

Supplementary Figures

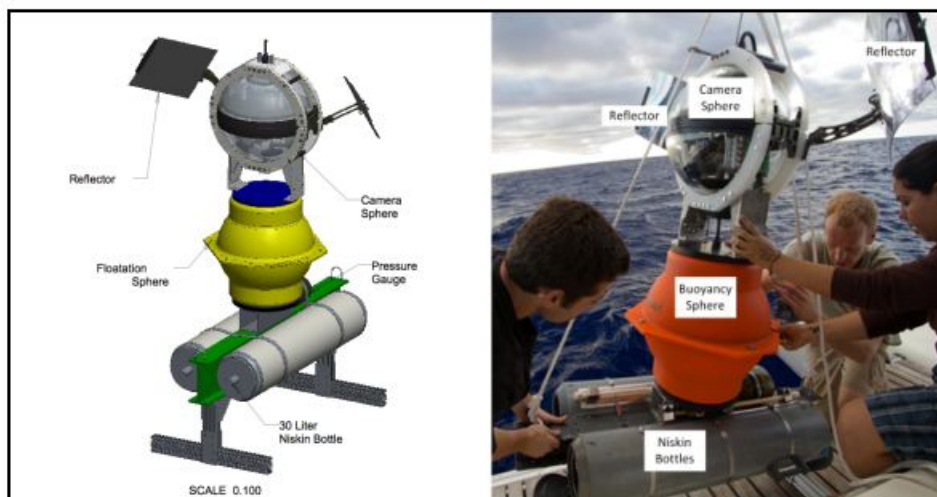


Figure S1. Free falling vehicle used to collect the ultra-deep seawater sample used in this study. The free falling vehicle (FFV) was designed and fabricated by National Geographic Remote Imaging. It contained a camera (HDR-XR520V, Sony, Tokyo, Japan), which captured high-definition video in 1080i format at 60 frames per second and recorded to an internal 240GB hard drive. Illumination was provided by two 3600 lumen LED arrays (BXRA-C4500, Bridgelux, Livermore, CA). A custom embedded computer commanded the camera and lighting based on pre-programmed timing. This system was encased in a polished 43 cm diameter, 2.5 cm thick borosilicate glass sphere with a depth rating of 12,000 m (Vitrovex, Nautilus Marine Service, GmbH, Buxtehude, Germany). A pair of external polycarbonate reflectors spread the illumination into the field of view of the camera. An external pressure gauge (DG25, Ashcroft, Stratford, CT) was used to measure the final depth that system achieved. To collect microbial samples the FFV was fitted with a pair of baited 30 l Niskin water sampling bottles and an additional 43 cm sphere to provide additional buoyancy. The FFV was weighted with a 22 kg external steel ballast attached via a timed-release burnwire. Dissolving magnesium links provided a redundant release (A2, Neptune Marine Products, Port Townsend, WA). The FFV had an onboard radio beacon transmitter (MK8, Telonics, Mesa, AZ), which facilitated recovery using locating antennae. A backup ST-21H-200L Telonics satellite transmitter

was used to determine position on the surface via the ARGOS satellite network. Video is available upon request.

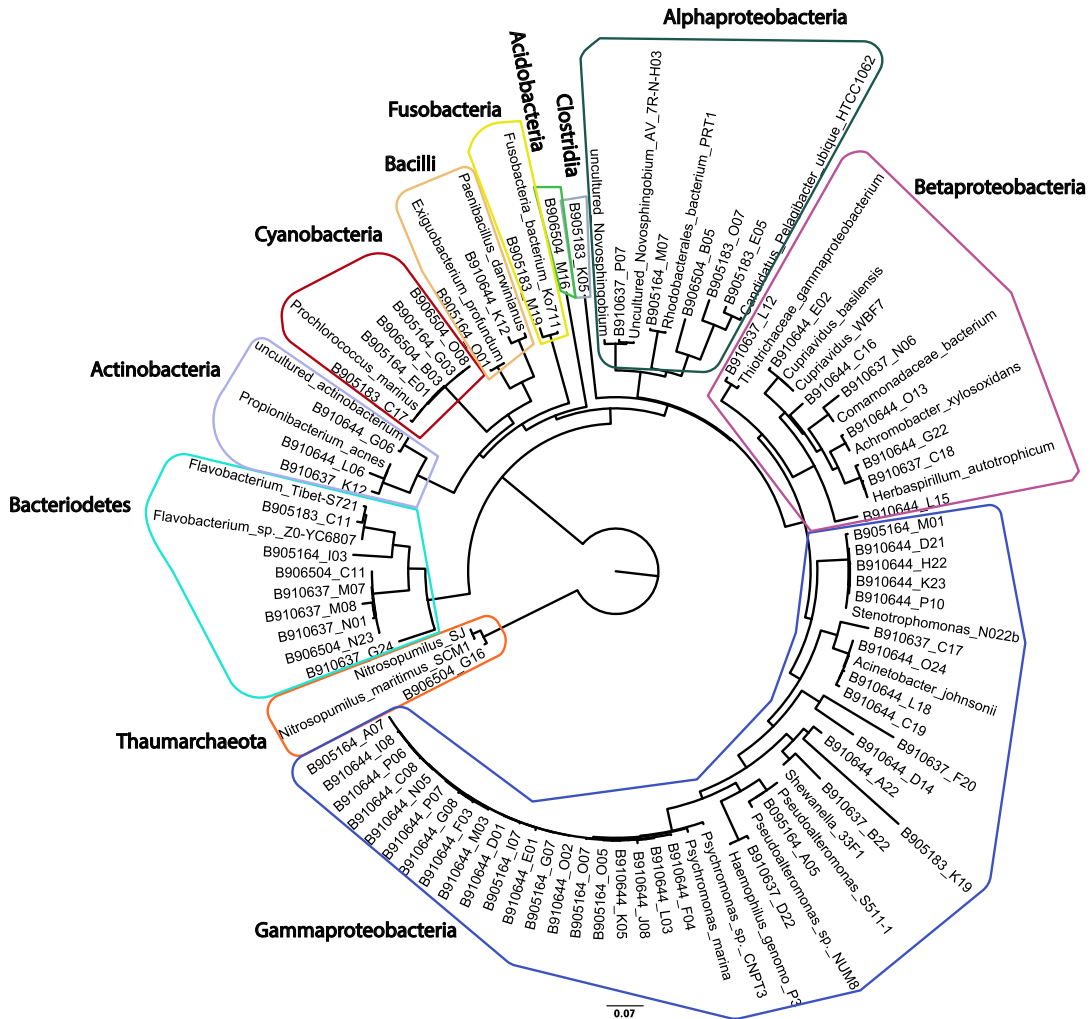


Figure S2. Phylogenetic tree of 16S rRNA gene sequences obtained from MDA amplifications. The maximum likelihood phylogenetic tree of 16S rRNA gene sequences obtained for 70 amplified SAG genomes are shown. Selected sequences are embedded within the amplified SAG for phylogenetic reference. The phylogenetic divisions of the relevant bacterial classes are highlighted.

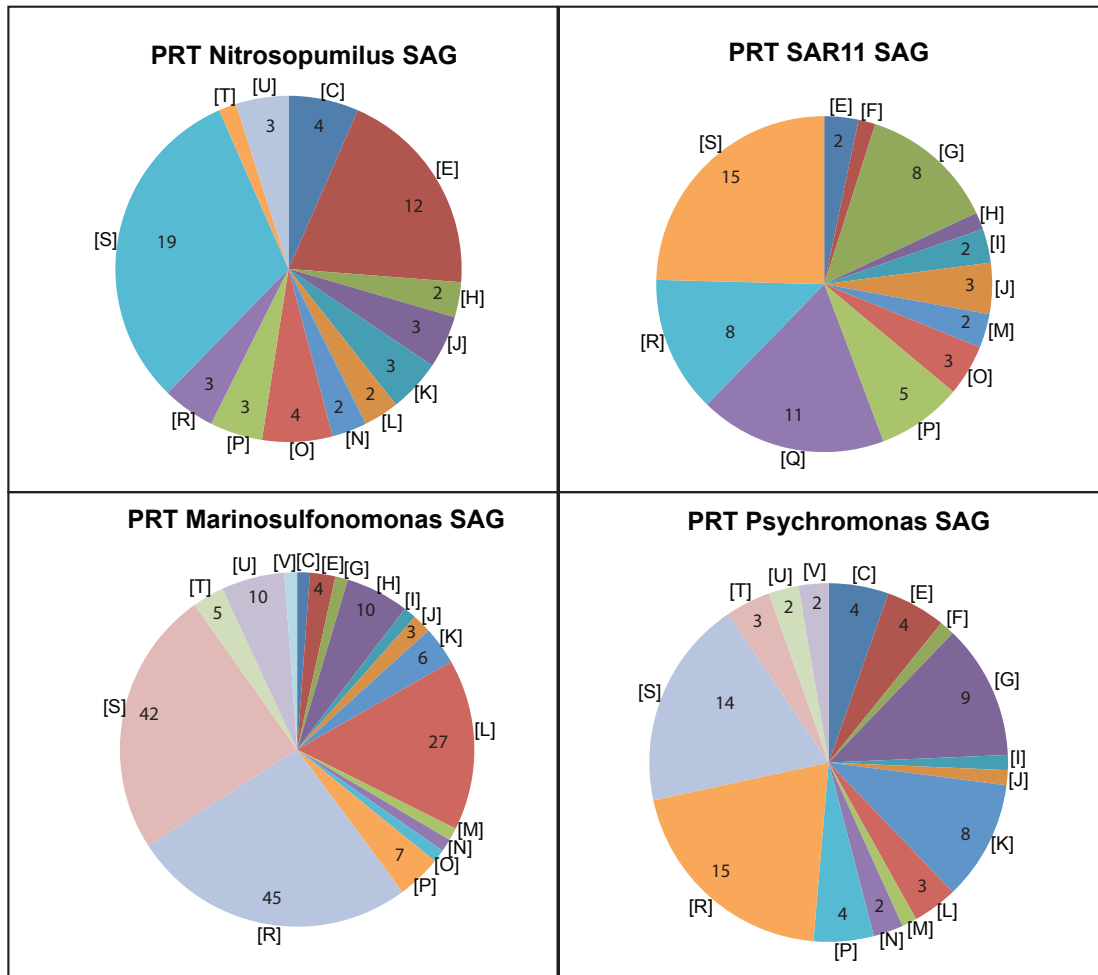


Figure S3. COG category distribution of unique genes when compared to SAGs most closely related genomes. The COG categories and their respective gene counts are displayed using pie charts for each SAG. Category legend: [E] Amino acid transport and metabolism, [G] Carbohydrate transport and metabolism, [D] Cell cycle control, cell division, chromosome partitioning, [N] Cell motility, [M] Cell wall/membrane/envelope biogenesis, [B] Chromatin structure and dynamics, dynamics, [H] Coenzyme transport and metabolism, [V] Defense mechanisms, [C] Energy production and conversion, [S] Function unknown, [R] General function prediction only, [P] Inorganic ion transport and metabolism, [U] Intracellular trafficking, secretion, and vesicular transport, [I] Lipid transport and metabolism, [F] Nucleotide transport and metabolism, [O] Posttranslational

modification, protein turnover, chaperones, [L] Replication, recombination and repair, [A] RNA processing and modification, [Q] Secondary metabolites biosynthesis, transport and catabolism, [T] Signal transduction mechanisms, [K] Transcription, [J] Translation, ribosomal structure and biogenesis.

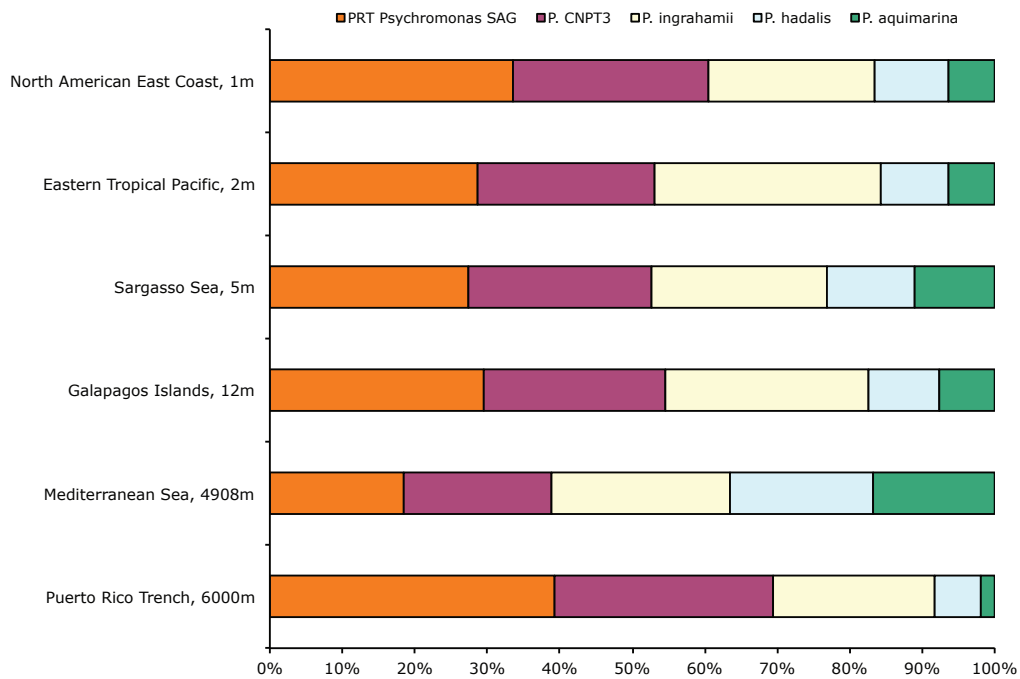
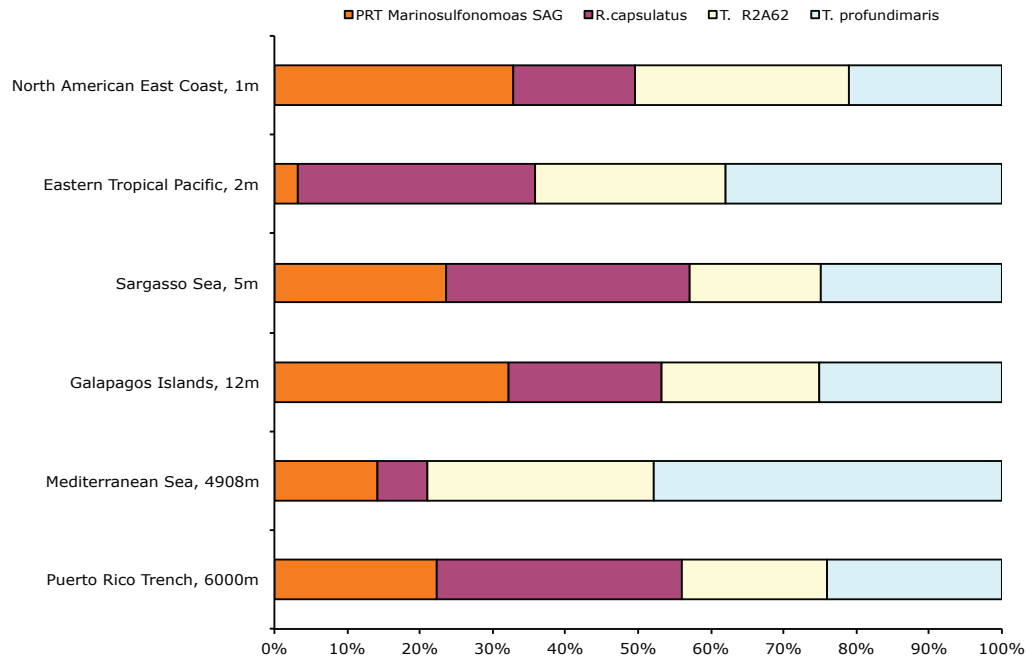


Figure S4. Reciprocal best blast for PRT *Marinosulfonomonas* SAG and PRT *Psychromonas* SAG. Relative abundance of PRT *Psychromonas* SAG and PRT *Marinosulfonomonas* SAG by reciprocal best blast analysis do not show a trend recruiting metagenome reads from deeper environments when compared to surface metagenomes. A) PRT *Psychromonas* SAG and related genomes: *P. CNPT3* - *Psychromonas sp. CNPT3*, *P. hadalis* - *Psychromonas hadalis* and *P. aquamarina* - *Psychromonas aquamarina*. B) PRT *Marinosulfonomonas* SAG and related genomes: *R. capsulatus* – *Rhodobacter capsulatus*, *T. R2A62* - *Thalassiosibium sp. R2A62*, *T. profundimaris* – *Thalassiosibium profundimaris*. RBB were normalized based on the genome size of the analyzed genome and total number of reads of the analyzed metagenome.

Supplementary Tables

Table S1. List of metagenomes used in read recruitment analyses. Full list of metagenomes is indicated and highlighted those use for comparisons shown in figure 2.

Geographic Location	NICKNAME	Depth
Galapagos Islands	IIGI	0.10
Galapagos Islands	PCGI	0.20
Indian Ocean	IOEZ	0.30
North American East Coast	GUME	1.00
North American East Coast	BBME	1.00
North American East Coast	BBNS	1.00
North American East Coast	BFNS	1.00
North American East Coast	NOME	1.00
North American East Coast	NHRI	1.00
North American East Coast	BNY	1.00
North American East Coast	CMNJ	1.00
North American East Coast	DBNJ	1.00
North American East Coast	CHSC	1.00
Polynesia Archipelagos	RAFP	1.00
Eastern Tropical Pacific	DRCR	1.10
Polynesia Archipelagos	TLFP	1.20
Polynesia Archipelagos	CBPa	1.40
Polynesia Archipelagos	CBFPb	1.40
Polynesia Archipelagos	MOFP	1.40
Indian Ocean	IOA	1.50
Indian Ocean	IOBa	1.50
Indian Ocean	IOBb	1.50
Indian Ocean	IOF	1.50
Indian Ocean	IOG	1.50
Indian Ocean	IOS	1.50
Indian Ocean	IOZ	1.50
Indian Ocean	IOWZ	1.50
Eastern Tropical Pacific	GUPA	1.60
Caribbean Sea	KWFL	1.70
Caribbean Sea	ROSA	1.70
Caribbean Sea	COPA	1.70
Galapagos Islands	WIGI	1.70
Tropical South Pacific	TSPE	1.70
Tropical South Pacific	FRPY	1.70
Eastern Tropical Pacific	EQPB	1.80
Tropical South Pacific	TSPA	1.80
Indian Ocean	CKLa	1.80
Indian Ocean	CKLb	1.80
Indian Ocean	IOC	1.80
Indian Ocean	IODa	1.80
Indian Ocean	IODb	1.80
Indian Ocean	IOE	1.80
Indian Ocean	IOSAa	1.80
Indian Ocean	IOSAb	1.80
Tropical South Pacific	TSPP	1.90
Tropical South Pacific	FRPX	1.90
Indian Ocean	IOYa	1.90
Indian Ocean	IOYb	1.90
North American East Coast	FXNS	2.00
Caribbean Sea	GMEX	2.00
Caribbean Sea	YUCA	2.00
Panama Canal	LGPA	2.00
Eastern Tropical Pacific	PCPA	2.00
Eastern Tropical Pacific	CICR	2.00
Galapagos Islands	NEGI	2.00
Galapagos Islands	FLGI	2.00
Tropical South Pacific	TSPB	2.00
Tropical South Pacific	TSPD	2.00
Tropical South Pacific	FRPZ	2.00
Indian Ocean	IORI	2.00
North American East Coast	CBVL	2.07
North American East Coast	NHNC	2.10
Galapagos Islands	SIGI	2.10
Galapagos Islands	SEGI	2.10
Galapagos Islands	CMGI	2.10
Galapagos Islands	DCGI	2.20
Tropical South Pacific	TSPP	2.20
Indian Ocean	IOX	2.20
Indian Ocean	IOM	2.80
Sargasso Sea	SARA	5.00
Sargasso Sea	SARA	5.00
Sargasso Sea	SARB	5.00
Sargasso Sea	SARB	5.00
Sargasso Sea	SARC	5.00
Sargasso Sea	SARD	5.00
Sargasso Sea	HYDA	5.00
Sargasso Sea	HYDB	5.00
Sargasso Sea	HYDC	5.00
Mediterranean Sea	ERR164407	5.00
Mediterranean Sea	ERR164409	5.00
Salish Sea	SRR944610	5.00
Salish Sea	SRR944614	5.00
Galapagos Islands	FIGI	12.00
North American East Coast	CBNJ	13.20
Galapagos Islands	RRGI	19.00
Tropical South Pacific	FRPW	30.00
Mediterranean Sea	SRR037008	50.00
Red Sea	SRR789380	50.00
Mediterranean Sea	ERR164408	56.00
Pacific Ocean, Chile Coast	SRR961671	70.00
Pacific Ocean, Chile Coast	SRR960580	70.00
Pacific Ocean, Chile Coast	SRR961675	110.00
Pacific Ocean, Chile Coast	SRR961673	110.00
Pacific Ocean, Chile Coast	SRR961677	200.00
Pacific Ocean, Chile Coast	SRR961676	200.00
Pacific Ocean, Chile Coast	SRR961679	1000.00
Pacific Ocean, Chile Coast	SRR961680	1000.00
Mid Atlantic Ridge	ERR133679	2320.00
Mid Atlantic Ridge	ERR133680	2320.00
Mid Atlantic Ridge	ERR133681	2320.00
Mediterranean Sea	DeepMed	3000.00
Hawaii Ocean Time Series	HOT	4000.00
Mediterranean Sea	SRR324677	4908.00
PRT		6000.00

Table S2. Unique genes for each SAG and their respective COG, KEGG, EC and Pfam classifications. See separate Table S2 file.