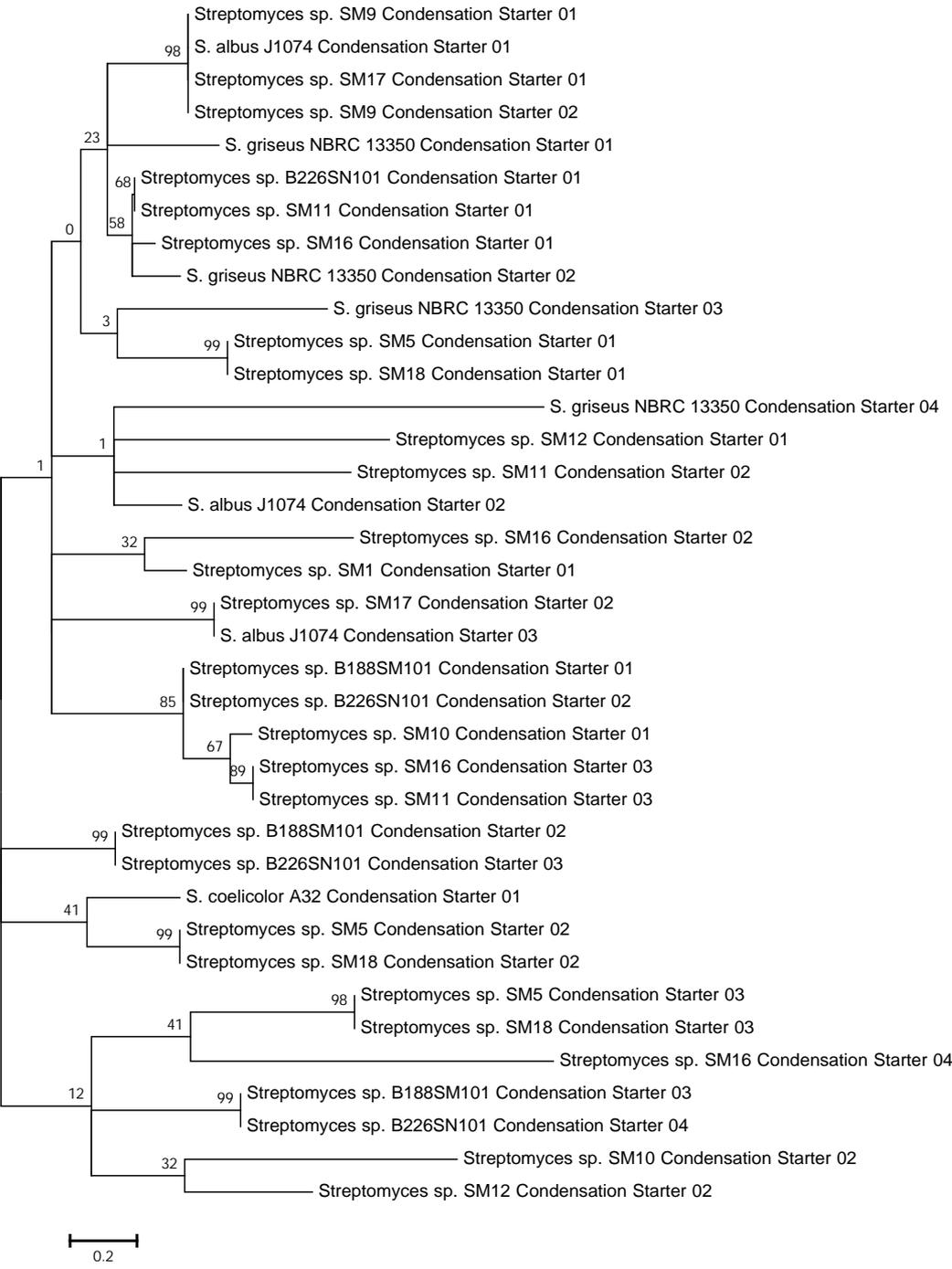
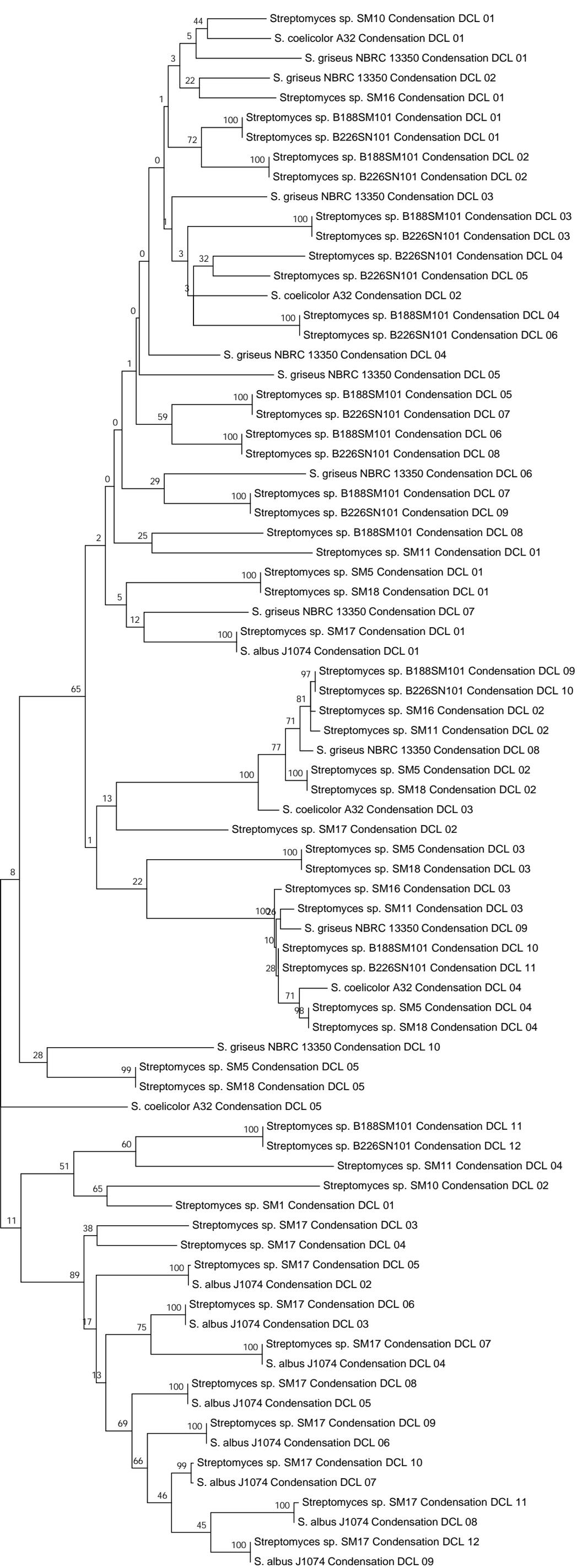




Supplementary Figure S1. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic tree of KS domain, deduced amino acid sequences of PKS gene clusters, from the genomes of marine *Streptomyces* spp. and from the genomes of selected reference terrestrial *Streptomyces* spp.

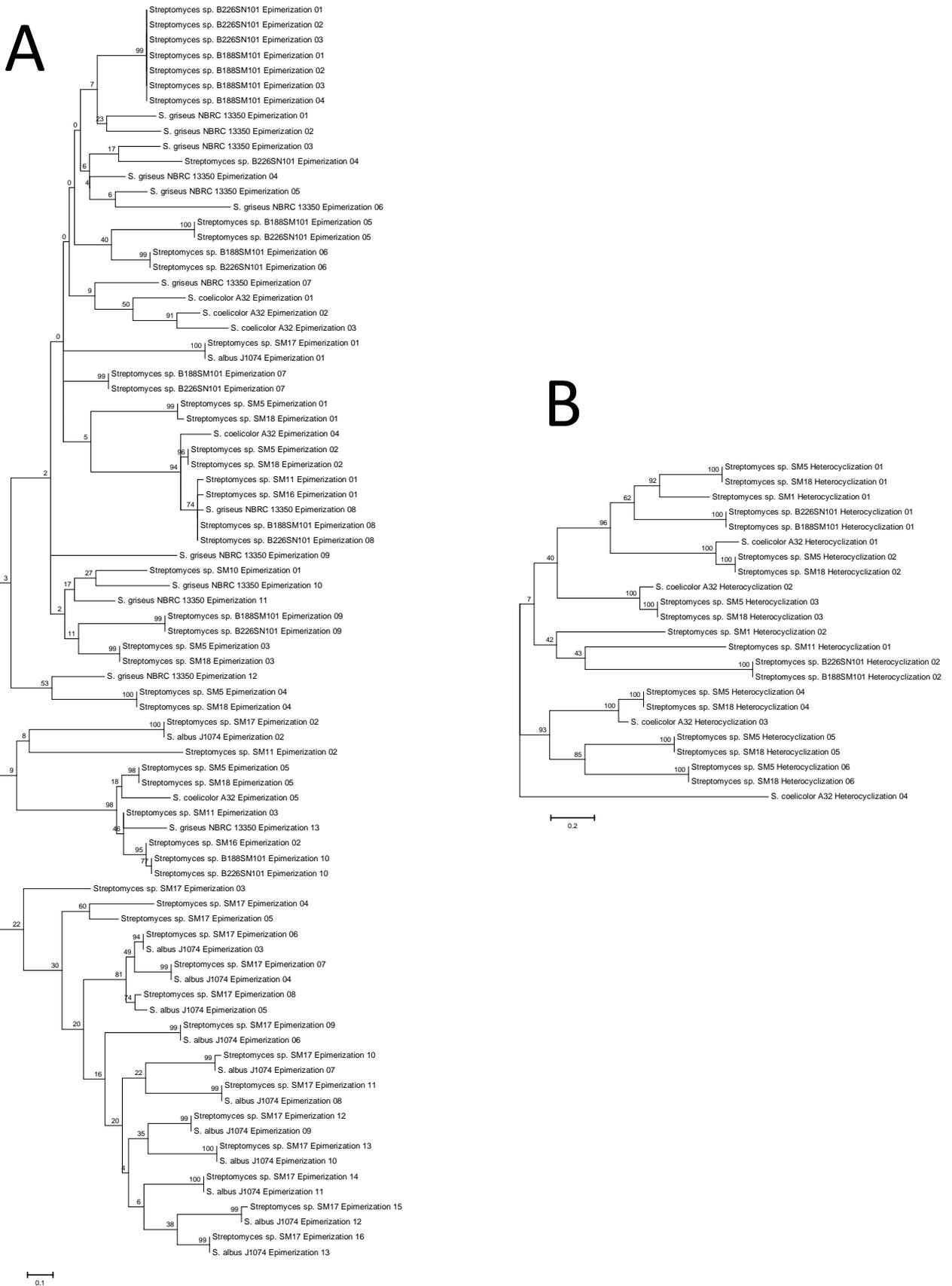


Supplementary Figure S2. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic tree of condensation starter domain, deduced amino acid sequences, of NRPS gene clusters, from the genomes of marine *Streptomyces* spp. and from the genomes of selected reference terrestrial *Streptomyces* spp.

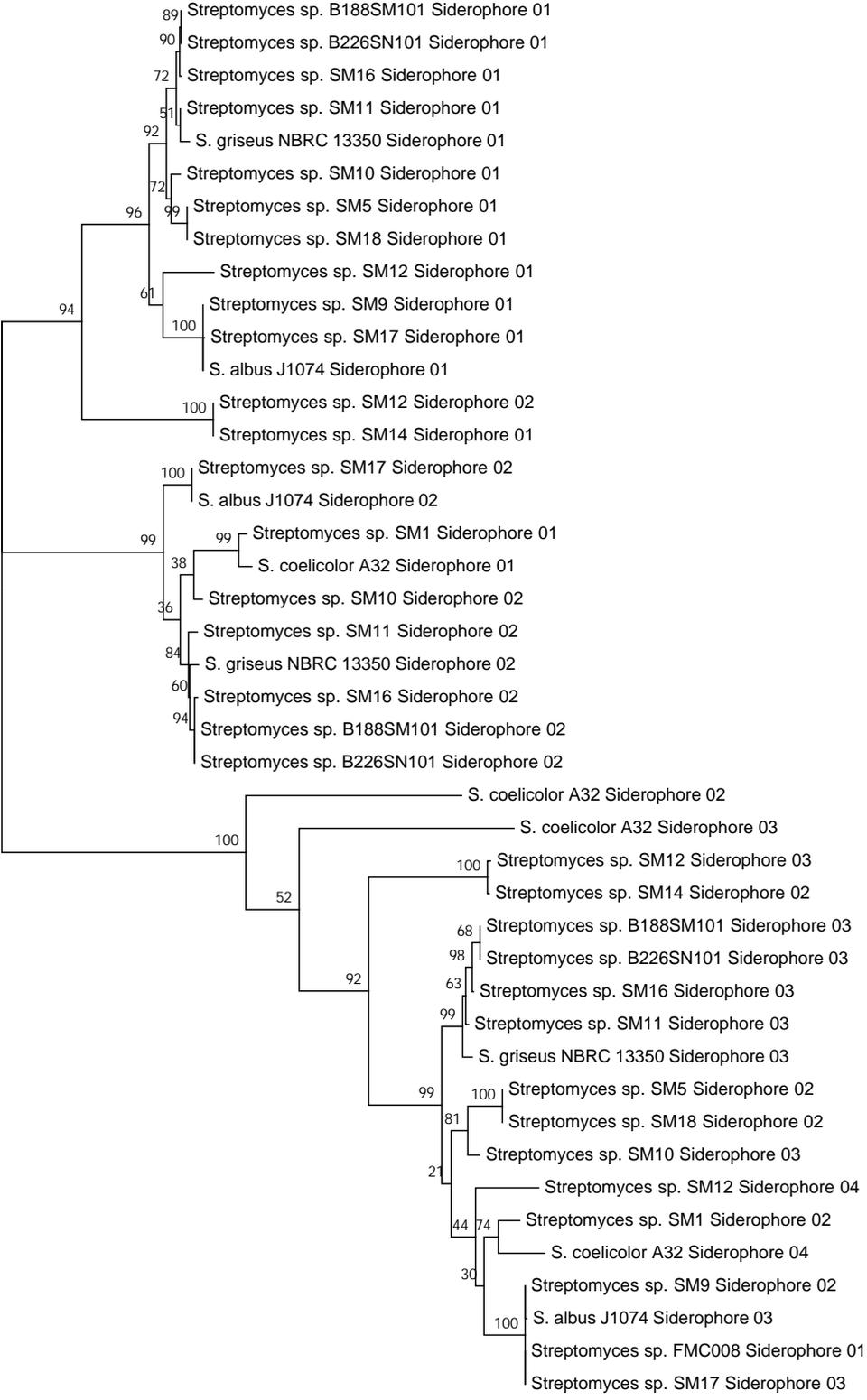


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Supplementary Figure S3. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic tree of condensation DCL domain, deduced amino acid sequences, of NRPS gene clusters, from the genomes of marine *Streptomyces* spp. and from the genomes of selected reference terrestrial *Streptomyces* spp.

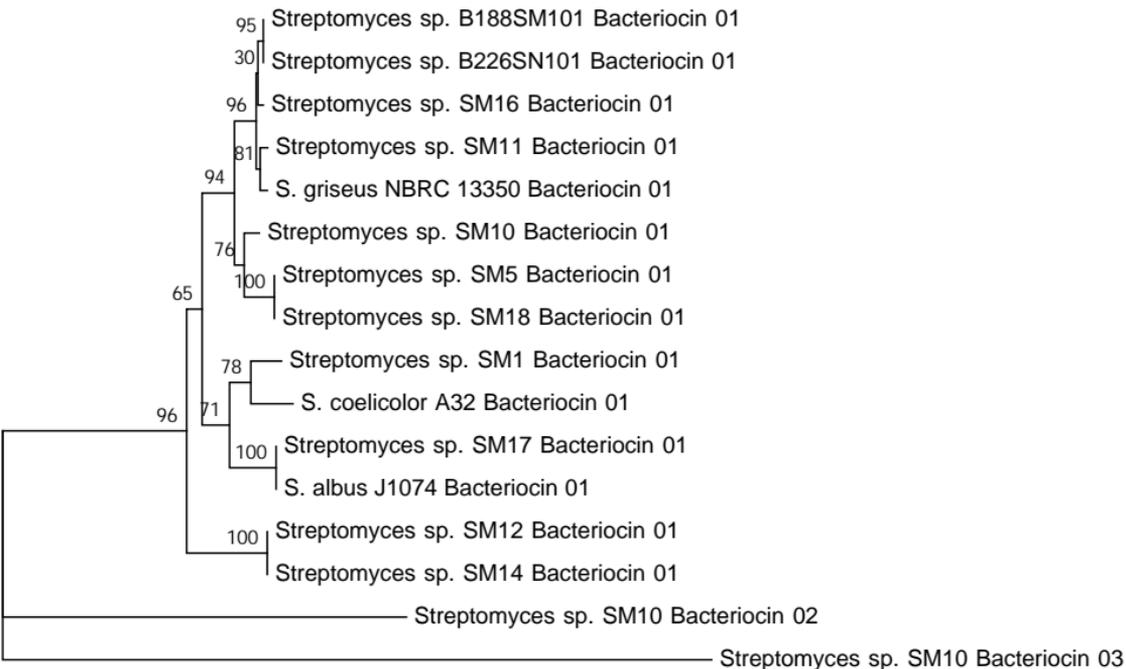


Supplementary Figure S5. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic trees of deduced amino acid sequences of (A) epimerization and (B) heterocyclization domains from NRPS gene clusters, from the genomes of marine *Streptomyces* spp. and from the genomes of selected reference terrestrial *Streptomyces* spp.



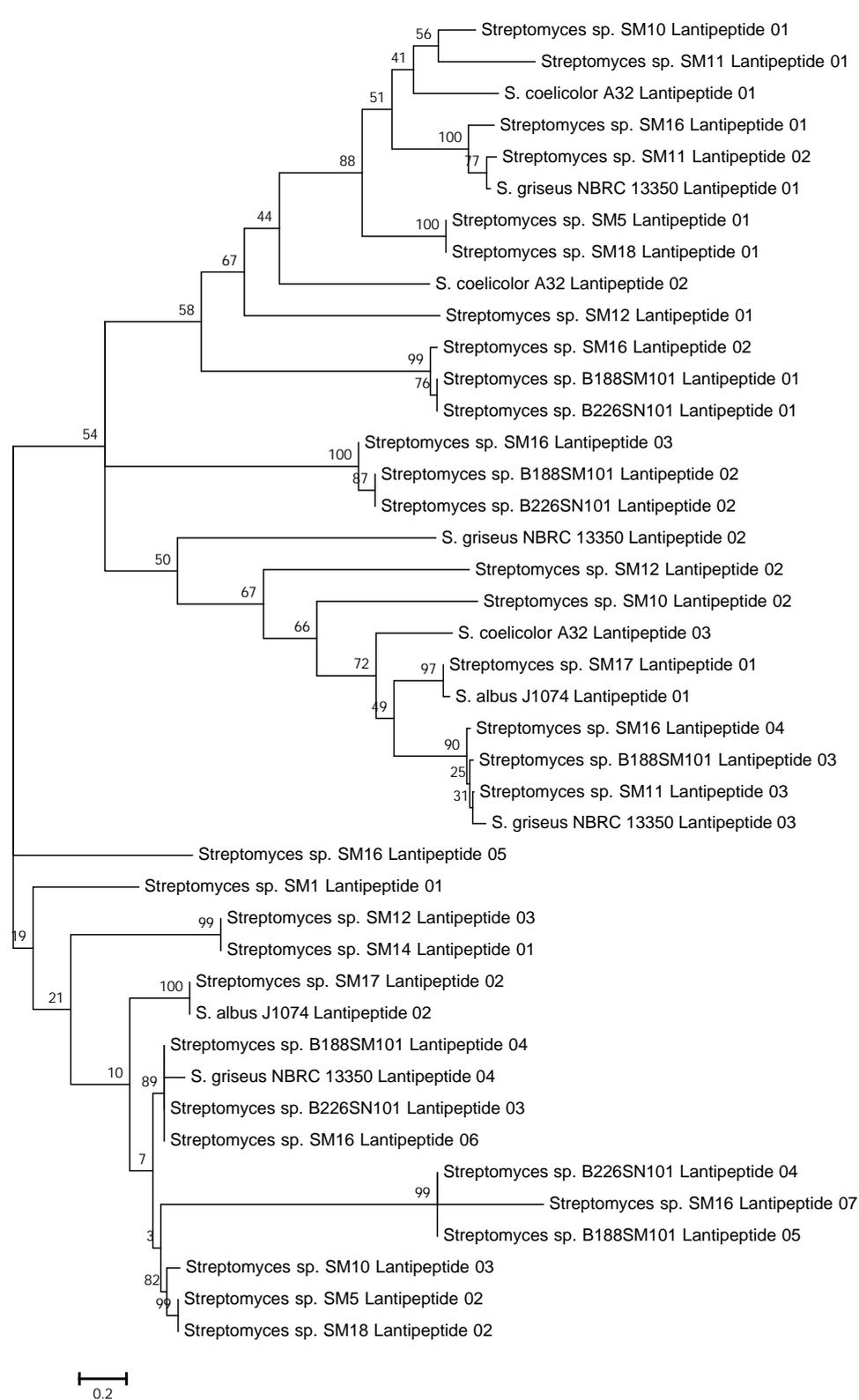
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Supplementary Figure S6. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic trees of deduced amino acid sequences of *lucA-lucC* domains from siderophore gene clusters, from the genomes of marine *Streptomyces* spp. and from the genomes of selected reference terrestrial *Streptomyces* spp.



0.2

Supplementary Figure S7. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic trees of deduced amino acid sequences of DUF692 domains from bacteriocin gene clusters, from the genomes of marine *Streptomyces* spp. and from the genomes of selected reference terrestrial *Streptomyces* spp.



Supplementary Figure S8. Bootstrap-consensus (n=100) Maximum Likelihood phylogenetic trees of deduced amino acid sequences of LanC-like domains from lantipeptide gene clusters, from the genomes of marine *Streptomyces* spp. and from the genomes of selected reference terrestrial *Streptomyces* spp.

Isolate ID	Percentage of sequences assigned to closest sequence in kraken classification with miniKraken database
SM1	31.7% <i>Streptomyces coelicolor</i> A3 (2) 18.1% <i>Streptomyces</i> root
SM5	83.91% <i>Streptomyces</i> sp. Sirex AA-E
SM9	97.4% <i>Streptomyces albus</i> J1074
SM10	55.5% <i>Streptomyces</i> sp. Sirex AA-E
SM11	78.7% <i>Streptomyces griseus</i> subsp. <i>griseus</i> NBRC 13350
SM12	33.3% <i>Streptomyces</i> root 47.5% assigned to various <i>Streptomyces</i> spp.
SM14	35.1% <i>Streptomyces</i> root 47.4% assigned to various <i>Streptomyces</i> spp.
SM16	80.45% <i>Streptomyces griseus</i> subsp. <i>griseus</i> NBRC 13350
SM17	97.8% <i>Streptomyces albus</i> J1074
SM18	84.5% <i>Streptomyces</i> sp. Sirex AA-E
FMC008	97.2% <i>Streptomyces albus</i> J1074
B188M101	82.7% <i>Streptomyces griseus</i> subsp. <i>griseus</i> NBRC 13350
B226SN101	82.22% <i>Streptomyces griseus</i> subsp. <i>griseus</i> NBRC 13350

Supplementary Table S1. Taxonomy of *Streptomyces* spp. isolates using KRAKEN.

B188M101			
Cluster no.	Cluster type	Most similar known cluster	% of genes showing similarity
1	NRPS	Heat Stable Antifungal Factor (HSAF)	62
2	Butyrolactone	Gamma - butyroactone	100
3	Siderophore	Desferrioxamine B	100
4	NRPS-T1PKS	Balhimycin	8
5	NRPS	none	0
6	Lasso peptide	SRO15-2005	80
7	Others KS	none	0
8	NRPS	Calcium-dependent antibiotic	5
9	Terpene	none	0
10	Ladderane-Arylpoyene	Skylamycin	12
11	Melanin	Melanin	100
12	Ectoine	Ectoine	100
13	Bacteriocin	none	0
14	Lantipeptide	none	0
15	T3-PKS	Alkylresorcinol	66
16	Bacteriocin	none	0
17	Others-Nrps-T1PKS	Zorbamycin	4
18	T1PKS-NRPS	none	0
19	NRPS	Thaxtomin	18
20	Terpene	none	0
21	Other	none	0
22	T1PKS	SGR-PTMs	33
23	NRPS	none	0
24	T3PKS	Herboxidiene	6
25	NRPS	none	0
26	Terpene	none	0
27	NRPS	Laspartomycin	6
28	NRPS	none	0
29	NRPS	Daptomycin	18
30	Lantipeptide	none	0
31	Phenazine	Lomofungin	26
32	NRPS	none	0
33	NRPS	Friulimicin	6
34	NRPS	Skylamycin	16
35	Terpene	Hopene	69
36	Siderophore	Kinamycin	8
37	NRPS	Friulimicin	15
38	Butyrolactone	Skylamycin	14
39	Ectoine	Kosinostatin	11
40	Lantipeptide	AmfS	60
41	NRPS	none	0
42	Thiopeptide-Lantipeptide	none	0
43	NRPS-OthersKS	Kirromycin	8
44	Lasso peptide	Chlortetracycline	5
45	NRPS	Griseobactin	52
46	Lantipeptide	Chalcomycin	9
47	NRPS	none	0
48	Terpene	Isorenieratene	100
49	NRPS	Friulimicin	18
50	NRPS	Coelichelin	72
51	NRPS	Daptomycin	4
52	NRPS	none	0
53	NRPS	none	0

Supplementary Table S2. Secondary metabolism gene cluster types in the draft genome of B188M101, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

B226SN101			
Cluster no.	Cluster type	Most similar known cluster	% of genes showing similarity
1	Bacteriocin	none	0
2	Terpene	none	0
3	Others KS	Eicosapentanoic acid	33
4	Arylpolyene-Ladderene	Skylamycin	12
5	NRPS-T1PKS	HSAF	75
6	Butyrolactone	Gamma Butyrolactone	100
7	NRPS	none	0
8	Siderophore	Desferrioxamine B	100
9	Melanin	Melanin	100
10	Terpene	none	0
11	NRPS-T1PKS	Zorbamycin	4
12	Ectoine	Kosinostatin	11
13	Lantipeptide	none	0
14	Bacteriocin	none	0
15	T3PKS	Herboxidiene	6
16	Other	none	0
17	NRPS	none	0
18	NRPS	none	0
19	NRPS	none	0
20	Terpene	Hopene	69
21	NRPS	Calcium-dependent antibiotic	7
22	Terpene	none	0
23	NRPS	Friulimicin	15
24	NRPS	none	0
25	Phenazine	Lomofungin	26
26	NRPS	Griseobactin	29
27	Lasso peptide	SRO15-2005	60
28	Lasso peptide	none	0
29	NRPS	none	0
30	Siderophore	Kinamycin	8
31	NRPS	Daptomycin	18
32	Lantipeptide	none	0
33	NRPS	none	0
34	NRPS	none	0
35	NRPS-T1PKS	Kanamycin	2
36	NRPS	Virginiamycin	11
37	Lantipeptide	Guadinomine	7
38	NRPS	Friulimicin	15
39	NRPS-Others KS	Kirromycin	8
40	Butyrolactone	Skylamycin	14
41	Ectoine	Ectoine	100
42	Thiopeptide-Lantipeptide	none	0
43	T3PKS	Alkylresorcinol	100
44	NRPS	Grisobactin	64
45	Terpene	Isorenieratene	100
46	NRPS	Coelichelin	72
47	NRPS	none	0
48	NRPS	Daptomycin	4
49	NRPS	WS9326	22
50	NRPS	Friulimicin	6
51	NRPS	none	0

Supplementary Table S3. Secondary metabolism gene cluster types in the draft genome of B226SN101, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

SM5			
Cluster no.	Cluster type	Most similar known cluster	% of genes showing similarity
1	Others-T1PKS	none	0
2	Others-KS	none	0
3	Terpene	Isorenieratene	42
4	Other	Gobichelin	11
5	NRPS	Coelichelin	72
6	Bacteriocin	none	0
7	NRPS	Coelichelin	27
8	NRPS	none	0
9	Terpene	Carbapenem_MM_4550	6
10	Terpene	Steffimycin	11
11	Thiopeptide-Lantipeptide	none	0
12	NRPS	none	0
13	Ectoine	Ectoine	100
14	Others-KS	A33853	34
15	T1PKS	Lasalocid	5
16	Butyrolactone	Lactonamycin	5
17	Terpene	none	0
18	T1PKS	Surfactin	8
19	Bacteriocin	none	0
20	NRPS	Mirubactin	50
21	Lantipeptide-Lassoptide	none	0
22	T1PKS	Bafilomycin	33
23	NRPS	Paenibactin	83
24	NRPS-T1PKS	Herboxidiene	15
25	Siderophore	Kinamycin	11
26	T1PKS-NRPS	Myxothiazol	42
27	Melanin	Istamycin	2
28	NRPS	Griseoviridin/Viridogrisien	2
29	Terpene	Carotenoid	27
30	T1PKS	Bafilomycin	83
31	Other KS	none	0
32	T2PKS-Terpene	Spore Pigment	75
33	NRPS	Coelibactin	90
34	Terpene	Hopene	69
35	T1PKS	Indanomycin	17
36	Lantipeptide	none	0
37	T2PKS-Oligosaccharide	Pristinamycin	25
38	NRPS	SW163	28

Supplementary Table S4. Secondary metabolism gene cluster types in the draft genome of SM5, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

SM10			
Cluster no.	Cluster type	Most similar known cluster	% of genes showing similarity
1	Beta-Lactam	Clavams	35
2	Ectoine	Ectoine	100
3	T1PKS	none	0
4	T1PKS	Tetronomycin	18
5	T1PKS	ECO-02301	39
6	Others-T2PKS	Cinerubin B	28
7	T1PKS	Micromonolactam	100
8	T1PKS	none	0
9	Siderophore	Desferrioxamine B	83
10	Terpene-T2PKS	Spore Pigment	83
11	Melanin	Istamycin	4
12	NRPS	Cystathiazole A	11
13	T3PKS	Tetronasin	11
14	T2PKS	Jadomycin	100
15	Lantipeptide	none	0
16	T1PKS	Lasalocid	13
17	Terpene	none	0
18	Siderophore	none	0
19	Bacteriocin	none	0
20	Butyrolactone	Zorbamycin	6
21	Terpene	Steffinycin	19
22	Lantipeptide	Fluostatin	4
23	T1PKS	none	0
24	T1PKS	none	0
25	Terpene	none	0
26	T1PKS	Sporolide	21
27	Bacteriocin	none	0
28	T1PKS	Aculeximycin	23
29	NRPS	Daptomycin	9
30	Bacteriocin	none	0
31	Thiopeptide	none	0
32	Bacteriocin	none	0
33	T1PKS-Bacteriocin	Hygrocin	29
34	Terpene	Hopene	76
35	Lantipeptide	Ansatrienin (mycotrienin)	7
36	NRPS	Tetronasin	3
37	Butyrolactone	Rabelomycin	12
38	Bacteriocin	none	0
39	Other	Laspartomycin	11
40	Oligosaccharide	none	0
41	T1PKS	Ebelactone	50
42	T1PKS	Thuggacin	15
43	T1PKS	none	0
44	T1PKS	none	0

Supplementary Table S5. Secondary metabolism gene cluster types in the draft genome of SM10, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

SM11			
Cluster no.	Cluster type	Most similar known cluster	% of genes showing similarity
1	Lasso peptide	none	0
2	NRPS	Coelichelin	81
3	Other	none	0
4	Melanin	Istamycin	4
5	Terpene	Steffimycin	11
6	Other	none	0
7	T1PKS	Bafilomycin	44
8	Lantipeptide	AmfS	100
9	Ectoïne	Ectoïne	75
10	Thiopeptide-Lantipeptide	none	0
11	NRPS	none	0
12	NRPS	none	0
13	Lantipeptide	none	0
14	T1PKS	Bafilomycin	83
15	T1PKS	Concanamycin A	21
16	NRPS	none	0
17	T3PKS	Alkylresorcinol	100
18	T1PKS	C-1027	18
19	NRPS	A47934	8
20	Terpene-Others KS	Pristinamycin	6
21	Ectoïne	Kosinostatin	11
22	Butyrolactone	none	0
23	Terpene	Platensimycin/Platencin	8
24	Terpene	Isorenieratene	100
25	T1PKS-NRPS	none	0
26	NRPS	Daptomycin	7
27	T1PKS	SGR-PTMs	66
28	T2PKS	Granaticin	21
29	NRPS	Streptolygidin	5
30	Lantipeptide	none	0
31	Other	none	0
32	NRPS	Tetronasin	3
33	T3PKS	Naringenin	100
34	T1PKS	none	0
35	Other KS	Arsenopolyketides	20
36	NRPS-T1PKS	Herboxidiene	4
37	NRPS	Kirromycin	28
38	Trans AT PKS-NRPS-T1PKS	Kirromycin	35
39	Terpene	none	0
40	Lasso peptide	SRO15-2005	80
41	Terpene	Hopene	69
42	Melanin	none	0
43	Bacteriocin	none	0
44	Siderophore	Desferrioxamine B	100
45	Siderophore	none	0
46	NRPS	Friulimicin	21
47	Other	Roseoflavin	100
48	NRPS	Griseobactin	58
49	Terpene	none	0
50	Butyrolactone	Gamma Butyrolactone	100
51	NRPS-Bacteriocin	C-1027	63
52	T2PKS	Chartreusin	33
53	Bacteriocin	none	0
54	Other	Actinomycin	7

Supplementary Table S6. Secondary metabolism gene cluster types in the draft genome of SM11, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

SM12			
Cluster no.	Cluster type	Most similar known cluster	% of genes showing similarity
1	T1PKS	Stambomycin	52
2	Bacteriocin	none	0
3	T1PKS	none	0
4	T1PKS	none	0
5	T1PKS	Guadinomine	7
6	T1PKS	none	0
7	NRPS	none	0
8	Lantipeptide	none	0
9	Other KS	none	0
10	Oligosaccharide	Pellastoren	16
11	T1PKS	none	0
12	T1PKS	none	0
13	Siderophore	none	0
14	T1PKS	none	0
15	Other KS	none	0
16	NRPS	Laspartomycin	6
17	Lantipeptide	none	0
18	T1PKS	none	0
19	Siderophore	none	0
20	Terpene	none	0
21	T1PKS	none	0
22	Lantipeptide	Kanamycin	3
23	T1PKS	Stambomycin	60
24	T1PKS	Nigericin	55
25	Butyrolactone	none	0
26	NRPS	none	0
27	T1PKS	none	0
28	Ectoine	Ectoine	100
29	T1PKS	Concanamycin	21
30	T3PKS	Zorbamycin	4
31	Siderophore	none	0
32	Siderophore	none	0
33	T1PKS	Sanglifehrin A	6
34	NRPS	Marfomycins	8
35	T1PKS	Thuggacin	15
36	NRPS	none	0
37	NRPS	none	0
38	NRPS	none	0
39	B-Lactam	Clavulanic acid	20
40	T1PKS	Concanamycin A	28

Supplementary Table S7. Secondary metabolism gene cluster types in the draft genome of SM12, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

SM16			
Cluster no.	Cluster type	Most similar known cluster	% of genes showing similarity
1	Terpene	Steffimycin	11
2	Lantipeptide	AmfS	40
3	Ectoine	Kosinostatin	9
4	Thiopeptide-Lantipeptide	none	0
5	Siderophore	Desferrioxamine B	100
6	NRPS	Oxazolomycin	6
7	Other	none	0
8	T3PKS	Alkylresorcinol	100
9	Terpene	Hopene	69
10	NRPS-T1PKS	Kanamycin	2
11	Bacteriocin-NRPS	Tetronasin	7
12	NRPS-T1PKS	Heat Stable Antifungal Factor (HSAF)	75
13	NRPS	none	0
14	Others KS-NRPS	Bacillibactin	15
15	Lantipeptide	Guadinomine	7
16	Terpene	Glycopeptidolipid	20
17	NRPS-T1PKS-Lantipeptide	none	0
18	Bacteriocin	none	0
19	T3PKS	Herboxidiene	6
20	Lantipeptide	none	0
21	Lasso peptide	SRO15-2015	80
22	Melanin	Melanin	100
23	Ectoine	Ectoine	100
24	Terpene	none	0
25	Terpene	none	0
26	Terpene	Isorenieratene	85
27	Other KS	Borrelidin	9
28	Other	BE-14106	10
29	Other KS-T1PKS-Terpene	Isorenieratene	85
30	Lantipeptide	SRO15-2015	100
31	Lantipeptide	Labyrinthopeptin	40
32	Butyrolactone	Gamma-Butyrolactone	100
33	Terpene	none	0
34	NRPS	Griseobactin	94
35	NRPS	Coelichelin	81
36	Siderophore	Kinamycin	11
37	NRPS	C-1027	37
38	T1PKS-Butyrolactone	Neocarzinostatin	52
39	NRPS	none	0

Supplementary Table S8. Secondary metabolism gene cluster types in the draft genome of SM16, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

SM17			
Cluster no.	Cluster type	Most similar known cluster	% of genes showing similarity
1	NRPS	none	0
2	Terpene	none	0
3	NRPS	none	0
4	NRPS	none	0
5	T1PKS	none	0
6	Terpene	Hopene	46
7	Lantipeptide	none	0
8	Bacteriocin	Carotenoid	18
9	NRPS	Mannopeptimycin	40
10	Other	Albachelin	20
11	Lantipeptide	SAL-2242	40
12	NRPS	none	0
13	NRPS-T1PKS	SGR-PTMs	10
14	NRPS	none	0
15	NRPS	none	0
16	Ectoine	Ectoine	75
17	T1PKS	FR-008	71
18	Lantipeptide-NRPS-T1PKS	Antimycin	26
19	Siderophore	none	0
20	Bacteriocin	none	0
21	NRPS	none	0
22	Terpene	Albaflavenone	100
23	Terpene	none	0
24	Bacteriocin	none	0
25	T1PKS	none	0
26	T1PKS	none	0
27	T1PKS	none	0
28	T1PKS	Indanomycin	21
29	NRPS	Desotamide	9
30	NRPS	Tertronasin	9
31	Siderophore	Desferrioxamine B	100
32	NRPS	none	0
33	T3PKS	Herboxidiene	12
34	Terpene	none	0
35	T1PKS	none	0
36	NRPS	none	0
37	NRPS	none	0
38	NRPS	none	0
39	NRPS	none	0
40	T1PKS	ECO-02301	25
41	NRPS	none	0
42	NRPS	none	0
43	T1PKS	none	0
44	T1PKS	none	0
45	T1PKS	none	0
46	Siderophore	none	0
47	T1PKS	Halstoctacosanolide	77
48	NRPS	none	0

Supplementary Table S9. Secondary metabolism gene cluster types in the draft genome of SM17, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

SM18			
Cluster no.	Cluster type	Most similar known cluster	% of genes showing similarity
1	Butyrolactone	Lactonamycin	5
2	Other KS	A33853	34
3	NRPS	Coelibactin	27
4	Terpene	Carotenoid	27
5	NRPS	Paenibactin	66
6	Melanin	Melanin	100
7	Lantipeptide	none	100
8	T1PKS	Lasalocid	5
9	Terpene	Steffimycin	13
10	Other KS	none	0
11	T1PKS	Kirromycin	3
12	NRPS	Coelichelin	27
13	NRPS	Coelichelin	72
14	Terpene	Isorenieratene	57
15	T1PKS-NRPS	Cystothiazole A	17
16	NRPS	none	0
17	Other KS-NRPS	SW-163	28
18	T1PKS	none	0
19	Other KS-T1PKS	none	0
20	NRPS	Mirubactin	50
21	Terpene	none	0
22	Siderophore	none	0
23	Lantipeptide-Lasso peptide	Lipopolysaccharide	5
24	T1PKS	Salinomycin	18
25	Terpene	Hopene	69
26	T1PKS	FD-891	62
27	NRPS-T1PKS	Herboxidiene	15
28	Oligosaccharide-T2PKS	Granaticin	43
29	Bacteriocin	none	0
30	Bacteriocin	none	0
31	T1PKS	Bafilomycin	83
32	NRPS	none	0
33	Ectoine	Ectoine	100
34	Terpene-T2PKS	Spore Pigment	75
35	Terpene	Carbapenem MM 4550	10
36	T1PKS	none	0
37	T1PKS	Bafilomycin	33
38	NRPS	Coelibactin	100
39	NRPS	Mannopectimycin	7
40	T1PKS	none	0
41	Lantipeptide	none	0

Supplementary Table S10. Secondary metabolism gene cluster types in the draft genome of SM18, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

SM1			
Cluster no.	Cluster type	Most similar known cluster	% of genes showing similarity
1	NRPS	none	0
2	Other KS	none	0
3	NRPS	none	0
4	NRPS	none	0
5	Lantipeptide	none	0
6	NRPS	Erythrochelin	42
7	Siderophore	Desferrioxamine B	100
8	Terpene	none	0
9	Siderophore	Kinamycin	8
10	NRPS	none	0
11	Terpene	Carotenoid	27
12	Lantipeptide	none	0
13	NRPS	none	0
14	T1PKS	Micromonolactam	100
15	T2PKS	Spore Pigment	83
16	Butyrolactone	none	0
17	Terpene	Isorenieratene	28
18	Terpene	Hopene	15
19	Other KS	none	0
20	Terpene	none	0
21	NRPS	none	0
22	Other	none	0
23	Bacteriocin	none	0
24	T1PKS	none	0
25	NRPS	none	0
26	T1PKS-NRPS	Myxalamid	45
27	T1PKS	none	0
28	Bacteriocin	none	0

Supplementary Table S11. Secondary metabolism gene cluster types in the draft genome of SM1, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

FMC008			
Cluster no.	Cluster type	Most similar known cluster	% of genes showing similarity
1	Terpene	none	0
2	Ectoine	Ectoine	100
3	NRPS	Complestatin	25
4	Other	Aureothin	22
5	Terpene	none	0
6	Siderophore	none	0
7	Bacteriocin	none	0
8	T1PKS	none	0
9	Terpene	Phosphonoglycans	6
10	NRPS	Desotamide	13
11	Other	Antimycin	13
12	NRPS	none	0
13	Terpene	none	0
14	Other	none	0
15	Terpene	none	0

Supplementary Table S12. Secondary metabolism gene cluster types in the draft genome of FMC008, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

SM14			
Cluster no.	Cluster type	Most similar known cluster	% of genes showing similarity
1	T1PKS	none	0
2	T1PKS	none	0
3	B-Lactam	Clavulanic acid	20
4	Siderophore	none	0
5	T1PKS	none	0
6	Lantipeptide	none	0
7	Oligosaccharide	Pellastoren	16
8	T1PKS	none	0
9	T1PKS	Aculeximycin	23
10	T1PKS	none	0
11	NRPS	Calium-dependent antibiotic	12
12	Thiopeptide=Lantipeptide	none	0
13	T3PKS	Zorbamycin	4
14	NRPS	Tetronasin	3
15	T1PKS	none	0
16	Siderophore	none	0
17	Bacteriocin	none	0

Supplementary Table S13. Secondary metabolism gene cluster types in the draft genome of SM14, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.

SM9			
Cluster no.	Cluster type	Most similar known cluster	% of genes showing similarity
1	Ectoine	Ectoine	100
2	Terpene	none	0
3	Siderophore	none	0
4	NRPS	Antimycin	20
5	T1PKS	Frontalamides	28
6	Terpene	Carotenoid	18
7	Terpene	none	0
8	Bacteriocin	none	0
9	Siderophore	none	0
10	Terpene	none	0
11	Other	none	0
12	Terpene	none	0
13	T1PKS	none	0
14	T1PKS	none	0
15	NRPS	Complestatin	25
16	Terpene	Hopene	15

Supplementary Table S14. Secondary metabolism gene cluster types in the draft genome of SM9, most similar known clusters and % of genes showing similarity to known clusters as determined by antiSMASH.