

Figure S1. Constructed vectors of *DIRan3A* and *DIRan3B*. **a** pCAMBIA1301 - 35S - *DIRan3A* (P35S_A). **b** pCAMBIA1301 - 35S - *DIRan3B* (P35S_B). **c** pCAMBIA1301 - pDIRan3A (1256bp)- *DIRan3A* (PA_A). **d** pCAMBIA1301 - pDIRan3B (1569bp) - *DIRan3B* (PB_B). **e** pDIRan3A (1256bp) – GUS (PA_GUS). **f** pCAMBIA1301 - pDIRan3B (1569bp) – GUS (PB_GUS).

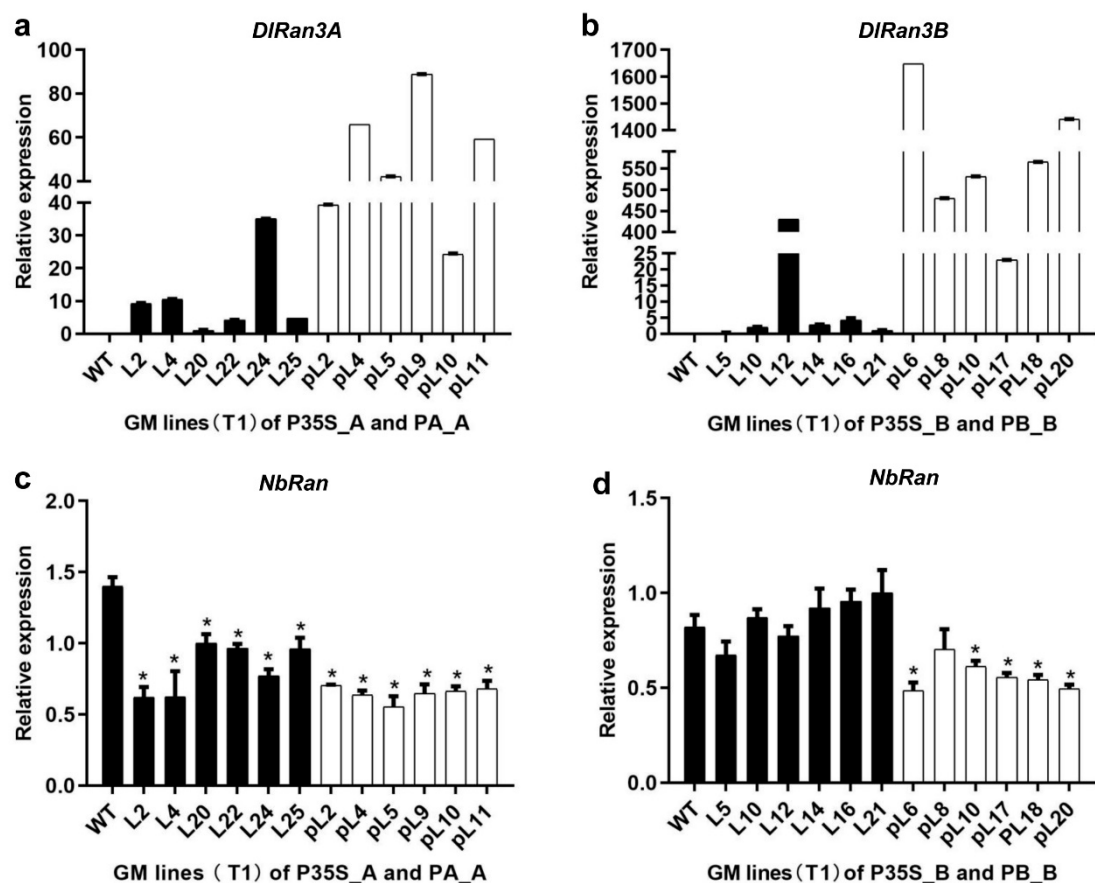


Figure S2. Gene relative expression in transgenic modified tobacco (T1 lines). a Relative expression of *DIRan3A* in P35S_A and PA_A T1lines; b Relative expression of *DIRan3B* in P35S_B and PB_B T1lines; c Relative expression of *NbRan* in P35S_A and PA_A T1lines; d Relative expression of *NbRan* in P35S_B and PB_B T1lines; significant differences in contrast to the control (WT) are indicated with an asterisk (*) and were assessed by a one-way ANOVA test (* $p < 0.05$)

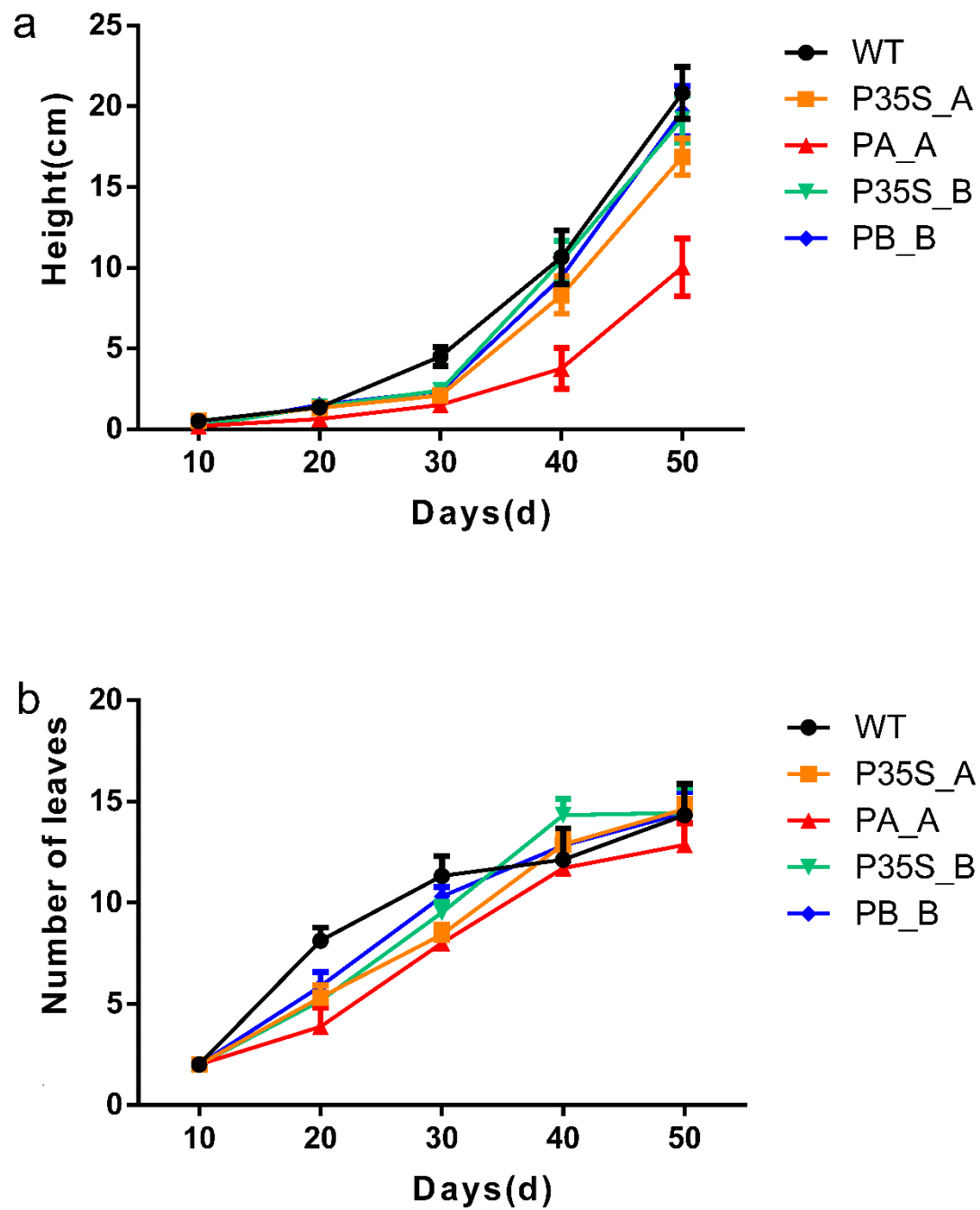


Figure S3. Height (a) and leaf number (b) of transgenic tobacco.

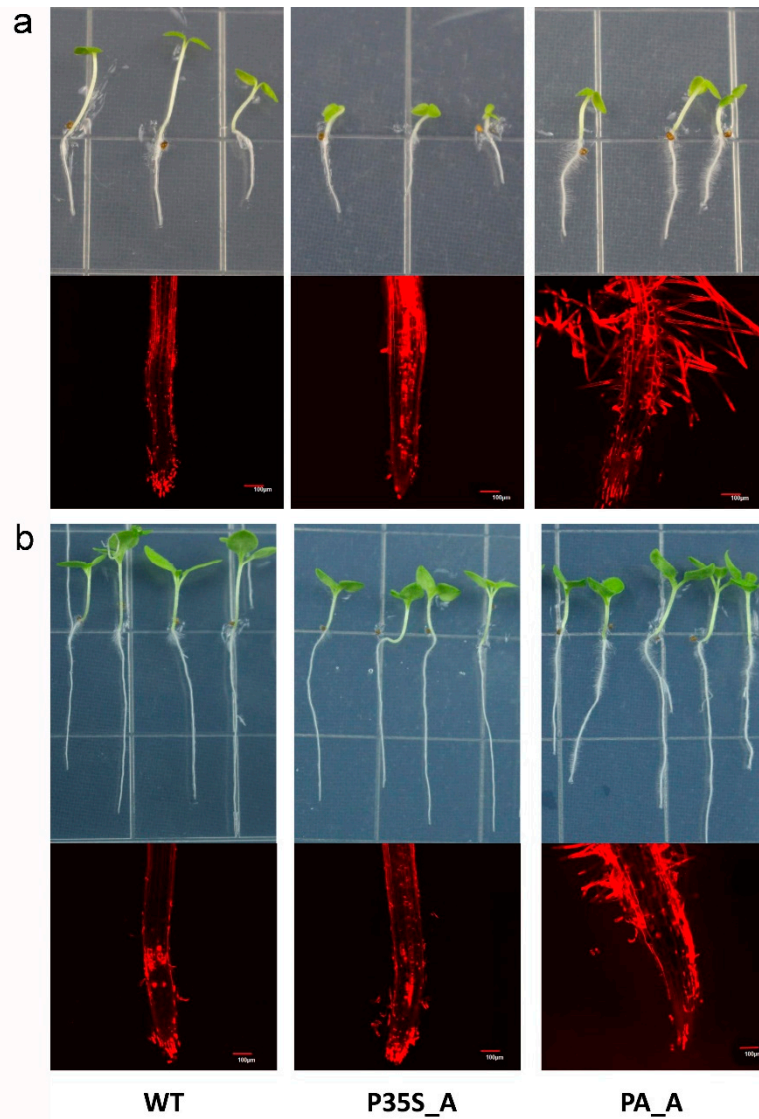


Figure S4. Phenotype of transgenic tobacco root (7d and 14d). Transgenic tobaccos were germinated and vertically cultivated for 7d (**a**) and 14d (**b**). WT and T2 lines of P35S_A and PA_A were displayed in the graph from left to right in turn. The upper images illustrated transgenic tobaccos germinated and vertically cultivated on MS medium for 7d and 14d, respectively, and the lower images illustrated the 7 day- and 14 day-cultivated tobacco roots stained with propidium iodide (bar =100 μ m), respectively.

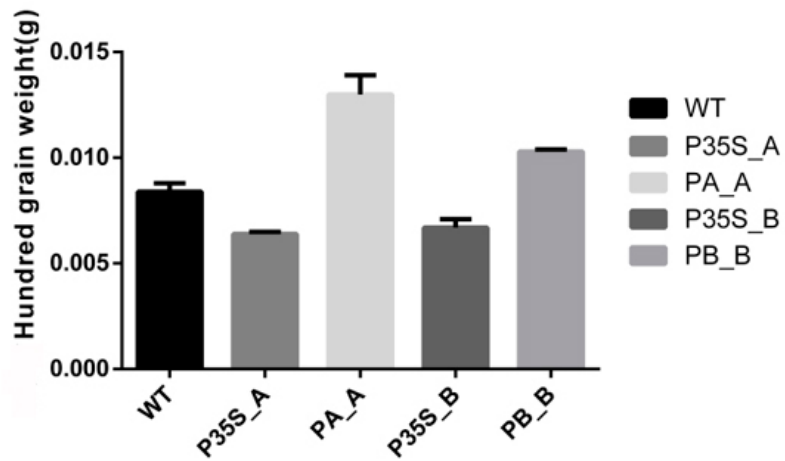


Figure S5. Hundred grain weight of transgenic tobacco.

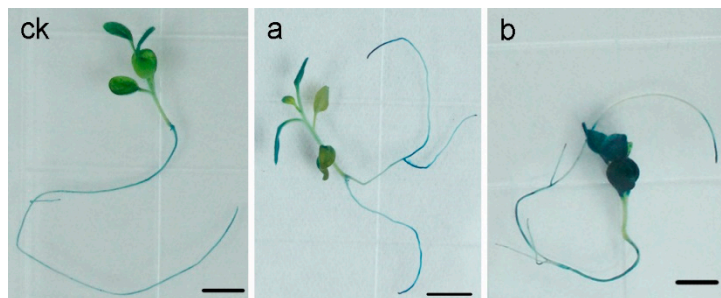


Figure S6. GUS staining of transgenic tobacco seedlings (T1 lines). ck: 1301. a: PA-GUS. b: PB-GUS. Bar = 5 mm.

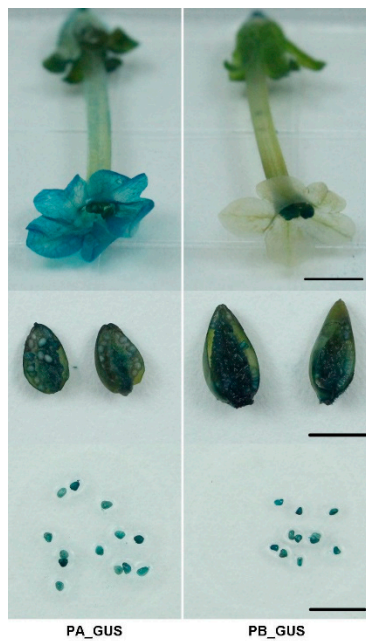


Figure S7. GUS staining of flowers, fruits and seeds of transgenic tobacco (T0 lines). Bar = 5 mm.

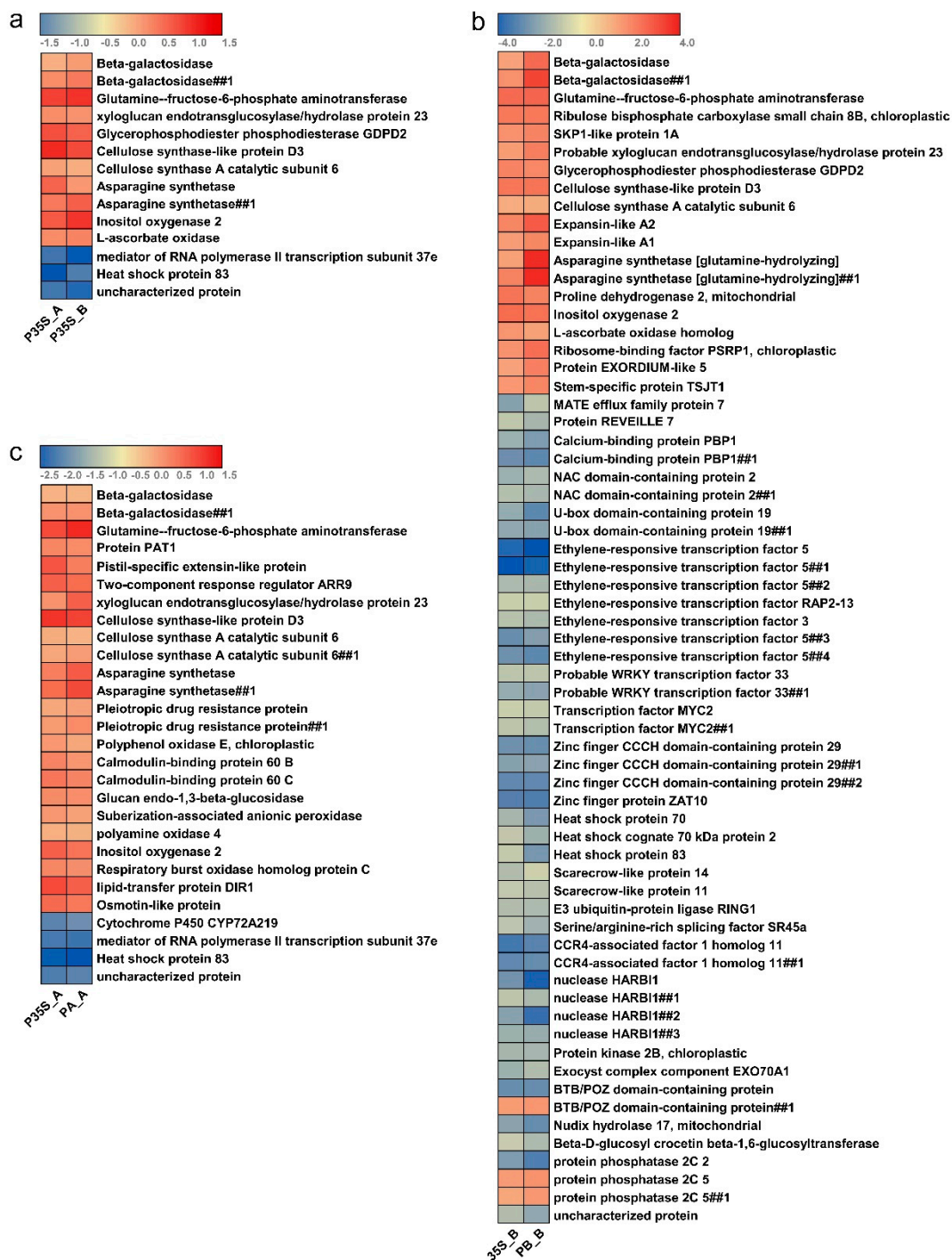


Figure S8. Expression profiles of the shared DEGs in transgenic lines.

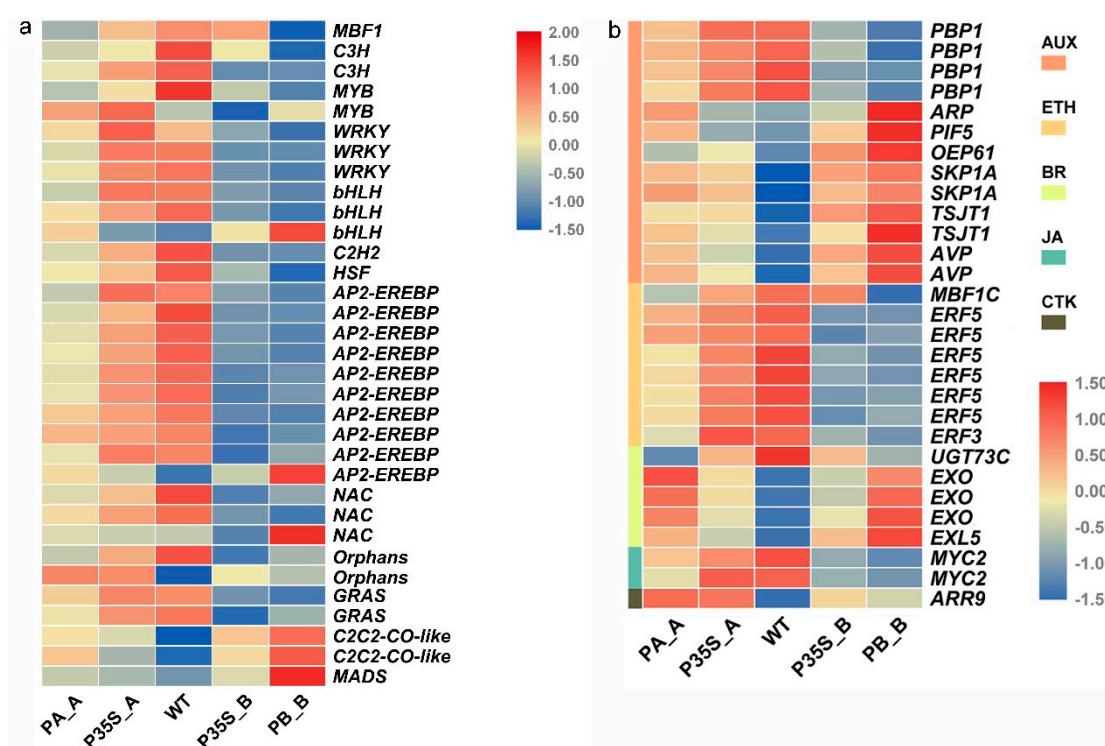


Figure S9. Expression profiles of the DEGs classified as genes encoding transcription factors (TFs) (a) and hormone-related genes (HRGs) (b).

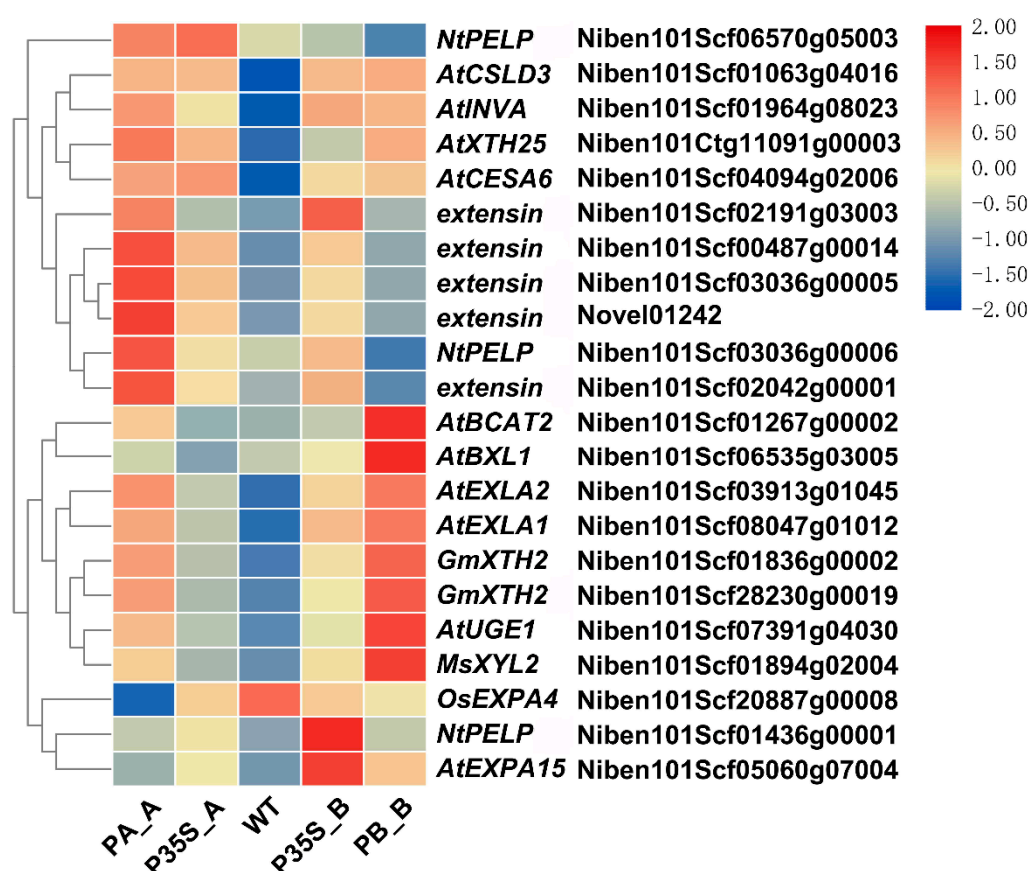


Figure S10. Expression profiles of DEGs involved in cell wall development.

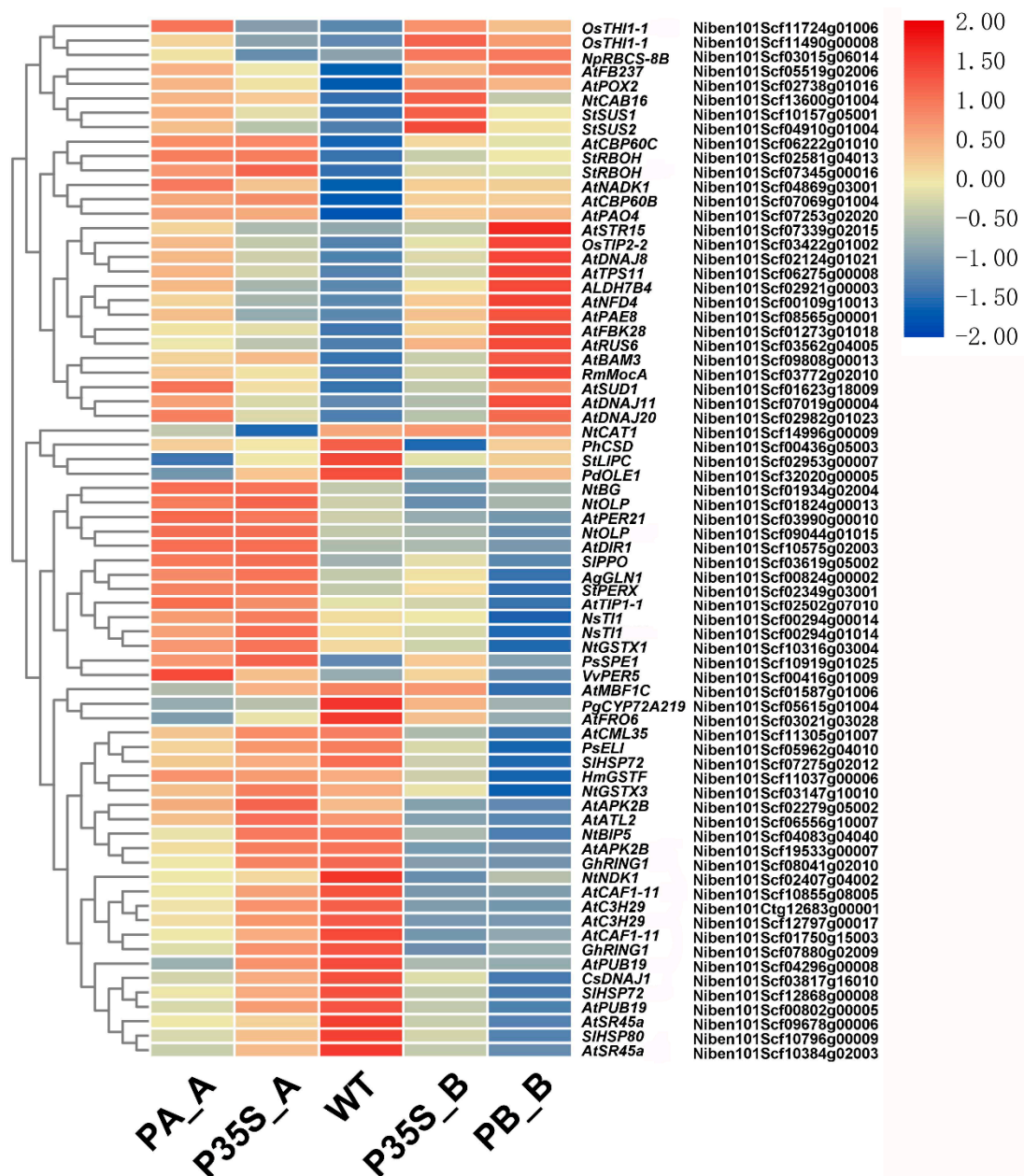


Figure S11. Expression profiles of stress-related DEGs.

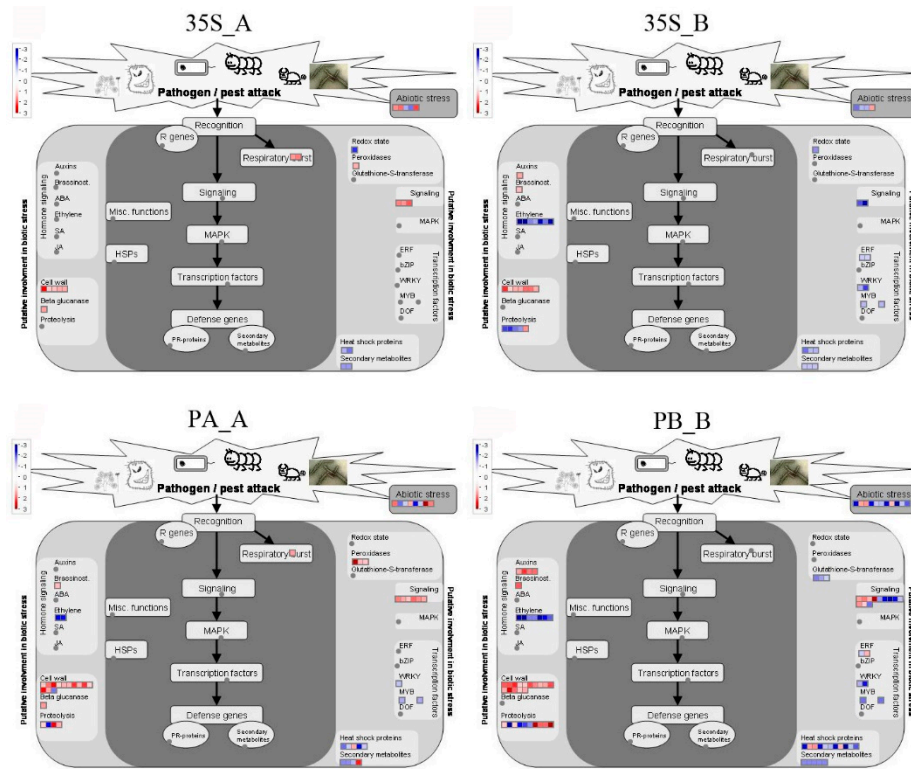


Figure S12. Mapman software visualization of stress-related genes. Genes differentially expressed ($|\text{Log}_2(\text{FC})| \geq 1$ and $\text{Padj} \leq 0.005$) of transgenic tobacco plants overexpressing longan Ran were represented according to their respective Log2 rescaled fold change. Red color represents up-regulated genes and blue color represents down-regulated genes. The dark gray rectangle includes genes directly involved in biotic stress responses and the light gray rectangle includes genes potentially involved in biotic stress responses. The medium gray rectangle includes genes involved in abiotic stress responses. ABA, abscisic acid; bZIP, basic region leucine zipper; DOF, DNA-binding with one finger; ERF, ethylene responsive factor; HSP, heat shock protein; JA, jasmonic acid; MAPK, mitogen activated protein kinase; MYB, v-myb avian myeloblastosis viral oncogene homolog; PR, pathogenesis-related; R, resistance; SA, salicylic acid.

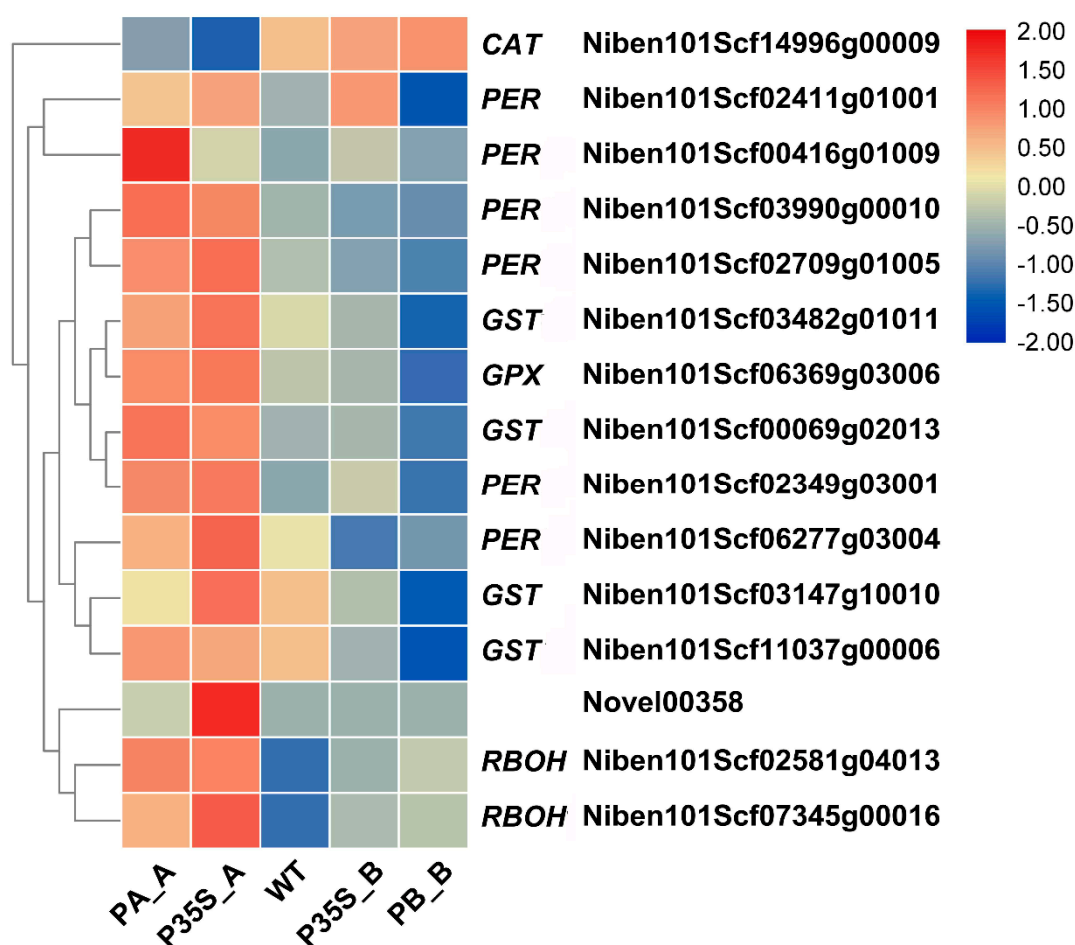


Figure S13. Expression profiles of the antioxidant-defense-related DEGs.

Table S1. Sequences of primers used for qPCR analysis of *DIran3A* and *DIran3B* in *longan*.

Primer Name	Primer Sequence (5'→3')
DIran3A-QF	GCATGAGGCTGAACTGCAA
DIran3A-QR	TCCCCATCCTGCTGTTTTAC
DIran3B-QF	CATCATGAAGCTGAGCTTGC
DIran3B-QR	CCAGCCTGCAACTGTTCTC
pre-miR167f3p (scaffold692)QF	TGAAGCTGCCAGCATGAT
pre-miR167f3p (scaffold692)QR	CCATCAATAGGTGAAACTGCC
pre-miR171f (scaffold760)QF	CGGTTTCGGTTCAATGAGAA
pre-miR171f (scaffold760)QR	GATATCGGCACGGCTCAA
pre-miR394a (scaffold3884)QF	CGCATCTGTCCACCTCC
pre-miR394a (scaffold3884)QR	AGAGAAGCCAACAGAGCTCAG

Table S2. Primers sequences used for *DIran3A* and *DIran3B* constructs for genetic transformation of *Nicotiana benthamiana*.

Primer name	Sequence (5'→3')
DIran3A-(BamHI)F	TGGTACCCGGGGATCCATGGCTCTACCGAATCAGC

DlRan3A-(Sall)R	AACGCTGCAGGTCGACTTACTCGAATGCATCATCATC
DlRan3B-(BamHI)F	TGGTACCCGGGGATCCATGGCTTTGCCAAATCAGC
DlRan3B-(Sall)R	AACGCTGCAGGTCGACCTATTCAAATGTGTCATCATCGTC
pDlRan3A-(EcoRI)F	CCATGATTACGAATTCCGGAGAGTGTTGAAGGCC
pDlRan3A-(KpnI)R	CTAGAGGATCCCCGGGTACCTTCTTCTTGGTTTGGTTCTGAG
pDlRan3B-(EcoRI)F	CCATGATTACGAATTCAACAACCTACCTACCAATGAGCG
pDlRan3B-(KpnI)R	CTAGAGGATCCCCGGGTACCGAGAGCTGTCCTTGAGAAAG C
pDlRan3A-(HindIII) F	GCAGGCATGCAAGCTTCGGAGAGTGTTGAAGGCC
pDlRan3A-(NcoI)R	CTCAGATCTACCATGGTTCTTCTTGGTTTGGTTCTG
pDlRan3B-(HindIII) F	GCAGGCATGCAAGCTTAACAACCTACCTACCAATGAG
pDlRan3B-(NcoI)R	CTCAGATCTACCATGGGAGAGCTGTCCTTGAG

Table S3. Sequences of primers used for qPCR detection in transgenic tobaccos.

Primer name	Sequence (5'→3')	Function
DlRan3A-QF1	GCAAGTGAAAGCCAAGCAA	<i>DlRan3A</i> primers used for qPCR detection of transgenic lines
DlRan3A-QR1	TGACTAGCAGCAGCTTGCACT	
DlRan3B-QF1	CCTAGCTTCAAGCTCGTCATC	<i>DlRan3B</i> primers used for qPCR detection of transgenic lines
DlRan3B-QR1	CCCAGCAGTAGAAACGGATT	
NbRanQF	GGCTTCTGAGGACTCTCTGTTC	Primers used for qPCR detection of endogenous <i>Ran</i> gene in transgenic lines
NbRanQR	CCAAATCGGTCCATCCAAAC	

Table S4. Primers sequences used for qPCR verification.

Primer name	Sequence (5'→3')	Gene ID
AtSKP1A-QF	CACTGACCCGCAAGCC	Niben101Scf02658g00012
AtSKP1A-QR	TCTCGCCGTCGGAAGCTC	
VrAVP-QF	TGAGATGGCTGGAATGAGC	Niben101Scf05220g00005
VrAVP-QR	AGAACCAATGGCAAATCCC	
AtCESA6-QF	CAAGGAAATGGGTCCCG	Niben101Scf04634g00004
AtCESA6-QR	CACGGCGTTCCCTCAC	
NtPELP-QF	TGCCACATTTGAGGTGTTG	Niben101Scf03036g00006
NtPELP-QR	GGTGGTGGAGAAGGAGAAGC	
SIPPO-QF	GGCAGAGTTCGCAGGAAG	Niben101Scf03619g05002
SIPPO-QR	CGGGACCAGAGTCACCAC	
NtBG-QF	TTCTCCCAACAAGCAGCC	Niben101Scf01934g02004

NtBG-QR	CCGAACTGTCCCAAACCTCC	
AtTIP1-1-QF	TTGGGCTGTTCGTGGC	Niben101Scf02502g07010
AtTIP1-1-QR	TTACCGCCAACAAACGC	
StRBOHC-QF	TGTCAAAGCCACAGGGC	Niben101Scf02581g04013
StRBOHC-QR	GCTGGCAAACCTCGGAG	
HmGSTF-QF	GCTTGGTCTAAGGCACTTGAG	Niben101Scf00069g02013
HmGSTF-QR	CAACAATCACGCCTCGG	
NtGSTX1-QF	TTGCTGCTTCCGCTCG	Niben101Scf10316g03004
NtGSTX1-QR	CTCTTGGGAGGCAACCC	
NtGPX4-QF	CCAGTTTGGTGGGCAGG	Niben101Scf06369g03006
NtGPX4-QR	CAGCCTTGAAGCGAGTGC	
AtPER21-QF	TGGGACGAGTTCATTGTGTG	Niben101Scf03990g00010
AtPER21-QR	GGTCAGGATTTGGTGTCCG	
AtPER10-QF	GCTCACACCATTGGATTTGC	Niben101Scf06277g03004
AtPER10-QR	GTGTCGGGTCAGGATTTCC	
AtMYB59-QF	GGAGGAAATCAGAAGAGGTCC	Niben101Scf39382g00003
AtMYB59-QR	GAGGAGTCATCTTGCCACG	

Table S5. Comparison of reads by transcriptome sequencing to reference genome.

Sample name	WT	P35S_A	PA_A	P35S_B	PB_B
Total reads	42684446	55087298	45622008	52717818	50937938
Total mapped	38262505 (89.64%)	49454712 (89.78%)	41298764 (90.52%)	47175126 (89.49%)	45959763 (90.23%)
Multiple mapped	2606302 (6.11%)	3418317 (6.21%)	2915443 (6.39%)	3462580 (6.57%)	3191092 (6.26%)
Uniquely mapped	35656203 (83.53%)	46036395 (83.57%)	38383321 (84.13%)	43712546 (82.92%)	42768671 (83.96%)
Read-1	18417835 (43.15%)	23749073 (43.11%)	19830398 (43.47%)	22584157 (42.84%)	21989665 (43.17%)
Read-2	17238368 (40.39%)	22287322 (40.46%)	18552923 (40.67%)	21128389 (40.08%)	20779006 (40.79%)

Reads map to '+'	17834532 (41.78%)	23031003 (41.81%)	19198815 (42.08%)	21864927 (41.48%)	21390603 (41.99%)
Reads map to '-'	17821671 (41.75%)	23005392 (41.76%)	19184506 (42.05%)	21847619 (41.44%)	21378068 (41.97%)
Non-splice reads	22857915 (53.55%)	29452865 (53.47%)	24625286 (53.98%)	27987161 (53.09%)	27375524 (53.74%)
Splice reads	12798288 (29.98%)	16583530 (30.1%)	13758035 (30.16%)	15725385 (29.83%)	15393147 (30.22%)

Table S6. Differentially expressed genes (DEGs) of the GM *N. benthamiana* lines.

Comparison of lines	All DEGs	Up-regulated DEGs	Down-regulated DEGs
P35S_A vs WT	56	46	10
PA_A vs WT	115	72	43
P35S_B vs WT	94	35	59
PB_B vs WT	186	107	79
P35S_A vs P35S_B	68	56	12
PA_A vs P35S_A	16	8	8
PB_B vs P35S_B	36	28	8
PA_A vs PB_B	82	59	23

Table S7. Shared DEGs between the P35S_A and P35S_B lines.

Gene ID	Gene Expression	Annotation
Niben101Scf02363g00015	UP	Beta-galactosidase
Niben101Scf10213g00009	UP	Beta-galactosidase
Niben101Scf03253g02010	UP	Glutamine--fructose-6-phosphate aminotransferase
Niben101Ctg13782g00003	UP	Probable xyloglucan endotransglucosylase/hydrolase protein 23
Niben101Scf00109g03008	UP	Glycerophosphodiester phosphodiesterase GDPD2
Niben101Scf03326g01009	UP	Cellulose synthase-like protein D3

Niben101Scf04634g00004	UP	Cellulose synthase A catalytic subunit 6 [UDP-forming]
Niben101Scf00573g01003	UP	Asparagine synthetase [glutamine-hydrolyzing]
Niben101Scf11860g00013	UP	Asparagine synthetase [glutamine-hydrolyzing]
Niben101Scf03307g06003	UP	Inositol oxygenase 2
Niben101Scf16156g00005	UP	L-ascorbate oxidase homolog
Niben101Scf00449g06008	DOWN	Heat shock protein 70
Niben101Scf06684g01005	DOWN	Heat shock protein 83
Niben101Scf02389g00013	DOWN	Protein of unknown function

Table S8. Shared DEGs between the P35S_A and PA_A lines.

Gene ID	Gene Expression	Annotation
Niben101Scf02363g00015	UP	Beta-galactosidase
Niben101Scf10213g00009	UP	Beta-galactosidase
Niben101Scf03253g02010	UP	Glutamine--fructose-6-phosphate aminotransferase
Niben101Scf06374g00021	UP	Protein PAT1 homolog 1
Niben101Scf06570g05003	UP	Pollen Ole e 1 allergen protein
Niben101Scf01785g04007	UP	Two-component response regulator ARR9
Niben101Ctg13782g00003	UP	Probable xyloglucan endotransglucosylase/hydrolase protein 23
Niben101Scf03326g01009	UP	Cellulose synthase-like protein D3
Niben101Scf04094g02006	UP	Cellulose synthase A catalytic subunit 6 [UDP-forming]
Niben101Scf04634g00004	UP	Cellulose synthase A catalytic subunit 6 [UDP-forming]
Niben101Scf11860g00013	UP	Asparagine synthetase [glutamine-hydrolyzing]
Niben101Scf00573g01003	UP	Asparagine synthetase [glutamine-hydrolyzing]
Niben101Scf01719g08001	UP	Pleiotropic drug resistance protein 1
Niben101Scf06583g03009	UP	Pleiotropic drug resistance protein 1
Niben101Scf03619g05002	UP	Polyphenol oxidase E, chloroplastic
Niben101Scf07069g01004	UP	Calmodulin-binding protein 60 B
Niben101Scf06222g01010	UP	Calmodulin-binding protein 60 C
Niben101Scf01934g02004	UP	Glucan endo-1,3-beta-glucosidase, basic vacuolar isoform GLB
Niben101Scf02349g03001	UP	Suberization-associated anionic peroxidase
Niben101Scf07253g02020	UP	Probable polyamine oxidase 4
Niben101Scf03307g06003	UP	Inositol oxygenase 2
Niben101Scf02581g04013	UP	Respiratory burst oxidase homolog protein C
Niben101Scf10575g02003	UP	Putative lipid-transfer protein DIR1
Niben101Scf09044g01015	UP	Osmotin-like protein
Niben101Scf05615g01004	DOWN	Cytochrome P450 CYP72A219
Niben101Scf00449g06008	DOWN	mediator of RNA polymerase II transcription subunit 37e
Niben101Scf06684g01005	DOWN	Heat shock protein 83
Niben101Scf01084g05013	DOWN	Protein of unknown function

Table S9. Shared DEGs between the P35S_B and PB_B lines.

Gene ID	Gene Expression	Annotation
Niben101Scf02363g00015	UP	Beta-galactosidase
Niben101Scf10213g00009	UP	Beta-galactosidase
Niben101Scf03253g02010	UP	Glutamine--fructose-6-phosphate aminotransferase
Niben101Scf03015g06014	UP	Ribulose biphosphate carboxylase small chain 8B, chloroplastic
Niben101Scf02658g00012	UP	SKP1-like protein 1A
Niben101Ctg13782g00003	UP	Probable xyloglucan endotransglucosylase/hydrolase protein 23
Niben101Scf00109g03008	UP	Glycerophosphodiester phosphodiesterase GDPD2
Niben101Scf03326g01009	UP	Cellulose synthase-like protein D3
Niben101Scf04634g00004	UP	Cellulose synthase A catalytic subunit 6 [UDP-forming]
Niben101Scf03913g01045	UP	Expansin-like A2
Niben101Scf08047g01012	UP	Expansin-like A1
Niben101Scf00573g01003	UP	Asparagine synthetase [glutamine-hydrolyzing]
Niben101Scf11860g00013	UP	Asparagine synthetase [glutamine-hydrolyzing]
Niben101Scf02738g01016	UP	Proline dehydrogenase 2, mitochondrial
Niben101Scf03307g06003	UP	Inositol oxygenase 2
Niben101Scf16156g00005	UP	L-ascorbate oxidase homolog
Niben101Scf15666g00009	UP	Ribosome-binding factor PSRP1, chloroplastic
Niben101Scf03822g00010	UP	Protein EXORDIUM-like 5
Niben101Scf10763g00008	UP	Stem-specific protein TSJT1
Niben101Scf04024g02024	DOWN	MATE efflux family protein 7
Niben101Scf00887g02002	DOWN	Protein REVEILLE 7
Niben101Scf01685g09002	DOWN	Calcium-binding protein PBP1
Niben101Scf05522g00002	DOWN	Calcium-binding protein PBP1
Niben101Scf00799g00011	DOWN	NAC domain-containing protein 2
Niben101Scf03028g01011	DOWN	NAC domain-containing protein 2

Niben101Scf00802g00005	DOWN	U-box domain-containing protein 19
Niben101Scf04296g00008	DOWN	U-box domain-containing protein 19
Niben101Scf00163g22002	DOWN	Ethylene-responsive transcription factor 5
Niben101Scf00163g22004	DOWN	Ethylene-responsive transcription factor 5
Niben101Scf00454g03001	DOWN	Ethylene-responsive transcription factor 5
Niben101Scf00846g02001	DOWN	Ethylene-responsive transcription factor RAP2-13
Niben101Scf01752g05003	DOWN	Ethylene-responsive transcription factor 3
Niben101Scf23241g00003	DOWN	Ethylene-responsive transcription factor 5
Niben101Scf08546g03002	DOWN	Ethylene-responsive transcription factor 5
Niben101Scf02362g02014	DOWN	Probable WRKY transcription factor 33
Niben101Scf02430g03006	DOWN	Probable WRKY transcription factor 33
Niben101Scf06822g04004	DOWN	Transcription factor MYC2
Niben101Scf15224g00002	DOWN	Transcription factor MYC2
Niben101Ctg12683g0000 1	DOWN	Zinc finger CCCH domain-containing protein 29
Niben101Scf02286g01005	DOWN	Zinc finger CCCH domain-containing protein 29
Niben101Scf12797g00017	DOWN	Zinc finger CCCH domain-containing protein 29
Niben101Scf00080g05006	DOWN	Zinc finger protein ZAT10
Niben101Scf00449g06008	DOWN	Heat shock protein 70
Niben101Scf12868g00008	DOWN	Heat shock cognate 70 kDa protein 2
Niben101Scf06684g01005	DOWN	Heat shock protein 83
Niben101Scf04867g00001	DOWN	Scarecrow-like protein 14
Niben101Scf06996g02005	DOWN	Scarecrow-like protein 11
Niben101Scf08041g02010	DOWN	E3 ubiquitin-protein ligase RING1
Niben101Scf09678g00006	DOWN	Serine/arginine-rich splicing factor SR45a
Niben101Scf01750g15003	DOWN	Probable CCR4-associated factor 1 homolog 11
Niben101Scf10855g08005	DOWN	Probable CCR4-associated factor 1 homolog 11
Niben101Scf00611g09003	DOWN	Putative nuclease HARBI1
Niben101Scf34484g00001	DOWN	Putative nuclease HARBI1
Niben101Scf05756g00005	DOWN	Putative nuclease HARBI1
Niben101Scf01109g03004	DOWN	Putative nuclease HARBI1
Niben101Scf19533g00007	DOWN	Protein kinase 2B, chloroplastic
Niben101Scf02303g00022	DOWN	Exocyst complex component EXO70A1
Niben101Scf11689g03003	DOWN	BTB/POZ domain-containing protein At5g41330
Niben101Scf00712g16028	UP	BTB/POZ domain-containing protein
Niben101Scf08804g02014	DOWN	Nudix hydrolase 17, mitochondrial
Niben101Scf09225g04002	DOWN	Beta-D-glucosyl crocetin beta-1,6-glucosyltransferase
Niben101Scf00573g00010	DOWN	Probable protein phosphatase 2C 2
Niben101Scf07040g00001	UP	Probable protein phosphatase 2C 5

Niben101Scf06383g01007	UP	Probable protein phosphatase 2C 5
Niben101Scf01109g03005	DOWN	Protein of unknown function

Table S10. Significant GO enrichment pathways of the genetically modified (GM) *N. benthamiana* lines.

Comparison group	GO pathway	GO ID	Gene Number	Corrected P-value
P35S_A vs WT	carbohydrate metabolic process	GO:0005975	13	0.027126
	oxidoreductase activity, acting on peroxide as acceptor	GO:0016684	5	0.034676
PA_A vs WT	structural constituent of cell wall	GO:0005199	6	8.70E-07
	plant-type cell wall organization	GO:0009664	6	1.22E-05
	plant-type cell wall organization or biogenesis	GO:0071669	6	1.22E-05
	cellular glucan metabolic process	GO:0006073	7	0.0013551
	glucan metabolic process	GO:0044042	7	0.0013551
	cell wall organization	GO:0071555	6	0.0046685
	carbohydrate metabolic process	GO:0005975	19	0.0046685
	external encapsulating structure organization	GO:0045229	6	0.0058503
	cellular carbohydrate metabolic process	GO:0044262	11	0.0094167
	cellulose synthase activity	GO:0016759	4	0.020978
	cellulose synthase (UDP-forming) activity	GO:0016760	4	0.020978
	cell wall organization or biogenesis	GO:0071554	6	0.032003
	transferase activity, transferring hexosyl groups	GO:0016758	9	0.03418
	cellulose biosynthetic process	GO:0030244	4	0.03418
	cellulose metabolic process	GO:0030243	4	0.036399
	cellular polysaccharide metabolic process	GO:0044264	9	0.036399
PB_B vs WT	carbohydrate metabolic process	GO:0005975	29	0.00065519
PA_A vs P35S_A	structural constituent of cell wall	GO:0005199	3	0.00020834
	plant-type cell wall organization	GO:0009664	3	0.00036911
	plant-type cell wall organization or biogenesis	GO:0071669	3	0.00036911
	cell wall organization	GO:0071555	3	0.0091721
	external encapsulating structure organization	GO:0045229	3	0.0091721
	cell wall organization or biogenesis	GO:0071554	3	0.024512
PB_B vs P35S_B	structural constituent of cell wall	GO:0005199	3	0.0091491
	plant-type cell wall organization	GO:0009664	3	0.016974
	plant-type cell wall organization or biogenesis	GO:0071669	3	0.016974
PA_A vs PB_B	structural constituent of cell wall	GO:0005199	7	2.99E-12
	plant-type cell wall organization	GO:0009664	7	9.95E-09
	plant-type cell wall organization or biogenesis	GO:0071669	7	9.95E-09

cell wall organization	GO:0071555	7	5.44E-05
cell wall organization or biogenesis	GO:0071554	8	5.44E-05
external encapsulating structure organization	GO:0045229	7	5.86E-05
peroxidase activity	GO:0004601	6	0.0035078
oxidoreductase activity, acting on peroxide as acceptor	GO:0016684	6	0.0042536
hydrolase activity, hydrolyzing O-glycosyl compounds	GO:0004553	9	0.016781
antioxidant activity	GO:0016209	6	0.020492
hydrolase activity, acting on glycosyl bonds	GO:0016798	9	0.022597
response to oxidative stress	GO:0006979	5	0.022628
beta-galactosidase complex	GO:0009341	3	0.02616
beta-galactosidase activity	GO:0004565	3	0.02616
galactosidase activity	GO:0015925	3	0.02616

Table S11. Significant KEGG enrichment pathways of the GM *N. benthamiana* lines.

Comparison Group	KEGG Pathway	KEGG ID	Gene Number	Corrected P-value
P35S_A vs WT	Alanine, aspartate and glutamate metabolism	sly00250	4	0.00130653
P35S_B vs WT	Alanine, aspartate and glutamate metabolism	sly00250	3	0.03924253
PA_A vs WT	Alanine, aspartate and glutamate metabolism	sly00250	4	0.01021507
PA_A vs PB_B	Glutathione metabolism	sly00480	6	0.00200214
	Alanine, aspartate and glutamate metabolism	sly00250	4	0.00477255
	Phenylalanine metabolism	sly00360	5	0.02537974
	Biosynthesis of secondary metabolites	sly01110	14	0.03550397
	Phenylpropanoid biosynthesis	sly00940	5	0.0378198