Supplementary material

Genomic-based taxonomic classification of the family *Erythrobacteraceae*

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Table S1. Currently validly-published genera and species belonging to the family *Erythrobacteraceae*.

Genus and species	Type strain	16S rRNA gene accession number	Source	Reference
Altererythrobacter				
Aeb. aerius	100921-2^{T}	KU311004.	Air	[1]
Aeb. aerophilus	Ery1^{T}	MG183676	Seawater	[2]
Aeb. aestiaquae	HDW-31^{T}	KJ658262	Seawater	[3]
Aeb. aestuarii	KYW147^{T}	FJ997597	Seawater	[4]
Aeb. amylolyticus	NS1^{T}	KX601069	Lake sediment	[5]
Aeb. aquaemixtae	JSSK-8^{T}	KY614064	Ocean and freshwater spring junction water	[6]
Aeb. aquiaggeris	KEM-3^{T}	KX812543	Estuary water	[7]
Aeb. aquimixticola	SSKS-13^{T}	MK194299	Ocean and freshwater spring junction sediment	[8]
Aeb. atlanticus	26DY36^{T}	KC018454	Marine sediment	[9]
Aeb. aurantiacus	O30^{T}	KF924607	Marine sediment	[10]
Aeb. buctensis	M0322^{T}	KJ599648	Mudstone core	[11]
Aeb. confluentis	KEM-4^{T}	KX129915	Estuary water	[12]
Aeb. deserti	THG-S3^{T}	KY287245	Desert sand	[13]
Aeb. dongtanensis	JM27^{T}	GU166344	Tidal flat	[14]
Aeb. endophyticus	BR75^{T}	KY310591	Salt marsh plant	[15]
Aeb. epoxidivorans	JCS350^{T}	DQ304436	Marine sediment	[16]
Aeb. flavus	MS1-4^{T}	KX099616	Mangrove sediment	[17]
Aeb. fulvus	S-54^{T}	KY117470	Soil	[18]
Aeb. gangjinensis	KJ7^{T}	JF751048	Tidal flat	[19]
Aeb. halimionae	CPA5^{T}	KY310593	Salt marsh plant	[15]

Genus and species	Type strain	16S rRNA gene accession number	Source	Reference
Aeb. indicus	MSSRF26^T	DQ399262	Wild rice	[20]
Aeb. insulae	BPTF-M16^T	MH206217	Tidal flat	[21]
Aeb. ishigakiensis	JPCCMB0017^T	AB363004	Marine sediment	[22]
Aeb. lauratis	YIM 75003^T	KX808673	Hot spring	[23]
Aeb. luteolus	SW-109^T	AY739662	Tidal flat	[24]
Aeb. lutipelagi	GH1-16^T	LT797153	Tidal flat	[25]
Aeb. mangrovi	C9-11^T	MF034045	Mangrove sediment	[26]
Aeb. marensis	MSW-14^T	FM177586	Seawater	[27]
Aeb. marinus	H32^T	EU726272	Seawater	[28]
Aeb. maritimus	HME9302^T	KF385494	Seawater	[29]
Aeb. namhicola	KYW48^T	FJ935793	Seawater	[4]
Aeb. oceanensis	Y2^T	KF924606	Marine sediment	[30]
Aeb. palmitatis	YIM 75004^T	KX808674	Hot spring	[23]
Aeb. rigui	WW3^T	KP997219	Freshwater	[31]
Aeb. salegens	XY-R17^T	KT886062	Marine sediment	[32]
Aeb. sediminis	CAU1172^T	KP779619	Marine sediment	[33]
Aeb. soli	MN-1^T	KT906300	Desert sand	[34]
Aeb. troitsensis	KMM 6042^T	AY676115	Sea urchin	[35]
Aeb. xiamenensis	LY02^T	KC520828	Seawater	[36]
Aeb. xinjiangensis	S3-63^T	HM028673	Desert sand	[37]
Aeb. xixiisoli	S36^T	KJ150597	Soil	[38]
Croceibacterium				

Genus and species	Type strain	16S rRNA gene accession number	Source	Reference
Crb. ferulae	SX2RGS8^T	KX289944	Medicinal plant	[39]
Crb. mercuriale	Coronado^T	KP122961	Stadium seat	[40]
Croceicoccus				
Ccc. marinus	E4A9^T	EF623998	Marine sediment	[41]
Ccc. mobilis	Ery22^T	KT383846	Marine sediment	[42]
Ccc. naphthovorans	PQ-2^T	KF145127	Marine biofilm	[43]
Ccc. pelagius	Ery9^T	KT383844	Marine sediment	[42]
Erythrobacter				
Erb. aquimaris	SW-110^T	AY461441	Tidal flat	[44]
Erb. aquimixticola	JSSK-14^T	KY614066	Ocean and freshwater spring junction water	[45]
Erb. arachoides	RC4-10-4^T	KU302715	Glacier	[46]
Erb. atlanticus	s31-N3^T	KP994305	Marine sediment	[47]
Erb. citreus	RE35F/1^T	AF118020	Seawater	[48]
Erb. flavus	SW-46^T	AF500004	Seawater	[49]
Erb. gaetbuli	SW-161^T	AY562220	Intertidal sediment	[50]
Erb. gangjinensis	K7-2^T	EU428782	Seawater	[51]
Erb. jejuensis	CNU001^T	DQ453142	Seawater	[52]
Erb. litoralis	T4^T	AF465836	Marine cyanobacterial mat	[53]
Erb. longus	OCh101^T	AF465835	Seaweed	[54]
Erb. luteus	KA37^T	KP197673	Mangrove sediment	[55]
Erb. lutimaris	S-5^T	KJ870094	Intertidal sediment	[56]
Erb. marinus	HWDM-33^T	HQ117934	Seawater	[57]

Genus and species	Type strain	16S rRNA gene accession number	Source	Reference
Erb. marisflavi	KEM-5^T	MK121890	Estuary water	[58]
Erb. nanhaisediminis	T30^T	FJ654473	Marine sediment	[59]
Erb. odishensis	JA747^T	HE680094	Saltern soil	[60]
Erb. pelagi	UST081027-248^T	HQ203045	Seawater	[61]
Erb. seohaensis	SW-135^T	AY562219	Intertidal sediment	[50]
Erb. spongiae	HN-E23^T	MG655147	Marine sponge	[62]
Erb. vulgaris	022-2-10^T	AY706935	Marine starfish	[63]
Erb. xanthus	SM1501^T	KU529278	Seawater	[64]
Erb. zhengii	V18^T	MG183678	Marine sediment	[65]
Erythromicrobium				
Erm. ramosum	E5^T	AF465837	Alkaline spring cyanobacterial spring	[53]
Porphyrobacter				
Por. algicida	2-22^T	KU981071	Seawater	[66]
Por. colymbi	TPW-24^T	AB702992	Swimming pool water	[67]
Por. cryptus	ALC-2^T	AF465834	Hot spring	[68]
Por. dokdonensis	DSW-74^T	DQ011529	Seawater	[69]
Por. donghaensis	SW-132^T	AY559428	Seawater	[70]
Por. neustonensis	ACM 2844^T	AB033327	Freshwater	[71]
Por. sanguineus	A91^T	AB021493	Seawater	[72]
Por. tepidarius	OT3^T	AB033328	Hot spring	[73]
Qipengyuania				
Qpy. sediminis	M1^T	KJ734993	Subterrestrial sediment	[74]

17

Table S2. Genomic completeness and contamination as well as rRNA and tRNA gene counts of obtained *Erythrobacteraceae* genomes.

Genomes	Genomic quality		Gene counts	
	Completeness (%)	Contamination (%)	rRNA gene	tRNA gene
Aeb. aerius 100921-2^{T}	99.4	0.1	3	48
Aeb. aerophilus Ery1^{T}	99.6	4.9	3	45
Aeb. aestiaquae KCTC 42006^{T}	98.5	0.2	3	42
Aeb. aestuarii JCM 16339^{T}	99.1	0.4	3	45
Aeb. amylolyticus NS1^{T}	99.5	0.3	3	45
Aeb. aquaemixtae KCTC 52763^{T}	99.0	1.1	3	45
Aeb. aquimixticola SSKS-13^{T}	98.8	0.2	3	45
Aeb. atlanticus 26DY36^{T}	99.5	1.8	6	47
Aeb. aurantiacus MCCC 1A09962^{T}	98.7	0.3	3	41
Aeb. buctensis M0322^{T}	98.9	0.5	3	47
Aeb. confluentis KCTC 52259^{T}	99.4	0.1	6	46
Aeb. dongtanensis KCTC 22672^{T}	99.5	0.2	3	47
Aeb. endophyticus LMG 29518^{T}	99.3	0.3	3	45
Aeb. epoxidivorans CGMCC 1.7731^{T}	99.2	1.3	3	43
Aeb. flavus MS1-4^{T}	99.1	1.0	4	46
Aeb. gangjinensis JCM 17802^{T}	99.2	0.1	3	42
Aeb. halimionae LMG 29519^{T}	99.2	0.5	3	44
Aeb. indicus DSM 18604^{T}	99.4	0.9	17	54
Aeb. insulae BPTF-M16^{T}	98.4	2.8	9	47
Aeb. ishigakiensis NBRC 107699^{T}	98.9	0.7	3	42
Aeb. luteolus SW-109^{T}	99.9	0.3	12	52

Genomes	Genomic quality		Gene counts	
	Completeness (%)	Contamination (%)	rRNA gene	tRNA gene
Aeb. lutipelagi GH1-16^T	99.6	0.6	3	44
Aeb. mangrovi C9-11^T	99.0	0.8	3	46
Aeb. marensis KCTC 22370^T	99.5	0.6	3	45
Aeb. marinus H32^T	99.4	0.3	3	46
Aeb. maritimus HME9302^T	99.2	1.7	3	43
Aeb. namhicola JCM 16345^T	99.5	0	3	44
Aeb. oceanensis MCCC 1A09965^T	99.2	0.2	3	45
Aeb. rigui KCTC 42620^T	99.3	0	3	49
Aeb. salegens MCCC 1K01500^T	99.3	0.7	3	47
Aeb. sediminis KCTC 42453^T	99.2	0.2	3	42
Aeb. soli MCCC 1K02066^T	99.6	0	3	48
Aeb. troitsensis JCM 17037^T	99.6	0.2	3	45
Aeb. xiamenensis CGMCC 1.12494^T	99.1	0.3	3	44
Aeb. xinjiangensis CCTCC AB 207166^T	97.8	0.7	3	47
Aeb. xixiisoli S36^T	99.4	2.4	3	48
Crb. ferulae SX2RGS8^T	97.6	1.1	3	51
Crb. mercuriale Coronado^T	98.1	0.4	3	48
Ccc. marinus E4A9^T	99.6	1.8	6	48
Ccc. mobilis Ery22^T	99.4	2.7	12	54
Ccc. naphthovorans PQ-2^T	99.5	0.3	3	45
Ccc. pelagius Ery9^T	99.3	0.5	9	51
Erb. aquimaris JCM 12189^T	99.6	0	3	45

Genomes	Genomic quality		Gene counts	
	Completeness (%)	Contamination (%)	rRNA gene	tRNA gene
Erb. aquimixticola JSSK-14^T	99.2	1.2	3	45
Erb. arachoides RC4-10-4^T	99.5	0.4	3	46
Erb. atlanticus s21-N3^T	99.1	1.1	3	45
Erb. citreus CGMCC 1.8703^T	99.8	0.4	12	52
Erb. gaetbuli DSM 16225^T	99.8	0.3	3	45
Erb. gangjinensis CGMCC 1.15024^T	99.2	0.6	3	43
Erb. jejuensis JCM 16677^T	98.3	4.8	6	61
Erb. litoralis DSM 8509^T	99.2	0.9	3	45
Erb. longus DSM 6997^T	99.6	0.6	3	42
Erb. luteus KA37^T	99.5	0	3	45
Erb. lutimaris S-5^T	99.5	0.3	11	44
Erb. marinus KCTC 23554^T	99.2	0.5	3	43
Erb. marisflavi KEM-5^T	99.9	0	3	43
Erb. nanhaisediminis CGMCC 1.7715^T	99.8	0.1	3	44
Erb. odishensis KCTC 23981^T	99.6	0.3	3	45
Erb. pelagi JCM 17468^T	99.5	0	3	44
Erb. seohaensis SW-135^T	99.8	0.1	3	44
Erb. spongiae HN-E23^T	99.8	0.5	3	45
Erb. vulgaris DSM 17792^T	98.9	0	3	45
Erb. xanthus CCTCC AB 2015396^T	99.2	0.5	12	55
Erb. zhengii V18^T	99.9	3.0	3	46
Erm. ramosum JCM 10282^T	99.5	1.1	3	44

Genomes	Genomic quality		Gene counts	
	Completeness (%)	Contamination (%)	rRNA gene	tRNA gene
Por. algicida KEMB 9005-328^T	99.9	1.0	3	47
Por. colymbi JCM 18338^T	99.3	0.9	3	44
Por. cryptus DSM 12079^T	99.5	0	3	44
Por. dokdonensis DSM 17193^T	99.3	0.8	3	44
Por. donghaensis DSM 16220^T	99.5	1.0	3	44
Por. neustonensis DSM 9434^T	99.5	0.3	6	47
Por. sanguineus JCM 20691^T	99.6	0.7	3	44
Por. tepidarius DSM 10594^T	99.7	0	3	44
Qpy. sediminis CGMCC 1.12928^T	99.5	0.2	3	44

Table S3. Sequence identities of annotated 16S rRNA genes within sequenced *Erythrobacteraceae* genomes in this study through the EzBioCloud web server. Red indicates that the type strain has multi-copy 16S rRNA genes.

Genome	Closest type strain	Identity (%)
Aeb. aerius 100921-2^{T}	*Aeb. aerius* 100921-2^{T}	99.2
Aeb. aestiaquae KCTC 42006^{T}	*Aeb. aestiaquae* HDW-31^{T}	100.0
Aeb. aestuarii JCM 16339^{T}	*Aeb. aestuarii* KYW147^{T}	100.0
Aeb. aquaemixtae KCTC 52763^{T}	*Aeb. aquaemixtae* JSSK-8^{T}	100.0
Aeb. aurantiacus MCCC 1A09962^{T}	*Aeb. aurantiacus* O30^{T}	99.9
Aeb. buctensis M0322^{T}	*Aeb. buctensis* M0322^{T}	100.0
Aeb. confluentis KCTC 52259^{T}	*Aeb. confluentis* KEM-4^{T}	100.0
	Aeb. confluentis KEM-4^{T}	100.0
Aeb. endophyticus LMG 29518^{T}	*Aeb. endophyticus* BR75^{T}	100.0
Aeb. gangjinensis JCM 17802^{T}	*Aeb. gangjinensis* KJ7^{T}	100.0
Aeb. halimionae LMG 29519^{T}	*Aeb. halimionae* CPA5^{T}	100.0
Aeb. indicus DSM 18604^{T}	*Aeb. indicus* MSSRF26^{T}	100.0
	Aeb. indicus MSSRF26^{T}	100.0
	Aeb. indicus MSSRF26^{T}	100.0
	Aeb. indicus MSSRF26^{T}	100.0
	Aeb. indicus MSSRF26^{T}	100.0
Aeb. luteolus SW-109^{T}	*Aeb. luteolus* SW-109^{T}	100.0
	Aeb. luteolus SW-109^{T}	100.0
	Aeb. luteolus SW-109^{T}	100.0
	Aeb. luteolus SW-109^{T}	100.0
Aeb. marinus H32^{T}	*Aeb. marinus* H32^{T}	100.0

Genome	Closest type strain	Identity (%)
Aeb. oceanensis MCCC 1A09965^T	*Aeb. oceanensis* Y2^T	100.0
Aeb. salegens MCCC 1K01500^T	*Aeb. salegens* XY-R17^T	100.0
Aeb. sediminis KCTC 42453^T	*Aeb. sediminis* CAU1172^T	100.0
Aeb. soli MCCC 1K02066^T	*Aeb. soli* MN-1^T	100.0
Aeb. xixiisoli S36^T	*Aeb. xixiisoli* S36^T	99.9
Erb. aquimaris JCM 12189^T	*Erb. aquimaris* SW-110^T	100.0
Erb. arachoides RC4-10-4^T	*Erb. arachoides* RC4-10-4^T	99.3
Erb. citreus CGMCC 1.8703^T	*Erb. citreus* RE35F/1^T *Erb. citreus* RE35F/1^T *Erb. citreus* RE35F/1^T *Erb. citreus* RE35F/1^T	100.0 100.0 100.0 100.0
Erb. gaetbuli DSM 16225^T	*Erb. gaetbuli* SW-161^T	100.0
Erb. jejuensis JCM 16677^T	*Erb. jejuensis* CNU001^T *Erb. jejuensis* CNU001^T	99.6 99.6
Erb. pelagi JCM 17468^T	*Erb. pelagi* JCM 17468^T	99.8
Erb. vulgaris DSM 17792^T	*Erb. vulgaris* 022 2-10^T	100.0
Erm. ramosum JCM 10282^T	*Erm. ramosum* DSM 8510^T	100.0
Por. algicida KEMB 9005-328^T	*Por. algicida* KEMB 9005-328^T	100.0

23 Table S4. Annotations of OCs for the phylogenomic analysis assigned to COG and KEGG databases and their best substitutional model.

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
1	SSU ribosomal protein S4p (S9e)	J	Ribosome	GTR+F+R5	LG+R4
2	Queuine tRNA-ribosyltransferase	J	Transfer RNA biogenesis	GTR+F+R6	LG+F+R5
3	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	J	Transfer RNA biogenesis	TIM3+F+R6	LG+F+R5
4	Peptidyl-prolyl cis-trans isomerase	O	Necroptosis	GTR+F+R5	LG+F+I+G4
5	Phosphopantetheine adenylyltransferase	H	Pantothenate and CoA biosynthesis	TVM+F+R5	LG+R5
6	(2E,6E)-farnesyl diphosphate synthase	H	Terpenoid backbone biosynthesis	TIM3+F+R5	LG+F+R5
7	Exodeoxyribonuclease VII small subunit	L	DNA repair and recombination proteins Mismatch repair	TIM3+F+R5	Dayhoff+I+G4
8	Phosphoribosylformylglycinamidine synthase, synthetase subunit	F	Nucleotide metabolism	GTR+F+R6	LG+F+R5
9	Phosphoserine phosphatase	E	Amino acid metabolism Energy metabolism	TIM3+F+R6	LG+F+R6
10	tRNA dimethylallyltransferase	J	Biosynthesis of secondary metabolites Transfer RNA biogenesis	TVM+F+R6	LG+F+I+G4
11	Ketol-acid reductoisomerase (NADP(+))	E	Amino acid metabolism Metabolism of cofactors and vitamins	GTR+F+R5	LG+R5
12	Phosphate transport ATP-binding protein PstB	P	ABC transporters	GTR+F+R5	LG+R5
13	Phosphate transport system regulatory protein PhoU	P	Signaling proteins	GTR+F+R5	LG+R4
14	Phosphate regulon transcriptional regulatory protein PhoB	T	Signaling proteins	GTR+F+R5	LG+R5
15	Inositol-1-monophosphatase	G	Inositol phosphate metabolism Phosphatidylinositol signaling system Streptomycin biosynthesis	GTR+F+R6	LG+R4

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
16	Translation elongation factor P	J	Translation factors	GTR+F+R5	LG+R3
17	Thiamine-phosphate pyrophosphorylase	H	Thiamine metabolism	GTR+F+I+G4	LG+F+R5
18	Transketolase	G	Pentose phosphate pathway	GTR+F+R6	LG+F+R6
19	ATP-dependent DNA helicase RecG	L	Homologous recombination	GTR+F+R6	LG+F+R5
20	Transcription-repair coupling factor	L	Nucleotide excision repair	GTR+F+R6	LG+F+R5
21	NAD kinase	G	Nicotinate and nicotinamide metabolism	GTR+F+R5	LG+I+G4
22	Protein translocase subunit SecA	U	Bacterial secretion system Quorum sensing	GTR+F+R6	LG+F+R6
23	Glutamate N-acetyltransferase (EC 2.3.1.35)	E	Arginine biosynthesis	TIM3+F+R6	LG+F+R5
24	Thioredoxin	O	Chaperones and folding catalysts	GTR+F+I+G4	LG+G4
25	Nucleotidyl transferase	M	Fructose and mannose metabolism	GTR+F+R6	LG+R5
26	Adenosylhomocysteinase	H	Cysteine and methionine metabolism	GTR+F+R6	LG+F+R5
27	Peroxiredoxin	O	Apoptosis	GTR+F+I+G4	LG+I+G4
28	Excinuclease ABC subunit C	L	Nucleotide excision repair	GTR+F+R6	LG+F+R5
29	Translation initiation factor 1	J	Translation factors	TIM2+F+R5	LG+R2
30	Septum formation protein Maf	D	Signaling proteins	GTR+F+R6	LG+F+R6
31	Phosphoribosylaminoimidazole-succinocarboxamide synthase	F	Purine metabolism	GTR+F+I+G4	LG+R5
32	Glutamine-fructose-6-phosphate aminotransferase	M	Alanine, aspartate and glutamate metabolism Amino sugar and nucleotide sugar metabolism	GTR+F+R6	LG+F+R6
33	Type II restriction adenine-specific methylase	L	Prokaryotic defense system	GTR+F+R6	LG+R6
34	Ribonuclease HII	L	DNA replication	GTR+F+R5	LG+F+R5
35	Topoisomerase IV subunit A	L	DNA replication	GTR+F+R5	LG+F+R5

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
			DNA repair and recombination		
36	Ferredoxin, 2Fe-2S	C	Energy metabolism	TIM3+F+R4	WAG+I+G4
37	Hydrolase SMc00528, alpha/beta fold family	S	Function unknown	TIM+F+R5	LG+R4
38	DNA-binding response regulator ChvI	T	Signaling proteins	GTR+F+R5	LG+R6
39	PTS system permease (IIAMan), nitrogen regulatory IIA protein	G	Galactose metabolism Phosphotransferase system	GTR+F+I+G4	LG+I+G4
40	Phosphocarrier protein, nitrogen regulation associated	G	Phosphotransferase system	TPM3u+F+I+G4	LG+I+G4
41	Recombination protein RecR	L	Homologous recombination	TIM3+F+R5	LG+R5
42	Methionyl-tRNA formyltransferase	J	Aminoacyl-tRNA biosynthesis One carbon pool by folate	GTR+F+R5	LG+F+I+G4
43	tRNA pseudouridine(38-40) synthase	J	Transfer RNA biogenesis	TVM+F+R5	WAG+F+R5
44	Argininosuccinate lyase	E	Alanine, aspartate and glutamate metabolism	GTR+F+R6	LG+F+R6
45	Diaminopimelate decarboxylase	E	Lysine biosynthesis	GTR+F+R6	LG+F+R5
46	Adenylosuccinate synthetase	F	Purine metabolism	GTR+F+R6	LG+R5
47	Replication-associated recombination protein RarA	L	DNA replication and repair	GTR+F+R6	LG+F+R6
48	Argininosuccinate synthase	E	Alanine, aspartate and glutamate metabolism	GTR+F+R5	WAG+R4
49	Excinuclease ABC subunit A	L	Nucleotide excision repair	GTR+F+R6	LG+R6
50	Malate dehydrogenase	C	Carbon fixation pathways in prokaryotes Citrate cycle Cysteine and methionine metabolism Glyoxylate and dicarboxylate metabolism Pyruvate metabolism	TIM+F+R5	LG+F+R4

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
51	2-oxoglutarate dehydrogenase E1 component	C	Citrate cycle	GTR+F+R6	LG+R5
52	E2 component of 2-oxoglutarate dehydrogenase complex	C	Citrate cycle Glycolysis / Gluconeogenesis Pyruvate metabolism	GTR+F+R6	LG+F+R5
53	LSU ribosomal protein L17p	J	Ribosome	TIM+F+I+G4	LG+I+G4
54	DNA-directed RNA polymerase alpha subunit	K	RNA polymerase	GTR+F+R5	LG+R4
55	SSU ribosomal protein S11p	L	Ribosome	TIM2+F+I+G4	LG+R2
56	SSU ribosomal protein S13p	J	Ribosome	TIM2+F+I+G4	LG+I+G4
57	Protein translocase subunit SecY	U	Bacterial secretion system Quorum sensing	GTR+F+R6	LG+F+R5
58	LSU ribosomal protein L15p	J	Ribosome	TIM3+F+I+G4	WAG+I+G4
59	LSU ribosomal protein L30p	J	Ribosome	GTR+F+I+G4	LG+R3
60	SSU ribosomal protein S5p	J	Ribosome	TIM3+F+R5	WAG+F+R4
61	LSU ribosomal protein L18p	J	Ribosome	TN+F+I+G4	WAG+I+R4
62	LSU ribosomal protein L6p	J	Ribosome	TIM+F+R5	LG+I+G4
63	SSU ribosomal protein S8p	J	Ribosome	TIM+F+R5	LG+R3
64	SSU ribosomal protein S14p	J	Ribosome	TIM2+F+I+G4	LG+R2
65	LSU ribosomal protein L5p	J	Ribosome	GTR+F+R5	LG+R4
66	LSU ribosomal protein L24p	J	Ribosome	TIM2+F+R4	LG+G4
67	LSU ribosomal protein L14p	J	Ribosome	TIM2+F+I+G4	LG+I+G4
68	SSU ribosomal protein S17p	J	Ribosome	TIM+F+I+G4	WAG+G4
69	LSU ribosomal protein L29p	J	Ribosome	TIM2+F+I+G4	LG+I+G4

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
70	LSU ribosomal protein L16	J	Ribosome	TIM2+F+R4	LG+R3
71	SSU ribosomal protein S3p	J	Ribosome	TIM2+F+R5	LG+R4
72	LSU ribosomal protein L22p	J	Ribosome	GTR+F+R5	LG+I+G4
73	SSU ribosomal protein S19p	J	Ribosome	GTR+F+R4	JTTDCMut+I+G4
74	LSU ribosomal protein L2p	J	Ribosome	GTR+F+R5	LG+R4
75	LSU ribosomal protein L23p	J	Ribosome	GTR+F+I+G4	LG+I+G4
76	LSU ribosomal protein L4p	J	Ribosome	GTR+F+R5	LG+I+G4
77	LSU ribosomal protein L3p	J	Ribosome	TIM2+F+R5	LG+F+R5
78	SSU ribosomal protein S10p	J	Ribosome	TIM2+F+I+G4	LG+R2
79	Translation elongation factor G	J	Translation factors	GTR+F+R6	LG+F+R5
80	SSU ribosomal protein S7p	J	Ribosome	GTR+F+I+G4	LG+I+G4
81	ApaG protein	P	Signaling proteins	GTR+F+R5	WAG+F+G4
82	RNA binding methyltransferase FtsJ like	J	Ribosome biogenesis	GTR+F+R6	LG+F+R6
83	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase II	E	Phenylalanine, tyrosine and tryptophan biosynthesis Quorum sensing	GTR+F+R6	LG+F+R5
84	NifU-like domain protein	O	Not assigned	TVM+F+R5	LG+F+I+G4
85	Ferric uptake regulation protein FUR	P	Transcription factors	GTR+F+R4	LG+R3
86	Metal-dependent hydrolase YbeY	S	Drug metabolism - other enzymes Pyrimidine metabolism	TIM3+F+R5	LG+F+I+G4
87	Phosphate starvation-inducible protein PhoH, predicted ATPase	T	Signaling proteins	GTR+F+R5	LG+R5
88	tRNA-i(6)A37 methylthiotransferase	J	Transfer RNA biogenesis	GTR+F+R6	LG+F+R5

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
89	A/G-specific adenine glycosylase	L	Base excision repair	GTR+F+R6	WAG+F+R6
90	3-Oxoacyl-[acyl-carrier-protein] synthase, KASIII	I	Fatty acid biosynthesis	TIM3+F+R6	LG+I+G4
91	Hypothetical metal-binding enzyme, YcbL homolog	S	Pyruvate metabolism	GTR+F+R5	LG+R5
92	Aerobic cobaltochelatase CobT subunit	H	Porphyrin and chlorophyll metabolism	GTR+F+R6	LG+F+R5
93	ATP synthase alpha chain	C	Oxidative phosphorylation Photosynthesis	GTR+F+R5	LG+R5
94	ATP synthase gamma chain	C	Oxidative phosphorylation Photosynthesis	GTR+F+R5	LG+F+R5
95	ATP synthase beta chain	C	Oxidative phosphorylation Photosynthesis	GTR+F+R5	LG+R4
96	ATP synthase epsilon chain	C	Oxidative phosphorylation Photosynthesis	GTR+F+R4	LG+R4
97	*N*-acetylglucosamine-1-phosphate uridyltransferase	M	Amino sugar and nucleotide sugar metabolism	GTR+F+R6	LG+F+R5
98	Octanoate-[acyl-carrier-protein]-protein-*N*-octanoyltransferase	H	Lipoic acid metabolism	GTR+F+R6	WAG+R5
99	Phosphoribosylformylglycinamidine cyclo-ligase	F	Purine metabolism	TIM3+F+R6	WAG+F+R5
100	Nucleoside diphosphate kinase	F	Drug metabolism - other enzymes Purine metabolism Pyrimidine metabolism	GTR+F+R5	WAG+I+G4
101	Cytosol aminopeptidase PepA	E	Glutathione metabolism	GTR+F+R6	LG+F+R6
102	4-hydroxythreonine-4-phosphate dehydrogenase	H	Vitamin B6 metabolism	TVM+F+R6	LG+F+R6
103	SSU rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase	J	Ribosome biogenesis	TPM3u+F+R6	LG+R5

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
104	GTP-binding protein TypA/BipA	T	Signaling proteins	GTR+F+R5	LG+R5
105	Excinuclease ABC subunit B	L	Nucleotide excision repair	GTR+F+R6	LG+F+R5
106	N(6)-L-threonylcarbamoyladenine synthase	O	Transfer RNA biogenesis	GTR+F+R6	LG+F+R5
107	Glycerol-3-phosphate dehydrogenase [NAD(P)+]	C	Glycerophospholipid metabolism	TVM+F+R6	LG+F+R5
108	Hypothetical protein	S	Not assigned	TIM3+F+I+G4	LG+G4
109	Hypothetical protein	Not assigned	Not assigned	TN+F+R5	LG+G4
110	Ribosomal protein S12p Asp88 methylthiotransferase	J	Ribosome biogenesis	GTR+F+R6	LG+F+R5
111	5'-nucleotidase SurE	F	Nicotinate and nicotinamide metabolism Purine metabolism Pyrimidine metabolism	GTR+F+R5	LG+R5
112	Seryl-tRNA synthetase	J	Aminoacyl-tRNA biosynthesis	GTR+F+R6	LG+F+R5
113	Aspartate carbamoyltransferase	F	Alanine, aspartate and glutamate metabolism Pyrimidine metabolism	GTR+F+R5	WAG+F+R5
114	ATP-dependent Clp protease proteolytic subunit	O	Cell cycle	GTR+F+R5	LG+R5
115	ATP-dependent Clp protease ATP-binding subunit ClpX	O	Cell cycle	GTR+F+R5	LG+R4
116	Ribosomal large subunit pseudouridine synthase D	J	Ribosome biogenesis	TVM+F+R5	LG+F+R6
117	*N*-acetylmuramoyl-L-alanine amidase	M	Unclassified: metabolism	GTR+F+R6	LG+F+R5
118	Sulfite exporter TauE/SafE	S	Function unknown	TVM+F+R5	LG+F+R5
119	Valyl-tRNA synthetase	J	Aminoacyl-tRNA biosynthesis	GTR+F+R6	LG+F+R6
120	Ribosomal large subunit pseudouridine synthase C	J	Ribosome biogenesis	GTR+F+R6	LG+F+R5
121	SSU ribosomal protein S21p	J	Ribosome	GTR+F+I+G4	LG+R2

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
122	Aspartyl-tRNA(Asn) amidotransferase subunit C	J	Aminoacyl-tRNA biosynthesis	GTR+F+R5	WAG+G4
123	Aspartyl-tRNA(Asn) amidotransferase subunit A	J	Aminoacyl-tRNA biosynthesis	GTR+F+R6	LG+F+R6
124	Aspartyl-tRNA(Asn) amidotransferase subunit B	J	Aminoacyl-tRNA biosynthesis	GTR+F+R5	LG+F+R5
125	ClpB protein	O	Chaperones and folding catalysts	GTR+F+R6	LG+F+R5
126	Ribonuclease HI	L	DNA replication	TIM3+F+I+G4	LG+I+G4
127	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	I	Terpenoid backbone biosynthesis	GTR+F+R5	LG+R5
128	Arginyl-tRNA synthetase	J	Aminoacyl-tRNA biosynthesis	GTR+F+R6	LG+F+R6
129	beta-*N*-acetylglucosaminidase	G	Amino sugar and nucleotide sugar metabolism Glycosaminoglycan degradation	TIM3+F+R6	LG+F+R6
130	Twin-arginine translocation protein TatC	U	Protein export	TPM3u+F+R5	LG+R6
131	Threonine dehydratase, catabolic	E	Glycine, serine and threonine metabolism	GTR+F+R6	LG+R6
132	Glutamine synthetase type I	E	Alanine, aspartate and glutamate metabolism Arginine biosynthesis Glyoxylate and dicarboxylate metabolism Nitrogen metabolism	GTR+F+R5	LG+R4
133	Nitrogen regulatory protein P-II	E	Two-component system	TVM+F+I+G4	LG+I+G4
134	Peptidase B	E	Glutathione metabolism	TIM3+F+R6	LG+F+I+G4
135	Methionine aminopeptidase	J	Peptidases and inhibitors	GTR+F+R5	LG+I+G4
136	Pterin-4-alpha-carbinolamine dehydratase	H	Folate biosynthesis	TIM3+F+R5	WAG+G4
137	16S rRNA (cytosine(1402)-N(4))-methyltransferase	M	Ribosome biogenesis	TIM3+F+R5	LG+F+I+G4
138	Phospho-*N*-acetylmuramoyl-pentapeptide-transferase	M	Peptidoglycan biosynthesis	GTR+F+R6	LG+F+R4
139	UDP-*N*-acetylmuramate--L-alanine ligase	M	D-Glutamine and D-glutamate metabolism	GTR+F+R6	LG+F+R6

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
			Peptidoglycan biosynthesis		
140	UDP-*N*-acetylenolpyruvoylglucosamine reductase	M	Amino sugar and nucleotide sugar metabolism Peptidoglycan biosynthesis	GTR+F+R5	LG+R5
141	GTP-binding protein Obg	S	Ribosome biogenesis	GTR+F+R6	LG+F+R5
142	Aerobic cobaltochelatase CobS subunit	H	Porphyrin and chlorophyll metabolism	GTR+F+R5	LG+R5
143	Putative pre-16S rRNA nuclease Yqg	L	Unclassified: metabolism	TIM3+F+R5	LG+F+I+G4
144	Pyridoxine 5'-phosphate synthase	H	Vitamin B6 metabolism	GTR+F+R6	LG+R4
145	Threonine synthase	E	Glycine, serine and threonine metabolism Vitamin B6 metabolism	GTR+F+R6	LG+F+R6
146	LSU ribosomal protein L27p	J	Ribosome	TIM+F+I+G4	DCMut+G4
147	Glutamate--cysteine ligase	H	Cysteine and methionine metabolism Glutathione metabolism	GTR+F+R6	LG+R5
148	Lysyl-tRNA synthetase (class I)	J	Aminoacyl-tRNA biosynthesis	GTR+F+R5	LG+F+R5
149	Energy-dependent translational throttle protein EttA	S	Transfer RNA biogenesis	GTR+F+R5	LG+R5
150	Transcriptional regulator, AsnC family	K	Transcription factors	GTR+F+R5	LG+R4
151	Biotin carboxylase of acetyl-CoA carboxylase	I	Carbon fixation pathways in prokaryotes Fatty acid biosynthesis Propanoate metabolism Pyruvate metabolism	GTR+F+R5	LG+R5
152	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	I	Carbon fixation pathways in prokaryotes Fatty acid biosynthesis Propanoate metabolism	TIM3+F+R6	LG+F+R5

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
			Pyruvate metabolism		
153	Two-component transcriptional response regulator, LuxR family	T	Two-component system	TIM+F+R5	WAG+R4
154	Decaprenyl diphosphate synthase	H	Terpenoid backbone biosynthesis	GTR+F+R5	LG+F+R6
155	DNA polymerase III subunits gamma and tau	L	DNA replication Homologous recombination Mismatch repair	GTR+F+R7	LG+F+R6
156	ATP-dependent protease La Type I	O	Cell cycle	GTR+F+R6	LG+F+R5
157	DNA-binding protein HU-beta	L	DNA replication	GTR+F+I+G4	Dayhoff+G4
158	SSU ribosomal protein S2p	J	Ribosome	TIM+F+R5	LG+R4
159	Translation elongation factor Ts	J	Translation factors	TIM2+F+R6	LG+F+R4
160	Uridine monophosphate kinase	F	Pyrimidine metabolism	GTR+F+R5	LG+R5
161	Ribosome recycling factor	J	Translation factors	GTR+F+R5	LG+I+G4
162	Undecaprenyl diphosphate synthase	I	Terpenoid backbone biosynthesis	TIM3+F+I+G4	LG+F+R6
163	1-deoxy-D-xylulose 5-phosphate reductoisomerase	I	Terpenoid backbone biosynthesis	GTR+F+R6	LG+F+R6
164	3-hydroxyacyl-[acyl-carrier-protein] dehydratase, FabZ form	I	Biotin metabolism Fatty acid biosynthesis	GTR+F+R5	LG+I+G4
165	LSU ribosomal protein L31p	J	Ribosome	TIM+F+I+G4	WAG+G4
166	Cytochrome c-type biogenesis protein CcmC, putative heme lyase for CcmE	O	ABC transporters	TVM+F+R5	mtZOA+F+R6
167	Signal recognition particle receptor FtsY	U	Protein export Quorum sensing	GTR+F+R5	LG+R4
168	Diaminopimelate epimerase	E	Lysine biosynthesis	GTR+F+R6	LG+F+R6

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
169	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	I	Glycerophospholipid metabolism	TVM+F+R6	LG+F+I+G4
170	Aspartyl-tRNA synthetase	J	Aminoacyl-tRNA biosynthesis	GTR+F+R6	LG+R6
171	Acyl carrier protein	I	Fatty acid biosynthesis	TIM2+F+I+G4	JTTDCMut+G4
172	3-oxoacyl-[acyl-carrier-protein] synthase, KASII	I	Biotin metabolism Fatty acid biosynthesis	GTR+F+R6	LG+R5
173	Thioredoxin reductase	O	Selenocompound metabolism	GTR+F+R6	WAG+R5
174	Psp operon transcriptional activator	K	Transcription factors	GTR+F+R6	LG+F+R6
175	5-aminolevulinate synthase	H	Glycine, serine and threonine metabolism Porphyrin and chlorophyll metabolism	GTR+F+R6	LG+R4
176	Acyl-phosphate:glycerol-3-phosphate O-acyltransferase PlsY	S	Glycerolipid metabolism Glycerophospholipid metabolism	GTR+F+R5	LG+F+R5
177	DNA topoisomerase I	L	NA repair and recombination DNA replication	GTR+F+R7	LG+F+R5
178	GTP-binding protein Era	K	Ribosome biogenesis	GTR+F+R6	LG+R5
179	ATP-dependent RNA helicase RhlE	L	RNA degradation	GTR+F+R6	LG+F+R5
180	3-dehydroquinate synthase	E	Phenylalanine, tyrosine and tryptophan biosynthesis	GTR+F+R6	LG+F+R6
181	Shikimate kinase I	E	Phenylalanine, tyrosine and tryptophan biosynthesis	TPM3+F+R5	LG+F+I+G4
182	Site-specific tyrosine recombinase XerD	L	Chromosome and associated proteins	TVM+F+R6	LG+F+R5
183	Acetyl-coenzyme A carboxyl transferase alpha chain	I	Carbon fixation pathways in prokaryotes Fatty acid biosynthesis	TIM3+F+R5	LG+R5

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
			Propanoate metabolism Pyruvate metabolism		
184	Transcription termination protein NusA	K	Transcription machinery	GTR+F+R6	LG+R5
185	23S rRNA (adenine(2503)-C(2))-methyltransferase	J	Ribosome biogenesis	GTR+F+R6	LG+F+R5
186	Translation initiation factor 2	J	Translation factors	GTR+F+R6	LG+F+R6
187	4-hydroxy-tetrahydrodipicolinate synthase	E	Lysine biosynthesis Monobactam biosynthesis	GTR+F+R6	LG+I+G4
188	tmRNA-binding protein SmpB	O	Unclassified: genetic information processing	TIM+F+R5	LG+R4
189	RecA protein	L	Homologous recombination	GTR+F+R5	LG+I+G4
190	Alanyl-tRNA synthetase	J	Aminoacyl-tRNA biosynthesis	GTR+F+R6	LG+F+R5
191	Isocitrate dehydrogenase [NADP]	C	Carbon fixation pathways in prokaryotes Citrate cycle Glutathione metabolism Peroxisome	GTR+F+R5	LG+R5
192	ATP-dependent RNA helicase Atu1833	L	RNA degradation	GTR+F+R6	LG+F+R6
193	ATP-dependent DNA helicase UvrD/PcrA	L	Mismatch repair Nucleotide excision repair	GTR+F+R6	LG+F+R6
194	Ribosomal large subunit pseudouridine synthase B	J	Ribosome biogenesis	GTR+F+R5	LG+R5
195	Ribosome-binding factor A	J	Ribosome biogenesis	GTR+F+R5	LG+R4
196	Acetyl-coenzyme A carboxyl transferase beta chain	H	Carbon fixation pathways in prokaryotes Fatty acid biosynthesis Propanoate metabolism	GTR+F+R6	LG+I+G4

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
			Pyruvate metabolism		
197	Tryptophan synthase alpha chain	E	Glycine, serine and threonine metabolism Phenylalanine, tyrosine and tryptophan biosynthesis	GTR+F+R5	WAG+R5
198	Tryptophan synthase beta chain	E	Glycine, serine and threonine metabolism Phenylalanine, tyrosine and tryptophan biosynthesis	GTR+F+R5	LG+R5
199	Phosphoribosylanthranilate isomerase	E	Phenylalanine, tyrosine and tryptophan biosynthesis	TVM+F+R5	LG+I+G4
200	Orotidine 5'-phosphate decarboxylase	F	Pyrimidine metabolism	GTR+F+R5	LG+R5
201	Adenylosuccinate lyase	F	Alanine, aspartate and glutamate metabolism Purine metabolism	GTR+F+R6	LG+F+R5
202	Hydroxyacylglutathione hydrolase	C	Pyruvate metabolism	TIM3+F+R6	WAG+I+R4
203	SSU ribosomal protein S1p	J	Ribosome	TIM+F+R5	LG+F+R5
204	Cytidylate kinase	F	beta-Alanine metabolism Pyrimidine metabolism Pantothenate and CoA biosynthesis	GTR+F+R5	WAG+F+R5
205	3-phosphoshikimate 1-carboxyvinyltransferase	E	Novobiocin biosynthesis Phenylalanine, tyrosine and tryptophan biosynthesis	GTR+F+R6	LG+F+R6
206	Signal recognition particle protein Ffh	U	Protein export Quorum sensing	GTR+F+R6	LG+F+R5
207	tRNA (guanine(37)-N(1))-methyltransferase	J	Transfer RNA biogenesis	GTR+F+R6	LG+I+G4

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
208	LSU ribosomal protein L19p	J	Ribosome	GTR+F+I+G4	LG+I+G4
209	Aspartate-semialdehyde dehydrogenase	E	Cysteine and methionine metabolism Glycine, serine and threonine metabolism Lysine biosynthesis Monobactam biosynthesis	GTR+F+R6	LG+R5
210	LSU ribosomal protein L9p	J	Ribosome	GTR+F+R5	LG+F+I+G4
211	SSU ribosomal protein S18p	J	Ribosome	TIM2+F+I+G4	rtREV+R3
212	SSU ribosomal protein S6p	J	Ribosome	TIM+F+I+G4	LG+R3
213	Malonyl CoA-acyl carrier protein transacylase	I	Fatty acid biosynthesis Prodigiosin biosynthesis	TIM3+F+R5	LG+F+R5
214	3-oxoacyl-[acyl-carrier protein] reductase	I	Biotin metabolism Fatty acid biosynthesis Prodigiosin biosynthesis	GTR+F+R5	LG+R4
215	DNA polymerase III beta subunit	L	DNA replication Homologous recombination Mismatch repair	GTR+F+R5	LG+F+R5
216	Translation elongation factor LepA	M	Legionellosis	GTR+F+R6	LG+R5
217	Competence lipoprotein ComL	M	Transporters	GTR+F+R5	LG+I+G4
218	SSU ribosomal protein S15p	J	Ribosome	GTR+F+I+G4	WAG+I+G4
219	DNA repair protein RecN	L	DNA repair and recombination	GTR+F+R6	LG+F+R5
220	DNA ligase (NAD(+))	L	Base excision repair DNA replication	GTR+F+R6	LG+F+R6

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
			Mismatch repair Nucleotide excision repair		
221	Polyribonucleotide nucleotidyltransferase	J	RNA degradation	GTR+F+R6	LG+F+R5
222	Succinate dehydrogenase flavoprotein subunit	C	Butanoate metabolism Carbon fixation pathways in prokaryotes Citrate cycle Oxidative phosphorylation	TIM+F+R5	LG+R5
223	Inosine-5'-monophosphate dehydrogenase	F	Drug metabolism - other enzymes Purine metabolism	GTR+F+R6	LG+F+R5
224	Adenosine (5')-pentaphospho-(5'')-adenosine pyrophosphohydrolase	J	RNA degradation	TIM3+F+R5	LG+I+R4
225	Amidophosphoribosyltransferase	F	Alanine, aspartate and glutamate metabolism Purine metabolism	GTR+F+R6	LG+R5
226	Lipoprotein-releasing system ATP-binding protein LolD	P	Transporters	TIM3+F+R5	LG+I+G4
227	DNA polymerase III alpha subunit	L	DNA replication Homologous recombination Mismatch repair	GTR+F+R6	LG+F+R6
228	Succinate dehydrogenase iron-sulfur protein	C	Butanoate metabolism Carbon fixation pathways in prokaryotes Citrate cycle Oxidative phosphorylation	GTR+F+R6	LG+R4
229	GTP-binding and nucleic acid-binding protein YchF	J	Ribosome biogenesis	GTR+F+R5	LG+F+R5
230	Hypothetical protein	S	Chromosome and associated proteins	TVM+F+I+G4	LG+I+G4
231	Peptidyl-tRNA hydrolase	J	Translation factors	GTR+F+R5	LG+R5

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
232	Glycyl-tRNA synthetase alpha chain	J	Aminoacyl-tRNA biosynthesis	GTR+F+R5	WAG+R4
233	Cysteine synthase	E	Cysteine and methionine metabolism Sulfur metabolism	GTR+F+R6	LG+R5
234	Tyrosyl-tRNA synthetase	J	Aminoacyl-tRNA biosynthesis	GTR+F+R6	LG+F+R6
235	Topoisomerase IV subunit B	L	DNA repair and recombination DNA replication	GTR+F+R6	LG+R5
236	16S rRNA (cytidine(1402)-2'-O)-methyltransferase	S	Ribosome biogenesis	GTR+F+R5	LG+F+I+G4
237	Glutathione synthetase	H	Cysteine and methionine metabolism Glutathione metabolism	GTR+F+R5	LG+R5
238	Radical SAM family enzyme	H	Porphyrin and chlorophyll metabolism	GTR+F+R6	LG+F+R5
239	Nucleoside 5-triphosphatase RdgB (dHAPTP, dITP, XTP-specific)	F	Purine metabolism	TIM3+F+R5	LG+F+R4
240	Ribonuclease PH	J	Transfer RNA biogenesis	GTR+F+R5	LG+R4
241	Chaperone protein DnaK	O	RNA degradation	GTR+F+R6	LG+F+R5
242	Chaperone protein DnaJ	O	Chaperones and folding catalysts Mitochondrial biogenesis	GTR+F+R5	LG+F+R5
243	DNA repair protein RadA	O	DNA repair and recombination	TIM3+F+R6	LG+F+R5
244	Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex	C	Citrate cycle Glycine, serine and threonine metabolism Glycolysis Glyoxylate and dicarboxylate metabolism Lysine degradation Propanoate metabolism	GTR+F+R5	LG+F+R5

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
			Pyruvate metabolism Tryptophan metabolism Valine, leucine and isoleucine degradation		
245	Methionyl-tRNA synthetase	J	Aminoacyl-tRNA biosynthesis Selenocompound metabolism	GTR+F+R6	LG+F+R6
246	Uncharacterized metal-dependent hydrolase YcfH	L	Unclassified: metabolism	TIM3+F+R6	LG+F+R5
247	Nucleoside triphosphate pyrophosphohydrolase MazG	F	Chromosome and associated proteins	GTR+F+R6	LG+F+R6
248	Ribosome LSU-associated GTP-binding protein HflX	S	Ribosome biogenesis	TIM3+F+R6	LG+F+R6
249	Nitrogen regulation protein NtrX	T	Two-component system	GTR+F+R6	LG+F+R6
250	tRNA-dihydrouridine synthase DusB	J	Transfer RNA biogenesis	GTR+F+R6	LG+F+R5
251	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	I	Terpenoid backbone biosynthesis	GTR+F+R7	WAG+F+R6
252	Nicotinamide-nucleotide amidase	S	Nicotinate and nicotinamide metabolism	TVM+F+R5	LG+R4
253	Lipoyl synthase	H	Lipoic acid metabolism	GTR+F+R9	LG+R5
254	DNA gyrase subunit A	L	DNA repair and recombination DNA replication	GTR+F+R6	LG+F+R6
255	Methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase TrmFO	J	Transfer RNA biogenesis	GTR+F+R6	LG+F+R5
256	Glutaredoxin 3 (Grx2)	O	Chaperones and folding catalysts	GTR+F+I+G4	WAG+I+G4
257	16 kDa heat shock protein A	O	Chaperones and folding catalysts	GTR+F+R5	LG+R5
258	CTP synthase	F	Pyrimidine metabolism	GTR+F+R6	LG+F+R5
259	Triosephosphate isomerase	G	Carbon fixation in photosynthetic organisms Fructose and mannose metabolism Glycolysis	TIM3+F+R6	LG+F+R5

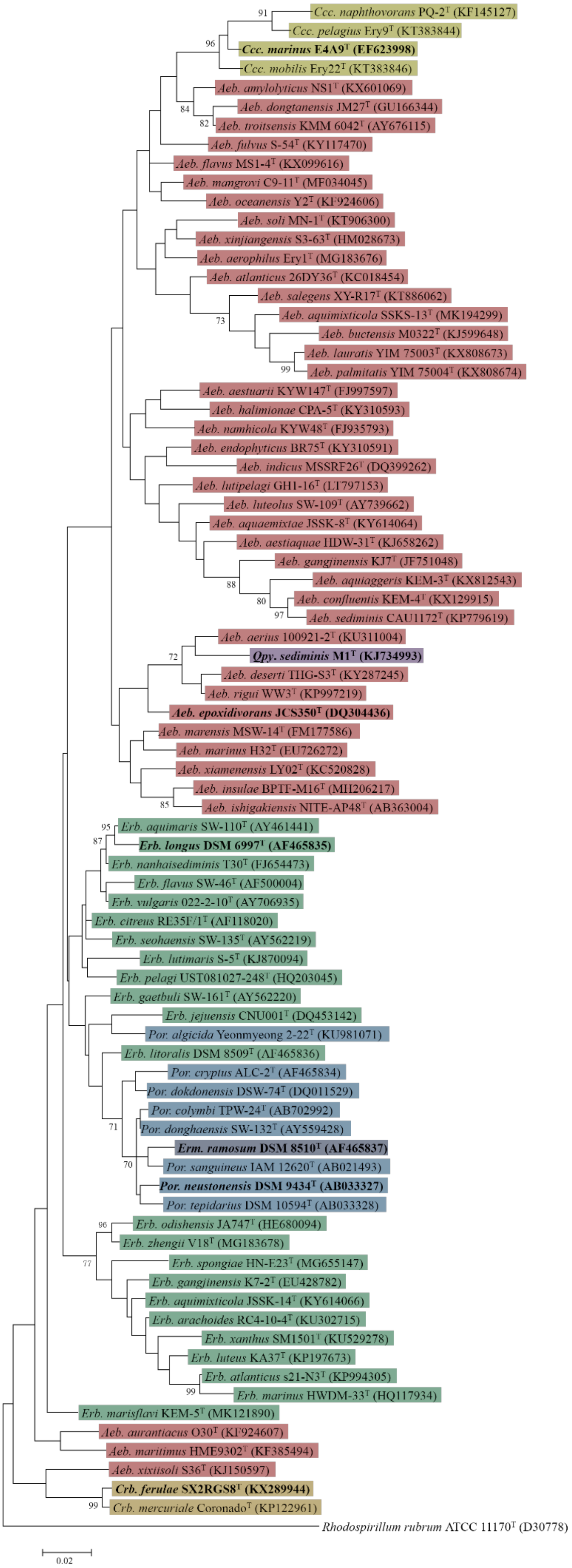
Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
			Inositol phosphate metabolism		
260	Anthranilate synthase, aminase component	E	Phenazine biosynthesis Phenylalanine, tyrosine and tryptophan biosynthesis Quorum sensing	GTR+F+R6	WAG+F+R6
261	Anthranilate synthase, amidotransferase component	E	Phenazine biosynthesis Phenylalanine, tyrosine and tryptophan biosynthesis Quorum sensing	GTR+F+R5	WAG+I+G4
262	Anthranilate phosphoribosyltransferase	E	Phenylalanine, tyrosine and tryptophan biosynthesis	GTR+F+R5	LG+F+R5
263	Indole-3-glycerol phosphate synthase	E	Phenylalanine, tyrosine and tryptophan biosynthesis	TIM3+F+R5	LG+F+I+G4
264	SOS-response repressor and protease LexA	K	DNA repair and recombination Peptidases and inhibitors	GTR+F+R6	LG+R5
265	Glutamyl-tRNA synthetase	J	Aminoacyl-tRNA biosynthesis Porphyrin and chlorophyll metabolism	TIM3+F+R6	LG+f+R5
266	Pantothenate kinase type III, CoaX-like	K	Pantothenate and CoA biosynthesis	GTR+F+R6	LG+R5
267	NADH-ubiquinone oxidoreductase chain N	C	Oxidative phosphorylation	TVM+F+R6	LG+F+R5
268	NADH-ubiquinone oxidoreductase chain M	C	Oxidative phosphorylation	GTR+F+R6	LG+F+R5
269	NADH-ubiquinone oxidoreductase chain L	C	Oxidative phosphorylation	GTR+F+R6	LG+F+R5
270	NADH-ubiquinone oxidoreductase chain K	C	Oxidative phosphorylation	TVM+F+I+G4	mtZOA+R4

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
271	NADH-ubiquinone oxidoreductase chain J	C	Oxidative phosphorylation	TVM+F+R5	LG+I+G4
272	NADH-ubiquinone oxidoreductase chain I	C	Oxidative phosphorylation	GTR+F+R5	LG+R3
273	NADH-ubiquinone oxidoreductase chain H	C	Oxidative phosphorylation	TIM+F+R6	LG+F+R5
274	NADH-ubiquinone oxidoreductase chain G	C	Oxidative phosphorylation	GTR+F+R6	LG+F+R5
275	NADH-ubiquinone oxidoreductase chain F	C	Oxidative phosphorylation	GTR+F+R6	LG+R4
276	NADH-ubiquinone oxidoreductase chain D	C	Oxidative phosphorylation	GTR+F+R6	LG+R4
277	NADH-ubiquinone oxidoreductase chain C	C	Oxidative phosphorylation	GTR+F+R6	WAG+I+G4
278	NADH-ubiquinone oxidoreductase chain B	C	Oxidative phosphorylation	TIM+F+R5	JTTDCMut+R5
279	3-ketoacyl-CoA thiolase	I	Benzoate degradation Butanoate metabolism Carbon fixation pathways in prokaryotes Fatty acid degradation Glyoxylate and dicarboxylate metabolism Lysine degradation Propanoate metabolism Pyruvate metabolism Synthesis and degradation of ketone bodies Terpenoid backbone biosynthesis Tryptophan metabolism Valine, leucine and isoleucine degradation	GTR+F+R6	LG+F+R5
280	Peptide chain release factor 2	J	Translation factors	TIM+F+R5	LG+F+R5
281	DNA mismatch repair protein MutL	L	Mismatch repair	TIM3+F+R6	LG+F+R6
282	Rod shape-determining protein MreB	D	Chromosome and associated proteins	GTR+F+R5	LG+R4

Group	Annotation	COG	KEGG	Best substitution model	
				Nucleotides	Amino acids
			Cytoskeleton proteins Prokaryotic defense system		
283	Enolase	G	Glycolysis Methane metabolism RNA degradation	GTR+F+R6	LG+F+R5
284	Transcription elongation factor GreA	K	Transcription machinery	GTR+F+R5	LG+I+G4
285	Carbamoyl-phosphate synthase large chain	F	Alanine, aspartate and glutamate metabolism Pyrimidine metabolism	GTR+F+R6	LG+F+R6
286	Carbamoyl-phosphate synthase small chain	F	Alanine, aspartate and glutamate metabolism Pyrimidine metabolism	GTR+F+R6	LG+R5
287	Transamidase GatB domain protein	S	Function unknown	TIM3+F+R5	LG+F+I+G4
288	RNA polymerase sigma factor RpoD	K	Transcription machinery	GTR+F+R6	LG+F+R5

24

Fig. S1. Maximum-likelihood tree based on 16S rRNA gene sequences showing the phylogenetic relationship of *Erythrobacteraceae* type strains. Bootstrap values are based on 1,000 replicates; only bootstrap values ≥70 % are shown. Bar, 0.02 substitutions per nucleotide position. Type species within the family *Erythrobacteraceae* are marked in bold. Red, orange, yellow, green, blue, indigo and purple represent the genera *Altererythrobacter*, *Croceibacterium*, *Croceicoccus*, *Erythrobacter*, *Erythromicrobium*, *Porphyrobacter* and *Qipengyuania*, respectively. *Rhodospirillum rubrum* ATCC 11170^T was used as an outgroup.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Aeb. gangjinensis KJ7^{T} (JF751048)
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Aeb. confluentis KEM-4^{T} (KX129915)
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Aeb. marinus H32^{T} (EU726272)
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Aeb. insulae BPTF-M16^{T} (MH206217)
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Aeb. ishigakiensis NITE-AP48^{T} (AB363004)
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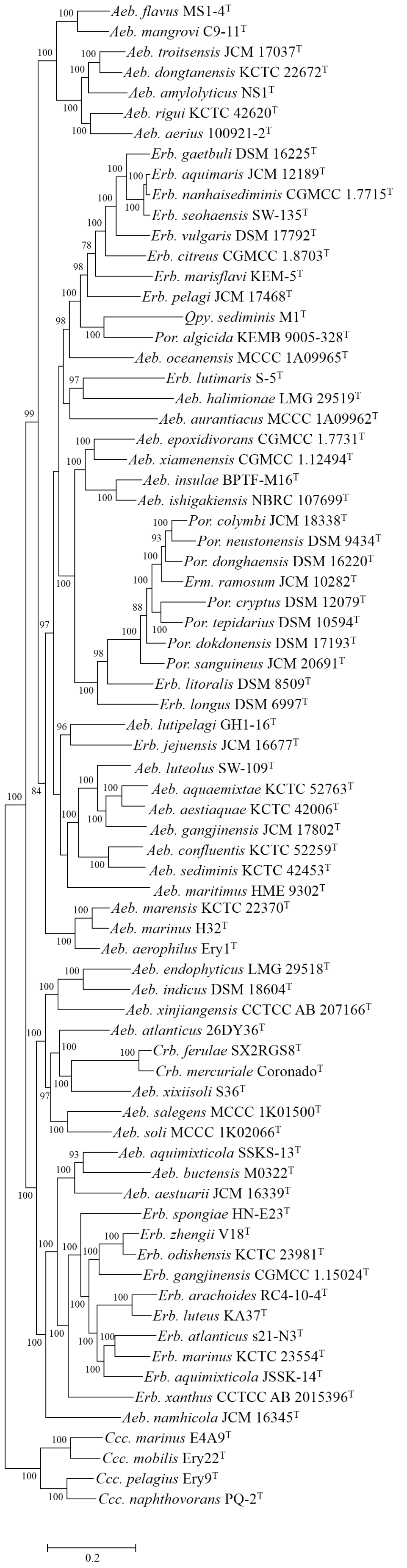
Fig. S2. Maximum-likelihood tree based on the concatenation of 288 single-copy OCs protein sequences showing the phylogenetic relationship of type strains belonging to the family *Erythrobacteraceae*. Bootstrap values are based on 100 replicates. Bar. 0.2 substitutions per amino acid position. *Rhodospirillum rubrum* ATCC 11170^T was used as an outgroup (not shown).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Erb. vulgaris DSM 17792^{T}
Erb. citreus CGMCC 1.8703^{T}
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Erb. pelagi JCM 17468^{T}
Qpy. sediminis M1^{T}
Por. algicida KEMB 9005-328^{T}
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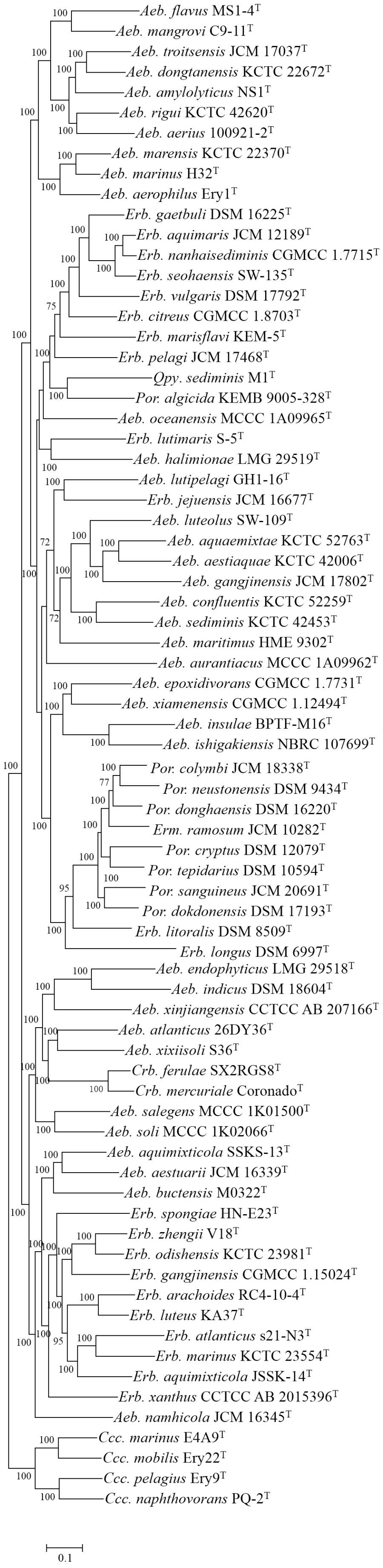
0.2

Fig. S3. Maximum-likelihood tree based on the partition of 288 single-copy OCs gene sequences showing the phylogenetic relationship of type strains belonging to the family *Erythrobacteraceae*. Bootstrap values are based on 100 replicates. Bar. 0.1 substitutions per nucleotide position. *Rhodospirillum rubrum* ATCC 11170^T was used as an outgroup (not shown).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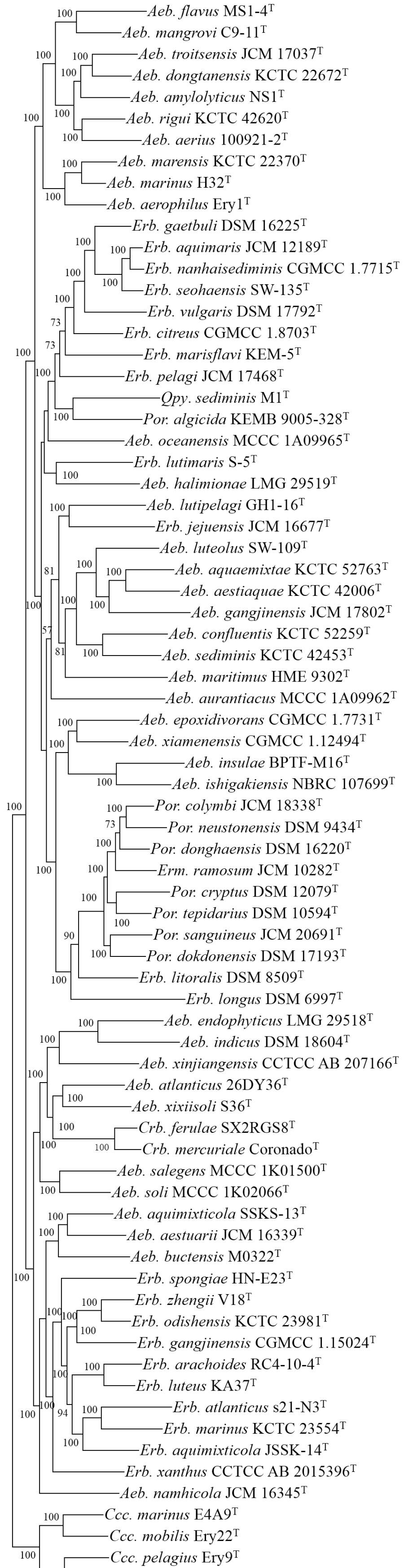
Ccc. marinus E4A9^{T}
Ccc. mobilis Ery22^{T}
Ccc. pelagius Ery9^{T}
Ccc. naphthovorans PQ-2^{T}
0.1

Fig. S4. Maximum-likelihood tree based on the concatenation of 288 single-copy OCs gene sequences showing the phylogenetic relationship of type strains belonging to the family *Erythrobacteraceae*. Bootstrap values are based on 100 replicates. Bar. 0.1 substitutions per nucleotide position. *Rhodospirillum rubrum* ATCC 11170^{T} was used as an outgroup (not shown).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Ccc. marinus E4A9^{T}
Ccc. mobilis Ery22^{T}
Ccc. pelagius Ery9^{T}
Ccc. naphthovorans PQ-2^{T}
0.1

Fig. S5. A heatmap of ANI values for 74 type strains within the family *Erythrobacteraceae*.

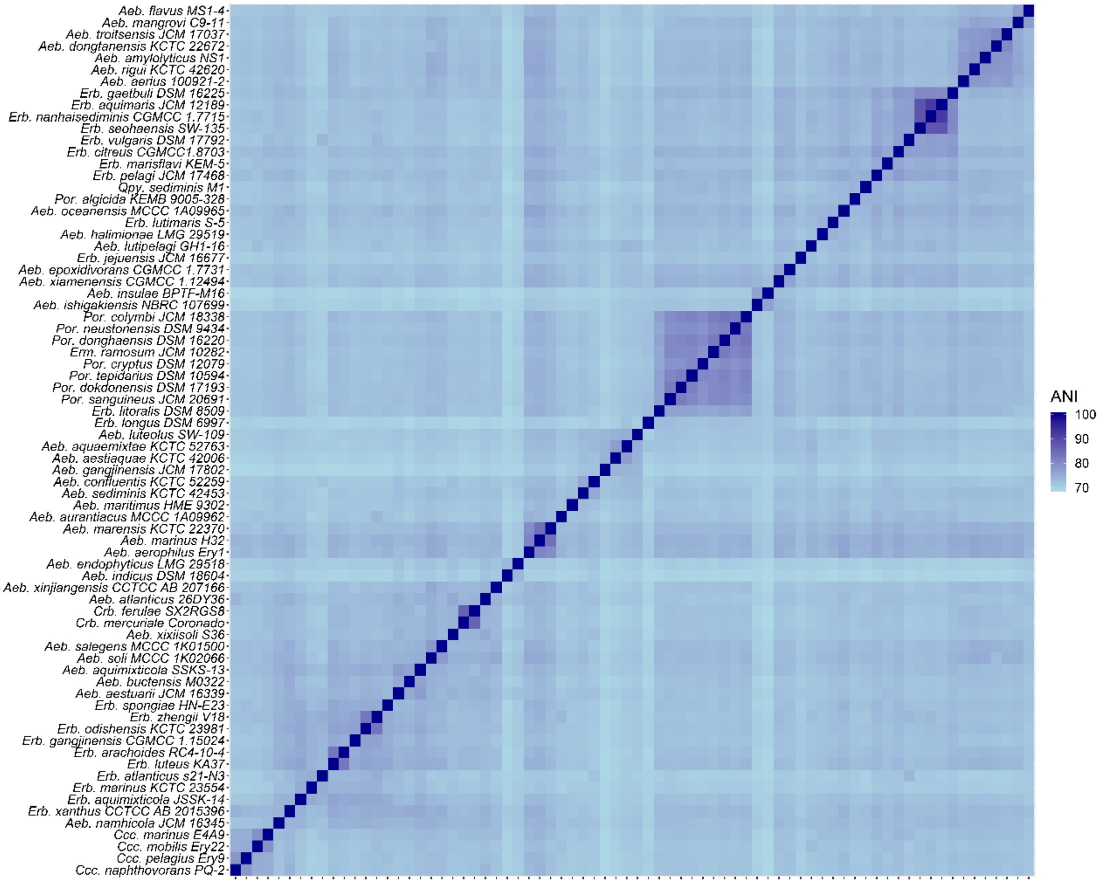


Fig. S6. A heatmap of AAI values for 74 type strains within the family *Erythrobacteraceae*.

Fig. S7. A heatmap of POCP values for 74 type strains within the family *Erythrobacteraceae*.

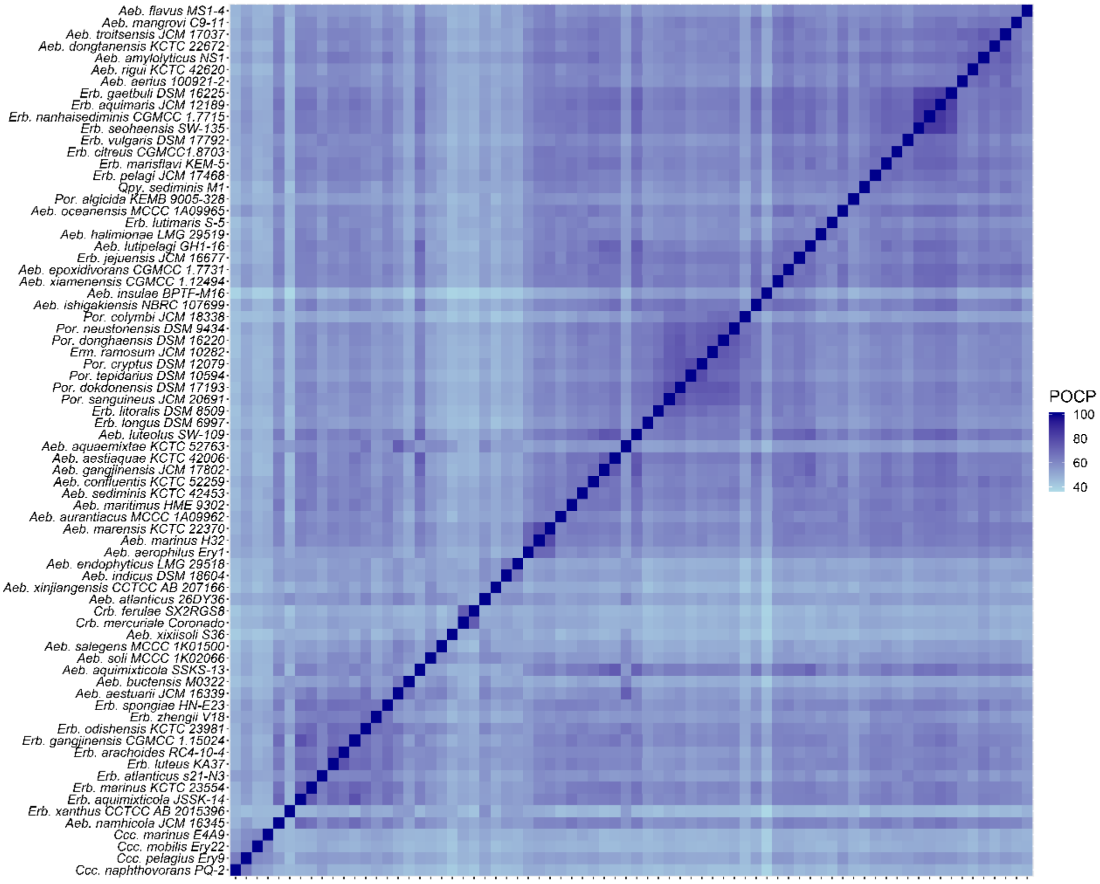
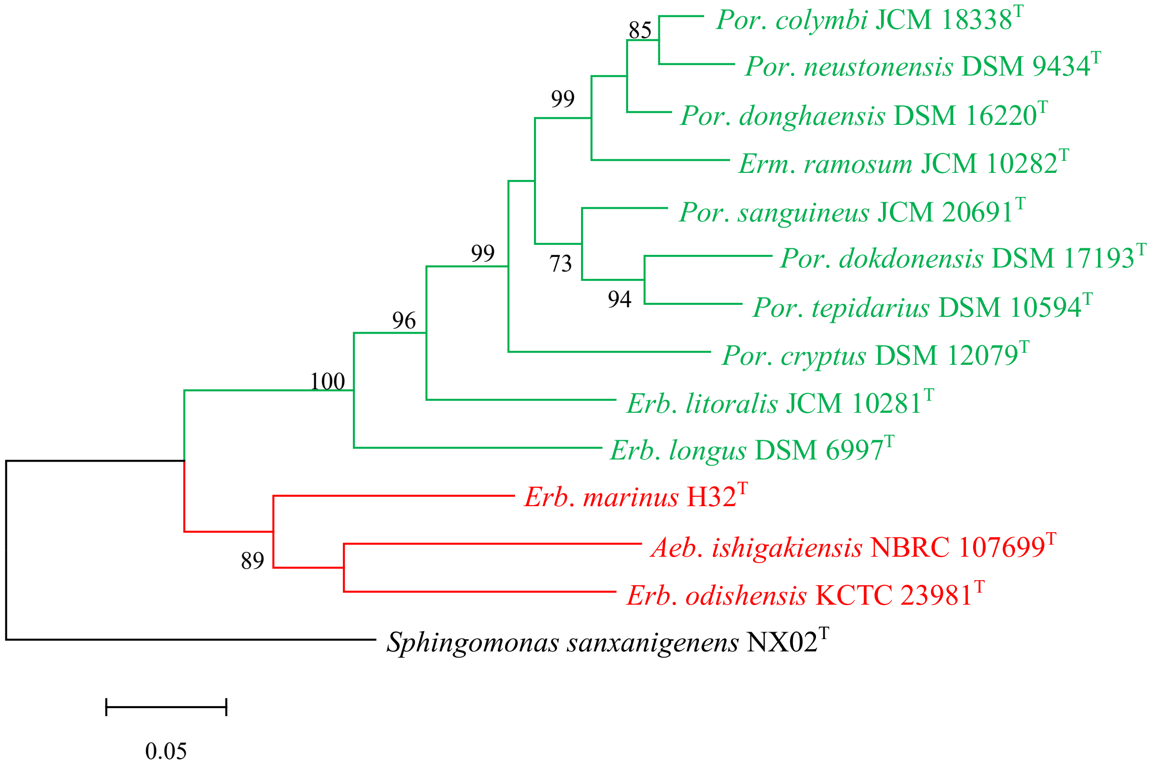


Fig. S8. Maximum-likelihood tree based on protein sequences of aerobic anoxygenic photosynthesis. Bootstrap values are based on 1,000 replicates; only bootstrap values ≥70 % are shown. Bar, 0.05 substitutions per amino acid position. *Sphingomonas sanxanigenens* NX02^T was used as an outgroup.



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