Supplemental Table S1. Significant GO terms enriched for the upregulated genes and for the downregulated genes by Al in SL cells under shaking condition. Using microarray data (**Supplemental Data Set 1**), the differentially expressed genes ($P < 0.05$) with changes of at least 2-fold under Al treatment over control in cells under shaking condition were assessed by GO enrichment analysis using AgriGO v2.0. The brief summary of the results is described in a box indicating the number of significant GO terms enriched for the upregulated genes (A) and the downregulated genes (B), respectively. The detailed information of each significant GO term is shown in this Table, including GO term, ontology (GO category, namely, biological process [P], molecular function [F], and cellular components [C]), description, the item number mapping the GO term in the query list and back ground, *p*-value, and FDR (false discovery rate). The GO term in this Table is ranked according to its FDR value. The GO terms localized at the bottom of the hierarchical network of these significant GO terms (see **Supplemental Fig. S1**) are highlighted in red, yellow, and green color for the P, F, and C category, respectively.

A

Species: *Nicotiana tabacum*
Genes: Upregulated by Al
GO type: Completed GO
Background/Reference: Agilent tobacco Genome Array (blast)
Annotated number in query list: 308
Annotated number in background/reference: 19042
Significant GO terms: 1

GO term	Ontology	Description	Number in input list	Number in BG/Ref	p-value	FDR
GO:0010200	P	response to chitin	11	118	7E-06	0.0056

B

Species: *Nicotiana tabacum*
Genes: Downregulated by Al
GO type: Completed GO
Background/Reference: Agilent tobacco Genome Array (blast)
Annotated number in query list: 497
Annotated number in background/reference: 19042
Significant GO terms: 15

GO term	Ontology	Description	Number in input list	Number in BG/Ref	p-value	FDR
GO:0010876	P	lipid localization	13	108	1.3E-05	0.0053
GO:0042547	P	cell wall modification during multidimensional cell growth	6	17	1.8E-05	0.0053
GO:0006869	P	lipid transport	13	104	8.9E-06	0.0053
GO:0009831	P	plant-type cell wall modification during multidimensional cell growth	6	16	1.4E-05	0.0053
GO:0009828	P	plant-type cell wall loosening	7	26	1.6E-05	0.0053
GO:0009827	P	plant-type cell wall modification	7	29	2.9E-05	0.007
GO:0006949	P	syncytium formation	5	12	0.00005	0.01
GO:0009664	P	plant-type cell wall organization	8	53	0.00015	0.024
GO:0009825	P	multidimensional cell growth	7	39	0.00015	0.024
GO:0005372	F	water transmembrane transporter activity	12	45	1.6E-08	0.0000039
GO:0015250	F	water channel activity	12	45	1.6E-08	0.0000039
GO:0015267	F	channel activity	14	129	1.8E-05	0.0017
GO:0022803	F	passive transmembrane transporter activity	14	129	1.8E-05	0.0017
GO:0022838	F	substrate-specific channel activity	14	127	1.5E-05	0.0017
GO:0012505	C	endomembrane system	59	1214	5.7E-06	0.0018

Supplemental Table S2. List of the genes annotated to the GO terms localized at the bottoms of hierarchical network of the GO terms significantly enriched for up- and down-regulated genes by Al in SL cells under shaking condition. The genes listed in (A) are the upregulated genes annotated to one GO term (response to chitin) of biological process (P) category. The genes listed in (B) are the downregulated genes annotated to four GO terms (plant-type cell wall loosening, plant-type cell wall modification during multidimensional cell growth, syncytium formation, lipid transport) of the P category, one GO term (water channel activity) of molecular function (F) category, and one GO term (endomembrane system) of cellular component (C) category. These GO terms were localized at the bottoms of the hierarchical network shown in **Supplemental Fig. S1**.

A Upregulated genes by Al

Biological process (**P**)

GO Accession: GO:0010200
Ontology: Biological Process
Description: response to chitin
Annotated/Total number in query list: 11/308
Annotated/Total number in background/reference: 118/19042

Name	**Description (Direct description or transfer from target)**	**Description (Agilent)**
A_95_P195572	ethylene responsive element binding factor 1 (ERF-1);	KL4B.101B01F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101B01, mRNA sequence [DV999109]
A_95_P032377	myb domain protein 15 (MYB15);	Nicotiana tabacum mRNA for myb-related transcription factor LBM2, complete cds [AB028650]
A_95_P087498	GRAS family transcription factor;	---
A_95_P004626	---	Nicotiana tabacum mRNA for WIPK, complete cds [D61377]
A_95_P006976	ethylene responsive element binding factor 1 (ERF-1);	Rep: Ethylene-responsive transcription factor 1 - Nicotiana tabacum (Common tobacco), complete [TC126973]
A_95_P162752	RESPONSIVE TO HIGH LIGHT 41 (RHL41); FUNCTIONS IN: sequence-specific DNA binding transcription factor activity, zinc ion binding, nucleic acid binding;	---
A_95_P269586	XERICO;	KF8C.103J07F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103J07, mRNA sequence [EB425527]
A_95_P312788	ethylene responsive element binding factor 2 (ERF2);	AGN_RNC108xf03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence [FG152342]
A_95_P161782	WRKY6;	Rep: WRKY protein - Solanum tuberosum (Potato), partial (23%) [TC132550]
A_95_P217077	heat shock transcription factor A4A (HSF A4A); FUNCTIONS IN: DNA binding, sequence-specific DNA binding transcription factor activity;	Nicotiana tabacum NtHSF2 mRNA for heat shock factor, complete cds [AB014484]
A_95_P082790	salt tolerance zinc finger (STZ);	Nicotiana tabacum osmotic stress-induced zinc-finger protein (zfp) mRNA, complete cds [AF053077]

B Downregulated genes by Al

Biological process (**P**)

GO Accession: GO:0009828
Ontology: Biological Process
Description: plant-type cell wall loosening
Annotated/Total number in query list: 7/497
Annotated/Total number in background/reference: 26/19042

Name	Description (Direct description or transfer from target)	Description (Agilent)
A_95_P188767	expansin A15 (EXPA15);	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA4) mRNA, complete cds [AF049353]
A_95_P032706	---	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA6) mRNA, partial cds [AF049355]
A_95_P032701	expansin 11 (EXPA11);	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA2) mRNA, complete cds [AF049351]
A_95_P188762	expansin A1 (EXPA1);	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA4) mRNA, complete cds [AF049353]
A_95_P020386	expansin 11 (EXPA11);	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA3) mRNA, complete cds [AF049352]
A_95_P172341	---	---
A_95_P011017	expansin A8 (EXPA8);	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA5) mRNA, partial cds [AF049354]

GO Accession: GO:0009831
Ontology: Biological Process
Description: plant-type cell wall modification during multidimensional cell growth
Annotated/Total number in query list: 6/497
Annotated/Total number in background/reference: 16/19042

Name	Description (Direct description or transfer from target)	Description (Agilent)
A_95_P188767	expansin A15 (EXPA15);	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA4) mRNA, complete cds [AF049353]
A_95_P032706	---	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA6) mRNA, partial cds [AF049355]
A_95_P032701	expansin 11 (EXPA11);	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA2) mRNA, complete cds [AF049351]
A_95_P020386	expansin 11 (EXPA11);	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA3) mRNA, complete cds [AF049352]
A_95_P172341	---	---
A_95_P011017	expansin A8 (EXPA8);	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA5) mRNA, partial cds [AF049354]

GO Accession: GO:0006949
Ontology: Biological Process
Description: syncytium formation
Annotated/Total number in query list: 5/497
Annotated/Total number in background/reference: 12/19042

Name	Description (Direct description or transfer from target)	Description (Agilent)
A_95_P011017	expansin A8 (EXPA8);	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA5) mRNA, partial cds [AF049354]
A_95_P188767	expansin A15 (EXPA15);	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA4) mRNA, complete cds [AF049353]
A_95_P032706	---	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA6) mRNA, partial cds [AF049355]
A_95_P188762	expansin A1 (EXPA1);	Nicotiana tabacum alpha-expansin precursor (Nt-EXPA4) mRNA, complete cds [AF049353]
A_95_P172341	---	---

GO Accession: GO:0006869
Ontology: Biological Process
Description: lipid transport
Annotated/Total number in query list: 13/497
Annotated/Total number in background/reference: 104/19042

Name	Description (Direct description or transfer from target)	Description (Agilent)
A_95_P102367	---	---
A_95_P004391	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein; FUNCTIONS IN: lipid binding;	CHO_SL015xl15f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH618856]
A_95_P205197	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein; FUNCTIONS IN: lipid binding;	KG9B.102L12F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102L12, mRNA sequence [EB677782]
A_95_P238389	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein; FUNCTIONS IN: lipid binding;	Nicotiana tabacum mRNA for P-rich protein EIG-I30, complete cds [AB041516]
A_95_P027676	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein; FUNCTIONS IN: lipid binding;	Rep: Hairy root 4 - Nicotiana tabacum (Common tobacco), partial (46%) [TC161742]
A_95_P107092	lipid transfer protein 1 (LP1); FUNCTIONS IN: calmodulin binding;	KL4B.109E17F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.109E17, mRNA sequence [DW000894]
A_95_P112022	---	CHO_SL015xl15f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH618856]
A_95_P113567	---	KR3B.101B06F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101B06, mRNA sequence [DW001775]
A_95_P034953	---	---
A_95_P109177	---	24B11 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', mRNA sequence [EH665607]
A_95_P189947	cell wall-plasma membrane linker protein (CWLP); FUNCTIONS IN: lipid binding;	Rep: 36.4 kDa proline-rich protein - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), partial (83%) [TC125764]
A_95_P000541	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein; FUNCTIONS IN: lipid binding;	TT-17_C07 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [FG636567]
A_95_P094703	---	Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vinifera (Grape), partial (9%) [TC159954]

Molecular function (**F**)

GO Accession: GO:0015250
Ontology: Molecular Function
Description: water channel activity
Annotated/Total number in query list: 12/497
Annotated/Total number in background/reference: 45/19042

Name	Description (Direct description or transfer from target)	Description (Agilent)
A_95_P283478	gamma tonoplast intrinsic protein (GAMMA-TIP); FUNCTIONS IN: water channel activity, urea transmembrane transporter activity;	N.tabacum mRNA for aquaporin 1 [Y08161]
A_95_P008181	tonoplast intrinsic protein 4;1 (TIP4;1); FUNCTIONS IN: water channel activity;	KL4B.104L20F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104L20, mRNA sequence [DW000053]
A_95_P007681	plasma membrane intrinsic protein 1C (PIP1C); FUNCTIONS IN: water channel activity;	Rep: Water channel protein - Nicotiana excelsior, complete [TC122983]
A_95_P126547	small and basic intrinsic protein 1A (SIP1A); FUNCTIONS IN: water channel activity;	KT7C.109N01F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109N01, mRNA sequence [EB451173]
A_95_P176972	plasma membrane intrinsic protein 1;4 (PIP1;4); FUNCTIONS IN: water channel activity;	FTP P15 Tobacco stigma cDNA Nicotiana tabacum cDNA similar to PIP1 aquaporin, mRNA sequence [CK720598]
A_95_P259616	RESPONSIVE TO DESICCATION 28 (RD28); FUNCTIONS IN: water channel activity;	---
A_95_P258766	plasma membrane intrinsic protein 1;4 (PIP1;4); FUNCTIONS IN: water channel activity;	KL4B.101O20F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101O20, mRNA sequence [DV999402]
A_95_P156997	plasma membrane intrinsic protein 1;4 (PIP1;4); FUNCTIONS IN: water channel activity;	---
A_95_P245117	plasma membrane intrinsic protein 1;4 (PIP1;4); FUNCTIONS IN: water channel activity;	KL4B.101O20F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101O20, mRNA sequence [DV999402]
A_95_P004971	gamma tonoplast intrinsic protein (GAMMA-TIP); FUNCTIONS IN: water channel activity, urea transmembrane transporter activity;	30F11 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', mRNA sequence [EH666154]
A_95_P144372	NOD26-like intrinsic protein 6;1 (NIP6;1);	KN6B.104B19F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104B19, mRNA sequence [EB439651]
A_95_P120157	---	---

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Cellular component (**C**)

GO Accession: GO:0012505
Ontology: Cellular Component
Description: endomembrane system
Annotated/Total number in query list: 59/497
Annotated/Total number in background/reference: 1214/19042

Name	Description (Direct description or transfer from target)	Description (Agilent)
A_95_P108772	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein; FUNCTIONS IN: molecular_function unknown;	---
A_95_P137142	Leucine-rich repeat (LRR) family protein;	KG9B.001F01F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001F01, mRNA sequence [DV157586]
A_95_P000796	TRANSPARENT TESTA 5 (TT5); FUNCTIONS IN: chalcone isomerase activity;	Nicotiana tabacum NtCHI1 mRNA for chalcone isomerase, complete cds [AB213651]
A_95_P254189	glycine-rich protein; FUNCTIONS IN: molecular_function unknown;	TT-27_C04 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG634819]
A_95_P139162	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein; FUNCTIONS IN: molecular_function unknown;	AGN_RPC015xi06f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence [FG144494]
A_95_P113277	Plant invertase/pectin methylesterase inhibitor superfamily protein; FUNCTIONS IN: enzyme inhibitor activity, pectinesterase inhibitor activity, pectinesterase activity;	---
A_95_P304168	unknown protein; FUNCTIONS IN: molecular_function unknown;	TT-21_P08 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG635257]
A_95_P247352	Phosphorylase superfamily protein; FUNCTIONS IN: catalytic activity;	KF8C.102I03F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102I03, mRNA sequence [EB425144]
A_95_P143147	Peroxidase superfamily protein; FUNCTIONS IN: peroxidase activity, heme binding;	KR2B.111L22F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.111L22, mRNA sequence [EB446486]
A_95_P001511	Gibberellin-regulated family protein;	Rep: RSI-1 protein precursor - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), partial (71%) [TC148460]
A_95_P128932	Concanavalin A-like lectin family protein; FUNCTIONS IN: carbohydrate binding, binding;	KF8B.202A20F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202A20, mRNA sequence [EB428698]
A_95_P107642	Protein of Unknown Function (DUF239);	KL4B.105E16F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105E16, mRNA sequence [DW000251]
A_95_P230364	FUNCTIONS IN: molecular_function unknown;	AGN_RPC017xe04f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence [FG143913]
A_95_P029251	Eukaryotic aspartyl protease family protein; FUNCTIONS IN: aspartic-type endopeptidase activity;	Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinifera (Grape), partial (63%) [TC137694]
A_95_P162182	Galactose mutarotase-like superfamily protein; FUNCTIONS IN: aldose 1-epimerase activity;	Rep: Aldose-1-epimerase-like protein - Nicotiana tabacum (Common tobacco), partial (65%) [TC164921]
A_95_P263216	Protein of Unknown Function (DUF239);	---
A_95_P205197	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein; FUNCTIONS IN: lipid binding;	KG9B.102L12F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102L12, mRNA sequence [EB677782]
A_95_P060695	Serine carboxypeptidase S28 family protein; FUNCTIONS IN: serine-type peptidase activity, peptidase activity;	---
A_95_P289943	alpha/beta-Hydrolases superfamily protein; FUNCTIONS IN: molecular_function unknown;	KP1B.108B22F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108B22, mRNA sequence [DV161443]
A_95_P188587	unknown seed protein like 1 (USPL1);	KF8C.102I24F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102I24, mRNA sequence [EB425160]
A_95_P128467	unknown protein; FUNCTIONS IN: molecular_function unknown;	KF8B.200G11F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200G11, mRNA sequence [EB428169]
A_95_P269786	EamA-like transporter family; FUNCTIONS IN: molecular_function unknown;	KF8C.106O13F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106O13, mRNA sequence [EB426716]
A_95_P163272	Leucine-rich repeat (LRR) family protein;	Rep: Chromosome chr3 scaffold_117, whole genome shotgun sequence - Vitis vinifera (Grape), partial (93%) [TC149187]
A_95_P190262	Subtilase family protein; FUNCTIONS IN: identical protein binding, serine-type endopeptidase activity;	KP1B.001C18F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001C18, mRNA sequence [DV162456]
A_95_P148302	RAN GTPase activating protein 2 (RANGAP2); FUNCTIONS IN: RAN GTPase activator activity;	Rep: RAN GTPase-activating protein 2 - Nicotiana benthamiana, complete [TC130291]
A_95_P004391	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein; FUNCTIONS IN: lipid binding;	CHO_SL015xl15f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH618856]
A_95_P009621	Leucine-rich repeat (LRR) family protein;	Rep: Chromosome chr3 scaffold_117, whole genome shotgun sequence - Vitis vinifera (Grape), partial (98%) [TC162010]
A_95_P119752	Pollen Ole e 1 allergen and extensin family protein; FUNCTIONS IN: molecular_function unknown;	Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vinifera (Grape), partial (84%) [TC139301]
A_95_P135282	Protein of Unknown Function (DUF239);	KN6B.101F20F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101F20, mRNA sequence [EB438655]
A_95_P135812	GDSL-like Lipase/Acylhydrolase superfamily protein; FUNCTIONS IN: hydrolase activity, acting on ester bonds, carboxylesterase activity;	Rep: BYJ15 - Nicotiana tabacum (Common tobacco), partial (91%) [TC142053]
A_95_P200987	Leucine-rich repeat (LRR) family protein;	KG9B.102E01F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102E01, mRNA sequence [EB677609]
A_95_P238389	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein; FUNCTIONS IN: lipid binding;	Nicotiana tabacum mRNA for P-rich protein EIG-I30, complete cds [AB041516]
A_95_P026031	xyloglucan endotransglucosylase/hydrolase 8 (XTH8); FUNCTIONS IN: hydrolase activity, acting on glycosyl bonds, xyloglucan:xyloglucosyl transferase activity, hydrolase activity, hydrolyzing O-glycosyl compounds;	KT7C.110J14F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110J14, mRNA sequence [EB451452]
A_95_P289433	---	KP1B.037C22F.050623T7 KP1B Nicotiana tabacum cDNA clone KP1B.037C22, mRNA sequence [DV159365]
A_95_P155982	---	Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vinifera (Grape), partial (37%) [TC136070]
A_95_P293763	---	BL12.104O01F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.104O01, mRNA sequence [EB437533]
A_95_P000541	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein; FUNCTIONS IN: lipid binding;	TT-17_C07 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [FG636567]
A_95_P146657	---	---
A_95_P281888	Glycosyltransferase family 29 (sialyltransferase) family protein; FUNCTIONS IN: sialyltransferase activity;	AM826065 seedling library, SL Nicotiana tabacum cDNA clone nt002243079, mRNA sequence [AM826065]
A_95_P190152	Carbohydrate-binding X8 domain superfamily protein; FUNCTIONS IN: molecular_function unknown;	TOBESTR062H06 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA sequence [FG626648]
A_95_P230954	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein; FUNCTIONS IN: molecular_function unknown;	CHO_SL024xf07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH622610]
A_95_P081895	GDSL-like Lipase/Acylhydrolase superfamily protein; FUNCTIONS IN: hydrolase activity, acting on ester bonds, carboxylesterase activity;	Rep: BYJ15 - Nicotiana tabacum (Common tobacco), partial (87%) [TC145798]
A_95_P141422	---	Rep: Chromosome undetermined scaffold_484, whole genome shotgun sequence - Vitis vinifera (Grape), partial (84%) [TC166366]
A_95_P228959	---	KP1B.107B02F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107B02, mRNA sequence [DV161085]
A_95_P027676	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein; FUNCTIONS IN: lipid binding;	Rep: Hairy root 4 - Nicotiana tabacum (Common tobacco), partial (46%) [TC161742]
A_95_P295188	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein; FUNCTIONS IN: molecular_function unknown;	AGN_PNL230bf1_e7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA sequence [FG200595]
A_95_P124987	unknown protein; FUNCTIONS IN: molecular_function unknown;	KR3B.109L01F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109L01, mRNA sequence [DW004773]
A_95_P186277	Pollen Ole e 1 allergen and extensin family protein; FUNCTIONS IN: molecular_function unknown;	KG9B.001I14F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001I14, mRNA sequence [DV157668]
A_95_P284098	---	Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vinifera (Grape), partial (52%) [TC165388]
A_95_P302013	Peroxidase superfamily protein; FUNCTIONS IN: peroxidase activity, heme binding;	TT-40_M13 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG640485]
A_95_P142412	---	Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vinifera (Grape), partial (35%) [TC141121]
A_95_P302493	GDSL-like Lipase/Acylhydrolase superfamily protein; FUNCTIONS IN: hydrolase activity, acting on ester bonds, carboxylesterase activity;	AGN_PNL209df1_a1.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA sequence [FG185597]
A_95_P102072	FAD-binding Berberine family protein; FUNCTIONS IN: electron carrier activity, oxidoreductase activity, FAD binding, catalytic activity;	Rep: Chromosome chr10 scaffold_50, whole genome shotgun sequence - Vitis vinifera (Grape), partial (69%) [TC131374]
A_95_P144842	PIN-FORMED 3 (PIN3); FUNCTIONS IN: auxin:hydrogen symporter activity, transporter activity;	Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinifera (Grape), partial (86%) [TC155446]
A_95_P142557	Protein of Unknown Function (DUF239);	Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinifera (Grape), partial (96%) [TC131482]
A_95_P207927	TRICHOME BIREFRINGENCE-LIKE 36 (TBL36);	KT7C.110N20F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110N20, mRNA sequence [EB451538]
A_95_P230614	Domain of unknown function (DUF303) ; FUNCTIONS IN: molecular_function unknown;	KF8C.104O14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104O14, mRNA sequence [EB425998]
A_95_P220957	Peroxidase superfamily protein; FUNCTIONS IN: peroxidase activity, heme binding;	KT7C.104O02F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104O02, mRNA sequence [EB449799]
A_95_P308028	Protein of Unknown Function (DUF239);	---

Supplemental Table S3. Primer sequences used for real-time RT-PCR analysis. The primer sets were designed based on the sequence information available on the NCBI site: Gene (https://www.ncbi.nlm.nih.gov/gene) and/or GenBank (https://www.ncbi.nlm.nih.gov/genbank). Some genes (*NtMYB3, NtEXPA4, NtEIG-C29, NtLTP3*) share a part of their sequence with their homologous or orthologous genes. In this case, the primer sets specific to these genes were designed based on the information described in references (*NtMYB3* [Sugimoto et al., 2000], *NtEXPA4* [Link and Cosgrove, 1998]) or in footnotes of this Table *(NtEIG-C29, NtLTP3)*. The sequence information of all the genes listed in this Table was reported to be determined by sequencing of cloned cDNAs, except for the *PDHK* sequence which was the Transcriptome Shotgun Assembly (TAS) sequence.

Gene name (Gene description)	Gene accession	Primer sequences (5' to 3')	Reference for sequences
NtMYB3 **(myb-related transcription factor*)*** **(formerly called *LBM2*)**	**AB028650**	**F ATGCGGGAAAAGTTGCAGAC** **R CCTTGGAATCATGATTTTTGGAGTGTC**	**This paper**
NtERF1 **(ethylene-responsive transcription factor 1)**	**D38123**	**F GGTTTGGCTTGGAACATACGA** **R GCCTTTCTTCTCCGTTTAGGTG**	**Tsuchiya et al. 2021**
WIPK **(wound-induced protein kinase)** **(mitogen-activated protein kinase 3-like)**	**D61377**	**F ATGTTTGGTCTGTCGGTTGC** **R TGCCAAGAAGCTCGGTTAAC**	**This paper**
NtEXPA4 **(α-expansin4)**	**AF049353**	**F GGCTCACACTCCAAAGAACATG** **R ATCCAACCTCCTCCACCATAAC**	**This paper**
NtEIG-C29 **(elicitor-inducible gene-C29)** **(14 kDa proline-rich protein DC2.15-like)**	**AB041519**	**F GCCCAAGTCCTAAACCAAAACC** **R GGTCAGCAACACCTTGAATGAG**	**This paper**
NtLTP3 **(non-specific lipid-transfer protein 2)**	**D13952**	**F ACAGACTGCTCTAAGGTCCAG** **R TGCACTACTGCCAAAGAGTG**	**This paper**
SUSY **(sucrose synthase)**	**AB055497**	**F CATAGCTCATGCGTTGGAGA** **R CCTGGAAAGTGCTGGTGATT**	**Tsuchiya et al. 2021**
LDH **(L-lactate dehydrogenase B-like)**	**KJ874422**	**F GATTCACCCTGTCTCAGTCCTC** **R TCACACCCAAAACTCCACTTC**	**Tsuchiya et al. 2021**
PDC1 **(pyruvate decarboxylase 1)**	**X81854**	**F AGTGTTGTGATTGCTGAGACG** **R TGTGCGTAACCAAGAGTTGC**	**Tsuchiya et al. 2021**
ADH1 **(alcohol dehydrogenase 1)**	**X81853**	**F TGGAGGTGTTGACCGAAGTG** **R CAGTTTTGGGCTTGTAGTTGC**	**Tsuchiya et al. 2021**
PDH_E1α **(pyruvate dehydrogenase E1 component subunit alpha, mitochondrial-like)**	**AB090281**	**F ATTGTTGGTGCTCAGGTTCC** **R GCTGTCCCCATTCCATAGTG**	**Tsuchiya et al. 2021**
PDHK **(pyruvate dehydrogenase [acetyl-transferring] kinase, mitochondrial-like)**	**XM_016621727**	**F TACAAAAATGTCCCCGTTGG** **R AAATCGCTCTTCCACAGCAC**	**Tsuchiya et al. 2021**
Actin9 **(actin)**	**X69885** **(GenBank)**	**F CTATTCTCCGCTTTGGACTTGGCA** **R AGGACCTCAGGACAACGGAAACG**	**Volkov et al. 2003**

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Footnotes

Sequence information of *NtEIG-C29* and *NtLTP3* genes. These genes are also listed in **Table 1B**. Regarding the sequence information, *NtEIG-C29* cDNA was provided with two accession IDs, GenBank (EH618856) and UniGene (Nta. 2978) (**Supplemental Table S2B, Supplemental Data Set 1**). The UniGene ID (Nta. 2978) was given to *NtEIG-C29* mRNA sequence (GenBank ID, AB041519; shown in **Table 1B**) which was submitted with a reference (Takemoto et al., 2003). On the other hand, the nucleotide sequence of GenBank ID (EH618856) includes the *NtEIG-C29* mRNA sequence (AB041519) in it, and was submitted later without reference. Similarly, regarding the sequence information of *NtLTP3* cDNA, the probe A_95_107092 was provided with two accession IDs, GenBank (DW000894) and UniGene (Nta. 1247) (**Supplemental Table S2B, Supplemental Data Set 1**). The nucleotide sequence of the GenBank ID is the *N. tabacum* cDNA clone KL4B.109E17, while that of the UniGene ID is *NtLTP3* mRNA sequence (GenBank ID, D13952; shown in **Table 1B**) submitted as *TOBLTP* with a reference (Masuta et al., 1992). The whole sequences of these two cDNAs are different, but partly share identical region which includes the region corresponding to the 'non-specific LTP' function (from 162 to 434 bases of the *NtLTP3* mRNA sequence). Thus, although the cDNA clone KL4B.109E17 also seems to encode LTP or LTP-like protein, we analyzed the expression of *NtLTP3* in this study by performing RT-PCR using the *NtLTP3*-specific primers shown in this Table (**Supplemental Table S3**).