

Identification of the common biosynthetic gene cluster for both antifungal 5-alkyl-1,2,3,4-tetrahydroquinolines and antimicrobial streptaminals.

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Table of contents

Tables

Table S1. ¹³ C incorporation pattern of 5aTHQ-10a.	Page S3
Table S2. ¹³ C incorporation pattern of 5aTHQ-9i.	Page S4
Table S3. ¹³ C incorporation pattern of 5aTHQ-9n.	Page S5
Table S4. ¹³ C incorporation pattern of 5aTHQ-8i.	Page S6
Table S5. ¹³ C incorporation pattern of 5aTHQ-8n.	Page S7
Table S6. Accession numbers for KSs used for phylogenetic analysis.	Page S8
Table S7. Primers used in this study.	Page S13

Figures

Figure S1. ¹³ C NMR spectra of 5aTHQ-10a (125 MHz, CDCl ₃).	Page S15
Figure S2. ¹³ C NMR spectra of 5aTHQ-9i (125 MHz, CDCl ₃).	Page S17
Figure S3. ¹³ C NMR spectra of 5aTHQ-9n (125 MHz, CDCl ₃).	Page S19
Figure S4. ¹³ C NMR spectra of 5aTHQ-8i (125 MHz, CDCl ₃).	Page S21
Figure S5. ¹³ C NMR spectra of 5aTHQ-8n (125 MHz, CDCl ₃).	Page S23
Figure S6. Comparison of the gene clusters identified in Gram-positive and Gram-negative bacteria. Conserved genes are colored as indicated.	Page S25

Figure S7. Sequence comparison of the KSs and CLFs of known type II PKSs. Page S26

Figure S8. MS (down) and MS/MS (top) spectra of authentic (A) and heterologously produced (B) STAMs-9i and -9n. Page S27

Figure S9. LC-MS profile of STAMs produced by the transformant and authentic ones.

Page S28

Figure S10. MS and MS/MS spectra of THQs.

Page S29

Figure S11. LC-MS analysis of the metabolites produced by the transformants cultured in GS medium.

Page S30

Table S1. ^{13}C incorporation pattern of 5aTHQ-10a.

No.	δ_c (ppm)	Peak area ^a		Intensity ratio ^c	J_{c-c} (Hz) [1,2- $^{13}\text{C}_2$] ^d
		[1- ^{13}C] ^b	unlabeled		
2	41.7	1.76	0.97	1.81	34.0
3	22.6	1.17	0.94	1.24	34.0
4	23.7	1.63	0.93	1.75	41.8
4a	119.8	0.44	0.36	1.22	41.8
5	141.9	0.72	0.39	1.85	43.0
6	118.3	1	1	1.00	55.4
7	126.4	1.55	0.87	1.78	55.4
8	112.6	1.11	0.85	1.31	61.8
8a	144.7	0.71	0.43	1.65	61.8
1'	33.0	1.14	0.95	1.20	43.0
2'	30.3	1.72	0.95	1.81	34.1
3'	30.0	3.12	2.00	1.56	34.4
4'	30.1				34.4
5'	27.1	1.10	0.89	1.24	34.4
6'	36.7	1.15	0.96	1.20	34.4 ^e
7'	34.5	1.07	0.88	1.22	34.6 ^e
8'	29.6	1.10	0.92	1.20	34.6 ^e
9'	11.5	1.21	0.90	1.34	34.9 ^e
10'	19.3	1.10	0.95	1.16	34.9 ^e

^aThe peak areas of each peak were normalized to that of C6.^bLabeled with [1- ^{13}C] sodium acetate.^cThe relative peak area labeled with [1- ^{13}C] sodium acetate was divided by that obtained in the unlabeled spectrum.^dLabeled with [1,2- $^{13}\text{C}_2$] sodium acetate.^eThe doublet signal was very weak.

Table S2. ^{13}C incorporation pattern of 5aTHQ-9i.

No.	δ_c (ppm)	Peak area ^a		Intensity ratio ^c	J_{c-c} (Hz) [1,2- $^{13}\text{C}_2$] ^d
		[1- ^{13}C] ^b	unlabeled		
2	41.8	1.46	1.09	1.34	34.0
3	22.4	0.96	1.08	0.89	34.4
4	23.7	1.31	1.07	1.22	41.8
4a	120.3	0.44	0.41	1.07	41.8
5	142.0	0.61	0.42	1.45	43.0
6	119.0	1	1	1	55.4
7	126.4	1.28	0.95	1.35	55.5
8	113.1	0.91	1.00	0.91	61.8
8a	143.9	0.55	0.46	1.20	61.8
1'	32.9	1.05	1.13	0.93	43.0
2'	30.3	1.45	1.09	1.33	34.3
3'	30.0	1.07	1.20	0.89	- ^e
4'	29.9	1.23	1.04	1.18	34.8
5'	27.4	0.99	1.07	0.93	34.5
6'	39.1	0.93	1.02	0.91	34.5 ^f
7'	28.0	0.86	0.93	0.92	34.9 ^f
8'	22.7	1.99	2.26	0.88	- ^e
9'					

^aThe peak areas of each peak were normalized to that of C6.^bLabeled with [1- ^{13}C] sodium acetate.^cThe relative peak area labeled with [1- ^{13}C] sodium acetate was divided by that obtained in the unlabeled spectrum.^dLabeled with [1,2- $^{13}\text{C}_2$] sodium acetate.^eNot determined.^fThe doublet signal was very weak.

Table S3. ^{13}C incorporation pattern of 5aTHQ-9n.

No.	δ_c (ppm)	Peak area ^a		Intensity ratio ^c	J_{c-c} (Hz) [1,2- $^{13}\text{C}_2$] ^d
		[1- ^{13}C] ^b	unlabeled		
2	41.8	1.54	1.13	1.36	34.0
3	22.5	1.11	1.10	1.01	34.1
4	23.7	1.67	1.07	1.56	41.8
4a	119.8	0.45	0.42	1.07	41.8
5	141.9	0.80	0.40	2.00	43.0
6	118.4	1	1	1	55.5
7	126.3	1.62	0.92	1.76	55.5
8	112.7	1.08	0.92	1.17	61.9
8a	144.6	0.76	0.44	1.73	61.9
1'	33.0	1.02	1.22	0.84	43.0
2'	30.3	1.67	1.15	1.45	34.1
3'	30.0	1.17	1.01	1.16	34.0
4'	29.7	3.30	2.37	1.39	- ^e
5'	29.7				- ^e
6'	29.4	1.84	1.07	1.72	34.5
7'	32.0	1.04	1.13	0.92	34.5
8'	22.8	1.99	1.09	1.83	34.5
9'	14.2	1.01	1.01	1.00	34.5

^aThe peak areas of each peak were normalized to that of C6.^bLabeled with [1- ^{13}C] sodium acetate.^cThe relative peak area labeled with [1- ^{13}C] sodium acetate was divided by that obtained in the unlabeled spectrum.^dLabeled with [1,2- $^{13}\text{C}_2$] sodium acetate.^eNot determined.

Table S4. ^{13}C incorporation pattern of 5aTHQ-8i.

No.	δ_c (ppm)	Peak area ^a		Intensity ratio ^c	J_{c-c} (Hz) [1,2- $^{13}\text{C}_2$] ^d
		[1- ^{13}C] ^b	unlabeled		
2	41.7	1.67	1.00	1.67	34.0
3	22.6	1.32	1.23	1.07	34.1
4	23.7	1.61	1.10	1.46	41.8
4a	119.6	0.36	0.45	0.80	- ^e
5	141.9	0.62	0.45	1.38	43.4
6	118.1	1	1	1	55.4
7	126.3	1.43	1.05	1.36	55.5
8	112.4	0.96	1.12	0.86	62.1
8a	145.0	0.67	0.46	1.46	61.8
1'	33.0	1.27	1.12	1.13	43.0
2'	30.3	1.61	1.01	1.59	34.0
3'	30.2	1.41	1.11	1.27	34.0
4'	27.4	1.18	1.07	1.10	- ^e
5'	39.1	1.23	1.16	1.06	- ^e
6'	28.1	1.03	0.94	1.10	34.9 ^f
7'	22.8	2.49	2.15	1.16	- ^e
8'					

^aThe peak areas of each peak were normalized to that of C6.^bLabeled with [1- ^{13}C] sodium acetate.^cThe relative peak area labeled with [1- ^{13}C] sodium acetate was divided by that obtained in the unlabeled spectrum.^dLabeled with [1,2- $^{13}\text{C}_2$] sodium acetate.^eNot determined.^fThe doublet signal was very weak.

Table S5. ^{13}C incorporation pattern of 5aTHQ-8n.

No.	δ_c (ppm)	Peak area ^a		Intensity ratio ^c	J_{c-c} (Hz) [1,2- $^{13}\text{C}_2$] ^d
		[1- ^{13}C] ^b	unlabeled		
2	41.7	1.60	1.06	1.51	34.1
3	22.6	1.08	1.15	0.94	34.1
4	23.7	1.49	1.07	1.39	41.8
4a	119.6	0.42	0.40	1.05	41.8
5	141.9	0.63	0.45	1.40	43.0
6	118.1	1	1	1	55.5
7	126.3	1.27	0.94	1.35	55.5
8	112.4	1.03	0.98	1.05	61.6
8a	145.0	0.67	0.52	1.29	61.8
1'	33.0	1.14	1.12	1.02	43.0
2'	30.3	1.56	1.03	1.51	34.5
3'	30.0	1.11	1.06	1.05	34.4
4'	29.6	1.44	1.10	1.31	34.4
5'	29.4	1.03	1.07	0.96	34.3
6'	32.0	1.40	1.00	1.40	34.4
7'	22.8	1.10	1.07	1.03	34.4
8'	14.2	0.96	1.01	0.95	34.5

^aThe peak areas of each peak were normalized to that of C6.^bLabeled with [1- ^{13}C] sodium acetate.^cThe relative peak area labeled with [1- ^{13}C] sodium acetate was divided by that obtained in the unlabeled spectrum.^dLabeled with [1,2- $^{13}\text{C}_2$] sodium acetate.

Table S6. Accession numbers for KSs used for phylogenetic analysis.

Name	Accession No.	Strain
ActI-ORF1	CAC44200	<i>Streptomyces coelicolor</i> A3(2)
ActI-ORF2	CAC44201	<i>Streptomyces coelicolor</i> A3(2)
AknB	AAF70106	<i>Streptomyces galilaeus</i>
AknC	AAF70107	<i>Streptomyces galilaeus</i>
AknE2	AAF70109	<i>Streptomyces galilaeus</i>
AmphC	AJE44524	<i>Streptomyces nodosus</i>
AsuC13	ADI58650	<i>Streptomyces nodosus</i> subsp. asukaensis
AsuC14	ADI58649	<i>Streptomyces nodosus</i> subsp. asukaensis
AviM KS	AAK83194	<i>Streptomyces viridochromogenes</i> Tue57
BenA	CAM58798	<i>Streptomyces</i> sp. 2991200
BenB	CAM58799	<i>Streptomyces</i> sp. 2991200
BenQ	CAM58805	<i>Streptomyces</i> sp. A2991200
BSQ33_10425	CP018835	<i>Vibrio gazogenes</i>
BSQ33_10430	CP018835	<i>Vibrio gazogenes</i>
BSQ33_10435	CP018835	<i>Vibrio gazogenes</i>
BSQ33_10440	CP018835	<i>Vibrio gazogenes</i>
Cal30	ALG65306	<i>Streptomyces calvus</i>
Cal31	ALG65305	<i>Streptomyces calvus</i>
Cal32	ALG65304	<i>Streptomyces calvus</i>
Cal33	ALG65303	<i>Streptomyces calvus</i>
CalE8	AAM94794	<i>Micromonospora echinospora</i>
CalO5	AAM70355.1	<i>Micromonospora echinospora</i>
ChIA3	AAZ77696.1	<i>Streptomyces antibioticus</i>
ChlB1	AAZ77673	<i>Streptomyces antibioticus</i>
ChmGII_KS1	AAS79460	<i>Streptomyces bikiniensis</i>
CmmP	Q70J88	<i>Streptomyces griseus</i> subsp. griseus
DauA	Q55225	<i>Streptomyces</i> sp.
ColC3	AIL50165	<i>Streptomyces aureus</i>
ColC4	AIL50166	<i>Streptomyces aureus</i>
ColC13	AIL50179	<i>Streptomyces aureus</i>
ColC14	AIL50180	<i>Streptomyces aureus</i>

DC74_4642	CP007574	<i>Streptomyces albulus</i>
DC74_4643	CP007574	<i>Streptomyces albulus</i>
DC74_4644	CP007574	<i>Streptomyces albulus</i>
DC74_4645	CP007574	<i>Streptomyces albulus</i>
DHA ORF8 KS	BAA89382	<i>Moritella marina</i> ATCC 15381
DpgA	AAM80548	<i>Streptomyces toyocaensis</i>
DpsA	AAA65206	<i>Streptomyces peucetius</i>
DpsB	AAA65207	<i>Streptomyces peucetius</i>
DpsC	AAA65208	<i>Streptomyces peucetius</i>
DynE8	ACB47048	<i>Micromonospora chersina</i>
EcFabB	EIQ69853	<i>Escherichia coli</i> EPEC C342-62
EcFabF	EGT67882	<i>Escherichia coli</i> O104:H4 str. C227-11
EcThiolase	ATOB_ECOLI	<i>Escherichia coli</i>
EncA	AIN46688	<i>Streptomyces qinglanensis</i>
EncB	AIN46689	<i>Streptomyces qinglanensis</i>
FscC_KS1	AAQ82564	<i>Streptomyces</i> sp. FR-008
FscD_KS1	AAQ82568	<i>Streptomyces</i> sp. FR-008
Gcs	Q9K464	<i>Streptomyces coelicolor</i> A3(2)
GdmAIII	AAO06918	<i>Streptomyces hygroscopicus</i>
H744_1c1529	CP005973	<i>Photobacterium gaetbulicola</i> Gung47
H744_1c1530	CP005973	<i>Photobacterium gaetbulicola</i> Gung47
H744_1c1531	CP005973	<i>Photobacterium gaetbulicola</i> Gung47
H744_1c1532	CP005973	<i>Photobacterium gaetbulicola</i> Gung47
Iga11	BAX64252	<i>Streptomyces</i> sp. MSC090213JE08
Iga12	BAX64253	<i>Streptomyces</i> sp. MSC090213JE08
JadA	AAB36562	<i>Streptomyces venezuelae</i> ATCC 10712
JadB	AAB36563	<i>Streptomyces venezuelae</i> ATCC 10712
KirAII_KS1	CAN89632.1	<i>Streptomyces collinus</i> Tu 365
LanA	AAD13536	<i>Streptomyces cyanogenus</i>
LanB	AAD13537	<i>Streptomyces cyanogenus</i>
LipPks2	ABB05103	<i>Streptomyces aureofaciens</i>
LipPks3	ABB05104	<i>Streptomyces aureofaciens</i>
LipPks4	ABB05105	<i>Streptomyces aureofaciens</i>
MdpB	ABY66019	<i>Actinomadura madurae</i>
MdpE_KS	AAQ17110	<i>Actinomadura madurae</i>

MerA KSQ	ABJ97437.1	<i>Streptomyces violaceusniger</i>
MerC KSQ	ABJ97439.1	<i>Streptomyces violaceusniger</i>
MonAI KSQ	AAO65796	<i>Streptomyces cinnamonensis</i>
MtmK	CAA61990	<i>Streptomyces argillaceus</i>
MtmP	CAA61989	<i>Streptomyces argillaceus</i>
NcsE KS_1	Q83TF5	<i>Streptomyces carzinostaticus</i> subsp. neocarzinostaticus
NidA2_KS1	AAC46024	<i>Streptomyces caelestis</i>
NysC	AF263912	<i>Streptomyces noursei</i> ATCC 11455
OxyA	AAZ78325	<i>Streptomyces rimosus</i>
OxyB	AAZ78326	<i>Streptomyces rimosus</i>
OxyD	AAZ78328	<i>Streptomyces rimosus</i>
OzmN	ABS90475	<i>Streptomyces albus</i>
PaFabF	4B7V	<i>Pseudomonas aeruginosa</i> PAO1
PctS_KS1	BAF92601	<i>Streptomyces pactum</i>
Sch_PfaA	AF378327	<i>Schizochytrium</i> sp. ATCC 20888
Pho_PfaA	AF409100	<i>Photobacterium profundum</i> SS9
PikAI_KS1	AAC69329	<i>Streptomyces venezuelae</i>
PikAI_KSQ	AAC69329	<i>Streptomyces venezuelae</i>
PimS3_KS1	CAC20920	<i>Streptomyces natalensis</i>
PksE	AAO25894.1	<i>Streptomyces macromomyceticus</i>
PokM1 KS	ACN64831	<i>Streptomyces diastatochromogenes</i>
PP_2778	AE015451	<i>Pseudomonas putida</i> KT2440
PP_2779	AE015451	<i>Pseudomonas putida</i> KT2440
PP_2780	AE015451	<i>Pseudomonas putida</i> KT2440
PP_2781	AE015451	<i>Pseudomonas putida</i> KT2440
Pput_2974	CP000712	<i>Pseudomonas putida</i> F1
Pput_2975	CP000712	<i>Pseudomonas putida</i> F1
Pput_2976	CP000712	<i>Pseudomonas putida</i> F1
Pput_2977	CP000712	<i>Pseudomonas putida</i> F1
PqsB	NP_249688	<i>Pseudomonas aeruginosa</i> PAO1
PqsC	NP_249689	<i>Pseudomonas aeruginosa</i> PAO1
PqsD	NP_249690	<i>Pseudomonas aeruginosa</i> PAO1
RapB KS1	CAA60459	<i>Streptomyces rapamycinicus</i> NRRL 5491
RedR	NP_630007	<i>Streptomyces coelicolor</i> A3(2)
RedX	NP_630000	<i>Streptomyces coelicolor</i> A3(2)

Res7	BAU09323	<i>Streptomyces roseoverticillatus</i>
RppA	ABY82172	<i>Triticum aestivum</i>
SAZ_24795	CP006871	<i>Streptomyces albulus</i> ZPM
SAZ_24800	CP006871	<i>Streptomyces albulus</i> ZPM
SAZ_24805	CP006871	<i>Streptomyces albulus</i> ZPM
SAZ_24810	CP006871	<i>Streptomyces albulus</i> ZPM
ScFabH	CAB62720	<i>Streptomyces coelicolor</i> A3(2)
SgcE_KS1	Q8GME1	<i>Streptomyces globisporus</i>
Sim-ORF2	AEU17884	<i>Streptomyces antibioticus</i>
Sim-ORF3	AEU17885	<i>Streptomyces antibioticus</i>
SimX5	AEU17889	<i>Streptomyces antibioticus</i>
Sky17	AEA30260	<i>Streptomyces</i> sp. Acta 2897
Sky18	AEA30261	<i>Streptomyces</i> sp. Acta 2897;
Sky19	AEA30262	<i>Streptomyces</i> sp. Acta 2897;
Sky22	AEA30265	<i>Streptomyces</i> sp. Acta 2897;
SmcKSI	ALT05933.1	<i>Kitasatospora</i> sp. 152608
SmcKSII	ALT05934.1	<i>Kitasatospora</i> sp. 152608
SmcX5	ALT05939.1	<i>Kitasatospora</i> sp. 152608
Snoa1	Q54495	<i>Streptomyces nogalater</i>
Snoa2	Q54496	<i>Streptomyces nogalater</i>
SpsA	Q55223	<i>Streptomyces</i> sp.
SaFabF	WP_006605824	<i>Streptomyces auratus</i>
ScFabF	WP_011028323	<i>Streptomyces</i> sp.
SNOUR_18675	CP011533	<i>Streptomyces noursei</i> ATCC 11455
SNOUR_18680	CP011533	<i>Streptomyces noursei</i> ATCC 11455
SNOUR_18685	CP011533	<i>Streptomyces noursei</i> ATCC 11455
SNOUR_18690	CP011533	<i>Streptomyces noursei</i> ATCC 11455
SvFabF	WP_015033414	<i>Streptomyces venezuelae</i>
TcmK	AAA67515	<i>Streptomyces glaucescens</i>
TcmL	AAA67516	<i>Streptomyces glaucescens</i> ;
UrdA	Q54173	<i>Streptomyces fradiae</i>
VirA_KS1	BAF50727	<i>Streptomyces virginiae</i>
WhiE CLF	CAB45607	<i>Streptomyces coelicolor</i> A3(2)
WhiE KS	CAB45606	<i>Streptomyces coelicolor</i> A3(2)
ZhuA	AAG30188	<i>Streptomyces</i> sp. R1128

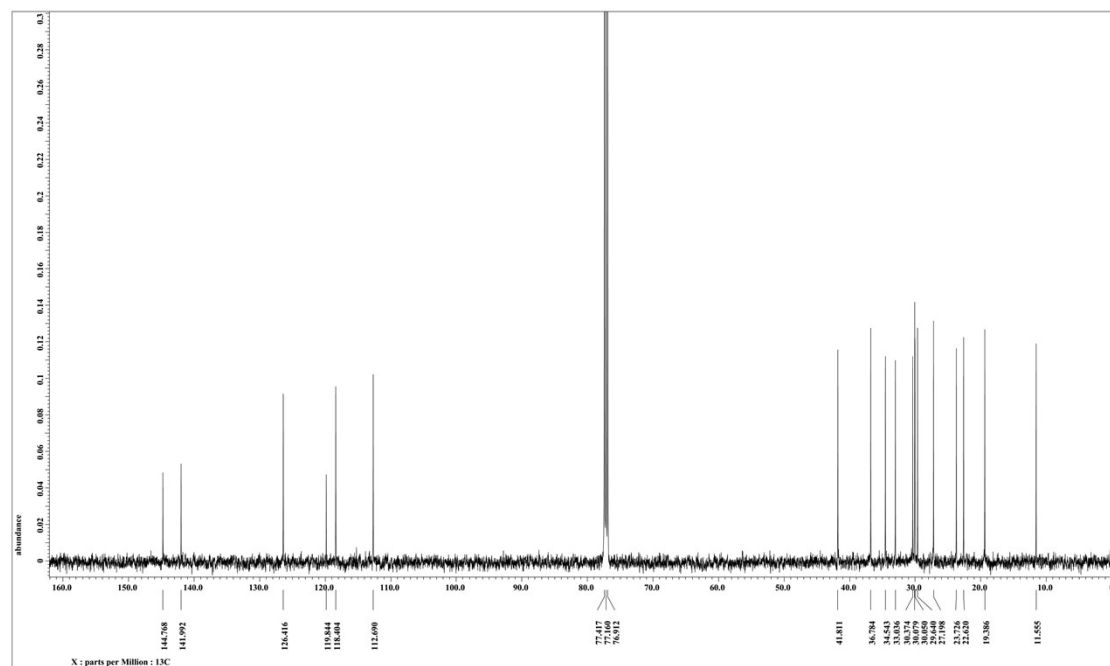
ZhuB	AAG30189	<i>Streptomyces</i> sp. R1128
ZhuH	AAG30195	<i>Streptomyces</i> sp. R1128

Table S7. Primers used in this study. Recognition sequence of restriction enzymes are underlined.

No.	Name	Sequence (5' to 3') (restriction enzymes)
1	THQ1-Fw-NdeI3	GGGTCTAGACATATGCAGAACCCCTACGAGGCAGAC (<u>XbaI</u> , <u>NdeI</u>)
2	THQ1-Rv-Hind	GGGAAGCTTTCAGTCCGTGTGCGGCCGCTG (<u>HindIII</u>)
3	pTHQdKS1-F	ACGCCTGCGCCGCGGGCGGGATGGCCATCGGCAGCGCGT ACCGCTACATCTCTAGACAGTGAGTTCGAGCGACTCGAGT (<u>XbaI</u>)
4	pTHQdKS1-R	ACGAACCCGGAGCGGTCTTGTCTGAACGGGCGGCTCAGCT CCGCCGCGTCTCTAGACTGGTACCGAGCGAACGCGTT (<u>XbaI</u>)
5	pTHQdKS3-F	CGCTGGCCGCCGGGATCGCGGCCGGCACCGGCTGCGCGG CCCGGCGCTGTCTAGACAGTGAGTTCGAGCGATCGAGT (<u>XbaI</u>)
6	pTHQdKS3-R	GAGCTACCAAAACCCGCCACCTCGGCATAGACGATCGCG CCGCGCCGCGTCTAGACTGGTACCGAGCGAACGCGTT (<u>XbaI</u>)
7	pTHQdAT-F	GCTGGCCCAGCGGCCGCACACGGACTGACGCACGAGGGG ACCACCAACACATGTCTAGACAGTGAGTTCGAGCGACTCG AGT (<u>XbaI</u>)
8	pTHQdAT-R	CTGGCCTTCGAATCCATGGTGTCTCTCGCGAGTCGGTG CGGTCCGGTCTCATCTAGACTGGTACCGAGCGAACGCGTT (<u>XbaI</u>)
9	pTHQdKR-F	GCCGCCGCATCGAGCTCTCCAGGGGACGTCTCCGACCC CGACGTGCCGTCTAGACAGTGAGTTCGAGCGACTCGAGT (<u>XbaI</u>)
10	pTHQdKR-R	ATGGCGTCGGTCATCTCCGTGTTGATGACGCCGGGGGCGA CCGCGTTGACTCTAGACTGGTACCGAGCGAACGCGTT (<u>XbaI</u>)
11	pTHQdSDR-F	TCGTCAAGGAGGCCGCCGGCCTGGGCGCCACCGCCGTGG CCGTCGCCGCGTCTAGACAGTGAGTTCGAGCGACTCGAGT (<u>XbaI</u>)
12	pTHQdSDR-R	GGGTCGGCGCCGATCTCGTCGGCCTGCGCGGCGAGTTCGC GGCGCAGCATCTAGACTGGTACCGAGCGAACGCGTT (<u>XbaI</u>)
13	pKS1-F	GGGGAATTCCATATGCAAGTGAACCCCCACATAC (<u>EcoRI</u>)

		<u>NdeI</u>)
14	pKS1-R	GGGAAGCTTTCACCCCGCCTGCGCCAG (<u>HindIII</u>)
15	pKS3-F	GGGGAATTCCATATGAGCCGCCGCGTCGTG (<u>EcoRI</u> , <u>NdeI</u>)
16	pKS3-R	GGGAAGCTTTCAGTCGTCATAACCGCGTACCA (<u>HindIII</u>)
17	pAT-F	GGGTCTAGACATATGTCGCAGTTCACCGAGTTC (<u>XbaI</u> , <u>NdeI</u>)
18	pAT-R	GGGAAGCTTTCAGACCGAGTGGGCGCTCTTG (<u>HindIII</u>)
19	pKR-F	GGGTCTAGACATATGGAATTCGAAGGCCAG (<u>XbaI</u> , <u>NdeI</u>)
20	pKR-R	GGGAAGCTTTCACGCCATCTTCAGGCC (<u>HindIII</u>)
21	pSDR-F	GGGTCTAGACATATGACCGATGACGTGACAAC (<u>XbaI</u> , <u>NdeI</u>)
22	pSDR-R	GGGAAGCTTCTACATTCCACGGGTGTAG (<u>HindIII</u>)

A



B

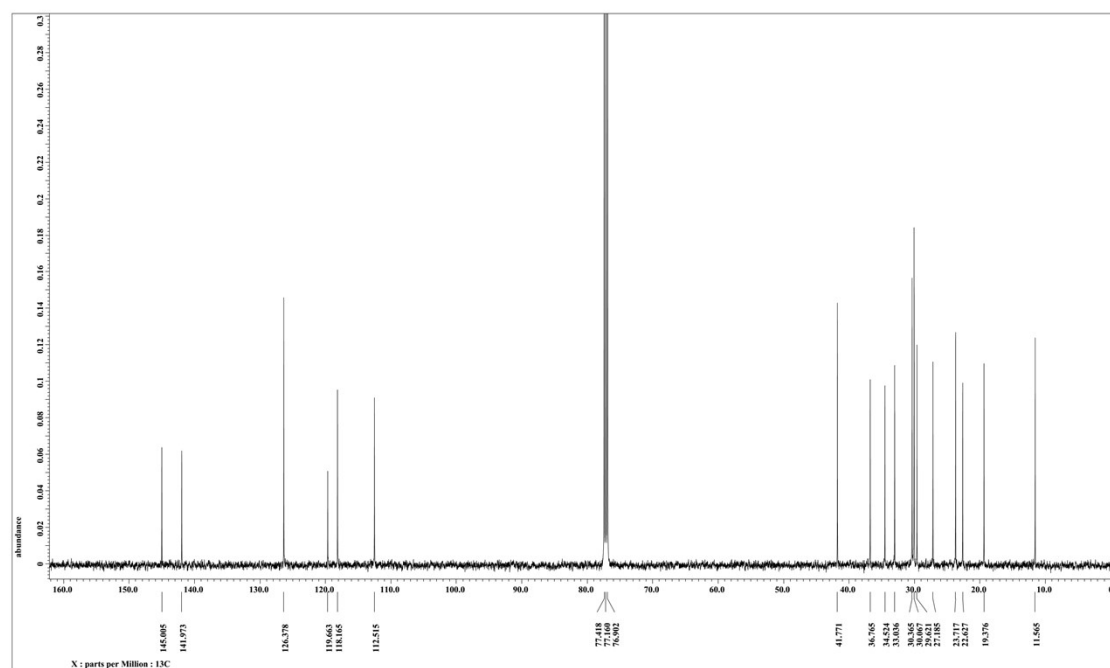
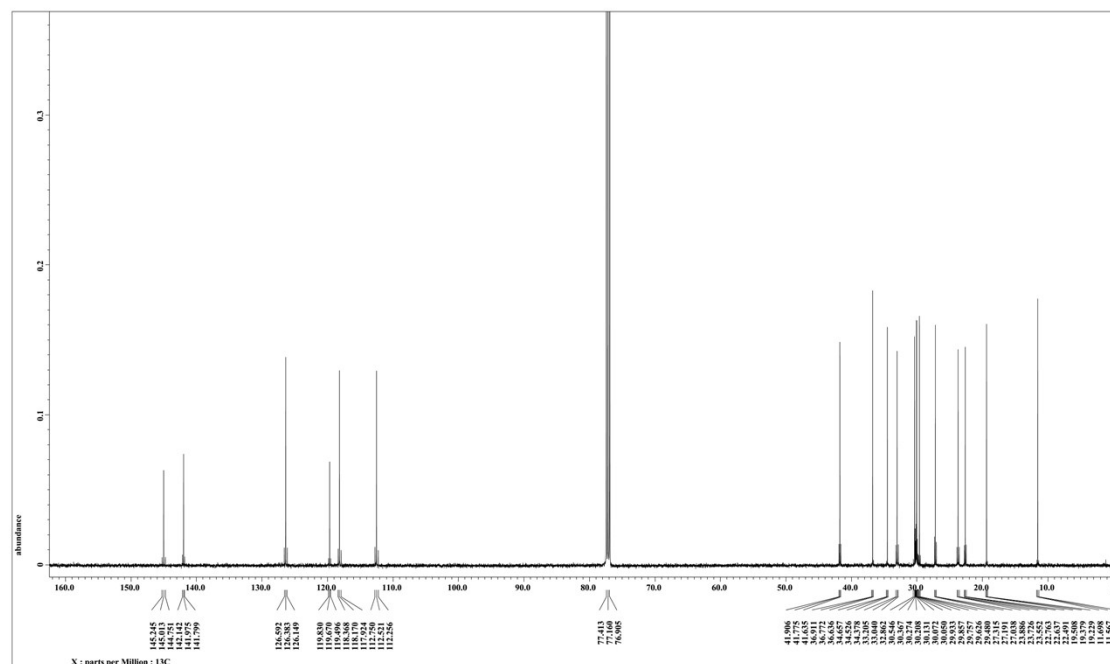


Figure S1. ¹³C NMR spectra of (A) unlabeled 5aTHQ-10a and (B) 5aTHQ-10a labeled with [1-¹³C] sodium acetate (125 MHz, CDCl₃).

C



D

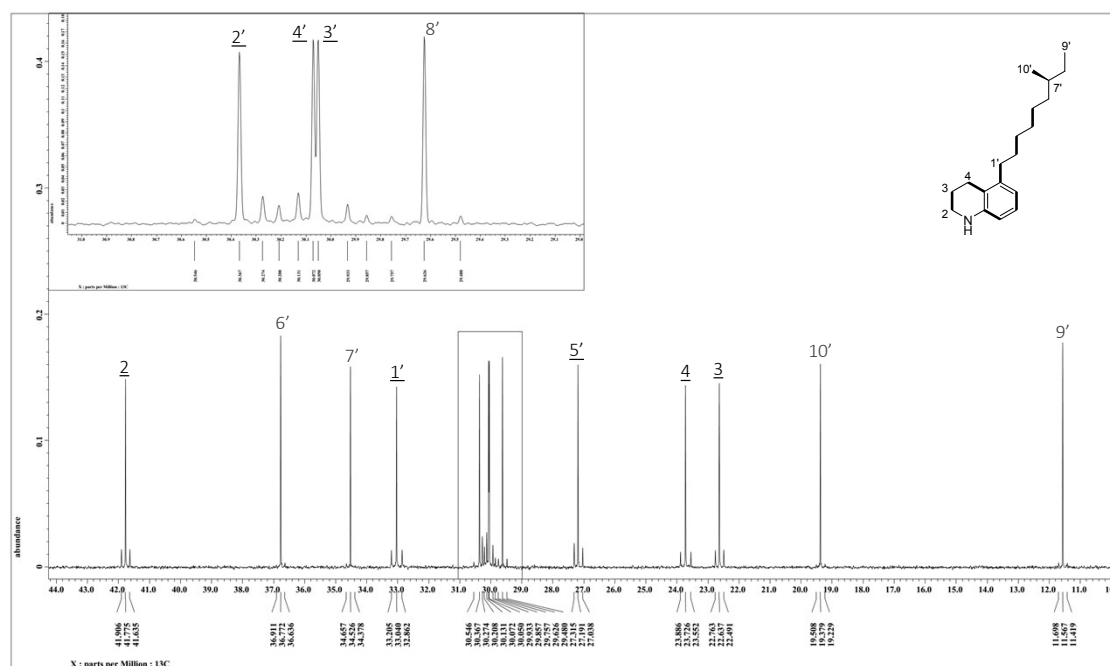
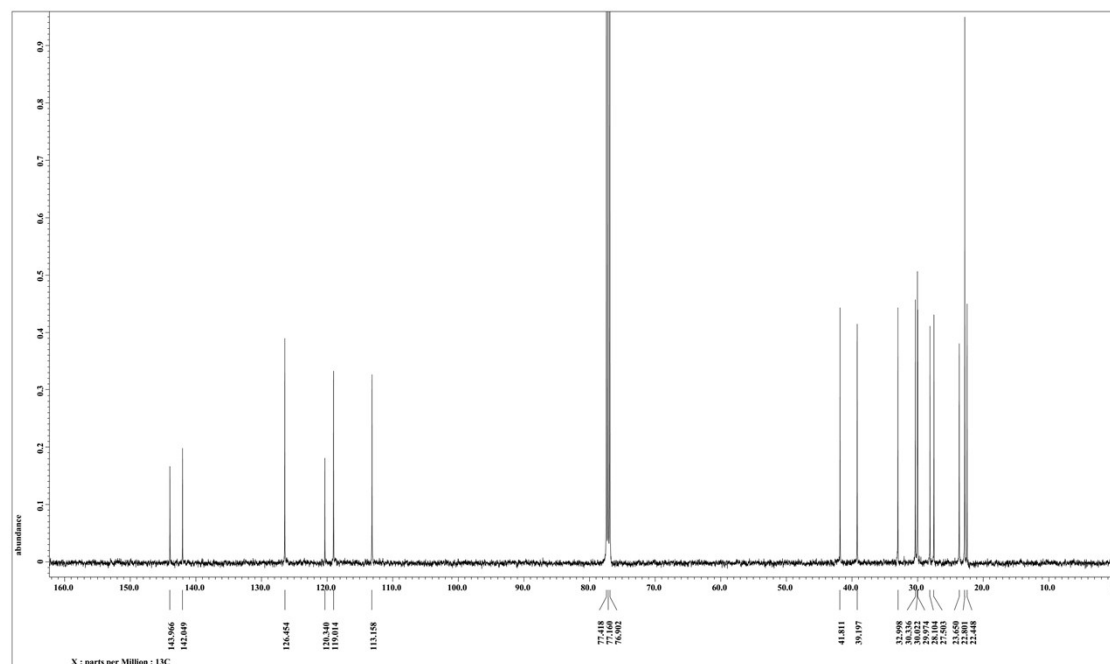


Figure S1 (continued). (C) Full scope and (D) upfield region of ^{13}C NMR spectrum of 5aTHQ-10a labeled with $[1,2-^{13}\text{C}_2]$ sodium acetate (125 MHz, CDCl_3). The positions where the acetate unit was incorporated more efficiently are underlined.

A



B

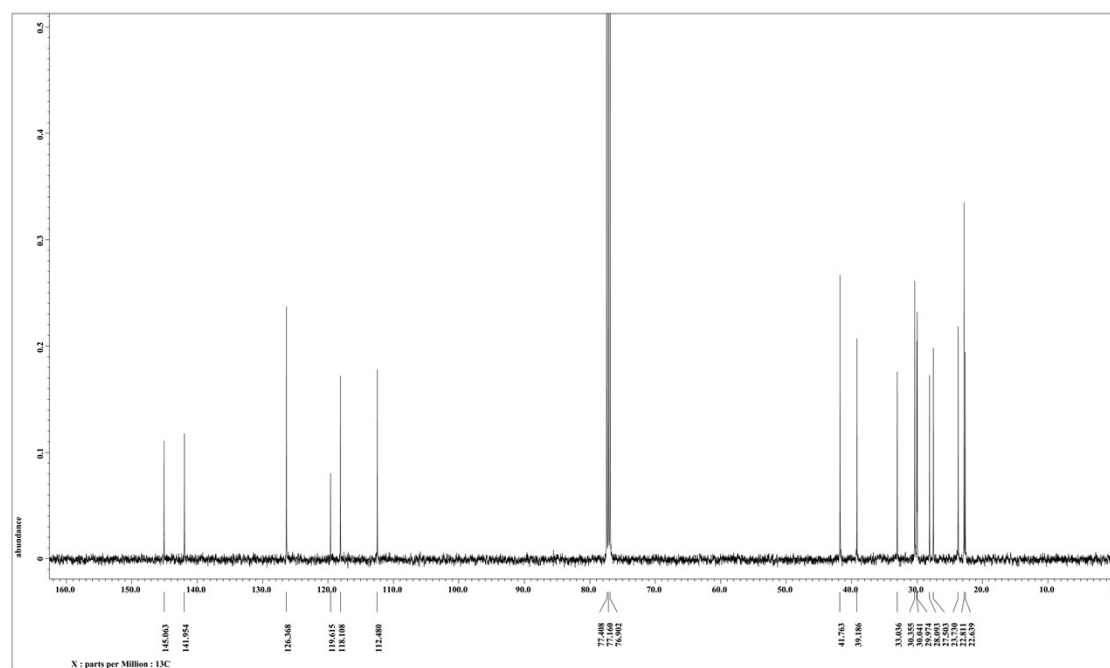
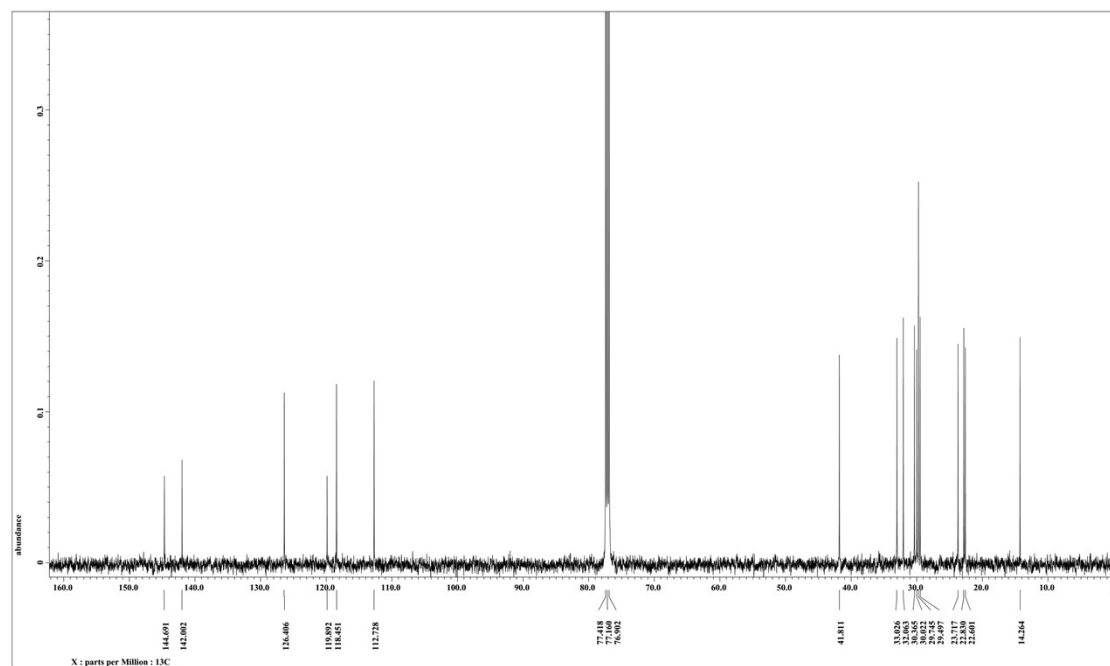


Figure S2. ¹³C NMR spectra of (A) unlabeled 5aTHQ-9i and (B) 5aTHQ-9i labeled with [1-¹³C] sodium acetate (125 MHz, CDCl₃).

A



B

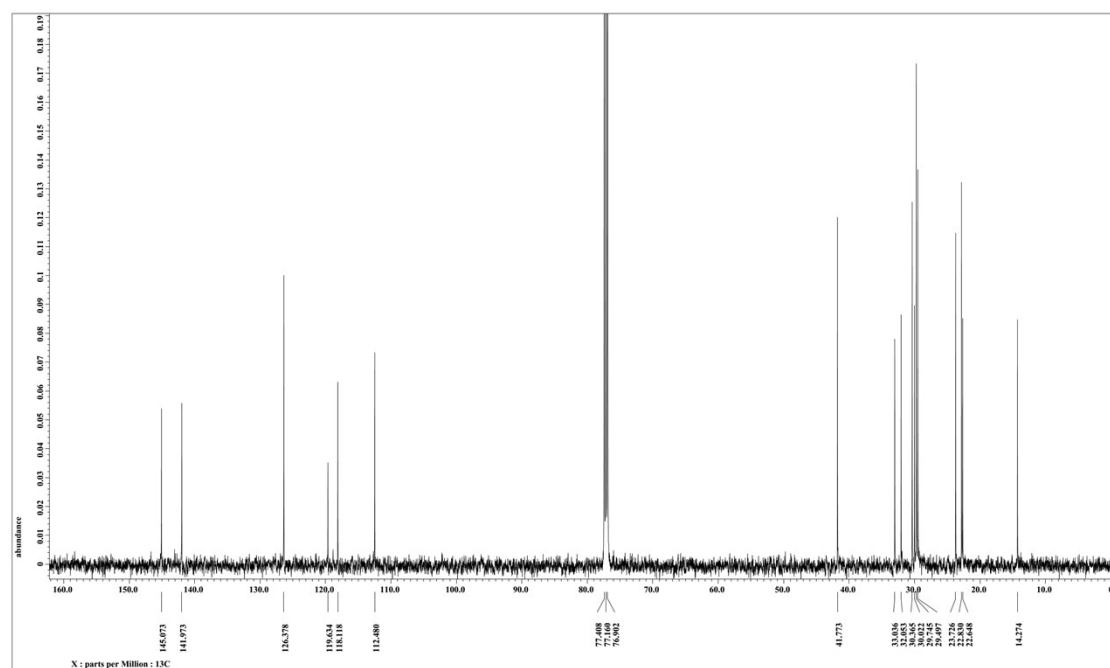
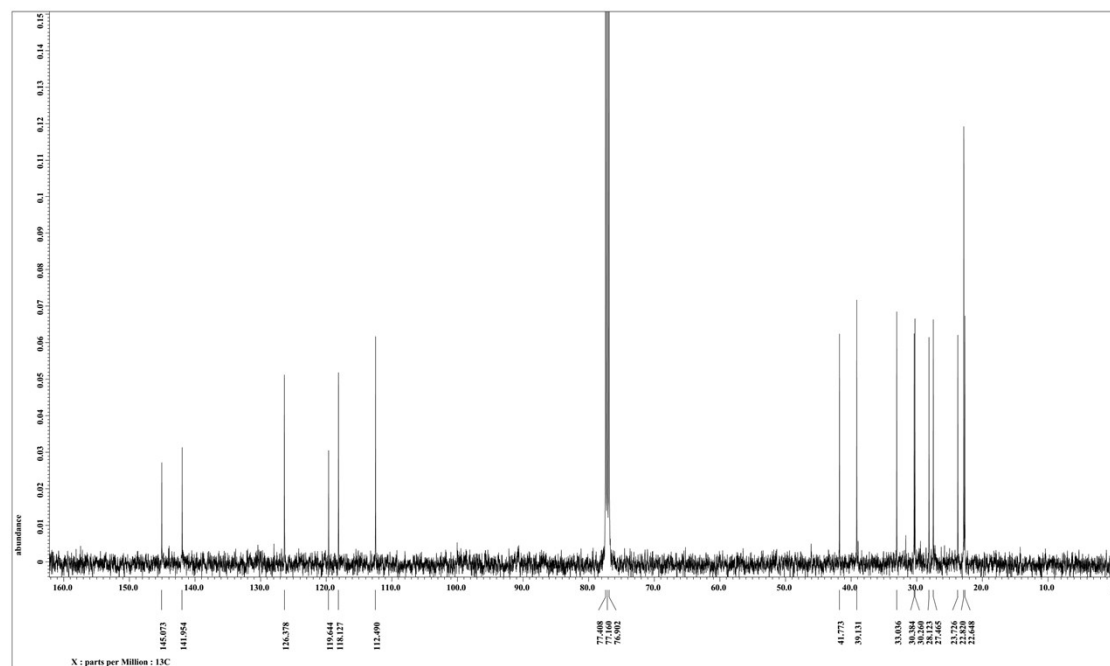


Figure S3. ¹³C NMR spectra of (A) unlabeled 5aTHQ-9n and (B) 5aTHQ-9n labeled with [1-¹³C] sodium acetate (125 MHz, CDCl₃).

A



B

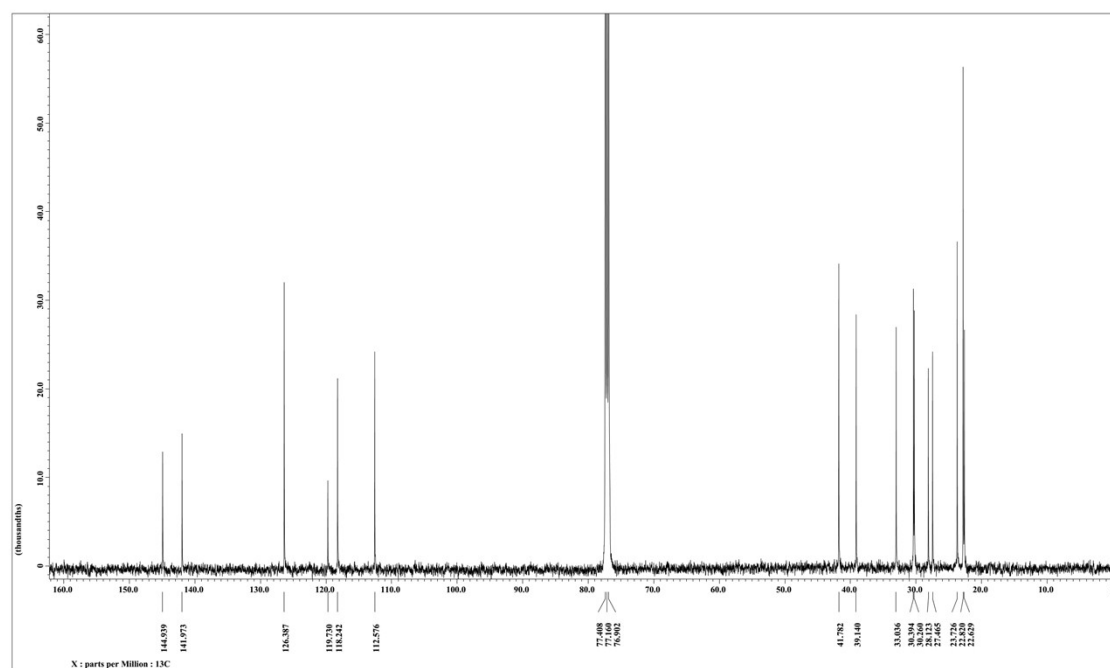


Figure S4. ¹³C NMR spectra of (A) unlabeled 5aTHQ-8i and (B) 5aTHQ-8i labeled with [1-¹³C] sodium acetate (125 MHz, CDCl₃).

Abundance

160.0 150.0 140.0 130.0 120.0 110.0 100.0 90.0 80.0 70.0 60.0 50.0 40.0 30.0 20.0 10.0

144.501
141.578
126.602
126.158
119.751
118.770
118.261
112.561
112.507
112.330
77.413
77.160
76.905
41.916
41.641
39.138
33.804
33.604
30.603
30.312
30.302
28.654
28.128
27.772
27.719
22.521
22.509
22.482
22.477

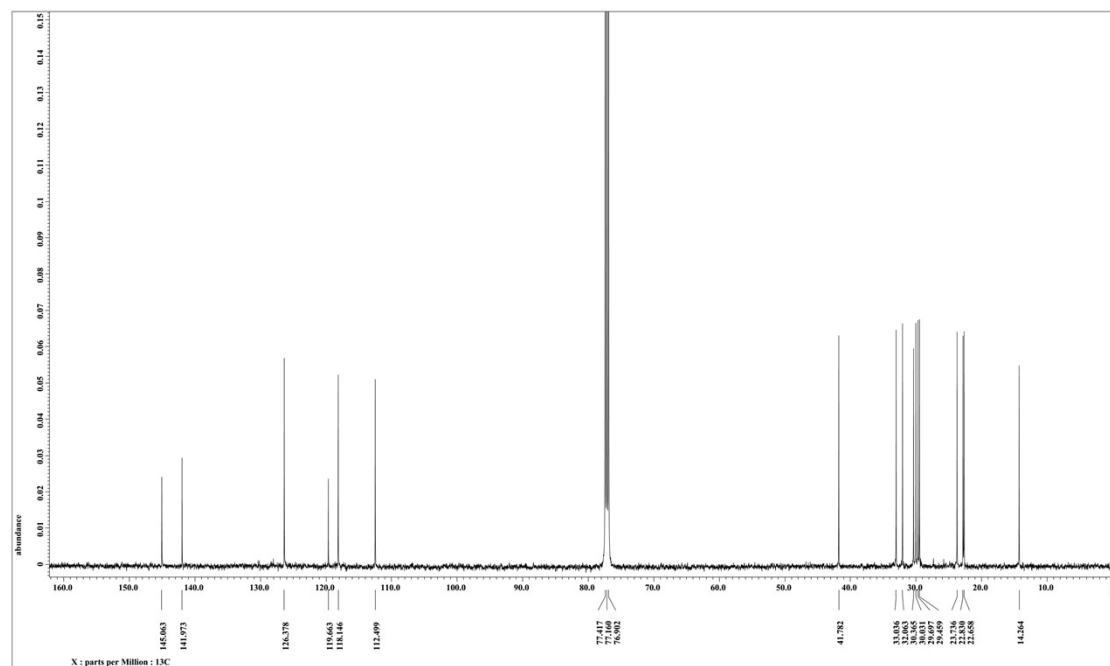
delta

X : parts per Million : 13C

[illegible]

S22

A



B

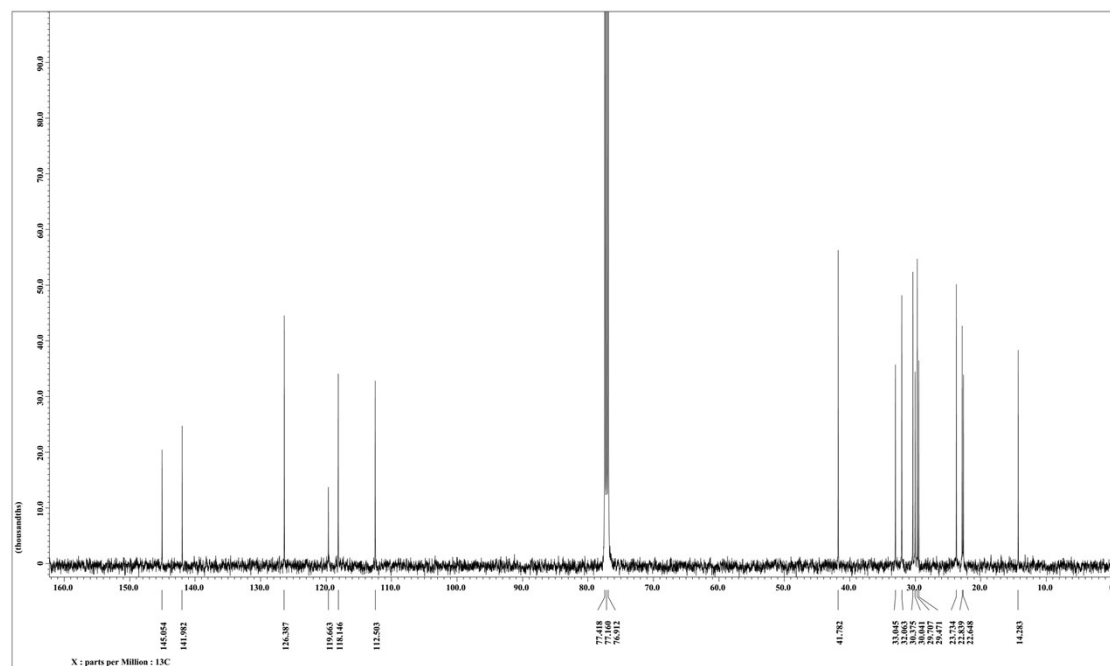


Figure S5. ¹³C NMR spectra of (A) unlabeled 5aTHQ-8n and (B) 5aTHQ-8n labeled with [1-¹³C] sodium acetate (125 MHz, CDCl₃).

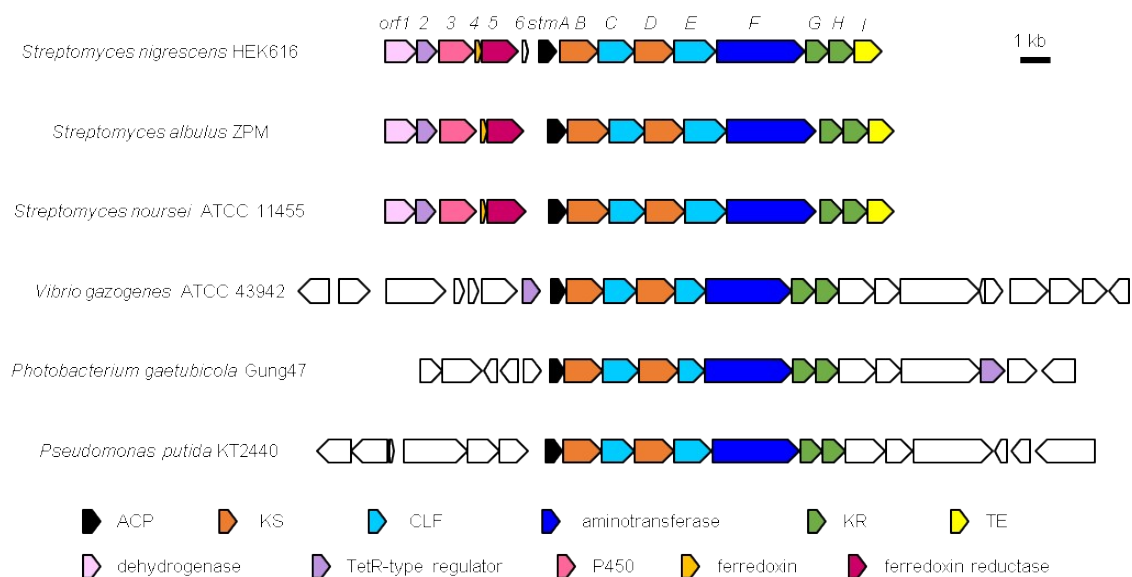


Figure S6. Comparison of the gene clusters identified in Gram-positive and Gram-negative bacteria. Conserved genes are colored as indicated. Accession numbers for each strain are following, CP006871; *S. alubulus* ZPM, CP011533; *S. noursei* ATCC 11455, CP018835; *Vibrio gazogenes* ATCC 43942, CP005973; *P. gaetubicola* Gung47, AE015451; *P. putida* KT2440.

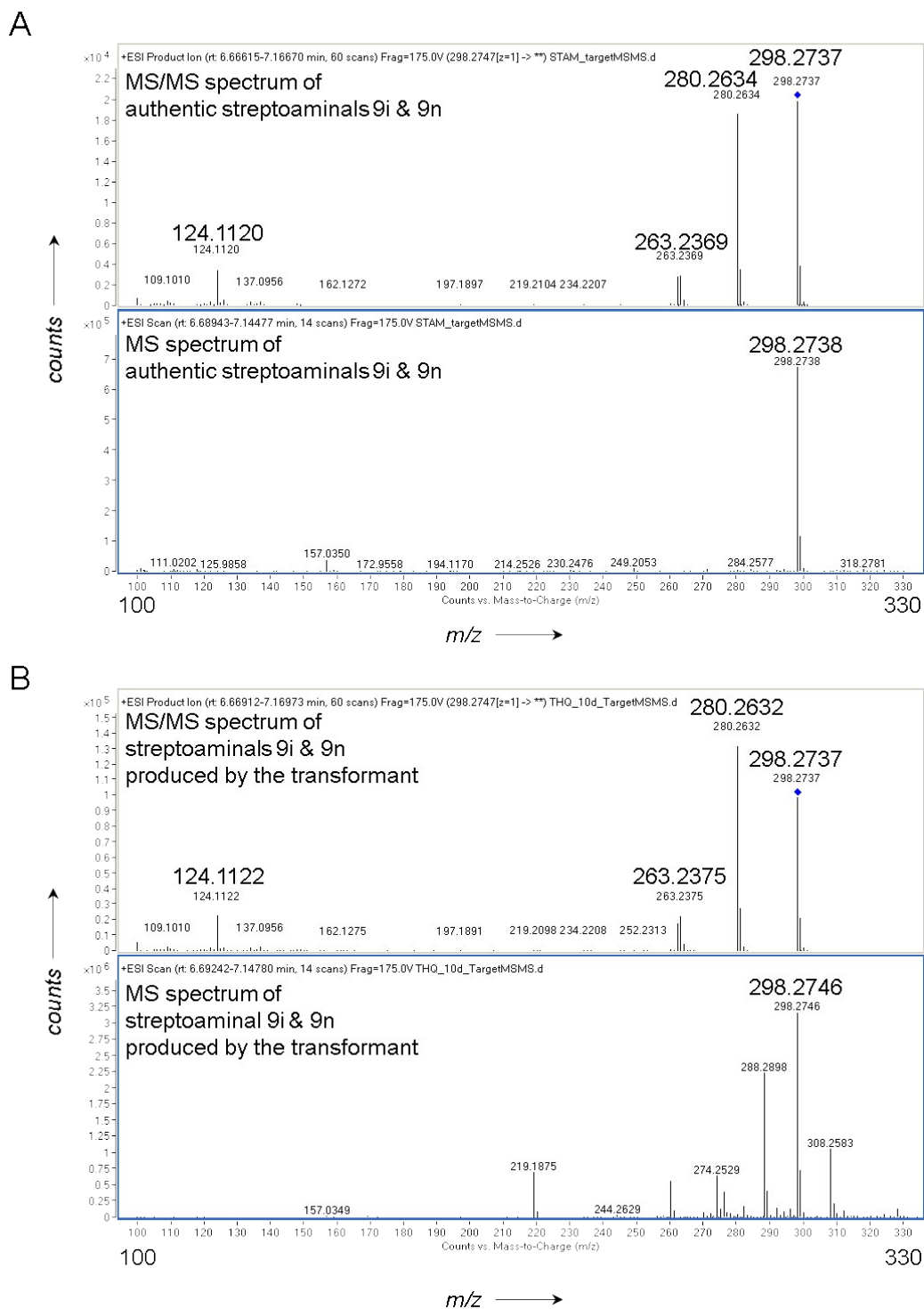
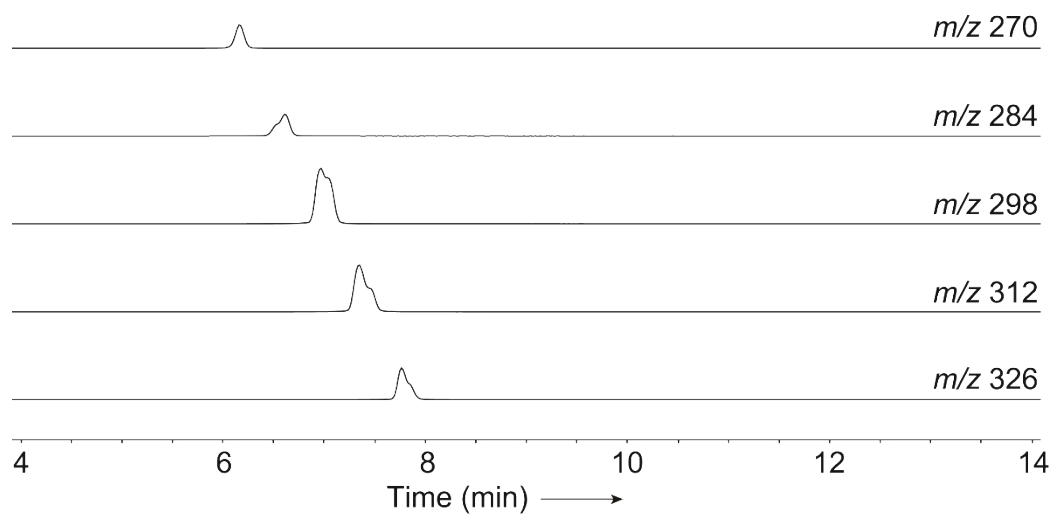


Figure S8. MS (down) and MS/MS (top) spectra of authentic (A) and heterologously produced (B) STAMS-9i and -9n.

authentic streptoaminals



S. lividans/pTYM19gt-*stm* + *T. pulmonis*

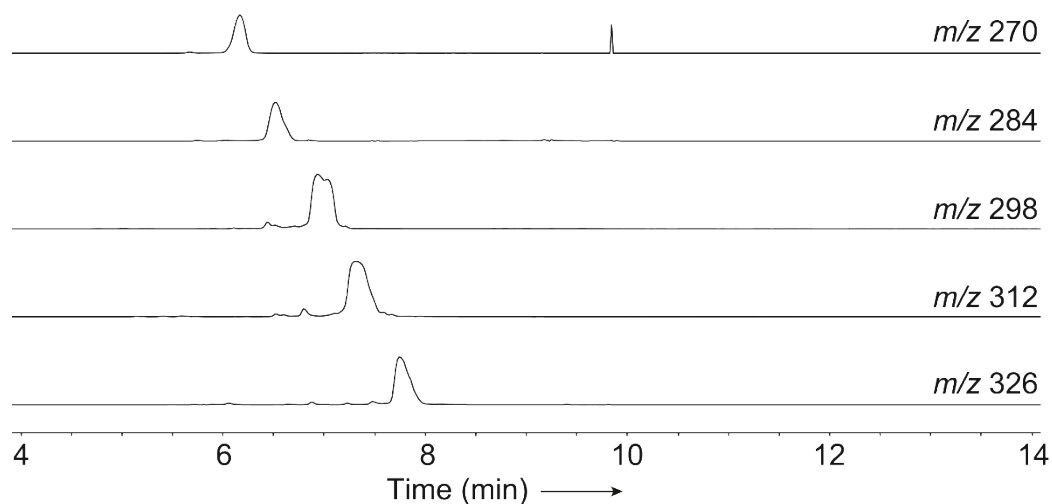


Figure S9. LC-MS profile of STAMs produced by the transformant and authentic ones. Chromatograms were extracted at m/z 270 (C_7 side chain), 284 (C_8), 298 (C_9), 312 (C_{10}), and 326 (C_{11}), which are corresponding to known STAMs.

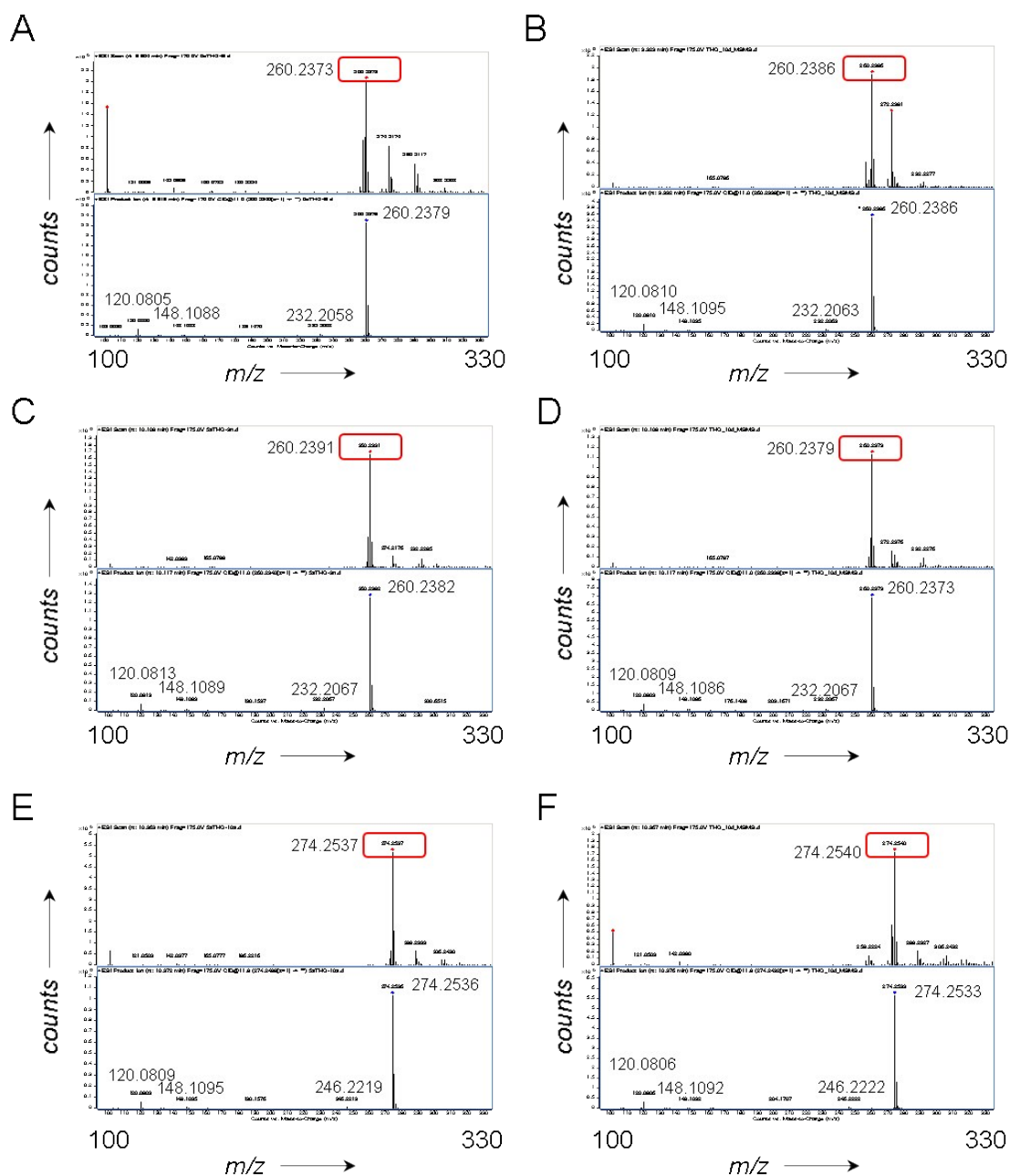
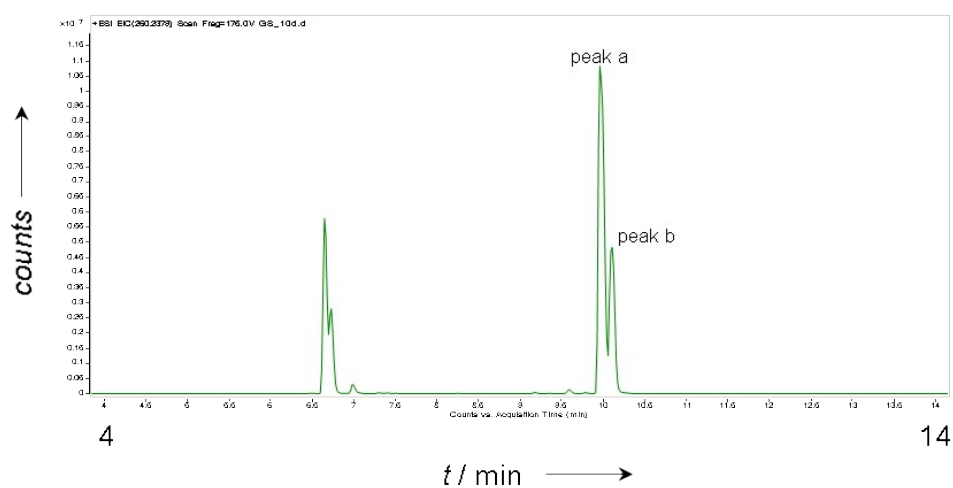
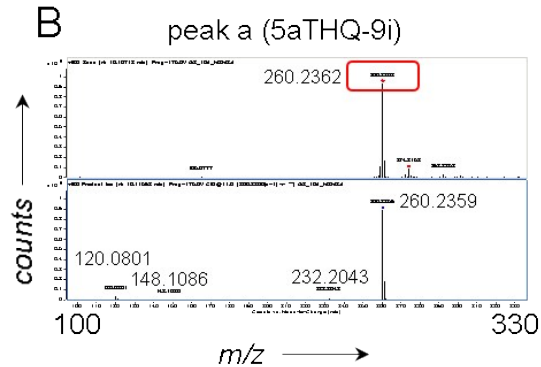


Figure S10. MS and MS/MS spectra of THQs. A, authentic THQ-9i. B, THQ-9i produced by *S. lividans*/pTYM19-*stm*. C, authentic THQ-9n. D, THQ-9n produced by *S. lividans*/pTYM19gt-*stm*. E, authentic THQ-10a. F, THQ-10a produced by *S. lividans*/pTYM19gt-*stm*. Upper panels show MS spectra and lower panels show MS/MS spectra of corresponding signal.

A



B



C

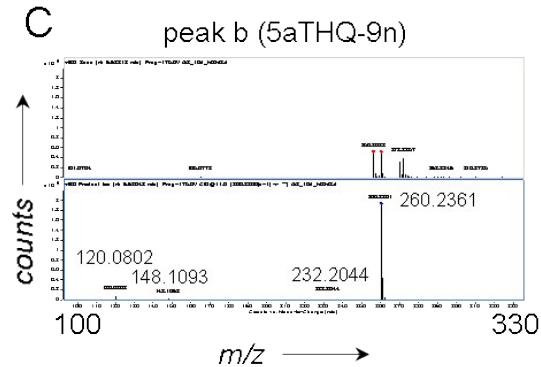


Figure S11. LC-MS analysis of the metabolites produced by the transformants cultured in GS medium. A, chromatograms extracted at m/z 260. B, MS and MS/MS spectra of peak a, which corresponds to 5aTHQ-9i. C, MS and MS/MS spectra of peak b, which corresponds to 5aTHQ-9n. Upper panels show MS spectra and lower panels show MS/MS spectra of corresponding signal.