## **Supporting Information**

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**Fig. S1.** Rank abundance curve of bacterial OTUs defined by 16S rDNA pyrosequencing of 25 Delaware coastal site surface water samples taken monthly over 3 y. Average () and maximum frequencies () of each OTU are plotted. The percentage of times the OTU frequency was equal to or above 1% ().



Fig. S2. Phylogenetic classification of bacterial OTUs found in Delaware coastal surface waters. Members of the (A) Alphaproteobacteria and (B) Bacteroidetes. The groups' percentage was divided into three categories: mostly abundant (occurring >50% of the time), cycling (<50% of the time), and always rare.



**Fig. S3.** To explore how different growth rates and ribosomal copy numbers affect the relationship between rRNA and rDNA, we took the original sequence numbers generated for the top 10 most-abundant ribotypes, because they had a wide distribution in abundance. The sequence numbers was assumed to approximate the number of cells in the actual community, and growth rates were assumed to be constant. We then changed the growth rate of individual ribotypes by varying the number of rRNA copies or varied the operon copy number by multiplying the rDNA by the indicated number of operons, as indicated by the table (*Lower*). The resulting absolute rRNA and rDNA numbers were transformed into relative percentages and plotted. Note that OTU types 1 or 8 started with the same number of cells, but either the relative growth rate or operon copy number was varied. All points >1 had relative growth rates >1, regardless of the operon copy number.



Fig. S4. Ratios of 16S rRNA:rDNA as a function of 16S rDNA rank in the tag dataset. Points marked in black have ratios significantly different from 1.



**Fig. S5.** To explore the effect of varying growth rates on the relationship between rRNA and rDNA, we took the original sequence numbers generated for all ribotypes. The community consisted of 685 ribotypes varying in abundance as described in the main text. This distribution of sequence numbers was assumed to approximate the distribution of ribotypes in the actual community, in effect assuming one operon per ribotype for this exercise. All of the ribotypes were assumed to grow at the same, constant growth rate, except for one ribotype whose growth rate was very high at low abundances and low at high abundances (*Upper*). The growth rates, i.e., rRNA:rDNA ratios (*Upper*), were then used to calculate the rRNA numbers as abundance varied. The absolute abundance of rRNA and rDNA was then used to calculate the percent of the total rRNA and the percent of total rDNA made up by all ribotypes (*Lower*). The data for two ribotypes are plotted, one whose growth rate, and it is greater than zero for the ribotype whose growth rate increases as abundance decreases.

## Table S1. Relationships of rRNA to rDNA of individual taxa over 3 y

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Family	OTU	$A/C/R^{\dagger}$	Best BLAST hit nearest isolate (%)	Slope	SE	CI	Int.	SE	r <sup>2</sup>
SAR11	10	А	P. ubique HTCC1002, AF510192 (100)	1.1	0.08	0.85–1.38	-0.56	0.25	0.88
	9*	А	<i>P. ubique</i> HTCC1002, AF510192 (98)	0.80	0.06	0.68–0.97	0.43	0.20	0.88
	12*	А	<i>P. ubique</i> HTCC1002, AF510192 (99)	0.75	0.05	0.61–0.88	0.07	0.09	0.89
	66*	А	P. ubique HTCC1002, AF510192 (99)	0.92	0.09	0.69–1.26	0.04	0.16	0.78
	63	С	P. ubique HTCC1002, AF510192 (99)	0.70	0.08	0.49-0.92	0.08	0.09	0.68
	188*	С	P. ubique HTCC1002, AF510192 (99)	1.34	0.15	0.94–2.0	-0.18	0.16	0.70
	716	R	P. ubique HTCC1002, AF510192 (98)	1.12	0.17	0.66–1.58	0.05	0.06	0.50
Rhodobacteraceae	51	А	Thalassobius sp., FJ196059 (98)	0.86	0.09	0.63–0.97	-0.31	0.25	0.75
	46	А	Paracoccus sp., EF575566 (97)	1.23	0.13	0.95–1.57	-0.30	0.27	0.73
	49*	А	Roseovarius aestuarii, EU156066 (98)	1.06	0.09	0.8–1.35	0.44	0.15	0.82
	308	С	Roseobacter sp., EU196325 (97)	1.30	0.04	0.93–1.41	0	0.05	0.98
	2,454*	С	Roseovarius aestuarii, EU156066 (97)	1.06	0.11	0.77-1.40	0.28	0.14	0.73
Flavobacteriaceae	29	А	Polaribacter sp., HM010401 (94)	0.73	0.09	0.44-1.04	0	0.01	0.66
	218	А	Ulvibacter sp., DQ660381 (93)	0.68	0.06	0.46-0.85	-0.04	0.10	0.83
	2,556	С	Flavobacterium sp., EU099872 (85)	0.67	0.04	0.60-0.75	0.02	0.06	0.91
	554	С	Ulvibacter antarcticus, EF554364 (95)	0.53	0.06	0.32-0.73	-0.06	0.08	0.73
	552	С	Ulvibacter antarcticus, EF554364 (93)	0.69	0.06	0.52-0.87	-0.10	0.08	0.82
Oceanospirillales	41	А	Nept. naphthovorans, FJ172035 (88)	1.28	0.16	0.92-1.62	-1.07	0.31	0.64
	39	А	Nept. naphthovorans, FJ172035 (87)	0.86	0.11	0.62-1.19	-0.13	0.16	0.60
	1,454	А	Nept. naphthovorans, FJ172035 (87)	0.80	0.10	0.56-1.11	-0.23	0.15	0.64
	3,115*	С	Thalassol. oleivorans, AM279755 (94)	1.36	0.10	1.04–1.85	-0.05	0.10	0.87
OMG group	4,354*	С	Marine str. HTCC2188, AY386344 (98)	0.85	0.09	0.59-1.09	0.13	0.14	0.72
	114*	R	Marine str. HTCC2080, AY386339 (100)	0.64	0.12	0.36-1.05	-0.07	0.11	0.24
Methylophilaceae	1,019	С	Methylophilus sp., AY436792 (92)	1.13	0.13	0.83–1.44	-0.07	0.12	0.69
	1,393*	С	Methylophilus sp., AY436792 (92)	1.04	0.11	0.87-1.50	0.17	0.10	0.72
	231	С	Methylophilus sp., EU194893 (92)	1.13	0.10	0.71–1.3	-0.06	0.08	0.79
	250*	С	Methylotenera mobila, DQ287786 (93)	0.96	0.11	0.70–1.23	0.06	0.08	0.71
Denitromonas	448*	С	Denitromonas sp., AM403171 (92)	0.83	0.13	0.49–1.45	0.02	0.01	0.42

Reduced major axis (RMA) regression analysis was used with slopes, intercepts (Int.), and SEs. Confidence intervals (CI) of slopes are also reported with bootstrapping at 99%. OTUs where 16S rRNA:rDNA ratios increase more than twofold as abundance decreases are indicated by an asterisk. Slopes significantly different from 1 and intercepts significantly different from zero are underlined. <sup>†</sup>Mostly abundant (A), cycling (C), or always rare (R).

## Table S2. OTUs, primers and qPCR conditions used to determine 16S rRNA and 16S rRNA gene copies in Delaware coastal water samples

ΟΤυ	No. of clones with expected sequence (%)	Primers	qPCR conditions* <sup>,†</sup>	Efficiency qPCR RT-qPCR	
Actinobacteria-960	8/9 (89)	F-5' AACACGTGAGAAATCTGCCCCT R-5' CTCCCTGACCGAAATTCTTTCT	42 °C, 3'; 95 °C, 5'; 35 cycles of 94 °C,15''; 58 °C, 30''; 72 °C, 30''; 40 °C, 1' melt	0.94	0.97
Rhodobacteria-51	11/11 (100)	F-5' ACGCGTGGGAATATACCCAG R-5' TCCAATTCCGATAAATCTTTCCC	Reverse transcription 50 °C	0.96	1.16
Bacteroidetes-29	9/11 (82)	F-5′ GTATTGTAAACTGGCATCGGTTT R-5′ GTTACCTTACCATCTAGCTAATAA	Extension 66 °C	0.94	0.95
Bacteroidetes-218	7/8 (88)	F-5′ GAATCTACCTTGTACTAGGG R-5′ GTCATCTTGTACCGTAACCT	Annealing 54 °C, extension 68 °C	0.96	0.96
Betaproteobacteria-448 10/11 (91)		F-5' ATGGCGAACGGGTGAGTA R-5' CCCACTTTCCTCCTCAGAGA	Reverse transcription 50 °C, annealing 56 °C, extension 68 °C	1.0	1.22

\*Quantitative PCR reactions had no RT or 40 °C step, and the initial denaturation step was 10 min.

<sup>†</sup>Only changes from Actinobacteria-960 PCR conditions are listed.