

Supplemental Figure S2. Alignment of α -terpineol synthases (ATERS) and γ -terpinene synthases (GTS) of the Lamiaceae. MI_15999 and MI_14850 are candidate monoterpene synthases characterized as part of the present study.

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GTS_ORIVU      RMSGNYQASIWNNNDYVSFNTN-QYKDEKHLKKKEELIAQV-KILLNTKMEAVKQLELIE 58
MI_14850      RMSGNYQPSLWDFDYIQSLNTH-HYKEERQLNREEELIIQVKKMLLGEKMEAVKQLELID 59
GTS4_THYCA    RMSGNYQPSLWDFNFIQSQPTH-HYEEERN--RKEDLIVHV-KTLLGTMKEAIEQLDFID 56
MI_15999      RMSGNYEPSLWDFDYIQSLDTH-RYKEEKHLIREEELIVQV-KMLLGKEMEAVKQLELID 58
ATERS1        RMSGNYEPSLWDFDFIQSLDNHHPYVKEEQLKREEELIVQV-KILLGTMKEAVKQLELID 59
ATERS2        RMSGNYEPSLWDFDFIQSLDNHHPYVKEEQLKREEELIVQV-KMLLGTMKEAVKQLELID 59
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GTS_ORIVU      DLRLNLGLTYFYFQDEVKKILTSIYNHDKCFKNEQVGDLYFTSLGFRLRLRHGFVDVSEEVFD 118
MI_14850      DLKNLGLSYFFQDEIKKILSCIYNEHNFQNNKVGDLHFTALGFRLLRHHGFVDVSQEIFD 119
GTS4_THYCA    DLRLNLGLSYFFLDEIKNILSFIYSENKCFQNNQAGDLYFTSLGFRLRLRHGFNVQSQEVFN 116
MI_15999      DLKNLGLSYFFQDEIKKILSCIYNEHNFQNNKVRDLHFTALGFRLLRHHGFVDVSQEIFD 118
ATERS1        DLKNLGLSYFFRDEIKTILTSIYNNSFENKNNQVGDLYFTSLGFRLRLRHGFNVQSDIFD 119
ATERS2        DLKNLGLSYFFRDEIKTILTSIYNNSFENKNNQVGDLYFTSLGFRLRLRHGFNVQSDIFD 119
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GTS_ORIVU      FFKNEDGSDFKA-SLGENIKDVLQLYEASFLIREGEVILEQARVFSTKHLEKKVDEGI-- 175
MI_14850      CFKNEEGSDFEKTLIGEDTKGMLQLYEASFLIREGEDTLELARKFSTKYLQKRVDGIRN 179
GTS4_THYCA    RFKNDDGSDFKA-SLGEDTKGILQLYEASFLIREGEDTLELARQFSTKYLQKKVDEKG-I 174
MI_15999      CFKNEEGSDFEKALIGEDMKGILQLYEASFLIREGEDTLELARKFSTKYLQKRVDGIIIN 178
ATERS1        CFKNEKGSDFDETIGEDTKATLQLYEASFHLREGEVILEQARVFSTKHLEKKVDEGI-- 175
ATERS2        CFKNEKGSDFDETIGEDTKATLQLYEVSFHLREGEVILEQARVFSTKHLEKKVDEGI-- 175
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GTS_ORIVU      ND--EKLAWIRHSLDLPLHWRIQRLEARWFLDAYRARKDMIPLIFELGKIDFHIIQETQ 233
MI_14850      DD--NNLLSWIRHSLDLPLHWRIQRLEARWFLDAYSRKDMNPLIFELAILDFNNIQAQ 237
GTS4_THYCA    DD--ENVLSWIRHSLDLPLHWRIQRLEARWFLDAYAARKDMNPLILELGKIDFNIIQATM 232
MI_15999      DDNNNNILSWIRHSLDLPLHWRIQRLEARWFLDAYSTRKDMNPLIFELSILDFNNIQA 238
ATERS1        DE---NLSSWIRHSLDLPLHWRIQRLEARWFLDAYAVREDKNPLIFELAKLDFNIIQA 236
ATERS2        DE---NLSSLWIRHSLDLPLHWRIQRLEARWFLDAYAAREDKNPLIFELAKLDFNIIQA 236
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Variable Region 1
GTS_ORIVU      LEELQEVSKWWTNSNLAELPFVRDRIVECYFWALGLFEPHEGYQRKMAAIIITFVTII 293
MI_14850      LEELKEVSRWWNSSCLAELPFVRDRIVECYFWALGLFEPHENGYQRKKAIIITFVTII 297
GTS4_THYCA    LDELKEVSRWWNSSCLAELPFVRDRIVECYFWALALFEPHQFGYQRKMAAIIITFVTI 292
MI_15999      ILELKEVSRWWNSSCLAELPFVRDRVVSFFWAAGLFEGHEGYQRKMAAIIITFVTI 298
ATERS1        QEELKEVSRGWNSCLAELPFVRDRVVSFVWGVGLFEGHEFGYQRKLTAAANTLLISAI 296
ATERS2        QEELKEVSRWWNSCLAELPFVRDRVVSFVWGVGLFEGHEFGYQRKLTAAANTLLISAI 296
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DDxxD Motif
GTS_ORIVU      DDVYDVYGTLDLDELQLFTDAIRKWDFQSISTLPYYMQVCYLALYTYASELAYDILKDQGFN 353
MI_14850      DDVYDVYGTLDLDELQLFTNTIQRWDTDTINQLPYYMQVCYLALYTFVSEMAVDILKEQGFN 357
GTS4_THYCA    DDVYDVYGTLDLDELQLFTDVRXWDTESISQLPYYMQVCYLALYTYVSELAYDILKDKGFN 352
MI_15999      DDVYDVYGTLDLDELQLFTDTIRRWDTESIDQLPYYMQVCYLALYNYVSNLAYDILKDRRFN 358
ATERS1        DDVYDVYGTLDLDELRLFTDVFRWDTESIDQLPYYMQVCYLALYNYVSGVAYDILKDHRRN 356
ATERS2        DDVYDVYGTLDLDELRLFTDVFRWDTESIDQLPYYMQVCYLALHNYVSGVAYDILKDHRRN 356
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Variable Region 2
GTS_ORIVU      SIAYLQRSWLSLVEGFFQEAQWYYAGYPTPTLAEYLENKVSISSTPIISQVYFTLPNSTE 413
MI_14850      SIPYLQKSWVSLVEGFFQEAQWYYKGYPTPTLEEYLNNAKISISSPTIISQYFTLPNSTE 417
GTS4_THYCA    SIPYLRSWLSLIEGFFQEAQWYYSGYPTPTLEEYLNNAKVSISSTPIISQVYFTLATSTE 412
MI_15999      TIPYLHKSWLCLVETYLKEAEWYESGYPTPTLEEYLSNAKISIGSLTILLQVELSLQKSTL 418
ATERS1        TIPYLQETWVELVEAYMKEAEWYKSGYTPSLEEYLTIAKISIASLTILLSVELSLPDSTI 416
ATERS2        TIPYLQETWVELVEAYMKEAEWYQSGYTPSLEEYLTIAKISIGSLPILLSVELSLPDSTI 416
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GTS_ORIVU      RTVVENVFGYHNILYLSGMILRLADDLGTTFELKRGDVPKAIQCYMKDNNATEKEGAEH 473
MI_14850      KTAIESLYEYHDILCLSGMILRLADDLGTTFELKRGDVPKAIQCYMKDRNSTEKEAQEH 477
GTS4_THYCA    KVVXESVYGYHNILYLSGTILRLADDLGTTFELKRGDVPKAVQCYMKDKNVTEKEAQEH 472

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Ml_15999	DRT--AFDLRHKILYLSALVSRLADDLGTAPSELKRGDVPNAIQCYMKDKNCSEEEARAH 476
ATERS1	DRA--TFDRRHKMFYLSATVSR LADDLGTAPSELERGDVPKAIQCYMKDTNASEEEARGH 474
ATERS2	DRA--TFDRRHKMFYLSATVSR LADDLGTAPSELERGDVPKAIQCYMKDTNASEEEAQGH 474
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GTS_ORIVU	VKYLIREAWKEMNTAMA--DPECPLSEDLVDAAANLGRASQFIYLEGDGHGVQHSEIHNQ 531
Ml_14850	VRFLIREAWKEMNTAMA--DSDCPFSEELVAAAANLGRAAQYIYLEGDGHGVQHSEIHKQ 535
GTS4_THYCA	VRYLIQEAWKEMNTAMA--EPDCPFSEELVTAAANLGRASQFIYLEGDGHGVQHSEIHKQ 530
Ml_15999	VRGMIGEVWKEMNTAMAVSDDDCPFTEQVVEAAAANLGRAAQFIYMEGDGHG--HSQIHEQ 534
ATERS1	VRFMIGETWKELNTAMAK-PDDCPFTEQVVEATANLGRAAQFIYREGDGHG--HFQIHHQ 531
ATERS2	VRFMIREAWKELNTAMAE-PDDCPFTEQVVEATANIGRAAQYIYREGDGHG--HFQIRQH 531
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GTS_ORIVU	MGGLIFEPYV	541
Ml_14850	MGGLIFEPYA	545
GTS4_THYCA	MGGLLFETYA	540
Ml_15999	MRSLLFHPYI	544
ATERS1	MGNLFFHPYV	541
ATERS2	VRNLFFHPYV	541
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