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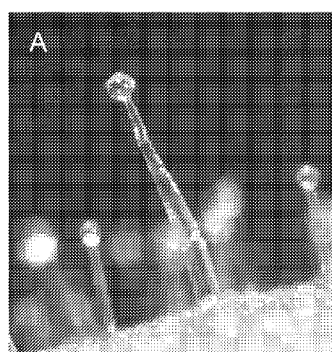
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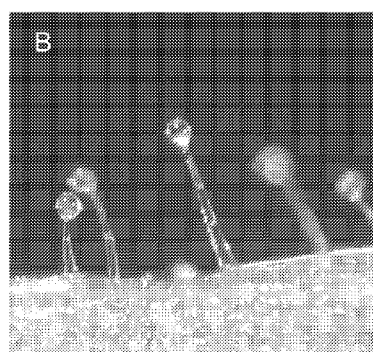
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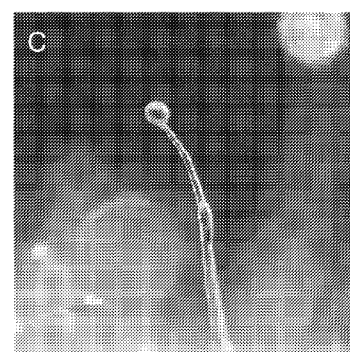
(54) Title: INCREASING TRICHOME DENSITY AND IMPROVING TRANSPORT OF METABOLITES IN PLANT TRICHOMES



N. benthamiana



N. tabacum 'TN90'



N. tabacum 'Izmir Ego'

Figure 1

(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.



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

**CROSS-REFERENCE TO RELATED APPLICATIONS AND INCORPORATION OF
SEQUENCE LISTING**

5 [0001] This application claims the benefit of U.S. Provisional Patent Application No. 63/145,259, filed February 3, 2021; U.S. Provisional Patent Application No. 63/145,262, filed February 3, 2021; and U.S. Provisional Patent Application No. 63/145,263, filed February 3, 2021, all of which are incorporated by reference herein in their entireties. This application also contains a Sequence Listing, which has been submitted electronically in ASCII format and is
10 hereby incorporated by reference in its entirety. Said ASCII copy, created on January 25, 2022, is named P335029WO00_SL.txt and is 141,791 bytes in size as measured in Microsoft Windows®.

FIELD

15 [0002] 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

20 [0003] 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.

25 [0004] 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
30 isopentenyl diphosphate [IPP]) most often by the sequential head-to-tail addition of DMAPP to IPP.

[0005] 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 artemisin (Matias-Hernandez *et al.*, *Plant Journal*, 90:520-534 (2017)).

[0006] 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)).

[0007] 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 trichome density will also improve transport of specialized metabolites in glandular trichomes.

SUMMARY

[0008] 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.

[0009] 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.

[0010] 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.

[0011] 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.

[0012] 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.

[0013] 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.

[0014] 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).

[0015] 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/

5 [0016] 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
10 operably linked to a heterologous promoter, to at least one plant cell.

[0017] 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
15 operably linked to a heterologous promoter, to at least one plant cell.

[0018] 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%
20 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.

25 BRIEF DESCRIPTION OF THE SEQUENCES

[0019] SEQ ID NOs: 1 to 12 are primers that can used for the cloning of nucleic acid sequences described herein for expression in transgenic plants.

[0020] 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*,
30 and *NtLTP1*.

- [0021] SEQ ID NOs: 18 to 22 are amino acid sequences corresponding to the nucleic acid sequences of SEQ ID NOs: 13 to 17.
- [0022] 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*,
5 and *NtLTP1*.
- [0023] 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*.
- [0024] SEQ ID NOs: 31 to 33 are amino acid sequences corresponding to the nucleic
10 acid sequences of SEQ ID NOs: 28 to 30.
- [0025] 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*.
- [0026] SEQ ID NOs: 37 is a nucleic acid sequence corresponding to the coding
15 sequence for sweet wormwood (*Artemisia annua*) specifically *MYB* transcription factor.
- [0027] SEQ ID NOs: 38 is an amino acid sequence corresponding to the nucleic acid sequence of SEQ ID NOs: 37.
- [0028] 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*,
20 *CBTS2a(HM)*, *GGPPS2* and *cis abienol synthase (ABS)*.
- [0029] 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)*.
- [0030] SEQ ID NOs: 49 to 53 are amino acid sequences corresponding to the nucleic
25 acid sequences of SEQ ID NOs: 39 to 43.
- [0031] 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.

[0032] 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 Figure 9. SEQ ID NO: 92 is the consensus amino acid sequence shown in Figure 9.

5 [0033] 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

SEQ ID NO	Sequence Description	Sequence Type
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>Artemisia annua</i>] KC118530.1	Nucleic acid, CDS
38	MYB transcription factor [<i>Artemisia annua</i>] AGR40501.1	Amino acid
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

SEQ ID NO	Sequence Description	Sequence Type
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
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 Figure 9 sequence	Amino acid
83	XP_016452099.1 Figure 9 sequence	Amino acid
84	XP_016496894.1 Figure 9 sequence	Amino acid
85	XP_016463157.1 Figure 9 sequence	Amino acid
86	XP_016504074.1 Figure 9 sequence	Amino acid
87	XP_016513187.1 Figure 9 sequence	Amino acid
88	LPT4_BAK19152 Figure 9 sequence	Amino acid
89	LTP3_BAK19151 Figure 9 sequence	Amino acid
90	LPT2_BAJ25798 Figure 9 sequence	Amino acid
91	LTP1_BAK19150 Figure 9 sequence	Amino acid
92	LTP Consensus Figure 9 sequence	Amino acid
93	Figure 8B consensus sequence	Amino acid

BRIEF DESCRIPTION OF THE DRAWINGS

- [0034] **Figure 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’.
- 5 [0035] **Figure 2** depicts the expression vector used for tobacco transformation.
- [0036] **Figure 3** comprises panels **Figure 3A** and **Figure 3B**. **Figure 3A** depicts a phylogenetic analysis of the DNA-binding domain of the MYB transcription factor family in tobacco plants (N=319). **Figure 3B** depicts protein sequence pairwise alignment of the tobacco *MYB86* gene (SEQ ID NO: 18, XP_016450602.1) 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 **Figure 3A** represents evolutionary distance used to infer the phylogenetic tree.
- 10 [0037] **Figure 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.
- 15 [0038] **Figure 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 trichome 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 trichome 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 10x magnification.
- 20 [0039] **Figure 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 160x magnification.
- 25 [0040] **Figure 7** comprises panels **Figure 7A** and **Figure 7B**. **Figure 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
- 30

Ego background compared to a wild-type *Nicotiana tabacum* variety Izmir Ego (a). Images are shown at 70x magnification with scale bar representing 1 mm. **Figure 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).

5 [0041] **Figure 8** comprises panels **Figure 8A** and **Figure 8B**. **Figure 8A** depicts a phylogenetic analysis of the LTP gene family, and the position of the NtLTP1 gene is marked by a filled circle. **Figure 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).

10 [0042] **Figure 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 $\geq 90\%$ of the NtLTPs identified.

[0043] **Figure 10** depicts the relative gene expression of *NtMYB86* (SEQ ID NO: 14) 15 in nine independent Izmir Ego transgenic lines in the T₀ generation. The relative gene expression was quantified following the $2^{-\Delta\Delta C(t)}$ method. See Livak and Schmittgen, *Methods*, 25:402-408 (2001) for information regarding the $2^{-\Delta\Delta C(t)}$ 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.

20 [0044] **Figure 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 $2^{-\Delta\Delta C(t)}$ 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.

[0045] **Figure 12** depicts the relative abundance of divatrienediol in leaves of T₀ Izmir 25 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).

[0046] **Figure 13** depicts the relative abundance of neophytadiene in leaves of T₀ Izmir 30 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] **Figure 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).

[0048] **Figure 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).

[0049] **Figure 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.

[0050] **Figure 16** 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

[0051] 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).

[0052] Any references cited herein, including, e.g., all patents, published patent applications, and non-patent publications, are incorporated herein by reference in their entirety.

[0053] 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.

[0054] 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.

[0055] 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.

[0056] 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.

[0057] 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.

[0058] 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.

[0059] 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.

[0060] Glandular trichomes (*see* Figure 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.

[0061] 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.

[0062] 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.

[0063] 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

[0064] 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, artemisin, 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)).

5 **Storage and transportation of metabolites in glandular trichome**

[0065] 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
10 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
15 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 Figure 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
20 cell expansion (Salminen *et al.*, 2016). The trichome-specific *NLTP1* 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

[0066] In an aspect, a plant provided herein is a modified plant. In an aspect, a seed
25 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
30 comprises a genetic modification. In an aspect, a modified plant, seed, or plant part is a transgenic plant, seed, or plant part.

[0067] 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.

[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%, 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.

[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 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, 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 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, 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 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, 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 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, 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 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, 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 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, 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 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, 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 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, 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 at least 99.9% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, 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 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, where the nucleic acid sequence is operably linked to a heterologous promoter.

[0070] 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.

[0071] 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.

[0072] 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.

[0073] 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.

[0074] 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.

[0075] 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.

[0076] 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
5 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
10 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.

15 **[0077]** 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
20 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.

[0078] 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
25 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
30 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.

[0079] 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.

[0080] 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.

- [0081] 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.
- 5
- [0082] 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.
- [0083] 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.
- 10
- [0084] 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*.
- 15
- [0085] 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*.
- 20
- [0086] 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*.
- 25
- [0087] 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
- 30

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.

[0088] 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.

[0089] 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.

[0090] This disclosure provides cells from plants provided herein.

[0091] 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.

[0092] 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.

[0093] 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.

[0094] 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.

[0095] 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

[0096] 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)	K 346	Reams 134
401 (TC 226)	K 346 (TC 569)	Reams 158
401 Cherry Red (TC 227)	K 358	Reams 713
401 Cherry Red Free (TC 228)	K 394 (TC 321)	Reams 744
Cash (TC 250)	K 399	Reams M1
Cash (TI 278)	K 399 (TC 322)	RG 11 (TC 600)
CC 101	K 730	RG 13 (TC 601)
CC 1063	Lonibow (TI 1573)	RG 17 (TC 627)
CC 13	Lonibow (TI 1613)	RG 22 (TC 584)
CC 143	McNair 10 (TC 330)	RG 8 (TC 585)
CC 200	McNair 135 (TC 337)	RG 81 (TC 618)
CC 27	McNair 30 (TC 334)	RG H51
CC 301	McNair 373 (TC 338)	RG4H 217
CC 33	McNair 944 (TC 339)	RGH 12
CC 35	MK94 (TI 1512)	RGH 4
CC 37	MS K 326	RGH 51
CC 400	MS NC 71	RGH 61
CC 500	MS NC 72	SC 58 (TC 400)
CC 600	NC 100	SC 72 (TC 403)
CC 65	NC 102	Sp. G-168
CC 67	NC 1071 (TC 364)	SPEIGHT 168
CC 700	NC 1125-2	Speight 168 (TC 633)
CC 800	NC 12 (TC 346)	Speight 172 (TC 634)
CC 900	NC 1226	Speight 178
Coker 139 (TC 259)	NC 196	Speight 179
Coker 139 yb1, yb2	NC 2326 (TC 365)	Speight 190
Coker 140 (TC 260)	NC 27 NF (TC 349)	Speight 196
Coker 176 (TC 262)	NC 291	SPEIGHT 220
Coker 187 (TC 263)	NC 297	SPEIGHT 225
Coker 187-Hicks (TC 265)	NC 299	SPEIGHT 227
Coker 209 (TC 267)	NC 37 NF (TC 350)	SPEIGHT 236
Coker 258 (TC 270)	NC 471	Speight G-10 (TC 416)
Coker 298 (TC 272)	NC 55	Speight G-102

Coker 316 (TC 273)	NC 567 (TC 362)	Speight G-108
Coker 319 (TC 274)	NC 60 (TC 352)	Speight G-111
Coker 347 (TC 275)	NC 606	Speight G-117
Coker 371-Gold (TC 276)	NC 6140	Speight G-126
Coker 411 (TC 277)	NC 71	Speight G-15 (TC 418)
Coker 48 (TC 253)	NC 72	Speight G-23
Coker 51 (TC 254)	NC 729 (TC 557)	Speight G-28 (TC 420)
Coker 86 (TC 256)	NC 810 (TC 659)	Speight G-33
CU 263 (TC 619)	NC 82 (TC 356)	Speight G-41
CU 561	NC 8640	Speight G-5
DH95-1562-1	NC 89 (TC 359)	Speight G-52
Dixie Bright 101 (TC 290)	NC 92	Speight G-58
Dixie Bright 102 (TC 291)	NC 925	Speight G-70
Dixie Bright 244 (TC 292)	NC 95 (TC 360)	Speight G-70 (TC 426)
Dixie Bright 27 (TC 288)	NC 98 (TC 361)	Speight G-80 (TC 427)
Dixie Bright 28 (TC 289)	NC EX 24	Speight NF3 (TC 629)
GF 157	NC PY 10 (TC 367)	STNCB
GF 318	NC TG 61	VA 182
GL 26H	Oxford 1 (TC 369)	VA 45 (TC 559)
GL 338	Oxford 1-181 (TC 370)	Vesta 30 (TC 439)
GL 350	Oxford 2 (TC 371)	Vesta 33 (TC 440)
GL 368	Oxford 207 (TC 632)	Vesta 5 (TC 438)
GL 395	Oxford 26 (TC 373)	Vesta 62 (TC 441)
GL 600	Oxford 3 (TC 372)	Virginia (TI 220)
GL 737	Oxford 414 NF	Virginia (TI 273)
GL 939	PD 611 (TC 387)	Virginia (TI 877)
GL 939 (TC 628)	PVH 03	Virginia 115 (TC 444)
Hicks (TC 310)	PVH 09	Virginia 21 (TC 443)
Hicks Broadleaf (TC 311)	PVH 1118	Virginia Bright (TI 964)
K 149 (TC 568)	PVH 1452	Virginia Bright Leaf (TC 446)
K 317	PVH 1600	Virginia Gold (TC 447)
K 326	PVH 2110	White Stem Orinoco (TC 451)
K 326 (TC 319)	PVH 2275	
K 340 (TC 320)	R 83 (Line 256-1) (TI 1400)	

[0097] 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.

[0098] 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.

10 [0099] 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	HB 4108P	KY 54 (TC 71)
AA-37-1	HB 4151P	KY 56 (TC 72)
Burley 21 (TC 7)	HB 4192P	KY 56 (TC 72)
Burley 49 (TC 10)	HB 4194P	KY 57 (TC 73)
Burley 64 (TC 11)	HB 4196	KY 58 (TC 74)
Burley Mammoth KY 16 (TC 12)	HB 4488	KY 8654 (TC 77)
Clay 402	HB 4488P	KY 8959
Clay 403	HB04P	KY 9 (TC 54)
Clay 502	HB 4488 LC	KY 907 LC
Clays 403	HIB 21	KY 908 (TC 630)
GR 10 (TC 19)	HPB 21	NBH 98 (Screened)
GR 10 (TC 19)	HY 403	NC 1206
GR 10A (TC 20)	Hybrid 403 LC	NC 129
GR 13 (TC 21)	Hybrid 404 LC	NC 2000 LC
GR 14 (TC 22)	Hybrid 501 LC	NC 2002 LC
GR 149 LC	KDH-959 (TC 576)	NC 3 LC
GR 153	KDH-960 (TC 577)	NC 5 LC
GR 17 (TC 23)	KT 200 LC	NC 6 LC
GR 17B (TC 24)	KT 204 LC	NC 7 LC
GR 18 (TC 25)	KT 206 LC	NC BH 129 LC
GR 19 (TC 26)	KT 209 LC	NC03-42-2
GR 2 (TC 15)	KT 210 LC	Newton 98
GR 24 (TC 27)	KT 212 LC	R 610 LC
GR 36 (TC 28)	KT 215 LC	R 630 LC
GR 38 (TC 29)	KY 1 (TC 52)	R 7-11
GR 38A (TC 30)	KY 10 (TC 55)	R 7-12 LC
GR 40 (TC 31)	KY 12 (TC 56)	RG 17
GR 42 (TC 32)	KY 14 (TC 57)	TKF 1801 LC
GR 42C (TC 33)	KY 14 x L8 LC	TKF 2002 LC
GR 43 (TC 34)	KY 15 (TC 58)	TKF 4024 LC
GR 44 (TC 35)	KY 16 (TC 59)	TKF 4028 LC
GR 45 (TC 36)	KY 17 (TC 60)	TKF 6400 LC
GR 46 (TC 37)	KY 19 (TC 61)	TKF 7002 LC
GR 48 (TC 38)	KY 21 (TC 62)	TKS 2002 LC
GR 5 (TC 16)	KY 22 (TC 63)	TN 86 (TC 82)
GR 53 (TC 39)	KY 24 (TC 64)	TN 90 LC
GR 6 (TC 17)	KY 26 (TC 65)	TN 97 Hybrid LC
GR 9 (TC 18)	KY 33 (TC 66)	TN 97 LC
GR139 NS	KY 34 (TC 67)	VA 116
GR139 S	KY 35 (TC 68)	VA 119
HB 04P	KY 41A (TC 69)	Virgin A Mutante (TI 1406)
HB 04P LC	KY 5 (TC 53)	Virginia 509 (TC 84)
HB 3307P LC	KY 52 (TC 70)	

[00100] 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)

5

[00101] 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 Paraguayan Passado, and any variety essentially derived from any one of the foregoing varieties.

10

[00102] 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.

15

20 **Table 5.** Dark Fire-Cured Tobacco Varieties

Black Mammoth (TC 461)	KY 171 (TC 475)	PD 7309 LC
Black Mammoth Small Stalk (TC 641)	KY 171 LC	PD 7312 LC
Certified Madole (TC 463)	KY 171 NS	PD 7318 LC
D-534-A-1 (TC 464)	KY 180 (TC 573)	PD 7319 LC

DAC ULT 302	KY 190 (TC 574)	Petico M PG04
DAC ULT 303	Little Crittenden	PY KY 160 (TC 612)
DAC ULT 306	Little Crittenden (TC 476)	PY KY 171 (TC 613)
DAC ULT 308	Little Crittenden LC (certified)	Shirey
DAC ULT 312	Little Crittenden PhPh	TI 1372
DF 300 (TC 465)	Lizard Tail Turtle Foot	TN D94
DF 485 (TC 466)	Madole (TC 478)	TN D94 (TC 621)
DF 516 (TC 467)	Madole (TC 479)	TN D 950
DF 911 (TC 468)	MS KY 171	TN D950 (PhPh)
DT 508	MS NL Madole LC	TN D950
DT 518 (Screened)	MS TN D950 LC	TN D950 (TC 622)
DT 538 LC	Nance (TC 616)	TR Madole (TC 486)
DT 592	Narrow Leaf Madole LC (certified)	VA 309
Improved Madole (TC 471)	Neal Smith Madole (TC 646)	VA 309 (TC 560)
Jernigan's Madole (TC 472)	Newtons VH Madole	VA 309 LC (certified)
KT 14LC	NL Madole	VA 310 (TC 487)
KT D17LC	NL Madole (PhPh)	VA 331 (TC 592)
KT D4 LC	NL Madole (TC 484)	VA 355 (TC 638)
KT D6 LC	NL Madole LC	VA 359
KT D8 LC	NL Madole LC (PhPh)	VA 359 (Screened)
KY 153 (TC 216)	NL Madole NS	VA 359 (TC 639)
KY 157 (TC 217)	One Sucker (TC 224)	VA 359 LC (certified)
KY 160	OS 400	VA 403 (TC 580)
KY 160 (TC 218)	PD 302H	VA 405 (TC 581)
KY 163 (TC 219)	PD 312H	VA 409 (TC 562)
KY 165 (TC 220)	PD 318H	VA 510 (TC 572)
KY 170 (TC 474)	PD 7302 LC	
KY 171 (PhPh)	PD 7305	

[00103] 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.

10 **Table 6.** Oriental Tobacco Varieties

Bafra (TI 1641)	Edirne (TI 1671)	Samsun (TC 536)
Bahce (TI 1730)	Ege (TI 1642)	Samsun 959 (TI 1570)
Bahia (TI 1416)	Ege-64 (TI 1672)	Samsun Evkaf (TI 1723)
Bahia (TI 1455)	Izmir (Akhisar) (TI 1729)	Samsun Holmes NN (TC 540)
Baiano (TI 128)	Izmir (Gavurkoy) (TI 1727)	Samsun Maden (TI 1647)
Basma	Izmir Ege 64	Samsun NO 15 (TC 541)

Basma (TI 1666)	Izmir-Incekara (TI 1674)	Samsun-BLK SHK Tol (TC 542)
Basma Drama	Izmir-Ozbas (TI 1675)	Samsun-Canik (TI 1678)
Basma Hybrid (PhPh)	Jaka Dzebel (TI 1326)	Samsun-Maden (TI 1679)
Basma Zihna I	Kaba-Kulak	Saribaptar 407 - Izmir Region
Bitlis (TI 1667)	Kagoshima Maruba (TI 158)	Smyrna (TC 543)
Bitlis (TI 1725)	Katerini	Smyrna No. 23 (TC 545)
Bubalovac (TI 1282)	Katerini S53	Smyrna No. 9 (TC 544)
Bursa (TI 1650)	Krumovgrad 58	Smyrna-Blk Shk Tol (TC 546)
Bursa (TI 1668)	MS Basma	Trabzon (TI 1649)
Canik (TI 1644)	MS Katerini S53	Trabzon (TI 1682)
Djebel 174 (TI 1492)	Nevrokop 1146	Trapezund 161 (TI 1407)
Djebel 359 (TI 1493)	Ozbas (TI 1645)	Turkish (TC 548)
Djebel 81	Perustitza (TI 980)	Turkish Angshit (TI 90)
Dubec 566 (TI 1409)	Prilep (TI 1291)	Turkish Samsun (TI 92)
Dubec 7 (TI 1410)	Prilep (TI 1325)	Turkish Tropizoid (TI 93)
Dubek 566 (TI 1567)	Prilep 12-2/1	Turkish Varotic (TI 89)
Duzce (TI 1670)	Prilep 23	Xanthi (TI 1662)

[00104] 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.

5 **Table 7.** Cigar Tobacco Varieties

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

[00105] 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.

10 **Table 8.** Other Tobacco Varieties

Chocoa (TI 319)
Hoja Parada (TI 1089)
Hoja Parado (Galpoa) (TI 1068)
Perique (St. James Parrish)
Perique (TC 556)
Perique (TI 1374)
Sylvestris (TI 984)

TI 179

[00106] 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.

[00107] 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.

[00108] 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.

[00109] 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.

[00110] 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.

[00111] 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 C x D hybrid, and a second hybrid can be made by crossing Variety E with Variety F to create an E x F hybrid. The first and second hybrids can be further crossed to create the higher order hybrid (C x D) x (E x F) comprising genetic information from all four parent varieties. In an aspect, a plant or seed provided herein is a hybrid plant or seed.

[00112] 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.

[00113] 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.

[00114] 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, undercutting, 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.

[00115] 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.

[00116] 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.

[00117] 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.

[00118] 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 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 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; 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 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; 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 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; 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 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; 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 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; and (b) selecting
5 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
10 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 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; 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
15 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
20 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; 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
25 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 sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof;
30 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.

[00119] 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 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, 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 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, 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 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, 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 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, 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 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, 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 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, 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 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, 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 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, 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 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, 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 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, 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.

[00120] In an 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 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; (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. In an 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 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; (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. In an 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 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; (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. In an 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 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; (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. In an 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 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; (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. In an 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 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; (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. In an 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 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; (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. In an 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 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; (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. In an 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 comprises a nucleic acid sequence at least 99.9% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36; (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. In an 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 comprises a nucleic acid sequence 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36; (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.

[00121] In an 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. In an 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 85% 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. In an 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 90% 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. In an 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 92.5% 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. In an 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 95% 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

5 (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. In an 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

10 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; (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

15 comparable conditions. In an 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 97%

20 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. In an 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

25 a recombinant nucleic acid comprising a heterologous promoter operably linked to a 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; (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

30 compared to a leaf from a control plant lacking the recombinant nucleic acid when grown under comparable conditions. In an 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 99%

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. In an 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 99.9% 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. In an 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 100% 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.

[00122] 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.

[00123] 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.

[00124] 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.

[00125] As used herein, the term “crossing” refers to the deliberate mating of two plants.
5 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
10 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.

[00126] 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
15 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

[00127] As used herein, “heterologous” refers to a sequence (nucleic acid or amino acid)
20 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
25 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
30 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.

[00128] 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.

[00129] 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.

[00130] 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 comprises a nucleic acid sequence at least 99.5% 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 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36.

[00131] In an aspect, this disclosure provides 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, this disclosure provides 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, this disclosure provides 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, this disclosure provides 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, this disclosure provides 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, this disclosure provides 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, this disclosure provides 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, this disclosure provides 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, this disclosure provides 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, this disclosure provides a nucleic acid sequence at least 99.5% 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, this disclosure provides a nucleic acid sequence 100% identical to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36.

[00132] In an aspect, a gene comprises 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. In an aspect, a gene comprises 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. In an aspect, a gene comprises 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. In an aspect, a gene comprises a nucleic acid sequence encoding 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 gene comprises 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. In an aspect, a gene comprises 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. In an aspect, a gene comprises 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. In an aspect, a gene comprises 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. In an aspect, a gene comprises 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. In an aspect, a gene comprises 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. In an aspect, a gene comprises 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.

[00133] In an aspect, this disclosure provides 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. In an aspect, this disclosure provides 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. In an aspect, this disclosure provides 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. In an aspect, this disclosure provides a nucleic acid sequence encoding 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, this disclosure provides 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. In an aspect, this disclosure provides 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. In an aspect, this disclosure provides 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. In an aspect, this disclosure provides 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. In an aspect, this disclosure provides 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. In an aspect, this disclosure provides 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. In an aspect, this disclosure provides 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.

[00134] In an aspect, a polypeptide comprises 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, 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.

[00135] 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%.

[00136] 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.”

[00137] 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 MA *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.

5 [00138] 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
10 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
15 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
20 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-
25 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%.

[00139] The use of the term "polynucleotide" or "nucleic acid molecule" is not intended to limit the present disclosure to polynucleotides comprising deoxyribonucleic acid (DNA).
30 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
5 aspect, a nucleic acid molecule provided herein is double-stranded. A nucleic acid molecule can encode a polypeptide or a small RNA.

[00140] 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
10 molecule formed by laboratory methods of genetic recombination.

[00141] 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
15 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
20 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
25 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
30 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, 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 polynucleotide, where nucleic acid sequence 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.

[00142] 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.

20 **[00143]** 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.

[00144] 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).

[00145] 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.

[00146] 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.

[00147] 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.

[00148] 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.

[00149] 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)).

[00150] 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.

[00151] 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.

[00152] In an aspect, a promoter is expressible in a plant cell.

Terpenes

[00153] 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, salvinorin A, cannabinoids, and curcuminoids.

[00154] 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.

[00155] Terpenoids are classified according to the number of isoprene units that comprise the parent terpene. A hemiterpenoid comprises one isoprene unit. A monoterpeneoid 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.

[00156] 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 levopimaric 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, levopimaric acid, and L-leucine. In an aspect, a terpene is selected from the group consisting of menthol or a related compound, a labdanoid, cembratrienediol, levopimaric acid, L-leucine, and neophytadiene. In an aspect, a terpene is selected from the group consisting of menthol, a labdanoid, cembratrienediol, levopimaric acid, and L-leucine. In an aspect, a terpene is selected from the group consisting of menthol, a labdanoid, cembratrienediol, levopimaric acid, L-leucine, and neophytadiene.

[00157] 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.

[00158] 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.

[00159] As used herein, “cebratrienediol” refers to the organic compound having a chemical formula of $C_{20}H_{34}O_2$ and the IUPAC name (1*R*,3*R*,4*Z*,8*Z*,12*S*,13*Z*)-1,5,9-trimethyl-12-propan-2-ylcyclotetradeca-4,8,13-triene-1,3-diol. Cembratrienediol is also referred to as “beta-Cembrenediol.”

[00160] As used herein, “levopimaric acid” refers to the organic compound having a chemical formula of $C_{20}H_{30}O_2$ and the IUPAC name (1*R*,4*aR*,4*bS*,10*aR*)-1,4*a*-dimethyl-7-propan-2-yl-2,3,4,4*b*,5,9,10,10*a*-octahydrophenanthrene-1-carboxylic acid. Levopimaric acid is also referred to as “L-Pimaric acid.”

[00161] As used herein, “L-leucine” refers to the amino acid having the chemical formula $C_6H_{12}NO_2$ and the IUPAC name (2*S*)-2-amino-4-methylpentanoic acid.

[00162] 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
5 (1*S*,2*S*,4*aS*,8*aR*)-2,5,5,8*a*-tetramethyl-1-[(3*R*)-3-methylpentyl]-1,2,3,4,4*a*,6,7,8-octahydronaphthalene.

[00163] 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
10 (1*R*,2*R*,4*aS*,8*aS*)-2,5,5,8*a*-tetramethyl-1-[(2*Z*)-3-methylpenta-2,4,-dienyl]-3,4,4*a*,6,7,8-hexahydro-1*H*-naphthalen-2-ol.

[00164] 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
15 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
20 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.

[00165] 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
25 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
30 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%.

[00166] 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%.

[00167] 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.

5 **Products**

[00168] 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.

[00169] 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.

[00170] “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. Patent 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.

[00171] 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.

[00172] 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.

[00173] 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 bright variety, a Burley variety, a Virginia variety, a Maryland variety, a dark variety, an Oriental variety, and a Turkish variety.

10 [00174] 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.

15 [00175] 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. Patent 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. Patent Nos. 4,528,993; 4,660,577; and 20 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.

[00176] 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.

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[00177] 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, 5 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.

[00178] 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 10 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).

[00179] 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 15 contribution to cigarette taste from processing flavor development using reactions between ammonia and sugars.

[00180] 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 20 capacity. It reduces the weight of tobacco used in cigarettes.

[00181] 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 30 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.

[00182] 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.

5 [00183] 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.

[00184] 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 10 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.

15 [00185] 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 vaping device.

[00186] In an aspect, a tobacco product of the present disclosure can be a blended tobacco product.

20 [00187] 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.

[00188] In an aspect, a tobacco blend comprises at least 5% cured tobacco by weight. In 25 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 30 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 aspect, a tobacco blend comprises at least 75% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 80% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 85% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 90% cured tobacco by weight. In an aspect, a tobacco blend comprises at least 95% cured tobacco by weight.

[00189] In an aspect, a tobacco blend comprises at least 5% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 10% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 15% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 20% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 25% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 30% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 35% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 40% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 45% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 50% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 55% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 60% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 65% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 70% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 75% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 80% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 85% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 90% cured tobacco by volume. In an aspect, a tobacco blend comprises at least 95% cured tobacco by volume.

[00190] In an aspect, this disclosure provides a cannabis product comprising material from a cannabis plant, cannabis seed, or cannabis plant part provided herein. In an aspect, a cannabis product is a smokeless product. In a further aspect, a smokeless cannabis product is an edible cannabis product. In a further aspect, a smokeless cannabis product is a fiber based product. In an aspect, a cannabis product is a smokable product. In an aspect, a cannabis product is derived from cannabis biomass. In an aspect, a cannabis product is a distillate derived from cannabis biomass.

[00191] In an aspect, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom 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. In an aspect, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom 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. In an aspect, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom 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. In an aspect, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom 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 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 method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom 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 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 method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom 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 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 method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom 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 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 method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom 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 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 method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom 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 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 method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom 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 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 method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous polynucleotide, where the nucleic acid sequence is selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, or a functional fragment thereof.

[00192] In an aspect, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco

plant or part therefrom, where the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a tobacco product producing using cured tobacco material from a modified tobacco plant or part therefrom, where the modified tobacco plant or part therefrom comprises a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence encodes an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, or a functional fragment thereof.

[00193] In an aspect, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom 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. In an aspect, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom

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. In an aspect, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom 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. In an aspect, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom 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 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 method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom 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 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 method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom 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 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 method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom 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 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 method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom 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 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 method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom 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 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 method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom 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 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 method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom comprises a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous polynucleotide, where nucleic acid sequence 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.

[00194] In an aspect, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified

cannabis plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom comprises a recombinant nucleic acid molecule comprising 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, this disclosure provides a method comprising preparing a cannabis product using material from a modified cannabis plant or part therefrom, where the modified cannabis plant or part therefrom comprises a recombinant nucleic acid molecule comprising a promoter operably linked to a heterologous nucleic acid sequence, where the nucleic acid sequence encodes an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, or a functional fragment thereof.

Transformation

[00195] 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 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; (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 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; (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 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;

5 (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

10 plant cell, 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; (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

15 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 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; (b) selecting at least one plant cell from step (a), where the at least one plant

20 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 is at least 96% identical to

25 a sequence selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, 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

30 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 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; (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 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; (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 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; (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 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; (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 is selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36, 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).

[00196] 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 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, 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 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, 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 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, 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 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, 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 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, 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 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, 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 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, 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 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, 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 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, a method provided herein
5 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 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, a method provided herein comprises transforming a plant cell
10 with a recombinant nucleic acid molecule, where the recombinant nucleic acid molecule comprises a promoter operably linked to a heterologous polynucleotide, where nucleic acid sequence 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.

[00197] In an aspect, this disclosure provides a method of generating a modified plant,
15 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 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; (b) selecting at least one plant cell from step (a), where the at
20 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
25 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; (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
30 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 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; (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 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; (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 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; (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 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; (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 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; (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 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; (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% 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).

[00198] 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 selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, or a functional fragment thereof.

[00199] 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 microprojectile 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.

[00200] 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 microprojectile bombardment with particles coated with recombinant DNA (*e.g.*, biolistic transformation) are found in U.S. Patent 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. Patent 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.

5 [00201] 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.

10 [00202] 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).

15 [00203] Any plant cell from which a fertile plant can be regenerated is contemplated as a useful recipient cell for practice of this disclosure.

20 [00204] 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.

25 [00205] 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.

5 [00206] 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
10 embryos, and subsequent regeneration of fertile transgenic plants) are disclosed, for example, in U. S. Patents 6,194,636 and 6,232,526 and U. S. Patent Application Publication 2004/0216189, all of which are incorporated herein by reference.

Embodiments

[00207] The following examples of non-limiting embodiments are envisioned:

- 15 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.
- 20 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.
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
25 SEQ ID NOs: 13-17, 23-30, and 34-36.
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.
5. The modified plant, seed, or plant part, of any one of embodiments 1-4, wherein said
30 nucleic acid sequence is selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36.
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.

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.
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.
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.
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.
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.
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.
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.
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.
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.
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.

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.
18. A tobacco product comprising the cured tobacco material of embodiment 16.
- 5 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.
- 10 20. The tobacco product of embodiment 19, wherein the tobacco product is a smokeless tobacco product.
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.
- 15 22. A reconstituted tobacco comprising the cured tobacco material of embodiment 16.
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.
- 20 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.
- 25 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.
- 30 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.

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.
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.
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.
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.
31. 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.
32. The method of embodiment 31, further comprising
- (d) harvesting plant material from a plant germinated from said at least one progeny seed; and
 - (e) producing a product comprising of or derived from said harvested plant material.
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.
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.

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*.
- 5 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.
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
10 31-33.
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.
39. The method of any one of embodiments 31-38, wherein said a recombinant nucleic acid
15 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.
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
20 ID NOs: 13-27 and 34-36.
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.
42. A method of generating a modified plant, the method comprising:
25 (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
30 comprises the recombinant nucleic acid molecule; and
(c) regenerating a modified plant from the at least one plant cell selected in step (b).
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.

- 5 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.
- 10 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.
- 15 46. 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; and
 - (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.
- 20
- 25

[00208] 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

[00209] Transcription factors involved in regulation of trichome initiation and
5 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 (Figures 3A and 3B)
and C2H2 (Figure 4). From these families, three transcription factors candidates are selected
10 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* Figures 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
15 NOs: 13-27 and 34-36). *See* Table 1.

Example 2. Construction of vectors

[00210] 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
20 GATEWAY expression vector, where the subcloned gene is fused with GREEN
FUORESCENCE PROTEIN (G3GFP) operably linked to a CaMV 35S promoter. *See* Figure
2.

Example 3. Transformation and regeneration of modified tobacco plants

[00211] Each of the vector constructs generated in Example 2 is separately transformed
25 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).

[00212] 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
30 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.

[00213] Leaf discs are transferred to co-cultivation Petri plates (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.

[00214] 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 subculture 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.

[00215] 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

[00216] 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 Figures 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.

[00217] Gene expression of *NtMYB* and *NbGIS* is also quantified in T₁ transgenic plants. See Figures 16 and 17, respectively.

5 **Example 5. Confirming modification of trichome density in modified tobacco plants**

[00218] 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
10 *NbGIS* show an increase in the number of glandular trichomes per unit area (i.e. increased trichome density) in leaf and stem tissues. (See Figures 5-7)

Example 6. Measuring terpene levels in modified tobacco plants

[00219] 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
15 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.

20 [00220] 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.

[00221] To identify secondary metabolites secreted from leaf trichomes, 1 gram of leaf
25 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 Figures 12-15.

CLAIMS

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.
5
2. The modified plant, seed, or plant part, of claim 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: 18-22 and 31-33.
- 10 3. The modified plant, seed, or plant part, of claim 1, 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.
4. The modified plant, seed, or plant part, of claim 1, 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.
15
5. The modified plant, seed, or plant part, of claim 1, wherein said nucleic acid sequence is selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36.
6. The modified plant, seed, or plant part, of claim 1, wherein said amino acid sequence is selected from the group consisting of SEQ ID NOs: 18-22 and 31-33.
- 20 7. The modified plant, seed, or part thereof of claim 1, wherein said modified plant, seed, or plant part is a tobacco plant, tobacco seed, or tobacco plant part.
8. The modified plant, seed, or part thereof of claim 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.
25
9. The modified plant, seed, or part thereof of claim 1, wherein the plant is male sterile or cytoplasmically male sterile.
10. The modified plant, seed, or part thereof of claim 1, wherein said modified plant, seed, or plant part is a cannabis plant, cannabis seed, or cannabis plant part.
- 30 11. The modified plant, seed, or plant part, of claim 1, 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.

12. The modified plant, seed, or plant part, of claim 1, 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.
13. The modified plant, seed, or plant part of claim 1, 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.
14. The modified plant, seed, or plant part of claim 1, 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.
15. The modified plant, seed, or plant part of claim 1, 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.
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.
17. The cured tobacco material of claim 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.
18. A tobacco product comprising the cured tobacco material of claim 16.
19. The tobacco product of claim 18, 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.
20. The tobacco product of claim 19, wherein the tobacco product is a smokeless tobacco product.
21. The tobacco product of claim 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.
22. A reconstituted tobacco comprising the cured tobacco material of claim 16.

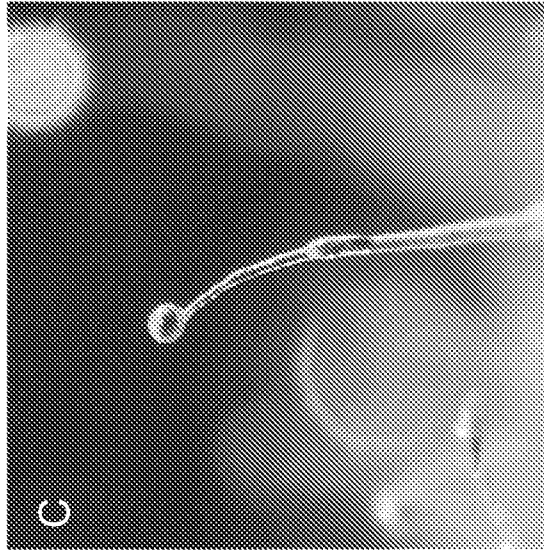
23. A tobacco product comprising material from a modified tobacco plant, tobacco seed, or tobacco plant part comprising a recombinant nucleic acid molecule comprising a nucleic acid sequence encoding an amino acid sequence at least 80% identical or similar to an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-22 and 31-33, wherein said nucleic acid sequence is operably linked to a heterologous promoter.
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.
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.
26. The recombinant nucleic acid molecule of claim 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.
27. The recombinant nucleic acid molecule of claim 25, 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.
28. The recombinant nucleic acid molecule of claim 25, 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.
29. The recombinant nucleic acid molecule of claim 25, wherein said nucleic acid sequence is selected from the group consisting of SEQ ID NOs: 13-17, 23-30, and 34-36.
30. The recombinant nucleic acid molecule of claim 25, wherein said nucleic acid sequence encodes a protein selected from the group consisting of SEQ ID NOs: 18-22 and 31-33.
31. 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.
- 5
32. The method of claim 31, further comprising
- (f) harvesting plant material from a plant germinated from said at least one progeny seed; and
- (g) producing a product comprising of or derived from said harvested plant material.
- 10
33. The method of claim 31, 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.
34. The method of claim 31, 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.
- 15
35. The method of claim 31, wherein said at least one plant is from a genus selected from the group consisting of *Nicotiana* and *Cannabis*.
36. The method of claim 31, wherein said at least one plant is from a genus selected from the group consisting of tobacco and cannabis.
- 20
37. The method of claim 31, 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.
38. The method of claim 31, 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.
- 25
39. The method of claim 31, 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.
- 30
40. The method of claim 31, 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.

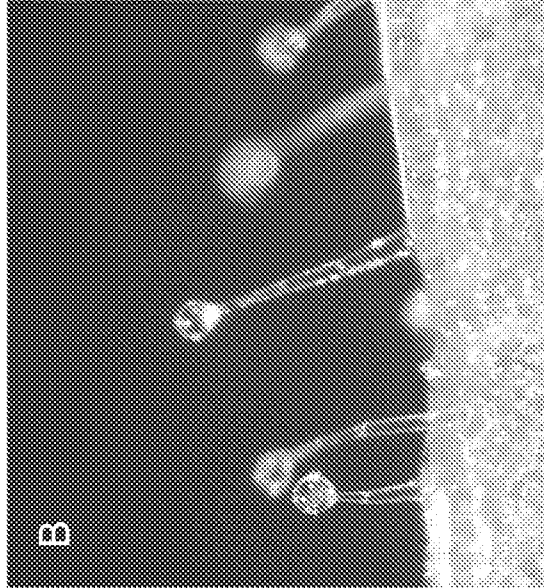
41. The method of claim 31, wherein said a recombinant nucleic acid molecule comprises a nucleic acid sequence encoding a protein selected from the group consisting of SEQ ID NOs: 18-22 and 31-33.
42. A method of generating a modified plant, the method comprising:
- 5 (a) introducing a recombinant nucleic 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
- 10 comprises the recombinant nucleic acid molecule; and
- (c) regenerating a modified plant from the at least one plant cell selected in step (b).
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
- 15 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.
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
- 20 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.
45. A method comprising transforming a plant cell with a recombinant nucleic acid
- 25 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.
46. A method for producing a plant with increased trichome density, the method
- 30 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; and

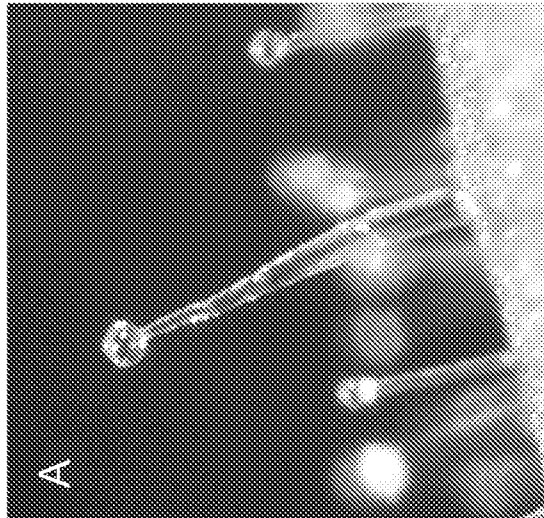
- 5 (b) regenerating a modified plant from the at least one plant cell in step (a), where the modified plant comprises an increased trichome density on at least one leaf as compared to a leaf from a control plant lacking the recombinant nucleic acid when grown under comparable conditions.



N. tabacum 'Izmir Ego'

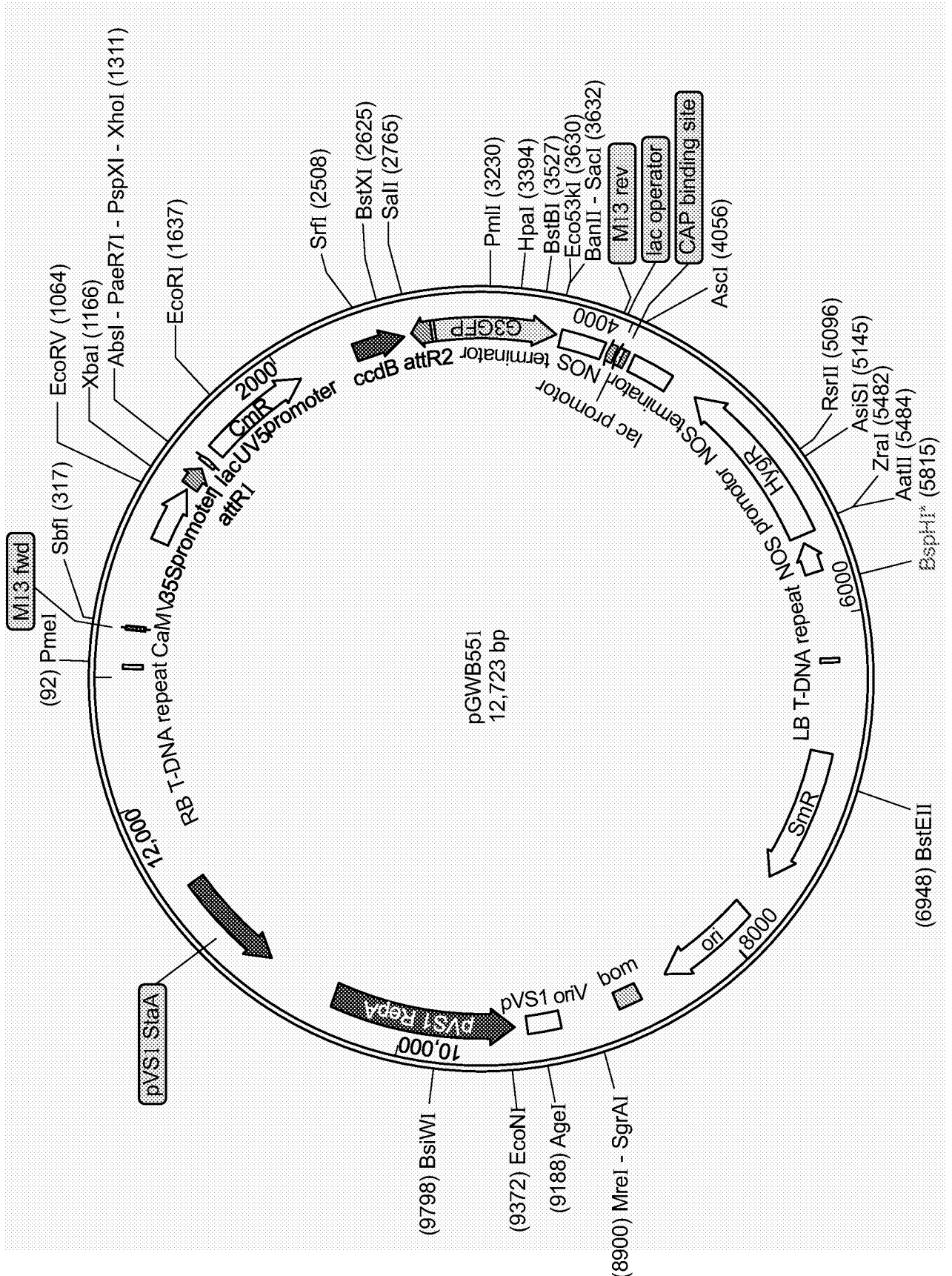


N. tabacum 'TN90'



N. benthamiana

Figure 1



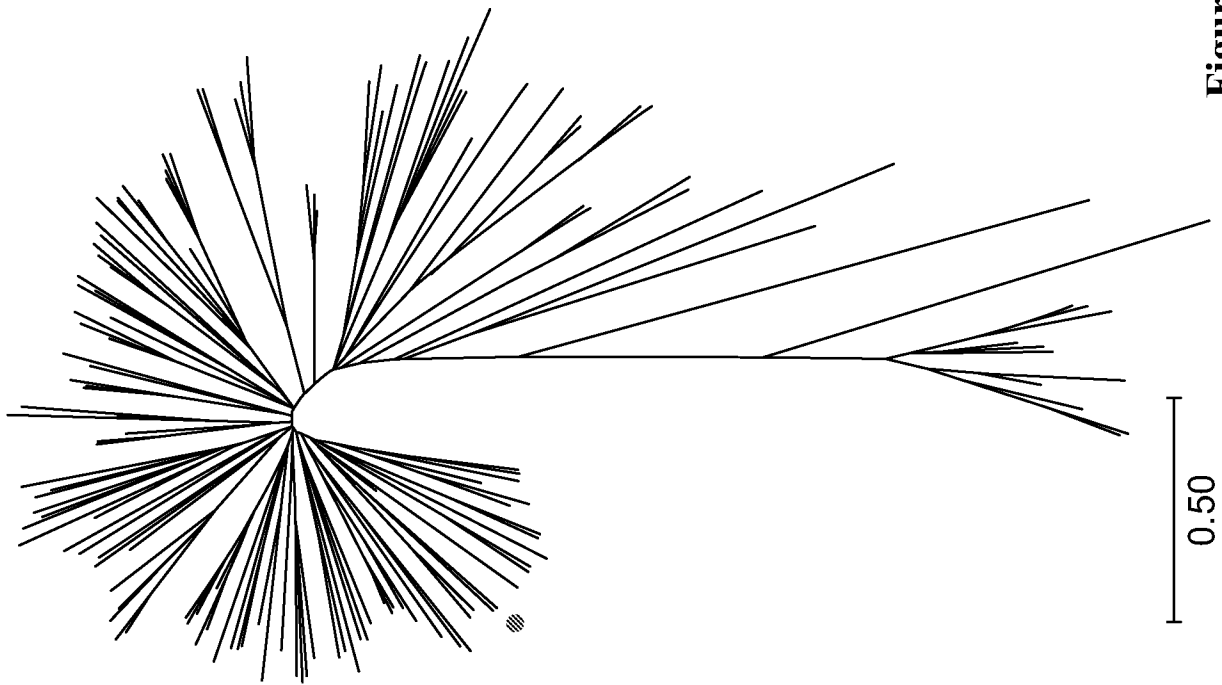
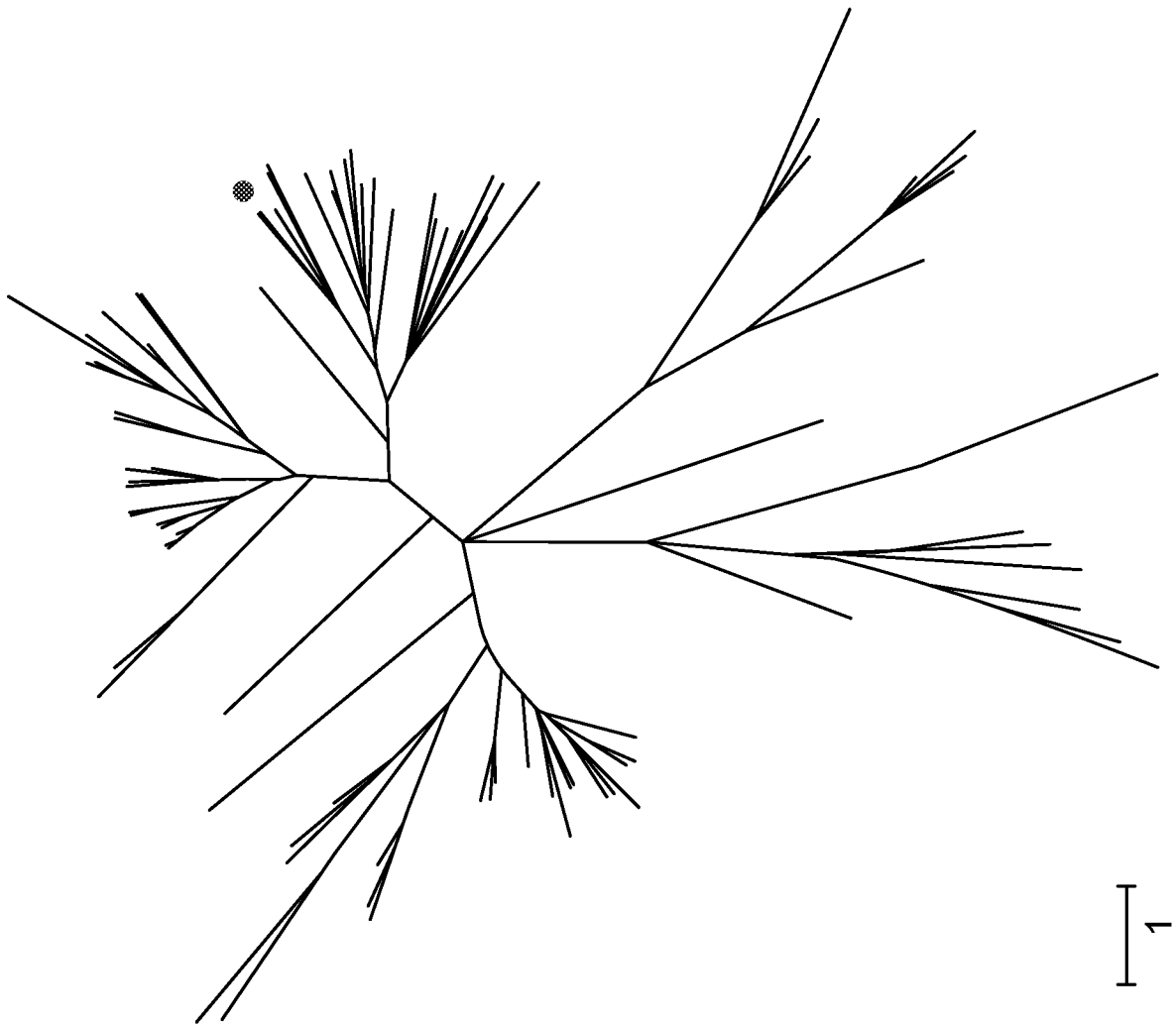


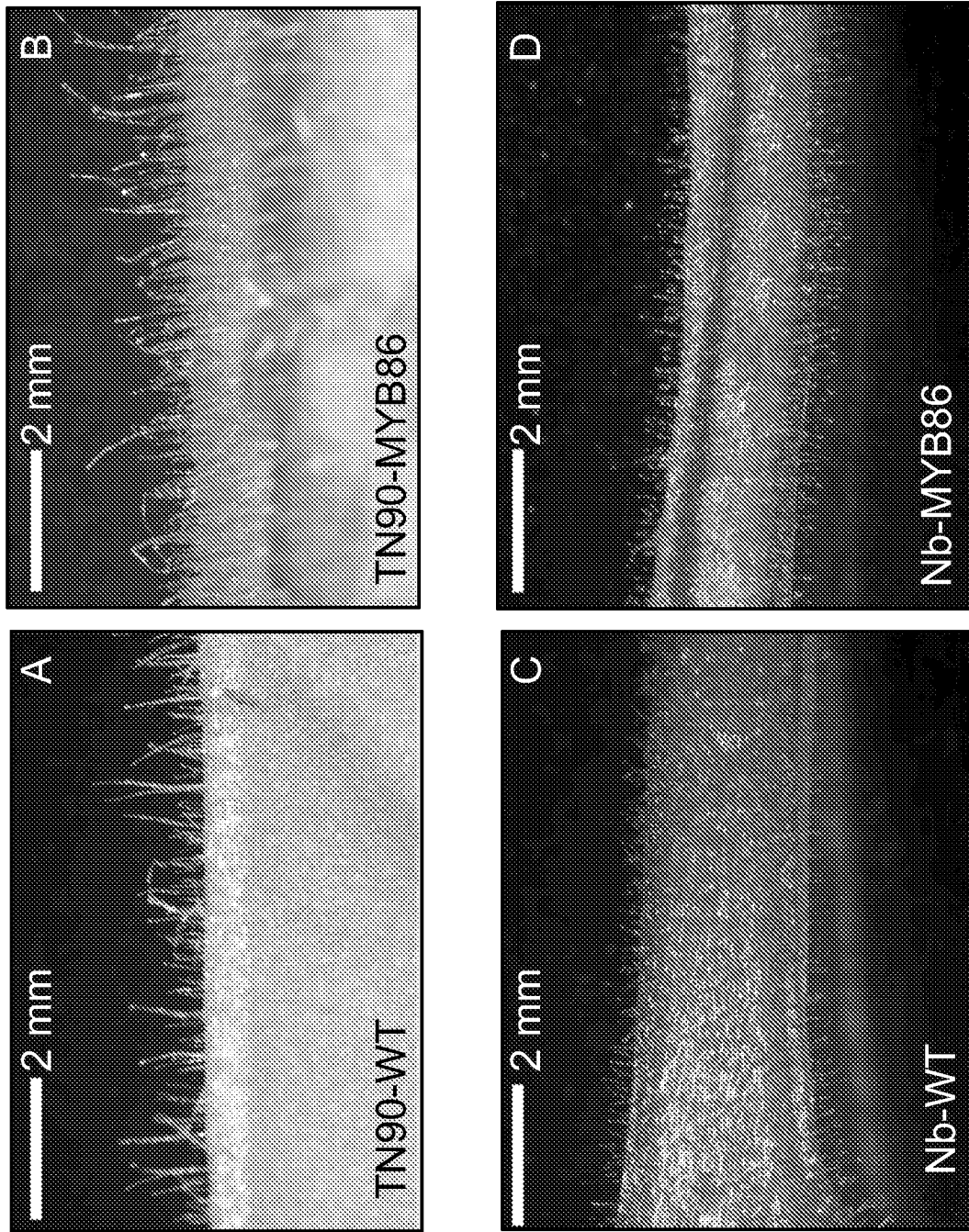
Figure 3A

	R2										R3																																																																																																						
	10	20	30	40	50	60	70	80	90	100	110	120	130	131	140	150	160	170	180	190	200	210	220	230	240	250	260																																																																																						
AGR40501.1	MARHSTCYKQ	LRKGLWSP	EEDEKLIKHITK	FGHGWSV	PKLAGL	RGCGSK	RLRWIYL	RPDL	KRGTF	SQEE	TIIV	ELH	AVL	GNK	WSQ	IAAQL	P	GR	T	DN	E	I	K	N	L	W	S	I	K	K	R	R	G	D	P	N	T	H	K	P	L	S																																																																							
XP_016450602	MGRHSCYKQ	LRKGLWSP	EEDEKLIKHITK	YGHGWSV	PKLAGL	RGCGSK	RLRWIYL	RPDL	KRGTF	SQEE	TIIV	ELH	AVL	GNK	WSQ	IAAARL	P	GR	T	DN	E	I	K	N	L	W	S	I	K	K	R	R	G	D	P	N	T	H	K	P	L	S																																																																							
Consensus	MARHSTCYKQ	LRKGLWSP	EEDEKLIKHITK	FGHGWSV	PKLAGL	RGCGSK	RLRWIYL	RPDL	KRGTF	SQEE	TIIV	ELH	AVL	GNK	WSQ	IAA	L	P	GR	T	DN	E	I	K	N	L	W	S	I	K	K	R	R	G	D	P	N	T	H	K	P	L	S																																																																						
AGR40501.1	DVENEDKPS	PRSMN	-----	KMHQ	TI	PS	IE	NP	S	LET	-----	HEFF	NR	FT	S	H	E	N	A	-----	N	L	A	S	H	T	D	T	K	H	N	T	D	Q	F	S	G	F	-----	L	D	F	A	N	D	P	P	E	S	-																																																															
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Consensus	ShHfFr	Smm	T#	T	S	I	S	W	p	q	T	m	d	s	S	iF	d	a	N	a	f	e	n	#	a	n	i	h	g	e	s	#	P	E	D	I	K	W	K	Y	L	O	S	P	N	F	G	G	A	T	L	O	S	R	V	L	C	N	E	T	R	P	D	L	G	M	S	I	M	M	H	I	I	-	-																																	
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Consensus	#	q	q	n	#	g	a	D	Y	N	K	I	O	R	I	C	A	A	%	O	F	S																																																																																									

Figure 3B

Figure 4





Leaf midvein
(abaxial)

Leaf pedicel

Figure 5

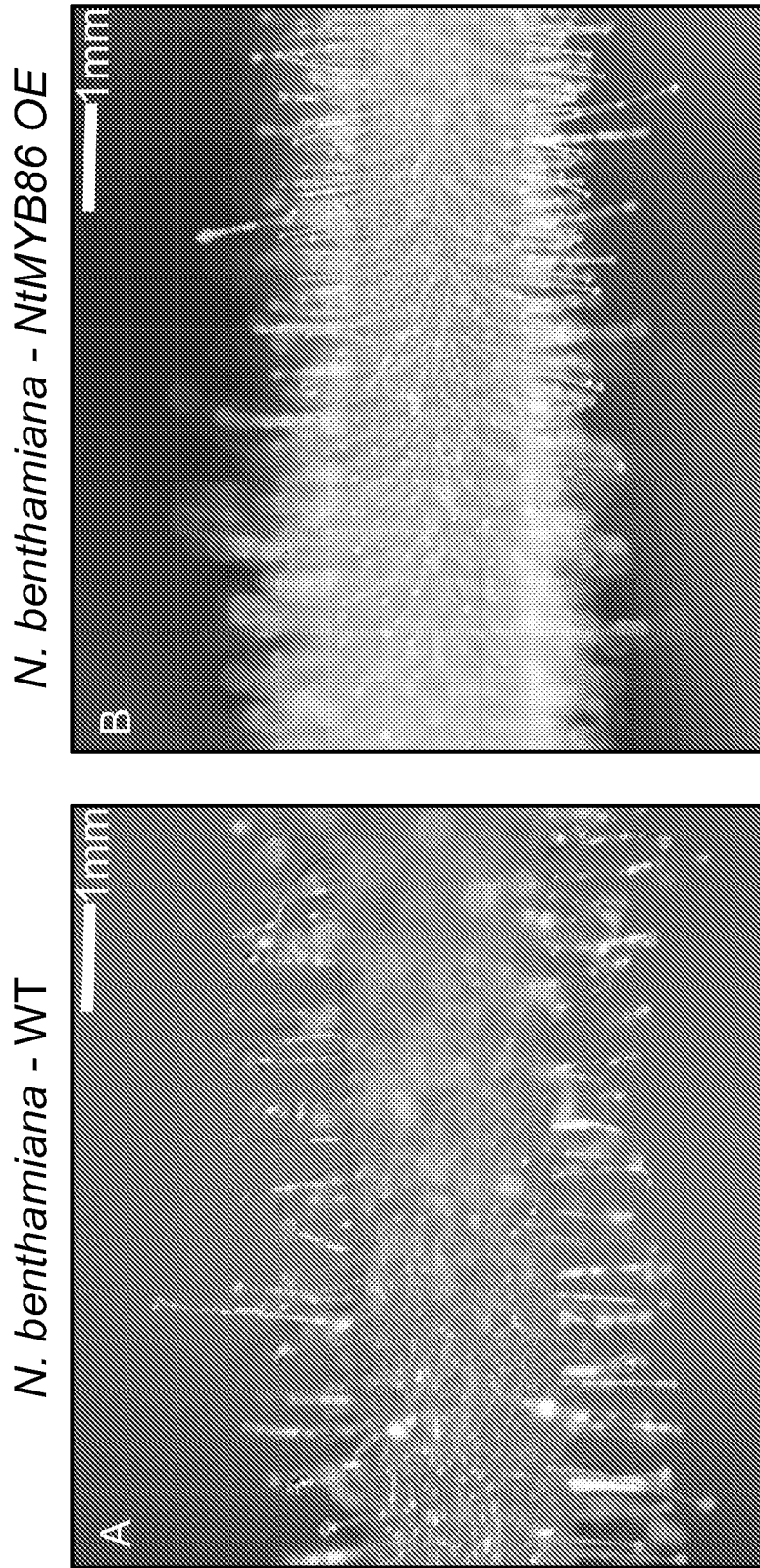


Figure 6

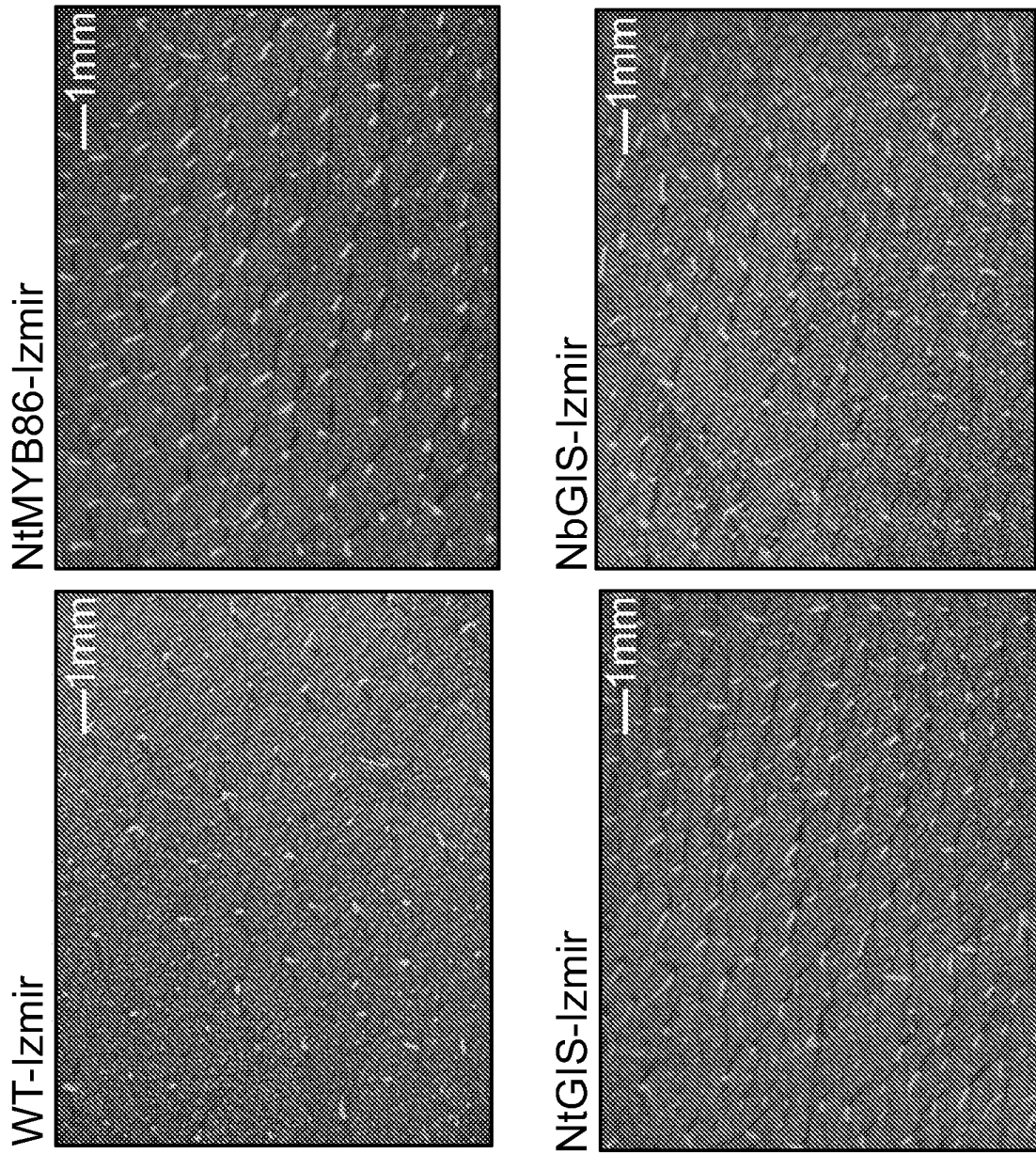


Figure 7A

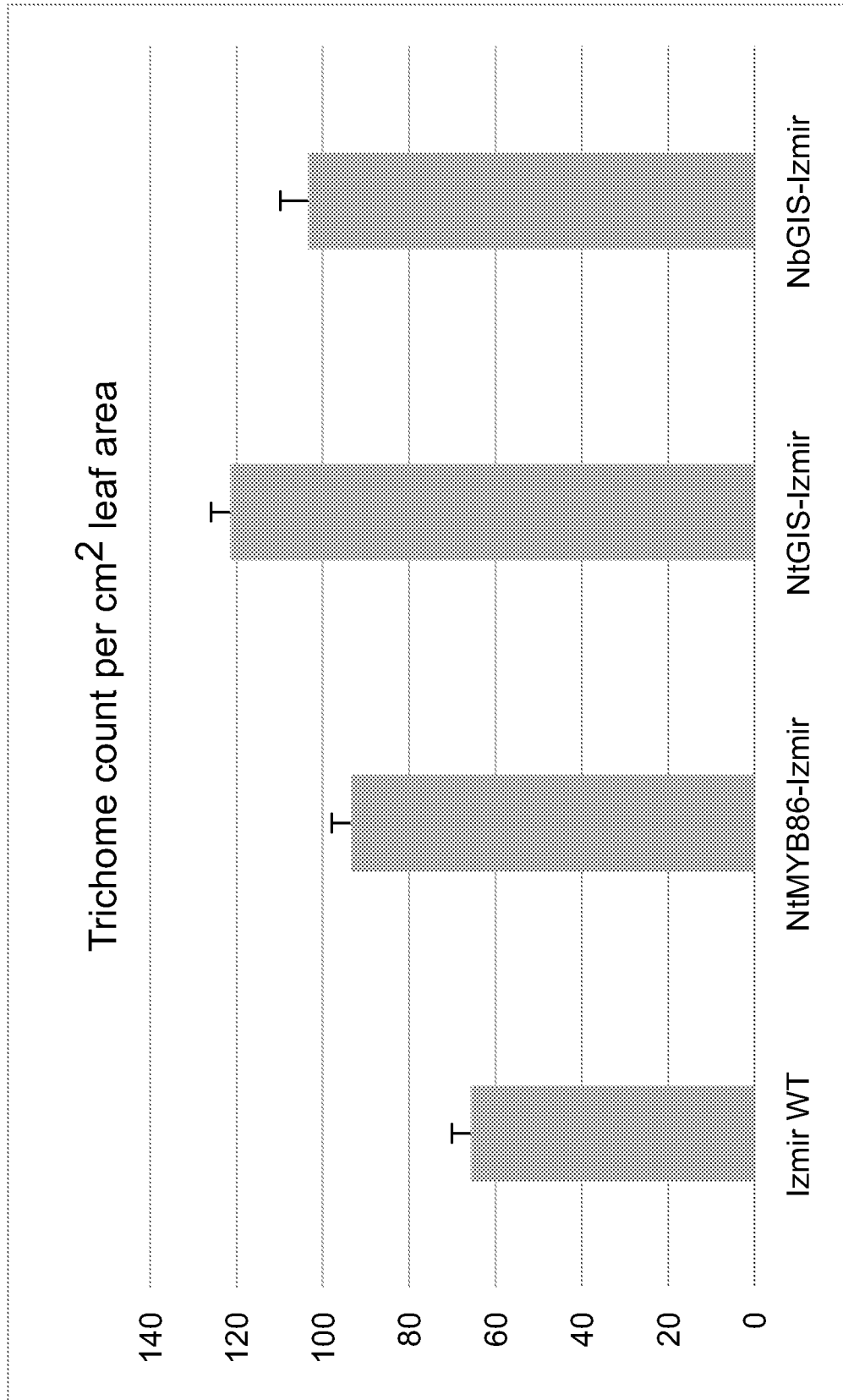


Figure 7B

10/20

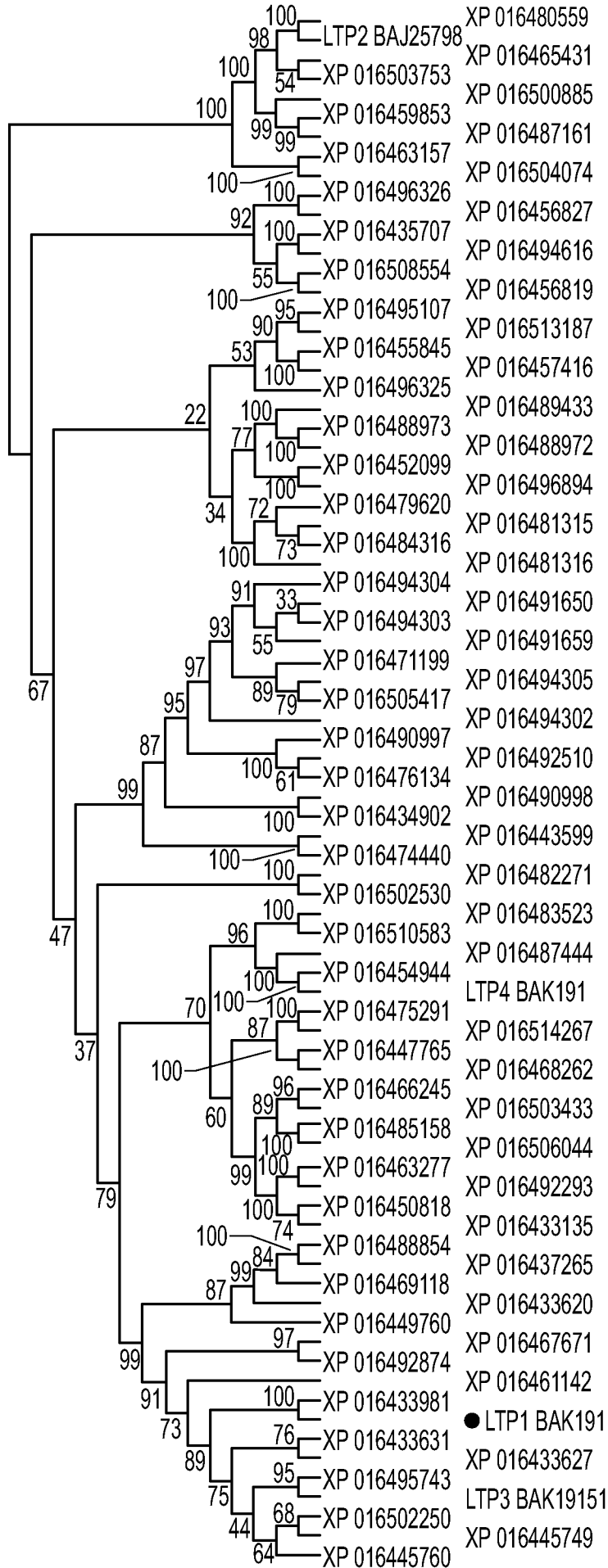


Figure 8A

Gene Structure of N+LTP1 isoforms

N+LTP1 isoform 1 (345 bp)

2 exons - 1 intron

- Exon 1 is 336 bp long
- Intron is 669 bp
- Exon 2 is 9 bp

N+LTP1 isoform 2 (489 bp)

2 exons - 1 intron

- Exon 1 is 480 bp long
- Intron is 669 bp
- Exon 2 is 9 bp

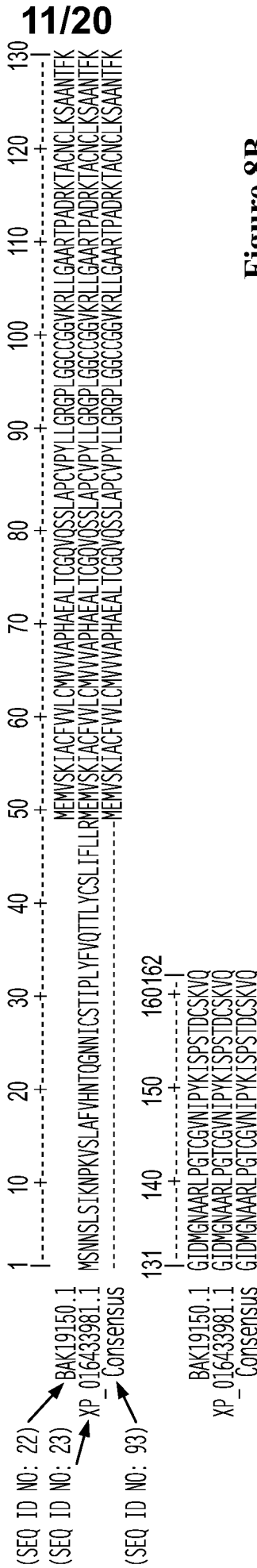


Figure 8B

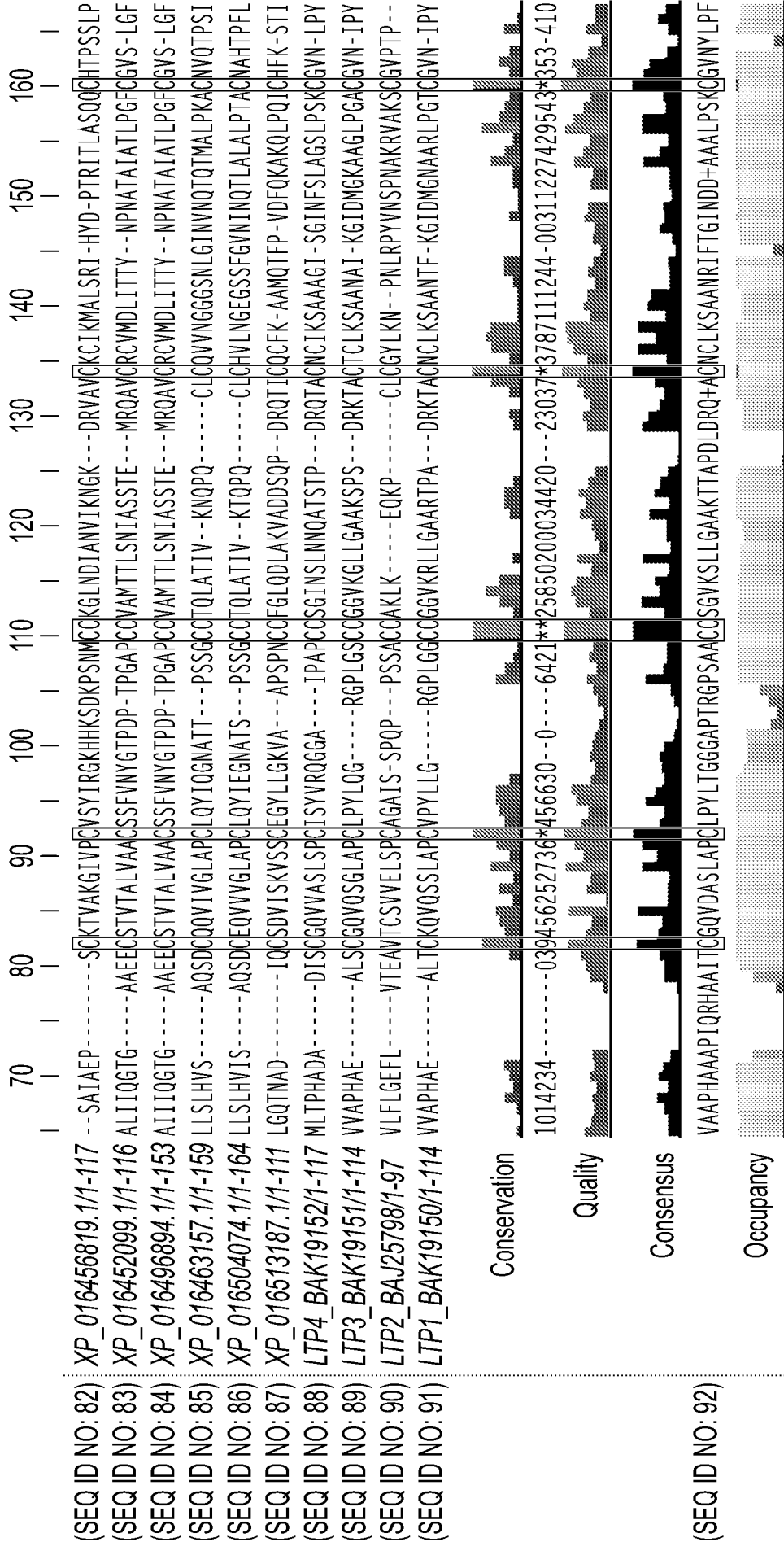


Figure 9

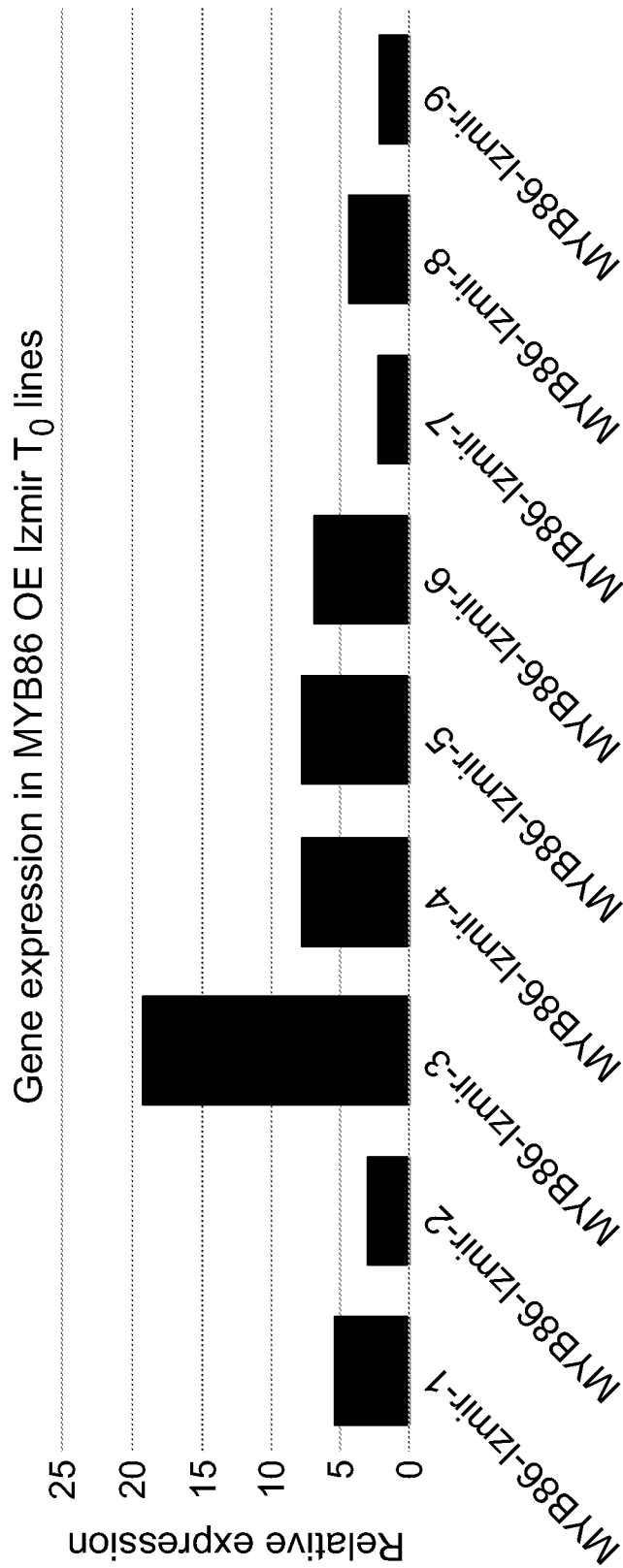


Figure 10

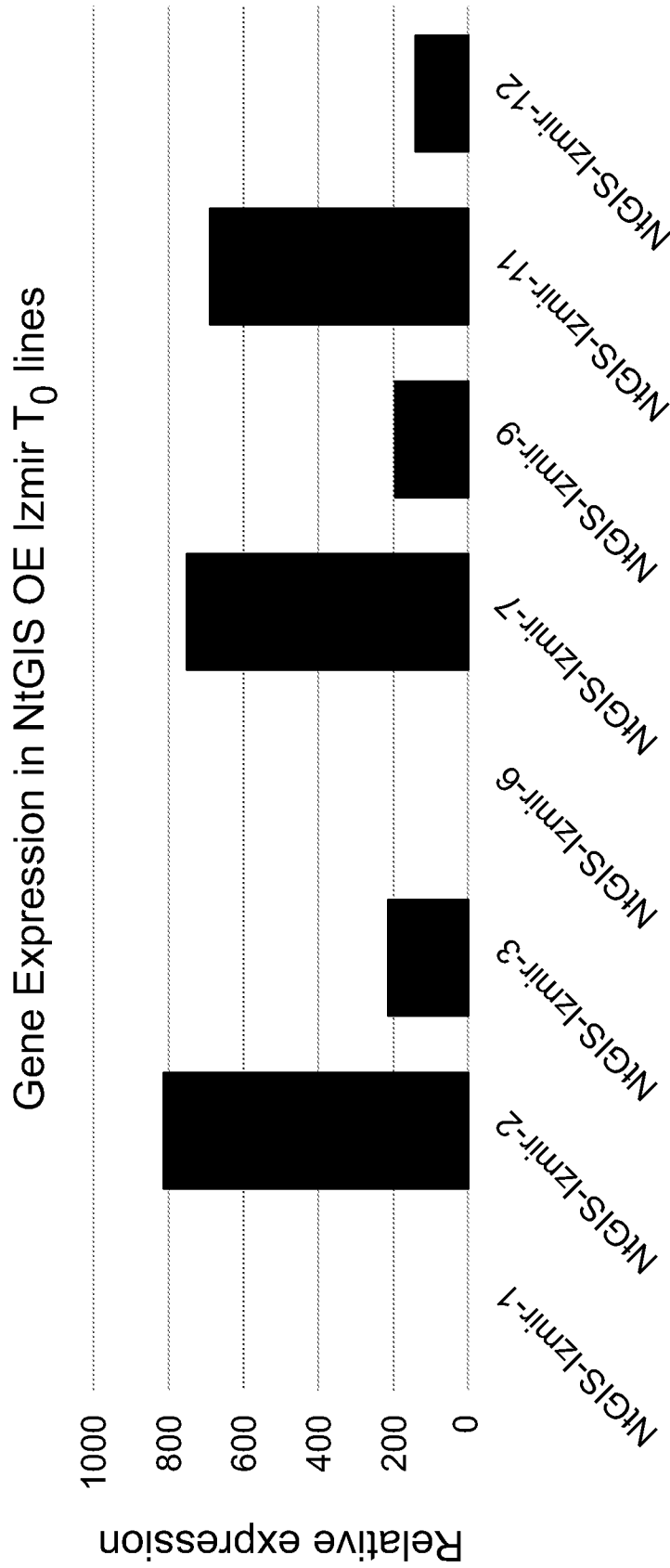


Figure 11

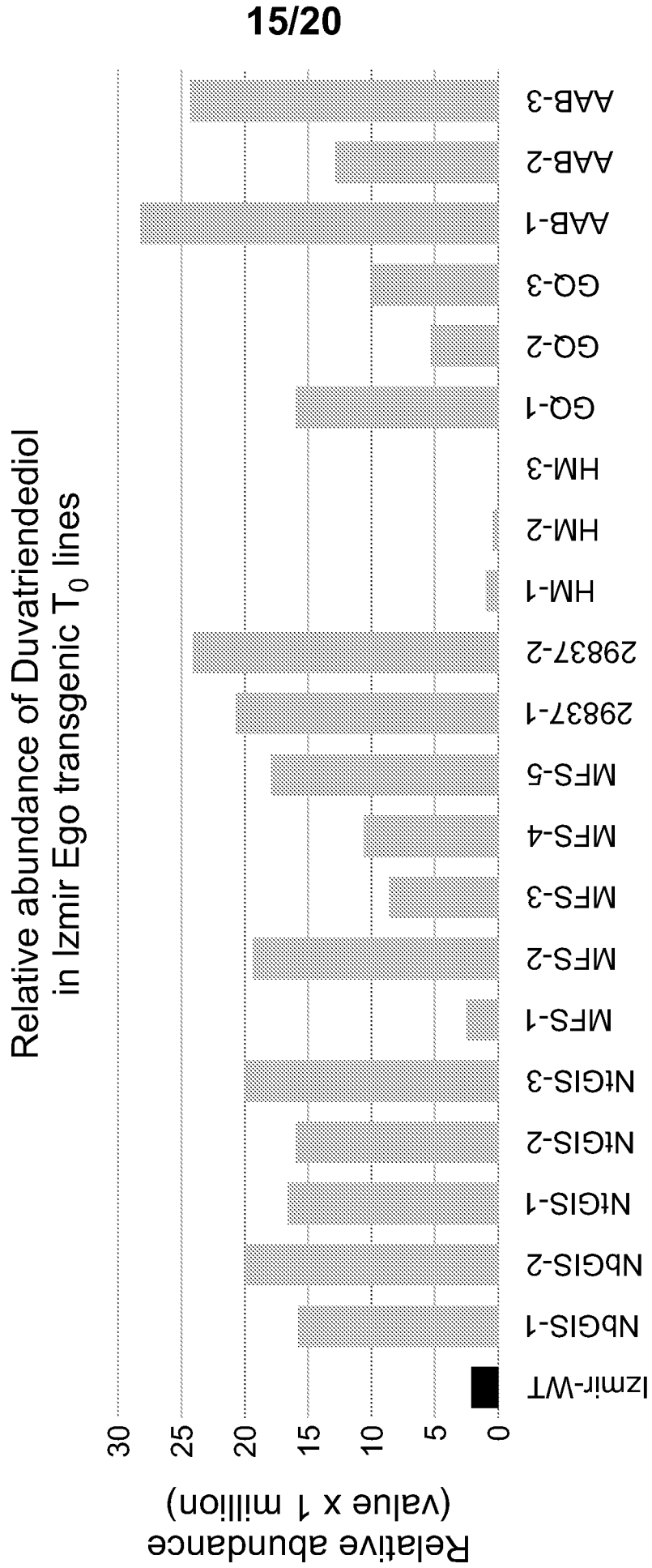


Figure 12

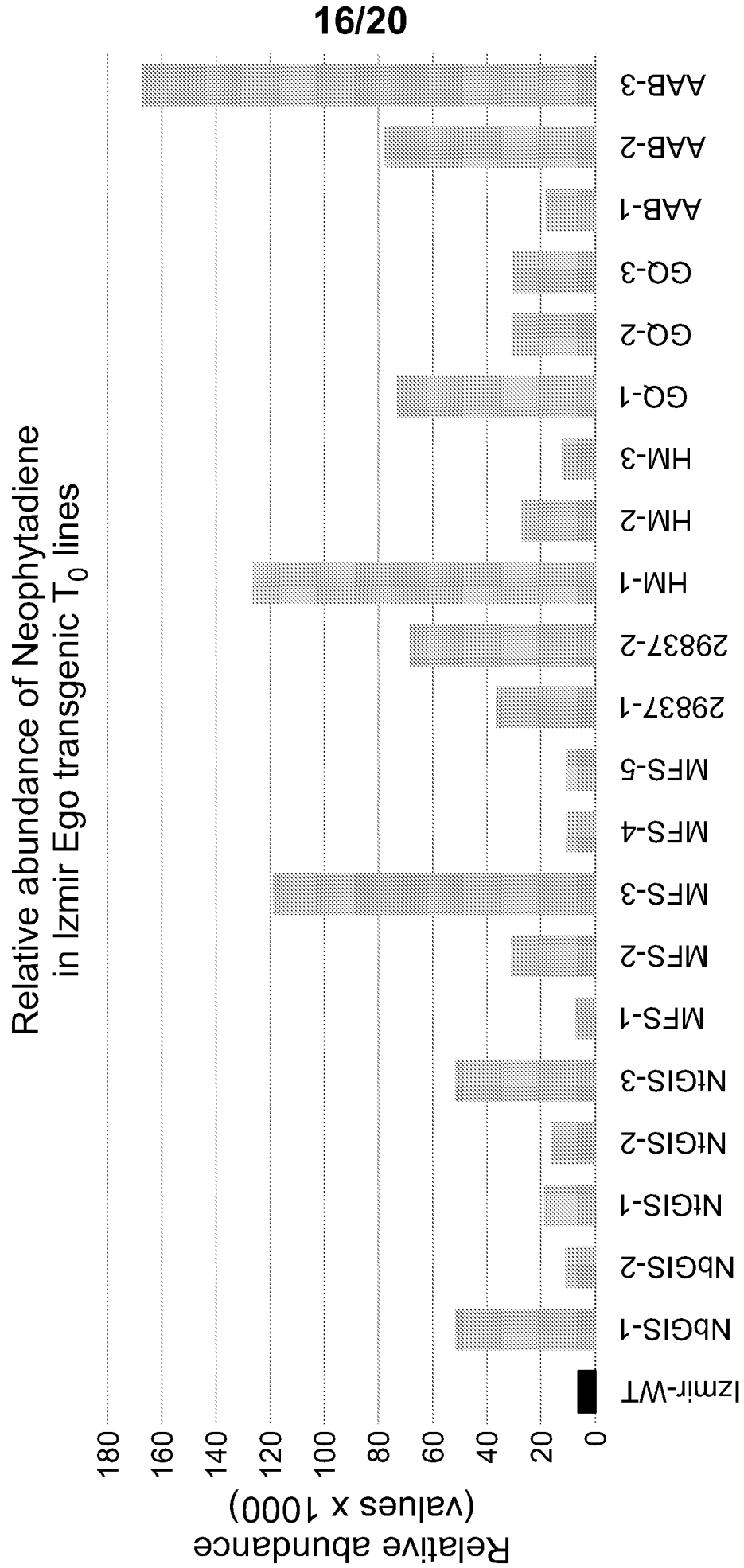


Figure 13

17/20

Relative abundance of 2,4-Dimethyl-1-heptene
in Izmir Ego transgenic T₀ lines

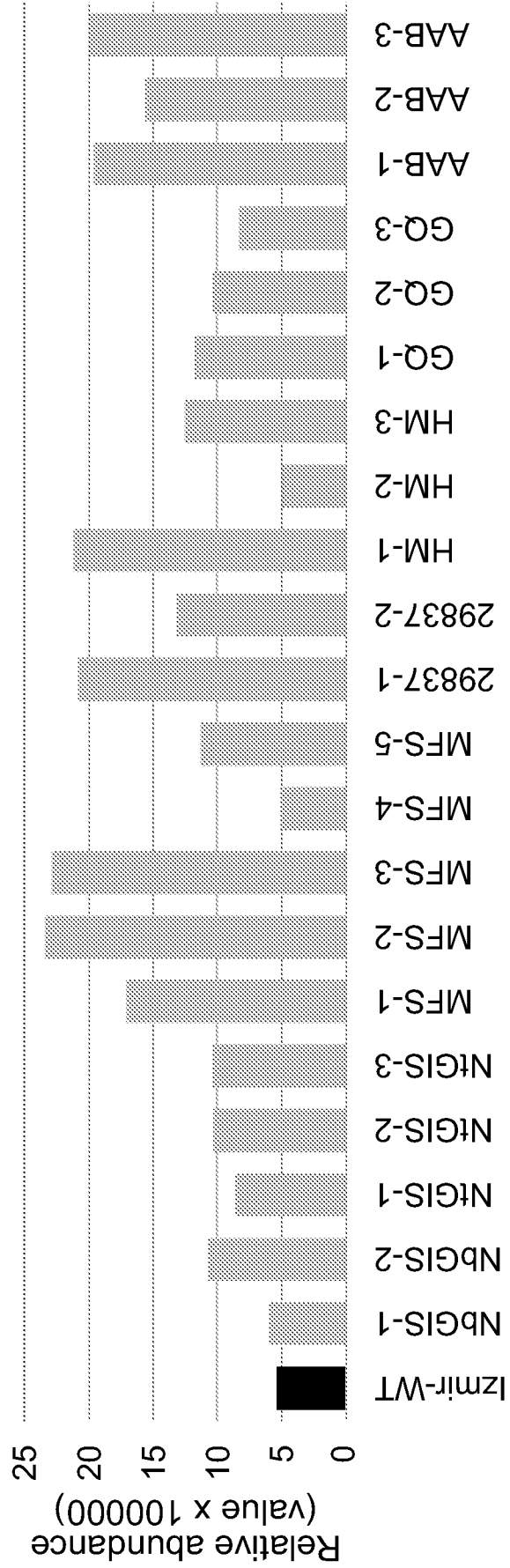


Figure 14

18/20

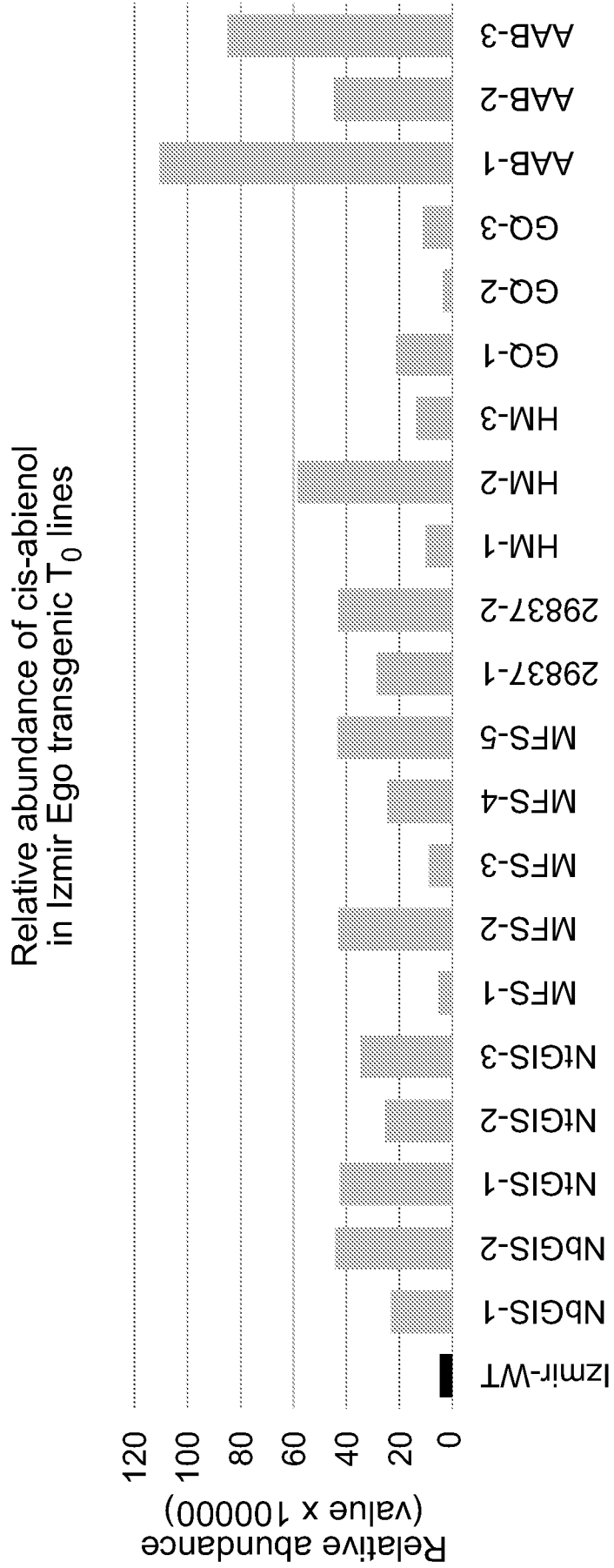
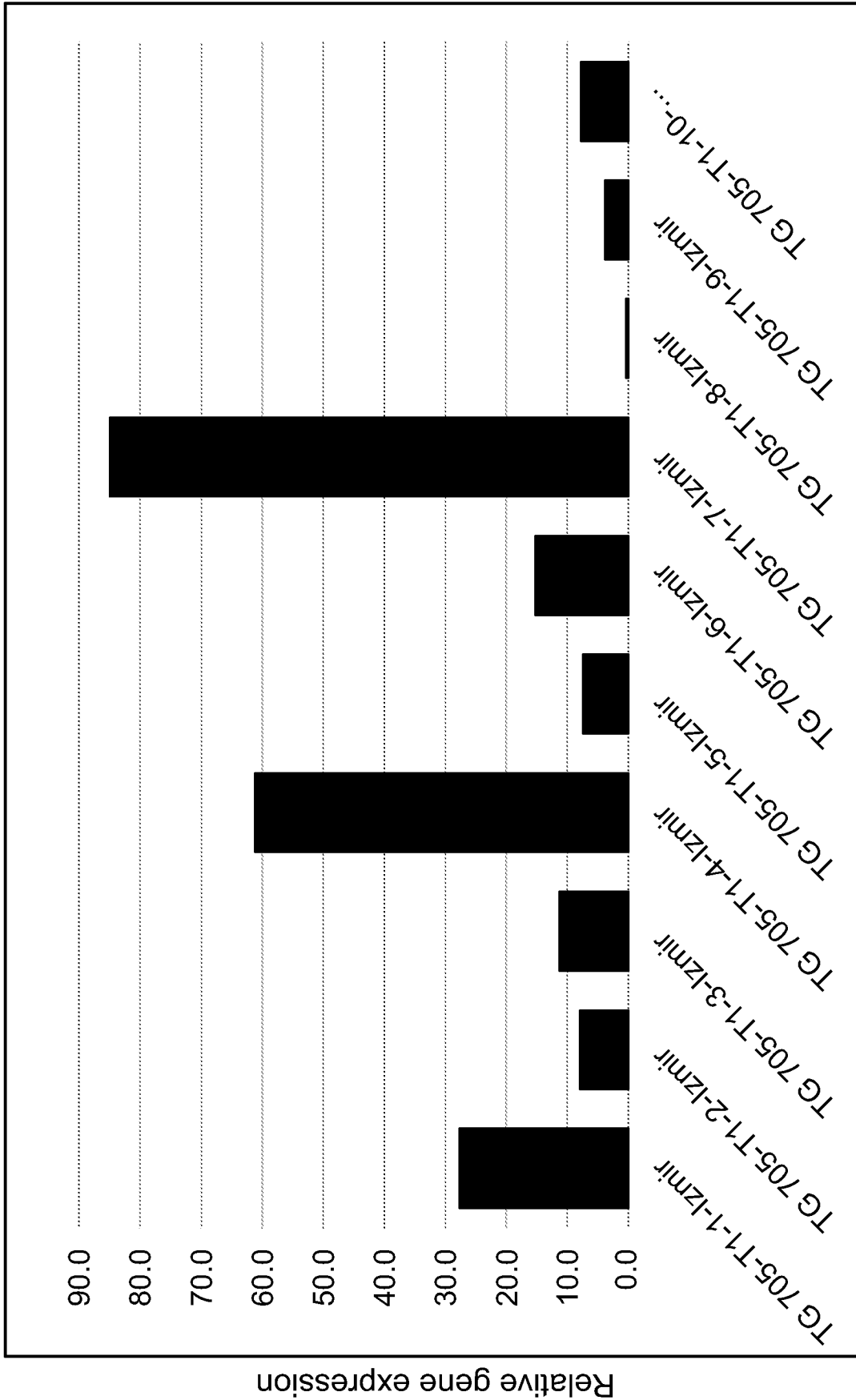
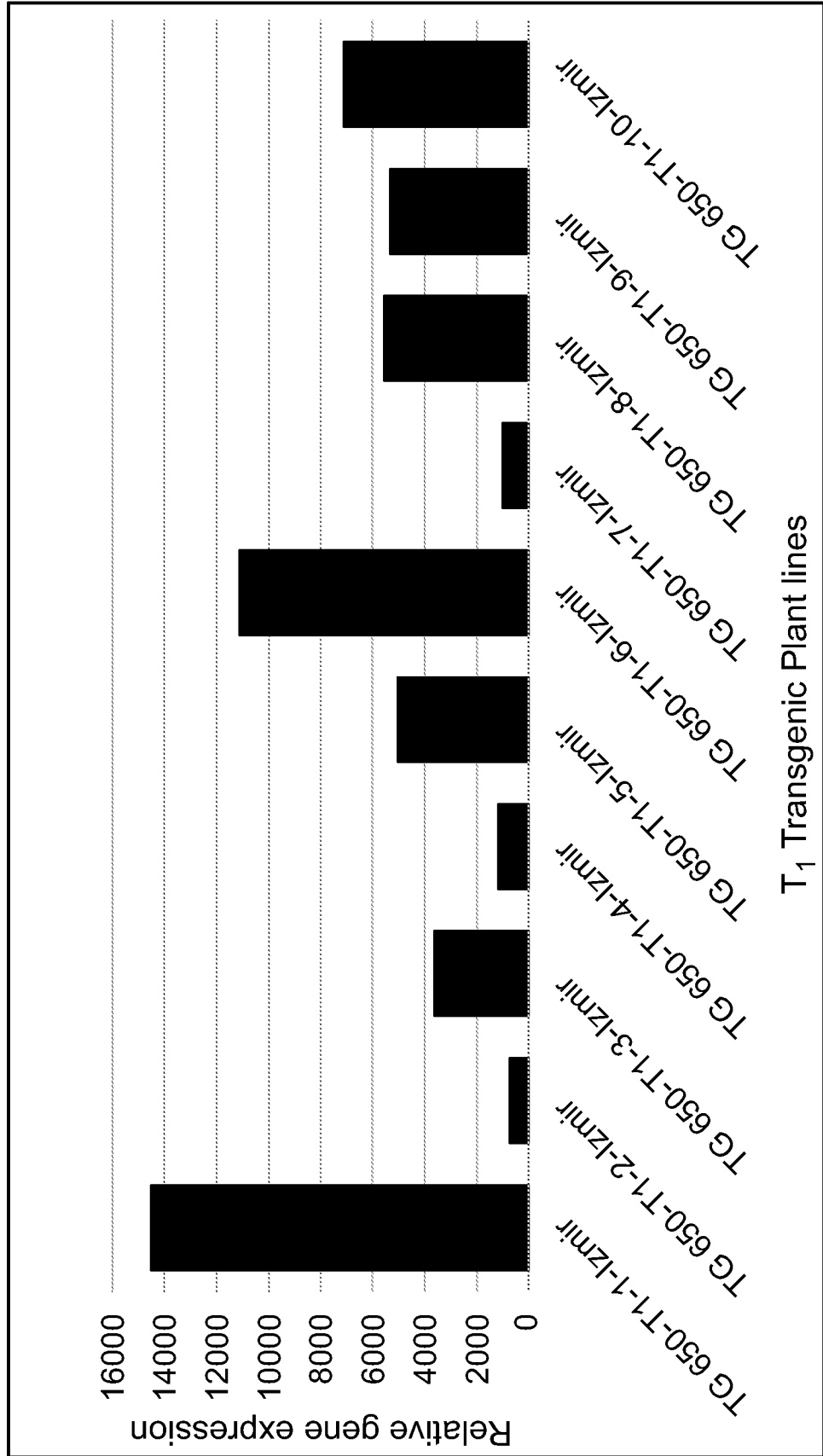


Figure 15



T₁ Transgenic Plant lines

Figure 16



T₁ Transgenic Plant lines

Figure 17

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2022/014898

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K14/415 C12N15/82
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, BIOSIS, Sequence Search, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 2019/147873 A2 (TRAIT BIOSCIENCES INC [US]) 1 August 2019 (2019-08-01) page 15, line 26 - page 16, line 9 -----	1-46
Y	CHANDRA MUKTESH ET AL: "Comparative transcriptome analysis to identify putative genes related to trichome development inspecies", MOLECULAR BIOLOGY REPORTS, SPRINGER NETHERLANDS, NL, vol. 47, no. 9, 28 August 2020 (2020-08-28), pages 6587-6598, XP037270588, ISSN: 0301-4851, DOI: 10.1007/S11033-020-05710-1 [retrieved on 2020-08-28] page 6595, right-hand column, paragraph 1 - paragraph 2 ----- -/--	1-46

Further documents are listed in the continuation of Box C.

See patent family annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier application or patent but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- "&" document member of the same patent family

Date of the actual completion of the international search

Date of mailing of the international search report

3 May 2022

08/07/2022

Name and mailing address of the ISA/
 European Patent Office, P.B. 5818 Patentlaan 2
 NL - 2280 HV Rijswijk
 Tel. (+31-70) 340-2040,
 Fax: (+31-70) 340-3016

Authorized officer

Kania, Thomas

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2022/014898

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>CHALVIN CAMILLE ET AL: "Genetic Control of Glandular Trichome Development", TRENDS IN PLANT SCIENCE, ELSEVIER, AMSTERDAM, NL, vol. 25, no. 5, 23 January 2020 (2020-01-23), pages 477-487, XP086137590, ISSN: 1360-1385, DOI: 10.1016/J.TPLANTS.2019.12.025 [retrieved on 2020-01-23] page 480, last paragraph - page 481, paragraph 3</p> <p style="text-align: center;">-----</p>	1-46
A	<p>DATABASE UniProtKB [Online]</p> <p>12 April 2017 (2017-04-12), Anonymous: "LOC107775392 - transcription factor MYB86-like - Nicotiana tabacum (Common tobacco) - LOC107775392 gene & protein", XP055917102, Database accession no. A0A1S3YF18 100% identity to present SEQ ID NO: 18; abstract</p> <p style="text-align: center;">-----</p>	1-46
A	<p>DATABASE NCBI [Online]</p> <p>18 May 2020 (2020-05-18), Anonymous: "transcription factor MYB61 isoform X1 [Cannabis sativa] - Protein - NCBI", XP055917107, Database accession no. XP_030504371 100% identity to present SEQ ID NO: 31; abstract</p> <p style="text-align: center;">-----</p>	1-46
A	<p>WO 2018/176055 A2 (TRAIT BIOSCIENCES INC [US]) 27 September 2018 (2018-09-27)</p> <p style="text-align: center;">-----</p>	1-46
A	<p>WO 2020/185865 A1 (AVANTGARDE LLC [US]) 17 September 2020 (2020-09-17)</p> <p style="text-align: center;">-----</p>	1-46
A	<p>WO 2017/181018 A1 (EBBU LLC [US]) 19 October 2017 (2017-10-19)</p> <p style="text-align: center;">-----</p>	1-46
A	<p>LUIS MATIAS-HERNANDEZ ET AL: "AaMYB1 and its orthologue AtMYB61 affect terpene metabolism and trichome development in Artemisia annua and Arabidopsis thaliana", THE PLANT JOURNAL, vol. 90, no. 3, 27 March 2017 (2017-03-27), pages 520-534, XP055636153, GB ISSN: 0960-7412, DOI: 10.1111/tpj.13509 cited in the application</p> <p style="text-align: center;">-----</p>	1-46
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INTERNATIONAL SEARCH REPORT

International application No

PCT/US2022/014898

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	CN 104 152 463 A (UNIV SHANGHAI JIAOTONG) 19 November 2014 (2014-11-19) -----	1-46
A	US 2021/010018 A1 (TANG KEXUAN [CN] ET AL) 14 January 2021 (2021-01-14) -----	1-46
A	JIESEN XU ET AL: "SlMYC1 Regulates Type VI Glandular Trichome Formation and Terpene Biosynthesis in Tomato Glandular Cells", THE PLANT CELL, vol. 30, no. 12, 1 December 2018 (2018-12-01), pages 2988-3005, XP055679205, US ISSN: 1040-4651, DOI: 10.1105/tpc.18.00571 -----	1-46
A	NAUTIYAL ABHISHEK KUMAR ET AL: "Comprehensive transcriptome analysis provides insights into metabolic and gene regulatory networks in trichomes of", PLANT MOLECULAR BIOLOGY, SPRINGER, DORDRECHT, NL, vol. 102, no. 6, 21 January 2020 (2020-01-21), pages 625-644, XP037057883, ISSN: 0167-4412, DOI: 10.1007/s11103-020-00968-2 [retrieved on 2020-01-21] -----	1-46
A	ALEXANDRE HUCHELMANN ET AL: "Plant Glandular Trichomes: Natural Cell Factories of High Biotechnological Interest", PLANT PHYSIOLOGY, vol. 175, no. 1, 19 July 2017 (2017-07-19) , pages 6-22, XP055665110, Rockville, Md, USA ISSN: 0032-0889, DOI: 10.1104/pp.17.00727 page 14, right-hand column, last paragraph - page 18, right-hand column, paragraph 4 -----	1-46

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2022/014898

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:
 - a. forming part of the international application as filed:
 - in the form of an Annex C/ST.25 text file.
 - on paper or in the form of an image file.
 - b. furnished together with the international application under PCT Rule 13ter.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.
 - c. furnished subsequent to the international filing date for the purposes of international search only:
 - in the form of an Annex C/ST.25 text file (Rule 13ter.1(a)).
 - on paper or in the form of an image file (Rule 13ter.1(b) and Administrative Instructions, Section 713).
2. In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.
3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2022/014898

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims;; it is covered by claims Nos.:

1-46 (partially)

Remark on Protest

- The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-46 (partially)

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 and 31 (MYB-like transcription factors), wherein said nucleic acid sequence is operable linked to a heterologous promoter, as well as related products and methods of their use as claimed.

1.1. claims: 1-46 (partially)

idem for SEQ ID NO: 18, 13, 23 (MYB86-like transcription factor from tobacco)

1.2. claims: 1-46 (partially)

idem for SEQ ID NO: 31, 28, 34 (MYB61-like transcription factor from Cannabis)

2. claims: 1-46 (partially)

idem for SEQ ID NOs: 19, 20, 32, 14, 15, 24, 25, 29, 35 (C2H2-like transcription factors)

3. claims: 1-46 (partially)

idem for SEQ ID NOs: 21, 22, 33, 16, 17, 26, 27, 30, 36 (LTP-like proteins)

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/US2022/014898

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2019147873	A2	01-08-2019	AU 2019208175 A1
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			WO 2020147113 A1
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