

Supplemental Figure S3. Alignment of bornyl diphosphate synthases (BPPS) of the Lamiaceae. MI_38055 is a candidate monoterpene synthase characterized as part of the present study.

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BPPS_SALOF      -----RRSGNYQPALWDSNYIQSLNTPYTEERHLDRKAE 34
BPPS_PHYDU      RRSNGYEPPIWNFNYSQSSSSQYTAGRRSGNYEAMWDFDIQSSSSQFTEDRYLERASE 60
M1_38055        -----RRSGNYKPTLWDFDRIQSLNSVYTEEKYATRASE 34
BPPSLAVAN       -----RRSGMYKPTLWDFDRIQSLNSVYTEEKYSTRACD 34
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BPPS_SALOF      LIVQVRILLKEKM-EPVQQLELIHDLKYLGLSDFFQDEIKEILGVIYNEHKCFH--NNEV 91
BPPS_PHYDU      LVVQVKKLEEEELTEPIQQLELIDDLQNMGVSYHFEDKQILKSMYDDRVKKYNSKDSK 120
M1_38055        LVVVVKKLLEES-SWFGQLELIDDLQRLGLSYHFEDKQILSSIYLLD-----KYCK 87
BPPSLAVAN       LIQQVKKLE-ES-DWFRQLQLIDDLQRLGLSYRFDDEINLILNTIYFEK-----KFCE 86
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BPPS_SALOF      EKMDLYFTALGFRLLRQHGFNISQDVFNCFKNEKGIDFKASLAQDTKGMLQLYEASFLLR 151
BPPS_PHYDU      NVRDLYSTALEFRLSRQHGFNISQEVFDCFKNNKG-GFEASLAEDTRGLLQLYEASFMLR 179
M1_38055        -KMDLYSTSLCFRLLRQHGFKVSQDVFNCFKNNKG-DFESSLGEDMKGLLELYEASFLT 145
BPPSLAVAN       KEMDLYSTSLAFRLLRQHGLKVSQEVFDCFKNEEG-DFEARLGDETNGILEMCEASFLAT 145
                  *** *:  *  *** *:  *:  *:  *:  *:  *:  *:  *:  *:  *:  *:  *:

BPPS_SALOF      KGEDTLELAREFATKCLQKKLDEGGN---EIDENLLLWIRHSLDLPLHWRIQSVEARWFI 208
BPPS_PHYDU      EGEETLEQAKEFATSFLKKLEDDTKHGILVDENLSLSVFHALELPIHWRTQRHNARWFI 239
M1_38055        HGEETLEQARVFSTNLLQKKLDDEG---IMDEHLLNLVRHSLRLPLHWSVQRPNARWFI 201
BPPSLAVAN       EGEETLELARLFTTNILQKKLDDERNELLIMDDYLRTLIRHSLDLPLYWRVQRP SARWFI 205
                  .*:  *:  *:  *:  *:  *:  *:  *:  *:  *:  *:  *:  *:  *:  *:  *:

BPPS_SALOF      DAYARR--PDMNPLIFELAKLNFNIIQATHQQELKDLRSRWSRLCFPEKLPFVRDLVES 266
BPPS_PHYDU      DAYEKR--SNRNSVLELAKVDFNIVQATYQQEIKHISRWEQTRLAEKLPFARDRLVEN 297
M1_38055        DACAKKRLNTNPILLELAKLDFNIVQAAHQELKHVSRWWEESKLAELKLPFARDRVVEN 261
BPPSLAVAN       EAYATR--SDMNPIMLELAKLDFNIVQATHQEELKQVSRWWKESRLAEKLPFARDRVVEN 263
                  :*  :  :  *  :  :  *:  *:  *:  *:  *:  *:  *:  *:  *:  *:  *:
                  Variable Region 1 DDxxD Motif

BPPS_SALOF      FFVAWGMFEPHQHGYQRKMAATIIIVLATVIDDIYDVYGTLDLELELFTDTFKRWDTESITR 326
BPPS_PHYDU      FLWTVGWLREPQYGYARIMCTKLFIFITYVDDIFDVYGTLEELQLFRDVIRRWDIAMGQ 357
M1_38055        YIWNVGLLFEPQYGYPRIMTKLFILITVDDISDVYGTLEETQLFNDTIQRWDTEGLDK 321
BPPSLAVAN       YLWNRGMLFPPQYGYPRIMNAKLFVLITVLDIYDVYGTLEETQLFTNLITRWDEVAIGQ 323
                  :*:  *  :  :  *:  *:  *  *  :  :  :  *  :  *:  *:  *:  *:  *:  *:

BPPS_SALOF      LPYYMQLCYWGVHNYISDAAYDILKEHGFFCLQYLRKSVVDLVEAYFHEAKWYHSGYTPS 386
BPPS_PHYDU      LPNYMQMCFLAIDNFINEMAYDVLKEQEFVVIIPHLRKMWADLCTSYCQEAWEYYNKYMPT 417
M1_38055        LPEYMQICYLALDSFIDEAAHYVLKEQGVLIIQDLRKSWADLCAAYAKEAEWYYTGKPT 381
BPPSLAVAN       LPEYMRICYMAIDNNINELAYEVLKQHGLLIIQDLRKFWADLCVAYGKEAEWYYTGKPT 383
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                  Variable Region 2

BPPS_SALOF      LDEYLNIAKISVASPAIISPTYFTFANASHDTAVIDSLYQYHDILCLAGIILRLPDDLGT 446
BPPS_PHYDU      MDEYINNACISISTPLILSNTYFVVTNPIE-EEVVQNFYKNPDVVRYSAMILRLADDLGT 476
M1_38055        LEEYMEVAWISISAHTILSYVFFLISNPIE-KDAENLRNYHNVIRCSAMVLRLADDLGT 440
BPPSLAVAN       LEEYLEVAWVSISAHLILGYMFFLTSNPIE-KEASQSLSNYHNIIRNSAMVLRLADDLGT 442
                  :  *:  :  *  :  *:  :  *:  :  :  *  :  *  .  .  :  :  :  :  :  :  :  :  :  :  :  :

BPPS_SALOF      SYFELARGDVPKTIQCYMKETNASEEEAVEHVKFLIREAWKDMNTAIAAG-YFPFDGMVA 505
BPPS_PHYDU      SEFEAERGDVPKAIIECYMNESGASREEAREHVKFMIWEAWKKINKELLSN-ASFPQFFLR 535
M1_38055        EPFEMRRGDVPKAVECYMNDTGASMEEGREYVKFMIRETWKETNEESFKEKLPFSEIFMR 500
BPPSLAVAN       SPYEMQRGDVPKAVECYMNENGASTEEAREYVKHLLREVWKETNGERFKE-SPFTPSFMR 501
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BPPS_SALOF      GAANIGRVAQFIYLGHDGFGVQHSKTYEHIAGLLFEPYA 544
BPPS_PHYDU      NAADLGRAGQFMYQHGDGFGVNPHHHKEDVSTLFFEPL- 573
M1_38055        SAADLGRQAQYMYQHGDGHGISNREMEERILGLIFEPIV 539
BPPSLAVAN       ICADLGRMAQFMYQHGDGHGIRNLQMEDRIQSLIFEPIV 540
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