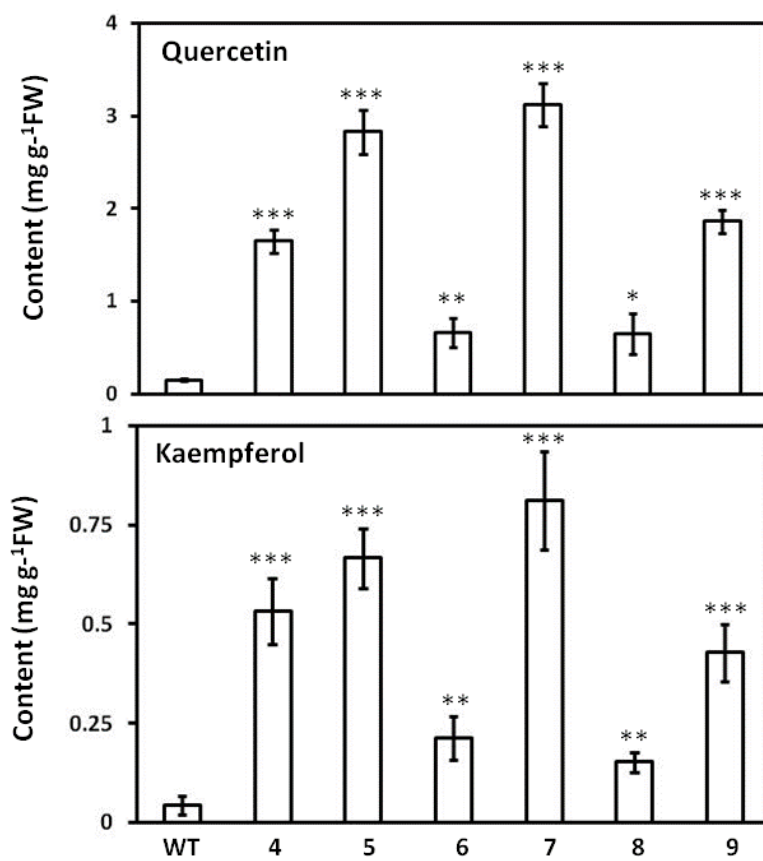
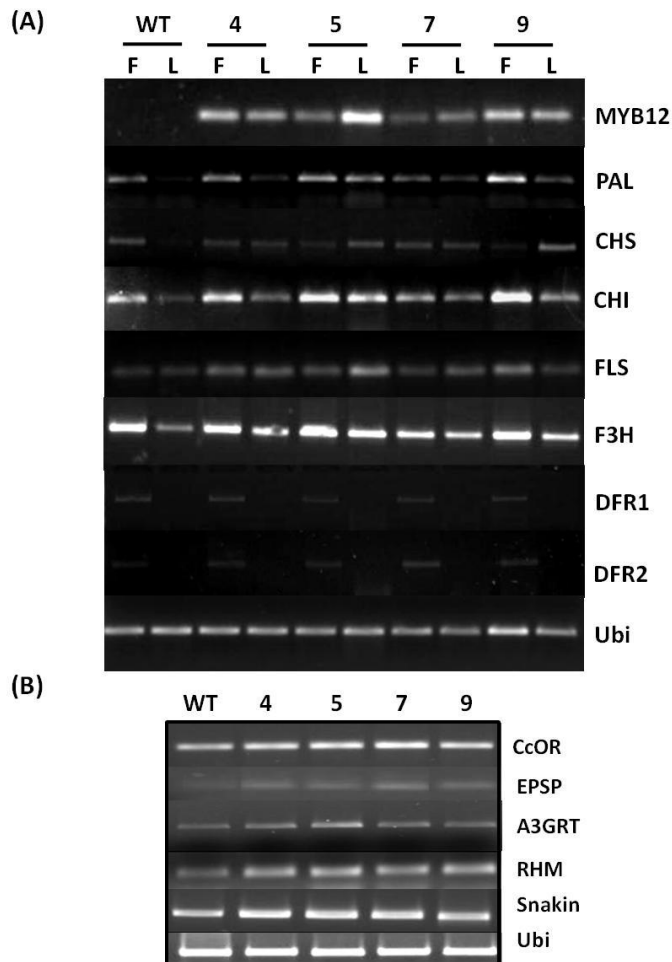


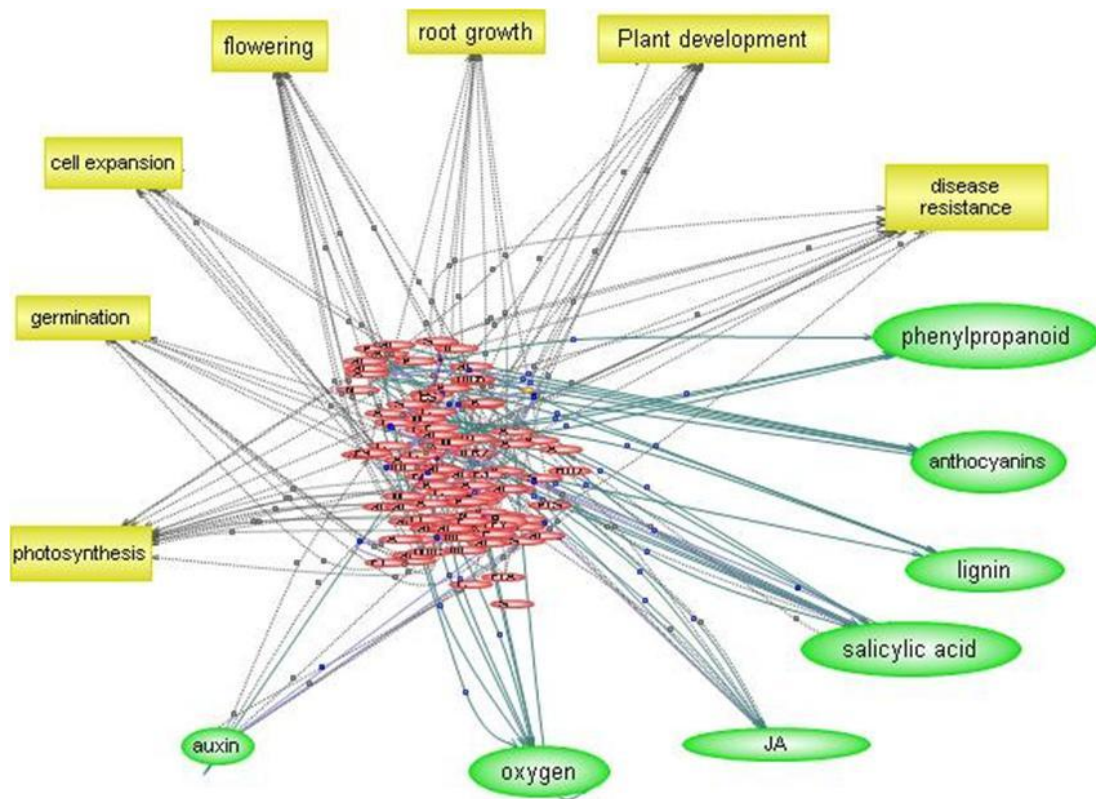
Supplementary Figure S1. Effect of *AtMYB12* expression on flower anthocyanin and leaf flavonoid content in transgenic tobacco lines (T4 to T9), as compared to control (WT).



Supplementary Figure S2. Effect of *AtMYB12* expression on leaf quercetin and kaempferol content in transgenic tobacco lines as compared to the control (WT). Analysis of the compounds was carried out after extraction by acid hydrolysis and quantification by HPLC.



Supplementary Figure S3. Semi-quantitative RTPCR analysis of genes up-regulated in *AtMYB12* expressing tobacco transgenic lines. Analysis was carried out for different genes involved in phenylpropanoid (A) and other pathways (B). MYB12, *AtMYB12*; PAL, Phenylalanine ammonia lyase; CHS, Chalcone synthase; CHI, Chalcone isomerase; FLS, Flavonol synthase; F3H, Flavonone-3-hydroxylase; DFR1, Dihydroflavonol 4-reductase 1; DFR2, Dihydroflavonol 4-reductase; CcOR, Cinnamoyl CoA reductase; EPSP, 5-enoylpyruvylshikimate-3-phosphate synthase; A3RT, Anthocyanin 3-O-glucoside rhamnosyltransferase; RHM, Rhamnose synthase; Snakin and Ubi, ubiquitin.



Supplementary Figure S4. Functional network predicted from the genes differentially regulated by *AtMYB12* in transgenic tobacco lines. *Arabidopsis* homologues of the differentially expressed genes in *AtMYB12* tobacco were identified to construct interactive network using Pathway Studio (Ariadne Genomics, USA).

Supplementary Table S1. List of up-regulated (\geq two-fold) genes in *AtMYB12*-expressing tobacco lines

Tobacco Accession No.	Putative annotation	TAIR locus id	Annotation in TAIR
EB427243	Anthocyanin 3-O-glucoside: rhamnosyltransferase [<i>Petunia hybrida</i>]	AT3G29630	Glycosyltransferase family protein; similar to glycosyltransferase family protein
EH622481	Basic beta-1,3-glucanase [<i>Nicotiana tabacum</i>]	AT4G16260	Glycosyl hydrolase family 17 protein; similar to BG1 (β -1,3-Glucanase 1),
AY061820	<i>Nicotiana tabacum</i> asparagine synthetase (din6) mRNA	AT5G65010	Asparagine biosynthetic process
BP129992	LBD37 (Lob Domain-Containing Protein 37)	AT5G67420	LBD37 (Lob domain containing protein)
EB425624	Chalcone synthase (<i>Solanum tuberosum</i>)	AT5G13930	Chalcone synthase
AY578143	<i>Nicotiana tabacum</i> 3-dehydroquinate dehydratase / shikimate dehydrogenase isoform 2 mRNA	AT3G06350	3-dehydroquinate dehydratase activity
BP533763	Unnamed protein product [<i>Vitis vinifera</i>]	AT4G10270	Wound-responsive protein, putative
EB432591	Snakin-2 (<i>Solanum tuberosum</i>)	AT1G75750	GASA5 (GAST1 protein homolog); similar to gibberellin-regulated family protein
BP134431	Hypothetical protein Paramecium	AT2G19806	Transposable element gene; Mariner-like transposase family,
DW001929	Phenylalanine ammonialyase 1 [<i>Petunia hybrida</i>]	AT2G37040	Encodes a protein similar to phenylalanine ammonia-lyase
EB431024	Flavanone 3-hydroxylase [<i>Nicotiana tabacum</i>]	AT3G51240	Encodes flavanone 3-hydroxylase
EB683796	PR protein; osmotin [<i>Nicotiana tabacum</i>]	AT4G11650	Osmotin-like protein
EH615405	Chalcone isomerase [<i>Nicotiana tabacum</i>]	AT5G05270	Chalcone-flavanone isomerase family protein
EB682906	Tonoplast intrinsic protein bobTIP26-2 [<i>Brassica oleracea</i>]	AT2G36830	Gamma tonoplast intrinsic protein
DV161807	RHM1 [<i>Arabidopsis thaliana</i>]	AT1G78570	RHM1 (Rhamnose biosynthesis 1); [<i>Arabidopsis thaliana</i>]
BP531184	Hypothetical protein BRAFLDRAFT_127937 [<i>Branchiostoma floridae</i>]	AT1G61610	S-locus lectin protein kinase family protein
BP526802	Hypothetical protein [<i>Vitis vinifera</i>]	AT1G42595	Transposable element gene; Mutator-like transposase family
EB678275	L-serine dehydratase, iron-sulfur-dependent, beta subunit [Dethiosulfovibrio peptidovorans DSM 11002]	AT3G22150	Pentatricopeptide (PPR) repeat-containing protein; similar to pentatricopeptide (PPR) repeat-containing protein
BP535514	Drm3-like protein [<i>Solanum tuberosum</i>]Auxin repressed	AT1G56220	Dormancy/auxin associated family protein; similar to dormancy/auxin associated protein-related
BP130879	EGL-Nine (EGLN) protein (ISS) [<i>Ostreococcus tauri</i>]	AT5G25190	Encodes a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family
EB427420	Unnamed protein product [<i>Vitis vinifera</i>]	AT4G16563	Aspartyl protease family protein; similar to aspartyl protease family protein
EB439864	Unnamed protein product [<i>Vitis vinifera</i>]	AT1G06550	Enoyl-CoA hydratase/isomerase family protein; similar to CHY1 (β -Hydroxyisobutryl-CoA Hydrolase 1)
Y07563	<i>N.tabacum</i> mRNA for hin1 gene	AT2G35460	Harpin-induced family protein / HINI family protein / harpin-responsive family protein
BP533176	No significant similarity found	AT3G09410	Pectinacetylerase family protein; similar to pectinacetylerase family protein
CV021144	Putative auxin-repressed protein [<i>Prunus armeniaca</i>]	AT1G56220	Dormancy/auxin associated family protein; similar to dormancy/auxin associated protein-related
EH620015	3-phosphoshikimate 1-carboxyvinyltransferase 1/ 5-	AT2G45300	Encodes 3-phosphoshikimate 1-carboxyvinyltransferase / 5-enolpyruvylshikimate-3-phosphate / EPSP synthase

	enolpyruvylshikimate-3-phosphate synthase		involved in chorismate biosynthesis
EH624008	Hypothetical protein [<i>Paramecium tetraurelia</i> strain d4-2]	AT5G10280	<i>AtMYB64</i> , <i>AtMYB92</i> , F18D22.50, F18D22_50
EB431117	No significant similarity found	AT5G03820	GDSL-motif lipase/hydrolase family protein; similar to carboxylesterase
EB443716	Thionin like protein [<i>Nicotiana tabacum</i>]	AT2G02130	Predicted to encode a PR (pathogenesis-related) protein. Belongs to the plant defensin
CN949753	Predicted protein [<i>Populus trichocarpa</i>]	AT1G49560	MYB family transcription factor,
EB442268	Hypothetical protein [<i>Vitis vinifera</i>]	AT1G48300	Unknown protein
EB450056	Unnamed protein product [<i>Vitis vinifera</i>]	AT2G46220	unknown protein
EB446913	Transaldolase [<i>Solanum tuberosum</i>]	AT5G13420	Transaldolase
EH615763	Cystatin-like protein [<i>Citrus paradisi</i>]	AT5G47550	Cysteine protease inhibitor, putative / cystatin, putative; Identical to cysteine proteinase inhibitor 5
CV016634	Predicted protein [<i>Populus trichocarpa</i>]	AT3G50770	Calmodulin-related protein, putative; Identical to Calmodulin-like protein 41 (CML41)
AB236952	Nicotiana tabacum C4H mRNA for trans-cinnamate 4-monooxygenase	AT2G30490	Cinnamate-4-hydroxylase
EB679296	Carboxylesterase [<i>Arabidopsis thaliana</i>]	AT5G45920	Carboxylesterase; similar to GDSL-motif lipase/hydrolase family protein
DW003994	Cinnamoyl CoA reductase [<i>Solanum tuberosum</i>]	AT1G80820	Cinnamoyl coA reductase
DW001734	Hypothetical protein [<i>Vitis vinifera</i>]	AT1G48300	Unknown protein
EB449778	Beta xylosidase [<i>Camellia sinensis</i>]	AT5G49360	Beta xylosidase 1
EH617140	Arginine decarboxylase [<i>Nicotiana tabacum</i>]	AT4G34710	encodes a arginine decarboxylase (ADC)
EB428594	Unnamed protein product [<i>Vitis vinifera</i>]	AT2G22250	Aspartate amino transferase
DV159582	Endo-xyloglucan transferase (EXGT) [<i>Nicotiana tabacum</i>]	AT5G13870	Endoxyloglucan transferase
EB449474	Hypothetical protein [<i>Vitis vinifera</i>]	AT2G17650	AMP-dependent synthetase and ligase family protein;
EB426371	DNAJ-like protein [<i>Solanum lycopersicum</i>]	AT2G17880	DNAJ heat shock protein
CN824871	SRC2-like protein [<i>Nicotiana benthamiana</i>]	AT1G09070	SRC2
EB679929	CYP84A14v1 [<i>Nicotiana tabacum</i>]	AT4G36220	Encodes ferulate 5-hydroxylase (F5H). Involved in lignin biosynthesis
EB677824	Unnamed protein product [<i>Vitis vinifera</i>]	AT5G08060	Unnamed protein product
BP128507	Conserved hypothetical protein [Bacteroides sp. D1]	AT1G05500	Synaptotagmin homolog
EH621485	Unnamed protein product [<i>Vitis vinifera</i>]	AT3G04140	Ankyrin repeat family protein; similar to ankyrin repeat family protein
EB437250	Ntdin [<i>Nicotiana tabacum</i>]	AT5G66040	Sulfur transferase protein
EB427781	Type 2 proly 4-hydroxylase [<i>Nicotiana tabacum</i>]	AT3G28480	Oxidoreductase, 2OG-Fe(II) oxygenase family protein; similar to oxidoreductase, 2OG-Fe(II) oxygenase family protein
EH621860	Avr9/Cf-9 rapidly elicited protein 169 [<i>Nicotiana tabacum</i>]	AT1G78410	VQ motif-containing protein; similar to unknown protein
EB441340	Hydrogen-exporting ATPase,	AT3G60330	Hydrogen-exporting ATPase

EH620838	regulator of gene silencing [<i>Nicotiana tabacum</i>]	AT1G76650	CML38; calcium ion binding; similar to calmodulin-related protein
EH621541	predicted protein [<i>Populus trichocarpa</i>]	AT4G37300	Maternal effect embryo arrest
BP527797	Glutamate synthase, putative [<i>Ricinus communis</i>]	AT5G53460	NADH-dependent glutamate synthase

Nucleotide sequences of all the probe ids were downloaded and homology search was carried out using BLASTx on the NCBI and TAIR databases.

Supplementary Table S2. List of down-regulated (\geq two-fold) genes in *AtMYB12*-expressing tobacco lines

Tobacco Accession No.	Putative annotation	TAIR locus id	Annotation in TAIR
EB450456	Unnamed protein product [<i>Vitis vinifera</i>]	AT1G09750	Aspartyl protease family protein
EB426001	Pectin methylesterase [<i>Nicotiana tabacum</i>]	AT3G05610	Pectinesterase family protein
EG649865	Unnamed protein product [<i>Vitis vinifera</i>]	AT3G33011	Transposable element gene
EH618693	Unnamed protein product [<i>Vitis vinifera</i>]	AT3G13610	Oxidoreductase, 2OG-Fe(II) oxygenase family protein
EB424996 xcxzcxczc	Putative caffeoyl-CoA 3-O-methyltransferase [<i>Nicotiana tabacum</i>]	AT4G34050	Caffeoyl-CoA 3-O-methyltransferase
BP533582	Aspartic proteinase nepenthesin-1 precursor, putative [<i>Ricinus communis</i>]	AT1G09750	Aspartic-type endopeptidase activity.
EB425297	Hypothetical protein PICST_51421	AT5G57050	ABA insensistive2 Encodes a protein phosphatase 2C and is involved in ABA signal transduction
DW000332	Betaine-aldehyde dehydrogenase, chloroplast	AT3G48170	Arabidopsis thaliana putative betaine aldehyde dehydrogenase
EH624390	Vetispiradiene synthase [<i>Solanum tuberosum</i>]	AT3G32030	Terpene synthase/cyclase family protein
BP533451	Arginine decarboxylase [<i>Cucumis sativus</i>]	AT4G15360	Cytochrome P450;Molecular Function: monooxygenase
DV159225	Heat-shock protein, putative [<i>Ricinus communis</i>]	AT5G12020	Heat shock protein
EB425990	Unnamed protein product [<i>Vitis vinifera</i>]	AT5G62350	Invertase/pectin methylesterase inhibitor family protein
EH617289	Probable glutathione S-transferase parA [<i>Nicotiana tabacum</i>]	AT1G78340	Encodes glutathione transferase belonging to the tau class of GSTs
EH665203	GEM-like 1 [<i>Vitis vinifera</i>]	AT1G28200	FH interacting protein
EB427383	Pectate lyase [<i>Nicotiana tabacum</i>]	AT5G15110	Pectate lyase family protein
EH619192	Predicted protein [<i>Populus trichocarpa</i>]	AT4G22990	SPX (SYG1/Pho81/XPR1) domain-containing protein
EB450187	Hypothetical protein [<i>Vitis vinifera</i>]	AT5G34965	Transposable element gene; copia-like retrotransposon family
EH618280	mRNA inducible by salicylic acid or by TMV during Systemic Acquired, Resistance response	AT5G04480	Molecular function unknown
EH616792	Predicted protein [<i>Populus trichocarpa</i>]	AT4G13010	Oxidoreductase/ zinc ion binding
EB678731	Hypothetical protein [<i>Vitis vinifera</i>]	AT1G71691	GDSL-motif lipase/hydrolase family protein
EB451837	Unnamed protein product [<i>Vitis vinifera</i>]	AT1G15410	Aspartate-glutamate racemase
BP526215	Ethylene receptor [<i>Petunia hybrida</i>]	AT3G23150	Ethylene response 2
DV159074	mRNA inducible by salicylic acid or by TMV during Systemic Acquired, Resistance response	AT3G54230	nucleic acid binding / nucleotide binding / zinc ion binding
DV999116	CYP82E4v6 [<i>Nicotiana tabacum</i>]	AT2G25160	CYP82F1

EB425362	Pollen tube RhoGDI2 [<i>Nicotiana tabacum</i>]	AT3G07880	Rho GDP-dissociation inhibitor family protein; Identical to Rho GDP-dissociation inhibitor 1 (GDI1)
EB446807	Conserved hypothetical protein [<i>Ricinus communis</i>]	AT2G02710	PAS/LOV Protein
DV158594	ECP31 protein [<i>Daucus carota</i>]	AT3G22490	Late embryogenesis abundant protein, putative / LEA protein, putative; similar to ATECP31 (late embryogenesis abundant)
DW003046	Asparaginase 2 [<i>Medicago truncatula</i>]	AT3G16150	L-asparaginase, putative / L-asparagine amidohydrolase, putative; Identical to Probable L-asparaginase 2 precursor
EB435318	Cytochrome P450 monooxygenase [<i>Nicotiana sylvestris</i>]	AT4G31940	CYP82C4
DW003245	Histone H3.1t [<i>Culex quinquefasciatus</i>]	AT4G40040	Histone H3.2
EG649865	Unnamed protein product [<i>Vitis vinifera</i>]	AT3G33011	Transposable element gene; copia-like retrotransposon family
EH619790	Sesquiterpene synthase [<i>Fabiana imbricate</i>]	AT1G64530	RWP-RK domain-containing protein; similar to RWP-RK domain-containing protein
EB450523	Auxin:hydrogen symporter, putative [<i>Ricinus communis</i>]	AT1G20925	Auxin efflux carrier family protein; similar to auxin efflux carrier family protein [<i>Arabidopsis thaliana</i>]
CV016966	DC1.2 homologue [<i>Nicotiana tabacum</i>] Pectin inverterse/Pectin methylestrase inhibitor	AT5G62350	Invertase/pectin methylesterase inhibitor family
EB450593	21 kDa protein precursor, putative [<i>Ricinus communis</i>]	AT2G01610	Invertase/pectin methylesterase inhibitor family protein
EB679611	Predicted protein [<i>Populus trichocarpa</i>]	AT2G05920	Subtilase family protein;
EB450636	Predicted protein [<i>Populus trichocarpa</i>]	AT2G41380	Embryo-abundant protein-related; similar to embryo-abundant protein-related, methyltransferase activity
BP132920	N-like protein [<i>Nicotiana tabacum</i>]	AT5G38350	Disease resistance protein
CV019874	Hypothetical protein [<i>Vitis vinifera</i>]	AT2G28740	Histone 4
EH623629	SAR8.2n [<i>Nicotiana tabacum</i>]	AT3G15350	Glycosyltransferase family
BP526993	Unknown [<i>Solanum tuberosum</i>]	AT2G34480	60S ribosomal protein L18A (RPL18aB); Identical to 60S ribosomal protein
EH619953	mRNA inducible by salicylic acid	AT2G27530	Encodes ribosomal protein L10aP. Identified in a screen for enhancers of as1.
EB428211	GLN1;5; glutamate-ammonia ligase	AT5G37600	encodes a cytosolic glutamine synthetase
EB442438	Pyruvate decarboxylase	AT5G54960	Pyruvate decarboxylase-2
EH666250	Conserved hypothetical protein [<i>Ricinus communis</i>]	AT5G46700	Encodes a transmembrane protein of the tetraspanin (TET) family
BP533219	Unnamed protein product [<i>Vitis vinifera</i>]	AT2G42580	Tetratricopeptide repeat thioredoxin like
EB443392	D-type cyclin family 3 subgroup 3 [<i>Solanum tuberosum</i>]	AT4G34160	D-type cyclin family 3 subgroup 3 [<i>Solanum tuberosum</i>]
CN949738	Patatin homolog [<i>Nicotiana tabacum</i>]	AT2G26560	Phospholipase A
EH619929	mRNA inducible by salicylic acid	AT4G01975	Transposable element gene; pseudogene,
EB428944	unnamed protein product [<i>Vitis vinifera</i>]	AT5G15180	Peroxidase
EB447918	Chromomethylase [<i>Nicotiana sylvestris</i>]	AT1G69770	Encodes a chromomethylase involved in methylating cytosine residues at non-CG sites
DV999922	Water channel protein [<i>Nicotiana excelsior</i>]	AT1G01620	A member of the plasma membrane intrinsic protein subfamily PIP1

EH623154	Lignan glucosyltransferase [<i>Sesamum indicum</i>]	AT4G15260	UDP-glucuronosyl/UDP-glucosyl transferase family protein; similar to UDP-glucuronosyl/UDP-glucosyl transferase
DW004106	Hypothetical protein [<i>Vitis vinifera</i>]	AT4G10310	Encodes a sodium transporter (HKT1)
EB451159	Putative PLA2 [<i>Nicotiana tabacum</i>]	AT1G77100	peroxidase, putative; Identical to Peroxidase 13 precursor (PER13)
EB447957	Geranylgeranyl pyrophosphate synthase 1 [<i>Solanum lycopersicum</i>]	AT4G36810	Geranyl geranyl pyrophosphate synthase1
BP530174	Putative transposase [<i>Ipomoea tricolor</i>]	AT5G34960	Transposable element gene; similar to unknown protein
BP528584	Os10g0170600 [<i>Oryza sativa</i> (japonica cultivar-group)]	AT1G37038	Transposable element gene; hAT-like transposase family
EB426609	Expansin [<i>Lycopersicon esculentum</i>]	AT2G03090	Expansin A 15
EB679635	Conserved hypothetical protein [<i>Ricinus communis</i>]	AT5G11420	Similar to unknown protein [<i>Arabidopsis thaliana</i>]
EB450241	Arylacetamide deacetylase, putative [<i>Ricinus communis</i>]	AT3G48700	Carboxyesterase
EB450706	Unnamed protein product [<i>Vitis vinifera</i>]	AT5G67210	Nucleic acid binding / pancreatic ribonuclease; similar to nucleic acid binding
EH618171	Predicted protein [<i>Populus trichocarpa</i>]	AT1G52760	Esterase/lipase/thioesterase family protein
BP535208	Unnamed protein product [<i>Vitis vinifera</i>]	AT3G54240	Hydrolase, alpha/beta fold family protein
DW001052	Unknown protein	AT4G00360	Encodes a member of the CYP86A subfamily of cytochrome p450 genes
BP135122	Hypothetical protein [<i>Vitis vinifera</i>]	AT5G39245	Transposable element gene; non-LTR retrotransposon family (LINE)
EB424922	predicted protein [<i>Populus trichocarpa</i>]	AT5G66440	Unknown protein
BP136490	No significant similarity	AT4G06196	Transposable element gene; CACTA-like transposase family (Tnp2/En/Spm)
EH665347	Expansin 6 [<i>Arabidopsis thaliana</i>]	AT2G28950	Expansin 6
EB428009	No significant similarity	AT2G42570	Similar to unknown protein
BP533987	Similar to histone protein Hist2h3c1 [<i>Monodelphis domestica</i>]	AT3G27360	Histone H3; Identical to Histone H3.2 (HTR1)
EB680266	Unnamed protein product [<i>Vitis vinifera</i>]	AT5G65380	Ripening-responsive protein, putative; similar to antiporter
DV999970	Conserved hypothetical protein [<i>Ricinus communis</i>]	AT4G27310	Zinc finger (B-box type) family protein; similar to zinc finger (B-box type) family protein
BP535208	Unnamed protein product [<i>Vitis vinifera</i>]	AT3G54240	Hydrolase, alpha/beta fold family protein; similar to hydrolase
EH620388	WRKY protein [<i>Solanum tuberosum</i>]	AT1G62300	WRKY6

EB447986	Peroxidase [Solanum lycopersicum]	AT1G05260	Encodes a cold-inducible cationic peroxidase that is involved in the stress response
EB683839	Unknown Protein (Picea sitchensis)	AT5G59970	Histone H4; Identical to Histone H4
EH618110	Cytochrome P450-dependent fatty acid hydroxylase [Nicotiana tabacum]	AT3G56630	CYP94D2
EB425727	Hypothetical protein [Vitis vinifera]	AT2G33750	Member of a family of proteins related to PUP1, a purine transporter
DQ448851	CK25 [Nicotiana tabacum]	AT4G28180	Unknown protein
BP533219	Unnamed protein product [Vitis vinifera]	AT2G42580	Encodes a member of the TTL family and contains a thioredoxin like domain and three tandem TPRs
EB679200	Unnamed protein product [Vitis vinifera]	AT2G44300	Lipid transfer protein-related; similar to protease inhibitor/seed storage/lipid transfer protein
EB643474	Unnamed protein product [Vitis vinifera]	AT5G18840	Sugar transporter, putative; Identical to Sugar transporter ERD6-like 16
EH624401	Catechol O-methyltransferase [Nicotiana tabacum]	AT5G54160	Caffeic acid/5-hydroxyferulic acid O-methyltransferase
BQ843156	Hypothetical protein [Vitis vinifera]	AT3G59840	Similar to conserved hypothetical protein [Medicago truncatula]
EB425616	Predicted protein [Populus trichocarpa]	AT1G13440	Glyceraldehyde-3-phosphate dehydrogenase
EB445882	DWARF1/DIMINUTO [Lycopersicon esculentum]	AT3G19820	Diminuto1, Dwarf1, Dwf1, Enhanced Very-Low-Fluence Responses1, Eve1, Mpn9.6
BP137261	Hypothetical protein RCOM_0939100 [Ricinus communis]	AT3G18990	Reduced vernalization response 1
DW001350	Predicted protein [Populus trichocarpa]	AT4G22070	WRKY31
AJ718251	Predicted protein [Populus trichocarpa]	AT3G46940	Deoxyuridine 5'-triphosphate nucleotidohydrolase family
EB428187	Conserved hypothetical protein [Ricinus communis]	AT1G15385	Unknown protein
DQ460184	Glucose-6-phosphate/phosphate-translocator [Arabidopsis thaliana]	AT1G61800	Glucose-6-phosphate transmembrane transporter

Nucleotide sequences of all the probe ids were downloaded and homology search was carried out using BLASTx on the NCBI and TAIR databases.

Supplementary Table S3. Insect bioassay on detached leaves of WT and *AtMYB12*-expressing transgenic tobacco plants

Line No	Mortality (%) after 3 days	Larval weight (mg±S.E)	Growth Reduction (%)
Control	10.00	10.6±0.43	--
T4	76	8.84±0.59	16.60
T5	80	4.75±0.78	55.20
T6	75	6.24±0.57	41.13
T7	80	4.58±0.78	56.79

Two day old larvae of *S. litura* were released on detached leaves. Observations on mortality and weight of surviving larvae were made after three days of feeding.

Supplementary Table S4. Insect bioassay on wild type and *AtMYB12* expressing transgenic tobacco lines

	WT	T5	T7
Mortality (%)	0	75	75
Average weight	90.22±3.16	5.77±2.40	18.95±4.3
Growth reduction (%)	0	93.6	79.6

Twenty five neonate larvae of *S. litura* were released per plant. Weight and survival of the larvae were measured after 10 days. Weight of surviving larvae was used to calculate percent growth reduction.

Supplementary Table S5. Larval growth reduction caused by feeding *Spodoptera litura* on diet supplemented with *AtMYB12*-expressing tobacco leaf extract

Treatment	Average larval weight (mg ± S.E)			
	3 rd day	5 th day	7 th day	10 th day
Normal diet	1.06±0.07 ^a	3.65±0.28 ^a	14.25±0.86 ^a	72.69 ± 3.12 ^a
Solvent	1.11±0.07 ^a	3.89±0.26 ^a	15.35±0.48 ^a	73.13 ± 2.43 ^a
Control extract (0.5mg/ml)	1.06±0.04 ^a	3.63±0.19 ^a	13.82±0.92 ^a	73.09 ± 2.29 ^a
Control extract (1mg/ml)	0.99±0.04 ^a	3.61±0.19 ^a	14.24±1.35 ^a	68.79 ± 1.07 ^a
Transgenic extract (0.5mg/ml)	0.83±0.06 ^b	2.30±0.26 ^b	5.08±0.21 ^b	8.66± 0.66 ^b
Transgenic extract (1mg/ml)	0.69±0.04 ^b	1.09±0.07 ^c	1.78±0.13 ^c	3.31 ± 0.16 ^c
Rutin (1mg/ml)	0.36±0.04 ^c	1.18±0.08 ^c	1.90±0.11 ^c	3.40 ± 0.19 ^c
Rutin (2mg/ml)	0.25±0.03 ^c	0.44±0.03 ^d	0.63±0.04 ^c	1.92 ± 0.07 ^c

Stock solutions of different extracts were mixed separately with 50 ml of semi synthetic diet before solidifying. Control consisted of 5 ml ethanol mixed with the diet. The medium was poured into the petriplates (60 mm) and kept open overnight to evaporate the solvent. Each treatment was replicated thrice. One-day-old larvae of *Spodoptera litura* were used. Weight of surviving larvae was recorded on different days. Means were compared using DMRT at $\alpha = 0.05$. Means within a column, superscribed with same alphabet are not significantly different.

Supplementary Table S6. Larval mortality caused by feeding *Spodoptera litura* on diet supplemented with *AtMYB12*-expressing tobacco leaf extract

Treatment	Per cent mortality (% Growth reduction)			
	3 rd day	5 th day	7 th day	10 th day
Normal diet	0.0 -	0.0 -	0.0 -	0.0 -
Solvent	0.0 (-4.70)	0.0 (-6.57)	0.0 (-16.70)	0.0 (0.60)
Control extract (0.5mg/ml)	0.0 (0.0)	0.0 (0.54)	0.0 (19.27)	0.0 (0.55)
Control extract (1mg/ml)	0.0 (6.60)	0.0 (0.93)	0.0 (0.07)	0.0 (0.53)
Transgenic extract (0.5mg/ml)	0.0 (21.88)	0.0 (36.16)	13.33 (64.35)	16.66 (88.08)
Transgenic extract (1mg/ml)	0.0 (34.90)	16.66 (70.13)	43.33 (87.50)	50.00 (95.45)
Rutin (1mg/ml)	0.0 (66.03)	10.00 (67.67)	30.0 (86.66)	46.66 (95.32)
Rutin (2mg/ml)	0.0 (76.41)	33.33 (87.94)	53.33 (95.57)	66.66 (97.35)

Data used in the analysis was utilized from supplementary table 6. Percent Growth Reduction was calculated by comparing weight of treated larvae with the controls (normal diet).

Growth Reduction (%) = 100 - (Weight of Larvae on supplemented diet/weight of larvae in control)*100

Supplementary Table S7. Larval growth reduction caused by feeding *Helicoverpa armigera* on diet supplemented with *AtMYB12*-expressing tobacco leaf extract

Treatment	Average larval weight (mg ± S.E)			
	3 rd day	5 th day	7 th day	10 th day
Normal diet	0.85±0.092 ^a	5.66±0.17 ^a	36.40±1.57 ^a	211.80 ± 11.14 ^a
Solvent	0.72±0.069 ^a	5.42±0.21 ^a	37.30±1.25 ^a	206.06 ± 10.33 ^b
Control extract (0.5mg/ml)	0.44±0.042 ^b	2.93±0.30 ^b	19.25±1.74 ^b	116.10 ± 11.21 ^c
Control extract (1mg/ml)	0.49±0.037 ^b	1.01±0.16 ^d	14.14±1.00 ^c	79.64 ± 8.20 ^c
Transgenic extract (0.5mg/ml)	0.16±0.016 ^d	0.55±0.10 ^d	4.40±0.65 ^d	5.06± 0.83 ^d
Transgenic extract (1mg/ml)	0.14±0.016 ^d	0.39±0.037 ^d	1.33±0.21 ^d	NA
Rutin (1mg/ml)	0.36±0.040 ^{bc}	1.49±0.088 ^d	1.99±0.14 ^d	4.05 ±0.89 ^d
Rutin (2mg/ml)	0.28±0.029 ^{cd}	1.00±0.28 ^d	0.63±0.04 ^d	NA

The diet and concentrations were prepared and analysis done as described in table 6. The larvae were released individually to avoid cannibalism.

Supplementary Table S8. Larval mortality caused by feeding *Helicoverpa armigera* on diet supplemented with *AtMYB12*-expressing tobacco leaf extract

Treatment	Per cent mortality (% Growth reduction)			
	3 rd day	5 th day	7 th day	10 th day
Normal diet	0.0 -	0.0 -	0.0 -	0.0 -
Solvent	0.0 (15.29)	0.0 (4.24)	0.0 (-2.47)	0.0 (2.44)
Control extract (0.5mg/ml)	0.0 (48.23)	0.0 (48.23)	0.0 (47.11)	0.0 (45.18)
Control extract (1mg/ml)	10.00 (42.35)	10.00 (82.15)	10.00 (61.15)	10.00 (62.39)
Transgenic extract (0.5mg/ml)	33.33 (81.17)	40.00 (90.28)	66.66 (87.91)	86.66 (97.60)
Transgenic extract (1mg/ml)	40.00 (83.52)	50.00 (93.10)	80.00 (96.88)	100 NA
Rutin (1mg/ml)	30.33 (57.64)	33.33 (73.67)	50.00 (94.53)	86.66 (98.08)
Rutin (2mg/ml)	50.00 (67.05)	50.00 (93.99)	83.33 (97.25)	100 NA

Data used in the analysis was utilized from supplementary table 8. Other details are same, as in table 7.

Supplementary Table S9. The primers used for semi-quantitative analysis of selected genes by RTPCR

S.No.	Gene name	Forward primer	Reverse primer
1.	NtUBI	TCCAGGACAAGGAGGGTAT	GAGACCTCAGTAGACAAAGC
2.	AtMYB12	AACCAAGGGAATCTCGACTGTCT	CGTCGTCATGATCTAACGGTTC
3.	NTPAL	GCCAACAGGATAAAAAGAATGC	CAAGAACATATAAGCACATTG
4.	NtCHS	CCTTTGGGAATTTCTGATTGG	TCCCACAATATAAGCCCAAGC
5.	NtF3H	AGCTAGAGACTACTCCAGGTG	AACCGTGATCCAAGTTTTGCCA
6.	NtCHI	GACGGGTAAGCAATACTCAGAGAAG	AACTAGACTCCAATTTCTGGAATG
7.	NtFLS	AAGTGATAAATCATGGAATCCAG	TCTTCACCACCTGCTGCCTCCATC
8.	NtDFR1	TCGAGTCCAAGGATCCTGAGAATG	CAACAACCAGCGGCGGTATGATG
9.	NtDFR2	TGACGAGACCAGCTGGAGCGAC	CCACATCATAGATGATAGCATG
10.	NtCcOR	CAATCCAGTGTTGGTGCTTG	CTGCAGGCTCTTCACCGTCTC
11.	NtEPSP	TCTGCATCAGTGGTCACTGCAC	ACAACCTTCCACGATTGCTC
12.	NtA3GRT	TCAAATCTATGTTGAATTCTGC	CTGAAGTGACAGAGGTGTGAGG
13.	NtRHM	CATCCTAGAATGCTGATGATG	CACCAGCAGCATTGAATACATG
14.	NtSnakin	CTTCTGGCAACACTGAAACTTG	CCAAGAGGAGAGGACACAATTC

Supplementary Table S10. Oligonucleotide primers used for mutagenising the scaffold of miRNA159a for designing artificial miRNAs for NtFLS

Candidate 1:

FLSmiF1

AAGATAGATCTAGATCTGACGATGGAAGGGCCATTGGTATGATGTCAAACATGAGTTGAGCAGGGT
A

FLSmiR1

AAAATAGAGCTCGTGAAAGAAGGGCCATTGGTATGATGTCAA AAAAGAAGAGTAAAAGCCATTA

Candidate 2:

FLSmiF2

AAGATAGATCTAGATCTGACGATGGAAGGGTGAAGATATTGTTTACTTACATGAGTTGAGCAGGGTA

FLSmiR2

AAAATAGAGCTCGTGAAAGAAGGGTGAAGATATTGTTTACTTAAAAGAAGAGTAAAAGCCATTA

Candidate 3:

FLSmiF3

AAGATAGATCTAGATCTGACGATGGAAGATACAGACATGTCCCATATAACATGAGTTGAGCAGGGTA

FLSmiR 3

AAAATAGAGCTCGTGAAAGAAGATACAGACATGTCCCATATAAAAAGAAGAGTAAAAGCCATTA