

Prupe.3G222200.1/1-630	1 · · · · · · · · · · · · · · · · · · ·	77
Prupe.3G222300.1/1-463	······································	
Prupe.3G234300.1/1-831	1 · · · · · · · · · · · · · · · MD LQ E S S V K N L V K V K QD L LA S S QV D V Y G L · · · · · · · · · V P P S P Y D T A WL SMV SN PQQ SD Q P L FQG C LD WV LQHQN RGG SWG EN I AH PT I · · EC LT ST LAC I V A LT T WN GHDA I C K GLA F I HAN T EK LL E EQNG SF L EWFA	IVFPAM 137
Prupe.3G234400.1/1-695	1 · · · · · · · · · · · · MDLQGSSVKYLVTKVKQDLLASSQVDVYGL · · · · · · · · VPSPYDTAWLSMVSNPQHSQQLFQGCLDWVLQHQNRGGFWGENIGHPTL · · ECLTSTLACIVALITWNVGHDAICKGLAFIHGNTERLLEEQNGSFPEWFA	IVFPAM 137
Prupe.3G234500.1/1-838	1 · · · · · · · · · · · · MD SQ E SLVKNLLMKVKQDHLASSEFDVYSL · · · · · · · · VPSPYDT AWLSMV PN PQQSDQPL FQGC LDWV LOHQNRGGFWGEN I AH PT I · · EC LT ST LAC I VA LTT WNVGHDA I CKGLAFI HGNT EKLL E EQNG SF PEWFA	IVFPAM 137
Prupe.4G029900.1/1-576	1	41
Prupe.4G030300.1/1-536	1 MAULQAHSASPNC	13
Prupe.4G030400.1/1-580	1	50
Prupe.4G125200.1/1-352	1 MD SK I N FQAN ERC RR SAN YK PN I	23
Prupe.4G125300.1/1-555	1	23
Prupe.4G125500.1/1-545	1	23
Prupe.4G126600.1/1-558	1	23
Prupe.4G128500.1/1-805	1 MSFSHLSTLKCSTFSLSSEKFYGNHILPQAASTIPTLDGEAEGNTAGLRNFESTKLRIKKMFNKVDLTVSSYDTAWVAMVPSTNSLKDPFFPECVNWLLGNQLYDGSWGPPNLHPLLMKDALLSTIACILALKRWSVGEEQINKGLHFIESNLASANDEELHS-PVGFN	IMFPVM 174
Prupe.4G128600.1/1-461	1 · · · · · · · · · · · · · · · · · · ·	IIFPAM 154
Prupe.4G190700.1/1-551	1 MSVQV SLA SAQPQ · · · · · · T PKAT PDDVN RRCAN F SPSM · · · · · · · · · · · · · · · · · · ·	33
Prupe.4G190800.1/1-359	1 MSV PV SL SSDQPQ · · · · · · · · · · · · · · · · · ·	33
Prupe.4G191000.1/1-564	1	33
Prupe.4G194100.1/1-562	1	29
Prupe.4G194200.1/1-599	1	67
Prupe.4G194300.1/1-558	1	29
Prupe.4G194400.1/1-458	1 MSVQVGSAAQ PONAK PDE LARRT AN FH PSI	30
Prupe.4G194500.1/1-559	1 MSVQVGSAAQ PONAK PDE LARRT AN FH PSI	30
Prupe.4G194600.1/1-471	1	62
Prupe.4G197900.1/1-559	1	26
Prupe.4G198000.1/1-485	1	28
Prupe.4G198200.1/1-583	1	49
Prupe.4G198500.1/1-522	1 MK EV ESLV PS <mark>RRT AN</mark> YHLSI	20
Prupe.4G198600.1/1-458		
Prupe.4G198700.1/1-437	1	30
Prupe.4G199000.1/1-565	1	30
Prupe.4G199200.1/1-563	1	32
Prupe.4G199300.1/1-458		

Terpene_synth (PF01397)

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Prupe.3G222200.1/1-630	78	WDKLIDSFT	TH HYTYELHATRLES KON VA ET L LAAST SNKGGSAS - TC SV LKLID SMORLGVA YHFEQ ET DAALLSLVSSS	T 159
Prupe.3G222300.1/1-463	1		MQYELHATRLESLKON VAETL LAAST SNKGGSAS-TC SV LKLID SMORLGVA YH F EQ ET DAALLSLV SSS	T 70
Prupe.3G234300.1/1-831	138 ELAETKGLRVYFSNGSTALVQQVFLERQQIFKTQF	WESGCDQQQYYPAGMLKYLEDG-LIQFPSAIA	A YA FMKT GNK EFFVR LNSIVQTCGYGV PTVYPFDE-DLVK IHLIDQTERLGLA EHFMEETTSLLGQV YR SY	1 274
Prupe 3G234400 1/1-695	138 ELAETKGLHVYFSNGLVEQVFLERGEILOTBE	WY SGCGQQQYYPALMLQYLEDG-LIQSPSALA	A YA FMKT GNK EFLYKHYYMEFFMYMT SCYRLLLPIPA YYPLDE-DLYNILLINO FTLGLAFHFMEFIK SLLAQYYR SC	1 279
Prune 3G234500 1/1-838	138 FLAFTKGLHVYFSNGLV	WY S GCGBOON YPALMLK YHEDG- LLOSPSALA		1 271
Prupe 4G029900 1/1-576	42	WKYSEFESLD	DSKYHEDDYKROSEK LIEDVKN-MIFVETEN-SIAOLELVDIJAK LGLTNHFEKEIKET DTIASVEI	N 116
Prupe 4G030300 1/1-536	14			A 73
Prupe 4G030400 1/1-580	51			T 122
Prupe.4G125200.1/1-352	24	WNDGFLES	LINNKYISEN LIED VKNMM	P 91
Prupe 4G125300 1/1-555	24	WKDGFLESLN		P 98
Prupe 4G125500 1/1-545	24	W	NNKY I GDDY SROFEN LYKDYKNMMFYKTED-LTAOLEL I DNI GKLGLTNHEEKELK FALDTY EN SN	P 98
Prune 4G126600 1/1-558	24	W		N 99
Prupe.4G128500.1/1-805	175 E SAMK LDMN L P L G A P T L D A L F H B R E R E L K S S YG SN SEG	WRAFLAYISEGFGK SODWELVMK YORKNOSL FNSPSTTA	AAAFTH LKNADC LKYLRTL LEK FGNAV PTVYPLENYARL SMVASLESLG JDRHFREELRSVLDET YRCW	L 321
Prupe 4G128600 1/1-461	155 ESAMN FDMYLPLGAPALDALFHBBDFELKBGYGSNSEG	WRAFLAYISEGLG-SODWELVMKFOKKNGSLENSPSTTA	AAAFTOLKNAHCIKYI BALLEKCGNAV PMVYPLDNYABI SVVASLESIG I DBHEBEE I BSVI DET YBCW	0 300
Prupe 4G190700 1/1-551	34	W	ASV FTNIKAKOBAO FLK FK VKMII	H 107
Prupe 4G190800 1/1-359	34	W	ASVETNIKAKORAQELKEKVKMIIMAPVKK. PSOKIDI IHD IQBIGVSHHEENELEELIQQIHTSS	H 107
Prupe 4G191000 1/1-564	34	W	ASV ETNIKAKORAOFIKEKVKMIIMAPVKK-PSOKIDI HDIORIGVSHHEENEIDELLOQIHTSSI	H 107
Prupe 4G194100 1/1-562	30	W	QUVITNARNOO EVONIK EV	B 106
Prune 4G194200 1/1-599	68	W	DONIT HAOKOVDELKEL VBREVETNI KAGGDG- FAHOLKI FALORIGVA YHEERELEFAL FRIHGTT	Y 146
Prupe 4G194300 1/1-558	30	W	ODITINARNOOFVNELKEV	B 106
Prupe 4G194400 1/1-458	31		OMITHANKOGOVDEL BEV VBBEV F TT SAGD. I SHOLKI IDA IOBI GVA VHEEBELEEAL ECMHTTU	H 108
Prupe 4G194500 1/1-559	31		OMITHAHKOGOVDELKEVVBBEVFTT SAGD. LSHOLK LDA LOBI GVA YHEET ELEFAL EBI	H 105
Prupe 4G194600 1/1-471	63		NON ITHYHDKO, VDELKEM	H 143
Prune 4G197900 1/1-559	27	W	ODITINARNO FEVEELKEV	H 103
Prupe 4G198000 1/1-485	29	W	SIGIT YDHMOOOVDOL KYT	H 106
Prupe 4G198200 1/1-583	50	CDOEMNY, VSE	TT SADD, ESNOWKI DALOPICYAYHEEKELEEALEHIYAAN	N 126
Prune 4G198500 1/1-522	21	W	EDITT VAHKOOFVEFLKLA	H 97
Prupe 4G198600 1/1-458	1		MODOVDOLKVA	H 59
Prupe 4G198700 1/1-437	31	W	EDMIT YAHKOOEVEELKIV	H 107
Prupe 4G199000 1/1-565	91	CDOEMNY DSV	TT SADD, ESNOMK I DA I OPLOVA VHEEKELEEALEH I YAANI	H 107
Prupe 4G199200 1/1-563	33	W	ASVET DIKA FOD VOELKEK	Y 107
Prune 4G199300 1/1-458	1			H 38
Prune 4G199500 1/1-566	31	CDOFMN V. DSF	EDITTAHKOOFVEELKIA	H 107
Prupe 4G200000 1/1-568	31	W	TTGAGD ESYOMK I DA I OR I GVA YHEEK EI EFAL EH I YAANI	B 107
Prupe 4G200100 1/1-564	31	CDOFINY DSE		H 107
Prupa 4G238400 1/1-504	47	ET AMK VORKNOSI EN SPSTTA		1 137
Prune 4G238000 1/1-525	28	W	ASVKTDIKA FORVOFIKEK VKGMI	¥ 102
Prupe 8G230000 1/1-608	117 I FLAD SINI EV DODCAVIHELVAMONIKITKIDDO IMHKV DTTILHSI EGMAGID	W		T 262
rupe.00203000.171-098	IN LETAISLEEF DOORTENET AMINICALITATION AND INTROPPETEL SLEEMAGE			202

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Prupe.3G222200.1/1-630		- DIYERD- NS KNL	LLELA 29
Prupe.3G222300.1/1-463		I - D I YERD - N S KN LA	LLELA 13
Prupe.3G234300.1/1-831	275 SCEEPKSMAKHALPLQLYTHSLAFRLLRLHGYRYSPR-KFCRFLEDEDIVTYIEEYHELFLSAMYNYYRATDVTFIGENQLKDARVFSRRILEKETIKN	- ERKET LG PWT GNALSYRLL SCOSNAT	LLQLA 42
Prupe.3G234400.1/1-695	280 SCKESKSMGKHAIPLOLYTHALSFHLLRLYGYRVSPR-KFCRFLEDEDIVTYIEEYHELFLSAMYNVYRATDVTFTGENOLEDARAFSRRILEKETMKNCTNLVRPISLTNLOGOIK-HELSIPWLARLDHLEHRRC	- ERKETLGPWTGNSLSYRLLACQSNAN	LLQLA 44
Prupe.3G234500.1/1-838	272 SCEEPKSMAKNAMPIQLYKHSLAFRLLR UG YRV SPR-NFCRFLEDEDIVAYIEEHRELFLSAMYNVYRATDVTFTGENQLEDTRAFSRRILEKETMKDCMNLVRPISMTNLQGQIK-HELSIPWLARLDHLEHRRC	I - ER E E S L G P WT A N A L S Y R L S S Q - S N A T	LLQLA 43
Prupe.4G029900.1/1-576	117 · · · · · · N SPC I S I T D D L Y T A L Y FK I L R Q G YK V SQD · L FR G FMD E E · · · G T L K K SH L S D V K GML E L FEA SN L A L E G E D · · · I L D E I KASSK VA L R D SN I C N · L · · · · · D N L A K H V V · HA L E L S SH R V R WF N V K GH	I - DAYEKDNHV NT I	LLELA 25
Prupe.4G030300.1/1-536	74 · · · · · · · YDNCNHOLLEVSLR FRLLROOG YHVT D · V FNK FKN I Q · · · D LK SGLDKD I EGLVGL YEA SHLSFOG ED · · ALD EA GKLSHOILT AWLPNN · L · · · · · · D DHRA PLVA · H SLKH FYHK SLT RFMAKNF	L - D Y FOGT EKW A S I	LQELA 20
Prupe.4G030400.1/1-580	123 S G SAH GANHH SD LH EV AV R FR L LROOG Y FV PDD - V FNK FK E - S - E G S FK OM L SED I K G LM SL Y EA SOL SI E G ED T L E E A GO F SWH L LN T SL - SH - L D HHQ A R V V G - NT L SN PHHK SL AT FMAKN F	FATN SRGTNNR WLN I	LQEVA 26
Prupe.4G125200.1/1-352	92 · · · · · · · · · · · · · · · · · · ·	I - HT YEKDNHA NT I U	LLELV 22
Prupe.4G125300.1/1-555	99 YIIENLYATALHFKILROHGYKY SQD - V FGGFMDEK GALKESNLWDVKGMLELLEASNLAFEGER ILDEAKASSTVALRGSKVWN - P DNNLAROVI - HALELSSHRRVGWFNVKSH	I - QA YEKDNHA NTVL	LLELA 23
Prupe.4G125500.1/1-545	99 CITENLYATALHFKILROHGYKVSQD - V FGGFMDEK GALKESN FWDVKGMLELLEATNLAFEGER ILDEAKASSTVALRGSKVWN - L DNNLAROVV - HALELFSHRRVGWFNVKWH	I - HA Y EKDNHA NT I L	LLELA 23
Prupe.4G126600.1/1-558	100 N D PHMT EN LYA I A LH FK I LROHG YK V SOD - V FDG FLD EK GML EK SH FSDVKGML EL LEA SN LA LDG EN V LD EA KA F ST LA LRD SN I CN I L DNN LA RHV V - HA LE LSSH RV GWFNVKWH	- HA <mark>Y</mark> EKDNHV KT	LLELA 23
Prupe.4G128500.1/1-805	322 HG DED I FSDAAT FAMA FRLLRVNG YD SAD - PLSOF SEDC FFN SLGGYLKD I GAALELLRA SEFI I HPDE SVMEKON YWT SHFLKOELSN - T LVOGH I FNKH I V LEV E - DV LKFP SYAN LGRLST RRA	I - K Y YNTD ST R I LK S S YR C L N I G <mark>N E</mark> D	FLKLA 47
Prupe.4G128600.1/1-461	301 QG EED IFSDAASCAMAFRLLRVHGYD ISAV - NFQK IVSSIPLGGYMKD IGAALELFKASEIIIHPDES - VLEKQNNWMSQFPETGV IQYFNSGSC	L - N I	FLKLA 40
Prupe.4G190700.1/1-551	108 C ST E SG D Q ET D N EL YT A A L R FR LL R Q Q YN I SC D - I FNN FKD SD GK FK E SL V N D V A L T FT T T H L E SA T HR L SPI L SK Q V T - HAM Y Q P FWK G L P R L ET R H Y	L - SL YQER - DS QNET	LLNFA 22
Prupe.4G190800.1/1-359	108 · · · CN PESG · · DQ ET DN EL YT AA LR FR LLRQQG YN I SCD · I FNN FKD SD · · · GK FK ES LVN DV VG LLS LYEATHLR I HGED · · · I LD EA LT FT TT HLESATHR L · · · · · · · · SPV LLKQV T · HA LYQ PFWKGL PR LET RHY	L - SL YQER - DS HNET	LLNFA 24
Prupe.4G191000.1/1-564	108 · · · CN PESG · · DQ ET DN EL YT AALR FRLLRQQG YN I SCD · I FNN FKD SD · · · GK FK ESLVNDVVGLLSLYEATHLR I HGED · · · I LD EALT FT TTHLESATHRL · · · · · · · SPV LLKQVT · HAL YQ PFWKGL PR LET RHY	L - SL YQER - DS HNET	LLNFA 24
Prupe.4G194100.1/1-562	107 · · · · · · DH · · A F SDDGDL YNVALG FRLLRQHG YK V SCD · V FNMFKD · K · · NG SFK ECL I ADV PGML SL YEAGHLGV RG EE · · · ILD EA LA FT TTHLD SAAKAH · V · · · · · · S YEHA EQ I T · QALER PLQKDLER LCARRY	M- SIYQHE-ASHNEA	LLKLA 24
Prupe.4G194200.1/1-599	147 · · · · · · HD · · N Y - · DGDLH SVALG FRLLROHG YN V SD · I FNO FKD · A · · NGN FK ESLTANV SGML SL YEATHLRVHG ED · · · I LEEALV FTTAHL ESK I · TH · V · · · · · · · RY SLAADIS · OALER PLLKCLER LGARNY	L - SI YQDE - AS HNET	LLKLA 27
Prupe.4G194300.1/1-558	107 ······ DHOGDLYNVALGFRLLROHGYKVSCD · V FNK FKDEN ··· GSFK ECLIADVPGMLSLYEAGHLGIRGEE ··· ILDEALAFTTTHLDSAAKAH · V ····· SYEHAEQIT · GALERPLRKDLERVCARRY	A- SI YQDE- AS HNEA	LLKLA 23
Prupe.4G194400.1/1-458	109 · · · · · DH · · DSDDDDDDLYNVALCFRLLROHGHNVSCD · I FNKFKD · E · · NGSFKESLIADMSGMLSFYEATHLR · · · · · · · · · · · · · · · · · · ·	I - SI YQDE-ASHNEC	LLKLA 22
Prupe.4G194500.1/1-559	106 ·····DSDDGDLYHVALCFRLLROHGHNVSCD-IFNKFKD-E-·NGSFKESLIADVSGMLSFYEATHLRVHGED···ILEEALAFTTHLESAT-TC-V······SNPLAAQIT-QALERPLRKSLERLGARRY	M- PIYQDE-ASHNEC	LLKLA 23
Prupe.4G194600.1/1-471	144 ······ DHAINDDDDGDLYNVALGFRLLROHGYNV SCD-MFNK FKD · A · · NGN F··· IVVDV SGMLSLYEATHLRVHGEY··· ILEEAFAFTTTQLIESKTTH·A······ TYSLAAQIT·QALERPLLKSPERLAARNY	A- SIYQDE-ASHNDA	VIELA 27
Prupe.4G197900.1/1-559	104 ····· DF SDDGDL YNVALG FRLLROHG YK I SCD · V FNK FKDEN ··· GSFK ECL IV DV PGMLSL YEAGHLGIRGEE ··· ILDEALA FTTTHLD SAAKTH · V ····· SYEHA ED IT · GALER PLRKDLERVCARRY	A-SIYQDE-ASHNEA	LLKLA 23
Prupe.4G198000.1/1-485	107 ····· DYDG-GDLYAVALGFRLLROHGFNVSCD-IFNKFKDKN-··GNFKESLTADVPGMLSFYEAAHLRKHGED···ILEEALVFTTTHLESAETTE-A······ RNPLALDIT-OALERPLRKGLERVCARGY	A- SI YQDD - A S H SEA	ILKLA 23
Prupe.4G198200.1/1-583	127 ····· FH·· DDDDDDDDDU YNVSLGFALLRQHGINA SCA- I FNK FKESK ·· NGGFKESL IADV PGMLSFYEATHLRVHGED ··· I LEEALV FT KHLESAT · TH· V······ SYQLAED I A· OAL EA PLRKSLEALCARR F	A-SIYQDE-ASHNEA	LLKLA 26
Prupe.4G198500.1/1-522	98 FHD - DDDCDCDCLYSVSLGFFLLFHHGINVSSG- I FNK FRDSK - NGGFKKSLIADVSGLLSFYEATHLRVHGED I LEEALVFTTKHLESAT - TH - V SYQLAEDIA - QALEFPLRKSLVFLCARFF	A-SIYQDE-ASHNEA	LLKLA 23
Prupe.4G198600.1/1-458	60 DYDG-GDLYTVALG FRLPRCHGENV SCO	A-SIYQDD-ASHSEA	ILKLA 18
Prupe.4G198700.1/1-437	108 ······ FHD · DDDDDDDDDDDDDDDDDDDDDDDDDD	A- ST YQDE-ASHNEA	LLKLA 24
Prupe.4G199000.1/1-565	108 ····· FHD · DDDDDDDDDDDDDDDDDDDDDDDDDDD	A- SI YODE- AS HNEA	LLKLA 24
Prupe.4G199200.1/1-563	108 GG- DEENDFDLFTTALRFHLLRGHGYEVSCTUMFNKFRUED GKFKETLVDDVVGLLSLYESTHLRMHGED LDEALTFTTTHLESVEAHR L	L-AIFEEEPHPANEI	LLILA 24
Prupe.4G199300.1/1-458	39 FH DDDDDDDDUYNYL G	A- STYQDE-ASHNEA	LLKLA 15
Prupe.4G199500.1/1-566	108 PHD-DD0D0D0LTWSLGFHLLHCHGHNVSCLGFFNKFNDIK-SGGFKESLIADVSGMLSFTEATHLRVHGEDILEEALVFTIKHLESAT-TH-VST0LAEUTL-OALEHPLHKGLEHLCANKT	A- SI YODE- GS HNEA	LLKLA 24
Prupe.4G200000.1/1-568	100 ···································	A SITUDE AS HNEA	LLALA 24
Prupe.4G200100.1/1-564	100	A SITUDE AS HNEA	A 24
Prupe.4G238400.1/1-525	138 QG. DEDITSDAALGAMATHEH	ALEEEDHI	FLKLA 28
Prupe.4G238900.1/1-525	103 - DECIDING DEPUTING A FALL DURING VERUSAGE VERUS		VI FLA 23
Prupe.8G239900.1/1-698	203 ·· EKGIGWA··HNSEYGUIDDIAMATHLLHUNGHHYBAD·VERIKKGNEFIGFAGGSIGA·VIGMTNLFHASGVLFFGEN···ILEEAKDFSIKFLREKGASDEL·LDKWITTKDLPGEVG·YALEVPWYASLPHLEIHFF	- EUTGGRUUVWIGKILYHMPYV-NNNV	TLELA 42

Terpene_synth_C (PF03936)

Prupe.3G222200.1/1-630	296 KLD YNLVOSV YQMEIK WMMEAKEEL P- EMMK PV YAAMLK GON ELADKV FKNNGLD-V LPYTKE WAMEAKEEL P- EMMK PV YAAMLK GON ELADKV FKNNGLD-V LPYTKE WAMEAKEEL P- EMMK PV YAAMLK GON ELADKV FKNNGLD-V LPYTKE
Prupe.3G222300.1/1-463	138 K DYN VOSY YGMETK
Prupe.3G234300.1/1-831	430 TENYT ROSVERNELK
Prupe.3G234400.1/1-695	447 IENYT LROSI FRNELK
Prupe.3G234500.1/1-838	438 TENYSLEQSIFRNELK
Prupe.4G029900.1/1-576	253 KLN FNMVQAKLQKQLR WOVGETEALP ECMKICFQVLVNTCELAHEIEEENGWNQVLPQLRKV WOVGETEALP ECMKICFQVLVNTCELAHEIEEENGWNQVLPQLRKV W A 394
Prupe.4G030300.1/1-536	206 KLELNVVESIIRNEIL
Prupe.4G030400.1/1-580	262 KTDFNIVOSLHQKELFWEIGDIEHLP-DYMKICFKALHDITNEISSKVYQKHQWN-PLRSLRKTWG402
Prupe.4G125200.1/1-352	224 KLNFNMVQAALQKDLRDRPVECFMLAVGLNFHEGYTSFRNLFSKVINLILIIDDVYDIYQSLEELKIFTNAVD-BWDVGVTEQLS-ECMKTCFQVLVNTTCEFAHEIEEESGWNLALPHLSKA
Prupe.4G125300.1/1-555	231 KLNFNMVQAALQKDLR EV SMWWNNLGLKEHLNFARDR PV ECFMFAVGLNFHHGYT SFRILLSKVINLILI IDDVYD YGSLEELKIFTNAVD-R WDVGATEQLP-ECMKTCFQVLVNTTCEFAHEIEEESGWNLALPHLSKA W
Prupe.4G125500.1/1-545	231 KLNFNMVQAALQNDLR EV SMWWNNLGLKEHLKFARDR PV EC FMFAVGLNFH PGYT SFRLLLSKVINLILIIDD KIFTNAVD-R WDV GVT EQLP. ECMKTC FQV LYNTTC EFAH EI EEEI GWNLALPHLSKA W A j82
Prupe.4G126600.1/1-558	235 KLNFNMVQATLQKDIK BASKWWNNLGHAEHLK FYRDRPVESFMSAVGLNFOPDYTSFRIRLTKVIYLILIIDDYYDYGSLEELKLFTNAVD-R WDVGETGQLP.DCMKICFQVLYNTTCEIAHEIEEENGWNLVLPHLSKV W
Prupe.4G128500.1/1-805	477 VDDFN ICOSIHREELNHLARWIEENRLD-KLNFARQKLAYCYFSAAATLFPPELSDANISWAKNGVLTTVVDDFD GGSEEELVNLIQLVE-KWDVNVSVDCCSEHVEIIFSALKDTINEIGVKAFKWOGRS-VTSHVIEIW.
Prupe.4G128600.1/1-461	406 V EDFN I COSI HHKELN HLSRWVV ENRLD-KLKFSRQKQA YCYFSAAANLFPPELSDA
Prupe.4G190700.1/1-551	224 KLDFNLLQQVHQRELSWDISAMDHLP-EYMKVCJQALLDVVVESYFWASGVHFEPQYYFAHITLCKVIALITIUNDIYD/YGTHEELELFTEAVE-BWDISAMDHLP-EYMKVCJQALLDVVVEIEENLANE-GNLYSIHYAREARLITWFGLSDK 373
Prupe.4G190800.1/1-359	246 KLDFNLLQQVHQRELS····································
Prupe.4G191000.1/1-564	246 KLDFNLLQQVHQRELS····································
Prupe.4G194100.1/1-562	242 KLDFNLVQCLHKKELS···································
Prupe.4G194200.1/1-599	279 KLDFNLVQSLHKKELS···································
Prupe.4G194300.1/1-558	238 KLDFNLVQSLHKKELS···································
Prupe.4G194400.1/1-458	224 KLDFNLVQPLHKKELQ···································
Prupe.4G194500.1/1-559	240 KLDFNLVQPLHKKELQ···································
Prupe.4G194600.1/1-471	278 KFDFNLVQSLHKKELS
Prupe.4G197900.1/1-559	239 KLDFNLVQSLHKNELS····································
Prupe.4G198000.1/1-485	239 KLDFN I VQSLHKKELS
Prupe.4G198200.1/1-583	262 K SDFNLVQSLHKQELS····································
Prupe.4G198500.1/1-522	234 K SDFNLVQSLHKQELS EITRWWKELDFERKLPFARNRIVELYCWIFGVYVEPQYLVGRKFLTKIIALISVNDDIYDAFGTFEELEIFTEAIHQR WHASCMEGLP-EYKQIFFHTLLNVFNEIEEEMVKE-GRAYRAHYAKEA W
Prupe.4G198600.1/1-458	185 KLDFSIVQSLHKKELS···································
Prupe.4G198700.1/1-437	244 KSDFNLVQSLHKQELS EI I RWWKELEFEKKLPFARDR I VELYFWVVQVYFEHQYLVGRKI LTKVMALLSINDD I YDAFGT FEELEI FT EA I Q. R WHVNCMDGL PAD YMQI FYHAVLNVFNE I EEEMMKE- GRAYRAN YAK EA W
Prupe.4G199000.1/1-565	244 KSDFNLVQSLHKQELS····································
Prupe.4G199200.1/1-563	245 KLDFNLVQVHQKELS····································
Prupe.4G199300.1/1-458	160 K SDFNLVQSLHKQELS EI I RWWKELDFGRKLPFARNR I VELYCSI LGVYFEPQYLVGRKFVTKI I ALMSVNDD I YHAFGT FEELEI FT EA I HQR WHANCMDGV P- DYMQI FFHT LLNV
Prupe.4G199500.1/1-566	245 KLDFNLVQSLHKQELS····································
Prupe.4G200000.1/1-568	243 K SDFNLVQSLHKQELS EFIRWWKEVDFKRKLPFARDRIVELYFWVVGVYFEPQYLVGRNILTKWIALLTANDDMYDAFGTFEELEIFTEAVO-RLDEFLWDVNCMDELP-EYMQIFYRTLLNVFNEIEEEMVKE-GRAYGAYYAKEA W
Prupe.4G200100.1/1-564	243 KSDFNLVQSLHKOELS
Prupe.4G238400.1/1-525	284 V ED YN FCO SI FYT SWRI O PFCKV LV LSLSLKLLCF I V WV V ENRLD-KLK FAROKOP YCYFSAAI SLFPPKL SDAR I SWAK SGFLLTV VND FFD GGSE EEL
Prupe.4G238900.1/1-525	232 KLDFNLVQQVHQKELS
Prupe.8G239900.1/1-698	425 KLDYNNCDALHLIEWDNIOKWYAECRLE-DYGLSTRSLLMAYFVAAASIFEPERANERVAWAKTTCLIETVGCHFKE-ETYEORGAFVHEFRTRKMNTNKKRO-GLIETLMATLHHFSLDANVAHGHDISHPLROA



	Terpene_synth_C (PF03936)	
Prupe.3G222200.1/1-630 Prupe.3G222300.1/1-463 Prupe.3G224300.1/1-631 Prupe.3G234400.1/1-695 Prupe.3G234500.1/1-636 Prupe.4G029900.1/1-576 Prupe.4G029900.300.1/1-536	437 NLCKSYLVEARWFYRGYT PT LOEYLDNAWT SVGGPGAL HAYLLOGLGSHLTKTSLESFK- HGSEIV YWSSLMTR LSDDL- GT SKAE SERGDVAKAV ECYMEEKGTS- EEEAGHYINDLTCYSWKKMNEESA- KT SRIPK- PIV- KMSLMMARTAHSIFGHGDGIGT	37 39 24 88 30 56 08
Prupe.4G030400.1/1-580 Prupe.4G125200.1/1-352 Prupe.4G125300.1/1-555 Prupe.4G125500.1/1-545 Prupe.4G126600.1/1-558	403 SIGNAFLVEAKWEKSGHLEKAEDYLKNGIVSSGVNVVNVHIFFLLGGG-ITKGSVELLN-ETPATISSAAAILELWDDL-GTAEDENGDGHDGSVIRCYINEHOGCSIKDAGEITINLISEEWKAENKELV-SPNPFEV-AFT-NASLNLAFMVPLMYSYDONGCL56 373 DFCKALLVEAEWYSRSYTPSLEEYLSNGCISSSVSVLNVHTFFSTTHRDGI-KEIADFLH-KNEDLVHNISLIVALTNDL-GTSTAEDERGDAPSAILCYMREMNAS-EDTAEAKIKGMIDNAWKKINGTCLRTPOOVPFLSPFINNIATNIAFMAHSLYOAGDGFGD	36 26 39
Prupe.4G128500.1/1-805 Prupe.4G128600.1/1-461 Prupe.4G190700.1/1-551 Prupe.4G190800.1/1-359 Prupe.4G191000.1/1-564	618 DLLKSMSKEAEWLENKSVPT MDE WATNAVISFALGPIVLPALVLVGPRLSEEVVENSEFYNLYRLMST SGRLLNDI GGFKRESAEGKLNALTLAMIHGRRVVT EEET IN EMKSVIT SKRRELLRIVLLEKGSIVP RACKDLFWMMSKVLHLFVAKNDGFTA	78 31 59 44
Prupe.4G194100.1/1-559 Prupe.4G194200.1/1-559 Prupe.4G194300.1/1-558 Prupe.4G194400.1/1-458 Prupe.4G194500.1/1-559 Prupe.4G194600.1/1-471	303 A IARA FD BARWLHEGG I PSMEEYMHVI ASVGNS - PLST SLLMGDIVTKEF EWLL - NPKILHASN IFRLUDDV - AGYKFD EHGHVASS DG MKUNGVS - BEELDVFNK OVDLWWD IN EELLIKFI VVH - PVL - MULLIKH VULLIKHGDGFH - 55 379 ALARA YF BARWNEGY FT MDEVL PAA IV SSGYP - MLSTV SLGMGDIVTKEF EWLF - SNPKILHASN IFRLUDDI - VSGOFE KERGHVASS ID CYMKOVGVS - BEETLDVFNK OVDLWWD IN EELLIKFI VVH - PVL - MULLIHKVOLLIKHGDGFH - 55 379 ALARA YF BARWNEGYT FT MDEVL PAA IV SSGYP - MLSTV SLGMGDIVTKEF EWLF - SNPKILHASN IFRLUNDI - VSGOFE KERGHVASSI DCYMKOVGVS - BEETLDVFNK OVDLWWD IN EELLIKFI VVH - PVL - MULLIHKVOLLIKKGDGFH - 55 379 ALARA YF BARWNEGYT FT MDEVL PAA IV SSGYP - MLSTV SLGMGDIVTKEF FEWLF - NDGK IVRASAT LCAF MDDI - VSGOFE KERGHVASSI DCYMKOVGVS - BEETLDVFNK OVDLWWD IN EEFL - RPTAAPM - AV L. MRVLNIKKV ID LUXKGDGFT 365 DGARSYFN BARWLEGRI PSMEEYMSVAT VSISYT - FLTTI SLLGMGDIVTNESFEWLL - NDPK IVRAANTIFRLUNDI - VSTOFF KERGHAASSVDCYI KQYCYS - BEETLOVFKKOIMDLWKD IN EEFL - RPTAVPM - AV L. MRVLNIKKV DLUXKGDGFTR 361 DGARSYFN BARWLGEGRI PSMEEYMSVAT VSISYT - FLTTI SLLGMGDIVTKESFEWLL - NDPK IVRAANTIFRLUNDI - VSTOFF KERGHAASSVDCYI KQYCYS - BEETLOVFKKOIMDLWKD IN EEFL - RPTAVPM - PVL - KRVLNITRVADLLYK GBGFTR 361 DGARSYFN BARWLGEGRI PSMEEYMSVAT VSISYT - FLTTI SLLGMGDIVTKESFEWLL - NDPK IVRAANTIFRLUDDI - VSTOFF KKRIMDDI - VSTOFF KKRIMDI - VSTOFF KKRIMDDI - VSTOFF KKRIMDDI - VSTOFF KKRI	79 37 55 39 52
Prupe. 4G197900. 1/1-559 Prupe. 4G198000. 1/1-485 Prupe. 4G198200. 1/1-483 Prupe. 4G198500. 1/1-522 Prupe. 4G198600. 1/1-458	380 AVARAYE EARWENEGY PTMEEYLPAAIVSTGYP-MISTVSLEMGDIVTKEIFEWLF-NDAKIVRASTTLFREMDDI-VTSKFEKERGHVACSIDCYMKGYGES-EQEALDALNKRVDUWKDINEEFL-RPTAAPM-AVL-MRVLNLTKVVDLUVKGDGGYTA 307 AOANYFAEAOWLKDYI PSMEEYMSVATACVGNT-LISITSLVGMGDIVTKEIFEWLL-NDPRILRASNIIFRLMDDI-SGYEFE KERGHVACSIDCYMKGYGP-EQEVLDINKKDINEEFL-RPTAPM-PU-MRVLNLTKVVDLUVKGDGGYTA 404 TITKAYFDEAKWFHEGCIPSMEEYMSVATSAASF-ALSTISLVGMGDIVTKESFEWLF-NDPKILRASNIIVRLMDDI-VSSKFEKERGHVACAIDCYMKGYGVSGSEGUIDVFNKKIVDSWKDINEEFL-RPTSMPM-PIL-ERIVNLTRVVDLUVKKDGAYTA 376 TITKAYFDEAKWFHEGCIPSMEEYMSVATSAASF-ALSTISLVGMGDIVTKESFEWLF-NDPKILRASNIIVRLMDDI-VSSKFEKERGHVACAIDCYMKGYGVSGEVEIDVFNKKIVDSWKDINEEFL-RPTSMPM-PIL-ERIVNLTRVVDLUVKKDGAYTA 376 TITKAYFDEAKWFHEGCIPSMEEYMSVATSAASF-ALSTISLVGMGDIVTKEFFEWLL-NDPRILRASNIIVRLMDDI-SGYEFEKERGYVACAIDCYMKGYGVSGEVEIDVFNKKIVDSWKDINEEFL-RPTSMPM-PIL-ERIVNLTRVVDLUVKKDGAYTA 376 TITKAYFDEAKWFHEGCIPSMEEYMSVATACVGATSAASF-ALSTISLVGMGDIVTKEFFEWLL-NDPRILRASNIIFRLMDDI-SGYEFEKERGYVACAIDCYMKGYGVSGEVEDIDVFNKKIVDSWKDINEEFL-RPTSMPM-RIL-ERIVNLTRVVDLUVKKDGAYTH	38 55 53 02 41
Prupe.4G198700.1/1-437 Prupe.4G199000.1/1-565 Prupe.4G199200.1/1-563 Prupe.4G199300.1/1-458 Prupe.4G199500.1/1-566 Prupe.4G199500.1/1-566	1 YT FNY I FL. 42 386 T I SAKA YFD EAK WFHEGC I PNMEEYMRV AT SVGNT 386 T I SAKA YFD EAK WFHEGC I PNMEEYMRV AT SAAF - ALSTT SLVGMGD I VTKESFEWLF - ND PK I LKASN I I VRLMDD I - V SSKFEKERGHVACA I DCYMKQYGV SD EQEI I DV FNKQI VD SWKD I NEEFL - RPT SMPM - PI L - ER I VNLTRVVDL KKYDA YTH - 5 386 CHVRG YFD EAK WLHGKY PT MD EYMAVA LGT SYK - MPLTT SFI GMRD I VTKESFEWLF - ND PK I LKASN I I VRLMDD M - K SHKFED KREHVACA I DCYMKQYGV SD EQEI I DV FNKQI VD SWKD I NEEFL - RPT SMPM - PI L - ER I VNLTRVVDL KKYDA YTH - 5 377 TI KAYFD EAK WFHEGC I PSMEEYMRV AAT SAAF - ALSTT SLVGMGD I VTKESFEWLF - ND PK I LKASN I I VRLMDD M - V SKKFEK ERGHVACA I DCYMKQYGV SD EQEI DV FNKQI VD SWKD I NEEFL - RPT SMPM - PI L - ER I VNLTRVVDL VKYDA YTH - 5 378 TAKAYFD EAK WFHEGC I PSMEEYMRV AAT SSGIF - GV STT SLVGMGD I VTKESFEWLF - ND PK I LKASN I I VRLMDD I - V SSKFEK GRGHVACA I DCYMKQYGV SD EQEI DV FNKQI VD SWKD I NEEFL - RPT SMPM - PI L - ER I VNLTRVVDL VKYDA YTH - 5 379 TAKAYFD EAK WFHEGC I PSMEEYMRV AAT SSGIF - GV STT SLVGMGD I VTKESFEWLF - ND PK I LKASN I I VRLMDD I - V SSKFEK GRGHVACA I DCYMKQYGV SD EQEI DV FNKQI VD SWKD I NEEFL - RPT SMPM - PI L - ER I VNLTRVVDL VKYDA YTH - 5 379 TAKAYFD EAK WFHEGC I PSMEEYMRV AAT SSGIF - GV STT SLVGMGD I VTKESFEWLF - ND PK I LKASN I I VRLMDD I - V SSKFEK GRGHVACA I DCYMKQYGV SD EQEI DV FNKQI VD SWKD I NEEFL - RPT SMPM - PI L - ER I VNLTRVVDL VKYDA YTH - 5 379 TAKAYFD EAK WFHEGC I PSMEEYMRV AAT SSGIF - GV STT SLVGMGD I VTKESFEWLF - ND PK I LRASN I VRLMAD I - V SSKFEK FER FWHEGV SND FER FUNDA I DV SNKO I NEEFL - RPT SMPM - PI L - ER I VNLTRVVDL VKYDA YTH - 5 370 TAKAYFD EAK WFHEGC I PSMEEYMRV AAT SSGIF - GV STT SLVGMGD I VTKESFEWLF - ND PK I LRASN I VRLMAD I - V SSKFEK FER FUNDA I DV SNKO I NEEFL - RPT SMPM - PI L - ER I VNLTRVVDL VKYDA YTH - 5 370 TAKAYFD EAK WFHEGV I DV SNKO I NEEFL - RPT SMPM - PI L - ER I VNLTRVVDL VKYDA YTH - 5 370 TAKAYFD EAK WFHEGV I DV SNKO I NEEFL - RPT SNPM - PI L - ER I VNLTRVVDL VKYDA YTH - 5 370 TAKAYFD EAK WFHEGV I DV SNKO I NEEFL - RPT SNPM - PI L - RVNLTRVVDL VKYDA Y	30 45 43 38 46 48
Prupe.46200100.1/1-564 Prupe.46238400.1/1-525 Prupe.46238900.1/1-525 Prupe.86239900.1/1-525	385 THARA YFD EAK WFH EGCI PSMEEVMRVA TA SAGHT - T LTTMSL GMGD IVTK ESF EWLL - ND PKI LRASN I GRUMDD I - V SSK FEKERGHVA SA I DC YRKOYEV SD EGEI I DA FHKO IVD SWKD IN EEFL - RPT SV PM - PLL - VRV LN LTRVAD LI VKKDD GLTH	44 06 05 81

NSE/DTE

Prupe.3G222200.1/1-630	598 SIGVT KDRLISLIAN P
Prupe.3G222300.1/1-463	440 SIGVTKHRLISLIASPIAIFHEH*
Prupe.3G234300.1/1-831	725 - PTELLADINKA I FDSLRVEDVQGSFMPLNSMQGTLGLKRDKSLA I HGKSHYSSSKPCNG I FESNCA I KVQGNSRKGLVTKPYSRIL SVKMRNPI I YPTFSNPKA YI*-
Prupe.3G234400.1/1-695	689 PT E SN F*
Prupe.3G234500.1/1-838	731 - PT EL LAH INKA I FD PLRV EDVQG SFM PLN SFQ ST LG LKKDK SLA SHGK SHYSSSKT CNG FFK ST CA I K LQGN SRKD LVTK PYSR I L SL EMRN PT I YTT FSK PKA Y I Y*
Prupe.4G029900.1/1-576	557 Q EKGT R I L I Q S L L V Q P L L L
Prupe.4G030300.1/1-536	509 - PSLEENMK SLLFD SFLAQG FQ SPGQTK
Prupe.4G030400.1/1-580	563 - PSLKEYMPSMLYET
Prupe 4G125200 1/1-352	349
Prupe 4G125300 1/1-555	537 - Q EQG SR L I Q SV L V E P
Prupe 4G125500 1/1-545	
Prupe 4G126600 1/1-558	540 - OFKGSBLIQSLIAFP.
Prupe 4G128500 1/1-805	
Prupe 4G128600 1/1-461	
Prupe 4G190700 1/1-551	
Prupe 4G100000 1/1-351	
Prupo 4G101000 1/1-509	
Prupe.4G191000.1/1-564	
Prupe.4G194100.1/1-562	
Prupe.4G194200.1/1-599	
Prupe.4G194300.1/1-558	38 VERVER ASHFIDE
Prupe.4G194400.1/1-458	
Prupe.4G194500.1/1-559	S40 VGKVTKDSTASVCTN
Prupe.4G194600.1/1-471	453 CNSCHSPMILAP AVVSPS
Prupe.4G197900.1/1-559	539 V GK V V K D K I A SH F I N P
Prupe.4G198000.1/1-485	466 V GK V MKD SVA SLFIEP · · · · · · · V PL ·
Prupe.4G198200.1/1-583	564 AGKVMNDCVASYFIDPAPV
Prupe.4G198500.1/1-522	503 GGKVMNDCIASYLIDPALV
Prupe.4G198600.1/1-458	442 VGKYMKDSVASVFINQ
Prupe.4G198700.1/1-437	431 HGRHCN*
Prupe.4G199000.1/1-565	546 GGKVMNDCIASYLIDL
Prupe.4G199200.1/1-563	544 AGVVLKDLLVSLFVNP
Prupe.4G199300.1/1-458	439 GGKVMNDCIASYLIDP
Prupe.4G199500.1/1-566	547 GGKVMNDCIALYLIDP
Prupe.4G200000.1/1-568	549 VGKVMKD SVA SYFIDP
Prupe.4G200100.1/1-564	545 VGKVMKD SVA SYFIDP
Prupe, 4G238400, 1/1-525	507 VGNEMMKDVNEVIDE
Prupe, 4G238900, 1/1-525	
Prupe.8G239900.1/1-698	682 GT I NHH LT KV F F E

Figure S1. Alignment of amino acid sequences of 38 PpTPSs. N-terminal conserved domain (PF01397) and C-terminal conserved domain (PF03936) are marked in red and green boxes, respectively. Three conserved motifs of RRX₈W, Asp-rich domain DDxxD and NSE/DTE are also labeled.



Figure S2. SDS-PAGE analysis of PpTPS3 protein.



Figure S3. Silencing of *PpPDS* (**Prupe.1G174100**) **gene in peach fruit.** Empty pTRV1 + pTRV2 vector was used as a control, and phytoene desaturase (*PDS*) was used as a reporter gene for VIGS. The arrow points to the injection hole. The photo was taken two weeks after the infiltration.



Figure S4. Expression of *AtTPS10* and *AtTPS14* in *PpTPS3* transgenic Arabidopsis. Relative expression levels were determined using qRT-PCR. Data are presented as the mean \pm SE from three independent biological replicates. Significant differences are indicated with asterisks above the bars (*, *P* < 0.05). N.D., Not Detected.



Figure S5. Changes in content of free linalool in *PpTPS3* transgenic tomato leaves. (a) Relative expression of *PpTPS3* in wild type and transgenic tomato leaves. (b) The content of linalool in wild type and transgenic tomato leaves. Volatiles were identified using gas chromatography–mass spectrometry (GC–MS). Data are presented as the mean \pm SE from three independent biological replicates. Wild-type (WT) plant was used as control. Significant differences are compared against controls and indicated with asterisks above the bars (**, *P* < 0.01). N.D., Not Detected.



Figure S6. Expression profiles of three bHLH genes and regulatory effect of PpbHLH1 on the promoter of *PpTPS1.* (a) Expression profiles of three bHLH genes during peach fruit ripening. The RNA-seq was conducted with three biological replicates. (b) Regulatory effect of PpbHLH1 on the promoter of *PpTPS1*. Relative LUC/REN value of the empty vector on *PpTPS1* promoter was used as the calibrator, set as 1. S.E.s were calculated from at six replicates. Statistical significance was determined by Student's two-tail *t* test.



Figure S7. PpbHLH1 binds to *PpTPS3* **promoter. (a)** The three probes sequences used for EMSA. (b) SDS-PAGE analysis of PpbHLH1 protein. (c) EMSA of PpbHLH1 binding to *PpTPS3* promoter. Presence or absence of specific probes is marked by symbol + or -.



Figure S8. Correlation between transcript and S-(+)-Linalool content in different peach cultivars. (a) Correlation between *PpTPS3* expression and S-(+)-Linalool content in peach cultivars. (b) Correlation between *PpbHLH1* expression and S-(+)-Linalool content in peach cultivars.

PpTPS3 RcLIN-NERS1 VvLIS/NES FaNES1 RcLIN-NERS2 MdLIS PpTPS1 Consensus	MALLQAHSASPNCPIVDFHVHAQKIKELKDALANVGE.D.ELLIAVDAMCHLGLDHH REETEAFLQKQYH.ARAYDNCNHQ .MAFILQAHSASSKSQTADLHVRHEEKIKELKETLANSGE.DQLQQUVWVDAMCRLGVAYY ODEIDAILEK YTR.SLAYNDNDDGNHQ .MGFSPÄFYACSIPPVGPNKFTELGQSKFNNVVLVPTAQKWSIAHDHTLVYKPLRKHNHQSQHL.STTDEFYIKHAQRIDEIRNVFSEVGE.DTLEGIMMIDAICRLGIDYHBKEETEAVUQKCYMKASTHG.ESIQD MASSSRAFFKVFNP.APKSIPRIGQSNLMQLTHKKQLPFFQRGIAED.SLLPSSTTPIELISYDTKIITKTMDDIFVQHCQKLELFRNVLRNVAELDALEGINMIDAVCRLGIDYHBCPEIDEILHKCMNSISVIGD .MEFSISQSSFATS.SSTPAAPEHLS.SQKWSIPEDHSLLS.TPLKPINVETKYT.SSKDGIICFQNEQKIDDLRALIKVGG.EAVESIDMIDAVCRLGIDYHBCDEIDQILQKCH.IISSTAHGAHHPTD MALFSMÄISAVYNAPKKIPHIQLTPKPS.SQQWSTAQDHGLLS.TPLHLLNSKTNYANTITKEDDDICFLHAKKIDVFRHVISKLGE.EAVEGINMIDAVCRLGIDHH QDEIDQILQKCHLIITSGSAHGANHHSD l da q lg f ei l q	80 87 134 135 137 126 134
PpTPS3 RcLIN-NERS1 VvLIS/NES FaNES1 RcLIN-NERS2 MdLIS PpTPS1 Consensus	LEVSIRFRLLRQQCYHVTTDVENKFKNIQ.DLKSCTDKDIEGIVGIYEASH SFQGEDALDEAGKISHQITTAW.PNNLDDHRAPIVAHSIKH YHKSITRFMAKNBLDYF.QGTE.KWASIIQELAKLELNVWESIIRNDIL LEASLRFRLLRQQGFFVTPDAEAGNQIKNNE.KLKSGIIAGDEDIKGIVEIGEASHIGFHGETIDEAGKISRQITTAWVPNNLKDHRAALASHTLEHEYHKSITRFMAKNBLDNF.QGQE.KWVCSIRELANLEFNNVESIIRNDIL IMEVALRFRLLRQEGYHVPADVINNFKNREGKFKQNUSKDIKGILGIYEASGISIEGEDIUEEAQRESSTINAGIE.HUDHHENTVVVHTLEHEYHKSITRFMAKNBLNNF.QGQE.KWVCSIRELANLEFNNVESIIRNDIL IMEVALRFRLLRQEGYHVPADVINNFKNREGKFKQNUSKDIKGILGIYEASGISIEGEDIUEEAQRESSTINAGIE.HUDHHENTVVVHTLEHEYHKSIFTRFMAKNBLKDF.QGY.GWT.QGIN.GWLTVLQELAKADFNNVGSIHQQELLQ IHEVALRFRLLRQGYFVPDVVNNFKNREGKFKQNIGEDIKGIMSIYEASGIGTEGEDIVEEKESGHLIKTSI.HUDHHENTVGNIFNEHHKSIASFMARNBFVT.QGIN.SWLALKKVAKTDFNNVGSIHQQELLQ IHEVALRFRLLRQGYFVPDVVNNFKESNGMFKQAIGEDIKGIMSIYEASGIGTEGEDIVEEKESGHLIKTSI.HUDHHQARVVGNTLGNIHKSIASFMARNBFVT.QGIN.TWSNLKEVAKTDFSNVGSIHQDIVQ IHEVALRFRLLRQGYFVPDVVNNFKESNGMFKQAIGEDIKGIMSIYEASGIGTEGEDIVEEKESGHLIKTSI.HUDHHQARVVGNTLGNIHKSIASFMARNBFVT.QGIN.TWSNLKEVAKTDFSNVGSIHQDIVQ IHEVALRFRLLRQGYFVPDVVNNFKESNGMFKQAIGEDIKGIMSIYEASGISIEGEVVIEEAGKFSGHTINSSIS.HUDHHQARVVGNTLRNHHKSIASFMARNBFVT.QGIN.TWSNLKEVAKTDFSNVGSIHQNEIVQ IHEVANRFRLLRQGYFVPDVVNNFKESGSFKQVISEDIKGIMSIYEASGISIEGEVVIEEAGKFSGHTINSSIS.HUDHQARVVGNTLRNHHKSIASFMARNBFVS.QGYNNWKIIIQVVAKTDINVCSIHQKUVQ IHEVANRFRLLRQGYFVPDVVNNFKNREGNFNQVIREDIKGIMSIYEASGISIEGEVVIEEAGKFSGHTINSSIS.HUDHQARVVGNTIRNHHKSIASFMARNBFVS.GTNNRWLNIIQVVAKTDINVCSIHQKUVQ IHEVANRFRLLRQQYFVPDVVNFKKESEGSFKQMISEDIKGIMSIYEASQISIEGEDTIEEQQFSWHILNTSIS.HUDHQARVVGNTISNHHKSIATFMAKNFFANSRTNNKUNIIQVVAKTDINVCSIHQKUKDF. I e rfrllrqg v n k 1 di ql 1 eas 1 1 h a 1 phksl fma f w 1 a v s e q	222 234 276 277 279 270 278
PpTPS3 RcLIN-NERS1 VvLIS/NES FaNES1 RcLIN-NERS2 MdLIS PpTPS1 Consensus	ISKWWRELGITKELNEVROOFIKWYTWPMACTTESISEERLEITKSISLVYIIDDIFD/HGTLDEIVLFYAAVERWDLDETDELEDYMKISFKAUYDITNETSDRAMKRHGWNPIESIKKSWAILGKAFTLEAGWERCGHENAEDYLK VSRWWRELGITKELKEVROOFIKWYTWPMASTVDERISDDRFELTKAISLVYIIDDIFD/HGTLDEIIFFAAVARWDTDTNDELENYMKTOFKALNEITNDISESVYEKHGWNPIESIKKSWAILGKAFTLEAGWERCGHENSEDYLK ISKWWQLGIAEDIKEARDORIKWHWWPMAVIPDISISECRVELTKPISMIYIDDIFD/HGTLDEIIFFAAVARWDTDTNDELENYMKTOFKALNEITNDISESVYEKHGWNPIESIKKSWAILGKAFTLEAGWERCGHENSEDYLK ISKWWCLGIAEDIKEARDORIKWHWPMAVIPDISISECRVELTKPISMIYIDDIFD/HGTLDEIIFFAAVARWDTDTNDELENYMKICFKIDEITNEISNKVYKEHGWNPUSIRKWMSLGNAFTVEAEWERGGIENSEDYLK ISKWWELGIAKELKEARDORIKWHWSMACHDEKISECRVELTKPISFIYIDDIFD/HGTLDEIIIFFEAVNRWEITAIDHEDYMKICFKIDEITNEISNKVYKEHGWNPUSIRKWMSLGNAFTVEAKWEASGIENSEC ISKWWELGIAKELKEARDORIKWIMSMACHDEKISECRVELTKPISFIYIDDIFD/YGTLDEIIIFFEAVNRWEITAIDHEDYMKICFKAIYDMTNEISCKVYKHGWNPLOSIKKWASLGNAFTVEAKWEASGIENSEC VSKWWELGIAKELKEARDORIKWIMSMACHDEKISERVELTKPISFIYIIDDIFD/YGTLDEIITLFFEAVNRWEIGIAEHLEDYMKICFKAIYDMTNEISCKVYKHGWNPLOSIKKWASLGNAFTVEAKWEASGIENSEC VSKWWELGICKELKEARDORIKWIMSMACHDENISDERIELTKPISFIYIIDDIFD/YGTLDEIITLFFEAVNRWEIGIAEHLEDYMKICFKAIYDMTNEISCKVYKHGWNPLOSIKKWASLGNAFTVEAKWEASGIENSEC VSKWWELGICKELKEARDORIKWIMSMACHDENISDERIELTKPISFIYIIDDIFD/YGTLDEIITLFFEAVNRWEIGIAEHLEDYMKICFKAIYDMTNEISCKVYKHGWNPLSKKWASLGNAFTVEAKWEKSCHLEMAEEYLK VSKWWELGICKELKEARDORIKWIMSMACHDENISDERIELTKPISFIYIIDDIFD/YGTLDEIILFFEAVNRWEIGSIEHLEDYMKICFKAIYDMTNEISCKVYKHGWNPLSKKWASLGNAFTVEAKWEKSCHLEMAEEYLK SKWWELGICKELKEARDORIKWIMSMACHDENISDERIELTKPISFIYIIDDIFD/YGTLDEIILFFEAVNRWEIGSIEHLEDYMKICFKAIHDITNEISCKVYKHGWNPLKSKKHGUNFLKAKWEKSCHLEMAEEYLK SKWWELGICKELKEARDORIKWIMSMACHDENSCHWEKSCHLEMAEEKSCHLEMAEEGYLK SKWWELGICKELKEARDORIKWIMSMACHDENISDERVELTKPISFIYIIDDIFD/YGTLDEIILFFEAVNRWEIGDIEHLEDYMKICFKAIHDITNEISCKVYKHGWNPLSKAUASGONAFTVEAKWEKSCHLEMAEEYLK SKWWELGIAKELKEARDORIKWIMSMACHAENSWEKSCHAFVEKSCHLEMAEEYLK SKWWELGIAKELKEARDORIKWIMSMACHAENSY SKWWELGICKELKEARDORIKWIMSMACHAENSY SKWWELGIAKELKEARDORIKWIMSMACHAENSY SKWWELGICKELKEARDORIKWENSKELGENKEKSCHEKKESCHEFKELKTWEGYLK SKWWELGIAKELKEARDORIKKYTYTTYT	372 384 426 427 429 420 428
PpTPS3 RcLIN-NERS1 VvLIS/NES FaNES1 RcLIN-NERS2 MdLIS PpTPS1 Consensus	NGVISTGV PAVLTHAFFILGRGTTQQAIDIVDNINTEGIISSTATIIRLWDIG SAKDE MONGYDGSYIQGYVNEHEGOSDEDARAYVIQKISDEWKRUNQECESSNEFSESTKLALNVARMVEMMYDYNTQHRUESLEDAMKSLUFDS NGTISSGV PAVLTHAFFILGRGTTQQAIDIVDNINTEGIISSTATITRUWDIG SAKDE KONGYDGSYVQGYMEEH POSSVEFAQAYVIRKISDEWKYLNGECESSNEFSESTKLALNVARMVEMMYDYNTQHRUESLEDAMKSLUFDS NGVISSGV HVULHLFFILGRGTTRGNVDLVDDEPSIISSTATITRUWDIG SAKDE KOLGHDGSYLEGYIKEH OGSSMENARQNVTYMISDUWKRUNKECLSQHLESTSTTKGSLNIARVPLMYSYDDNQSLEHLEEHMKSLUFEA NGVISSGVNVULHHEFILGRGTTRGNVDLVDDEPSIISSTATITRUWDIG SAKDE KOLGHDGSYLEGYIKEH OGSSMENARQNVTYMISDUWKRUNKECLSQHLESTSTTKGSLNIARVPLMYSYDDNQSLEHLEEHMKSLUFEA NGVISSGVNVULHHEFILGRGTTRGNVDLVDDEPSIISSTATIRUWDIG SAKDE KOLGHDGSYLEGYIKELEEHECCSIEBAREKTINNISDEWKKUNRELLSPNFFPATTIASINLARVPLMYSYDDNQSLEHLEEHMKSLUFEA NGVISSGVNVVLVHIFFILGQNITKSVELLN.DTPTIISSTATIRUWDIG SAKDE KOLGHDGSYLRGYLEEHECCSIEBAREKTINNISDEWKKUNRELLSPNFFPATTIASINLARVPLMYSYDGNQCLESUKEYMKSUTYT NGISSGVNVVMVHIFFILGGSTTNGSVEELN.GTPAIISSTATIRUWDIG SAKDE KOENDGSYLRGYLEEHECCSIEBAREKTINNISDEWKKUNRELLSPNFFPATTIASINLARVPLMYSYDGNQCLESUKEYMKSMIYET NGISSGVNVVMVHIFFILGGSTTNGSVEELN.GTPAIISSTAATIRUWDIG SAKDE KOENDGSYLRGYLEEHECCSIEBAREKTINNISDEWKKUNRELSPNFFPATTIASINLARVPLMYSYDGNQCLESUKEYMKSMIYET NGISSGVNVVMVHIFFILGGSTTNGSVEELN.GTPAIISSTAATIRUWDIG SAKDE KOENDGSYLRGYLEEHECCSIEBAREKTINNISDEWKKUNRELSPNFFPATTASINLARVPLMYSYDDNQCLESUKEYMKSMIYET NGISSGVNVVMVHIFFILGGSTTNGSVEELN.GTPAIISSTAATIRUWDIG SAKDE KOENDGSYLRGYNRMLENGCCTING SUFTINISDEWKKUNRELSPNFFPATTASINLARVPLMYSYDDNQCLESUKEYMKSMIYET NGISSGVNVMVHIFFILGGSTTNGSVELLN.ETPAIISSTAATIRUWDIG TAEDE KOENDGSYIRGYINEHCCCSIKDAQEITINIISEEWKKUNKELSPNFFPATTASINLARVPLMYSYDDNQCLESUKEYMKSMIYET NGISSGVNVMVHIFFILGGSTTNGSVELLN.ETPAIISSTAATIRUWDIG AKDE KOENDGSYIRGYINEHCCCSIKDAQEITINIISEEWKKUNKELSPNFFPATTASINLARVPLMYSYDDNQCLESUKEYMKSMIYET NGISSGVNVMVHIFFILGGSTTNGSVELLN.ETPAIISSTAATIRUWDIG AD GOG GYVRYLEHEGOSTINGSTNGGTINGSTNGSTNGTNATATINGSTNGTNGT NGISSGVNVMVHIFFILGGSTTNGSVELLN.ETPAIISSTAATIRUWDIG AD GOG GYGYNGYDAGGYIRGYINGGCG SIKDAGEITINISEEWKKUNKELSPNFFPATTASINLARVPLMYSNDONGCLESUKEYMKSMIYET NGVNVMVHIFFILG	522 534 574 575 577 567 576
PpTPS3 RcLIN-NERS1 VvLIS/NES FaNES1 RcLIN-NERS2 MdLIS PpTPS1 Consensus	FLAQGFQSPGQT NSE/DTE FLSKGITHG FPL VSM VSM ESV	534 543 577 578 580 567 579

Figure S9. Alignment of amino acid sequence of PpTPS3 with closely related sequences from TPS-g subfamily. Two conserved motifs of Asp-rich domain DDxxD and (N, D) Dxx (S, T) xxxE (NSE/DTE) are marked.



Figure S10. Phylogenetic tree constructed using the sequences of bHLH proteins from both peach and Arabidopsis with some bHLH proteins which regulate linalool or terpene formation in other species.



Figure S11. Changes in content of linalyl- β -d-glucoside and linalool oxide in *PpTPS3* and *PpbHLH1* transgenic tomato fruits. (a) Content of linalyl- β -d-glucoside in wild type and *PpTPS3* transgenic tomato fruits. (b) Content of linalyl- β -d-glucoside in wild type and *PpbHLH1* transgenic tomato fruits. (c) Content of *cis*-linalool oxide in wild type and *PpbHLH1* transgenic tomato fruits. (c) Content of *cis*-linalool oxide in wild type and *PpbHLH1* transgenic tomato fruits. Significant transgenic tomato fruits. Data are presented as the mean \pm SE from three independent biological replicates. Significant differences are compared against controls and indicated with asterisks above the bars (**, *P* < 0.01 and ***, *P* < 0.001).

	Compound (ng/gEW)	Days after bloom (DAB)				
	Compound (ng/g F w)	34 (S1)	71 (S2)	94 (S3)	108 (S4)	111 (S5)
	α-Pinene	UD	UD	2.13±2.13	UD	6.35±6.35
	β-Pinene	4.20±2.69	4.76±2.38	7.07±5.31	4.73±2.72	4.89±2.45
	Myrcene	UD	3.20 ± 1.68	8.10±4.22	5.16±2.60	9.16±4.64
	D-Limonene	58.51 ± 17.52	73.37 ± 30.62	57.19±18.96	29.27±9.51	34.62±0.73
	γ-Terpinene	UD	UD	1.13 ± 1.13	1.35 ± 1.35	UD
Tomonos	(Z)-Ocimene	UD	UD	UD	UD	14.03±7.16
Terpenes	α-terpinene	11.98 ± 10.24	UD	0.47 ± 0.47	4.59±4.59	11.29 ± 11.29
	2-Carene	UD	UD	UD	2.20±2.20	UD
	2-Camphene	UD	UD	7.71±0.32	3.36±3.36	5.97 ± 5.97
	Terpinolene	UD	UD	7.69±3.87	12.80±6.71	22.7 ± 11.50
	α-Phellandrene	UD	UD	1.03 ± 1.03	UD	UD
	Caryophyllene	UD	0.77±0.77	UD	UD	UD
	Linalool	UD	3.97±1.99	140.66±12.88	428.24±45.96	580.11±82.82
	α-Terpineol	0.90±0.90	0.77 ± 0.77	UD	4.65±4.65	UD
Terpenoids	Nerolidol	UD	UD	2.36±2.36	UD	UD
	farnesol	UD	UD	3.56±1.79	UD	UD
	Cedrol	19.56±14.36	6.07±4.42	2.14±0.27	2.96±0.18	7.89±6.35
	β-Damascenone	21.28 ± 11.21	13.3±0.24	20.92 ± 1.21	22.76±4.30	17.12±4.52
Norisoprenoids	Dihydro-β-Ionone	UD	UD	36.43±4.83	35.11 ± 11.14	45.95 ± 15.27
	β-Ionone	70.84 ± 19.06	29.42±4.90	6.37±3.19	6.88±6.88	9.97±9.97

Table S1. Content of volatiles in peach fruit during development and ripening.

UD, under the limit of detection.

Abbraviation	GenBank	Abbraviation	GenBank	Abbreviation	GenBank	Abbraviation	GenBank
Abbieviation	accession	Abbieviation	accession	Abbieviation	accession	Addieviation	accession
VvLIS/NES	ADR74212	NaLIS	NIATv7_g00838	LoTPS1	AHD24667	PfLIS	AAL38029
VvCSLinNer	HM807393	OfTPS2	AMB57286	MaLIS	AAP40638	PfGES/LIS	ACN42011
VvRiLinNer	JQ062931	LiS-LINS	MG870571	MdOCS	JX848733	PcLIS	AAX16075
VvPNLinNer1	ADR74210	AmNES/LIS-1	ABR24417	BcLS	BAG82825	MdCAR	JX848729
VvPNLNG11	ADR74213	AmNES/LIS-2	ABR24418	AaLIS	Q9SPN1	MdGDS	JX848730
CsLIS/NES	AGX26045	AmMS	AAO41727	AaQH1	AF154125	MdPIN/CAM	JX848732
AaLS1	ADD81294	AmOS	Q84NC8.1	AaQH5	AAF13356	Pt5	AAO61226
ApLS1	GQ338154	CoLIS	AFQ20812	GhLin2	AJT59543	PaLIS	AAS47693
CuLIS	BAP75559	OsLIS	ACF05530	CaTPS2	CCM43928	PcTPS-Lin-1	ADZ45501
MdLIS	AGB14629	LoTPS3		PtTPS1	AII32476	PcTPS-Lin-2	ADZ45502
RcLIN-NERS2	MG673511	PITPS3	ARG42161	SITPS5	AAX69063	CbLIS	AAC49395
FaNES1	P0CV94	ObLIS	AY693647	CsLINS	AHC54051	CbLIS2	AAD19840
PtTPS3	AEI52903	ObGES	Q6USK1	HcTPS8	AGY49283	ZmTPS1	AAO18435
GhTPS12	AJT59541	CrGES	AFD64744	AtTPS10	At2g24210	AtCPS1	NP_192187
RcLIN-NERS1	MG673510	OfTPS1	AMB57285	PdLIS	ATY48639	CmCPS	AAD04292
MtTPS3	AAV36466	OeGES1	AFI47926	MsLS	AAC37366	SITPS40	JN412074
PITPS4	ARG42162	RcLINS	MG673509	LaRLin	ABD77417	SrCPS	AAB87091
AtTPS14	At1g61680	VvPNRLin	ADR74209	LaLINS	ABB73045		
SITPS37	AEP82769	PtTPS4	AEI52904	McLIS	AY083653		
SITPS39	AEP82767	McTPS1	ART66980	MaLin	AAL99381		

 Table S2. Accession numbers for plant TPSs used for sequence analysis in Figure 2.

TF families	Species	Description	Gene ID	Peach ID	Name	References
		AaNAC1	KF319046	Prupe.4G187100	PpNAC1	
NAC	Actividia arouta	AaNAC2	KF319047	Prupe.4G040900	PpNAC2	Nieuwenhuizen et al.,
	Actiniata arguia	AaNAC3	KF319048	Prupe.4G040900	PpNAC2	2015
		AaNAC4	KF319049	Prupe.1G220400	PpNAC4	
	Actinidia deliciosa	AdNAC6/7	Achn208181/Achn077531	Prupe.5G196000	PpNAC6	Wang et al., 2019
	Artemisia annua	AaNAC1	KX082975	Prupe.1G493100	PpNAC8	Lv et al., 2016
		FhMYB21L1	QNC43969	Prupe.5G222400	PpMYB1	
МҮВ	Freesia hybrida	FhMYB21L2	QNC43970	Prupe.5G031700	Not expressed in peach	Yang <i>et al.</i> , 2020
	Mentha spicata	MsMYB	KY081780	Prupe.8G164300	PpMYB2	Reddy et al., 2017
	Catharanthus roseus	CrBPF1	AJ251686	Prupe.2G237100	PpMYB3	Li et al., 2015
	Artemisia annua	AaWRKY1	FJ390842	Prupe.5G117000	PpWRKY1	Ma et al., 2009
	Gossypium arboreum	GaWRKY1	AY507929	Prupe.1G393000	PpWRKY2	Xu et al., 2004
	Solanum lycopersicum	SIWRKY73	Solyc03g113120.2.1	Prupe.5G187800	PpWRKY73	Spyropoulou et al., 2014
	Oryza sativa	WRKY45	AK066255	Prupe.6G295100	PpWRKY45	Akagi <i>et al.</i> , 2014; Shimono <i>et al.</i> , 2007
WRKY		WRKY53	AB190436	Prupe.6G286000	PpWRKY53	
		WRKY76	AK068337	Prupe.6G230600	PpWRKY76	Schluttenhofer and Yuan,
	Nicotiana benthamiana	WRKY8	AB445392	Prupe.6G046900	PpWRKY8	2015
	Panax quinquefolius	PqWRKY1	JF508376	Prupe.1G431100	PpWRKY3	
	Catharanthus roseus	CrWRKY1	HQ646368	Prupe.6G295100	PpWRKY4	Suttipanta et al., 2011
	Arabidopsis thaliana	AtMYC2	At1g32640	Prupe.5G035400	PpMYC2	Hong et al., 2012
ьні н	Artemisia annua	AabHLH1	AGH25053	Prupe.5G035400	PpMYC2	Ji et al., 2014
UIILII	Catharanthus roseus	CrMYC1	AF283506	Prupe.8G095700	PpMYC1	Chatel et al., 2003
	Catharanthus roseus	CrMYC2	AF283507	Prupe.5G035400	PpMYC2	Zhang <i>et al.</i> , 2011

Table S3. Peach homologues of transcription factors that regulate terpenoid formation.

		CrBIS1	KM409646	Prupe.8G157500	PpbHLH1	van Moerkercke <i>et al.</i> , 2015
		CrBIS2	KM409645	Prupe.6G211900	PpbHLH2	van Moerkercke <i>et al.,</i> 2016
	Oryza sativa	OsbHLH025 (DPF)	Os01g0196300	Prupe.7G207500	PpbHLH25	Yamamura et al., 2015
	Medicago truncatula	TSAR1-2	Medtr7g080780 Medtr4g066460	Prupe.6G212000	PpbHLH3	Mertens et al., 2016
	Phalaenopsis bellina	PbbHLH4	KY979199	Prupe.5G143200	PpbHLH4	Chuang et al., 2018
	Taxus cuspidata	TcMYC1, TcJAMYC1/2/4	FJ608574/JX519289 /JX519290	Prupe.5G035400	PpMYC2	Lenka et al., 2015
	Cucumis sativus	Bl Bt	Csa5G156220	Prupe.2G286100	Not expressed in peach	Shang et al. 2014
	Cucumis suivus	Di, Di	Csa5G157230	Prupe.2G286000	Not expressed in peach	Shang et u., 2014
	Freesia hybrida	FhMYC2	QNC43971	Prupe.5G035400	PpMYC2	Yang et al., 2020
	Solanum lycopersicum	SIMYC1	KF430611	Prupe.5G035400	РрМҮС2	Spyropoulou <i>et al.</i> , 2014; Xu <i>et al.</i> , 2019
	Malus domestica	MdMYC2	MDP0000029168	Prupe.5G035400	PpMYC2	Wang et al., 2020
		AaERF1	JN162091	Prupe.5G061800	PpERF1	Vu at al. 2012
	Artemisia annua	AaERF2	JN162092	Prupe.2G272400	PpERF2	1 u <i>el ul.</i> , 2012
		AaORA	JQ797708	Prupe.2G129400	PpERF3	Lu et al., 2013
	Catharanthus roseus	CrORCA3	CAB96899	Prupe.2G129300	Not expressed	van der Fits and Memelink, 2000
ERF		CrORCA4/CrORCA5	KR703577/KR703578	Prupe.2G129300	in peach	Paul et al., 2017
	Zea mays	ZmEREB58	NP_001170395.1	Prupe.1G037900	PpEREB58	Li et al., 2015
		CitAP2.10	orange1.1t02867.1	Prupe.3G104100	PpAP2	Shen et al., 2016
	Citrus sinensis Osbeck	CitERF71	orange1.1g047100m	Prupe.2G129300	Not expressed in peach	Li et al., 2017
	Malus domestica	MdERF3	MDP0000787281	Prupe.5G061800	PpERF1	Wang et al., 2020
EII	Actividia chinorcia	AcEIL1	KF319041	Prupe.2G058400	DraEII 1	Nieuwenhuizen et al.,
EIL	Actinidia chinensis	AcEIL2	KF319042	Prupe.2G058400	грецет	2015

		AcEIL3	KF319043	Prupe.6G018200		
		AcEIL4	KF319044	Prupe.6G018200	PpEIL3	
	Actinidia arguta	AaEIL4	KF319045	Prupe.6G018200		
	Artemisia annua	AabZIP1	contig131774	Prupe.1G434500	PpbZIP1	Zhang et al., 2015
bZIP	Oryza sativa	OsTGAP1	AK073715	Prupe.1G307300	PpbZIP2	Okada et al., 2009
		OsbZIP79	Os11g0152700	Prupe.6G129100	PpbZIP79	Miyamoto et al., 2015
EOT	Solanum lycopersicum	SIEOT1	AGW27396.1	Prupe.1G371500	PpEOT1	Spyropoulou et al., 2014
VADDV	Mentha spicata	MsYABBY5	AMA07776	Prupe.7G245200	DnVADDV5	Wang et al., 2016
YABBY	Artemisia annua	AaYABBY5	MK675289	Prupe.7G245200	гріявніз	Kayani <i>et al.</i> , 2019

Bold indicates transcription factors associated with linalool synthesis.

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Family	Peach ID	Correlation	Name	Primer-SK (5')	Primer-SK (3')
		with <i>PpTPS3</i>			
	Prupe.4G077100	0.85456	PpbHLH5	agaactagtggatccATGCAGAGGGACCAACAGTT	cccctcgaggtcgacTTAGTCATTCAAATTCTCAA
LUI U	Prupe.1G173300	0.80985	PpbHLH6	agaactagtggatccATGGGAAAAGACAGAACAGC	cccctcgaggtcgacTTATAGCTCAACTTTCATCT
UNLN	Prupe.6G343400	0.70216	PpbHLH7	agaactagtggatccATGGCGGGAAATCCGCCTGA	cccctcgaggtcgacCTATGAAGAGGAGTTTGATT
	Prupe.1G207100	0.66293	PpbHLH8	agaactagtggatccATGATTGTTAGCTCTCTCTG	cccctcgaggtcgacTCAATGGAATTGTGAGATGG
	Prupe.1G369300	0.82833	PpbZIP3	agaactagtggatccATGGAGGGCAGTGATGAAAC	cccctcgaggtcgacCTATTCGCTTGACTCGTGCT
	Prupe.8G091600	0.79739	PpbZIP4	agaactagtggatccATGGCTTCTTCTAGTGGGAC	cccctcgaggtcgacTCAGTAATGAAACATCTCTG
	Prupe.2G263700	0.77684	PpbZIP5	agaactagtggatccATGCAAGATCCGGCGAACCC	cccctcgaggtcgacTCAAAATCTCCTGTTGCTTT
bZIP	Prupe.8G267100	0.77304	PpbZIP6	agaactagtggatccATGTCTTCAGTTCAGCAGCA	cccctcgaggtcgacTCAGCCGAGAAACATGTCGG
	Prupe.1G374400	0.76511	PpbZIP7	agaactagtggatccATGGCTTCCTCTAGTGGGAA	cccctcgaggtcgacTTAGTATTGATGGAGCATGT
	Prupe.5G211200	0.58722	PpbZIP8	agaactagtggatccATGGAGCCAAATGAATCAAA	cccctcgaggtcgacTCATGGGGTACTGGAATCTT
	Prupe.1G478400	0.58511	PpbZIP9	agaactagtggatccATGCAAGAGCAAGCGACGAG	cccctcgaggtcgacCTATAAGGATCCTTCTGCAT
	Prupe.3G032300	0.83867	PpERF4	agaactagtggatccATGTGTGGAGGTGCTATAAT	cccctcgaggtcgacTCAGAAACCTCCCCCAATCA
	Prupe.4G051200	0.79244	PpERF5	agaactagtggatccATGGCGACTGCTTCTTCATC	cccctcgaggtcgacTCACAGCCACAAGGGTGGGG
ERF	Prupe.8G264900	0.60191	PpERF6	agaactagtggatccATGTGTGGCGGTGCTATTCT	cccctcgaggtcgacTTACGGAGCAGAAACGCGGT
	Prupe.5G090000	0.5465	PpERF7	agaactagtggatccATGGACATGTTCTCCGCTCA	cccctcgaggtcgacTCAGATAGAGAAACTCCATA
	Prupe.5G117800	0.51657	PpERF61	agaactagtggatccATGGACACAATGCAAGACAG	cccctcgaggtcgacCTAATTAGCAAGAACTTCCC
	Prupe.1G531700	0.74244	PpMADS1	agaactagtggatccATGATGAGGGAGAAGATCAA	cccctcgaggtcgacCTAGGGAAGCCCCAGTTTGA
MADS	Prupe.1G531600	0.70606	PpMADS2	agaactagtggatccATGATGAGGAATAAGATCAA	cccctcgaggtcgacTCACCCCAGTTTGAGAGACA

Table S4. Primers of TFs which have expression correlation with *PpTPS3* during peach fruit ripening.

MYB	Prupe.3G045300	0.79317	PpMYB4 agaactagtggatccATGGGAAACCAAAAGCAAAA cccctcgaggtcgacCTACGCCAAGGCGACAACTT	
	Prupe.6G255800	0.60963	PpMYB5 agaactagtggatccATGGAAATGAAGGAGAGACA cccctcgaggtcgacTCACCGGCCATTAGGCTCAG	
	Prupe.4G053300	0.81331	PpNAC9 agaactagtggatccATGACATGGTGCAATGACTC cccctcgaggtcgacCTATTTTCTCTCAAGCTTTC	
NAC	Prupe.4G187100	0.7711	PpNAC1 agaactagtggatccATGGAGAGCACCGACTCCTC cccctcgaggtcgacCTATCCCAAATTGGACTCAG	
	Prupe.7G001400	0.71459	PpNAC10 agaactagtggatccATGGAACAAAACATGGTGGT cccctcgaggtcgacTCAGAAGTCCCACAAGCCTT	
WRKY	Prupe.6G230600	0.8711	PpWRKY76 agaactagtggatccATGGCTGTAGATTTTATGGG cccctcgaggtcgacCTAAGACGATTCTAGAATGA	
	Prupe.1G431100	0.73225	PpWRKY3 agaactagtggatccATGGCTGTGGAGCTCATGAT cccctcgaggtcgacTTAAGATGATTCGAGGACGA	
	Prupe.5G117000	0.70191	PpWRKY1 agaactagtggatccATGGATTCTAGTAAGAGCTG cccctcgaggtcgacTTATGAGAAAATTCCTGTGG	
	Prupe.6G286000	0.56201	PpWRKY53 agaactagtggatccATGACTTCCTCTTTCACTCA cccctcgaggtcgacTTAGAACTCTGGAAATCCAT	

Lowercase letters indicate sequences on the vector.

Motif	Motif sequence	Position	Number	Organism	Short function
ACE	GACACGTATG	1472 +	9	Petroselinum crispum	cis-acting element involved in light responsiveness
3-AF1 binding site	TAAGAGAGGAA	313 +	10	Solanum tuberosum	light responsive element
Box 4	ATTAAT	120 +	6	Petroselinum crispum	part of a conserved DNA module involved in light responsiveness
	ATTAAT	196 +	6	Petroselinum crispum	part of a conserved DNA module involved in light responsiveness
	ATTAAT	1037 +	6	Petroselinum crispum	part of a conserved DNA module involved in light responsiveness
	ATTAAT	1041 +	6	Petroselinum crispum	part of a conserved DNA module involved in light responsiveness
	ATTAAT	1720 -	6	Petroselinum crispum	part of a conserved DNA module involved in light responsiveness
	ATTAAT	2003 -	6	Petroselinum crispum	part of a conserved DNA module involved in light responsiveness
	ATTAAT	2068 -	6	Petroselinum crispum	part of a conserved DNA module involved in light responsiveness
G-Box	CACGTG	1606 -	6	Pisum sativum	<i>cis</i> -acting regulatory element involved in light responsiveness
	CAGACGTGGCA	1471 -	10	Nicotiana plumbaginifolia	<i>cis</i> -acting regulatory element involved in light responsiveness
	CACGTC	1474 +	6	Zea mays	<i>cis</i> -acting regulatory element involved in light responsiveness
	CACGTG	1606 -	6	Arabidopsis thaliana	<i>cis</i> -acting regulatory element involved in light responsiveness
	TACGTG	1709 +	6	Arabidopsis thaliana	<i>cis</i> -acting regulatory element involved in light responsiveness
GT1-motif	GGTTAA	629 -	6	Arabidopsis thaliana	light responsive element
Box II	TGGTAATAA	1956 +	9	Solanum tuberosum	part of a light responsive element

Table S5. The light response-related *cis*-acting elements of *PpbHLH1* promoter.

Table S6. Statistic of whole-genome bisulfite sequencing reads from peach fruit at different development stages and under UV-B treatment.

Comple	Clean Deede	n Dooda Cloon Dooo	Q20	Q30	GC Content	Unique mapped	Mapping rate	BS Conversion
Sample	Clean Reads	Clean Base	(%)	(%)	(%)	Reads	(%)	Rate (%)
S 1	52228515	15625465236	97.57	94.33	22.25	34159457	65.40	99.55
S2	45297379	13511144752	97.49	94.10	22.08	29991889	66.21	99.57
S 3	29082640	8671179212	97.22	93.55	21.85	19063507	65.55	99.49
S 4	73842467	22084452994	97.64	94.65	21.27	49699965	67.31	99.53
S 5	31362921	9373582598	96.47	92.02	21.55	20678550	65.93	99.51
Control	47046165	13984776940	97.20	93.56	22.31	30512795	64.86	99.67
UV-B	39321501	11729996560	96.98	93.09	22.05	25050159	63.71	99.68

Samula	A your as donth	Covering ratio	Covering ratio	Covering ratio
Sample	Average deput	$1 \times (\%)$	5×(%)	10×(%)
S 1	46	92.77	89.65	87.24
S 2	41	92.16	88.85	86.03
S 3	26	91.75	87.33	82.28
S 4	67	92.89	90.08	88.11
S 5	28	91.72	87.37	82.46
Control	41	93.07	90.15	87.69
UV-B	33	92.95	89.62	86.41

Table S7. Statistic of sequencing depth and covering in peach fruit at different development stages and under UV-B treatment.

Peach ID	Name	Primer-SK (5')	Primer-SK (3')
Prupe.4G187100	PpNAC1	agaactagtggatccATGGAGAGCACCGACTCCTC	cccctcgaggtcgacCTATCCCAAATTGGACTCAG
Prupe.4G040900	PpNAC2	agaactagtggatccATGGAGAGCACAGATTCATC	cccctcgaggtcgacCTATGAATTCCAATTCATAC
Prupe.1G220400	PpNAC4	agaactagtggatccATGGAGAGGCTTAATTTTGT	cccctcgaggtcgacCTACTGTTTTCTTCTAAAGT
Prupe.5G196000	PpNAC6	agaactagtggatccATGGAACACGTTCCAGCTGG	cccctcgaggtcgacTTAATAATTCCAAAAATTAT
Prupe.1G493100	PpNAC8	agaactagtggatccATGTCGTCCTCCGATTTACA	cccctcgaggtcgacTCAATACGGCTTCTGTAGGT
Prupe.5G222400	PpMYB1	agaactagtggatccATGTCTAGTAATACTAAAAGC	cccctcgaggtcgacTTAGCTCCTACTTTGCCACA
Prupe.8G164300	PpMYB2	agaactagtggatccATGGGAAGATCTCCTTGCTG	cccctcgaggtcgacTCATTTCATCTCCAAGCTTC
Prupe.2G237100	PpMYB3	agaactagtggatccATGGTGTTGAAGAAGAGGCT	cccctcgaggtcgacTCAGCTCCATGTCTTATCAG
Prupe.5G117000	PpWRKY1	agaactagtggatccATGGATTCTAGTAAGAGCTG	cccctcgaggtcgacTTATGAGAAAATTCCTGTGG
Prupe.1G393000	PpWRKY2	agaactagtggatccATGGACTCAGAATGGGTGAA	cccctcgaggtcgacTCACCAATTTCCCATCCGAG
Prupe.5G187800	PpWRKY73	agaactagtggatccATGGAGGCTGCTCTGGGAAA	cccctcgaggtcgacCTATAAACTTTTGTGATCTC
Prupe.6G295100	PpWRKY45	agaactagtggatccATGGAGTTGTCTTGGCCGGA	cccctcgaggtcgacTCAAAATTCATATTGCAAAA
Prupe.6G286000	PpWRKY53	agaactagtggatccATGACTTCCTCTTTCACTCA	cccctcgaggtcgacTTAGAACTCTGGAAATCCAT
Prupe.6G230600	PpWRKY76	agaactagtggatccATGGCTGTAGATTTTATGGG	cccctcgaggtcgacCTAAGACGATTCTAGAATGA
Prupe.6G046900	PpWRKY8	agaactagtggatccATGGCCTCCTCTTCTGGGAG	cccctcgaggtcgacTCAGCATAGCAATGATTCAA
Prupe.1G431100	PpWRKY3	agaactagtggatccATGGCTGTGGAGCTCATGAT	cccctcgaggtcgacTTAAGATGATTCGAGGACGA
Prupe.6G295100	PpWRKY4	agaactagtggatccATGGAGTTGTCTTGGCCGGA	cccctcgaggtcgacTCAAAATTCATATTGCAAAA
Prupe.8G095700	PpMYC1	agaactagtggatccATGAACAGAGCGTTGCCGGA	cccctcgaggtcgacTCACATCTCCATCTTTAAAT
Prupe.5G035400	PpMYC2	agaactagtggatccATGACGGACTATCGGATACC	cccctcgaggtcgacACCTCTTCTTCTTGCTGTTG
Prupe.8G157500	PpbHLH1	agaactagtggatccATGGAGATTTCGTCGATAGG	cccctcgaggtcgacTCACATGAACATGTCGAAAG
Prupe.6G211900	PpbHLH2	agaactagtggatccATGGACATATCATCAGCCAA	cccctcgaggtcgacTCACATGAACTTCAGCAGAG
Prupe.7G207500	PpbHLH25	agaactagtggatccATGGACACTGCCTTCCAGCT	cccctcgaggtcgacTCATTGATTGCGGCAATTAT
Prupe.6G212000	PpbHLH3	agaactagtggatccATGGACATGATTTCATCAGC	cccctcgaggtcgacTCACACAAACTTGAGCAATG
Prupe.5G143200	PpbHLH4	agaactagtggatccATGCTGCCTAGGCTGAACGG	cccctcgaggtcgacCTATATCAAGCCATGGAACC
Prupe.5G061800	PpERF1	agaactagtggatccATGTTCGGACAGAGTGGAAC	cccctcgaggtcgacTCAGCTCACTAATAACTGCT
Prupe.2G272400	PpERF2	agaactagtggatccATGGCAACAGAGCATGAAGA	cccctcgaggtcgacTTATGTAACCATAAGCTGAG
Prupe.2G129400	PpERF3	agaactagtggatccATGTTAGGAGATGAAAAAAG	cccctcgaggtcgacCTACTTCTTCGGTGAGCCAC

Table S8. Primers of TFs which homologues of transcription factors that regulate terpenoid formation.

Prupe.1G037900	PpEREB58	agaactagtggatccATGAATTACTCAATCTTCCA	cccctcgaggtcgacTCAACGATTAGGTGTGGCAG
Prupe.3G104100	PpAP2	agaactagtggatccATGGCGAAAACCTCACAGCA	cccctcgaggtcgacTCAGGCATCAAGTTCACAAT
Prupe.2G058400	PpEIL1	agaactagtggatccATGGGGATCTTTGAAGAAAT	cccctcgaggtcgacTCAGATCCAAAATGCATCTT
Prupe.6G018200	PpEIL3	agaactagtggatccATGGGTGACGTTGAAGAGGT	cccctcgaggtcgacTTATGCCGCAAAGTATTCCA
Prupe.1G434500	PpbZIP1	agaactagtggatccATGGGTACCAACATGAACTT	cccctcgaggtcgacTTACCATGGACCGGTCTGCG
Prupe.1G307300	PpbZIP2	agaactagtggatccATGCAGAGCTTCAAAGCAGC	cccctcgaggtcgacTTAGTCCCTAGGACGTGCCA
Prupe.6G129100	PpbZIP79	agaactagtggatccATGGCTTTCATTTCTGCCAC	cccctcgaggtcgacTCAGAAGGATGAGAAGTGAT
Prupe.1G371500	PpEOT1	agaactagtggatccATGGCTGGCTTGTTTTGCTT	cccctcgaggtcgacTCAATCATAATCATCCTCTC
Prupe.7G245200	PpYABBY5	agaactagtggatccATGACCAGCTGCATCGATGT	cccctcgaggtcgacTCATTTATTCAGCAGTGCAG

Lowercase letters indicate sequences on the vector.

Primers	Sequence $(5' \rightarrow 3')$	Description
pET-PpTPS3-FP	aaggcetetgtegacATGGCCCTTCTTCAAGCTCA	pET vector cloning of <i>PpTPS3</i>
pET- <i>PpTPS3</i> -RP	agaattcgcaagcttTTATTTCGTCTGGCCTGGGG	pET vector cloning of <i>PpTPS3</i>
SK-PpTPS3-FP	agaactagtggatccATGGCCCTTCTTCAAGCTCA	pGreen-SK vector cloning of <i>PpTPS3</i>
SK-PpTPS3-RP	cccctcgaggtcgacTTATTTCGTCTGGCCTGGGG	pGreen-SK vector cloning of <i>PpTPS3</i>
pBI121-PpTPS3-FP	acgggggactctagaATGGCCCTTCTTCAAGCTCA	pBI121 vector cloning of <i>PpTPS3</i>
pBI121-PpTPS3-RP	accacccggggatccTTTCGTCTGGCCTGGGGGACT	pBI121 vector cloning of <i>PpTPS3</i>
eGFP-PpTPS3-FP	ggtacccggggatccATGGCCCTTCTTCAAGCTCA	35S-eGFP vector cloning of <i>PpTPS3</i>
eGFP-PpTPS3-RP	gctcaccatgtcgacTTTCGTCTGGCCTGGGGACT	35S-eGFP vector cloning of <i>PpTPS3</i>
LUC-ProPpTPS3-FP	ggtatcgataagcttAAGATAGAAGTCAGCTGGAA	pGreen-LUC vector cloning of PpTPS3 promoter
LUC-ProPpTPS3-RP	tggcgtcttccatggGTCGTTAATATGCCGAGTAT	pGreen-LUC vector cloning of PpTPS3 promoter
LUC-ProPpTPS1-FP	ggtatcgataagcttACCGGCCTAAATAACTAGAT	pGreen-LUC vector cloning of PpTPS1 promoter
LUC-ProPpTPS1-RP	tggcgtcttccatggTTTTACTAGAGCAATTGCAG	pGreen-LUC vector cloning of PpTPS1 promoter
LUC-ProNtLIS-FP	ggtatcgataagcttAGTCAAATTTGATCCTTTTC	pGreen-LUC vector cloning of NtLIS promoter
LUC-ProNtLIS-RP	tggcgtcttccatggGTAAAAGATTATTTTGCTGT	pGreen-LUC vector cloning of NtLIS promoter
LUC-ProAtTPS10-FP	ggtatcgataagcttTCTCACTTTGGTTTCCCAAC	pGreen-LUC vector cloning of AtTPS10 promoter
LUC-ProAtTPS10-RP	tggcgtcttccatggATTGAATAAATGTATTATTA	pGreen-LUC vector cloning of AtTPS10 promoter
pAbAi-Pro <i>PpTPS3-</i> FP	tgaattgaaaagcttAAGATAGAAGTCAGCTGGAA	pAbAi vector cloning of PpTPS3 promoter
pAbAi-Pro <i>PpTPS3-</i> RP	cgacagatccccgggGTCGTTAATATGCCGAGTAT	pAbAi vector cloning of PpTPS3 promoter
AD-PpbHLH1-FP	gaggccagtgaattcATGGAGATTTCGTCGATAGG	pGADT7 vector cloning of PpbHLH1
AD-PpbHLH1-RP	gagetcgatggatccTCACATGAACATGTCGAAAG	pGADT7 vector cloning of PpbHLH1
pGEX-PpbHLH1-FP	gttccgcgtggatccATGGAGATTTCGTCGATAGG	pGEX-4T-1 vector cloning of PpbHLH1
pGEX-PpbHLH1-RP	tcgacccgggaattcTCACATGAACATGTCGAAAG	pGEX-4T-1 vector cloning of PpbHLH1
eGFP-PpbHLH1-FP	ggtacccggggatccATGGAGATTTCGTCGATAGG	35S-eGFP vector cloning of <i>PpbHLH</i>
eGFP-PpbHLH1-RP	gctcaccatgtcgacCATGAACATGTCGAAAGCAG	35S-eGFP vector cloning of <i>PpbHLH</i>
pBI121-PpbHLH1-FP	acgggggactctagaATGGAGATTTCGTCGATAGG	pBI121 vector cloning of PpbHLH1
pBI121-PpbHLH1-RP	accacccggggatccCATGAACATGTCGAAAGCAG	pBI121 vector cloning of PpbHLH1
attB1-PpbHLH1-FP	ggggacaagtttgtacaaaaaagcaggctATGGAGATTTCGTCGATAGG	pBIN19-E8 vector cloning of <i>PpbHLH1</i>

 Table S9. Other primer sequences used in the present study.

ottD) DubUIUI DD	a = a = a = a = a = a = a = a = a = a =	pPIN10 E8 vector cloping of PphUI U1
Probe1-FP-biotin		Probe for EMSA
Probe1-RP-biotin	GTTTTCCAGGCCATATATCCATGTGCTTATCATCATTTCA	Probe for EMSA
Probe2-FP-biotin	GGTTGGTACGACCACGTGAAATTACGTTATGGTATTTCGT	Probe for EMSA
Probe2-RP-biotin	ACGAAATACCATAACGTAATTTCACGTGGTCGTACCAACC	Probe for EMSA
Probe3-FP-biotin	ATCAATCCTTTCAAGCGGACAATCACATGATGCGTCGTCG	Probe for EMSA
Probe3-RP-biotin	CGACGACGCATCATGTGATTGTCCGCTTGAAAGGATTGAT	Probe for EMSA
Probe1-FP	TGAAATGATGATAAGCACATGGATATATGGCCTGGAAAAC	Probe for EMSA
Probe1-RP	GTTTTCCAGGCCATATATCCATGTGCTTATCATCATTTCA	Probe for EMSA
Mutant-Probe1-FP-biotin	TGAAATGATGATAAGAGTGGAGATATATGGCCTGGAAAAC	Probe for EMSA
Mutant-Probe1-FP-biotin	GTTTTCCAGGCCATATATCTCCACTCTTATCATCATTTCA	Probe for EMSA
TRV2-PpPDS-FP	tgcccgggcctcgagATGTCTCAGTGGGCTTGTGT	pTRV2 vector cloning of <i>PpPDS</i> for VIGS
TRV2-PpPDS-RP	cctccatggggatccCTCTTGCTTCCAGTAAGATA	pTRV2 vector cloning of <i>PpPDS</i> for VIGS
TRV2-PpTPS3-FP	tgcccgggcctcgagTACATAATAGATGATATTTT	pTRV2 vector cloning of <i>PpTPS3</i> for VIGS
TRV2-PpTPS3-RP	cctccatggggatccTTGGTTCTCATCCTTGGCAC	pTRV2 vector cloning of <i>PpTPS3</i> for VIGS
TRV2-PpbHLH1-FP	tgcccgggcctcgagACACTTGAGGAACAGACCAG	pTRV2 vector cloning of <i>PpbHLH1</i> for VIGS
TRV2-PpbHLH1-RP	cctccatggggatccTTGACAAGTTCCTTCACTGA	pTRV2 vector cloning of <i>PpbHLH1</i> for VIGS
qPCR-PpTPS3-FP	GGTCGCGGTATAACTCAGCA	RT-qPCR of <i>PpTPS3</i>
qPCR-PpTPS3-RP	CAAAGTCATCCCAGAGCCGT	RT-qPCR of <i>PpTPS3</i>
qPCR-PpbHLH1-FP	CCCCTTTGAGGAGACACTGC	RT-qPCR of <i>PpbHLH1</i>
qPCR-PpbHLH1-RP	TGTCGAAAGCAGAGCGTAGA	RT-qPCR of <i>PpbHLH1</i>
qPCR-AtTPS10-FP	ATCGTACAAGCTATTCATCAAGAGGAACT	RT-qPCR of AtTPS10
qPCR-AtTPS10-RP	ACCTAAACCTGTCTCCATCCACC	RT-qPCR of AtTPS10
qPCR-AtTPS14-FP	GTCATTGACTCAAGGAGAAATGTCTCAAAC	RT-qPCR of AtTPS14
qPCR-AtTPS14-RP	GCTTCTTGCCTTCTCCACATCTTT	RT-qPCR of AtTPS14
qPCR-SITPS5-FP	CTTCGGATGAACTGAAAAGAGG	RT-qPCR of SITPS5
qPCR-SITPS5-RP	GTGGAGAATTTTTGCTTTGAGC	RT-qPCR of <i>SlTPS5</i>
qPCR-NtLIS-FP	ATGGATGGGGAAGAAGCACC	RT-qPCR of <i>NtLIS</i>
qPCR-NtLIS-RP	CGGCTTCTGTGAAGAGGGTT	RT-qPCR of <i>NtLIS</i>

PpTEF2-FP	GGTGTGACGATGAAGAGTGATG	RT-qPCR of house-keeping gene PpTEF
PpTEF2-RP	TGAAGGAGAGGGAAGGTGAAAG	RT-qPCR of house-keeping gene PpTEF
AtEF1α-FP	TGAGCACGCTCTTCTTGCTTTCA	RT-qPCR of house-keeping gene $AtEF1\alpha$
<i>AtEF1α</i> - R P	GGTGGTGGCATCCATCTTGTTACA	RT-qPCR of house-keeping gene $AtEF1\alpha$
SlActin-FP	TGTCCCTATTTACGAGGGTTATGC	RT-qPCR of house-keeping gene SlActin
SlActin-RP	CAGTTAAATCACGACCAGCAAGAT	RT-qPCR of house-keeping gene SlActin
<i>NtEF1-α</i> -FP	GCCCAACACTTCTTGATGCTC	RT-qPCR of house-keeping gene NtEF1
<i>NtEF1-α</i> -RP	GACACCAGTTTCCACACGAC	RT-qPCR of house-keeping gene NtEF1

Lowercase letters indicate sequences on the vector.