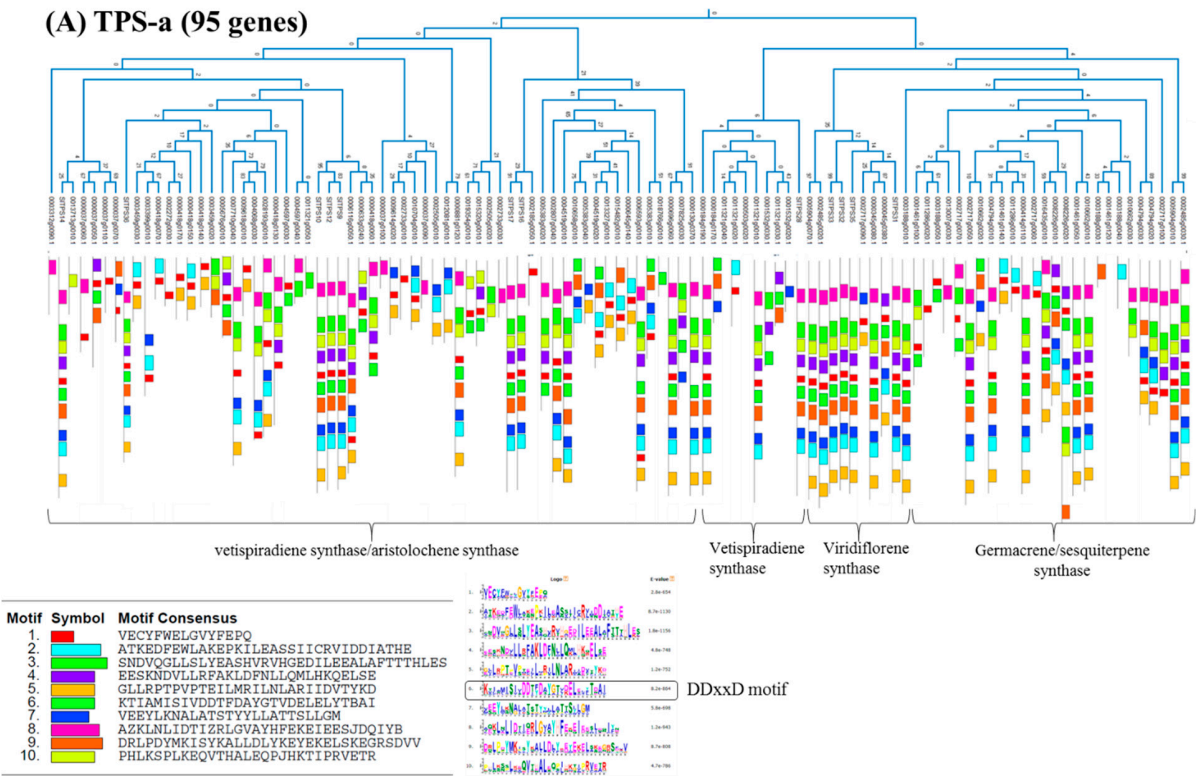
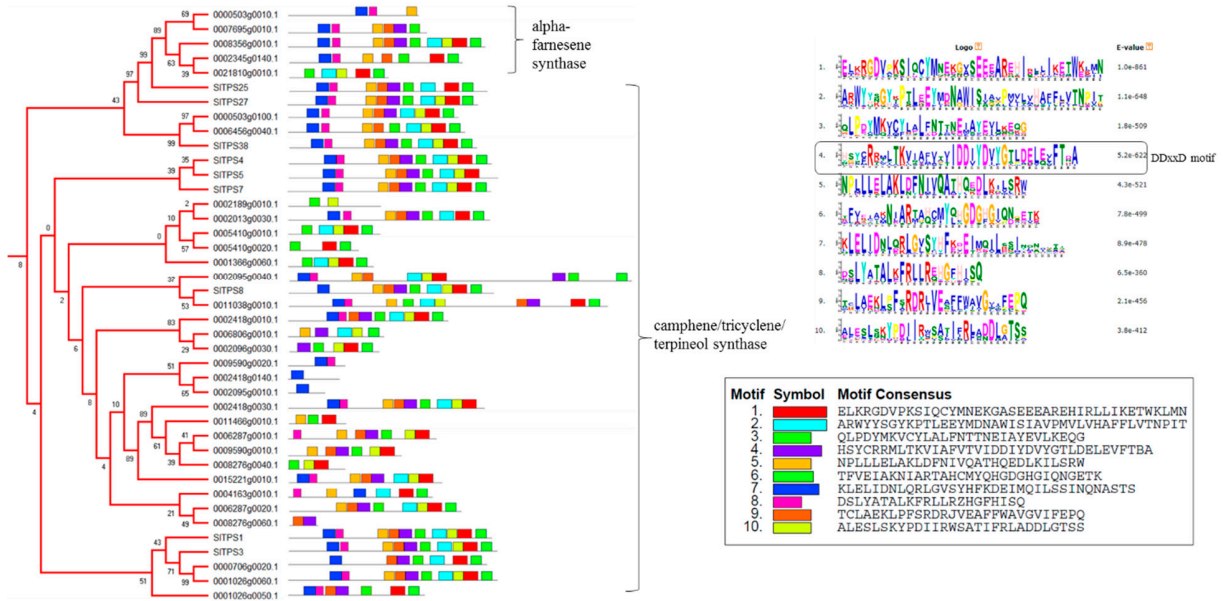


Supplementary Data

Supplementary Figure S1. Identified consensus motif in each member of the *TPS* clades (A) TPS-a (B) TPS-b (C) TPS-c (D) TPS-e/f and (E) TPS-g.

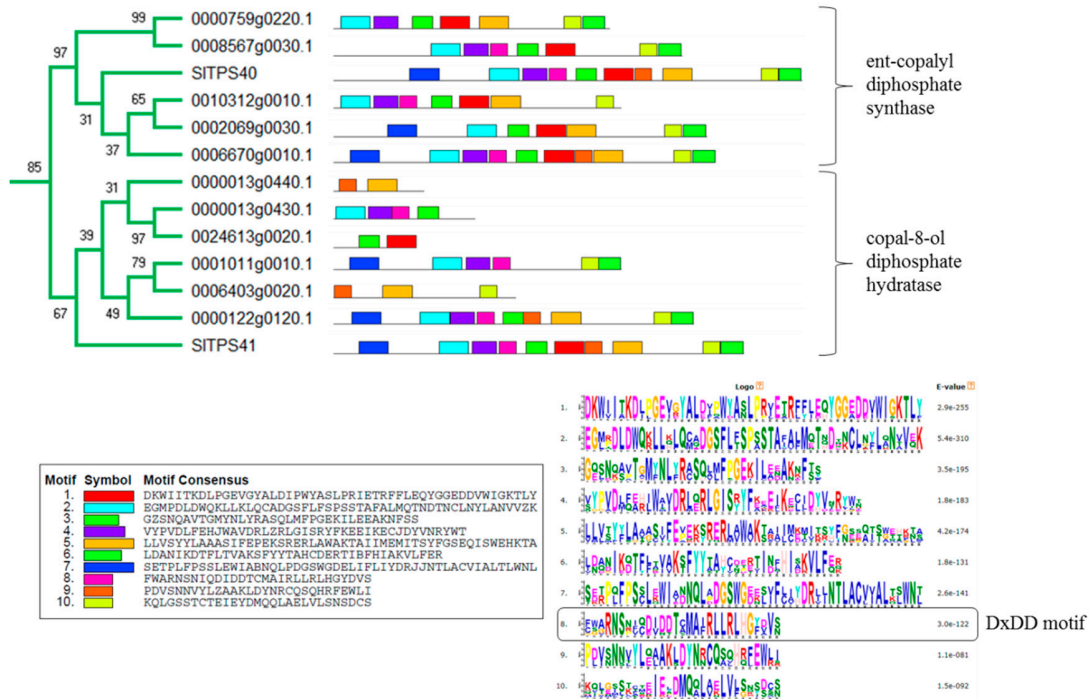


(B) TPS-b (32 genes)

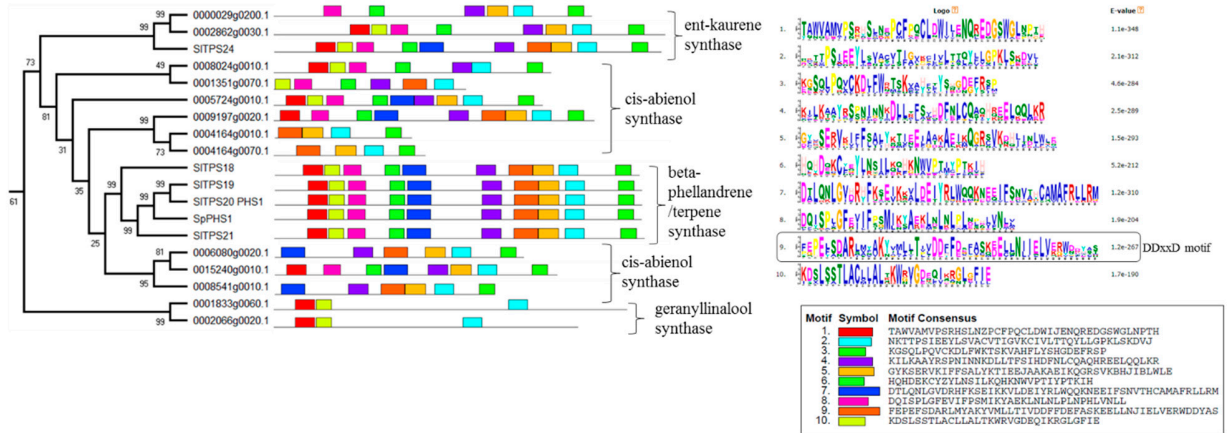


RRX ₅ W motif	
0000503g0010	GRKGMCHRTNKLHSTIKKQSLPERSKICTYKPNIWKYDHLIT
0000503g0100	MDLRRSGNYKPSIWEDGYVQS
0000706g0020	PLNHS-TISTNQSSFS--LNPIRRSGNYEPTTWDFEY--IQSIHND
0001026g0060	PLNHS-TISTNQSSSD--LNPIRRSGNYEPTTWDFEY--IQSIHND
0002013g0030	NSTSPKAEPLSHSSIPNTMNTDRRSGNYKPTWDFEY--IESISND
0002345g0140	SNKRQSTTKKQSLPERKISTYKPNIWKYDHLIT
0002418g0010	LSTKTEPSPNQYSAISASDQNPTRRSGNYQPTMWDFEY--IQSIHND
0002418g0030	LSTKTEPSPNQYSAISASDQNLTRRSGNYQPTMWDFEY--IQSIHND
0006456g0040	MDLRRSGNYKPSIWEDGYVQS
0008356g0010	TKKLHSTIKKQSHPERKISTYKPNIWKYDHLIT
0009590g0020	FSTKTEPSPHQYSAISASDQNPTRRSGNYQPTMWDFEY--IQSIHND
SlTPS1	IIITKHSHPISATRRSGNYKPTLWDFQF--IESLHNP
SlTPS3	PLNYSPISTNIISSSNGIINPIRRSGNYEPTMWNYEY--IQSTHNP
SlTPS4	INGGKPSLLIVVSKASSNPPTTRRSGNYKPTMWDFQF--IQSVNNL
SlTPS5	LRRSANN-IIITKHSHP-ISTTRRSGNYKPTMWDFQF--IQLHNP
SlTPS7	LHHSISARGAINNISTP-ISATRRSGNYKPTMWDFQF--IQLHNP
SlTPS27	TTSFRKSNIDETLIGRRNANYKPNIWKYDILQS
SlTPS38	MLQSCISTMDIRRSGNYKPSIWEDGYVQS

(C) TPS-c (11 genes)



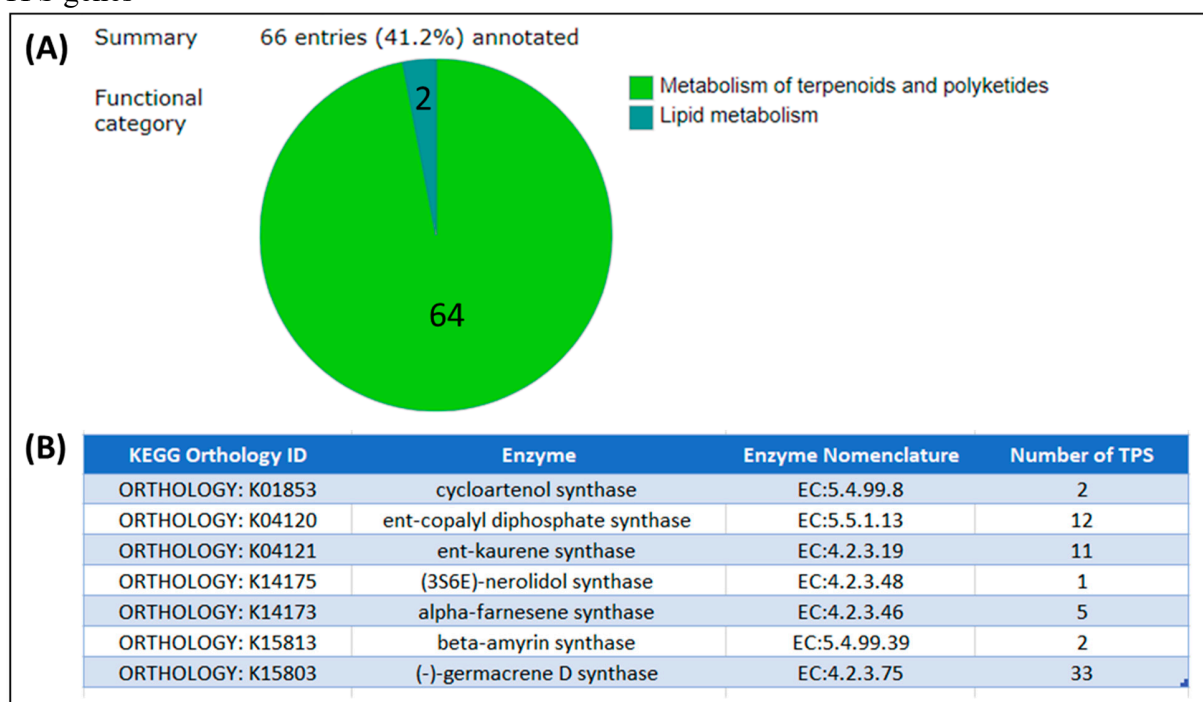
(D) TPS-e/f (13 genes)



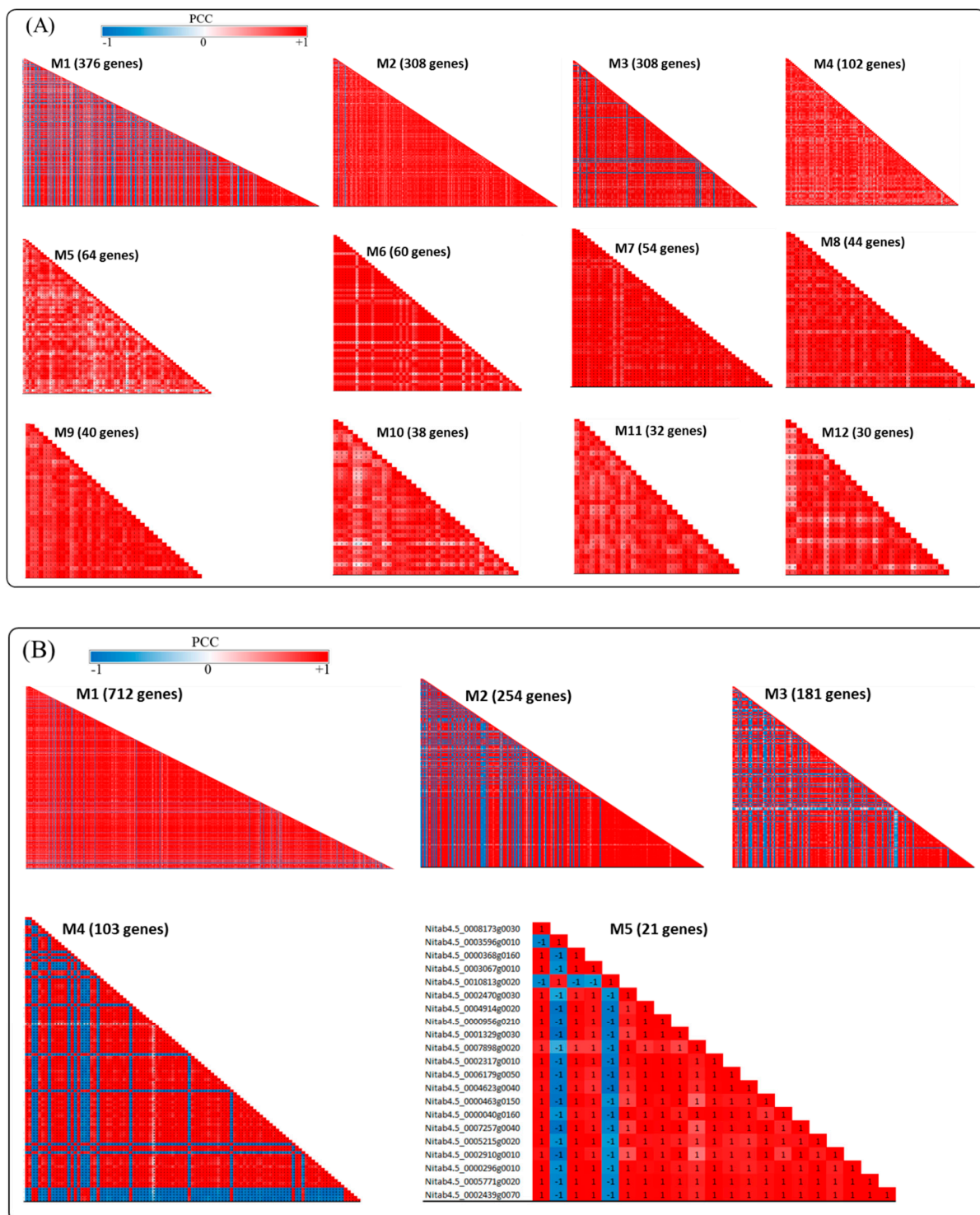
(E) TPS-g (1 gene)



Supplementary Figure S2. KEGG annotation of the 160 TPS identified in the tobacco genome. Functional classification of the annotated TPS (A). KEGG orthology (KO) annotation of the 66 TPS genes



Supplementary Figure S3. Heatmap of Pearson correlation coefficient (PCC) analysis of gene expression of members of each identified co-expression module in (A) diurnal global transcriptome and (B) topping transcriptome of tobacco genes.



Supplementary Figure S4. Pearson correlation coefficient (PCC) analysis of gene expression of members of each terpene-related biosynthetic gene clusters in diurnal global transcriptome of tobacco genes. Cluster number represents the cluster number indicated in Supplementary Table S1.

Supplementary Table S1. Gene members of each terpene-related metabolic gene clusters (MGCs) in tobacco genome.

Member Number	Cluster ID	Chromosome Number	Gene ID	Annotation
1	Cluster 9	Nt07	Nitab4.5_0001026g0020	Expansin/pollen allergen, DPBB domain, RlpA-like double-psi beta-barrel domain, Major pollen allergen Lol pI, Expansin, cellulose-binding-like domain, Expansin/Lol pI, Barwin-like endoglucanase
2		Nt07	Nitab4.5_0001026g0060	Terpenoid synthase, Terpene synthase, N-terminal domain, Terpene synthase, metal-binding domain, Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid
3		Nt07	Nitab4.5_0001026g0050	Terpenoid synthase, Terpene synthase, N-terminal domain, Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid, Terpene synthase, metal-binding domain
4		Nt07	Nitab4.5_0001026g0040	Peptidase C48, SUMO/Sentrin/Ubl1
5		Nt07	Nitab4.5_0001026g0030	
6		Nt07	Nitab4.5_0001026g0070	GDP dissociation inhibitor, Rab GDI protein
1	Cluster 18	Nt10	Nitab4.5_0003002g0010	Chloramphenicol acetyltransferase-like domain, Transferase
2		Nt10	Nitab4.5_0003002g0020	Homeodomain-like
3		Nt10	Nitab4.5_0003002g0030	Chloramphenicol acetyltransferase-like domain, Transferase
4		Nt10	Nitab4.5_0004942g0020	
5		Nt10	Nitab4.5_0004942g0010	
6		Nt10	Nitab4.5_0000696g0060	Terpenoid synthase, Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid, Terpene synthase, metal-binding domain, Terpene synthase, N-terminal domain
7		Nt10	Nitab4.5_0000696g0050	
8		Nt10	Nitab4.5_0000696g0040	
1	Cluster 21	Nt13	Nitab4.5_0000404g0170	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid, Prenyltransferase/squalene oxidase

2	Cluster 22	Nt13	Nitab4.5_0000404g0180	Protein kinase-like domain, Protein kinase domain, Serine/threonine- / dual specificity protein kinase, catalytic domain, Protein kinase, ATP binding site, Serine/threonine-protein kinase, active site, Glycosyl transferase, family 1, Concanavalin A-like lectin/glucanase, subgroup
3		Nt13	Nitab4.5_0000404g0190	Pentatricopeptide repeat
4		Nt13	Nitab4.5_0000404g0200	Cytochrome P450, Cytochrome P450, E-class, group I, Cytochrome P450, conserved site
5		Nt13	Nitab4.5_0000404g0240	rRNA-processing arch domain, Helicase, superfamily 1/2, ATP-binding domain, Helicase, C-terminal, DSH, C-terminal, RNA helicase, ATP-dependent, SK12/DOB1, P-loop containing nucleoside triphosphate hydrolase, DNA/RNA helicase, DEAD/DEAH box type, N-terminal
1		Nt13	Nitab4.5_0001461g0040	NAC domain
2		Nt13	Nitab4.5_0001461g0060	Lactate/malate dehydrogenase, N-terminal, NAD(P)-binding domain, Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal, Malate dehydrogenase, type 2, Malate dehydrogenase, active site, Lactate/malate dehydrogenase, C-terminal
3		Nt13	Nitab4.5_0001461g0050	Terpenoid synthase, Terpene synthase, metal-binding domain, Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid, Terpene synthase, N-terminal domain
4		Nt13	Nitab4.5_0001461g0070	Cytochrome P450, Cytochrome P450, E-class, group I, Cytochrome P450, conserved site
5		Nt13	Nitab4.5_0001461g0080	
6		Nt13	Nitab4.5_0001461g0110	
7		Nt13	Nitab4.5_0001461g0090	
8		Nt13	Nitab4.5_0001461g0140	Terpenoid synthase, Terpene synthase, metal-binding domain
9		Nt13	Nitab4.5_0001461g0120	Terpenoid synthase, Terpene synthase, metal-binding domain
10		Nt13	Nitab4.5_0001461g0100	Terpenoid synthase, Terpene synthase, metal-binding domain, Terpene synthase, N-terminal domain, Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid

11	Cluster 23	Nt13	Nitab4.5_0001461g0130	Cytochrome P450, Cytochrome P450, E-class, group I, Cytochrome P450, conserved site
12		Nt13	Nitab4.5_0004794g0010	Terpene synthase, N-terminal domain, Terpene synthase, metal-binding domain, Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid, Terpenoid synthase
13		Nt13	Nitab4.5_0004794g0030	Terpenoid synthase, Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid, Terpene synthase, metal-binding domain, Terpene synthase, N-terminal domain
14		Nt13	Nitab4.5_0004794g0020	Terpenoid synthase, Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid, Terpene synthase, N-terminal domain, Terpene synthase, metal-binding domain
15		Nt13	Nitab4.5_0004794g0040	AMP-binding, conserved site, AMP-binding enzyme C-terminal domain, AMP-dependent synthetase/ligase
1		Nt14	Nitab4.5_0000037g0010	Pentatricopeptide repeat, Tetratricopeptide-like helical
2		Nt14	Nitab4.5_0000037g0030	AMP-binding, AMP-binding, conserved site, AMP-dependent synthetase/ligase
3		Nt14	Nitab4.5_0000037g0020	Leucine-rich repeat-containing N-terminal, type 2, Protein kinase domain, Protein kinase, ATP binding site, Protein kinase-like domain, Serine/threonine- / dual specificity protein kinase, catalytic domain, Serine/threonine-protein kinase, active site, Leucine-rich repeat, Concanavalin A-like lectin/glucanase, subgroup, Leucine-rich repeat, typical subtype
4		Nt14	Nitab4.5_0000037g0060	Terpene synthase, metal-binding domain, Terpenoid synthase, Terpene synthase, N-terminal domain, Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid
5		Nt14	Nitab4.5_0000037g0070	Terpenoid synthase, Terpene synthase, metal-binding domain
6		Nt14	Nitab4.5_0000037g0040	Ribosomal protein S18
7		Nt14	Nitab4.5_0000037g0050	Terpenoid synthase, Terpene synthase, metal-binding domain
8		Nt14	Nitab4.5_0000037g0080	Terpenoid synthase, Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid
1	Cluster 24	Nt14	Nitab4.5_0000037g0100	Terpene synthase, N-terminal domain, Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid
2		Nt14	Nitab4.5_0000037g0110	Terpenoid synthase, Terpene synthase, metal-binding domain
3		Nt14	Nitab4.5_0000037g0120	

4	Cluster 32	Nt14	Nitab4.5_0000037g0150	Nucleic acid-binding, OB-fold
5		Nt14	Nitab4.5_0000037g0130	Nucleic acid-binding, OB-fold
6		Nt14	Nitab4.5_0000037g0140	EF-Hand 1, calcium-binding site, UDP-glucuronosyl/UDP-glucosyltransferase
7		Nt14	Nitab4.5_0000037g0170	
8		Nt14	Nitab4.5_0000037g0180	Xyloglucan endotransglucosylase/hydrolase, Xyloglucan endo-transglycosylase, C-terminal, Glycoside hydrolase, family 16, Concanavalin A-like lectin/glucanase, subgroup, Glycoside hydrolase, family 16, active site, Concanavalin A-like lectin/glucanases superfamily
9		Nt14	Nitab4.5_0000037g0190	Tic22-like
10		Nt14	Nitab4.5_0000037g0160	Zinc finger, C2H2
11		Nt14	Nitab4.5_0000037g0200	Cytochrome P450, Cytochrome P450, conserved site, Cytochrome P450, E-class, group I
12		Nt14	Nitab4.5_0000037g0210	Cytochrome P450, E-class, group I, Cytochrome P450
13		Nt14	Nitab4.5_0000037g0230	
14		Nt14	Nitab4.5_0000037g0220	
1		Nt22	Nitab4.5_0000418g0010	Cytochrome P450, Cytochrome P450, conserved site, Cytochrome P450, E-class, group I
2		Nt22	Nitab4.5_0000418g0020	
3		Nt22	Nitab4.5_0000418g0030	Zinc finger, CW-type, SET domain, Post-SET domain
4		Nt22	Nitab4.5_0000418g0050	Transcription factor, K-box, Transcription factor, MADS-box
5		Nt22	Nitab4.5_0000418g0040	GDP-fucose protein O-fucosyltransferase
6		Nt22	Nitab4.5_0000418g0060	Terpenoid synthase, Terpene synthase, metal-binding domain, Terpene synthase, N-terminal domain, Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid

7	Nt22	Nitab4.5_0000418g0070	Terpene synthase, metal-binding domain, Terpenoid synthase
8	Nt22	Nitab4.5_0000418g0080	
9	Nt22	Nitab4.5_0000418g0090	Cytochrome P450
10	Nt22	Nitab4.5_0000418g0100	Cytochrome P450
11	Nt22	Nitab4.5_0000418g0110	Decaprenyl diphosphate synthase-like
12	Nt22	Nitab4.5_0000418g0120	Ribonuclease H-like domain
13	Nt22	Nitab4.5_0000418g0130	Terpene synthase, metal-binding domain, Terpene synthase, N-terminal domain, Terpenoid synthase, Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid
14	Nt22	Nitab4.5_0000418g0170	Terpenoid synthase, Terpene synthase, metal-binding domain
15	Nt22	Nitab4.5_0000418g0150	Terpene synthase, metal-binding domain, Terpenoid synthase
16	Nt22	Nitab4.5_0000418g0140	Terpenoid synthase, Terpene synthase, metal-binding domain
17	Nt22	Nitab4.5_0000418g0160	Decaprenyl diphosphate synthase-like, Di-trans-poly-cis-decaprenylcistransferase-like, conserved site
18	Nt22	Nitab4.5_0003459g0020	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid, Terpene synthase, N-terminal domain, Terpenoid synthase, Terpene synthase, metal-binding domain
19	Nt22	Nitab4.5_0003459g0030	Terpenoid synthase, Terpene synthase, metal-binding domain
20	Nt22	Nitab4.5_0003459g0010	Cytochrome P450, E-class, group I, Cytochrome P450, Cytochrome P450, conserved site