

Supplementary Information

Diversity and function of terpene synthases in the production of carrot aroma and flavor compounds

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SUPPLEMENTARY TABLES

Supplementary Table S1. Volatile terpenes from carrot tissues (n=3, three individual plants) quantified by GC-FID using multi point internal standard calibration curves of authentic α -pinene and α -humulene. Identification was based on comparison to mass spectral libraries (NIST, Wiley) and comparison (*) to authentic standards or compounds in an Opopanax essential oil. Values are reported as micrograms per gram fresh weight.

Compound	Leaf	Petiole	Root	Root Phloem	Root Xylem
α -pinene*	6.00 ± 0.39	3.71 ± 0.12	1.19 ± 0.01	1.01 ± 0.01	1.06 ± 0.00
camphene*	0.26 ± 0.07	0.17 ± 0.09	trace	trace	trace
β -pinene*	0.59 ± 0.00	0.30 ± 0.00	0.21 ± 0.02	0.07 ± 0.00	0.07 ± 0.02
β -myrcene*	3.54 ± 0.44	0.40 ± 0.35	0.07 ± 0.07	0.08 ± 0.04	0.10 ± 0.04
p-cymene	0.06 ± 0.20	0.05 ± 0.02	0.05 ± 0.03	trace	trace
limonene*	0.46 ± 0.00	0.29 ± 0.05	0.09 ± 0.00	0.05 ± 0.02	0.08 ± 0.03
(E)- β -ocimene*	1.87 ± 0.4	0.43 ± 0.1	trace	trace	trace
α -terpinolene*	0.1 ± 0.02	0.06 ± 0.03	0.85 ± 0.10	0.03 ± 0.00	0.02 ± 0.02
γ -terpinene*	0.88 ± 0.30	0.76 ± 0.05	0.41 ± 0.20	0.39 ± 0.09	0.39 ± 0.20
(E)- β -caryophyllene*	12.73 ± 0.10	5.61 ± 0.20	2.13 ± 1.17	1.22 ± 0.40	1.70 ± 1.40
δ -elemene	4.57 ± 0.60	1.41 ± 0.06	0.05 ± 0.00	0.07 ± 0.02	0.20 ± 0.01
α -humulene*	0.92 ± 0.02	0.36 ± 0.03	0.12 ± 0.08	0.12 ± 0.06	0.17 ± 0.13
germacrene-D*	4.26 ± 0.93	0.68 ± 0.15	0.02 ± 0.00	0.03 ± 0.01	0.04 ± 0.03
β -bisabolene*	1.34 ± 0.02	0.45 ± 0.06	0.08 ± 0.00	0.13 ± 0.03	0.35 ± 0.02

Supplementary Table S2. Predicted transit peptides based on ChloroP (v1.1) analysis of predicted full-length *DcTPS* proteins.

Name	Length	cTP	cTP-length (amino acids)
<i>DcTPS01</i>	560	-	-
<i>DcTPS02</i>	594	Y	36
<i>DcTPS03</i>	589	Y	40
<i>DcTPS04</i>	608	Y	43
<i>DcTPS05</i>	550	-	-
<i>DcTPS07</i>	563	-	-
<i>DcTPS09</i>	589	Y	33
<i>DcTPS10</i>	588	Y	34
<i>DcTPS11</i>	551	-	-
<i>DcTPS12</i>	551	-	-
<i>DcTPS13</i>	566	-	-
<i>DcTPS14</i>	647	-	-
<i>DcTPS15</i>	577	-	-
<i>DcTPS16</i>	632	-	-
<i>DcTPS17</i>	551	-	-
<i>DcTPS19</i>	562	Y	37
<i>DcTPS21</i>	551	-	-
<i>DcTPS23</i>	553	-	-
<i>DcTPS25</i>	826	Y	59
<i>DcTPS26</i>	570	-	-
<i>DcTPS27</i>	593	Y	44
<i>DcTPS28</i>	769	-	-
<i>DcTPS29</i>	836	-	-
<i>DcTPS30</i>	609	Y	43
<i>DcTPS32</i>	554	-	-

<i>DcTPS33</i>	593	Y	17
<i>DcTPS38</i>	567	-	-
<i>DcTPS42</i>	541	-	-
<i>DcTPS43</i>	562	-	-
<i>DcTPS44</i>	582	-	-
<i>DcTPS45</i>	517	-	-
<i>DcTPS46</i>	534	-	-
<i>DcTPS47</i>	512	-	-
<i>DcTPS48</i>	587	Y	39
<i>DcTPS52</i>	587	Y	26
<i>DcTPS53</i>	560	-	-
<i>DcTPS54</i>	588	Y	43
<i>DcTPS55</i>	598	Y	34
<i>DcTPS56</i>	804	-	-
<i>DcTPS57</i>	763	Y	78
<i>DcTPS59</i>	772	-	-
<i>DcTPS60</i>	554	-	-
<i>DcTPS62</i>	506	-	-

Supplementary Table S3. qRT-PCR primers used in this study.

Primer Name	Primer Seq	Tm	Amplicon (bp)
<i>DcTPS01F_int</i>	CAACATCTTCAGCTTCTACC	53.7	281
<i>DcTPS01R_int</i>	CATACGCTGCAACACAGC	57.2	281
<i>DcTPS02F_int</i>	CTAACACTTGTGCTCTAAACC	55.3	248
<i>DcTPS02R_int</i>	CAGCAGCTCCAGCTTGTC	58.4	248
<i>DcTPS32F_int</i>	GTTTGGGAGGTTCAAAGATG	54.5	391
<i>DcTPS32R_int</i>	CCATGCTCCCTGAGC	52.9	391
<i>DcTPS45F_int</i>	CTTTGAATTGCGGAAAACCTC	54.6	276
<i>DcTPS45R_int</i>	CTTGATCCATTGCCTTATACTGGC	59.8	276
<i>DcTPS46F_int</i>	GGTGAAGAACGTGGTACG	55.5	218
<i>DcTPS46R_int</i>	CGAAGTTGTAAAAACATCTGC	57.1	218
<i>DcTPS19F_int</i>	GATATGGCAAATATTAAGCGTG	53.8	384
<i>DcTPS19R_int</i>	GCGGCTCAAGTATTCA	52.5	384
<i>DcTPS25F_int</i>	CCATCCCTCCTCCTCC	53.9	301
<i>DcTPS25R_int</i>	CGACGAATGAAGCTTAGTGTTC	58.9	301
<i>DcTPS30F_int</i>	GCATGAGGTTCTCTTCATTG	54.4	292
<i>DcTPS30R_int</i>	CTCACAAATTCTCTTCAATCC	52.1	292
<i>DcTPS09F_int</i>	GCTGCACCTCCCCG	55.8	251
<i>DcTPS09R_int</i>	GCATGGATCAGAACGCTCG	56.5	251
<i>DcTPS04F_int</i>	GTGAGTGTGGTATGAGTTTCTG	58.6	286
<i>DcTPS04R_int</i>	CCTTCAAATCCCTGC	51.2	286
<i>DcTPS26F_int</i>	CTGCACTAGGAATGATACTGC	56.2	325
<i>DcTPS26R_int</i>	CCACTTGTCAATTCTGTTAC	55.4	325
<i>DcTPS56F_int</i>	CAGGGGAGAAAAGAAAGAACATC	54.2	297
<i>DcTPS56R_int</i>	CTCAAGAAAATGTGTACCCC	53.9	297
<i>DcTPS28F_int</i>	CTTTCACCCAAATTCTTACATAC	53.7	281
<i>DcTPS28R_int</i>	CATCCTTAAGTTGATTTCCAATATC	55	281
<i>DcTPS14F_int</i>	CACGGTCTTTTCCCC	52.8	334
<i>DcTPS14R_int</i>	GCCTATGAACAGAGTCGAG	54.8	334
<i>DcTPS17F_int</i>	CACACACTGCCAGTTC	52.1	291
<i>DcTPS17R_int</i>	GATTTCCCAGTGATTATTATTTG	52.5	291
<i>DcTPS57F_int</i>	CATTCCACGTCTTCTTACTTGC	58.3	345
<i>DcTPS57R_int</i>	CAGAACATTTATCTCCATCGTC	55.9	345
<i>DcTPS59F_int</i>	GACATAATTACACAGGATTG	53.1	326
<i>DcTPS59R_int</i>	CTTGAAGGGAACATAGGTAGTCC	58	326
<i>DcTPS23F_int</i>	GTTAGGCAAGAACTCAAGG	53.3	355
<i>DcTPS23R_int</i>	CTTCATCTTCTATCCTCAGC	52.6	355

DcTPS60F_int	GCTAATAACAAGGTAGGAATCG	54.5	331
DcTPS60R_int	GTTCCTCACTAGCTTCTCCTTG	59.9	331
DcTPS44F_int	GCCTTGGATCATTCAGTTG	55.7	303
DcTPS44R_int	CAATAAGCTCCAACCTTCCC	55.1	303
DcTPS29F_int	CTCTCCACAGCTACAAATTG	54.6	335
DcTPS29R_int	CTGAAAAACGATGGTAAAC	52.8	335
DcTPS16F_int	GAACCTTCCTCAGTTGGG	55.6	289
DcTPS16R_int	CTAAATCATTGATACTCCACGC	55.1	289
DcTPS15F_int	GTTCTCACACATAAGGCTG	58.6	307
DcTPS15R_int	CAAAGCTCATGATACGAATC	52.2	307
DcTPS38F_int	GGAACAAAATGCTGGGG	53.2	329
DcTPS38R_int	CGACCATGAAAAGGCC	52.2	329
DcTPS42F_int	CAGTCTCGGCCATTGCG	58.2	319
DcTPS42R_int	CTTAAGATTGGAAGTAAAGTGC	55.7	319
DcTPS10F_int	CATCTATAATTTCCCAGTTCAAC	54.7	330
DcTPS10R_int	CAACTCTCTGCAACTGATC	53.4	330
DcTPS11F_int	GCTAAAACAGGAAGTGAAG	51.4	395
DcTPS11R_int	GAGAGGTGTTAAATTCAAGAG	53.7	395
DcTPS03F_int	CTATAGTCCACATTCTCCCC	54.9	377
DcTPS03R_int	CTTCAGGCACGTTCTATTTC	55.3	377
DcTPS07F_int	CATACTGTAACTCGTCGC	52.8	338
DcTPS07R_int	GTTGTTGTCCTGAACTTGTAG	55.5	338
DcTPS53F_int	GTAAACGCTGCAACTGG	53.8	353
DcTPS53R_int	CTTAGTGCAACATCATGAAATTATC	55.3	353
DcTPS12F_int	GCTGCCTGTTATTAGACG	52.9	339
DcTPS12R_int	CCATGTTGTCAGAGTC	53	339
DcTPS48F_int	CTCCATTAGTCACCTGCTGC	58.3	282
DcTPS48R_int	GATCTAGCGGCTAACAG	54.9	282
DcTPS13F_int	GTGTGCCTGAGATTGTCG	56.7	339
DcTPS13R_int	GTAAACCGGAAGCAAAGAG	53.1	339
DcTPS21F_int	CAGGCGTTGGGAATTAC	58.6	361
DcTPS21R_int	CATAAAACTCTGAATATCTTC	51.6	361

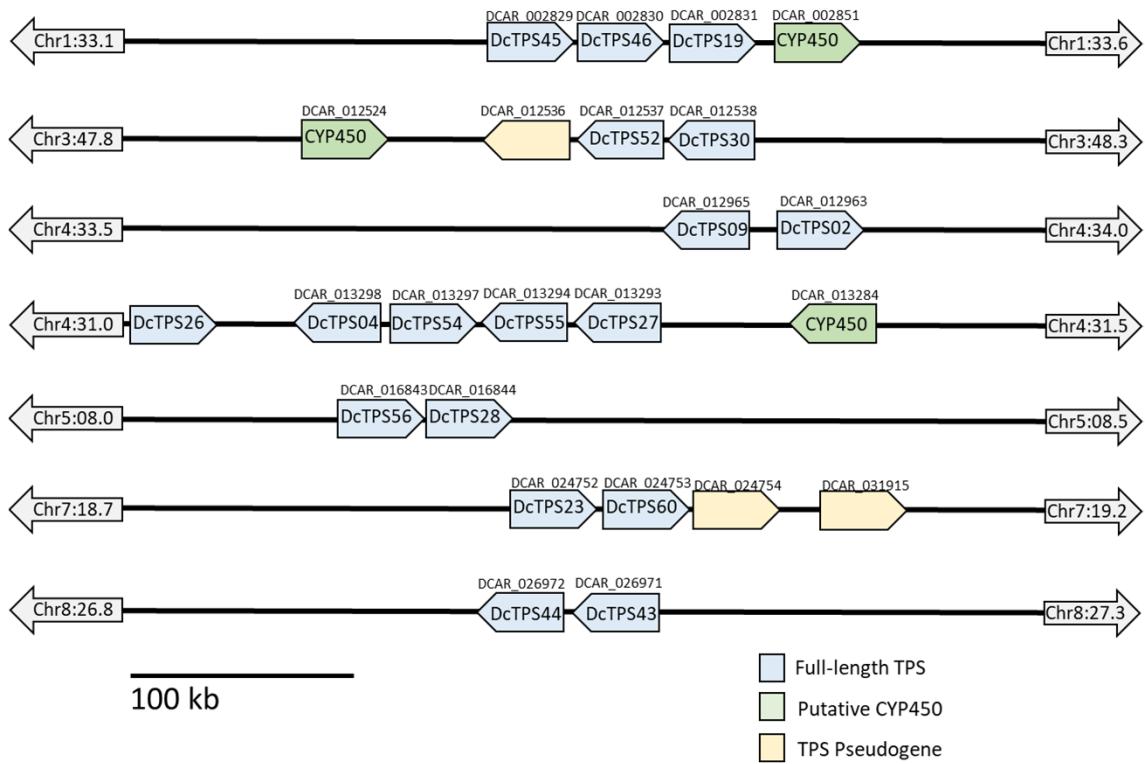
Supplementary Table S4. Primers for gene cloning.

Primer Name	Primer Seq	Purpose
DcActin_F	CGGTATTGTGTTGGACTCTGGTGAT	Housekeeping gene
DcActin_R	CAGCAAGGTCAAGACGGAGTATGG	Housekeeping gene
DcPP2A_F	GTGTATCAATGTACCACCAGCAACT	Housekeeping gene
DcPP2A_R	GCTCACCAAGGAACATGACTTCTT	Housekeeping gene
Tubulin_F	TCTTGGAGGTGGCACAGGAT	Housekeeping gene
Tubulin_R	ACCTTAGGAGACGGAACACAGA	Housekeeping gene
DcTPS1_F	ATGTCTCTCAATGTTCTGGC	Control TPS
DcTPS1_R	TGATGGAACCCGATCAATGA	Control TPS
DcTPS19_F	GGATCCATGTTAACACAGGCACAAG	Cloning
DcTPS19_R	CTCGAGTCACAAATTAAAGGTAAAAC	Cloning
DcTPS25_F	GGATCCATGACTGCAGTTCAAG	Cloning
DcTPS25_R	CTCGAGTTACATCCTACGGCC	Cloning
DcTPS23_F	GGATCCATGGCGATTGTTAGG	Cloning
DcTPS23_R	CTCGAGCTAGAACAAATTGTTCCC	Cloning
DcTPS16_F	GGATCCATGGCTGCAGTACTG	Cloning
DcTPS16_R	CTCGAGTTAACCAAGAGTTAC	Cloning
DcTPS04_TCF	GGATCCATGATGGAAAGAGTTCTTG	Cloning
DcTPS04_TCR	CTCGAGTCAGGTGATCGAAAGAGGTTC	Cloning
DcTPS05F_TC	GAATTCATGAGTACTCTTATTGTGAATC	Cloning
DcTPS05R_TC	GTCGACTTACAGAAGAACAGG	Cloning
DcTPS03F_TC	GGATCCATGGTTCTCAATCC	Cloning

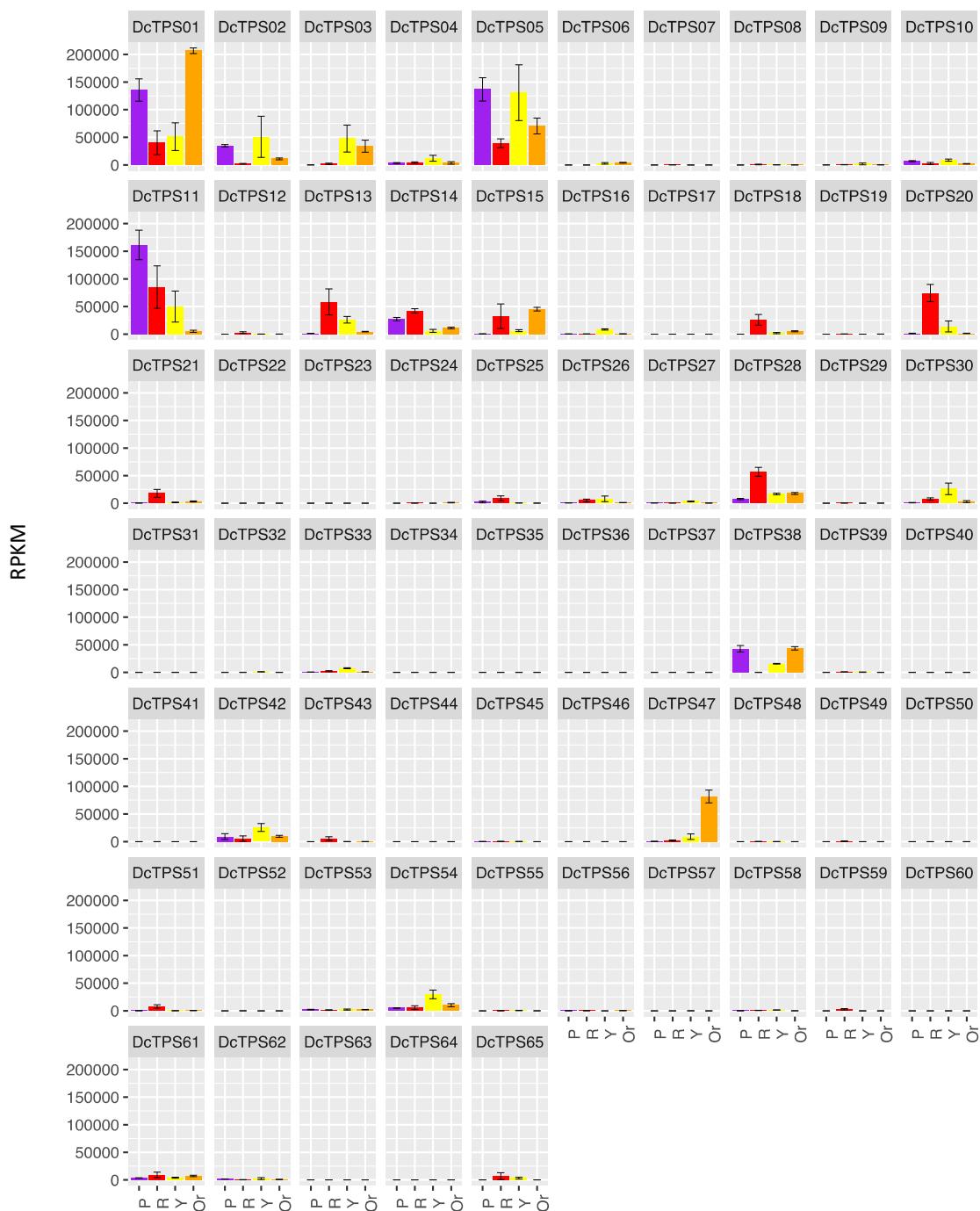
DcTPS03R_TC	GTCGACTCATATATCGATGGGGTC	Cloning
DcTPS07R_TC	GGATCCATGAATTCTACTTCTGG	Cloning
DcTPS07F_TC	CTCGAGTTATAGGAAAAGGGTC	Cloning
DcTPS53R_TC	GGATCCATGGCTATGTATGTTAACG	Cloning
DcTPS53F_TC	CTCGAGTTATGCTGGAATCGGATC	Cloning
DcTPS03B_TCF	GGATCCATGTCCATGGGAATTCTG	Cloning
DcTPS03B_TCR	GTCGACTCAGTCAATATCGATGGGG	Cloning
DcTPS53B_TCR	CTCGAGTTACCCCTGAAATCGGATC	Cloning
DcTPS48_F	GGATCCATGGAGGGATCTGTCACCAAG	Cloning
DcTPS48_R	GTCGACTCATATAGGCTAACAAAGAAGGG	Cloning
DcTPS14_R	CTCGAGTCACTCATTAAGAGTGAAGG	Cloning
DcTPS42_F	GAGCTCATGAGCAGCCAGTCTCG	Cloning
DcTPS42_R	GTCGACTCATATCGGTATCGGATCCACC	Cloning
DcTPS11_F	GGATCCATGGCTCAAGTGTGGG	Cloning
DcTPS42_R	CTCGAGTTATGCTGGAATGGGATTATG	Cloning
DcTPS10_F	CTCGAGATGGCGCTGAAACAAAC	Cloning
DcTPS10_R	GTCGACTCAGAGAGGGATGGGCTC	Cloning
DcTPS30_F	GGATCCATGTGCAGTAGCAGTAGTCATG	Cloning
DcTPS30_R	CTCGAGCTATAGAGGTATGGGTCAAC	Cloning
DcTPS15_F	GAGCTCATGTCGTGTTCTCAGGC	Cloning
DcTPS15_R	GTCGACTCATATTGAGATGGATCCACTAG	Cloning
DcTPS38_F	CTCGAGATGTCGGCTTCAGCAGG	Cloning
DcTPS38_R	GTCGACTTAGACAAGTTGTCAGG	Cloning
DcTPS28_F	GGATCCATGGCCTACTGGAGTC	Cloning
DcTPS28_R	CTCGAGCTATACTGGTAATAGGTTG	Cloning

Supplementary Table S5. Terpene compounds identified from random forest analysis and Boruta variable selection of colored carrot root tissue. ANOVAs comparing the concentrations of the selected compounds among groups are reported (F-statistic and p value). All compounds were identified by comparison to authentic standards or compounds in an Opopanax essential oil except bornyl acetate, which was identified by comparison to mass spectral libraries.

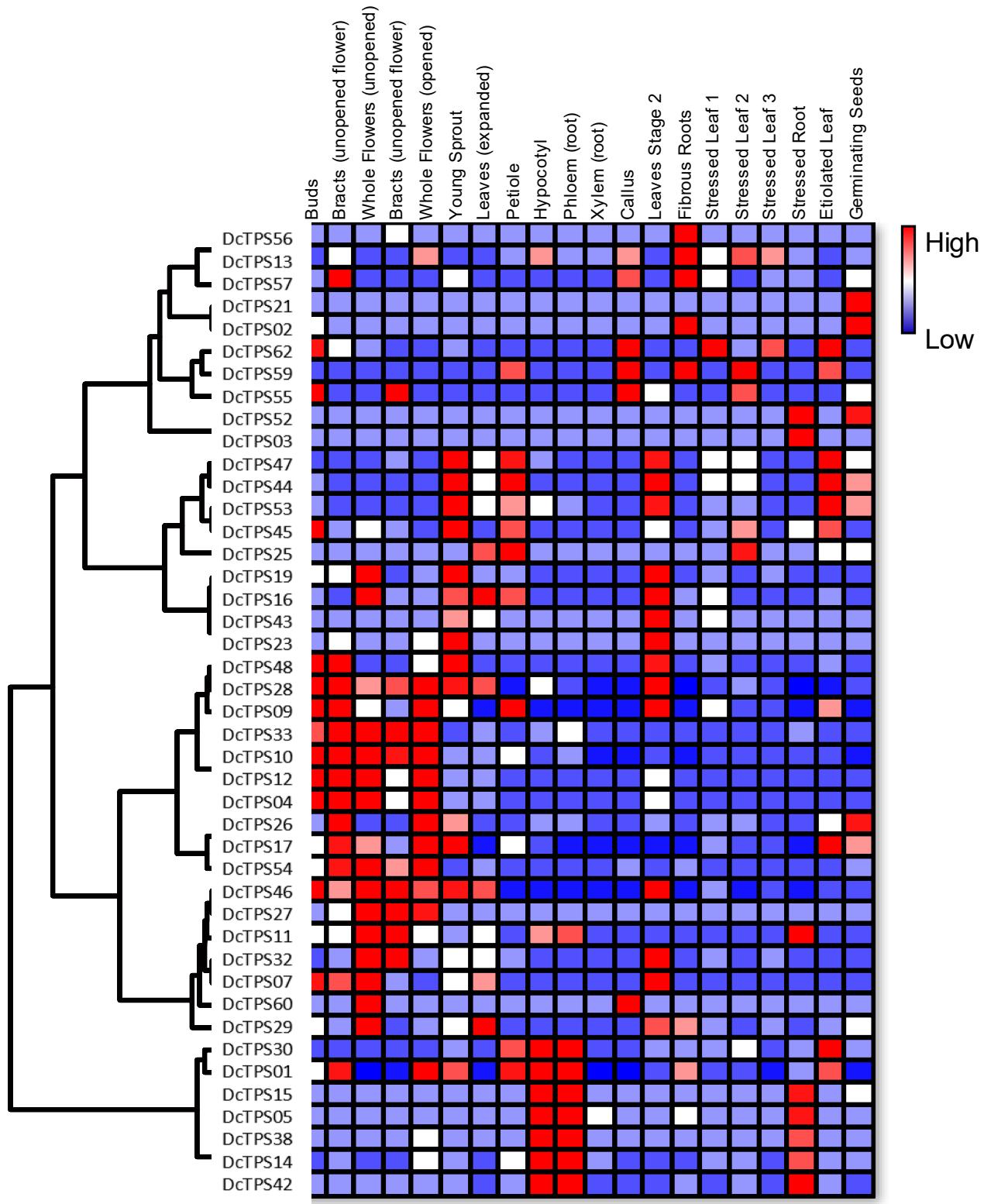
Compound	Boruta IMP Factor	F Value	p Value
α -pinene	4.7437306	3.6368	6.40E-02
β -pinene	4.9868365	4.7613	3.448e-02*
α -terpinolene	7.2058394	4.1936	4.659e-02*
bornyl acetate	8.1511563	20.344	4.228e-04***
(E)- β -farnesene	8.003681	21.099	3.721e-04***
(E)- β -caryophyllene	7.2949134	42.36	2.955e-05***
α -humulene	5.5921902	30.176	1.034e-04***
β -bisabolene	4.4540192	12.795	2.022e-03**
(E)- γ -bisabolene	6.7570118	8.3796	7.506e-03**



Supplementary Figure S1. Diagram of 7 gene clusters identified in the DH1 carrot genome. Full-length TPSs are highlighted in blue and cluster by TPS sub-family. TPS pseudogenes are highlighted in yellow and putative cytochromes P450 clustered in the similar chromosomal region are listed. Chromosomal positions are indicated by gray arrows in Mbp.



Supplementary Figure S2. RNA-seq analysis of the 65 TPS gene models predicted by Keilwagen et al.¹⁹ across four colored carrot varieties. Gene expression is presented as reads per kilobase of transcript per million mapped reads (RPKM). P: purple (cv. P7262), R: red (cv. R6637), Y: yellow (cv. Y9244A) and O: orange (cv. B493B).



Supplementary Figure S3. Hierarchical cluster analysis of TPS gene expression profiles across DH1 carrot tissues. Heat map comparing relative transcript abundance for all 43 TPS genes candidate in FPKM (Fragments Per Kilobase of transcript per Million mapped reads) in 20 tissues. Specific gene expression data sets are from Iorizzo et al.¹⁸.

Supplementary Figure S4. Amino acid sequence alignment of proteins in the carrot TPS-a subfamily and other select TPSs of this subfamily. Alignments were performed using Clustal W⁴³ and visualized with BoxShade (v3.21, https://embnet.vital-it.ch/software/BOX_form.html); At, *Arabidopsis thaliana*; Aa, *Artemisia annua*; Dc, *Daucus carota*.

DcTPS16	1	-----MAAVLHALSSVGRQCSLFETDILDAPRFSNYLHKPGRVQOMAGLQFIATRRHEKCQSCYTSNR
At_mycene_s	1	-----MATLCIGSAPIYQNACIHNFLQRPRFISKSM
DcTPS14	1	MPIFKLRRSQLIFNYFFHLERCIYEIWCNLCEENKIYNKLLTYRIQKRSFSCQTIPKQMALHGLFSPFLVTAPSRAIPSSNAPKLCAS
DcTPS09	1	-----MVMAVQGLFSSFLIAAPPRI-PPLPFARTGSKI
DcTPS32	1	-----MCLGGSKMTR-----
DcTPS33	1	-----MALKGLSSTLLVTLALPRSSVPSSGRNH-NKSF
DcTPS02	1	-----MALPALFSTFIVTAPPRTSLSLARNP--SNT
DcTPS62	1	-----MPAITSVIVH-----
Sf_cineole_s	1	-----MSSLIMQVVIPKPAKIFHHNNLFSVISKRHRFSTTITTR
Mc_linalool_s	1	-----MCTIISVNHHHVAILSKPKVKLFHTKNKRSASINLPWSLSPSS
So_bornylPP_s	1	-----MSIISMNVSIILSKPLNCLHNLERPSKALVPCAT
DcTPS26	1	-----MHHTSSHCTR-----
DcTPS55	1	-----MSSSATRMVKAFAASLTLQOPPSKAIHTTISTCCTS
DcTPS54	1	-----MALISTVSLGMSFSATRF-MVKPAASLTLLKPPSTKAIHNTSIRSTS
DcTPS04	1	-----MVLVSTVSVGMSFSATRFMVKAFAASFTLLKPPSTKAIHNTSIRCTSN
DcTPS27	1	-----MAVISTVSLGVVISATRLLKPPSTKAIHNTSIRCTGN
DcTPS30	1	-----MAISMSVNLGMRFSSLHSMILKETSFTCVNPSSNAKKVFVEGIRCS
DcTPS52	1	-----MLKPTSFASVNRSTTAGKV-----
DcTPS17	1	-----MNRLLAHDHT-----
DcTPS21	1	-----MSTLIADQ1F-----
DcTPS05	1	-----MSTLIVNHS-----
DcTPS12	1	-----MSTLIAKHQ-----
DcTPS03	1	-----MAASTIVHISPLTIGSQSTLPLRTPGITKSVACKS
DcTPS48	1	-----MASAFILNSPLVTCNCNRRLSPLCKPKFLTLSKS
DcTPS10	1	-----MASIIFPVSTLINQRFITCKPKAATACKS
DcTPS47	1	-----MWKLEKFRFSDFVLMNDNHIHTLIVQLASC-----
DcTPS16	63	ESIQPVSAASESQATVIPAASEVASAQSVAAPA
At_mycene_s	34	-----W SINDLAAQLKFKNYKQDEVYEQMATEKIEIEIRMTIEDEMASNPNINFELIDNIER
DcTPS14	34	NPLDLRRSGNYQPSSW-DHSYLLSIENK-YV-NKEVITRHVLKKVKKMPEEVETKSRLEKLELDDLCK
DcTPS09	91	K-----PVQCITTPVTTTDHQGSASRRNANYVPSW-DYNVWVKSLSSEN-YD-EKKYEMQVEVKRLIHA-ETDVEPLAKLELDDSVHR
DcTPS32	33	CATKPVCQCIKTTDV-----HQGSGSRRNANYPPSSW-DYNFVKSLSND-FT-EK-YARQDLEKDDVVKRLIYA-ETDVEPLAKLELDDSVQR
DcTPS33	11	-----DQGAALRRRNANYPPSSW-DYNFVKSLSND-FT-EK-YARQDLEKDDVVKRLIYA-ETDVEPLAKLELDDSVQR
DcTPS02	31	ATERSVOC1KTATTATIDQDGAALRRRNANYPPSSW-DYNFVKSLSND-YT-EK-YARQDLEKDDVVKRLIHAETDPP-LAKLELDDSVQR
DcTPS62	30	CALKPVQCIMTNPKTNPDQGTPSRRNANYAPSWE-DYSFVKSLSND-YA-EK-YVKQVDDELKDVKSLIHA-ETEV-LDKLELDDSVQR
Sf_cineole_s	11	-----YOLQF---IIIYQNLNVIYFS-GSKICKAG-----
Mc_linalool_s	39	GGRWAHCQLQMG-----NEIQTGRRUHGQYOPTIW-DFSTIQLFDSE-YK-EKHLMRRAAGMIAQVNMLQE-EVDS-IQRLELDDLRR
So_bornylPP_s	45	AASRPICSISSKLYTISSAQEEETRRSGNYHPSW-DPDTIQLSDT-DHYK-EKQLEEEELVKLGA-KMEA-TKOELLEDDLON
DcTPS26	37	TARLRASCSKL-----QEAHQIIRRSGNYOPAW-----DNVYIQLSLNP-YT-EK-HLDRLKAELIVORVRLIKE-KMEP-VQQLLELHDLYK
DcTPS55	12	DTALVNNDTACV-----DDKSIVRRSGNFPPPIW-DDDFVQSLTSD-FK-GEICNKYAGDLKEVRMMLNKEEDTDN-LKKLELVDVSQR
DcTPS54	38	DTALVSRGDACV-----DDKSIVRRSGNYPPPIW-DDDFVQSLASD-FK-GEICNKYAGDLKEVRMMLNKEEDTDN-LRKLELVDVSQR
DcTPS04	48	DTALVSRGDACV-----DGKSIVRRSGNYPPPIW-DDDFVQSLASD-FK-GEICNKYAGDLKEVRMMLNKEEDTDN-LKKLELVDVSQR
DcTPS27	49	DTALLSRGDACV-----DDKSIVRRSGNYPPPIW-DDDFVQSLASD-FK-GEICNKYAGDLKEVRMMLNKEEDTDN-LKKLELVDVSQR
DcTPS30	46	SSSHDSAVVSTGNVS-----DEVSDGRRSGNYPPSW-DYDFFQSLSSD-FK-GEICNKKANGLKEIVRMMLDKEEDLDS-LHKLELIDTIQR
DcTPS52	20	VKISSIRCSTR-----DKSIGRRSGNSYPSYPPSW-DYDFEIQSLASS-FK-GEICSRQACELKENVRFELNEDLDS-LHKLELVDAIQR
DcTPS17	11	-----PVLLRSGNYKPCBFRHNNNIVQSLITE-YK-IERFKGRVDKLREDVEMFND-VSEP-LDQLELDDLQR
DcTPS21	11	-----PVVRRSGNSYKPCWFRDNNNIVQSLND-FK-VERFKERVDELFVGMFAD-IIKS-LDQLELIDALQR
DcTPS05	11	-----PVVRRSGNSYKPCW-DADEFVQTLADL-YT-GERFNGRVNELKGNIGMIND-VAKPNIDRLELIDYLQR
DcTPS12	11	-----PVIIRRSANYOPCW-TNDFVQSLTTD-YT-GERFNGRVNELKENVIEMLND-VAKPNIDRLELIDNLQR
DcTPS03	37	VLIRSSMGISV-----TPEPIIRRSANYOPCW-DNKEIQSLKSD-YT-GEGSKEPASELKEVVRFMKN-VEEP-LDQLEFIDHLQR
DcTPS48	34	VVEFVTGNEGSV-----SPEPIIRRSANYOPCW-DNNEIQSLKTN-YT-GENPANASMLKEEVRMLFDD-AVEP-LDQLELDDLQR
DcTPS10	31	VITSAETTKLPV-----PAEPIVRRSENYKPCW-YT-GEAVDARASELKEBVRMIFNN-VAGP-LEQLELIDQLQR
DcTPS47	30	-----HMW-----KLKKKNRFSDF-----GEAIDARASELKEBVRMIFKN-VAEP-LDQLELIDQLQR
DcTPS16	153	LGIQYRFKEKDISTAFTK-----MVSLEGAPEYHN-----SLHSTALFRLLREHGYEVSO-----DVFQSFKDE-NC-AEPMPL-LADVKG
At_mycene_s	110	LGWSYHFFQEEINNIETN-----FHLENGKNIWKCDEKD-----LHATALEFRLRQHGFVSE-----DIFDVIIDKIESNIEFK----SDNITS
DcTPS14	174	LGINYQOFQDKIJKQATDRI-----CEADSQGN-----DLHSTALFRFLREHGYEVSO-----DVFQKFTDE-TG-KFKANL-CEDVKG
DcTPS09	116	LGIKHLKKDIKQAVDAI-Y-----NNSVDAWLS-----DLHSTALFRFLREHGYEVSO-----DVFQKFTDE-TG-NFKENL-CGDVKG
DcTPS32	79	LGINYQOFQNDVKQAVDVI-Y-----NNISDASLSD-----DLYTALQFRFLREHGYEVSO-----DVFQKFTDE-TG-NFKANL-CEDVKG
DcTPS33	117	LGINHFRQNDVKQAVDVI-Y-----NNINDAWLSD-----DLYTALQFRFLREHGYEVSO-----DVFQKFTDE-TG-NFKANL-CEDVKG
DcTPS02	115	LGIKYQOFQDKIMQAVDVI-----HNNNNNSADAWLSD-----DLYTALQFRFLREHGYEVSO-----DVFQKFTDE-TG-NFKANL-CEDVKG
DcTPS62	37	LGKQYQFQDLKQAVDVI-Y-----NDSADAWLSD-----DLYSTALKFRFLREHGYEVSO-----DVFQKFTDE-TG-NFKANL-CEDVKG
Sf_cineole_s	118	LGESCHFDREIVEITNSKY-----YTNNNEIDES-----DLYSTALKFRFLREHGYEVSO-----DVFQKFTDE-TG-NFKANL-CEDVKG
Mc_linalool_s	131	LGDSYFFRDEIKNI-----NSI-----YKIFQNNNSTKVG-----DLHFVTSGLFRLLRQHGFVSO-----DVFQKFTDE-TG-NFKANL-CEDVKG
So_bornylPP_s	116	LGDSDFQDEIKEI-----GVI-----MNEHKCFHNNNEVEKM-----DLYFTALGFRFLRQHGFVSO-----DVFQKFTDE-TG-NFKANL-CEDVKG
DcTPS26	92	LGVGHFFKNEIIRI-----BEAV-----NKNNDKWDGKD-----NLQANSLKFRLLRQHGFVPO-----EFGDCPKNE-HGSDFEKTIIGEDTRG
DcTPS55	118	LGVGYHFKNEIIRI-----BEAV-----NNEKQYGKD-----NLHATSLKFRLLRQHGFVPO-----EAFSGFLNE-SG-KFKISI-TSDMKG
DcTPS54	116	LGVGYHFKNEIIRI-----BEAV-----STEKWDGQD-----NLHATSLKFRLLRQHGFVPO-----QAFSGFLNE-LG-KFKISI-TSDMKG
DcTPS04	128	LGVGYHFKNEIIRI-----BEAV-----STEKWDGQD-----NLHATSLKFRLLRQHGFVPO-----EAFNGFLNE-SG-KFKISI-TSDMKG
DcTPS27	129	LG-----NNEKWDGQD-----NLHATSLKFRLLRQHGFVPO-----EAFNGFLNE-SG-EFKISI-TSDMKG
DcTPS30	129	LGVGYHFEDEIKR-----BEAI-----HIADEKLSS-----ELNATSLKFRLLRQHGFVPO-----EIFEEFMD-E-SG-KFKISI-SKDMKS
DcTPS52	100	LGVSYHFFKNEIIRI-----BEAV-----YNNNEKFLNSQ-----NLHATSLKFRLLRQHGFVPO-----EAFNGFLNE-SG-KFKISI-TSDMKG
DcTPS17	76	LGVAYYFDEIKR-----BEKI-----FE-DQNNNNHWEIK-----DLHATALKFRLLRQHGFVPO-----DVLSEFMEN-G-SIKECL-WDDVKG
DcTPS21	76	LGIANHFFDEIKR-----KRI-----FE-NRTSDLWEIK-----DLHATALKFRLLRQHGFVPO-----DIFEFMVN-G-SFKEG-SKFCGCL-CEDAKG
DcTPS05	76	LGIGYHFEQEIKS-----TMM-----DPSYETLERN-----DLHGNALFRFLRQHGFVPO-----NVFEYFMEN-G-SFKGCL-CEDAKG
DcTPS12	76	LGIGYHFEQEIKS-----MKI-----MEDDQSSSETLERN-----DLHAAALKFRLLRQHGFVPO-----DVFKYFMEN-G-SFKGCL-CEDAKG
DcTPS03	115	LGVAYHFFDEIKA-----KKI-----HSDDTNNDKWER-----NLHATALKFRLLRQHGFVPO-----EDEKGFTEN-E-RFKESI-DEDVKG
DcTPS48	113	LGTAYHYEEIQRT-----KKI-----QNGEINVDDREK-----DLHATALEFRLFRQHGFVPO-----EGPKQFMSN-G-NPMCS-GADIKG
DcTPS10	111	VGVDYHYRDEINRA-----KSI-----HQNAETWEK-----DLHATALEFRLFRQHGFVPO-----EGFNKFTEN-G-SENKSI-HSDVRG
DcTPS47	81	VGIDYHFQDEIKH-----KSI-----QHNGQNSETTS-----NLHATALKFRLLRQHGFVPO-----

Supplementary Figure S5. Amino acid sequence alignment of proteins in the carrot TPS-b subfamily and other select TPSs of this subfamily. Alignments were performed using Clustal W⁴³ and visualized with BoxShade (v3.21, https://embnet.vital-it.ch/software/BOX_form.html); At, *Arabidopsis thaliana*; Dc, *Daucus carota*; Mc, *Mentha citrata*; Sf, *Salvia fruticosa*; So, *Salvia officinalis*.

DcTPS16 226 LLSLYEASFLAFOQGTTFEDDEI-RSIFARQGZEYVMQKTT---ESKLAKLIGTIAALPWFRTLSEAFRPAHQWYSRM---EDS-NEL-
At_myrcene_s 186 IETLTLAASVLSLKTSKDTKLHKVIRP-AEQIRNPFVDDDESETYNIMPREMAIATIETDHWYRMMRNLWVYDADANKK---HDL-NLF-
DcTPS14 245 LGGLYEAASFIGFOQGEDIIMDOA-KAASEHCKNLLQGNN---LSPIMARKHCHADMPMLWVKEPFWVAVV-----TQE---QNK-IDN-
DcTPS09 189 LLSLYEASFIGFKGDEDIIMDKA-KA-SATHCKNAVERE---ISPDMARRVNHADMPMLWVLAARVEARMYIDYTHEE---BNV-LPN-
DcTPS32 152 LLSLYEASFIGFKDGDIDDLA-KA-SATHCKNAVEGK---ISPDMARAKVNHADMPMLWVLAARVEARMYIDYTHEE---QNM-NDN-
DcTPS33 190 LLSLYEASFIGFOQGEDVIDEKA-KA-SATHCKNAVQGK---ICPNMRAKVNHAADMPMLWVLAIRVEARMYIDYTHEE---QNI-NSN-
DcTPS02 192 LLSLYEASFIGFKDGDIDDEA-KA-SRTHCKNALGKGE---ISPDMARKVNHAADMPMLWVLAIRVEARMYISNYQD---DNM-NQN-
DcTPS62 110 LLSLYEASFIGFOQGEDIDDOA-KA-SATHCKNALGK---VSPEHAGKVNHAADMPMLWVLAIRVEARMYIDYTHEE---HNV-FQD-
Sf_cineole_s 191 LLLQLEASFLSAQGQGETLHLA-RDIAATVTHKRVLVD---KQINLSSIERAYELP-TWNRQMPN-SPIDIAKRR---PDM-NPL-
Mc_linalool_s 208 VLLQLEASFLLRKGEDTLEVA-RK-SATELEEKELKAGI---DGDNLSSSIGEPLWVLRQFQD-VFEDAYSRR---PDM-NPL-
Sc_bornylPP_s 194 MLLQLEASFLLRKGEDTLELA-RK-SATELEEKELKAGI---DGDNLSSSIGEPLWVLRQFQD-VFEDAYSRR---PDM-NPL-
DcTPS26 164 MLLYEAASFLSKTKNCKILDEA-QH-DATGCHMRDYYVNNNNKNS-KDEKLSKLVSHEAHLPLMTESRMEARMYIDYFERSMLADDIKSD-
DcTPS55 190 MLLYEAASFLSKTKNCKILDEA-QH-DATGCHMRDYYVNNNNKNS-KDEKLSKLVSHEAHLPLMTESRMEARMYIDYFERSMLADDIKSD-
DcTPS54 181 MLLYEAASFLSKTKNCKILDEA-QH-DATGCHMRDYYVNNNNKNS-KDEKLSKLVSHEAHLPLMTESRMEARMYIDYFERSMLADDIKSD-
DcTPS04 200 MLLYEAASFLSKTKNCKILDEA-QH-DATGCHMRDYYVNNNNKNS-KDEKLSKLVSHEAHLPLMTESRMEARMYIDYFERSMLADDIKSD-
DcTPS27 184 MLLYEAASFLSKTKNCKILDEA-QRATGCHMTDYINNSNTKNDKSKLVSHEAHLPLMTESRMEARMYIDYFERSMLADDIKSD-
DcTPS30 201 VUNLQLEASFHCKKNCKIMDEA-QD-DATGCHMKDLYDNTNNKNDENLVKLVSHEAHLPLMTESRMEARMYIDYFERSMLADDIKSD-
DcTPS52 180 LVQLYEAASYLSKNEBIMDEA-QD-DATGCHMTDYINDISC-KDENLVKLVSHEAHLPLMTESRMEARMYIDYFERSMLADDIKSD-
DcTPS17 149 LSLLYEAASYLSKNEBIMDEA-MC-DATGCHMTREHDDI---IDPILSCKVREALKSPDWRPFLKARMYIDYVYISRC---NNM-NPA-
DcTPS21 149 TSLSLYEAASYLSKNEBIMDEA-WRLASCLGRERSDDI---VDPDNLGIKURHEALKSPDWRPFLKARMYIDYVYISRC---SDM-NPA-
DcTPS05 149 VSLSLYEAASYLSKNEBIMDEA-WSLTSLSLSLKENLDDI-IDPILDMDKVKURHEALKSPDWRPFLKARMYIDYVYISRC---NNM-NPA-
DcTPS12 150 VSLSLYEAASYLSKNEBIMDEA-WSLTSLSLKENLDDI-IDPILDMDKVKURHEALKSPDWRPFLKARMYIDYVYISRC---NNM-NPA-
DcTPS03 188 LLSLYEASMSIEGDSLMDA-CC-ASEI-KERVNSI---DDWDLSMRKRAELPTQWRPFLKARMYIDYVYISRC---ODV-IE-VPK
DcTPS48 185 MLLSLEASMSIEGDSLMDA-WC-TNLSRESPHNV-TDWVQIQVRYHQLVRIAGYDIAHNLQRS---SDV-IEA-VPK
DcTPS10 181 LLSLYEASYLSIQGDSLMDA-WSLTSLSLKDCKLKNI-NDLNLQMRQVRAELPLPQWRPFLKARMYIDYVYISRC---GHHVV-AVPL
DcTPS47 133 -GEGLSLEMBA-SLLTSRLKECLENT---MDSDELEMQVRAELPLPQWRPFLKARMYIDYVYISRC---GVV-IEA-VPK
DcTPS47 1 -MWKLEKFRPSDFDVLMDNHEHTLIVQASC

DcTPS16 307 LAKLDYENIVQASALQDDEAQVQVMRHNQICLGSKLSPSTEDSLLQCPPLTIGSFEPHLSDS-BISLTLATPLWVTDLYDDEGSVBLRLL
At_myrcene_s 271 FAKKEDIVIVQZAHQEDDVRYVSCM-KETGIGSQDPLV-RDRRIVENYF-LVGMIYEPQFGVIRIVAAVALLVIDDLYDYGTPPELELP
DcTPS14 326 LAKLDYENIVQSVHOKVSKLASHM-VD1GQG-NPFL-RDRLRIVENYF-LVGMIYEPQFGVIRIVAAVALLVIDDLYDYGTPPELELP
DcTPS09 270 LAKLDYENIVQSVKQVSKLASHM-VD1GQI-OKMFIA-RDRLRIVENYF-LVGMIYEPQFGVIRIVAAVALLVIDDLYDYGTPPELELP
DcTPS32 233 FAKKEDIVIVQSVQKQVSKLASHM-VETGJ-DKMSFA-RDRLRIVENYF-LVGMIYEPQFGVIRIVAAVALLVIDDLYDYGTPPELELP
DcTPS33 272 FAKKEDYENIVQSVKQVSKLASHM-VETGJ-DKMSFA-RDRLRIVENYF-LVGMIYEPQFGVIRIVAAVALLVIDDLYDYGTPPELELP
DcTPS02 273 LAKLDYENIVQSVKQVSKLASHM-VETGJ-DKMSFA-RDRLRIVENYF-LVGMIYEPQFGVIRIVAAVALLVIDDLYDYGTPPELELP
DcTPS62 191 LAKLDYENIVQSVKQVSKLASHM-MDMGL-DKMSFA-RDRLRIVENYF-LVGMIYEPQFGVIRIVAAVALLVIDDLYDYGTPPELELP
Sf_cineole_s 272 LAKLDYENIVQSVKQVSKLASHM-MDMGL-DKMSFA-RDRLRIVENYF-LVGMIYEPQFGVIRIVAAVALLVIDDLYDYGTPPELELP
Mc_linalool_s 290 LAKLDYENIVQATQBLKDLRSLNNDSS-PQKPLV-RDRLRIVENYF-LVGMIYEPQFGVIRIVAAVALLVIDDLYDYGTPPELELP
Sc_bornylPP_s 278 LAKLDYENIVQATQBLKDLRSLNRLLCFPEKLPF-RDRLRIVENYF-LVGMIYEPQFGVIRIVAAVALLVIDDLYDYGTPPELELP
DcTPS26 251 FAKKEDIVMLQAYQDEBLKENSRM-KS1QWAEKLSFA-PARLVCFCM-SLGQMAPDQVSKYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS55 277 FAKKEDYMLQAYQDEBLKENSRM-KG1QWEECFNFS-GCTLVOGFY-SLGIXIGSKFVAVNLSALNVFII-TIDDIYDVGTLEEL
DcTPS54 269 FAKKEDYMLQAYQDEBLKESSRM-KS1QWAEKLSFA-PARLVCFCM-SLGQMAPDQVSKYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS04 287 FAKKEDYMLQAYQDEBLKESSRM-KS1QWAEKLSFA-PARLVCFCM-SLGQMAPDQVSKYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS27 272 FAKKEDYMLQAYQDEBLKESSRM-KS1QWAEKLSFA-PARLVCFCM-SLGQMAPDQVSKYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS30 288 FAKKEDYMLQAYQDEBLKESSRM-KS1QWAEKLSFA-PARLVCFCM-SLGQMAPDQVSKYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS52 266 FAKKEDYMLQAYQDEBLKLSKLM-KTDENGE-LGFA-RDRLRIVENYF-SLGQMAPDQVSKYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS17 230 LAKLDYENIVQGVYQEDDLKFSRF-NELGLANRSLFA-RDRLRIVENYF-SLGQMAPDQVSKYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS21 230 LAKLDYENIVQGVYQEDDLKFSRF-NELGLANRSLFA-RDRLRIVENYF-SLGQMAPDQVSKYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS05 230 LAKLDYENIVQGVYQEDDLKFSRF-NELGLANRSLFA-RDRLRIVENYF-SLGQMAPDQVSKYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS12 231 LAKLDYENIVQGVYQEDDLKFSRF-NELGLANRSLFA-RDRLRIVENYF-SLGQMAPDQVSKYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS03 269 FAKKEDIVMLQALNQBLKDLRSLNKTSPGDKLFA-RDRLRIVENYF-LVGQTEPONGCQLQIQAQIQSIVDLYDVGTLEEL
DcTPS48 266 FAKKEDIVMLROCNQBLKDLRSLNCTLGRMELVATL-SLGQMAPDQVSKYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS10 264 FAKKEDIVMLROCNQBLKDLRSLNRLDNGKELPFA-RDRLRIVENYF-SLGQMAPDQVSKYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS47 201 FAKKEDIVMLROCNQBLKELSSMTRLDNGKELPFA-RDRLRIVENYF-SLGQMAPDQVSKYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS47 30 -ENM--KLKKKRNRFSD--QAIADARASLAEV-MIFKN-VAEP-EDOLELIDOLQR

DcTPS16 397 QNSVRRWWVDAVDDLEPDLSLRLFFLALATVNEAIDALKEHGENPLPFLKQVWGDQCOALPFTKHEKSIPSEDDIVVWGRWISSCVV
At_myrcene_s 360 QAMVQNDINRLDSDPEYMMICPLFELI-AMGCDVLUKCKNNDVPLFKA-SADLQKAWAKYVKGKYPSPVYEMOJAMWISIAPI
DcTPS14 414 QYVDRMDITEIDKPLMHEI-TVLVIAFPVYRIGWTM-ERDFNITPZLQ-AN-CAYEPRATVYESGKYPSPVYEMEIASVIGCL
DcTPS09 358 RYFVERMHDITQIDKPLMHEI-TVLVIAFPVYRIGWTM-ERDFNITPZLQ-VNC-CYKAKWISOCBPLLE-HEV-NAVS-GVQI
DcTPS32 321 RYVDRMDITEIDRPLKPLMHEI-TVLVIAFPVYRIGWTM-ERDFNITPZLQ-TYMC-PLKAKWYTSGYKPLLEYMB-GAVS-SAPD
DcTPS33 360 RYVDRMDITEIDRPLKPLMHEI-TVLVIAFPVYRIGWTM-ERDFNITPZLQ-TYMC-PLKAKWYTSGYKPLLEYMB-GAVS-SAPD
DcTPS02 361 RYVDRMDITEIDRPLKPLMHEI-TVLVIAFPVYRIGWTM-ERDFNITPZLQ-VYLCQAKWYTSGYKPLLEYMB-GAVS-SAPD
DcTPS62 279 RYVTRMDITEIDRPLKPLMHEI-TVLVIAFPVYRIGWTM-ERDFNITPZLQ-PLKQKWMNSAKPKTDYEIQIAPVSIQADP
Sf_cineole_s 361 QTAIQERMDIESMKOLPPYNOICLPLFVMEAIYDILKDFGPNSTPLKQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
Mc_linalool_s 379 RYVIRANDTESATOSIPLFVYQKLYFVYIPLFVSEWAHLK-EGFISIPLRHRVQVWVYDQVWVYDQVWVYDQVWVYDQVW
Sc_bornylPP_s 367 RYTFKQANDTESITRPLFVYQKLYFVYIPLFVSEWAHLK-EGFISIPLRHRVQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS26 340 RYLTKSMDAELDOLPDPFMIICPTEFYIPLKQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS55 366 RYLTKSMDAELDOLPDPFMIICPFDLYKINEEVANVFQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS54 358 RYLTKSMDAELDOLPDPFMIICPFDLYKINEEVANVFQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS04 376 RYLTKSMDAELDOLPDPFMIICPFDLYKINEEVANVFQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS27 361 RYLTKSMDAELDOLPDPFMIICPFDLYKINEEVANVFQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS30 377 RYSTKRDVAELODPLPDPFMIICPFDLYKINEEVANVFQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS52 355 RYLSKRDVAELODPLPDPFMIICPFDLYKINEEVANVFQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS17 319 RYAIERMDINSIEQBLPDPFMIICPFDLYKINEEVANVFQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS21 319 RYAIERMDINSIEBLPNYMKVCPFLALYKINEEVANVFQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS05 319 RYAIERMDINSQPLPDPFMIICPFDLYKINEEVANVFQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS12 320 RYAIERMDINSQPLPDPFMIICPFDLYKINEEVANVFQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS03 358 RYVIERMDITAMSBLPDPFMIICPFDLYKINEEVANVFQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS48 355 RYVVKRDVSAIKEBLPNYMKVCPFLSPYVPHETSFBLKQNTEEBLKQNTEEBLKQNTEEBLKQNTEEBLKQNTEEBLKQNTEEBL
DcTPS10 353 RYVTKRDVHALNEBLPDPFMIICPFDLYKINEEVANVFQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS47 290 RYVVRQMDINAMEKBLPDPFMIICPFDLYKINEEVANVFQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVWVYDQVW
DcTPS47 81 YGLDKEFQDSEKHAUJKS1QHNGQNSETTSDF--NLAIALEPFRLLQHCHISSL

Figure S5. Continued

DcTPS16 487 IIAAHAFPLRSQ-NFTKMAIDIL-AKDHHLLKWSSMVFRLCNELASFTREKSKEETANGVTSIYTHNGVSSEDVIREHKNLDDANQNS-
At_myrcene_s 450 MLIHFICAFSG-QISVQILESLVQQQDVRVCSATVLRFLANDLAEPEDEKAGDVLKSVQCYIMHETGVSEFPLRTHVQOMISH-NDENMY
DcTPS14 504 MDFCAIYLTAE-KITVCAALDFI-DKVPSPNWCPSLIRLTNDLGTSAAEARGDILKAVQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS09 448 LIFCAIYLTAE-KITVCAALDYV-DKVPSPNWCPSLIVRLTNDLGTSAAEARGDILKAVQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS32 411 VIFCAIYLTAE-KITVCAALDYI-DKLPSPNWCSSMILRLTNDLGTSSEBARGDLSLAVQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS33 450 VIFCAIYLTAE-KITVCAALDYV-DKLPSPNWCSSMILRLTNDLGTSSEBARGDLSLAVQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS02 451 AIFCAIYLTAE-QTVADYI-DKLPSPNWCPSLIVRLTNDLGTSSEBARGDLSLAVQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS62 363 AIFCAIYLTAE-KITVCAALDYI-DKLPSPNWCPSLIVRLTNDLGTSSEBARGDLSLAVQCYIMNDGOSSEVSRKHWVDLVHITWKID-
Sf_cineole_s 451 IISHLFIRLTD-SLEEDDAESM-HKYHDVTRACSTILRLAADDMDGSSEVSRKHWVDLVHITWKID-
Mc_linalool_s 469 VISQIYMLAK-SKEKPVIEST-KEYDEEIRLSGLMLVLPFDDLGZLPFEMKRGDVAKSICQHMEKONATRSEEEHVRSLIDQWNCMS-
So_bornylPP_s 457 LISPTVTFANASHDTAVIDL-SQYHDLCLAGIILRLPDDLGZSYFPLRGDVPKSIQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS26 430 INTYLTAD-SVKEEDQCL-MTYPNLRRSATILRLAADDMDGSSEVSRKHWVDLVHITWKID-
DcTPS55 456 VTHMLLKPN-SVKEEDLCL-MTCPNVLRLSATILRLAADDMDGSSEVSRKHWVDLVHITWKID-
DcTPS54 448 LETHLKVPKPNSLKHEDQCL-MTYPNLRHSATILRLAADDMDGSSEVSRKHWVDLVHITWKID-
DcTPS04 466 LETHLKVPKPNSLKHEDQCL-MACPNIURHSATILRLAADDMDGSSEVSRKHWVDLVHITWKID-
DcTPS27 451 LETHLKVPKPNSLKHEDQCL-MACPNIURHSATILRLAADDMDGSSEVSRKHWVDLVHITWKID-
DcTPS30 467 LETHLKVPLSTT-SFTDPAOSI-WDPYKHLRLAAILRLAADDMDGSSEVSRKHWVDLVHITWKID-
DcTPS52 445 VTHMLLKTEP-SFTDPAOSI-MNCPKHVRLVSMHIRETDDINSDGZLKGDPKLIQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS17 409 CIVQNLCSSEN-PVRRRAFTFL-MDMMPNLSACALLGIGDNGTSSHEARGDVPKSIQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS21 409 CIVQNLCSMNP-VFDRLAZELF-MNMPEVLLSACALLGIGDNGTSSHEARGDVPKSIQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS05 409 VMLSYTCSAN-PIKKE-PIKEF-EDMPDMLNSLKLGRDNGTSSHEARGDVPKSIQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS12 410 VVIQSCSICAN-PIKEFIECL-LAMPYHQLGTGLCIREDDYDGTSSHEARGDVPKSIQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS03 448 IALQSCTCSAN-PIKKE-PIKEFIECL-PIKEFIVLASEIFPLRDYDGTSSHEARGDVPKSIQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS48 445 GULVYICTAD-RIKEFIEFI-EGPLDPLVRLACEILRLADDYDGTSSHEARGDVPKSIQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS10 443 VMLYALIGTAD-FIKEFIEFI-EDFPDPLVRLACEVFRISDDIPLRDYDGTSSHEARGDVPKSIQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS47 380 VALYAIXTAN-PIKKE-PIKEFIEF-ENFSIDLIRLAYEIPFRESDDYDGTSSHEARGDVPKSIQCYIMNDGOSSEVSRKHWVDLVHITWKID-
DcTPS47 1 -----MWKLEKFRSFDFVLMDNHHTLIVOLASC-----

DcTPS16 574 EARVSLEP--QFSTSPTTEAAINLRLSHSAIYGSQ-DDHRI-PDKKAKKQKQIFSLLEWPFPTVTLG*-EILATPLFVWIDDYDDHGSVDELELF-
At_myrcene_s 539 EARTAARSSSLRRFVETAMLARMSOCMHQEC-DGHCCPDKAKIIVDRVOTLVEPIPD--AIWAALIVVIDDYDDHGSVDELELF-
DcTPS14 591 KDLGLSY--PPSEPPLSANSPLHARTSQTFIQG-DGHCH-PQHWTNDHUKSLVFTIHE--MIVCLITVDDYDDHGSVDELELF-
DcTPS09 535 KDLLEYY--PPGEVVAANPDMRAGQFPIQG-DGHCH-PQHRTDHDH-SALLVEPFTLHE--MIVISLVEHIDDYDDHGSVDELELF-
DcTPS32 498 EDLGLSY--PPSEPPLTANPLIARTTOSFYIQG-DGLGMQ-PQWNIKDLKSLLVEPFTLHE--MIVICLIVVIDDYDDHGSVDELELF-
DcTPS33 537 EDLGLSH--PPSEPPLTANPLIARTTOSFYIQG-DGLGMQ-PQWNMKDLKSLLVEPFTLHE--MIVICLIVVIDDYDDHGSVDELELF-
DcTPS02 538 KDLGLSY--PPSEPPLTANPLIARTTOSFYIQG-DGHCH-PQHWTNDHUKSLLVEPFTLSS*-EILCLITVIDDYDDHGSVDELELF-
DcTPS62 450 KDLGLSY--PPGEPPITANPLIARTTOSFYIQG-DGHCH-PQHWTNDHUKSLLVEPFTLSS*-EILCLITVIDDYDDHGSVDELELF-
Sf_cineole_s 538 KEMMTS--SPSKYIIVQVSAIILRMAQWIIQHESDGFQH-QHSLVNUKMRGQFDFRYE--MIVALVVEVIDDYDDHGSVDELELF-
Mc_linalool_s 556 TMAAANS-DLRGDVVMAAAIGRDAQFMYLQD-DG--NHSQLOQRHIANLFPNTYV--AIITLILADDYDDHGSVDELELF-
DcTPS26 517 BECAES--PPFKSPTRENCLHLARIACCIVLYC-DGHCH-PSSRDKEPLFLFVPIPL*-SALNVFIFVIDDYDDHGSVDELELF-
DcTPS55 543 BECAES--PPSKPPIENCLHLARIASCIVLYC-DGHCH-PGSRDKEPLFLFVPIPL*-RAVNAFVYVIDDYDDHGSVDELELF-
DcTPS54 535 BECAES--PPSKPPIENCLHLARIASCIVLYC-DGHCH-PSSRDKEPLFLFVPIPL*-RAVNAFVYVIDDYDDHGSVDELELF-
DcTPS04 553 EESAES--PPSKPPIENCLHLARIASCIVLYC-DGHCH-PGSRDKEPLFLFVPIPL*-PVNAFVYVIDDYDDHGSVDELELF-
DcTPS27 538 EECAES--PPSKPPIENCLHLARIASCIVLYC-DGHCH-PGSRDKEPLFLFVPIPL*-PVNAFVYVIDDYDDHGSVDELELF-
DcTPS30 554 EKIIIAEE-TFSKPFIMEMCMIGRIALYMC-DGHCH-PTLKDVERSTYFVPIPL*-AAATAFVYVIDDYDDHGSVDELELF-
DcTPS52 532 EEMQAES-IFSKPFIDVCLHLARIITTAIYMC-DGHCH-PNAKIDRSTYFVPIPL*-LAVTFVYVIDDYDDHGSVDELELF-
DcTPS17 496 KYRLQNN-ALFLQVWYIYDFDURATHYDRC-DGSFQWDHGKSKILLSLALIVEPIPG--AQOQFPLVIDDYDDHGSVDELELF-
DcTPS21 496 KCRLODT--PWPLQAVDWFYIFDULRATHYDRC-DGYSVQHEGKS-LLNALALIVEPIPM--AQOQMICVYIDDYDDHGSVDELELF-
DcTPS05 496 ACRARDM--PWVCPCTEFMLCARSSHYIYTTS-DGFAV-HDDRSANTFSLWVOPVLY--AIIQINSVIDDYDDHGSVDELELF-
DcTPS12 497 ACRARDM--PWRSSSVEMILVTSKCVVNAACNDGFCV---EDEEAFLPSFLPIDPIDI--AIQINSVIDDYDDHGSVDELELF-
DcTPS03 535 QCRYSKDY--PLSWHIVIILWVTSKCVVNAACNDGFCV---EDEEAFLPSFLPIDPIDI--AIQINSVIDDYDDHGSVDELELF-
DcTPS48 532 KCRFSDNQN-PLSWHIVDMLLIVRAAACMINACEDGQYAD-EDGISRDTFFSLLVEPI--LIGIELCVYDDYDDHGSVDELELF-
DcTPS10 530 KLRFSEXGNPQWSRFVDTMLLIVRSGHCLYNAEDGFSV-EDVVAKESLVSLLVEPIPL--LIGIELCVYDDYDDHGSVDELELF-
DcTPS47 454 KLRFSEYYNNPWSRHYDMLLIVTRIAHYLYNACEDNYCV-EDGLVKAISLVEPIPL--ASVELLIGVYDDYDDHGSVDELELF-
DcTPS47 30 -----HM-LKKKKRNFSDF-CEAIDARASAHAEVWIFRN-VAPB-LDQLELIDQDFP

DcTPS16 397 EDSVRRNVDAVDLDPDSLRLFPLALYNTVEMALIDALKHEGENPLPLFNVWGDLCMLOETKMKWESKISPEELDDIVEWGRSSSSVV
At_myrcene_s 360 ZAMVQNDINRLEDELPSYIMKLCPLTFEBINAMGCDVLCKKNIDWIPYKNSADICKAYLVEAKWYKGGYKPSVEMQWISISAFT
DcTPS14 414 EDYVDRMDIEKLPMLMIKHTVFLAMPFLVNEGILMTMOERDFNHPYIPLQMANCKAYLEATMHSGYKPTVEELMENPSVIGCLL
DcTPS09 358 EDFVERMDITQIKLPMLMIKTVLAMPFLTNEIGLMTMOERDFNHPYIPLQBLVNLCKYLMKAWKNSCHQPTLLEMEVAIVSIVGVOI
DcTPS32 321 EDYVDRMDITBEIRLPKLLKTVLAMPFLTQIGMTLOERDFNHPYIPLQMTKQPLAKWYKNSCHQPTLLEMEVAIVSIVGVOI
DcTPS33 360 EDYVDRDYTEIKLPKLLKTVLAMPFLTQIGMTLOERDFNHPYIPLQMTKQPLAKWYKNSCHQPTLLEMEVAIVSIVGVOI
DcTPS02 361 EDYVERMDIAEELKLPMLMIKTVLAMPFLTNEIGLMTMOERDFNHPYIPLQMTKQPLAKWYKNSCHQPTLLEMEVAIVSIVGVOI
DcTPS27 279 EDYVTRMDIEESKMLPMLMIKTVLAMPFLTNEIGLMTMOERDFNHPYIPLQMTKQPLAKWYKNSCHQPTLLEMEVAIVSIVGVOI
Sf_cineole_s 361 ATAIQRMDIEESKMLPMLMIKTVLAMPFLTNEIGLMTMOERDFNHPYIPLQMTKQPLAKWYKNSCHQPTLLEMEVAIVSIVGVOI
Mc_linalool_s 379 QHVIIRMDTESALTOPLYVHILKELGFVFLVPLFEGFISIPLFPLRHWVNLVEGILQEAHKWYTKTIPMEEZYLNASITIGAFA
So_bornylPP_s 367 EDTFKRDTESTIRLPYIPLQCLWVGVLWISDARALDILMGGFFCQYIPLQSVVSDUVEAFLPEAKWYHSGYIPLSDLYLNLKISVASA
DcTPS26 340 KLTKSMDAAELDOLPDMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
DcTPS55 366 KLTKSMDAAELDOLPDMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
DcTPS54 358 KLTKSMDAAELDOLPDMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
DcTPS04 376 KLTKSMDAAELDOLPDMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
DcTPS27 361 KLTKSMDAAELDOLPDMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
DcTPS30 377 EESTKRDVADLEQPEEIKVCFVVFYIINNAVDAIAEHLGVNLPHLQDWTDFEAYLVEAKWYHSGYKPLSRZYLDNWVTSQFV
DcTPS52 355 EKLSKRNDVAEELDOLPDMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
DcTPS17 319 EDAIERNDINSIEQLPDMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
DcTPS21 319 EDAIERNDINSIEQLPDMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
DcTPS05 319 EDAIERNDINSIEQLPDMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
DcTPS12 320 EDAIERNDINSIEQLPDMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
DcTPS03 358 EKVIERNDITAMESELQPLPDMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
DcTPS48 355 EAVVKRNDVSAIKELPNMMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
DcTPS10 353 EAVVKRNDUNALNESELQPLPDMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
DcTPS47 290 ENVORNDINAMELQPLPDMKICPTEFSEINKLDVAQHGSVSLPQIOWMTGFEAVLWAKWNSGKIPFSSSLLDNWVTSQFV
81 VQGDYHODIICHALKSHOHNGQNSETSDK---NLHATALEFRLRQHGHIYIGS-----

Figure S5. Continued

<i>nerolidol_s_Med</i>	1	-MSNKTSNILEY-----NKTNLDSVFN-QIHIPK-----SGKCKDDLHIR-----HEKALDEVKQ
<i>myrcene_snapdra</i>	1	MIYIWCIFYLOTTLFPCSLSTRTKFATCANTSKLHRAAYXTSRNNIFCGVGSTPPPSKLHQALCLNEHLSCLMAELPMID-----YECKIKETRH
<i>ocimene_snapdra</i>	1	--MAFCISYLGAVPFSSLSPRTKFAIFHNT-SKHAAYKTCRWNIPRGSTPPPSKLHQALCLNAHTSCMAELPMID-----YECKIKETRH
DcTPS23	1	-----MEFLSMPSSIADTWCIKRDLL-SLVSKNRAQIFSFRPPKITT-----S-----EDYOK-----QSQNMAIVRO
DcTPS60	1	-----MQFLSMPSSIADTWCIKRDLL-SLVSKNRAQIFSFRPPKITT-----S-----EDYOK-----QSQNMAIVRO
DcTPS19	1	-----MYSFAFDMRNTQLCRTTN-----MPEPKWNSNTDLPV-----VWRCEKNVFFSKKVSFGFLTRTFADMANKR
DcTPS45	1	-----MLPSINPHDSITKQCCC-----FSREGEAT-----SLSCL-KCHPK-----LAQHVKDICKH
DcTPS46	1	-----MLPSINPHDSITKQCCC-----FSREGEAT-----LISI-----HDYFP-----QAQDMEEIKH
<i>nerolidol_s_Med</i>	49	-VFVRN-IRKNTDECISMVDSIQRLGMEYNFEEEIEATLERKHTMLRFQNFQRNEYQGTSQAAQFQFRMLRQEYVYISPLIFDKFCDNKGLK--YTFSED
<i>myrcene_snapdra</i>	90	LIHLKG---ENDPIESLIFVDATLRLGVNHHFQKEEIEILRKSYATMKSICK---YHTEDVSVIFFRINRQHGRYVSADVFNNEKGESGRFKEELKR--D
<i>ocimene_snapdra</i>	85	LIHLKG---ENDPIESLIFVDATLRLGVNHHFQKEEIEILRKSYATMKSICK---YHTEDVSVIFFRINRQHGRYVSADVFNNEKGESGRFKEELKR--D
DcTPS23	56	ELKASNKVGDYDTYOSITLIDAVQRIGIDHIFFKDEIEQVLERQYMAISGFFK--NNDICLACSLCFRLRQOHYHVADAFDKEMNEDKKLVRKLLRGES
DcTPS60	58	ELKANNKVGIDDEYOSITVDAEQRIGIDYHFKEDEIEQVLERQYMTI-SPVFFK--NNDICLACSLCFRLRQOHYHVADAFDKEMDKEKFLVRKLLRGES
DcTPS19	67	ELMVKN-IGRDPYKDLIMVVVQRLGIDYBFEKEEIEQVLERQYTAI--DELVN--NNDKDYFVSVLCFRLRQHQYVSADAFNNEVNKTRNLE---IRGES
DcTPS45	35	ELMVKN-MGR---GLIMVDVQRLGIDYFEEIEIIVLDSQYKAM--DQV--EPYIVFVSLCFRLRQHYYVSADAFDKP--INNKRELE--IAGNS
DcTPS46	46	ELMVKN-VVR---GLIMVDVQRLGIDYFKEEIEQVLERQYTAI--DELVN--HKDIFYFVSLCFRLRQHYYVSADAFDKP--INNKRELE--IAGNS
<i>nerolidol_s_Med</i>	145	INGMIALFEASQLIEGEDDLDNWSSTFHGPQAKFVAHTLMWTHKPLSREFPTIMQSIAQFSKIDTQMWSSSHKK
<i>myrcene_snapdra</i>	184	TRGLIVELYAQLSBEGERILDEAENFSRQILHGHNLAGM-EDNLLRSVCNKLRLVEFHISIARFTGRNY-DDDLGCMYEWGKTRELALMDLQVERSVOE
<i>ocimene_snapdra</i>	179	TRGLIVELYAQLSBEGERILDEAENFSRQILHGHNLAGM-EDNLLRSVCNKLRLVEFHISIARFTGRNY-DDDLGCMYEWGKTRELALMDLQVERSVOE
DcTPS23	153	TEALTSLYEASQLRIEDDVLDEAEFSQCQLNERIKFL-NHHPHWSVRNTIAHPLHRSIAGFTKHNHYKDVIRGKARGKALQELAYIDRAFMQAHQRR
DcTPS60	155	TEALMSLYEASQLRIEDDVLDEAEFSQCQLNERIKFL-NHHPHWSVRNTIAHPLHRSIAGFTKHNHYKDVIRGKARGKALQELAYIDRAFMQAHQRR
DcTPS19	159	NDALMSLYEASQLRIEDDVLDEAEFSQCQLNERIKFL-NHDPQSIATKNTLAHPLHRSIAGFTKHNHYKDVIRGKARGKALQELAYIDRAFMQAHQRR
DcTPS45	120	NALMSLYEASQLRIEGEDVLDEAEFSQCQLNERIKFL-NHDPQSIATKNTLAHPLHRSIAGFTKHNHYKDSFARISSKGHLQGNVFD-NEYGKALQELAYIDRAFMQAHQRR
DcTPS46	134	NDALMSLYEASQLRIEGEDVLDEAEFSQCQLNERIKFL-NHDPQSIATKNTLAHPLHRSIAGFTKHNHYKDSFARISSKGHLQGNVFD-NEYGKALQELAYIDRAFMQAHQRR
<i>nerolidol_s_Med</i>	241	E1FAVSKWWKDGLLPKDLLEFARDEPIKWSWSMACLPLD-BQFSEERIELTKPLSIIYIIDDIFDYEYGNIDEETLFTDAVKRWDLSATEBOLPDCMKVCEKA
<i>myrcene_snapdra</i>	282	ELLOVSKWWNGLGYKKLNPARNRPEEYFWSMVILADYINLSEQRVELTKSVAIFIYIIDDIFDYEYGTDELIFTTEAVNWKDYSATDTPDNMKVCMMT
<i>ocimene_snapdra</i>	277	ELLOVSKWWNGLGYKKLNPARNRPEEYFWSMVILADYINLSEQRVELTKSVAIFIYIIDDIFDYEYGTDELIFTTEAVNWKDYSATDTPDNMKVCMMT
DcTPS23	252	ELSEFSRWNGLRDLAEKLYARNQPLKWFWSMALLTDPLSSEERIELSKAIFIYIIDDIFDYEYGTDELIFTTEAVNWKDYSATDTPDNMKVCMMT
DcTPS60	254	ELSEFSRWNGLRDLAEKLYARNQPLKWFWSMALLTDPLSSEERIELSKAIFIYIIDDIFDYEYGTDELIFTTEAVNWKDYSATDTPDNMKVCMMT
DcTPS19	258	ELSAVSRWNGLGLOELKLVDRDQPLKWWYWTTLTDPLSSEERIELSKAIFIYIIDDIFDYEYGTDELIFTTEAVNWKDYSATDTPDNMKVCMMT
DcTPS45	217	ELSTFSRWNGLGLOELKLVDRDQPLKWWYWTTLTDPLSSEERIELSKAIFIYIIDDIFDYEYGTDELIFTTEAVNWKDYSATDTPDNMKVCMMT
DcTPS46	234	ELSAVSRWNGLGLOELKLVDRDQPLKWWYWTTLTDPLSSEERIELSKAIFIYIIDDIFDYEYGTDELIFTTEAVNWKDYSATDTPDNMKVCMMT
<i>nerolidol_s_Med</i>	340	HYDITNEFALRTYIKHGWNPPLTSLLKSWVRLNNAFQEAQFWASGNVPKSEEYLKNAIVSTGTVHVLVHAEFFCMQ-GITEKTVS-TMDDFTIIST-A
<i>myrcene_snapdra</i>	382	LLDTINGTSQRTYKRGYNPIDSLLTTWRSLCSAFLVEAKWSASGSPLSANEYIENERWSGVVVVLLVFLCINGLGSRSGIE--INDTQBLMSI-A
<i>ocimene_snapdra</i>	377	LLDTINGTSQRTYKRGYNPIDSLLTTWRSLCSAFLVEAKWSASGSPLSANEYIENERWSGVVVVLLVFLCINGLGSRSGIE--INDTQBLMSI-A
DcTPS23	351	LHEITNEIGYKVKKHGFNPIDYLAKTWAALKCTAFLEEKWFAASGHLPAEEYIKNGIGNSGVHVALVMMFLIGDHGSTKDIAE-SVRLDTCLI-SYNVIA
DcTPS60	353	LHEITNEIGYKVKKHGFNPIDYLAKTWAALKCTAFLEEKWFAASGHLPAEEYIKNGIGNSGVHVALVMMFLIGDHGSTKDIAE-SVRLDTCLI-SYNVIA
DcTPS19	357	LHENITNEIGYKVKKHGFNPIDYLAKTWAALKCTAFLEEKWFAASGHLPAEEYIKNGIGNSGVHVALVMMFLIGDHGSTKDIAE-SVRLDTCLI-SYNVIA
DcTPS45	316	LLENITNEIGYKLYKKVGLNPIDYLKWSKLCNSAFLDESKWFFSGLHPAEEYIKNGIGNSGVHVALVMMFLIGDHGSTKDIAE-SVRLDTCLI-SYNVIA
DcTPS46	333	LLNITNEIGYKLYKKVGLNPIDYLKWSKLCNSAFLDESKWFFSGLHPAEEYIKNGIGNSGVHVALVMMFLIGDHGSTKDIAE-SVRLDTCLI-SYNVIA
<i>nerolidol_s_Med</i>	437	KILRLCDDLEGKD KV NCE GNDGSYSKCYMDNPGVSIGLTKEHMSEQISDAWKQLNKECLNTNPLP-SSETKRLCLNAARMVPLMYNYDGNTP-SKLEEVV
<i>myrcene_snapdra</i>	479	IIFRLWNLGSAKNEBONGRGSYLNCKYKEHINLTAAGFHEHALELVIAEWKRINKESBNLNHDSVSSFKQAAALNARMVPLMYSDBNQRGEVLEEVV
<i>ocimene_snapdra</i>	474	IIFRLWNLGSAKNEBONGRGSYLNCKYKEHINLTAAGFHEHALELVIAEWKRINKESBNLNHDSVSSFKQAAALNARMVPLMYSDBNQRGEVLEEVV
DcTPS23	450	AIRLRWDDLGSAKDENODGKDGGSYVACYMKHHKEASIEAREQVSKMISETWKQLNKECISPNQYS-KFPIKGSLNARMVPLMYTYDQSPLLLEEVY
DcTPS60	451	AIRLRWDDLGSAKDENODGKDGGSYVACYMKHHKEASIEAREKVSFMSITWKQLNKECISPNQYS-KFPIKGSLNARMVPLMYTYDQSPLLLEEVY
DcTPS19	454	AIRLRWDDLGSAKDENQKGDGSYVTCYMKHHCEVSVERARKHODMISDTWKRLNKECFSPPNYS-KFPIKGSLNARMVPLMYTYDQSPLLLEEVY
DcTPS45	414	AIRLRWDDLGSAKDENQKGDGSYVTCYMKHHCEVSVERARKHVENMISDTWKRLNKECFSPPNYS-KFPIKGSLNARMVPLMYTYDQSPLLLEEVY
DcTPS46	431	AIRLRWDDLGSAKDENQKGDGSYVTCYMKHHCEVSVERARKHVENMISDTWKRLNKECFSPPNYS-KFPIKGSLNARMVPLMYTYDQSPLLLEEVY
<i>nerolidol_s_Med</i>	535	ESSLINDGGYLQSIHSPTSEHSTV
<i>myrcene_snapdra</i>	579	KEMIISD-----
<i>ocimene_snapdra</i>	574	KEMIISD-----
DcTPS23	549	REQLF*-----
DcTPS60	550	REQLF*-----
DcTPS19	553	RSMFVL-----PLNC*
DcTPS45	513	RGMFL*-----
DcTPS46	530	RGMFI*-----

Supplementary Figure S6. Amino acid sequence alignment of proteins in the carrot TPS-g sub-family and other select TPSs of this subfamily. Alignments were performed using Clustal W⁴³ and visualized with BoxShade (v3.21, https://embnet.vital-it.ch/software/BOX_form.html). Dc, *Daucus carota*; Med, *Medicago truncatula*; snapdra, *Antirrhinum majus*.

AT4G02780_1 1 -----MRMALCIHINSTNQN-----RSFLISTIIT-----QV|QENLHRRFSTWVFYVARINLVVEVVYFECFA-----DLAVONKL
DcTPS59 1 -----MESVYHPSSPS-----DOKFPPATFTESVSV--SVSENVSPNHFSGPNAVKGDIWVKLRFGVOCATAVSRSRTEYEYAESLKSPL
DcTPS25 1 MLRHLQQTTMYSSTSTKTMSPSHSTSSIAEFTISPTFTSPPLLFPOKLFCNIRDLAFSVDSVNGDKRKVLRYSACQSASRSHT-----ATVVEKNL
DcTPS57

AT4G02780_1 10 PLIHEWQOLQGEDAPQISVG-SNSNAFKEAVKSVKTILRNLTGEITISAYDTAWVALIDAGDKT--PAFPSAVKWIAENQLSDGSWGDAYLFSYHDRLI
DcTPS59 68 PAIVNWQKILEPHKIRKDK-RCFSPW-----TTELVITISAYDTAWVALVEDSDKTGFMFPSSLEWIADNQLDGSWGDDKLFLAHDRL
DcTPS25 82 PAVINWOEILESDKKGENTKLHSISIKIICKINSREMFRSMDDCAISLSAYDTAWVALVEDMNEPGWFOFPASLQWIVSNQLDGSWGDDKLFLAHDRL
DcTPS57 96 SSIVYWQBRILESHPKQEEOTKIREFTKL----IREIFNSMDGDINVSAYDTAWVALVEDNKTKG|PQFPSSLQWIVADNQLDGSWGDDKNVFLAYERIL

AT4G02780_1 107 NTLACCVVALRSWNLFPHQCNKGITFFRENIKGLEDENDEHMPIGFEVAFPSLIEIARGINID-VPVYDPSVLUKDIYAKKEELKLTRIPKEIMHK|PTTLLHS
DcTPS59 154 NTLACCVVALKTWVHPQKMERGLLFIRENINKLADVKIEETTMGFELVFPFLVEVAESLNIE-IPKNDLPIKEIYAQRDLKRSRIPKDQMHEVPTTLLHS
DcTPS25 182 NTLACVIALALKSWNVHPEKMERGLLFINENISKLDEEMEMHMPIGFEVAFPSLVEIAETLNIC-IPKDLPLILOEIYAQRDLKLSRIPKDTMHKVPTTLLHS
DcTPS57 190 CTLACCVVALRTWNHPONMERGLLFIRENINKLDEMEHMHTIGFEVAFPSLVEIAETLNIVSKLPLIOP|YAQRDLKLS-----

AT4G02780_1 206 LEGMRDLDWEKLLKLQSQDGDSFLFSPSSTAFAFMQTRDSDNCLERYLRNAVKRFNGGVPNVFPVD|FEHIWLTVDRLQRLGISRYYEEIKEC|DYVFRYWT
DcTPS59 253 LEGMVDLKWEKLLKLRCEDGSFLSPSSTAVALMOTKDAFCDFYLISKAQKFNGGVNTYPVDMFEHNWWVDRLERLGTSRHFFPEIKECMDDYVFRYWT
DcTPS25 281 LEGMAEMEWEKLLKLQCEDGSFLFSPSSTAFAFMQTRDSDNCLERYLRNAVKRFNGGVPNVFPVD|FEHIWVWDRLERLGTSRYFKSEIKECMDYVFRYWT
DcTPS57 273 -----NSVPNAYPVDMFEHWAVDRLERLCLVSRYFKYEIKDCMDYYVFRYWT

AT4G02780_1 306 NGICWARCSHVQDIDDTAMAFRLRQHGYQVSADVFKNFKEGEFFCFVGQSNQAVTGMFNLRYRASOAFPREFILKNAKEFSYNYLLEKREREELIDKW
DcTPS59 353 KGICWARCPFLNITIDDDTAMAFRLRLLHGYSVSPDVFNRFESNGKPFALACBSNQAVTGMNLRLRVSNQSFPEEELLSAAKKS|DFLRSKRADEQLLDKW
DcTPS25 381 OGICWARNTRVNIDDDTAMAFRLRLLHGYSVSPDVFNRFESKGEPVCFAQGSNQAVTGMFLRLRASQVVFPEEALLECAKKS|EFLRCKQAENOLFDKW
DcTPS57 320 KGICWGGRNINIAIDDDTSMARLRLHGYNVSQDVFRNFESKGEPWAAGOSNQAVTGMDDLKASQVMLPGENVLEAKTFSYEFLRKQANOLLDKW

AT4G02780_1 406 IIMKDLPGEIFALEIPWYASLPRVETRFYLDQYGGENDWVIGKTLRYRMPVUNNNYGELELAKQDYNNCQAOHQLEWDIFQKWYEENRLSEWGVRRSEL
DcTPS59 453 IITKDLQGEVEYGLDIPWYASLPRLETFCYLDHYGGEDDWVIGKTLRYRMPVUNNNYLEAKLDYAKCQTIIHQEWYMKWEPFAHSKLEQFGMNENSLLL
DcTPS25 481 IITKDLPGEVGYALDIPWYASLPRLETSF|LDQYGGEDDWVIGKTLRYRMPVUNNNYLEAKLTDYAKCQTIIQLEWNQMKEWCANSLKFGLSETSLLL
DcTPS57 420 IIMKDLPGEVEXALDIPWYASLPRLETCFYLDQYGGEDDWVIGKTLRYRMPVUNNNYLEAKLTDYAKCQTIIHQLEWSHMKEWCARSNLIDKGLSENSLLL

AT4G02780_1 506 CYYLAAATIFESERSHERMWAKSSVLVKAISSSFEGE---SSDSRFSFSDQFHEYIANARRSDHHFNDRNMRLLDRPGSVQAS--RLAGVLIGTLINQMSFD
DcTPS59 553 SYYLAASSLFEPEPDHSQRFWAKATEALVETIGSPEENMSEQRKAF-----KLVGTVLQKLTLLN
DcTPS25 581 SYYLAASSLVEPESSNLRFRAWAKTEALIETIRLYEGNIESAEQRBAFVDYMK-----PTENLYVSPGRYKSPRKKLLGTVGH|LQLMLD
DcTPS57 520 SYYLAASSLFEPEVSNLRFRAWAKTDALVETIRSYPGNLERSVEQRKAFAPBEEN-----TSEN SYFANHGRYSIE-KKLLGTVATLQLI

AT4G02780_1 601 LFMSHGRDVNNLILYLSWCDWMEWKWLKG--DEGEGEGLMVKMIIILMKNNDLTN-FFTHTHFVRJAEITINRCL--PROYLKARRDEKEKTIKS----M
DcTPS59 617 AKSAHGIDIYFQLHQAWLWVQEDGNVDKAQLLEB|INICAGRL|SEEILSHPQYKTLSTITNRICHOLR|FQ-KVQNQNNNCNGNTCAITTAEI
DcTPS25 669 AMVAHGIDIHOQLHQAWGMWLTWQEEGVDKAQLLEPTINICAGRL|SEEILSNPOYRNLSKITNQLCHOLGPFOYGKLNEDSSDREIRGITAMEI
DcTPS57 607 AKSAHGIDIYFQLHQAWTMWLLKQEEGVDKAQLLEPTINICAGRL|SNEILSHPHYKTLSTITNRICHOLSI|F-R-KVONEKSRTSRGGITTMEI

AT4G02780_1 690 EKEMGKMWELAISESDTFRDVSIIT--FLDVAKAFYYFALFG-DHLQTHISKVLFQKV---
DcTPS59 715 ESDMQELVQSVFCNSPDSLDPEFKQIFFMARTFYYTAYCDPNTINDHICKVLFGT-RM*
DcTPS25 769 ESKMQUELVKLVLCNSPDGLDPELKQIFFT|ARTFYYTAYCDPITINSHISKVLFGT-RM*
DcTPS57 705 ESDMRELVRLVFCNSEDS1HPELKH|FFMVARTFYYTAYCDVDTVNGH|KVLGSGTRM*

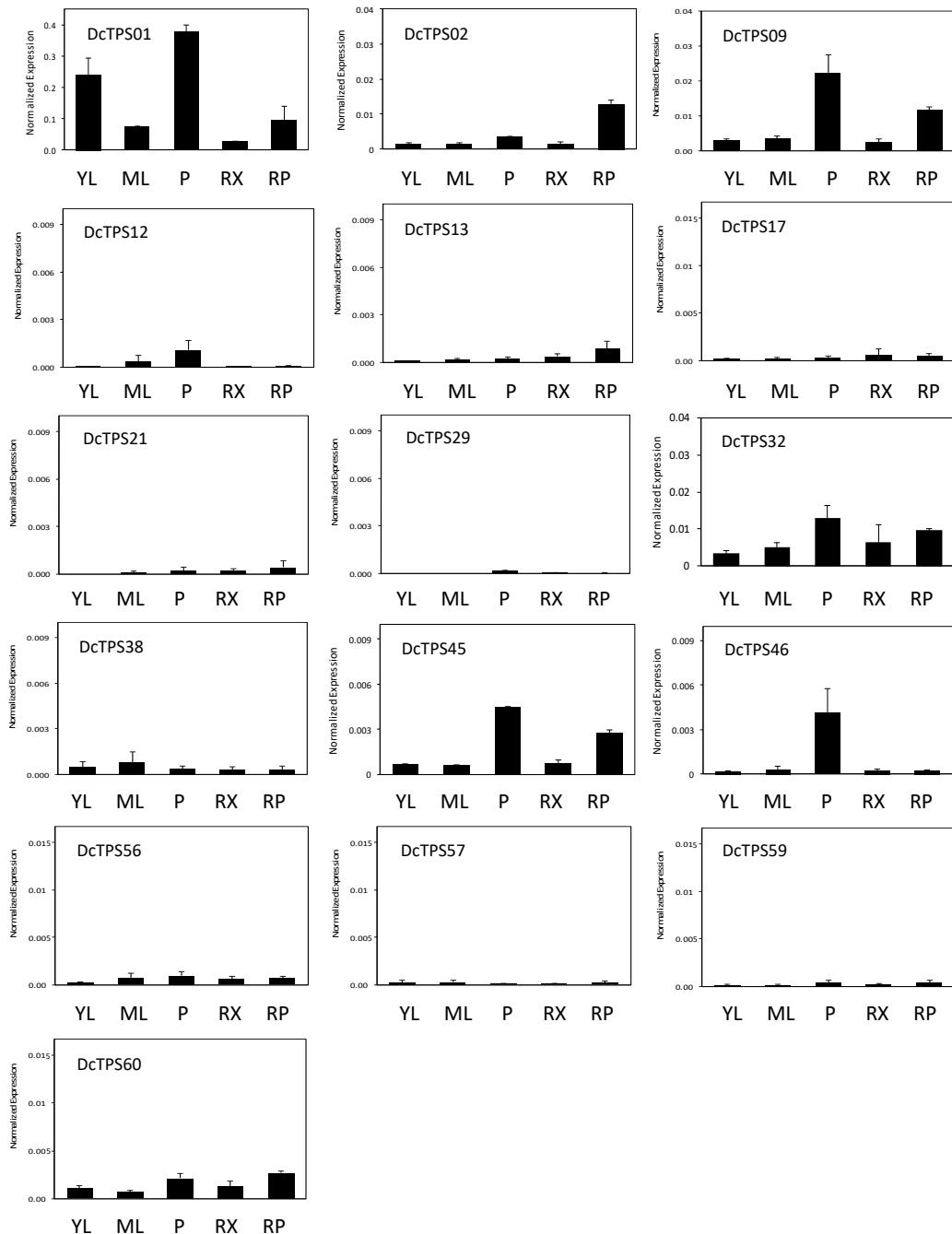
Supplementary Figure S7. Amino acid sequence alignment of proteins in the carrot TPS-c sub-family and other select TPSs of this subfamily. Alignments were performed using Clustal W⁴³ and visualized with BoxShade (v3.21, https://embnet.vital-it.ch/software/BOX_form.html); At, *Arabidopsis thaliana*; Dc, *Daucus carota*.

At1g79460	1	-----MSINLRSSGCSSPISATERRI-----	DSEVQTRANNVSFOTEKIRKMLEKVELSVSAYDTSWVAMVPSPPSONAPLEPOC
DcTPS28	1	-----MIPPTILLYL-----	SIFILLFERKVTEESKEIRRLERKVELSVSAYDTAWVAMVPSPPHSHAPCFSGC
DcTPS56	1	MIYKFDFRANLPVKYQTFSKQN PVVSYPACLFSTSKPVAFHINSIL ILITHLSQD	HGKRERIRSLFSKVELSVSAYDTAWVAMVPSPRHSOTPCFSNC
At1g79460	79	VKWLLDNOHE <u>DGSWGLDNHDHOSLKKDVLSSTLASILALKWCIGEROINKGQFIELNSALVTDETIQKPTGFDIIFPGMILKYARDLNLTIPLGSEVV</u> D	D
DcTPS28	68	<u>VDWILENQIKDGSWGLPQOSVRILKDD</u>	SISSTLACVALALKRWDVGEEHINKGIRFLKSNFASVTDNNQSSPQGFDIIFPGMLEYANDLGTLKPVEOTLLN
DcTPS56	101	<u>VDWILENQNDGSWGLPHENQWLKD</u>	LSSTLACILALKRWDVGKHEINRGCHFLELNFGSAIDDSQAPVGFDIIFPGMLEYATTLDLKLPIDOTTFN
At1g79460	179	<u>DMDIKRDLILKCDSEKFSSKGREAYLAYVLEGTRNLKDWLIVKYQORKNGSLFDS</u> PAFTAATQFTQFGNDCCCLRYLCSSLQKFEEAVPGVYPFDQYARLSII	D
DcTPS28	167	<u>TVLNKRAQEIKRCSENRPESEAYLAYSEGGMNLQNNDMV</u> I	KYQORKNGSLFNSPSTTAAYLNHIQNTGCLNYLSHLEKFGNAVPTVYPFDIYAHLCMV
DcTPS56	200	<u>DMILRKRDREIKRYSERQSQSEAYLAYSEGGMNSQNNDM</u> ICRFQORKNGSLFNSPSTTAASLSHTQNTGCLNYLRGVLKKFGDAVPTVYPFDIYARLCMV	
At1g79460	279	<u>VTLESLGIDRDFKDEIKSMLDDETYRYWLRGDEEICLDPLATCALAFRILLAHGVDVSYDPLKPF</u> AEESGFSDTLEGYVKNTFSVLELFKAQS- -YPHESA	D
DcTPS28	267	<u>DTLEPLGIDRHFKDEIRSVLDEAVSCWLQDDEELFMDVDT</u> CALAFRILEMNGYNVLSDKLTRIAKECYLNSLGENLKDTEALOLYRASEAIIYNSESA	
DcTPS56	300	<u>DNLDRGLIDWHFRQEI</u> RVLDDEEIKFDVATCALAFRILRVNGYDVS	PKLTOVAQEDYYCNSHGGHLNDTMEALELYRASQNIYPNETA
At1g79460	377	<u>LKKOCCWTKOYLEMELSSWVKTTSVRDKYLK---KEVEDALAAFSYASLERSDHRRKELNGSAVENTRVTKTSYRLHNICTSDILKLA</u> VDDFNFCQSTIHERE	D
DcTPS28	367	<u>LEKQNSWSNRFLEIKLSN--GSVHLDRCARIIFQEVH</u> DALKFFEHNSLERMVNRNIEQYEADSIRILKTSYSSPNISNAEVYRAGEDFNVCQSIQOK	
DcTPS56	400	<u>LEKQNSWSNRFLEIKLNN--RSVHSDKYUTSAMFQEVETALKFPYYATL</u> ERVVHRRSIEQYNTGNLIRLKTCLSENISNMFPRFAMEDFNTSQSIYQE	
At1g79460	474	<u>EMERPLDRWIVENRPLQELKFARQKILACYFSGAATLFSPELSDARISWAKGGVLT</u> TTVVDDFFDVGGSKEEELNLIHLVEKWDLNGVPPEYSSSEHVEIIIFS	D
DcTPS28	464	<u>ELKLLESWTVI</u> ESSPDKLKFARQKILACYFSSAAATLFSPELSDARISWAKNGILTTVVDDFFDVGGSEELNLIOLV	EKWDVNEETTECCSEHVRIIIFSAL
DcTPS56	497	<u>ELKLLESWTVDNKIRKTEFAREKRNVYCYFCAAATIFPPEL</u> HEARITWARYSILTAKVDDFFDNGGSPEELNLQIPLFRKWNVDVHTECCSENVRIEAL	
At1g79460	574	<u>RDTILETGDKAFTMQGRNVTHHTVKIWLDL</u> IKSMLREAEWSSDKSTPSLEDYMEANAYISFALGPIVLPA	D
DcTPS28	564	<u>HHTICEIIGESAFKROAWHVT</u> THITEIWLELLNSMLKEAEWTRDSYVPLDEYMSNGFISFALGPIVLPTV	YLDQYQNLKLVSTMGR
DcTPS56	597	<u>RSTICETVDPWASKQGRNVTHM</u> IEIWMEVLDMLKEAEWARGLYVPKMDEYENGIVS	FALGPIVLFTIYLVGPOLSES
At1g79460	674	<u>LNDIQGFKRESAEGKLNNAVSLHMKHERDNRSK</u> EVITIESMKGLAERKREELHNVLLEERGSVVPRECKEAFLKMSKVLNLFYRKDDGFTSN	D
DcTPS28	664	<u>LNDIQSFKRESKEGKLNNAVSLYMIH</u> T-DATTEEDAINBIKCAFEINRRELLOLVLQEKDSVVERACKDLFWKMRVHHQFY	IMLSLVRSL
DcTPS56	697	<u>LNDIQSYKRESKOKLNYVBLHMINT</u> -DSSSEEDAVGEIKRITDDORRELQR	KDDGFTSEDMGAVKDIL
At1g79460	774	VEPVSLQEEESLT	
DcTPS28	763	YKPT*RV*- --	
DcTPS56	796	HKPISSDLK*- --	

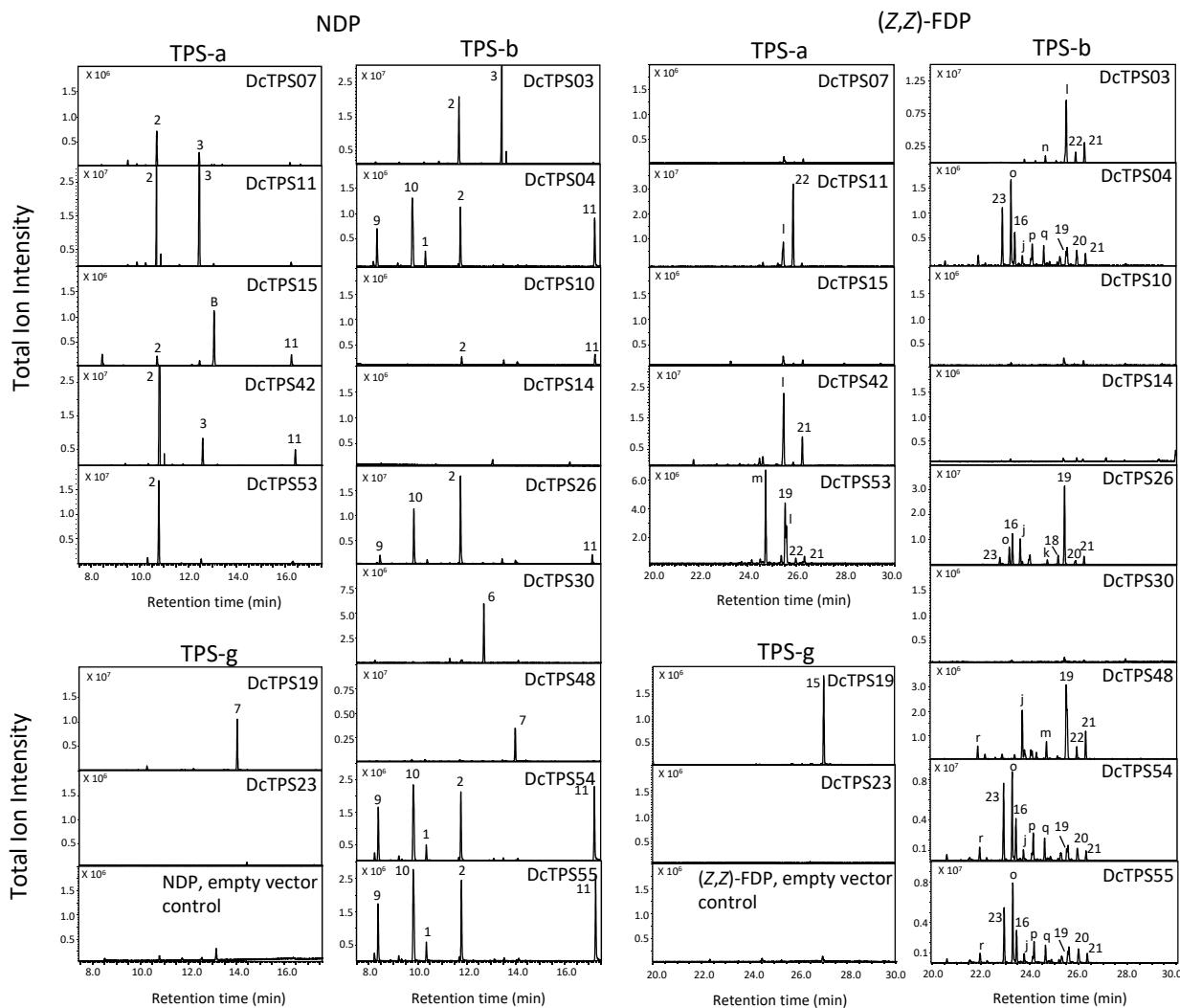
Supplementary Figure S8. Amino acid sequence alignment of proteins in the carrot TPS-e sub-family and other select TPSs of this subfamily. Alignments were performed using Clustal W⁴³ and visualized with BoxShade (v3.21, https://embnet.vital-it.ch/software/BOX_form.html); At, *Arabidopsis thaliana*; Dc, *Daucus carota*.

At1g61120_geran	1 -	[KSSYGSNSNDIHA[PNEIKGETIQLSNINLDPYSFVSPSAYDTAWLNTIEEDINVDDNELKEPMFOGCLDWIMCNCNAREGFWMNSTSYTTVADGRDED
DcTPS29	1 -	[KESYTSAAVIQVLVKEHQQLFSPQLONSSE--SPSAYDTAWLAMIPDS---NNTKNPMEKSCVQWILNNKE-GGEWG-----D
linalool_s_C_br	1	MQLITNFSSSSSBLQFLVDKVPRESISSSSNTQNIELSTSPYDTAWLAPIPHPOHHHHHGRPMFEKCLQWILHNOTP-QGFWAAAGDNIS----DTD
At1g61120_geran	99	GEKDMCILSTLACVVALOKWNIGCFHLHKGTRYIPRNTEMIIGKVINEEGSYPRWFHAKFTGMLLELAOKLGLHFVFSRSRCIEMIKGMFYQHOEIIOREK
DcTPS29	77	EDYLIHTLSSTLACILELIALATWNVGPKNIQOLCKSYVVVNAKKLLD---GNDRKLPRWFTJVFPAMLEQSERVDLHLNLPREIKALVSSFN----VGREK
linalool_s_C_br	94	DPVTLDCILSTLACLVALKRWQIAPDMIHKGLEEVNTERIVMK--QKPSDVPRWFTMFPAMLELGASSPRVDFSENINRILVEISQNRDDLTREE
At1g61120_geran	199	LVHDCNWKELLAYLEVELSKLYVTNOEDIIVVKSLDSMDGSLSFQSPSATAASFMLTRNTKCLAYIQLNVQKCPN-GVFQKYPLNEDLIKLSMVNLIESSTGL
DcTPS29	168	IDPNEHHSLLT-LSCPEAHFSACNIKLUHLVKNFEDGKLFKSFPEASAGYMP-TGHPAILKLYIESVVKFPC-GVPSVYPVDEDLIKLCIDKLINLGL
linalool_s_C_br	192	VDEKKOYSELLLELEALPAQSMDNDVILKOTIDKNSLNDGSILQSPSATARAYMTGNTTCLSLYHSLTNCSNGVPSFYPVDDDIHDLVMVNOLTRSGL
At1g61120_geran	298	GEPFGIEIEHVLPQVYSPVEERDF-PRMPMSYLADQIHKDSLAFRMLRHGRDVSPRSFCWFINDOEITRNHLPNIDPSFLIVILSVYRATDLMFGEHDL
DcTPS29	266	ABYBAVEIBETLACTYRSYVKNRAREQEDIHALVNIVKZLAFRLRGHGFDVTPCTFCWFEDHKNEMDHLSNSDIPASTIYNYRASDITFPGETEL
linalool_s_C_br	292	TEHLIPEIDHLLKVKQKNYKYKNA-SPKSLYSIAABLYRDSLAFLQRLRVNNHWSPSIFCWFLDDDEIRDHETNYEEFAVLLNVYRATDLMFGEVOL
At1g61120_geran	397	QEAREYTRNLLERRRSIKE-----KMTMHELSPTFWIARLKHDHRMWIEDKNSNVISMERASFLRLHSSYSDPLTHLAARNFPEQOAKYCRE
DcTPS29	366	DDPKRSFSRRLPBPIVSV-EYDRYGDNEQSFKOMIKRELINPWIARVDHLDHRMWIEENAPLICLERSFSFSRLSCLDDIDQIOLSVONYMFRQSLERRE
linalool_s_C_br	391	VEARSFATKNLEKILATGNIKTNADESSLSBKMIDPELVRPVWTARMHDHEVNREWIEEASSALWFGKSYSLRSLSCFHKMSIQLAVKNYTTROLVYRDE
At1g61120_geran	484	LEELTMWVKKGSDIIGFGREKTTTCYFATVTSPLPYEYAIFGKLAAKTAILITHADDFFDEKGFSNFDLEGTLKAVLRWEGEELKSYGNIIIFRALDIVR
DcTPS29	465	LEELIKSWSKRQLGIADMGFGREKTTTCYFACVCGTMYSHEHSITRKIVTKSAILITVADDFFDMDMEGSTBTFQFLTEAVQRWDGEGLTGPKSIIIFDALDFHVR
linalool_s_C_br	491	LAEVERWSKSERGICDMGFCREKTYGYCYAFAASTCIPWSIDVRLVITKAAVVITVADDFFDVEGSMVDFLEKLTDAVRWRDABGLGSISKTIREALDDLVN
At1g61120_geran	584	ETNTNTCRTTHEKTDIIVHPRNIWGETFPSWLREAEWSRKGH-----SSMDEYMRNGMISIAAHTIALSI-SCLMEOCPFPHKL-KPGNYDSITLTLMIIPRLL
DcTPS29	565	DMAEFLDHERNEMNNRIOTLWKETFVSWMETTWGETGVY---PSADEYIDVGMTSIAAHTIALPASCLLNORMPAEI-VNYDNETITNLMMNARLL
linalool_s_C_br	591	EVRLKCFQONGQDIIKNLQQLWYETFWSWLMEAKWGR-GTDSKPSVDVYICNAAMTSIAAHTMVLTA-SCLLGPFGPVHOTWSQRRHQDITSLLMVITRL
At1g61120_geran	680	NDLQSYOKEQEOGKMNCSVLLHMKNHPGLEITEDSTAHIEKITTDSKRKFELBVLDGLSLPLPKCKEIHMSCKVFEMFFNKKNRYDSNTEMIDIKKALY
DcTPS29	662	NDIQSYEKEQEEGKNNVLLBDKENLNADIDSINKVKEIDNENRMEFLERVLGNDSBMSKECKNLHSCLKVFEMFFNSSNLFDSKTALEIDIKAIY
linalool_s_C_br	689	NDIQSYLKEEDEGKINVWMYMIENNOASIDDSVREHQTINVKRCFELRVLSDOHCNLPKSIFDIDTDLLDIDIRAEAV
At1g61120_geran	780	DPIINVYELSEMEPMPLMAHGDYIMILLNLSLPNIIDEFKFRKD-----YGAMKTSMCFCRSYRVNKRVMASQLDDQHKBLKIVASQRKPVPMQSIFFP--
DcTPS29	762	IPPERNPLLRTTIX-P-----NCTSASMEFPKKG---FPKMLSENW-HGCRNMNRIGQK---LSRPHSSHCRVHIAEOLTTTG--
linalool_s_C_br	789	SPPQVPKFNPHEKPP-----HQLPATIOPPQHQPOQIMVNKKVENVY-KSYHHPFKVPTL---QKQSSGHT---MNEFASILAGPN
At1g61120_geran	875	---
DcTPS29	835	--FE*
linalool_s_C_br	865	IKLCEFS

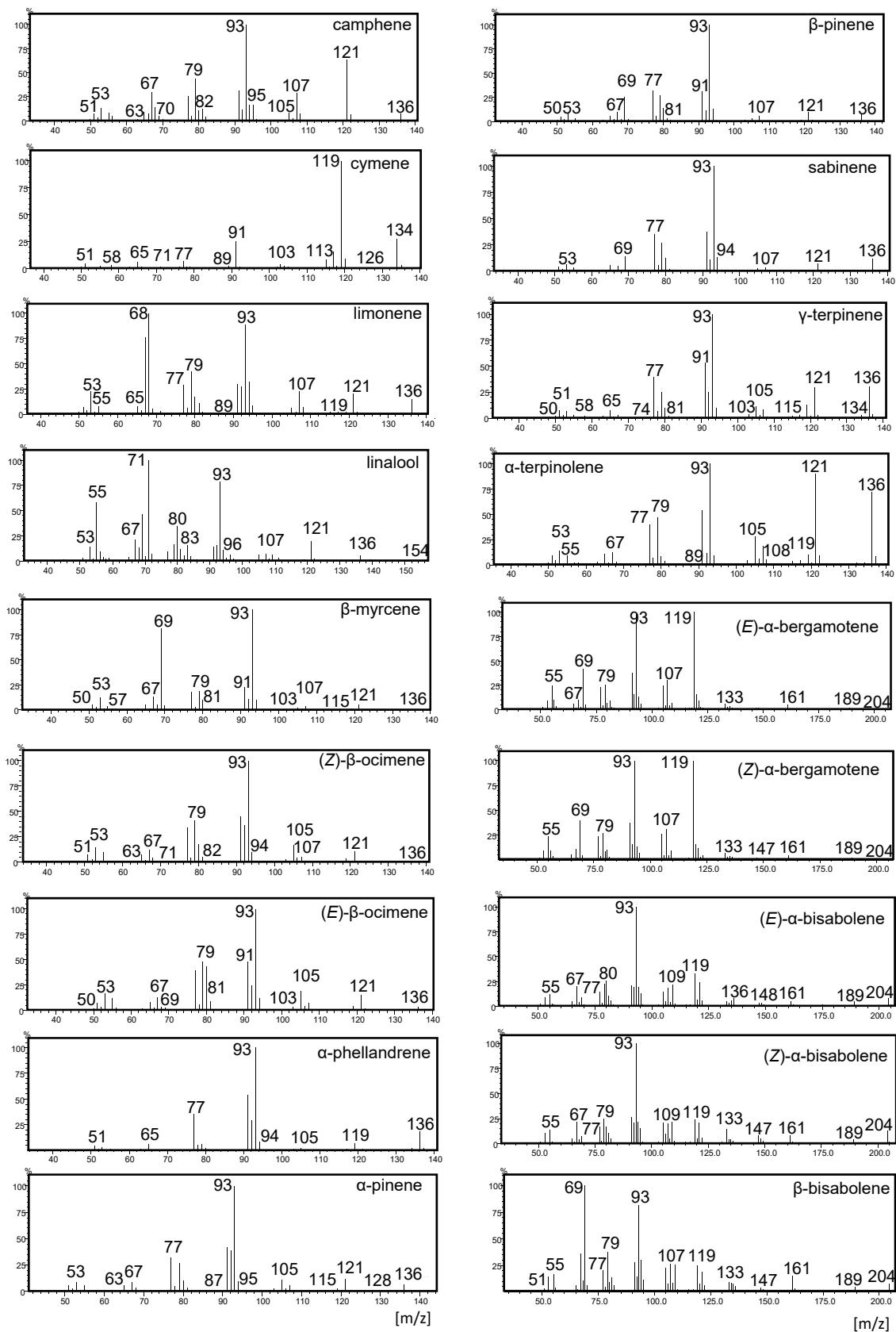
Supplementary Figure S9. Amino acid sequence alignment of proteins in the carrot TPS-f sub-family and other select TPSs of this subfamily. Alignments were performed using Clustal W⁴³ and visualized with BoxShade (v3.21, https://embnet.vital-it.ch/software/BOX_form.html); At, *Arabidopsis thaliana*; Cb, *Clarkia breweri*; Dc, *Daucus carota*.



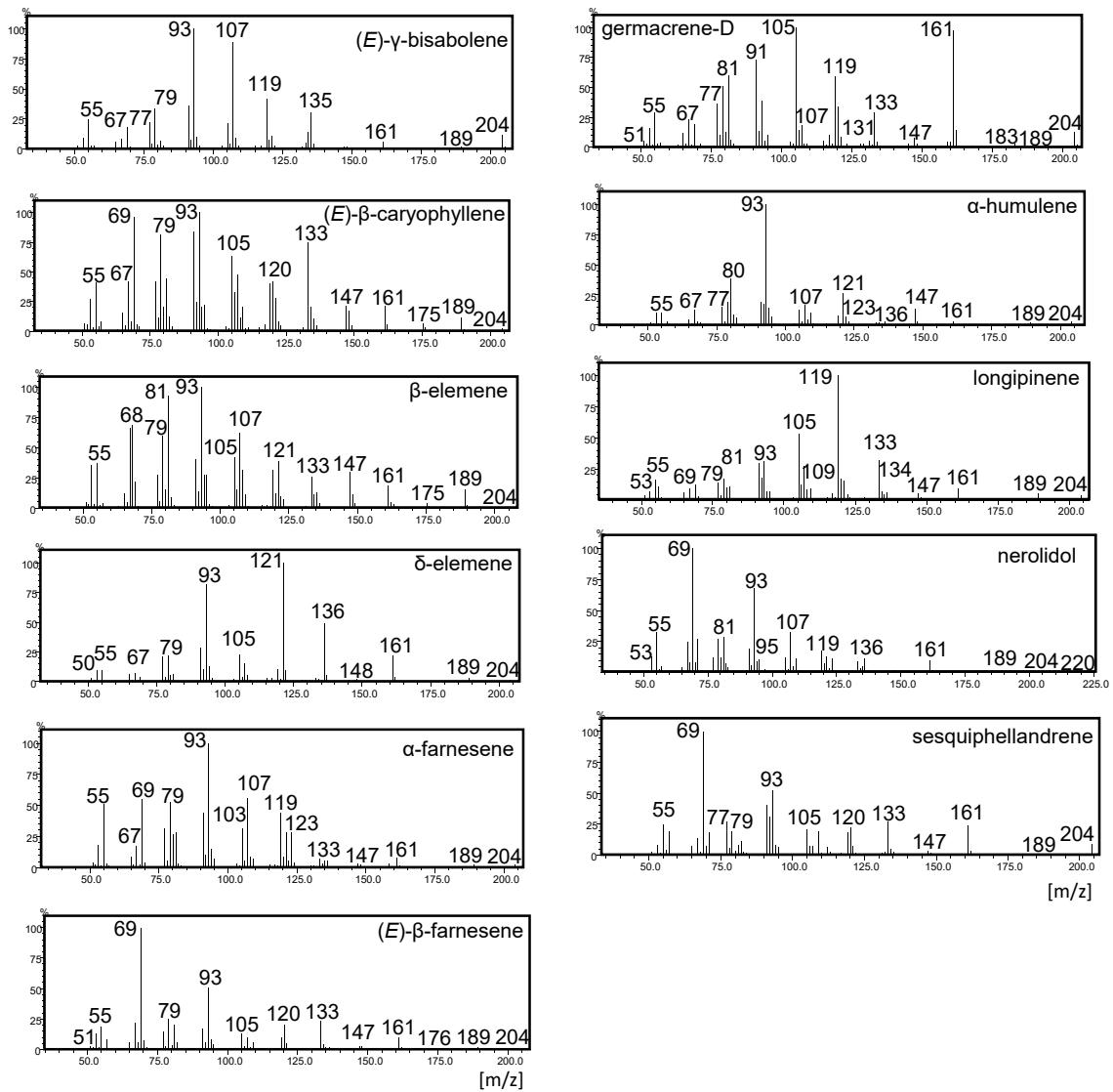
Supplementary Figure S10. qRT-PCR analysis of transcript abundance of TPS genes that were identified previously¹⁷ or not functionally characterized in this study. Relative expression levels across tissues for each gene were calculated using the $\Delta\Delta C_T$ standard method normalized to expression of actin. Amplifications were performed in biological and technical triplicate and error bars indicate standard deviation from the mean. YL: young leaf, ML: mature leaf, P: petiole, RX: root xylem and RP: root phloem.



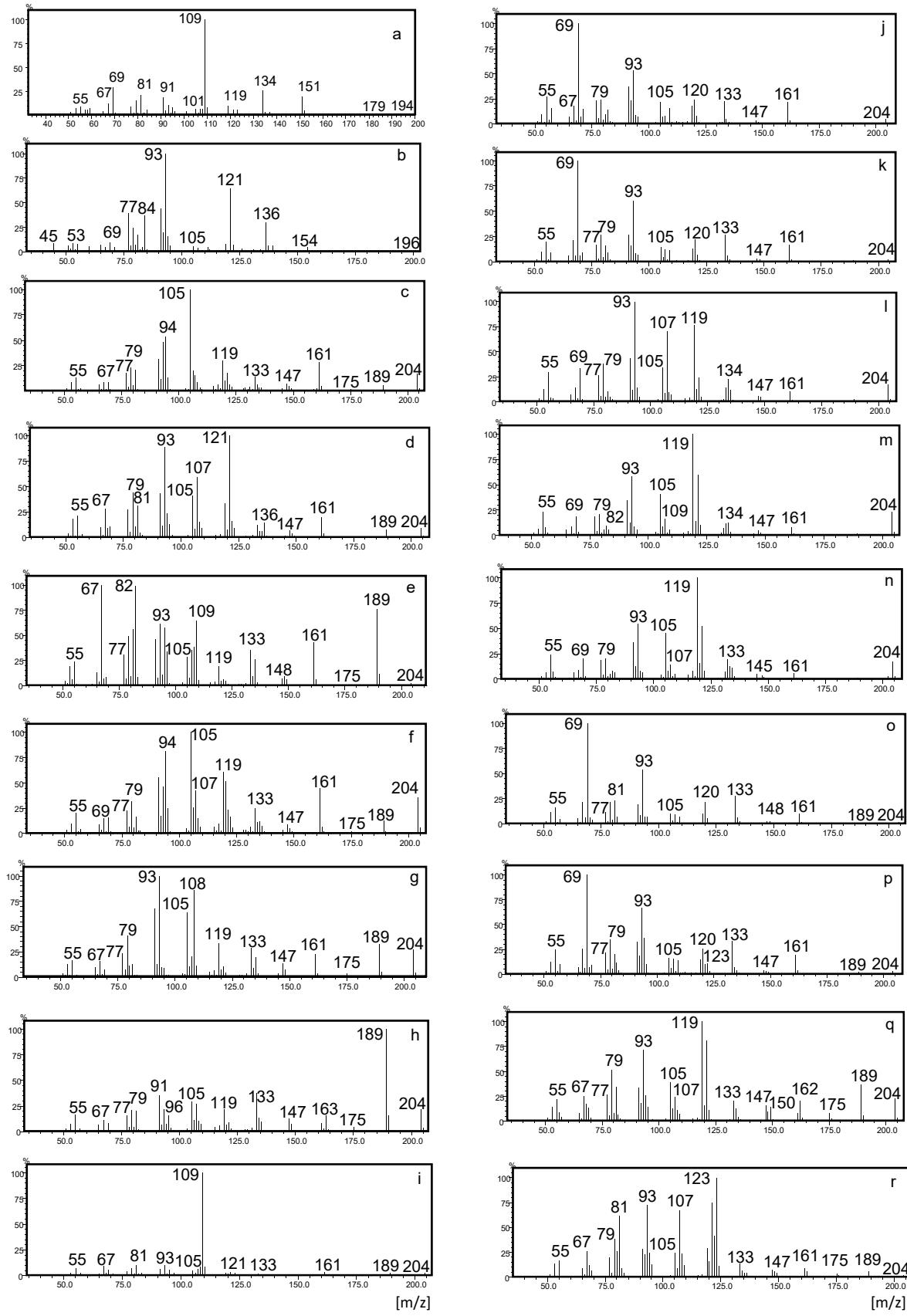
Supplementary Figure S11. SPME-GC-MS analysis of terpene products from assays with recombinant TPS enzymes. Partially purified proteins were incubated in the presence of NDP or (Z,Z)-FDP. Numbering of compounds matches that of Figure 4. 1: β -myrcene*, 2: limonene*, 3: α -terpinolene*, 6: γ -terpinene*, 7: linalool*, 9: α -pinene*, 10: sabinene*, 11: α -terpineol*, 15: nerolidol*, 16: (E)- α -bergamotene*, 18: (Z)- α -bisabolene*, 19: β -bisabolene*, 20: sesquiphellandrene*, 21: (E)- α -bisabolene*, 22: (E)- γ -bisabolene*, 23: (Z)- α -bergamotene*. * indicates compounds that were identified with authentic standards or by comparison with compounds of Opopanax oil. Mass spectra of these compounds are shown in Supplementary Figure S12. Lower case letters indicate additional terpene compounds with identification confidence levels <90%. Mass spectra of these compounds are depicted in Supplementary Figure S13. Note that retention times of products obtained from TPS-a enzymes with NDP are shifted by 1 min due to difference in column condition. B; SPME fiber-related background occurring in some assays.



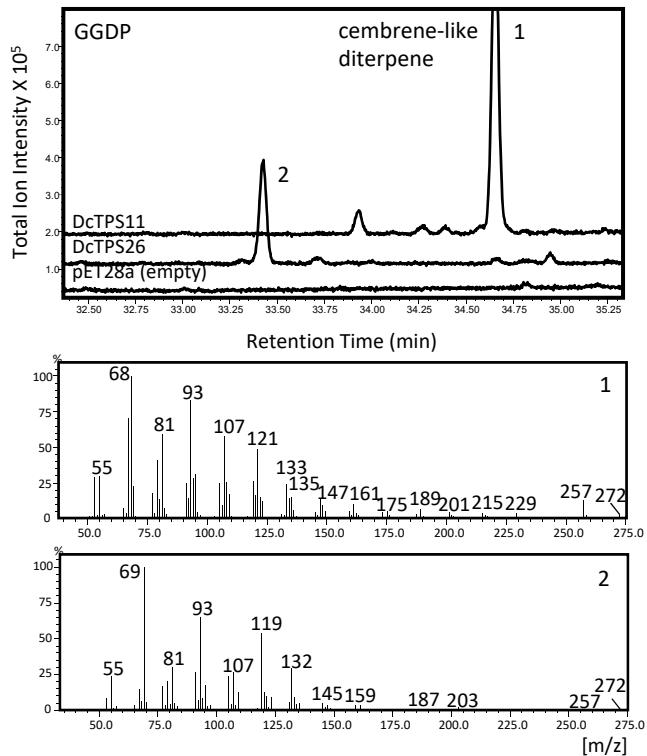
Supplementary Figure S12. Mass spectra of enzymatic products identified by comparison to authentic standards and components of Opopanax oil.



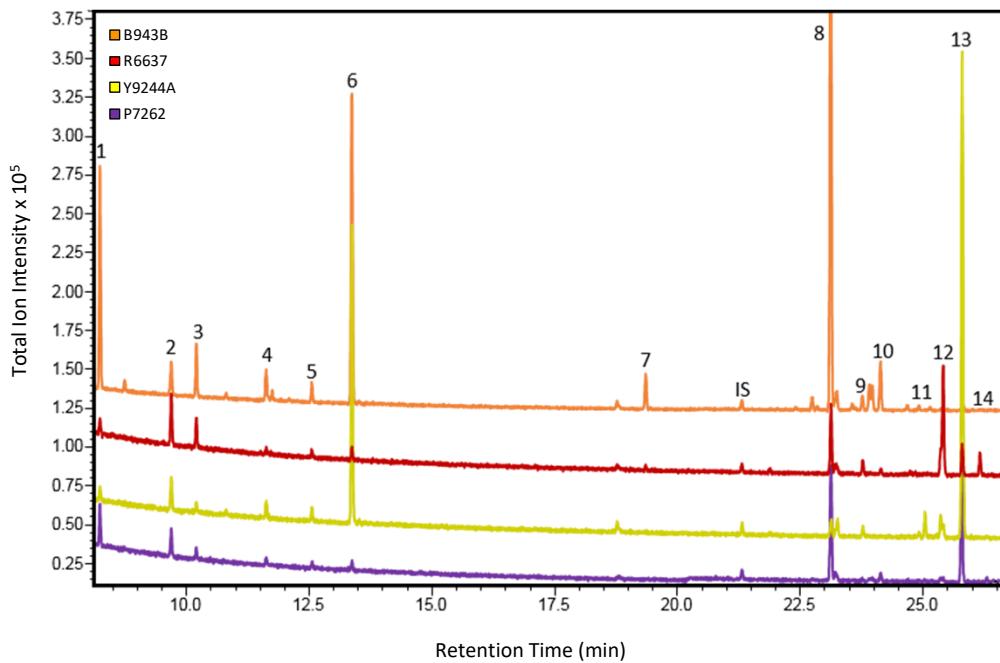
Supplementary Figure S12 continued.



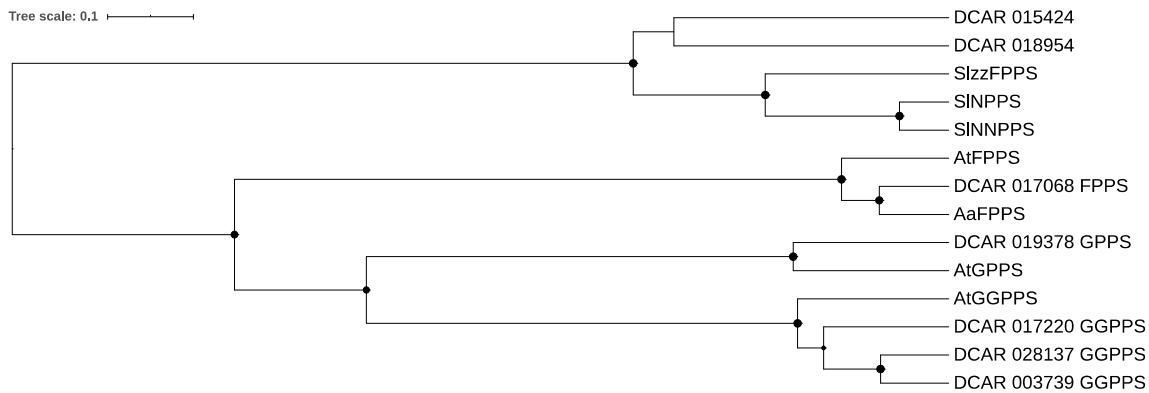
Supplementary Figure S13. Mass spectra of enzymatic sesquiterpene products with identification confidence levels <90%. The letters refer to compound peaks shown in Figure 4 and Supplementary Figure S11. Compounds j, n, and o are putative farnesene isomers. Compound k is a putative bisabolene isomer.



Supplementary Figure S14. SPME-GC-MS analysis of enzyme assays with GGDP and partially purified recombinant *DcTPS11* and *DcTPS26* protein or empty vector control. Assays were incubated for 5 min in the presence of a SPME fiber prior to thermal desorption. Putative compound identification is based on comparisons to reference libraries (NIST and Wiley). Mass spectra of putative diterpene products 1 and 2 are presented below.



Supplementary Figure S15. GC-MS analysis of hexane extracts from roots of 11-week old, field grown colored carrot cultivars. 1: α -pinene*, 2: β -pinene*, 3: β -myrcene*, 4: limonene*, 5: γ -terpinene*, 6: α -terpinolene*, 7: bornyl acetate, 8: (*E*)- β -caryophyllene*, 9: (*E*)- β -farnesene*, 10: α -humulene*, 11: β -bisabolene*, 12: Putative bisabolene isomer, 13: (*E*)- γ -bisabolene*, 14: (*E*)- α -bisabolene*, IS: internal standard 1-bromodecane. *indicates compounds that were identified with authentic standards or by comparison with compounds of Opopanax oil. Other labeled compounds were identified by library comparison only. Purple (cv. P7262), Red (cv. R6637), Yellow (cv. Y9244A) and Orange (cv. B493B).



Supplementary Figure S16. Maximum-likelihood phylogenetic tree of putative carrot (DCAR) *trans*- and *cis*-IDSs and known *trans*- and *cis*-IDS from other plant species. Circles indicate bootstrap support of > 80% where bootstrap replicates = 500. At, *Arabidopsis thaliana*; Aa, *Artemisia annua*; Sl, *Solanum lycopersicum*. GPPS, geranyl diphosphate synthase; FPPS, farnesyl diphosphate synthase; GGPPS, geranylgeranyl diphosphate synthase; NPPS, neryl diphosphate synthase; NNPPS, nerylneryl diphosphate synthase.