TABLE S1**.** MAR4 isolates from Channel Island sediments.

Strain number	**Location**	**Processing method**	**Isolation media**	**NCBI accession number**
CNY-714	34° 02.67’ N, 119° 32.67’ W	dry, stamp	trace mineral + cycloheximide	KC261606
CNY-715	33° 58.39’ N, 118° 57.22’ W	no pretreatment	sea water agar + cycloheximide	KC261604
CNY-716	34° 02.67’ N, 119° 32.67’ W	enrichment culture	1/5 A1 + cycloheximide	KC261615
CNY-717	34° 01.99’ N, 119° 42.14’ W	dry, stamp	trace mineral + cycloheximide	KC261622
CNY-718	33° 58.39’ N, 118° 57.22’ W	no pretreatment	sea water agar + cycloheximide	KC261611

TABLE S2. Primers used in study.

Primer name	Forward or Reverse	Specificity	Sequence 5’- 3’
FC27	F	General bacteria	AGAGTTTGATCCTGGCTGGCTCAG
RC1492	R	General bacteria	TACGGCTACCTTGTTACGACTT
F7	F	Actinobacteria	TGCACTCTGGGACAAGCCCT
MAR4_R3	R	MAR4	AGTCTCCCGTGAGTCCCCAC
MAR4_F5	F	MAR4	ACYWYYGGGCGCATGYCTG
MAR4_F6	F	MAR4	WYYGGGCGCATGYCTGDKR

TABLE S3. Primers used for nested PCR amplification of MAR4 16S rRNA gene sequences from environmental samples. + Indicates primers sets that yielded PCR products. In some cases, two separate nested PCR reactions were performed using different second round primers.

Sample no.	**1st round FC27/RC1492**	**1st round F7/MAR4_R3**	**2nd round MAR4_F5/ MAR4_R3**	**2nd round MAR4_F6/ MAR4_R3**
26	+	-	-	+
153	-	+	-	+
280	-	+	+	+
407	+	-	+	+

TABLE S4. Cultured and cloned MAR4 sequences. Bold locations indicate strains isolated from marine samples. Strain numbers beginning with "CN" are maintained in the SIO culture collection. References for strains that were not isolated as a part of this study are indicated when available. *All cloned sequences are from Santa Cruz Island except where indicated. ** Strains included in secondary metabolite analysis.

OTU no.	No. clones* (accession no.)	Cultured strains (accession no.)	Source of cultured strains	Reference
1	0	CNX-435 (KC261602)**	**California**	
2	2	0	-	
3	0	CNS-776 (EU214946)**	**California**	Prieto-Davo et al., 2008
4	0	CNY-715 (KC261604)**	**California**	
		CNP-082 (KC261603)**	**California**	
5	Washington (HM186499)	0	-	Lin et al., 2011
6	1	0	-	
7	3	CNB-632 (KC261626)**	**California**	
8	0	(EF121313)	Egypt sand dune	Hozzein et al., 2007
9	2	CNH-099 (KC261627)**	**California**	
		CNQ-181 (EU214926)**	**California**	Prieto-Davo et al., 2008
10	7	0	-	
11	1	0	-	
12	8	(JQ014483)	Lechuguilla Cave	
		(JQ014364)	Lechuguilla Cave	

		CNQ-329 (KC261610)	**California**	
		CNS-581 (KC261621)**	**California**	
		CNQ-509 (EF581384)**	**California**	Prieto-Davo et al., 2008
		CNS-686 (EU214957)**	**California**	Prieto-Davo et al., 2008
		CNQ-384 (KC261605)	**California**	
		CNR-925 (DQ448742)	**Palau**	Gontang et al., 2007
		CNQ-766 (AY464546)**	**Guam**	Jensen and Fenical, 2005
13	105	(NR_041166)	Japan soil	Labeda et al., 2012
		CNQ-260 (KC261613)	**California**	
		CNQ-525 (EF177816)**	**California**	Soria-Mercado et al., 2005
		CNY-716 (KC261615)**	**California**	
		CNQ-139 (KC261614)**	**California**	
14	0	(JQ014513)	Lechuguilla Cave	
		(JQ014571)	Lechuguilla Cave	
		CNH-070 (KC261625)	**California**	
		CNX-496 (KC261624)	**Palmyra**	
		(EU741176)	**Caribbean beach sand**	Solano et al., 2009
		(JQ014418)	Lechuguilla Cave	
		CNT-371 (KC261612)	**Fiji**	
		CNQ-904 (KC261616)	**Guam**	
		(HQ537077)	**sponge, South China Sea**	Wang et al., 2011
		(HQ992743)	unknown	

		(JQ782978)	**Yellow Sea**	
		(JF346436)	**marine sponge**	
		CNY-717 (KC261622)**	**California**	
		CNQ-031 (KC261620)	**California**	
		(EU741167)	**Caribbean beach sand**	Solano et al., 2009
		(EU741161)	**Caribbean beach sand**	Solano et al., 2009
		(FJ263416)	**mangrove**	
		CNS-580 (KC261618)	**Fiji**	
		CNY-718 (KC261611)**	**California**	
		CNQ-428 (KC261608)	**California**	
		(FJ261966)	**mangrove**	
		CNQ-865 (KC261619)**	**Guam**	
		CNX-232 (KC261623)	**California**	
		CNQ-381 (KC261617)	**California**	
		(FJ615277)	plant endophyte	Qin et al., 2009
		CNQ-907 (KC261609)	**Guam**	
		CNS-335 (KC261607)**	**Fiji**	
		CNY-714 (KC261606)**	**California**	
15	0	(EF538742)	**mangrove**	
		(EU267797)	**Xiaoping Islands**	Zhao et al., 2009
		(AB373966)	Japan soil	
16	1	0	-	
17	37	CNX-198 (KC261629)**	**California**	

		CNS-284 (KC261628)**	**Palau**
18	3	0	**-**
19	0	(X87316)	unknown
20	0	(JQ014508)	Lechuguilla Cave
21	1	0	-
22	1	0	-
23	1	0	-
24	1	0	-
25	1	0	-
26	1	0	-
27	1	0	-
28	2	0	-

FIGURE S1. 16S rRNA gene maximum likelihood phylogeny of MAR4 strains and BLAST matches. The MAR4 clade is highlighted in blue. No conflicting nodes were detected using parsimony methods. Red asterisks indicate nodes supported by ≥50% using both maximum likelihood (bootstrap) and parsimony (jackknife) methods. A purple asterisk indicates nodes supported by only one of these methods.

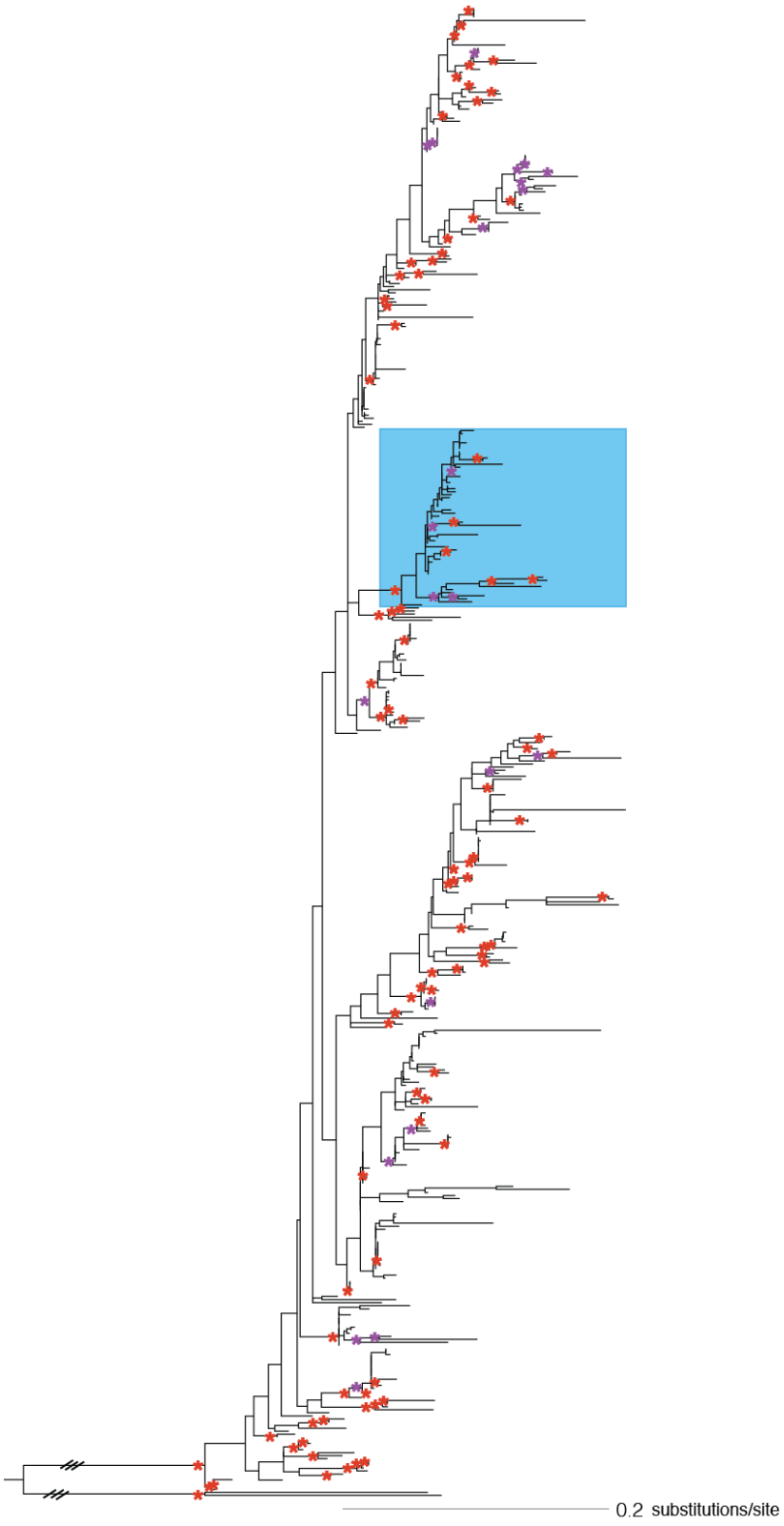


FIGURE S2. UV spectra for compounds in culture extracts (blue) in comparison with known HIs (red). (A) napyradiomycin A2, match score = 983; (B) lavanducyanin, match score = 989; (C) marinone, match score = 996; and (D) nitropyrrolin A, match score = 983. Match scores >900 were considered positive identification for that compound class. Match scores ranged from 903-999 and averaged 969.

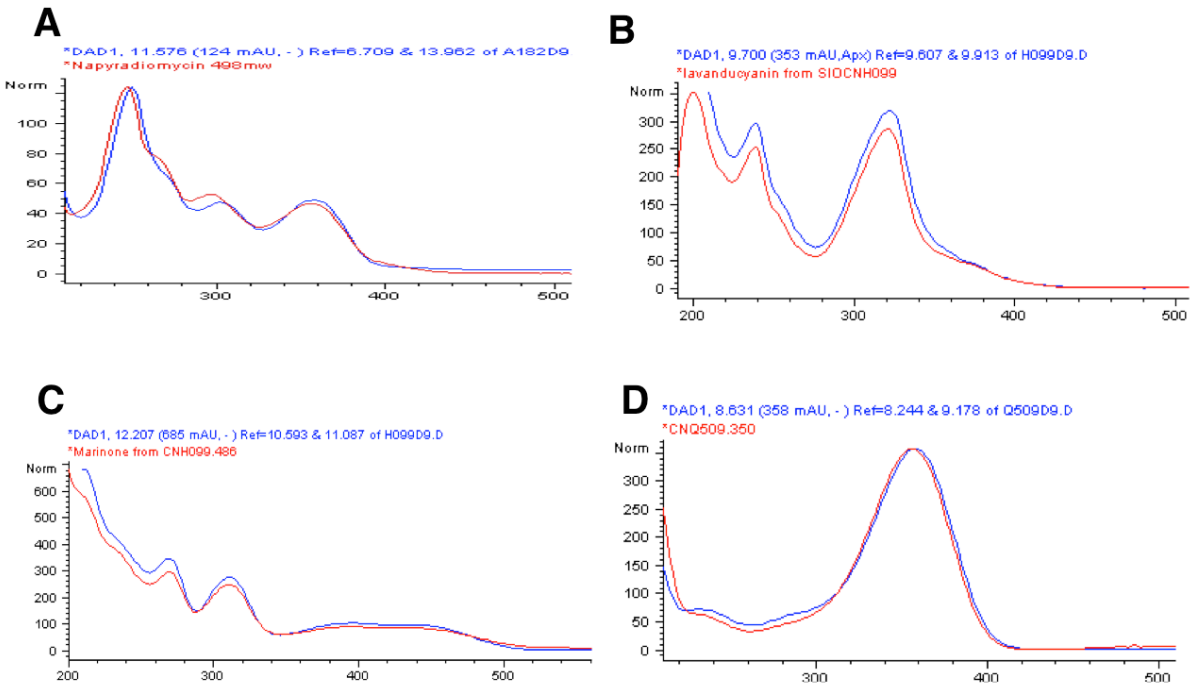
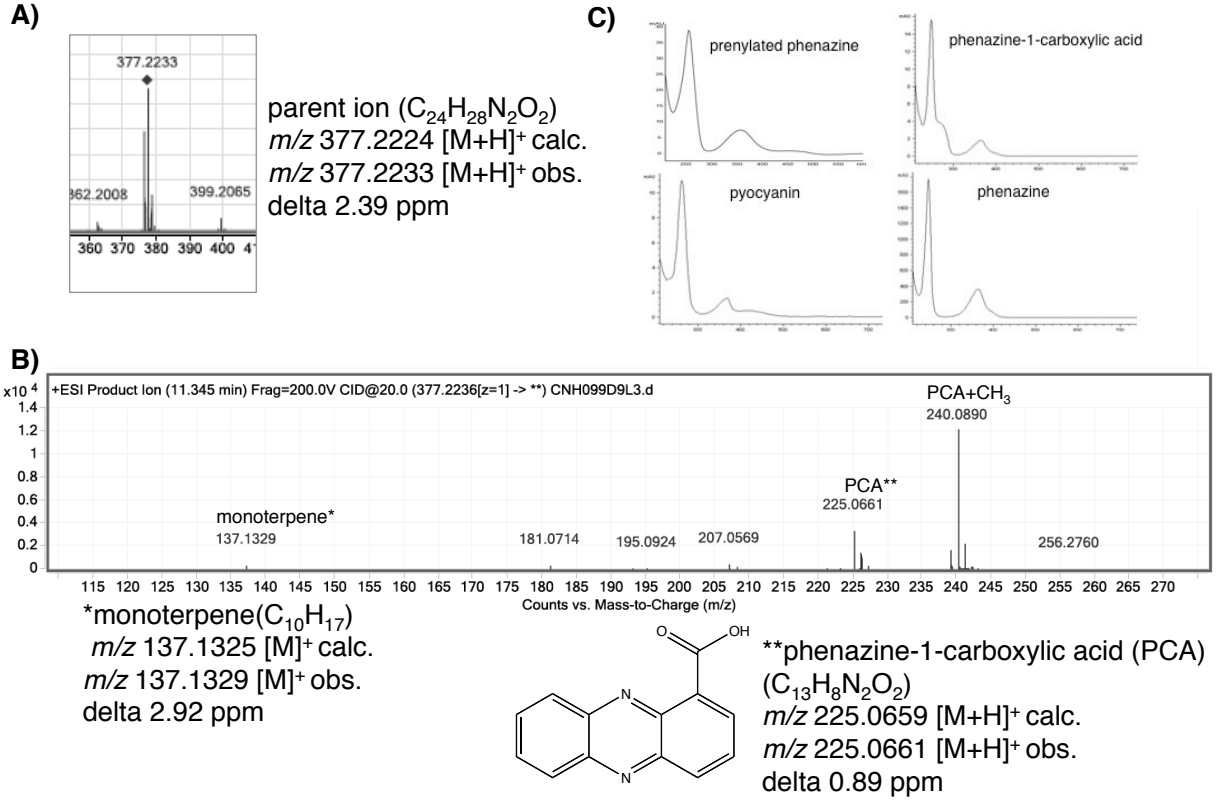


FIGURE S3**.** Identification of prenylated phenazine. (A) Parent ion. (B) MS2 fragmentation of parent ion. Fragments coresponding to a monoterpene*, phenazine-1-carboxylic acid (PCA**), and PCA with a methyl substituent are observed. (C) UV spectra for the prenylated phenazine observed in this study and related compounds (Moree et. al., 2012).



References

Gontang EA, Fenical W, Jensen PR (2007). Phylogenetic diversity of gram-positive bacteria cultured from marine sediments. Applied and Environmental Microbiology 73: 3272-3282.

Hozzein WN, Goodfellow M (2007). Streptomyces synnematoformans sp nov., a novel actinomycete isolated from a sand dune soil in Egypt. International Journal of Systematic and Evolutionary Microbiology 57: 2009-2013.

Jensen PR, Fenical W (2005). New natural-product diversity from marine actinomycetes. Natural Products: Drug Discovery and Therapeutic Medicine: 315-328.

Labeda DP, Goodfellow M, Brown R, Ward AC, Lanoot B, Vanncanneyt M et al (2012). Phylogenetic study of the species within the family Streptomycetaceae. Antonie Van Leeuwenhoek International Journal of General and Molecular Microbiology 101: 73-104.

Lin X, Kennedy D, Fredrickson J, Bjornstad B, Konopka A (2012). Vertical stratification of subsurface microbial community composition across geological formations at the Hanford Site. Environmental Microbiology 14.

Moree WJ, Phelan VV, Wu C-H, Bandeira N, Cornett DS, Duggan BM et al (2012). Interkingdom metabolic transformations captured by microbial imaging mass spectrometry. Proceedings of the National Academy of Sciences 109: 13811-13816.

Prieto-Davo A, Fenical W, Jensen PR (2008). Comparative actinomycete diversity in marine sediments. Aquatic Microbial Ecology 52: 1-11.

Qin S, Li J, Chen H-H, Zhao G-Z, Zhu W-Y, Jiang C-L et al (2009). Isolation, Diversity, and Antimicrobial Activity of Rare Actinobacteria from Medicinal Plants of Tropical Rain Forests in Xishuangbanna, China. Applied and Environmental Microbiology 75: 6176-6186.

Solano G, Rojas-Jimenez K, Jaspars M, Tamayo-Castillo G (2009). Study of the diversity of culturable actinomycetes in the North Pacific and Caribbean coasts of Costa Rica. Antonie Van Leeuwenhoek International Journal of General and Molecular Microbiology 96: 71-78.

Soria-Mercado IE, Prieto-Davo A, Jensen PR, Fenical W (2005). Antibiotic terpenoid chloro-dihydroquinones from a new marine actinomycete. Journal of Natural Products 68: 904-910.