Table S1. Primers for plasmid construction

Primer name	Sequence (5′–3′)	Purpose
GST-TaGAD2-F	GGGACTCTTGACCATGGTAATGGTGATCTCGCACGCGAGC	Constructing the *pGEX-4T-GST-TaGAD2* plasmid
GST-TaGAD2-R	TCAGTCACGATGCGGCCGCGCAGACTCCGGCCTTCTT	Constructing the *pGEX-4T-GST-TaGAD2* plasmid
GST-TaGAD2△C-R	TCAGTCACGATGCGGCCGCGGCGGCGGCGTTGGACA	Constructing the *pGEX-4T-GST-TaGAD2△C* plasmid
1302-TaGAD2-F	GGGACTCTTGACCATGGTAATGGTGATCTCGCACGCG	Constructing the *35S*$_{pro}$*:TaGAD2-GFP* plasmid
1302-TaGAD2-R	GCTCACCATCCTAGGACTAGTGCAGACTCCGGCCTTCTT	Constructing the *35S*$_{pro}$*:TaGAD2-GFP* plasmid
1302-TaGAD2△C-R	CTCACCATCCTAGGACTAGTGGCGGCGGCGTTGGACA	Constructing the *35S*$_{pro}$*:TaGAD2△C-GFP* plasmid
CUB-TaGAD2-F	GAAAAAGAGGGGGATTAACTAGTATGGTGATCTCGCACGCG	Constructing the *pCUB-TaGAD2-3×Flag* plasmid
CUB-TaGAD2-R	ACCGCTACCACCGCTACCGAGCTCGCAGACTCCGGCCTTCTT	Constructing the *pCUB-TaGAD2-3×Flag* plasmid
CUB-TaGAD2△C-R	ACCGCTACCACCGCTACCGAGCTCGGCGGCGGCGTTGGACAG	Constructing the *pCUB-TaGAD2△C-3×Flag* plasmid
TaGAD2-Sen-F	CTTGTTCTTTGAAAAAGAGGGGGATTAggatccGTAAACATGATAGCTCACTTGTTC	Constructing the *pCUB-TaGAD2△C-RNAi* plasmid
TaGAD2-Sen-R	GACGCGAAGCGGGTAGATATCactagtGCAAACCTGAACATTTGCACC	
TaGAD2-Ant-F	GATCGAATTCCTGCAGcccgggGCAAACCTGAACATTTGCACC	
TaGAD2-Ant-R	TGAACGATCGGGGAAATTCgagctcGTAAACATGATAGCTCACTTGTTC	

Table S2. Primers used in qRT-PCR

Primer name	**Sequence (5′–3′)**
TaGAD2-RT-F1	CCGGTACCGGATGCCGGAGGGG
TaGAD2-RT-R1	GATAGCAGTCTCATCCTCGCCG
TaGAD2-RT-F2	TTCTTCAGCCGGAGCTTGAA
TaGAD2-RT-R2	GTGCAATGATCTGGCTAGCACC
TaActin-F	ACCTTCAGTTGCCCAGCAAT
TaActin-R	CAGAGTCGAGCACAATACCAGTTG

Table S3 Effects of *Rht5* on internodes elongation and spike length

Groups	Genotypes	I5 length	I4 length	I3 length	I2 length	Peduncle length	Spike length	Plant height
T1 VS D1	T1	5.69±2.48	14.38±1.87	17.19±1.31	23.62±1.04	24.00±0.37	8.71±0.60	93.75±6.39
	D1	3.9±0.91	9.25±1.65	13.62±0.94	17.43±1.19	17.04±3.40	7.52±0.49	67.87±3.65
	Effect	-31.43%	-35.65%	-20.76%	-26.22%	-29.00%	-13.69%	-22.67%
	Contribute rate	6.91%	19.80%	13.78%	23.94%	26.89%	4.61%	100.00%
T2 VS D2	T2	9.75±1.98	15.94±1.27	18.31±1.71	22.56±1.52	19.56±8.14	8.10±0.40	94.36±4.73
	D2	3.55±1.64	9.65±2.30	13.46±1.74	19.09±1.36	15.79±5.85	8.50±0.64	70.03±3.06
	Effect	-63.59%	-39.45%	-26.50%	-15.39%	-19.28%	4.94%	-23.38%
	Contribute rate	25.48%	25.84%	19.94%	14.27%	15.50%	-1.64%	100.00%
T3 VS D3	T3	3.07±1.21	10.85±1.28	16.93±2.52	20.64±3.54	25.71±2.46	7.94±0.62	85.46±4.60
	D3	2.85±1.45	7.81±3.16	12.24±1.67	15.72±1.59	14.03±5.55	7.86±0.49	60.12±1.92
	Effect	-7.21%	-28.07%	-27.70%	-23.85%	-45.44%	-1.04%	-27.45%
	Contribute rate	0.87%	12.03%	18.50%	19.43%	46.12%	0.33%	100.00%
Average	Effect	-34.08%	-34.39%	-24.98%	-21.82%	-31.24%	-3.26%	-24.50%
	Contribute rate	11.09%	19.22%	17.41%	19.21%	29.50%	1.10%	100.00%

Note: Data are presented as mean ± SE (standard error). Effect (%) = (Mean of dwarf lines − Mean of tall lines)/Mean of tall lines × 100%; Contribute rate (%) = (Tall internode length − Dwarf internode length)/(Tall plant height − Dwarf plant height) × 100%.

Table S4. Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs)

GO accession	Term type	Term	Number	*P*-value	FDR	Rich Factor
GO:0009986	CC	Cell surface	23	4.80×10^{-07}	3.20×10^{-04}	0.032348805
GO:0010008	CC	Endosome membrane	27	1.10×10^{-05}	2.20×10^{-03}	0.024085638
GO:0048471	CC	Perinuclear region of cytoplasm	14	1.20×10^{-05}	2.20×10^{-03}	0.038888889
GO:0044440	CC	Endosomal part	27	1.30×10^{-05}	2.20×10^{-03}	0.023893805
GO:0003700	MF	Transcription factor activity, sequence-specific DNA binding	119	7.40×10^{-15}	6.10×10^{-12}	0.01981352
GO:0001071	MF	Nucleic acid binding transcription factor activity	119	7.50×10^{-15}	6.10×10^{-12}	0.019810221
GO:0019901	MF	Protein kinase binding	32	4.30×10^{-10}	2.40×10^{-07}	0.035087719
GO:0052641	MF	Benzoic acid glucosyltransferase activity	18	1.50×10^{-09}	3.40×10^{-07}	0.059602649
GO:0052638	MF	Indole-3-butyrate beta-glucosyltransferase activity	18	1.50×10^{-09}	3.40×10^{-07}	0.059602649
GO:1901700	BP	Response to oxygen-containing compound	323	1.50×10^{-39}	1.40×10^{-35}	0.018641427
GO:0009719	BP	Response to endogenous stimulus	294	4.70×10^{-36}	2.30×10^{-32}	0.018872769
GO:0009696	BP	Salicylic acid metabolic process	80	1.70×10^{-35}	5.70×10^{-32}	0.054570259
GO:0009607	BP	Response to biotic stimulus	253	2.50×10^{-34}	6.10×10^{-31}	0.020111288
GO:0010200	BP	Response to chitin	100	3.90×10^{-34}	7.70×10^{-31}	0.040749796

Note: Term type represents GO category (BP, biological process; MF, molecular function; CC, cellular component); *P*-values were calculated using a hypergeometric test and adjusted for multiple testing using the false discovery rate (FDR); FDR represents the multiple testing–adjusted *P*-value. Rich Factor indicates the enrichment strength of each GO term.

Table S5. KEGG pathway enrichment of the differentially expressed genes (DEGs)

ID	KEGG name	Number	*P*-value	*Q*-value	KEGG_class
KO04016	MAPK signaling pathway - plant	24	5.23×10^{-10}	4.18×10^{-08}	Signal transduction
KO00360	Phenylalanine metabolism	14	3.18×10^{-09}	1.27×10^{-07}	Amino acid metabolism
KO01110	Biosynthesis of secondary metabolites	85	2.42×10^{-08}	6.46×10^{-07}	Global and overview maps
KO04626	Plant-pathogen interaction	26	1.67×10^{-07}	3.33×10^{-06}	Environmental adaptation
KO00940	Phenylpropanoid biosynthesis	23	2.03×10^{-05}	3.25×10^{-04}	Biosynthesis of other secondary metabolites
KO00591	Linoleic acid metabolism	5	3.39×10^{-04}	4.51×10^{-03}	Lipid metabolism
KO00750	Vitamin B6 metabolism	3	6.89×10^{-03}	7.29×10^{-02}	Metabolism of cofactors and vitamins
KO00592	alpha-Linolenic acid metabolism	6	7.29×10^{-03}	7.29×10^{-02}	Lipid metabolism
KO00904	Diterpenoid biosynthesis	5	8.89×10^{-03}	7.90×10^{-02}	Metabolism of terpenoids and polyketides
KO00220	Arginine biosynthesis	4	1.41×10^{-02}	1.13×10^{-01}	Amino acid metabolism
KO00944	Flavone and flavonol biosynthesis	3	1.61×10^{-02}	1.17×10^{-01}	Biosynthesis of other secondary metabolites
KO00910	Nitrogen metabolism	5	1.89×10^{-02}	1.26×10^{-01}	Energy metabolism
KO01210	2-Oxocarboxylic acid metabolism	5	2.92×10^{-02}	1.63×10^{-01}	Global and overview maps
KO00460	Cyanoamino acid metabolism	7	3.01×10^{-02}	1.63×10^{-01}	Metabolism of other amino acids
KO00410	beta-Alanine metabolism	4	3.05×10^{-02}	1.63×10^{-01}	Metabolism of other amino acids

Note: *P*-value is the raw enrichment *P*-value, and *Q*-value is the multiple testing-adjusted *P*-value. “KEGG_class” denotes the functional category assigned by KEGG.

Table S6. Transcripts per million (TPM) values of phytohormone-related DEGs

Pathway	**Gene ID**	**Gene description**	**TPMs**								
			JM47	**Marfed M**	**T1**	**T2**	**T3**	**Mean**	**D1**	**D2**	**D3**
GA	*TraesCS7D02G539200*	GA biosynthesis enzyme *TaCPS-D*	1.14	4.33	1.16	1.15	1.47	1.26	2.48	2.06	3.72
	TraesCS3D02G293800	Gibberellin 2-beta-dioxygenase *TaGA2ox-D3*	1.28	3.24	10.05	14.95	30.75	18.59	8.24	6.08	4.50
	TraesCS1D02G127000	Gibberellin 2-beta-dioxygenase *TaGA2ox-D10*	2.63	1.38	4.65	4.56	5.75	4.98	2.45	1.66	2.16
	TraesCS3B02G141800	GA biosynthesis enzyme *TaGA3ox-B2*	48.13	3.16	64.89	28.55	47.62	47.02	34.96	50.94	7.73
	TraesCS3D02G124500	GA biosynthesis enzyme *TaGA3ox-D2*	30.14	3.42	29.97	9.99	23.58	21.18	22.20	34.61	7.44
	TraesCS1A02G255100	Gibberellin Receptor *GID1-A*	8.56	10.79	15.14	42.89	60.43	39.48	26.77	31.28	6.97
	TraesCS4A02G271000	Green revolution gene *Rht-A1*(DELLA protein GRA)	133.16	67.38	111.87	88.11	73.97	91.32	87.74	94.07	62.00
	TraesCS4B02G043100	Green revolution gene *Rht-B1*	113.77	67.27	102.42	76.51	61.13	80.02	91.76	96.95	63.60
	TraesCS4D02G040400	Green revolution gene *Rht-D1*	96.71	52.80	71.66	59.15	47.02	59.27	62.71	66.36	57.20
BR	*TraesCS6B02G334600*	Transcription factor *ILI5*	11.74	39.11	14.61	15.51	7.22	12.45	21.22	16.05	37.48
	TraesCS6D02G285300	Transcription factor *ILI5*	24.84	80.71	31.63	29.73	10.94	24.10	42.69	33.29	96.31
	TraesCS4D02G282100	Serine/threonine protein phosphatase *PP2A-4* catalytic subunit	40.50	54.67	39.14	67.22	54.79	53.71	63.59	60.66	58.23
	TraesCS4D02G221200	Protein TPR3	24.53	32.33	30.38	38.03	31.92	33.45	47.10	46.98	33.46
	TraesCS3A02G055600	14-3-3-like protein B	191.25	264.84	133.12	124.83	123.95	127.30	189.33	147.89	281.06
	TraesCS4A02G268700	14-3-3-like protein A	312.89	380.74	288.00	269.76	251.65	269.81	348.13	305.97	389.39
	TraesCS4B02G045500	14-3-3-like protein A	310.53	358.22	269.67	237.02	240.81	249.16	348.21	285.03	360.04
	TraesCS4D02G046400	14-3-3-like protein A	393.33	450.59	339.93	312.69	305.78	319.46	397.35	367.19	447.00
AUX	*TraesCS6B02G260800*	Bifunctional nitrilase/nitrile hydratase *NIT4*	9.71	54.22	49.89	27.21	48.36	41.82	31.35	37.17	55.26
	TraesCS6D02G215300	Bifunctional nitrilase/nitrile hydratase *NIT4*	25.55	41.66	26.94	34.14	35.94	32.34	27.68	36.91	40.67
	TraesCS4B02G193200	Pyruvate decarboxylase 2	46.85	6.50	36.90	42.06	136.54	71.83	41.37	124.07	5.65
	TraesCS4D02G194200	Pyruvate decarboxylase 2	54.58	79.68	68.49	395.26	288.67	250.81	112.41	264.59	103.81
	TraesCS5D02G517000	IAA-amino acid hydrolase ILR1-like 4	11.97	34.13	18.83	20.28	17.29	18.80	19.39	23.17	26.57

CTK	*TraesCS2A02G113600*	Very-long-chain enoyl-CoA reductase	2.81	1.04	0.09	0.16	0.10	0.12	1.59	0.95	3.10
	TraesCS3A02G103800	Cytochrome *P450 90D2*	2.31	1.93	7.86	5.40	11.77	8.34	2.54	4.21	0.92
	TraesCS5A02G500000	DIMBOA UDP-glucosyltransferase *BX8*	6.22	29.04	7.12	6.98	12.05	8.72	11.11	8.09	17.71
	TraesCS3B02G156600	UDP-glycosyltransferase *76F1*	5.88	9.56	9.51	12.48	11.45	11.15	9.87	9.22	6.85
	TraesCS3D02G139300	UDP-glycosyltransferase *85A7*	4.80	9.53	9.60	12.67	11.07	11.11	9.52	9.09	7.76
	TraesCS6A02G288100	Transcription factor *BIM2*	2.45	4.88	6.29	13.83	12.90	11.01	5.57	5.07	2.70
	TraesCS6D02G270900	Transcription factor *BIM2*	0.96	3.01	3.08	5.35	5.33	4.59	2.33	2.39	1.95
	TraesCS5D02G428400	Transcription factor Phytochrome-interacting factor-like 13	2.28	2.01	1.80	4.81	6.66	4.42	2.33	2.87	2.58
ETH	*TraesCS2B02G436300*	Ethylene-responsive transcription factor 2	1.79	15.38	11.62	19.90	35.07	22.20	7.02	5.62	3.86
	TraesCS2D02G414600	Ethylene-responsive transcription factor 2	0.31	3.86	2.32	5.29	14.47	7.36	1.28	1.16	0.95
	TraesCS2A02G307100	Mitogen-activated protein kinase kinase kinase 3	3.27	16.80	3.46	6.87	7.73	6.02	5.56	4.91	11.53
	TraesCS4B02G039300	Probable ethylene response sensor 1	7.17	15.35	7.58	9.01	8.95	8.52	11.06	9.45	12.91
	TraesCS4D02G036400	Probable ethylene response sensor 1	8.81	13.33	6.92	9.35	8.05	8.11	10.46	8.67	11.62
	TraesCS6A02G169300	S-adenosylmethionine synthase	32.52	54.51	50.20	43.07	41.10	44.79	58.43	60.11	52.40
	TraesCS6B02G197300	S-adenosylmethionine synthase	30.13	45.25	43.06	42.48	40.81	42.12	49.85	53.80	43.47

Note: T1, T2, T3 indicate the tall *Rht5* RILs. D1, D2 and D3 indicate three independent dwarf *Rht5* RILs. GA = Gibberellin pathway, BR = Brassinosteroid pathway, AUX = Auxin pathway, CTK = Cytokinin pathway, ETH = Ethylene pathway.

Table S7. TPM values of DEGs involving in phytohormone pathway related to stress responses

Function	Gene description	Gene ID	TPMs								
			JM47	Marfed M	T1	T2	T3	Mean	D1	D2	D3
SA	*TraesCS3B02G045900*	Calmodulin-binding protein 60 B	0.29	22.35	2.29	15.01	16.38	11.23	4.38	2.79	6.00
	TraesCS3D02G041800	Calmodulin-binding protein 60 B	0.39	10.62	4.67	12.07	12.88	9.87	7.02	3.68	3.66
	TraesCS4A02G216100	Lipase-like *PAD4*	5.37	29.43	9.56	17.45	20.03	15.68	8.48	7.31	6.51
	TraesCS4B02G100100	Lipase-like *PAD4*	6.35	17.40	6.99	10.01	12.51	9.84	9.84	7.30	6.67
	TraesCS4D02G096400	Lipase-like *PAD4*	6.76	40.71	6.96	15.56	16.58	13.03	9.37	7.30	12.24
	TraesCS7B02G187600	NAC domain-containing protein 14	5.99	13.81	8.64	15.93	13.29	12.62	10.77	8.99	12.11
	TraesCS3B02G371200	NAC domain-containing protein 68	0.47	7.13	6.35	16.88	26.36	16.53	2.35	4.03	1.80
	TraesCS3A02G339600	NAC domain-containing protein 68	0.32	8.12	5.51	18.70	29.21	17.81	2.64	5.04	1.25
	TraesCS3D02G333100	NAC domain-containing protein 68	0.03	10.19	4.84	16.27	24.96	15.36	1.99	2.71	1.98
	TraesCS6D02G327600	Pathogenesis-related protein PR-1	17.95	6.95	12.46	2.73	2.51	5.90	11.90	15.14	7.91
	TraesCS5A02G183300	Pathogenesis-related protein PRB1-3	0.00	0.00	6.74	6.97	6.90	6.87	0.38	4.84	0.00
	TraesCS7D02G161200	Pathogenesis-related protein PRB1-3	0.00	0.00	10.32	8.57	8.79	9.23	0.33	7.29	0.00
	TraesCS7B02G105100	Pathogenesis-related protein PRMS	0.24	0.00	15.21	21.37	18.73	18.44	0.92	5.26	0.00
	TraesCS5A02G225500	WRKY transcription factor WRKY62	0.00	37.94	0.00	0.00	0.00	0.00	9.78	0.73	52.68
	TraesCS5D02G232700	WRKY transcription factor WRKY62	0.00	22.50	0.12	0.00	0.25	0.12	6.15	0.40	30.62
	TraesCS5B02G224100	WRKY transcription factor WRKY76	0.00	11.35	0.12	0.18	0.49	0.26	1.61	0.78	8.98
	TraesCS5A02G225600	WRKY transcription factor WRKY76	0.00	82.21	0.04	0.42	1.24	0.57	14.70	2.57	68.27
	TraesCS5B02G224000	WRKY transcription factor WRKY76	0.31	75.12	0.50	0.94	1.28	0.91	12.66	2.29	73.22
	TraesCS5D02G232800	WRKY transcription factor WRKY76	0.41	82.28	0.52	0.30	1.06	0.63	11.38	1.17	62.60
	TraesCS5D02G232900	WRKY transcription factor WRKY76	0.08	62.92	0.00	0.13	1.27	0.47	13.89	2.07	63.62

ABA	*TraesCS5D02G038800*	9-cis-epoxycarotenoid dioxygenase *NCED5*	0.18	1.69	0.11	0.26	0.32	0.23	0.67	1.23	1.38
	TraesCS7B02G269600	Abscisic acid receptor *PYL9*	2.65	1.55	2.52	4.19	7.94	4.88	1.15	2.49	1.21
	TraesCS2A02G099400	ABSCISIC ACID-INSENSITIVE 5-like protein 3	7.49	5.13	8.41	6.76	7.30	7.49	5.82	6.54	3.39
	TraesCS6A02G160500	Potassium channel *KAT1*	4.82	8.35	7.77	10.69	10.21	9.55	10.81	19.07	9.40
	TraesCS4B02G079300	Serine/threonine protein kinase *SAPK10*	4.16	0.34	4.52	4.28	8.08	5.63	3.60	2.87	0.49
JA	*TraesCS6A02G185100*	Allene oxide synthase 4	6.31	1.60	10.62	8.03	8.48	9.04	8.06	7.11	1.93
	TraesCS3A02G145300	Probable indole-3-acetic acid-amido synthetase	3.39	12.14	3.03	3.74	4.40	3.72	5.30	6.71	8.66
	TraesCS5A02G212800	Protein TIFY 10c	1.37	13.20	20.51	33.41	33.35	29.09	20.90	23.03	9.39
	TraesCS5B02G211000	Protein TIFY 10c	0.00	4.29	4.75	11.98	14.98	10.57	3.17	2.57	2.70
	TraesCS5D02G219300	Protein TIFY 10c	0.33	13.36	14.11	30.67	38.85	27.88	7.77	7.51	12.23
	TraesCS3B02G284800	Transcription factor *MYC2*	0.81	1.48	2.38	13.41	16.02	10.60	2.02	1.44	0.58
	TraesCS3D02G253700	Transcription factor *MYC2*	0.92	3.83	3.13	16.57	21.64	13.78	2.26	1.24	1.07
	TraesCS3D02G341100	WRKY DNA-binding transcription factor 70	0.49	2.54	6.95	25.02	31.24	21.07	3.14	3.68	0.89
	TraesCS3B02G379200	WRKY transcription factor *WRKY24*	0.31	2.59	8.58	26.33	34.99	23.30	4.52	3.99	0.95

Note: T1, T2, T3 indicate the tall *Rht5* RILs. D1, D2 and D3 indicate three independent dwarf *Rht5* RILs. SA = Salicylic acid pathway ABA = Abscisic acid pathway, JA = Jasmonic acid pathway

Table S8. TPM values of plant growth- and development-associated DEGs

Name	Gene ID	Gene description	TPMs								
			JM47	**Marfed M**	**T1**	**T2**	**T3**	**Mean**	**D1**	**D2**	**D3**
TaSPL17	*TraesCS7A02G246500*	Squamosa promoter-binding protein	2.89	4.72	1.38	3.35	1.79	2.17	3.32	1.80	4.59
	TraesCS5D02G273900		2.46	1.05	1.95	2.45	1.89	2.10	1.49	1.48	0.90
TaPKs	*TraesCS5A02G131100*	Pyruvate kinase	72.40	46.59	62.79	89.05	66.45	72.77	54.28	72.44	54.75
	TraesCS5B02G131000		84.98	47.79	72.92	85.66	68.96	75.85	61.44	77.85	57.55
	TraesCS5D02G138800		73.85	55.28	67.76	88.87	69.01	75.21	57.85	74.41	68.39
TaDEP3	*TraesCS7A02G464400*	Erect and dense spike gene; glycoprotein-associated phospholipase A	2.82	4.40	15.08	16.12	35.60	22.27	9.01	6.57	1.76
	TraesCS7B02G364900		2.22	5.51	9.53	12.52	30.11	17.39	5.32	5.00	1.49
	TraesCS7D02G452000		5.34	8.22	25.24	27.10	59.39	37.24	13.40	12.90	3.76
TaIDD14	*TraesCS4A02G074700*	Zinc finger protein SHOOT GRAVITROPISM 5	6.32	0.47	5.16	3.41	3.93	4.16	2.44	3.32	1.52
	TraesCS4D02G232000		6.02	0.53	6.82	5.56	4.70	5.69	2.28	3.85	0.80
TaMAPK6	*TraesCS7A02G111300*	Mitogen-activated protein kinase	8.36	26.90	15.24	11.23	21.35	15.94	14.42	18.80	7.76
	TraesCS7B02G009200		31.69	27.94	27.02	29.93	27.02	27.99	33.92	35.37	34.23
	TraesCS7D02G106400		39.40	31.84	32.37	34.81	31.79	32.99	38.91	40.55	37.07
TaBC2	*TraesCS5A02G161600*	Brittle culm gene	43.21	54.50	41.57	45.56	39.32	42.15	56.45	55.53	56.06
	TraesCS5B02G159100		35.23	40.19	36.72	42.24	32.21	37.06	44.23	46.47	41.50
	TraesCS5D02G167500		46.95	44.29	47.57	45.10	39.89	44.19	57.53	58.94	45.81
	TraesCS6D02G291700		52.62	36.98	37.30	32.80	28.50	32.87	39.83	42.46	32.54
	TraesCS7A02G198100		16.20	19.59	15.03	17.11	16.19	16.11	16.86	18.05	17.78
	TraesCS7B02G104500		17.75	19.86	15.60	19.38	17.19	17.39	19.03	19.68	19.70
TaUPL2	*TraesCS5B02G112800*	E3 ubiquitin ligase	11.13	13.33	9.68	14.38	12.50	12.18	15.05	12.30	13.15
	TraesCS5D02G118000		11.95	14.54	10.50	14.13	12.73	12.45	15.67	13.08	14.10

TaMHZ4	*TraesCS3B02G039800*	Protein MAO HUZI 4, chloroplastic	3.01	1.02	6.31	12.02	12.32	10.22	0.63	1.20	0.96
TaMADS 15	*TraesCS2A02G261200*	MADS-box gene	28.41	31.15	28.30	26.91	27.45	27.55	38.35	37.00	27.92
	TraesCS2B02G281000		53.67	63.86	54.44	62.77	60.96	59.39	77.24	74.41	62.98
	TraesCS2D02G262700		27.82	30.60	29.92	36.93	32.82	33.22	39.95	43.06	37.26
TaWRKYs	*TraesCS1B02G088900*	WRKY transcription factor	0.03	9.75	13.29	45.35	46.35	34.99	6.72	6.43	2.83
	TraesCS1D02G072900		0.00	5.89	13.46	52.40	44.41	36.76	7.66	6.79	1.03
TaGAD2	*TraesCS3A02G022600*	Glutamate decarboxylase	50.10	59.17	37.05	41.25	39.14	39.15	57.05	61.05	50.14
	TraesCS3B02G022900		8.78	68.98	5.41	5.88	7.65	6.31	63.55	65.97	66.40
	TraesCS3D02G023900		162.69	71.42	86.53	59.22	57.45	67.73	85.46	97.51	77.55
TaPSS1	*TraesCS3A02G021500*	Shortened uppermost internode;phosphatidylserine synthase	0.92	0.98	2.68	2.94	3.42	3.01	2.64	1.04	3.76
	TraesCS3B02G024600		0.22	2.01	0.34	0.10	0.42	0.29	1.51	1.50	2.03
	TraesCS3D02G025400		1.71	2.92	2.59	2.79	3.30	2.89	2.03	1.61	2.18

Note:T1, T2, T3 indicate the tall *Rht5* RILs. D1, D2 and D3 indicate three independent dwarf *Rht5* RILs.

Table S9. Accession numbers of the GAD homologs used for phylogenetic analysis

Species	Gene symbol	Gene ID
Zea mays	*ZmGAD1*	*Zm00001eb081600*
Zea mays	*ZmGAD2*	*Zm00001eb055490*
Zea mays	*ZmGAD3*	*Zm00001eb037690*
Zea mays	*ZmGAD4*	*Zm00001eb081550*
Zea mays	*ZmGAD5*	*Zm00001eb399220*
Glycine max	*GmGAD1*	*GLYMA_18G043600*
Glycine max	*GmGAD2*	*GLYMA_16G218500*
Glycine max	*GmGAD3*	*GLYMA_14G211100*
Glycine max	*GmGAD4*	*GLYMA_11G213000*
Glycine max	*GmGAD5*	*GLYMA_09G168900*
Glycine max	*GmGAD6*	*GLYMA_08G091300*
Glycine max	*GmGAD7*	*GLYMA_08G091400*
Glycine max	*GmGAD8*	*GLYMA_08G091500*
Glycine max	*GmGAD9*	*GLYMA_05G136100*
Glycine max	*GmGAD10*	*GLYMA_02G241400*
Triticum aestivum L.	*TaGAD1*	*TraesCS3B02G583600*
Triticum aestivum L.	*TaGAD2*	*TraesCS3B02G022900*
Triticum aestivum L.	*TaGAD3*	*TraesCS3A02G022600*
Triticum aestivum L.	*TaGAD4*	*TraesCS3A02G515300*
Triticum aestivum L.	*TaGAD5*	*TraesCS3D02G023900*
Triticum aestivum L.	*TaGAD6*	*TraesCS3D02G523200*
Triticum aestivum L.	*TaGAD7*	*TraesCS2A02G315300*
Triticum aestivum L.	*TaGAD8*	*TraesCS2A02G315800*
Triticum aestivum L.	*TaGAD9*	*TraesCS2B02G333700*
Triticum aestivum L.	*TaGAD10*	*TraesCS2B02G334000*
Triticum aestivum L.	*TaGAD11*	*TraesCS2D02G313500*
Triticum aestivum L.	*TaGAD12*	*TraesCS2D02G313800*
Triticum aestivum L.	*TaGAD13*	*TraesCS4A02G075600*
Triticum aestivum L.	*TaGAD14*	*TraesCS4A02G262600*
Triticum aestivum L.	*TaGAD15*	*TraesCS4A02G369200*
Triticum aestivum L.	*TaGAD16*	*TraesCS4B02G052300*
Triticum aestivum L.	*TaGAD17*	*TraesCS4B02G231400*
Triticum aestivum L.	*TaGAD18*	*TraesCS4D02G052500*
Triticum aestivum L.	*TaGAD19*	*TraesCS4D02G232700*
Oryza sativa	*OsGAD1*	*Os08g0465800*
Oryza sativa	*OsGAD2*	*Os04g0447800*
Oryza sativa	*OsGAD3*	*Os03g0236200*
Oryza sativa	*OsGAD4*	*Os03g0720300*

Oryza sativa	*OsGAD5*	*Os04g0447400*
Arabidopsis thaliana	*AtGAD1*	*AT5G17330*
Arabidopsis thaliana	*AtGAD2*	*AT1G65960*
Arabidopsis thaliana	*AtGAD3*	*AT2G02000*
Arabidopsis thaliana	*AtGAD4*	*AT2G02010*
Arabidopsis thaliana	*AtGAD5*	*AT3G17760*
Arabidopsis thaliana	*AtGAD6*	*AT3G17720*

Note: Ta = *Triticum aestivum* L., Gm = *Glycine max*, Os = *Oryza sativa,* Zm = *Zea mays and* At = *Arabidopsis thaliana.*