

Supplementary Materials

Supplementary Tables

Supplementary Table 1. The Metagenome clean data basic information of all samples

Sample	Clean reads	Contig Number	Assembly Length (bp)	N50 (bp)	N90 (bp)	Average Size (bp)
H12swf	18,102.80	445,562	484,836,788	1,144	559	1,088.15
H12swp	17,146.84	697,891	577,983,922	797	537	828.19
H12bwf	17,284.13	618,026	624,733,236	1,029	558	1,010.85
H12bwp	19,123.78	530,280	486,698,637	895	544	917.81
H12m	31,111.29	629,979	476,040,823	714	527	755.65
HS5swf	24,185.83	863,242	850,874,056	985	555	985.67
HS5swp	19,029.69	889,673	769,763,410	843	541	865.22
HS5bwf	21,933.21	673,037	695,929,207	1,058	557	1,034.01
HS5bwp	20,299.88	593,214	564,627,774	946	548	951.81
HS5m	27,270.10	774,309	641,952,542	786	534	829.07
H25	106,194,046	145,672	145,893,739	994	551	1001
B41	80,741,206	32,622	31,980,432	999	562	980
B45	81,015,472	46,645	47,686,773	1041	564	1022
B47	85,342,684	29,036	23,917,017	793	540	823
B50	116,539,140	212,671	222,127,826	1061	557	1044
T1	86,968,070	135,574	79,410,337	587	348	586
TVG5-3	70,534,322	3,923	2,661,870	638	520	678
TVG11-2	81,951,240	33,259	24,135,629	701	529	725
TVGS5-3	119,612,348	404,396	447,323,409	1,166	565	1106
TVGS11-2	113,860,692	109,320	101,722,206	923	551	930

Supplementary Table 2. Information of high completion MAGs

Bins	completeness(%)	contamination (%)	Taxonomy	Genes involved in DMSP cycling	Accession numbers
H12bwf_bin.29	91.45	2.14	k_Bacteria; p_Actinobacteria; c_Actinobacteria	<i>dddP, dmdB, dmdC, tmm</i>	SAMN13828863
H12bwf_bin.44	90.94	4.21	k_Bacteria; p_Bacteroidetes	<i>acuH, dmdD</i>	SAMN13828865
H12bwp_bin.25	94.02	1.68	k_Bacteria; p_Planctomycetes; c_Planctomycetacia	<i>dmdD</i>	SAMN13828867
H12swf_bin.13	97.35	1.45	k_Bacteria; p_Proteobacteria; c_Alphaproteobacteria	<i>acuH, dmdB, dmdC, dmoA</i>	SAMN13828871
H12swf_bin.4	96.96	0.68	k_Bacteria; p_Verrucomicrobia		SAMN13828870
HS5bwf_bin.44	95.54	4.08	k_Bacteria; p_Verrucomicrobia; c_Verrucomicrobiae; o_Verrucomicrobiales; f_Verrucomicrobiaceae		SAMN13828881
HS5bwp_bin.22	95.33	3.91	k_Bacteria; p_Verrucomicrobia; c_Verrucomicrobiae; o_Verrucomicrobiales; f_Verrucomicrobiaceae		SAMN13828882
HS5bwp_bin.32	93.96	4.66	k_Bacteria; p_Planctomycetes; c_Planctomycetacia	<i>dmdD</i>	SAMN13828884
HS5swf_bin.18	93.03	1.78	k_Bacteria; p_Proteobacteria; c_Alphaproteobacteria	<i>acuH, dmdB, dmdC</i>	SAMN13828889
HS5swf_bin.3	92.26	4.73	k_Bacteria; p_Bacteroidetes	<i>acuH, dmdD</i>	SAMN13828886
HS5swf_bin.30	90.12	2.31	k_Bacteria; p_Proteobacteria	<i>dmdB, dmdC</i>	SAMN13828891
HS5swf_bin.63	90.21	2.57	k_Bacteria; p_Bacteroidetes	<i>acuH</i>	SAMN13828893
HS5swp_bin.4	90.47	0.77	k_Bacteria; p_Planctomycetes; c_Planctomycetacia		SAMN13828895
H12BWF_bin.23	89.69	3.08	k_Bacteria; p_Chloroflexi; c_Dehalococcoidia; o_Dehalococcoidales	<i>dddP</i>	SAMN13828862
HS5SWF_bin.65	89.41	0.54	k_Bacteria; p_Bacteroidetes		SAMN13828894
H12SWP_bin.13	89.34	0.11	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria	<i>dmdB, dmdC</i>	SAMN13828874
H12BWP_bin.35	88.89	0.63	k_Bacteria; p_Bacteroidetes		SAMN13828869
HS5BWF_bin.23	88.65	3.23	k_Bacteria; p_Planctomycetes; c_Planctomycetacia	<i>dmdD</i>	SAMN13828878
HS5BWP_bin.26	87.63	0.36	k_Bacteria; p_Bacteroidetes		SAMN13828883
HS5SWF_bin.26	87.1	3.06	k_Bacteria; p_Bacteroidetes	<i>dddP, dddQ, dmdA, dmdB, dmdC</i>	SAMN13828890
H12BWF_bin.34	86.55	4.8	k_Bacteria; p_Verrucomicrobia; c_Verrucomicrobiae;		SAMN13828864

			o_Verrucomicrobiales		
H12BWP_bin.26	86.52	4.37	k_Bacteria; p_Actinobacteria;	<i>dddP, dmdB,</i>	SAMN13828868
			c_Actinobacteria	<i>dmdC, tmm</i>	
HS5BWF_bin.2	85.25	2.98	k_Bacteria; p_Proteobacteria;	<i>acuH, dmdB,</i>	SAMN13828876
			c_Alphaproteobacteria;	<i>dmdC</i>	
			o_Rhodobacterales		
HS5BWF_bin.36	85.04	0.8	k_Archaea; p_Euryarchaeota	<i>AcuH</i>	SAMN13828880
H12SWP_bin.12	84.78	1.55	k_Bacteria; Cyanobacteria;		SAMN13828873
			o_Synechococcales		
H12SWP_bin.2	84.02	3	k_Bacteria; p_Bacteroidetes		SAMN13828872
HS5BWF_bin.1	84	2.4	k_Archaea; p_Euryarchaeota		SAMN13828875
H12BWF_bin.49	83.82	8.97	k_Bacteria; p_Actinobacteria;	<i>dmdB, dmdC,</i>	SAMN13828866
			c_Actinobacteria	<i>dmoA</i>	
H12BWF_bin.3	83.69	1.61	k_Bacteria; p_Planctomycetes;	<i>dmdD</i>	SAMN13828858
			c_Planctomycetacia		
HS5SWF_bin.35	83.33	6.8	k_Bacteria; p_Proteobacteria	<i>dmdB, dmdC</i>	SAMN13828892
HS5SWF_bin.10	83.16	4.29	k_Bacteria; p_Proteobacteria	<i>dmdB, dmdC</i>	SAMN13828887
HS5SWF_bin.12	82.39	4.59	k_Bacteria; p_Proteobacteria;	<i>AcuH, dmdB,</i>	SAMN13828888
			c_Alphaproteobacteria	<i>dmdC</i>	
H12BWF_bin.21	82.29	2.2	k_Bacteria	<i>acuH, dmdB</i>	SAMN13828861
H12BWF_bin.10	82.08	0	k_Bacteria	<i>dmdC</i>	SAMN13828859
H12BWF_bin.14	81.2	2.4	k_Archaea; p_Euryarchaeota		SAMN13828860
HS5BWF_bin.10	80.73	0.54	k_Bacteria; p_Actinobacteria;	<i>acuH, dmdB</i>	SAMN13828877
			c_Actinobacteria;		
			o_Actinomycetales		
HS5BWF_bin.30	80.56	0.36	k_Bacteria; p_Bacteroidetes		SAMN13828879
HS5M_bin.12	80.14	8.84	k_Bacteria; p_Proteobacteria	<i>acuH, dddP,</i>	SAMN13828885
				<i>dmdB, dmdC</i>	
B_bin.47	95	2.9	k_Bacteria; p_Proteobacteria;	<i>ddhA, dmdB,</i>	SAMN13826822
			c_Gammaproteobacteria	<i>dmdC, mtoX</i>	
B_bin.98	94.84	8.11		<i>acuH, dddP,</i>	SAMN13826828
			k_Bacteria; p_Proteobacteria;	<i>dmdB, dmdC,</i>	
			c_Gammaproteobacteria	<i>DMSOR</i>	
B_bin.4	91.87	2.7	k_Bacteria; p_Proteobacteria;	<i>acuH, dddP,</i>	SAMN13826814
			c_Gammaproteobacteria	<i>dddQ, dmdA,</i>	
				<i>dmdB, dmdC,</i>	
				<i>tmm</i>	
B_bin.33	90.91	2	k_Bacteria	<i>acuH, dddD,</i>	SAMN13826819
				<i>dmdB, mddA</i>	
B_bin.18	90.88	0.72	k_Bacteria		SAMN13826817
B_bin.9	90.27	2.02	k_Bacteria; p_Proteobacteria;	<i>dmdB, dmdC,</i>	SAMN13826815
			c_Gammaproteobacteria	<i>DMSOR</i>	
B_bin.42	90.04	6.85	k_Bacteria; p_Proteobacteria;	<i>acuH, dddD,</i>	SAMN13826821
			c_Alphaproteobacteria	<i>dddP, dddQ,</i>	

				<i>dmdA, dmdB, dmdC</i>	
B_bin.62	87.69	2.69	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria	<i>dmdB,</i>	SAMN13826823
B_bin.79	87.54	1.94	k_Archaea		SAMN13826824
B_bin.86	87.05	2.76	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria	<i>dddL, dmdB, dmdC, dmdD,</i>	SAMN13826825
B_bin.40	86.69	2.64	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria	<i>dmdB, mddA</i>	SAMN13826820
B_bin.93	86.6	1.36	k_Bacteria		SAMN13826827
B_bin.87	86.14	3.58	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria	<i>dmdC</i>	SAMN13826826
B_bin.24	86.65	2.55	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria	<i>dmdB, dmdC</i>	SAMN13826818
B_bin.12	81.84	6.47	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria	<i>ddhA, mtoX</i>	SAMN13826816
OT_bin.97	97.44	4.27	Wang et al., unpublished		SAMN13826949
OT_bin.31	96.7	2.75	Wang et al., unpublished		SAMN13826934
OT_bin.83	95.31	0.84	Wang et al., unpublished		SAMN13826947
OT_bin.105	93.64	1.62	Wang et al., unpublished		SAMN13826950
OT_bin.72	95.3	8.78	Wang et al., unpublished	<i>dmdB</i>	SAMN13826943
OT_bin.123	92.21	0.75	Wang et al., unpublished	<i>dmdB</i>	SAMN13826952
OT_bin.67	92.02	4.25	Wang et al., unpublished	<i>dmdB</i>	SAMN13826941
OT_bin.92	91.48	2.27	Wang et al., unpublished		SAMN13826948
OT_bin.74	90.91	0	Wang et al., unpublished		SAMN13826944
OT_bin.119	90.34	0.84	Wang et al., unpublished	<i>dmdC</i>	SAMN13826951
OT_bin.57	89.83	2.7	Wang et al., unpublished		SAMN13826938
OT_bin.35	89.78	3.85	Wang et al., unpublished		SAMN13826935
OT_bin.50	88.18	2.91	Wang et al., unpublished		SAMN13826937
OT_bin.18	87.94	2.44	Wang et al., unpublished	<i>dmdB, dmdC</i>	SAMN13826933
OT_bin.126	85.61	3.35	Wang et al., unpublished	<i>dmdB, dmdC</i>	SAMN13826953
OT_bin.78	84.4	2.2	Wang et al., unpublished		SAMN13826946
OT_bin.66	84.38	1.35	Wang et al., unpublished	<i>dmdB, dmdC</i>	SAMN13826940
OT_bin.128	83.94	0	Wang et al., unpublished		SAMN13826955
OT_bin.42	82.91	0	Wang et al., unpublished	<i>dmoA</i>	SAMN13826936
OT_bin.127	82.78	4.23	Wang et al., unpublished	<i>acuH</i>	SAMN13826954
OT_bin.77	82.62	0.24	Wang et al., unpublished		SAMN13826945
OT_bin.62	82.17	5.08	Wang et al., unpublished	<i>dmdB</i>	SAMN13826939
OT_bin.6	81.18	5.08	Wang et al., unpublished	<i>dmdB, dmdC</i>	SAMN13826931
OT_bin.15	80.44	0	Wang et al., unpublished		SAMN13826932
OT_bin.69	80.25	5.04	Wang et al., unpublished		SAMN13826942

H: Yellow Sea; B: Bohai Sea; OT: Okinawa Trough; swf: surface water free-living; swp: surface water particle; bwf: bottom water free-living; bwp: bottom water particle; m: sediment; k: kingdom; p: phylum; c: class; o: order; f: family.

Supplementary Table 3. Reference protein sequences of the ratified proteins

Protein	Source	NCBI Accession	Reference
DsyB	<i>Labrenzia aggregata</i> IAM 12614	EAV42226	Curson et al., 2017
	<i>Labrenzia aggregata</i> LZB033	WP_075282486.1	Curson et al., 2017
	<i>Pseudooceanicola batsensis</i> HTCC2597	EAQ04968	Curson et al., 2017
	<i>Pelagibaca bermudensis</i> HTCC2601	EAU45958	Curson et al., 2017
	<i>Amorphus coralli</i> DSM 19760	WP_018697905	Curson et al., 2017
	<i>Sediminimonas qiaohouensis</i> DSM 21189	WP_018697905	Curson et al., 2017
	<i>Sagittula stellate</i> E37	WP_005854984.1	Curson et al., 2017
	<i>Thalassobaculum salexigens</i> DSM 19539	WP_084618911.1	Curson et al., 2017
MmtN	<i>Thalassospira profundimaris</i> PB8B	OAZ15224	Seebeck et al., 2019
	<i>Novosphingobium</i> sp. MBES04	GAM03459	Williams et al., 2019
	<i>Roseovarius indicus</i> B108	KRS18724	Williams et al., 2019
	<i>Nocardiopsis chromatogenes</i> YIM 90109	WP_017624909	Williams et al., 2019
	<i>Streptomyces mobaraensis</i> DSM 40847	EME99407	Williams et al., 2019
DSYB	<i>Prymnesium parvum</i> CCAP946/6	NA	Curson et al., 2018
	<i>Chrysochromulina tobin</i> CCMP291	KOO32714	Curson et al., 2018
	<i>Lingulodinium polyedrum</i> CCMP1936	NA	Curson et al., 2018
	<i>Alexandrium tamarense</i> ATSP1-B	NA	Curson et al., 2018
	<i>Acropora cervicornis</i>	NA	Curson et al., 2018
	<i>Fragilariopsis cylindrus</i> CCMP1102	OEU17621	Curson et al., 2018
	<i>Symbiodinium microadriaticum</i>	OLQ07620	Curson et al., 2018
	CCMP2467		
DmdA	<i>Ruegeria pomeroyi</i> DSS-3	AAV95190	Howard et al., 2006
	<i>Pelagibacter ubique</i> HTCC1062	WP_011281570	Howard et al., 2006
	<i>Dinoroseobacter shibae</i> DFL 12	WP_012178987	Howard et al., 2008
	<i>marine gammaproteobacterium</i>	WP_007233625	Howard et al., 2008
	HTCC2080		
	<i>Candidatus Pelagibacter</i> sp. HTCC7211	WP_008546106	Howard et al., 2010
	<i>Candidatus Puniceispirillum marinum</i>	WP_013044947	Curson et al., 2011b
DmdB	IMCC1322		
	<i>Ruegeria pomeroyi</i>	WP_011047771.1	Reisch et al., 2011
	<i>Ruegeria pomeroyi</i>	WP_011046428.1	Reisch et al., 2011
	<i>Candidatus Pelagibacter ubique</i>	WP_011281571.1	Reisch et al., 2011

DmdC	<i>Ruegeria pomeroyi</i>	WP_011049476.1	Reisch et al., 2011
	<i>Burkholderia thailandensis</i> E264	WP_009892931.1	Reisch et al., 2011
	<i>Ruegeria lacuscaerulensis</i> ITI-1157	EEX10128.1	Reisch et al., 2011
	<i>Ruegeria pomeroyi</i> DSS-3	WP_011048615.1	Reisch et al., 2011
	<i>Pseudomonas aeruginosa</i> PAO1	WP_003114720.1	Reisch et al., 2011
	<i>Pseudomonas aeruginosa</i> PAO1	WP_003114561.1	Reisch et al., 2011
	<i>Burkholderia thailandensis</i> E264	WP_009889880.1	Reisch et al., 2011
	<i>Ruegeria lacuscaerulensis</i> ITI-1157	EEX08676.1	Reisch et al., 2011
DmdD	<i>Ruegeria pomeroyi</i>	Q5LLW6.1	Reisch et al., 2011 Tan et al., 2013
AcuH	<i>Ruegeria lacuscaerulensis</i> ITI-1157	EEX08788.1	Cao et al., 2017
	<i>Ruegeria pomeroyi</i> DSS-3	AAV93475.1	Cao et al., 2017
DddD	<i>Marinomonas</i> sp.	WP_012071702.1	Todd et al., 2007
	<i>Oceanimonas doudoroffii</i>	WP_094199898.1	Curson et al., 2012
	<i>Psychrobacter</i> sp. J466	ACY02894	Curson et al., 2010
	<i>Halomonas</i> sp.	ACV84065	Todd et al., 2010
	<i>Burkholderia ambifaria</i>	WP_011659284	Curson et al., 2010
	<i>Pseudomonas</i> sp. J465	ACY01992	Todd et al., 2007
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> IAM12614	WP_006936138.1	Curson et al., 2017
	<i>Fulvimarina pelagi</i>	WP_007067665.1	Curson et al., 2008
	<i>Pseudooceanicola batsensis</i>	WP_009805827.1	Curson et al., 2008
	<i>Ahrensia marina</i> LZD062	KP639183	Liu et al., 2018
DddP	<i>Roseovarius nubinhibens</i>	EAP77700	Kirkwood et al., 2010
	<i>Ruegeria pomeroyi</i> DSS-3	WP_044029245.1	Todd et al., 2011
	<i>Fusarium graminearum</i> PH-1	XP_389272	Todd et al., 2009
	<i>Oceanimonas</i> P1	WP_094198963.1	Curson et al., 2012
	<i>Oceanimonas</i> P2	WP_094200218.1	Curson et al., 2012
DddQ	<i>Ruegeria pomeroyi</i> DSS-3	WP_011047333	Todd et al., 2011
	<i>Roseovarius nubinhibens</i> 1	WP_009814827.1	Todd et al., 2011
	<i>Roseovarius nubinhibens</i> 2	WP_009814826.1	Todd et al., 2011
	<i>Ruegeria lacuscaerulensis</i>	WP_005978225	Li et al., 2014
	GOS databases 1	ECW91654	Todd et al., 2011
	GOS databases 2	EBP74803	Todd et al., 2011

	GOS databases 3	ECX82089	Todd et al., 2011
DddW	<i>Ruegeria pomeroyi</i> DSS-3	AAV93771	Todd et al., 2012
DddY	<i>Alcaligenes faecalis</i> M3A	ADT64689	Curson et al., 2012
	<i>Shewanella putrefaciens</i> CN-32	ABP77243	Curson et al., 2012
	<i>Candidatus Pelagibacter ubique</i> HTCC1062	WP_011281678.1	Schnicker et al., 2017
	<i>Alphaproteobacterium</i> HIMB5	WP_014953073.1	Schnicker et al., 2017
	<i>Candidatus Pelagibacter ubique</i> HTCC1002	WP_006997514.1	Schnicker et al., 2017
DddK	<i>Pelagibacteraceae bacterium</i> BACL20	KRP06000.1	Schnicker et al., 2017
	<i>Candidatus Pelagibacter ubique</i> 4	WP_027306832.1	Schnicker et al., 2017
	<i>Candidatus Pelagibacter ubique</i> 2	WP_018413735.1	Schnicker et al., 2017
	<i>Candidatus Pelagibacter ubique</i> 3	WP_028037226.1	Schnicker et al., 2017
Alma1	<i>Emiliania huxleyi</i> CCMP1516	XP_005784450	Alcolombri et al., 2015
	<i>Emiliania huxleyi</i> CCMP1516	XP_005763983	Alcolombri et al., 2015
	<i>Symbiodinium</i> sp. clade D	P0DN22	Alcolombri et al., 2015
MddA	<i>Mycobacterium tuberculosis</i> H37Rv	WP_003416945.1	Carrión et al., 2015
	<i>Bradyrhizobium diazoefficiens</i> USDA 110	WP_011084036.1	Carrión et al., 2015
	<i>Bradyrhizobium diazoefficiens</i> USDA 110	WP_011088485.1	Carrión et al., 2015
	<i>Pseudomonas</i> sp. GM41	WP_008148420.1	Carrión et al., 2015
	<i>Pseudomonas deceptionensis</i>	WP_048359798.1	Carrión et al., 2015
	<i>Sulfurovum</i> sp. NBC37-1	WP_011980608.1	Carrión et al., 2015
DmoA	<i>Hyphomicrobium sulfonivorans</i> 6AK1_A	NA	Boden et al., 2011
	<i>Hyphomicrobium</i> sp.	ATJ26742.1	Lee et al., 2002
MTO	<i>Methylophaga thiooxydans</i>	WP_008290534.1	Eyice et al., 2018

	<i>Ruegeria pomeroyi</i>	WP_011242048.1	Eyice et al., 2018
DdhA	<i>Ruegeria pomeroyi</i> DSS-3	WP_011242048.1	McDevitt et al., 2002
	<i>Rhodovulum sulfidophilum</i>	WP_060833690.1	McDevitt et al., 2002
Tmm	<i>Methylocella silvestris</i> BL2	ACK52489.1	Lidbury et al., 2016
	<i>Ruegeria pomeroyi</i> DSS-3	AAV94838.1	Lidbury et al., 2016
	<i>Roseovarius</i> sp. 217	EAQ26624.1	Lidbury et al., 2016
	<i>Rhodobacter capsulatus</i> 1DMR_A	NA	Satoh and Kurihara., 1987
DMSOR	<i>Escherichia coli</i>	WP_097479356.1	Sambasivarao and Weiner., 1991
	<i>Rhodobacter sphaeroides</i>	AAB94874.1	Mcewan et al., 1991

NA: not available. The protein sequences were as follows.

DSYB:

>Prymnesium_parvum_CCAP_946/6

MLRLAPRLPTRALVRHALRAHALPLARPALPSGTRLFASAPADDIDVDNVAYGFMASQALFTGLE
MGLFDAIAAGPEAGLNIDELKAAANCSAPRLQTLVTSLVAIKSLKRTPDGRYTLSPNTARFLVQSSK
QYYGDYLYKYQMGRQFYHRMGALPDVMTSGEAPSYASWFSDPETAATYTQAQHNGSVATAKYLI
KKKLQLGDAATMLDVGGGSGAFSYVFTEATPGLSSTVLELPEVCRTGEAIKAKQPVSVQERVKLV
ELDATSPDWPVNDAAYDVVLMSYISGSPESIIGALYANAYKALKPGGRLLVHDFMVDNSLDGPP
LGALWALQHVTVNADGLGLCPQGVIERMGSAGFDPSACETMEMITGLTKLIVAYKP

>Lingulodinium_polyedrum_CCMP1936

MAFAPRTSPLLARAVTRAWPRAQRSAAAALRSWARPALAAKPPLASRAFARTSWDEGEDVDLDS
VAYGFMASQALFTGLELGIFDHIAAAGAGGLSAAGIGKACGIEAPRVQTLTSLVAVKCLKRDASA
MYTLSPNTAQYMTSSRHFGDYLYRYQIGRQFYHRMGALPEVMTSGKAPSYASWFSDEPVARTY
TQAQHNGSVATAKYLIKKKLQLGGISAMLDVGGGSGAFSYVFTQATPGLHASKVLELPEVCRTGEGI
RAKQPEDVRSRVSFVELDASSPTWPVDDSAFDVVLMSYISGSPPEIIGSLYANAMKALRPGGRLL
VHDFMVDNSLDGPALGALWGLQHVTVNADGLGLCPKEIISRMGTAGFDTSKCTMEMIHMGTML
IVGYKN

>Alexandrium_tamarense_ATSP1B_1

MPPSRAWRRLLAVSAQQILPSIVQGTSSDVLDAAYGFMASQALFSALELGIFDHLAACPATAPEL
GSACGIPTQLRLTLLTALVASRCLRLDAESLKYTNSPNVARFMVSNKSYGYDYLYKQIGWLFYHR
MGRITEVMKGGALDYQTFWSDPHVADTYTSAQHNGSLATARALMRKVDLSRVTCLLDAGGGS
GAFSIAAARAVPGLEATVLELPEVCKTGSRIVEQAGLSGRIRYVELDATSPDWPVHGGSFQAVLMS
YLSGSVPAHAIVGLYSNAYKALGPGGRLLVHDFMVDNSLDGPQLGALWALQHVTVNPDGLGLCP
GHVVSRMRTAGFARTETLDLIGGMTKVVGKYD

>Acropora_cervicornis

MAAAFAAARGLTRAISRCASKRVPEQALFSRLSAPAPPALAAALPGVRAFSRTSWESGDDVDLDSVA
YGFMASQALFSALELGIFDKVAAAGEKGCAAKDVQQACGVEGPRLTLLTALTAVKCLRRSDEGL
YTLSPNTAQYMVSSSRHYGYDYLYQYQIGRQFYHRMGALPEVMTTGKAPSYASWFSDEPVAKTYT

QAQHNGSVATAKYLVRRKKLDLGGISSMLDVGGGSGAFSYVFTEATPGLKSTVLELPEVCRTGEGIK
AQQPQDIQDRVSFVELDATSPDWPVSDSNYDIVLMSYISGSVPESVILPLYKNAFKALRPGGRLLVH
DFMVNDSLDGPALGALWGLQHVTVNAQGLGLCPAEVIRMAQAGFEENKCQTHEMIHGMTKLI
VAHKA

DmoA:

> *Hyphomicrobium_sulfonivorans_6AK1_A*

MKKRIVLNAFDMTCVSHQSAGTWRHPSSQAARYNDLEYWTNMAMELERGCFDCLFIADVGVY
DVYRGS AEMALRDADQVPVNDPFGAISAMAAVTEHVGFGVTAAITFEQPYLLARRLSTLDHLTKG
RVAWNVVS SYLNSAALNIGMDQQLAHDERYEMADEYMEV MYKLWEGSWEDDAVKRDKKSGVF
TDGSKVHPINHQQKYYKVPGFHICEPSPQRTPVIFQAGASGRGSKFAASNAEGMFILTTSVEQARQI
TTDIRNQAEAAGRSRDSIKIFMLLTVITGDSDEAAEAKYQEYLSYANPEGMLALYGGWTGIDFAKL
DPDEPLQAMENDSLRTTLESLTHGENAKKWTVRDVIRERCIGGLGPVLVGGPQKVADELERWVDE
GGVDGFNLAYAVTPGSVTD FIDYIVPELRRKRGRAQDSYKPGSLRRKLIGTNDGRVESTHPAAQYRD
AYVGKESVADRTQPSPFANAKAPVAE

DMSOR

> *Rhodobacter Capsulatus 1DMR_A*

MTKFSGNELRAELYRRAFLSYSVAPGALGMFGRSLLAKGARA EALANGTVMSGSHWGVFTATVENGR
ATAFTPWEKDPHPSPMLAGVLD SIYSPTRIKYPMVRREFLEKGVNADRSTRGN GDFVRVSWDQALDLV
AAEVKRVEETYGPEGVF GGSYGWKSPGRLHNCTTLLRRMLTLAGGYVNGAGDYSTGAAQVIMPHVV
GTLEVYEQQTAWPVLAENTEVMVFWAADPIKTSQIGWVIPEHGAYPGLEALKAKGTKVIVIDPVRTKT
VEFFGAEHITPKPQTDVAIMLGMAHTLVAEDLYDKDFIANYTSGFDKFLPYLDGETDSTPKTAEWAEGIS
GVPAETIKELARLFESKRTMLAAGWSMQRMHHGEQAHWMLVTLASMLGQIGLPGGGFGLSYHYS GG
GTPSTSGPALAGITDGGAATKGPEWLAASGASVIPVARVVDMLENPGA EFDNFNGTRSKFPDVKMAYWV
GGNPFVHHQDRNRMVKAWEKLET FVVHDFQWTP TARHADIVLPATT SYERNDIETIGDYSNTGILAMK
KIVEPLYEARSDYDIFA AEAERLGKGAEFTEGKDEMGWIKSFYDDAAKQGKAAGVQMPAFDAFWAEGI
VEFPVTDGAD FVRYASFREDPLL NPLGTPTGLIEIYSKNIEKMGYDDCPAHPTWMEPLERLDGPGAKYP
LHIAASHPFNRLHSQLNGTVLREGYAVQGHEPCLMHPDDAAARGIADGDVVRVHNDRGQILTGVKVT
DAVMKGVIQIYEGGWYDPSDVTEPGTLDKYGDVNVLSADIGTSKLAQGNCGQTVLAEVEKYTGPAVT
LTGFVAP

Supplementary Table 4. The information of key proteins involved in cycling DMSP and related compounds.

Enzyme	Polypeptide class	Reaction catalysed	E-value used in this study	Reference
DddP	M24B metallopeptidase family	DMSP cleavage to DMS and acrylate, plus a proton	$E \leq 1 \times 10^{-83}$	Todd et al., 2009 Curson et al., 2011 Lei et al., 2018
DddQ	Cupin superfamily	DMSP cleavage to DMS and acrylate, plus a proton	$E < 1 \times 10^{-20}$	Todd et al., 2011 Curson et al., 2011 Lei et al., 2018
DddW	Cupin superfamily	DMSP cleavage to DMS and acrylate, plus a proton	$E < 1 \times 10^{-49}$	Todd et al., 2012 Curson et al., 2011 Lei et al., 2018
DddY	Cupin superfamily	DMSP cleavage to DMS and acrylate, plus a proton	$E \leq 1 \times 10^{-64}$	Curson et al., 2011a Li et al., 2017 Lei et al., 2018
DddL	Cupin superfamily	DMSP cleavage to DMS and acrylate, plus a proton	$E \leq 1 \times 10^{-33}$	Curson et al., 2008 Lei et al., 2018 Curson et al., 2011
DddK	Cupin superfamily	DMSP cleavage to DMS and acrylate, plus a proton	$E \leq 1 \times 10^{-35}$	Schnicker et al., 2017 Lei et al., 2018
DddD	Class III CoA transferase family	DMSP cleavage to DMS and 3HP, probably involving a DMSP-CoA intermediate	$E \leq 1 \times 10^{-97}$	Todd et al., 2007 Curson et al., 2011 Lei et al., 2018
Alma1 (eukaryotic)	Aspartic acid/glutamic acid/ethylurea racemase superfamily	DMSP cleavage to DMS and acrylate	$E \leq 1 \times 10^{-26}$	Alcolombri et al., 2015 Lei et al., 2018
DmdA	Glycine cleavage system T family	DMSP demethylation to MMPA	$E \leq 1 \times 10^{-130}$	Reisch et al., 2008 Curson et al., 2011b González et al., 2019
DmdB	AMP combinase superfamily	Catalyze MMPA to MMPA-CoA	$E \leq 1 \times 10^{-75}$	Reisch et al., 2011
DmdC	Acyl CoA dehydrogenase superfamily	MMPA-CoA dehydrogenation to MTA-CoA	$E \leq 1 \times 10^{-100}$	Reisch et al., 2011
DmdD	Allyl hydrase superfamily	MTA-CoA hydration to acetaldehyde	$E < 1 \times 10^{-30}$	Reisch et al., 2011 Tan et al., 2013
AcuH	Allyl hydrase superfamily	MTA-CoA hydration to acetaldehyde	$E \leq 1 \times 10^{-56}$	Cao et al., 2017

DsyB	SAM-dependent methyltransferase	MTHB methylation to DMSHB	$E \leq 1 \times 10^{-67}$	Curson et al., 2017
MmtN (MSMT)	Met-methylating enzymes	Methionine methylation to SMM	$E \leq 1 \times 10^{-98}$	Seebeck et al., 2019 Williams et al., 2019
DSYB (eukaryotic)	SAM-dependent methyltransferase	MTHB methylation to DMSHB	$E \leq 1 \times 10^{-30}$	Curson et al., 2018
MddA	Methanethiol S-methyltransferase	Catalyzes MeSH to DMS	$E < 1 \times 10^{-30}$	Carrión et al., 2015
DmoA	Dimethylsulfide monooxygenase	DMS assimilation to MeSH	$E \leq 1 \times 10^{-34}$	Boden et al., 2011
MTO	Methanethiol oxidase	MeSH oxidation to Formaldehyde	phylogenetic tree and re-blast	Lee et al., 2002 Eyice et al., 2018
DdhA	Dimethylsulfide dehydrogenase	DMS oxidation to DMSO	phylogenetic tree and re-blast	McDevitt et al., 2002
Tmm	Trimethylamine monooxygenase	DMS oxidation	phylogenetic tree and re-blast	Lidbury et al., 2016
DMSOR	Dimethyl sulfoxide reductase	DMSO reduction to DMS	$E \leq 1 \times 10^{-94}$	Satoh and Kurihara., 1987 Sambasivarao and Weiner., 1991 Mcewan et al., 1991

Note: 3HP, 3-hydroxypropionate; DMS, dimethyl sulfide; DMSP, dimethylsulfoniopropionate; MMPA, methylmercaptopropionate; MTHB, 4-methylthio-2-hydroxybutyrate; DMSHB, 4-dimethylsulfonio-2-hydroxybutyrate; SMM, S-methylmethionine. MeSH, methanethiol; MTA-CoA, methylthioacryloyl-CoA.

Supplementary Table 5. The numbers of gene homologues in metagenomes from different samples.

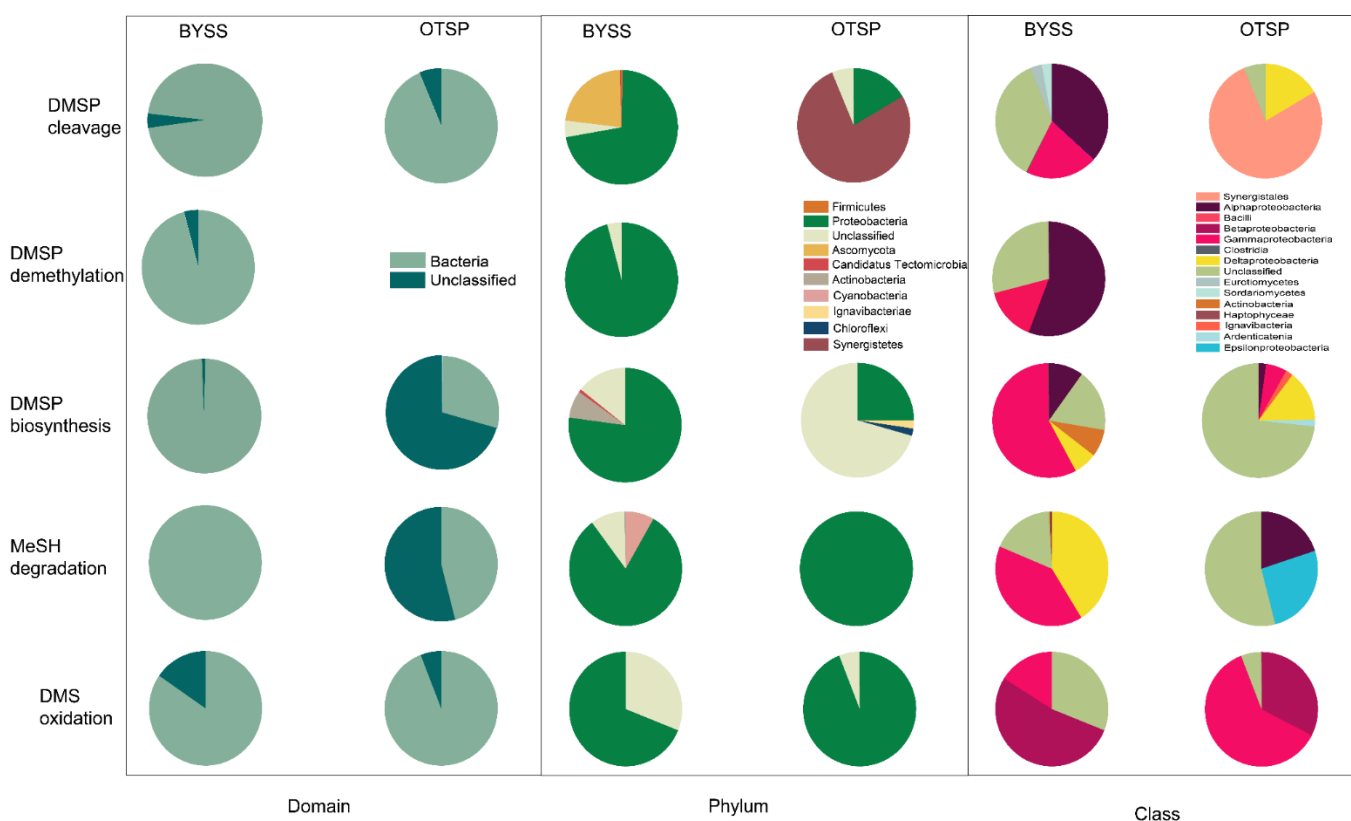
Station	<i>dsyB</i>	<i>mmtN</i>	<i>DSYB</i>	<i>AlmaI</i>	<i>dddD</i>	<i>dddK</i>	<i>dddL</i>	<i>dddP</i>	<i>dddQ</i>	<i>dmdA</i>	<i>dmdB</i>	<i>dmdC</i>	<i>dmdD</i>	<i>AcuH</i>	<i>mddA</i>	<i>dmoA</i>	<i>ddhA</i>	<i>mtaX</i>	<i>tmm</i>	<i>DMSOR</i>	<i>recA</i>	β - <i>Actin</i>
H12m	9	NT	NT	NT	43	NT	NT	712	94	212	796	841	43	375	211	33	10	NT	NT	44	1593	296
H12sw	24	NT	6	512	49	275	1	520	471	1562	955	1525	59	296	21	74	NT	9	4	149	3331	5537
H12bw	23	NT	1	NT	2	269	11	596	297	1798	2218	1616	133	384	12	169	67	29	26	320	4929	502
HS5m	34	NT	NT	NT	112	NT	13	827	99	172	1157	939	69	451	324	69	89	7	20	52	2180	402
HS5sw	16	NT	38	1149	35	80	NT	151	241	1703	1240	1649	72	343	6	42	NT	8	8	214	4042	6968
HS5bw	25	NT	10	175	9	282	7	643	360	2151	3026	2143	136	553	39	103	3	37	37	385	6214	2577
H25	22	NT	NT	NT	49	NT	85	611	54	139	1106	779	2	247	171	10	12	22	19	27	2084	1
B41	21	NT	NT	2	59	NT	36	527	78	128	801	589	0	258	194	8	29	13	19	31	1560	93
B45	37	NT	NT	2	81	NT	20	970	143	297	1137	898	0	382	256	14	24	5	52	52	2262	218
B47	16	NT	NT	NT	73	NT	43	637	31	89	553	429	0	317	116	5	6	45	14	28	1404	125
B50	34	NT	NT	NT	64	NT	47	816	120	239	1395	936	7	380	216	14	23	16	29	61	2574	1
T1	1	NT	NT	NT	NT	NT	NT	NT	NT	NT	34	75	0	39	21	NT	NT	5	NT	NT	293	NT
TVG11-2	8	NT	NT	NT	NT	NT	NT	NT	NT	NT	137	109	7	57	19	15	68	NT	NT	23	1547	NT
TVG5-3	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	225	248	7	148	44	36	85	NT	NT	3	1276	NT
TVGS11-2	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	63	5	6	18	1	5	1	NT	NT	NT	1723	NT
TVGS5-3	29	NT	NT	NT	NT	NT	NT	1	NT	NT	34	202	3	137	4	6	72	NT	NT	11	1508	NT

Note: m, sediment; sw, surface seawater; bw, bottom seawater; TVG, sediment; TVGS, polymetallic sulfide; NT, not detected.

Supplementary Figures

$$G_k = \frac{r_k}{L_k} \cdot \frac{1}{\sum_{i=1}^n \frac{r_i}{L_i}}$$

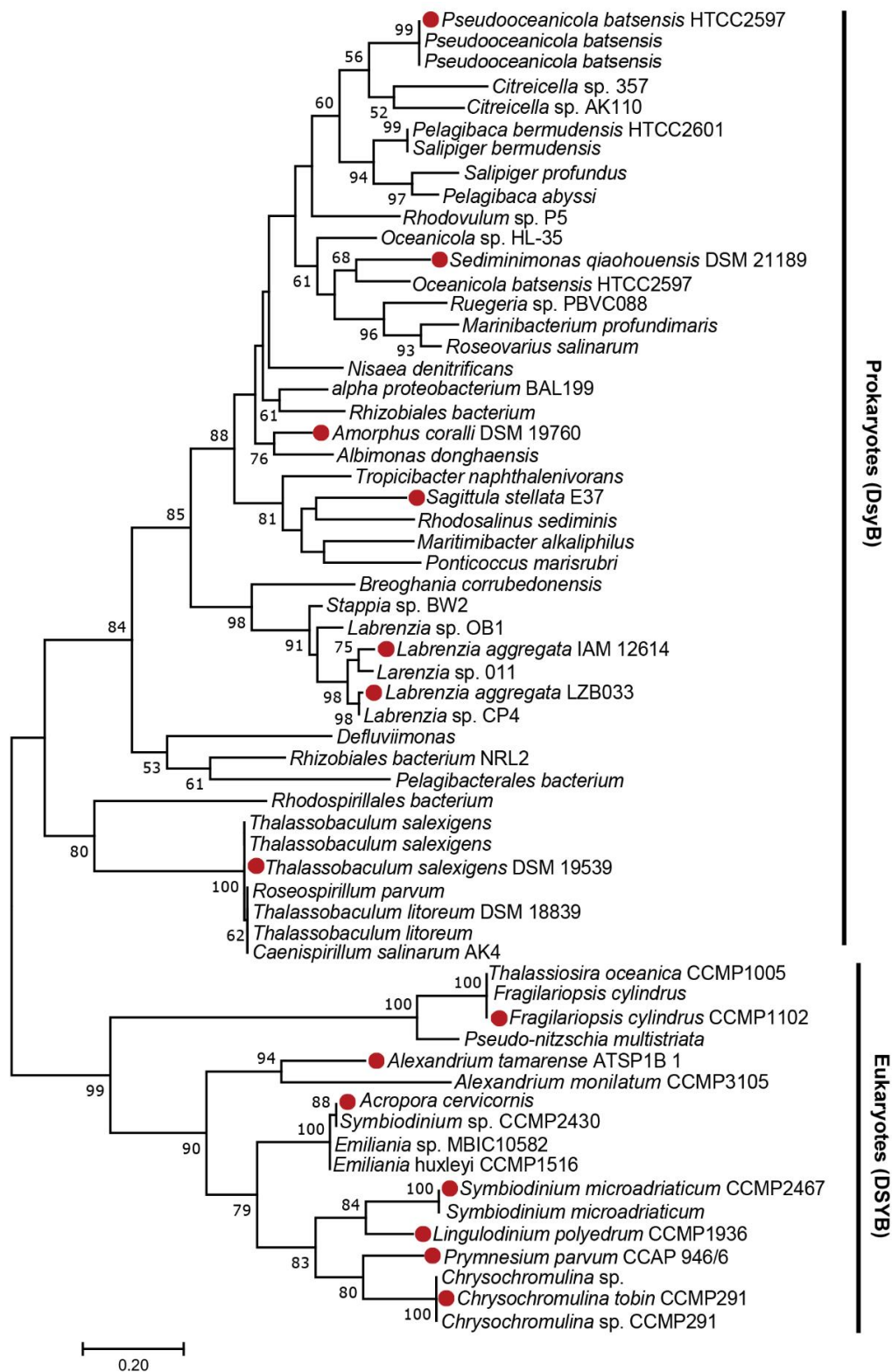
Supplementary Figure 1. Metagenomics non-redundant gene set (Unigenes/protein) abundance calculation method. G_k represents the relative abundance of the gene k in the sample, r_k is the number of times the gene k is detected in the sample, equal to the number of aligned reads, L_k is the length of gene k , the total number of r_i samples and the total length of L_i samples (Villar et al., 2015).



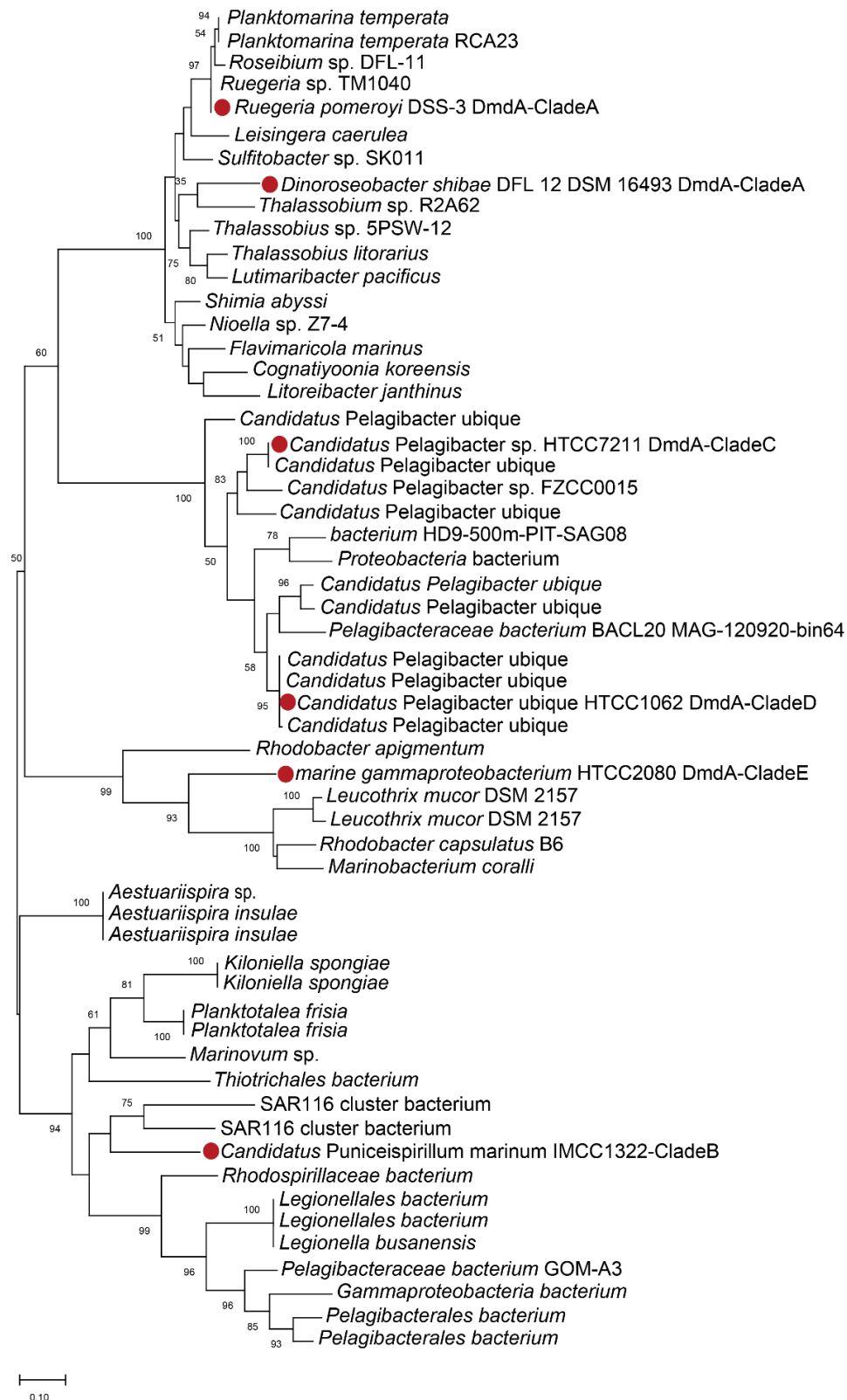
Supplementary Figure 2. The taxa implicated in the production and cycling of DMSP and related compounds at Domain, Phylum and Class taxonomic levels in metagenomics data from eathern Chinese marginal sea sediment samples. BYSS, sediment of the Yellow Sea and the Bohai Sea; OTSP, sediment and polymetallic sulfide of the Okinawa Trough.



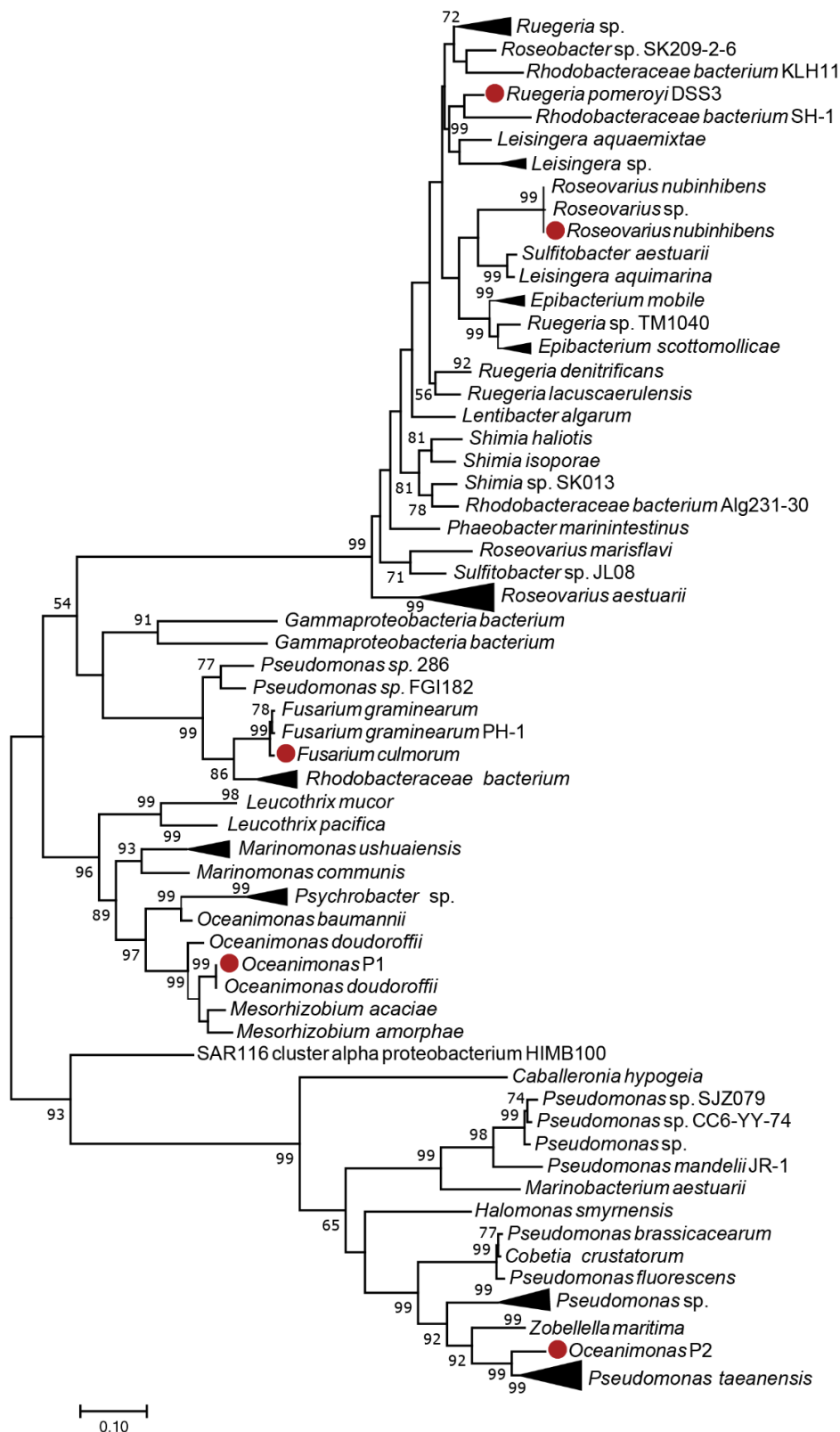
Supplementary Figure 3. The most abundant genera involved in the production and cycling of DMSP and related compounds in the Yellow Sea seawater samples (sites H12 and HS5). A: The most abundant genera possessing “*ddd*” genes; B: The most abundant genera possessing *dmdA*; C: The most abundant genera possessing *dsyB* with red, the most abundant genera of MeSH degradation with yellow and the most abundant genera of DMS oxidation with green; D: The most abundant genera possessing *Alma1* with blue, The most abundant genera possessing *DSYB* with red.



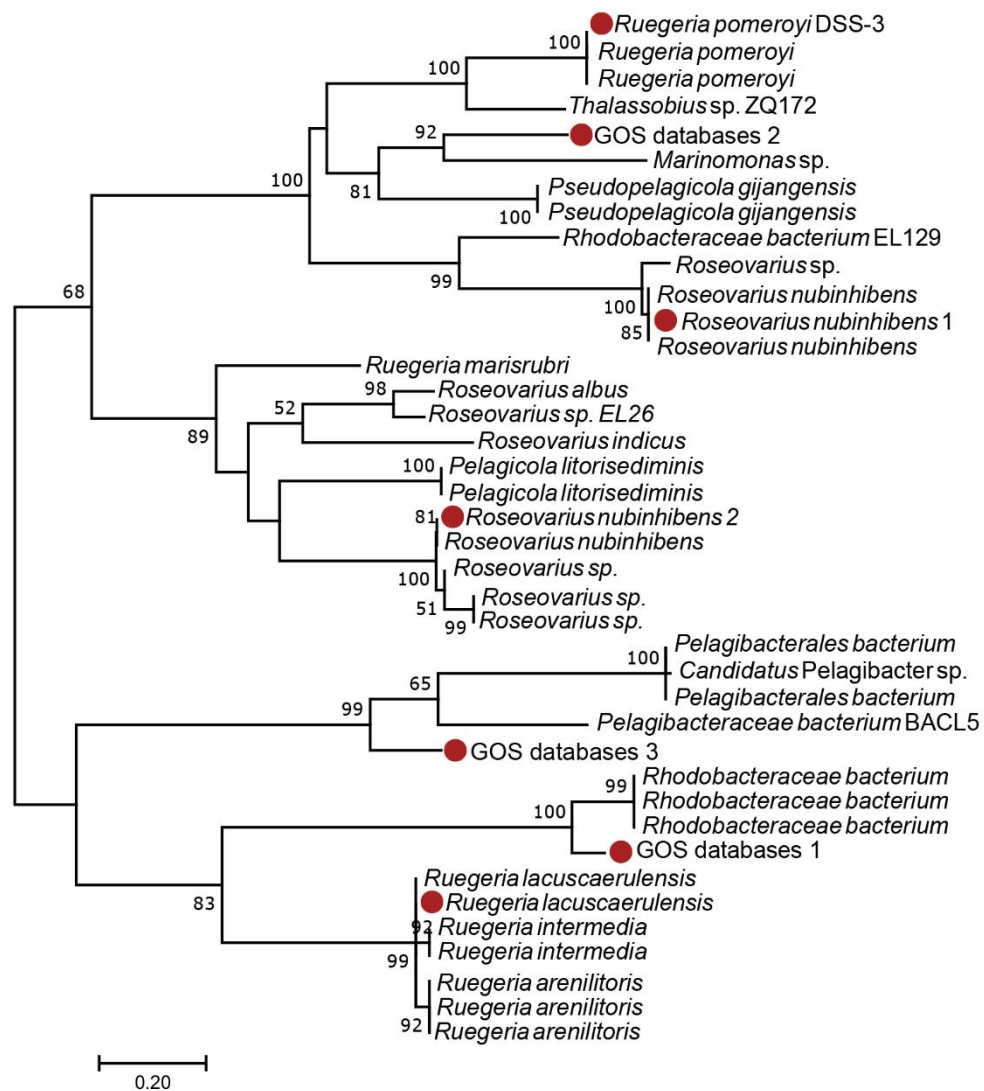
Supplementary Figure 4. Maximum likelihood phylogenetic tree of DsyB and DSYB proteins. Ratified proteins of DsyB and DSYB (Supplementary Material Table 3) available from NCBI alongside the newly retrieved sequences from metagenomes were used for phylogenetic tree reconstruction. The ratified proteins were marked with a red solid circle. Bootstrap support for nodes is marked.



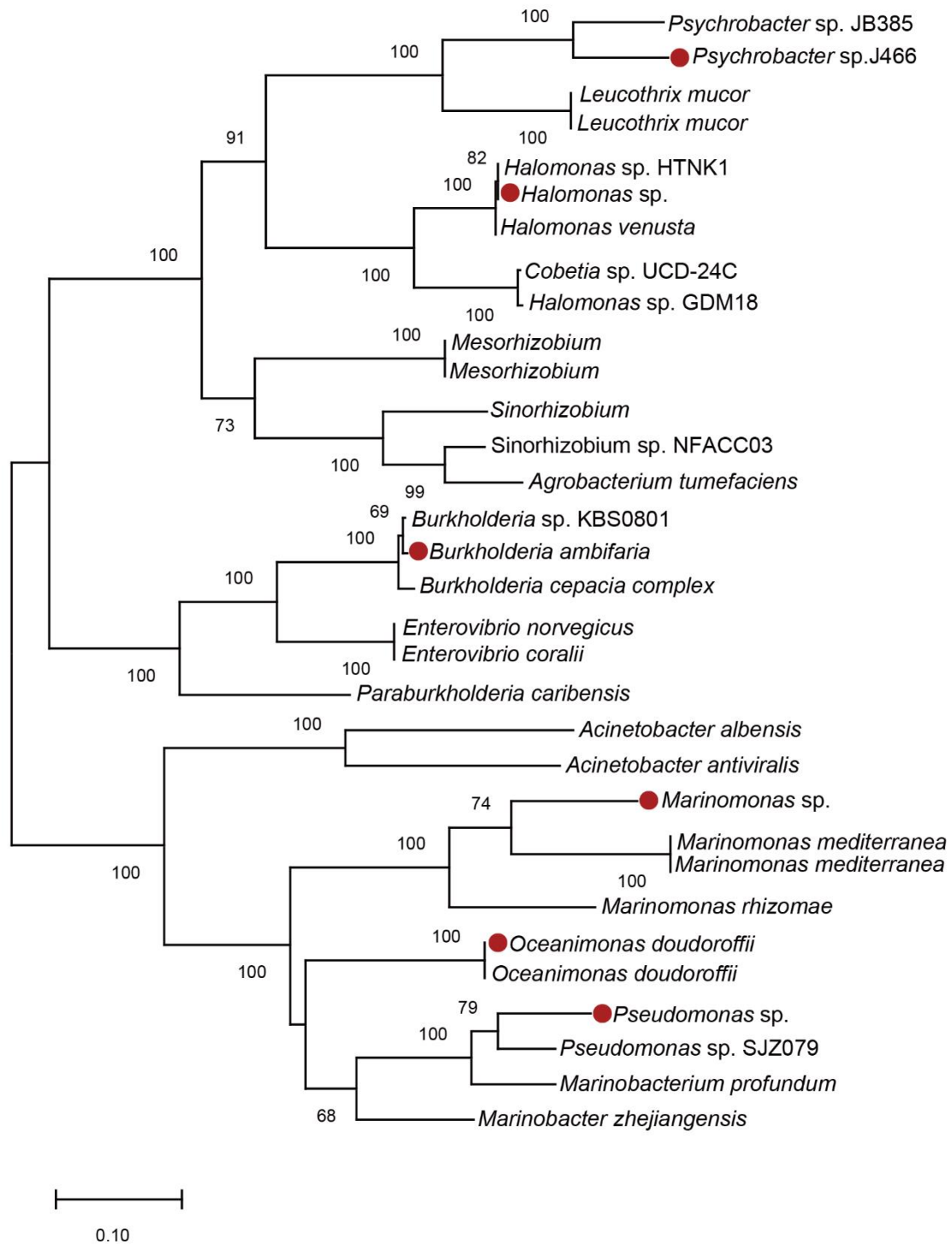
Supplementary Figure 5. Maximum likelihood phylogenetic tree of DmdA proteins. Ratified proteins of DmdA (Supplementary Material Table 3) available from NCBI alongside the newly retrieved sequences from metagenomes were used for phylogenetic tree reconstruction. The ratified proteins were marked with a red solid circle. Bootstrap support for nodes is marked.



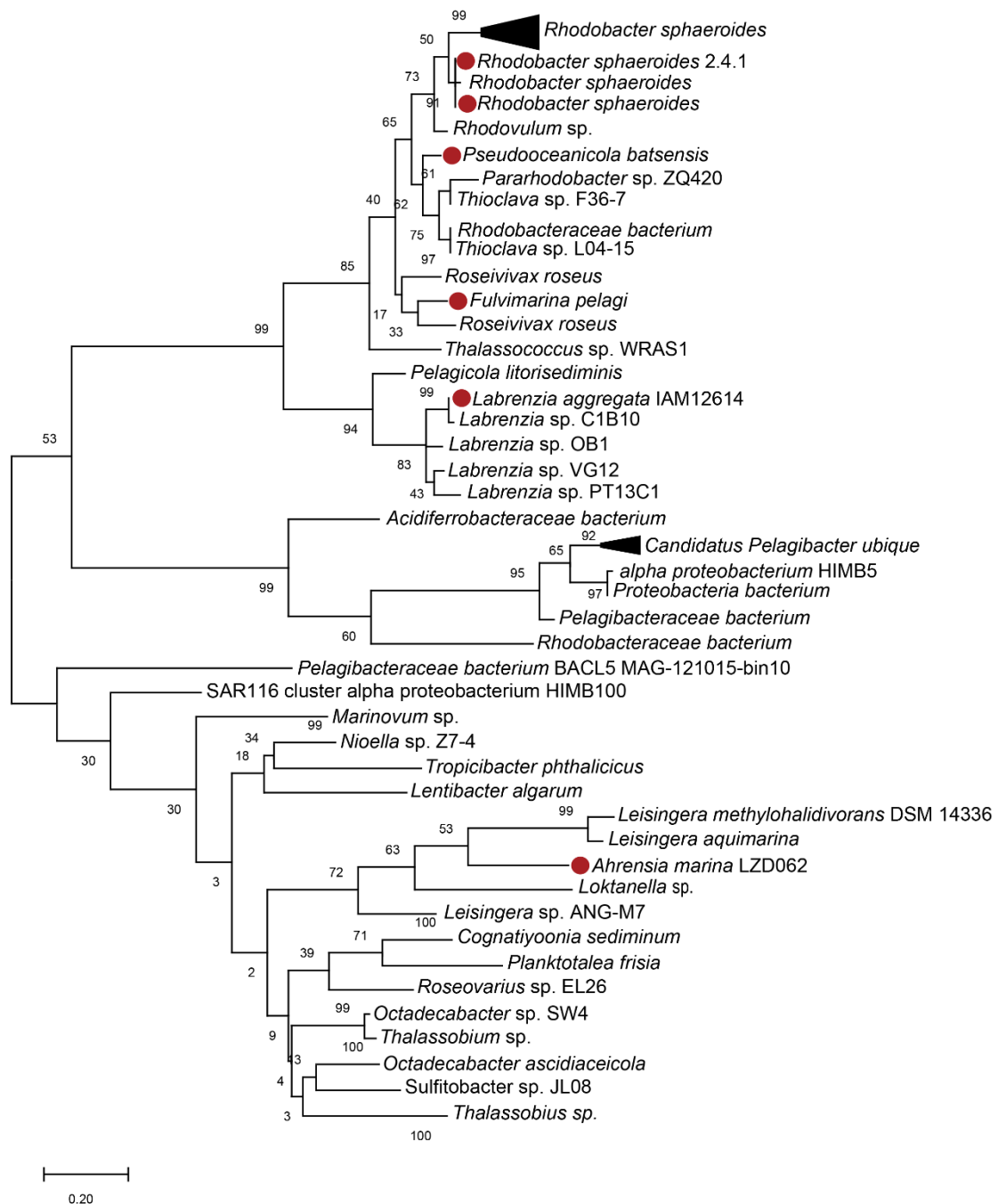
Supplementary Figure 6. Maximum likelihood phylogenetic tree of DddP proteins. Ratified proteins of DddP (Supplementary Material Table 3) available from NCBI alongside the newly retrieved sequences from metagenomes were used for phylogenetic tree reconstruction. The ratified proteins were marked with a red solid circle. Bootstrap support for nodes is marked.



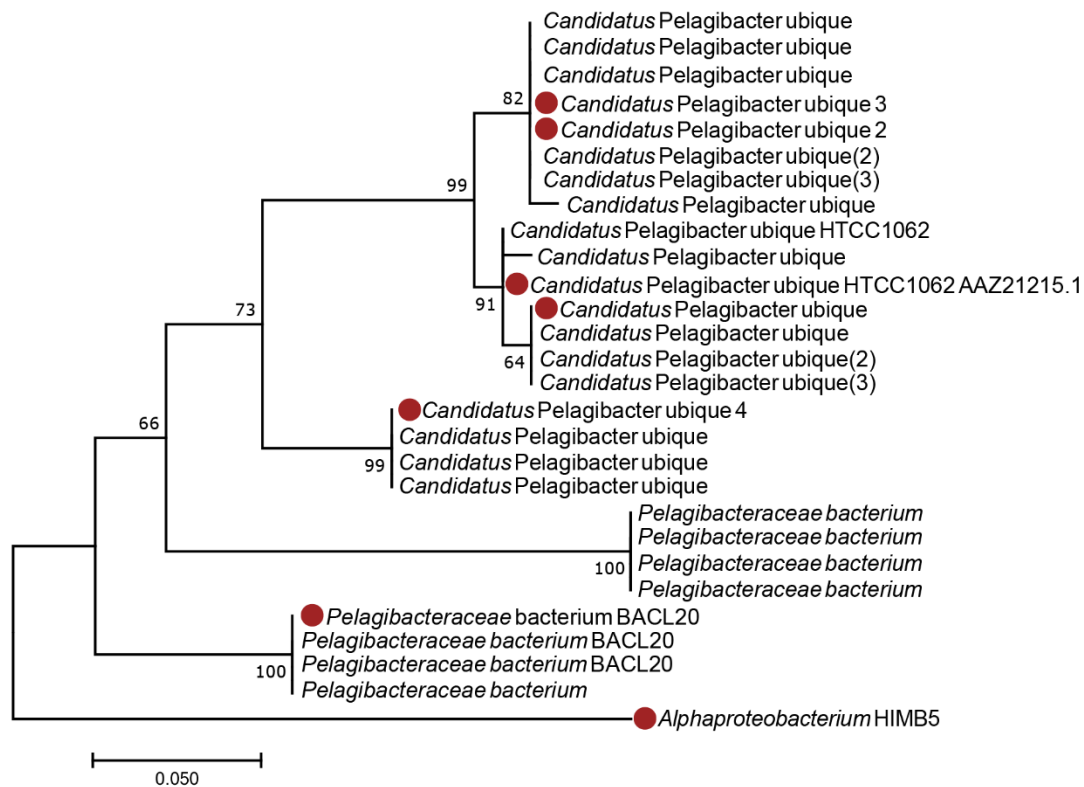
Supplementary Figure 7. Maximum likelihood phylogenetic tree of DddQ proteins. Ratified proteins of DddQ (Supplementary Material Table 3) available from NCBI alongside the newly retrieved sequences from metagenomes were used for phylogenetic tree reconstruction. The ratified proteins were marked with a red solid circle. Bootstrap support for nodes is marked.



Supplementary Figure 8. Maximum likelihood phylogenetic tree of DddD proteins. Ratified proteins of DddD (Supplementary Material Table 3) available from NCBI alongside the newly retrieved sequences from metagenomes were used for phylogenetic tree reconstruction. The ratified proteins were marked with a red solid circle. Bootstrap support for nodes is marked.



Supplementary Figure 9. Maximum likelihood phylogenetic tree of DddL proteins. Ratified proteins of DddL (Supplementary Material Table 3) available from NCBI alongside the newly retrieved sequences from metagenomes were used for phylogenetic tree reconstruction. The ratified proteins were marked with a red solid circle. Bootstrap support for nodes is marked.



Supplementary Figure 10. Maximum likelihood phylogenetic tree of DddK proteins. Ratified proteins of DddK (Supplementary Material Table 3) available from NCBI alongside the newly retrieved sequences from metagenomes were used for phylogenetic tree reconstruction. The ratified proteins were marked with a red solid circle. Bootstrap support for nodes is marked.

References for supplementary materials

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