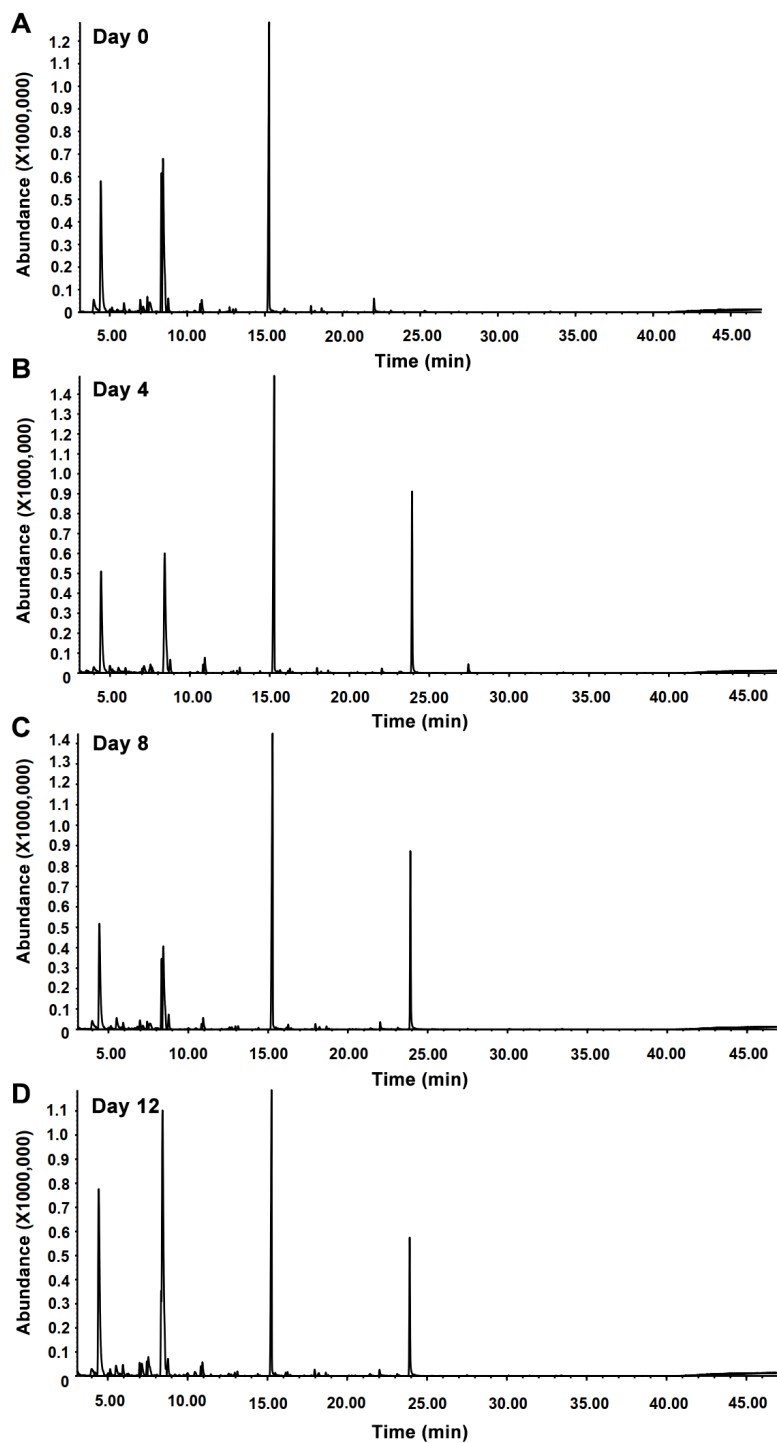
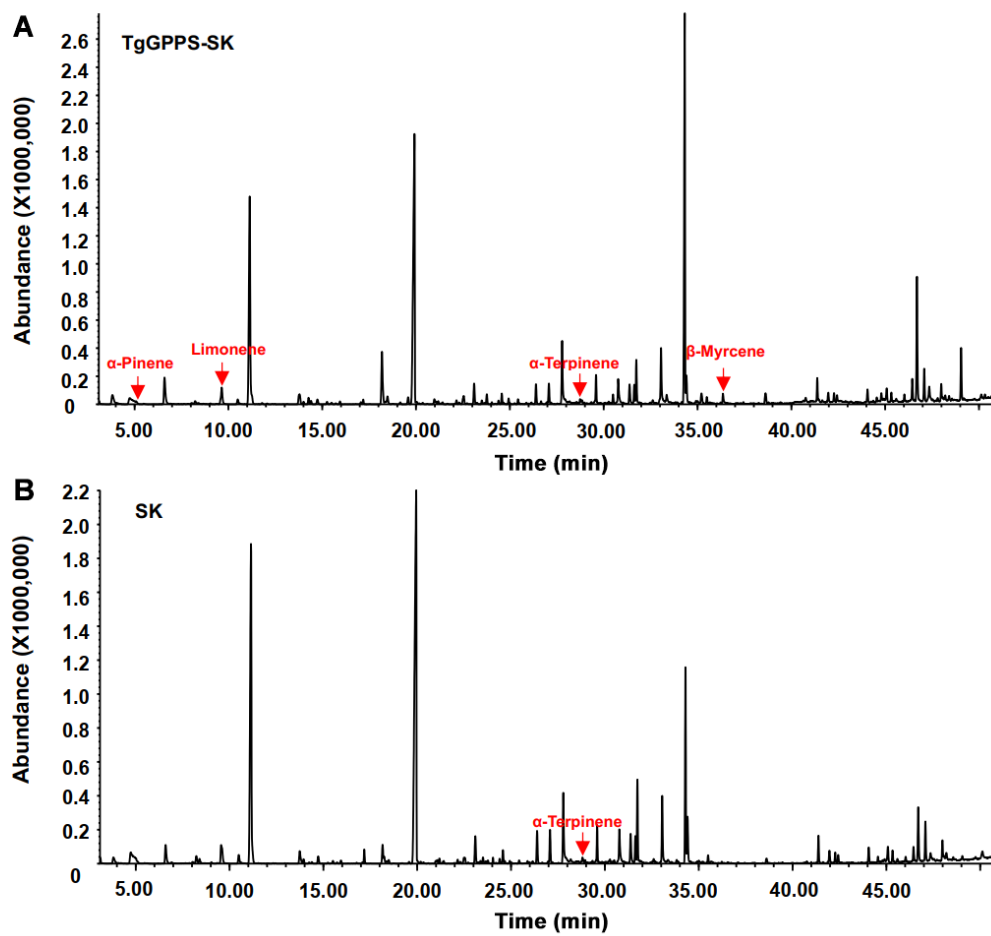


1 **Supplemental Data**



2

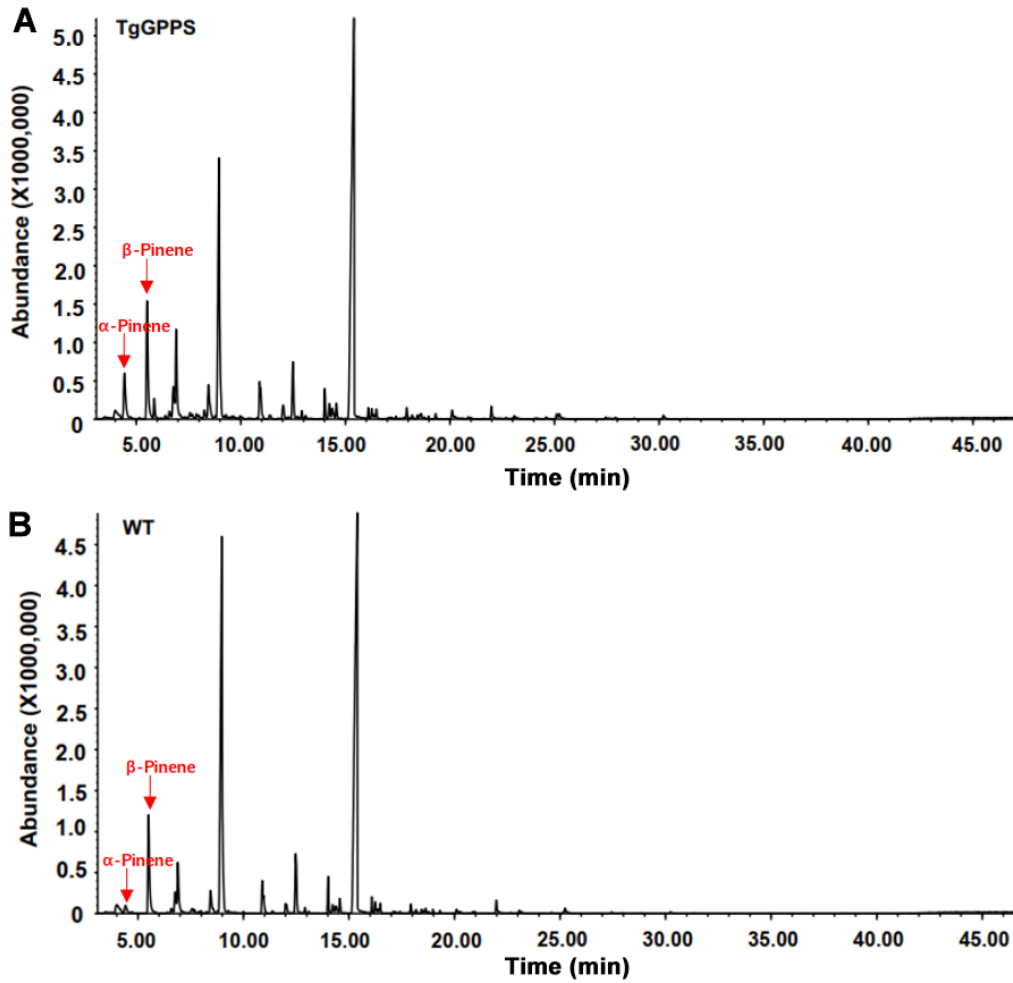
3 **Supplemental Figure S1.** Gas chromatography-mass spectrometry (GC-MS)
4 chromatogram of volatiles in xiangfei (*Torreya grandis*) nuts determined on different
5 days during the postharvest ripening stage. Note: A, day 0 of ripening time; B, day 4 of
6 ripening time; C, day 8 of ripening time; D, day 12 of ripening time.



13

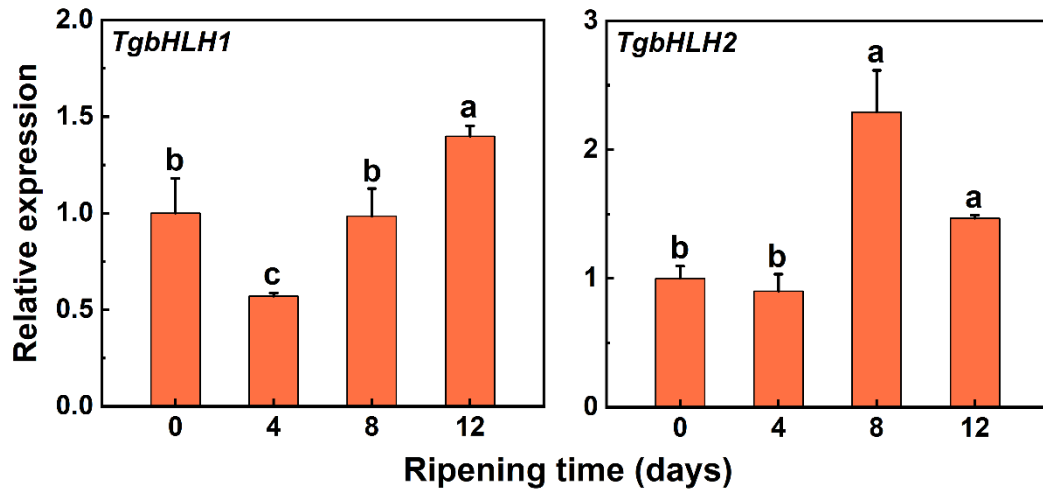
14 **Supplemental Figure S3.** GC-MS chromatogram of volatiles determined 7 days after
 15 infiltration of tobacco (*Nicotiana tabacum*) leaves. A, GC-MS chromatogram of
 16 volatiles after TgGPPS-SK infiltration. B, GC-MS chromatogram of volatiles after
 17 empty vector SK infiltration.

18



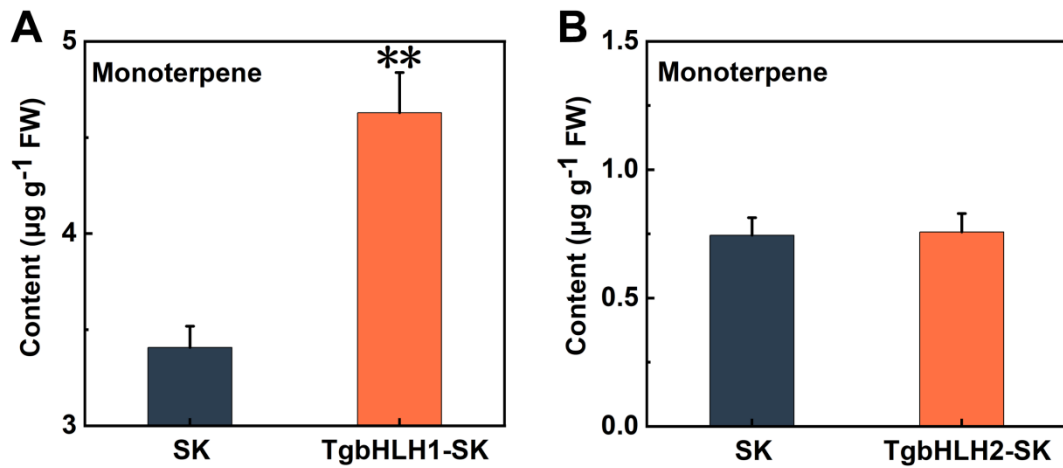
19

20 **Supplemental Figure S4.** GC-MS chromatogram of volatiles determined 7 days after
 21 the breaker stage of tomato (*Solanum lycopersicum*, cv *MicroTom*) fruit. A, GC-MS
 22 chromatogram of volatiles in *TgGPPS* overexpressing tomato fruit. B, GC-MS
 23 chromatogram of volatiles in wild type (WT) tomato fruit.



24

25 **Supplemental Figure S5.** Relative expression of *TgbHLH1* and *TgbHLH2* on days 0-
26 12 during the postharvest ripening stage of xiangfei nuts. Bars represent the average +
27 SE values obtained from three biological replicates. Different letters indicate significant
28 differences ($P < 0.05$) during the postharvest ripening stage by Duncan's multiple range
29 test.



30

31 **Supplemental Figure S6.** Transient overexpression of *TgbHLHs* in tobacco (*Nicotiana*
 32 *tabacum*) leaves. A, Transient overexpression of *TgbHLH1* showed an increase in total
 33 monoterpene contents in tobacco leaves. B, Transient overexpression of *TgbHLH2*
 34 showed no change in total monoterpene contents in tobacco leaves. The relative content
 35 of monoterpenes after 7 days of infection was calculated according to the peak area of
 36 the internal standard (2-octanol). SE values were obtained from three biological
 37 replicates. Significant differences are indicated with asterisks using Students's test (**
 38 $P < 0.01$). FW, fresh weight.

39 **Supplemental Table S1.** Isolated and identified transcription factors involved in
 40 regulating terpenes biosynthesis in different plant species.

Type	Species	Transcription factors	Targeted genes
AP2/ERF	<i>Artemisia annua</i>	AaERF1/2	ADS, CYP71AV1
		AaORA	ADS, CYP71AV1, DBR2, AaERF1
	<i>Citrus sinensis</i>	CitAP2.10/CitERF76	CsTPS1/CitTPS16
	<i>Zea mays</i>	ZmEREB58	ZmTPS10
bHLH	<i>Artemisia annua</i>	AabHLH1	ADS, CYP71AV1
	<i>Arabidopsis thaliana</i>	AtMYC2	AtTPS1, AtTPS21
MYB	<i>Arabidopsis thaliana</i>	MYB21, MYB24	AtTPS11, AtTPS21
	<i>Mentha spicata</i>	MsMYB	MsGPPS.LSU
NAC	<i>Artemisia annua</i>	AaNAC1	ADS, DBR2, ALDH1
	<i>Actinidia arguta</i>	NAC3	AcTPS1
WRKY	<i>Gossypium arboreum</i>	GaWRKY1	GaCAD1-A
	<i>Artemisia annua</i>	AaWRKY1	ADS
bZIP	<i>Artemisia annua</i>	AabZIP1	ADS, CYP71AV1
	<i>Oryza sativa</i>	TGAP1	OsCPS4, OsKSL4, CYP99A2, CYP99A3, OsMAS, OsDXS3
Others	<i>Mentha spicata</i>	MsYABBY5	
	<i>Artemisia annua</i>	EIN3	ADS, DBR2, CYP71AV1, AaORA
	<i>Actinidia arguta</i>	AaEIL1	AaTPS1

42 **Supplemental Table S2.** The fragments per kilobase of exon per million mapped
43 fragments (FPKM) value of all terpenoid synthesis genes from the 2-C-methyl-D-
44 erythritol 4-phosphate (MEP) and mevalonate (MVA) pathways through annotation in
45 the *T. grandis* transcriptome database. Among them, those marked in red had higher
46 relative expression, and were selected as candidate genes from the heat map in Figure
47 2. C4 indicates samples on day 4, C8 indicates samples on day 8, C12 indicates samples
48 on day 12, CK-1, 2, 3 indicate control samples with three biological replicates.

Gene	gene ID	C4-AVE	C8-AVE	C12-AVE	CK-1	CK-2	CK-3
TPS	cluster_contig41508	445.38	58.9	68.71	2855.9	2245.48	2653.26
	cluster_contig107675	18.37	5.87	6.38	2.17	1.42	1.45
	Unigene1071683	9.87	4.59	4.239	1.8	1.26	0.81
	Unigene1138992	3.25	0.27	0.72	0.95	2.1	0.73
	cluster_contig107677	2.88	0.79	0.90	1.22	1.87	1.41
	Unigene1244643	4.08	1.57	1.12	1.08	1.09	0.91
	Unigene1071684	4.74	3.11	2.89	1.6	1.08	1.45
	cluster_contig28483	2.37	1.04	1.07	0.33	0.28	0.35
	Unigene1169816	0.64	0.03	0.08	0.57	0.77	0.24
	Unigene1169581	1.72	0.55	0.16	1.23	0.95	0.75
	cluster_contig107673	0.48	0.41	0.11	0.27	0.67	0.45
	cluster_contig28484	0.53	0.30	0.16	0.06	0.11	0.09
	cluster_contig107678	0.80	0.55	0.40	0.28	0.22	0.18
	cluster_contig110610	0.06	0.02	0.04	0	0.04	0.04
	cluster_contig122705	0.33	0.55	1.74	0.79	0.30	0.49
	cluster_contig107676	0.85	0.25	0.03	0	0	0.08
	Unigene1030463	0.08	0.03	0	0	0	0
	Unigene1052201	0.33	0.45	0.20	0.15	0.25	0.25
	Unigene1055505	1.93	0	0.40	0	0	0
	Unigene1111750	0.05	0	0	0.11	0.07	0.11
Unigene1138993	0.53	0.62	0.92	0.51	0.23	0.24	
cluster_contig107674	0.28	0.20	0.20	0.15	0.14	0.34	

Unigene1169815	0.97	0.38	0.04	0	0.03	0	
Unigene1216764	0	0	0	0	0	0	
Unigene1223088	0.04	0	0	0	0	0	
Unigene1229165	0.23	0.32	0.34	0.24	0.17	0.15	
Unigene1230466	0	0	0	0	0	0	
cluster_contig29037	0.04	0.06	0.02	0.02	0	0.02	
cluster_contig47588	0.17	0.01	0.01	0	0	0	
cluster_contig86232	0.05	0.01	0	0	0.02	0.04	
cluster_contig106440	0	0	0	0	0	0	
cluster_contig107672	0.04	0.08	0	0	0.27	0.06	
Unigene1013840	0	0	0	0	0	0	
Unigene1030127	0	0	0	0	0	0	
Unigene1030462	3.40	0.62	0	0	0	0	
Unigene1036911	0	0	0	0	0	0	
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GPPS	cluster_contig30179	5.14	6.7	7.55	6.39	6.04	6.73
	Unigene1220367	2.32	1.93	2.48	1.64	1.5	1.7
	cluster_contig70933	7.14	5.17	6.97	13.33	12.44	13.57
	cluster_contig111709	1.58	1.26	1.72	1.11	1.06	1.31
	cluster_contig118960	2.23	1.99	2.73	1.48	1.54	1.64
	Unigene1143830	0	0	0			
	cluster_contig89056	0.01	0	0.04	0	0	0.03
	cluster_contig69789	0.01	0.17	0.03	0.06	0	0.06
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	Unigene1133129	68.23	75.68	87.52	56.52	59.87	59.68
	cluster_contig81183	8.84	10.31	11.38	8.19	8.34	8.13
HDR	cluster_contig81184	15.10	17.28	19.15	12.35	12.84	12.59
	cluster_contig81185	16.06	19.51	21.80	14.33	15.23	13.94
	cluster_contig69353	0.01	0.04	0.05	0	0	0.02
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	Unigene1134183	30.82	30.34	24.01	19.02	19.57	20.52
HDS	cluster_contig81234	14.43	14.08	10.83	8.79	8.67	8.61
	cluster_contig81235	10.08	9.52	7.85	5.48	6.21	6.2

	cluster_contig104705	21.37	21.01	16.84	12.54	13.46	12.83
	Unigene1222427	17.11	16.87	13.40	10.75	11.27	10.8
	Unigene1167278	24.19	19.66	13.59	18.96	15.67	18.28
	cluster_contig93362	7.63	6.20	4.56	6.75	5.45	6.42
	Unigene1223957	6.60	6.36	3.66	5.14	4.81	5.53
	cluster_contig93371	1.68	2.36	1.10	1.62	1.24	1.72
	Unigene1124563	2.03	2.02	3.17	2.09	2.19	2.13
MDS	cluster_contig91897	0.98	1.30	1.61	0.72	1.08	0.81
	cluster_contig114151	0.92	1.2	1.18	0.72	1.12	0.86
	Unigene1046800	0.06	0.16	0.08	0.05	0.02	0.04
	Unigene1056177	0	0	0	0	0	0
	Unigene1134643	0.50	0.82	0.99	0.64	0.8	0.88
	cluster_contig27809	0.04	0.16	0.04	0.01	0	0.03
	cluster_contig27810	0.01	0.18	0.07	0	0	0.07
	cluster_contig97353	581.04	614.43	560.70	718.65	781.59	758.55
CMK	cluster_contig6554	10.17	11.11	9.23	0	0	0
	cluster_contig127572	0.11	0.33	0.04	0.05	0	0.09
	Unigene1052694	5.89	6.10	5.93	4.84	4.28	4.39
	Unigene1113803	2.35	2.85	2.60	2.2	1.6	1.54
MCT	Unigene1139466	3.72	4.22	3.41	3.49	2.42	3.58
	Unigene1174511	4.74	5.68	4.65	4.25	3.61	3.73
	Unigene1222041	4.08	4.44	4.13	4.07	2.96	3
	Unigene1133829	15.48	15.03	18.21	11.42	11.49	11.69
	cluster_contig121684	8.03	7.92	9.86	6.17	6.34	6.16
	cluster_contig121687	7.98	7.73	9.21	5.61	5.81	5.76
DXR	Unigene1225548	2.34	2.65	2.87	1.55	1.94	1.81
	cluster_contig121686	2.26	2.67	2.97	1.76	1.97	1.72
	Unigene1053578	0.04	0.15	0.09	0.01	0.05	0.07
	Unigene1063629	0.06	0.26	0.05	0.1	0.05	0
	cluster_contig37222	0.07	0.20	0.12	0.06	0.08	0.13

	Unigene1131741	38.46	26.78	19.55	9.97	9.49	9.62
	cluster_contig132342	25.74	17.68	13.04	6.74	6.2	6.95
	cluster_contig113973	20.69	15.24	10.60	5.26	5.59	5.92
	Unigene1230286	20.31	15.05	10.41	5.28	5.67	5.26
	Unigene1129266	13.75	9.71	6.87	3.45	3.57	3.45
	cluster_contig132790	1.43	2.46	2.26	1.46	1.41	1.33
DXS	cluster_contig102724	1.04	1.09	2.80	1.27	1.26	1.39
	Unigene1106877	0.97	0.8	2.35	1.1	1.2	0.91
	Unigene1187813	0.64	1.01	0.98	0.5	0.56	0.61
	cluster_contig77178	0.53	0.86	0.88	0.41	0.45	0.38
	cluster_contig18484	0.51	0.81	0.68	0.32	0.4	0.38
	cluster_contig14348	0.47	0.46	1.30	0.57	0.64	0.54
	cluster_contig8962	0	0	0.1	0	0	0
	cluster_contig45735	7.7	3.78	4.54	6.99	5.66	6.62
MVD	cluster_contig14056	1.19	0.73	0.83	1.14	0.92	1.19
	Unigene1064877	0	0.057	0.06	0.05	0.05	0.03
	cluster_contig2092	18.03	24.76	20.22	31.81	35.8	34.76
	Unigene1173569	6.42	9.43	8.63	13.08	13.46	14.59
	Unigene1067755	6.07	8.22	7.09	10.11	10.64	10.84
PMK	cluster_contig5009	5.2	8.07	6.87	9.69	9.13	9.28
	cluster_contig2627	2.83	4.29	3.54	5.26	5.83	5.55
	Unigene1193858	2.69	4.20	3.05	4.53	5.29	5.8
	cluster_contig47753	0.05	0.18	0.06	0.05	0.04	0
	Unigene1243203	4.66	5.12	5.43	7.26	6.45	7.22
	cluster_contig107843	1.17	1.31	0.96	1.03	1.05	1.05
MVK	cluster_contig107844	1.15	1.54	1.33	2.08	1.74	1.9
	Unigene1055110	1.34	1.56	1.28	1.36	1.03	1.04
	Unigene1055113	0.2	0.27	0.12	0.35	0.11	0.57
	cluster_contig66474	52.35	13.26	1.27	2.37	2.69	2.1
	Unigene1027186	37.80	7.8	0.8	1.35	1.24	0.87

HMGR	cluster_contig66468	11.66	2.67	0.77	1.3	1.24	1.21
	Unigene1223684	14.34	3.19	0.55	0.72	0.63	0.7
	cluster_contig66471	25.34	6.23	0.80	1.05	0.9	0.83
	Unigene1193836	17.84	4.51	0.61	1.11	1.46	0.51
	cluster_contig66472	1.22	1.35	1.31	4.67	4.6	4.64
	cluster_contig112291	9.62	2.81	0.57	0.89	1.43	1.18
	Unigene1141625	1.08	1.40	1.20	5.71	5.51	6.09
	cluster_contig45995	0.19	0	0	0.04	0.07	0.03
	cluster_contig66467	0.22	0.28	0.22	0.54	0.32	0.32
	cluster_contig66469	0.22	0.04	0.30	0.55	0.81	0.58
	cluster_contig66473	1.12	0.35	0.36	0.15	0.26	0.18
	cluster_contig17085	0.51	0.29	0.32	0.49	0.31	0.32
	cluster_contig74862	0.58	0	0.03	0	0.08	0
	cluster_contig84896	4.89	0.99	0	0.05	0.09	0.05
	cluster_contig106108	0	0	0.03	0	0	0
	Unigene1026281	6.01	1.42	0	0	0.16	0
	Unigene1055278	0.96	0.05	0	0.14	0.4	0
	Unigene1055279	0.14	0	0	0	0	0
	Unigene1072160	0	0	0	0	0	0.71
	Unigene1072161	1.01	0.12	0	0	0.15	0
	Unigene1102935	0	0	0	0	0	0
	Unigene1120547	0.07	0.07	0.04	0.13	0	0
	Unigene1141624	1.01	0	0	0	0	0
	Unigene1220775	0.47	0.11	0	0	0	0
	Unigene1245029	0	0	2.58	0	0	0
	Unigene1136698	17.93	20.77	21.14	13.31	13.25	13.89
	cluster_contig50852	19.86	8.03	4.47	5.71	9.4	5.66
HMGS	cluster_contig43562	5.71	4.71	4.38	2.91	3.01	2.78
	cluster_contig99384	4.38	4.08	3.95	2.8	2.99	2.72
	cluster_contig122767	6.52	3.01	1.63	2.14	2.44	2.28

	Unigene1136697	3.46	1.55	0.89	1.34	1.47	1.41
	cluster_contig122766	1.08	0.44	0.29	0.32	0.4	0.38
	cluster_contig123082	0	0.11	0.07	0	0	0.01
	Unigene1043935	1.49	1.38	1.32	0.85	1.02	0.95
	Unigene1043936	0	0	0.03	0	0	0
	Unigene1235014	0	0	0	0	0	0
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	Unigene1132446	38.19	38.99	35.52	22.1	23.73	23.29
	cluster_contig67828	12.50	13.48	12.35	8.17	7.7	8.07
	cluster_contig125937	12.37	12.81	12.15	7.23	7.47	7.46
	Unigene1033526	1.10	1.36	1.21	0.66	0.72	0.65
AACT	Unigene1075230	0	0	0	0	0	0
	Unigene1150027	0	1.11	0	0	0	0
	Unigene1156688	0	0.30	0	0	0	0
	Unigene1199643	0	0	0	0	0	0
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50 **Supplemental Table S3.** Primers used for RT-qPCR.

Gene	Forward (5'-3')	Reverse (5'-3')
<i>TgActin</i>	TGGCATCTCTCAGCACATTCCA	TGCCAACATCTCAAGCAAGCAC
<i>TgGPPS</i>	CGAGAGGATTCGTCGTTGTA	ACCTCCCTAAGCCTCACTTA
<i>TgbHLH1</i>	TGAGGCAAATAGAGACGTGC	GTCACGGAAGATTGCTGGAA
<i>TgbHLH2</i>	GTCGCTGTTTTTCAACCAGG	GTTATATTCGCCGCCTCCAA
<i>TgbHLH95</i>	TGGATCCAATGTTGTGGGAA	TGCTGACTATTGCCCTTGGA
<i>TgbZIP44</i>	ATGGGCAGGCCTACTGAAT	GGCTGAGAAATGGAAGGCTG

51

Primer name	Sequence (5'-3')
LUC: `	
TgGPPSpro-LUC-FP-BamHI	CAGCCCGGGG <u>GATCCT</u> GTGATTGAAGAGCCCACAC
TgGPPSpro-LUC-RP-NcoI	TGGCGTCTT <u>CCATGG</u> CTTGCCTTCTGAAACAAAAA
pAbAi:	
TgGPPSpro-pAbAi-FP-SacI	AAGCTTGAATTC <u>GAGCTCT</u> GTGATTGAAGAGCCCACAC
TgGPPSpro-pAbAi-RP-XhoI	AGCACATGCCT <u>CGAGCT</u> TGCCTTCTGAAACAAAAA
GFP:	
TgGPPS-GFP-FP-KpnI	GTACCCGGGG <u>GATCC</u> ATGTCTTTGAGGTGCTCAGTAAGAAA
TgGPPS-GFP-RP-SalI	GCTCACCAT <u>GTCGAC</u> CTTTTTCTAGTGGTACTTTTTTCAGT
TgbHLH95-GFP-FP-KpnI	GAGCTC <u>GGTACC</u> ATGTCAACTTACAGAGGCTC
TgbHLH95-GFP-RP-SalI	GCTCACCAT <u>GTCGAC</u> TTCTTCATGACTAGTTA
TgbZIP44-GFP-FP-KpnI	GAGCTC <u>GGTACC</u> ATGGCTCCTCCATCAAATTT
TgbZIP44-GFP-RP-SalI	GCTCACCAT <u>GTCGAC</u> CTGATAAATTTCTTGAG
pGADT7:	
TgbHLH130-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGTTAACAATCAAGGGCA
TgbHLH130-AD-RP-BamHI	GAGCTCGAT <u>GGATCC</u> TCAGAACCATGCATTGCAAA
TgbHLH1-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGACGGTGCTAACATTGCG
TgbHLH1-AD-RP-BamHI	CTCGAT <u>GGATCC</u> TTACTGCAACCTTTTCAGCTA
TgbHLH2-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGGAGTCTTACAAGGCGAT
TgbHLH2-AD-RP-BamHI	GAGCTCGAT <u>GGATCC</u> CTACATTGCCATCTGACTGC
TgbHLH30-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGGCTATGTTTACGGACA
TgbHLH30-AD-RP-BamHI	GAGCTCGAT <u>GGATCC</u> TTACCCTGAAACACTTCGA
TgbHLH95-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGTCAACTTACAGAGGCTC
TgbHLH95-AD-RP-BamHI	GAGCTCGAT <u>GGATCC</u> TCATTCTTCATGACTAGTTA
TgbZIP44-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGGCTCCTCCATCAAAT
TgbZIP44-AD-RP-BamHI	GAGCTCGAT <u>GGATCC</u> CTACTGATAAATTTCTTGA
TgERF1B-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGTGTCCGCTGTCTCTTCG
TgERF1B-AD-RP-BamHI	GAGCTCGAT <u>GGATCC</u> TCAAGATGGAGGAAGAGGGG
TgERF1-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGGCGACGGAGGAAGATGG
TgERF1-AD-RP-BamHI	GAGCTCGAT <u>GGATCC</u> TTATGCCCCGAATGTGGGACT
TgERF2-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGCTCCGGCGGGTAAATTG
TgERF2-AD-RP-BamHI	GAGCTCGAT <u>GGATCC</u> TTAATAAGTGCTGTCTTTTT

TgMADS16-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGTTTCATGGTGCTAGGTGT
TgMADS16-AD-RP-BamHI	GAGCTCGAT <u>GGATCC</u> TATCCCCAAATAGAAGATA
TgMYB3-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGCCATGGAGTGAGGAA
TgMYB3-AD-RP-BamHI	GAGCTCGAT <u>GGATCC</u> TACACCACTCTGATAAT
TgRAV1-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGGGATTGACTTTGGGTTT
TgRAV1-AD-RP-BamHI	GAGCTCGAT <u>GGATCC</u> TCAGCCGCTATTCGCTTTGT
TgRAV3-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGAAATTCAGGGCAAGAG
TgRAV3-AD-RP-BamHI	GAGCTCGAT <u>GGATCC</u> CAATTCTGCCCTCCGCTA
TgGTE4-AD-FP-EcoRI	GAGGCCAGT <u>GAAATTC</u> ATGGCTTCCGCTCTGCTGGC
TgGTE4-AD-RP-BamHI	GAGCTCGAT <u>GGATCC</u> TCAAAGAGAAAACCCAACCT

SK:

TgbHLH130-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGTTTAAACAATCAAGGGCA
TgbHLH130-SK-RP-EcoRI	GCTTGATATCGAATTCCTCAGAACCATGCATTGCAAA
TgbHLH1-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGACGGTGCTAACATTGCG
TgbHLH1-SK-RP-EcoRI	GCTTGATATCGAATTCCTTACTGCAACCTTTCAGCTA
TgbHLH2-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGGAGTCTTACAAGGCGAT
TgbHLH2-SK-RP-EcoRI	GCTTGATATCGAATTCCTACATTGCCATCTGACTGC
TgbHLH30-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGGCTATGTTTACGGACA
TgbHLH30-SK-RP-EcoRI	GCTTGATATCGAATTCCTTACCCTGAAACACTTCGA
TgbHLH95-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGTCAACTTACAGAGGCTC
TgbHLH95-SK-RP-EcoRI	GCTTGATATCGAATTCCTCATTCTTCATGACTAGTTA
TgbZIP44-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGGCTCCTCCATCAAAT
TgbZIP44-SK-RP-EcoRI	GCTTGATATCGAATTCCTACTGATAAATTTCTTGA
TgERF1B-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGTGTCCGCTGTCTCTTCG
TgERF1B-SK-RP-EcoRI	GCTTGATATCGAATTCCTCAAGATGGAGGAAGAGGGG
TgERF1-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGGCGACGGAGGAAGATGG
TgERF1-SK-RP-EcoRI	GCTTGATATCGAATTCCTTATGCCCCGAATGTGGGACT
TgERF2-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGCTCCGGCGGGTAAATTG
TgERF2-SK-RP-EcoRI	GCTTGATATCGAATTCCTTAATAAGTGCTGTCTTTTT
TgTGE4-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGGCTTCCGCTCTGCTGGC
TgTGE4-SK-RP-EcoRI	GCTTGATATCGAATTCCTCAAAGAGAAAACCCAACCT
TgMADS16-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGTTTCATGGTGCTAGGTGT
TgMADS16-SK-RP-EcoRI	GCTTGATATCGAATTCCTATCCCCAAATAGAAGATA
TgMYB3-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGCCATGGAGTGAGGAA
TgMYB3-SK-RP-EcoRI	GCTTGATATCGAATTCCTCACACCACTCTGATAAT

TgRAV1-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGGGATTGACTTTGGGTTT
TgRAV1-SK-RP-EcoRI	GCTTGATATCGAATTCTCAGCCGCTATTCGCTTTGT
TgRAV3-SK-FP-BamHI	TAGAACTAGT <u>GGATCC</u> ATGAAATTTTCAGGGCAAGAG
TgRAV3-SK-RP-EcoRI	GCTTGATATCGAATTCTCAATTCTGCCCTCCGCTA
BiFC:	
TgbHLH95-2YCN-FP-PacI	TACGAACGATAGT <u>TAAATTA</u> ATATGTCAACTTACAGAGGCT
TgbHLH95-2YCN-RP-AscI	TCCTCCACTAGTGGCGCGCCCTTCTTCATGACTA
TgbZIP44-2YCN-FP-PacI	TACGAACGATAGT <u>TAAATTA</u> ATATGGCTCCTCCATCAAAT
TgbZIP44-2YCN-RP-AscI	TCCTCCACTAGTGGCGCGCCCTGATAAATTTCTTGA
LCI:	
TgbHLH95-cLUC-FP-KpnI	TACGCGTCCCGGGGCGGT <u>ACC</u> ATGTCAACTTACAGAGGCT
TgbHLH95-cLUC-RP-SalI	ACGAAAGCTCTGCAGGT <u>CGACT</u> CATTCTTCATGACTAGTT
TgbZIP44-cLUC-FP-KpnI	TACGCGTCCCGGGGCGGT <u>ACC</u> ATGGCTCCTCCATCAAAT
TgbZIP44-cLUC-RP-SalI	ACGAAAGCTCTGCAGGT <u>CGACT</u> CTACTGATAAATTTCTTGA
TgbHLH95-nLUC-FP-KpnI	ACGGGGGACGAGCTC <u>GGTACC</u> ATGTCAACTTACAGAGGCT
TgbHLH95-nLUC-RP-SalI	CGCGTACGAGATCTGGT <u>CGACT</u> TCTTCATGACTAGTTA
TgbZIP44-nLUC-FP-KpnI	ACGGGGGACGAGCTC <u>GGTACC</u> ATGGCTCCTCCATCAAAT
TgbZIP44-nLUC-RP-SalI	CGCGTACGAGATCTGGT <u>CGACT</u> CTGATAAATTTCTTGA
Co-IP:	
TgbHLH95-Flag-FP-BamHI	GTACCCGGGGATCCATGTCAACTTACAGAGGC
TgbHLH95-Flag-RP-HindIII	GTGACTAGTA <u>AAGCTT</u> TCTTCATGACTAGTTA
TgbZIP44-GFP2-FP-KpnI	GTACAAGGGT <u>ACC</u> ATGGCTCCTCCATCAAAT
TgbZIP44-GFP2-RP-BamHI	TTCATCTAGAGGATCCCTGATAAATTTCTTGA
GST pull-down:	
TgbHLH95-pGEX-FP-EcoRI	CCTGGGATCCCCGGA <u>ATTC</u> ATGTCAACTTACAGAGGC
TgbHLH95-pGEX-RP-NotI	AGTCACGATGCGGCGCTTCTTCATGACTAGTTA
TgbZIP44-pET32a-FP-NcoI	GACAAGGCCATGGATGGCTCCTCCATCAAAT
TgbZIP44-pET32a-RP-XhoI	GGTGGTGCTCGAGCTGATAAATTTCTTGA
EMSA:	
Probe-FP-biotin	ATCATCCCATTTCGTATCCAACGTGAGACATACTCGGACCA
Probe-RP-biotin	TGGTCCGAGTATGTCTCACGTTGGATACGAATGGGATGAT
Mutant-Probe-FP-biotin	ATCATCCCATTTCGTATCCAAAAAGAGACATACTCGGACCA
Mutant-Probe-RP-biotin	TGGTCCGAGTATGTCTCTTTTGGATACGAATGGGATGAT

Supplemental Table S5. The full-length sequences of *TFs* and *TgGPPS*.

>TgGPPS

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