

Supplemental Figures

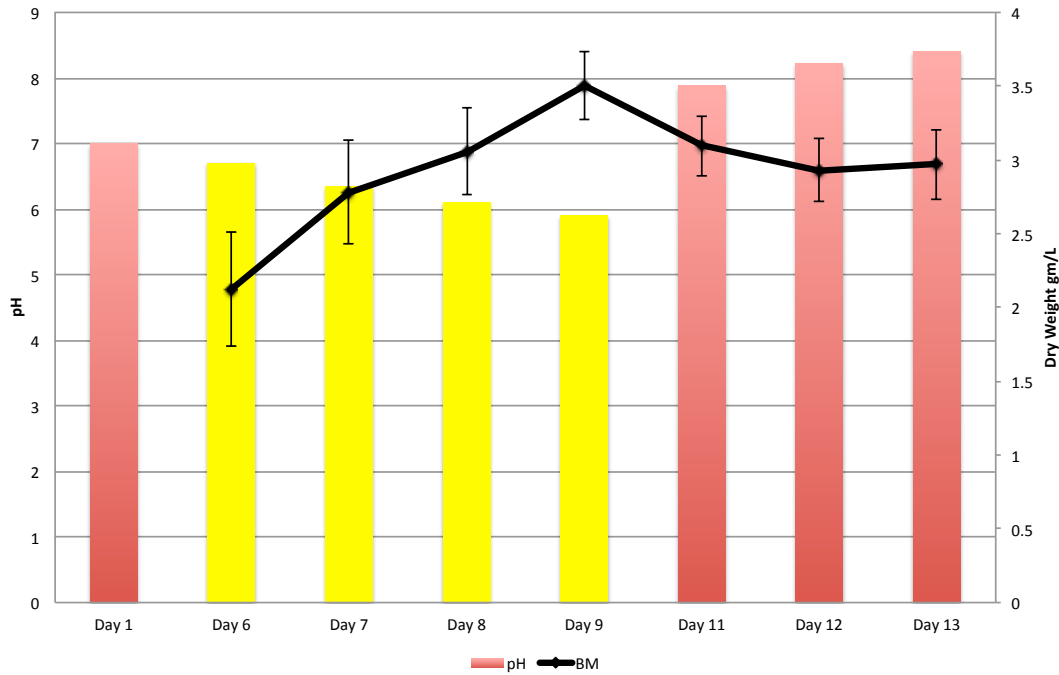


Figure S1, Related to Figure 1. Representative phenol red growth curve (*S. tropica* strain CNY-681). The culture pH dropped below 7 at day 6, which corresponded to a phenol red color change from red to yellow. Upon entering stationary phase after day 9, the pH increased to above 7, which resulted in a color change from yellow back to red. All cultures were extracted when this yellow to red color change was observed. Standard deviations around the mean were calculated for the dry weight biomasses (BM) from three independent cultures.

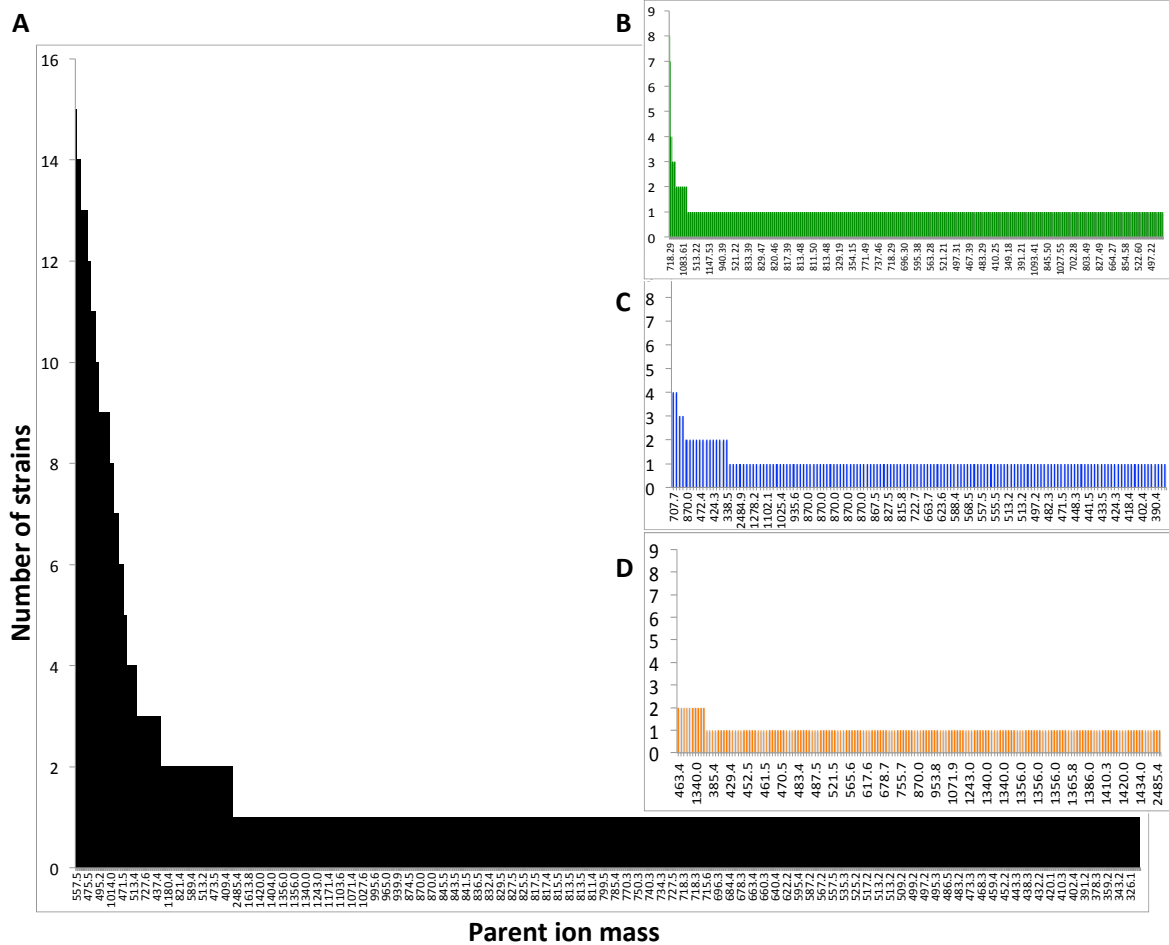


Figure S2, Related to Figure 2. Rank-abundance curve of parent ion distributions. A) Excluding media components, a total of 1114 parent ions were observed of which 85.3 % were detected in only one strain. B) *S. arenicola* parent ion distribution among 12 strains. C) *S. pacifica* parent ion distribution among 17 strains. D) *S. tropica* parent ion distribution among 7 strains. Note: Y-axis = number of strains for figures B-C; scales vary among figures.

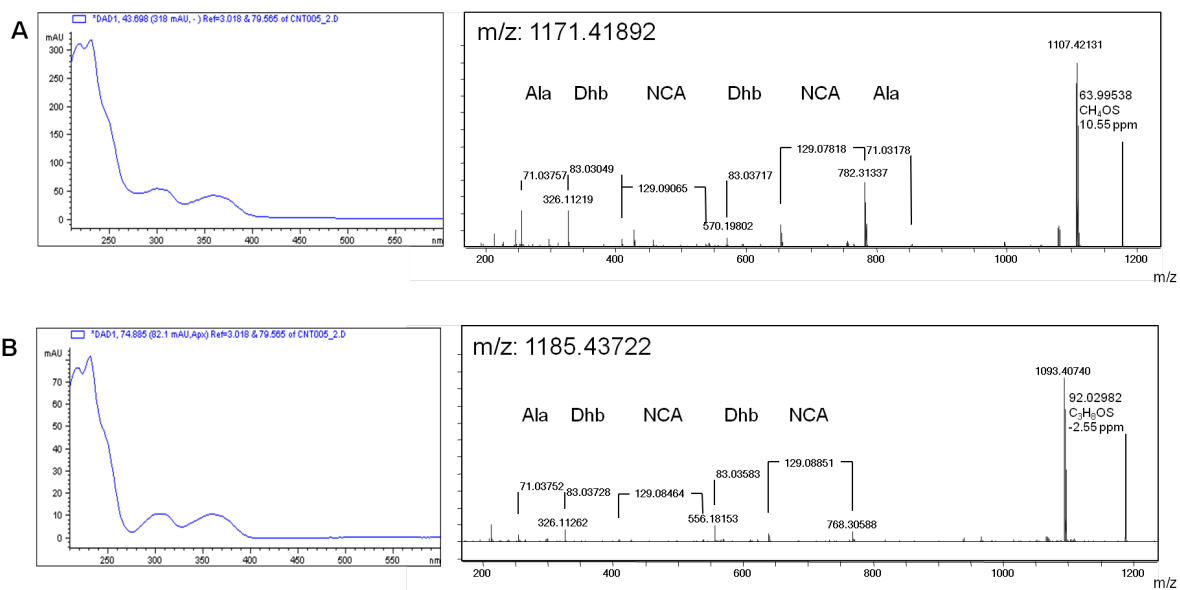


Figure S3. Related to Figure 5. : UV-Vis spectra and MS2 fragmentation patterns for (A) retimycin A and (B) the retimycin m/z 1185 analogue.

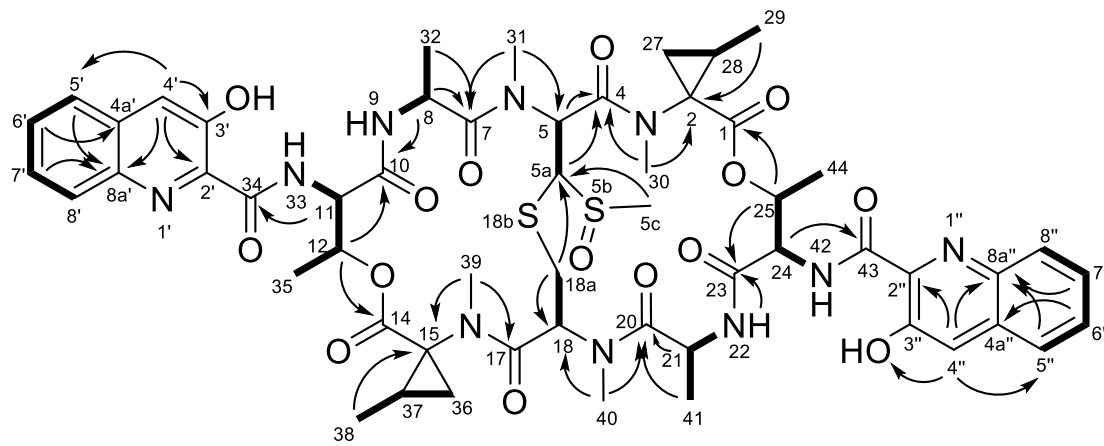
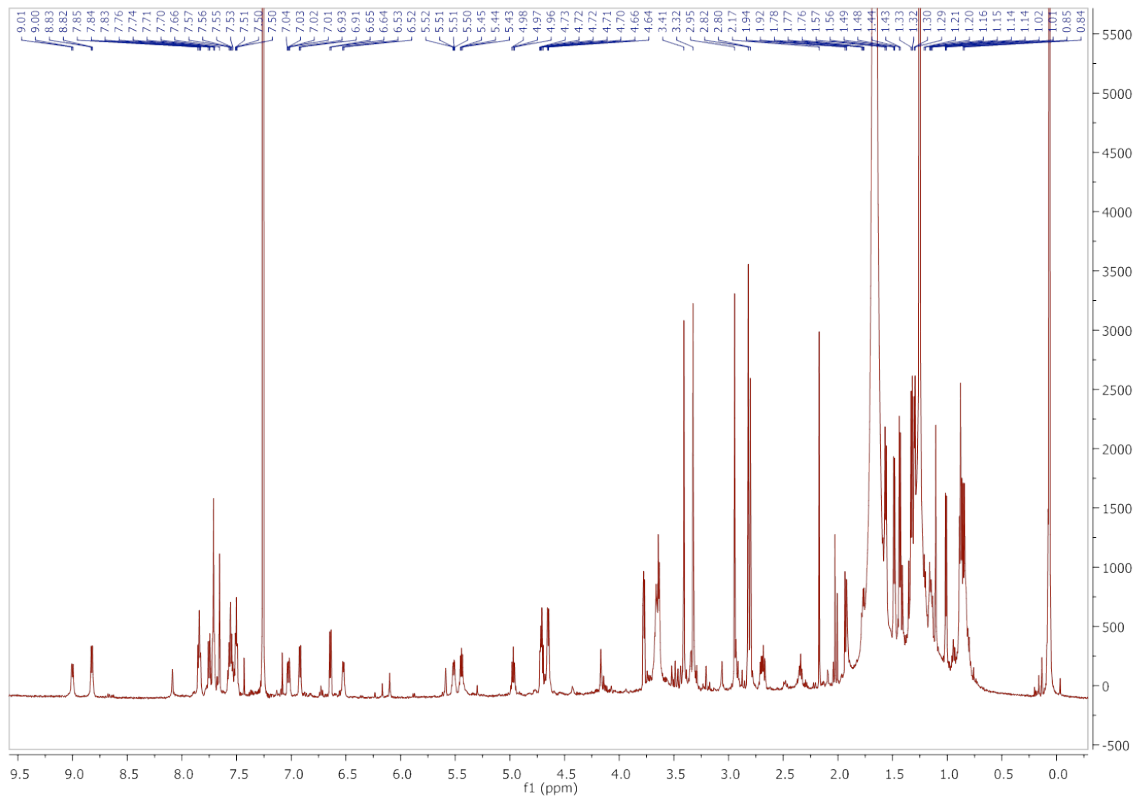
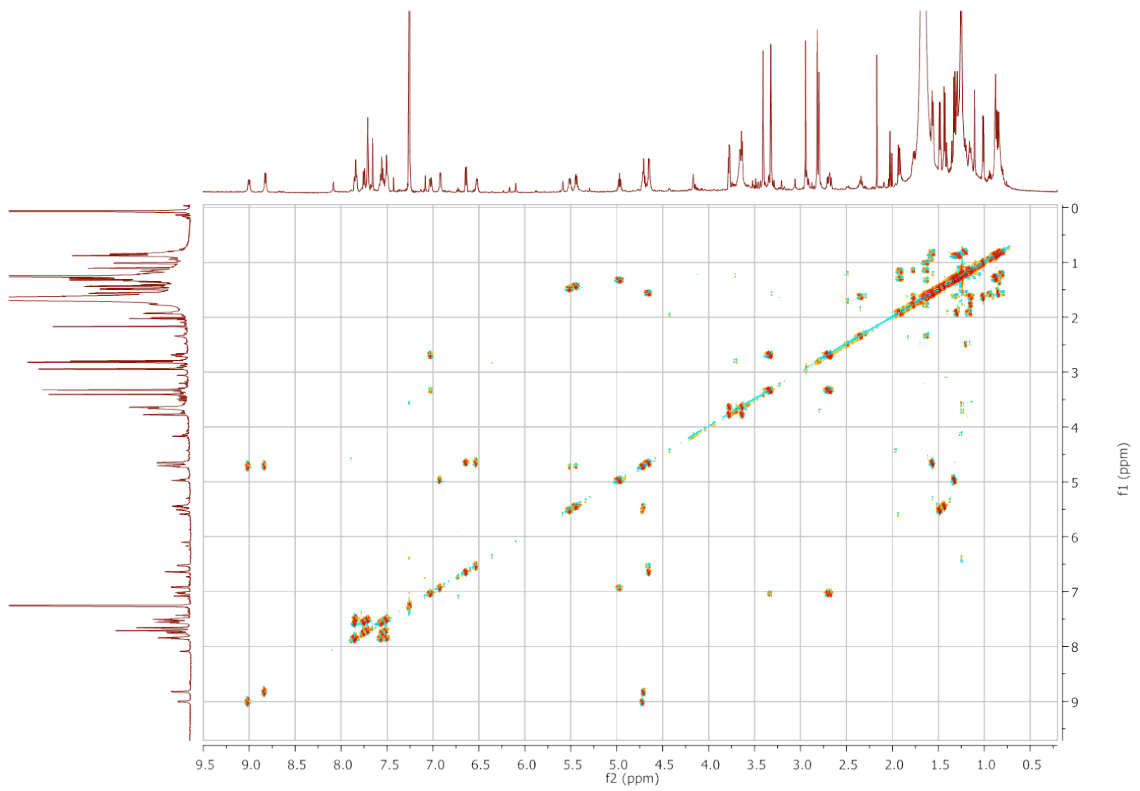


Figure S4, Related to Figure 5. $^1\text{H}-^1\text{H}$ COSY (bold lines) and key HMBC (arrows) correlations of retimycin A

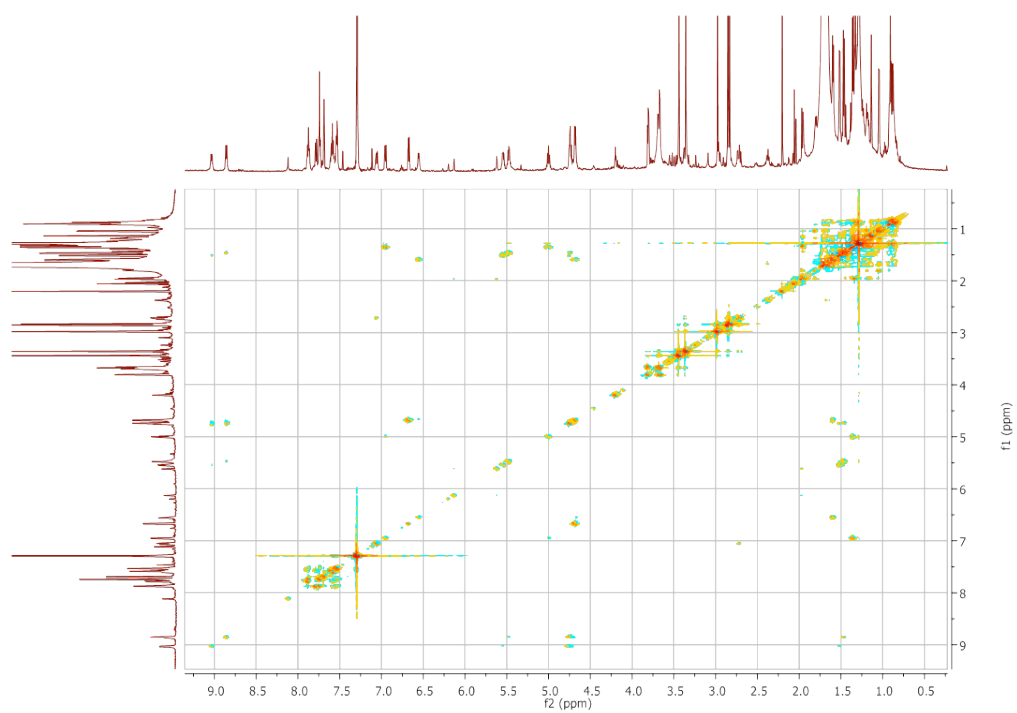
A)



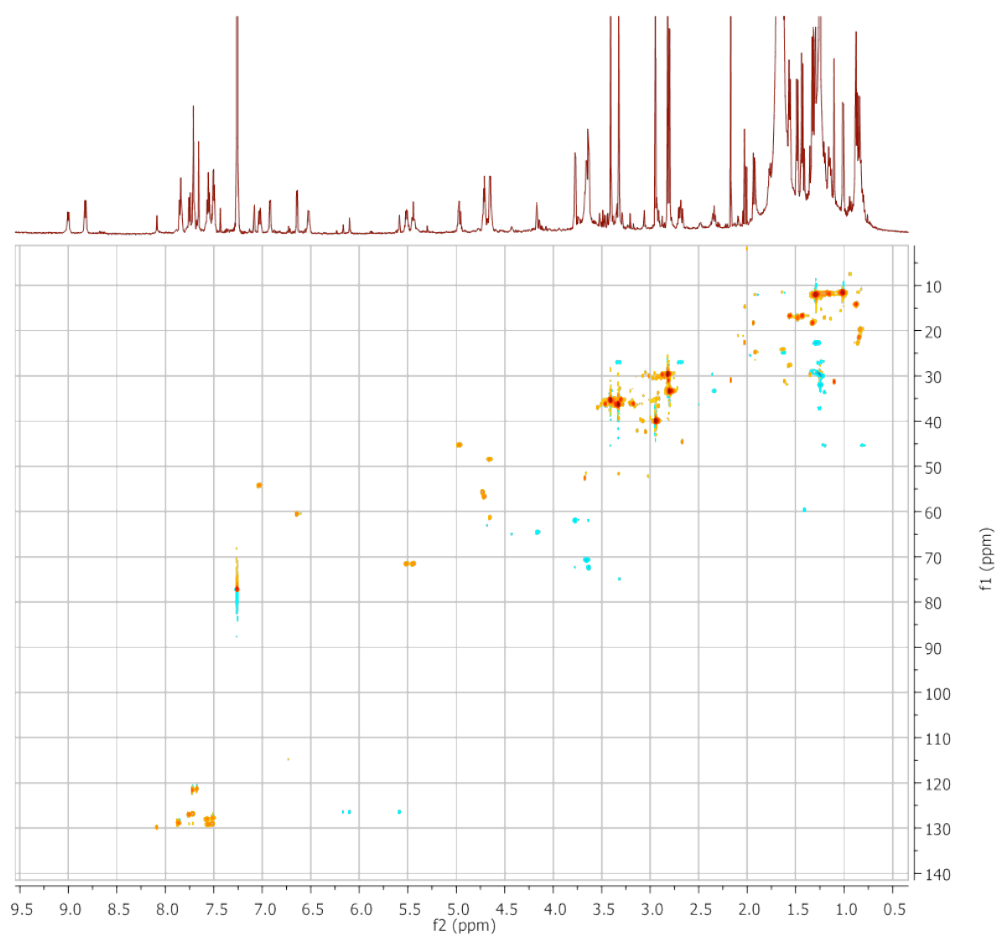
B)



C)



D)



E)

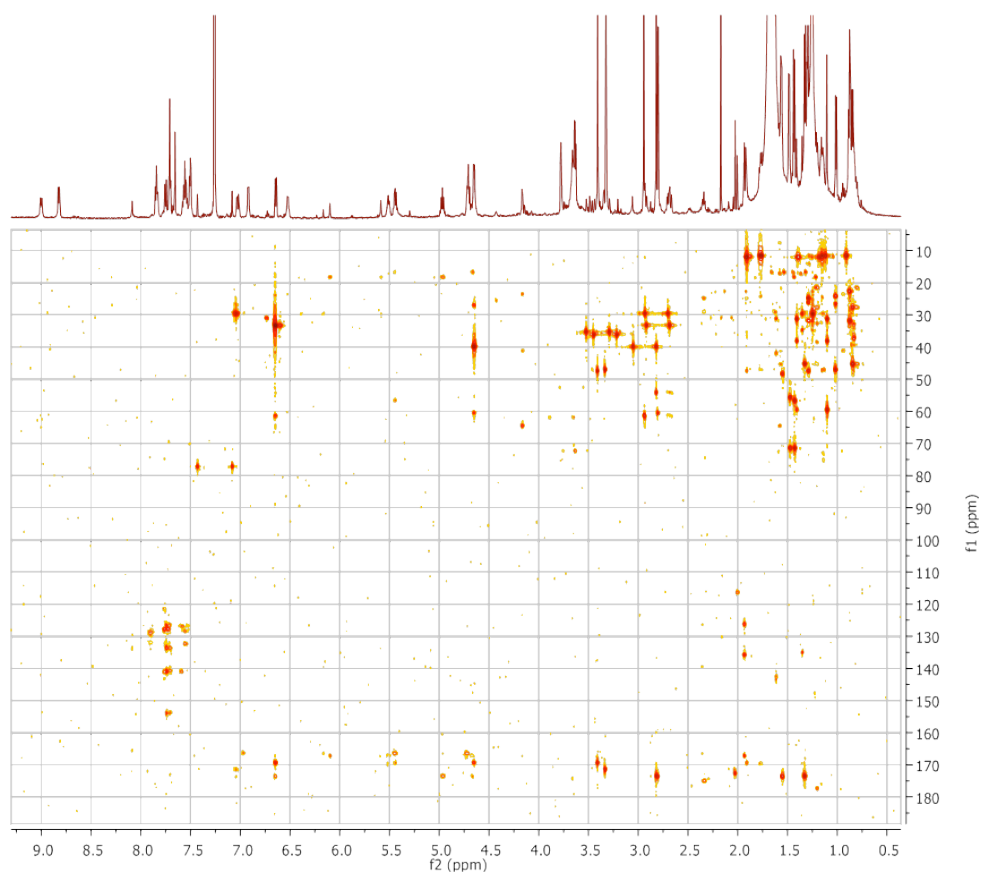


Figure S5, Related to Figure 5. A) ^1H NMR spectrum of retemycin A (CDCl_3 , 600 MHz). B) DQF-COSY spectrum of retemycin A (CDCl_3 , 600 MHz). C) TOCSY spectrum of retemycin A (CDCl_3 , 600 MHz). D) HSQC spectrum of retemycin A (CDCl_3 , 600 MHz). E) HMBC spectrum of retemycin A (CDCl_3 , 600 MHz).

Supplemental Tables

Table S1, Related to Table 1. *Salinispora* strains used in this study. NA = not available, IMG = Integrated Microbial Genomes (<http://img.jgi.doe.gov/>).

Number of strains	Species	Strain	Location	16S Sequence type ^a (accession number)	Extraction time (days)	Genome sequence	New to this study	IMG Genome ID
1	<i>S. arenicola</i>	CNB-527	Bahamas	ST (JN999716)	19	Yes	No	2515154093
2	<i>S. arenicola</i>	CNH-646	Bahamas	ST (AY040620)	13	Yes	No	2515154181
3	<i>S. arenicola</i>	CNH-725	Red Sea	ST (AY040621)	19	No	NA	NA
4	<i>S. arenicola</i>	CNH-996	Sea of Cortez	A (JN999727)	30	Yes	Yes	2561511104
5	<i>S. arenicola</i>	CNP-188	US Virgin Islands	ST (KM205629)	17	No	NA	NA
6	<i>S. arenicola</i>	CNP-193	Sea of Cortez	B (NA)	18	Yes	No	2518285552
7	<i>S. arenicola</i>	CNQ-748	Guam	ST (NA)	18	Yes	No	2515154180
8	<i>S. arenicola</i>	CNR-647	Bahamas	ST (FJ887039)	19	No	NA	NA
9	<i>S. arenicola</i>	CNS-205	Palau	ST (NR_074612)	11	Yes	No	641228504
10	<i>S. arenicola</i>	CNT-005	Fiji	ST (JN161827)	19	Yes	No	2517572137
11	<i>S. arenicola</i>	CNT-849	Hawaii	ST (NA)	15	Yes	No	2518285550
12	<i>S. arenicola</i>	CNX-508	Palmyra	ST (NA)	15	Yes	No	2515154188
13	<i>S. pacifica</i>	CNR-894	Palau	ST (NA)	14	Yes	No	2515154194
14	<i>S. pacifica</i>	CNR-114	Guam	ST (DQ224161)	13	Yes	No	2515154178
15	<i>S. pacifica</i>	CNR-551	Guam	A (HQ642881)	13	No	NA	NA
16	<i>S. pacifica</i>	CNR-942	Palau	E (HQ642877)	11	Yes	No	2518285561
17	<i>S. pacifica</i>	CNS-055	Palau	A (DQ224159)	13	Yes	No	2518285562
18	<i>S. pacifica</i>	CNS-237	Palau	B (HQ642850)	13	Yes	Yes	2524614807
19	<i>S. pacifica</i>	CNS-863	Fiji	C (HQ642851)	25	Yes	No	2517572194
20	<i>S. pacifica</i>	CNT-003	Fiji	ST (NA)	30	Yes	No	2515154126
21	<i>S. pacifica</i>	CNT-029	Fiji	F (HQ642852)	13	Yes	No	2515154177
22	<i>S. pacifica</i>	CNT-138	Fiji	C (HQ642853)	16	Yes	No	2516493032
23	<i>S. pacifica</i>	CNT148	Fiji	A (HQ642899)	29	Yes	No	2517287023
24	<i>S. pacifica</i>	CNT-150	Fiji	B (HQ642900)	24	Yes	No	2517434008
25	<i>S. pacifica</i>	CNT-851	Hawaii	D (NA)	14	Yes	No	2517572162

26	<i>S. pacifica</i>	CNT-855	Hawaii	A (NA)	14	Yes	No	2515154128
27	<i>S. pacifica</i>	CNY-202	Sea of Cortez	K (HQ873948)	21	Yes	Yes	2528311034
28	<i>S. pacifica</i>	CNY-330	Sea of Cortez	ST (NA)	19	Yes	No	2518645626
29	<i>S. pacifica</i>	CNY-368	Sea of Cortez	C (HQ873947)	19	No	NA	NA
30	<i>S. tropica</i>	CNB-440	Bahamas	ST (AY040617)	11	Yes	No	640427140
31	<i>S. tropica</i>	CNB-536	Bahamas	ST (AY040618)	9	Yes	No	2517572212
32	<i>S. tropica</i>	CNS-197	Bahamas	ST (JN999709)	15	Yes	No	2515154163
33	<i>S. tropica</i>	CNY-012	Bahamas	ST (NA)	16	Yes	Yes	2540341192
34	<i>S. tropica</i>	CNY-678	Yucatan	ST (NA)	24	Yes	Yes	2561511109
35	<i>S. tropica</i>	CNY-681	Yucatan	ST (NA)	14	Yes	Yes	2561511108

a) Sequence types defined as per Freel et al., 2012.

Table S2, Related to Figure 5. The retimycin gene cluster (NRPS40) from *S. arenicola* CNT-005. Genes are listed as presented from left to right in Figure 5D for NRPS40.

Gene	Size (aa)	Annotation	Closest homolog [source] (% similarity/identity)	Predicted function
<i>rtmA</i>	488	Amino acid adenylation domain	ribosomal peptide synthetase [<i>Streptomyces davawensis</i>] (61/49)	Unknown
<i>rtmB</i>	236	Tryptophan 2,3-dioxygenase	tryptophan 2,3-dioxygenase [uncultured bacterium esnapd9] (90/83)	HQA biosynthesis
<i>rtmC</i>	421	Aspartate/tyrosine/aromatic aminotransferase	kynurenine aminotransferase [<i>Micromonospora</i> sp. ML1] (83/76)	HQA biosynthesis
<i>rtmD</i>	240	Dehydrogenase	NAD or NADP oxidoreductase [<i>Micromonospora</i> sp. ML1] (83/75)	HQA biosynthesis
<i>rtmE</i>	423	Cytochrome P450	quinaldate 3-hydroxylase [<i>Micromonospora</i> sp. ML1] (85/77)	HQA biosynthesis
<i>rtmF</i>	528	(2,3-dihydroxybenzoyl) adenylation synthase	putative 3-hydroxy-quinaldate-AMP-Ligase [<i>Micromonospora</i> sp. ML1] (89/76)	HQA biosynthesis
<i>rtmG</i>	599	Amino acid adenylation domain	NRPS protein [<i>Micromonospora</i> sp. ML1] (78/70)	HQA biosynthesis
<i>rtmH</i>	391	Cytochrome P450	cytochrome P450 [<i>Saccharopolyspora spinosa</i>] (80/68)	Core oxygenation
<i>rtmI</i>	385	Kynurenine aminotransferase	putative aminotransferase [<i>Streptomyces</i> sp. SNA15896] (83/77)	NCA biosynthesis
<i>rtmJ</i>	634	Fe-S oxidoreductase	hypothetical protein [<i>Streptomyces</i> sp. SNA15896] (88/81)	NCA biosynthesis
<i>rtmK</i>	237	Methyltransferase	putative SAM-dependent methyltransferase [<i>Streptomyces</i> sp. SNA15896] (78/64)	Methylation
<i>rtmL</i>	661	Fe-S oxidoreductase	radical SAM protein [<i>Saccharomonospora</i> sp. CNQ490] (79/66)	Thioacetal formation
<i>rtmM</i>	244	Thioesterase	putative thioesterase [<i>Streptomyces</i> sp. SNA15896] (83/74)	HQA biosynthesis
<i>rtmN</i>	820	Excinuclease ATPase subunit	UvrA-like protein [<i>Streptomyces</i> sp. SNA15896] (89/80)	Unknown
<i>rtmO</i>	2565	Non-ribosomal peptide synthetase	long-chain-fatty-acid--CoA ligase [uncultured bacterium esnapd9] (77/67)	Peptide backbone formation
<i>rtmP</i>	3126	Non-ribosomal peptide synthetase	putative non-ribosomal peptide synthetase [<i>Streptomyces</i> sp. SNA15896] (85/77)	Peptide backbone formation
<i>rtmQ</i>	70	MbtH-like protein	MbtH-like protein [<i>Streptomyces</i> sp. SNA15896] (85/77)	Peptide backbone formation
<i>rtmR</i>	167	Signal transduction response regulator, C-terminal	MbtH-like protein [<i>Streptomyces</i> sp. SNA15896] (90/71) OmpR family regulator [<i>Micromonospora</i> sp. ML1] (85/74)	Unknown

Table S3, related to Figure 5. ^1H and ^{13}C -NMR spectroscopic data of retimycin A^a ($[\alpha] - 12.2^\circ$ (c.0.2, CHCl_3))

no.	δ_{H}^b	δ_{C}^c	no.	δ_{H}^b	δ_{C}^c
1		169.4	33-NH	9.00 (1H, d, 7.5)	
2		47.4	34		167.8
4		169.3	35	1.48 (3H, d, 6.5)	17.1
5	6.64 (1H, d, 6.9)	60.5	36	1.80 (1H, m)	26.6
5a	4.66 (1H, d, 6.9)	61.4		1.18 (1H, m)	
5c	2.95 (3H, s)	39.9	37	1.64 (1H, m)	24.0
7		173.6	38	1.04 (3H, d, 6.2)	11.3
8	4.67 (1H, m)	48.3	39	3.32 (3H, s)	36.2
9-NH	6.53 (1H, br s)		40	2.82 (3H, s)	29.5
10		167.1	41	1.33 (1H, d, 6.8)	18.2
11	4.72 (1H, m)	55.7	42-NH	8.82 (1H, d, 7.5)	
12	5.51 (1H, m)	71.5	43		167.5
14		169.5	44	1.43 (1H, d, 6.5)	16.7
15		47.1	2'		133.6
17		171.5	3'		153.9
18	7.03 (1H, dd, 10.2, 3.9)	54.2	4'	7.66 (1H, s)	121.1
18a	3.35 (1H, dd, 15.3, 3.9)	26.9	4a'		132.4
	2.72 (1H, dd, 15.3, 10.2)		5'	7.71 (1H, m)	126.9
20		173.5	6'	7.50 (1H, m)	129.0
21	4.97 (1H, m)	45.2	7'	7.55 (1H, m)	127.6
22-NH	6.92 (1H, d, 7.4)		8'	7.84 (1H, m)	128.9
23		166.3	8a'		140.8
24	4.71 (1H, m)	56.7	2''		133.6
25	5.44 (1H, m)	71.5	3''		153.9
27	1.92 (1H, m)	25.9	4''	7.71 (1H, m)	121.4
	1.18 (1H, m)		4a''		132.4
28	1.90 (1H, m)	24.7	5''	7.75 (1H, m)	127.0
29	1.30 (3H, d, 6.2)	11.9	6''	7.51 (1H, m)	129.2
30	3.41 (3H, s)	35.2	7''	7.57 (1H, m)	127.9
31	2.80 (3H, s)	33.3	8''	7.85 (1H, m)	129.1
32	1.56 (3H, d, 6.9)	16.7	8a''		141.0

^a NMR data obtained in CDCl_3 . Assignments are based on ^1H - ^1H COSY, HSQC, and HMBC spectroscopic data. The assignments for the two 3-hydroxyquinaldic acid rings are interchangeable due to the absence of HMBC correlations from 33-NH and 42-NH protons ^b Measured at 600 MHz for ^1H NMR; δ in ppm, (mult. J in Hz). ^c Deduced from HSQC and HMBC spectroscopic data; δ in ppm.