Supporting Information

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SI Materials and Methods

Bioinformatics. Bacterial genome sequence data (total of 8,759,463 proteins and 5,152 strains) were obtained from the National Center for Biotechnology Information (ftp://ftp.ncbi.nih.gov/genomes/Bacteria; 8,617,057 proteins and 5,132 strains), the Broad Institute (olive.broadinstitute.org/collections/actinomycetales_group.1/strains; 104,911 proteins and 15 strains), and in-house draft genome data (37,495 proteins and 5 strains). The construction of the HMM by aligned protein sequences and searching of the protein databases used binary programs made by the compilation of a source package of HMMs for biological sequence analysis, hmmer-3.1b1 (ftp://selab.janelia.org/pub/software/hmmer3/3.1b1). Alignment of sequences was analyzed by using MAFFT (1), version 7.182 (mafft.cbrc.jp/alignment/software/source.html). Phylogenetic analysis of aligned sequences was done by the bootstrap method (bootstrap number, 1,000; seed number, 111) of CLUSTALW (2), version 2.1 (ftp://ftp.ebi.ac.uk/pub/software/clustalw2/2.1). Drawing of the bootstrap tree was carried out with MEGA, version 6.06 (www.megasoftware.net). The third generation HMM specific for bacterial terpene synthases was prepared as follows: 140 presumptive terpene synthases obtained from a previous study (3) using a second generation HMM were aligned by the MAFFT program. Conserved regions (about 260 aa, including the metal-binding motif and the NxxxSxxxE triad motif) of the aligned sequence were extracted by an in-house Perl script program. Extracted sequences were realigned, and the newly aligned sequences were converted to HMM by the hmmbuild program in the hmmer-3.1b1 package. The newest bacterial protein sequence databases described above were processed by the hmmsearch program (E values less than 10^{-3}) in the hmmer-3.1b1 package using the above-described third generation HMM. A web-based program for searching bacterial terpene synthases using the third generation HMM is available from our website (avermitilis.ls.kitasato-u.ac.jp/pfam-ts).

Cloning of Terpene Synthase Genes. Each presumptive terpene synthase gene was amplified by PCR from the total DNA preparation obtained from individual *Streptomyces* microorganisms using a pair of forward and reverse primers to introduce XbaI and HindIII restriction sites flanking the ribosome-binding sites and stop codons, respectively (Table S2). Initial denaturation at 96 °C for 180 s was followed by 25 cycles (95 °C for 30 s, 60 °C for 30 s, and 72 °C for the length of amplified fragment (kilobases) × 60 s) and then final incubation at 72 °C for 5 min using the Expand High-Fidelity PCR System (Roche Diagnostics) or Phusion DNA polymerase (New England Biolabs). After amplification, the reaction mixture was treated with XbaI and HindIII. The digested fragment was ligated into XbaI/HindIII-cut pKU1021*gps* (AB982124), pKU1021*fps* (AB982125), or pKU1021*ggs* (AB982126) by using T4 DNA ligase at 12 °C overnight. The ligation mixture was used to transform *Escherichia coli* DH5α under standard conditions. The recombinant plasmids were isolated from individual colonies after overnight cultivation at 30 °C in LB kanamycin (50 μg/mL), purified and screened by restriction digestion, and sequenced to confirm the integrity of the inserted DNA sequences. Terpene synthase genes from in-house draft genome data were deposited in GenBank as follows: *scya_02107* (accession no. AB981710), *slt18_1078* (accession no. AB981711), *slt18_1246* (accession no. AB981719), *slt18_1718* (accession no. AB981720), *slt18_593* (accession no. AB981721), *slt18_1880* (accession no. AB981722), *slt11_214* (accession no. AB981723), *scya_02397* (accession no. AB981724), *scya_00859* (accession no. AB981725), *scya_02852* (accession no. AB981726), *sspSK5794* (accession no. AB981727), *sspSK6539* (accession no. AB981728), *sspSK3051* (accession no. AB981729), *sspSK6215* (accession no. AB981730), *nd90_2698* (accession no. AB981731), *nd90_4926* (accession no. AB981732), *nd90_4247* (accession no. AB981733), *nd90_2413* (accession no. AB981734), *nd90_0354* (accession no. AB981735), and *nd90_0246* (accession no. AB981736).

Genes encoding Ava_1982 (*Anabaena variabilis* ATCC 29413; AB983201), Haur_2987 (*Herpetosiphon aurantiacus* DSM 785; AB983202), Haur_2988 (*H. aurantiacus* DSM 785; AB983203), Alr4685 (*Nostoc* sp. PCC 7120; AB983204), Npun_R3832 (*Nostoc punctiforme* PCC 73102; AB983205), Rcas_0622 (*Roseiflexus castenholzii* DSM 13941; AB983206), *roseRS_3509* (*Roseiflexus* sp. RS-1; AB983207), *sce6369* (*Sorangium cellulosum* 'So ce 56'; AB983208), *sce8552* (*S. cellulosum* 'So ce 56'; AB983209), MMAR_3220 (*Mycobacterium marinum* M; AB983210), and Rxyl_0493 (*Rubrobacter xylanophilus* DSM 9941, AB983211) were synthesized (Eurofins Genomics) according to *Streptomyces avermitilis* codon use, and restriction sites XbaI plus ribosome-binding site and HindIII were added at the 5′ and 3′ ends, respectively. Each synthetic gene was digested with XbaI and HindIII, and the digested fragment was ligated into XbaI/HindIII-cut pKU1021*fps* or pKU1021*ggs* by using T4 DNA ligase at 12 °C overnight. The resultant recombinant plasmids were introduced into *E. coli* GM2929 *hsdS::*Tn*10* to prepare unmethylated DNA. The unmethylated DNA preparations were transformed into *S. avermitilis* SUKA22 by PEG-assisted protoplast transformation as described previously (4).

Cultivation of *S. avermitilis* SUKA22 for the Generation of Terpenes. Spores of *S. avermitilis* SUKA22 transformants carrying the gene encoding a terpene synthase were used to inoculate a 100-mL flask containing 10 mL vegetative medium (5), and the culture was allowed to grow while shaking at 30 °C for 2 d. A 1-mL portion of the vegetative culture was used to inoculate a 500-mL flask containing 100 mL production medium (5), and the culture was allowed to grow while shaking at 28 °C for 5 d. When more than 5 L culture was required, a jar fermentor was used. A 70-mL portion of the vegetative culture grown in a 500-mL flask containing 100 mL vegetative medium at 30 °C for 2 d was used to inoculate a 10-L jar fermentor containing 7 L production medium. The conditions of the fermentation were incubation temperature of 28 °C, sterile airflow of 7 L/min, and rotation at 200 rpm.

Physicochemical Analysis of Terpene Metabolites. Both 1D and 2D NMR (^{1}H: 500 MHz; ^{13}C: 125 MHz) spectra were obtained on a JEOL JNM-ECP 500 FT NMR System. Chemical shifts are referenced to $CDCl_3$ at room temperature. Abbreviations in ^{1}H NMR signals are as follows: singlet (s), multiplet (m), doublet (d), triplet (t), double doublet (dd), double-double doublet (ddd), broad singlet (brs), and broad doublet (brd) signals. High-resolution mass spectra (HRMS) by electron ionization (EI) mode were obtained on a JEOL JMS-700 Mstation. Optical rotations were recorded on a JASCO DIP-1000 polarimeter (c indicates the concentration of compound as wt/vol %).

Isolation of (−)-Drimenol from *S. avermitilis* SUKA22 Carrying *sclav_p0067-sclav_p0068*. One liter culture was centrifuged at 5,000 × *g* for 15 min; then, sedimented mycelium was extracted with 500 mL methanol. The methanol extract was reextracted two times with 100 mL *n*-hexane, and the *n*-hexane extract was

washed with 100 mL 0.1 N NaOH to remove free fatty acids. The organic layer was dried over anhydrous Na_2SO_4, and *n*-hexane extract was evaporated to dryness. The residual brown syrupy material was dissolved in a small volume of *n*-pentane, and the solution was subjected to silica gel column chromatography. After the column was washed with *n*-pentane, the mixture of *n*-pentane-dichloromethane was applied. The (−)-drimenol (1.8 mg), which was eluted by dichloromethane, gave NMR data that matched those previously reported for this compound (6).

(−)-Drimenol: ^{1}H NMR ($CDCl_3$, 500 MHz) δ 5.54 (m, 1H, H-7), 3.84 (m, 1H, H-11), 3.75 (m, 1H, H-11), 2.02 (m, 1H, H-6), 1.98 (m, 1H, H-1), 1.95 (m, 1H, H-6), 1.84 (m, 1H, H-9), 1.79 (s, 3H, H-15), 1.46 (m, 1H, H-2), 1.44 (m, 1H, H-3), 1.24 (m, 1H, H-5), 1.22 (m, 1H, H-3), 1.21 (m, 1H, H-2), 1.06 (m, 1H, H-1), 0.89 (s, 3H, H-13), 0.86 (s, 3H, H-12), 0.85 (s, 3H, H-14); ^{13}C NMR ($CDCl_3$, 125 MHz) δ 133.0 (C, C-8), 124.3 (CH, C-7), 61.2 (CH_2, C11), 57.5 (CH, C-9), 50.1 (CH, C-5), 42.4 (CH_2, C-3), 40.2 (CH_2, C-1), 36.4 (C, C-10), 33.6 (CH_3, C-12), 33.2 (C, C-4), 23.9 (CH_2, C-6), 22.1 (CH_3, C-15), 21.9 (CH_3, C-13), 18.8 (CH_2, C-2), 15.9 (CH_3, C-14); HRMS (EI) calculated for $C_{15}H_{26}O$ [M^+] was 222.19837; found 222.19838.

Isolation of Hydropyrene, Hydropyrenol, Isoelisabethatriene B, and Isoelisabethatriene from *S. avermitilis* SUKA22 Carrying *sclav_p0765*. After centrifugation of the 35-L culture at 5,000 × *g* for 15 min, the supernatant was discarded, and the sedimented mycelium was extracted with 10 L methanol. The mycelium was removed by suction on the filter paper, and the resulting methanolic extract was evaporated under reduced pressure to a volume of ∼2 L. The concentrated methanol extract was then reextracted two times with 200 mL *n*-hexane, and the *n*-hexane layer was then washed with 200 mL 0.1 N NaOH. The *n*-hexane extract was dried over anhydrous Na_2SO_4 and evaporated to dryness. The residual brownish syrup was dissolved in a small volume of *n*-pentane, and the extract was subjected to silica gel chromatography developing with *n*-pentane/dichloromethane (1:0–1:1). Hydropyrene (51.7 mg) was eluted by *n*-pentane, isoelisabethatriene (8.0 mg) was eluted by *n*-pentane/dichloromethane (20:1), isoelisabethatriene B (4.8 mg) was eluted by *n*-pentane/dichloromethane (10:1), and hydropyrenol (22.3 mg) was eluted by dichloromethane. The 1D and 2D ^{1}H and ^{13}C NMR assignments of the structures of the previously unknown compounds hydropyrene, hydropyrenol, and isoelisabethatriene B are described in a separate publication (7). Isoelisabethatriene displayed ^{1}H and ^{13}C NMR data corresponding to those previously reported for the compound isolated from sea plumes (8).

Isoelisabethatriene: ^{1}H NMR ($CDCl_3$, 500 MHz) δ 5.59 (s, 1H, H-5), 5.12 (t, J = 7.1 Hz, 1H, H-14), 2.17 (m, 1H, H-8), 2.15 (m, 1H, H-1), 2.10 (m, 1H, H-4), 2.02 (m, 1H, H-8), 1.96 (m, 2H, H-13), 1.91 (m, 2H, H-7), 1.80 (m, 1H, H-2), 1.79 (s, 3H, H-19), 1.78 (m, 1H, H-11), 1.68 (s, 3H, H-17), 1.61 (s, 3H, H-16), 1.58 (m, 1H, H-3), 1.32 (m, 1H, H-12), 1.31 (m, 1H, H-3), 1.24 (m, 1H, H-12), 1.13 (m, 1H, H-2), 0.94 (d, J = 7.8 Hz, 1H, H-20), 0.64 (d, J = 7.8 Hz, 1H, H-18); ^{13}C NMR ($CDCl_3$, 125 MHz) δ 133.2 (C, C-9), 132.6 (C, C-6), 131.1 (C, C-15), 129.7 (C, C-10), 125.1 (CH, C-14), 122.0 (CH, C-5), 40.5 (CH, C-4), 35.3 (CH_2, C-12), 34.1 (CH, C-11), 33.7 (CH, C-1), 31.1 (CH_2, C-2), 28.8 (CH_2, C-7), 27.0 (CH_2, C-13), 26.5 (CH_2, C-8), 25.9 (CH_3, C-17), 23.2 (CH_3, C-19), 20.6 (CH_2, C-3), 19.1 (CH_3, C-20), 17.8 (CH_3, C-16), 14.7 (CH_3, C-18); HRMS (EI) calculated for $C_{20}H_{32}$ [M^+] was 272.2504; found 272.2506.

Isolation of African-1-Ene and African-2-Ene from *S. avermitilis* SUKA22 Carrying *sclav_p0985*. A 1-L culture was centrifuged at 5,000 × *g* for 15 min, and the supernatant was discarded. The sedimented mycelium was extracted with 500 mL methanol, and the mycelium was removed by filtration. The methanol extract was extracted two times with 100 mL *n*-hexane, and the *n*-hexane layer was washed with 100 mL 0.1 N NaOH to remove free fatty acids. The organic layer was collected and dried over anhydrous Na_2SO_4. The *n*-hexane extract was evaporated to dryness, and the resulting brownish syrup was dissolved in a small volume of *n*-pentane. The extract was subjected to silica gel column chromatography developing with *n*-pentane. The effluent was concentrated, and the concentrate was subjected to 10% (wt/vol) silver nitrate-treated silica gel column chromatography. The column was developed with *n*-pentane/dichloromethane (10:0–10:1). African-1-ene (3.0 mg) was eluted by *n*-pentane/dichloromethane (100:1), and african-2-ene (3.2 mg) was eluted by *n*-pentane/dichloromethane (50:1). The ^{1}H and ^{13}C NMR spectra of african-1-ene (9, 10) and african-2-ene (11) matched those previously reported for the same compounds extracted from plant sources.

African-1-ene: ^{1}H NMR ($CDCl_3$, 500 MHz) δ 4.93 (dd, J = 2.4 Hz, J = 4.5 Hz, 1H, H-1), 2.48 (m, 1H, H-6), 2.27 (m, 1H, H-3), 1.78 (m, 1H, H-5), 1.68 (m, 1H, H-10), 1.67 (m, 1H, H-4), 1.60 (m, 1H, H-5), 1.54 (m, 1H, H-10), 1.20 (m, 1H, H-4), 1.04 (s, 3H, H-14), 1.01 (d, J = 7.0 Hz, 3H, H-15), 0.92 (s, 3H, H-13), 0.91 (s, 3H, H-12), 0.57 (m, 1H, H-9), 0.45 (dd, J = 4.5 Hz, J = 8.0 Hz, 1H, H-8), 0.27 (ddd, J = 4.5 Hz, 1H, H-8); ^{13}C NMR ($CDCl_3$, 125 MHz) δ 146.2 (C, C-2), 129.6 (CH, C-1), 45.4 (CH, C-6), 40.5 (CH_2, C-10), 40.1 (CH, C-3), 37.5 (C, C-11), 33.9 (CH_2, C-4), 32.9 (CH_3, C-13), 28.0 (CH_3, C-14), 26.7 (CH_2, C-5), 23.8 (C, C-7), 22.1 (CH_2, C-8), 20.7 (CH_3, C-12), 20.6 (CH, C-9), 19.2 (CH_3, C-15); HRMS (EI) calculated for $C_{15}H_{24}$ [M^+] was 204.1878; found 204.1878.

African-2-ene: ^{1}H NMR ($CDCl_3$, 500 MHz) δ 2.33 (m, 1H, H-4), 2.23 (s, 1H, H-1), 2.12 (m, 1H, H-6), 2.09 (m, 1H, H-4), 1.82 (m, 2H, H-5), 1.80 (s, 1H, H-1), 1.72 (d, J = 13.5 Hz, 1H, H-10), 1.62 (s, 3H, H-15), 1.09 (dd, J = 10.5 Hz, J = 13.5 Hz, 1H, H-10), 0.91 (s, 3H, H-14), 0.88 (s, 3H, H-13), 0.86 (s, 3H, H-12), 0.49 (dd, J = 4.5 Hz, J = 8.0 Hz, 1H, H-8), 0.45 (m, 1H, H-9), 0.15 (ddd, J = 4.4 Hz, 1H, H-8); ^{13}C NMR ($CDCl_3$, 125 MHz) δ 136.2 (C, C-2), 132.1 (C, C-3), 53.5 (CH, C-6), 43.0 (CH_2, C-1), 42.5 (CH_2, C-10), 37.7 (CH_2, C-4), 34.6 (C, C-11), 32.2 (CH_3, C-13), 26.4 (CH_2, C-5), 26.3 (CH_3, C-14), 22.7 (CH_2, C-8), 21.9 (CH, C-9), 20.5 (CH_3, C-12), 20.4 (C, C-7), 13.7 (CH_3, C-15); HRMS (EI) calculated for $C_{15}H_{24}$ [M^+] was 204.1878; found 204.1878.

Isolation of Clavulatrienes A and B, Prenylgermacrene, Prenylgermacrene B, Prenyl-β-Elemene, and Lobophytumin C from *S. avermitilis* SUKA22 Carrying *sclav_p1169*. Seven liters culture was centrifuged at 5,000 × *g* for 15 min to remove the supernatant. The sedimented mycelium was extracted with 2 L methanol. The mycelium was removed by filtration, and the methanol extract was reextracted two times with 200 mL *n*-hexane. The *n*-hexane extract was washed with 100 mL 0.1 N NaOH to remove free fatty acids. The organic phase was dried over anhydrous Na_2SO_4 and then evaporated to dryness. The residual brownish syrup was dissolved in a small volume of *n*-pentane and subjected to silica gel column chromatography developing with *n*-pentane/dichloromethane (1:0–1:1). Fraction 1 containing clavulatriene B, prenylgermacrene, clavulatriene A, and lobophytumin C was eluted with *n*-pentane. Fraction 2 containing prenyl-β-elemene and prenylgermacrene B was eluted with *n*-pentane/dichloromethane (20:1). Fraction 1 was concentrated under reduced pressure, and the concentrate was subjected to 10% (wt/vol) silver nitrate-treated silica gel column chromatography developing with *n*-pentane/dichloromethane (1:0–0:1) and dichloromethane/methanol (1:0–10:1). Clavulatriene B (4.2 mg) was eluted with *n*-pentane/dichloromethane (1:1), prenylgermacrene (1.2 mg) was eluted with *n*-pentane/dichloromethane (1:20), and clavulatriene A and lobophytumin C were eluted with dichloromethane/methanol (10:1). The fraction containing clavulatriene A and lobophytumin C was concentrated to a small volume, and the concentrate was subjected to 10% (wt/vol) silver nitrate-treated silica gel column chromatography developing with dichloromethane/methanol (50:1).

The faster eluted fraction contained clavulatriene A (22.3 mg), whereas lobophytumin C (4.8 mg) eluted later. Fraction 2 containing prenyl-β-elemene and prenylgermacrene B was concentrated, and the concentrate was subjected to 10% (wt/vol) silver nitrate-treated silica gel column chromatography developing with dichloromethane/methanol (1:0–1:1). Prenyl-β-elemene (0.9 mg) was eluted with dichloromethane/methanol (20:1), and prenylgermacrene B (1.3 mg) was eluted with dichloromethane/methanol (1:1). The 1D and 2D ^{1}H and ^{13}C NMR assignments of the structures of the previously unknown compounds clavulatriene A, clavulatriene B, and prenylgermacrene B are described in a separate publication (7). The ^{1}H and ^{13}C NMR spectra of prenylgermacrene and lobophytumin C both matched those previously reported for the compounds isolated from plant and soft coral (12, 13).

Prenylgermacrene: ^{1}H NMR ($CDCl_3$, 500 MHz) δ 5.13 (m, 1H, H-14), 4.79 (brs, 1H, H-18), 4.74 (brd, J = 11.0 Hz, 1H, H-5), 4.73 (d, J = 1.5 Hz, 1H, H-18), 4.52 (d, J = 10.0 Hz, 1H, H-5), 2.18 (m, 1H, H-2), 2.11 (m, 1H, H-9), 2.08 (m, 1H, H-6), 2.07 (m, 2H, H-12), 2.04 (m, 1H, H-2), 2.01 (m, 2H, H-3), 1.97 (m, 1H, H-9), 1.86 (m, 1H, H-6), 1.69 (s, 3H, H-16), 1.61 (s, 3H, H-17), 1.49 (s, 3H, H-20), 1.44 (m, 1H, H-8), 1.40 (s, 3H, H-19), 1.36 (m, 1H, H-8); ^{13}C NMR ($CDCl_3$, 125 MHz) δ 154.3 (C, C-11), 135.2 (C, C-10), 134.1 (C, C-4), 131.2 (C, C-15), 126.8 (CH, C-1), 126.0 (CH, C-5), 124.1 (CH, C-14), 105.1 (CH_2, C-18), 47.2 (CH, C-7), 39.9 (CH_2, C-9), 38.2 (CH_2, C-3), 35.1 (CH_2, C-12), 31.7 (CH_2, C-2), 30.3 (CH_2, C-8), 29.7 (CH_2, C-6), 26.1 (CH_3, C-16), 26.0 (CH_2, C-13), 17.8 (CH_3, C-17), 16.8 (CH_3, C-20), 16.5 (CH_3, C-19); HRMS (EI) calculated for $C_{20}H_{32}$ [M^+] was 272.2504; found 272.2506.

Lobophytumin C: ^{1}H NMR ($CDCl_3$, 500 MHz) δ 5.13 (m, 1H, H-14), 4.80 (brs, 1H, H-18), 4.74 (d, J = 1.5 Hz, 1H, H-18), 4.7 (d, J = 1.45 Hz, 1H, H-20), 4.44 (d, J = 1.5 Hz, 1H, H-20), 2.31 (m, 1H, H-3), 2.13 (m, 2H, H-13), 2.08 (m, 2H, H-12), 2.01 (m, 1H, H-3), 1.95 (m, 1H, H-7), 1.81 (d, J = 10.0 Hz, 1H, H-5), 1.69 (s, 3H, H-16), 1.62 (s, 3H, H-17), 1.61 (m, 2H, H-8), 1.58 (m, 1H, H-2), 1.53 (m, 1H, H-9), 1.51 (m, 1H, H-9), 1.45 (m, 1H, H-1), 1.27 (m, 1H, H-6), 1.25 (m, 1H, H-1), 0.76 (s, 3H, H-19); ^{13}C NMR ($CDCl_3$, 125 MHz) δ 155.0 (C, C-11), 151.3 (C, C-4), 131.5 (C, C-15), 124.4 (CH, C-14), 107.1 (CH_2, C-20), 105.4 (CH_2, C-18), 50.2 (CH, C-5), 44.7 (CH, C-7), 42.0 (CH_2, C-1), 41.4 (CH_2, C-9), 37.0 (CH_2, C-3), 36.1 (C, C-10), 35.0 (CH_2, C-12), 29.8 (CH_2, C-6), 27.4 (CH_2, C-8), 26.9 (CH_2, C-13), 25.7 (CH_3, C-16), 23.5 (CH_2, C-2), 17.8 (CH_3, C-19), 16.5 (CH_3, C-17); HRMS (EI) calculated for $C_{20}H_{32}$ [M^+] was 272.2504; found 272.2506.

Isolation of Isohirsut-1-Ene from *S. avermitilis* SUKA22 Carrying *sclav_p1407*. Four liters culture was centrifuged at 5,000 × *g* for 15 min, and the mycelium was harvested. The mycelium was extracted with 2 L methanol, and the mycelium was removed by filtration. The methanol extract was reextracted two times with 200 mL *n*-hexane. The upper *n*-hexane layer was collected and washed with 0.1 N NaOH to remove free fatty acids. After the organic phase was dried over anhydrous Na_2SO_4, the extract was concentrated under reduced pressure. The concentrate was subjected to silica gel column chromatography developing with *n*-pentane/dichloromethane (1:0–1:1). Isohirsut-1-ene (1.7 mg) was eluted with *n*-pentane. The 1D and 2D ^{1}H and ^{13}C NMR assignment of the structure of the previously unknown compound isohirsut-1-ene is described in a separate publication (7).

Isolation of Cyclooctat-7(8),10(14)-Diene from *S. avermitilis* SUKA22 Carrying *slt18_1078*. Seven liters culture was centrifuged at 5,000 × *g* for 15 min to remove the supernatant. The sedimented mycelium was extracted with 2 L methanol, and the mycelium was removed by filtration. The methanol extract was reextracted two times with 200 mL *n*-hexane, and the upper *n*-hexane layer was collected and washed with 100 mL 0.1 N NaOH. The organic phase was collected and dried over anhydrous Na_2SO_4, and the extract was evaporated to dryness. The residual brownish syrup was subjected to silica gel column chromatography developing with *n*-pentane/ethyl acetate (1:0–1:1). Cyclooctat-7(8),10(14)-diene (23.9 mg) was eluted with *n*-pentane/ethyl acetate (9:1). The 1D and 2D ^{1}H and ^{13}C NMR assignment of the structure of the previously undescribed compound cyclooctat-7(8),10(14)-diene is described in a separate publication (7).

Isolation of Isohirsut-4-Ene from *S. avermitilis* SUKA22 Carrying *slt18_1880*. Two liters culture was centrifuged at 5,000 × *g* for 15 min, and the supernatant was discarded. The mycelium was extracted with 1 L methanol and then removed by filtration. The methanol extract was reextracted two times with 100 mL *n*-hexane. The upper *n*-hexane layer was collected and washed with 0.1 N NaOH to remove free fatty acids. After the organic phase was dried over anhydrous Na_2SO_4, the extract was concentrated under the reduced pressure. The concentrate was subjected to silica gel column chromatography developing with *n*-pentane/dichloromethane (1:0–1:1). Isohirsut-4-ene (1.8 mg) was eluted with *n*-pentane. The 1D and 2D ^{1}H and ^{13}C NMR assignment of the structure of the previously unknown compound isohirsut-4-ene is described in a separate publication (7).

Isolation of (+)-Dauca-8,11-Diene from *S. avermitilis* SUKA22 Carrying *sven_0552*. Two liters culture was centrifuged at 5,000 × *g* for 15 min. The sedimented mycelium was extracted with 1 L methanol, and the mycelium was removed by filtration. The methanol extract was reextracted two times with 100 mL *n*-hexane. The upper *n*-hexane layer was collected and washed with 100 mL 0.1 N NaOH to remove free fatty acid. The organic phase was dried over anhydrous Na_2SO_4, and the extract was concentrated under reduced pressure. The concentrate was subjected to silica gel column chromatography developing with *n*-pentane/dichloromethane (1:0–1:1). (+)-Dauca-8,11-diene (1.3 mg) was eluted with *n*-pentane/dichloromethane (20:1). Chamigrene was eluted with *n*-pentane/dichloromethane (10:1). The ^{1}H and ^{13}C NMR spectra of (+)-dauca-8,11-diene matched those previously reported for the compound isolated from plants (14, 15).

(+)-Dauca-8,11-diene: ^{1}H NMR ($CDCl_3$, 500 MHz) δ 5.36 (t, J = 6.3 Hz, 1H, H-8), 4.76 (brd, J = 2.0 Hz, 1H, H-12), 4.69 (brd, J = 2.0 Hz, 1H, H-12), 2.93 (m, 1H, H-3), 2.07 (m, 1H, H-9), 2.06 (m, 1H, H-6), 1.99 (m, 1H, H-6), 1.82 (m, 1H, H-9), 1.77 (m, 1H, H-4), 1.72 (s, 3H, H-14), 1.69 (s, 3H, H-13), 1.54 (m, 1H, H-2), 1.51 (m, 1H, H-5), 1.50 (m, 1H, H-1), 1.45 (m, 1H, H-1), 1.25 (m, 1H, H-2), 1.23 (m, 1H, H-5), 0.79 (s, 3H, H-15); ^{13}C NMR ($CDCl_3$, 125 MHz) δ 148.2 (C, C-11), 138.9 (C, C-7), 122.8 (CH, C-8), 112.7 (CH_2, C-12), 56.9 (CH, C-4), 50.4 (CH, C-3), 42.6 (C, C-10), 42.5 (CH_2, C-9), 42.1 (CH_2, C-1), 35.4 (CH_2, C-6), 28.4 (CH_2, C-2), 27.7 (CH_3, C-14), 23.1 (CH_3, C-13), 23.0 (CH_2, C-5), 19.4 (CH_3, C-15); HRMS (EI) calculated for $C_{15}H_{24}$ [M^+] was 204.1878; found 204.1878.

Isolation of Tsukubadiene from *S. avermitilis* SUKA22 Carrying *stsu_20912*. Two liters culture was centrifuged at 5,000 × *g* for 15 min; the sedimented mycelium was extracted with 1 L methanol. The methanol extract was reextracted two times with 200 mL *n*-hexane. The upper *n*-hexane layer was washed with 100 mL 0.1 N NaOH to remove free fatty acids. The organic phase was collected and dried over anhydrous Na_2SO_4, and the extract was evaporated to dryness. The residual brownish syrup was dissolved in a small volume of *n*-pentane, and the extract was subjected to silica gel column chromatography developing with *n*-pentane/dichloromethane (1:0–1:1). Tsukubadiene (9.4 mg) was eluted with *n*-pentane/dichloromethane (20:1). The 1D and 2D ^{1}H and ^{13}C NMR assignment of the structure of the previously unknown compound tsukubadiene is described in a separate publication (7).

Isolation of Odyverdienes A and B from *S. avermitilis* SUKA22 Carrying *nd90_0354*. Two liters culture was centrifuged at 5,000 × *g* for 15 min. The sedimented mycelium was extracted with 2 L methanol, and the mycelium was removed by filtration. The methanol extract was reextracted two times with 200 mL *n*-hexane. The upper *n*-hexane layer was collected and washed with 100 mL 0.1 N NaOH. The organic phase was dried over Na_2SO_4 and evaporated to dryness. The residue was dissolved in a small volume of *n*-pentane, and the extract was subjected to silica gel column chromatography developing with *n*-pentane. The effluent was concentrated under reduced pressure, and the concentrate was subjected to 10% (wt/vol) silver nitrate-treated silica gel column chromatography developing with *n*-pentane/dichloromethane (1:0–1:1). Odyverdiene A (1.2 mg) was eluted with *n*-pentane/dichloromethane (10:1), and odyverdiene B (1.2 mg) was eluted with *n*-pentane/dichloromethane (1:1). The 1D and 2D ^1H and ^{13}C NMR assignments of the structures of the previously unknown compounds odyverdienes A and B are described in a separate publication (7).

Isolation of Allohedycaryol (Germacradien-11-ol) from *S. avermitilis* SUKA22 Carrying *mmar_3220*. Two liters culture was centrifuged at 5,000 × *g* for 15 min. The supernatant was discarded, and sedimented mycelium was extracted with 1 L methanol. After the mycelium was removed by filtration, the methanol extract was reextracted two times with 200 mL *n*-hexane, and the upper *n*-hexane layer was washed with 100 mL 0.1 N NaOH. The organic phase was dried over Na_2SO_4 and then concentrated under reduced pressure. The concentrate was subjected to silica gel column chromatography developing with *n*-pentane/dichloromethane (1:0–0:1). Allohedycaryol [(*4S,7S*)-germacra-1(10)*E*,5*E*-diene-11-ol; 3.7 mg] was eluted with dichloromethane. The ^1H and ^{13}C NMR spectra as well as optical rotation of allohedycaryol matched those previously reported for the compound isolated from *Ferula communis* (16). The allohedycaryol is the diastereomer of the germacradienol [(*4S,7R*)-germacra-1(10)*E*,5*E*-diene-11-ol] produced by *Streptomyces* geosmin synthases.

Allohedycaryol: $[\alpha]_D^{22}$ +150.7° ($CHCl_3$, c = 0.10); ^1H NMR ($CDCl_3$, 500 MHz) δ 5.10 (dd, *J* = 9.4 Hz, *J* = 15.0 Hz, 1H, H-5), 5.09 (dd, *J* = 9.4 Hz, *J* = 15.0 Hz, 1H, H-6), 4.96 (brd, *J* = 11.0 Hz, 1H, H-1), 2.38 (m, 1H, H-2), 2.27 (m, 2H, H-9), 2.18 (m, 1H, H-7), 2.17 (m, 1H, H-4), 2.10 (m, 1H, H-2), 1.56 (m, 1H, H-3), 1.55 (s, 3H, H-15), 1.49 (m, 1H, H-8), 1.32 (m, 1H, H-8), 1.25 (m, 1H, H-3), 1.15 (s, 3H, H-13), 1.06 (s, 3H, H-12), 0.90 (d, *J* = 6.6 Hz, 3H, H-14); ^{13}C NMR ($CDCl_3$, 125 MHz) δ 144.0 (CH, C-5), 132.1 (C, C-10), 130.4 (CH, C-1), 127.1 (CH, C-6), 71.5 (C, C-11), 58.8 (CH, C-7), 41.2 (CH_2, C-9), 40.5 (CH, C-4), 35.6 (CH_2, C-3), 28.4 (CH_2, C-8), 26.8 (CH_3, C-13), 26.2 (CH_3, C-12), 22.8 (CH_2, C-8), 22.7 (CH_3, C-14), 16.8 (CH_3, C-15); HRMS (EI) calculated for $C_{15}H_{26}O$ [M^+] was 222.19837; found 222.19838.

Isolation of Cembrene C from *S. avermitilis* SUKA22 Carrying *rxyl_0493*. Fourteen liters culture was centrifuged at 5,000 × *g* for 15 min, and the supernatant was discarded. The sedimented mycelium was extracted with 4 L methanol. After the mycelium was removed by filtration, the methanol extract was reextracted two times with 400 mL *n*-hexane. The upper *n*-hexane layer was collected and washed with 200 mL 0.1 N NaOH to remove free fatty acids. The *n*-hexane extract was dried over Na_2SO_4, and the extract was evaporated to dryness. The residual brownish syrup was dissolved in a small volume of *n*-pentane, and the material was subjected to silica gel column chromatography developing with *n*-pentane/dichloromethane (1:0–1:1). Cembrene C (2.0 mg) was eluted with *n*-pentane/dichloromethane (20:1). The ^1H and ^{13}C NMR spectra of cembrene C matched those previously reported for the compound isolated from soft coral (17).

Cembrene C: ^1H NMR ($CDCl_3$, 500 MHz) δ 6.09 (d, *J* = 11.0 Hz, 1H, H-2), 5.99 (dd, *J* = 1.5 Hz, *J* = 10.0 Hz, 1H, H-3), 5.09 (m, 1H, H-7), 5.08 (m, 1H, H-11), 2.36 (m, 1H, H-15), 2.35 (m, 2H, H-14), 2.22 (m, 2H, H-6), 2.21 (m, 2H, H-5), 2.20 (m, 2H, H-9), 2.18 (m, 2H, H-10), 2.14 (m, 2H, H-13), 1.79 (s, 3H, H-20), 1.63 (s, 3H, H-18), 1.54 (d, *J* = 3.5 Hz, 3H, H-19), 1.10 (d, *J* = 6.8 Hz, 3H, H-16), 1.09 (d, *J* = 6.8 Hz, 3H, H-17); ^{13}C NMR ($CDCl_3$, 125 MHz) δ 147.0 (C, C-1), 134.5 (C, C-4), 134.3 (C, C-8), 134.2 (C, C-12), 125.0 (CH, C-7), 124.1 (CH, C-11), 122.0 (CH, C-3), 118.2 (CH, C-2), 39.0 (CH_2, C-13), 38.9 (CH_2, C-5), 38.5 (CH_2, C-9), 33.5 (CH, C-15), 28.0 (CH_2, C-14), 25.7 (CH_2, C-6), 24.4 (CH_2, C-10), 22.4 (CH_2, C-16), 22.3 (CH_3, C-17), 17.1 (CH_3, C-18), 17.0 (CH_3, C-20), 15.5 (CH_3, C-19); HRMS (EI) calculated for $C_{20}H_{32}$ [M^+] was 272.2504; found 272.2506.

Isolation of Obscuronatin from *S. avermitilis* SUKA22 Carrying *haur_2987*. Two liters of culture was centrifuged at 5,000 × *g* for 15 min, and the supernatant was discarded. The sedimented mycelium was extracted with 1 L methanol. The methanol extract was reextracted two times with 200 mL *n*-hexane. The organic layer was collected and washed with 100 mL 0.1 N NaOH. The organic layer was collected, dried over anhydrous Na_2SO_4, and evaporated to dryness. The residual brownish syrup was dissolved in a small volume of *n*-pentane, and the extract was subjected to silica gel column chromatography developing with *n*-pentane/dichloromethane (1:0–1:10). Obscuronatin (5.8 mg) was eluted with *n*-pentane/dichloromethane (1:10). The ^1H and ^{13}C NMR spectra of obscuronatin matched those previously reported for the compound isolated from soft coral (18).

Obscuronatin: ^1H NMR ($CDCl_3$, 500 MHz) δ 5.24 (d, *J* = 15.0 Hz, 1H, H-5), 5.19 (dd, *J* = 9.5 Hz, *J* = 16.0 Hz, 1H, H-6), 5.09 (m, 1H, H-14), 4.99 (d, *J* = 10.5 Hz, 1H, H-1), 2.48 (m, 1H, H-2), 2.26 (m, 2H, H-9), 2.14 (m, 2H, H-13), 2.04 (m, 1H, H-7), 1.95 (m, 1H, H-2), 1.68 (s, 3H, H-20), 1.66 (m, 1H, H-11), 1.63 (m, 1H, H-3), 1.59 (s, 3H, H-19), 1.58 (m, 1H, H-3), 1.55 (s, 3H, H-17), 1.50 (m, 1H, H-11), 1.39 (m, 2H, H-8), 1.34 (m, 1H, H-12), 1.20 (s, 3H, H-16), 1.14 (m, 1H, H-12), 0.83 (d, *J* = 6.5 Hz, 3H, H-18); ^{13}C NMR ($CDCl_3$, 125 MHz) δ 140.0 (CH, C-5), 132.4 (C, C-10), 130.2 (C, C-15), 129.4 (CH, C-6), 126.1 (CH, C-1), 125.7 (CH, C-14), 73.0 (C, C-4), 51.8 (CH, C-7), 41.8 (CH_2, C-9), 40.0 (CH_2, C-3), 38.1 (CH_2, C-12), 33.5 (CH_2, C-8), 31.0 (CH_3, C-16), 26.0 (CH, C-11), 25.9 (CH_3, C-20), 25.6 (CH_2, C-13), 23.7 (CH_2, C-2), 17.8 (CH_3, C-19), 17.1 (CH_3, C-18), 16.5 (CH_3, C-17); HRMS (EI) calculated for $C_{20}H_{34}O$ [M^+] was 290.2610; found 290.2612.

Locus Tags and Accession Numbers in Fig. 2. Locus tags or accession numbers are as follows: Acix8; *Granulicella mallensis* MP5ACTX8, ACO31274; terpene synthase (*Streptomyces platensis* MA7327), ADD83014; terpene synthase (*S. platensis* MA7339), AMED; *Amycolatopsis mediterranei* U32, BAL14866; germacradien-4-ol synthase (*Streptomyces citricolor* NBRC 13005), BAL14867; *epi*-α-bisabolol synthase (*S. citricolor* NBRC 13005), SCAT; *Streptomyces cattleya* NRRL 8057, ABY50951; germacradienol synthase (*Streptomyces peucetius* ATCC 27952), ACG70951; terpene synthase (*Planobispora rosea* ATCC 53773), ADO85594; pentalenene synthase (PenA of *Streptomyces exfoliatus* UC5319), Amir; *Actinosynnema mirum* DSM 43827, B446; *Streptomyces collinus* Tü 365, BAD86798; diterpene synthase (*Streptomyces* sp. KO-3988), BAI44338; cyclooctat-9-ene-7-ol synthase (*Streptomyces melanosporofaciens* MI614-43F2), BAI77423; 2-methylisoborneol synthase (*Streptomyces lasaliensis* NRRL 3382), BAK26793; 2-methylisoborneol synthase (*Micromonospora olivasterospora* NRRL 8178), BN159; *Streptomyces davawensis* JCM 4913, BN6; *Saccharothrix espanaensis* DSM 44229, Caci; *Catenulispora acidiphila* DSM 44928, CYC2_KITGR; *Kitasatospora griseola*, FRAAL; *Frankia alni* ACN14a, Francci3; *Frankia* sp. CcI3, Franean1; *Frankia* sp.

EAN1pec, Kfla; *Kribbella flavida* DSM 17836, KSE; *Kitasatospora setae* KM-6054, M271; *Streptomyces rapamycinicus* NRRL 5491, MCAG; *Micromonospora* sp. ATCC 39149, MMAR; *M. marinum* M, ND90; *Streptomyces* sp. ND90, Ndas; *Nocardiopsis dassonvillei* subsp. *dassonvillei* DSM 43111, O3I; *Nocardia brasiliensis* ATCC 700358, Rxyl; *xylanophilus* DSM 9941, SACE; *Saccharopolyspora erythraea* NRRL 2338, SACTE; *Streptomyces* sp. SirexAA-E, SAM; *Streptomyces ambofaciens* ATCC 23877, Sare; *Salinispora arenicola* CNS-205, SAV; *S. avermitilis* ATCC 31267, SBD; *Streptomyces bottropensis* ATCC 2543, SBI; *Streptomyces bingchenggensis* BCW-1, SCAB; *Streptomyces scabiei* 87.22, SCLAV; *Streptomyces clavuligerus* ATCC 27064, SCO; *Streptomyces coelicolor* A3(2), SCYA; *Streptomyces cyaneogriseus* susp. *noncyanogenus* NRRL 15773, Sfla; *Streptomyces flavogriseus* ATCC 33331, SFUL; *Streptomyces fulvissimus* DSM 40593, SGR; *Streptomyces griseus* IFO 13550, SHJG; *Streptomyces hygroscopicus* subsp. *jinggangensis* 5008, SLT; *Streptomyces lactacystinaeus* OM-6519, Snas; *Stackebrandtia nassauensis* DSM 44728, SRIM; *Streptomyces rimosus* subsp. *rimosus* ATCC 10970, Sros; *Streptosporangium roseum* DSM 43021, SSAG; *Streptomyces* sp. Mg1, SSBG; *Streptomyces* sp. SPB74, SSDG; *Streptomyces pristinaespiralis* ATCC 25486, SSEG; *Streptomyces sviceus* ATCC 29083, SSFG; *Streptomyces ghanaensis* ATCC 14672, SSGG; *Streptomyces roseosporus* NRRL 11379, SSLG; *Streptomyces* sp. SPB78, SSMG; *Streptomyces* sp. AA4, SSNG; *Streptomyces* sp. C, SSOG; *Streptomyces himastatinicus* ATCC 53653, SSPG; *Streptomyces lividans* TK24, SspSK; *Stpreomyces* sp. SK 1894, SSQG; *Streptomyces viridochromogenes* DSM 40736, SSRG; *Streptomyces griseoflavus* Tü4000, SSTG; *Streptomyces* sp. e14, Strvi; *Streptomyces violaceusniger* Tü 4113, STSU; *Streptomyces tsukubaensis* NRRL18488, SVEN; *Streptomyces venezuelae* ATCC 10712, Tcur; *Thermomospora curvata* DSM 43183, VAB18032; *Verrucosispora maris* AB-18–032, XNR; *Streptomyces albus* J1074, BN77; *Rhizobium mesoamericanum* STM3625, BURPS1106A; *Burkholderia pseudomallei* 1106a, BURPS1710b; *B. pseudomallei* 1710b, BURPS668; *B. pseudomallei* 668, Wcw; *Waddlia chondrophila* WSU 86–1044, Haur; *Herpetosiphon aurantiacus* DSM 785, Rcas; *R. castenholzii* DSM 13941, RoseRS; *Roseiflexus* sp. RS-1, ABU93239; sesquiterpene synthase (*Phormidium* sp. P2r), ADU79148; 2-methylisoborneol synthase (*Pseudanabaena limnetica* str. Castaic Lake), ADU79149; 2-methylisoborneol synthase (*Pseudanabaena* sp. NIVA-CYA 111), ADU79150; 2-methylisoborneol synthase (*Oscillatoria limosa* LBD 305b), AEA03338; geosmin synthase (*Anabaena ucrainica* CHAB1432), AEA03341; geosmin synthase (*A. ucrainica* CHAB2155), AEK21533; monoterpene cyclase (*Pseudanabaena* sp. dqh15), AEK21537; monoterpene cyclase (*Planktothricoides raciborskii* CHAB3331), Alr; *Nostoc* sp. PCC 7120, Ava; *A. variabilis* ATCC 29413, Cylst; *Cylindrospermum stagnale* PCC 7417, Npun; *N. punctiforme* PCC 73102, COCOR; *Corallococcus coralloides* DSM 2259, Hoch; *Haliangium ochraceum* DSM 14365, LILAB; *Myxococcus fulvus* HW-1, MXAN; *Myxococcus xanthus* DK 1622, MYSTI; *Myxococcus stipitatus* DSM 14675, PPSIR1; *Plesiocystis pacifica* SIR-1, Sce; *Sorangium cellulosum* 'So ce 56,' STAUR; *Stigmatella aurantiaca* DW4/3–1, STIAU; *St. aurantiaca* DW4/3–1, PMI13; *Chryseobacterium* sp. CF314, Pfl01; *Pseudomonas fluorescens* Pf0-1, Thimo; *Thioflavicoccus mobilis* 8321, Krac; *Ktedonobacter racemifer* DSM 44963, Cpin; *Chitinophaga pinensis* DSM 2588.

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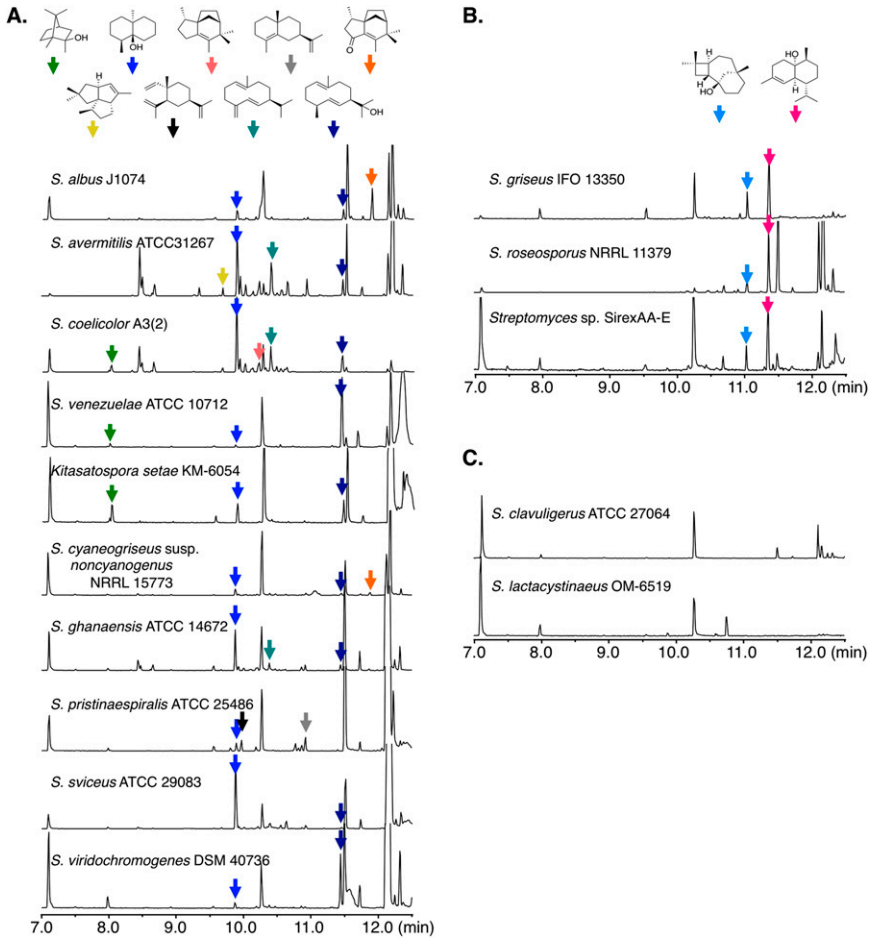

Fig. S1. GC-MS analysis of *n*-hexane extracts of *Streptomycetaceae* microorganisms. Microorganisms were classified into (*A*) group A (geosmin producers), (*B*) group B [(+)-caryolan-1-ol and *epi*-cubenol producers but not producing geosmin], and (*C*) group C (terpene nonproducers). Terpenes in *A* from left to right are 2-methylisoborneol (green arrow), pentalenene (yellow arrow), geosmin (blue arrow), β-elemene (black arrow), *epi*-isozizaene (salmon-pink arrow), germacrene D (teal-blue arrow), selina-4(15),7(11)-diene (gray arrow), germacradienol (deep-blue arrow), and albaflavenone (orange arrow). Terpenes in *B* from left to right are (+)-caryolan-1-ol (light-blue arrow) and *epi*-cubenol (pink arrow).

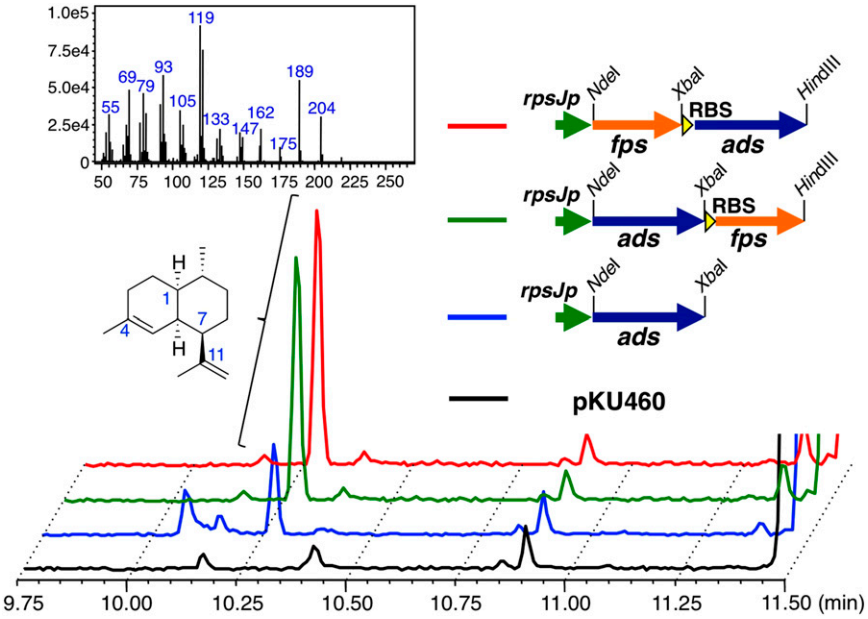

Fig. S2. GC-MS of an *n*-hexane extract of *S. avermitilis* SUKA22 carrying pKU460 (negative control; black), pKU1021::*ads* (blue), pKU1021::*ads*::*fps* (green), and pKU1021::*fps*::*ads* (red). Integrating vector pKU1021 (1) consists of pKU460 (4) and a constitutively expressed promoter *rpsJp*; *ads* indicates a synthetic gene (AB530988) encoding the amorpha-4,11-diene synthase of *Artemisia annua* (Q9AR04), *fps* indicates SAV_2997, and RBS indicates ribosome-binding site.

Table S1. Terpene metabolites produced by heterologous expression in *S. avermitilis*

ORF*	Expression vector	Product(s)	Molecular formula
SCLAV_p0068	pKU1021*fps*	(+)-T-muurolol	$C_{15}H_{26}O$
SCLAV_p0068	pKU1021*fps*	(−)-Drimenol[†]	$C_{15}H_{26}O$
SCLAV_p0328	pKU1021*fps*	δ-Cadinene	$C_{15}H_{24}$
SCLAV_p0635	pKU1021*fps*	β-Elemene[‡]	$C_{15}H_{24}$
SCLAV_p0635	pKU1021*fps*	Selina-4,11-diene	$C_{15}H_{24}$
SCLAV_p0635	pKU1021*fps*	Selina-11-ene-4α-ol	$C_{15}H_{26}O$
SCLAV_p0765	pKU1021*ggs*	Hydropyrene[§]	$C_{20}H_{32}$
SCLAV_p0765	pKU1021*ggs*	Hydropyrenol[§]	$C_{20}H_{34}O$
SCLAV_p0765	pKU1021*ggs*	Isoelisabethatriene	$C_{20}H_{32}$
SCLAV_p0765	pKU1021*ggs*	Isoelisabethatriene B[§]	$C_{20}H_{32}$
SCLAV_p0982	pKU1021*gps*	1,8-Cineole[¶]	$C_{10}H_{18}O$
SCLAV_p0982	pKU1021*gps*	β-Pinene[‖]	$C_{10}H_{16}$
SCLAV_p0982	pKU1021*gps*	Camphene[‖]	$C_{10}H_{16}$
SCLAV_p0985	pKU1021*fps*	African-1-ene	$C_{15}H_{24}$
SCLAV_p0985	pKU1021*fps*	African-2-ene	$C_{15}H_{24}$
SCLAV_p0985	pKU1021*fps*	α-Gurjunene	$C_{15}H_{24}$
SCLAV_p0985	pKU1021*fps*	α-Humulene	$C_{15}H_{24}$
SCLAV_p0985	pKU1021*fps*	9-*epi*-Caryophylene	$C_{15}H_{24}$
SCLAV_p1169	pKU1021*ggs*	Clavulatriene A[§]	$C_{20}H_{32}$
SCLAV_p1169	pKU1021*ggs*	Clavulatriene B[§]	$C_{20}H_{32}$
SCLAV_p1169	pKU1021*ggs*	Prenyl-β-elemene[§]	$C_{20}H_{32}$
SCLAV_p1169	pKU1021*ggs*	Prenylgermacrene	$C_{20}H_{32}$
SCLAV_p1169	pKU1021*ggs*	Prenylgermacrene B[§]	$C_{20}H_{32}$
SCLAV_p1169	pKU1021*ggs*	Lobophytumin C	$C_{20}H_{32}$
SCLAV_p1185	pKU1021*gps*	(*3R*)-linalool	$C_{10}H_{18}O$
SCLAV_p1407	pKU1021*fps*	Isohirsut-1-ene[§]	$C_{15}H_{24}$
SGR_2079	pKU1021*fps*	(+)-Caryolan-1-ol	$C_{15}H_{26}O$
SGR_6065	pKU1021*fps*	α-Copaene	$C_{15}H_{24}$
SGR_6065	pKU1021*fps*	(+)-Caralene	$C_{15}H_{24}$
SGR_6065	pKU1021*fps*	α-Muurolene	$C_{15}H_{24}$
SGR_6065	pKU1021*fps*	Cadina-1(10),4-diene	$C_{15}H_{24}$
SGR_6065	pKU1021*fps*	Cadina-1,4-diene	$C_{15}H_{24}$
SGR_6065	pKU1021*fps*	*epi*-Cubenol	$C_{15}H_{26}O$
SspSK_3051	pKU1021*fps*	γ-Elemene[‡]	$C_{15}H_{24}$
SspSK_3051	pKU1021*fps*	β-Maaliene	$C_{15}H_{24}$
SspSK_3051	pKU1021*fps*	Selina-3,7(11)-diene	$C_{15}H_{24}$
SspSK_3051	pKU1021*fps*	Selina7(11)-ene-4-ol	$C_{15}H_{26}O$
SLT18_1078	pKU1021*ggs*	Cyclooctat-7(8),10(14)-diene[§]	$C_{20}H_{32}$
SLT18_1246	pKU1021*fps*	Germacradien-4-ol	$C_{15}H_{26}O$
SLT18_1246	pKU1021*fps*	α-Copaene	$C_{15}H_{24}$
SLT18_1246	pKU1021*fps*	β-Elemene[‡]	$C_{15}H_{24}$
SLT18_1246	pKU1021*fps*	β-Aromadendrene	$C_{15}H_{24}$
SLT18_1246	pKU1021*fps*	Viridiflorene	$C_{15}H_{24}$
SLT18_1246	pKU1021*fps*	γ-Cadinene	$C_{15}H_{24}$
SLT18_1246	pKU1021*fps*	α-Cubebene	$C_{15}H_{24}$
SLT18_1246	pKU1021*fps*	β-Cubebene	$C_{15}H_{24}$
SLT18_1246	pKU1021*fps*	β-Cadinene	$C_{15}H_{24}$
SLT18_1246	pKU1021*fps*	α-Cadinene	$C_{15}H_{24}$
SLT18_1246	pKU1021*fps*	T-Cadinol	$C_{15}H_{26}O$
SLT18_1880	pKU1021*fps*	Isohirsut-4-ene[§]	$C_{15}H_{24}$
SVEN_0552	pKU1021*fps*	(+)-Dauca-8,11-diene	$C_{15}H_{24}$
STSU_20912	pKU1021*ggs*	Tsukubadiene[§]	$C_{20}H_{32}$
ND90_0354	pKU1021*ggs*	Odyverdiene A[§]	$C_{20}H_{32}$
ND90_0354	pKU1021*ggs*	Odyverdiene B[§]	$C_{20}H_{32}$
MMAR_3220	pKU1021*fps*	γ-Elemene[‡]	$C_{15}H_{24}$
MMAR_3220	pKU1021*fps*	β-Elemene[‡]	$C_{15}H_{24}$
MMAR_3220	pKU1021*fps*	Allohedycaryol	$C_{15}H_{26}O$
Rxyl_0493	pKU1021*ggs*	Cembrene C	$C_{20}H_{32}$
Ava_1982	pKU1021*fps*	β-Elemene[‡]	$C_{15}H_{24}$
Ava_1982	pKU1021*fps*	Germacrene A	$C_{15}H_{24}$
Alr4685	pKU1021*fps*	β-Elemene[‡]	$C_{15}H_{24}$
Alr4685	pKU1021*fps*	Germacrene A	$C_{15}H_{24}$
Haur_2987	pKU1021*ggs*	Obscuronatin	$C_{20}H_{32}$

Table S1. Cont.

ORF*	Expression vector	Product(s)	Molecular formula
Haur_2988	pKU1021*fps*	β-Elemene[‡]	$C_{15}H_{24}$
Haur_2988	pKU1021*fps*	α-Selinene	$C_{15}H_{24}$
Npun_R3832	pKU1021*fps*	Selina-4,11-diene	$C_{15}H_{24}$
Npun_R3832	pKU1021*fps*	8a-*epi*-α-Selinene	$C_{15}H_{24}$
Rcas_0622	pKU1021*fps*	(+)-T-muurolol	$C_{15}H_{26}O$
RoseRS_3509	pKU1021*fps*	(+)-T-muurolol	$C_{15}H_{26}O$
Sce6369	pKU1021*fps*	α-Cubebene	$C_{15}H_{24}$
Sce6369	pKU1021*fps*	β-Cubebene	$C_{15}H_{24}$
Sce6369	pKU1021*fps*	Cadina-3,5-diene	$C_{15}H_{24}$
Sce6369	pKU1021*fps*	Bicyclosesquiphellandrene	$C_{15}H_{24}$
Sce8552	pKU1021*fps*	Eremophilene	$C_{15}H_{24}$

*Each locus tag is indicated in Fig. 2.
[†]The gene *sclav_p0068* was coexpressed with *sclav_p0067* encoding cytochrome P450.
[‡]Generated from germacrene A or B by Cope rearrangement in the injection port of the GC apparatus.
[§]Metabolites that have not previously been reported.
[¶]Product extracted from culture broth.
[‖]Product extracted from mycelium.

Table S2. Lists of primers for PCR amplification of terpene synthase genes

Gene	Sequence (5′–3′)	Direction
sclav_p0068	CGGCTCTAGATGCGAGGTCGACATGTCCCTGAAC	Forward
sclav_p0068	GGTCACAAGCTTCGGGCAGCTCCCGGATGAAGT	Reverse
sclav_p0067-p0068	GGGTTCTAGACAGAGGTGATGTGGACGGTCTAGCC	Forward
sclav_p0067-p0068	GGTCACAAGCTTCGGGCAGCTCCCGGATGAAGT	Reverse
sclav_p0328	GCTCTAGAGGGAACGGAGCGGTGTCGACC	Forward
sclav_p0328	CTCGAGAAGCTTACCGCGTGGCCCAGGAAGGGAAGA	Reverse
sclav_p0571	GCTCTAGAGTCCGGAGGTATGTGGTGCCGCAGG	Forward
sclav_p0571	CTCGAGAAGCTTAACAGGCGGCACCGGGTCAGAGG	Reverse
sclav_p0574	CGCTCTAGACCCTCGGCACGGTAAGCGCCCATG	Forward
sclav_p0574	CTCGAGAAGCTTTCCGGTGGGACGCGTGGTTCGTGTG	Reverse
sclav_p0635	CCGGGCTCTAGAACATAGGCTCCGGACATGAATCCC	Forward
sclav_p0635	GTGGAGAAGCTTGCGACCGCCGTCCTCTACG	Reverse
sclav_p0765	CCTTCTAGAGGAGGACCATATGACCATCTCCGTTCCCCAGCTC	Forward
sclav_p0765	CGCCCAAGCTTGGCCGAGCGCGTTCCTGAC	Reverse
sclav_p0982	CGGCCTCTAGACCACAGGAGCAGCGCACATGCCCG	Forward
sclav_p0982	CTCGAGAAGCTTCGGAGGGACGGGCGGGTCACCAAG	Reverse
sclav_p0985	CGCTCTAGACGCGGTCGTGAGGAGTGAACCCTG	Forward
sclav_p0985	GAGCACAAGCTTTATCCCGGCGGGCAGGTCACG	Reverse
sclav_p1169	CGGTCTAGAGGAGGACCATATGCGCGGAGCCGGTCCCGGGAGC	Forward
sclav_p1169	CGCCGTGAAGCTTGGGCCGGGGTCGCTACCAGGGGGTGAACAC	Reverse
sclav_p1173	CGTCTAGAGGAGGACCATATGCACCCACTGGACCTGCCACCGC	Forward
sclav_p1173	CCCCGAAGCTTCGCCACGCTCACCCCGGAGGACAC	Reverse
sclav_p1185	GCCGTCTAGACGAGAGTTGGGGTCATTGATGCAG	Forward
sclav_p1185	CTCGAGAAGCTTCAGCTCGAACCGGCGTGAGA	Reverse
sclav_p1407	CCTCTAGACGGGAGGGGCTGGGATGCCGCAGG	Forward
sclav_p1407	GCTCAGAAGCTTCACCGGGCGGGGCGTCCGGATCAT	Reverse
sgr2079	GCTCTAGACGAGGGGCAGCAATGAGCCAGATC	Forward
sgr2079	GGTGAGAAGCTTAAACATTCGATGGGCGCGGTAGCC	Reverse
sgr6065	CGGCTCTAGACTGGGGCACACCGTTTGACCGGAG	Forward
sgr6065	ACCGGAAAGCTTGCGAGGCCCCCGATCCGTTCC	Reverse
sspsk_3051	GCTCTGCGACGGAGGCCCGCGCATGACCACCACTTC	Forward
sspsk_3051	CTCGAGAAGCTTCGGCCCGGCTCCGTTCCGGTGGAT	Reverse
sspsk_5794	GCTCTAGATGAGGTGATCCAGGGTGGGACCCCATTTGACC	Forward
sspsk_5794	CTCGAGAAGCTTCCCTGACAGCAGGAGCCGGAGGAC	Reverse
slt18_1078	GCTCTAGAAGGGATTTTTGGCATGACAACCGTGCGCCGCACACTTGGC	Forward
slt18_1078	CTCGAGAAGCTTTCACTTCTCCAACTGGTCCCACCACCAGGCGATC	Reverse
slt17_1246	GCTCTAGACGGGAGTCCGATGTCTGACGACACC	Forward
slt17_1246	CTCGAGAAGCTTCGCGTCGGTGGGGCTGTTC	Reverse
slt18_1718	CCCTCCGTCTAGAGGAGGACCATATGTCTGACGACACCTCACTTCAG	Forward
slt18_1718	GGTCCAAGCTTCACGCCGGTCAGACCGCGTGGTAC	Reverse
slt18_1880	CCCTCTAGAGGAGGACCATATGACAACCACGGCAGAGATCCTC	Forward
slt18_1880	GGGGCAAGCTTGTACGACGGGAGGCGGGAAG	Reverse
sven_0552	CGGCTCTAGACGAGGAAGAAGGAGGCTGGTCCCG	Forward
sven_0552	CTCGAGAAGCTTCCACCTGGCGTACGAGGGTCATGC	Reverse
stsu_20912	GGCCTCTAGACGGAGGGAACAAATGATTGAGGTA	Forward
stsu_20912	CTCGAGAAGCTTTCCTTAATGCTGCGATTGACAGAC	Reverse
nd90_0354	GGCTCTAGAGTGAGGAGCCCTTCATGCCGTTCGTC	Forward
nd90_0354	CTCGAGAAGCTTACCAGAGCAGTGACGCGGGCCCTA	Reverse