Genome mining, microbial interactions and molecular networking reveals new dibromoalterochromides from strains of *Pseudoalteromonas* of Coiba National Park- Panama.

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Table S1. Identified BGC in *Pseudoalteromonas* by antiSMASH

Cluster	Input accession number	Input name *Pseudoalteromonas* sp.	Gene cluster type	from	to	Most similar known cluster (MIBiG)	Similarity	MIBiG BGC-ID
1	c00002_NODE_7_length_275579_cov_91.798942	CO109Y	putative	209438	216420	-		
2	c00008_NODE_27_length_28775_cov_95.895672	CO109Y	putative	12029	20440	Exopolysaccharide	13%	BGC0000766_c1
3	c00013_NODE_28_length_27831_cov_96.346797	CO109Y	putative	8665	25857	Emulsan	13%	BGC0000760_c1
4	c00022_NODE_8_length_245287_cov_75.255230	CO109Y	fatty acid	156299	177372	-		-
5	c00025_NODE_5_length_301484_cov_74.847426	CO109Y	bacteriocin	74499	85362	-		-
6	c00025_NODE_5_length_301484_cov_74.847426	CO109Y	fatty acid	269827	291725	Xenocyloins	25%	BGC0000189_c1
7	c00028_NODE_2_length_436453_cov_71.787067	CO109Y	saccharide	120799	160399	Taxlllaid	4%	BGC0001133_c1
8	c00028_NODE_2_length_436453_cov_71.787067	CO109Y	putative	194074	198925	-		-
9	c00028_NODE_2_length_436453_cov_71.787067	CO109Y	putative	292380	299876	-		-
10	c00028_NODE_2_length_436453_cov_71.787067	CO109Y	putative	319275	326198	-		-
11	c00034_NODE_6_length_297666_cov_83.368656	CO109Y	putative	124035	140946	-		-
12	c00035_NODE_3_length_421190_cov_82.305811	CO109Y	siderophore	98509	110908	Desferrioxamine B	60%	BGC0000941_c1
13	c00035_NODE_3_length_421190_cov_82.305811	CO109Y	fatty acid	373851	395065	Alterochromides	9%	BGC0000299_c1
14	c00039_NODE_4_length_315195_cov_104.192787	CO109Y	putative	173020	188999	-		-
15	c00042_NODE_1_length_523833_cov_79.969463	CO109Y	putative	24028	39627	-		-
16	c00042_NODE_1_length_523833_cov_79.969463	CO109Y	putative	82738	88707	-		-
17	c00042_NODE_1_length_523833_cov_79.969463	CO109Y	arylpolyene	123335	166888	APE Vf	45%	BGC0000837_c1
18	c00042_NODE_1_length_523833_cov_79.969463	CO109Y	putative	222628	230409	-		-
19	c00044_NODE_17_length_70298_cov_94.478190	CO109Y	putative	49844	55847	-		-
1	c00001_NODE_16_length_57928_cov_96.696012	CO133X	putative	36924	43300	-		-
2	c00002_NODE_6_length_314560_cov_90.082326	CO133X	fatty acid	298607	314560	Alterochromides	9%	BGC0000299_c1
3	c00004_NODE_8_length_185114_cov_100.635624	CO133X	resorcinol	15829	56938	-		-
4	c00004_NODE_8_length_185114_cov_100.635624	CO133X	putative	161210	174968	-		-

Table S1. Identified BGC in *Pseudoalteromonas* by antiSMASH (*Continuation*)

Cluster	Input accession number	Input name *Pseudoalteromonas* sp.	Gene cluster type	from	to	Most similar known cluster (MIBiG)	Similarity	MIBiG BGC-ID
5	c00005_NODE_4_length_398869_cov_98.406831	CO133X	putative	186350	199672	Lipopolysaccharide	18%	BGC0000773_c1
6	c00005_NODE_4_length_398869_cov_98.406831	CO133X	saccharide	214996	242108	O-antigen	10%	BGC0000788_c1
7	c00011_NODE_5_length_322967_cov_90.495317	CO133X	fatty acid	36504	60082	-		-
8	c00017_NODE_14_length_75731_cov_85.392815	CO133X	bacteriocin	1	6155	-		-
9	c00018_NODE_2_length_617072_cov_80.445482	CO133X	fatty acid	151522	173420	Xenocyloins	25%	BGC0000189_c1
10	c00018_NODE_2_length_617072_cov_80.445482	CO133X	saccharide	303578	343175	Taxlllaid	4%	BGC0001133_c1
11	c00018_NODE_2_length_617072_cov_80.445482	CO133X	putative	374102	378942	-		
12	c00018_NODE_2_length_617072_cov_80.445482	CO133X	putative	493014	511833	Capsular polysaccharide	18%	BGC0000729_c1
13	c00018_NODE_2_length_617072_cov_80.445482	CO133X	putative	519770	526669	-		-
14	c00022_NODE_1_length_907290_cov_84.548418	CO133X	putative	189606	195351	-		-
15	c00022_NODE_1_length_907290_cov_84.548418	CO133X	fatty acid	523690	544763	-		-
16	c00022_NODE_1_length_907290_cov_84.548418	CO133X	siderophore	583940	595802	Desferrioxamine B	40%	BGC0000941_c1
17	c00022_NODE_1_length_907290_cov_84.548418	CO133X	putative	705428	711382	-		-
18	c00022_NODE_1_length_907290_cov_84.548418	CO133X	arylpolyene	749445	792998	APE Vf	40%	BGC0000837_c1
19	c00026_NODE_3_length_446844_cov_94.819338	CO133X	putative	227732	233664	-		-
1	c00003_NODE_3_length_435531_cov_70.772293	CO302Y	saccharide	122027	161624	Taxlllaid	4%	BGC0001133_c1
2	c00003_NODE_3_length_435531_cov_70.772293	CO302Y	putative	192551	197391	-		-
3	c00003_NODE_3_length_435531_cov_70.772293	CO302Y	putative	311463	330282	Capsular polysaccharide	18%	BGC0000729_c1
4	c00003_NODE_3_length_435531_cov_70.772293	CO302Y	putative	338219	345118	-		-
5	c00008_NODE_17_length_57928_cov_86.112064	CO302Y	putative	36924	43300	-		-
6	c00009_NODE_4_length_398869_cov_88.401239	CO302Y	putative	186350	199672	Lipopolysaccharide	18%	BGC0000773_c1
7	c00009_NODE_4_length_398869_cov_88.401239	CO302Y	saccharide	214996	242108	O-antigen	10%	BGC0000788_c1
8	c00016_NODE_15_length_75743_cov_75.636783	CO302Y	bacteriocin	1	6167	-		-

Table S1. Identified BGC in *Pseudoalteromonas* by antiSMASH (*Continuation*)

Cluster	Input accession number	Input name *Pseudoalteromonas* sp.	Gene cluster type	from	to	Most similar known cluster (MIBiG)	Similarity	MIBiG BGC-ID
9	c00021_NODE_6_length_314546_cov_79.228725	CO302Y	fatty acid	298607	314546	Alterochromides	9%	BGC0000299_c1
10	c00022_NODE_1_length_907290_cov_75.576858	CO302Y	putative	189606	195351	-		-
11	c00022_NODE_1_length_907290_cov_75.576858	CO302Y	fatty acid	523690	544763	-		-
12	c00022_NODE_1_length_907290_cov_75.576858	CO302Y	siderophore	583940	595802	Desferrioxamine B	40%	BGC0000941_c1
13	c00022_NODE_1_length_907290_cov_75.576858	CO302Y	putative	705428	711382	-		-
14	c00022_NODE_1_length_907290_cov_75.576858	CO302Y	arylpolyene	749445	792998	APE Vf	40%	BGC0000837_c1
15	c00023_NODE_8_length_185114_cov_91.426385	CO302Y	resorcinol	15829	56938	-		-
16	c00023_NODE_8_length_185114_cov_91.426385	CO302Y	putative	161210	174968	-		-
17	c00024_NODE_5_length_322967_cov_79.767407	CO302Y	fatty acid	36504	60082	-		-
18	c00026_NODE_2_length_446850_cov_83.984274	CO302Y	putative	227738	233670	-		-
19	c00029_NODE_9_length_181499_cov_73.333543	CO302Y	fatty acid	151545	173443	Xenocyloins	25%	BGC0000189_c1
1	c00003_NODE_10_length_161627_cov_96.675339	CO325X	fatty acid	53745	74857	-		
2	c00009_NODE_1_length_593470_cov_98.282885	CO325X	siderophore	137198	149594	Desferrioxamine B	60%	BGC0000941_c1
3	c00009_NODE_1_length_593470_cov_98.282885	CO325X	resorcinol	206269	247369	-		
4	c00009_NODE_1_length_593470_cov_98.282885	CO325X	putative	275440	284485	-		
5	c00009_NODE_1_length_593470_cov_98.282885	CO325X	putative	544910	551250	-		
6	c00012_NODE_8_length_195902_cov_86.100876	CO325X	putative	163725	172598	-		
7	c00013_NODE_2_length_386893_cov_96.205092	CO325X	putative	204103	211799	-		
8	c00013_NODE_2_length_386893_cov_96.205092	CO325X	putative	299298	307528	-		
9	c00019_NODE_5_length_274675_cov_86.289230	CO325X	putative	15853	23851	-		
10	c00019_NODE_5_length_274675_cov_86.289230	CO325X	putative	205727	212760	-		
11	c00022_NODE_3_length_311950_cov_92.901688	CO325X	fatty acid	11490	32704	Alterochromides	9%	BGC0000299_c1
12	c00028_NODE_15_length_91940_cov_92.735744	CO325X	arylpolyene	1	30285	APE Vf	40%	BGC0000837_c1

Table S1. Identified BGC in *Pseudoalteromonas* by antiSMASH (*Continuation*)

Cluster	Input accession number	Input name *Pseudoalteromonas* sp.	Gene cluster type	from	to	Most similar known cluster (MIBiG)	Similarity	MIBiG BGC-ID
13	c00029_NODE_29_length_18399_cov_109.616308	CO325X	putative	1320	8776	-		
14	c00034_NODE_16_length_88477_cov_89.274378	CO325X	bacteriocin	34655	45500	-		
15	c00035_NODE_6_length_236743_cov_103.452938	CO325X	saccharide	179287	220707	O-antigen	22%	BGC0000784_c1
16	c00036_NODE_11_length_132357_cov_94.488917	CO325X	putative	32163	37566	-		
1	c00002_NODE_22_length_77183_cov_56.043421	CO342X	fatty acid	1	21213	-		-
2	c00013_NODE_39_length_6543_cov_70.826632	CO342X	nrps	1	6543	-		-
3	c00014_NODE_13_length_160050_cov_62.437136	CO342X	putative	44802	64448	-		-
4	c00017_NODE_11_length_173480_cov_64.738107	CO342X	putative	93837	96329	-		-
5	c00019_NODE_42_length_4032_cov_72.488496	CO342X	nrps	1	4032	-		-
6	c00020_NODE_21_length_80338_cov_74.548211..	CO342X	nrps	1	47394	Bacillibactin	60%	BGC0001185_c1
7	c00022_NODE_45_length_2030_cov_70.160266	CO342X	nrps	1	2030	-		-
8	c00026_NODE_20_length_90752_cov_57.841643	CO342X	nrps	1	27150	-		-
9	c00028_NODE_14_length_148454_cov_76.387250	CO342X	lantipeptide-nrps	11199	96314	-		-
10	c00032_NODE_7_length_243401_cov_61.083120	CO342X	bacteriocin	63360	74310	-		-
11	c00032_NODE_7_length_243401_cov_61.083120	CO342X	bacteriocin	154005	164835	-		-
12	c00032_NODE_7_length_243401_cov_61.083120	CO342X	nrps	191175	243401	-		-
13	c00034_NODE_17_length_138819_cov_71.084877	CO342X	putative	44698	51855	-		-
14	c00034_NODE_17_length_138819_cov_71.084877	CO342X	t1pks-nrps	67464	138819	-		-
15	c00036_NODE_43_length_3161_cov_133.473735	CO342X	nrps	1	3161	-		-
16	c00038_NODE_12_length_162668_cov_63.201819	CO342X	acyl_amino_acids	62686	123579	-		-
17	c00039_NODE_16_length_138882_cov_54.400915	CO342X	t1pks-nrps	14743	64084	-		-
18	c00039_NODE_16_length_138882_cov_54.400915	CO342X	putative	95443	104283	-		-
19	c00040_NODE_2_length_465641_cov_53.519119	CO342X	putative	186168	197739	-		-

Table S1. Identified BGC in *Pseudoalteromonas* by antiSMASH (*Continuation*)

Cluster	Input accession number	Input name *Pseudoalteromonas* sp.	Gene cluster type	from	to	Most similar known cluster (MIBiG)	Similarity	MIBiG BGC-ID
20	c00040_NODE_2_length_465641_cov_53.519119	CO342X	thiopeptide	316700	354922	-		-
21	c00041_NODE_1_length_550994_cov_55.846605	CO342X	fatty acid	792	21862	-		-
22	c00041_NODE_1_length_550994_cov_55.846605	CO342X	putative	305432	310734	-		-
23	c00041_NODE_1_length_550994_cov_55.846605	CO342X	putative	477403	497639	-		-
24	c00043_NODE_26_length_59499_cov_66.152620	CO342X	saccharide	1	45690	O-antigen	16%	BGC0000784_c1
25	c00044_NODE_3_length_376664_cov_66.543338	CO342X	putative	35353	40268	-		-
26	c00044_NODE_3_length_376664_cov_66.543338	CO342X	putative	354091	367115	-		-
27	c00046_NODE_8_length_214299_cov_75.176270	CO342X	nrps	430	55842	-		-
28	c00046_NODE_8_length_214299_cov_75.176270	CO342X	putative	77260	95787	-		-
29	c00048_NODE_9_length_203384_cov_56.489186	CO342X	fatty acid	16889	38103	-		-
30	c00048_NODE_9_length_203384_cov_56.489186	CO342X	fatty acid	155577	176815	-		-
31	c00049_NODE_5_length_307095_cov_59.338703	CO342X	bacteriocin	113978	124814	-		-
32	c00049_NODE_5_length_307095_cov_59.338703	CO342X	putative	192643	205171	-		-
33	c00049_NODE_5_length_307095_cov_59.338703	CO342X	ladderane-nrps	267716	307095	Alterochromides	95%	BGC0000299_c1
34	c00051_NODE_19_length_119059_cov_73.997319	CO342X	putative	20924	29279	Bacillomycin	20%	BGC0001090_c1
35	c00053_NODE_10_length_200666_cov_58.759807	CO342X	putative	65829	81657	-		-
36	c00054_NODE_18_length_133308_cov_62.288101	CO342X	nrps	1	27212	Bromoalterochromides	14%	BGC0000314_c1
37	c00057_NODE_40_length_6534_cov_70.430695	CO342X	other	1	6534	-		-
1	c00004_NODE_9_length_211179_cov_70.167979	CO348	putative	188544	201621	-		-
2	c00005_NODE_14_length_148729_cov_72.514134	CO348	putative	35116	40031	-		-
3	c00006_NODE_3_length_380609_cov_76.711850	CO348	nrps	533	55945	-		-
4	c00006_NODE_3_length_380609_cov_76.711850	CO348	putative	81457	94510	-		-
5	c00006_NODE_3_length_380609_cov_76.711850	CO348	lantipeptide-nrps	239295	318184	-		

Table S1. Identified BGC in *Pseudoalteromonas* by antiSMASH (*Continuation*)

Cluster	Input accession number	Input name *Pseudoalteromonas* sp.	Gene cluster type	from	to	Most similar known cluster (MIBiG)	Similarity	MIBiG BGC-ID
6	c00007_NODE_1_length_503294_cov_63.287991	CO348	putative	477	9977	-		-
7	c00007_NODE_1_length_503294_cov_63.287991	CO348	t1pks-nrps	174883	224224	-		-
8	c00007_NODE_1_length_503294_cov_63.287991	CO348	putative	255943	264782	-		-
9	c00007_NODE_1_length_503294_cov_63.287991	CO348	fatty acid	326556	347794	-		-
10	c00007_NODE_1_length_503294_cov_63.287991	CO348	fatty acid	465210	486424	-		-
11	c00008_NODE_8_length_219423_cov_61.386497	CO348	putative	53017	64740	-		-
12	c00012_NODE_6_length_264646_cov_73.560581	CO348	saccharide	41594	91570	Emulsan	18%	BGC0000760_c1
13	c00012_NODE_6_length_264646_cov_73.560581	CO348	fatty acid-t1pks-nrps	160825	264646	-		-
14	c00016_NODE_10_length_208930_cov_69.532763	CO348	putative	71189	90845	-		-
15	c00018_NODE_4_length_314892_cov_66.600618	CO348	bacteriocin	121569	132405	-		-
16	c00018_NODE_4_length_314892_cov_66.600618	CO348	putative	200538	213066	-		-
17	c00018_NODE_4_length_314892_cov_66.600618	CO348	ladderane-nrps	275404	314892	Alterochromides	95%	BGC0000299_c1
18	c00019_NODE_45_length_1795_cov_171.722870	CO348	other	1	1795	-		-
19	c00027_NODE_18_length_122393_cov_75.665127	CO348	t1pks-nrps	605	85780	Enterobactin	8%	BGC0000343_c1
20	c00029_NODE_7_length_262814_cov_66.321357	CO348	putative	18754	24056	-		-
21	c00029_NODE_7_length_262814_cov_66.321357	CO348	putative	192593	214183	-		-
22	c00035_NODE_15_length_133296_cov_67.349675	CO348	nrps	1	26760	Bromoalterochromides	14%	BGC0000314_c1
23	c00036_NODE_19_length_112961_cov_63.342390	CO348	fatty acid	772	21842	-		-
24	c00038_NODE_40_length_7178_cov_89.174722	CO348	nrps	1	7178	-		-
25	c00043_NODE_13_length_149429_cov_69.951951	CO348	putative	92383	99345	-		-
26	c00043_NODE_13_length_149429_cov_69.951951	CO348	putative	111972	121333	-		-
27	c00046_NODE_2_length_401822_cov_70.165380	CO348	bacteriocin	250977	261927	-		-
28	c00046_NODE_2_length_401822_cov_70.165380	CO348	bacteriocin	338107	348937	-		-

Table S1. Identified BGC in *Pseudoalteromonas* by antiSMASH (*Continuation*)

Cluster	Input accession number	Input name *Pseudoalteromonas* sp.	Gene cluster type	from	to	Most similar known cluster (MIBiG)	Similarity	MIBiG BGC-ID
29	c00046_NODE_2_length_401822_cov_70.165380	CO348	nrps	373078	401822	-		-
30	c00048_NODE_23_length_78873_cov_67.657046	CO348	other	1	22050	-		-

Table S2. MultiGeneBlast Results per category

Query Cluster	Query antiSMASH category	Hit Cluster	Hit antiSMAH Category	Total Score	Cumulative Blast score	BGC similarity (%) *
CO342X_Cluster002	NRPS	CO342X_Cluster002	NRPS	4.5	3991	100
		CO348_cluster29	NRPS	3	750	31
		CO348_cluster005	lantipeptide-nrps	2	1634	40
		CO342X_cluster009	lantipeptide-nrps	2	1633	40
		CO342X_cluster014	T1pks-nrps	2	1460	40
		CO348_cluster013	Fatty acid-T1pks-nrps	2	1442	40
		CO342X_cluster012	NRPS	2	1341	35
		CO342X_cluster027	NRPS	2	1118	53
		CO348_cluster003	NRPS	2	1107	46
		CO348_cluster019	T1pks-nrps	2	438	45
		CO342X_cluster006	NRPS	2	201	47
		CO348_cluster24	NRPS	1	678	39
		CO342X_cluster006	NRPS	1	50	32
CO342X_Cluster005	NRPS	CO348_cluster005	Lantipeptide-nrps	1	1490	41
		CO342X_cluster009	Lantipeptide-nrps	1	1484	40
		CO342X_cluster014	T1pks-nrps	1	1331	34
		CO348_cluster013	Fatty acid-T1pks-nrps	1	1325	34
		CO342X_cluster012	NRPS	1	1203	31
		CO342X_cluster002	NRPS	1	1170	52
		CO348_cluster24	NRPS	1	674	39
		CO348_cluster019	T1pks-nrps	1	409	31
		CO348_cluster019	T1pks-nrps	1	64	36
CO342X_Cluster006	NRPS	CO342X_cluster006	NRPS	54	29779	100
		CO348_cluster019	T1pks-nrps	25.5	10344	46
		CO342X_cluster014	T1pks-nrps	2	330	37
		CO348_cluster013	Fatty acid-T1pks-nrps	2	325	37
		CO348_cluster24	NRPS	2	259	31
		CO342X_cluster002	NRPS	2	250	32
		CO342X_cluster027	NRPS	1	168	37
		CO348_cluster003	NRPS	1	165	44
		CO348_cluster29	NRPS	1	123	34
		CO348_cluster013	Fatty acid-T1pks-nrps	1	108	33

* The BGC similarity percentage is shown for the core biosynthetic gene.

Table S2. MultiGeneBlast Results per category (*Continuation*)

Query Cluster	Query antiSMASH category	Hit Cluster	Hit antiSMAH Category	Total Score	Cumulative Blast score	BGC similarity (%) *
CO342X_Cluster007	NRPS	CO348_cluster019	T1pks-nrps	1	150	45
CO342X_Cluster008	NRPS	CO342X_Cluster008	NRPS	25.5	17615	100
		CO348_cluster019	T1pks-nrps	4	700	43
CO342X_Cluster009	Lantipeptide-nrps	CO342X_Cluster009	Lantipeptide-nrps	82	52530	100
		CO348_cluster005	Lantipeptide-nrps	69	49011	99
		CO348_cluster019	T1pks-nrps	4	582	33
		CO342X_cluster014	Lantipeptide-nrps	3	2213	32
		CO348_cluster013	Fatty acid-T1pks-nrps	3	2212	32
		CO342X_cluster002	NRPS	3	1612	34
		CO348_cluster29	NRPS	3	259	0
		CO342X_cluster012	NRPS	2	1318	31
		CO348_cluster24	NRPS	2	1214	32
		CO342X_cluster008	NRPS	1	443	0
CO342X_Cluster012	NRPS	CO342X_cluster012	NRPS	40.5	28518	100
		CO348_cluster29	NRPS	12	3883	99
		CO342X_cluster002	NRPS	3	1338	34
		CO342X_cluster009	Lantipeptide-nrps	3	1317	31
		CO348_cluster005	Lantipeptide-nrps	3	1316	31
		CO348_cluster019	T1pks-nrps	3	157	33
		CO348_cluster24	NRPS	2	481	34
		CO348_cluster013	Fatty acid-T1pks-nrps	2	310	0
		CO348_cluster019	T1pks-nrps	1	268	0
CO342X_Cluster014	T1pks-nrps	CO342X_cluster014	T1pks-nrps	59	46127	100
		CO348_cluster013	Fatty acid-T1pks-nrps	55	43681	97
		CO348_cluster019	T1pks-nrps	4.5	1507	40
		CO342X_cluster009	Lantipeptide-nrps	3	2244	32
		CO348_cluster005	Lantipeptide-nrps	3	2241	31
		CO342X_cluster002	NRPS	3	1461	35
		CO348_cluster24	NRPS	2	872	32
		CO342X_cluster008	NRPS	1	516	0
		CO342X_cluster006	NRPS	1	71	32

* The BGC similarity percentage is shown for the core biosynthetic gene.

Table S2. MultiGeneBlast Results per category (*Continuation*)

Query Cluster	Query antiSMASH category	Hit Cluster	Hit antiSMAH Category	Total Score	Cumulative Blast score	BGC similarity (%) *
CO342X_Cluster015	NRPS	CO348_cluster005	Lantipeptide-nrps	1	1311	38
		CO342X_cluster009	Lantipeptide-nrps	1	1309	38
		CO342X_cluster014	T1pks-nrps	1	1277	39
		CO348_cluster013	Fatty acid-T1pks-nrps	1	1268	39
		CO348_cluster019	T1pks-nrps	1	1244	31
		CO342X_cluster002	NRPS	1	1185	55
		CO342X_cluster012	NRPS	1	1111	32
		CO342X_cluster027	NRPS	1	972	35
		CO348_cluster003	NRPS	1	969	35
		CO348_cluster24	NRPS	1	585	31
CO342X_Cluster017	T1pks-nrps	CO342X_Cluster017	T1pks-nrps	56	31418	100
		CO348_cluster007	T1pks-nrps	37.5	24594	98
CO342X_Cluster027	NRPS	CO342X_cluster027	NRPS	68.5	35514	100
		CO348_cluster003	NRPS	65.5	34569	99
		CO348_cluster017	ladderane-nrps	4	1057	34
		CO342X_cluster002	NRPS	3	1112	31
		CO342X_cluster033	ladderane-nrps	3	752	34
CO342X_Cluster033	ladderane-nrps	CO342X_cluster033	ladderane-nrps	31	17938	100
		CO348_cluster017	ladderane-nrps	29.5	17701	99
		CO348_cluster003	NRPS	2	752	34
		CO342X_cluster027	NRPS	2	752	34
		CO348_cluster013	Fatty acid-T1pks-nrps	2	256	32
		CO348_cluster013	Fatty acid-T1pks-nrps	1	434	32
CO342X_Cluster036	NRPS	CO342X_cluster036	NRPS	25	16740	100
		CO348_cluster22	NRPS	16	11798	98
		CO342X_cluster027	NRPS	8.5	4403	0
		CO348_cluster019	T1pks-nrps	1	286	0
		CO348_cluster019	T1pks-nrps	1	58	37
CO348_Cluster003	NRPS	CO348_cluster003	NRPS	66.5	35149	100
		CO342X_cluster027	NRPS	64	345117	99
		CO348_cluster017	ladderane-nrps	4	1054	34
		CO342X_cluster002	NRPS	3	1099	31
		CO342X_cluster033	ladderane-nrps	3	753	34

[*] The BGC similarity percentage is shown for the core biosynthetic gene.

Table S2. MultiGeneBlast Results per category (*Continuation*)

Query Cluster	Query antiSMASH category	Hit Cluster	Hit antiSMAH Category	Total Score	Cumulative Blast score	BGC similarity (%) *
CO348_Cluster005	Lantipeptide-nrps	CO348_cluster005	Lantipeptide-nrps	71.5	50088	100
		CO342X_cluster009	Lantipeptide-nrps	69	49060	99
		CO348_cluster019	T1pks-nrps	4	1010	31
		CO342X_cluster014	T1pks-nrps	3	2209	32
		CO348_cluster013	fatty_acid-T1pks-nrps	3	2207	32
		CO342X_cluster002	NRPS	3	1617	35
		CO342X_cluster012	NRPS	3	1316	31
		CO348_cluster24	NRPS	2	1211	36
		CO348_cluster29	NRPS	2	117	32
		CO342X_cluster008	NRPS	1	443	36
CO348_Cluster007	T1pks-nrps	CO348_Cluster007	T1pks-nrps	62	30669	100
		CO342X_cluster017	T1pks-nrps	37.5	24594	98
CO348_Cluster013	Fatty acid-T1pks-nrps	CO348_cluster013	Fatty acid-T1pks-nrps	109.5	64829	100
		CO342X_cluster014	T1pks-nrps	55	43696	95
		CO348_cluster019	T1pks-nrps	4	1220	34
		CO342X_cluster009	Lantipeptide-nrps	3	2241	31
		CO348_cluster005	Lantipeptide-nrps	3	2238	31
		CO342X_cluster002	NRPS	3	1444	35
		CO348_cluster024	NRPS	2	869	33
		CO348_cluster017	ladderane-nrps	2	563	34
		CO342X_cluster033	ladderane-nrps	2	562	34
		CO342X_cluster006	NRPS	2	362	31
		CO342X_cluster012	NRPS	2	310	0
		CO342X_cluster008	NRPS	1	515	0
		CO342X_cluster006	NRPS	1	70	37
CO348_Cluster017	ladderane-nrps	CO348_cluster017	ladderane-nrps	29.5	17854	100
		CO342X_cluster033	ladderane-nrps	29.5	17701	99
		CO348_cluster003	NRPS	2	755	34
		CO342X_cluster027	NRPS	2	755	34
		CO348_cluster005	Lantipeptide-nrps	2	382	34
		CO348_cluster013	fatty_acid-T1pks-nrps	2	259	32
		CO348_cluster013	fatty_acid-T1pks-nrps	1	436	32

[*] The BGC similarity percentage is shown for the core biosynthetic gene.

Table S2. MultiGeneBlast Results per category (*Continuation*)

Query Cluster	Query antiSMASH category	Hit Cluster	Hit antiSMAH Category	Total Score	Cumulative Blast score	BGC similarity (%) *
CO348_Cluster019	T1pks-nrps	CO348_cluster019	T1pks-nrps	73	58406	100
		CO342X_cluster006	NRPS	39.5	17351	42
		CO342X_cluster002	NRPS	6	438	36
		CO342X_cluster014	T1pks-nrps	4.5	1508	37
		CO348_cluster005	Lantipeptide-nrps	4	1013	34
		CO348_cluster013	fatty_acid-T1pks-nrps	3	1219	36
		CO342X_cluster008	NRPS	3	706	31
		CO342X_cluster009	Lantipeptide-nrps	3	583	34
		CO348_cluster29	NRPS	2.5	434	33
		CO342X_cluster012	NRPS	2	425	33
		CO348_cluster003	NRPS	2	119	32
		CO342X_cluster027	NRPS	1	119	32
CO348_Cluster022	NRPS	CO342X_cluster036	NRPS	25	16200	98
		CO348_cluster22	NRPS	16	12030	100
		CO342X_cluster027	NRPS	8.5	4511	0
		CO348_cluster019	T1pks-nrps	1	58	36
CO348_Cluster024	NRPS	CO348_cluster24	NRPS	2.5	3746	100
		CO342X_cluster014	T1pks-nrps	2.5	1116	33
		CO342X_cluster009	Lantipeptide-nrps	2	1215	36
		CO348_cluster005	Lantipeptide-nrps	2	1211	33
		CO348_cluster013	fatty_acid-T1pks-nrps	2	863	33
		CO348_cluster019	T1pks-nrps	2	507	33
		CO342X_cluster012	NRPS	2	481	34
		CO342X_cluster006	NRPS	1	46	31
CO348_Cluster029	NRPS	CO348_cluster029	NRPS	40	16127	100
		CO342X_cluster012	NRPS	12	3883	99
		CO348_cluster019	T1pks-nrps	2.5	434	33
		CO342X_cluster002	NRPS	2	740	31
		CO348_cluster005	Lantipeptide-nrps	1	80	0
		CO342X_cluster009	Lantipeptide-nrps	1	44	0

[*] The BGC similarity percentage is shown for the core biosynthetic gene.

Table S2. MultiGeneBlast Results per category (*Continuation*)

Query Cluster	Query antiSMASH category	Hit Cluster	Hit antiSMAH Category	Total Score	Cumulative Blast score	BGC similarity (%) *
CO109Y_cluster005	Bacteriocin	CO109Y_cluster005	Bacteriocin	16	6168	100
		CO348_cluster015	Bacteriocin	16	3394	72
		CO342X_cluster031	Bacteriocin	15.5	3411	72
		CO325X_cluster014	Bacteriocin	11.5	2108	72
		CO302Y_cluster008	Bacteriocin	8.5	3025	83
		CO302Y_cluster008	Bacteriocin	8.5	3025	83
CO133X_cluster008	Bacteriocin	CO133X_cluster008	Bacteriocin	10	3569	100
		CO302Y_cluster008	Bacteriocin	10	3567	100
		CO109Y_cluster005	Bacteriocin	8.5	3026	83
		CO348_cluster015	Bacteriocin	8.5	2023	69
		CO342X_cluster031	Bacteriocin	8	2043	70
		CO325X_cluster014	Bacteriocin	4	738	68
CO302Y_cluster008	Bacteriocin	CO302Y_cluster008	Bacteriocin	10	3569	100
		CO133X_cluster008	Bacteriocin	10	3567	100
		CO109Y_cluster005	Bacteriocin	8.5	3026	83
		CO348_cluster015	Bacteriocin	8.5	2023	69
		CO342X_cluster031	Bacteriocin	8	2043	70
		CO325X_cluster014	Bacteriocin	4	738	68
CO325X_cluster014	Bacteriocin	CO325X_cluster014	Bacteriocin	16	5199	100
		CO109Y_cluster005	Bacteriocin	11.5	2193	72
		CO342X_cluster031	Bacteriocin	9.5	1802	70
		CO348_cluster015	Bacteriocin	9.5	1796	69
		CO302Y_cluster008	Bacteriocin	4	738	68
		CO133X_cluster008	Bacteriocin	4	738	68
CO342X_cluster010	Bacteriocin	CO342X_cluster010	Bacteriocin	8.5	5220	100
		CO348_cluster27	Bacteriocin	8.5	4831	97
CO342X_cluster011	Bacteriocin	CO342X_cluster011	Bacteriocin	13	4748	100
		CO348_cluster28	Bacteriocin	10.5	4450	98

* The BGC similarity percentage is shown for the core biosynthetic gene.

Table S2. MultiGeneBlast Results per category (*Continuation*)

Query Cluster	Query antiSMASH category	Hit Cluster	Hit antiSMAH Category	Total Score	Cumulative Blast score	BGC similarity (%) *
CO342X_cluster031	Bacteriocin	CO342X_cluster031	Bacteriocin	17.5	6219	100
		CO348_cluster015	Bacteriocin	15.5	5922	98
		CO109Y_cluster005	Bacteriocin	15.5	3556	72
		CO325X_cluster014	Bacteriocin	9.5	1818	70
		CO302Y_cluster008	Bacteriocin	8	2043	70
		CO133X_cluster008	Bacteriocin	8	2043	70
CO348_cluster015	Bacteriocin	CO348_cluster015	Bacteriocin	16	6090	100
		CO109Y_cluster005	Bacteriocin	16	3547	72
		CO342X_cluster031	Bacteriocin	15.5	5938	98
		CO325X_cluster014	Bacteriocin	9.5	1810	69
		CO302Y_cluster008	Bacteriocin	8.5	2028	69
		CO133X_cluster008	Bacteriocin	8.5	2028	69
CO348_cluster027	Bacteriocin	CO348_cluster027	Bacteriocin	8.5	5229	100
		CO342X_cluster010	Bacteriocin	8.5	4831	97
CO348_cluster028	Bacteriocin	CO348_cluster028	Bacteriocin	14.5	4931	100
		CO342X_cluster011	Bacteriocin	10.5	4450	98

* The BGC similarity percentage is shown for the core biosynthetic gene.

Table S2. MultiGeneBlast Results per category (*Continuation*)

Query Cluster	Query antiSMASH category	Hit Cluster	Hit antiSMAH Category	Total Score	Cumulative Blast score	BGC similarity (%) *
CO109Y_cluster012	Siderophore	CO109Y_cluster012	Siderophore	16	7274	100
		CO325X_cluster002	Siderophore	5	2506	73
		CO302Y_cluster012	Siderophore	3.5	1417	42
		CO133X_cluster016	Siderophore	3.5	1417	42
CO133X_cluster016	Siderophore	CO302Y_cluster012	Siderophore	13	7098	100
		CO133X_cluster016	Siderophore	13	7098	100
		CO109Y_cluster012	Siderophore	3.5	1443	42
		CO325X_cluster002	Siderophore	3	1085	41
CO302Y_cluster012	Siderophore	CO302Y_cluster012	Siderophore	13	7098	100
		CO133X_cluster016	Siderophore	13	7098	100
		CO109Y_cluster012	Siderophore	3.5	1443	42
		CO325X_cluster002	Siderophore	3	1085	41
CO325X_cluster002	Siderophore	CO325X_cluster002	Siderophore	8.5	6544	100
		CO109Y_cluster012	Siderophore	5	22522	73
		CO302Y_cluster012	Siderophore	2	1063	41
		CO133X_cluster016	Siderophore	2	1063	41

* The BGC similarity percentage is shown for the core biosynthetic gene.

Table S3. Summary of BGC found in *Pseudoalteromonas* species according to antiSMASH database

Categories	**Number of BCG**	**Found in**	**Most similar MIBiG clusters**
Aryl polyene	45	*P. agarivorans, P. aliena ,P. arabiensis, P. gelatinilytica, P. haloplanktis, P. lipolytica, P. luteoviolaceae, P. nigrifaciens,P. piratica, P. prydzensis, P. ruthenica, P. shioyasakiensis, P. spongiae, P.translucida Pseudoalteromonas* sp. (unclassified)	APEVf
Bacteriocin or other unspecified RiPP	186	*P. agarivorans, P. aliena, P. amylolytica, P. arabiensis, P. arctica, P. atlantica, P. byunsanensis, P. carrageenovora, P. citrea, P. denitrificans, P. elyakovii, P. espejiana, P. flavipulchra, P. fuliginea, P. gelatinilytica, P. haloplanktis, P. issachenkonii, P. lipolytica, P. luteaoviolaceae, P. marina,P. neustonica, P. nigrifaciens , P. phenolica P. piratica, P. piscicida, P. porphyrae,P. prydzensis, P. rubra, P. ruthenica, P. shioyasakiensis, P. spongiae, P. teatraodonis, P. translucida, P. tunicata, P. undina, Pseudoalteromonas* sp. (unclassified).	
Homoserine lactone	12	*P. atlantica, P. luteoviolaceae, P. rubra, Pseudoalteromonas* sp. (unclassified)	
Hybrid cluster: Aryl polyene & Lanthipeptide	1	*P. denitrificans*	APEVf
Hybrid cluster: Aryl polyene & Nonribosomal peptide	9	*P. flavipulchra, P. luteoviolaceae, P. piscicida Pseudoalteromonas* sp. (unclassified)	APEVf, Alterochromides, Bromoalterochromides
Hybrid cluster: Aryl polyene & Resorcinol	9	*P. arctica, P. neustonica,P. porphyrae, P. spongiae, Pseudoalteromonas* sp. (unclassified)	APEVf, Flexirubin
Hybrid cluster: Bacteriocin or other unspecified RiPP & Nonribosomal peptide	1	*P. aliena*	
Hybrid cluster: Bacteriocin or other unspecified RiPP & Nonribosomal peptide & Type I polyketide	1	*P. rubra*	
Hybrid cluster: Butyrolactone & Homoserine lactone & Nonribosomal peptide	1	*Pseudoalteromonas sp.* (unclassified)	
Hybrid cluster: Butyrolactone & Type I polyketide	1	*P. byunsanensis*	
Hybrid cluster: hglE-type polyketide & Nonribosomal peptide & Trans-AT polyketide	2	*P. luteoviolaceae*	Thiomarinol, Calyculin
Hybrid cluster: hglE-type polyketide & Polyunsaturated fatty acid	1	*P. denitrificans*	Eicosapentaenoicacid-like compound
Hybrid cluster: hglE-type polyketide & Polyunsaturated fatty acid & Type I polyketide	1	*Pseudoalteromonas sp.* (unclassified)	Eicosapentaenoicacid-like compound
Hybrid cluster: Homoserine lactone & N-acyl amino acid cluster	1	*P. luteoviolaceae*	

Table S3. Summary of BGC found in *Pseudoalteromonas* species according to antiSMASH database *(Continuation)*

Categories	**Number of BCG**	**Found in**	**Most similar MIBiG clusters**
Hybrid cluster: Homoserine lactone & Type I polyketide	2	*P. citrea, Pseudoalteromonas* sp. (unclassified)	
Hybrid cluster: Indole & Type III polyketide	5	*P. luteoviolaceae*	Violacein
Hybrid cluster: Ladderane & Lanthipeptide	1	*P. luteoviolaceae*	
Hybrid cluster: Ladderane & Nonribosomal peptide	7	*P. elyakovii, P. piscicida, P. luteoviolaceae Pseudoalteromonas* sp. (unclassified)	Altherochromides, Bromoalterochromides
Hybrid cluster: Lanthipeptide & Nonribosomal peptide	6	*P. elyakovii, P. piscicida, P. rubra, Pseudoalteromonas* sp. (unclassified)	
Hybrid cluster: Lanthipeptide & Nonribosomal peptide & Type I polyketide	2	*P. piscicida*	Colibactin
Hybrid cluster: Lanthipeptide & Trans-AT polyketide	1	*P. luteoviolaceae*	Cystobactamide
Hybrid cluster: Nonribosomal peptide & Thiopeptide	1	*P. rubra*	
Hybrid cluster: Nonribosomal peptide & Trans-AT polyketide	1	*P. rubra*	
Hybrid cluster: Nonribosomal peptide & Type I polyketide	70	*P. amylolytica, P. byunsanensis, P. citrea, P. denitrificans, P. elyakovii, P. flavipulchra, P. luteoviolaceae, P. piscicida, P. prydzensis, P. rubra, Pseudoalteromonas* sp. (unclassified)	Turnerbactin,Streptomycin, Serobactins, Hectochlorin, Cystobactamide, Griseobactin,Enterobactin, Pyoverdine,
Hybrid cluster: Nonribosomal peptide & Type III polyketide	2	*P. luteoviolaceae, P. piscicida*	Feglymycin
Indole	10	*P. amylolytica, P. byunsanensis, P. luteoviolaceae, P. tunicata, Pseudoalteromonas* sp. (unclassified)	Violacein
Lanthipeptide	23	*P. amylolytica, P. byunsanensis, P. citrea, P. espejiana, P. flavipulchra, P. haloplanktis, P. luteoviolaceae, P. phenolica, P. piscicida, P. rubra, Pseudoalteromonas* sp. (unclassified)	Xenocyloins
N-acyl amino acid cluster	4	*P. elyakovii, P. piscicida, P. luteoviolaceae, Pseudoalteromonas* sp. (unclassified)	

Table S3. Summary of BGC found in *Pseudoalteromonas* species according to antiSMASH database *(Continuation)*

Categories	**Number of BCG**	**Found in**	**Most similar MIBiG clusters**
Nonribosomal Peptide	178	*P. amylolytica, P. byunsanensis, P. citrea, P. denitrificans, P. elyakovii, P. flavipulchra,P. fuliginea, P. luteoviolaceae,P. neustonica, P. phenolica, P. piscicida, P. porphyrae, P. rubra, P. tunicata Pseudoalteromonas* sp. (unclassified)	Taxlllaid, Syringomycin, Bacillibactin, Bromoalterochromides, Orfamide, Colibactin, Cupriachelin, Alterochromides, Cahuitamycins, Dorrigocin/migrastatin,Stenothricin, Kalimantacin/batumin, Turnerbactin, Vibrobactin, Bongkrekicacid, Pyoverdine, Vulnibactin, Enterobactin, Griseobactin, Bacitracin,Heterobactin, Nunapeptin/nunamycin, Griselimycin, Syringomycin, Mycobactin, WAP-8294A2(lotilibcin), Syringopeptin
Other	35	*P. amylolytica, P. byunsanensis, P. citrea, P. fuliginea, P. luteoviolaceae ,P. nigrifaciens, P. piscicida, P. rubra, P. tunicata, Pseudoalteromonas* sp. (unclassified)	Pyoverdine, Auricindeoxysugarmoieties, Indigoidine, Prodigiosin
Phosphonate	1	*P. byunsanensis*	
Polybrominated diphenyl ether	1	*P. phenolica*	Bromophenols/bromopyrroles
Resorcinol	3	*P. ruthenica*	
Siderophore	50	*P. agarivorans, P. aliena ,P. amylolytica, P. arabiensis,P. byunsanensis, P. carrageenovora, P. espejiana, P. gelatinilytica, P. haloplanktis, P. issachenkonii, P. lipolytica,P. piratica, P. prydzensis, P. ruthenica, P. shioyasakiensis, P. spongiae, P. tetraodonis ,P. tunicata, Pseudoalteromonas* sp. (unclassified)	DesferrioxamineB
Thiopeptide	7	*P. citrea,P. elyakovii, P. flavipulchra, P. luteaoviolaceae, Pseudoalteromonas* sp. (unclassified)	
Type I polyketide	3	*P. citrea, P. luteaoviolaceae, P. rubra*	
Type II polyketide	4	*P. luteoviolaceae*	
Type III polyketide	10	*P. citrea, P. luteaoviolaceae, P. rubra, Pseudoalteromonas* sp. (unclassified)	

Table S4. MS1 peaks considered for MS2 fragmentation data.

Time	Collision RF	Transfer Time	Collision
0	450.0	70.0	125
25	550.0	75.0	100
50	800.0	90.0	100
75	1100.0	95.0	75

Table S5. Collision-induced dissociation (CID) energies for MS/MS data acquisition

Type	Mass	Width	Collision	Charge State
Base	100.00	4.00	22.00	1
Base	100.00	4.00	18.00	2
Base	300.00	5.00	27.00	1
Base	300.00	5.00	22.00	2
Base	500.00	6.00	35.00	1
Base	500.00	6.00	30.00	2
Base	1000.00	8.00	45.00	1
Base	1000.00	8.00	35.00	2
Base	2000.00	10.00	50.00	1
Base	2000.00	10.00	50.00	2

Table S6. Observed CID fragment ions for characterized bromoalterochromides

Open species	Fragment*	Bromoalterochromide A/A' m/z 844.2900 [M + H]$^+$ (1,2)	Dibromoalterochromide A/A' m/z 922.1996 [M + H]$^+$ (3,4)	Bromoalterochromide B/B' m/z 870.3061[M + H]$^+$ (5,6)	Dibromoalterochromide B/B' m/z 948.2175 [M + H]$^+$ (7,8)	Bromoalterochromide D/D' m/z 858.3049 [M + H]$^+$ (9,10)	Dibromoalterochromide D/D' m/z 936.2157 [M + H]$^+$ (11,12)
Dehydration	M-OH	827/829	905/907/909	853/855	931/933/935	841/843	919/921/923
Isomeric open specie A	a_1	-	435/437/439	-	-	358/360 (low)	-
	a_2	457/459	535/537/539	483/485	561/563/565	471/473	549/551/553
	a_4	685/687	763/765/767 (low)	-	-	699/701	777/779/781 (low)
	a_5	798/800	-	-	-	-	-
	b_0	303/305	381/383/385	329/331	406/408/410	303/305	380/382/384
	b_1	386/388	464/466/468	412/414	489/491/493	386/388	464/466/468
	b_2	485/487	563/565/567	511/513	589/591/593 (low)	499/501	577/579/581
	b_3	599/601	677/679/681	625/627	703/705/707 (low)	613/615	691/693/695
	b_4	713/715	791/793/795	-	-	727/729	805/807/809
	y_1	131	131	131	131	131	131
	y_2	246	246	246	246	246	246
	y_3	360	360	360	360	360	360
	y_4	459	459	459	459	473	473
	y_5	542	542	542	542	556	556
	c_1	404/406	482/484/486	-	-	404/406	482/484/486
	c_3	617/619	-	-	-	631/633 (low)	-
	c_4	731/733	-			-	-
	z_2	229	229	229	229	229	229
	z_3	343	343	343	343	343	343
	z_4	442	442	442	442	456	456
	z_5	525	525	525	525	539	539
	w_3	300	300	300 (low)	300	-	-
	v_2	-	187	-	187	187	-
	v_5	514 (low)	514 (low)	-	-	-	-
Isomeric open specie B	b_0	303/305	381/383/385	329/331	406/408/410	303/305	380/382/384
	b_1	404/406	482/484/486	-	-	404/406	482/484/486
	b_3	616/618 (low)	-	-	-	631/633 (low)	-
	b_4	731/733	809/811/813	-	-	745/747 (low)	823/825/827
	y_2	228 (low)	228	228	228	228	228
	y_3	342	342	342	342	342	342
	y_4	441 (low)	441	441	441	455	455
	y_5	542	542	542	542	556	556
	z_3	325 (low)	325 (low)	325 (low)	325 (low)	325	325
	z_4	424 (low)	424 (low)	424 (low)	424 (low)	438	438
	z_5	525	525	525	525	539	539
	v_3	283	-	283	-	-	-
	v_4	397	397	397	397	-	-
Aromatic elimination	$C_9H_6BrO^+$	208/210	-	-	-	208/210	-
	$C_9H_5Br_2O^+$	-	286/288/290	-	-	-	286/288/290
	$C_{11}H_8BrO^+$	-	-	234/236	-	-	-
	$C_{11}H_7Br_2O^+$	-	-	-	312/314/316	-	-

*Fragmentation cleavage sites according to Kalinovskaya et al. 2008. We included b_0 as a side chain cleavage; and side chain sub-fragmentation rearrangements. Low less than 5% intensity

Table S7. Pairwise comparisons of *Pseudoalteromonas* strains genomes vs type strain genomes in Type (Strain) Genome Server (TSGS)

Query strain	**Subject strain**	**dDDH* (d0, in %)**	**C.I.** (d0, in %)**	**dDDH (d4, in %)**	**C.I. (d4, in %)**	**dDDH (d6, in %)**	**C.I. (d6, in %)**	**G+C content difference (in %)**
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	100	[100.0 - 100.0]	100	[100.0 - 100.0]	100	[100.0 - 100.0]	0
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas maricaloris LMG 19692	95.4	[93.3 - 96.9]	92.9	[90.9 - 94.4]	96.8	[95.3 - 97.8]	0.15
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas shioyasakiensis JCM 18891	92.1	[89.2 - 94.3]	87	[84.4 - 89.2]	93.7	[91.5 - 95.4]	0.01
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	82.5	[78.7 - 85.8]	79	[76.0 - 81.7]	84.9	[81.7 - 87.6]	0.06
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas maricaloris LMG 19692	79.6	[75.7 - 83.1]	78.8	[75.8 - 81.5]	82.4	[79.1 - 85.3]	0.1
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas ruthenica LMG 19699	87.7	[84.2 - 90.5]	78.6	[75.7 - 81.3]	89	[86.1 - 91.3]	0.28
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas piscicida ATCC 15057	81	[77.1 - 84.4]	68.8	[65.8 - 71.6]	81.6	[78.3 - 84.6]	0.02
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas piscicida ATCC 15057	81.3	[77.4 - 84.7]	68.7	[65.7 - 71.5]	81.8	[78.5 - 84.8]	0.04
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas arabiensis JCM 17292	86.4	[82.8 - 89.4]	64.1	[61.1 - 66.9]	85	[81.9 - 87.8]	0.06
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas arabiensis JCM 17292	86.5	[82.8 - 89.4]	64.1	[61.1 - 66.9]	85.1	[81.9 - 87.8]	0.06
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas gelatinilytica NH153	85.1	[81.4 - 88.2]	52	[49.3 - 54.7]	80.5	[77.1 - 83.5]	0.12
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Kangiella profundi FT102	12.6	[10.0 - 15.9]	36	[33.6 - 38.5]	13	[10.7 - 15.8]	3.44
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Salinimonas sediminis KCTC 62440	12.8	[10.1 - 16.1]	33.1	[30.7 - 35.7]	13.2	[10.9 - 16.0]	0.96
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Salinimonas sediminis KCTC 62440	12.6	[9.9 - 15.8]	31.5	[29.1 - 34.0]	13	[10.7 - 15.7]	6.93
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	59.2	[55.5 - 62.7]	29	[26.6 - 31.5]	50.1	[47.0 - 53.1]	0.4
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	59.1	[55.5 - 62.7]	29	[26.6 - 31.5]	50.1	[47.0 - 53.1]	0.4
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas gelatinilytica NH153	55.1	[51.6 - 58.6]	29	[26.6 - 31.5]	47.3	[44.3 - 50.4]	0.52
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas gelatinilytica NH153	55.1	[51.6 - 58.6]	29	[26.6 - 31.5]	47.3	[44.3 - 50.4]	0.51
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas shioyasakiensis JCM 18891	56.4	[52.8 - 59.9]	28.9	[26.5 - 31.4]	48.2	[45.1 - 51.2]	0.39
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas shioyasakiensis JCM 18891	56.4	[52.9 - 59.9]	28.9	[26.5 - 31.4]	48.2	[45.2 - 51.2]	0.39
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas arabiensis JCM 17292	55.4	[51.9 - 58.9]	28.3	[25.9 - 30.8]	47.2	[44.2 - 50.2]	0.34
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Salinimonas sediminis KCTC 62440	12.6	[9.9 - 15.9]	26.3	[23.9 - 28.8]	13	[10.7 - 15.7]	5.01

'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Salinimonas sediminis KCTC 62440	12.6	[9.9 - 15.9]	25.1	[22.8 - 27.6]	13	[10.7 - 15.8]	7.33
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Salinimonas sediminis KCTC 62440	12.6	[9.9 - 15.9]	25	[22.7 - 27.5]	13	[10.7 - 15.8]	7.32
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas donghaensis KCTC22219	55.4	[51.9 - 58.9]	24.6	[22.3 - 27.1]	45	[42.0 - 48.0]	0.32
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Kangiella profundi FT102	12.6	[9.9 - 15.8]	24.5	[22.2 - 27.0]	13	[10.6 - 15.7]	2.93
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Kangiella profundi FT102	12.6	[9.9 - 15.8]	24.5	[22.1 - 26.9]	13	[10.6 - 15.7]	2.92
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas lipolytica CGMCC 1.8499	55	[51.4 - 58.4]	24.5	[22.2 - 27.0]	44.6	[41.6 - 47.7]	0.2
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Salinimonas sediminis KCTC 62440	12.6	[9.9 - 15.9]	24.3	[21.9 - 26.7]	13	[10.7 - 15.8]	4.95
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas peptidolytica NBRC 101021	35.7	[32.3 - 39.2]	24	[21.7 - 26.4]	31.6	[28.7 - 34.7]	0.82
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas donghaensis KCTC22219	48.9	[45.5 - 52.3]	24	[21.7 - 26.4]	40.5	[37.5 - 43.5]	0.72
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas donghaensis KCTC22219	48.9	[45.5 - 52.3]	24	[21.7 - 26.4]	40.5	[37.5 - 43.5]	0.72
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas peptidolytica NBRC 101021	36.3	[32.9 - 39.8]	23.9	[21.6 - 26.3]	32	[29.1 - 35.1]	0.76
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas lipolytica CGMCC 1.8499	48.7	[45.3 - 52.2]	23.8	[21.5 - 26.3]	40.3	[37.3 - 43.3]	0.59
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas lipolytica CGMCC 1.8499	48.7	[45.3 - 52.2]	23.8	[21.5 - 26.3]	40.3	[37.3 - 43.3]	0.6
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Vibrio panuliri LBS2	12.6	[9.9 - 15.9]	23.6	[21.3 - 26.1]	13	[10.7 - 15.8]	2.14
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas piratica OCN003	13.2	[10.5 - 16.5]	22.8	[20.5 - 25.2]	13.5	[11.2 - 16.3]	7.29
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas piratica OCN003	13.3	[10.6 - 16.7]	22.5	[20.3 - 25.0]	13.7	[11.3 - 16.5]	3.24
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas phenolica KCTC 12086	13.4	[10.7 - 16.8]	22	[19.7 - 24.4]	13.8	[11.4 - 16.6]	6.67
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas piratica OCN003	13.4	[10.6 - 16.7]	22	[19.8 - 24.5]	13.7	[11.3 - 16.5]	3.3
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas ruthenica LMG 19699	13.4	[10.6 - 16.7]	21.8	[19.5 - 24.2]	13.7	[11.3 - 16.5]	4.33
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Kangiella profundi FT102	12.6	[9.9 - 15.8]	21.8	[19.6 - 24.3]	13	[10.6 - 15.7]	2.53
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas ruthenica LMG 19699	13.4	[10.7 - 16.7]	21.7	[19.4 - 24.1]	13.7	[11.4 - 16.5]	4.27
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas citrea NCIMB 1889	13.4	[10.7 - 16.7]	21.5	[19.3 - 23.9]	13.7	[11.4 - 16.5]	6.13
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas spongiae JCM 12884	13.3	[10.5 - 16.6]	21.5	[19.3 - 24.0]	13.6	[11.2 - 16.4]	2.39
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas amylolytica JW1	13.5	[10.7 - 16.8]	21.5	[19.3 - 24.0]	13.8	[11.4 - 16.6]	3.9
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas spongiae JCM 12884	13.3	[10.6 - 16.6]	21.4	[19.1 - 23.8]	13.6	[11.2 - 16.4]	2.45

'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas maricaloris LMG 19692	13.3	[10.6 - 16.6]	21.3	[19.0 - 23.7]	13.6	[11.3 - 16.4]	4.14
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	13.3	[10.5 - 16.6]	21.2	[18.9 - 23.6]	13.6	[11.2 - 16.4]	4.05
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas piratica OCN003	13.9	[11.1 - 17.3]	21.2	[18.9 - 23.6]	14.2	[11.8 - 17.0]	1.32
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas agarivorans DSM 14585	13.6	[10.8 - 16.9]	21.1	[18.8 - 23.5]	13.9	[11.5 - 16.7]	2.42
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas agarivorans DSM 14585	13.6	[10.9 - 17.0]	21.1	[18.8 - 23.5]	13.9	[11.5 - 16.7]	2.36
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas tetraodonis DSM 9166	13.6	[10.9 - 17.0]	21.1	[18.9 - 23.5]	13.9	[11.5 - 16.7]	6.94
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas issachenkonii KCTC 12958	13.6	[10.8 - 16.9]	21	[18.8 - 23.4]	13.9	[11.5 - 16.7]	6.96
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas piscicida ATCC 15057	13.3	[10.5 - 16.6]	20.9	[18.7 - 23.4]	13.6	[11.2 - 16.4]	4.03
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas espejiana ATCC 29659	13.6	[10.9 - 17.0]	20.9	[18.6 - 23.3]	13.9	[11.5 - 16.7]	2.9
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas tetraodonis DSM 9166	19.6	[16.4 - 23.2]	20.9	[18.7 - 23.3]	19	[16.3 - 22.0]	0.97
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas rubra ATCC 29570	13.2	[10.5 - 16.5]	20.9	[18.6 - 23.3]	13.6	[11.2 - 16.4]	0.54
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas phenolica KCTC 12086	14.5	[11.7 - 17.9]	20.8	[18.6 - 23.2]	14.7	[12.3 - 17.6]	2.62
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas spongiae JCM 12884	13.7	[11.0 - 17.1]	20.8	[18.6 - 23.3]	14	[11.6 - 16.8]	0.08
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas spongiae JCM 12884	13.2	[10.5 - 16.5]	20.8	[18.6 - 23.3]	13.5	[11.2 - 16.3]	6.44
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas maricaloris LMG 19692	14.3	[11.4 - 17.6]	20.8	[18.6 - 23.3]	14.5	[12.0 - 17.3]	1.82
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas spongiae JCM 12884	13.7	[11.0 - 17.1]	20.8	[18.6 - 23.2]	14	[11.6 - 16.8]	0.08
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas espejiana ATCC 29659	13.7	[10.9 - 17.1]	20.8	[18.5 - 23.2]	14	[11.6 - 16.8]	2.96
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas phenolica KCTC 12086	14.5	[11.7 - 17.9]	20.8	[18.5 - 23.2]	14.7	[12.3 - 17.6]	0.31
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas phenolica KCTC 12086	14.5	[11.7 - 17.9]	20.8	[18.5 - 23.2]	14.7	[12.3 - 17.6]	0.3
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas carrageenovora ATCC 43555	13.6	[10.9 - 17.0]	20.8	[18.6 - 23.2]	13.9	[11.5 - 16.7]	3.78
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas issachenkonii KCTC 12958	19.6	[16.5 - 23.2]	20.8	[18.6 - 23.2]	19	[16.3 - 22.0]	0.99
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas tetraodonis DSM 9166	13.8	[11.0 - 17.1]	20.8	[18.5 - 23.2]	14.1	[11.6 - 16.9]	2.95
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas spiralis DSM 16099	19.2	[16.1 - 22.8]	20.8	[18.6 - 23.3]	18.7	[16.0 - 21.7]	1.14
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	13.3	[10.6 - 16.6]	20.7	[18.4 - 23.1]	13.6	[11.3 - 16.4]	3.99
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas tetraodonis DSM 9166	13.8	[11.1 - 17.2]	20.7	[18.4 - 23.1]	14.1	[11.7 - 16.9]	2.89

'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas agarivorans DSM 14585	18.9	[15.8 - 22.5]	20.7	[18.5 - 23.1]	18.4	[15.8 - 21.4]	0.45
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas atlantica NBRC 103033	18.9	[15.7 - 22.5]	20.6	[18.4 - 23.0]	18.4	[15.7 - 21.4]	0.53
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas ruthenica LMG 19699	13.9	[11.1 - 17.2]	20.6	[18.4 - 23.1]	14.1	[11.7 - 17.0]	6.64
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas luteoviolacea DSM 6061	13.6	[10.8 - 16.9]	20.6	[18.4 - 23.0]	13.9	[11.5 - 16.7]	0.89
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas luteoviolacea DSM 6061	13.2	[10.5 - 16.5]	20.6	[18.3 - 23.0]	13.6	[11.2 - 16.3]	5.48
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas luteoviolacea DSM 6061	13.6	[10.8 - 16.9]	20.6	[18.4 - 23.0]	13.9	[11.5 - 16.7]	0.88
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas ruthenica LMG 19699	13.9	[11.1 - 17.2]	20.6	[18.4 - 23.1]	14.1	[11.7 - 17.0]	6.64
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas issachenkonii KCTC 12958	13.8	[11.0 - 17.2]	20.6	[18.3 - 23.0]	14.1	[11.7 - 16.9]	2.97
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas phenolica KCTC 12086	14.6	[11.8 - 18.0]	20.5	[18.3 - 22.9]	14.8	[12.3 - 17.7]	2.68
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas telluritireducens DSM 16098	18.9	[15.8 - 22.5]	20.5	[18.2 - 22.9]	18.4	[15.7 - 21.4]	0.37
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas spiralis DSM 16099	13.6	[10.9 - 17.0]	20.5	[18.3 - 22.9]	13.9	[11.5 - 16.7]	7.1
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas carrageenovora ATCC 43555	19.2	[16.1 - 22.8]	20.5	[18.3 - 22.9]	18.6	[16.0 - 21.7]	1.87
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas piratica OCN003	13.9	[11.1 - 17.2]	20.5	[18.3 - 22.9]	14.1	[11.7 - 17.0]	0.92
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas haloplanktis ATCC 14393	21.9	[18.6 - 25.5]	20.5	[18.3 - 23.0]	20.7	[18.0 - 23.8]	0.44
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas piratica OCN003	13.9	[11.1 - 17.2]	20.5	[18.3 - 22.9]	14.1	[11.7 - 17.0]	0.92
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas rubra ATCC 29570	13.3	[10.6 - 16.7]	20.4	[18.2 - 22.8]	13.7	[11.3 - 16.5]	6.91
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas issachenkonii KCTC 12958	13.8	[11.0 - 17.2]	20.4	[18.2 - 22.9]	14.1	[11.7 - 16.9]	2.91
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas rubra ATCC 29570	13.3	[10.6 - 16.7]	20.4	[18.2 - 22.8]	13.7	[11.3 - 16.5]	6.9
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas spiralis DSM 16099	13.8	[11.0 - 17.1]	20.4	[18.2 - 22.8]	14	[11.6 - 16.9]	3.11
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas byunsanensis JCM 12483	13.6	[10.8 - 16.9]	20.4	[18.2 - 22.8]	13.9	[11.5 - 16.7]	4.77
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Vibrio panuliri LBS2	12.7	[10.1 - 16.0]	20.4	[18.2 - 22.8]	13.1	[10.8 - 15.9]	4.22
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Vibrio panuliri LBS2	12.7	[10.1 - 16.0]	20.4	[18.2 - 22.8]	13.1	[10.8 - 15.9]	4.23
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas phenolica KCTC 12086	14.7	[11.8 - 18.1]	20.4	[18.1 - 22.8]	14.8	[12.4 - 17.7]	0.7
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas espejiana ATCC 29659	19.8	[16.6 - 23.4]	20.4	[18.2 - 22.8]	19	[16.4 - 22.1]	0.99
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas telluritireducens DSM 16098	13.6	[10.8 - 16.9]	20.4	[18.2 - 22.8]	13.9	[11.5 - 16.7]	2.28

'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas peptidolytica NBRC 101021	13.3	[10.6 - 16.6]	20.4	[18.2 - 22.8]	13.7	[11.3 - 16.4]	4.81
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas neustonica PAMC 28425	20.1	[16.9 - 23.7]	20.4	[18.2 - 22.8]	19.3	[16.6 - 22.4]	1.56
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas prydzensis DSM 14232	21.6	[18.4 - 25.2]	20.3	[18.1 - 22.7]	20.5	[17.7 - 23.5]	0.13
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas tetraodonis DSM 9166	19.2	[16.0 - 22.8]	20.3	[18.1 - 22.7]	18.6	[15.9 - 21.6]	0.58
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	14.1	[11.3 - 17.4]	20.3	[18.1 - 22.7]	14.3	[11.9 - 17.1]	2.31
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	14.1	[11.3 - 17.4]	20.3	[18.1 - 22.7]	14.3	[11.9 - 17.1]	2.32
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas agarivorans DSM 14585	19.5	[16.3 - 23.1]	20.3	[18.1 - 22.7]	18.8	[16.1 - 21.8]	0.05
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas peptidolytica NBRC 101021	13.8	[11.0 - 17.1]	20.3	[18.1 - 22.7]	14	[11.6 - 16.9]	1.15
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas agarivorans DSM 14585	19.5	[16.3 - 23.1]	20.3	[18.1 - 22.7]	18.8	[16.1 - 21.8]	0.05
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas tetraodonis DSM 9166	19.2	[16.0 - 22.8]	20.3	[18.1 - 22.7]	18.6	[15.9 - 21.6]	0.58
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas donghaensis KCTC22219	14.1	[11.3 - 17.4]	20.3	[18.1 - 22.7]	14.3	[11.9 - 17.1]	1.6
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas espejiana ATCC 29659	19.9	[16.7 - 23.5]	20.3	[18.1 - 22.7]	19.1	[16.4 - 22.2]	0.59
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas espejiana ATCC 29659	19.9	[16.7 - 23.5]	20.3	[18.1 - 22.7]	19.1	[16.4 - 22.1]	0.59
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas piscicida ATCC 15057	14	[11.2 - 17.4]	20.2	[18.0 - 22.6]	14.3	[11.9 - 17.1]	2.34
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	14.1	[11.3 - 17.4]	20.2	[18.0 - 22.6]	14.3	[11.9 - 17.1]	2.37
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas carrageenovora ATCC 43555	19.7	[16.5 - 23.3]	20.2	[18.0 - 22.6]	19	[16.3 - 22.0]	1.47
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas donghaensis KCTC22219	14.1	[11.3 - 17.5]	20.2	[18.0 - 22.7]	14.4	[11.9 - 17.2]	1.66
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas issachenkonii KCTC 12958	19.1	[16.0 - 22.7]	20.2	[18.0 - 22.6]	18.5	[15.9 - 21.5]	0.6
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas carrageenovora ATCC 43555	19.6	[16.5 - 23.3]	20.2	[18.0 - 22.6]	18.9	[16.3 - 22.0]	1.47
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas maricaloris LMG 19692	14	[11.2 - 17.4]	20.2	[18.0 - 22.7]	14.3	[11.9 - 17.1]	2.22
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas carrageenovora ATCC 43555	13.8	[11.0 - 17.1]	20.2	[18.0 - 22.6]	14	[11.6 - 16.8]	3.84
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas agarivorans DSM 14585	13.8	[11.0 - 17.1]	20.2	[18.0 - 22.6]	14	[11.6 - 16.9]	6.41
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas maricaloris LMG 19692	14	[11.2 - 17.4]	20.2	[18.0 - 22.7]	14.3	[11.9 - 17.1]	2.22
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas issachenkonii KCTC 12958	19.1	[16.0 - 22.7]	20.2	[18.0 - 22.6]	18.5	[15.9 - 21.5]	0.59
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas piscicida ATCC 15057	14	[11.2 - 17.4]	20.2	[18.0 - 22.6]	14.3	[11.9 - 17.1]	2.34

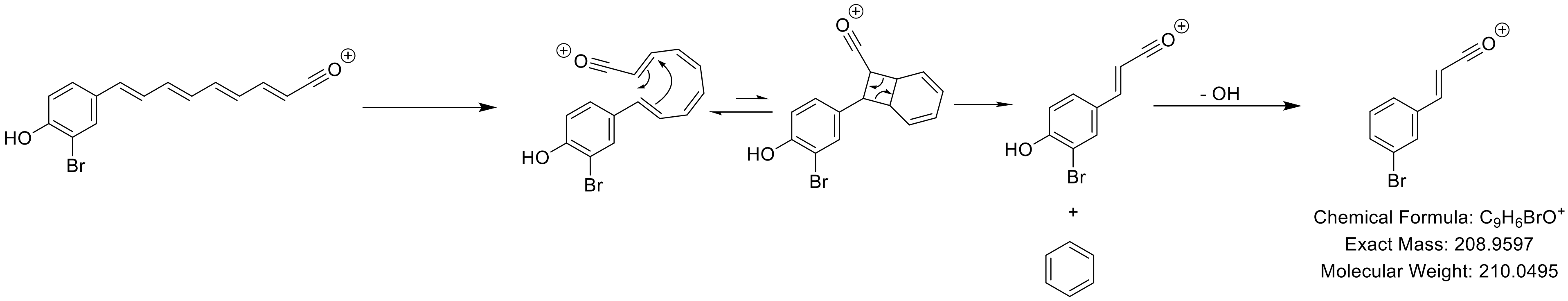
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas spiralis DSM 16099	13.7	[11.0 - 17.1]	20.2	[18.0 - 22.6]	14	[11.6 - 16.8]	3.05
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas gelatinilytica NH153	14	[11.2 - 17.4]	20.1	[17.9 - 22.5]	14.3	[11.8 - 17.1]	1.8
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas gelatinilytica NH153	14.1	[11.3 - 17.5]	20.1	[17.8 - 22.5]	14.3	[11.9 - 17.1]	1.86
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas spiralis DSM 16099	19	[15.9 - 22.6]	20.1	[17.9 - 22.5]	18.4	[15.8 - 21.4]	0.74
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas byunsanensis JCM 12483	14.8	[11.9 - 18.2]	20.1	[17.9 - 22.5]	14.9	[12.5 - 17.8]	0.73
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas arctica DSM 18437	19	[15.9 - 22.6]	20.1	[17.9 - 22.5]	18.4	[15.7 - 21.4]	2.24
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas telluritireducens DSM 16098	13.6	[10.8 - 16.9]	20.1	[17.9 - 22.5]	13.9	[11.5 - 16.7]	2.34
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas spiralis DSM 16099	19	[15.9 - 22.6]	20.1	[17.9 - 22.5]	18.4	[15.8 - 21.4]	0.74
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Vibrio panuliri LBS2	12.7	[10.0 - 16.0]	20.1	[17.9 - 22.6]	13.1	[10.8 - 15.9]	3.83
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Kangiella profundi FT102	12.6	[9.9 - 15.9]	20.1	[17.9 - 22.5]	13	[10.7 - 15.7]	0.55
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	14.1	[11.3 - 17.4]	20.1	[17.9 - 22.6]	14.3	[11.9 - 17.1]	2.37
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas atlantica NBRC 103033	19.2	[16.0 - 22.8]	20.1	[17.9 - 22.5]	18.6	[15.9 - 21.6]	0.13
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas rubra ATCC 29570	13.5	[10.7 - 16.8]	20.1	[17.9 - 22.5]	13.8	[11.4 - 16.6]	6.51
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas espejiana ATCC 29659	13.7	[10.9 - 17.0]	20.1	[17.9 - 22.6]	14	[11.6 - 16.8]	6.95
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas atlantica NBRC 103033	19.2	[16.0 - 22.8]	20.1	[17.9 - 22.5]	18.6	[15.9 - 21.6]	0.13
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas marina mano4	19.2	[16.1 - 22.8]	20.1	[17.9 - 22.5]	18.6	[15.9 - 21.6]	1.63
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas citrea NCIMB 1889	14.1	[11.3 - 17.4]	20	[17.8 - 22.4]	14.3	[11.9 - 17.1]	0.24
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Kangiella profundi FT102	12.6	[9.9 - 15.9]	20	[17.7 - 22.4]	13	[10.7 - 15.7]	0.61
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas arctica DSM 18437	18.8	[15.7 - 22.4]	20	[17.7 - 22.4]	18.2	[15.6 - 21.2]	1.84
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas citrea NCIMB 1889	14.1	[11.3 - 17.4]	20	[17.8 - 22.4]	14.3	[11.9 - 17.1]	0.24
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas luteoviolacea DSM 6061	14.3	[11.5 - 17.7]	20	[17.8 - 22.4]	14.5	[12.1 - 17.3]	1.49
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas ruthenica LMG 19699	14	[11.2 - 17.3]	20	[17.8 - 22.4]	14.2	[11.8 - 17.0]	6.24
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas telluritireducens DSM 16098	19.9	[16.7 - 23.5]	20	[17.8 - 22.4]	19.1	[16.4 - 22.1]	0.03
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas byunsanensis JCM 12483	14.7	[11.9 - 18.2]	20	[17.7 - 22.4]	14.9	[12.4 - 17.7]	0.78
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas luteoviolacea DSM 6061	13.7	[11.0 - 17.1]	20	[17.8 - 22.4]	14	[11.6 - 16.8]	0.49

'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas haloplanktis ATCC 14393	13.4	[10.7 - 16.8]	20	[17.8 - 22.4]	13.7	[11.4 - 16.5]	6.41
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas donghaensis KCTC22219	13.9	[11.1 - 17.3]	20	[17.8 - 22.4]	14.1	[11.7 - 17.0]	5.65
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas neustonica PAMC 28425	20.3	[17.1 - 23.9]	20	[17.8 - 22.4]	19.4	[16.7 - 22.4]	1.16
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas neustonica PAMC 28425	20.3	[17.1 - 23.9]	20	[17.8 - 22.4]	19.4	[16.7 - 22.4]	1.16
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas arabiensis JCM 17292	14	[11.2 - 17.3]	20	[17.8 - 22.4]	14.2	[11.8 - 17.0]	2.25
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas undina NCIMB 2128	19.4	[16.2 - 23.0]	20	[17.8 - 22.4]	18.7	[16.0 - 21.7]	1.34
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas telluritireducens DSM 16098	19.9	[16.7 - 23.5]	20	[17.8 - 22.4]	19.1	[16.4 - 22.1]	0.03
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas undina NCIMB 2128	13.6	[10.8 - 16.9]	20	[17.8 - 22.4]	13.9	[11.5 - 16.7]	3.26
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas arctica DSM 18437	18.8	[15.7 - 22.4]	19.9	[17.7 - 22.4]	18.2	[15.6 - 21.2]	1.84
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas spongiae JCM 12884	14	[11.2 - 17.3]	19.9	[17.7 - 22.4]	14.2	[11.8 - 17.0]	0.48
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas arabiensis JCM 17292	14	[11.2 - 17.3]	19.9	[17.7 - 22.4]	14.2	[11.8 - 17.0]	2.31
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas rubra ATCC 29570	14.5	[11.6 - 17.8]	19.9	[17.7 - 22.3]	14.6	[12.2 - 17.5]	4.59
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas luteoviolacea DSM 6061	14.2	[11.4 - 17.6]	19.9	[17.7 - 22.3]	14.4	[12.0 - 17.3]	1.43
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Vibrio panuliri LBS2	12.8	[10.1 - 16.0]	19.9	[17.7 - 22.3]	13.1	[10.8 - 15.9]	1.91
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	13.9	[11.1 - 17.2]	19.9	[17.7 - 22.3]	14.1	[11.7 - 16.9]	6.36
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas haloplanktis ATCC 14393	21.6	[18.4 - 25.2]	19.9	[17.7 - 22.3]	20.4	[17.7 - 23.5]	0.04
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas amylolytica JW1	14.3	[11.5 - 17.7]	19.9	[17.7 - 22.3]	14.5	[12.1 - 17.3]	2.46
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	13.9	[11.1 - 17.2]	19.9	[17.7 - 22.3]	14.1	[11.7 - 16.9]	6.36
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas haloplanktis ATCC 14393	21.6	[18.4 - 25.2]	19.9	[17.7 - 22.3]	20.4	[17.7 - 23.5]	0.04
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas undina NCIMB 2128	19.7	[16.5 - 23.3]	19.9	[17.7 - 22.3]	18.9	[16.3 - 22.0]	0.94
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas undina NCIMB 2128	19.7	[16.5 - 23.3]	19.9	[17.7 - 22.3]	18.9	[16.3 - 22.0]	0.94
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas amylolytica JW1	14.3	[11.5 - 17.7]	19.9	[17.7 - 22.3]	14.5	[12.1 - 17.3]	2.46
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas arabiensis JCM 17292	13.8	[11.0 - 17.2]	19.9	[17.7 - 22.3]	14.1	[11.7 - 16.9]	6.3
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas amylolytica JW1	14.9	[12.0 - 18.3]	19.9	[17.7 - 22.3]	15	[12.5 - 17.9]	0.09
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas amylolytica JW1	14.5	[11.6 - 17.9]	19.8	[17.6 - 22.2]	14.6	[12.2 - 17.5]	2.06

'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas undina NCIMB 2128	13.6	[10.9 - 17.0]	19.8	[17.6 - 22.2]	13.9	[11.5 - 16.7]	3.31
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas byunsanensis JCM 12483	14.4	[11.5 - 17.7]	19.8	[17.6 - 22.2]	14.5	[12.1 - 17.4]	1.19
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas shioyasakiensis JCM 18891	13.8	[11.0 - 17.2]	19.8	[17.6 - 22.3]	14.1	[11.7 - 16.9]	5.97
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	14.1	[11.3 - 17.5]	19.8	[17.6 - 22.2]	14.3	[11.9 - 17.1]	1.92
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas neustonica PAMC 28425	13.4	[10.6 - 16.7]	19.8	[17.6 - 22.2]	13.7	[11.3 - 16.5]	7.52
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas prydzensis DSM 14232	22.4	[19.1 - 26.0]	19.8	[17.6 - 22.2]	21	[18.2 - 24.1]	0.27
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas prydzensis DSM 14232	22.4	[19.1 - 26.0]	19.8	[17.6 - 22.2]	21	[18.2 - 24.1]	0.27
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas denitrificans DSM 6059	13.1	[10.4 - 16.4]	19.7	[17.5 - 22.1]	13.5	[11.1 - 16.2]	6.16
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas lipolytica CGMCC 1.8499	14	[11.2 - 17.4]	19.7	[17.5 - 22.1]	14.2	[11.8 - 17.1]	1.72
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas denitrificans DSM 6059	12.8	[10.1 - 16.1]	19.7	[17.5 - 22.1]	13.2	[10.9 - 16.0]	8.48
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas amylolytica JW1	14.9	[12.0 - 18.3]	19.7	[17.5 - 22.1]	15	[12.6 - 17.9]	0.15
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas undina NCIMB 2128	13.5	[10.7 - 16.8]	19.7	[17.5 - 22.1]	13.8	[11.4 - 16.6]	7.3
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas gelatinilytica NH153	13.9	[11.1 - 17.3]	19.7	[17.5 - 22.1]	14.2	[11.7 - 17.0]	5.85
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas marina mano4	13.6	[10.8 - 16.9]	19.7	[17.5 - 22.1]	13.9	[11.5 - 16.7]	3.55
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas shioyasakiensis JCM 18891	14.1	[11.3 - 17.5]	19.7	[17.5 - 22.1]	14.3	[11.9 - 17.1]	1.92
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas atlantica NBRC 103033	13.6	[10.8 - 16.9]	19.7	[17.5 - 22.1]	13.9	[11.5 - 16.7]	2.5
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas denitrificans DSM 6059	13.1	[10.4 - 16.4]	19.7	[17.5 - 22.1]	13.5	[11.1 - 16.2]	6.16
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas shioyasakiensis JCM 18891	14.1	[11.3 - 17.5]	19.7	[17.5 - 22.1]	14.3	[11.9 - 17.2]	1.98
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	14.1	[11.3 - 17.5]	19.7	[17.5 - 22.1]	14.3	[11.9 - 17.2]	1.98
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas atlantica NBRC 103033	13.6	[10.8 - 16.9]	19.7	[17.5 - 22.1]	13.9	[11.5 - 16.7]	2.44
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas citrea NCIMB 1889	14.5	[11.6 - 17.8]	19.6	[17.4 - 22.0]	14.6	[12.2 - 17.5]	2.14
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas piscicida ATCC 15057	14.1	[11.3 - 17.5]	19.6	[17.4 - 22.0]	14.3	[11.9 - 17.1]	1.94
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas carrageenovora ATCC 43555	13.8	[11.0 - 17.2]	19.6	[17.4 - 22.0]	14.1	[11.6 - 16.9]	7.83
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas byunsanensis JCM 12483	14.4	[11.5 - 17.8]	19.6	[17.4 - 22.0]	14.5	[12.1 - 17.4]	1.59
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas lipolytica CGMCC 1.8499	14	[11.2 - 17.4]	19.6	[17.4 - 22.0]	14.3	[11.8 - 17.1]	1.78

'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas haloplanktis ATCC 14393	13.7	[10.9 - 17.0]	19.6	[17.4 - 22.0]	14	[11.6 - 16.8]	2.36
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas marina mano4	19.1	[16.0 - 22.7]	19.6	[17.4 - 22.0]	18.5	[15.8 - 21.5]	1.24
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas marina mano4	19.1	[16.0 - 22.7]	19.6	[17.4 - 22.0]	18.5	[15.8 - 21.5]	1.23
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas arctica DSM 18437	13.5	[10.7 - 16.8]	19.6	[17.4 - 22.0]	13.8	[11.4 - 16.6]	4.21
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas rubra ATCC 29570	14.4	[11.6 - 17.8]	19.6	[17.4 - 22.0]	14.6	[12.2 - 17.5]	4.53
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas byunsanensis JCM 12483	14.4	[11.5 - 17.8]	19.6	[17.4 - 22.0]	14.5	[12.1 - 17.4]	1.59
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas denitrificans DSM 6059	13.1	[10.4 - 16.4]	19.6	[17.4 - 22.0]	13.5	[11.1 - 16.2]	6.56
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas haloplanktis ATCC 14393	13.6	[10.9 - 17.0]	19.6	[17.4 - 22.0]	13.9	[11.5 - 16.7]	2.42
'Pseudoalteromonas sp. CO302Y' (NZ SGPF00000000.1)	Pseudoalteromonas peptidolytica NBRC 101021	14	[11.2 - 17.3]	19.5	[17.3 - 21.9]	14.2	[11.8 - 17.0]	1.55
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas marina mano4	13.7	[10.9 - 17.0]	19.5	[17.3 - 21.9]	13.9	[11.5 - 16.8]	3.61
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	Pseudoalteromonas citrea NCIMB 1889	14.2	[11.4 - 17.6]	19.5	[17.3 - 21.9]	14.4	[12.0 - 17.3]	0.16
'Pseudoalteromonas sp. CO109Y' (NZ SGPD00000000.1)	'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	13.9	[11.1 - 17.2]	19.5	[17.3 - 21.9]	14.1	[11.7 - 16.9]	5.97
'Pseudoalteromonas sp. CO133X' (NZ SGPE00000000.1)	Pseudoalteromonas peptidolytica NBRC 101021	14	[11.2 - 17.3]	19.5	[17.3 - 21.9]	14.2	[11.8 - 17.0]	1.55
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas prydzensis DSM 14232	13.9	[11.1 - 17.2]	19.5	[17.3 - 21.9]	14.1	[11.7 - 16.9]	2.11
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas arctica DSM 18437	13.5	[10.7 - 16.8]	19.4	[17.2 - 21.8]	13.8	[11.4 - 16.5]	4.15
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas telluritireducens DSM 16098	13.7	[10.9 - 17.0]	19.4	[17.2 - 21.8]	13.9	[11.5 - 16.8]	6.33
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas citrea NCIMB 1889	14.5	[11.6 - 17.9]	19.4	[17.2 - 21.8]	14.6	[12.2 - 17.5]	2.08
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas atlantica NBRC 103033	13.6	[10.8 - 16.9]	19.3	[17.1 - 21.7]	13.9	[11.5 - 16.7]	6.49
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas neustonica PAMC 28425	13.6	[10.8 - 16.9]	19.3	[17.1 - 21.7]	13.9	[11.5 - 16.7]	3.53
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas neustonica PAMC 28425	13.6	[10.8 - 16.9]	19.2	[17.0 - 21.6]	13.9	[11.5 - 16.7]	3.48
'Pseudoalteromonas sp. CO348' (NZ SGPI00000000.1)	Pseudoalteromonas prydzensis DSM 14232	13.8	[11.0 - 17.2]	19.2	[17.0 - 21.6]	14.1	[11.6 - 16.9]	2.05
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas prydzensis DSM 14232	13.7	[10.9 - 17.0]	19.2	[17.1 - 21.6]	13.9	[11.5 - 16.7]	6.1
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas arctica DSM 18437	13.5	[10.7 - 16.8]	19.2	[17.0 - 21.6]	13.8	[11.4 - 16.6]	8.2
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Pseudoalteromonas denitrificans DSM 6059	12.9	[10.2 - 16.2]	19.1	[16.9 - 21.5]	13.3	[10.9 - 16.0]	8.53
'Pseudoalteromonas sp. CO342X' (NZ SGPH00000000.1)	Vibrio panuliri LBS2	12.8	[10.1 - 16.1]	19.1	[16.9 - 21.5]	13.2	[10.8 - 15.9]	1.85

'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas lipolytica CGMCC 1.8499	13.8	[11.0 - 17.2]	19.1	[17.0 - 21.5]	14.1	[11.7 - 16.9]	5.77
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas denitrificans DSM 6059	12.8	[10.1 - 16.1]	19	[16.8 - 21.4]	13.2	[10.9 - 16.0]	12.53
'Pseudoalteromonas sp. CO325X' (NZ SGPG00000000.1)	Pseudoalteromonas marina mano4	13.6	[10.8 - 16.9]	19	[16.8 - 21.4]	13.9	[11.5 - 16.7]	7.6



Chemical Formula: $C_9H_6BrO^+$
Exact Mass: 208.9597
Molecular Weight: 210.0495

Figure S1. Aromatic elimination of aryl polyenes

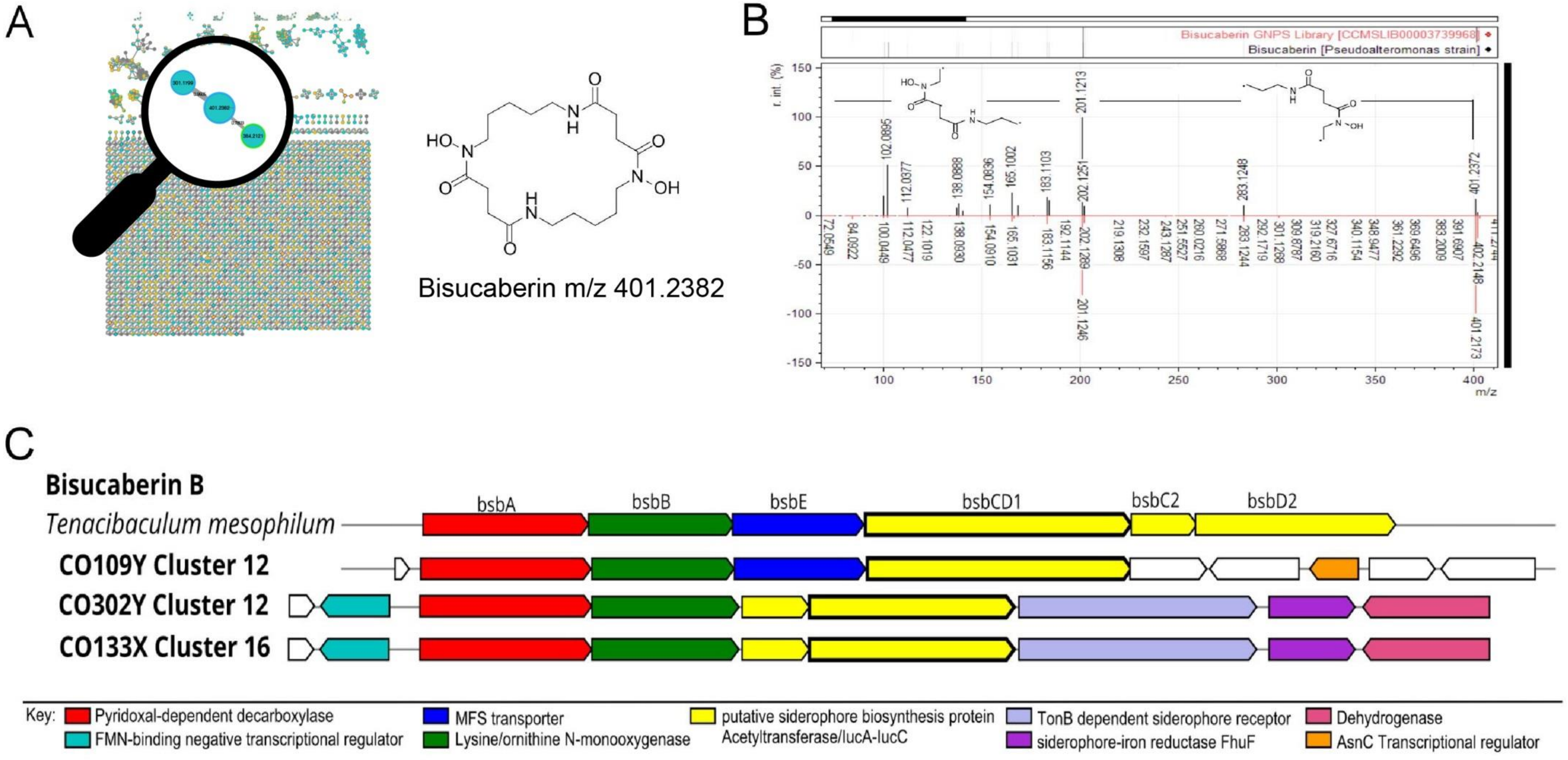
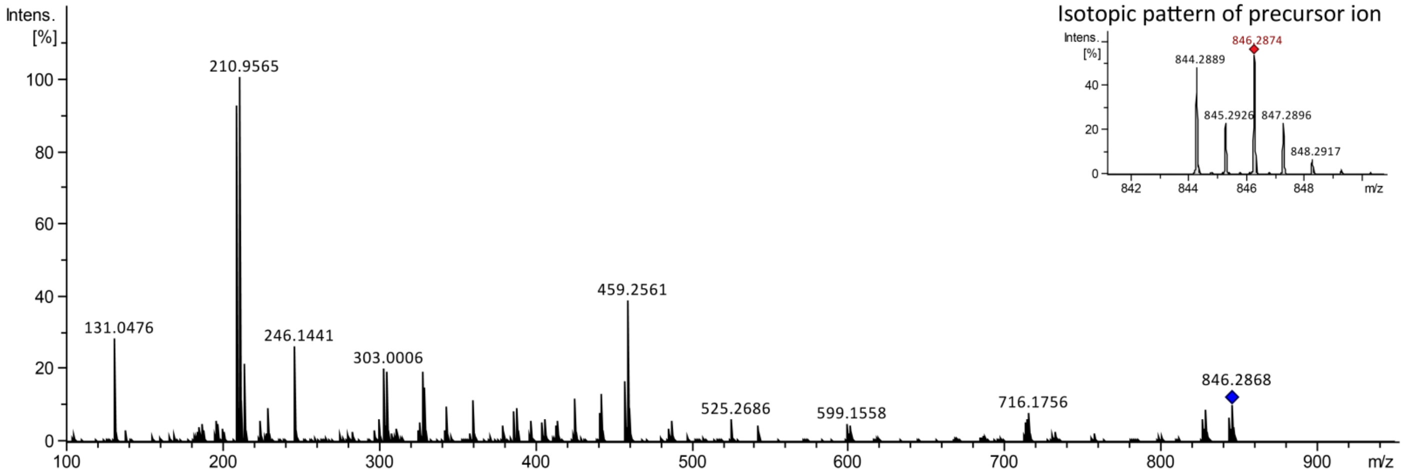


Figure S2. Bisucaberin A) Node of bisucaberin in the molecular network and its molecular structure. B) MS/MS fragmentation patterns of Bisucaberin. C) Synteny map of bisucaberin B BGC (*Tenacibaculum mesophilum* NBCR 16307) compared with clusters of non-pigmented strains, all homologous genomic regions were identified by MultiGeneBlast. The most similar BGC is showed immediately below the cluster. The core biosynthetic genes are shown in bold.

Bromoalterochromide A/A′

HRMS:m/z 844.2889 (calcd. 844.2875 for $[M+H]^+$, $C_{38}H_{50}BrN_7O_{10}$; error 1.6 ppm)



Dibromoalterochromide A/A′

HRMS:m/z 922.1996 (calcd. 922.1980 for $[M+H]^+$, $C_{38}H_{50}Br_2N_7O_{10}$; error -1.7 ppm)

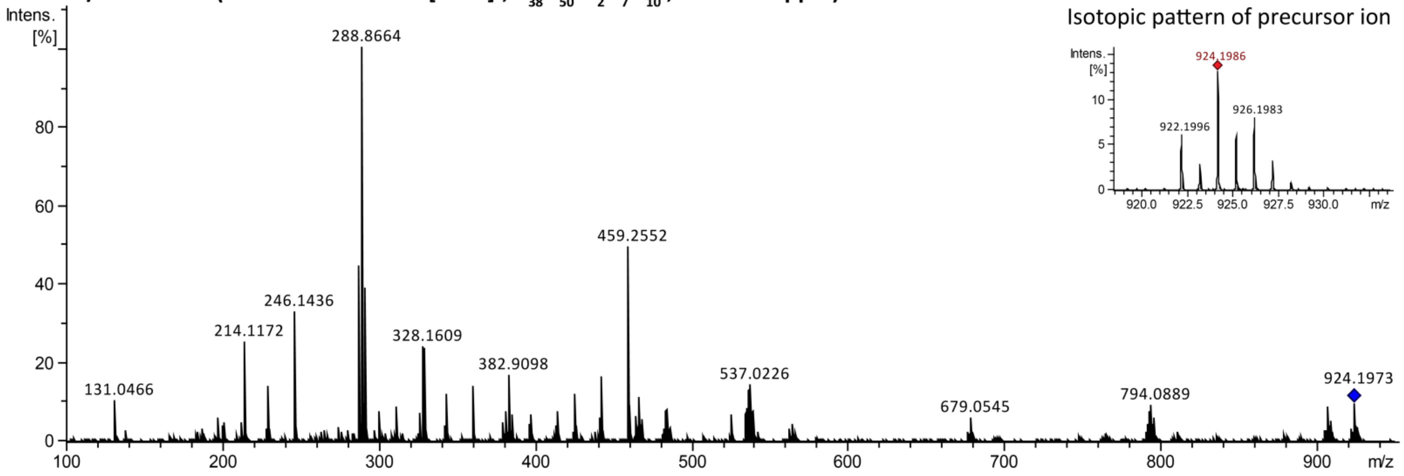
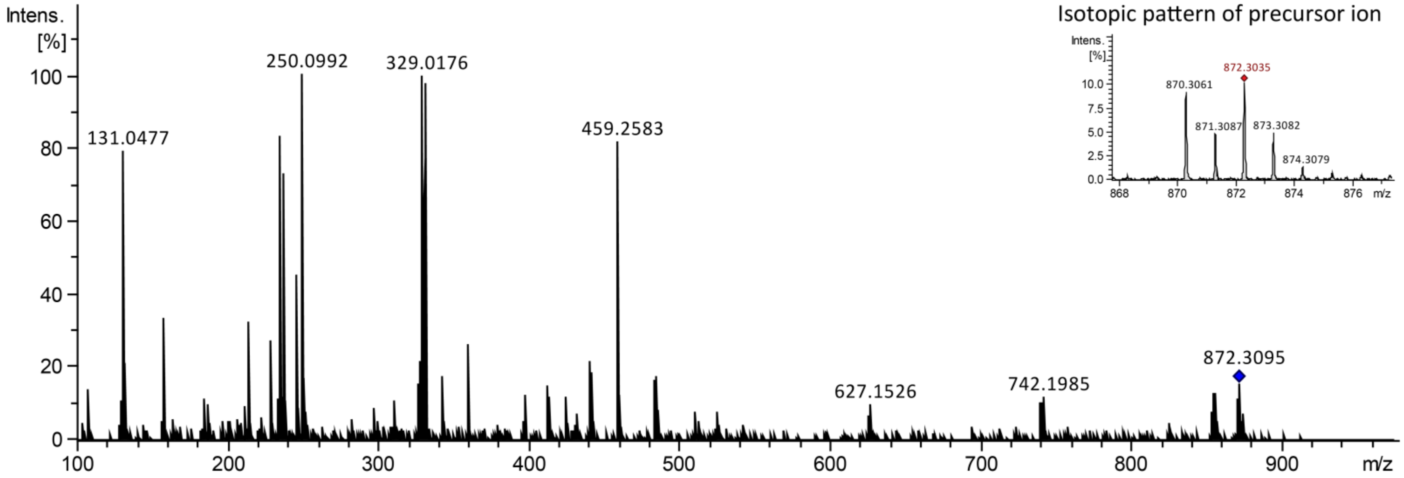


Figure S3. MS/MS spectra for bromoalterochromide A/A′ (**1**,**2**) and dibromoalterochromide A/A′ (**3**,**4**).

Bromoalterochromide B/B′
HRMS:m/z 870.3061 (calcd. 870.3032 for $[M+H]^+$, $C_{40}H_{53}BrN_7O_{10}$; error 3.4 ppm)



Dibromoalterochromide B/B′
HRMS:m/z 948.2175 (calcd. 948.2137 for $[M+H]^+$, $C_{40}H_{52}Br_2N_7O_{10}$; error -4.1 ppm)

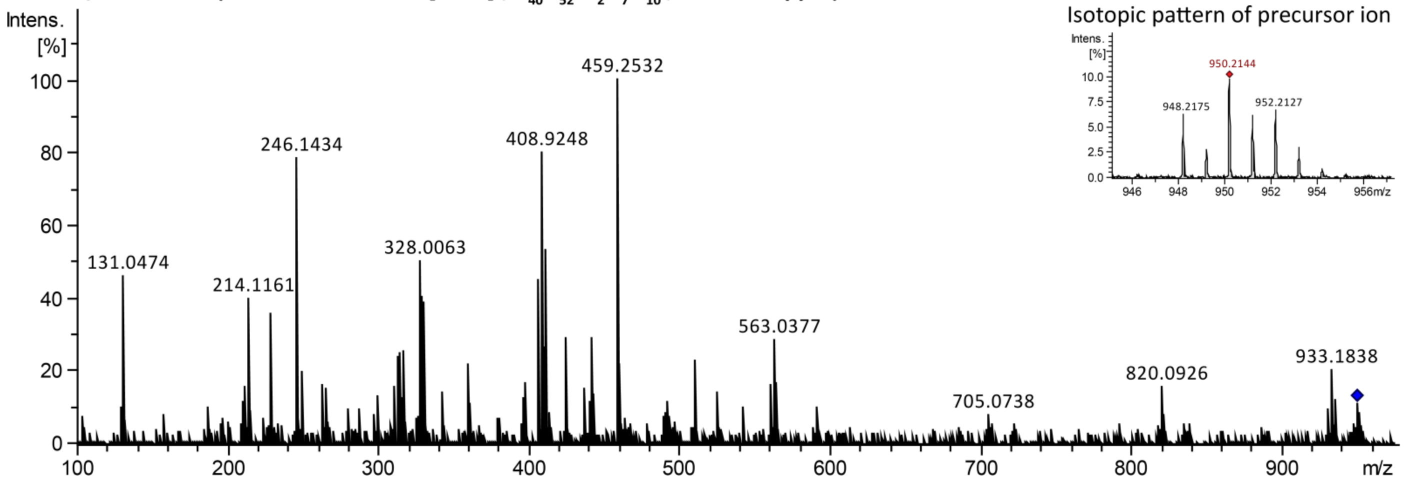


Figure S4. MS/MS spectra for bromoalterochromide B/B′ (**5**,**6**) and dibromoalterochromide B/B′ (**7**,**8**).

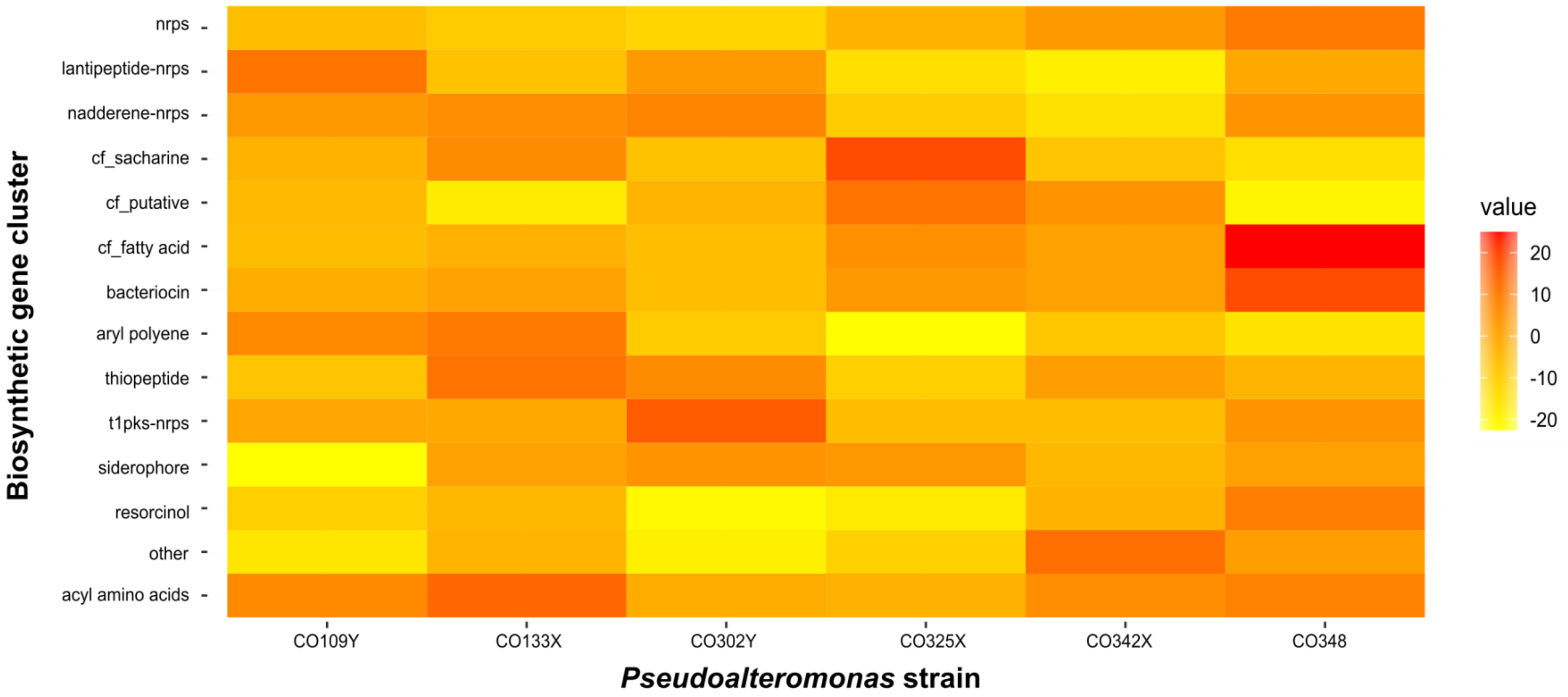


Figure S5. Heatmap containing BGCs categories predicted by AntiSMASH in *Pseudoalteromonas* strains genomes.

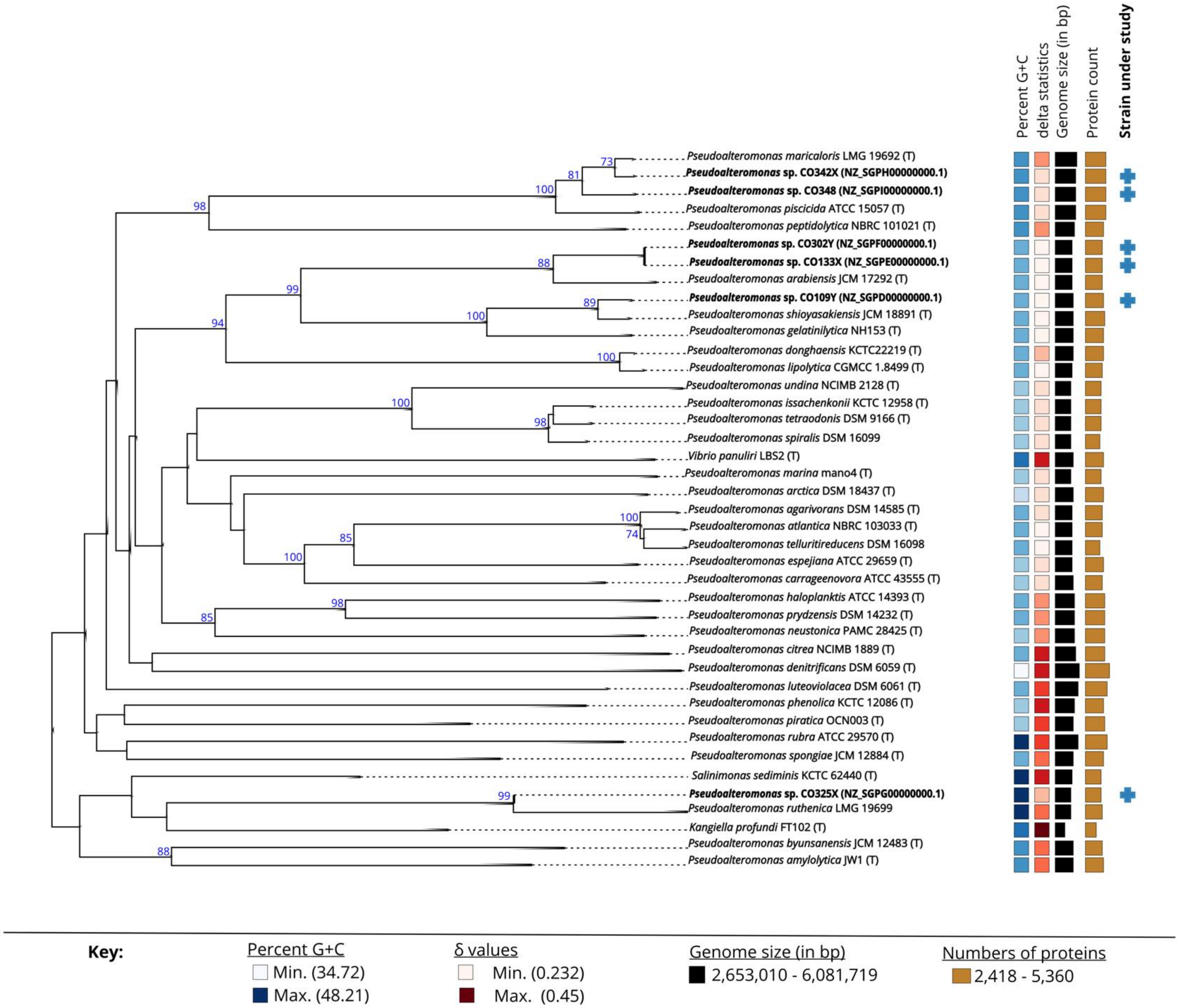


Figure S6. Genome Blast Distance Phylogeny (GBDP) of *Pseudoalteromonas* strains from Coiba. Tree inferred with FastME 2.1.6.1 from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula d5. The numbers above branches are GBDP pseudo-bootstrap support values (> 70% are shown next to its respective branch). Leaf labels are annotated by affiliation to species, genomic G+C content, δ values, overall genome sequence length, and number of proteins. *Pseudoalteromonas* strains genomes from Coiba National Park are highlighted in bold and with a blue cross in the last annotations column.