High efficacy of the Volatile Organic Compounds of *Streptomyces yanglinensis* 3-10 in Suppression of *Aspergillus* Contamination on Peanut Kernels

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I. Supplementary Tables

Supplementary Table S1. List of the microbial isolates used in this study.

Test fungus and isolates	Host and/or origin*
Actinomycetes	
Streptomyces yanglinensis 3-10	Rice (*Oryza sativa*), HZAU
Fungi	
Alteraria alternata TBS-3	Tobacco (*Nicotiana tabacum*), HZAU
Aspergillus flavus NRRL3357	Peanut (*Arachis hypogaea*), NRRL
Aspergillus parasiticus MO527	Rice Rice (*Oryza sativa*), CGMCC
Botrytis cinerea RoseBC-3	Rose (*Rosa chinensis*), HZAU
Bipolaris maydis MB-1	Maize (*Zea mays*), HZAU
Curvularia lunata CFW-4	Rice (*Oryza sativa*), HZAU
Colletotrichum siamense Nj-2	Strawberry (*Fragaria×ananassa*), HAAS
Drechslera graminea BGW014	Barley (*Hordeum vulgare*), HZAU
Fusarium moniliforme WF-3	Rice (*Oryza sativa*) , HZAU
Fusarium oxysporum f. sp. *vasinfectum* FO-25	Cotton (*Gossypium hirsutum*), HAAS
Gaeumanomyces graminis var. *tritici*	Wheat (*Triticum aestivum* L.), HnAAS
Monilia fructigena BT15-56	Peach (*Amygdalus persica*), HZAU
Mucor hiemails WHT-1	Tomato (*Lycopersicon esculentum*), HZAU
Pestalotia theae DMZ21	Rice (*Oryza sativa*), HZAU
Pyricularia oryzae PB-1	Rice (*Oryza sativa*), HZAU
Rhizoctonia solani WH-1	Rice (*Oryza sativa*), HZAU
Rhizopus stolonifer WHS-1	Strawberry (*Fragaria* × *ananassa*), HZAU
Sclerotinia minor Lc-45	Lettuce *(Lactuca sativa)*, HZAU
Sclerotinia sclerotiorum Ss-1	Oilseed rape (*Brassica napus*), HZAU
Sclerotium rolfsii B-1	Plumepoppy (*Macleaya cordata*), HZAU
Oomycetes	
Pythium ultimum WLOW2F	Watermelon (*Citrullus lanatus*), WAAST
Pythium aphanidermatum Py-xg	Watermelon (*Citrullus lanatus*), WAAST

*NRRL = Agricultural Research Service Culture Collection, United States Department of Agriculture; CGMCC = China General Microbiological Culture Collection Center, Beijing, China: HbAAS = Hubei Academy of Agricultural Sciences, Wuhan, China; HnAAS = Henan Academy of Agricultural Sciences, Zhengzhou, China; HZAU = Huazhong Agricultural University, Wuhan, China: WAAST = Wuhan Academy of Agricultural Science and Technology, Wuhan, China.

Supplementary Table S2. List of the oligonucleotide primers for RT- PCR amplification in this study.

Gene	GenBank Acc. No.	Sequence (5'-3')	Thermal program in RT-PCR	Size of the RT-PCR product
2-MIB synthase gene	MK861971	Forward: TGGTTGTGGATCTCGACACTG Reverse: ACCTCGTCACGGCCTACTAC	Initial denaturation: 95℃ for 5 min; 32 cycles: 95℃ for 30s, 56℃ for 30s, 72℃ for 1 min 15s;	1107 bp
Methyltransfer-ase gene	MK861972	Forward: AGAAACGGTTCTTCGACCCC Reverse: CTGAGGAGAACCCGGTCAAC	Initial denaturation: 95℃ for 5 min; 32 cycles: 95℃ for 30s, 56℃ for 30s, 72℃ for 1 min;	876 bp
Geosmin synthase gene	MK861973	Forward: CTCGTGCCAGGTGAGGATGCC Reverse: CGCGTTCTACGTGCCGTACC	Initial denaturation: 95℃ for 5 min; 32 cycles: 95℃ for 30s, 56℃ for 30s, 72℃ for 2 min 15s;	2277 bp
Aryl-alcohol dehydrogenase gene	MK861974	Forward: GATGTGCCGGACCGACC Reverse: GATGAGCTGGTCGAAGGGGAA	Initial denaturation: 95℃ for 5 min; 32 cycles: 95℃ for 30s, 56℃ for 30s, 72℃ for 1min; final	1066 bp
(+)-β-caryophyllene synthase gene	MK861975	Forward: CAGATCACCTTACCGGCGTT Reverse: TCGATCAGTTCCCTTTCCGC	Initial denaturation: 95℃ for 5 min; 32 cycles: 95℃ for 30s, 55℃ for 30s, 72℃ for 1 min;	975 bp
gyrB gene	MK861976	Forward: GAGGTCGTGCTGACCGTGCTGCACGCGGGCGGCAAGTTCGGC Reverse: GTTGATGTGCTGGCCGTCGACGTCGGCGTCCGCCAT	Initial denaturation: 95℃ for 5 min; 32 cycles: 95℃ for 30s, 65℃ for 30s, 72℃ for 1 min 30s; final extension: 72℃ for 10 min.	1284 bp

Supplementary Table S3. List of the oligonucleotide primers for qRT- PCR analysis in this study.

Gene name	**Gene functions**	**Primers used in the qRT-PCR**
aflR	Pathway regulator	F:AGCACTACAAACACTGACCCAC R:CCAGCACCTTGAGAACGATAA
aflCa	Noranthrone monooxygenase, Norsolorinate-anthrone to norsolorinate	F: GCACCAATGGAGCCGTAT R: GCGGTGTTCGTAGCGTTC
aflA	FAS alpha subunit, Acetate to polyketide	F: CGTGAGGTCAAGGCATTCCT R: GACTTGGCCCCCCTTCTGT
aflS	Transcription enhancer, Pathway regulator	F: CCGAAGATTCCGCTTGGA R: TGAAGACATGCAGCAAAAGGA
aflO	O-methyltransferase B, dihydrodemethylsterigmatocystin to dihydrosterigmatocystin	F: TGCTGTGGCATCCATTCAAA R: GGACTGCGTCTTCCAAAAGG
aflD	NOR reductase, norsolorinic acid to averantin	F: ACTGCGACTCGGAAACTGATG R: TGCTCCTCCCGCAATGTC
aflP	O-methyltransferase A, sterigmatocystin to O-methylsterigmatocystin	F: TGTGTCGAGTGATGTGGGACTAG R: GCCACCCAGCTCAACCTACA
aflF	NOR dehydrogenase, norsolorinic acid to averantin	F: AAGATGCTGGGCACGTTTG R: CATGGGTGAGGACGAATTGG
aflQ	Oxydoreductase, O-methylsterigmatocystin to AFB_1 and AFG1, dihydro-Omethylsterigmatocystin to AFB_2 and AFG_2	F: TTGCTGGGCTTGTGGATTC R: GAGGAGGACGCGTGTCTTTG
aflX	Monooxygenase/oxidase, VA to DMST	F: ACCGCGTTGCACATCGT R: TGGGTGTCCACAACCTTCGT
AccC	Acetyl-CoA carbosylase, Acetyl-CoA to Malonlyl-CoA	F: ATGGTAAGACCTGCCTGCTA R: AGCGAGGATACCGAGGAT
β-tubulin	Endogenous control, Reference gene	F: AGCAGGCGAAGAAGGAGG R: ACGCCACGCATTTGATCTTC

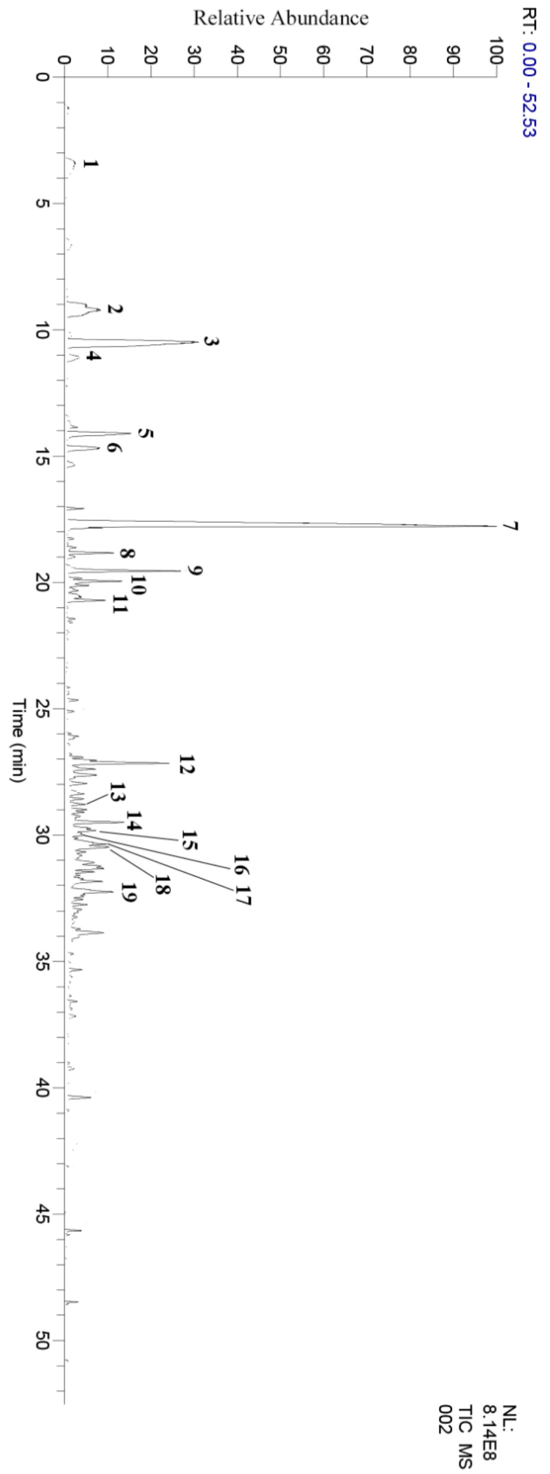
Reference: Gong, A. D., Wu, N. N., Kong, X. W., Zhang, Y. M., Hu, M. J., Gong, S. J., Dong. F. Y., Wang, J. H., Zhao, Z. Y., and Liao, Y. C. (2019) Inhibitory effect of volatiles emitted from *Alcaligenes faecalis* N1-4 on *Aspergillus flavus* and aflatoxins in storage. *Front. Microbiol.* 10:1419. doi: 10.3389/fmicb.2019.01419

Supplementary Table S4. Effects of the volatile organic compounds (VOCs) from the autoclaved wheat grains (AWG) cultures of *Streptomyces yanglinensis* 3-10 and soil amendment with the AWG cultures of this strain on peanut seedlings growth.

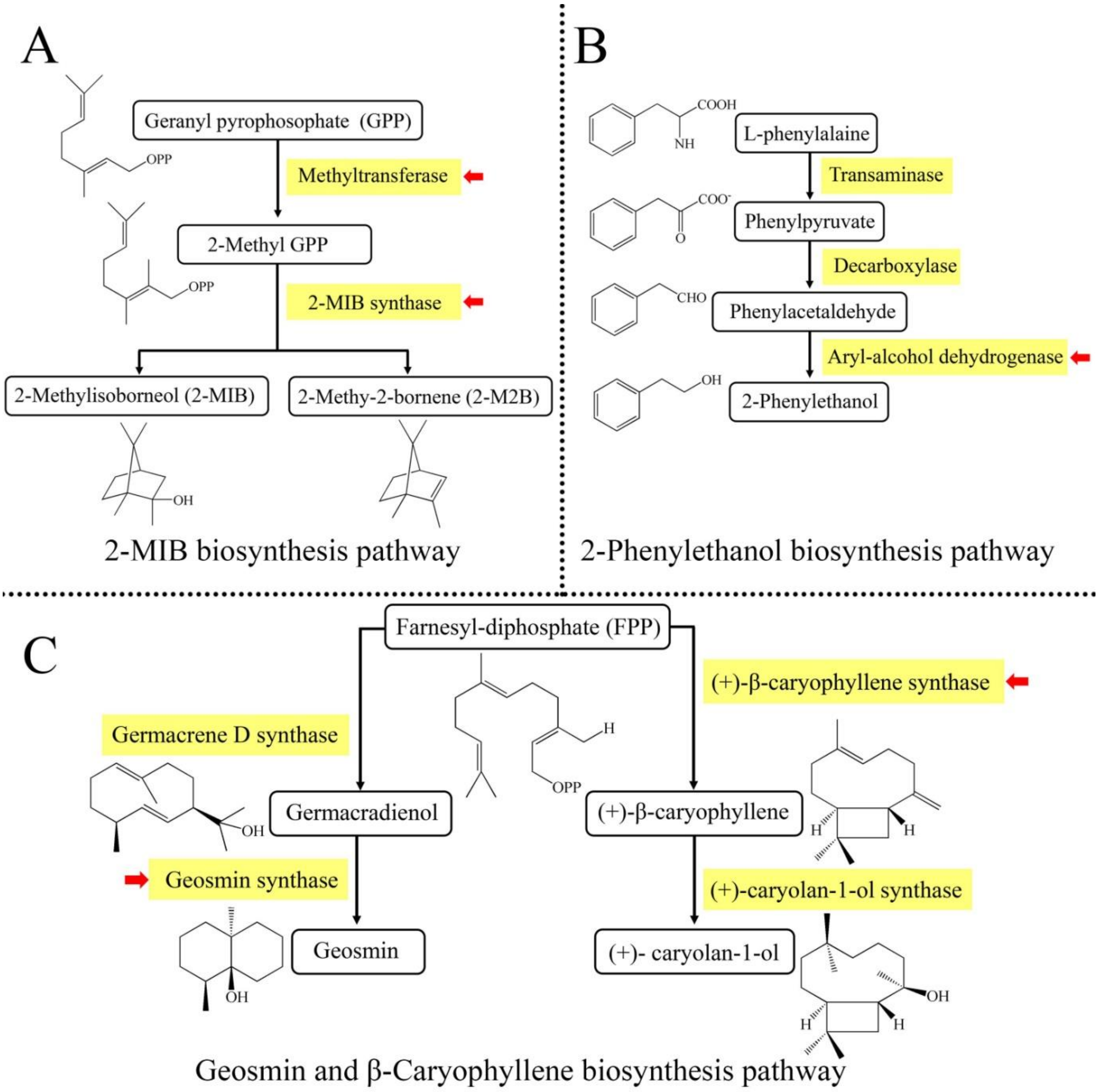
Character	Fumigation with the VOCs			Soil amendment with live culture of *S. yanglinensis* 3-10	
	AWG culture of *S. yanglinensis* 3-10 at 12 g/L *n* =16	AWG culture of *S. yanglinensis* 3-10 at 34 g/L *n* =16	Fresh AWG *n* =16	AWG culture of *S. yanglinensis* 3-10 at 5% (w/w) *n* =16	Fresh AWG *n* =16
Height (cm)	14.1 ± 1.9	11.8 ± 2.2*	14.9 ± 1.70	16.1 ± 4.6	16.7 ± 3.2
TDW (g per seedling)	0.39 ± 0.09	0.38 ± 0.10	0.41 ± 0.11	1.02 ± 0.25	1.05 ± 0.26

*Significantly different ($P < 0.05$) in comparison with that in the control treatment according to Student's *T* test. TDW =Total dry weight

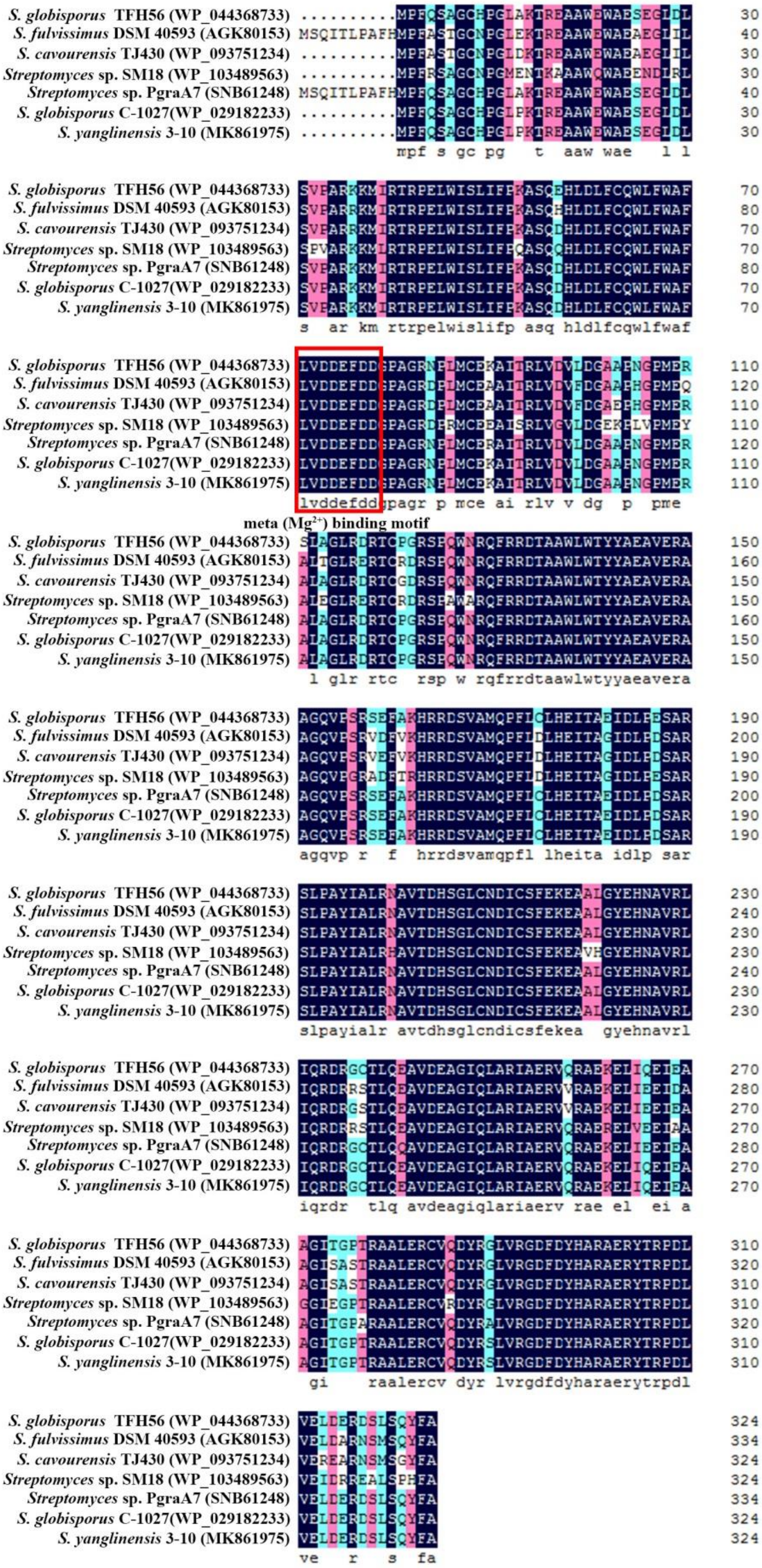
II. Supplementary Figures



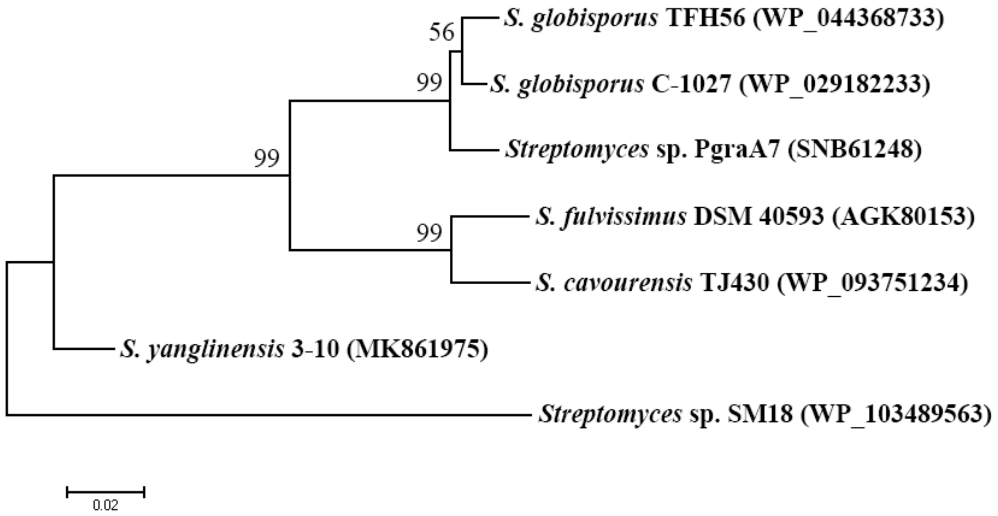
Supplementary Figure S1. A SPME-GC-MS chromatogram showing 19 volatile organic compounds (VOCs) emitted from a 10-day-old AWG culture of *Streptomyces yanglinensis* 3-10 (AWG = autoclaved wheat grains). Chemical identity of the labeled VOCs was listed in Table 1. **Peak 1**, methyl 2-methylbutyrate (M2M); **Peak 3** = 2-methyl-2-bornene (2-M2B); **Peak 6**, 2-Phenylethanol (2-PE); **Peak 7**, 2-methylisoborneol (2-MIB); **Peak 12**, *trans*-1,10-dimethyl-*trans*-9-decalinol (geosmin); **Peak 13**, (+)-β-caryophyllene



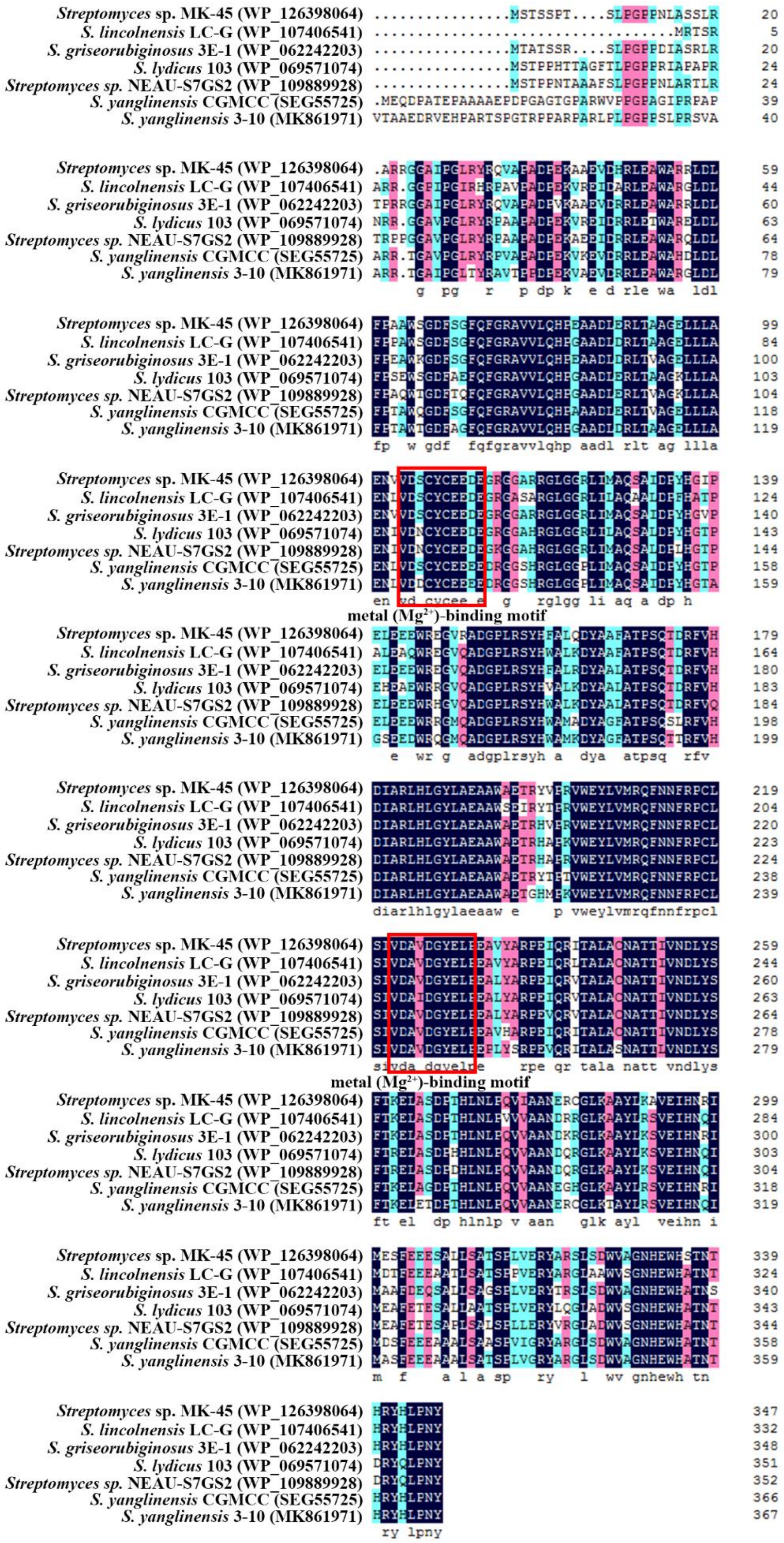
Supplementary Figure S2. Biosynthesis pathways of selected VOCs from *S. yanglinensis* 3-10. The red arrows indicate the genes used for detection of expression by RT-PCR. References for the biosynthesis pathways: **A**, from Komatsu et al. 2008. Proceedings of the National Academy of Sciences of the United States of America, 105: 7422-7427; **B**: from Zhang et al. 2014, BMC Biotechnology 14: 30; **C**, from Jiang et al. 2007. Nature Chemical Biology 3: 711-715; and Nakano et al. 2011. The Journal of Biological Chemistry 286: 27980-27987.



Supplementary Figure S3. (+)-beta-Caryophyllene synthase AA sequence alignment



Supplementary Figure S4. A phylogenetic tree based on AA sequence of (+)-beta-caryophyllene synthase using the maximum likelihood method. The numbers at the nodes in that tree indicate the bootstrap percentages (*n* = 1, 000). The bar indicates the average nucleotide change per site.



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S. lincolnensis LC-G (WP_107406541)         ...................................MRTSR    5
S. griseorubiginosus 3E-1 (WP_062242203)    ................MTATSSR....SLPGPPDIASRLR    20
S. lydicus 103 (WP_069571074)               ................MSTPPHTTAGFTLPGPPRIAPAPR    24
Streptomyces sp. NEAU-S7GS2 (WP_109889928)  ................MSTPPNTAAAFSLPGPPNLARTLR    24
S. yanglinensis CGMCC (SEG55725)            .MEQDPATEPAAAAEPDPGAGTGPARWVPPGPAGIPRPAP    39
S. yanglinensis 3-10 (MK861971)             VTAAEDRVEHPARTSPGTRPPARPARLPLPGPPSLPRSVA    40

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S. lincolnensis LC-G (WP_107406541)         ARR.GGPIPGIRHRPAVPADPEKVREIDARLEAWARGLDL    44
S. griseorubiginosus 3E-1 (WP_062242203)    TPRRGGAIPGLRYRQVAPADPVKAAEVDRRLEAWARRLDL    60
S. lydicus 103 (WP_069571074)               NRR.GGAVPGLRYRPAAPADPEKVREIDRRLETWARELDL    63
Streptomyces sp. NEAU-S7GS2 (WP_109889928)  TRPPGGAVPGLRYRPAAPADPEKAEEIDRRLEAWARQLDL    64
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S. yanglinensis 3-10 (MK861971)             ARR.TGAIPGLTYRAVTPPDPEKVAEVDRRLEAWARGLDL    79
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S. griseorubiginosus 3E-1 (WP_062242203)    FPEAWKGDFSGFQFGRAVVLQHPEAADLDRLTVAGELLLA    100
S. lydicus 103 (WP_069571074)               FPSEWSGDFAEFQFGRAVVLQHPGAADLERLTAAGKLLLA    103
Streptomyces sp. NEAU-S7GS2 (WP_109889928)  FPAQWTGDFTQFQFGRAVVLQHPGAADLERLTVAGKLLLA    104
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S. lydicus 103 (WP_069571074)               ENIVDNCYCEEDEGRGGAHRGLGGRLILAQSALDPYHGTP    143
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S. lincolnensis LC-G (WP_107406541)         ALEAQWREGVQADGPLRSYHWALKDYAAFATPSQTDRFVH    164
S. griseorubiginosus 3E-1 (WP_062242203)    ELEEEWREGVQADGPLRSYHFALRDYAALATPSQTDRFVH    180
S. lydicus 103 (WP_069571074)               EHEAEWRRGVQADGPLRSYHVALKDYAALATPSQTDRFVH    183
Streptomyces sp. NEAU-S7GS2 (WP_109889928)  ELEEEWRHGVQADGPLRSYHWALKDYAALATPSQTDRFVQ    184
S. yanglinensis CGMCC (SEG55725)            ELEEEWRRGMQADGPLRSYHWAMADYAGFATPSQSLRFVH    198
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S. griseorubiginosus 3E-1 (WP_062242203)    DIARLHLGYLAEAAWAETRHVPRVWEYLVMRQFNNFRPCL    220
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                                            diarlhlgylaeaaw e    p vweylvmrqfnnfrpcl

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S. lincolnensis LC-G (WP_107406541)         SIVDAVDGYELPEAVYARPEIQRLTALACNATTIVNDLYS    244
S. griseorubiginosus 3E-1 (WP_062242203)    SIVDAVDGYELPEALYARPEIQRVTALACNATTIVNDLYS    260
S. lydicus 103 (WP_069571074)               SIVDAIDGYELPEALYARPEIQRVTALACNATTIVNDLYS    263
Streptomyces sp. NEAU-S7GS2 (WP_109889928)  SIVDAVDGYELPEALYARPEVQRVTALACNATTIVNDLYS    264
S. yanglinensis CGMCC (SEG55725)            SIVDAVDGYELPEAVHARPEIQRITALACNATTIVNDLYS    278
S. yanglinensis 3-10 (MK861971)             SIVDAVDGYELPEPLYSRPEVQRITALASNATTLVNDLYS    279
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S. griseorubiginosus 3E-1 (WP_062242203)    FTKELASDPTHLNLPQVVAANDKRGLKAAYLKSVEIHNRI    300
S. lydicus 103 (WP_069571074)               FTRELASDPHHLNLPQVVAANDQRGLKAAYLKSVEIHNQI    303
Streptomyces sp. NEAU-S7GS2 (WP_109889928)  FTRELASDPDHLNLPQVVAANDQRGLKAAYLKSVEIHNQI    304
S. yanglinensis CGMCC (SEG55725)            FTKELAGDPTHLNLPQVVAANEGHGLKAAYLRSVEIHNRI    318
S. yanglinensis 3-10 (MK861971)             FTKELETDPTHLNLPQVVAANERCGLKTAYLRSVEIHNQI    319
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S. lincolnensis LC-G (WP_107406541)         MDTFEEEAATLSATSPPVERYARGLAAWVSGNHEWHATNT    324
S. griseorubiginosus 3E-1 (WP_062242203)    MAAFDEQSALLSAGSPLVERYTRSLSDWVAGNHEWHATNS    340
S. lydicus 103 (WP_069571074)               MEAFETESALLAATSPLVERYLQGLADWVSGNHEWHATNT    343
Streptomyces sp. NEAU-S7GS2 (WP_109889928)  MEAFETESAPLSALSPLLERYVRGLADWVSGNHEWHATNT    344
S. yanglinensis CGMCC (SEG55725)            MDSFEEEAAALSAASPVIGRYARGLSDWVAGNHEWHATNT    358
S. yanglinensis 3-10 (MK861971)             MASFEEEAAALSATSPLVGRYARGLSDWVAGNHEWHATNT    359
                                            m  f    a l a sp   ry   l  wv gnhewh tn

Streptomyces sp. MK-45 (WP_126398064)       HRYHLPNY                                    347
S. lincolnensis LC-G (WP_107406541)         HRYHLPNY                                    332
S. griseorubiginosus 3E-1 (WP_062242203)    HRYHLPNY                                    348
S. lydicus 103 (WP_069571074)               DRYQLPNY                                    351
Streptomyces sp. NEAU-S7GS2 (WP_109889928)  DRYQLPNY                                    352
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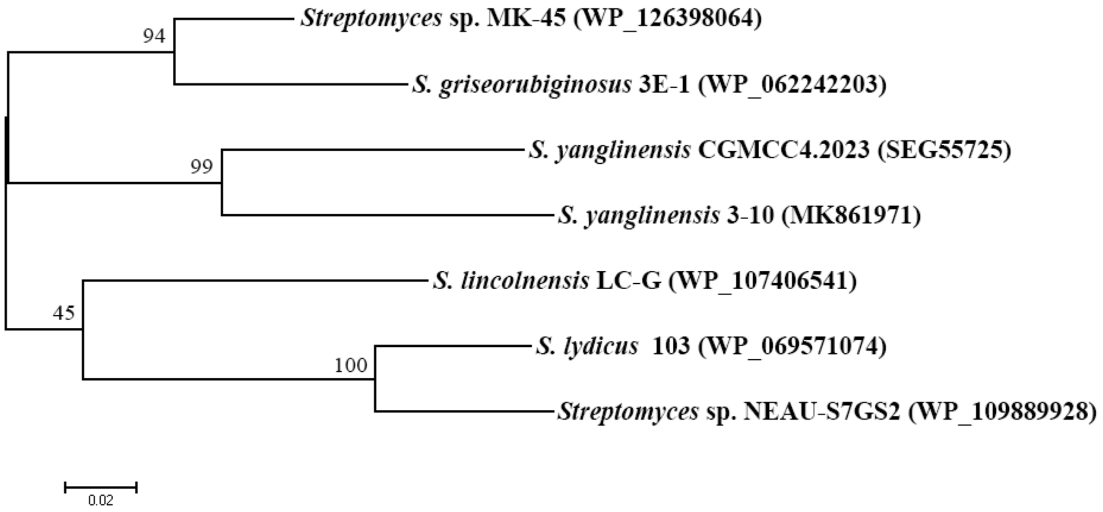
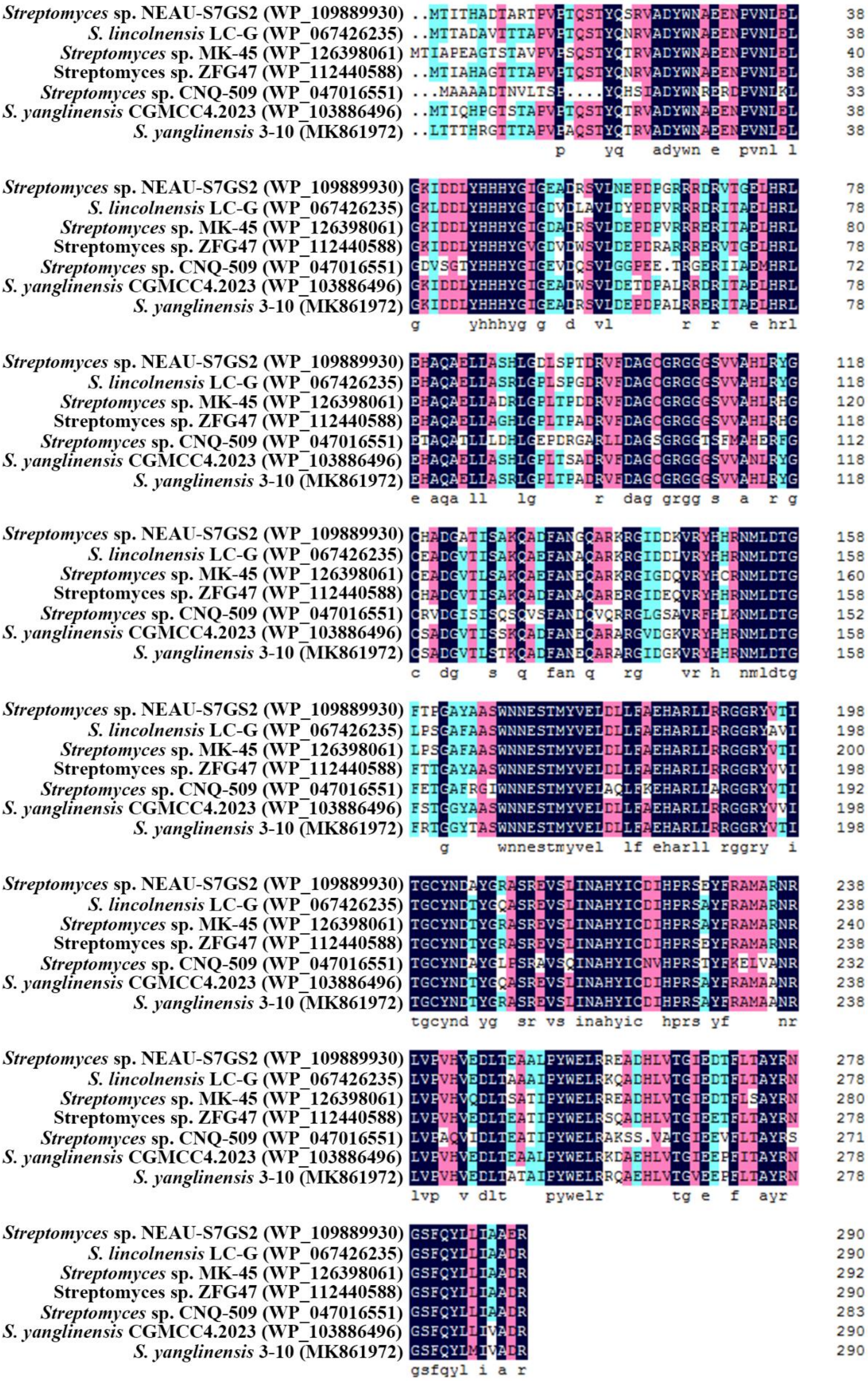
Supplementary Figure S5. Alignment of the amino acid sequences of 2-MIB synthase in *Streptomyces* species



Supplementary Figure S6. A phylogenetic tree inferred based on the amino acid sequences of 2-MIB synthase in *Streptomyces* using the maximum likelihood method. The numbers at the nodes in that tree indicate the bootstrap percentages (*n* = 1, 000). The bar indicates the average nucleotide change per site.



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     Streptomyces sp. ZFG47 (WP_112440588) ..MTIAHAGTTTAPVPTQSTYQNRVADYWNAEENPVNLEL    38
   Streptomyces sp. CNQ-509 (WP_047016551) ...MAAAADTNVLTSP....YQHSIADYWNRERDPVNLKL    33
S. yanglinensis CGMCC4.2023 (WP_103886496) ..MTIQHPGTSTAPVPTQSTYQTRVADYWNAEENPVNLEL    38
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                                                          p    yq   adywn e  pvnl l

Streptomyces sp. NEAU-S7GS2 (WP_109889930) GKIDDLYHHHYGIGEADRSVLNEPDPGRRRDRVTGELHRL    78
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     Streptomyces sp. MK-45 (WP_126398061) GKIDDLYHHHYGIGDADRSVLDEPDPVRRRERITAELHRL    80
     Streptomyces sp. ZFG47 (WP_112440588) GKIDDLYHHHYGVGDVDWSVLDEPDRARRRERVTGELHRL    78
   Streptomyces sp. CNQ-509 (WP_047016551) GDVSGTYHHHYGIGEVDQSVLGGPEE.TRGERIIAEMHRL    72
S. yanglinensis CGMCC4.2023 (WP_103886496) GKIDDLYHHHYGIGEADWSVLDETDPALRRDRITAELHRL    78
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                                           e aqa ll   lg      r  dag grgg s  a  r g

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   Streptomyces sp. CNQ-509 (WP_047016551) CRVDGISISQSQVSFANDQVQRRGLGSAVRFHLKNMLDTG   152
S. yanglinensis CGMCC4.2023 (WP_103886496) CSADGVTISSKQADFANEQARARGVDGKVRYHHRNMLDTG   158
           S. yanglinensis 3-10 (MK861972) CSADGVTLSTKQADFANEQARARGIDGKVRYHHRNMLDTG   158
                                           c  dg   s  q  fan q   rg    vr h  nmldtg

Streptomyces sp. NEAU-S7GS2 (WP_109889930) FTPGAYAASWNNESTMYVELDLLFAEHARLLRRGGRYVTI   198
       S. lincolnensis LC-G (WP_067426235) LPSGAFAASWNNESTMYVELDLLFAEHARLLRRGGRYAVI   198
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     Streptomyces sp. ZFG47 (WP_112440588) FTTGAYAASWNNESTMYVELDLLFAEHARLLRRGGRYVVI   198
   Streptomyces sp. CNQ-509 (WP_047016551) FETGAFRGIWNNESTMYVELAQLFKEHARLLARGGRYVTI   192
S. yanglinensis CGMCC4.2023 (WP_103886496) FSTGGYAASWNNESTMYVELDLLFAEHARLLRRGGRYVVI   198
           S. yanglinensis 3-10 (MK861972) FRTGGYTASWNNESTMYVELDLLFAEHARLLRRGGRYVTI   198
                                              g     wnnestmyvel  lf eharll rggry  i

Streptomyces sp. NEAU-S7GS2 (WP_109889930) TGCYNDAYGRASREVSLINAHYICDIHPRSEYFRAMARNR   238
       S. lincolnensis LC-G (WP_067426235) TGCYNDTYGQASREVSLINAHYICDIHPRSAYFRAMARNR   238
     Streptomyces sp. MK-45 (WP_126398061) TGCYNDTYGRASREVSLINAHYICDIHPRSAYFRAMARNR   240
     Streptomyces sp. ZFG47 (WP_112440588) TGCYNDTYGRASREVSLINAHYICDIHPRSEYFRAMARNR   238
   Streptomyces sp. CNQ-509 (WP_047016551) TGCYNDAYGLPSRAVSQINAHYICNVHPRSTYFKELVANR   232
S. yanglinensis CGMCC4.2023 (WP_103886496) TGCYNDTYGQASREVSLINAHYICDIHPRSAYFRAMAANR   238
           S. yanglinensis 3-10 (MK861972) TGCYNDTYGRASREVSLINAHYICDIHPRSAYFRAMAANR   238
                                           tgcynd yg  sr vs inahyic  hprs yf     nr

Streptomyces sp. NEAU-S7GS2 (WP_109889930) LVPVHVEDLTEAALPYWELRREADHLVTGIEDTFLTAYRN   278
       S. lincolnensis LC-G (WP_067426235) LVPVHVEDLTAAAIPYWELRKQADHLVTGIEDTFLTAYRN   278
     Streptomyces sp. MK-45 (WP_126398061) LVPVHVQDLTSATIPYWELRREADHLVTGIEDTFLSAYRN   280
     Streptomyces sp. ZFG47 (WP_112440588) LVPVHVEDLTEATIPYWELRSQADHLVTGIEETFLTAYRN   278
   Streptomyces sp. CNQ-509 (WP_047016551) LVPAQVIDLTEATIPYWELRAKSS.VATGIEEVFLTAYRS   271
S. yanglinensis CGMCC4.2023 (WP_103886496) LVPVHVEDLTEAALPYWELRKDAEHLVTGIEEPFITAYRN   278
           S. yanglinensis 3-10 (MK861972) LVPVHVEDLTATAIPYWELRRQAEHLVTGVEEPFLTAYRN   278
                                           lvp  v dlt    pywelr       tg e  f  ayr

Streptomyces sp. NEAU-S7GS2 (WP_109889930) GSFQYLLIAAER                               290
       S. lincolnensis LC-G (WP_067426235) GSFQYLLIAADR                               290
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   Streptomyces sp. CNQ-509 (WP_047016551) GSFQYLLIAADR                               283
S. yanglinensis CGMCC4.2023 (WP_103886496) GSFQYLLIVADR                               290
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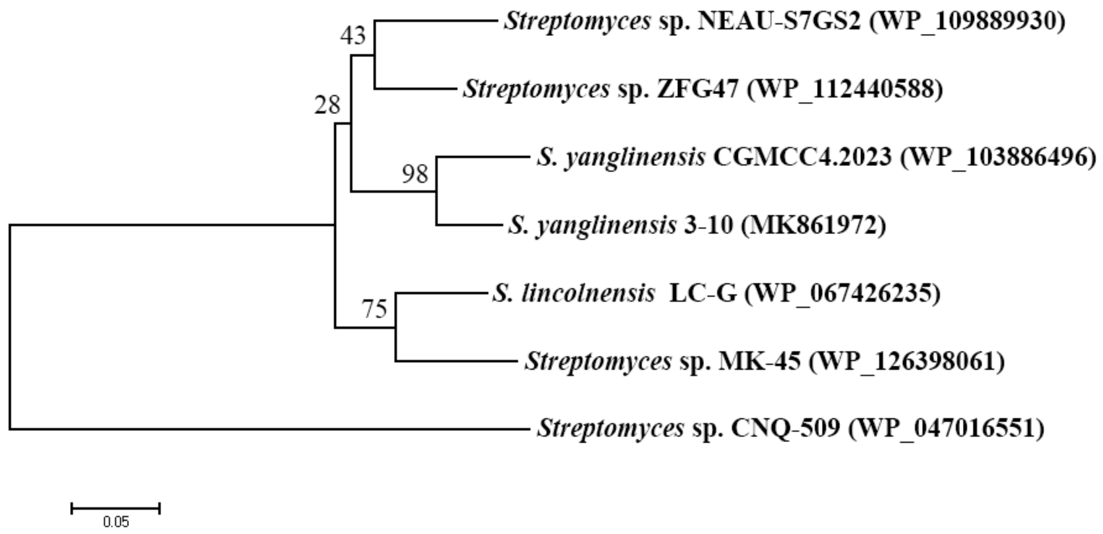
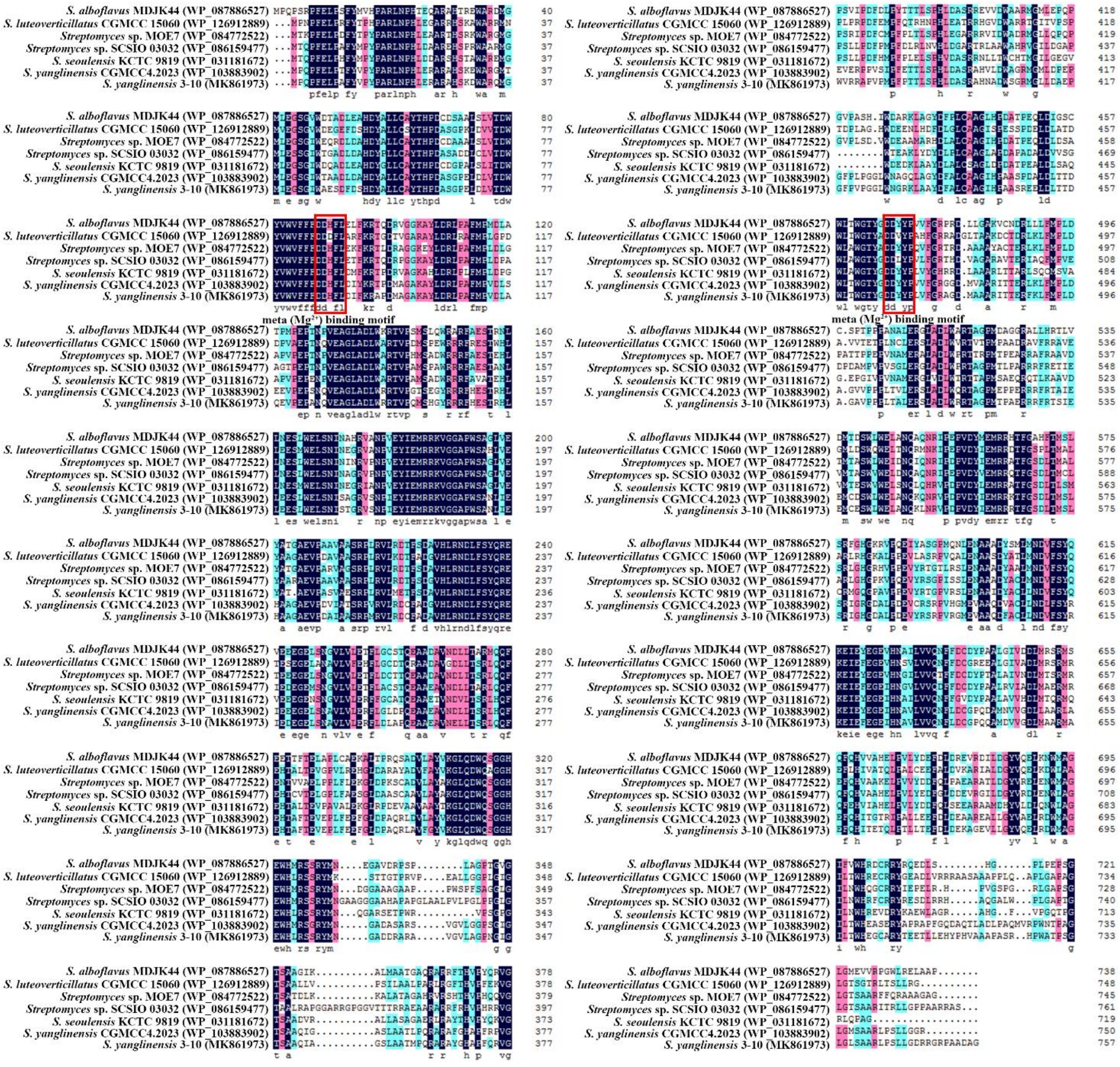
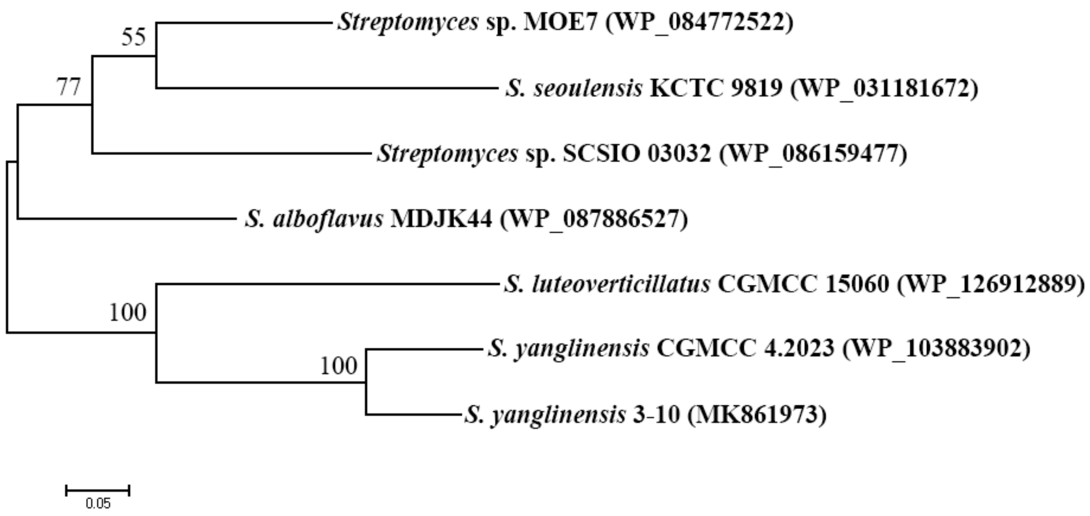
Supplementary Figure S7. Methyltransferase AA sequence alignment



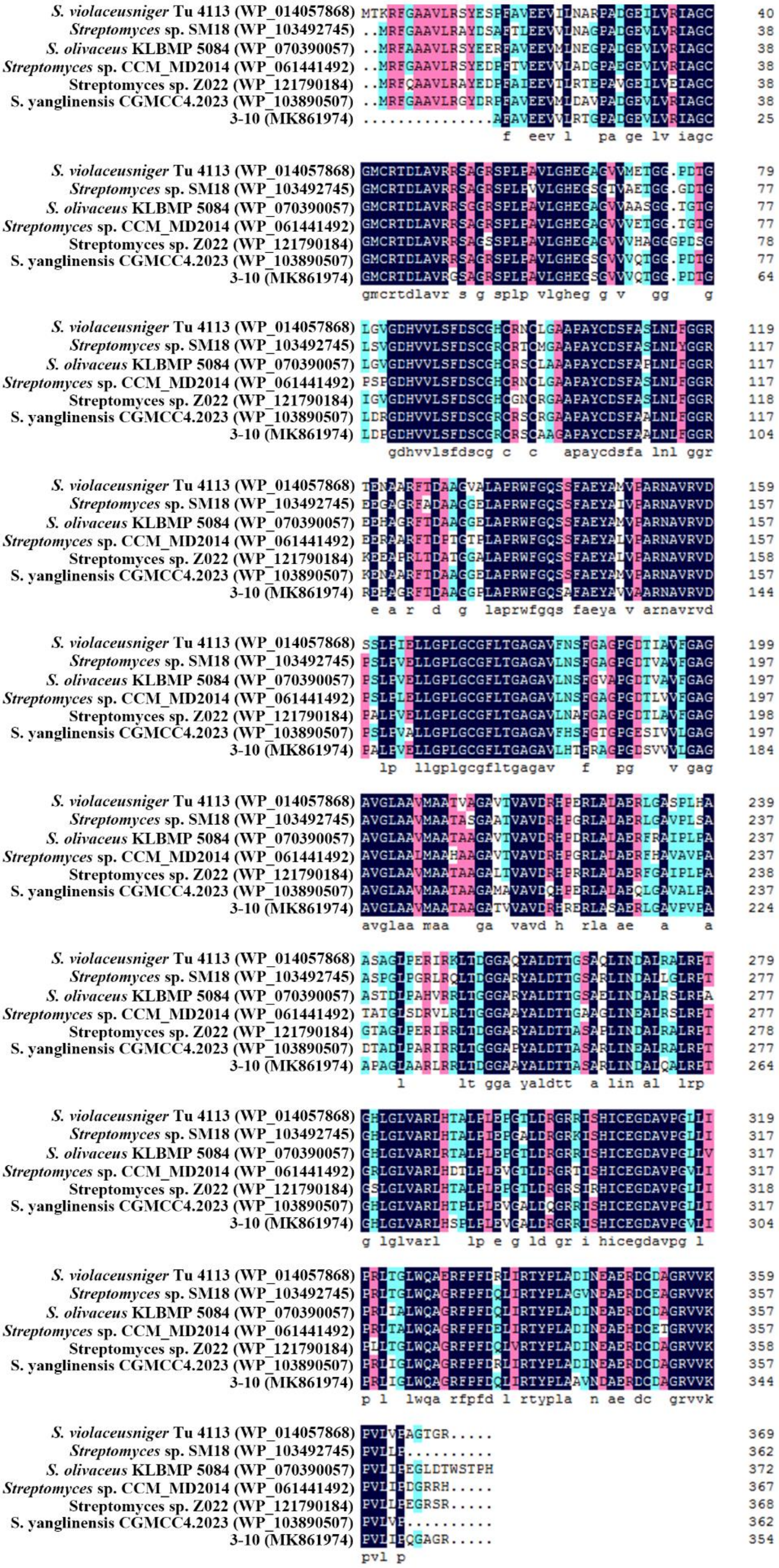
Supplementary Figure S8. A phylogenetic tree based on AA sequence of methyltransferase using the maximum likelihood method. The numbers at the nodes in that tree indicate the bootstrap percentages (*n* = 1, 000). The bar indicates the average nucleotide change per site.



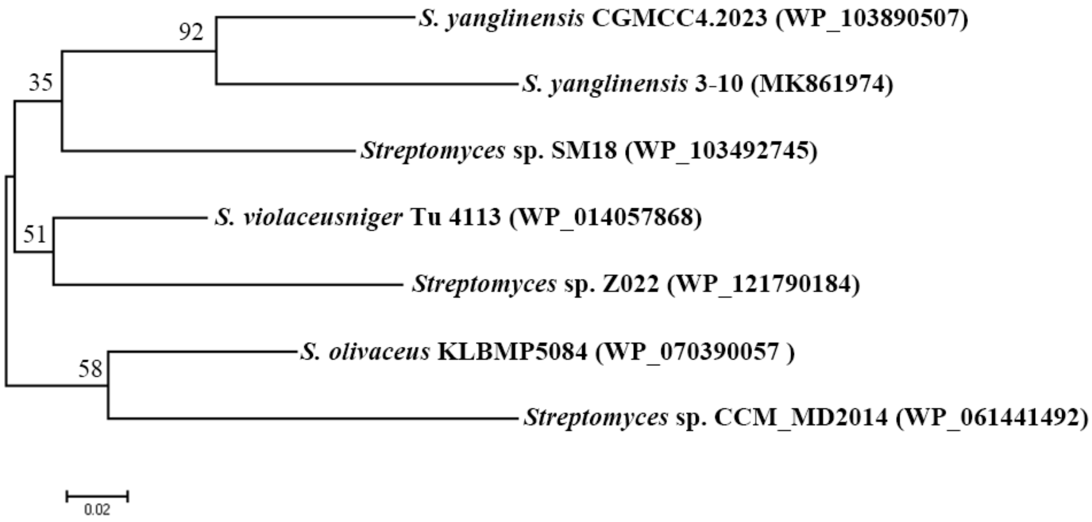
Supplementary Figure S9. Geosmin synthase AA sequence alignment



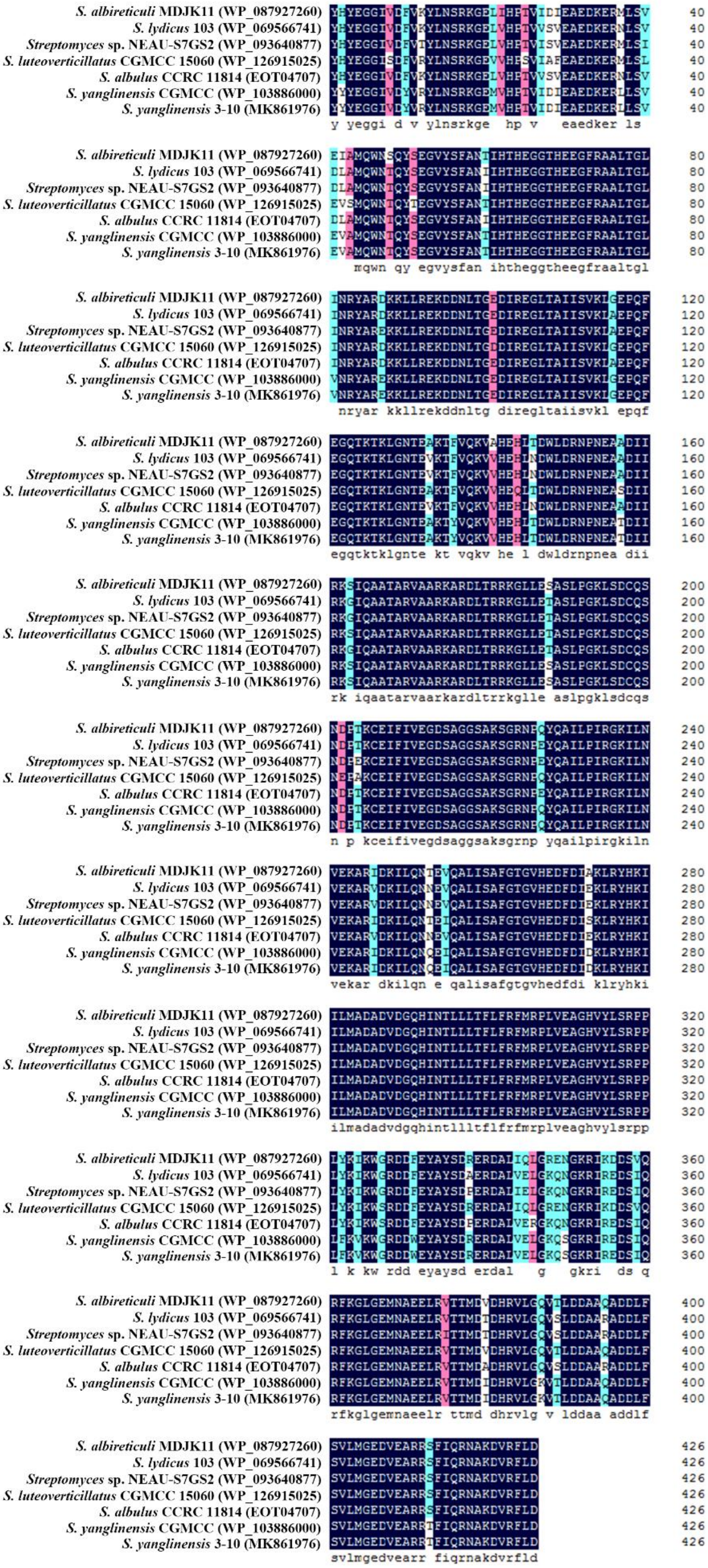
Supplementary Figure S10. A phylogenetic tree based on AA sequence of geosmin synthase using the maximum likelihood method. The numbers at the nodes in that tree indicate the bootstrap percentages (*n* = 1, 000). The bar indicates the average nucleotide change per site.



Supplementary Figure S11. Aryl-alcohol dehydrogenase (2-phenylethanol synthase) AA sequence alignment



Supplementary Figure S12. A phylogenetic tree based on AA sequence of Aryl-alcohol dehydrogenase (2-phenylethanol synthase) using the maximum likelihood method. The numbers at the nodes in that tree indicate the bootstrap percentages (*n* = 1, 000). The bar indicates the average nucleotide change per site.



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                   S. lydicus 103 (WP_069566741) YHYEGGIVDFVKYLNSRKGELVHPTVVSVEAEDKERNLSV    40
     Streptomyces sp. NEAU-S7GS2 (WP_093640877) YHYEGGIVDFVTYLNSRKGELVHPTVISVEAEDKERMLSI    40
S. luteoverticillatus CGMCC 15060 (WP_126915025) YHYEGGISDFVRYLNSRKGEVVHPSVIAFEAEDKERMLSL    40
                S. albulus CCRC 11814 (EOT04707) YHYEGGIVDFVKYLNSRKGELVHPTVVSVEAEDKERNLSV    40
             S. yanglinensis CGMCC (WP_103886000) YYYEGGIVDYVRYLNSRKGEMVHPTVIDIEAEDKERLLSV    40
                  S. yanglinensis 3-10 (MK861976) YYYEGGIVDYVRYLNSRKGEMVHPTVIDIEAEDKERLLSV    40
                                                 y yeggi d v ylnsrkge  hp v   eaedker ls

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                   S. lydicus 103 (WP_069566741) DLAMQWNTQYSEGVYSFANIIHTHEGGTHEEGFRAALTGL    80
     Streptomyces sp. NEAU-S7GS2 (WP_093640877) DLAMQWNTQYSEGVYSFANIIHTHEGGTHEEGFRAALTGL    80
S. luteoverticillatus CGMCC 15060 (WP_126915025) EVSMQWNTQYTEGVYSFANTIHTHEGGTHEEGFRAALTGL    80
                S. albulus CCRC 11814 (EOT04707) DLAMQWNTQYSEGVYSFANIIHTHEGGTHEEGFRAALTGL    80
             S. yanglinensis CGMCC (WP_103886000) EVAMQWNTQYSEGVYSFANTIHTHEGGTHEEGFRAALTGL    80
                  S. yanglinensis 3-10 (MK861976) EVAMQWNTQYSEGVYSFANTIHTHEGGTHEEGFRAALTGL    80
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S. luteoverticillatus CGMCC 15060 (WP_126915025) INRYARDKKLLREKDDNLTGDDIREGLTAIISVKLGEPQF   120
                S. albulus CCRC 11814 (EOT04707) INRYARDKKLLREKDDNLTGEDIREGLTAIISVKLAEPQF   120
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     Streptomyces sp. NEAU-S7GS2 (WP_093640877) EGQTKTKLGNTEVKTFVQKVVHEHLNDWLDRNPNEAADII   160
S. luteoverticillatus CGMCC 15060 (WP_126915025) EGQTKTKLGNTEAKTFVQKVVHEQLTDWLDRNPNEASDII   160
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S. luteoverticillatus CGMCC 15060 (WP_126915025) RKSIQAATARVAARKARDLTRRKGLLETASLPGKLSDCQS   200
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             S. yanglinensis CGMCC (WP_103886000) RKSIQAATARVAARKARDLTRRKGLLESASLPGKLSDCQS   200
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S. luteoverticillatus CGMCC 15060 (WP_126915025) ILMADADVDGQHINTLLLTFLFRFMRPLVEAGHVYLSRPP   320
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                  S. yanglinensis 3-10 (MK861976) ILMADADVDGQHINTLLLTFLFRFMRPLVEAGHVYLSRPP   320
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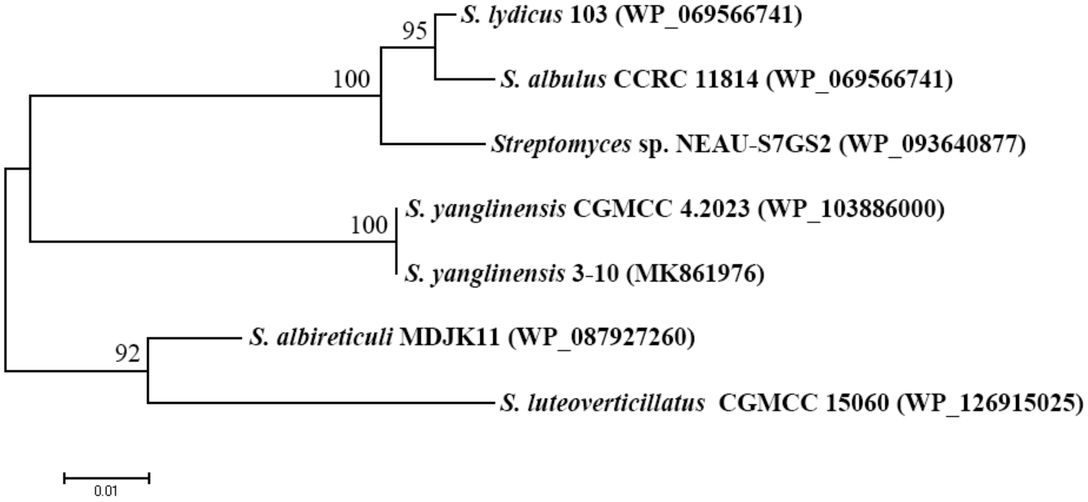
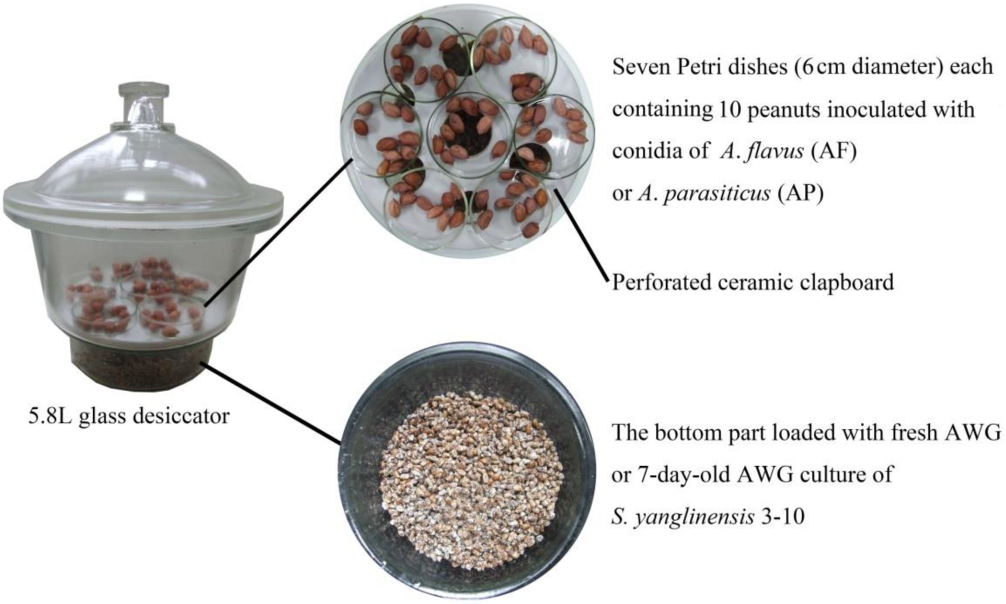
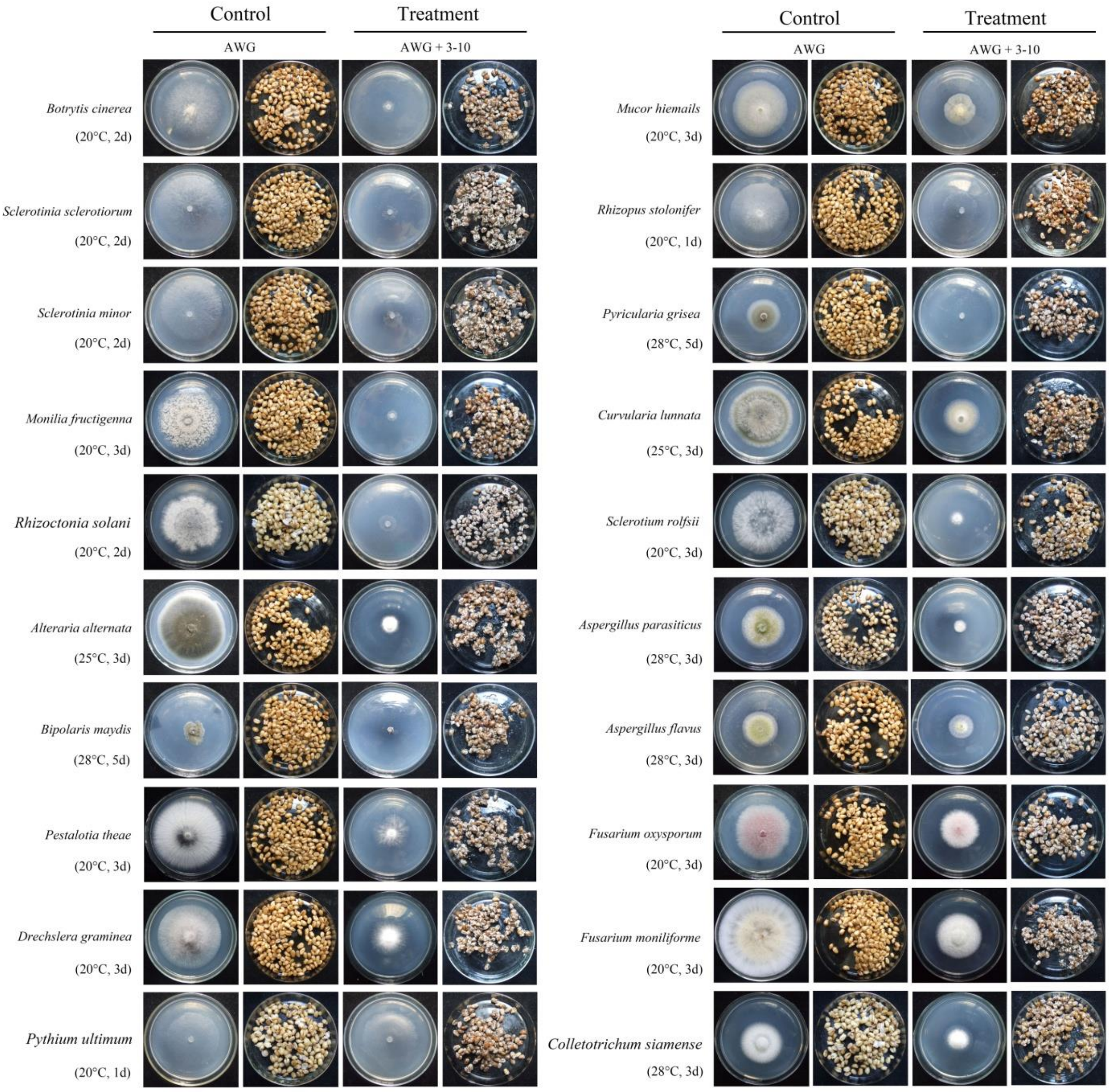
Supplementary Figure S13. gyrB subunit AA sequence alignment



Supplementary Figure S14. A phylogenetic tree based on AA sequence of gyrB subunit using the maximum likelihood method. The numbers at the nodes in that tree indicate the bootstrap percentages (*n* = 1, 000). The bar indicates the average nucleotide change per site.



Supplementary Figure S15. A glass desiccator showing set-up of the bioassay for determination of the efficacy of the volatiles from *Strptomyces yanglinensis* 3-10 in suppression of colonization of peanut kernels by *Aspergillus flavus* and *A. parasiticus*.



Supplementary Figure S16. Antifungal spectrum of the VOCs from *Streptomyces yanglinensis* 3-10.

Control = fresh AWG, Treatment = fumigated with the VOCs from the AWG cultures of *S. yanglinensis* 3-10

Supplementary Figure S17. Effect of the VOCs from the 7-day-old AWG culture of *Streptomyces yanglinensis* 3-10 ($\mathrm{VOCs}^{\mathrm{3\text{-}10AWG}}$). AWG = autoclaved wheat grains. The seedlings were fumigated for seven days under the VOCs from fresh AWG or the AWG culture of *Streptomyces yanglinensis* 3-10.