

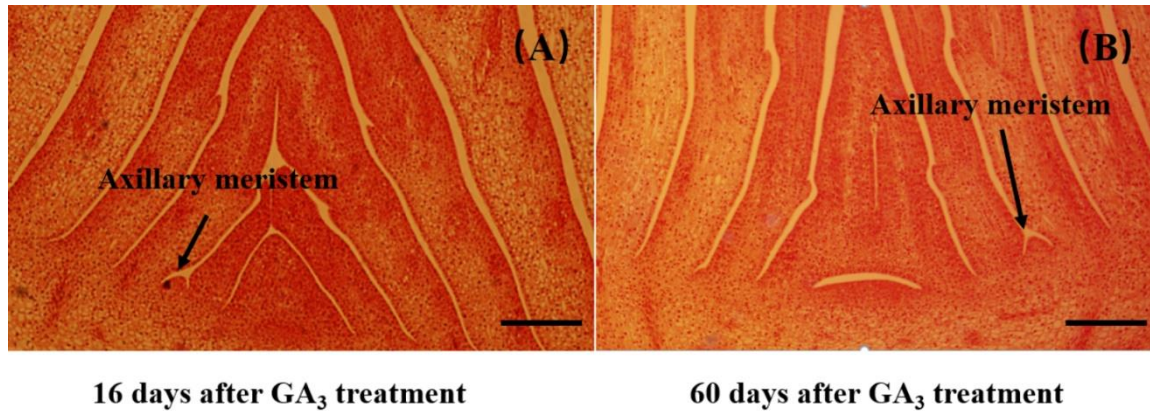


Figure S1 Histological studies on axillary meristem development of GA₃-treated plant. (A), axillary meristem arose at 16 days after GA₃ treatment. (B), axillary meristem arose at 60 days after GA₃ treatment. Scale bars in A and B are 200 μm in length.

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1  ATG GAC TCC ATT TTT CTC CCC GGC CCT TCA TTG AAT TTC AAC AAA GAT GCG AAG AAA AAC GAT CTC TAC ATC AAC AGT GGA GCG ATA TTT 90
1  Met Asp Ser Ile Phe Leu Pro Gly Pro Ser Leu Asn Phe Asn Lys Asp Ala Lys Lys Asn Asp Leu Tyr Ile Asn Ser Gly Ala Ile Phe 30

91  GAT TCA TCT ACA CTC CAC AAA CAA TCA AAA ATA CCC AAA CAC TTC ATT TGG CCC CAA GCC CAA AGG CCC ACA AAA ACA CTA CAA GAG CTT 180
31  Asp Ser Ser Thr Leu His Lys Gln Ser Lys Ile Pro Lys His Phe Ile Trp Pro Gln Ala Gln Arg Pro Thr Lys Thr Leu Gln Glu Leu 60

181  GAT GCA CCA ATT ATA GAT CTT CGA GTA TTT GAC AAT GGA CAT CAA GAA TCA ATA CTA CAA ACA CTG GAC CTT ATA AGA AAA GCT TGC TCC 270
61  Asp Ala Pro Ile Ile Asp Leu Arg Val Phe Asp Asn Gly His Gln Glu Ser Ile Leu Gln Thr Leu Asp Leu Ile Arg Lys Ala Cys Ser 90

271  ACA CAT GGA TTT TTC CAA GTT ATC AAT CAT GGC ATA GAT GCA ACA TTA TGT AGC AAT GCA TTA GGT TAC CTC GAC CAT CTC TTT AAG GAT 360
91  Thr His Gly Phe Phe Gln Val Ile Asn His Gly Ile Asp Ala Thr Leu Cys Ser Asn Ala Leu Gly Tyr Leu Asp His Leu Phe Lys Asp 120

361  TTA TCA AGT GAT GGA AAG CTA CAA GCA CAC AGA AAG CCA GGA AGC ACT TGG GGA TAT GCA GGT GCA CAT AGC GAC CGT TTC TCT TCC AAG 450
121  Leu Ser Ser Asp Gly Lys Leu Gln Ala His Arg Lys Pro Gly Ser Thr Trp Gly Tyr Ala Gly Ala His Ser Asp Arg Phe Ser Ser Lys 150

451  TTG CCT TGG AAA GAG ACA TTT TCA TTT GAG TAT TCA TGT AGC GAA AAT GAA AAG ACA ATG GTG GAC TAC TTT GTA TCT GTA CTA GGC AAG 540
151  Leu Pro Trp Lys Glu Thr Phe Ser Phe Glu Tyr Ser Cys Ser Glu Asn Glu Lys Thr Met Val Asp Tyr Phe Val Ser Val Leu Gly Lys 180

541  GAT TTC GAA GAT ATT GGA GTT GTG TAC CAA AAA TAT TGT CGA GAA ATG TTC AAG CTC TCC CTA AAG CTA ATG GAA GTT TTA GGA GTA AGT 630
181  Asp Phe Glu Asp Ile Gly Val Val Tyr Gln Lys Tyr Cys Arg Glu Met Phe Lys Leu Ser Leu Lys Leu Met Glu Val Leu Gly Val Ser 210

631  TTA GGA CTT GAA AAA GGC TAT TGC AGA GAA CTA TTT CAA GAT GGT AGC GGC ATA TTG AGA TGC AAC TAT TAT CCA TCA TGC AAA GAA CCA 720
211  Leu Gly Leu Glu Lys Gly Tyr Cys Arg Glu Leu Phe Gln Asp Gly Ser Gly Ile Leu Arg Cys Asn Tyr Tyr Pro Ser Cys Lys Glu Pro 240

721  GAA CTT ACC CTT GGA ACC GGA CCA CAT TGT GAT CCA ACA GCA TTG ACC ATC TTG CAG CAA GAT CAA GTT GGA GGC CTT GAA GTG TTT GCC 810
241  Glu Leu Thr Leu Gly Thr Gly Pro His Cys Asp Pro Thr Ala Leu Thr Ile Leu Gln Gln Asp Gln Val Gly Gly Leu Glu Val Phe Ala 270

811  AAC GGC AGT TGG CAA ACT GTT AAA CCT ATG AGA GGT GCC TTA GTT ATC AAT ATT GGT GAC ACA TTT ATG GCG CTA ACG AAT GGC CAC TAC 900
271  Asn Gly Ser Trp Gln Thr Val Lys Pro Met Arg Gly Ala Leu Val Ile Asn Ile Gly Asp Thr Phe Met Ala Leu Thr Asn Gly His Tyr 300

901  AAG AGT TGC CTT CAT CGA GCA GTG GTG AAT CCT TAC AGA GAA AGA AAA TCT ATT GCC TTC TTT CTA AAT CCA AAA GGT GAT AAA ACA ATT 990
301  Lys Ser Cys Leu His Arg Ala Val Val Asn Pro Tyr Arg Glu Arg Lys Ser Ile Ala Phe Phe Leu Asn Pro Lys Gly Asp Lys Thr Ile 330

991  AAA CCA CCA AGC ATA CTG TGC TCA AAC TCA GTG GAT AGA ATG TAC GTA GAT TTT ACA TGG TCT GAG CTG TTG GAG TTC ACC CAA AAG TAT 1080
331  Lys Pro Pro Ser Ile Leu Cys Ser Asn Ser Val Asp Arg Met Tyr Val Asp Phe Thr Trp Ser Glu Leu Leu Glu Phe Thr Gln Lys Tyr 360

1081  TAT AGA GCA GAC ACA AGA ACA CTA CAA AAT TTC TCA AAT TGG ATT AAA AGA ACT GGA AAT ATG TGA 1146
361  Tyr Arg Ala Asp Thr Arg Thr Leu Gln Asn Phe Ser Asn Trp Ile Lys Arg Thr Gly Asn Met End

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Figure S2 The nucleotide sequence and the deduced amino acid sequence of *AsGA20ox* CDS.

1	ATG	TCT	TCG	TTT	AGA	GAC	TTG	GAG	TCG	CCT	CCT	TTG	TCT	TCC	CTT	TCT	CCT	CTC	CTT	CCT	CCG	GAG	GAA	TCC	GCT	CCT	CGG	AAA	TCG	AAA	90
1	Met	Ser	Ser	Phe	Arg	Asp	Leu	Glu	Ser	Pro	Pro	Leu	Ser	Ser	Leu	Ser	Pro	Leu	Pro	Pro	Glu	Glu	Ser	Ala	Pro	Arg	Lys	Ser	Lys	30	
91	AAG	GGG	TAC	TTC	GTA	TCG	GCC	GCT	CTC	ATG	CTT	CTG	ACG	CTT	GCA	GGC	TTG	GCC	GCG	TTC	GTT	TAC	CTC	TCG	GGT	ACG	GAT	ATA	ACG	GGC	180
31	Lys	Ala	Tyr	Phe	Val	Ser	Ala	Ala	Leu	Met	Leu	Leu	Thr	Leu	Ala	Gly	Leu	Ala	Ala	Phe	Val	Tyr	Leu	Ser	Gly	Thr	Asp	Ile	Thr	Gly	60
181	TTG	GAT	CCG	ATT	CAT	CCG	GAT	CCG	ATC	GTG	ATG	GAT	CCG	GGT	GTT	AAA	GCC	GGG	GTG	TCG	ATG	AAG	GGT	TCG	GGT	ACG	GGT	ATG	TTG	AAA	270
61	Leu	Asp	Pro	Ile	His	Arg	Asp	Pro	Ile	Val	Met	Asp	Arg	Gly	Val	Lys	Ala	Gly	Val	Ser	Met	Lys	Gly	Ser	Gly	Thr	Gly	Met	Leu	Lys	90
271	CCG	GGT	CCG	TAT	CCG	TGG	ACT	AAT	CAG	ATG	CTG	CTG	TGG	CAG	AGA	AGC	GGA	TTC	CAT	TTT	CAA	CCC	GAG	AAG	AAT	TGG	ATG	AAC	GAT	CCG	360
91	Ala	Gly	Ala	Tyr	Pro	Trp	Thr	Asn	Gln	Met	Leu	Leu	Trp	Gln	Arg	Ser	Gly	Phe	His	Phe	Gln	Pro	Glu	Lys	Asn	Trp	Met	Asn	Asp	Pro	120
361	AAT	GGC	CCA	ATG	TAT	TAC	AAT	GGA	TGG	TAC	CAT	TTC	TTT	TAC	CAA	TAC	AAC	CCG	GAT	GGA	GCA	GTA	TGG	GGA	AAC	ATA	GCG	TGG	GGC	CAT	450
121	Asn	Gly	Pro	Met	Tyr	Tyr	Asn	Gly	Trp	Tyr	His	Phe	Phe	Tyr	Gln	Tyr	Asn	Pro	Asp	Gly	Ala	Val	Trp	Gly	Asn	Ile	Ala	Trp	Gly	His	150
451	GCA	GTC	TCA	AAA	GAC	CTT	CTA	AAC	TGG	GTT	CAC	CTG	CCC	TTA	GCC	ATG	GTA	CCA	GAC	CCG	TCC	TAT	GAC	GCA	GAC	GGT	GTC	TGG	ACC	GGT	540
151	Ala	Val	Ser	Lys	Asp	Leu	Leu	Asn	Trp	Val	His	Leu	Pro	Leu	Ala	Met	Val	Pro	Ala	Ser	Lys	Tyr	Asp	Ala	Asp	Gly	Val	Trp	Thr	Gly	180
541	TCA	GCC	ACA	ATT	TTA	CCC	GAT	GGA	GCG	ATC	ATA	ATG	ATC	TAC	ACT	GGT	CTC	TTA	GTT	GGC	ACA	GAC	GTC	CAA	GTT	CAA	AAC	ATA	GCA	GTT	630
181	Ser	Ala	Thr	Ile	Leu	Pro	Asp	Gly	Arg	Ile	Ile	Met	Ile	Tyr	Thr	Gly	Leu	Leu	Val	Gly	Thr	Asp	Val	Gln	Val	Gln	Asn	Ile	Ala	Val	210
631	CCA	GCA	AAT	TTG	TCC	GAT	CCT	TTA	TTA	CTA	GAC	TGG	GTC	AAA	ATC	GAC	GAA	ATC	AAC	CCA	GTC	ATA	CTT	CCA	CCA	CCT	GGT	GTC	GGG	GGT	720
211	Pro	Ala	Asn	Leu	Ser	Asp	Pro	Leu	Leu	Leu	Asp	Trp	Val	Lys	Ile	Asp	Glu	Ile	Asn	Pro	Val	Ile	Leu	Pro	Pro	Pro	Gly	Val	Gly	Ala	240
721	GGC	GAC	TTG	AGA	GAC	CCC	AGC	GCG	TGG	TTG	GAA	CCC	TCC	GAC	TCC	ACA	TGG	CGT	TTT	ACT	ATT	GGC	TCA	AAA	GAT	GCA	TTA	AAC	AAG	810	
241	Gly	Asp	Phe	Arg	Asp	Pro	Ser	Thr	Ala	Trp	Phe	Glu	Pro	Ser	Asp	Ser	Thr	Trp	Arg	Phe	Thr	Ile	Gly	Ser	Lys	Asp	Ala	Leu	Asn	Lys	270
811	GGT	ATC	GCT	CTT	GTG	TAT	AGC	ACC	AAG	GAC	TTC	AGA	ACC	TTC	ACA	CTC	CTT	CCC	AAC	ACC	TTA	CAC	GGA	GTT	GAA	AAA	GTG	GGT	ATG	TGG	900
271	Gly	Ile	Ala	Leu	Val	Tyr	Ser	Thr	Lys	Asp	Phe	Arg	Thr	Phe	Thr	Leu	Leu	Pro	Asn	Thr	Leu	His	Gly	Val	Glu	Lys	Val	Gly	Met	Trp	300
901	GAG	TGT	ATT	GAT	TTC	TAC	CCT	ATT	GCC	ACC	TCT	GAG	GCC	GGA	GCA	AAC	AAG	GGC	CTG	GAC	CCT	TCC	GAA	GGC	CCG	AGT	TTG	GAA	ACA	AAG	990
301	Glu	Cys	Ile	Asp	Phe	Tyr	Pro	Ile	Ala	Thr	Ser	Glu	Ala	Gly	Ala	Asn	Lys	Gly	Leu	Asp	Pro	Ser	Glu	Gly	Pro	Ser	Leu	Glu	Thr	Lys	330
1081	GTC	GAG	AGC	CTT	CAC	GTT	GGT	CTT	GGG	TTG	ACA	TAC	GAC	TGG	GGA	AGG	TTC	TAC	GCT	TCT	AAG	ACA	TTT	TAC	GAT	AAT	CTC	AAG	CAA	AGA	1170
361	Val	Glu	Ser	Leu	Asp	Val	Gly	Leu	Gly	Leu	Arg	Tyr	Asp	Trp	Gly	Arg	Phe	Tyr	Ala	Ser	Lys	Thr	Phe	Tyr	Asp	Asn	Val	Lys	Gln	Arg	390
1171	AGG	ATT	CTA	TGG	GGT	TGG	GTT	AAA	GAG	GCC	GAT	AGC	GAG	AGC	GCT	GAT	ATT	GCC	AAA	GGC	TGG	GCT	TCT	CTT	CAG	GGA	ATT	CCT	GGA	TCA	1260
391	Arg	Ile	Leu	Trp	Gly	Trp	Val	Lys	Glu	Ala	Asp	Ser	Glu	Ser	Ala	Asp	Ile	Ala	Lys	Gly	Trp	Ala	Ser	Leu	Gln	Gly	Ile	Pro	Arg	Ser	420
1261	GTG	TTG	TAC	GAT	TTG	AAC	ACG	AAG	ACG	CAC	CTA	TTG	ACA	TGG	CCA	GTG	GAG	GAG	GTG	GAG	AAG	TTA	AGA	GCA	GAA	CAT	ATG	GAT	TTG	AGT	1350
421	Val	Leu	Tyr	Asp	Leu	Asn	Thr	Lys	Thr	His	Leu	Leu	Thr	Trp	Pro	Val	Glu	Glu	Val	Glu	Lys	Leu	Arg	Ala	Glu	His	Met	Asp	Phe	Ser	450
1351	GGA	ATT	ACA	GTG	GAT	GCA	GGG	AAA	ACT	GTG	GAG	CTC	AAA	GTA	GGC	GGT	GCT	GCA	CAG	TTG	GAT	GTT	GAA	GTT	CAA	TTT	ACC	ATA	GAG	GAA	1440
451	Gly	Ile	Thr	Val	Asp	Ala	Gly	Lys	Thr	Val	Glu	Leu	Lys	Val	Gly	Gly	Ala	Ala	Gln	Leu	Asp	Val	Glu	Val	Glu	Phe	Thr	Ile	Glu	Glu	480
1441	AAG	GCA	TTA	GAA	TTG	GCA	ACT	GAA	GAG	GTT	GTT	GAG	TAT	GAA	TGC	ATC	AAA	AGC	AAC	GGT	GCA	GCA	CAG	CGT	GGA	CTG	CTC	GGA	CCG	TTT	1530
481	Lys	Ala	Leu	Glu	Leu	Ala	Thr	Glu	Glu	Val	Val	Glu	Tyr	Glu	Cys	Ile	Lys	Ser	Asn	Gly	Ala	Ala	Gln	Arg	Gly	Leu	Leu	Gly	Pro	Phe	510
1531	GGT	TTG	CTT	GTG	CTT	GGG	AAT	GAG	GAT	TTG	ACT	GAA	CAG	ACC	CCG	ACT	TAC	TTC	TAC	GTT	AGC	AAG	AAA	TCA	GAT	GGC	GGT	TTG	GTT	ACA	1620
511	Gly	Leu	Leu	Val	Leu	Ala	Asn	Glu	Asp	Leu	Thr	Glu	Gln	Thr	Ala	Thr	Tyr	Phe	Tyr	Val	Ser	Lys	Lys	Ser	Asp	Gly	Gly	Leu	Val	Thr	540
1621	CAT	TTT	TGT	CAG	GAT	GAA	TTA	AGA	TCT	TCC	AAA	GCG	ACT	GAC	ACC	ATT	ACT	CAA	ATC	GTT	GGG	CAT	ACC	GTT	CCG	GTT	CTT	AAT	GGA	GAA	1710
541	His	Phe	Cys	Gln	Asp	Glu	Leu	Arg	Ser	Ser	Lys	Ala	Thr	Asp	Thr	Ile	Thr	Gln	Ile	Val	Gly	His	Thr	Val	Pro	Val	Leu	Asn	Gly	Glu	570
1711	TCC	TTC	ACG	CTT	AGA	GTG	CTG	ATT	GAT	CAC	TCT	ATC	GTG	GAG	AGT	TTT	GCA	CAA	GGA	GGG	AGA	GCT	AGC	GCG	ACA	TCT	AGA	GTG	TAT	CCG	1800
571	Ser	Phe	Thr	Leu	Arg	Val	Leu	Ile	Asp	His	Ser	Ile	Val	Glu	Ser	Phe	Ala	Gln	Glu	Glu	Arg	Ala	Ser	Ala	Thr	Ser	Arg	Val	Tur	Pro	600
1801	ACA	GAG	GCG	ATT	TAT	GGG	GAT	GCA	GCG	TTG	TTT	GTC	TTT	AAT	AAT	CCG	ACC	GGT	GCT	TCC	ATT	ACG	GCA	TCG	AGT	TTG	AAT	TTA	TGG	CAT	1890
601	Thr	Glu	Ala	Ile	Tur	Gly	Asp	Ala	Arg	Leu	Phe	Val	Phe	Asn	Asn	Ala	Thr	Gly	Ala	Ser	Ile	Thr	Ala	Ser	Ser	Leu	Asn	Leu	Trp	His	630
1891	ATG	AAC	TCC	GCA	TCA	AAC	AGT	AAC	CTA	ATG	GAT	CTC	TAG																	1929	
631	Met	Asn	Ser	Ala	Ser	Asn	Ser	Asn	Leu	Met	Asp	Leu	End																		

Figure S3 The nucleotide sequence and the deduced amino acid sequence of *AsINV* CDS.

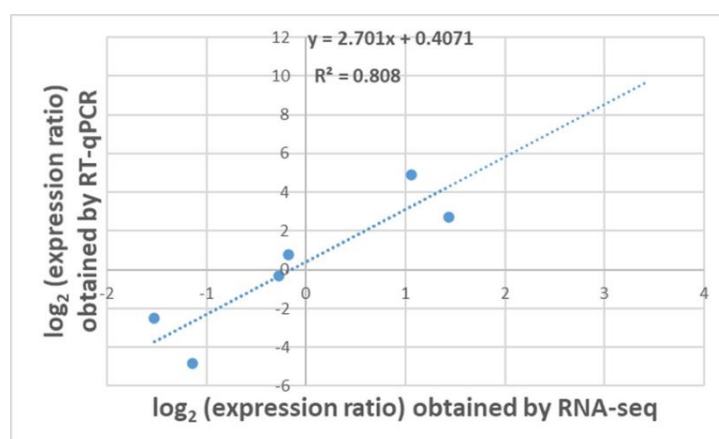


Figure S4 Comparison between the log2 of expression ratios of DGEs obtained from RNA-seq and RT-qPCR.

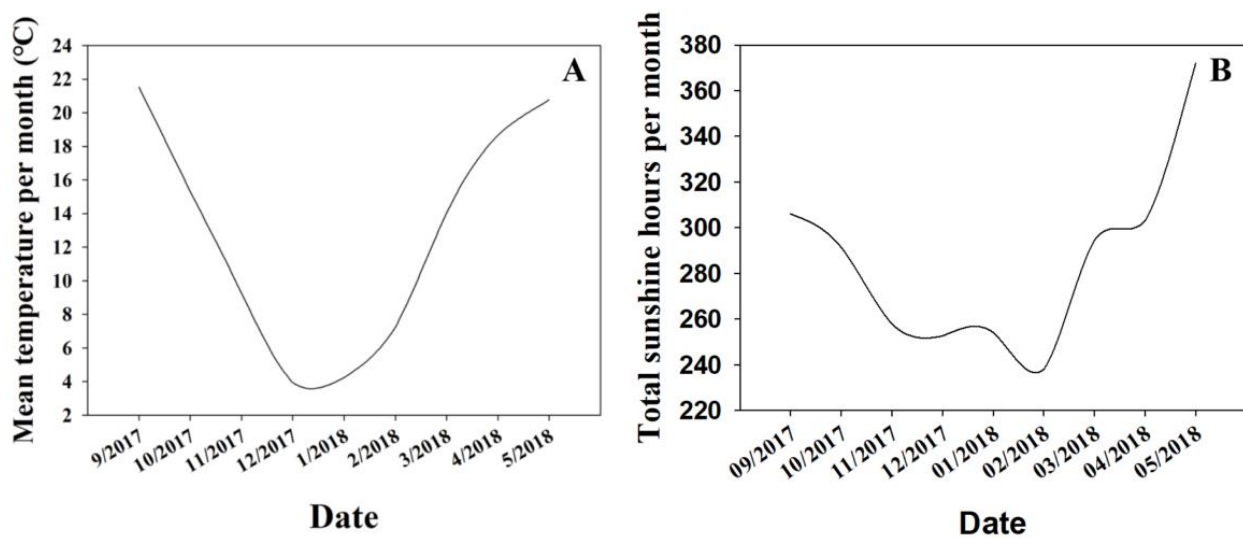


Figure S5 Average temperature per month and total sunshine hours per month in the plastic tunnel. The data show the mean of air temperature within a month (A) and the total hours of illumination intensity higher than 2 klux within a month (B).



Figure S6 Sample for measuring endogenous plant hormone level, sugars content, soluble protein content and related genes expression in 1 cm-thick stem containing shoot apical meristem.

Table S1 List of 159 DEGs in this study

gene_id	GA_readcount	CK_readcount	Swissprot annotation
Cluster-32430.84552	121.5226452	0	Putative casein kinase II subunit beta-4
Cluster-32430.98519	67.49916236	0	Protein Rf1, mitochondrial
Cluster-66662.0	0.308096439	60.57114749	None
Cluster-32430.176693	0	51.36034364	None
Cluster-32430.107041	0.308096439	48.52239553	ATP-dependent zinc metalloprotease
Cluster-32430.135820	42.25128969	0	None
Cluster-32430.126776	0	61.17712304	Armadillo repeat-containing kinesin-like protein 1
Cluster-32430.71626	0	38.61313743	None
Cluster-32430.96634	37.23079965	0	None
Cluster-66662.1	58.81173229	0	None
Cluster-32430.83417	0	77.77617466	U-box domain-containing protein 44
Cluster-32430.192010	0	34.74414326	None
Cluster-32430.107551	23.65590037	192.7729235	Retrovirus-related Pol polyprotein from transposon TNT 1-94
Cluster-32430.132687	0	31.07604787	Alliin lyase
Cluster-32430.75749	31.25506638	0	Retrovirus-related Pol polyprotein from transposon TNT 1-94
Cluster-32430.30318	0	30.49094931	Pentatricopeptide repeat-containing protein
Cluster-32430.139928	29.46271667	0	None
Cluster-32430.93908	39.08297361	0	None
Cluster-32430.124207	0	27.65046076	Protein PHYLLLO, chloroplastic
Cluster-32430.76732	0	27.75531509	None
Cluster-32430.94502	27.76571514	0	None
Cluster-32430.4608	0	67.33953135	Beta-glucosidase 25
Cluster-32430.132255	0	26.45207389	None
Cluster-32430.64383	0	51.98272839	Transcription factor bHLH121
Cluster-32430.80726	15.54530596	92.97608668	OTU domain-containing protein
Cluster-32430.81837	32.37499427	0.608515183	OTU domain-containing protein
Cluster-32430.147003	86.34561334	0	None
Cluster-32430.86775	42.79196066	0.377786653	None
Cluster-32430.71391	1.232385756	35.41500125	Gibberellin 20 oxidase 2
Cluster-32430.76615	8.557363811	68.96448585	None
Cluster-32430.155576	25.13024238	0	Probable phospholipid-transporting ATPase 5
Cluster-32430.45689	26.64544957	0	None
Cluster-32430.90497	3.379414339	44.61029633	ABC transporter G family member 28
Cluster-32430.54290	111.4511526	0.304257591	Probable leucine-rich repeat receptor-like protein kinase
Cluster-32430.80743	28.97679345	134.5901905	None
Cluster-32430.26814	0	24.12823491	None

Cluster-32430.181365	222.8903063	27.49475682	Premnaspirodiene oxygenase
Cluster-32430.66296	10.47527892	74.57476166	None
Cluster-32430.77681	244.6628103	68.90960028	Trans-cinnamate 4-monooxygenase
Cluster-32430.182348	23.51444168	0	None
Cluster-32430.80765	130.4146582	30.66156694	Receptor-like protein kinase BRI1-like 3
Cluster-32430.167555	23.17176142	0	RING domain-containing protein 2
Cluster-32430.61256	53.34746574	5.469630021	None
Cluster-32430.147617	0	26.32247068	Auxin response factor 23
Cluster-32430.116955	0.308096439	40.61288753	Sodium/hydrogen exchanger 2
Cluster-32430.124946	22.65475002	0	None
Cluster-32430.95809	34.20384633	0	None
Cluster-32430.69004	28.16953199	0.608515183	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 homolog
Cluster-30209.1	0	22.25376551	None
Cluster-32430.187776	22.25331987	0	None
Cluster-32430.36768	0	21.42734725	None
Cluster-32430.72346	12.32385756	76.53617908	Leucine-rich repeat receptor-like protein kinase
Cluster-32430.103842	4.621446584	47.43273568	SNF2 domain-containing protein CLASSY 1
Cluster-32430.93247	26.10081104	0	Uncharacterized mitochondrial protein
Cluster-32430.114245	89.22539073	13.23894443	None
Cluster-32430.22715	0	24.02278629	None
Cluster-32430.149248	21.64549571	0	None
Cluster-32430.81481	6.399410971	51.8841443	Uncharacterized protein
Cluster-32430.118496	1.257491922	48.8704969	None
Cluster-32430.179614	30.27690026	0	None
Cluster-32430.59832	0	20.7836349	None
Cluster-44018.0	0	20.69041744	None
Cluster-32430.163095	0	20.84597771	None
Cluster-32430.144527	0	20.60406292	None
Cluster-27356.0	0	20.53157877	None
Cluster-32430.163964	0	46.46372469	None
Cluster-32430.36115	76.87501498	13.56184551	LINE-1 retrotransposable element ORF2 protein
Cluster-32430.124571	26.79121349	110.201541	Protein RADIALIS-like 5
Cluster-32430.149181	49.9394496	2.43406073	None
Cluster-32430.147993	0	19.68592273	None
Cluster-32430.119078	625.5650297	1613.708747	6.4 kDa proline-rich protein
Cluster-32430.125552	19.98563354	0	Retrovirus-related Pol polyprotein from transposon TNT 1-94
Cluster-32430.41247	0	19.52126602	None
Cluster-32430.59195	20.35580667	0	None
Cluster-32430.74146	5.047645236	58.70339815	Pentatricopeptide repeat-containing protein

Cluster-32430.105335	110.556808	26.25117511	None
Cluster-32430.140355	0	18.90424869	None
Cluster-32430.185285	31.76387789	2.102063209	Polyadenylate-binding protein 1
Cluster-32430.79704	193.1201302	42.02559293	UPF0481 protein
Cluster-32430.178547	36.24443365	3.400079873	None
Cluster-32430.168371	500.4407479	181.9179282	Cytochrome P450 84A1
Cluster-41012.1	0	19.06622129	None
Cluster-32430.199547	57.42867496	5.780894234	None
Cluster-32430.141273	48.73677458	5.780894234	E3 ubiquitin-protein ligase
Cluster-32430.187970	18.72357162	0	None
Cluster-32430.110011	72165.29051	15263.4717	RNA replication protein
Cluster-32430.110201	4416.3668	10728.67305	Osmotin-like protein
Cluster-32430.71737	0	37.01504201	None
Cluster-37193.0	0	18.44920396	None
Cluster-29862.0	18.69103683	0	Phosphoinositide phospholipase C 2
Cluster-32430.201933	28.84255623	0	None
Cluster-30209.2	18.48464283	0	None
Cluster-32430.167775	18.43916932	0	None
Cluster-32430.110907	0.924289317	2213.893168	RNA replication protein
Cluster-32430.143893	0	20.44522505	Fanconi anemia group D2 protein homolog
Cluster-32430.145506	53.07869196	7.656408545	None
Cluster-32430.188659	29.06619418	0	None
Cluster-66303.0	34.90816216	2.812892291	Calreticulin
Cluster-32430.174186	1.232385756	26.62195514	None
Cluster-32430.52972	19.09135805	85.7170103	None
Cluster-32430.181484	6.329303223	47.20737457	DNA repair protein XRCC2 homolog
Cluster-32430.1018	28.1851605	0.304257591	None
Cluster-32430.41607	18.03441237	82.03414253	None
Cluster-32430.30225	17.94709525	0	None
Cluster-32430.90492	35.61876311	3.777866526	ABC transporter G family member 28
Cluster-32430.115147	234.5853279	78.47819465	Protein FAM214B
Cluster-32430.111587	0	42.40204732	Phototropin-2
Cluster-32430.87832	49.24289631	8.017190112	Protein trichome birefringence-like 3
Cluster-32430.116589	49.22757089	158.9023207	Scarecrow-like protein 3
Cluster-32430.110475	867344.2706	94345.10504	RNA replication protein
Cluster-32430.102725	45.54449585	6.683976278	Myosin-12
Cluster-32430.123770	42.6926795	0.912772774	None
Cluster-32430.124484	22.92906848	92.90837645	None
Cluster-32430.142231	41.33614036	4.563863869	Phospholipase D delta
Cluster-32430.108883	1.278968195	5520.159918	RNA replication protein
Cluster-32430.118311	186.8979399	50.50006047	None
Cluster-32430.201934	17.09449454	0	None
Cluster-32430.181457	17.0479121	0	None

Cluster-32430.179674	0	16.72492741	None
Cluster-32430.138137	4.114047095	49.36491684	LINE-1 retrotransposable element ORF2 protein
Cluster-32430.108836	6.858178985	16378.4296	RNA replication protein
Cluster-32430.135972	0	30.09496978	Putative E3 ubiquitin-protein ligase LIN-1
Cluster-32430.182902	37.3550873	4.322993993	Pentatricopeptide repeat-containing protein
Cluster-32430.40997	0	16.33968352	None
Cluster-41012.0	16.84134926	0	None
Cluster-32430.92390	8.448535848	49.22845148	Cytochrome c biogenesis CcmF C-terminal-like mitochondrial protein
Cluster-32430.109922	0.924289317	1219.682155	Uncharacterized ORF4 protein
Cluster-32430.130078	35.08723213	3.458694458	Pentatricopeptide repeat-containing protein
Cluster-32430.161717	16.76603076	0	None
Cluster-2331.2	20.79511287	0	None
Cluster-32430.12585	0	16.04288316	None
Cluster-32430.48385	0	15.93206712	Plastidal glycolate/glycerate translocator 1
Cluster-54685.2	0	15.95071061	None
Cluster-32430.134404	803.4489562	338.9334031	Cytosolic sulfotransferase 17
Cluster-32430.87908	0	15.84839671	None
Cluster-58617.2	15.91722878	0	Pentatricopeptide repeat-containing protein
Cluster-32430.132754	71.17991985	15.3187788	1,4-alpha-glucan-branching enzyme 3
Cluster-32430.187390	30.66888733	2.471347715	Major sperm protein isoform beta
Cluster-32430.202065	17.38854333	0	None
Cluster-32430.197702	32.02061849	1.51114661	None
Cluster-32430.121303	0	25.35913485	Protein PHYLLO, chloroplastic
Cluster-32430.68939	17.90286494	0	None
Cluster-37193.1	15.54107363	0	None
Cluster-32430.77837	24.26661773	0	None
Cluster-32430.183150	55.95403361	11.33359958	ATP-dependent DNA helicase pif1
Cluster-32430.49325	11.00933086	56.48902338	None
Cluster-32430.127388	0	14.99423852	Uncharacterized mitochondrial protein
Cluster-32430.109798	0.308096439	1156.016297	RNA replication protein
Cluster-32430.17630	1.2491232	22.89420026	None
Cluster-32430.62985	0	21.04464379	None
Cluster-32430.190012	8.643437735	49.39847561	Beta-glucosidase 31
Cluster-32430.110626	27.9508017	97.41794825	Cyclin-dependent kinase G-2
Cluster-20050.0	0	14.76142017	None
Cluster-32430.76189	20.32609593	0.755573305	None
Cluster-32430.108837	0.316465161	478.0593421	RNA replication protein
Cluster-32430.121	15.1217971	0	None
Cluster-32430.161747	15.13601359	0	None
Cluster-32430.86339	0.632930322	22.03153913	None
Cluster-32430.59769	14.97731095	0	None

Table S2 Primers used in this study

Gene symbol	Forward primer (5' to 3')	Reverse primer (5' to 3')	Purpose
<i>AsGA20ox</i>	ATGGACTCCATTTTTCTCCCC	TCACATATTTCCAGTTCTTTTAATC	CDS clone
<i>AsGA20ox</i>	TATCAAGTGATGGAAAGCTACAA	AGAGAAACGGTCGCTATGTG	RT-qPCR
<i>AsINV</i>	ATGTCTTCGTTTAGAGACTTGGAG	CTAGAGATCCATTAGGTTACTGTTTG	CDS clone
<i>AsINV</i>	TCTCATGCTTCTGACGCTTG	ATACGCACCCGCTTTC AAC	RT-qPCR
<i>AsCYP735</i>	GTTCTAACTGGCAGTATAGTCGA	TGATCATCTCAGTGTC CGTCA	RT-qPCR
<i>AsAHK</i>	TGGAAGGAGGAAAGATGTCA	GATCTGT TAAACCAGGCAAAC	RT-qPCR
<i>AsAUX</i>	GAGAAGCATTGGAGGTTTAGAAT	CTTTAGCAATGGGTCGATCA	RT-qPCR
<i>AsBGLU31</i>	GTATTTGCTGTTACCTGTGGCT	TCCAAAGCTGCTCCTTCTAC	RT-qPCR
<i>ACT</i>	CAGGAGTTATGGTTGGAATGG	AGCACGGGATGTTCTTCA	RT-qPCR