

**Table S1.** Environmental parameters of ME3, P11 and P03 seawater and oxic surface sediment samples

Sample	Sampling time	Location	Depth (m)	Salinity (PSU)	DO (mg·L <sup>-1</sup> )	NO <sub>3</sub> <sup>-</sup> (μmol·L <sup>-1</sup> )	NO <sub>2</sub> <sup>-</sup> (μmol·L <sup>-1</sup> )	NH <sub>3</sub> (μmol·L <sup>-1</sup> )	PO <sub>4</sub> <sup>3-</sup> (μmol·L <sup>-1</sup> )
ME3 SW	Jul. 2013	28.7 °N, 122.6 °E	3 59	33.63 34.41	6.70 5.03	1.18 7.28	0.42 0.49	0.39 0.39	0.42 0.93
P11 SW	Jul. 2013	28.7 °N, 126.9 °E	3 193	33.61 34.39	6.09 4.75	0.29 18.29	0.16 0.18	0.54 0.23	0.16 1.54
P03 SW	Oct. 2015	32.0 °N, 123.6 °E	4 50	30.13 33.73	7.00 4.73	— —	— —	— —	— —
P03 OSS			52	—	—	—	—	—	—

**Table S2.** Chl-*a* and DMSP-related factors of ME3, P11 and P03 seawater and oxic surface sediment samples

Sample	Chl- <i>a</i> ( $\mu\text{g}\cdot\text{L}^{-1}$ )	DMSPt ( $\text{nmol}\cdot\text{mL}^{-1}$ or $\text{g}^{-1}$ )	DMSPp > 0.7 $\mu\text{m}$ ( $\text{nmol}\cdot\text{mL}^{-1}$ or $\text{g}^{-1}$ )	DMSPp > 3 $\mu\text{m}$ ( $\text{nmol}\cdot\text{mL}^{-1}$ or $\text{g}^{-1}$ )	DMSPp 0.22–3 $\mu\text{m}$ ( $\text{nmol}\cdot\text{mL}^{-1}$ or $\text{g}^{-1}$ )
ME3 SW	0.35	$0.0384 \pm 0.0016$	$0.0317 \pm 0.0022$	$0.0334 \pm 0.0043$	$0.0029 \pm 0.0008$
ME3 NBW	0.02	$0.0115 \pm 0.0007$	$0.0082 \pm 0.0010$	$0.0080 \pm 0.0023$	$0.0016 \pm 0.0007$
P11 SW	0.07	$0.0102 \pm 0.0007$	$0.0077 \pm 0.0009$	$0.0073 \pm 0.0020$	$0.0011 \pm 0.0006$
P11 NBW	0.01	$0.0032 \pm 0.0002$	$0.0022 \pm 0.43$	$0.0020 \pm 0.0004$	$0.0005 \pm 0.0002$
P03 SW	0.69	$0.0884 \pm 0.0054$	$0.0838 \pm 0.0050$	$0.0810 \pm 0.0082$	$0.0044 \pm 0.0009$
P03 NBW	0.07	$0.0086 \pm 0.0007$	$0.0060 \pm 0.0003$	$0.0058 \pm 0.0007$	$0.0009 \pm 0.0002$
P03 OSS	0.11	$16.29 \pm 1.07$		$14.19 \pm 1.70$	

Abbreviation: SW, surface seawater; NBW, near bottom seawater; OSS, oxic surface sediment; PSU, practical salinity unit; DO, dissolved oxygen; Chl-*a*, Chlorophyll *a*; DMSPt, total DMSP; DMSPp, particulate DMSP.

**Table S3.** Proportion of phytoplankton plastid sequences in total 16S rRNA gene data from amplicon sequencing analysis.

	P03 SW	P03 NBW	P03 SS	ME3 SW	ME3 NBW	P11 SW	P11 NBW
Phytoplanktonic sequences proportion	0.8% ± 0.02%	0.4% ± 0.05%	0.05 ± 0.00%	0.5% ± 0.05%	0.1% ± 0.06%	0.5% ± 0.1%	0.1% ± 0.02%

**Table S4.** The phytoplankton community structures of ME3 & P11 derived from flow cytometry.

Phylum/Species/Group*	Phytoplankton abundance (cells/ml) †			
	ME3SW	ME3NBW	P11SW	P11NBW
<b>Bacillariophyta</b>	<b>360.56</b>	<b>4.47</b>	<b>1.70</b>	<b>3.98</b>
<i>Thalassiosira curviseriata</i>	138.89 (22.2%)	0.21 (3.7%)	-	-
<i>Pseudo-nitzschia delicatissima</i>	127.78 (20.4%)	-	-	-
<i>Skeletonema</i> sp.	35.00 (5.6%)	-	-	-
<i>Leptocylindrus minimus</i>	16.67 (2.7%)	-	-	-
<i>Thalassionema nitzschiooides</i>	13.33 (2.1%)	0.43 (7.5%)	-	-
<i>Paralia sulata</i>	-	2.45 (42.7%)	-	3.01 (26.4%)
<i>Plagiogramma</i> sp.	1.11 (0.2%)	0.21 (3.7%)	-	-
<i>Coscinodiscus decrescens</i>	-	0.21 (3.7%)	-	-
<i>Nitzschia panduriformis</i>	-	0.21 (3.7%)	-	-
<i>Chaetoceros compressus</i>	-	-	0.43 (0.8%)	0.22 (1.9%)
<b>Chlorophyta</b>	<b>100.00</b>	-	<b>0.21</b>	-
<i>Pachysphaera</i> spp.	100.00 (16.0%)	-	-	-
<b>Dinophyta</b>	<b>88.89</b>	<b>1.06</b>	<b>32.3</b>	<b>3.44</b>
<i>Karlodinium veneficum</i>	35.00 (5.6%)	0.11 (1.9%)	12.1 (23.7%)	1.72 (15.1%)
<i>Scrippsiella trochoidea</i>	23.89 (3.8%)	0.21 (3.7%)	5.53 (10.8)	0.32 (2.8%)
<i>Gyrodinium spirale</i>	-	0.21 (3.7%)	-	-
<i>Akashiwo sanguinea</i>	-	-	2.34 (4.6%)	-
<i>Heterocapsa circularisquama</i>	-	-	1.81 (3.5)	0.32 (2.8%)
<i>Prorocentrum minimum</i>	-	-	1.38 (2.7%)	0.11 (1.0%)
<i>Katodinium glaucum</i>	-	-	1.17 (2.3%)	0.11 (1.0%)

<i>Prorocentrum donghaiense</i>	-	-	0.74 (1.4%)	0.22 (1.9%)
<i>Alexandrium catenella</i>	-	-	0.21 (0.4%)	0.22 (1.9%)
<b>Cryptophyta</b>	<b>34.44</b>	-	<b>6.7</b>	<b>0.22</b>
<i>Hemiselmis</i> sp.	26.67 (4.3%)	-	2.34 (4.6)	-
<i>Plagioselmis prolonga</i>	-	-	2.98 (5.8%)	0.11 (1.0%)
<b>Prymnesiophyta</b>	<b>30.00</b>	<b>0.21</b>	<b>10.3</b>	<b>3.55</b>
Coccolithaceae spp.	23.89 (3.8%)	0.21 (3.7%)	1.91 (3.7%)	0.32 (2.8%)
Coccolithaceae (ovoid, species uncertain)	-	-	7.66 (14.9%)	2.80 (24.6%)
<i>Algirosphaera robusta</i>	-	-	0.11 (0.2%)	0.22 (1.9%)
<b>Euglenophyta</b>	<b>11.11</b>	-	-	<b>0.22</b>
<b>Chrysophyta</b>	<b>1.11</b>	-	-	-
<b>Picoeukaryotes‡</b>	<b><math>1.87 \times 10^4</math></b>	<b><math>0.10 \times 10^4</math></b>	<b>NT\$</b>	<b>NT\$</b>

\*Phytoplankton abundance was listed at phylum level; the top ten most abundant species in each sample were listed (dominant species)

†Percentage indicated contribution of the species to the total phytoplankton abundance in the sample

‡Data were obtained by flow cytometry

\$Not determined

**Table S5.** DMSP concentrations before and after enrichment incubation.

Samples	DMSP concentration (pmol/µg protein)	
	T1C	T1
P03 SW	36.32	494.15
P03 NBW	32.72	232.49
P03 OSS	34.88	118.45

**Table S6.** qPCR and RT-qPCR analysis of *dsyB* and *mmtN* in P03 seawater and sediment samples. Data were obtained on two or three independent samples (n=2 or n=3) and expressed as mean ± SD.

Sample	<i>dsyB</i> (copies·mL <sup>-1</sup> or g <sup>-1</sup> )	<i>mmtN</i> (copies·mL <sup>-1</sup> or g <sup>-1</sup> )	16s rRNA (copies·mL <sup>-1</sup> or g <sup>-1</sup> )	<i>rpoB</i> (copies·mL <sup>-1</sup> or g <sup>-1</sup> )	Relative abundance of DMSP producer (%)
<b>qPCR</b>					
SW	2.46E+03 ± 7.86E+01	2.75E+02 ± 2.85E+02	5.13E+05 ± 1.32E+04	ND	0.5
	4.60E+03 ± 1.96E+02	2.13E+01 ± 8.63E-01	7.54E+05 ± 3.07E+04	ND	0.6
NBW	6.68E+06 ± 3.63E+05	1.07E+03 ± 3.91E+02	7.42E+08 ± 3.12E+07	ND	0.9
<b>RT-qPCR</b>					
SW	8.17E+00 ± 7.03E+00	1.40E+00 ± 4.20E-01	ND	1.81E+03 ± 3.06E+03	0.5
	8.16E+00 ± 8.67E-02	6.08E+00 ± 4.34E-01	ND	3.75E+02 ± 1.78E+01	3.7
NBW	2.96E+04 ± 5.76E+03	1.99E+04 ± 1.12E+04	ND	1.08E+06 ± 6.07E+04	4.5
ND: not determined.					

**Table S7.** Characteristics of DMSP-producing bacterial isolates.

Strain code	Closest taxonomically related species	Isolation source\$	Growth medium*	DMSP production (pmol µg protein <sup>-1</sup> )	Estimated intracellular DMSP concentration (mM)	DsyB and/or MmtN presentation.	Detection Method
ADSW12	<i>Amorphus suaedaee</i>	P03 SW T1	MB MBM (minimal, 1 mM NH <sub>4</sub> Cl)	6.5 ± 0.5 N.G. <sup>†</sup>	1.0 ± 0.07 N.G.	DsyB	degenerate PCR
ADSW13	<i>Amorphus suaedaee</i>	P03 SW T1	MB MBM (minimal, 1 mM NH <sub>4</sub> Cl)	5.4 ± 0.1 N.G.	0.9 ± 0.02 N.G.	DsyB	degenerate PCR
ADSW14	<i>Amorphus suaedaee</i>	P03 SW T1	MB MBM (minimal, 1 mM NH <sub>4</sub> Cl)	6.6 ± 0.3 N.G.	1.0 ± 0.05 N.G.	DsyB	degenerate PCR
ADSW24	<i>Amorphus suaedaee</i>	P03 SW T1	MB MBM (minimal, 1 mM NH <sub>4</sub> Cl)	6.0 ± 0.4 N.G.	0.9 ± 0.06 N.G.	DsyB	degenerate PCR
ADSW25-1	<i>Amorphus suaedaee</i>	P03 SW T1	MB MBM (minimal, 1 mM NH <sub>4</sub> Cl)	10.4 ± 0.6 N.G.	1.6 ± 0.1 N.G.	DsyB	degenerate PCR
ADSW29	<i>Acuticoccus yangtzensis</i>	P03 SW T1	MB MBM (minimal, 1 mM NH <sub>4</sub> Cl)	89.9 ± 11.5 79.5 ± 5.2	14.1 ± 1.8 12.4 ± 0.8	DsyB	degenerate PCR
ADBW18	<i>Pelagibaca bermudensis</i>	P03 NBW T1	MB	55.3 ± 1.3	8.6 ± 0.2	DsyB	degenerate PCR

			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	9.7 ± 0.7	1.5 ± 0.1		
ADSS11-1	<i>Stappia taiwanensis</i>	P03 OSS T1	MB	7.9 ± 0.8	1.2 ± 0.1	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	22.9 ± 0.9	3.6 ± 0.1		
ADSS19	<i>Stappia taiwanensis</i>	P03 OSS T1	MB	9.6 ± 0.8	1.5 ± 0.1	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	25.3 ± 0.1	4.0 ± 0.02		
ADSS20	<i>Stappia taiwanensis</i>	P03 OSS T1	MB	12.7 ± 1.1	2.0 ± 0.2	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	25.4 ± 1.3	4.0 ± 0.2		
ADSS28	<i>Stappia taiwanensis</i>	P03 OSS T1	MB	14.5 ± 1.8	2.3 ± 0.3	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	23.0 ± 0.6	3.6 ± 0.1		
AESS21	<i>Labrenzia suaedae</i>	P03 OSS T1	MB	131.1 ± 2.6	20.5 ± 0.4	DsyB	degenerate PCR & genome sequencing
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	6.1 ± 0.1	1.0 ± 0.02		
AESS44	<i>Labrenzia suaedae</i>	P03 OSS T1	MB	169.2 ± 5.0	26.5 ± 0.8	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	6.0 ± 0.3	0.9 ± 0.05		
AESS46	<i>Labrenzia suaedae</i>	P03 OSS T1	MB	186.0 ± 22.5	29.1 ± 3.5	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	6.1 ± 0.02	1.0 ± 0.003		
AESS41	<i>Marinobacter lipolyticus</i>	P03 OSS T1	MB	6.3 ± 0.3	1.0 ± 0.05	N.D.	degenerate PCR & genome sequencing
			MBM (minimal, 1	N.D. <sup>‡</sup>	N.D.		

mM NH <sub>4</sub> Cl)							
AE551-2	<i>Marinobacter adhaerens</i>	P03 OSS T1	MB	1.9 ± 0.1	0.3 ± 0.02	N.D.	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	N.D.	N.D.		
BDSW03	<i>Pseudooceanicola antarcticus</i>	P03 SW T1	MB	148.8 ± 23.6	23.3 ± 3.7	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	36.5 ± 7.2	5.7 ± 1.1		
BDSW11	<i>Pseudooceanicola antarcticus</i>	P03 SW T1	MB	189.6 ± 4.3	29.7 ± 0.7	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	29.6 ± 1.1	4.6 ± 0.2		
BDSW15	<i>Pseudooceanicola antarcticus</i>	P03 SW T1	MB	191.3 ± 6.6	29.9 ± 1.0	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	30.9 ± 3.5	4.8 ± 0.5		
BDSW19	<i>Pseudooceanicola antarcticus</i>	P03 SW T1	MB	150.3 ± 29.0	23.5 ± 4.5	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	31.3 ± 3.0	4.9 ± 0.5		
BDSW30	<i>Pseudooceanicola antarcticus</i>	P03 SW T1	MB	196.3 ± 22.3	30.7 ± 3.5	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	17.8 ± 0.4	2.8 ± 0.1		
BDBW05	<i>Pelagibaca bermudensis</i>	P03 NBW T1	MB	28.7 ± 2.9	4.5 ± 0.5	DsyB	degenerate PCR

				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	11.2 ± 0.5	1.8 ± 0.1		
BDBW16	<i>Pelagibaca bermudensis</i>	P03 T1	NBW	MB	32.0 ± 4.4	5.0 ± 0.7	DsyB	degenerate PCR
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	9.5 ± 0.3	1.5 ± 0.05		
BDSS02	<i>Sulfitobacter dubis</i>	P03 OSS T1		MB	2.9 ± 0.04	0.5 ± 0.007	DsyB	genome sequencing
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	N.G.	N.G.		
BDSS04	<i>Sulfitobacter dubis</i>	P03 OSS T1		MB	2.8 ± 0.4	0.4 ± 0.06	N.D.	degenerate PCR
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	N.G.	N.G.		
BDSS12	<i>Labrenzia aggregata</i>	P03 OSS T1		MB	44.0 ± 1.3	6.9 ± 0.2	DsyB	degenerate PCR
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	20.2 ± 0.8	3.2 ± 0.1		
BDSS19	<i>Sulfitobacter dubis</i>	P03 OSS T1		MB	3.2 ± 0.4	0.5 ± 0.06	N.D.	degenerate PCR
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	N.G.	N.G.		
BEBW06	<i>Thalassospira profundimaris</i>	P03 T1	NBW	MB	1.2 ± 0.1	0.2 ± 0.02	MmtN	degenerate PCR
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	85.5 ± 6.3	13.4 ± 1.0		
BEBW11	<i>Thalassospira profundimaris</i>	P03 T1	NBW	MB	1.1 ± 0.3	0.2 ± 0.04	MmtN	degenerate PCR
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	81.6 ± 1.6	12.8 ± 0.2		
BEBW19	<i>Thalassospira</i>	P03	NBW	MB	1.3 ± 0.1	0.2 ± 0.02	MmtN	degenerate PCR

profoundimaris							
T1							
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	86.0 ± 2.1	13.5 ± 0.3	
BEBW25-2	<i>Thalassospira profundimaris</i>	P03	NBW	MB	1.2 ± 0.01	0.2 ± 0.001	MmtN
		T1		MBM (minimal, 1 mM NH <sub>4</sub> Cl)	81.9 ± 0.7	12.8 ± 0.1	degenerate PCR
BEBW28	<i>Thalassospira tepidiphila</i>	P03	NBW	MB	8.6 ± 0.2	1.4 ± 0.04	MmtN
		T1		MBM (minimal, 1 mM NH <sub>4</sub> Cl)	339.9 ± 2.8	53.2 ± 0.4	degenerate PCR & genome sequencing
BEBW31-1	<i>Thalassospira profundimaris</i>	P03	NBW	MB	1.2 ± 0.04	0.2 ± 0.01	MmtN
		T1		MBM (minimal, 1 mM NH <sub>4</sub> Cl)	84.5 ± 1.0	13.2 ± 0.2	degenerate PCR
BEBW31-2	<i>Thalassospira profundimaris</i>	P03	NBW	MB	1.3 ± 0.1	0.2 ± 0.02	MmtN
		T1		MBM (minimal, 1 mM NH <sub>4</sub> Cl)	391.6 ± 27.1	61.3 ± 4.2	degenerate PCR
BEBW32	<i>Thalassospira tepidiphila</i>	P03	NBW	MB	8.0 ± 0.1	1.3 ± 0.02	MmtN
		T1		MBM (minimal, 1 mM NH <sub>4</sub> Cl)	336.6 ± 9.4	52.6 ± 1.5	degenerate PCR
BESS04	<i>Labrenzia suaedae</i>	P03 OSS T1		MB	73.3 ± 0.4	11.5 ± 0.1	DsyB.
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	5.0 ± 0.03	0.8 ± 0.004	degenerate PCR
BESS05	<i>Labrenzia suaedae</i>	P03 OSS T1		MB	84.7 ± 2.1	13.2 ± 0.3	DsyB
							degenerate PCR

			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	4.9 ± 0.1	0.8 ± 0.01		
BESS10	<i>Labrenzia suaedae</i>	P03 OSS T1	MB	136.1 ± 6.0	21.3 ± 0.9	N.D.	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	4.7 ± 0.1	0.7 ± 0.02		
BESS13	<i>Labrenzia suaedae</i>	P03 OSS T1	MB	77.8 ± 2.2	12.2 ± 0.3	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	4.7 ± 0.3	0.7 ± 0.04		
BESS15	<i>Labrenzia suaedae</i>	P03 OSS T1	MB	72.6 ± 4.0	11.4 ± 0.6	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	4.4 ± 0.3	0.7 ± 0.04		
BESS17	<i>Labrenzia suaedae</i>	P03 OSS T1	MB	133.7 ± 3.8	20.9 ± 0.6	DsyB	degenerate PCR of
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	14.0 ± 1.6	2.2 ± 0.2		
BESS24	<i>Labrenzia alexandrii</i>	P03 OSS T1	MB	47.6 ± 0.7	7.4 ± 0.1	DsyB	degenerate PCR of <i>dsyB</i>
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	11.7 ± 0.4	1.8 ± 0.06		
BESS25	<i>Labrenzia suaedae</i>	P03 OSS T1	MB	130.4 ± 0.03	20.4 ± 0.01	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	11.1 ± 0.01	1.7 ± 0.002		
DSW02	<i>Labrenzia aggregata</i>	P03 SW T0	MB	68.0 ± 7.3	10.6 ± 1.1	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	28.6 ± 0.06	4.5 ± 0.009		
DSW17	<i>Poseidonocella pacifica</i>	P03 SW T0	MB	49.0 ± 3.9	7.7 ± 0.6	DsyB	degenerate PCR
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	33.8 ± 1.3	5.3 ± 0.2		

DSW18	<i>Marinobacter salarius</i>	P03 SW T0	MB	1.4 ± 0.3	0.2 ± 0.05	N.D.	degenerate PCR & genome sequencing
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	N.G.	N.G.		
EBW16	<i>Oceanicola litoreus</i>	P03 NBW T0	MB	4.3 ± 0.1	0.7 ± 0.02	DsyB	degenerate PCR & genome sequencing
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	N.D.	N.D.		
ESS08	<i>Bacillus boroniphilus</i>	P03 OSS T0	MB	0.9 ± 0.2	0.1 ± 0.03	N.D.	degenerate PCR & genome sequencing
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	N.G.	N.G.		
ZYFB032	<i>Pelagibaca bermudensis</i>	P11 SW T0	MB	86.9 ± 2.2	13.6 ± 0.3	DsyB	degenerate PCR
			MBM (minimal, 10 mM NH <sub>4</sub> Cl)	3.4 ± 0.1	0.5 ± 0.02		
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	10.7 ± 1.1	1.7 ± 0.2		
			MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	91.0 ± 3.6	14.2 ± 0.6		
LZB033	<i>Labrenzia aggregata</i>	ME3 SW T0	MB	62.4 ± 0.6	9.8 ± 0.1	DsyB	degenerate PCR & genome sequencing
			MBM (minimal, 10 mM NH <sub>4</sub> Cl)	4.9 ± 0.3	0.8 ± 0.05		
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	25.7 ± 0.3	4.0 ± 0.1		
			MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	99.8 ± 1.2	15.6 ± 0.2		

mM NH <sub>4</sub> Cl)							
LZB062	<i>Pseudooceanicola nanhaiensis</i>	ME3 SW T0	MB	43.6 ± 0.6	6.8 ± 0.1	DsyB	degenerate PCR
LZD001	<i>Pelagibaca bermudensis</i>	ME3 NBW T0	MBM (minimal, 10 mM NH <sub>4</sub> Cl)	8.4 ± 0.1	1.3 ± 0.02		
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	132.6 ± 12.2	20.7 ± 1.9		
			MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	3051.2 ± 52.9	477.2 ± 8.3		
LZD012	<i>Halomonas saccharevitans</i>	ME3 NBW T0	MB	63.8 ± 3.5	10.0 ± 0.5	DsyB	degenerate PCR
			MBM (minimal, 10 mM NH <sub>4</sub> Cl)	5.0 ± 0.4	0.8 ± 0.1		
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	11.5 ± 0.7	1.8 ± 0.1		
			MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	145.2 ± 0.8	22.7 ± 0.1		
LZD019	<i>Pelagibaca bermudensis</i>	ME3 NBW T0	MB	1.4 ± 0.2	0.2 ± 0.02	N.D.	degenerate PCR & genome sequencing
			MBM (minimal, 10 mM NH <sub>4</sub> Cl)	N.D.	N.D.		
			MBM (minimal, 1 mM NH <sub>4</sub> Cl)	N.D.	N.D.		
			MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	N.D.	N.D.		

LZD031	<i>Pelagibaca bermudensis</i>	ME3	NBW	MBM (minimal, 10 mM NH <sub>4</sub> Cl)	5.1 ± 0.1	0.8 ± 0.01	
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	10.8 ± 0.4	1.7 ± 0.06	
				MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	130.3 ± 2.7	20.4 ± 0.4	
		T0	MB	MBM (minimal, 10 mM NH <sub>4</sub> Cl)	5.1 ± 0.1	0.8 ± 0.02	DsyB
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	11.6 ± 0.2	1.8 ± 0.03	degenerate PCR
				MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	162.2 ± 2.1	25.4 ± 0.3	
LZD033	<i>Pelagibaca bermudensis</i>	ME3	NBW	MBM (minimal, 10 mM NH <sub>4</sub> Cl)	4.6 ± 0.3	0.7 ± 0.05	
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	9.2 ± 0.1	1.4 ± 0.02	DsyB
				MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	165.0 ± 1.7	25.8 ± 0.3	degenerate PCR
		T0	MB	MBM (minimal, 10 mM NH <sub>4</sub> Cl)	66.9 ± 2.2	10.5 ± 0.3	
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	69.1 ± 0.1	10.8 ± 0.02	DsyB
				MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	5.5 ± 0.5	0.9 ± 0.08	
LZD040	<i>Pelagibaca bermudensis</i>	ME3	NBW	MBM (minimal, 1 mM NH <sub>4</sub> Cl)	9.7 ± 0.1	1.5 ± 0.01	
				MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)			degenerate PCR

				mM NH <sub>4</sub> Cl)			
LZD042	<i>Pelagibaca bermudensis</i>	ME3 NBW	T0	MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	120.3 ± 3.2	18.8 ± 0.5	
				MB	72.0 ± 1.0	11.3 ± 0.2	DsyB
				MBM (minimal, 10 mM NH <sub>4</sub> Cl)	10.0 ± 0.5	1.6 ± 0.08	degenerate PCR
			T0	MBM (minimal, 1 mM NH <sub>4</sub> Cl)	19.9 ± 2.1	3.1 ± 0.3	
				MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	218.2 ± 5.5	34.1 ± 0.9	
				MB	53.7 ± 1.7	8.4 ± 0.3	DsyB
LZD043	<i>Pelagibaca bermudensis</i>	ME3 NBW	T0	MBM (minimal, 10 mM NH <sub>4</sub> Cl)	N.D.	N.D.	
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	22.3 ± 3.9	3.5 ± 0.6	degenerate PCR
				MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	125.1 ± 2.1	19.6 ± 0.3	
			T0	MB	76.4 ± 0.1	12.0 ± 0.02	DsyB
				MBM (minimal, 10 mM NH <sub>4</sub> Cl)	4.4 ± 0.4	0.7 ± 0.05	degenerate PCR
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	10.4 ± 0.3	1.6 ± 0.05	
LZD044	<i>Pelagibaca bermudensis</i>	ME3 NBW	T0	MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	163.7 ± 3.4	25.6 ± 0.5	
				MB	76.4 ± 0.1	12.0 ± 0.02	DsyB
				MBM (minimal, 10 mM NH <sub>4</sub> Cl)	4.4 ± 0.4	0.7 ± 0.05	degenerate PCR
			T0	MBM (minimal, 1 mM NH <sub>4</sub> Cl)	10.4 ± 0.3	1.6 ± 0.05	
				MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	163.7 ± 3.4	25.6 ± 0.5	

LZD059	<i>Marinobacter algicola</i>	ME3	NBW	MB	1.7 ± 0.1	0.3 ± 0.02	N.D.	degenerate PCR
		T0		MBM (minimal, 10 mM NH <sub>4</sub> Cl)	N.D.	N.G.		
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	N.D.	N.G.		
				MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	N.D.	N.G.		
LZD060	<i>Marinobacter salsuginis</i>	ME3	NBW	MB	2.0 ± 0.5	0.3 ± 0.07	N.D.	degenerate PCR
		T0		MBM (minimal, 10 mM NH <sub>4</sub> Cl)	N.D.	N.G.		
				MBM (minimal, 1 mM NH <sub>4</sub> Cl)	N.D.	N.G.		
				MBM (minimal, 0.5 mM NH <sub>4</sub> Cl)	N.D.	N.G.		

The values for DMSP production and estimated intracellular DMSP concentration are the averages of three biological replicates with the s.d. being shown.

“SW”, ‘NBW’ and “OSS” present surface seawater, near bottom seawater and oxic surface sediment, respectively; T0 and T1 present natural and DMSP production process enriching samples, respectively.

\*No added methylated sulfur compounds unless stated otherwise; 2 mM succinate + 2 mM glucose + 2 mM sucrose + 2 mM pyruvate + 2 mM glycerol were used as carbon source mixture for MBM media.

†N.G., no growth.

‡N.D., not detected.

**Table S8.** MAGs recovered from the metagenomic data.

MAGs	Sample	Taxonnamy	Completeness	Contamination	DMSP biosynthesis gene
MAG1	ME3 SW T0	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Rhodobacterales.f_Rhodobacteraceae	99.7	0.55	<i>dsyB</i>
MAG2	P03 NBW T1	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Rhodospirillales.f_Rhodospirillaceae	100	0	<i>mmtN</i>
MAG3	P03 OSS T1	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria	99.29	0.85	<i>dsyB</i>
MAG4	P03 SW T1	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria	90.1	2.36	<i>dsyB</i>
MAG5	P03 SW T1C	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria	96.55	4.34	<i>dsyB</i>
MAG6	P03 SW T1C	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Oceanospirillales.f_Halomonadaceae	98.71	0.43	
MAG7	P03 SW T1C	d_Bacteria.p_Bacteroidetes.c_Cytophagia.o_Cytophagales	99.26	0.63	
MAG8	P03 SW T1C	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Oceanospirillales.f_Halomonadaceae	96.1	1.08	
MAG9	P03 SW T1C	d_Bacteria.p_Plantomycetes.c_Plantomycetacia.o_Plantomycetales.f_Plantomycetaceae	96.55	4.34	
MAG10	P03 SW T1C	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Alteromonadales.f_Alteromonadaceae.g_Alteromonas.s_macleodii	87.55	1.67	
MAG11	P03 SW T1C	d_Bacteria.p_Bacteroidetes	100	0	
MAG12	P03 SW T1C	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Rhodospirillales.f_Rhodospirillaceae	94.98	1.49	
MAG13	P03 SW T1	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Rhodobacterales.f_Rhodobacteraceae	99.6	1.51	
MAG14	P03 SW T1	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Rhodobacterales.f_Hyphomonadaceae	99.68	1.3	

MAG15	P03 SW T1	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Oceanospirillales.f_Halomonadaceae	94.7	1.03
MAG16	P03 SW T1	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Rhodospirillales.f_Rhodospirillaceae	97.64	0
MAG17	P03 SW T0	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria	84.88	1.51
MAG18	P03 SW T0	d_Bacteria.p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobales.f_Verrucomicrobiaceae	95.89	3.63
MAG19	P03 SW T0	d_Bacteria.p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobales.f_Verrucomicrobiaceae	96.6	0.68
MAG20	P03 SW T0	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria	89.14	2.23
MAG21	P03 OSS T1C	d_Bacteria.p_Bacteroidetes	98.68	0.85
MAG22	P03 OSS T1C	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Rhodobacteriales.f_Hyphomonadaceae	99.38	1.04
MAG23	P03 OSS T1C	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Rhodobacteriales.f_Hyphomonadaceae	89.26	1.73
MAG24	P03 OSS T1C	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Oceanospirillales	97.39	1.52
MAG25	P03 OSS T1C	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Vibrionales.f_Vibrionaceae.g_Vibrio	95.27	0.87
MAG26	P03 OSS T1C	d_Bacteria.p_Bacteroidetes.c_Flavobacteria.o_Flavobacteriales.f_Flavobacteriaceae	98.42	0.25
MAG27	P03 OSS T1C	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Aeromonadales	90.09	0.54
MAG28	P03 OSS T1	d_Bacteria.p_Bacteroidetes	90.44	1.64
MAG29	P03 OSS T1	d_Bacteria.p_Bacteroidetes.c_Flavobacteria.o_Flavobacteriales.f_Flavobacteriaceae	93.15	3.12
MAG30	P03 OSS T1	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Alteromon	99.84	0.24

MAG31	P03 OSS T1	adales.f_Alteromonadaceae.g_Alteromonas.s_macleodii d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria	99.9	1.4
MAG32	P03 OSS T1	d_Bacteria.p_Bacteroidetes.c_Flavobacteria.o_Flavobacteriales.f_Flavobacteriaceae	97.3	5.22
MAG33	P03 OSS T1	d_Bacteria.p_Bacteroidetes	98.51	0.99
MAG34	P03 OSS T1	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Alteromonadales.f_Idiomarinaceae.g_Idiomarina	98.65	0.39
MAG35	P03 OSS T1	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Oceanospirillales	96.18	4.74
MAG36	P03 OSS T1	d_Bacteria.p_Bacteroidetes	98.99	0.52
MAG37	P03 OSS T1	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Oceanospirillales.f_Halomonadaceae	99.29	0.85
MAG38	P03 OSS T1	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Alteromonadales.f_Alteromonadaceae.g_Marinobacter	95.49	0.68
MAG39	P03 OSS T1	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria	93.29	0.7
MAG40	P03 OSS T1	d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Rhodobacterales.f_Rhodobacteraceae	99.54	0.83
MAG41	P03 OSS T1	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Vibrionales.f_Vibrionaceae.g_Vibrio	97.78	1.12
MAG42	P03 NBW T1C	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Oceanospirillales	99.14	0.21
MAG43	P03 NBW T1C	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Oceanospirillales	99.14	0.64
MAG44	P03 NBW T1C	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Oceanospirillales.f_Halomonadaceae	98.37	1.51
MAG45	P03 NBW T1C	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Alteromonadales.f_Alteromonadaceae.g_Alteromonas.s_macleodii	99.55	1.53

MAG46	P03 NBW T1C	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Oceanospirillales.f_Halomonadaceae	90.04	1.36
MAG47	P11 NBW T0	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Oceanospirillales.f_Halomonadaceae	94.85	3.1
MAG48	P11 NBW T0	d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria	98.07	1.27
MAG49	P11 NBW T0	d_Bacteria.p_Actinobacteria.c_Actinobacteria	97.09	0
MAG50	ME3 SW T0	d_Bacteria.p_Actinobacteria.c_Actinobacteria	91.25	3.79

**Table S9.** Basic information of metagenomic data.

Sample	Clean reads	Contig	Assembly	N50 (bp)	N75(bp)	CDS number
		Number	Length (bp)			
P11SWT0	18,474,140	94,043	68,751,933	699	576	899,663
P11NBWT0	17,723,312	28,681	21,594,513	723	582	279,816
ME3SWT0	18,962,344	53,042	40,923,951	747	588	560,755
ME3NBWT0	12,614,636	57,887	43,451,151	717	579	670,752
P03SWT0	14,570,444	39,499	49,367,974	1,359	699	604,531
P03NBWT0	20,865,496	947	673,425	696	582	31,750
P03OSST0	8,960,848	3,320	2,422,894	661	561	385,897
P03SWT1	20,746,884	16,633	41,182,818	32,366	1,442	105,705
P03NBWT1	21,760,928	13,566	39,374,403	12,644	1,916	82,333
P03OSST1	21,305,296	73,162	143,688,576	3,604	1,128	393,315
P03SWT1C	22,489,728	29,829	77,961,891	13,605	1,613	171,540
P03NBWT1C	22,230,216	6,494	15,074,973	90,873	1,189	50,053
P03OSST1C	22,015,280	31,582	80,915,269	7,185	1,690	186,178

**Table S10.** Composition of normal or modified MBM medium

Basal Media* (pH 7.5)	Tris	34.61 g
	K <sub>2</sub> HPO <sub>4</sub>	0.17 g
	H <sub>2</sub> O	1000 ml
1 M NH <sub>4</sub> Cl stock solution	NH <sub>4</sub> Cl	5.35 g
	H <sub>2</sub> O	100 ml
FeEDTA stock solution*	FeEDTA	0.05 g
	H <sub>2</sub> O	100 ml
0.5 M L-methionine (L-Met) stock solution†	L-Met	7.46 g
	H <sub>2</sub> O	100 ml
Carbon source stock solution†	Disodium succinate hexahydrate	54 g
	Glucose	36.3 g
	Sucrose	68.4 g
	Sodium pyruvate	22 g
	Glycerol	14.6 g
	H <sub>2</sub> O	985.4 ml
Normal MBM (pH 7.0)	Sea Salts (Sigma-Aldrich, UK)	35 g
	Basal Media	250 ml
	FeEDTA stock	50 ml
	NH <sub>4</sub> Cl stock	10 ml
	Vitamin supplement stock†§	10 ml
	Carbon source stock solution	10 ml
	H <sub>2</sub> O	670 ml
For modified MBM (pH 7.0)	Sea Salts (Sigma-Aldrich, UK)	50 g
	Basal Media	250 ml
	FeEDTA stock	50 ml
	NH <sub>4</sub> Cl stock	1 ml
	L-Met stock	1 ml
	Vitamin supplement stock†§	10 ml
	Carbon source stock solution	10 ml
	H <sub>2</sub> O	678 ml

\*Autoclaving to sterilize

†Filtering to sterilize

§Balch et al., 1979

**Table S11.** Reference protein sequences of the functionally ratified DMSP degradation and biosynthesis enzymes

Protein	Source	NCBI Accession Number	Reference
DsyB	<i>Labrenzia aggregata</i> IAM 12614	EAV42226	Curson <i>et al.</i> , 2017
	<i>Pseudooceanicola batsensis</i> HTCC2597	EAQ04968	Curson <i>et al.</i> , 2017
	<i>Pelagibaca bermudensis</i> HTCC2601	EAU45958	Curson <i>et al.</i> , 2017
	<i>Amorphus coralli</i> DSM 19760	WP_018697905	Curson <i>et al.</i> , 2017
MmtN	<i>Thalassospira profundimaris</i> PB8B	OAZ15224	Williams <i>et al.</i> , 2019
	<i>Novosphingobium</i> sp. MBES04	GAM03459	Williams <i>et al.</i> , 2019
	<i>Roseovarius indicus</i> B108	KRS18724	Williams <i>et al.</i> , 2019
	<i>Nocardiopsis chromatogenes</i> YIM 90109	WP_017624909	Williams <i>et al.</i> , 2019
	<i>Streptomyces mobaraensis</i> DSM 40847	EME99407	Williams <i>et al.</i> , 2019
DSYB	<i>Prymnesium parvum</i> CCAP946/6	N.A.*	Curson <i>et al.</i> , 2018
	<i>Chrysochromulina tobin</i> CCMP291	KOO32714	Curson <i>et al.</i> , 2018
	<i>Lingulodinium polyedrum</i> CCMP1936	N.A.	Curson <i>et al.</i> , 2018
	<i>Alexandrium tamarensense</i> ATSP1-B	N.A.	Curson <i>et al.</i> , 2018
	<i>Acropora cervicornis</i>	N.A.	Curson <i>et al.</i> , 2018
	<i>Fragilariaopsis cylindrus</i> CCMP1102	OEU17621	Curson <i>et al.</i> , 2018
	<i>Symbiodinium microadriaticum</i> CCMP2467	OLQ07620	Curson <i>et al.</i> , 2018
TpMMT	<i>Thalassiosira pseudonana</i> CCMP1335	Tp23128	Kageyama <i>et al.</i> , 2018
DmdA	<i>Ruegeria pomeroyi</i> DSS-3	AAV95190	Howard <i>et al.</i> , 2006
	<i>Pelagibacter ubique</i> HTCC1062	WP_011281570	Howard <i>et al.</i> , 2006
	<i>Dinoroseobacter shibae</i> DFL 12	WP_012178987	Howard <i>et al.</i> , 2008
	marine gammaproteobacterium HTCC2080	WP_007233625	Howard <i>et al.</i> , 2008
	<i>Candidatus Pelagibacter</i> sp. HTCC7211	WP_008546106	Howard <i>et al.</i> , 2011
	<i>Candidatus Puniceispirillum marinum</i> IMCC1322	WP_013044947	Howard <i>et al.</i> , 2011
DddD	<i>Marinomonas</i> sp. MWYL1	ABR72937	Todd <i>et al.</i> , 2007

	<i>Oceanimonas doudoroffii</i>	AEQ39135	Curson et al., 2012
	<i>Psychrobacter</i> sp. J466	ACY02894	Curson et al., 2010
	<i>Halomonas</i> sp. HTNK1	ACV84065	Todd et al., 2010
	<i>Sinorhizobium fredii</i> NGR234	AAQ87407	Todd et al., 2007
	<i>Burkholderia ambifaria</i> AMMD	WP_011659284	Todd et al., 2007
	<i>Pseudomonas</i> sp. J465	ACY01992	Curson et al., 2010
	<i>Sagittula stellata</i> E-37	EBA08656	Curson et al., 2011a
DddL	<i>Sulfitobacter</i> sp. EE-36	ADK55772	Curson et al., 2008
	<i>Rhodobacter sphaeroides</i> 2.4.1	YP_351475	Curson et al., 2008
	<i>Labrenzia aggregata</i> LZB033	KP639184	Curson et al., 2017
	<i>Ahrensius marina</i> LZD062	KP639183	Curson et al., 2017
DddP	<i>Roseovarius nubinhibens</i> ISM	EAP77700	Todd et al., 2009
	<i>Ruegeria pomeroyi</i> DSS-3	WP_044029245	Todd et al., 2011
	<i>Phaeobacter inhibens</i> DSM 17395	AFO91571	Burkhardt et al., 2017
	<i>Oceanimonas doudoroffii</i> DSM 7028	AEQ39091	Curson et al., 2012
	<i>Oceanimonas doudoroffii</i> DSM 7028	AEQ39103	Curson et al., 2012
	<i>Aspergillus oryzae</i> RIB40	BAE62778	Todd et al., 2009
	<i>Fusarium graminearum</i> PH-1	XP_389272	Todd et al., 2009
	<i>Candidatus Puniceispirillum marinum</i>	WP_013046297	Choi et al., 2015
	<i>Ruegeria lacuscaerulensis</i> ITI-1157	WP_005982191	Wang et al., 2015
DddQ	<i>Ruegeria pomeroyi</i> DSS-3	WP_011047333	Todd et al., 2011
	<i>Roseovarius nubinhibens</i> ISM	EAP76002	Todd et al., 2011
	<i>Roseovarius nubinhibens</i> ISM	EAP76001	Todd et al., 2011
	<i>Ruegeria lacuscaerulensis</i> ITI-1157	WP_005978225	Li et al., 2014
	GOS databases	ECW91654	Todd et al., 2011
	GOS databases	EBP74803	Todd et al., 2011

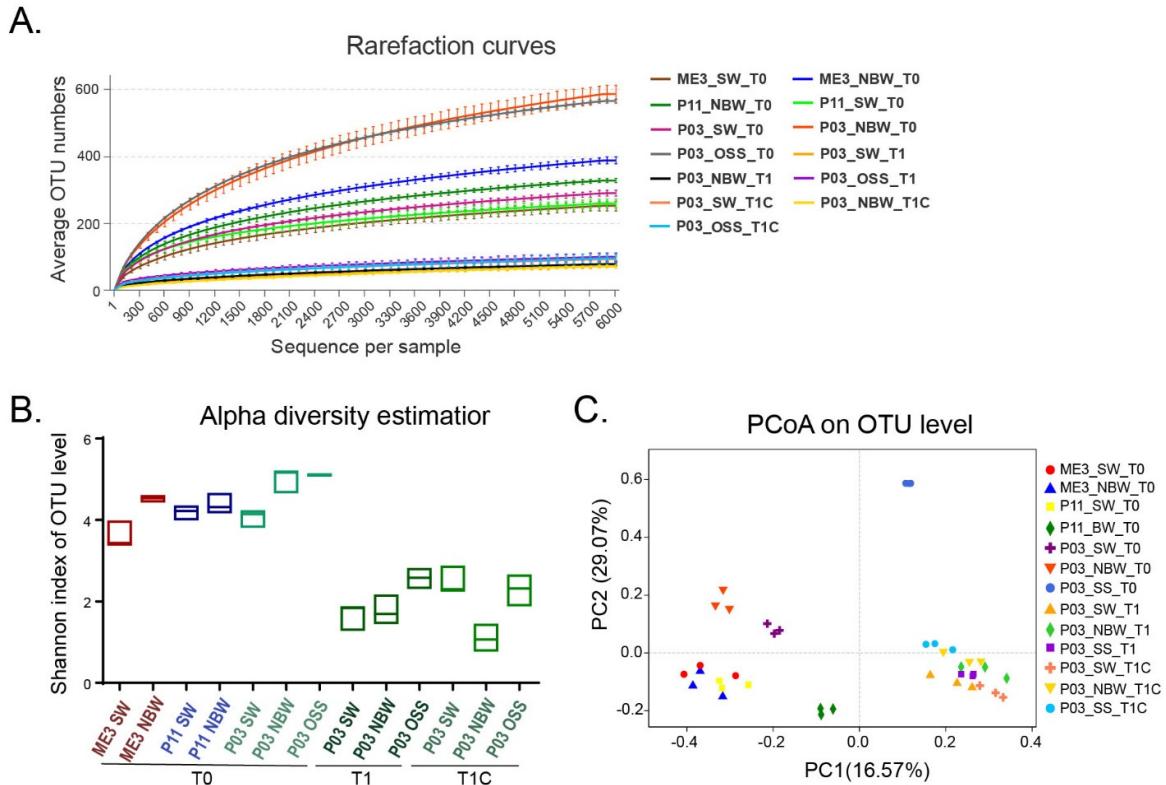
	GOS databases	ECX82089	Todd <i>et al.</i> , 2011
DddW	<i>Ruegeria pomeroyi</i> DSS-3	AAV93771	Todd <i>et al.</i> , 2012
DddY	<i>Alcaligenes faecalis</i> M3A	ADT64689	Souza <i>et al.</i> , 1995; Curson <i>et al.</i> , 2011a; Lei <i>et al.</i> , 2018
	<i>Shewanella putrefaciens</i> CN-32	ABP77243	Curson <i>et al.</i> , 2011b; Lei <i>et al.</i> , 2018
	<i>Desulfovibrio acrylicus</i>	SHJ73420	Van Der Maarel <i>et al.</i> , 1996; Lei <i>et al.</i> , 2018
	<i>Ferrimonas kyonanensis</i> DSM 18153	WP_028114584	Lei <i>et al.</i> , 2018
	<i>Acinetobacter bereziniae</i>	ENV21217	Li <i>et al.</i> , 2017
DddK	<i>Candidatus Pelagibacter ubique</i> HTCC1062	AAZ21215	Sun <i>et al.</i> , 2016
	<i>Alphaproteobacterium HIMB5</i>	AFS47241	Sun <i>et al.</i> , 2016
	<i>Candidatus Pelagibacter ubique</i> HTCC9022	WP_028037226	Sun <i>et al.</i> , 2016
Alma1	<i>Emiliania huxleyi</i> CCMP1516	XP_005784450	Alcolombri <i>et al.</i> , 2015
	<i>Emiliania huxleyi</i> CCMP1516	XP_005763983	Alcolombri <i>et al.</i> , 2015
	<i>Symbiodinium</i> sp. clade D	P0DN22	Alcolombri <i>et al.</i> , 2015

\*N.A., not available.

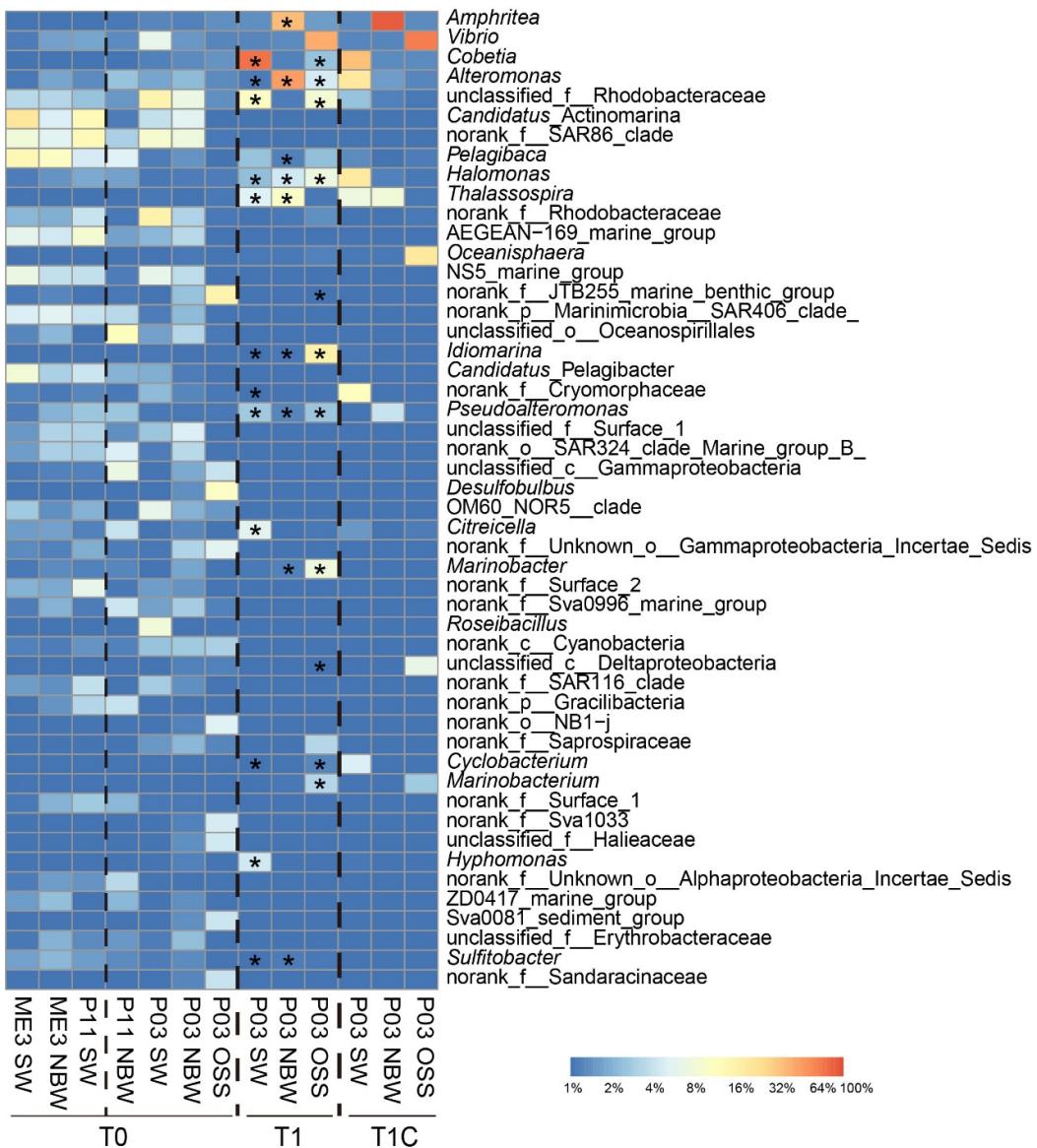
**Table S12.** Oligonucleotide primers used in this study.

Primer name	Sequence (5' to 3')	Use	Reference
27F	AGAGTTGATCCTGGCTCAG	Amplification of	DeLong, 1992;
1492R	GGTTACCTTGTACGACTT	cultivated strain's 16S rRNA gene	Lane et al., 1985
515F	GTGCCAGCMGCCGCGG	Preparing partial 16S	Caporaso et al.,
806R	GGACTACHVGGGTWTCTAAT	rRNA genes amplicon for pyrosequencing	2012
Eub338F	ACTCCTACGGGAGGCAGCAG	qPCR of 16S rRNA gene	Yin et al., 2013
Eub518R	ATTACCGCGGCTGCTGG		
dsyBF	CATGGGSTCSAAGGCSTKTT	Degenerate primers for	Williams et al.,
dsyBR	GCAGRTARTCGCCGAAATCGTA	dsyB detection in DMSP	2019
		producing bacterial	
		isolates and qPCR of dsyB	
mmtNF	CCGAGGTGGTCATGAAYTTYGG	Degenerate primers for	Williams et al.,
mmtNR	CCGAGGTGGTCATGAAYTTYGG	mmtN detection in DMSP	2019
		producing bacterial	
		isolates and qPCR and RT-	
		qPCR of mmtN	

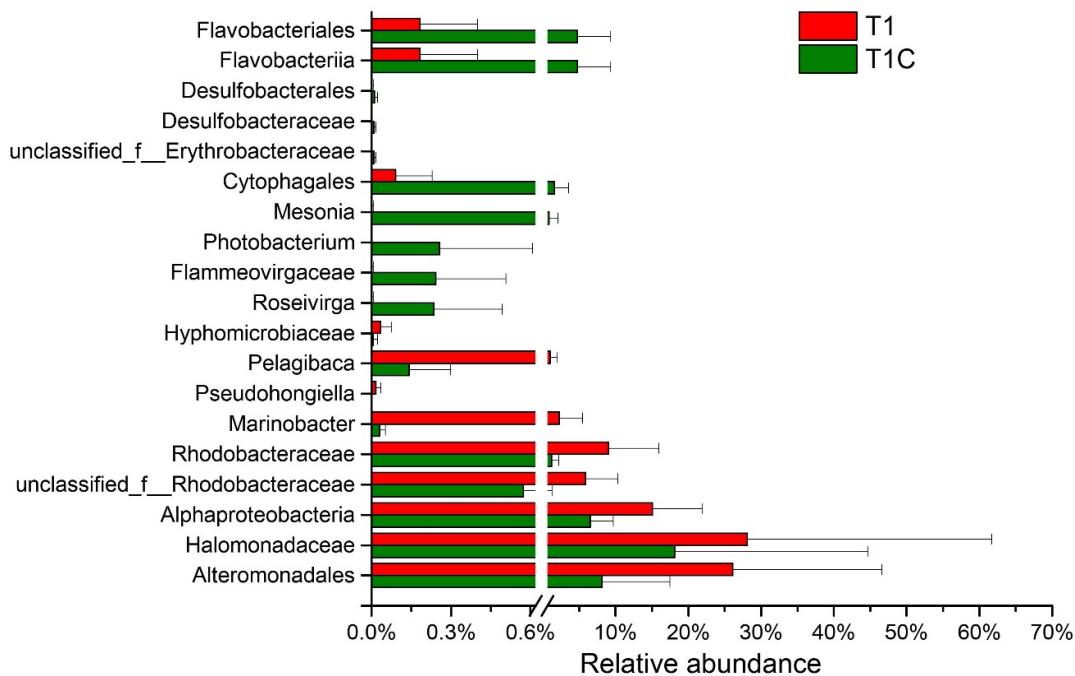
**Fig. S1** Alpha- and beta diversity analyses from 16S rRNA amplicon sequencing data. All samples were rarefied to an even depth of 5,861 sequences per sample. Data shown are the averages of three biological samples. A, Rarefaction curves depicting the mean number of OTUs in each group of samples as a function of the number of sequences. B, Box plots illustrating Shannon Index diversity in each group. C, PCoA plot calculated using Bray-Curtis dissimilarity matrix. ME3, P11, and P03 refer to the different sample sites. SW: sea water; NBW: near sea water; OSS: oxic surface sediment; T0: natural samples; T1: enriched samples in the incubation experiment; T1C: control in the incubation experiment.



**Fig. S2** Heatmap depicting the 50 most abundant genera from the 16S rRNA gene amplicon sequencing data from natural ECS samples (T0), the enriched (T1) and control incubation experiments after 14 days. \*, p < 0.05 in Student's t-test comparing to the TIC samples.



**Fig. S3** Relative abundance for each significant taxon in the LEfSe analysis of T1 & T1C samples.  
Error bars represent standard deviation from the mean value.



**Fig. S4** Composition of eukaryotic plastid 16S rRNA genes in P03 SW and NBW samples. Total numbers of eukaryotic plastid 16S rRNA sequences identified in P03 SW and NBW were  $339 \pm 302$  and  $383 \pm 230$ .

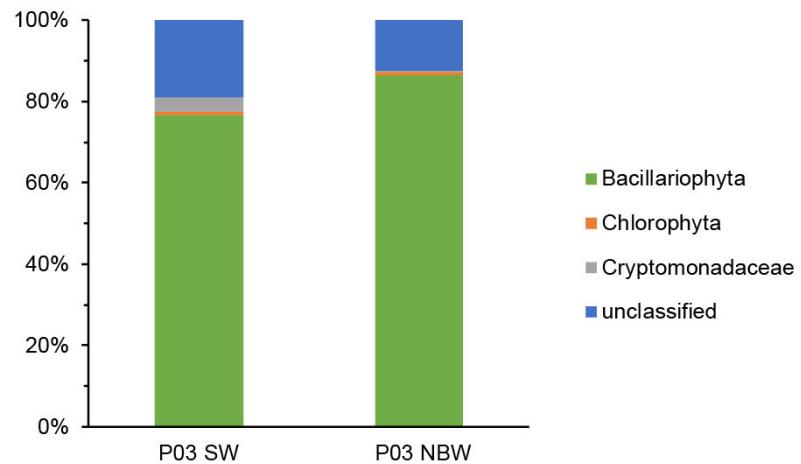


Fig. S5 Canonical correspondence analysis (CCA) on bacterial communities at family level in samples of incubation experiments.

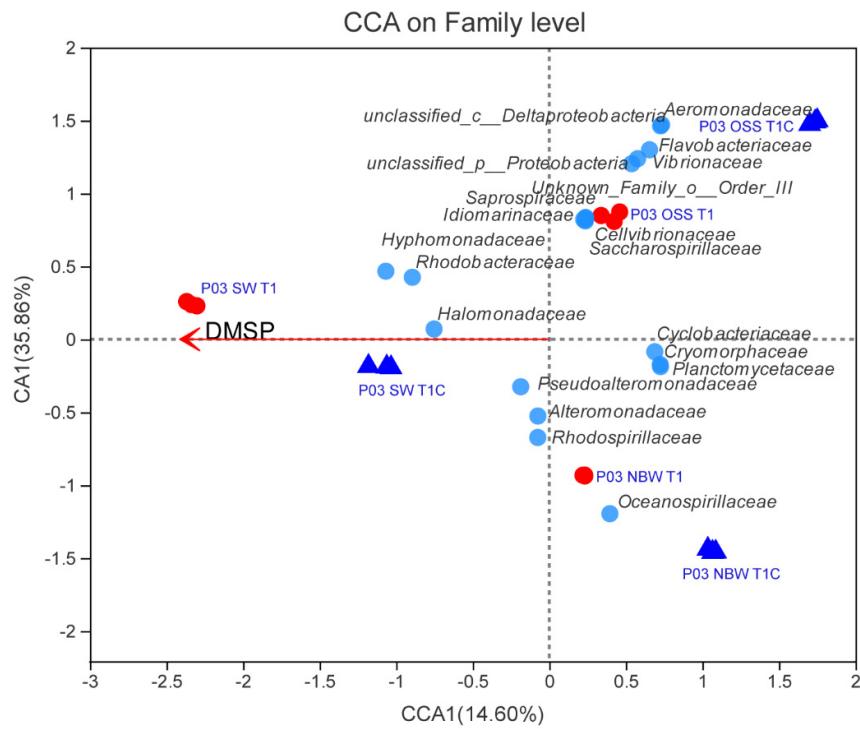
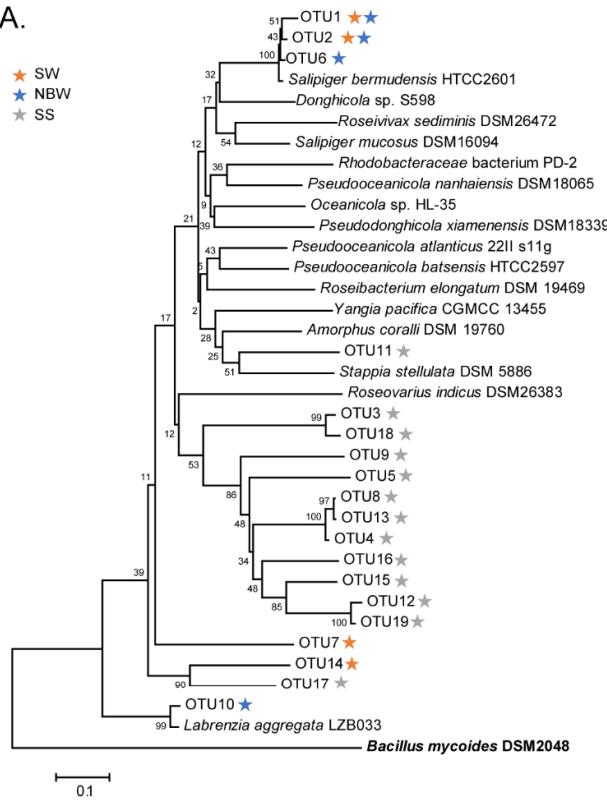
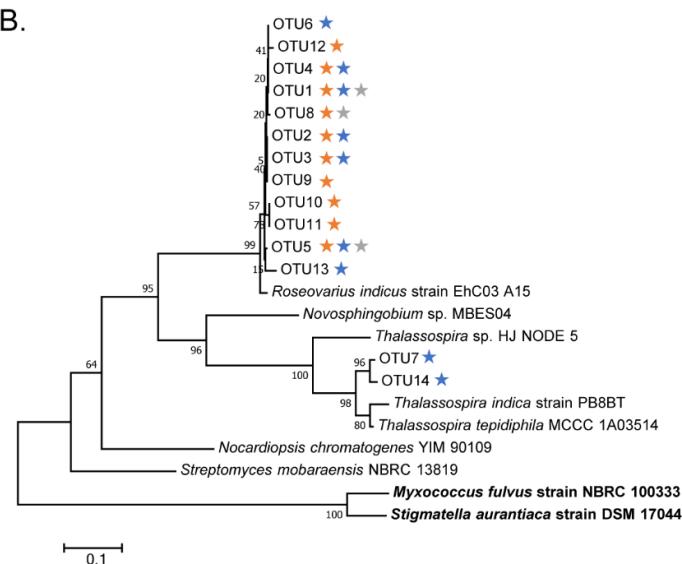


Fig. S6 Amino acid tree of representative DsyB and MmtN OTU sequences from clone libraries. Stars represent the source of different DsyB and MmtN OTUs. Non-functional DsyB and MmtN sequences were indicated in bold. Branch lengths are measured in the number of substitutions per site, as indicated on the scale bar.

A.



B.



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