosphatase BSU1 seem to participate in this process. Phosphorylation also appears to affect BZR1's transcriptional activities.
GRMZM2G016756 bhlh60 - bHLH-transcription factor 60	indel GGCG	indel GGCGCGCG frameshift_variant	0/0	0/0	1/1	AT2G43010.1 (PIF4, SRL2) phytochrome interacting factor 4 Isolated as a semidominant mutation defective in red -light responses. Encodes a nuclear localized bHLH protein that interacts with active PhyB protein. Negatively regulates phyB mediated red light responses. Involved in shade avoidance response. Protein abundance is negatively regulated by PhyB.
GRMZM2G042666 idd7 - indeterminate1 domain7	CCCGGCC	CCCGGCCGGCCGCC frameshift_variant	0/0	0/0	1/1	AT2G02080.1 (AtIDD4, IDD4) indeterminate(ID)-domain 4 C2H2 BIRD transcription factor family.
GRMZM2G046290	indel ACG	indel ACGGCGAGTCG frameshift_variant	0/0	1/1	0/0	AT3G13810.1 (AtIDD11, IDD11) indeterminate(ID)-domain 11
GRMZM2G089736 zim23 - ZIM-transcription factor 23	indel TTGT	indel TT frameshift_variant	1/1	1/1	0/0	AT1G74950.1 (JAZ2, TIFY10B) TIFY domain/Divergent CCT motif family protein JAZ2 - JASMONATE-ZIM-DOMAIN PROTEIN 2

GRMZM2G065374 bhlh47 - bHLH- transcription factor 47	indel		1/1	0/0	0/0	AT3G59060.2 (PIF5, PIL6) phytochrome interacting factor 3-like 6 Encodes a novel Myc-related bHLH transcription factor, which physically associated with APRR1/TOC1 and is a member of PIF3 transcription factor family. Involved in shade avoidance. Functions as negative regulator of PhyB. Protein levels are modulated by phytochrome B.
	ACTGCTGCGTGCTGCTGC	ACTGCTGC frameshift_variant				
	SNP		0/0	1/1	0/0	
C	T splice_donor_variant & intron_variant					
GRMZM2G123094	indel		0/0	1/1	0/0	AT1G25250.1 (AtIDD16, IDD16) indeterminate(ID)-domain 16 Encodes a transcription factor that, together with IDD14 and IDD15, regulates auxin biosynthesis and transport and thus aerial organ morphogenesis and gravitropic responses.
	TCTCGTACTCGTAC	TCTCGTAC splice_donor_variant&splice_ region_variant & 3_prime_UTR_variant & intron_variant				
	SNP		0/1	0/1	0/0	
C	A stop_gained					
GRMZM2G179677 iddp1 - indeterminate domain p1	indel		0/0	0/0	1/1	AT3G50700.1 (AtIDD2, IDD2) indeterminate(ID)-domain 2
	CGT	CGTGT frameshift_variant				
	indel		0/0	0/0	1/1	
	G	GA frameshift_variant				
	SNP		0/0	0/0	1/1	
C	T stop_gained					
GRMZM2G016605 Gibberellin receptor GID1A	SNP		0/0	1/1	0/0	LOC_Os05g33730.1 gibberellin receptor GID1L2 putative expressed
	C	T stop_gained				