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(54) **INCREASING TRICHOME DENSITY AND IMPROVING TRANSPORT OF METABOLITES IN PLANT TRICHOMES**

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(60) Provisional application No. 63/145,259, filed on Feb. 3, 2021, provisional application No. 63/145,262, filed on Feb. 3, 2021, provisional application No. 63/145,263, filed on Feb. 3, 2021.

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(52) **U.S. Cl.**

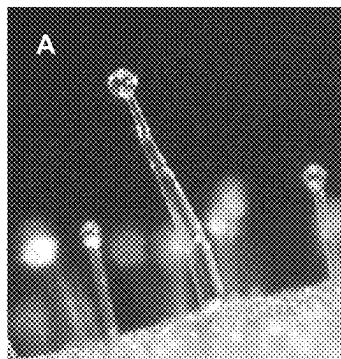
CPC **C12N 15/8262** (2013.01); **C12N 15/8223** (2013.01); **C12N 15/8243** (2013.01); **C07K 14/415** (2013.01); **C12N 2800/22** (2013.01); **C12P 5/007** (2013.01)

(57)

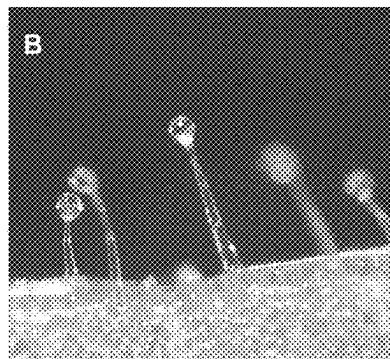
ABSTRACT

The present disclosure relates to compositions and methods related to modification of trichome density and transport of metabolite and their uses in plants, including tobacco and *cannabis*. The provided transcription factors enable the increase in trichome density in plants.

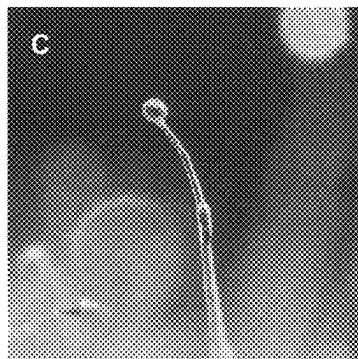
Specification includes a Sequence Listing.



N. benthamiana

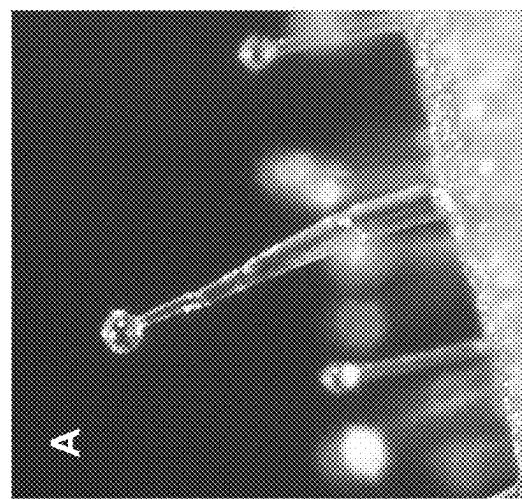
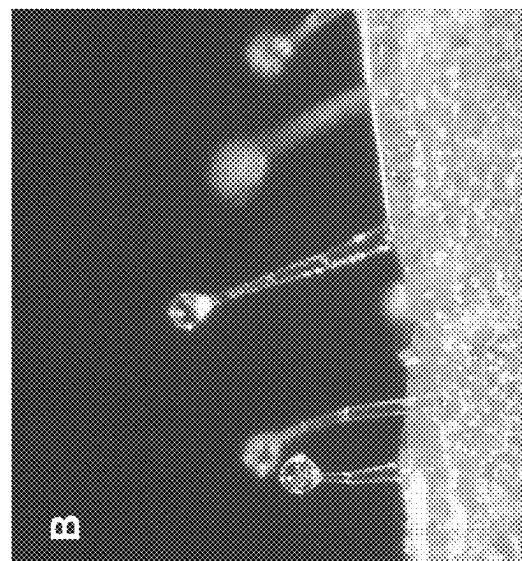
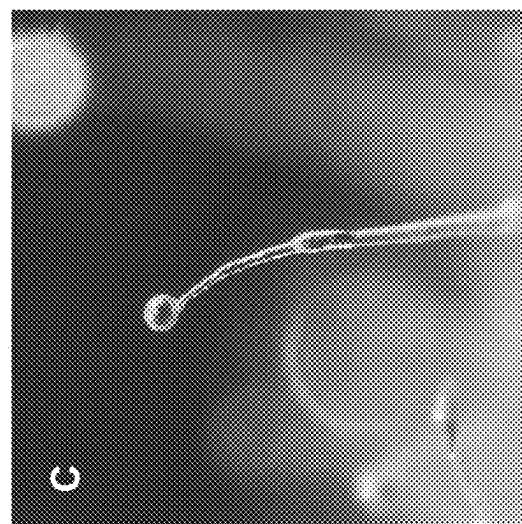


N. tabacum 'TN90'



N. tabacum 'Izmir Ego'

Figure 1



N. benthamiana

N. tabacum 'TN90'

N. tabacum 'Izmir Ego'

Figure 2

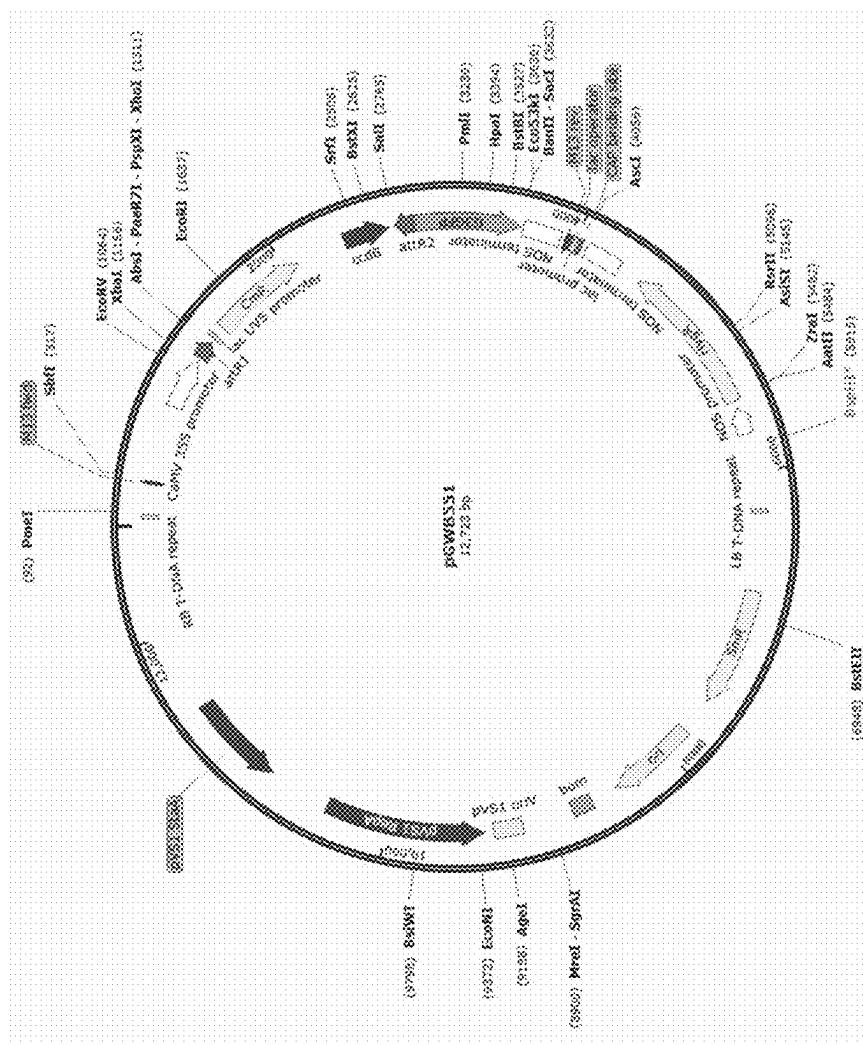


Figure 3

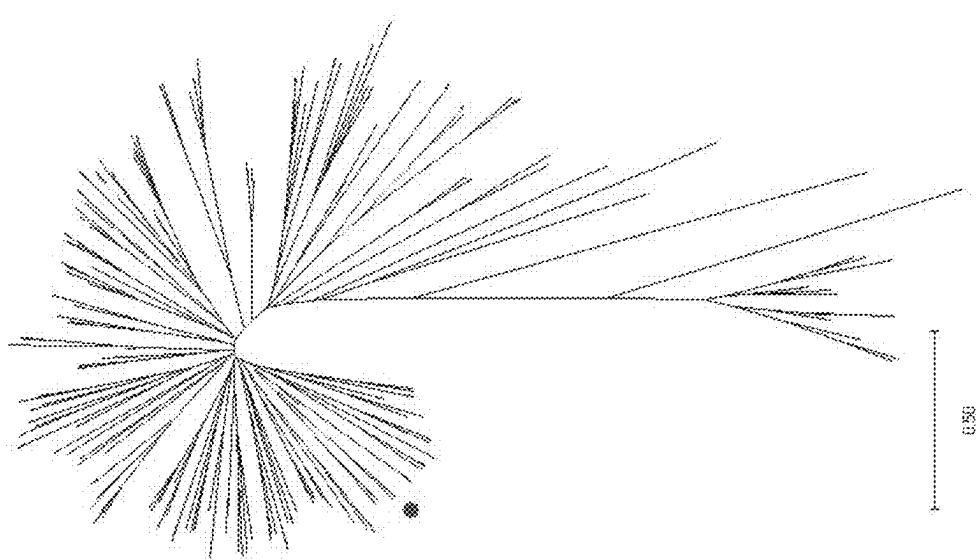


Figure 3A

Figure 3C

Figure 3B

	R2		R3										
	10	20	30	40	50	60	70	80	90	100	110	120	130
8838405001,1 NP_016450002	100	200	300	400	500	600	700	800	900	1000	1100	1200	1300
8838405001,1 NP_016450002	131	140	150	160	170	180	190	200	210	220	230	240	250
8838405001,1 NP_016450002	261	270	280	290	300	310	320	330	340	350	360	370	380
8838405001,1 NP_016450002	311	320	330	340	350	360	370	380	390	400	410	420	430
8838405001,1 NP_016450002	391	400	410	420	430	440	450	460	470	480	490	500	510

Figure 4

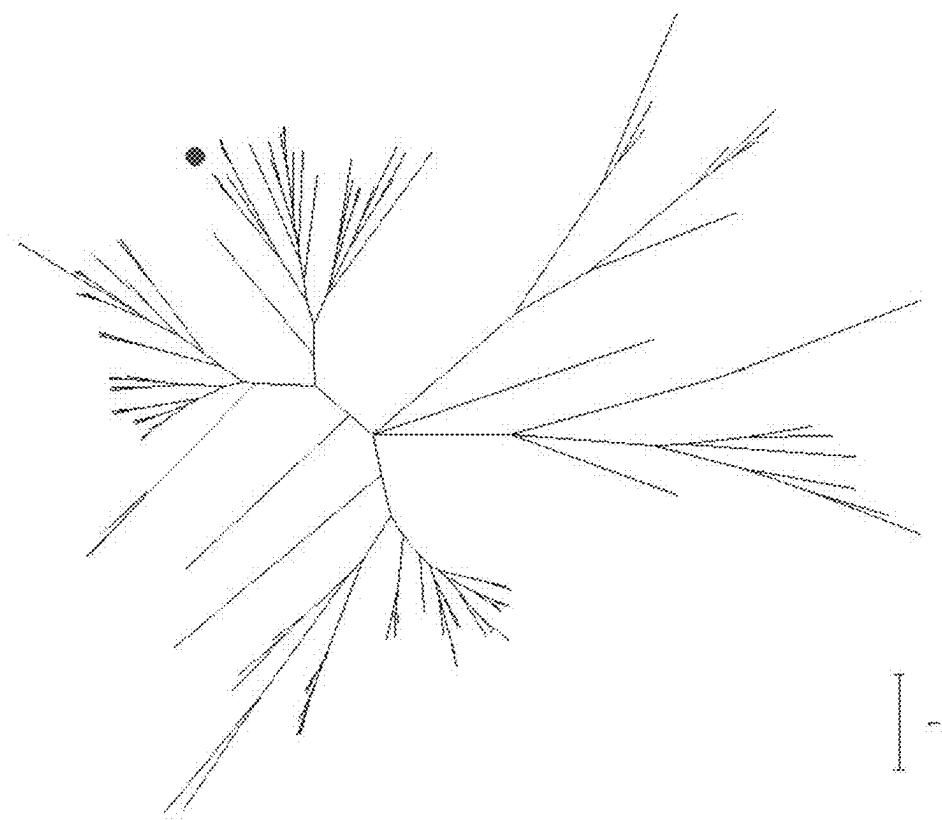


Figure 5

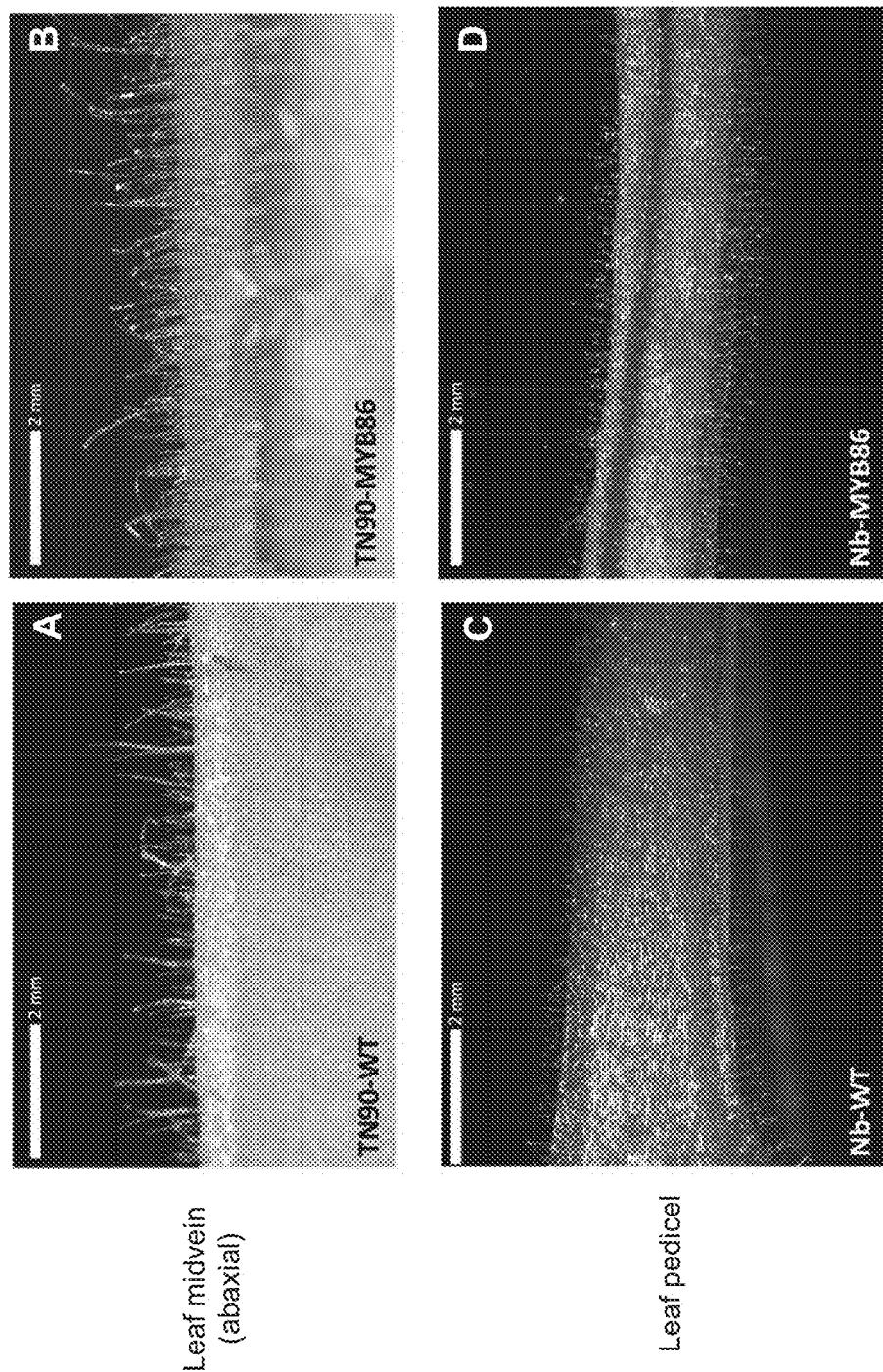


Figure 6

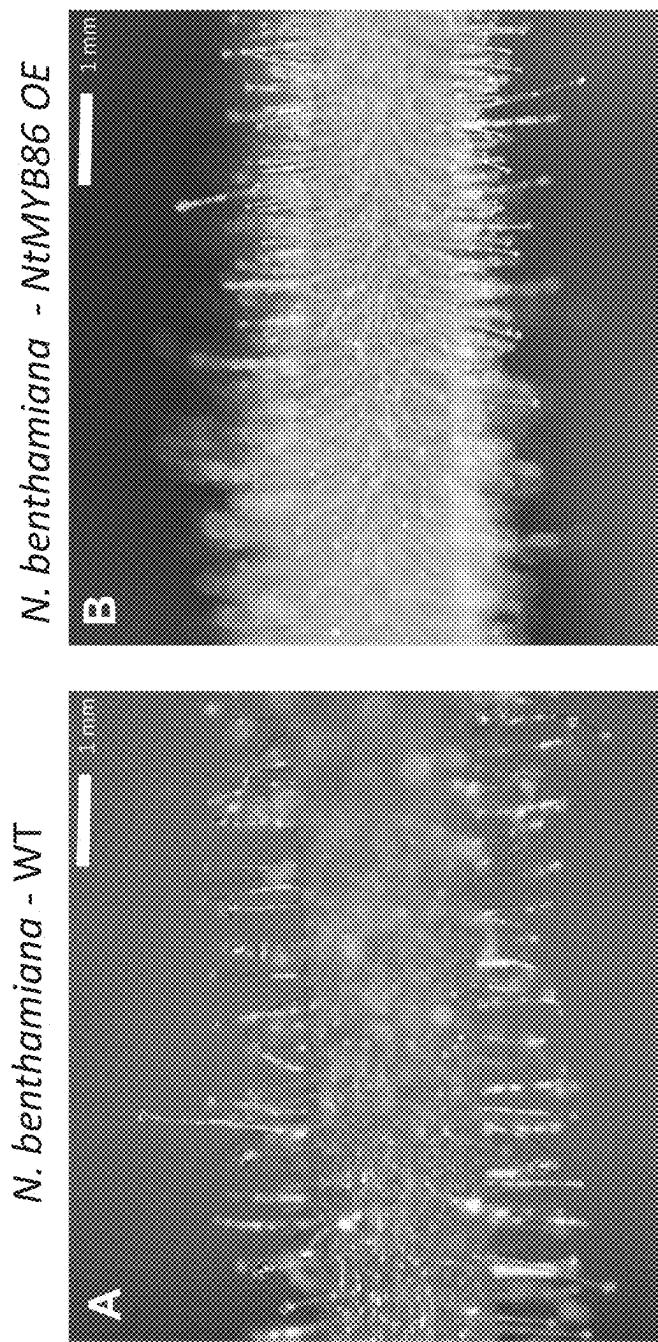


Figure 7

Figure 7A

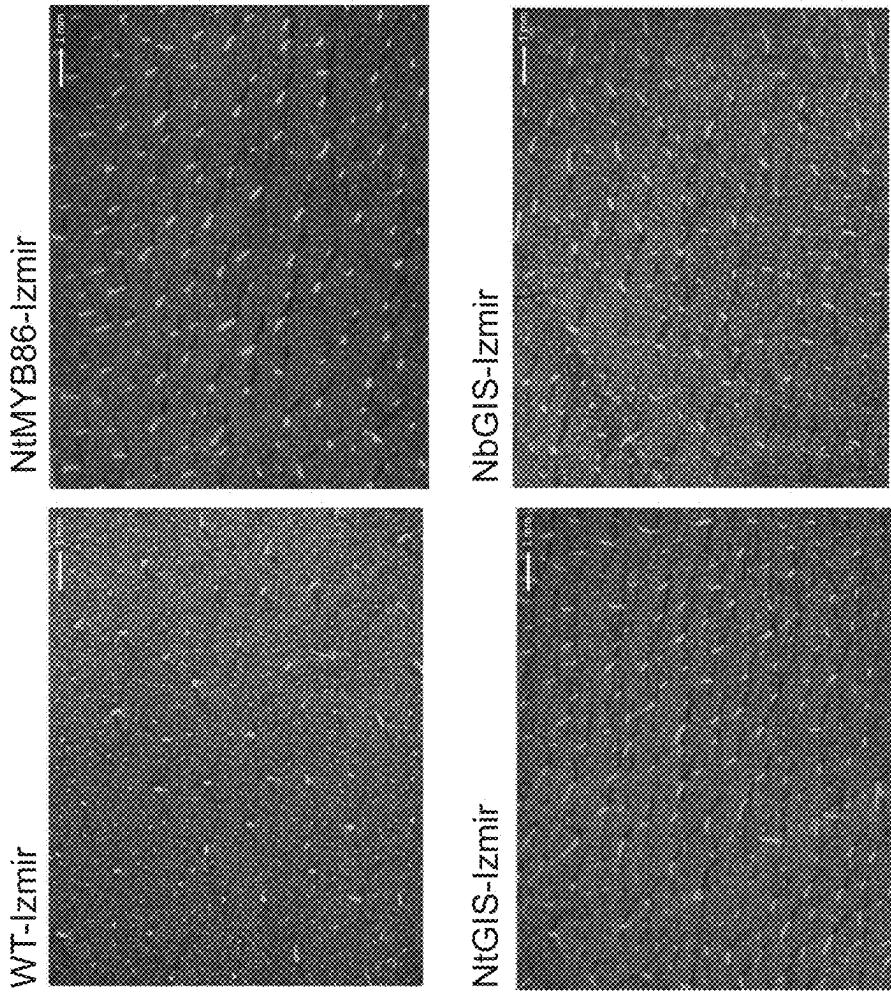


Figure 7

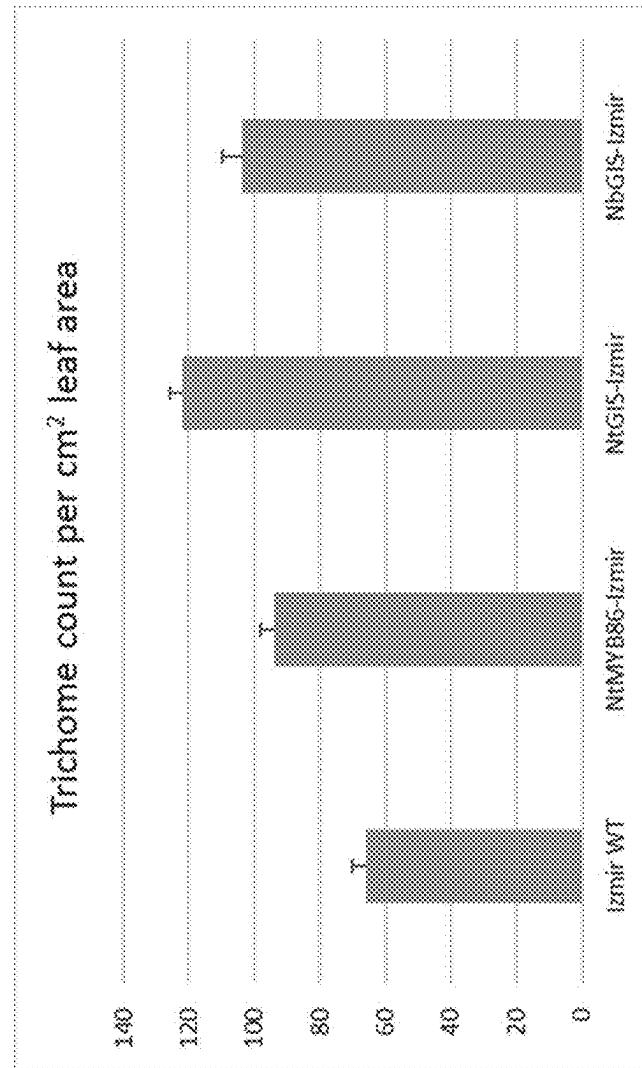


Figure 7B

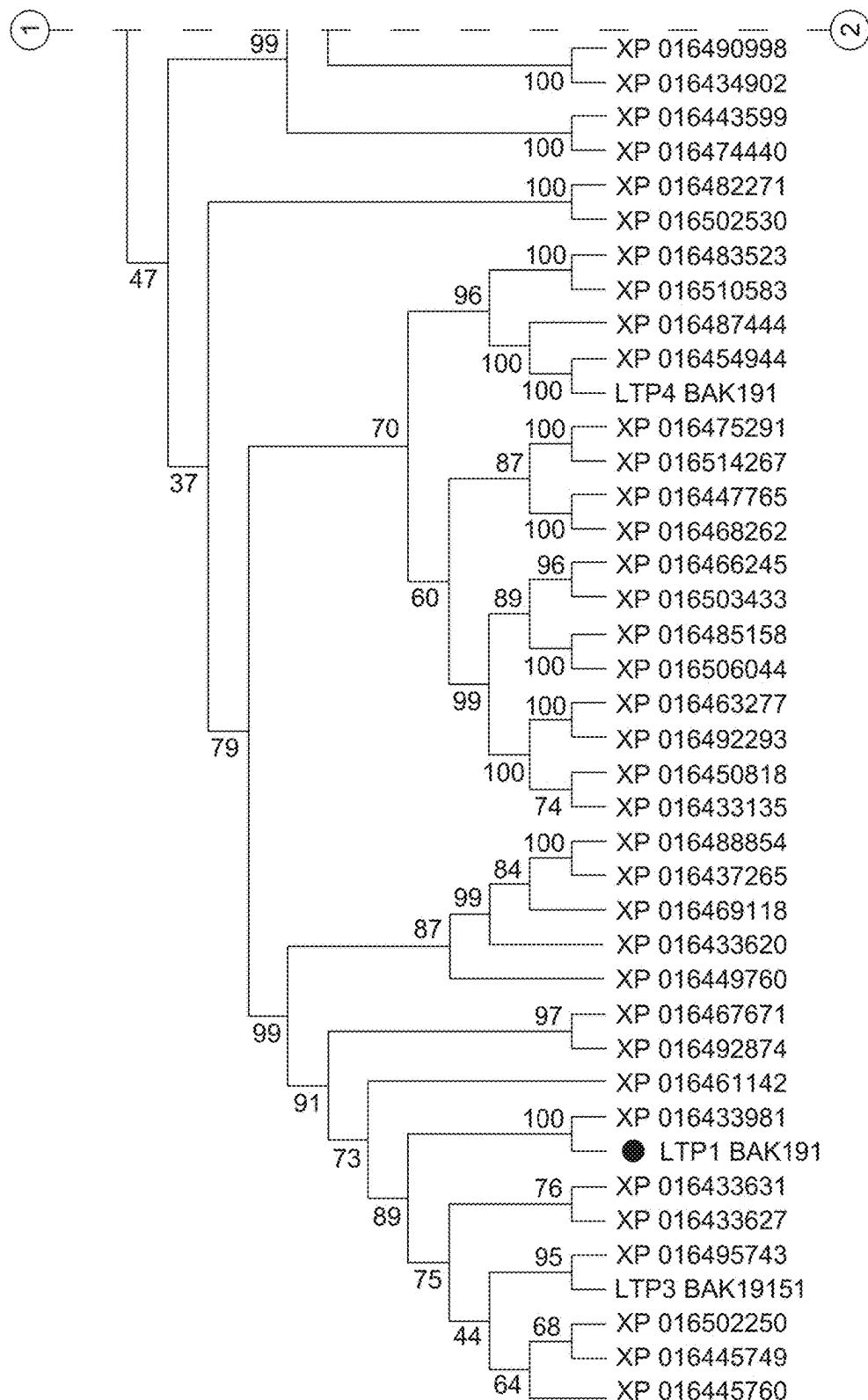


Figure 8A

Figure 8

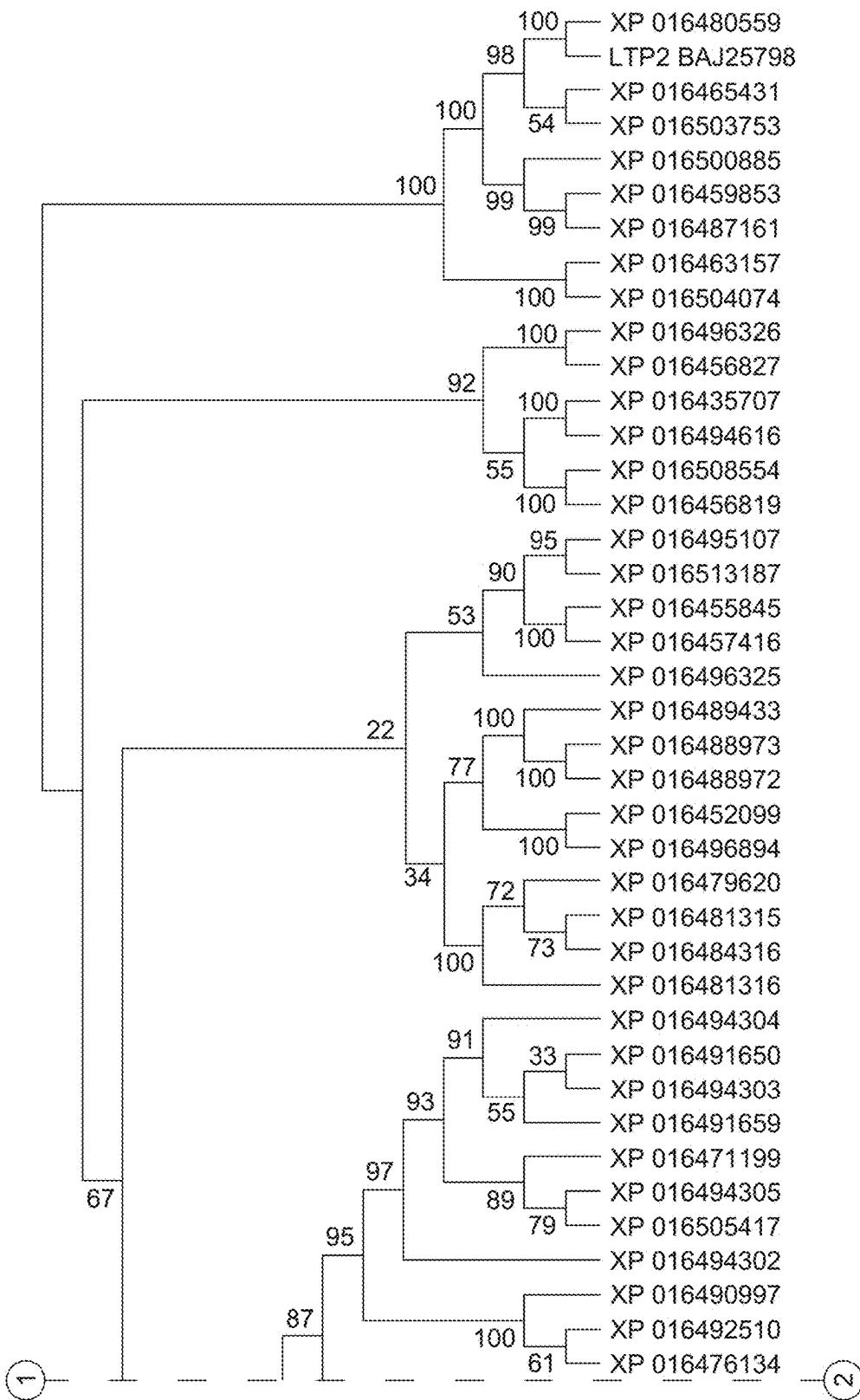


Figure 8A (Continued)

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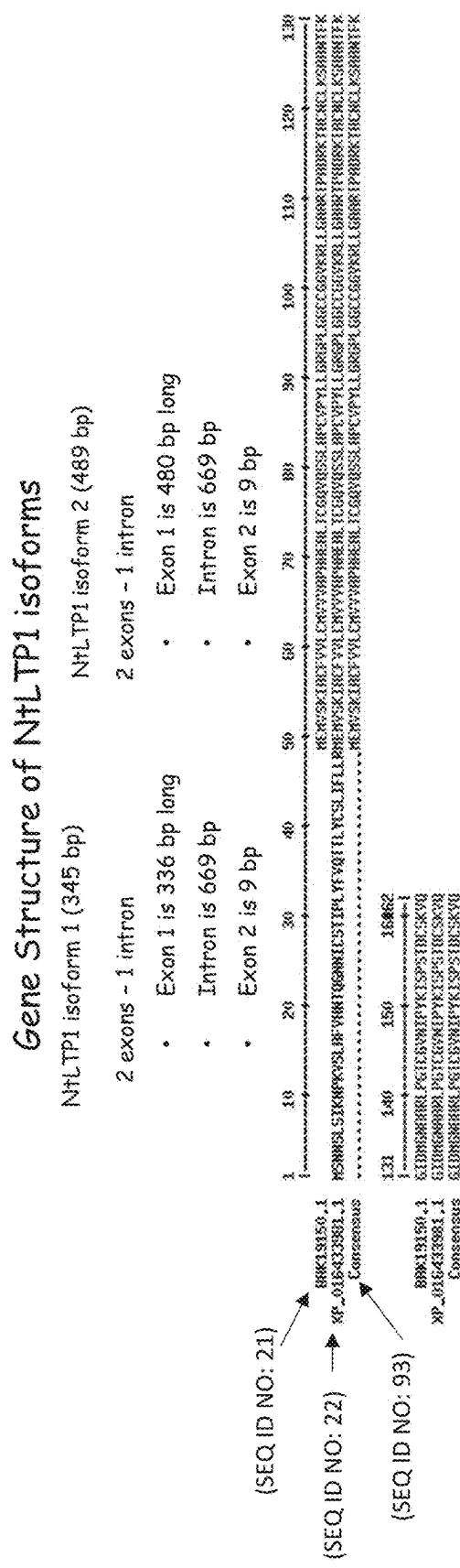


Figure 8B

Figure 9

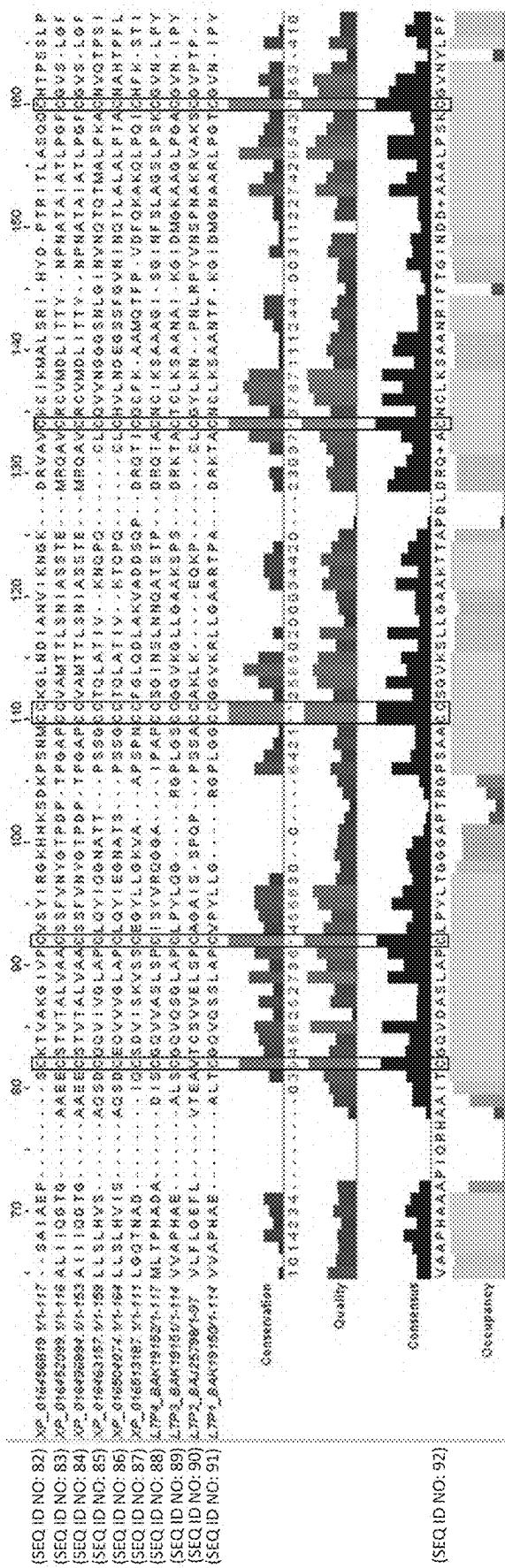


Figure 10

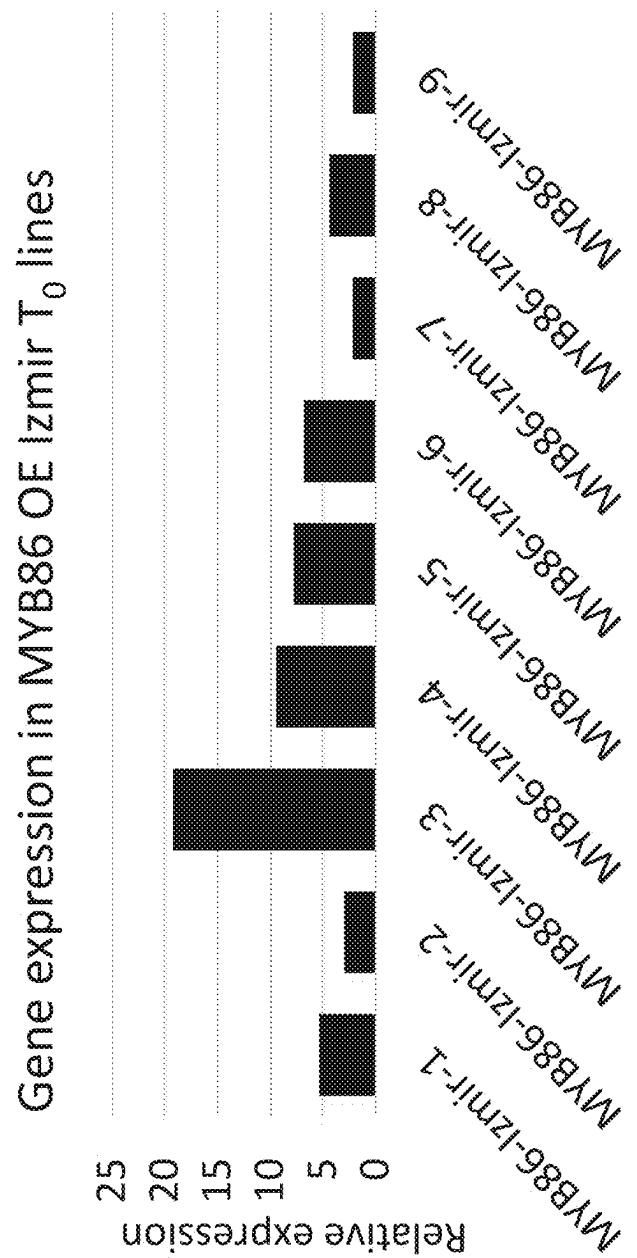


Figure 11

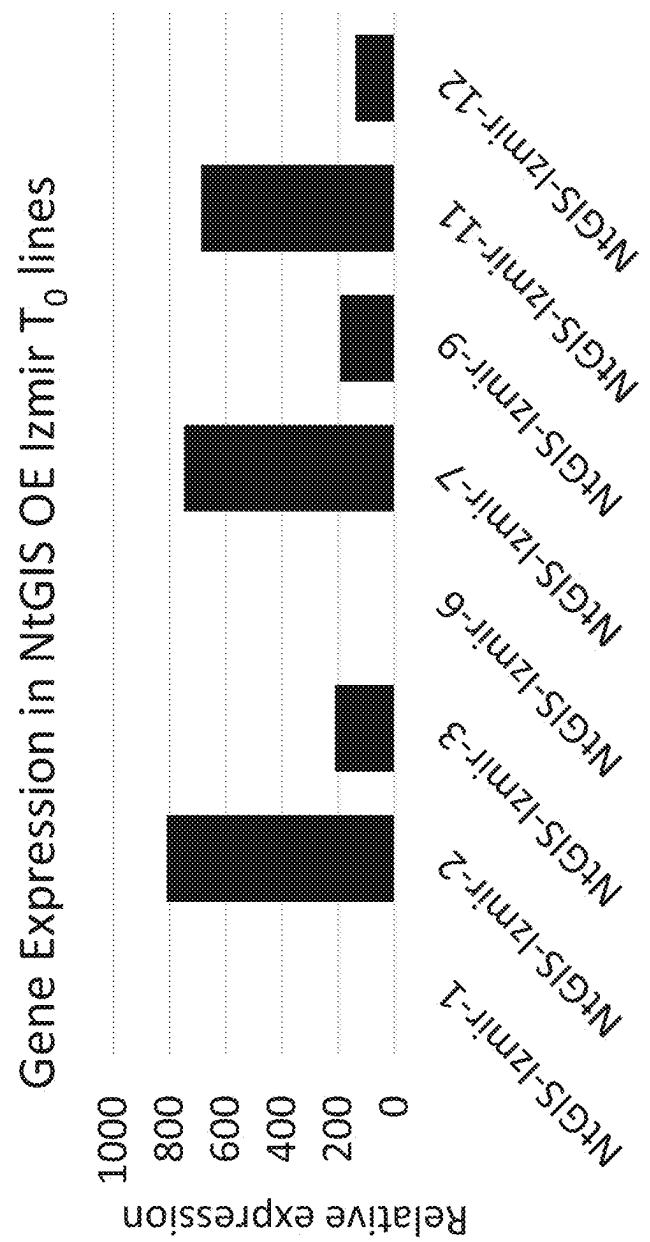


Figure 12

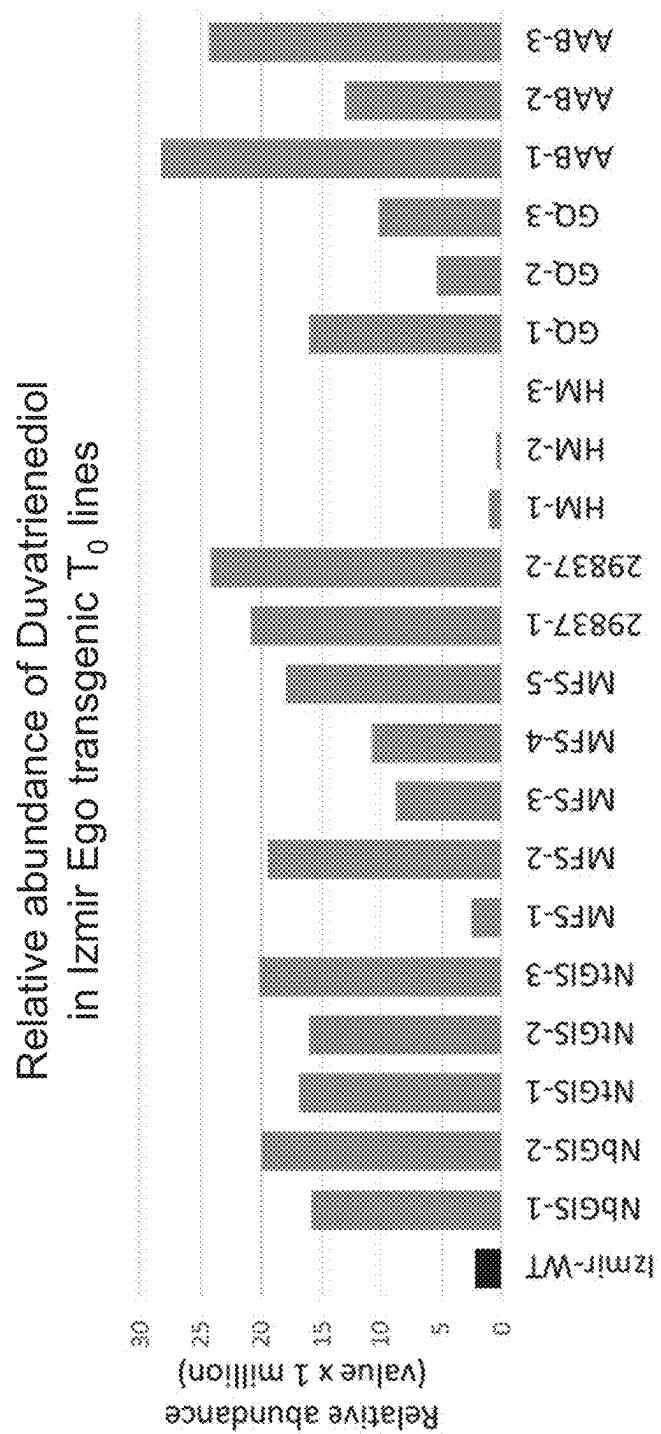


Figure 13

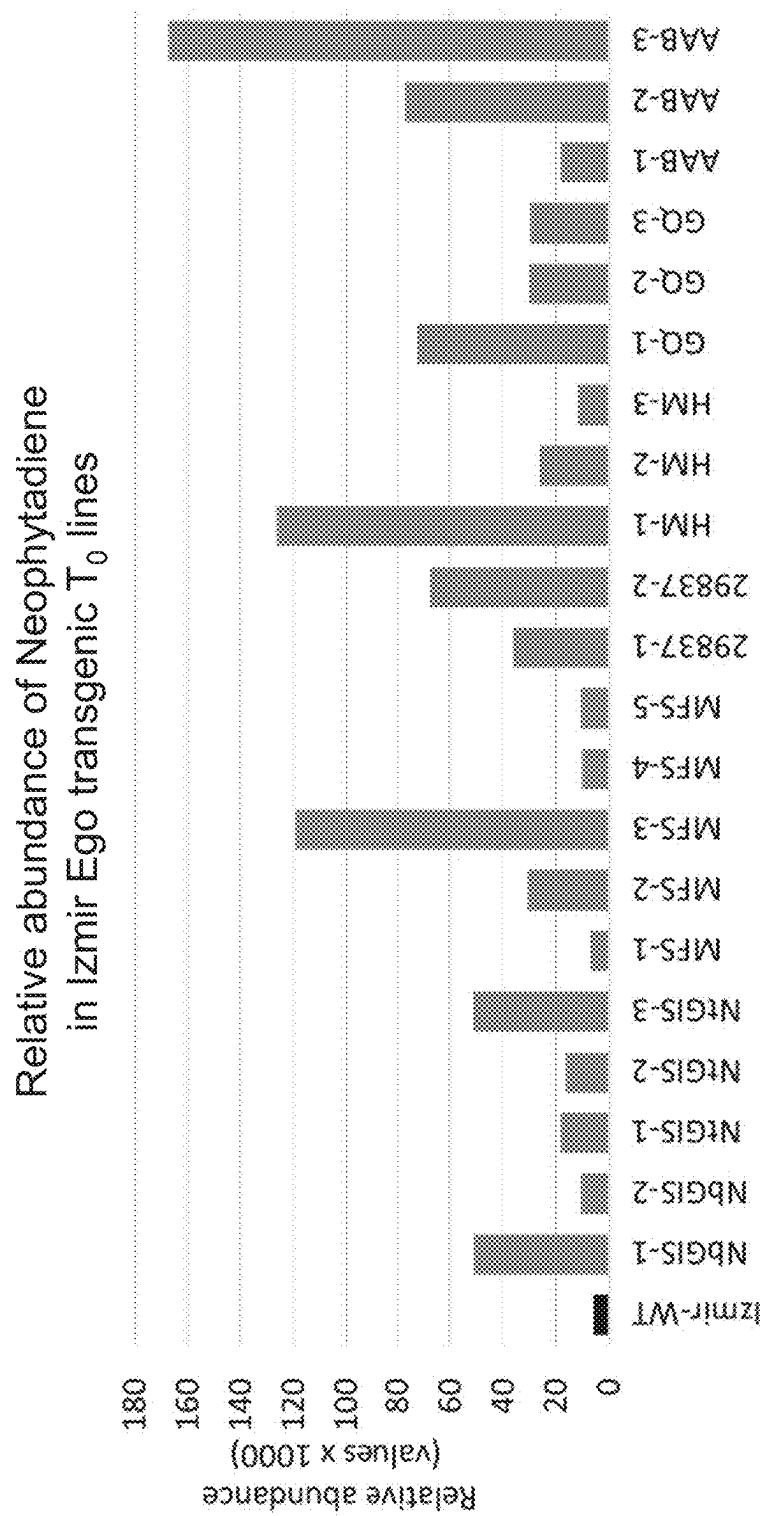


Figure 14

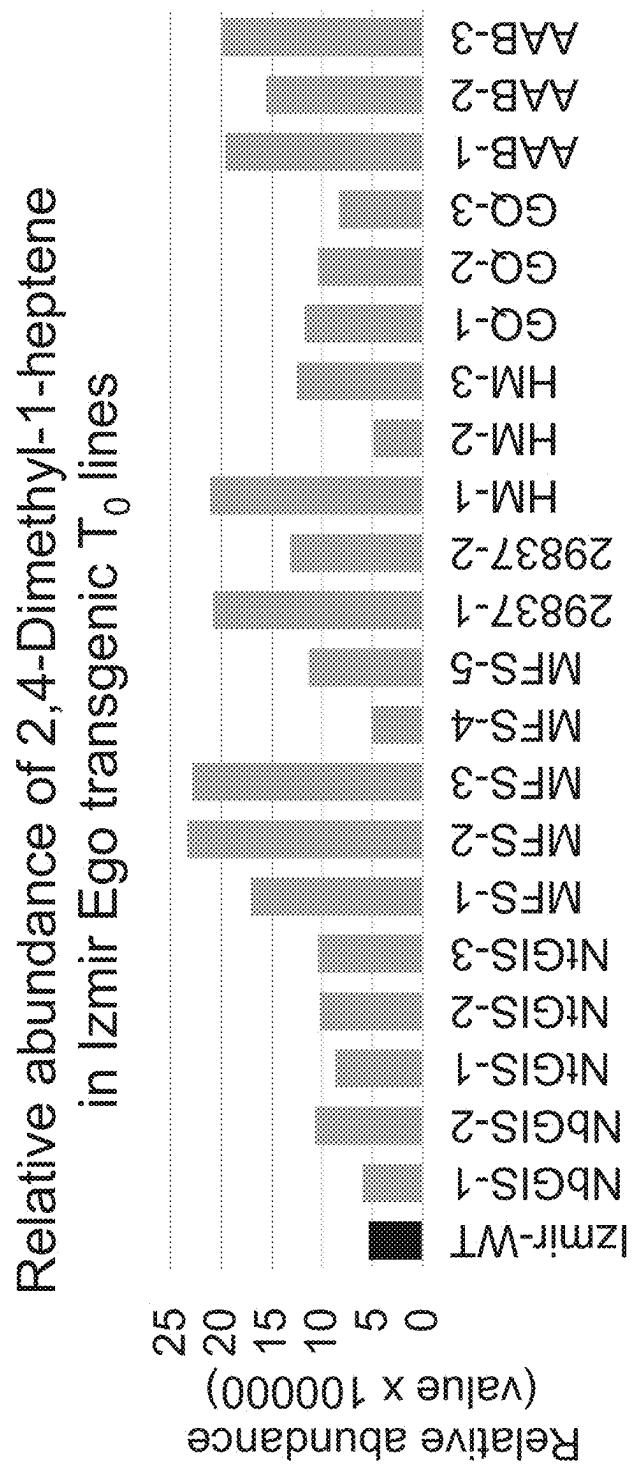


Figure 15

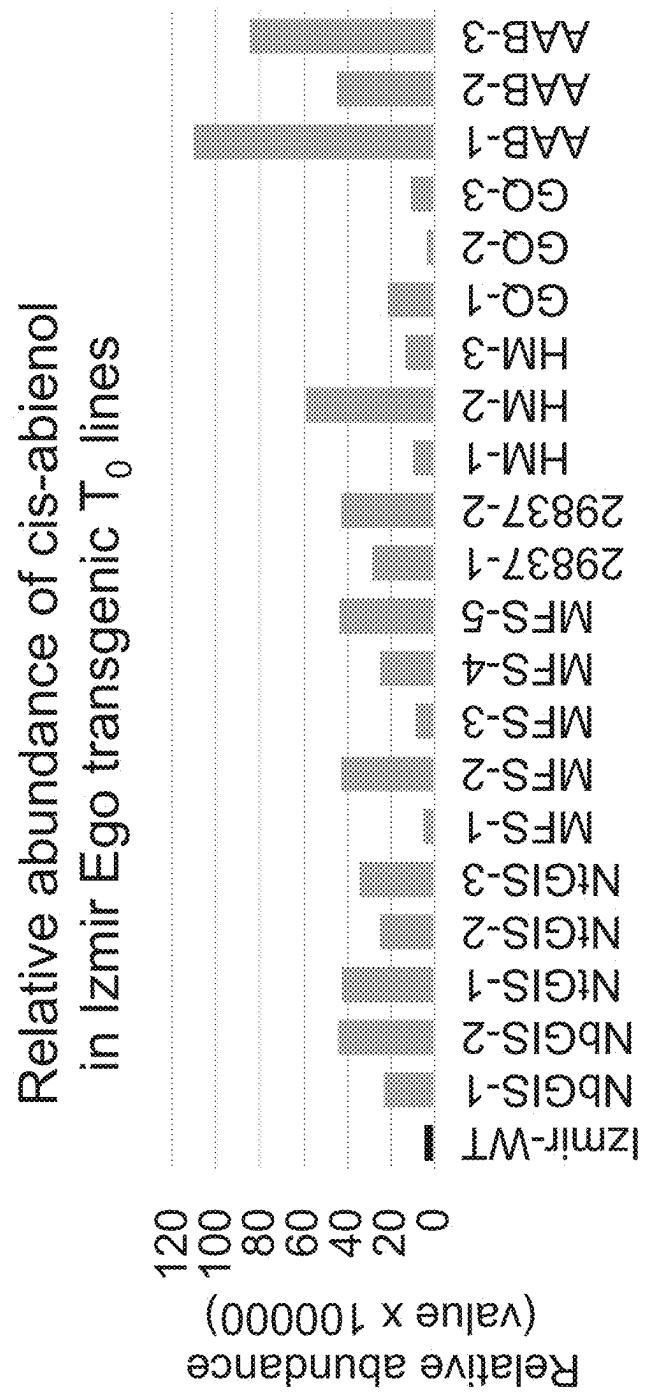


Figure 16

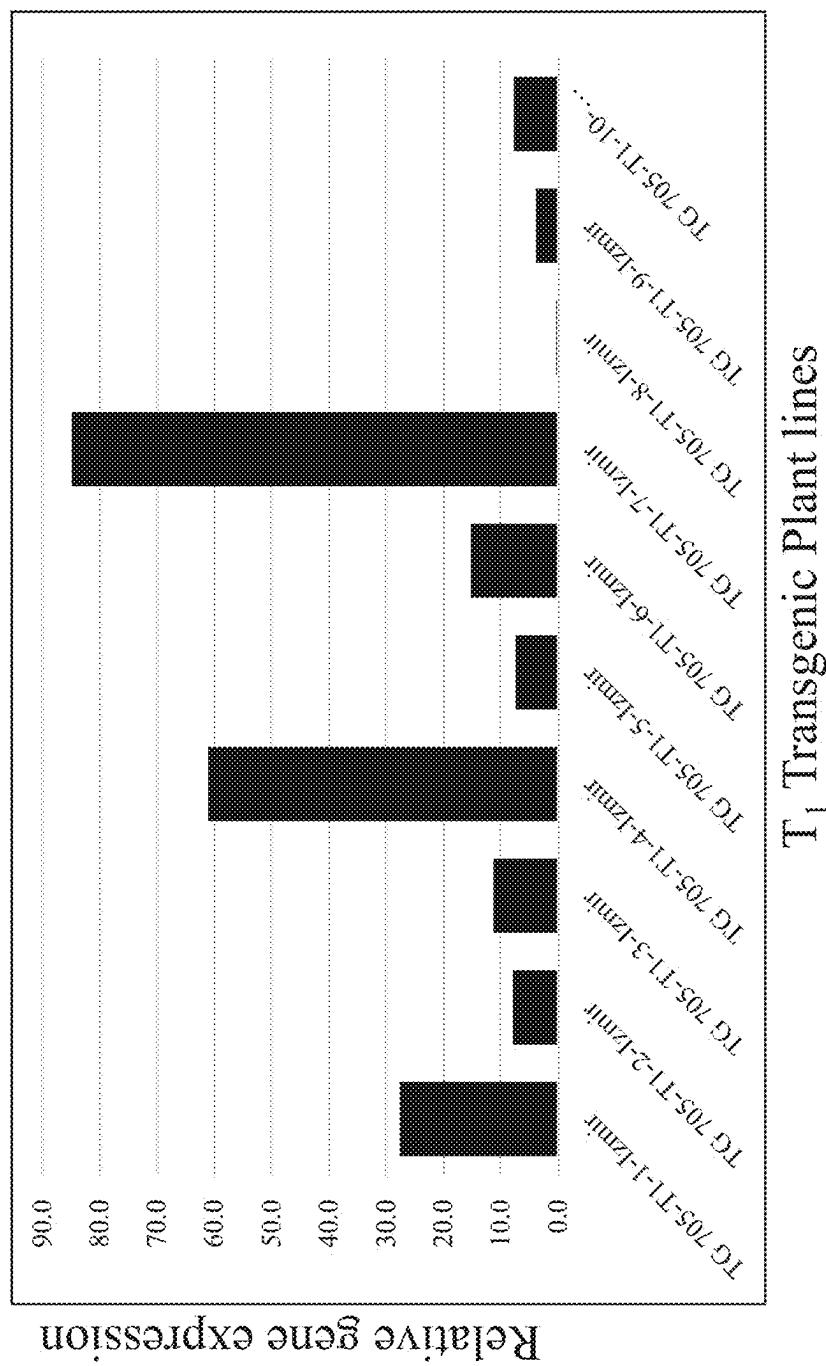
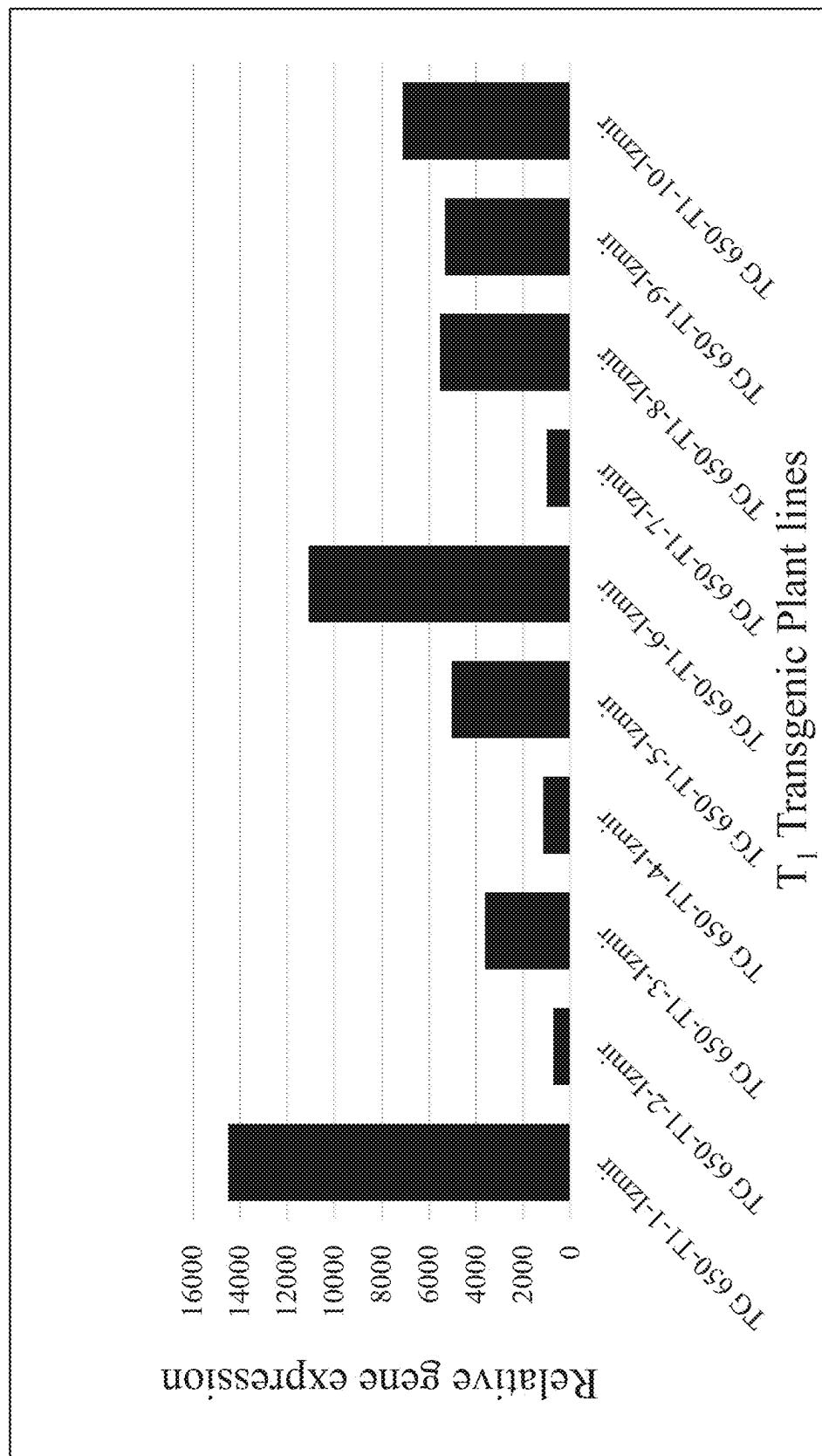


Figure 17



INCREASING TRICHOME DENSITY AND IMPROVING TRANSPORT OF METABOLITES IN PLANT TRICHOMES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation of U.S. patent application Ser. No. 17/591,057, filed Feb. 2, 2022, which claims the benefit of U.S. Provisional Patent Application No. 63/145,259, filed Feb. 3, 2021; U.S. Provisional Patent Application No. 63/145,262, filed Feb. 3, 2021; and U.S. Provisional Patent Application No. 63/145,263, filed Feb. 3, 2021, all of which are incorporated by reference herein in their entireties.

INCORPORATION OF SEQUENCE LISTING

[0002] A sequence listing contained in the file named "P35029US01_SL.xml" which is 147,545 bytes (measured in operating system MS-Windows®), created on May 5, 2025, containing a total number of 93 sequences, starting from SEQ ID NO: 1 to SEQ ID NO: 93, is filed electronically herewith and incorporated by reference in its entirety.

FIELD

[0003] The present disclosure relates to enhancing trichome initiation and development on the surface of plant tissues as well as improving the transport of specialized metabolites into trichomes, the exudation of specialized metabolites from trichomes, and the application of such to change the chemical composition in plants, including tobacco.

BACKGROUND

[0004] Glandular trichomes are epidermal outgrowths in plants that are the site of metabolic compound synthesis and storage. Their presence on stem, leaf, and floral tissues provides protection for plants against various biotic and abiotic stresses. Glandular trichomes also play a role in the biosynthesis, storage, and secretion of specialized or secondary metabolites.

[0005] Metabolites produced and secreted by glandular trichomes are often hydrophobic (e.g., fatty acid derivatives, flavonoids, terpenoids). Terpenoids constitute the largest and most diverse class of plant metabolites. The olefinic backbone of terpenoids is made of multiples of the five-carbon (C) isoprene unit, with the major groups being monoterpenes (10C), sesquiterpenes (15C), and diterpenes (20C). These terpenoids are produced through the condensation of five-carbon isoprene units (dimethylallyl diphosphate [DMAPP] and isopentenyl diphosphate [IPP]) most often by the sequential head-to-tail addition of DMAPP to IPP.

[0006] The amount of secondary metabolites produced is often tightly correlated to the glandular trichome density present on the plant epidermis (Chalvin et al., *Cell*, 25:477-487 (2020)). One way to increase the amount of secondary metabolite production in plants is to increase the density of trichomes present on the plant epidermis. Transcriptional regulation of trichome initiation has been shown to involve members of MYB and C2H2 zinc-finger family of transcription factors. Transgenic overexpression of *Artemisia annua* MYB1 (AaMYB1) was shown to increase trichome density and subsequently the production of artemisinin (Matias-Hernandez et al., *Plant Journal*, 90:520-534 (2017)).

[0007] Lipid transfer proteins (LTPs) are important in the transport of specialized metabolites in glandular trichomes. Studies have shown that overexpression of LTPs leads to an increase of exudates in plants glandular trichomes (Choi et al., *Plant Journal*, 70:480-491 (2012)).

[0008] Due to the important role of glandular trichomes in the biosynthesis and secretion of terpenoids, there is a need for a greater understanding of the genes, regulatory factors, and signaling mechanisms involved in the control of trichome initiation and development in plants. It is also important to understand the mode of secretion of these specialized metabolites into the cuticle of trichomes. In this disclosure, candidate genes are provided that can be used to modify trichome density in plants. Modification of trichrome density will also improve transport of specialized metabolites in glandular trichomes.

SUMMARY

[0009] In one aspect, this disclosure provides a modified plant, seed, or plant part, comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, wherein said nucleic acid sequence is operably linked to a heterologous promoter.

[0010] In one aspect, this disclosure provides cured tobacco material from a modified tobacco plant or tobacco plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence at encoding an amino acid sequence least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, wherein said nucleic acid sequence is operably linked to a heterologous promoter.

[0011] In one aspect, this disclosure provides a tobacco product comprising material from a modified tobacco plant, tobacco seed, or tobacco plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, wherein said nucleic acid sequence is operably linked to a heterologous promoter.

[0012] In one aspect, this disclosure provides a *cannabis* product comprising material from a modified *cannabis* plant, *cannabis* seed, or *cannabis* plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, wherein said nucleic acid sequence is operably linked to a heterologous promoter.

[0013] In one aspect, this disclosure provides a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, wherein said nucleic acid sequence is operably linked to a heterologous promoter.

[0014] In one aspect, this disclosure provides a method for producing a plant, the method comprising: (a) obtaining at least one plant comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence at least 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, wherein said nucleic acid sequence is operably linked to a heterologous promoter; (b) crossing said at least one plant with at least one plant of a second variety to produce at least one progeny seed; and (c) selecting said at least one progeny seed produced in step (b), or a plant germinated therefrom, wherein said at least one progeny seed or plant germinated therefrom comprises said recombinant nucleic acid molecule.

[0015] In one aspect, this disclosure provides a method of generating a modified plant, the method comprising: (a) introducing a recombinant nucleic acid molecule comprising a nucleic acid sequence at least 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, wherein said nucleic acid sequence is operably linked to a heterologous promoter, to at least one plant cell; (b) selecting at least one plant cell from step (a), wherein the at least one plant cell comprises the recombinant nucleic acid molecule; and (c) regenerating a modified plant from the at least one plant cell selected in step (b).

[0016] In one aspect, this disclosure provides a method comprising preparing a tobacco product using cured tobacco material from a modified tobacco plant or part therefrom, wherein the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprises a nucleic acid sequence at least 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, wherein said nucleic acid sequence is operably linked to a heterologous promoter, to at least one plant cell/

[0017] In one aspect, this disclosure provides a method comprising preparing a *cannabis* product using material from a modified *cannabis* plant or part therefrom, wherein the modified *cannabis* plant or part therefrom comprises a recombinant nucleic acid molecule comprises a nucleic acid sequence at least 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, wherein said nucleic acid sequence is operably linked to a heterologous promoter, to at least one plant cell.

[0018] In one aspect, this disclosure provides a method comprising transforming a plant cell with a recombinant nucleic acid molecule, wherein the recombinant nucleic acid molecule comprises a nucleic acid sequence at least 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, wherein said nucleic acid sequence is operably linked to a heterologous promoter, to at least one plant cell.

[0019] In one aspect, this disclosure provides a method for producing a plant with increased trichome density, the method comprising: (a) providing to at least one plant cell a recombinant nucleic acid comprising a heterologous promoter operably linked to a polynucleotide, where the polynucleotide encodes an amino acid sequence at least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33; (b) regenerating a modified plant from the at least one plant cell in step (a), where the modified plant comprises an increased trichome density on at least one leaf as compared to a leaf from a control plant lacking the recombinant nucleic acid when grown under comparable conditions.

BRIEF DESCRIPTION OF THE SEQUENCES

[0020] SEQ ID NOs: 1 to 12 are primers that can be used for the cloning of nucleic acid sequences described herein for expression in transgenic plants.

[0021] SEQ ID NOs: 13 to 17 are nucleic acids sequences corresponding to the coding sequences for tobacco genes of interest described herein, specifically NtMYB86, NtGIS, NbGIS, and NtLTP1.

[0022] SEQ ID NOs: 18 to 22 are amino acid sequences corresponding to the nucleic acid sequences of SEQ ID NOs: 13 to 17.

[0023] SEQ ID NOs: 23 to 27 are nucleic acid sequences corresponding to the genomic sequences for tobacco genes of interest described herein, specifically NtMYB86, NtGIS, NbGIS, and NtLTP1.

[0024] SEQ ID NOs: 28 to 30 are nucleic acid sequences corresponding to the coding sequences for *cannabis* genes of interest described herein, specifically MYB61, GIS3, and non-specific lipid transfer protein 1-like.

[0025] SEQ ID NOs: 31 to 33 are amino acid sequences corresponding to the nucleic acid sequences of SEQ ID NOs: 28 to 30.

[0026] SEQ ID NOs: 34 to 36 are nucleic acid sequences corresponding to the genomic sequences for *cannabis* genes of interest described herein, specifically MYB61, GIS3, and non-specific lipid transfer protein 1-like.

[0027] SEQ ID NOs: 37 is a nucleic acid sequence corresponding to the coding sequence for sweet wormwood (*Artemisia annua*) specifically MYB transcription factor.

[0028] SEQ ID NOs: 38 is an amino acid sequence corresponding to the nucleic acid sequence of SEQ ID NOs: 37.

[0029] SEQ ID NOs: 39 to 43 are nucleic acid sequences corresponding to the coding sequences for tobacco genes of interest described herein, specifically MFS, NMD, CBTS2a (HM), GGPPS2 and cis abienol synthase (ABS).

[0030] SEQ ID NOs: 44 to 48 are nucleic acid sequences corresponding to the genomic sequences for tobacco genes of interest described herein, specifically MFS, NMD, CBTS2a(HM), GGPPS2 and cis abienol synthase (ABS).

[0031] SEQ ID NOs: 49 to 53 are amino acid sequences corresponding to the nucleic acid sequences of SEQ ID NOs: 39 to 43.

[0032] SEQ ID NOs: 54 to 62 and 63 to 71 are nucleic acid sequences corresponding to coding sequences and genomic sequences, respectively, for tobacco LTP genes.

[0033] SEQ ID NOs: 72 to 80 are amino acid sequences corresponding to the nucleic acid sequences of SEQ ID NOs: 54 to 62. SEQ ID NO: 81 is a consensus LTP amino acid sequence. SEQ ID NOs: 82 to 91 are subsequences of SEQ ID NOs: 21 and 72 to 80 as shown in FIG. 9. SEQ ID NO: 92 is the consensus amino acid sequence shown in FIG. 9.

[0034] Table 1 provides nucleic acid sequences and amino acid sequences used in this disclosure.

TABLE 1

Sequences used in this disclosure		
SEQ ID NO	Sequence Description	Sequence Type
1	NtMYB86-Fwd	Nucleic acid
2	NtMYB86-Rev	Nucleic acid
3	Nb/NtGIS-Fwd	Nucleic acid
4	Nb/NtGIS-Rev	Nucleic acid
5	qNtMYB86-Fwd2	Nucleic acid
6	qNtMYB86-Rev2	Nucleic acid
7	qNbGIS-Fwd	Nucleic acid
8	qNbGIS-Rev	Nucleic acid
9	NtLTP1isoform1-Fwd	Nucleic acid
10	NtLTP1isoform1-Rev	Nucleic acid
11	NtLTP1isoform2-Fwd	Nucleic acid
12	NtLTP1isoform2-Rev	Nucleic acid
13	NtMYB86 (XM_016595116)	Nucleic acid, CDS
14	NtGIS (XM_016590730)	Nucleic acid, CDS
15	NbGIS (Niben101Ctg13716g00003)	Nucleic acid, CDS
16	NtLTP1isoform1 (AB625593)	Nucleic acid, CDS
17	NtLTP1isoform2 (XM_016578495)	Nucleic acid, CDS
18	NtMYB86 (XP_016450602)	Amino acid
19	NtGIS (XP_016446216)	Amino acid
20	NbGIS	Amino acid
21	NtLTP1isoform1 (BAK19150)	Amino acid
22	NtLTP1isoform2 (XP_016433981)	Amino acid
23	NtMYB86 (XM_016595116)	Nucleic acid, genomic
24	NtGIS (XM_016590730)	Nucleic acid, genomic
25	NbGIS (Niben101Ctg13716g00003)	Nucleic acid, genomic
26	NtLTP1isoform1 (AB625593)	Nucleic acid, genomic
27	NtLTP1isoform2 (XM_016578495)	Nucleic acid, genomic
28	MYB61 (<i>Cannabis sativa</i>)	Nucleic acid, CDS
29	Zinc finger protein GIS3 (<i>Cannabis sativa</i>)	Nucleic acid, CDS
30	Non-specific lipid-transfer protein 1-like (<i>Cannabis sativa</i>)	Nucleic acid, CDS
31	MYB61 (<i>Cannabis sativa</i>)	Amino acid
32	Zinc finger protein GIS3 (<i>Cannabis sativa</i>)	Amino acid
33	Non-specific lipid-transfer protein 1-like (<i>Cannabis sativa</i>)	Amino acid
34	MYB61 (<i>Cannabis sativa</i>)	Nucleic acid, genomic
35	Zinc finger protein GIS3 (<i>Cannabis sativa</i>)	Nucleic acid, genomic
36	Non-specific lipid-transfer protein 1-like (<i>Cannabis sativa</i>)	Nucleic acid, genomic
37	MYB transcription factor [<i>Artemesia annua</i>]	Nucleic acid, CDS
	KC118530.1	
38	MYB transcription factor [<i>Artemesia annua</i>]	Amino acid
	AGR40501.1	
39	Cytochrome P450_menthofuran synthase (g96188/MFS)	Nucleic acid, CDS
40	(+)-neomenthol dehydrogenase/ menthone_reductase_(NMD/g29837)	Nucleic acid, CDS
41	Cembratrienol synthase 2a (CBTS-2a/HM/g58533)	Nucleic acid, CDS
42	Geranylgeranyl diphosphate synthase (g49326/GGPPS2/GQ911584)	Nucleic acid, CDS
43	Cis-abienol synthase_Isoform 1 (g2330/AAB)	Nucleic acid, CDS
44	Cytochrome P450_menthofuran synthase (g96188/MFS)	Nucleic acid, genomic
45	(+)-neomenthol dehydrogenase/ menthone_reductase_(NMD/g29837)	Nucleic acid, genomic
46	Cembratrienol synthase 2a (CBTS-2a/HM/g58533)	Nucleic acid, genomic
47	Geranylgeranyl diphosphate synthase (g49326/GGPPS2/GQ911584)	Nucleic acid, genomic
48	Cis-abienol synthase_Isoform 1 (g2330/AAB)	Nucleic acid, genomic
49	Cytochrome P450_menthofuran synthase (g96188/MFS)	Amino acid
50	(+)-neomenthol dehydrogenase/ menthone_reductase_(NMD/g29837)	Amino acid
51	Cembratrienol synthase 2a (CBTS-2a/HM/g58533)	Amino acid
52	Geranylgeranyl diphosphate synthase (g49326/GGPPS2/GQ911584)	Amino acid
53	Cis-abienol synthase_Isoform 1 (g2330/AAB)	Amino acid
54	XM_016601333.1 (XP_016456819.1)	Nucleic acid, CDS
55	XM_016596613.1 (XP_016452099.1)	Nucleic acid, CDS
56	XM_016641408.1 (XP_016496894.1)	Nucleic acid, CDS
57	XM_016607671.1 (XP_016463157.1)	Nucleic acid, CDS
58	XM_016648588.1 (XP_016504074.1)	Nucleic acid, CDS
59	XM_016657701.1 (XP_016513187.1)	Nucleic acid, CDS
60	LTP4 (AB625595.1)	Nucleic acid, CDS
61	LTP3 (AB625594.1)	Nucleic acid, CDS
62	LTP2 (AB518680.1)	Nucleic acid, CDS
63	XM_016601333.1 (XP_016456819.1)	Nucleic acid, genomic
64	XM_016596613.1 (XP_016452099.1)	Nucleic acid, genomic
65	XM_016641408.1 (XP_016496894.1)	Nucleic acid, genomic

TABLE 1-continued

Sequences used in this disclosure		
SEQ ID NO	Sequence Description	Sequence Type
66	XM_016607671.1 (XP_016463157.1)	Nucleic acid, genomic
67	XM_016648588.1 (XP_016504074.1)	Nucleic acid, genomic
68	XM_016657701.1 (XP_016513187.1)	Nucleic acid, genomic
69	LTP4 (AB625595.1)	Nucleic acid, genomic
70	LTP3 (AB625594.1)	Nucleic acid, genomic
71	LTP2 (AB518680.1)	Nucleic acid, genomic
72	XP_016456819.1	Amino acid
73	XP_016452099.1	Amino acid
74	XP_016496894.1	Amino acid
75	XP_016463157.1	Amino acid
76	XP_016504074.1	Amino acid
77	XP_016513187.1	Amino acid
78	LTP4 (BAK19152)	Amino acid
79	LTP3 (BAK19151)	Amino acid
80	LTP2 (BAJ25798)	Amino acid
81	LTP Consensus sequence	Amino acid
82	XP_016456819.1 FIG. 9 sequence	Amino acid
83	XP_016452099.1 FIG. 9 sequence	Amino acid
84	XP_016496894.1 FIG. 9 sequence	Amino acid
85	XP_016463157.1 FIG. 9 sequence	Amino acid
86	XP_016504074.1 FIG. 9 sequence	Amino acid
87	XP_016513187.1 FIG. 9 sequence	Amino acid
88	LPT4_BAK19152 FIG. 9 sequence	Amino acid
89	LTP3_BAK19151 FIG. 9 sequence	Amino acid
90	LPT2_BAJ25798 FIG. 9 sequence	Amino acid
91	LTP1_BAK19150 FIG. 9 sequence	Amino acid
92	LTP Consensus FIG. 9 sequence	Amino acid
93	FIG. 8B consensus sequence	Amino acid

BRIEF DESCRIPTION OF THE DRAWINGS

[0035] FIG. 1 comprises Panels A, B, and C. Panel A depicts glandular trichomes in *Nicotiana benthamiana*. Panel B depicts glandular trichomes in *Nicotiana tabacum* variety 'TN90', and Panel C depicts glandular trichomes in *Nicotiana tabacum* variety 'Izmir Ego'.

[0036] FIG. 2 depicts the expression vector used for tobacco transformation.

[0037] FIG. 3 comprises panels FIG. 3A and FIG. 3B. FIG. 3A depicts a phylogenetic analysis of the DNA-binding domain of the MYB transcription factor family in tobacco plants (N=319). FIG. 3B depicts protein sequence pairwise alignment of the tobacco MYB86 gene (SEQ ID NO: 18, XP_016450602) and sweet wormwood (*Artemisia annua*) MYB (SEQ ID NO: 38, AGR40501.1), highlighting the R2 and R3 DNA-binding domains (enclosed in boxes) specifically. The filled circle indicates MYB86 on the cladogram. The scale bar in FIG. 3A represents evolutionary distance used to infer the phylogenetic tree.

[0038] FIG. 4 depicts a phylogenetic analysis of the Glabrous Inflorescence Stems (GIS) family of C2H2 transcription factors in tobacco plants (N=247). The filled circle indicates NtGIS gene (SEQ ID NO: 19) on the cladogram. The scale bar represents evolutionary distance used to infer the phylogenetic tree.

[0039] FIG. 5 comprises Panels A, B, C, and D. Panel A depicts glandular trichome density in the abaxial leaf midvein of wild-type (WT) TN90. Panel B depicts glandular trichome density in the abaxial midvein of TN90 overexpressing NtMYB86 (SEQ ID NO: 13) under the control of a CaMV 35S promoter, demonstrating an increase in glandular trichrome density compared to wild-type TN90. An abaxial view of the leaf pedicle of wild-type (WT) *N. benthamiana* is shown in Panel C. Panel D depicts an

increase in glandular trichrome density in *N. benthamiana* overexpressing NtMYB86 under the control of a CaMV 35S promoter as compared to wild-type (Panel C). Images are light micrographs shown at 10 \times magnification.

[0040] FIG. 6 comprises Panel A and Panel B. Panel A depicts the glandular trichome density in the main vegetative stem of wild-type (WT) *Nicotiana benthamiana*. Panel B depicts the glandular trichome density in the main vegetative stem of *N. benthamiana* overexpressing NtMYB86 (SEQ ID NO: 18). Images are light micrographs shown at 160 \times magnification.

[0041] FIG. 7 comprises panels FIG. 7A and FIG. 7B. FIG. 7A depicts the light micrographs of glandular trichome density of a tobacco leaf overexpressing NtMYB86 (SEQ ID NO: 18) (b), NtGIS (SEQ ID NO: 19) (c), and NbGIS (SEQ ID NO: 20) (c) in Izmir Ego background compared to a wild-type *Nicotiana tabacum* variety Izmir Ego (a). Images are shown at 70 \times magnification with scale bar representing 1 mm. FIG. 7B depicts leaf trichome counts of Izmir Ego WT, Izmir Ego T₀ transgenic lines overexpressing NtMYB86 (SEQ ID NO: 18), NtGIS (SEQ ID NO: 19), and NbGIS (SEQ ID NO: 20).

[0042] FIG. 8 comprises panels FIG. 8A and FIG. 8B. FIG. 8A depicts a phylogenetic analysis of the LTP gene family, and the position of the NtLTP1 gene is marked by a filled circle. Publicly available GenBank Accession numbers are provided for each LTP gene family member. FIG. 8B depicts a sequence alignment and gene structure comparison in tobacco plants of two NtLTP1 isoforms (SEQ ID NOS: 21, 22, and 93, respectively, in order of appearance).

[0043] FIG. 9 depicts the conserved motifs of a representative number of NtLTP of the 76 that were identified in the *Nicotiana tabacum* genome following ClustalW multiple

sequence alignment algorithm. Six conserved cysteine residues (enclosed in boxes) are notably conserved in >90% of the NtLTPs identified.

[0044] FIG. 10 depicts the relative gene expression of NtMYB86 (SEQ ID NO: 14) in nine independent Izmir Ego transgenic lines in the T₀ generation. The relative gene expression was quantified following the 2^{(-ΔΔC(t))} method. See Livak and Schmittgen, *Methods*, 25:402-408 (2001) for information regarding the 2^{(-ΔΔC(t))} method. Expression of NtMYB86 in a wildtype control Izmir Ego plant is used as a baseline (e.g., wildtype expression is set to 1), and is not shown.

[0045] FIG. 11 depicts the relative gene expression of NtGIS (SEQ ID NO: 16) in eight independent Izmir Ego transgenic lines in the T₀ generation. The relative gene expression was quantified following the 2^{-ΔΔCT} method. Expression of NtGIS in a wildtype control Izmir Ego plant is used as a baseline (e.g., wildtype expression is set to 1), and is not shown.

[0046] FIG. 12 depicts the relative abundance of duvatrienediol in leaves of T₀ Izmir Ego transgenic lines overexpressing NbGIS (SEQ ID NO: 20), NtGIS (SEQ ID NO: 19), NtMFS (SEQ ID NO: 39), NtNMD (29837; SEQ ID NO: 40), *Nicotiana sylvestris* cembratrienol synthase 2a (HM; SEQ ID NO: 41), geranylgeranyl diphosphate synthase (GQ; SEQ ID NO: 42), and cis-abienol synthase (AAB; SEQ ID NO: 43).

[0047] FIG. 13 depicts the relative abundance of neophytadiene in leaves of T₀ Izmir Ego transgenic lines overexpressing NbGIS (SEQ ID NO: 20), NtGIS (SEQ ID NO: 19), NtMFS (SEQ ID NO: 39), NtNMD (29837; SEQ ID NO: 40), *Nicotiana sylvestris* cembratrienol synthase 2a (HM; SEQ ID NO: 41), geranylgeranyl diphosphate synthase (GQ; SEQ ID NO: 42), and cis-abienol synthase (AAB; SEQ ID NO: 43).

[0048] FIG. 14 depicts the relative abundance of 2,4-Dimethyl-1-heptene in leaves of T₀ Izmir Ego transgenic lines overexpressing NbGIS (SEQ ID NO: 20), NtGIS (SEQ ID NO: 19), NtMFS (SEQ ID NO: 39), NtNMD (29837; SEQ ID NO: 40), *Nicotiana sylvestris* cembratrienol synthase 2a (HM; SEQ ID NO: 41), geranylgeranyl diphosphate synthase (GQ; SEQ ID NO: 42), and cis-abienol synthase (AAB; SEQ ID NO: 43).

[0049] FIG. 15 depicts the relative abundance of cis-abienol in leaves of T₀ Izmir Ego transgenic lines overexpressing NbGIS (SEQ ID NO: 20), NtGIS (SEQ ID NO: 19), NtMFS (SEQ ID NO: 39), NtNMD (29837; SEQ ID NO: 40), *Nicotiana sylvestris* cembratrienol synthase 2a (HM; SEQ ID NO: 41), geranylgeranyl diphosphate synthase (GQ; SEQ ID NO: 42), and cis-abienol synthase (AAB; SEQ ID NO: 43).

[0050] FIG. 16 depicts the relative gene expression levels of NtMYB86 (SEQ ID NO: 13) under control of a CaMV 35S promoter in T₁ transgenic tobacco lines in the Izmir Ego variety.

[0051] FIG. 17 depicts the relative gene expression levels of NbGIS (SEQ ID NO: 15) under control of a CaMV 35S promoter in T₁ transgenic tobacco lines in the Izmir Ego variety.

DETAILED DESCRIPTION

[0052] Unless defined otherwise, all technical and scientific terms used have the same meaning as commonly understood by one of ordinary skill in the art to which this

disclosure belongs. Where a term is provided in the singular, the inventors also contemplate aspects of the disclosure described by the plural of that term. Where there are discrepancies in terms and definitions used in references that are incorporated by reference, the terms used in this application shall have the definitions given herein. Other technical terms used have their ordinary meaning in the art in which they are used, as exemplified by various art-specific dictionaries, for example, "The American Heritage® Science Dictionary" (Editors of the American Heritage Dictionaries, 2011, Houghton Mifflin Harcourt, Boston and New York), the "McGraw-Hill Dictionary of Scientific and Technical Terms" (6th edition, 2002, McGraw-Hill, New York), or the "Oxford Dictionary of Biology" (6th edition, 2008, Oxford University Press, Oxford and New York).

[0053] Any references cited herein, including, e.g., all patents, published patent applications, and non-patent publications, are incorporated herein by reference in their entirety.

[0054] When a grouping of alternatives is presented, any and all combinations of the members that make up that grouping of alternatives is specifically envisioned. For example, if an item is selected from a group consisting of A, B, C, and D, the inventors specifically envision each alternative individually (e.g., A alone, B alone, etc.), as well as combinations such as A, B, and D; A and C; B and C; etc. The term "and/or" when used in a list of two or more items means any one of the listed items by itself or in combination with any one or more of the other listed items. For example, the expression "A and/or B" is intended to mean either or both of A and B—i.e., A alone, B alone, or A and B in combination. The expression "A, B and/or C" is intended to mean A alone, B alone, C alone, A and B in combination, A and C in combination, B and C in combination, or A, B, and C in combination.

[0055] When a range of numbers is provided herein, the range is understood to inclusive of the edges of the range as well as any number between the defined edges of the range. For example, "between 1 and 10" includes any number between 1 and 10, as well as the number 1 and the number 10.

[0056] When the term "about" is used in reference to a number, it is understood to mean plus or minus 10%. For example, "about 100" would include from 90 to 110.

[0057] As used herein, the singular form "a," "an," and "the" include plural references unless the context clearly dictates otherwise. For example, the term "a compound" or "at least one compound" may include a plurality of compounds, including mixtures thereof.

[0058] Any tobacco plant, or part thereof, provided herein is specifically envisioned for use with any method provided herein. Similarly, any modified tobacco plant, or part thereof, is specifically envisioned for use with any method provided herein. Any nucleic acid sequence, amino acid sequence, or other composition provided herein is specifically envisioned for use with any method provided herein.

[0059] Any *cannabis* plant, or part thereof, provided herein is specifically envisioned for use with any method provided herein. Similarly, any modified *cannabis* plant, or part thereof, is specifically envisioned for use with any method provided herein. Any nucleic acid sequence, amino acid sequence, or other composition provided herein is specifically envisioned for use with any method provided herein.

[0060] Trichomes, in general, are hair-like epidermal outgrowths covering most aerial plant tissues. Trichomes tend to be multicellular, but unicellular trichomes are known as well. Multiple types of trichomes can be found on an individual plant, and trichomes vary in shape, size, and cellular organization. An individual trichome can be classified as a glandular trichome or a non-glandular trichome.

[0061] Glandular trichomes (see FIG. 1) are characterized by the presence of a head made of cells that can secrete or store large quantities of specialized metabolites (e.g., terpenes). Within the group of glandular trichomes, a trichome can be further characterized as being peltate or capitate. A capitate glandular trichome typically possesses a stalk with a length that is more than twice the height of the head, and the number of cells in the trichome is highly variable. A peltate trichome is a short-stalked trichome with a large head made of between four and eighteen cells arranged in one or two concentric circles.

[0062] In an aspect, a trichome is a glandular trichome. In an aspect, a glandular trichome is a capitate glandular trichome. In an aspect, a glandular trichome is a peltate glandular trichome. In an aspect, a glandular trichome is selected from the group consisting of a capitate glandular trichome and a peltate glandular trichome.

[0063] In an aspect, glandular trichome initiation and development is regulated by several transcription factors including, but not limited to, genes belonging to MYB and C2H2 transcription factor gene families.

[0064] In an aspect, this disclosure provides a modified plant, seed, or plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide operably linked to a heterologous promoter for the initiation and development of trichome to improve its density. In another aspect, this disclosure provides a modified plant, seed, or plant part comprising a nucleic acid sequence encoding a polypeptide operably linked to a heterologous promoter for improving secretion of metabolites to the trichome cuticles. In a further aspect, a modified plant, seed, or plant part is a plant, seed or plant part of the *Nicotiana* genus. In a further aspect, a modified plant, seed, or plant part is a plant, seed or plant part of the *Cannabis* genus.

Transcription Factors Regulation of Trichome Initiation

[0065] Transcription factors are known regulators of various biological processes involved in plants growth and development. Several transcription factors have been identified as regulators of glandular trichome initiation. These include, but are not limited to, the transcription factors gene families R2R3-MYB, HD-ZIP IV, MYC, and C2H2 (Chavlin et al., 2020). Overexpression of MYB1 (AaMYB1) in *Artemisia annua* significantly increase production of a sesquiterpene lactone, artemisinin, as well as increased trichome density (Matias-Hernandez et al., 2017). Another transcription factor that regulates trichome development as well as terpene biosynthesis is MYC1, a basic helix-loop-helix (bHLH). Knockdown of MYC1 (SiMYC1) in tomato led to significant reduction in monoterpenes as well as the ectopic development of smaller Type VI glandular trichomes at low densities (Xu et al., *Plant Cell*, 30:2988-3005 (2018)). A transcription factor belonging to the C2H2 gene family is also involved in the regulation of trichome development in tobacco. Overexpression of GIS in *Nicotiana benthamiana*

(NbGIS) resulted in the increase of glandular trichome density in transgenic lines (Liu et al., *Plant Molecular Biology*, 98:153-167 (2018)).

Storage and Transportation of Metabolites in Glandular Trichome

[0066] Glandular trichomes produce large amount of metabolites which can account for up to 20% of leaf dry weight (Tissier et al., *Trends in Plant Science*, 22:930-938 (2017)). Trichomes develop morphological features enabling the storage of secondary metabolites. The type, shape, and size of these morphological features depends on the type of glandular trichomes. Nonvolatile compounds, including diterpenoids, are typically produced by capitate glandular trichomes and directly secreted from the tip of the trichome while glandular trichomes that produce volatile compounds have dedicated structures for secretion and storage (Tissier et al., 2017). Transport of hydrophobic molecules in trichomes requires transporters and lipid transfer proteins (LTPs) that facilitate movement of volatile organic compounds to across hydrophilic cell walls and to prevent VOC repartitioning into the plasma membrane (Tissier et al., 2017). LTPs are small (about 10 kDa), soluble proteins that are characterized by a highly conserved cysteine-rich motif (Salminen et al., *Planta*, 244:971-997 (2016)). See FIG. 10. LTPs are involved in various functions during plant growth and development including, but not limited to, cuticular wax accumulation, pollen and seed development, and cell expansion (Salminen et al., 2016). The trichome-specific NtLTP1 was reported to increase secretion in trichome exudates in tobacco plants as well increasing protection against insect pests when overexpressed (Choi et al., 2012).

Plants

[0067] In an aspect, a plant provided herein is a modified plant. In an aspect, a seed provided herein is a modified seed. In an aspect, a plant part provided herein is a modified plant part. As used herein, "modified," in the context of a plant, seed, or plant part, refers to a plant, seed, or plant part, comprising a genetic alteration introduced for certain purposes and beyond natural polymorphisms. Without being limiting, a modified plant, seed, or plant part comprises a recombinant nucleic acid molecule. In another aspect, a modified plant, seed, or plant part comprises a genetic modification. In an aspect, a modified plant, seed, or plant part is a transgenic plant, seed, or plant part.

[0068] In an aspect, this disclosure provides a modified plant, seed, or plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, where the nucleic acid sequence is operably linked to a heterologous promoter. In an aspect, this disclosure provides a modified plant, seed, or plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 85% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, where the nucleic acid sequence is operably linked to a heterologous promoter. In an aspect, this disclosure provides a modified plant, seed, or plant part comprising a recombinant nucleic acid molecule comprising

a nucleic acid sequence encoding an amino acid sequence at least 90% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, where the nucleic acid sequence is operably linked to a heterologous promoter. In an aspect, this disclosure provides a modified plant, seed, or plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 95% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, where the nucleic acid sequence is operably linked to a heterologous promoter. In an aspect, this disclosure provides a modified plant, seed, or plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 96% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, where the nucleic acid sequence is operably linked to a heterologous promoter. In an aspect, this disclosure provides a modified plant, seed, or plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 97% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, where the nucleic acid sequence is operably linked to a heterologous promoter. In an aspect, this disclosure provides a modified plant, seed, or plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 98% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, where the nucleic acid sequence is operably linked to a heterologous promoter. In an aspect, this disclosure provides a modified plant, seed, or plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 99% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, where the nucleic acid sequence is operably linked to a heterologous promoter. In an aspect, this disclosure provides a modified plant, seed, or plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 99.9% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, where the nucleic acid sequence is operably linked to a heterologous promoter. In an aspect, this disclosure provides a modified plant, seed, or plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence 100% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, where the nucleic acid sequence is operably linked to a heterologous promoter.

[0069] In an aspect, this disclosure provides a modified plant, seed, or plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 72-81, where the nucleic acid sequence is operably linked to a heterologous promoter.

[0071] In an aspect, this disclosure provides a modified plant, seed, or plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99%, or 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 54-71, where the nucleic acid sequence is operably linked to a heterologous promoter.

[0072] In an aspect, at least one leaf of a modified plant comprises a greater average trichome density as compared to a leaf of a control plant grown under comparable conditions. In an aspect, at least one leaf of a modified plant comprises a greater average trichome density on the abaxial side of the leaf as compared to the abaxial side of a leaf of a control plant grown under comparable conditions. In an aspect, at least one leaf of a modified plant comprises a greater average trichome density on the adaxial side of the leaf as compared to the adaxial side of a leaf of a control plant grown under comparable conditions.

[0073] In an aspect, at least two leaves of a modified plant comprise a greater average trichome density as compared to two leaves of a control plant grown under comparable conditions. In an aspect, a majority of the leaves of a modified plant comprise a greater average trichome density as compared to the same number of leaves of a control plant grown under comparable conditions. In an aspect, all of the leaves of a modified plant comprise a greater average trichome density as compared to all of the leaves of a control plant grown under comparable conditions.

[0074] In an aspect, at least one stem of a modified plant comprises a greater average trichome density as compared to a stem of a control plant grown under comparable conditions. In an aspect, at least one flower of a modified plant comprises a greater average trichome density as compared to a flower of a control plant grown under comparable conditions. In an aspect, at least one root of a modified plant comprises a greater average trichome density as compared to a root of a control plant grown under comparable conditions.

[0075] In an aspect, a modified plant comprises a greater average density of glandular trichomes as compared to a control plant. In an aspect, a modified plant comprises a greater average density of non-glandular trichomes as compared to a control plant.

[0076] In an aspect, a leaf of a modified tobacco plant comprises at least 70 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises at least 75 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises at least 80 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises at least 85 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises at least 90 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises at least 95 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises at least 100 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises at least 105 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises at least 110 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises at least 115 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises at least 120 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant

comprises at least 125 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises at least 130 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises at least 140 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises at least 150 trichomes per square centimeter.

[0077] In an aspect, a leaf of a modified tobacco plant comprises between 60 and 200 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 60 and 190 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 60 and 180 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 60 and 170 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 60 and 160 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 60 and 150 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 60 and 140 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 60 and 130 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 60 and 120 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 60 and 110 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 60 and 100 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 60 and 90 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 60 and 80 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 60 and 70 trichomes per square centimeter.

[0078] In an aspect, a leaf of a modified tobacco plant comprises between 80 and 130 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 80 and 120 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 80 and 100 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 75 and 140 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 75 and 130 trichomes per square centimeter. In an aspect, a leaf of a modified tobacco plant comprises between 75 and 125 trichomes per square centimeter.

[0079] In an aspect, a leaf of a modified tobacco plant comprises at least 1% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 5% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 10% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 15% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant

comprises at least 20% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 25% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 30% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 40% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 50% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 60% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 70% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 80% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 90% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 100% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 110% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 125% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 150% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions. In an aspect, a leaf of a modified tobacco plant comprises at least 200% more trichomes per square centimeter as compared to a control leaf of the same age when grown under comparable conditions.

[0080] It will be understood that, unless otherwise specified, a comparison between a modified leaf and a leaf from a control plant grown under comparable conditions must use leaves that are of the same leaf number (e.g., a modified V5 leaf must be compared to a control V5 leaf) on the modified and control plants.

[0081] In an aspect, a plant is a tobacco plant. In an aspect, a plant is a *Nicotiana* plant. In an aspect, a tobacco plant is a *Nicotiana tabacum* plant.

[0082] In an aspect, a *Nicotiana* plant, seed, or plant part is selected from the group consisting of *Nicotiana tabacum*, *Nicotiana amplexicaulis* PI 271989; *Nicotiana benthamiana* PI 555478; *Nicotiana bigelovii* PI 555485; *Nicotiana debneyi*; *Nicotiana excelsior* PI 224063; *Nicotiana glutinosa* PI 555507; *Nicotiana goodspeedii* PI 241012; *Nicotiana gossei*

PI 230953; *Nicotiana hesperis* PI 271991; *Nicotiana knightiana* PI 555527; *Nicotiana maritima* PI 555535; *Nicotiana megalosiphon* PI 555536; *Nicotiana nudicaulis* PI 555540; *Nicotiana paniculata* PI 555545; *Nicotiana plumbaginifolia* PI 555548; *Nicotiana repanda* PI 555552; *Nicotiana rustica*; *Nicotiana suaveolens* PI 230960; *Nicotiana sylvestris* PI 555569; *Nicotiana tomentosa* PI 266379; *Nicotiana tomentosiformis*; and *Nicotiana trigonophylla* PI 555572.

[0083] In an aspect, a seed is a tobacco seed. In an aspect, a seed is a *Nicotiana* seed. In an aspect, a tobacco seed is a *Nicotiana tabacum* or *Nicotiana benthamiana* seed.

[0084] In an aspect, a plant part is a tobacco plant part. In an aspect, a plant part is a *Nicotiana* plant part. In an aspect, a tobacco plant part is a *Nicotiana tabacum* plant part or a *Nicotiana benthamiana* plant part.

[0085] In an aspect, a plant is a *cannabis* plant. In an aspect, a plant is a *Cannabis* plant. In an aspect, a *cannabis* plant is a *Cannabis sativa* plant. In an aspect, a *cannabis* plant is a *Cannabis indica* plant. In an aspect, a *cannabis* plant is a *Cannabis ruderalis* plant. In an aspect, a *cannabis* plant is selected from the group consisting of *Cannabis sativa*, *Cannabis indica*, and *Cannabis ruderalis*.

[0086] In an aspect, a seed is a *cannabis* seed. In an aspect, a seed is a *Cannabis* seed. In an aspect, a *cannabis* seed is a *Cannabis sativa* seed. In an aspect, a *cannabis* seed is a *Cannabis indica* seed. In an aspect, a *cannabis* seed is a *Cannabis ruderalis* seed. In an aspect, a *cannabis* seed is selected from the group consisting of *Cannabis sativa*, *Cannabis indica*, and *Cannabis ruderalis*.

[0087] In an aspect, a plant part is a *cannabis* plant part. In an aspect, a plant part is a *Cannabis* plant part. In an aspect, a *cannabis* plant part is a *Cannabis sativa* plant part. In an aspect, a *cannabis* plant part is a *Cannabis indica* plant part. In an aspect, a *cannabis* plant part is a *Cannabis ruderalis* plant part. In an aspect, a *cannabis* plant part is selected from the group consisting of *Cannabis sativa*, *Cannabis indica*, and *Cannabis ruderalis*.

[0088] In an aspect, a plant part provided includes, but is not limited to, a leaf, a stem, a root, a trichome, a seed, a flower, pollen, an anther, an ovule, a pedicel, a fruit, a meristem, a cotyledon, a hypocotyl, a pod, an embryo, endosperm, an explant, a callus, a tissue culture, a shoot, a cell, and a protoplast. In an aspect, a plant part does not include a seed. In an aspect, this disclosure provides plant cells, tissues, and organs that are not reproductive material and do not mediate the natural reproduction of the plant. In another aspect, this disclosure also provides plant cells, tissues, and organs that are reproductive material and mediate the natural reproduction of the plant. In another aspect, this disclosure provides plant cells, tissues, and organs that cannot maintain themselves via photosynthesis. In another aspect, this disclosure provides somatic plant cells. Somatic cells, contrary to germline cells, do not mediate plant reproduction.

[0089] Cells, tissues and organs can be from seed, fruit, leaf, cotyledon, hypocotyl, meristem, embryos, endosperm, root, shoot, stem, trichome, pod, flower, inflorescence, stalk, pedicel, style, stigma, receptacle, petal, sepal, pollen, anther, filament, ovary, ovule, pericarp, phloem, vascular tissue. In another aspect, this disclosure provides a plant chloroplast. In a further aspect, this disclosure provides epidermal cells, stomata cell, leaf or root hairs, a storage root, or a tuber. In another aspect, this disclosure provides a tobacco protoplast.

[0090] Skilled artisans understand that tobacco and *cannabis* plants naturally reproduce via seeds, not via asexual reproduction or vegetative propagation. In an aspect, this disclosure provides plant endosperm.

[0091] This disclosure provides cells from plants provided herein.

[0092] As used herein, a “progeny plant” or “progeny seed” can be from any filial generation, e.g., F₁, F₂, F₃, F₄, F₅, F₆, F₇, etc.

[0093] In an aspect, a tobacco plant, seed, or plant part, is of a tobacco variety selected from the group consisting of a flue-cured variety, a bright variety, a Burley variety, a Virginia variety, a Maryland variety, a dark variety, a Galpão variety, an Oriental variety, and a Turkish variety.

[0094] In an aspect, a tobacco cell is of a tobacco variety selected from the group consisting of a flue cured variety, a bright variety, a Burley variety, a Virginia variety, a Maryland variety, a dark variety, a Galpão variety, an Oriental variety, and a Turkish variety.

[0095] In an aspect, a tobacco leaf is of a tobacco variety selected from the group consisting of a flue cured variety, a bright variety, a Burley variety, a Virginia variety, a Maryland variety, a dark variety, a Galpão variety, an Oriental variety, and a Turkish variety.

[0096] In an aspect, a cured tobacco leaf or plant part is of a tobacco variety selected from the group consisting of a flue cured variety, a bright variety, a Burley variety, a Virginia variety, a Maryland variety, a dark variety, a Galpão variety, an Oriental variety, and a Turkish variety. Skilled artisans further understand that cured tobacco does not constitute a living organism and is not capable of growth or reproduction.

[0097] Flue-cured tobaccos (also called “Virginia” or “bright” tobaccos) amount to approximately 40% of world tobacco production. Flue-cured tobaccos are often also referred to as “bright tobacco” because of the golden-yellow to deep-orange color it reaches during curing. Flue-cured tobaccos have a light, bright aroma and taste. Flue-cured tobaccos are generally high in sugar and low in oils. Major flue-cured tobacco growing countries are Argentina, Brazil, China, India, Tanzania and the United States of America. In one aspect, tobacco plants, seeds, or plant parts provided herein are of a flue-cured tobacco variety selected from the group consisting of the varieties listed in Table 2, and any variety essentially derived from any one of the foregoing varieties. See WO 2004/041006 A1. In a further aspect, tobacco plants, seeds, or plant parts provided herein are in a flue-cured variety selected from the group consisting of K326, K346, and NC196.

TABLE 2

Flue-cured Tobacco Varieties
400 (TC 225)
401 (TC 226)
401 Cherry Red (TC 227)
401 Cherry Red Free (TC 228)
Cash (TC 250)
Cash (TI 278)
CC 101
CC 1063
CC 13
CC 143
CC 200
CC 27
CC 301
CC 33

TABLE 2-continued

Flue-cured Tobacco Varieties
CC 35
CC 37
CC 400
CC 500
CC 600
CC 65
CC 67
CC 700
CC 800
CC 900
Coker 139 (TC 259)
Coker 139 yb1, yb2
Coker 140 (TC 260)
Coker 176 (TC 262)
Coker 187 (TC 263)
Coker 187-Hicks (TC 265)
Coker 209 (TC 267)
Coker 258 (TC 270)
Coker 298 (TC 272)
Coker 316 (TC 273)
Coker 319 (TC 274)
Coker 347 (TC 275)
Coker 371-Gold (TC 276)
Coker 411 (TC 277)
Coker 48 (TC 253)
Coker 51 (TC 254)
Coker 86 (TC 256)
CU 263 (TC 619)
CU 561
DH95-1562-1
Dixie Bright 101 (TC 290)
Dixie Bright 102 (TC 291)
Dixie Bright 244 (TC 292)
Dixie Bright 27 (TC 288)
Dixie Bright 28 (TC 289)
GF 157
GF 318
GL 26H
GL 338
GL 350
GL 368
GL 395
GL 600
GL 737
GL 939
GL 939 (TC 628)
Hicks (TC 310)
Hicks Broadleaf (TC 311)
K 149 (TC 568)
K 317
K 326
K 326 (TC 319)
K 340 (TC 320)
K 346
K 346 (TC 569)
K 358
K 394 (TC 321)
K 399
K 399 (TC 322)
K 730
Lonibow (TI 1573)
Lonibow (TI 1613)
McNair 10 (TC 330)
McNair 135 (TC 337)
McNair 30 (TC 334)
McNair 373 (TC 338)
McNair 944 (TC 339)
MK94 (TI 1512)
MS K 326
MS NC 71
MS NC 72
NC 100
NC 102
NC 1071 (TC 364)
NC 1125-2

TABLE 2-continued

Flue-cured Tobacco Varieties
NC 12 (TC 346)
NC 1226
NC 196
NC 2326 (TC 365)
NC 27 NF (TC 349)
NC 291
NC 297
NC 299
NC 37 NF (TC 350)
NC 471
NC 55
NC 567 (TC 362)
NC 60 (TC 352)
NC 606
NC 6140
NC 71
NC 72
NC 729 (TC 557)
NC 810 (TC 659)
NC 82 (TC 356)
NC 8640
NC 89 (TC 359)
NC 92
NC 925
NC 95 (TC 360)
NC 98 (TC 361)
NC EX 24
NC PY 10 (TC 367)
NC TG 61
Oxford 1 (TC 369)
Oxford 1-181 (TC 370)
Oxford 2 (TC 371)
Oxford 207 (TC 632)
Oxford 26 (TC 373)
Oxford 3 (TC 372)
Oxford 414 NF
PD 611 (TC 387)
PVH 03
PVH 09
PVH 1118
PVH 1452
PVH 1600
PVH 2110
PVH 2275
R 83 (Line 256-1) (TI 1400)
Reams 134
Reams 158
Reams 713
Reams 744
Reams M1
RG 11 (TC 600)
RG 13 (TC 601)
RG 17 (TC 627)
RG 22 (TC 584)
RG 8 (TC 585)
RG 81 (TC 618)
RG H51
RG4H 217
RGH 12
RGH 4
RGH 51
RGH 61
SC 58 (TC 400)
SC 72 (TC 403)
Sp. G-168
SPEIGHT 168
Speight 168 (TC 633)
Speight 172 (TC 634)
Speight 178
Speight 179
Speight 190
Speight 196
SPEIGHT 220
SPEIGHT 225
SPEIGHT 227

TABLE 2-continued

Flue-cured Tobacco Varieties
SPEIGHT 236
Speight G-10 (TC 416)
Speight G-102
Speight G-108
Speight G-111
Speight G-117
Speight G-126
Speight G-15 (TC 418)
Speight G-23
Speight G-28 (TC 420)
Speight G-33
Speight G-41
Speight G-5
Speight G-52
Speight G-58
Speight G-70
Speight G-70 (TC 426)
Speight G-80 (TC 427)
Speight NF3 (TC 629)
STNCB
VA 182
VA 45 (TC 559)
Vesta 30 (TC 439)
Vesta 33 (TC 440)
Vesta 5 (TC 438)
Vesta 62 (TC 441)
Virginia (TI 220)
Virginia (TI 273)
Virginia (TI 877)
Virginia 115 (TC 444)
Virginia 21 (TC 443)
Virginia Bright (TI 964)
Virginia Bright Leaf (TC 446)
Virginia Gold (TC 447)
White Stem Orinoco (TC 451)

[0098] Air-cured tobaccos include “Burley,” “Maryland,” and “dark” tobaccos. The common factor linking air-cured tobaccos is that curing occurs primarily without artificial sources of heat and humidity. Burley tobaccos are light to dark brown in color, high in oil, and low in sugar. Burley tobaccos are typically air-cured in barns. Major Burley growing countries include Argentina, Brazil, Italy, Malawi, and the United States of America.

[0099] Maryland tobaccos are extremely fluffy, have good burning properties, low nicotine and a neutral aroma. Major Maryland growing countries include the United States of America and Italy.

[0100] In one aspect, tobacco plants, seeds, or plant parts provided herein are of a Burley tobacco variety selected from the group consisting of the tobacco varieties listed in Table 3, and any variety essentially derived from any one of the foregoing varieties. In a further aspect, tobacco plants, seeds, or plant parts provided herein are in a Burley variety selected from the group consisting of TN 90, KT 209, KT 206, KT212, and HB 4488.

TABLE 3

Burley Tobacco Varieties
4407 LC
AA-37-1
Burley 21 (TC 7)
Burley 49 (TC 10)
Burley 64 (TC 11)
Burley Mammoth KY 16 (TC 12)

TABLE 3-continued

Burley Tobacco Varieties
Clay 402
Clay 403
Clay 502
Clays 403
GR 10 (TC 19)
GR 10 (TC 19)
GR 10A (TC 20)
GR 13 (TC 21)
GR 14 (TC 22)
GR 149 LC
GR 153
GR 17 (TC 23)
GR 17B (TC 24)
GR 18 (TC 25)
GR 19 (TC 26)
GR 2 (TC 15)
GR 24 (TC 27)
GR 36 (TC 28)
GR 38 (TC 29)
GR 38A (TC 30)
GR 40 (TC 31)
GR 42 (TC 32)
GR 42C (TC 33)
GR 43 (TC 34)
GR 44 (TC 35)
GR 45 (TC 36)
GR 46 (TC 37)
GR 48 (TC 38)
GR 5 (TC 16)
GR 53 (TC 39)
GR 6 (TC 17)
GR 9 (TC 18)
GR 139 NS
GR 139 S
HB 04P
HB 04P LC
HB 3307P LC
HB 4108P
HB 4151P
HB 4192P
HB 4194P
HB 4196
HB 4488
HB 4488P
HB04P
HB 4488 LC
HIB 21
HPB 21
HY 403
Hybrid 403 LC
Hybrid 404 LC
Hybrid 501 LC
KDH-959 (TC 576)
KDH-960 (TC 577)
KT 200 LC
KT 204 LC
KT 206 LC
KT 209 LC
KT 210 LC
KT 212 LC
KT 215 LC
KY 1 (TC 52)
KY 10 (TC 55)
KY 12 (TC 56)
KY 14 (TC 57)
KY 14 x L8 LC
KY 15 (TC 58)
KY 16 (TC 59)
KY 17 (TC 60)
KY 19 (TC 61)
KY 21 (TC 62)
KY 22 (TC 63)
KY 24 (TC 64)
KY 26 (TC 65)
KY 33 (TC 66)

TABLE 3-continued

Burley Tobacco Varieties
KY 34 (TC 67)
KY 35 (TC 68)
KY 41A (TC 69)
KY 5 (TC 53)
KY 52 (TC 70)
KY 54 (TC 71)
KY 56 (TC 72)
KY 56 (TC 72)
KY 57 (TC 73)
KY 58 (TC 74)
KY 8654 (TC 77)
KY 8959
KY 9 (TC 54)
KY 907 LC
KY 908 (TC 630)
NBH 98 (Screened)
NC 1206
NC 129
NC 2000 LC
NC 2002 LC
NC 3 LC
NC 5 LC
NC 6 LC
NC 7 LC
NC BH 129 LC
NC03-42-2
Newton 98
R 610 LC
R 630 LC
R 7-11
R 7-12 LC
RG 17
TKF 1801 LC
TKF 2002 LC
TKF 4024 LC
TKF 4028 LC
TKF 6400 LC
TKF 7002 LC
TKS 2002 LC
TN 86 (TC 82)
TN 90 LC
TN 97 Hybrid LC
TN 97 LC
VA 116
VA 119
Virgin A Mutante (TI 1406)
Virginia 509 (TC 84)

[0101] In another aspect, tobacco plants, seeds, or plant parts provided herein are of a Maryland tobacco variety selected from the group consisting of the tobacco varieties listed in Table 4, and any variety essentially derived from any one of the foregoing varieties.

TABLE 4

Maryland Tobacco Varieties
Maryland 10 (TC 498)
Maryland 14 D2 (TC 499)
Maryland 201 (TC 503)
Maryland 21 (TC 500)
Maryland 341 (TC 504)
Maryland 40
Maryland 402
Maryland 59 (TC 501)
Maryland 601
Maryland 609 (TC 505)
Maryland 64 (TC 502)
Maryland 872 (TC 506)
Maryland Mammoth (TC 507)

[0102] Dark air-cured tobaccos are distinguished from other tobacco types primarily by its curing process, which gives dark air-cured tobacco its medium-brown to dark-brown color and a distinct aroma. Dark air-cured tobaccos are mainly used in the production of chewing tobacco and snuff. In one aspect, tobacco plants, seeds, or plant parts provided herein are of a dark air-cured tobacco variety selected from the group consisting of Sumatra, Jatim, Dominican Cubano, Besuki, One sucker, Green River, Virginia sun-cured, and Paraguan Passado, and any variety essentially derived from any one of the foregoing varieties.

[0103] Dark fire-cured tobaccos are generally cured with low-burning wood fires on the floors of closed curing barns. Dark fire-cured tobaccos are typically used for making pipe blends, cigarettes, chewing tobacco, snuff, and strong-tasting cigars. Major growing regions for dark fire-cured tobaccos are Tennessee, Kentucky, and Virginia in the United States of America. In one aspect, tobacco plants, seeds, or plant parts provided herein are of a dark fire-cured tobacco variety selected from the group consisting of the tobacco varieties listed in Table 5, and any variety essentially derived from any one of the foregoing varieties.

TABLE 5

Dark Fire-Cured Tobacco Varieties
Black Mammoth (TC 461)
Black Mammoth Small Stalk (TC 641)
Certified Madole (TC 463)
D-534-A-1 (TC 464)
DAC ULT 302
DAC ULT 303
DAC ULT 306
DAC ULT 308
DAC ULT 312
DF 300 (TC 465)
DF 485 (TC 466)
DF 516 (TC 467)
DF 911 (TC 468)
DT 508
DT 518 (Screened)
DT 538 LC
DT 592
Improved Madole (TC 471)
Jemigan's Madole (TC 472)
KT 14LC
KT D17LC
KT D4 LC
KT D6 LC
KT D8 LC
KY 153 (TC 216)
KY 157 (TC 217)
KY 160
KY 160 (TC 218)
KY 163 (TC 219)
KY 165 (TC 220)
KY 170 (TC 474)
KY 171 (PhPh)
KY 171 (TC 475)
KY 171 LC
KY 171 NS
KY 180 (TC 573)
KY 190 (TC 574)
Little Crittenden
Little Crittenden (TC 476)
Little Crittenden LC (certified)
Little Crittenden PhPh
Lizard Tail Turtle Foot
Madole (TC 478)
Madole (TC 479)
MS KY 171
MS NL Madole LC

TABLE 5-continued

Dark Fire-Cured Tobacco Varieties

MS TN D950 LC
Nance (TC 616)
Narrow Leaf Madole LC (certified)
Neal Smith Madole (TC 646)
Newtons VH Madole
NL Madole
NL Madole (PhPh)
NL Madole (TC 484)
NL Madole LC
NL Madole LC (PhPh)
NL Madole NS
One Sucker (TC 224)
OS 400
PD 302H
PD 312H
PD 318H
PD 7302 LC
PD 7305
PD 7309 LC
PD 7312 LC
PD 7318 LC
PD 7319 LC
Petico M PG04
PY KY 160 (TC 612)
PY KY 171 (TC 613)
Shirey
TI 1372
TN D94
TN D94 (TC 621)
TN D950
TN D950 (PhPh)
TN D950
TN D950 (TC 622)
TR Madole (TC 486)
VA 309
VA 309 (TC 560)
VA 309 LC (certified)
VA 310 (TC 487)
VA 331 (TC 592)
VA 355 (TC 638)
VA 359
VA 359 (Screened)
VA 359 (TC 639)
VA 359 LC (certified)
VA 403 (TC 580)
VA 405 (TC 581)
VA 409 (TC 562)
VA 510 (TC 572)

[0104] Oriental tobaccos are also referred to as Greek, aroma and Turkish tobaccos due to the fact that they are typically grown in eastern Mediterranean regions such as Turkey, Greece, Bulgaria, Macedonia, Syria, Lebanon, Italy, and Romania. The small plant size, small leaf size, and unique aroma properties of Oriental tobacco varieties are a result of their adaptation to the poor soil and stressful climatic conditions in which they have been developed. In one aspect, tobacco plants, seeds, or plant parts provided herein are of an Oriental tobacco variety selected from the group consisting of the tobacco varieties listed in Table 6, and any variety essentially derived from any one of the foregoing varieties.

TABLE 6

Oriental Tobacco Varieties

Bafra (TI 1641)
Bahce (TI 1730)
Bahia (TI 1416)

TABLE 6-continued

Oriental Tobacco Varieties
Bahia (TI 1455)
Baiano (TI 128)
Basma
Basma (TI 1666)
Basma Drama
Basma Hybrid (PhPh)
Basma Zihna I
Bitlis (TI 1667)
Bitlis (TI 1725)
Bubalovac (TI 1282)
Bursa (TI 1650)
Bursa (TI 1668)
Canik (TI 1644)
Djebel 174 (TI 1492)
Djebel 359 (TI 1493)
Djebel 81
Dubec 566 (TI 1409)
Dubec 7 (TI 1410)
Dubek 566 (TI 1567)
Duzee (TI 1670)
Edime (TI 1671)
Ege (TI 1642)
Ege-64 (TI 1672)
Izmir (Akhisar) (TI 1729)
Izmir (Gavurkoy) (TI 1727)
Izmir Ege 64
Izmir-Incekara (TI 1674)
Izmir-Ozbas (TI 1675)
Jaka Dzebel (TI 1326)
Kaba-Kulak
Kagoshima Mamba (TI 158)
Katerini
Katerini S53
Krumovgrad 58
MS Basma
MS Katerini S53
Nevrokop 1146
Ozbas (TI 1645)
Perustitza (TI 980)
Prilep (TI 1291)
Prilep (TI 1325)
Prilep 12-2/1
Prilep 23
Samsun (TC 536)
Samsun 959 (TI 1570)
Samsun Evkaf (TI 1723)
Samsun Holmes NN (TC 540)
Samsun Maden (TI 1647)
Samsun NO 15 (TC 541)
Samsun-BLK SHK Tol (TC 542)
Samsun-Canik (TI 1678)
Samsun-Maden (TI 1679)
Saribaptar 407 - Izmir Region
Smyrna (TC 543)
Smyrna No. 23 (TC 545)
Smyrna No. 9 (TC 544)
Smyma-Blk Shk Tol (TC 546)
Trabzon (TI 1649)
Trabzon (TI 1682)
Trapezund 161 (TI 1407)
Turkish (TC 548)
Turkish Anghit (TI 90)
Turkish Samsun (TI 92)
Turkish Tropizoid (TI 93)
Turkish Varotic (TI 89)
Xanthi (TI 1662)

[0105] In an aspect, tobacco plants, seeds, or plant parts provided herein are of a cigar tobacco variety selected from the group consisting of the tobacco varieties listed in Table 7, and any variety essentially derived from any one of the foregoing varieties.

TABLE 7

Cigar Tobacco Varieties
Bahai (TI 62)
Beinhart 1000
Beinhart 1000 (TI 1562)
Beinhart 1000-1 (TI 1561)
Bergerac C
Bergerac C (TI 1529)
Big Cuban (TI 1565)
Castillo Negro, Blanco, Pina (TI 448)
Castillo Negro, Blanco, Pina (TI 448A)
Castillo Negro, Blanco, Pina (TI 449)
Caujaro (TI 893)
Chocoa (TI 289)
Chocoa (TI 313)
Connecticut 15 (TC 183)
Connecticut Broadleaf
Connecticut Broadleaf (TC 186)
Connecticut Shade (TC 188)
Criollo, Colorado (TI 1093)
Enshu (TI 1586)
Florida 301
Florida 301 (TC 195)
PA Broadleaf (TC 119)
Pennsylvania Broadleaf
Pennsylvania Broadleaf (TC 119)
Petite Havana SR1
Petite Havana SR1 (TC 105)

[0106] In an aspect, tobacco plants, seeds, or plant parts provided herein are of a tobacco variety selected from the group consisting of the tobacco varieties listed in Table 8, and any variety essentially derived from any one of the foregoing varieties.

TABLE 8

Other Tobacco Varieties
Chocoa (TI 319)
Hojas Paradas (TI 1089)
Hojas Paradas (Galpoa) (TI 1068)
Perique (St. James Parrish)
Perique (TC 556)
Perique (TI 1374)
Sylvestris (TI 984)
TI 179

[0107] In an aspect, a tobacco plant or plant part is from a variety selected from the group consisting of the tobacco varieties listed in Table 2, Table 3, Table 4, Table 5, Table 6, Table 7, and Table 8. In another aspect, a tobacco plant or plant part is from a variety listed in Table 2. In another aspect, a tobacco plant or plant part is from a variety listed in Table 3. In another aspect, a tobacco plant or plant part is from a variety listed in Table 4. In another aspect, a tobacco plant or plant part is from a variety listed in Table 5. In another aspect, a tobacco plant or plant part is from a variety listed in Table 6. In another aspect, a tobacco plant or plant part is from a variety listed in Table 7. In another aspect, a tobacco plant or plant part is from a variety listed in Table 8.

[0108] In an aspect, a tobacco seed is from a variety selected from the group consisting of the tobacco varieties listed in Table 2, Table 3, Table 4, Table 5, Table 6, Table 7, and Table 8. In another aspect, a tobacco seed is from a variety listed in Table 2. In another aspect, a tobacco seed is from a variety listed in Table 3. In another aspect, a tobacco seed is from a variety listed in Table 4. In another aspect, a

tobacco seed is from a variety listed in Table 5. In another aspect, a tobacco seed is from a variety listed in Table 6. In another aspect, a tobacco seed is from a variety listed in Table 7. In another aspect, a tobacco seed is from a variety listed in Table 8.

[0109] In an aspect, a tobacco cell is from a variety selected from the group consisting of the tobacco varieties listed in Table 2, Table 3, Table 4, Table 5, Table 6, Table 7, and Table 8. In another aspect, a tobacco cell is from a variety listed in Table 2. In another aspect, a tobacco cell is from a variety listed in Table 3. In another aspect, a tobacco cell is from a variety listed in Table 4. In another aspect, a tobacco cell is from a variety listed in Table 5. In another aspect, a tobacco cell is from a variety listed in Table 6. In another aspect, a tobacco cell is from a variety listed in Table 7. In another aspect, a tobacco cell is from a variety listed in Table 8.

[0110] All foregoing mentioned specific varieties of flue-cured, dark air-cured, Burley, Maryland, dark fire-cured, cigar, or Oriental type are listed only for exemplary purposes. Any additional flue-cured, dark air-cured, Burley, Maryland, dark fire-cured, cigar, or Oriental varieties are also contemplated in the present application.

[0111] In an aspect, a plant or variety provided herein is an inbred plant or variety. As used herein, an “inbred” variety is a variety that has been bred for genetic homogeneity.

[0112] As used herein, a “hybrid” is created by crossing two plants from different varieties or species, such that the progeny comprises genetic material from each parent. Skilled artisans recognize that higher order hybrids can be generated as well. For example, a first hybrid can be made by crossing Variety C with Variety D to create a CxD hybrid, and a second hybrid can be made by crossing Variety E with Variety F to create an ExF hybrid. The first and second hybrids can be further crossed to create the higher order hybrid (CxD)×(ExF) comprising genetic information from all four parent varieties. In an aspect, a plant or seed provided herein is a hybrid plant or seed.

[0113] In an aspect, a tobacco plant provided herein is an inbred tobacco plant. In an aspect, a tobacco seed provided herein is an inbred tobacco seed. In an aspect, a tobacco plant provided herein is a hybrid tobacco plant. In another aspect, a tobacco seed provided herein is a hybrid tobacco seed.

[0114] In an aspect, a *cannabis* plant provided herein is an inbred *cannabis* plant. In an aspect, a *cannabis* seed provided herein is an inbred *cannabis* seed. In an aspect, a *cannabis* plant provided herein is a hybrid *cannabis* plant. In an aspect, a *cannabis* seed provided herein is a hybrid *cannabis* seed.

[0115] Unless specified otherwise, all comparisons to control plants require similar growth conditions or comparable growth conditions for the two plants being compared. As used herein, “grown under comparable conditions,” “similar growth conditions” or “comparable growth conditions” refer to similar environmental conditions and/or agronomic practices for growing and making meaningful comparisons between two or more plant genotypes so that neither environmental conditions nor agronomic practices would contribute to or explain any difference observed between the two or more plant genotypes. Environmental conditions include, for example, light, temperature, water (humidity), and nutrition (e.g., nitrogen and phosphorus). Agronomic practices include, for example, seeding, clipping, undercut-

ting, transplanting, topping, and suckering. See Chapters 4B and 4C of *Tobacco, Production, Chemistry and Technology*, Davis & Nielsen, eds., Blackwell Publishing, Oxford (1999), pp 70-103.

[0116] As used herein, a “control plant” refers to a plant of identical, or nearly identical, genetic makeup as the modified plant being compared, except for the recombinant nucleic acid molecule provided herein that was introduced to the modified plant.

[0117] In an aspect, a plant or variety provided herein is male sterile. In another aspect, a plant or variety provided herein is cytoplasmic male sterile (CMS). Male sterile plants can be produced by any method known in the art. Methods of producing male sterile tobacco are described in Wernsman, E. A., and Ruffy, R. C. 1987. Chapter Seventeen. *Tobacco*. Pages 669-698 In: *Cultivar Development. Crop Species*. W. H. Fehr (ed.), MacMillan Publishing Co., Inc., New York, N.Y. 761 pp.

[0118] In another aspect, a plant or variety provided herein is female sterile. As a non-limiting example, female sterile plants can be made by mutating the STIG1 gene. See, for example, Goldman et al. 1994, *EMBO Journal* 13:2976-2984.

[0119] In an aspect, this disclosure provides a method for producing a plant, the method comprising: (a) crossing at least one plant of a first variety with at least one plant of a second variety to produce at least one progeny seed, where the at least one plant of the first variety comprises a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof; and (b) selecting at least one progeny seed produced in step (a), or a plant germinated therefrom, where the at least one progeny seed or plant germinated therefrom comprises the recombinant nucleic acid molecule. In an aspect, this disclosure provides a method for producing a plant, the method comprising: (a) crossing at least one plant of a first variety with at least one plant of a second variety to produce at least one progeny seed, where the at least one plant of the first variety comprises a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 85% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof; and (b) selecting at least one progeny seed produced in step (a), or a plant germinated therefrom, where the at least one progeny seed or plant germinated therefrom comprises the recombinant nucleic acid molecule. In an aspect, this disclosure provides a method for producing a plant, the method comprising: (a) crossing at least one plant of a first variety with at least one plant of a second variety to produce at least one progeny seed, where the at least one plant of the first variety comprises a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 90% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof; and (b) selecting at least one progeny seed produced in step (a), or a plant germinated therefrom, where the at least one progeny seed or plant germinated therefrom comprises the recombinant nucleic acid molecule. In an

acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33; (b) regenerating a modified plant from the at least one plant cell in step (a), where the modified plant comprises an increased trichome density on at least one leaf as compared to a leaf from a control plant lacking the recombinant nucleic acid when grown under comparable conditions.

[0123] In an aspect, a first plant variety and a second plant variety are the same variety. In an aspect, a first plant variety and a second plant variety are two different varieties. In an aspect, a second plant variety comprises a recombinant nucleic acid molecule.

[0124] In an aspect, a first plant variety is heterozygous for a recombinant nucleic acid molecule. In an aspect, a first plant variety is hemizygous for a recombinant nucleic acid molecule. In an aspect, a first plant variety is homozygous for a recombinant nucleic acid molecule. In an aspect, a second plant variety is heterozygous for a recombinant nucleic acid molecule. In an aspect, a second plant variety is hemizygous for a recombinant nucleic acid molecule. In an aspect, a second plant variety is homozygous for a recombinant nucleic acid molecule. In an aspect, a progeny seed, or a plant germinated therefrom, is heterozygous for a recombinant nucleic acid molecule. In an aspect, a progeny seed, or a plant germinated therefrom, is hemizygous for a recombinant nucleic acid molecule. In an aspect, a progeny seed, or a plant germinated therefrom, is homozygous for a recombinant nucleic acid molecule.

[0125] In an aspect, a first plant variety is a tobacco plant variety. In an aspect, a second plant variety is a tobacco plant variety. In an aspect, a first plant variety is a *cannabis* plant variety. In an aspect, a second plant variety is a *cannabis* plant variety.

[0126] As used herein, the term "crossing" refers to the deliberate mating of two plants. In an aspect, crossing comprises pollination and/or fertilization of a first plant by a second plant. The two plants being crossed can be distantly related, closely related, or identical. In an aspect, the two plants being crossed are both modified plants. In an aspect, the two plants being crossed are of the same variety. In an aspect, the two plants being crossed are of two different varieties. In an aspect, one of the two plants being crossed is male sterile. In an aspect, one of the two plants being crossed is female sterile. In an aspect, at least one of the two plants being crossed is a hybrid tobacco plant. In an aspect, at least one of the two plants being crossed is a modified plant.

[0127] In an aspect, a plant of a first variety is the male parent in a crossing step. In an aspect, a plant of a first variety is the female parent in a crossing step. In an aspect, a plant of a second variety is the male parent in a crossing step. In an aspect, a plant of a second variety is the female parent in a crossing step.

Nucleic Acids and Amino Acids

[0128] As used herein, "heterologous" refers to a sequence (nucleic acid or amino acid) that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention. The term also is applicable to nucleic acid constructs, also referred to herein as "polynucleotide constructs." In this manner, a "heterologous" nucleic acid construct is intended to mean a construct that originates from a foreign species, or, if from the same

species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention. Heterologous nucleic acid constructs include, but are not limited to, recombinant nucleotide constructs that have been introduced into a plant or plant part thereof, for example, via transformation methods or subsequent breeding of a transgenic plant with another plant of interest. It will be appreciated that an endogenous promoter can be considered heterologous to an operably linked endogenous gene if the endogenous promoter and endogenous gene are not naturally operably linked (e.g., human intervention is required to put them in operable linkage). As used herein, an "endogenous" nucleic acid sequence refers to a nucleic acid sequence that occurs naturally in the genome of an organism.

[0129] In an aspect, a heterologous polynucleotide comprises a gene. In an aspect, a heterologous polynucleotide encodes a small RNA molecule or a precursor thereof. In an aspect, a heterologous polynucleotide encodes a polypeptide.

[0130] As used herein, a "gene" refers to a polynucleotide that can produce a functional unit (e.g., without being limiting, for example, a polypeptide, or a small RNA molecule). A gene can comprise a promoter, an enhancer sequence, a leader sequence, a transcriptional start site, a transcriptional stop site, a polyadenylation site, one or more exons, one or more introns, a 5'-UTR, a 3'-UTR, or any combination thereof. A "gene sequence" can comprise a polynucleotide sequence encoding a promoter, an enhancer sequence, a leader sequence, a transcriptional start site, a transcriptional stop site, a polyadenylation site, one or more exons, one or more introns, a 5'-UTR, a 3'-UTR, or any combination thereof. In one aspect, a gene encodes a small RNA molecule or a precursor thereof. In another aspect, a gene encodes a polypeptide.

[0131] In an aspect, a gene comprises a nucleic acid sequence at least 80% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36. In an aspect, a gene comprises a nucleic acid sequence at least 85% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36. In an aspect, a gene comprises a nucleic acid sequence at least 90% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36. In an aspect, a gene comprises a nucleic acid sequence at least 92.5% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36. In an aspect, a gene comprises a nucleic acid sequence at least 95% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36. In an aspect, a gene comprises a nucleic acid sequence at least 96% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36. In an aspect, a gene comprises a nucleic acid sequence at least 97% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36. In an aspect, a gene comprises a nucleic acid sequence at least 98% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36. In an aspect, a gene comprises a nucleic acid sequence at least 99% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36. In an aspect, a gene com-

acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, a polypeptide comprises an amino acid sequence at least 85% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, a polypeptide comprises an amino acid sequence at least 90% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, a polypeptide comprises an amino acid sequence at least 92.5% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, a polypeptide comprises an amino acid sequence at least 95% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, a polypeptide comprises an amino acid sequence at least 96% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, a polypeptide comprises an amino acid sequence at least 97% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, a polypeptide comprises an amino acid sequence at least 98% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, a polypeptide comprises an amino acid sequence at least 99% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, a polypeptide comprises an amino acid sequence at least 99.9% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, a polypeptide comprises an amino acid sequence 100% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33.

[0136] The terms “percent identity” or “percent identical” as used herein in reference to two or more nucleotide or amino acid sequences is calculated by (i) comparing two optimally aligned sequences (nucleotide or amino acid) over a window of comparison (the “alignable” region or regions), (ii) determining the number of positions at which the identical nucleic acid base (for nucleotide sequences) or amino acid residue (for proteins and polypeptides) occurs in both sequences to yield the number of matched positions, (iii) dividing the number of matched positions by the total number of positions in the window of comparison, and then (iv) multiplying this quotient by 100% to yield the percent identity. If the “percent identity” is being calculated in relation to a reference sequence without a particular comparison window being specified, then the percent identity is determined by dividing the number of matched positions over the region of alignment by the total length of the reference sequence. Accordingly, for purposes of the present application, when two sequences (query and subject) are optimally aligned (with allowance for gaps in their alignment), the “percent identity” for the query sequence is equal to the number of identical positions between the two sequences divided by the total number of positions in the query sequence over its length (or a comparison window), which is then multiplied by 100%.

[0137] When percentage of sequence identity is used in reference to amino acids it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are

substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity can be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have “sequence similarity” or “similarity.”

[0138] For optimal alignment of sequences to calculate their percent identity, various pair-wise or multiple sequence alignment algorithms and programs are known in the art, such as ClustalW or Basic Local Alignment Search Tool® (BLAST™), etc., that can be used to compare the sequence identity or similarity between two or more nucleotide or amino acid sequences. Although other alignment and comparison methods are known in the art, the alignment and percent identity between two sequences (including the percent identity ranges described above) can be as determined by the ClustalW algorithm, see, e.g., Chenna et al., “Multiple sequence alignment with the Clustal series of programs,” *Nucleic Acids Research* 31: 3497-3500 (2003); Thompson et al., “Clustal W: Improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice,” *Nucleic Acids Research* 22: 4673-4680 (1994); Larkin M A et al., “Clustal W and Clustal X version 2.0,” *Bioinformatics* 23: 2947-48 (2007); and Altschul et al. “Basic local alignment search tool.” *J. Mol. Biol.* 215:403-410 (1990), the entire contents and disclosures of which are incorporated herein by reference.

[0139] The terms “percent complementarity” or “percent complementary” as used herein in reference to two nucleotide sequences is similar to the concept of percent identity but refers to the percentage of nucleotides of a query sequence that optimally base-pair or hybridize to nucleotides a subject sequence when the query and subject sequences are linearly arranged and optimally base paired without secondary folding structures, such as loops, stems or hairpins. Such a percent complementarity can be between two DNA strands, two RNA strands, or a DNA strand and a RNA strand. The “percent complementarity” can be calculated by (i) optimally base-pairing or hybridizing the two nucleotide sequences in a linear and fully extended arrangement (i.e., without folding or secondary structures) over a window of comparison, (ii) determining the number of positions that base-pair between the two sequences over the window of comparison to yield the number of complementary positions, (iii) dividing the number of complementary positions by the total number of positions in the window of comparison, and (iv) multiplying this quotient by 100% to yield the percent complementarity of the two sequences. Optimal base pairing of two sequences can be determined based on the known pairings of nucleotide bases, such as G-C, A-T, and A-U, through hydrogen binding. If the “percent complementarity” is being calculated in relation to a reference sequence without specifying a particular comparison window, then the percent identity is determined by dividing the number of complementary positions between the two linear sequences by the total length of the reference sequence. Thus, for purposes of the present application, when two sequences (query and subject) are optimally base-paired (with allowance for mismatches or non-base-paired nucleotides), the “percent complementarity” for the query sequence is equal to the number of base-paired positions

between the two sequences divided by the total number of positions in the query sequence over its length, which is then multiplied by 100%.

[0140] The use of the term “polynucleotide” or “nucleic acid molecule” is not intended to limit the present disclosure to polynucleotides comprising deoxyribonucleic acid (DNA). For example, ribonucleic acid (RNA) molecules are also envisioned. Those of ordinary skill in the art will recognize that polynucleotides and nucleic acid molecules can comprise ribonucleotides and combinations of ribonucleotides and deoxyribonucleotides. Such deoxyribonucleotides and ribonucleotides include both naturally occurring molecules and synthetic analogues. The polynucleotides of the present disclosure also encompass all forms of sequences including, but not limited to, single-stranded forms, double-stranded forms, hairpins, stem-and-loop structures, and the like. In an aspect, a nucleic acid molecule provided herein is a DNA molecule. In another aspect, a nucleic acid molecule provided herein is an RNA molecule. In an aspect, a nucleic acid molecule provided herein is single-stranded. In another aspect, a nucleic acid molecule provided herein is double-stranded. A nucleic acid molecule can encode a polypeptide or a small RNA.

[0141] As used herein, a “recombinant nucleic acid molecule” refers to a nucleic acid molecule formed by laboratory methods of genetic recombination, such as, without being limiting, molecular cloning. Similarly, a “recombinant DNA construct” refers to a DNA molecule formed by laboratory methods of genetic recombination.

[0142] In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 85% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 90% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 92.5% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 95% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 96% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 97% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof. In an aspect,

aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 97% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 98% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 99% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 99.9% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence is at least 100% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof.

[0143] In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous polynucleotide, where the polynucleotide encodes an amino acid sequence at least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous polynucleotide, where the polynucleotide encodes an amino acid sequence at least 85% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous polynucleotide, where the polynucleotide encodes an amino acid sequence at least 90% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous polynucleotide, where the polynucleotide encodes an amino acid sequence at least 95% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous polynucleotide, where the polynucleotide encodes an amino acid sequence at least 96% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous polynucleotide, where the polynucleotide encodes an amino acid sequence at least 97% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33. In an aspect, this disclosure provides

a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous polynucleotide, where the polynucleotide encodes an amino acid sequence at least 98% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous polynucleotide, where the polynucleotide encodes an amino acid sequence at least 99% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous polynucleotide, where the polynucleotide encodes an amino acid sequence at least 99.9% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33. In an aspect, this disclosure provides a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous polynucleotide, where the polynucleotide encodes an amino acid sequence 100% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33.

[0144] Nucleic acids can be isolated using techniques routine in the art. For example, nucleic acids can be isolated using any method including, without limitation, recombinant nucleic acid technology, and/or the polymerase chain reaction (PCR). General PCR techniques are described, for example in PCR Primer: A Laboratory Manual, Dieffenbach & Dveksler, Eds., Cold Spring Harbor Laboratory Press, 1995. Recombinant nucleic acid techniques include, for example, restriction enzyme digestion and ligation, which can be used to isolate a nucleic acid. Isolated nucleic acids also can be chemically synthesized, either as a single nucleic acid molecule or as a series of oligonucleotides. Polypeptides can be purified from natural sources (e.g., a biological sample) by known methods such as DEAE ion exchange, gel filtration, and hydroxyapatite chromatography. A polypeptide also can be purified, for example, by expressing a nucleic acid in an expression vector. In addition, a purified polypeptide can be obtained by chemical synthesis. The extent of purity of a polypeptide can be measured using any appropriate method, e.g., column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

[0145] In one aspect, this disclosure provides methods of detecting recombinant nucleic acids and polypeptides in plant cells. Without being limiting, nucleic acids also can be detected using hybridization. Hybridization between nucleic acids is discussed in detail in Sambrook et al. (1989, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

[0146] As used herein, the term "polypeptide" refers to a chain of at least two covalently linked amino acids. Polypeptides can be encoded by polynucleotides provided herein. Proteins provided herein can be encoded by nucleic acid molecules provided herein. Proteins can comprise polypeptides provided herein. As used herein, a "protein" refers to a chain of amino acid residues that is capable of providing structure or enzymatic activity to a cell.

[0147] Polypeptides can be detected using antibodies. Techniques for detecting polypeptides using antibodies include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. An antibody provided herein can be a polyclonal antibody or a monoclonal antibody. An antibody having

specific binding affinity for a polypeptide provided herein can be generated using methods well known in the art. An antibody provided herein can be attached to a solid support such as a microtiter plate using methods known in the art. [0148] Detection (e.g., of an amplification product, of a hybridization complex, of a polypeptide) can be accomplished using detectable labels. The term "label" is intended to encompass the use of direct labels as well as indirect labels. Detectable labels include enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials.

[0149] In an aspect, this disclosure provides a promoter. In an aspect, a promoter is heterologous to an operably linked nucleic acid sequence. As used herein, "operably linked" refers to a functional linkage between two or more elements. For example, an operable linkage between a polynucleotide of interest and a regulatory sequence (e.g., a promoter) is a functional link that allows for expression of the polynucleotide of interest. Operably linked elements may be contiguous or non-contiguous.

[0150] Promoters that drive enhanced expression in certain tissues of an organism relative to other tissues of the organism are referred to as "tissue-preferred" promoters. Thus, a "tissue-preferred" promoter causes relatively higher or preferential expression in a specific tissue(s) of a plant, but with lower levels of expression in other tissue(s) of the plant. In an aspect, a promoter is a tissue-preferred promoter. In an aspect, a tissue-preferred promoter is a leaf tissue-preferred promoter. In an aspect, a tissue-preferred promoter is a flower tissue-preferred promoter such as the promoter of gene that encode anthocyanidin synthase (NtANS1) (Lim et al., *Plant Cell Tissue Organ Cult* 114(3):373-383 (2013)). In an aspect, a tissue-preferred promoter is a root tissue-preferred promoter such as the promoter of extension-like protein (NtREL1) (Zhang et al. *Plant Cell Rep* 35, 757-769 (2016)). In an aspect, a promoter is an epidermal tissue-preferred promoter such as the promoter of gene that encodes lipid transfer protein (Ntltp1) in root epidermis (Canevascini et al., *Plant Physiol* 112(2) 513-524 (1996)).

[0151] Promoters that drive expression in all or most tissues of the plant are referred to as "constitutive" promoters. In an aspect, a promoter is a constitutive promoter. In an aspect, a constitutive promoter is selected from the group consisting of a Cauliflower Mosaic Virus 35S promoter, a ubiquitin promoter, an actin promoter, an opine promoter, and an alcohol dehydrogenase promoter.

[0152] An "inducible" promoter is a promoter that initiates transcription in response to an environmental stimulus such as heat, cold, drought, light, or other stimuli, such as wounding or chemical application. In an aspect, a promoter is an inducible promoter.

[0153] In an aspect, a promoter is expressible in a plant cell.

Terpenes

[0154] Terpenes are a class of aromatic organic compounds produced by plants and some insects. Terpenes are hydrocarbon molecules that are often used by plants to either directly deter herbivory or to attract predators or parasites of plant herbivores. Non-limiting examples of terpenes include citral, menthol, camphor, salvianin A, cannabinoids, and curcuminooids.

[0155] In an aspect, a terpene is a terpenoid. Terpenoids (also referred to as isoprenoids) are modified terpenes that

contain additional functional groups, which can include oxygen. Terpenoids, which can be cyclic or acyclic, vary in size from five-carbon hemiterpenes to long complex molecules containing thousands of isoprene units. Terpenoids are produced through the condensation of five-carbon isoprene units (e.g., dimethylallyl diphosphate (DMAPP) and isopentenyl diphosphate (IPP)), most often by the sequential head-to-tail addition of DMAPP to IPP. The initial cyclization processes are catalyzed by different terpene synthases and enzyme variation leads to variation in monoterpene structure.

[0156] Terpenoids are classified according to the number of isoprene units that comprise the parent terpene. A hemiterpenoid comprises one isoprene unit. A monoterpenoid comprises two isoprene units. A sesquiterpenoid comprises three isoprene units. A diterpenoid comprises four isoprene units. A sesterterpenoid comprises five isoprene units. A triterpenoid comprises six isoprene units. A tetraterpenoid comprises eight isoprene units. A polyterpenoid comprises more than eight isoprene units.

[0157] In an aspect, a terpene is menthol. In an aspect, a terpene is menthol or a related compound. In an aspect, a terpene is a labdanoid. In an aspect, a terpene is cembratrienediol. In an aspect, a terpene is levopimamic acid. In an aspect, a terpene is L-leucine. In an aspect, a terpene is neophytadiene. In an aspect, a labdanoid is cis-abienol. In an aspect, a terpene is selected from the group consisting of menthol or a related compound, a labdanoid, cembratrienediol, levopimamic acid, L-leucine, and neophytadiene. In an aspect, a terpene is selected from the group consisting of menthol, a labdanoid, cembratrienediol, levopimamic acid, L-leucine, and neophytadiene. In an aspect, a terpene is selected from the group consisting of menthol, a labdanoid, cembratrienediol, levopimamic acid, L-leucine, and neophytadiene.

[0158] As used herein, "menthol" refers to the organic compound having a chemical formula of $C_{10}H_{20}O$ and the International Union of Pure and Applied Chemistry (IUPAC) name 5-Methyl-2-(propan-2-yl)cyclohexan-1-ol. Menthol is also referred to as "(-)-Menthol." Related compounds of menthol include, but are not limited to, (+)-Menthol, (+)-Isomenthol, (+)-Neomenthol, (+)-Neoisomenthol, (-)-Isomenthol, (-)-Neomethol, and (-)-Neoisomenthol. In an aspect, a related compound of menthol is selected from the group consisting of (+)-Menthol, (+)-Isomenthol, (+)-Neomenthol, (+)-Neoisomenthol, (-)-Isomenthol, (-)-Neomethol, and (-)-Neoisomenthol.

[0159] As used herein, "neophytadiene" refers to the organic compound having a chemical formula of $C_{20}H_{38}$ and the IUPAC name of 7,11,15-trimethyl-3-methylidenehexadec-1-ene.

[0160] As used herein, "cembratrienediol" refers to the organic compound having a chemical formula of $C_{20}H_{34}O_2$ and the IUPAC name (1R,3R,4Z,8Z,12S,13Z)-1,5,9-trimethyl-12-propan-2-ylcyclotetradeca-4,8,13-triene-1,3-diol. Cembratrienediol is also referred to as "beta-Cembrene-diol."

[0161] As used herein, "levopimamic acid" refers to the organic compound having a chemical formula of $C_{20}H_{30}O_2$ and the IUPAC name (1R,4aR,4bS,10aR)-1,4a-dimethyl-7-

propan-2-yl-2,3,4,4b,5,9,10,10a-octahydrophenanthrene-1-carboxylic acid. Levopimamic acid is also referred to as "L-Pimamic acid."

[0162] As used herein, "L-leucine" refers to the amino acid having the chemical formula $C_6H_{12}NO_2$ and the IUPAC name (2S)-2-amino-4-methylpentanoic acid.

[0163] As used herein, a "labdanoid" refers to a terpenoid derivative of the fundamental parent labdane, a diterpene. A labdane has the chemical formula $C_{20}H_{38}$ and the IUPAC name (1S,2S,4aS,8aR)-2,5,5,8a-tetramethyl-1-[(3R)-3-methylpentyl]-1,2,3,4,4a,6,7,8-octahydronaphthalene.

[0164] A non-limiting example of a labdanoid is cis-abienol. As used herein, "cis-abienol" refers to the organic compound having a chemical formula of $C_{20}H_{34}O$ and the IUPAC name (1R,2R,4aS,8aS)-2,5,5,8a-tetramethyl-1-[(2Z)-3-methylpenta-2,4,-dienyl]-3,4,4a,6,7,8-hexahydro-1H-naphthalen-2-ol.

[0165] In an aspect, a modified plant, seed, or plant part comprising a recombinant nucleic acid provided herein comprises an increased amount of at least one terpene as compared to a control plant, seed, or plant part lacking the recombinant nucleic acid molecule when grown under comparable conditions. In an aspect, a modified tobacco plant, tobacco seed, or tobacco plant part comprising a recombinant nucleic acid provided herein comprises an increased amount of at least one terpene as compared to a control tobacco plant, tobacco seed, or tobacco plant part lacking the recombinant nucleic acid molecule when grown under comparable conditions. In an aspect, a modified *cannabis* plant, *cannabis* seed, or *cannabis* plant part comprising a recombinant nucleic acid provided herein comprises an increased amount of at least one terpene as compared to a control *cannabis* plant, *cannabis* seed, or *cannabis* plant part lacking the recombinant nucleic acid molecule when grown under comparable conditions.

[0166] In an aspect, an increased amount of at least one terpene comprises an increase of at least 0.5%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 1%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 2%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 3%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 4%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 5%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 10%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 12.5%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 15%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 17.5%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 20%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 25%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 30%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 40%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 50%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 60%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 70%. In an aspect, an increased amount

of at least one terpene comprises an increase of at least 80%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 90%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 100%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 150%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 200%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 250%. In an aspect, an increased amount of at least one terpene comprises an increase of at least 500%.

[0167] In an aspect, an increased amount of at least one terpene comprises an increase of between 0.5% and 500%. In an aspect, an increased amount of at least one terpene comprises an increase of between 0.5% and 250%. In an aspect, an increased amount of at least one terpene comprises an increase of between 0.5% and 100%. In an aspect, an increased amount of at least one terpene comprises an increase of between 0.5% and 75%. In an aspect, an increased amount of at least one terpene comprises an increase of between 0.5% and 50%. In an aspect, an increased amount of at least one terpene comprises an increase of between 0.5% and 25%. In an aspect, an increased amount of at least one terpene comprises an increase of between 0.5% and 10%. In an aspect, an increased amount of at least one terpene comprises an increase of between 0.5% and 5%. In an aspect, an increased amount of at least one terpene comprises an increase of between 0.5% and 500%. In an aspect, an increased amount of at least one terpene comprises an increase of between 5% and 250%. In an aspect, an increased amount of at least one terpene comprises an increase of between 5% and 100%. In an aspect, an increased amount of at least one terpene comprises an increase of between 5% and 50%. In an aspect, an increased amount of at least one terpene comprises an increase of between 25% and 500%. In an aspect, an increased amount of at least one terpene comprises an increase of between 25% and 250%. In an aspect, an increased amount of at least one terpene comprises an increase of between 50% and 100%. In an aspect, an increased amount of at least one terpene comprises an increase of between 100% and 500%.

[0168] The amount of terpenes in a plant can be measured using any method known in the art, including, without being limiting, gas chromatography mass spectrometry (GC-MS), Nuclear Magnetic Resonance Spectroscopy, and liquid chromatography-linked mass spectrometry. See The Handbook of Plant Metabolomics, edited by Weckwerth and Kahl, (Wiley-Blackwell) (May 28, 2013). In an aspect, an amount of at least one terpene refers to the concentration of the at least one terpene in the tissue sampled.

Products

[0169] In an aspect, this disclosure provides cured plant material from any plant or plant part provided herein. In an aspect, this disclosure provides cured tobacco material from any tobacco plant or tobacco plant part provided herein.

[0170] In an aspect, cured plant material is made by a curing process selected from the group consisting of flue curing, air curing, fire curing, and sun curing. In an aspect, cured tobacco material is made by a curing process selected from the group consisting of flue curing, air curing, fire curing, and sun curing.

[0171] "Curing" is the aging process that reduces moisture and brings about the destruction of chlorophyll giving tobacco leaves a golden color and by which starch is converted to sugar. Cured tobacco therefore has a higher reducing sugar content and a lower starch content compared to harvested green leaf. In one aspect, tobacco plants or plant components provided herein can be cured using conventional means, (e.g., flue-cured, barn-cured, fire-cured, air-cured or sun-cured). See, for example, Tso (1999, Chapter 1 in Tobacco, Production, Chemistry and Technology, Davis & Nielsen, eds., Blackwell Publishing, Oxford) for a description of different types of curing methods. Cured tobacco is usually aged in a wooden drum (e.g., a hogshead) or cardboard cartons in compressed conditions for several years (e.g., two to five years), at a moisture content ranging from 10% to about 25%. See, U.S. Pat. Nos. 4,516,590 and 5,372,149. Cured and aged tobacco then can be further processed. Further processing includes conditioning the tobacco under vacuum with or without the introduction of steam at various temperatures, pasteurization, and fermentation.

[0172] Information regarding the harvesting of burley and dark tobacco varieties can be found in the 2019-2020 *Burley and Dark Tobacco Production Guide* (December 2018) published by the University of Kentucky, The University of Tennessee, Virginia Tech, and North Carolina State University, which is incorporated herein by reference in its entirety.

[0173] In an aspect, cured tobacco material comprises tobacco material selected from the group selected from cured leaf material, cured stem material, cured bud material, cured flower material, and cured root material. In an aspect, cured tobacco material comprises cured leaf material, cured stem material, or both. In an aspect, cured tobacco material comprises cured leaf material. In an aspect, cured tobacco material comprises cured stem material.

[0174] In an aspect, cured tobacco material comprises flue-cured tobacco material. In an aspect, cured tobacco material comprises air-cured tobacco material. In an aspect, cured tobacco material comprises fire-cured tobacco material. In an aspect, cured tobacco material comprises sun-cured tobacco material. In an aspect, cured tobacco material provided herein is selected from the group consisting of air-cured tobacco material, fire-cured tobacco material, sun-cured tobacco material, and flue-cured tobacco material. In an aspect, cured tobacco material is from a tobacco variety selected from the group consisting of a flue-cured variety, a Burley variety, a Virginia variety, a Maryland variety, a dark variety, an Oriental variety, and a Turkish variety.

[0175] In an aspect, cured tobacco leaf provided herein is selected from the group consisting of air-cured tobacco leaf, fire-cured tobacco leaf, sun-cured tobacco leaf, and flue-cured tobacco leaf. In an aspect, cured tobacco leaf is from a tobacco variety selected from the group consisting of a flue-cured variety, a bright variety, a Burley variety, a Virginia variety, a Maryland variety, a dark variety, an Oriental variety, and a Turkish variety.

[0176] Fermentation typically is characterized by high initial moisture content, heat generation, and a 10 to 20% loss of dry weight. See, for example, U.S. Pat. Nos. 4,528,993, 4,660,577, 4,848,373, 5,372,149; U.S. Publication No. 2005/0178398; and Tso (1999, Chapter 1 in Tobacco, Production, Chemistry and Technology, Davis & Nielsen, eds., Blackwell Publishing, Oxford). Cured, aged, and fermented

tobacco can be further processed (e.g., cut, shredded, expanded, or blended). See, for example, U.S. Pat. Nos. 4,528,993; 4,660,577; and 4,987,907. In an aspect, this disclosure provides fermented tobacco material from any tobacco plant, or part thereof, provided herein. In another aspect, this disclosure provides fermented tobacco material from any modified tobacco plant, or part thereof, provided herein.

[0177] Tobacco material obtained from the tobacco lines, varieties or hybrids of the present disclosure can be used to make tobacco products. As used herein, “tobacco product” is defined as any product made or derived from tobacco that is intended for human use or consumption. In an aspect, this disclosure provides a tobacco product comprising plant material from a tobacco plant provided herein. In another aspect, this disclosure provides a tobacco product comprising plant material from a modified tobacco plant provided herein. In another aspect, this disclosure provides a tobacco product comprising cured tobacco material. In another aspect, this disclosure provides a tobacco product comprising fermented tobacco material. In another aspect, this disclosure provides a tobacco product comprising a tobacco blend.

[0178] Tobacco products include, without limitation, cigarette products (e.g., cigarettes and bidi cigarettes), cigar products (e.g., cigar wrapping tobacco and cigarillos), pipe tobacco products, products derived from tobacco, tobacco-derived nicotine products, smokeless tobacco products (e.g., moist snuff, dry snuff, and chewing tobacco), films, chewables, tabs, shaped parts, gels, consumable units, insoluble matrices, hollow shapes, reconstituted tobacco, expanded tobacco, and the like. See, e.g., U.S. Patent Publication No. US 2006/0191548.

[0179] As used herein, “cigarette” refers a tobacco product having a “rod” and “filler”. The cigarette “rod” includes the cigarette paper, filter, plug wrap (used to contain filtration materials), tipping paper that holds the cigarette paper (including the filler) to the filter, and all glues that hold these components together. The “filler” includes (1) all tobaccos, including but not limited to reconstituted and expanded tobacco, (2) non-tobacco substitutes (including but not limited to herbs, non-tobacco plant materials and other spices that may accompany tobaccos rolled within the cigarette paper), (3) casings, (4) flavorings, and (5) all other additives (that are mixed into tobaccos and substitutes and rolled into the cigarette).

[0180] In an aspect, a tobacco product comprises reconstituted tobacco. In another aspect, this disclosure provides reconstituted tobacco comprising cured tobacco material. As used herein, “reconstituted tobacco” refers to a part of tobacco filler made from tobacco dust and other tobacco scrap material, processed into sheet form and cut into strips to resemble tobacco. In addition to the cost savings, reconstituted tobacco is very important for its contribution to cigarette taste from processing flavor development using reactions between ammonia and sugars.

[0181] In an aspect, a tobacco product comprises expanded tobacco. As used herein, “expanded tobacco” refers to a part of tobacco filler which is processed through expansion of suitable gases so that the tobacco is “puffed” resulting in reduced density and greater filling capacity. It reduces the weight of tobacco used in cigarettes.

[0182] Tobacco products derived from plants of the present disclosure also include cigarettes and other smoking

articles, particularly those smoking articles including filter elements, where the rod of smokable material includes cured tobacco within a tobacco blend. In an aspect, a tobacco product of the present disclosure is selected from the group consisting of a kretek, a bidi cigarette, a cigarillo, a non-ventilated recess filter cigarette, a vented recess filter cigarette, a cigar, snuff, pipe tobacco, cigar tobacco, cigarette tobacco, chewing tobacco, leaf tobacco, hookah tobacco, shredded tobacco, and cut tobacco.

[0183] In an aspect, a tobacco product of the present disclosure is selected from the group consisting of a cigarette, a heated tobacco product, a kretek, a bidi cigarette, a cigar, a cigarillo, a non-ventilated cigarette, a vented recess filter cigarette, pipe tobacco, snuff, snus, chewing tobacco, moist smokeless tobacco, fine cut chewing tobacco, long cut chewing tobacco, pouched chewing tobacco product, gum, a tablet, a lozenge, and a dissolving strip.

[0184] In an aspect, a tobacco product of the present disclosure is a smokeless tobacco product. In an aspect, a smokeless tobacco product is selected from the group consisting of loose leaf chewing tobacco, plug chewing tobacco, moist snuff, nasal snuff, dry snuff, and snus.

[0185] Smokeless tobacco products are not combusted and include, but not limited to, chewing tobacco, moist smokeless tobacco, snus, and dry snuff. Chewing tobacco is coarsely divided tobacco leaf that is typically packaged in a large pouch-like package and used in a plug or twist. Moist smokeless tobacco is a moist, more finely divided tobacco that is provided in loose form or in pouch form and is typically packaged in round cans and used as a pinch or in a pouch placed between an adult tobacco consumer's cheek and gum. Snus is a heat-treated smokeless tobacco. Dry snuff is finely ground tobacco that is placed in the mouth or used nasally.

[0186] In yet another aspect, a tobacco product of the present disclosure is selected from the group consisting of an electronically heated cigarette, an e-cigarette, an electronic vaporizing device.

[0187] In an aspect, a tobacco product of the present disclosure can be a blended tobacco product.

[0188] In another aspect, this disclosure provides a tobacco blend comprising cured tobacco material. A tobacco blend can comprise any combination of cured tobacco, uncured tobacco, fermented tobacco, unfermented tobacco, expanded tobacco, and reconstituted tobacco.

[0189] In an aspect, a tobacco blend comprises at least 5% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 10% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 15% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 20% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 25% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 30% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 35% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 40% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 45% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 50% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 55% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 60% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 65% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 70% cured tobacco by weight. In an

sequence to at least one plant cell, where the nucleic acid sequence encodes an amino acid sequence at least 99% identical or similar to a sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment thereof; (b) selecting at least one plant cell from step (a), where the at least one plant cell comprises the recombinant nucleic acid molecule; and (c) regenerating a modified plant from the at least one plant cell selected in step (b). In an aspect, this disclosure provides a method of generating a modified plant, the method comprising: (a) introducing a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence to at least one plant cell, where the nucleic acid sequence encodes an amino acid sequence at least 99.9% identical or similar to a sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment thereof; (b) selecting at least one plant cell from step (a), where the at least one plant cell comprises the recombinant nucleic acid molecule; and (c) regenerating a modified plant from the at least one plant cell selected in step (b). In an aspect, this disclosure provides a method of generating a modified plant, the method comprising: (a) introducing a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence to at least one plant cell, where nucleic acid sequence encodes a protein selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment thereof; (b) selecting at least one plant cell from step (a), where the at least one plant cell comprises the recombinant nucleic acid molecule; and (c) regenerating a modified plant from the at least one plant cell selected in step (b).

[0199] In an aspect, a method provided herein comprises transforming a plant cell with a recombinant nucleic acid molecule, where the recombinant nucleic acid molecule comprises a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence encodes an amino acid sequence at least 80% identical or similar to a sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment thereof. In an aspect, a method provided herein comprises transforming a plant cell with a recombinant nucleic acid molecule, where the recombinant nucleic acid molecule comprises a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence encodes an amino acid sequence at least 85% identical or similar to a sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment thereof. In an aspect, a method provided herein comprises transforming a plant cell with a recombinant nucleic acid molecule, where the recombinant nucleic acid molecule comprises a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence encodes an amino acid sequence at least 90% identical or similar to a sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment thereof. In an aspect, a method provided herein comprises transforming a plant cell with a recombinant nucleic acid molecule, where the recombinant nucleic acid molecule comprises a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence encodes an amino acid sequence at least 92.5% identical or similar to a sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment

thereof. In an aspect, a method provided herein comprises transforming a plant cell with a recombinant nucleic acid molecule, where the recombinant nucleic acid molecule comprises a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence encodes an amino acid sequence at least 95% identical or similar to a sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment thereof. In an aspect, a method provided herein comprises transforming a plant cell with a recombinant nucleic acid molecule, where the recombinant nucleic acid molecule comprises a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence encodes an amino acid sequence at least 96% identical or similar to a sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment thereof. In an aspect, a method provided herein comprises transforming a plant cell with a recombinant nucleic acid molecule, where the recombinant nucleic acid molecule comprises a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence encodes an amino acid sequence at least 97% identical or similar to a sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment thereof. In an aspect, a method provided herein comprises transforming a plant cell with a recombinant nucleic acid molecule, where the recombinant nucleic acid molecule comprises a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence encodes an amino acid sequence at least 98% identical or similar to a sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment thereof. In an aspect, a method provided herein comprises transforming a plant cell with a recombinant nucleic acid molecule, where the recombinant nucleic acid molecule comprises a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence encodes an amino acid sequence at least 99% identical or similar to a sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment thereof. In an aspect, a method provided herein comprises transforming a plant cell with a recombinant nucleic acid molecule, where the recombinant nucleic acid molecule comprises a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence encodes an amino acid sequence at least 99.9% identical or similar to a sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment thereof. In an aspect, a method provided herein comprises transforming a plant cell with a recombinant nucleic acid molecule, where the recombinant nucleic acid molecule comprises a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence encodes an amino acid sequence at least 99.99% identical or similar to a sequence selected from the group consisting of SEQ ID NOS: 18-22 and 31-33, or a functional fragment thereof.

[0200] Numerous methods for “introducing” a recombinant nucleic acid molecule to a plant cell are known in the art, which can be used according to methods of the present application to produce a modified plant cell, plant, seed, or plant part. As used herein, the terms “introducing” and “transforming” can be used interchangeably. Any suitable method or technique for transformation of a plant cell known in the art can be used according to present methods.

Effective methods for transformation of plants include bacterially mediated transformation, such as *Agrobacterium*-mediated or *Rhizobium*-mediated transformation and micro-projectile bombardment-mediated transformation. A variety of methods are known in the art for transforming explants with a transformation vector via bacterially mediated transformation or microprojectile bombardment and then subsequently culturing, etc., those explants to regenerate or develop transgenic plants. Other methods for plant transformation, such as microinjection, electroporation, vacuum infiltration, pressure, sonication, silicon carbide fiber agitation, polyethylene glycol (PEG)-mediated transformation, etc., are also known in the art. Modified plants produced by these transformation methods can be chimeric or non-chimeric for the transformation event depending on the methods and explants used.

[0201] Methods of transforming plant cells are well known by persons of ordinary skill in the art. For instance, specific instructions for transforming plant cells by micro-projectile bombardment with particles coated with recombinant DNA (e.g., biolistic transformation) are found in U.S. Pat. Nos. 5,550,318; 5,538,880 6,160,208; 6,399,861; and 6,153,812 and *Agrobacterium*-mediated transformation is described in U.S. Pat. Nos. 5,159,135; 5,824,877; 5,591,616; 6,384,301; 5,750,871; 5,463,174; and 5,188,958, all of which are incorporated herein by reference. Additional methods for transforming plants can be found in, for example, Compendium of Transgenic Crop Plants (2009) Blackwell Publishing. Any appropriate method known to those skilled in the art can be used to transform a plant cell (e.g., tobacco cell, *cannabis* cell) with any of the nucleic acid molecules provided herein.

[0202] In an aspect, a method of introducing a recombinant nucleic acid molecule to a plant cell comprises *Agrobacterium*-mediated transformation. In another aspect, a method of introducing a recombinant nucleic acid molecule to a plant cell comprises PEG-mediated transformation. In another aspect, a method of introducing a recombinant nucleic acid molecule to a plant cell comprises biolistic transformation. In another aspect, a method of introducing a recombinant nucleic acid molecule to a plant cell comprises liposome-mediated transfection (lipofection). In another aspect, a method of introducing a recombinant nucleic acid molecule to a plant cell comprises lentiviral transfection.

[0203] Lipofection is described in e.g., U.S. Pat. Nos. 5,049,386, 4,946,787; and 4,897,355) and lipofection reagents are sold commercially (e.g., Transfectam™ and Lipofectin™) Cationic and neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides include those of WO 91/17424 and WO 91/16024. Delivery can be to cells (e.g. *in vitro* or *ex vivo* administration) or target tissues (e.g. *in vivo* administration).

[0204] Any plant cell from which a fertile plant can be regenerated is contemplated as a useful recipient cell for practice of this disclosure.

[0205] In an aspect, a recombinant nucleic acid molecule is introduced to a tobacco cell. In an aspect, a recombinant nucleic acid molecule is introduced to a tobacco protoplast cell. In another aspect, a recombinant nucleic acid molecule is introduced to a tobacco callus cell. In an aspect, a recombinant nucleic acid molecule is introduced to a tobacco cell selected from the group consisting of a seed cell, a fruit cell, a leaf cell, a cotyledon cell, a hypocotyl cell, a meristem cell, an embryo cell, an endosperm cell, a root

cell, a shoot cell, a stem cell, a flower cell, an inflorescence cell, a stalk cell, a pedicel cell, a style cell, a stigma cell, a receptacle cell, a petal cell, a sepal cell, a pollen cell, an anther cell, a filament cell, an ovary cell, an ovule cell, a pericarp cell, and a phloem cell.

[0206] In an aspect, a recombinant nucleic acid molecule is introduced to a *cannabis* cell. In an aspect, a recombinant nucleic acid molecule is introduced to a *cannabis* protoplast cell. In another aspect, a recombinant nucleic acid molecule is introduced to a *cannabis* callus cell. In an aspect, a recombinant nucleic acid molecule is introduced to a *cannabis* cell selected from the group consisting of a seed cell, a fruit cell, a leaf cell, a cotyledon cell, a hypocotyl cell, a meristem cell, an embryo cell, an endosperm cell, a root cell, a shoot cell, a stem cell, a flower cell, an inflorescence cell, a stalk cell, a pedicel cell, a style cell, a stigma cell, a receptacle cell, a petal cell, a sepal cell, a pollen cell, an anther cell, a filament cell, an ovary cell, an ovule cell, a pericarp cell, and a phloem cell.

[0207] Callus can be initiated from various tissue sources, including, but not limited to, immature embryos or parts of embryos, seedling apical meristems, microspores, and the like. Those cells which are capable of proliferating as callus can serve as recipient cells for transformation. Practical transformation methods and materials for making transgenic plants of this disclosure (e.g., various media and recipient target cells, transformation of immature embryos, and subsequent regeneration of fertile transgenic plants) are disclosed, for example, in U.S. Pat. Nos. 6,194,636 and 6,232,526 and U. S. Patent Application Publication 2004/0216189, all of which are incorporated herein by reference.

Embodiments

[0208] The following examples of non-limiting embodiments are envisioned:

[0209] 1. A modified plant, seed, or plant part, comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, wherein said nucleic acid sequence is operably linked to a heterologous promoter.

[0210] 2. The modified plant, seed, or plant part, of embodiment 1, wherein said nucleic acid sequence comprises a sequence at least 90% identical or similar to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36.

[0211] 3. The modified plant, seed, or plant part, of embodiment 1 or 2, wherein said nucleic acid sequence is at least 95% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36.

[0212] 4. The modified plant, seed, or plant part, of any one of embodiments 1-3, wherein said nucleic acid sequence encodes a protein at least 90% identical or similar to a sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33.

[0213] 5. The modified plant, seed, or plant part, of any one of embodiments 1-4, wherein said nucleic acid sequence is selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36.

[0214] 6. The modified plant, seed, or plant part, of any one of embodiments 1-5, wherein said amino acid sequence is selected from the group consisting of SEQ ID NOs: 18-22 and 31-33.

[0215] 7. The modified plant, seed, or part thereof of any one of embodiments 1-6, wherein said modified plant, seed, or plant part is a tobacco plant, tobacco seed, or tobacco plant part.

[0216] 8. The modified plant, seed, or part thereof of embodiment 7, wherein the tobacco plant, tobacco seed, or plant part is of a tobacco variety selected from the group consisting of a flue-cured variety, a bright variety, a Burley variety, a Virginia variety, a Maryland variety, a dark variety, a Galpão variety, an Oriental variety, and a Turkish variety.

[0217] 9. The modified plant, seed, or part thereof of any one of embodiments 1-8, wherein the plant is male sterile or cytoplasmically male sterile.

[0218] 10. The modified plant, seed, or part thereof of any one of embodiments 1-6, wherein said modified plant, seed, or plant part is a *cannabis* plant, *cannabis* seed, or *cannabis* plant part.

[0219] 11. The modified plant, seed, or plant part, of any one of embodiments 1-10, wherein said plant or plant part comprises an amount of at least one terpene that is increased by at least 5% as compared to a control plant lacking said recombinant nucleic acid molecule.

[0220] 12. The modified plant, seed, or plant part, of any one of embodiments 1-11, wherein the heterologous promoter is selected from the group consisting of a constitutive promoter, an inducible promoter, and a tissue-preferred or tissue-specific promoter.

[0221] 13. The modified plant, seed, or plant part of any one of embodiments 1-12, wherein at least one leaf of the modified plant comprises a greater average trichome density as compared to a leaf of a control plant grown under comparable conditions.

[0222] 14. The modified plant, seed, or plant part of any one of embodiments 1-12, wherein at least one leaf of the modified plant comprises a greater average trichome density on the abaxial side of the leaf as compared to the abaxial side of a leaf of a control plant grown under comparable conditions.

[0223] 15. The modified plant, seed, or plant part of any one of embodiments 1-12, wherein at least one leaf of the modified plant comprises a greater average trichome density on the adaxial side of the leaf as compared to the adaxial side of a leaf of a control plant grown under comparable conditions.

[0224] 16. Cured tobacco material from a modified tobacco plant or tobacco plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence at encoding an amino acid sequence least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, wherein said nucleic acid sequence is operably linked to a heterologous promoter.

[0225] 17. The cured tobacco material of embodiment 16, wherein the cured tobacco material is selected from the group consisting of flue cured tobacco material, air cured tobacco material, fire cured tobacco material, and sun cured tobacco material.

[0226] 18. A tobacco product comprising the cured tobacco material of embodiment 16.

[0227] 19. The tobacco product of embodiment 18 or 23, wherein the tobacco product is selected from the group consisting of a kretek, a bidi cigarette, a cigarillo, a non-ventilated recess filter cigarette, a vented recess filter cigarette, a cigar, pipe tobacco, cigar tobacco, cigarette tobacco,

chewing tobacco, moist snuff, nasal snuff, dry snuff, snus, leaf tobacco, hookah tobacco, shredded tobacco, and cut tobacco.

[0228] 20. The tobacco product of embodiment 19, wherein the tobacco product is a smokeless tobacco product.

[0229] 21. The tobacco product of embodiment 20, wherein the smokeless tobacco product is selected from the group consisting of loose leaf chewing tobacco, plug chewing tobacco, moist snuff, nasal snuff, dry snuff, and snus.

[0230] 22. A reconstituted tobacco comprising the cured tobacco material of embodiment 16.

[0231] 23. A tobacco product comprising material from a modified tobacco plant, tobacco seed, or tobacco plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, wherein said nucleic acid sequence is operably linked to a heterologous promoter.

[0232] 24. A *cannabis* product comprising material from a modified *cannabis* plant, *cannabis* seed, or *cannabis* plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, wherein said nucleic acid sequence is operably linked to a heterologous promoter.

[0233] 25. A recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, wherein said nucleic acid sequence is operably linked to a heterologous promoter.

[0234] 26. The recombinant nucleic acid molecule of embodiment 25, wherein said nucleic acid sequence encodes a protein at least 90% identical or similar to a sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33.

[0235] 27. The recombinant nucleic acid molecule of embodiment 25 or 26, wherein said nucleic acid sequence is at least 90% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36.

[0236] 28. The recombinant nucleic acid molecule of any one of embodiments 25-27, wherein said nucleic acid sequence encodes a protein at least 95% identical or similar to a sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33.

[0237] 29. The recombinant nucleic acid molecule of any one of embodiments 25-28, wherein said nucleic acid sequence is selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36.

[0238] 30. The recombinant nucleic acid molecule of any one of embodiments 25-29, wherein said nucleic acid sequence encodes a protein selected from the group consisting of SEQ ID NOs: 18-22 and 31-33.

[0239] 31. A method for producing a plant, the method comprising:

[0240] (a) obtaining at least one plant comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence at least 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, wherein said nucleic acid sequence is operably linked to a heterologous promoter;

- [0241] (b) crossing said at least one plant with at least one plant of a second variety to produce at least one progeny seed; and
- [0242] (c) selecting said at least one progeny seed produced in step (b), or a plant germinated therefrom, wherein said at least one progeny seed or plant germinated therefrom comprises said recombinant nucleic acid molecule.
- [0243] 32. The method of embodiment 31, further comprising
- [0244] (d) harvesting plant material from a plant germinated from said at least one progeny seed; and
- [0245] (e) producing a product comprising or derived from said harvested plant material.
- [0246] 33. The method of embodiment 31 or 32, wherein a plant grown from said at least one progeny seed further comprises an amount of at least one terpene that is increased by at least 5% as compared to a control plant lacking said recombinant nucleic acid molecule.
- [0247] 34. The method of any one of embodiments 31-33, wherein a plant grown from said at least one progeny seed further comprises an amount of at least one terpene that is increased by at least 10% as compared to a control plant lacking said recombinant nucleic acid molecule.
- [0248] 35. The method of any one of embodiments 31-34, wherein said at least one plant is from a genus selected from the group consisting of *Nicotiana* and *Cannabis*.
- [0249] 36. The method of any one of embodiments 31-35, wherein said at least one plant is from a genus selected from the group consisting of tobacco and *cannabis*.
- [0250] 37. The method of any one of embodiments 31-36, wherein said a recombinant nucleic acid molecule comprises a nucleic acid sequence encoding a protein at least 80% identical or similar to a sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33.
- [0251] 38. The method of any one of embodiments 31-37, wherein said a recombinant nucleic acid molecule comprises a nucleic acid sequence at least 90% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-27 and 34-36.
- [0252] 39. The method of any one of embodiments 31-38, wherein said a recombinant nucleic acid molecule comprises a nucleic acid sequence encoding a protein at least 90% identical or similar to a sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33.
- [0253] 40. The method of any one of embodiments 31-39, wherein said a recombinant nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-27 and 34-36.
- [0254] 41. The method of any one of embodiments 31-40, wherein said a recombinant nucleic acid molecule comprises a nucleic acid sequence encoding a protein selected from the group consisting of SEQ ID NOs: 18-22 and 31-33.
- [0255] 42. A method of generating a modified plant, the method comprising:
- [0256] (a) introducing a recombinant nucleic acid molecule comprising a nucleic acid sequence at least 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, wherein said nucleic acid sequence is operably linked to a heterologous promoter, to at least one plant cell;
- [0257] (b) selecting at least one plant cell from step (a), wherein the at least one plant cell comprises the recombinant nucleic acid molecule; and
- [0258] (c) regenerating a modified plant from the at least one plant cell selected in step (b).
- [0259] 43. A method comprising preparing a tobacco product using cured tobacco material from a modified tobacco plant or part therefrom, wherein the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprises a nucleic acid sequence at least 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, wherein said nucleic acid sequence is operably linked to a heterologous promoter, to at least one plant cell.
- [0260] 44. A method comprising preparing a *cannabis* product using material from a modified *cannabis* plant or part therefrom, wherein the modified *cannabis* plant or part therefrom comprises a recombinant nucleic acid molecule comprises a nucleic acid sequence at least 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, wherein said nucleic acid sequence is operably linked to a heterologous promoter, to at least one plant cell.
- [0261] 45. A method comprising transforming a plant cell with a recombinant nucleic acid molecule, wherein the recombinant nucleic acid molecule comprises a nucleic acid sequence at least 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, wherein said nucleic acid sequence is operably linked to a heterologous promoter, to at least one plant cell.
- [0262] 46. A method for producing a plant with increased trichome density, the method comprising:
- [0263] (a) providing to at least one plant cell a recombinant nucleic acid comprising a heterologous promoter operably linked to a polynucleotide, where the polynucleotide encodes an amino acid sequence at least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33; and
- [0264] (b) regenerating a modified plant from the at least one plant cell in step (a), where the modified plant comprises an increased trichome density on at least one leaf as compared to a leaf from a control plant lacking the recombinant nucleic acid when grown under comparable conditions.
- [0265] Having now generally described the disclosure, the same will be more readily understood through reference to the following examples that are provided by way of illustration, and are not intended to be limiting of the present disclosure, unless specified.

EXAMPLES

Example 1. Identification of Candidate Transcription Factors for Trichome Density Modification

[0266] Transcription factors involved in regulation of trichome initiation and development were used as query in a search of the National Center for Biotechnology Information (NCBI) database. A similar approach is utilized to identify lipid transfer proteins in tobacco. The resulting sequences were then extracted from a second, internal database. This methodology identified members of the transcription factor families MYB (FIGS. 3A and 3B) and C2H2 (FIG. 4). From these families, three transcription factors candidates are selected for modification of trichome density in plants. This approach also identified 86 members of the

lipid transfer protein (LTP) family in tobacco and subsequently led to identification of two variant isoforms of LTP1, isoform two (SEQ ID NO:27) having a 5' extension compared to isoform 1 (SEQ ID NO:26). See FIGS. 8A and 8B. This approach allowed the curation of a list of candidate genes that are trichome-specific and involved in metabolite transport (SEQ ID NOS: 13-27 and 34-36). See Table 1.

Example 2. Construction of Vectors

[0267] The candidate genes identified in Example 1 (e.g., SEQ ID NOS: 13-27 and 34-36) are cloned using the PCR Cloning System with GATEWAY™ Technology (ThermoFisher Scientific, Catalog Number 12535029). The cloned genes are subsequently subcloned into a GATEWAY™ expression vector, where the subcloned gene is fused with GREEN FLUORESCENCE PROTEIN (G3GFP) operably linked to a CaMV 35S promoter. See FIG. 2.

Example 3. Transformation and Regeneration of Modified Tobacco Plants

[0268] Each of the vector constructs generated in Example 2 is separately transformed into tobacco cells in separate experiments. Briefly, the vectors are introduced into tobacco leaf discs via *Agrobacterium* transformation. See, for example, Mayo et al., *Nat. Protoc.*, 1:1105-1111 (2006); and Horsch et al., *Science*, 227:1229-1231 (1985).

[0269] Transformed tobacco plants (variety 'TN90' and 'Izmir Ego') and *N. benthamiana* are grown in Magenta™ GA-7 boxes and leaf discs are cut and placed into Petri plates. *Agrobacterium tumefaciens* cells comprising a transformation vector are collected by centrifuging a 20 mL cell suspension in a 50 mL centrifuge tube at 3500 RPM for 10 minutes. The supernatant is removed, and the *Agrobacterium tumefaciens* cell pellet is re-suspended in 40 mL liquid re-suspension medium. Tobacco leaves, avoiding the midrib, are cut into eight 0.6 cm discs with a #15 razor blade and placed upside down in a Petri plate. A thin layer of Murashige & Skoog (MS) with B5 vitamin liquid re-suspension medium is added to the Petri plate and the leaf discs are poked uniformly with a fine point needle. About 25 mL of the *Agrobacterium tumefaciens* suspension is added to the Petri plate and the leaf discs are incubated in the suspension for 10 minutes.

[0270] Leaf discs are transferred to co-cultivation Petri plates ($\frac{1}{2}$ MS medium) and discs are placed upside down in contact with filter paper overlaid on the co-cultivation TOM medium (MS medium with 30 g/L sucrose; 0.1 mg/L 1-naphthaleneacetic acid (NAA); and 1 mg/L 6-benzyl aminopurine (BAP)). The Petri plate is sealed with parafilm and incubated in the dark for two days.

[0271] After incubation, leaf discs are transferred to regeneration/selection TOM K medium Petri plates (TOM medium plus 200 mg/L cefotaxime and 50 mg/L hygromycin). Calli formed from leaf discs are sub-cultured bi-weekly to fresh TOM-Hyg medium in dim light (between 60 and 80 mE/ms) with photoperiods of 18 hours light, 6 hours dark, at 24° C. until shoots (plantlets) become excisable. Plantlets formed from calli are removed with forceps and subcultured into MS rooting medium (MS medium with 3 g/L sucrose, 7 g/L dextrose with 200 mg/L cefotaxime and 50 mg/L hygromycin). Shoots on MS basal medium with 50 mg/L hygromycin are incubated with the same lighting (approximately 60-80 mE/ms) with photoperiods of 18 hours light, 6 hours dark, at 24° C. to induce rooting.

[0272] When plantlets comprising both shoots and roots grow large enough (e.g., over half the height of a Magenta™ GA-7 box), they are transferred to Jiffy peat pellets for acclimatization in the growth room. Once established, seedlings are transferred to a greenhouse for further growth, breeding, and analysis.

Example 4. Confirming Expression of Candidate Genes in Modified Tobacco Plants

[0273] During the vegetative stage of growth, RNA is extracted from young leaves of modified tobacco plants produced in Example 3, and from control tobacco plants lacking the recombinant nucleic acid constructs grown under comparable conditions. The extracted RNA is used to generate cDNA. Gene expression of NtMYB and NtGIS is quantified using quantitative real-time PCR (qRT-PCR) in T₀ transgenic plants (see FIGS. 10 and 11). To confirm the constructs are expressing the recombinant nucleic acids, expression of NtMYB and NtGIS in the modified plants is compared to control tobacco plants.

[0274] Gene expression of NtMYB and NbGIS is also quantified in T₁ transgenic plants. See FIGS. 16 and 17, respectively.

Example 5. Confirming Modification of Trichome Density in Modified Tobacco Plants

[0275] During the vegetative stage of growth, samples of transgenic lines of NtMYB86, NtGIS, and NbGIS from various tobacco backgrounds are examined under a stereomicroscope (model/type) to identify changes in trichome density in various plant parts compared with control plants. The results demonstrate that transgenic plants comprising NtMYB86, NtGIS, or NbGIS show an increase in the number of glandular trichomes per unit area (i.e. increased trichome density) in leaf and stem tissues. (See FIGS. 5-7)

Example 6. Measuring Terpene Levels in Modified Tobacco Plants

[0276] During the vegetative stage of growth, young leaves are harvested from the modified tobacco plants from Examples 3, 4, and 5, and from control tobacco plants lacking the recombinant nucleic acid constructs grown under comparable conditions, for use in a qualitative metabolic profile analysis following the protocol outlined by Jiang et al. (*Curr Protoc Plant Biol.* 2016; 1:345-358). Leaf samples are ground in liquid nitrogen, and then the samples are mixed with 60:40 hexane:ethyl acetate (v/v), supplemented with heptadecanol (an internal standard) and incubated overnight with shaking.

[0277] The solvent extracts are concentrated in a refrigerated SpeedVac™ (ThermoFisher Scientific) and placed into a silica column. The column is washed with hexane and allowed to flow through into collection tubes. Samples are aliquoted from the collection tubes and used for gas chromatography-mass spectrometry (GC-MS) analysis of metabolites.

[0278] To identify secondary metabolites secreted from leaf trichomes, 1 gram of leaf samples from transgenic lines are cut into small sections and soaked into hexane supplemented with heptadecanol (an internal standard) and incubated overnight with shaking. The extract is filtered and used for analysis of metabolic profile in gas chromatography-mass spectrometry (GC-MS). See FIGS. 12-15.

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 cgtatgttcc ttggacgtatc tactcgatc tatggaaatc gtcatgttta taatggtagc 420
 cattttctc aagctcataataatgtt agtgccttgg cttttttggaa aagtcttct 480
 tttcccttctt ctaattatgtc tgcgttccatc tcaatgtatc tagatccat tccatgttgc 540
 gttatgttggaa atttgcacat caataacaggc tgcgttccatc taaggccat tgggtatgtaa 600
 cagaagcaag aagtccaaatc tcatgttgatc ttatgtatc acttgttgc 648

SEQ ID NO: 26 moltype = DNA length = 1014
 FEATURE Location/Qualifiers
 source 1..1014
 mol_type = genomic DNA
 organism = Nicotiana tabacum

SEQUENCE: 26 atggaaatgg taagcaatgt tgcatgtttc gtgggttgc gcatgggttgc gtttgcaccc 60
 catgcagagg cactgacatc cggccagggtt cagtcatacc tggctcttgc cgtcccttat 120
 ttgtgtggcc cggcccccgggggggtt tggccggcc ttaaaatgtt gttgggtgttgc 180
 gtcgcaccc cagccggacc aaaaactgtca tgcataatgtcc tggaaatcagc cgtatataact 240
 ttaaaggccca ttgtatgttgc caacccgcgtt cgttcccttgc gatcttgcgttgc cttttttt 300
 ccctacaaga tcagtccttc cactgacttc tccaaatgttgc tttttcaactt tttttttttt 360
 ttatgtatgttgc ttatgtatgttgc ttccatgttac attgttaaaga atttttgcattt gtcagggttgc 420
 aattttgttgc acaacaagaa gtaatgtttt attgttgcacat aaaaataaaat aatgtatgtca 480
 tcaaaatata atgtatgttgc taatgtaaaaaa aatgttacat tccctttgtt atcttacac 540
 tacccatatt ttcatgttca ttcatttgc tttttccgg cttccacttta attgtatgttgc 600
 ttggccctttt ttatgtatgttgc ttatgtatgttgc ttatgtatgttgc ttatgtatgttgc 660
 caaagaaagaa cttaaaaatgttgc tttccaaatgttgc gtaaaaggttgc ggtactatgttgc 720
 ttatgtatgttgc tgaatgttgc aaaaatgttgc tttatgtatgttgc ttatgtatgttgc 780
 attatattaa aaaaatgttgc cccatgttgc tttatgtatgttgc ttatgtatgttgc ttatgtatgttgc 840
 tggatcgaaatc ttgtatgttgc ttatgtatgttgc ttatgtatgttgc ttatgtatgttgc 900
 acgacactgttgc attggctgttgc aatgttgcatttgc atttatttttgc tttatgtatgttgc ttatgtatgttgc 960
 ggtgtcgatc ttatgtatgttgc ttatgtatgttgc ttatgtatgttgc ttatgtatgttgc 1014

SEQ ID NO: 27 moltype = DNA length = 1158
 FEATURE Location/Qualifiers
 source 1..1158
 mol_type = genomic DNA
 organism = Nicotiana tabacum

SEQUENCE: 27 atgttccaaatc atttctcttc tataaaaaac ctttttttttgc ttttttttttgc ttttttttttgc 60
 actcaaggca ataacatgttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 120
 ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 180
 ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 240
 ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 300
 ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 360
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 ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 480
 ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 540
 aaaaatgttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 600

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acataaaaaaa ataaagtaat gctatcaa atataactgat atgataatgt aaaaaaactt 660
aatctccctt tgctatccctt acactaccca tattttcatt cttacttcaa ttttactttt 720
cccgctccac tttaattgtat tttttggcc ttttttagat tatagatcat tattttgata 780
ataatgtat gatttttttg atatcaaga agaactaaaa aaattttcca aagtgtcccc 840
tggagtaaaaq agttqgacta tctgttattt ttaatgaaca attaaqaqgq atataaaaaag 900
ttaatatgtat taatttttt attaattaat attaaaaaagc gaaccctta atatgagtga 960
aaacaaccaa ataatcaatt aaagtggatc ggaagaagca atcacttgaa agtgtgttaa 1020
catgatataat aatccacatat ttatcacaca ctgaattggc tggtaagtga gaagatttt 1080
attcataacc aatgcgtttt ttttgggtgt cgatggggat taatgttgggtt tttcatgtga 1140
caatgcaggg tcacgtgtca 1158

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SEQ ID NO: 28          moltype = DNA  length = 1566
FEATURE                Location/Qualifiers
source                 1..1566
                      mol_type = genomic DNA
                      organism = Cannabis sativa
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SEQ ID NO: 29          moltype = DNA  length = 705
FEATURE              Location/Qualifiers
source               1..705
                     mol_type = genomic DNA
                     organism = Cannabis sativa
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SEQUENCE: 29

	organism = cannabis sativa					
atggcggagc	tagaataccaa	aattaccaaa	aacccaactc	caaccaccac	gcgcgttaaaa	60
ctatcggtt	tcaacgtttc	agacgactac	gaagaaggcc	tagtgtactc	agcaaaaaacg	120
acgcgcgttc	gttcacccggaa	atccggcaaa	ggatttcaga	actccgggttgc	ccggaaataac	180
gagtgtcagt	actgttgtag	agaatttcgt	aattcccaag	cccttaggtgg	ccatcaaaaac	240
gtcataaaa	aagaaagaca	acagctttaa	cgagcttcgc	ttcaagcgag	ccgaaacgcgc	300
ggccgttttc	acgtcttttt	cccgataatc	tcgggttttg	ccgcgcgcgc	gcatctttttc	360
tcgcgcgttc	gacaggttat	ggtacccggcg	gcttcttcctt	ctgggtttttc	ttgtccccgt	420
tcggcttc	cttccacgt	gtcgcatggc	tgtgttttc	cttcgtgtat	gaacgggtggg	480
agaggtgcga	gttcagtttt	gttategtat	ggtagccgtat	tagggatata	ttctacatttgc	540
acgtatgggtt	ctcaaggttca	acaacaacaa	caacacttcac	ggggccatata	ttttaagggttgc	600
atggggccctt	ctggtagat	atttcggaaa	ggagatgtgt	ggcccaattt	tgatgtatgc	660
ttggggccctgg	acttgcattt	tagtcttgc	cccgctgtctc	catgaa		705

SEQ ID NO: 30 moltype = DNA length = 357
FEATURE Location/Qualifiers
source 1..357
mol_type = genomic DNA
organism = Cannabis sativa

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SEQUENCE: 30
                                         organism = Cannabis sativa
atggcctcaa actcttcaag catgaagcta ctctgatgg tggcatgggatgggtggta 60
gttgcaccaa cgacacatgc cctaacatgt ggccaagtgt cttagcgtct tagcccatgc 120
atcaactact tcaagagccg cgggtgtcgc ccttcacatgttataatgg gatcaggctcg 180
ctgaaacatgtt cggccaaagac cccagggcgc cgcaaaactgttcatggatgttcttgc 240
ggccggccgca gcatcaactaa aacctcgcgg cgggatcttcc tggaaatgttgc 300
gggtgtcaatgtttccatcacaa gatcgttcc tccaccatttgc gcaacatgttgc 357

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SEQ ID NO: 31 moltype = AA length = 521
 FEATURE Location/Qualifiers
 source 1..521
 mol_type = protein
 organism = Cannabis sativa

SEQUENCE: 31
 MGRHSCCYKQ KLRKGLWSPE EDEKLNNYT KHGHGCVSSW PKLAGLQRCG KCSRRLRWINY 60
 LRPDLKRGPF SQQEENNLIE LHAVLGNRWS QIAAQLPGRD DNEIKNWLNS C1KKKLQRKG 120
 IDPNTHKPLS EVENDIGNKL ENKGNKAATN NNNNNENINNS TVRASSLGNL SNDHHHHHHH 180
 HLNLAQDSQP SMAAINRYPY LEVSSSTPPT QEFFFIEKSTD TRSSPSIISSS SPCDFSTYFS 240
 FHSNNNYNTTS SAAAAAAVSH HQDQNQQNNNM ASFCFNINQN STRPPQHHHH NMQISMNLIQP 300
 LQQQVSPSST TTASSSSPPS NIPRVRKPNIS LPLLSDHQSN SNSTTTTTT TTGAVQNWET 360
 STFSNSNGSSS SSCNIELQCN NNNNNNNNFED HNTNSTAAQQ AAAAPNNPNFW GLVNESTVGS 420
 IKSDDPEDIK WSEYLHSPFL LGGGISNTNN QNSSSSHLQ PILYSNIVKP ESHFSNTTA 480
 TGSNPTWHHQ NDHHQLQAAS SEIMYTNKDL QRLAVAFGQT L 521

SEQ ID NO: 32 moltype = AA length = 234
 FEATURE Location/Qualifiers
 source 1..234
 mol_type = protein
 organism = Cannabis sativa

SEQUENCE: 32
 MAELEYQITK NPTPTTTTRLK LFGFNVQDDY EEAIVADSAKT TPSGSPESGN GPQNSGDRKY 60
 ECQYCCREFA NSQALGGHQH AHKKERQQLK RAQLQASRNA AVSYARNSI SAFAPPHPHLL 120
 SPAGQVMVPA ASPSWVYVPR SAPFPFHVSHG CVFPPVMING RGASSVGLPY GSVDGDNSTL 180
 TMGSQVQQQQ QHSRAHNLRV DGPSLSRSFK GDGGPNFDDA LGLDLHLSLA PAAP 234

SEQ ID NO: 33 moltype = AA length = 118
 FEATURE Location/Qualifiers
 source 1..118
 mol_type = protein
 organism = Cannabis sativa

SEQUENCE: 33
 MASNNSSMKL LCMVVVMVMV VAPTTHALTC GQVSSSLSPC INYLGKSGGAV PSPCCNGIRS 60
 LNSAAKTPAD RKTACKCLQS AAGSIKGLNL NLAALPGK C GVNPVKISP STNCNSVQ 118

SEQ ID NO: 34 moltype = DNA length = 1768
 FEATURE Location/Qualifiers
 source 1..1768
 mol_type = genomic DNA
 organism = Cannabis sativa

SEQUENCE: 34
 atggggaggc actcttgttg ttacaaggcag aaactgagaa aagggttgtg gtcaccagaa 60
 gaagatgaga aacctcttaa ttatataacc aagcatggac atggctctg gagctctgtc 120
 cctaactgat ctggattaaa ttctactt actactatca atgctataaa ttctgtatg 180
 ttgcatacca aattagttac atattttatc atattaattt ttttatgaca ggtcttcaga 240
 gatgtgaaaa aagtggcagg ctaagggtga taaattattt gaggccgtt ttgaaaaagag 300
 gcccatttc acaacaagag gagaatttga taattgaact tcattgcagg ttggcaaca 360
 ggtaattaa tactttgttt ttgagaaaaa agaagaatga cattaattt gagttgttaat 420
 tcattttctgg gtactttatg aaataattt gtcggcaattt ttccatgtt cacagattgc 480
 agctcgatgtt ccaggaaagaa cagataatgtt gataaaaaac ttatggaaat ttgcattaa 540
 gaagaaaactg aggcaaaaag ggattgaccc aaatactcat aagccattat ttgaggtaga 600
 aatgacatt ggttaataaa tggagaaaaa gggtaaaaaa gtcgcacca ataacaacaa 660
 caatgagata attaataattt atactgttag agcttgcattt tttagaaaaact tatccaatg 720
 tcatcatcatcatcatcattt atcatctggaa ttctatgttgc cagtcacaaat catcaatggc 780
 ggccatcaat cgttaccacat tattggaaat ttccatctca actccggcga cacaagaatt 840
 cttcatagaa aatcaacat ataccagatc atcaccatca atatcatcat catcacattt 900
 tgattttttccatcttccatca aacaataatc aatacggcgtt cgttccgtt 960
 tgcagctgtc gctgtttctt atcatcaaga tcaaaaaacaa aacaacaaca tggccaggtt 1020
 ctgcgttcaac attaatcaaa atcaacttag acctccacat caccatcatc ataatcagat 1080
 gatttagat ctcatccagc cactacaaca acaagttatca ctttcatcaaa caacaacagc 1140
 atcatcatca tcacccatctt ccaatattt acgtgttaag cccctccatca gtctccctt 1200
 attatctgtat caccaaaaaca acgtaatag ctactactt actactatcaaa caactactgg 1260
 agccgttacaa aattggggaaa ctatgtactt cagcaacaaac ggaagttttt gtagtactgg 1320
 caatatcgaa ttacaaggta ataaaaatcaa caacaacaaac aacttctttt atcacaacac 1380
 taattccacc gccggggccg ccggccggccg cgctcttaat aacttctgtt ggggatttagt 1440
 caatgaaatg actgttgttgc gcataaaatc tgatgacccaa gaagacataaa aatgggttgc 1500
 atatccatcat agccctttt ttcttgggg aggaaattttt aatactataa atcaaaatc 1560
 ttcttcttctt tcacatcttca aaccatcttgc atcaacttagt atgtgaaac cagaatcaca 1620
 cttagtaat actactactg ctacaggatc aaacccccacg tggccatcatc agaacgtatca 1680
 tcatcagatca caagcggcgtt catcagaaat aatgtacact aatcaaagatc tacagagact 1740
 tgctgtatc ttggacaga cccttttg 1768

SEQ ID NO: 35 moltype = DNA length = 705
 FEATURE Location/Qualifiers

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ttgcccctcat	cggaaaacaaa	gaaaaattct	ccaccatctc	cttcaaagct	tccgttaatc	120
ggtcacttcc	acaaaactagg	cttacaacct	caccgttctc	tacaaaact	atcaaatgaa	180
catgggtccca	tgatgtatgc	tcaatccgt	agcgtaactg	tgcgttatcgc	ttcatcagct	240
gaagctgott	ccggaaatcat	gaaaacccaa	gatttgcctt	ttgcaaacaa	accatttca	300
accatttcta	gcaagctttt	cttcggccca	aaggacgttg	cttcacccc	atatgggat	360
tactggagga	atgcggagaag	catttgcatg	cttcagctt	tgaacaaacaa	aagagtccag	420
tcttttcgaa	agataaggga	agaagagact	tcttttcttc	ttcagaggat	taggaaatcg	480
ccaaatttcg	aagtccattt	aacggagctg	ttcggttcca	tgactaaacga	catagtttc	540
agggtggcct	taggaaggaa	gtattgtat	ggggagaag	ggaggaaatt	caagtcttg	600
ctgttagagt	tttgtggatt	gttggggat	tttacatttgc	gagattacat	gccgtggct	660
gcatggatga	atcgtttca	tggttgaat	gccaatgttg	ataaagtggc	gaaagat	720
gatgcatttt	ttggaggatgt	gatttggagaa	cacggaggaa	ataagaatc	agacactgaa	780
gctgaagggg	cagactcgt	ggatatatta	ttcaggtt	acaaagaaa	caaggctgg	840
tttcaagtcg	aatgtggatc	aatcaaagct	attatcatgg	atattgttc	tgccggaaaca	900
gatacaactt	ccacgttct	agagtggaca	atgaacgagc	tcttaagaaa	tccaaaacaa	960
ttaaataatg	tgagagatga	ggtggagacaa	gtgactcaag	ggaagacaga	ggttaacagag	1020
gatgacttag	agaaaatgcc	gtatthaaga	gcagcgtt	aggagatgc	caggctacac	1080
tctccagtc	cacttctacc	tcgagaagca	attaaggat	caaagggtt	gggcgtacat	1140
atagctcgag	ggactcaagt	cctcttgc	ccatggggca	tctcaagaga	tccaaacctt	1200
tggaaaatc	catggagat	tcaacctgaa	agatttctgg	atactccat	agattacaaa	1260
ggtttacatt	tcgagttat	tccattcggt	gcaggtcgga	ggggttgccc	tggcatcaca	1320
tttgctaagt	tttgtgaatg	gctagcattt	gcaagattaa	tgttccattt	tgatttctcg	1380
ctacccaaag	gagttaaagca	tgaggatttgc	gacgtggagg	aagctgtcg	aattactgtt	1440
agaaggaatg	ttccccctttt	agccgtcgcc	actccatgt	cgtga		1485

SEQ ID NO: 40	moltype = DNA	length = 966				
FEATURE	Location/Qualifiers					
source	1..966					
	mol_type = genomic DNA					
	organism = Nicotiana tabacum					
SEQUENCE: 40						
atggcagaaa	aaatcaccag	ccacggagac	acaaggatgt	cagtgggtac	agggggaaat	60
aaaggaaatg	gatatgaaac	atgcaggca	ctagcaaagg	aaggaaatgt	ggtagtgg	120
acagcaagg	atgaaaggag	aggaattgaa	gctctcgaa	agctcaagga	agagtactca	180
agoaataaaa	ctgtatgtat	tcagatttt	tttcatcaac	ttgatgttat	ggatccagat	240
agtatttctt	ctcttgcgaa	cttcatcaaa	actaaatttg	gaaagtcga	tattctgtt	300
aacaacgcog	ggatttgcgg	attaatggta	gaaggagatg	ttgttataat	aaaagat	360
atagaaggag	acttcgtaac	catttctgt	gaaaatgggg	aaaggatgg	tattaagaaa	420
tcaatttgcg	gtatttgcgg	tattttcaat	gattatgtat	tgacaaaacaa	atgcctggag	480
acaacacttct	atggtgcggaa	agaatgatt	gaagcattt	ttccccctct	tcagctct	540
aactccccc	gatattgtta	tgcgttctt	ttcttgggg	agttaaaatgt	attgtgcac	600
caatgggcta	taggaatgt	aagtgtatgc	aaaagcgtga	gagaagaaag	ggtggatgaa	660
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gttacgaaat	atccaaat	tcggat	tctgtgtgc	ctggattttt	caaaacagac	840
gtgaactgc	atactgggag	cttaactgt	gaagaagtg	ctgaaagctt	ggtgaagctt	900
gttttgcgtc	caatgtatgg	accctctgtt	cttttctttt	atagaaagga	ggtcaccc	960
ttttga						966

SEQ ID NO: 41	moltype = DNA	length = 1797				
FEATURE	Location/Qualifiers					
source	1..1797					
	mol_type = genomic DNA					
	organism = Nicotiana sylvestris					
SEQUENCE: 41						
atgagtcaat	caatttctcc	attatctgt	tctcaatttgc	cgaaaattca	gtcgaatatt	60
tggagatgca	atacttctca	actcagatgtt	atacactcat	catatgcctc	ttttgggg	120
agaagaaaag	agagagatgt	aagaatgtat	cgagcaatgg	atctttcttc	aagctctcg	180
catttgcgat	attttccctc	aacaatttgg	ggtgaccatt	ttctctcc	caatttgcgaa	240
ataacagaaa	tttacttccca	agagaaaaat	gaacatgaa	tgcgttgc	aatatgttgc	300
aaaatgttgg	tagaaatcttcc	agataatgt	acacaaaac	tagtctgt	tgacacatt	360
caaagatgg	gatttagcata	tcatttcaat	gtatgtatgt	aaaactccat	tcaaaacatc	420
tttaatttgt	ttccaaatag	tgaagatgt	gtatgtatgt	ttgtgtctt	480	
cgtttgcgc	tttgcggggca	acaaggatgt	tatcatgtt	cagatgttgc	caagcaattc	540
actaaccatg	acggaaaattt	caaggatgt	cataactatg	atgttcaagg	attattgtat	600
ttgtatgtat	gaggtgcac	gacggggaaa	ttctgtatgt	agctttatc	660	
tttaccacgt	ctcatatgc	gtccgtatc	ccgaaatttgc	gcaactgt	taaggatcaa	720
gttactgtat	ctttaagggca	tccttattcg	aaagctatac	caagggtgg	agcaaggaaa	780
tacatacaca	tatgtaaaa	catttgcgaa	cataatgtt	tacttttgc	attttgc	840
ttggacttca	acatgttaca	aaagcttcat	cgaaaagac	ttaacgtat	aacaagctgg	900
tggaaagatt	tggatgtgc	aaacaaat	ccatatgc	aggacatgt	agtagaaat	960
tacttttgc	cggtggaaat	atatttgc	cctcaatata	gtcgatca	aatgttgc	1020
acaacaaatgt	tcaaaatgt	ctccattt	gtatgtatgt	tgcaactt	1080	
gtatgtatgt	tgcttttgc	ggatgtgc	caaagatgg	acgaagggtgc	catggat	1140
ttaccgcacat	atctgatgt	tatttgc	ggccttctcg	acgttttgc	tgaaatggaa	1200
gaagtatttgc	ccaaagaagg	taaaggatgt	cacatctact	atgcgaaaaa	agagatgt	1260

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aagggtggcg	aagtctatt	taaggaagct	gaatgggtga	atgctaacta	cattccaaaa	1320
tgcgaggagt	atatgaaaaa	tggacttgt	agcttaccc	gtcccgatgt	tggaaaattt	1380
tcttttgtt	ttatggagga	attataaca	aaagaggctt	ttaatgggtt	gacaatggaa	1440
ccttgatttc	tttcgagotgc	atcaacaatt	tgtatggat	tgtatggat	ggctgtatcat	1500
gaagttgaa	aacaaagagg	acatgttgc	tcattttgtt	agtgtatcat	gaaagaatat	1560
ggagtttcaa	agcaagaagc	atatgttgc	atgcggaaaa	aaatcacaaa	tgctggaaaa	1620
gatataaaat	aggaacttct	ggccctact	gcgtatccaa	tgtttatct	cgaacgtatc	1680
ttaatttt	caagatgtgc	cgtacatatt	tttggaaatgt	atgtatggata	cacaatcccc	1740
aatccaaag	ttaaagactt	gattgttcg	ttgtttgtcg	aatgttcgaa	catatgtat	1797

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SEQ ID NO: 42 moltype = DNA length = 1098
FEATURE Location/Qualifiers
source 1..1098
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQUENCE: 42
atggcatttt tggctaccat ttctggccat gaaaatatgc ttcttccaa taccctaaac 60
aataacttta ttttcagttt aaaaccccca cagagacatt ctatagtt cctcccccaag 120
aaaatccagg ccagaagttt tgcaactca tcctaaaacat ttcaagtcaa agaagaagaa 180
ttctcatcta agacagagaa attcatcttgc cctaaaggttt accttgaaga atatatgaaa 240
atgaaggccca ttaaggataaa caaaagacta gatgtgcata taccatgcgaa agagcctata 300
aaaatttcatg aaggccatggc atacttcattt ctatcggtttt gaaaacgcgtt ccggccgtatc 360
ctatcgatgg cttcttgatggc agtagtagga gggggatgaaat ccttagatct tccctgcgtt 420
tgctcggtt agatgtatccca caccatgtca ctcatccacg acgatcttcc ttgcatggac 480
aacatgtatgc tacgtcggtt caagcccaacg agcccaacgg ctttcggggaa agacactgtca 540
gttctaaacag gggatgcact ttgtcttttgc gccttggaaat atgtatgttcc caaagataaa 600
gtatgtgcaccc cccaaagatgtt ggttcacggc gttggccat tgggttcgcg cgttggctcg 660
aaaggggcttggc tggcgccggca gattgtggac atagctatgtt agggaaaaca agtgagccata 720
actgaatttag agtacatccca caaccatggc acaggggaaat tattggggggc tgcgttgcgtt 780
tgtggggccaa taattgggggg aggaaatggc atttgggttggc agagaaatggc gaactatgtt 840
agatgttgcgttggc gactgtttttgc tcaatgttgc gatgtatgttcc ttgtatgttac taatgtatca 900
gaagagttggc gaaagacggc tggtaaaggac ctatgtactg ataaggctac atatccatgg 960
ttgtatggggc tagaaaaaaacg tcggggagtc gccggagagc tgggtggctaa ggcctatggat 1020
gagctgtatgttgc tgccaaaggcg gcacccctttt atcattttgc taatttatatt 1080
ccacatccccca aatgtatgttgc 1098

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SEQ ID NO: 43          moltype = DNA  length = 2379
FEATURE              Location/Qualifiers
source               1..2379
                     mol_type = genomic DNA
                     organism = Nicotiana sp.
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SEQ ID NO: 44 moltype = DNA length = 1792
FEATURE Location/Qualifiers
source 1..1792
mol_type = genomic DNA
organism = Nicotiana sp.

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                      organism = Nicotiana sp.
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organism = Nicotiana sp

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FEATURE              Location/Qualifiers
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FEATURE Location/Qualifiers
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organism = Nicotiana sp.

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Organism = Nicotiana sp.
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YWRNARSIKM	LQLNNKVRQ	SFRKIREEET	SLLLQRRIRES	PNSEVDLTEL	FVSMTNNDIVC	180
RVALGRKYCD	GEEGGRKFKSL	LLEFVELLGV	FNIGDYMMPWL	AWMNRFNGLN	AKVDKVAKEF	240
DAFLDEDVIEE	HGGNKKSDTE	AEGADFVDIL	LQVHKENKAG	FQVEMDAIKA	IIMDMFAAGT	300
DTTSTLLEWT	MNELLRNPKT	LNKLRDEVHQ	VTOGKTEVTE	DDLEKMPYL	AAVKESSRLH	360
SPVPLLPREA	I KDAKAVLYD	IAAGTQVLVC	PWAISRDPNL	WENPEEFQPE	RFLDTSIDYK	420
GLHFELIPREG	AGRRGCPGIT	FAFKVNELAL	ARLMFHFDPS	LPKGVKHEDL	DVEEAAGITV	480
RRKFPLLA	TPCS					
						494
 SEQ ID NO: 50		moltype = AA	length = 321			
FEATURE		Location/Qualifiers				
source		1..321				
		mol_type = protein				
		organism = Nicotiana tabacum				
SEQUENCE: 50						
MAEKITSHEN	TRYAVVTGGN	KGIGYETCRQ	LAKEGIVVVL	TARDERRGIE	ALEKLKEEYS	60
SNKTDDQIL	FHQLDVMDPA	SISSLVDFIK	TKEPGKLDILV	NNAGIGGLMV	EGDVVIICKDL	120
IEGDFVTISA	ENGEEDSYNKE	SIEGLERIVT	DYEPLITKQCLE	TNFYGAKRMI	EAFIPLQLS	180
NSPRIVNVAS	FLGKLKLLCN	QWAIGMLSDA	KSLREERVDE	VLINEFIKDFK	EKSIEAKGWP	240
TYFSAYKVSK	ASLIAVTRVL	ATKYPNFRIN	SVCPEGCKTD	VNCNTGSLTA	EEGAESLVKL	300
ALVPNDGPSG	LFFYRKEVTS	F				
						321
 SEQ ID NO: 51		moltype = AA	length = 598			
FEATURE		Location/Qualifiers				
source		1..598				
		mol_type = protein				
		organism = Nicotiana sylvestris				
SEQUENCE: 51						
MSQSISPLIC	SHFAKPQSNI	WRCNTSQLRV	IHSYASPGG	RRKERVRRMN	RAMDLSSSSR	60
HIALDFPSTIW	GDHFLSYNSE	ITEITTQEKN	EHEMLKEIVR	KMLVETPDNS	TQKLVLIDTI	120
QRLGLAYHFN	DEIENSQNI	FNLSQNSEDD	DEHNLYVAAL	RPFLRARQGY	YMSSDVFKQF	180
TNHDGKFKEN	HTNDVQGLLS	LYEAHHMRVH	DEEILEEALI	FTTTTHLESVI	PNLNSNLSKVQ	240
VTEALSHPIR	KAIPRVGARK	YIHIYENIGT	HNDLLLKFAK	LDFNMLQKLH	RKELNELTSW	300
WKDLDLDRANKF	PYAKDRLVEA	YFWFTVGIYE	PQYSRSRSLV	TKVVKMNSII	DDTYDAYATF	360
DELVLFLTDI	QRWDEGAMDL	LPTYLRLPIYQ	GLLDVFNEME	EVLAKEGKAD	HIYYAKKEMK	420
KVAEVYFKEA	EWLNANYIPK	CEEYMKNGLV	SSTGPMYGI	SLVVMEEEIT	KEAFEWLTNE	480
PLILRAASTI	CRIMDDMADH	EVEQQRGHVA	SFVECYMK	GVSKQEAYVE	MRKKITNAWK	540
DINKELLRT	AVPMFILERS	LNFSLRADTF	LKDDDGYTNP	KSKVKDLIAS	LFVESVDI	598
 SEQ ID NO: 52		moltype = AA	length = 792			
FEATURE		Location/Qualifiers				
source		1..792				
		mol_type = protein				
		organism = Nicotiana tabacum				
SEQUENCE: 52						
MVLGLRSKII	PLPDHKLGN	KLGSVTTNAIC	HRCRVRCSH	STASSMEEAK	ERIRETFGKI	60
ELSPRSSYDTA	WVAMVPSRYS	MNQCPFPQCL	DWILENQRED	GSWGLNPSHP	LLVKDSLSSST	120
LASLLALRKW	RIGDNQVQRG	LGFIEHTHWGA	VDNQDQISPL	GFEIIFPCMI	NYAEKLNLLDL	180
PLDPNLVNM	LCERELTTIER	ALKNEFEGNM	ANVEYFAEGL	GELCHWKEMM	LRQRHNGSLF	240
DSPATTAAAL	IYHQYDEKCF	GYLNSILKLH	DNWVPTICPT	KIHSNLFLVD	ALQNLGVDRY	300
FKTEVKRVL	EIYRLWLEK	EEIFSDVVAHC	AMAFRLLRMN	NYEVSSSEEL	GFVQEHFFT	360
TSSGKLMNHV	AILELHRASQ	VAIHERKDHI	LDKISTWTRN	FMEQKLLDKH	IPDRSKKEME	420
FAMRKFYGT	DRVETTRYIE	SYKMDSFKIL	KAAYRSGGIN	NIDLLKFSEH	DFNLCQTRHK	480
EELQQMKRWF	TDCCKLEQVGL	SQQYLYTSYF	IIAAILFEPE	YADARLAYAK	YAIITAVDD	540
FFDCFICKEE	LQNIIELVER	WEGYSTVGR	SERVRIFFLA	LYKMVEEIAA	KAETKQGRCV	600
KDHLINLWID	MLKCMVLELD	LWKIKSTTPS	IEEYLSVACV	TIGVPCFVLT	SLYLLGPKLS	660
KDVISSSEVS	ALCNCTAAVA	RLINDIHSYK	REQAESSTM	VSILITQSQG	TISEEEAIRQ	720
IKEMMMEKRR	ELLGMVLQNK	ESQLPQVCKD	LFWTTINAAY	SIHTHGHDYR	FPEEFKNHIN	780
DVIYKPLNQY	SP					
						792
 SEQ ID NO: 53		moltype = AA	length = 365			
FEATURE		Location/Qualifiers				
source		1..365				

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mol_type = protein
organism = Nicotiana sp.

SEQUENCE: 53
MAFLATISGH ENMLLSNTLN NNFIFSGKPP QRHSYSFLPK KIQARSVANS SKTFQVKEEE 60
FSSKTEKFIL PKFDFEYEMK MKAIVNKAL DDAIPMQEPI KIHEAMRYSL LAGGKRVRPI 120
LCMASCEVVG GDESLAIPAA CSVEMIHTMS LIHDDLPCMD NDDLRRGKPT SHKAFGEDTA 180
VLTDGDALLSL AFEHVASKTK DVTPQRVVQA VGELGSAVGS KGLVAGQIVD IASEGKVSL 240
TELEYIHNNHK TGKLLEAAVV CGAIIIGGGNE IEVERMRNYA RCLGLLFQVV DDILDVTKSS 300
EELGKTAGKD LVTDKATYPK LMGLEKAREL AGELVAKAMD ELSYFDAAKA APLYHFANYI 360
AHQN                                              365

SEQ ID NO: 54      moltype = DNA length = 354
FEATURE           Location/Qualifiers
source            1..354
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQUENCE: 54
atggctaggc tattctatac tatgatcatt ctcttgcttg ctttagcaac atcagcaatt 60
gctgaacattt cttgtaaaaac tgttgcaaaa gggatagtagc cttgtgtgtc ttatattaga 120
gggaaacatc ataaatccga caaggccatca aatatgtgtc gcaaaggact gaatgacata 180
gccaatgtga taaaaaatgg caaggatcggt gtatgtgtt gcaagtgtat aaatggcga 240
cttcacgtta ttcattatga tccccacttgt atcacacttg cttcacacaaca gtgtcatacg 300
ccttcatctc tgcccttcggc tggccaaaaac actaattgtg caagggcgcgt ctgca 354

SEQ ID NO: 55      moltype = DNA length = 351
FEATURE           Location/Qualifiers
source            1..351
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQUENCE: 55
atggcaagag agaaaatctgt aatgtgtatg gtatgtgtt tgggggttgc cttattttt 60
caggggcactg gtgtgtctga agaatgttagc acatgtgcac cactgtgtc agcatgtcc 120
agctttgtga actatggcac accagatccg actccagggtg cgccatgtcg cgtgtctatg 180
acgaccctaa gcaacatagc tagtccaccg gaaatgcgcg aggccgtctg tagatgtgtt 240
atggaccccta ttactactta caacccaaat gctactgcgc ttgccactt gcctggtttc 300
tgtgggtttt ctcttggttt caccattgac cctaacaactg actgtgaata g 351

SEQ ID NO: 56      moltype = DNA length = 462
FEATURE           Location/Qualifiers
source            1..462
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQUENCE: 56
atggcaagag agaaaatctgt aatgtgtatg gtatgtgtt tgggggttgc cttatataatt 60
caggggcactg gaggtgtctga agaatgttagc acatgtgcac cactgtgtc agcatgtcc 120
agctttgtga actatggcac accagatcca actccagggtg caccatgtcg cgtcgctatg 180
acgaccctaa gcaacatagc tagtccaccg gaaatgcgcg aggccgtctg tagatgtgtt 240
atggaccccta ttactactta caacccaaat gctactgcgc ttgccactt gcctggtttc 300
tgtgggtttt ctcttggttt caccattgac cctaacaactg actccatccg atattcaagg 360
tccactggc tcattaatcg tgattgtctc tggttaaga agttctctac tcccgggtgt 420
ctcataacaacaa tatggctctc ggaaagtgtat gctgaagaat ga 462

SEQ ID NO: 57      moltype = DNA length = 480
FEATURE           Location/Qualifiers
source            1..480
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQUENCE: 57
atgaagatgt tagttagtgc aagtcaatt ttgttagtgc ttgtcccttc ttcattacat 60
gttagtgc tc atcggtttt ccaacaagggtt tagtgggtt tagcccggtg tctgtcaataac 120
attcaaggaa atgcgacaaac cccatcatca ggtatgttgc ctcaacttgc tactataatg 180
aaaaaatcagc cacaatgttt atgtcaatgtt gttatgtgtt gtgggttcaaa tttaggaatt 240
aatgttaatc aaacacacagac tatggctttt cccaaagctt gtaatgtcca aacaccctct 300
attagcctttt gcaaaagggtac tactcctca gggttccacggg ggtctccatc cactcctca 360
gggtggatcga aggggtgaccc aagtggaaat tcatcaggaa actcagtcaa gatgccatc 420
tctcttttat ttacccttgcg atgatctcgcc ttttcggca caccatctga 480

SEQ ID NO: 58      moltype = DNA length = 495
FEATURE           Location/Qualifiers
source            1..495
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQUENCE: 58
atgcagatat cagcgagcac aataagtgcataaatagttt tggcagtggc tcttcttca 60
ttatcatgtca tcagcgctca atcggattgc gaacagggttgg ttgttgggtt agctccgtgc 120
ctgcaataaca tagaaggggaa tgccacgcgc ccgtcatcag gatgtcgac tcagctcgcc 180

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actatagtga agacgcagcc tcagtgcctt tgcacgtt tgaatggca gggctcatcc 240
ttggaggta atataatca gacatgtc ttggctcttc ctacagctg taatgcccac 300
actcccttc ttactctatg taaaactcactg tccccaaactg gtctccggaa aatctctccg 360
tccattctt caggagacag atattcaaga ttttcgccaatgatgc attgaagctg 420
cagccatact ctctgttatt tacccttaat gtgcactatgt cacaatattc 480
agctccatct tataa 495

SEQ ID NO: 59      moltype = DNA length = 336
FEATURE           Location/Qualifiers
source            1..336
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQUENCE: 59
atggcaaaaa tccttatagc tttgtttgtc ttgtctctaa tttaggcca aacaaatgca 60
gatattcgt gtagtgcgt tataatcaaaa gtgagcttgc ttgtcgatgt 120
aaatgttcgac cacctagccc aaatgttgc ttggatgc aagatggc taaatgtggc 180
gtgactcac aaccagatcg tcaaactatt tgcaatgc tttaagatgc catgcaaaact 240
ttccctgtgg acttccaaaa agctaaacaa cttcctcaga ttgcattt caagatgtact 300
ataccaatgg aaccaatgt tgattgtca aagtaa 336

SEQ ID NO: 60      moltype = DNA length = 354
FEATURE           Location/Qualifiers
source            1..354
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQUENCE: 60
atggctaaag tagcattgtt gggtgtgttgc tgcatggcaag cagtagctgt gatgataacg 60
ccccatcgac acgctgacat ctcttgggg cagggttgc ttggatgc accatgcatt 120
agctatgtga ggcaaggtgg tgctattca gcaccatgc gcagtgaaat taattccctc 180
aacaaccaag ctaccagcac tcctgatgcg cagacgggtt gtaactgtat taaatctgct 240
gtgcggcggc tcagtgccat caactctgtt ctgtgttgc ttgcattt cttatgtggt 300
gtcaatcttcc ttataaagat tagcccttc attgactgtt ccacgggtca gtaa 354

SEQ ID NO: 61      moltype = DNA length = 345
FEATURE           Location/Qualifiers
source            1..345
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQUENCE: 61
atggaaatgg taggtaaatgt tgcatgtttt gtgggtttgtt gcatgggttgg ggttgcaccc 60
catgcagagg cactgagctg cggccaaatgtt cagtcgggtt tggctcttgc tctcccttat 120
ttgcaggggc gccccctt gggggatgtt tgggtgttgc tttaagggtct gttgggtgca 180
gccaaggccc catctgaccg gaagactgc tgcaacttgcc tggaaatccggc tgctaattgt 240
attaagggtt ttgatatggg caaagccgtt ggttccctgtt gttgtgtgg tgcataacatt 300
ccttacaagaatggccctc cacaactgc tctaagggttca agtaa 345

SEQ ID NO: 62      moltype = DNA length = 294
FEATURE           Location/Qualifiers
source            1..294
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQUENCE: 62
atgaagaagg gtggtaattt ttttgcggca ataatctgg ttgtgacact agtcctttt 60
cttggcgaat ttcttagtgac agaggcgtt acgtgcgtt tcgtggagctt gagtcgtgt 120
gccccggccgat ttcctgtccac acagccaccc ttttcggcat gttgcgtttaa gttgaaagag 180
cagaaggccc ttctttgtgg tgcataatggg aatccaaacc taaggccctt tgcataatct 240
ccttacaatgcataa agagactgttca taaatctgtt ggatgttccca ctcccaatgtt ttag 294

SEQ ID NO: 63      moltype = DNA length = 354
FEATURE           Location/Qualifiers
source            1..354
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQUENCE: 63
atggcttaggc tattctatac tatgtatcatt ctcttgcctt cttagcaac atcagcaatt 60
gtctgaacctt cttgtaaaac ttttgcggcaaaa gggatgttac ctgtgtgtc ttatattgtt 120
ggggaaacatc ataaatcgga caagccatca aatatgtgtt gcaaaaggactt gaatgcata 180
gccaatgtga taaaaaatggt caaggatgtt gtagctgtttt gcaatgttataa agatggca 240
ctttcaatgcataa ttcattatgtt tccactgtt atcacacttgc ctgcataaca gttgcatacg 300
ccttcatctc tgccttcgtt tggccaaaacttactaattgttca agggccgtt ctgt 354

SEQ ID NO: 64      moltype = DNA length = 351
FEATURE           Location/Qualifiers
source            1..351
mol_type = genomic DNA
organism = Nicotiana tabacum

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SEQUENCE: 64
atggcaagag agaaatctgt aatgtgtatg gtgatggttt tgggggttgc cttattttttt 60
cagggcactg gtgctgctga aagaatgttagc acatgtacag cactggtagc agcatgtcc 120
atgtttgtatg actatggcac accagatccg actccagggtg cgccatgtctg cgttgtatg 180
acgacccttaa gcaacatagc tagtccaccacc gaaatggccc aggccgtctg tagatgttt 240
atggacatcta ttactacta caaaaaaaaactgtactggccatggcttgcggtttc 300
ttttttttttt ctctttttttt cattttttttt cttttttttt cttttttttt cttttttttt 351

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```
SEQ ID NO: 65          moltype = DNA  length = 655
FEATURE                  Location/Qualifiers
source                   1..655
                         mol_type = genomic DNA
                         organism = Nicotiana tabacum
```

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SEQUENCE: 65
atggcaag agaaatctgt aatgtgtatg gtgtatggttt tgggggttgc cataataatt 60
caggggactg gagctgtctga aagaatgtacg acagtgcacg cactgttagc agcatgtcc 120
acgtttgtca actatggcac accagatcca actccagggtc caccatgtcg cgtcgatcg 180
acgaccctaa gcaacatagc tagctccacc gagatgcgcc aggcgtctg tagatgcgtg 240
atggacctta ttactactt caacccaaat gctactgcga ttgcacactt gcctgtttt 300
tgtgtgtttt ctcttggtt caccattgac cctaacaatcg actgtgaata gtaaaga 360
caaccataag ttcttcatac cctaataattt catactttgt ttgtgtgtt ggcatcccg 420
tattcaagg t ccactgggtcc tattaatctgt gatttgcctt ggttaaagaa gttctctact 480
ccccgggttca aaacccggaaa acctttgttt aagagggttgc ggtttaatcaa ccatccacca 540
cacaccttgg tggtaataat tttatctgttatacataatc tttgtatcaat tttttttttt 600
ctctttgcag tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 665

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```
SEQ ID NO: 66          moltype = DNA  length = 1174
FEATURE                Location/Qualifiers
source                  1..1174
                        mol_type = genomic DNA
                        organism = Nicotiana tabacum
```

SEQ ID NO: 67 moltype = DNA length = 1817
FEATURE Location/Qualifiers
source 1..1817
mol_type = genomic DNA
organism = Nicotiana tabacum

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aattacacag	cctggtaatt	acgttagtatt	gtaattaca	tggctgttt	gttgtcatg	1080
gtgttaattac	agtgttaatta	catgtgtcat	gtttgggtgt	acaagtgtaa	ttatataaat	1140
aaataataat	tttttaactgt	atgataaaa	tttatatgt	taatagata	taataactat	1200
tatataattga	aaaaaaaaa	aggaatttga	aagggtgcct	caccaaattc	tttaccgcct	1260
tttggaaat	ggagagtgta	attaccctt	cccaattaca	ctcaattcat	caccaatcaa	1320
ataatttactt	ggtttaataaa	atatgcacaa	gtgtataatt	acacccaatt	acacttaatt	1380
tcaatttcga	tgtgggtttc	caaacaggct	ctaagggtt	gcaactgtt	tgcccttctt	1440
tcttttttat	ttttcccgaa	gcttttcat	tcccttcta	tatgacgaaa	gatcttattt	1500
ttaatattgtt	ctgtgtat	aaacatttca	gcaacttccc	caactggttc	tccggaaatc	1560
tctccgttca	ttcccttcagg	tacgaatacg	aacaatcgt	gcaactgtaa	aactgcactt	1620
tttccatgtt	ttttttccctg	caccaatttc	aacatttata	taatgggtgt	gagaattata	1680
tacttgtgttgc	cgcaggagac	agatatttca	gattttgcct	aaatggagat	tcattgaagc	1740
tgccagccata	ctctctgtt	tttaccctt	atgtagccac	tttgcata	gtcacaatat	1800
tcagctccat	tttataaa					1817

SEQ ID NO: 68 moltype = DNA length = 336
FEATURE Location/Qualifiers
source 1..336
mol_type = genomic DNA
organism = Nicotiana tabacum

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SEQUENCE: 68
atggcaaaaa tccttatagc tttgtttgtc ttgtctcaa ttttaggcca aacaaatgca 60
gatattcagt gtagtgatgt tataatcaaaa gtgagcttt gtgaagggtt tttgttaggt 120
aaatgttcgc caccttagccc aaattgttgc ttggatgtc aagatgttgc taaatgtggc 180
gtatgttcac aaccatgtc tcaaaatct tggtaatgtc ttaaaatgtc catgtcaact 240
ttccctgtgg atttccaaaa agcttacaaa ctccctcaga ttggccatcc caagatgtc 300
ataccaattt aaccatgtc tgattgtca aagtaa 336

```

SEQ ID NO: 69 moltype = DNA length = 354
FEATURE Location/Qualifiers
source 1..354
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQUENCE: 69		organism = Nicotiana tabacum
atggctaaag	tagcattgtt	60
cccatgcacg	acgctgacat	120
agctatgtca	ggcaaaagggg	180
aacaaccaaa	ctaccaggcac	240
gtgcaggcata	cgtggccat	300
gtcaatcttc	cctataaagat	354
atggctaaag	tagcattgtt	60
cccatgcacg	acgctgacat	120
agctatgtca	ggcaaaagggg	180
aacaaccaaa	ctaccaggcac	240
gtgcaggcata	cgtggccat	300
gtcaatcttc	cctataaagat	354

SEQ ID NO: 70 moltype = DNA length = 345
FEATURE Location/Qualifiers
source 1..345
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQ ID NO: 71 moltype = DNA length = 294
FEATURE Location/Qualifiers
source 1..294
mol_type = genomic DNA
organism = Nicotiana tabacum

SEQUENCE: 71
atgaagaagg gtggtaattc ttttgcggca ataatcttg agtgcacact agtccctttt 60
cttggcgaat ttctagtgac agaggcagta acgtgcgtg tcgtggagct gaggccgtgt 120
gcggggggca tctcgtcggc acaggcaccc tcttcgtact gttgcgtaa gttgaagag 180
caagaacctt gtctttttgg gtacccaaat aatccaaacc taaggcccta tgtaattct 240
cctaatacgcca aqaqadttqc taaaatccctgt qqqaqtaccca ctcccaqctq ttaq 294

SEQ ID NO: 72 moltype = AA length = 117
FEATURE Location/Qualifiers
source 1..117
mol_type = protein
organism = Nicotiana tabacum

SEQUENCE: 72
 MARLFYTMII LLLLALATSAI EAPSCKTVAK GIVPCVSYIR GKHHKSDPKS NMCKGLNDI 60
 ANVILKNGDP RAVVCKC1KMA LSPRTHYDPTV TLTASOCOTR PSSLLPSVGON TNCAEPAI 117

SEQ ID NO: 73 moltype = AA length = 116

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FEATURE	Location/Qualifiers
source	1..116
	mol_type = protein
	organism = Nicotiana tabacum
SEQUENCE: 73	
MAREKSVCM VMVLGVALII QGTGAAECS TVTALVAACS SFVNYGTPDP TPGAPCCVAM 60	
TTLSNIASTT EMRQAVCRCV MDLITTYNPN ATAIATLPGF CGVSLGFTID PNTDCE 116	
SEQ ID NO: 74	moltype = AA length = 153
FEATURE	Location/Qualifiers
source	1..153
	mol_type = protein
	organism = Nicotiana tabacum
SEQUENCE: 74	
MAREKSVCM VMVLGVAlIII QGTGAAECS TVTALVAACS SFVNYGTPDP TPGAPCCVAM 60	
TTLsNIASTT EMRQAVCRCV MDLITTYNPN ATAIATLPGF CGVSLGFTID PNTDSIRYSR 120	
STGPINRDLW LKKFSTPGC LITIWSLESD AEE 153	
SEQ ID NO: 75	moltype = AA length = 159
FEATURE	Location/Qualifiers
source	1..159
	mol_type = protein
	organism = Nicotiana tabacum
SEQUENCE: 75	
MKMLASASSI FVAIVLLSLH VSAQSDCQQV IVGLAPCLQY IQGNATTSSS GCCTQLATIV 60	
KNQPOCLCQV VNNGGSNLGI NVNQTQTMAL PKACNVQTPS ISLCKGTTPS GSPGSPSTPS 120	
GGSKGEPSGN SSGNSVKMPY SLLFTLVAIA FFATVFTTI 159	
SEQ ID NO: 76	moltype = AA length = 164
FEATURE	Location/Qualifiers
source	1..164
	mol_type = protein
	organism = Nicotiana tabacum
SEQUENCE: 76	
MQISASTISA IIIVAVALLS LHVISAQSDC EQVVVGLAPC LOYIEGNATS PSSGCCTQLA 60	
TIVKTQPQCL CHVLNCEGSS FGVNINQTLA LALPTACNAH TPFLTLCKAT SPTGSPEISP 120	
SIPSGDRYSR FSPNGDSLKL QPYSLLFTLN VATLSYVTIF SSIL 164	
SEQ ID NO: 77	moltype = AA length = 111
FEATURE	Location/Qualifiers
source	1..111
	mol_type = protein
	organism = Nicotiana tabacum
SEQUENCE: 77	
MAKILIALFA LSLILGQTN DIQCSDVISK VSSCEGYLLG KVAAPSPNCC FGLQDLAKVA 60	
DDSQPDRQTI CQCFKAAMQT FPVDFQKAKQ LPQICHFKST IPIEPNVDCS K 111	
SEQ ID NO: 78	moltype = AA length = 117
FEATURE	Location/Qualifiers
source	1..117
	mol_type = protein
	organism = Nicotiana tabacum
SEQUENCE: 78	
MAKVALLVVV CMAAVAVMLT PHADADISCG QVVASLSPCI SYVRQGGAIP APCCSGINS 60	
NNQATSTPDR QTACNCIKSA AAGISGINFS LAGSLPSKCG VNLPYKISPS IDCSTVQ 117	
SEQ ID NO: 79	moltype = AA length = 114
FEATURE	Location/Qualifiers
source	1..114
	mol_type = protein
	organism = Nicotiana tabacum
SEQUENCE: 79	
MEMVGKIACF VVLCMVVVAP HAEALSCGVF QSGLAPCLPY LQGRGPLGSC CGGVKGLLGA 60	
AKSPSDRKTA CTCLKSAANA IKGIDMGKAA GLPGACGVNI PYKISPSTDc SKVQ 114	
SEQ ID NO: 80	moltype = AA length = 97
FEATURE	Location/Qualifiers
source	1..97
	mol_type = protein
	organism = Nicotiana tabacum
SEQUENCE: 80	
MKKGGNSFAA IILVVTLVLF LGEFLVTEAV TCSVVELSPC AGAISSPQPP SSACCAKLKE 60	
QKPCLCGYLK NPNLRPYVNS PNAKRAKSC GVPTPSC 97	
SEQ ID NO: 81	moltype = AA length = 229
FEATURE	Location/Qualifiers

-continued

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REGION          1..229
                note = Description of Sequence: Synthetic polypeptide
source          1..229
                mol_type = protein
                organism = synthetic construct
SEQUENCE: 81
MSNNNSLSIKN PKVSLAFVML PKANMWKETK LKISIMLNQ LFMNAKNIMKE MVGSIACLLV 60
LCMVVAAPHA AAPIQRHAAI TCGQVDASLA PCLPYLTGGG APTRGPSAAC CSGVKSLG 120
AKTTAPDLDR QAAACNLKSA ANRIFTGIND DAAAALPSKC GVNYLPFKIS PSTEPVDCSK 180
IQMSTPSGDR DGLFSYKFSG DSCKIQPYSI LFTLEVAHAF FATIFPSIL 229

SEQ ID NO: 82      moltype = AA length = 88
FEATURE          Location/Qualifiers
source           1..88
                mol_type = protein
                organism = Nicotiana tabacum
SEQUENCE: 82
SAIAEPEPCKT VAKGIVPCVS YIRGKHHKSD KPSNMCCKGL NDIANVIKNG KDRVAVCKCI 60
KMALSRIHYD PTRITLASQQ CHTPSSLP 88

SEQ ID NO: 83      moltype = AA length = 91
FEATURE          Location/Qualifiers
source           1..91
                mol_type = protein
                organism = Nicotiana tabacum
SEQUENCE: 83
AIIIQGTGAA EECSTVTALV AACSSFVNNG TPDPTPGAPC CVAMTLSNI ASSTEMRQAV 60
CRCVMDLITT YNPNATAIAT LPGFCGVSLG F 91

SEQ ID NO: 84      moltype = AA length = 91
FEATURE          Location/Qualifiers
source           1..91
                mol_type = protein
                organism = Nicotiana tabacum
SEQUENCE: 84
AIIIQGTGAA EECSTVTALV AACSSFVNNG TPDPTPGAPC CVAMTLSNI ASSTEMRQAV 60
CRCVMDLITT YNPNATAIAT LPGFCGVSLG F 91

SEQ ID NO: 85      moltype = AA length = 86
FEATURE          Location/Qualifiers
source           1..86
                mol_type = protein
                organism = Nicotiana tabacum
SEQUENCE: 85
LLSLHVSAQD DCQQVIVGLA PCLQYIQQNA TPPSSGCCTQ LATIVKNQPQ CLCQVVNGGG 60
SNLGINVNQT QTMALPKACN VQTPSI 86

SEQ ID NO: 86      moltype = AA length = 87
FEATURE          Location/Qualifiers
source           1..87
                mol_type = protein
                organism = Nicotiana tabacum
SEQUENCE: 86
LLSLHVSAQD SDCEQVVVGL APCLQYIEGN ATSPSSGCCT QLATIVKTQP QCLCHVLNGE 60
GSSFGVNVINQ TLALALPTAC NAHTPFL 87

SEQ ID NO: 87      moltype = AA length = 87
FEATURE          Location/Qualifiers
source           1..87
                mol_type = protein
                organism = Nicotiana tabacum
SEQUENCE: 87
LGQTNADIQC SDVISKVSSC EGYLLGKVAAP PSPNCCFGLQ DLAKVADDSQ PDRQTICQCF 60
KAAMQTFPPVD EQKAKQLPQI CHFKSTI 87

SEQ ID NO: 88      moltype = AA length = 88
FEATURE          Location/Qualifiers
source           1..88
                mol_type = protein
                organism = Nicotiana tabacum
SEQUENCE: 88
MLTPHADADI SCGQVVVASLS PCISYVRQGG AIPAPCCSGI NSLNNQATST PDRQTACNCI 60
KSAAAGISGI NFSLAGSLPS KCGVNLPI 88

SEQ ID NO: 89      moltype = AA length = 86
FEATURE          Location/Qualifiers

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-continued

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source          1..86
               mol_type = protein
               organism = Nicotiana tabacum

SEQUENCE: 89
VVAPHAEALS CGQVQSGLAP CLPYLQGRGP LGSCCGGVKG LLGAAKSPSD RKTACTCLKS 60
AANAIAKGIDM GKAAGLPGAC GVNIKY                         86

SEQ ID NO: 90      moltype = AA length = 78
FEATURE          Location/Qualifiers
source           1..78
               mol_type = protein
               organism = Nicotiana tabacum

SEQUENCE: 90
VLFGLGEFLVT EAVTCVVEL SPCAGAISSP QPPSSACCAK LKEQKPCLCG YLKNPNLRPY 60
VNNSPAKRAV KSCGVPTP                         78

SEQ ID NO: 91      moltype = AA length = 86
FEATURE          Location/Qualifiers
source           1..86
               mol_type = protein
               organism = Nicotiana tabacum

SEQUENCE: 91
VVAPHAEALT CGQVQSSLAP CVPYLLGRGP LGGCCGGVKR LLGAARTPAD RKTACNCLKS 60
AANTFKGIDM GNAARLPGTC GVNIKY                         86

SEQ ID NO: 92      moltype = AA length = 103
FEATURE          Location/Qualifiers
REGION           1..103
               note = Description of Sequence: Synthetic polypeptide
source           1..103
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 92
VAAPAHAAPI QRHAAITCGQ VDASLAPCLP YLTGGGAPTR GPSAACCSGV KSLLGAAKTT 60
APDLDRQAAC NCLKSAANRI FTGINDDAAA ALPSKCGVNY LPF             103

SEQ ID NO: 93      moltype = AA length = 162
FEATURE          Location/Qualifiers
REGION           1..162
               note = Description of Sequence: Synthetic polypeptide
VARIANT          1..48
               note = This region may be absent
source           1..162
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 93
MSMNNSLSIKN PKVSLAFVHN TQGNNICSTI PLYFVQTTLI CSLIFLLRME MVSKIACFVV 60
LCMVVVAHPA EALTCGQVQS SLAPCPVYLL GRGPLGGCCG GVKRLLGAAR TPADRKTACN 120
CLKSAANTFK GIDMGNAARL PGTCGVNIPY KISPSTDCKV QO                         162

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1-46. (canceled)

47. A modified tobacco plant, tobacco seed, or tobacco plant part comprising a recombinant nucleic acid molecule comprising heterologous promoter operably linked to a nucleic acid sequence encoding an amino acid sequence at least 95% identical to the amino acid sequence of SEQ ID NO: 19, and wherein at least one leaf of the modified tobacco plant comprises a greater average trichome density as compared to a leaf of a control tobacco plant grown under comparable conditions.

48. The modified tobacco plant, tobacco seed, or tobacco plant part of claim **47**, wherein the amino acid sequence is identical to the amino acid sequence of SEQ ID NO: 19.

49. The modified tobacco plant, tobacco seed, or tobacco plant part, of claim **47**, wherein the nucleic acid sequence is at least 95% identical to the nucleic acid sequence of SEQ ID NO: 14 or SEQ ID NO: 24.

50. The modified tobacco plant, tobacco seed, or tobacco plant part, of claim **47**, wherein the nucleic acid sequence is identical to the nucleic acid sequence of SEQ ID NO: 14 or SEQ ID NO: 24.

51. The modified tobacco plant, tobacco seed, or tobacco plant part thereof of claim **47**, wherein the tobacco plant, tobacco seed, or tobacco plant part is of a tobacco variety selected from the group consisting of a flue-cured variety, a bright variety, a Burley variety, a Virginia variety, a Maryland variety, a dark variety, a Galpão variety, an Oriental variety, and a Turkish variety.

52. The modified tobacco plant, tobacco seed, or tobacco plant part thereof of claim **47**, wherein the modified tobacco plant is male sterile or cytoplasmically male sterile.

53. The modified tobacco plant, tobacco seed, or tobacco plant part, of claim **47**, wherein the heterologous promoter is selected from the group consisting of a constitutive promoter, an inducible promoter, a tissue-preferred promoter, and a tissue-specific promoter.

54. The modified tobacco plant, tobacco seed, or tobacco plant part of claim **47**, wherein at least one leaf of the modified tobacco plant comprises a greater average trichome density on the abaxial side of the at least one leaf of the modified tobacco plant as compared to the abaxial side of a leaf of a control tobacco plant grown under comparable conditions.

55. The modified plant, seed, or plant part of claim **47**, wherein at least one leaf of the modified tobacco plant comprises a greater average trichome density on the adaxial side of the at least one leaf of the modified tobacco plant as compared to the adaxial side of a leaf of a control tobacco plant grown under comparable conditions.

56. The modified tobacco plant, tobacco seed, or tobacco plant part of claim **47**, wherein the greater average trichome density comprises a greater average density of glandular trichomes.

57. The modified tobacco plant, tobacco seed, or tobacco plant part of claim **47**, wherein the at least one leaf of the modified tobacco plant comprises at least 110 glandular trichomes per square centimeter.

58. Cured tobacco material from a modified tobacco plant or tobacco plant part comprising a recombinant nucleic acid molecule comprising a heterologous promoter operably linked to a nucleic acid sequence encoding an amino acid sequence least 95% identical to the amino acid sequence of SEQ ID NO: 19, and wherein at least one leaf of the modified tobacco plant comprises a greater average trichome density as compared to a leaf of a control tobacco plant grown under comparable conditions.

59. The cured tobacco material of claim **58**, wherein the amino acid sequence is identical to the amino acid sequence of SEQ ID NO: 19.

60. The cured tobacco material of claim **58**, wherein the nucleic acid sequence is at least 95% identical to the nucleic acid sequence of SEQ ID NO: 14 or SEQ ID NO: 24.

61. The cured tobacco material of claim **58**, wherein the cured tobacco material is selected from the group consisting of flue-cured tobacco material, air-cured tobacco material, fire-cured tobacco material, and sun-cured tobacco material.

62. The cured tobacco material of claim **58**, wherein the cured tobacco material is selected from the group consisting of cured leaf material and cured stem material.

63. A tobacco product comprising the cured tobacco material of claim **58**.

64. The tobacco product of claim **63**, wherein the tobacco product is selected from the group consisting of a kretek, a bidi cigarette, a cigarillo, a non-ventilated recess filter cigarette, a vented recess filter cigarette, a cigar, pipe tobacco, cigar tobacco, cigarette tobacco, chewing tobacco, moist snuff, nasal snuff, dry snuff, snus, leaf tobacco, hookah tobacco, shredded tobacco, and cut tobacco.

65. The tobacco product of claim **63**, wherein the tobacco product is a smokeless tobacco product.

66. The tobacco product of claim **65**, wherein the smokeless tobacco product is selected from the group consisting of loose leaf chewing tobacco, plug chewing tobacco, moist snuff, nasal snuff, dry snuff, and snus.

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