

Table S1 Sequences of primers used for qRT-PCR in this study

Primer name	Primer Sequence (5'→3')	Gene name
Os01g0646300 qRT-F	TTGCCGTCCACTTCACCA	<i>SLN1</i>
Os01g0646300 qRT-R	GCGAACTTGAGGTAGGGACA	
Os01g0763200 qRT-F	ATAATGGCAGCGTGCAAGACA	<i>OsTCP5</i>
Os01g0763200 qRT-R	CCAAGGAAAGCAGTGAAGGGA	
Os04g0618600 qRT-F	CCTCCTGAGCTGCAACAATACA	<i>PIF1</i>
Os04g0618600 qRT-R	GAAATCCGACTCGACGTTAGAC	
Os11g0700500 qRT-F	AATCCTGCCCTCTAGATACTGTG	<i>MYBAS1</i>
Os11g0700500 qRT-R	TGCTTTGTCTTTCCCTTCATC	
Os06g0110000 qRT-F	CAGCAACGCAGAACGGATTA	<i>KAO</i>
Os06g0110000 qRT-R	ACGGAAGGACACGAAGGAGA	
Os01g0206700 qRT-F	GCTTCTCAACGGTGATCCTAAT	<i>CIPK5</i>
Os01g0206700 qRT-R	GTCTTGCGGTGTCATACTCTTT	
Os01g0864000 qRT-F	GCAGATGGTGGTGGAGAAG	<i>OFP8</i>
Os01g0864000 qRT-R	AAGGCGTGGAGGATGAGA	
Os07g0580500 qRT-F	AGCACTGCGACAACAACGAG	<i>BZR1</i>
Os07g0580500 qRT-R	CGGCGGCTTACATCCCT	
Os09g0293500 qRT-F	CCCAATCACCTTCCTCTTCC	<i>BRL1</i>
Os09g0293500 qRT-R	ACTGGTCCAATCCCTTCATCC	
Os01g0190300 qRT-F	CAGATGTTCATCGCCACCG	<i>IAA2</i>
Os01g0190300 qRT-R	TGCCCTCTCTCTGCTCCCT	
Os02g0643800 qRT-F	AGAAGGCGGTGCTCAAGTG	<i>SAUR36</i>
Os02g0643800 qRT-R	CAGCGGGTGGTTGAAGTAGA	
Os01g0764800 qRT-F	TGCCGACGATAGAAGATGAGC	<i>GH3.2</i>
Os01g0764800 qRT-R	GGGCGGTGCTTGAAGTGAT	
Os06g0713800 qRT-F	CGCCTACATCCTCACCCAT	<i>AMY2A</i>
Os06g0713800 qRT-R	GCGATCTGCTCCTTTAACCC	
Os08g0473600 qRT-F	GGCGGGTGGTACAACCTTTCT	<i>AMY1.4</i>
Os08g0473600 qRT-R	TGCCTCGATCAGCGACTTG	
Os09g0414500 qRT-F	GCGGCAACAGCACAAGC	<i>MIF3</i>
Os09g0414500 qRT-R	ACCCTGCGGTGGAAGCT	
Os11g0128300 qRT-F	ATGGGGCCTCAGCAAGAC	<i>MIF1</i>
Os11g0128300 qRT-R	CCTGTACCGCACCCCTT	
Os05g0500900 qRT-F	TCGTGGCAGGGCATCAT	<i>GH3.4</i>
Os05g0500900 qRT-R	CGAAGTAGCACTCGGAGGA	
Os05g0143800 qRT-F	TGCGGCGTTCATCATTG	<i>GH3.6</i>
Os05g0143800 qRT-R	CGAGCAGCTTGCTTCCAT	
Os11g0528700 qRT-F	CCGCAATCCGGTTCGT	<i>GH3.13</i>
Os11g0528700 qRT-R	TCCTCGGAGGTCTTGTCGGT	
Os08g0342300 qRT-F	GCAGTTTGCTTTCTCCGTAA	<i>BRL3</i>
Os08g0342300 qRT-R	AAGATCATGCTCCCATTGTTTC	
Os02g0233200 qRT-F	TCCGAAGCACTGCGACAA	<i>BZR4</i>
Os02g0233200 qRT-R	GGCGGCTTGCATCCTTTTG	
Os03g0718100 qRT-F	GACTCTGGTGTGGTGTGTCAGC	<i>Actin I</i>
Os03g0718100 qRT-R	GCTGGAAGAGGACCTCAGG	

Table S2 Basic information for the transcriptomic data by HisSeq2500

Sample	Clean reads	Clean bases	Error %	Q20 %	Q30 %	Total mapped	Multiple mapped	Uniquely mapped
GAPT (0)-1	47721614	7124628344	0.025	98.10	94.00	46211608(96.84%)	1762091(3.69%)	44449517(93.14%)
GAPT (0)-2	46609118	6939761724	0.022	98.14	94.22	44935864(96.41%)	1837638(3.94%)	43098226(92.47%)
GAPT (0)-3	43109142	6431358671	0.026	97.82	93.34	41646989(96.61%)	1439115(3.34%)	40207874(93.27%)
GAPT (10)-1	65667948	9767088115	0.012	98.53	95.59	63522788(96.73%)	2553430(3.89%)	60969358(92.84%)
GAPT (10)-2	60011250	8936233283	0.012	98.52	95.55	57970639(96.60%)	1874186(3.12%)	56096453(93.48%)
GAPT (10)-3	53658204	7990606660	0.012	98.54	95.61	51893753(96.71%)	2886968(5.38%)	49006785(91.33%)
GAPT (50)-1	52816176	7866147265	0.012	98.56	95.66	51173259(96.89%)	5370267(10.17%)	45802992(86.72%)
GAPT (50)-2	65026990	9685582232	0.012	98.54	95.61	63035052(96.94%)	5033239(7.74%)	58001813(89.20%)
GAPT (50)-3	58844720	8758029667	0.012	98.47	95.42	56991470(96.85%)	2134334(3.63%)	54857136(93.22%)

Table S3 Correlation coefficient range among different samples based on FPKM values under all three treatments

	GAPT (0)-1	GAPT (0)-2	GAPT (0)-3	GAPT (10)-1	GAPT (10)-2	GAPT (10)-3	GAPT (50)-1	GAPT (50)-2	GAPT (50)-3
GAPT (0)-1	1.00	0.96	0.96	0.96	0.95	0.95	0.94	0.95	0.95
GAPT (0)-2	0.96	1.00	0.96	0.95	0.95	0.94	0.94	0.95	0.95
GAPT (0)-3	0.96	0.96	1.00	0.95	0.95	0.95	0.95	0.95	0.95
GAPT (10)-1	0.95	0.95	0.95	1.00	0.96	0.96	0.96	0.96	0.96
GAPT (10)-2	0.95	0.95	0.95	0.96	1.00	0.96	0.96	0.96	0.96
GAPT (10)-3	0.95	0.94	0.95	0.96	0.96	1.00	0.96	0.96	0.96
GAPT (50)-1	0.94	0.94	0.95	0.96	0.96	0.96	1.00	0.96	0.96
GAPT (50)-2	0.95	0.95	0.95	0.96	0.96	0.96	0.96	1.00	0.96
GAPT (50)-3	0.95	0.95	0.95	0.96	0.96	0.96	0.96	0.96	1.00

Table S4 Gene ontology (GO) enrichment analysis of the effect of GAPT (10) and GAPT (50) on rice mesocotyl under deep-sowing conditions

	Number	GO ID	Term Type	Description	Ratio_in_study	P value_uncorrected	P value_corrected
GAPT(10)	24	GO:0009404	BP	toxin metabolic process	24/3093	6.78633E-11	0
/GAPT(0)	5	GO:0034470	BP	ncRNA processing	5/3093	1.38997E-10	0
	88	GO:0019748	BP	secondary metabolic process	88/3093	1.47982E-10	0
	9	GO:0034660	BP	ncRNA metabolic process	9/3093	1.77869E-10	0
	8	GO:0006259	BP	DNA metabolic process	8/3093	1.97094E-10	0
	28	GO:0043933	BP	macromolecular complex subunit organization	28/3093	2.18662E-10	0
	16	GO:0006396	BP	RNA processing	16/3093	2.30473E-10	0
	19	GO:0090305	BP	nucleic acid phosphodiester bond hydrolysis	19/3093	2.30516E-10	0
	18	GO:1902589	BP	single-organism organelle organization	18/3093	2.35471E-10	0
	37	GO:0006996	BP	organelle organization	37/3093	2.35528E-10	0
	130	GO:0016043	BP	cellular component organization	130/3093	3.81243E-10	0
	292	GO:0006468	BP	protein phosphorylation	292/3093	3.85601E-10	0
	372	GO:0055114	BP	oxidation-reduction process	372/3093	4.29925E-10	0
	240	GO:0090304	BP	nucleic acid metabolic process	240/3093	4.54491E-10	0
	329	GO:0006725	BP	cellular aromatic compound metabolic process	329/3093	5.15626E-10	0
	51	GO:0044550	BP	secondary metabolite biosynthetic process	51/3093	5.31185E-10	0
	420	GO:0006807	BP	nitrogen compound metabolic process	420/3093	5.48139E-10	0
	271	GO:0006139	BP	nucleobase-containing compound metabolic process	271/3093	5.49384E-10	0
	362	GO:0034641	BP	cellular nitrogen compound metabolic process	362/3093	5.52247E-10	0
	21	GO:0033554	BP	cellular response to stress	21/3093	6.60542E-09	0
	333	GO:0016310	BP	phosphorylation	333/3093	8.47315E-09	0
	30	GO:0006412	BP	translation	30/3093	1.95181E-07	0
	35	GO:0043604	BP	amide biosynthetic process	35/3093	2.53402E-07	0
	30	GO:0051716	BP	cellular response to stimulus	30/3093	2.64767E-07	0
	84	GO:1901566	BP	organonitrogen compound biosynthetic process	84/3093	2.86191E-07	0
	10	GO:0006325	BP	chromatin organization	10/3093	9.45163E-07	0

1378	GO:0009987	BP	cellular process	1378/3093	1.10726E-06	0
47	GO:0072593	BP	reactive oxygen species metabolic process	47/3093	1.12449E-06	0
5	GO:0006397	BP	mRNA processing	5/3093	1.72102E-06	0.002
18	GO:0045491	BP	xylan metabolic process	18/3093	2.05878E-06	0.002
6	GO:0016568	BP	chromatin modification	6/3093	2.07858E-06	0.002
4	GO:0016569	BP	covalent chromatin modification	4/3093	2.6089E-06	0.002
4	GO:0010629	BP	negative regulation of gene expression	4/3093	3.79188E-06	0.002
34	GO:0008037	BP	cell recognition	34/3093	4.8598E-06	0.004
34	GO:0048544	BP	recognition of pollen	34/3093	4.8598E-06	0.004
3	GO:0010608	BP	posttranscriptional regulation of gene expression	3/3093	8.87924E-06	0.004
827	GO:0043170	BP	macromolecule metabolic process	827/3093	1.48431E-05	0.006
8	GO:0051128	BP	regulation of cellular component organization	8/3093	1.62328E-05	0.006
60	GO:0098869	BP	cellular oxidant detoxification	60/3093	1.68096E-05	0.008
60	GO:0098754	BP	detoxification	60/3093	1.68096E-05	0.008
22	GO:0032259	BP	methylation	22/3093	1.9608E-05	0.01
7	GO:0006399	BP	tRNA metabolic process	7/3093	2.04329E-05	0.01
7	GO:0008380	BP	RNA splicing	7/3093	2.04329E-05	0.01
19	GO:1901071	BP	glucosamine-containing compound metabolic process	19/3093	2.11712E-05	0.01
13	GO:0046274	BP	lignin catabolic process	13/3093	2.21658E-05	0.012
13	GO:0046271	BP	phenylpropanoid catabolic process	13/3093	2.21658E-05	0.012
8	GO:0022402	BP	cell cycle process	8/3093	2.22966E-05	0.012
2	GO:0018205	BP	peptidyl-lysine modification	2/3093	2.71941E-05	0.016
7	GO:0006470	BP	protein dephosphorylation	7/3093	2.95097E-05	0.022
27	GO:0010410	BP	hemicellulose metabolic process	27/3093	2.97951E-05	0.022
33	GO:0044036	BP	cell wall macromolecule metabolic process	33/3093	3.25018E-05	0.022
8	GO:0009853	BP	photorespiration	8/3093	3.32767E-05	0.022
17	GO:0071822	BP	protein complex subunit organization	17/3093	3.33187E-05	0.022

248	GO:0009056	BP	catabolic process	248/3093	3.37213E-05	0.022
273	GO:0006355	BP	regulation of transcription, DNA-templated	273/3093	3.89253E-05	0.028
3	GO:0006417	BP	regulation of translation	3/3093	4.04917E-05	0.028
38	GO:0072330	BP	monocarboxylic acid biosynthetic process	38/3093	4.27134E-05	0.03
4	GO:0016570	BP	histone modification	4/3093	5.14103E-05	0.048
27	GO:0048522	BP	positive regulation of cellular process	27/3093	5.17559E-05	0.048
37	GO:1990904	CC	ribonucleoprotein complex	37/3093	2.31024E-10	0
37	GO:0030529	CC	intracellular ribonucleoprotein complex	37/3093	2.31024E-10	0
24	GO:0044428	CC	nuclear part	24/3093	2.47204E-10	0
52	GO:0043228	CC	non-membrane-bounded organelle	52/3093	3.37325E-10	0
52	GO:0043232	CC	intracellular non-membrane-bounded organelle	52/3093	3.37325E-10	0
91	GO:0043234	CC	protein complex	91/3093	4.5494E-10	0
173	GO:0044422	CC	organelle part	173/3093	4.67796E-10	0
126	GO:0032991	CC	macromolecular complex	126/3093	4.74178E-10	0
171	GO:0044446	CC	intracellular organelle part	171/3093	5.20805E-10	0
344	GO:0044444	CC	cytoplasmic part	344/3093	6.1149E-10	0
665	GO:0043226	CC	organelle	665/3093	6.45377E-10	0
662	GO:0043229	CC	intracellular organelle	662/3093	7.04126E-10	0
6	GO:0044445	CC	cytosolic part	6/3093	8.46137E-10	0
889	GO:0044424	CC	intracellular part	889/3093	8.49058E-10	0
1222	GO:0044464	CC	cell part	1222/3093	8.54933E-10	0
8	GO:0044432	CC	endoplasmic reticulum part	8/3093	1.68604E-09	0
217	GO:0005886	CC	plasma membrane	217/3093	1.22786E-08	0
24	GO:0098796	CC	membrane protein complex	24/3093	1.2664E-08	0
40	GO:0044435	CC	plastid part	40/3093	1.58855E-08	0
40	GO:0044434	CC	chloroplast part	40/3093	3.61551E-08	0
632	GO:0043227	CC	membrane-bounded organelle	632/3093	7.06687E-08	0
9	GO:0044391	CC	ribosomal subunit	9/3093	7.29304E-08	0

629	GO:0043231	CC	intracellular membrane-bounded organelle	629/3093	7.65279E-08	0
5	GO:0005789	CC	endoplasmic reticulum membrane	5/3093	1.75345E-07	0
68	GO:0031090	CC	organelle membrane	68/3093	8.68728E-07	0
85	GO:0009507	CC	chloroplast	85/3093	2.00484E-06	0.002
88	GO:0009536	CC	plastid	88/3093	2.1269E-06	0.002
1193	GO:0016020	CC	membrane	1193/3093	2.34373E-06	0.002
50	GO:0005622	CC	intracellular	50/3093	2.92728E-06	0.002
34	GO:1902494	CC	catalytic complex	34/3093	2.96244E-06	0.002
16	GO:1990234	CC	transferase complex	16/3093	4.2234E-06	0.004
27	GO:0005840	CC	ribosome	27/3093	6.3171E-06	0.004
10	GO:0031975	CC	envelope	10/3093	6.82971E-06	0.004
10	GO:0031967	CC	organelle envelope	10/3093	6.82971E-06	0.004
11	GO:0044427	CC	chromosomal part	11/3093	7.23254E-06	0.004
7	GO:0005730	CC	nucleolus	7/3093	7.41097E-06	0.004
49	GO:0098588	CC	bounding membrane of organelle	49/3093	1.0195E-05	0.004
9	GO:0044451	CC	nucleoplasm part	9/3093	1.7266E-05	0.008
16	GO:0009532	CC	plastid stroma	16/3093	3.43225E-05	0.022
1033	GO:0031224	CC	intrinsic component of membrane	1033/3093	4.37581E-05	0.03
16	GO:0009570	CC	chloroplast stroma	16/3093	4.66031E-05	0.038
46	GO:0080043	MF	quercetin 3-O-glucosyltransferase activity	46/3093	1.03838E-10	0
46	GO:0080044	MF	quercetin 7-O-glucosyltransferase activity	46/3093	1.03838E-10	0
15	GO:0004519	MF	endonuclease activity	15/3093	1.47266E-10	0
17	GO:0004518	MF	nuclease activity	17/3093	2.31766E-10	0
149	GO:0046906	MF	tetrapyrrole binding	149/3093	2.3513E-10	0
147	GO:0020037	MF	heme binding	147/3093	2.41971E-10	0
86	GO:0016788	MF	hydrolase activity, acting on ester bonds	86/3093	3.44572E-10	0
39	GO:0003723	MF	RNA binding	39/3093	3.72985E-10	0
292	GO:0004672	MF	protein kinase activity	292/3093	3.75078E-10	0

94	GO:0004497	MF	monooxygenase activity	94/3093	3.93814E-10	0
359	GO:0016491	MF	oxidoreductase activity	359/3093	4.70612E-10	0
305	GO:0016773	MF	phosphotransferase activity, alcohol group as acceptor	305/3093	5.80452E-10	0
339	GO:0003676	MF	nucleic acid binding	339/3093	6.18911E-10	0
176	GO:0004674	MF	protein serine/threonine kinase activity	176/3093	5.1153E-09	0
326	GO:0016301	MF	kinase activity	326/3093	8.8847E-09	0
98	GO:0030246	MF	carbohydrate binding	98/3093	1.05188E-08	0
138	GO:0005515	MF	protein binding	138/3093	2.42391E-08	0
56	GO:0001871	MF	pattern binding	56/3093	2.87396E-08	0
56	GO:0030247	MF	polysaccharide binding	56/3093	2.87396E-08	0
26	GO:0005198	MF	structural molecule activity	26/3093	4.07685E-08	0
51	GO:0017111	MF	nucleoside-triphosphatase activity	51/3093	3.10226E-07	0
107	GO:0016705	MF	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	107/3093	3.76515E-07	0
58	GO:0016817	MF	hydrolase activity, acting on acid anhydrides	58/3093	4.0278E-07	0
46	GO:0016709	MF	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	46/3093	4.55701E-07	0
56	GO:0016462	MF	pyrophosphatase activity	56/3093	6.31966E-07	0
58	GO:0016818	MF	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	58/3093	8.16157E-07	0
53	GO:0016684	MF	oxidoreductase activity, acting on peroxide as acceptor	53/3093	9.13691E-07	0
52	GO:0004601	MF	peroxidase activity	52/3093	1.62476E-06	0.002
11	GO:0005525	MF	GTP binding	11/3093	1.98149E-06	0.002
11	GO:0032561	MF	guanyl ribonucleotide binding	11/3093	1.98149E-06	0.002

11	GO:0019001	MF	guanyl nucleotide binding	11/3093	1.98149E-06	0.002
144	GO:0001071	MF	nucleic acid binding transcription factor activity	144/3093	2.05473E-06	0.002
144	GO:0003700	MF	transcription factor activity, sequence-specific DNA binding	144/3093	2.05473E-06	0.002
3	GO:0004386	MF	helicase activity	3/3093	2.68723E-06	0.002
395	GO:0016787	MF	hydrolase activity	395/3093	2.96652E-06	0.002
6	GO:0003924	MF	GTPase activity	6/3093	2.97212E-06	0.002
676	GO:0016740	MF	transferase activity	676/3093	3.20417E-06	0.002
50	GO:0008270	MF	zinc ion binding	50/3093	3.69195E-06	0.002
1540	GO:0003824	MF	catalytic activity	1540/3093	4.02018E-06	0.004
24	GO:0003735	MF	structural constituent of ribosome	24/3093	4.36997E-06	0.004
16	GO:0016682	MF	oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor	16/3093	4.84233E-06	0.004
335	GO:0016772	MF	transferase activity, transferring phosphorus-containing groups	335/3093	5.02424E-06	0.004
18	GO:0010333	MF	terpene synthase activity	18/3093	5.32668E-06	0.004
467	GO:0032559	MF	adenyl ribonucleotide binding	467/3093	6.29552E-06	0.004
50	GO:0035251	MF	UDP-glucosyltransferase activity	50/3093	6.73258E-06	0.004
467	GO:0030554	MF	adenyl nucleotide binding	467/3093	7.35241E-06	0.004
21	GO:0016741	MF	transferase activity, transferring one-carbon groups	21/3093	8.90741E-06	0.004
7	GO:0008757	MF	S-adenosylmethionine-dependent methyltransferase activity	7/3093	1.01037E-05	0.004
51	GO:0046527	MF	glucosyltransferase activity	51/3093	1.03256E-05	0.004
98	GO:0005506	MF	iron ion binding	98/3093	1.40699E-05	0.006
60	GO:0016209	MF	antioxidant activity	60/3093	1.68096E-05	0.008
14	GO:0044877	MF	macromolecular complex binding	14/3093	1.96351E-05	0.01
13	GO:0052716	MF	hydroquinone:oxygen oxidoreductase activity	13/3093	2.21658E-05	0.012
938	GO:0043167	MF	ion binding	938/3093	2.22224E-05	0.012

	4	GO:0008135	MF	translation factor activity, RNA binding	4/3093	2.5565E-05	0.016
	26	GO:0004364	MF	glutathione transferase activity	26/3093	2.67311E-05	0.016
	21	GO:0008168	MF	methyltransferase activity	21/3093	2.75407E-05	0.016
	9	GO:0005372	MF	water transmembrane transporter activity	9/3093	2.89267E-05	0.022
	9	GO:0015250	MF	water channel activity	9/3093	2.89267E-05	0.022
	7	GO:0004721	MF	phosphoprotein phosphatase activity	7/3093	2.95097E-05	0.022
	18	GO:0016838	MF	carbon-oxygen lyase activity, acting on phosphates	18/3093	4.05605E-05	0.028
	18	GO:0008061	MF	chitin binding	18/3093	4.05605E-05	0.028
GAPT(50)	9	GO:0034470	BP	ncRNA processing	9/3213	1.55838E-10	0
/GAPT(0)	31	GO:0006396	BP	RNA processing	31/3213	2.01236E-10	0
	18	GO:0009451	BP	RNA modification	18/3213	2.05756E-10	0
	16	GO:0034660	BP	ncRNA metabolic process	16/3213	3.41351E-10	0
	707	GO:0044260	BP	cellular macromolecule metabolic process	707/3213	7.8585E-10	0
	419	GO:0034641	BP	cellular nitrogen compound metabolic process	419/3213	1.64323E-09	0
	32	GO:0046907	BP	intracellular transport	32/3213	2.19364E-09	0
	348	GO:0043412	BP	macromolecule modification	348/3213	2.26449E-09	0
	23	GO:0045184	BP	establishment of protein localization	23/3213	6.23707E-09	0
	474	GO:0006807	BP	nitrogen compound metabolic process	474/3213	9.82232E-09	0
	285	GO:0090304	BP	nucleic acid metabolic process	285/3213	1.29625E-08	0
	333	GO:0006139	BP	nucleobase-containing compound metabolic process	333/3213	1.32496E-08	0
	352	GO:0055114	BP	oxidation-reduction process	352/3213	1.56413E-08	0
	23	GO:0015031	BP	protein transport	23/3213	1.58557E-08	0
	36	GO:0051649	BP	establishment of localization in cell	36/3213	1.82162E-08	0
	833	GO:0043170	BP	macromolecule metabolic process	833/3213	2.89808E-08	0
	37	GO:0090305	BP	nucleic acid phosphodiester bond hydrolysis	37/3213	3.04876E-08	0
	27	GO:0033036	BP	macromolecule localization	27/3213	3.58641E-08	0
	26	GO:0008104	BP	protein localization	26/3213	3.69673E-08	0
	1043	GO:0044237	BP	cellular metabolic process	1043/3213	6.13465E-08	0

24	GO:1902582	BP	single-organism intracellular transport	24/3213	1.70351E-07	0
368	GO:0046483	BP	heterocycle metabolic process	368/3213	2.04109E-07	0
380	GO:0006725	BP	cellular aromatic compound metabolic process	380/3213	2.10437E-07	0
389	GO:1901360	BP	organic cyclic compound metabolic process	389/3213	2.61395E-07	0
22	GO:0006259	BP	DNA metabolic process	22/3213	5.90118E-07	0
17	GO:0016192	BP	vesicle-mediated transport	17/3213	6.20495E-07	0
17	GO:0006886	BP	intracellular protein transport	17/3213	2.12112E-06	0.002
19	GO:0018193	BP	peptidyl-amino acid modification	19/3213	2.84737E-06	0.002
284	GO:0006355	BP	regulation of transcription, DNA-templated	284/3213	7.89253E-06	0.002
30	GO:0010410	BP	hemicellulose metabolic process	30/3213	2.92723E-06	0.002
31	GO:0006869	BP	lipid transport	31/3213	3.05639E-06	0.002
1441	GO:0009987	BP	cellular process	1441/3213	3.78886E-06	0.002
237	GO:0006950	BP	response to stress	237/3213	4.08891E-06	0.002
30	GO:0010383	BP	cell wall polysaccharide metabolic process	30/3213	4.20351E-06	0.002
8	GO:0006364	BP	rRNA processing	8/3213	7.52714E-06	0.006
26	GO:0009733	BP	response to auxin	26/3213	7.89714E-06	0.006
4	GO:0043414	BP	macromolecule methylation	4/3213	1.15894E-05	0.014
258	GO:0016070	BP	RNA metabolic process	258/3213	1.20888E-05	0.014
7	GO:0006397	BP	mRNA processing	7/3213	1.36243E-05	0.014
25	GO:0010817	BP	regulation of hormone levels	25/3213	1.59827E-05	0.018
17	GO:0045491	BP	xylan metabolic process	17/3213	1.75821E-05	0.018
17	GO:0022402	BP	cell cycle process	17/3213	1.96782E-05	0.02
19	GO:0051301	BP	cell division	19/3213	2.05891E-05	0.02
9	GO:0016072	BP	rRNA metabolic process	9/3213	2.25537E-05	0.024
9	GO:0009742	BP	brassinosteroid mediated signaling pathway	9/3213	2.34857E-05	0.024
73	GO:0005976	BP	polysaccharide metabolic process	73/3213	2.83859E-05	0.028
381	GO:0044267	BP	cellular protein metabolic process	381/3213	3.06094E-05	0.028
63	GO:0043933	BP	macromolecular complex subunit organization	63/3213	3.44804E-05	0.03

41	GO:0072593	BP	reactive oxygen species metabolic process	41/3213	4.01808E-05	0.038
1107	GO:0044238	BP	primary metabolic process	1107/3213	5.04248E-05	0.044
479	GO:0019538	BP	protein metabolic process	479/3213	5.29413E-05	0.048
2	GO:0008033	BP	tRNA processing	2/3213	5.8351E-05	0.05
72	GO:0042651	CC	thylakoid membrane	72/3213	7.82462E-11	0
72	GO:0034357	CC	photosynthetic membrane	72/3213	7.82462E-11	0
82	GO:0044436	CC	thylakoid part	82/3213	1.36868E-10	0
69	GO:0009535	CC	chloroplast thylakoid membrane	69/3213	1.49477E-10	0
69	GO:0055035	CC	plastid thylakoid membrane	69/3213	1.49477E-10	0
53	GO:0044428	CC	nuclear part	53/3213	3.40715E-10	0
209	GO:0032991	CC	macromolecular complex	209/3213	5.8236E-10	0
54	GO:1990904	CC	ribonucleoprotein complex	54/3213	4.9811E-09	0
54	GO:0030529	CC	intracellular ribonucleoprotein complex	54/3213	4.9811E-09	0
156	GO:0043234	CC	protein complex	156/3213	6.83627E-09	0
55	GO:0009579	CC	thylakoid	55/3213	5.50476E-08	0
326	GO:0044422	CC	organelle part	326/3213	2.6132E-07	0
324	GO:0044446	CC	intracellular organelle part	324/3213	2.84352E-07	0
13	GO:0044432	CC	endoplasmic reticulum part	13/3213	3.92049E-07	0
130	GO:0044434	CC	chloroplast part	130/3213	4.50454E-07	0
130	GO:0044435	CC	plastid part	130/3213	1.32066E-06	0
189	GO:0009507	CC	chloroplast	189/3213	2.26331E-06	0.002
192	GO:0009536	CC	plastid	192/3213	3.76496E-06	0.002
1100	GO:0044424	CC	intracellular part	1100/3213	8.61916E-06	0.008
1229	GO:0016020	CC	membrane	1229/3213	9.6034E-06	0.008
67	GO:0031226	CC	intrinsic component of plasma membrane	67/3213	1.03935E-05	0.01
27	GO:0031976	CC	plastid thylakoid	27/3213	2.13317E-05	0.024
27	GO:0009534	CC	chloroplast thylakoid	27/3213	2.13317E-05	0.024
9	GO:0005789	CC	endoplasmic reticulum membrane	9/3213	2.25537E-05	0.024

490	GO:0044444	CC	cytoplasmic part	490/3213	2.64786E-05	0.026
9	GO:0005730	CC	nucleolus	9/3213	3.14816E-05	0.03
190	GO:0005737	CC	cytoplasm	190/3213	4.15007E-05	0.032
87	GO:0043228	CC	non-membrane-bounded organelle	87/3213	5.79501E-05	0.05
87	GO:0043232	CC	intracellular non-membrane-bounded organelle	87/3213	5.79501E-05	0.05
77	GO:0003723	MF	RNA binding	77/3213	4.11654E-10	0
412	GO:0003676	MF	nucleic acid binding	412/3213	5.61784E-09	0
36	GO:0004518	MF	nuclease activity	36/3213	7.25734E-08	0
330	GO:0016491	MF	oxidoreductase activity	330/3213	9.40726E-08	0
29	GO:0004519	MF	endonuclease activity	29/3213	1.0871E-07	0
40	GO:0080043	MF	quercetin 3-O-glucosyltransferase activity	40/3213	5.19163E-07	0
40	GO:0080044	MF	quercetin 7-O-glucosyltransferase activity	40/3213	5.19163E-07	0
133	GO:0046906	MF	tetrapyrrole binding	133/3213	6.70298E-07	0
54	GO:0016209	MF	antioxidant activity	54/3213	6.90282E-07	0
42	GO:0004601	MF	peroxidase activity	42/3213	7.50136E-07	0
6	GO:0003924	MF	GTPase activity	6/3213	1.32803E-06	0
99	GO:0004553	MF	hydrolase activity, hydrolyzing O-glycosyl compounds	99/3213	2.8848E-06	0.002
4	GO:0008135	MF	translation factor activity, RNA binding	4/3213	1.10782E-05	0.012
123	GO:0020037	MF	heme binding	123/3213	1.50761E-05	0.018
14	GO:0005525	MF	GTP binding	14/3213	1.84132E-05	0.02
14	GO:0032561	MF	guanyl ribonucleotide binding	14/3213	1.84132E-05	0.02
14	GO:0019001	MF	guanyl nucleotide binding	14/3213	1.84132E-05	0.02
106	GO:0016798	MF	hydrolase activity, acting on glycosyl bonds	106/3213	1.99377E-05	0.024
135	GO:0001071	MF	nucleic acid binding transcription factor activity	135/3213	2.69355E-05	0.03
135	GO:0003700	MF	transcription factor activity, sequence-specific DNA binding	135/3213	2.69355E-05	0.03
79	GO:0004497	MF	monooxygenase activity	79/3213	5.90211E-05	0.05

9	GO:0008757	MF	S-adenosylmethionine-dependent methyltransferase activity	9/3213	6.05837E-05	0.05
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GO terms with the corrected p value less than 0.05 are shown. The red color indicates GO terms significantly enriched in both GAPT (10) / GAPT (0) and GAPT (50) / GAPT (0) comparisons, while the green color indicates GO terms significantly enriched only in GAPT (50) / GAPT (0) comparison. GAPT (0), priming treatment with 0 mg/L GA3; GAPT (10), priming treatment with 10 mg/L GA3; GAPT (50), priming treatment with 50 mg/L GA3. BP: biological process; MF: molecular function; CC: cellular component.

Table S5 Expression profiles of some focused genes related with phytohormones signaling or synthesis in response to GAPT under deep sowing condition

Gene id	Gene annotation	GAPT	GAPT	GAPT	Average	GAPT	GAPT	GAPT	Average	GAPT	GAPT	GAPT	Average	
		(0)-1	(0)-2	(0)-3		(10)-1	(10)-2	(10)-3		(50)-1	(50)-2	(50)-3		
Auxin	OS01G0764800	GH3.2	9.22	9.04	15.62	11.29	42.14	66.34	50.61	53.03	38.49	44.39	66.26	49.71
	OS05G0500900	GH3.4	11.98	9.55	10.12	10.55	26.78	26.26	27.40	26.81	22.53	23.50	27.30	24.45
	OS05G0143800	GH3.6	0.74	0.42	0.69	0.62	1.133	1.98	1.49	1.53	1.40	2.05	1.71	1.72
	OS11G0528700	GH3.13	1.49	1.77	1.92	1.73	3.55	3.96	3.72	3.74	4.76	5.09	4.48	4.78
	OS09G0437400	auxin-responsive protein SAUR36-like	5.45	9.15	7.95	7.52	3.03	4.69	3.01	3.57	2.68	4.56	2.61	3.28
	OS04G0537100	auxin-responsive protein SAUR36	9.29	7.76	5.58	7.54	3.32	3.62	1.45	2.80	2.38	2.14	3.21	2.58
	OS02G0643800	auxin-responsive protein SAUR36	23.27	22.20	11.11	18.89	3.22	4.09	1.70	3.00	1.66	2.96	2.96	2.53
	OS06G0166500	IAA20	18.70	44.71	32.65	32.02	67.47	55.74	75.58	66.26	72.50	63.80	67.05	67.78
	OS08G0109400	IAA25	2.97	3.58	3.68	3.41	4.02	4.89	4.56	4.49	7.21	8.07	10.16	8.48
	OS03G0633800	IAA12	118.31	71.69	117.03	102.34	252.61	253.04	259.97	255.21	239.00	233.12	238.12	236.75
	OS01G0190300	IAA2	8.13	7.66	5.02	6.94	14.30	10.38	24.42	16.37	25.86	12.04	20.08	19.33
	OS03G0742900	IAA13	168.58	219.57	504.11	297.42	502.26	491.53	692.47	562.09	703.00	429.81	331.07	487.96
	OS05G0447200	auxin transporter-like protein 2	10.80	7.37	9.78	9.32	15.77	19.07	14.41	16.41	16.074	27.106	25.78	22.99
	OS06G0671150	auxin-responsive protein SAUR71	5.38	3.30	3.04	3.91	0.99	1.44	0.94	1.12	1.02	1.21	0.94	1.06
	OS10G0147400	auxin transporter-like protein 3	11.32	10.93	13.41	11.89	4.93	4.07	3.25	4.08	1.48	4.58	4.09	3.38
	OS04G0662200	indole-3-acetic acid-induced protein ARG7	5.03	14.12	9.18	9.44	4.30	4.12	4.25	4.22	3.62	3.35	3.55	3.51
	OS03G0244600	auxin transporter-like protein 3	3.42	2.63	3.31	3.12	2.12	1.54	1.84	1.84	0.43	1.54	1.58	1.18
	OS08G0118500	auxin-induced protein 15A	10.81	55.69	28.40	31.64	9.50	3.17	3.42	5.36	5.79	1.53	6.31	4.54
	OS06G0137400	auxin-responsive protein SAUR50	21.81	59.18	44.89	41.96	23.72	13.62	25.49	20.95	11.80	14.72	16.85	14.46
	OS04G0617050	auxin-responsive protein SAUR71	6.12	11.28	10.79	9.40	5.32	3.01	2.76	3.70	5.58	3.85	2.75	4.06
	OS02G0445600	auxin-responsive protein SAUR50	6.35	12.68	10.02	9.68	5.68	4.31	4.13	4.71	3.37	5.31	3.87	4.18
	OS03G0797800	auxin-responsive protein IAA14-like	79.39	121.78	90.81	97.33	44.13	28.45	54.42	42.33	26.43	24.11	31.66	27.40
	OS06G0597000	auxin-responsive protein IAA23-like	22.44	20.14	20.69	21.09	8.40	11.02	8.12	9.18	8.39	7.05	7.52	7.65

BR	OS08G0342300	BRL3	1.74	1.81	1.10	1.55	5.15	5.05	5.06	5.09	3.53	5.99	4.07	4.53
	OS09G0293500	BRL1	0.85	0.80	1.04	0.90	2.24	2.49	2.34	2.36	2.08	3.25	2.11	2.48
	OS07G0580500	BZR1	32.36	44.32	49.75	42.14	56.03	52.95	40.31	49.76	134.98	135.46	130.44	133.62
	OS02G0233200	BZR4	2.57	2.36	2.41	2.44	5.05	5.95	3.86	4.95	12.51	18.61	19.91	12.51
	OS01G0864000	OFP8	14.07	15.13	19.29	16.16	5.10	5.31	3.78	4.73	2.58	3.93	4.23	3.58
	OS02G0794500	serine carboxypeptidase 24	15.24	19.30	18.84	17.79	9.38	7.05	8.99	8.47	7.60	6.12	8.01	7.24
	OS05G0139100	APG	18.13	23.53	19.75	20.47	10.51	9.43	7.13	9.02	12.73	8.07	10.69	10.50
	OS06G0127800	DLT	10.73	8.18	9.53	9.48	3.73	2.66	2.58	2.99	0.80	3.59	2.74	2.38
	OS03G0171300	ILI6	4.56	8.22	7.24	6.68	1.55	1.83	3.14	2.17	1.34	1.15	1.98	1.49
	GA	Os06G0110000	KAO	8.42	7.14	9.25	8.27	10.62	8.78	8.92	9.44	19.41	22.67	16.92
OS01G0646300		gibberellin response modulator-like (SLN1)	9.72	13.31	13.51	12.18	4.60	5.19	3.96	4.58	2.10	3.00	3.59	2.90
ABA	OS02G0551100	SAPK6; Osmotic stress/abscisic acid-activated protein kinase 6	5.70	7.36	5.57	6.21	15.36	18.26	19.91	17.84	16.53	15.48	13.19	15.07
	OS03G0390200	SAPK1;Osmotic stress/abscisic acid-activated protein kinase 1	5.26	5.35	4.52	5.04	9.12	11.57	13.53	11.40	12.81	13.42	12.82	13.02
	OS03G0297600	abscisic acid receptor PYL4	46.59	66.48	53.13	55.40	20.12	16.03	24.91	20.35	13.61	19.58	17.01	16.73
	OS10G0573400	abscisic acid receptor PYL10-like	110.33	93.095	135.24	112.89	48.153	47.20	43.88	46.41	34.23	61.34	64.12	53.230
JA	OS03G0180900	TIFY11C	8.62	5.04	3.44	5.70	39.02	28.15	52.60	39.93	19.66	6.49	23.83	16.66
	OS09G0439200	TIFY10C	9.70	7.35	3.83	6.96	17.71	10.97	29.49	19.38	20.55	10.33	15.37	15.42
	OS10G0392400	TIFY11D	37.67	23.76	14.97	25.47	38.11	44.79	64.01	48.97	33.44	12.47	22.70	22.87
	OS03G0402800	TIFY10A	60.31	41.07	31.75	44.38	81.84	66.91	115.77	88.171	73.96	42.70	64.96	60.54
	OS03G0181100	TIFY11B	109.99	55.84	20.22	62.02	42.86	37.57	43.63	41.35	27.08	18.11	26.73	23.98
	OS07G0687700	TGA2.1	21.22	26.96	22.64	23.61	38.26	45.16	47.11	43.51	44.59	45.06	38.98	42.88
	OS09G0280500	TGAL7	0.94	1.38	1.51	1.27	2.90	3.39	3.38	3.22	3.12	4.29	2.89	3.47
	OS11G0152700	TGAL4	3.48	2.99	3.09	3.19	3.68	4.33	4.48	4.16	3.99	14.06	7.62	8.56
	OS03G0318600	TGA2.2	17.46	22.63	18.58	19.55	34.86	43.55	49.51	42.64	35.49	37.39	33.48	35.46

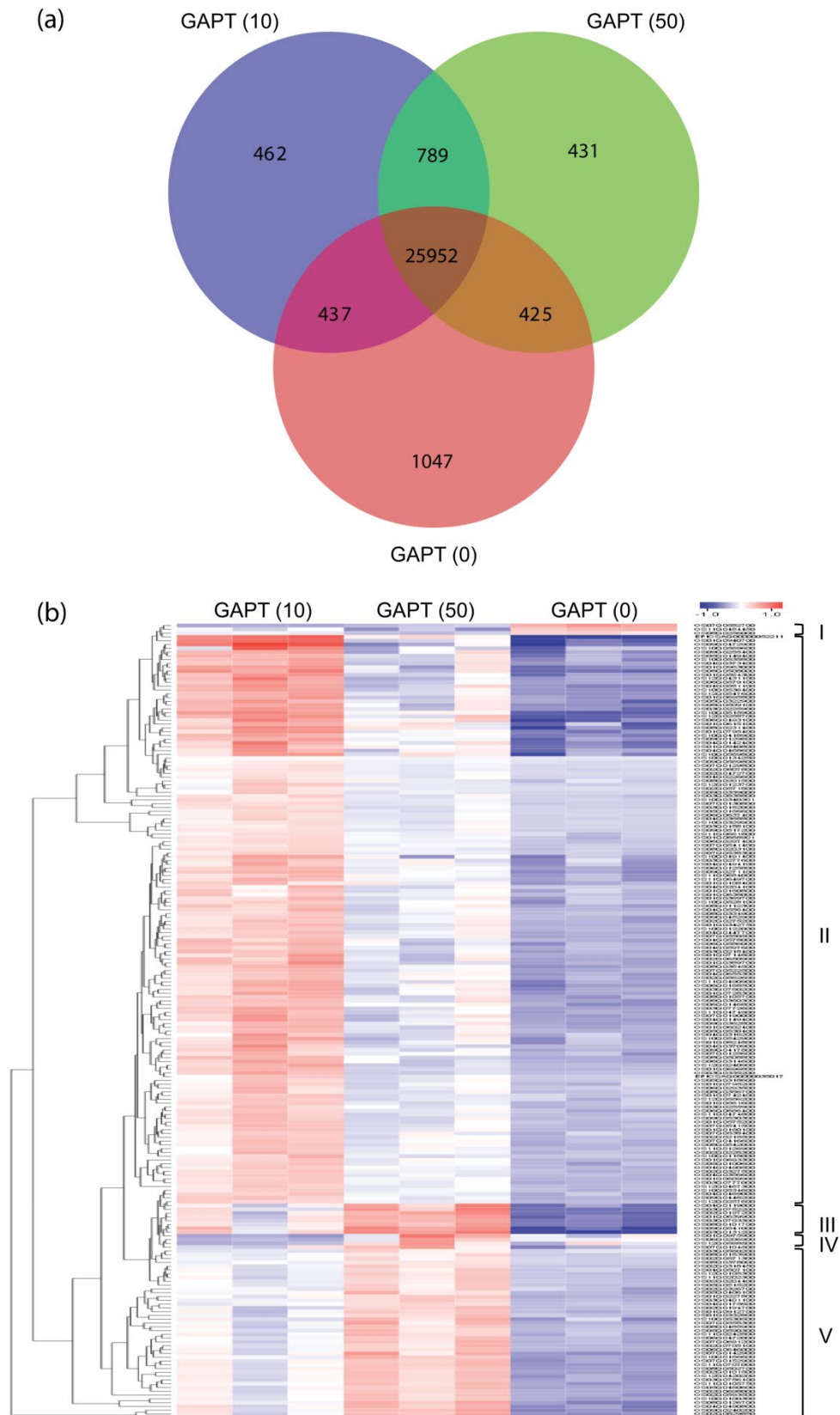
OS04G0637000	TGAL6	8.92	8.81	9.46	9.06	13.49	22.40	19.27	18.39	22.87	32.22	22.26	25.78
OS06G0614100	TGAL8	0.28	0.26	0.33	0.29	0.55	1.46	0.64	0.88	0.39	0.40	0.58	0.46
OS12G0152900	TGAL11	3.13	4.10	4.26	3.83	3.14	6.34	6.37	5.28	5.22	13.56	5.65	8.14
OS09G0489500	TGA2	0.47	0.35	0.42	0.41	0.65	0.91	1.45	1.00	0.42	1.02	0.92	0.79
OS06G0265400	TGAL3	5.41	5.72	4.77	5.30	1.76	1.66	1.39	1.60	0.67	2.04	2.26	1.66
OS06G0211200	bZIP transcription factor 46-like	32.51	38.06	35.59	35.39	17.32	13.87	12.05	14.41	14.52	13.43	11.41	13.12

The purple, red, green, pink, and blue colors indicate genes related with auxin, BRs, GA, ABA, and JA signaling or synthesis, respectively. The boldface in the "Gene id" column highlight the genes which were upregulated after GAPT. Gene annotations were extracted from the NCBI database. GAPT (0), priming treatment with 0 mg/L GA₃; GAPT (10), priming treatment with 10 mg/L GA₃; GAPT (50), priming treatment with 50 mg/L GA₃. Expression profiles were showed as FPKM values. The values in the "Average" column were shown as means of three biological replicates.

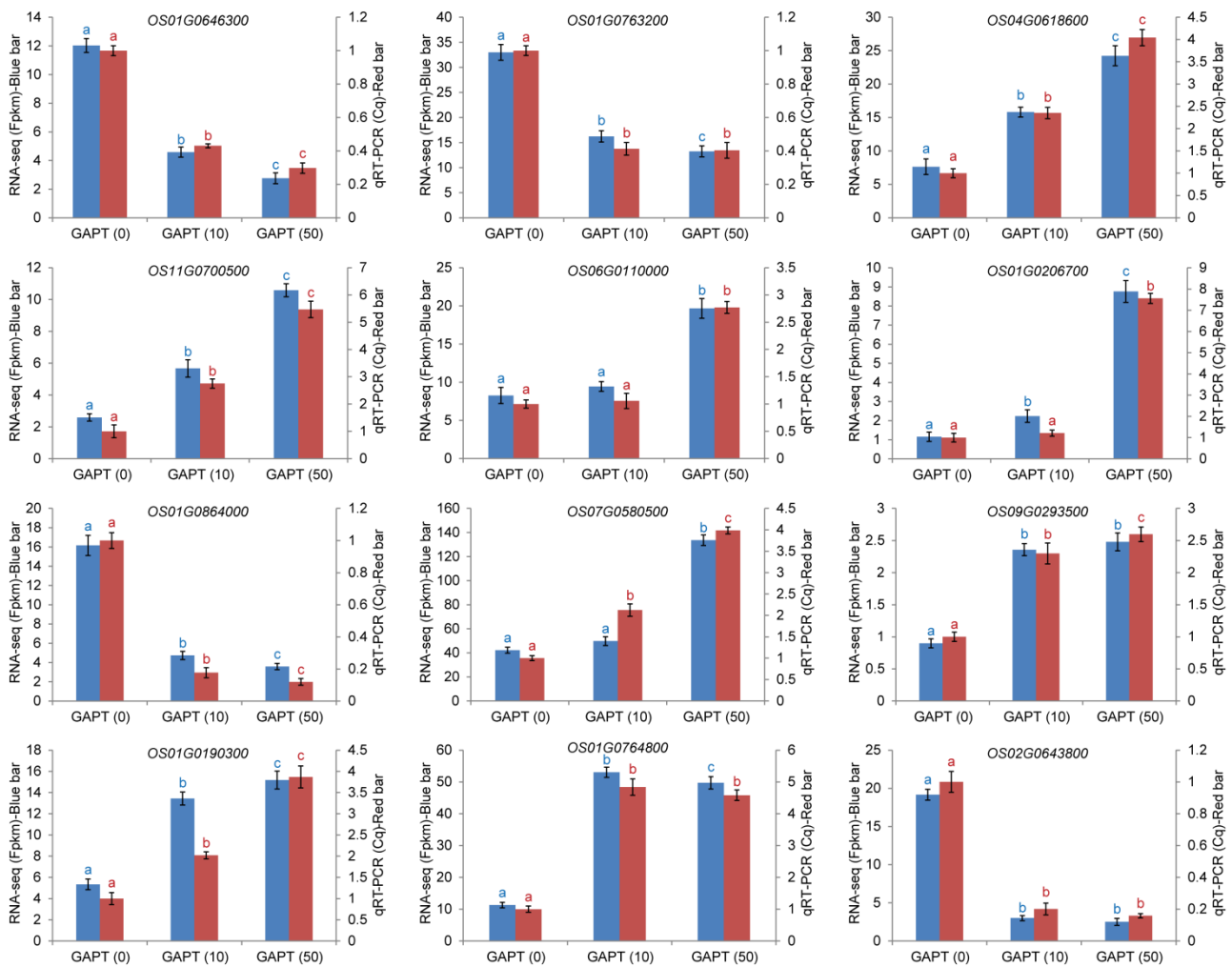
Table S6 Expression profiles of 23 genes related with starch and sucrose metabolism in response to GAPT under deep sowing condition

Gene id	Gene name	GAPT (0)-1	GAPT (0)-2	GAPT (0)-3	Average	GAPT (10)-1	GAPT (10)-2	GAPT (10)-3	Average	GAPT (50)-1	GAPT (50)-2	GAPT (50)-3	Average
OS10G0323500	BGLU34	0.39	0.72	0.59	0.57	1.30	2.20	2.54	2.02	1.28	3.12	1.26	1.89
OS09G0511700	beta-glucosidase 32-like	13.97	14.87	13.93	14.26	28.20	48.55	51.98	42.91	22.12	31.21	38.11	30.48
OS07G0421300	alpha-glucosidase 2	0.34	0.75	0.34	0.48	0.97	1.19	0.772	0.98	0.99	2.108	1.81	1.64
OS01G0930800	BGLU5	9.40	7.41	5.84	7.55	18.68	9.95	10.78	13.14	34.66	20.97	35.51	30.38
OS05G0365700	beta-glucosidase 20-like	1.67	1.7	1.36	1.40	2.85	5.05	4.28	4.06	3.15	5.07	3.32	3.85
OS06G0683300	beta-glucosidase 25-like	4.95	5.71	3.85	4.84	5.85	7.26	10.24	7.78	11.21	14.66	7.86	11.24
OS05G0365600	BGLU19	1.34	2.01	0.90	1.41	2.46	1.93	1.22	1.87	4.61	3.79	5.55	4.65
OS08G0224500	glucan endo-1,3-beta-glucosidase 6	4.38	3.51	4.38	4.09	7.00	5.14	6.28	6.14	9.30	7.19	7.71	8.07
OS09G0511600	beta-glucosidase 31-like	13.95	16.42	14.88	15.09	46.92	61.86	83.35	64.05	33.72	26.81	60.05	40.19
OS07G0510200	glucan endo-1,3-beta-glucosidase 1	37.10	41.35	40.48	39.65	22.54	21.20	17.08	20.27	18.98	17.43	22.49	19.63
OS03G0703000	BGLU7	627.85	843.43	700.73	724.00	467.92	375.85	433.27	425.68	393.16	346.16	363.65	367.66
OS03G0221500	glucan endo-1,3-beta-glucosidase 3	31.80	34.17	33.60	33.19	18.07	10.91	10.13	13.03	3.66	19.41	15.21	12.76
OS06G0713800	AMY2A	1.06	1.86	2.65	1.86	4.97	10.98	10.36	8.77	7.06	9.82	5.17	7.35
OS08G0473600	AMY1.4; alpha-amylase isozyme 3E	0.14	0.10	0.23	0.15	1.11	1.13	1.10	1.11	3.13	3.49	3.95	3.52
OS01G0633100	ADP-glucose pyrophosphorylase large subunit isoform	3.74	3.27	2.49	3.16	4.13	4.56	2.55	3.75	8.549	3.86	7.64	6.69
OS03G0735000	ADP glucose pyrophosphorylase	17.67	21.65	16.66	18.66	36.68	18.91	25.46	27.02	63.61	32.69	46.11	47.47
OS01G0190400	HXK8	3.30	3.61	6.48	4.46	2.35	3.48	3.304	3.043	3.071	46.66	17.44	22.39
OS01G0919400	probable sucrose-phosphate synthase 1	2.45	1.06	2.73	2.08	3.65	2.37	3.245	3.085	6.048	15.04	10.10	10.39
OS03G0340500	SUS4	12.71	15.91	12.58	13.73	25.89	39.19	31.63	32.24	32.55	37.56	24.46	31.52
OS04G0249500	sucrose synthase 7-like	0.88	0.67	0.57	0.70	0.92	1.45	0.97	1.12	1.46	1.07	2.05	1.52
OS04G0413500	CIN2	79.63	74.59	81.89	78.70	33.07	21.42	21.49	25.33	9.12	26.63	27.49	21.08
OS09G0376800	alpha, alpha-trehalose-phosphate synthase [UDP-forming] 10	16.04	16.16	16.96	16.39	24.25	30.33	36.16	30.25	33.41	38.55	27.07	33.01
OS06G0256500	glucose-6-phosphate isomerase	36.27	30.19	32.19	32.88	55.13	65.16	90.31	70.20	49.05	67.87	91.44	69.452

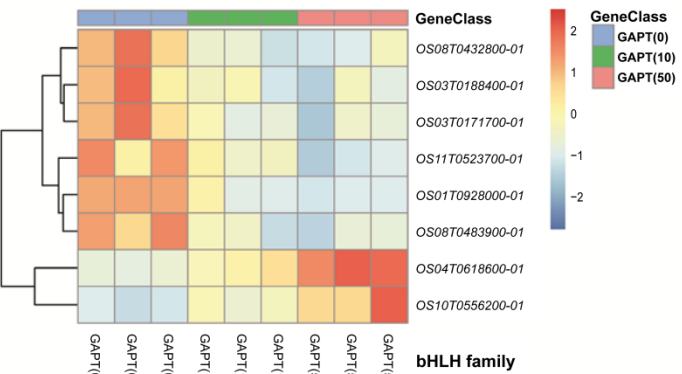
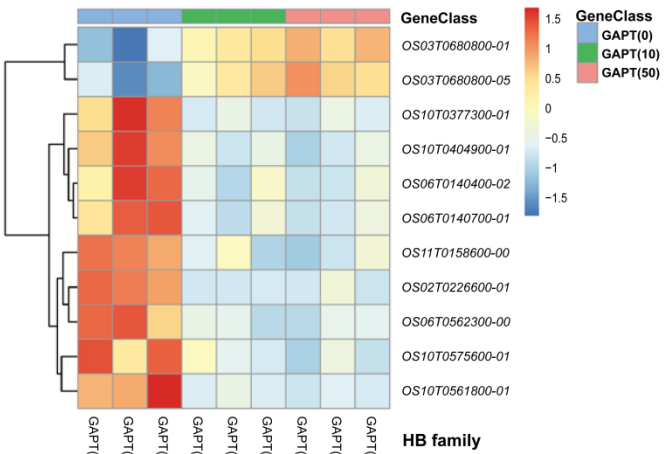
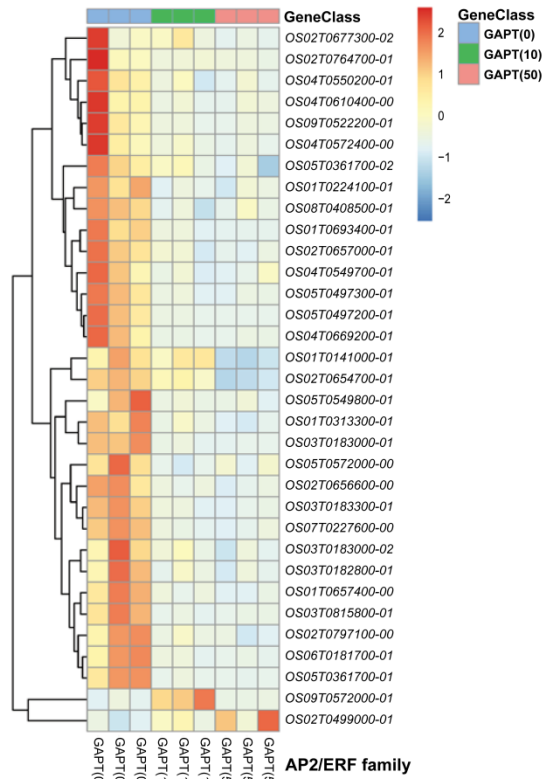
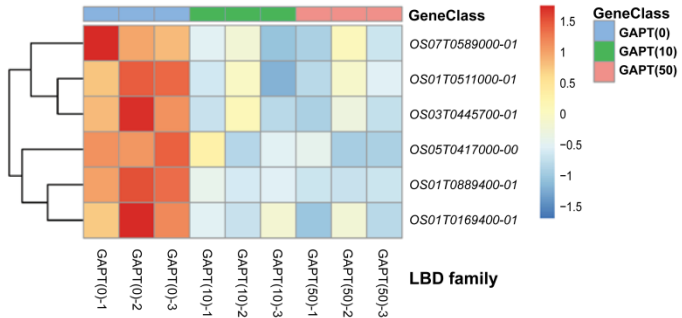
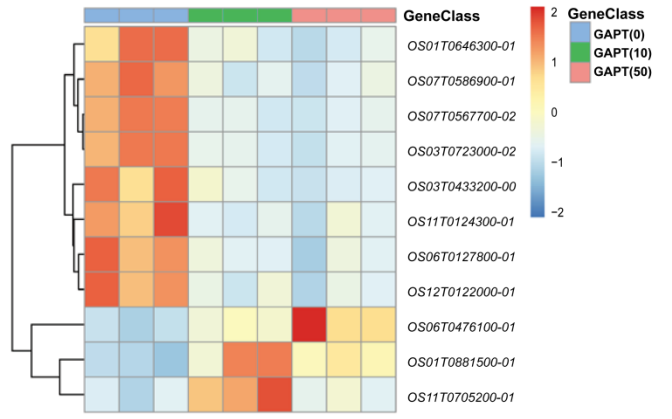
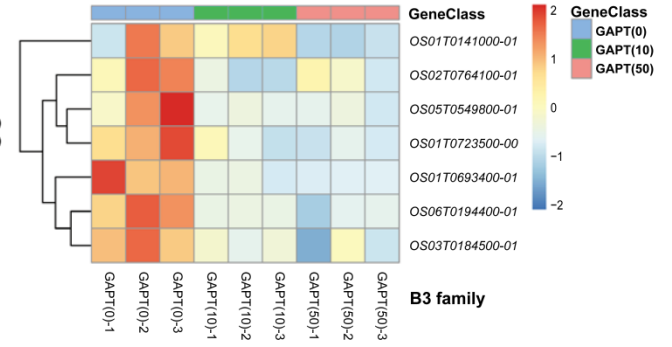
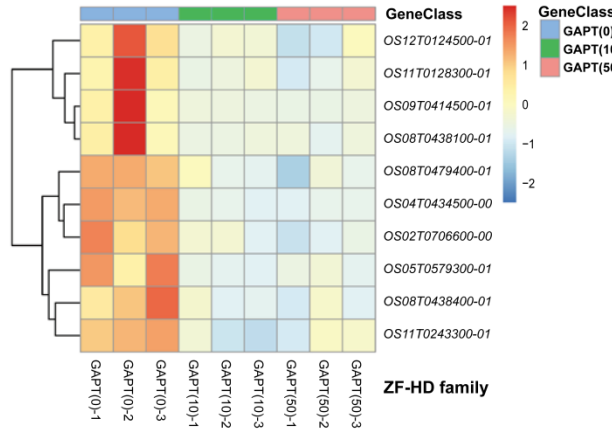
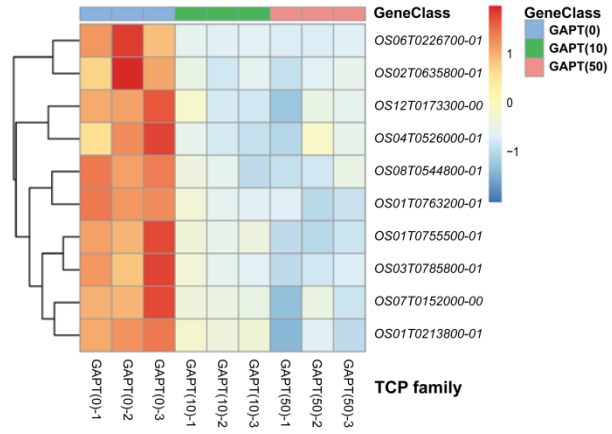
The boldface in the “Gene id” column highlighted the genes which were upregulated after GAPT. Gene annotations were extracted from the NCBI database. GAPT (0), priming treatment with 0 mg/L GA₃; GAPT (10), priming treatment with 10 mg/L GA₃; GAPT (50), priming treatment with 50 mg/L GA₃. Expression profiles were showed as FPKM values. The values in the “Average” column were shown as means of three biological replicates.

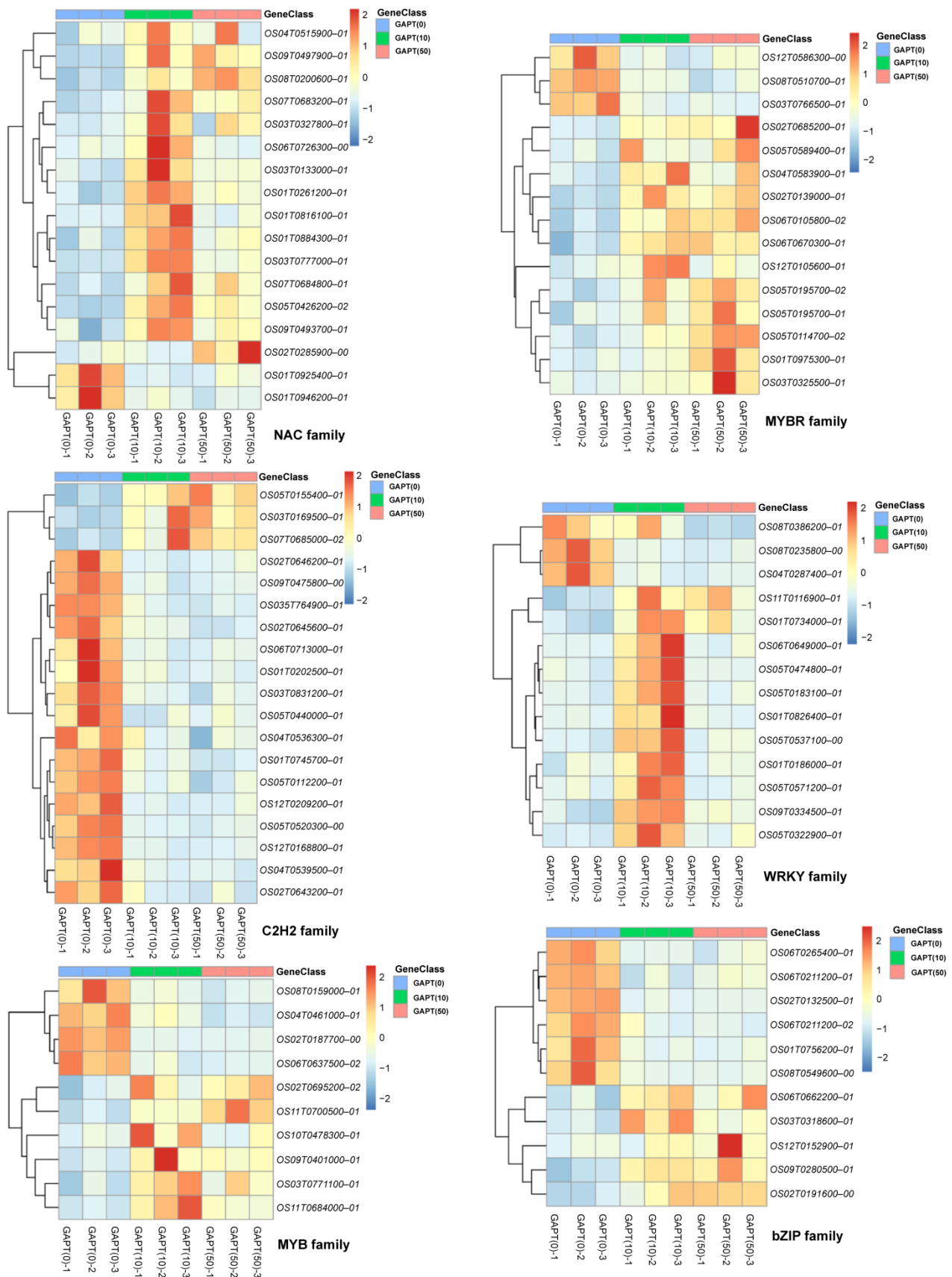


Figs. S1 (a) Venn diagram showing the distribution of expressed genes from rice mesocotyl after GAPT (0), GAPT (10) and GAPT (50). (b) Hierarchical clustering analysis of the co-expressed DEGs among GAPT (0), GAPT (10) and GAPT (50). The DEGs used here meet three criteria: FDR value <0.05 , $|\log_2(\text{fold change})| \geq 1$ and average FPKM >0.2 as this figure shows. The color bar on the right represents the \log_2 FPKM values. Blue, pink, and red colors indicate low, medium, and high FPKM values, respectively. GAPT, priming treatment with GA₃; DEG, differentially expressed gene; FDR, false discovery rate; FPKM, fragments per kilobase of exon per million mapped read.

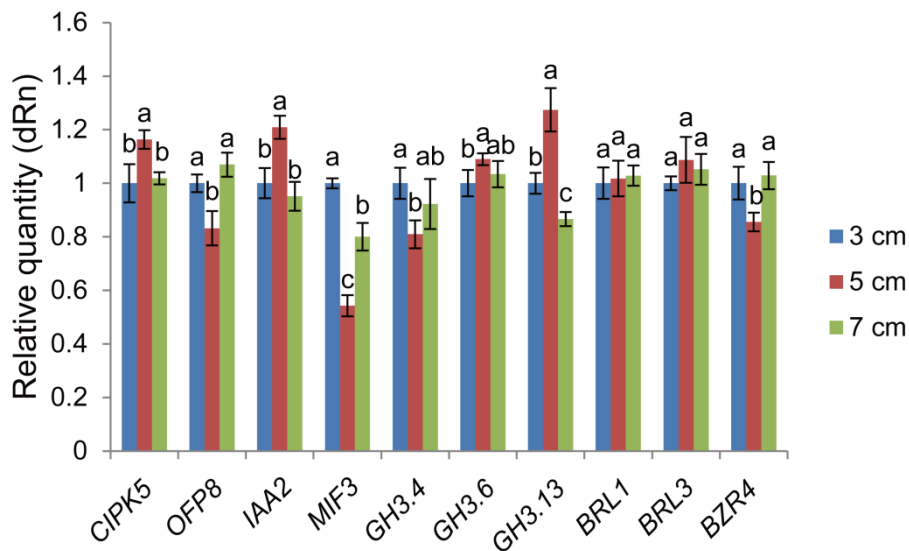


Figs. S2 Comparison of qRT-PCR (red bar) and RNA-seq (blue bar) data for selected genes. Values are shown as mean±SD of three biological replicates. Different lowercase letters represent significant differences among samples with different treatments at $P < 0.05$ by Duncan's test. FPKM, fragments per kilobase of exon per million mapped read; qRT-PCR, quantitative real-time polymerase chain reaction; Cq, quantitative cycle; GAPT, priming treatment with GA₃; SD, standard deviation.





Figs. S3 Detailed expression profile of DEGs related to transcription factors after GAPT under deep sowing condition. Heat maps illustrating the relative expression levels of genes encoding transcription factor obtained from the plant transcription factor database (<http://plantfdb.cbi.pku.edu.cn/>). The DEGs used here met three criteria: FDR value <0.05 , $|\log_2 \text{foldchange}| \geq 1$ and average FPKM >0.2 as this figure shows. Red and blue colors depict up- and down-regulation, respectively. GAPT, priming treatment with GA₃; DEG, differentially expressed gene; FDR, false discovery rate; FPKM, fragments per kilobase of exon per million mapped read.



Figs. S4 The expression patterns of *CIPK5*, *OFP8*, *IAA2*, *MIF3*, *GH3.4*, *GH3.6*, *GH3.13*, *BRL1*, *BRL3* and *BZR4* under different sowing depths. Values are shown as mean±SD of three biological replicates. Different lowercase letters represent significant differences in samples under different sowing depths at $P < 0.05$ based on the Duncan's test. dRn: delta normalized reporter; CIPK5, calcineurin B-like protein interacting protein kinase 5; OFP8, ovate family protein 8-like; IAA2, indole-3-acetic acid 2; MIF3, mini zinc finger 3; GH: gretchen hagen; BRL1/3, BR insensitive 1/3-like receptor kinase; BZR4, brassinazole-resistant 4; SD, standard deviation.