

Supplementary Table S1 List of few well-known secondary metabolite biosynthesis pathways and associated unigenes identified from the transcriptome of *Pistacia weinmannifolia*

No.	KO number	Description of entry enzyme	Representative gene ID
<i>Metabolism of terpenoids and polyketides</i>			
00902 Monoterpenoid biosynthesis			
1	K15095	(+)-neomenthol dehydrogenase [EC:1.1.1.208]	CYM04337 (3)
2	K15096	(R)-limonene synthase [EC:4.2.3.20]	CYM16691 (1)
3	K20618	CYP76A26; nepetalactol monooxygenase [EC:1.14.14.161]	CYM07294 (1)
00906 Carotenoid biosynthesis			
1	K00514	ZDS, crtQ; zeta-carotene desaturase [EC:1.3.5.6]	CYM01659 (1)
2	K02291	crtB; 15-cis-phytoene synthase [EC:2.5.1.32]	CYM07106 (1)
3	K02293	PDS, crtP; 15-cis-phytoene desaturase [EC:1.3.5.5]	CYM09154 (1)
4	K06443	lycB, crtL1, crtY; lycopene beta-cyclase [EC:5.5.1.19]	CYM14878 (1)
5	K06444	lycE, crtL2; lycopene epsilon-cyclase [EC:5.5.1.18]	CYM05364 (1)
6	K09835	crtISO, crtH; polycopene isomerase [EC:5.2.1.13]	CYM12975 (1)
7	K09837	LUT1, CYP97C1; carotenoid epsilon hydroxylase [EC:1.14.14.158]	CYM01360 (1)
8	K09838	ZEP, ABA1; zeaxanthin epoxidase [EC:1.14.15.21]	CYM16372 (1)
9	K09839	VDE, NPQ1; violaxanthin de-epoxidase [EC:1.23.5.1]	CYM12093 (1)
10	K09840	NCED; 9-cis-epoxycarotenoid dioxygenase [EC:1.13.11.51]	CYM03673 (3)
11	K09841	ABA2; xanthoxin dehydrogenase [EC:1.1.1.288]	CYM14125 (1)
12	K09843	CYP707A; (+)-abscisic acid 8'-hydroxylase [EC:1.14.14.137]	CYM00968 (3)
13	K14595	AOG; abscisate beta-glucosyltransferase [EC:2.4.1.263]	CYM16263 (1)
14	K15744	Z-ISO; zeta-carotene isomerase [EC:5.2.1.12]	CYM03775 (1)
15	K15746	crtZ; beta-carotene 3-hydroxylase [EC:1.14.15.24]	CYM13904 (1)
16	K15747	LUT5, CYP97A3; beta-ring hydroxylase [EC:1.14.-.-]	CYM18691 (1)
00904 Diterpenoid biosynthesis			
1	K04122	GA3, CYP701; ent-kaurene oxidase [EC:1.14.14.86]	CYM17555 (1)
2	K04123	KAO; ent-kaurenoic acid monooxygenase [EC:1.14.14.107]	CYM14941 (1)
3	K04125	GA2ox; gibberellin 2-beta-dioxygenase [EC:1.14.11.13]	CYM11230 (4)
4	K05282	GA20ox; gibberellin-44 dioxygenase [EC:1.14.11.12]	CYM18507 (1)
00909 Sesquiterpenoid and triterpenoid biosynthesis			
1	K00511	SQLE, ERG1; squalene monooxygenase [EC:1.14.14.17]	CYM01183 (1)
2	K00801	FDFT1; farnesyl-diphosphate farnesyltransferase [EC:2.5.1.21]	CYM01386 (1)
3	K14175	NES1; (3S,6E)-nerolidol synthase [EC:4.2.3.48]	CYM13924 (1)
4	K15803	GERD; (-)-germacrene D synthase [EC:4.2.3.75]	CYM00030 (4)
5	K15813	LUP4; beta-amyrin synthase [EC:5.4.99.39]	CYM00574 (2)
6	K15891	FLDH; NAD+-dependent farnesol dehydrogenase [EC:1.1.1.354]	CYM18064 (1)
7	K22064	CJFS; beta-farnesene synthase [EC:4.2.3.47]	CYM06988 (1)
<i>Biosynthesis of other secondary metabolites</i>			
00941 Flavonoid biosynthesis			
1	K00475	F3H; naringenin 3-dioxygenase [EC:1.14.11.9]	CYM01197 (1)
2	K00487	CYP73A; trans-cinnamate 4-monooxygenase [EC:1.14.14.91]	CYM07919 (1)
3	K00588	Caffeoyl-CoA O-methyltransferase [EC:2.1.1.104]	CYM01855 (2)
4	K00660	CHS; chalcone synthase [EC:2.3.1.74]	CYM02945 (3)
5	K01859	Chalcone isomerase [EC:5.5.1.6]	CYM10653 (2)
6	K05277	ANS; anthocyanidin synthase [EC:1.14.20.4]	CYM03902 (1)

Supplementary Table S1 List of few well-known secondary metabolite biosynthesis pathways and associated unigenes identified from the transcriptome of *Pistacia weinmannifolia* (continued)

No.	KO number	Description of entry enzyme	Representative gene ID
7	K05278	FLS; flavonol synthase [EC:1.14.20.6]	CYM10124 (2)
8	K05280	CYP75B1; flavonoid 3'-monooxygenase [EC:1.14.14.82]	CYM02025 (1)
9	K08243	CHR; chalcone reductase	CYM01109 (2)
10	K08695	ANR; anthocyanidin reductase [EC:1.3.1.77]	CYM15847 (1)
11	K09754	CYP98A, C3'H; 5-O-(4-coumaroyl)-D-quinic acid 3'-monooxygenase [EC:1.14.14.96]	CYM05132 (1)
12	K13065	HCT; shikimate O-hydroxycinnamoyltransferase [EC:2.3.1.133]	CYM01370 (5)
13	K13081	LAR; leucoanthocyanidin reductase [EC:1.17.1.3]	CYM08005 (1)
14	K13082	DFR; bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase [EC:1.1.1.219 1.1.1.234]	CYM16712 (1)
15	K13083	CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	CYM11875 (1)
00944 Flavone and flavonol biosynthesis			
1	K05280	CYP75B1; flavonoid 3'-monooxygenase [EC:1.14.14.82]	CYM02025 (1)
2	K13083	CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	CYM11875 (1)
3	K13269	Kaempferol 3-O-beta-D-galactosyltransferase [EC:2.4.1.234]	CYM02768 (1)
4	K22772	FG2; flavonol-3-O-glucoside L-rhamnosyltransferase [EC:2.4.1.159]	CYM16729 (1)
00950 Isoquinoline alkaloid biosynthesis			
1	K00276	AOC3, AOC2, tynA; primary-amine oxidase [EC:1.4.3.21]	CYM18640 (1)
2	K00811	ASP5; aspartate aminotransferase, chloroplastic [EC:2.6.1.1]	CYM13014 (1)
3	K00815	TAT; tyrosine aminotransferase [EC:2.6.1.5]	CYM13346 (1)
4	K01593	DDC, TDC; aromatic-L-amino-acid/L-tryptophan decarboxylase [EC:4.1.1.28]	CYM09227 (1)
5	K14454	GOT1; aspartate aminotransferase, cytoplasmic [EC:2.6.1.1]	CYM06660 (1)
6	K14455	GOT2; aspartate aminotransferase, mitochondrial [EC:2.6.1.1]	CYM14476 (1)
7	K15849	PAT, AAT; bifunctional aspartate aminotransferase and glutamate/aspartate	CYM05564 (1)
00940 Phenylpropanoid biosynthesis			
1	K00083	CAD; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	CYM06799 (4)
2	K00430	Peroxidase [EC:1.11.1.7]	CYM02003 (14)
3	K00487	CYP73A; trans-cinnamate 4-monooxygenase [EC:1.14.14.91]	CYM07919 (1)
4	K00588	Caffeoyl-CoA O-methyltransferase [EC:2.1.1.104]	CYM01855 (2)
5	K01904	4CL; 4-coumarate-CoA ligase [EC:6.2.1.12]	CYM00266 (8)
6	K09753	CCR; cinnamoyl-CoA reductase [EC:1.2.1.44]	CYM00461 (1)
7	K09754	CYP98A, C3'H; 5-O-(4-coumaroyl)-D-quinic acid 3'-monooxygenase [EC:1.14.14.96]	CYM05132 (1)
8	K09755	CYP84A, F5H; ferulate-5-hydroxylase [EC:1.14.-.-]	CYM06350 (1)
9	K10775	PAL; phenylalanine ammonia-lyase [EC:4.3.1.24]	CYM01401 (4)
10	K12355	REF1; coniferyl-aldehyde dehydrogenase [EC:1.2.1.68]	CYM16572 (1)
11	K13065	HCT; shikimate O-hydroxycinnamoyltransferase [EC:2.3.1.133]	CYM01370 (5)
12	K13066	COMT; caffeic acid 3-O-methyltransferase / acetylserotonin O-methyltransferase [EC:2.1.1.68 2.1.1.4]	CYM04212 (3)
13	K18368	CSE; caffeoylshikimate esterase [EC:3.1.1.-]	CYM01325 (3)
14	K22395	K22395; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	CYM14440 (1)

*Numbers in parenthesis indicate the number of homologous unigenes identified from *Pistacia weinmannifolia* transcriptome. KO, Kyoto Encyclopedia of Genes and Genomes Orthology.

Supplementary Table S2 Identification of repetitive sequences from the transcriptome of *Pistacia weinmannifolia* (17,080,830 bp)

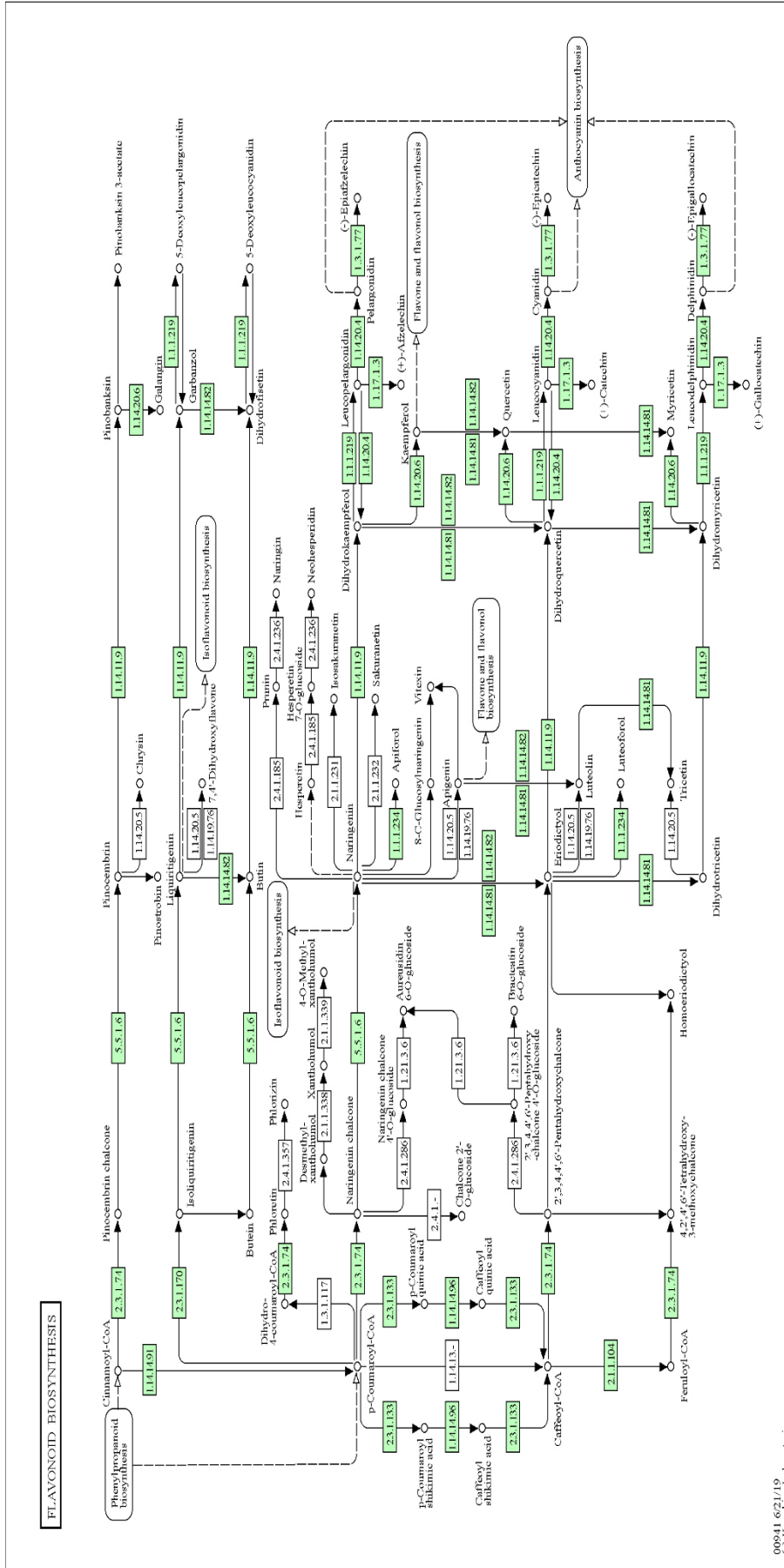
Type of repeat	Number of elements	Sequence occupied (bp)	Percentage of sequence (%)
Retroelements	16	1,067	0.01
SINEs	1	69	0.00
LINEs:	13	766	0.00
LTR elements:	2	222	0.00
DNA transposons	9	561	0.00
hobo-Activator:	6	348	0.00
Tc1-IS630-Pogo:	3	213	0.00
Total interspersed repeats:	50	1,628	0.01
Small RNA:	2	545	0.00
Simple repeats:	2,618	114,244	0.67
Low complexity:	592	31,890	0.19
Total bases masked		148,307	0.87

SINEs, short interspersed nuclear elements; LINEs, long interspersed nuclear elements; LTR, long terminal repeat.

Supplementary Table S3 Distribution and comparison of SSRs from unigenes of *Pistacia chinensis* and *Pistacia weinmannifolia* based on repeat motifs

Motifs	Number of motif repeats (Pistacia chinensis/Pistacia weinmannifolia)												Sum	SSRs per 1.0 Mb
	4	5	6	7	8	9	10	11	≥ 12					
A/T	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	29/35	29/35	1.8/2
AC/GT	0/0	0/0	4/4	2/2	1/0	1/1	1/1	0/0	0/0	0/0	0/0	9/8	9/8	0.6/0.5
AG/CT	0/0	0/0	53/39	16/11	12/16	7/12	12/12	10/6	13/15	13/15	10/6	123/111	123/111	7.6/6.5
AT/AT	0/0	0/0	3/7	2/2	2/0	1/2	0/0	1/0	1/0	1/0	1/0	10/11	10/11	0.6/0.6
AAC/GTT	130/132	49/58	21/18	8/4	5/6	1/2	0/0	0/0	1/0	1/0	0/0	215/220	215/220	13.3/12.9
AAG/CTT	480/476	130/113	41/56	27/26	21/19	0/1	4/2	0/3	1/3	1/3	0/0	704/699	704/699	43.5/40.9
AAT/ATT	46/54	12/18	11/5	3/1	3/1	0/0	0/1	1/1	0/0	0/0	0/0	76/81	76/81	4.7/4.7
ACC/GGT	221/211	94/77	26/30	19/17	5/6	1/1	0/2	0/0	3/2	3/2	0/0	369/346	369/346	22.8/20.3
ACG/CGT	37/35	13/11	7/3	3/3	0/0	0/0	0/0	0/0	0/0	0/0	0/0	60/52	60/52	3.7/3
ACT/AGT	20/18	5/8	0/2	0/1	3/1	0/0	0/0	0/0	0/0	0/0	0/0	28/30	28/30	1.7/1.8
AGC/GCT	172/169	41/42	16/12	3/5	1/2	0/0	0/0	0/0	0/0	0/0	0/0	233/230	233/230	14.4/13.5
AGG/CCT	137/127	39/45	18/21	13/9	5/2	1/0	1/1	0/0	0/0	0/0	0/0	214/205	214/205	13.2/12
ATC/GAT	272/279	62/75	23/29	20/12	9/13	1/1	2/2	0/1	0/0	0/0	0/0	389/412	389/412	24/24.1
CCG/CGG	44/43	10/10	1/4	0/2	0/0	0/0	0/0	0/0	0/0	0/0	0/0	55/59	55/59	3.4/3.5
AAAC/GTTT	1/1	0/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	1/2	1/2	0.1/0.1
AAAG/CTTT	7/3	1/3	2/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	10/7	10/7	0.6/0.4
AAGC/CTTG	1/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	1/0	1/0	0.1/0
AAGG/CCTT	1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	1/1	1/1	0.1/0.1
AATC/ATTG	0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	1/0	1/0	0.1/0
ACAG/CTGT	0	0/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/1	0/1	0.0/0.1
ACCG/CGGT	0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	1/0	1/0	0.1/0
ACTC/AGTG	1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	3/1	3/1	0.2/0.1
AGCG/CGCT	0	0/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/1	0/1	0.0/0.1
≥ penta-	85/66	6/7	2/10	1/1	0/2	1/1	0/0	2/0	0/0	0/0	0/0	97/87	97/87	6/5.1
Sum	1,659/1,616	462/470	228/241	117/96	67/68	14/21	20/21	14/11	48/55	2,629/2,599	162.5/152.2			

SSR, simple sequence repeat.



Supplementary Fig. S1 Flavonoid biosynthesis pathway reconstructed based on unigenes of *Pistacia weinmannifolia* associated with flavonoid biosynthesis. The map was drawn using Kyoto Encyclopedia of Genes and Genomes pathway mapper. Unigenes used for map reconstruction included caffeoyl-CoA O-methyltransferase [EC:2.1.1.104], chalcone synthase [EC:2.3.1.74], chalcone isomerase (E5.5.1.6) [EC:5.5.1.6], anthocyanidin synthase [EC:1.14.20.4], flavonol synthase [EC:1.14.20.6], flavonoid 3'-monooxygenase [EC:1.14.14.82], chalcone reductase, anthocyanidin reductase [EC:1.3.1.77], 5-O-(4-coumaroyl)-D-quinic acid 3'-monooxygenase [EC:1.14.14.96], shikimate O-hydroxycinnamoyltransferase [EC:2.3.1.133], leucoanthocyanidin reductase [EC:1.1.1.3], bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase [EC:1.1.1.219], and flavonoid 3',5'-hydroxylase [EC:1.14.14.81]

Supplementary Data List of unigenes associated with plant resin (Mastic) biosynthesis

>CYM02514

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>CYM15186

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Supplementary Data List of unigenes associated with plant resin (Mastic) biosynthesis (continued)

>CYM00763

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