

Table S2. Marine microbe genome data (see methods), amino acid usage and theoretical Nitrogen contents of proteins and DNA.

General Genomic Information										Median ARSC		
Genus Species	Strain	PID	Genome Size	Percent of Open Ocean	Percent of Open Ocean Standard Deviation	Percent of Coastal Ocean	Percent of Coastal Ocean Standard Deviation	GC %	Num Of ORF Analyzed	Median Mass Per Residue	N	C:N
<i>Candidatus Pelagibacter</i> sp.	HTCC7211	19339	1456888	6.14%	0.17%	4.91%	0.14%	29.00	1447	113.175	0.345	8.999
<i>Candidatus Pelagibacter</i> sp.	HTCC1002	13577	1326089	2.89%	0.12%	2.25%	0.13%	29.70	1387	113.084	0.340	9.121
<i>Candidatus Pelagibacter</i> sp.	HTCC1062	13989	1308759	1.85%	0.16%	1.41%	0.15%	29.68	1354	112.993	0.339	9.106
<i>Prochlorococcus marinus</i>	AS9601	13548	1674733	1.40%	0.09%	0.40%	0.04%	31.33	1921	113.268	0.344	9.043
<i>Unnamed alphaproteobacterium</i>	BAL199	19281	6101023	1.31%	0.08%	1.09%	0.08%	65.02	6128	108.553	0.376	7.441
<i>Prochlorococcus marinus</i>	MIT9301	15746	1642753	1.24%	0.07%	0.36%	0.04%	31.34	1907	113.256	0.344	8.994
<i>Unnamed SAR11 alphaproteobacterium</i>	HIMB114	41237	1294666	0.87%	0.07%	0.66%	0.05%	29.61	1425	113.453	0.349	8.948
<i>Prochlorococcus marinus</i>	MIT9312	13910	1709204	0.69%	0.06%	0.19%	0.03%	31.21	1810	113.117	0.345	9.012
<i>Prochlorococcus marinus</i>	MIT9202	19343	1691453	0.57%	0.05%	0.16%	0.03%	31.00	1890	113.302	0.348	8.976
<i>Unnamed gammaproteobacterium</i>	HTCC2143	13605	3925629	0.50%	0.05%	0.49%	0.06%	47.00	3662	110.414	0.340	8.544
<i>Prochlorococcus marinus</i>	MIT9215	18633	1738790	0.50%	0.04%	0.15%	0.03%	31.15	1982	113.328	0.345	9.011
<i>Microscilla marina</i>	ATCC23134	13411	9771226	0.44%	0.06%	0.42%	0.07%	40.60	8319	113.817	0.367	8.586
<i>Unnamed Flavobacteriales bacterium</i>	HTCC2170	13595	3873100	0.42%	0.05%	0.48%	0.07%	37.00	3478	113.028	0.329	9.399
<i>Kordia algicida</i>	OT-1	19315	5019836	0.37%	0.05%	0.43%	0.05%	34.00	4514	113.735	0.336	9.320
<i>Unnamed gammaproteobacterium</i>	HTCC2207	16658	2619777	0.36%	0.05%	0.43%	0.05%	51.00	2388	110.015	0.333	8.623
<i>Unnamed gammaproteobacterium</i>	HTCC2080	18487	3576081	0.36%	0.05%	0.54%	0.06%	51.82	3185	109.410	0.340	8.382
<i>Janibacter</i> sp.	HTCC2649	13546	4228723	0.35%	0.04%	0.31%	0.04%	68.00	4078	106.863	0.347	7.852
<i>Algiphagus</i> sp.	PR1	18947	4776234	0.34%	0.04%	0.31%	0.06%	38.72	4215	112.858	0.320	9.664
<i>Unnamed gammaproteobacterium</i>	HTCC2148	30725	4325790	0.33%	0.04%	0.37%	0.04%	51.25	3827	109.944	0.343	8.417
<i>Labrenzia aggregata</i>	IAM12614	18315	6561391	0.33%	0.04%	0.28%	0.04%	59.00	6314	109.136	0.349	8.138
<i>Prochlorococcus marinus</i>	CCMP1986	213	1657990	0.32%	0.04%	0.06%	0.02%	30.80	1717	113.007	0.345	8.998
<i>Unnamed Flavobacteriales bacterium</i>	ALC-1	19307	3825707	0.32%	0.05%	0.40%	0.06%	32.40	3445	113.344	0.326	9.537
<i>Pseudovibrio</i> sp.	JE062	19345	5726521	0.32%	0.04%	0.26%	0.04%	52.53	5225	109.800	0.335	8.604
<i>Unnamed Rhodobacterales bacterium</i>	HTCC2255	17677	4809064	0.30%	0.04%	0.31%	0.04%	39.00	2240	110.616	0.333	8.768
<i>Labrenzia alexandrii</i>	DFL-11	19367	5502380	0.30%	0.04%	0.25%	0.03%	56.41	5385	109.055	0.341	8.341
<i>Hoeflea photophotica</i>	DFL-43	19311	4458057	0.30%	0.04%	0.25%	0.04%	59.81	4357	108.587	0.348	8.024
<i>Unnamed Verrucomicrobiae bacterium</i>	DG1235	19391	5770561	0.29%	0.05%	0.29%	0.05%	54.26	4909	110.820	0.347	8.517
<i>Aciduliprofundum boonei</i>	T469	38403	2967866	0.28%	0.04%	0.27%	0.04%	39.14	1544	113.733	0.345	8.992
<i>Neptuniibacter caesariensis</i>	MED92	13561	4039111	0.26%	0.04%	0.24%	0.04%	47.00	3687	111.277	0.341	8.623
<i>Unnamed Rhodobacterales bacterium</i>	HTCC2150	18973	3582902	0.26%	0.05%	0.24%	0.05%	49.06	3667	109.492	0.340	8.413
<i>Planctomyces maris</i>	DSM8797	15662	7775452	0.26%	0.04%	0.24%	0.04%	50.45	6480	111.511	0.364	8.143
<i>Unnamed gammaproteobacterium</i>	NOR51-B	31355	3261541	0.26%	0.04%	0.34%	0.05%	57.00	2930	109.402	0.348	8.190
<i>Leeuwenhoeekia blandsensis</i>	MED217	13573	4238065	0.24%	0.04%	0.26%	0.04%	40.00	3735	112.831	0.328	9.373
<i>Marinobacter algicola</i>	DG893	19321	4412179	0.24%	0.04%	0.23%	0.03%	56.98	4127	110.370	0.366	7.879
<i>Croceibacter atlanticus</i>	HTCC2559	13570	2951152	0.24%	0.07%	0.24%	0.06%	34.00	2702	112.887	0.325	9.470
<i>Plesiocystis pacifica</i>	SIR-1	19341	10585045	0.23%	0.04%	0.20%	0.04%	70.66	8450	107.915	0.370	7.499
<i>Unnamed Actinobacterium</i>	PHSC20c1	13373	2766287	0.23%	0.05%	0.29%	0.05%	59.00	2668	107.336	0.330	8.393
<i>Limnobacter</i> sp.	MED105	19317	3390271	0.22%	0.08%	0.22%	0.08%	52.18	3245	109.910	0.349	8.298
<i>Alcanivorax</i> sp.	DG881	19279	3800634	0.22%	0.03%	0.20%	0.03%	58.23	3337	110.145	0.364	7.927
<i>Unnamed gammaproteobacterium</i>	NOR5-3	31353	4206598	0.21%	0.04%	0.22%	0.04%	56.31	3671	109.624	0.356	7.999
<i>Unnamed Flavobacterium</i>	BAL38	18953	2803466	0.21%	0.06%	0.24%	0.06%	31.43	2612	113.579	0.323	9.735
<i>Reinekea</i> sp.	MED297	13534	4506331	0.21%	0.03%	0.19%	0.03%	52.00	4194	111.149	0.358	8.240
<i>Marinomonas</i> sp.	MED121	13587	5121076	0.21%	0.03%	0.19%	0.03%	42.00	4803	111.532	0.333	8.914
<i>Pedobacter</i> sp.	BAL39	19337	5788054	0.21%	0.03%	0.21%	0.03%	44.92	5101	112.348	0.338	9.045
<i>Unnamed Rhodobacterales bacterium</i>	HTCC2083	13508	4015194	0.20%	0.03%	0.24%	0.03%	53.30	4179	109.163	0.340	8.307
<i>Oceanicoccus alexandrii</i>	HTCC2633	13448	3166372	0.20%	0.04%	0.17%	0.03%	64.00	3028	108.432	0.354	7.921
<i>Carboxydibrachium pacificum</i>	JM (DSM12653)	19289	2311713	0.20%	0.03%	0.15%	0.03%	38.47	1686	112.574	0.322	9.589
<i>Polaribacter dokdonensis</i>	MED152	13543	2967100	0.19%	0.04%	0.22%	0.04%	31.00	2611	113.402	0.329	9.530
<i>Prochlorococcus marinus</i>	MIT9515	13617	1710076	0.19%	0.03%	0.06%	0.02%	30.80	1906	113.389	0.349	8.959
<i>Blastopirellula marina</i>	DSM3645	13488	6653746	0.19%	0.03%	0.19%	0.04%	57.00	5686	110.174	0.367	7.887
<i>Bacillus</i> sp.	SG-1	19283	3944880	0.19%	0.03%	0.15%	0.03%	42.09	4337	112.816	0.330	9.238
<i>Congregibacter litoralis</i>	KT71	13585	4325534	0.19%	0.03%	0.20%	0.03%	58.00	3939	109.721	0.358	7.957
<i>Hydrogenivira</i> sp.	128-5-R1-1	19313	2275409	0.19%	0.03%	0.16%	0.03%	43.00	3808	113.762	0.346	9.094
<i>Roseobacter litoralis</i>	Och 149	19357	4678915	0.18%	0.06%	0.20%	0.06%	57.25	4746	108.882	0.345	8.150
<i>Dokdonia donghaensis</i>	MED134	13544	3298531	0.18%	0.04%	0.20%	0.04%	38.00	2944	112.439	0.323	9.432
<i>Lentisphaera araneosa</i>	HTCC2155	13437	6021958	0.18%	0.03%	0.17%	0.05%	40.95	5104	113.133	0.358	8.563
<i>Microcoleus chthonoplastes</i>	PCC7420	19325	8651623	0.18%	0.05%	0.16%	0.04%	45.43	8294	112.039	0.367	8.227
<i>Roseobacter</i> sp.	AzwK-3b	19361	4209812	0.18%	0.03%	0.20%	0.03%	61.85	4145	108.947	0.365	7.697
<i>Octadecabacter antarcticus</i>	238	19331	5388160	0.18%	0.06%	0.14%	0.05%	55.21	5834	109.637	0.372	7.692
<i>Psychroflexus torquis</i>	ATCC700755	13542	4312844	0.17%	0.04%	0.19%	0.04%	35.26	4032	114.028	0.334	9.366
<i>Lyngbya</i> sp.	PCC8106	13409	7037511	0.17%	0.04%	0.14%	0.04%	41.00	6142	112.420	0.356	8.524
<i>Sagittula stellata</i>	E-37	18971	5261741	0.17%	0.03%	0.18%	0.03%	64.97	5067	108.424	0.354	7.898
<i>Nitrosococcus oceanii</i>	AFC-27	13547	3469829	0.17%	0.03%	0.17%	0.03%	50.31	3396	111.468	0.385	7.776
<i>Marinobacter</i> sp.	ELB17	18955	4893590	0.17%	0.03%	0.16%	0.02%	54.24	4850	110.309	0.369	7.819
<i>Alteromonas macleodii</i>	'deep ecotype'	13374	4408257	0.17%	0.03%	0.16%	0.03%	45.00	4072	110.961	0.338	8.744
<i>Methylophaga thiooxidans</i>	DMS010	19323	3047652	0.17%	0.03%	0.17%	0.03%	46.16	3001	111.287	0.353	8.312
<i>Silicibacter lacuscaeruleus</i>	ITI-1157	37681	3523710	0.16%	0.03%	0.17%	0.03%	63.00	3611	109.031	0.364	7.749
<i>Trichodesmium erythraeum</i>	IMS101	318	7750108	0.16%	0.07%	0.14%	0.06%	34.14	4451	112.960	0.353	8.778
<i>Bermanellia marisrubri</i>	13562	3527084	0.16%	0.03%	0.15%	0.03%	43.96	2542	111.945	0.350	8.511	
<i>Unnamed Rhodobacterales bacterium</i>	HTCC2654	13614	4529231	0.16%	0.03%	0.14%	0.03%	65.00	4500	108.620	0.348	8.064
<i>Unnamed Flavobacterium</i>	SCB49	19389	3202734	0.16%	0.03%	0.18%	0.04%	34.04	2948	112.859	0.318	9.666

Unnamed gammaproteobacterium	HTCC5015	19309	2622479	0.15%	0.03%	0.14%	0.03% 54.05	2459	110.775 0.370 7.881
Aurantimonas sp.	SI85-9A1	13607	4325257	0.15%	0.03%	0.13%	0.02% 67.00	3607	108.005 0.362 7.614
Fulvimarina pelagi	HTCC2506	13506	3800929	0.15%	0.03%	0.12%	0.03% 66.00	3754	108.911 0.358 7.872
Bacillus sp.	NRRL B-14911	13545	5072318	0.15%	0.03%	0.13%	0.03% 45.72	4522	112.049 0.331 9.145
Unnamed Alteromonadales bacterium	TW-7	18465	4101856	0.15%	0.03%	0.12%	0.03% 40.00	3783	111.356 0.331 8.954
Unnamed betaproteobacterium	KB13	13602	1334326	0.15%	0.04%	0.16%	0.04% 35.37	1318	112.884 0.340 9.043
Oceanicola granulosus	HTCC2516	13450	4039111	0.15%	0.03%	0.13%	0.03% 70.00	3784	107.948 0.360 7.665
Cyanothece sp.	CCY0110	18951	5816986	0.14%	0.03%	0.13%	0.03% 36.69	6475	113.223 0.352 8.768
Roseovarius nubinhibens	ISM	13464	3668667	0.14%	0.03%	0.15%	0.03% 65.00	3543	108.611 0.358 7.828
Thermococcus barophilus	MP (DSMZ11836)	19379	2056187	0.14%	0.03%	0.14%	0.03% 41.66	2146	113.483 0.341 9.301
Bacillus sp.	B14905	18949	4495626	0.14%	0.03%	0.12%	0.02% 37.58	4624	112.565 0.326 9.350
Roseovarius sp.	HTCC2601	13574	5425920	0.14%	0.03%	0.15%	0.04% 61.00	5452	108.317 0.354 7.887
Thalassioibium sp.	R2A62	37677	3488453	0.14%	0.03%	0.17%	0.03% 55.00	3696	108.973 0.342 8.255
Nitrococcus mobilis	Nb-231	13475	3617638	0.14%	0.03%	0.13%	0.03% 60.00	3487	110.509 0.420 6.912
Stenotrophomonas sp.	SKA14	19369	5017753	0.13%	0.04%	0.14%	0.03% 66.35	4469	108.696 0.386 7.293
Unnamed Rhodobacteraceae bacterium	KLH11	31351	4486463	0.13%	0.03%	0.15%	0.03% 57.64	4274	109.339 0.357 7.968
Synechococcus sp.	WH8109	37911	2118903	0.13%	0.03%	0.49%	0.07% 60.00	2577	109.490 0.378 7.467
Roseobacter sp.	SK209-2-6	18997	4555826	0.13%	0.02%	0.14%	0.03% 57.05	4537	109.236 0.351 8.095
Roseovarius sp.	TM1035	19363	4209812	0.13%	0.03%	0.13%	0.03% 60.98	4102	108.465 0.358 7.810
Polaribacter irgensii	23-P	13451	2745458	0.13%	0.03%	0.15%	0.03% 35.00	2553	113.088 0.329 9.452
Sphingomonas sp.	SKA58	13584	3948000	0.12%	0.03%	0.10%	0.02% 63.00	3835	108.208 0.371 7.540
Idiomarina baltica	OS145	13408	2715224	0.12%	0.03%	0.11%	0.02% 47.00	2313	111.497 0.367 8.096
Mariprofundus ferrooxydans	PV-1	13615	2869318	0.12%	0.03%	0.10%	0.02% 54.00	2866	110.314 0.364 7.925
Parvularcula bermudensis	HTCC2503	13509	2907177	0.12%	0.03%	0.09%	0.02% 61.00	2733	108.463 0.357 7.901
Nodularia spumigena	CCY9414	13447	5314247	0.12%	0.02%	0.10%	0.02% 42.00	4860	111.841 0.355 8.536
Loktanella vestfoldensis	SKA53	13444	3062158	0.12%	0.03%	0.12%	0.02% 60.00	3067	108.077 0.347 7.999
Moritella sp.	PE36	13535	5164151	0.12%	0.03%	0.12%	0.04% 42.00	4781	111.094 0.329 8.975
Roseobacter sp.	CCS2	18995	3497325	0.12%	0.03%	0.12%	0.03% 55.47	3660	108.795 0.337 8.339
Roseobacter sp.	GAI-101	30723	4521165	0.12%	0.02%	0.11%	0.02% 58.74	4203	108.574 0.341 8.199
Unnamed Flavobacterium	BBFL7	13604	3076732	0.12%	0.03%	0.14%	0.04% 35.00	2587	112.971 0.330 9.280
Synechococcus sp.	WH7805	13553	2618810	0.12%	0.05%	0.12%	0.04% 56.00	2882	109.523 0.381 7.450
Nitrobacter sp.	Nb-311A	13538	4104352	0.12%	0.03%	0.09%	0.02% 62.00	2225	109.079 0.387 7.353
Oceanicola batsensis	HTCC2597	13449	4437668	0.11%	0.03%	0.12%	0.03% 67.00	3373	108.521 0.366 7.647
Unnamed Methylophilales bacterium	HTCC2181	18317	1304428	0.11%	0.02%	0.21%	0.04% 38.00	1338	111.950 0.336 9.009
Erythrobacter litoralis	HTCC2594	13480	3053035	0.11%	0.03%	0.09%	0.02% 63.00	3011	108.642 0.355 7.887
Shewanella benthica	KT99	13387	4325175	0.11%	0.03%	0.13%	0.03% 46.00	4235	111.189 0.342 8.629
Citreicella sp.	SE45	37679	5523231	0.11%	0.02%	0.12%	0.03% 67.00	5427	108.312 0.363 7.694
Roseovarius sp.	217	13576	4762632	0.11%	0.03%	0.11%	0.02% 61.00	4769	108.755 0.361 7.797
Thermococcus sp.	AM4	19381	2084088	0.11%	0.03%	0.11%	0.03% 54.79	2168	112.597 0.355 8.752
Synechococcus sp.	RS9916 (= RCC555)	13557	2664465	0.11%	0.13%	0.08%	0.04% 61.00	2961	109.082 0.378 7.474
Brevundimonas sp.	BAL3	19287	3639246	0.11%	0.02%	0.09%	0.02% 67.37	3470	107.579 0.365 7.544
Synechococcus sp.	PCC7335	19377	5965029	0.11%	0.02%	0.10%	0.02% 48.24	5586	110.709 0.350 8.415
Unnamed Rhodobacterales bacterium	Y4I	19349	4344244	0.10%	0.02%	0.12%	0.02% 64.43	4133	108.345 0.355 7.911
Octadecabacter antarcticus	307	19333	4892946	0.10%	0.02%	0.11%	0.02% 54.62	5495	109.484 0.361 7.885
Silicibacter sp.	TrichCH4B	37909	4689084	0.10%	0.03%	0.12%	0.03% 59.00	4735	109.008 0.359 7.891
Erythrobacter sp.	NAP1	13512	3264238	0.10%	0.02%	0.09%	0.02% 61.00	3177	108.514 0.346 8.084
Prochlorococcus marinus	NATL2A	13911	1842899	0.10%	0.04%	0.07%	0.04% 35.12	2162	112.171 0.345 8.822
Photobacterium profundum	3TCK	13563	6096989	0.10%	0.02%	0.08%	0.02% 42.00	5407	111.210 0.333 8.887
Synechococcus sp.	RS9917 (= RCC556)	13555	2579542	0.10%	0.08%	0.08%	0.06% 61.00	2770	109.159 0.396 7.158
Roseobacter sp.	MED193	13590	4652716	0.09%	0.02%	0.10%	0.02% 58.00	3999	108.984 0.349 8.097
Ruegeria sp.	R11	13635	3821839	0.09%	0.02%	0.09%	0.02% 60.01	3656	108.629 0.352 7.955
Vibrio shilonii	AK1	13937	5698984	0.09%	0.02%	0.08%	0.02% 43.98	5360	111.226 0.333 8.848
Erythrobacter sp.	SD-21	19305	2969154	0.09%	0.02%	0.08%	0.02% 62.86	2941	108.799 0.358 7.840
Oceanibulbus indolifex	HEL-45	19327	4105524	0.09%	0.02%	0.10%	0.03% 59.52	4153	108.645 0.347 8.009
Caminibacter mediatlanticus	TB-2 DSM16658	19293	1662141	0.08%	0.02%	0.07%	0.02% 27.13	1826	114.889 0.331 9.822
Carnobacterium sp.	AT7	19299	2442118	0.08%	0.02%	0.07%	0.02% 35.34	2388	112.373 0.314 9.659
Prochlorococcus marinus	MIT9211	13551	1688863	0.07%	0.03%	0.04%	0.02% 39.00	1855	111.513 0.353 8.512
Vibrio campbellii	AND4	13564	4254674	0.07%	0.03%	0.07%	0.04% 44.66	3935	111.554 0.344 8.662
Vibrio alginolyticus	12G01	13571	5152585	0.06%	0.02%	0.05%	0.02% 45.00	4655	111.517 0.339 8.748
Prochlorococcus marinus	MIT9303	13496	2681398	0.06%	0.04%	0.06%	0.05% 50.02	2997	110.167 0.373 7.735
Phaeobacter gallaeciensis	BS107	19355	4231299	0.06%	0.02%	0.08%	0.02% 59.81	4059	108.718 0.354 7.912
Psychromonas sp.	CNPT3	13583	2937686	0.06%	0.02%	0.06%	0.02% 39.00	2697	111.871 0.340 8.859
Synechococcus sp.	BL107	13559	2283377	0.06%	0.02%	0.09%	0.02% 55.00	2507	109.810 0.376 7.617
Vibrio splendidus	12B01	13568	5587386	0.05%	0.04%	0.05%	0.04% 46.00	5067	111.462 0.335 8.852
Vibrio parahaemolyticus	16	19395	4523781	0.05%	0.02%	0.05%	0.01% 46.00	4035	111.339 0.339 8.706
Photobacterium sp.	SKA34	13566	4945266	0.05%	0.02%	0.04%	0.02% 41.00	4310	111.708 0.342 8.724
Prochlorococcus marinus	NATL1A	15660	1865534	0.05%	0.02%	0.03%	0.02% 35.02	2193	112.214 0.345 8.776
Sulfitobacter sp.	NAS-14.1	13591	4002069	0.05%	0.02%	0.05%	0.02% 61.00	3431	108.745 0.350 8.027
Phaeobacter gallaeciensis	2.1	19353	4157399	0.05%	0.01%	0.05%	0.02% 60.00	3948	108.622 0.352 7.945
Unnamed Vibionales bacterium	SWAT-3	19399	5830607	0.04%	0.02%	0.05%	0.02% 44.48	5408	111.521 0.337 8.769
Synechococcus sp.	WH5701	13554	2858742	0.04%	0.01%	0.04%	0.01% 66.00	3127	108.612 0.383 7.371
Sulfitobacter sp.	EE-36	13501	3547243	0.04%	0.02%	0.04%	0.01% 61.00	2975	108.551 0.344 8.120
Cyanobium sp.	PCC7001	19301	2832412	0.04%	0.01%	0.03%	0.01% 68.74	2771	108.041 0.387 7.236
Prochlorococcus marinus	CCMP1375	419	1751080	0.04%	0.01%	0.02%	0.01% 36.44	1883	111.659 0.352 8.541
Vibrio angustum	S14	13567	5082513	0.04%	0.03%	0.04%	0.02% 40.00	4430	111.542 0.339 8.766
Prochlorococcus marinus	MIT9313	220	2410873	0.03%	0.02%	0.02%	0.02% 50.74	2269	109.954 0.373 7.712
Pseudoalteromonas tunicata	D2	13456	4973283	0.03%	0.01%	0.03%	0.01% 40.00	1374	111.611 0.333 9.000
Vibrio sp.	MED222	13616	4882030	0.03%	0.01%	0.03%	0.02% 45.00	4525	111.404 0.334 8.856