

Peculiar features of the plastids of the colourless alga *Euglena longa* and photosynthetic euglenophytes unveiled by transcriptome analyses

Kristína Záhonová, Zoltán Füßy, Erik Birčák, Anna M. G. Novák Vanclová, Vladimír Klimeš, Matej Vesteg, Juraj Krajčovič, Miroslav Oborník, Marek Eliáš

SUPPLEMENTARY FIGURES S1 – S8

SUPPLEMENTARY DATA S1

BUSCO Assessment Results

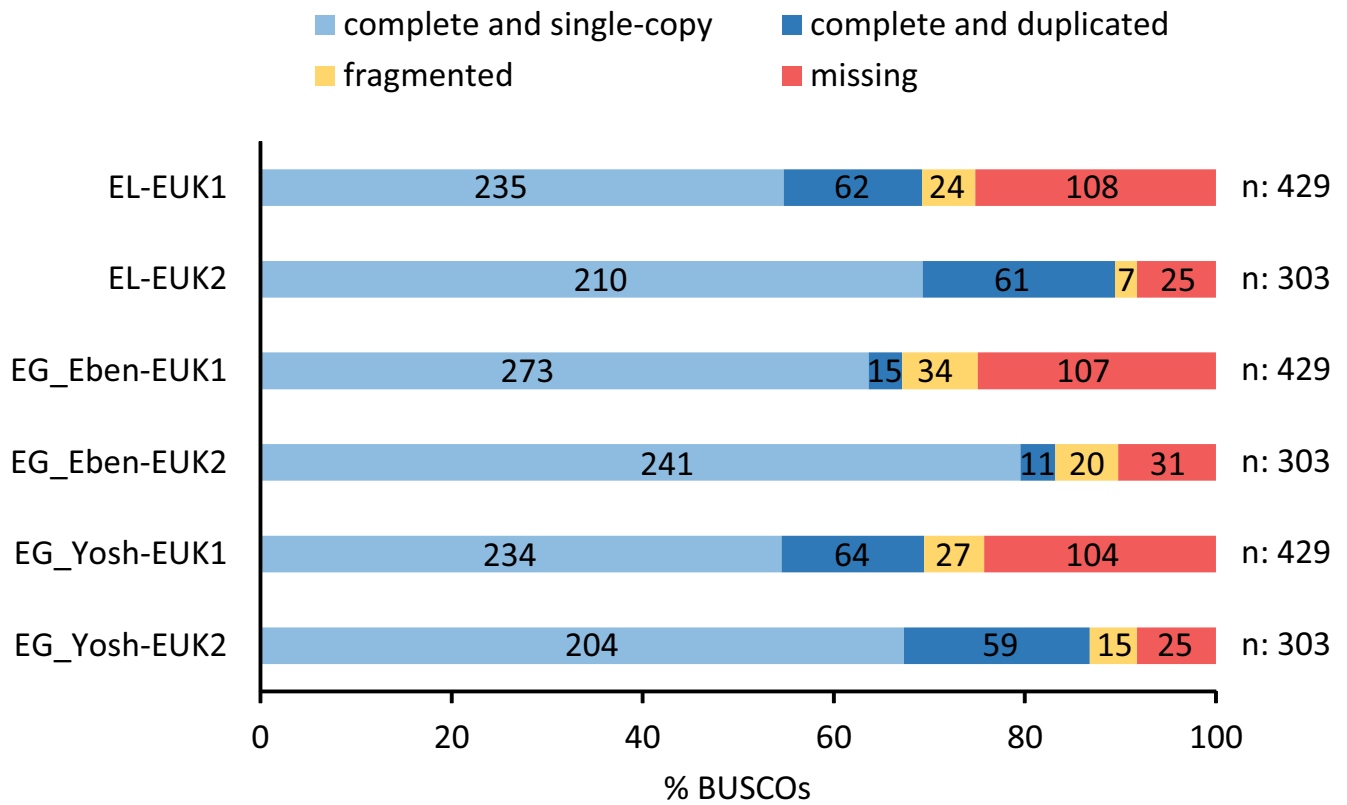


Figure S1: BUSCO analysis of the transcriptomic data from *Euglena* spp. Two sets of conserved eukaryotic orthologs (EUK1 and EUK2) were used to assess the completeness of the *E. longa* transcriptome, compared to publicly available data from *E. gracilis*. EG_Eben, *E. gracilis* from [7]; EG_Yosh, *E. gracilis* from [9]; EL, *E. longa* from this work; n, number of orthologs in the BUSCO dataset.

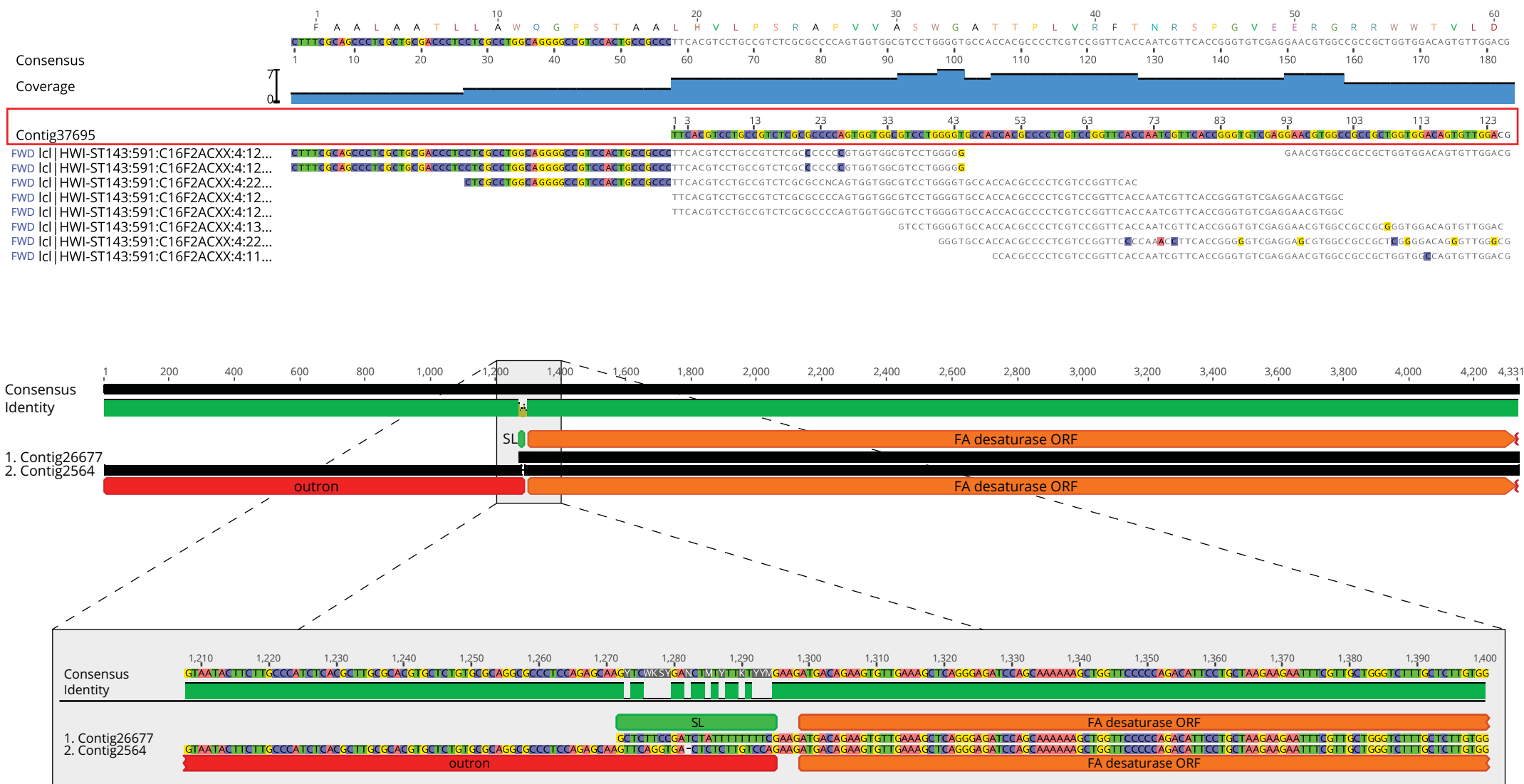


Figure S2: Examples of *E. longa* contigs lacking the 5'-end SL sequence due to truncation or incomplete splicing. A) Although iterative read mapping extended the assembled Contig37695 (arginyl-tRNA synthetase) towards its 5'-end, it did not yield the full open reading frame (indicated by protein sequence above the consensus sequence). B) Alignment of two contigs encoding the same protein (fatty acid desaturase; orange box) is presented. Contig26677 bears a SL sequence (green box) at its 5'-end, whereas Contig2564 represents the same transcript before trans-splicing of the outon (red box) and the SL-RNA.

rps2	rpl2	rrn5S	mat2	rps18	psaI	psbJ	ycf4	psaI
rps3	rpl5	rrn16S	roaA	atpA	psaM	psbK		ycf65
rps4	rpl12	rrn23S		atpB	psbA	psbL		mat5
rps7	rpl14	rbcl		atpE	psbB	psbN		
rps8	rpl16	rpoA		atpF	psbC	psbT		
rps9	rpl20	<u>rpoB</u>		atpH	psbD	psbZ		
rps11	rpl22	<u>rpoC1</u>		atpI	psbE	psb30		
rps12	rpl23	<u>rpoC2</u>		psaA	psbF	chlI		
rps14	rpl32	<u>tufA</u>		psaB	psbH	petB		
rps19	rpl36	ycf13	<i>E. longa</i>	psaC	psbI	petG	<i>E. gracilis</i>	<i>M. parapyrum</i>
								<i>Eur. anabaena</i>
								<i>T. volvocina</i>
								<i>S. acuminata</i>

Figure S3: Genes in euglenophyte plastid genomes. For simplicity, only selected euglenophytes (*E. longa*, *E. gracilis*, and species with the maximum plastid-encoded genes found) are included. *E. longa* genes fully covered by the transcriptomic data obtained are in bold, genes with only a partial coverage are underlined.

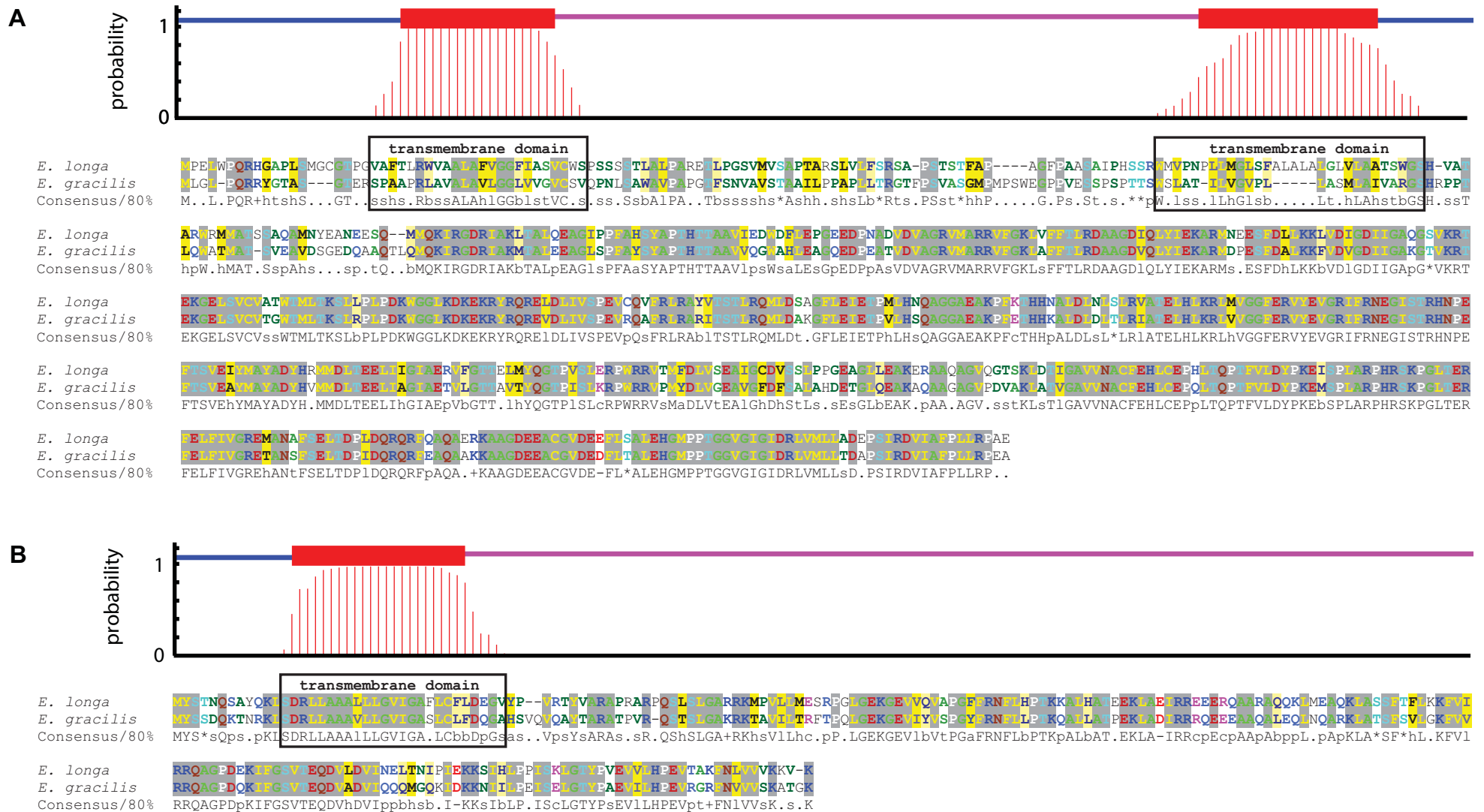


Figure S4: Two classes of plastid-targeting bipartite topogenic signals (BTs) in *Euglena*. The figure shows two proteins exemplifying the two classes of plastid-protein presequences (or BTs) that can be found in *Euglena* spp. The alignments were prepared using MAFFT v7 and processed for visualization using Chroma v1.0. Class I BTs (A; represented by lysyl-tRNA synthetase) contains two transmembrane domains (boxed), while class II (B; represented by ribosomal protein L9) has one. The first domain overlaps with the signal peptide, and is trailed by the transit peptide that is (Class I) or is not (Class II) followed by the second transmembrane domain presumably serving as a membrane anchor during the ER-to-plastid trafficking. Following the two-step cleavage of the presequence, the mature protein is released to the stroma (or possibly inserted into the inner envelope membrane via the so-called stop-transfer pathway). Note the high sequence similarity between the presequences of orthologous proteins from *E. gracilis* and *E. longa*.

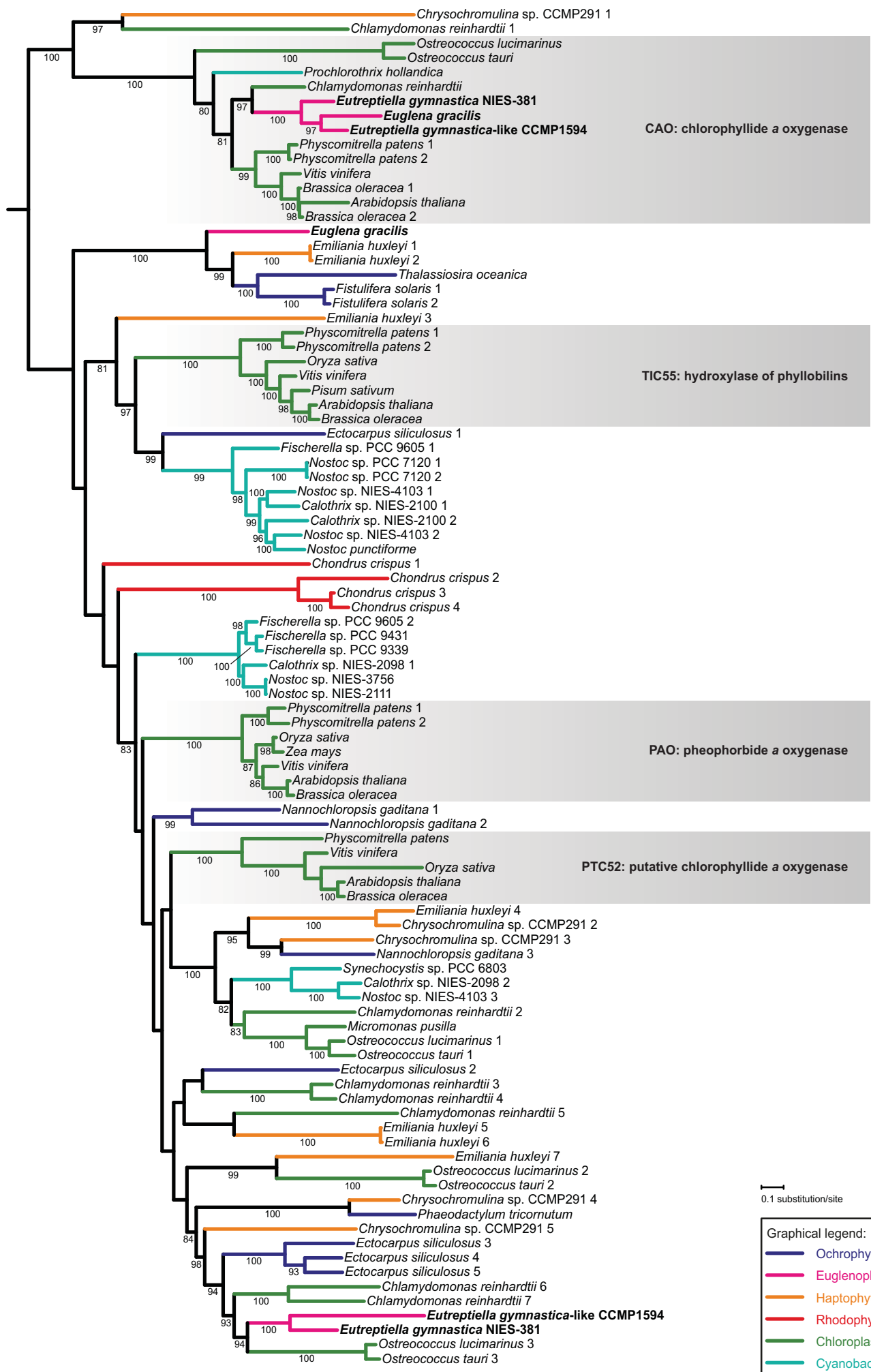


Figure S5: Phylogenetic analysis of Tic55 family proteins. The maximum likelihood phylogenetic tree documents that neither of the euglenophyte Tic55 homologs is a *bona fide* TIC55 protein (grey box named TIC55: hydroxylase of phyllobilins). Three sequences belong to the group of CAO (chlorophyllide *a* oxygenase) proteins, while others represent different branches of the broader family. Bootstrap support values are given when ≥ 80 .

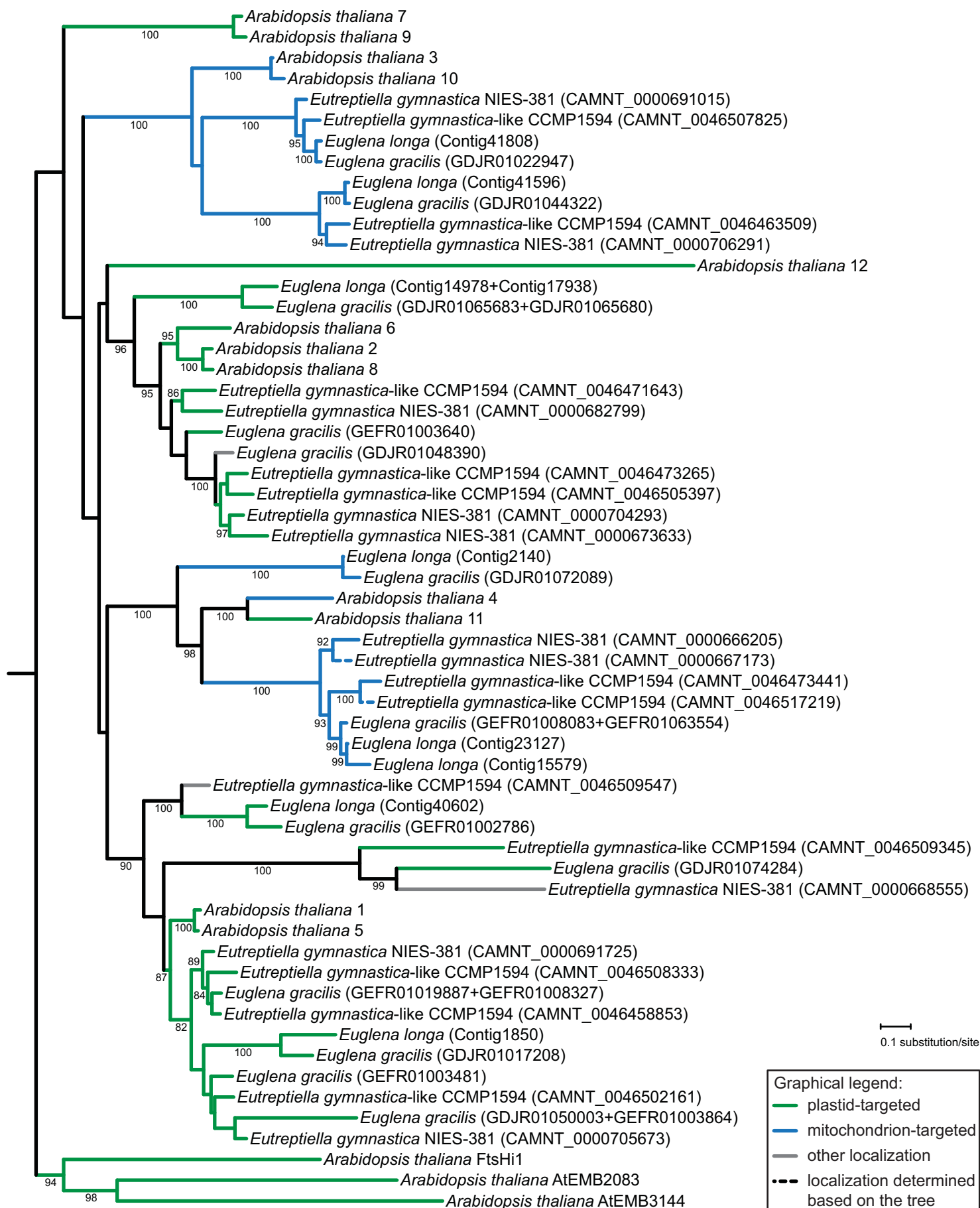


Figure S6: Phylogenetic analysis of FTSH proteases. The maximum likelihood tree was inferred from an alignment of all identified euglenophyte FTSH proteases and the previously described FTSH protease family members from *Arabidopsis thaliana*. Note the reduction of the repertoire of plastid-targeted FTSH proteases in *E. longa* and the absence of euglenophyte orthologs of the *A. thaliana* FTSH12. Dashed lines indicate incomplete sequences whose targeting was indirectly inferred from their position in the tree. Bootstrap support values are given when ≥ 80 .

Euglena longa
Euglena gracilis
Eutreptiella gymnastica NIES-381
Eutreptiella gymnastica-like CCMP1594
Candidatus Lambdaproteobacteria bacterium isolate PCRbin3
Candidatus Lambdaproteobacteria bacterium RIF0XYD2_FULL_50_16
Deltaproteobacteria bacterium UBA1014
Proteobacteria bacterium TMED154
SAR324 cluster bacterium REDSEA-S11_B7
SAR324 cluster bacterium REDSEA-S06_B4
SAR324 cluster bacterium JCVI-SC AAA005
"UBA10388"
Deltaproteobacteria bacterium UBA1121
SAR324 cluster bacterium REDSEA-S33_B4
SAR324 cluster bacterium SAR324-CTD10
"UBA12577"
Consensus/80%

IQEIN^{ED}EEHHKK^{CP}DD^{ETPLF}ESRR^IENQ⁻⁻QELLPRV^{VD}VTVE^{MG}QRAL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
IAAIN^{ED}EEHHKK^{CP}DD^{ETPLF}ENRR^IERK^Q--QELLPRV^{VD}VTVE^{MG}QRAL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
QKQINY^{ED}EEAAAG^{TV}ED^{ETPLF}DRMRK^{ET}LDPN^{HL}VR^{VD}TTT^{PL}GL^{QR}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
DKIN^{EA}EEKSKG^{KP}DE^{ETPLF}ERR^RETRS⁻⁻SD^{VL}TR^{VD}AT^{LG}FS^{QR}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
VESIN^{ED}EEELSK^{DP}ED^{ETPLF}EYER^RTE^{SG}KK⁻⁻EHLT^{SR}VDVVP^{IG}KQ^{RL}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
VEKIN^{ED}EEEMSK^{DKT}DN^{ETPLF}YEGIK^{ER}KD⁻⁻SM^{TA}TRI^{DM}FC^QQ^{RL}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
VEEVN^{KS}DIASEK^{LD}DN^{ETPLF}ENNR^KERG^D--RDM^{TT}RI^{DA}AP^{IG}MQ^{RL}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
VEEVN^{KS}DIASEK^{LD}DN^{ETPLF}ENNR^KERG^D--RDM^{TT}RI^{DA}AP^{IG}MQ^{RL}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
VEEVN^{KS}DIASEK^{LD}DN^{ETPLF}ENNR^KERG^D--RDM^{TT}RI^{DA}AP^{IG}MQ^{RL}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
VEEVN^{KS}DIASEK^{LD}DN^{ETPLF}ENNR^KERG^D--RDM^{TT}RI^{DA}AP^{IG}MQ^{RL}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
VEEVN^{RP}DDAF^{EK}LD^{DN}ETPL^FEYEE^{PS}ERG^D--KDL^{TR}VM^{DA}AP^{IG}KQ^{RL}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
VEEVN^{RP}DDAF^{EK}LD^{DN}ETPL^FEYEE^{PS}ERG^D--KDL^{TR}VM^{DA}AP^{IG}KQ^{RL}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
VEEIN^{QP}DMV^{FD}K^{LD}DN^{ETPLF}EYER^KKD⁻⁻KDM^{TS}RV^{VD}VSP^{IG}KQ^{RL}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
VEEIN^{SD}TKAF^{EK}LD^{DN}ETPL^FEQH^RERG^D--NDL^{TR}RV^{VD}VSP^{IG}KQ^{RL}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
VEEINRDTKAF^{EK}LD^{DN}ETPL^FEQH^RERG^D--NDL^{TR}RV^{VD}VSP^{IG}KQ^{RL}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
VEEINRDTKAF^{EK}LD^{DN}ETPL^FEQH^RERG^D--NDL^{TR}RV^{VD}VSP^{IG}KQ^{RL}AL^VAPPR^{KG}IV^{MQ}IAN^{SS}AE^{NH}FN^{IN}LIVLL^{DER}EE^{VE}EQ^{RS}KGE^VISST^{DE}HP
V-c1NfCps-pb.t.CkILFDsLTPLaPp+LPLeP.c.pdbssRIIDLssPIGBGQRTIVAPPRGTGTbILQtIANStspNH-VDLIVLLIDERPEEVT-MpRSVCGEIVLSTDEPA

Euglena longa
Euglena gracilis
Eutreptiella gymnastica NIES-381
Eutreptiella gymnastica-like CCMP1594
 Candidatus Lambdaproteobacteria bacterium isolate PCRbin3
 Candidatus Lambdaproteobacteria bacterium RIFOXD2_FULL_50_16
 Deltaproteobacteria bacterium UBA1014
 Proteobacteria bacterium TMED154
 SAR324 cluster bacterium REDSEA-S11_B7
 SAR324 cluster bacterium REDSEA-S06_B4
 SAR324 cluster bacterium JCVI-SC AAA005
 "UBA10388"
 Deltaproteobacteria bacterium UBA1121
 SAR324 cluster bacterium REDSEA-S33_B4
 SAR324 cluster bacterium SAR324-CTD10
 "UBA12577"
 Consensus/80%

AIDINRSGGRKEEDLFFSTEEQATIRVRKSSFFVYDAMHLHLERLQKPTTEAARQHVRE-----APPPSKDPDGSAAAMSTSSSDQRQSPDRDGSLLHGPRRDGSA--RRSGSRGRNE
AIDINRSGGRKEEDLFFSPKEEALVCIQRRTTSFYVDAMYLLEKLKLPTEAARQHVREQLQGLYLAAPPNADSSASNAAMDANSRDRRGGGRNGYSYGGGRSDRDRDRDRKGRGRDRSP
AIDINKSGGRKEEDLLELPEGEKQVKKRRRTTSVWVDAMDLLKQMGKTPSSRTTEAVDQHVGV-----DTTGMRPEEPTQKQRY-----SQPSYRERDRDRDRY-----
AIDVNGSGGRKEEELPEVEVGQVITRRRLAPFYVDALILLDRVQRTSSNDEAGIVIEKGL-----SQPSYRERDRDRDRY-----
AIDINKSGGRKEEDLTPKKQDRIIVVRKVSSSPVSEMEIMQEKLFKDSNENIDMMDK-----
ALPIEKGAIRKEEELLP--NADVVKRRISATKSQDGLFYLLDKMKKKTNDLQLQMVNS-----
SIDINKSGGRKEEELIEKGDDRIIVVRKVASNVVEAMELFDKMEKKNNEEIHMMDK-----
SIDINKSGGRKEEELIEKGDDRIIVVRKVASNVVEAMELFDKMEKKNNEEIH-----
SIDINKSGGRKEEELIEKGDDRIIVVRKVASNVVEAMELFDKMEKKNNEEIHMMDK-----
SIDINKSGGRKEEELIEKGDDRIIVVRKVASNVVEAMELFDKMEKKNNEEIHMMDK-----
SIDINKSGGRKEEELIEKGDDRIIVVRKVASNVVEAMELFDKMEKKNNEEIHMMDK-----
AIDINKSGGRKEEELMEKNDRIIVVRKVQAQSAIESMEIMVEKLSKKSNEKIDMMDK-----
AIDINKSGGRKEEELMEKNDRIIVVRKVQAQSSIESMEIMVEKLSKKSNEKIDMMDK-----
AIDINKSGGRKEEELIEKADRIIVVRKVQSQNVVEAMELIDKMKSKKENSEIDMMDK-----
AIDLSKSGGRKEEELIEKANDDRIIVVRKVQSQNVVEAMELIDKMKSKKENSEIDMMDK-----
AIDLSKSGGRKEEELVEKADRIIVVRKVQSQNVVEAMELIDKMEKKENVNIDMMDK-----
AIDLSKSGGRKEEELVDKADRIIVVRKVQSQNVVEAMELIEKMEKKENVNIDMMDK-----
tIdLSKSGTRKEELLbp. --LcpIw.LR+LlTPl.vS-tbEFbb-KbpKFcSnPpPLpbhcc.

GPRDGGNRQNSGHRWGGSGLLMGGH
DRGRDYGKRRRSSGR-----

.....

Figure S7: Sequences of the euglenophyte translation-termination factor Rho and their comparison to bacterial homologs. The multiple sequence alignments includes Rho factor sequences from all four euglenophytes analysed and their closest bacterial homologs resolved by a phylogenetic analysis (see Fig. 6). Note the high similarity of the euglenophyte and bacterial sequences, indicative of a conserved function. The euglenophyte sequences exhibit an N-terminal extension bearing all characteristics of a plastid-targeting BTS (note the presence of the two predicted transmembrane domains). The sequence from *Eutreptiella gymnastica*-like CCMP1594 is truncated at the N-terminus.

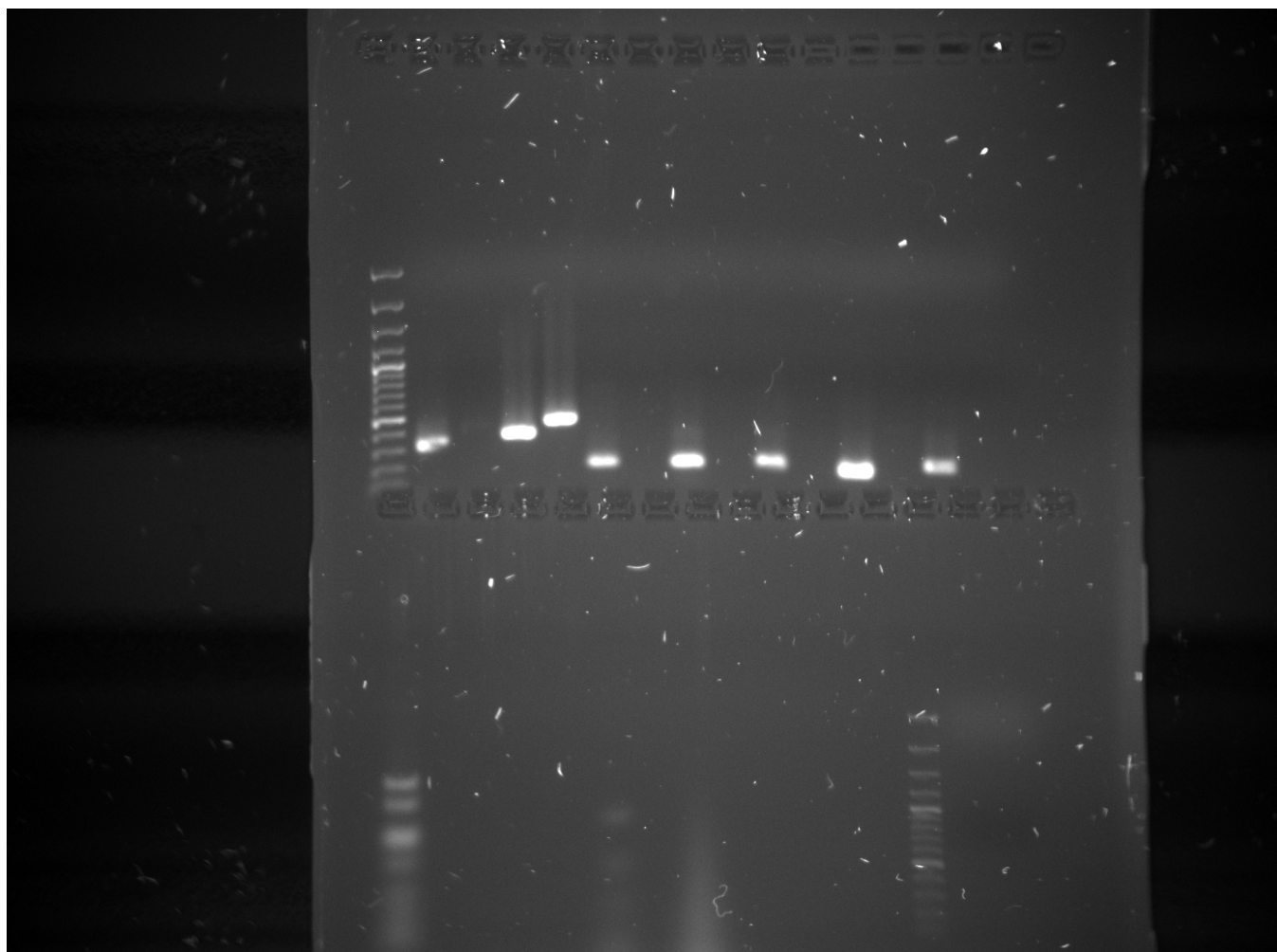


Figure S8: Full original version of the electrophoretic gel, whose part is shown (with an inverted greyscale) in Fig. 1A.

SUPPLEMENTARY DATA S1 - Rho factor full tree Newick

(Euglena longa:0.2454073866,Euglena gracilis:0.1071609403,((Eutreptiella gymnastica-like CCMF1594:0.3737283808,(((OGG94779.1:0.1685048508,Candidatus Lambdaproteobacteria bacterium RIFOXYC1_FULL_56_13__Candidatus Lambdaproteobacteria__Proteobacteria_Bacteria:0.1008004207)55:0.068073,SAR324 cluster bacterium__SAR324 cluster_Deltaproteobacteria__Proteobacteria_Bacteria:0.1991998136)100:0.296532,((((SAR324 cluster bacterium SAR324-CTD10 Contig82360 d_Bacteria_p_SAR324_c_SAR324_o_SAR324_f_NAC60-12_g_Arctic96AD-7_s_Arctic96AD-7 sp1:0.0000023338,UBA12577 d_Bacteria_p_SAR324_c_SAR324_o_SAR324_f_NAC60-12_g_Arctic96AD-7_s_Arctic96AD-7 sp2:0.0135532591)100:0.016115,SAR324 cluster bacterium REDSEA-S33_B4 scaffold91 d_Bacteria_p_SAR324_c_SAR324_o_SAR324_f_NAC60-12_g_Arctic96AD-7_s_Arctic96AD-7 sp3:0.0310352670)100:0.175969,Deltaproteobacteria bacterium UBA1121 UBA1121_contig_52842 d_Bacteria_p_SAR324_c_SAR324_o_SAR324_f_NAC60-12_g_UBA8110_s_UBA8110 sp1:0.0842116089)100:0.031041,(SAR324 cluster bacterium JCVI-SC AAA005 ctg_270 d_Bacteria_p_SAR324_c_SAR324_o_SAR324_f_NAC60-12_g_JCVI-SCAAA005_s_JCVI-SCAAA005 sp1:0.0042855830,UBA10388 d_Bacteria_p_SAR324_c_SAR324_o_SAR324_f_NAC60-12_g_JCVI-SCAAA005_s_JCVI-SCAAA005 sp2:0.0138762315)100:0.112689)99:0.038696,(Deltaproteobacteria bacterium UBA1014 UBA1014_contig_2062 d_Bacteria_p_SAR324_c_SAR324_o_SAR324_f_NAC60-12_g_UBA1014_s_UBA1014 sp1:0.0045134975,((SAR324 cluster bacterium REDSEA-S11_B7 scaffold89 d_Bacteria_p_SAR324_c_SAR324_o_SAR324_f_NAC60-12_g_UBA1014_s_UBA1014 sp2:0.0000023338,SAR324 cluster bacterium REDSEA-S06_B4 scaffold119 GTDB Taxonomy_Undefined_Failed Quality Check_1 mismatch from_s_UBA1014 sp2:0.0000023338)69:0.000003,Proteobacteria bacterium TMED154__Proteobacteria_Bacteria:0.0000023338)99:0.004285)99:0.128756)31:0.039085,Candidatus Lambdaproteobacteria bacterium isolate PCRbin3 scaffold145:0.1944772611)32:0.034464)19:0.076709,(((Geothermobacter sp. HR-1__Geothermobacter_Geobacteraceae_Desulfuromonadales_Deltaproteobacteria__Proteobacteria_Bacteria:0.0921128103,(Geoalkalibacter ferrihydriticus__Geoalkalibacter_Geobacteraceae_Desulfuromonadales_Deltaproteobacteria__Proteobacteria_Bacteria:0.0919029214,(Desulfuromonas acetoxidans DSM 684__Desulfuromonas_Desulfuromonadaceae_Desulfuromonadales_Deltaproteobacteria__Proteobacteria_Bacteria:0.1359627243,Deltaproteobacteria bacterium HGW-Deltaproteobacteria-4__Deltaproteobacteria__Proteobacteria_Bacteria:0.0866248835)98:0.021889)98:0.022295)58:0.010264,(((Pelobacter acetylenicus__Pelobacter_Desulfuromonadaceae_Desulfuromonadales_Deltaproteobacteria__Proteobacteria_Bacteria:0.0843323056,Pelobacter sp. SFB93__Pelobacter_Desulfuromonadaceae_Desulfuromonadales_Deltaproteobacteria__Proteobacteria_Bacteria:0.0444400910)98:0.033698,((Desulfuromonadales bacterium C00003093__Desulfuromonadales_Deltaproteobacteria__Proteobacteria_Bacteria:0.0994831335,Desulfuromusa kysingii__Desulfuromusa_Desulfuromonadaceae_Desulfuromonadales_Deltaproteobacteria__Proteobacteria_Bacteria:0.1113619984)100:0.029728,Geopsychrobacter electrodiphilus__Geopsychrobacter_Geobacteraceae_Desulfuromonadales_Deltaproteobacteria__Proteobacteria_Bacteria:0.1461550384)100:0.100917)42:0.002964,Desulfuromonas sp.__Desulfuromonas_Desulfuromonadaceae_Desulfuromonadales_Deltaproteobacteria__Proteobacteria_Bacteria:0.0715751841)43:0.012854,(((Desulfuromonas sp.__Desulfuromonas_Desulfuromonadaceae_Desulfuromonadales_Deltaproteobacteria__Proteobacteria_Bacteria:0.0494176536,Desulfuromonas sp. DDH964__Desulfuromonas_Desulfuromonadaceae_Desulfuromonadales_Deltaproteobacteria__Proteobacteria_Bacteria:0.0257743651)99:0.020152,Desulfuromonas sp.__Desulfuromonas_Desulfuromonadaceae_Desulfuromonadales_Deltaproteobacteria__Proteobacteria_Bacteria:0.0367949605)98:0.013216,Desulfuromonas sp.__Desulfuromonas_Desulfuromonadaceae_Desulfuromonadales_Deltaproteobacteria__Proteobacteria_Bacteria:0.0703874259)98:0.028793)32:0.010314)100:0.125524,((((((((((((Ga mmaproteobacteria bacterium__Gammaproteobacteria__Proteobacteria_Bacteria:0.0986601772,Methylophaga aminisulfidivorans__Methylophaga_Piscirickettsiaceae_Thiotrichales_Gammaproteobacteria__Proteobacteria_Bacteria:0.1165975437)100:0.266530,((((Gammaproteobacteria bacterium SG8_15__Gammaproteobacteria__Proteobacteria_Bacteria:0.1138794890,((((Algicola sagamiensis__Algicola_Pseudoalteromonadaceae_Alteromonadales_Gammaproteobacteria__Proteobacteria_Bacteria:0.0452406947,Pseudoalteromonas ulvae__Pseudoalteromonas_Pseudoalteromonadaceae_Alteromonadales_Gammaproteobacteria__Proteobacteria_Bacteria:0.0871108950)100:0.043128,Ferrimonas balearica__Ferrimonas_Ferrimonadaceae_Alteromonadales_Gammaproteobacteria__Proteobacteria_Bacteria:0.0775566822)100:0.019877,Idiomarina xiamenensis__Idiomarina_Idiomarinaceae_Alteromonadales_Gammaproteobacteria__Proteobacteria_Bacteria:0.0741299547)100:0.140580,((Endozoicomonas elysicola__Endozoicomonas_Hahellaceae_Oceanospirillales_Gammaproteobacteria__Proteobacteria_Bacteria:0.0817556924,(Motiliproteus sp. MSK22-1__Motiliproteus_Oceanospirillales_Gammaproteobacteria__Proteobacteria_Bacteria:0.1197722849,(Thalassolituus sp. CG17_big_fil_post_rev_8_21_14_2_50_53_8__Thalassolituus_Oceanospirillales_Gammaproteobacteria__Proteobacteria_Bacteria:0.0691289361,Bacterioplanes sanyensis__Bacterioplanes_Oceanospirillales_Gammaproteobacteria__Proteobacteria_Bacteria:0.0616847998)100:0.185081)78:0.082321)100:0.069361,Legionella sp.__Legionella_Legionellaceae_Legionellales_Gammaproteobacteria__Proteobacteria_Bacteria:0.3179032408)95:0.025615)81:0.022432,Coxiella sp. DG_40__Coxiella_Coxiellaceae_Legionellales_Gammaproteobacteria__Proteobacteria_Bacteria:0.1891986449)94:0.057402,Gammaproteobacteria bacterium TMED36__Gammaproteobacteria__Proteobacteria_Bacteria:0.4180340603)62:0.016645)71:0.014564,Candidatus Tenderia electrophaga__Candidatus Tenderia_Chromatiaceae_Chromatiales_Gammaproteobacteria__Proteobacteria_Bacteria:0.1408187123)76:0.019681,(bacterium BMS3Bbin12 Bacteria:__.0.1342390854,Candidatus Competibacter denitrificans__Candidatus Competibacter_Competibacteraceae_Gammaproteobacteria__Proteobacteria_Bacteria:0.1394531005)94:0.036123)87:0.028733,Candidatus Thiomargarita nelsonii__Thiomargarita_Thiotrichaceae_Thiotrichales_Gammaproteobacteria__Proteobacteria_Bacteria:0.2386490942)87:0.025091,Nitrosococcus watsonii__Nitrosococcus_Chromatiaceae_Chromatiales_Gammaproteobacteria__Proteobacteria_Bacteria:0.1648962600)87:0.033480)89:0.050122,Acidithiobacillales bacterium SG8_45__Acidithiobacillales_Acidithiobacillia__Proteobacteria_Bacteria:0.2580088435)97:0.068953,(Thermithiobacillus tepidarius__Thermithiobacillus_Thermithiobacillaceae_Acidithiobacillales_Acidithiobacillia__Proteobacteria_Bacteria:0.0477045728,(Acidithiobacillus caldus SM-1__Acidithiobacillus_Acidithiobacillaceae_Acidithiobacillales_Acidithiobacillia__Proteobacteria_Bacteria:0.0259065974,Acidithiobacillus ferrovirans SS3__Acidithiobacillus_Acidithiobacillaceae_Acidithiobacillales_Acidithiobacillia__Proteobacteria_Bacteria:0.0423585202)100:0.149970)100:0.116524)100:0.147834,((((((((Candidatus Puniceispirillum marinum IMCC1322__Candidatus Puniceispirillum_SAR116 cluster_Alphaproteobacteria__Proteobacteria_Bacteria:0.0498443321,Candidatus Puniceispirillum sp. TMED52__Candidatus Puniceispirillum_SAR116 cluster_Alphaproteobacteria__Proteobacteria_Bacteria:0.1551220806)100:0.100896,Candidatus Endolissoclinum sp. TMED26__Candidatus Endolissoclinum_Rhodospirillaceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.1120899188)66:0.037005,((Oceanibaculum nanhaiense__Oceanibaculum_Rhodospirillaceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0344470375,Oceanibaculum pacificum__Oceanibaculum_Rhodospirillaceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0121975962)100:0.070893,Magnetospirillum gryphiswaldense MSR-1__Magnetospirillum_Rhodospirillaceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.1001418173)52:0.013088)85:0.016306,(Rhodospirillales bacterium 47_12_T64__unclassified Rhodospirillales_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.1167871838,Fodinicurvata fenggangensis__Fodinicurvata_Rhodospirillaceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.1467474263)78:0.071493)57:0.025346,(((Rhodospirillales bacterium 20-60-12__unclassified Rhodospirillales_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0588527495,(((Acidocella aminolytica__Acidocella_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0162773844,Acidocella__Acetobacteraceae_Rhodospirillales_Alphaproteo bacteria__Proteobacteria_Bacteria:0.0207487411)100:0.097883,Rhodospirillales bacterium 20-64-7__unclassified Rhodospirillales_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0358830522)100:0.051927,(Acidiphilium sp. 21-60-14__Acidiphilium_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0382987101,Acidiphilium__Acetobacteraceae_Rhodospirillales_Alphaproteobact eria__Proteobacteria_Bacteria:0.03877232149)100:0.061550)100:0.038417)100:0.038632,(((Neoasaia chiangmaiensis__Neoasaia_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0044869253,Gluconobacter morbifer G707__Gluconobacter_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0521219162)98:0.009084,(Kozakia baliensis__Kozakia_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0178704978,Tanticharoenia sakaeratisensis__Tanticharoenia_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0534773389)86:0.000002)100:0.033190,((((((Acetobacter syzygii__Acetobacter_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0000000000,Acetobacter okinawensis__Acetobacter_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0000000000)0.000000,Acetobacter__Acetobacteraceae_Rhodospirillale s__Alphaproteobacteria__Proteobacteria_Bacteria:0.0000000000)0.000000,Acetobacter okinawensis__Acetobacter_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0000000000)0.000002,Acetobacter ghanensis__Acetobacter_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0000023226)100:0.009000,Acetobacter pasteurianus__Acetobacter_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0000023873)100:0.038796,Acetobacter__Acetobacteraceae_Rhodospir illales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0370842235)100:0.025413,(Acetobacter aceti__Acetobacter subgen. Acetobacter__Acetobacter_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0386657182,Acetobacter nitrogenifigens__Acetobacter_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0230264661)100:0.017113)99:0.010994)99:0.016672,(Gluconacetoba cter diazotrophicus__Gluconacetobacter_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0146084425,Komagataeibacter hansenii__Komagataeibacter_Acetobacteraceae_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.0581890264)86:0.009187)100:0.068339)98:0.031623,Elioraea tepidiphila__Elioraea_unclassified Rhodospirillales_Rhodospirillales_Alphaproteobacteria__Proteobacteria_Bacteria:0.1303361735)99:0.056071)40:0.005224,((((Alphaproteobacteria

bacterium GWF2_58_20__Alphaproteobacteria__Proteobacteria__Bacteria:0.2246958872,Tistrella mobilis__Tistrella_Rhodospirillaceae_Rhodospirillales__Alphaproteobacteria__Proteobacteria__Bacteria:0.2112129639)73:0.038188,(Niveispirillum irakense__Niveispirillum_Rhodospirillaceae_Rhodospirillales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1242406603,(Azospirillum brasiliense__Azospirillum_Rhodospirillaceae_Rhodospirillales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0171597909,Azospirillum sp. B510__Azospirillum_Rhodospirillaceae_Rhodospirillales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0365239112)100:0.070888)92:0.037312)64:0.024839,(((uncultured Alphaproteobacteria bacterium__environmental samples__Alphaproteobacteria__Proteobacteria__Bacteria:0.0940811313,(Rhodospira trueperi__Rhodospira_Rhodospirillaceae_Rhodospirillales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0000023338,Rhodospira trueperi__Rhodospira_Rhodospirillaceae_Rhodospirillales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0000023338)100:0.140556)70:0.024915,(Roseospirillum parvum__Roseospirillum_Rhodobiaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1209480895,(Caedibacter sp. 37-49__Caedibacter_Holosporales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1791261950,Caedimonas varicaedens__Caedimonas_Caedimonadaceae_Holosporales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1461191493)100:0.086544)82:0.030803)80:0.008090,Novispirillum itersonii__Novispirillum_Rhodospirillaceae_Rhodospirillales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1587071602)74:0.012414)56:0.010706,Rhodospirillaceae bacterium__Rhodospirillaceae_Rhodospirillales__Alphaproteobacteria__Proteobacteria__Bacteria:0.2128820915)52:0.004947,Alphaproteobacteria bacterium 41-28__Alphaproteobacteria__Proteobacteria__Bacteria:0.2403200494)47:0.011673)86:0.027436,(Candidatus Endolissoclinum sp. TMED37__Candidatus Endolissoclinum_Rhodospirillaceae_Rhodospirillales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1845069516,((Rhodospirillaceae bacterium TMED167__Rhodospirillaceae_Rhodospirillales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1406525887,Rhodospirillales bacterium RIFCSLOWO2_02_FULL_58_16__unclassified Rhodospirillales_Rhodospirillaceae_Rhodospirillales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1441072809)96:0.038206,Terasakiella sp. PR1__Terasakiella_Methylocystaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1643566526)92:0.022754)84:0.008095)86:0.019541,(Candidatus Odysella thessalonicensis__Candidatus Odysella_Candidatus Paracaedibacteraceae_Holosporales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0316406648,Candidatus Paracaedibacter acanthamoebae__Candidatus Paracaedibacter__Candidatus Paracaedibacteraceae_Holosporales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0298210916)100:0.154240)76:0.014297,(Alphaproteobacteria bacterium CG11_big_fil_rev_8_21_14_0_20_39_49__Alphaproteobacteria__Proteobacteria__Bacteria:0.3295106307,Alphaproteobacteria bacterium__Alphaproteobacteria__Proteobacteria__Bacteria:0.2648058121)89:0.062353)90:0.045239,(((((((Xanthobacter autotrophicus__Xanthobacter__Xanthobacteraceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0350845326,(Rhizobiales bacterium 39-66-18__Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0138435142,(Rhizobiales bacterium 17-65-6__Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0000023229,Rhizobiales bacterium 12-68-15__Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0045683792)100:0.022777)100:0.014069)99:0.019688,(Bosea sp. 117__Bosea_Bradyrhizobiaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0088674355,Ancylobacter__Xanthobacteraceae_Rhizobiales__Alphaproteobacteria__Proteo bacteria__Bacteria:0.0387871387)100:0.029007)81:0.013376,(((unclassified Rhizobiales miscellaneous__Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0631798976,Rhizobiales bacterium 65-9__Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1195467254)72:0.015637,((Chelatococcus__Chelatococcaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacter ia:0.0089305922,Chelatococcus__Chelatococcaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0000024009)100:0.015425,(Microvirga sp. BSC39__Microvirga_Methylobacteriaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0467770492,(Methylobacterium extorquens PA1__Methylobacterium_Methylobacteriaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0139693550,Methylobacterium sp. ARG-1__Methylobacterium_Methylobacteriaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0188343604)100:0.090373)100:0.057546)49:0.016317)44:0.012631,(Labrys sp. WJW__Labrys__Xanthobacteraceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0966241714,Bosea sp. AAP35__Bosea_Bradyrhizobiaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1275957014)37:0.016184)51:0.007788)97:0.031464,(((Pseudoxanthobacter soli__Pseudoxanthobacter__Xanthobacteraceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0481594487,(Amorphus coralli__Amorphus_Rhodobiaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0573703605,(Labrenzia sp. OB1__Labrenzia_Rhodobacteraceae_Rhodobacterales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0715041443,Roseibium sp. TrichSKD4__Roseibium_Rhodobacteraceae_Rhodobacterales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0325397934)100:0.036286)85:0.013999,Pleomorphomonas oryzae__Pleomorphomonas_Methylocystaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0788598110)86:0.022115)86:0.012155,Kaistia adipata__Kaistia_Rhizobiaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1123501610)72:0.026856,(((Hyphomicrobium sp. CS18SMeth3__Hyphomicrobium__Hyphomicrobiaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0574145180,Hyphomicrobium sp. 12-62-95__Hyphomicrobium__Hyphomicrobiaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0707576194)100:0.011555,Filomicrobium__Hyphomicrobiaceae_Rhizobiales__A lphaproteobacteria__Proteobacteria__Bacteria:0.0420769487)100:0.026890,Hyphomicrobium nitrativorans__Hyphomicrobium__Hyphomicrobiaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0297195832)100:0.130202,((Methylophil sp. M107__Methylophil_Methylocystaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0229072534,Methylophil sp. Yamaguchi__Methylophil_Methylocystaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0127006852)100:0.082743,(((Thermopetrobacter sp. TC1__Thermopetrobacter__Alphaproteobacteria__Proteobacteria__Bacteria:0.1635864021,Methyloceanibacter caenitepidi__Methyloceanibacter_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0844607735)83:0.020111,(alpha proteobacterium Mf 1.05b.01__Alphaproteobacteria__Proteobacteria__Bacteria:0.0994613699,((Chelativorans sp. BNC1__Chelativorans_Phyllobacteriaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0391582233,Bartonella ancashensis__Bartonella_Bartonellaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1663572522)98:0.016448,Rhizobiales bacterium__Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1088843830)100:0.091151)98:0.025898)75:0.016614,Lutibaculum baratangense__Lutibaculum_Rhodobiaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1277504102)63:0.010540,Rhizobiales bacterium__Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1223725732)68:0.021961)45:0.006458)43:0.002938)53:0.005772,(alpha proteobacterium IMCC14465__Alphaproteobacteria__Proteobacteria__Bacteria:0.1678268706,((Pelagibacterium__Hyphomicrobiaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.04279 53452,Maritalea myrionectae__Maritalea__Hyphomicrobiaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0816329179)99:0.028903,Cucumbacter marinus__Cucumbacter__Hyphomicrobiaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0318978221)100:0.026765)92:0.045451)57:0.010530)67:0.026029,Rhodopla nes sp. 22-YC6860__Rhodoplanes__Rhodobiaceae_Rhizobiales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0893523308)84:0.053634,(Euryhalocalis caribicus__Euryhalocalis__Hyphomonadaceae_Rhodobacterales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1862010712,((Phaeobacter gallaeciensis DSM 26640__Phaeobacter_Rhodobacteraceae_Rhodobacterales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0446750251,Rhodobacteraceae bacterium__Rhodobacteraceae_Rhodobacterales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1228101965)100:0.054753,Natronohydrobacter thiooxidans__Natronohydrobacter_Rhodobacteraceae_Rhodobacterales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1218103360)100:0.115785,Henriciella marina__Henriciella__Hyphomonadaceae_Rhodobacterales__Alphaproteobacteria__Proteobacteria__Bacteria:0.2480282869)98:0.067780)96:0.027087)100:0.034297,Candidatus Fonsibacter ubiquis__Candidatus Fonsibacter__Pelagibacterales__Alphaproteobacteria__Proteobacteria__Bacteria:0.3332872955)95:0.043206,(alpha proteobacterium Q-1__Alphaproteobacteria__Proteobacteria__Bacteria:0.2039494600,(Kordiimonas lipolytica__Kordiimonas_Kordiimonadaceae_Kordiimonadales__Alphaproteobacteria__Proteobacteria__Bacteria:0.0589549690,Kordiimonadales bacterium__unclassified Kordiimonadales_Kordiimonadales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1202066705)100:0.044735)99:0.095697)40:0.010808)74:0.034023,Sneathiella glossodoripedis__Sneathiella__Sneathiellaceae__Sneathiellales__Alphaproteobacteria__Proteobacteria__Bacteria:0.1477933350)100:0.134104,Magnetococcus marinus MC-1__Magnetococcus_Magnetococcaceae__Alphaproteobacteria__Proteobacteria__Bacteria:0.3441493265)97:0.063271)100:0.113416,(Desulfocurvus vexinensis__Desulfocurvus__Desulfovibrionaceae__Desulfovibrionales__Deltaproteobacteria__Proteobacteria__Bacteria:0.1462724611,(((Desulfovibrio vulgaris DP4__Desulfovibrio__Desulfovibrionaceae__Desulfovibrionales__Deltaproteobacteria__Proteobacteria__Bacteria:0.0333687768,uncultured delta proteobacterium__environmental samples__Deltaproteobacteria__Proteobacteria__Bacteria:0.1004683414)89:0.024185,Desulfovibrio alaskensis G20__Desulfovibrio__Desulfovibrionaceae__Desulfovibrionales__Deltaproteobacteria__Proteobacteria__Bacteria:0.0680554098)100:0.053844,Desulfovibrio gigas__Desulfovibrio__Desulfovibrionaceae__Desulfovibrionales__Deltaproteobacteria__Proteobacteria__Bacteria:0.1546105983)100:0.085566,Pseudodesulfovibrio piezophilus__Desulfovibrionaceae__Desulfovibrionales__Deltaproteobacteria__Proteobacteria__Bacteria:0.1277208097)98:0.024508)100:0.233356)86:0.029152,Calditerrivibrio nitroreducens__Deferribacteraceae__Deferribacterales__Deferribacteres__Bacteria:0.4437533724)80:0.035880,(((Deltaproteobacteria bacterium__Deltaproteobacteria__Proteobacteria__Bacteria:0.2665441810,Deferriisoma camini__Deferriisoma__Deltaproteobacteria__Proteobacteria__Bacteria:0.1300821288)100:0.170451,((bacterium TMED88__Bacteria:0.0980147109,Opitutales bacterium TMED158__Opitutales__Opitutae__Verrucomicrobia__Bacteria:0.1261885810)100:0.316931,Deltaproteobacteria bacterium CG11_big_fil_rev_8_21_14_0_20_45_16__Deltaproteobacteria__Proteobacteria__Bacteria:0.3174104369)79:0.034986)87:0.035110,Thermodesulfator autotrophicus__Thermodesulfator__Thermodesulfobacteriaceae__Thermodesulfobacterales__Thermodesulfobacteria__Bacteria:0.2950632627)79:0.009288)88:0.042923,(Desulfuromona dales bacterium C00003096__Desulfuromonadales__Deltaproteobacteria__Proteobacteria__Bacteria:0.0507118991,delta proteobacterium ML8_D__Deltaproteobacteria__Proteobacteria__Bacteria:0.0681258153)100:0.149495)85:0.020354,((((((((Bdellovibrio sp. ArH5__Bdellovibrio__Bdellovibrionaceae__Bdellovibrionales__Oligoflexia__Proteobacteria__Bacteria:0.0000024991,Bdellovibrio bacteriovorus__Bdellovibrio__Bdellovibrionaceae__Bdellovibrionales__Oligoflexia__Proteobacteria__Bacteria:0.0045387848)94:0.011123,Bdellovibrio

bacteriovorus__Bdellovibrio__Bdellovibrionaceae__Bdellovibrionales__Oligoflexia__Proteobacteria__Bacteria:0.0219394113)87:0.000002,Bdellovibrio sp.
SKB1291214__Bdellovibrio__Bdellovibrionaceae__Bdellovibrionales__Oligoflexia__Proteobacteria__Bacteria:0.0496003256)91:0.030350,(Bdellovibrionales bacterium
RIFCSPHIGHO2_01_FULL_40_29__Bdellovibrionales__Oligoflexia__Proteobacteria__Bacteria:0.0456552348,Bdellovibrio
exovorus__Bdellovibrio__Bdellovibrionaceae__Bdellovibrionales__Oligoflexia__Proteobacteria__Bacteria:0.0236143380)100:0.102753)98:0.053656,Bdellovibrionales bacterium
RBG_16_40_8__Bdellovibrionales__Oligoflexia__Proteobacteria__Bacteria:0.0918313466)81:0.057989,Proteobacteria bacterium
SG_bin7__Proteobacteria__Bacteria:0.1243390132)100:0.245016,(Deltaproteobacteria bacterium
RIFCSPHIGHO2_02_FULL_40_28__Deltaproteobacteria__Proteobacteria__Bacteria:0.1324667156,Deltaproteobacteria bacterium
GWA2_45_12__Deltaproteobacteria__Proteobacteria__Bacteria:0.1281335154)100:0.058937)71:0.040673,Deltaproteobacteria bacterium
GWA2_50_8__Deltaproteobacteria__Proteobacteria__Bacteria:0.2599246407)60:0.022501,((((Deltaproteobacteria bacterium
CG11_big_fil_rev_8_21_14_0_20_49_13__Deltaproteobacteria__Proteobacteria__Bacteria:0.1471892094,((Deltaproteobacteria bacterium
CG11_big_fil_rev_8_21_14_0_20_47_16__Deltaproteobacteria__Proteobacteria__Bacteria:0.1542711604,Deltaproteobacteria bacterium
RIFCSPLOWO2_02_FULL_46_8__Deltaproteobacteria__Proteobacteria__Bacteria:0.1915122991)35:0.013831,(Deltaproteobacteria bacterium
RIFOXYA12_FULL_58_15__Deltaproteobacteria__Proteobacteria__Bacteria:0.2295464401,(Deltaproteobacteria bacterium HGW-Deltaproteobacteria-
22__Deltaproteobacteria__Proteobacteria__Bacteria:0.2269099291,Sorangium
cellulosum__Sorangium__Polyangiaceae__Soranginiaceae__Myxococcales__Deltaproteobacteria__Proteobacteria__Bacteria:0.1934235167)100:0.073812)34:0.038088)31:0.023290)39:0.036256,
Deltaproteobacteria bacterium GWA2_38_16__Deltaproteobacteria__Proteobacteria__Bacteria:0.2505789521)80:0.011482,Deltaproteobacteria bacterium
CG2_30_63_29__Deltaproteobacteria__Proteobacteria__Bacteria:0.2922298236)92:0.042038,Deltaproteobacteria bacterium
RIFOXYA12_FULL_61_11__Deltaproteobacteria__Proteobacteria__Bacteria:0.2629192672)56:0.014781)89:0.034538,Deltaproteobacteria bacterium
RBG_16_64_85__Deltaproteobacteria__Proteobacteria__Bacteria:0.3622680686)84:0.039905)77:0.025891,((((((Deltaproteobacteria bacterium
GWA2_54_12__Deltaproteobacteria__Proteobacteria__Bacteria:0.1581972302,Deltaproteobacteria bacterium
RBG_19FT_COMBO_52_11__Deltaproteobacteria__Proteobacteria__Bacteria:0.1946167818)93:0.062909,(Deltaproteobacteria bacterium
CG_4_10_14_0_8_um_filter_43_12__Deltaproteobacteria__Proteobacteria__Bacteria:0.1701002973,(Syntrophaceae bacterium
CG2_30_49_12__Syntrophaceae__Syntrophobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.0665133599,Syntrophus
gentianae__Syntrophus__Syntrophaceae__Syntrophobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.0922717722)100:0.247682)96:0.036871)85:0.021404,(Desulfomonile
tiedjei__Desulfomonile__Syntrophaceae__Syntrophobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.2197415918,Nitrospirae bacterium
CG2_30_53_67__Nitrospirae__Bacteria:0.1920216297)99:0.066751)83:0.013422,Candidatus Adiutrix intracellularis__Candidatus
Adiutrix__Deltaproteobacteria__Proteobacteria__Bacteria:0.2402750606)81:0.011450,(((Treponema
denticola__Treponema__Spirochaetaceae__Spirochaetales__Spirochaetes__Bacteria:0.1891072552,Salinispira
pacificus__Salinispira__Spirochaetaceae__Spirochaetales__Spirochaetes__Bacteria:0.2330715326)46:0.053545,((Treponema
medium__Treponema__Spirochaetaceae__Spirochaetales__Spirochaetes__Bacteria:0.0043182815,Treponema sp. OMZ
838__Treponema__Spirochaetaceae__Spirochaetales__Spirochaetes__Bacteria:0.0000026402)84:0.013638,Treponema
vincentii__Treponema__Spirochaetaceae__Spirochaetales__Spirochaetes__Bacteria:0.0038850260)99:0.109471)100:0.424313,(((((((candidate division TA06 bacterium 32_111__candidate
division TA06__Bacteria:0.3279608007,bacterium Candidatus Stahlbacteria CG08_land_8_20_14_0_20_40_26__Bacteria:0.4778332100)82:0.109378,candidate division TA06 bacterium
DG_24__candidate division TA06__Bacteria:0.1834356653)73:0.032908,candidate division Zixibacteria bacterium SM23_81__Bacteria:0.1713383481)74:0.050475,((Chlorobi bacterium
OLB4__Chlorobi__Bacteria:0.3993155556,Candidatus Edwardsbacteria bacterium RifOxyC12_full_54_24__Candidatus Edwardsbacteria__Bacteria:0.3513310629)44:0.027065,(Candidatus
Marinimicrobia bacterium CG_4_10_14_0_2_um_filter_48_9__Candidatus Marinimicrobia__Bacteria:0.4229485787,(Candidatus Desantisbacteria bacterium CG1_02_38_46__Candidatus
Desantisbacteria__Bacteria:0.0720381704,Candidatus Desantisbacteria bacterium CG1_02_49_89__Candidatus
Desantisbacteria__Bacteria:0.1122155838)100:0.262259)59:0.043578)69:0.030600)86:0.035820,Candidatus Handelsmanbacteria bacterium RIFCSPLOWO2_12_FULL_64_10__Candidatus
Handelsmanbacteria__Bacteria:0.4002748422)54:0.043873,candidate division KSB1_4572_119__candidate division KSB1__Bacteria:0.2494705240)53:0.031613,(Omnitrophica WOR_2
bacterium RIFCSPHIGHO2_02_FULL_67_20__Candidatus Omnitrophica__Bacteria:0.4009188528,candidate division BRC1 bacterium HGW-BRC1-1__candidate division
BRC1__Bacteria:0.5080218811)72:0.091161)47:0.052189)82:0.061434)72:0.015326,(Deltaproteobacteria bacterium
GWA2_47_9__Deltaproteobacteria__Proteobacteria__Bacteria:0.2214337505,(((Deltaproteobacteria bacterium
RIFOXYD12_FULL_57_12__Deltaproteobacteria__Proteobacteria__Bacteria:0.1306269046,((Desulfobulbus propionicus DSM
2032__Desulfobulbus__Desulfobulbaceae__Desulfobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.1651982890,Desulfobulbaceae bacterium
A2__Desulfobulbaceae__Desulfobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.0887179335)100:0.059141,uncultured Desulfofustis sp. PB-SRB1__environmental
samples__Desulfofustis__Desulfobulbaceae__Desulfobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.2742562389)99:0.043148)100:0.132386,Desulfurivibrio
alkaliphilus__Desulfurivibrio__Desulfobulbaceae__Desulfobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.1737932720)100:0.139995,Silvanigrella
aquatica__Silvanigrella__Silvanigrellaceae__Silvanigrellales__Oligoflexia__Proteobacteria__Bacteria:0.4280545308)63:0.029849)75:0.045679)73:0.015898,((Desulfobacca
acetoxidans__Desulfobacca__Syntrophaceae__Syntrophobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.0872884193,Deltaproteobacteria bacterium
CG07_land_8_20_14_0_80_60_11__Deltaproteobacteria__Proteobacteria__Bacteria:0.1414834968)100:0.049874,((((Syntrophobacter
fumaroxidans__Syntrophobacter__Syntrophobacteraceae__Syntrophobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.0879689584,Syntrophobacteraceae bacterium
CG2_30_61_12__Syntrophobacteraceae__Syntrophobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.1672422678)99:0.021217,Thermodesulfurhobdus
norvegica__Thermodesulfurhobdus__Syntrophobacteraceae__Syntrophobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.1005898737)100:0.087155,Desulfobacteraceae
bacterium__Desulfobacteraceae__Desulfobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.1658513963)83:0.039633,delta proteobacterium
NaphS2__Deltaproteobacteria__Proteobacteria__Bacteria:0.2175088750)79:0.019620,((Desulfobacteriales bacterium
C00003060__Desulfobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.1620010079,(Desulfatibacillum alkenivorans AK-
01__Desulfatibacillum__Desulfobacteraceae__Desulfobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.1053438653,(Deltaproteobacteria bacterium
RBG_13_49_15__Deltaproteobacteria__Proteobacteria__Bacteria:0.1169203918,Deltaproteobacteria bacterium
SG8_13__Deltaproteobacteria__Proteobacteria__Bacteria:0.1971839586)100:0.083459)99:0.037957)99:0.054001,Desulfobacteriales bacterium
C00003106__Desulfobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.1713345599)99:0.040460)97:0.029192)71:0.019362)65:0.009598)59:0.005929,(Desulfarculus
baarsii__Desulfarculus__Desulfarculaceae__Desulfarculales__Deltaproteobacteria__Proteobacteria__Bacteria:0.0427871644,Desulfocarbo
indianensis__Desulfocarbo__Desulfarculaceae__Desulfarculales__Deltaproteobacteria__Proteobacteria__Bacteria:0.1430210482)100:0.127853)40:0.005963,(((candidate division KSB3
bacterium__candidate division KSB3__Bacteria:0.2718774751,(((Acidobacteriaceae bacterium KBS
96__Acidobacteriaceae__Acidobacteriales__Acidobacteria__Bacteria:0.0541000245,Bryobacter
aggregatus__Bryobacter__Bryobacteraceae__Solibacteriales__Solibacteres__Acidobacteria__Bacteria:0.0911619013)100:0.020931,Candidatus Solibacter usitatus__Candidatus
Solibacter__Solibacteraceae__Solibacteres__Acidobacteria__Bacteria:0.0488250844)100:0.066670,Chloracidobacterium
thermophilum__Chloracidobacterium__Blastocatellia__Acidobacteria__Bacteria:0.2631521082)89:0.032984,(Acidobacteria bacterium
13_1_40CM_56_16__Acidobacteria__Bacteria:0.1079176011,(((Acidobacteria bacterium 13_1_40CM_2_64_6__Acidobacteria__Bacteria:0.0312824685,((Acidobacteria bacterium
RIFCSPLOWO2_02_FULL_67_36__Acidobacteria__Bacteria:0.0846616797,(Acidobacteria bacterium 13_1_40CM_4_65_8__Acidobacteria__Bacteria:0.0400292146,Acidobacteria bacterium
RIFCSPLOWO2_02_FULL_64_15__Acidobacteria__Bacteria:0.0342133810)100:0.017232)100:0.013185,Acidobacterium
sp.__Acidobacterium__Acidobacteriaceae__Acidobacteriales__Acidobacteria__Bacteria:0.1187126300)100:0.011827)100:0.048699,Acidobacteria bacterium SCN 69-
37__Acidobacteria__Bacteria:0.0607420381)100:0.041316,Luteitalea pratensis__Luteitalea__Acidobacteria subdivision 6__Acidobacteria__Bacteria:0.1537071063)98:0.026824,Acidobacteria
bacterium Mor1__Acidobacteria subdivision 22__Acidobacteria__Bacteria:0.4377377382)82:0.031578)64:0.017705)70:0.046524)77:0.024645,(Acidobacteria
bacterium__Acidobacteria__Bacteria:0.3482349585,Geothrix
fermentans__Geothrix__Holophagaceae__Holophagales__Holophagae__Acidobacteria__Bacteria:0.4421640344)85:0.142677)89:0.028170,(Nitrospirae bacterium
CG11_big_fil_rev_8_21_14_0_20_56_8__Nitrospirae__Nitrospirae/Tectomicrobia group__Bacteria:0.2050183352,Candidatus Tectomicrobia bacterium
RIFCSPLOWO2_02_FULL_70_19__Candidatus Tectomicrobia__Nitrospirae/Tectomicrobia group__Bacteria:0.2938620159)100:0.091709)90:0.056499,((Nitrospirae bacterium
RIFCSPHIGHO2_01_FULL_66_17__Nitrospirae__Bacteria:0.1280805528,Nitrospirae bacterium
RIFCSPLOWO2_12_FULL_63_8__Nitrospirae__Bacteria:0.1913097410)99:0.097974,Leptospirillum
ferriphilum__Leptospirillum__Nitrospiraceae__Nitrospirales__Nitrospirae__Bacteria:0.3476712558)100:0.103313)40:0.022361)38:0.017477,bacterium BMS3Abin14
Bacteria:0.2963687996)77:0.028820,(Deltaproteobacteria bacterium RBG_13_65_10__Deltaproteobacteria__Proteobacteria__Bacteria:0.1732689782,Syntrophorhabdus
aromaticivorans__Syntrophorhabdus__Syntrophorhabdaceae__Syntrophobacteriales__Deltaproteobacteria__Proteobacteria__Bacteria:0.3248785955)89:0.029314)83:0.060062)98:0.058281)
99:0.304507)100:0.124960,Eutrepitella gymnastica NIES-381:0.2337393534)100:0.459214);