Table S1.

(A). Gene number (predicted for ancestral nodes), and predicted number of gene families gained, lost, expanded, and contracted in the Roseobacter and SAR11 clade genomes. The ancestral reconstruction is based on an alphaproteobacterial tree estimated using the NDCH model in P4. Note that the gain of a gene family or expansion of an existing gene family could be a result of either lateral gene transfer or gene duplication. The relative contribution of these two mechanisms is presented in Fig. 3.

Node	Gene #	Gain	Loss	Expansion	Contraction
Phaeobacter gallaeciensis BS107	4220	294	135	48	8
Jannaschia sp. CCS1	4369	491	4332	84	194
Dinoroseobacter shibae DFL 12	3743	281	4900	50	197
Ruegeria pomeroyi DSS-3	3954	211	2072	60	100
Sulfitobacter sp. EE36	3680	161	301	28	15
Roseobacter sp. GAI101	4325	452	1025	108	63
Oceanibulbus indolifex HEL-45	4245	501	1329	108	69
Rhodobacteraceae bacterium HTCC2083	4281	687	4512	77	202
Rhodobacterales bacterium HTCC2255	2327	165	5556	47	110
Roseovarius nubinhibens ISM	3662	278	1963	69	90
Rhodobacteraceae bacterium KLH11	4332	715	572	101	23
Roseobacter sp. MED193	4675	543	631	112	67
Sulfitobacter sp. NAS-14.1	4019	284	123	112	4
Octadecabacter arcticus 238	4730	1039	602	247	11
Octadecabacter antarcticus 307	5011	1197	509	221	6
Oceanicola batsensis HTCC2597	4297	519	3957	105	194
Roseobacter denitrificans OCh114	4148	288	527	43	37
Roseobacter litoralis Och149	4872	553	149	88	3
Oceanicola granulosus HTCC2516	3857	427	4434	111	170
Phaeobacter gallaeciensis 2.10	4154	245	145	25	6
Ruegeria sp. R11	3858	291	531	39	32
Pelagibaca bermudensis HTCC2601	5448	872	694	171	61
Roseobacter sp. R2A57	4522	944	4440	98	177
Thalassiobium sp. R2A62	3818	591	1514	78	79
Roseobacter sp. AzwK-3b	4143	591	1512	113	78
Rhodobacterales bacterium HTCC2150	3770	489	5133	72	203
Maritimibacter alkaliphilus HTCC2654	4792	865	4330	140	189
Roseobacter sp. CCS2	3849	440	542	58	27
Roseovarius sp. 217	4822	545	263	136	4
Roseobacter sp. SK209-2-6	4646	573	687	83	33

Citreicella sp. SE45	5488	876	662	147	57
Loktanella sp. SE62	4757	867	898	105	56
Loktanella vestfoldensis SKA53	3191	249	936	68	39
Ruegeria lacuscaerulensis ITI-1157	3847	383	671	30	48
Sagittula stellata E-37	5100	686	1346	131	121
Roseovarius sp. TM1035	4269	369	579	74	36
Ruegeria sp. TM1040	3187	192	1051	30	42
Ruegeria sp. TrichCH4B	4922	820	137	96	3
Phaeobacter sp. Y4I	4284	394	1990	55	130
R1	4041	125	204	13	13
R2	4128	24	1319	2	83
R3	4769	21	454	0	13
R4	5810	0	42	0	2
R5	4154	59	1733	0	119
R6	6065	0	0	0	0
R7	6075	60	426	6	9
R8	4168	22	680	0	33
R9	6013	6	141	0	3
R10	6589	20	1589	13	49
R11	3838	63	1060	4	54
R12	4961	13	129	0	0
R13	5173	24	2802	8	112
R14	4417	153	3853	29	252
R15	8596	5	0	0	0
R16	8584	0	0	0	0
R17	8644	3	0	2	0
R18	5248	122	630	21	22
R19	5840	73	2326	13	73
R20	8689	0	0	0	0
R21	4502	123	516	25	35
R22	5159	0	119	0	1
R23	5469	24	284	1	10
R24	8134	3	1	4	0
R25	8454	0	2	0	1
R26	8689	32	76	3	2
R27	4237	122	539	0	24
R28	4766	5	478	0	5
R29	3915	0	323	1	5
R30	4760	67	922	1	8
R31	7391	0	3	1	0
R32	8341	19	155	0	9
R33	8957	5	0	0	0
R34	8680	0	1	0	0

R35	8935	0	0	0	0
R36	8935	0	24	0	1
R37	8986	292	2	1	0
R38	8374	127	1179	30	44
alpha proteobacterium HIMB5	1588	198	300	18	8
alpha proteobacterium HIMB114	1353	73	137	12	5
Alphaproteobacterium HIMB59	1625	247	647	20	20
Candidatus Pelagibacter ubique HTCC1002	1441	49	44	5	0
Candidatus Pelagibacter ubique HTCC1062	1408	16	40	4	1
Candidatus Pelagibacter sp. HTCC7211	1489	95	285	22	5
Candidatus Pelagibacter sp. IMCC9063	1498	219	154	15	1
S52	1425	0	465	2	8
S53	1435	45	297	1	6
S54	1703	0	3	0	0
S55	1712	1	209	0	1
S56	1953	172	284	0	4
S57	2045	35	210	5	2

(B) Gene number (predicted for ancestral nodes), and predicted number of gene families gained, lost, expanded, and contracted in the Roseobacter and SAR11 clade genomes. The ancestral reconstruction is based on an alphaproteobacterial tree estimated using RAxML. Note that the gain of a gene family or expansion of an existing gene family could be a result of either lateral gene transfer or gene duplication. The relative contribution of these two mechanisms is presented in Fig. S3.

Node	Gene #	Gain	Loss	Expansion	Contraction
Phaeobacter gallaeciensis BS107	4220	280	137	49	8
Jannaschia sp. CCS1	4369	519	3047	93	88
Dinoroseobacter shibae DFL 12	3743	287	3371	67	106
Ruegeria pomeroyi DSS-3	3954	210	2070	62	91
Sulfitobacter sp. EE36	3680	161	300	29	15
Roseobacter sp. GAI101	4325	456	1019	109	65
Oceanibulbus indolifex HEL-45	4245	499	1324	112	66
Rhodobacteraceae bacterium HTCC2083	4281	688	4552	80	184
Rhodobacterales bacterium HTCC2255	2327	166	5364	48	103
Roseovarius nubinhibens ISM	3662	279	1867	71	79
Rhodobacteraceae bacterium KLH11	4332	719	569	103	23
Roseobacter sp. MED193	4675	546	630	113	67
Sulfitobacter sp. NAS-14.1	4019	285	123	112	3
Octadecabacter arcticus 238	4730	1043	595	251	11
Octadecabacter antarcticus 307	5011	1204	505	223	5
Oceanicola batsensis HTCC2597	4297	525	1103	85	89
Roseobacter denitrificans OCh114	4148	288	529	42	37
Roseobacter litoralis Och149	4872	551	149	87	4
Oceanicola granulosus HTCC2516	3857	445	3472	120	124
Phaeobacter gallaeciensis 2.10	4154	243	159	25	5
Ruegeria sp. R11	3858	287	536	39	32
Pelagibaca bermudensis HTCC2601	5448	876	690	171	57
Roseobacter sp. R2A57	4522	940	4729	96	184
Thalassiobium sp. R2A62	3818	595	1439	77	70
Roseobacter sp. AzwK-3b	4143	590	1486	115	73
Rhodobacterales bacterium HTCC2150	3770	492	5003	75	176
Maritimibacter alkaliphilus HTCC2654	4792	924	1062	114	93
Roseobacter sp. CCS2	3849	442	523	59	26
Roseovarius sp. 217	4822	547	263	138	4
Roseobacter sp. SK209-2-6	4646	573	683	85	35
Citreicella sp. SE45	5488	880	658	153	56
Loktanella sp. SE62	4757	871	895	103	49
Loktanella vestfoldensis SKA53	3191	254	920	68	39

Ruegeria lacuscaerulensis ITI-1157	3847	385	666	31	47
Sagittula stellata E-37	5100	694	1351	140	119
Roseovarius sp. TM1035	4269	369	577	74	34
Ruegeria sp. TM1040	3187	193	1046	26	43
Ruegeria sp. TrichCH4B	4922	825	136	93	4
Phaeobacter sp. Y4I	4284	394	1988	58	123
R1	4059	125	206	12	14
R2	4138	23	1661	2	101
R3	4761	21	772	0	19
R4	4147	62	1678	1	109
R5	5988	0	0	0	0
R6	6038	0	17	0	1
R7	6076	67	435	7	8
R8	4162	22	682	0	34
R9	6024	6	131	0	3
R10	6581	16	1582	12	45
R11	4419	153	3890	29	224
R12	3836	64	1053	4	51
R13	4951	13	128	0	0
R14	5170	24	2774	7	105
R15	8635	5	0	0	0
R16	8625	0	0	2	0
R17	8718	3	0	1	0
R18	4499	129	511	27	34
R19	5127	0	123	0	2
R20	5405	25	1786	3	22
R21	5236	126	624	21	21
R22	5817	75	532	10	2
R23	4863	0	1139	14	14
R24	7077	2	178	0	9
R25	8582	1	7	2	1
R26	8778	1	0	0	0
R27	8773	37	37	9	1
R28	3898	0	338	1	6
R29	4749	67	636	1	7
R30	7189	0	1	0	0
R31	4225	127	513	0	21
R32	4689	5	1161	0	6
R33	7984	18	194	2	8
R34	8799	1	0	0	0
R35	7170	5	51	0	0
R36	8793	0	18	0	1

R37	8838	301	2	0	0
R38	8153	132	1115	57	32
alpha proteobacterium HIMB5	1588	205	287	18	10
alpha proteobacterium HIMB114	1353	74	128	13	5
alpha proteobacterium HIMB59	1625	253	565	16	23
Candidatus Pelagibacter ubique	1441	51	41	5	1
Candidatus Pelagibacter ubique	1408	19	38	3	1
Candidatus Pelagibacter sp. HTCC7211	1489	102	272	20	6
Candidatus Pelagibacter sp. IMCC9063	1498	228	153	15	0
S52	1680	0	3	0	0
S53	1429	50	283	0	6
S54	1688	1	174	0	2
S55	1414	0	441	2	10
S56	1912	186	255	0	0
S57	1954	38	104	49	1

(C) Gene number (predicted for ancestral nodes), and predicted number of gene families gained, lost, expanded, and contracted in the Roseobacter and SAR11 clade genomes. The ancestral reconstruction is based on an alphaproteobacterial tree estimated using the CAT model in PhyloBayes. Note that the gain of a gene family or expansion of an existing gene family could be a result of either lateral gene transfer or gene duplication. The relative contribution of these two mechanisms is presented in Fig. S3.

Node	Gene #	Gain	Loss	Expansion	Contraction
Phaeobacter gallaeciensis BS107	4220	294	134	49	5
Jannaschia sp. CCS1	4369	524	4328	93	174
Dinoroseobacter shibae DFL 12	3743	289	4650	54	151
Ruegeria pomeroyi DSS-3	3954	215	2027	65	86
Sulfitobacter sp. EE36	3680	164	298	29	16
Roseobacter sp. GAI101	4325	460	998	109	60
Oceanibulbus indolifex HEL-45	4245	506	1311	112	64
Rhodobacteraceae bacterium	4281	690	4547	77	179
Rhodobacterales bacterium	2327	169	5208	48	91
Roseovarius nubinhibens ISM	3662	283	1838	72	82
Rhodobacteraceae bacterium KLH11	4332	731	566	102	22
Roseobacter sp. MED193	4675	554	612	113	64
Sulfitobacter sp. NAS-14.1	4019	287	120	111	3
Octadecabacter arcticus 238	4730	1050	589	248	10
Octadecabacter antarcticus 307	5011	1210	498	223	6
Oceanicola batsensis HTCC2597	4297	530	1009	83	60
Roseobacter denitrificans OCh114	4148	290	524	42	35
Roseobacter litoralis Och149	4872	556	147	89	4
Oceanicola granulosus HTCC2516	3857	463	3439	120	112
Phaeobacter gallaeciensis 2.10	4154	246	145	28	5
Ruegeria sp. R11	3858	291	529	39	31
Pelagibaca bermudensis HTCC2601	5448	887	685	173	55
Roseobacter sp. R2A57	4522	953	4391	97	171
Thalassiobium sp. R2A62	3818	599	1410	79	66
Roseobacter sp. AzwK-3b	4143	598	1455	115	71
Rhodobacterales bacterium	3770	500	4882	78	165
Maritimibacter alkaliphilus	4792	925	964	116	68
Roseobacter sp. CCS2	3849	445	514	62	24
Roseovarius sp. 217	4822	554	263	138	4
Roseobacter sp. SK209-2-6	4646	589	673	87	33
Citreicella sp. SE45	5488	885	647	155	52
Loktanella sp. SE62	4757	881	883	108	45
Loktanella vestfoldensis SKA53	3191	255	909	68	35

Ruegeria lacuscaerulensis ITI-1157	3847	388	654	31	44
Sagittula stellata E-37	5100	702	1312	144	109
Roseovarius sp. TM1035	4269	369	570	74	34
Ruegeria sp. TM1040	3187	197	1034	27	42
Ruegeria sp. TrichCH4B	4922	837	132	96	4
Phaeobacter sp. Y4I	4284	396	1929	58	114
R1	4040	127	202	12	14
R2	4126	23	1616	2	100
R3	4732	21	724	0	18
R4	4129	62	1633	1	109
R5	5923	0	0	0	0
R6	5953	0	20	0	1
R7	6005	71	411	10	11
R8	4144	22	680	0	38
R9	5966	6	104	0	3
R10	6491	20	1366	10	37
R11	3831	68	1036	4	50
R12	4921	13	138	0	0
R13	5145	23	2675	6	100
R14	4412	158	3748	30	216
R15	8461	5	0	0	0
R16	8457	3	16	0	1
R17	8614	0	0	0	0
R18	4494	133	496	27	33
R19	5078	0	131	0	4
R20	5374	26	1705	3	22
R21	5217	127	617	20	22
R22	5783	76	1866	11	37
R23	8361	0	0	0	0
R24	4788	0	2527	14	54
R25	8384	0	0	0	0
R26	8418	2	40	0	1
R27	8614	33	38	24	0
R28	4210	128	500	0	18
R29	4655	5	1165	0	6
R30	3885	0	362	1	6
R31	4727	69	650	1	5
R32	7130	0	1	0	0
R33	7874	20	188	2	8
R34	8649	3	0	0	0
R35	8635	0	0	0	0
R36	8634	0	18	0	1

R37	8688	278	3	1	0
R38	7976	136	1039	24	17
alpha proteobacterium HIMB5	1588	213	281	18	8
alpha proteobacterium HIMB114	1353	76	126	12	5
alpha proteobacterium HIMB59	1625	268	542	23	11
Candidatus Pelagibacter ubique	1441	53	41	5	0
Candidatus Pelagibacter ubique	1408	19	36	4	1
Candidatus Pelagibacter sp.	1489	105	261	22	5
Candidatus Pelagibacter sp.	1498	230	151	15	1
S49	1409	0	432	2	8
S50	1427	50	270	0	6
S51	1665	0	4	0	0
S52	1676	1	171	0	2
S53	1902	190	245	0	1
S54	1928	39	4285	8	45