

Figure S1. Euler diagram comparing sediment metabolome composition at five sites. Total number of nodes (parent ions) per site is listed in parentheses after the site ID.

Spectra	Retention time	Mass
Monactin (standard)	11.0 min	773.443
Sediment match	11.0 min	773.450

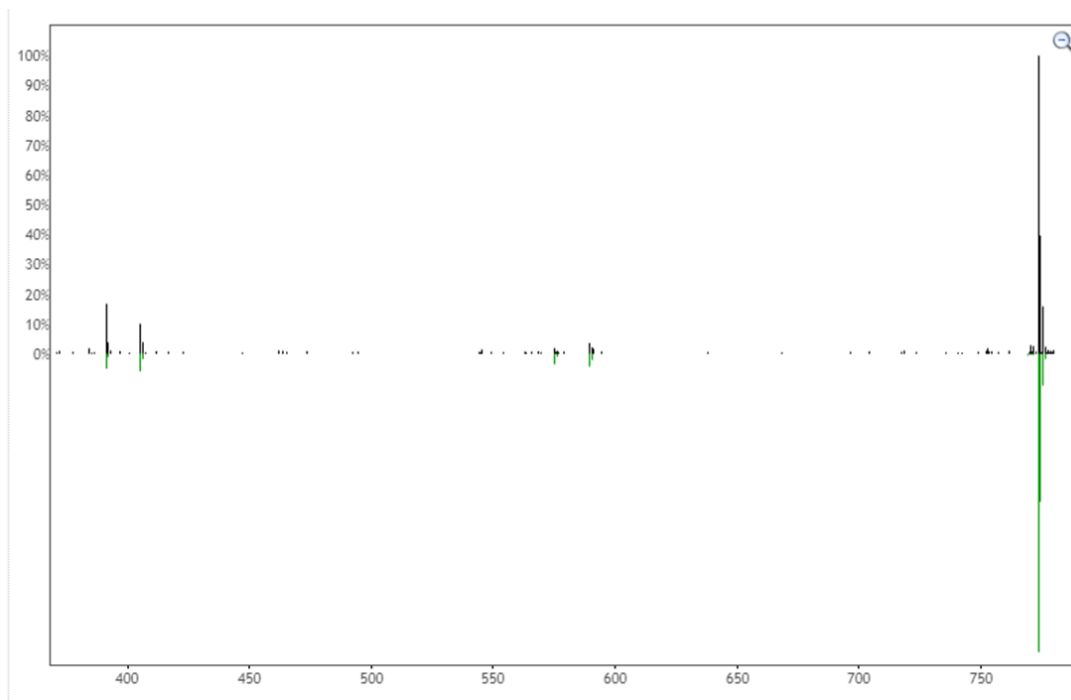


Figure S2. Retention time, mass, and mirror plot fragmentation spectral matching for monactin standard (green) and the parent ion detected (black).

Spectra	Retention time	Mass
Staurosporine (standard)	5.08 min	467.434
Sediment match	5.02 min	467.549

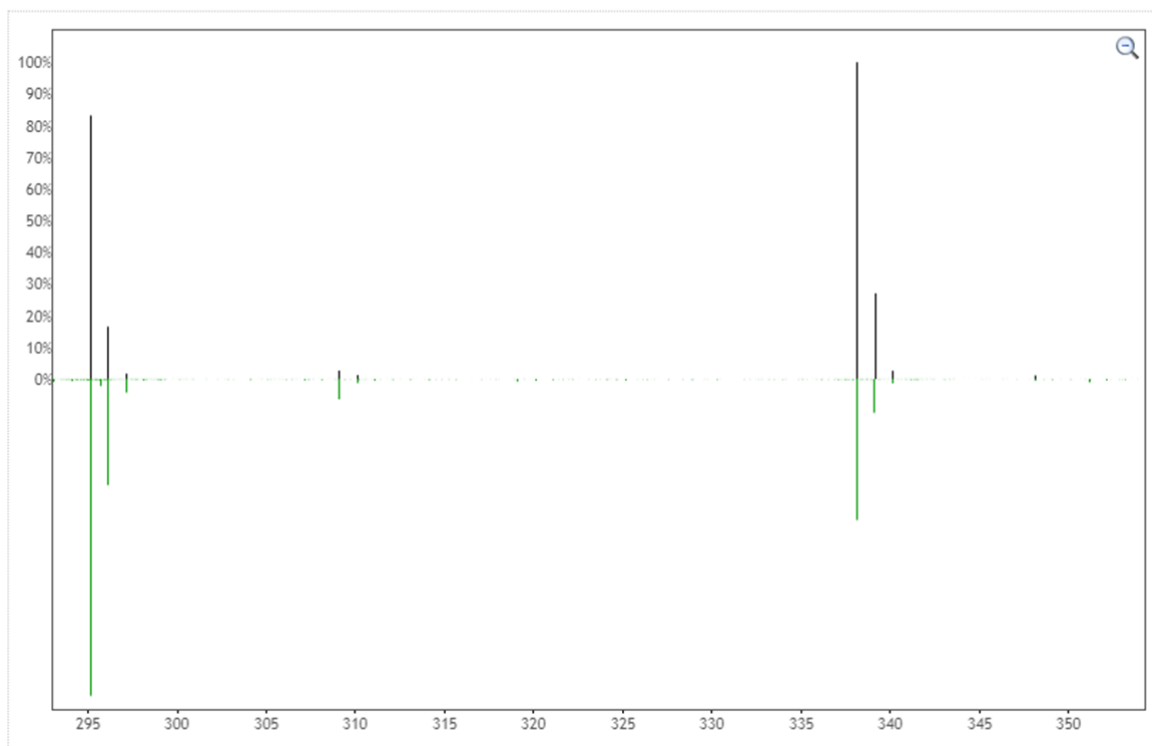


Figure S3. Retention time, mass, and mirror plot fragmentation spectral matching for staurosporine standard (green) and the parent ion detected (black).

Spectra	Retention time	Mass
Cocamidopropyl Betaine (standard)	6.12 min	343.259
Sediment match	6.11 min	343.293

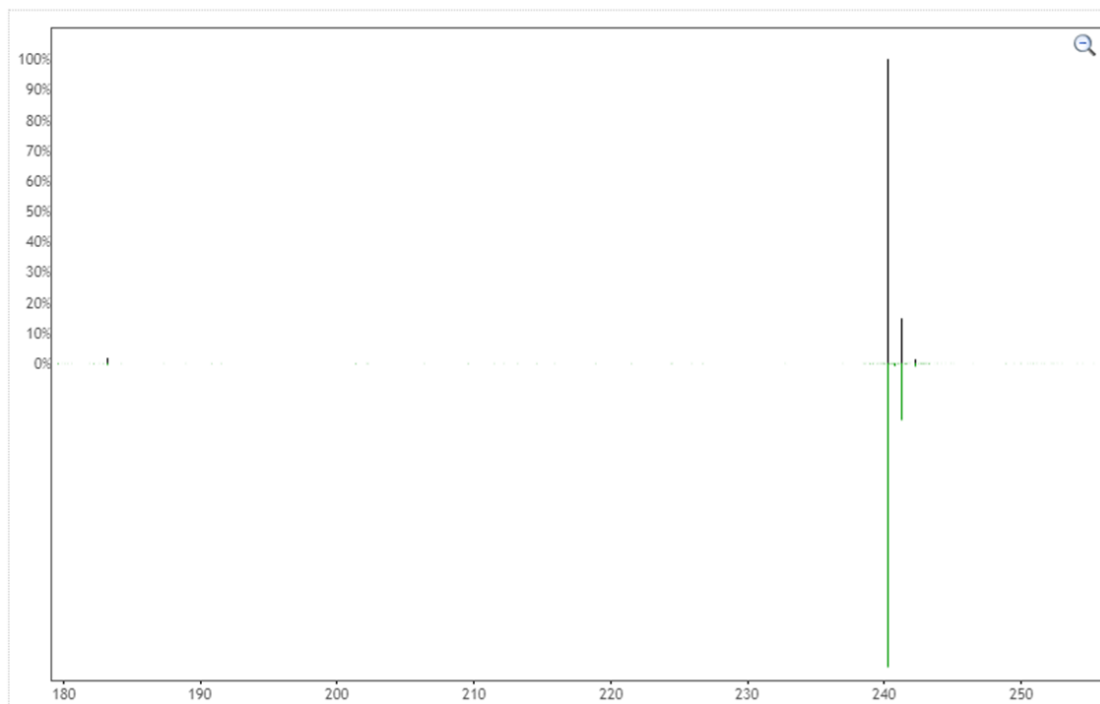


Figure S4. Retention time, mass, and mirror plot fragmentation spectral matching for cocamidopropyl betaine standard (green) and the parent ion detected (black).

Spectra	Retention time	Mass
Erucamide (standard)	11.61 min	338.342
Sediment match	11.62 min	338.341

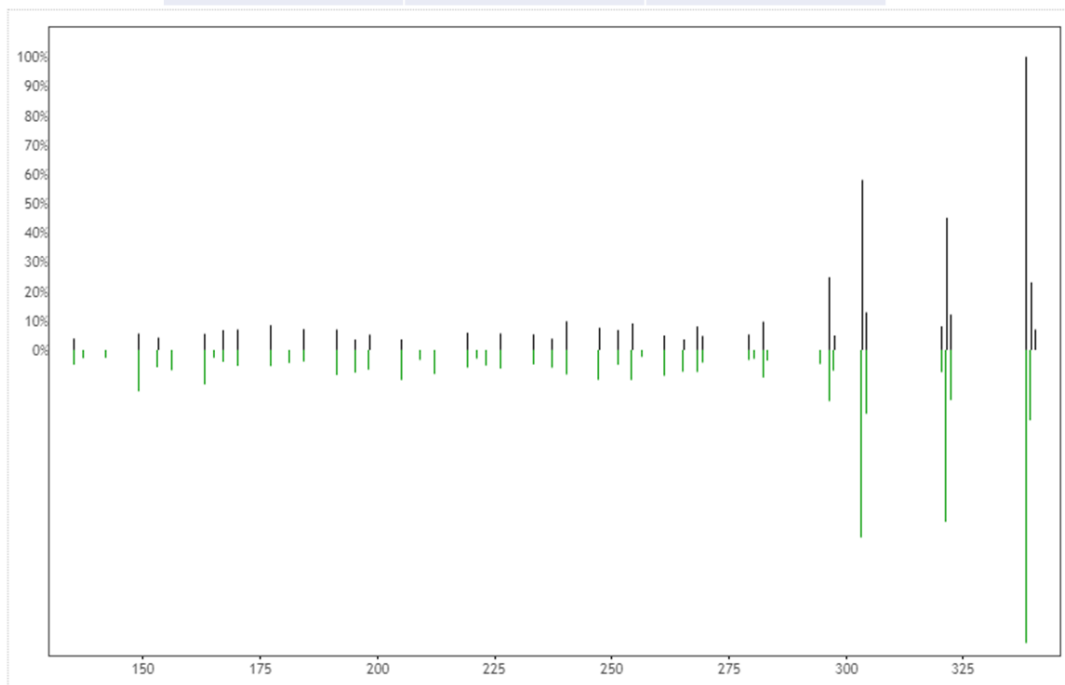


Figure S5. Retention time, mass, and mirror plot fragmentation spectral matching for erucamide standard (green) and the parent ion detected (black).

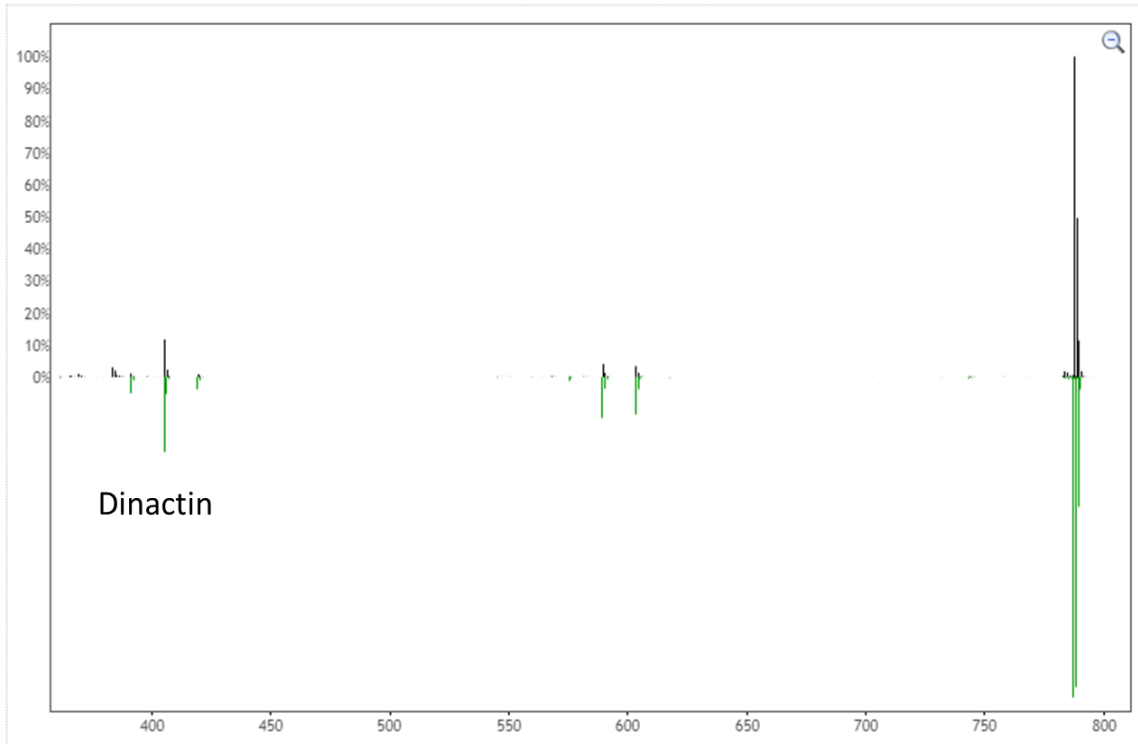


Figure S6. Mirror plot showing the fragmentation spectrum for dinactin from the GNPS library (green) against the matching parent ion from a sediment sample (black).

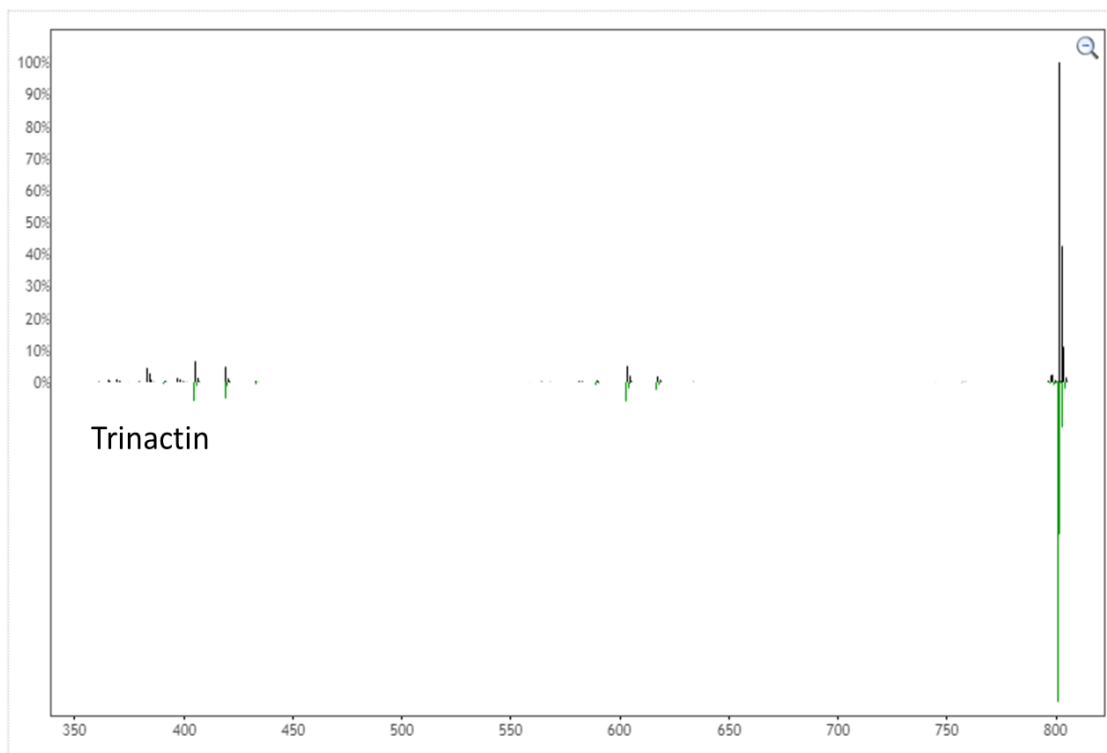


Figure S7. Mirror plot showing the fragmentation spectrum for trinactin from the GNPS library (green) against the matching parent ion from a sediment sample (black).

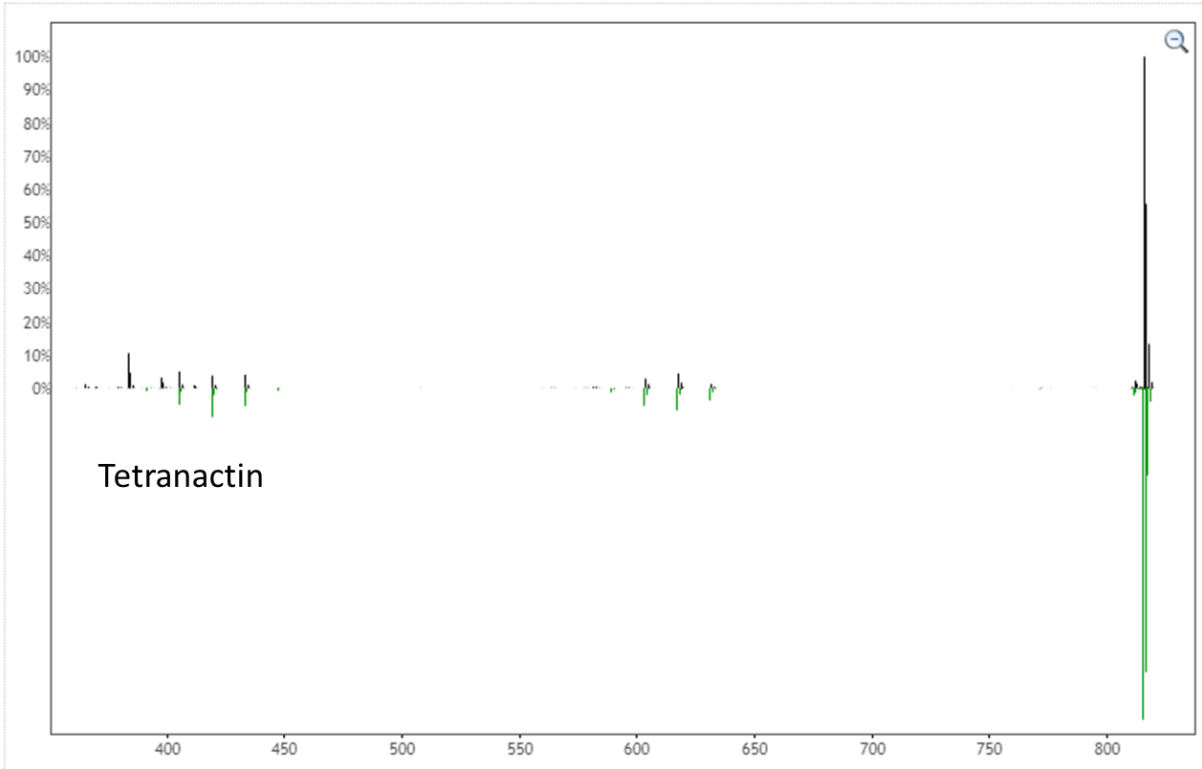


Figure S8. Mirror plot showing the fragmentation spectrum for tetranactin from the GNPS library (green) against the matching parent ion from a sediment sample (black).

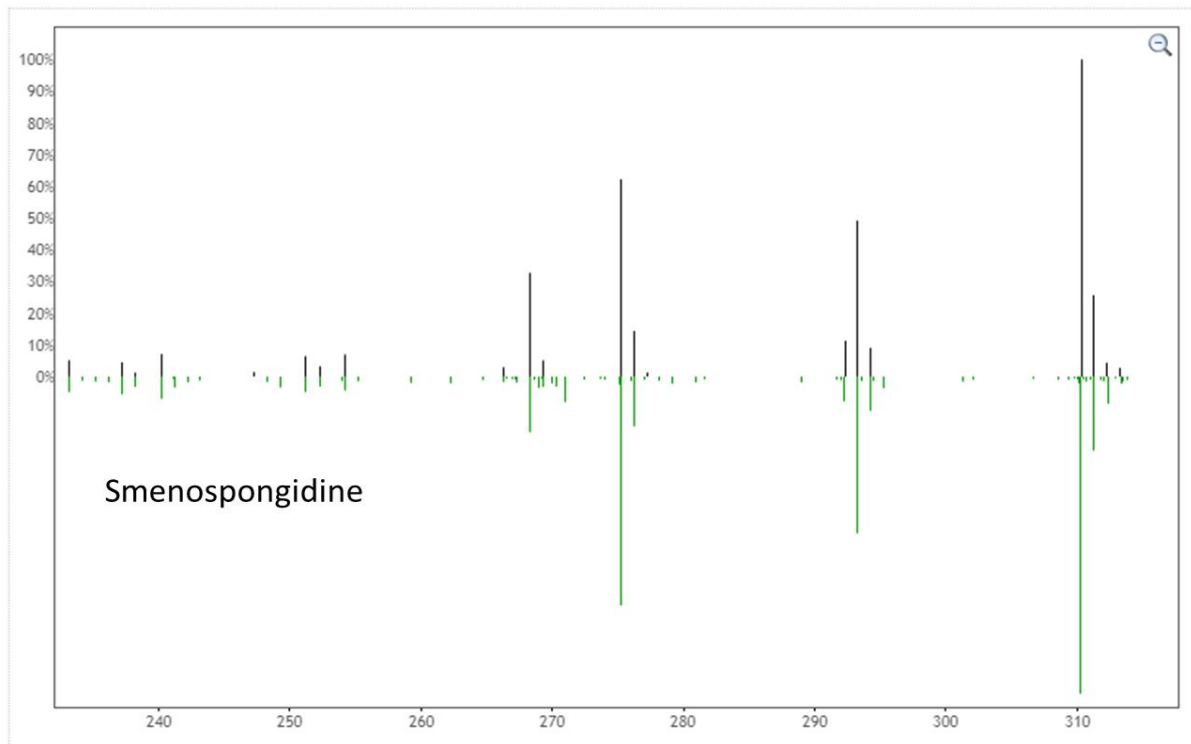


Figure S9. Mirror plot showing the fragmentation spectrum for smenospongidine from the GNPS library (green) against the matching parent ion from a sediment sample (black).

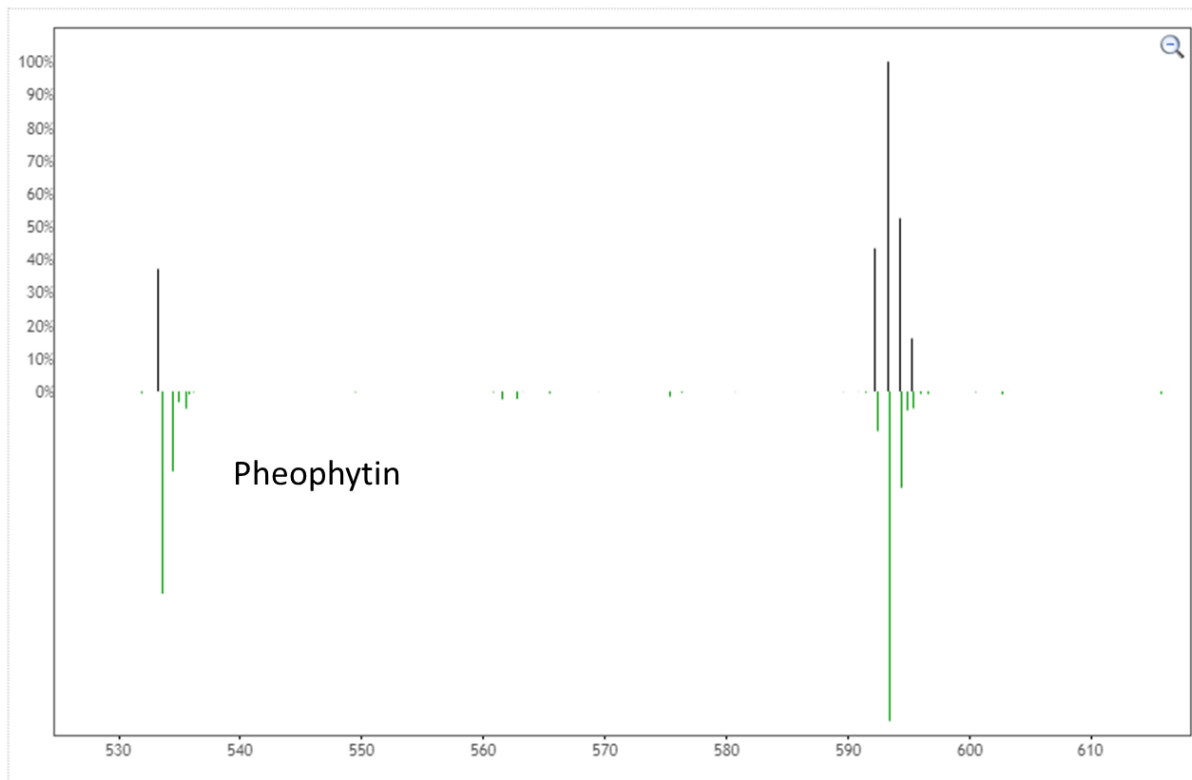


Figure S10. Mirror plot showing the fragmentation spectrum for phaeophytin from the GNPS library (green) against the matching parent ion from a sediment sample (black).

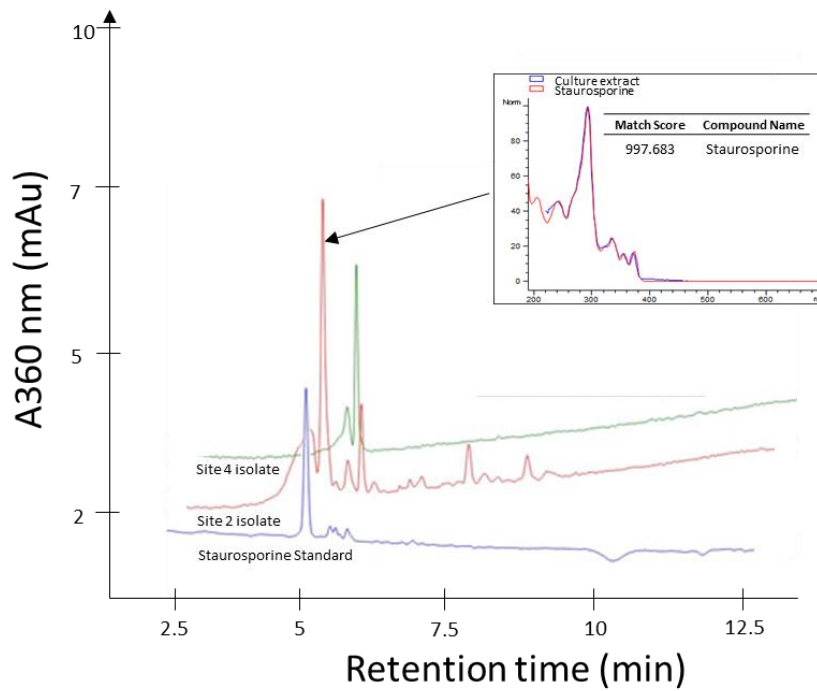


Figure S11. Staurosporine production by *S. arenicola* strains. LC traces (360 nm) of culture extracts show peaks at 5 min with UV absorbance spectra that closely match that of a staurosporine standard.

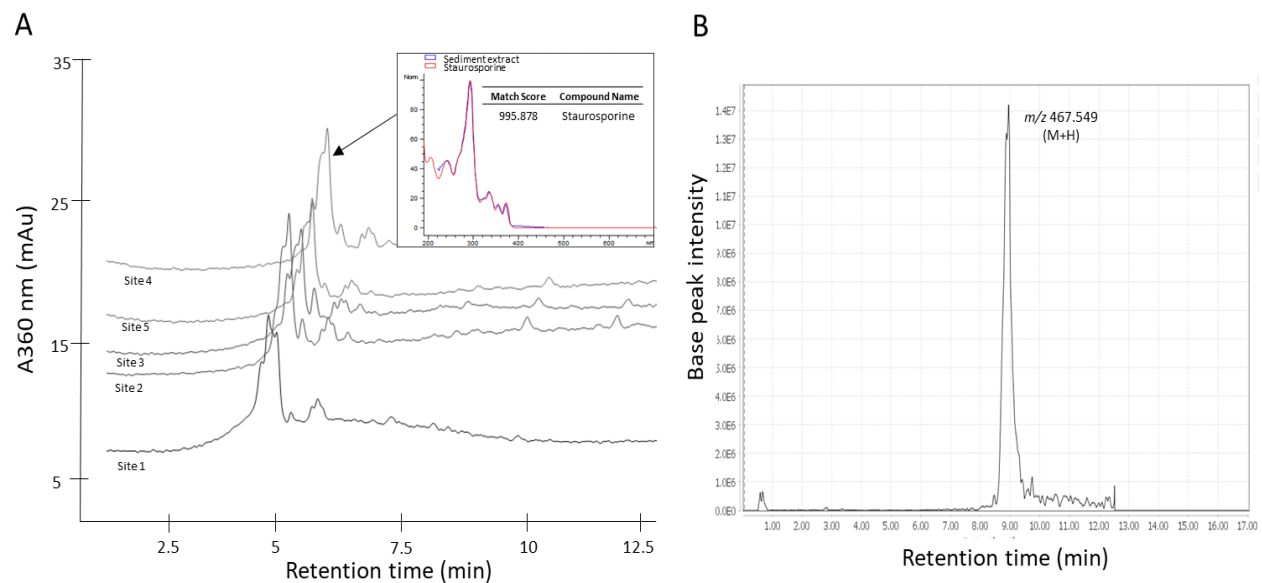


Figure S12. Staurosporine detection A) UV trace (360 nm) for sediment extracts from all five sites. Inset: absorbance spectrum corresponding to the major peak is shown with a high match score to a staurosporine library standard. B) Extracted ion chromatogram from the site 4 sediment extract for mass range 466.80-467.80 with the major peak matching staurosporine (exact mass 466.531).

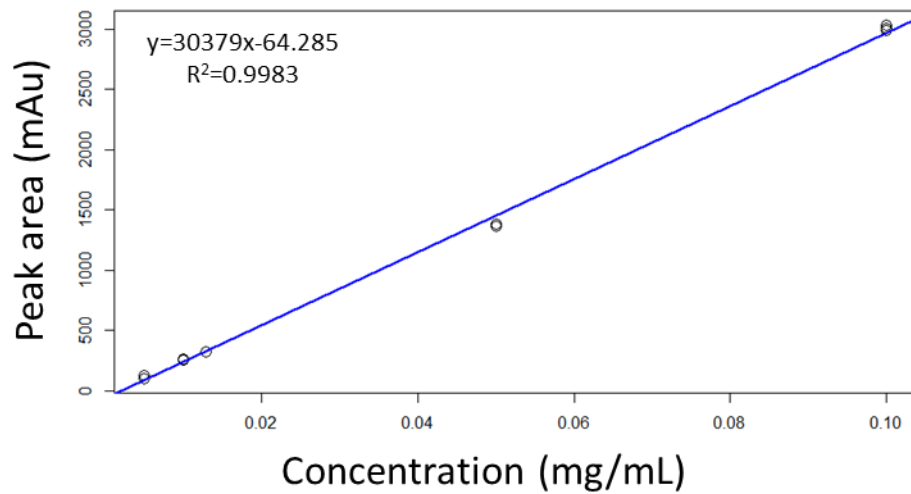


Figure S13. Staurosporine standard curve, linear regression equation, and R^2 value.

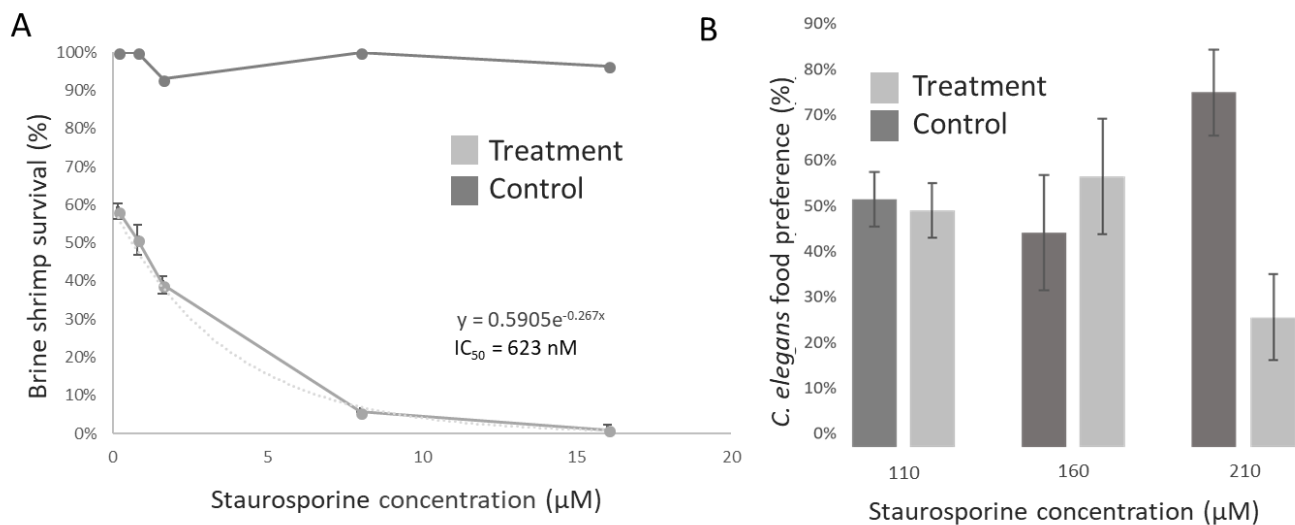


Figure S14. *C. elegans* and brine shrimp assays. A) Effects of staurosporine concentration on brine shrimp survival. Error bars are +/- one standard deviation of the mean. The exponential regression line and equation are shown as well as the calculated IC₅₀ value. B) Effects of staurosporine concentration on *C. elegans* feeding preference. *C. elegans* were given a choice between control (solvent only) and treatment (solvent + staurosporine) food sources at three different concentrations. Results presented as % *C. elegans* feeding on treatment (black) vs. control (grey). The asterisk indicates a significant difference (t-test, p-value <0.05).

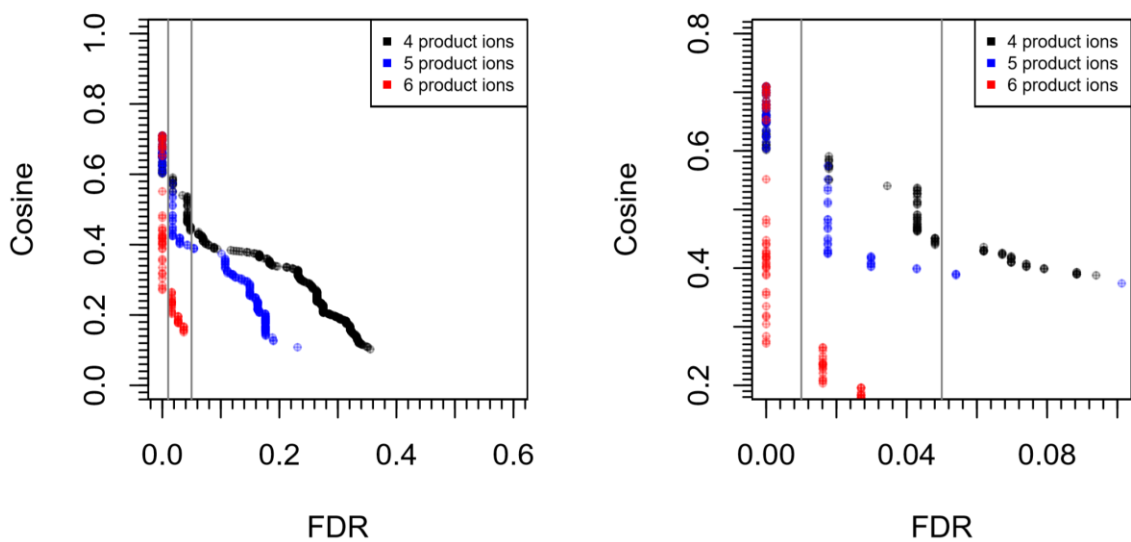


Figure S19. Estimated false discovery rates based on the minimum number of product ions used to match sediment spectra to library spectra for different cosine (similarity) scores. Lines are drawn at 1% and 5% FDR rates.

Table.S1. BLAST analysis of actinomycete strains. Both isolates had a 100% match for *S. arenicola* strain CNH-643.

Isolate from site	BLAST match	Max score	Total score	Query cover	E value	Sequence length	Identity	Accession number
2	<i>S. arenicola</i> (CNH-643)	2420	2420	100%	0	1306	100%	MH036184
4	<i>S. arenicola</i> (CNH-643)	2420	2420	100%	0	1324	100%	MH036185

Table S2. Average staurosporine concentration per site. Biologically relevant concentrations were calculated by dividing the percent organic material by the total volumetric concentration.

Site	Staurosporine concentration ($\mu\text{M} \pm$ standard deviation)	% Inorganic	Biologically relevant staurosporine concentration ($\mu\text{M} \pm$ standard deviation)
1	1.63 ± 1.22	67.3 ± 3.2	4.98 ± 2.04
2	5.56 ± 1.29	67.6 ± 2.5	17.17 ± 2.15
3	1.56 ± 0.95	62.6 ± 2.8	4.18 ± 1.58
4	5.51 ± 1.21	58.6 ± 3.1	13.32 ± 2.02
5	2.06 ± 1.27	59.7 ± 3.0	5.15 ± 2.12

Table S3. BLAST analysis of house-keeping genes flanking eight biosynthetic gene clusters (BGCs) assembled from the metagenome. Shown is the name of the house keeping gene, the four top BLAST hits, and the percent identity.

BGC	House keeping gene	Related species	% identity
1	Single stranded DNA specific exonuclease <i>recJ</i>	<i>Pleurocapsa</i>	72
		<i>Myxosarcina</i>	70
		<i>chondrocystis</i>	67
		<i>Stanieria</i>	64
2	Phycocerythrobilin: ferredoxin oxidoreductase	<i>Pleurocapsa</i> sp PCC 7319	84
		<i>Xenococcus</i> sp PCC 7305	80
		<i>chondrocystis</i> sp NIES-4102	78
		<i>Stanieria</i> sp NIES -3757	79
3	GGDEF domain-containing protein	<i>Pleurocapsa</i> sp. PCC 7319	68
		<i>Chondrocystis</i> sp. NIES-4102	65
		<i>Pleurocapsa</i> sp. CCALA 161	64
		<i>Stanieria cyanosphaera</i>	69
4	Ergothioneine biosynthesis protein <i>egtB</i>	<i>Myxosarcina</i> sp. G11	67
		<i>Hydrococcus rivularis</i>	62
		<i>Cyanobacteria bacterium</i> QH_1_48_107	62
		<i>Pleurocapsa minor</i>	62
5	Holliday junction branch migration DNA helicase <i>ruvB</i>	<i>Myxosarcina</i> sp. G11	85
		<i>Pleurocapsa</i> sp. PCC 7319	80
		<i>Chondrocystis</i> sp. NIES-4102	79
		<i>Pleurocapsa</i> sp. CCALA 161	74
6	UTP-glucose-1-phosphate uridylyltransferase	<i>Moorea producens</i>	73
		<i>Moorea producens</i>	72
		<i>Moorea producens</i>	73
		<i>Moorea bouillonii</i>	73
7	Group II intron reverse transcriptase/maturase	<i>Trichodesmium erythraeum</i>	81
		<i>Oscillatoria nigro-viridis</i>	67
		<i>Oscillatoria nigro-viridis</i>	67
		<i>Lynbya</i> sp. PCC 8106	65
8	Pyruvate phosphate dikinase PEP/pyruvate-binding protein	<i>Myxosarcina</i> sp. G11	68
		<i>Pleurocapsa</i> sp. CCALA 161	67
		<i>Chondrocystis</i> sp. NIES-4102	68
		<i>Stanieria cyanosphaera</i>	66