Supplementary Information

The domain composition of sequences from *Laurencia dendroidea* that were annotated as terpene synthases and presented in Table 2 of the main manuscript were obtained through search for conserved domains using the NCBI Conserved Domain Database (CDD, [1]) and compared with the domain composition of corresponding sequences available in the SwissProt/UniProt and PlantCycDB databases. Analyzing the tables and figures below, we reinforce the Blast annotations presented in Table 2 of the main manuscript text, although biochemical and gene cloning approaches are necessary to prove these *in silico* identifications. For two of the 21 terpene synthase sequences from *Laurencia* (identified as nerolidol synthase and (+)-delta-cadinene synthase), we were not able to identify conserved domains, possibly because they were partial sequences. In the case of alpha-bisabolene synthase, we provide the domain composition of a reference sequence and the alignment of the sequence from *L. dendroidea* with this reference, showing a high similarity between them.

Table S1. List of domain hits for a putative (3*R*)-linalool synthase gene from *L. dendroidea*.

Name	Accession	Description	Interval	E-Value
rad1	TIGR00596	DNA repair protein (rad1); All proteins in this family for which functions are known are ...	1–51	1.04e-15

Figure S1. Conserved domains detected in a putative (3*R*)-linalool synthase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S2. List of domain hits for the (3R)-linalool synthase gene from *Zea mays mays* (GDQC-116173-MONOMER—PlantCycDB).

Name	Accession	Description	Interval	E-Value
Terpene_cyclase_plant_C1	cd00684	Plant Terpene Cyclases, Class 1; This CD includes a diverse group of monomeric plant terpene ...	1377–1833	9.57e-107
ERCC4	pfam02732	ERCC4 domain; This domain is a family of nucleases. The family includes EME1 which is an ...	732–859	2.10e-28
rad1	TIGR00596	DNA repair protein (rad1); All proteins in this family for which functions are known are ...	88–933	0e+00

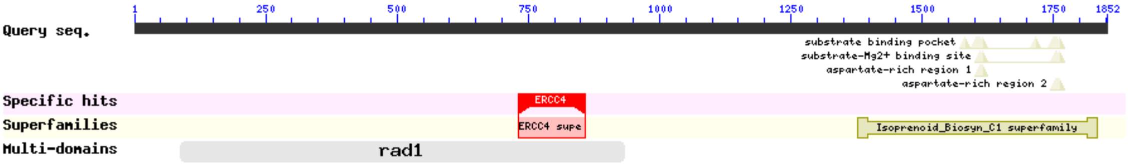

Figure S2. Conserved domains detected in the (3R)-linalool synthase gene from *Zea mays mays* (GDQC-116173-MONOMER—PlantCycDB) (edited from the NCBI CDD database, [1]).

Table S3. List of domain hits for a putative (+)-trans-carveol dehydrogenase gene from *L. dendroidea*.

Name	Accession	Description	Interval	E-value
CR_SDR_c	cd08936	Porcine peroxisomal carbonyl reductase like, classical (c) SDR; This subgroup contains porcine ...	17–272	1.05e-91
PRK05875	PRK05875	short chain dehydrogenase; Provisional	11–267	2.12e-39
adh_short_C2	pfam13561	Enoyl-(Acyl carrier protein) reductase;	22–268	1.19e-35
PLN02730	PLN02730	enoyl-[acyl-carrier-protein] reductase	85–262	3.56e-14
sepiapter_red	TIGR01500	sepiapterin reductase; This model describes sepiapterin reductase, a member of the short chain ...	17–201	5.40e-06
PKS_KR	smart00822	This enzymatic domain is part of bacterial polyketide synthases; It catalyses the first step ...	19–167	2.88e-04
fabG	PRK07231	3-ketoacyl-(acyl-carrier-protein) reductase; Provisional	17–267	2.43e-77
FabG	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) ...	14–267	4.59e-61
3oxo_ACP_reduc	TIGR01830	3-oxoacyl-(acyl-carrier-protein) reductase; This model represents 3-oxoacyl-[ACP] reductase, ...	18–267	3.80e-55
adh_short	pfam00106	short chain dehydrogenase; This family contains a wide variety of dehydrogenases.	17–185	4.24e-25
PLN02253	PLN02253	xanthoxin dehydrogenase	10–267	3.65e-18
Se_ygfK	TIGR03315	putative selenate reductase, YgfK subunit; Members of this protein family are YgfK, predicted ...	6–63	5.85e-03

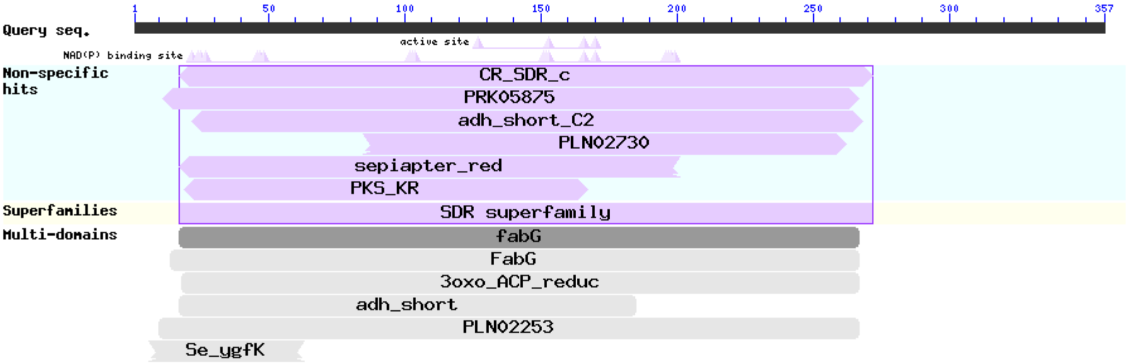

Figure S3. Conserved domains detected in a putative (+)-trans-carveol dehydrogenase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S4. List of domain hits for the (+)-trans-carveol dehydrogenase gene from *Mentha piperita* (sp|Q5C9I9|ISPD_MENPI).

Name	**Accession**	**Description**	**Interval**	**E-Value**
secoisolariciresinol-DH_like_SDR_c	cd05326	secoisolariciresinol dehydrogenase (secoisolariciresinol-DH)-like, classical (c) SDRs;	6–255	4.43e-70
PRK06947	PRK06947	glucose-1-dehydrogenase; Provisional	10–254	1.34e-28
adh_short_C2	pfam13561	Enoyl-(Acyl carrier protein) reductase;	16–255	1.75e-19
PLN00015	PLN00015	protochlorophyllide reductase	13–102	3.87e-10
PKS_KR	smart00822	This enzymatic domain is part of bacterial polyketide synthases; It catalyses the first step ...	10–124	5.58e-09
LPOR	TIGR01289	light-dependent protochlorophyllide reductase; This model represents the light-dependent,	12–101	3.14e-06
PLN02253	PLN02253	xanthoxin dehydrogenase	3–257	2.86e-63
PRK08324	PRK08324	short chain dehydrogenase; Validated	1–255	4.79e-61
FabG	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) ...	6–255	1.64e-50
RhaD_aldol-ADH	TIGR02632	rhamnulose-1-phosphate aldolase/alcohol dehydrogenase;	1–255	3.70e-45
adh_short	pfam00106	short chain dehydrogenase; This family contains a wide variety of dehydrogenases.	10–178	4.18e-20

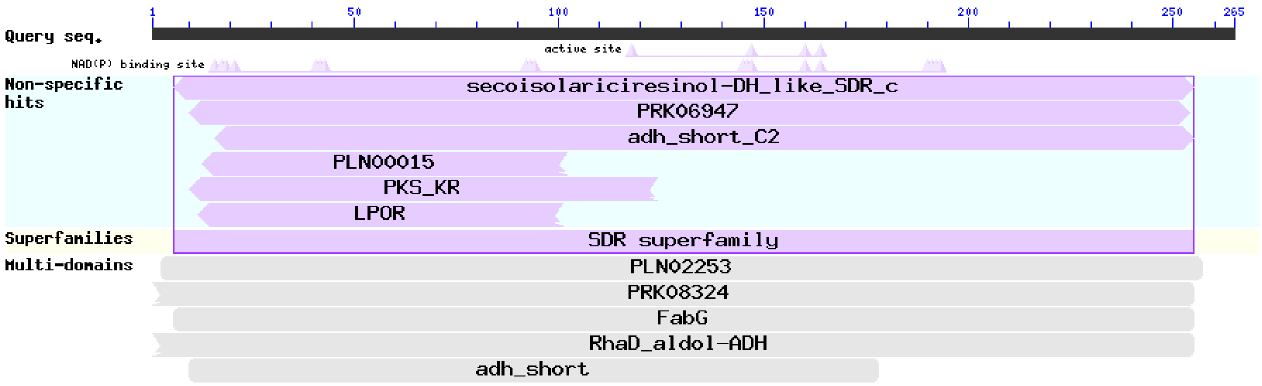

Figure S4. Conserved domains detected in the (+)-trans-carveol dehydrogenase gene from *Mentha piperita* (sp|Q5C9I9|ISPD_MENPI) (edited from the NCBI CDD database, [1]).

Table S5. List of domain hits for a putative (+)-pulegone reductase gene from *L. dendroidea*.

Name	Accession	Description	Interval	E-Value
PGDH	cd05288	Prostaglandin dehydrogenases; Prostaglandins and related eicosanoids are metabolized by the ...	1–293	9.21e-128
leukotriene_B4_DH_like	cd08294	13-PGR is a bifunctional enzyme with delta-13 15-prostaglandin reductase and leukotriene B4 12 ...	14–294	1.49e-74
double_bond_reductase_like	cd08295	Arabidopsis alkenal double bond reductase and leukotriene B4 12-hydroxydehydrogenase; This ...	1–295	7.02e-73
PTGR2	cd08293	Prostaglandin reductase; Prostaglandins and related eicosanoids are metabolized by the ...	1–294	3.04e-65
Mgc45594_like	cd08250	Mgc45594 gene product and other MDR family members; Includes Human Mgc45594 gene product of ...	28–294	1.18e-48
QOR1	cd08241	Quinone oxidoreductase (QOR); QOR catalyzes the conversion of a quinone + NAD(P)H to a ...	29–294	1.89e-39
p53_inducible_oxidoreductase	cd05276	PIG3 p53-inducible quinone oxidoreductase; PIG3 p53-inducible quinone oxidoreductase, a medium ...	53–293	9.65e-29
zeta_crystallin	cd08253	Zeta-crystallin with NADP-dependent quinone reductase activity (QOR); Zeta-crystallin is a eye ...	65–295	6.42e-27
MDR_like_2	cd05289	alcohol dehydrogenase and quinone reductase-like medium chain degydrogenases/reductases; ...	45–293	5.28e-26
Zn_ADH_like1	cd08266	Alcohol dehydrogenases of the MDR family; This group contains proteins related to the ...	85–295	9.64e-24

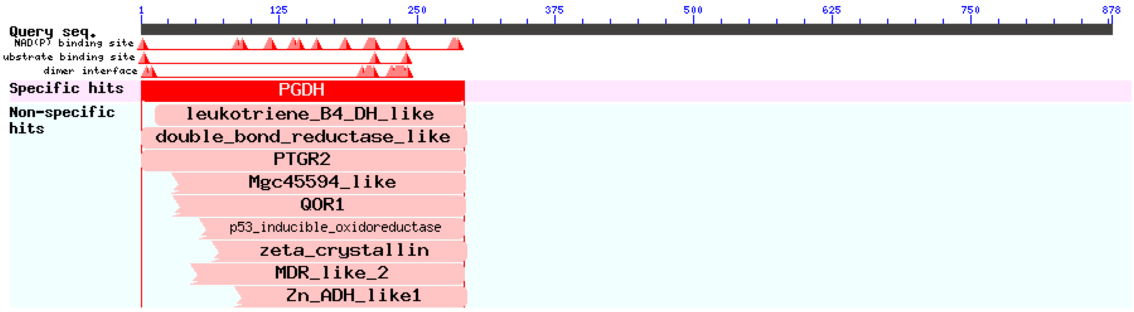

Figure S5. Conserved domains detected in a putative (+)-pulegone reductase gene from *L. dendroidea* (edited from the NCBI CDD database [1]).

Table S6. List of domain hits for the (+)-pulegone reductase gene from *Mentha piperita* (sp|Q6WAU0|PULR_MENPI).

Name	**Accession**	**Description**	**Interval**	**E-Value**
double_bond_reductase_like	cd08295	Arabidopsis alkenal double bond reductase and leukotriene B4 12-hydroxydehydrogenase; This ...	2–339	0e+00
PGDH	cd05288	Prostaglandin dehydrogenases; Prostaglandins and related eicosanoids are metabolized by the ...	3–337	1.06e-144
leukotriene_B4_DH_like	cd08294	13-PGR is a bifunctional enzyme with delta-13 15-prostaglandin reductase and leukotriene B4 12 ...	2–339	1.23e-104
PTGR2	cd08293	Prostaglandin reductase; Prostaglandins and related eicosanoids are metabolized by the ...	3–339	3.91e-65
Mgc45594_like	cd08250	Mgc45594 gene product and other MDR family members; Includes Human Mgc45594 gene product of ...	137–337	7.60e-47
zeta_crystallin	cd08253	Zeta-crystallin with NADP-dependent quinone reductase activity (QOR); Zeta-crystallin is a eye ...	29–283	3.04e-28
MDR	cd05188	Medium chain reductase/dehydrogenase (MDR)/zinc-dependent alcohol dehydrogenase-like family; ...	94–297	9.69e-27
p53_inducible_oxidoreductase	cd05276	PIG3 p53-inducible quinone oxidoreductase; PIG3 p53-inducible quinone oxidoreductase, a medium ...	138–307	1.44e-25
MDR_like_2	cd05289	alcohol dehydrogenase and quinone reductase-like medium chain degydrogenases/reductases; ...	31–323	3.42e-25
ADH_zinc_N	pfam00107	Zinc-binding dehydrogenase;	16–298	3.91e-21

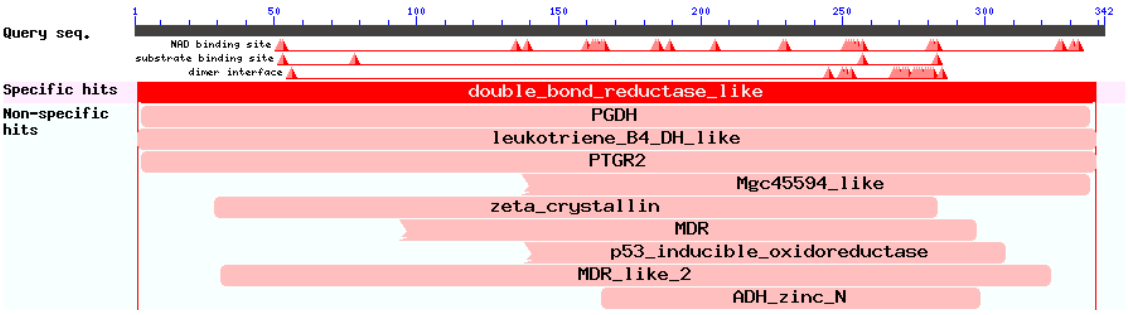

Figure S6. Conserved domains detected in the (+)-pulegone reductase gene from *Mentha piperita* (sp|Q6WAU0|PULR_MENPI) (edited from the NCBI CDD database, [1]).

Table S7. List of domain hits for a putative (−)-isopiperitenone reductase gene from *L. dendroidea*.

Name	Accession	Description	Interval	E-Value
17beta-HSD1_like_SDR_c	cd05356	17-beta-hydroxysteroid dehydrogenases (17beta-HSDs) types -1, -3, and -12, -like, classical (c) ...	34–146	3.56e-31
PRK08339	PRK08339	short chain dehydrogenase; Provisional	27–112	1.20e-09
sepiapter_red	TIGR01500	sepiapterin reductase; This model describes sepiapterin reductase, a member of the short chain ...	37–119	3.85e-06
DltE	COG0300	Short-chain dehydrogenases of various substrate specificities [General function prediction ...	32–146	7.97e-29
PLN02780	PLN02780	ketoreductase/oxidoreductase	14–146	7.50e-23
fabG	PRK07666	3-ketoacyl-(acyl-carrier-protein) reductase; Provisional	37–145	3.61e-17
23BDH	TIGR02415	acetoin reductases; One member of this family, as characterized in Klebsiella terrigena, is ...	37–145	3.62e-12
adh_short	pfam00106	short chain dehydrogenase; This family contains a wide variety of dehydrogenases.	36–145	1.50e-09

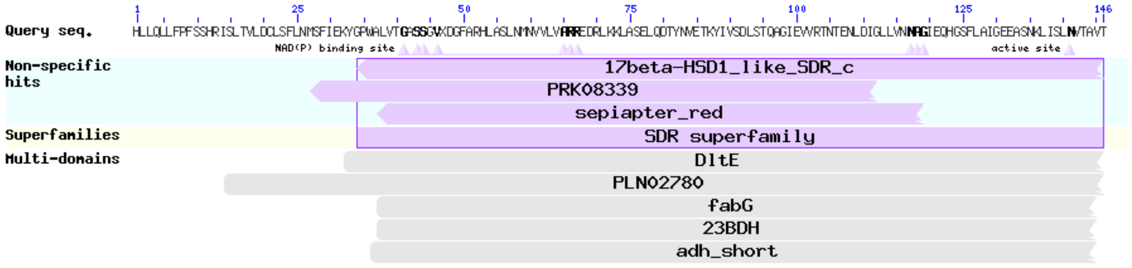

Figure S7. Conserved domains detected in a putative (−)-isopiperitenone reductase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S8. List of domain hits for the (−)-isopiperitenone reductase gene from *Mentha piperita* (sp|Q6WAU1|IPIPR_MENPI).

Name	Accession	Description	Interval	E-Value
carb_red_PTCR-like_SDR_c	cd05324	Porcine testicular carbonyl reductase (PTCR)-like, classical (c) SDRs; PTCR is a classical SDR ...	6–311	1.99e-74
PRK05854	PRK05854	short chain dehydrogenase; Provisional	6–96	4.90e-15
adh_short_C2	pfam13561	Enoyl-(Acyl carrier protein) reductase;	15–126	4.28e-11
PKS_KR	smart00822	This enzymatic domain is part of bacterial polyketide synthases; It catalyses the first step ...	9–96	8.02e-11
sepiapter_red	TIGR01500	sepiapterin reductase; This model describes sepiapterin reductase, a member of the short chain ...	7–120	1.78e-06

Table S8. *Cont.*

PLN00015	PLN00015	protochlorophyllide reductase	9–96	1.60e-03
PRK12939	PRK12939	short chain dehydrogenase; Provisional	6–299	2.99e-15
FabG	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) .	8–300	4.86e-27
adh_short	pfam00106	short chain dehydrogenase; This family contains a wide variety of dehydrogenases.	8–138	3.61e-19

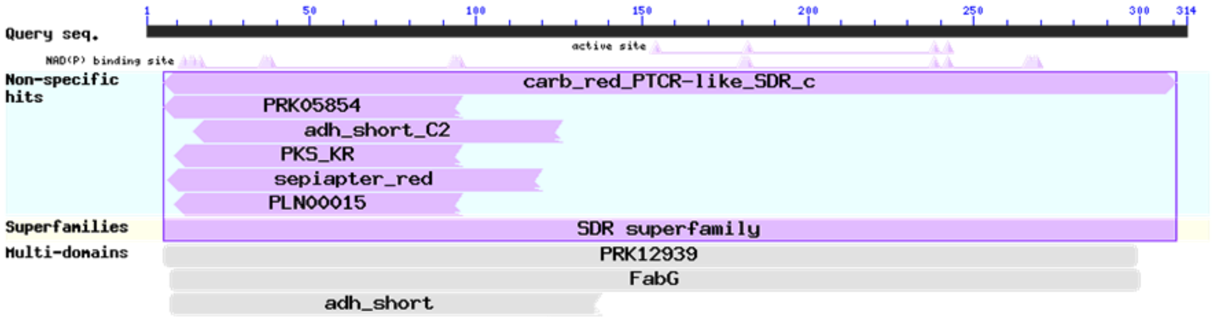

Figure S8. Conserved domains detected in the (−)-isopiperitenone reductase gene from *Mentha piperita* (sp|Q6WAU1|IPIPR_MENPI) (edited from the NCBI CDD database, [1]).

Table S9. List of domain hits for a putative secologanin synthase gene from *L. dendroidea*.

Name	Accession	Description	Interval	E-Value
p450	pfam00067	Cytochrome P450; Cytochrome P450s are haem-thiolate proteins involved in the oxidative	160–384	2.32e-29
CypX	COG2124	Cytochrome P450 [Secondary metabolites biosynthesis, transport, and catabolism]	13–378	2.81e-25
PLN02290	PLN02290	cytokinin trans-hydroxylase	170–351	8.00e-17
PLN02169	PLN02169	fatty acid (omega-1)-hydroxylase/midchain alkane hydroxylase	168–356	8.21e-17
PLN03195	PLN03195	fatty acid omega-hydroxylase; Provisional	167–378	9.71e-15
PLN02426	PLN02426	cytochrome P450, family 94, subfamily C protein	168–370	6.50e-14
PLN00168	PLN00168	Cytochrome P450; Provisional	160–356	7.30e-14
PLN02936	PLN02936	epsilon-ring hydroxylase	162–380	1.74e-13
PLN02687	PLN02687	flavonoid 3′-monooxygenase	159–344	6.33e-09
PLN02655	PLN02655	ent-kaurene oxidase	160–378	1.04e-07
PLN00110	PLN00110	flavonoid 3′,5′-hydroxylase (F3′5′H); Provisional	154–300	6.62e-07
PTZ00404	PTZ00404	cytochrome P450; Provisional	164–359	7.19e-07
PLN02183	PLN02183	ferulate 5-hydroxylase	160–298	1.08e-06
PLN03018	PLN03018	homomethionine *N*-hydroxylase	155–349	1.21e-06
PLN03112	PLN03112	cytochrome P450 family protein; Provisional	172–300	3.83e-06
PLN02971	PLN02971	tryptophan *N*-hydroxylase	157–357	5.06e-06
PLN02966	PLN02966	cytochrome P450 83A1	157–338	5.44e-06
PLN03234	PLN03234	cytochrome P450 83B1; Provisional	144–345	1.74e-05
PLN02394	PLN02394	trans-cinnamate 4-monooxygenase	178–380	2.89e-04
PLN02302	PLN02302	ent-kaurenoic acid oxidase	152–359	4.88e-04
PLN02774	PLN02774	brassinosteroid-6-oxidase	159–361	6.03e-03

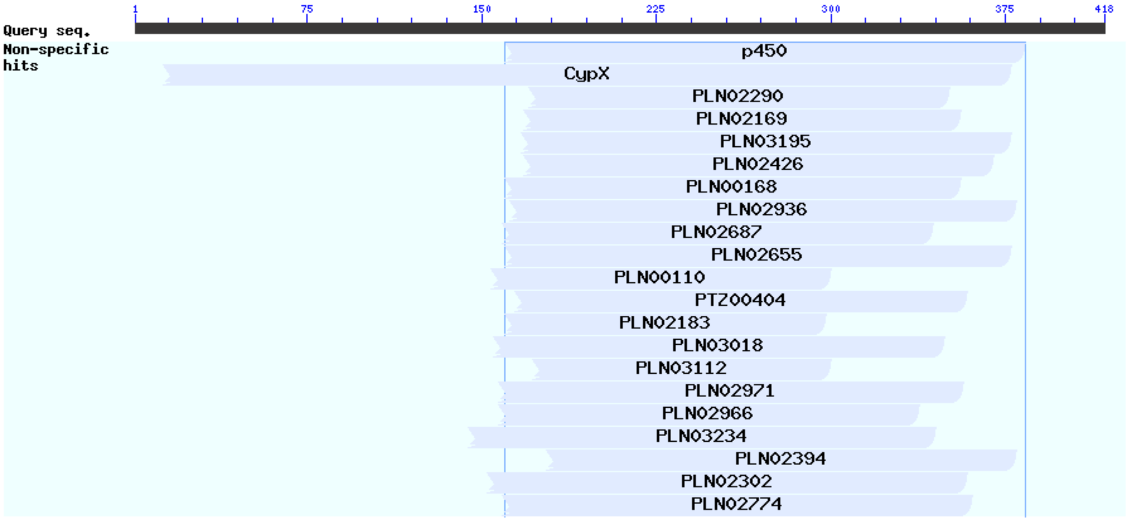

Figure S9. Conserved domains detected in a putative secologanin synthase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S10. List of domain hits for the secologanin synthase gene from *Catharanthus roseus* (sp|Q05047|C72A1_CATRO).

Name	Accession	Description	Interval	E-Value
PLN02290	PLN02290	cytokinin trans-hydroxylase	5–524	2.05e-129
p450	pfam00067	Cytochrome P450; Cytochrome P450s are haem-thiolate proteins involved in the oxidative ...	102–497	4.56e-82
CypX	COG2124	Cytochrome P450 [Secondary metabolites biosynthesis, transport, and catabolism]	114–521	3.87e-50
PLN02936	PLN02936	epsilon-ring hydroxylase	100–497	3.71e-41
PLN02687	PLN02687	flavonoid 3′-monooxygenase	190–496	2.09e-26
PLN02426	PLN02426	cytochrome P450, family 94, subfamily C protein	260–503	2.27e-26
PTZ00404	PTZ00404	cytochrome P450; Provisional	64–493	7.42e-24
PLN03195	PLN03195	fatty acid omega-hydroxylase; Provisional	110–497	8.36e-24
PLN02302	PLN02302	ent-kaurenoic acid oxidase	88–507	3.89e-23
PLN02183	PLN02183	ferulate 5-hydroxylase	208–495	8.15e-23
PLN03112	PLN03112	cytochrome P450 family protein; Provisional	93–497	1.07e-21
PLN02169	PLN02169	fatty acid (omega-1)-hydroxylase/midchain alkane hydroxylase	260–521	1.98e-21
PLN02655	PLN02655	ent-kaurene oxidase	228–491	2.30e-21
PLN02966	PLN02966	cytochrome P450 83A1	183–495	8.06e-19
PLN03234	PLN03234	cytochrome P450 83B1; Provisional	164–495	2.81e-18
PLN00168	PLN00168	Cytochrome P450; Provisional	314–497	3.95e-16
PLN02987	PLN02987	Cytochrome P450, family 90, subfamily A	223–493	2.87e-15
PLN02971	PLN02971	tryptophan *N*-hydroxylase	242–498	3.03e-15
PLN02394	PLN02394	trans-cinnamate 4-monooxygenase	332–491	1.33e-14
PLN00110	PLN00110	flavonoid 3′,5′-hydroxylase (F3′5′H); Provisional	247–491	6.65e-12
PLN02500	PLN02500	cytochrome P450 90B1	272–496	1.01e-11
PLN03018	PLN03018	homomethionine *N*-hydroxylase	150–522	3.32e-11
PLN02774	PLN02774	brassinosteroid-6-oxidase	107–494	4.36e-11

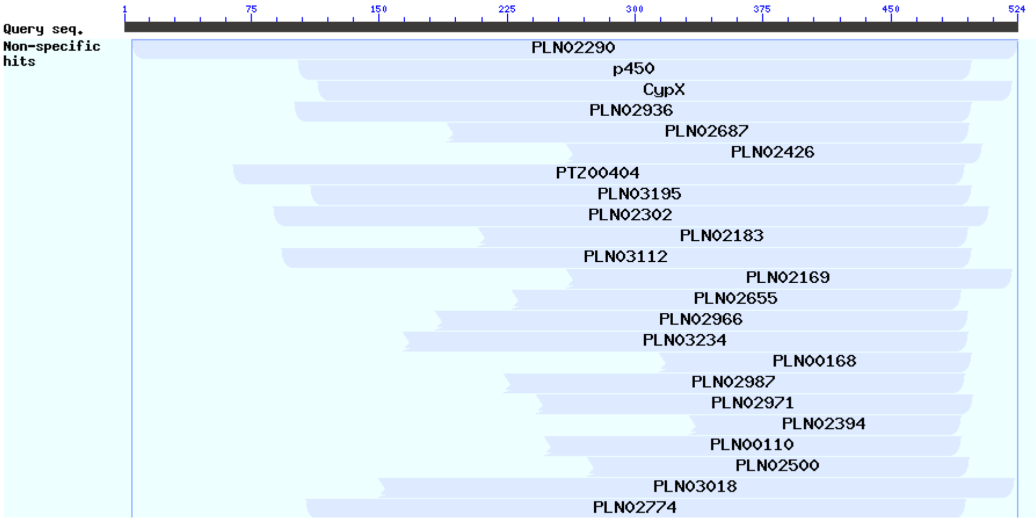

Figure S10. Conserved domains detected in the secologanin synthase gene from *Catharanthus roseus* (sp|Q05047|C72A1_CATRO) (edited from the NCBI CDD database, [1]).

Table S11. List of domain hits for a putative farnesyl-diphosphate farnesyltransferase gene from *L. dendroidea*.

Name	Accession	Description	Interval	E-Value
squal_synth	TIGR01559	farnesyl-diphosphate farnesyltransferase; This model describes farnesyl-diphosphate ...	139–411	1.00e-104
Trans_IPPS_HH	cd00683	Trans-Isoprenyl Diphosphate Synthases, head-to-head; These trans-Isoprenyl Diphosphate ...	165–364	2.49e-47
SQS_PSY	pfam00494	Squalene/phytoene synthase;	158–361	1.01e-37
ERG9	COG1562	Phytoene/squalene synthetase [Lipid metabolism]	180–370	2.86e-35
Trans_IPPS	cd00867	Trans-Isoprenyl Diphosphate Synthases; Trans-Isoprenyl Diphosphate Synthases (Trans_IPPS) of ...	179–286	1.13e-17
Isoprenoid_Biosyn_C1	cd00385	Isoprenoid Biosynthesis enzymes, Class 1; Superfamily of trans-isoprenyl diphosphate synthases ...	174–325	4.43e-17
HpnD	TIGR03465	squalene synthase HpnD; The genes of this family are often found in the same genetic locus ...	193–275	1.41e-08
PLN02632	PLN02632	phytoene synthase	185–275	4.93e-07

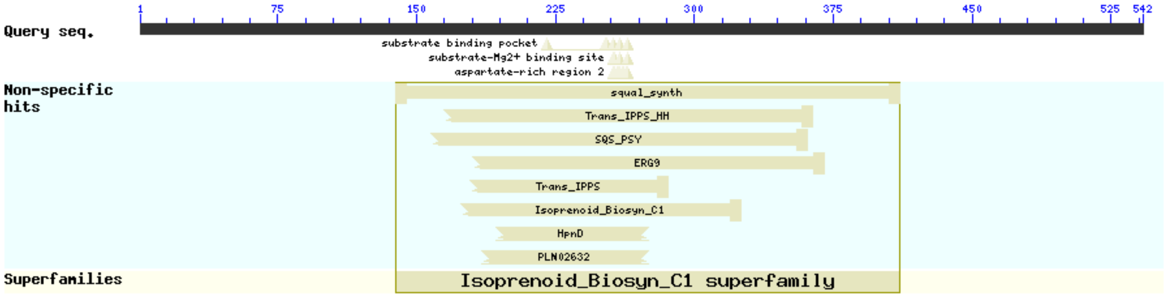

Figure S11. Conserved domains detected in a putative farnesyl-diphosphate farnesyltransferase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S12. List of domain hits for the farnesyl-diphosphate farnesyltransferase gene from *Scheffersomyces stipitis* (tr|A3LTQ5|A3LTQ5_PICST).

Name	**Accession**	**Description**	**Interval**	**E-value**
Trans_IPPS_HH	cd00683	Trans-Isoprenyl Diphosphate Synthases, head-to-head; These trans-Isoprenyl Diphosphate ...	40–333	2.34e-74
squal_synth	TIGR01559	farnesyl-diphosphate farnesyltransferase; This model describes farnesyl-diphosphate ...	39–381	0e+00
ERG9	COG1562	Phytoene/squalene synthetase [Lipid metabolism]	39–342	1.08e-57
SQS_PSY	pfam00494	Squalene/phytoene synthase;	48–329	5.08e-48
PLN02632	PLN02632	phytoene synthase	170–242	9.10e-07

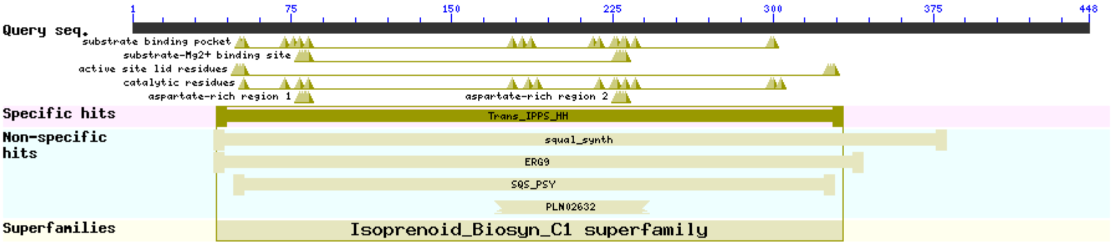

Figure S12. Conserved domains detected in the farnesyl-diphosphate farnesyltransferase gene from *Scheffersomyces stipitis* (tr|A3LTQ5|A3LTQ5_PICST) (edited from the NCBI CDD database, [1]).

Table S13. List of domain hits for a putative squalene monooxygenase gene from *L. dendroidea*.

Name	**Accession**	**Description**	**Interval**	**E-Value**
SE	pfam08491	Squalene epoxidase; This domain is found in squalene epoxidase (SE) and related proteins which ...	11–258	2.16e-101
PRK07608	PRK07608	ubiquinone biosynthesis hydroxylase family protein; Provisional	100–200	3.03e-04
COQ6	TIGR01989	ubiquinone biosynthesis monooxygenase COQ6; This model represents the monooxygenase ...	110–198	7.59e-03
PTZ00367	PTZ00367	squalene epoxidase; Provisional	15–275	2.05e-68
PLN02985	PLN02985	squalene monooxygenase	30–275	6.46e-56
UbiH	COG0654	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases [Coenzyme ...	16–205	7.72e-12
PRK07045	PRK07045	putative monooxygenase; Reviewed	114–185	1.84e-04

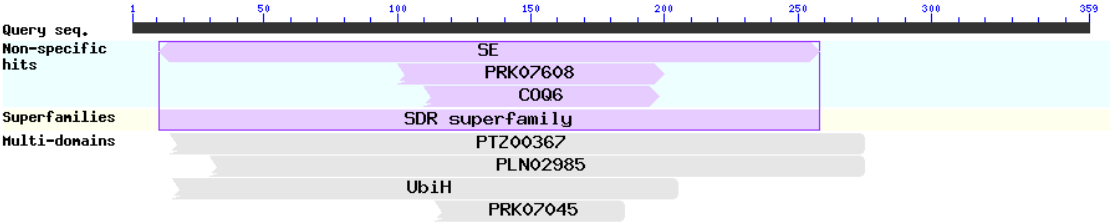

Figure S13. Conserved domains detected in a putative squalene monooxygenase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S14. List of domain hits for the squalene monooxygenase gene from *Arabidopsis thaliana* (sp|O65403|ERG13_ARATH).

Name	Accession	Description	Interval	E-value
SE	pfam08491	Squalene epoxidase; This domain is found in squalene epoxidase (SE) and related proteins which ...	195–472	2.27e-124
PRK08773	PRK08773	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase; Validated	40–364	3.79e-09
NAD_binding_8	pfam13450	NAD(P)-binding Rossmann-like domain;	48–74	5.95e-07
PRK12834	PRK12834	putative FAD-binding dehydrogenase; Reviewed	44–105	1.76e-06
THI4	COG1635	Ribulose 1,5-bisphosphate synthetase, converts PRPP to RuBP, flavoprotein [Carbohydrate ...	44–76	2.60e-05
PLN02661	PLN02661	Putative thiazole synthesis	44–74	3.21e-03
PTZ00383	PTZ00383	malate:quinone oxidoreductase; Provisional	25–74	5.01e-03
PLN02985	PLN02985	squalene monooxygenase	1–515	0e+00
PTZ00367	PTZ00367	squalene epoxidase; Provisional	6–499	3.11e-86
UbiH	COG0654	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases [Coenzyme ...	44–439	6.61e-36

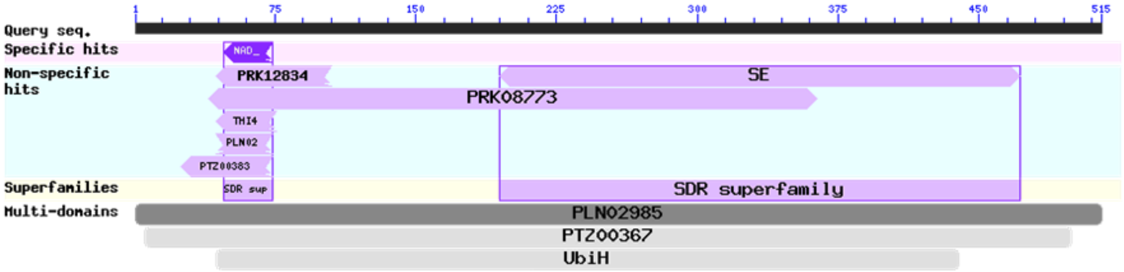

Figure S14. Conserved domains detected in the squalene monooxygenase gene from *Arabidopsis thaliana* (sp|O65403|ERG13_ARATH) (edited from the NCBI CDD database, [1]).

Table S15. List of domain hits for a putative squalene-hopene/tetraprenyl-beta-curcumene cyclase gene from *L. dendroidea*.

Name	Accession	Description	Interval	E-value
SQCY_1	cd02892	Squalene cyclase (SQCY) domain subgroup 1; found in class II terpene cyclases that have an ...	1–363	5.98e-143
SQCY	cd02889	Squalene cyclase (SQCY) domain; found in class II terpene cyclases that have an alpha 6— ...	24–363	8.74e-126
ISOPREN_C2_like	cd00688	This group contains class II terpene cyclases, protein prenyltransferases beta subunit, two ...	1–363	6.47e-39
Prenyltrans	pfam00432	Prenyltransferase and squalene oxidase repeat;	207–240	3.26e-04
SQCY_1	cd02892	Squalene cyclase (SQCY) domain subgroup 1; found in class II terpene cyclases that have an ...	207–274	4.34e-03
Prenyltrans_2	pfam13249	Prenyltransferase-like;	211–331	7.97e-09
Prenyltrans_2	pfam13249	Prenyltransferase-like;	134–275	5.74e-08

Table S15. *Cont.*

squalene_cyclas	TIGR01787	squalene/oxidosqualene cyclases; This family of enzymes catalyzes the cyclization of the ...	3–363	1.19e-117
PLN03012	PLN03012	Camelliol C synthase	3–363	1.41e-106
PLN02993	PLN02993	lupeol synthase	3–369	4.48e-97
osq_cycl	TIGR03463	2,3-oxidosqualene cyclase; This model identifies 2,3-oxidosqualene cyclases from Stigmatella ...	1–361	1.37e-91
SqhC	COG1657	Squalene cyclase [Lipid metabolism]	3–367	4.95e-56
hopene_cyclase	TIGR01507	squalene-hopene cyclase; SHC is an essential prokaryotic gene in hopanoid (triterpenoid) ...	5–369	9.84e-30
squa_tetra_cyc	TIGR04277	squalene--tetrahymanol cyclase; This enzyme, also called squalene--tetrahymanol cyclase, ...	126–363	2.76e-10
Prenyltrans_1	pfam13243	Prenyltransferase-like;	207–274	1.62e-08
Prenyltrans_2	pfam13249	Prenyltransferase-like;	83–224	1.02e-03
Prenyltrans_1	pfam13243	Prenyltransferase-like;	129–270	1.31e-03

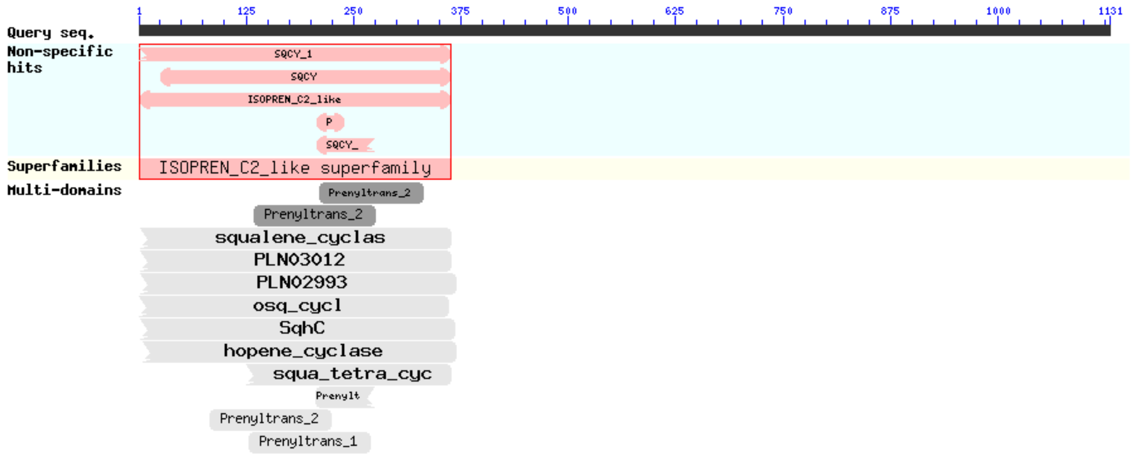

Figure S15. Conserved domains detected in a putative squalene-hopene/tetraprenyl-beta-curcumene cyclase gene from *L. dendroidea*, (edited from the NCBI CDD database, [1]).

Table S16. List of domain hits for the squalene-hopene/tetraprenyl-beta-curcumene cyclase gene from *Bradyrhizobium* sp. (tr|A4Z167 A4Z167_BRASO).

Name	**Accession**	**Description**	**Interval**	**E-Value**
SQCY_1	cd02892	Squalene cyclase (SQCY) domain subgroup 1; found in class II terpene cyclases that have an ...	26–677	0e+00
SQCY	cd02889	Squalene cyclase (SQCY) domain; found in class II terpene cyclases that have an alpha 6—...	332–676	8.79e-130
ISOPREN_C2_like	cd00688	This group contains class II terpene cyclases, protein prenyltransferases beta subunit, two ...	326–677	9.84e-39
SQCY	cd02889	Squalene cyclase (SQCY) domain; found in class II terpene cyclases that have an alpha 6— ...	26–375	3.52e-08

Table S16. *Cont.*

ISOPREN_C2_like	cd00688	This group contains class II terpene cyclases, protein prenyltransferases beta subunit, two ...	26–410	7.38e-08
SQCY	cd02889	Squalene cyclase (SQCY) domain; found in class II terpene cyclases that have an alpha 6— ...	18–97	1.79e-07
SQCY_1	cd02892	Squalene cyclase (SQCY) domain subgroup 1; found in class II terpene cyclases that have an ...	23–96	9.72e-07
ISOPREN_C2_like	cd00688	This group contains class II terpene cyclases, protein prenyltransferases beta subunit, two ...	17–132	4.24e-05
SQCY	cd02889	Squalene cyclase (SQCY) domain; found in class II terpene cyclases that have an alpha 6— ...	17–129	8.21e-05
SQCY_1	cd02892	Squalene cyclase (SQCY) domain subgroup 1; found in class II terpene cyclases that have an ...	17–129	1.16e-04
Prenyltrans	pfam00432	Prenyltransferase and squalene oxidase repeat;	493–535	3.52e-04
Prenyltrans	pfam00432	Prenyltransferase and squalene oxidase repeat;	541–583	5.36e-04
hopene_cyclase	TIGR01507	squalene-hopene cyclase; SHC is an essential prokaryotic gene in hopanoid (triterpenoid) ...	26–676	0e+00
squalene_cyclas	TIGR01787	squalene/oxidosqualene cyclases; This family of enzymes catalyzes the cyclization of the ...	25–676	1.99e-157
SqhC	COG1657	Squalene cyclase [Lipid metabolism]	110–683	9.16e-74
squa_tetra_cyc	TIGR04277	squalene—tetrahymanol cyclase; This enzyme, also called squalene—tetrahymanol cyclase, ...	77–681	6.52e-61
osq_cycl	TIGR03463	2,3-oxidosqualene cyclase; This model identifies 2,3-oxidosqualene cyclases from Stigmatella ...	33–676	1.09e-49
PLN02993	PLN02993	lupeol synthase	18–566	6.57e-33
PLN03012	PLN03012	Camelliol C synthase	24–675	9.97e-33
Prenyltrans_2	pfam13249	Prenyltransferase-like;	431–562	4.07e-16
Prenyltrans_1	pfam13243	Prenyltransferase-like;	495–614	2.09e-14

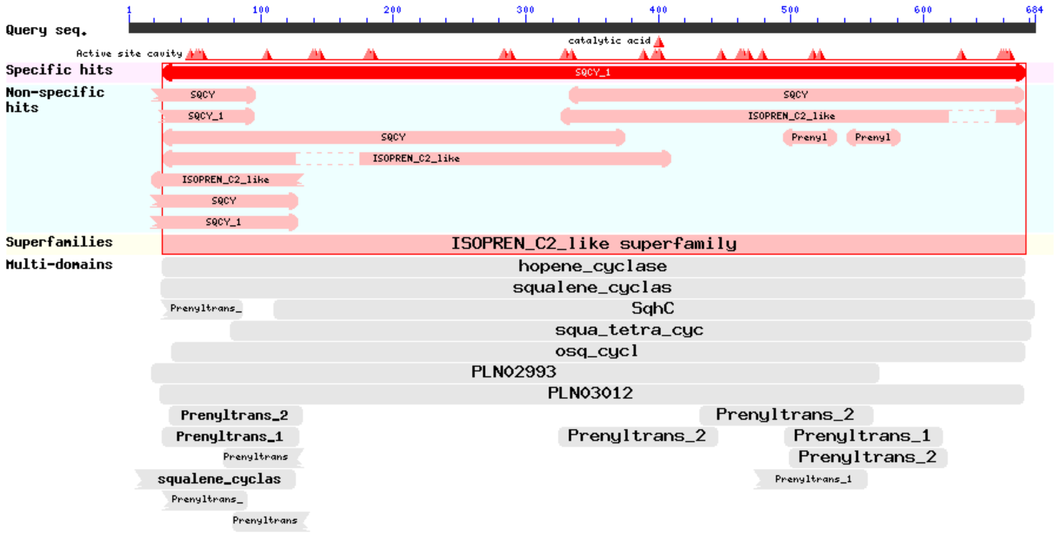

Figure S16. Conserved domains detected in the squalene-hopene/tetraprenyl-beta-curcumene cyclase gene from *Bradyrhizobium sp* (tr|A4Z167 A4Z167_BRASO) (edited from the NCBI CDD database, [1]).

Table S17. List of domain hits for a putative lupeol synthase 1 gene from *L. dendroidea*.

Name	Accession	Description	Interval	E-Value
SQCY_1	cd02892	Squalene cyclase (SQCY) domain subgroup 1; found in class II terpene cyclases that have an ...	1363	5.98e-143
SQCY	cd02889	Squalene cyclase (SQCY) domain; found in class II terpene cyclases that have an alpha 6 - ...	24–363	8.74e-126
ISOPREN_C2_like	cd00688	This group contains class II terpene cyclases, protein prenyltransferases beta subunit, two ...	1–363	6.47e-39
Prenyltrans	pfam00432	Prenyltransferase and squalene oxidase repeat;	207–240	3.26e-04
SQCY_1	cd02892	Squalene cyclase (SQCY) domain subgroup 1; found in class II terpene cyclases that have an ...	207–274	4.34e-03
Prenyltrans_2	pfam13249	Prenyltransferase-like;	211–331	7.97e-09
Prenyltrans_2	pfam13249	Prenyltransferase-like;	134–275	5.74e-08
squalene_cyclas	TIGR01787	squalene/oxidosqualene cyclases; This family of enzymes catalyzes the cyclization of the ...	3–363	1.19e-117
PLN03012	PLN03012	Camelliol C synthase	3–363	1.41e-106
PLN02993	PLN02993	lupeol synthase	3–369	4.48e-97
osq_cycl	TIGR03463	2,3-oxidosqualene cyclase; This model identifies 2,3-oxidosqualene cyclases from Stigmatella ...	1–361	1.37e-91
SqhC	COG1657	Squalene cyclase [Lipid metabolism]	3–367	4.95e-56

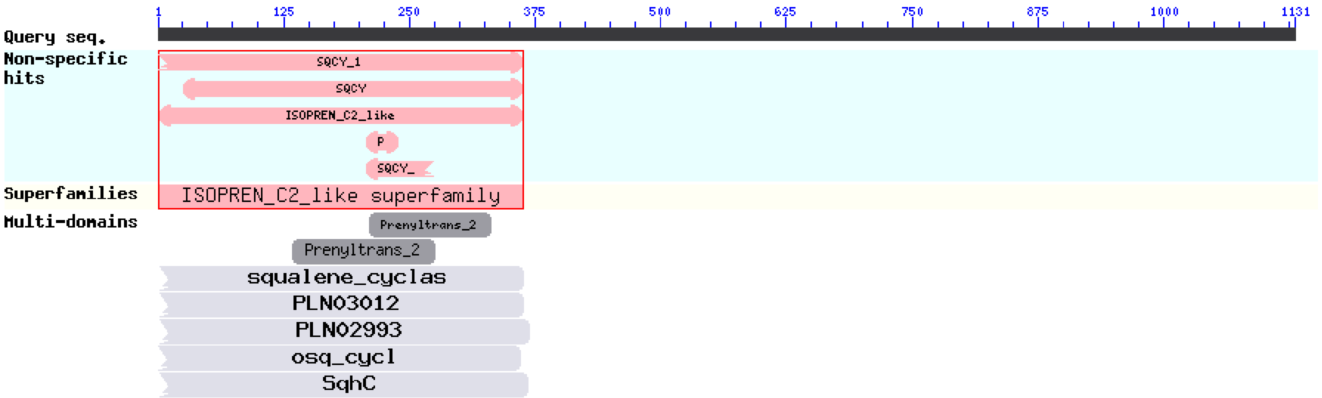

Figure S17. Conserved domains detected in a putative lupeol synthase 1 gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S18. List of domain hits for the lupeol synthase 1 gene from *Arabidopsis thaliana* (sp|Q9C5M3|LUP1_ARATH).

Name	Accession	Description	Interval	E-Value
SQCY_1	cd02892	Squalene cyclase (SQCY) domain subgroup 1; found in class II terpene cyclases that have an ...	99–749	0e+00
Prenyltrans	pfam00432	Prenyltransferase and squalene oxidase repeat;	589–629	1.24e-07
PLN02993	PLN02993	lupeol synthase	1–757	0e+00
squalene_cyclas	TIGR01787	squalene/oxidosqualene cyclases; This family of enzymes catalyzes the cyclization of the ...	98–751	0e+00
SqhC	COG1657	Squalene cyclase [Lipid metabolism]	186–749	3.47e-59
Prenyltrans_2	pfam13249	Prenyltransferase-like	593–717	5.37e-15

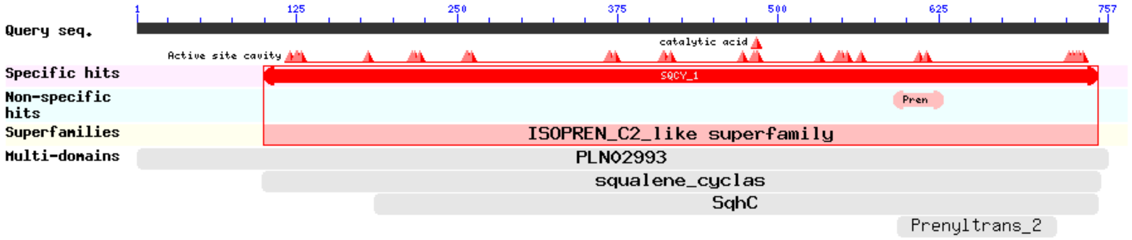

Figure S18. Conserved domains detected in the lupeol synthase 1 gene from *Arabidopsis thaliana* (sp|Q9C5M3|LUP1_ARATH) (edited from the NCBI CDD database, [1]).

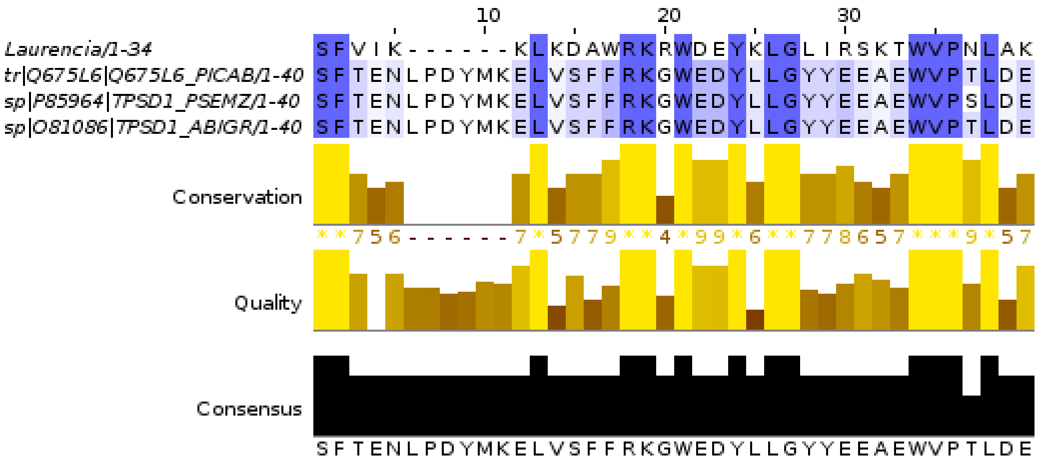

Figure S19. Multiple alignment analysis between a putative alpha-bisabolene synthase from *L. dendroidea* and alpha-bisabolene synthase reference sequences from *Picea abies*, *Pseudotsuga menziesii* and *Abies grandis* downloaded from Uniprot. The alignment was done using Muscle software [2] and visualized with Jalview [3].

Table S19. List of domain hits for the alpha-bisabolene synthase gene from *Picea abies* (tr|Q675L6 Q675L6_PICAB).

Name	**Accession**	**Description**	**Interval**	**E-Value**
Terpene_cyclase_plant_C1	cd00684	Plant Terpene Cyclases, Class 1; This CD includes a diverse group of monomeric plant terpene ...	271–804	0e+00
Terpene_synth_C	pfam03936	Terpene synthase family, metal binding domain; It has been suggested that this gene family be ...	481–751	1.09e-97
Terpene_cyclase_C1	cd00868	Terpene cyclases, Class 1; Terpene cyclases, Class 1 (C1) of the class 1 family of isoprenoid ...	495–775	3.12e-89
Terpene_synth	pfam01397	Terpene synthase, *N*-terminal domain; It has been suggested that this gene family be designated ...	246–439	6.37e-66
Isoprenoid_Biosyn_C1	cd00385	Isoprenoid Biosynthesis enzymes, Class 1; Superfamily of trans-isoprenyl diphosphate synthases ...	534–771	1.28e-29
PLN02150	PLN02150	terpene synthase/cyclase family protein	714–807	1.15e-07
ISOPREN_C2_like	cd00688	This group contains class II terpene cyclases, protein prenyltransferases beta subunit, two ...	73–156	3.94e-03
PLN02279	PLN02279	ent-kaur-16-ene synthase	60–807	5.06e-148
PLN02592	PLN02592	ent-copalyl diphosphate synthase	57–713	4.31e-165
Prenyltrans_1	pfam13243	Prenyltransferase-like;	99–157	9.07e-04
Prenyltrans_1	pfam13243	Prenyltransferase-like;	78-154	1.33e-03

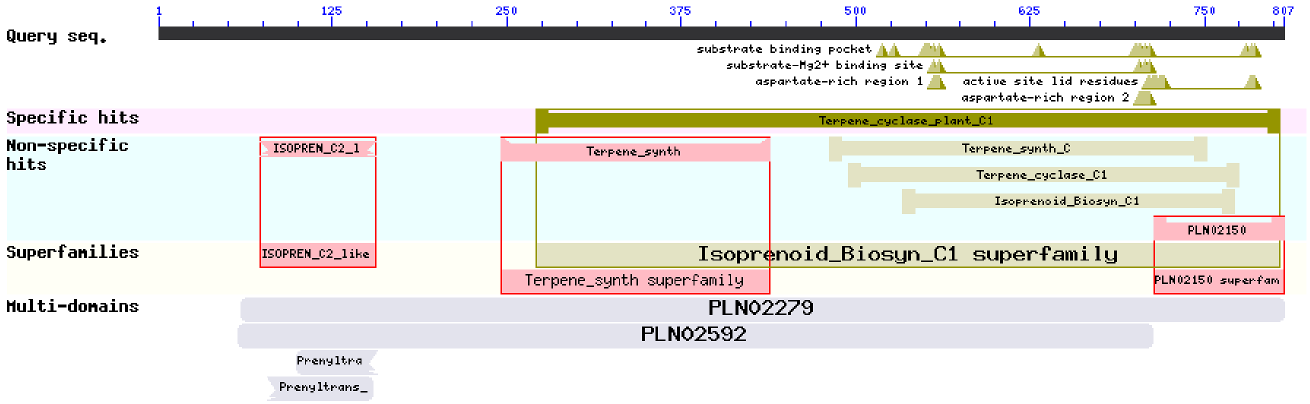

Figure S20. Conserved domains detected in the alpha-bisabolene synthase gene from *Picea abies* (tr|Q675L6 Q675L6_PICAB) (edited from the NCBI CDD database, [1]).

Table S20. List of domain hits for a putative germacrene-*A* synthase gene from *L. dendroidea*.

Name	Accession	Description	Interval	E-Value
Terpene_cyclase_nonplant_C1	cd00687	Non-plant Terpene Cyclases, Class 1; This CD includes terpenoid cyclases such as pentalenene ...	56-353	8.36e-25
Terpene_cyclase_C1	cd00868	Terpene cyclases, Class 1; Terpene cyclases, Class 1 (C1) of the class 1 family of isoprenoid ...	60-349	2.45e-11
Terpene_synth_C	pfam03936	Terpene synthase family, metal binding domain; It has been suggested that this gene family be ...	56-314	1.07e-04

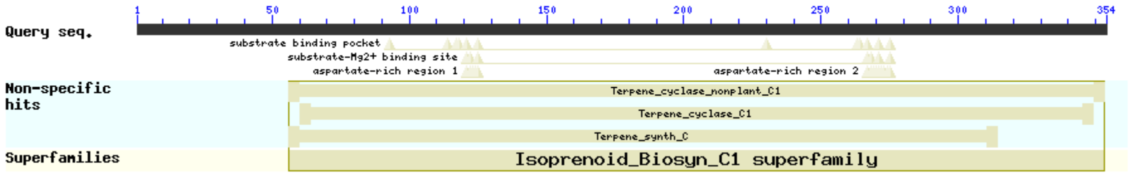

Figure S21. Conserved domains detected in a putative germacrene-*A* synthase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S21. List of domain hits for the germacrene-*A* synthase gene from *Nostoc punctiforme* (sp|B2J4A4 GERAS_NOSP7).

Name	Accession	Description	Interval	E-Value
Terpene_cyclase_nonplant_C1	cd00687	Non-plant Terpene Cyclases, Class 1; This CD includes terpenoid cyclases such as pentalenene ...	10–309	3.27e-123
Terpene_cyclase_C1	cd00868	Terpene cyclases, Class 1; Terpene cyclases, Class 1 (C1) of the class 1 family of isoprenoid ...	23–305	7.93e-51
Terpene_synth_C	pfam03936	Terpene synthase family, metal binding domain; It has been suggested that this gene family be ...	31–264	1.87e-20

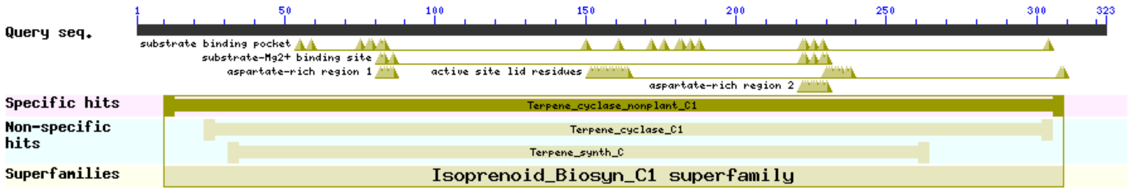

Figure S22. Conserved domains detected in the germacrene-A synthase gene from *Nostoc punctiforme* (sp|B2J4A4 GERAS_NOSP7) (edited from the NCBI CDD database, [1]).

Table S22. List of domain hits for a putative germacrene *A* oxidase gene from *L. dendroidea*.

Name	Accession	Description	Interval	E-Value
p450	pfam00067	Cytochrome P450; Cytochrome P450s are haem-thiolate proteins involved in the oxidative ...	367–564	1.03e-44
CypX	COG2124	Cytochrome P450 [Secondary metabolites biosynthesis, transport, and catabolism]	367–535	3.07e-31
PLN02687	PLN02687	flavonoid 3′-monooxygenase	370–531	6.05e-21
PTZ00404	PTZ00404	cytochrome P450; Provisional	370–539	3.35e-18
PLN02738	PLN02738	carotene beta-ring hydroxylase	370–534	1.21e-17

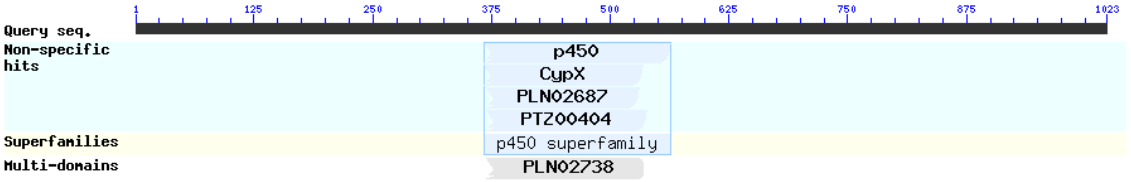

Figure S23. Conserved domains detected in a putative germacrene *A* oxidase gene from *L. dendroidea* (edited from the NCBI CDD database [1]).

Table S23. List of domain hits for the germacrene *A* oxidase gene from *Cichorium intybus* (sp|D5JBW8|GAO_CICIN).

Name	Accession	Description	Interval	E-value
PLN02687	PLN02687	flavonoid 3′-monooxygenase	5–486	4.19e-134
p450	pfam00067	Cytochrome P450; Cytochrome P450s are haem-thiolate proteins involved in the oxidative ...	33–460	7.76e-99
PTZ00404	PTZ00404	cytochrome P450; Provisional	5–477	1.31e-56
CypX	COG2124	Cytochrome P450 [Secondary metabolites biosynthesis, transport, and catabolism]	67–460	1.34e-38
PLN02738	PLN02738	carotene beta-ring hydroxylase	31–487	6.67e-29

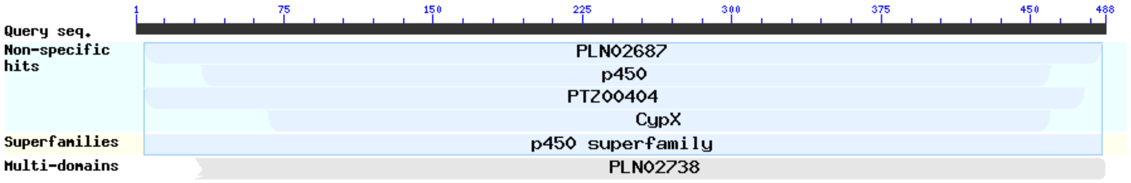

Figure S24. Conserved domains detected in the germacrene *A* oxidase gene from *Cichorium intybus* (sp|D5JBW8|GAO_CICIN) (edited from the NCBI CDD database, [1].

Table S24. List of domain hits for a putative aristolochene synthase gene from *L. dendroidea*.

Name	Accession	Description	Interval	E-Value
Terpene_cyclase_nonplant_C1	cd00687	Non-plant Terpene Cyclases, Class 1; This CD includes terpenoid cyclases such as pentalenene	56–353	8.36e-25
Terpene_cyclase_C1	cd00868	Terpene cyclases, Class 1; Terpene cyclases, Class 1 (C1) of the class 1 family of isoprenoid	60–349	2.45e-11
Terpene_synth_C	pfam03936	Terpene synthase family, metal binding domain; It has been suggested that this gene family be	56–314	1.07e-04

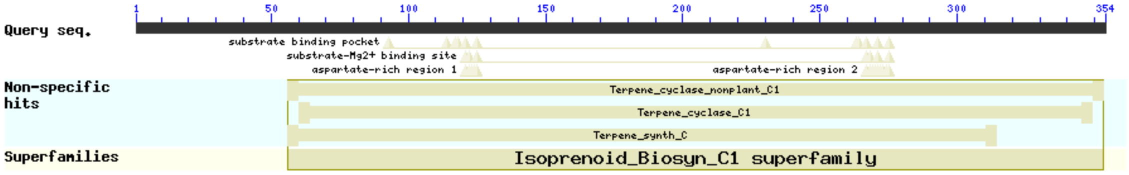

Figure S25. Conserved domains detected in a putative aristolochene synthase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S25. List of domain hits for the aristolochene synthase gene from *Aspergillus terreus* (sp|Q9UR08 ARIS_ASPTE).

Name	Accession	Description	Interval	E-Value
Terpene_cyclase_nonplant_C1	cd00687	Non-plant Terpene Cyclases, Class 1; This CD includes terpenoid cyclases such as pentalenene	18–312	1.26e-98
Terpene_cyclase_C1	cd00868	Terpene cyclases, Class 1; Terpene cyclases, Class 1 (C1) of the class 1 family of isoprenoid	28–308	6.00e-32
Terpene_synth_C	pfam03936	Terpene synthase family, metal binding domain; It has been suggested that this gene family be	21–269	2.55e-30
Isoprenoid_Biosyn_C1	cd00385	Isoprenoid Biosynthesis enzymes, Class 1; Superfamily of trans-isoprenyl diphosphate synthases	63–280	6.29e-09

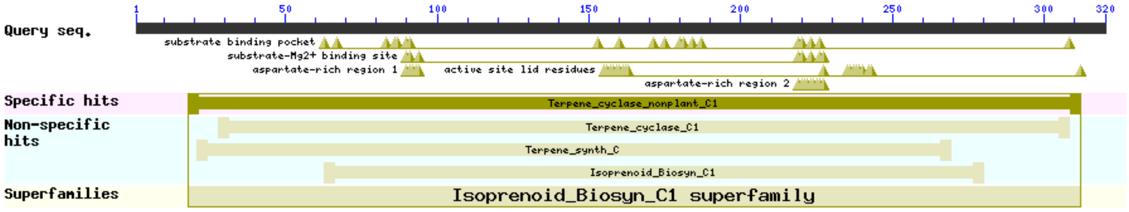

Figure S26. Conserved domains detected in the aristolochene synthase gene from *Aspergillus terreus* (sp|Q9UR08 ARIS_ASPTE) (edited from the NCBI CDD database, [1]).

Table S26. List of domain hits for a putative 5-epiaristolochene 1,3-dihydroxylase gene from *L. dendroidea*.

Name	**Accession**	**Description**	**Interval**	**E-Value**
p450	pfam00067	Cytochrome P450; Cytochrome P450s are haem-thiolate proteins involved in the oxidative ...	367–564	1.10e-44
CypX	COG2124	Cytochrome P450 [Secondary metabolites biosynthesis, transport, and catabolism]	367–535	3.30e-31
PLN02687	PLN02687	flavonoid 3′-monooxygenase	370–531	5.92e-21
PLN02183	PLN02183	ferulate 5-hydroxylase	367–530	2.79e-20
PLN02302	PLN02302	ent-kaurenoic acid oxidase	384–551	1.27e-19
PLN02966	PLN02966	cytochrome P450 83A1	367–548	3.18e-19
PLN02394	PLN02394	trans-cinnamate 4-monooxygenase	373–521	8.60e-19
PLN02655	PLN02655	ent-kaurene oxidase	371–517	2.94e-18
PTZ00404	PTZ00404	cytochrome P450; Provisional	370–539	3.54e-18
PLN03195	PLN03195	fatty acid omega-hydroxylase; Provisional	367–529	1.14e-17
PLN03234	PLN03234	cytochrome P450 83B1; Provisional	367–526	1.40e-16
PLN02290	PLN02290	cytokinin trans-hydroxylase	373–540	5.60e-16
PLN02936	PLN02936	epsilon-ring hydroxylase	370–529	6.75e-16
PLN02196	PLN02196	abscisic acid 8′-hydroxylase	367–538	1.04e-15
PLN00110	PLN00110	flavonoid 3′,5′-hydroxylase (F3′5′H); Provisional	367–521	1.60e-15
PLN02169	PLN02169	fatty acid (omega-1)-hydroxylase/midchain alkane hydroxylase	367–537	4.63e-15
PLN02426	PLN02426	cytochrome P450, family 94, subfamily C protein	367–545	6.97e-15
PLN02500	PLN02500	cytochrome P450 90B1	413–536	3.43e-14
PLN03112	PLN03112	cytochrome P450 family protein; Provisional	370–524	9.26e-13
PLN02987	PLN02987	Cytochrome P450, family 90, subfamily A	367–536	1.95e-12
PLN03141	PLN03141	3-epi-6-deoxocathasterone 23-monooxygenase; Provisional	365–535	4.81e-09
PLN02774	PLN02774	brassinosteroid-6-oxidase	367–524	5.38e-09
PLN00168	PLN00168	Cytochrome P450; Provisional	371–525	2.91e-08
PLN03018	PLN03018	homomethionine *N*-hydroxylase	384–520	4.02e-08
PLN02971	PLN02971	tryptophan *N*-hydroxylase	370–522	4.17e-08
PLN02648	PLN02648	allene oxide synthase	412–489	8.49e-08
PLN02738	PLN02738	carotene beta-ring hydroxylase	370–534	1.28e-17

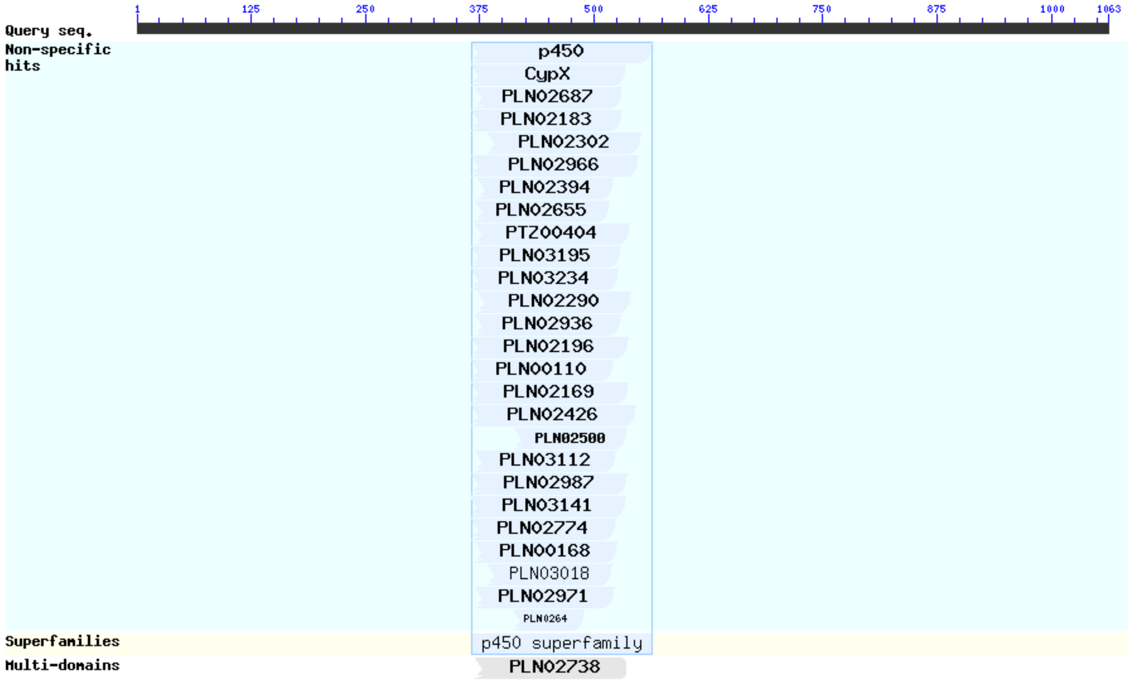

Figure S27. Conserved domains detected in a putative 5-epiaristolochene 1,3-dihydroxylase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S27. List of domain hits for the 5-epiaristolochene 1,3-dihydroxylase gene from *Nicotiana tabacum* (sp|Q94FM7|C71DK_TOBAC).

Name	**Accession**	**Description**	**Interval**	**E-Value**
PLN02183	PLN02183	ferulate 5-hydroxylase	33–488	9.91e-128
PLN02687	PLN02687	flavonoid 3′-monooxygenase	30–498	5.87e-123
PLN03112	PLN03112	cytochrome P450 family protein; Provisional	4–498	6.11e-114
p450	pfam00067	Cytochrome P450; Cytochrome P450s are haem-thiolate proteins involved in the oxidative ...	33–494	2.34e-109
PLN03234	PLN03234	cytochrome P450 83B1; Provisional	23–499	4.35e-109
PLN02966	PLN02966	cytochrome P450 83A1	22–494	2.38e-103
PLN00110	PLN00110	flavonoid 3′,5′-hydroxylase (F3′5′H); Provisional	29–498	2.76e-102
PLN02394	PLN02394	trans-cinnamate 4-monooxygenase	31–483	1.57e-81
PLN02971	PLN02971	tryptophan *N*-hydroxylase	25–468	5.45e-60
PLN02655	PLN02655	ent-kaurene oxidase	34–498	8.16e-59
PLN00168	PLN00168	Cytochrome P450; Provisional	20–466	4.94e-57
PLN03018	PLN03018	homomethionine *N*-hydroxylase	25–477	8.67e-54
PTZ00404	PTZ00404	cytochrome P450; Provisional	24–486	1.12e-53
CypX	COG2124	Cytochrome P450 [Secondary metabolites biosynthesis, transport, and catabolism]	33–470	4.01e-43
PLN02936	PLN02936	epsilon-ring hydroxylase	62–497	5.84e-36
PLN02302	PLN02302	ent-kaurenoic acid oxidase	234–463	4.10e-28
PLN03195	PLN03195	fatty acid omega-hydroxylase; Provisional	27–463	5.47e-27

Table S27. Cont.

PLN02290	PLN02290	cytokinin trans-hydroxylase	219–463	1.48e-25
PLN02987	PLN02987	Cytochrome P450, family 90, subfamily A	31–465	2.75e-23
PLN02196	PLN02196	abscisic acid 8′-hydroxylase	3–467	2.78e-21
PLN02774	PLN02774	brassinosteroid-6-oxidase	233–463	1.42e-20
PLN02169	PLN02169	fatty acid (omega-1)-hydroxylase/midchain alkane hydroxylase	230–470	3.80e-20
PLN03141	PLN03141	3-epi-6-deoxocathasterone 23-monooxygenase; Provisional	234–465	1.83e-18
PLN02426	PLN02426	cytochrome P450, family 94, subfamily C protein	122–444	3.98e-15
PLN02500	PLN02500	cytochrome P450 90B1	233–467	2.22e-14
PLN02648	PLN02648	allene oxide synthase	331–418	7.72e-06
PLN02738	PLN02738	carotene beta-ring hydroxylase	269–497	3.46e-34

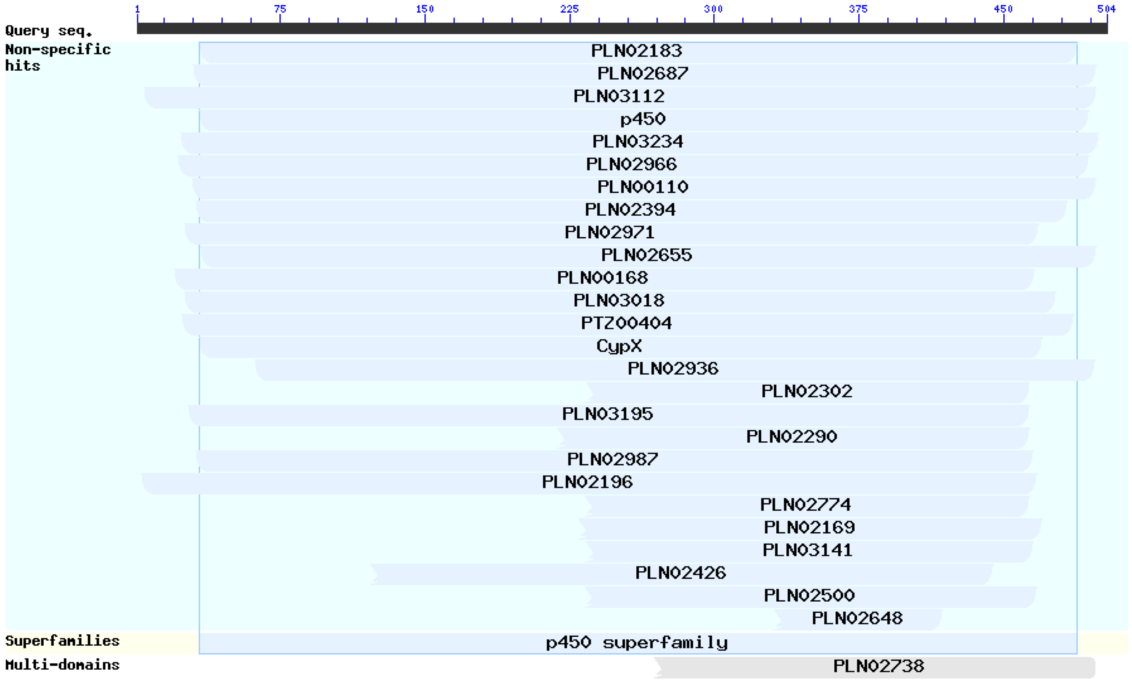

Figure S28. Conserved domains detected in the 5-epiaristolochene 1,3-dihydroxylase gene from *Nicotiana tabacum* (sp|Q94FM7|C71DK_TOBAC) (edited from the NCBI CDD database, [1]).

Table S28. List of domain hits for a putative pentalenene synthase gene from *L. dendroidea*.

Name	Accession	Description	Interval	E-value
Terpene_cyclase_nonplant_C1	cd00687	Non-plant Terpene Cyclases, Class 1; This CD includes terpenoid cyclases such as pentalenene ...	11–298	3.90e-21
Terpene_cyclase_C1	cd00868	Terpene cyclases, Class 1; Terpene cyclases, Class 1 (C1) of the class 1 family of isoprenoid ...	15–282	4.15e-09
Terpene_synth_C	pfam03936	Terpene synthase family, metal binding domain; It has been suggested that this gene family be ...	15–262	2.96e-04

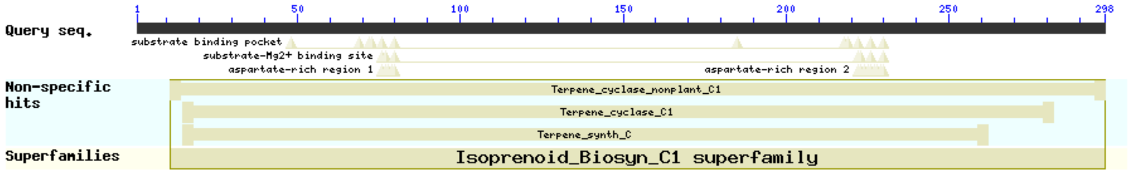

Figure S29. Conserved domains detected in a putative pentalenene synthase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S29. List of domain hits for the pentalenene synthase gene from *Streptomyces exfoliatus* (sp|Q55012 PENA_STREX).

Name	Accession	Description	Interval	E-Value
Terpene_cyclase_nonplant_C1	cd00687	Non-plant Terpene Cyclases, Class 1; This CD includes terpenoid cyclases such as pentalenene ...	8–313	2.37e-108
Terpene_cyclase_C1	cd00868	Terpene cyclases, Class 1; Terpene cyclases, Class 1 (C1) of the class 1 family of isoprenoid ...	19–309	4.49e-41
Terpene_synth_C	pfam03936	Terpene synthase family, metal binding domain; It has been suggested that this gene family be ...	29–265	1.57e-34
Isoprenoid_Biosyn_C1	cd00385	Isoprenoid Biosynthesis enzymes, Class 1; Superfamily of trans-isoprenyl diphosphate synthases ...	72–292	9.90e-10

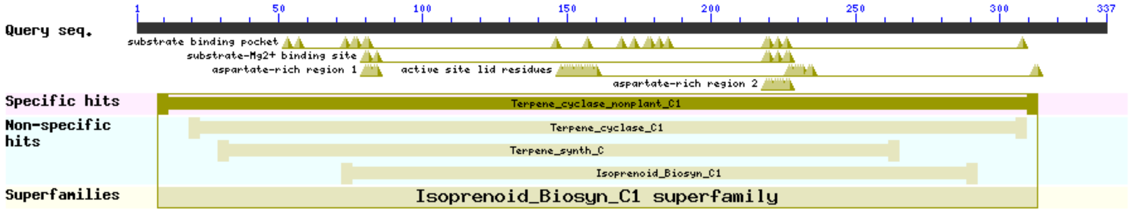

Figure S30. Conserved domains detected in the pentalenene synthase gene from *Streptomyces exfoliatus* (sp|Q55012 PENA_STREX) (edited from the NCBI CDD database, [1]).

Table S30. List of domain hits for a putative zerumbone synthase gene from *L. dendroidea*.

Name	Accession	Description	Interval	E-Value
SDR_c	cd05233	classical (c) SDRs; SDRs are a functionally diverse family of oxidoreductases that have a ...	44–275	1.22e-32
fabG	PRK06550	3-ketoacyl-(acyl-carrier-protein) reductase; Provisional	41–233	4.23e-17
adh_short_C2	pfam13561	Enoyl-(Acyl carrier protein) reductase;	51–278	1.00e-07

Table S30. *Cont.*

PKS_KR	smart00822	This enzymatic domain is part of bacterial polyketide synthases; It catalyses the first step ...	42–132	1.88e-05
FabG	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) ...	39–278	2.19e-34
fabG	PRK05565	3-ketoacyl-(acyl-carrier-protein) reductase; Provisional	38–242	7.99e-26
PHB_DH	TIGR01963	3-hydroxybutyrate dehydrogenase; This model represents a subfamily of the short chain ...	41–279	1.08e-22
adh_short	pfam00106	short chain dehydrogenase; This family contains a wide variety of dehydrogenases.	42–209	1.95e-16
PLN02253	PLN02253	xanthoxin dehydrogenase	36–224	2.44e-13
secoisolariciresinol-DH_like_SDR_c	cd05326	secoisolariciresinol dehydrogenase (secoisolariciresinol-DH)-like, classical (c) SDRs;	38–225	1.86e-15

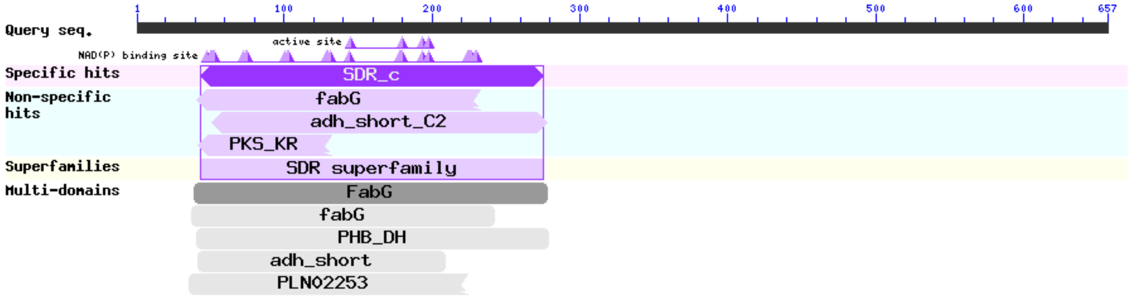

Figure S31. Conserved domains detected in a putative zerumbone synthase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S31. List of domain hits for the zerumbone synthase gene from *Zingiber zerumbet* (sp|F1SWA0|ZERSY_ZINZE).

Name	Accession	Description	Interval	E-Value
secoisolariciresinol-DH_like_SDR_c	cd05326	secoisolariciresinol dehydrogenase (secoisolariciresinol-DH)-like, classical (c) SDRs; ...	2–257	5.98e-118
PRK07069	PRK07069	short chain dehydrogenase; Validated	8–257	5.07e-52
adh_short_C2	pfam13561	Enoyl-(Acyl carrier protein) reductase;	12–257	2.29e-27
PKS_KR	smart00822	This enzymatic domain is part of bacterial polyketide synthases; It catalyses the first step ...	6–151	2.29e-08
PLN02730	PLN02730	enoyl-[acyl-carrier-protein] reductase	122–255	1.58e-04

Table S31. *Cont.*

PLN02253	PLN02253	xanthoxin dehydrogenase	2–267	1.11e-165
fabG	PRK07231	3-ketoacyl-(acyl-carrier-protein) reductase; Provisional	1–258	4.45e-76
FabG	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) ...	1–257	9.62e-59
3oxo_ACP_reduc	TIGR01830	3-oxoacyl-(acyl-carrier-protein) reductase; This model represents 3-oxoacyl-[ACP] reductase, ...	8–255	2.40e-55
adh_short	pfam00106	short chain dehydrogenase; This family contains a wide variety of dehydrogenases.	6–173	4.49e-30

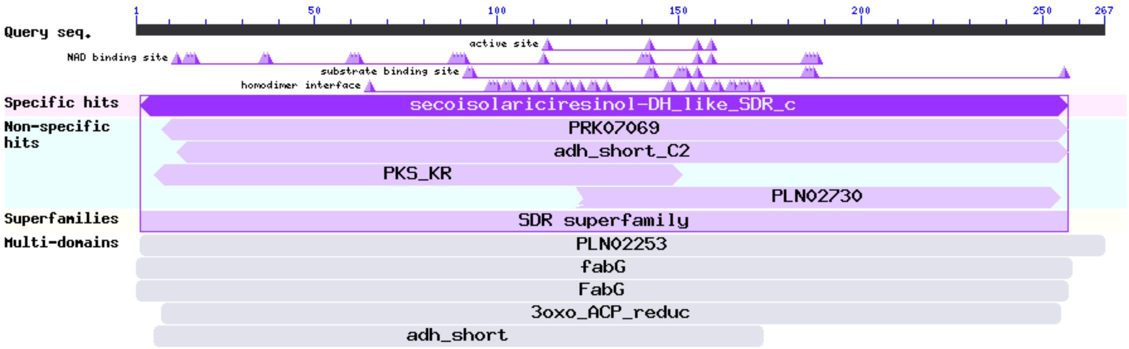

Figure S32. Conserved domains detected in the zerumbone synthase gene from *Zingiber zerumbet* (sp|F1SWA0|ZERSY_ZINZE) (edited from the NCBI CDD database, [1]).

Table S32. List of domain hits for a putative gibberelin 20-oxidase gene from *L. dendroidea*.

Name	**Accession**	**Description**	**Interval**	**E-Value**
DIOX_N	pfam14226	non-haem dioxygenase in morphine synthesis *N*-terminal; This is the highly conserved *N*-terminal ...	2129–2401	2.84e-12
2OG-FeII_Oxy	pfam03171	2OG-Fe(II) oxygenase superfamily; This family contains members of the 2-oxoglutarate (2OG) and ...	1616–1954	7.56e-09
PTZ00273	PTZ00273	oxidase reductase; Provisional	1508–2443	8.96e-24
PcbC	COG3491	Isopenicillin N synthase and related dioxygenases [General function prediction only]	1595–2419	5.94e-29
PLN02485	PLN02485	Oxidoreductase	1511–2497	2.50e-19
PLN03002	PLN03002	oxidoreductase, 2OG-Fe(II) oxygenase family protein	1508–2362	6.26e-18
PLN02750	PLN02750	oxidoreductase, 2OG-Fe(II) oxygenase family protein	1517–2443	1.70e-12
PLN02393	PLN02393	leucoanthocyanidin dioxygenase like protein	1529–2521	1.25e-11
PLN02276	PLN02276	gibberellin 20-oxidase	1598–2497	1.94e-10

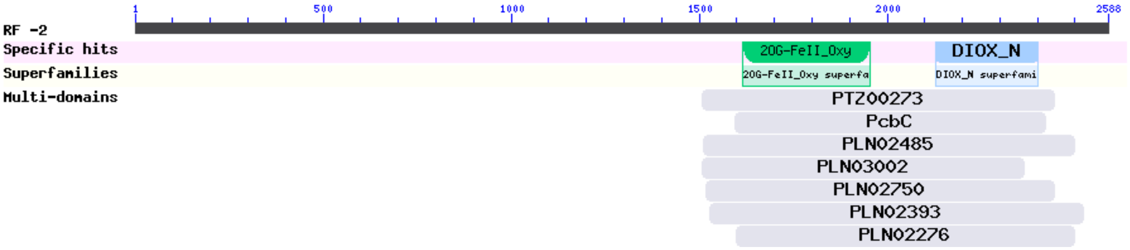

Figure S33. Conserved domains detected in a putative gibberelin 20-oxidase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S33. List of domain hits for the gibberelin 20-oxidase gene from *Arabidopsis thaliana* (gi|60390168|sp|Q39112.1|GAOX3_ARATH).

Name	Accession	Description	Interval	E-value
2OG-FeII_Oxy	pfam03171	2OG-Fe(II) oxygenase superfamily; This family contains members of the 2-oxoglutarate (2OG) and ...	222–321	3.06e-39
DIOX_N	pfam14226	non-haem dioxygenase in morphine synthesis *N*-terminal; This is the highly conserved *N*-terminal ...	58–160	3.86e-21
PLN03176	PLN03176	flavanone-3-hydroxylase; Provisional	41–137	1.49e-05
PLN02276	PLN02276	gibberellin 20-oxidase	17–380	0e+00
PLN02393	PLN02393	leucoanthocyanidin dioxygenase like protein	37–334	9.01e-65
PLN02254	PLN02254	gibberellin 3-beta-dioxygenase	22–360	7.45e-62
PLN03178	PLN03178	leucoanthocyanidin dioxygenase; Provisional	37–354	5.59e-61
PLN02912	PLN02912	oxidoreductase, 2OG-Fe(II) oxygenase family protein	36–370	4.36e-60
PLN02639	PLN02639	oxidoreductase, 2OG-Fe(II) oxygenase family protein	26–350	4.80e-58
PLN02758	PLN02758	oxidoreductase, 2OG-Fe(II) oxygenase family protein	37–360	6.27e-57
PLN02750	PLN02750	oxidoreductase, 2OG-Fe(II) oxygenase family protein	37–353	3.35e-53
PcbC	COG3491	Isopenicillin *N* synthase and related dioxygenases [General function prediction only]	54–361	5.21e-52

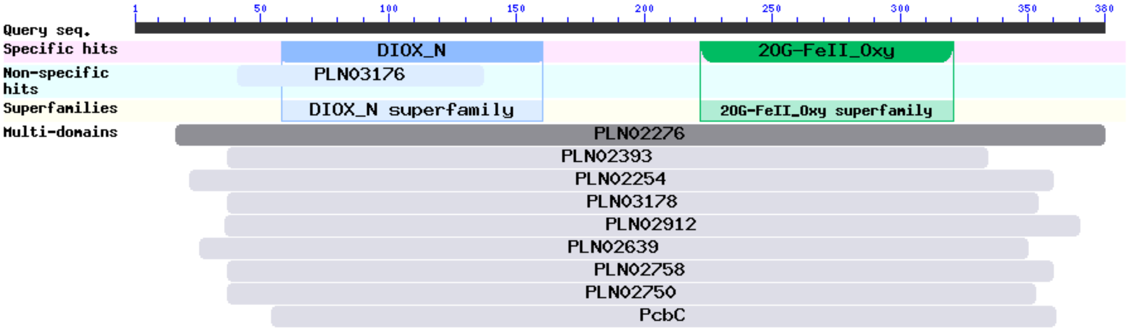

Figure S34. Conserved domains detected in the gibberelin 20-oxidase gene from *Arabidopsis thaliana* (gi|60390168|sp|Q39112.1|GAOX3_ARATH) (edited from the NCBI CDD database, [1]).

Table S34. List of domain hits for a putative gibberelin 2-oxidase gene from *L. dendroidea*.

Name	**Accession**	**Description**	**Interval**	**E-Value**
DIOX_N	pfam14226	non-haem dioxygenase in morphine synthesis *N*-terminal; This is the highly conserved *N*-terminal ...	97–471	4.75e-09
2OG-FeII_Oxy	pfam03171	2OG-Fe(II) oxygenase superfamily; This family contains members of the 2-oxoglutarate (2OG) and ...	610–927	4.13e-07
PTZ00273	PTZ00273	oxidase reductase; Provisional	94–1035	1.91e-32
PcbC	COG3491	Isopenicillin *N* synthase and related dioxygenases [General function prediction only]	85–948	1.05e-32
PLN02485	PLN02485	oxidoreductase	91–873	1.63e-15
PLN03002	PLN03002	oxidoreductase, 2OG-Fe(II) oxygenase family protein	214–1056	2.60e-09
PLN02156	PLN02156	gibberellin 2-beta-dioxygenase	79–873	3.20e-08

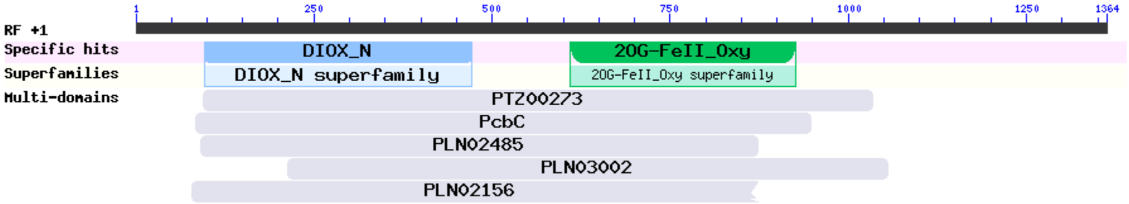

Figure S35. Conserved domains detected in a putative gibberelin 2-oxidase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S35. List of domain hits for the the gibberelin 2-oxidase gene from *Arabidopsis thaliana*.

Name	**Accession**	**Description**	**Interval**	**E-Value**
2OG-FeII_Oxy	pfam03171	2OG-Fe(II) oxygenase superfamily; This family contains members of the 2-oxoglutarate (2OG) and ...	157–269	3.98e-28
DIOX_N	pfam14226	non-haem dioxygenase in morphine synthesis *N*-terminal; This is the highly conserved *N*-terminal ...	15–108	9.31e-20
PLN03176	PLN03176	flavanone-3-hydroxylase; Provisional	9–71	3.40e-09
PcbC	COG3491	Isopenicillin *N* synthase and related dioxygenases [General function prediction only]	13–309	1.14e-49
PLN02156	PLN02156	gibberellin 2-beta-dioxygenase	15–316	7.18e-98

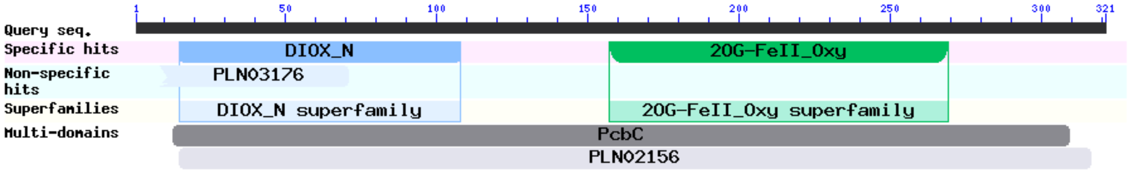

Figure S36. Conserved domains detected in the gibberelin 2-oxidase gene from *Arabidopsis thaliana* (gi|75308865|sp|Q9C7Z1.1|G2OX4_ARATH) (edited from the NCBI CDD database, [1]).

Table S36. List of domain hits for a putative abietadienol/ abietadienal oxidase gene from *L. dendroidea*.

Name	**Accession**	**Description**	**Interval**	**E-Value**
PLN02936	PLN02936	epsilon-ring hydroxylase	135–620	5.82e-141
p450	pfam00067	Cytochrome P450; Cytochrome P450s are haem-thiolate proteins involved in the oxidative ...	139–613	6.45e-78
CypX	COG2124	Cytochrome P450 [Secondary metabolites biosynthesis, transport, and catabolism]	154–620	2.27e-42
PLN02290	PLN02290	cytokinin trans-hydroxylase	207–618	1.36e-32
PLN03195	PLN03195	fatty acid omega-hydroxylase; Provisional	179–620	3.59e-31
PLN02302	PLN02302	ent-kaurenoic acid oxidase	381–579	1.91e-27
PLN02183	PLN02183	ferulate 5-hydroxylase	394–594	1.27e-24
PLN00110	PLN00110	flavonoid 3′,5′-hydroxylase (F3′5′H); Provisional	382–594	1.17e-23
PLN02655	PLN02655	ent-kaurene oxidase	370–623	1.76e-23
PLN02426	PLN02426	cytochrome P450, family 94, subfamily C protein	387–620	1.04e-22
PLN02687	PLN02687	flavonoid 3′-monooxygenase	326–621	1.89e-22
PLN02394	PLN02394	trans-cinnamate 4-monooxygenase	399–589	3.07e-22
PTZ00404	PTZ00404	cytochrome P450; Provisional	139–597	1.17e-21
PLN03112	PLN03112	cytochrome P450 family protein; Provisional	359–624	1.27e-21
PLN03234	PLN03234	cytochrome P450 83B1; Provisional	129–615	3.95e-21
PLN02169	PLN02169	fatty acid (omega-1)-hydroxylase/midchain alkane hydroxylase	179–621	1.62e-19
PLN02966	PLN02966	cytochrome P450 83A1	372–624	2.70e-18
PLN02987	PLN02987	Cytochrome P450, family 90, subfamily A	382–598	3.61e-18
PLN02500	PLN02500	cytochrome P450 90B1	380–597	2.47e-17
PLN02196	PLN02196	abscisic acid 8'-hydroxylase	358–620	1.48e-16
PLN00168	PLN00168	Cytochrome P450; Provisional	145–591	5.93e-16
PLN02774	PLN02774	brassinosteroid-6-oxidase	380–588	1.93e-12
PLN03018	PLN03018	homomethionine N-hydroxylase	386–588	4.15e-11
PLN03141	PLN03141	3-epi-6-deoxocathasterone 23-monooxygenase; Provisional	386–622	1.97e-10
PLN02971	PLN02971	tryptophan *N*-hydroxylase	386–624	1.99e-10
PLN02738	PLN02738	carotene beta-ring hydroxylase	135–633	2.48e-167

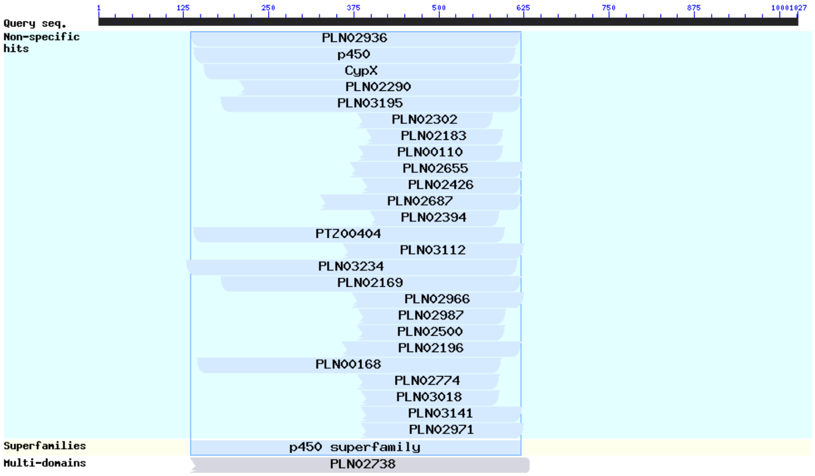

Figure S37. Conserved domains detected in a putative abietadienol/abietadienal oxidase gene from *L. dendroidea* (edited from the NCBI CDD database, [1]).

Table S37. List of domain hits for the abietadienol/abietadienal oxidase gene from *Pinus taeda* (sp|Q50EK6] C72B1_PINTA).

Name	**Accession**	**Description**	**Interval**	**E-Value**
PLN03141	PLN03141	3-epi-6-deoxocathasterone 23-monooxygenase; Provisional	45–481	4.09e-132
PLN02987	PLN02987	Cytochrome P450, family 90, subfamily A	5–481	1.47e-130
PLN02500	PLN02500	cytochrome P450 90B1	1–477	9.23e-117
PLN02774	PLN02774	brassinosteroid-6-oxidase	5–477	5.51e-104
PLN02302	PLN02302	ent-kaurenoic acid oxidase	5–477	6.93e-82
PLN02196	PLN02196	abscisic acid 8′-hydroxylase	3–477	9.81e-71
p450	pfam00067	Cytochrome P450; Cytochrome P450s are haem-thiolate proteins involved in the oxidative ...	46–454	7.80e-49
CypX	COG2124	Cytochrome P450 [Secondary metabolites biosynthesis, transport, and catabolism]	60–477	3.30e-46
PTZ00404	PTZ00404	cytochrome P450; Provisional	18–452	1.33e-17
PLN02936	PLN02936	epsilon-ring hydroxylase	283–459	3.81e-17
PLN02183	PLN02183	ferulate 5-hydroxylase	46–454	8.12e-17
PLN02290	PLN02290	cytokinin trans-hydroxylase	229–460	1.01e-15
PLN02687	PLN02687	flavonoid 3′-monooxygenase	248–458	5.51e-14
PLN03112	PLN03112	cytochrome P450 family protein; Provisional	8–447	8.67e-13
PLN02966	PLN02966	cytochrome P450 83A1	39–436	1.26e-11
PLN00168	PLN00168	Cytochrome P450; Provisional	239–459	6.04e-09
PLN02426	PLN02426	cytochrome P450, family 94, subfamily C protein	251–481	1.59e-08
PLN03234	PLN03234	cytochrome P450 83B1; Provisional	265–453	2.81e-08
PLN03195	PLN03195	fatty acid omega-hydroxylase; Provisional	3–480	1.77e-07
PLN00110	PLN00110	flavonoid 3′,5′-hydroxylase (F3′5′H); Provisional	254–454	4.65e-07
PLN02655	PLN02655	ent-kaurene oxidase	330–453	5.28e-06
PLN02971	PLN02971	tryptophan *N*-hydroxylase	32–459	6.10e-06
PLN02169	PLN02169	fatty acid (omega-1)-hydroxylase/midchain alkane hydroxylase	264–442	1.52e-05
PLN02394	PLN02394	trans-cinnamate 4-monooxygenase	279–451	2.37e-05
PLN03018	PLN03018	homomethionine *N*-hydroxylase	4–100	2.90e-04
PLN02738	PLN02738	carotene beta-ring hydroxylase	256–461	4.83e-23

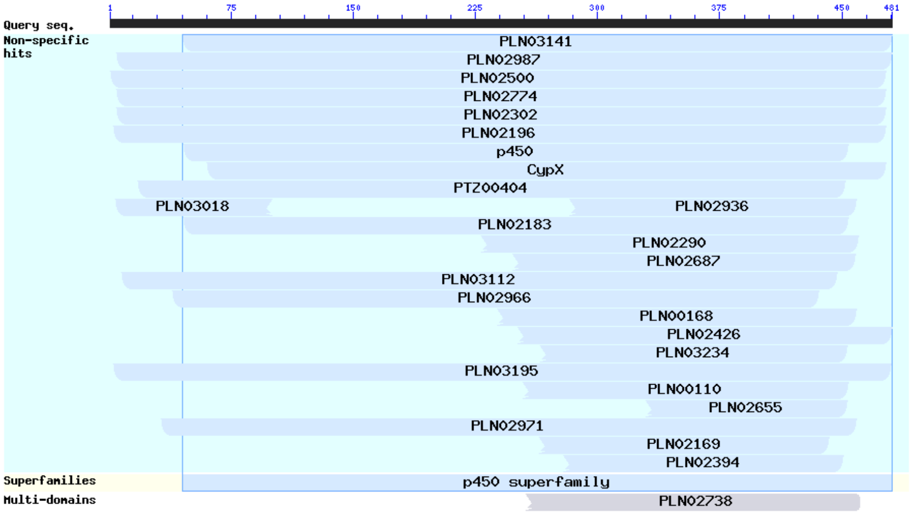

Figure S38. Conserved domains detected in the abietadienol/abietadienal oxidase gene from *Pinus taeda* (sp|Q50EK6] C72B1_PINTA) (edited from the NCBI CDD database, [1]).

References

1. Conserved Domain Database (CDD). Available online: http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi (accessed on 15 September 2014).
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