

Supplementary Information:

Article title: Taurine is a major carbon and energy source for marine prokaryotes in the North Atlantic Ocean off the Iberian Peninsula

Journal name: Microbial Ecology

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Table S1. Parameters to validate the HPLC method.

DFAA ^a	Linearity [nM]	R^2	LOD/LOQ [nM]	Recovery/RSD [$n = 5$, %]		
				1nM	5nM	10nM
ASP	0.02-100	0.999	0.02/0.06	90/6.3	104/1.6	101/0.5
GLU	0.01-100	0.999	0.01/0.04	100/8.2	104/4.1	100/0.1
ASN	0.01-100	0.999	0.01/0.04	98/0.7	105/3.6	95/0.5
SER	0.02-100	0.999	0.02/0.06	104/2.3	86.7/5.7	87/22
GLN	0.04-100	0.999	0.04/0.12	95/1.4	106/3.6	101/1.1
HIS	0.06-100	0.999	0.06/0.18	97/1.4	108/4.9	102/1.4
GLY	0.01-100	0.998	0.01/0.03	97/2.0	96/2.5	98.8/1.1
ARG	0.01-100	0.999	0.01/0.03	103/2.0	109/6.5	101/1.1
THR	0.06-100	0.999	0.06/0.20	96/3.7	108/7.2	100/1.0
ALA	0.01-100	0.999	0.01/0.05	102/0.9	100/2.9	100/5.4
TAU	0.01-100	0.998	0.01/0.05	99/0.5	100/0.2	101/2.9
GABA	0.01-100	0.999	0.01/0.05	95/3.6	89/3.6	100/0.1
TYR	0.04-100	0.999	0.04/0.12	97/5.7	80/3.6	100/0.32
VAL/MET	0.03-100	0.999	0.03/0.09	102/4.2	102/6.4	100/7.8
TRP	0.02-100	0.998	0.02/0.06	101/3.2	102/0.9	99/3.5
PHE	0.01-100	0.997	0.01/0.04	98/5.2	105/1.9	90/16.4
ILE	0.01-100	0.999	0.01/0.03	100/4.1	103/2.8	99/6.2
LEU	0.01-100	0.999	0.01/0.03	102/1.7	106/2.3	104/10.3
LYS	0.03-100	0.999	0.03/0.10	100/0.9	107/2.7	102/1.9

^a DFAA species abbreviations: R^2 , correlation coefficient; LOD, limit of detection; LOQ, limit of quantification; RSD, relative standard deviation; Asp, Aspartic acid; Glu, Glutamic acid; Asn, Asparagine; Ser, Serine; Gln, Glutamine; His, Histidine; Gly, Glycine; Arg, Arginine; Thr, Threonine; Ala, Alanine; Tau, Taurine; GABA, gamma aminobutyric acid; Tyr, Tyrosine; Met, Methionine; Val, Valine; Trp, Tryptophan; Phe, Phenylalanine; Ile, Isoleucine; Leu, Leucine; Lys, Lysine

Table S2. Probes and hybridization conditions used for MICRO-CARD-FISH analyses. Hyb. Temp: Hybridization temperature.

Probe name	Sequence (5' – 3')	Target group	Formamide [%]	Hyb. Temp. [°C]	Reference
NON338	ACTCCTACGGGAGGCAGC	negative control probe	55	35	Amann et al. (1995) [1]
EUB 338 I	GCTGCCTCCCGTAGGAGT	most Bacteria	55	35	Amann et al. (1990) [2]
EUB 338 II	GCAGCCACCCGTAGGTGT	Planctomycetales	55	35	Daims et al. (1999) [3]
		Verrucomicrobiales,			
EUB 338 III	GCTGCCACCCGTAGGTGT	Chloroflexi	55	35	Daims et al. (1999) [3]
SAR11-152R	ATTAGCACAAGTTTCCYCGTGT	SAR 11 cluster	45	35	Morris et al. (2002) [4]
SAR11-441R	TACAGTCATTTTCTTCCCGAC	SAR 11 cluster	45	35	Morris et al. (2002) [4]
SAR11-542R	TCCGAACTACGCTAGGTC	SAR 11 cluster	45	35	Morris et al. (2002) [4]
SAR11-732R	GTCAGTAATGATCCAGAAAGYTG	SAR 11 cluster	45	35	Morris et al. (2002) [4]
CREN 537	TGACCATTGAGGTGCTG	Thaumarchaeota	20	35	Teira et al. (2004) [5]
CREN 554	TTAGGCCCAATAATCMTCT	Thaumarchaeota	20	35	Woebken (2007) [6]
EURY 806	CACAGCGTTTACACCTAG	Euryarchaeota	20	35	Teira et al. (2004) [5]

Table S4a. Dissolved free amino acids (DFAA) throughout the water column at the stations occupied during the MODUPLAN cruise in the North Atlantic Ocean. The total DFAA and the percentages of dissolved taurine and leucine to the total DFAA [%] are also indicated. Concentrations between the detection and quantification limits are marked in grey. Abbreviations: Asp, Aspartic acid; Glu, Glutamic acid; Asn, Asparagine; Ser, Serine; Gln, Glutamine; His, Histine; Gly, Glycine; Arg, Arginine; Thr, Threonine; Ala, Alanine; Tau, Taurine; GABA, gamma aminobutyric acid; Tyr, Tyrosine; Met, Methionine; Val, Valine; Trp, Tryptophan; Phe, Phenylalanine; Ile, Isoleucine; Leu, Leucine; Lys, Lysine.

Station	Depth	ASP	GLU	ASN	SER	GLN	HIS	GLY	ARG	THR	ALA	TAU	GABA	TYR	VAL/MET	TRP	PHE	ILE	LEU	LYS	total DFAA	Tau/DFAA [%]	Leu/DFAA [%]
5	5	2.45	6.13	8.42	4.28	6.64	7.00	4.66	1.79	2.17	11.36	15.66	1.48	0.45	1.28	-	0.42	1.24	0.78	0.98	77.18	20.29	1.01
5	9	1.16	3.25	6.50	7.95	2.32	1.95	7.93	2.02	0.78	7.39	4.39	0.24	0.52	1.05	-	0.50	1.39	0.91	1.08	51.33	8.56	1.76
5	40	0.89	2.48	5.02	9.78	0.46	1.37	5.82	1.86	0.25	3.87	2.04	0.05	0.42	0.83	-	0.84	2.42	0.76	0.96	40.12	5.09	1.88
5	100	1.95	2.66	4.29	5.56	0.74	1.36	2.82	0.86	0.08	1.41	0.27	0.05	0.17	0.37	0.20	0.50	0.19	0.24	-	23.71	1.13	1.02
5	202	1.56	2.88	4.05	6.51	0.45	0.93	3.31	0.25	1.10	2.13	1.59	0.54	0.30	0.68	-	0.10	0.30	0.58	0.54	27.80	5.73	2.07
8	3	1.54	2.97	5.89	7.38	1.47	1.94	4.70	1.50	0.31	2.35	1.44	0.83	-	0.54	0.01	0.24	0.26	0.48	0.62	34.48	4.17	1.39
8	21	1.30	3.57	5.39	8.88	1.08	1.10	2.82	1.60	0.40	3.35	2.39	0.10	0.41	0.67	-	0.13	0.71	0.71	0.87	35.49	6.74	1.99
8	100	2.93	6.82	4.65	13.59	0.94	2.51	4.05	2.47	0.13	4.25	0.67	0.13	0.48	0.62	0.29	0.41	0.56	1.25	1.77	48.52	1.38	2.58
8	250	2.82	10.70	4.63	9.95	4.11	10.86	15.07	8.09	0.38	13.28	0.54	0.08	1.58	2.14	0.50	1.31	1.84	2.14	4.76	94.80	0.57	2.26
8	450	2.65	5.89	2.48	13.35	0.26	1.75	7.16	2.05	0.10	3.82	0.26	0.79	0.43	0.58	-	0.31	0.52	0.79	1.14	44.32	0.60	1.78
8	1050	1.70	4.10	2.48	11.17	0.65	1.95	5.82	1.61	0.05	3.19	0.08	0.73	-	0.46	0.18	0.32	0.39	1.21	2.71	38.82	0.22	3.12
8	1800	1.49	2.64	1.15	6.74	0.29	0.82	3.84	1.15	-	-	0.25	-	-	2.57	0.17	0.01	0.71	0.77	0.50	23.09	1.06	3.33
11	5	1.61	1.83	6.03	2.93	0.69	0.29	1.81	0.37	0.15	0.66	0.63	0.50	-	0.17	-	-	0.19	0.24	0.14	18.23	3.45	1.29
11	45	1.64	2.64	4.58	3.30	0.18	0.66	2.50	0.62	0.12	1.17	0.74	0.55	-	0.29	-	-	0.36	0.31	0.25	19.91	3.74	1.53
11	100	1.52	1.90	4.41	2.93	0.28	0.42	1.96	0.17	0.25	0.87	0.50	-	-	0.15	0.02	0.14	0.03	0.30	0.28	16.14	3.12	1.85
11	250	2.96	5.53	3.75	17.25	0.48	3.55	6.90	0.54	8.55	1.55	0.18	4.95	1.23	0.95	0.85	0.87	0.77	0.87	1.31	63.02	0.28	1.38
11	500	1.32	1.53	2.92	2.24	0.26	0.29	1.15	0.37	0.06	0.45	0.41	0.45	-	0.16	0.03	-	0.49	0.22	0.10	12.43	3.28	1.75
11	1150	1.00	2.22	2.12	6.99	0.22	0.86	4.17	0.63	0.26	1.89	0.28	-	-	0.66	-	0.06	0.24	0.70	1.08	23.39	1.21	2.99
11	1900	1.43	2.39	2.29	5.65	0.18	0.76	3.45	0.74	0.12	19.29	0.19	-	-	0.46	-	0.26	0.20	0.75	1.64	39.79	0.48	1.89
11	2750	1.89	3.68	1.73	7.37	0.20	0.95	4.41	0.93	0.11	2.01	0.12	-	0.23	0.58	-	0.10	0.55	0.53	0.72	26.13	0.44	2.05
14	5	1.21	2.67	4.98	5.35	0.64	0.44	4.35	1.41	0.59	2.57	2.56	0.08	0.28	0.92	-	0.13	0.20	0.54	0.53	29.44	8.70	1.82
14	50	1.22	3.38	4.14	10.92	0.88	2.03	5.05	0.74	1.93	5.43	0.80	0.03	0.41	1.12	0.44	0.27	0.37	0.65	0.74	40.55	1.97	1.60
14	101	0.97	1.60	3.91	5.92	0.67	0.88	3.39	1.24	0.04	1.60	0.31	-	-	0.95	0.50	0.61	1.48	0.43	0.46	24.95	1.23	1.71
14	250	1.51	0.85	3.16	1.81	0.27	0.25	0.37	0.44	0.41	0.59	0.32	0.03	0.02	0.03	-	-	0.31	0.20	0.13	10.70	2.95	1.82
14	500	0.91	1.16	2.36	2.63	0.52	0.76	1.38	0.51	0.11	0.67	0.56	-	0.05	0.24	-	1.61	1.35	0.25	0.25	15.32	3.65	1.62
14	1150	1.04	1.72	2.42	5.00	0.29	0.11	3.02	0.83	-	1.71	0.18	7.54	0.31	1.29	-	2.60	0.22	0.48	0.59	29.33	0.60	1.62
14	1950	1.29	2.79	2.08	9.40	0.92	0.40	4.89	2.09	0.21	3.05	0.21	0.96	-	0.80	0.14	0.15	0.50	0.83	1.10	31.82	0.67	2.60
14	2750	1.40	2.77	5.86	3.44	0.98	0.26	2.13	0.62	0.27	1.36	1.10	0.19	0.12	0.30	-	0.06	0.54	0.32	0.26	22.00	5.02	1.46

Station	Depth	ASP	GLU	ASN	SER	GLN	HIS	GLY	ARG	THR	ALA	TAU	GABA	TYR	VAL/MET	TRP	PHE	ILE	LEU	LYS	total DFAA	Tau/DFAA [%]	Leu/DFAA [%]
16	5	1.31	1.84	4.77	2.65	0.31	0.77	2.51	0.46	0.19	1.02	1.12	0.08	0.15	0.41	0.51	0.54	0.05	0.35	0.44	19.49	5.75	1.80
16	50	1.93	3.33	5.28	3.33	0.92	1.38	2.67	0.23	0.09	1.17	1.58	0.01	0.12	0.34	0.09	0.54	0.10	0.56	0.81	24.50	6.45	2.28
16	100	1.43	2.11	5.82	1.33	0.58	0.95	2.07	0.38	0.06	1.37	0.38	0.05	0.03	0.79	0.09	0.22	0.51	0.33	0.43	18.91	1.99	1.73
16	250	2.45	3.92	8.62	2.35	0.28	1.14	4.26	2.05	0.24	2.32	0.39	0.03	0.20	0.76	-	0.29	0.49	0.56	0.41	30.75	1.27	1.83
16	500	1.40	1.20	2.12	2.18	0.23	-	1.15	0.15	0.02	0.44	0.08	0.41	-	0.15	0.36	0.12	-	0.24	0.01	10.24	0.82	2.37
16	1100	1.39	1.17	2.84	1.65	0.18	0.29	1.08	0.15	0.01	0.50	0.40	0.08	-	0.27	-	-	0.36	0.29	0.22	10.89	3.71	2.64
16	1800	1.17	2.14	2.38	5.74	0.21	0.26	4.84	1.21	0.07	1.75	0.15	0.00	0.17	1.50	0.34	0.35	0.21	-	0.51	23.01	0.66	-
16	2300	1.25	2.11	5.67	5.41	0.99	1.31	3.34	1.01	0.44	2.04	1.39	0.20	0.30	0.47	-	0.23	0.92	0.48	0.50	28.05	4.95	1.72
16	3950	1.47	2.35	5.91	10.08	0.70	1.48	10.42	3.82	0.74	4.20	1.62	-	0.48	0.71	-	-	0.37	0.60	0.66	45.62	3.56	1.32
103	5	1.64	2.43	6.24	2.76	1.90	0.60	3.71	0.74	0.66	3.08	2.87	4.37	0.30	0.97	-	2.90	0.35	0.40	0.16	36.08	7.96	1.11
103	20	1.28	3.69	6.02	7.23	1.28	1.31	8.20	2.30	1.27	8.47	5.56	0.11	0.94	0.41	0.17	1.11	1.50	2.62	2.25	55.70	9.97	4.71
103	45	1.42	2.22	4.22	3.17	0.75	1.16	2.97	-	0.42	1.19	1.02	0.09	0.12	0.61	1.29	1.08	3.90	0.47	0.19	26.28	3.88	1.78
103	70	2.95	10.61	4.83	30.77	0.98	4.67	18.53	1.12	4.83	10.07	2.26	3.69	2.19	1.66	0.78	2.28	1.52	1.85	2.35	107.95	2.10	1.72
108	3	2.09	2.63	5.85	2.00	0.48	0.77	0.92	0.14	0.28	0.69	0.83	0.11	0.06	0.24	0.11	0.06	0.77	0.24	0.34	18.61	4.47	1.31
108	5	1.92	2.09	5.80	1.82	1.39	0.61	0.92	0.19	0.18	0.58	0.66	0.81	0.04	0.17	0.33	0.24	-	0.14	0.04	17.92	3.70	0.76
108	50	2.06	4.66	5.41	15.72	0.78	2.46	8.86	3.02	0.24	5.44	1.31	0.11	0.61	1.19	0.59	0.85	0.68	0.87	1.16	56.02	2.34	1.55
108	100	1.48	1.81	4.37	4.07	0.92	0.76	2.41	1.14	0.04	1.85	0.23	7.82	0.13	0.61	-	1.18	1.71	0.46	0.07	31.07	0.73	1.47
108	250	2.76	9.93	4.98	28.16	0.42	3.34	13.24	0.50	4.68	0.73	0.54	0.98	-	1.91	1.25	1.49	1.46	2.05	1.82	80.25	0.67	2.56
108	400	1.64	2.04	3.45	2.90	0.01	0.44	1.82	0.38	0.41	1.13	0.31	0.06	0.04	0.15	4.01	0.08	0.08	0.47	0.06	19.48	1.58	2.39
108	1000	1.21	2.09	2.36	1.98	0.18	0.40	1.54	0.32	0.04	0.58	0.35	0.03	-	0.35	-	-	0.22	0.26	0.04	11.95	2.91	2.19
108	1800	1.28	1.36	2.49	1.31	0.37	0.56	1.10	0.05	0.31	0.42	0.20	0.04	-	0.16	0.04	0.20	-	0.19	0.15	10.23	1.92	1.86
108	2750	1.27	1.43	2.20	2.04	0.45	0.74	1.39	0.08	0.24	0.53	-	0.04	0.01	0.27	-	-	0.25	0.35	0.25	11.54	-	2.99
108	4200	1.32	2.08	1.63	4.38	0.35	0.86	2.46	0.63	0.07	1.08	0.08	0.03	0.07	0.45	-	-	0.12	0.46	0.14	16.20	0.49	2.83
109	5	1.83	2.35	6.34	3.74	1.07	1.26	14.45	0.64	0.50	1.77	3.96	0.21	0.17	0.52	-	1.13	1.37	0.35	0.59	42.26	9.36	0.82
109	50	2.85	5.26	4.56	5.09	0.44	0.92	2.75	0.70	0.27	1.83	0.97	0.14	0.20	0.51	-	0.65	0.88	0.48	0.41	28.91	3.35	1.66
109	100	2.64	5.44	4.05	11.63	0.37	1.59	4.03	2.14	2.17	3.52	0.73	-	0.48	0.33	0.55	0.59	0.47	0.84	0.98	42.57	1.72	1.97
109	250	1.20	2.70	3.47	9.96	0.25	1.36	5.15	1.53	0.12	2.81	0.36	0.22	0.38	0.59	0.44	0.63	0.40	0.77	0.67	33.00	1.08	2.35
109	500	0.96	1.70	2.95	5.55	0.70	1.22	3.33	1.25	0.12	1.60	0.61	0.09	0.14	0.43	0.47	0.30	0.12	0.44	0.30	22.29	2.75	1.96
109	1000	0.76	0.74	2.05	1.75	0.19	0.28	0.23	0.22	0.33	0.44	0.25	0.03	-	-	0.18	0.13	-	0.21	0.53	8.32	3.06	2.55
109	1800	1.43	1.78	2.65	2.60	0.58	0.89	0.79	0.01	0.59	0.52	0.21	0.03	0.05	0.08	-	0.09	0.14	0.30	0.01	12.75	1.66	2.39
109	2750	1.81	1.40	3.27	2.15	0.60	0.45	1.00	0.26	0.03	0.64	1.23	0.01	-	-	0.18	0.13	-	-	0.53	13.70	9.01	-
109	5000	1.00	1.87	1.80	6.03	0.47	1.30	2.13	0.69	1.28	1.68	0.14	0.03	0.20	0.51	0.25	0.23	0.22	0.51	0.30	20.61	0.66	2.46
111	8	2.76	4.11	3.04	7.22	0.75	0.43	2.49	0.85	0.32	1.88	1.91	0.12	0.21	0.45	-	0.10	0.15	0.37	0.77	27.95	6.84	1.33
111	50	2.12	4.34	7.04	5.25	0.88	0.85	3.50	1.02	0.41	2.66	1.96	0.10	0.22	0.49	0.14	0.28	0.22	0.51	0.41	32.40	6.05	1.57
111	100	1.57	2.24	3.82	2.37	0.31	0.16	1.51	0.20	0.03	0.68	0.90	0.04	0.07	0.02	0.01	0.02	-	0.35	0.17	14.47	6.22	2.42
111	250	1.93	2.14	3.64	2.42	0.54	0.53	1.25	0.29	0.86	0.54	0.30	0.03	0.02	0.03	0.36	0.36	0.02	0.18	0.51	15.95	1.91	1.15
111	500	1.49	1.71	2.88	2.82	0.69	0.81	1.48	0.38	-	0.53	2.44	-	0.02	-	0.25	0.28	-	0.54	1.26	17.60	13.86	3.07
111	1000	1.29	1.58	2.14	2.88	0.64	0.86	1.33	0.67	-	0.67	0.31	-	0.04	0.52	0.33	0.65	0.00	0.34	0.02	14.28	2.19	2.38
111	1800	1.33	1.83	2.24	2.75	0.60	0.77	1.24	0.37	-	0.59	0.22	-	0.03	0.16	-	-	-	0.35	0.04	12.51	1.76	2.76
111	2750	2.51	4.19	1.74	8.83	0.17	0.96	5.00	1.73	0.03	2.33	0.21	0.03	0.53	0.47	0.08	0.43	0.42	0.76	0.60	31.04	0.69	2.45
111	4000	2.28	4.88	1.42	11.92	0.17	1.31	6.23	0.52	0.96	3.21	0.22	0.01	0.69	0.77	0.18	0.56	0.61	1.08	0.87	37.91	0.59	2.84
111	4830	1.07	1.74	1.54	5.39	0.42	1.01	2.84	0.75	0.02	1.46	0.17	0.02	0.23	0.48	0.27	0.49	0.25	0.56	1.24	19.95	0.86	2.83

Station	Depth	ASP	GLU	ASN	SER	GLN	HIS	GLY	ARG	THR	ALA	TAU	GABA	TYR	VAL/MET	TRP	PHE	ILE	LEU	LYS	total DFAA	Tau/DFAA [%]	Leu/DFAA [%]
56	6	1.55	2.50	7.87	5.10	0.81	0.80	4.20	1.26	0.97	1.91	2.10	0.14	0.30	0.72	0.04	0.22	0.21	0.53	0.60	31.82	6.60	1.66
56	60	1.76	4.11	4.21	5.59	2.19	3.28	3.95	0.59	0.76	3.20	9.38	0.20	0.36	0.45	0.12	0.16	0.17	0.47	0.58	41.52	22.59	1.14
56	90	1.22	1.89	5.36	2.90	0.19	0.58	1.38	0.37	10.34	0.83	0.81	0.06	0.08	-	-	0.01	2.20	0.27	0.13	28.61	2.82	0.93
56	100	1.58	2.75	4.44	4.10	0.93	1.14	0.53	1.49	0.74	1.08	0.36	0.06	0.04	0.09	-	0.16	-	0.28	0.15	19.89	1.79	1.39
56	250	1.32	2.06	3.57	2.94	0.51	-	1.66	0.41	0.03	0.92	0.42	0.03	0.06	0.18	-	0.36	0.04	0.21	0.13	14.84	2.80	1.42
56	500	1.53	2.78	2.12	5.11	0.63	1.12	2.10	0.24	0.89	1.34	0.45	0.04	0.17	0.12	-	0.11	0.08	0.35	0.26	19.42	2.33	1.80
56	1000	0.91	0.86	2.42	1.55	0.10	0.31	0.26	0.41	0.36	0.42	0.43	0.05	0.02	-	-	-	-	0.39	0.01	8.50	5.08	4.59
56	2070	0.82	1.00	1.92	3.61	0.48	0.87	2.57	0.52	0.25	1.03	0.40	-	0.40	0.08	-	-	0.06	0.35	0.20	14.57	2.77	2.40
56	2750	0.94	1.57	1.41	4.13	0.34	0.68	2.21	0.48	0.25	0.94	0.26	0.06	0.17	0.24	0.25	0.43	0.07	0.43	0.18	15.07	1.75	2.87
57	6	1.39	1.26	6.40	1.61	1.43	0.66	0.07	-	1.29	0.59	4.23	0.07	-	0.08	0.31	0.24	-	0.12	0.14	19.89	21.24	0.61
57	50	2.19	3.04	5.56	1.63	0.08	0.75	0.71	0.22	0.38	0.87	1.50	-	-	0.14	-	-	0.64	0.19	0.24	18.14	8.29	1.07
57	100	1.22	1.69	3.95	2.47	0.52	0.76	0.94	0.36	0.07	0.69	0.92	-	-	0.43	0.22	0.15	-	0.19	0.16	14.74	6.26	1.31
57	250	0.89	0.80	2.81	1.66	0.63	0.46	0.28	0.03	0.01	0.27	0.64	0.03	-	0.23	0.14	0.13	-	0.18	0.07	9.26	6.93	1.92
57	500	0.89	0.80	2.40	0.70	0.29	0.21	0.20	-	-	0.21	0.63	-	-	0.26	-	-	-	0.12	0.19	6.88	9.09	1.68
57	1000	0.68	0.63	0.68	0.28	0.32	0.19	-	-	-	-	0.27	-	-	0.02	-	-	-	0.13	-	3.19	8.40	4.02
57	1900	0.95	0.73	1.02	-	-	-	-	-	-	-	0.28	0.03	-	-	-	-	-	0.03	-	3.04	9.24	0.93
57	2750	0.90	1.22	1.24	3.71	-	0.55	1.87	0.56	0.11	1.19	0.42	-	-	1.41	0.23	0.09	-	0.41	0.18	14.07	2.95	2.90
57	3150	0.97	0.78	1.42	1.07	0.17	0.25	0.13	0.03	-	0.12	0.28	0.03	-	0.03	-	0.03	0.21	0.19	0.19	5.90	4.69	3.23
58	5	1.73	1.67	7.36	-	-	-	0.04	-	0.46	0.61	1.10	-	-	0.05	0.05	-	0.17	0.36	-	13.61	8.06	2.63
58	60	1.38	1.63	5.56	1.04	-	0.95	0.39	-	0.27	0.55	1.19	0.03	-	0.13	-	0.53	-	0.14	-	13.78	8.66	1.01
58	100	1.20	6.26	3.68	20.13	-	-	10.55	3.97	-	5.49	1.57	-	-	1.26	1.08	1.74	1.18	1.88	2.23	62.23	2.52	3.03
58	250	0.94	0.49	3.72	0.56	-	-	-	-	-	-	0.80	0.04	-	0.09	-	0.82	-	-	-	7.46	10.69	-
58	500	0.78	1.51	2.67	6.20	-	1.61	3.03	2.01	0.48	2.00	0.61	0.03	-	0.49	-	0.14	0.08	0.54	0.43	22.62	2.69	2.38
58	1000	0.68	0.39	1.86	0.50	-	0.31	-	-	0.00	0.01	0.59	-	-	-	-	-	0.10	0.13	-	4.57	12.86	2.79
58	1800	1.18	1.41	1.70	1.06	-	0.46	0.49	-	0.14	0.24	0.39	-	-	0.02	-	-	-	0.17	0.11	7.38	5.29	2.37
59	5	1.46	1.49	8.03	1.39	2.04	0.49	1.12	0.51	1.17	2.08	3.36	-	-	0.10	-	-	-	0.15	0.15	23.53	14.26	0.63
59	70	2.60	2.26	5.79	7.60	0.47	1.79	4.46	1.49	0.34	2.78	1.89	-	-	0.38	0.26	0.23	0.19	0.38	1.17	34.07	5.55	1.11
59	100	0.92	0.72	4.34	0.58	0.73	0.73	0.17	-	0.11	0.22	1.16	-	-	-	0.87	-	-	0.13	-	10.67	10.86	1.23
59	250	0.74	0.51	3.09	-	-	0.34	-	-	0.29	-	0.39	-	-	-	-	0.02	-	0.10	-	5.47	7.13	1.77
59	500	0.89	0.91	4.41	-	-	0.72	0.27	-	0.24	0.12	0.36	-	-	0.23	0.11	0.05	-	0.14	-	8.45	4.21	1.66
59	100	1.05	0.95	3.88	0.04	-	0.59	0.65	0.21	-	0.65	0.23	-	-	0.32	-	0.61	-	0.20	0.18	9.56	2.41	2.07
59	1900	0.98	1.15	3.12	1.59	0.40	0.67	0.85	0.22	0.01	0.67	0.20	0.04	-	0.11	0.12	0.08	-	0.30	0.25	10.75	1.83	2.78
59	2700	0.94	0.86	1.12	1.33	0.15	0.41	0.47	0.17	0.04	0.37	0.35	-	-	0.16	0.09	0.03	-	0.20	0.06	6.74	5.23	2.94

Station	Depth	ASP	GLU	ASN	SER	GLN	HIS	GLY	ARG	THR	ALA	TAU	GABA	TYR	VAL/MET	TRP	PHE	ILE	LEU	LYS	total DFAA	Tau/DFAA [%]	Leu/DFAA [%]
60	5	1.90	2.52	7.83	3.18	1.36	0.75	3.20	0.73	0.43	1.39	2.91	-	0.10	0.44	0.38	0.42	0.23	0.47	0.53	28.77	10.12	1.63
60	60	1.22	1.50	5.71	2.65	0.76	0.75	0.85	0.29	0.14	0.91	0.86	-	-	0.17	-	0.38	0.06	0.23	0.26	16.73	5.15	1.36
60	100	1.11	1.38	9.19	0.44	0.82	1.36	2.21	0.85	0.37	1.45	0.95	0.12	-	0.18	-	0.28	0.04	0.31	0.20	21.26	4.48	1.47
60	250	0.86	1.82	8.69	-	-	0.81	2.38	0.24	0.31	1.53	0.79	0.05	-	0.18	-	0.78	0.07	0.28	0.37	19.16	4.14	1.49
60	500	0.87	0.86	2.70	0.59	-	0.49	-	0.84	0.18	-	-	0.03	-	0.28	0.30	0.10	-	0.17	-	7.42	-	2.31
60	1000	1.40	1.99	2.55	2.42	0.63	0.77	0.77	0.03	0.30	0.64	1.08	-	-	4.66	-	0.94	0.14	0.28	0.17	18.77	5.75	1.50
60	1900	0.83	0.93	3.49	1.06	0.48	0.68	0.78	0.38	0.41	0.60	0.18	0.01	-	1.07	0.39	-	0.37	0.32	0.32	12.32	1.50	2.59
60	2450	1.37	2.35	4.37	1.85	0.43	0.88	1.84	0.89	0.09	1.22	0.19	0.03	-	0.21	-	-	0.08	0.38	0.58	16.77	1.12	2.26
62	5	1.54	1.93	8.68	1.70	2.67	1.28	8.63	0.43	1.08	2.11	4.94	0.09	-	0.15	0.16	0.09	0.06	0.14	0.68	36.37	13.57	0.39
62	30	1.41	2.36	6.66	1.28	1.91	0.31	2.72	0.11	0.48	0.52	5.88	-	-	0.18	-	-	0.24	0.19	0.33	24.60	23.92	0.75
62	50	1.18	1.53	5.08	0.83	1.51	0.55	1.29	-	0.33	0.84	3.70	0.03	-	0.06	0.02	0.04	-	0.14	-	17.13	21.63	0.80
62	75	1.56	1.55	4.06	0.65	0.07	0.28	0.30	-	0.01	0.32	0.76	-	-	0.06	-	0.10	-	0.13	-	9.84	7.68	1.32
62	220	0.79	0.55	3.60	0.55	0.63	0.58	0.06	-	0.06	0.14	1.87	-	-	-	-	0.12	-	0.17	-	9.13	20.52	1.84
64	5	1.67	4.06	8.12	3.23	1.50	1.80	9.34	0.59	0.70	1.97	5.55	-	0.02	0.47	0.49	0.91	0.08	0.48	0.51	41.51	13.38	1.15
64	10	1.30	3.76	14.83	0.51	0.84	2.02	14.41	1.62	1.09	4.87	6.88	0.12	0.10	0.59	0.17	0.44	0.18	0.52	0.73	54.98	12.51	0.95
64	20	1.79	1.56	4.69	2.18	0.58	0.49	3.03	0.31	0.20	0.27	1.33	0.07	-	0.13	0.04	0.03	-	0.18	0.06	16.94	7.86	1.08
64	50	2.30	6.20	19.48	1.99	0.71	2.68	7.81	2.35	1.30	5.28	1.37	0.09	0.37	1.08	0.63	0.71	0.67	0.94	2.77	58.72	2.33	1.60
114	4	2.86	3.13	6.69	3.63	0.81	0.66	2.21	1.04	0.90	1.14	1.66	0.03	0.22	0.25	-	0.14	0.13	0.38	0.35	26.24	6.34	1.46
114	70	1.60	3.43	5.19	3.23	0.75	0.30	2.20	0.36	0.51	1.59	2.51	-	0.10	0.33	-	0.16	0.05	0.25	-	22.56	11.13	1.09
114	100	1.42	2.42	4.06	2.64	0.97	1.19	2.19	0.51	0.22	0.98	0.92	-	0.06	0.10	-	0.06	0.56	0.30	0.11	18.71	4.92	1.58
114	250	0.96	1.24	5.09	2.11	0.70	0.89	1.56	0.25	0.15	0.58	0.45	0.06	0.08	-	-	-	0.19	0.24	0.06	14.61	3.09	1.66
114	500	0.72	0.51	4.06	1.73	0.70	0.75	1.33	0.16	0.01	0.47	0.38	0.05	-	0.17	-	0.01	-	0.18	0.02	11.25	3.34	1.63
114	1000	1.10	1.52	2.13	1.59	0.46	0.69	1.20	0.00	0.13	0.51	0.25	0.08	-	0.05	-	-	0.73	0.25	-	10.70	2.32	2.34
114	1760	1.76	1.31	2.66	2.01	0.48	0.34	1.16	0.29	-	0.35	0.21	0.03	-	-	-	0.03	-	0.17	0.18	10.99	1.89	1.54
114	2750	1.40	1.98	1.95	3.70	0.49	0.88	2.20	0.51	0.12	0.84	0.18	0.09	0.09	0.20	-	0.27	0.08	0.39	0.13	15.51	1.17	2.52
114	3700	0.97	2.07	2.11	3.98	0.27	1.63	2.63	1.57	0.10	1.88	0.28	0.12	0.40	0.51	-	0.73	0.33	0.66	0.58	20.81	1.36	3.16
115	10	1.98	2.09	6.14	5.07	1.43	1.23	2.69	0.54	0.66	1.40	0.84	0.06	0.15	0.21	-	-	1.02	0.49	0.54	26.55	3.15	1.84
115	50	1.95	2.70	5.92	2.34	0.99	1.11	2.18	0.21	0.09	1.28	1.24	0.20	0.13	0.36	0.50	0.42	1.31	0.23	0.82	23.99	5.17	0.94
115	100	1.49	1.50	5.01	2.20	0.05	0.30	1.44	0.13	0.34	0.70	1.03	0.04	0.01	0.02	-	-	-	0.40	0.02	14.69	7.00	2.74
115	250	1.46	1.67	4.51	2.56	0.72	0.92	1.48	-	0.34	0.28	0.44	0.27	0.07	0.05	-	-	0.29	0.31	0.26	15.64	2.81	1.98
115	500	1.06	1.45	4.90	2.58	0.57	1.01	2.11	0.51	0.16	1.28	0.55	0.03	0.09	0.17	-	-	0.19	0.42	0.14	17.21	3.18	2.47
115	1000	1.53	1.68	2.69	2.06	0.01	0.30	1.37	0.23	-	0.54	0.39	0.05	-	0.12	-	0.15	-	0.21	-	11.32	3.47	1.85
115	2000	1.36	2.18	3.93	0.88	0.39	0.66	1.60	0.33	0.05	0.78	0.18	0.05	0.02	0.01	0.09	0.03	-	0.37	0.33	13.23	1.32	2.79
115	2750	1.31	1.22	1.93	1.95	0.53	0.61	-	0.75	0.38	0.31	0.25	-	-	0.21	0.13	0.49	-	0.31	-	10.36	2.43	2.99
115	3950	1.32	1.35	1.50	4.23	0.22	0.31	2.29	0.89	0.10	1.17	0.20	0.03	0.13	0.31	-	0.05	0.10	0.31	0.24	12.47	1.57	2.49

Table S4b. Dissolved free amino acids (DFAA) throughout the water column at the stations occupied during the RadProf cruise in the North Atlantic Ocean. The total DFAA and the percentages of dissolved taurine and leucine to the total DFAA [%] are also indicated. Concentrations between the detection and quantification limits are marked grey. Abbreviations: Asp, Aspartic acid; Glu, Glutamic acid; Asn, Asparagine; Ser, Serine; Gln, Glutamine; His, Histine; Gly, Glycine; Arg, Arginine; Thr, Threonine; Ala, Alanine; Tau, Taurine; GABA, gamma aminobutyric acid; Tyr, Tyrosine; Met, Methionine; Val, Valine; Trp, Tryptophan; Phe, Phenylalanine; Ile, Isoleucine; Leu, Leucine; Lys, Lysine.

Station	Depth	ASP	GLU	ASN	SER	GLN	HIS	GLY	ARG	THR	ALA	TAU	GABA	TYR	VAL/MET	TRP	PHE	ILE	LEU	LYS	total DFAA	Tau/DFAA [%]	Leu/DFAA [%]
8	5	2.48	2.82	11.14	0.52	0.51	0.35	2.62	0.08	0.57	2.75	5.72	0.10	0.07	0.59	-	0.25	0.40	1.29	0.25	32.51	17.58	3.98
8	50	3.40	3.85	10.66	-	0.86	0.77	3.07	0.28	0.49	2.58	5.96	0.29	-	0.50	1.08	0.51	0.03	1.67	0.39	36.37	16.38	4.59
8	100	2.53	15.13	7.70	1.60	0.21	0.10	1.42	0.45	-	0.40	0.83	0.28	0.20	0.50	-	-	0.01	0.56	0.25	32.16	2.58	1.73
8	250	1.85	2.43	8.15	2.03	-	-	0.12	-	-	0.07	0.93	0.21	0.14	0.14	-	-	-	0.05	-	16.12	5.79	0.30
8	500	1.59	1.15	7.78	-	0.17	-	0.91	0.14	-	0.20	0.73	0.20	0.11	-	-	-	-	0.23	0.39	13.60	5.36	1.71
8	1000	1.27	1.47	6.27	0.79	0.44	-	0.06	-	0.06	0.03	0.77	0.28	0.12	-	-	0.91	0.50	0.01	-	12.97	5.95	0.09
8	1900	1.38	1.34	5.74	1.42	0.43	0.05	0.38	0.10	0.09	0.26	1.36	0.17	0.07	-	-	0.22	0.36	0.58	-	13.96	9.77	4.17
11	5	0.79	2.34	10.49	4.04	0.58	0.25	1.39	0.73	0.07	1.09	1.35	0.03	0.09	0.31	0.98	0.36	0.41	1.19	0.12	26.60	5.08	4.46
11	100	1.40	2.40	13.14	1.40	0.49	0.14	-	3.70	0.88	1.16	0.62	0.39	0.21	0.56	1.84	0.39	0.17	0.46	0.55	29.91	2.06	1.52
11	250	1.73	2.25	9.24	-	-	-	0.98	0.19	0.06	0.35	0.63	0.25	0.12	0.35	0.66	0.20	0.06	0.29	0.25	17.59	3.59	1.63
11	400	2.87	1.88	8.00	0.06	-	-	0.81	0.05	0.09	-	0.45	0.03	0.04	0.33	0.35	0.23	-	0.23	0.16	15.56	2.87	1.45
11	700	3.78	3.66	6.06	2.07	2.08	0.80	-	-	-	0.50	0.74	0.10	0.11	0.50	1.28	0.66	0.06	0.29	0.53	23.22	3.19	1.26
11	1000	1.68	1.60	6.48	0.43	1.61	-	-	3.85	0.53	1.03	0.52	0.27	0.24	0.42	1.42	0.36	0.06	0.43	0.52	21.42	2.41	1.99
11	1800	2.13	1.45	6.29	1.42	0.12	0.30	1.58	0.65	0.10	0.83	0.29	0.26	0.12	0.60	1.34	0.34	0.08	0.47	0.34	18.72	1.55	2.53
11	2500	2.03	1.25	7.45	-	-	-	0.85	0.09	-	0.07	0.25	-	0.01	0.53	1.36	0.97	0.03	0.22	0.50	15.62	1.58	1.41
16	5	1.12	2.01	4.00	2.61	0.21	0.36	1.35	0.80	0.27	0.72	1.20	0.19	0.06	-	0.42	0.80	0.38	1.40	0.41	18.31	6.55	7.65
16	38	1.31	2.29	10.11	6.48	1.68	0.60	-	1.16	0.08	-	0.85	-	-	0.33	0.03	-	0.41	-	-	25.33	3.34	-
16	100	2.03	2.92	11.29	-	0.19	0.45	1.40	0.20	0.07	0.46	1.14	0.20	0.18	0.28	0.89	0.40	0.04	0.41	0.20	22.74	5.03	1.79
16	350	2.11	2.61	7.92	1.63	0.53	0.21	1.06	0.23	0.09	0.42	1.01	0.14	0.15	0.36	-	-	-	0.49	0.21	19.14	5.26	2.54
16	600	1.18	1.70	6.40	1.32	0.21	-	0.71	0.13	0.10	0.13	0.28	0.15	0.12	0.33	0.42	0.18	-	0.33	0.09	13.79	2.01	2.38
16	1000	2.30	2.12	5.79	2.03	0.12	0.25	1.34	0.57	0.13	0.78	0.42	0.22	0.12	0.48	-	-	0.13	0.41	0.29	17.49	2.37	2.36
16	2000	0.77	0.78	3.99	-	-	-	-	-	-	0.94	0.96	-	0.01	0.20	-	0.14	0.27	2.04	2.80	12.90	7.44	15.84
16	2450	1.92	1.52	5.22	1.83	0.13	0.21	1.14	0.35	0.09	0.55	0.28	0.25	0.24	0.21	0.55	0.33	-	0.61	0.25	15.69	1.80	3.91

Station	Depth	ASP	GLU	ASN	SER	GLN	HIS	GLY	ARG	THR	ALA	TAU	GABA	TYR	VAL/MET	TRP	PHE	ILE	LEU	LYS	total DFAA	Tau/DFAA [%]	Leu/DFAA [%]
108	5	1.03	1.25	4.97	9.77	0.17	0.96	6.07	3.03	0.40	3.50	1.22	1.02	0.28	1.24	3.11	0.26	0.91	1.44	3.86	44.47	2.73	3.23
108	100	1.90	4.81	9.06	5.86	0.29	0.83	2.88	1.73	0.31	2.01	0.92	0.37	0.37	0.42	1.82	0.34	0.30	0.60	0.83	35.63	2.57	1.69
108	400	2.26	3.12	7.83	1.21	0.56	0.30	1.12	0.18	0.13	0.43	1.03	0.11	0.17	0.35	1.06	0.41	-	0.26	0.26	20.78	4.94	1.26
108	550	1.19	1.88	5.95	1.73	0.19	0.22	1.12	0.42	0.18	0.61	0.59	0.23	0.15	0.20	0.51	0.09	0.10	0.36	0.44	16.15	3.66	2.20
108	1000	1.35	1.54	-	3.01	1.08	-	-	1.31	0.26	0.19	0.21	0.16	0.10	0.33	1.01	0.36	0.08	0.30	0.25	11.55	1.80	2.64
108	2000	2.02	4.57	5.67	-	-	-	0.81	0.28	0.17	0.14	0.40	0.04	0.01	0.46	0.56	0.10	-	1.41	0.22	16.86	2.37	8.35
108	2750	1.92	1.85	4.29	1.47	0.08	0.06	1.09	0.41	0.03	0.74	-	0.13	0.07	0.24	0.40	0.09	0.12	0.56	0.54	14.08	-	3.97
108	4000	3.09	2.69	4.10	1.53	0.17	0.19	0.89	0.35	0.06	0.34	0.09	0.16	0.08	0.21	0.62	0.15	0.06	0.43	0.25	15.45	0.58	2.79
111	5	3.81	11.00	52.78	2.59	0.98	3.07	11.31	2.12	2.33	9.91	3.16	0.46	2.22	0.79	0.74	1.49	0.64	5.60	0.17	115.18	2.74	4.86
111	100	7.49	5.90	24.09	0.30	1.46	1.99	2.17	3.32	2.27	2.74	0.47	1.83	2.46	0.68	2.12	1.17	0.77	0.94	0.97	63.16	0.74	1.48
111	300	7.49	5.90	9.81	0.80	0.10	0.34	2.25	0.74	0.09	1.31	0.53	0.10	0.12	0.41	1.09	0.24	0.04	2.35	0.41	34.10	1.56	6.89
111	1000	1.79	3.77	7.48	-	0.33	-	0.41	0.01	0.02	0.03	0.63	-	0.06	0.26	0.50	0.19	-	0.14	0.10	15.71	4.04	0.86
111	2000	1.74	2.30	6.34	-	-	0.35	0.57	0.05	0.03	0.11	0.19	0.07	-	0.29	0.73	0.54	0.03	0.44	0.15	13.93	1.38	3.19
111	2750	1.36	4.03	3.98	0.78	0.26	-	0.23	0.10	-	0.95	1.63	0.25	0.09	0.29	1.40	0.02	0.19	0.93	0.25	16.72	9.72	5.56
111	3200	1.47	1.99	3.88	0.03	0.76	-	-	-	-	0.17	0.16	0.12	-	0.21	0.66	-	0.01	0.42	-	9.87	1.62	4.28
111	4500	1.47	2.17	3.44	0.23	0.16	-	0.14	-	0.02	0.31	0.20	0.03	-	0.41	-	-	0.03	0.12	-	8.73	2.33	1.35

Table S5. Slope, coefficient of determination (R^2) and number of stations (n) from the correlation between depth and taurine assimilation and respiration, leucine incorporation and prokaryotic abundance. Abbreviations: SD, standard deviation. (Transect 1 = MODUPLAN + RADPROF).

	<i>n</i> <i>Transect 1</i>	<i>Slope</i> <i>Transect 1</i> (Mean $\pm$ SD)	R^2 <i>Transect 1</i> (Mean $\pm$ SD)	<i>n</i> <i>Transect 2</i>	<i>slope</i> <i>Transect 2</i> (Mean $\pm$ SD)	R^2 <i>Transect 2</i> (Mean $\pm$ SD)
<i>Taurine assimilation</i>	11	-0.86 $\pm$ 0.12	0.802 $\pm$ 0.11	7	-0.96 $\pm$ 0.28	0.741 $\pm$ 0.07
<i>Taurine respiration</i>	11	-1.23 $\pm$ 0.38	0.740 $\pm$ 0.22	7	-0.92 $\pm$ 0.13	0.742 $\pm$ 0.06
<i>Leucine incorporation</i>	14	-0.82 $\pm$ 0.22	0.815 $\pm$ 0.15	9	-0.85 $\pm$ 0.27	0.748 $\pm$ 0.18
<i>Prokaryotic abundance</i>	14	-1.82 $\pm$ 0.76	0.822 $\pm$ 0.12	9	-1.55 $\pm$ 0.19	0.869 $\pm$ 0.07

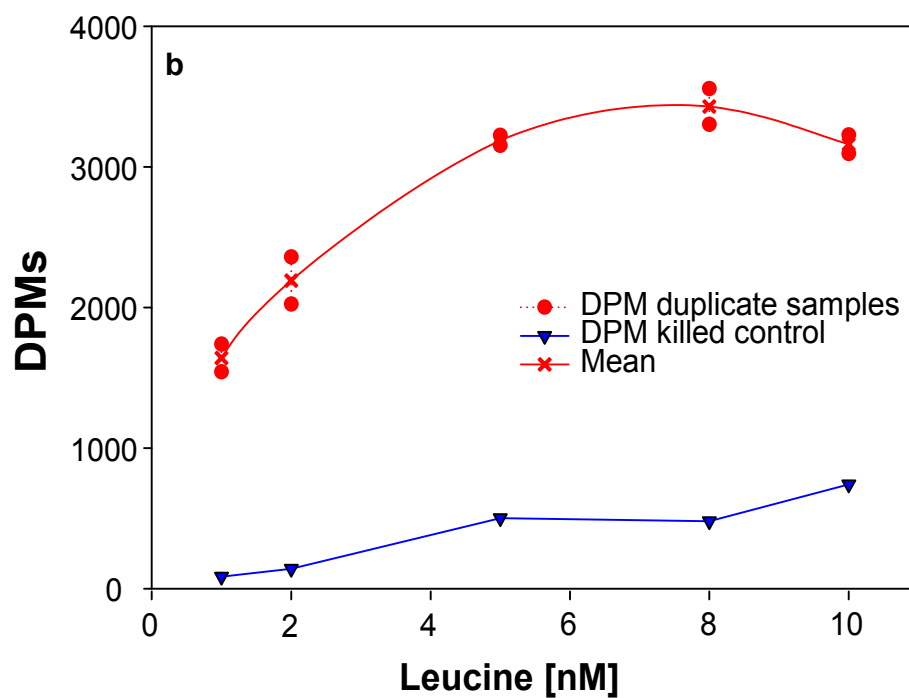
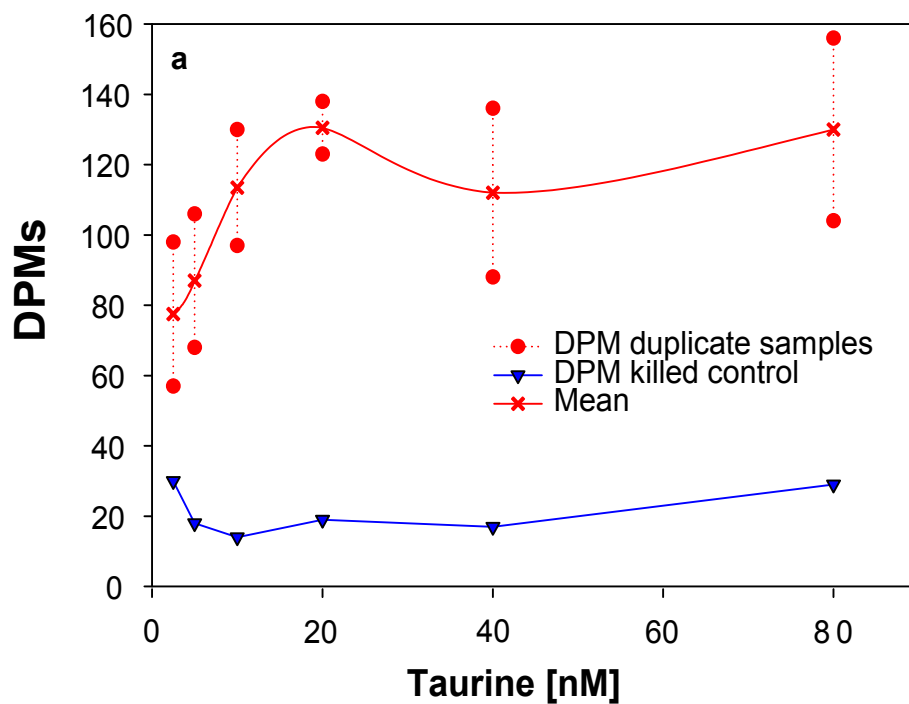


Fig. S1. Saturation curve for (a) taurine and (b) leucine assimilation of prokaryotic communities collected at 2000 m depth. Measured rates correspond to 0.015 nmol taurine L⁻¹d⁻¹ and 0.0005 nmol leucine L⁻¹ d⁻¹, respectively.

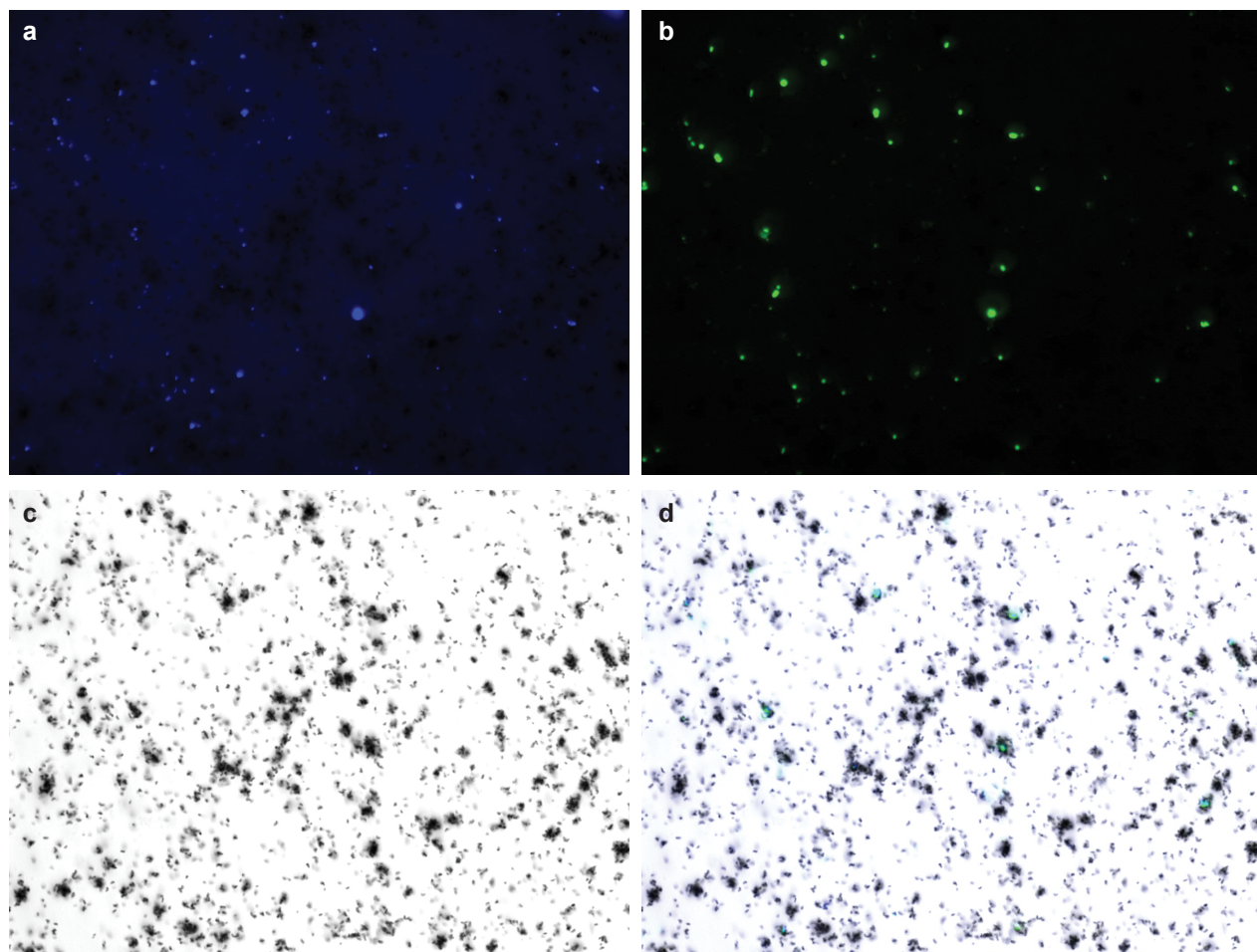
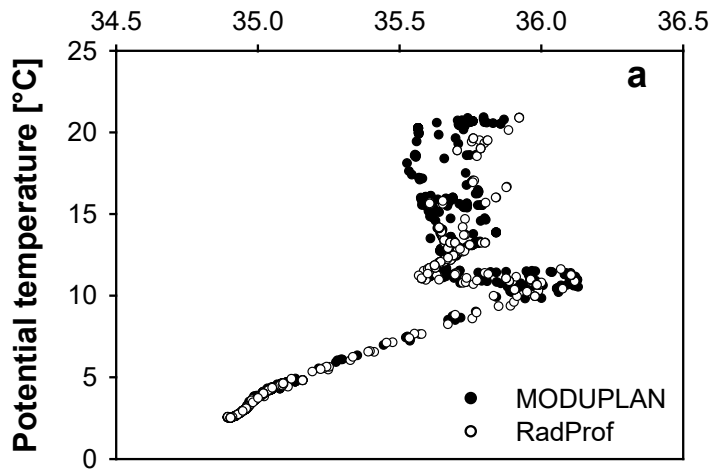


Fig. S2. MICRO-CARD-FISH image of (a) DAPI-stained prokaryotic cells (blue), (b) Bacteria labelled by CARD-FISH (green), (c) silver grains (black), and (d) overlay of the three images. Sample was collected at 5 m depth at Station 8.

TRANSECT 1

Salinity



TRANSECT 2

Salinity

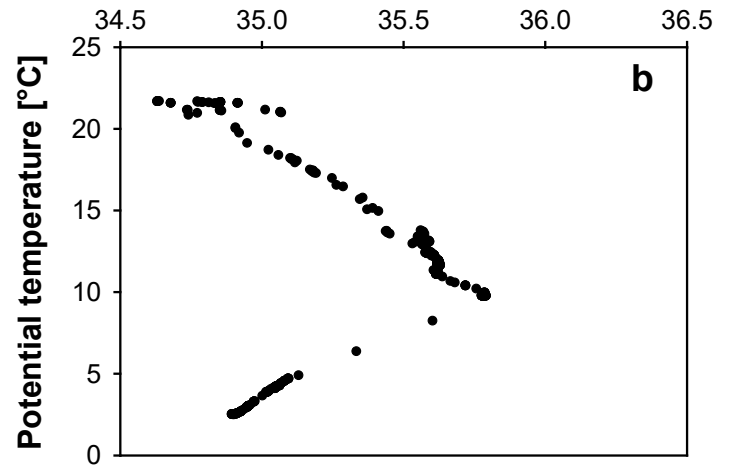


Fig. S3. Temperature-salinity diagrams (Transect 1: a; Transect 2: b) throughout the water column at the stations occupied during the MODUPLAN and the RadProf cruise in the North Atlantic. The data for the MODUPLAN cruise were published in Clifford et al. [7].

TRANSECT 1

TRANSECT 2

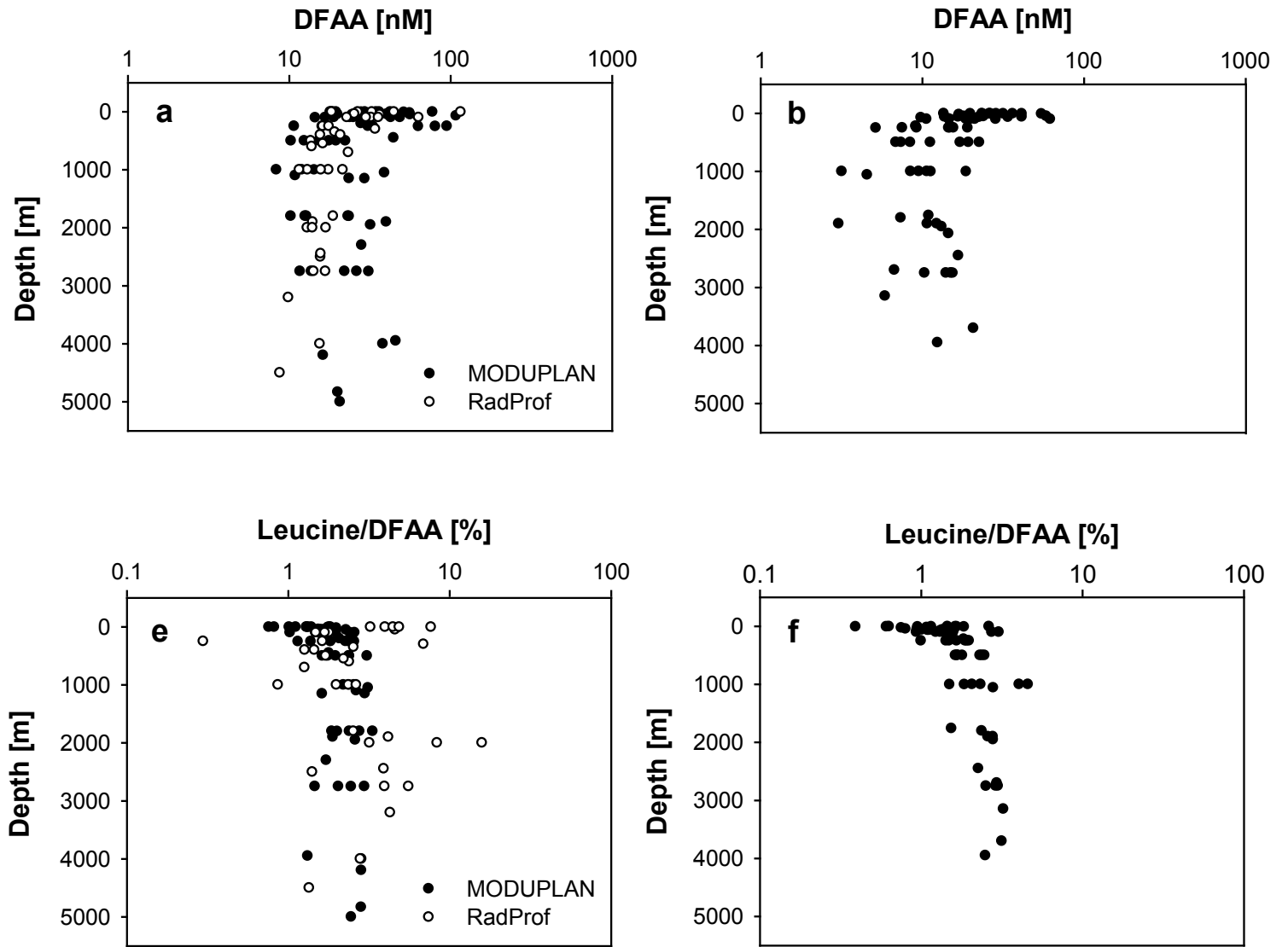


Fig. S4. Dissolved free amino acids (DFAA) concentrations (a, b), and Leucine/DFAA % (c, d) throughout the water column at the stations occupied during the MODUPLAN and the RadProf cruise in the North Atlantic. Data of Transect 1 are shown in the left panels, and data of Transect 2 are shown in the right panels.

TRANSECT 1

TRANSECT 2

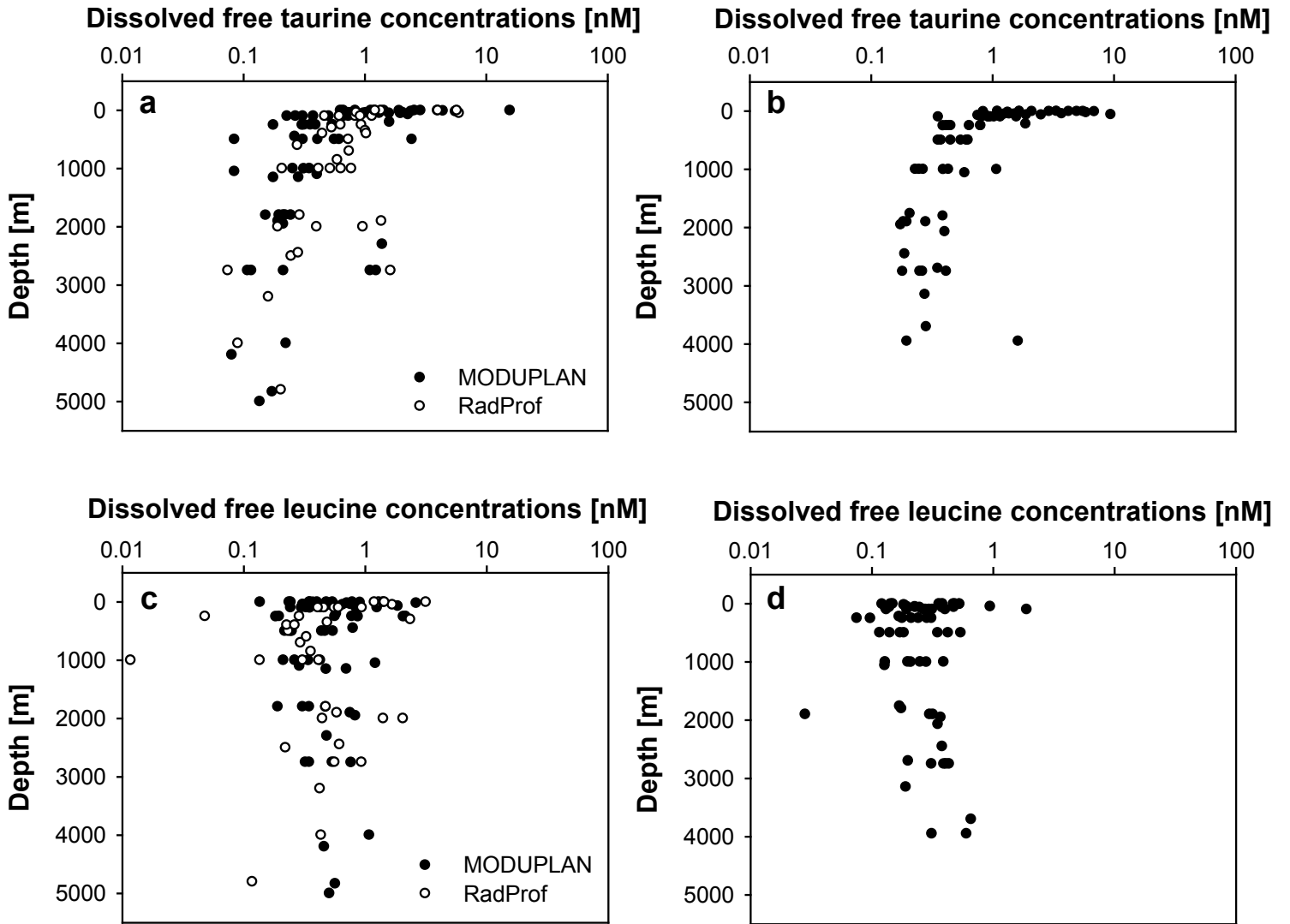


Fig. S5. Dissolved free taurine (a, b) and dissolved free leucine (c, d) concentrations throughout the water column at the stations occupied during the MODUPLAN and the RadProf cruise in the North Atlantic. Left panels show data for Transect 1 and the right panels for Transect 2. The taurine concentrations of the MODUPLAN cruise are from Clifford et al. [7].

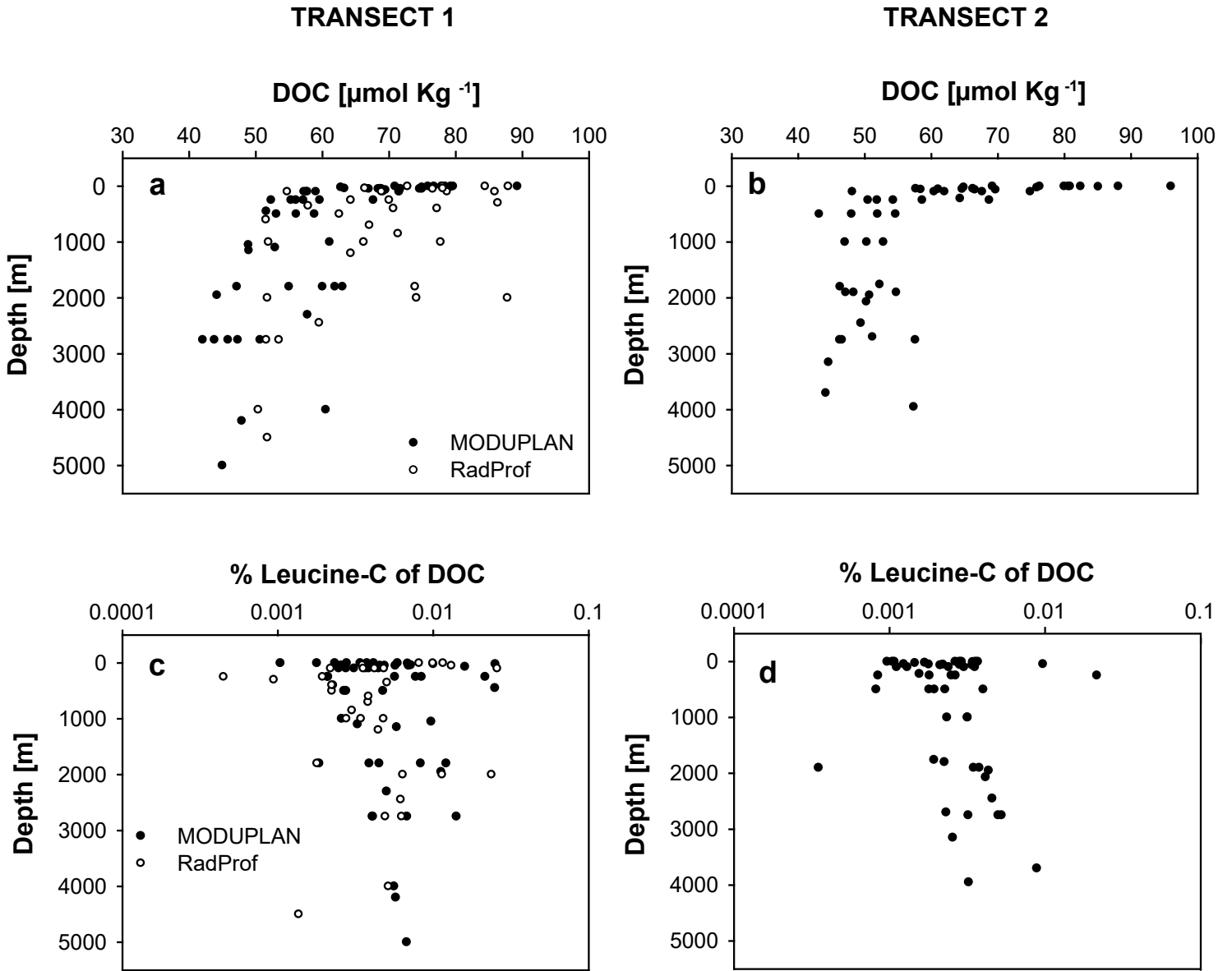


Fig. S6. Dissolved organic matter (DOC) concentrations (a, b), % Leucine-C of DOC (c, d) throughout the water column at the stations occupied during the MODUPLAN and the RadProf cruise in the North Atlantic. Data of Transect 1 are shown in the left panels and data of Transect 2 in the right panels.

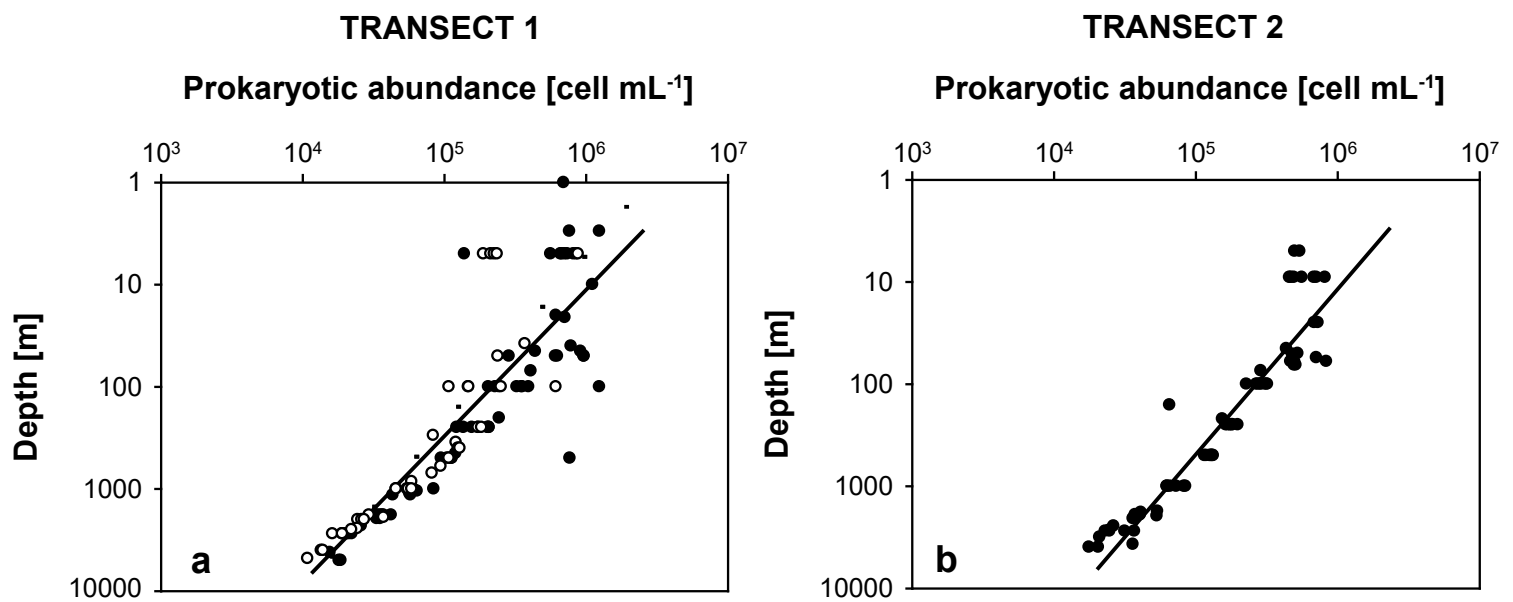


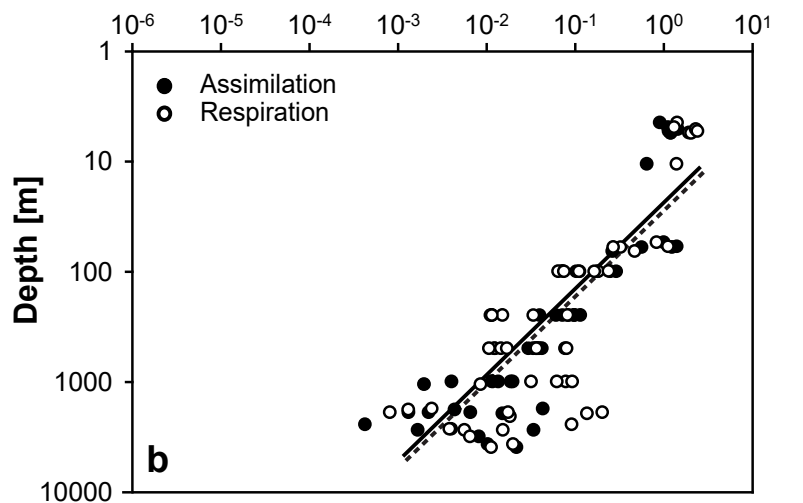
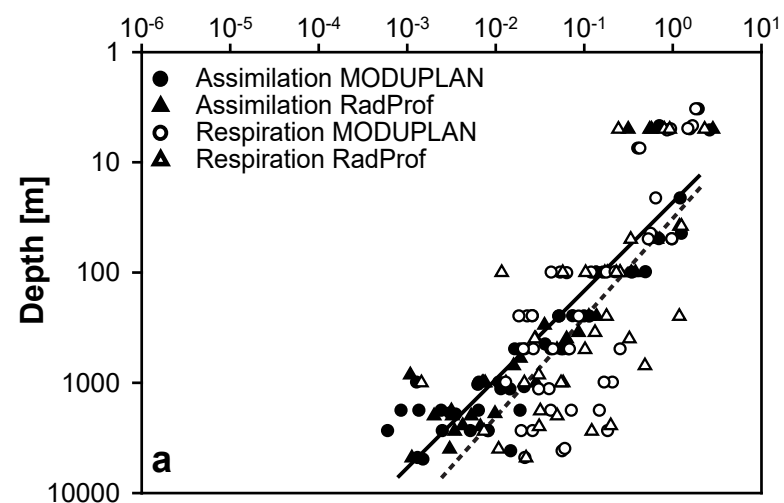
Fig. S7. Log - log plots of prokaryotic abundance determined via flow cytometry (FCM) throughout the water column of (a) Transect 1 (MODUPLAN - epipelagic: $n = 31$; mesopelagic: $n = 18$, bathypelagic: $n = 21$; RadProf - epipelagic: $n = 12$; mesopelagic: $n = 15$, bathypelagic: $n = 12$) and (b) Transect 2 (MODUPLAN - epipelagic: $n = 30$; mesopelagic: $n = 21$, bathypelagic: $n = 17$) at the stations occupied during the MODUPLAN and the RadProf Cruise in the North Atlantic Ocean. The full lines represent the trend-lines of the prokaryotic abundance with depth. The mean slopes and the mean coefficients of determination (R^2) are given in Table S5.

TRANSECT 1

TRANSECT 2

Taurine assimilation and respiration [$\text{nmol L}^{-1}\text{d}^{-1}$]

Taurine assimilation and respiration [$\text{nmol L}^{-1}\text{d}^{-1}$]



Leucine incorporation rate [$\text{nmol L}^{-1}\text{d}^{-1}$]

Leucine incorporation rate [$\text{nmol L}^{-1}\text{d}^{-1}$]

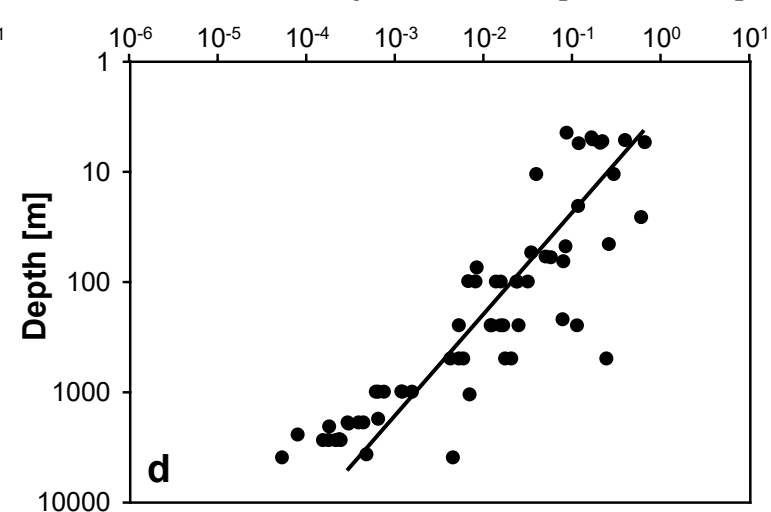
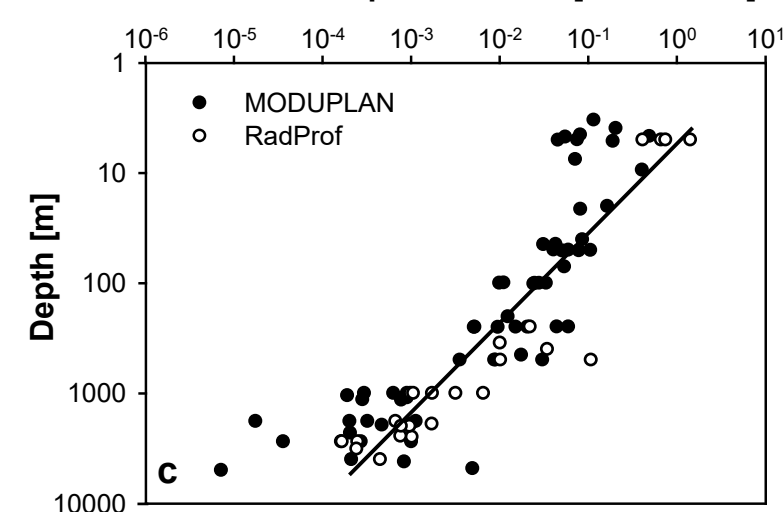


Fig. S8. Log – log plots of taurine assimilation and respiration rates (average of duplicates) throughout the water column of (a) Transect 1 and (b) Transect 2; leucine incorporation rates (average of duplicates) throughout the water column of (c) Transect 1 and (d) Transect 2 at the stations occupied during the MODUPLAN and the RadProf Cruise in the North Atlantic (Fig. 1). The full and dotted lines in a and b represent the trend-lines of taurine assimilation and respiration rates of the entire data sets with depth, respectively. The full lines in c and d represent the trend-lines of leucine incorporation rates with depth. The slopes and the coefficients of determination (R^2) for taurine assimilation and respiration and leucine incorporation rates are indicated in Table S5.

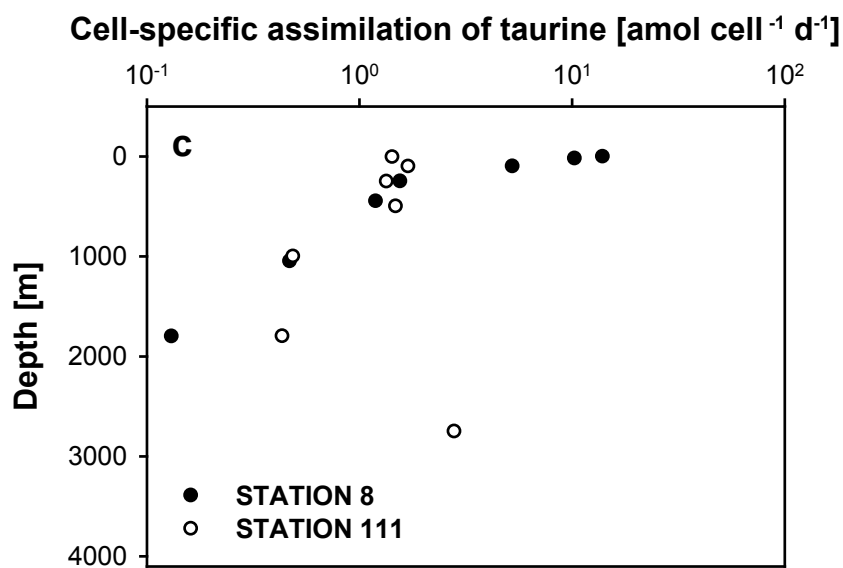
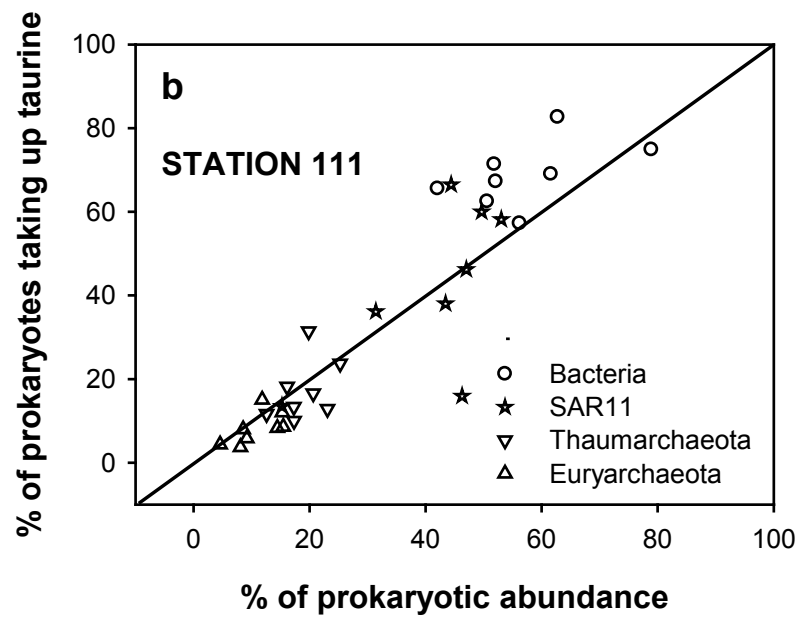
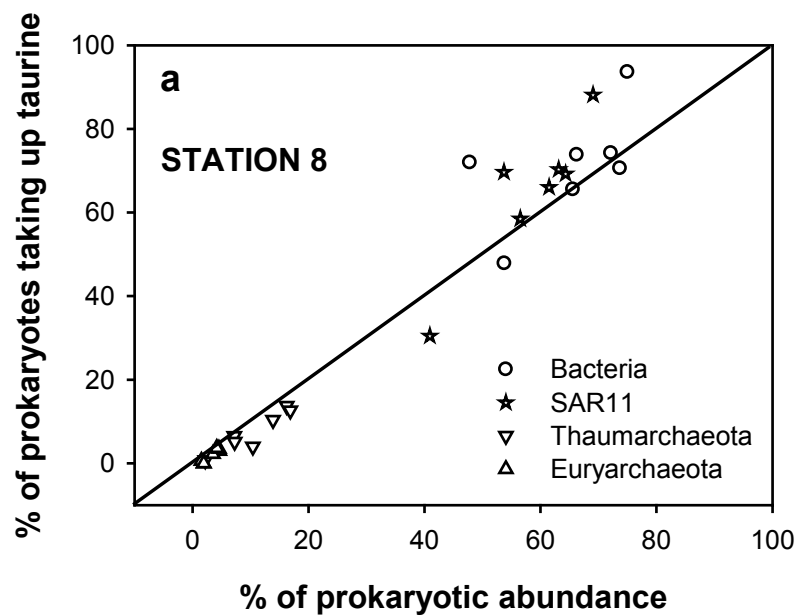


Fig. S9. The contribution of prokaryotes taking up taurine of the respective prokaryotic taxa *versus* their contribution to the abundance of prokaryotes (based on DAPI-counts): (a) Station 8, (b) Station 111. Cell-specific assimilation of taurine *versus* depth at Stations 8 and 111 (c)

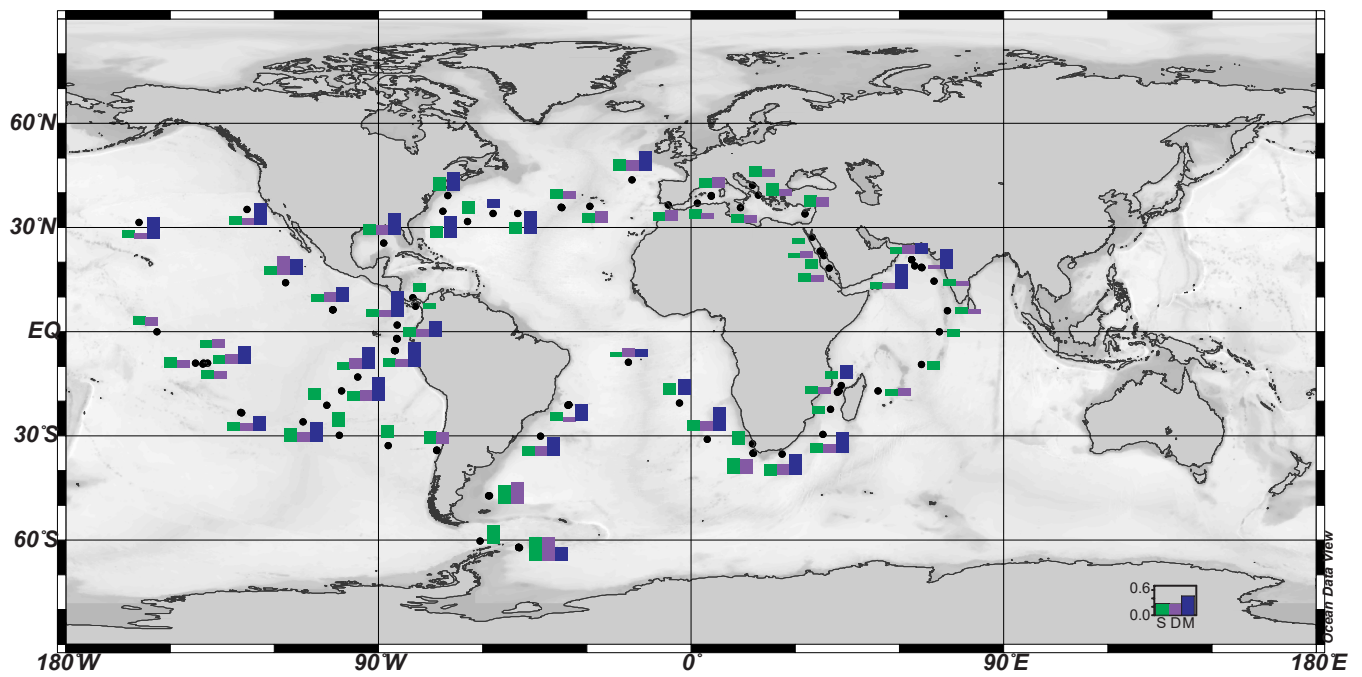


Fig. S10. Ratio between the abundance of taurine transporters (tauA + tauB + tauC) and the housekeeping gene of recombinases (recA and radA) in the Tara Oceans dataset [8]. Sampling locations are marked by full circles, bar charts depict the relative abundances for different depth layers according to the scale indicated in the graph in the bottom right corner. S, subsurface, D, deep chlorophyll maximum (DCM) (Table S3), M, mesopelagic

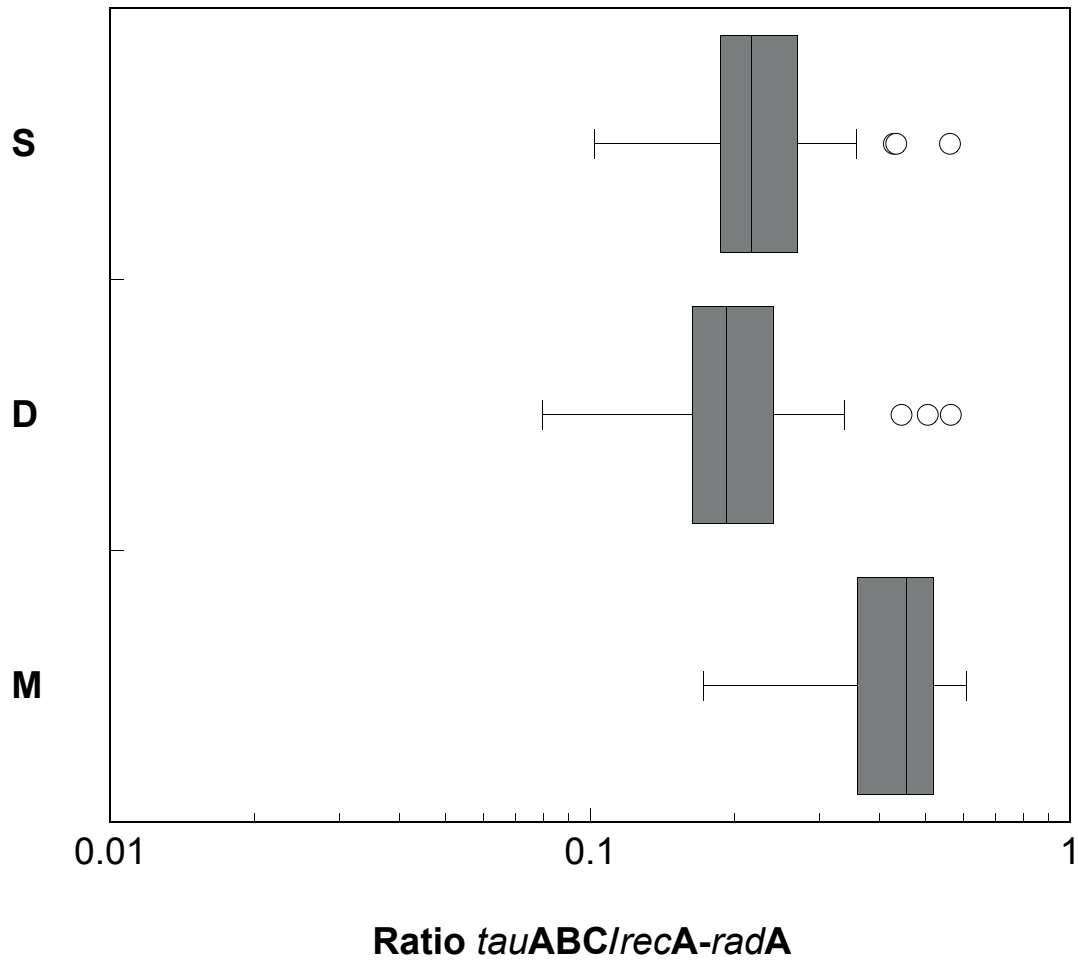


Fig. S11. Boxplot depicting the ratio between the sum of taurine transporters and *recA-radA* gene abundances in different depth layers of the Tara Oceans dataset [8]. The vertical line in the box represents the median, the lower box border represents the 25th percentile and the upper box border the 75th percentile, the whiskers represent the minimum and maximum values within the data set that fall within an acceptable range, and circles indicate outliers. The four samples identified as mixed layer in the dataset (Table S3) have been included in the DCM data. Abbreviations: S, subsurface water; D, deep chlorophyll maximum; M, mesopelagic.

1. Amann RI, Ludwig W, Schleifer KH (1995) Phylogenetic identification and in situ detection of individual microbial cells without cultivation. *Microbiol Rev* 59:143–69
2. Amann RI, Binder BJ, Olson RJ, et al (1990) Combination of 16S rRNA-targeted oligonucleotide probes with flow cytometry for analyzing mixed microbial populations. *Appl Environ Microbiol* 56:1919–25
3. Daims H, Brühl A, Amann R, et al (1999) The domain-specific probe EUB338 is insufficient for the detection of all Bacteria: development and evaluation of a more comprehensive probe set. *Syst Appl Microbiol* 22:434–44 . doi: 10.1016/S0723-2020(99)80053-8
4. Morris RM, Rappé MS, Connon SA, et al (2002) SAR11 clade dominates ocean surface bacterioplankton communities. *Nature* 420:806–810 . doi: 10.1038/nature01240
5. Teira E, Reinthaler T, Pernthaler A, et al (2004) Combining catalyzed reporter deposition-fluorescence in situ hybridization and microautoradiography to detect substrate utilization by bacteria and archaea in the deep ocean. *Appl Environ Microbiol* 70:4411–4414 . doi: 10.1128/AEM.70.7.4411-4414.2004
6. Woebken D, Fuchs BM, Kuypers MMM, Amann R (2007) Potential interactions of particle-associated anammox bacteria with bacterial and archaeal partners in the Namibian upwelling system. *Appl Environ Microbiol* 73:4648–4657 . doi: 10.1128/AEM.02774-06
7. Clifford EL, Hansell DA, Varela MM, et al (2017) Crustacean zooplankton release copious amounts of dissolved organic matter as taurine in the ocean. *Limnol Oceanogr* 62:2745–2758 . doi: 10.1002/lno.10603
8. Sunagawa S, Coelho LP, Chaffron S, et al (2015) Structure and function of the global ocean microbiome. *Science* 348:1261359 . doi: 10.1126/science.1261359