Table S1 : Summary table of number of peaks (visible and major) observed for each microbial extract in HPLC-DAD-CAD analysis.

Microbial strain	Code extract	Culture conditions			Number of peaks detected by HPLC-DAD-CAD	
		Medium	Support	Days	Visible peaks (Height > 5 pA)	Major peaks (Height > 30 pA)
Micromonospora sp. SH-82	82 A1 S 7 Ac	A1	Solid	7	13	2
	82 A1 S 14 Ac			14	19	9
	82 A1 S 21 Ac			21	21	12
	82 A1 L 7 Ac		Liquid	7	14	5
	82 A1 L 14 Ac			14	20	5
	82 A1 L 21 Ac			21	22	7
	82 MB S 14 Ac	MB	Solid	14	10	1
	82 MB L 14 Ac		Liquid	14	16	10
Micromonospora sp. SH-57	57 A1 S 7 Ac	A1	Solid	7	4	0
	57 A1 S 14 Ac			14	4	0
	57 A1 S 21 Ac			21	6	1
	57 A1 L 7 Ac		Liquid	7	4	0
	57 A1 L 14 Ac			14	4	0
	57 A1 L 21 Ac			21	10	2
	57 MB S 14 Ac	MB	Solid	14	1	0
	57 MB L 14 Ac		Liquid	14	3	0
Salinispora arenicola SH-78	78 A1 S 7 Ac	A1	Solid	7	7	0
	78 A1 S 14 Ac			14	7	0
	78 A1 S 21 Ac			21	7	0
	78 A1 L 14 Ac		Liquid	14	8	1

Table S2 : Detailed of observed peaks in the HPLC-CAD chromatographic profiles of microbials extracts from *Micromonospora* sp. SH-82.

Culture conditions									
Medium		A1						MB	
Support		Solid			Liquid			Solid	Liquid
Days		7	14	21	7	14	21	14	14
Code extract		82 A1 S 7 Ac	82 A1 S 14 Ac	82 A1 S 21 Ac	82 A1 L 7 Ac	82 A1 L 14 Ac	82 A1 L 21 Ac	82 MB S 14 Ac	82 MB L 14 Ac
Peaks code	**Retention Time (min)**	**Height of peaks (pA)**							
		82 A1 S 7 Ac	**82 A1 S 14 Ac**	**82 A1 S 21 Ac**	**82 A1 L 7 Ac**	**82 A1 L 14 Ac**	**82 A1 L 21 Ac**	**82 MB S 14 Ac**	**82 MB L 14 Ac**
P 82.1	10.0	-	17	32	-	-	-	-	8
P 82.2	10.8	-	48	64	-	-	-	-	21
P 82.3	11.0	-	23	34	-	-	-	-	38
P 82.4	11.5	17	38	47	10	10	11	-	31
P 82.5	11.8	-	73	91	46	50	52	8	45
P 82.6	12.3	20	44	60	45	46	46	5	42
P 82.7	13.0	11	15	15	20	20	24	-	-
P 82.8	14.1	8	25	26	9	9	8	-	-
P 82.9	15.4	6	23	13	8	8	7	-	-
P 82.10	19.0	75	149	187	37	59	115	39	114
P 82.11	19.3	-	17	17	5	7	7	-	11
P 82.12	20.7	29	63	81	46	64	60	11	44
P 82.13	21.5	7	28	30	26	27	20	5	30
P 82.14	21.7	8	25	28	20	30	29	-	12
P 82.15	22.8	54	114	132	55	60	57	26	62
P 82.16	24.1	-	5	6	7	9	7	-	-
P 82.17	24.7	-	-	-	8	18	15	-	-
P 82.18	25.0	-	-	-	-	7	6	-	-
P 82.19	25.3	-	-	7	-	7	6	9	8
P 82.20	26.4	-	-	-	-	9	11	-	-

Table S2 : *Continued*

Culture conditions									
Medium		A1						MB	
Support		Solid			Liquid			Solid	Liquid
Days		7	14	21	7	14	21	14	14
Code extract		82 A1 S 7 Ac	82 A1 S 14 Ac	82 A1 S 21 Ac	82 A1 L 7 Ac	82 A1 L 14 Ac	82 A1 L 21 Ac	82 MB S 14 Ac	82 MB L 14 Ac
Peaks code	**Retention Time (min)**	**Height of peaks (pA)**							
		82 A1 S 7 Ac	**82 A1 S 14 Ac**	**82 A1 S 21 Ac**	**82 A1 L 7 Ac**	**82 A1 L 14 Ac**	**82 A1 L 21 Ac**	**82 MB S 14 Ac**	**82 MB L 14 Ac**
P 82.21	27.1	-	-	-	-	6	6	-	-
P 82.22	27.5	-	-	-	-	5	7	-	-
P 82.23	32.7	-	-	15	-	-	-	15	-
P 82.24	33.2	9	10	14	-	-	7	-	8
P 82.25	34.7	8	49	48	-	7	34	11	50
P 82.26	35.3	14	66	72	-	5	32	45	37

Table S3 : Summary table of annotations from the Ion Identity Molecular Network of the different extracts of *Micromonospora sp.* SH-82.

Compound ID	Retention Time (min)	*m/z* [+Adduct]	Molecular formula	Compound name or InChIKey [1,2,3]	Chemical class	Similarity [1,2,3]
C82.1	6.14	877.5648 $[M+H]^+$	$C_{44}H_{80}N_2O_{15}$	Megalomicin A [1,3]	Organooxygen compounds	92% [1] / 0.05 [3]
C82.2	6.34	919.5754 $[M+H]^+$	$C_{45}H_{78}N_2O_{17}$	Megalomicin B [1,3]		89% [1] / 0.05 [3]
C82.3	6.52	933.5939 $[M+H]^+$	$C_{47}H_{84}N_2O_{16}$	4′-Propionylmegalomicin A [1]		89% [1]
C82.4	6.59	961.5883 $[M+H]^+$	$C_{48}H_{84}N_2O_{17}$	Megalomicin C1 [1,3]		87% [1] / 0.05 [3]
C82.5	6.77	975.6046 $[M+H]^+$	$C_{49}H_{86}N_2O_{17}$	Megalomicin C2 [1,3]		84% [1] / 0.05 [3]
C82.6	7.26	776.4797 $[M+H]^+$	$C_{39}H_{69}NO_{14}$	2′-*O*-Acetylerythromycin A [1]	Organooxygen compounds	83% [1]
C82.7	6.75	720.4529 $[M+H]^+$	$C_{36}H_{65}NO_{13}$	Erythromycin C [1]		98% [1]
C82.8	7.24	720.4536 $[M+H]^+$	$C_{36}H_{65}NO_{13}$	13-Deethyl-13-methylerythromycin [1]		96% [1]
C82.9	7.08	704.4586 $[M+H]^+$	$C_{36}H_{65}NO_{12}$	Erythromycin D [1]		93% [1]
C82.10	7.25	718.4717 $[M+H]^+$	$C_{37}H_{67}NO_{12}$	Erythromycin B [1,3]		91% [1] / 0.05 [3]
C82.11	6.98	690.4431 $[M+H]^+$	$C_{36}H_{65}NO_{12}$	6-Desmethyl erythromycin D [1,3]		92% [1] / 0.05 [3]
C82.12	6.92	560.3782 $[M+H]^+$	$C_{29}H_{53}NO_9$	3-*O*-De(3-C,3-O-dimethyl-2,6-dideoxy-alpha-L-ribo-hexopyranosyl)-6-deoxyerythromycin [1]		85,3% [1]
C82.13	6.72	560.3782 $[M+H]^+$	$C_{29}H_{53}NO_9$			
C82.14	7.35	704.4521 $[M+H]^+$	$C_{36}H_{65}NO_{12}$	6-Deoxy-3'-*O*-demethylerythromycin [1]		89% [1]
C82.15	6.67	706.4521 $[M+H]^+$	$C_{35}H_{63}NO_{13}$	Norerythromycin [1]		89% [1]
C82.16	7.54	385.2577 $[M-H_2O+H]^+$	$C_{21}H_{38}O_7$	Erythronolide B [1]	Macrolides and analogues	62% [1]
C82.17	7.30	371.2423 $[M-H_2O+H]^+$	$C_{20}H_{36}O_7$	2-Desmethyl-2-hydroxy-6-deoxyerythronolide B [1]		69% [1]
C82.18	7.99	529.3367 $[M-H_2O+H]^+$	$C_{28}H_{50}O_{10}$	3-*O*-alpha-mycarosylerythronolide B [1]		68% [1]
C82.19	7.71	515.3209 $[M-H_2O+H]^+$	$C_{27}H_{48}O_{10}$	3-*O*-(alpha-L-olivosyl)erythronolide B [1]		75% [1]
C82.20	7.89	515.3183 $[M-H_2O+H]^+$				75% [1]
C82.21	8.25	369.2626 $[M-H_2O+H]^+$	$C_{21}H_{38}O_6$	6-Deoxyerythronolide B [1,3]		63% [1] / 0.05 [3]

Data from [1] SIRIUS, [2] GNPS or [3] ISDB timaR bioinformatics tools.
Each score is independent and associated with the specific workflow from which it originates.

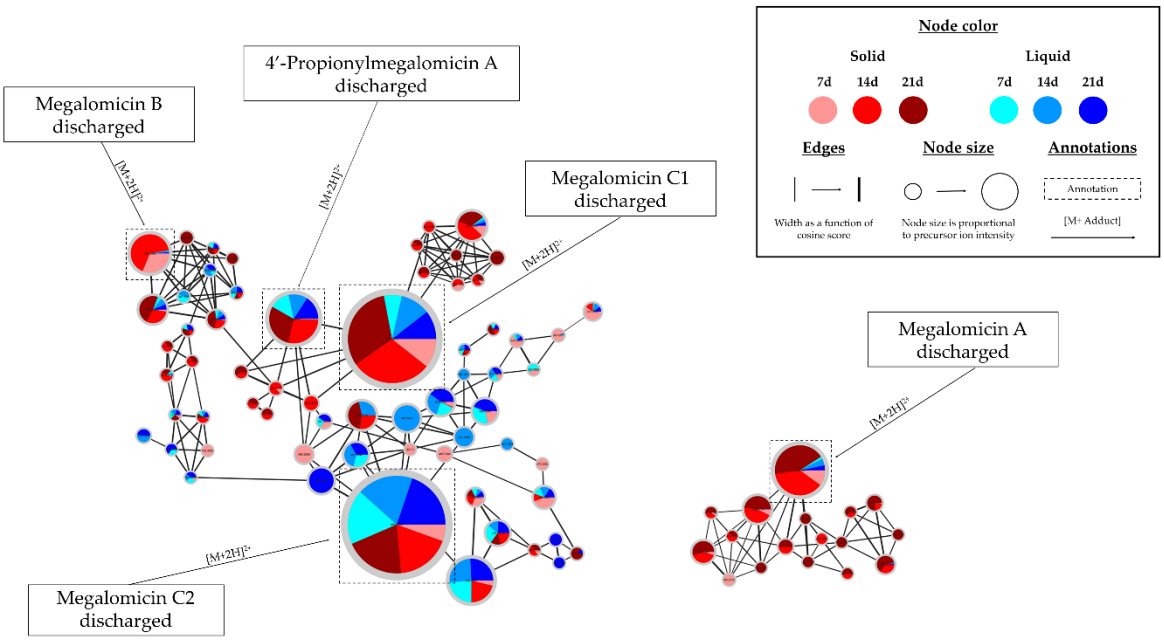

Figure S1 : Cluster of *Micromonospora* sp. SH-82 containing discharged ions representing the megalomicins.

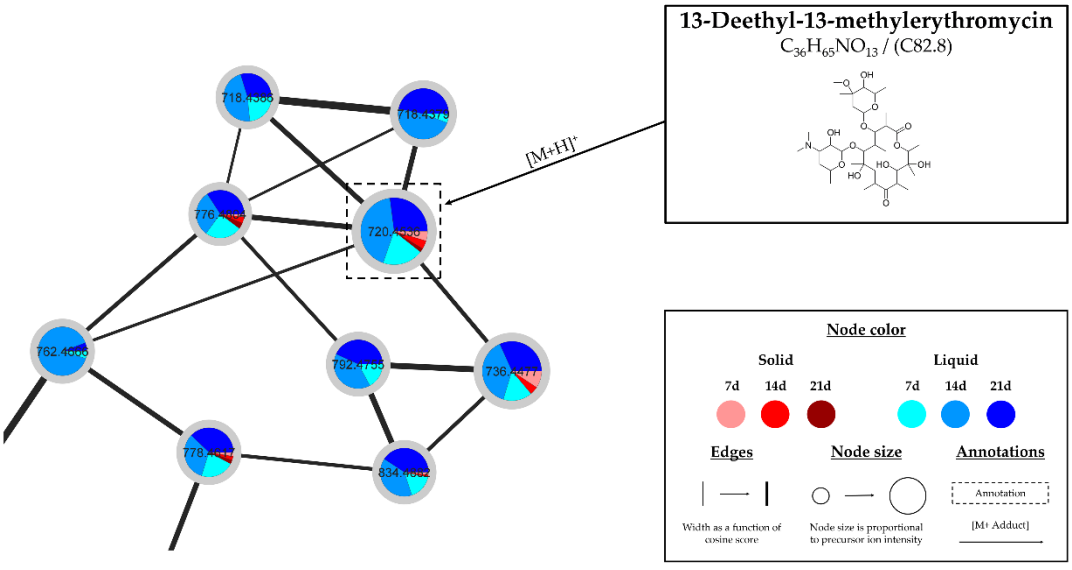

Figure S2 : Zoom-in on cluster of *Micromonospora* sp. SH-82 containing erythromycin annotation.

Table S4 : Detailed of observed peaks in the HPLC-CAD chromatographic profiles of microbials extracts from *Micromonospora* sp. SH-57.

Culture conditions									
Medium		A1						MB	
Support		Solid			Liquid			Solid	Liquid
Days		7	14	21	7	14	21	14	14
Code extract		57 A1 S 7 Ac	57 A1 S 14 Ac	57 A1 S 21 Ac	57 A1 L 7 Ac	57 A1 L 14 Ac	57 A1 L 21 Ac	57 MB S 14 Ac	57 MB L 14 Ac
Peaks code	**Retention Time (min)**	**Height of peaks (pA)**							
		57 A1 S 7 Ac	**57 A1 S 14 Ac**	**57 A1 S 21 Ac**	**57 A1 L 7 Ac**	**57 A1 L 14 Ac**	**57 A1 L 21 Ac**	**57 MB S 14 Ac**	**57 MB L 14 Ac**
P 57.1	12.2	-	-	6	12	11	8	-	10
P 57.2	16.4	-	-	-	10	14	6	-	-
P 57.3	26.7	-	-	-	-	-	5	-	-
P 57.4	26.9	-	-	-	-	-	5	-	-
P 57.5	31.4	9	5	16	15	19	20	-	21
P 57.6	34.4	13	13	16	-	-	17	8	-
P 57.7	35.3	22	17	32	6	6	43	-	5
P 57.8	36.4	12	18	25	-	-	36	-	-
P 57.9	37.6	-	-	-	-	-	9	-	-
P 57.10	39.1	-	-	7	-	-	24	-	-

Table S5 : Summary table of annotations from the Ion Identity Molecular Network of the different extracts of *Micromonospora* sp. SH-57.

Compound ID	Retention Time (min)	*m/z* [+Adduct]	Molecular formula	Compound name or InChIKey [1,2,3]	Chemical class	Similarity [1,2,3]
C57.1	1.08	266.1245 $[M+H]^+$	$C_{11}H_{15}N_5O_3$	2-Deoxy-*N*6-methyladenosine [1]	Purine nucléoside	93% [1]
C57.2	3.45	234.1351 $[M+H]^+$	$C_{11}H_{15}N_5O$	SXIDRQQQIPLCTJ [1]		81% [1]
C57.3	8.48	264.1277 $[M+H]^+$	$C_{11}H_{13}N_5O_3$	UHYRJPGYRFMFLT [1]		75% [1]
C57.4	6.08	218.1400 $[M+H]^+$	$C_{11}H_{15}N_5$	9-cyclopentyl-*N*-methylpurin-6-amine [1]		75% [1]
C57.5	7.12	280.1225 $[M+H]^+$	$C_{12}H_{17}N_5OS$	INPAYTORGXXLMB [1]		66% [1]
C57.6	6.19	335.163 $[M+H]^+$	$C_{14}H_{26}N_2O_5S$	JDNYVZBVEBRRCT [1]	Carboxylic acids and derivatives	86% [1]
C57.7	5.38	343.1292 $[M+Na]^+$	$C_{13}H_{24}NO_5S$	(?)-*S*-Acetylpantetheine [1]		77% [1]
C57.8	7.31	375.1949 $[M+H]^+$	$C_{17}H_{30}N_2O_5S$	ZCNIMMSEOJFZKZ [1]		81% [1]
C57.9	7.32	397.1772 $[M+H]^+$	$C_{19}H_{28}N_2O_5S$	IXKOTSUCYPEFPP [1]		78% [1]
C57.10	8.53	130.0652 $[M+H-H_2O]^+$	C_9H_9NO	Indole-3-carbinol [1,2]	Indoles and derivatives	88% [1]/ 0.77 [2]
C57.11	8.40	130.0653 $[M+H-H_2O]^+$				
C57.12	6.72	233.0812 $[M+H]^+$	$C_{13}H_{12}O_4$	Aloesone [1]	Benzopyrans	71% [1]
C57.13	6.52	235.0967 $[M+H]^+$	$C_{13}H_{14}O_4$	Aloesol [1]		83% [1]
C57.14	9.70	310.1803 $[M+H]^+$	$C_{20}H_{23}NO_2$	Carbazoquinocin C [1,3]	Indoles and derivatives	71% [1]/ 0.05 [3]
C57.15	10.00	324.1958 $[M+H]^+$	$C_{21}H_{25}NO_2$	Carbazoquinocin E [1,3]		61% [1]/ 0.05 [3]
C57.16	10.30	338.2111 $[M+H]^+$	$C_{22}H_{27}NO_2$	Carbazoquinocin F [1,3]		58% [1]/ 0.05 [3]
C57.17	10.60	366.2423 $[M+H]^+$	$C_{24}H_{31}NO_2$	12-Carbazol-9-yldodecanoic acid [1]		53% [1]

Data from [1] SIRIUS, [2] GNPS or [3] ISDB timaR bioinformatics tools.
Each score is independent and associated with the specific workflow from which it originates.

Table S6 : Detailed of observed peaks in the HPLC-CAD chromatographic profiles of microbials extracts from *Salinispora arenicola* SH-78.

Culture conditions					
Medium		A1			
Support		Solide			Liquid
Days		7	14	21	14
Code extract		78 A1 S 7 Ac	78 A1 S 14 Ac	78 A1 S 21 Ac	78 A1 L 14 Ac
Peaks code	**Retention Time (min)**	**Height of peaks (pA)**			
		78 A1 S 7 Ac	**78 A1 S 14 Ac**	**78 A1 S 21 Ac**	**78 A1 L 14 Ac**
P 78.1	13.4	12	16	12	10
P 78.2	20.3	5	10	5	9
P 78.3	20.8	7	11	5	11
P 78.4	24.8	10	10	6	15
P 78.5	26.8	10	17	7	12
P 78.6	28.3	-	-	-	38
P 78.7	29.5	8	12	6	15
P 78.8	34.5	10	15	5	96

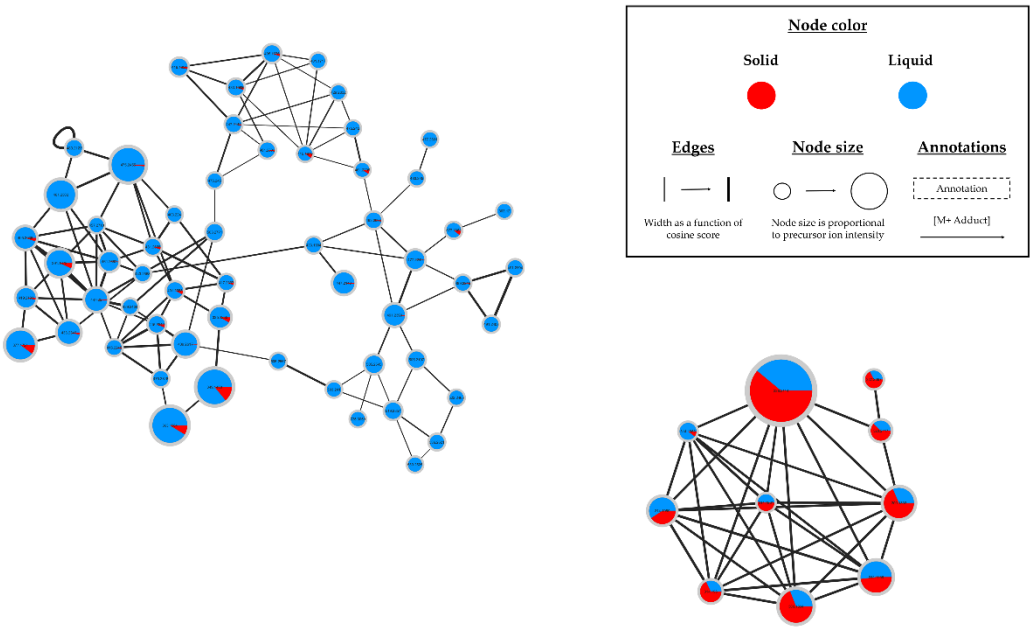

Figure S3 : Zoom-in on two largest cluster of *Salinispora arenicola* SH-78 is not clearly annotated.

Table S7: Summary table of annotations from the Ion Identity Molecular Network of the different extracts of *Salinispora arenicola* SH-78.

Compound ID	Retention Time (min)	*m/z* [+Adduct]	Molecular formula	Compound name or InChIKey [1,2,3]	Chemical class	Similarity [1,2,3]
C78.1	7.20	483.2028 $[M+H]^+$	$C_{28}H_{26}N_4O_4$	OH staurosporine [1,2,3]	Indoles and derivatives	85 % [1] / 0,79 [2] / 0.1 [3]
C78.2	7.33	467.2085 $[M+H]^+$	$C_{28}H_{26}N_4O_3$	Staurosporine [1,2,3]		98% [1] / 0,96 [2] / 0.1 [3]
C78.3	7.30	497.2192 $[M+H]^+$	$C_{29}H_{28}N_4O_4$	4'-*N*-methyl-5'-hydroxy-staurosporine [1]		78% [1]
C78.4	7.53	497.1825 $[M+H]^+$	$C_{28}H_{24}N_4O_5$	4'-demethyl-Af-formyl-7V-hydroxy-staurosporine [1]		74% [1]
C78.5	9.70	696.3022 $[M+H]^+$	$C_{37}H_{45}NO_{12}$	Rifamycin S [1,2,3]	Macrolactams	75% [1] / 0,74 [2] / 0.05 [3]
C78.6	9.24	682.2866 $[M+H]^+$	$C_{36}H_{43}NO_{12}$	16-demethyl rifamycin S [3]		0.1 [3]
C78.7	8.40	640.3113 $[M+H]^+$	$C_{35}H_{45}NO_{10}$	34a-deoxy-rifamycin W [1]		62% [1]
C78.8	9.75	640.3119 $[M+H]^+$				58% [1]
C78.9	8.30	624.3190 $[M+H]^+$	$C_{35}H_{45}NO_9$	Proansamycin B [1,3]		64% [1] / 0.05 [3]
C78.10	9.39	624.3164 $[M+H]^+$				54%[1]
C78.11	8.73	622.2658 $[M-H_2O+H]^+$	$C_{34}H_{41}NO_{11}$	Demethyl-desacetyl-rifamycin S [1]		71% [1]
C78.12	9.57	712.2971 $[M+H]^+$	$C_{37}H_{45}NO_{13}$	20-hydroxyrifamycin S [1,3]		74% [1] / 0.05 [3]
C78.13	7.61	672.3036 $[M+H]^+$	$C_{35}H_{42}NO_{12}$	30-hydroxyrifamycin W [1]		59% [1]
C78.14	7.84	396.2745 $[M+H]^+$	$C_{22}H_{37}NO_5$	Saliniketal A [1,3]	Prenol lipids	43% [1] / 0.05 [3]
C78.15	6.90	412.2693 $[M+H]^+$	$C_{22}H_{37}NO_6$	Saliniketal B [1,3]		49% [1] / 0.13 [3]

Data from [1] SIRIUS, [2] GNPS or [3] ISDB timaR bioinformatics tools.
Each score is independent and associated with the specific workflow from which it originates.

Table S7: *Continued*

Compound ID	Retention Time (min)	*m/z* [+Adduct]	Molecular formula	Compound name or InChIKey [1,2,3]	Chemical class	Similarity [1,2,3]
C78.16	6.47	155.0703 $[M+H]^+$	$C_8H_{10}O_3$	Salinilactone D [3]	Lactones	0.13 [3]
C78.17	6.88	169.0858 $[M+H]^+$	$C_9H_{12}O_3$	Salinilactone E [3]		0.13 [3]
C78.18	7.28	169.086 $[M+H]^+$				0.13 [3]
C78.19	7.67	183.1016 $[M+H]^+$	$C_{10}H_{14}O_3$	Salinilactone A [3]		0.13 [3]
C78.20	7.79	183.1016 $[M+H]^+$				0.13 [3]
C78.21	7.95	183.1017 $[M+H]^+$				0.13 [3]
C78.22	8.44	197.1174 $[M+H]^+$	$C_{11}H_{16}O_3$	Salinilactone C [3]		0.13 [3]
C78.23	8.84	211.1332 $[M+H]^+$	$C_{12}H_{18}O_3$	Salinilactone H [3]		0.13 [3]

Data from [1] SIRIUS, [2] GNPS or [3] ISDB timaR bioinformatics tools.
Each score is independent and associated with the specific workflow from which it originates.

Table S8: Batch mode use for data processing with MzMine 3.

1) Mass detection

Scan MS1 centroid ; noise level : 3^E3
Scan MS2 centroid ; noise level : 0^E0

2) ADAP Chromatogram Builder

Min group size in # of scans : 3
Group intensity threshold : 3^E3
Min highest intensity : 5^E3
Scan to scan accuracy : 0.0050 *m*/*z* or 20 ppm

3) Local minimum feature resolver

MS/MS scan pairing: retention time (RT) tolerance : 0.2 min
MS1 to MS2 precursor tolerance : 0.0050 *m*/*z* or 20 ppm
Chromatographic threshold : 85%
Minimum search range RT : 0.080 min
Minimum relative height : 0%
Minimum absolute height : 2.503
Min ratio of peak top/edge : 1.7
Peak duration range: 0-2 min
Min # of data points : 3

4) 13C isotope filter

m/*z* tolerance : 0.005 *m*/*z* or 20 ppm
RT tolerance : 0.08 min
Maximum charge : 2
Representative isotope most intense

5) Join aligner

m/*z* tolerance : 0.005 *m*/*z* or 20 ppm
Weight for *m*/*z* : 3
RT tolerance : 0.08 min
Weight for RT : 1

6) Feature list blank subtraction

Minimum # of detection in blanks : 1

7) metaCorrelate

RT : 0.05 min
Min height : 3^E3
Intensity correlation threshold : 3^E3
Correlation grouping
Feature height correlation

8) Ion identity molecular networking

m/*z* tolerance 0.005 *m*/*z* or 20 ppm
Min height 3^E3

9) Export feature list GNPS

Feature intensity : peak area
CSV export simple

Table S9: Parameters use for molecular network with GNPS.

1) Basic options

Precursor Ion Mass Tolerance : 0.02 Da
Fragment Ion Mass Tolerance : 0.02 Da

2) Advanced network options

Min paris cos : 0.70
Network TopK : 7
Minimum Matched Fragment Ions : 12

3) Advanced Library Search Options

Library Search Min Matched Peaks : 6
Score Threshold : 0.7