Convergent patterns in the evolution of mealybug symbioses involving different intrabacterial symbionts

Gitta Szabó, Frederik Schulz, Elena R. Toenshoff, Jean-Marie Volland, Omri M. Finkel, Shimshon Belkin, Matthias Horn

Supplementary Information

Supplementary Materials and Methods

Microscopy

Mealybugs were fixed in 4% paraformaldehyde solution for 4 hours at 4°C, washed twice in 1:1 solution of PBS and ethanol, and stored in this solution at 4°C on the day of sampling for subsequent fluorescence *in situ* hybridization (FISH). FISH was performed on dissected specimens as described earlier (Toenshoff *et al.*, 2012). We employed a general bacterial probe (EUB-338I: 5'-GCT GCC TCC CGT AGG AGT-3') (Amann *et al.*, 1990), a general gammaproteobacterial probe (Gam42a: 5'-GCC TTC CCA CAT CGT TT-3') and an unlabeled competitor probe (Bet42a: 5'-GCC TTC CCA CTT CGT TT-3') (Manz *et al.*, 1992) together with a probe specific to the 16S rRNA of the gammaproteobacterial symbiont of *T. manniapara* (Trabutinella-300: 5'-CAG TGT GGC TGT TTA TCC-3') using 20v/v% formamide in the hybridization buffer. Samples were hybridized for at least 1.5 hours and were analyzed on a Leica Sp8 confocal laser-scanning microscope.

Frozen egg sacs of *T. mannipara* stored at -80°C were dissected and individual insects were fixed under vacuum in 2.5% glutaraldehyde and 2% paraformaldehyde in 0.1M phosphate buffer at pH 7.2 for two days at 4°C. The mealybugs were cut open on the sides to improve the penetration of the fixative. Samples were then washed in the buffer under vacuum for 4h and post-fixed in 2% osmium tetroxide in 0.1M phosphate buffer. They were subsequently dehydrated in an ethanol series, substituted in acetone and embedded in Agar Low Viscosity Resin®. Polymerization was performed at 60°C for two days. Semi-thin sections (0.5µm) were cut on a Leica® EM UC7, mounted on slides and stained

with a solution of 0.25% azure II, 0.25% methylene blue, 0.25% toluidine blue in 0.25% sodium borate. The slides were observed on a Zeiss® Axio plan-2 light microscope. For ultrastructure observation ultrathin sections (70 nm) were stained with 0.5% uranyl acetate and 3% lead citrate prior observations with a Zeiss® Libra 120 transmission electron microscope.

Genome annotation pipeline

The following steps were performed in the ConsPred genome annotation pipeline (Weinmaier *et al.*, unpublished; available at https://sourceforge.net/p/conspred/). Coding sequences (CDSs) were predicted based on intrinsic signals by Glimmer (Salzberg *et al.*, 1998), GeneMark (Lukashin & Borodovsky, 1998), Prodigal (Hyatt *et al.*, 2010) and Critica (Badger & Olsen, 1999), as well as based on sequence homology using blastx searches against the non-redundant protein database (nr) of the National Center for Biotechnology Information (NCBI). RNAmmer (Lagesen *et al.*, 2007), tRNA-scan SE (Lowe & Eddy, 1997), and Infernal (Nawrocki & Eddy, 2013) together with the Rfam database (Griffiths-Jones *et al.*, 2003) were applied to identify ribosomal RNAs, tRNAs and non-coding RNAs. CRISPR repeats were inferred by PILER-CR (Edgar, 2007). InterProScan annotated conserved domains in the consensus CDSs (Zdobnov & Apweiler, 2001). Functional assignment was according to the best blastp hits against the UniProt Swiss-Prot and TrEMBL databases (Bairoch *et al.*, 2005). Pathways and representation of main functional categories were predicted by sequence homology searches against the KEGG (Kanehisa & Goto, 2000) and eggNOG (Jensen *et al.*, 2008) databases, respectively.

References

Amann RI, Binder BJ, Olson RJ, Chisholm SW, Devereux R, Stahl DA. (1990). Combination of 16S rRNA-targeted oligonucleotide probes with flow cytometry for analyzing mixed microbial populations. Appl Environ Microbiol 56: 1919–1925.

Badger JH, Olsen GJ. (1999). CRITICA: coding region identification tool invoking comparative analysis. Mol Biol Evol 16: 512–524.

Bairoch A, Apweiler R, Wu CH, Barker WC, Boeckmann B, Ferro S, *et al.* (2005). The universal protein resource (UniProt). Nucleic Acids Res 33: D154–D159.

Edgar RC. (2007). PILER-CR: fast and accurate identification of CRISPR repeats. BMC Bioinformatics 8: 18.

Griffiths-Jones S, Bateman A, Marshall M, Khanna A, Eddy SR. (2003). Rfam: an RNA family database. Nucleic Acids Res 31: 439–441.

Hyatt D, Chen G-L, LoCascio PF, Land ML, Larimer FW, Hauser LJ. (2010). Prodigal: prokaryotic gene recognition and translation initiation site identification. BMC Bioinformatics 11: 119.

Jensen LJ, Julien P, Kuhn M, Mering C von, Muller J, Doerks T, *et al.* (2008). eggNOG: automated construction and annotation of orthologous groups of genes. Nucleic Acids Res 36: D250–D254.

Kanehisa M, Goto S. (2000). KEGG: Kyoto Encyclopedia of Genes and Genomes. Nucleic Acids Res 28: 27–30.

Lagesen K, Hallin P, Rødland EA, Stærfeldt H-H, Rognes T, Ussery DW. (2007). RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res 35: 3100–3108.

Lowe TM, Eddy SR. (1997). tRNAscan-SE: a program for improved detection of transfer rna genes in genomic sequence. Nucleic Acids Res 25: 0955–0964.

Lukashin AV, Borodovsky M. (1998). GeneMark.hmm: new solutions for gene finding. Nucleic Acids Res 26: 1107–1115.

Manz W, Amann R, Ludwig W, Wagner M, Schleifer K-H. (1992). Phylogenetic oligodeoxynucleotide probes for the major subclasses of Proteobacteria: Problems and Solutions. Syst Appl Microbiol 15: 593–600.

Nawrocki EP, Eddy SR. (2013). Infernal 1.1: 100-fold faster RNA homology searches. Bioinforma Oxf Engl 29: 2933–2935.

Salzberg SL, Delcher AL, Kasif S, White O. (1998). Microbial gene identification using interpolated Markov models. Nucleic Acids Res 26: 544–548.

Toenshoff ER, Penz T, Narzt T, Collingro A, Schmitz-Esser S, Pfeiffer S, *et al.* (2012). Bacteriocyte-associated gammaproteobacterial symbionts of the *Adelges nordmannianae*/*piceae* complex (Hemiptera: Adelgidae). ISME J 6: 384–396.

Zdobnov EM, Apweiler R. (2001). InterProScan – an integration platform for the signature-recognition methods in InterPro. Bioinformatics 17: 847–848.

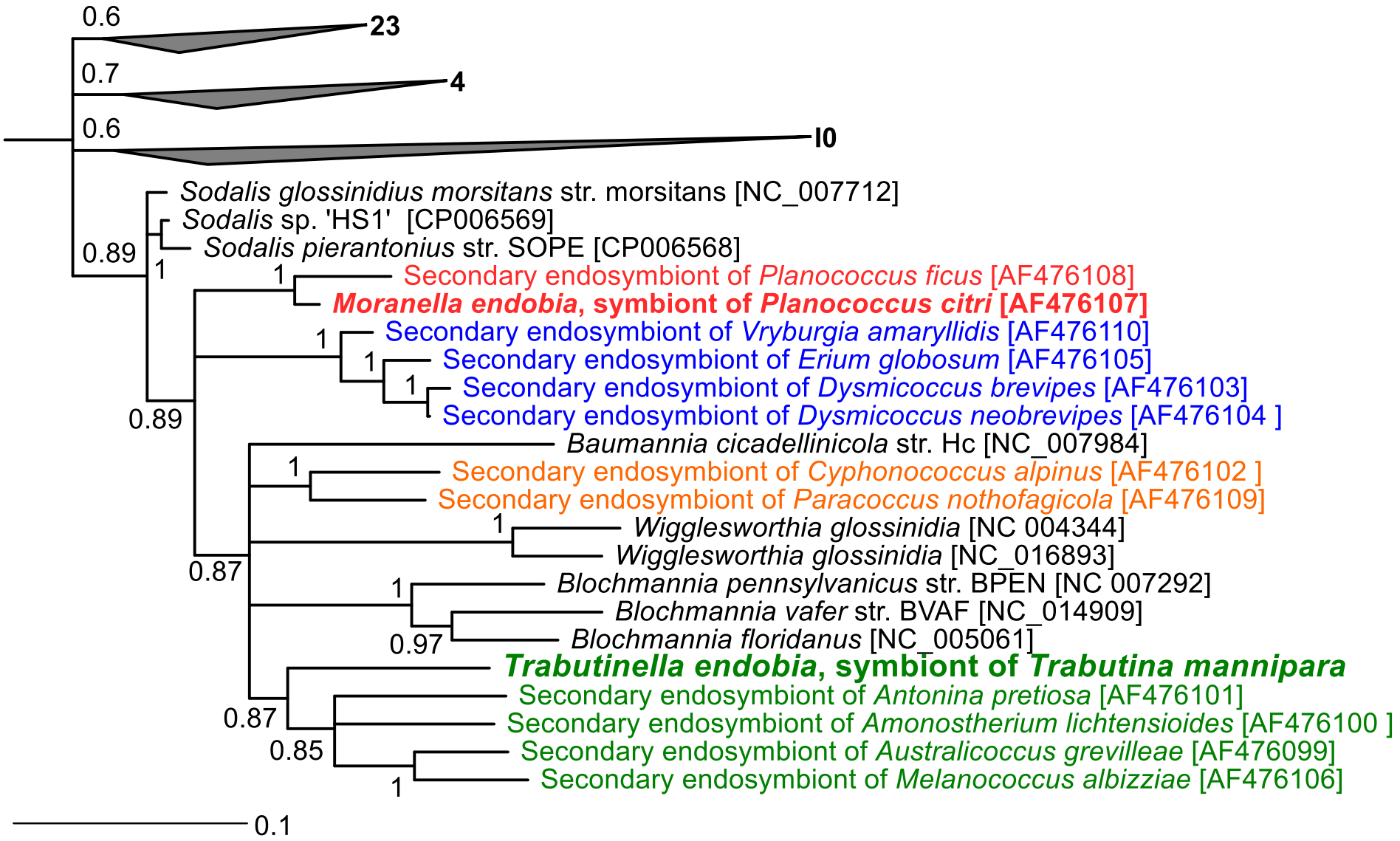

Figure S1. MrBayes tree based on 16S rRNA sequences showing the relation of '*Candidatus* Trabutinella endobia' to other symbionts of mealybugs. *Trabutinella* groups with secondary symbionts of other mealybugs within the tribe Trabutinini. Selected members of non-enterobacterial *Gammaproteobacteria* were used as outgroups (NC_000907, NC_003902, AB194327, NC_002516, NC_002505).

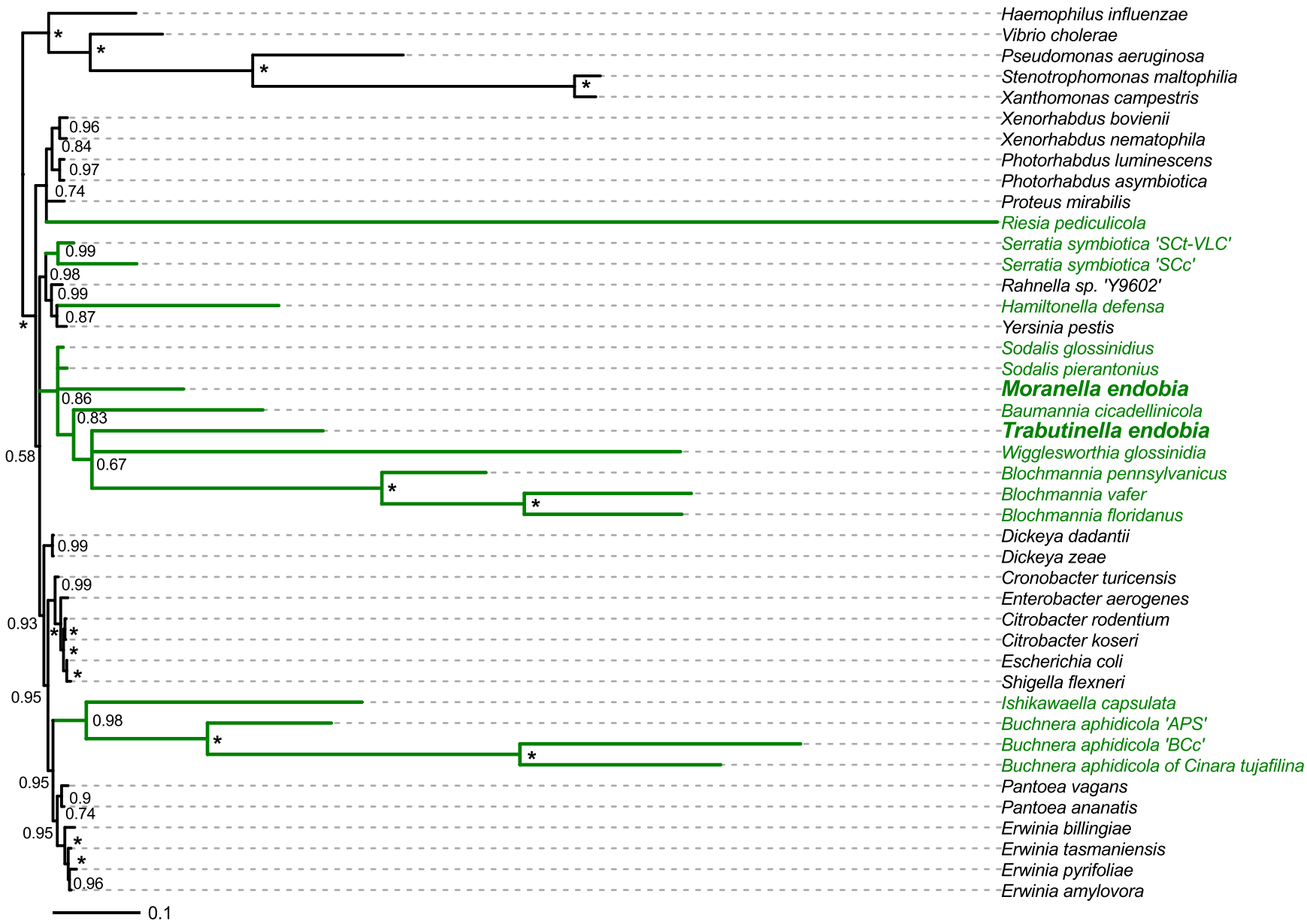

Figure S2. Phylobayes tree showing the relation of '*Candidatus* Trabutinella endobia' to free-living bacteria and other insect symbionts. Insect symbiont lineages are colored in green. The analysis is based on a concatenated set of 34 ribosomal proteins. Posterior probabilities are shown on the internal nodes; asterisks imply posterior probabilities equal to 1. Nodes with a support of 0.5 or below are collapsed.

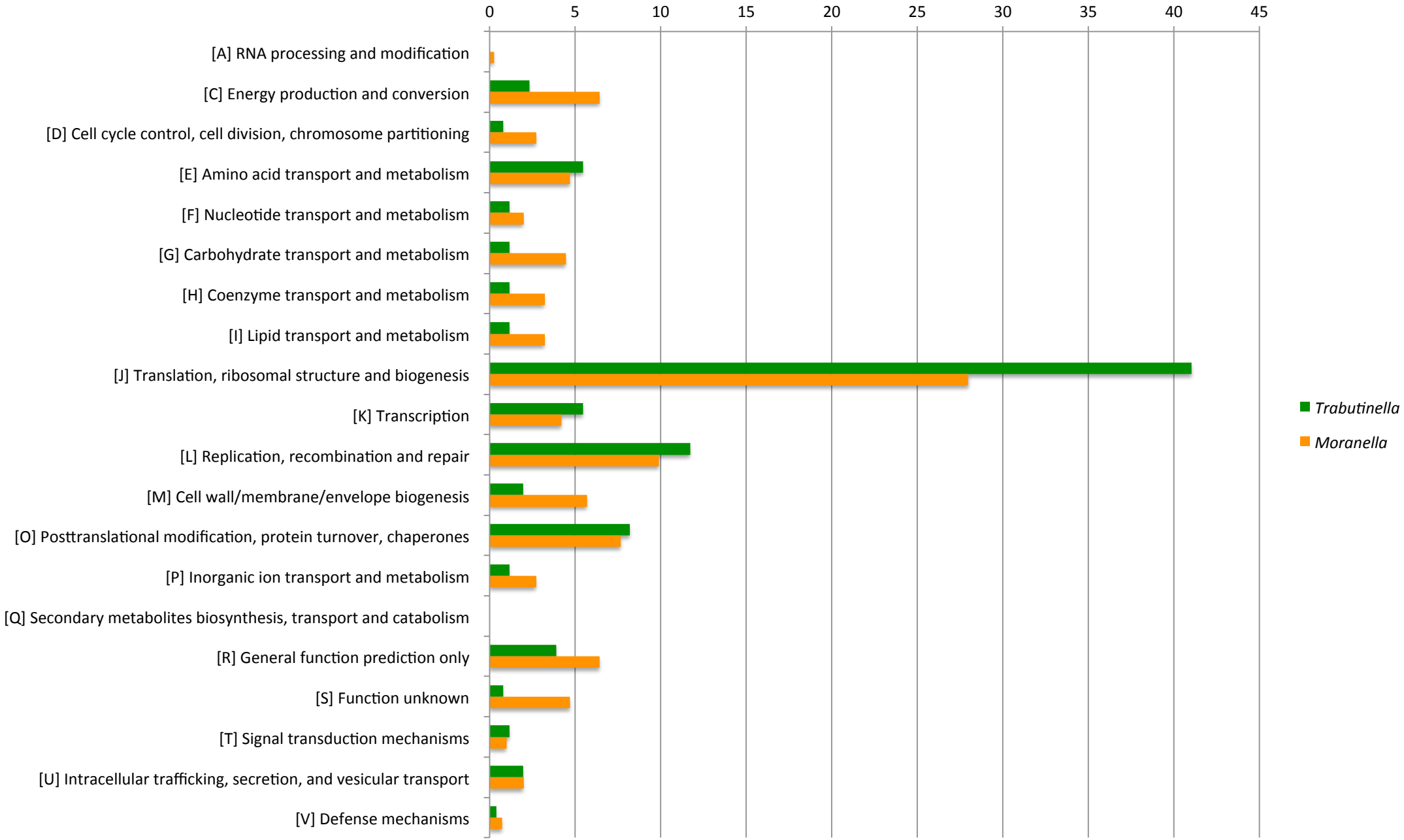

Figure S3. Percental distribution of genes among main functional categories according to the EggNOG classification in *Trabutinella* versus *Moranella*

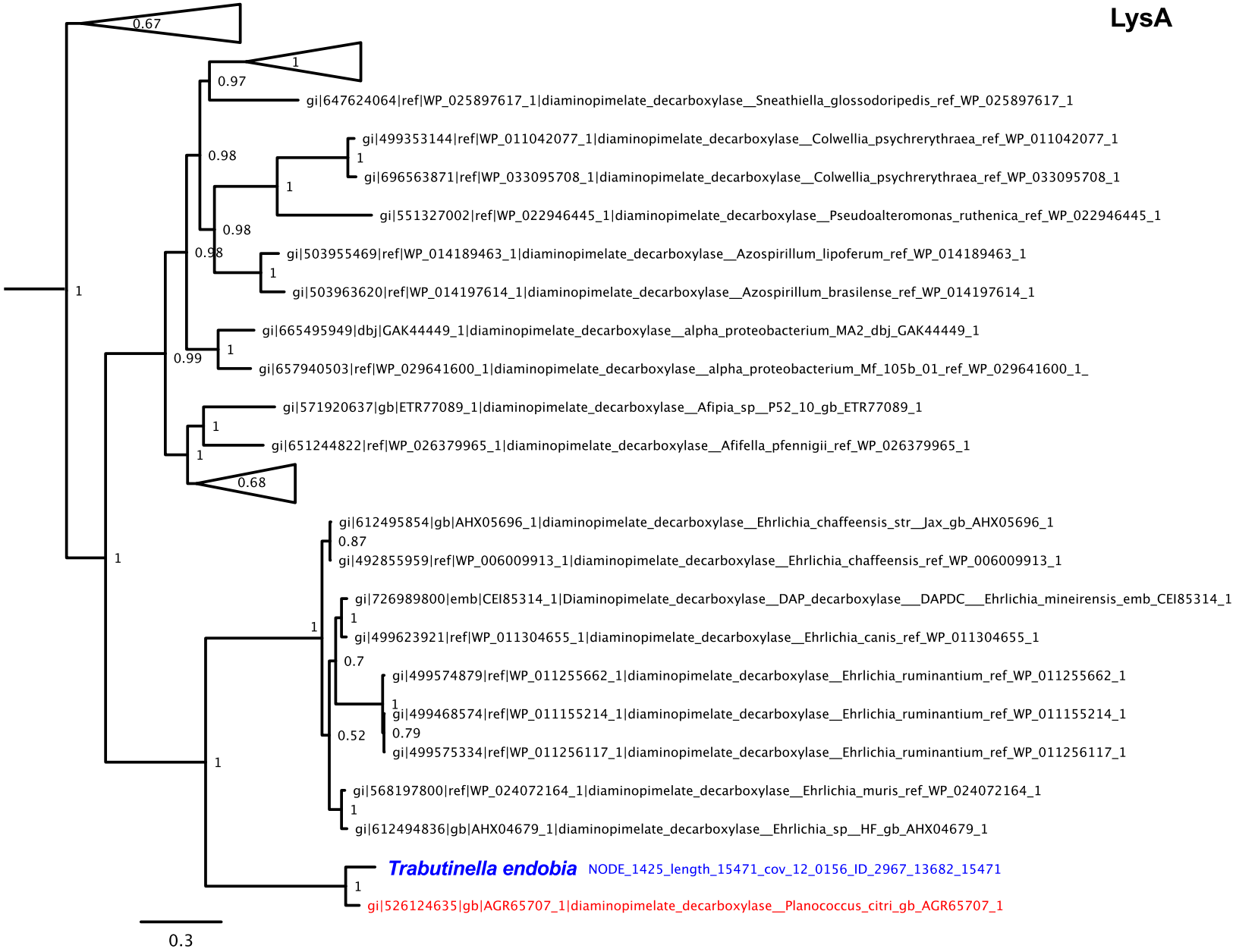

Figure S4 (A-I) MrBayes trees showing the phylogenetic relationships of the products of *lysA*, *dapF*, *cysK*, *ribA*, *ribD*, *bioA*, *bioB*, *bioD* and *tms1*, horizontally acquired genes in the genome of *Trabutina mannipara*.

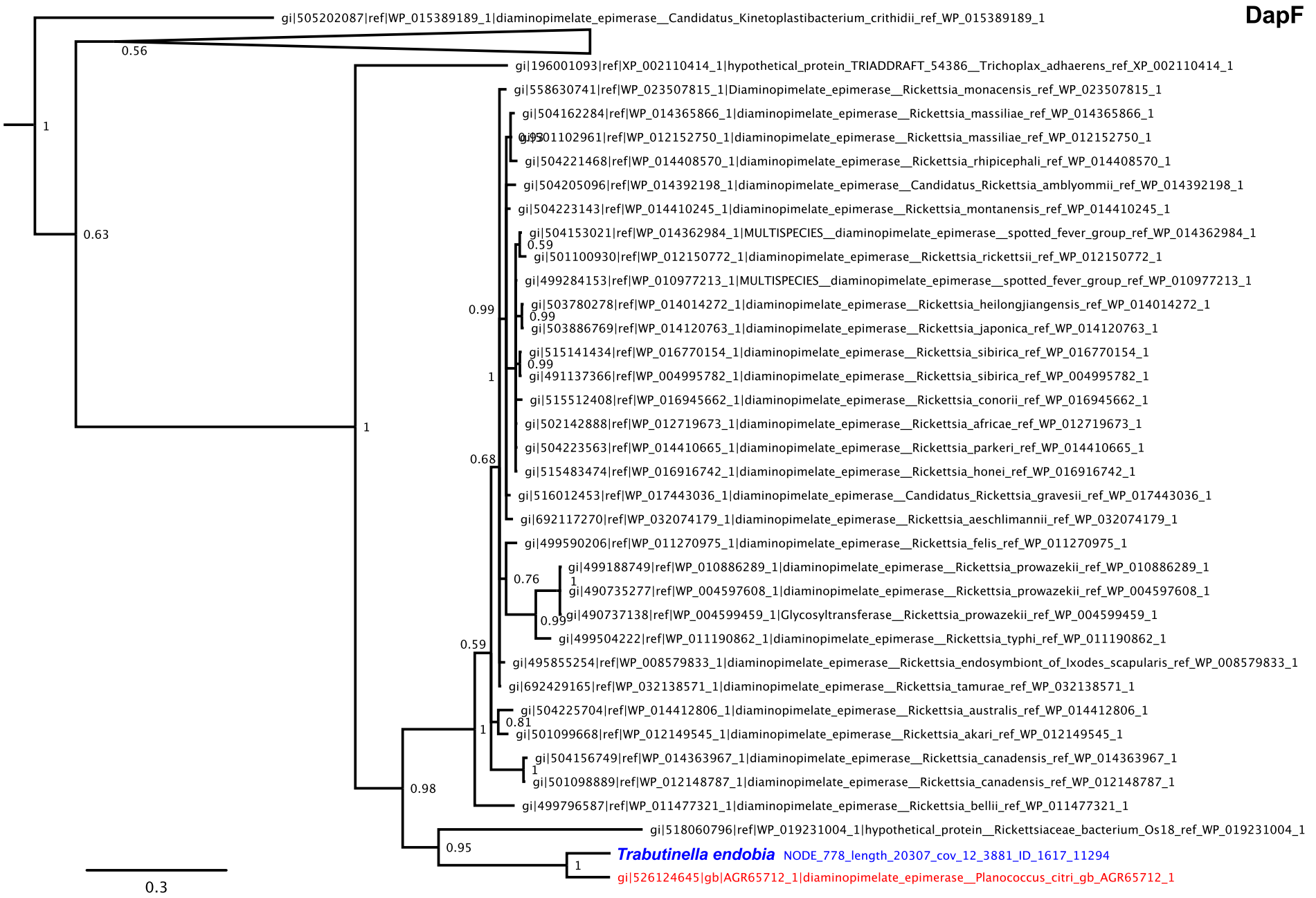
DapF
gi|505202087|ref|WP_015389189_1|diaminopimelate_epimerase__Candidatus_Kinetoplastibacterium_crithidii_ref_WP_015389189_1
gi|196001093|ref|XP_002110414_1|hypothetical_protein_TRIADDRAFT_54386__Trichoplax_adhaerens_ref_XP_002110414_1
gi|558630741|ref|WP_023507815_1|Diaminopimelate_epimerase__Rickettsia_monacensis_ref_WP_023507815_1
gi|504162284|ref|WP_014365866_1|diaminopimelate_epimerase__Rickettsia_massiliae_ref_WP_014365866_1
gi|501102961|ref|WP_012152750_1|diaminopimelate_epimerase__Rickettsia_massiliae_ref_WP_012152750_1
gi|504221468|ref|WP_014408570_1|diaminopimelate_epimerase__Rickettsia_rhipicephali_ref_WP_014408570_1
gi|504205096|ref|WP_014392198_1|diaminopimelate_epimerase__Candidatus_Rickettsia_amblyommii_ref_WP_014392198_1
gi|504223143|ref|WP_014410245_1|diaminopimelate_epimerase__Rickettsia_montanensis_ref_WP_014410245_1
gi|504153021|ref|WP_014362984_1|MULTISPECIES__diaminopimelate_epimerase__spotted_fever_group_ref_WP_014362984_1
gi|501100930|ref|WP_012150772_1|diaminopimelate_epimerase__Rickettsia_rickettsii_ref_WP_012150772_1
gi|499284153|ref|WP_010977213_1|MULTISPECIES__diaminopimelate_epimerase__spotted_fever_group_ref_WP_010977213_1
gi|503780278|ref|WP_014014272_1|diaminopimelate_epimerase__Rickettsia_heilongjiangensis_ref_WP_014014272_1
gi|503886769|ref|WP_014120763_1|diaminopimelate_epimerase__Rickettsia_japonica_ref_WP_014120763_1
gi|515141434|ref|WP_016770154_1|diaminopimelate_epimerase__Rickettsia_sibirica_ref_WP_016770154_1
gi|491137366|ref|WP_004995782_1|diaminopimelate_epimerase__Rickettsia_sibirica_ref_WP_004995782_1
gi|515512408|ref|WP_016945662_1|diaminopimelate_epimerase__Rickettsia_conorii_ref_WP_016945662_1
gi|502142888|ref|WP_012719673_1|diaminopimelate_epimerase__Rickettsia_africae_ref_WP_012719673_1
gi|504223563|ref|WP_014410665_1|diaminopimelate_epimerase__Rickettsia_parkeri_ref_WP_014410665_1
gi|515483474|ref|WP_016916742_1|diaminopimelate_epimerase__Rickettsia_honei_ref_WP_016916742_1
gi|516012453|ref|WP_017443036_1|diaminopimelate_epimerase__Candidatus_Rickettsia_gravesii_ref_WP_017443036_1
gi|692117270|ref|WP_032074179_1|diaminopimelate_epimerase__Rickettsia_aeschlimannii_ref_WP_032074179_1
gi|499590206|ref|WP_011270975_1|diaminopimelate_epimerase__Rickettsia_felis_ref_WP_011270975_1
gi|499188749|ref|WP_010886289_1|diaminopimelate_epimerase__Rickettsia_prowazekii_ref_WP_010886289_1
gi|490735277|ref|WP_004597608_1|diaminopimelate_epimerase__Rickettsia_prowazekii_ref_WP_004597608_1
gi|490737138|ref|WP_004599459_1|Glycosyltransferase__Rickettsia_prowazekii_ref_WP_004599459_1
gi|499504222|ref|WP_011190862_1|diaminopimelate_epimerase__Rickettsia_typhi_ref_WP_011190862_1
gi|495855254|ref|WP_008579833_1|diaminopimelate_epimerase__Rickettsia_endosymbiont_of_Ixodes_scapularis_ref_WP_008579833_1
gi|692429165|ref|WP_032138571_1|diaminopimelate_epimerase__Rickettsia_tamurae_ref_WP_032138571_1
gi|504225704|ref|WP_014412806_1|diaminopimelate_epimerase__Rickettsia_australis_ref_WP_014412806_1
gi|501099668|ref|WP_012149545_1|diaminopimelate_epimerase__Rickettsia_akari_ref_WP_012149545_1
gi|504156749|ref|WP_014363967_1|diaminopimelate_epimerase__Rickettsia_canadensis_ref_WP_014363967_1
gi|501098889|ref|WP_012148787_1|diaminopimelate_epimerase__Rickettsia_canadensis_ref_WP_012148787_1
gi|499796587|ref|WP_011477321_1|diaminopimelate_epimerase__Rickettsia_bellii_ref_WP_011477321_1
gi|518060796|ref|WP_019231004_1|hypothetical_protein__Rickettsiaceae_bacterium_Os18_ref_WP_019231004_1
Trabutinella endobia NODE_778_length_20307_cov_12_3881_ID_1617_11294
gi|526124645|gb|AGR65712_1|diaminopimelate_epimerase__Planococcus_citri_gb_AGR65712_1
0.3

Figure S4B

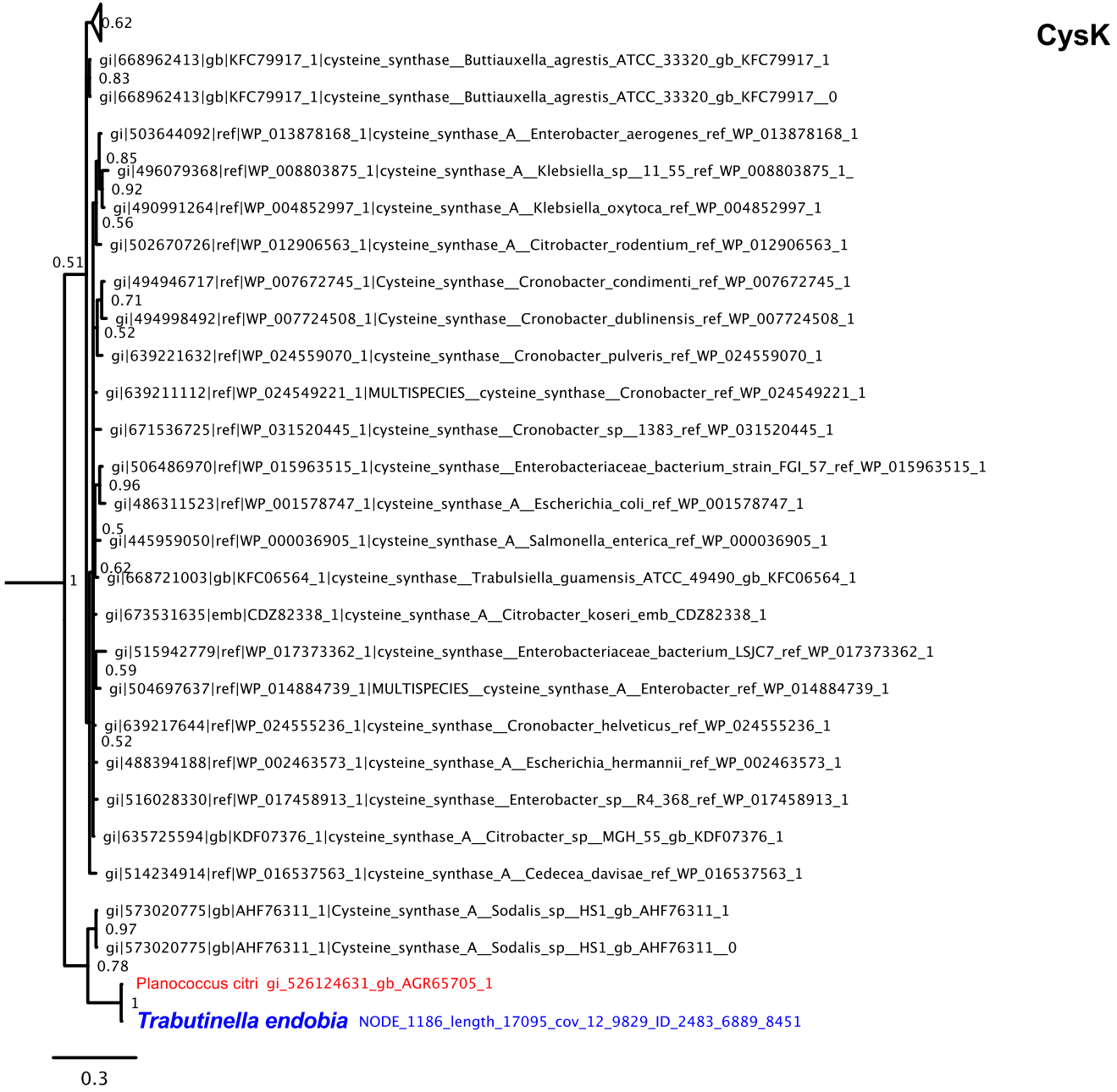
CysK
0.62
gi|668962413|gb|KFC79917_1|cysteine_synthase__Buttiauxella_agrestis_ATCC_33320_gb_KFC79917_1
0.83
gi|668962413|gb|KFC79917_1|cysteine_synthase__Buttiauxella_agrestis_ATCC_33320_gb_KFC79917__0
gi|503644092|ref|WP_013878168_1|cysteine_synthase_A__Enterobacter_aerogenes_ref_WP_013878168_1
0.85
gi|496079368|ref|WP_008803875_1|cysteine_synthase_A__Klebsiella_sp__11_55_ref_WP_008803875_1_
0.92
gi|490991264|ref|WP_004852997_1|cysteine_synthase_A__Klebsiella_oxytoca_ref_WP_004852997_1
0.56
gi|502670726|ref|WP_012906563_1|cysteine_synthase_A__Citrobacter_rodentium_ref_WP_012906563_1
0.51
gi|494946717|ref|WP_007672745_1|Cysteine_synthase__Cronobacter_condimenti_ref_WP_007672745_1
0.71
gi|494998492|ref|WP_007724508_1|Cysteine_synthase__Cronobacter_dublinensis_ref_WP_007724508_1
0.52
gi|639221632|ref|WP_024559070_1|cysteine_synthase__Cronobacter_pulveris_ref_WP_024559070_1
gi|639211112|ref|WP_024549221_1|MULTISPECIES__cysteine_synthase__Cronobacter_ref_WP_024549221_1
gi|671536725|ref|WP_031520445_1|cysteine_synthase__Cronobacter_sp__1383_ref_WP_031520445_1
gi|506486970|ref|WP_015963515_1|cysteine_synthase__Enterobacteriaceae_bacterium_strain_FGI_57_ref_WP_015963515_1
0.96
gi|486311523|ref|WP_001578747_1|cysteine_synthase_A__Escherichia_coli_ref_WP_001578747_1
0.5
gi|445959050|ref|WP_000036905_1|cysteine_synthase_A__Salmonella_enterica_ref_WP_000036905_1
0.62
1
gi|668721003|gb|KFC06564_1|cysteine_synthase__Trabulsiella_guamensis_ATCC_49490_gb_KFC06564_1
gi|673531635|emb|CDZ82338_1|cysteine_synthase_A__Citrobacter_koseri_emb_CDZ82338_1
gi|515942779|ref|WP_017373362_1|cysteine_synthase__Enterobacteriaceae_bacterium_LSJC7_ref_WP_017373362_1
0.59
gi|504697637|ref|WP_014884739_1|MULTISPECIES__cysteine_synthase_A__Enterobacter_ref_WP_014884739_1
gi|639217644|ref|WP_024555236_1|cysteine_synthase__Cronobacter_helveticus_ref_WP_024555236_1
0.52
gi|488394188|ref|WP_002463573_1|cysteine_synthase_A__Escherichia_hermannii_ref_WP_002463573_1
gi|516028330|ref|WP_017458913_1|cysteine_synthase__Enterobacter_sp__R4_368_ref_WP_017458913_1
gi|635725594|gb|KDF07376_1|cysteine_synthase_A__Citrobacter_sp__MGH_55_gb_KDF07376_1
gi|514234914|ref|WP_016537563_1|cysteine_synthase_A__Cedecea_davisae_ref_WP_016537563_1
gi|573020775|gb|AHF76311_1|Cysteine_synthase_A__Sodalis_sp__HS1_gb_AHF76311_1
0.97
gi|573020775|gb|AHF76311_1|Cysteine_synthase_A__Sodalis_sp__HS1_gb_AHF76311__0
0.78
Planococcus citri gi_526124631_gb_AGR65705_1
1
Trabutinella endobia NODE_1186_length_17095_cov_12_9829_ID_2483_6889_8451
0.3

Figure S4C

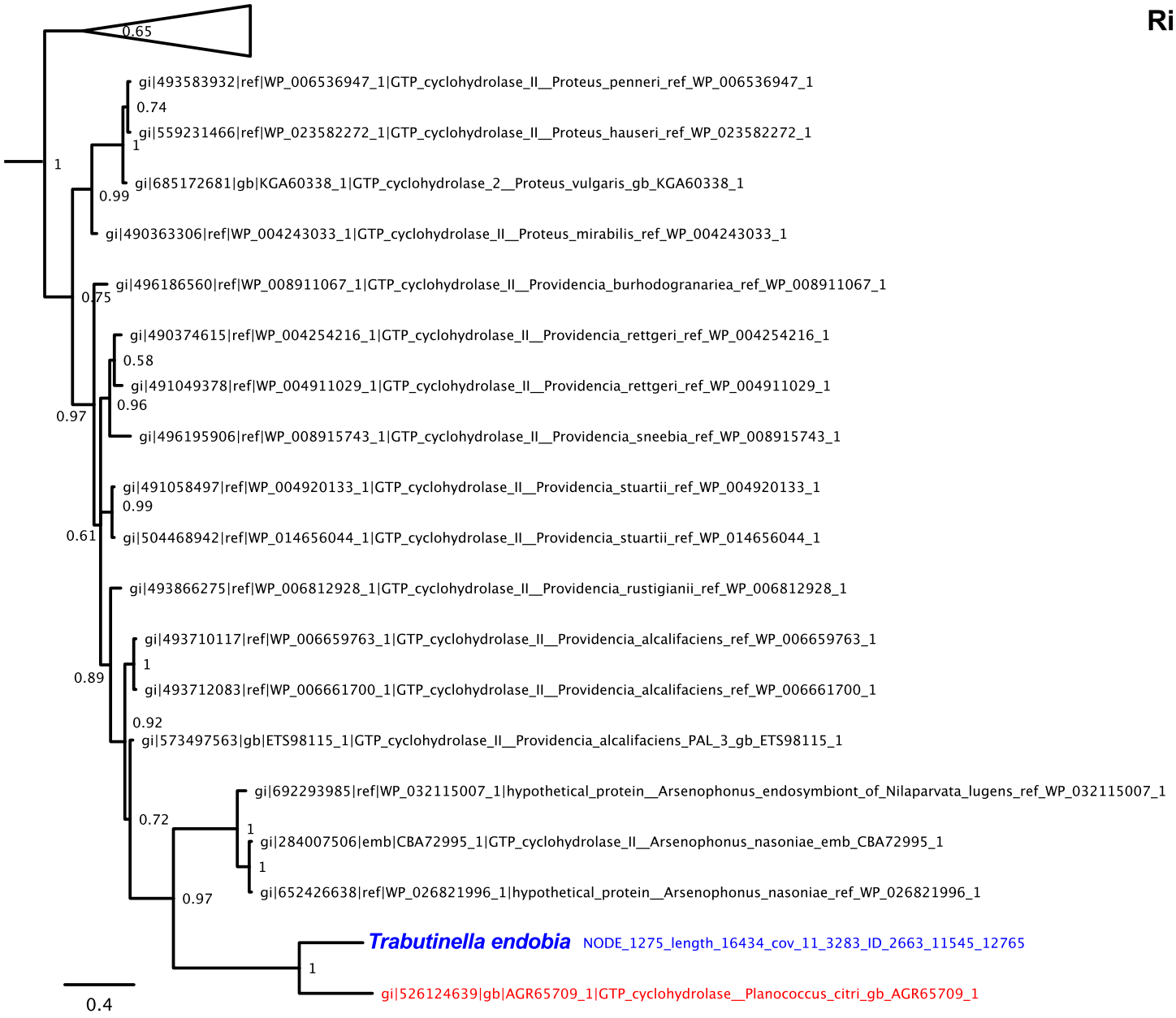
RibA
0.65
gi|493583932|ref|WP_006536947_1|GTP_cyclohydrolase_II__Proteus_penneri_ref_WP_006536947_1
0.74
gi|559231466|ref|WP_023582272_1|GTP_cyclohydrolase_II__Proteus_hauseri_ref_WP_023582272_1
1
1
gi|685172681|gb|KGA60338_1|GTP_cyclohydrolase_2__Proteus_vulgaris_gb_KGA60338_1
0.99
gi|490363306|ref|WP_004243033_1|GTP_cyclohydrolase_II__Proteus_mirabilis_ref_WP_004243033_1
gi|496186560|ref|WP_008911067_1|GTP_cyclohydrolase_II__Providencia_burhodogranariea_ref_WP_008911067_1
0.75
gi|490374615|ref|WP_004254216_1|GTP_cyclohydrolase_II__Providencia_rettgeri_ref_WP_004254216_1
0.58
gi|491049378|ref|WP_004911029_1|GTP_cyclohydrolase_II__Providencia_rettgeri_ref_WP_004911029_1
0.96
0.97
gi|496195906|ref|WP_008915743_1|GTP_cyclohydrolase_II__Providencia_sneebia_ref_WP_008915743_1
gi|491058497|ref|WP_004920133_1|GTP_cyclohydrolase_II__Providencia_stuartii_ref_WP_004920133_1
0.99
0.61
gi|504468942|ref|WP_014656044_1|GTP_cyclohydrolase_II__Providencia_stuartii_ref_WP_014656044_1
gi|493866275|ref|WP_006812928_1|GTP_cyclohydrolase_II__Providencia_rustigianii_ref_WP_006812928_1
gi|493710117|ref|WP_006659763_1|GTP_cyclohydrolase_II__Providencia_alcalifaciens_ref_WP_006659763_1
1
0.89
gi|493712083|ref|WP_006661700_1|GTP_cyclohydrolase_II__Providencia_alcalifaciens_ref_WP_006661700_1
0.92
gi|573497563|gb|ETS98115_1|GTP_cyclohydrolase_II__Providencia_alcalifaciens_PAL_3_gb_ETS98115_1
gi|692293985|ref|WP_032115007_1|hypothetical_protein__Arsenophonus_endosymbiont_of_Nilaparvata_lugens_ref_WP_032115007_1
0.72
1
gi|284007506|emb|CBA72995_1|GTP_cyclohydrolase_II__Arsenophonus_nasoniae_emb_CBA72995_1
1
gi|652426638|ref|WP_026821996_1|hypothetical_protein__Arsenophonus_nasoniae_ref_WP_026821996_1
0.97
Trabutinella endobia NODE_1275_length_16434_cov_11_3283_ID_2663_11545_12765
1
gi|526124639|gb|AGR65709_1|GTP_cyclohydrolase__Planococcus_citri_gb_AGR65709_1
0.4

Figure S4D

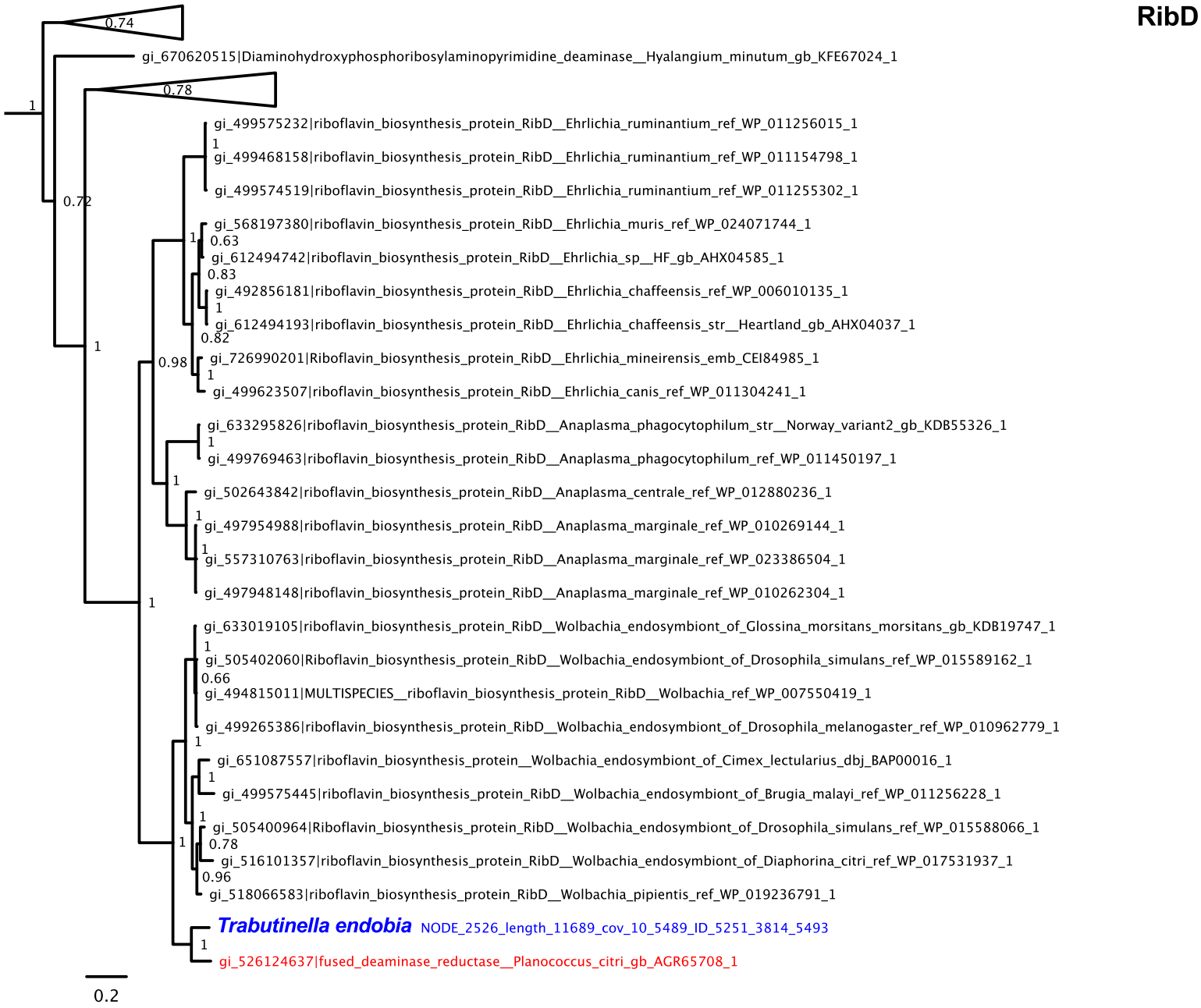
RibD
0.74
gi_670620515|Diaminohydroxyphosphoribosylaminopyrimidine_deaminase__Hyalangium_minutum_gb_KFE67024_1
0.78
gi_499575232|riboflavin_biosynthesis_protein_RibD__Ehrlichia_ruminantium_ref_WP_011256015_1
gi_499468158|riboflavin_biosynthesis_protein_RibD__Ehrlichia_ruminantium_ref_WP_011154798_1
gi_499574519|riboflavin_biosynthesis_protein_RibD__Ehrlichia_ruminantium_ref_WP_011255302_1
gi_568197380|riboflavin_biosynthesis_protein_RibD__Ehrlichia_muris_ref_WP_024071744_1
gi_612494742|riboflavin_biosynthesis_protein_RibD__Ehrlichia_sp__HF_gb_AHX04585_1
gi_492856181|riboflavin_biosynthesis_protein_RibD__Ehrlichia_chaffeensis_ref_WP_006010135_1
gi_612494193|riboflavin_biosynthesis_protein_RibD__Ehrlichia_chaffeensis_str__Heartland_gb_AHX04037_1
gi_726990201|Riboflavin_biosynthesis_protein_RibD__Ehrlichia_mineirensis_emb_CEI84985_1
gi_499623507|riboflavin_biosynthesis_protein_RibD__Ehrlichia_canis_ref_WP_011304241_1
gi_633295826|riboflavin_biosynthesis_protein_RibD__Anaplasma_phagocytophilum_str__Norway_variant2_gb_KDB55326_1
gi_499769463|riboflavin_biosynthesis_protein_RibD__Anaplasma_phagocytophilum_ref_WP_011450197_1
gi_502643842|riboflavin_biosynthesis_protein_RibD__Anaplasma_centrale_ref_WP_012880236_1
gi_497954988|riboflavin_biosynthesis_protein_RibD__Anaplasma_marginale_ref_WP_010269144_1
gi_557310763|riboflavin_biosynthesis_protein_RibD__Anaplasma_marginale_ref_WP_023386504_1
gi_497948148|riboflavin_biosynthesis_protein_RibD__Anaplasma_marginale_ref_WP_010262304_1
gi_633019105|riboflavin_biosynthesis_protein_RibD__Wolbachia_endosymbiont_of_Glossina_morsitans_morsitans_gb_KDB19747_1
gi_505402060|Riboflavin_biosynthesis_protein_RibD__Wolbachia_endosymbiont_of_Drosophila_simulans_ref_WP_015589162_1
gi_494815011|MULTISPECIES__riboflavin_biosynthesis_protein_RibD__Wolbachia_ref_WP_007550419_1
gi_499265386|riboflavin_biosynthesis_protein_RibD__Wolbachia_endosymbiont_of_Drosophila_melanogaster_ref_WP_010962779_1
gi_651087557|riboflavin_biosynthesis_protein__Wolbachia_endosymbiont_of_Cimex_lectularius_dbj_BAP00016_1
gi_499575445|riboflavin_biosynthesis_protein_RibD__Wolbachia_endosymbiont_of_Brugia_malayi_ref_WP_011256228_1
gi_505400964|Riboflavin_biosynthesis_protein_RibD__Wolbachia_endosymbiont_of_Drosophila_simulans_ref_WP_015588066_1
gi_516101357|riboflavin_biosynthesis_protein_RibD__Wolbachia_endosymbiont_of_Diaphorina_citri_ref_WP_017531937_1
gi_518066583|riboflavin_biosynthesis_protein_RibD__Wolbachia_pipientis_ref_WP_019236791_1
Trabutinella endobia NODE_2526_length_11689_cov_10_5489_ID_5251_3814_5493
gi_526124637|fused_deaminase_reductase__Planococcus_citri_gb_AGR65708_1
0.2

Figure S4E


BioA
1
0.88
0.9
0.86
0.9
gi|406941334|gb|EKD73856_1|hypothetical_protein_ACD_45C00171G0005__uncultured_bacterium_gb_EKD73856_1
1
gi|518061146|ref|WP_019231354_1|hypothetical_protein__Rickettsiaceae_bacterium_Os18_ref_WP_019231354_1
0.66
gi|612501694|gb|AHX11530_1|adenosylmethionine_8_amino_7_oxononanoate_transaminase__Neorickettsia_helminthoeca_str__Oregon_gb_AHX11530_1
0.96
1
gi|499771270|ref|WP_011452004_1|adenosylmethionine_8_amino_7_oxononanoate_aminotransferase__Neorickettsia_sennetsu_ref_WP_011452004_1
1
gi|506296687|ref|WP_015816462_1|adenosylmethionine_8_amino_7_oxononanoate_aminotransferase__Neorickettsia_risticii_ref_WP_015816462_1
1
gi|503716903|ref|WP_013950979_1|adenosylmethionine_8_amino_7_oxononanoate_aminotransferase__Candidatus_Midichloria_mitochondrii_ref_WP_013950979_1
gi|575431086|gb|AHG63392_1|adenosylmethionine_8_amino_7_oxononanoate_aminotransferase__Advenella_mimigardefordensis_DPN7_gb_AHG63392_1
1
gi|504564270|ref|WP_014751372_1|adenosylmethionine_8_amino_7_oxononanoate_aminotransferase__Advenella_kashmirensis_ref_WP_014751372_1
1
0.59
gi|665876585|ref|WP_031243791_1|adenosylmethionine_8_amino_7_oxononanoate_aminotransferase__partial__Advenella_kashmirensis_ref_WP_031243791_1
1
gi|565406167|gb|ETF00509_1|adenosylmethionine_8_amino_7_oxononanoate_aminotransferase__Advenella_kashmirensis_W13003_gb_ETF00509_1
gi|651087684|dbj|BAP00143_1|adenosylmethionine_8_amino_7_oxononanoate_transaminase__Wolbachia_endosymbiont_of_Cimex_lectularius_dbj_BAP00143_1
1
gi|656322965|dbj|BAP01370_1|adenosylmethionine_8_amino_7_oxononanoate_aminotransferase__Wolbachia_sp__KTCN_dbj_BAP01370_1
0.67
1
gi|504747611|ref|WP_014934713_1|adenosylmethionine_8_amino_7_oxononanoate_aminotransferase__Cardinium_endosymbiont_of_Encarsia_pergandiella_ref_WP_014934713_1
1
0.82
gi|612065053|emb|CDG50084_1|Adenosylmethionine_8_amino_7_oxononanoate_aminotransferase__Cardinium_endosymbiont_cBtQ1_of_Bemisia_tabaci_emb_CDG50084_1
gi|495856878|ref|WP_008581457_1|adenosylmethionine_8_amino_7_oxononanoate_aminotransferase__Rickettsia_endosymbiont_of_Ixodes_scapularis_ref_WP_008581457_1
1
0.75
gi|499845776|ref|WP_011526510_1|adenosylmethionine_8_amino_7_oxononanoate_aminotransferase__Lawsonia_intracellularis_ref_WP_011526510_1
gi|546194982|ref|WP_021827225_1|hypothetical_protein__Holospora_obtusa_ref_WP_021827225_1
1
gi|493330790|ref|WP_006287973_1|adenosylmethionine_8_amino_7_oxononanoate_aminotransferase__Holospora_undulata_ref_WP_006287973_1
0.69
Trabutinella endobia NODE_819_length_19994_cov_12_2516_ID_1701_39_1919
1
gi|526124647|gb|AGR65713_1|adenosylmethionine_8_amino_7_oxononanoate_transaminase__Planococcus_citri_gb_AGR65713_1
0.2

Figure S4F

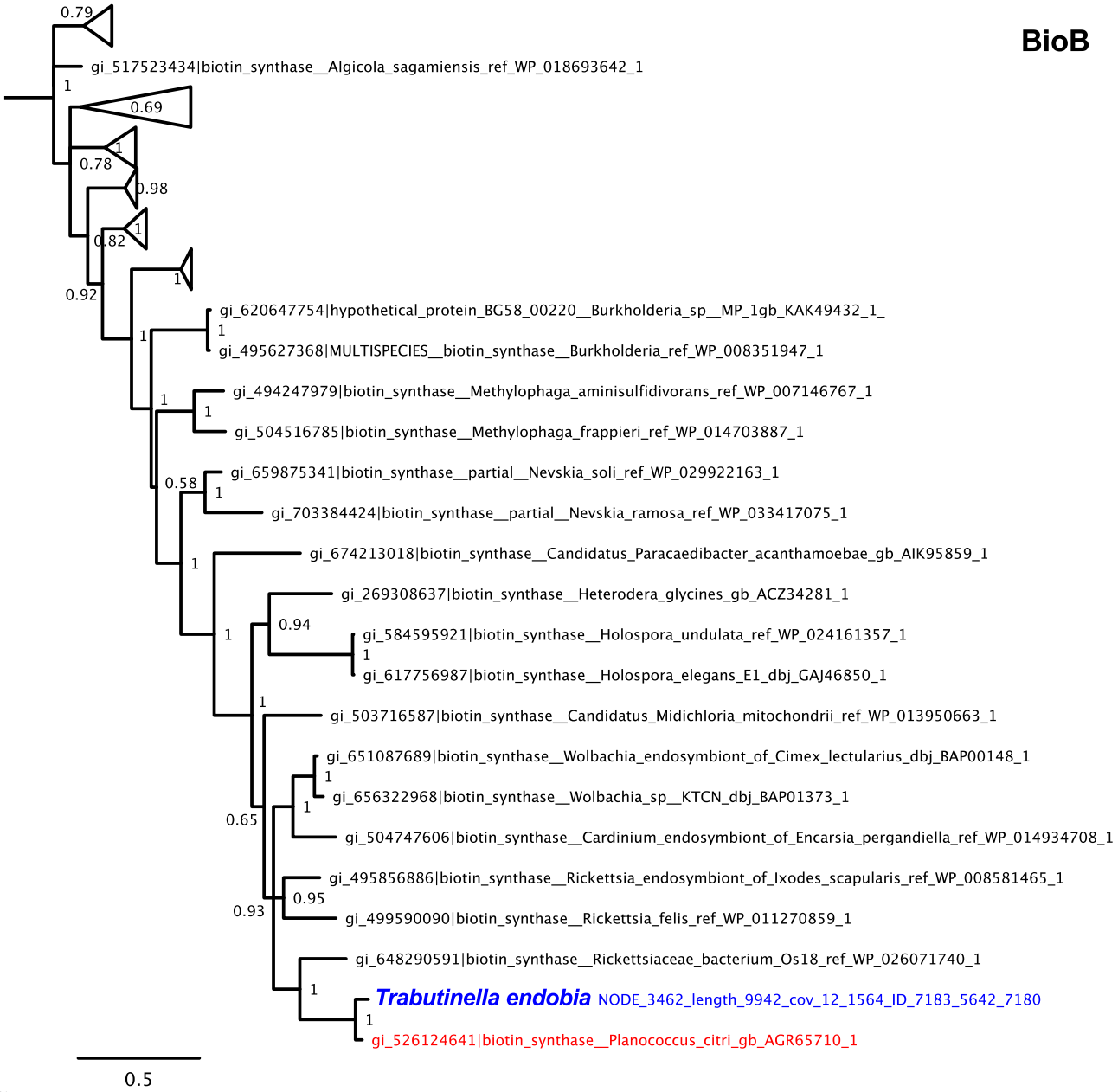
BioB
0.79
gi_517523434|biotin_synthase__Algicola_sagamiensis_ref_WP_018693642_1
1
0.69
1
0.78
0.98
1
0.82
1
0.92
gi_620647754|hypothetical_protein_BG58_00220__Burkholderia_sp__MP_1gb_KAK49432_1_
1
gi_495627368|MULTISPECIES__biotin_synthase__Burkholderia_ref_WP_008351947_1
gi_494247979|biotin_synthase__Methylophaga_aminisulfidivorans_ref_WP_007146767_1
1
gi_504516785|biotin_synthase__Methylophaga_frappieri_ref_WP_014703887_1
0.58
gi_659875341|biotin_synthase__partial__Nevskia_soli_ref_WP_029922163_1
1
gi_703384424|biotin_synthase__partial__Nevskia_ramosa_ref_WP_033417075_1
gi_674213018|biotin_synthase__Candidatus_Paracaedibacter_acanthamoebae_gb_AIK95859_1
gi_269308637|biotin_synthase__Heterodera_glycines_gb_ACZ34281_1
0.94
gi_584595921|biotin_synthase__Holospora_undulata_ref_WP_024161357_1
1
gi_617756987|biotin_synthase__Holospora_elegans_E1_dbj_GAJ46850_1
gi_503716587|biotin_synthase__Candidatus_Midichloria_mitochondrii_ref_WP_013950663_1
gi_651087689|biotin_synthase__Wolbachia_endosymbiont_of_Cimex_lectularius_dbj_BAP00148_1
1
gi_656322968|biotin_synthase__Wolbachia_sp__KTCN_dbj_BAP01373_1
0.65
gi_504747606|biotin_synthase__Cardinium_endosymbiont_of_Encarsia_pergandiella_ref_WP_014934708_1
gi_495856886|biotin_synthase__Rickettsia_endosymbiont_of_Ixodes_scapularis_ref_WP_008581465_1
0.95
0.93
gi_499590090|biotin_synthase__Rickettsia_felis_ref_WP_011270859_1
gi_648290591|biotin_synthase__Rickettsiaceae_bacterium_Os18_ref_WP_026071740_1
1
Trabutinella endobia NODE_3462_length_9942_cov_12_1564_ID_7183_5642_7180
1
gi_526124641|biotin_synthase__Planococcus_citri_gb_AGR65710_1
0.5

Figure S4G

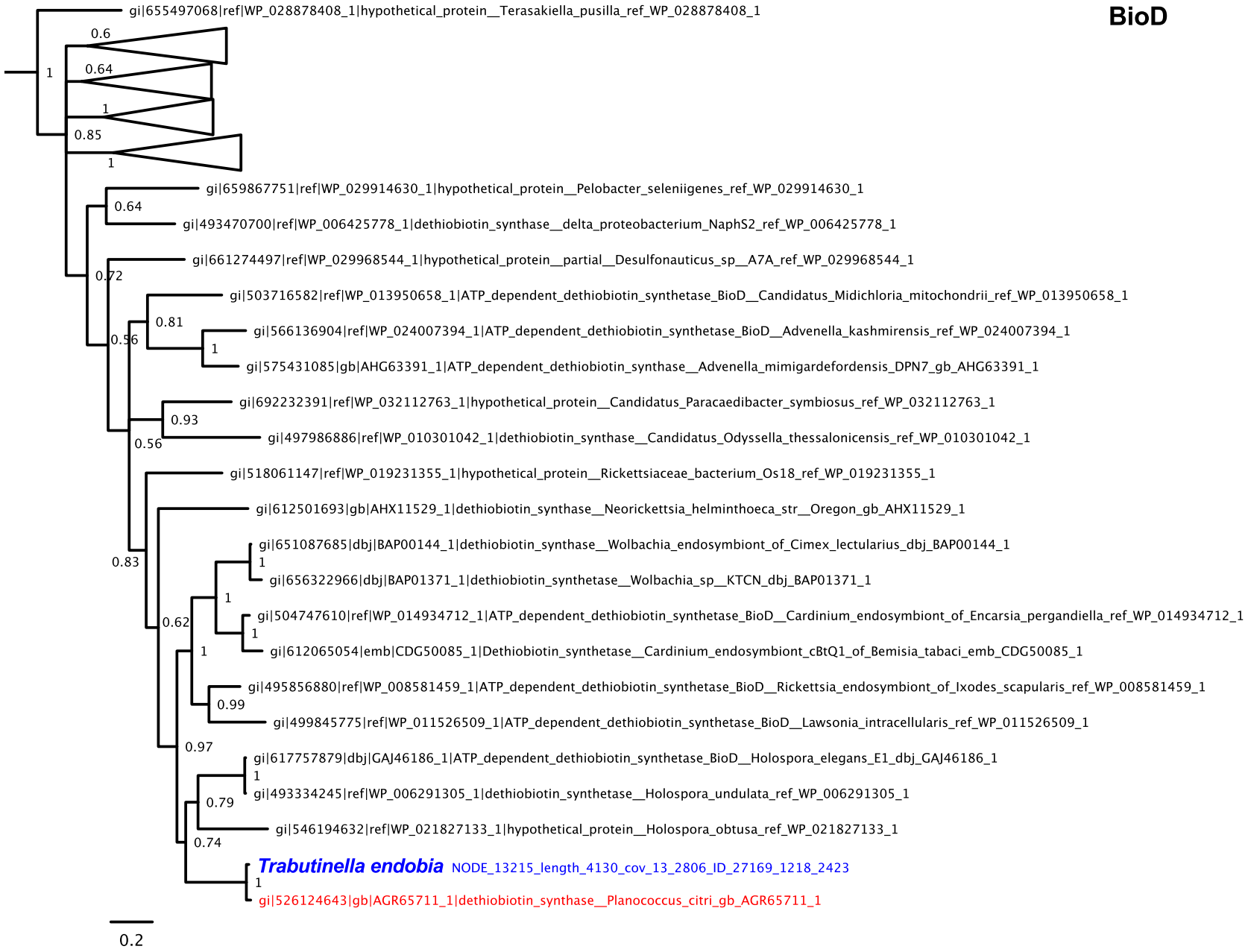
BioD
gi|655497068|ref|WP_028878408_1|hypothetical_protein__Terasakiella_pusilla_ref_WP_028878408_1
0.6
0.64
1
0.85
1
1
gi|659867751|ref|WP_029914630_1|hypothetical_protein__Pelobacter_seleniigenes_ref_WP_029914630_1
0.64
gi|493470700|ref|WP_006425778_1|dethiobiotin_synthase__delta_proteobacterium_NaphS2_ref_WP_006425778_1
gi|661274497|ref|WP_029968544_1|hypothetical_protein__partial__Desulfonauticus_sp__A7A_ref_WP_029968544_1
0.72
gi|503716582|ref|WP_013950658_1|ATP_dependent_dethiobiotin_synthetase_BioD__Candidatus_Midichloria_mitochondrii_ref_WP_013950658_1
0.81
0.56
gi|566136904|ref|WP_024007394_1|ATP_dependent_dethiobiotin_synthetase_BioD__Advenella_kashmirensis_ref_WP_024007394_1
1
gi|575431085|gb|AHG63391_1|ATP_dependent_dethiobiotin_synthase__Advenella_mimigardefordensis_DPN7_gb_AHG63391_1
gi|692232391|ref|WP_032112763_1|hypothetical_protein__Candidatus_Paracaedibacter_symbiosus_ref_WP_032112763_1
0.93
0.56
gi|497986886|ref|WP_010301042_1|dethiobiotin_synthase__Candidatus_Odyssella_thessalonicensis_ref_WP_010301042_1
gi|518061147|ref|WP_019231355_1|hypothetical_protein__Rickettsiaceae_bacterium_Os18_ref_WP_019231355_1
gi|612501693|gb|AHX11529_1|dethiobiotin_synthase__Neorickettsia_helminthoeca_str__Oregon_gb_AHX11529_1
gi|651087685|dbj|BAP00144_1|dethiobiotin_synthase__Wolbachia_endosymbiont_of_Cimex_lectularius_dbj_BAP00144_1
0.83
1
gi|656322966|dbj|BAP01371_1|dethiobiotin_synthetase__Wolbachia_sp__KTCN_dbj_BAP01371_1
1
gi|504747610|ref|WP_014934712_1|ATP_dependent_dethiobiotin_synthetase_BioD__Cardinium_endosymbiont_of_Encarsia_pergandiella_ref_WP_014934712_1
0.62
1
1
gi|612065054|emb|CDG50085_1|Dethiobiotin_synthetase__Cardinium_endosymbiont_cBtQ1_of_Bemisia_tabaci_emb_CDG50085_1
gi|495856880|ref|WP_008581459_1|ATP_dependent_dethiobiotin_synthetase_BioD__Rickettsia_endosymbiont_of_Ixodes_scapularis_ref_WP_008581459_1
0.99
gi|499845775|ref|WP_011526509_1|ATP_dependent_dethiobiotin_synthetase_BioD__Lawsonia_intracellularis_ref_WP_011526509_1
0.97
gi|617757879|dbj|GAJ46186_1|ATP_dependent_dethiobiotin_synthetase_BioD__Holospora_elegans_E1_dbj_GAJ46186_1
1
gi|493334245|ref|WP_006291305_1|dethiobiotin_synthetase__Holospora_undulata_ref_WP_006291305_1
0.79
gi|546194632|ref|WP_021827133_1|hypothetical_protein__Holospora_obtusa_ref_WP_021827133_1
0.74
Trabutinella endobia NODE_13215_length_4130_cov_13_2806_ID_27169_1218_2423
1
gi|526124643|gb|AGR65711_1|dethiobiotin_synthase__Planococcus_citri_gb_AGR65711_1
0.2

Figure S4H

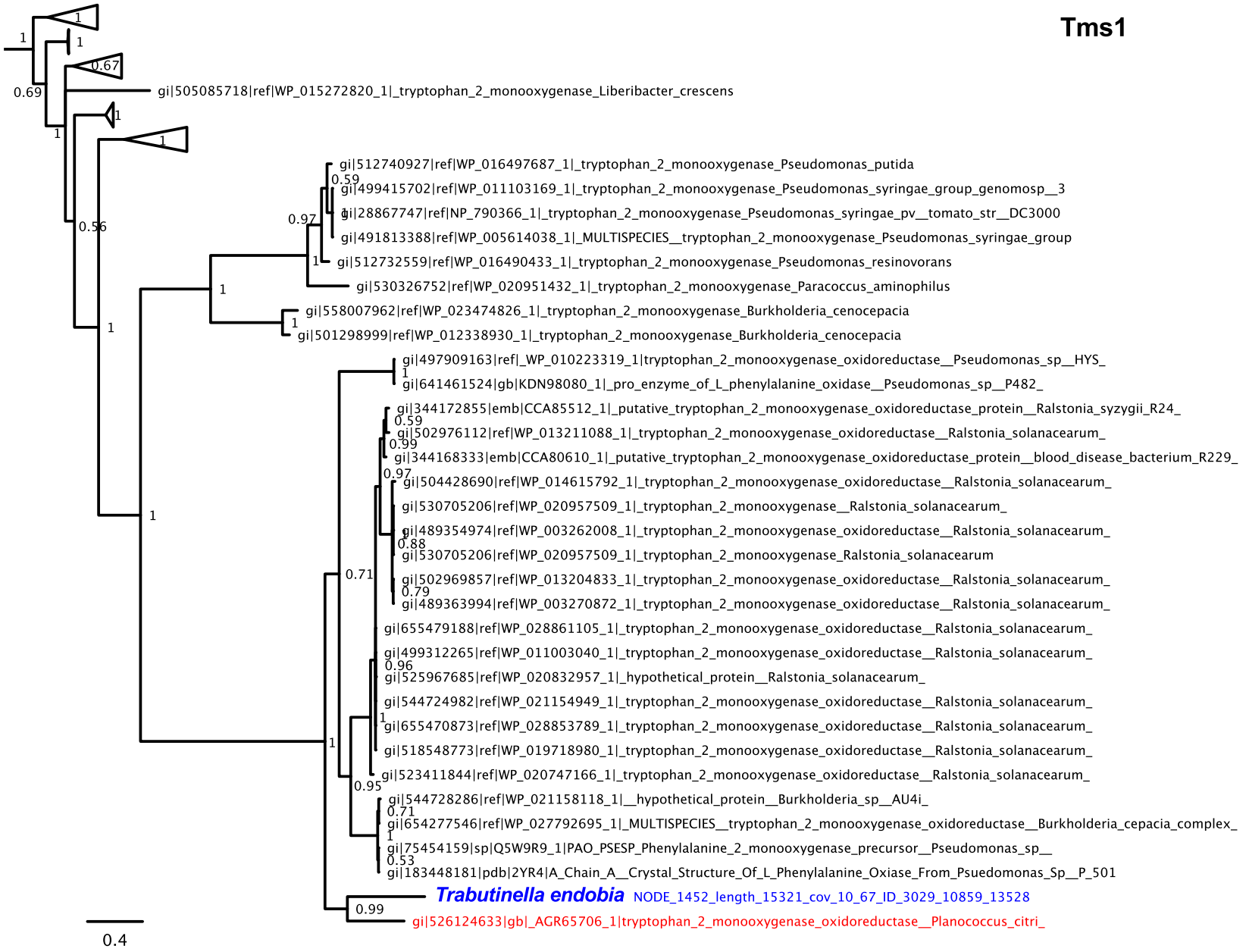
Tms1
gi|505085718|ref|WP_015272820_1|_tryptophan_2_monooxygenase_Liberibacter_crescens
gi|512740927|ref|WP_016497687_1|_tryptophan_2_monooxygenase_Pseudomonas_putida
gi|499415702|ref|WP_011103169_1|_tryptophan_2_monooxygenase_Pseudomonas_syringae_group_genomosp__3
gi|28867747|ref|NP_790366_1|_tryptophan_2_monooxygenase_Pseudomonas_syringae_pv__tomato_str__DC3000
gi|491813388|ref|WP_005614038_1|_MULTISPECIES__tryptophan_2_monooxygenase_Pseudomonas_syringae_group
gi|512732559|ref|WP_016490433_1|_tryptophan_2_monooxygenase_Pseudomonas_resinovorans
gi|530326752|ref|WP_020951432_1|_tryptophan_2_monooxygenase_Paracoccus_aminophilus
gi|558007962|ref|WP_023474826_1|_tryptophan_2_monooxygenase_Burkholderia_cenocepacia
gi|501298999|ref|WP_012338930_1|_tryptophan_2_monooxygenase_Burkholderia_cenocepacia
gi|497909163|ref|_WP_010223319_1|tryptophan_2_monooxygenase_oxidoreductase__Pseudomonas_sp__HYS_
gi|641461524|gb|KDN98080_1|_pro_enzyme_of_L_phenylalanine_oxidase__Pseudomonas_sp__P482_
gi|344172855|emb|CCA85512_1|_putative_tryptophan_2_monooxygenase_oxidoreductase_protein__Ralstonia_syzygii_R24_
gi|502976112|ref|WP_013211088_1|_tryptophan_2_monooxygenase_oxidoreductase__Ralstonia_solanacearum_
gi|344168333|emb|CCA80610_1|_putative_tryptophan_2_monooxygenase_oxidoreductase_protein__blood_disease_bacterium_R229_
gi|504428690|ref|WP_014615792_1|_tryptophan_2_monooxygenase_oxidoreductase__Ralstonia_solanacearum_
gi|530705206|ref|WP_020957509_1|_tryptophan_2_monooxygenase__Ralstonia_solanacearum_
gi|489354974|ref|WP_003262008_1|_tryptophan_2_monooxygenase_oxidoreductase__Ralstonia_solanacearum_
gi|530705206|ref|WP_020957509_1|_tryptophan_2_monooxygenase_Ralstonia_solanacearum
gi|502969857|ref|WP_013204833_1|_tryptophan_2_monooxygenase_oxidoreductase__Ralstonia_solanacearum_
gi|489363994|ref|WP_003270872_1|_tryptophan_2_monooxygenase_oxidoreductase__Ralstonia_solanacearum_
gi|655479188|ref|WP_028861105_1|_tryptophan_2_monooxygenase_oxidoreductase__Ralstonia_solanacearum_
gi|499312265|ref|WP_011003040_1|_tryptophan_2_monooxygenase_oxidoreductase__Ralstonia_solanacearum_
gi|525967685|ref|WP_020832957_1|_hypothetical_protein__Ralstonia_solanacearum_
gi|544724982|ref|WP_021154949_1|_tryptophan_2_monooxygenase_oxidoreductase__Ralstonia_solanacearum_
gi|655470873|ref|WP_028853789_1|_tryptophan_2_monooxygenase_oxidoreductase__Ralstonia_solanacearum_
gi|518548773|ref|WP_019718980_1|_tryptophan_2_monooxygenase_oxidoreductase__Ralstonia_solanacearum_
gi|523411844|ref|WP_020747166_1|_tryptophan_2_monooxygenase_oxidoreductase__Ralstonia_solanacearum_
gi|544728286|ref|WP_021158118_1|__hypothetical_protein__Burkholderia_sp__AU4i_
gi|654277546|ref|WP_027792695_1|_MULTISPECIES__tryptophan_2_monooxygenase_oxidoreductase__Burkholderia_cepacia_complex_
gi|75454159|sp|Q5W9R9_1|PAO_PSESP_Phenylalanine_2_monooxygenase_precursor__Pseudomonas_sp__
gi|183448181|pdb|2YR4|A_Chain_A__Crystal_Structure_Of_L_Phenylalanine_Oxiase_From_Psuedomonas_Sp__P_501
Trabutinella endobia
NODE_1452_length_15321_cov_10_67_ID_3029_10859_13528
gi|526124633|gb|_AGR65706_1|tryptophan_2_monooxygenase_oxidoreductase__Planococcus_citri_
0.4

Figure S4I