

Supplemental figures

Identification of three monofunctional diterpene synthases with specific enzyme activities expressed during heartwood formation in Western redcedar (*Thuja plicata*) trees

Sifat Tasnim, Regine Gries and Jim Mattsson

>*TpdiTPS1* (MT468207)

```
CTTCTAATGCCTACTGAAACAAATTTGATCTCTATTTTATCAAAATGGCTCAGAAGATGTTTTCTCCGTCCATTTCA
GTTTCCAAGTCTCGAGGATGGATTTCAACCAAAACCTCTGGATTTTACCCATTGGAAAGTACTCGCGCTCAAAGAG
TCTGGCTTGCCACAACATGCCATCTGCTGTTGTTGTTGGAGAGGATGCTAAGACTCTTCAGGCTTTGAGAATAGCGC
ATAAGGAGAGTAAAATCAATCCTAATCACGCGAAACCAGATTATGTTCACTCTGTTTCAACATTTGAGGAGGCACCC
TTTGATGAGATGGATAAGAGAATAGAGGAATTGGTTACAGAGATCAAAGGGCTTTTTAATTCGATGGAAGATGGGGA
AATAAGTCCCTCTGCTTACGATACTGCGTGGGTAGCGAGAGTTCATGCCATTGATGGCTCTGTTAAACCCCAATTTT
CTCAAATGGTGGACTGGATTCTTCAAAATCAGTTACCGGACGGTTCTTGGGGAGAAAAGAGTCGCTTTTTAGCGTGT
GATAGACTGCTCAATACTCTTTCCTGCTTAGTTACTCTCTCCATCTGGGGCGTTGGAAACAATCAAGTGAACAGGGG
TCTTAATTTCTTGAGGAGAAATACAGAAGGAATGATTAAAGAAGCACTCGGTCATCATCAACCAAGGGATTGACA
TGGTCTTTCTGTACTGCTGAATGAAGCCAAACTTTTGGGTTTGATCTTCTTATGGGCTATATATCGTTAAACAA
ATACGCGAAAAGCCAGACTTGGAATTGAAAAAGTATTTGTTGAAGAGCTACACGGTCATCCCTCAACAATGTTACA
GTGTCTGGAAGGCGTACAAGAAATAATTGATTGGAAGGGTCTGAAACTGCAATCCAAGGATGGATCTTCTCTG
GCTCGCCAGCATCTACAGCTTGCGTATTTATGCACACAGGAGACATTAAATCTCTCCAATTTTTGACGAGCCTTGT
AAAAAGTTTGAGACCATGTGCCGAGCATGTATCCGGTGGATATAGCGGAGCGTTTAAGAGCCGTGGATTGCGTTGA
GCGTCTTGGAAGTGAACGCCATTTTCAAACGGAATTAACAAGCAATGGATTATGTGTTCCAGTACTGGAGTGAAA
GAGGCATTGGATTTGGAAGGGAAAGCCTGGTTCCTGATATTGATATTACAGCCACTGCCTTCAGGCTTCTCAGAACC
TTCGGCTACTCTGTATCTTCCGAGGTTCTGCAAAACATTAAAGCCGAGGCTGAAGAAGTCTTAAAGCTGTCTGGTAA
CGAAAACAGCGCAGGAATAATCGGAATATTGAGCCTGTATAGATCTTCACAGCTTAACTTTCCGGGCGAAATTGTAA
TGAAGGAAATAGATTGCTTTGCAAAAGATTACCTGGCTGAATTCCTGCAAAACCAAGAAGTCTTCTCAGGTGAAGGTT
GTCAAGGAAAACCTTCCCGAAGAGGTTGAATATGCTTTGTCTGCTCAATGGAATAGAAATATGCCAAGGCTGATGTC
TAGAAATCAGATAGAATTGTTTAAATCCCAATGACCTATGGCTGGGGAAGACATTATATCACCTGCCAAATGCTAGCA
ATGACAAGTATTTAGAATTGGCCAAACTCGACTTCAACCGCATTTCAGGCTACACACAGATTGAAATACAACGAATA
CAGAGATGGTACAAGGATTGCAATTTCCCGCGGTTGGATTTTACTCGTCACAGAGAAGTGGCAGTTTACTGGACCTC
TTCAGCGGTGATGTTTGAACCACAATACACCGATTGCAGACTCGATTACGCAAAAGCCGGACTCCTGGCTACTATCA
CAGACGACCTCTATGAATCCTATGCAACTCTCAACCAACTCAAGCTTTTCAATGAAGCTTTGAAAGATGGGATCCA
TTAATGAGCGAGCAACTGCCAGAGGACATGAAAATAGTTTTTATGGGAATCTATAACACTTTGACCGATATTTCTGA
GCGAGCACTGAAGGTTCAAGGTCGTGATGTGCTTCTTACCTGCGCCAACAGTGGTTAAATCTGTTGTTTCAAGTTTCA
CAAAGGAAAGAGAGTGGATGGAAAGAAGTTATTCGCCATCATTGGATGAATACTGGGCGAATGCAGAAGTGTGATA
GCACTGGAAACAATATCCTGTGCGCAATATTTTCTACGGGAAATTTTCTTCTGATCGCATTCTGGAGAAGATTAA
CTTTCTGGATCTGGTCAAGTCAAAACAGGGCGTCTTATGAACGACGTTAGAACTTTCCAGAAGGAAAGAGATCGCGGG
AATTGGCTTCATTTCGTAGAATGCTACAAAAATGAGCTCCATGGATGCACTGAAGAAGAAGCCCTGAATTACATGGAG
AGAATGAACGAAGAGGCCCTTATCAATTTGAACTACCATTTTCTAATGCGATCAGACATACCTAAGTGCTACAGAAC
ACTTCTTTTCAACACGGCTAGGATAATGCAATGATTTACAGGAAGGAAGACGGTTTTTCGAAATGCCGCGGAGTACC
TCGAAGATTCAATTAATAAATCTCTGTACGAACAGTGCTGTAACAGATTACTATTCTGTAGTGTTGAAATTCGAAC
ATCAGTCAAATAAAAAAATTTTCCAAATGTTAATAAATATTTTTTATTACTAAAAAAGGCATCATTACAATCAT
GGTAATATTATTAGTTAATTTTCTGCAAAAAA
```

>TpdiTPS1

MAQKMFSFSPISVSKSRGWISTKTSGFSPIGKYSRSLACHNMPSAVVVGEDAKTLQALRIAHKESKINPNHAKPDY
VHSVSTFEEAPFDEMCKRIEELVTEIKGLFNSMEDGEISPSAYDTAWVARVHAIDGSVKPQFPQMVWDWILQNLPLDG
SWGEKSRFLACDRLNLNTLSCLVTL SIWGVGNQVNRGLNFLRRNTEGMIKEALGHHQPKGFDMVFPVLLNEAKLLGL
DLPYGLYIVKQIREKPDLELKKVFVEELHGH PSTMLQCLEGVQEIIDWKRVLKLQSKDGSFSGSPASTACVMHTGD
IKSLQFLTSLVKKFGDHVPSMPVDIAERLRAVDCVERLGLERHFQTEIKQAMDYVFQYWSERGIGFGRESLVPDID
ITATAFRLRLRTFGYSVSSEVLQNIKAEAEELLKLSGNENSAGIIGILSLYRSSQLNFPGEIVMKEIDCFADYLAEF
LQTKNFSQVKVVKENLPEEVEYALSAQWNRNMPRLMSRNQIELFNPNDLWLGKTLYHLPNASNDKYLELAKLDFNRI
QATHRFEIQIRIQRYKDCNFPRLDFTRHREVAVYWTSSAVMFEPQYTDCLDYAKAGLLATITDDLYESYATLNQLK
LFNEAFERWDPLMSEQLPEDMKIVFMGIYNTLTDISERALKVQGRDVLPLYRQQWLNLLFSFTKEREWMSRYSYPSL
DEYWANA EVSIALETTILSPIFSTGNFLPDRILEKINFLDLVSQTGRMLMNDVRTFQKERDRGELASFVECYKNELHG
CTEEELNYMERMNEEALINLNYHFLMRSDIPKCYRTLLFNTARIMQMIYRKEDGFRNAAEYLEDSEIKKSLYEPVL

>TpdiTPS2 (MT468208)

GGAATCTAATTGAGATTTGGCAGGGTATGCCCTGTGCAGCTCCGATAAAACCTCTCTCTCTCTACTCCCCATGGGA
TTCAAAGTCTTCTTCAACAGGCGACATCTAATTTGTTAAAAATGTCCCAGAGTTTGTGTCCGCGCCTCAGTTTGT
TCGAAGCCTACTACCAAATCCACACAACGTCTTTCCAATACTTCTCTGCCTTTTACAACTACGCTCGCATTAAAGAG
CATAGATTGCTACAACATGACATCTGCTCCTGCTCTTGGCGACAATGCGAAAACACTTCACGCTGCAGCGATTGCGC
ATCCGGAGCCCAAATCTATCCTAATGCTGGGAAGCCAGATTATGTTTATTCTAATTCAACATTTGAGGAGGCACCG
TTGGAGGAGATGGATAAGCGAATAGAGGCATTGGTTGCGGAGATCAAAGAGCTGTTTTATTCAATGGAAGATGGGGA
AATAAGTCCTTCCGCATACGATACTGCGTGGGTAGCGAGAGTGCCTGCCATTGATGCCTCCGCTCAACCCCAATTC
CCCAATTGCTGGACTGGATTCTTCAGAATCAGTTAGCGGACGGTTTCTGGGGCCAGCAGAGTCGCTTTTTAGCGTCT
GATAGGTTCTCTCAATACTCTTGCCTGCCTCCTTACTCTCACCTTCTGGGGCGTTGGAAACAATCAAGTGCAGAGAGG
TCTTCATTTCTTAAGAGGAAATATGGAAGCAATGGTTAAAGAAGCTGTAGCATTTCGGTCATCAAGGATTTCGAGATGG
TTTTGCCTGCACTGTTGAATGAAGCCAAACATTTGGGCTTGGATCTTCCTTACGAGCTACCTATCATCCAGCAAATA
AACAAAAAGAGGGACTCCGAATTGAAAAAGGTATCTGTTGAGGAGCTACACACGCATCCGACAGCAATGTTGCAGTG
TCTGGAAAGCATACAAGAAGTAGTCGATTGGAAAGACATCCTGAAATTGCAATCGAAGGATGGGTCTTTCTCAGGCT
CGCCAGCATCTACAGCTTGTGTATTTATGCACACCGGAGATAAGAAATGCCTACGATTCTTGGCGGGTCTTGTGTA
AAGTTTGAAGACTATGTCCCCTGCATGTATCCAGTGGACATAGCAGAGCGTTTGGAGGCGGTGGATAGTGTGAACG
TCTGGGGCTTGAACGCCATTTCCAAACGGAGATCAAACAAGCCTTGGACTATGTGTTCCAGTACTGGGGTGAAAGAG
GAGTTGGATTTGGAAGGGACAGCCTGGTTCCGGATATTGATGTACAGCCACGGGCTTCAGGCTTCTCAGGATGTTT
GGCTACACTGTGTCTCCAGACTTTCTGCAAAACATCAAAGACGAAGCTGAAGAACTCTGTAAGCTGTCTGATGGTG
AAACAGGGGAAGAGTAATCGACATGCTGAGCCTGTATAGATGCTCACAGATTAACCTTTCCGGGAGAAAATGTAATGA
GAGAAATAGGTGCATTTGCCAAAGATTACTTGGCCGAATCCCTGCAAGCAACAACCTTTTCTCAGGCGACGGCTGTC
AAGGATAACCTTCGCCAAGAGGTGCAATATGCTTTGTTTGCCAGATGGAATAGAAATATGCCGAGACTGGTGATTAT
AAATAACATAGAAGTGTGTTAATCCCGATGACTTATGGCTGGGGAAGACATTATATCAAATGCCAAATGCGAGCAACG
GCAAGTATTTAGAATTGGCCAACTCGAGTTCAACCGCACTCAGGCTATACACAGATCCGAAATACAACATATTAAG
AGATGGTACAAGGCTTGCAATTTCCCCCAGCTGGAATTTACTCGTCACAGAGAAGTGGCAATCTACTGGACTGCGGC
AGCGGTAATGCCCGATCCCCAATACACCGACTGTAGACTCGCTTATGCAAAAGCAGGAATCATGGCTGTTATCACAG
ACGACTTGTATGACACCTGTGCAACTCTGGAGCAGGCCAAGCTCTTCAACGAAGCTTTTGAAAGGTGCGCGCTTTA
ATCCCCATCTCAGTTAATGCGAATAAGGAATTGGAATCGGCGATATTAACATTGATTGTGTTTATGGGGTGCAGATG
GGATACAGAGCAAATCGAGCATCTACCAGAGGAGATGAGAATAGTATTTATGGGGCTGTACAACACTTTGAGGGAGA
TATCTGAAGGAGCGCGGGAGGTCCAAGGGCGTGATGTGCTTCCTTACCTGCGGCAAAAGTGGTTGGATCTGTTTACAG
AGATACACGAAAGAAACAGAGTGGATGGAAGGAGGCATTTCGCCGTCATTAGAAGAATACTGGGAGAACGCGGTGGA
GTCGATAGCACTGGGAGTCACTACCCTCACCCCAATATTCTCTACCCAAGATCTTCTTCTGATCATCTCCTCCAGA
AATTTGACTTCCGCGCAGACTTTCTGAATCTCGTCAGTCTCACGGGGCGCCTCATTAACGACGTGAGAACTTTCCAG
GAGGAAAGAGATCGGGGGGAATTGGCTTCATGCGTGCAATGCTACAGAAATGATAATCCGGGATGCACGGAAGAAGA
AGCCCTGAATTATCTGTACGGGGTGAATGAGGACGCCCTGACTAAATTGAATTATCAGTTTTTTGATGCGTGAAGACA
TTCCCAAGAGCTTCAGAACTGTTCTTTTCAACACGGCCAGGGTAATGCAATTGTTTTACAGGAACATTGACGGCTTT
CTAAATGCCGCCGAAGAGATGAAAGTCTTCATTAAAAAGACTCTCTATGAACCCCTGCTCTAATAAATTGCTCTATT
GGATGAACTGTGTAATAAATGAAATTCCATTTTTTTTTTAGTTTTTGGTGAATATATTTGAAGGAGAACTTATTAA
TGTACACTTCAATTTATGAAAGGATAACGAATCAAATTTACTATCATT

>TpdiTPS2

MSQSLCPRLSLFSKPTTKSTQRLSNTSLPFTNYARIKSIDCYNMTSAPALGDNAKTLHAAAIAHPEPKIYPNAGKPD
YVHSNSTFEEAPLEEMDKRIEALVAEIKELFYSMEDGEISPSAYDTAWVARVPAIDASAQPQFPQLLDWILQNQLAD
GSWGQQSRFLASDRFLNTLACLTLTFWGVGNQVQRGLHFLRGNMEAMVKEAVAFGHQGFEMVLPALLNEAKHLGL
DLPYELPIIQQINKKRDELKKSVEELHHTPTAMLQCLESIQEVVDWKDILKLQSKDGSFSGSPASTACVMHTGD
KKCLRFLAGLVTKFEDYVPCMPVDIAERLRAVDSVERLGLERHFQTEIKQALDYVFQYWGERGVGFRDSLVPDID
VTATGFRLLRMFGYTVSPDFLQNIKDEAEELCKLSDGENRGRVIDMLSLYRCSQINFPGENVMREIGAFKDYLAES
LQSNFNSQATAVKDNLRQEVEYALFARWNRNMPRLVIINNIEVFNPDDLWLGKTLYQMPNASNGKYLELAKLEFNRT
QAIHRSEIQHIKRWKACNFPQLEFTRHREVAIYWTAAVMPDPQYTDCLAYAKAGIMAVITDDLYDTCATLEQAK
LFNEAFERSPLIPISVNANKELESAILTLIVFDGCRWDTEQIEHLPEEMRIVFMGLYNTLREISEGAREVQGRDVL
PYLRQKWLDFRRYTKETEWMMERRHSPSLEEYWENAVESIALGVTTLTPIFSTQDLLPDHLLQKFDFRADFLNLVSL
TGRLINDVRTFQEERDRGELASCVQCYRNDNPGCTEEEEALNYLYGVNEDALTKLNYQFLMREDIPKSFRTVLFNNTAR
VMQLFYRNIDGFLNAAEEMKVFIKKTLYEPLL

>TpdiTPS3 (MT468209)

CTCTTAACACCTATTTCATTGAGGTCGCTGACAAATTTGAAAGGCAGGTGCAATTGGGACTTATCAGCTGAACAGTGC
AAAAGCTTAAAAACATACCAGTATTTTTCTTCTTCTTCTTCTTCTAACTTAGAGAAAATGGCTCAATCTTTGATTTT
TTCGGCCAATTCTTGTATTGCAAAGACTCGACTTTTCAGATGTTAATGGCAGAACAGAGCTCAACAGATCTCGACCAT
TATCATTTTTCATTTTTCTCTCTAAGCTGGTGAAGAGGCAATGGAATAAGCAGTCAGCTGGTTTTGGTTTTGGCTTGT
CTTGAGATTCCAGGCGTTCTTCTTCCCCTGCTGCTACAGGGGCTGCCACTGCTTCTACATCGGTGAAACGAGAGTA
CCCTCCAGCAGTTTGAATGATGACGTGATCAATTCTCTGATATCAACTTATAAATCTGCAGATGTAGCAGAGCAGG
AGAAAAGGTCTGAGACATTGATAGCGGAGATAAAGGGCATGTTTAAATCAATGGGGGATGGTGAAACGAATCCTTCT
GCCTATGATACTGCTTGGGTTGCAAGGATACCTGCTGTGGATGGCTCTAATGGCCCTCAGTTTCTCAGACGCTTCA
ATGGATTCTGCAAACAGTTGAGCGATGGTTCCTGGGGCGAAGAATTGTGCTTCTTGACATATGACCGTGCTCTGG
CTACTCTTGCTGTGTTATTACGCTCTCTCTGTGGAATACAGGGGAAGAACAAGTGAACAAAGGTGTTGAATTTATA
AAGAAACATGCTGAGCGAATGGAAGGAGAAGCGGACAATCACCGCCAAGTGGATTGCAAATTTGTTTTCATTTCAAT
GCTCAACGAAGCTAAGACTCTAGGATTGGATCTACCTTATGATCTGCCTTTCTTTAAGCAGATTAATGAAATGCGCG
AAACTAAGCTTAAAAAGATTCTTTGAATGTTGTCCACGCCATTATACACAACAATTCTGTACTCGTTGGAGGGGTTG
CAGGAAATAATAGACTGGGACAAGATAATGAAGCTTCAATCCAAGGATGGATCCTTCTTAGCTCCCCTGCTTCCAC
AGCAGCCGTGTTTCATGCGCACAGGAGACAAAAAGTGCTTAGACTTTTTGAGCTTCGTTCTCAACAAATTTCAAGATC
ATGCTCCTTGTCACTATCCTCTTGATCTCTTCGAGCGTCTATGGGCTGTTGACACTTGCCAACGCCTGGGAATCGAT
CGCCATTTCAAAGACGAGATCAAAGATACTCTAGATTATGTCTACAGCTATTGGAACGATAGAGGCATCGGATGGGC
AAGAGAAAATGCAGTTGGTGATATTGATGATACTGTCTATGGGCCTTCGCCTCCTCAGACTTAGCGGATACAATGTGT
CATCAGATGCACTGAAAACCTTTAGAGACGAGAATGGAGAATTTCTTTGCTTCATGGGTCAAACACAGAGAGGAGTT
ACAGACATGTTAAACGTTTCATCGCGGCTCACAAGTTGCATATCCAGGCGAAACAGTCATGGAAGAAGCAAAACAGTG
CACGCTCAGATATTTGACCAGCGCTCTTGAAAATGTGCGCGCTTTTGACAAATGGGCCCTGAAAAAGGATCTTCAAG
GAGAGGTGGAATACGTGCTTAGATATCCATGGCATAGAAGCCTGCCAAGACTGGAGGCAAGGAACTACGTAGAACAG
TACGGTGCAAATGATGTGTGGCTTGGAAGTCCATGTACCTGATGTATTACGTAAGCAATCAGAAATATTTAGAGCT
GGCCCAAATAGACTTCAACAAGGTTCAAGCGGTACACCAAAAGGAAATTCAGGAGCTTCAGAGGTGGTGGAATCAT
CTGGTTTTCAAAAGCTCAATTTACGCCTGAACGTGTGGTTGAAATCTATTTTGAGTGGCGCGACCATGTTTGAG
CCAGAGCTAGCTACACTAAGAGCTGTTTACACCAAAACTTCAATCTTTTCTGTCAATTCTCAGCGATCTCTATGAAGC
GCAGGGATCAACTCACAACATGGCGTTGTTCTCTGAAGCAGTCAAAGATGGGATATGTCAATGTTGACCGCATGC
CAGAAGAAATGAAAATCTGCTTCAAGGGCTTGATGAAACAGTCAATGAATTCGAGAGGAAGGAAGGAAGAGACAA
GGGCGTGACGTATTGCCTTACCTCCGAAACCTGTGGGAGGTTGAGTTGGAATCCTACCAAGGAAGCAAAAATGGC
TCAGGCCAAATACATGCCTTCTTCCAAGAGTACATGGAGAATGCCAAGTATCAATGGGACTAGCCACCATAGTTT
TGACCTCAGCTCTCTTTACAGGAGATCTTCTATCTGATGAAACACTTTCCAAAATGGGCTATGATTCCAAATTTGTC
CAATTAATGGTTTTCAACAGGGCGTTTGGTTTTGTGATACAAAACCTTACCAGGAGAAACAAGAGAGAGGTCTCCCTTC
AGCTGTACAATGCTACATGAAAGACCATCTGAAATCTCAGAAAAAGAAGCTTTAGACCATATCTACTCAGTACTGC
AGAATCCCTGCTGGAATTGAATTGGGAACCTGTTAACAACAGAGAAATGCCAGAGACTTGTAAGAAGCCTGGTTTTT
AACACAGCAAGAATAATGCAGCTATTTTACATGGAGAGAGATGGTTTTATTATGTCCCATCTAGAAATGCAACAACT

TGTGAGAAAGTGCCTTTTCGAGCCAGTGGCAGTATAGAAATCAAAC TAGACAAAGACCAACATTTTTTTTTCTGTCT
TAGGCATACAATATCCATGATGGGTCTCTCAGAAACTACCTTTTTTCTCGCAAATTCTTTCTTTTTTCTAGGATAC
TTCAGACTTCCATCAATTCGCTGCAAAAATAAATGCAAGTTGTATAGATTAGGTGAATCTACTCTTGCCTGATATGA
CCCTCACTTGGAGAGGGATTTGGGAAGACTTTTACACTCACATATGTGGGTTTTATTTACGCTAGTTATGTAAATTC
CATACTAGTTTGAATAATTGTTATACATATTCACATCAAATATTTTGGTGAACATTTTTATATAAGTCCAAGCTCT

>TpdiTPS3

MAQSLISSANSKIAKTRLSDVNGRTELNRSRPLSFSFSSSKLVKRQWNKQSAGLVLAACLGDSRRSSSPAATGAATAS
TSVKREYPPAVWNDDVINSLISTYKSADVAEQEKRSSETLIAEIKGMFKSMGDGETNPSAYDTAWVARI PAVDGSNGP
QFPQTLQWILQNQLSDGSWGEELCFLTYDRALATLACVITLSLWNTGEEQVNKGVEFIKKHAERMEGEADNHRPSGF
EIVFISMLNEAKTLGLDLPYDL PFFKQINEMRETKLKKIPLNVVHAIHTTILYSLEGLQEIIDWDKIMKLQSKDGSF
LSSPASTAAVFMRTGDKKCLDFLSFVLNKFQDHAPCHYPLDLFERLWAVDTCQRLGIDRHFKDEIKDTLDYVYSYWN
DRGIGWARENAVGDIDDTVMGLRLLRLSGYNVSSDALKTFRDENGEFFCFMGQTQRGVTDMLNVHRGSQVAYPGETV
MEEAKQCTLRYLTSALENVGAFDKWALKKDLQGEVEYVLRYPWHRSLRLEARNYVEQYGANDVWLKSMYLMYYVS
NQKYLELAQIDFNKVQAVHQKEIQELQRWWKSSGFTKLNFTPERVVEIYFGVAATMFEPELATLRVYTKTSIFSVI
LSDLYEAQGSTHNMA LFSEAVKRWDMSMVD RMPEEMKICFKGLYETVNEFAEEGRKRQGRDVL PYLRNLWEVQLESY
TKEAKMAQAKYMPSFQEYME NAKVSMGLATIVLTSALFTGDLLSDETL SKMGYDSKFVQLMVSTGRLVCDTKTYQEK
QERGLPSAVQCYMKDHPEISEKEALDHIYSVLQNSLLELNWELVNNREMPETCRSLVFNTARIMQLFYMERDGFIMS
HLEMQQLVRKCLFEPVAV

Supplemental figure S1. Nucleotide and predicted amino acid sequences of three *Thuja plicata* diterpene synthases described in this study.

PtIAS	~~~~MALPSSSS~LSSQ~-----HTGATTCQIPHHCGLNAGTSAGRRSLYLWKGPFKI-----VACAGQPPSVTTLVKREFPPGF	74
PcIAS2	~~~~MALPSSSS~LSSQ~-----HTGATTCQIPHHCGLNAGTSAGRRSLYLWKGPFKI-----VACAGQPPSVTTLVKREFPPGF	74
PbmIso1	~~~~MAMPSYSSSSHSIT-TTHTRPHPIFFPCYDQSIPIRRFISSTSSASQCNLYLRLSRKLIAGVREGATSLSSHSDMKMTSSPDPPLAKRDFPPGF	100
PcmIso1	~~~~MAMPSYSSSSHSIT-TTHTRPHPIFFPCYDQSIPIRRFISSTSSASQCNLYLRLSRKLIAGVREGATSLSSHSDMKMTSSPDPPLAKRDFPPGF	100
TpdiTPS1	MAQKMFSPSISVSKSR--GWISTKISGFSPIGKSRSSK-----LACHNMPHVVVGEDAKTLQALR-I----AHKESKINPN-----H	72
TpdiTPS2	MSQS-LCPRLSLEFKPTTKSTQRLNNTSLPFTNARIKS-----IDCYNMTAFALGDNAKTLHAAA-I----AHPEKXIYPN-----A	73
PtIAS	WKDEHVIESIMPYSYKVAI--SDEKRIETLITEIKNMFRSMGYGETNPSAYDTAWVARIFAVDGSSEKPFQFETLEWILQNQLMDGSWGEEFYFLAYDRILATLACII	177
PcIAS2	WKDEHVIESIMPYSYKVAI--SDEKRIETLITEIKNMFRSMGYGETNPSAYDTAWVARIFAVDGSSEKPFQFETLEWILQNQLMDGSWGEEFYFLAYDRILATLACII	177
PbmIso1	WKDDIIDSIMSSNKVAA--ADSERVELLISEIKSMFHCMDGETTPSAYDTAWVAKIFALDGSDDHHPFQTLQWILLNQLMDGSWGEEHHFLTIDRLATLACII	203
PcmIso1	WKDDIIDSIMSSNKVAA--ADSERVELLISEIKSMFHCMDGETTPSAYDTAWVAKIFALDGSDDHHPFQTLQWILLNQLMDGSWGEEHHFLTIDRLATLACII	203
TpdiTPS1	AKPIYVHSV-STEEAFEDMDKRIEELVTEIKGLFNEMEDGEISPSAYDTAWVARVHAIDGSVKPFQFQMDWILQNQLPDGSWGEEKSRFLACDRLLNTLSCLV	176
TpdiTPS2	GRPIYVHSN-STEEAFLEEMDKRIEELVAEIKLEFYSMDGEISPSAYDTAWVARVFAILAAQPFQQLDWILQNQLADGSWGQSRFLASDRFLNTLACL	177
PtIAS	TLTIWQCGTQVQKGIEFFKTCI--SKIEEEASHRPSGGLVIVFAMLKEARALGIALPYELPFIQIITEKREAKLQRLPDLLALPTLLYLSLEGLQEIVWEK	281
PcIAS2	TLTIWQCGTQVQKGIEFFKTCI--SKIEEEASHRPSGGLVIVFAMLKEARALGIALPYELPFIQIITEKREAKLQRLPDLLALPTLLYLSLEGLQEIVWEK	281
PbmIso1	TLTIWVRGKTQVQKGIEFFKHA--SMMEDKAIHRQPSGGLVIVFAMINEAKSLCLDLPYELPFIQIITEKREAKLRITDOLLNTPVTFFLYLEGLQEIVWEK	307
PcmIso1	TLTIWVRGKTQVQKGIEFFKHA--AMMEDKAIHRQPSGGLVIVFAMINEAKSLCLDLPYELPFIQIITEKREAKLRITDOLLNTPVTFFLYLEGLQEIVWEK	307
TpdiTPS1	TLTIWVGGINQVNRGLNFRNTEEMIKALGHQCPKGFIVFVLLNEAKLLGLDLPYELPFIQIITEKREAKLRITDOLLNTPVTFFLYLEGLQEIVWEK	281
TpdiTPS2	TLTIWVGGINQVNRGLNFRNTEEMIKALGHQCPKGFIVFVLLNEAKLLGLDLPYELPFIQIITEKREAKLRITDOLLNTPVTFFLYLEGLQEIVWEK	281
PtIAS	IMKLQSKDGSFLSSEASTAAVFMRTGNKKCLEFLNVLKKGFNHVPCHYPLDLFERLAVDTVLRLGIDHIFKEETKLDALDYVYSHWDERGIGWARENPVFDID	386
PcIAS2	IMKLQSKDRSFLSSEASTAAVFMRTGNKKCLEFLNVLKKGFNHVPCHYPLDLFERLAVDTVLRLGIDHIFKEETKLDALDYVYSHWDERGIGWARENPVFDID	386
PbmIso1	IIKLQSKDGSFLSSEASTAAVFMSTGNTKCLEFLNVLKKGFNHVPCHYPIDLLERLAVDTVLRLGIDYFKEEIKALDYIYSHWGERGIGWARENPVADIG	412
PcmIso1	IIKLQSKDGSFLSSEASTAAVFMSTGNTKCLEFLNVLKKGFNHVPCHYPIDLLERLAVDTVLRLGIDYFKEEIKALDYIYSHWGERGIGWARENPVADIG	412
TpdiTPS1	VLKLQSKDGSFSGSFACVEMHTGDIKSLQFLTSLVKKFGDHPVSMYPVDIAERLRAVDCTVERLGLERHFQTEIKQAMDYVYQWNSERGIGFGRSILVFDID	386
TpdiTPS2	ILKLQSKDGSFSGSFACVEMHTGDIKSLQFLTSLVKKFGDHPVSMYPVDIAERLRAVDCTVERLGLERHFQTEIKQALDYVYQWNGERGIGFGRSDILVFDID	386
PtIAS	TAMGLRILRLHGYNVSSDLKTFERDENGEEFFCLQ--TQRGVTIMLNVNRCSHVAFPGETIMEEARLCTERYLRNALEDGCSKWKALKKNIRGEVEYALKYPWH	490
PcIAS2	TAMGLRILRLHGYNVSSDLKTFERDENGEEFFCLQ--TQRGVTIMLNVNRCSHVAFPGETIMEEARLCTERYLRNALEDGCSKWKALKKNIRGEVEYALKYPWH	490
PbmIso1	TAMGLRILRLHGYNVSSDLRTFRDENGEEFFSFMGQ--TERGVITMLNLRCSHVAFPGETVMEEAHCTERYLRNALEDVLDLKKGLKNIRGEVEYALKYPWL	516
PcmIso1	TAMGLRILRLHGYNVSSDLRTFRDENGEEFFSFMGQ--TERGVITMLNLRCSHVAFPGETVMEEAHCTERYLRNALEDVLDLKKGLKNIRGEVEYALKYPWL	516
TpdiTPS1	TATAFRLLRTFGYSVSEVLQNIHAAEELLLKLSNENSAGIILSLIYRSSQLNFPGEIVMKEIDCFADYLAELFQTKFSSQVVKVKNLPPEVEYALSAQWN	491
TpdiTPS2	TATFRLLRMFSYTVSFFLQNIKEFAEELCKLSDGNGRGRVILMLSLIYRCSQINFPGENVMREIGAFADYLAESLQSNFSCATAVDNLIRGEVEYALFARN	491
PtIAS	RSMPRLARSYIENYGPNVDWLKGTMYMFPNISNEKYLELAKLDFNRVQFFHHQELDIRRWNNSSGFSQLGFTTRERVAEIIYFSPASFLFEPEFATCRVAYTKTS	595
PcIAS2	RSMPRLARSYIENYGPNVDWLKGTMYMFPNISNEKYLELAKLDFNRVQFFHHQELDIRRWNNSSGFSQLGFTTRERVAEIIYFSPASFLFEPEFATCRVAYTKTS	595
PbmIso1	RSPLRLARSYIENYGPNLAWLGTMYIMHYINNGKYLELAKLDFNNQSIHQELRELRLRWKSSGFAELNFTDRVAEIIFFSIASSMFEPELATCRVAYTKTS	621
PcmIso1	RSPLRLARSYIENYGPNLAWLGTMYIMHYINNGKYLELAKLDFNNQSIHQELRELRLRWKSSGFAELNFTDRVAEIIFFSIASSMFEPELATCRVAYTKTS	621
TpdiTPS1	RNMPRIMSINQIELFNPNLDWLKGTLYHLENAANDKYLELAKLDFNRVQFFHHQELDIRRWNNSSGFSQLGFTTRERVAEIIYFSPASFLFEPEFATCRVAYTKTS	596
TpdiTPS2	RNMPRVIINNIEVENPDDLWLKGTLYCMENANGKYLELAKLENNFTCAIHSEIHIKRWYACNFPQLEFTRHREVAIYWTAAVMPDPOITDCRLAARAG	596
PtIAS	NFTVILDDLYLAHGTLDNLKLFSESVR-----WDLSLVDCMPQIMKICFKGFYNTFNEIAEEGRKKQGRDVLISYIQVWE	671
PcIAS2	NFTVILDDLYLAHGTLDNLKLFSESVR-----WDLSLVDCMPQIMKICFKGFYNTFNEIAEEGRKKQGRDVLISYIQVWE	671
PbmIso1	ICTVILDDLYLAHGSVEDIKLFNEAVRR-----WDLFLLRMPEHIKICFLGLYNLVNEIAEEGRKKQGRDVLISYIQVWE	697
PcmIso1	ICTVILDDLYLAHGSVEDIKLFNEAVRR-----WDLFLLRMPEHIKICFLGLYNLVNEIAEEGRKKQGRDVLISYIQVWE	697
TpdiTPS1	LATITDDLYESYATINQLKLFNEAFER-----WDPLMSEQLPEIMKIVFMGIYNTITDISERALKVQGRDVLISYIQVWE	672
TpdiTPS2	IMAVITDDLYTCATLECAKLFNEAFERSPLRIPISVNANKELESAILTLIVFDGCRNTEQTEHLPEMRIVFMGLYNTIAREISGAREVQGRDVLISYIQVWE	701
PtIAS	VQLLAYTKEAEWSAVRYVPSYDEYIGNASVSIALGTVVLSALFTGEILTDILSKIGRDSRFLYIMGLTGRLVNDTKTYCAERGQGEVASAVQCYMKDHPFISE	776
PcIAS2	VQLLAYTKEAEWSAVRYVPSYDEYIGNASVSIALGTVVLSALFTGEILTDILSKIGRDSRFLYIMGLTGRLVNDTKTYCAERGQGEVASAVQCYMKDHPFISE	776
PbmIso1	IQLTITMKEAEWSAKYVPSHEYIETASVSIAAGATLVFGVLTGCVLTDHILAQIDYRSKFAYIMGLTGRLVNDTKTYCAERGQGEVASAVQCYMKDHPFISE	802
PcmIso1	IQLTITMKEAEWSAKYVPSHEYIETASVSIAAGATLVFGVLTGCVLTDHILAQIDYRSKFAYIMGLTGRLVNDTKTYCAERGQGEVASAVQCYMKDHPFISE	802
TpdiTPS1	NLFSFTKEREMMERSSPSLDEYWARAEISIAETLISFSTGQNFPLDRILEK----NFLDLVSQTRGLMNVRTFQKERDRGELASFVECYKNELHGCTE	773
TpdiTPS2	DLFRFYTKETEMMERSHSPSLEEYENAVESIALGVTTITLFSSTQDLPLDHLICDFRADFLNLVSTGRGLINVRTFQKERDRGELASCVQCYRNELHGCTE	806
PtIAS	EEALKHVVYTIMNALDELREFVNNRDVPITCRLVFEIARIMQLFVMDGDGLTSHNMEIKEHVKNCLFQPA	850
PcIAS2	EEALKHVVYTIMNALDELREFVNNRDVPITCRLVFEIARIMQLFVMDGDGLTSHNMEIKEHVKNCLFQPA	850
PbmIso1	EEALKQIYTIMENALADKEEFKARDVPCKKRLVFTYARSMLFVYQSDGGLTAPNMEIKQHVKKILFEPVP	876
PcmIso1	EEALKQIYTIMENALADKEEFKARDVPCKKRLVFTYARSMLFVYQSDGGLTAPNMEIKQHVKKILFEPVP	876
TpdiTPS1	EEALNYEMRMENALINLYHFMRSDIKCYRTLFFNTARIMCMYRKEDGGRNAA-EYLEDISKSLYEPVL	846
TpdiTPS2	EEALNYLVGNLALTKLYQFMREDIPKSFRTVLENTARVMQLFERNIDGLNAA-EEMKVFIEKTLYEPL	879

Supplemental figure S2. Amino acid alignment of *Thuja plicata* monofunctional diTPS1 (TpdiTPS1) and diTPS2 (TpdiTPS2) with *Pinus taeda* bifunctional levopimaradiene synthase (PtLAS, Q50EK2), *Pinus contorta* bifunctional levopimaradiene/abietadiene synthase (PcLAS2, JQ240311), *Pinus banksiana* (PbmIso1, JQ240313), and *Pinus contorta* (PcmIso1, JQ240314) monofunctional class I isopimaradiene synthase1.

TpdiTPS3	Y AQS L I S S --NS AKT L S D V N G R T E L N R S F S F S S S K V K R Q W N K S A S L V A L G D S R R S S F A A T G A A T A S T S V K E E P F A V W N D I V I N S L I S T Y E	102
PgCPS	~ M P E T A S --F Q C V T I F G C P A ~~~~S A A D A C P I L -G G R P F L H H A R R R P C P F M I S S P P Y F A S T ~~~~~D Q I E T ~~~~~E	29
OsCPSsyn	~ M P E T A S --F Q C V T I F G C P A ~~~~S A A D A C P I L -G G R P F L H H A R R R P C P F M I S S P P Y F A S T ~~~~~D Q I E T ~~~~~E	69
OsCPS2ent	N C H Q V L T A S S L P A T I L -F A ~~~~~A A E F ~~~~~V R Q S T L Q C A R P I R P S I M L C A A L Q --G C ~~~~~S T R E R S Q --L -D I D E H A R P P G G	74
TpdiTPS3	S A D V A E C K R S E T I A E I N C M F K S --M G D G E T N P S A Y D T A W V A R I E A V D G S N --S P Q F F Q T L Q W I L Q N Q L S D G S W G E E C F L T Y D R A L A T L A C V I T L S L W N T G E	202
PgCPS	N L C I S T A M M K W I E T V K Y I I Q S --N E D G E I T T S A Y D T A W I A L V E A L N G S S --E P Q F P S S L Q W L I N N Q L Q D G S W G T E I N F L I R D R T I I N T L A C V I A L K T W N I H S	129
OsCPSsyn	H E H T D L R E T T T N I D G I R T A L R S --L G E G E I S I S A Y D T S L V A L L K R L D G S L --S P Q F P S T I L W I V Q N Q L S D G S W G L A S F M M G D R I M S T L A C V A L K S W N I H T	169
OsCPS2ent	I D V V A S T S E L P Y I E S I K S K L E A A R N S L G E T V S A Y D T A W I A L V N R L D G S G E R S P Q F F E A L D W I A R N Q L S D G S W G L A C H F I N Q D R L I I N T L G C V V A L A T W G V H E	178
TpdiTPS3	E Q V N K G V E F I K K H A E R M E G L A D N H R S G F E I V E I M L N E A K T L G L D L Y D L F F F Q I N E M R T K L K K I P I N V V H A H T T I L Y S L E G L E I I D W L K I M K I S S K D G	306
PgCPS	L G N K G L S F L T Y P R M N D H I A H T E V G F E I V E A L M D A I M E L D L R Y T A E F Q K I Y D E R I R M K R I P M K V L H E F S T L L S L E G L R K V N W E L L K L Q S K N G	233
OsCPSsyn	D K C E R G L L F I G E N M R L A E E E W M L G F E I A L P S L L E M A K D L D I P Y D E F A L A I Y A E R E R K I A K I P D L H A M P T L L S L E G M V L -L D W E R L L K R L D G	272
OsCPS2ent	E Q R A R G L A I Y I D N L W R L G E D D E W M M G F E I T F V L L K A R N L G L D I N Y D I A L Q D I Y A K R O K L A K I P E A L H A R T T L L S L E G M E N -L D W E R L L Q F K C F A G	281
TpdiTPS3	S L I S F A S T A A V M R T E D K R C I D F L S F V I N F Q D H A P H Y P L D L F E R L W A V D T C Q R L G I D R F K D E I K D L E Y V Y S W N D R F G I G W A R E N A V G D I D D T V M G I R L L	410
PgCPS	S L F S F A S T A C I A C T S D T N C I R Y L N E I T K R Y D G G A R N V Y P V D L F E R L W T V D R I E R L G I A R Y F E S E I T D S L E Y V Y R Y W N Q G I G W A R S F V R D V D D T S M A F R L L	337
OsCPSsyn	S F I C S F A S T A T A R Q C T G D C K C F E Y L G I V K F N G G V P C I Y P L D V Y E R L W A V D R I T R L G I S R H F T S E I E C L D Y I F R N W T P D G I A H T K N C P V K D I D D T A M G F R L L	376
OsCPS2ent	S L I S S F A S A Y A L S E T G D E L E Y L E T A I N N F D G G A P T Y P V N F R L W S V D R I R R L G S R Y F T S E I E Y L E Y A Y H L S P D G M S G G L C P V K D I D D T A M A F R L L	385
TpdiTPS3	R L S G Y I V S S D A L T F R D E N G E F F C E M G Q T Q -R G V T I M L N V H R G S Q A Y P G E T -M E E A R Q C T L R Y L T S A L E N V G A F D K W A L K K D L Q S E V E Y V L R Y P W H R S P R L	512
PgCPS	R S H G F I V A E A F N F K -Q D D F F C F G Q T K -Q V T G M I N L P A S Q S F S P G E S -L E E A R V T I N F L E K F A E K Q L S D K W I I A N G L K E E V E Y A L K F P W Y S Q P R I	438
OsCPSsyn	R Y G Y Q V D P C V L R F E -R D K F F L H G E S N P S V T I M Y N I Y R A S Q K F P G D G L G R E V F C S F L D R H G N M K D K W I A K I D I P G E V E Y A M Y P W K A S P R I	479
OsCPS2ent	R L G Y I V S S V I N I F E -R D G Y F C A G Q S S -S L T A M A N S Y R A S Q V F P G D L D G L E I A Y C A F L E E R A T G N L R D K W I A N G L S E V E Y A L F P W K A S L P R V	487
TpdiTPS3	I A R N Y V E Q Y L -N D V W L G M S M L M Y Y S N Q K Y L E A Q I D F N K V C A V H Q K E Q E L Q R W W S S F T R I N F P -R R V E I Y F G V A A T M F E P E I A T L R A V Y T K T S I F	613
PgCPS	D R M Y I N Q Y R V -D D V W I G H A L R M F T I N N K T Y I E L A K A D F N I C Q S L H T E H G I I R W Y E S G D E L Q I R -D Q I V K S Y F L A A I A I Y E F T M A S A R A W A K S A V E	539
OsCPSsyn	E T R L Y L D Q Y G S G D W I G V L R M T L F C N D L Y L R A K A D F S N Q E C R V E I N S L R R W Y L S N L E F F G T D P Q T I L M T Y F L A S A N I F E P N R A A E R L G W A R V A L E	583
OsCPS2ent	E T R V Y L E Q Y G A S E L A W I G H L R M T L V N N D I Y L E A K A D E T N Q R I S R L E W L S L R W Y I N N L A H E V T E -Q S V L A Y F L A A N I F E P N R A A E R L G W A R T A I E	589
TpdiTPS3	S V I L D L E A G S T H ~~~~~M A L F S E V K R W M S M V R M E E M I C K G L E T V N E A E E R K R Q G R D V L P Y L R N L W V Q L E S Y T K A K M A Q A K Y M P S F Q E Y	711
PgCPS	M A I R I F S G N C F A ~~~~~H H R R Q F I D ~~~~~A F T R W D C A M R D S T N S A R L E S C L R M N I S D E V V A C R D I S G D L R H R W E H I A S E A D I L D A Q D H ~~~~~	631
OsCPSsyn	A D A V S S H F R I C G P K ~~~~~~T S N L E ~~~~~E L I S L V P D D A Y S G S L R E A W K W I A N T A K E S S Q ~~~~~	640
OsCPS2ent	A E I A S H L Q Y S A N G A A D G M T E R I S G L S H L W W E S N D S ~~~~~A A S L Y L A D ~~~~~E L I D H A T G N -A S L S R E A W K W I M S W T N ~~~~~S Q ~~~~~G ~~~~~	672
TpdiTPS3	M E N A R V S M G L I -T I V L T S A L F T G D L L S D E -T A S R M G Y D S F V I M V S T G S L V C D T K T Y D E K Q E R G L P S A V C --Y M K D H P E I S E K E A L D H I Y S V L Q S L L E L N W	811
PgCPS	---K T E A E -I V V L T -A A L G E T I S P -D I S H P D S S I M K V N T V G S L L R I A T Y K E E C -I S P S G T E D D R L K R R A E E G H G L V R A V Y R H Q Y S-----	720
OsCPSsyn	---S E G D T A I L L V R A E L C G R H V L G C R -F D I W E Y S Q L E G L T S I C R N L Y R R V L A C E N K -S-----E K W E I D Q Q L D L E M Q L T A R V L Q G C -S-----	726
OsCPS2ent	---S T G D T A L L L V R T E L C G R H G A E Q S K S E D A R L E Q I A S M G S K L A T K I L A N -G -S M-----D N E G I D Q E V D E M K E L C R V I G S S S-----	759
TpdiTPS3	E L V N N R M E E T C R S I V F T A R I N Q L F Y M E R D G F I M S H L M Q Q L V R C L F E P V A V	865
PgCPS	-----P V E S G V K R L C I V ~~~~~G K S F Y I A ~~~~~A H C N N E V G N A V E T L F Q P V Y ~~~~~	761
OsCPSsyn	-----A I N R L T R E T L H ~~~~~V K S F C Y V ~~~~~A Y C S P E T I D N H I D K V I F Q V I ~~~~~	767
OsCPS2ent	-----D V S S V T R G T F L D ~~~~~V K S F C Y V ~~~~~A H C S P E T I D G I S I V L F E D V N ~~~~~	800

Supplemental figure S3. Amino acid alignment of *Thuja plicata* monofunctional diTPS3 (TpdiTPS3) with *Picea glauca* monofunctional *ent*-copalyl diphosphate synthase (PgCPS, GU045755), *Oryza sativa syn*-copalyl diphosphate synthase (OsCPS_{syn}, AY530101) and *Oryza sativa ent*-copalyl diphosphate synthase (OsCPS2_{ent}, AY602991).

Tree scale: 1

Colored ranges

- Diterpene synthases
- Sesquiterpene synthases
- Monoterpene synthases



Supplemental figure S4: Phylogenetic relationships of conifer terpene synthases. The number of bootstrap replications was 100. The abbreviation of species are as follows: *Physcomitrella patens* (Pp) was used to root the tree. *Picea glauca* (Pg), *Picea sitchensis* (Ps), *Picea abies* (Pa), *Physcomitrella patens* (Pp), *Abies grandies* (Ag), *Pinus taeda* (Pt), *Pinus contorta* (Pc), *Pinus banksiana* (Pb), *Taiwania cryptomerioides* (Tc), *Abies balsamea* (Ab), *Chamaecyparis obtuse* (Co), *Chamaecyparis formosensis* (Cf), *Pseudotsuga menziesii* (Pm), *Cycas taitangensis* (Ct).

Supplemental Table S1: Primers used for nested PCR and SLIC-based cloning into expression plasmid.

<i>Gene ID</i>	<i>Primer set</i>	<i>Forward primer (5'-3')</i>	<i>Reverse primer (5'-3')</i>
<i>TpdiTPS1</i>	Set1	TCAAAATGGCTCAGAAGATGT	CCATGATTGTAATGATGCCTTTT
	Set2	TACTTCCAATCCAATGCAAAGACTCTTCAGGCTTTGAG	TTATCCACTTCCAATGTTATTACAGCACTGGTTCGTACA
<i>TpdiTPS2</i>	Set1	TACTCCCATGGGATTCAAA	CACAGTTCATCCAATAGAGCAA
	Set2	TACTTCCAATCCAATGCAGCGAAAACACTTCACGCTG	TTATCCACTTCCAATGTTATTAGAGCAGGGGTTTCATAGA
<i>TpdiTPS3</i>	Set1	CTGGTTTGGTTTGGCTTGT	CCAAATCCCTCTCCAAGTGA
	Set2	TACTTCCAATCCAATGCAGCTGCCACTGCTTCTACATCG	TTATCCACTTCCAATGTTACTATACTGCCACTGGCTCGA

Supplemental Table S2: Kovats Retention indices of identified diterpene compounds

Gene Name	Compound Name	Retention index
TpdiTPS1	sandaracopimaradiene	1986
	<i>syn</i> -stemod-13(17)-ene	2119
	unknown diterpene	1981
TpdiTPS2	levopimaradiene	2039
TpdiTPS3	normal-copalol	2293