

Table. S1. The organisms used in this study, isolation sources and genome accession numbers

Organisms	Source of Isolation	Accession number
<i>Rhodobacter capsulatus</i> DSM 1710 ^T	Sewage plants, eutrophic ponds	QKZO00000000
<i>Rhodobacter viridis</i> JA737 ^T	Mud of a stream	QJTK00000000
<i>Rhodobacter maris</i> JA276 ^T	Marine sediment	OBMT00000000
<i>Rhodobacter aestuarii</i> JA296 ^T	Estuarine environment	FTOG00000000
<i>Rhodobacter sphaeroides</i> 2.4.1 ^T	Sewage plants, eutrophic ponds	CP030271 and CP030272
<i>Rhodobacter johrii</i> JA192 ^T	Rhizosphere soil	MABH00000000
<i>Rhodobacter megalophilus</i> JA194 ^T	Soil, Himalayas	FZOV00000000
<i>Rhodobacter azotoformans</i> KA25 ^T	Sludge for waste water treatment	QAOT00000000
<i>Rhodobacter ovatus</i> JA234 ^T	Polluted pond	OAQO00000000
<i>Rhodobacter vinaykumarii</i> JA123 ^T	Seawater	OBMN00000000
<i>Rhodobacter veldkampii</i> ATCC 35703 ^T	Freshwater	PZKF00000000
<i>Rhodobacter blasticus</i> DSM 2131T	Eutrophic pond	PZKE00000000
<i>Cereibacter changlensis</i> JA139 ^T	Snow sample	PZKG00000000
<i>Defluviimonas denitrificans</i> DSM 18921 ^T	Marine aquaculture	PVEP00000000
<i>Falsirhodobacter</i> sp. alg1	Brown algae	BBJC00000000
<i>Haematobacter missouriensis</i> CCUG 52307 ^T	Septicemic patient	JFGS00000000
<i>Paenirhodobacter enshiensis</i> DW2-9 ^T	Soil	JFZB00000000
<i>Pseudorhodobacter ferrugineus</i> DSM 5888 ^T	Seawater of the Baltic Sea	ATVN00000000
<i>Thioclava pacifica</i> DSM 10166 ^T	Near-shore sulfidic hydrothermal area	AUND00000000
<i>Gemmobacter aquatilis</i> DSM 3857 ^T	Fresh water	FOCE00000000
<i>Pararhodobacter aggregans</i> DSM 18938 ^T	Marine aquaculture	QBKF00000000
<i>Rhodobaca barguzinensis</i> alga-05 ^T	Sediments of a saline	CP024899
<i>Roseicitreum antarcticum</i> CGMCC 1.8894 ^T	Sandy intertidal sediment	FNOM00000000
<i>Roseinatronobacter thiooxidans</i> DSM 13087 ^T	Soda lakes	MEHT00000000
<i>Rhodovulum sulfidophilum</i> DSM 1374 ^T	Sea sediment	CP015418
<i>Albimonas donghaensis</i> DSM 17890 ^T	Seawater	FNMZ00000000
<i>Paracoccus denitrificans</i> DSM 413 ^T	Soil	FNEA00000000
<i>Roseobacter litoralis</i> Och 149 ^T	Seaweed	CP002623
<i>Escherichia coli</i> ATCC 11775 ^T	Human, urine, cystitis	JMST00000000
<i>Pseudomonas aeruginosa</i> DSM 50071 ^T	Soil and water	JYLC00000000
<i>Sinorhodobacter ferrireducens</i> CCTCC AB2012026 ^T	Microbial fuel cell	SAVB00000000
<i>Roseibaca ekhonensis</i> CECT 7235 ^T	Lake water	UIHC00000000

Table S2. 16S rRNA gene sequence pairwise similarity percentages among the genus *Rhodobacter*

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	100															
2	100	100														
3	99.9	99.9	100													
4	98.1	98.1	98.1	100												
5	98.5	98.5	98.5	98.8	100											
6	98.4	98.4	98.5	97.5	98.1	100										
7	95.6	95.6	95.7	95.4	95.5	95.8	100									
8	95.7	95.7	95.7	94.8	95.0	94.7	95.7	100								
9	95.8	95.8	95.8	94.8	95.1	94.8	95.6	99.5	100							
10	95.4	95.4	95.4	94.4	94.7	94.4	95.3	99.5	99.9	100						
11	94.9	94.9	94.9	93.8	94.1	93.8	94.6	98.9	99.3	99.4	100					
12	95.1	95.1	95.1	94.4	94.8	95.0	94.4	96.8	97.0	96.7	96.2	100				
13	95.0	95.0	94.9	94.0	94.8	94.5	94.9	97.5	97.3	97.1	96.4	97.8	100			
14	93.9	93.9	93.9	92.8	93.8	93.5	93.7	96.5	97.0	97.0	96.9	96.8	98.4	100		
15	94.8	94.8	94.7	94.8	94.7	94.7	94.6	94.8	94.7	94.5	94.0	95.6	95.0	94.5	100	
16	95.9	95.9	95.9	95.0	95.6	95.5	95.2	96.3	96.4	96.1	95.5	97.8	96.5	95.9	95.9	100

1- *Rhodobacter sphaeroides* 2.4.1^T; 2- *Rhodobacter megalophilus* JA194^T; 3- *Rhodobacter johrii* JA192^T; 4- *Rhodobacter azotoformans* KA25^T; 5- *Rhodobacter ovatus* JA234^T; 6- *Rhodobacter alkalitolerans* JA916^T; 7- *Rhodobacter blasticus* DSM 2131^T; 8- *Rhodobacter capsulatus* ATCC 11166^T; 9- *Rhodobacter viridis* JA737^T; 10- *Rhodobacter sediminis* N1^T; 11- *Rhodobacter azollae* JA912^T; 12- *Rhodobacter aestuarii* JA296^T; 13- *Rhodobacter maris* JA276^T; 14- *Rhodobacter lacus* JA826^T; 15- *Rhodobacter veldkampii* ATCC 35703^T; 16- *Rhodobacter vinaykumarii* JA123^T.

Table S3. Genomic information of species/strains of genus *Rhodobacter*.

Organism name	Genome size (Mb)	Genome GC%	No of Genes	No. of proteins
<i>Rhodobacter sensu stricto</i> clade				
<i>Rba. capsulatus</i> DSM 1710 ^T	3.66	66.5	3495	3346
Strain SB1003	3.87	66.6	3660	3531
Strain DSM 938	3.86	66.3	3742	3593
Strain DE442	3.76	66.6	3593	3446
Strain B6	3.80	66.4	3607	3403
Strain YW1	3.64	66.6	3497	3354
Strain YW2	3.77	66.4	3576	3414
Strain R121	3.76	66.6	3588	3446
Strain Y262	3.84	66.5	3683	3528
Strain B41	3.67	66.5	3480	3331
Strain A52	3.60	66.5	3411	3357
<i>Rba. viridis</i> JA737 ^T	3.86	65.3	3701	3481
<i>Rba. maris</i> JA276 ^T	3.83	65	3745	3557
<i>Rba. aestuarii</i> JA296 ^T	3.84	61	3695	3544
<i>Rba. sphaeroides</i> Clade				
<i>Rba. sphaeroides</i> ATH 2.4.1 ^T	4.60	68.7	4474	4280
Strain ATCC 17025	4.55	68.2	4547	4280
Strain ATCC 17029	4.48	68.9	4338	4170
Strain KD131	4.71	69.1	4530	4367
Strain MBTLJ-8	4.66	68.7	4580	4374
Strain MBTLJ-13	4.64	68.7	4561	4360
Strain MBTLJ-20	4.65	68.7	4596	4365
Strain EBL0706	4.43	68.3	4387	4024
Strain AB25	4.58	69.1	4489	4279
Strain AB27	4.4	69.0	4381	4084
Strain AB29	4.54	69.0	4502	4192
Strain AB24	4.74	69.0	4692	4389
Strain WS8N	4.41	69.1	4317	4164
<i>Rba. johrii</i> JA192 ^T	4.51	69.0	4458	4093
Strain CDR-SL7Cii	4.68	69.1	4496	4330
<i>Rba. megalophilus</i> JA194 ^T	4.86	68.8	4690	4552
<i>Rba. azotoformans</i> KA25 ^T	4.41	68.4	4369	4112
Strain YLK20	4.32	68.5	4327	3980
<i>Rba. ovatus</i> JA234 ^T	3.81	66.5	3668	3422
<i>Rba. veldkampii</i> Clade				
<i>Rba. veldkampii</i> DSM 11550 ^T	3.26	65	3273	3019
<i>Rba. vinaykumarii</i> JA123 ^T	3.48	68.2	3281	3122
<i>Rba. blasticus</i> Clade				
<i>Rba. blasticus</i> DSM 2131 ^T	3.58	66.5	3455	3441
Strain 28/5	3.70	66.4	3595	3494

Table S4: BPGA of all 12 species of genus *Rhodobacter*

Organism name	No. of core genes	No. of accessory genes	No. of unique genes	No. of exclusively absent genes
12 species of genus <i>Rhodobacter</i>				
<i>Rba. aestuarii</i> JA296	1239	1655	699	9
<i>Rba. azotoformans</i> KA25	1239	2233	730	7
<i>Rba. blasticus</i> ATCC 33485	1239	1127	1113	57
<i>Rba. capsulatus</i> ATCC11166	1239	1791	421	2
<i>Rba. johrii</i> JA192	1239	2594	262	34
<i>Rba. maris</i> JA276	1239	1832	554	5
<i>Rba. megalophilus</i> JA194	1239	2961	269	0
<i>Rba. ovatus</i> JA234	1239	1655	588	8
<i>Rba. sphaeroides</i> ATH 2.4.1	1239	2478	130	3
<i>Rba. veldkampii</i> ATCC 35703	1239	1127	657	48
<i>Rba. vinaykumarii</i> JA123	1239	1184	720	26
<i>Rba. viridis</i> JA737	1239	1776	543	8
Pan-genome analysis of <i>Rba. sphaeroides</i> clade				
<i>Rba. azotoformans</i> KA25	2294	1082	820	66
<i>Rba. johrii</i> JA192	2294	1508	293	90
<i>Rba. megalophilus</i> JA194	2294	1827	345	2
<i>Rba. ovatus</i> JA234	2294	437	748	531
<i>Rba. sphaeroides</i> ATH 2.4.1	2294	1402	149	30
Pan-genome analysis of <i>Rba. capsulatus</i> clade				
<i>Rba. aestuarii</i> JA296	2225	571	791	130
<i>Rba. capsulatus</i> ATCC11166	2225	684	537	53
<i>Rba. maris</i> JA276	2225	665	727	87
<i>Rba. viridis</i> JA737	2225	668	663	80
Pan-genome analysis of <i>Rba. veldkampii</i> clade				
<i>Rba. vinaykumarii</i> JA123	2014	0	1123	1004
<i>Rba. veldkampii</i> ATCC 35703	2014	0	1004	1123

Taxa; 1- *Rhodobacter capsulatus* ATCC 11166^T; 2- *Rhodobacter viridis* JA737^T; 3- *Rhodobacter maris* JA276^T; 4- *Rhodobacter aestuarii* JA296^T; 5- *Rhodobacter sphaeroides* 2.4.1^T; 6- *Rhodobacter johrii* JA192^T; 7- *Rhodobacter megalophilus* JA194^T; 8- *Rhodobacter azotoformans* KA25^T; 9- *Rhodobacter ovatus* JA234^T; 10- *Rhodobacter vinaykumarii* JA123^T; 11- *Rhodobacter veldkampii* ATCC 35703^T; 12- *Rhodobacter blasticus* DSM 213^T; 13- *Cereibacter changlensis* JA139^T; 14- *Defluviimonas denitrificans* DSM 18921^T; 15- *Falsirhodobacter* sp. alg1; 16- *Haematobacter missouriensis* CCUG 52307^T; 17- *Paenirhodobacter enshiensis* DW2-9^T; 18- *Pseudorhodobacter ferrugineus* DSM 5888^T; 19- *Thioclava pacifica* DSM 10166^T; 20- *Gemmobacter aquatilis* DSM 3857^T; 21- *Pararhodobacter aggregans* DSM 18938^T; 22- *Rhodobaca barguzinensis* alga-05^T; 23- *Roseicitreum antarcticum* CGMCC 1.8894^T; 24- *Roseinatronobacter thiooxidans* DSM 13087^T; 25- *Rhodovulum sulfidophilum* DSM 1374^T; 26- *Albimonas donghaensis* DSM 17890^T; 27- *Paracoccus denitrificans* DSM 413^T; 28- *Roseobacter litoralis* Och 149^T; 29- *Escherichia coli* ATCC 11775^T; 30- *Pseudomonas aeruginosa* DSM 50071^T; 31- *Sinorhodobacter ferrireducens* CCTCC AB2012026^T; 32- *Roseibaca ekhonensis* CECT 7235^T. *Rba. sphaeroides* clade member values in red color; *Rba. capsulatus* clade member values in light brown color; *Rba. veldkampii* clade (*Rba. veldkampii* and *Rba. vinaykumarii*) member values in pink color.

Taxa; 1- *Rhodobacter capsulatus* ATCC 11166^T; 2- *Rhodobacter viridis* JA737^T; 3- *Rhodobacter maris* JA276^T; 4- *Rhodobacter aestuarii* JA296^T; 5- *Rhodobacter sphaeroides* 2.4.1^T; 6- *Rhodobacter johrii* JA192^T; 7- *Rhodobacter megalophilus* JA194^T; 8- *Rhodobacter azotoformans* KA25^T; 9- *Rhodobacter ovatus* JA234^T; 10- *Rhodobacter vinaykumarii* JA123^T; 11- *Rhodobacter veldkampii* ATCC 35703^T; 12- *Rhodobacter blasticus* DSM 213^T; 13- *Cereibacter changlensis* JA139^T; 14- *Defluviimonas denitrificans* DSM 18921^T; 15- *Falsirhodobacter* sp. alg1; 16- *Haematobacter missouriensis* CCUG 52307^T; 17- *Paenirhodobacter enshiensis* DW2-9^T; 18- *Pseudorhodobacter ferrugineus* DSM 5888^T; 19- *Thioclava pacifica* DSM 10166^T; 20- *Gemmobacter aquatilis* DSM 3857^T; 21- *Pararhodobacter aggregans* DSM 18938^T; 22- *Rhodobaca barguzinensis* alga-05^T; 23- *Roseicitreum antarcticum* CGMCC 1.8894^T; 24- *Roseinatronobacter thiooxidans* DSM 13087^T; 25- *Rhodovulum sulfidophilum* DSM 1374^T; 26- *Albimonas donghaensis* DSM 17890^T; 27- *Paracoccus denitrificans* DSM 413^T; 28- *Roseobacter litoralis* Och 149^T; 29- *Escherichia coli* ATCC 11775^T; 30- *Pseudomonas aeruginosa* DSM 50071^T; 31- *Sinorhodobacter ferrireducens* CCTCC AB2012026^T; 32- *Roseibaca ekhonensis* CECT 7235^T. *Rba. sphaeroides* clade member values in red color; *Rba. capsulatus* clade member values in light brown color; *Rba. veldkampii* clade (*Rba. veldkampii* and *Rba. vinaykumarii*) member values in pink color.