

Supplementary Information

Table S1. List of phylogenetic groups identified from clustering of rDNA and rRNA clone sequences obtained from each depth (25m, 500m, 3000m). Phylogenetic group or phylotype: A clone group with sequence similarity higher than 97%. D, 16S rDNA-derived sequences; R, 16S rRNA-derived sequences. Abbreviation used: OD1 (candidate division OD1); MGI (Marine Group I); MBG (Marine Benthic Group); MGII (Marine Group II); MHVG (Marine Hydrothermal Vent Group).

Phylum or class or family	25-D	25-R	500-D	500-R	3000-D	3000-R
<i>Gammaproteobacteria</i>	30	7	56	23	40	77
<i>Alphaproteobacteria</i>	33	5	16	13	19	14
<i>Deltaproteobacteria</i>	4	3	8	0	3	0
<i>Bacteroidetes</i>	2	3	0	0	0	0
<i>Planctomycetes</i>	0	0	0	5	6	3
<i>Verrucomicrobia</i>	7	3	11	7	2	0
SAR406	0	0	0	0	10	0
<i>Acidobacteria</i>	0	0	0	5	10	3
<i>Nitrospirae</i>	0	0	5	4	3	0
<i>Mycobacteriaceae</i>	0	0	0	2	0	0
<i>Chloroflexi</i>	0	0	5	12	2	3
OD1	0	0	0	0	2	0
<i>Cyanobacteria</i>	19	79	0	29	2	0
MGI	36	4	77	75	88	95
MBG	0	0	2	7	0	0
PSL12	0	0	11	19	6	3
MGII	64	96	10	0	6	3
MHVG	0	0	0	0	0	1



Figure S1. Phylogenetic affiliation of 16S rDNA (in bold) and rRNA (in red) clone sequences affiliated to Gammaproteobacteria obtained from the three water masses sampled (25 represented the MAW, whereas 500 and 3000 the LIW and TDW masses). Gen Bank accession numbers are in parentheses. Neighbour-joining analysis using 1000 bootstrap replicates was used to infer tree topology. Bootstrap values are indicated at branch points as open (50%–75%) and closed (>75%) circles. This is a part of the phylogenetic tree representing Eubacteria sequences obtained by ARB using Cenarchaeum symbiosium 1.1a as outgroup. The scale bar represents the expected numbers of changes per nucleotide position.

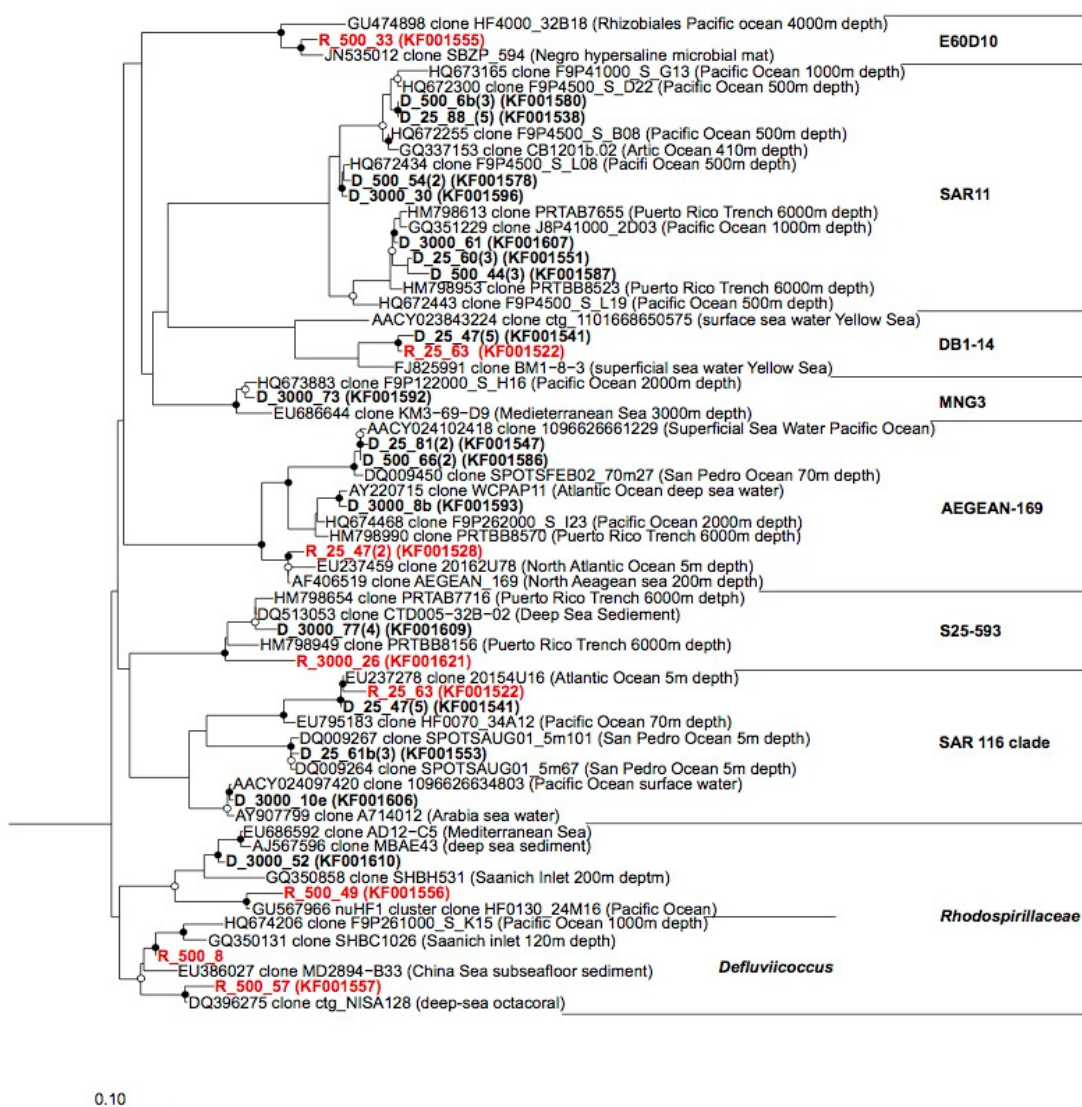


Figure S2. Phylogenetic affiliation of 16S rDNA (in bold) and rRNA (in red) clone sequences affiliated to Alphaproteobacteria obtained from the three water masses sampled (25 represented the MAW, whereas 500 and 3000 the LIW and TDW masses). Gen Bank accession numbers are in parentheses. Neighbour-joining analysis using 1000 bootstrap replicates was used to infer tree topology. Bootstrap values are indicated at branch points as open (50%–75%) and closed (>75%) circles. This is a part of the phylogenetic tree representing Eubacteria sequences obtained by ARB using *Cenarchaeum symbiosum* 1.1a as outgroup. The scale bar represents the expected numbers of changes per nucleotide position.

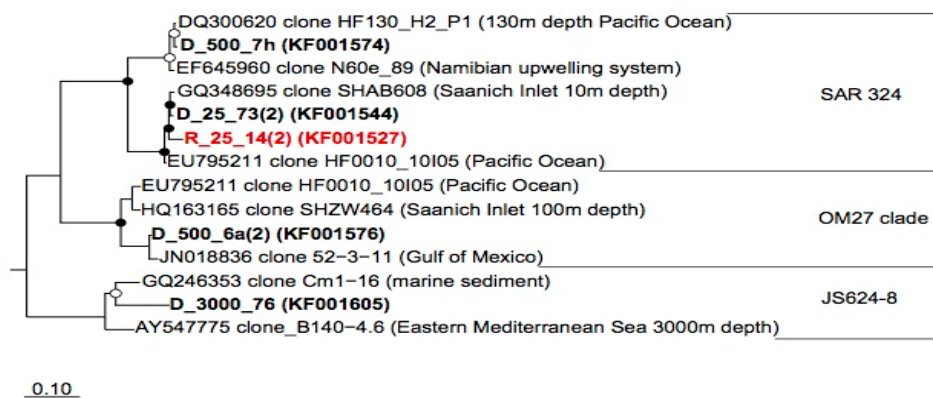


Figure S3. Phylogenetic affiliation of 16S rDNA (in bold) and rRNA (in red) clone sequences affiliated to Deltaproteobacteria obtained from the three water masses sampled (25 represented the MAW, whereas 500 and 3000 the LIW and TDW masses). Gen Bank accession numbers are in parentheses. Neighbour-joining analysis using 1000 bootstrap replicates was used to infer tree topology. Bootstrap values are indicated at branch points as open (50%–75%) and closed (>75%) circles. This is a part of the phylogenetic tree representing Eubacteria sequences obtained by ARB using *Cenarchaeum symbiosium* 1.1a as outgroup. The scale bar represents the expected numbers of changes per nucleotide position.

Table S2. Diversity indices calculated for the clone libraries from different depths in stations Vector; (D: 16S rDNA derived library; R: 16S rRNA derived library). Phylogenetic group or phylotype (Taxa): A clone group with sequence similarity higher than 97%.

Clone library	Taxa	Individuals	Dominance	Shannon (h)	Simpson (d)	Equitability (e)	Coverage (c)	Singletons	Dobletons	Chao1	Chao2
sup-D	50	89	0.036	3.616	0.964	0.934	0.663	32	8	114	105.1
sup-R	33	77	0.098	2.844	0.902	0.828	0.718	23	4	99.1	83.6
500-D	37	64	0.050	3.375	0.950	0.928	0.610	24	9	69	64.6
500-R	34	62	0.102	3.064	0.898	0.855	0.548	25	6	86.1	76.9
deep-D	33	56	0.124	2.855	0.876	0.831	0.536	27	2	215.3	150
deep-R	31	70	0.081	3.039	0.919	0.855	0.606	25	1	343.5	181
A-sup-D	19	36	0.091	2.674	0.909	0.908	0.667	12	4	307.0	32.2
A-sup-R	13	40	0.126	2.280	0.874	0.889	0.875	5	2	38.0	16.3
A-500-D	13	70	0.170	2.097	0.830	0.818	0.943	4	1	21.0	16.0
A-500-R	10	49	0.334	1.597	0.666	0.693	0.918	4	0	10.0	16.0
A-deep-D	5	45	0.794	0.497	0.206	0.309	0.933	3	1	9.5	6.5
A-deep-R	11	73	0.200	1.849	0.800	0.771	0.932	5	1	23.5	16.0



Figure S4. Phylogenetic affiliation of 16S rDNA (in bold) and rRNA (in red) clone sequences affiliated to the remaining Eubacteria group obtained from the three water masses sampled (25 represented the MAW, whereas 500 and 3000 the LIW and TDW masses). Gen Bank accession numbers are in parentheses. Neighbour-joining analysis using 1000 bootstrap replicates was used to infer tree topology. Bootstrap values are indicated at branch points as open (50%–75%) and closed (>75%) circles. This is a part of the phylogenetic tree representing Eubacteria sequences obtained by ARB using *Cenarchaeum symbiosum* 1.1a as outgroup. The scale bar represents the expected numbers of changes per nucleotide position.

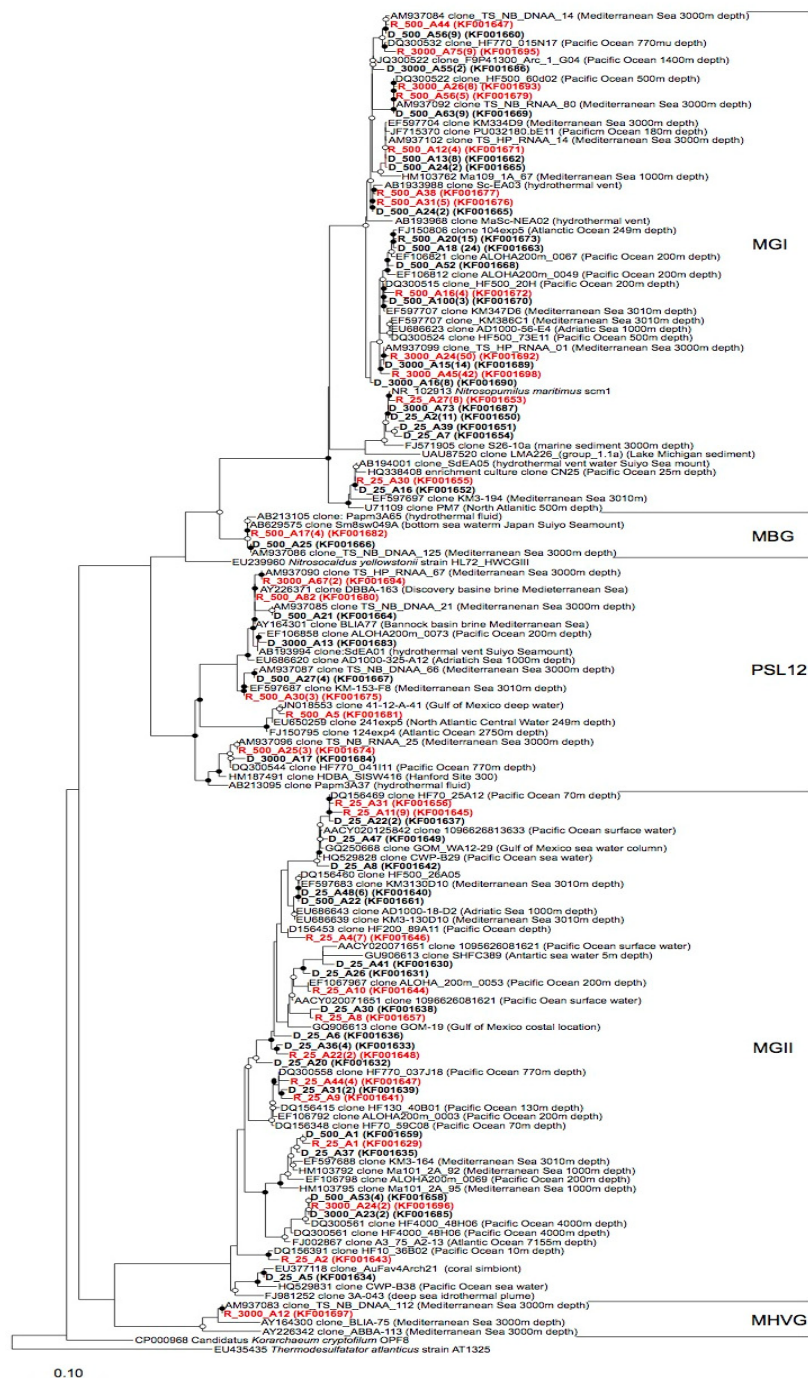


Figure S5. Phylogenetic affiliation of 16S rDNA (in bold) and rRNA (in red) clone sequences affiliated to Archaeal group obtained from the three water masses sampled (25 represented the MAW, whereas 500 and 3000 the LIW and TDW masses). Gen Bank accession numbers are in parentheses. Abbreviation used: MGI, Marine Group I; MBG, Marine Benthic Group; MGII, Marine Group II; MHVG, Marine Hydrothermal Vent Group. Neighbour-joining analysis using 1000 bootstrap replicates was used to infer tree topology. Bootstrap values are indicated at branch points as open (50%–75%) and closed (>75%) circles. This phylogenetic tree was obtained by ARB using *Thermodesulfator atlanticus* strain AT1325 as outgroup. The scale bar represents the expected numbers of changes per nucleotide position.