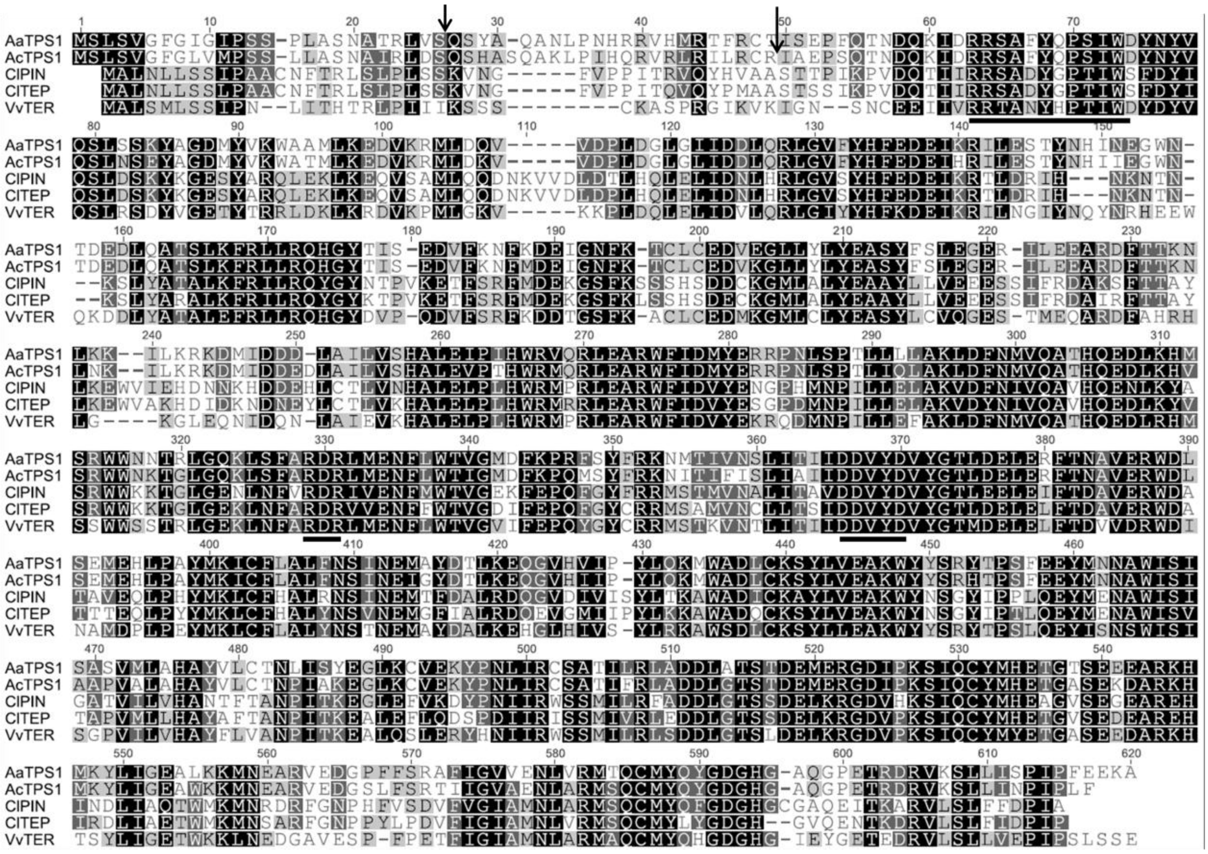
A)



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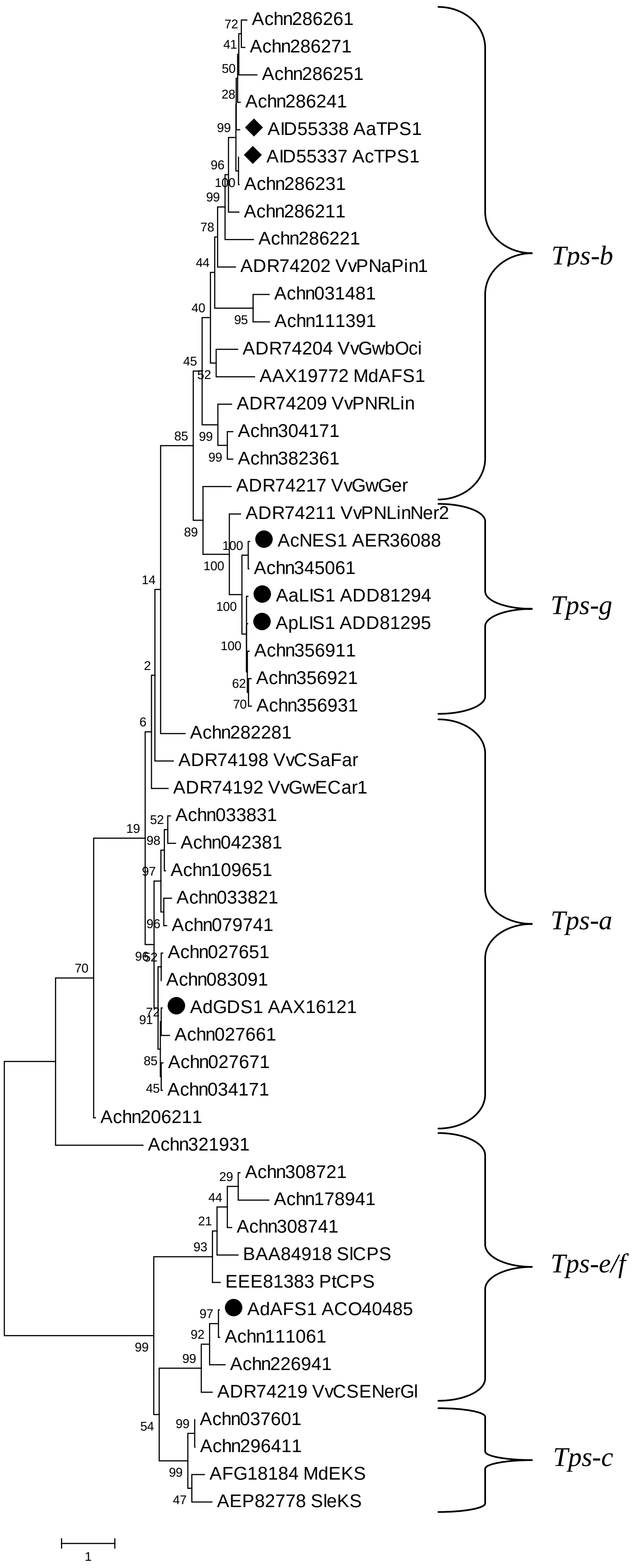
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28 Achn286241
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◆ AID55337 AcTPS1
96
100 Achn286231
99 Achn286211
78 Achn286221
44 ADR74202 VvPNaPin1
Achn031481
40
95 Achn111391
ADR74204 VvGwbOci
45
52 AAX19772 MdAFS1
ADR74209 VvPNRLin
85
99 Achn304171
99 Achn382361
ADR74217 VvGwGer
ADR74211 VvPNLinNer2
89
100 ● AcNES1 AER36088
100 Achn345061
14
100 ● AaLIS1 ADD81294
● ApLIS1 ADD81295
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ADR74192 VvGwECar1
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96 52 Achn027651
Achn083091
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Achn206211
Achn321931
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21 Achn308741
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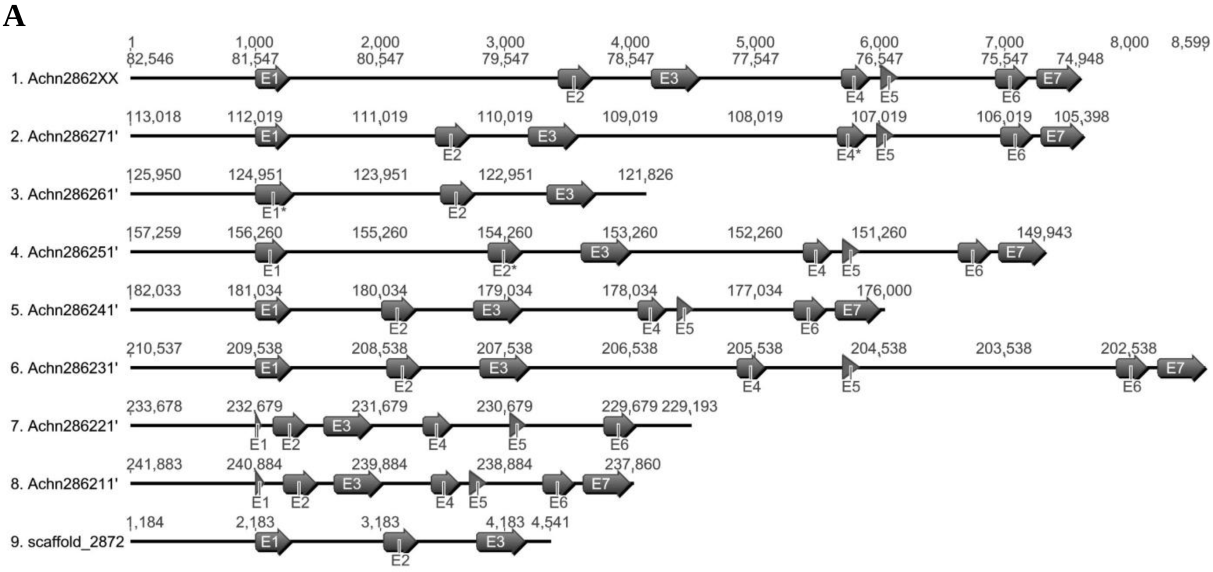
EEE81383 PtCPS
97 ● AdAFS1 ACO40485
92 Achn111061
99
99 Achn226941
ADR74219 VvCSENerGl
54
99 Achn037601
Achn296411
99 AFG18184 MdEKS
47 AEP82778 SleKS
1
Tps-b
Tps-g
Tps-a
Tps-e/f
Tps-c

Figure S1.
(A) Alignment of the deduced amino acid sequences of *AaTPS1* and *AcTPS1* and other *Tps-b* subfamily terpene synthases. Abbreviations with GenBank accessions in brackets: AaTPS1 (*Actinidia arguta* terpene synthase 1 - AID55338), AcTPS1 (*A. chinensis* terpene synthase 1 - AID55337), ClPIN (*Citrus limon* (-)-β-pinene synthase - AAM53945), ClTEP (*Citrus limon* γ-terpinene synthase - AAM53943) and VvTER (*Vitis vinifera* (-)-α-terpineol synthase - AAS79351). The highly conserved metal cofactor binding region (DDXXD) as well as the conserved RXR and RRX_8W motifs are underlined. The cleavage sites of the predicted chloroplast targeting peptides (ChloroP predictions) are marked with arrowheads. Sequence alignments were constructed using ClustalX (Thompson, 1997) and visualized using MEGA5 (Tamura et al., 2011).

(B) Unrooted Maximum Likelihood tree of *AcTPS1* and *AaTPS1* with other terpene synthases from kiwifruit, grape, apple, tomato and poplar. *AcTPS1* and *AaTPS1* from this work are indicated by black diamonds. Previously published functionally characterized kiwifruit TPS sequences are indicated by black circles. Thirty-five TPS gene models (Achn numbers) were identified in the kiwifruit 'Hongyang' genome (Huang et al., 2013) using BLASTP searches (cut-off < $1e^{-2}$) using full length TPS protein sequences from grape, tomato, apple, poplar as query sequences. The evolutionary history was inferred by using the Maximum Likelihood method based on the Dayhoff matrix based model (Schwarz and Dayhoff, 1979). The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 55 amino acid sequences. There were a total of 2260 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 (Tamura et al., 2013). Multiple amino acid sequence alignments of the TPS genes were first performed with ClustalW using the using Geneious® v6.1.6 (www.geneious.com), the alignment was then exported in Phylip format and imported in MEGA6 for the analysis. Bootstrap values are shown as a percentage based on 1000 replicates. The scale bar represents expected changes per site. TPS families are bases on (Bohlmann et al., 1998; Dudareva et al., 2003).

Abbreviations with GenBank accessions in brackets are as follows: AaTPS1 = *Actinidia arguta* terpene synthase 1 (AID55338); AcTPS1 = *A. chinensis* terpene synthase 1 (AID55337); AdAFS1 = *A. deliciosa* (E,E)-α-farnesene synthase (ACO40485); AdGDS1 = *A. deliciosa* (+)-germacreneD synthase (AAX16121); AaLIS1 = *A. arguta* linalool synthase (ADD81294); ApLIS1 = *A. polygama* linalool synthase (ADD81295); AcNES1 = *A. chinensis* nerolidol syntase (AER36088); VvGwECar1 = *Vitis vinifera* (E)-β-caryophyllene synthase (ADR74192), VvCSaFar = (E,E)-α-farnesene synthase (ADR74198), VvPNRLin = (3R)-linalool synthase (ADR74209), VvPNaPin1 = pinene synthase (ADR74202), VvGwbOci = (E)-β-ocimene synthase (ADR74204), VvGwGer = geraniol synthase (ADR74217), VvPNLinNer2 = (3S)-linalool/(E)-nerolidol synthase (ADR74211), VvCSENerGl = P(E)-nerolidol/(E,E)-geranyl linalool synthase (ADR74219); MdAFS1 = *Malus domestica* (E,E)-α-farnesene synthase (AAX19772), MdEKS = ent-kaurene synthase (AFG18184); SleKS = *Solanum lycopersicum* ent-kaurene synthase (AEP82778), SlCPS = copalyl diphosphate synthase (BAA84918); PtCPS = *Populus trichocarpa* copalyl diphosphate synthase (EEE81383).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76,547
75,547
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E4
E5
E6
E7
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106,019
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E5
E6
E7
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122,951
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E3
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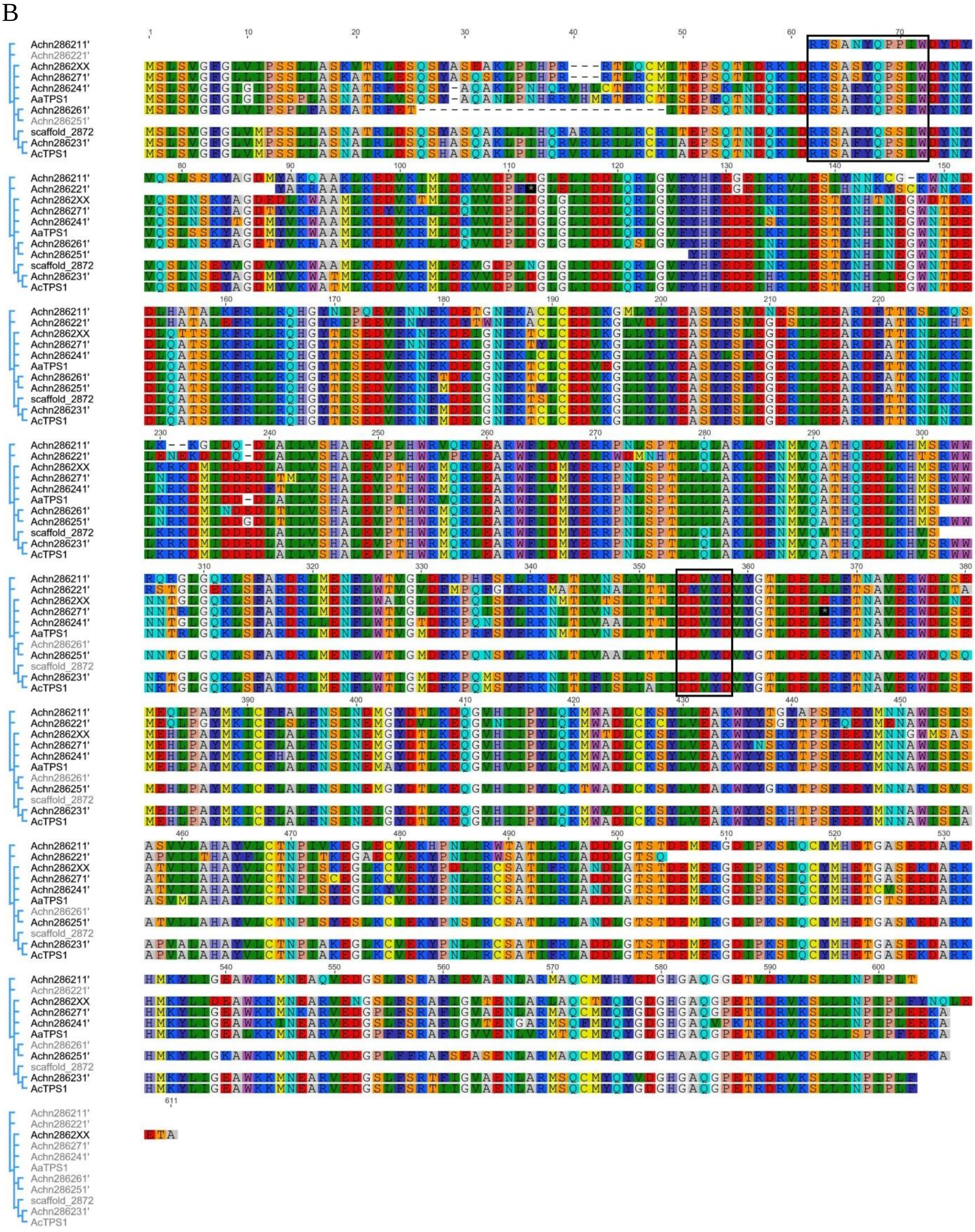
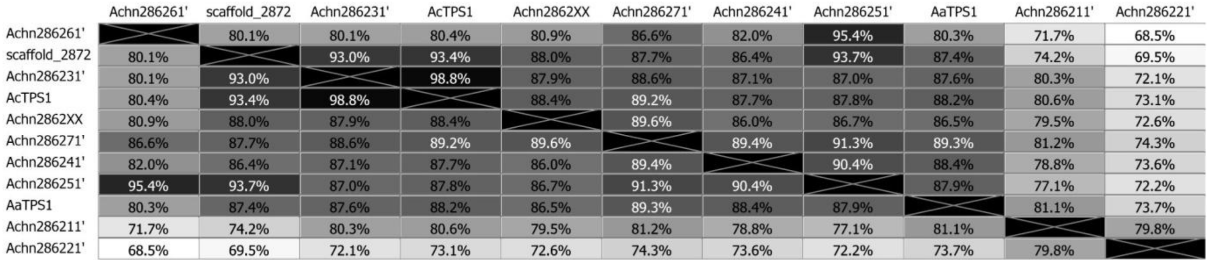
E2
E3


B
Achn286211'
Achn286221'
Achn2862XX
Achn286271'
Achn286241'
AaTPS1
Achn286261'
Achn286251'
scaffold_2872
Achn286231'
AcTPS1

C



	Achn286261'	scaffold_2872	Achn286231'	AcTPS1	Achn2862XX	Achn286271'	Achn286241'	Achn286251'	AaTPS1	Achn286211'	Achn286221'
Achn286261'		80.1%	80.1%	80.4%	80.9%	86.6%	82.0%	95.4%	80.3%	71.7%	68.5%
scaffold_2872	80.1%		93.0%	93.4%	88.0%	87.7%	86.4%	93.7%	87.4%	74.2%	69.5%
Achn286231'	80.1%	93.0%		98.8%	87.9%	88.6%	87.1%	87.0%	87.6%	80.3%	72.1%
AcTPS1	80.4%	93.4%	98.8%		88.4%	89.2%	87.7%	87.8%	88.2%	80.6%	73.1%
Achn2862XX	80.9%	88.0%	87.9%	88.4%		89.6%	86.0%	86.7%	86.5%	79.5%	72.6%
Achn286271'	86.6%	87.7%	88.6%	89.2%	89.6%		89.4%	91.3%	89.3%	81.2%	74.3%
Achn286241'	82.0%	86.4%	87.1%	87.7%	86.0%	89.4%		90.4%	88.4%	78.8%	73.6%
Achn286251'	95.4%	93.7%	87.0%	87.8%	86.7%	91.3%	90.4%		87.9%	77.1%	72.2%
AaTPS1	80.3%	87.4%	87.6%	88.2%	86.5%	89.3%	88.4%	87.9%		81.1%	73.7%
Achn286211'	71.7%	74.2%	80.3%	80.6%	79.5%	81.2%	78.8%	77.1%	81.1%		79.8%
Achn286221'	68.5%	69.5%	72.1%	73.1%	72.6%	74.3%	73.6%	72.2%	73.7%	79.8%	

Figure S2.
(A) Mapping of *AcTPS1* exons 1-7 onto scaffolds in the kiwifruit genome. To improve the TPS gene models identified in the kiwifruit genome, exons 1-7 of *AcTPS1* were used as BLASTn query sequences against the kiwifruit genome scaffold database (http://bioinfo.bti.cornell.edu/cgi-bin/kiwi/home.cgi). A schematic showing the structure of eight tandemly repeated, full-length and partial TPS1-like gene models (Achn286211'-XX) identified on scaffold_575 (length 316,842 bp) is shown. Scaffold_2872 (length 5307 bp) also contained a portion homologous to *AcTPS1* exons 1-3.

(B) Amino acid alignment of manually curated kiwifruit TPS1-like gene models. Exons 1-7 for each TPS1-like gene model were extracted from the kiwifruit scaffold database, joined together, translated into protein and aligned using Geneious® v6.1.6/ClustalW/default settings (www.geneious.com). Sequences were manually curated to maximise alignment and the designated with a prime (') symbol. Only three genes (Achn286231', Achn286241' and Achn2862XX) showed an intact structure of seven complete exons and no in-frame stop codons (asterisks). The conserved RRX8W and DDXXD domains are boxed.

C) Sequence identity table of aligned kiwifruit TPS1-like amino acid sequences.

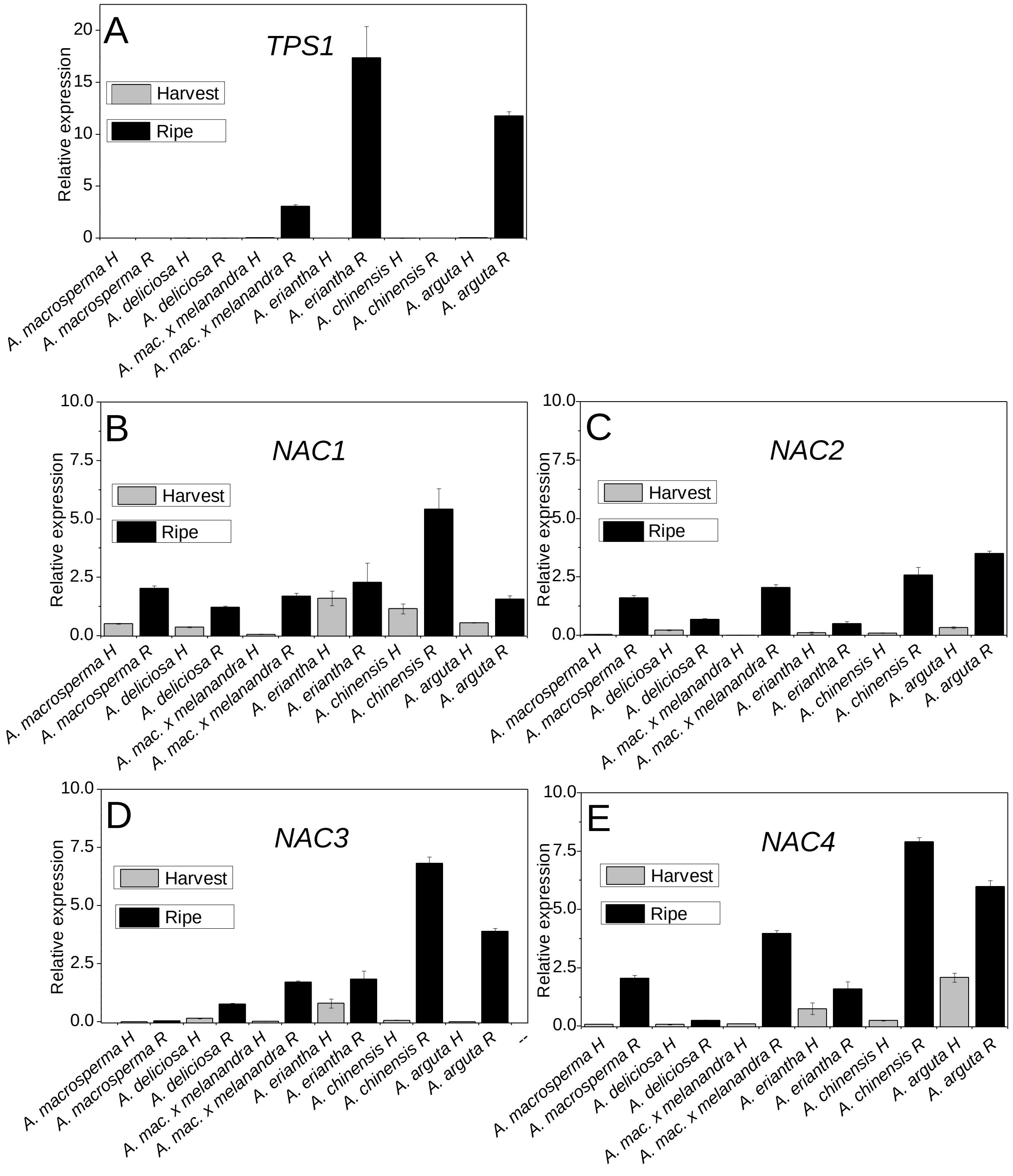


Figure S3.
Real-time qPCR analysis of *TPS1* (A) and *NAC1-4* (B-E) gene expression levels in harvest (H) and ripe (R) fruit for six *Actinidia* species. Analyses were performed on pooled fruit samples using gene specific primers given in Table S2. The *TPS1* primers were designed to amplify both *AaTPS1* and *AcTPS1*. Achn286241 and Achn2862XX expression was also tested using gene specific primers but both were not expressed in harvest or ripe fruit. Error bars are based on four technical replicates and data were normalized against the housekeeping gene EF1α. The *A. mac.* x *melanandra* sample represent fruit from an interspecific cross between *A. macrosperma* and *A. melanandra*.

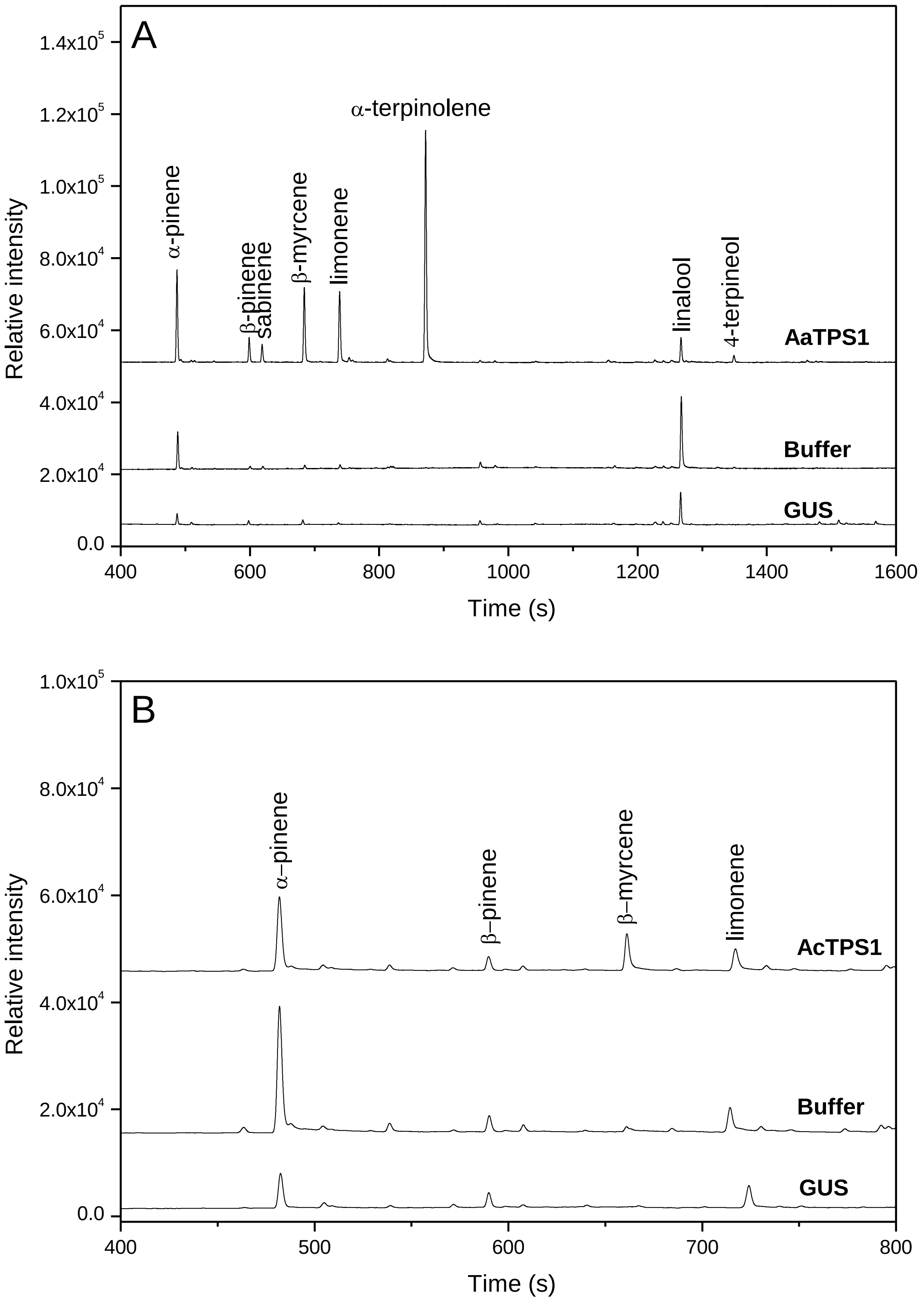
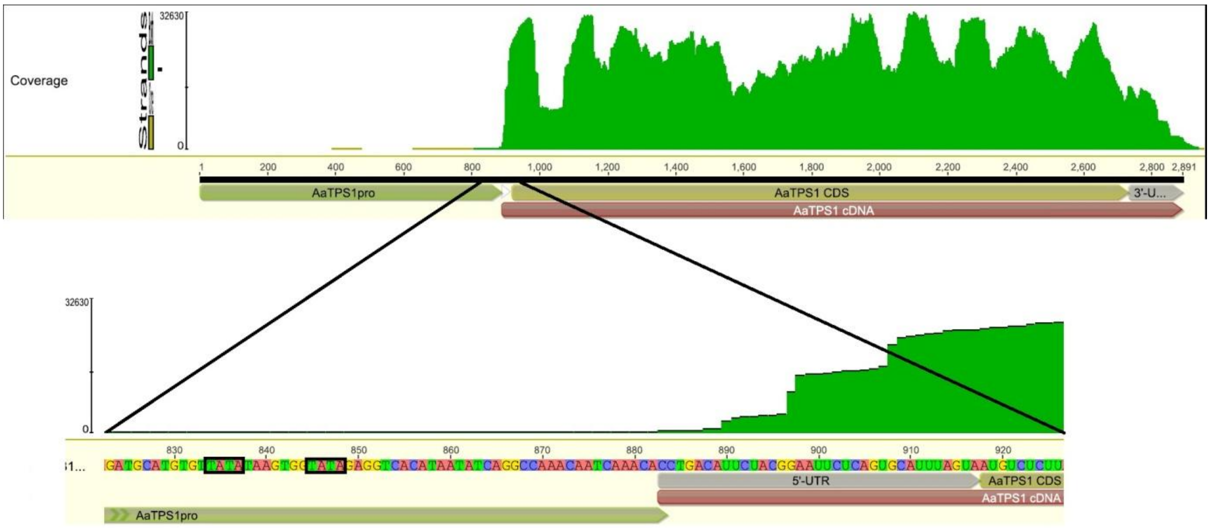

A
Relative intensity
1.4x10^5
1.2x10^5
1.0x10^5
8.0x10^4
6.0x10^4
4.0x10^4
2.0x10^4
0.0
α-pinene
β-pinene
sabinene
β-myrcene
limonene
α-terpinolene
linalool
4-terpineol
AaTPS1
Buffer
GUS
400
600
800
1000
1200
1400
1600
Time (s)
B
Relative intensity
1.0x10^5
8.0x10^4
6.0x10^4
4.0x10^4
2.0x10^4
0.0
α–pinene
β–pinene
β–myrcene
limonene
AcTPS1
Buffer
GUS
400
500
600
700
800
Time (s)

Figure S4. GC-MS analysis of the monoterpenes produced by transient expression of *AaTPS1* and *AcTPS1 in planta*. The complete open reading frames of *AaTPS1* and *AcTPS1* were cloned into the binary vector pHEX2 and transformed into *Agrobacterium tumefaciens*. Bacterial cell suspensions were injected into the abaxial side of three young *Nicotiana benthamiana* leaves and volatiles were assayed 2 weeks after injection by dynamic headspace sampling of detached leaves. Leaves were infiltrated with buffer-only and with a vector expressing the *GUS* reporter gene (pHEX2-GUS) as controls. (A) *AaTPS1* - upper trace; buffer-only (mock infiltrated) - middle trace; *GUS* - lower trace. (B) *AcTPS1* - upper trace; buffer-only - middle trace; *GUS* - lower trace. Analyses were made in triplicate with only a single representative trace shown for each treatment.

A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AaTPS1pro
AaTPS1 CDS
3'-U...
AaTPS1 cDNA
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850
860
870
880
890
900
910
920
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AaTPS1 cDNA
AaTPS1pro

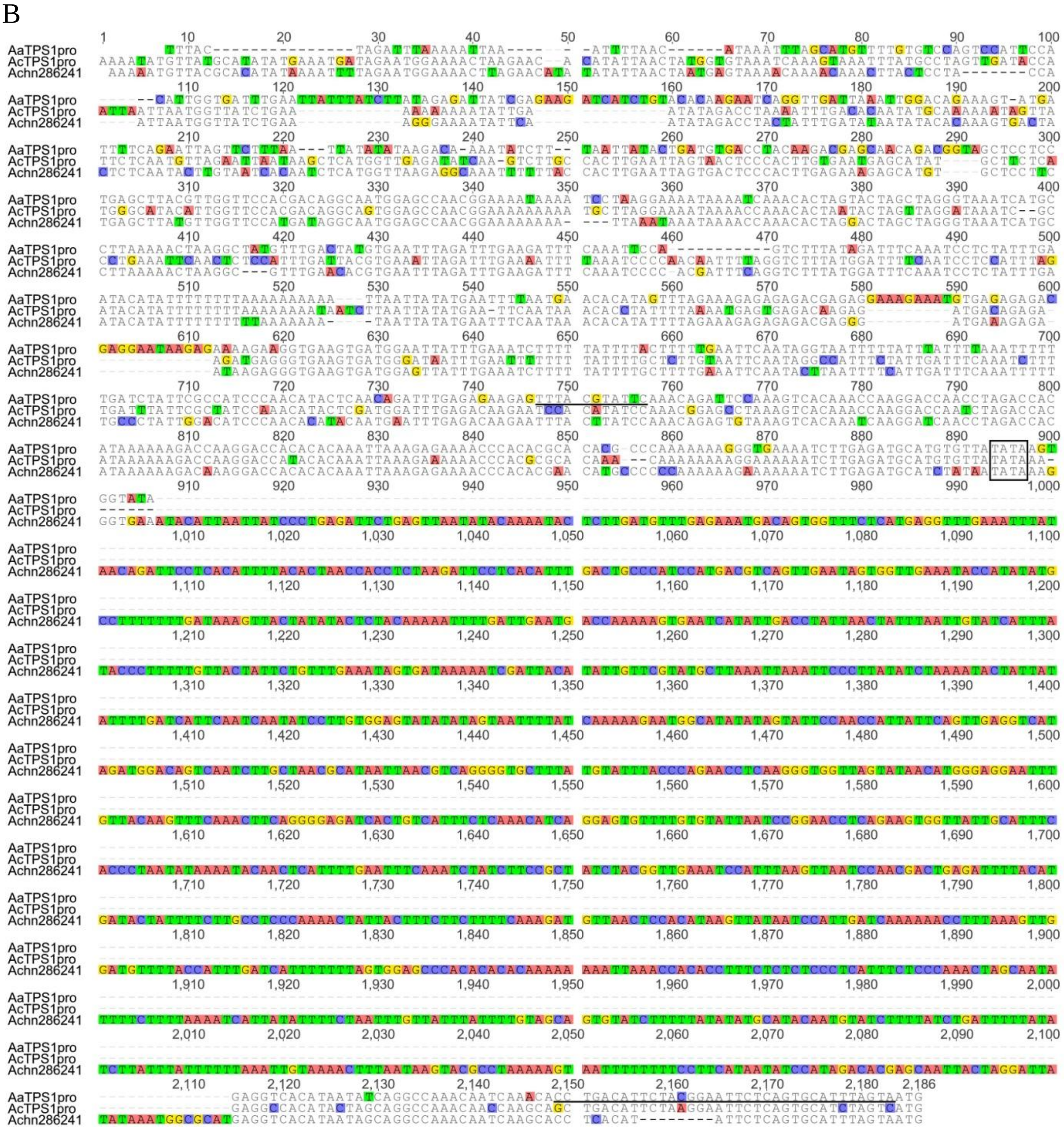
B
AaTPS1pro
AcTPS1pro
Achn286241

Figure S5.

(A) Identifying the transcriptional start site in the 5’-UTR of *AaTPS1*. Illumina sequencing data derived from *Actinidia arguta* fruit mRNA (ripening stage C3, Fig 2) was read mapped against the *AaTPS1* gene (*AaTPS1* promoter fused to the *AaTPS1* cDNA). Boxed sequences = putative TATA boxes. The 5’-UTR (in grey) is estimated to be 35 bp from the ATG (start of translation). Read mapping was performed using Geneious® v6.1.6/Align/Assemble/Map to reference. Parameters: Custom, Word length 30, Index word length 15, ignore words repeated more than 12 times, Max mismatch per read 10%, Maximum ambiguity 4, No gaps allowed. Library size: 37,154,393 reads (41-88 bp post trimming).

(B) Sequence alignment of *AaTPS1*, *AcTPS1* and *Achn286241* promoter regions. The kiwifruit genome scaffold database (http://bioinfo.bti.cornell.edu/cgi-bin/kiwi/home.cgi) was searched using BLASTn to identify regions of homology to the *AaTPS1* promoter. The *AaTPS1* promoter sequence (~0.9 kb) was then aligned with the *AcTPS1* (~0.9 kb) and *Achn286241* (~2.2 kb) upstream regions using Geneious® v6.1.6/Muscle align/default settings (www.geneious.com). The *AaTPS1* promoter shares significant sequence identity to the *AcTPS1* (68%) and *Achn286241* promoter (71%, excluding insertion) but not to other TPS1-like genes on scaffold_575. *Achn286241* shows an insertion of ~1.2 kb around the predicted TATA region (boxed), while *AcTPS1* shows significant divergence in the predicted NAC binding site (underlined at bp 750). The 5’-UTR in *AaTPS1* is underlined upstream of the ATG start codon (as determined above). The *AcTPS1* promoter sequence used in this work is 99% identical to the 3 kb Achn286231 upstream region.

```
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                  GCT CTC TG GC TAC TTGGTTCCACGACAGGCA TGGAGCCAACGGAAAA AAAAT
AcTPS1pro-648   1 GCTTCTCATGGGCATACATTGGTTCCACGACAGGCAGTGGAGCCAACGGAAAAAAAAATG 60

AaTPS1pro-668  61 CTAAGGAAAATAAAATCAAACACTAGTACTAGCTAGGGTAAATCATGCCTTAAAAACTAA 120
                  CT AGGAAAATAAAA CAAACACTA TACTAG TAGG TAAATC  GCC T AAA   AA
AcTPS1pro-648  61 CTTAGGAAAATAAAACCAAACACTAATACTAGTTAGGATAAATC--GCCCTGAAATTCAA 118

AaTPS1pro-668  121 GGCTATGTTTGACTATGTGAATTTAGATTTGAAGATTTCAAATTCC-----------AGT 169
                   CT     TTTGA TA GTGAA TTAGATTTGAA ATTT AAAT CC            GT
AcTPS1pro-648  119 CTCTCCATTTGATTACGTGAAATTAGATTTGAAAATTTTAAATCCCCAACAATTTTAGGT 178

AaTPS1pro-668  170 CTTTATAGATTTCAAATCCTCTATTTGAATACATATTTTTTTTAAAAAAAAAA---TTAA 226
                   CTTTAT GATTT  AATCCTC ATTT  ATACATATTTTTTTTAAAAAAAA A   TTAA
AcTPS1pro-648  179 CTTTATGGATTTTCAATCCTCCATTTAGATACATATTTTTTTTAAAAAAAATAATCTTAA 238

AaTPS1pro-668  227 TTATATGAATTTTAATGAACACATAGTTTAGAAAGAGAGAGACGAGAGGAAAGAAATGTG 286
                   TTATATGAA TT AAT AACAC TA TTTA AA GAG GAGAC AGAG          TG
AcTPS1pro-648  239 TTATATGAA-TTCAATAAACACCTATTTTAAAATGAGTGAGACAAGAG---------ATG 288

AaTPS1pro-668  287 AGAGAGACGAGGAATAAGAGAAAAGAAGGTGAAGTGATGGAATTATTTGAAATCTTTTTA 346
                   A AGAGA             A A GA GGTGAAGTGATGG AT ATTTGAA T TTTTTA
AcTPS1pro-648  289 ACAGAGA-------------AGATGAGGGTGAAGTGATGGGATAATTTGAATTTTTTTA 335

AaTPS1pro-668  347 TTTTACTTTTTGAATTCAATAGGTAATTTTTATTTATTTTAAATTTTTTGATCTATTCGC 406
                   TTTT CT TT  AATTCAATAGG  ATTT TATT ATTT AAAT TTTTGAT TATTCGC
AcTPS1pro-648  336 TTTTGCTCTTGTAATTCAATAGGCCATTTCTATTGATTTCAAATCTTTTGATTTATTCGC 395

AaTPS1pro-668  407 CATCCCAACATACTCAACAGATTTGAGAGAAGAGTTTACGTATTCAAACAGATTCCAAAG 466
                    ATCC AACATACTC A  GATTTGAGA AAGA T  AC TAT CAAAC GA  C AAAG
AcTPS1pro-648  396 TATCCAAACATACTCGATGGATTTGAGACAAGAATCCACATATCCAAACGGAGCCTAAAG 455

AaTPS1pro-668  467 TCACAAACCAAGGACCAACCTAGACCACATAAAAAAGACCAAGGACCACACACAAATTAA 526
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AcTPS1pro-648  456 TCACAAACCAAGGACCAATCTAGACCACATAAAAAAGACCAAGGACCATACACAAATTAA 515

AaTPS1pro-668  527 AGAGAAAACCCACACGCACACGCCCAAAAAAAGGGTGAAAATCTTGAGATGCATGTGTTA 586
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AcTPS1pro-648  516 AGAAAAAACCCACGCGCACAAA--CAAAAAAAAGGAAAAAATCTTGAGATGCATGTGTTA 573

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AaTPS1pro-668  647 GGAATTCTCAGTGCATTTAGCCATG 671
                   GGAATTCTCAGTGCAT TAGCCATG
AcTPS1pro-648  627 GGAATTCTCAGTGCATCTAGCCATG 651
```
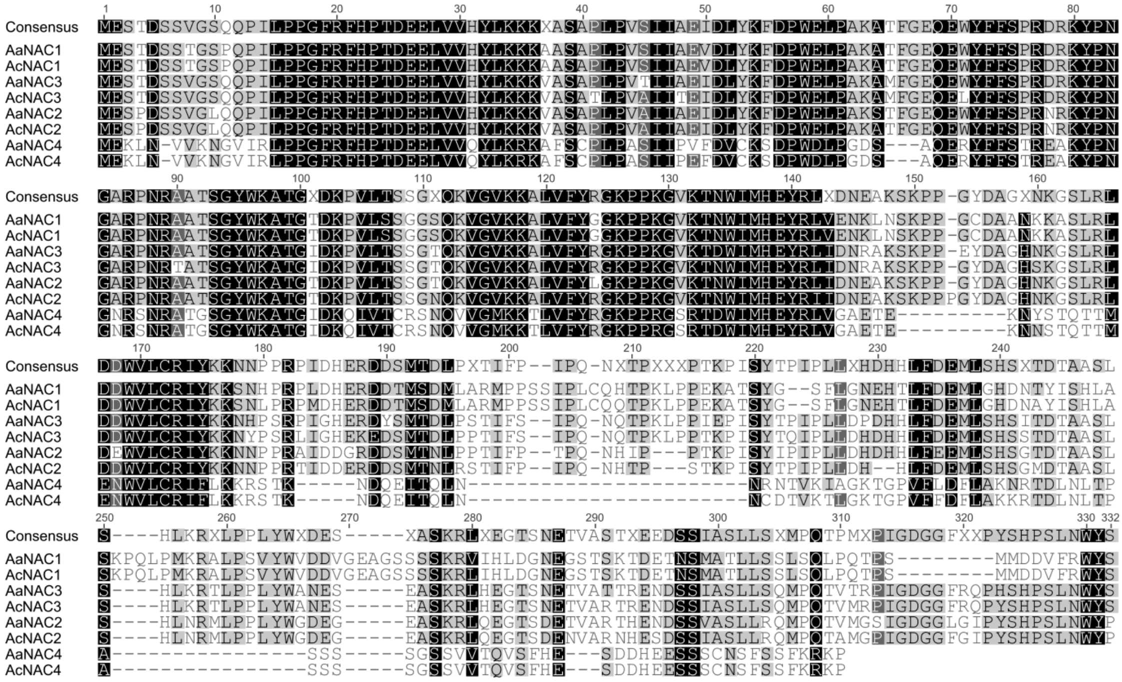

Figure S6. Binding sites in the *AaTPS1* and *AcTPS1* promoter regions. The translational start codon is indicated in bold. Highlighted promoter elements are: EIN3 binding site AYGWAYCT (Kosugi and Ohashi, 2000); EIN3 binding site ATGCATCT (Boutrot et al., 2010); NAC binding site YACGTAABY (Fig 6); Ethylene Response Elements (EREs) AWTTCAAA (Montgomery et al., 1993; Itzhaki et al., 1994; Tapia et al., 2005). Underlined: 5’-untranslated region (5’-UTR) based on Fig. S5A (*AaTPS1*) or available EST information (*AcTPS1*).

A)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AaNAC1 MESTDSSTGSPQPILPPGFRFHPTDEELVVHYLKKKAASAPLPVSIIAEVDLYKFDPWELPAKATFGEQEWYFFSPRDRKYPN
AcNAC1 MESTDSSTGSPQPILPPGFRFHPTDEELVVHYLKKKAASAPLPVSIIAEVDLYKFDPWELPAKATFGEQEWYFFSPRDRKYPN
AaNAC3 MESTDSSVGSQQPILPPGFRFHPTDEELVVHYLKKKVASAPLPVTIIAEIDLYKFDPWELPAKAMFGEQEWYFFSPRDRKYPN
AcNAC3 MESTDSSVGSQQPILPPGFRFHPTDEELVVHYLKKKVASATLPVAIITEIDLYKFDPWELPAKAMFGEQELYFFSPRDRKYPN
AaNAC2 MESPDSSVGLQQPILPPGFRFHPTDEELVVHYLKKKVASAPLPVAIIAEIDLYKFDPWELPAKSTFGEQEWYFFSPRNRKYPN
AcNAC2 MESPDSSVGLQQPILPPGFRFHPTDEELVVHYLKKKVASAPLPVAIIAEIDLYKFDPWELPAKATFGEQEWYFFSPRNRKYPN
AaNAC4 MEKLN-VVKNGVIRLPPGFRFHPTDEELVVQYLKRKAFSCPLPASIIPVFDVCKSDPWDLPGDS---AQERYFFSTREAKYPN
AcNAC4 MEKLN-VVKNGVIRLPPGFRFHPTDEELVVQYLKRKAFSCPLPASIIPEFDVCKSDPWDLPGDS---AQERYFFSTREAKYPN
90 100 110 120 130 140 150 160
Consensus GARPNRAATSGYWKATGXDKPVLTSSGXQKVGVKKALVFYRGKPPKGVKTNWIMHEYRLXDNEAKSKPP-GYDAGXNKGSLRL
AaNAC1 GARPNRAATSGYWKATGTDKPVLSSGGSQKVGVKKALVFYGGKPPKGVKTNWIMHEYRLVENKLNSKPP-GCDAANKKASLRL
AcNAC1 GARPNRAATSGYWKATGTDKPVLSSGGSQKVGVKKALVFYGGKPPKGVKTNWIMHEYRLVENKLNSKPP-GCDAANKKASLRL
AaNAC3 GARPNRAATSGYWKATGIDKPVLTSSGTQKVGVKKALVFYRGKPPKGVKTDWIMHEYRLIDNRAKSKPP-EYDAGHNKGSLRL
AcNAC3 GARPNRTATSGYWKATGIDKPVLTSSGTQKVGVKKALVFYRGKPPKGVKTNWIMHEYRLIDNRAKSKPP-GYDAGHSKGSLRL
AaNAC2 GARPNRAATSGYWKATGTDKPVLTSSGTQKVGVKKALVFYLGKPPKGVKTNWIMHEYRLIDNEAKSKPP-GYDAGHNKGSLRL
AcNAC2 GARPNRAATSGYWKATGTDKPVLTSSGNQKVGVKKALVFYRGKPPKGVKTNWIMHEYRIIDNEAKSKPPPGYDAGHNKGSLRL
AaNAC4 GNRSNRATGSGYWKATGIDKQIVTCRSNQVVGMKKTLVFYRGKPPRGSRTDWIMHEYRLVGAETE---------KNYSTQTTM
AcNAC4 GNRSNRATGSGYWKATGIDKQIVTCRSNQVVGMKKTLVFYRGKPPRGSRTDWIMHEYRLVGAETE---------KNNSTQTTM
170 180 190 200 210 220 230 240
Consensus DDWVLCRIYKKNNPPRPIDHERDDSMTDLPXTIFP--IPQ-NXTPXXXPTKPISYTPIPLLXHDHHLFDEMLSHSXTDTAASL
AaNAC1 DDWVLCRIYKKSNHPRPLDHERDDTMSDMLARMPPSSIPLCQHTPKLPPEKATSYG--SFLGNEHTLFDEMLGHDNTYISHLA
AcNAC1 DDWVLCRIYKKSNLPRPMDHERDDTMSDMLARMPPSSIPLCQQTPKLPPEKATSYG--SFLGNEHTLFDEMLGHDNAYISHLA
AaNAC3 DDWVLCRIYKKNHPSRPIGHERDYSMTDLPSTIFS--IPQ-NQTPKLPPIEPISYTPIPLLDPDHHLFDEMLSHSITDTAASL
AcNAC3 DDWVLCRIYKKNYPSRLIGHEKEDSMTDLPPTIFS--IPQ-NQTPKLPPTKPISYTQIPLLDHDHHLFDEMLSHSSTDTAASL
AaNAC2 DEWVLCRIYKKNNPPRAIDDGRDDSMTNLPPTIFP--TPQ-NHIP---PTKPISYIPIPLLDHDHHLFEEMLSHSGTDTAASL
AcNAC2 DDWVLCRIYKKNNPPRTIDDERDDSMTNLRSTIFP--IPQ-NHTP---STKPISYTPIPLLDH--HLFDEMLSHSGMDTAASL
AaNAC4 ENWVLCRIFLKKRSTK-----NDQEITQLN-----------------------NRNTVKIAGKTGPVFLDFLAKNRTDLNLTP
AcNAC4 ENWVLCRIFLKKRSTK-----NDQEITQLN-----------------------NCDTVKTLGKTGPVFFDFLAKKRTDLNLTP
250 260 270 280 290 300 310 320 330 332
Consensus S----HLKRXLPPLYWXDES-----XASKRLXEGTSNETVASTXEEDSSIASLLSXMPQTPMXPIGDGGFXXPYSHPSLNWYS
AaNAC1 SKPQLPMKRALPSVYWVDDVGEAGSSSSKRVIHLDGNEGSTSKTDETNSMATLLSSLSQLPQTPS--------MMDDVFRWYS
AcNAC1 SKPQLPMKRALPSVYWVDDVGEAGSSSSKRLIHLDGNEGSTSKTDETNSMATLLSSLSQLPQTPS--------MMDDVFRWYS
AaNAC3 S----HLKRTLPPLYWANES-----EASKRLHEGTSNETVATTRENDSSIASLLSQMPQTVTRPIGDGGFRQPHSHPSLNWYS
AcNAC3 S----HLKRTLPPLYWANES-----EASKRLHEGTSNETVARTRENDSSIASLLSQMPQTVMRPIGDGGFRQPYSHPSLNWYS
AaNAC2 S----HLNRMLPPLYWGDEG-----EASKRLQEGTSDETVARTHENDSSVASLLRQMPQTVMGSIGDGGLGIPYSHPSLNWYP
AcNAC2 S----HLNRMLPPLYWGDEG-----EASKRLQEGTSDENVARNHESDSSIASLLRQMPQTAMGPIGDGGFGIPYSHPSLNWYP
AaNAC4 A----------------SSS-----SGSSVVTQVSFHE---SDDHEESSSCNSFSSFKRKP
AcNAC4 A----------------SSS-----SGSSVVTQVSFHE---SDDHEESSSCNSFSSFKRKP

B)

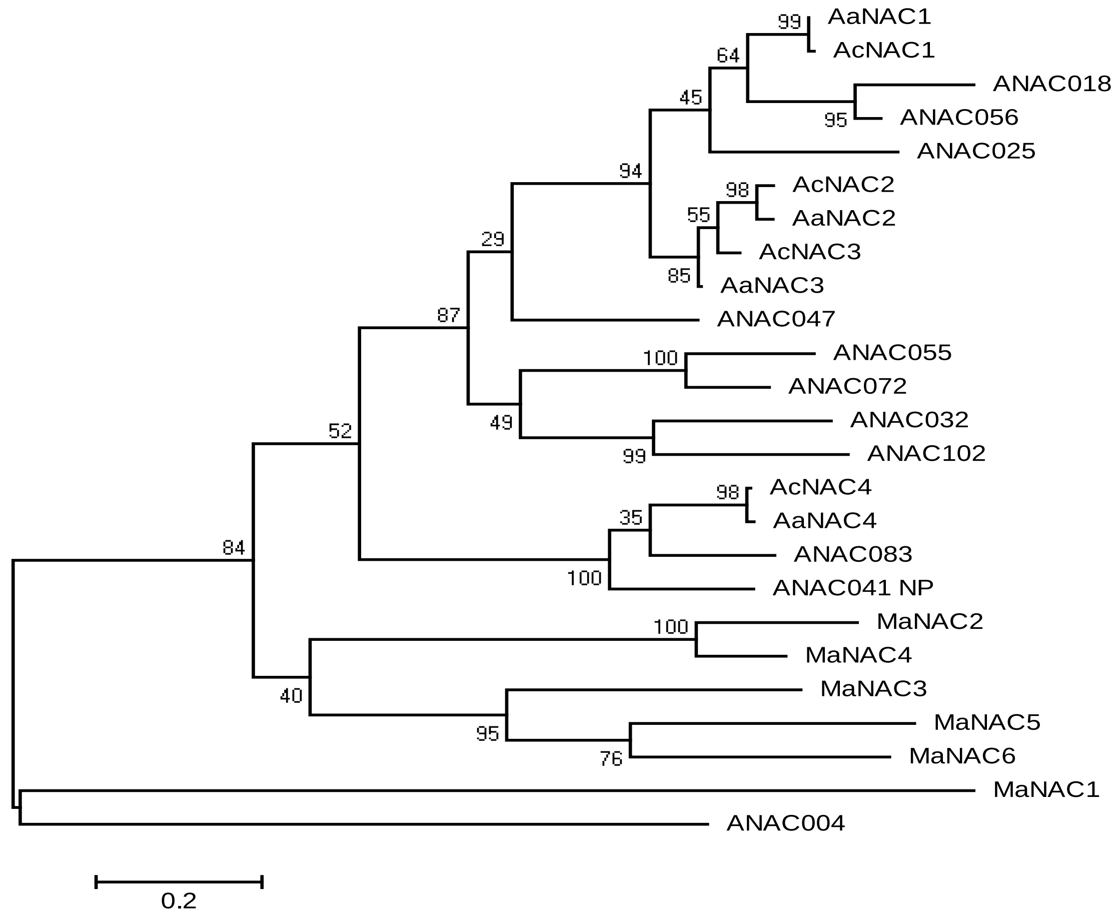
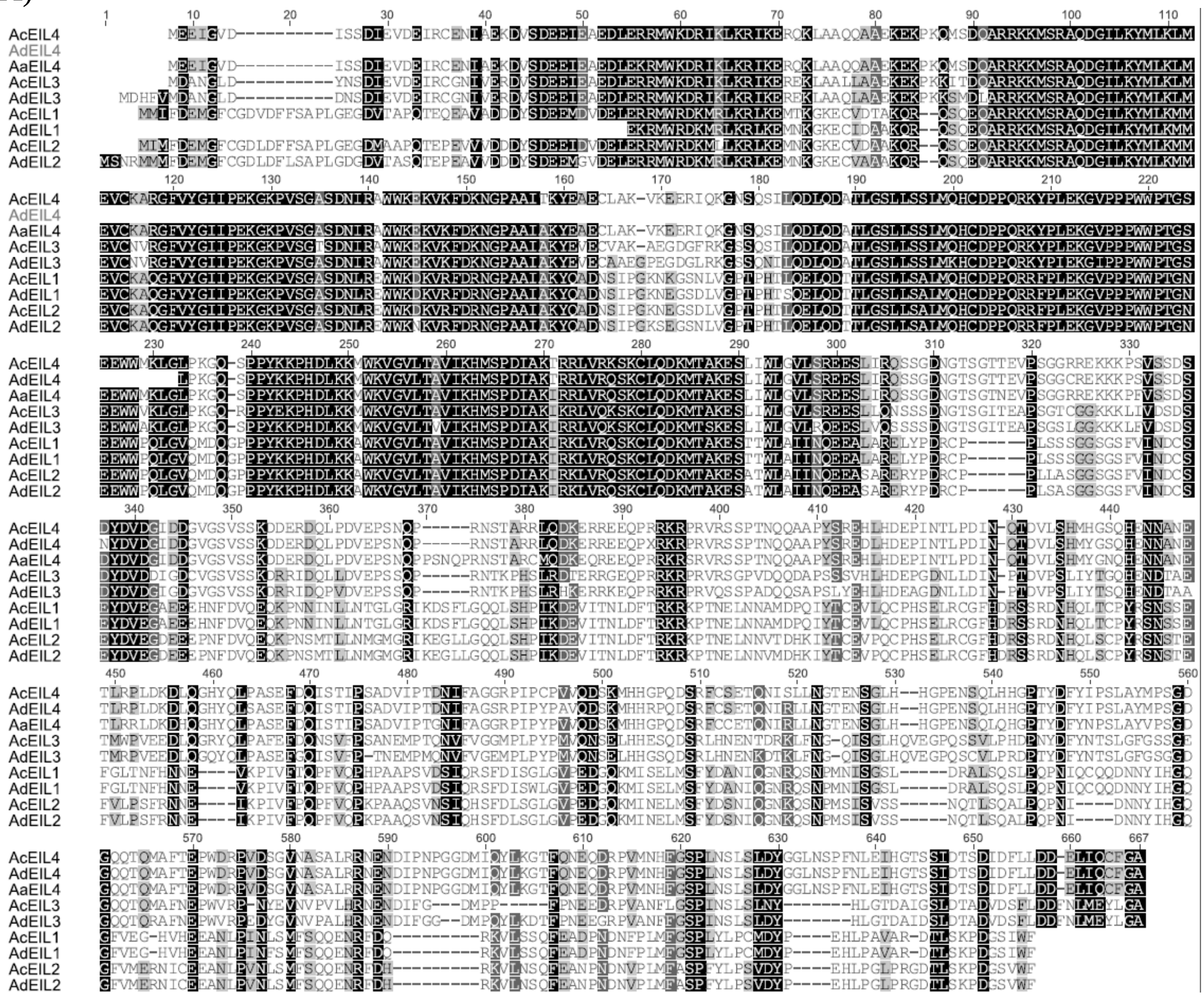


Figure S7.
(A) ClustalW alignment of the *Actinidia chinensis* (Ac) and *A. arguta* (Aa) *NAC1-4* proteins.

(B) Unrooted Maximum Likelihood tree of selected *Arabidopsis thaliana* (Ooka et al., 2003), *A. arguta* (Aa) and *A. chinensis* (Ac) NACs. *A. arguta*: AaNAC1 (KF319046), AaNAC2 (KF319047), AaNAC3 (KF319048), AaNAC4 (KF319049), *A. chinensis*: AcNAC1 (KF319050), AcNAC2 (KF319051), AcNAC3 (KF319052), AcNAC4 (KF319053). The evolutionary history was based on the JTT matrix-based model (Jones et al., 1992). The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. All positions containing gaps and missing data were eliminated. There were a total of 158 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 (Tamura et al., 2011).

A)


AcEIL4
AdEIL4
AaEIL4
AcEIL3
AdEIL3
AcEIL1
AdEIL1
AcEIL2
AdEIL2
1
10
20
30
40
50
60
70
80
90
100
110
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430
440
450
460
470
480
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640
650
660
667

B)

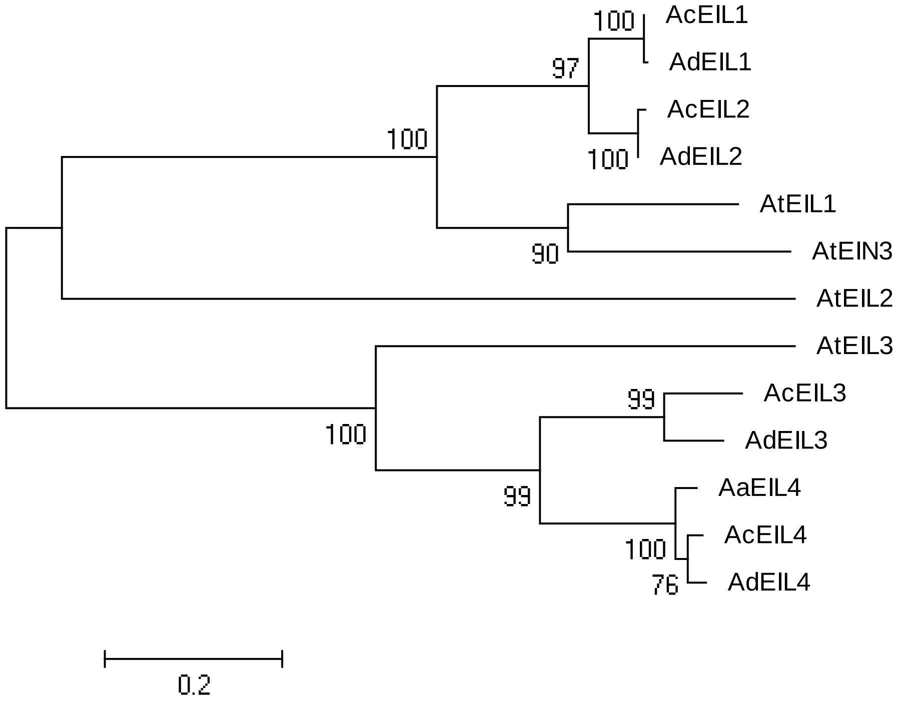
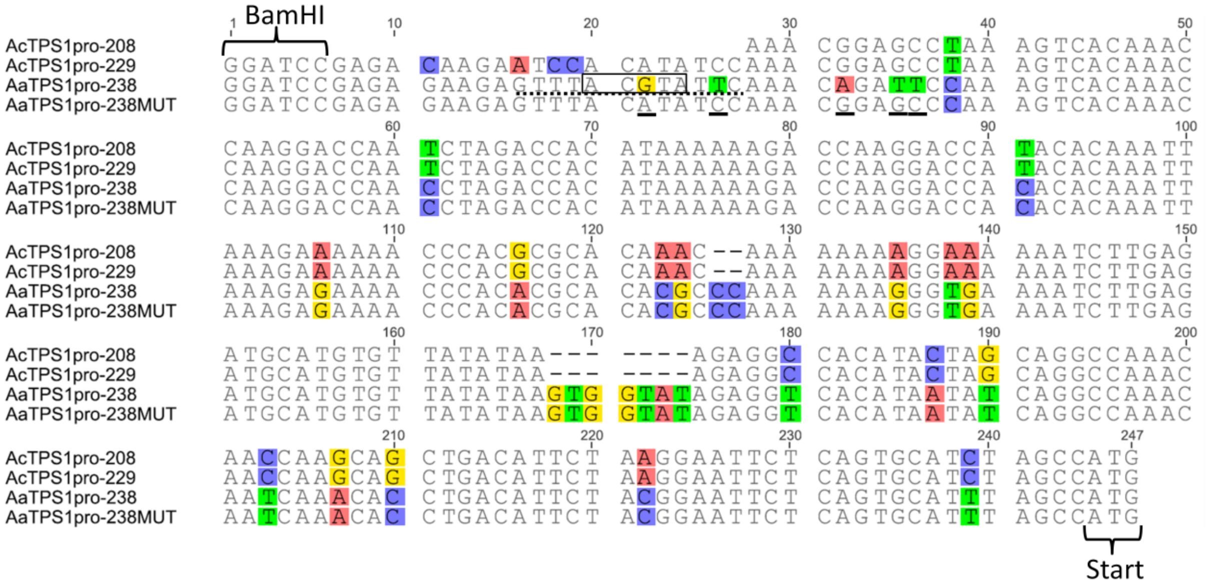


Figure S8.
(A) ClustalW alignment of the *Actinidia deliciosa* (Ad), *A. chinensis* (Ac) and *A. arguta* (Aa) *EIL1-4* proteins.

(B) Unrooted Maximum Likelihood tree of *A. deliciosa* (Ad), *A. arguta* (Aa) and *A. chinensis* (Ac) EIN3-like (EIL) transcription factors compared to *Arabidopsis thaliana*. Arabidopsis (At) EIN3 (GenBank AAC49749), EIL1 (AAC49746), EIL2 (AAC49747) and EIL3 (AAC49748), *A. deliciosa* (Yin et al., 2010): AdEIL1 (EU170633), AdEIL2 (EU887511), AdEIL3 (EU887512), AdEIL4 (EU887513), *A. chinensis*: AcEIL1 (KF319041), AcEIL2 (KF319042), AcEIL3 (KF319043), AcEIL4 (KF319044), *A. arguta*: AaEIL4 (KF319045). The tree was generated as described in Fig S7. There were a total of 239 positions in the final dataset.



```
                     1         10         20         30         40         50
AcTPS1pro-208                                         AAA CGGAGCCTAA AGTCACAAAC
AcTPS1pro-229       GGATCCGAGA CAAGAATCCA CATATCCAAA CGGAGCCTAA AGTCACAAAC
AaTPS1pro-238       GGATCCGAGA GAAGAGTTTA CGTATTCAAA CAGATTCCAA AGTCACAAAC
AaTPS1pro-238MUT    GGATCCGAGA GAAGAGTTTA CATATCCAAA CGGAGCCCAA AGTCACAAAC
                            60         70         80         90        100
AcTPS1pro-208       CAAGGACCAA TCTAGACCAC ATAAAAAAGA CCAAGGACCA TACACAAATT
AcTPS1pro-229       CAAGGACCAA TCTAGACCAC ATAAAAAAGA CCAAGGACCA TACACAAATT
AaTPS1pro-238       CAAGGACCAA CCTAGACCAC ATAAAAAAGA CCAAGGACCA CACACAAATT
AaTPS1pro-238MUT    CAAGGACCAA CCTAGACCAC ATAAAAAAGA CCAAGGACCA CACACAAATT
                           110        120        130        140        150
AcTPS1pro-208       AAAGAAAAAA CCCACGCGCA CAAAC--AAA AAAAAGGAAA AAATCTTGAG
AcTPS1pro-229       AAAGAAAAAA CCCACGCGCA CAAAC--AAA AAAAAGGAAA AAATCTTGAG
AaTPS1pro-238       AAAGAGAAAA CCCACACGCA CACGCCCAAA AAAAGGGTGA AAATCTTGAG
AaTPS1pro-238MUT    AAAGAGAAAA CCCACACGCA CACGCCCAAA AAAAGGGTGA AAATCTTGAG
                           160        170        180        190        200
AcTPS1pro-208       ATGCATGTGT TATATAA--- ----AGAGGC CACATACTAG CAGGCCAAAC
AcTPS1pro-229       ATGCATGTGT TATATAA--- ----AGAGGC CACATACTAG CAGGCCAAAC
AaTPS1pro-238       ATGCATGTGT TATATAAGTG GTATAGAGGT CACATAATAT CAGGCCAAAC
AaTPS1pro-238MUT    ATGCATGTGT TATATAAGTG GTATAGAGGT CACATAATAT CAGGCCAAAC
                           210        220        230        240     247
AcTPS1pro-208       AACCAAGCAG CTGACATTCT AAGGAATTCT CAGTGCATCT AGCCATG
AcTPS1pro-229       AACCAAGCAG CTGACATTCT AAGGAATTCT CAGTGCATCT AGCCATG
AaTPS1pro-238       AATCAAACAC CTGACATTCT ACGGAATTCT CAGTGCATTT AGCCATG
AaTPS1pro-238MUT    AATCAAACAC CTGACATTCT ACGGAATTCT CAGTGCATTT AGCCATG
```

Figure S9. Sequence alignment of minimal Aa *TPS*1_{pro} and Ac *TPS*1_{pro} promoter fragments. The conserved NAC binding core ACGTA is boxed in Aa *TPS*1_{pro}-238 and substitutions in $_{pro}$-238Mut are underlined. The NAC 12 bp (GTTTACGTATTC) sequence fused to Ac *TPS*1_{pro}-208 (see Fig 8E) is highlighted with a dotted line. The translational ATG start codon and *Bam*HI cloning site are highlighted.

Table S1. Characteristics of *Actinidia arguta* 'Hortgem Tahi' and *A. chinensis* 'Hort16A' ripening fruit. SSC: soluble solids content. nd: not determined

Species	**ripening stage**	**firmness (N)**	**fruit weight (g)**	**SSC (**°Brix**)**
A. arguta	a0	7.80 ± 0.33	13.46 ± 0.57	nd
A. arguta	a1	2.50 ± 0.02	14.74 ± 0.44	11.74 ± 0.19
A. arguta	a2	1.72 ± 0.02	15.50 ± 0.46	12.13 ± 0.30
A. arguta	a3	1.26 ± 0.01	14.10 ± 0.41	12.42 ± 0.22
A. arguta	a4	0.83 ± 0.02	13.53 ± 0.54	13.76 ± 0.81
A. arguta	a5	0.63 ± 0.01	13.29 ± 0.44	13.20 ± 0.67
A. chinensis	c0	31.1 ± 3.0	nd	16.66 ± 0.42
A. chinensis	c1	8.4 ± 0.5		19.11 ± 0.22
A. chinensis	c2	6.5 ± 0.3		18.83 ± 0.26
A. chinensis	c3	3.1 ± 0.2		19.33 ± 0.34
A. chinensis	c4	2.6 ± 0.1		18.89 ± 0.34

Table S2. Cloning and PCR primers

Primer	**Sequence**
***A) Transient terpene synthase and MEP pathway gene over-expression of pHEX2 vector in* Nicotiana benthamiana**	
AacTPS1_F1	CACCATGTCTCTTAGTGTTGGTTTTGG
AaTPS1_R1	CTAAGCTTTCTCCTCAAAGGGAATGGGACTGATTAGTAG
AcTPS1_R1	TTAAAAAAGGGGAATGGGATTGATTAGTAGTGACTTGACTCG
AdHDRF1	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGATGATTTCTCTGCAATTCTG
AdHDRR1	GGGGACCACTTTGTACAAGAAAGCTGGGTCTAAGCCAATTGCAGGGC
AcDXSF	CACCATGGCTGCTAGTGTTGTTCTC
AcDXSR	CAAGGATTATTCTTAGTTGAAAGGA
AaDXRF1	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGGCTCTAAATTTGCTATCCC
AaDXRR1	GGGGACCACTTTGTACAAGAAAGCTGGGTTCATACAGGAACAGGACTC
AaIDIF1	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGTCCCTCTCTCTCTCC
AaIDIR1	GGGGACCACTTTGTACAAGAAAGCTGGGTTTAAGTCAATTTGTGAATGGTTTTCAT
B) NAC and EIL plant over-expression in pHEX2	
pH_AacNAC1F	AAAAAGCAGGCTCCATGGAGAGCACGGATTCG
pH_AacNAC1R	AGAAAGCTGGGTCTAGGAGTACCATCGAAAG
pH_AacNAC2F	AAAAAGCAGGCTCCATGGAGAGCCCGGATTCG
pH_AacNAC2R	AGAAAGCTGGGTTAGGGTACCAATTCAAGCTAG
pH_AacNAC3F	AAAAAGCAGGCTCCATGGAGAGCACGGATTCA
pH_AacNAC3R	AGAAAGCTGGGTCTAAGAGTACCAATTCAAGCTAG
pH_AacNAC4F	AAAAAGCAGGCTCCATGGAGAAGCTCAACGTTG
pH_AacNAC4R	AGAAAGCTGGGTCTAAGGTTTTCTTTTAAAGGATGAG
pH_AcEIL1F	AAAAAGCAGGCTGGATGATGATATTTGATGAAATGGGG
pH_AcEIL1R	AGAAAGCTGGGTCTAGAACCAAATCGAGCC
pH_AcEIL2F	AAAAAGCAGGCTGGATGATAATGTTTGACGAGATGGG
pH_AcEIL2R	AGAAAGCTGGGTCTAGAACCATACTGAGCC
pH_AcEIL3F	AAAAAGCAGGCTGGATGGATGCCAATGGGTTG
pH_AcEIL3R	AGAAAGCTGGGTCTATGCCCCAAGGTATTC
pH_AacEIL4F	AAAAAGCAGGCTGGATGGAAGAGATTGGAGTTGATAT
pH_AacEIL4R	AGAAAGCTGGGTTTATGCACCAAAGCATTGGATC
C) Real time PCR analysis	
TPS genes	
TPSRTF1 (Fig. 2)	CGTTGAGAGGTGGGATCTGAGTGAA
TPSRTR1 (Fig. 2)	GACACCTTGCTCCTTTAGGGTGTCA
TPSUF (Fig. S9)	TTGCCATATTGGTGAGTCATGCCTT
TPSUR ((Fig. S9)	TGTGGGACTCAAATTAGGTCTTCTCTCA
MEP genes	
DXS_F1	GCCTCCCTGTTTGAAGAACTTGGAT
DXS_R1	CAGGCATGGCCTTGACCTTCTT
DXR_F1	TGCAAGCTTGGGTCACTGACATTT
DXR_R1	CGGCTTTCTCATTTGCAGCACTAA
MCT_F1	CACTCGCATCTGCAGCTAACCAGTT
MCT_R1	TCCACAGCCTTGGCAGAGCAA
CMK_F1	TATTGTCCACGGCTTGCAGCAA
CMK_R1	CAATGATTTGGAACCTCCTGCATTT
MDS_F1	TCGAGCCAGGTTACCCTCTCATCAT

MDS_R1	GGCGCCCAAAATTGCATCAA
HDS_F1	TGGAGCACCACCAACATACCCAA
HDS_R1	TGCCCGGTGTTTCTATTGCCAT
HDS_F2	CCGTCTTTGTATTCCTCATCCTGCA
HDS_R2	TAGATGGTCTTGGAGATGGCATTCT
HDR_F1	CACAATAGGGGTAACATCTGGTGCC
HDR_R1	CAATTGCAGGGCTTCTTCTCGTTTA
HDR_F2	ATGATGTTGTGGTTTTGCCTGCAT
HDR_R2	CCAAACCTTAGAAACCCATGGACAA
IDI_F1	CGAACCCTGATGAAGTTGCTGACAT
IDI_R1	TGAACCATGGGGACAGCTTCAAA
ssuGDPSII_F1	CTTCGAGCCCATGCACCACCTA
ssuGDPSII_R1	CTCACACGCGGCGACGCATA
ssuGDPSII_F2	CCCGTCTCTTCCATGGCCGTAT
ssuGDPSII_R2	CGGAACTAGCCTTGTGGACCATGTA

NAC genes

AcNAC1F	AAGAGCAACCTCCCAAGACCAA
AaNAC1F	AAGAGCAACCACCCACGACCAT
NAC1R	GAAGGTGGCATTCTTGCAAGCAT
NAC2F	CCGGTGGCGATCATAGCTGAAAT
NAC2R	CCGGTTCCTCGGACTGAAAAAAT
NAC3F	CAAACCCCAAAACTCCCACCAA
NAC3R	GCTGTGACTGAGCATTTCGTCGAA
NAC4F	TAGGACTGATTGGATCATGCACGAA
NAC4R	CGGCAAAGAACCCAATTCTCCATA

EIL genes

AcEIL1F	GAGAATCGGTTTGATCAGCGCAA
AcEIL1R	CCGAACATCAAGGGGAAGTTATCATT
AcEIL2F	GGGCAAAAAATGATCAACGAGCTT
AcEIL2R	GAAGAAACTGAGATGCTCATGGGATTT
AcEIL3F	ACACAGAACGTATTTGTTGGTGGCAT
AcEIL3R	TGAGATTCATGATGCAACTCGGAGTT
AcEIL4F	ACCGGATGTGGAACCATCTAATCAA
AcEIL4R	CTCTCGTCGCTCTTTGTCTTGCAA
AaEIL4F	AATCAACCACCATCTAATCAACCTCGA
AaEIL4R	AGGGCTTGATCTTACTCGTGATCTTTTT

Reference

AdEF1F	GCACTGTCATTGATGCTCCT
AdEF1R	CCAGCTTCAAAACCACCAGT

D) Bacterial protein expression of Ac- and AaTPS1 in the pET200 vector

p200_AcTPS1F	CACCGAAAACCTGTATTTTCAGGGAATTGCGGAGCCTAGCCAAACC
p200_AcTPS1R	TTAAAAAAGGGGAATGGGATTGATTAGTAGTGACTTGACTCG
p200_AaTPS1F	CACCAGGCGATCCGCGTTCTACCAACCTTC
p200_AaTPS1R	CTAAGCTTTCTCCTCAAAGGGAATGGGACTGATTAGTAG

E) Promoter constructs of pGreenII 0800-LUC

F1_717	AAACATAGTGCATATTGTGCGTCCTGA
F2_757	AATCGATCGTAACATTCACACAACCG
R1_131	GGTTCCGAAATCGTGCATCGAA

R2_101	CGCATATGTACCCTTCGATGATTGG
AaproF	TTAAGGATCCTTTACTAGATTTAAAAATTAAATTTTAACATA
AaproR	TTAACCATGGCTAAATGCACTGAGAATTC
AcproF	TTAAGGATCCCTCCTAAAATAGAGTTACAAAAAA
AcproR	TTAACCATGGCTAGATGCACTGAG
F-238	TTAAGGATCCGAGAGAAGAGTTTACGTATTCAA
F-229	TTAAGGATCCGAGACAAGAATCCACATATCC
F-238mut	TTAAGGATCCGAGAGAAGAGTTTACATATCCAAACGGAGCCCAAAGTCACAAACCAA
F-600	AAAAGGATCCTAAGGAAAATAAAAYCAAACACTA
208 (I)F	TTAAGGATCCGTTTACGTATTCAAACGGAGCCTAAAGTCACA
208 (II)F	TTAAGGATCCGTTTACGTATTCGTTTACGTATTCGTTTACGTATTCAAACGGAGCCTAAAGTCACA
208 (III)F	TTAAGGATCCGTTTACGTATTCGTTTACGTATTCGTTTACGTATTCGTTTACGTATTCGTTTACGTATTCAAACGGAGCCTAAAGTCACA

F) Bacterial protein expression of the NAC DNA binding domains in pET300

AaNAC1DBF	AAAAAGCAGGCTCCATGGAGAGCACGGATTCG
AaNAC1DBR	AGAAAGCTGGGTTCATGGTCGTGGGTGGTT
AaNAC2DBF	AAAAAGCAGGCTCCATGGAGAGCCCGGATTCG
AaNAC2DBR	AGAAAGCTGGGTTCAGGCTCTTGGTGGGTT
AaNAC3DBF	AAAAAGCAGGCTCCATGGAGAGCACGGATTCA
AaNAC3DBR	AGAAAGCTGGGTTCAGGGTCTTGATGGGTG
AaNAC4DBF	AAAAAGCAGGCTCCATGGAGAAGCTCAACGTTG
AaNAC4DBR	AGAAAGCTGGGTTCAATTTTTAGTACTTCTTTTCTTCAAAAATA

Table S3. Ripe fruit headspace terpene compounds in fourteen kiwifruit species. Headspace volatile levels were determined by dynamic headspace sampling of pulped fruit for 20 minutes and compounds were identified by GC-MS.

Compound (ng . $g^{-1} \cdot h^{-1}$)	DB WAX Retention index (s)	Species (# accessions)																											
		A. arguta AVERAGE	(n=15) MAX	*A. chinensis* AVERAGE	(n=8) MAX	*A. chrysantha* AVERAGE	(n=2) MAX	*A. deliciosa* AVERAGE	(n=3) MAX	*A. eriantha* AVERAGE	(n=5) MAX	*A. glaucophylla* AVERAGE	(n=1) MAX	*A. indochinensis* AVERAGE	(n=2) MAX	*A. latifolia* AVERAGE	(n=3) MAX	*A. macrosperma* AVERAGE	(n=3) MAX	*A. melanandra* AVERAGE	(n=3) MAX	*A. polygama* AVERAGE	(n=5) MAX	*A. purpurea* AVERAGE	(n=4) MAX	*A. rufa* AVERAGE	(n=2) MAX	*A. setosa* AVERAGE	n=1
unknown 1	1021	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.0	6.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
pinene, alpha-	1026	245.7	3248.5	0.6	7.2	68.2	157.4	0.0	0.0	33.9	63.8	144.4	159.5	2.2	6.5	0.0	0.0	0.0	0.0	24.1	46.5	38.6	87.6	13.9	55.4	27.7	55.4	0.0	0.0
thujene, alpha-	1033	5.2	42.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.1	4.5	30.4	191.8	55.3	213.3	110.6	213.3	0.0	0.0
fenchene, alpha-	1051	0.0	0.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
camphene	1063	2.4	26.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.6	1.7	0.6	2.5	1.4	5.4	2.7	5.4	0.0	0.0
pinene, beta-	1107	137.7	1654.2	2.4	83.3	11.9	29.2	0.0	0.0	27.1	84.2	11.1	16.5	0.0	0.0	0.0	0.0	0.0	0.0	9.0	20.1	20.0	48.1	14.4	28.9	24.9	28.9	3.9	7.8
terpinene, beta or sabinene	1121	151.3	2022.5	0.4	5.1	0.0	0.0	0.0	0.0	2.3	13.9	156.0	168.8	0.0	0.0	0.0	0.0	0.0	0.0	2.1	5.0	66.8	200.0	1.0	4.0	2.0	4.0	0.0	0.0
menthene, p-	1132	0.0	0.0	5.3	82.7	2.9	7.2	2.6	15.5	2.0	11.9	0.0	0.0	6.8	20.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
terpinene, alpha-	1172	63.8	1084.6	0.2	5.3	5.7	22.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.7	2.1	0.4	1.6	0.0	0.0	0.0	0.0	0.0	0.0
myrcene, beta-	1169	879.8	7596.4	0.0	0.0	16.7	34.7	0.0	0.0	6.9	41.1	22.3	35.3	0.0	0.0	0.0	0.0	0.0	0.0	97.4	187.6	155.7	535.2	37.4	95.4	27.2	51.5	47.7	95.4
limonene	1198	289.8	3331.0	1.0	18.7	223.6	558.9	0.0	0.0	18.8	64.2	72.6	93.8	3.3	9.8	0.0	0.0	0.0	0.0	80.4	144.0	58.5	168.6	17.7	67.7	33.9	67.7	1.6	3.2
phellandrene, beta-	1215	26.6	455.7	0.0	0.0	2.4	9.5	0.0	0.0	0.0	0.0	2.0	2.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	8.1	44.9	0.0	0.0	0.0	0.0	0.0	0.0
eucalyptol	1216	427.9	7529.0	66.7	333.2	6.4	25.6	0.0	0.0	0.0	0.0	0.0	0.0	19.1	57.2	0.0	0.0	0.0	0.0	0.0	0.0	63.2	144.1	0.0	0.0	0.0	0.0	0.0	0.0
unknown 2	1217	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	68.5	271.3	135.7	271.3	1.4	2.7
ocimene, (*Z*)-beta-	1230	9.1	107.2	0.0	0.0	1.7	6.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	8.4	36.7	146.7	0.0	0.0	73.4	146.7
terpinene, gamma-	1250	146.8	2455.1	0.6	12.0	2.7	9.2	0.0	0.0	0.0	0.0	15.5	19.2	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.5	10.5	25.4	0.4	1.5	0.8	1.5	0.0	0.0
ocimene, (*E*)-beta-	1230	9.1	107.2	0.0	0.0	1.7	6.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	8.4	36.7	146.7	0.0	0.0	73.4	146.7
unknown 3	1267	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.7	2.6	0.0	0.0	1.3	2.6
cymene, p-	1268	163.9	2729.0	17.4	260.0	10.5	26.2	1.0	6.0	0.2	0.9	73.7	101.0	0.0	0.0	0.0	0.0	0.0	0.0	4.3	13.0	9.5	25.9	1.9	7.5	3.8	7.5	0.0	0.0
dimethylstyrene	1278	161.9	1755.7	0.2	9.1	253.2	571.7	0.0	0.0	24.3	120.8	20.6	29.8	0.0	0.0	9.6	23.4	4.0	16.0	0.0	0.0	4.8	21.0	0.0	0.0	0.0	0.0	0.0	0.0
terpinolene	1285	1132.8	7546.9	0.7	13.0	160.7	537.5	29.4	176.2	253.4	869.5	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.9	489.1	1193.2	0.0	0.0	174.5	697.8	348.9	697.8	0.0	0.0
terpinolene, iso-	1286	45.7	391.5	0.2	3.2	2300.1	5208.5	0.0	0.0	38.3	134.8	12.9	16.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9	3.3	2.5	9.8	4.9	9.8	0.0	0.0
unknown 4	1408	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.7	37.1	0.0	0.0	0.0	0.0	0.0	0.0
perillen	1409	1.4	25.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.9	8.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
unknown 5	1414	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.8	2.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
mentha-1,3,8-triene, p	1399	12.1	128.5	0.0	0.0	1.9	7.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	1.5	0.0	0.0	0.3	1.0	0.5	1.0	0.0	0.0
unknown 6	1461	0.6	11.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
linalool	1538	0.4	5.7	0.0	0.0	12.9	35.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.6	10.3	0.0	0.0	16.0	51.1	0.0	0.0	0.0	0.0	0.0	0.0
linalool acetate	1538	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.4	1.5	0.0	0.0	1.4	9.8	0.0	0.0	0.0	0.0	0.0	0.0
unknown 8	1560	0.0	0.0	0.0	0.0	55.8	193.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.7	11.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
unknown 9	1582	1.4	24.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.5	4.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
terpine-4-ol	1600	74.5	1341.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Unknown 10	1620	1.3	23.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.3	6.8	0.0	0.0	0.0	0.0	0.0	0.0
terpineol, alpha-	1695	124.0	1988.3	0.0	0.0	5.4	17.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	31.4	118.9	0.0	0.0	0.0	0.0	0.0	0.0
citral	1704	1.2	15.3	0.0	0.0	19.6	52.9	0.0	0.0	0.0	0.0	10.8	16.3	0.0	0.0	0.0	0.0	0.0	0.0	3.3	8.7	0.1	1.0	1.1	4.4	2.2	4.4	0.0	0.0
geranylacetone	1835	0.0	0.0	16.3	192.4	0.0	0.0	8.0	21.5	0.0	0.0	0.0	0.0	1.7	5.1	2.8	8.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
cymen-8-ol, p-	1851	1.6	24.1	0.0	0.0	42.1	103.5	0.0	0.0	0.0	0.0	1.9	3.8	0.0	0.0	0.0	0.0	0.0	0.0	3.3	9.1	0.5	3.2	1.9	7.4	3.7	7.4	0.0	0.0
geranylacetone	1855	3.0	15.7	3.3	125.0	3.5	9.0	0.0	0.0	2.5	13.9	0.0	0.0	11.5	29.8	2.9	5.7	2.7	8.9	0.0	0.0	5.8	18.1	0.0	0.0	0.0	0.0	0.0	0.0

Key:		
	>10	ng . $g^{-1} \cdot h^{-1}$
	>100	ng . $g^{-1} \cdot h^{-1}$

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