Three novel bacteria associated with two centric diatom species from the Mediterranean Sea, *Thalassiosira rotula* and *Skeletonema marinoi*

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Supplementary Figures

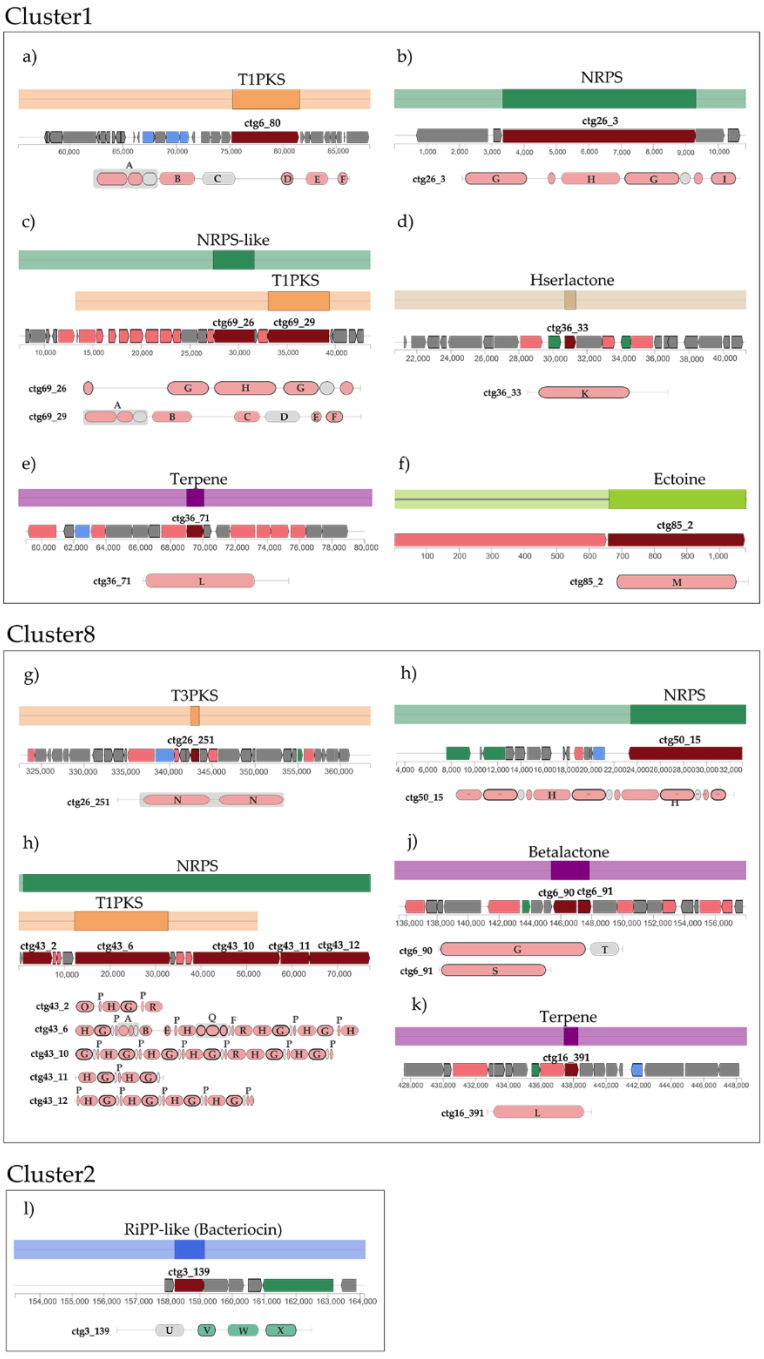
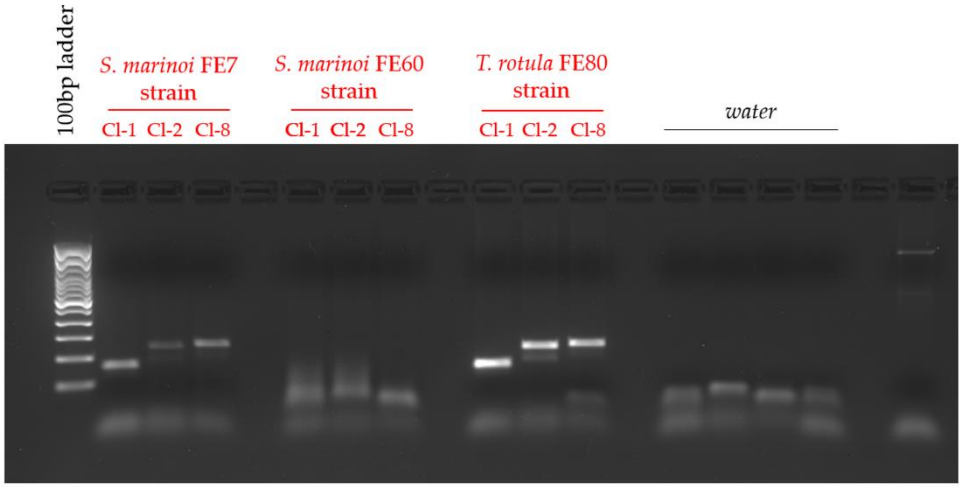


Figure S1. Analysis of MAG secondary metabolite pathways predicted using antiSMASH. Representative clusters organization of pathways related to Cluster1 *(a-f)*, Cluster8 *(g-k)* and Cluster2 (l). The genes constituting the clusters in the pathways are represented in different colors: red for core biosynthetic genes, pink for additional biosynthetic genes, blue for transport-related genes, green for regulatory genes and grey for other genes. The pfam domains constituting each core biosynthetic gene are also represented under the total cluster and are indicated by the letters ctg associated to numbers (i.e. ctg3_139). Domain abbreviations: A= ketoacyl synthase (KS), B= acyltransferase (AT), C= polyketide synthase dehydratase (PS-DH), D= Enoylreductase (ER), E= ketoreductase (KR), F= phosphopantetheine attachment site (PP), G= AMP-binding, H= condensation, I= thioesterase (TE), J= Bac_luciferase, K= Autoinducer synthase, L= squalene/phytoene synthase (SQS_PSY), M= Ectoine synthase, N= Chalchone and stylbene synthase, O= Co-enzyme A ligase (CAL), P= Peptidyl carrier protein (PCP), Q= Adenylation domain with integrated oxidase domain (A-OX), R= Epimerization, S=HMGL-like, T= C-terminal, U= Pkinase domain-containing protein 9 (PAS_9), V= His Kinase A (phosphoacceptor) domain (HisKA), W= Histidine kinase-like ATPases (HATPase c), X= Response regulator.

a



b

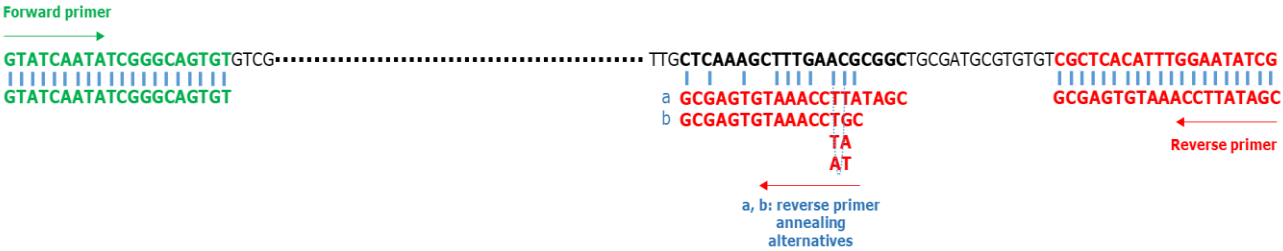


Figure S2. Confirmation of Cls presence in diatoms xenic cultures.

a. Uncropped image showing the MAG presence in different diatom species and strains. PCR amplification from 50ng of free-living bacterial fraction (FL) genomic DNA (gDNAs) with MAG-specific primers. gDNAs were extracted from the FL fraction of *Thalassiosira rotula* FE80 strain, *Skeletonema marinoi* FE7 and FE60 strains harvested at day 7 of growth. Abbreviations: Cl-1= Cluster1, Cl-2= Cluster2, Cl-8= Cluster8. 100bp ladder: from bottom to top: 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000 bps.

b. Cl-2 reverse primer alternative annealing sites responsible for the lower band visible in panel **a-** lanes *S. marinoi* FE7 strain and *T. rotula* FE80 strain, Cl-2. The reverse primer has some aspecific annealing possibilities forward in the sequence, in respect to the original primer site chosen for the amplification. Sequencing of the lower band confirmed its specificity as Cl-2 contig_82 and its derivation from a second annealing site of the reverse primer.

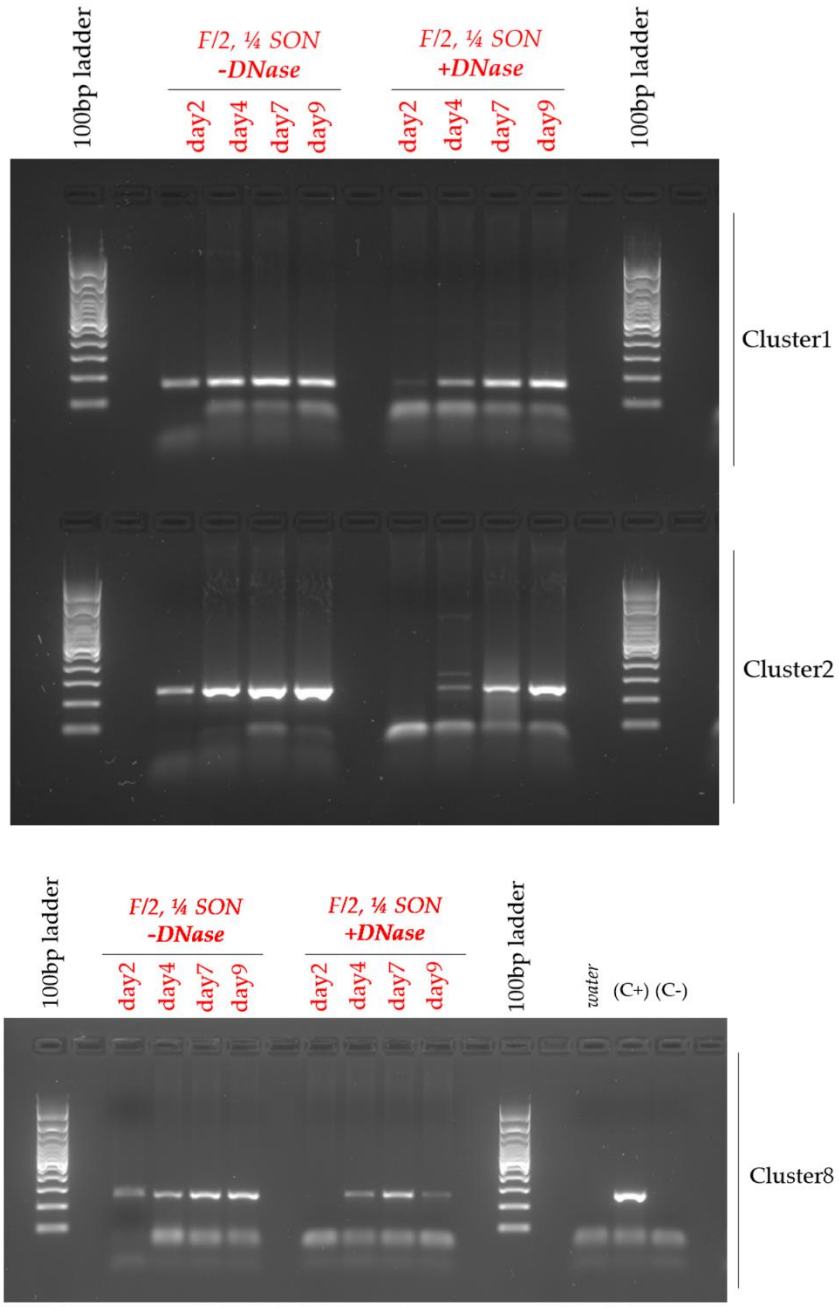


Figure S3. Uncropped image showing the detection of MAG following the introduction of *S. marinoi* FE7-FL bacteria into axenic *T. rotula* FE80 cultures. MAG PCR amplification from 50ng of strictly-associated (SA) and FL fractions gDNAs collected from *T. rotula* FE80 cultures in which FE7-FL bacteria were reintroduced. MAG presence was inspected after 1 (FE80_1), 3 (FE80_3), 6 (FE80_6) and 8 (FE80_8) months from the bacterial reintroduction. All the cultures were harvested at day 7 of growth. Abbreviations: (C-) = mixed gDNA from FE80 culture in which bacteria were not added, (C+) = mixed gDNA from FE7 culture. 100bp ladder: from bottom to top: 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000 bps.

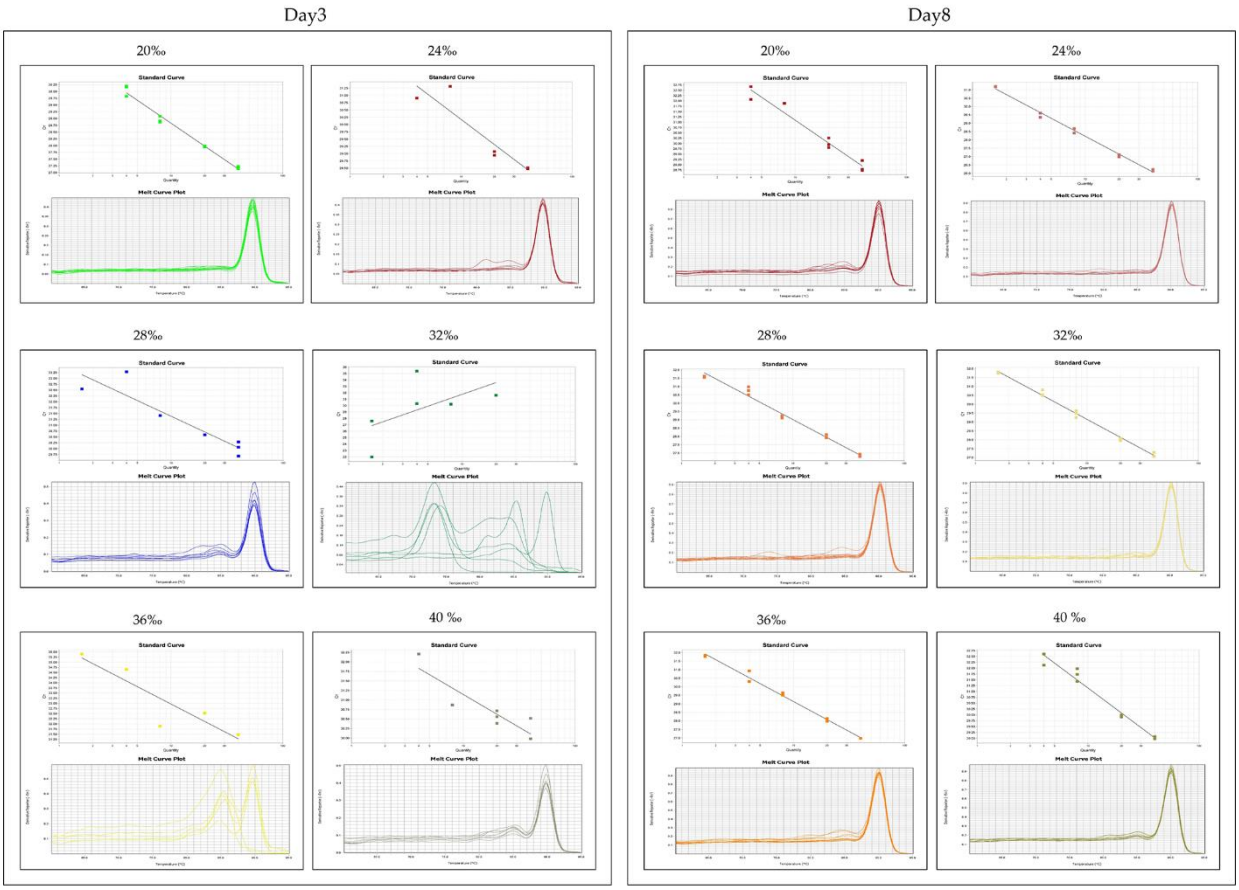


Figure S4. qPCR Standard Curves and their Melt Curve Plots with specific primers for the evaluation of Cl-1 abundance in SA fraction of cultures grown in different salinities. A standard curve was made for each salinity both at day 3 and day 8 of growth.

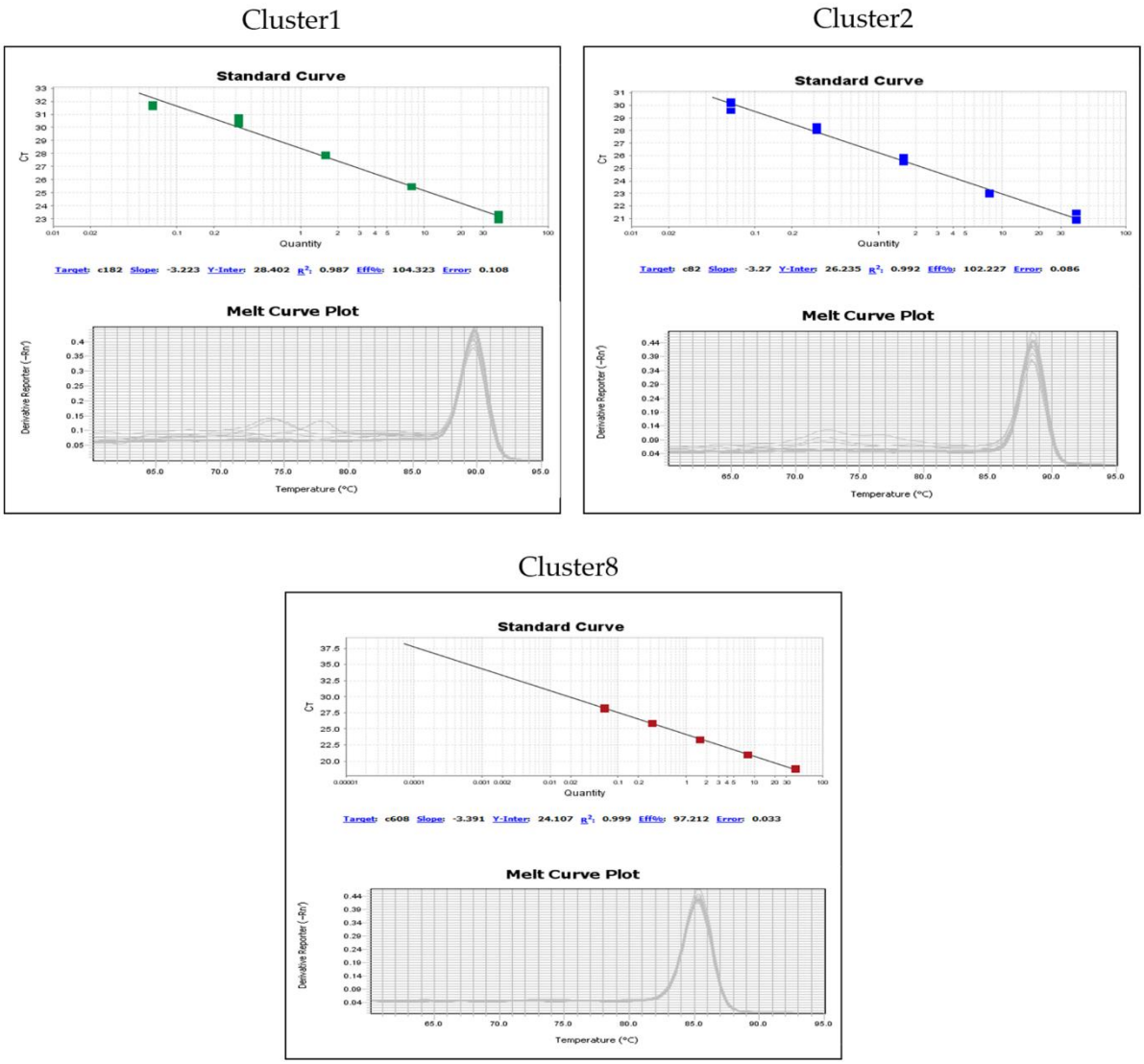


Figure S5. qPCR Standard Curve and its Melt Curve Plot with specific primers for the evaluation of MAG abundance in SA-FL culture fractions

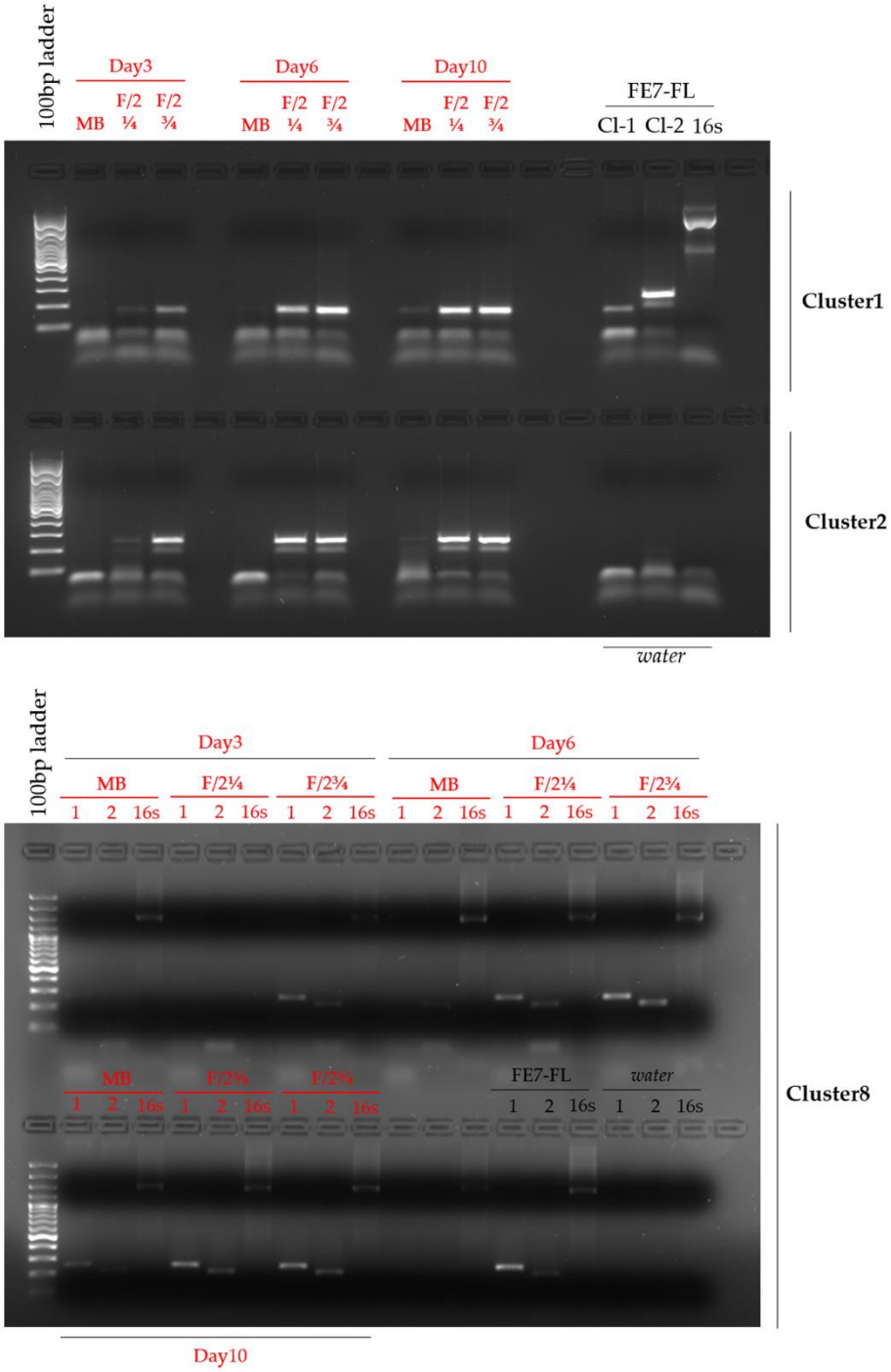


Figure S6. Uncropped image showing the detection of MAG growth in different types of media. PCR amplifications with MAG-specific primers on gDNA (50ng) of FE7-FL grown in the following types of medium: Marine Broth supplemented with FE7 spent culture medium (MB), F/2 supplemented with two different sonicated diatoms concentrations (¼ and ¾). Bacterial growth was followed along ten days. Abbreviations: Cl-1= Cluster1, Cl-2= Cluster2, 16s= E9/ U1510 universal primer. For Cluster8 were used two primer pairs (1= C8_c988; 2= C8_c450). 100bp ladder: from bottom to top: 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000 bps.

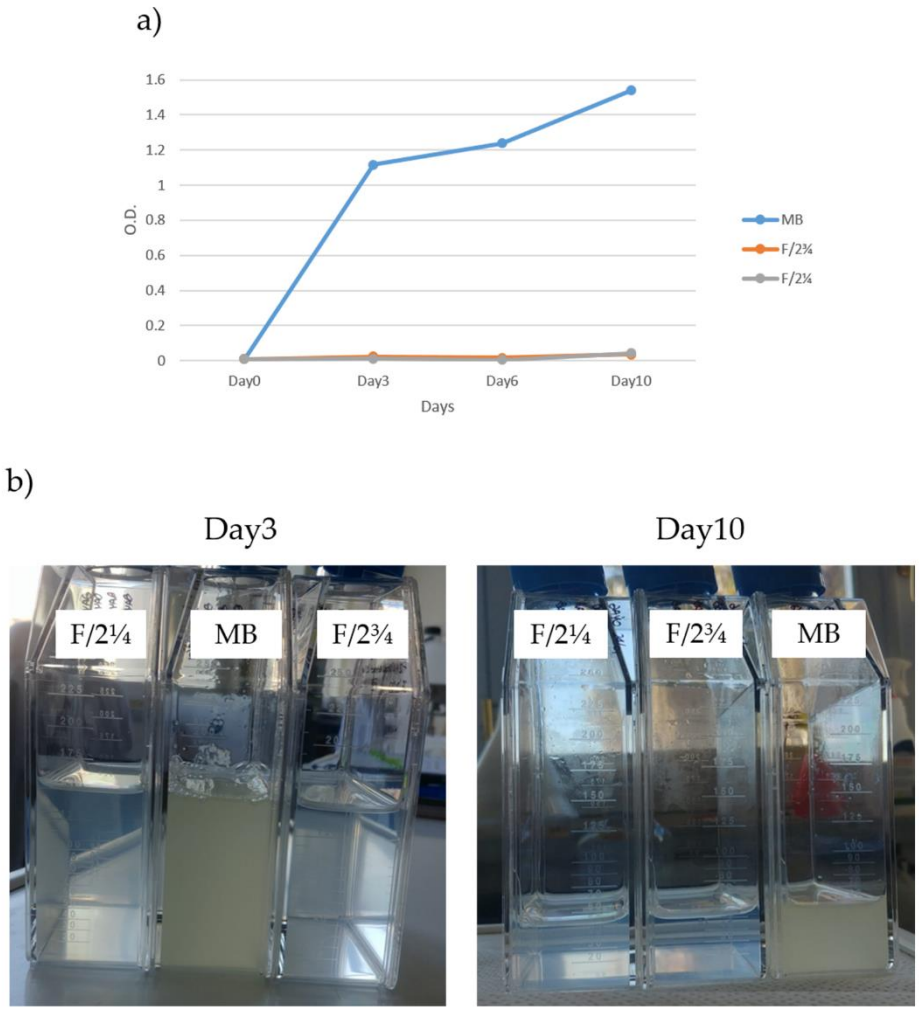


Figure S7. Optical density (OD) measurement and visual inspection of cultures grown in different types of media. **a)** OD reading of the FE7-FL total bacteria grown in MB or F/2 with the two sonicate concentrations. The OD were normalized on the blank (only MB or only F/2 without bacteria) and the means of three reads for each time point are reported in the graph; **b)** Visual inspection of the total FE7-FL bacteria growing in the three different media at day3 (starting sampling point) and day10 (final sampling point).

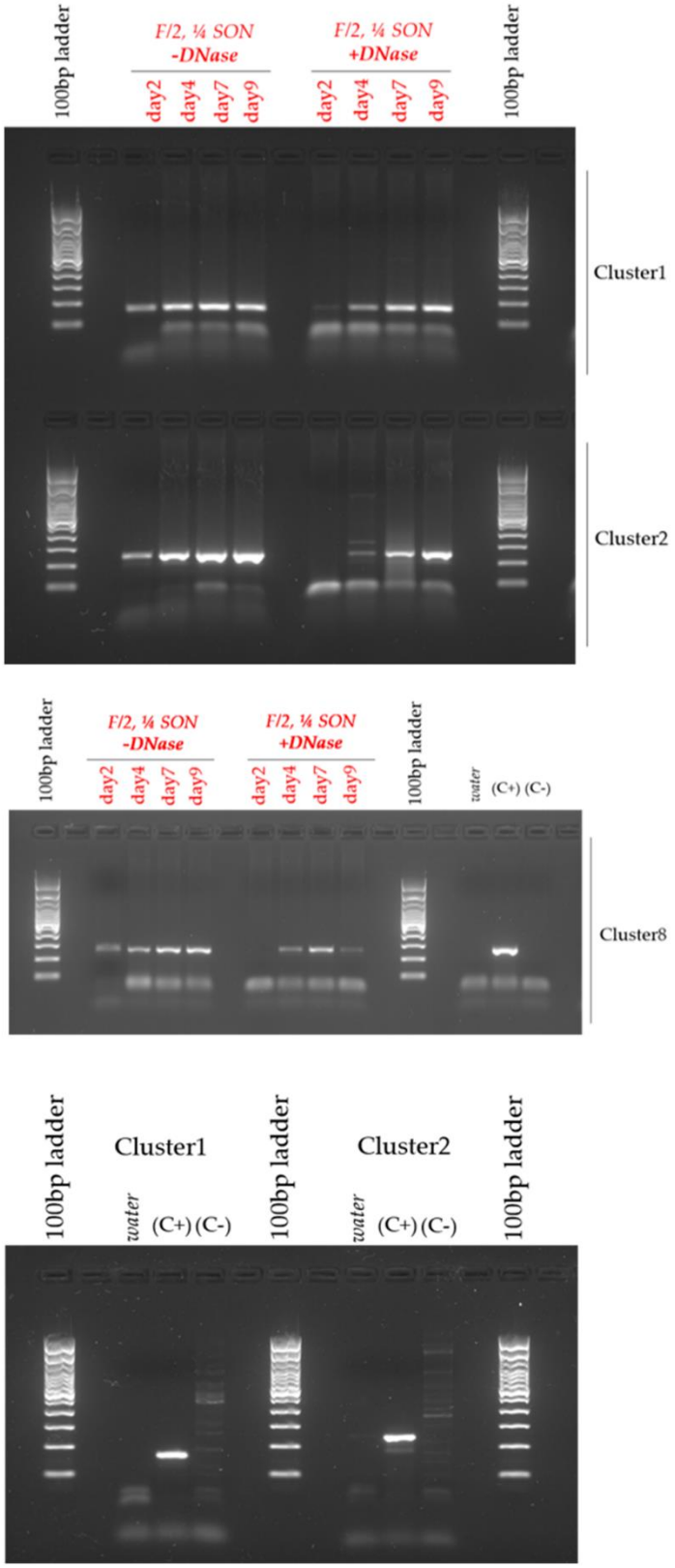


Figure S8. Uncropped image showing MAG detection in a medium F/2¼ with and without DNase treatment over nine days. PCR-based MAG detection in medium F/2¼ with and without DNase treatment over nine days. PCR amplifications with MAG-specific primers on gDNA (50ng) from FE7-FL bacteria grown in F/2¼ medium with (+DNase) and without (-DNase) the addiction of DNase. MAG presence was evaluated along nine days of culture growth. Abbreviations: (C-)= mixed gDNA from FE80 culture before the reintroduction of the bacteria, (C+)= mixed gDNA from FE7 culture. 100bp ladder: from bottom to top: 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000 bps.

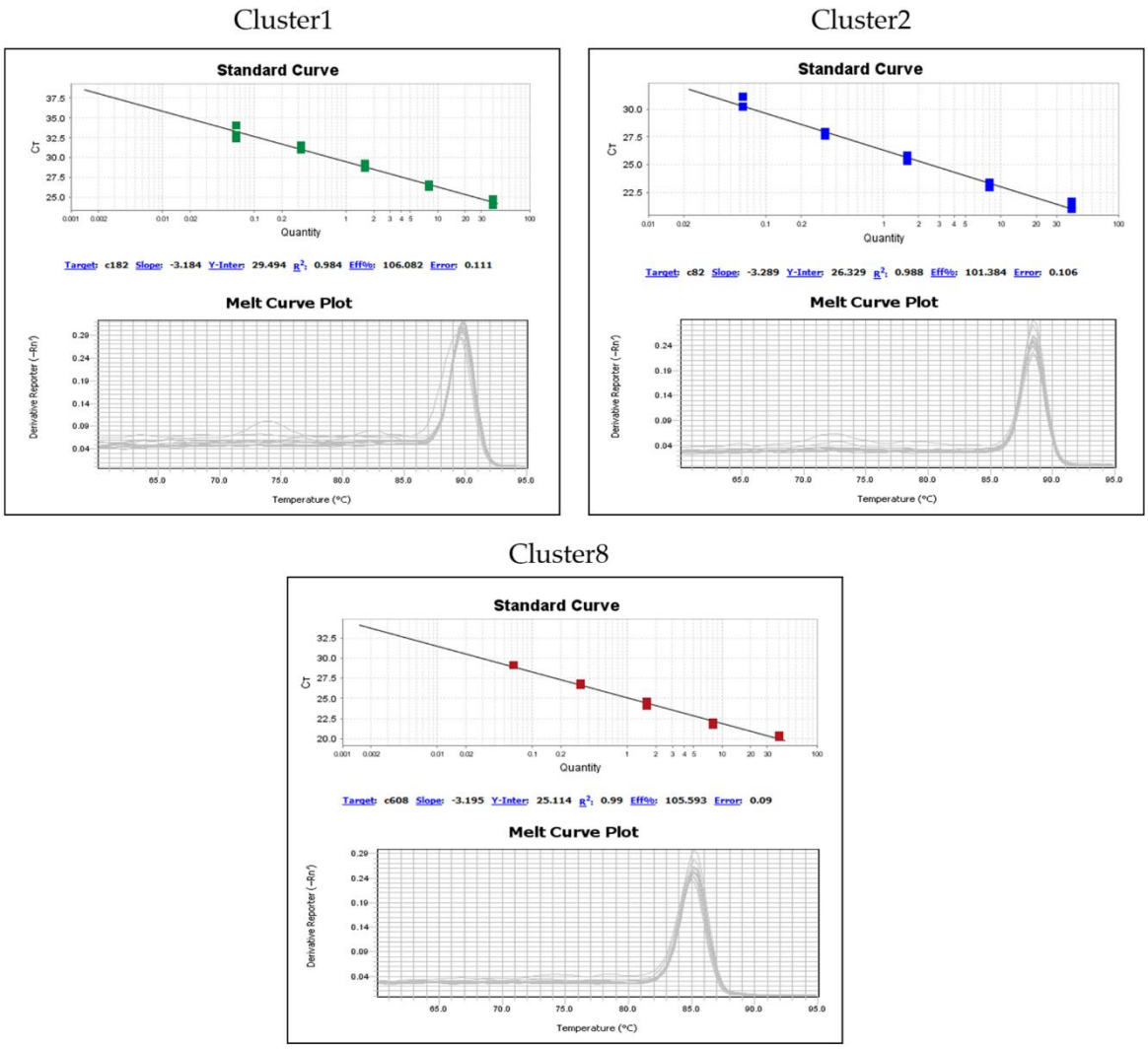


Figure S9. qPCR Standard Curve and its Melt Curve Plot with specific primers for the evaluation of MAG abundance in different media cultures.

Supplementary Tables

Table S1. General genome features and MIxS of the Cluster1.

Items	Description
General features	
Classification Cluster1	Domain *Bacteria* Phylum *Proteobacteria* Class *Alphaproteobacteria* Order *Rhodobacterales* Family *Rhodobacteraceae* Genus *Aestuariivita* Species *sp.*
Gram stain	Negative
Cell shape	NA
Motility	Motile
Sporulation	NA
Temperature Range; Optimum	18°C
pH range; optimum	NA
Salinity range; optimum	36ppm
Carbon source	NA
MIGS data	
Investigation_type	Bacteria
Project_name	Genome sequence of three bacteria associated with the diatom *Thalassiosira rotula*
Lat_lon	40°48.5′N, 14°15′E
Depth	NA
Alt_elev	NA
Geo_loc_name	Mediterranean sea: Central Tyrrhenian sea: East Sector
Collection_date	2011
Env_biome	marine biome [ENVO:00000447]
Env_feature	alga [ENVO:02500019]
Env_material	water [ENVO:00002006]
Env_package	host-associated environment [ENVO:01001000]
Ref_biomaterial	NA
Pathogenicity	NA
Biotic_relationship	Both free living and strictly associated
Trophic_level	Photoheterotroph
Rel_to_oxygen	Aerobic
Isol_growth_condt	NA
Samp_store_temp	18°C
Sediment_type	NA
Genome assembly data	

Seq_meth	Illumina MiSeq
Assembly	CLC Genomics
Finishing_strategy	N/A
Annot_source	PGAP (NCBI)

MAG Genome attribute

Total number of reads before trimming	20,505,104
Total number of reads after trimming	19,519,539
Average read length	239,5
Number of reads in contigs	17,286,414
Number of contigs >5kb	416
N50 (bp)	146,992
Assembly size (Mb)	22,15
Maximum contig length (bp)	952,220

Table S2. General genome features and MIxS of the Cluster2.

Items	Description
General features	
Classification Cluster2	Domain *Bacteria* Phylum *Proteobacteria* Class *Alphaproteobacteria* Order *Parvibaculales* Family *Parvibaculaceae* Genus *Mf105b01* Species *sp.*
Gram stain	Negative
Cell shape	NA
Motility	Motile
Sporulation	NA
Temperature Range; Optimum	18°C
pH range; optimum	NA
Salinity range; optimum	36ppm
Carbon source	NA
MIGS data	
Investigation_type	Bacteria
Project_name	Genome sequence of three bacteria associated with the diatom *Thalassiosira rotula*
Lat_lon	40°48.5'N, 14°15'E
Depth	NA
Alt_elev	NA
Geo_loc_name	Mediterranean sea: Central Tyrrhenian sea: East Sector
Collection_date	2011
Env_biome	marine biome [ENVO:00000447]
Env_feature	alga [ENVO:02500019]
Env_material	water [ENVO:00002006]
Env_package	host-associated environment [ENVO:01001000]
Ref_biomaterial	NA
Pathogenicity	NA
Biotic_relationship	Both free living and strictly associated
Trophic_level	
Rel_to_oxygen	Aerobic
Isol_growth_condt	NA
Samp_store_temp	18°C
Sediment_type	NA
Genome assembly data	
Seq_meth	Illumina MiSeq
Assembly	CLC Genomics

Finishing_strategy	N/A
Annot_source	PGAP (NCBI)
MAG Genome attribute	
Total number of reads before trimming	20,505,104
Total number of reads after trimming	19,519,539
Average read length	239,5
Number of reads in contigs	17,286,414
Number of contigs >5kb	416
N50 (bp)	146,992
Assembly size (Mb)	22,15
Maximum contig length (bp)	952,220

Table S3. General genome features and MIxS of the Cluster8.

Items	Description
General features	
Classification Cluster8	Domain *Bacteria* Phylum *Bacteroidota* Class *Bacteroidia* Order *Cytophagales* Family *Cyclobacteriaceae* Genus *Roseivirga_A* Species *sp.*
Gram stain	Negative
Cell shape	NA
Motility	Nonmotile
Sporulation	NA
Temperature Range; Optimum	18°C
pH range; optimum	NA
Salinity range; optimum	36ppm
Carbon source	NA
MIGS data	
Investigation_type	Bacteria
Project_name	Genome sequence of three bacteria associated with the diatom *Thalassiosira rotula*
Lat_lon	40°48.5′N, 14°15′E
Depth	NA
Alt_elev	NA
Geo_loc_name	Mediterranean sea: Central Tyrrhenian sea: East Sector
Collection_date	2011
Env_biome	marine biome [ENVO:00000447]
Env_feature	alga [ENVO:02500019]
Env_material	water [ENVO:00002006]
Env_package	host-associated environment [ENVO:01001000]
Num_replicons	
Ref_biomaterial	NA
Pathogenicity	NA
Biotic_relationship	Both free living and strictly associated
Trophic_level	Chemoorganotroph
Rel_to_oxygen	Aerobic
Isol_growth_condt	NA
Samp_store_temp	18°C
Sediment_type	NA
Genome assembly data	
Seq_meth	Illumina MiSeq

Assembly	CLC Genomics
Finishing_strategy	N/A
Annot_source	PGAP (NCBI)
MAG Genome attribute	
Total number of reads before trimming	20,505,104
Total number of reads after trimming	19,519,539
Average read length	239,5
Number of reads in contigs	17,286,414
Number of contigs >5kb	416
N50 (bp)	146,992
Assembly size (Mb)	22,15
Maximum contig length (bp)	952,220

Table S4. PRISM *T. rotula* Metagenome-Assembled Genomes (MAG) Cluster annotation.

				***T. rotula* MAG-Cluster1**			
Biosynthetic Cluster	PK		NRP	acyl homoserine lactone	Acyl homoserine lactone	PK, NRP	Ectoine
Biosynthetic assemblies (ORF #)	71, 75	56, 60, 62	37626, 3	33, 50261	25	23, 24, 26	2
ORFs Domains	71: Phosphopantetheinyltransferase; 75: Ketosynthase, Acyltransferase, Dehydratase, Enoylreductase, Ketoreductase, Thiolation.	56: Ketosynthase; 60: Thiolation; 62: Acyltransferase.	37626: Lasso peptide precursor; 3: Acyl adenylating enzyme, Thiolation, Condensation, Adenylation, Thiolation, Thioesterase.	33: Acyl homoserine lactone synthase; 50261: Dehydratase.	25: Acyl homoserine lactone synthase.	23: Phosphopantetheinyltransferase; 24: Formyltransferase, Adenylation, Adenylation, Thiolation; 26: Ketosynthase, Acyltransferase, Ketoreductase, Dehydratase, Thiolation, Thioesterase.	2: Ectoine synthase.
				***T. rotula* MAG-Cluster2**			
Biosynthetic Cluster	PK						
Biosynthetic assemblies (ORFs #)	352, 355, 356						
ORFs Domains	352: Acyltransferase; 355: Thiolation; 356: Ketosynthase.						
				***T. rotula* MAG-Cluster8**			
Biosynthetic Cluster	PK, NRP		NRP	lasso peptide			
Biosynthetic assemblies (ORFs #)	2, 3,_6,_8,_10,_11, 12		13, 17	178, 80751, 188, 80664, 191, 192			
ORFs Domains	2: Acyl adenylating enzyme, Thiolation, Condensation, Adenylation, Thiolation, Epimerization. 3: 2,3-diaminopropionate biosynthesis protein SbnA. 6: Condensation, Adenylation, Thiolation, Ketosynthase, Acyltransferase, Ketoreductase, Ketoreductase, Thiolation, Condensation, Adenylation, Adenylation, Thiolation, Epimerization, Condensation, Adenylation, Thiolation, Condensation, Adenylation, Thiolation, Condensation. 8: Amidotransferase. 10: Adenylation, Thiolation, Condensation, Adenylation, Thiolation, Condensation,		13: Thioesterase. 17: Condensation, Adenylation, Thiolation, Condensation, Adenylation, Thiolation, Condensation, Adenylation, Thioesterase.	178: Lasso peptide transglutaminase homolog; 80751: Putative lasso peptide precursor; 188: Sulfotransfera-se; 80664: Putative lasso peptide precursor; 191: Sulfotransfera-se; 192: Lasso peptide asparagine synthase homolog			

	Adenylation, Thiolation, Condensation, Adenylation, Thiolation, Epimerization, Condensation, Adenylation, Thiolation, Condensation, Adenylation, Thiolation.
	11: Condensation, Adenylation, Thiolation, Condensation, Adenylation.
	12: Thiolation, Condensation, Adenylation, Thiolation, Condensation, Adenylation, Thiolation, Condensation, Adenylation, Thiolation, Condensation, Adenylation, Thiolation, Condensation.

Table S5. qPCR quantization of Cl-1 abundance in SA fraction of cultures grown in different salinities.

Cluster1

Day3

	20‰		**24‰**		**28‰**	
Sample name	Quantity mean	Quantity SD	Quantity mean	Quantity SD	Quantity mean	Quantity SD
Replicate_1	14.5112409591674	0.798255980014801	8.16201210021972	0.606226086616516	N/D	N/D
Replicate_2	11.9483919143676	2.14905190467834	11.9473886489868	2.53087162971496	N/D	N/D
Replicate_3	12.2064056396484	3.06914186477661	12.0288705825805	3.67823576927185	N/D	N/D
	32‰		**36‰**		**40‰**	
Sample name	Quantity mean	Quantity SD	Quantity mean	Quantity SD	Quantity mean	Quantity SD
Replicate_1	N/D	N/D	N/D	N/D	N/D	N/D
Replicate_2	N/D	N/D	N/D	N/D	N/D	N/D
Replicate_3	N/D	N/D	N/D	N/D	N/D	N/D

Day8

	20‰		**24‰**		**28‰**	
Sample name	Quantity mean	Quantity SD	Quantity mean	Quantity SD	Quantity mean	Quantity SD
Replicate_1	31.6183595657348	5.80254477802653	6.68693971633911	0.831853449344635	11.7782106399536	3.32517790794372
Replicate_2	10.9883317947387	1.28338074684143	20.596580505371	1.56980264186859	39.6703758239746	1.72131192684173
Replicate_3	10.3919868469238	1.23993575572967	8.58546638488769	1.17350924015045	12.7557649612426	1.61978256702423
	32‰		**36‰**		**40‰**	
Sample name	Quantity mean	Quantity SD	Quantity mean	Quantity SD	Quantity mean	Quantity SD
Replicate_1	22.0469570159912	0.88727593421936	13.7929029464721	1.13168704509735	20.7034702301025	2.02587294578552
Replicate_2	14.0322103500366	3.17058825492858	30.1682376861572	3.14465661499737	11.9415206909179	0.597728669643402
Replicate_3	15.5249853134155	1.89186143875122	26.3027057647705	2.68924212455749	20.1522417068481	1.68568107645698

N/D – Not detected

Table S6. qPCR Slope, R^2 and % of Efficiency with specific primers for the evaluation of Cl-1 abundance in cultures with different salinities.

Cluster1

	Day3			**Day8**		
Standard curves	**Slope**	**R^2**	**Efficiency (%)**	**Slope**	**R^2**	**Efficiency (%)**
20‰	-2.816	0.983	126.497	-3.574	0.962	90.458
24‰	-2.877	0.872	122.655	-3.564	0.994	90.792
28‰	-2.228	0.852	181.147	-3.536	0.982	91.763
32‰	6.121	0.332	-31.351	-3.366	0.991	98.197
36‰	-2.812	0.803	126.801	-3.503	0.992	92.965
40‰	-1.722	0.799	280.820	-3.538	0.971	91.717

Table S7. qPCR quantization of MAG abundance in SA and FL fractions. Quantity Mean and Quantity Standard Deviations (SD) of the three MAG calculated via qPCR data analysis. Abbreviations: SA= strictly associated bacterial fraction; FL= free-living bacterial fraction; Day4= fourth day of culture growth; Day7= seventh day of culture growth.

Cluster1

	SA		FL	
Days	Quantity Mean	Quantity SD	Quantity Mean	Quantity SD
Day4	2.850962639	0.088266894	3.204114914	0.439069539
Day7	9.169445038	1.758309007	1.82853353	0.187807962

Cluster2

	SA		FL	
Days	Quantity Mean	Quantity SD	Quantity Mean	Quantity SD
Day4	4.156836987	0.520205617	0.114571519	0.026290052
Day7	12.14747334	0.741565466	0.185813785	0.033655368

Cluster8

	SA		FL	
Days	Quantity Mean	Quantity SD	Quantity Mean	Quantity SD
Day4	5.457804203	0.176898703	0.44285664	0.11048381
Day7	9.304740906	1.28759563	3.954962969	0.157003194

Table S8. qPCR Slope, R^2 and % of Efficiency with specific primers for the evaluation of MAG abundance in SA-FL culture fractions samples.

Primer name	Slope	R^2	Efficiency (%)
Cluster8_c608	-3.291	0.999	97.212
Cluster2_c82	-3.270	0.992	102.227
Cluster1_c182	-3.223	0.987	104.323

Table S9. qPCR quantization of MAG abundance in FE7-FL grown in different media.

Cluster1

	MB		F/2¼		F/2¾	
Days	Quantity Mean	Quantity SD	Quantity Mean	Quantity SD	Quantity Mean	Quantity SD
Day3	1.280346274	0.130211171	0.027051291	0.036026332	1.242784977	0.166221648
Day6	0.029285605	0.006642076	13.66777325	0.425333649	16.20821953	1.267161489
Day10	0.009822866	0.011881083	29.6822567	3.296260118	42.63631821	2.170769453

Cluster2

	MB		F/2¼		F/2¾	
Days	Quantity Mean	Quantity SD	Quantity Mean	Quantity SD	Quantity Mean	Quantity SD
Day3	0.032683714	0.016084398	0.024166935	0.002645122	4.377933025	0.241250709
Day6	0.061404854	0.039326753	18.35878563	0.782420158	30.27388763	2.298482418
Day10	0.090489812	0.004574142	24.60587311	0.367527306	39.92933273	3.180368423

Cluster8

	MB		F/2¼		F/2¾	
Days	Quantity Mean	Quantity SD	Quantity Mean	Quantity SD	Quantity Mean	Quantity SD
Day3	0.1362793	0.038577229	0.008	0.00915	2.689586878	0.452325106
Day6	0.129597649	0.034835324	18.79345703	3.886913193	14.20588303	1.957057476
Day10	0.095607392	0.018735146	27.99685478	2.574785471	39.20956039	2.05914402

Table S10. qPCR quantization of MAG abundance in FE7-FL grown in F/2¼ medium supplemented with DNase-treated sonicate.

F/2¼ (sonicate treated with DNase)

	Cluster1		Cluster2		Cluster8	
Days	Quantity Mean	Quantity SD	Quantity Mean	Quantity SD	Quantity Mean	Quantity SD
Day2	0.096502073	0.042068169	N/D	N/D	0.000123611	6.98944E-05
Day4	0.410697669	0.012779716	N/D	N/D	0.195641135	0.02719987
Day7	1.694224715	0.283904761	4.922961235	0.426027685	0.537181735	0.017694673
Day9	2.03311801	0.131902337	8.805378914	0.84562999	0.418001503	0.036180586

N/D – Not detected

Table S11. qPCR Slope, R^2 and % of Efficiency with specific primers for the evaluation of MAG abundance in different media.

Primer name	Slope	R^2	Efficiency (%)
Cluster8_c608	-3.195	0.990	105.593
Cluster2_c82	-3.289	0.988	101.384
Cluster1_c182	-3.184	0.984	106.082

Table S12. antiSMASH detection of biosynthetic clusters in the whole metagenome.

Whole metagenome biosynthetic clusters	
n° of Biosynthetic clusters	**Type of Biosynthetic clusters**
2	Ectoine
5	Terpenes
3	T1PKS
1	T3PKS
9	NRPS
3	Bacteriocin
1	RRE-containing
2	hserlactone
1	betalactone
1	Ranthipeptide
1	arylpolyene
1	Redox-cofactor

Table S13. List of primers used for amplification of the selected gene clusters.

Primer Name	Forward Sequence	Reverse Sequence	Tm (°C)	Amplicon length (bp)
C8_c988	AGCTTCAAACGTATCGATCA	CTCAAACAGGCAATTGGATG	59.9/63.1	206
C8_c608	GCTCCAGTGTTTTAACCGG	CCATCTATTCTGCCGACC	62.1/60.7	251
C8_c450	TCGCCAATACTGATTATGCT	GTCGTAGTTCCTAAGGTCAC	59.7/55.3	169
C1_c182	CTGATCTGTTATATGATGCGGA	GACATGACAGTGATGCATTG	61.3/60.2	161
C2_c82	GTATCAATATCGGGCAGTGT	CGATATTCCAAATGTGAGCG	58.9/63.0	243
E9/ U1510 (16s)	GAGTTTGATCCTGGCTCAG	GGCTTACCTTGTTACGACTT	60/53.1	1500

Supplementary information: Sequences of the cluster-specific genes.

C8_c988

>Diatom_S1_L001_R1_001_(paired)_unmapped_reads_[Diatom_S1_L001_R1_001] (paired)_trimmed_(paired)_not_merged_contig_988 Average coverage: 35.51

AGCTTCAAACGTATCGATCAAAAGCCACTTGGTCATACCCTCATATTTACGATAGTGGTGGTAAGAGTAGGTTTTTCCAT
CTTCTGAAAAGACATGCTCCCTGCGTACCTCAAACTTTCCGGTCTCGTCCTTCACAGAGTCTTCATACAGGAGTTTTTTA
CCTTTGAATTTCAAAGAGATTTGATCCATCCAATTGCCTGTTTGAG

C8_c608

>Diatom_S1_L001_R1_001_(paired)_unmapped_reads_[Diatom_S1_L001_R1_001] (paired)_trimmed_(paired)_not_merged_contig_608 Average coverage: 28.01

GCTCCAGTGTTTTAACCGGTTCTGGTTCAGGAGCTGGGGTGATTGCCTCTTTTGTTTCCTGTCCTGCTTCCGTTTTAGCC
TCTTCTTCTTTTTGCTCTTTTAGTGCCGCTGGTGCCGGCACTATAGGCGCTACTGCCACTGGCGTTTCAACCTGAGCAAC
GGCAACGACCGTCTCTTCTACAACGGTTGCAAAATCATGCTCATCCATAATAATGGCTTTGAGCAAGGCACGGTCGGCAG
AATAGATGG

C8_c450

>Diatom_S1_L001_R1_001_(paired)_unmapped_reads_[Diatom_S1_L001_R1_001] (paired)_trimmed_(paired)_not_merged_contig_450 Average coverage: 39.94

TCGCCAATACTGATTATGCTTTAAGTAATGCTACCATTACCATTCTGGACGGAGCCACAACCGGTATGATCACTTTTACT
ATTCAGGATGATGCGGATATTGAAGGAGACGAGACCGCTACTTTGACGCTCAGCAATCCATCAGCAGGTGTGACCTTAGG
AACTACGAC

C1_c182

>Diatom_S1_L001_R1_001_(paired)_unmapped_reads_[Diatom_S1_L001_R1_001] (paired)_trimmed_(paired)_not_merged_contig_182 Average coverage: 738.28

CTGATCTGTTATGATGCGGAATTCCCCTTGCTGGCGCGCGCTGGCGGAGGCCGACATCATTCTGGTGCCCTCGTGCAC
CGACGCGTTGTCGGGCTATTGGCGGGTGCGAATCGGGGCTATGGCCCGCGCGTTGGAAGGGCAATGCATCACTGTCATGT
C

C2_c82

>Diatom_S1_L001_R1_001_(paired)_unmapped_reads_[Diatom_S1_L001_R1_001] (paired)_trimmed_(paired)_not_merged_ contig_82 Average coverage: 66.46

GTATCAATATCGGGCAGTGTGTCGAGAAGGGCGACGCGGGCGTCTTTCAGATTGGCGCGGGTATCGGCGAGCGCATGTTC
CGTTGACCAGCGCACATTGTCGAAGATCGAGCGCACATGAGGAAAACGCTTCAGGCCCACCAGCCAATAGCCGCCGTCTT
CCGCCGGCCCAAAGACAGCATCATGATTGCTCAAAGCTTTGAACGCGGCTGCGATGCGTGTGTCGCTCACATTTGGAATA
TCG