

```

20          40          60          80
IrcPS1  -----MASSTMHNNHSPASRRRMSAAAAAHLMPCTTITKS-AWM-NNNTENTNYC--NHK-KISVACNRYATDAPQVH 79
SmCPS1  -----MASSSSTSSPAARR-TPASA-LHHPCA-T-S-AWMSSSNLSLSTQ--NHK-KISYA---TDAPQVH 68
SmCPS2  -----MTSLS-NSRAPATSRRL-Q-TPA-LHHPSELA-W-AWNSSTPSPSTQ--RRK-HLSVTEC-RVASDEVQVSE 73
IrcPS2
SmCPS3  MSLSCILGMSLITLTPNYSYSLGEGKN-L-LSA-KLQLPQSL---T-G-TW-L-KNRETFANNO-SHRL-RKH-IL---RYLNNVAH 74
IrcPS3  -----MSSSSNNTSLRPTTAAAGPRQMRNNSCNWYSAKAGGNTNPNGNK-CYEEVHR-SRQVAAAKSRE 76
IrcPS4  -----MGLMSASNAATGRIPLTTC-VYPS-PLRKNAGGSSS--GNMK-CYGLGR-SRVAVAA-SGRT 62
SmCPS4
IrcPS5  -----MPLASNPVAVPSSSTAHGRLPAAAA-SRSSAGCQOLCRPLTPTSSQ-CNAL-SRPTEE-LIDVYONGPVIK 70
SmCPS5
IrkSL1
SmKSL1
IrkSL3
IrkSL2  -----MSTKRLPPTSTSDKQK-----S-GRTSIIIG 25
SmKSL2  -----MSLSSNSALVGPK-RSSRI-----SHASA-S 26
-----MAPPSTCIIHPKSSRR-----CSPASAAS 30

100          120          140          160          180
IrcPS1  ODDSTENQGHDAVNNI-FDPI-E-NRTITRTMGGRISVSPDTAWYALKDLNGDAPQVSSLEWYVNOQDQSGWGD-D-KKCVY 166
SmCPS1  HGTITVHQGHDAVNNI-FDPI-E-NRTITRTMGGRISVSPDTAWYAMKDLNGDAPQVSSLEWYVNOQDQSGWGD-Q-KKCVY 155
SmCPS2  HGTITVHQGHDAVNNI-FDPI-E-NRTITRTMGGRISVSPDTAWYALKDLNGDAPQVSSLEWYVNOQDQSGWGD-Q-KKCVY 158
IrcPS2
SmCPS3  EFGSTAEAVENNNI-RDMK-S-CIKLIMTKEGRISVSAATAWYALKDLNGDAPQVSSLEWYVNOQDQSGWGD-Q-HHSVY 160
IrcPS3  GNGGEPQPFQKLNQKQKML-ECITITQSGGGRISVSAATAWYALKDYVNDLPIVPSWVWVSNQVRSWGD-R-DHSPV 115
IrcPS4  H-TKPTNQDQVSSK-MRVYK-N-ETMLQNMDEGEISVSPDTAWYALVETDGR--PQPTSEWVSNQVRSWGD-R-K-KVY 157
SmCPS4  W-SN-P--E-YESK-MKEM---LWYMRDMDDGEVNSAATAWYALVETDGR--PQPTSEWVSNQVRSWGD-R-K-KVY 141
IrcPS5
SmCPS5  WH-EIVVEDDAEKDQSPK-GEERD-AVRSMRSMGGEISVSPDTAWYALVADLGR-PQPSSHWVSTNQLAGSWWGD-H-ATST 156
SmCPS5
IrkSL1
SmKSL1
IrkSL3  GR-CCQITGPRITTK-QSKIVLKRIRRSNGKVFETASADTAWYAMPSREMSGRPSPECDWVWENQNPVGSWGD-N--P- 112
IrkSL2  H-LGQRATSPONAS-MATCEETKGRARLHKNESSSTDTAWYAMPSPTSSPECPACINWVLENGCHGSWARPHHH-MKKK 116
SmKSL2  H-SGHSATSAKIAS-MPTCEETKGRARLHKNESSSTDTAWYAMPSPTSSPECPACINWVLENGCHGSWARPHHH-MKKK 120

200          220          240          260
IrcPS1  VNTACVYALRSWYHDDKIKKGTIYKENVE-KRDNNEHMTGCEVYVYALQVACGLIEDLPI-DSPFQGEVHSROOKRIPMEM 257
SmCPS1  VNTACVYALRSWYHDDKIKKGTIYKENVE-KRDNNEHMTGCEVYVYALQVACGLIEDLPI-DSPFQGEVHSROOKRIPMEM 246
SmCPS2  VNTACVYALRSWYHDDKIKKGTIYKENVE-KRDNNEHMTGCEVYVYALQVACGLIEDLPI-DSPFQGEVHSROOKRIPMEM 249
IrcPS2
SmCPS3  VNTMACVYALRSWYHDDKIKKGTIYKENVE-KRDNNEHMTGCEVYVYALQVACGLIEDLPI-DSPFQGEVHSROOKRIPMEM 247
IrcPS3  VNTACVYALRSWYHDDKIKKGTIYKENVE-KRDNNEHMTGCEVYVYALQVACGLIEDLPI-DSPFQGEVHSROOKRIPMEM 206
IrcPS4  VNTACVYALRSWYHDDKIKKGTIYKENVE-KRDNNEHMTGCEVYVYALQVACGLIEDLPI-DSPFQGEVHSROOKRIPMEM 248
SmCPS4  VNTACVYALRSWYHDDKIKKGTIYKENVE-KRDNNEHMTGCEVYVYALQVACGLIEDLPI-DSPFQGEVHSROOKRIPMEM 231
IrcPS5  ---MACVYALRSWYHDDKIKKGTIYKENVE-KRDNNEHMTGCEVYVYALQVACGLIEDLPI-DSPFQGEVHSROOKRIPMEM 86
SmCPS5  VNTACVYALRSWYHDDKIKKGTIYKENVE-KRDNNEHMTGCEVYVYALQVACGLIEDLPI-DSPFQGEVHSROOKRIPMEM 246
IrkSL1
SmKSL1  -----MSIA-EN-6
IrkSL3  SCTACVYALRSWYHDDKIKKGTIYKENVE-KRDNNEHMTGCEVYVYALQVACGLIEDLPI-DSPFQGEVHSROOKRIPMEM 201
IrkSL2  SSTACVYALRSWYHDDKIKKGTIYKENVE-KRDNNEHMTGCEVYVYALQVACGLIEDLPI-DSPFQGEVHSROOKRIPMEM 205
SmKSL2  SSTACVYALRSWYHDDKIKKGTIYKENVE-KRDNNEHMTGCEVYVYALQVACGLIEDLPI-DSPFQGEVHSROOKRIPMEM 209

280          300          320          340          360
IrcPS1  M-HXVPTSLSLEGLENLWELK-LQADGSLTSPSSATAAMQT-KDEEC-QIKNTI-ETNGGAPHTPVDYGRWAVDQ 344
SmCPS1  M-HXVPTSLSLEGLENLWELK-LQADGSLTSPSSATAAMQT-KDEEC-QIKNTI-ETNGGAPHTPVDYGRWAVDQ 333
SmCPS2  M-HXVPTSLSLEGLENLWELK-LQADGSLTSPSSATAAMQT-KDEEC-QIKNTI-ETNGGAPHTPVDYGRWAVDQ 336
IrcPS2
SmCPS3  M-HXVPTSLSLEGLENLWELK-LQADGSLTSPSSATAAMQT-KDEEC-QIKNTI-ETNGGAPHTPVDYGRWAVDQ 334
IrcPS3  L-HXKPTSLSLEGLENLWELK-LQADGSLTSPSSATAAMQT-KDEEC-QIKNTI-ETNGGAPHTPVDYGRWAVDQ 294
IrcPS4  L-HXKPTSLSLEGLENLWELK-LQADGSLTSPSSATAAMQT-KDEEC-QIKNTI-ETNGGAPHTPVDYGRWAVDQ 334
SmCPS4  L-HXKPTSLSLEGLENLWELK-LQADGSLTSPSSATAAMQT-KDEEC-QIKNTI-ETNGGAPHTPVDYGRWAVDQ 317
IrcPS5  M-HXVPTSLSLEGLENLWELK-LQADGSLTSPSSATAAMQT-KDEEC-QIKNTI-ETNGGAPHTPVDYGRWAVDQ 173
SmCPS5  M-HXVPTSLSLEGLENLWELK-LQADGSLTSPSSATAAMQT-KDEEC-QIKNTI-ETNGGAPHTPVDYGRWAVDQ 333
IrkSL1  L-RVH-PPSGH-TL-QSRGGLP-H---ES-PMITTPAAKCSITISDPMGRKRNKGRVHSPATTHSADTPSNCLIDTQR 88
SmKSL1  P-AAT-ASGN-GA-SRRRNPHTKTYVVG-FPM-NKSSAANKNTIT-TDMGR-AEKKGEVNSPAAAAQPAADTPSNCLIDTQR 93
IrkSL3  K-WEL-VGEG-GA-SGNWNOQRHQS-RN-GSINSPATAAAAHC-RHHC-DLISAM-NKNGWAPTVPMDIARCMQDTE 284
IrkSL2  S-AEKVYWAHTAEQMGKIQWESMMKQRR-NGSINSPATAAAAIAL-RNSDC-NLHHAALKKGNASAPDIDISOLCTVNE 293
SmKSL2  S-SETEVYWAHTAEQMGKIQWESMMKQRR-NGSINSPATAAAAIAL-RNSDC-NLHHAALKKGNASAPDIDISOLCTVNE 297

380          400          420          440          460
IrcPS1  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 433
SmCPS1  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 423
SmCPS2  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 426
IrcPS2  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 48
SmCPS3  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 423
IrcPS3  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 384
IrcPS4  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 423
SmCPS4  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 406
IrcPS5  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 263
SmCPS5  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 422
IrkSL1  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 168
SmKSL1  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 173
IrkSL3  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 368
IrkSL2  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 376
SmKSL2  GSRFEESEAECAHHTKWTENYVSGRESECDIDDTSMGRRLKMHGDVDPNLYRKK-K-DN-SCGG-QMESPSPNINRA 380

480          500          520          540
IrcPS1  SOLR-PPGEEEDANKANNQEKLA-NNOQDKWYSHKHPDEKKGMEPWATPRVEARVYQVAGSGDYWGKTLRMPESNDT 524
SmCPS1  SOLR-PPGEEEDANKANNQEKLA-NNOQDKWYSHKHPDEKKGMEPWATPRVEARVYQVAGSGDYWGKTLRMPESNDT 514
SmCPS2  SOLR-PPGEEEDANKANNQEKLA-NNOQDKWYSHKHPDEKKGMEPWATPRVEARVYQVAGSGDYWGKTLRMPESNDT 517
IrcPS2  SOLR-PPGEEEDANKANNQEKLA-NNOQDKWYSHKHPDEKKGMEPWATPRVEARVYQVAGSGDYWGKTLRMPESNDT 139
SmCPS3  SOLR-PPGEEEDANKANNQEKLA-NNOQDKWYSHKHPDEKKGMEPWATPRVEARVYQVAGSGDYWGKTLRMPESNDT 514
IrcPS3  SOLR-PPGEEEDANKANNQEKLA-NNOQDKWYSHKHPDEKKGMEPWATPRVEARVYQVAGSGDYWGKTLRMPESNDT 476
IrcPS4  SOLR-PPGEEEDANKANNQEKLA-NNOQDKWYSHKHPDEKKGMEPWATPRVEARVYQVAGSGDYWGKTLRMPESNDT 514
SmCPS4  SOLR-PPGEEEDANKANNQEKLA-NNOQDKWYSHKHPDEKKGMEPWATPRVEARVYQVAGSGDYWGKTLRMPESNDT 484
IrcPS5  SOLR-PPGEEEDANKANNQEKLA-NNOQDKWYSHKHPDEKKGMEPWATPRVEARVYQVAGSGDYWGKTLRMPESNDT 354
SmCPS5  SOLR-PPGEEEDANKANNQEKLA-NNOQDKWYSHKHPDEKKGMEPWATPRVEARVYQVAGSGDYWGKTLRMPESNDT 513
IrkSL1  ADRITTEESTKKTWTSTKQQL-TBA-PDK-KH-EQ-VG-T-LK-N-HGLRMGVRSS-DL-D-GHKTKAAAGCSN-CD 253
SmKSL1  ADRITTEESTKKTWTSTKQQL-TBA-PDK-KH-EQ-VG-T-LK-N-HGLRMGVRSS-DL-D-GHKTKAAAGCSN-CD 258
IrkSL3  SGTATTEESTKKTWTSTKQQL-TBA-PDK-KH-EQ-VG-T-LK-N-HGLRMGVRSS-DL-D-GHKTKAAAGCSN-CD 453
IrkSL2  SGTATTEESTKKTWTSTKQQL-TBA-PDK-KH-EQ-VG-T-LK-N-HGLRMGVRSS-DL-D-GHKTKAAAGCSN-CD 462
SmKSL2  SGTATTEESTKKTWTSTKQQL-TBA-PDK-KH-EQ-VG-T-LK-N-HGLRMGVRSS-DL-D-GHKTKAAAGCSN-CD 470

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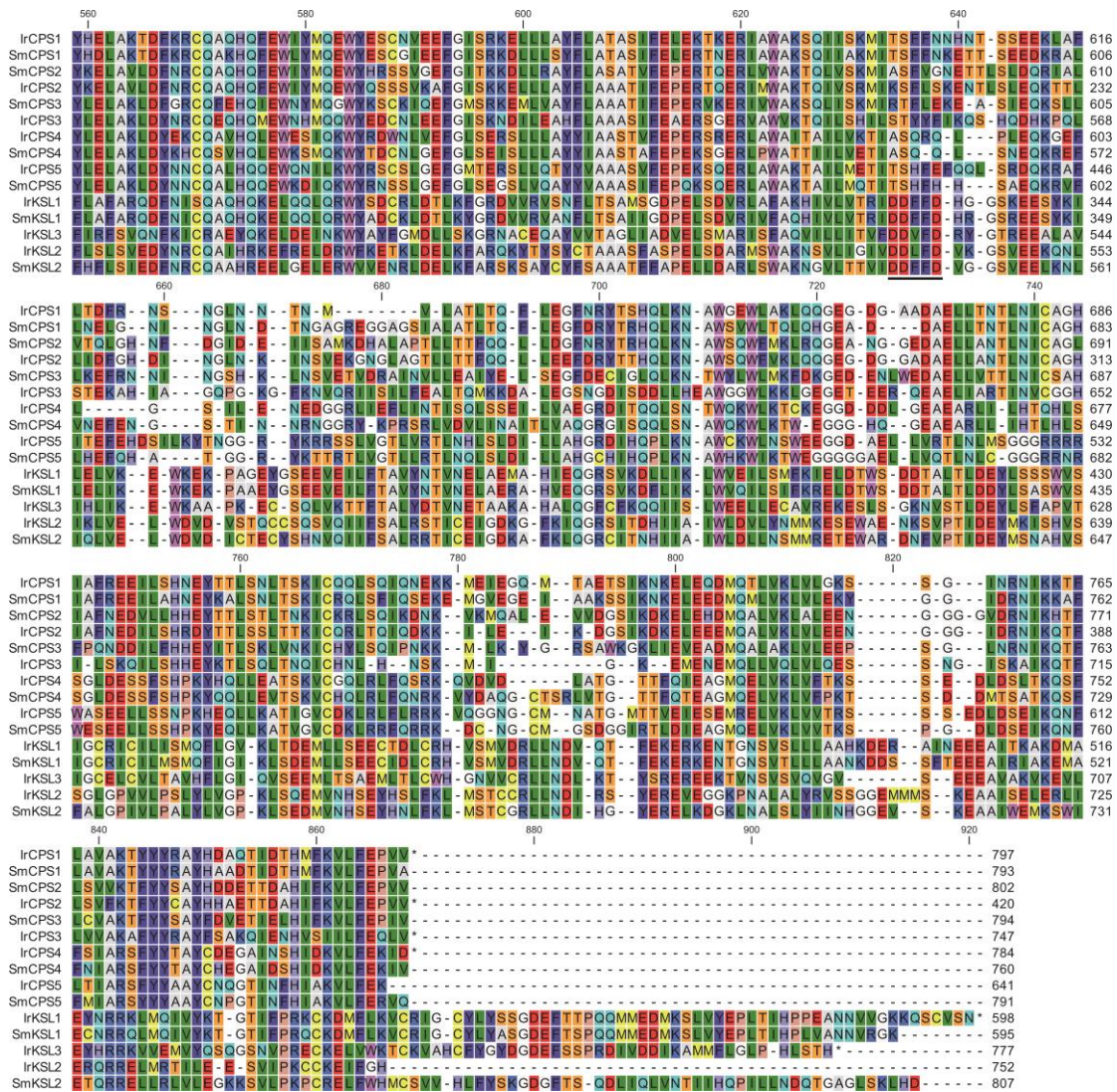


Figure S1. Amino acid alignment of diterpene synthase in *I. rubescens* and *S. miltiorrhiza*. The catalytic DXDD and DDXD motif was underlined. It was aligned and displayed with CLC sequence viewer 6.7.1 software.

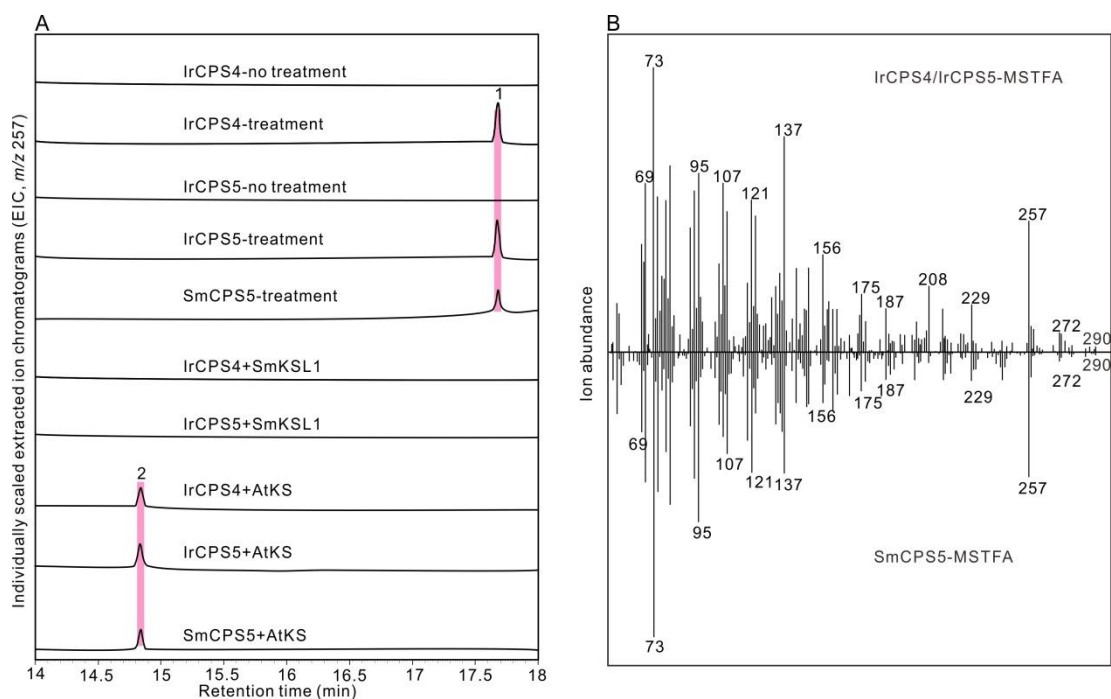


Figure S2. GC-MS analysis of in vitro assays of IrCPS4 and IrCPS5 on a TR-5ms capillary column

(A) EIC of m/z 257 of in vitro assays with IrCPS4 and IrCPS5 alone or with combination with AtKS (specific to *ent*-CPP) and SmKSL1 (specific to normal-CPP). “Treatment” means to dephosphorylate the product of CPS with 75 U bacterial alkaline phosphatase, and further derivatized with 80 μ L N-methyl-N-(trimethylsilyl) trifluoroacetamide (MSTFA) at 80 $^{\circ}$ C for 40 minutes. (B) EI mass spectrum of the dephosphorylated product of IrCPS4 and SmCPS5 after derivatization. 1. copalol, 2. *ent*-kaurene.

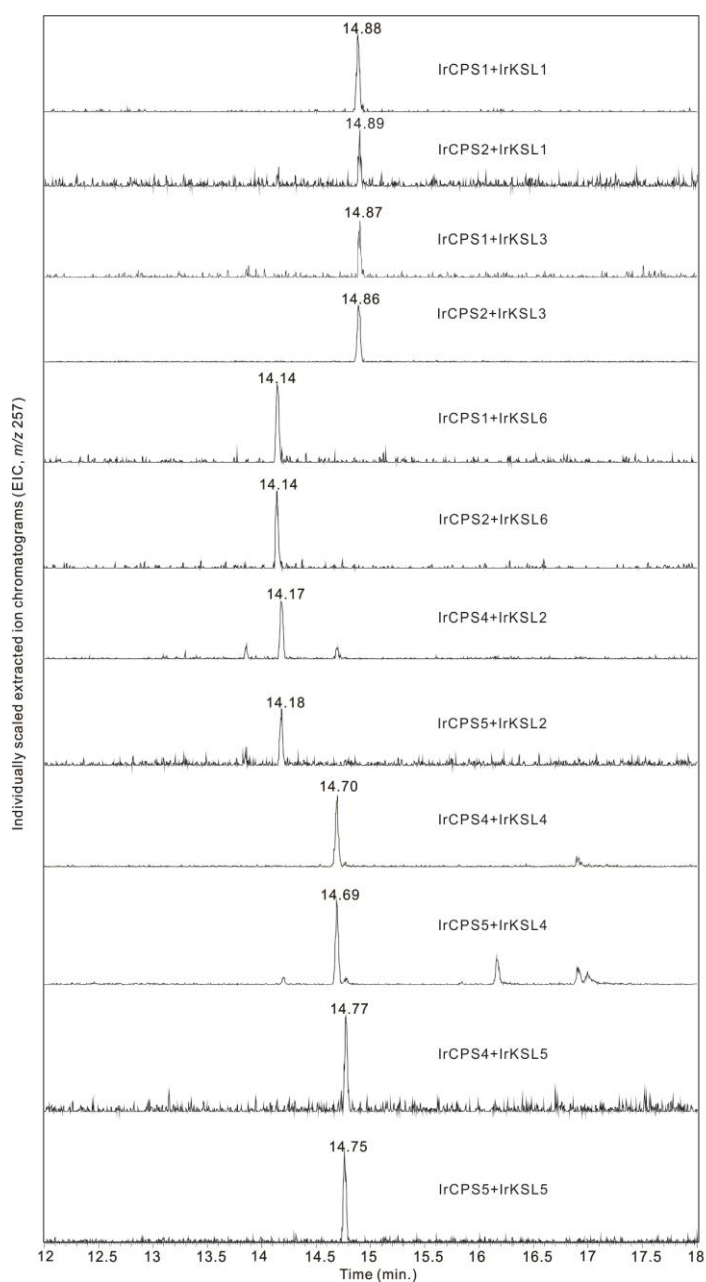


Figure S3. GC-MS analysis of different clade of IrKSL with the corresponding IrCPS on a TR-5ms capillary column. Extracted ion chromatograms (EIC) of m/z 257 of in vitro assays of the Lamiaceae-specialized CPS clade IrCPS1 and IrCPS2 combined with IrKSL1, IrKSL3 and IrKSL6, together with the IrCPS4 and IrCPS5, which was involved in the *ent*-CPP mediated biosynthetic pathway, to combine with IrKSL2, IrKSL4 and IrKSL5.

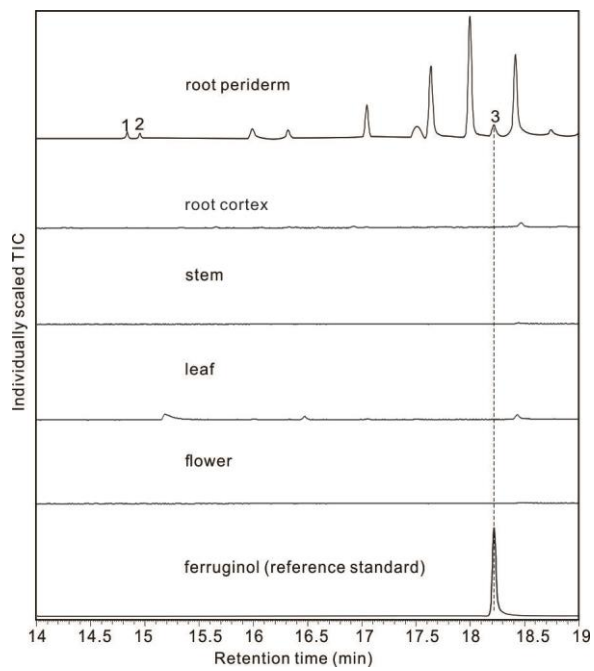


Figure S4. GC-MS detection of abietane diterpenoids in different organs. Total ion chromatograms (TIC) of diterpenoids in the hexane extract of the root periderm, stem, leaf, flower and the authentic standard of ferruginol. (1) abietatriene, (2) miltiradiene and (3) ferruginol.

IrCYP76AH30	ME T I A L L A A L F F I . A L T C F L T S G R R R N L P P G P Y P L P I I G N M L Q L G S N P H Q S F A Q L S K K Y G	59
SmCYP76AH1	M D S F P L L A A L F F I A A T I T F L S F R R R R N L P P G P F P Y P I V G N M L Q L G A N P H Q V F A K L S K R Y G	60
RoCYP76AH22	M D S F P L L A T L F F I L A A T W F I S F R R R R N L P P G P F P Y P I V G N M L Q L G S Q P H E T F A K L S K K Y G	60
RoCYP76AH23	M D S F P L L A T L F F I L A A T W F I S F R R R R N L P P G P F P Y P I V G N M L Q L G S Q P H E T F A K L S K K Y G	60
SfCYP76AH24	M D P F P L V A A A L F I . A A T W F I T F R R R R N L P P G P F P Y P I V G N M L Q L G S Q P H E T F A K L S K K Y G	59
Consensus	m l a f i a f r r r n l p p g p p i g n m l q l g p h f a l s k y g	
IrCYP76AH30	P L M S I H L G S L Y T V I V S S P E M A K E I L L H K H G Q A F S G R T I A Q A V H A C D H D K I S M G F L P V T S V W	119
SmCYP76AH1	P L M S I H L G S L Y T V I V S S P E M A K E I L L R H G Q V F S G R T I A Q A V H A C D H D K I S M G F L P V A S E W	120
RoCYP76AH22	P L M S I H L G S L Y T V I V S S P E M A K E I M H K Y G Q V F S G R T V A Q A V H A C G H D K I S M G F L P V G G E W	120
RoCYP76AH23	P L M S I H L G S L Y T V I V S S P E M A K E I M H K Y G Q V F S G R T V A Q A V H A C G H D K I S M G F L P V G G E W	120
SfCYP76AH24	P L M S I H L G S L Y T V I I S S P E M A K E I M H K Y G Q V F S G R T I A Q A V H A C D H D K I S M G F L P V G A E W	119
Consensus	p l m s i h l g s l y t v i s s p e m a k e i h g q f s g r t a q a v h a c h d k i s m g f l p v w	
IrCYP76AH30	R D L R K I C K E Q M F S H Q S L E A S E G L R H Q K L Q L L D Y A Q K C E T G R A V D I R E A S F I T T L N L M S	179
SmCYP76AH1	R D M R K I C K E Q M F S N Q S M E A S Q G L R R Q K L Q L L D H V Q K C S D S G R A V D I R E A A F I T T L N L M S	180
RoCYP76AH22	R D M R K I C K E Q M F S H Q S M E D S Q G L R K Q K L Q L L D Y A Q K C S E R G R A I D I R E A A F I T T L N L M S	180
RoCYP76AH23	R D M R K I C K E Q M F S H Q S M E D S Q G L R K Q K L Q L L D Y A Q K C S E R G R A I D I R E A A F I T T L N L M S	180
SfCYP76AH24	R D M R K I C K E Q M F S H Q S M E D S O N L R K Q K L Q L L E Y A Q K C S E E G R G I D I R E A A F I T T L N L M S	179
Consensus	r d r k i c k e q m f s q s e s l r q k l q l l q k c g r d i r e a f i t t l n l m s	
IrCYP76AH30	A T M F S T Q A T E F F S E A T K E F K E I I E G V A T I V G V P N F A D Y F P I L R P F D L Q G I K R Q A D G Y F G R	239
SmCYP76AH1	A T L F S S Q A T E F D S K A T M E F K E I I E G V A T I V G V P N F A D Y F P I L R P F D P Q G V K R R A D V Y F G K	240
RoCYP76AH22	A T L F S M Q A T E F D S K V T M E F K E I I E G V A S I V G V P N F A D Y F P I L R P F D P Q G V K R R A D V Y F G R	240
RoCYP76AH23	A T L F S M Q A T E F D S K V T M E F K E I I E G V A S I V G V P N F A D Y F P I L R P F D P Q G V K R R A D V Y F G R	240
SfCYP76AH24	A T L F S M Q A T E F D S K V T M E F K E I I E G V A S I V G V P N F A D Y F P I L R P F D P Q G V K R R A D V Y F G R	239
Consensus	a t f s q a t e f s t e f k e i e g v a i v g v p n f a d y f p i l r p f d q g k r a d f g	
IrCYP76AH30	L L K K I E G Y L N E R V E S R R L N P D A P R K N D F L E T I V V D T I E A D E Y K L T D H L T H L M L D L F V G G S	299
SmCYP76AH1	L L A K I E G Y L N E R L E S K R A N P N A P K K D D F L E I V V D I I Q A N E F K L K T H F T H L M L D L F V G G S	300
RoCYP76AH22	L L A M I E G F L N E R V E S R R T N P N A P K K D D F L E T L V D I L E A N D C K L K T D H L T H L M L D L F V G G S	300
RoCYP76AH23	L L A M I E G F L N E R V E S R R T N P N A P K K D D F L E T L V D I L E A N D C K L K T D H L T H L M L D L F V G G S	300
SfCYP76AH24	L L G L I E G Y L N E R I E F R K A N P N A P K K D D F L E T L V D A L D A K D Y K L K T B E L T H L M L D L F V G G S	299
Consensus	l l i e g l n e r e n p a p k d f l e v d a k l t h t h l m l d l f v g g s	
IrCYP76AH30	E T N T S I E W I M S E L V I N E D K M A R V K D E I K S V V G D K K I V D E S E M P R L P Y L Q A I K E V L R I H	359
SmCYP76AH1	D T N T S I E W A M S E L V M N E D K M A R L K A E L K S V A G D E K I V D E S A M P K L P Y L Q A V I K E V M R I H	360
RoCYP76AH22	E T S T E I E W I M W E L I A H P D K M V K V K A E L K S V M G E E K V V D E S N M P R L P Y L Q A V V K E S M R L H	360
RoCYP76AH23	E T S T E I E W I M W E L I A H P D K M V K V K A E L K S V M G E E K V V D E S N M P R L P Y L Q A V V K E S M R L H	360
SfCYP76AH24	E T S T E I E W I M W E L L A S P E K M A K V K A E L K S V M G E E K V V D E S M M P R L P Y L Q A V V K E S M R L H	359
Consensus	t t t e w m e l p k m k e k s v g k v d e s m p r l p y l q a k e r h	
IrCYP76AH30	P P G P L L L P R R A E I D Q E V N G Y L I P K G T Q I L I N A W A T G R D P S I W K N P D S F E P E R F L D Q T V D F	419
SmCYP76AH1	P P G P L L L P R K A B S D Q E V N G Y L I P K G T Q I L I N A Y A T G R D P S I W T D P E T F D P E R F L D N K I D F	420
RoCYP76AH22	P P G P L L L P R K A B S D Q V V N G Y L I P K G T Q V L I N A W A M G R D P S I W K N P D S F E P E R F L D Q K I D F	420
RoCYP76AH23	P P G P L L L P R K A B S D Q V V N G Y L I P K G T Q V L I N A W A M G R D P S I W K N P D S F E P E R F L D Q K I D F	420
SfCYP76AH24	P P G P L L L P R K A B S D Q V V N G Y L I P K G A Q V L I N A W A M G R D P S I W K N P D S F E P E R F L D Q K I D F	419
Consensus	p p g p l l l p r a e d q v n g y l i p k g q l n a a g r d p s w p f e r f l d q t v d f	
IrCYP76AH30	K G D Y E L I P F G S G R R I C P G M P L A N R I L H M T A T L V H N F D W K L E E E T A N . A D H Q D E L F G L A	478
SmCYP76AH1	K G O D Y E L L P F G S G R R V C P G M P L A T R I L H M A T A T L V H N F D W K L E D D S T A A A D H A G E L F G V A	480
RoCYP76AH22	K G O D Y E L I P F G S G R R V C P G M P L A N R I L H T V T A T L V H N F H W E L E R P D A S H A E H Q G V L F G F A	480
RoCYP76AH23	K G O D Y E L I P F G S G R R V C P G M P L A N R I L H T V T A T L V H N F H W E L E R P D A S H A E H Q G V L F G F A	480
SfCYP76AH24	K G T D Y E L I P F G S G R R V C P G M P L A N R I L H T V T A T L V H N F D W K L E R P E A S . D A H K G V L F G F A	478
Consensus	k g d e l p f g s g r r c p g m p l a r i l h t a t l v h n f w l e h l f g a	
IrCYP76AH30	V R R A V P L K I I P L R P .	492
SmCYP76AH1	V R R A V P L R I I P I V K S	495
RoCYP76AH22	V R R A V P L K I V P F K A .	494
RoCYP76AH23	V R R A V P L K I V P F K A .	494
SfCYP76AH24	V R R A V P L K I V P I K A .	492
Consensus	v r r a v p l i p	

Figure S5. Amino acid alignment of CYP76AH30 with CYP76AH1 and CYP76AH22-24. CYP76AH1 from *S. multiorrhiza*, and CYP76AH22-24 from *Rosmarinus officinalis* and *S. fruticosa*. The three active sites involved in reciprocal activity changes from ferruginol synthase to hydroxyferruginol synthase were marked with an asterisk. It was aligned and displayed with DNAMAN.

Table S1. The number and length of all of the unigenes obtained by RNA-Seq

Sample	sequences	bases	Min	Max	Average	N50	(A+T)%	(C+G)%
All_unigene	60483	53581114	201	12119	885.89	1469	57.32	42.68

Table S2. Unigenes annotated as copalyl diphosphate synthase and kaurene synthase genes

Gene_ID	NR_protein_ID	Description	Identity	Evalue	Score	geneLength	expected_count	FPKM
c892_g1_i1	gi 347546059 gb AEP03177.1	copalyl diphosphate synthase [<i>Isodon eriocalyx</i>]	98.26	0	586	866	14	1.65
c3974_g1_i1	gi 347546057 gb AEP03176.1	putative copalyl diphosphate synthase [<i>I. eriocalyx</i>]	66.41	1.00E-43	157	359	3	0.97
c5635_g1_i1	gi 374639391 gb AEZ55684.1	copalyl diphosphate synthase 2 [<i>Salvia miltiorrhiza</i>]	77.63	0	577	1252	26	2.06
c12262_g1_i1	gi 347546057 gb AEP03176.1	putative copalyl diphosphate synthase [<i>I.eriocalyx</i>]	68.57	5.00E-24	100	268	4	1.9
c19290_g1_i1	gi 157488863 gb ABV57835.1	copalyl diphosphate synthase [<i>S. miltiorrhiza</i>]	82.32	0	1014	1829	206	10.96
c23032_g2_i1	gi 347546055 gb AEP03175.1	copalyl diphosphate synthase [<i>I. eriocalyx</i>]	96.38	0	815	1284	172.49	13.31
c23032_g1_i2	gi 347546055 gb AEP03175.1	copalyl diphosphate synthase [<i>I. eriocalyx</i>]	74.1	1.00E-125	385	936	97.94	10.6
c31669_g1_i1	gi 347546059 gb AEP03177.1	copalyl diphosphate synthase [<i>I. eriocalyx</i>]	99.15	3.00E-76	245	353	3	1
c36297_g1_i1	gi 374639403 gb AEZ55690.1	copalyl diphosphate synthase 4, partial [<i>S. miltiorrhiza</i>]	83.58	2.00E-32	119	202	1	0.71
c37986_g1_i1	gi 157488863 gb ABV57835.1	copalyl diphosphate synthase [<i>S. miltiorrhiza</i>]	57.43	2.00E-99	314	748	10	1.38
c38849_g1_i1	gi 359479685 ref XP_002272869.2	PREDICTED: <i>ent</i> -copalyl diphosphate synthase, chloroplastic [<i>Vitis vinifera</i>]	35.15	5.00E-15	77.4	451	10	2.46
c44161_g1_i1	gi 374639391 gb AEZ55684.1	copalyl diphosphate synthase 2 [<i>S. miltiorrhiza</i>]	91.84	2.00E-59	199	296	2	0.83
c7500_g1_i1	gi 374639401 gb AEZ55689.1	kaurene synthase 2, partial [<i>S. miltiorrhiza</i>]	72.95	2E-49	174	467	65	15.36
c8557_g1_i1	gi 374639401 gb AEZ55689.1	kaurene synthase 2, partial [<i>S. miltiorrhiza</i>]	85.2	5.00E-118	364	900	41	4.63
c9905_g1_i1	gi 374639401 gb AEZ55689.1	kaurene synthase 2, partial [<i>S. miltiorrhiza</i>]	69.41	3.00E-25	105	333	34	12.14
c18094_g1_i1	gi 157072589 gb ABV08817.1	kaurene synthase [<i>S. miltiorrhiza</i>]	78.69	0	937	2084	167	7.76
c20365_g1_i2	gi 157072589 gb ABV08817.1	kaurene synthase [<i>S. miltiorrhiza</i>]	36.23	2.00E-73	250	1469	30.87	2.07
c20365_g1_i5	gi 157072589 gb ABV08817.1	kaurene synthase [<i>S. miltiorrhiza</i>]	38.32	2.00E-78	262	1403	0	0
c20365_g1_i6	gi 157072589 gb ABV08817.1	kaurene synthase [<i>S. miltiorrhiza</i>]	36.64	2E-59	134	1572	113.32	7.06
c21382_g1_i1	gi 374639401 gb AEZ55689.1	kaurene synthase 2, partial [<i>S. miltiorrhiza</i>]	74.3	9.00E-91	291	795	188	24.3
c21382_g2_i1	gi 374639401 gb AEZ55689.1	kaurene synthase 2, partial [<i>S. miltiorrhiza</i>]	58.09	6E-74	251	1097	29.46	2.69
c21382_g2_i2	gi 374639401 gb AEZ55689.1	kaurene synthase 2, partial [<i>S. miltiorrhiza</i>]	65.55	0	524	1624	97.99	5.9
c21382_g2_i3	gi 374639401 gb AEZ55689.1	kaurene synthase 2, partial [<i>S. miltiorrhiza</i>]	67.06	9.00E-176	518	1231	112.36	9.06
c21382_g2_i4	gi 374639401 gb AEZ55689.1	kaurene synthase 2, partial [<i>S. miltiorrhiza</i>]	71.35	1.00E-74	245	552	2.64	0.51

c21382_g2_i6	gi 374639401 gb AEZ55689.1	kaurene synthase 2, partial [<i>S. miltiorrhiza</i>]	69.25	0	700	1523	299.59	19.31
c21382_g2_i8	gi 374639401 gb AEZ55689.1	kaurene synthase 2, partial [<i>S. miltiorrhiza</i>]	80.95	0	742	1317	146.97	11.04
c30148_g1_i1	gi 29825615 gb AAO92305.1	<i>ent</i> -kaurene synthase [<i>Nicotiana sylvestris</i>]	50.71	3.00E-29	110	384	7	2.09
c33438_g1_i1	gi 157072589 gb ABV08817.1	kaurene synthase [<i>S. miltiorrhiza</i>]	44.32	2.00E-100	318	1269	25	1.95
c40624_g1_i1	gi 157072589 gb ABV08817.1	kaurene synthase [<i>S. miltiorrhiza</i>]	40.35	1.00E-19	89.4	355	3	0.99

Table S3. Information of diTPS gene family in *I. rubescens*

Gene	Accession No.	Length		Function annotation
		cDNA (bp)	Protein(aa)	
CPS1	KU180499	2391	796	copalyl diphosphate synthase
CPS2	KU180500	2400	799	copalyl diphosphate synthase
CPS3	KU180501	2241	746	unknown
CPS4	KU180502	2352	783	<i>ent</i> -copalyl diphosphate synthase
CPS5	KU180503	2454	817	<i>ent</i> -copalyl diphosphate synthase
KSL1	KU180504	1794	597	miltiradiene synthase/manoyl oxide synthase
KSL2	KU180505	2382	793	<i>ent</i> -isopimaradiene synthase
KSL3	KU180506	2331	776	miltiradiene synthase/manoyl oxide synthase
KSL4	KX580633	2421	806	<i>ent</i> -atisrene synthase
KSL5	KX580634	2385	794	<i>ent</i> - kaurene synthase
KSL6	KX580635	2328	775	isopimaradiene synthase

Table S4. Blast result of genes identified from this paper to the reference transcriptome sequencing dataset (Zerbe et al. 2013)

Query genes	seq. in reference	Score	Expect	Identities
IrCPS1*	IRL_24072012_comp91626_c0_seq8	4668 bits (2355)	0	2382/2391(99)
IrCPS2	IRL_24072012_comp91626_c0_seq8	363 bits (183)	3.00E-98	527/641 (82%)
IrCPS3	IRL_24072012_comp82593_c0_seq1	4349 bits (2194)	0	2231/2242 (99%)
	IRL_24072012_comp97718_c1_seq26	2759 bits (1392)	0	1431/1444 (99%)
IrCPS4	IRL_24072012_comp78356_c3_seq1	763 bits (385),	0	394/397 (99%)
	IRL_24072012_comp97718_c1_seq35	759 bits (383)	0	383/383 (100%)
IrCPS5	IRL_24072012_comp62394_c0_seq1	2123 bits (1071)	0	1074/1075 (99%)
	IRL_24072012_comp1867024_c0_seq1	519 bits (262)	e-145	268/270 (99%)
IrKSL1*	IRL_24072012_comp96546_c0_seq4	3503 bits (1767)	0	1789/1795 (99%)
IrKSL2	IRL_24072012_comp98782_c3_seq4	1877 bits (947)	0	1193/1275 (93%)
IrKSL3*	IRL_24072012_comp87946_c0_seq1	4409 bits (2224)	0	2307/2334 (98%)
IrKSL4	IRL_24072012_comp98782_c3_seq4	2305 bits (1163)	0	1467/1569 (93%)
IrKSL5	IRL_24072012_comp98782_c3_seq2	2282 bits (1151)	0	1773/1977 (89%)
IrKSL6	IRL_24072012_comp833254_c0_seq1	345 bits (174)	6.00E-93	181/182 (99%)

* indicate genes with the full length in the reference dataset (Zerbe et al., 2013).

Table S5. List of plant DiTPS involved in this paper

Gene	Species	GenBank Accession	Funtional Annotation*	Ref.
AgAS	<i>Abies grandis</i>	AAB05407	abietadiene synthase	Vogel et al.,1996
AbCAS	<i>Abies balsamea</i>	AEL99953	cis-abienol synthase	Zerbe et al., 2012
AtCPS	<i>Arabidopsis thaliana</i>	AAA53632	ent-copalylidiphosphatesynthas	Sun et al., 1994
AtKSL	<i>A. thaliana</i>	AAC39443	ent-kaurene synthase	Yamaguchi et al., 1998
CcCLS	<i>Cistus creticus</i>	ADJ93862	copal-8-ol diphosphate synthase	Falara et al., 2010
CfTPS1	<i>Coleus forskohlii</i>	KF444506	copalylidiphosphate synthase	Pateraki et al., 2014
CfTPS14	<i>C. forskohlii</i>	AGN70881	ent-kaurene synthase	Zerbe et al., 2013
CfTPS2	<i>C. forskohlii</i>	KF444507	copal-8-ol diphosphate synthase	Pateraki et al., 2014
CfTPS3	<i>C. forskohlii</i>	KF444508	(13R) manoyl oxide synthase	Pateraki et al., 2014
CfTPS4	<i>C. forskohlii</i>	KF444509	miltiradiene synthase	Pateraki et al., 2014
CmCPS1	<i>Cucurbita maxima</i>	AAD04292	ent-copalylidiphosphate synthase	Smith et al.,1998
CmCPS2	<i>C. maxima</i>	AAD04293	ent-copalylidiphosphate synthase	Smith et al.,1998
CmKS	<i>C. maxima</i>	AAB39482	ent-kaurene synthase	Yamaguchi et al., 1996
EpTPS1	<i>Euphorbia peplus</i>	KC702395	ent-kaurene synthase	Zerbe et al., 2013
EpTPS23	<i>E. peplus</i>	KP889108	<i>Class I diTPS</i>	Andersen-Ranberg et al., 2016
EpTPS7	<i>E. peplus</i>	AGN70883	ent-copalylidiphosphate synthase	Zerbe et al., 2013
EpTPS8	<i>E. peplus</i>	KP889107	<i>Class I diTPS</i>	Andersen-Ranberg et al., 2016
GbLS	<i>Ginkgo biloba</i>	AAL09965	levopimaradiene synthase	Schepmann et al., 2001
GrTPS1	<i>Grindelia robusta</i>	AGN70886	13-labden-8,15-diol pyrophosphate synthase	Zerbe et al., 2013
GrTPS2	<i>G. robusta</i>	KR089902	labda-7,13E-dienyl diphosphate synthase	Zerbe et al., 2015
GrTPS4	<i>G. robusta</i>	KR089903	ent-kaurene synthase	Zerbe et al., 2015
GrTPS6	<i>G. robusta</i>	AGN70887	manoyl oxide	Zerbe et al., 2013
HvCPS	<i>Hordeum vulgare</i>	AAT49065	ent-copalylidiphosphate synthase	Spielmeyer et al., 2004
HvKSL1	<i>H. vulgare</i>	AAT49066	ent-kaurene synthase	Spielmeyer et al., 2004
IeCPS1	<i>Isodon eriocalyx</i>	AEP03177	ent-copalylidiphosphate synthase	Li et al., 2012
IeCPS2	<i>I. eriocalyx</i>	AEP03175	ent-copalylidiphosphate synthase	Li et al., 2012
LsCPS	<i>Lactuca sativa</i>	BAB12440	ent-kaurene synthase	Sawada et al., 2008

LsKS	<i>L. sativa</i>	BAB12441	<i>ent</i> -kaurene synthase	Sawada et al., 2008
MvCPS1	<i>Marrubium vulgare</i>	KJ584450	peregrinol diphosphate synthase	Zerbe et al., 2014
MvCPS3	<i>M. vulgare</i>	KJ584452	copalyl diphosphate synthase	Zerbe et al., 2014
MvEKS	<i>M. vulgare</i>	KJ584453	<i>ent</i> -kaurene synthase	Zerbe et al., 2014
MvELS	<i>M. vulgare</i>	KJ584454	9,13-epoxy-labd-14-en synthase	Zerbe et al., 2014
NtABS	<i>Nicotiana tabacum</i>	CD33019	cis-abienol synthase	Sallaud et al., 2012
NtCPS2	<i>N. tabacum</i>	CCD33018	copal-8-ol diphosphate synthase	Sallaud et al., 2012
OsCPS1	<i>Oryza sativa</i>	BAD42449	<i>ent</i> -copalyldiphosphate synthase	Otomo et al., 2004
OsCPS2	<i>O. sativa</i>	AAT11021	<i>ent</i> -copalyldiphosphate synthase	Prisic et al., 2004
OsCPS4	<i>O. sativa</i>	AAS98158	<i>syn</i> -copalyldiphosphate synthase	Xu et al., 2004
OsKLS8	<i>O. sativa</i>	Q6BDZ9	stemar-13-ene synthase	Nemoto et al., 2004
OsKS1	<i>O. sativa</i>	AAQ72559	<i>ent</i> -kaurene synthase	Margis-Pinheiro et al., 2005
OsKSL10	<i>O. sativa</i>	Q2QQJ5	<i>ent</i> -sandaracopimara-8(14),15-diene synthase	Peters. 2006
OsKSL11	<i>O. sativa</i>	Q1AHB2	stemod-13(17)-ene synthase	Morrone et al., 2006
OsKSL4	<i>O. sativa</i>	AAU05906	pimara-7,15-diene synthase	Wilderman et al., 2004
OsKSL5	<i>O. sativa</i>	Q6Z5J6	<i>ent</i> -pimara-8(14),15-diene synthase	Margis-Pinheiro et al., 2005
OsKSL6	<i>O. sativa</i>	A4KAG8	<i>ent</i> -isokaur-15-ene synthase	Xu et al., 2007
OsKSL7	<i>O. sativa</i>	BAC56714	<i>ent</i> -cassa-12,15-diene synthase	Cho et al., 2004
PaIso	<i>Picea abies</i>	AAS47690	isopimaradiene synthase	Martin et al., 2004
PaLAS	<i>P. abies</i>	AAS47691	levopimaradiene/abietadiene synthase	Martin et al., 2004
PgCPS	<i>P. glauca</i>	ADB55707	<i>ent</i> -copalyldiphosphate synthase	Keeling et al., 2010
PgKS	<i>P. glauca</i>	ADB55708	<i>ent</i> -kaurene synthase	Keeling et al., 2010
PpCPS/KS	<i>Physcomitrella patens</i>	BAF61135	<i>ent</i> -kaurene synthase	Hayashi et al., 2006
PsaCPS	<i>Pisum sativum</i>	AAB58822	Bifunctional <i>ent</i> -copalyldiphosphate synthase	Ait-Ali et al., 1997
PsCPS	<i>P. sitchensis</i>	ADB55709	<i>ent</i> -copalyldiphosphate synthase	Keeling et al., 2010
PsIso	<i>P. sitchensis</i>	ADZ45512	Isopimaradiene synthase	Keeling et al., 2011
PsKS	<i>P. sitchensis</i>	ADB55710	<i>ent</i> -kaurene synthase	Keeling et al., 2010
PsLAS	<i>P. sitchensis</i>	ADZ45517	Levopimaradiene/abietadiene synthase	Keeling et al., 2011
PtKS	<i>Populus trichocarpa</i>	XP_002311286	<i>ent</i> -kaurene synthase	Tuskan et al., 2006

RcKSL1	<i>Ricinus communis</i>		<i>ent</i> -kaurene synthase	Jackson et al., 2014
RcKSL2	<i>R. communis</i>		<i>ent</i> -trachylobane synthase	Jackson et al., 2014
RcKSL3	<i>R. communis</i>		<i>ent</i> -sandaracopimaradiene synthase	Jackson et al., 2014
RcKSL4	<i>R. communis</i>		<i>ent</i> -beyerene synthase	Jackson et al., 2014
RoCPS1	<i>Rosmarinus officinalis</i>	KF805857	copalyl diphosphate synthase	Brückner et al., 2014
RoKSL1	<i>R. officinalis</i>	KF805858	multiradiene synthase	Brückner et al., 2014
RoKSL2	<i>R. officinalis</i>	KF805859	multiradiene synthase	Brückner et al., 2014
SdCPS	<i>Scoparia dulcis</i>	BAD91286	<i>ent</i> -copalyldiphosphate synthase	Nakagiri et al., 2005
ShSBS	<i>S. habrochaites</i>	B8XA41	santalene and bergamotene synthase	Sallaud et al., 2009
SIPHS	<i>Solanum lycopersicum</i>	ACO56896	phellandrene synthase	Schillmiller et al., 2009
SITPS14	<i>S. lycopersicum</i>	JN412091	<i>ent</i> -kaurene synthase	Falara et al., 2011
SITPS40	<i>S. lycopersicum</i>	JN412074	<i>ent</i> -copalyldiphosphate synthase	Falara et al., 2011
SmCPS1	<i>S. miltiorrhiza</i>	KC814639	copalyl diphosphate synthase	Gao et al., 2009
SmCPS2	<i>S. miltiorrhiza</i>	KC814640	copalyl diphosphate synthase	Cui et al., 2015
SmCPS3	<i>S. miltiorrhiza</i>	KC814641	No function	Cui et al., 2015
SmCPS4	<i>S. miltiorrhiza</i>	KP063138	labd-13-en-8-ol diphosphate synthase	Cui et al., 2015
SmCPS5	<i>S. miltiorrhiza</i>	KC814642	<i>ent</i> -copalyldiphosphate synthase	Cui et al., 2015
SmKSL1	<i>S. miltiorrhiza</i>	ABV08817	multiradiene synthase	Gao et al., 2009
SmKSL2	<i>S. miltiorrhiza</i>	KC814643	<i>ent</i> -kaurene synthase	Cui et al., 2015
SmMDS	<i>Selaginella moellendorffii</i>	AB668998	multiradiene synthase	Sugai et al., 2011
SrCPS	<i>Stevia rebaudiana</i>	AAB87091	<i>ent</i> -copalyldiphosphate synthase	Richman et al., 1999
SrKS1	<i>S. rebaudiana</i>	AAD34294	<i>ent</i> -kaurene synthase	Richman et al., 1999
SrKS2	<i>S. rebaudiana</i>	AAD34295	<i>ent</i> -kaurene synthase	Richman et al., 1999
SsLPS	<i>Salvia sclarea</i>	AET21247	copal-8-ol diphosphate synthase	Schalk et al., 2012
SsScS	<i>S. sclarea</i>	AET21246	sclareol synthase	Schalk et al., 2012
TaKSL5	<i>Triticum aestivum</i>	BAL41692	nerolidol synthase	Hillwig et al., 2011
TcTS	<i>Taxus brevifolia</i>	AAC49310	taxadiene synthase	Wildung and Croteau. 1996
TwTPS14	<i>Tripterygium Wilfordii</i>	KP889111	<i>Class II diTPS</i>	Andersen-Ranberg et al., 2016
TwTPS2	<i>T. Wilfordii</i>	KP889109	<i>Class I diTPS</i>	Andersen-Ranberg et al., 2016

TwTPS21	<i>T. Wilfordii</i>	KP889112	Class II diTPS	Andersen-Ranberg et al., 2016
TwTPS28	<i>T. Wilfordii</i>	KP889113	Class II diTPS	Andersen-Ranberg et al., 2016
TwTPS7	<i>T. Wilfordii</i>	KP889110	Class I diTPS	Andersen-Ranberg et al., 2016
ZmAn1	<i>Zea mays</i>	AAA73960	ent-copalyl diphosphate synthase	Bensen et al., 1995
ZmAn2	<i>Z. mays</i>	AAT70083	ent-copalyl diphosphate synthase	Bensen et al., 1995
ZmTPS1	<i>Zea mays</i>	NP_001105097	sesquiterpene synthase	Schnee et al., 2002
SfCPS	<i>S. fruticosa</i>	KP091840	copalyl diphosphate synthase	Božić et al., 2015
SfKSL	<i>S. fruticosa</i>	KP091841	multiradiene synthase	Božić et al., 2015
SdCPS1	<i>S. divinorum</i>	KX424876	ent-copalyl diphosphate synthase	Pelot et al., 2017
SdCPS2	<i>S. divinorum</i>	KX424877	clerodienyl diphosphate	Pelot et al., 2017
SdKSL1	<i>S. divinorum</i>	KY057342	ent-kaurene synthase like	Pelot et al., 2017

*Functional annotation is based on the main terpenoid product(s) of recombinant enzymes expressed in *E. coli*. Many TPSs produced multiple products.

Supplemental References

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Table S6. Primers used in this study

Name	Sequence(5'to 3')
RACE primer	
IrCPS2-5'-RACE1	TGCCACATAATCCTCTCTTGTGTTTCG
IrCPS2-5'-RACE2	CCGTTCTCAGTCCACACGTTATTGATGTGA
IrCPS5-5'-RACE	AGGCCTGCCATTTCCTTCCAAGCTATG
IrKSL2-5'-RACE	GGATAGTCGAGAGCGTGCTTCACTACTG
IrKSL2-3'-RACE3	TCCATTTCCTTACATATGAGGGACGTC
IrKSL4-5'-RACE	TCCGTCCTCCGCCGACCCATTCTCGGTA
IrKSL4-3'-RACE3	CTGTGAGGTTGGAGACAGAGCACACC
IrKSL5-3'-RACE	TATCCAGAGGAAAGAGATCTGGACCA
IrKSL5-5'-RACE	TATGTTGGTCCAGATCTCTTTCTCTGGA
IrKSL6-5'-RACE	TTGGCGAGTCATGAGATCTTGGGCCGTC
qRT-PCR primers for gene expression	
IrCPS1F	CCACATTGCTTTCAGAGAAGAAAT
IrCPS1R	TTAATACTAGTTTCCGCGGTCATCT
IrCPS2F	GGTCATATTGCCTTCAACGAAGAC
IrCPS2R	TCCTTATCTTTTATGCTCCCATCCT
IrCPS3F	ATAGATGCCAAGAACAACATCAGA
IrCPS3R	TTTACCGGGTTGGCCGGCAATGT
IrCPS4F	CGGTTGGCTTGGGCTATAACAGCA
IrCPS4R	TGCTTCTCCTAAATCATCATCACC
IrCPS5F	TCGTGATGCAGCTCGTTTCTCTGCC
IrCPS5R	CATCGTCATCACCGCCGTAAGTGT
IrKSL1F	TAACAGGAGACAACCTGATGCAGA
IrKSL1R	TTTGCCAACCACATTGTTAGC
IrKSL2F	CGTGTTGTCGTCTTCTAAATGA
IrKSL2R	ATCAATTCTCTCCTTTGCCTCT
IrKSL3F	ATGATCTCAAGACCTACAGCAGAG
IrKSL3R	CCTTGCAGGTCTTCCACACCAGCTCCT
IrKSL4F	TAACAGGAGACAACCTGATGCAGA
IrKSL4R	TTTGCCAACCACATTGTTAGC
IrKSL5F	CGTGTTGTCGTCTTCTAAATGA
IrKSL5R	ATCAATTCTCTCCTTTGCCTCT
IrKSL6F	ATGATCTCAAGACCTACAGCAGAG
IrKSL6R	CCTTGCAGGTCTTCCACACCAGCTCCT
IractinF	ATGGAGCCTCCAATCCAGACACTGT
IractinR	ATTCCGTTGCCCTGAGGTGCTCTT
Full length cloning primers for <i>E. coli</i> expression	
IrCPS1F	GGATCCATGGCCAGCCTGAGTAC
IrCPS1R	CTCGAGTTAAACCACAGGTTTCGAA
IrCPS2F+NotI	TTGCGGCCGCATGACCTCTATGTCATCATCTCTAAAC
IrCPS2R+XhoI	CCCTCGAGTCATACTGTTCAAATAGTACTTTG
IrCPS3F+BamHI	CGGGATCCATGGATGATAATTATCGTATTTTC

IrCPS3R+NotI	ATTTGCGGCCGCCTACACAAGCTGCTCAAATAGTATA
IrCPS4F	ATGAGCAGCAGCAGCAATGTG
IrCPS4R	TTAGTCAATTTTTTCGAACAGCAC
IrCPS5F+BamHI	CGGGATCCATGTCTATTGCTTCCACCGTCTC
IrCPS5R+NotI	TTGCGGCCGCTCAGAGTACTTTTTCAAAGAGCAC
IrKSL1F	ATGAGCTTAGCCTTCAATCTGCG
IrKSL1R	CTCGAGTTAGTTGCTAACACAACCTC
IrKSL2F+BamHI	CGGGATCCATGTCTCTTCTGCTCTCCAATTCTG
IrKSL2R+XhoI	CCCTCGAGTTAATTGAGAAGAATAGGGTCGTG
IrKSL3F+BamHI	CGGGATCCATGTCTACTCTCAAACCTAATCCCCTTC
IrKSL3R+NotI	TTGCGGCCGCTAATGAGTTGAAAGATGAGGAAGGC
IrKSL4F+BamHI	CGGGATCCATGTCTCTTATTCTCTCCTCTTTCC
IrKSL4R+XhoI	CCCTCGAGTTAGAAGTGGTTGAGGAGAATAGGT
IrK5F+BamHI	CGGGATCCATGTCTCTTCTGCTCTCCAATTCTG
IrKSL5R+XhoI	CCCTCGAGTCAA AATTGATTTAAGACAATCGGT
IrKSL6F+BamHI	CGGGATCCATGTTTTCTTCGAGTCTAAAACCTCAA
IrKSL6R+XhoI	CCCTCGAGTTAAGGAGTTGTTTTCAATACTGGA
Full length cloning primers for yeast identification	
IrCYP76AH30+BamHI	CGGGATCCATGGAAACCATTGCTCTTCTC
IrCYP76AH30+Sall	GCGTCGACTCATGGCCTAAGTGGGAATGATCT