



Figure S1. Alphaproteobacterial branch order frequencies. Each observed tree is shown with an associated table below for the corresponding missing data percentage(s) (rows) and gap-removal parameter(s) (columns: C- conservative, L- liberal, R- remgaps). † - Rhodospirillales paraphyletic. Totals for branch order are in the box at bottom right. * - bootstrap support for that node < 51%. Ana- Anaplasmataceae, Rick- Rickettsiaceae, Rhodosp- Rhodospirillales, Sph- Sphingomonadales, CHP- Caulobacterales, Hyphomonadaceae, Parvularculales, Rhod- Rhodobacteraceae.

Table S1. Bacterial taxa used in the analyses represented in Figs. 1a, 4, S1

NCBI taxon ID	Complete	Strain	Family	Order	Class	Protein coding	G+C %
573065	no	Asticcacaulis excentricus CB 48	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	3842	59.52
190650	yes	Caulobacter crescentus CB15	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	3737	67.21
565050	yes	Caulobacter crescentus NA1000	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	3876	67.17
366602	yes	Caulobacter sp. K31	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	5443	67.35
450851	yes	Phenylobacterium zucineum HLK1	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	3854	71.1
314260	no	Parvularcula bermudensis HTCC2503	Parvularculaceae	Parvularculales	Alphaproteobacteria	2733	60.66
314269	no	Aurantimonas sp. SI85-9A1	Aurantimonadaceae	Rhizobiales	Alphaproteobacteria	3650	66.74
314231	no	Fulvimarina pelagi HTCC2506	Aurantimonadaceae	Rhizobiales	Alphaproteobacteria	3754	61.23
360095	yes	Bartonella bacilliformis KC583	Bartonellaceae	Rhizobiales	Alphaproteobacteria	1322	38.24
634504	yes	Bartonella grahamii as4aup	Bartonellaceae	Rhizobiales	Alphaproteobacteria	1768	38.04
283166	yes	Bartonella henselae Houston-1	Bartonellaceae	Rhizobiales	Alphaproteobacteria	1611	38.23
283165	yes	Bartonella quintana Toulouse	Bartonellaceae	Rhizobiales	Alphaproteobacteria	1306	38.8
382640	yes	Bartonella tribocorum CIP 105476	Bartonellaceae	Rhizobiales	Alphaproteobacteria	2121	38.82
395963	yes	Beijerinckia indica indica ATCC 9039	Beijerinckiaceae	Rhizobiales	Alphaproteobacteria	3788	59.68
395965	yes	Methylocella silvestris BL2	Beijerinckiaceae	Rhizobiales	Alphaproteobacteria	3917	63.08
224911	yes	Bradyrhizobium japonicum USDA 110	Bradyrhizobiaceae	Rhizobiales	Alphaproteobacteria	8317	64.06
288000	yes	Bradyrhizobium sp. BTAi1	Bradyrhizobiaceae	Rhizobiales	Alphaproteobacteria	7741	64.81
323097	yes	Nitrobacter hamburgensis X14	Bradyrhizobiaceae	Rhizobiales	Alphaproteobacteria	4673	61.62
323098	yes	Nitrobacter winogradskyi Nb-255	Bradyrhizobiaceae	Rhizobiales	Alphaproteobacteria	3143	62.05
504832	yes	Oligotropha carboxidovorans OM5	Bradyrhizobiaceae	Rhizobiales	Alphaproteobacteria	3722	62.4
395960	yes	Rhodopseudomonas palustris TIE-1	Bradyrhizobiaceae	Rhizobiales	Alphaproteobacteria	5318	64.86
430066	yes	Brucella abortus S19	Bruceaceae	Rhizobiales	Alphaproteobacteria	3000	57.22
483179	yes	Brucella canis ATCC 23365	Bruceaceae	Rhizobiales	Alphaproteobacteria	3335	57.24
546272	yes	Brucella melitensis ATCC 23457	Bruceaceae	Rhizobiales	Alphaproteobacteria	3136	57.22
568815	yes	Brucella microti CCM 4915	Bruceaceae	Rhizobiales	Alphaproteobacteria	3282	57.25
444178	yes	Brucella ovis ATCC 25840	Bruceaceae	Rhizobiales	Alphaproteobacteria	3112	57.19
470137	yes	Brucella suis ATCC 23445	Bruceaceae	Rhizobiales	Alphaproteobacteria	3346	57.21
439375	yes	Ochrobactrum anthropi ATCC 49188	Bruceaceae	Rhizobiales	Alphaproteobacteria	4856	56.13
641118	no	Ochrobactrum intermedium LMG 3301	Bruceaceae	Rhizobiales	Alphaproteobacteria	4363	57.74
582899	no	Hyphomicrobium denitrificans ATCC 51888	Hyphomicrobiaceae	Rhizobiales	Alphaproteobacteria	3495	60.84
440085	yes	Methylobacterium chloromethanicum	Methylobacteriaceae	Rhizobiales	Alphaproteobacteria	5771	68.08

CM4							
272630	yes	Methylobacterium extorquens AM1	Methylobacteriaceae	Rhizobiales	Alphaproteobacteria	6216	68.48
460265	yes	Methylobacterium nodulans ORS 2060	Methylobacteriaceae	Rhizobiales	Alphaproteobacteria	8791	68.44
441620	yes	Methylobacterium populi BJ001	Methylobacteriaceae	Rhizobiales	Alphaproteobacteria	5464	69.36
426355	yes	Methylobacterium radiotolerans JCM 2831	Methylobacteriaceae	Rhizobiales	Alphaproteobacteria	6431	71.04
411684	no	Hoeflea phototrophica DFL-43	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	4357	59.81
266835	yes	Mesorhizobium loti MAFF303099	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	7272	62.51
402881	yes	Parvibaculum lavamentivorans DS-1	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	3654	62.33
311403	yes	Agrobacterium radiobacter K84	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	6684	59.87
176299	yes	Agrobacterium tumefaciens C58 (Cereon)	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	5288	59.04
311402	yes	Agrobacterium vitis S4	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	5389	57.47
537021	yes	Candidatus Liberibacter asiaticus str. psy62	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	1109	36.48
347834	yes	Rhizobium etli CFN 42	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	6030	61.03
395492	yes	Rhizobium leguminosarum bv. trifolii WSM2304	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	6581	61.18
366394	yes	Sinorhizobium medicae WSM419	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	6518	61.15
266834	yes	Sinorhizobium meliloti 1021	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	6212	62.17
438753	yes	Azorhizobium caulinodans ORS 571	Xanthobacteraceae	Rhizobiales	Alphaproteobacteria	4717	67.32
78245	yes	Xanthobacter autotrophicus Py2	Xanthobacteraceae	Rhizobiales	Alphaproteobacteria	5095	67.35
582402	yes	Hirschia baltica ATCC 49814	Hyphomonadaceae	Rhodobacterales	Alphaproteobacteria	3222	45.19
228405	yes	Hyphomonas neptunium ATCC 15444	Hyphomonadaceae	Rhodobacterales	Alphaproteobacteria	3520	61.93
394221	yes	Maricaulis maris MCS10	Hyphomonadaceae	Rhodobacterales	Alphaproteobacteria	3079	62.73
314254	no	Oceanicaulis alexandrii HTCC2633	Hyphomonadaceae	Rhodobacterales	Alphaproteobacteria	3029	63.59
398580	yes	Dinoroseobacter shibae DFL 12	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4219	65.52
290400	yes	Jannaschia sp. CCS1	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4283	62.24
314232	no	Loktanella vestfoldensis SKA53	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3068	59.96
391624	no	Oceanibulbus indolifex HEL-45	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4153	59.52
252305	no	Oceanicola batsensis HTCC2597	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4212	66.1
314256	no	Oceanicola granulosus HTCC2516	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3792	70.41
318586	yes	Paracoccus denitrificans PD1222	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	5077	66.7
383629	no	Phaeobacter gallaeciensis 2.10	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3948	59.78
391619	no	Phaeobacter gallaeciensis BS107	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4059	59.81
349102	yes	Rhodobacter sphaeroides ATCC 17025	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4397	68.23
388401	no	Rhodobacterales bacterium HTCC2150	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3667	49.05
314271	no	Rhodobacterales bacterium HTCC2654	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4712	64.13

373154	no	Rhodobacterales sp. HTCC2255	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4507	38.9
375451	yes	Roseobacter denitrificans OCH 114	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4146	58.88
391595	no	Roseobacter litoralis Och 149	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4746	57.25
89187	no	Roseovarius nubinhibens ISM	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3547	63.91
314265	no	Roseovarius sp. HTCC2601	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	5452	66.44
391613	no	Roseovarius sp. TM1035	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4102	60.98
388399	no	Sagittula stellata E-37	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	5067	65.05
246200	yes	Silicibacter pomeroyi DSS-3	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4283	64.07
292414	yes	Silicibacter sp. TM1040	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3870	60.06
384765	no	Stappia aggregata IAM 12614	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	6314	59.38
52598	no	Sulfitobacter sp. EE-36	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3474	60.31
314267	no	Sulfitobacter sp. NAS-14.1	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3962	60.05
634452	yes	Acetobacter pasteurianus IFO 3283-01	Acetobacteraceae	Rhodospirillales	Alphaproteobacteria	3050	53.1
349163	yes	Acidiphilium cryptum JF-5	Acetobacteraceae	Rhodospirillales	Alphaproteobacteria	3637	67.1
272568	yes	Gluconacetobacter diazotrophicus PAI 5	Acetobacteraceae	Rhodospirillales	Alphaproteobacteria	3566	66.32
290633	yes	Gluconobacter oxydans 621H	Acetobacteraceae	Rhodospirillales	Alphaproteobacteria	2664	60.82
391165	yes	Granulobacter bethesdensis CGDNIH1	Acetobacteraceae	Rhodospirillales	Alphaproteobacteria	2437	59.07
	yes	Candidatus Puniceispirillum marinum IMCC1322	Rhodospirillaceae	Rhodospirillales	Alphaproteobacteria	2546	48.85
342108	yes	Magnetospirillum magneticum AMB-1	Rhodospirillaceae	Rhodospirillales	Alphaproteobacteria	4559	65.09
331869	no	Nisaea sp. BAL199	Rhodospirillaceae	Rhodospirillales	Alphaproteobacteria	6128	65.02
414684	yes	Rhodospirillum centenum SW	Rhodospirillaceae	Rhodospirillales	Alphaproteobacteria	4002	70.46
269796	yes	Rhodospirillum rubrum ATCC 11170	Rhodospirillaceae	Rhodospirillales	Alphaproteobacteria	3850	65.38
320483	yes	Anaplasma marginale Florida	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	940	49.77
234826	yes	Anaplasma marginale St. Maries	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	963	49.76
212042	yes	Anaplasma phagocytophilum HZ	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	1291	41.64
269484	yes	Ehrlichia canis Jake	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	942	28.96
332415	no	Ehrlichia chaffeensis Sapulpa	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	805	29.98
302409	yes	Ehrlichia ruminantium Gardel	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	950	27.41
434131	yes	Neorickettsia risticii str. Illinois	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	892	41.27
222891	yes	Neorickettsia sennetsu Miyayama	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	935	41.08
314261	yes	HTCC1062	Pelagibacteraceae	Rickettsiales	Alphaproteobacteria	1393	29.76
335992	yes	HTCC1002	Pelagibacteraceae	Rickettsiales	Alphaproteobacteria	1354	29.68
439493	yes	HTCC7211	Pelagibacteraceae	Rickettsiales	Alphaproteobacteria	1541	29.03
198252	no	HTCC9565	Pelagibacteraceae	Rickettsiales	Alphaproteobacteria	1352	28.93
684719	no	HIMB114	Pelagibacteraceae	Rickettsiales	Alphaproteobacteria	1321	29.59

28211	no	HIMB5	Pelagibacteraceae	Rickettsiales	Alphaproteobacteria	1431	28.63
744985	no	HIMB59			Alphaproteobacteria	1393	32.26
357244	yes	Orientia tsutsugamushi Boryong	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	2141	30.53
334380	yes	Orientia tsutsugamushi Ikeda	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1967	30.51
347255	yes	Rickettsia africae ESF-5	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1041	32.41
293614	yes	Rickettsia akari Hartford	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1259	32.33
391896	yes	Rickettsia bellii OSU 85-389	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1476	31.63
293613	yes	Rickettsia canadensis McKiel	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1093	31.05
272944	yes	Rickettsia conorii Malish 7	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1376	32.44
315456	yes	Rickettsia felis URRWXCa2	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1512	32.51
416276	yes	Rickettsia massiliae MTU5	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1396	32.53
562019	yes	Rickettsia peacockii str. Rustic	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	947	32.6
272947	yes	Rickettsia prowazekii Madrid E	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	835	29
392021	yes	Rickettsia rickettsii Sheila Smith	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1345	32.47
272951	no	Rickettsia sibirica 246	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1234	32.47
257363	yes	Rickettsia typhi Wilmington	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	880	28.92
569881	no	Wolbachia endosymbiont of Culex quinquefasciatus JHB	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1378	34.19
163164	yes	Wolbachia endosymbiont of Drosophila melanogaster	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1268	35.23
292805	yes	Wolbachia endosymbiont TRS of Brugia malayi	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	900	34.18
955	yes	Wolbachia pipientis wPip	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1275	34.19
66084	yes	Wolbachia sp. wRi	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1150	35.16
314225	yes	Erythrobacter litoralis HTCC2594	Erythrobacteraceae	Sphingomonadales	Alphaproteobacteria	3011	63.07
237727	no	Erythrobacter sp. NAP1	Erythrobacteraceae	Sphingomonadales	Alphaproteobacteria	3177	60.97
279238	yes	Novosphingobium aromaticivorans DSM 12444	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	3957	65.11
314266	no	Sphingomonas sp. SKA58	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	3914	63.19
392499	yes	Sphingomonas wittichii RW1	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	5399	67.9
317655	yes	Sphingopyxis alaskensis RB2256	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	3208	65.46
264203	yes	Zymomonas mobilis mobilis ZM4	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	1998	46.33
		outgroup					
243231	yes	Geobacter sulfurreducens PCA	Geobacteraceae	Desulfuromonadales	Deltaproteobacteria	3465	60.94
316385	yes	Escherichia coli K12 DH10B	Enterobacteriaceae	Enterobacterales	Gammaproteobacteria	4126	50.78

243365	yes	Chromobacterium violaceum ATCC 12472	Neisseriaceae	Neisseriales	Betaproteobacteria	4407	64.83	
272843	yes	Pasteurella multocida multocida Pm70	Pasteurellaceae	Pasteurellales	Gammaproteobacteria	2015	40.4	
196600	yes	Vibrio vulnificus YJ016	Vibrionaceae	Vibrionales	Gammaproteobacteria	5024	46.68	
267608	yes	Ralstonia solanacearum GMI1000	Burkholderiaceae	Burkholderiales	Betaproteobacteria	5120	66.98	
							55.1	avg
		low GC outgroup						
641147	no	Simonsiella muelleri ATCC 29453	Neisseriaceae	Neisseriales	Betaproteobacteria	2416	41.33	
583345	yes	Methylotenera mobilis JLW8	Methylophilaceae	Methylophilales	Betaproteobacteria	2348	45.51	
272843	yes	Pasteurella multocida multocida Pm70	Pasteurellaceae	Pasteurellales	Gammaproteobacteria	2015	40.4	
233412	yes	Haemophilus ducreyi 35000HP	Pasteurellaceae	Pasteurellales	Gammaproteobacteria	1762	38.22	
412965	yes	Candidatus Vesicomysocius okutanii HA			Gammaproteobacteria	939	31.59	
363253	yes	Lawsonia intracellularis PHE/MN1-00	Desulfovibrionaceae	Desulfovibrionales	Deltaproteobacteria	1344	33.08	
							38.4	avg
		high GC outgroup						
290397	yes	Anaeromyxobacter dehalogenans 2CP-C	Myxococcaceae	Myxococcales	Deltaproteobacteria	4361	74.91	
243365	yes	Chromobacterium violaceum ATCC 12472	Neisseriaceae	Neisseriales	Betaproteobacteria	4407	64.83	
267608	yes	Ralstonia solanacearum GMI1000	Burkholderiaceae	Burkholderiales	Betaproteobacteria	5120	66.98	
208964	yes	Pseudomonas aeruginosa PAO1	Pseudomonadaceae	Pseudomonadales	Gammaproteobacteria	5568	66.56	
190485	yes	Xanthomonas campestris pv. campestris ATCC 33913	Xanthomonadaceae	Xanthomonadales	Gammaproteobacteria	4181	65.07	
349124	yes	Halorhodospira halophila SL1	Ectothiorhodospiraceae	Chromatiales	Gammaproteobacteria	2407	67.98	
							67.7	avg

Table S2. Bacterial taxa used in the analyses represented in Figs. 1b, 2, 5

NCBI taxon ID	Complete	Strain	Family	Order	Class	Protein coding	G+C %
320483	yes	Anaplasma marginale Florida	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	940	49.77
234826	yes	Anaplasma marginale St. Maries	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	963	49.76
517436	no	Anaplasma marginale str. Mississippi	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	885	49.79
517437	no	Anaplasma marginale str. Puerto Rico	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	965	49.8
403779	no	Anaplasma marginale str. Virginia	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	961	49.79
212042	yes	Anaplasma phagocytophilum HZ	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	1291	41.64
269484	yes	Ehrlichia canis Jake	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	942	28.96
205920	yes	Ehrlichia chaffeensis Arkansas	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	1114	30.1
332415	no	Ehrlichia chaffeensis Sapulpa	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	805	29.98
302409	yes	Ehrlichia ruminantium Gardel	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	950	27.41
254945	yes	Ehrlichia ruminantium Welgevonden (ARC-OVI)	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	920	27.48
254945	yes	Ehrlichia ruminantium Welgevonden (CIRAD)	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	958	27.48
434131	yes	Neorickettsia risticii str. Illinois	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	892	41.27
222891	yes	Neorickettsia sennetsu Miyayama	Anaplasmataceae	Rickettsiales	Alphaproteobacteria	935	41.08
314261	yes	HTCC1062	Pelagibacteraceae	Rickettsiales	Alphaproteobacteria	1393	29.76
335992	yes	HTCC1002	Pelagibacteraceae	Rickettsiales	Alphaproteobacteria	1354	29.68
439493	yes	HTCC7211	Pelagibacteraceae	Rickettsiales	Alphaproteobacteria	1541	29.03
198252	no	HTCC9565	Pelagibacteraceae	Rickettsiales	Alphaproteobacteria	1352	28.93
684719	no	HIMB114	Pelagibacteraceae	Rickettsiales	Alphaproteobacteria	1321	29.59
28211	no	HIMB5	Pelagibacteraceae	Rickettsiales	Alphaproteobacteria	1431	28.63
744985	no	HIMB59			Alphaproteobacteria	1393	32.26
357244	yes	Orientia tsutsugamushi Boryong	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	2141	30.53
334380	yes	Orientia tsutsugamushi Ikeda	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1967	30.51
347255	yes	Rickettsia africae ESF-5	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1041	32.41
293614	yes	Rickettsia akari Hartford	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1259	32.33
391896	yes	Rickettsia bellii OSU 85-389	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1476	31.63
336407	yes	Rickettsia bellii RML369-C	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1429	31.65
293613	yes	Rickettsia canadensis McKiel	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1093	31.05
272944	yes	Rickettsia conorii Malish 7	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1376	32.44
315456	yes	Rickettsia felis URRWXCal2	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1512	32.51

416276	yes	<i>Rickettsia massiliae</i> MTU5	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1396	32.53
562019	yes	<i>Rickettsia peacockii</i> str. Rustic	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	947	32.6
272947	yes	<i>Rickettsia prowazekii</i> Madrid E	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	835	29
452659	yes	<i>Rickettsia rickettsii</i> Iowa	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1384	32.45
392021	yes	<i>Rickettsia rickettsii</i> Sheila Smith	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1345	32.47
272951	no	<i>Rickettsia sibirica</i> 246	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1234	32.47
257363	yes	<i>Rickettsia typhi</i> Wilmington	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	880	28.92
292805	yes	<i>Wolbachia endosymbiont</i> TRS of <i>Brugia malayi</i>	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	900	34.18
569881	no	<i>Wolbachia endosymbiont</i> of <i>Culex quinquefasciatus</i> JHB	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1378	34.19
307502	no	<i>Wolbachia endosymbiont</i> of <i>Drosophila ananassae</i>	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1802	35.71
163164	yes	<i>Wolbachia endosymbiont</i> of <i>Drosophila melanogaster</i>	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1268	35.23
77038	no	<i>Wolbachia endosymbiont</i> of <i>Drosophila simulans</i>	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	760	35.4
955	yes	<i>Wolbachia pipientis</i> wPip	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1275	34.19
66084	yes	<i>Wolbachia</i> sp. wRi	Rickettsiaceae	Rickettsiales	Alphaproteobacteria	1150	35.16
634452	yes	<i>Acetobacter pasteurianus</i> IFO 3283-01	Acetobacteraceae	Rhodospirillales	Alphaproteobacteria	3050	53.1
349163	yes	<i>Acidiphilium cryptum</i> JF-5	Acetobacteraceae	Rhodospirillales	Alphaproteobacteria	3637	67.1
272568	yes	<i>Gluconacetobacter diazotrophicus</i> PAI 5	Acetobacteraceae	Rhodospirillales	Alphaproteobacteria	3566	66.32
290633	yes	<i>Gluconobacter oxydans</i> 621H	Acetobacteraceae	Rhodospirillales	Alphaproteobacteria	2664	60.82
391165	yes	<i>Granulobacter bethesdensis</i> CGDNIH1	Acetobacteraceae	Rhodospirillales	Alphaproteobacteria	2437	59.07
342108	yes	<i>Magnetospirillum magneticum</i> AMB-1	Rhodospirillaceae	Rhodospirillales	Alphaproteobacteria	4559	65.09
331869	no	<i>Nisaea</i> sp. BAL199	Rhodospirillaceae	Rhodospirillales	Alphaproteobacteria	6128	65.02
414684	yes	<i>Rhodospirillum centenum</i> SW	Rhodospirillaceae	Rhodospirillales	Alphaproteobacteria	4002	70.46
269796	yes	<i>Rhodospirillum rubrum</i> ATCC 11170	Rhodospirillaceae	Rhodospirillales	Alphaproteobacteria	3850	65.38
314225	yes	<i>Erythrobacter litoralis</i> HTCC2594	Erythrobacteraceae	Sphingomonadales	Alphaproteobacteria	3011	63.07
237727	no	<i>Erythrobacter</i> sp. NAP1	Erythrobacteraceae	Sphingomonadales	Alphaproteobacteria	3177	60.97
161528	no	<i>Erythrobacter</i> sp. SD-21	Erythrobacteraceae	Sphingomonadales	Alphaproteobacteria	2941	62.86
279238	yes	<i>Novosphingobium aromaticivorans</i> DSM 12444	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	3957	65.11
314266	no	<i>Sphingomonas</i> sp. SKA58	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	3914	63.19
392499	yes	<i>Sphingomonas wittichii</i> RW1	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	5399	67.9
317655	yes	<i>Sphingopyxis alaskensis</i> RB2256	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	3208	65.46
264203	yes	<i>Zymomonas mobilis mobilis</i> ZM4	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	1998	46.33

555217	no	Zymomonas mobilis subsp. mobilis ATCC 10988	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	1845	46.1
573065	no	Asticcacaulis excentricus CB 48	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	3842	59.52
190650	yes	Caulobacter crescentus CB15	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	3737	67.21
565050	yes	Caulobacter crescentus NA1000	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	3876	67.17
366602	yes	Caulobacter sp. K31	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	5443	67.35
450851	yes	Phenylobacterium zucineum HLK1	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	3854	71.1
314260	no	Parvularcula bermudensis HTCC2503	Parvularculaceae	Parvularculales	Alphaproteobacteria	2733	60.66
582402	yes	Hirschia baltica ATCC 49814	Hyphomonadaceae	Rhodobacterales	Alphaproteobacteria	3222	45.19
228405	yes	Hyphomonas neptunium ATCC 15444	Hyphomonadaceae	Rhodobacterales	Alphaproteobacteria	3520	61.93
394221	yes	Maricaulis maris MCS10	Hyphomonadaceae	Rhodobacterales	Alphaproteobacteria	3079	62.73
314254	no	Oceanicaulis alexandrii HTCC2633	Hyphomonadaceae	Rhodobacterales	Alphaproteobacteria	3029	63.59
388401	no	Rhodobacterales bacterium HTCC2150	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3667	49.05
314271	no	Rhodobacterales bacterium HTCC2654	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4712	64.13
398580	yes	Dinoroseobacter shibae DFL 12	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4219	65.52
290400	yes	Jannaschia sp. CCS1	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4283	62.24
314232	no	Loktanella vestfoldensis SKA53	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3068	59.96
391624	no	Oceanibulbus indolifex HEL-45	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4153	59.52
252305	no	Oceanicola batsensis HTCC2597	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4212	66.1
314256	no	Oceanicola granulosus HTCC2516	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3792	70.41
318586	yes	Paracoccus denitrificans PD1222	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	5077	66.7
383629	no	Phaeobacter gallaeciensis 2.10	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3948	59.78
391619	no	Phaeobacter gallaeciensis BS107	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4059	59.81
272943	yes	Rhodobacter sphaeroides 2.4.1	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4304	68.79
349102	yes	Rhodobacter sphaeroides ATCC 17025	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4397	68.23
349101	yes	Rhodobacter sphaeroides ATCC 17029	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4183	68.98
557760	yes	Rhodobacter sphaeroides KD131	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4569	69.09
375451	yes	Roseobacter denitrificans OCh 114	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4146	58.88
391595	no	Roseobacter litoralis Och 149	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4746	57.25
351016	no	Roseobacter sp. AzwK-3b	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4145	61.85
391593	no	Roseobacter sp. CCS2	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3660	55.47
314262	no	Roseobacter sp. MED193	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4535	57.45
388739	no	Roseobacter sp. SK209-2-6	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4537	57.02
89187	no	Roseovarius nubinhibens ISM	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3547	63.91
314264	no	Roseovarius sp. 217	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4772	60.81
314265	no	Roseovarius sp. HTCC2601	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	5452	66.44

391613	no	Roseovarius sp. TM1035	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4102	60.98	
388399	no	Sagittula stellata E-37	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	5067	65.05	
246200	yes	Silicibacter pomeroyi DSS-3	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4283	64.07	
292414	yes	Silicibacter sp. TM1040	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3870	60.06	
384765	no	Stappia aggregata IAM 12614	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	6314	59.38	
52598	no	Sulfitobacter sp. EE-36	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3474	60.31	
314267	no	Sulfitobacter sp. NAS-14.1	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	3962	60.05	
373154	no	Rhodobacterales sp. HTCC2255	Rhodobacteraceae	Rhodobacterales	Alphaproteobacteria	4507	38.9	
		outgroup						
243365	yes	Chromobacterium violaceum ATCC 12472	Neisseriaceae	Neisseriales	Betaproteobacteria	4407	64.83	
272843	yes	Pasteurella multocida multocida Pm70	Pasteurellaceae	Pasteurellales	Gammaproteobacteria	2015	40.4	
							52.6	avg
		low GC outgroup						
641147	no	Simonsiella muelleri ATCC 29453	Neisseriaceae	Neisseriales	Betaproteobacteria	2416	41.33	
272843	yes	Pasteurella multocida multocida Pm70	Pasteurellaceae	Pasteurellales	Gammaproteobacteria	2015	40.4	
							40.9	avg
		high GC outgroup						
243365	yes	Chromobacterium violaceum ATCC 12472	Neisseriaceae	Neisseriales	Betaproteobacteria	4407	64.83	
349124	yes	Halorhodospira halophila SL1	Ectothiorhodospiraceae	Chromatiales	Gammaproteobacteria	2407	67.98	
							66.4	avg

Table S3. Mitochondrial taxa used in the study

a

accession	organism	clade	Super Group	length	protein-coding	G+C %
AY359242	<i>Pseudendoclonium akinetum</i>	Chlorophyta	Archaeplastida	95880	72	39.34
CR954200	<i>Ostreococcus tauri</i>	Chlorophyta	Archaeplastida	44237	43	38.23
AF110138	<i>Nephroselmis olivacea</i>	Chlorophyta	Archaeplastida	45223	40	32.81
AP006444	<i>Brassica napus</i>	Embryophyta	Archaeplastida	221853	79	45.19
M68929	<i>Marchantia polymorpha</i>	Embryophyta	Archaeplastida	186609	76	42.41
EF463011	<i>Chlorokybus atmophyticus</i>	Embryophyta	Archaeplastida	201763	58	39.8
AF494279	<i>Chaetosphaeridium globosum</i>	Embryophyta	Archaeplastida	56574	46	34.41
AY267353	<i>Chara vulgaris</i>	Embryophyta	Archaeplastida	67737	46	40.9
AF353999	<i>Mesostigma viride</i>	Embryophyta	Archaeplastida	42424	41	32.22
D89861	<i>Cyanidioschyzon merolae strain 10D</i>	Rhodophyta	Archaeplastida	32211	34	27.07
AF114794	<i>Porphyra purpurea</i>	Rhodophyta	Archaeplastida	36753	31	33.49
EU651892	<i>Hemiselmis andersenii</i>	Cryptophyta	Chromalveolata	60553	44	28.73
AF288090	<i>Rhodomonas salina</i>	Cryptophyta	Chromalveolata	48063	44	29.83
AJ277126	<i>Pylaiella littoralis</i>	Stramenopiles	Chromalveolata	58507	52	37.99
DQ832717	<i>Phytophthora sojae</i>	Stramenopiles	Chromalveolata	42977	47	21.7
AF288092	<i>Naegleria gruberi</i>	Heterolobosea	Excavata	49843	46	22.25
AF007261	<i>Reclinomonas americana</i>	Jakobida	Excavata	69034	67	26.13
AF295546	<i>Malawimonas jakobiformis</i>	Malawimonadidae	Excavata	47328	49	26.12

b

accession	organism	clade	Super Group	length	protein-coding	G+C %
AY359242	<i>Pseudendoclonium akinetum</i>	Chlorophyta	Archaeplastida	95880	72	39.34
CR954200	<i>Ostreococcus tauri</i>	Chlorophyta	Archaeplastida	44237	43	38.23
AF110138	<i>Nephroselmis olivacea</i>	Chlorophyta	Archaeplastida	45223	40	32.81
FJ859351	<i>Micromonas sp. RCC299</i>	Chlorophyta	Archaeplastida	47425	39	34
DQ365900	<i>Oltmannsiellopsis viridis</i>	Chlorophyta	Archaeplastida	56761	36	33
U02970	<i>Prototheca wickerhamii</i>	Chlorophyta	Archaeplastida	55328	36	25
AY506529	<i>Zea mays</i>	Embryophyta	Archaeplastida	569630	163	43
BA000042	<i>Nicotiana tabacum</i>	Embryophyta	Archaeplastida	430597	156	44

BA000009	Beta vulgaris	Embryophyta	Archaeplastida	368801	140	43
Y08501	Arabidopsis thaliana	Embryophyta	Archaeplastida	366924	117	44
AP006444	Brassica napus	Embryophyta	Archaeplastida	221853	79	45.19
M68929	Marchantia polymorpha	Embryophyta	Archaeplastida	186609	76	42.41
FM179380	Vitis vinifera	Embryophyta	Archaeplastida	773279	74	44
FJ999996	Pleurozia purpurea	Embryophyta	Archaeplastida	168526	69	45
EF463011	Chlorokybus atmophyticus	Embryophyta	Archaeplastida	201763	58	39.8
BA000029	Oryza sativa (japonica cultivar-group)	Embryophyta	Archaeplastida	490520	53	43
EU660574	Megaceros aenigmaticus	Embryophyta	Archaeplastida	184908	48	46
AF494279	Chaetosphaeridium globosum	Embryophyta	Archaeplastida	56574	46	34.41
AY267353	Chara vulgaris	Embryophyta	Archaeplastida	67737	46	40.9
AB251495	Physcomitrella patens	Embryophyta	Archaeplastida	105340	42	40
AF353999	Mesostigma viride	Embryophyta	Archaeplastida	42424	41	32.22
AP011076	Oryza rufipogon	Embryophyta	Archaeplastida	559045	41	44
EU431224	Carica papaya	Embryophyta	Archaeplastida	476890	39	45
GQ856147	Citrullus lanatus	Embryophyta	Archaeplastida	379236	39	45
AP008982	Triticum aestivum	Embryophyta	Archaeplastida	452528	39	44
D89861	Cyanidioschyzon merolae strain 10D	Rhodophyta	Archaeplastida	32211	34	27.07
AF114794	Porphyra purpurea	Rhodophyta	Archaeplastida	36753	31	33.49
Z47547	Chondrus crispus	Rhodophyta	Archaeplastida	25836	29	27
X15917	Paramecium aurelia	Alveolata	Chromalveolata	40469	46	41
DQ927303	Tetrahymena malaccensis	Alveolata	Chromalveolata	47691	45	19
AF396436	Tetrahymena thermophila	Alveolata	Chromalveolata	47577	45	20
DQ927304	Tetrahymena paravorax	Alveolata	Chromalveolata	47496	44	18
DQ927305	Tetrahymena pigmentosa	Alveolata	Chromalveolata	46990	44	18
AF160864	Tetrahymena pyriformis	Alveolata	Chromalveolata	47296	44	21
EU651892	Hemiselmis andersenii	Cryptophyta	Chromalveolata	60553	44	28.73
AF288090	Rhodomonas salina	Cryptophyta	Chromalveolata	48063	44	29.83
AJ277126	Pylaiella littoralis	Stramenopiles	Chromalveolata	58507	52	37.99
DQ832717	Phytophthora sojae	Stramenopiles	Chromalveolata	42977	47	21
AF287134	Ochromonas danica	Stramenopiles	Chromalveolata	41035	44	26
DQ832718	Phytophthora ramorum	Stramenopiles	Chromalveolata	39314	43	21.7
AY534144	Saprolegnia ferax	Stramenopiles	Chromalveolata	46930	43	23
AB546636	Chattonella marina	Stramenopiles	Chromalveolata	44772	41	28
U17009	Phytophthora infestans	Stramenopiles	Chromalveolata	37957	40	22
AY500367	Desmarestia viridis	Stramenopiles	Chromalveolata	39049	39	36

AJ344328	Laminaria digitata	Stramenopiles	Chromalveolata	38007	39	35
AF288092	Naegleria gruberi	Heterolobosea	Excavata	49843	46	22.25
AF007261	Reclinomonas americana	Jakobida	Excavata	69034	67	26.13
AF295546	Malawimonas jakobiformis	Malawimonadidae	Excavata	47328	49	26.12

Table S4. Mitochondrial OCs used in Figs. 3, 7

Bn_007jUWG	gi 112253866 ref YP_717122.1 ribosomal protein S7 [Brassica napus]
Bn_00V5ePU	gi 112253916 ref YP_717170.1 ribosomal protein S14 [Brassica napus]
Bn_025PoQH	gi 112253893 ref YP_717148.1 cytochrome c biogenesis ccmB [Brassica napus]
Bn_0173Zt4	gi 112253922 ref YP_717175.1 ribosomal protein S4 [Brassica napus]
Bn_00PhgdH	gi 112253903 ref YP_717158.1 hypothetical protein BrnapMp061 [Brassica napus]
Bn_01wlDwc	gi 112253902 ref YP_717157.1 ribosomal protein L2 [Brassica napus]
Bn_02rGfAv	gi 112253889 ref YP_717144.1 ATPase subunit 9 [Brassica napus]
Bn_01pvmuC	gi 112253892 ref YP_717147.1 ribosomal protein S12 [Brassica napus]
Ca_02f6Hav	gi 150406489 ref YP_001315105.1 ribosomal protein S7 [Chlorokybus atmophyticus]
Ca_04c1Q64	gi 150406484 ref YP_001315133.1 ribosomal protein S14 [Chlorokybus atmophyticus]
Ca_03CKkmb	gi 150406481 ref YP_001315102.1 ribosomal protein S11 [Chlorokybus atmophyticus]
Ca_02wFhA6	gi 150406491 ref YP_001315099.1 succinate:cytochrome c oxidoreductase subunit 3 [Chlorokybus atmophyticus]
Ca_02XXFwo	gi 150406492 ref YP_001315098.1 succinate:cytochrome c oxidoreductase subunit 4 [Chlorokybus atmophyticus]
Ca_01kFW5g	gi 150406488 ref YP_001315127.1 ribosomal protein S4 [Chlorokybus atmophyticus]
Ca_01zj566	gi 150406465 ref YP_001315126.1 SecY-independent transporter protein [Chlorokybus atmophyticus]
Ca_04dUtdp	gi 150406477 ref YP_001315121.1 ribosomal protein L2 [Chlorokybus atmophyticus]
Ca_03sDHm5	gi 150406483 ref YP_001315132.1 ribosomal protein S13 [Chlorokybus atmophyticus]
Ca_01FHhQb	gi 150406460 ref YP_001315109.1 ATP synthase F0 subunit 9 [Chlorokybus atmophyticus]
Ca_00Gp4uT	gi 150406482 ref YP_001315103.1 ribosomal protein S12 [Chlorokybus atmophyticus]
Ca_0164TvG	gi 150406485 ref YP_001315122.1 ribosomal protein S19 [Chlorokybus atmophyticus]
Cg_00An5iK	gi 22550362 ref NP_689373.1 ribosomal protein S7 [Chaetosphaeridium globosum]
Cg_00QhCva	gi 22550357 ref NP_689358.1 ribosomal protein S14 [Chaetosphaeridium globosum]
Cg_00fmY6J	gi 22550354 ref NP_689355.1 ribosomal protein S11 [Chaetosphaeridium globosum]
Cg_03n6g9y	gi 22550363 ref NP_689350.1 succinate:cytochrome c oxidoreductase subunit 3 [Chaetosphaeridium globosum]
Cg_04KtkKh	gi 22550364 ref NP_689351.1 succinate:cytochrome c oxidoreductase subunit 4 [Chaetosphaeridium globosum]
Cg_03akIMF	gi 22550361 ref NP_689354.1 ribosomal protein S4 [Chaetosphaeridium globosum]
Cg_00ZKtTH	gi 22550365 ref NP_689353.1 SecY-independent transporter protein [Chaetosphaeridium globosum]
Cg_00VF0Cq	gi 22550349 ref NP_689363.1 ribosomal protein L2 [Chaetosphaeridium globosum]
Cg_049ivfM	gi 22550356 ref NP_689356.1 ribosomal protein S13 [Chaetosphaeridium globosum]
Cg_02BiB6m	gi 22550334 ref NP_689389.1 ATP synthase F0 subunit 9 [Chaetosphaeridium globosum]
Cg_04lg0gF	gi 22550355 ref NP_689372.1 ribosomal protein S12 [Chaetosphaeridium globosum]

Cg_00Lfy6A gi|22550358|ref|NP_689362.1| ribosomal protein S19 [Chaetosphaeridium globosum]

Cm_03V1xZK gi|8954382|ref|NP_059371.1| 30S ribosomal protein S14 [Cyanidioschyzon merolae]
Cm_00YGOWO gi|8954380|ref|NP_059369.1| 30S ribosomal protein S11 [Cyanidioschyzon merolae]
Cm_03pPHq8 gi|8954360|ref|NP_059349.1| succinate dehydrogenase cytochrome B560 subunit [Cyanidioschyzon merolae]
Cm_01vbZ3q gi|8954387|ref|NP_059376.1| ORF267 [Cyanidioschyzon merolae]
Cm_00YcRFH gi|8954376|ref|NP_059366.1| cytochrome c1 ABC transporter ATP-binding subunit [Cyanidioschyzon merolae]
Cm_04d4g9U gi|8954388|ref|NP_059377.1| ATP synthase F0 subunit 9 [Cyanidioschyzon merolae]
Cm_018tqtS gi|8954390|ref|NP_059379.1| ribosomal protein S12 [Cyanidioschyzon merolae]

Cv_01ktvfr gi|38638301|ref|NP_943687.1| ribosomal protein S7 [Chara vulgaris]
Cv_04a4M5p gi|38638296|ref|NP_943670.1| ribosomal protein S14 [Chara vulgaris]
Cv_02m78na gi|38638294|ref|NP_943668.1| ribosomal protein S11 [Chara vulgaris]
Cv_00rTACc gi|38638302|ref|NP_943707.1| succinate:cytochrome c oxidoreductase subunit 3 [Chara vulgaris]
Cv_00k2VO6 gi|38638303|ref|NP_943706.1| succinate:cytochrome c oxidoreductase subunit 4 [Chara vulgaris]
Cv_01L94bF gi|38638309|ref|NP_943698.1| channel subunit of ABC transporter for cytochrome c1 [Chara vulgaris]
Cv_00NWYQj gi|38638300|ref|NP_943664.1| ribosomal protein S4 [Chara vulgaris]
Cv_04cy8Bx gi|38638306|ref|NP_943665.1| SecY-independent transporter protein [Chara vulgaris]
Cv_02Zhzcl gi|38638289|ref|NP_943676.1| ribosomal protein L2 [Chara vulgaris]
Cv_02TrYhk gi|38638274|ref|NP_943666.1| ATP synthase F0 subunit 9 [Chara vulgaris]
Cv_04WDNVb gi|38638295|ref|NP_943688.1| ribosomal protein S12 [Chara vulgaris]
Cv_02fKMMF gi|38638297|ref|NP_943675.1| ribosomal protein S19 [Chara vulgaris]

Ha_01WJ79G gi|186920139|ref|YP_001874793.1| ribosomal protein S7 [Hemiselms andersenii]
Ha_02iAJP0 gi|186920145|ref|YP_001874799.1| ribosomal protein S14 [Hemiselms andersenii]
Ha_04f9Z6k gi|186920120|ref|YP_001874774.1| ribosomal protein S11 [Hemiselms andersenii]
Ha_01vk2Ut gi|186920110|ref|YP_001874764.1| succinate:cytochrome c oxidoreductase subunit 4 [Hemiselms andersenii]
Ha_00CFqt2 gi|186920146|ref|YP_001874800.1| hypothetical protein HAM_072 [Hemiselms andersenii]
Ha_0290Flw gi|186920132|ref|YP_001874786.1| ribosomal protein S4 [Hemiselms andersenii]
Ha_02dfNsA gi|186920134|ref|YP_001874788.1| sec-independent protein translocase protein TatC [Hemiselms andersenii]
Ha_00q2P9p gi|186920119|ref|YP_001874773.1| ribosomal protein S13 [Hemiselms andersenii]
Ha_02Byllf gi|186920133|ref|YP_001874787.1| ATP synthase F0 subunit 9 [Hemiselms andersenii]
Ha_02CHcKn gi|186920138|ref|YP_001874792.1| ribosomal protein S12 [Hemiselms andersenii]
Ha_02NiSBb gi|186920140|ref|YP_001874794.1| ribosomal protein S19 [Hemiselms andersenii]

Mj_03lxX1Q gi|11466644|ref|NP_066327.1| ribosomal protein S7 [Malawimonas jakobiformis]

Mj_01HVjda	gi 11466631 ref NP_066314.1 ribosomal protein S14 [Malawimonas jakobiformis]
Mj_04IgdI6	gi 11466638 ref NP_066321.1 ribosomal protein S11 [Malawimonas jakobiformis]
Mj_019vYL0	gi 11466639 ref NP_066322.1 ribosomal protein S4 [Malawimonas jakobiformis]
Mj_04KtGIQ	gi 11466636 ref NP_066319.1 ribosomal protein L20 [Malawimonas jakobiformis]
Mj_01ezVUC	gi 11466665 ref NP_066348.1 SecY-independent transporter protein [Malawimonas jakobiformis]
Mj_02P7IGE	gi 11466652 ref NP_066335.1 ribosomal protein L2 [Malawimonas jakobiformis]
Mj_022V2CQ	gi 11466637 ref NP_066320.1 ribosomal protein S13 [Malawimonas jakobiformis]
Mj_01iMQYf	gi 11466660 ref NP_066343.1 ATP synthase F0 subunit 9 [Malawimonas jakobiformis]
Mj_03BCjDE	gi 11466627 ref NP_066310.1 ribosomal protein L11 [Malawimonas jakobiformis]
Mj_01T4vbO	gi 39656299 ref NP_945313.1 ribosomal protein L36 [Malawimonas jakobiformis]
Mj_03vgtSK	gi 11466647 ref NP_066330.1 ribosomal protein S12 [Malawimonas jakobiformis]
Mj_02K7noH	gi 11466659 ref NP_066342.1 ribosomal protein S19 [Malawimonas jakobiformis]
Mp_01kXiPU	gi 11467105 ref NP_054406.1 ribosomal protein S7 [Marchantia polymorpha]
Mp_01bdy2G	gi 11467122 ref NP_054423.1 ribosomal protein S14 [Marchantia polymorpha]
Mp_00KriuB	gi 11467126 ref NP_054427.1 ribosomal protein S11 [Marchantia polymorpha]
Mp_01OfIEg	gi 11467108 ref NP_054409.1 succinate dehydrogenase subunit 3 [Marchantia polymorpha]
Mp_04KEg8O	gi 11467130 ref NP_054431.1 succinate dehydrogenase subunit 4 [Marchantia polymorpha]
Mp_01PE7mN	gi 11467164 ref NP_054465.1 ABC transporter channel subunit [Marchantia polymorpha]
Mp_00bbFw9	gi 11467160 ref NP_054461.1 ribosomal protein S4 [Marchantia polymorpha]
Mp_03SfSrD	gi 11467132 ref NP_054433.1 Sec-Y independent protein translocase component TatA [Marchantia polymorpha]
Mp_01qx8fV	gi 11467117 ref NP_054418.1 ribosomal protein L2 [Marchantia polymorpha]
Mp_01mIDij	gi 11467125 ref NP_054426.1 ribosomal protein S13 [Marchantia polymorpha]
Mp_03xzYvj	gi 11467161 ref NP_054462.1 ATP synthase F0 subunit 9 [Marchantia polymorpha]
Mp_03sYYXB	gi 11467104 ref NP_054405.1 ribosomal protein S12 [Marchantia polymorpha]
Mp_02e6g0M	gi 11467118 ref NP_054419.1 ribosomal protein S19 [Marchantia polymorpha]
Mv_04HCy0C	gi 110225709 ref YP_665714.1 ribosomal protein S7 [Mesostigma viride]
Mv_00PNDJf	gi 110225714 ref YP_665719.1 ribosomal protein S14 [Mesostigma viride]
Mv_0182JaN	gi 110225717 ref YP_665722.1 ribosomal protein S11 [Mesostigma viride]
Mv_00q9tgi	gi 110225706 ref YP_665711.1 succinate:cytochrome c oxidoreductase subunit 3 [Mesostigma viride]
Mv_04Rk5Tp	gi 110225697 ref YP_665702.1 succinate:cytochrome c oxidoreductase subunit 4 [Mesostigma viride]
Mv_03fX8t0	gi 110225704 ref YP_665709.1 ribosomal protein S4 [Mesostigma viride]
Mv_04YBfn8	gi 110225690 ref YP_665695.1 SecY-independent transporter protein [Mesostigma viride]
Mv_024oUz9	gi 110225694 ref YP_665699.1 ribosomal protein S13 [Mesostigma viride]
Mv_00hXvin	gi 110225679 ref YP_665684.1 ATP synthase F0 subunit 9 [Mesostigma viride]

Mv_02ZTI9P	gi 110225708 ref YP_665713.1 ribosomal protein S12 [Mesostigma viride]
Mv_00R7fyT	gi 110225698 ref YP_665703.1 ribosomal protein S19 [Mesostigma viride]
Ng_039eYQw	gi 11466203 ref NP_066526.1 ribosomal protein S14 [Naegleria gruberi]
Ng_03K6reH	gi 11466197 ref NP_066520.1 ribosomal protein L2 [Naegleria gruberi]
Ng_04TKZBo	gi 11466207 ref NP_066530.1 ribosomal protein S13 [Naegleria gruberi]
Ng_01M3e8j	gi 11466219 ref NP_066542.1 ATP synthase F0 subunit 9 [Naegleria gruberi]
Ng_00FOp6c	gi 11466196 ref NP_066519.1 ribosomal protein L11 [Naegleria gruberi]
Ng_01EBXRx	gi 11466181 ref NP_066504.1 ribosomal protein S12 [Naegleria gruberi]
Ng_01BE57k	gi 11466198 ref NP_066521.1 ribosomal protein S19 [Naegleria gruberi]
No_03Tnlx	gi 110225669 ref YP_665675.1 ribosomal protein S7 [Nephroselmis olivacea]
No_00ygecl	gi 110225650 ref YP_665656.1 ribosomal protein S14 [Nephroselmis olivacea]
No_00AXo9L	gi 110225646 ref YP_665652.1 ribosomal protein S11 [Nephroselmis olivacea]
No_04JhIer	gi 110225639 ref YP_665646.1 ribosomal protein S4 [Nephroselmis olivacea]
No_02T1oGT	gi 110225670 ref YP_665676.1 Ymf16 [Nephroselmis olivacea]
No_040liKg	gi 110225647 ref YP_665653.1 ribosomal protein S13 [Nephroselmis olivacea]
No_00qg2q9	gi 110225645 ref YP_665651.1 ATP synthase F0 subunit 9 [Nephroselmis olivacea]
No_04exJTX	gi 110225657 ref YP_665663.1 ribosomal protein S12 [Nephroselmis olivacea]
No_00vPIBt	gi 110225655 ref YP_665661.1 ribosomal protein S19 [Nephroselmis olivacea]
Ov_00IXn4T	gi 113170501 ref YP_717292.1 Rps7 [Ostreococcus tauri]
Ov_029m0mG	gi 113170481 ref YP_717272.1 Rps14 [Ostreococcus tauri]
Ov_043aZug	gi 113170477 ref YP_717268.1 Rps11 [Ostreococcus tauri]
Ov_04VBMNd	gi 113170474 ref YP_717265.1 Rps4 [Ostreococcus tauri]
Ov_04CIF96	gi 113170475 ref YP_717266.1 Ymf16 [Ostreococcus tauri]
Ov_03DEM9o	gi 113170478 ref YP_717269.1 Rps13 [Ostreococcus tauri]
Ov_015fJDq	gi 113170476 ref YP_717267.1 Atp9 [Ostreococcus tauri]
Ov_04Nmj4U	gi 113170500 ref YP_717291.1 Rps12 [Ostreococcus tauri]
Ov_003iWgW	gi 113170486 ref YP_717277.1 Rps19 [Ostreococcus tauri]
Pa_04U75i5	gi 49147157 ref YP_025759.1 ribosomal protein S14 [Pseudodoelium akinetum]
Pa_04g0661	gi 49147178 ref YP_025771.1 ribosomal protein S11 [Pseudodoelium akinetum]
Pa_03CFq6o	gi 49147226 ref YP_025819.1 ribosomal protein S13 [Pseudodoelium akinetum]
Pa_02BWjz8	gi 49147211 ref YP_025804.1 ATP synthase F0 subunit 9 [Pseudodoelium akinetum]
Pa_03mluoT	gi 49147222 ref YP_025815.1 ribosomal protein S12 [Pseudodoelium akinetum]

Pa_00Zpgbw gi|49147179|ref|YP_025772.1| ribosomal protein S19 [Pseudendoclonium akinetum]

Pl_02jnk00 gi|15150725|ref|NP_150391.1| ribosomal protein S7 [Pylaiella littoralis]
Pl_02e3ZCB gi|15150751|ref|NP_150417.1| ribosomal protein S14 [Pylaiella littoralis]
Pl_02JmKkp gi|15150735|ref|NP_150401.1| ribosomal protein S11 [Pylaiella littoralis]
Pl_02ErAZg gi|15150718|ref|NP_150384.1| ribosomal protein S4 [Pylaiella littoralis]
Pl_03pbHzE gi|15150720|ref|NP_150386.1| SecY-independent protein translocase component tatC [Pylaiella littoralis]
Pl_03sawjQ gi|15150733|ref|NP_150399.1| ribosomal protein L2 [Pylaiella littoralis]
Pl_03tgzry gi|15150734|ref|NP_150400.1| ribosomal protein S13 [Pylaiella littoralis]
Pl_01qDC10 gi|15150714|ref|NP_150380.1| ATP synthase F0 subunit c [Pylaiella littoralis]
Pl_042ra5U gi|15150724|ref|NP_150390.1| ribosomal protein S12 [Pylaiella littoralis]
Pl_00opkvt gi|15150732|ref|NP_150398.1| ribosomal protein S19 [Pylaiella littoralis]

Pp_048lhJU gi|11465649|ref|NP_049320.1| ribosomal protein S11 [Porphyra purpurea]
Pp_02S9vap gi|11465650|ref|NP_049321.1| succinate:cytochrome c oxidoreductase subunit 3 [Porphyra purpurea]
Pp_02gsjd4 gi|11465634|ref|NP_049305.1| succinate:cytochrome c oxidoreductase subunit 4 [Porphyra purpurea]
Pp_034ZvSe gi|11465646|ref|NP_049317.1| SecY-independent transporter protein [Porphyra purpurea]
Pp_01NiK8B gi|11465630|ref|NP_049301.1| ATP synthase F0 subunit 9 [Porphyra purpurea]
Pp_03hOMc3 gi|11465645|ref|NP_049316.1| ribosomal protein S12 [Porphyra purpurea]

Ps_01nLmqg gi|145932343|ref|YP_001165391.1| ribosomal protein S7 [Phytophthora sojae]
Ps_04Akg5 gi|145932370|ref|YP_001165419.1| ribosomal protein S14 [Phytophthora sojae]
Ps_04K2Ktr gi|145932362|ref|YP_001165411.1| ribosomal protein S11 [Phytophthora sojae]
Ps_04JxNJO gi|145932374|ref|YP_001165423.1| ribosomal protein S4 [Phytophthora sojae]
Ps_030c22f gi|145932360|ref|YP_001165409.1| Sec-independent transporter protein [Phytophthora sojae]
Ps_02sLFHQ gi|145932364|ref|YP_001165413.1| ribosomal protein L2 [Phytophthora sojae]
Ps_01BthCd gi|145932363|ref|YP_001165412.1| ribosomal protein S13 [Phytophthora sojae]
Ps_046oWe5 gi|145932339|ref|YP_001165387.1| ATP synthase F0 subunit 9 [Phytophthora sojae]
Ps_03uiQII gi|145932344|ref|YP_001165392.1| ribosomal protein S12 [Phytophthora sojae]
Ps_00KJ0GQ gi|145932365|ref|YP_001165414.1| ribosomal protein S19 [Phytophthora sojae]

Ra_01dNkl3 gi|11466503|ref|NP_044752.1| ribosomal protein S7 [Reclinomonas americana]
Ra_0172tNp gi|11466516|ref|NP_044765.1| ribosomal protein S14 [Reclinomonas americana]
Ra_02r3fo7 gi|11466522|ref|NP_044771.1| ribosomal protein S11 [Reclinomonas americana]
Ra_03ED77I gi|11466547|ref|NP_044796.1| succinate:ubiquinone oxidoreductase subunit 3 [Reclinomonas americana]
Ra_00KhtbV gi|11466548|ref|NP_044797.1| succinate:ubiquinone oxidoreductase subunit 4 [Reclinomonas americana]

Ra_00CCuOp	gi 11466542 ref NP_044791.1 ABC transporter channel subunit [Reclinomonas americana]
Ra_03ixFpP	gi 11466526 ref NP_044775.1 ribosomal protein S4 [Reclinomonas americana]
Ra_043ZwUx	gi 11466537 ref NP_044786.1 ribosomal protein L20 [Reclinomonas americana]
Ra_00salxs	gi 11466520 ref NP_044769.1 SecY-type transporter protein [Reclinomonas americana]
Ra_04IWTQX	gi 11466529 ref NP_044778.1 Sec-independent protein translocase component TatC [Reclinomonas americana]
Ra_039BzL2	gi 11466510 ref NP_044759.1 ribosomal protein L2 [Reclinomonas americana]
Ra_047zpfq	gi 11466521 ref NP_044770.1 ribosomal protein S13 [Reclinomonas americana]
Ra_04DsiQT	gi 11466543 ref NP_044792.1 ABC transporter ATP-binding subunit [Reclinomonas americana]
Ra_01UFZwZ	gi 11466528 ref NP_044777.1 ATP synthase F0 subunit 9 [Reclinomonas americana]
Ra_01zzsJw	gi 11466497 ref NP_044746.1 ribosomal protein L11 [Reclinomonas americana]
Ra_00BaFnz	gi 11466498 ref NP_044747.1 ribosomal protein L1 [Reclinomonas americana]
Ra_023mnAd	gi 11466538 ref NP_044787.1 ribosomal protein L27 [Reclinomonas americana]
Ra_036TVB7	gi 11466502 ref NP_044751.1 ribosomal protein S12 [Reclinomonas americana]
Ra_02FpcVP	gi 11466511 ref NP_044760.1 ribosomal protein S19 [Reclinomonas americana]
Rs_04D0CII	gi 11466599 ref NP_066489.1 ribosomal protein S7 [Rhodomonas salina]
Rs_000Zlja	gi 11466572 ref NP_066462.1 ribosomal protein S14 [Rhodomonas salina]
Rs_03R7M4I	gi 11466591 ref NP_066481.1 ribosomal protein S11 [Rhodomonas salina]
Rs_00COm2F	gi 11466582 ref NP_066472.1 succinate:cytochrome c oxidoreductase subunit 3 [Rhodomonas salina]
Rs_00M2ojj	gi 11466581 ref NP_066471.1 succinate:cytochrome c oxidoreductase subunit 4 [Rhodomonas salina]
Rs_01SgCsj	gi 11466566 ref NP_066456.1 ribosomal protein S4 [Rhodomonas salina]
Rs_03Z7oVD	gi 11466594 ref NP_066484.1 SecY-independent transporter protein [Rhodomonas salina]
Rs_02fsUwZ	gi 11466590 ref NP_066480.1 ribosomal protein S13 [Rhodomonas salina]
Rs_00zJmnK	gi 11466567 ref NP_066457.1 ATP synthase F0 subunit 9 [Rhodomonas salina]
Rs_03RfOf9	gi 11466598 ref NP_066488.1 ribosomal protein S12 [Rhodomonas salina]
Rs_0188lae	gi 11466600 ref NP_066490.1 ribosomal protein S19 [Rhodomonas salina]