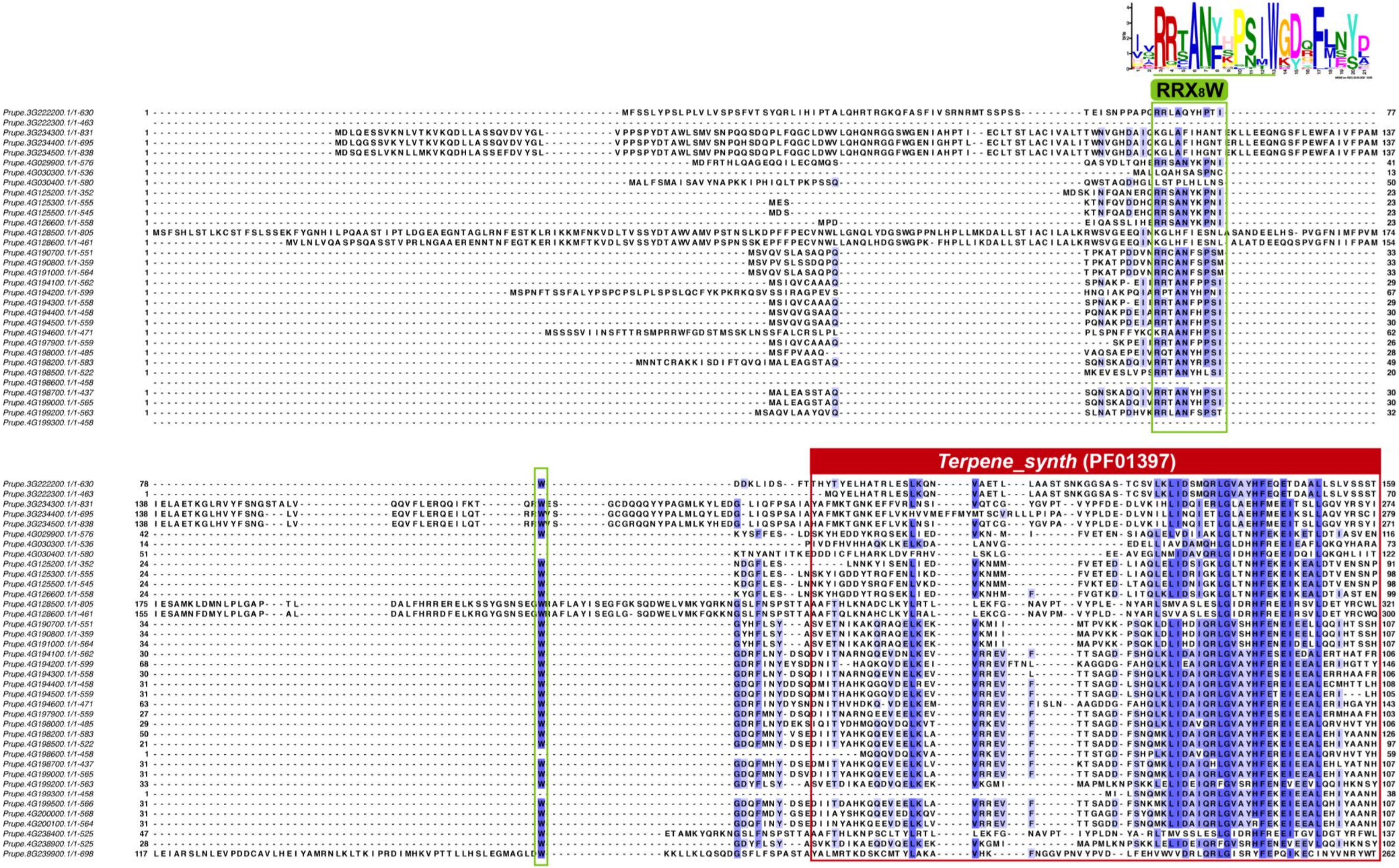
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Prupe.4G198700.1/1-437
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Prupe.4G199500.1/1-566
Prupe.4G200000.1/1-568
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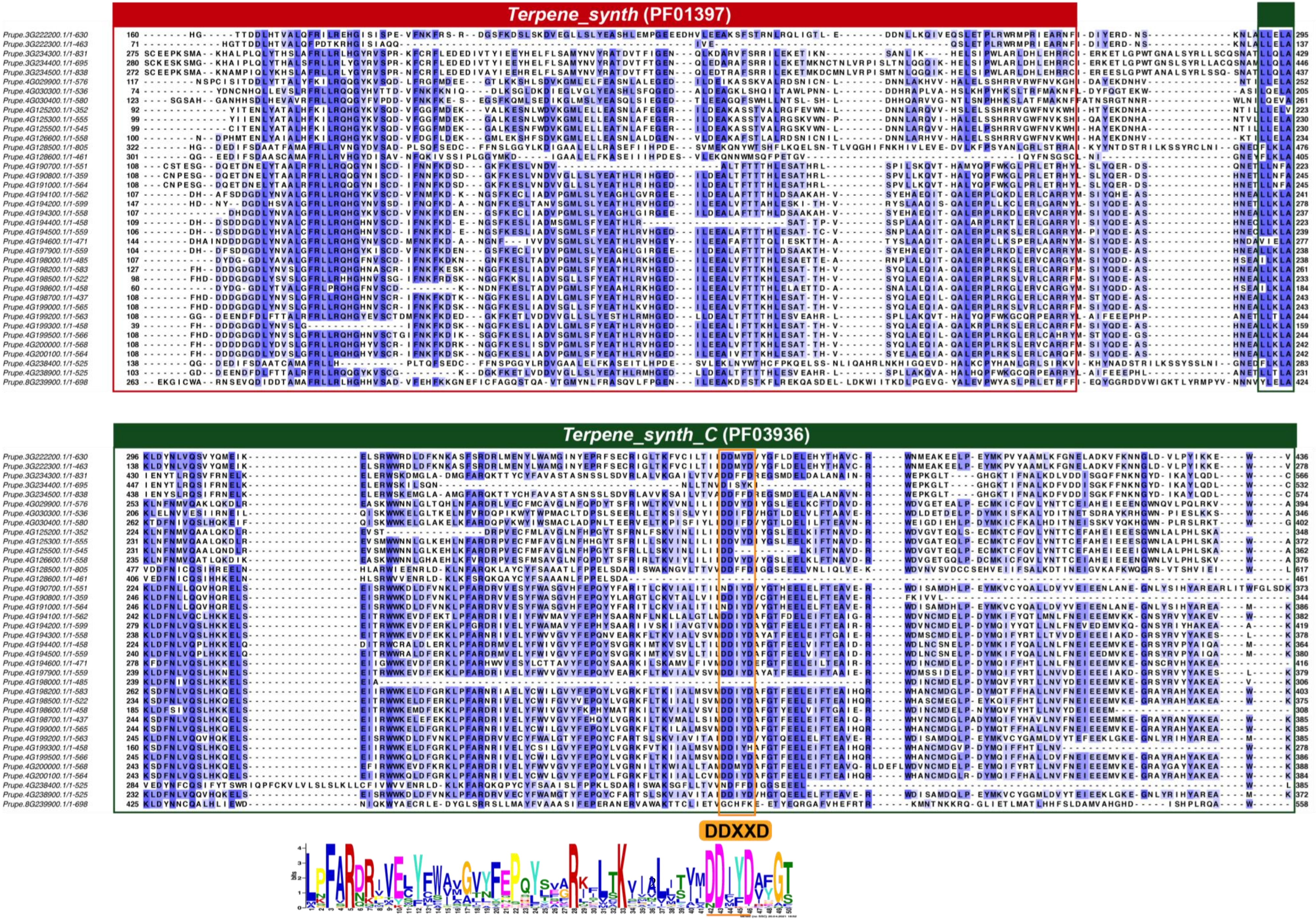
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Prupe.4G199000.1/1-565
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Prupe.4G200000.1/1-568
Prupe.4G200100.1/1-564
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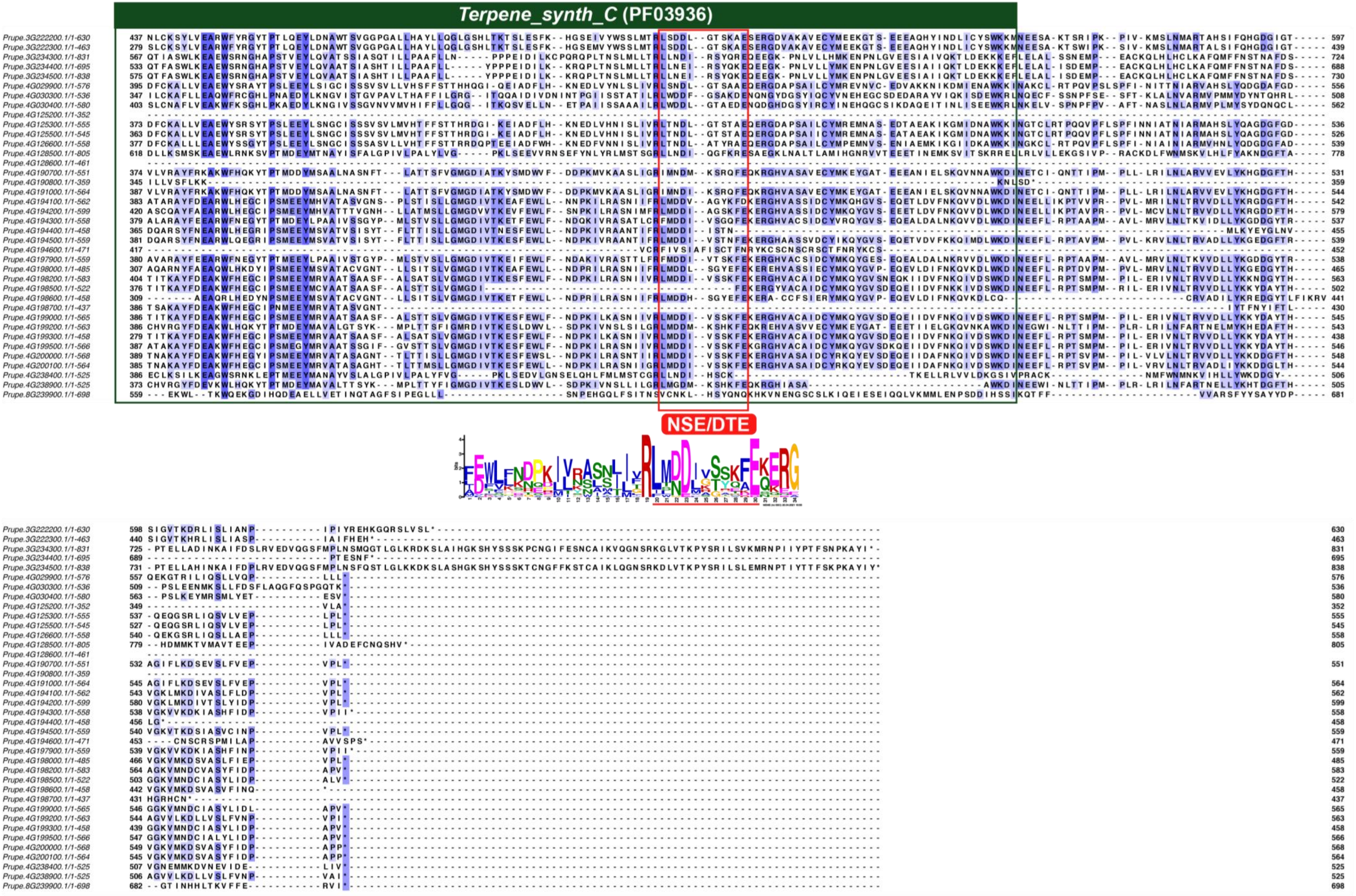
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Prupe.3G234500.1/1-838
Prupe.4G029900.1/1-576
Prupe.4G030300.1/1-536
Prupe.4G030400.1/1-580
Prupe.4G125200.1/1-352
Prupe.4G125300.1/1-555
Prupe.4G125500.1/1-545
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Prupe.4G238400.1/1-525
Prupe.4G238900.1/1-525
Prupe.8G239900.1/1-698

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 RRX$_8$W, Asp-rich domain DDxxD and NSE/DTE are also labeled.

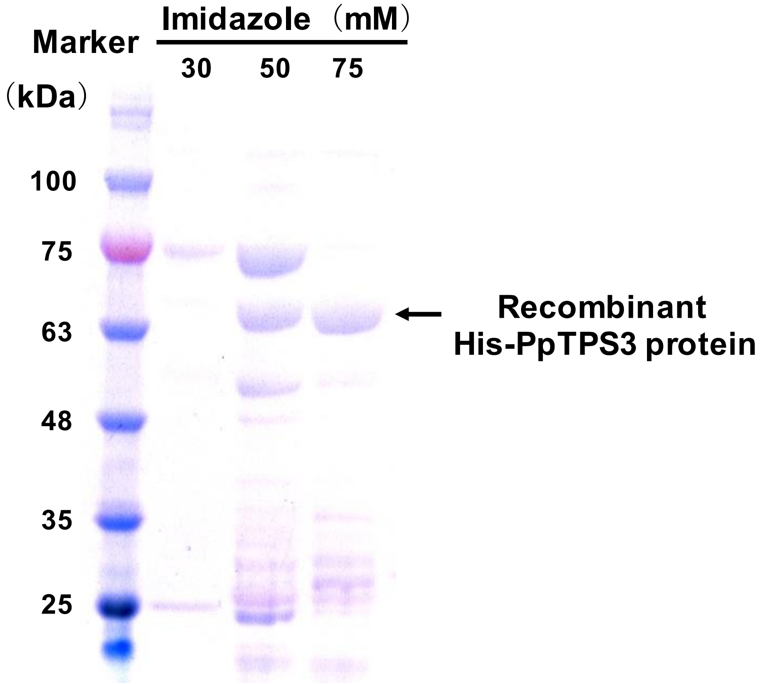

Figure S2. SDS-PAGE analysis of PpTPS3 protein.

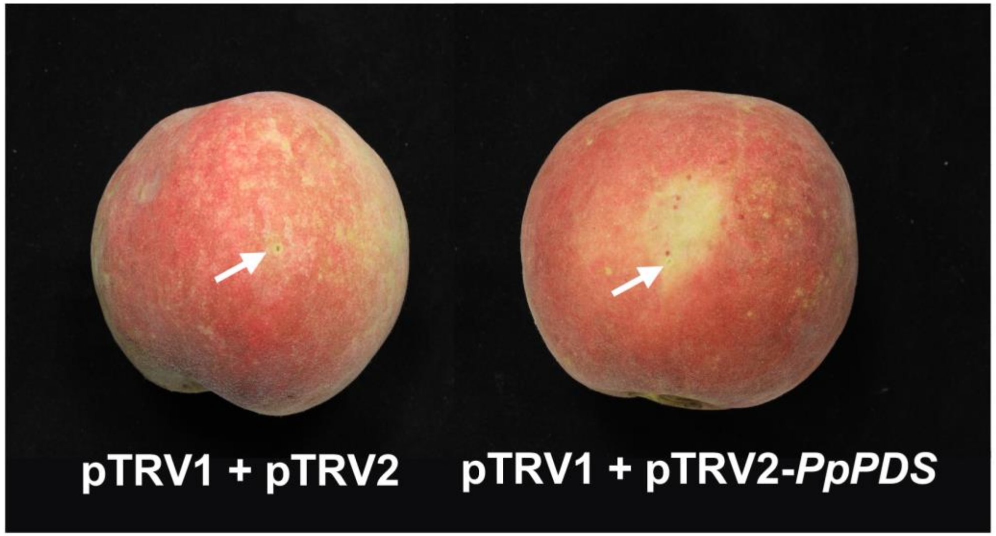

Figure S3. Silencing of *PpPDS* (Prupe.1G174100) gene in peach fruit. Empty pTRV1 + pTRV2 vector was used as a control, and phytoene desaturase (*PDS*) was used as a reporter gene for VIGS. The arrow points to the injection hole. The photo was taken two weeks after the infiltration.

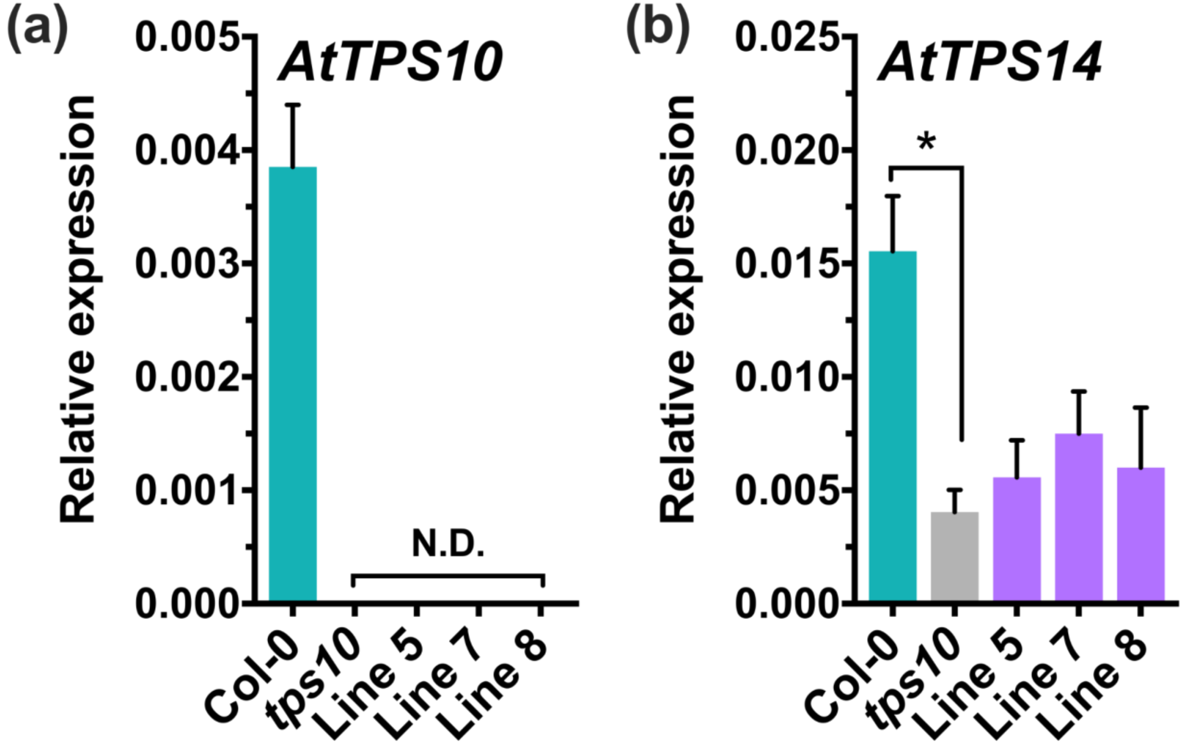

Figure S4. Expression of *AtTPS10* and *AtTPS14* in *PpTPS3* transgenic Arabidopsis. Relative expression levels were determined using qRT-PCR. Data are presented as the mean ± SE from three independent biological replicates. Significant differences are indicated with asterisks above the bars (*, $P 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

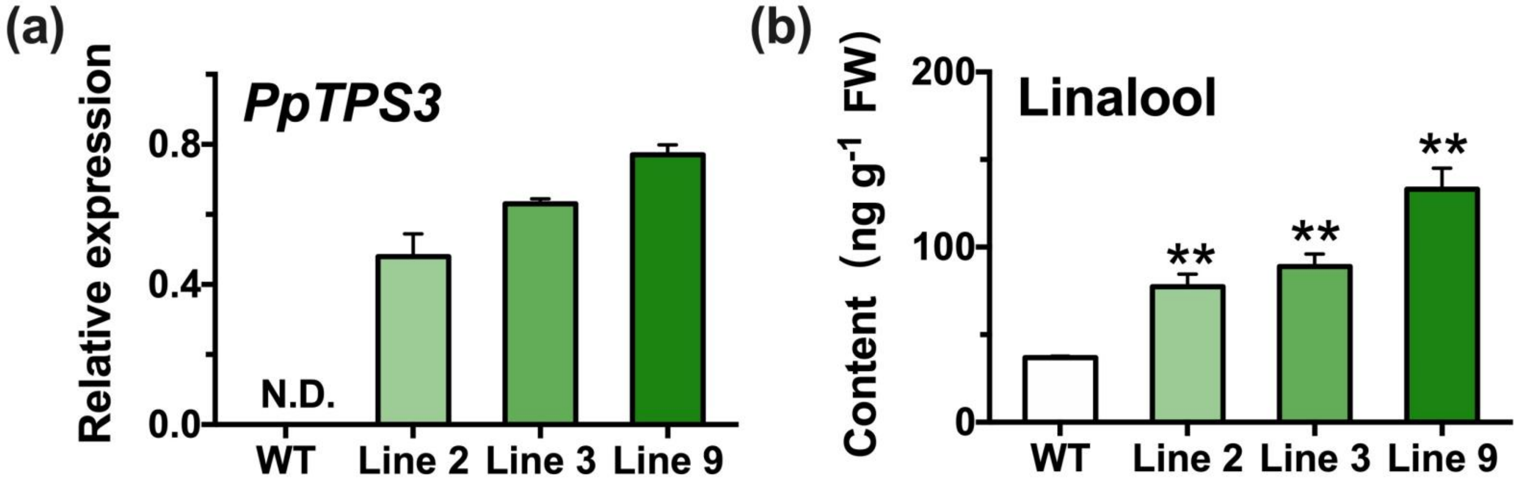

Figure S5. Changes in content of free linalool in *PpTPS3* transgenic tomato leaves. (a) Relative expression of *PpTPS3* in wild type and transgenic tomato leaves. **(b)** The content of linalool in wild type and transgenic tomato leaves. Volatiles were identified using gas chromatography–mass spectrometry (GC–MS). Data are presented as the mean ± 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.

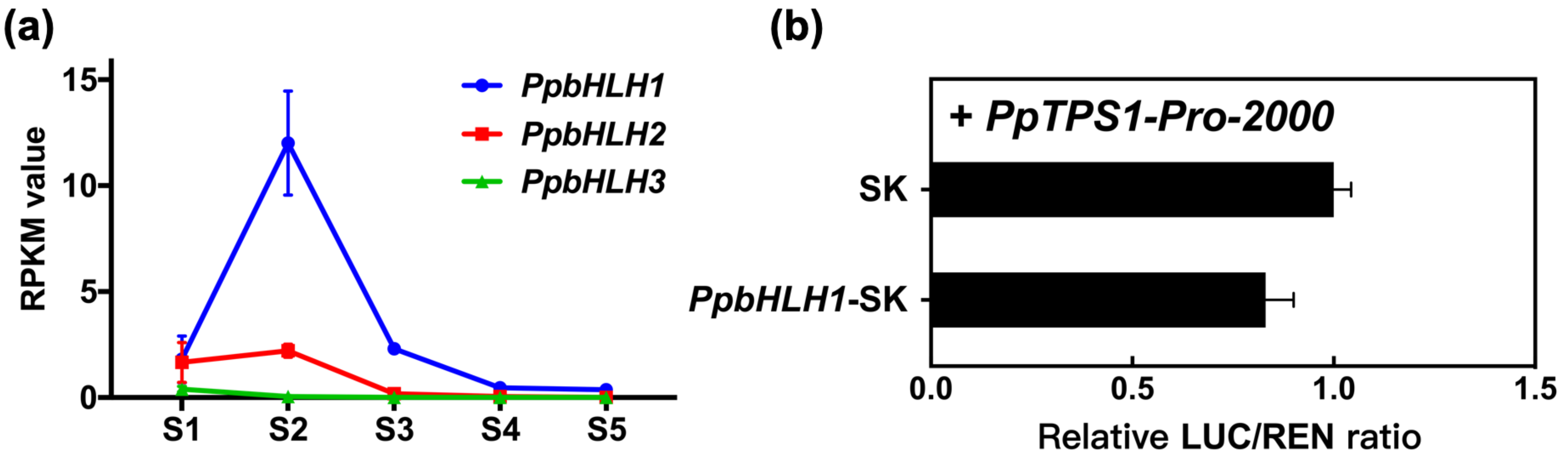

Figure S6. Expression profiles of three bHLH genes and regulatory effect of PpbHLH1 on the promoter of *PpTPS1*. **(a)** Expression profiles of three bHLH genes during peach fruit ripening. The RNA-seq was conducted with three biological replicates. **(b)** Regulatory effect of PpbHLH1 on the promoter 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.

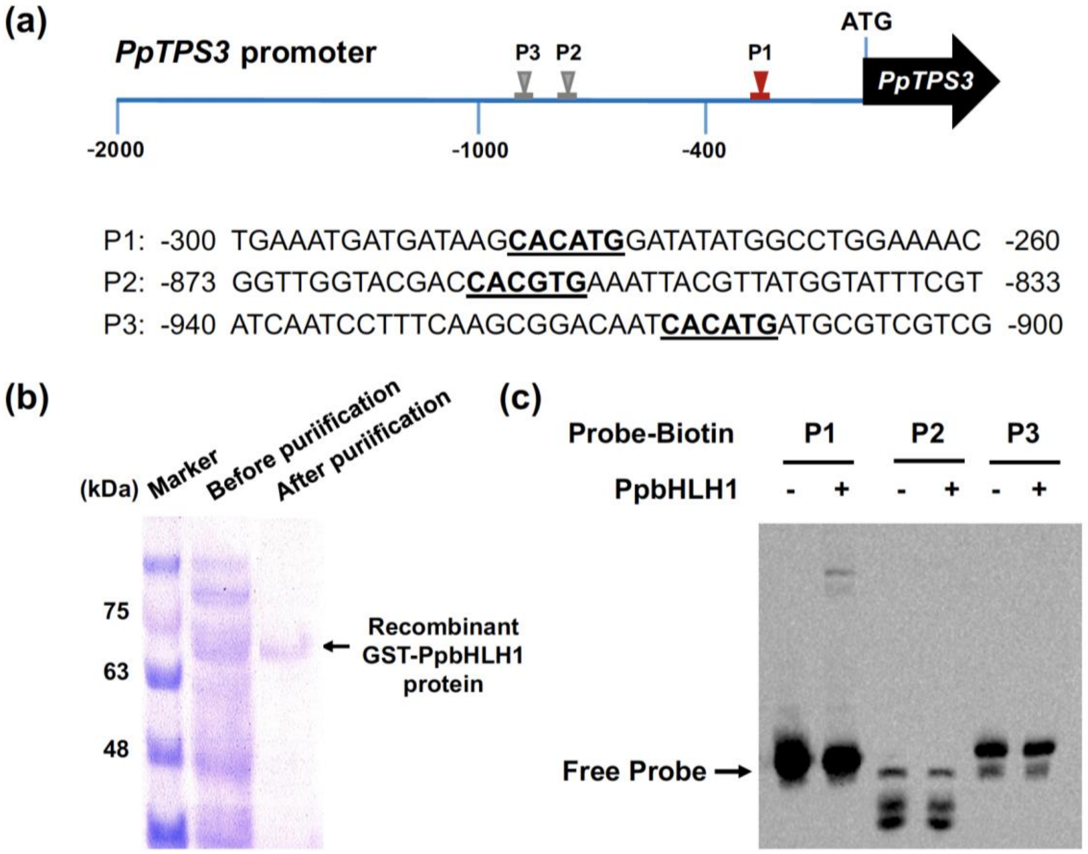

Figure S7. PpbHLH1 binds to *PpTPS3* promoter. (a) The three probes sequences used for EMSA. **(b)** SDS-PAGE analysis of PpbHLH1 protein. **(c)** EMSA of PpbHLH1 binding to *PpTPS3* promoter. Presence or absence of specific probes is marked by symbol + or -.

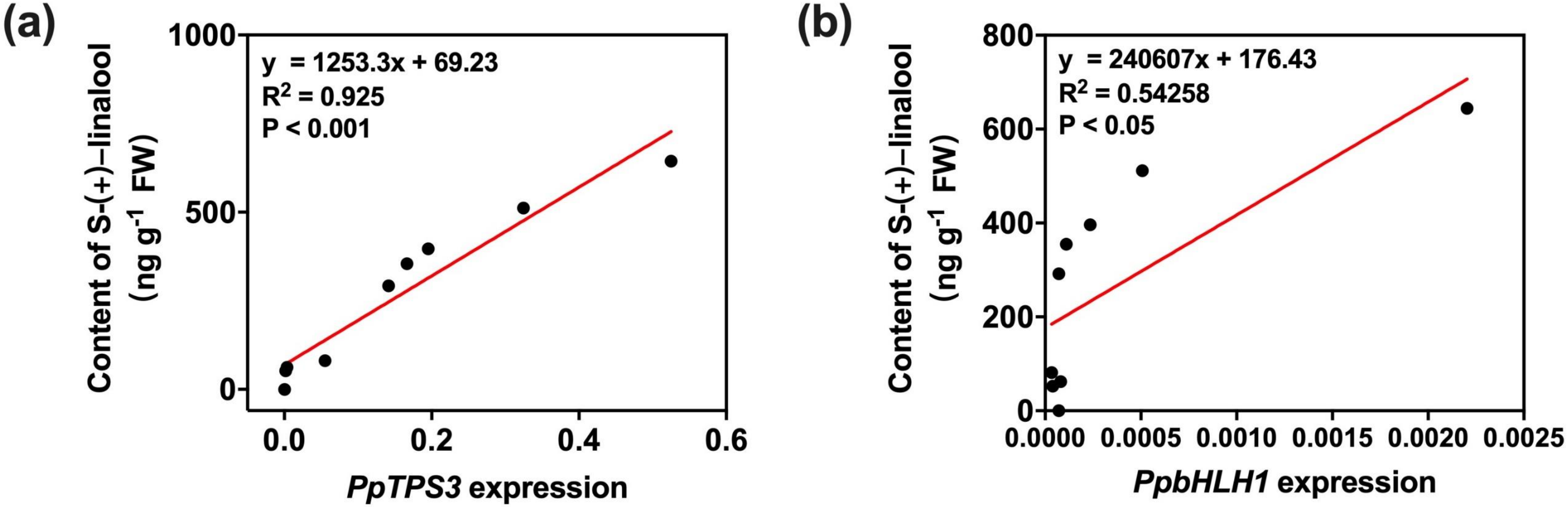

Figure S8. Correlation between transcript and S-(+)-Linalool content in different peach cultivars. **(a)** Correlation between *PpTPS3* expression and S-(+)-Linalool content in peach cultivars. **(b)** Correlation between *PpbHLH1* expression and S-(+)-Linalool content in peach cultivars.

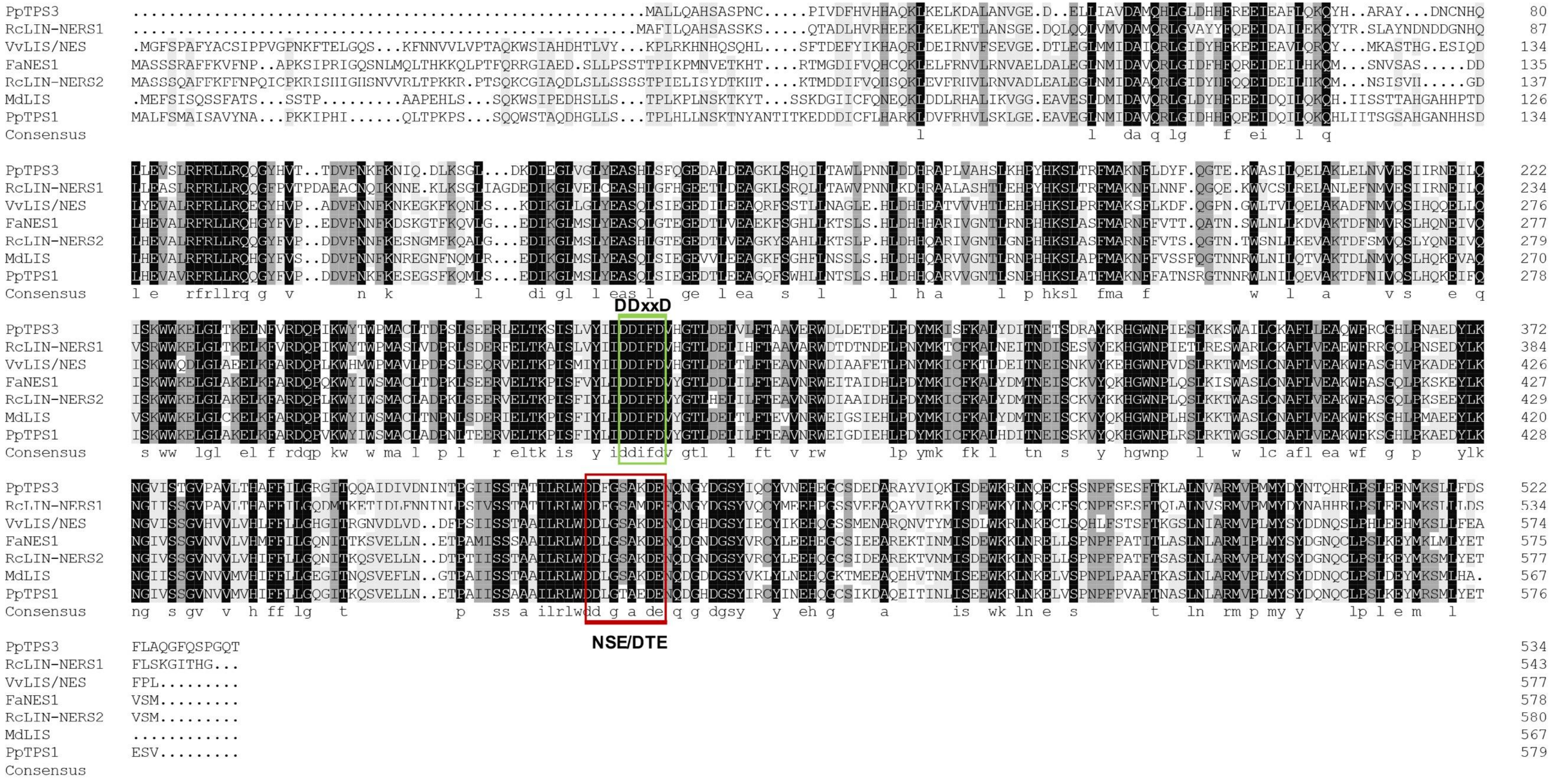

Figure S9. Alignment of amino acid sequence of PpTPS3 with closely related sequences from TPS-g subfamily. Two conserved motifs of Asp-rich domain DDxxD and (N, D) Dxx (S, T) xxxE (NSE/DTE) are marked.

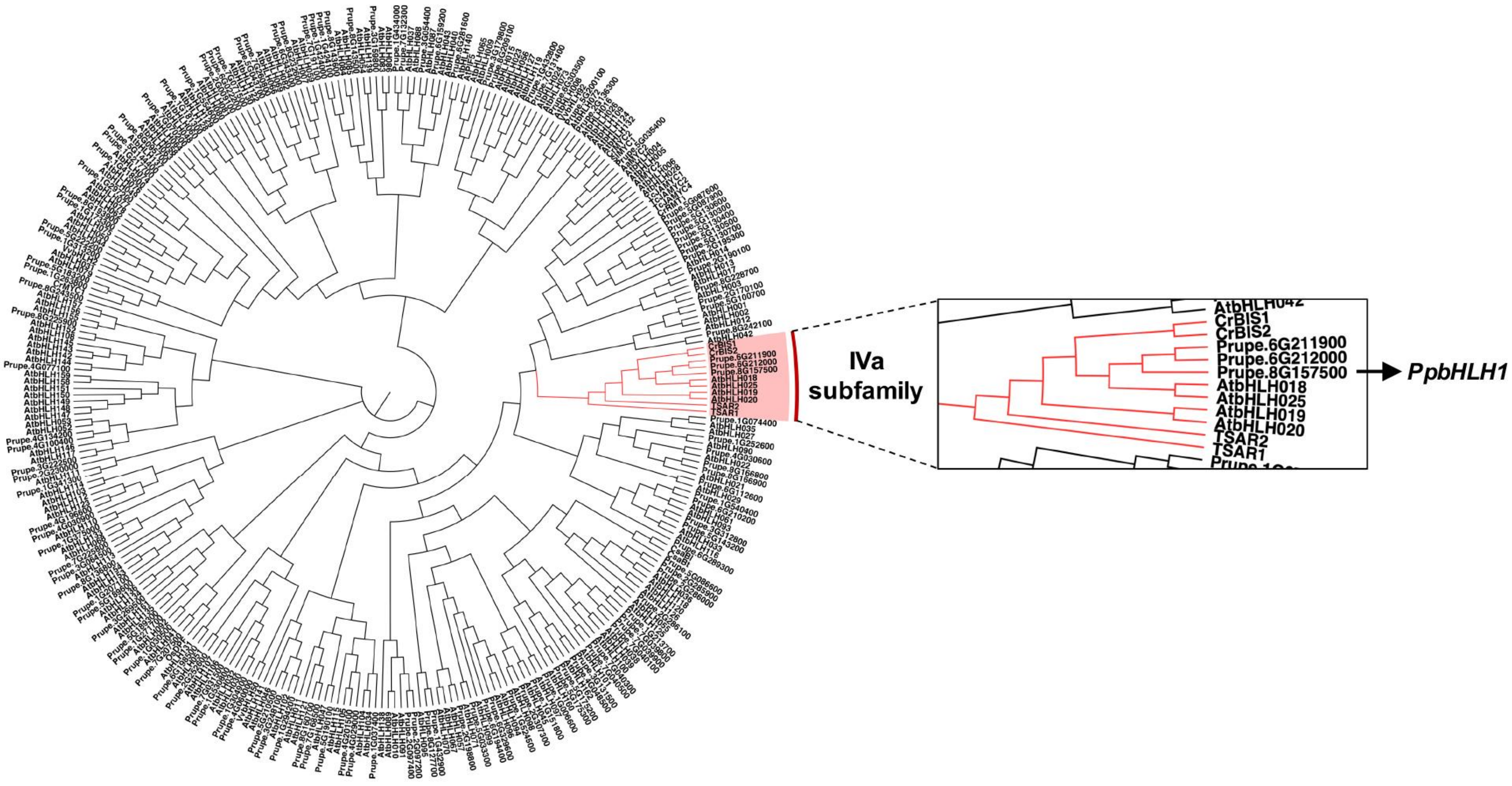

Figure S10. Phylogenetic tree constructed using the sequences of bHLH proteins from both peach and Arabidopsis with some bHLH proteins which regulate linalool or terpene formation in other species.

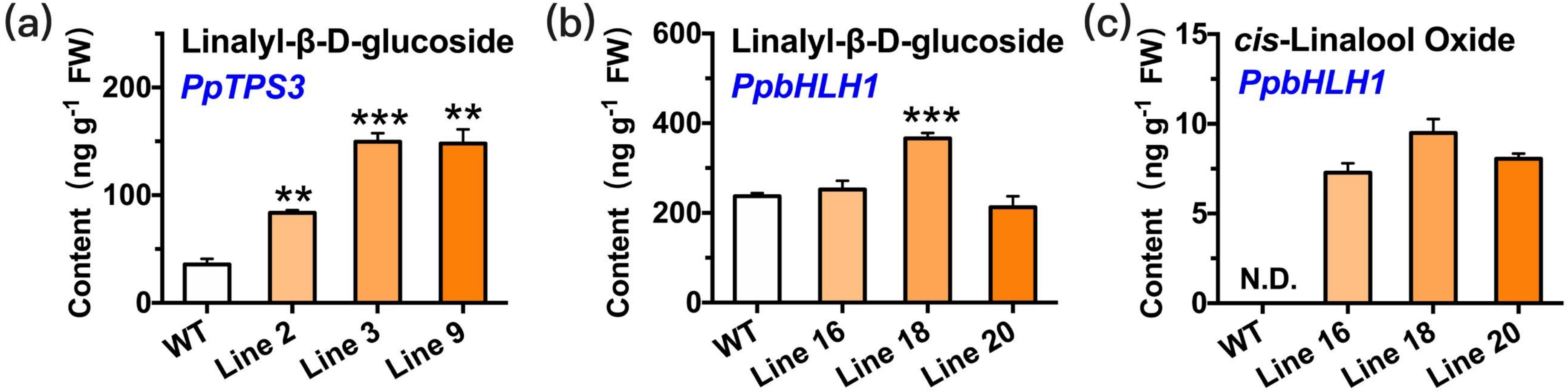

Figure S11. Changes in content of linalyl-β-d-glucoside and linalool oxide in *PpTPS3* and *PpbHLH1* transgenic tomato fruits. (a) Content of linalyl-β-d-glucoside in wild type and *PpTPS3* transgenic tomato fruits. **(b)** Content of linalyl-β-d-glucoside in wild type and *PpbHLH1* transgenic tomato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

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

Compound (ng/g FW)		Days after bloom (DAB)				
		34 (S1)	71 (S2)	94 (S3)	108 (S4)	111 (S5)
Terpenes	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
	(Z)-Ocimene	UD	UD	UD	UD	14.03±7.16
	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
Terpenoids	**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
	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
Norisoprenoids	β-Damascenone	21.28±11.21	13.3±0.24	20.92±1.21	22.76±4.30	17.12±4.52
	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

UD, under the limit of detection.

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

Abbreviation	GenBank accession	Abbreviation	GenBank accession	Abbreviation	GenBank accession	Abbreviation	GenBank 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
VvPNLNGl1	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	PlTPS3	ARG42161	SlTPS5	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	SlTPS40	JN412074
PlTPS4	ARG42162	RcLINS	MG673509	LaRLin	ABD77417	SrCPS	AAB87091
AtTPS14	At1g61680	VvPNRLin	ADR74209	LaLINS	ABB73045		
SlTPS37	AEP82769	PtTPS4	AEI52904	McLIS	AY083653		
SlTPS39	AEP82767	McTPS1	ART66980	MaLin	AAL99381		

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

TF families	Species	Description	Gene ID	Peach ID	Name	References
NAC	*Actinidia arguta*	AaNAC1	KF319046	Prupe.4G187100	PpNAC1	Nieuwenhuizen *et al.*, 2015
		AaNAC2	KF319047	Prupe.4G040900	PpNAC2	
		AaNAC3	KF319048	Prupe.4G040900	PpNAC2	
		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
MYB	*Freesia hybrida*	**FhMYB21L1**	**QNC43969**	**Prupe.5G222400**	**PpMYB1**	Yang *et al.*, 2020
		FhMYB21L2	**QNC43970**	**Prupe.5G031700**	Not expressed in peach	
	Mentha spicata	MsMYB	KY081780	Prupe.8G164300	PpMYB2	Reddy *et al.*, 2017
	Catharanthus roseus	CrBPF1	AJ251686	Prupe.2G237100	PpMYB3	Li *et al.*, 2015
WRKY	*Artemisia annua*	AaWRKY1	FJ390842	Prupe.5G117000	PpWRKY1	Ma *et al.*, 2009
	Gossypium arboreum	GaWRKY1	AY507929	Prupe.1G393000	PpWRKY2	Xu *et al.*, 2004
	Solanum lycopersicum	**SlWRKY73**	**Solyc03g113120.2.1**	**Prupe.5G187800**	**PpWRKY73**	Spyropoulou *et al.*, 2014
	Oryza sativa	WRKY45	AK066255	Prupe.6G295100	PpWRKY45	Akagi *et al.*, 2014; Shimono *et al.*, 2007
		WRKY53	AB190436	Prupe.6G286000	PpWRKY53	Schluttenhofer and Yuan, 2015
		WRKY76	AK068337	Prupe.6G230600	PpWRKY76	
	Nicotiana benthamiana	WRKY8	AB445392	Prupe.6G046900	PpWRKY8	
	Panax quinquefolius	PqWRKY1	JF508376	Prupe.1G431100	PpWRKY3	
	Catharanthus roseus	CrWRKY1	HQ646368	Prupe.6G295100	PpWRKY4	Suttipanta *et al.*, 2011
bHLH	*Arabidopsis thaliana*	AtMYC2	At1g32640	Prupe.5G035400	PpMYC2	Hong *et al.*, 2012
	Artemisia annua	AabHLH1	AGH25053	Prupe.5G035400	PpMYC2	Ji *et al.*, 2014
	Catharanthus roseus	CrMYC1	AF283506	Prupe.8G095700	PpMYC1	Chatel *et al.*, 2003
		CrMYC2	AF283507	Prupe.5G035400	PpMYC2	Zhang *et al.*, 2011

		CrBIS1	**KM409646**	**Prupe.8G157500**	**PpbHLH1**	van Moerkercke *et al.*, 2015
		CrBIS2	KM409645	Prupe.6G211900	PpbHLH2	van Moerkercke *et al.*, 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
			Csa5G157230	Prupe.2G286000	Not expressed in peach	
	Freesia hybrida	FhMYC2	QNC43971	Prupe.5G035400	PpMYC2	Yang *et al.*, 2020
	Solanum lycopersicum	**SlMYC1**	**KF430611**	**Prupe.5G035400**	**PpMYC2**	Spyropoulou *et al.*, 2014; Xu *et al.*, 2019
	Malus domestica	MdMYC2	MDP0000029168	Prupe.5G035400	PpMYC2	Wang *et al.*, 2020
ERF	*Artemisia annua*	AaERF1	JN162091	Prupe.5G061800	PpERF1	Yu *et al.*, 2012
		AaERF2	JN162092	Prupe.2G272400	PpERF2	
		AaORA	JQ797708	Prupe.2G129400	PpERF3	Lu *et al.*, 2013
	Catharanthus roseus	CrORCA3	CAB96899	Prupe.2G129300	Not expressed in peach	van der Fits and Memelink, 2000
		CrORCA4/CrORCA5	KR703577/KR703578	Prupe.2G129300		Paul *et al.*, 2017
	Zea mays	ZmEREB58	NP_001170395.1	Prupe.1G037900	PpEREB58	Li *et al.*, 2015
	Citrus sinensis Osbeck	CitAP2.10	orange1.1t02867.1	Prupe.3G104100	PpAP2	Shen *et al.*, 2016
		CitERF71	orange1.1g047100m	Prupe.2G129300	Not expressed in peach	Li *et al.*, 2017
	Malus domestica	MdERF3	MDP0000787281	Prupe.5G061800	PpERF1	Wang *et al.*, 2020
EIL	*Actinidia chinensis*	AcEIL1	KF319041	Prupe.2G058400	PpEIL1	Nieuwenhuizen *et al.*, 2015
		AcEIL2	KF319042	Prupe.2G058400		

		AcEIL3	KF319043	Prupe.6G018200	PpEIL3	
		AcEIL4	KF319044	Prupe.6G018200		
	Actinidia arguta	AaEIL4	KF319045	Prupe.6G018200		
bZIP	*Artemisia annua*	AabZIP1	contig131774	Prupe.1G434500	PpbZIP1	Zhang *et al*., 2015
	Oryza sativa	OsTGAP1	AK073715	Prupe.1G307300	PpbZIP2	Okada *et al*., 2009
		OsbZIP79	Os11g0152700	Prupe.6G129100	PpbZIP79	Miyamoto *et al*., 2015
EOT	*Solanum lycopersicum*	**SlEOT1**	**AGW27396.1**	**Prupe.1G371500**	**PpEOT1**	Spyropoulou *et al*., 2014
YABBY	*Mentha spicata*	MsYABBY5	AMA07776	Prupe.7G245200	PpYABBY5	Wang *et al*., 2016
	Artemisia annua	AaYABBY5	MK675289	Prupe.7G245200		Kayani *et al*., 2019

Bold indicates transcription factors associated with linalool synthesis.

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

Family	Peach ID	Correlation with *PpTPS3*	Name	Primer-SK (5’)	Primer-SK (3’)
bHLH	Prupe.4G077100	0.85456	PpbHLH5	agaactagtggatccATGCAGAGGGACCAACAGTT	cccctcgaggtcgacTTAGTCATTCAAATTCTCAA
	Prupe.1G173300	0.80985	PpbHLH6	agaactagtggatccATGGGAAAAGACAGAACAGC	cccctcgaggtcgacTTATAGCTCAACTTTCATCT
	Prupe.6G343400	0.70216	PpbHLH7	agaactagtggatccATGGCGGGAAATCCGCCTGA	cccctcgaggtcgacCTATGAAGAGGAGTTTGATT
	Prupe.1G207100	0.66293	PpbHLH8	agaactagtggatccATGATTGTTAGCTCTCTCTG	cccctcgaggtcgacTCAATGGAATTGTGAGATGG
bZIP	Prupe.1G369300	0.82833	PpbZIP3	agaactagtggatccATGGAGGGCAGTGATGAAAC	cccctcgaggtcgacCTATTCGCTTGACTCGTGCT
	Prupe.8G091600	0.79739	PpbZIP4	agaactagtggatccATGGCTTCTTCTAGTGGGAC	cccctcgaggtcgacTCAGTAATGAAACATCTCTG
	Prupe.2G263700	0.77684	PpbZIP5	agaactagtggatccATGCAAGATCCGGCGAACCC	cccctcgaggtcgacTCAAAATCTCCTGTTGCTTT
	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
ERF	Prupe.3G032300	0.83867	PpERF4	agaactagtggatccATGTGTGGAGGTGCTATAAT	cccctcgaggtcgacTCAGAAACCTCCCCCAATCA
	Prupe.4G051200	0.79244	PpERF5	agaactagtggatccATGGCGACTGCTTCTTCATC	cccctcgaggtcgacTCACAGCCACAAGGGTGGGG
	Prupe.8G264900	0.60191	PpERF6	agaactagtggatccATGTGTGGCGGTGCTATTCT	cccctcgaggtcgacTTACGGAGCAGAAACGCGGT
	Prupe.5G090000	0.5465	PpERF7	agaactagtggatccATGGACATGTTCTCCGCTCA	cccctcgaggtcgacTCAGATAGAGAAACTCCATA
	Prupe.5G117800	0.51657	PpERF61	agaactagtggatccATGGACACAATGCAAGACAG	cccctcgaggtcgacCTAATTAGCAAGAACTTCCC
MADS	Prupe.1G531700	0.74244	PpMADS1	agaactagtggatccATGATGAGGGAGAAGATCAA	cccctcgaggtcgacCTAGGGAAGCCCCAGTTTGA
	Prupe.1G531600	0.70606	PpMADS2	agaactagtggatccATGATGAGGAATAAGATCAA	cccctcgaggtcgacTCACCCCAGTTTGAGAGACA

MYB	Prupe.3G045300	0.79317	PpMYB4	agaactagtggatccATGGGAAACCAAAAGCAAAA	cccctcgaggtcgacCTACGCCAAGGCGACAACTT
	Prupe.6G255800	0.60963	PpMYB5	agaactagtggatccATGGAAATGAAGGAGAGACA	cccctcgaggtcgacTCACCGGCCATTAGGCTCAG
NAC	Prupe.4G053300	0.81331	PpNAC9	agaactagtggatccATGACATGGTGCAATGACTC	cccctcgaggtcgacCTATTTTCTCTCAAGCTTTC
	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.

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

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*	*cis*-acting regulatory element involved in light responsiveness
	CAGACGTGGCA	1471	-	10	*Nicotiana plumbaginifolia*	*cis*-acting regulatory element involved in light responsiveness
	CACGTC	1474	+	6	*Zea mays*	*cis*-acting regulatory element involved in light responsiveness
	CACGTG	1606	-	6	*Arabidopsis thaliana*	*cis*-acting regulatory element involved in light responsiveness
	TACGTG	1709	+	6	*Arabidopsis thaliana*	*cis*-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 S6. Statistic of whole-genome bisulfite sequencing reads from peach fruit at different development stages and under UV-B treatment.

Sample	Clean Reads	Clean Base	Q20 (%)	Q30 (%)	GC Content (%)	Unique mapped Reads	Mapping rate (%)	BS Conversion Rate (%)
S1	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
S3	29082640	8671179212	97.22	93.55	21.85	19063507	65.55	99.49
S4	73842467	22084452994	97.64	94.65	21.27	49699965	67.31	99.53
S5	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

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

Sample	Average depth	Covering ratio 1×(%)	Covering ratio 5×(%)	Covering ratio 10×(%)
S1	46	92.77	89.65	87.24
S2	41	92.16	88.85	86.03
S3	26	91.75	87.33	82.28
S4	67	92.89	90.08	88.11
S5	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 S8. Primers of TFs which homologues of transcription factors that regulate terpenoid formation.

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

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.

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

Primers	Sequence (5’→3’)	Description
pET-*PpTPS3*-FP	aaggcctctgtcgacATGGCCCTTCTTCAAGCTCA	pET vector cloning of *PpTPS3*
pET-*PpTPS3*-RP	agaattcgcaagcttTTATTTCGTCTGGCCTGGGG	pET vector cloning of *PpTPS3*
SK-*PpTPS3*-FP	agaactagtggatccATGGCCCTTCTTCAAGCTCA	pGreen-SK vector cloning of *PpTPS3*
SK-*PpTPS3*-RP	cccctcgaggtcgacTTATTTCGTCTGGCCTGGGG	pGreen-SK vector cloning of *PpTPS3*
pBI121-*PpTPS3*-FP	acgggggactctagaATGGCCCTTCTTCAAGCTCA	pBI121 vector cloning of *PpTPS3*
pBI121-*PpTPS3*-RP	accacccggggatccTTTCGTCTGGCCTGGGGACT	pBI121 vector cloning of *PpTPS3*
eGFP-*PpTPS3*-FP	ggtacccggggatccATGGCCCTTCTTCAAGCTCA	35S-eGFP vector cloning of *PpTPS3*
eGFP-*PpTPS3*-RP	gctcaccatgtcgacTTTCGTCTGGCCTGGGGACT	35S-eGFP vector cloning of *PpTPS3*
LUC-Pro*PpTPS3*-FP	ggtatcgataagcttAAGATAGAAGTCAGCTGGAA	pGreen-LUC vector cloning of *PpTPS3 promoter*
LUC-Pro*PpTPS3*-RP	tggcgtcttccatggGTCGTTAATATGCCGAGTAT	pGreen-LUC vector cloning of *PpTPS3 promoter*
LUC-Pro*PpTPS1*-FP	ggtatcgataagcttACCGGCCTAAATAACTAGAT	pGreen-LUC vector cloning of *PpTPS1 promoter*
LUC-Pro*PpTPS1*-RP	tggcgtcttccatggTTTTACTAGAGCAATTGCAG	pGreen-LUC vector cloning of *PpTPS1 promoter*
LUC-Pro*NtLIS*-FP	ggtatcgataagcttAGTCAAATTTGATCCTTTTC	pGreen-LUC vector cloning of *NtLIS promoter*
LUC-Pro*NtLIS*-RP	tggcgtcttccatggGTAAAAGATTATTTTGCTGT	pGreen-LUC vector cloning of *NtLIS promoter*
LUC-Pro*AtTPS10*-FP	ggtatcgataagcttTCTCACTTTGGTTTCCCAAC	pGreen-LUC vector cloning of *AtTPS10 promoter*
LUC-Pro*AtTPS10*-RP	tggcgtcttccatggATTGAATAAATGTATTATTA	pGreen-LUC vector cloning of *AtTPS10 promoter*
pAbAi-Pro*PpTPS3*-FP	tgaattgaaaagcttAAGATAGAAGTCAGCTGGAA	pAbAi vector cloning of *PpTPS3 promoter*
pAbAi-Pro*PpTPS3*-RP	cgacagatccccgggGTCGTTAATATGCCGAGTAT	pAbAi vector cloning of *PpTPS3 promoter*
AD-*PpbHLH1*-FP	gaggccagtgaattcATGGAGATTTCGTCGATAGG	pGADT7 vector cloning of *PpbHLH1*
AD-*PpbHLH1*-RP	gagctcgatggatccTCACATGAACATGTCGAAAG	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 *PpbHLH*
eGFP-*PpbHLH1*-RP	gctcaccatgtcgacCATGAACATGTCGAAAGCAG	35S-eGFP vector cloning of *PpbHLH*
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 *PpbHLH1*

attB2-*PpbHLH1*-RP	ggggaccactttgtacaagaaagctgggtCATGAACATGTCGAAAGCAG	pBIN19-E8 vector cloning of *PpbHLH1*
Probe1-FP-biotin	TGAAATGATGATAAGCACATGGATATATGGCCTGGAAAAC	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 *PpPDS* for VIGS
TRV2-*PpPDS*-RP	cctccatggggatccCTCTTGCTTCCAGTAAGATA	pTRV2 vector cloning of *PpPDS* for VIGS
TRV2-*PpTPS3*-FP	tgcccgggcctcgagTACATAATAGATGATATTTT	pTRV2 vector cloning of *PpTPS3* for VIGS
TRV2-*PpTPS3*-RP	cctccatggggatccTTGGTTCTCATCCTTGGCAC	pTRV2 vector cloning of *PpTPS3* for VIGS
TRV2-*PpbHLH1*-FP	tgcccgggcctcgagACACTTGAGGAACAGACCAG	pTRV2 vector cloning of *PpbHLH1*for VIGS
TRV2-*PpbHLH1*-RP	cctccatggggatccTTGACAAGTTCCTTCACTGA	pTRV2 vector cloning of *PpbHLH1* for VIGS
qPCR-*PpTPS3*-FP	GGTCGCGGTATAACTCAGCA	RT-qPCR of *PpTPS3*
qPCR-*PpTPS3*-RP	CAAAGTCATCCCAGAGCCGT	RT-qPCR of *PpTPS3*
qPCR-*PpbHLH1*-FP	CCCCTTTGAGGAGACACTGC	RT-qPCR of *PpbHLH1*
qPCR-*PpbHLH1*-RP	TGTCGAAAGCAGAGCGTAGA	RT-qPCR of *PpbHLH1*
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-*SlTPS5*-FP	CTTCGGATGAACTGAAAAGAGG	RT-qPCR of *SlTPS5*
qPCR-*SlTPS5*-RP	GTGGAGAATTTTTGCTTTGAGC	RT-qPCR of *SlTPS5*
qPCR-*NtLIS*-FP	ATGGATGGGGAAGAAGCACC	RT-qPCR of *NtLIS*
qPCR-*NtLIS*-RP	CGGCTTCTGTGAAGAGGGTT	RT-qPCR of *NtLIS*

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 *AtEF1α*
AtEF1α-RP	GGTGGTGGCATCCATCTTGTTACA	RT-qPCR of house-keeping gene *AtEF1α*
SlActin-FP	TGTCCCTATTTACGAGGGTTATGC	RT-qPCR of house-keeping gene *SlActin*
SlActin-RP	CAGTTAAATCACGACCAGCAAGAT	RT-qPCR of house-keeping gene *SlActin*
NtEF1-*α*-FP	GCCCAACACTTCTTGATGCTC	RT-qPCR of house-keeping gene *NtEF1*
NtEF1-*α*-RP	GACACCAGTTTCCACACGAC	RT-qPCR of house-keeping gene *NtEF1*

Lowercase letters indicate sequences on the vector.