

Additional File 5. Candidate LGT from prokaryotes to eukaryotes

Each tree is a Bayesian consensus tree, based on an alignment of homologues from one or more of the target taxa studied in this survey, where LGT from prokaryotes to eukaryotes is the most parsimonious explanation for the resulting tree topology. The key for the symbols used to differentiate the taxonomy of the analyses sequences and provide taxonomic contextualization for the candidate LGTs is indicated just after the list of trees. A parallel phylogenetic analyses was performed with pairwise maximum likelihood distances calculated with the same model used for the Bayesian analysis and bootstrap values estimated and mapped onto the Bayesian consensus tree. Only well-supported branches are indicated (posterior probabilities ≥ 0.95 , bootstrap ≥ 0.7) on the trees with all other branches being collapsed into polytomies. The LGTs supported by at least one node (trees numbered ONXXX) or at least two nodes (trees numbered TNXXX) separating the target taxa from other eukaryotes are illustrated. Datasets where the target taxa are the only eukaryote (or with closely related taxa, the latter suggesting deep LGT prior speciation events) among prokaryotic sequences are also labeled as TNXXX. The accession number and annotations of the sequences from the target taxa (boxed in the trees) are indicated. A PHOBIUS analysis investigated the potential presence of a signal peptide (SP) and transmembrane domains (TMD).

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21 September, 2012

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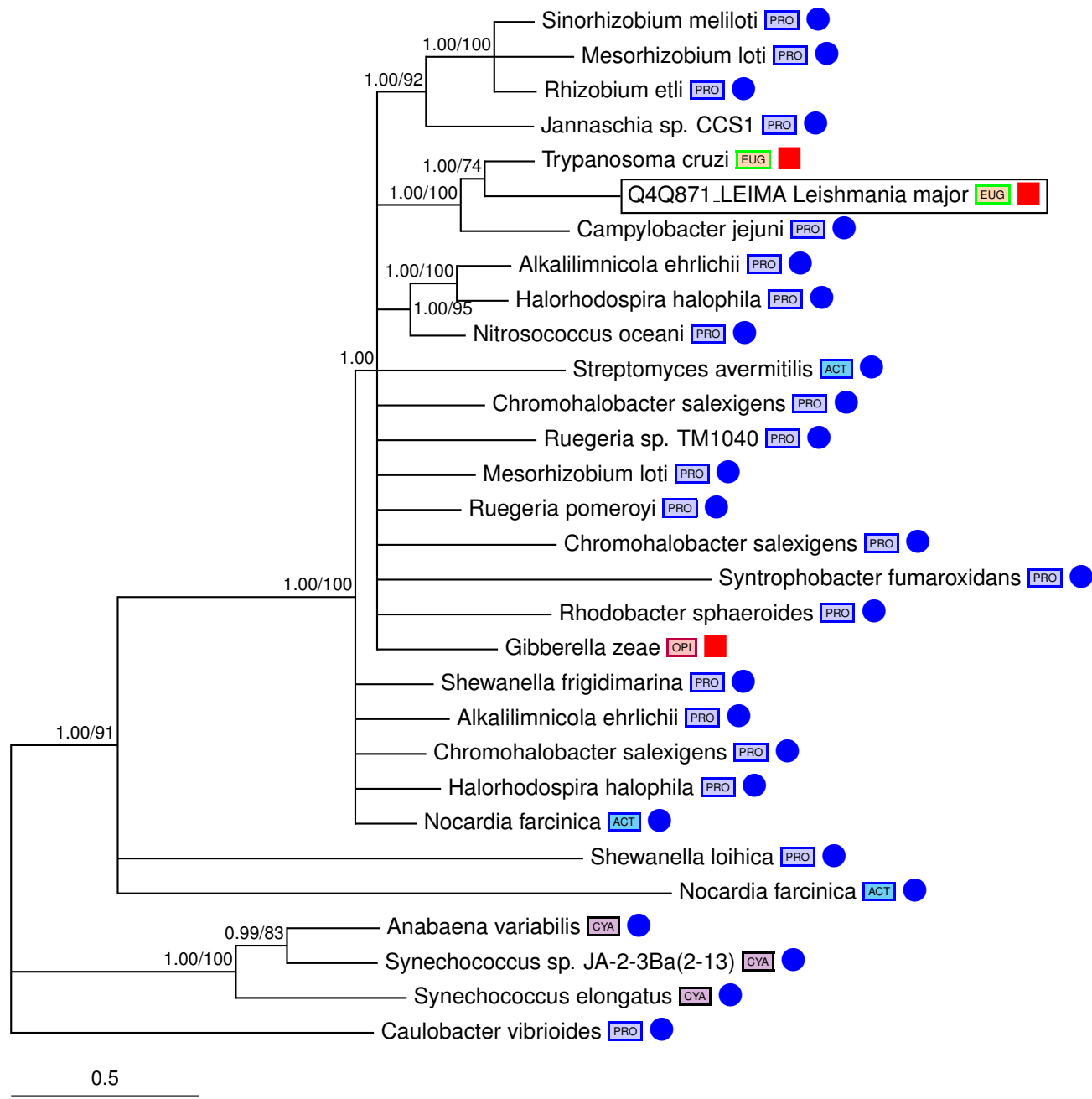
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ON027	29	TN030	95	TN096	161	TN164	227	TN230	293
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ON050	52	TN053	118	TN120	184	TN187	250	TN253	316
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ON053	55	TN056	121	TN123	187	TN190	253	TN256	319
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ON056	58	TN059	124	TN126	190	TN193	256	TN259	322
ON057	59	TN060	125	TN127	191	TN194	257	TN260	323
ON058	60	TN061	126	TN128	192	TN195	258	TN261	324
ON059	61	TN062	127	TN129	193	TN196	259	TN262	325
ON060	62	TN063	128	TN131	194	TN197	260	TN263	326
ON061	63	TN064	129	TN132	195	TN198	261	TN264	327
ON062	64	TN065	130	TN133	196	TN199	262	TN265	
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TN001	66	TN067	132	TN135	198	TN201	264		
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Taxa group color key

Bacteria		
ACT	Actinobacteria	
AQU	Aquificae	
BC	Bacteroidetes/Chlorobi group	
CAL	Caldiserica	
C-V	Chlamydiae/Verrucomicrobia group	
CHL	Chloroflexi	
CHR	Chrysiogenetes	
CYA	Cyanobacteria	
DEF	Deferribacteres	
D-T	Deinococcus-Thermus	
DIC	Dictyoglomi	
ELU	Elusimicrobia	
F-A	Fibrobacteres/Acidobacteria group	
FIR	Firmicutes	
FUS	Fusobacteria	
GEM	Gemmatimonadetes	
NIT	Nitrospirae	
PLA	Planctomycetes	
PRO	Proteobacteria	
SPI	Spirochaetes	
SYN	Synergistetes	
TEN	Tenericutes	
THED	Thermodesulfobacteria	
THET	Thermotogae	
UB	unclassified Bacteria	
EB	environmental samples	
Archaea		
CRE	Crenarchaeota	
EUR	Euryarchaeota	
KOR	Korarchaeota	
NAN	Nanoarchaeota	
THA	Thaumarchaeota	
UA	unclassified Archaea	
EA	environmental samples	
Eukaryotes		
AMO	Amoebozoa	
OPI	Opisthokonta	
NUC	Nucleariidae	
CEN	Centroheliiozoa	
APU	Apusozoa	
KAT	Katablepharidophyta	
RHI	Rhizaria	
HET	Heterolobosea	
FOR	Fornicata	
MAL	Malawimonadidae	
EUG	Euglenozoa	
JOK	Jakobida	
OXY	Oxymonadida	
PAR	Parabasalia	
HAP	Haptophyceae	
CRY	Cryptophyta	
ALV	Alveolata	
STR	stramenopiles	
RHO	Rhodophyta	
GLA	Glaucocystophyceae	
VIR	Viridiplantae	
UE	unclassified eukaryotes	
EE	environmental samples	
Superkingdoms		
●	Bacteria	
▲	Archaea	
■	Eukaryotes	
✱	Viruses	

ON001

Candy accession: Q4Q871_LEIMA
RefSeq accession: XP_001684477.1
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Species affected: LM,TC, FUNGI
Adjacent taxa in tree: Proteobacteria - Campylobacter
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: X-pro, dipeptidyl-peptidase,serine
peptidase, Clan SC, family S15
Name of enzyme/protein: NonD putative hydrolase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction

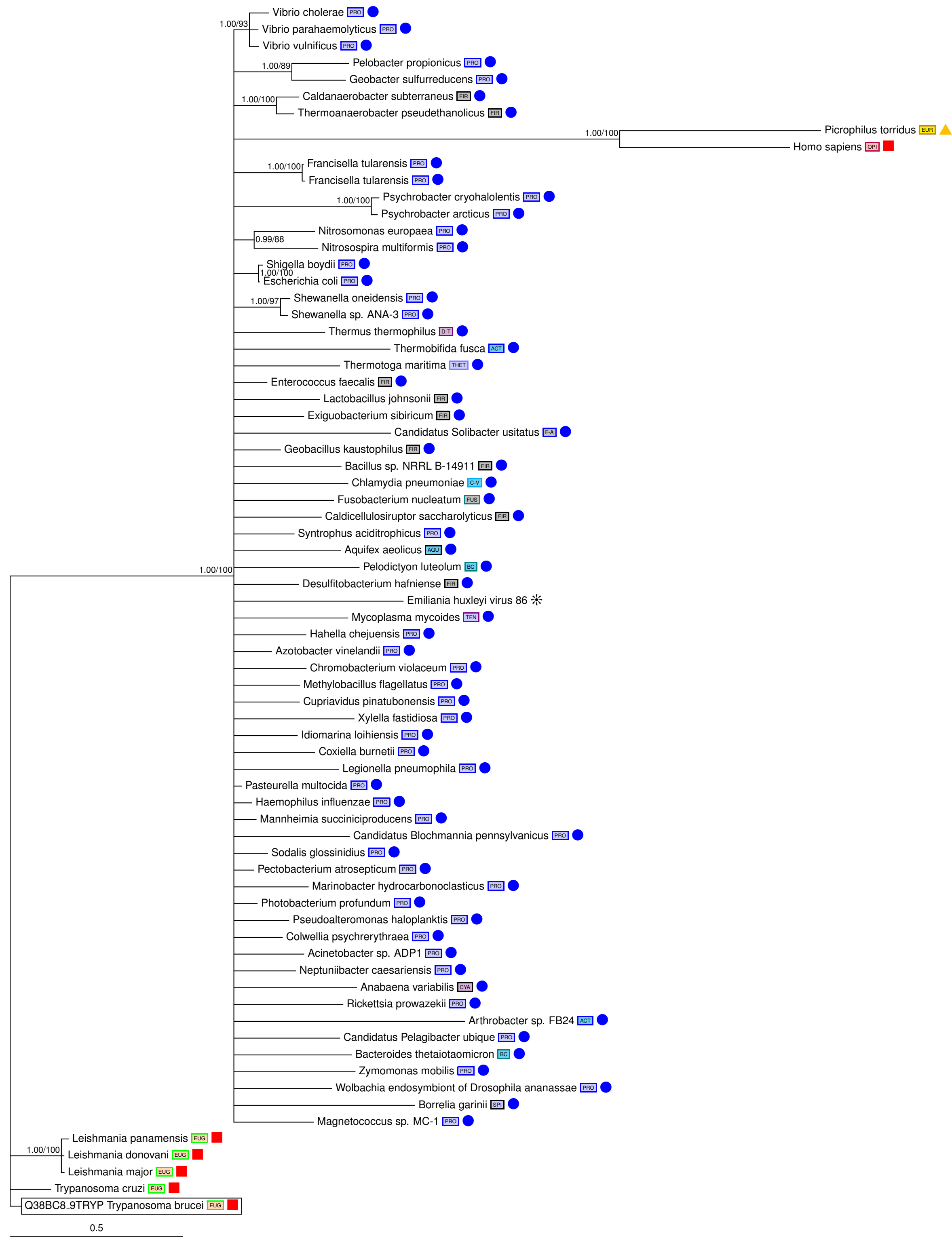


ON002

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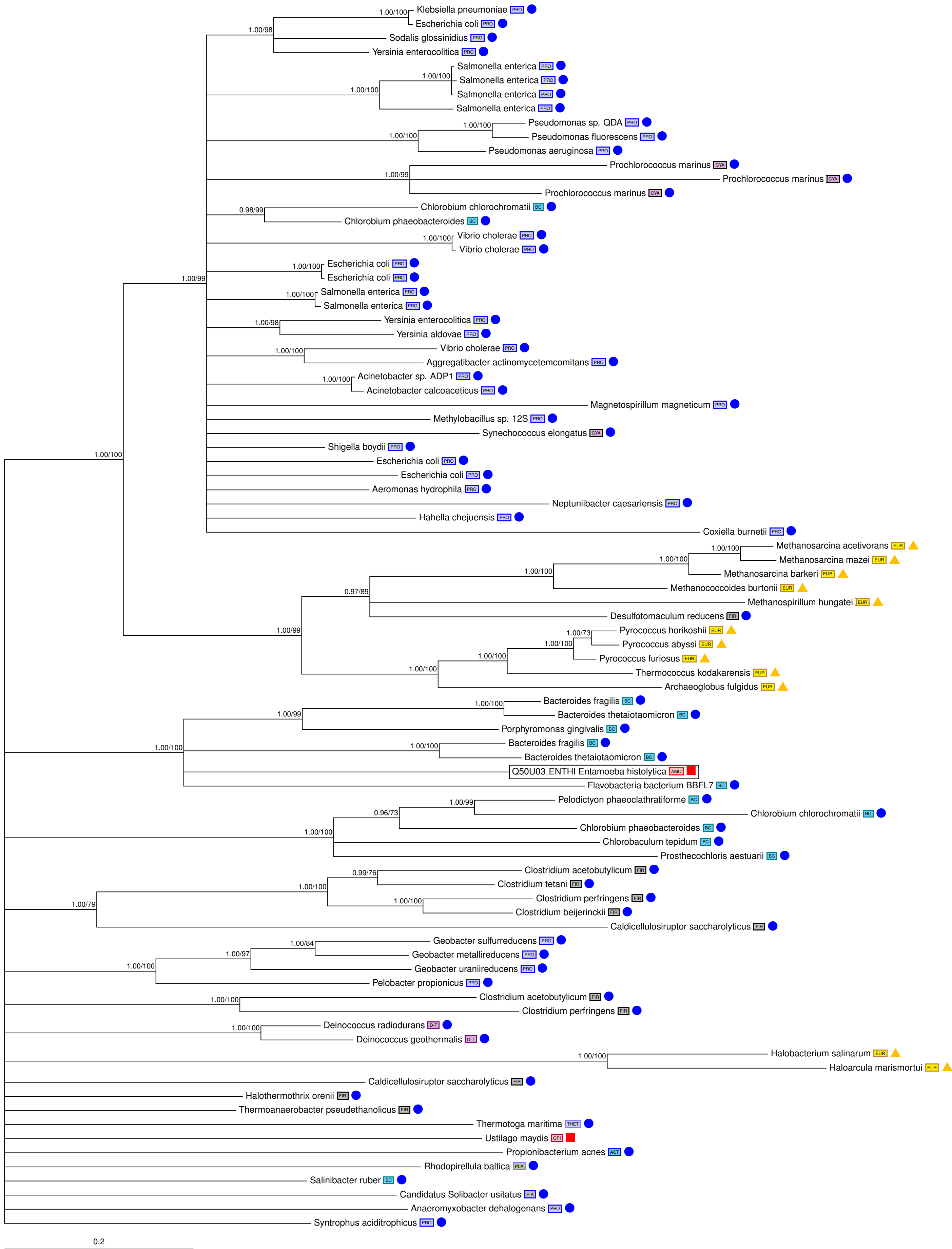
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      Adjacent taxa in tree: Bacteria
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      PHOBIUS SP: 0
      PHOBIUS TMD: 0
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      Name of enzyme/protein: Ribonuclease H
      KEGG PATHWAY - level 1: Reaction
      KEGG PATHWAY - level 2: Reaction

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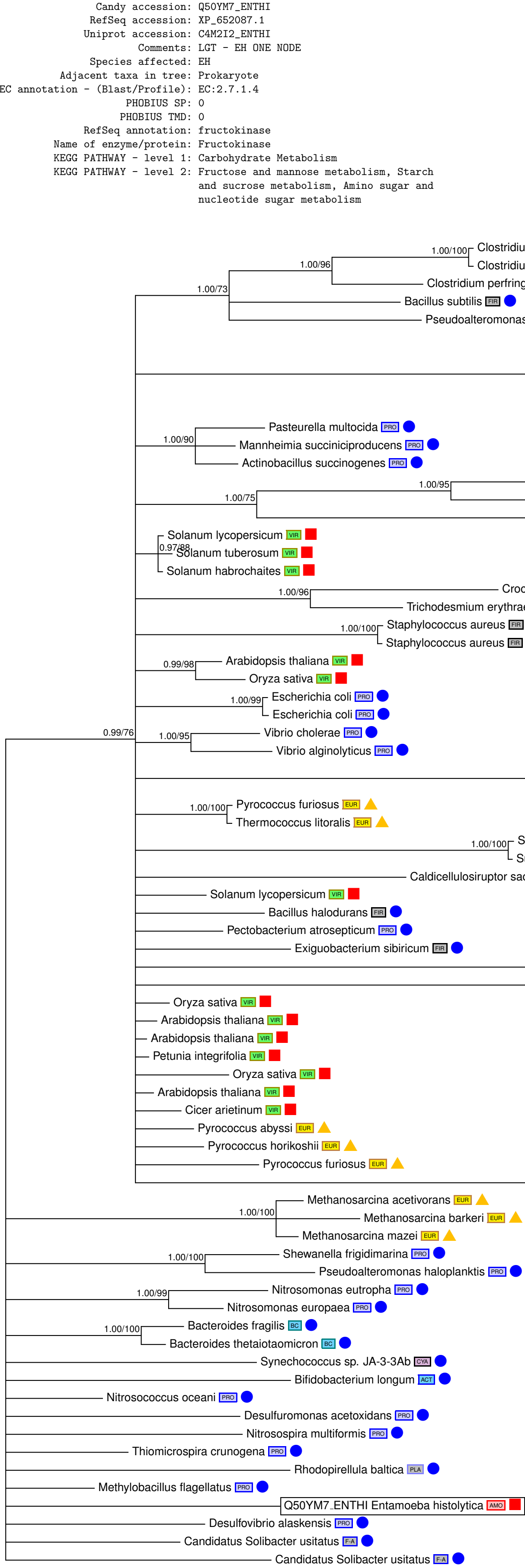
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RefSeq accession: XP_650453.1
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Species affected: EH
Adjacent taxa in tree: Bacteroidetes/Chlorobi
EC annotation - (Blast/Profile): EC:2.7.7.22
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: mannose-1-phosphate guanylyltransferase
Name of enzyme/protein: mannose-1-phosphate guanylyltransferase (GDP)
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Fructose and mannose metabolism, Amino sugar and nucleotide sugar metabolism

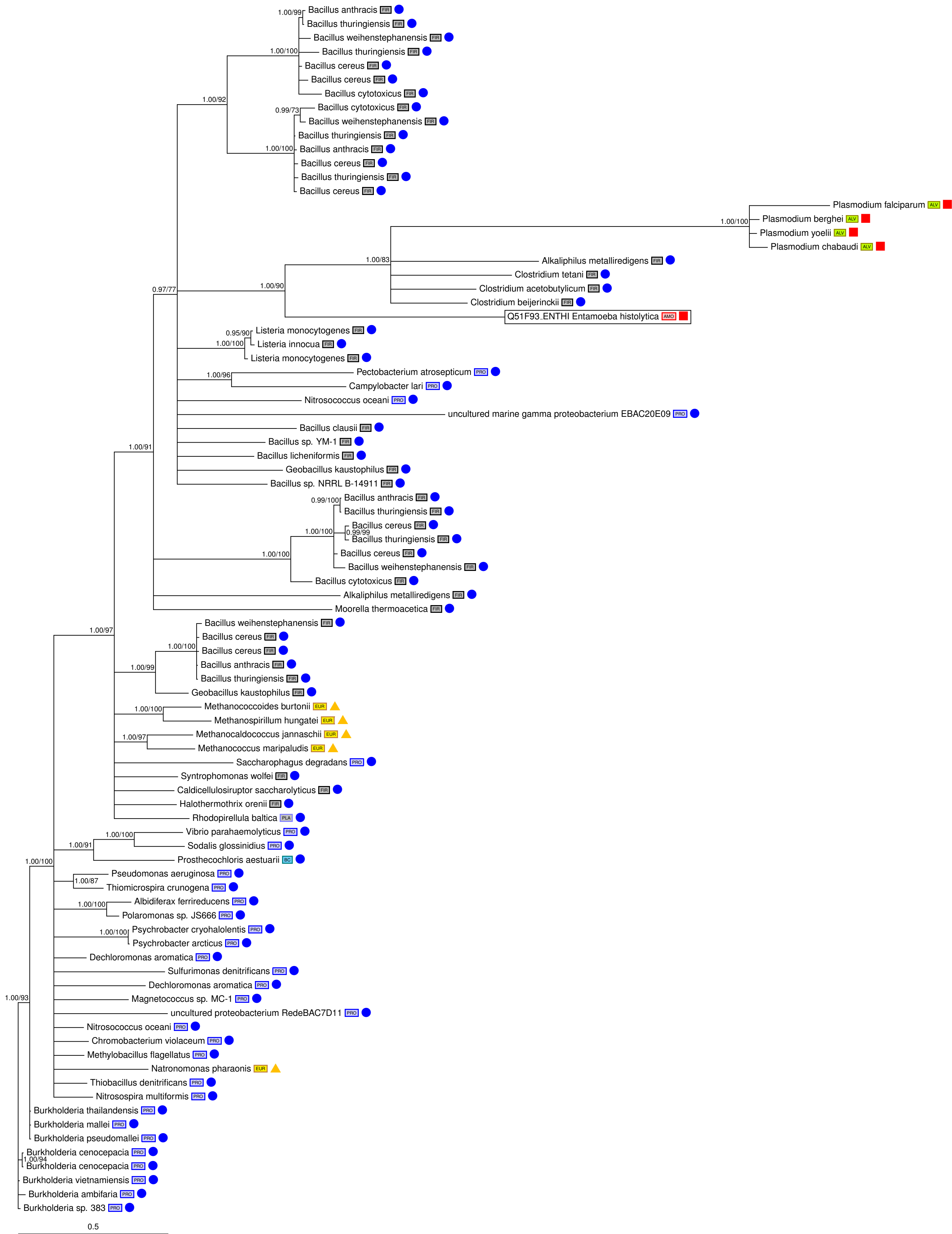


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ON004

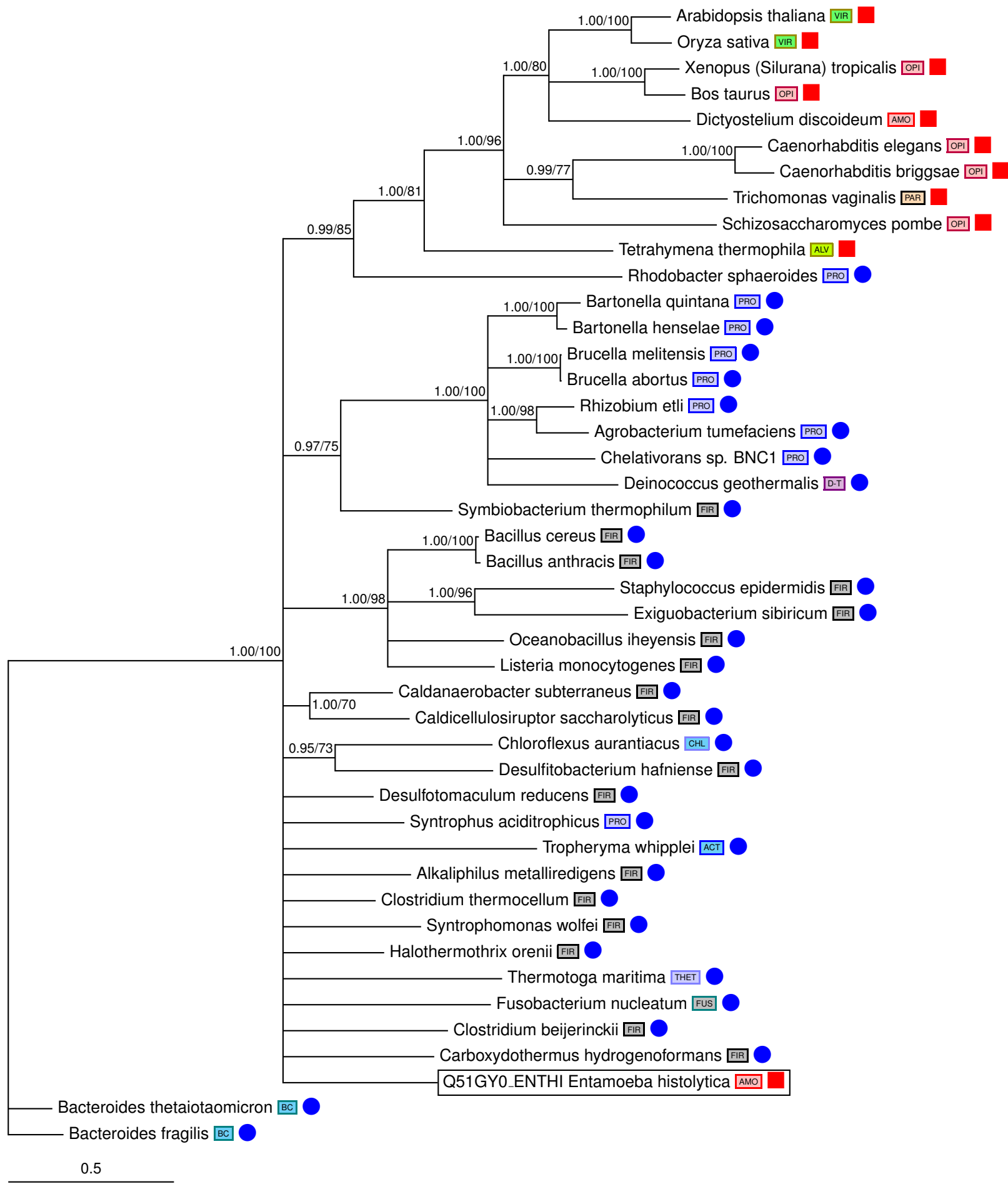


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RefSeq accession: XP_656980.1
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Species affected: EH,PF,PY
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): EC:2.6.1.42
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: branched-chain amino acid aminotransferase
Name of enzyme/protein: Branched-chain amino acid aminotransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Valine, leucine and isoleucine degradation, Valine, leucine and isoleucine biosynthesis, Pantothenate and CoA biosynthesis



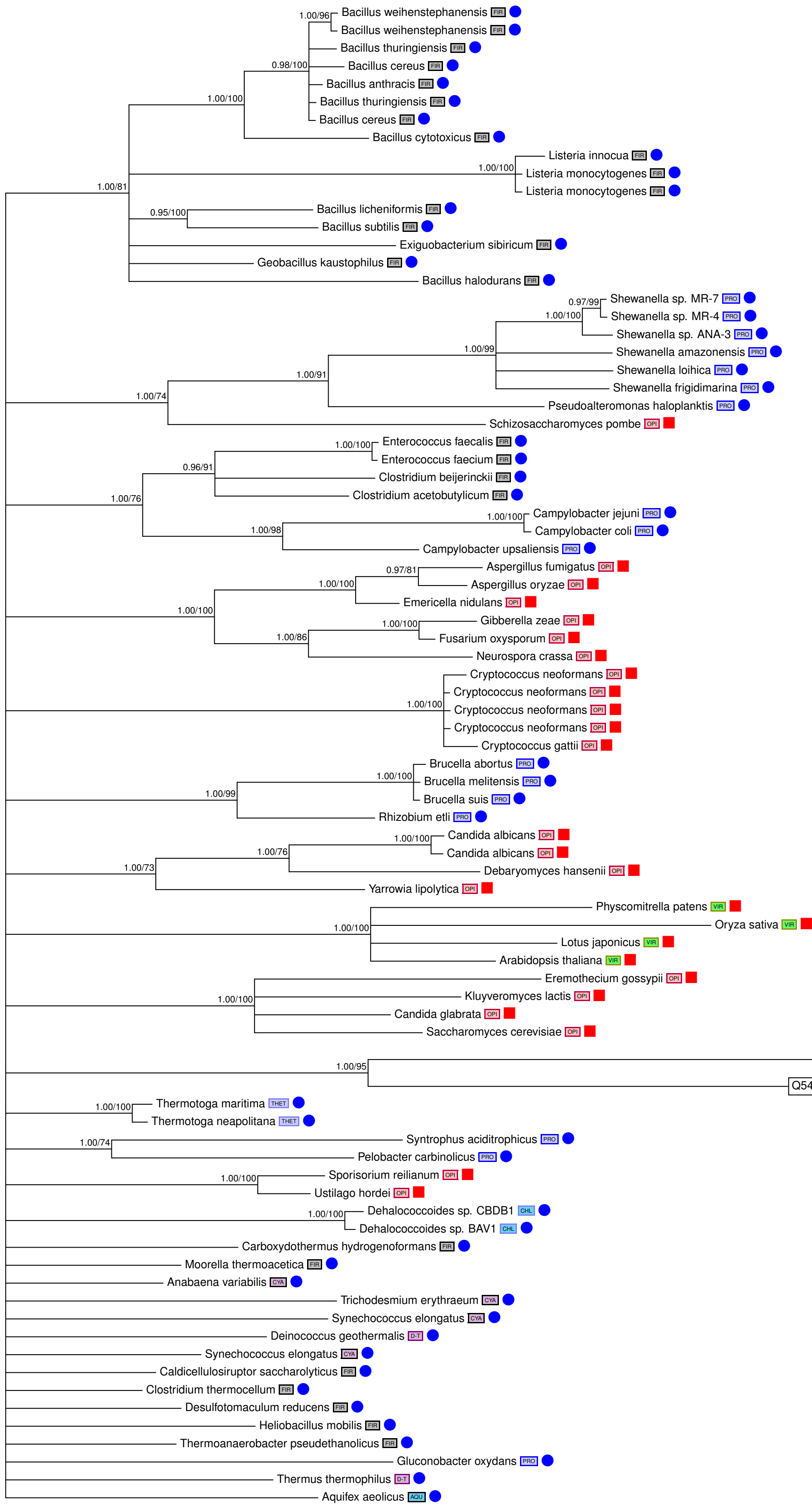
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Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.7.6.2
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: thiamine pyrophosphokinase
Name of enzyme/protein: Thiamine pyrophosphokinase
KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Thiamine metabolism



ON007

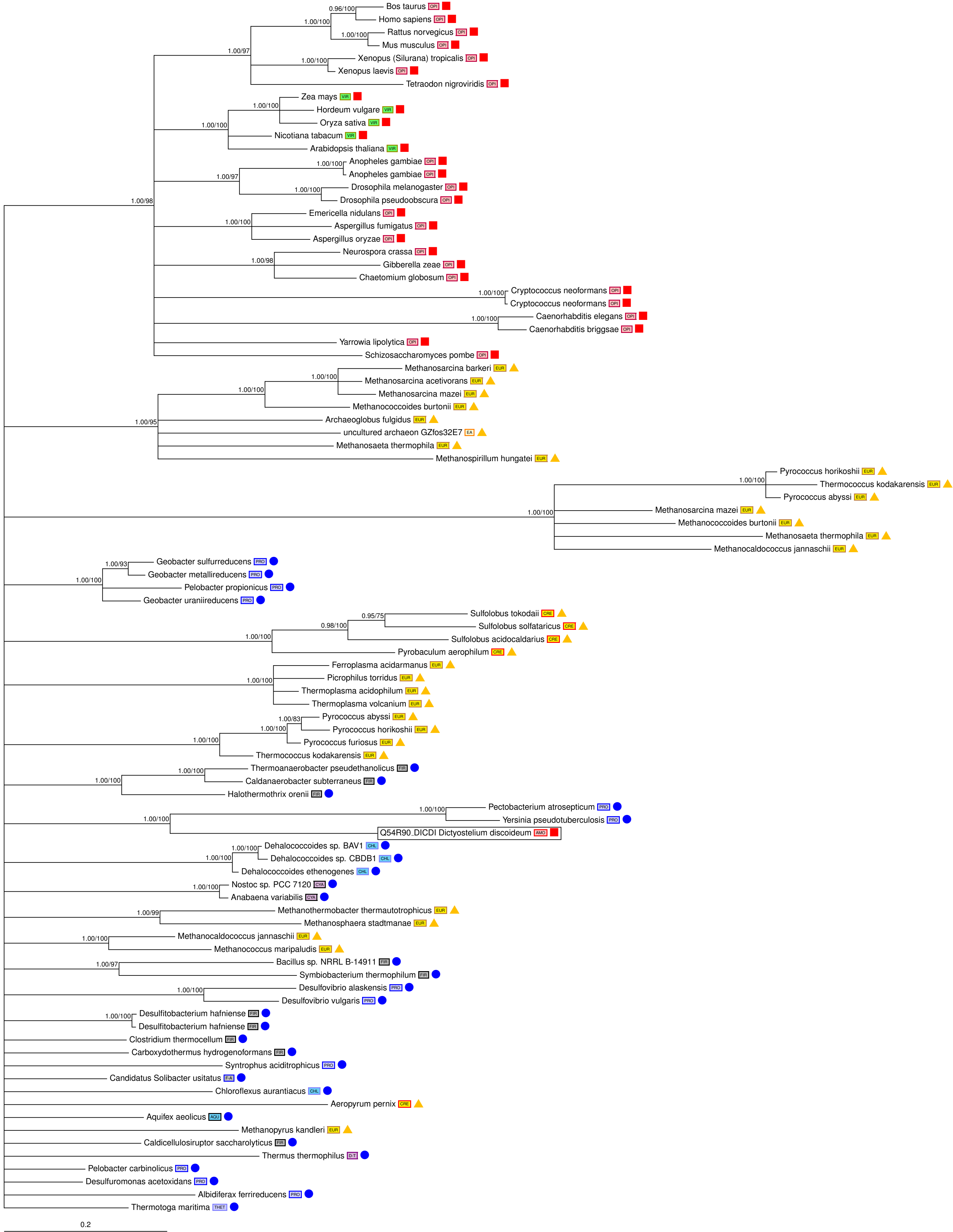
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Adjacent taxa in tree: Proteobacteria - Francisella
EC annotation - (Blast/Profile): EC:6.3.2.1
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: pantoate-beta-alanine ligase
Name of enzyme/protein: Pantoate-beta-alanine ligase
KEGG PATHWAY - level 1: Metabolism of Other Amino Acids,
Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: beta-Alanine metabolism, Pantothenate
and CoA biosynthesis



0.2

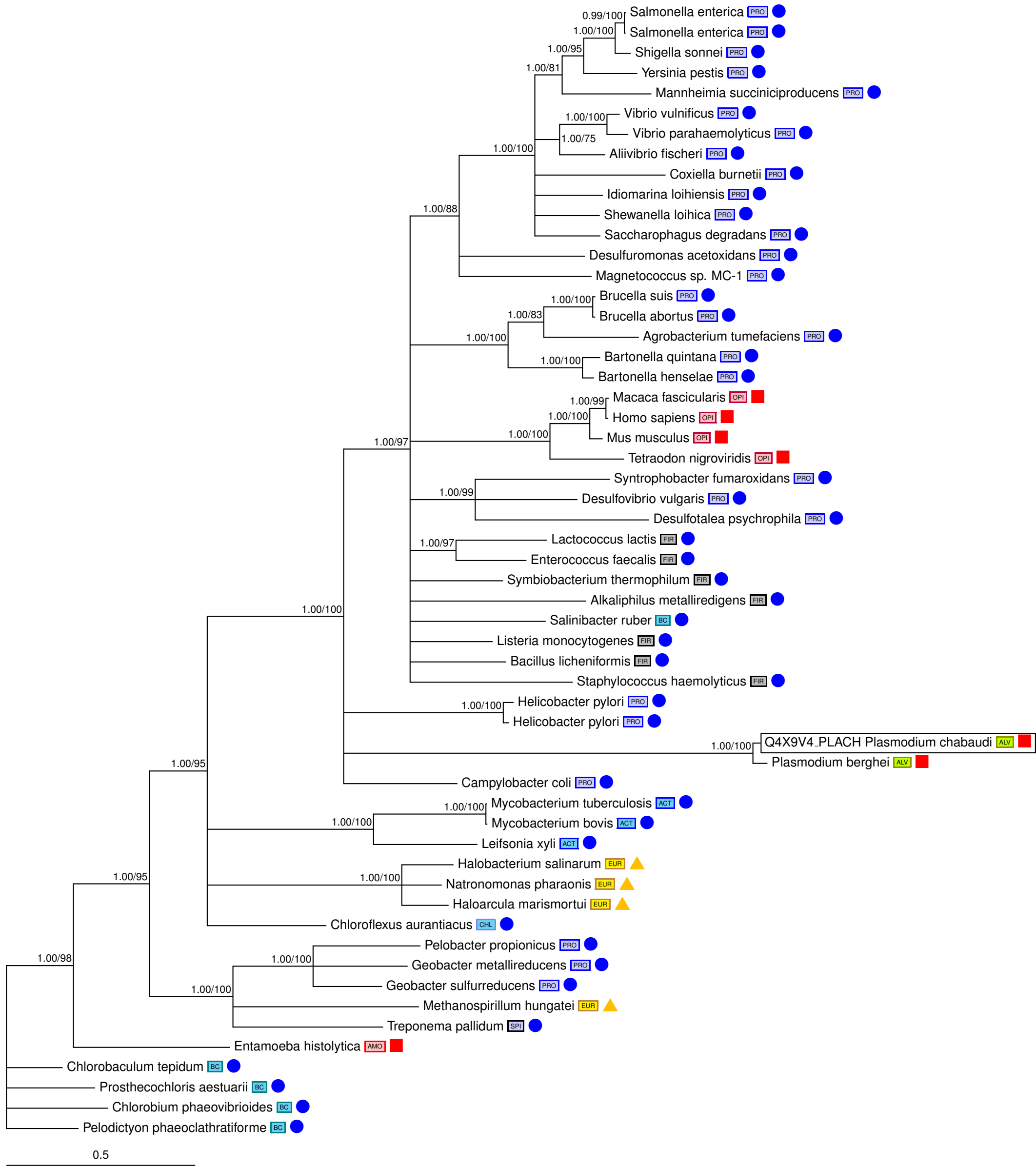
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Species affected: DD
Adjacent taxa in tree: Protobacteria
EC annotation - (Blast/Profile): EC:5.3.1.23
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: translation initiation factor eIF-2B
alpha subunit
Name of enzyme/protein: S-methyl-5-thioribose-1-phosphate
isomerase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Cysteine and methionine metabolism



ON009

Candy accession: Q4X9V4_PLACH
RefSeq accession: XP_735375.1
Uniprot accession: Q4X9V4_PLACH
Comments: LGT - EH ONE NODE
Species affected: PC,PB
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:3.2.2.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: A/G-specific adenine glycosylase
Name of enzyme/protein: purine nucleosidase
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Purine metabolism, Nicotinate and nicotinamide metabolism



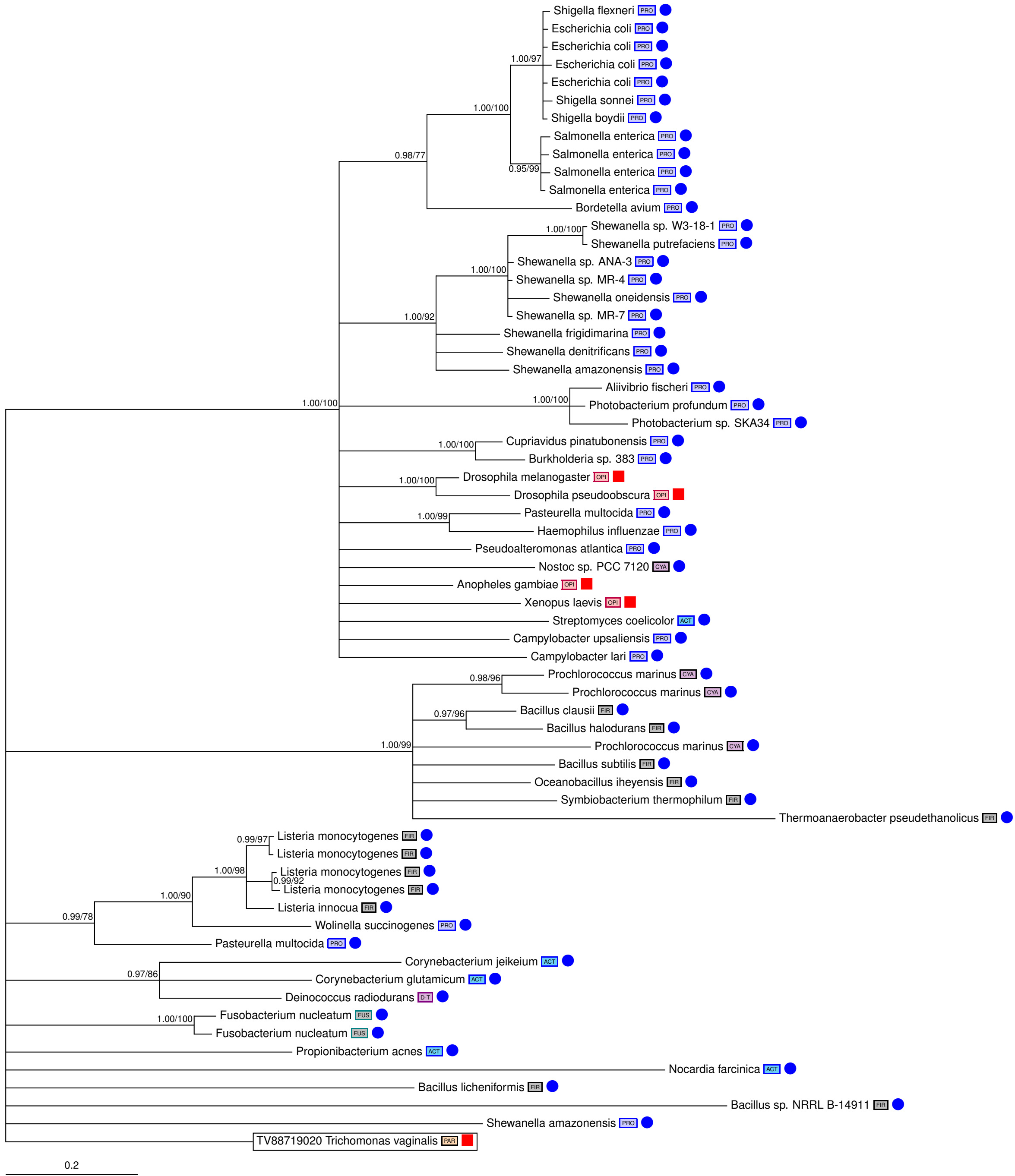
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Comments: LGT - TV ONE NODE
Species affected: TV
Adjacent taxa in tree: Bacteroides
EC annotation - (Blast/Profile): EC:3.1.1.31
PHOBIUS SP: 0
PHOBIUS TMD: 0
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Name of enzyme/protein: 6-phosphogluconolactonase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pentose phosphate pathway



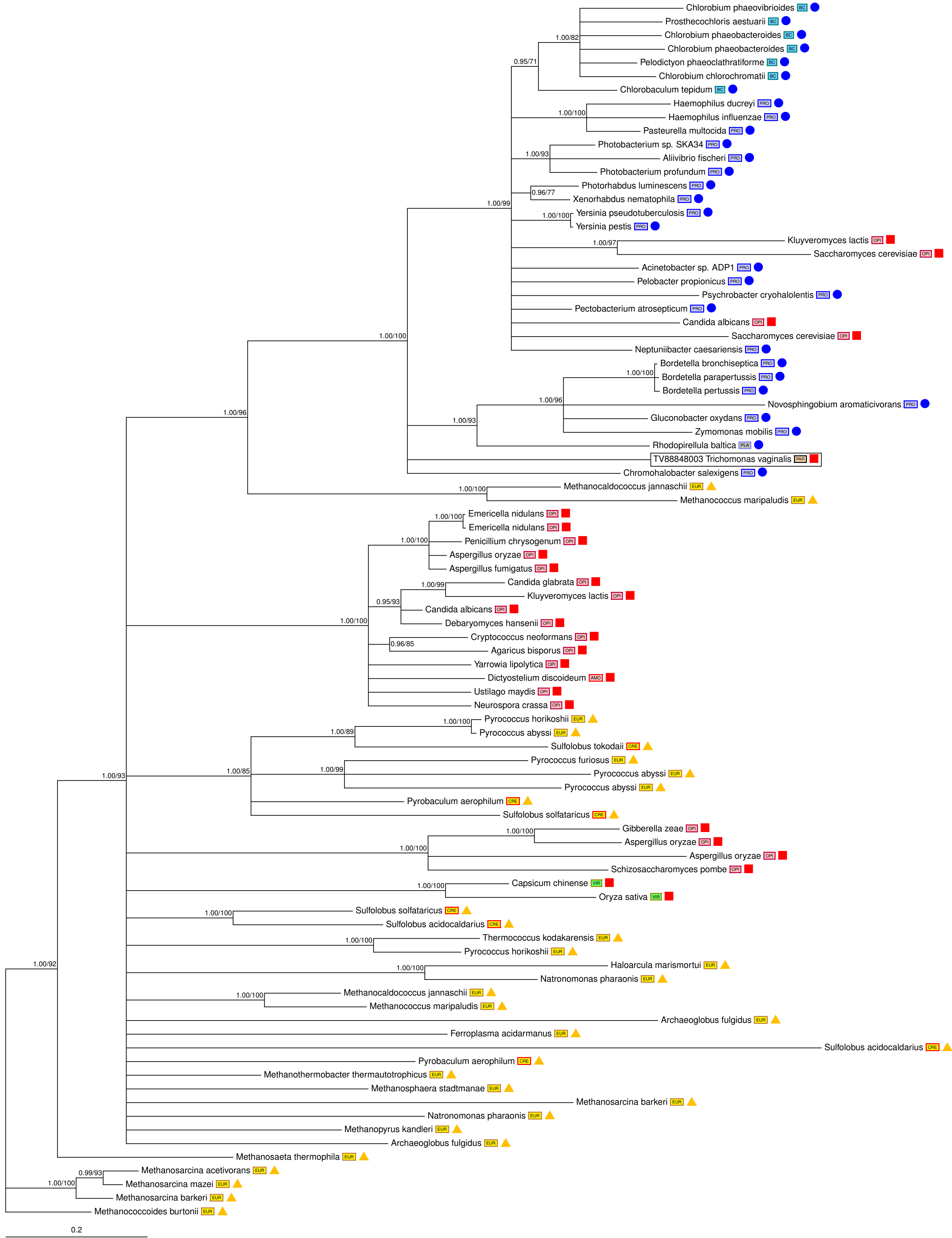
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Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.4.13.21
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Clan PC(S), family S51, peptidase E-like
serine peptidase
Name of enzyme/protein: dipeptidase E
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



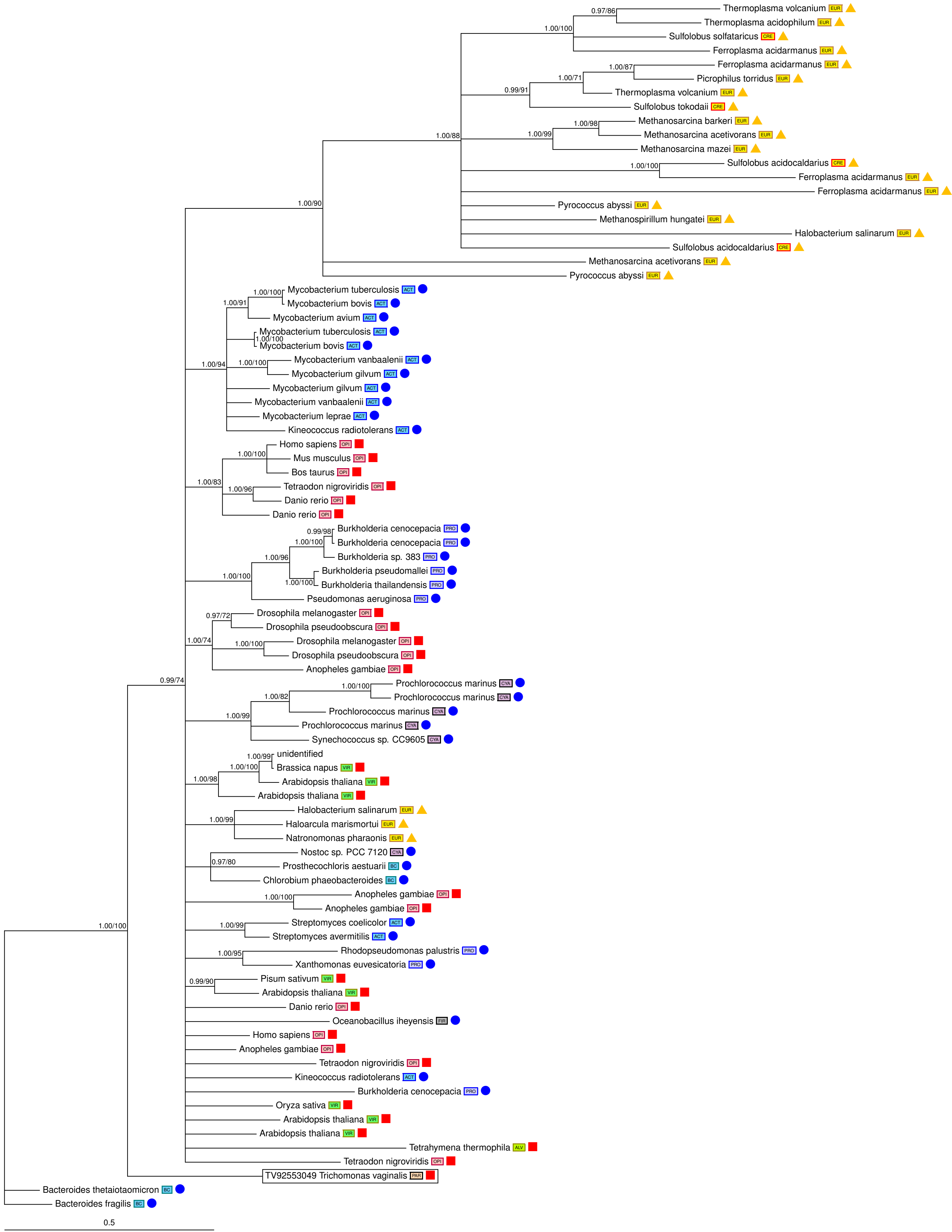
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Uniprot accession: A2GPY4_TRIVA
Comments: LGT - TV ONE NODE - LGT INTO FUNGI
Species affected: TV,FUNGI
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:2.6.1.62
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: adenosylmethionine-8-amino-7-oxononanoat
e aminotransferase family protein
Name of enzyme/protein: adenosylmethionine-8-amino-7-oxononanoat
e transaminase
KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Biotin metabolism



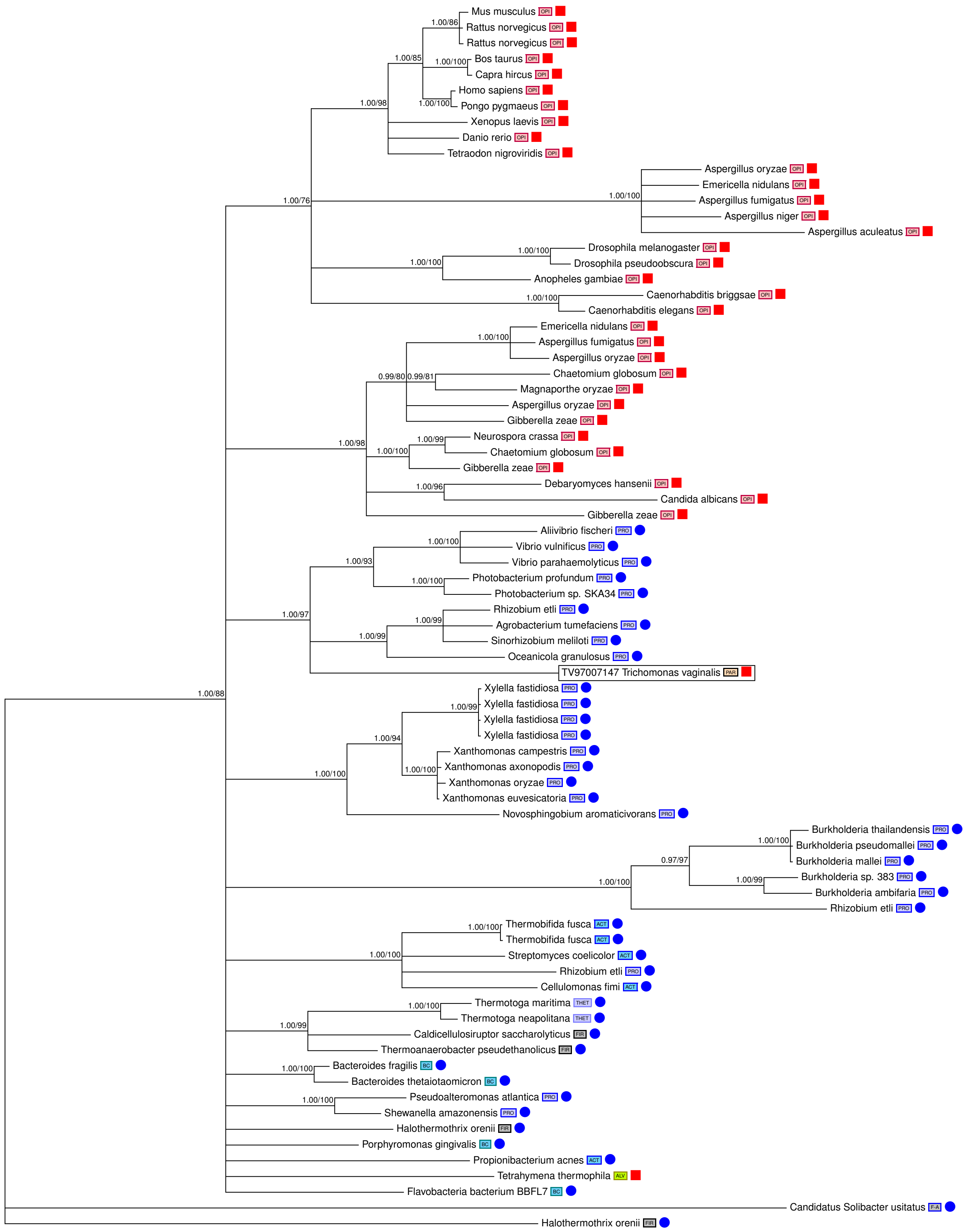
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Candy accession: TV92553049
RefSeq accession: XP_001308730.1
Uniprot accession: A2FH32_TRIVA
Comments: LGT - TV ONE NODE - 3 DOMAIN TREE
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:1.1.1.-
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: oxidoreductase, short chain
dehydrogenase/reductase family protein
Name of enzyme/protein: Oxidoreductase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



ON015

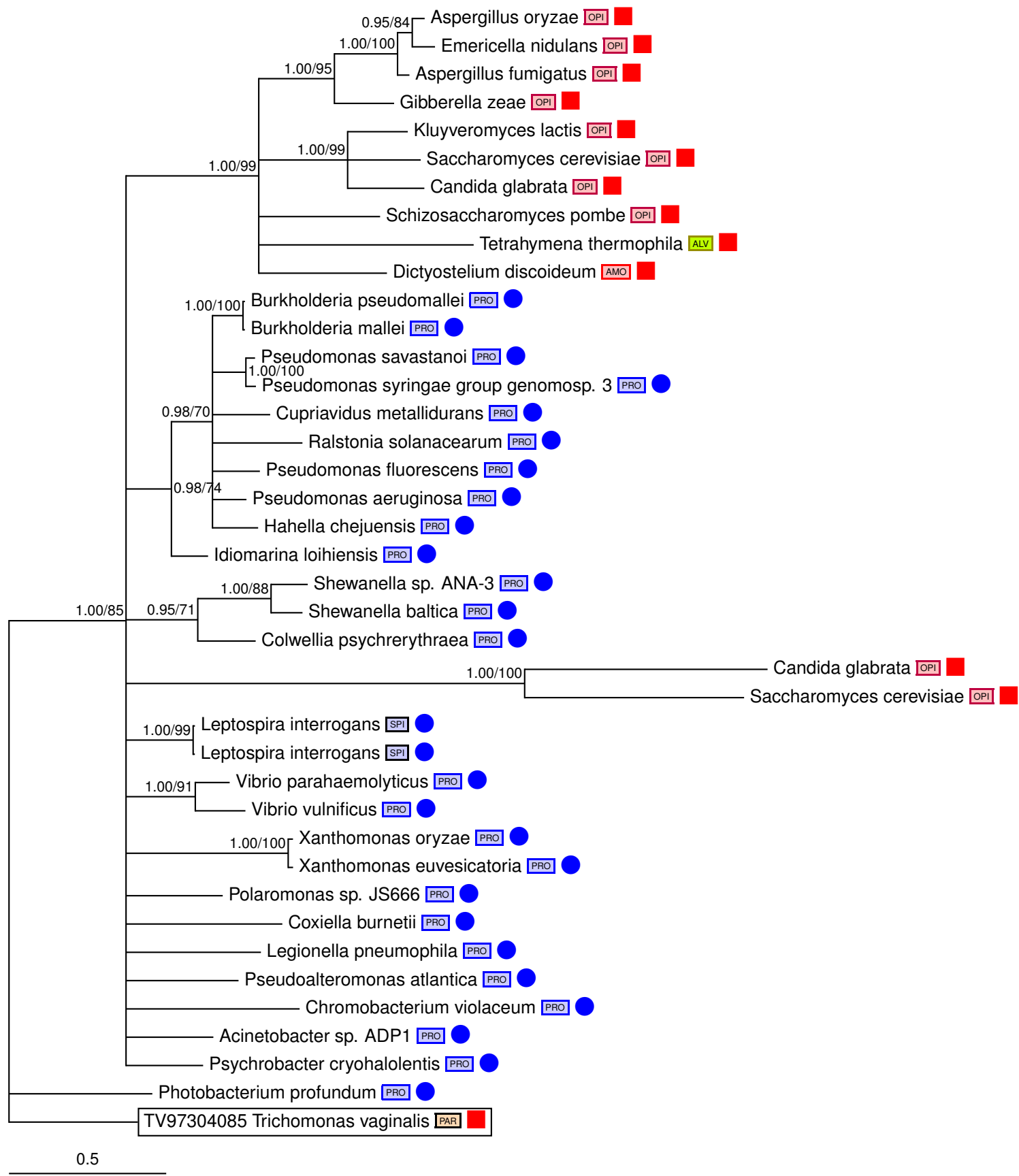
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EC annotation - (Blast/Profile): EC:3.2.1.25
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glycosyl hydrolase
Name of enzyme/protein: beta-mannosidase
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism
KEGG PATHWAY - level 2: Other glycan degradation



0.5

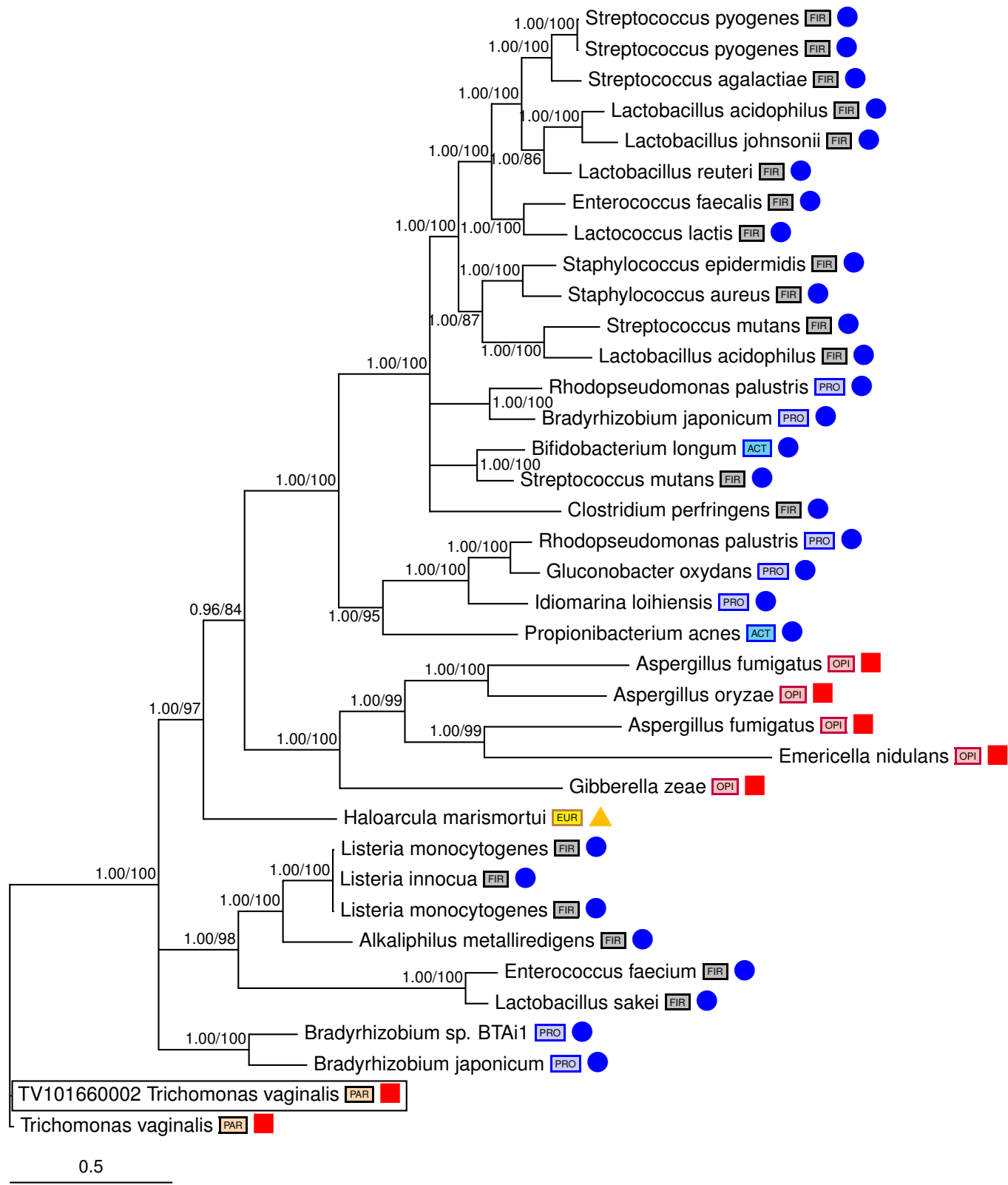
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Adjacent taxa in tree: Photobacterium
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 4
RefSeq annotation: PRS2 protein-related protein
Name of enzyme/protein: Protein containing DUF962
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



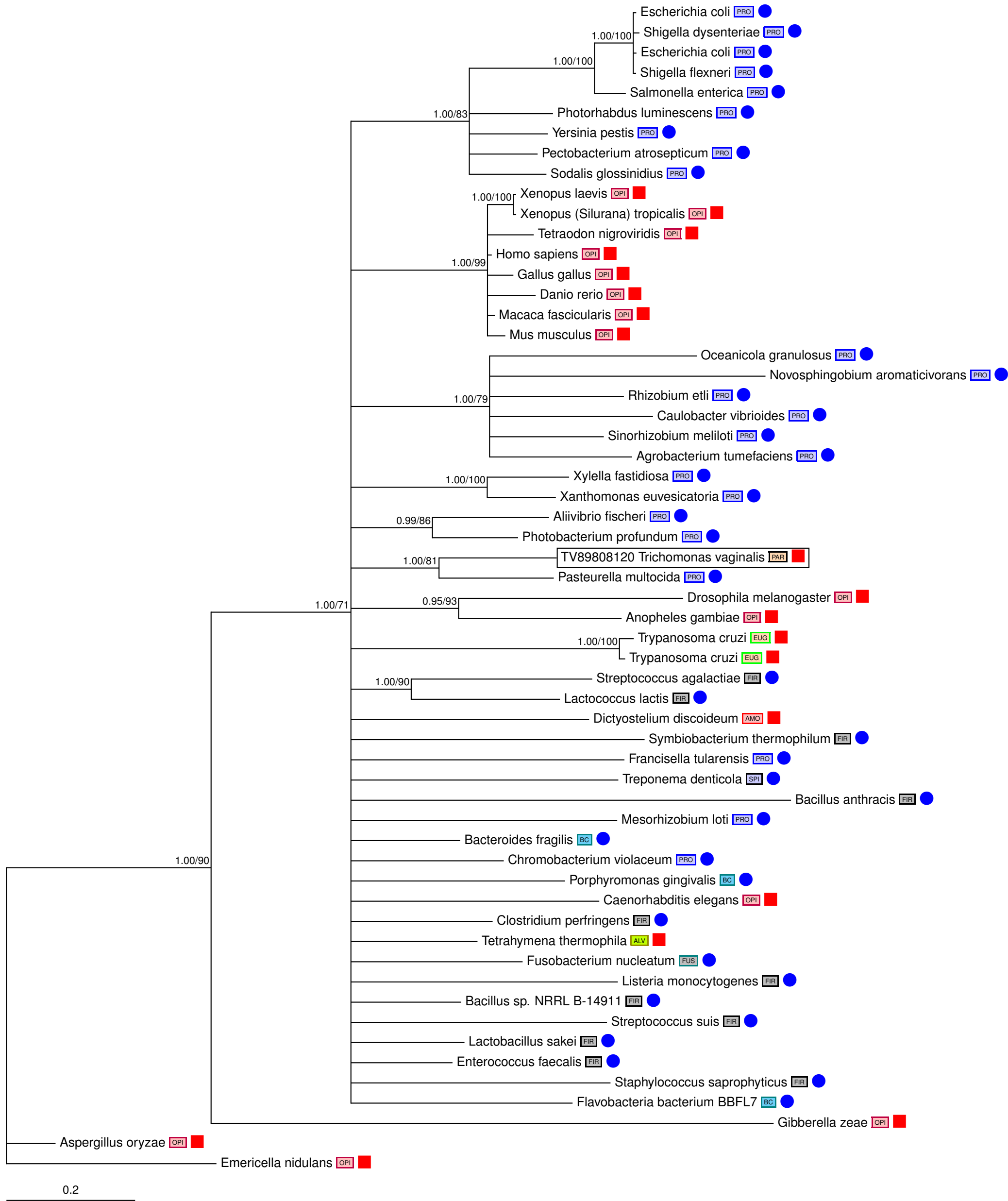
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Comments: LGT - TV ONE NODE
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 1
RefSeq annotation: antigen, 67 kD-related protein
Name of enzyme/protein: Predicted myosin-cross-reactive antigen
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KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

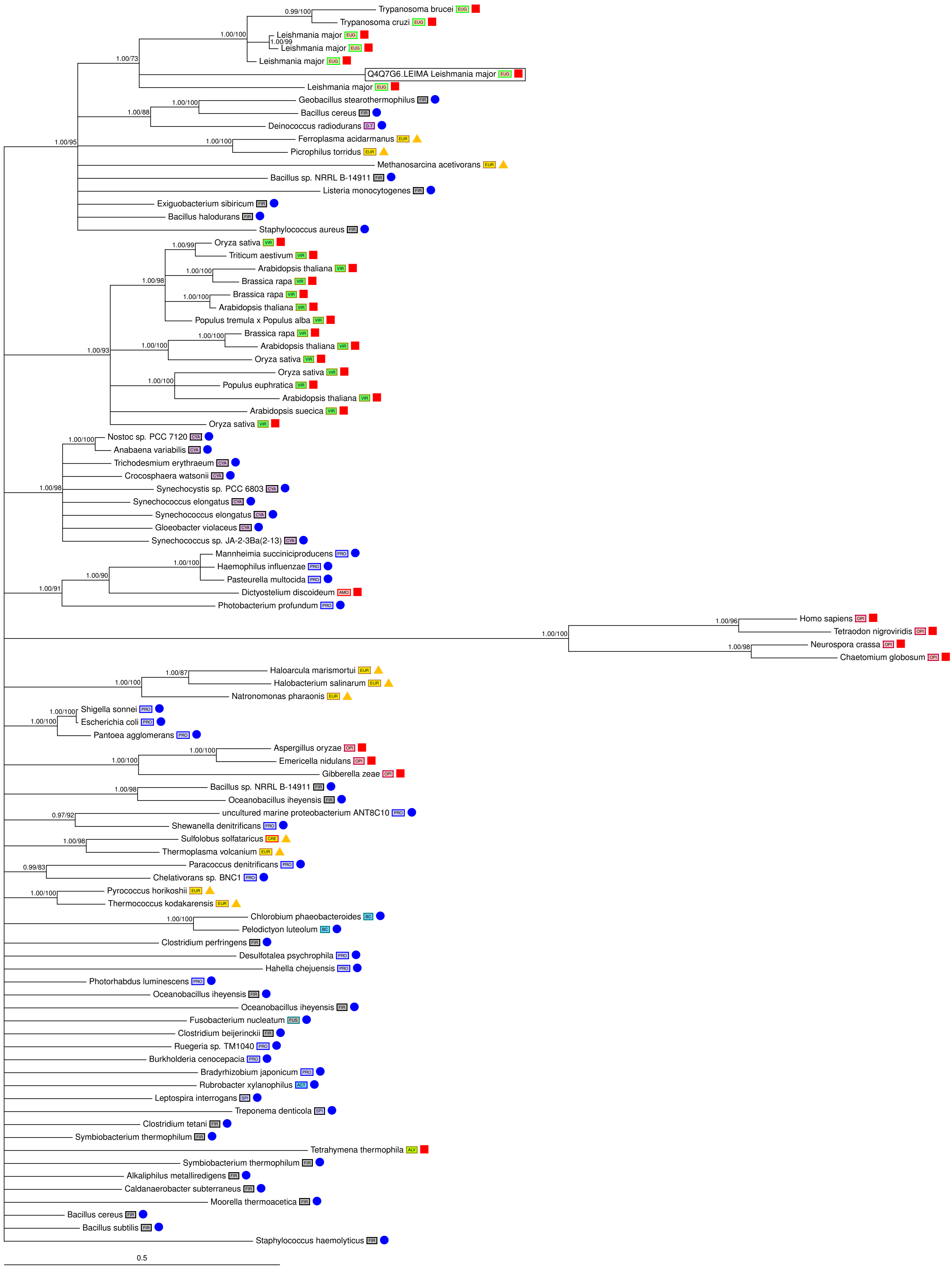


ON018

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Uniprot accession: A2F3H3_TR1VA
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Species affected: TV
Adjacent taxa in tree: Protobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: CutC family protein
Name of enzyme/protein: Predicted CutC Uncharacterized protein
involved in copper resistance
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

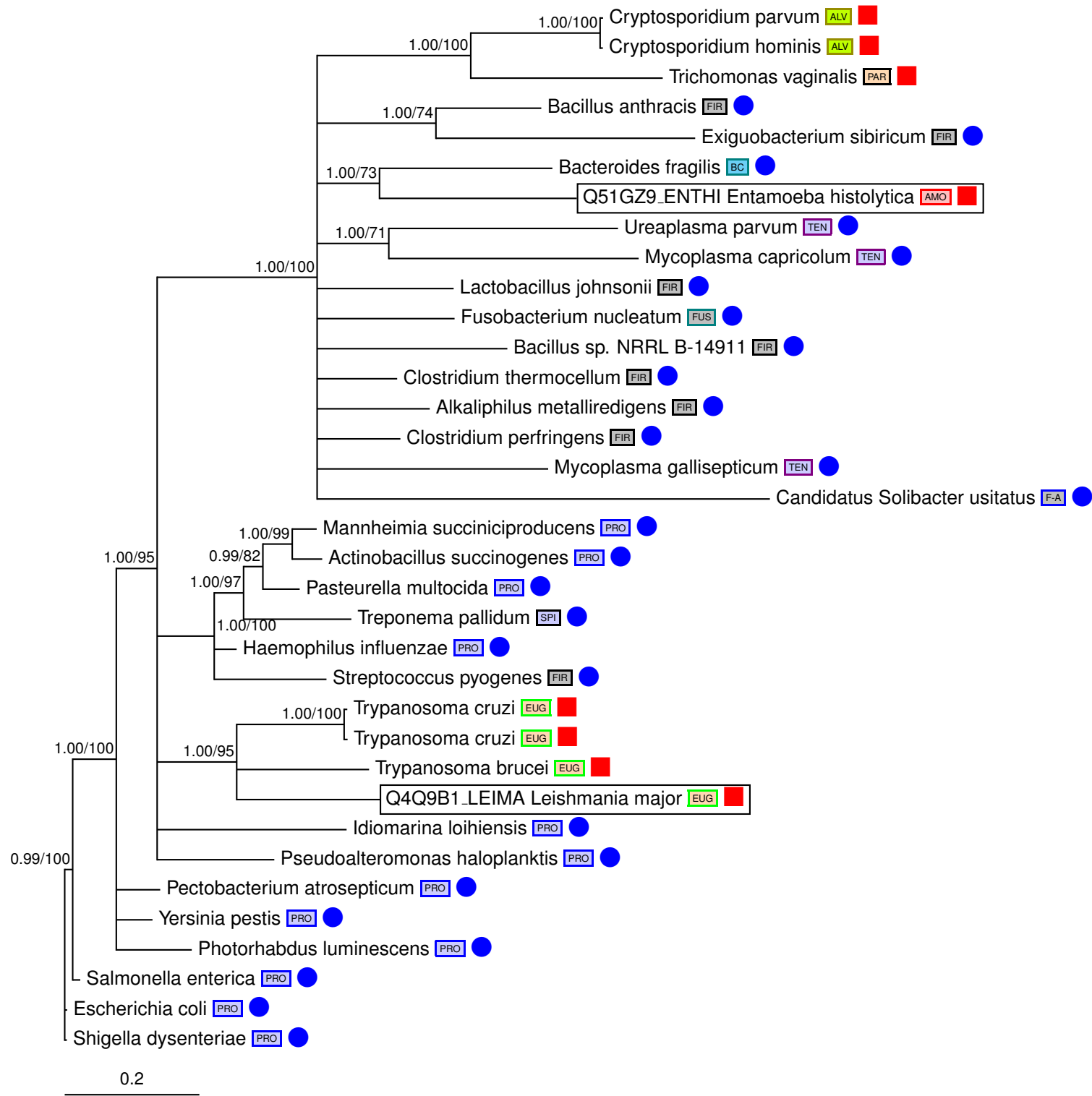


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DUPLICATIONS IN LM
Species affected: LM,TB,TC
Adjacent taxa in tree: Prokaryote
EC annotation - (Blast/Profile): EC:3.5.1.14
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: n-acyl-l-amino acid amidohydrolase
Name of enzyme/protein: aminocylase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism



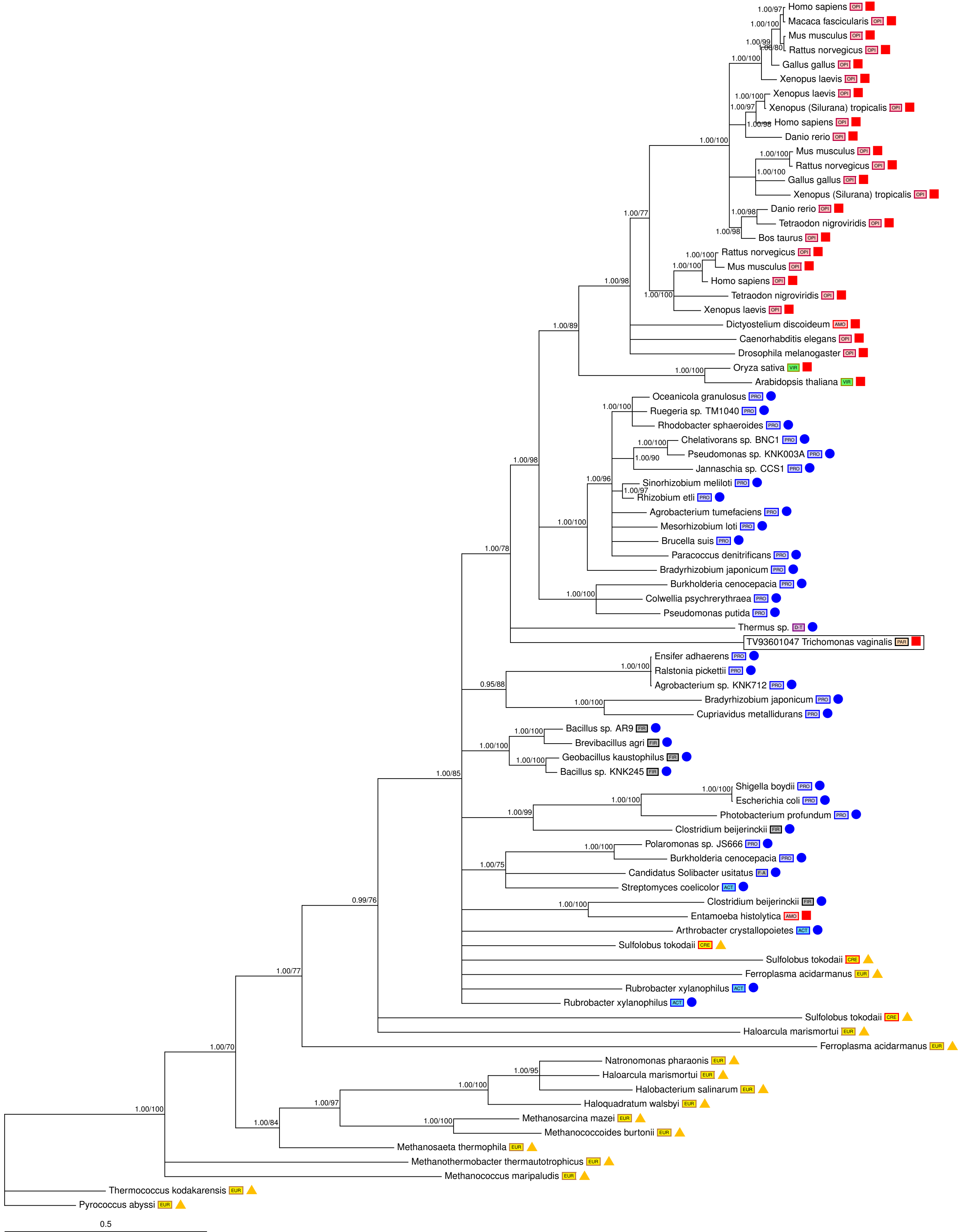
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Adjacent taxa in tree: Proteobacteria
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PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: asparagine synthetase a; aspartate--ammonia ligase
Name of enzyme/protein: aspartate-ammonia ligase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Metabolism of Other Amino Acids, Energy Metabolism
KEGG PATHWAY - level 2: Alanine, aspartate and glutamate metabolism, Cyanoamino acid metabolism, Nitrogen metabolism

Candy accession: Q51GZ9_ENTHI
RefSeq accession: XP_657492.1
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Species affected: EH
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:6.3.1.1
PHOBIUS SP: 0
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RefSeq annotation: aspartate--ammonia ligase
Name of enzyme/protein: aspartate-ammonia ligase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Metabolism of Other Amino Acids, Energy Metabolism
KEGG PATHWAY - level 2: Alanine, aspartate and glutamate metabolism, Cyanoamino acid metabolism, Nitrogen metabolism



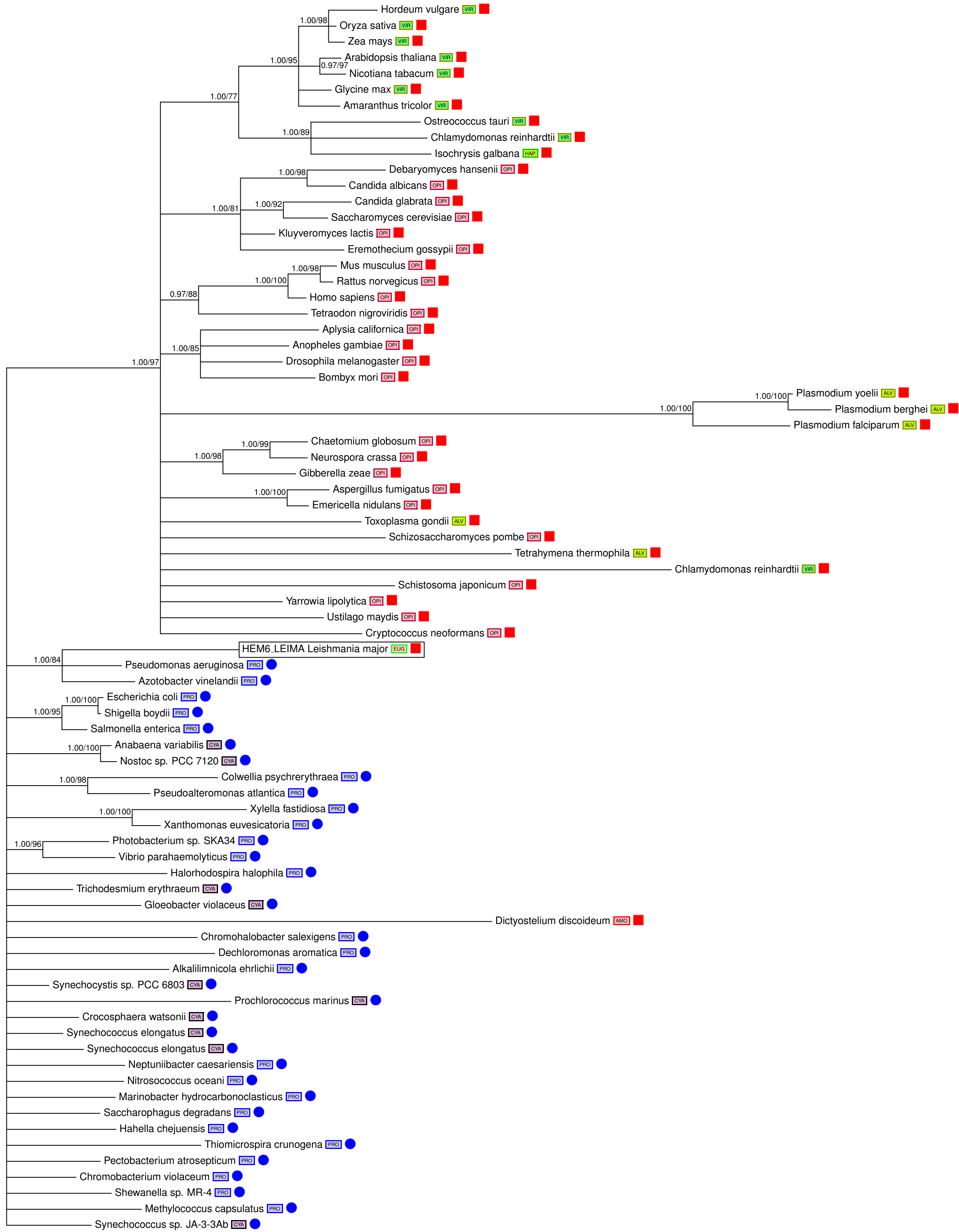
ON021

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Adjacent taxa in tree: Ambiguous
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PHOBIUS SP: 0
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RefSeq annotation: D-hydantoinase family protein
Name of enzyme/protein: dihydropyrimidinase
KEGG PATHWAY - level 1: Nucleotide Metabolism, Metabolism of Other Amino Acids, Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Pyrimidine metabolism, beta-Alanine metabolism, Pantothenate and CoA biosynthesis



ON022

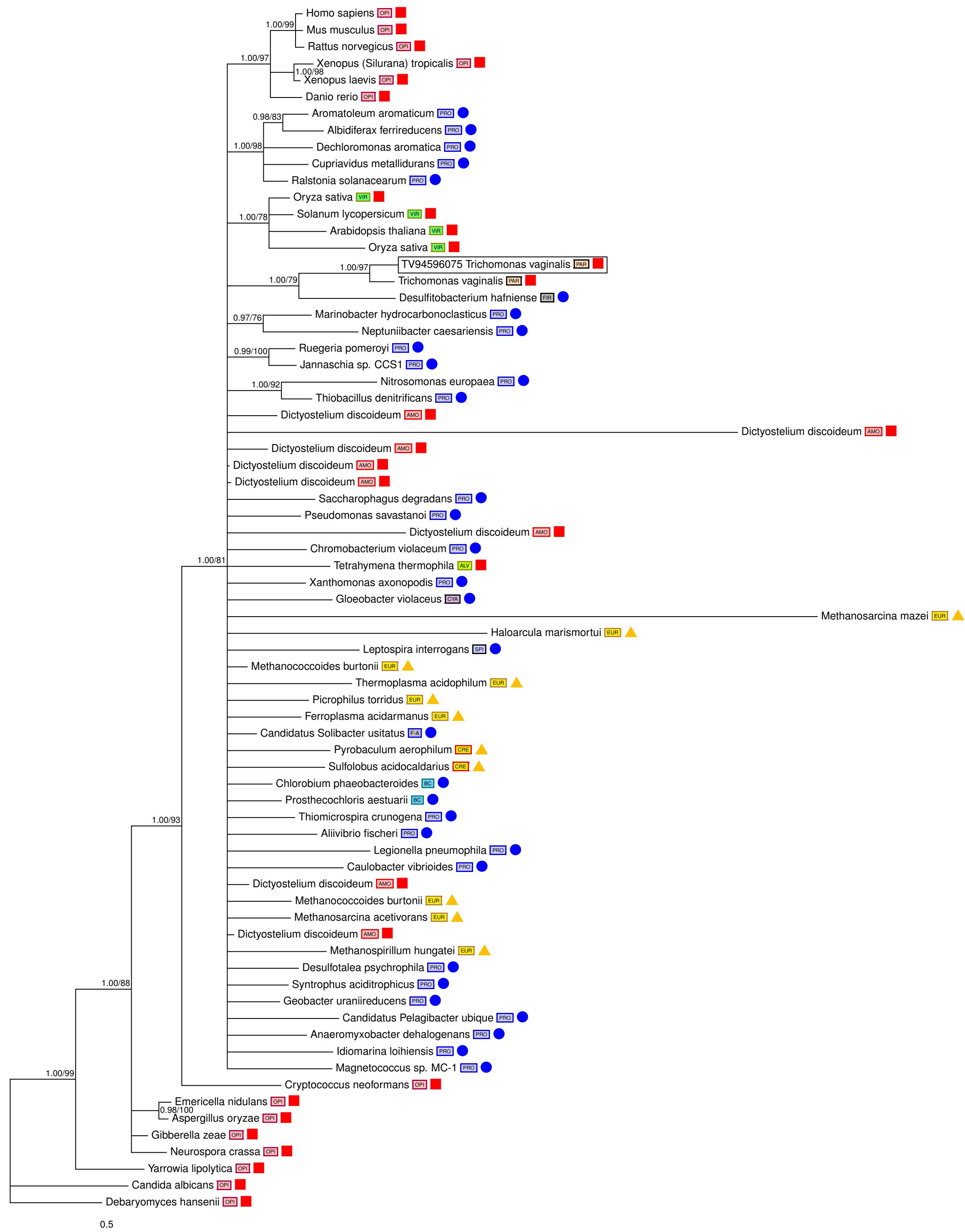
Candy accession: HEM6_LEIMA
RefSeq accession: XP_001680900.1
Uniprot accession: HEM6_LEIMA
Comments: LGT - ML ONE NODE
Species affected: DD
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:1.3.3.3
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: coproporphyrinogen iii oxidase
Name of enzyme/protein: coproporphyrinogen oxidase
KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Porphyrin and chlorophyll metabolism



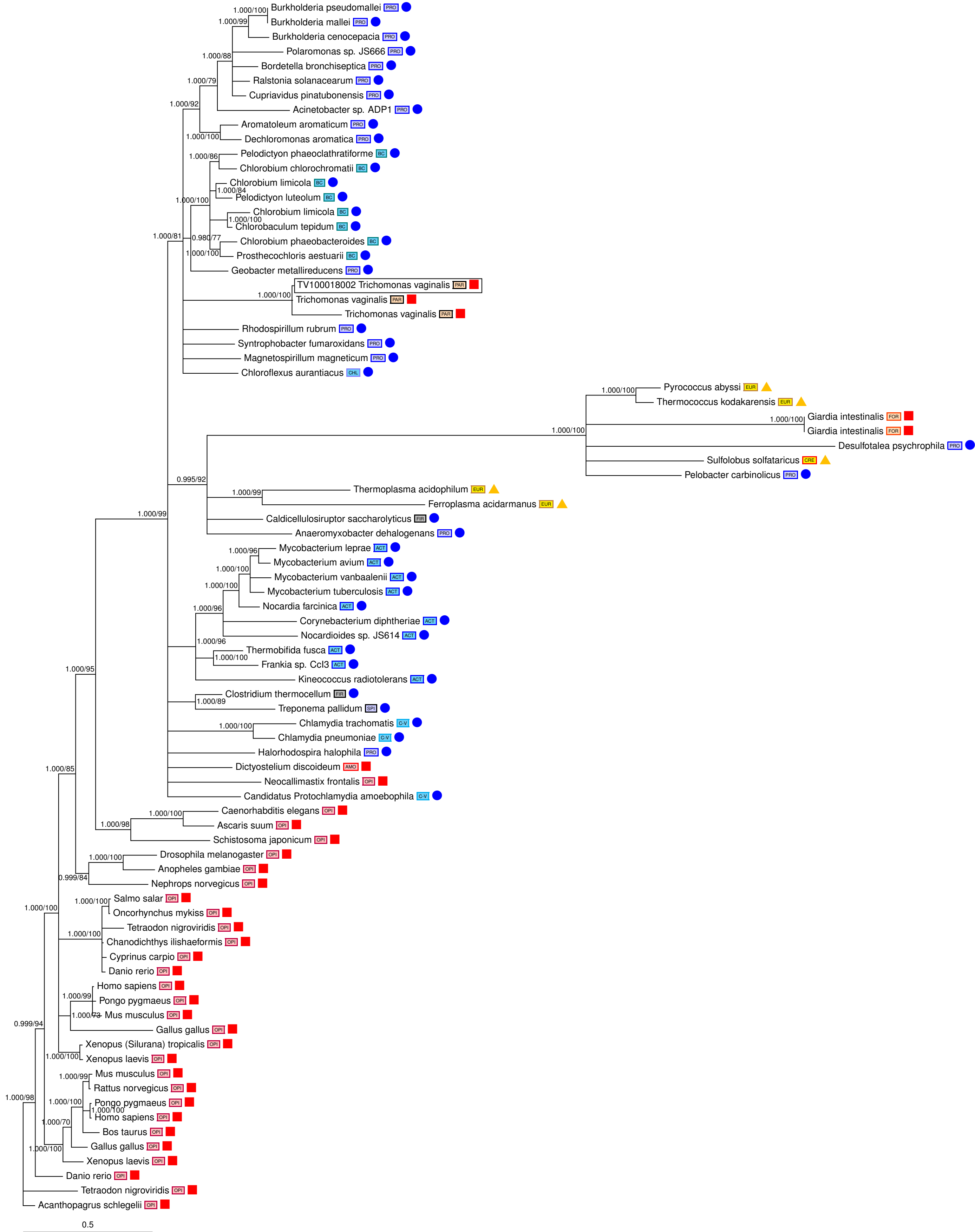
0.2

ON023

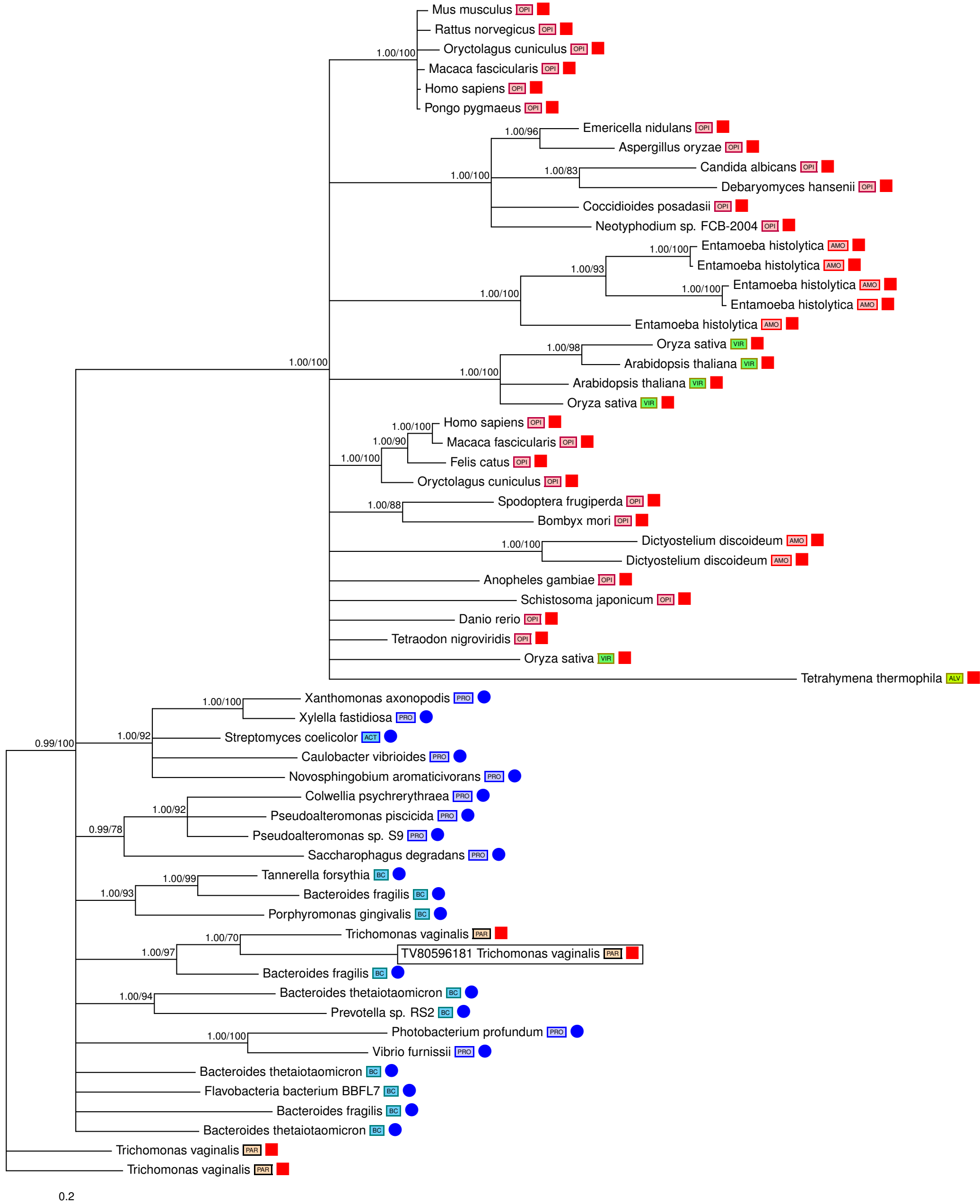
Candy accession: TV94596075
RefSeq accession: XP_001315334.1
Uniprot accession: A2EW75.TRIVA
Comments: LGT - ONE NODE 3 DOMAIN TREE
Species affected: TV
Adjacent taxa in tree: Firmicutes - Desulfitobacterium
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted pirin-like protein
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



Candy accession: TV100018002
RefSeq accession: XP_001307119.1
Uniprot accession: A2FLL6_TRIVA
Comments: LGT - TV ONE NODE
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:4.1.1.32
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: phosphoenol pyruvate carboxykinase
Name of enzyme/protein: phosphoenolpyruvate carboxykinase (GTP)
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Pyruvate metabolism

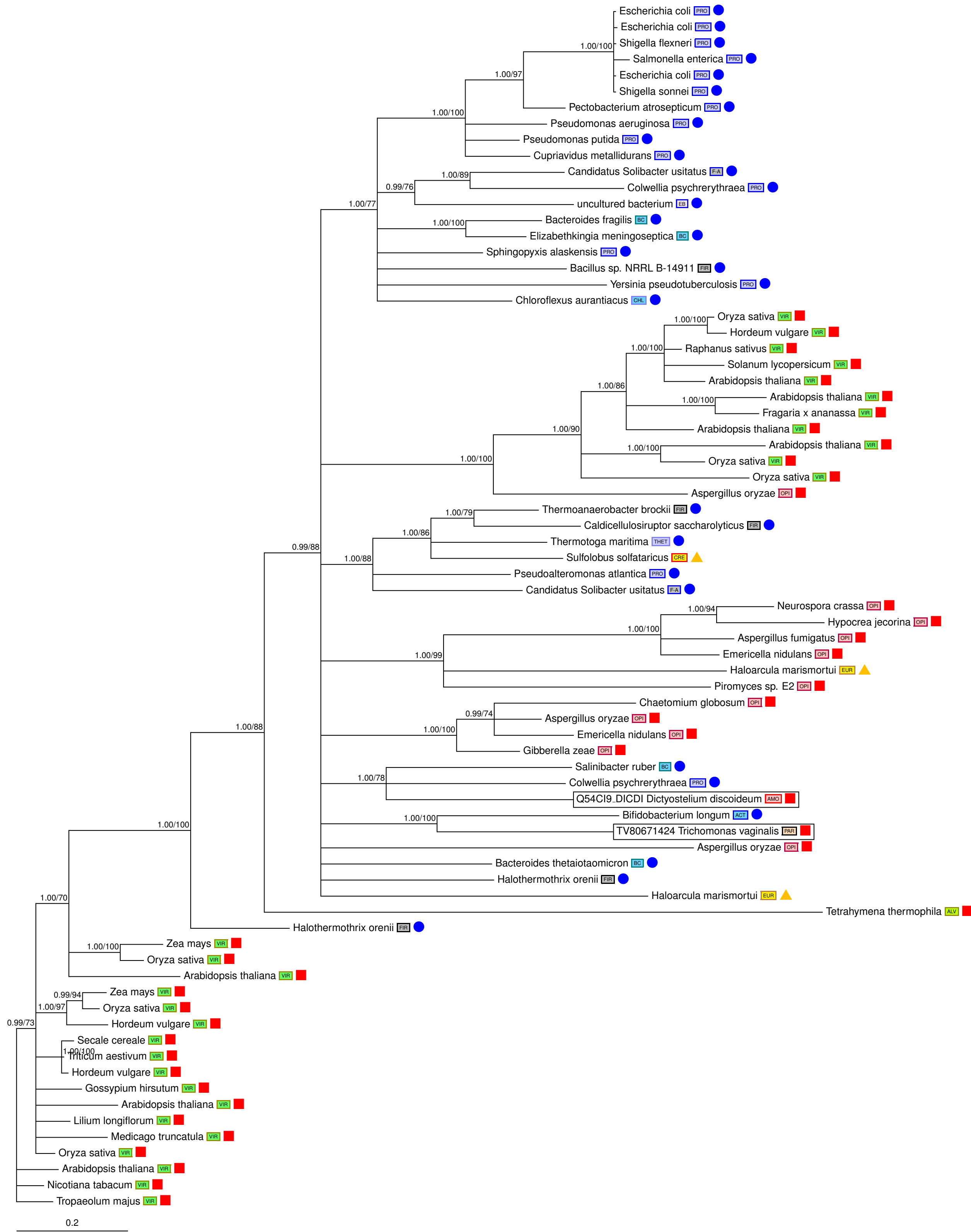


Candy accession: TV80596181
RefSeq accession: XP_001329989.1
Uniprot accession: A2DP05_TRIVA
Comments: LGT - TV ONE NODE WITH BACTEROIDES
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:3.2.1.52
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glycosyl hydrolase
Name of enzyme/protein: beta-N-acetylhexosaminidase
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism, Carbohydrate Metabolism
KEGG PATHWAY - level 2: Other glycan degradation, Various types of N-glycan biosynthesis, Amino sugar and nucleotide sugar metabolism



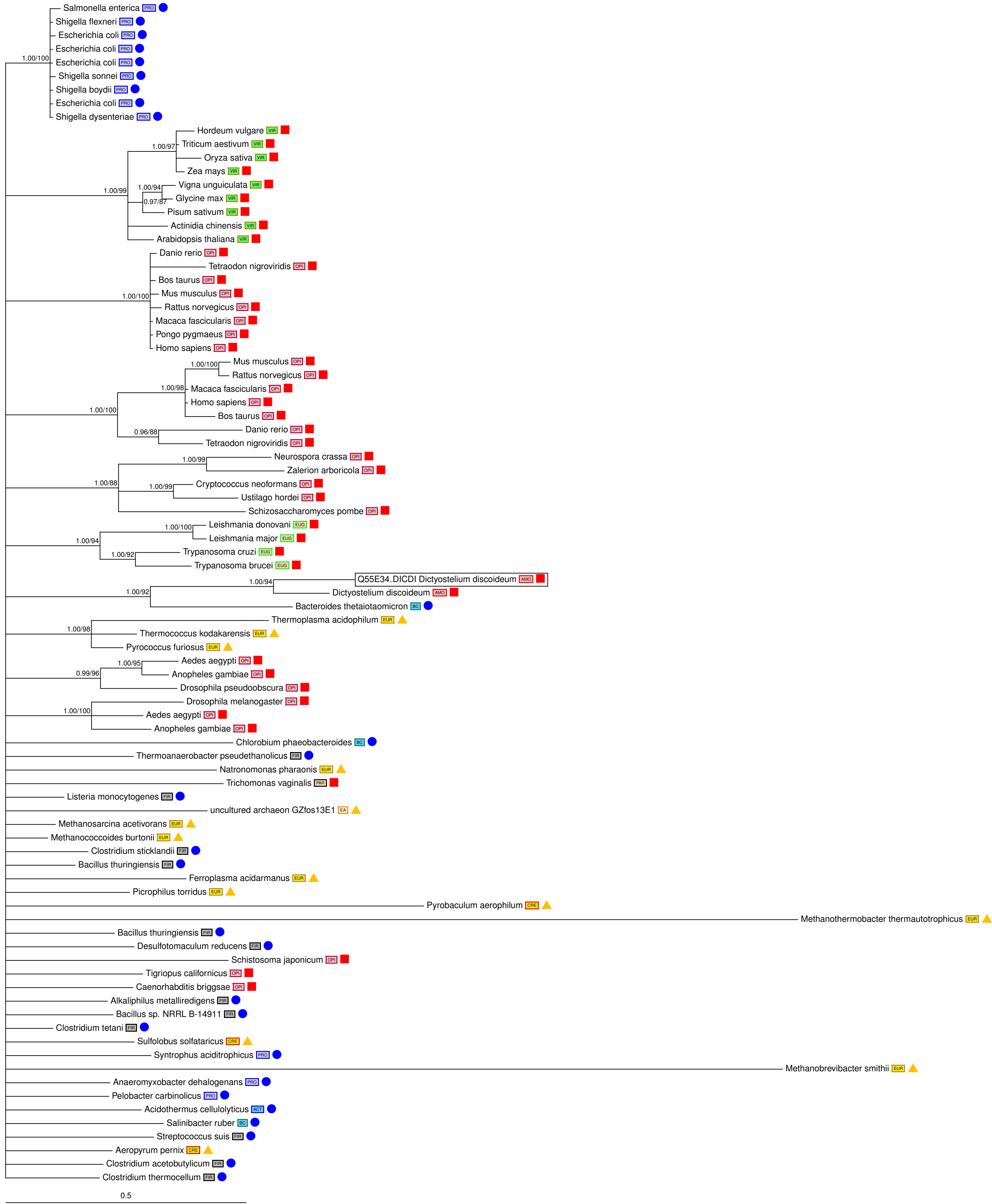
Candy accession: Q54CI9_DICDI
RefSeq accession: XP_629427.1
Uniprot accession: GLUA_DICDI
Comments: LGT - DD ONE NODE
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.2.1.21
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: beta glucosidase
Name of enzyme/protein: beta-glucosidase
KEGG PATHWAY - level 1: Metabolism of Other Amino Acids, Carbohydrate Metabolism, Biosynthesis of Other Secondary Metabolites
KEGG PATHWAY - level 2: Cyanoamino acid metabolism, Starch and sucrose metabolism, Phenylpropanoid biosynthesis

Candy accession: TV80671424
RefSeq accession: XP_001582566.1
Uniprot accession: A2DDA1_TRIVA
Comments: LGT - TV ONE NODE
Species affected: TV
Adjacent taxa in tree: Actinobacteria - Bifidobacterium
EC annotation - (Blast/Profile): EC:3.2.1.21
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glycosyl hydrolase
Name of enzyme/protein: beta-glucosidase
KEGG PATHWAY - level 1: Metabolism of Other Amino Acids, Carbohydrate Metabolism, Biosynthesis of Other Secondary Metabolites
KEGG PATHWAY - level 2: Cyanoamino acid metabolism, Starch and sucrose metabolism, Phenylpropanoid biosynthesis

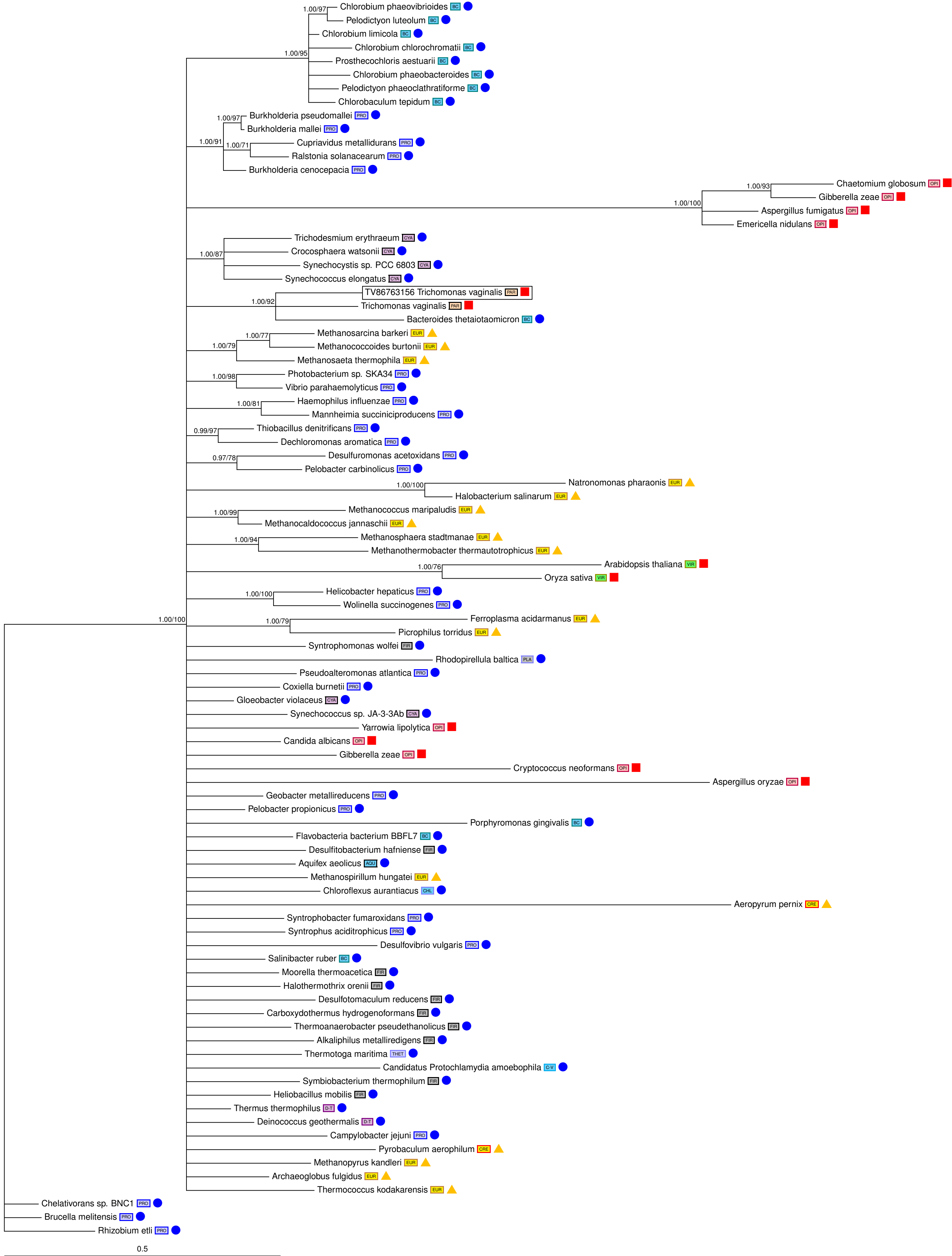


ON027

Candy accession: Q55E34_DICDI
RefSeq accession: XP_645947.1
Uniprot accession: P5CR2_DICDI
Comments: LGT - DD ONE NODE
Species affected: DD
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:1.5.1.2
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: pyrroline-5-carboxylate reductase
Name of enzyme/protein: pyrroline-5-carboxylate reductase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism,

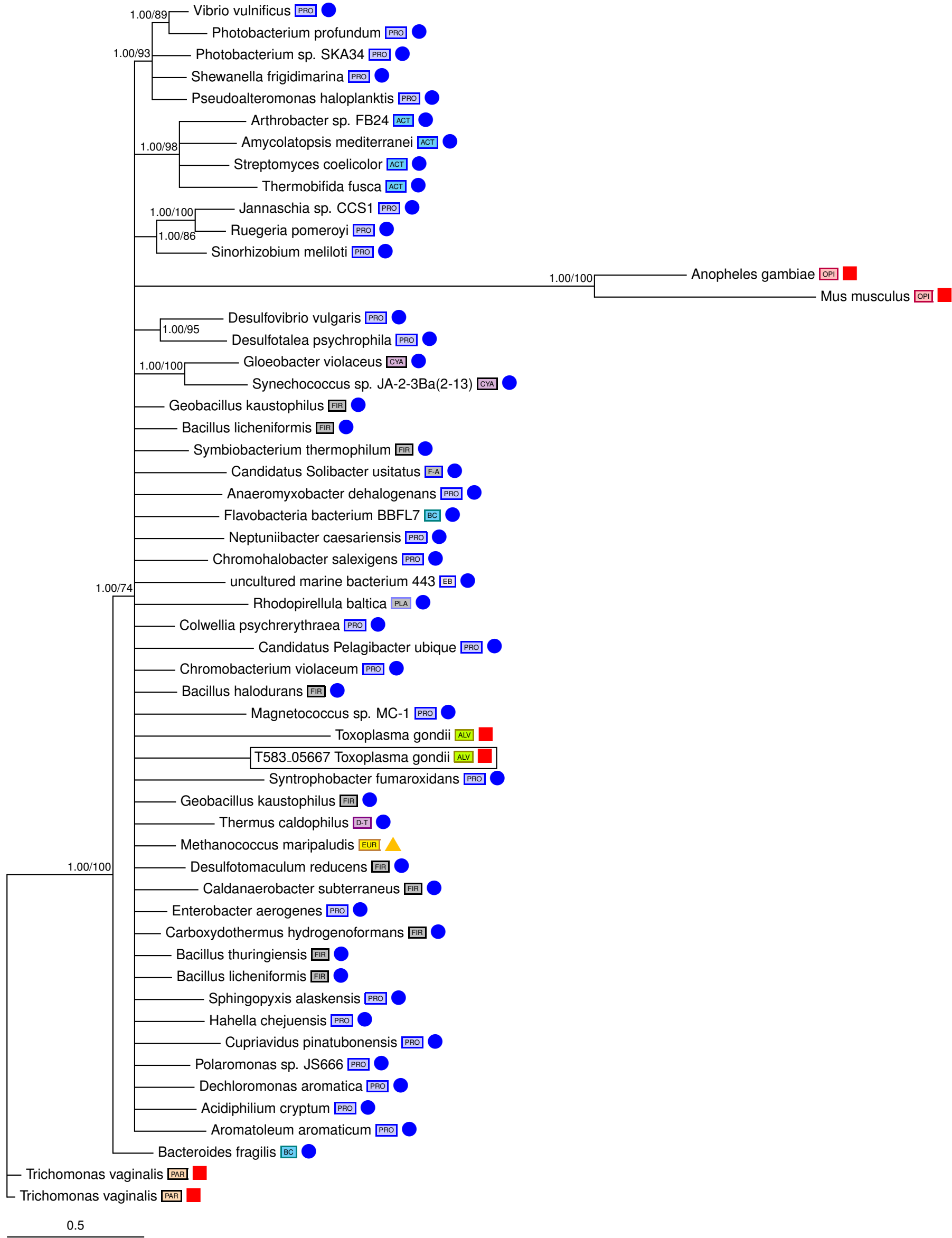


Candy accession: TV86763156
RefSeq accession: XP_001316223.1
Uniprot accession: A2ETN2_TRIVA
Comments: LGT - TV ONE NODE WITH BACTEROIDES
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:3.1.3.5
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Acid phosphatase surE
Name of enzyme/protein: 5'-nucleotidase
KEGG PATHWAY - level 1: Nucleotide Metabolism, Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Purine metabolism, Pyrimidine metabolism, Nicotinate and nicotinamide metabolism



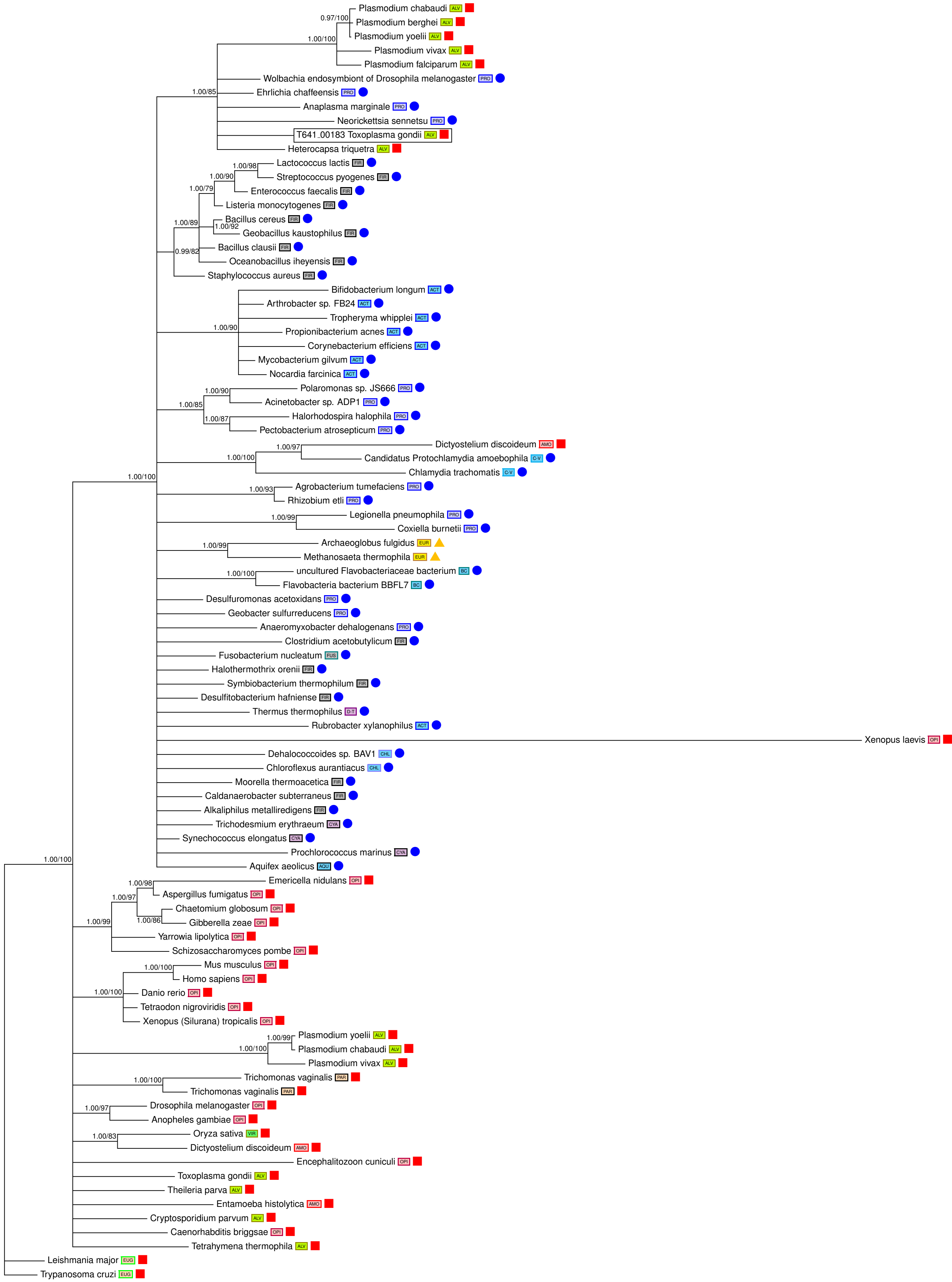
ON029

Candy accession: T583_05667
RefSeq accession: XP_002364705.1
Uniprot accession: B6K9I1_TOXGO
Comments: LGT - TV ONE NODE WITH BACTEROIDES
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:1.4.1.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: alanine dehydrogenase, putative
Name of enzyme/protein: alanine dehydrogenase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Metabolism of Other Amino Acids
KEGG PATHWAY - level 2: Alanine, aspartate and glutamate metabolism, Taurine and hypotaaurine metabolism



ON030

Candy accession: T641_00183
RefSeq accession: XP_002369919.1
Uniprot accession: B6KPP7_TOXGO
Comments: LGT - APICOMPLEXA + HETEROCAPSA ONE NODE
Species affected: PF,PV,PY,PC,TG,HT
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:2.4.2.29
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: queuine tRNA-ribosyltransferase,
putative
Name of enzyme/protein: tRNA-guanine transglycosylase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



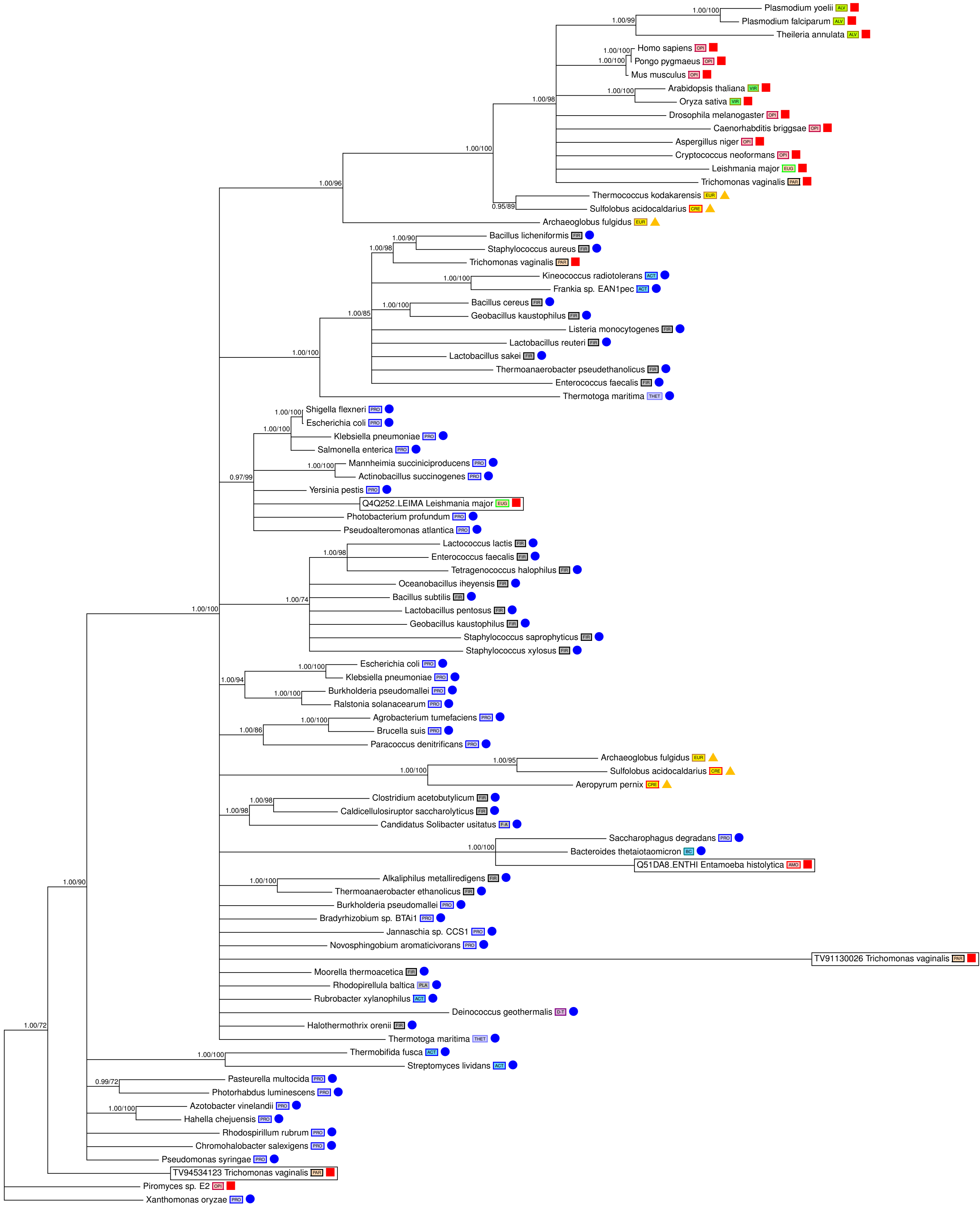
ON031

Candy accession: TV94534123
RefSeq accession: XP_001321965.1
Uniprot accession: A2EC65_TRIVA
Comments: LGT - TV ONE NODE - WITH ANAEROBIC FUNGI
- 3 DOMAIN ToL
Species affected: TV,FUNGI
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.7.1.17
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: xylulokinase family protein
Name of enzyme/protein: Xylulokinase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pentose and glucuronate interconversions

Candy accession: TV91130026
RefSeq accession: XP_001302338.1
Uniprot accession: A2G0B1_TRIVA
Comments: LGT - TV ONE NODE - 3 DOMAIN ToL
Species affected: TV
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): EC:2.7.1.17
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: FGGY family of carbohydrate kinases, N-terminal domain containing protein
Name of enzyme/protein: Xylulokinase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pentose and glucuronate interconversions

Candy accession: Q4Q252_LEIMA
RefSeq accession: XP_001686596.1
Uniprot accession: Q4Q252_LEIMA
Comments: LGT - LM ONE NODE -3 DOMAIN ToL
Species affected: LM
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:2.7.1.17
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: xylulokinase
Name of enzyme/protein: Xylulokinase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pentose and glucuronate interconversions

Candy accession: C4LTL6_ENTHI
RefSeq accession: XP_656185.1
Uniprot accession: C4LTL6_ENTHI
Comments: LGT - EH ONE NODE - 3 DOMAIN ToL
Species affected: EH
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.7.1.17
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: xylulose kinase
Name of enzyme/protein: Xylulokinase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pentose and glucuronate interconversions

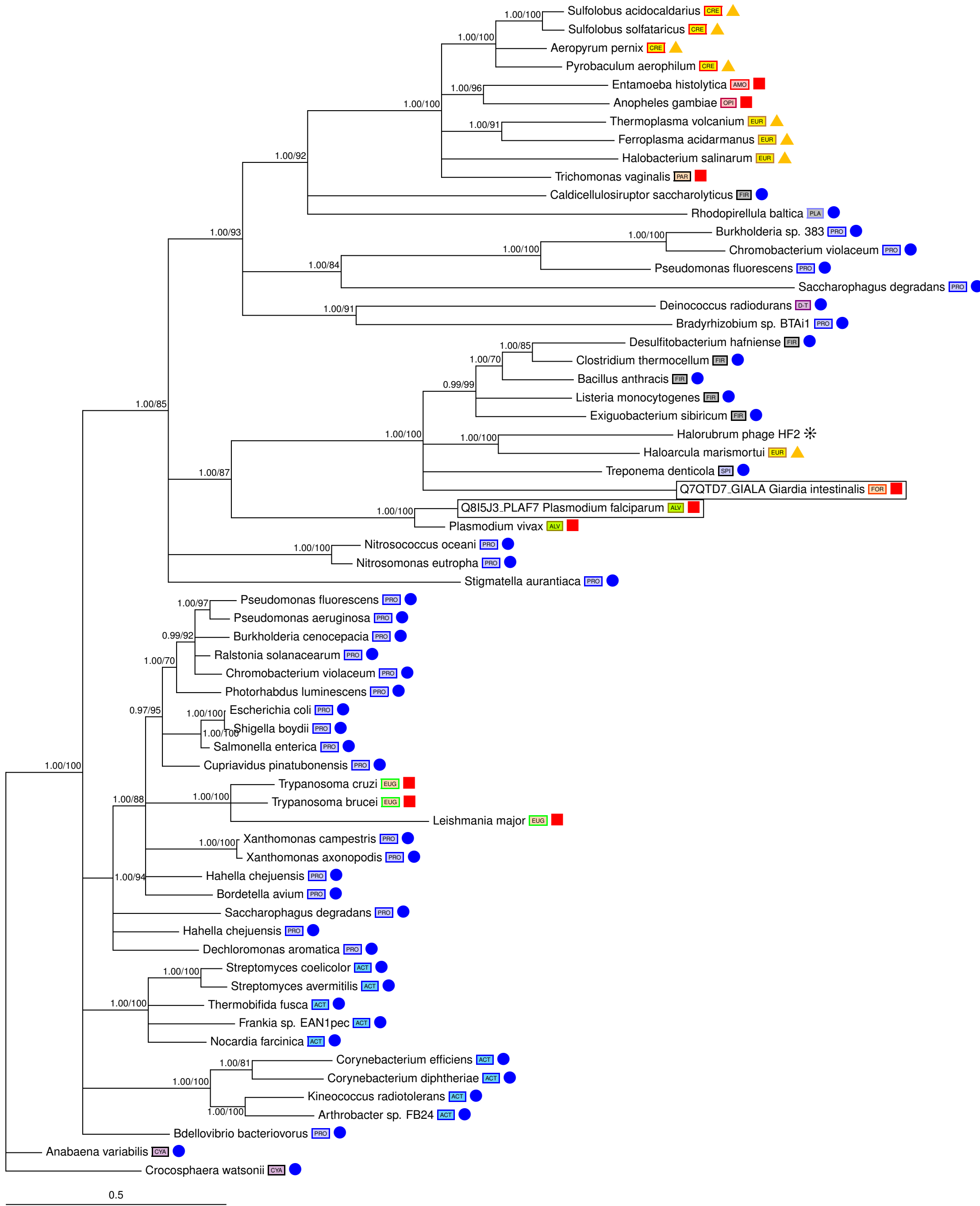


0.5

ON032

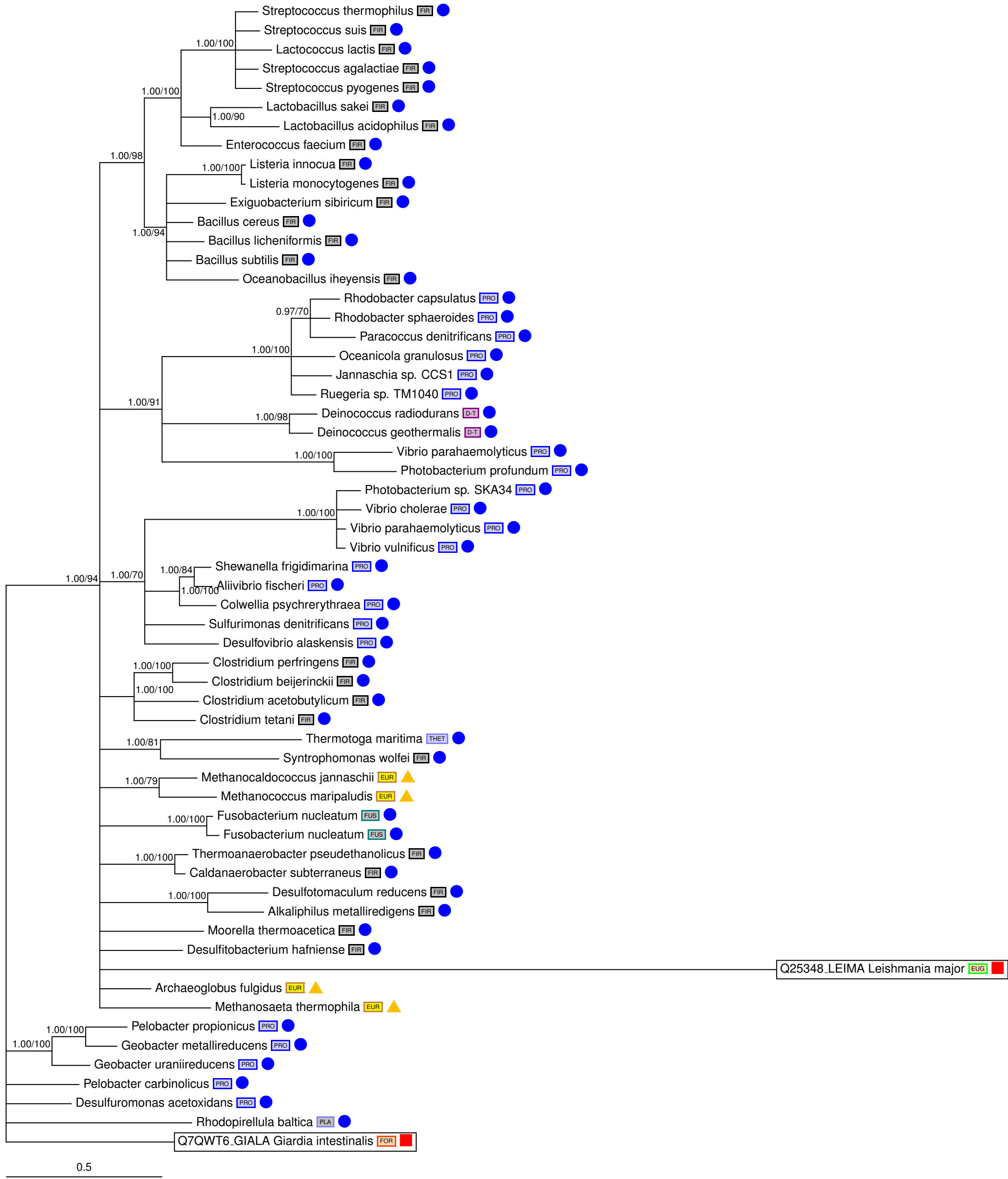
Candy accession: Q8I5J3_PLAF7
RefSeq accession: XP_001350618.1
Uniprot accession: Q8I5J3_PLAF7
Comments: LGT - PF, PV ONE NODE - 3 DOMAIN ToL
Species affected: PF,PV
Adjacent taxa in tree: Ambiguous
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: conserved protein
Name of enzyme/protein: Uncharacterised conserved protein family
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na

Candy accession: Q7QTD7_GIALA
RefSeq accession: XP_001709735.1
Uniprot accession: A8B4Z5_GIALA
Comments: LGT - GI ONE NODE - ODD TAXONOMIC SAMPLE
Species affected: GI
Adjacent taxa in tree: Prokaryote/Phage
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: RTCB PROTEIN
Name of enzyme/protein: Uncharacterised conserved protein family
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



Candy accession: Q25348_LEIMA
RefSeq accession: XP_001687423.1
Uniprot accession: E9AC20_LEIMA
Comments: LGT - LM ONE NODE
Species affected: LM
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:3.6.1.11
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: acidocalcisomal exopolyphosphatase
Name of enzyme/protein: exopolyphosphatase
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Purine metabolism

Candy accession: Q7QWT6_GIALA
RefSeq accession: XP_001709297.1
Uniprot accession: A8B5T0_GIALA
Comments: LGT - GI ONE NODE
Species affected: GI
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.6.1.11
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Manganese-dependent inorganic pyrophosphatase, putative
Name of enzyme/protein: exopolyphosphatase
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Purine metabolism

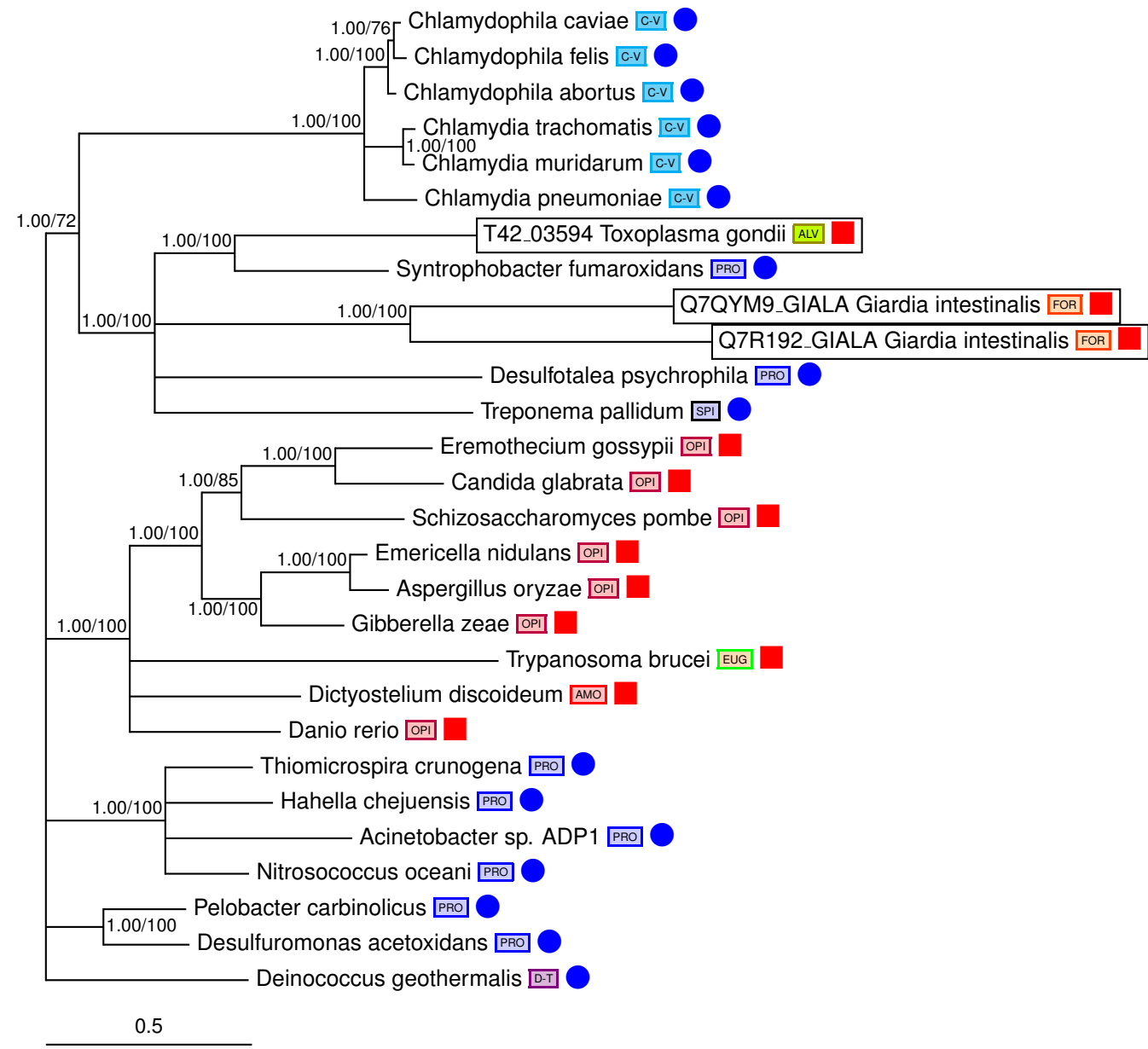


ON034

Candy accession: Q7R192_GIALA
RefSeq accession: XP_001704875.1
Uniprot accession: A8BTG2_GIALA
Comments: LGT - GI ONE NODE
Species affected: GI,TG
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Metalloprotease, insulinase family
Name of enzyme/protein: Predicted Zn-dependent peptidases, insulinase-like
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

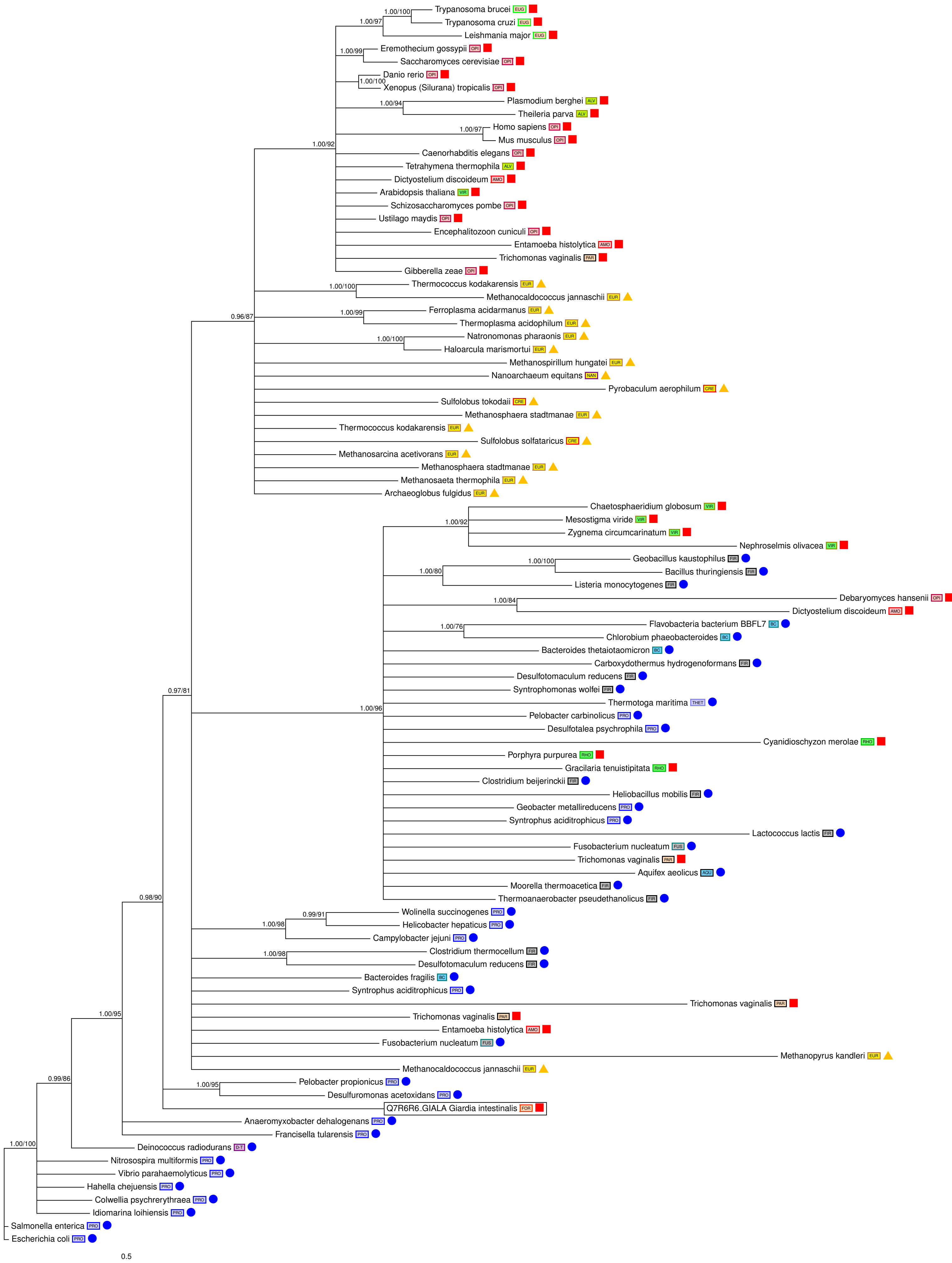
Candy accession: Q7QYM9_GIALA
RefSeq accession: XP_001705918.1
Uniprot accession: A8BN11_GIALA
Comments: LGT - GI ONE NODE
Species affected: GI,TG
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Metalloprotease, insulinase family
Name of enzyme/protein: Predicted Zn-dependent peptidases, insulinase-like
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

Candy accession: T42_03594
RefSeq accession: XP_002366418.1
Uniprot accession: B6KEZ5_TOXGO
Comments: LGT - TG ONE NODE
Species affected: TG
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: zinc metalloprotease 2, putative
Name of enzyme/protein: Predicted Zn-dependent peptidases, insulinase-like
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



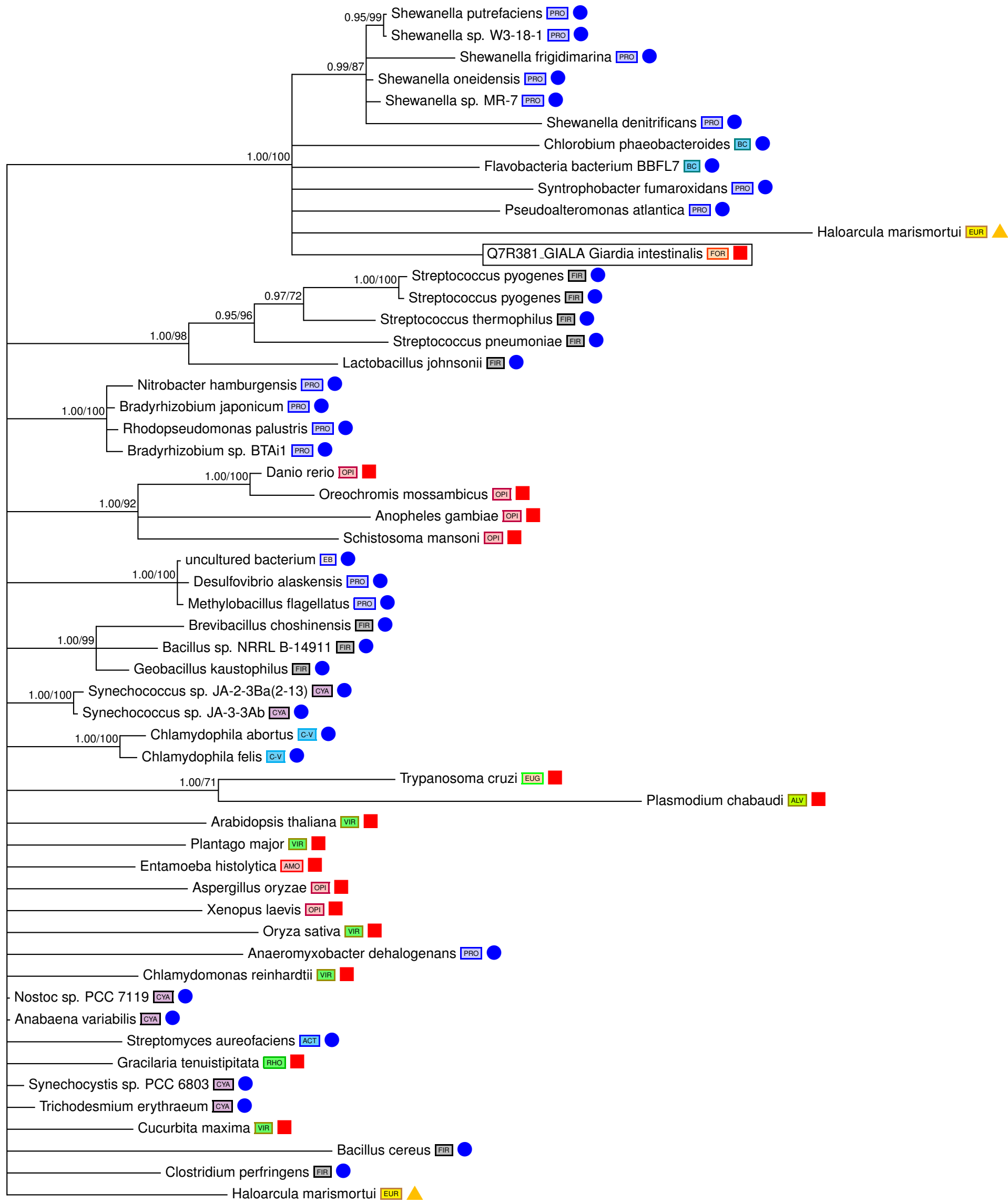
ON035

Candy accession: Q7R6R6_GIALA
RefSeq accession: XP_001707847.1
Uniprot accession: A8BC83_GIAIC
Comments: LGT - GI ONE NODE
Species affected: GI
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: ATPases of the PP-loop superfamily
Name of enzyme/protein: Predicted Adenine nucleotide alpha
hydrolase/ATPases of the PP-loop
superfamily
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



ON036

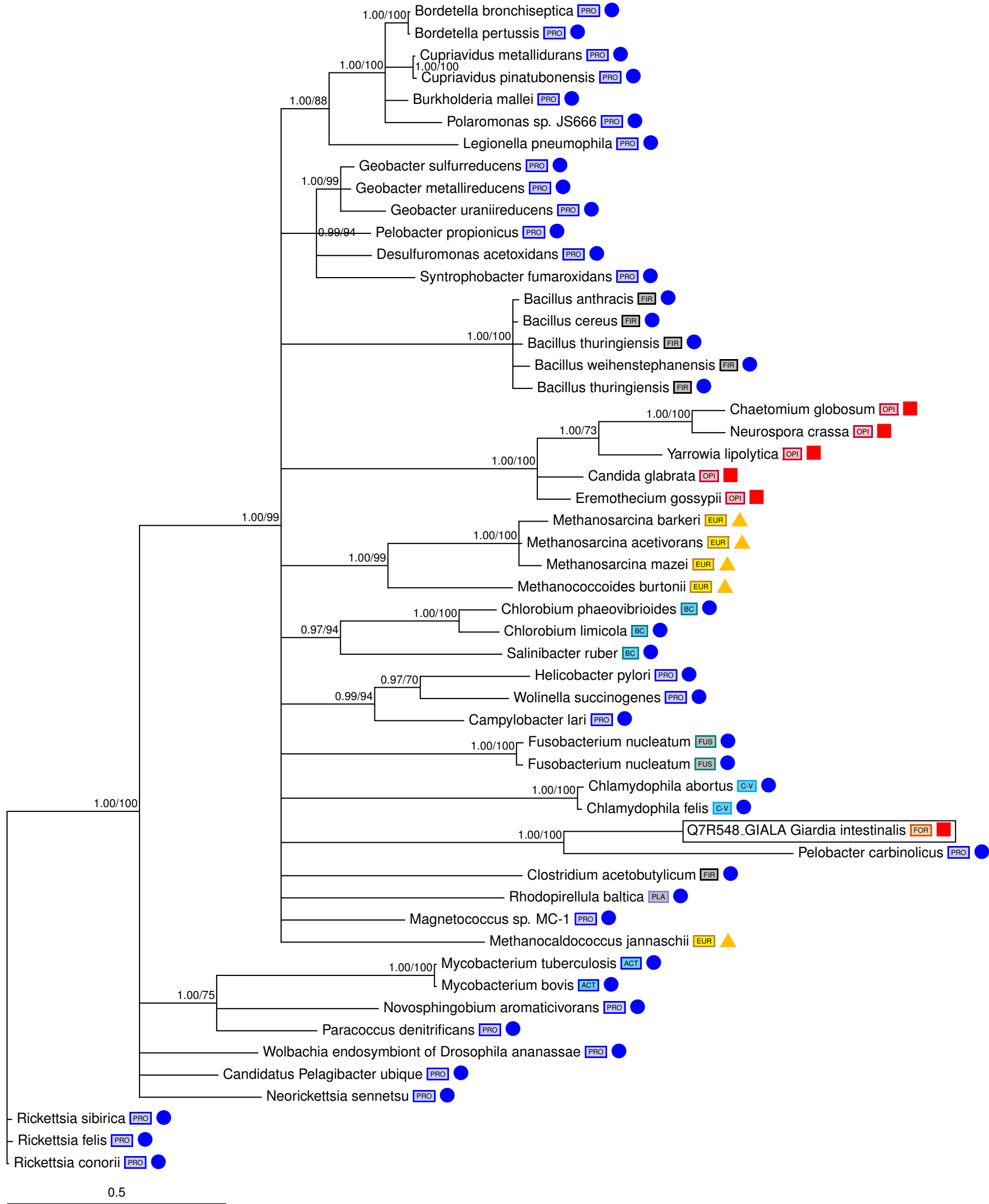
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RefSeq accession: XP_001709207.1
Uniprot accession: A8B5E9_GIAIC
Comments: LGT - GI ONE NODE
Species affected: GI
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: Hypothetical protein GL50803_3910
Name of enzyme/protein: Protein containing thioredoxin domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



0.2

ON037

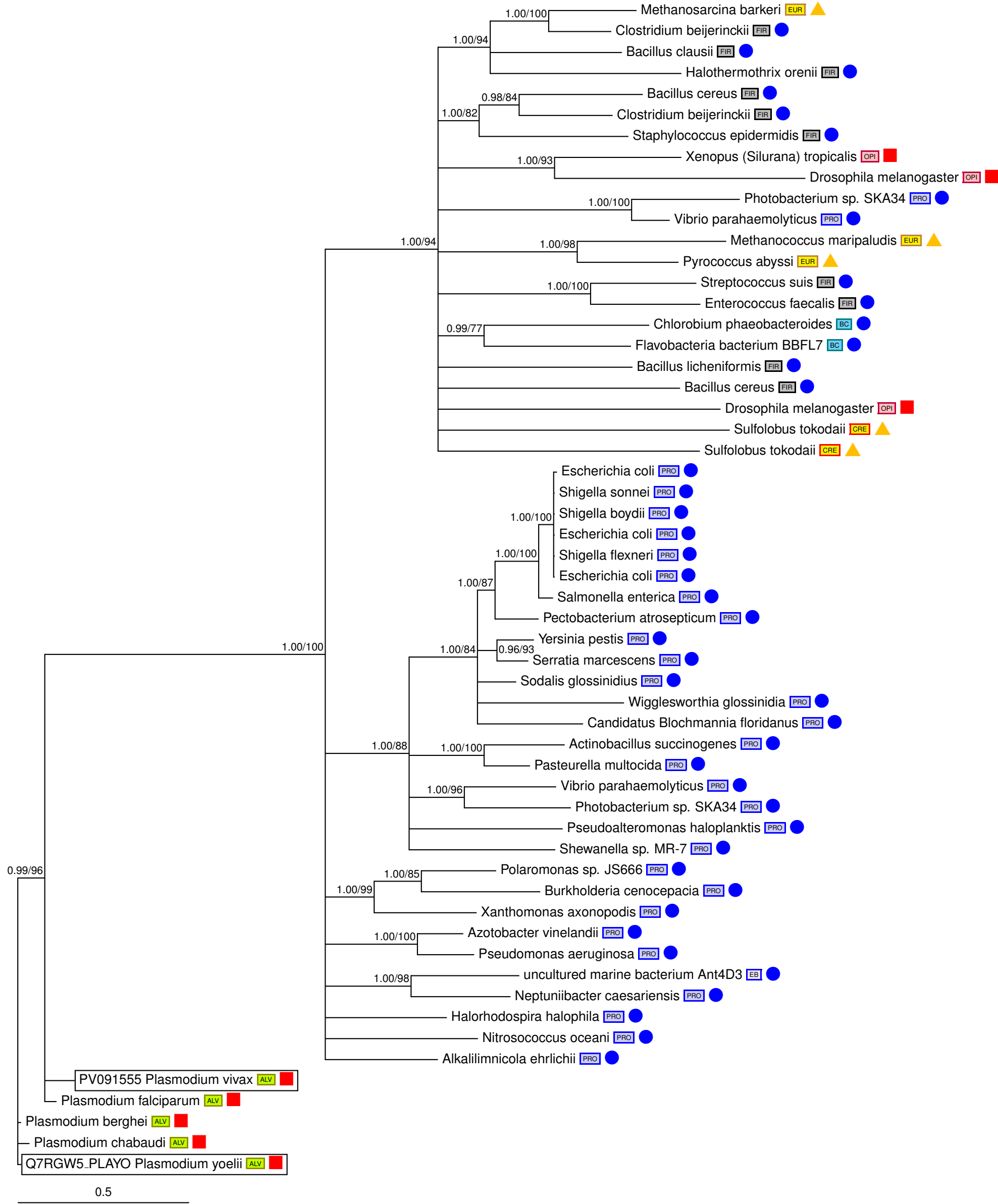
Candy accession: Q7R548_GIALA
RefSeq accession: XP_001707737.1
Uniprot accession: A8BD82_GIALA
Comments: LGT - GI ONE NODE
Species affected: GI
Adjacent taxa in tree: Pelobacter
EC annotation - (Blast/Profile): EC:2.7.8.8
PHOBIUS SP: 0
PHOBIUS TMD: 15
RefSeq annotation: Hypothetical protein GL50803_17427
Name of enzyme/protein: CDP-diacylglycerol-serine
O-phosphatidyltransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Lipid Metabolism
KEGG PATHWAY - level 2: Glycine, serine and threonine
metabolism, Glycerophospholipid
metabolism



ON038

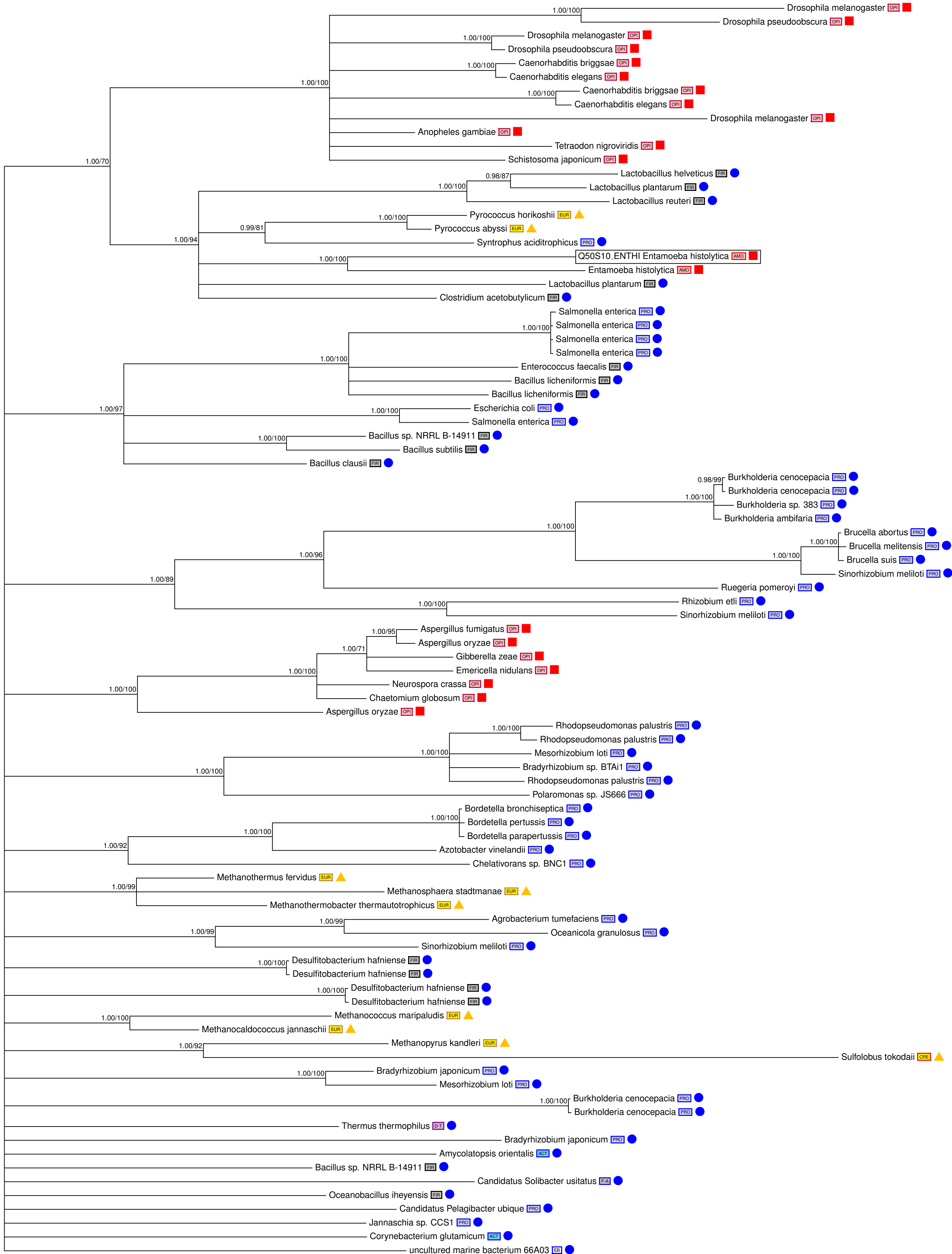
Candy accession: Q7RGW5_PLAYO
RefSeq accession: XP_724496.1
Uniprot accession: Q7RGW5_PLAYO
Comments: LGT - APICOMPLEXA ONE NODE
Species affected: PF,PV,PY
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted flavin mononucleotide
phosphatase, haloacid dehalogenase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

Candy accession: PV091555
RefSeq accession: XP_001615302.1
Uniprot accession: A5K4J7_PLAVS
Comments: LGT - APICOMPLEXA ONE NODE
Species affected: PF,PV,PY
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.8.1.2
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: haloacid dehalogenase-like hydrolase
Name of enzyme/protein: (S)-2-haloacid dehalogenase
KEGG PATHWAY - level 1: Xenobiotics Biodegradation and
Metabolism
KEGG PATHWAY - level 2: Chlorocyclohexane and chlorobenzene
degradation, Chloroalkane and
chloroalkene degradation



ON039

Candy accession: Q50S10_ENTHI
RefSeq accession: XP_649756.2
Uniprot accession: C4M213_ENTHI
Comments: LGT - EH ONE NODE
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:1.1.1.37
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: malate dehydrogenase
Name of enzyme/protein: Malate dehydrogenase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Citrate cycle (TCA cycle), Pyruvate metabolism, Glyoxylate and dicarboxylate metabolism

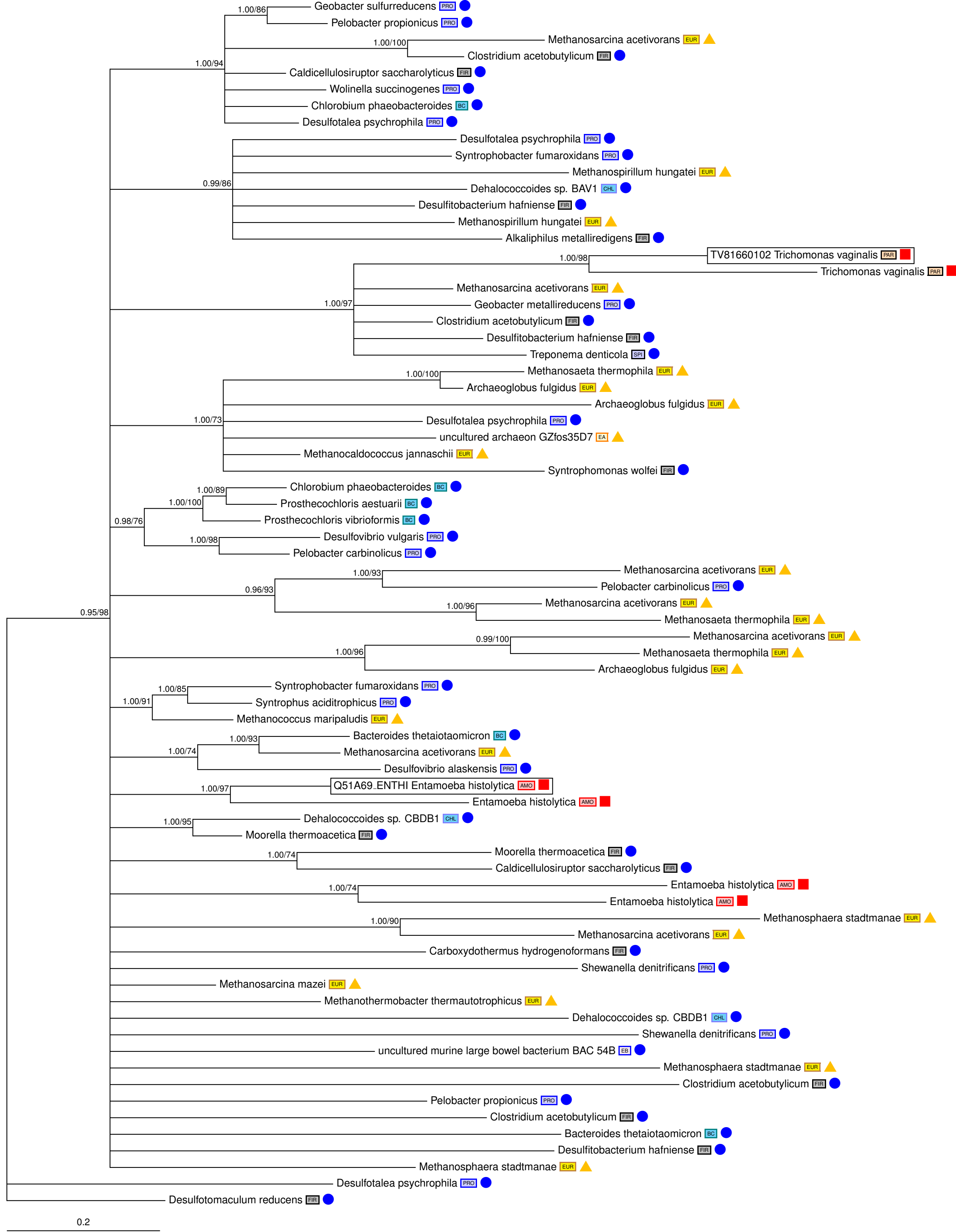


0.2

ON040

Candy accession: TV81660102
RefSeq accession: XP_001317174.1
Uniprot accession: A2EQX7_TRIVA
Comments: LGT - TV ONE NODE
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted multimeric flavodoxin WrbA,
NADPH-dependent FMN reductase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

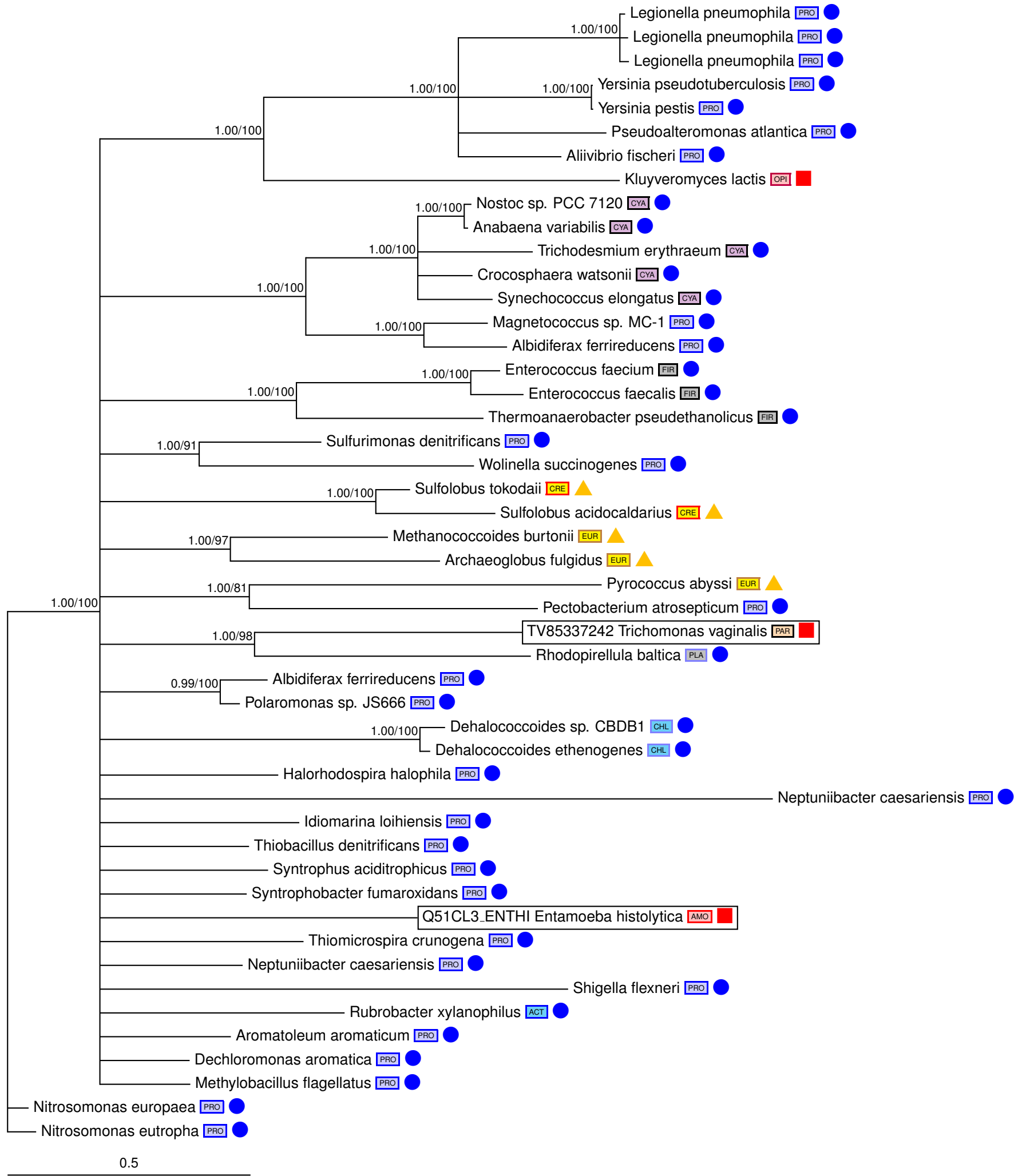
Candy accession: Q51A69_ENTHI
RefSeq accession: XP_655130.1
Uniprot accession: C4M3J0_ENTHI
Comments: LGT - EH ONE NODE
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: iron-sulfur flavoprotein
Name of enzyme/protein: Predicted multimeric flavodoxin WrbA,
NADPH-dependent FMN reductase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



ON041

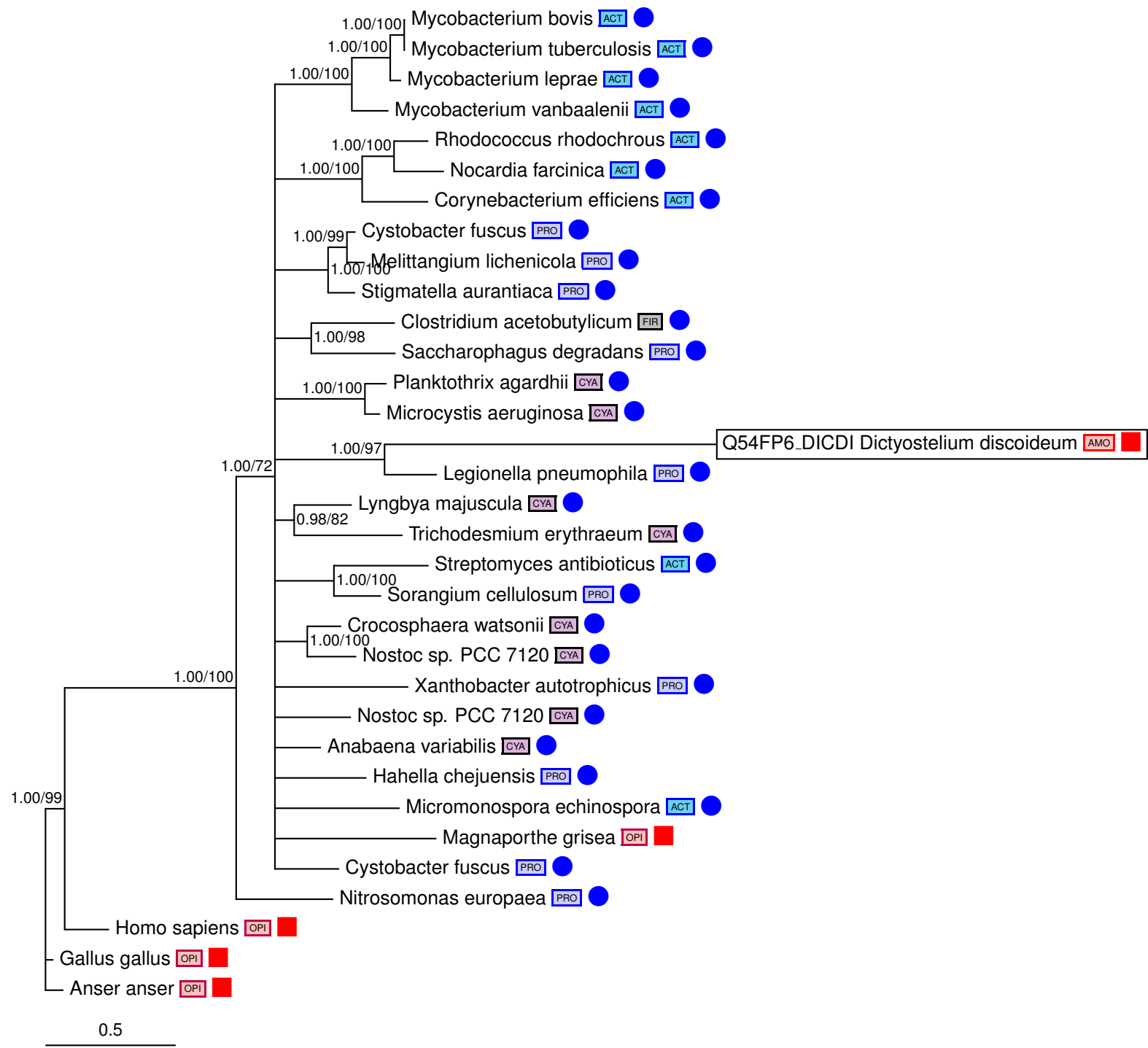
Candy accession: TV85337242
RefSeq accession: XP_001329114.1
Uniprot accession: A2DRU4_TRIVA
Comments: LGT - TV ONE NODE + FUNGI ONE NODE
Species affected: TV
Adjacent taxa in tree: Planctomycetes - Rhodopirellula
EC annotation - (Blast/Profile): EC:3.1.-.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Sulphohydrolase/Glycosulfatase, Zn-dependent hydrolase
Name of enzyme/protein: Protein containing beta-lactamase superfamily domain
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction

Candy accession: Q51CL3_ENTHI
RefSeq accession: XP_656005.1
Uniprot accession: C4M1A9_ENTHI
Comments: LGT - EH ONE NODE + FUNGI ONE NODE
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:3.1.-.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: metallo-beta-lactamase family protein
Name of enzyme/protein: Protein containing beta-lactamase superfamily domain
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



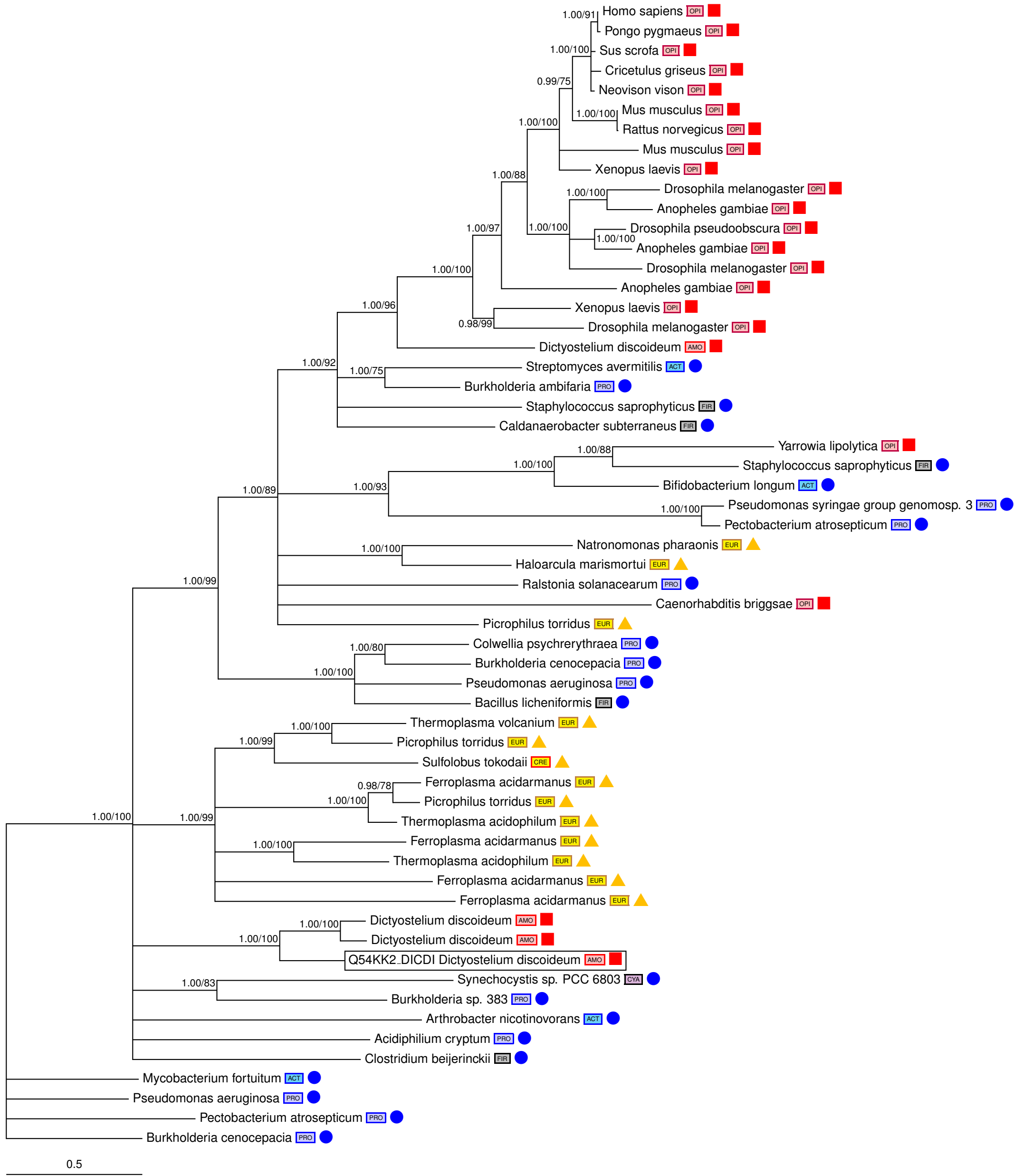
ON042

Candy accession: Q54FP6_DICDI
RefSeq accession: XP_635590.1
Uniprot accession: PKS31_DICDI
Comments: LGT - DD ONE NODE
Species affected: DD
Adjacent taxa in tree: Proteobacteria - Legionella
EC annotation - (Blast/Profile): EC:2.3.1.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0290703
Name of enzyme/protein: Transferases
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



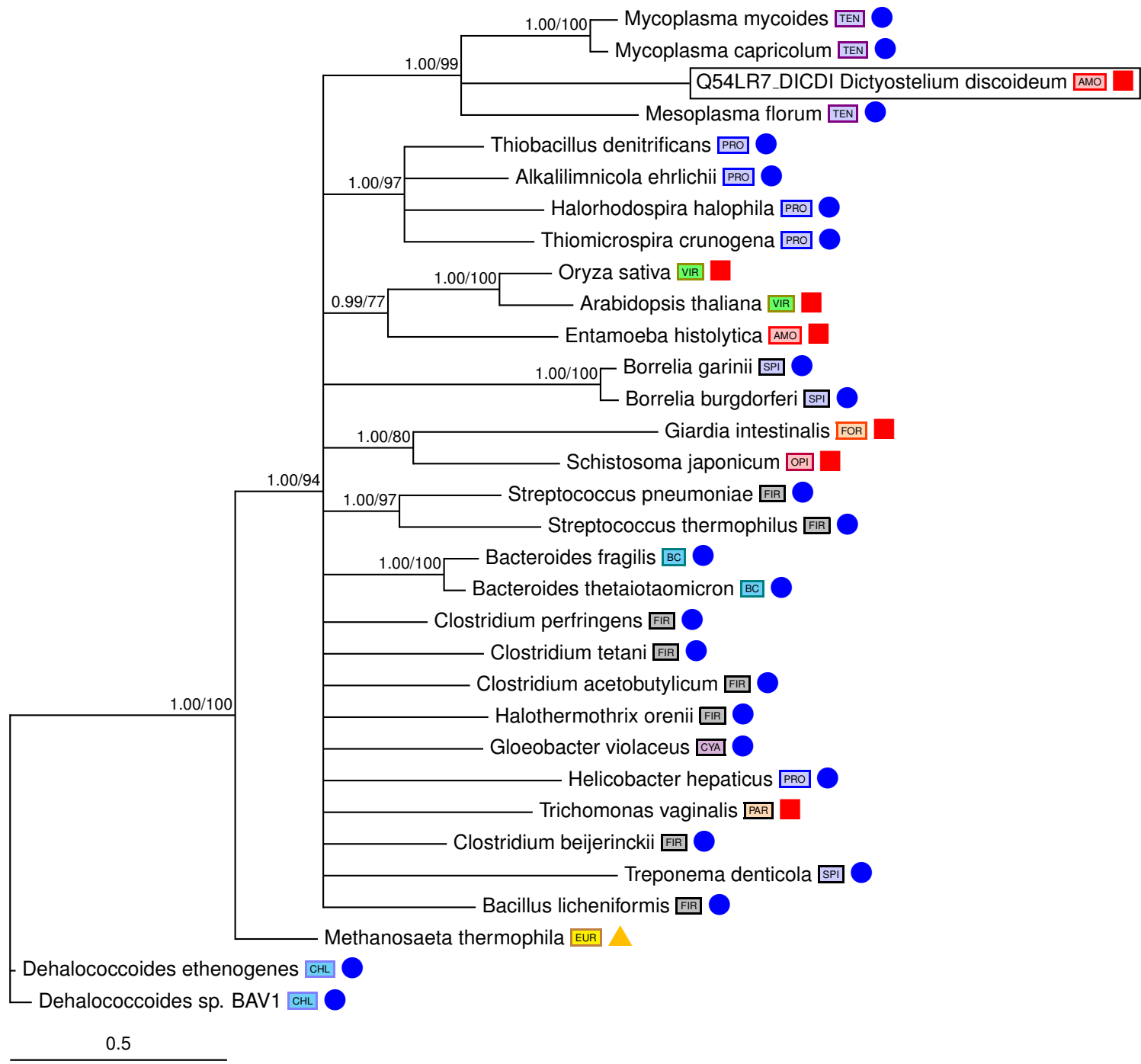
ON043

Candy accession: Q54KK2_DICDI
RefSeq accession: XP_637221.1
Uniprot accession: Q54KK2_DICDI
Comments: LGT - DD ONE NODES + LGT YL FUNGI TWO NODES
Species affected: DD,FUNGI
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 12
RefSeq annotation: hypothetical protein DDB_G0287303
Name of enzyme/protein: Predicted cationic amino acid transport permease
KEGG PATHWAY - level 1: Other function - Membrane transport
KEGG PATHWAY - level 2: na



ON044

Candy accession: Q54LR7_DICDI
RefSeq accession: XP_637763.1
Uniprot accession: Q54LR7_DICDI
Comments: LGT - DD ONE NODE
Species affected: DD
Adjacent taxa in tree: Tenericute
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0286443
Name of enzyme/protein: Protein containing Type 1 glutamine
amidotransferase (GATase1)-like domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



ON045

Candy accession: TV95721149
RefSeq accession: XP_001323199.1
Uniprot accession: A2E8N7_TRIVA
Comments: LGT - TV ONE NODE
Species affected: TV
Adjacent taxa in tree: Bacteroides

EC annotation - (Blast/Profile): EC:1.1.1.-
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: oxidoreductase, short chain
dehydrogenase/reductase family

Name of enzyme/protein: Oxidoreductases
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction

Candy accession: Q54PT0_DICDI
RefSeq accession: XP_638574.1
Uniprot accession: Q54PT0_DICDI
Comments: LGT - DD ONE NODE
Species affected: DD
Adjacent taxa in tree: Bacteria

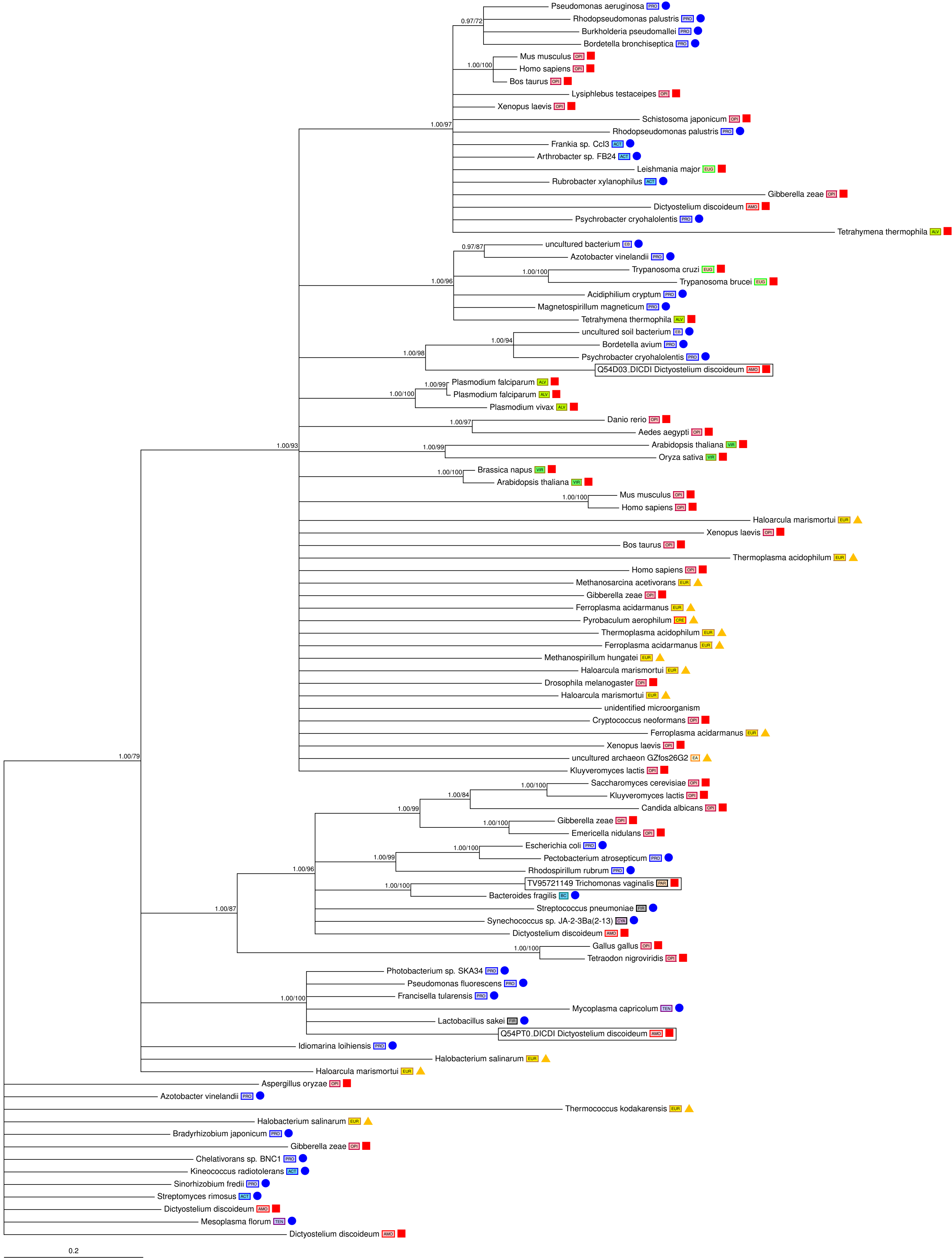
EC annotation - (Blast/Profile): EC:1.1.1.-
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0284351

Name of enzyme/protein: Oxidoreductases
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction

Candy accession: Q54D03_DICDI
RefSeq accession: XP_629517.1
Uniprot accession: 54D03_DICDI
Comments: LGT - DD ONE NODE
Species affected: DD
Adjacent taxa in tree: Bacteria

EC annotation - (Blast/Profile): EC:1.1.1.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0292602

Name of enzyme/protein: Oxidoreductases
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction

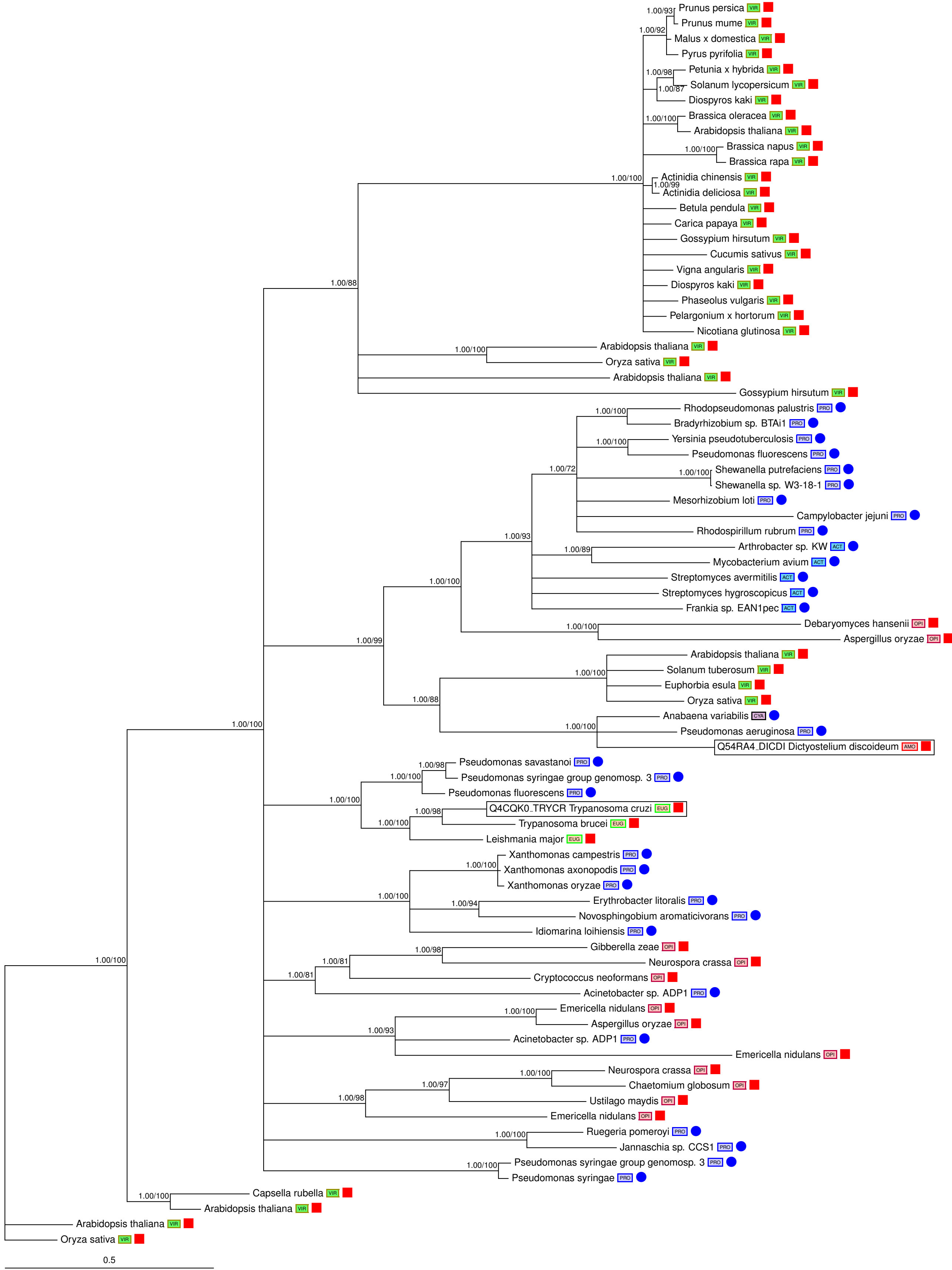


0.2

ON046

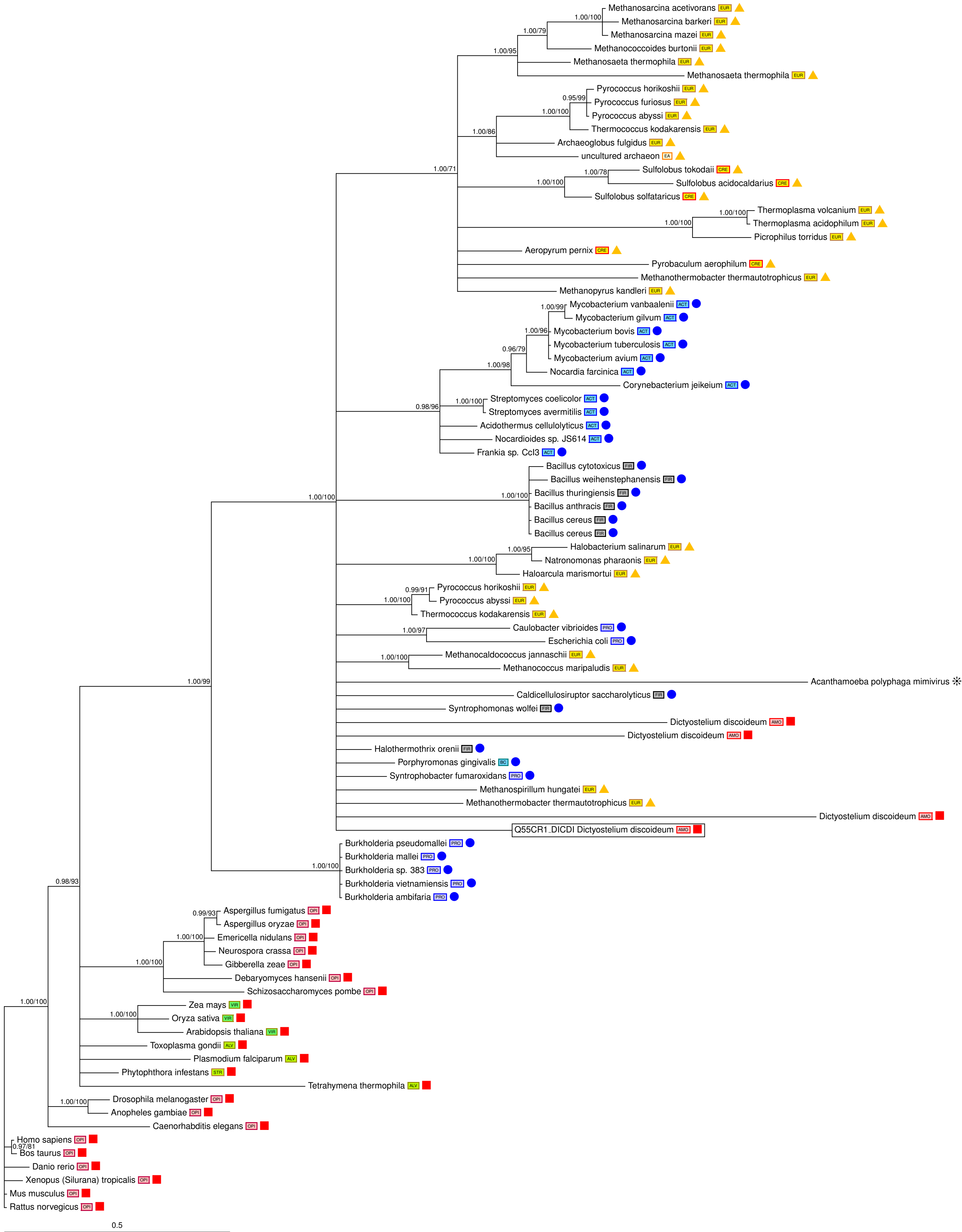
Candy accession: Q54RA4_DICDI
RefSeq accession: XP_639143.1
Uniprot accession: Y3291_DICDI
Comments: LGT - DD ONE NODE
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:1.21.3.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0283291
Name of enzyme/protein: isopenicillin-N synthase
KEGG PATHWAY - level 1: Biosynthesis of Other Secondary Metabolites
KEGG PATHWAY - level 2: Penicillin and cephalosporin biosynthesis

Candy accession: Q4CQK0_TRYCR
RefSeq accession: XP_804402.1
Uniprot accession: Q4CQK0_TRYCR
Comments: LGT - KINETOPLASTIDS ONE NODE
Species affected: TC,TB,LM
Adjacent taxa in tree: Pseudomonas
EC annotation - (Blast/Profile): EC:1.2.3.4
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: oxidoreductase
Name of enzyme/protein: oxalate oxidase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Glyoxylate and dicarboxylate metabolism



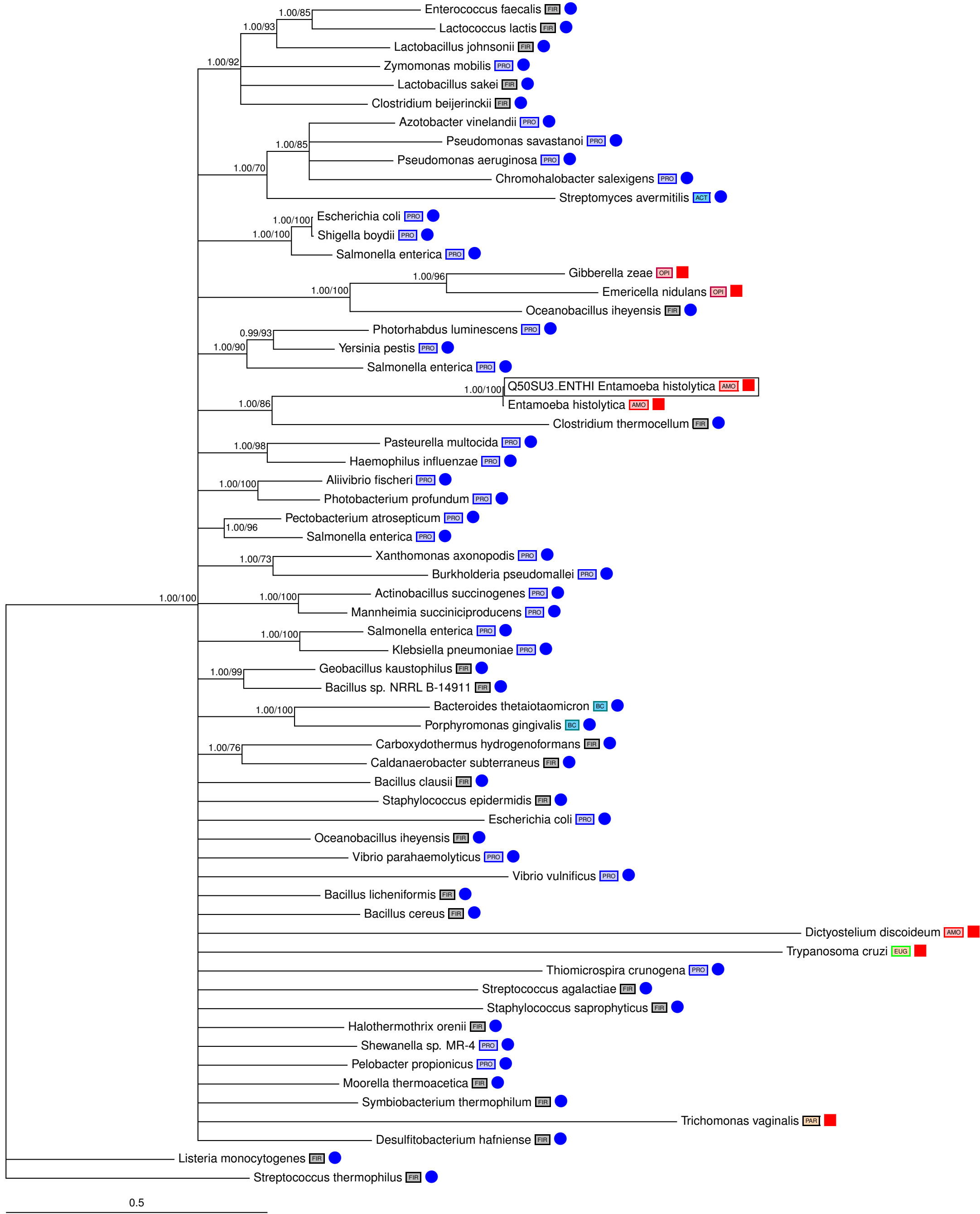
ON047

Candy accession: Q55CR1_DICDI
RefSeq accession: XP_646420.1
Uniprot accession: Q55CR1_DICDI
Comments: LGT - DD ONE NODE - 3 DOMAIN
Species affected: DD
Adjacent taxa in tree: Prokaryote
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 1
RefSeq annotation: hypothetical protein DDB_G0270694
Name of enzyme/protein: Predicted subgroup of the band 7 domain
of flotillin (reggie) like proteins
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



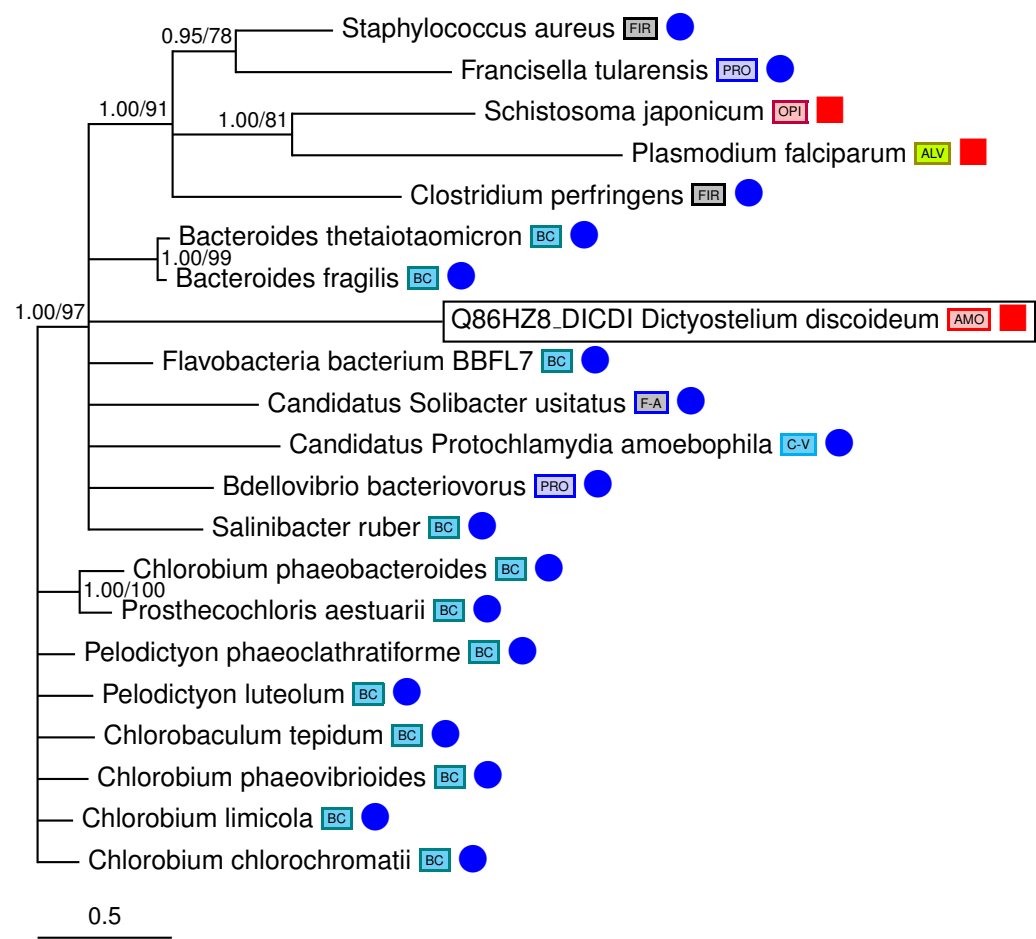
ON048

Candy accession: Q50SU3_ENTHI
RefSeq accession: XP_650055.1
Uniprot accession: Q401L6_ENTHI
Comments: LGT - EH ONE NODE + FUNGI ONE NODE
Species affected: EH
Adjacent taxa in tree: Firmicutes - Clostridium
EC annotation - (Blast/Profile): EC:2.7.1.31
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glycerate kinase
Name of enzyme/protein: Glycerate kinase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Lipid Metabolism, Carbohydrate Metabolism
KEGG PATHWAY - level 2: Glycine, serine and threonine metabolism, Glycerophospholipid metabolism, Glyoxylate and dicarboxylate metabolism



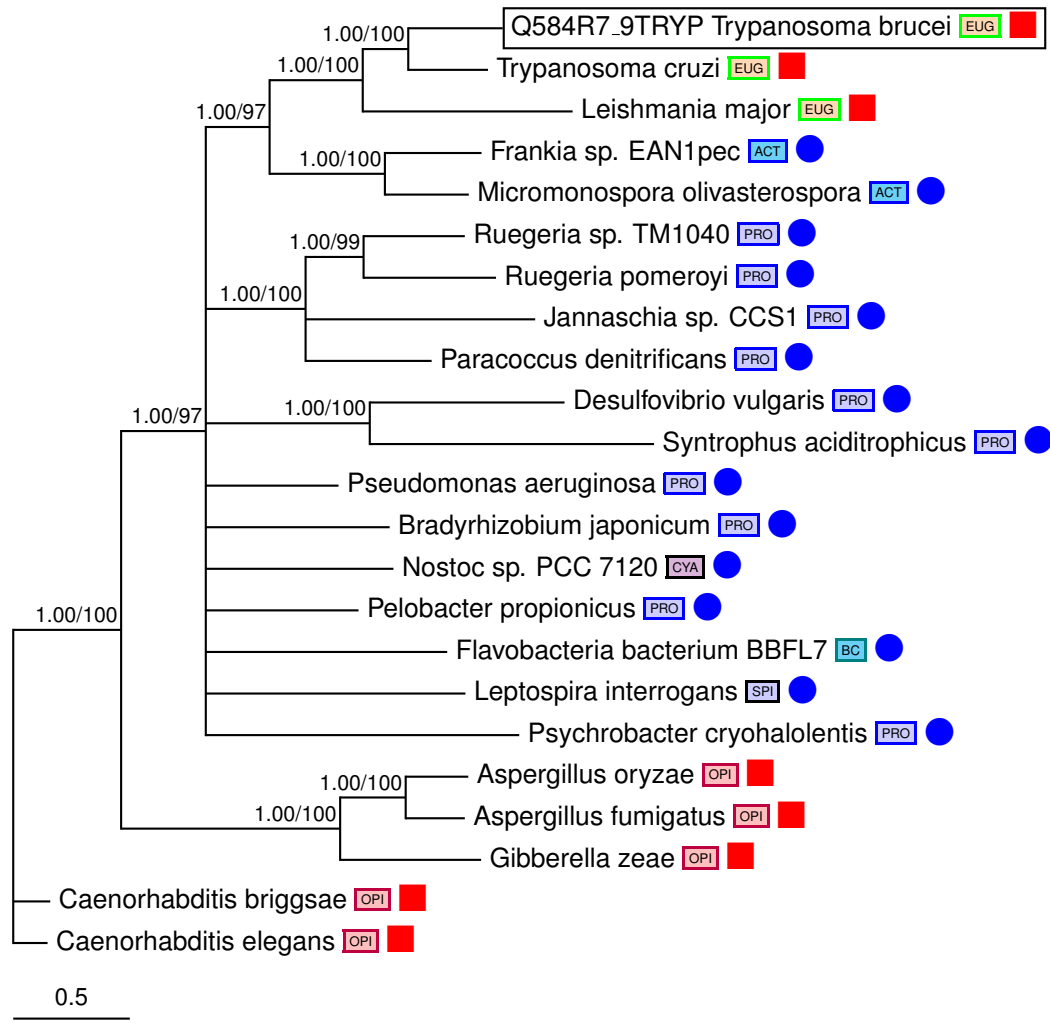
ON049

Candy accession: Q86HZ8_DICDI
RefSeq accession: XP_644821.1
Uniprot accession: Q557D9_DICDI
Comments: LGT - DD ONE NODE
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.1.1.34
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0273135
Name of enzyme/protein: tRNA
(guanosine18-2'-O)-methyltransferase
KEGG PATHWAY - level 1: Translation - Genetic Information
Processing
KEGG PATHWAY - level 2: Transfer RNA biogenesis



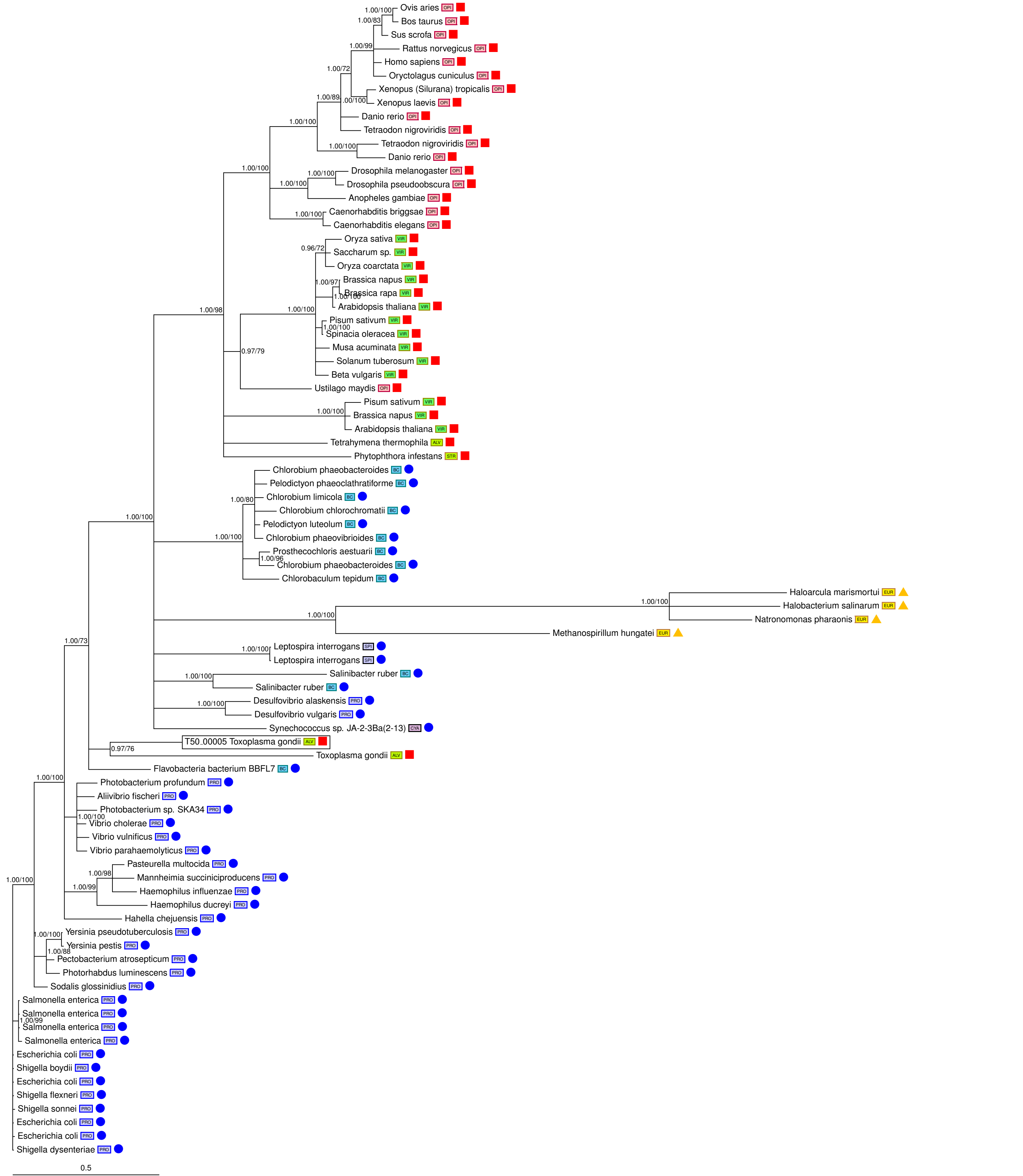
ON050

Candy accession: Q584R7_9TRYP
RefSeq accession: XP_845360.1
Uniprot accession: Q584R7_9TRYP
Comments: LGT - ONE NODE TB,TC,LM
Species affected: LM,TB,TC
Adjacent taxa in tree: Actinobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Hypothetical proteins
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



ON051

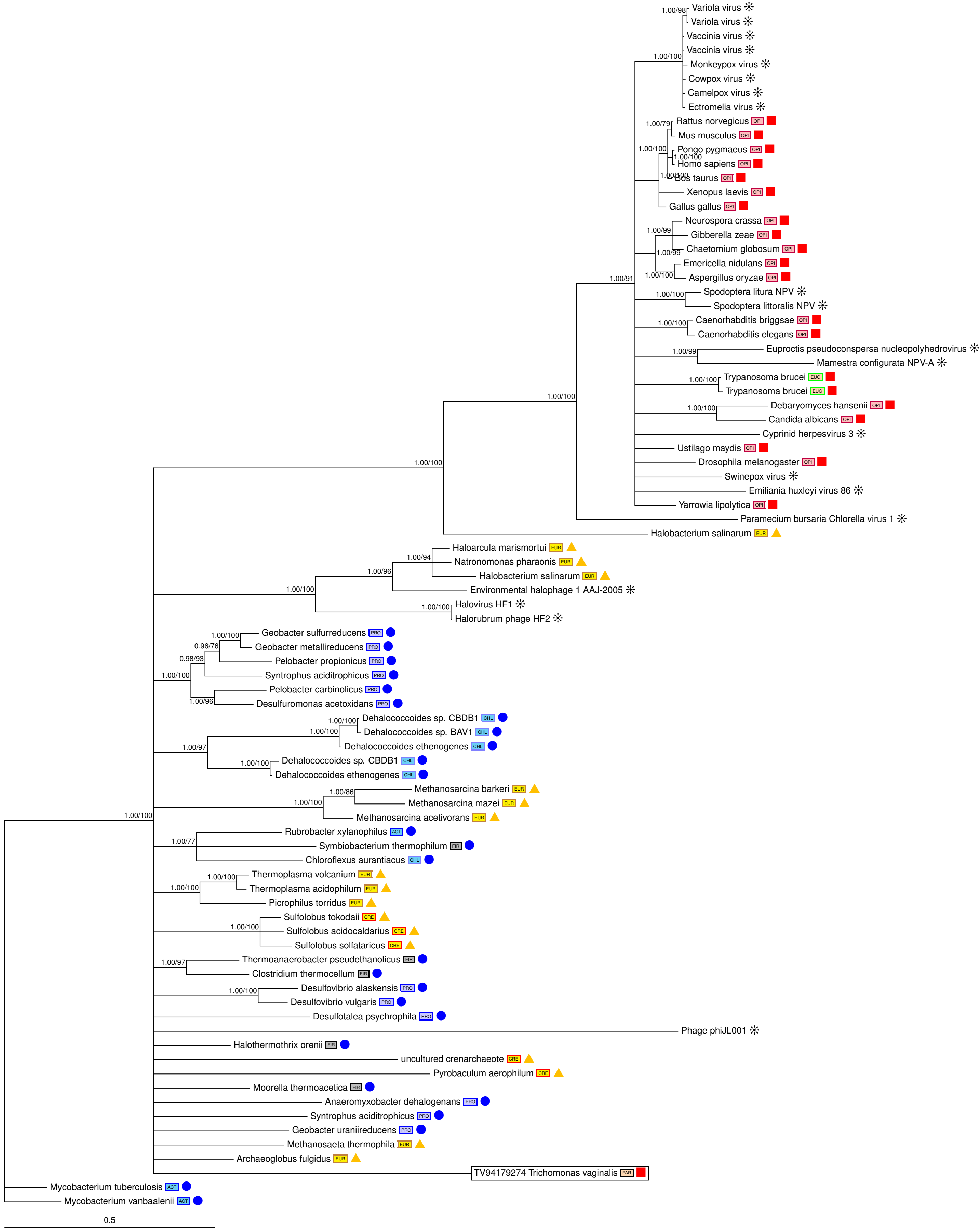
Candy accession: T50_00005
RefSeq accession: XP_002367118.1
Uniprot accession: B6KGZ5_TOXGO
Comments: LGT - TG ONE NODE -3 DOMAIN ToL
Species affected: TG
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.1.3.11
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: fructose-1,6-bisphosphatase, putative
Name of enzyme/protein: fructose-bisphosphatase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Glycolysis / Gluconeogenesis, Pentose phosphate pathway, Fructose and mannose metabolism



Candy accession: T59_03682
RefSeq accession: XP_002365950.1
Uniprot accession: B6KDM7_TOXGO
Comments: LGT - APICOMPLEXA ONE NODE + FUNGI
Species affected: PF,PV,PY,TG,CP
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:6.3.1.2
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: glutamine synthetase, putative
Name of enzyme/protein: glutamate-ammonia ligase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Energy Metabolism
KEGG PATHWAY - level 2: Alanine, aspartate and glutamate metabolism, Arginine and proline metabolism, Nitrogen metabolism

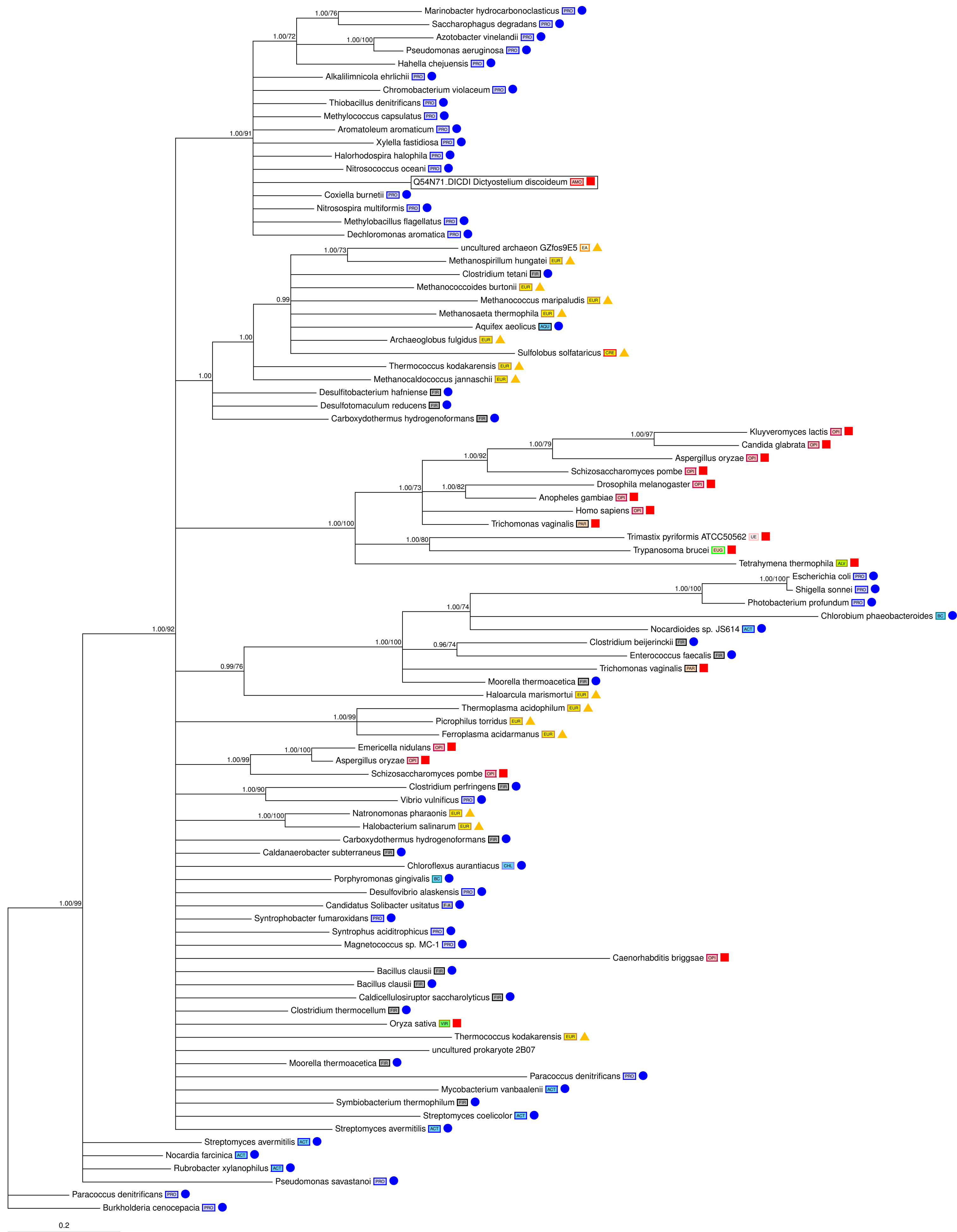


Candy accession: TV94179274
RefSeq accession: XP_001580988.1
Uniprot accession: A2DI13_TRIVA
Comments: LGT - TV ONE NODE + PHAGES + VIRUSES - 3 DOMAIN ToL
Species affected: TV
Adjacent taxa in tree: Prokaryotes/Phages
EC annotation - (Blast/Profile): EC:1.17.4.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Ribonucleotide reductase, all-alpha domain containing protein
Name of enzyme/protein: Ribonucleoside-diphosphate reductase alpha chain
KEGG PATHWAY - level 1: Nucleotide Metabolism, Metabolism of Other Amino Acids
KEGG PATHWAY - level 2: Purine metabolism, Pyrimidine metabolism, Glutathione metabolism

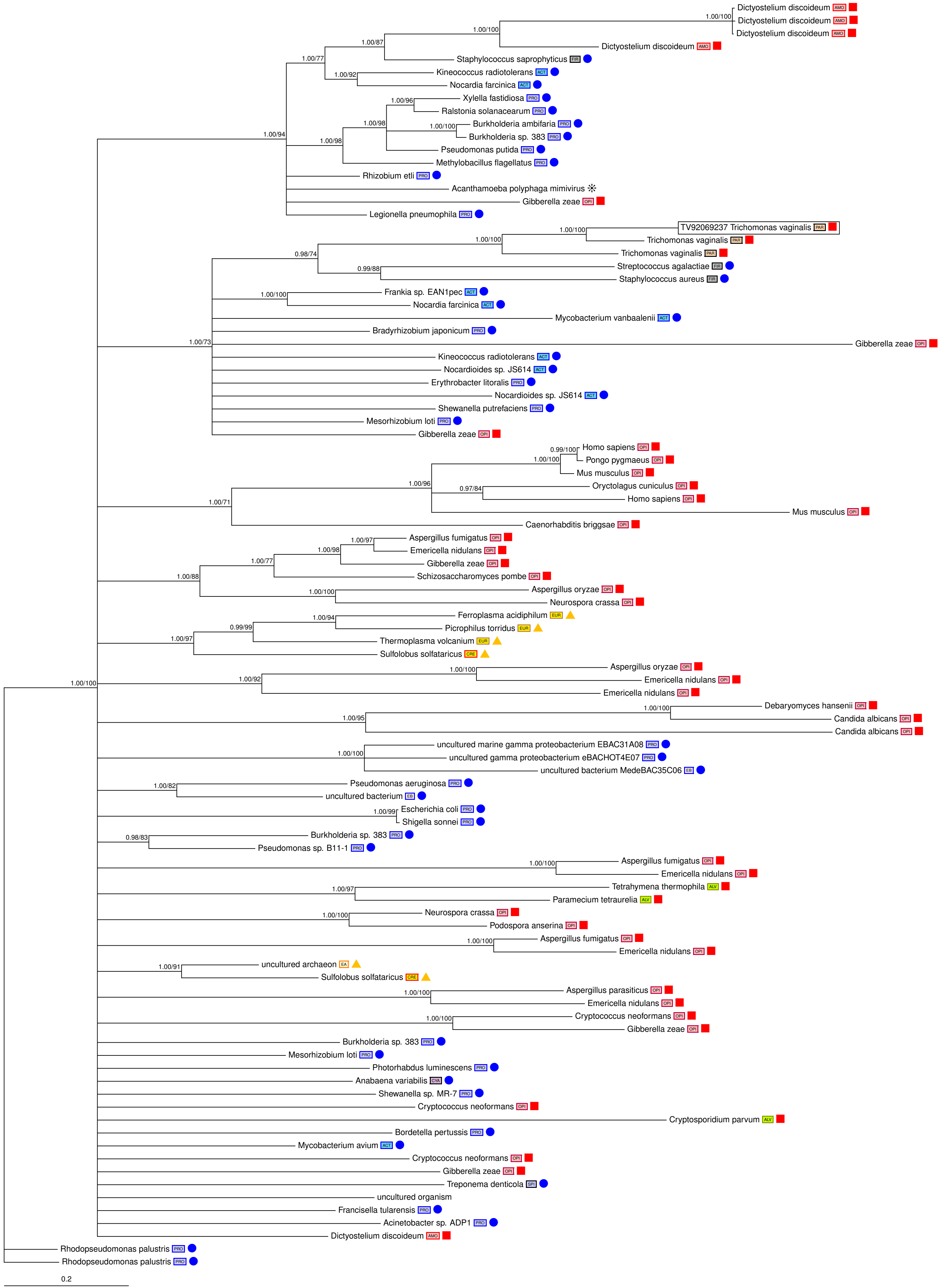


ON054

Candy accession: Q54N71.D1CDI
RefSeq accession: XP_638072.1
Uniprot accession: Q54N71.D1CDI
Comments: LGT - DD ONE NODES
Species affected: DD
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:3.5.99.3
PHOBUS SP: 0
PHOBUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0285467
Name of enzyme/protein: hydroxydechloroatrazine
ethylaminohydrolase
KEGG PATHWAY - level 1: Xenobiotics Biodegradation and
Metabolism
KEGG PATHWAY - level 2: Atrazine degradation

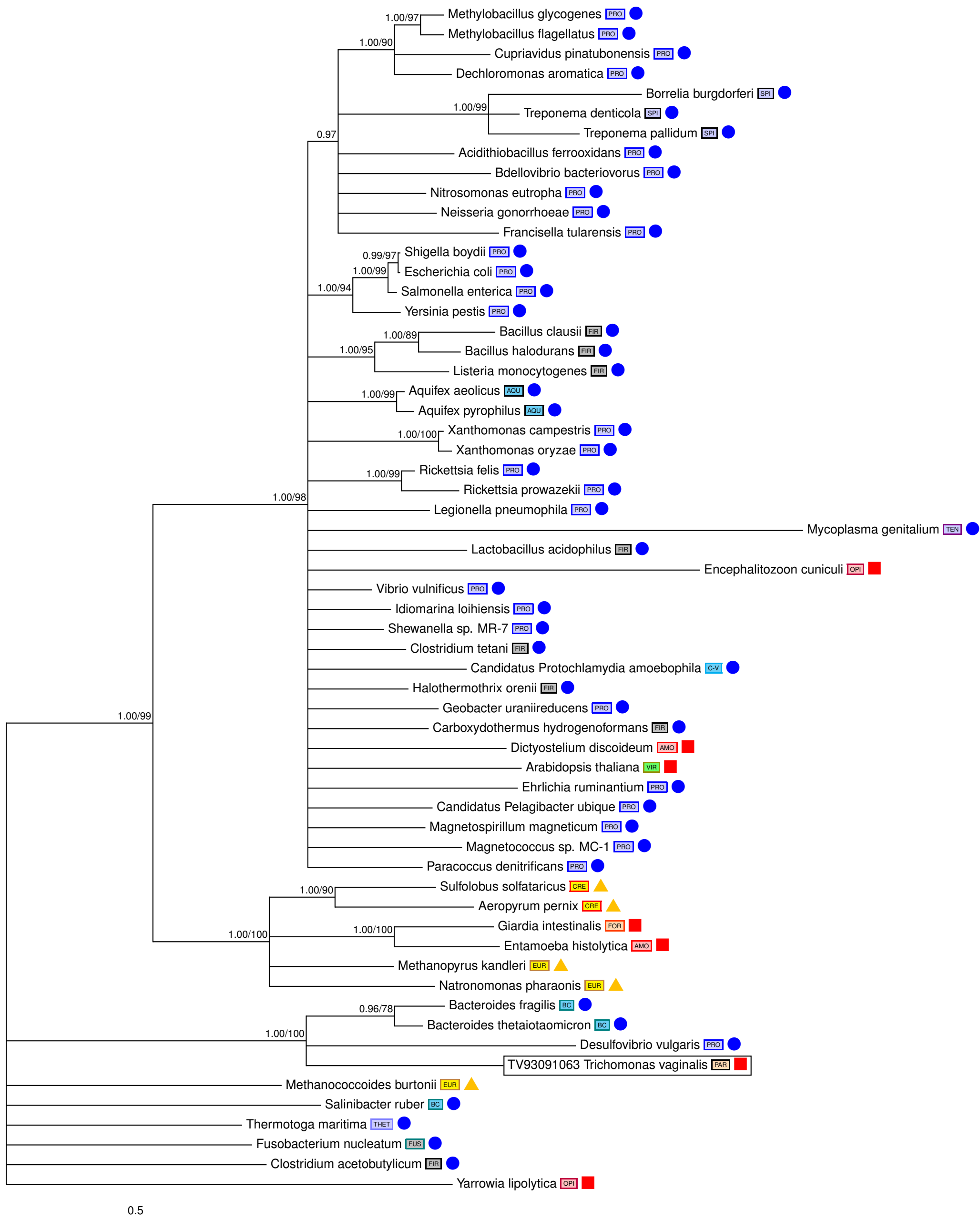


Candy accession: TV92069237
RefSeq accession: XP_001328466.1
Uniprot accession: A2DTU6_TRIVA
Comments: LGT - TV ONE NODE FROM FUNGI
Species affected: TV,DD
Adjacent taxa in tree: Firmicutes - Streptococcus
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted Esterase/lipase; alpha/beta
hydrolase fold
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



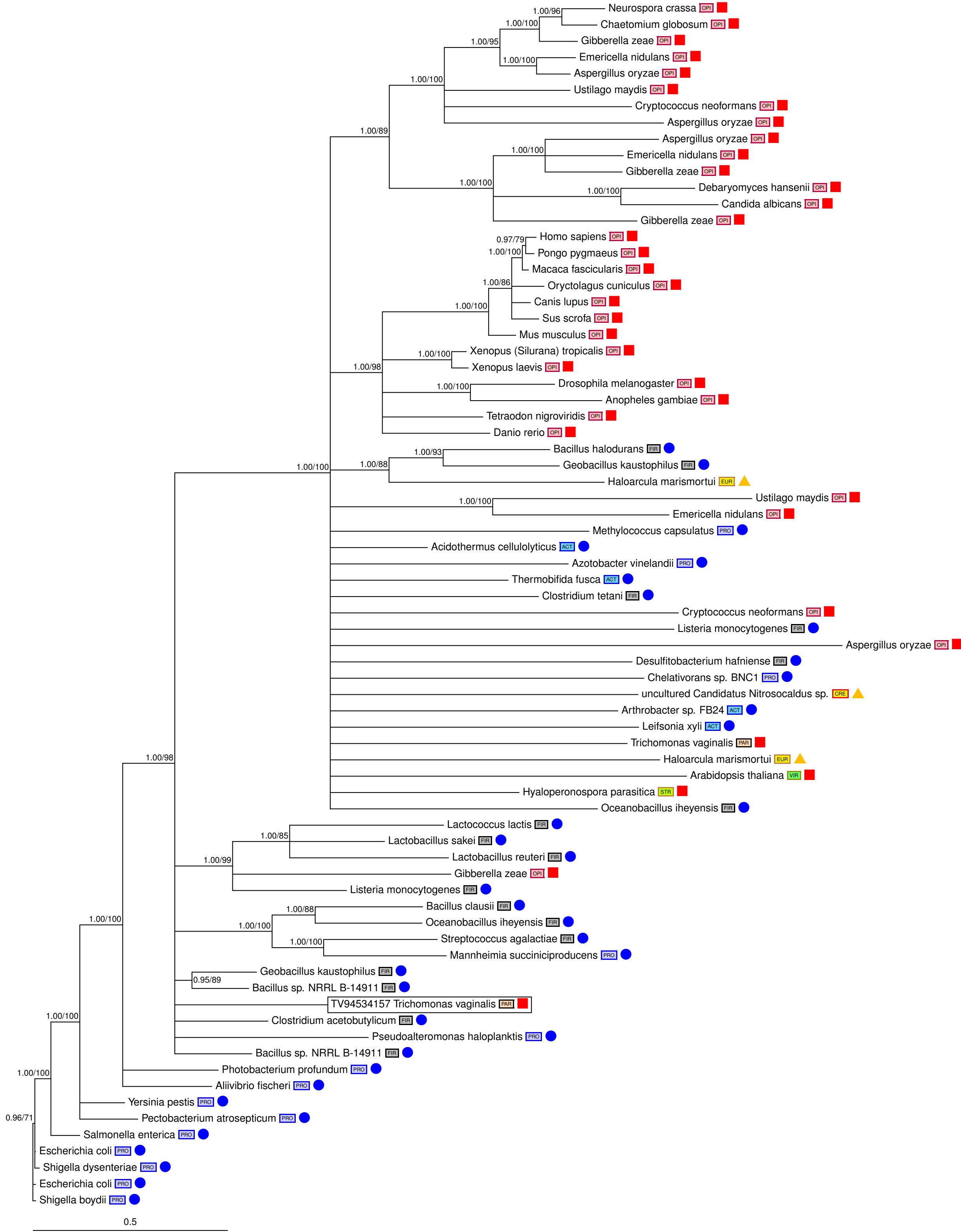
ON056

Candy accession: TV93091063
RefSeq accession: XP_001308954.1
Uniprot accession: A2FGG0_TRIVA
Comments: LGT - TV ONE NODE
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:6.1.1.7
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Probable R-RNA methyltransferase
KEGG PATHWAY - level 1: Translation - Genetic Information Processing
KEGG PATHWAY - level 2: Aminoacyl-tRNA biosynthesis



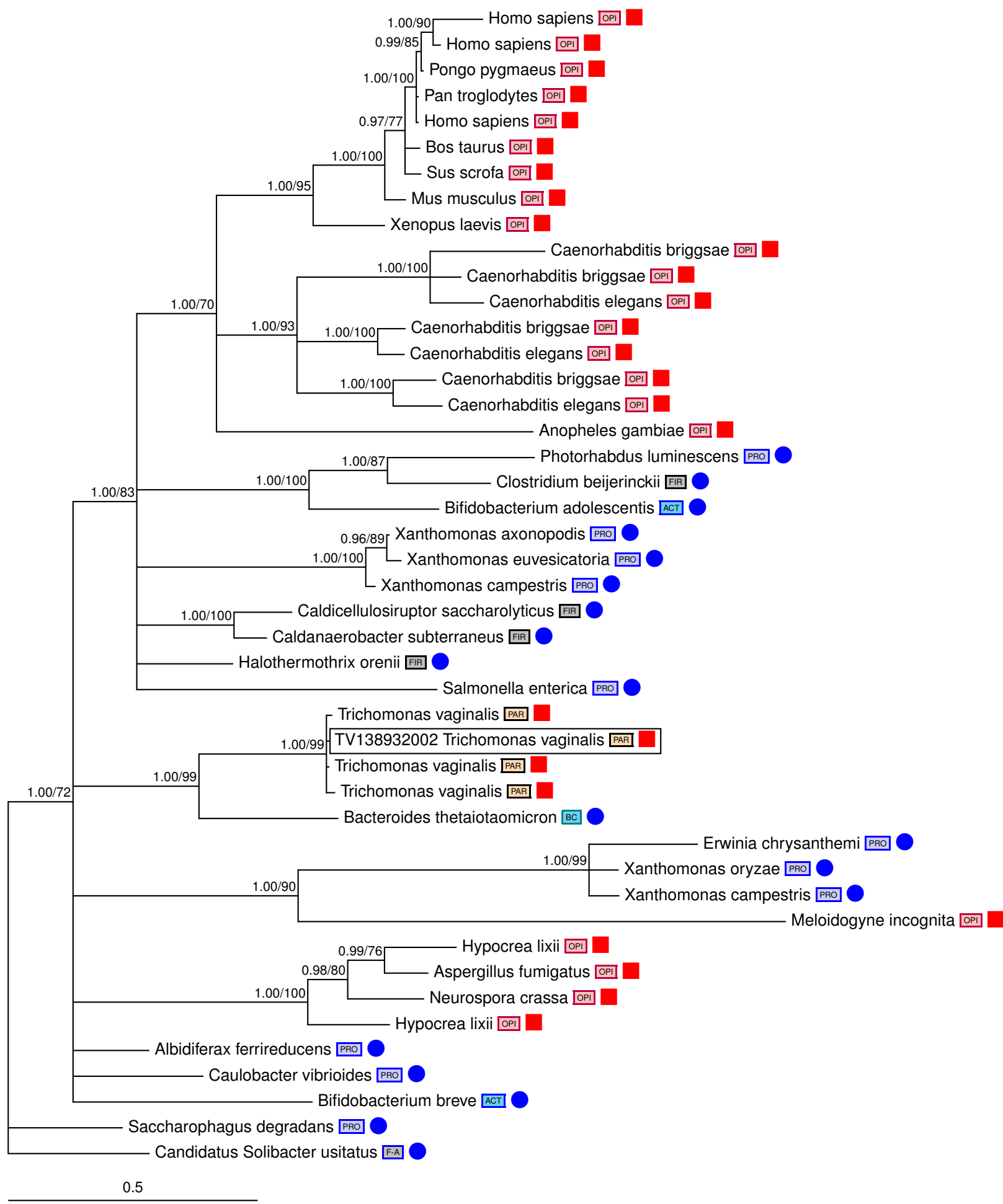
ON057

Candy accession: TV94534157
RefSeq accession: XP_001321975.1
Uniprot accession: A2EC75_TRIVA
Comments: LGT - TV ONE NODE
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:1.3.1.20
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Oxidoreductase family, NAD-binding
Rossmann fold containing protein
Name of enzyme/protein: trans-1,2-dihydrobenzene-1,2-diol
dehydrogenase
KEGG PATHWAY - level 1: Xenobiotics Biodegradation and
Metabolism
KEGG PATHWAY - level 2: Metabolism of xenobiotics by cytochrome
P450



ON058

Candy accession: TV138932002
RefSeq accession: XP_001279673.1
Uniprot accession: A2HV24_TRIVA
Comments: LGT - TV ONE NODE
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:3.2.1.45
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glucosylceramidase precursor
Name of enzyme/protein: glucosylceramidase
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism, Lipid Metabolism
KEGG PATHWAY - level 2: Other glycan degradation, Sphingolipid metabolism



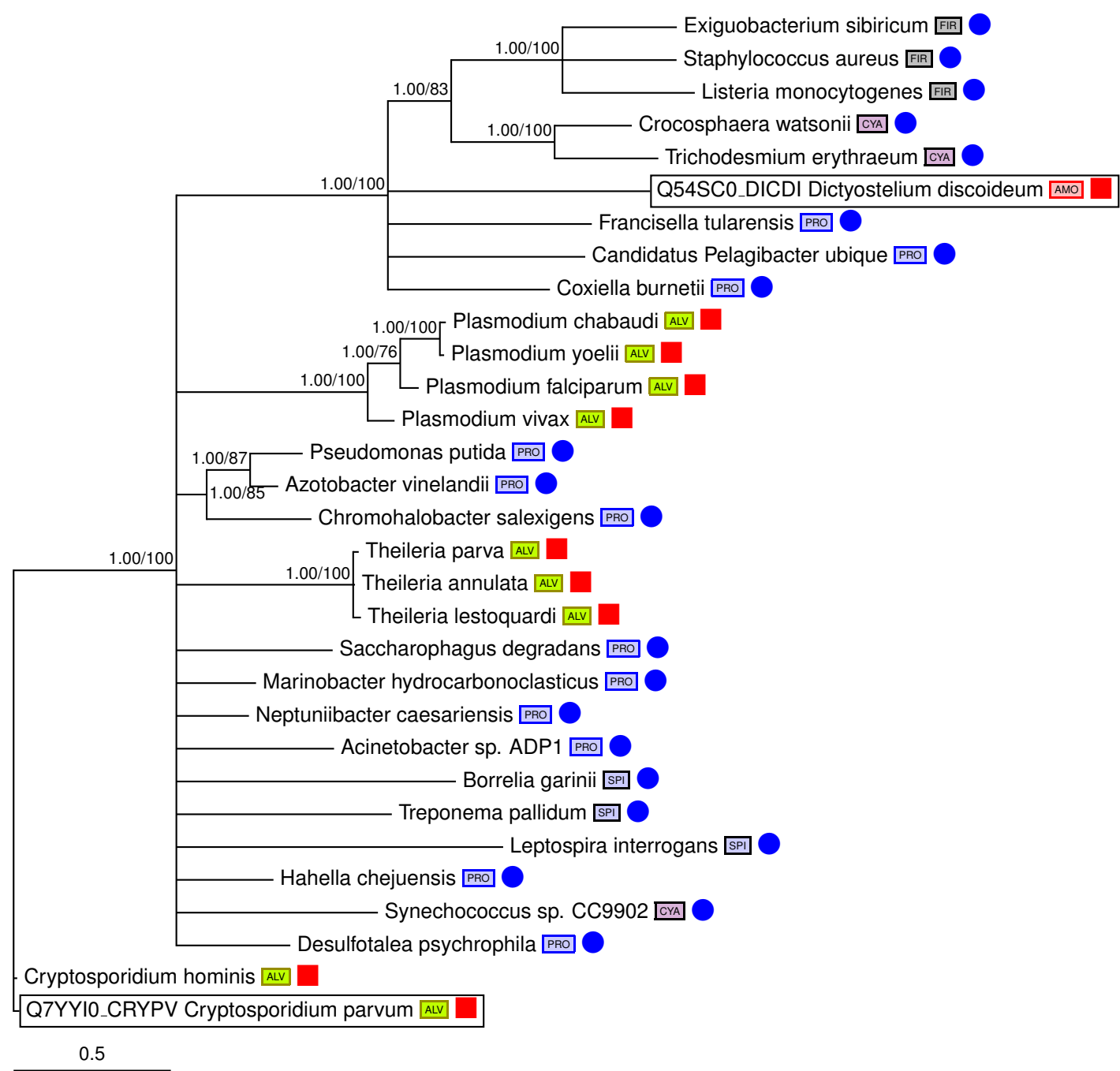
ON059

Candy accession: Q7YYI0_CRYPV
RefSeq accession: XP_627573.1
Uniprot accession: Q7YYI0_CRYPV
Comments: LGT - APICOMPLEXA ONE NODE
Species affected: CP,CH,TP,TA,TL,PC,PY,PF,PV
Adjacent taxa in tree: Bacteria

EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted R-RNA methyltransferase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

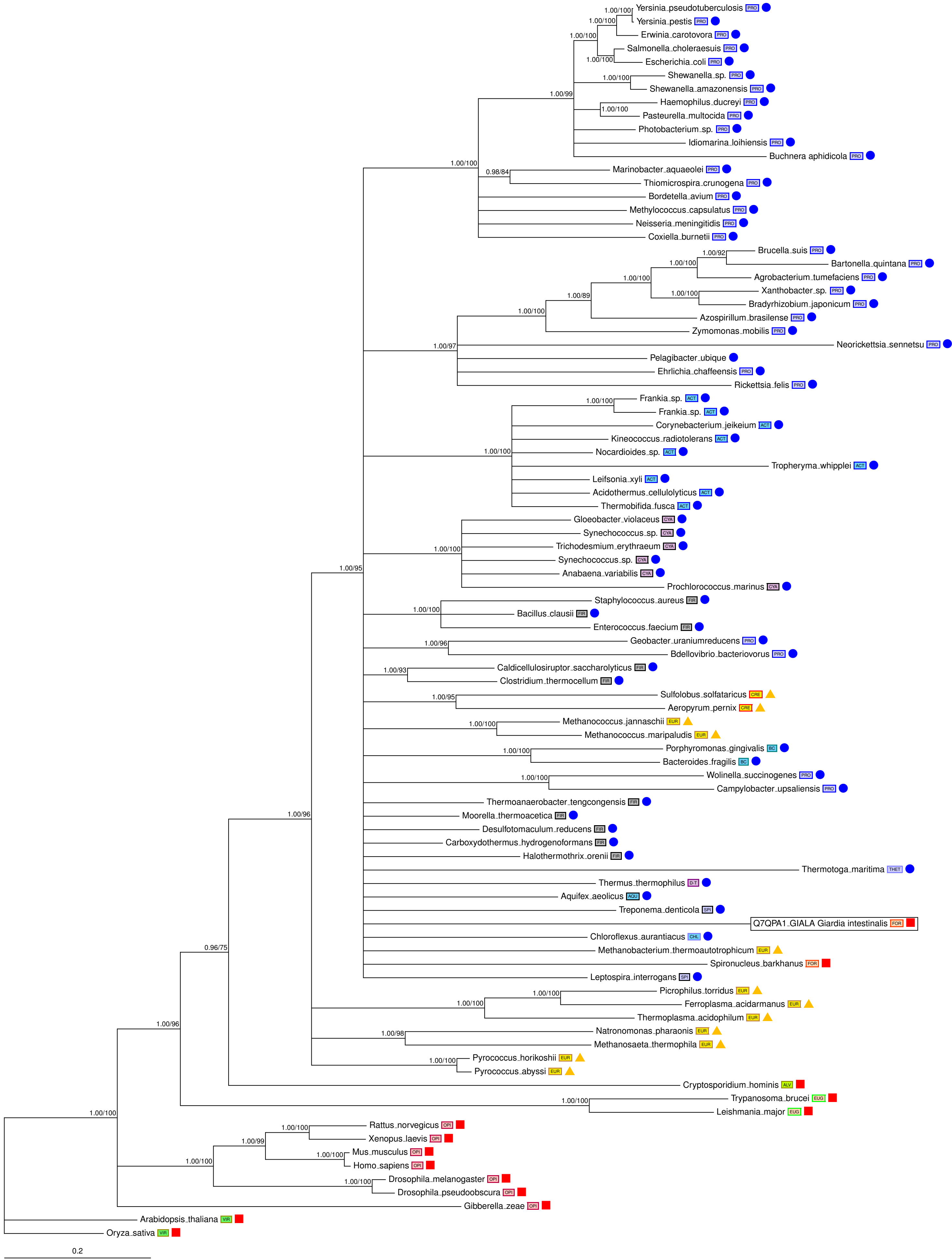
Candy accession: Q54SC0_DICDI
RefSeq accession: XP_640119.1
Uniprot accession: Q54SC0_DICDI
Comments: LGT - DD ONE NODE
Species affected: DD
Adjacent taxa in tree: Bacteria

EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0282549
Name of enzyme/protein: Predicted R-RNA methyltransferase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



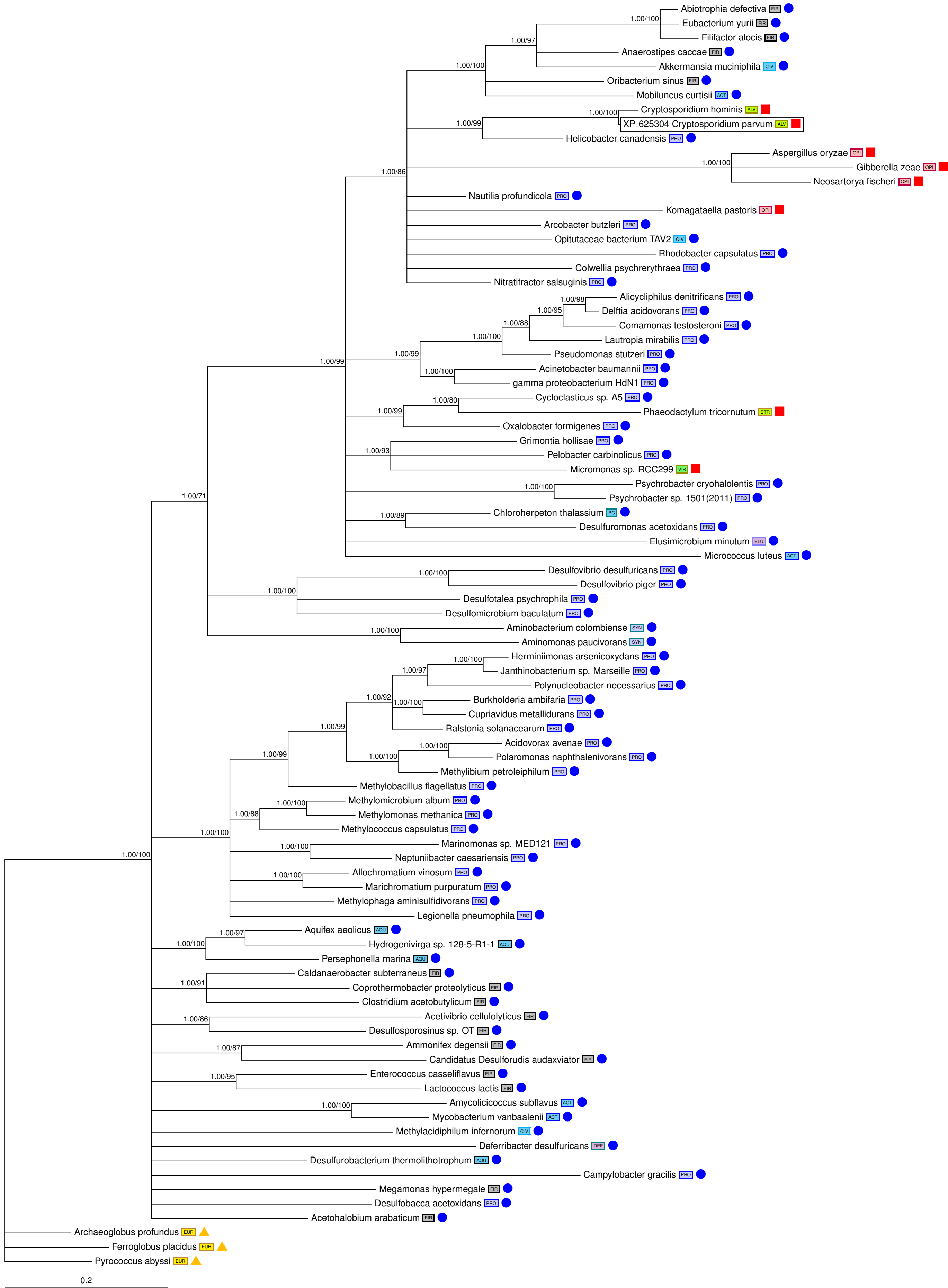
ON060

Candy accession: Q7QPA1_GIALA
RefSeq accession: XP_001709668.1
Uniprot accession: Q7QPA1_GIALA
Comments: LGT - GI, SB ONE NODE - 3 DOMAIN ToL
Species affected: GI,SB
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:6.3.4.2
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: CTP synthase
Name of enzyme/protein: CTP synthase
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Pyrimidine metabolism



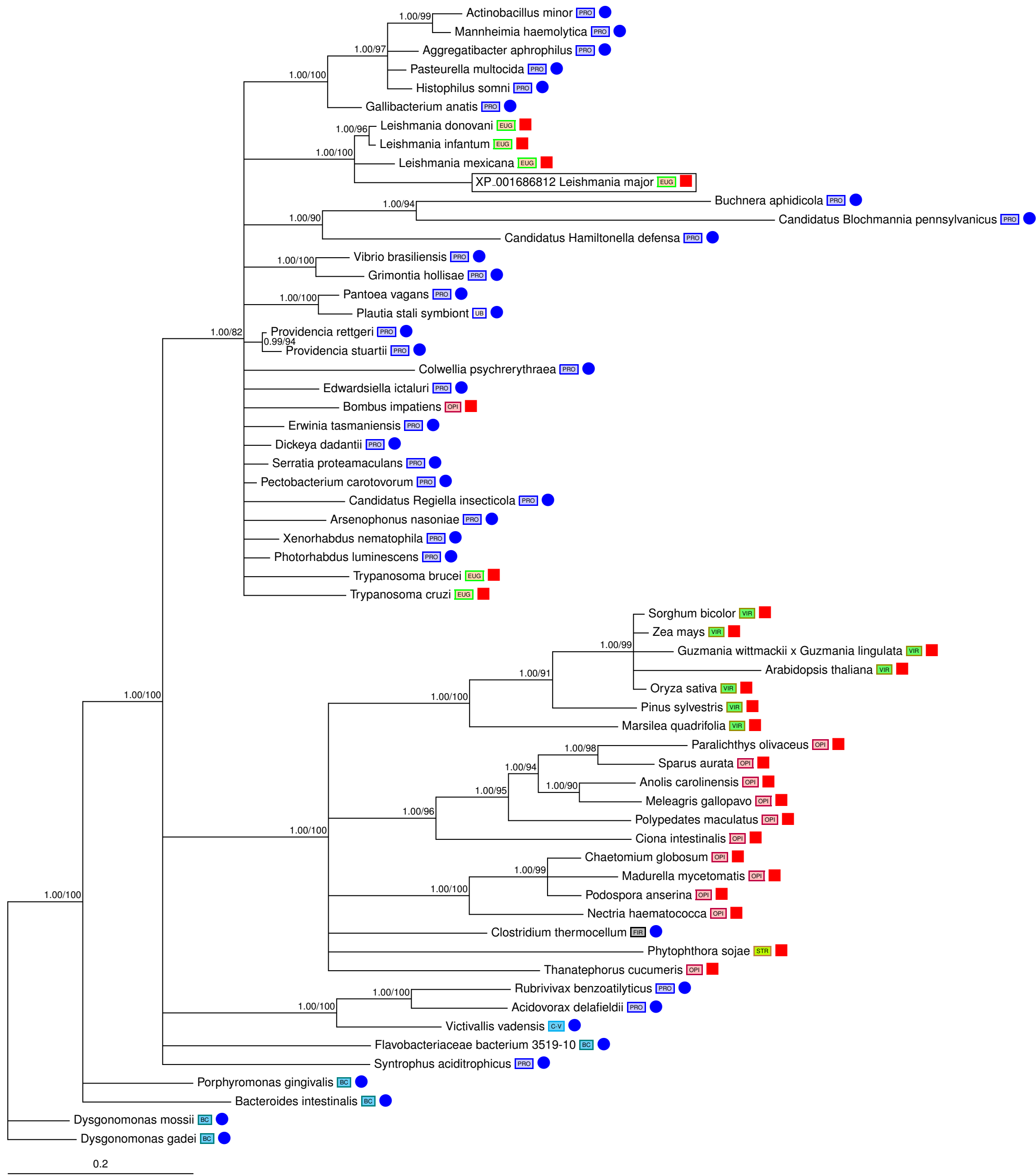
ON061

Candy accession: XP_625304
RefSeq accession: XP_625304
Uniprot accession: Q5CPD7_CRYPV
Comments: LGT - CP ONE NODE
Species affected: CP,FUNGI,PLANT, STRAMENOPILE
Adjacent taxa in tree: Proteobacteria - Campylobacter
EC annotation - (Blast/Profile): EC:4.2.1.20
PHOBIUS SP: 0
PHOBIUS TMD: 1
RefSeq annotation: tryptophan synthase trpB of possible bacterial origin
Name of enzyme/protein: Tryptophan synthase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Glycine, serine and threonine metabolism, Phenylalanine, tyrosine and tryptophan biosynthesis



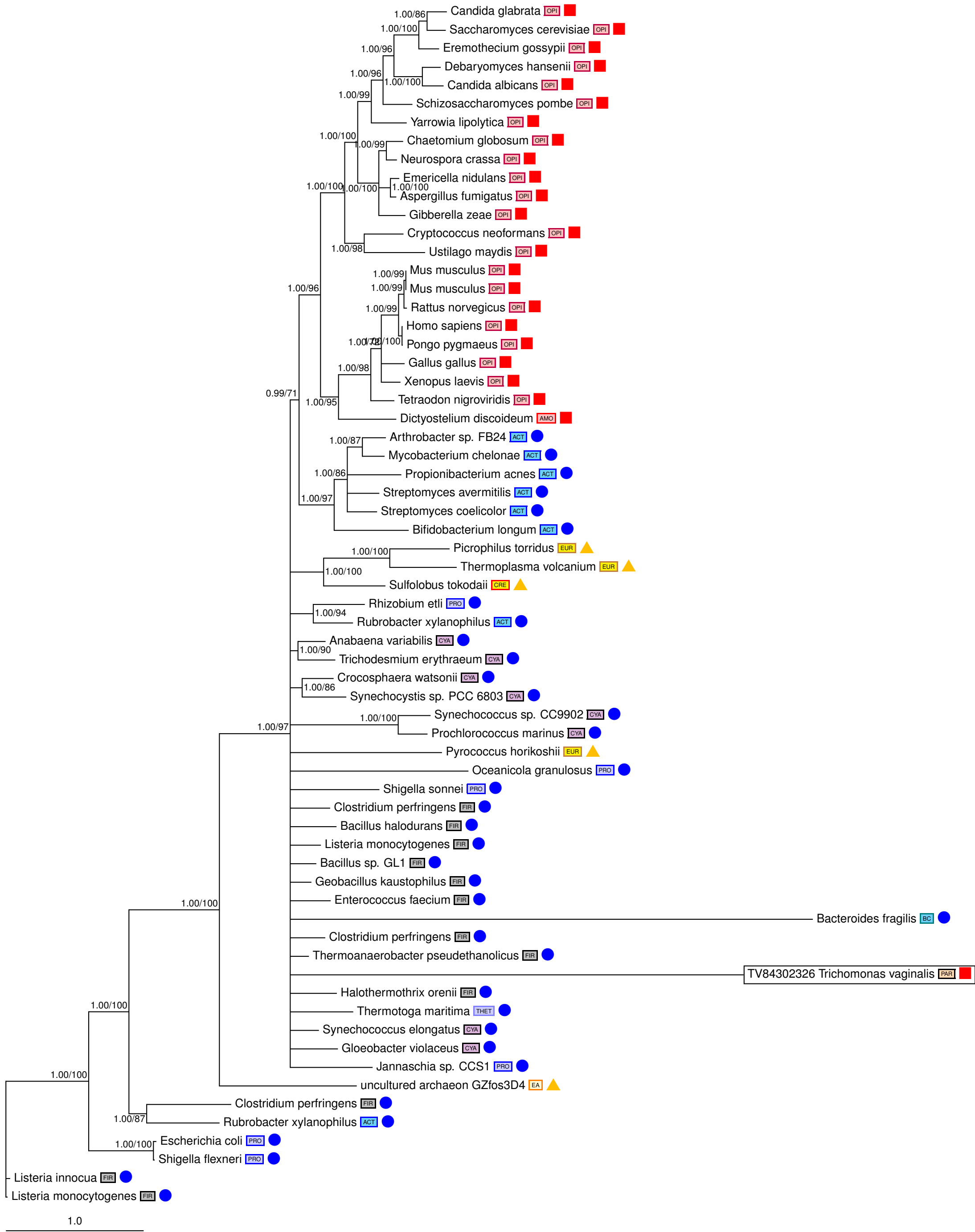
ON062

Candy accession: XP_001686812
RefSeq accession: XP_001686812
Uniprot accession: Q4Q1I6_LEIMA
Comments: LGT - KINETOPLASTIDS (plus LGT into
 bumblebee Bombus impatiens?)
Species affected: LM, TB, TC
Adjacent taxa in tree: g-proteobacteria
EC annotation - (Blast/Profile): EC:1.2.1.12
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: glyceraldehyde 3-phosphate
 dehydrogenase, cytosolic
Name of enzyme/protein: Glyceraldehyde 3-phosphate dehydrogenase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Glycolysis / Gluconeogenesis



ON063

Candy accession: TV84302326
RefSeq accession: XP_001579222.1
Uniprot accession: A2DN59_TRIVA
Comments: LGT - TV ONE NODE
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:3.2.1.24
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glycosyl hydrolase
Name of enzyme/protein: a-mannosidase
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism
KEGG PATHWAY - level 2: Other glycan degradation

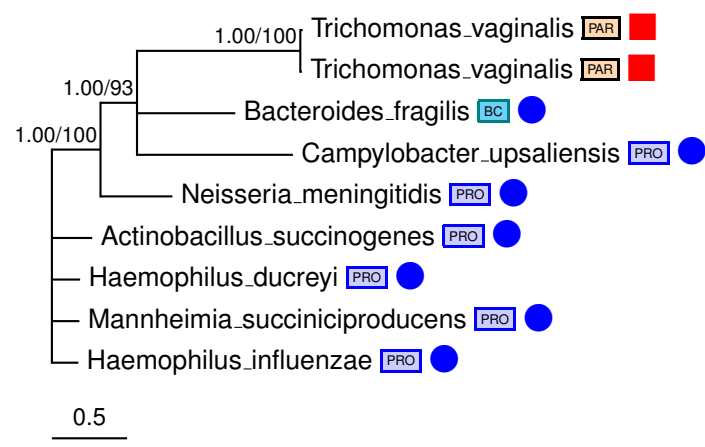


TN001

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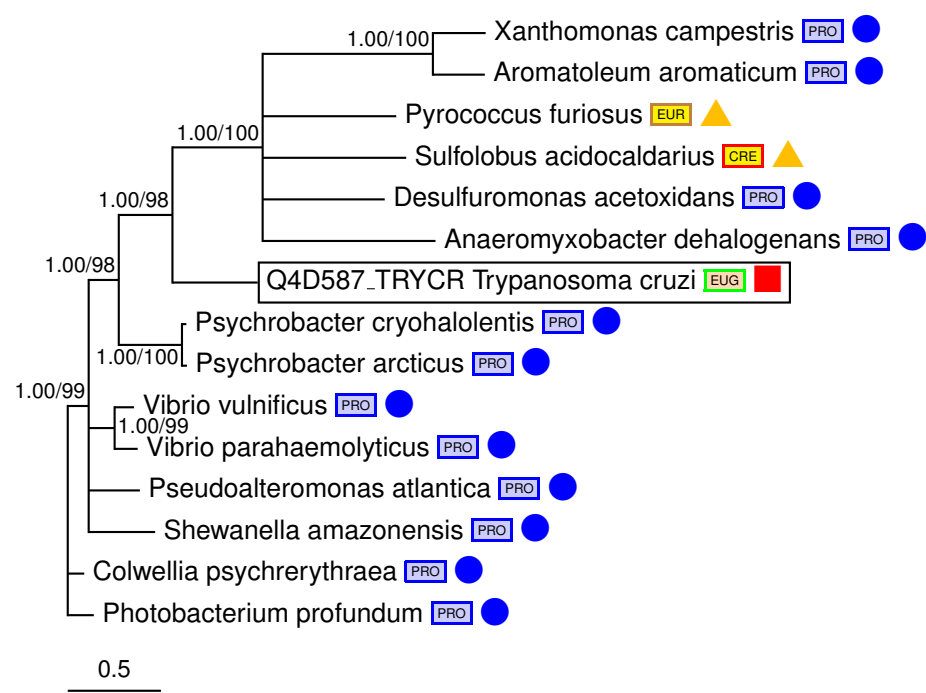
Candy accession: TV122580003
RefSeq accession: XP_001285086.1
Uniprot accession: A2HEL1_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted D12 class N6 adenine-specific
DHA methyltransferase
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na

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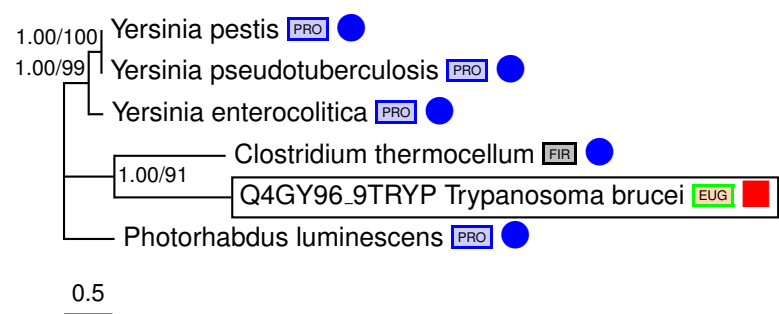
TN002

Candy accession: Q4D587_TRYCR
RefSeq accession: XP_809539.1
Uniprot accession: Q4D587_TRYCR
Comments: LGT - TC ONLY
Species affected: TC
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: metallo-beta-lactamase superfamily
Name of enzyme/protein: Predicted metallo-beta-lactamase protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



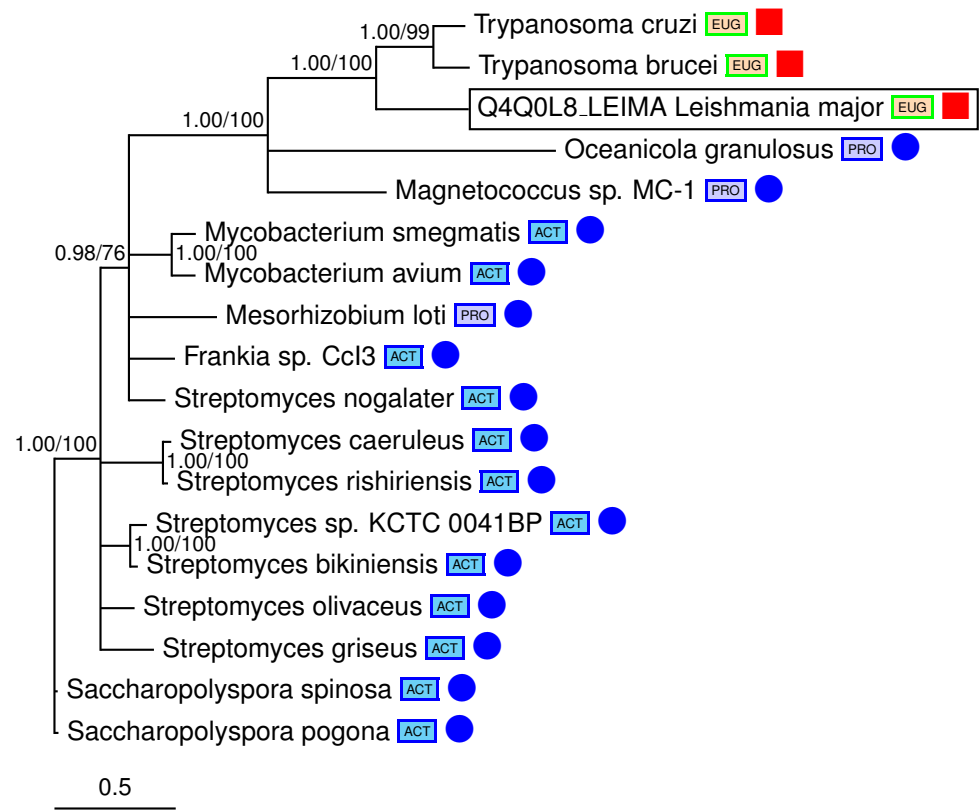
TN003

Candy accession: Q4GY96_9TRYP
RefSeq accession: XP_001219175.1
Uniprot accession: Q4GY96_9TRYP
Comments: LGT - TB ONLY
Species affected: TB
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.1.1.32
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: phospholipase A1
Name of enzyme/protein: phospholipase A1
KEGG PATHWAY - level 1: Lipid Metabolism
KEGG PATHWAY - level 2: Glycerophospholipid metabolism, alpha-Linolenic acid metabolism



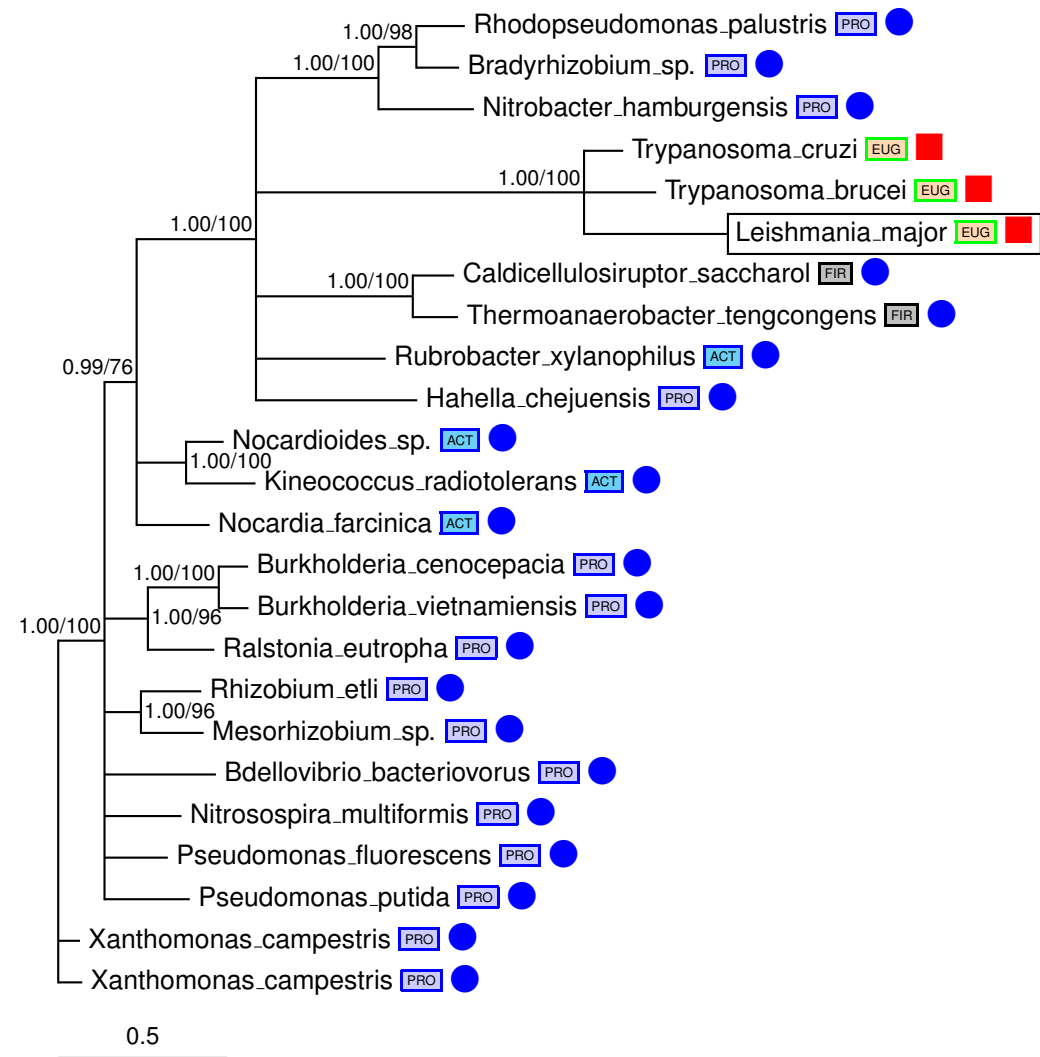
TN004

Candy accession: Q4Q0L8_LEIMA
RefSeq accession: XP_001687130.1
Uniprot accession: Q4Q0L8_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB,TC
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Macrocin-0-methyltransferase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



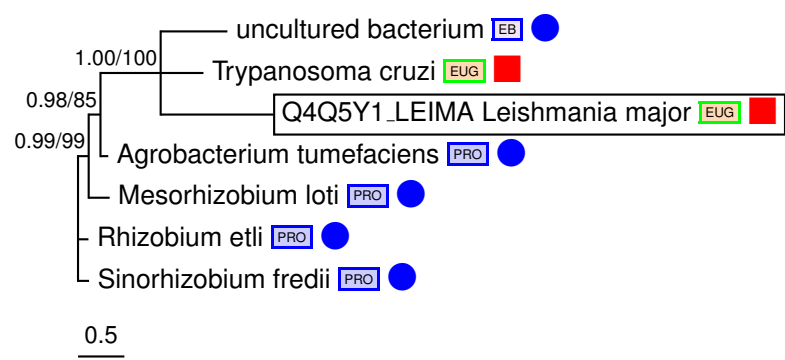
TN005

Candy accession: Q4Q1L6_LEIMA
RefSeq accession: XP_001686782.1
Uniprot accession: Q4Q1L6_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB,TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Hypothetical protein
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



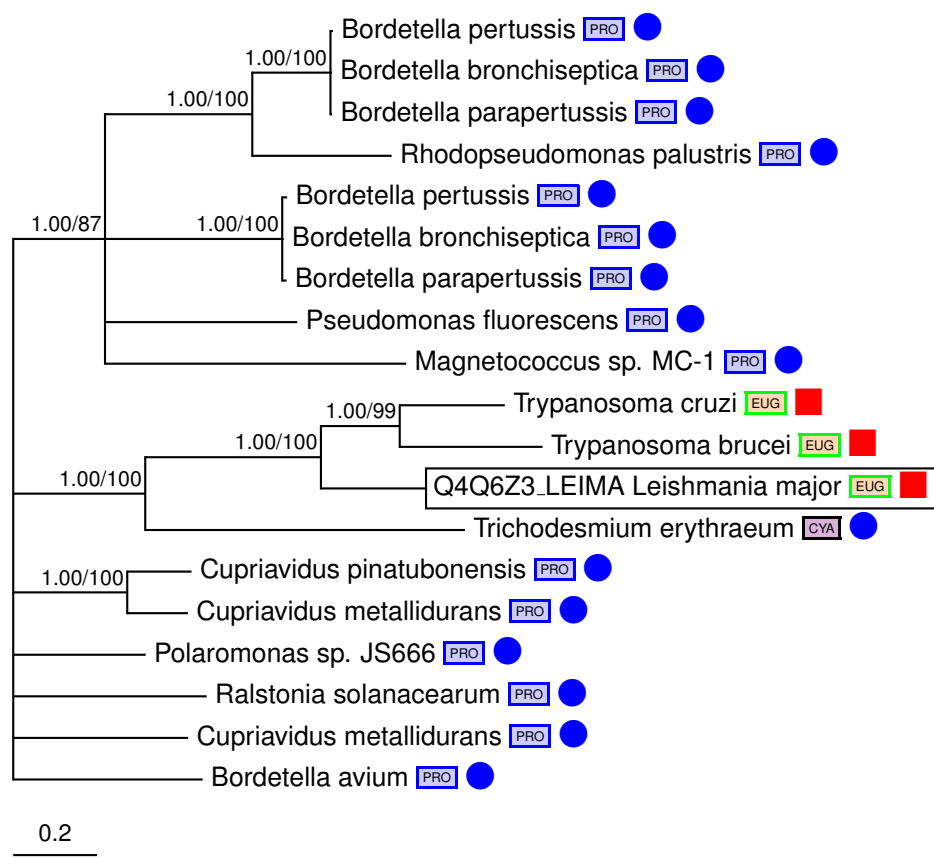
TN006

Candy accession: Q4Q5Y1_LEIMA
RefSeq accession: XP_001685267.1
Uniprot accession: Q4Q5Y1_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.5.1.16
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: acetylornithine deacetylase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism



TN007

Candy accession: Q4Q6Z3_LEIMA
RefSeq accession: XP_001684905.1
Uniprot accession: Q4Q6Z3_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB,TC
Adjacent taxa in tree: Cyanobacteria - Trichodesmium
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 1
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing peptidase M14-like domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



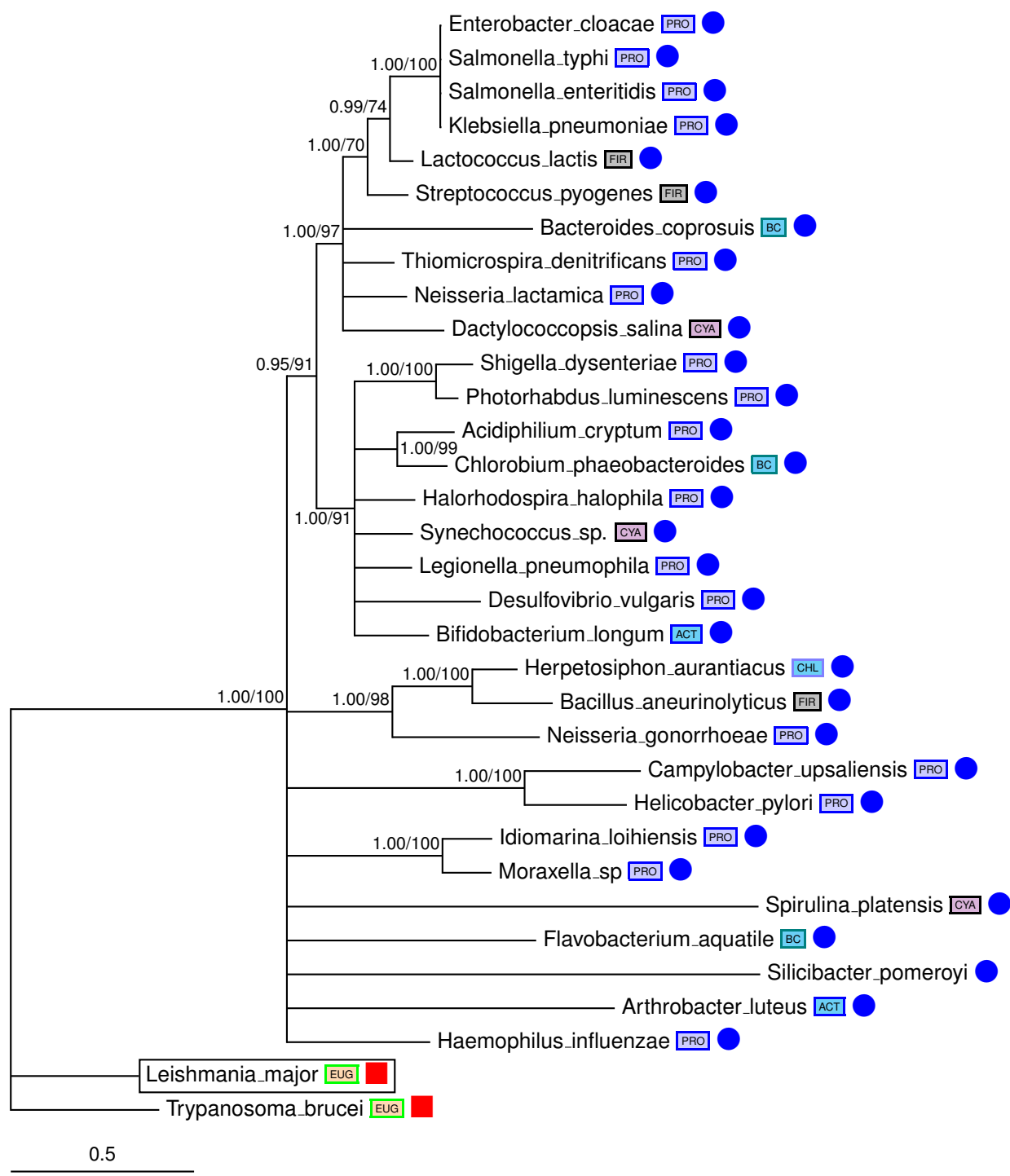
TN008

Candy accession: Q4Q8D2_LEIMA
RefSeq accession: XP_001684416.1
Uniprot accession: Q4Q8D2_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB,TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Putative hydrolase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



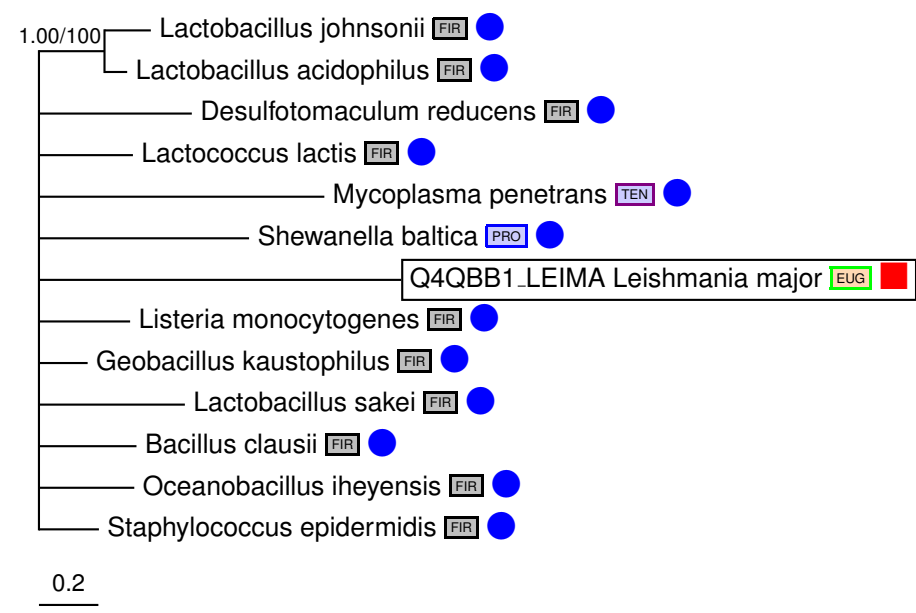
TN009

Candy accession: Q4Q9X3_LEIMA
RefSeq accession: XP_001683875.1
Uniprot accession: Q4Q9X3_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: TB, LM
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.1.1.37
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: modification methylase-like protein
Name of enzyme/protein: DNA (cytosine-5-)-methyltransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Cysteine and methionine metabolism



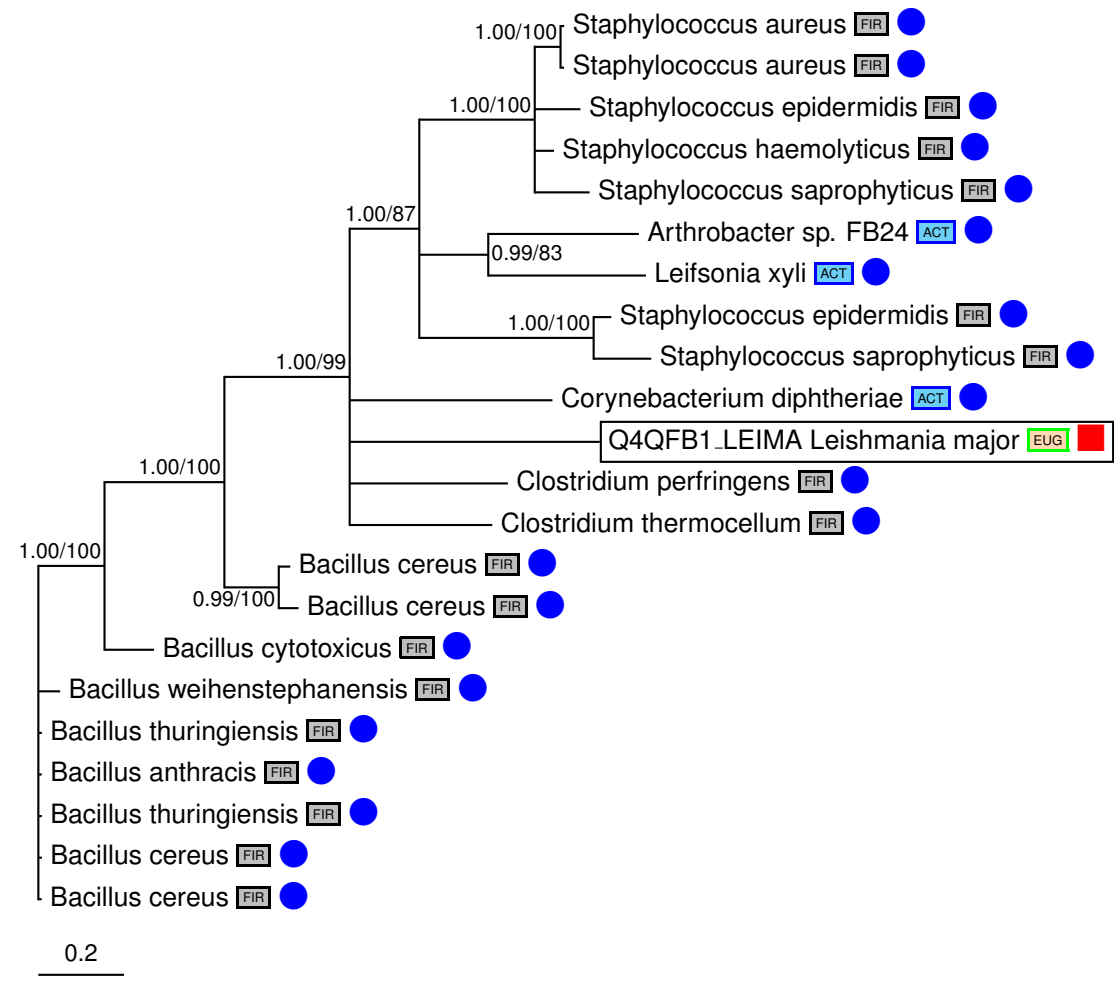
TN010

Candy accession: Q4QBB1_LEIMA
RefSeq accession: XP_001683387.1
Uniprot accession: Q4QBB1_LEIMA
Comments: LGT - LM ONLY
Species affected: LM
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:6.1.1.20
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: phenylalanyl-tRNA synthetase beta chain
KEGG PATHWAY - level 1: Translation - Genetic Information
Processing
KEGG PATHWAY - level 2: Aminoacyl-tRNA biosynthesis



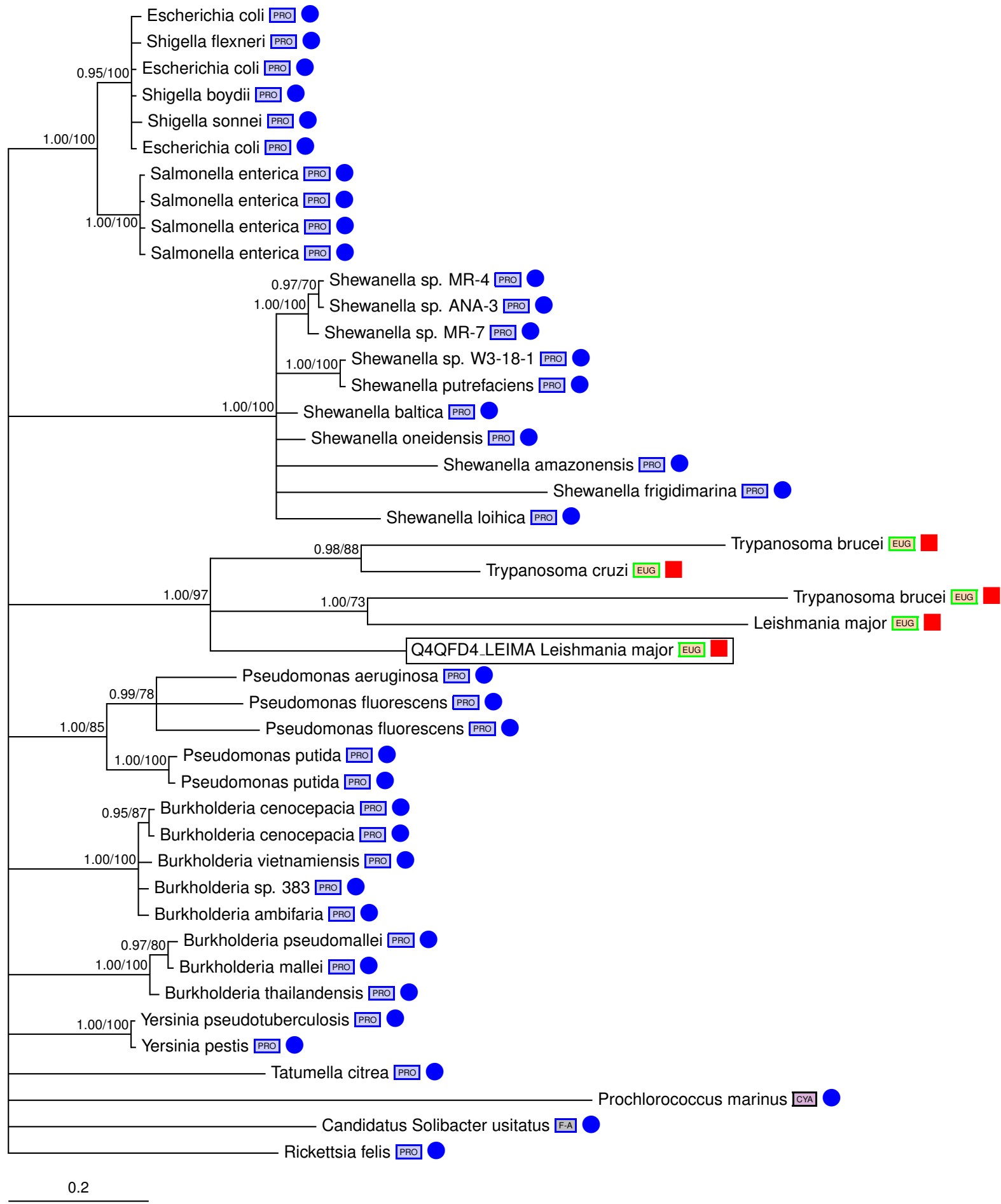
TN011

Candy accession: Q4QFB1_LEIMA
RefSeq accession: XP_001681987.1
Uniprot accession: Q4QFB1_LEIMA
Comments: LGT - LM ONLY
Species affected: LM
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 4
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF2871
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



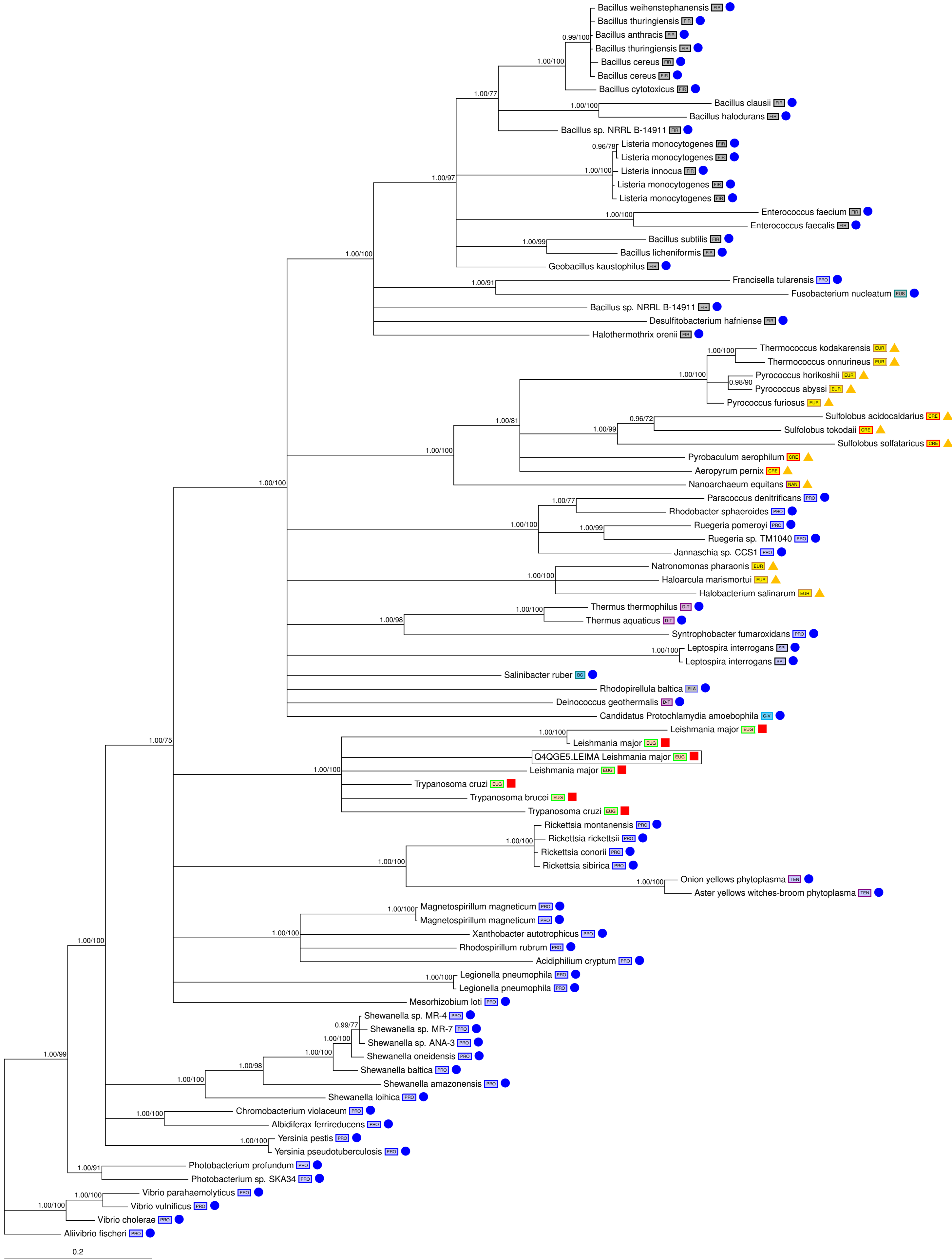
TN012

Candy accession: Q4QFD4_LEIMA
RefSeq accession: XP_001681964.1
Uniprot accession: ECOT2_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB,TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: ecotin
Name of enzyme/protein: ecotin
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



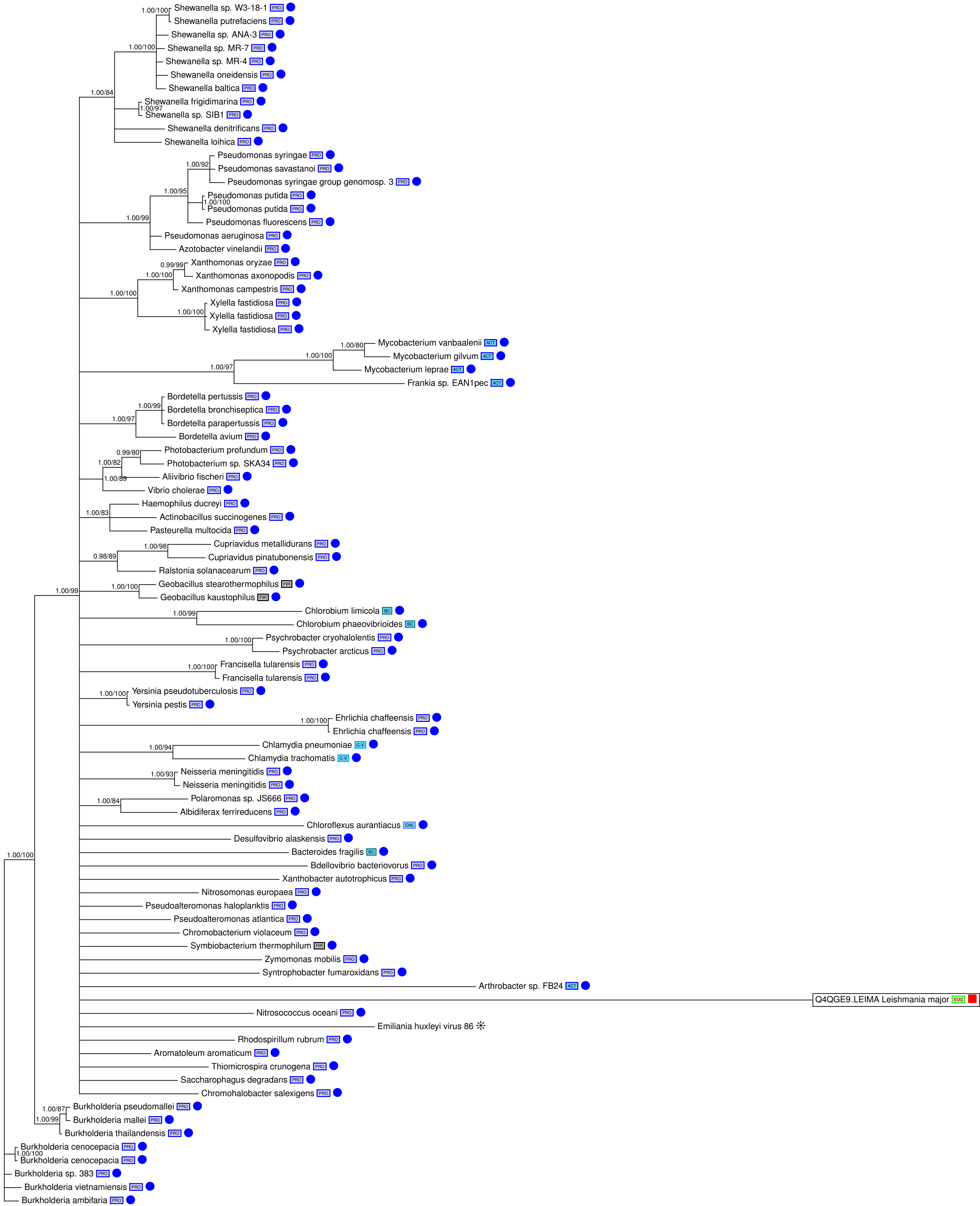
TN013

Candy accession: Q4QGE5_LEIMA
RefSeq accession: XP_001681753.1
Uniprot accession: Q4QGE5_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB,TC
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:3.4.17.19
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: carboxypeptidase; metallo-peptidase, Clan MA(E), family 32
Name of enzyme/protein: Metallo-peptidase, Clan MA(E), family 32
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



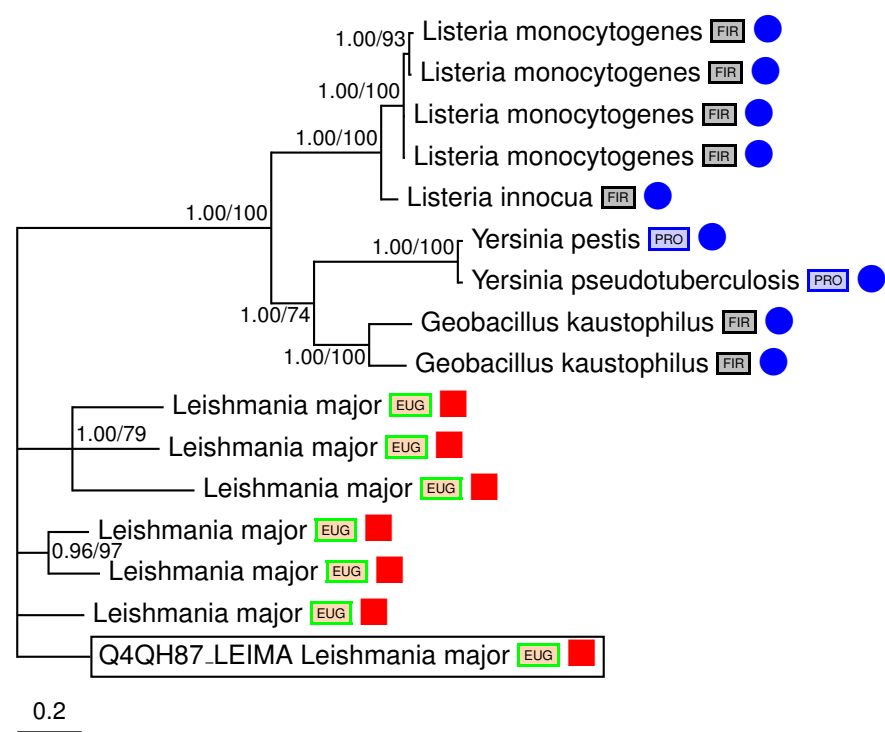
TN014

Candy accession: Q4QGE9_LEIMA
RefSeq accession: XP_001681749.1
Uniprot accession: Q4QGE9_LEIMA
Comments: LGT - LM ONLY
Species affected: LM
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:3.1.26.4
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: ribonuclease hii
Name of enzyme/protein: ribonuclease HII
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



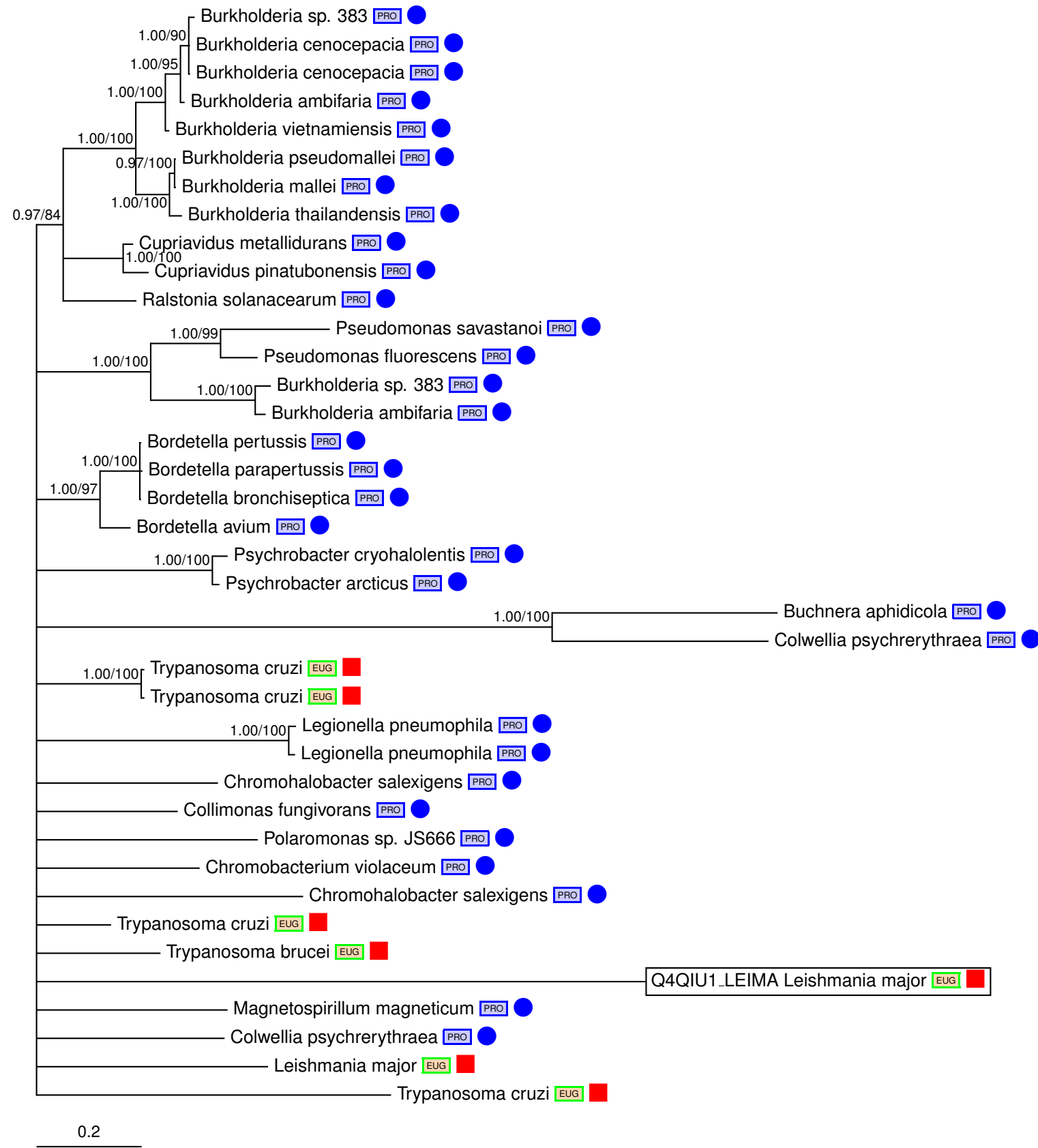
TN015

Candy accession: Q4QH87_LEIMA
RefSeq accession: XP_001681461.1
Uniprot accession: Q4QH87_LEIMA
Comments: LGT - LM ONLY
Species affected: LM
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF1861
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



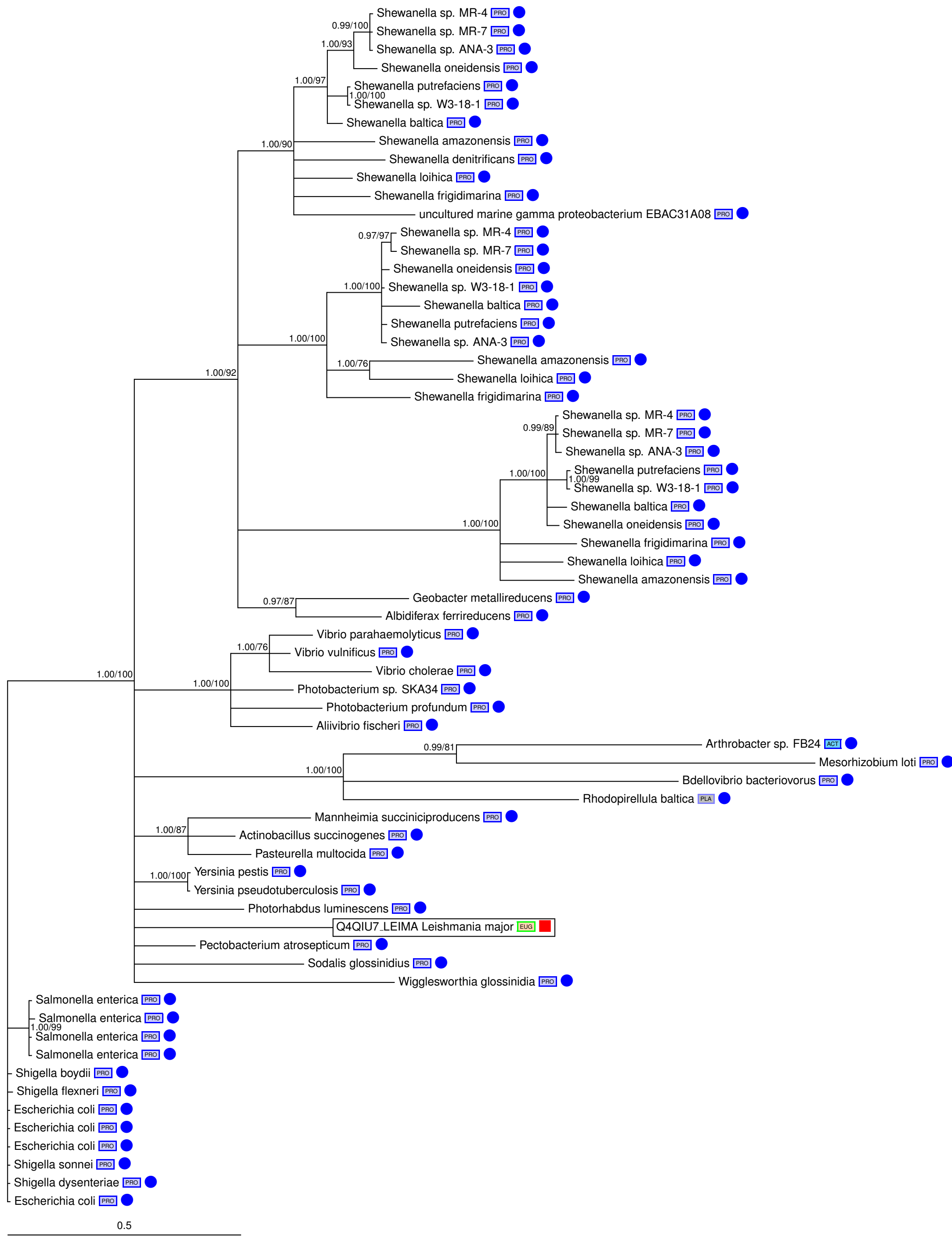
TN016

Candy accession: Q4QIU1_LEIMA
RefSeq accession: XP_001680907.1
Uniprot accession: Q4QIU1_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB,TC
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:3.5.1.16
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: acetylornithine deacetylase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism



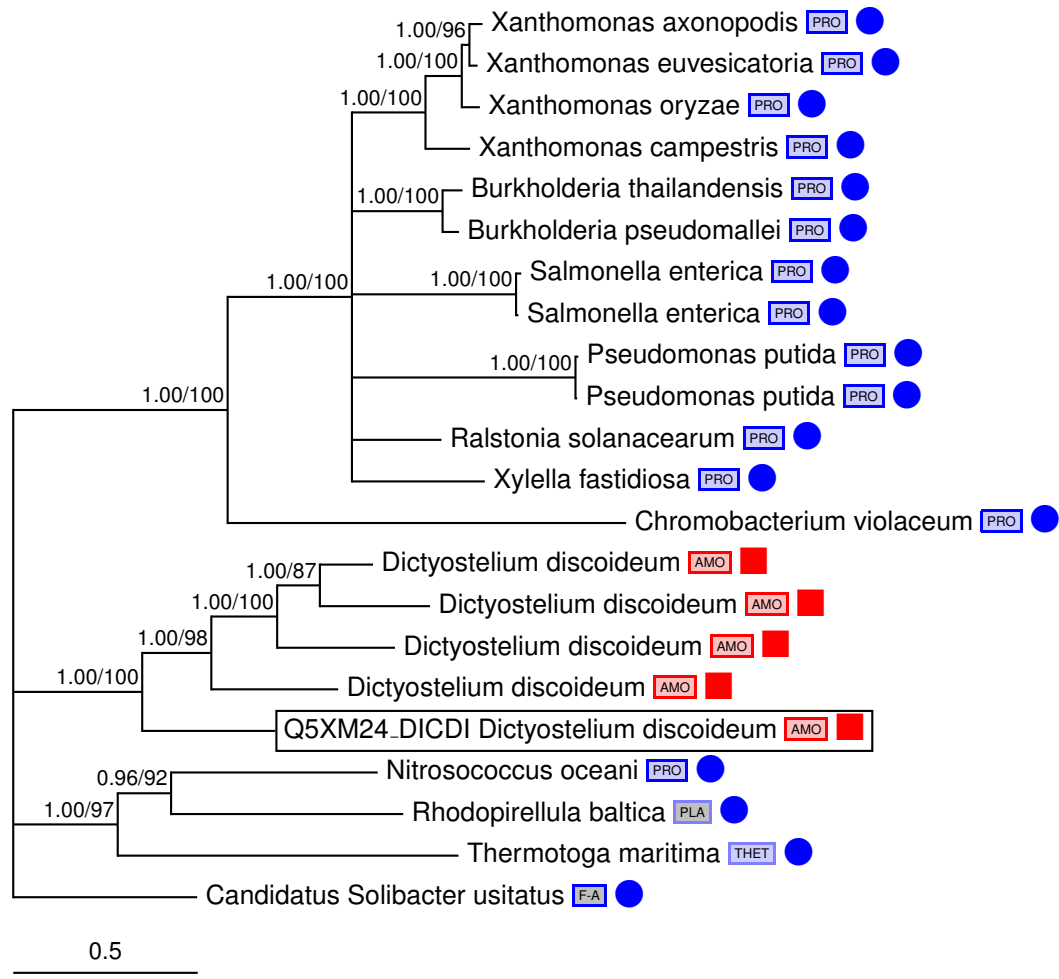
TN017

Candy accession: Q4QIU7_LEIMA
RefSeq accession: XP_001680901.1
Uniprot accession: Q4QIU7_LEIMA
Comments: LGT - LM ONLY
Species affected: LM
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:1.3.3.4
PHOBIOUS SP: 0
PHOBIOUS TMD: 1
RefSeq annotation: protoporphyrinogen oxidase-like protein
Name of enzyme/protein: protoporphyrinogen oxidase
KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Porphyrin and chlorophyll metabolism



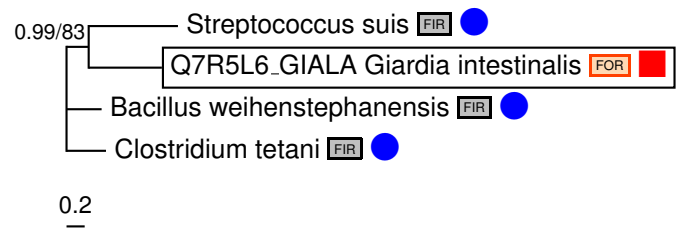
TN018

Candy accession: Q5XM24_DICDI
RefSeq accession: XP_640566.1
Uniprot accession: APRA_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: PhoPQ-activated pathogenicity-related protein
Name of enzyme/protein: PhoPQ-activated pathogenicity-related protein
KEGG PATHWAY - level 1: Other function - Signal Transduction
KEGG PATHWAY - level 2: na



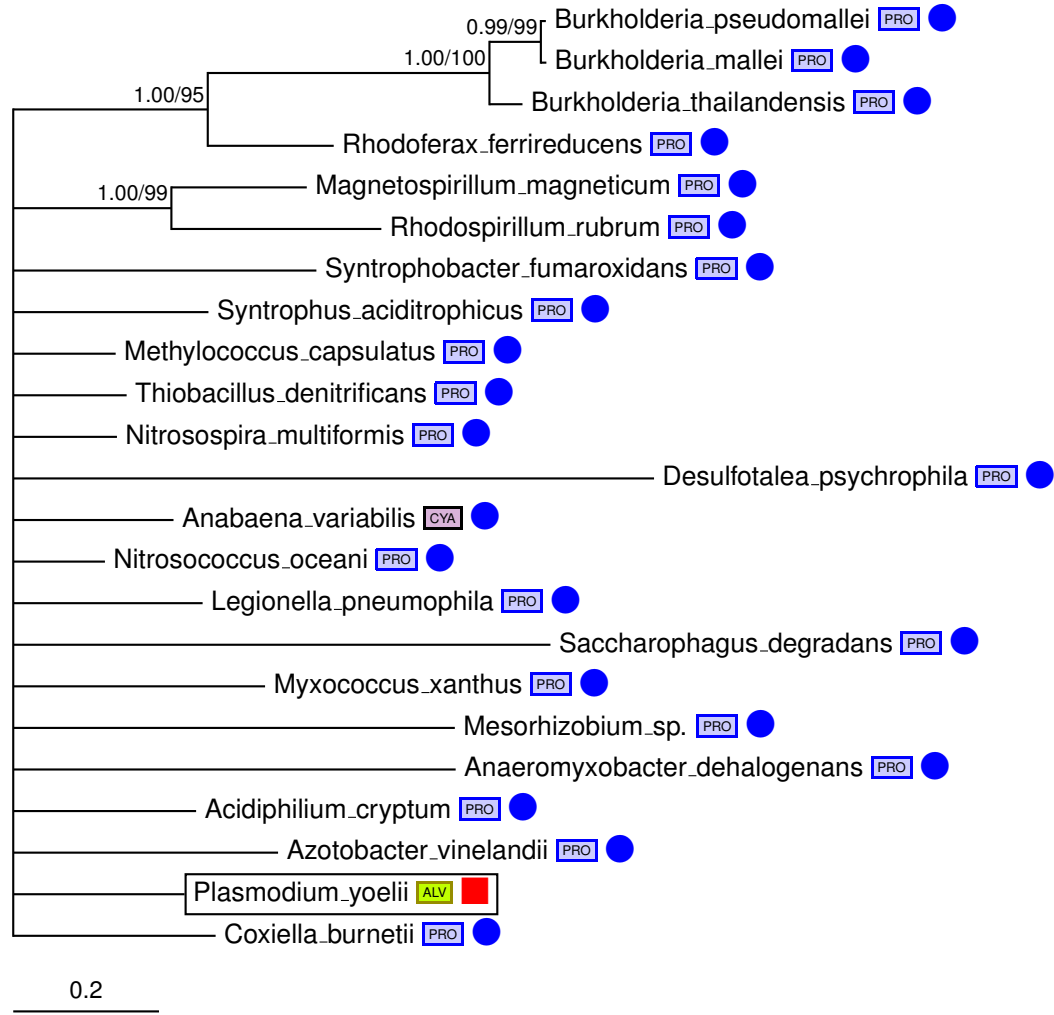
TN019

Candy accession: Q7R5L6_GIALA
RefSeq accession: XP_001707536.1
Uniprot accession: A8BDW4_GIALA
Comments: LGT - GI ONLY
Species affected: GI
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Transglutaminase/protease, putative
Name of enzyme/protein: Transglutaminase/protease, putative
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



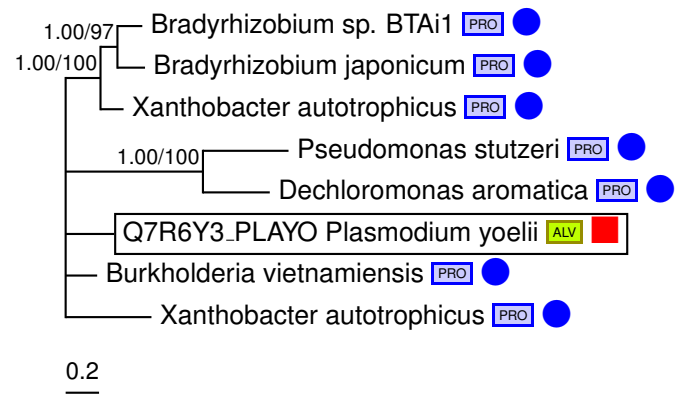
TN020

Candy accession: Q7R6X5_PLAY0
RefSeq accession: XP_728783.1
Uniprot accession: Q7R6X5_PLAY0
Comments: LGT - PY ONLY
Species affected: PY
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Putative ribosomal subunit interface protein; sigma-54 modulation protein family
KEGG PATHWAY - level 1: Other function - Genetic Information Processing
KEGG PATHWAY - level 2: na



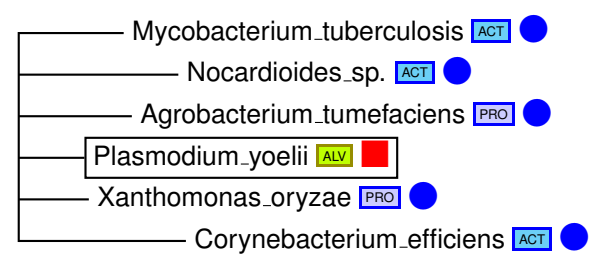
TN021

Candy accession: Q7R6Y3_PLAYO
RefSeq accession: XP_728775.1
Uniprot accession: Q7R6Y3_PLAYO
Comments: LGT - PY ONLY
Species affected: PY
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Hypothetical protein
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



TN022

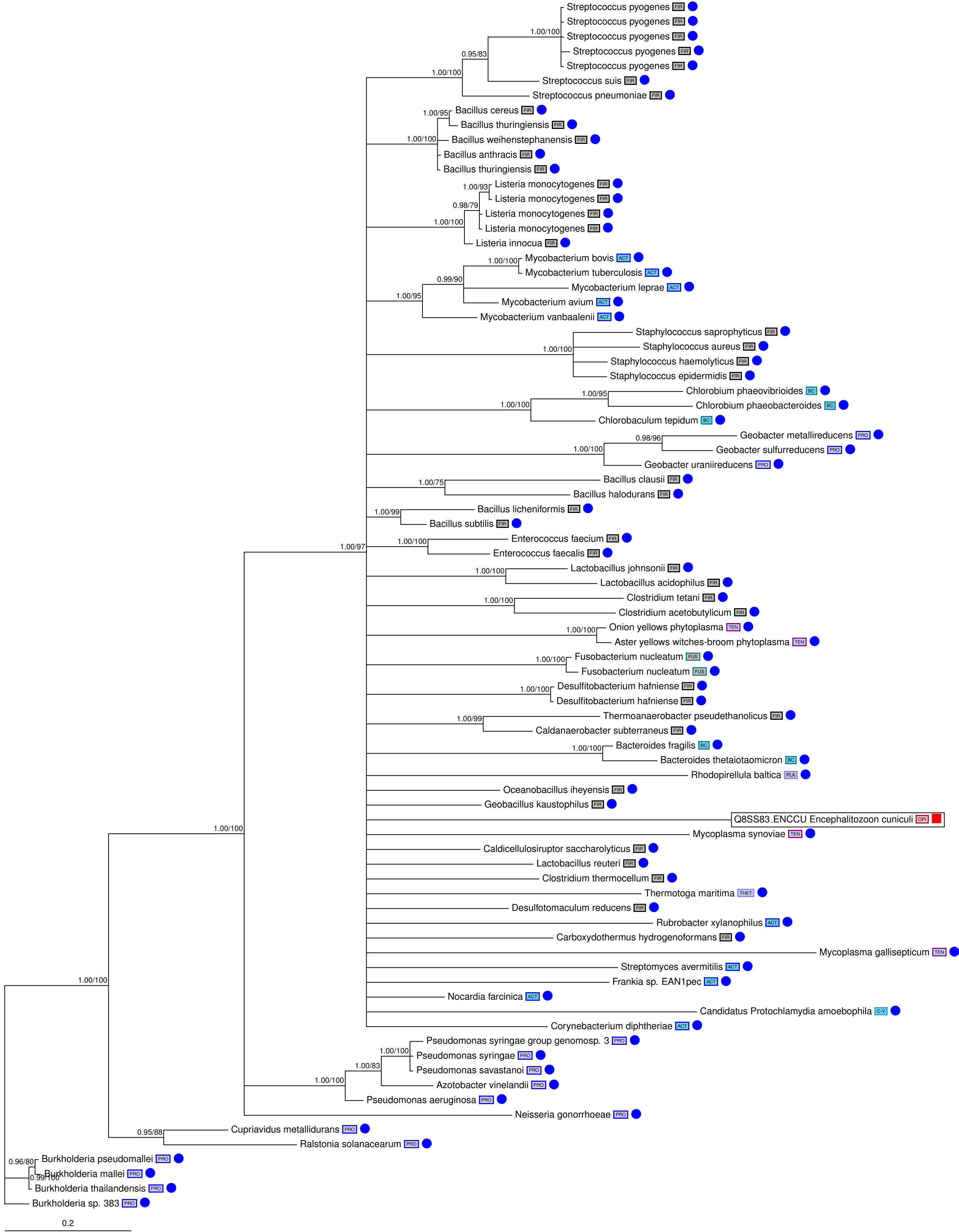
Candy accession: Q7R799_PLAY0
RefSeq accession: XP_728635.1
Uniprot accession: Q7R799_PLAY0
Comments: LGT - PY ONLY
Species affected: PY
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF2699
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



0.2

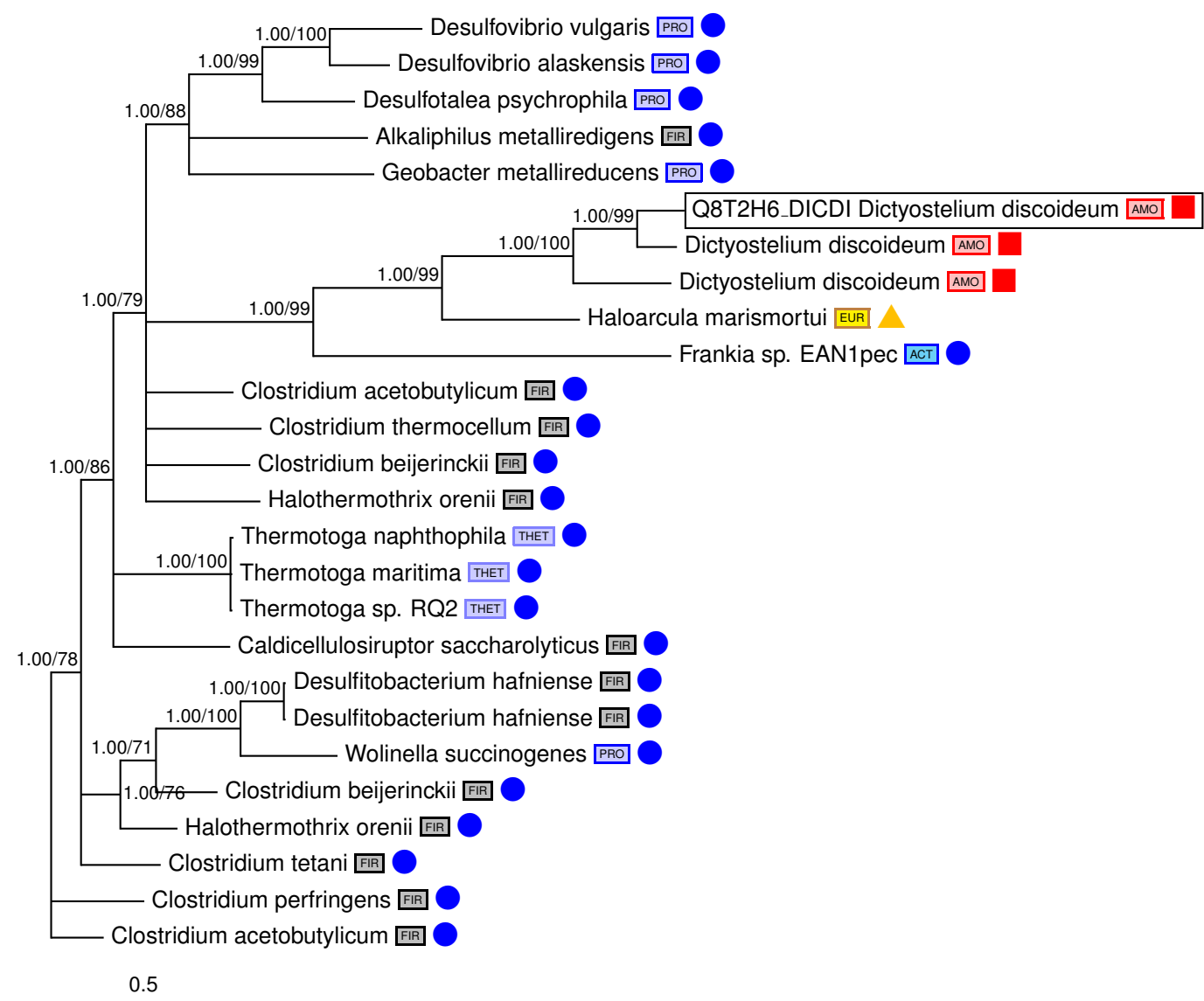
TN023

Candy accession: Q8SS83_ENCCU
RefSeq accession: NP_597635.1
Uniprot accession: KCY_ENCCU
Comments: LGT - EC ONLY
Species affected: EC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.7.4.14
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: CYTIDYLATE KINASE
Name of enzyme/protein: cytidylate kinase
KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins, Metabolism of Other Amino Acids, Nucleotide Metabolism
KEGG PATHWAY - level 2: Pyrimidine metabolism, beta-Alanine metabolism



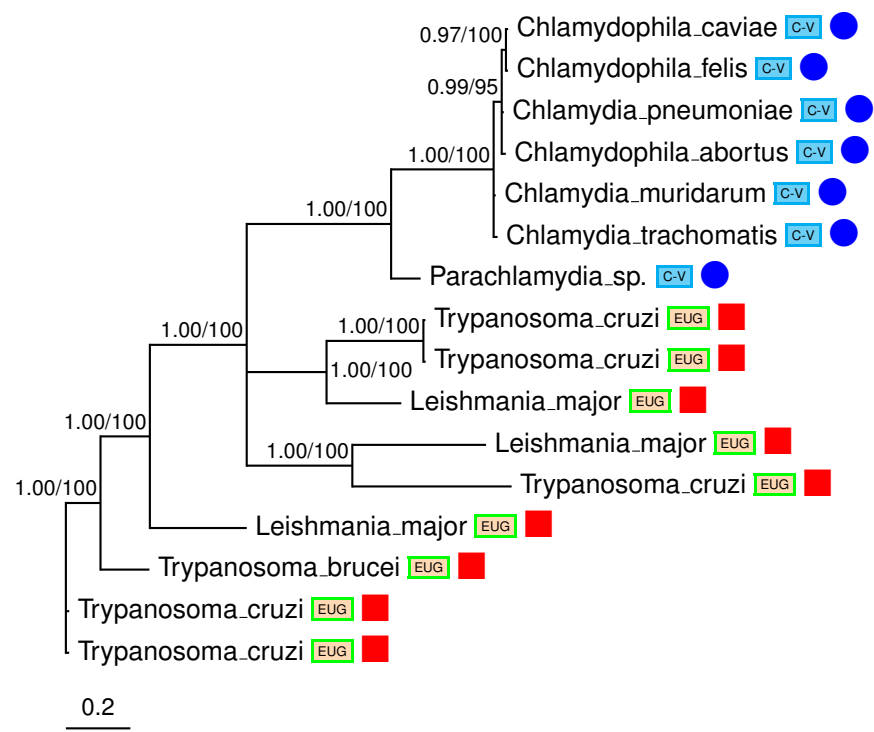
TN024

Candy accession: Q8T2H6_DICDI
RefSeq accession: XP_642591.1
Uniprot accession: Q8T2H6_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Achraea - Haloarcula
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0277409
Name of enzyme/protein: Protein containing DUF162
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



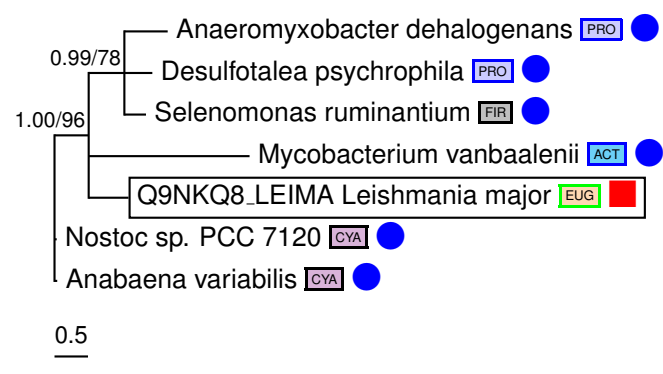
TN025

Candy accession: Q9BHG3_LEIMA
RefSeq accession: XP_001685059.1
Uniprot accession: Q9BHG3_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY - THE PROTEINS
POSSESS THE BACTERIAL CEST DOMAIN HENCE
IT IS CONSIDERED AS A CANDIDATE B->E LGT
Species affected: LM,TB,TC
Adjacent taxa in tree: Chlamydiae/Verrucomicrobia
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Secretion chaperone CesT
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na



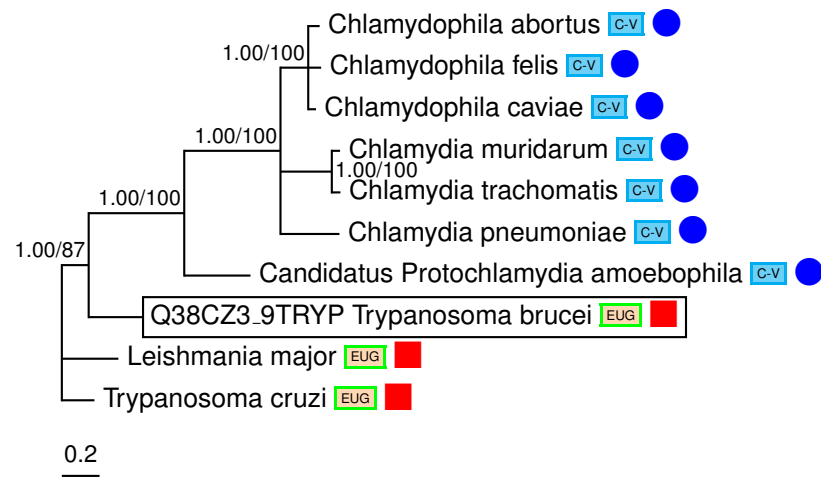
TN026

Candy accession: Q9NKKQ8_LEIMA
RefSeq accession: XP_001687362.1
Uniprot accession: Q9NKKQ8_LEIMA
Comments: LGT - LM ONLY
Species affected: LM
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:4.2.1.75
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: uroporphyrinogen-III synthase
KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Porphyrin and chlorophyll metabolism



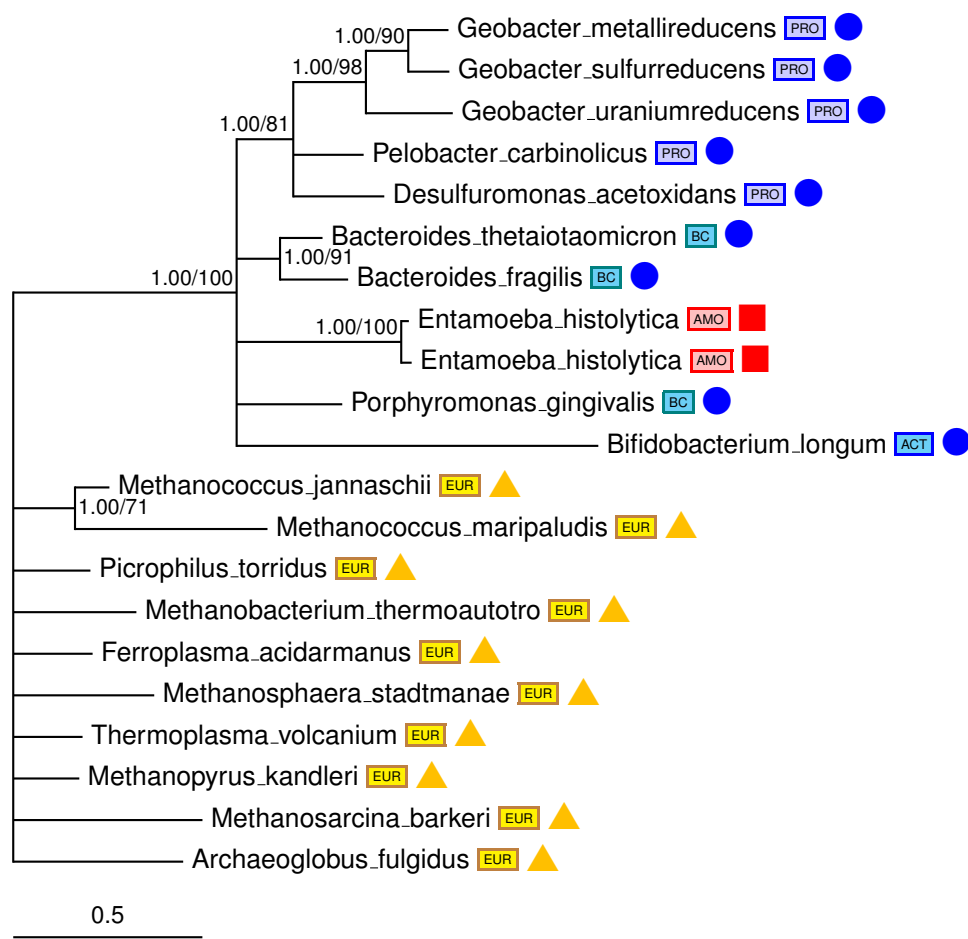
TN027

Candy accession: Q38CZ3_9TRYP
RefSeq accession: XP_827657.1
Uniprot accession: Q38CZ3_9TRYP
Comments: LGT - KINETOPLASTIDS ONLY - ADDITIONAL
BACTERIA TAXA ARE RECOVERED BUT
COREPSOND TO MUCH WEAKER HITS HENCE IT
IS CONSIDERED AS A CANDIDATE B->E LGT
Species affected: LM,TB,TC
Adjacent taxa in tree: Chlamydiae/Verrucomicrobia
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted Rossmann fold nucleotide-
binding protein
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na



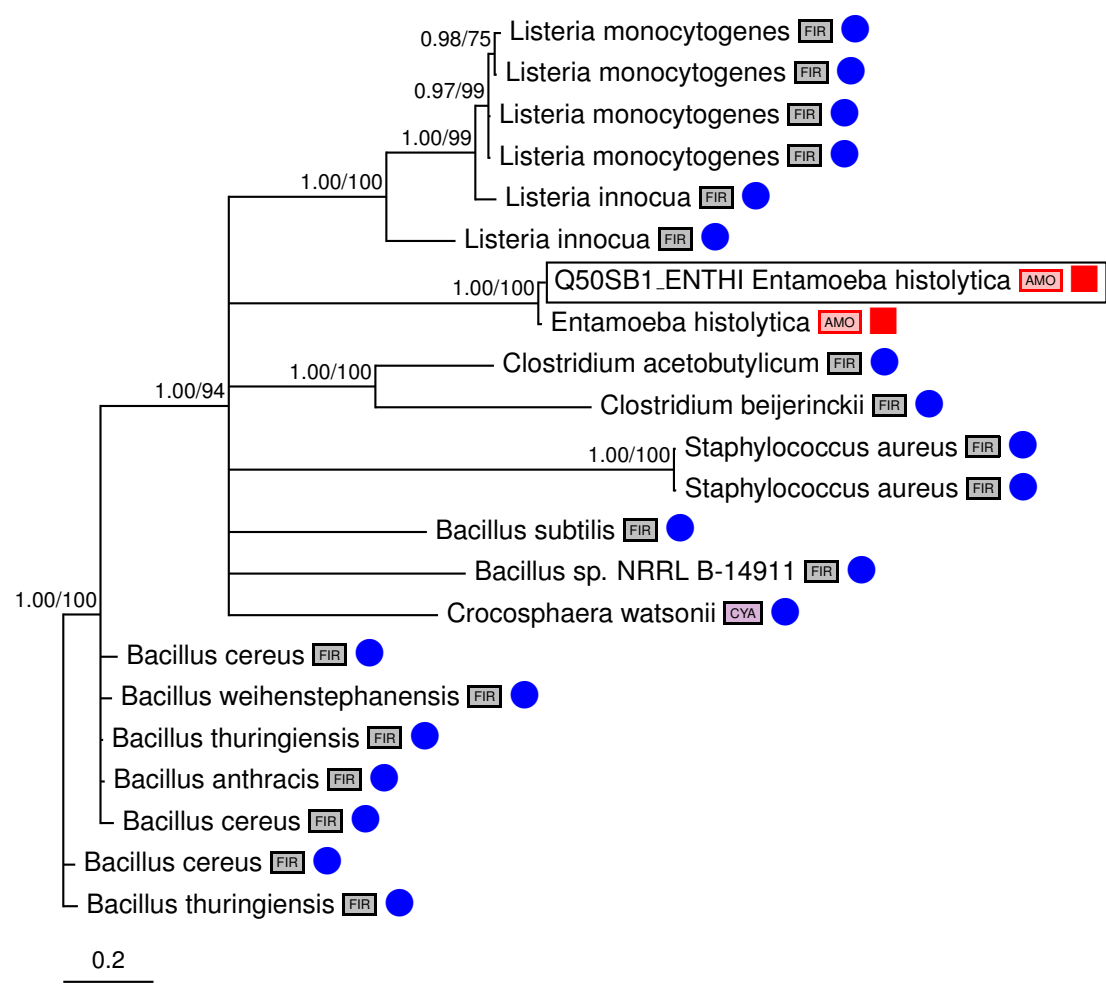
TN028

Candy accession: Q50LR6_ENTHI
RefSeq accession: XP_650165.1
Uniprot accession: C4MAL3_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted tRNA 2'-O-methylase; Predicted
HD superfamily hydrolase
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na



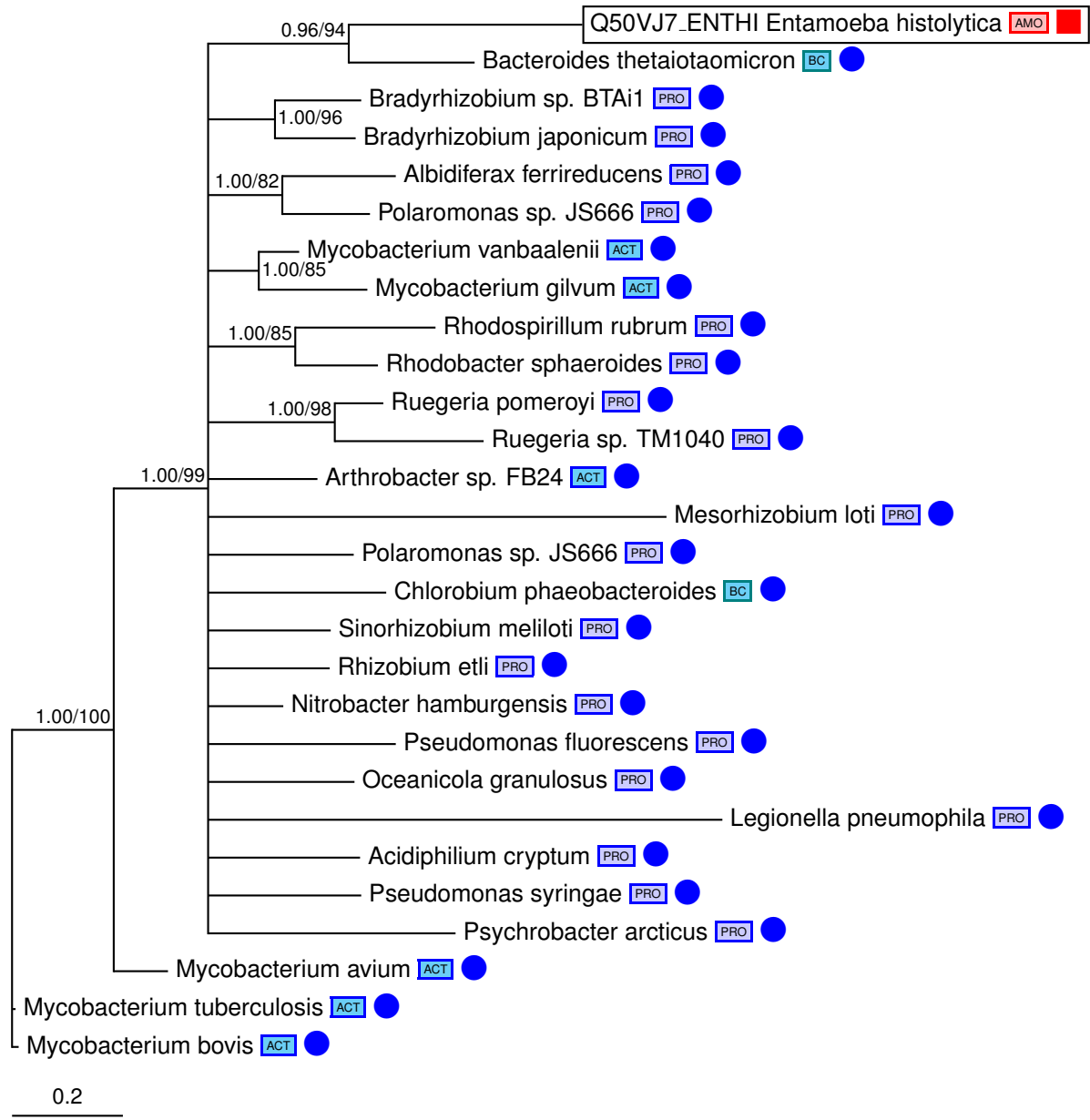
TN029

Candy accession: Q50SB1_ENTHI
RefSeq accession: XP_649873.2
Uniprot accession: C4M1J6_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF1963
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



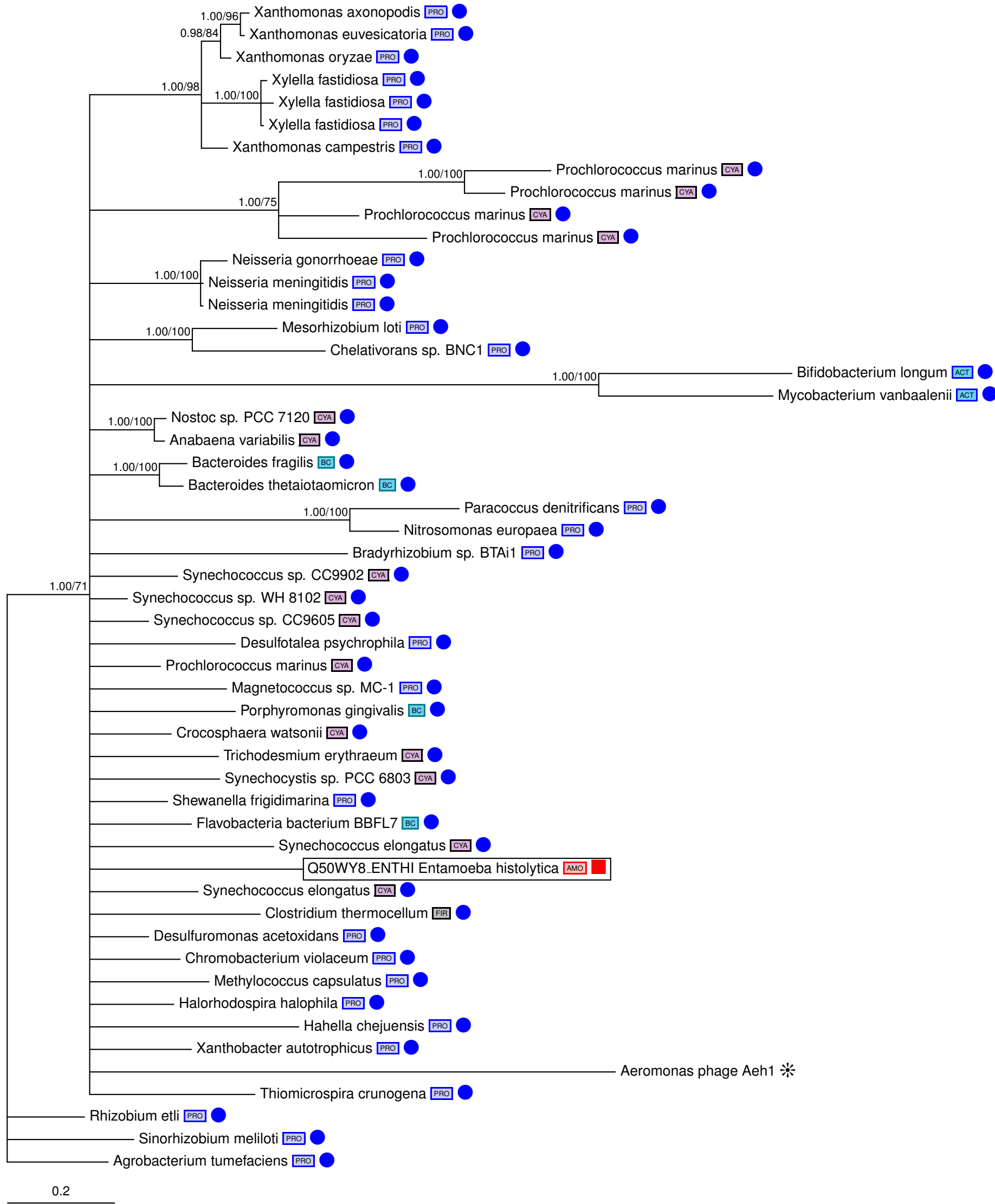
TN030

Candy accession: Q50VJ7_ENTHI
RefSeq accession: XP_651004.1
Uniprot accession: C4MBP5_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Bacteroides
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF1810
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



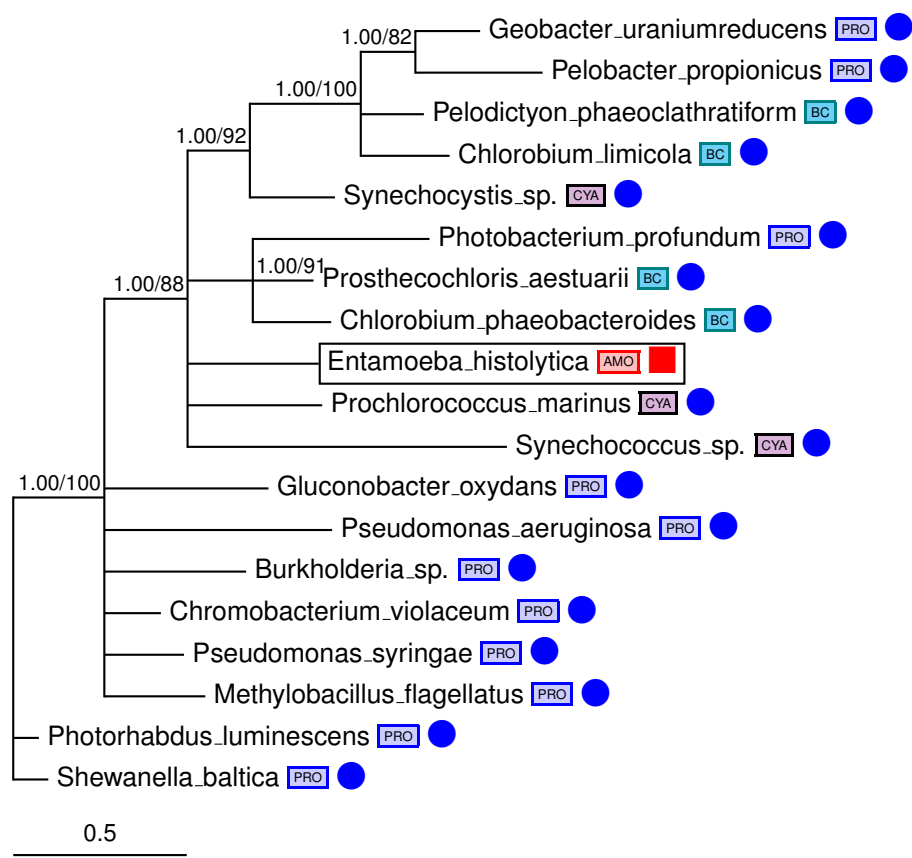
TN031

Candy accession: Q50WY8_ENTHI
RefSeq accession: XP_651498.1
Uniprot accession: C4M560_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:4.6.1.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: adenylate cyclase
KEGG PATHWAY - level 1: Nucleotide Metabolism, Signal Transduction
KEGG PATHWAY - level 2: Purine metabolism - several other entries



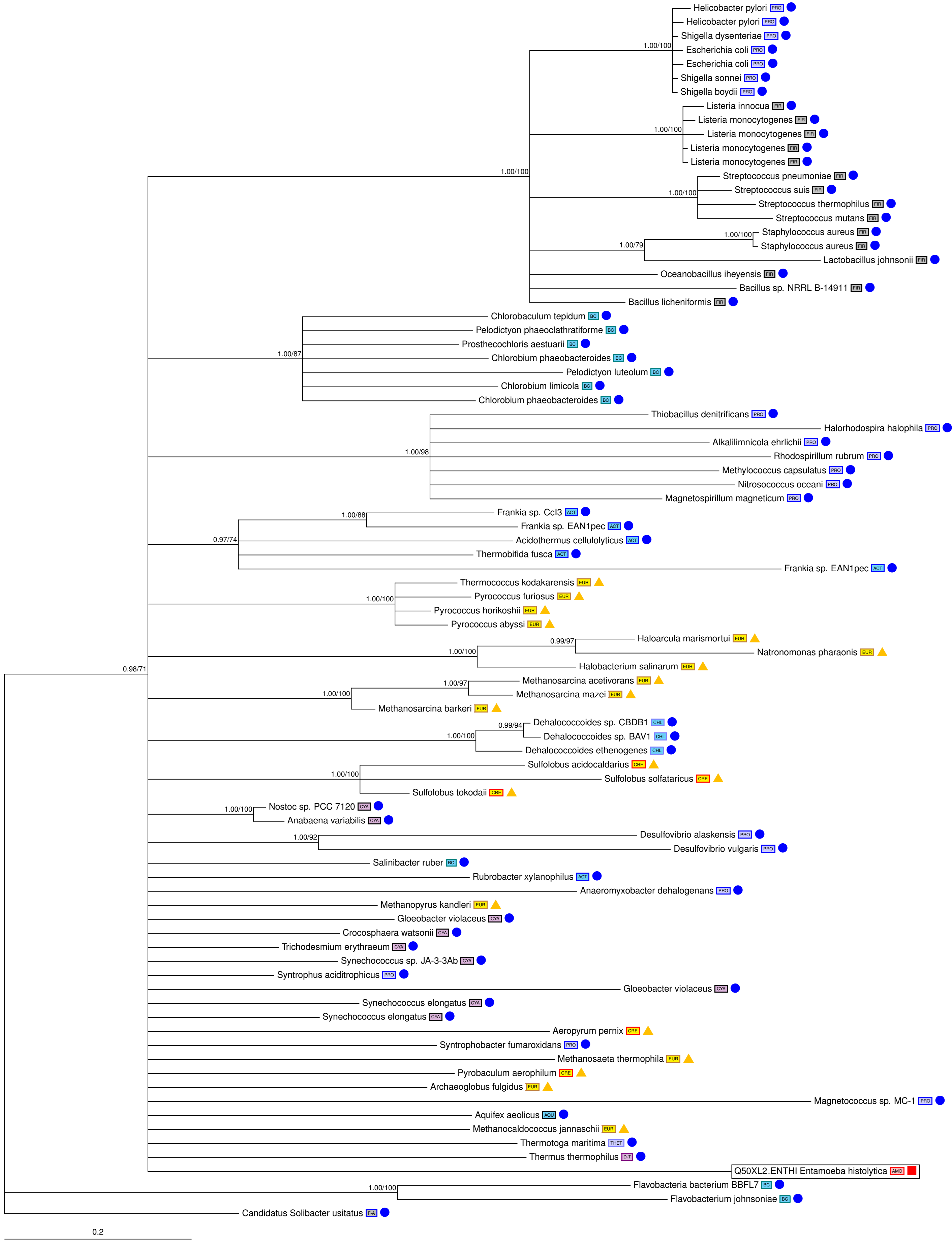
TN032

Candy accession: Q50XL0_ENTHI
RefSeq accession: XP_651699.1
Uniprot accession: C4MOV4_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing cupin-like fold and
unknown function
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



TN033

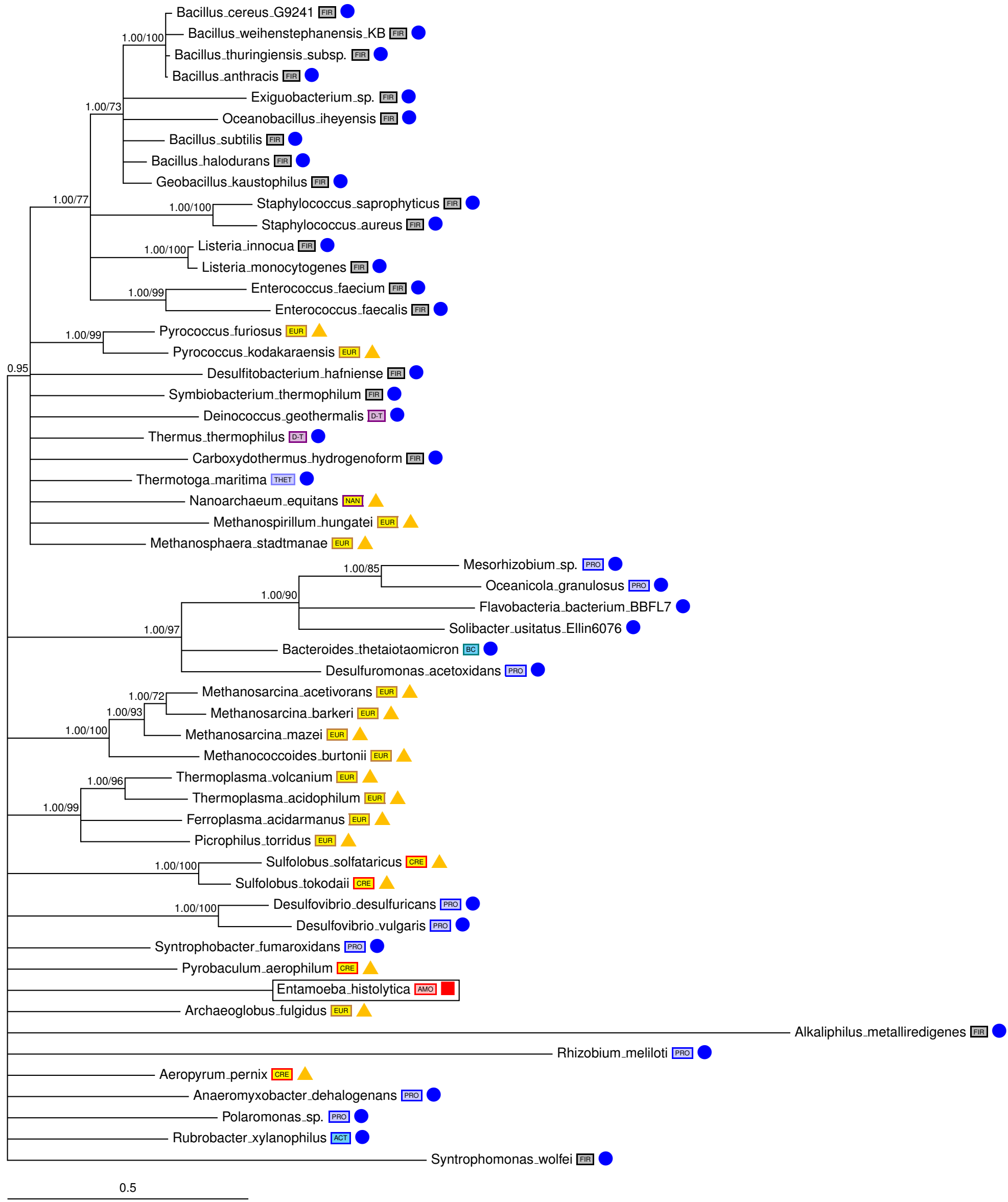
Candy accession: Q50XL2_ENTHI
RefSeq accession: XP_651697.1
Uniprot accession: C4MOV6_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted S-adenosyl-l-methionine
hydroxide adenosyltransferase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



0.2

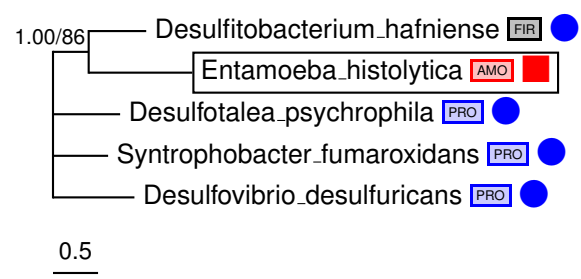
TN034

Candy accession: Q50YL9_ENTHI
RefSeq accession: XP_652065.1
Uniprot accession: C4M2I8_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: metal dependent hydrolase
Name of enzyme/protein: Predicted metal dependent hydrolase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



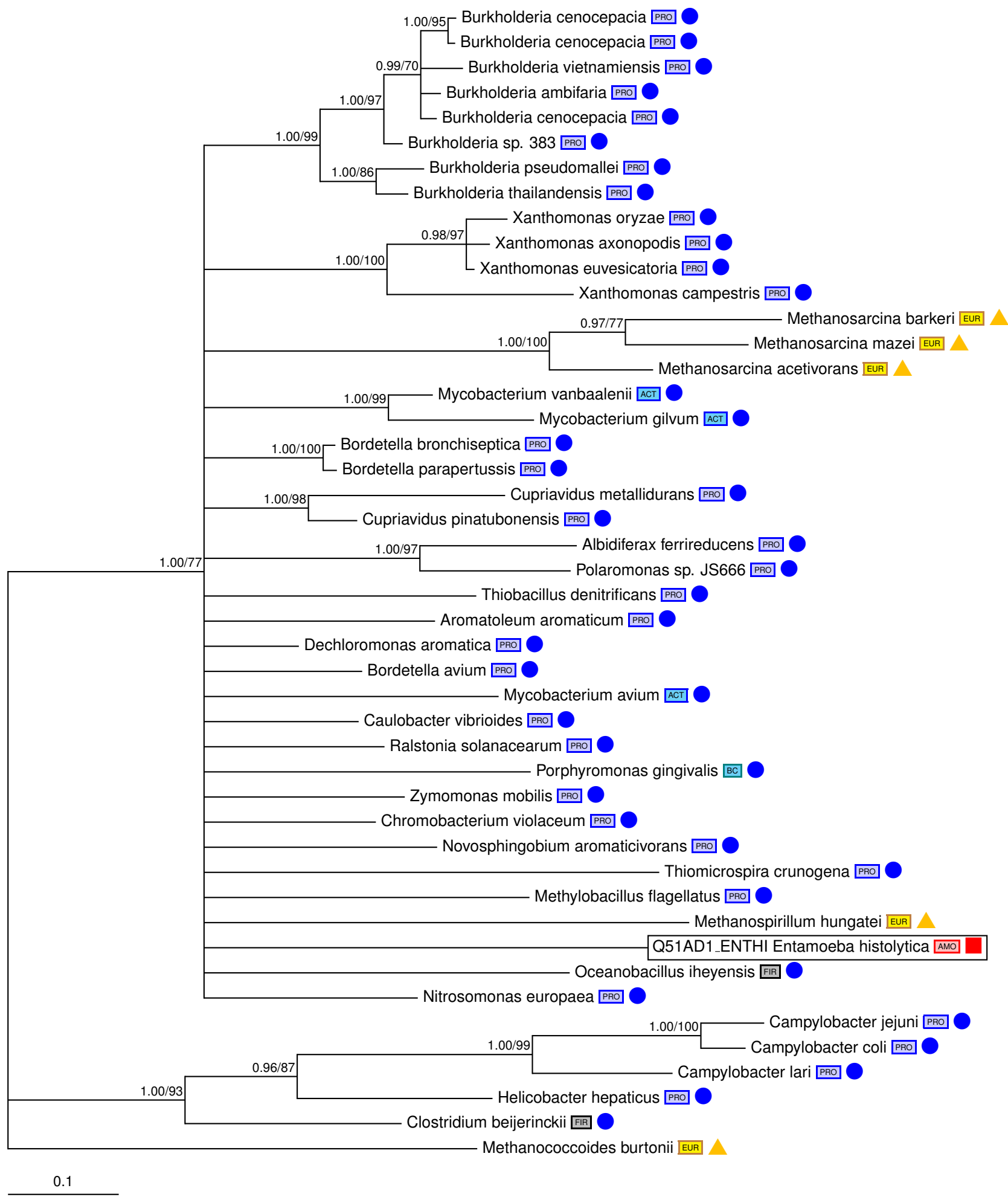
TN035

Candy accession: Q50YZ1_ENTHI
RefSeq accession: XP_652209.1
Uniprot accession: C4M3K4_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing uncharacterized domain HDIG
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



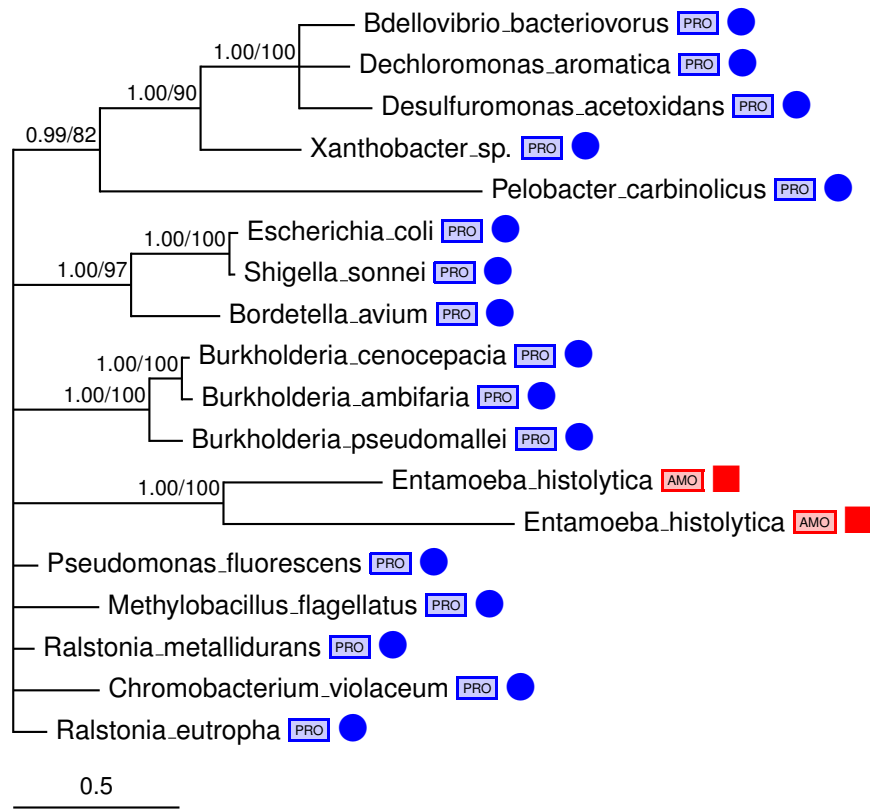
TN036

Candy accession: Q51AD1_ENTHI
RefSeq accession: XP_655177.1
Uniprot accession: C4LWRO_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted Mug G:T/U mismatch-specific
DNA glycosylase
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na



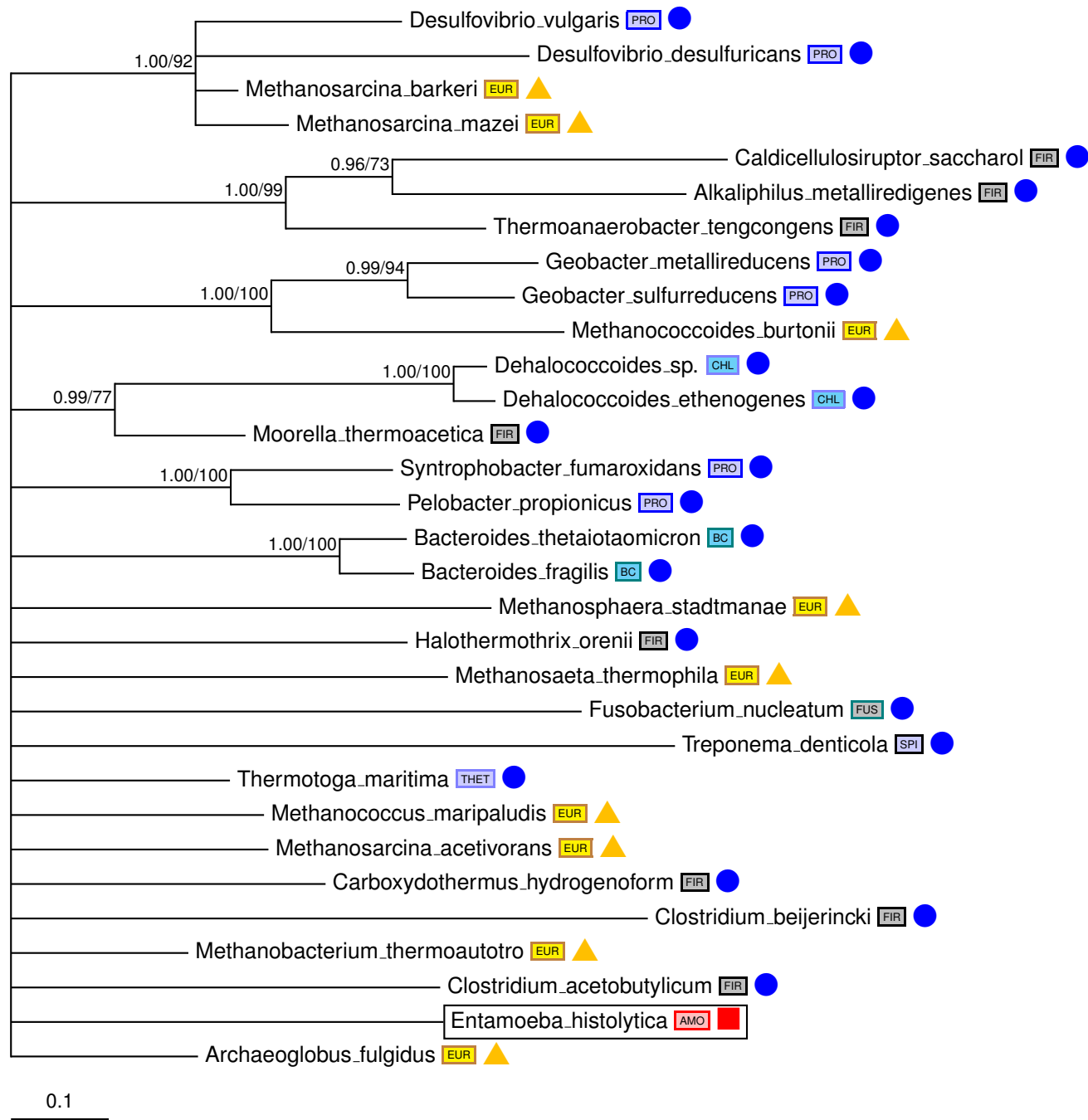
TN037

Candy accession: Q51AD5_ENTHI
RefSeq accession: XP_655200.1
Uniprot accession: C4LWQ7_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted flavoprotein, FMN binding,
electron transport
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



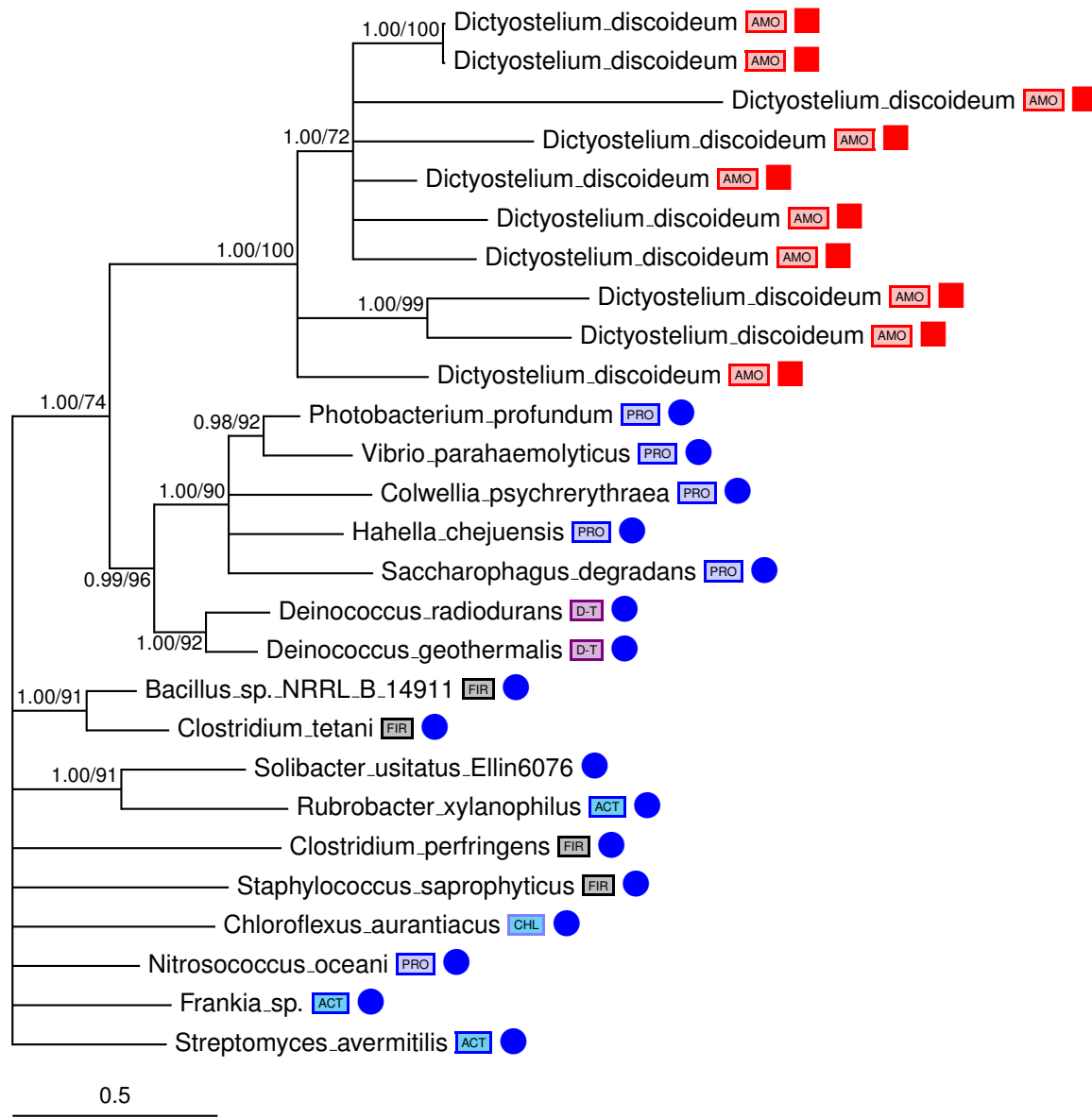
TN038

Candy accession: Q51DS8_ENTHI
RefSeq accession: XP_656375.1
Uniprot accession: C4LSD2_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:1.-.-.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: nitroreductase family protein
Name of enzyme/protein: nitroreductase family protein
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



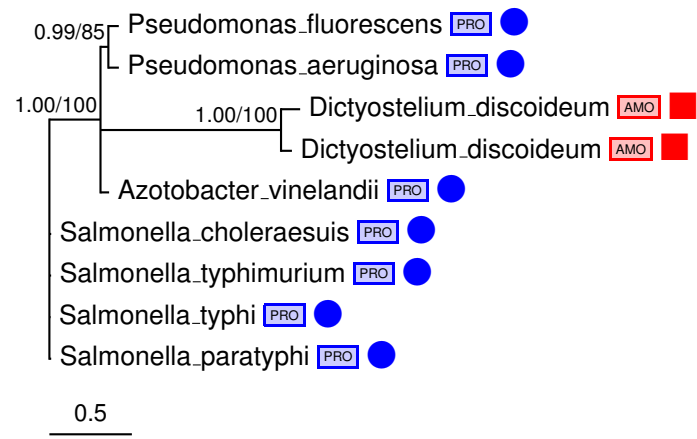
TN039

Candy accession: Q54DG5_DICDI
RefSeq accession: XP_629676.1
Uniprot accession: Q54DG5_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Protobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 1
RefSeq annotation: hypothetical protein DDB_G0292288
Name of enzyme/protein: Uncharacterized protein with SCP/PR1 domains
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



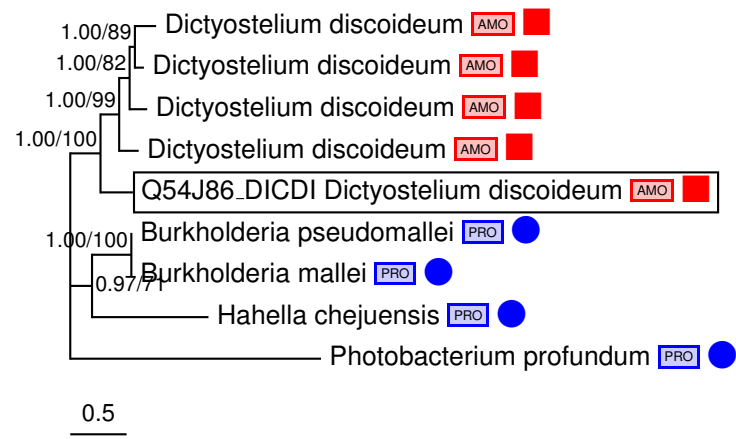
TN040

Candy accession: Q54I75_DICDI
RefSeq accession: XP_636504.1
Uniprot accession: Q54I75_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Protobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0288943
Name of enzyme/protein: Protein containing DUF796
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



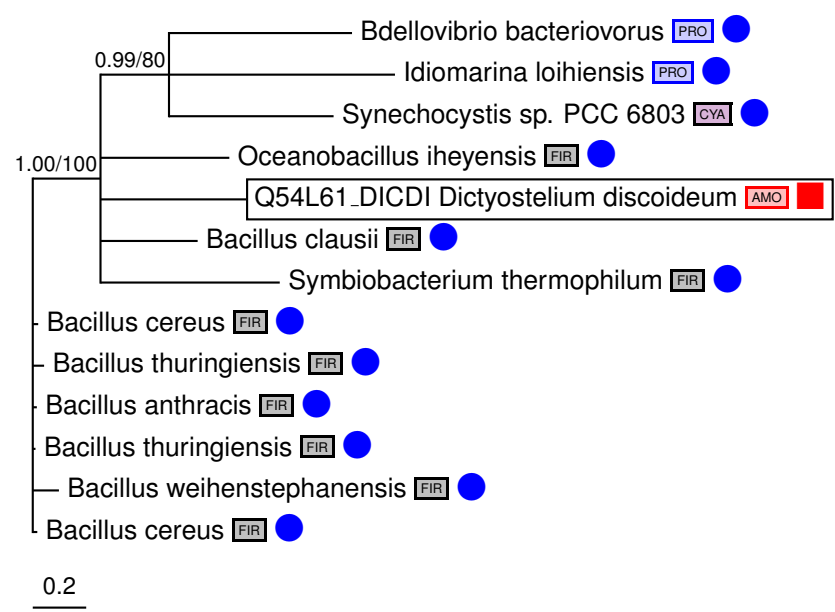
TN041

Candy accession: Q54J86_DICDI
RefSeq accession: XP_636850.1
Uniprot accession: DTML1_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0288219
Name of enzyme/protein: Protein containing peptidase M66 domain
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



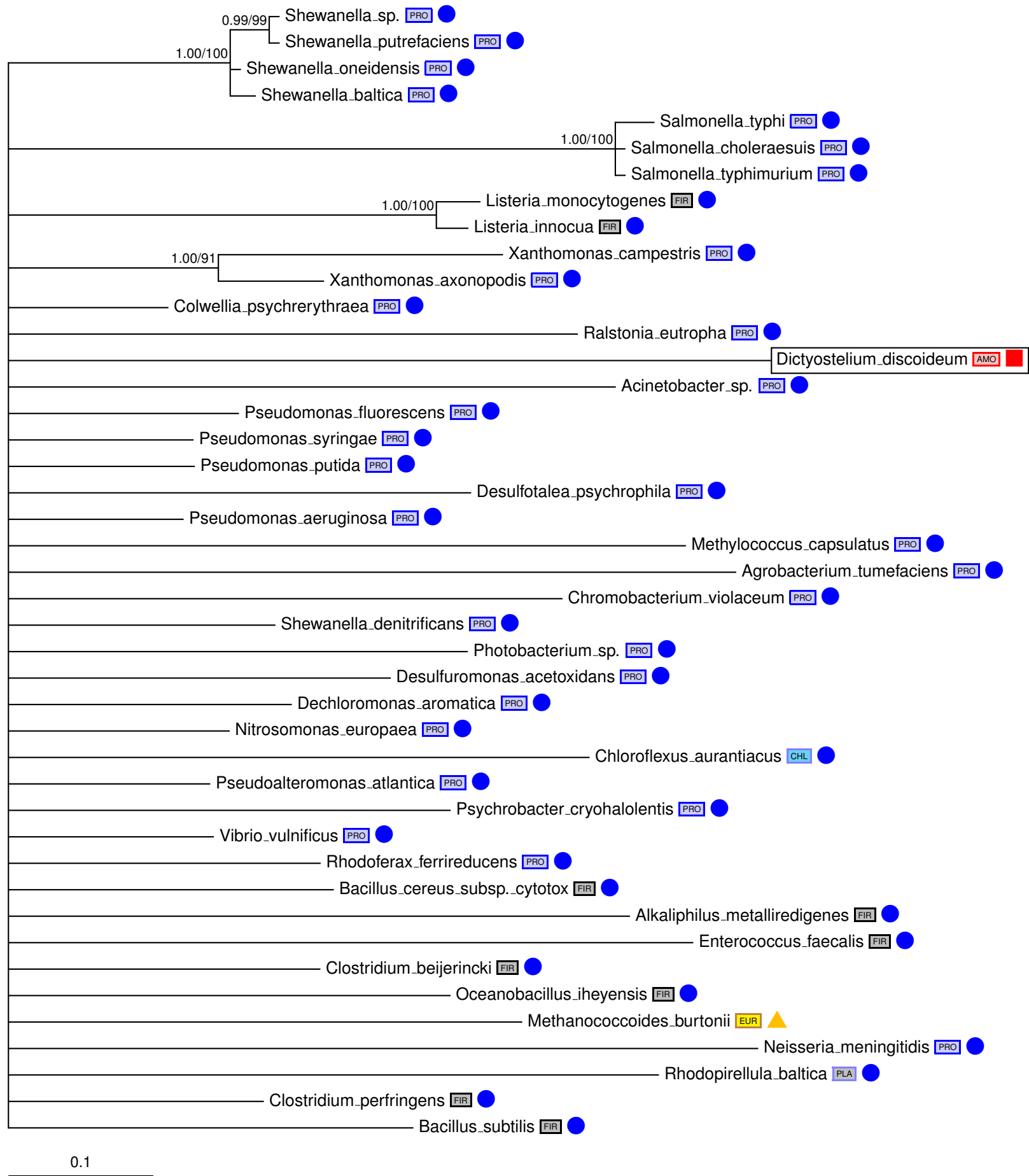
TN042

Candy accession: Q54L61_DICDI
RefSeq accession: XP_637502.1
Uniprot accession: Q54L61_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0286879
Name of enzyme/protein: Hypothetical protein
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



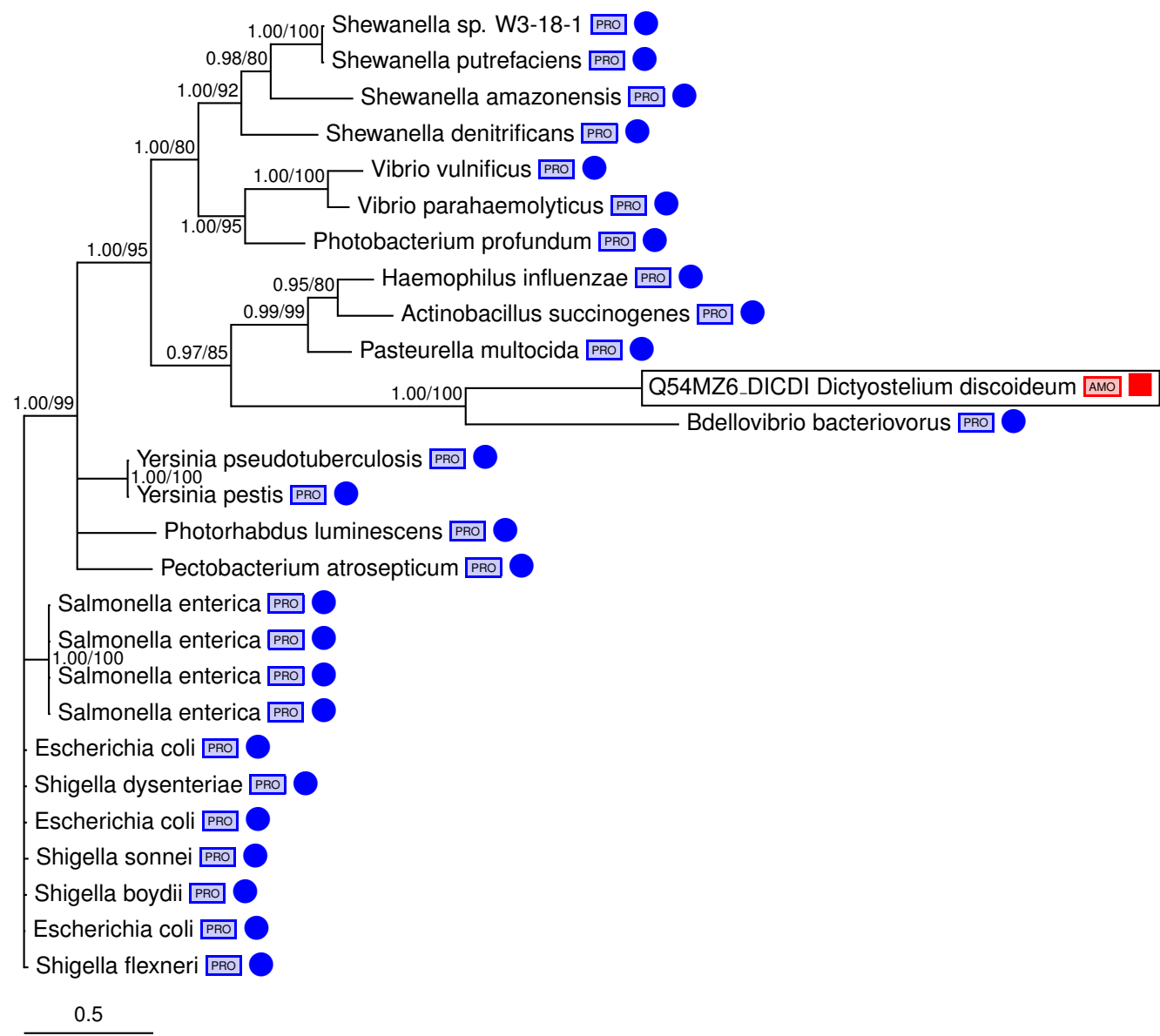
TN043

Candy accession: Q54MN5_DICDI
RefSeq accession: XP_638042.1
Uniprot accession: Q54MN5_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 3
RefSeq annotation: hypothetical protein DDB_G0285825
Name of enzyme/protein: Protein containing DUF1294
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



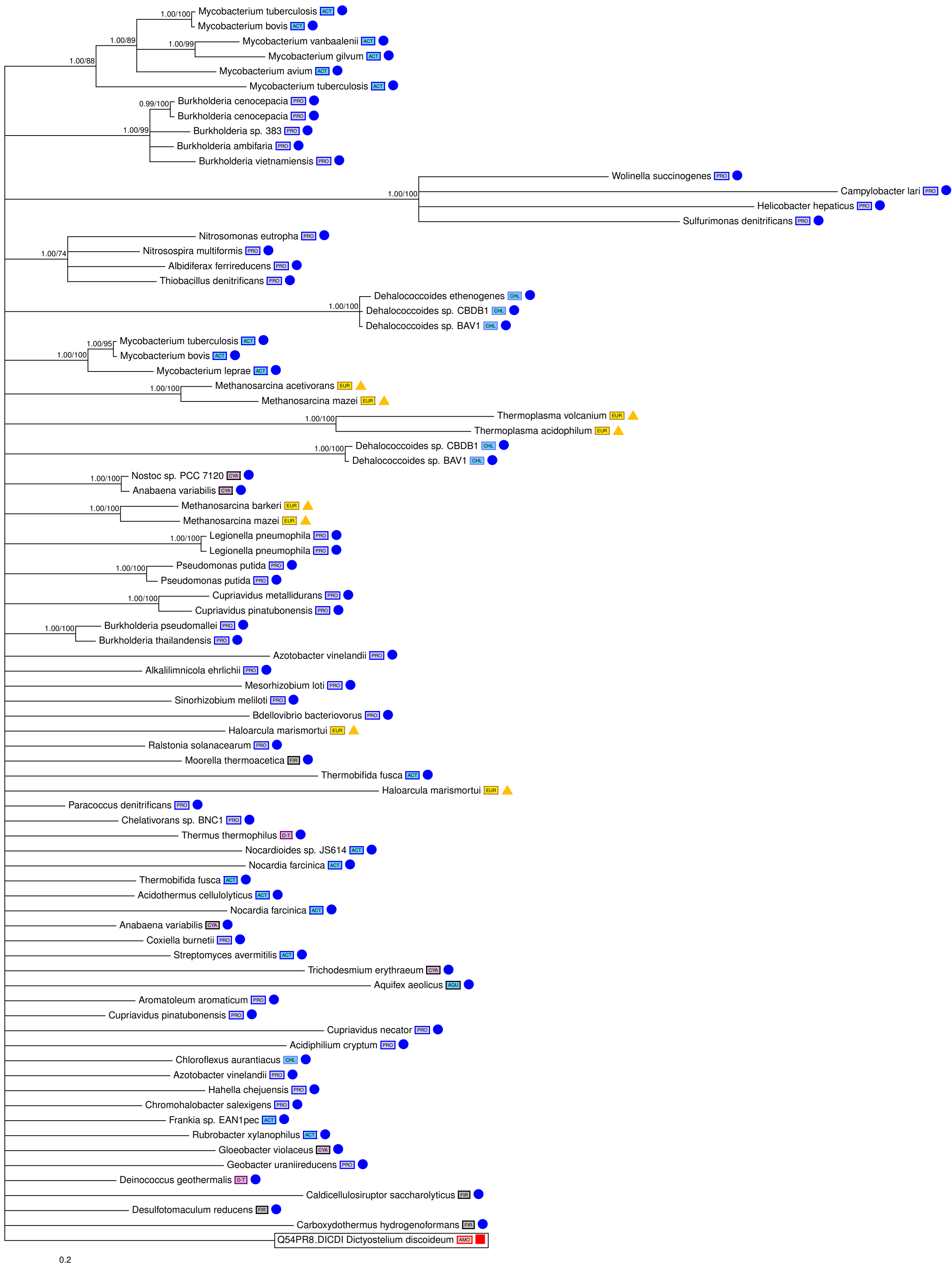
TN044

Candy accession: Q54MZ6_DICDI
RefSeq accession: XP_638147.1
Uniprot accession: Q54MZ6_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Proteobacteria - Bdellovibrio
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: dihydroxybiphenyl dioxygenase domain-
containing protein
Name of enzyme/protein: dihydroxybiphenyl dioxygenase domain-
containing protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



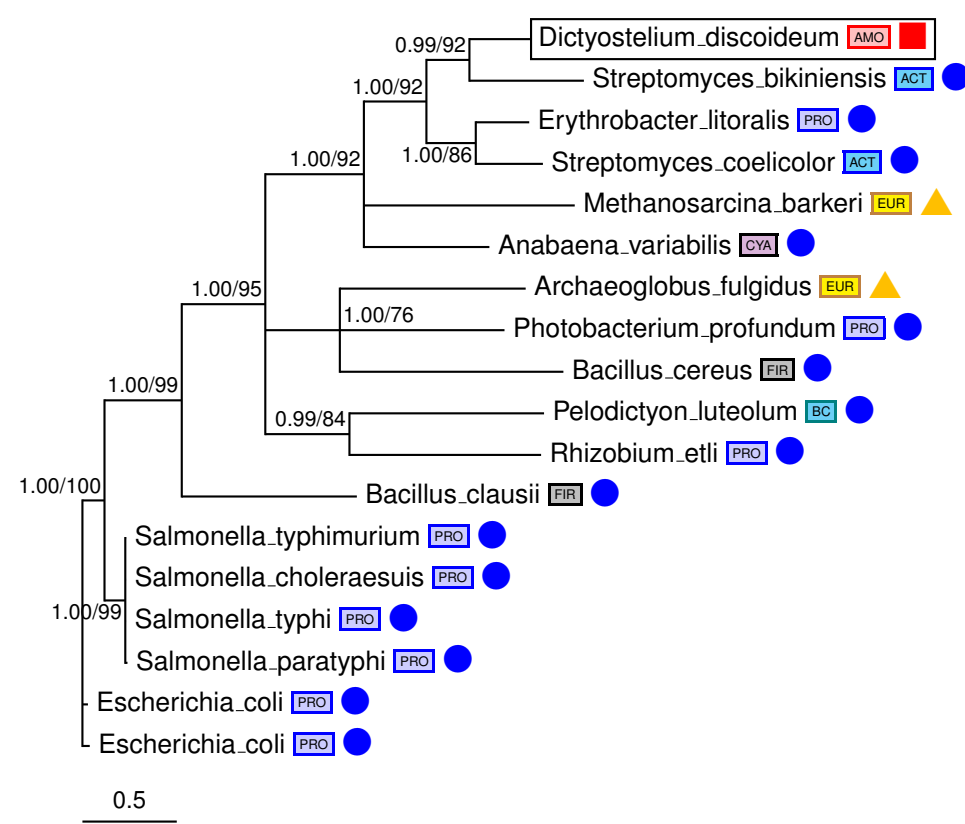
TN045

Candy accession: Q54PR8_DICDI
RefSeq accession: XP_638586.1
Uniprot accession: Q54PR8_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:2.4.2.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0284365
Name of enzyme/protein: phosphoribosyltransferase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



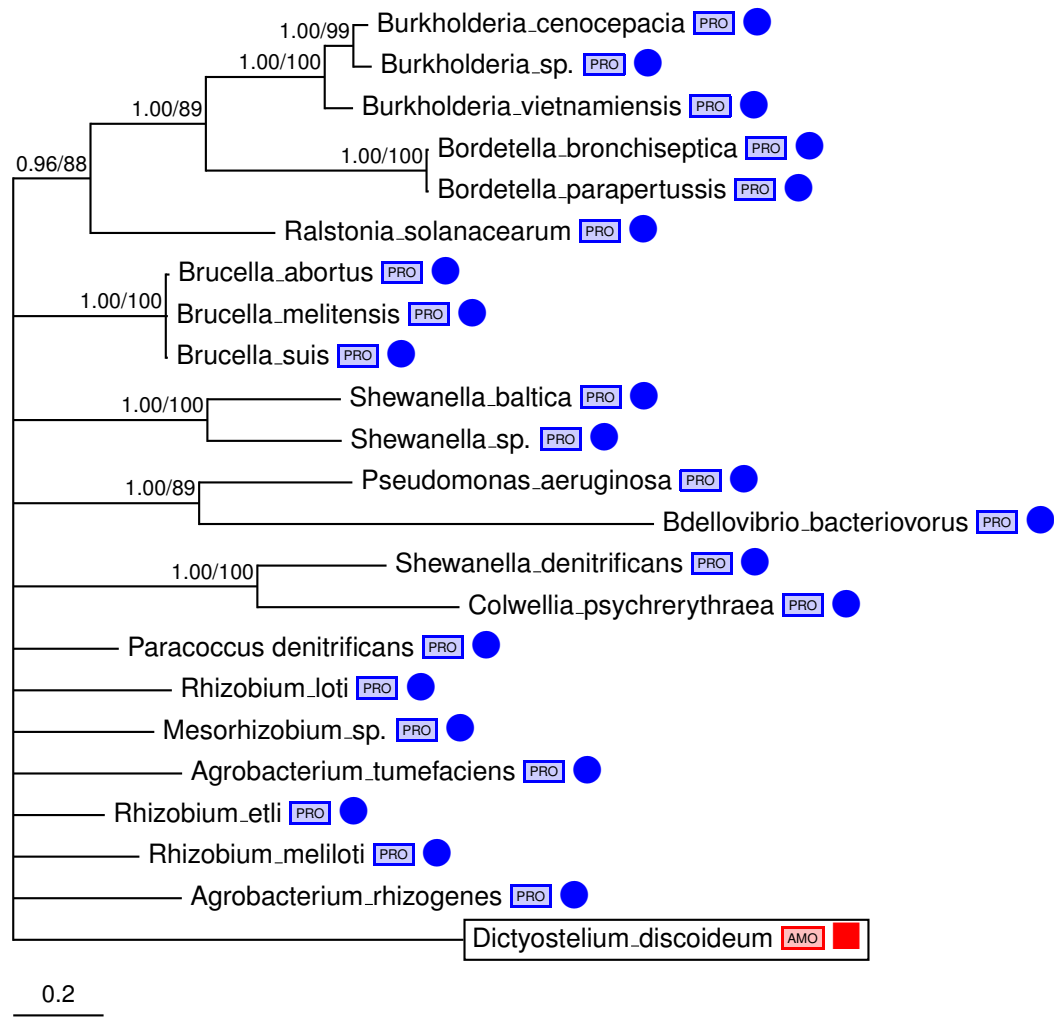
TN046

Candy accession: Q54QA3_DICDI
RefSeq accession: XP_638841.1
Uniprot accession: Q54QA3_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Actinobacteria - Streptomyces
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0283975
Name of enzyme/protein: Protein containing methyltransferase domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



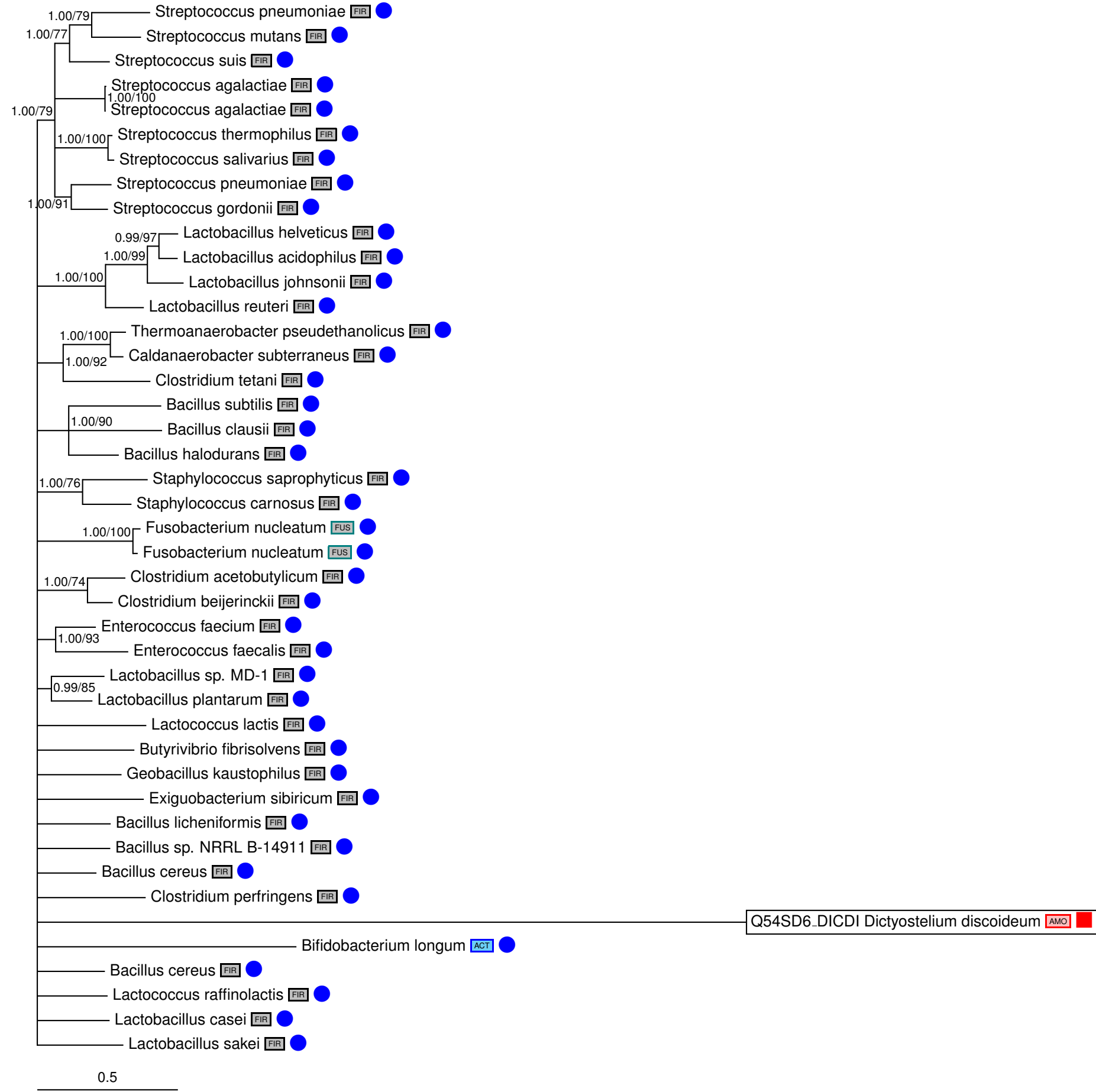
TN047

Candy accession: Q54RW2_DICDI
RefSeq accession: XP_639375.1
Uniprot accession: Q54RW2_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0282879
Name of enzyme/protein: Predicted protein of unknown function
HutD
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



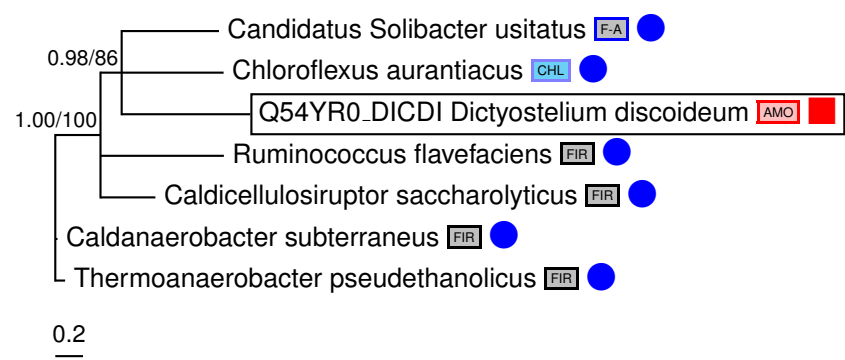
TN048

Candy accession: Q54SD6_DICDI
RefSeq accession: XP_640103.1
Uniprot accession: Q54SD6_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.7.7.12
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0282525
Name of enzyme/protein: UDPglucose--hexose-1-phosphate
 uridylyltransferase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Galactose metabolism, Amino sugar and
 nucleotide sugar metabolism



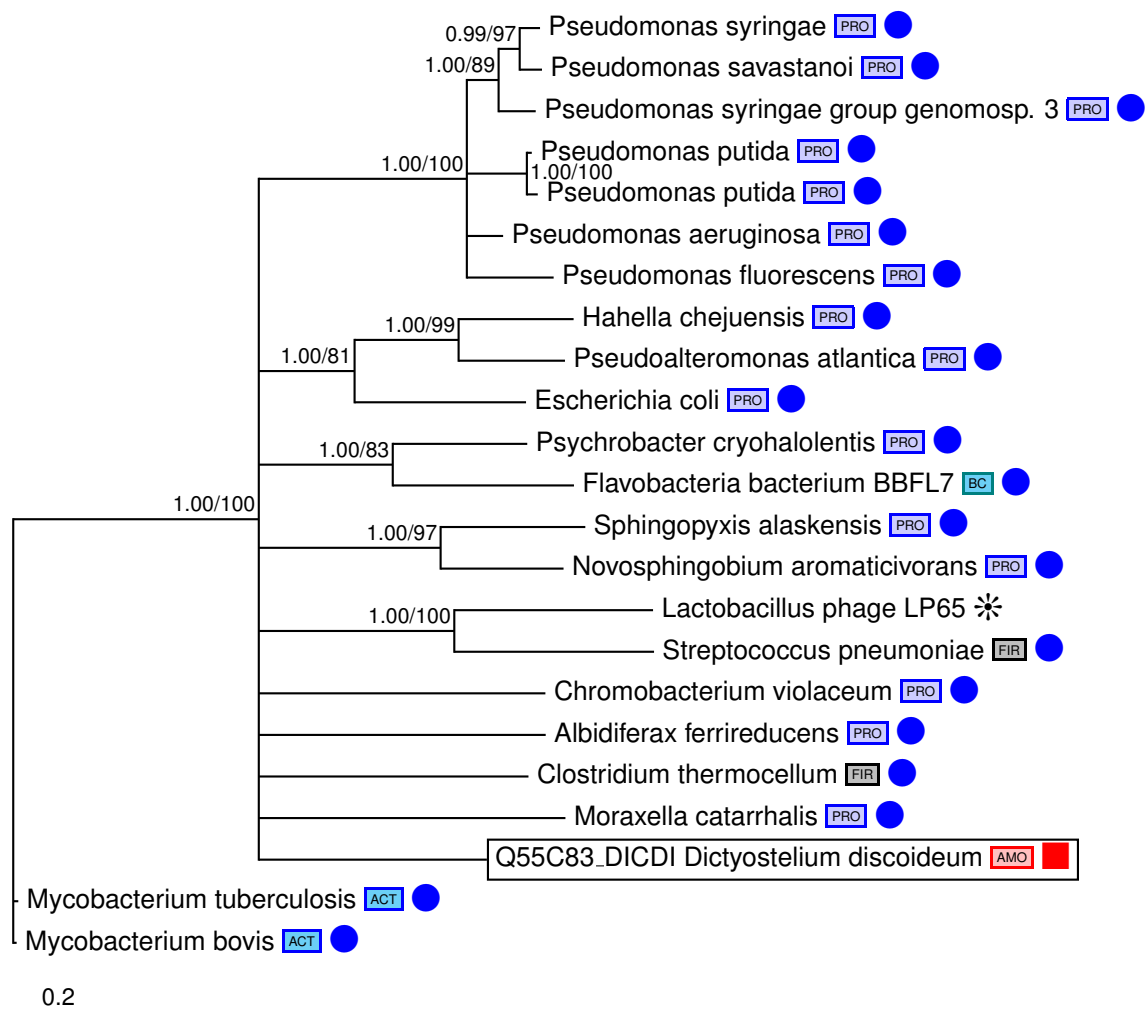
TN049

Candy accession: Q54YR0_DICDI
RefSeq accession: XP_002649169.1
Uniprot accession: C7G007_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.3.1.128
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0295725
Name of enzyme/protein: Ribosomal-protein-alanine
N-acetyltransferase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



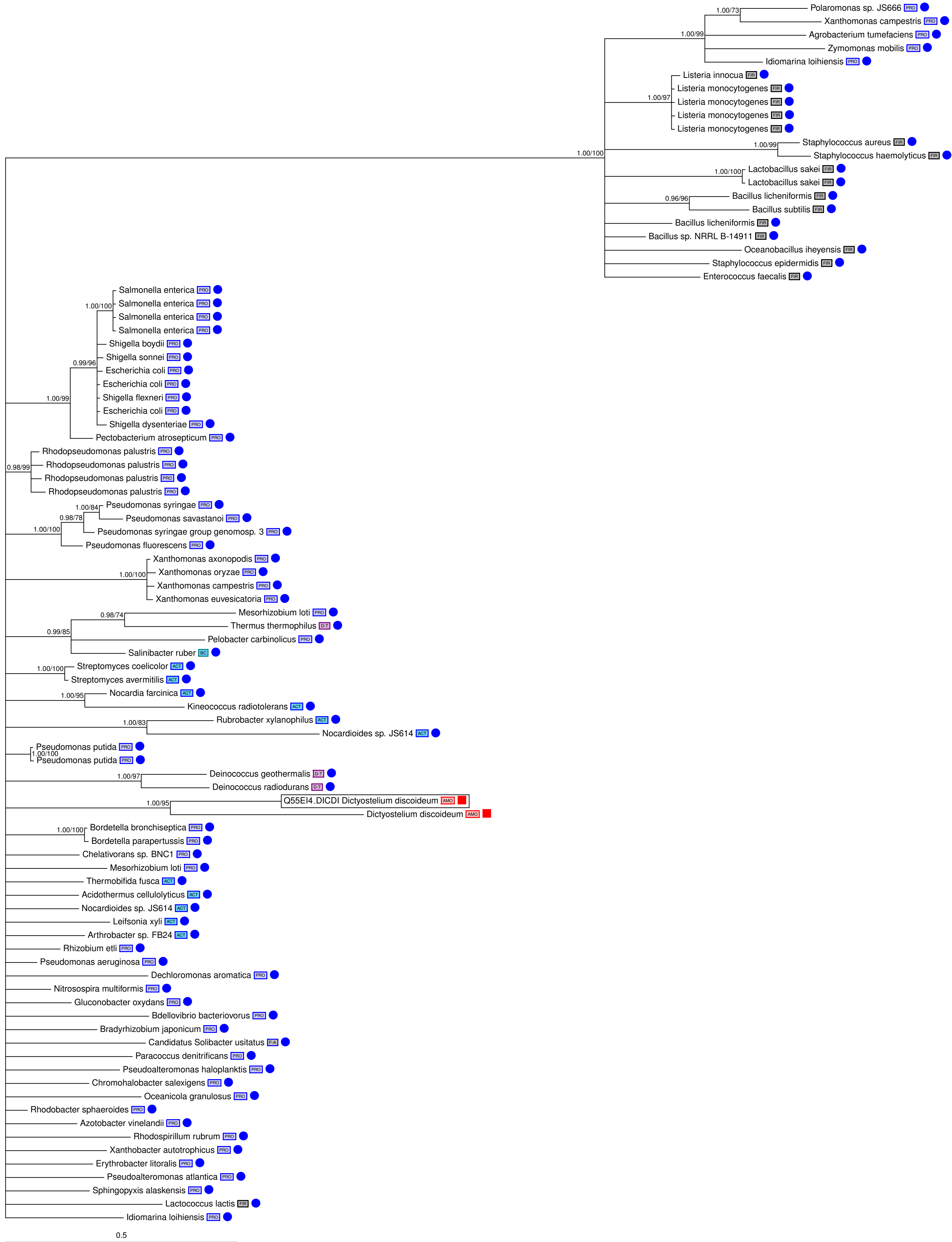
TN050

Candy accession: Q55C83_DICDI
RefSeq accession: XP_646598.1
Uniprot accession: Q55C83_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0270172
Name of enzyme/protein: Protein containing bifunctional DNA-binding transcriptional repressor/nicotinamide-nucleotide adenyllyltransferase
KEGG PATHWAY - level 1: Other function - Genetic Information Processing
KEGG PATHWAY - level 2: na



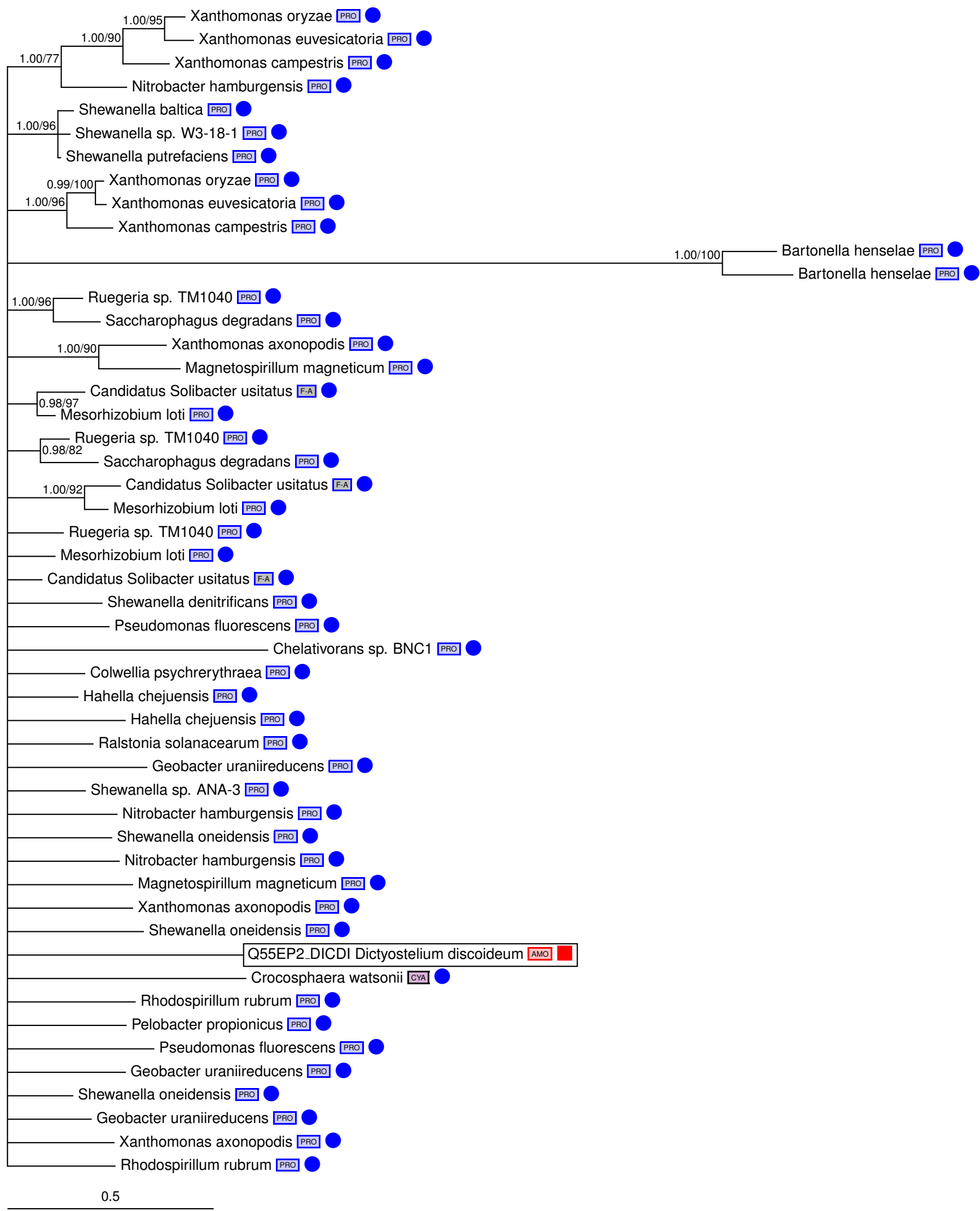
TN051

Candy accession: Q55EI4_DICDI
RefSeq accession: XP_647036.1
Uniprot accession: Q55EI4_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:1.11.1.15
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: osmotically inducible family protein
Name of enzyme/protein: peroxiredoxin, thioredoxin peroxidase
KEGG PATHWAY - level 1: Metabolism of Other Amino Acids
KEGG PATHWAY - level 2: Glutathione metabolism



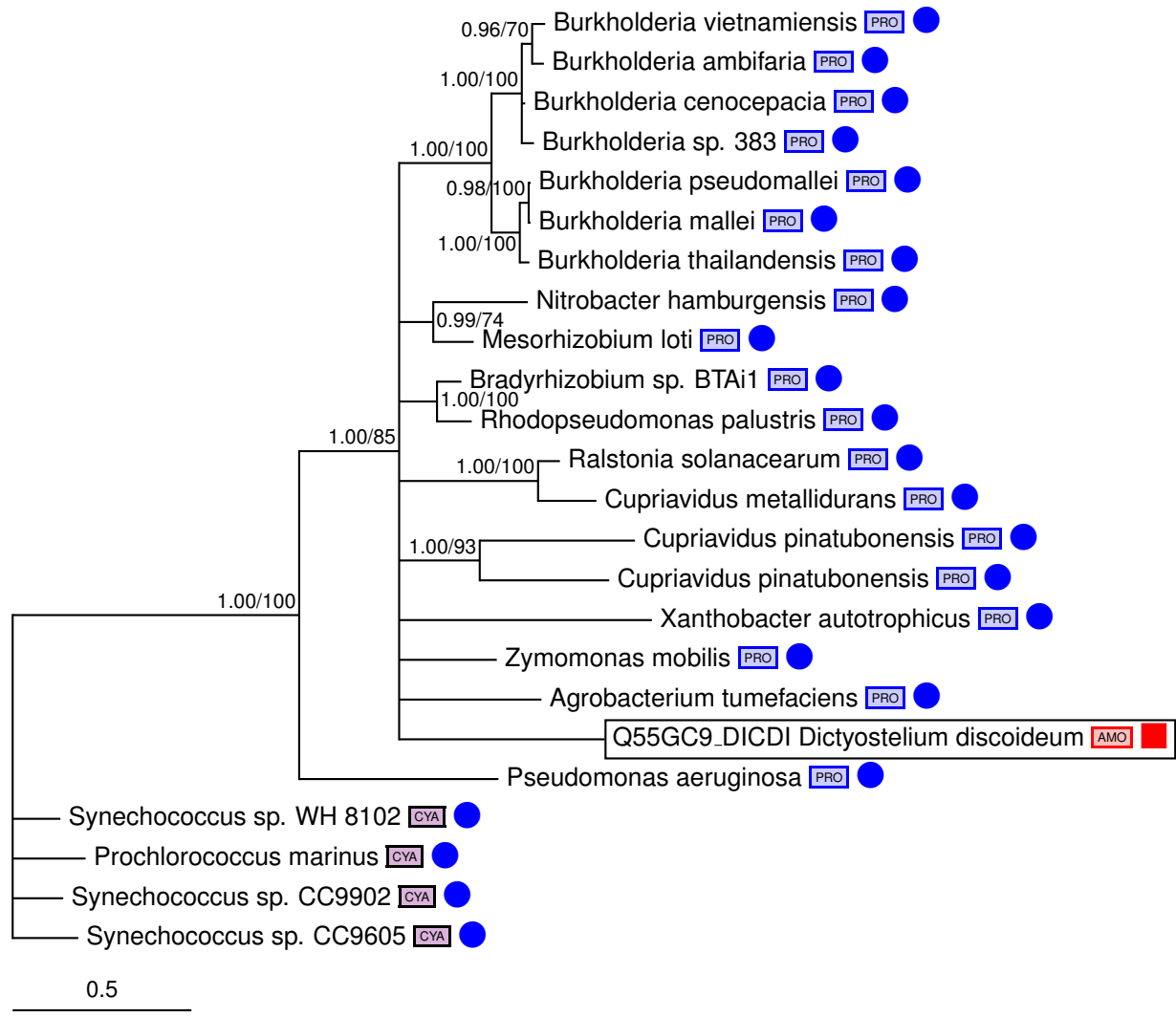
TN052

Candy accession: Q55EP2_DICDI
RefSeq accession: XP_646978.1
Uniprot accession: Q55EP2_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0269088
Name of enzyme/protein: Protein containing Phage Tail Collar
Domain/MdpB Microcystin-dependent
domains
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



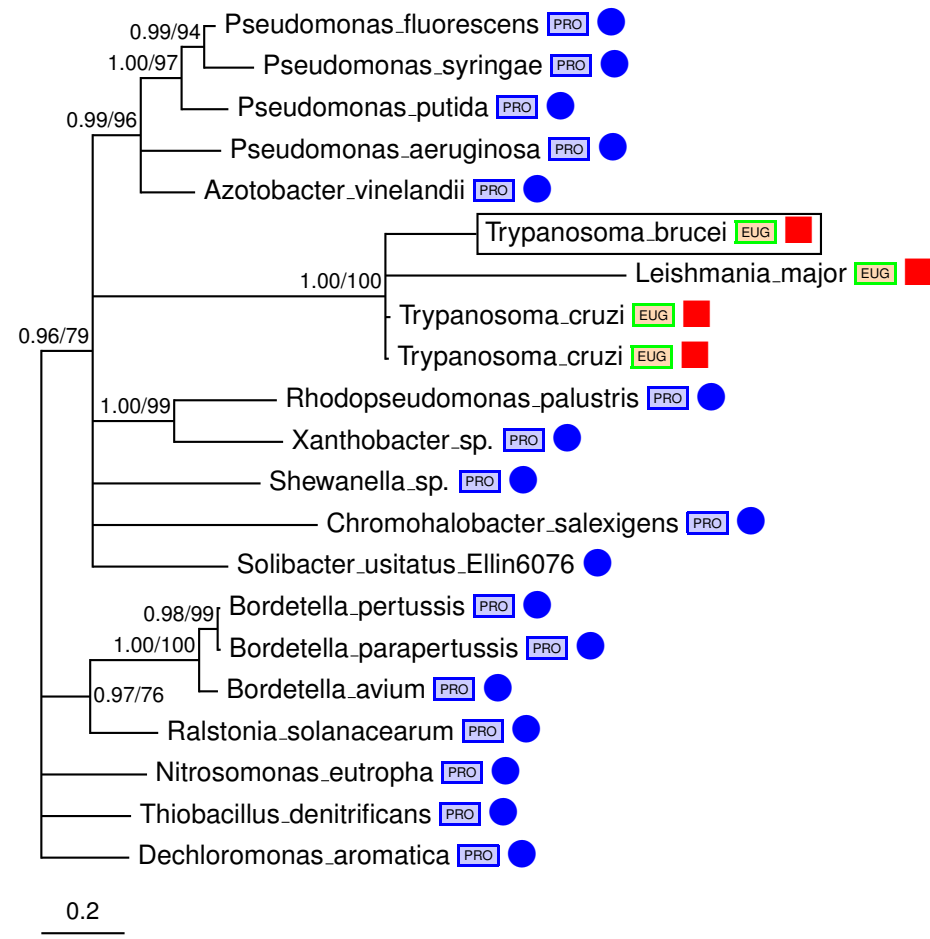
TN053

Candy accession: Q55GC9_DICDI
RefSeq accession: XP_647255.1
Uniprot accession: Q55GC9_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0267722
Name of enzyme/protein: Putative ParB-like nuclease
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na



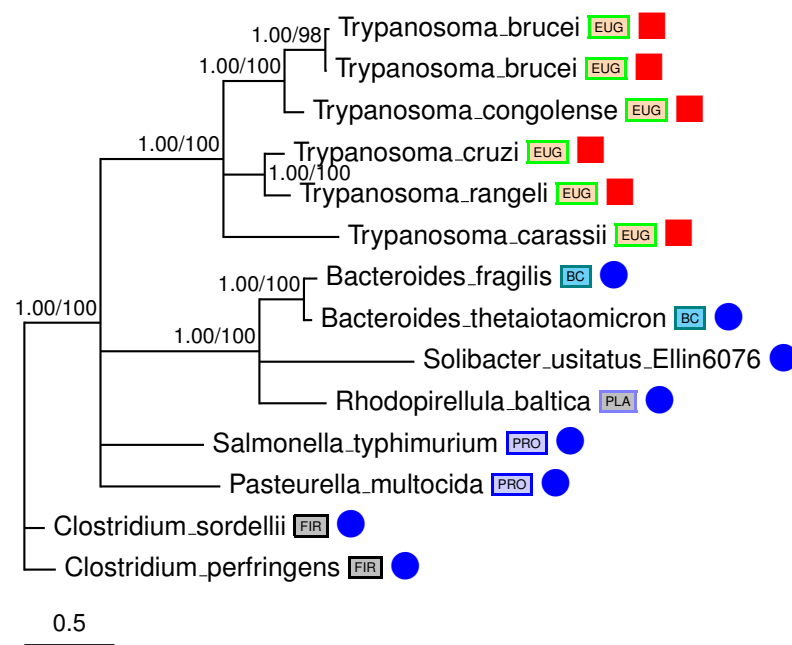
TN054

Candy accession: Q57WT0_9TRYP
RefSeq accession: XP_845744.1
Uniprot accession: Q57WT0_9TRYP
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB,TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF525
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



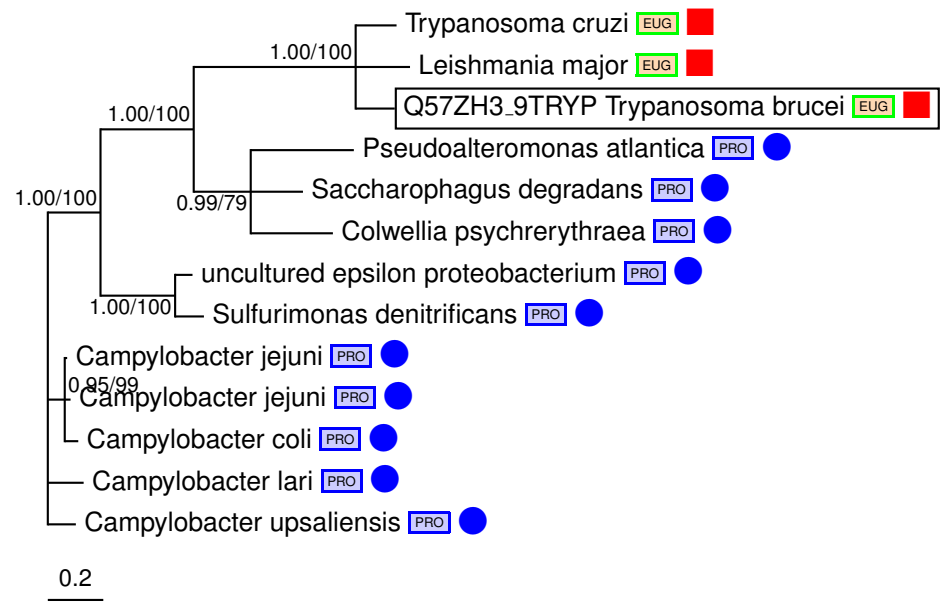
TN055

Candy accession: Q57Y46_9TRYP
RefSeq accession: XP_846303.1
Uniprot accession: Q57Y46_9TRYP
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: TB,TC,TCO,TR,TCAR
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.2.1.18
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: trans-sialidase
Name of enzyme/protein: exo-alpha-sialidase; neuraminidase; sialidase
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism, Lipid Metabolism
KEGG PATHWAY - level 2: Other glycan degradation, Sphingolipid metabolism



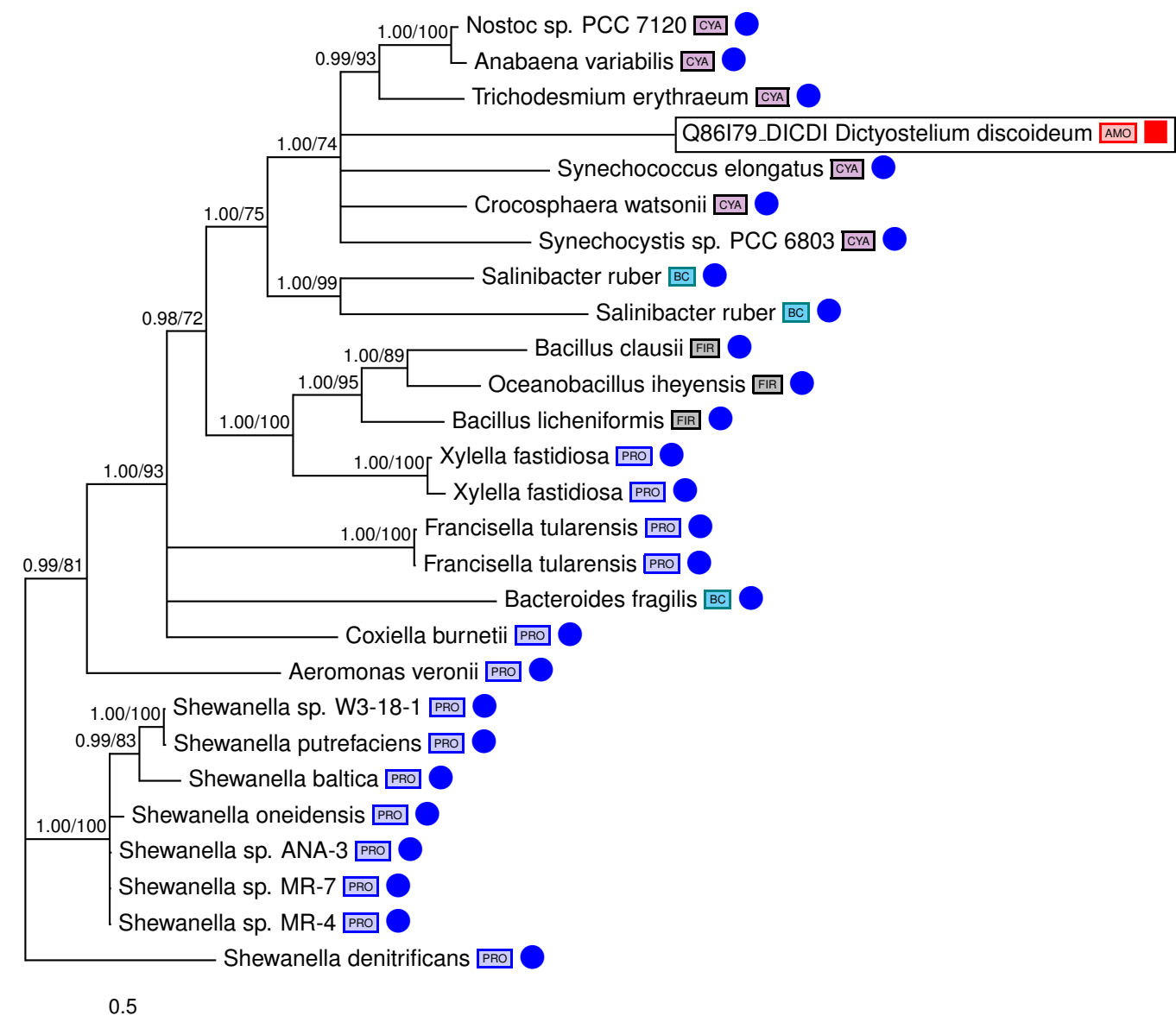
TN056

Candy accession: Q57ZH3_9TRYP
RefSeq accession: XP_846139.1
Uniprot accession: Q57ZH3_9TRYP
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB,TC
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:3.6.1.23
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: deoxyuridine triphosphatase
Name of enzyme/protein: dUTP pyrophosphatase
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Pyrimidine metabolism



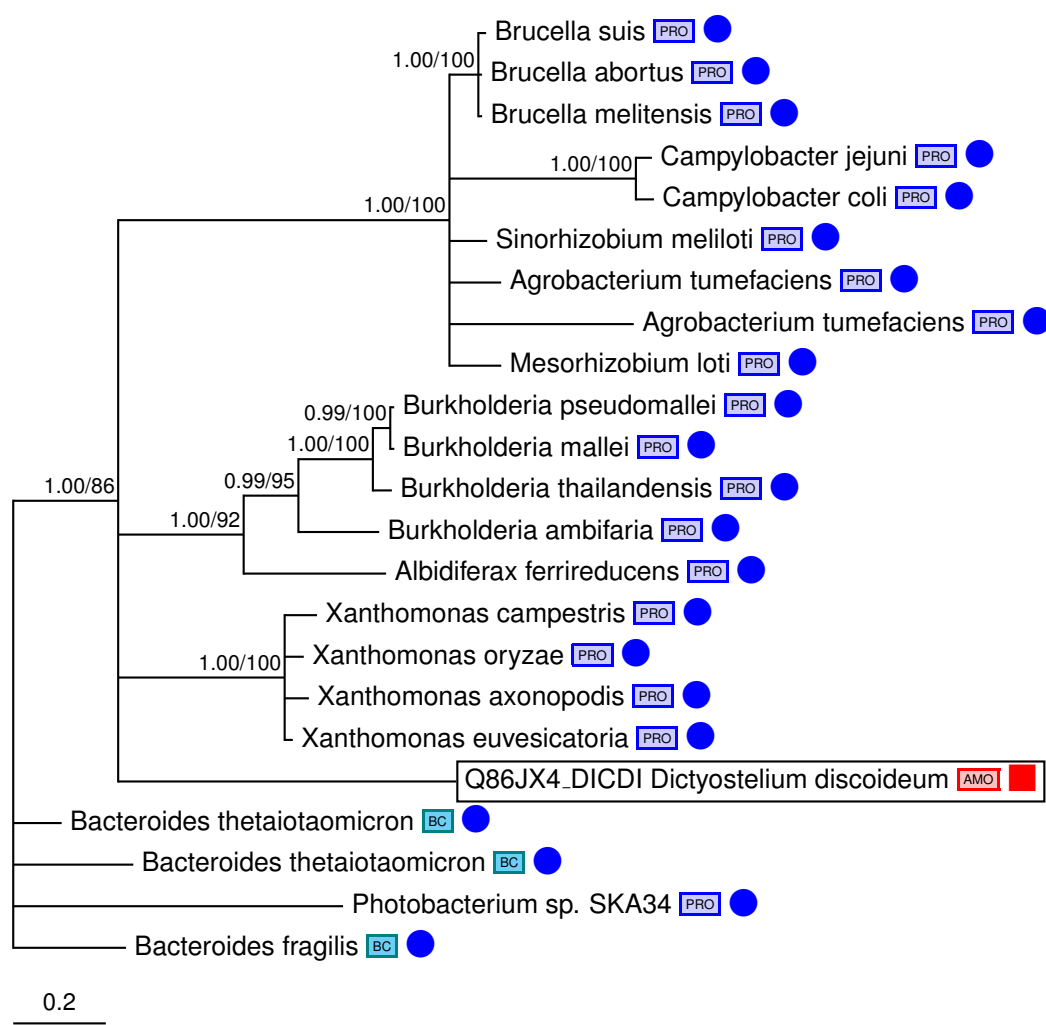
TN057

Candy accession: Q86179_DICD1
RefSeq accession: XP_645397.1
Uniprot accession: PSCA_DICD1
Comments: LGT - DD - POTENTIAL CYANOBACTERIA DONOR
Species affected: DD
Adjacent taxa in tree: Cyanobacteria
EC annotation - (Blast/Profile): EC:3.4.16.4
PHOBIOUS SP: Y
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein DBB_G0271902
Name of enzyme/protein: serine-type D-Ala-D-Ala carboxypeptidase
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism
KEGG PATHWAY - level 2: Peptidoglycan biosynthesis



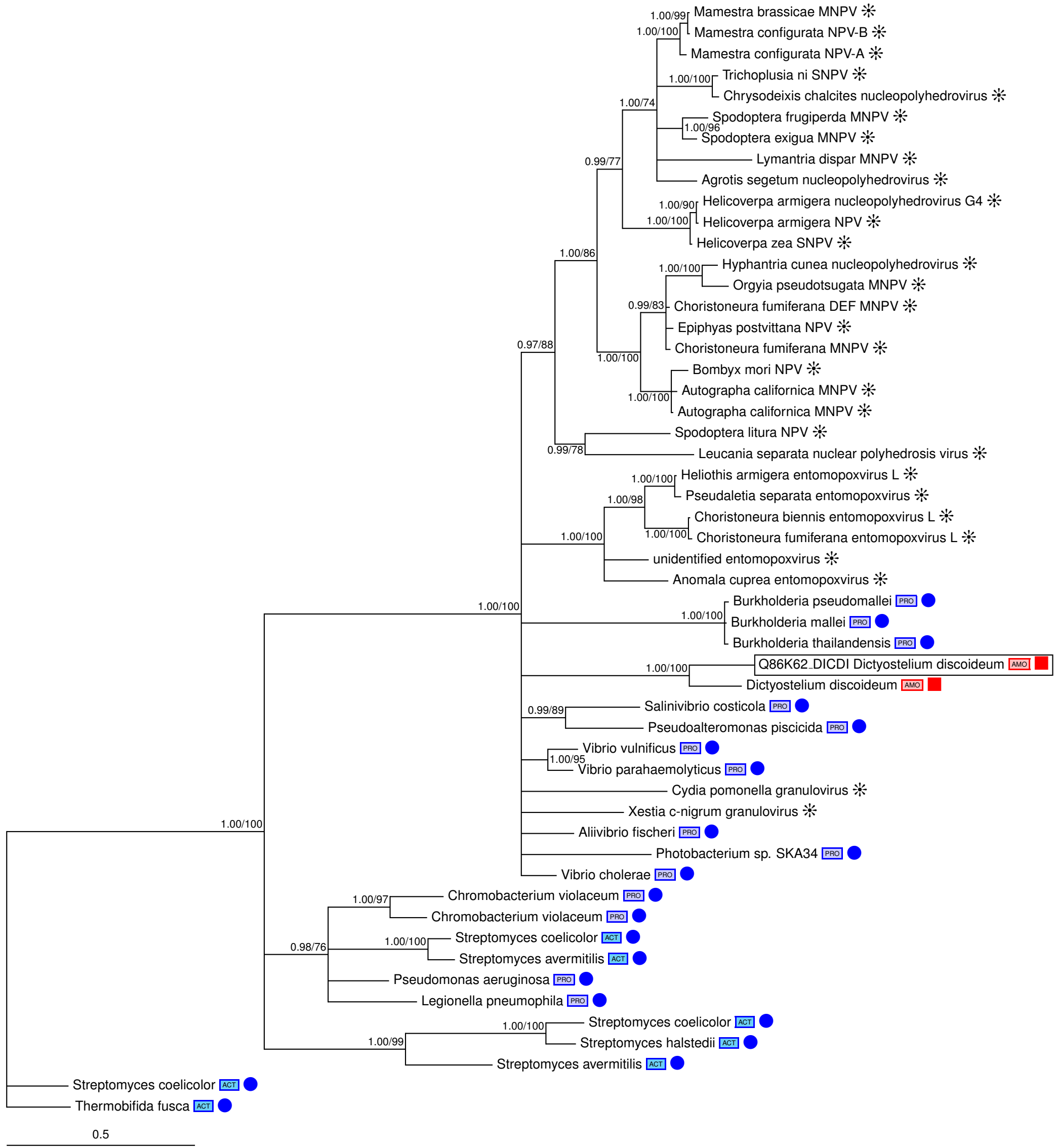
TN058

Candy accession: Q86JX4_DICDI
RefSeq accession: XP_644699.1
Uniprot accession: Y3871_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0273177
Name of enzyme/protein: Predicted rhamnose mutarotase
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



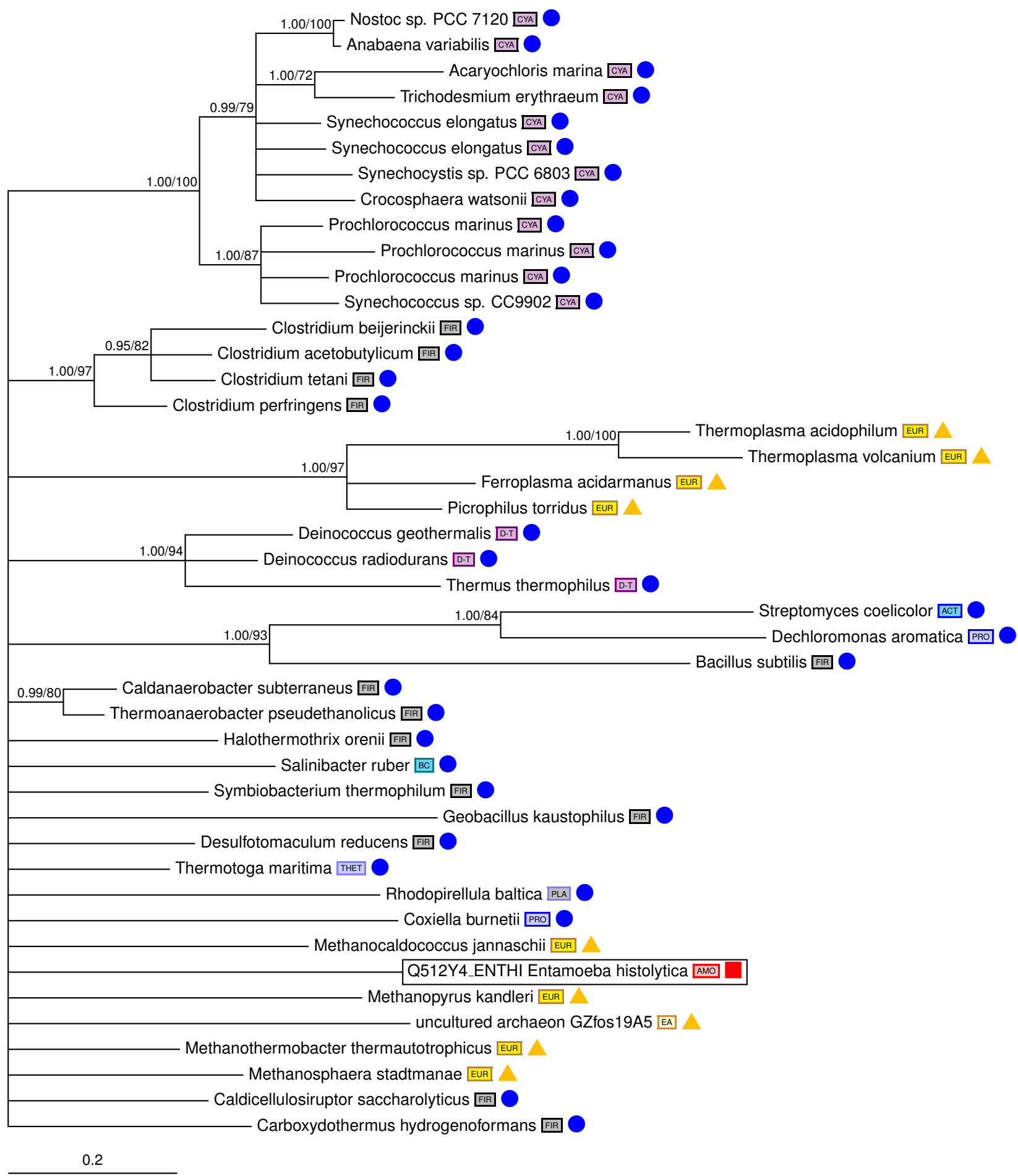
TN059

Candy accession: Q86K62_DICDI
RefSeq accession: XP_642725.1
Uniprot accession: Q86K62_DICDI
Comments: LGT - DD ONLY - MANY VIRUSES
Species affected: DD
Adjacent taxa in tree: Proteobacteria & phage
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0277201
Name of enzyme/protein: Predicted N-acetylglucosamine-binding protein; Chitin-binding protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



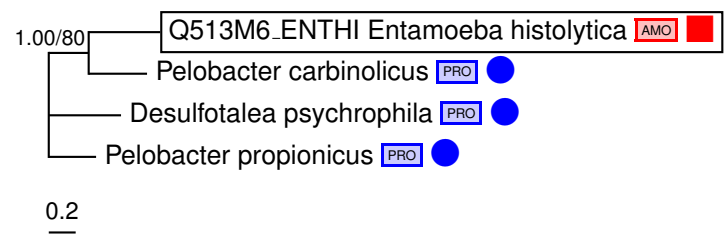
TN060

Candy accession: Q512Y4_ENTHI
RefSeq accession: XP_653291.1
Uniprot accession: C4LWV3_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:3.1.3.71
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: 2-phosphosulfolactate phosphatase
Name of enzyme/protein: 2-phosphosulfolactate phosphatase
KEGG PATHWAY - level 1: Energy Metabolism
KEGG PATHWAY - level 2: Methane metabolism



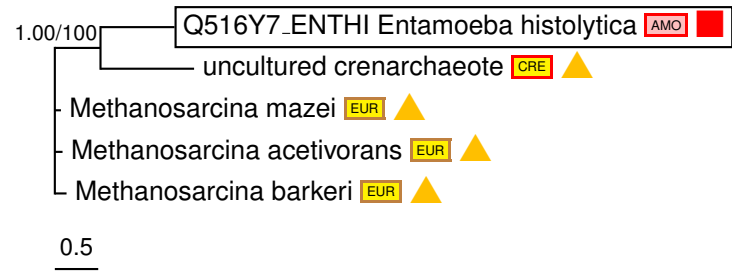
TN061

Candy accession: Q513M6_ENTHI
RefSeq accession: XP_653421.1
Uniprot accession: C4M2N2_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Proteobacteria - Pelobacter
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Putative redox-active protein
(C_GCAxxG_C_C)
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



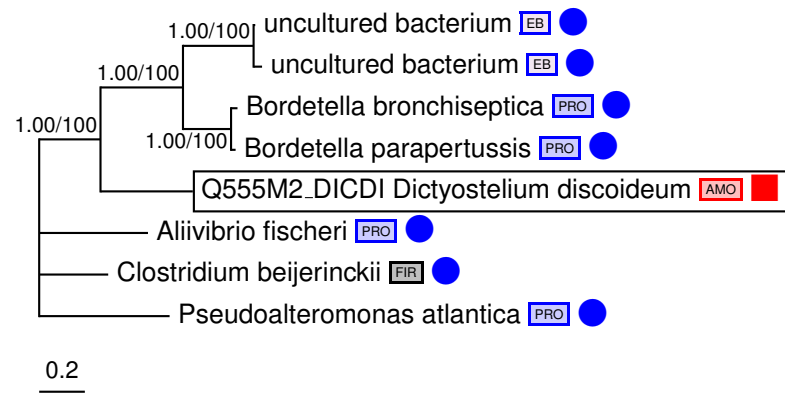
TN062

Candy accession: Q516Y7_ENTHI
RefSeq accession: XP_654288.1
Uniprot accession: C4M6B4_ENTHI
Comments: LGT - EH ONLY with 4 Archaea
Species affected: EH
Adjacent taxa in tree: Archaea
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted phosphohydrolase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



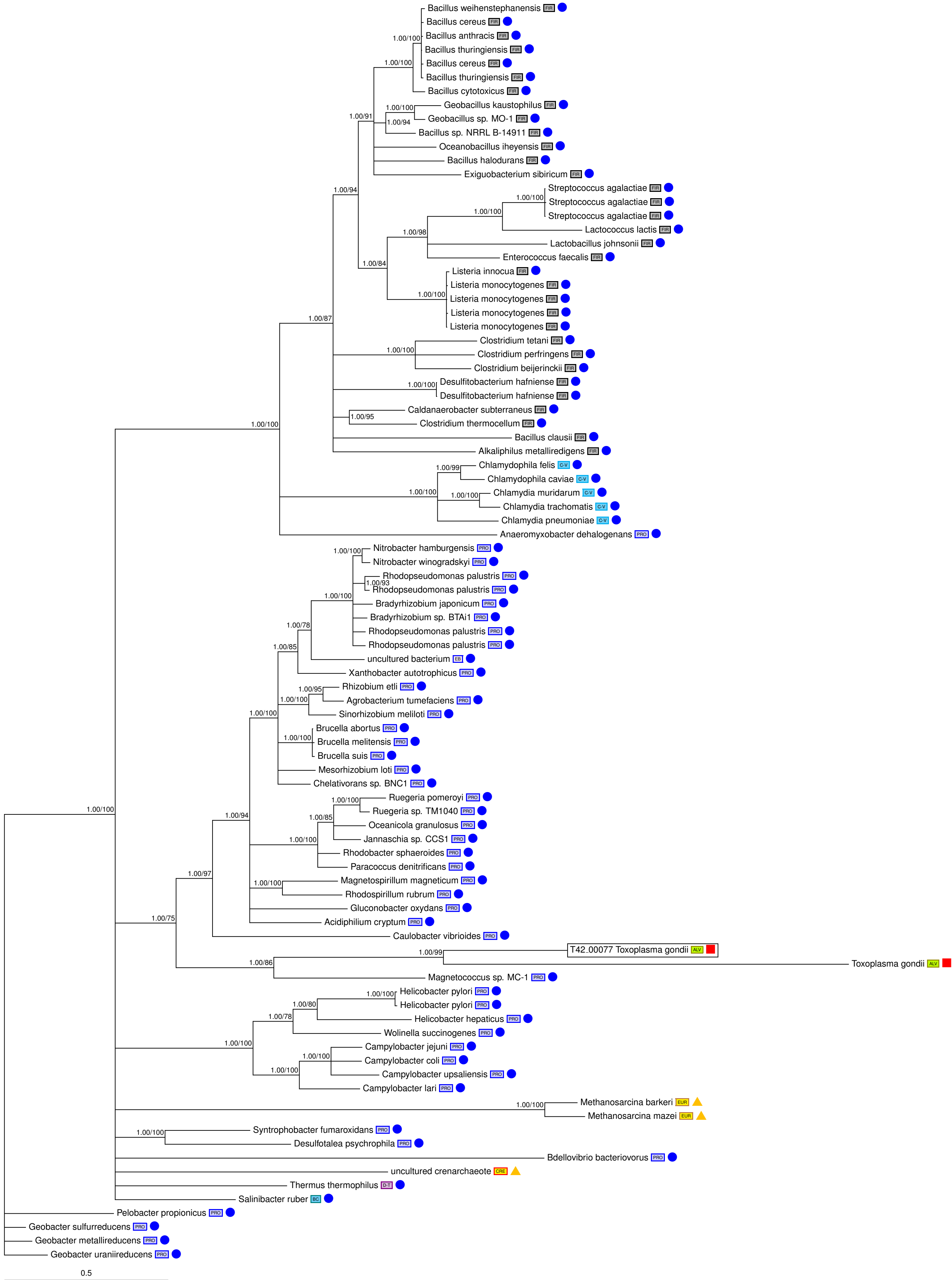
TN063

Candy accession: Q555M2_DICDI
RefSeq accession: XP_644044.1
Uniprot accession: Q555M2_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0274701
Name of enzyme/protein: Predicted Lincosamide
nucleotidyltransferase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



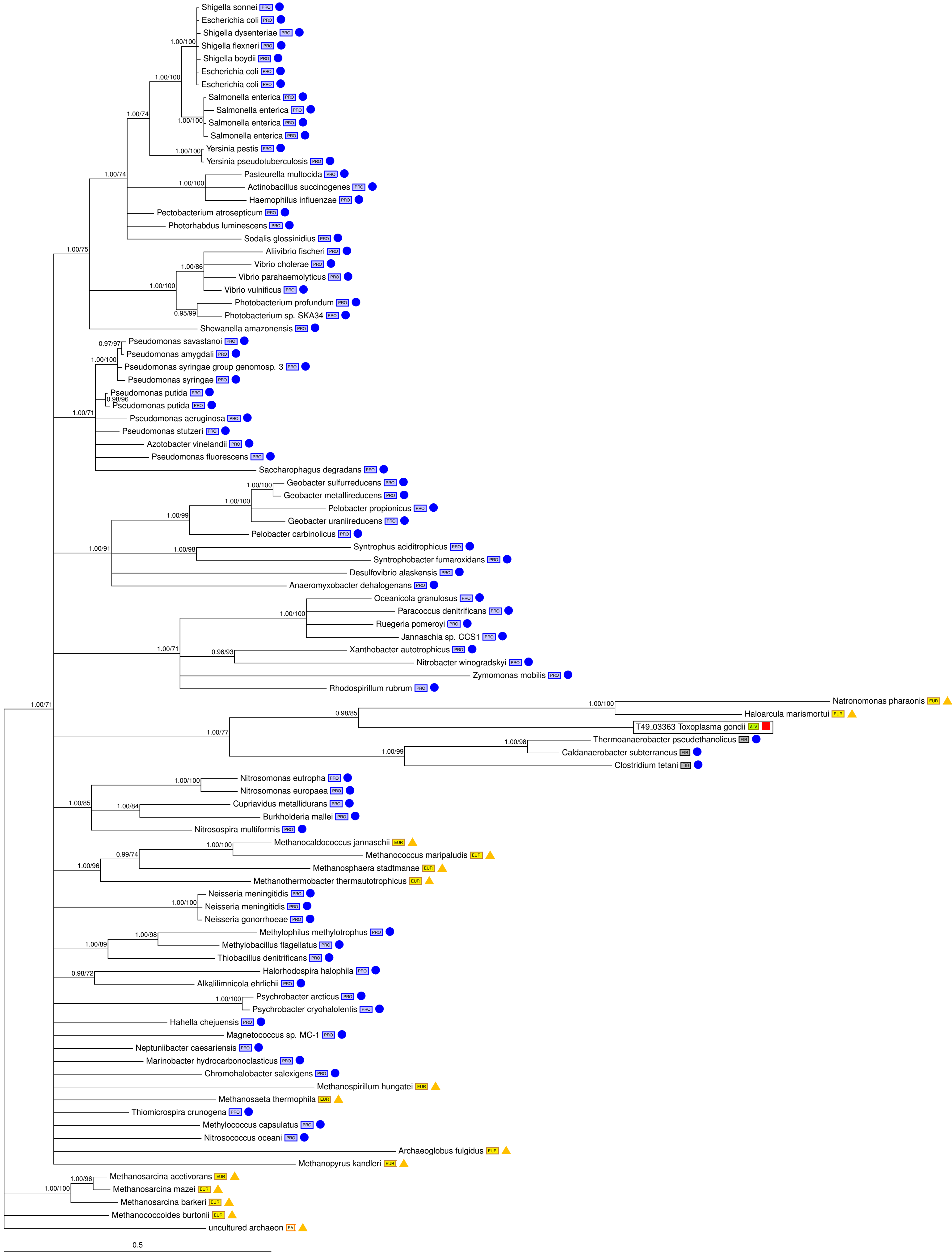
TN064

Candy accession: T42_00077
RefSeq accession: XP_002366295.1
Uniprot accession: B6KEM2_TOXGO
Comments: LGT - TG ONLY
Species affected: TG
Adjacent taxa in tree: Proteobacteria - Magnetococcus
EC annotation - (Blast/Profile): EC:3.4.24.15
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: oligoendopeptidase F, putative
Name of enzyme/protein: thimet oligopeptidase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



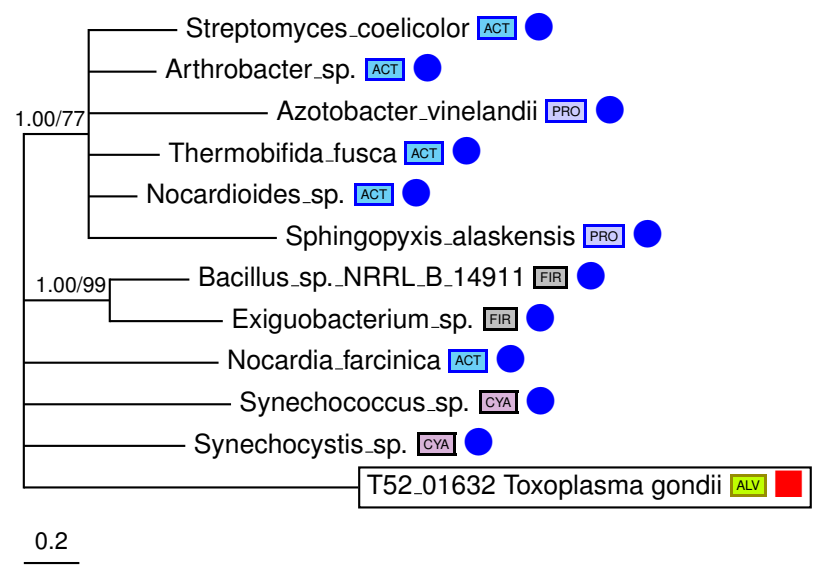
TN065

Candy accession: T49_03363
RefSeq accession: XP_002366867.1
Uniprot accession: B6KFY6_TOXGO
Comments: LGT - TG ONLY
Species affected: TG
Adjacent taxa in tree: Archaea
EC annotation - (Blast/Profile): EC:1.3.1.26
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: dihydrodipicolinate reductase, putative
Name of enzyme/protein: dihydrodipicolinate reductase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Lysine biosynthesis



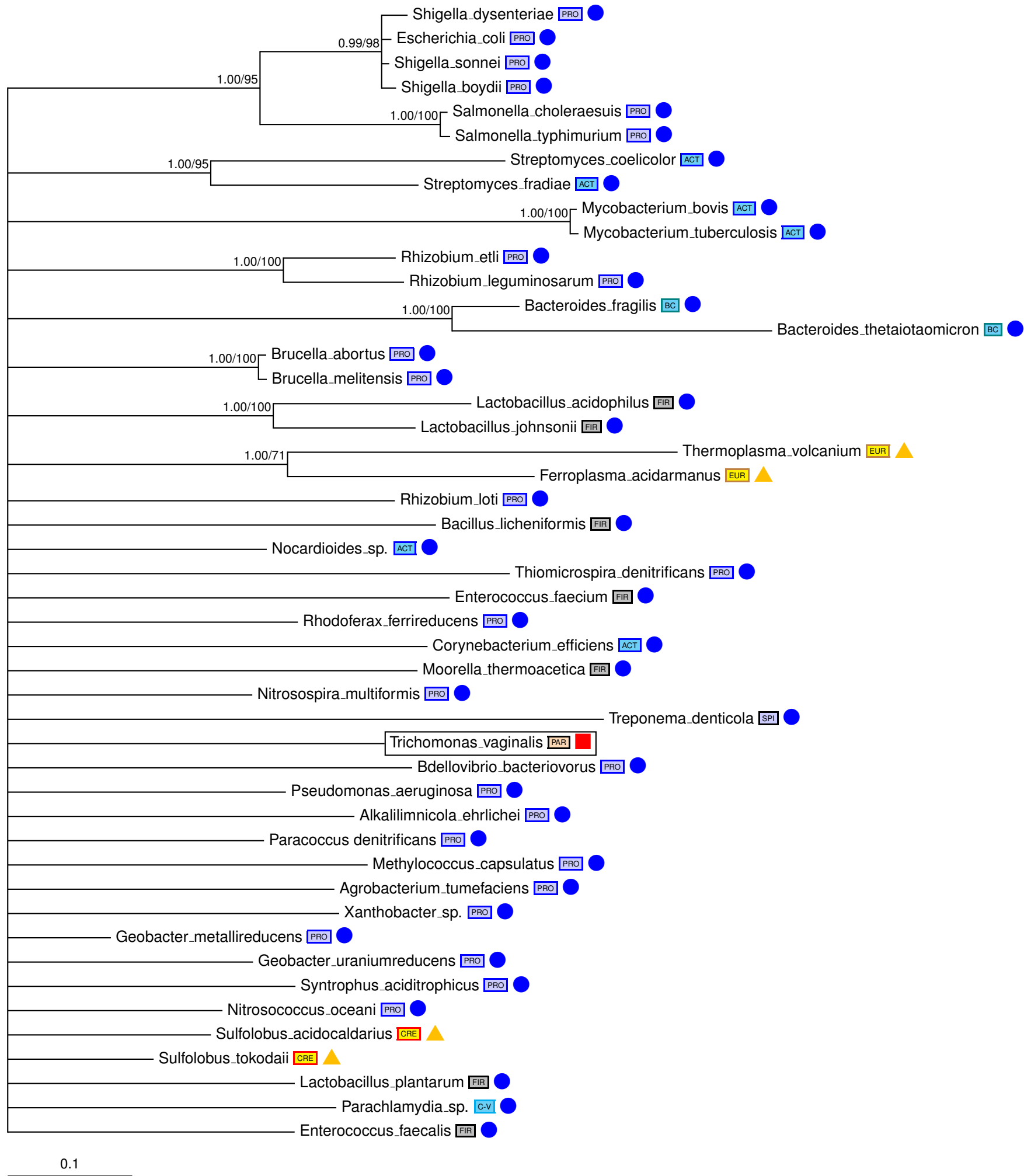
TN066

Candy accession: T52_01632
RefSeq accession: XP_002369463.1
Uniprot accession: B6KNP0_TOXGO
Comments: LGT - TG ONLY
Species affected: TG
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 7
RefSeq annotation: zinc transporter ZIP domain-containing protein
Name of enzyme/protein: zinc transporter ZIP domain-containing protein
KEGG PATHWAY - level 1: Other function - Membrane transport
KEGG PATHWAY - level 2: na



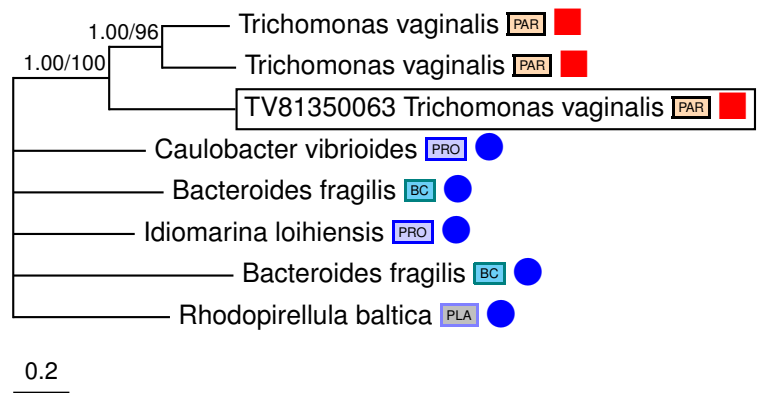
TN067

Candy accession: TV80361101
RefSeq accession: XP_001314405.1
Uniprot accession: A2EZT6_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF488
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



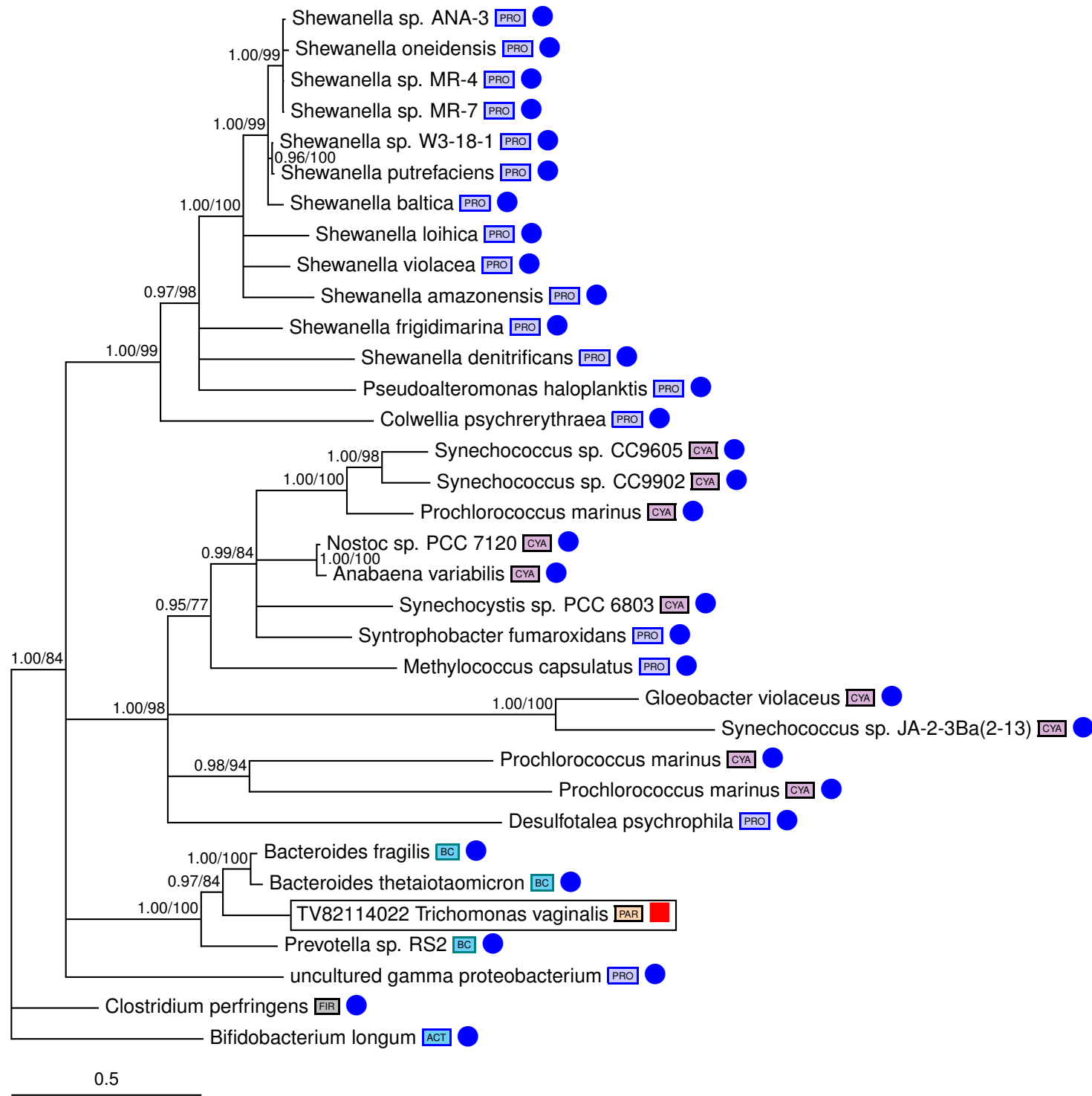
TN068

Candy accession: TV81350063
RefSeq accession: XP_001307357.1
Uniprot accession: A2FKX3_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 12
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Hypothetical protein
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



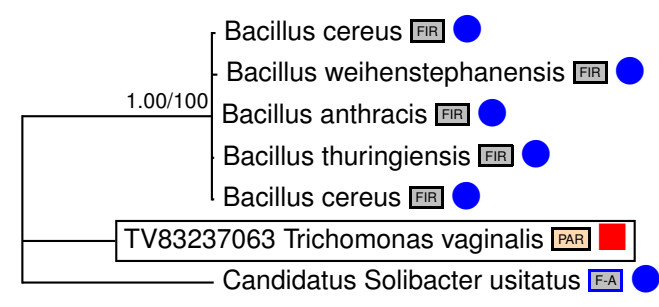
TN069

Candy accession: TV82114022
RefSeq accession: XP_001301892.1
Uniprot accession: A2G1K4_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:2.7.1.162
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: N-acetylhexosamine 1-kinase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



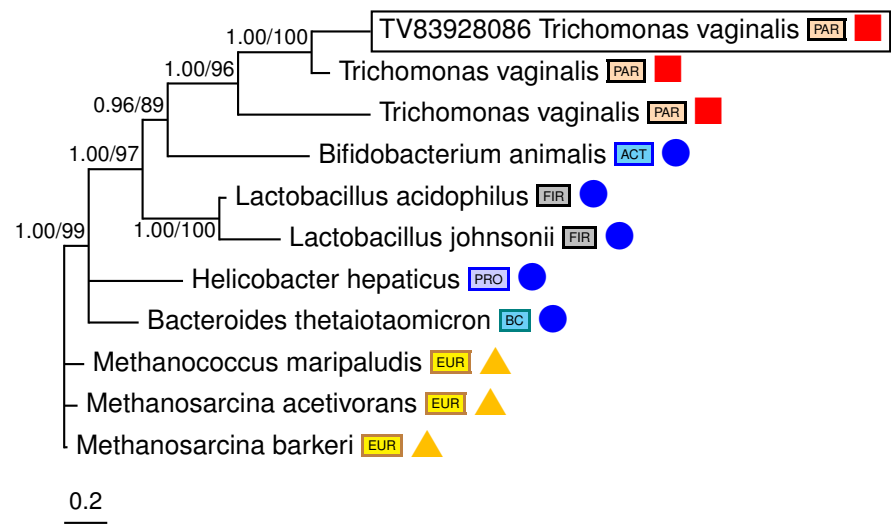
TN070

Candy accession: TV83237063
RefSeq accession: XP_001309866.1
Uniprot accession: A2FDT7_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containg DUF3111
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



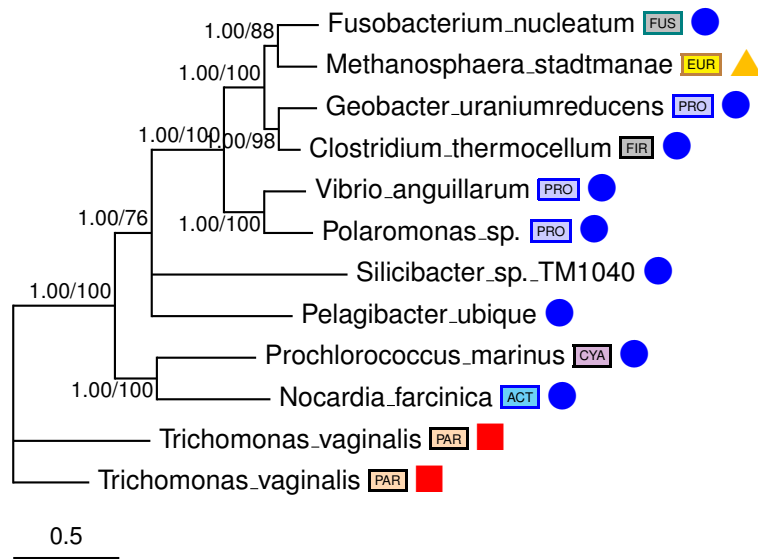
TN071

Candy accession: TV83928086
RefSeq accession: XP_001309751.1
Uniprot accession: A2FE49_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Actinobacteria - Bifidobacterium
EC annotation - (Blast/Profile): EC:4.1.1.44
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: 4-carboxymuconolactone decarboxylase
Name of enzyme/protein: 4-carboxymuconolactone decarboxylase
KEGG PATHWAY - level 1: Xenobiotics Biodegradation and Metabolism
KEGG PATHWAY - level 2: Benzoate degradation



TN072

Candy accession: TV84285194
RefSeq accession: XP_001323014.1
Uniprot accession: A2E9A6_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: NDP-hexose 3,4-dehydratase
Name of enzyme/protein: Predicted 3-amino-5-hydroxybenzoic acid synthase family
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



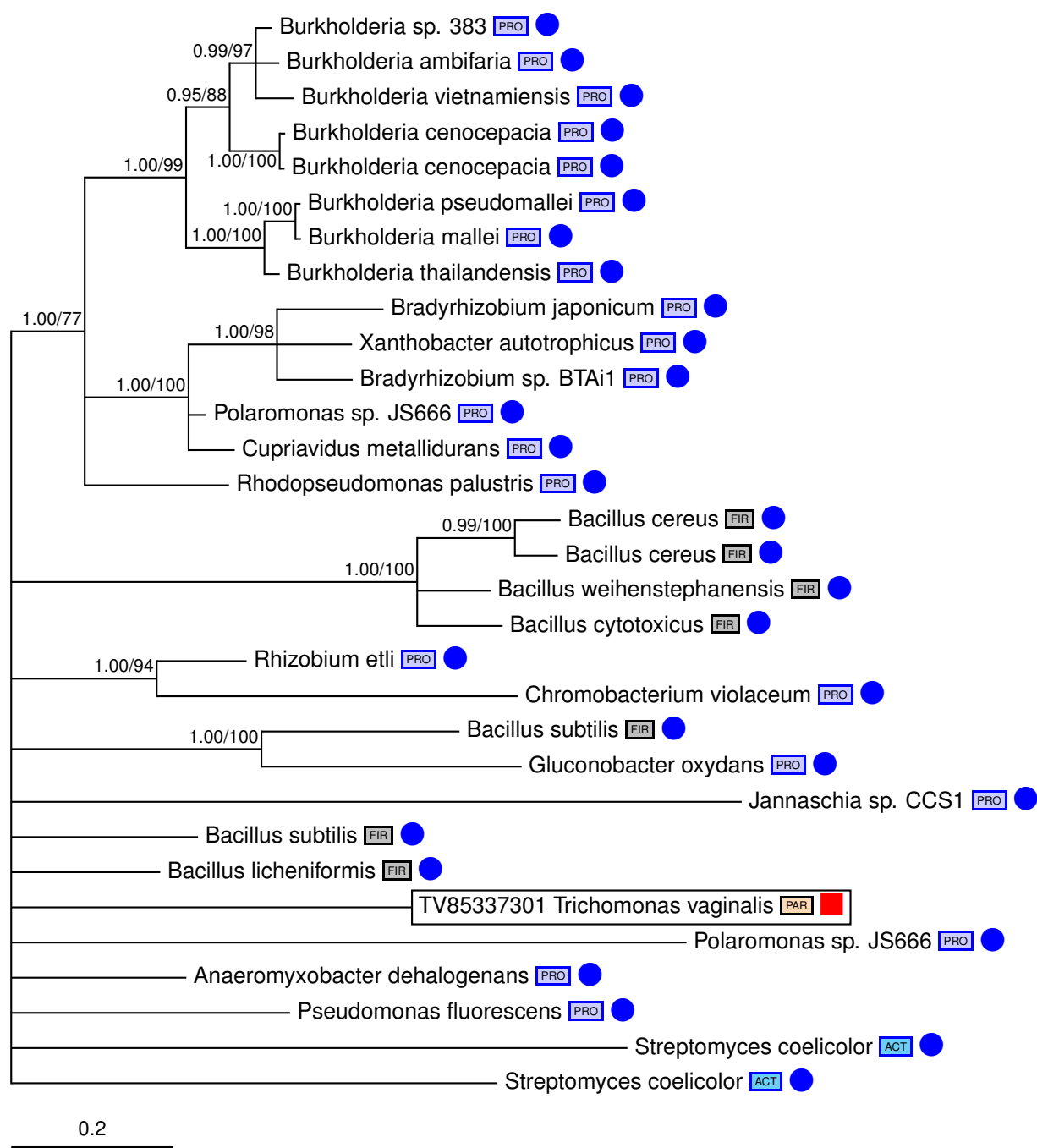
TN073

Candy accession: TV85232129
RefSeq accession: XP_001320703.1
Uniprot accession: A2EFS9_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:4.4.1.5
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glyoxalase
Name of enzyme/protein: lactoylglutathione lyase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pyruvate metabolism



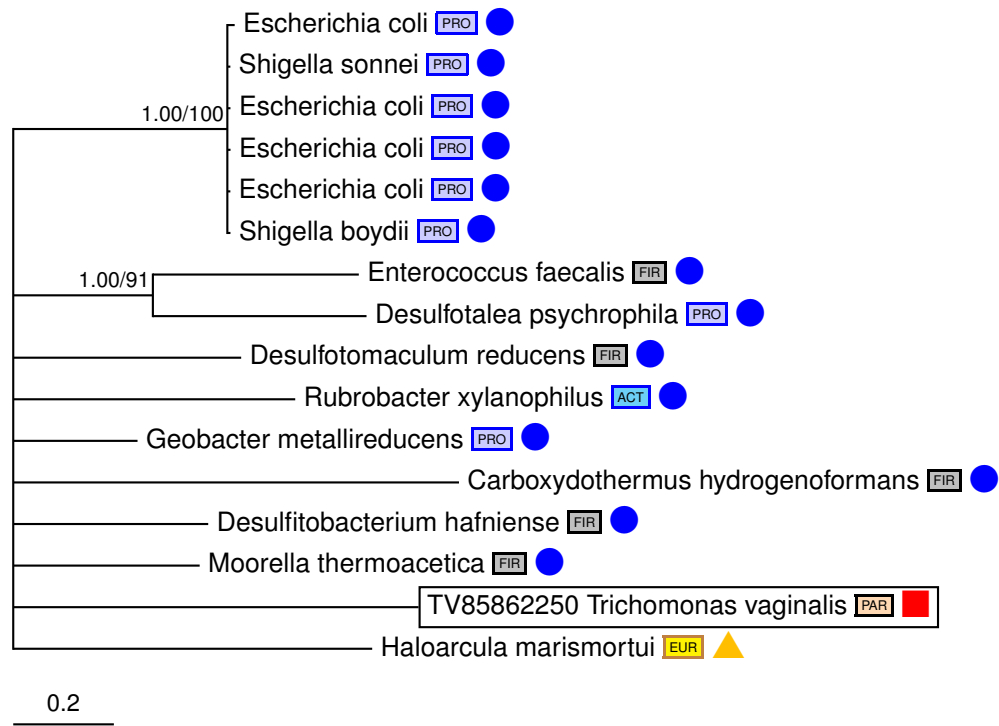
TN074

Candy accession: TV85337301
RefSeq accession: XP_001329100.1
Uniprot accession: A2DRTO_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:5.3.2.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Tautomerase enzyme family protein
Name of enzyme/protein: Tautomerase enzyme family protein
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



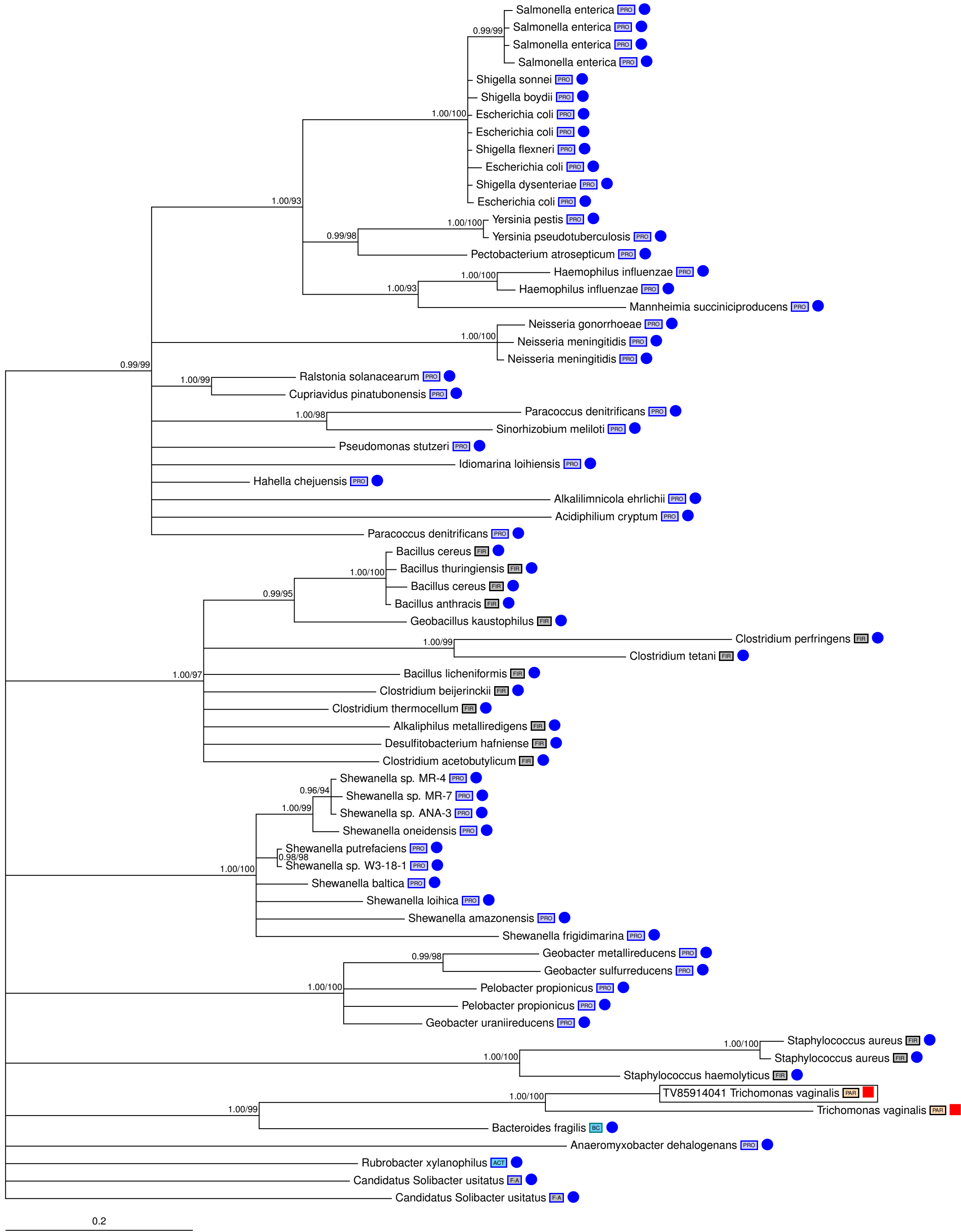
TN075

Candy accession: TV85862250
RefSeq accession: XP_001325565.1
Uniprot accession: A2E1Z3_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted selenium-dependent hydroxylase
accessory protein YqeC
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



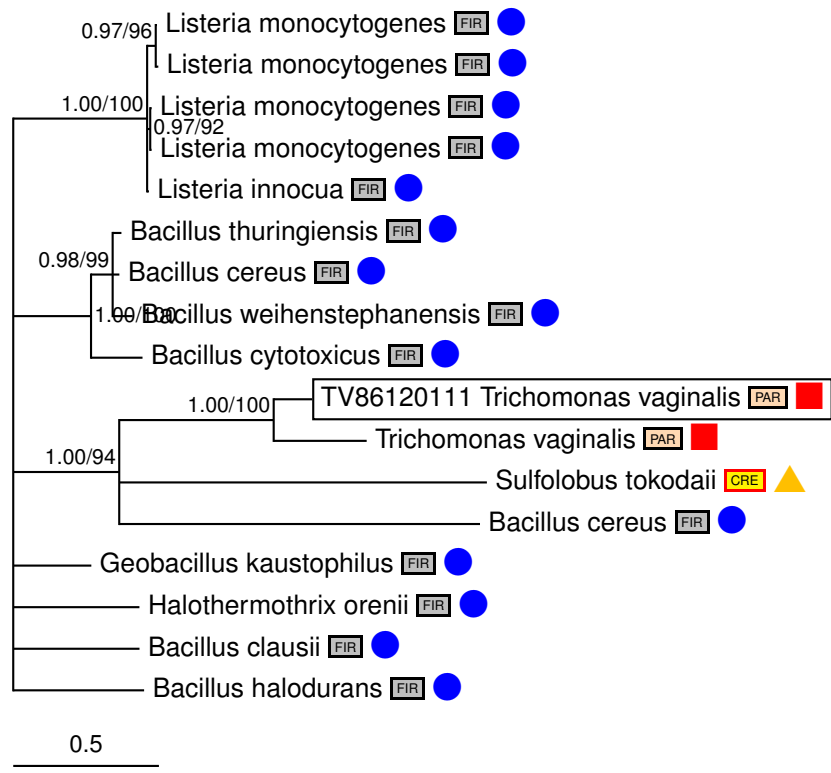
TN076

Candy accession: TV85914041
RefSeq accession: XP_001307232.1
Uniprot accession: A2FLC1_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteroides
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted iron-sulfur cluster repair di-iron protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



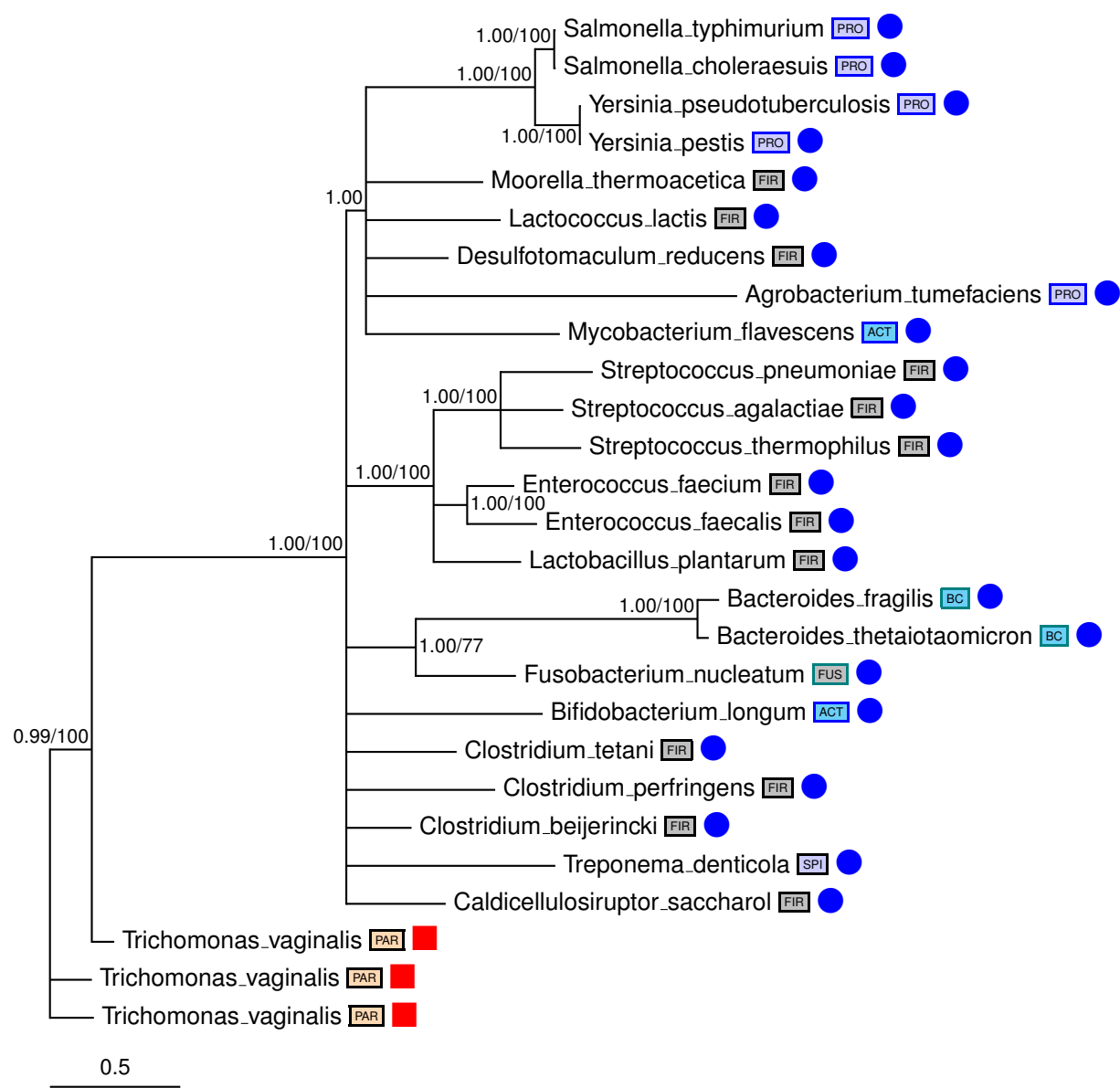
TN077

Candy accession: TV86120111
RefSeq accession: XP_001315078.1
Uniprot accession: A2EWU0_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: acetyltransferase, GNAT family-related protein
Name of enzyme/protein: Predicted acetyltransferase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



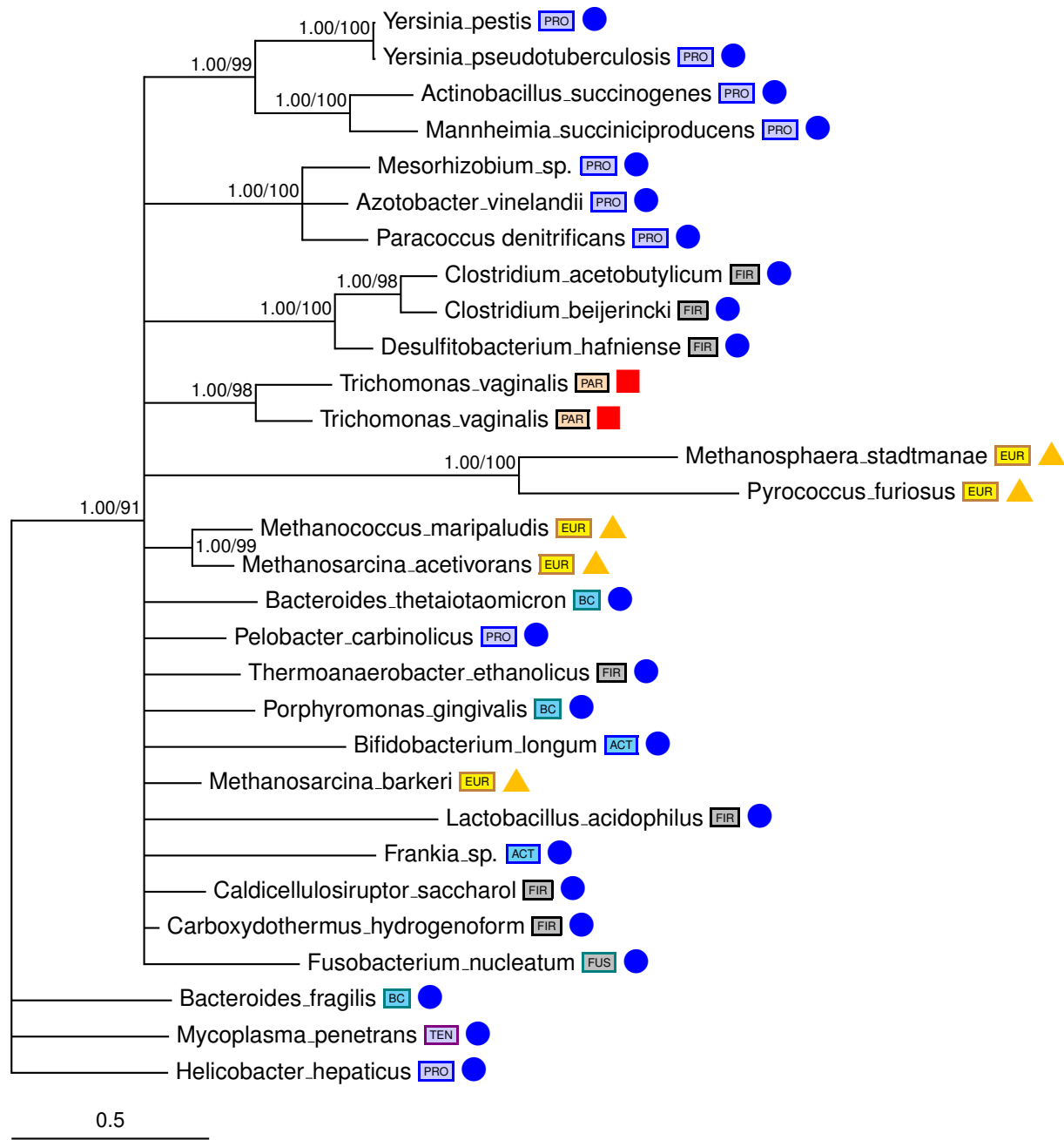
TN078

Candy accession: TV86507075
RefSeq accession: XP_001305824.1
Uniprot accession: A2FQA4_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 2
RefSeq annotation: TrkA-C domain containing protein
Name of enzyme/protein: TrkA-C domain containing protein
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



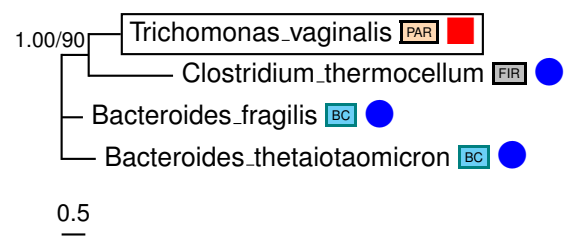
TN079

Candy accession: TV86576190
RefSeq accession: XP_001327976.1
Uniprot accession: A2DV26_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted flavodoxin
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



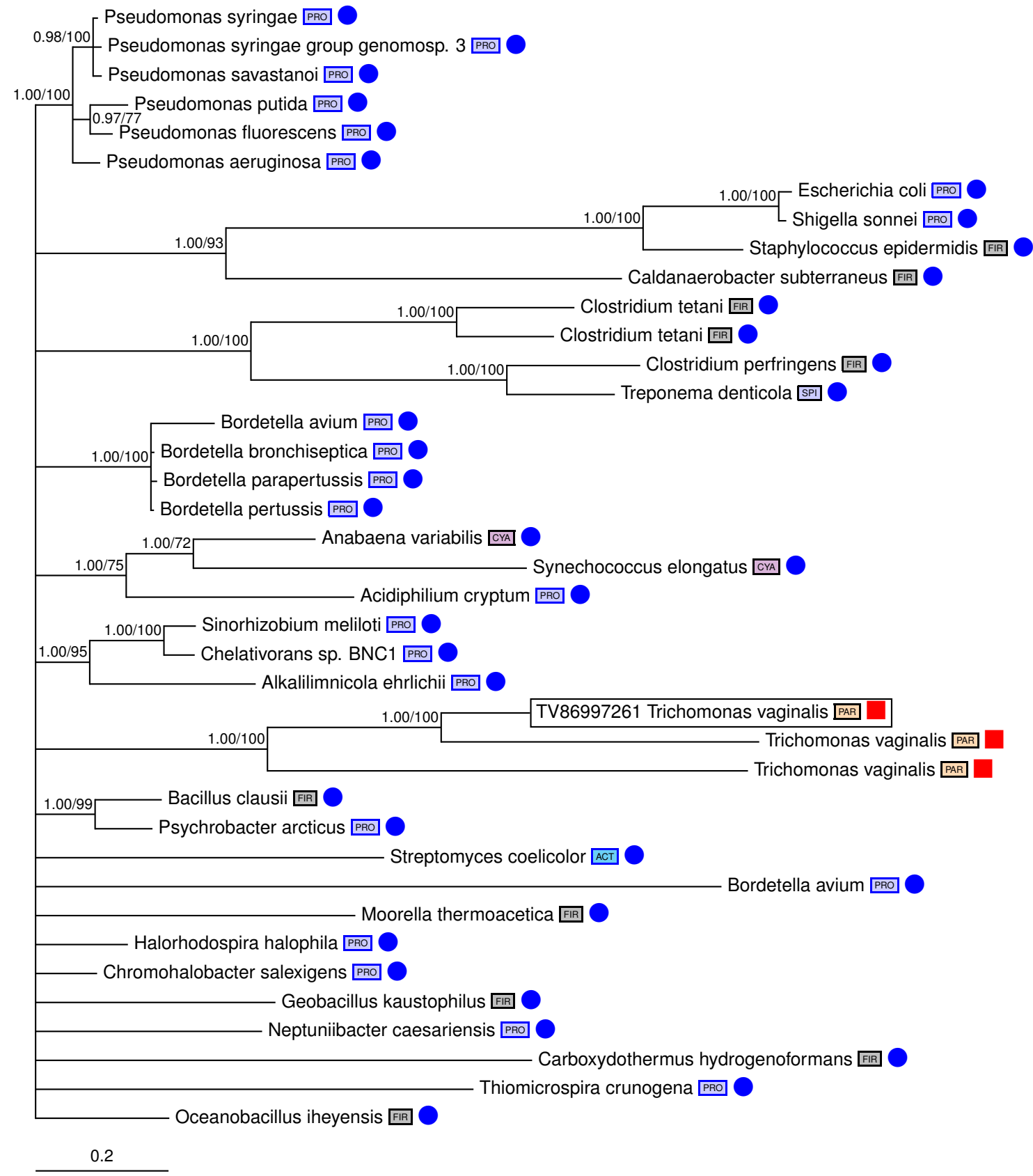
TN080

Candy accession: TV86997188
RefSeq accession: XP_001327447.1
Uniprot accession: A2DWN9_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): EC:3.2.1.4
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: xylanase
Name of enzyme/protein: endo-1,4-beta-D-glucanase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Starch and sucrose metabolism

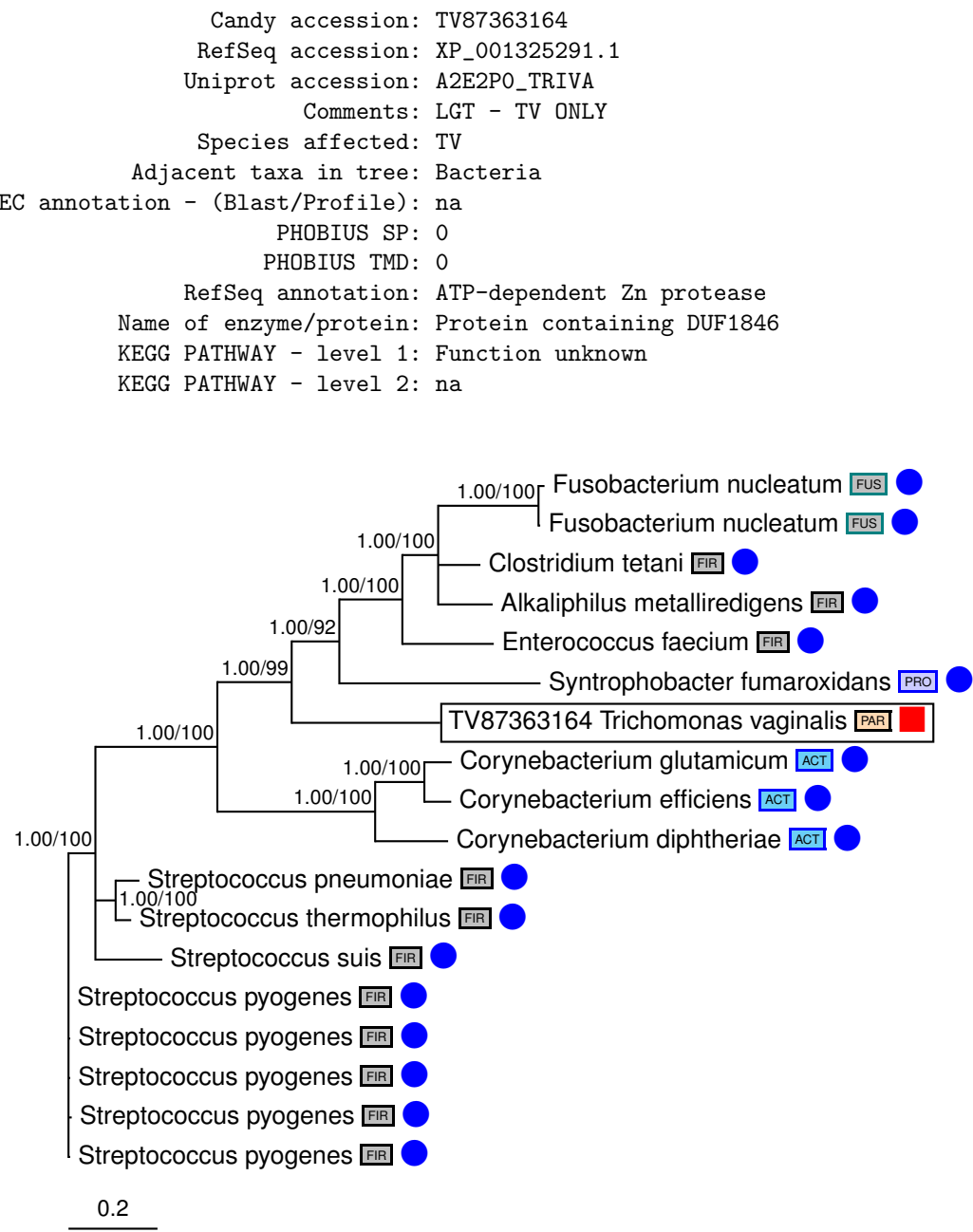


TN081

Candy accession: TV86997261
RefSeq accession: XP_001327422.1
Uniprot accession: A2DWL4_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 10
RefSeq annotation: YeeE/YedE family protein
Name of enzyme/protein: YeeE/YedE family protein
KEGG PATHWAY - level 1: Other function - Membrane transport
KEGG PATHWAY - level 2: na

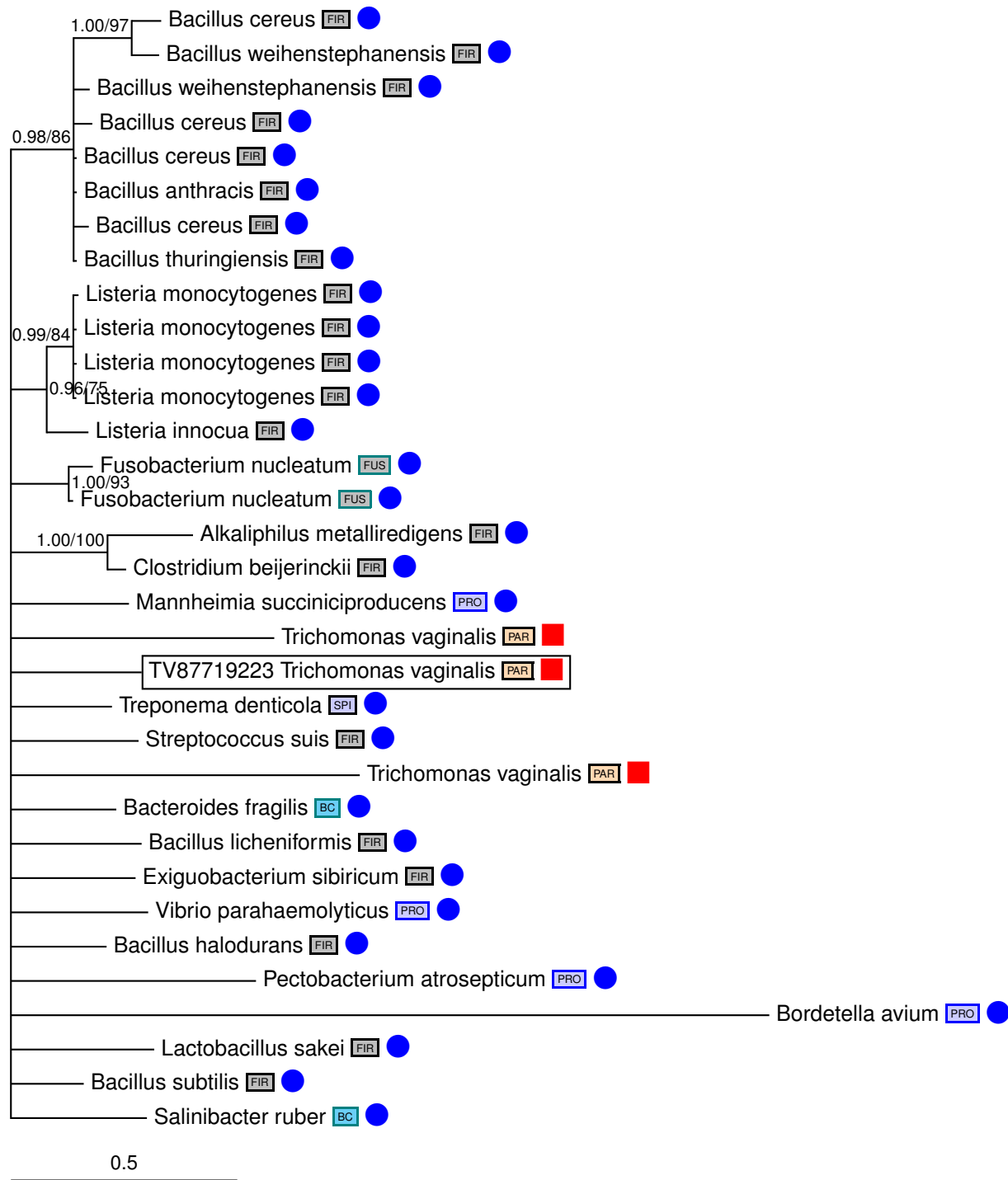


TN082



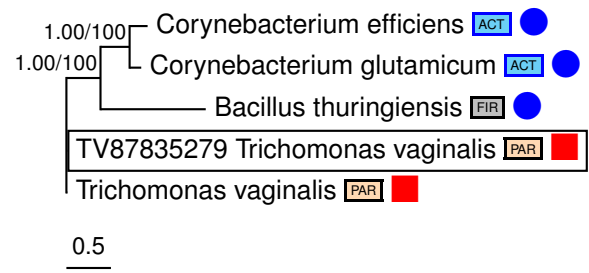
TN083

Candy accession: TV87719223
RefSeq accession: XP_001325053.1
Uniprot accession: A2E3D9_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:4.4.1.5
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Lactoylglutathione lyase
Name of enzyme/protein: lactoylglutathione lyase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pyruvate metabolism



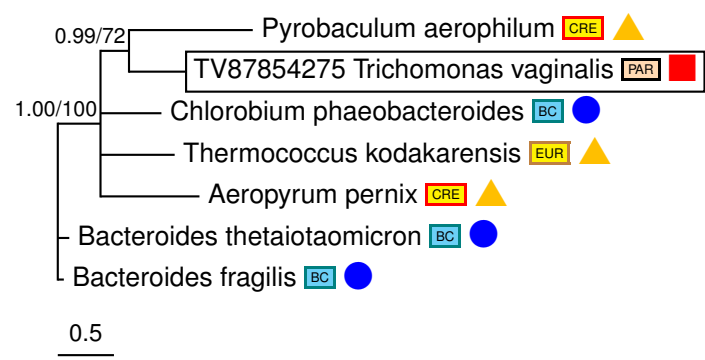
TN084

Candy accession: TV87835279
RefSeq accession: XP_001327568.1
Uniprot accession: A2DW44_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Hypothetical protein
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



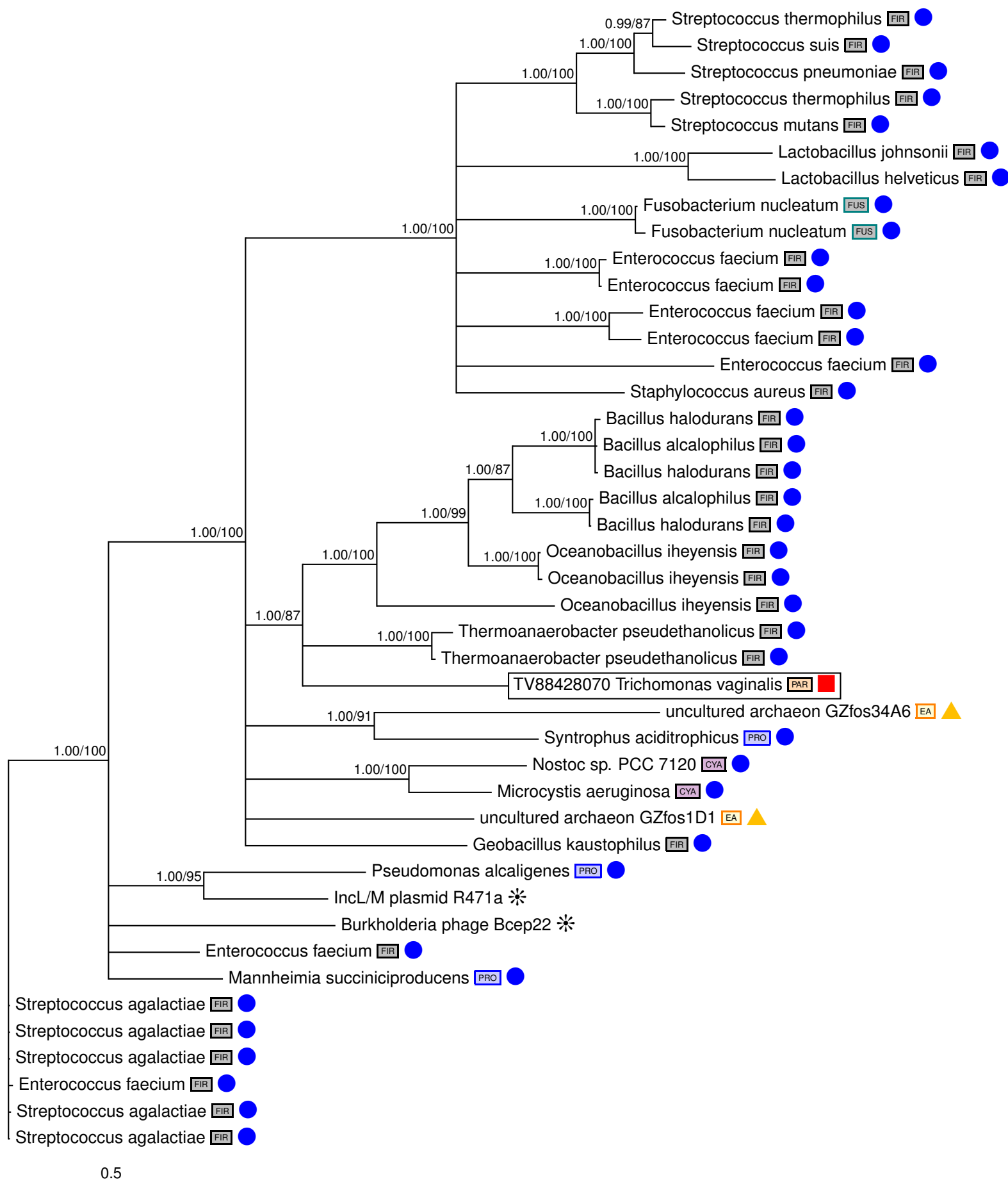
TN085

Candy accession: TV87854275
RefSeq accession: XP_001578953.1
Uniprot accession: A2DNX2_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Archaea - Pyrobaculum
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted L-ara-isomerases L-fucose
isomerase (FucIase) and L-arabinose
isomerase (AI) family
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



TN086

Candy accession: TV88428070
RefSeq accession: XP_001307942.1
Uniprot accession: A2FJ98_TRIVA
Comments: LGT - TV ONLY - ONE PHAGE, ONE PLASMID
Species affected: TV
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Transposase family protein
Name of enzyme/protein: Transposase family protein
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na



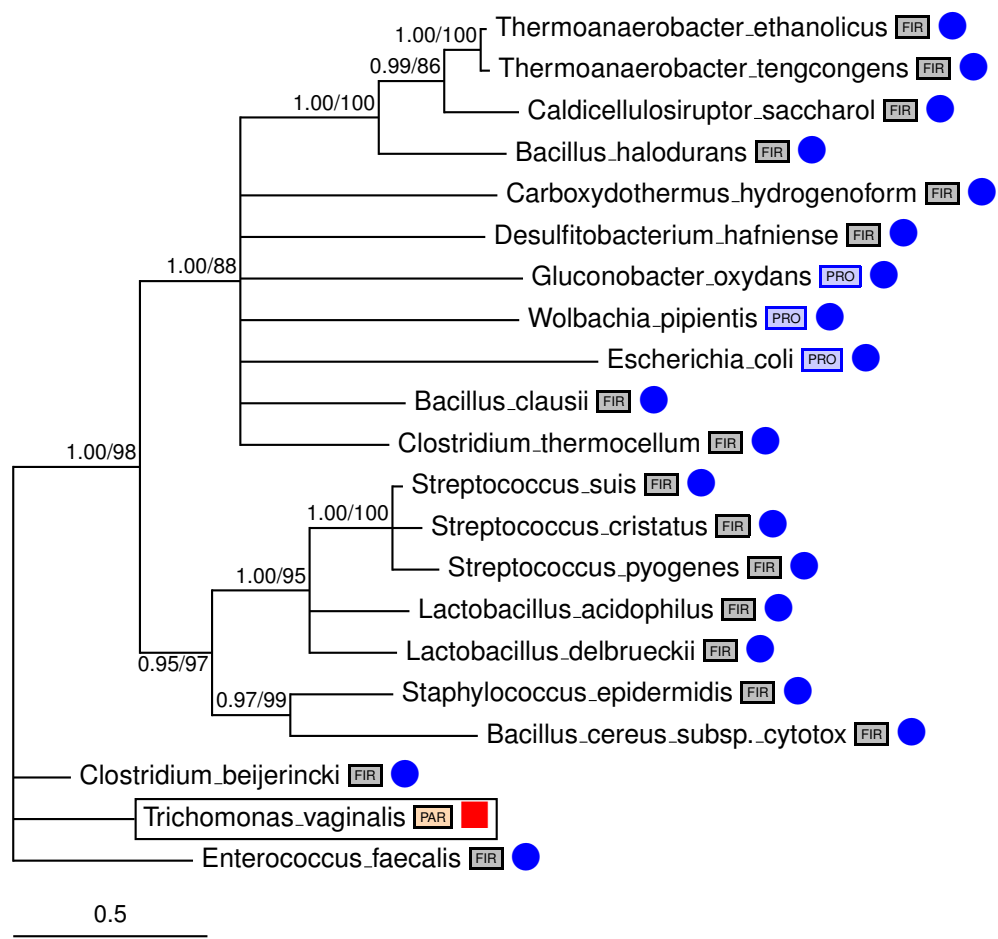
TN087

Candy accession: TV88428077
RefSeq accession: XP_001307936.1
Uniprot accession: A2FJ92_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.6.1.5
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: transcriptional regulator, gntR family protein
Name of enzyme/protein: tyrosine transaminase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Tyrosine metabolism



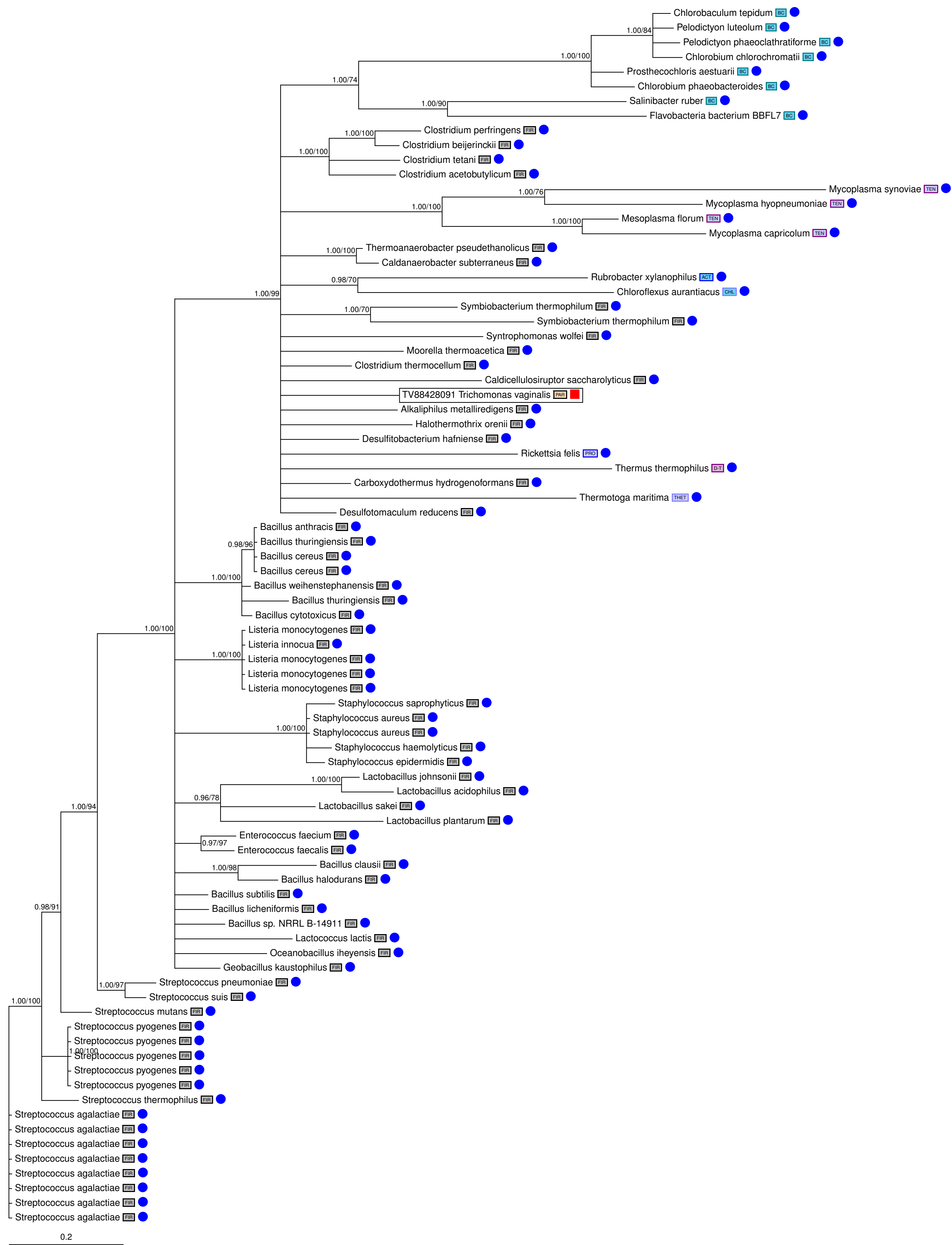
TN088

Candy accession: TV88428086
RefSeq accession: XP_001307935.1
Uniprot accession: A2FJ91_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Transposase IS116/IS110/IS902 family protein
Name of enzyme/protein: Transposase IS116/IS110/IS902 family protein
KEGG PATHWAY - level 1: Other function - Genetic Information Processing
KEGG PATHWAY - level 2: na



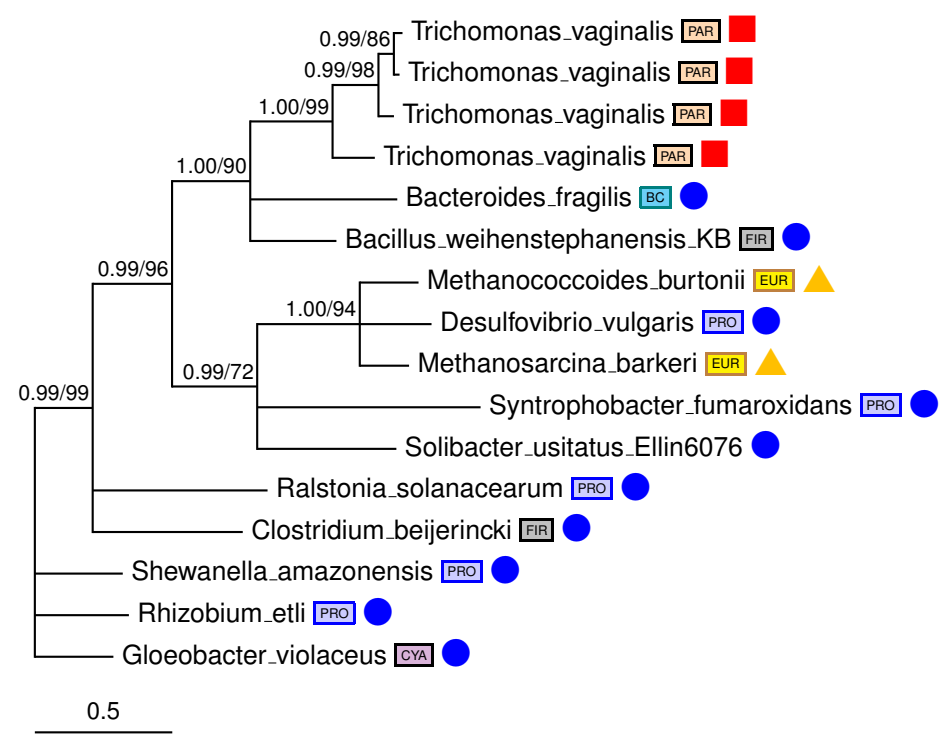
TN089

Candy accession: TV88428091
RefSeq accession: XP_001307960.1
Uniprot accession: A2FJB6_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: transcription elongation factor
Name of enzyme/protein: Predicted transcription elongation factor
KEGG PATHWAY - level 1: Other function - Genetic Information Processing
KEGG PATHWAY - level 2: na



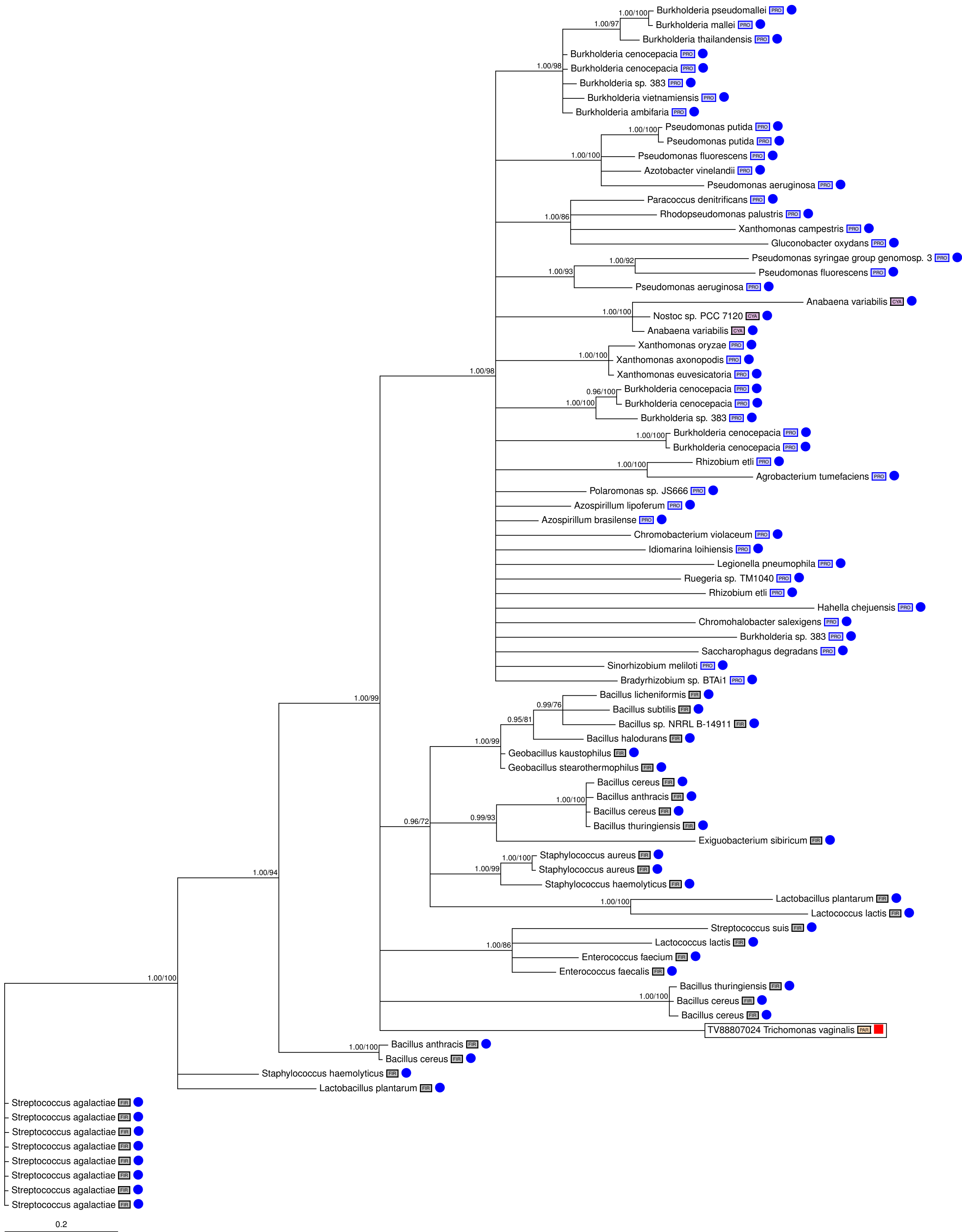
TN090

Candy accession: TV88613086
RefSeq accession: XP_001316524.1
Uniprot accession: A2ESRO_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted Zn-binding protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



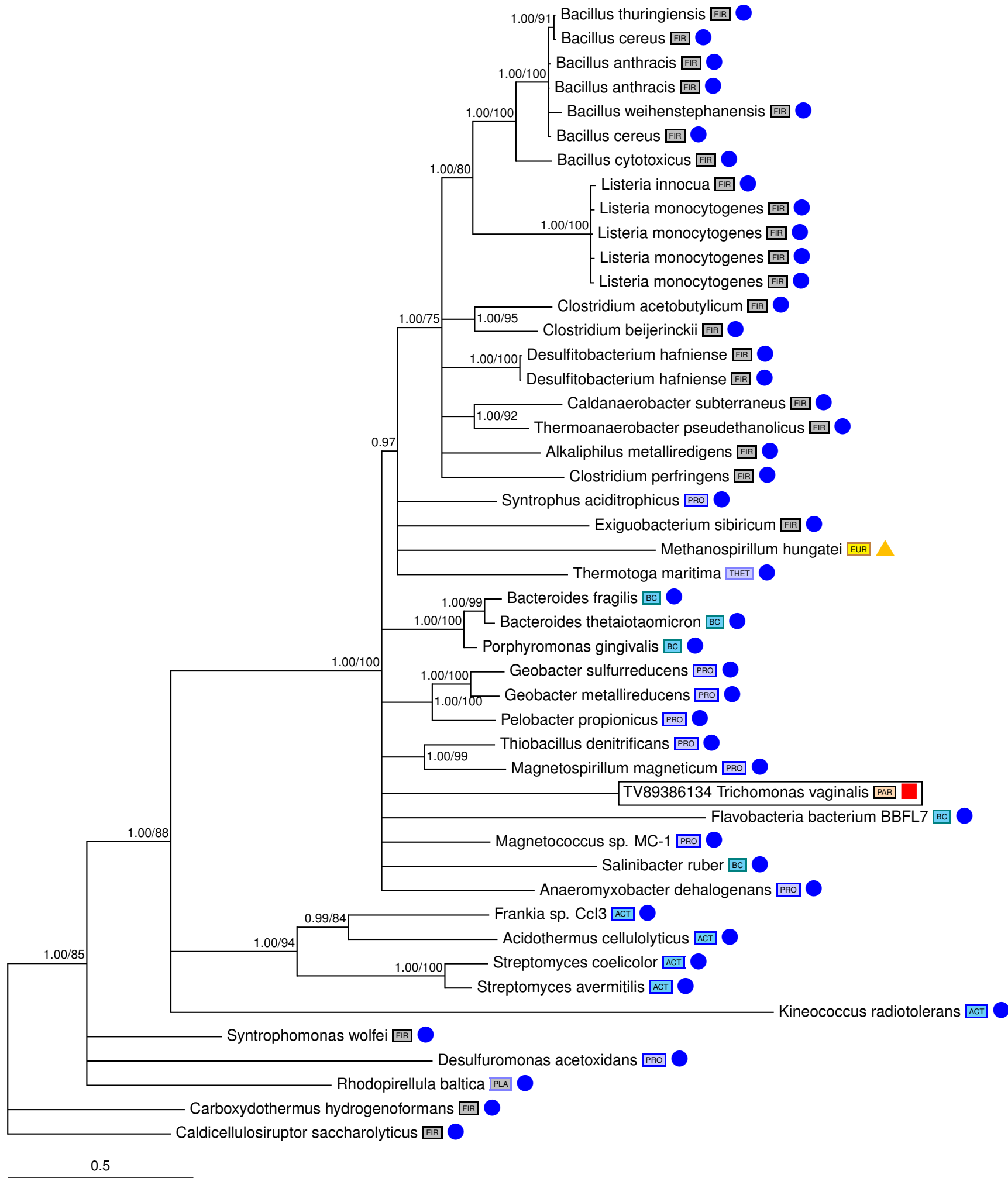
TN091

Candy accession: TV88807024
RefSeq accession: XP_001302201.1
Uniprot accession: A2G0P6_TRIPLA
Comments: LCT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): EC:3.1.4.14
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: Flavodoxin-like fold family protein
Name of enzyme/protein: Phosphodiesterase
KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Pantothenate and CoA biosynthesis



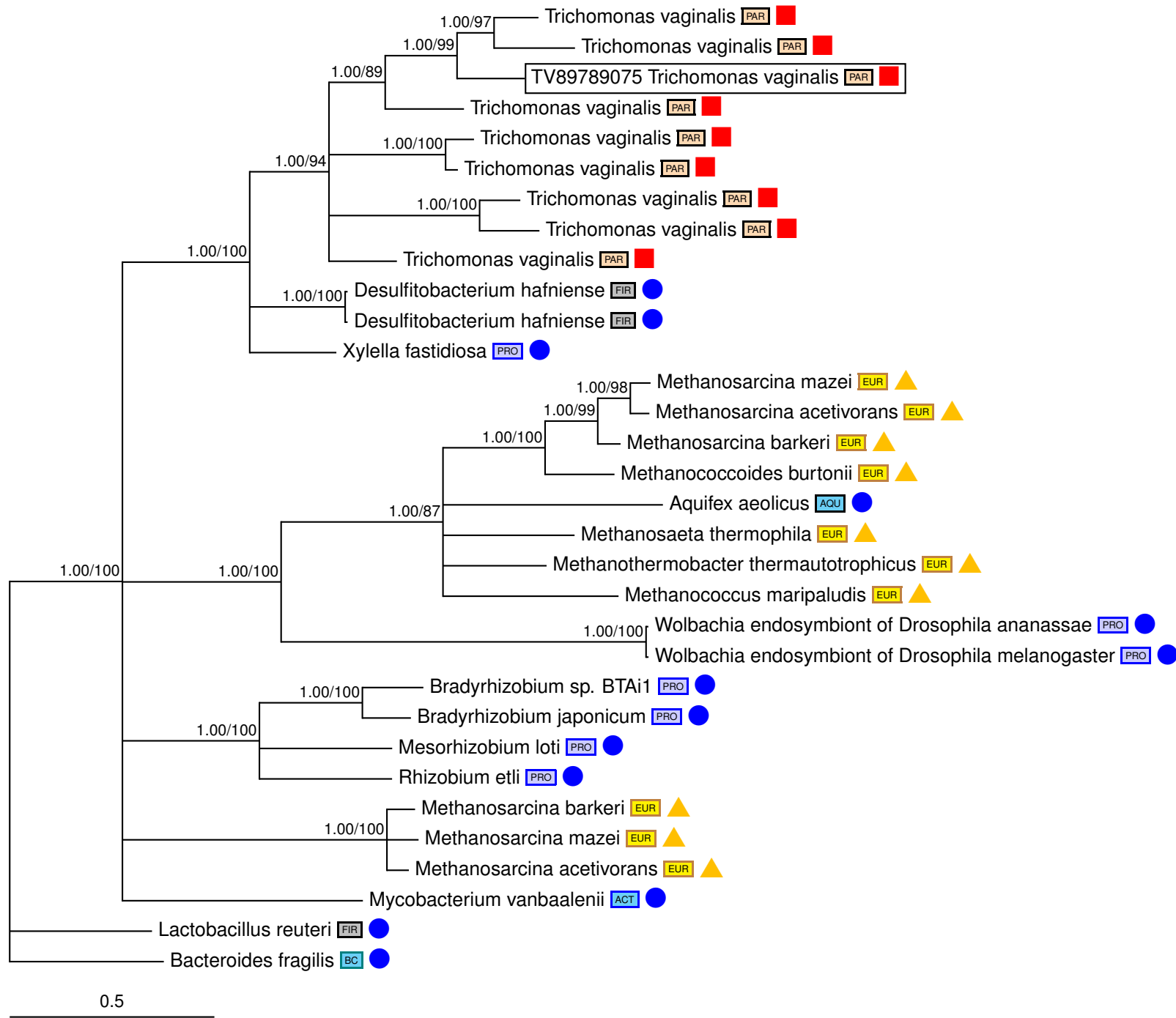
TN092

Candy accession: TV89386134
RefSeq accession: XP_001322324.1
Uniprot accession: A2EB55_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF1015
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



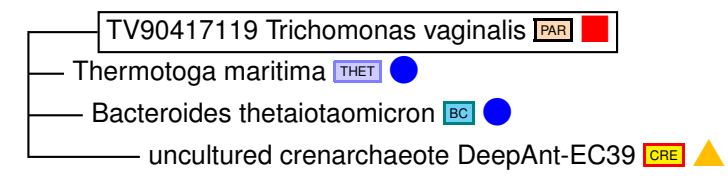
TN093

Candy accession: TV89789075
RefSeq accession: XP_001306702.1
Uniprot accession: A2FMV5_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:1.1.1.193
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: RibD C-terminal domain containing protein
Name of enzyme/protein: 5-amino-6-(5-phosphoribosylamino)uracil reductase
KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Riboflavin metabolism



TN094

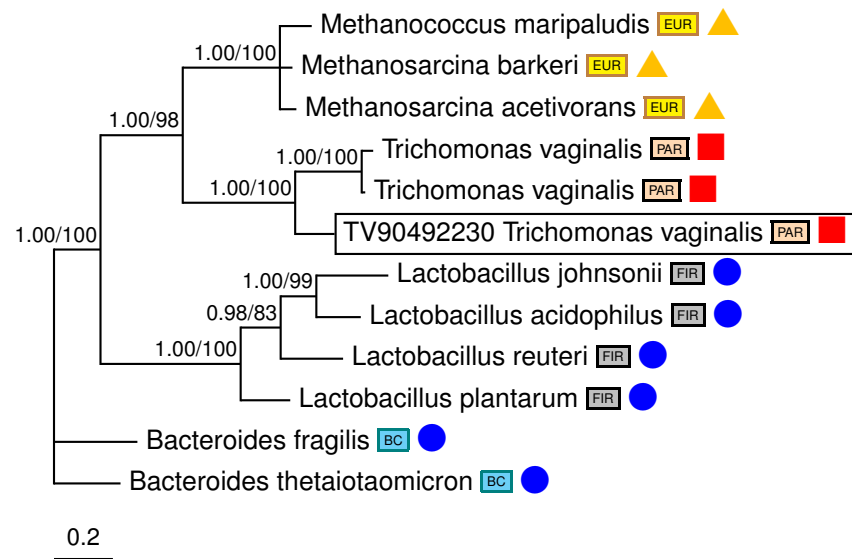
Candy accession: TV90417119
RefSeq accession: XP_001320377.1
Uniprot accession: A2EGR6_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing carbohydrate kinase domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



0.2

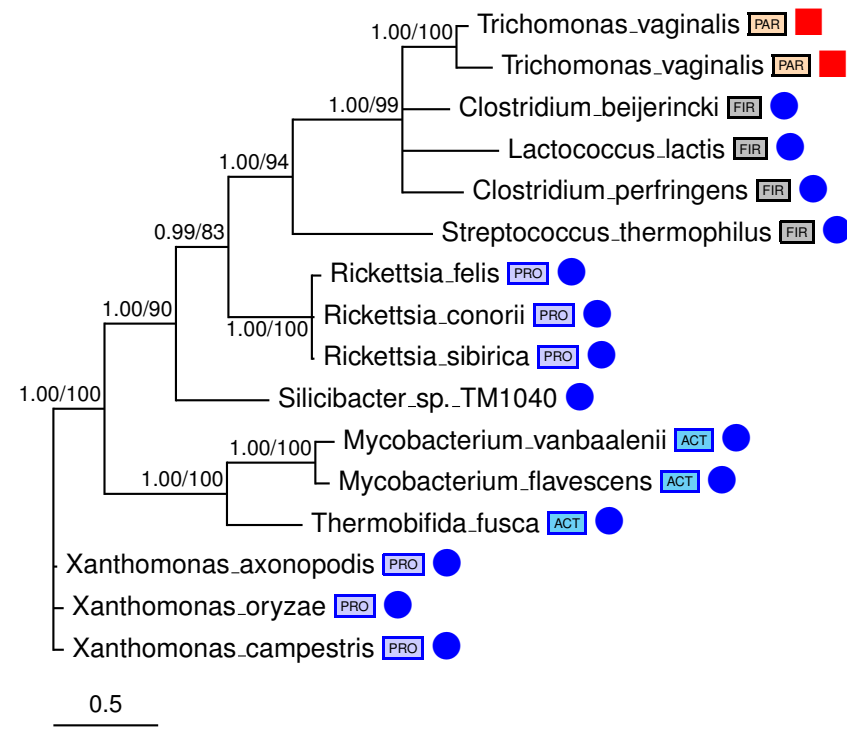
TN095

Candy accession: TV90492230
RefSeq accession: XP_001579117.1
Uniprot accession: A2DNE3_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Archaea
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF3737
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



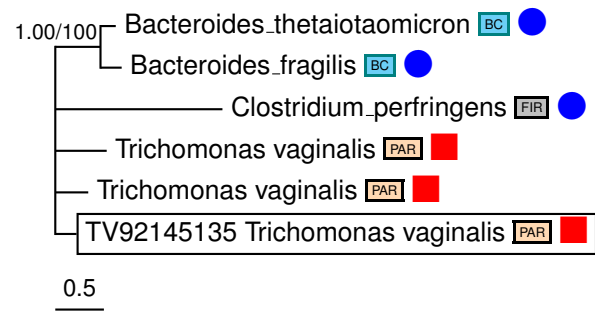
TN096

Candy accession: TV90569185
RefSeq accession: XP_001320437.1
Uniprot accession: A2EGL9_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Firmicutes - Clostridia
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hydrolase, NUDIX family protein
Name of enzyme/protein: Putative hydrolase, NUDIX family protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



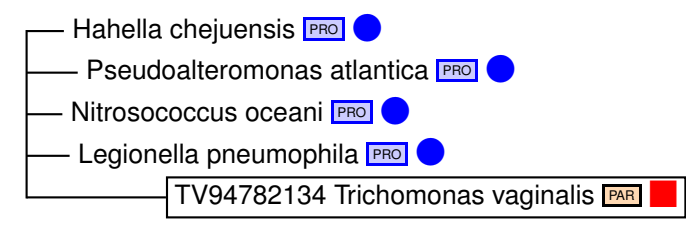
TN097

Candy accession: TV92145135
RefSeq accession: XP_001319335.1
Uniprot accession: A2EJN8_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: beta-N-acetylhexosaminidase
Name of enzyme/protein: Protein containig F5/8 type C domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



TN098

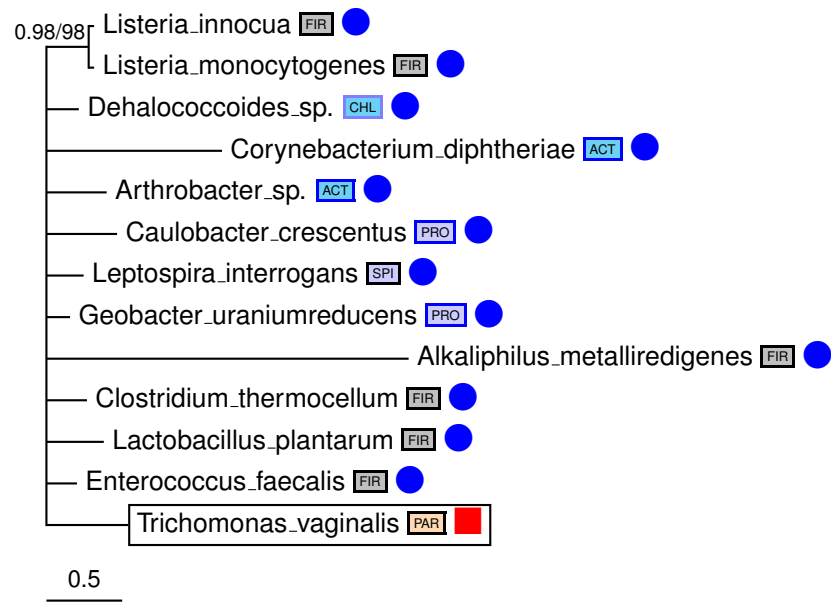
Candy accession: TV94782134
RefSeq accession: XP_001321629.1
Uniprot accession: A2ED51_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 1
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted disintegrin and metalloprotease-like protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



0.2

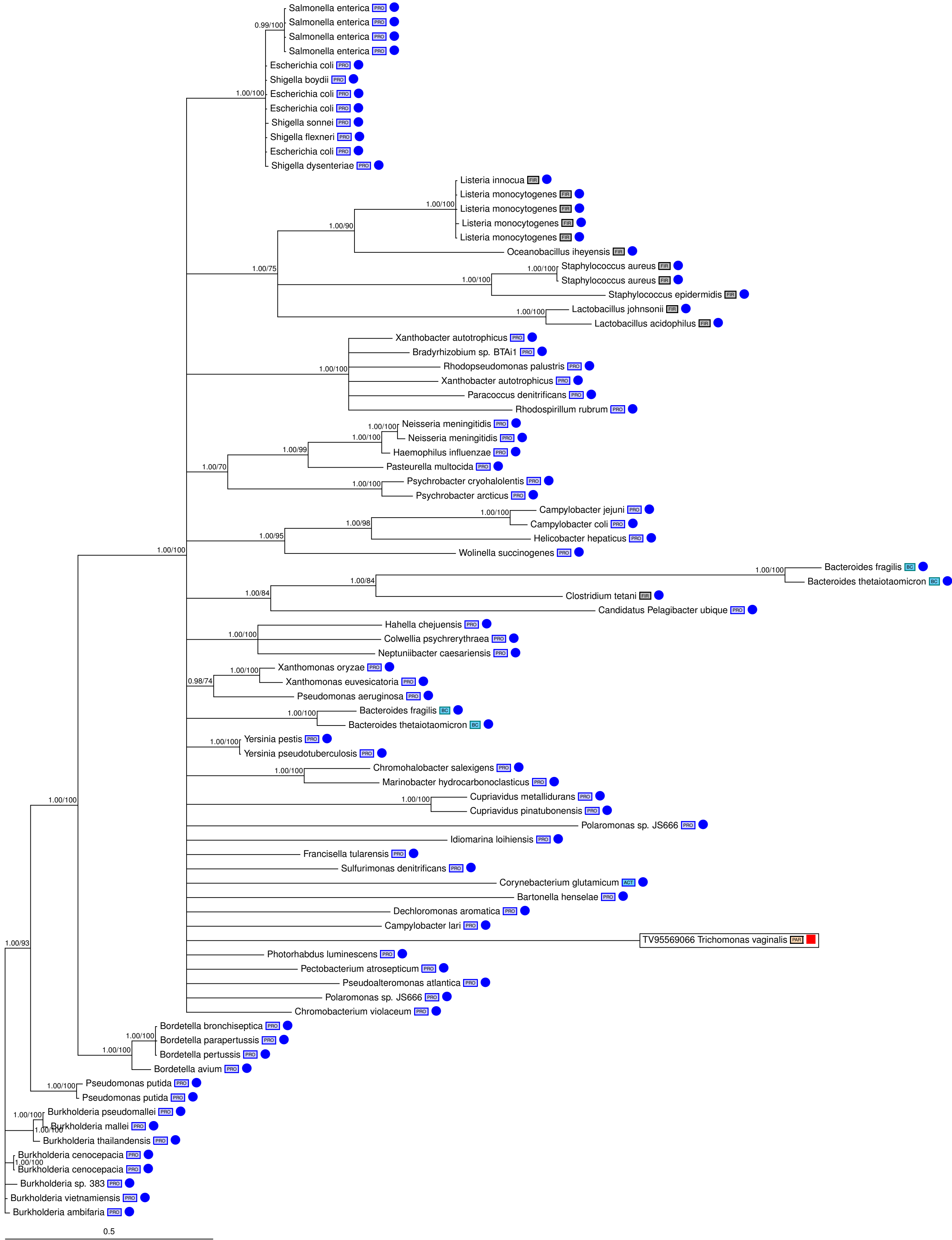
TN099

Candy accession: TV95240171
RefSeq accession: XP_001325131.1
Uniprot accession: A2E398_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF1801
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



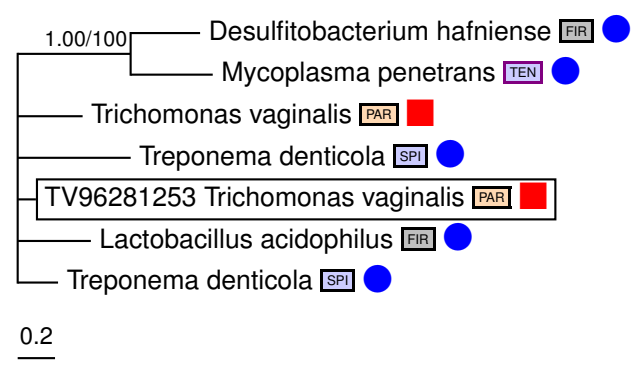
TN100

Candy accession: TV95569066
RefSeq accession: XP_001307274.1
Uniprot accession: A2FL88_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 10
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted 2-keto-3-deoxygluconate permease
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



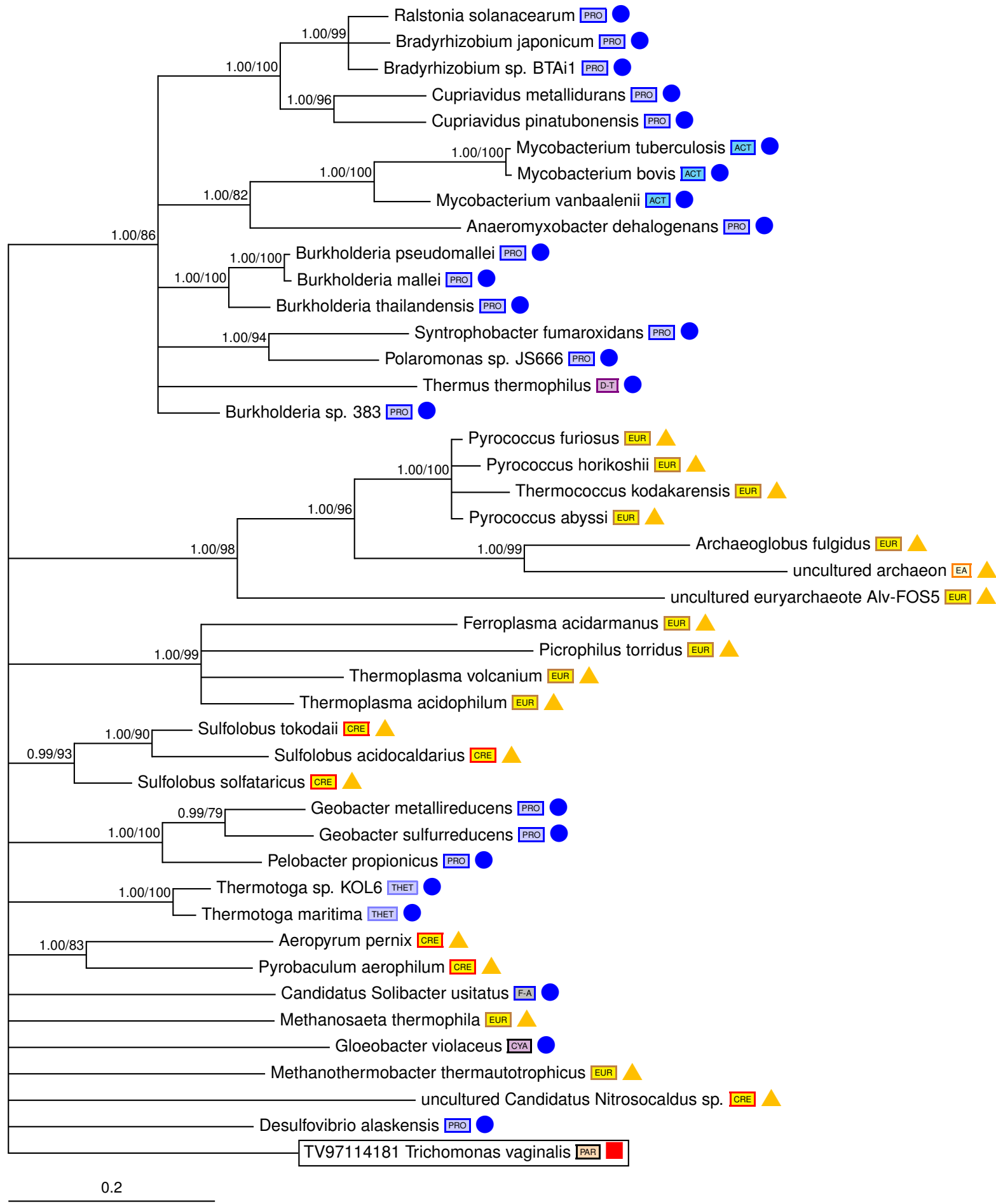
TN101

Candy accession: TV96281253
RefSeq accession: XP_001328362.1
Uniprot accession: A2DTZ2_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF369
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



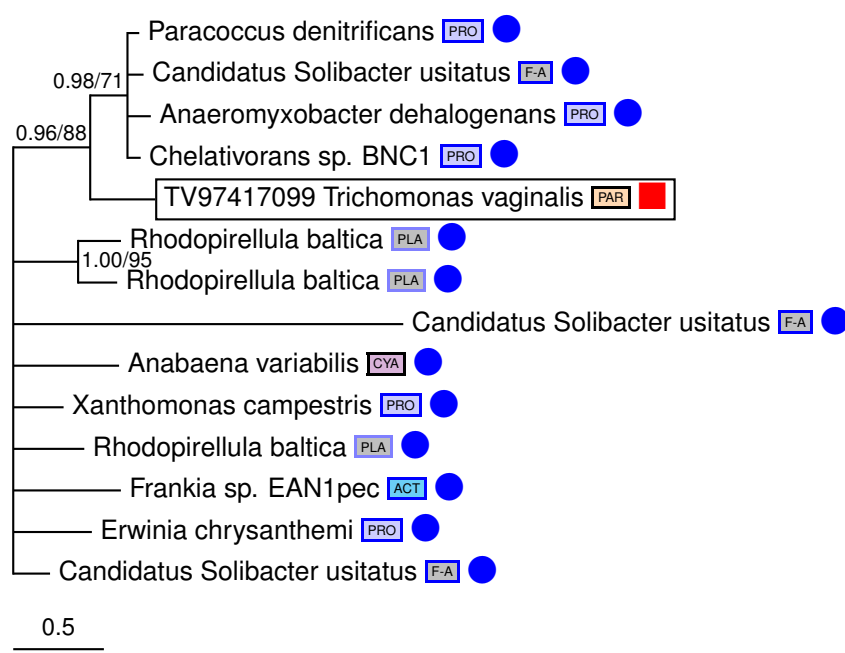
TN102

Candy accession: TV97114181
RefSeq accession: XP_001326490.1
Uniprot accession: A2DZD8_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted adenosine specific kinase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



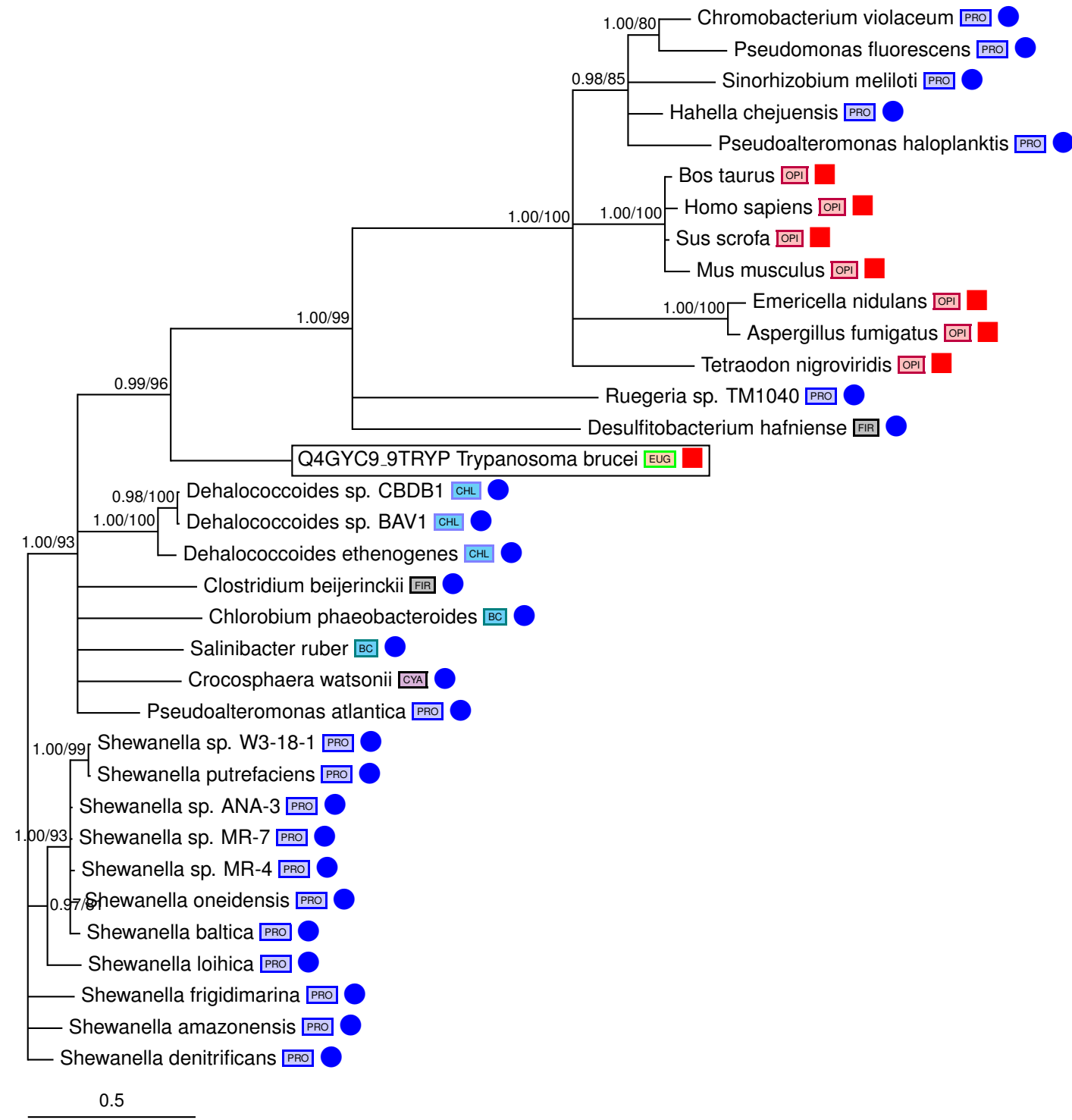
TN103

Candy accession: TV97417099
RefSeq accession: XP_001320324.1
Uniprot accession: A2EGW7_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.2.1.8
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: endo-1,4-beta-xylanase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



TN104

Candy accession: Q4GYC9_9TRYP
RefSeq accession: XP_001219142.1
Uniprot accession: Q4GYC9_9TRYP
Comments: LGT - TB
Species affected: TB
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.3.1.57
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: acetyltransferase
Name of enzyme/protein: diamine N-acetyltransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism



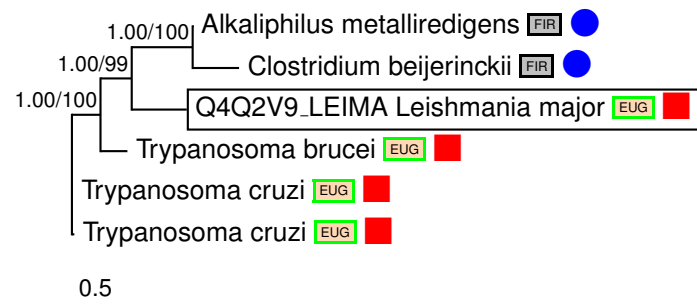
TN105

Candy accession: Q4Q014_LEIMA
RefSeq accession: XP_001687164.1
Uniprot accession: Q4Q014_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: TB,TC,Lm
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted mechanosensitive channel protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



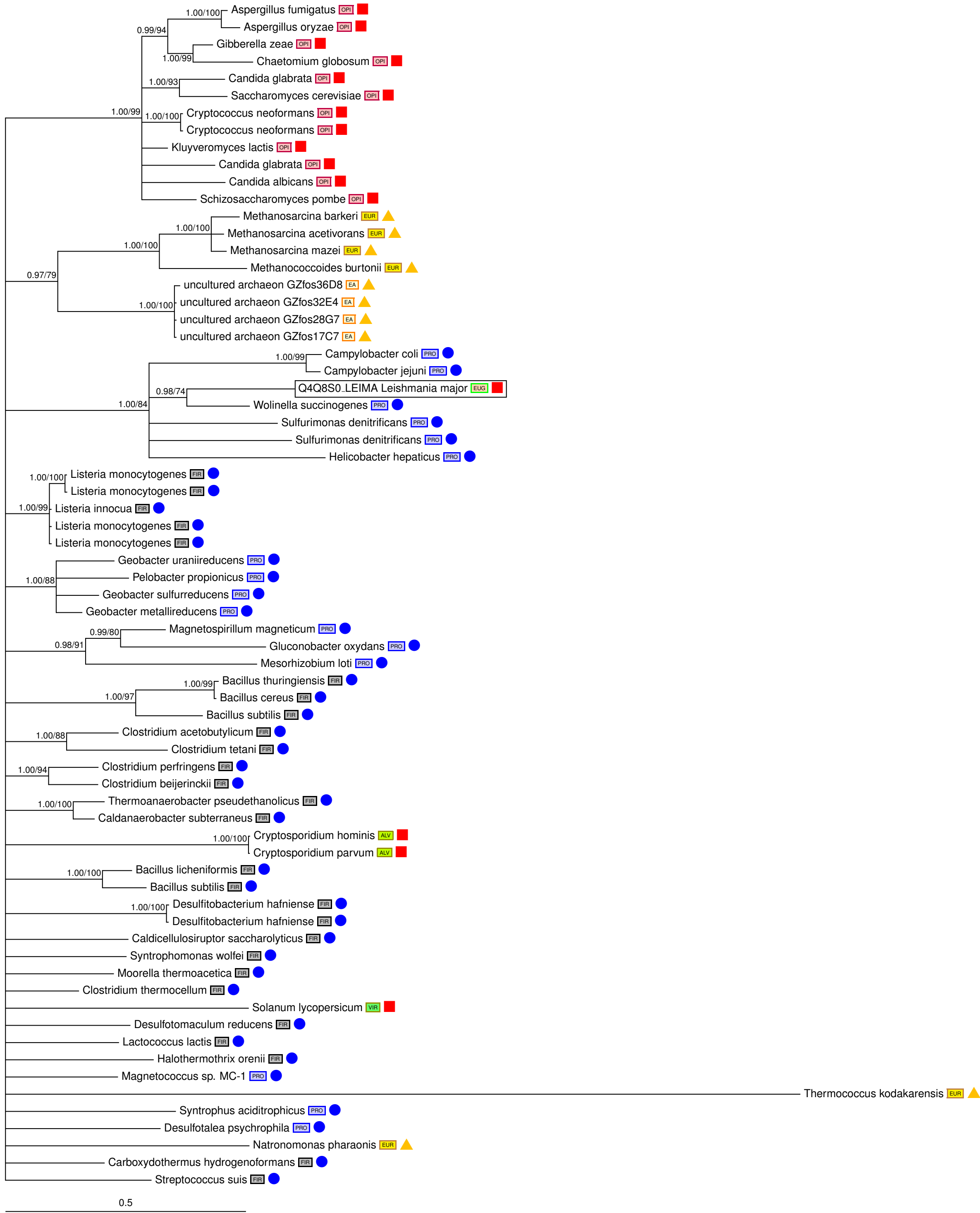
TN106

Candy accession: Q4Q2V9_LEIMA
RefSeq accession: XP_001686339.1
Uniprot accession: Q4Q2V9_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB,TC
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): EC:2.6.1.42
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: branched-chain amino acid aminotransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Valine, leucine and isoleucine degradation and biosynthesis, Pantothenate and CoA biosynthesis



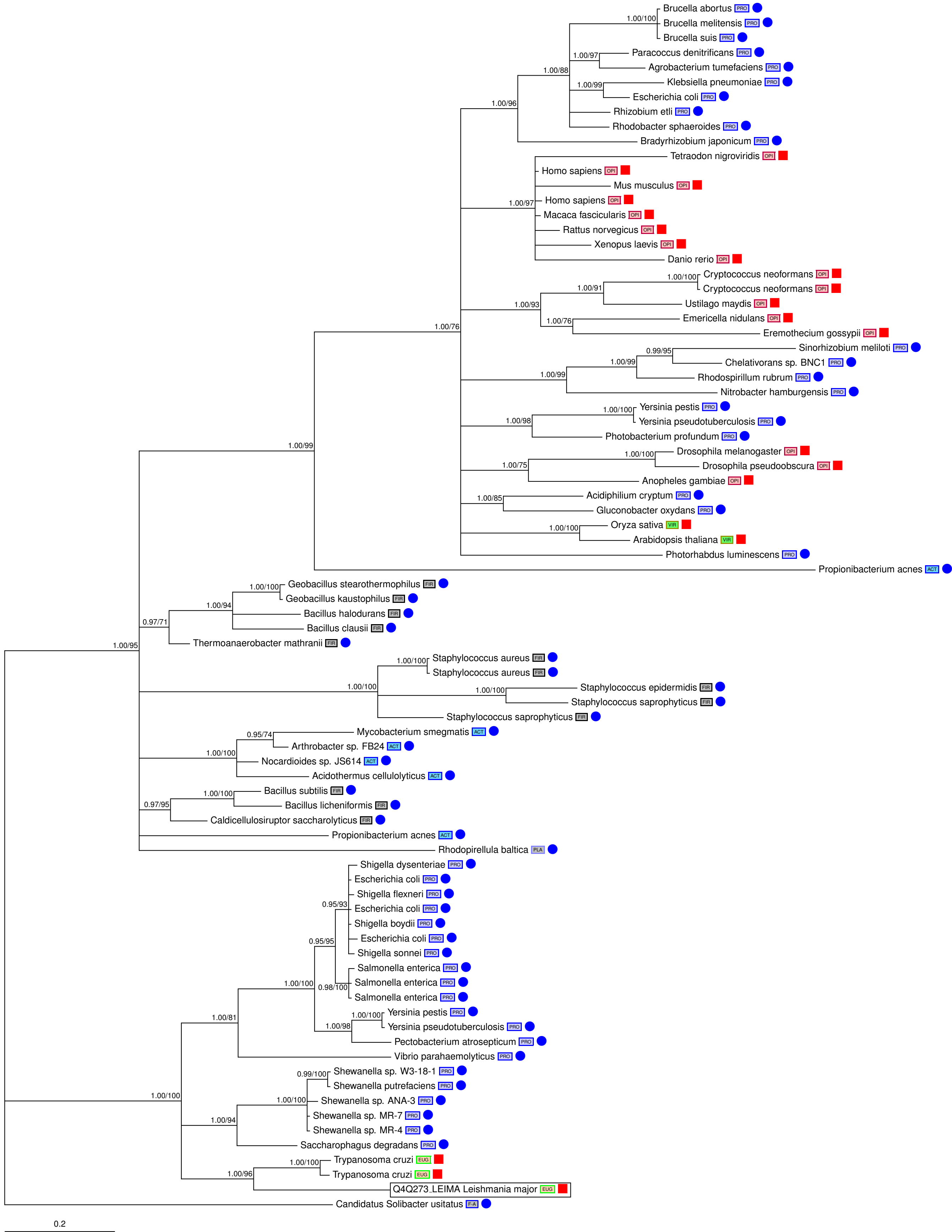
TN107

Candy accession: Q4Q8S0_LEIMA
RefSeq accession: XP_001684278.1
Uniprot accession: Q4Q8S0_LEIMA
Comments: LGT - LM TWO NODES
Species affected: LM
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:2.7.2.11
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glutamate 5-kinase
Name of enzyme/protein: Glutamate 5-kinase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism



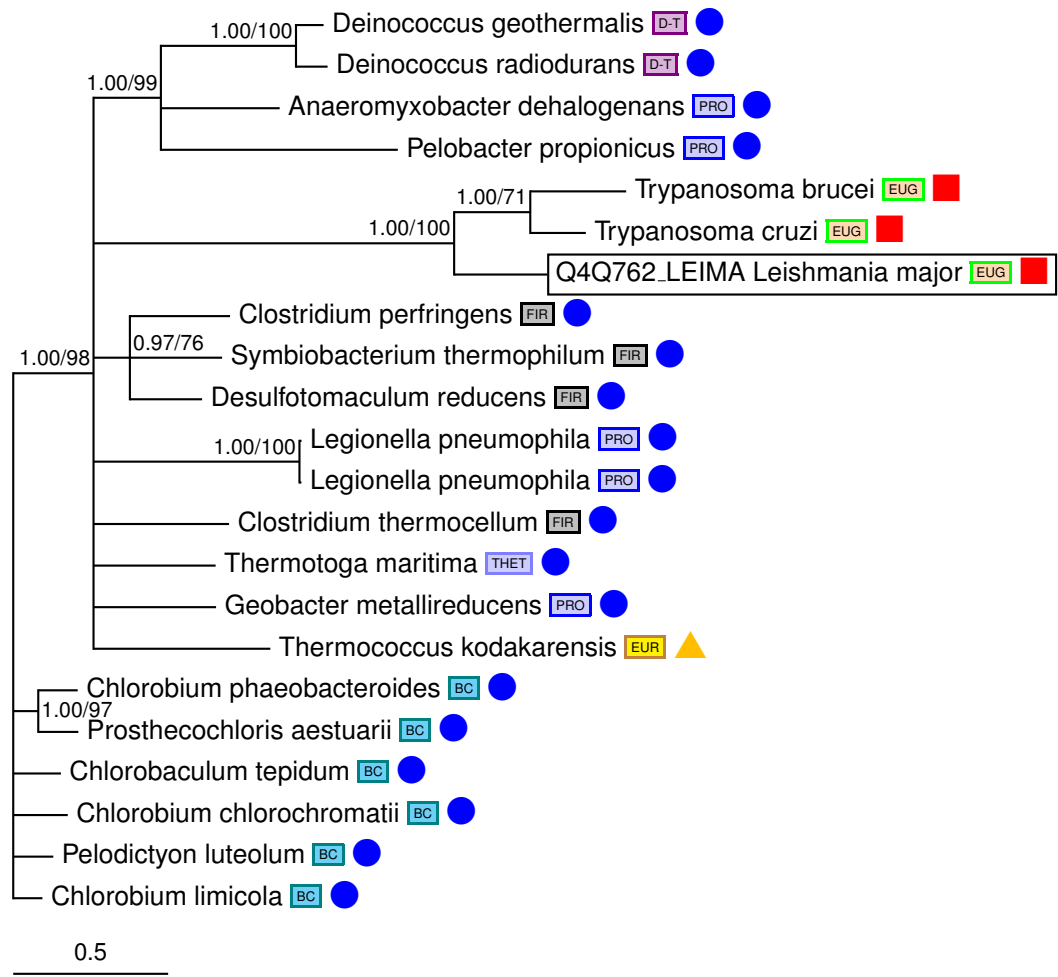
TN108

Candy accession: Q4Q273_LEIMA
RefSeq accession: XP_001686575.1
Uniprot accession: Q4Q273_LEIMA
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM, TC
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:2.7.1.16
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: L-ribulokinase
Name of enzyme/protein: L-ribulokinase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pentose and glucuronate interconversions



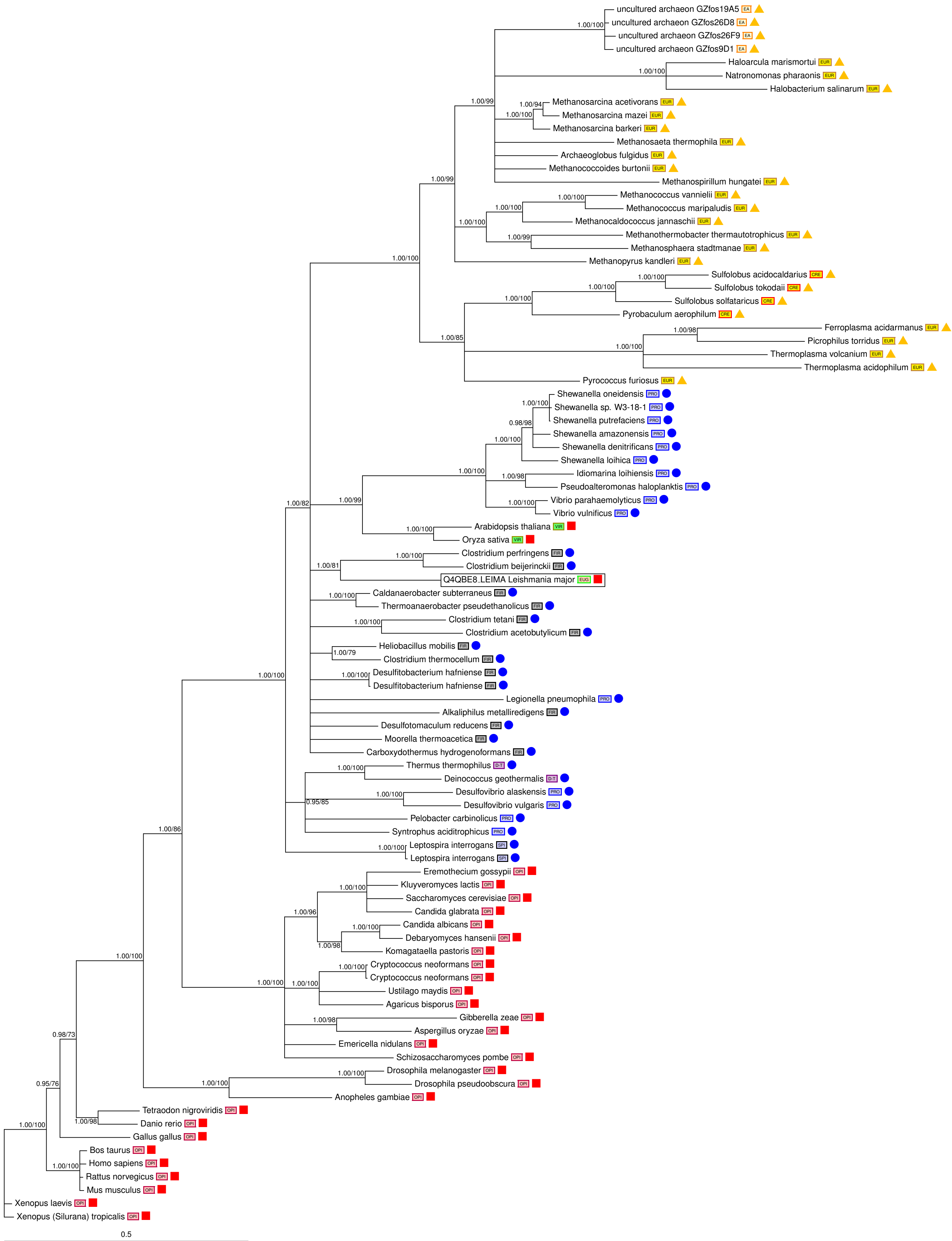
TN109

Candy accession: Q4Q762_LEIMA
RefSeq accession: XP_001684836.1
Uniprot accession: Q4Q762_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: TB,TC,LM
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:2.1.1.173
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: 23S rRNA
(guanine2445-N2)-methyltransferase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



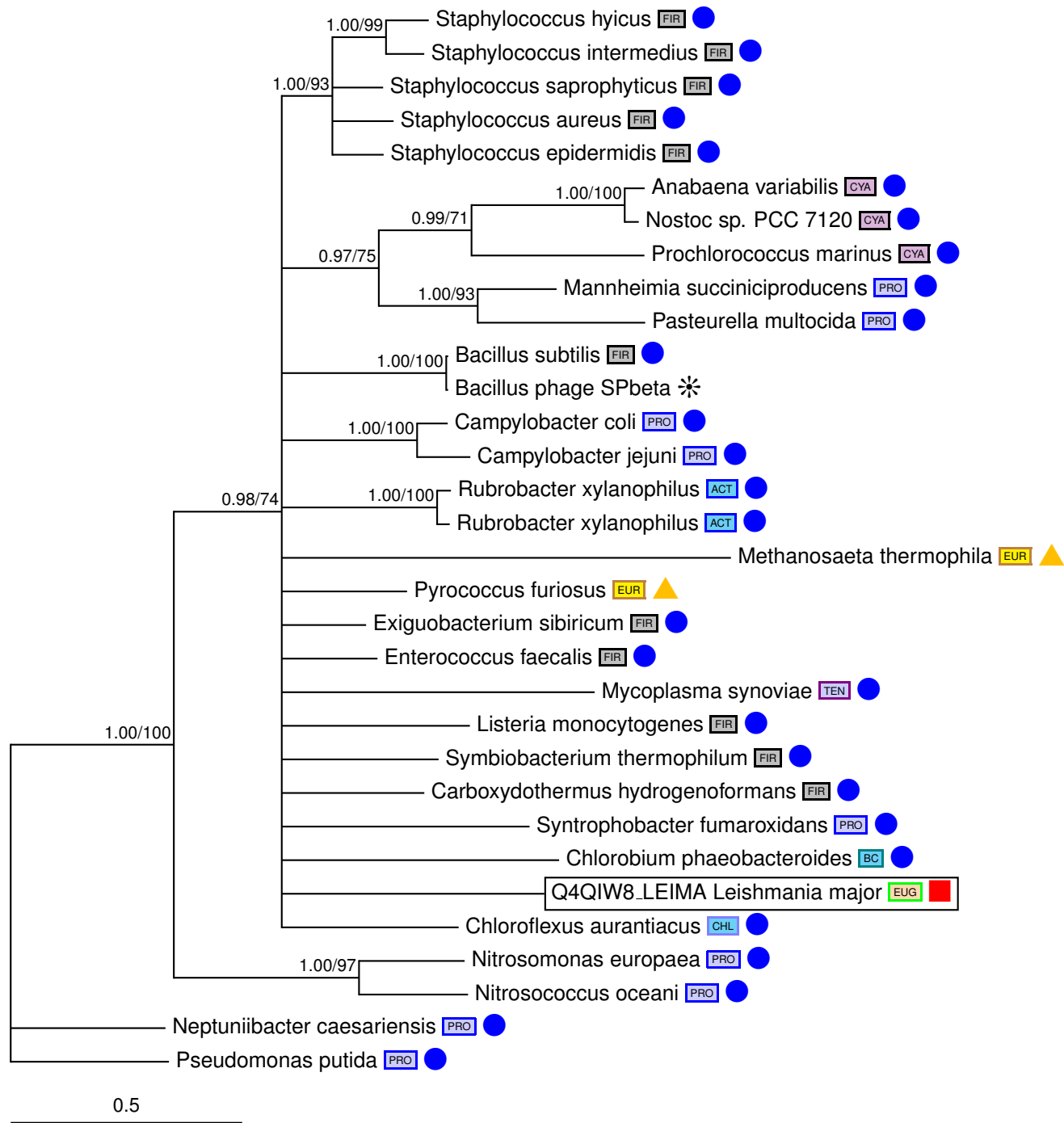
TN110

Candy accession: Q4QBE8_LEIMA
RefSeq accession: XP_001683350.1
Uniprot accession: Q4QBE8_LEIMA
Comments: LGT - LM TWO NODES - 3 DOMAIN TREE
Species affected: LM
Adjacent taxa in tree: Firmicutes - Clostridia
EC annotation - (Blast/Profile): EC:6.3.4.5
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: argininosuccinate synthase
Name of enzyme/protein: Argininosuccinate synthase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Alanine and aspartate metabolism, Arginine and proline metabolism



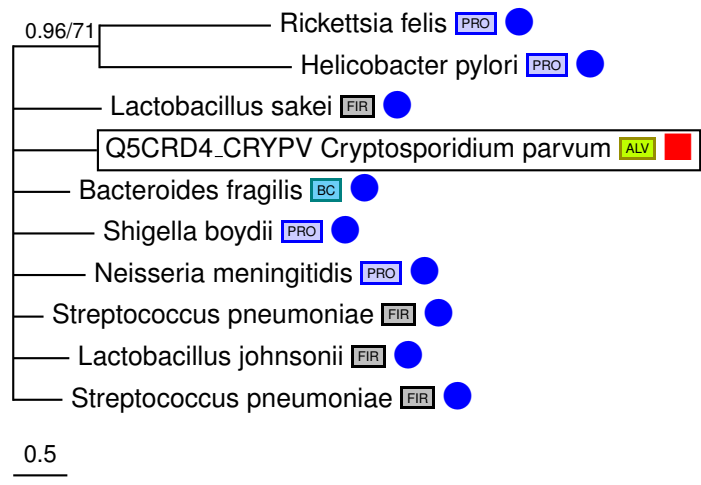
TN111

Candy accession: Q4QIW8_LEIMA
RefSeq accession: XP_001680880.1
Uniprot accession: Q4QIW8_LEIMA
Comments: LGT - LM ONLY
Species affected: LM
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:3.1.31.1
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: micrococcal nuclease
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



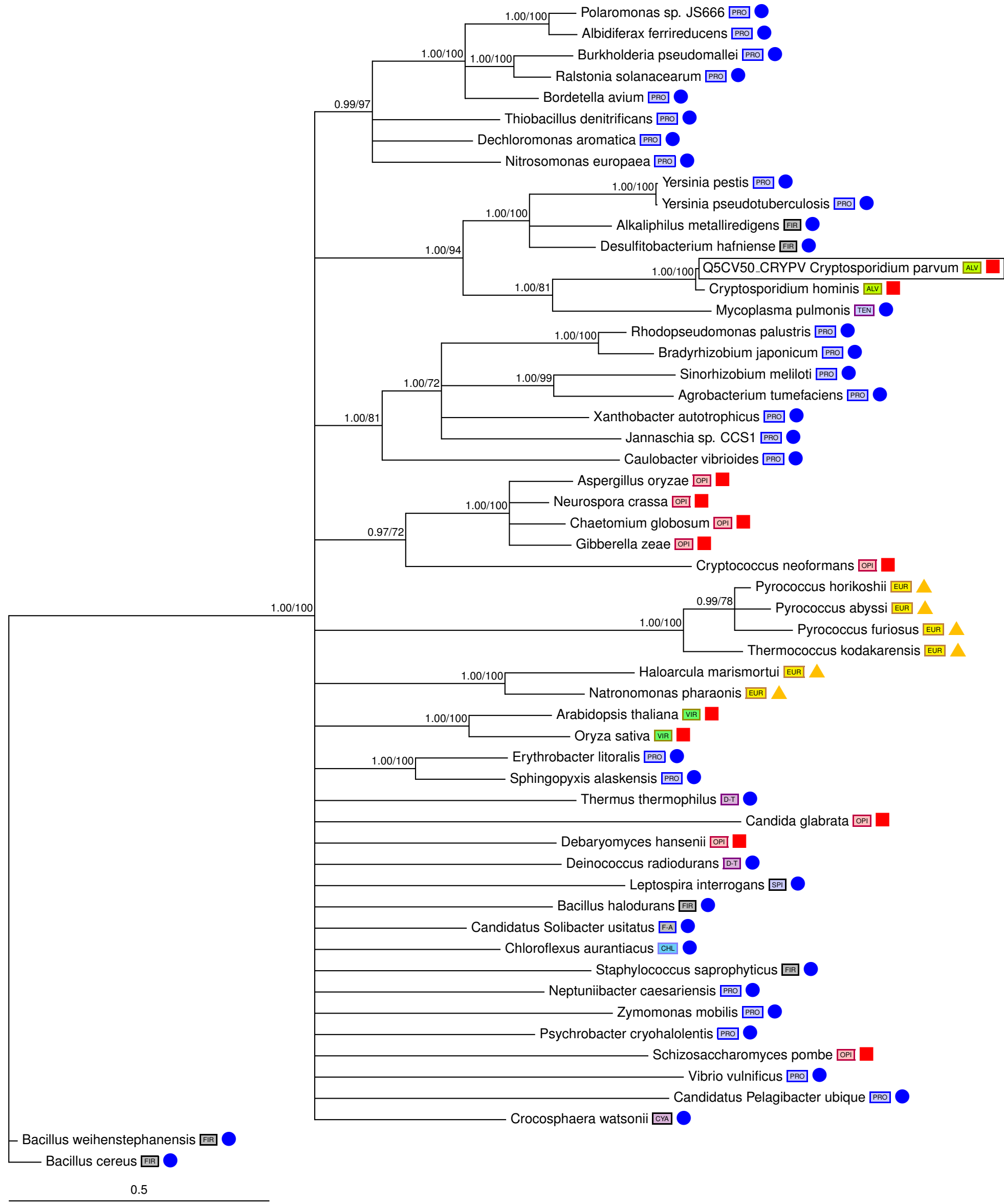
TN112

Candy accession: Q5CRD4_CRYPV
RefSeq accession: XP_626252.1
Uniprot accession: Q5CRD4_CRYPV
Comments: LGT - CP ONLY
Species affected: CP
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.4.1.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: secreted lipopolysaccharide sugar
transferase like family 8
glycosyltransferase
Name of enzyme/protein: lipopolysaccharide
1,2-glycosyltransferase
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism
KEGG PATHWAY - level 2: Lipopolysaccharide biosynthesis



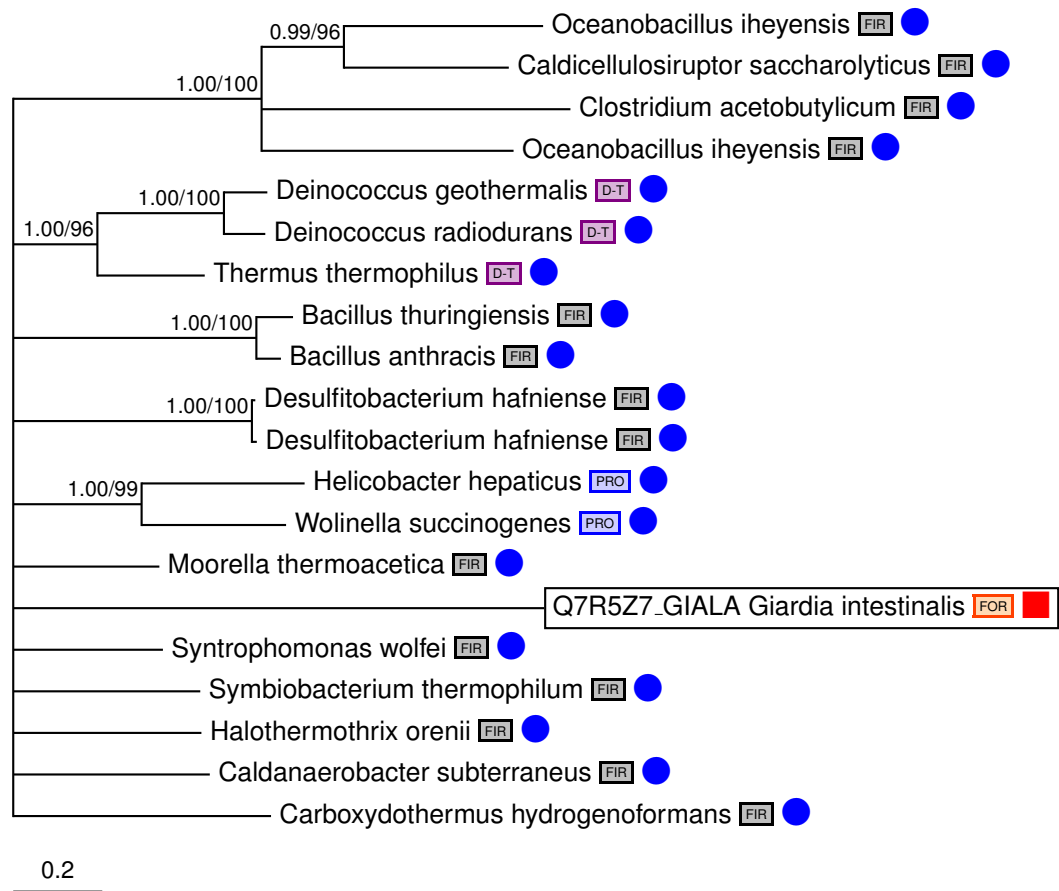
TN113

Candy accession: Q5CV50_CRYPV
RefSeq accession: XP_627419.1
Uniprot accession: Q5CV50_CRYPV
Comments: LGT - CP AND CH TWO NODES
Species affected: CP
Adjacent taxa in tree: Tenericutes - Mycoplasma
EC annotation - (Blast/Profile): EC:3.2.2.21
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: DNA-3-methyladenine glycosidase
Name of enzyme/protein: DNA-3-methyladenine glycosidase II
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



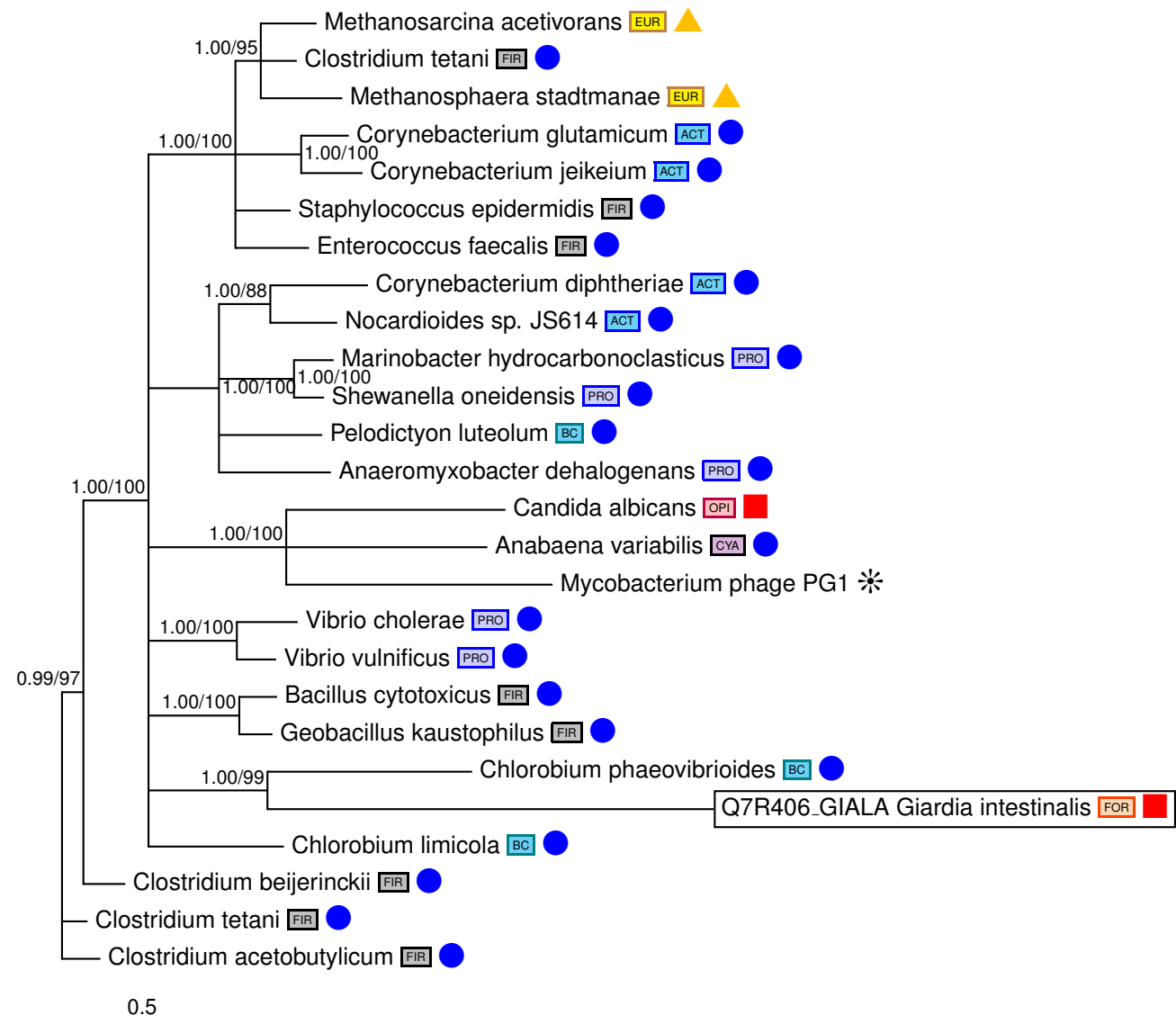
TN115

Candy accession: Q7R5Z7_GIALA
RefSeq accession: XP_001706848.1
Uniprot accession: A8BII9_GIALA
Comments: LGT - GI ONLY
Species affected: GI
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.1.3.15
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: Histidinol-phosphatase, putative
Name of enzyme/protein: Histidinol-phosphatase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Histidine metabolism



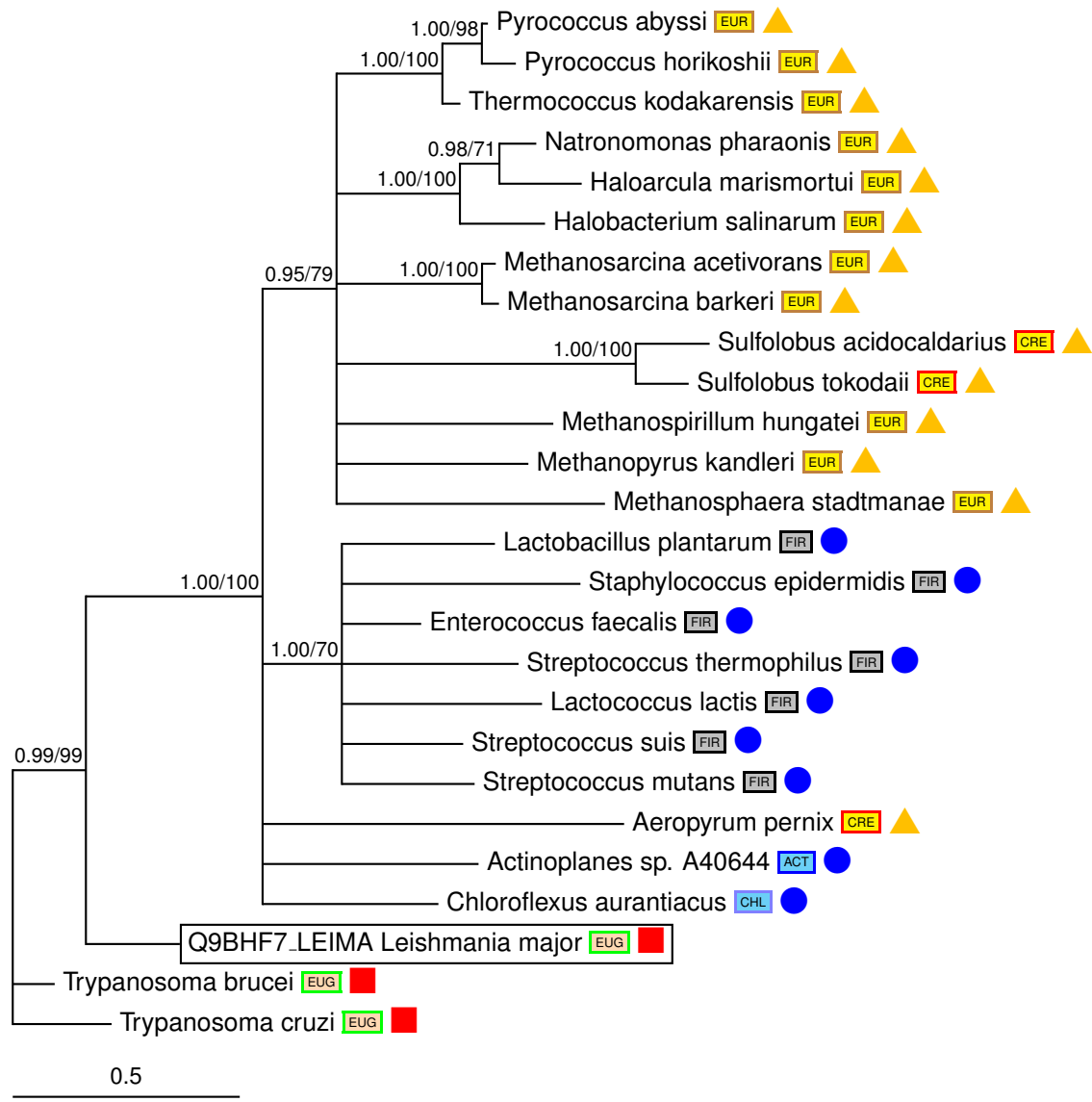
TN116

Candy accession: Q7R406_GIALA
RefSeq accession: XP_001709106.1
Uniprot accession: A8B707_GIALA
Comments: LGT - GI + ONE CANDIDA AND PHAGE
Species affected: GI
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Chlorobium
EC annotation - (Blast/Profile): EC:3.6.1.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Helicase-related protein
Name of enzyme/protein: DNA/RNA helicase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



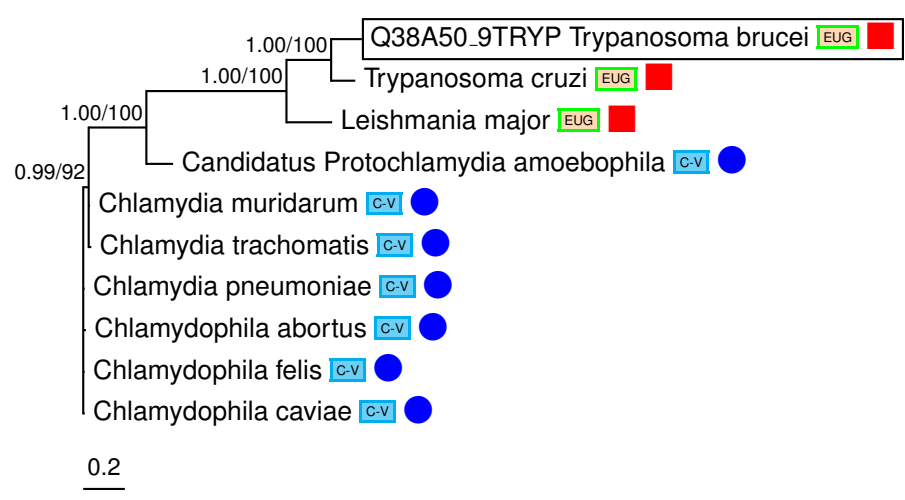
TN117

Candy accession: Q9BHF7_LEIMA
RefSeq accession: XP_001685041.1
Uniprot accession: Q9BHF7_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB,TC
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:2.7.1.36
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: mevalonate kinase
Name of enzyme/protein: mevalonate kinase
KEGG PATHWAY - level 1: Metabolism of Terpenoids and Polyketides
KEGG PATHWAY - level 2: Terpenoid backbone biosynthesis



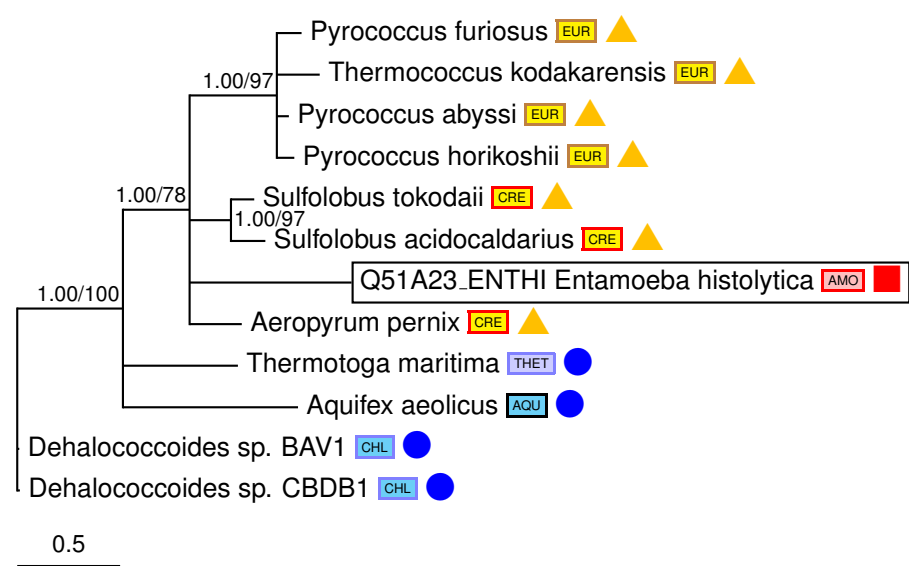
TN118

Candy accession: Q38A50.9TRYP
RefSeq accession: XP_823148.1
Uniprot accession: Q38A50.9TRYP
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB,TC
Adjacent taxa in tree: Chlamydiae/Verrucomicrobia -
Protochlamydia
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted CesT Tir chaperone protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



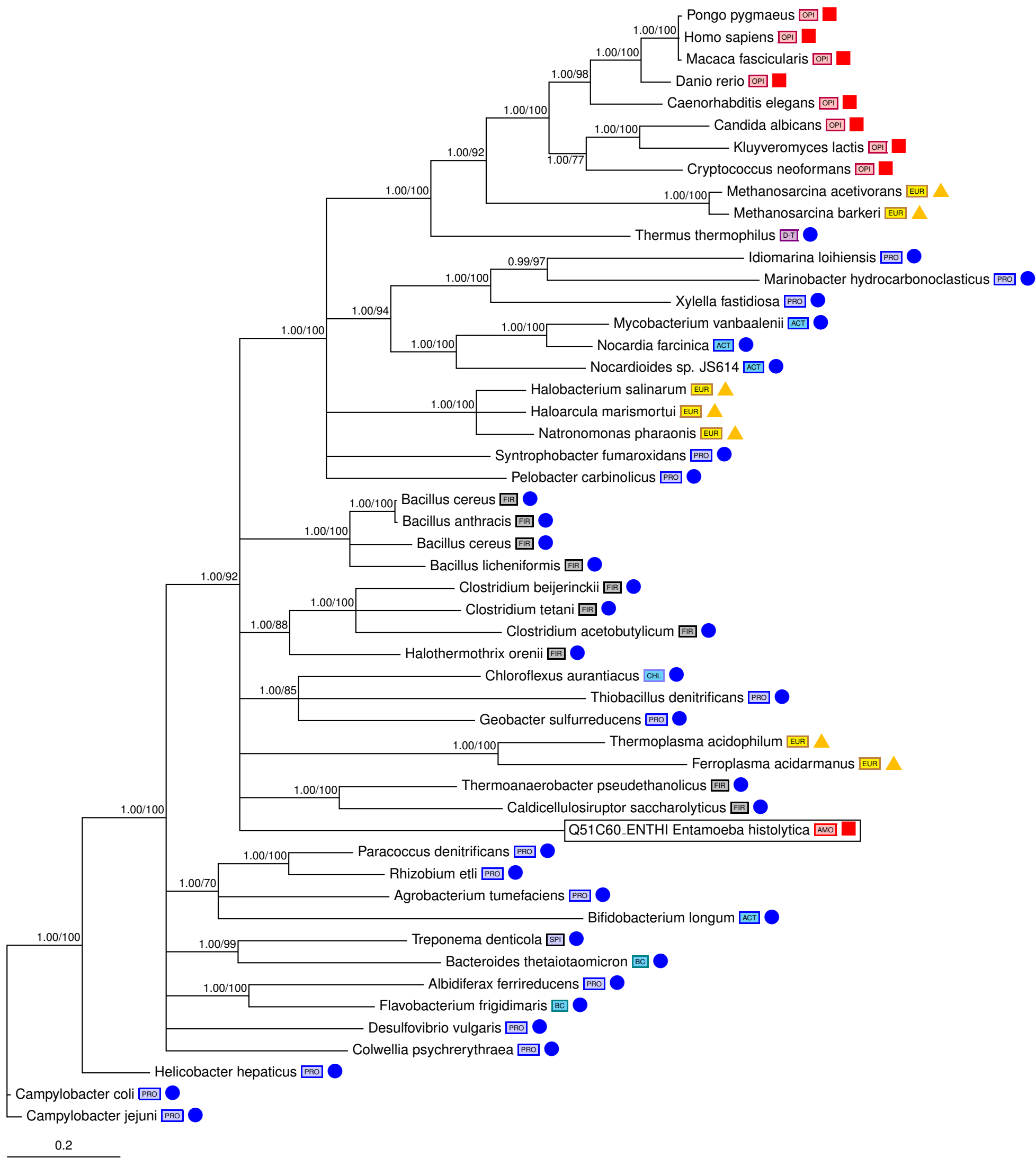
TN119

Candy accession: Q51A23_ENTHI
RefSeq accession: XP_655080.2
Uniprot accession: C4LXS0_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Archaea
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF82
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



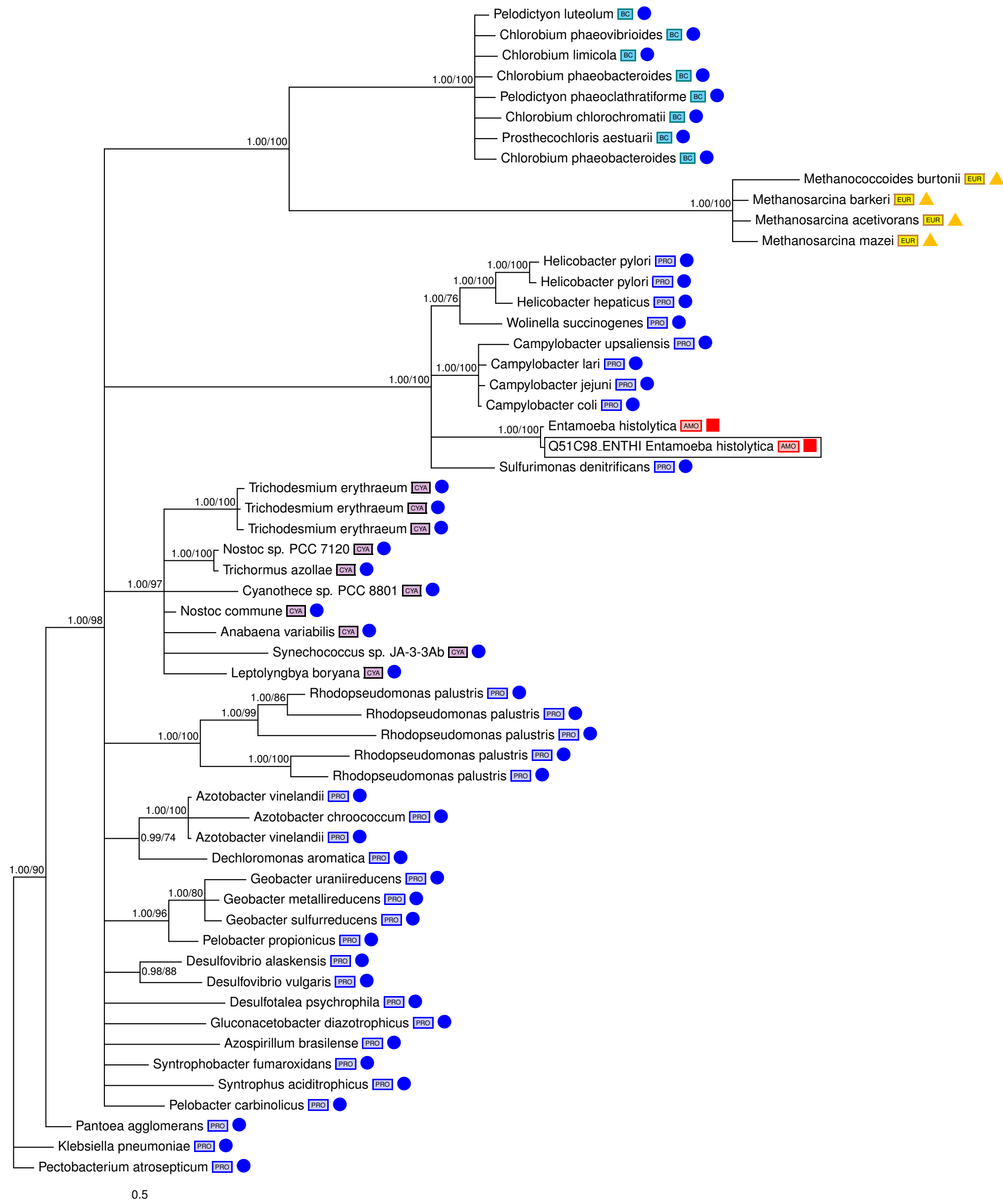
TN120

Candy accession: Q51C60_ENTHI
RefSeq accession: XP_655826.2
Uniprot accession: C4M220_ENTHI
Comments: LGT - EH - PLUS ANIMAL FUNGI CLADE
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:4.3.1.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: aspartate ammonia-lyase
Name of enzyme/protein: aspartate ammonia-lyase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Energy Metabolism
KEGG PATHWAY - level 2: Alanine, aspartate and glutamate metabolism, Nitrogen metabolism



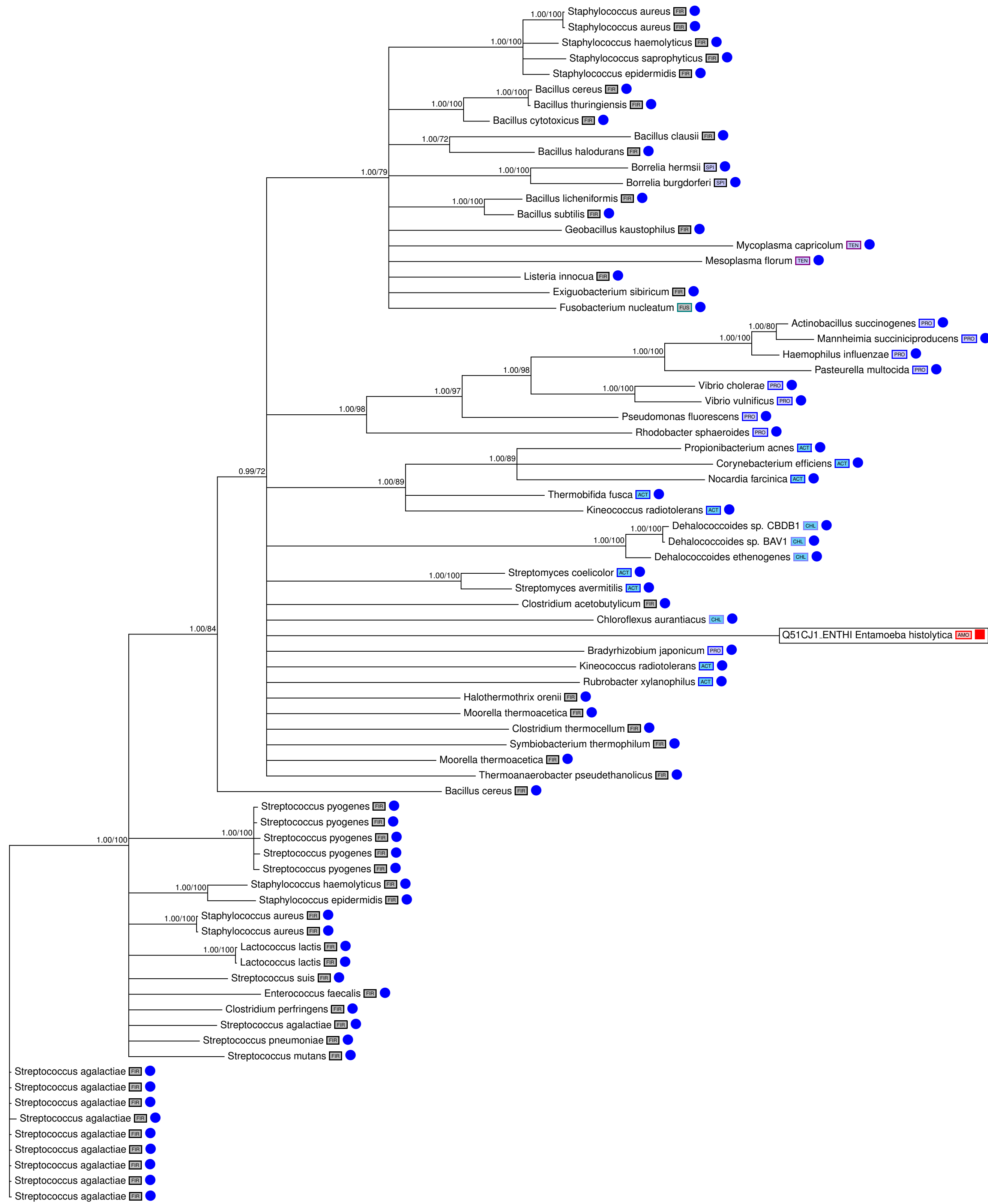
TN121

Candy accession: Q51C98_ENTHI
RefSeq accession: XP_655888.1
Uniprot accession: Q8MU40_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:1.7.1.4
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: Fe-S cluster assembly protein NifU
Name of enzyme/protein: nitrite reductase [NAD(P)H]
KEGG PATHWAY - level 1: Energy Metabolism
KEGG PATHWAY - level 2: Nitrogen metabolism



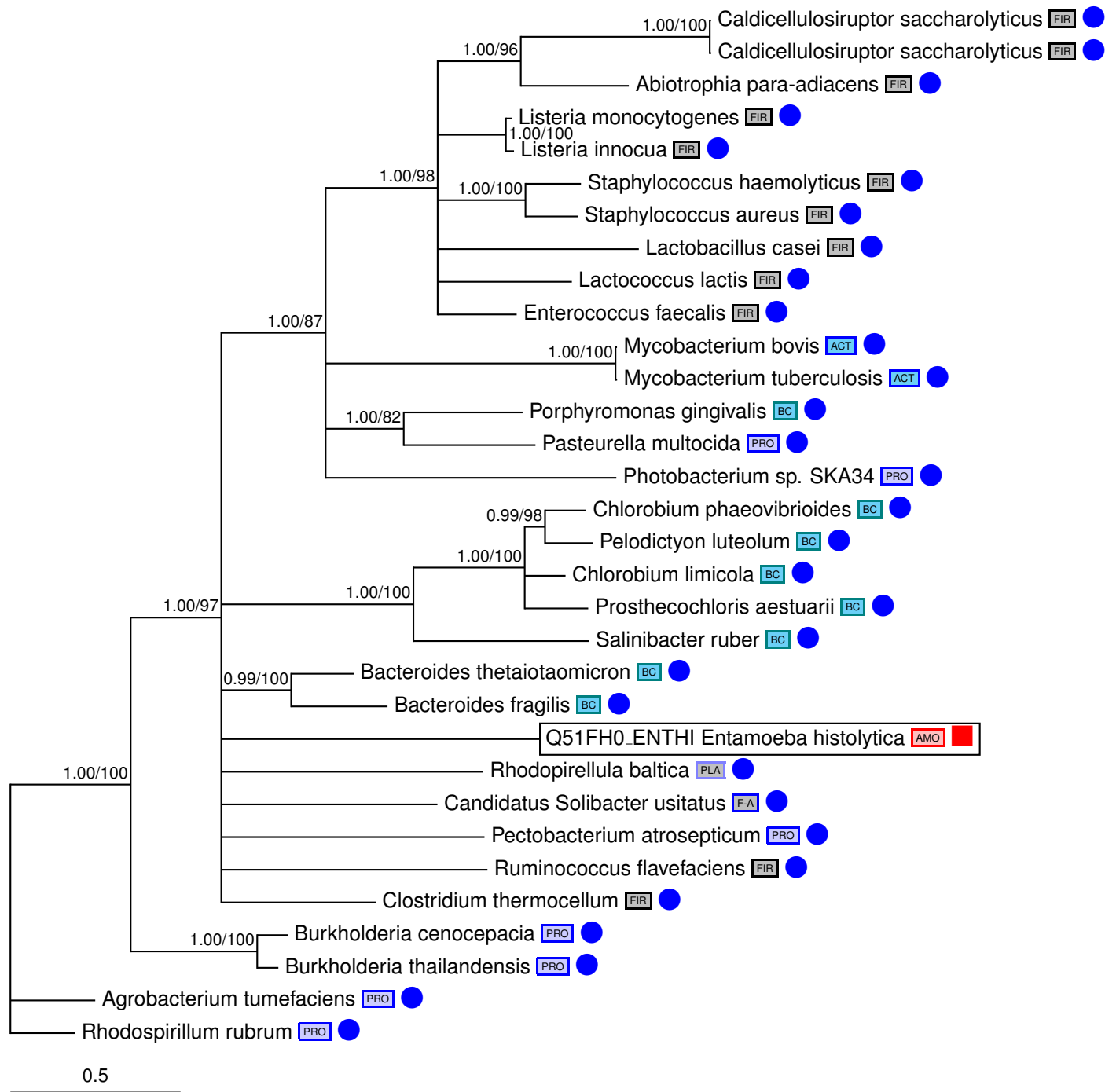
TN122

Candi accession: Q51CJ1_ENTH1
 RefSeq accession: XP_655905.1
 Uniprot accession: C4LZG3_ENTH1
 Comments: LGT - EH ONLY
 Species affected: EH
 Adjacent taxa in tree: Bacteria
 EC annotation - (Blast/Profile): EC:2.7.1.144
 PHOBIUS SP: 0
 PHOBIUS TMD: 0
 RefSeq annotation: tagatose-6-phosphate kinase
 Name of enzyme/protein: tagatose-6-phosphate kinase
 KEGG PATHWAY - level 1: Carbohydrate Metabolism
 KEGG PATHWAY - level 2: Galactose metabolism



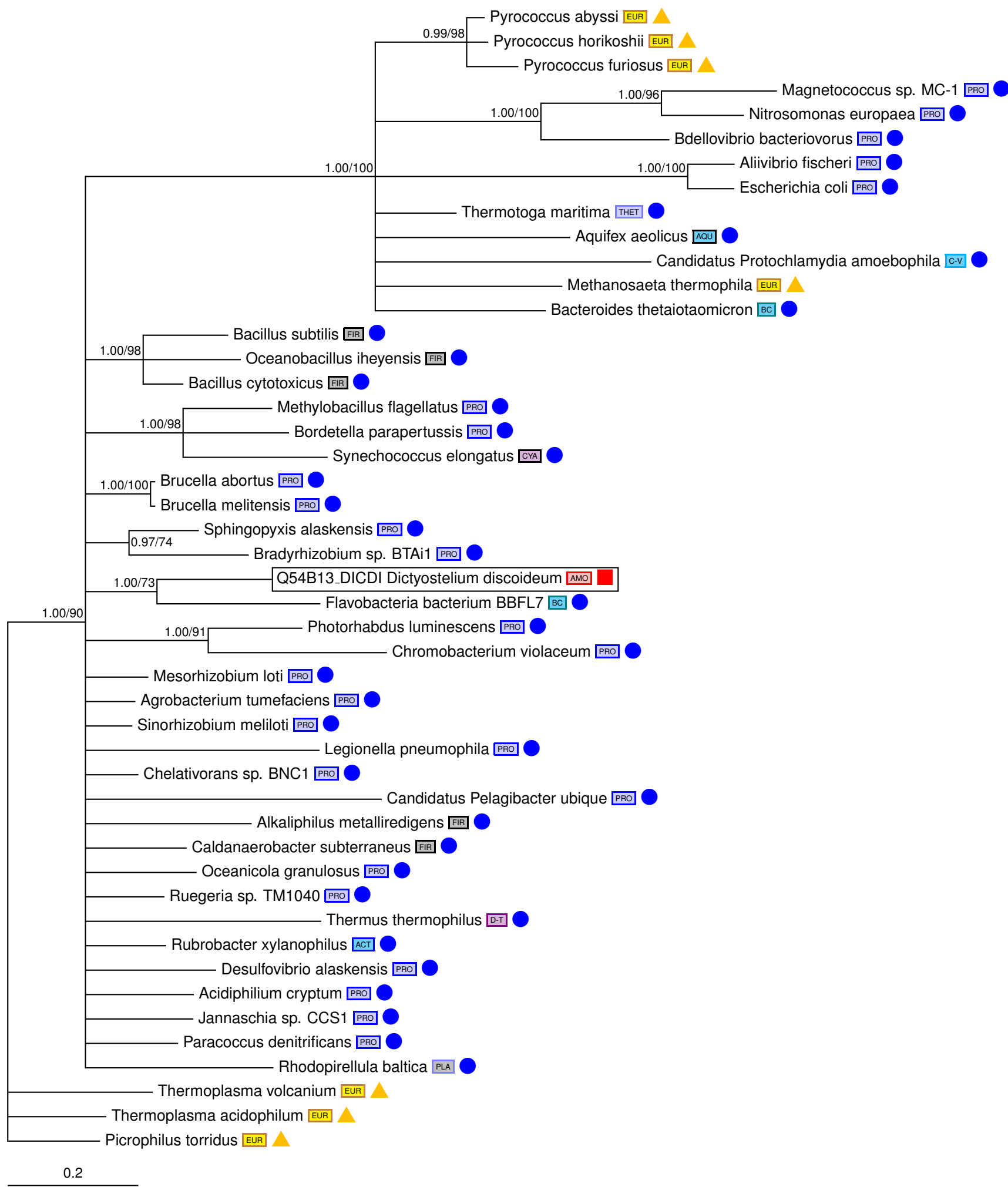
TN123

Candy accession: Q51FH0_ENTHI
RefSeq accession: XP_656903.1
Uniprot accession: C4LWE1_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.2.1.8
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: endo-1,4-beta-xylanase
Name of enzyme/protein: endo-1,4-beta-xylanase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



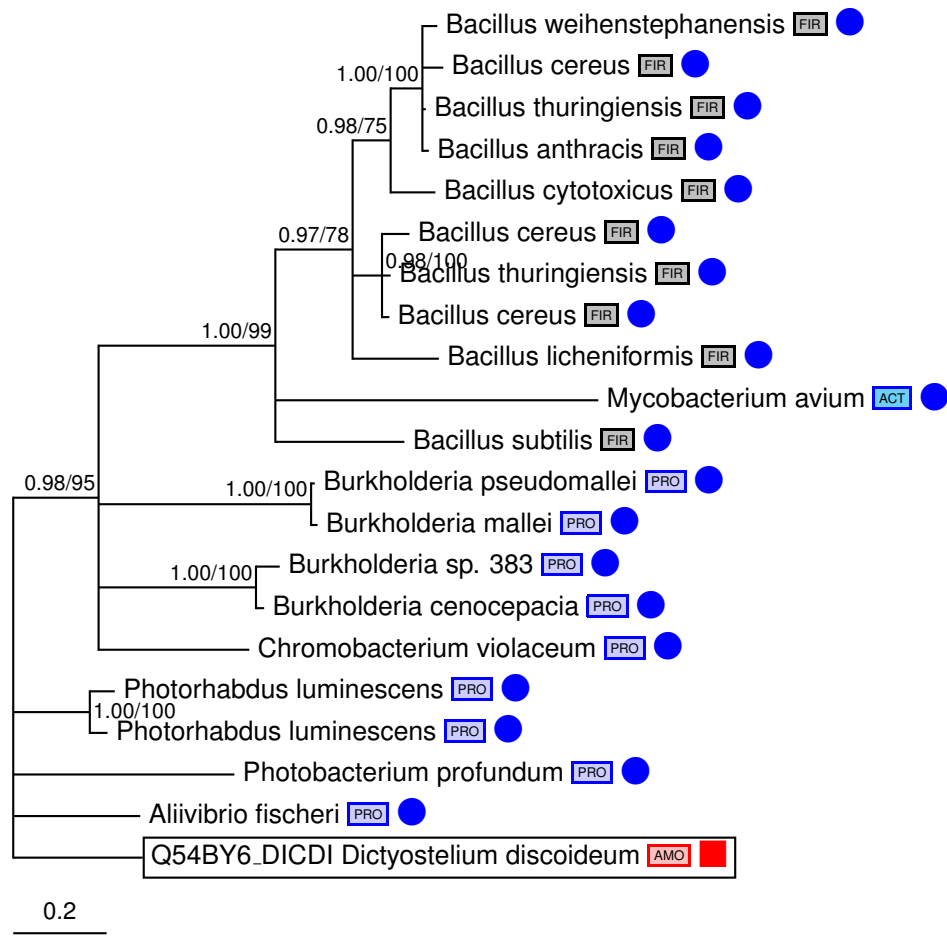
TN124

Candy accession: Q54B13_DICDI
RefSeq accession: XP_628903.1
Uniprot accession: Q54B13_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Flavobacterium
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0293956
Name of enzyme/protein: Predicted tRNA-binding protein
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na



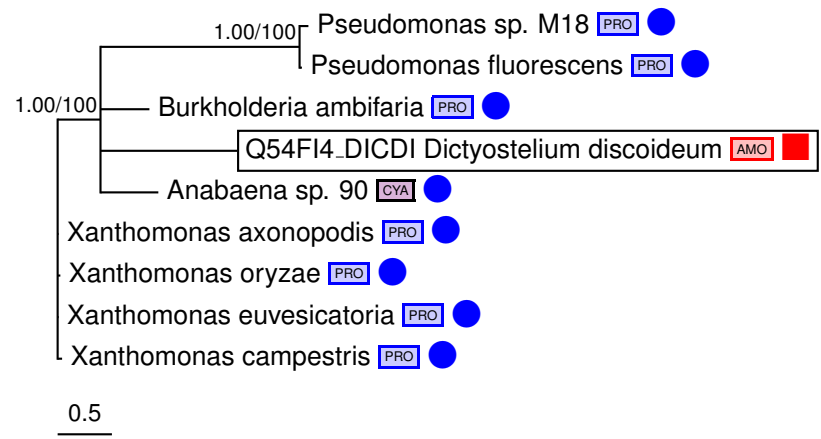
TN125

Candy accession: Q54BY6_DICDI
RefSeq accession: XP_629205.1
Uniprot accession: Q54BY6_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:3.4.21.26
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0293330
Name of enzyme/protein: Hypothetical protein
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



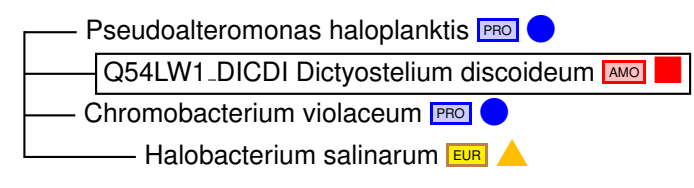
TN126

Candy accession: Q54FI4_DICDI
RefSeq accession: XP_635556.1
Uniprot accession: Q54FI4_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.8.1.1
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0290825
Name of enzyme/protein: alkylhalidase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



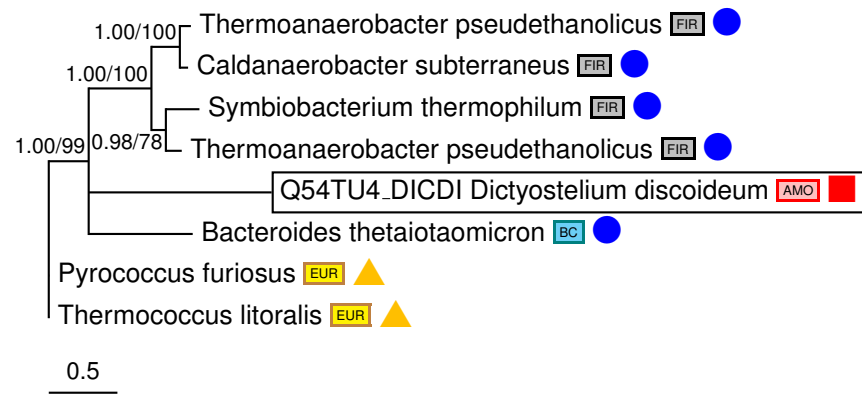
TN127

Candy accession: Q54LW1_DICDI
RefSeq accession: XP_637719.1
Uniprot accession: Q54LW1_DICDI
Comments: LGT - DD ONLY + 2 BACT + ONE ARCHAEA
Species affected: DD
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0286383
Name of enzyme/protein: Protein containing GAF domain
KEGG PATHWAY - level 1: Other function - Signal Transduction
KEGG PATHWAY - level 2: na



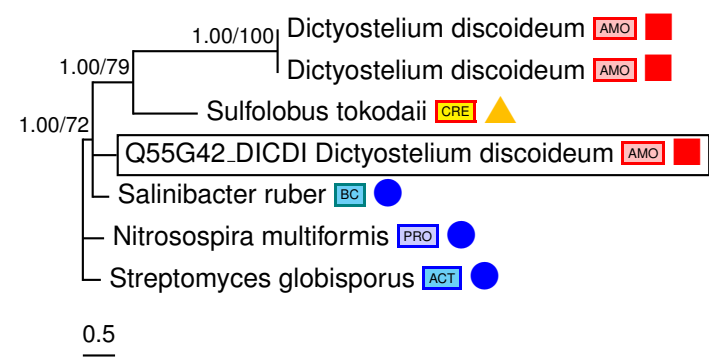
TN128

Candy accession: Q54TU4_DICDI
RefSeq accession: XP_640717.1
Uniprot accession: Q54TU4_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0281495
Name of enzyme/protein: Protein containing DUF377
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



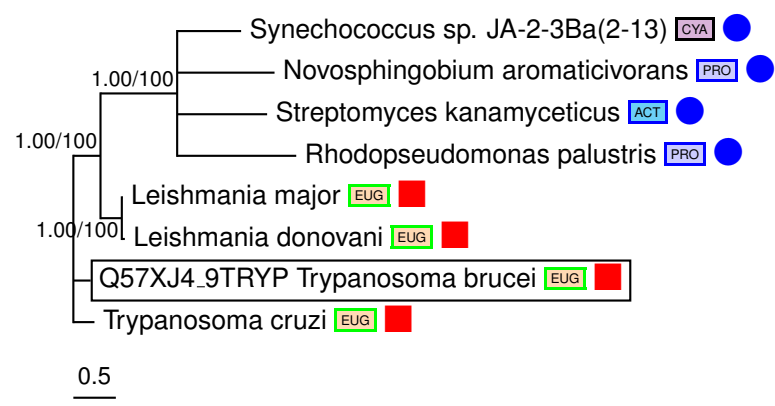
TN129

Candy accession: Q55G42_DICDI
RefSeq accession: XP_647341.1
Uniprot accession: Q55G42_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:2.1.1.14
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0267834
Name of enzyme/protein: 5-methyltetrahydropteroyltriglutamate--
homocysteine S-methyltransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Cysteine and methionine metabolism



TN131

Candy accession: Q57XJ4_9TRYP
RefSeq accession: XP_843936.1
Uniprot accession: Q57XJ4_9TRYP
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,LD,TE,TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing phytanoyl-CoA
dioxygenase domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

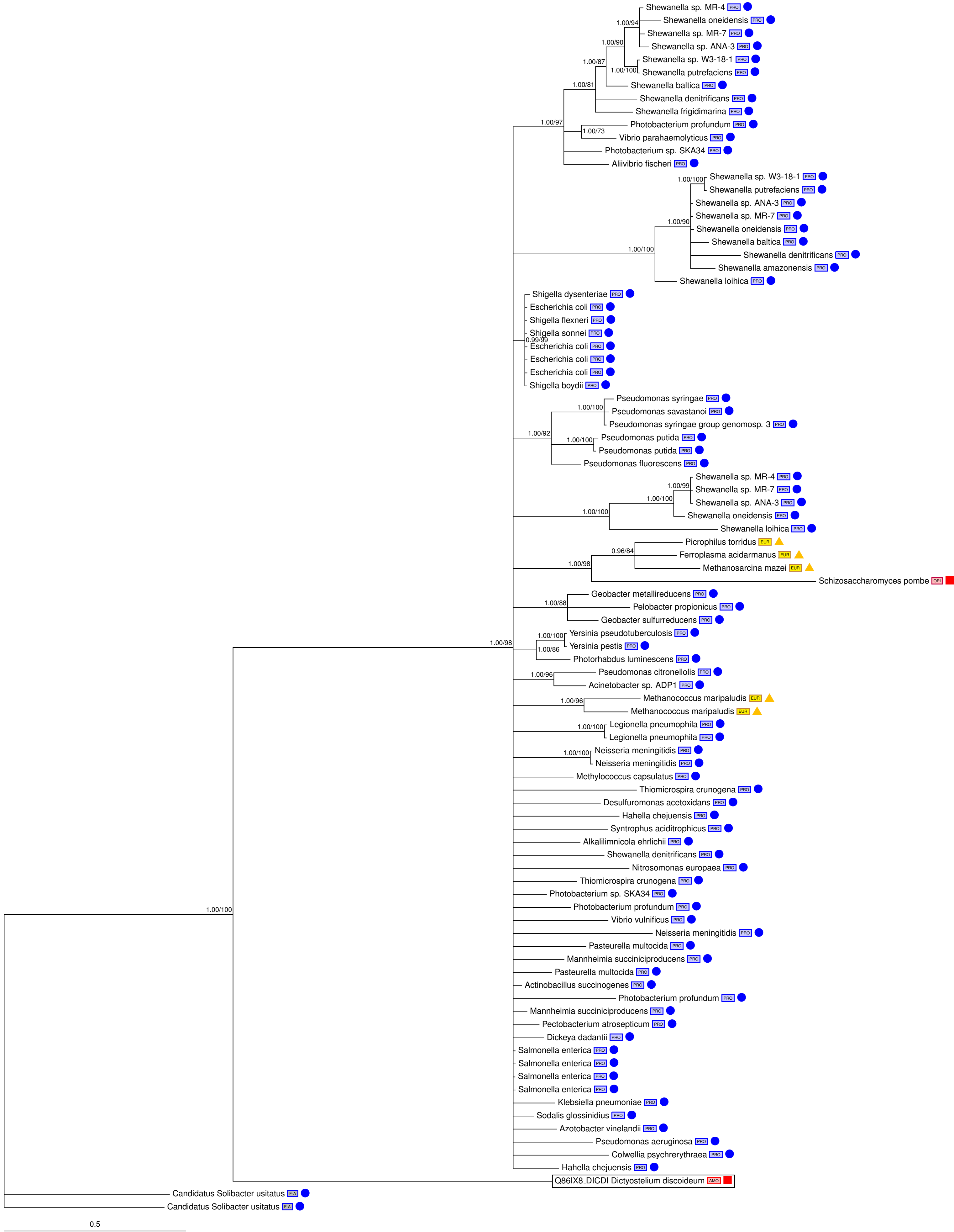


TN132

Candy accession: Q57XW9_9TRYP
RefSeq accession: XP_843730.1
Uniprot accession: Q57XW9_9TRYP
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:2.1.1.37
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: cytosine-specific DNA methylase
Name of enzyme/protein: DNA (cytosine-5-)-methyltransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Methionine metabolism



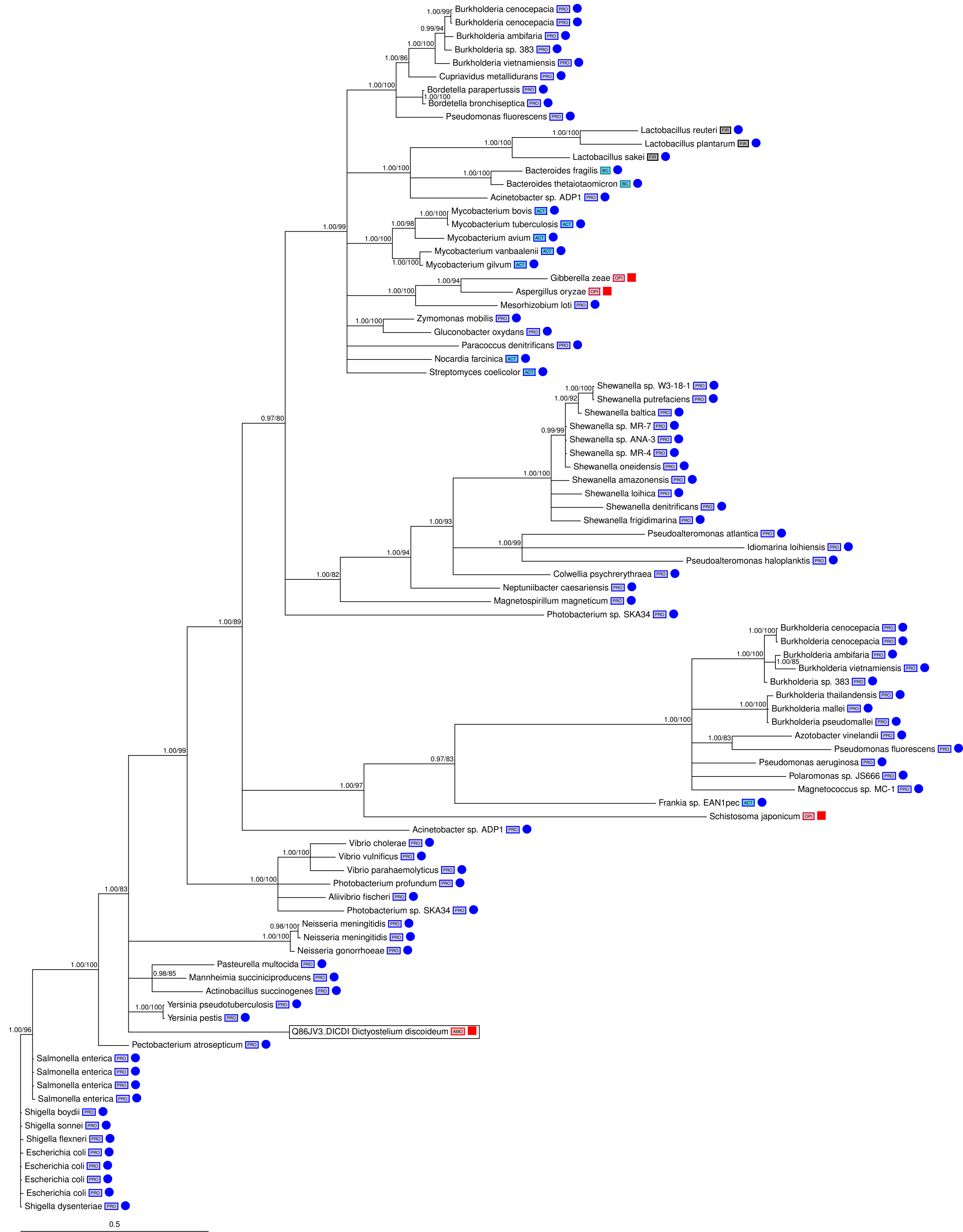
Candy accession: Q86IX8_DICDI
RefSeq accession: XP_643917.1
Uniprot accession: Q86IX8_DICDI
Comments: LGT - DD AND ONE FUNGI
Species affected: DD,SP
Adjacent taxa in tree: Fibrobacteres/Acidobacteria - Solibacter
EC annotation - (Blast/Profile): EC:5.2.1.8
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: cyclophilin-type peptidylprolyl cis-trans isomerase
Name of enzyme/protein: peptidylprolyl isomerase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



0.5

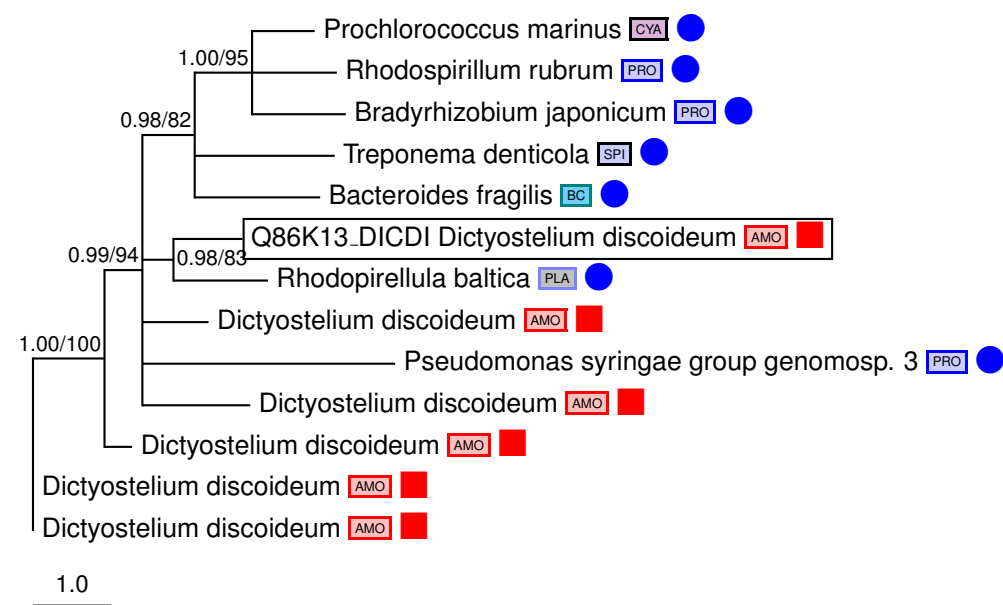
TN134

Candy accession: Q86JV3.DICDI
 RefSeq accession: XP_644739.1
 Uniprot accession: Q556V8.DICDI
 Comments: LGT - DD TWO NODES - LGT INTO FUNGI AND
 SCHISTOSOMA
 Species affected: DD, FUNGI, SJ
 Adjacent taxa in tree: Proteobacteria
 EC annotation - (Blast/Profile): na
 PHOBIUS SP: 0
 PHOBIUS DD: 0
 RefSeq annotation: Dyp-type peroxidase family protein
 Name of enzyme/protein: Predicted Dyp-type peroxidase family
 protein
 KEGG PATHWAY - level 1: Other function
 KEGG PATHWAY - level 2: na



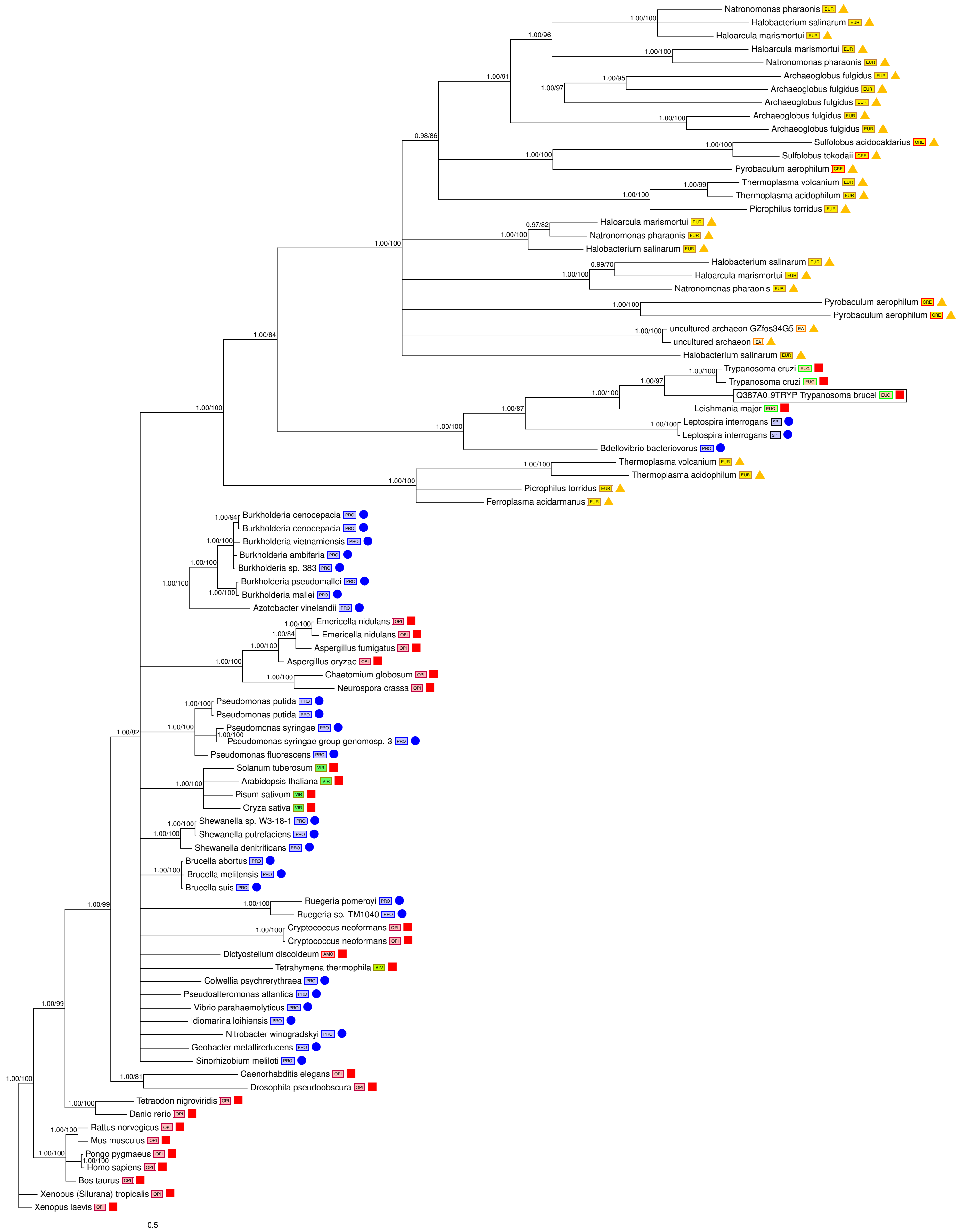
TN135

Candy accession: Q86K13_DICDI
RefSeq accession: XP_645041.1
Uniprot accession: Q556I6_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0272612
Name of enzyme/protein: Predicted transglutaminase-like superfamily
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



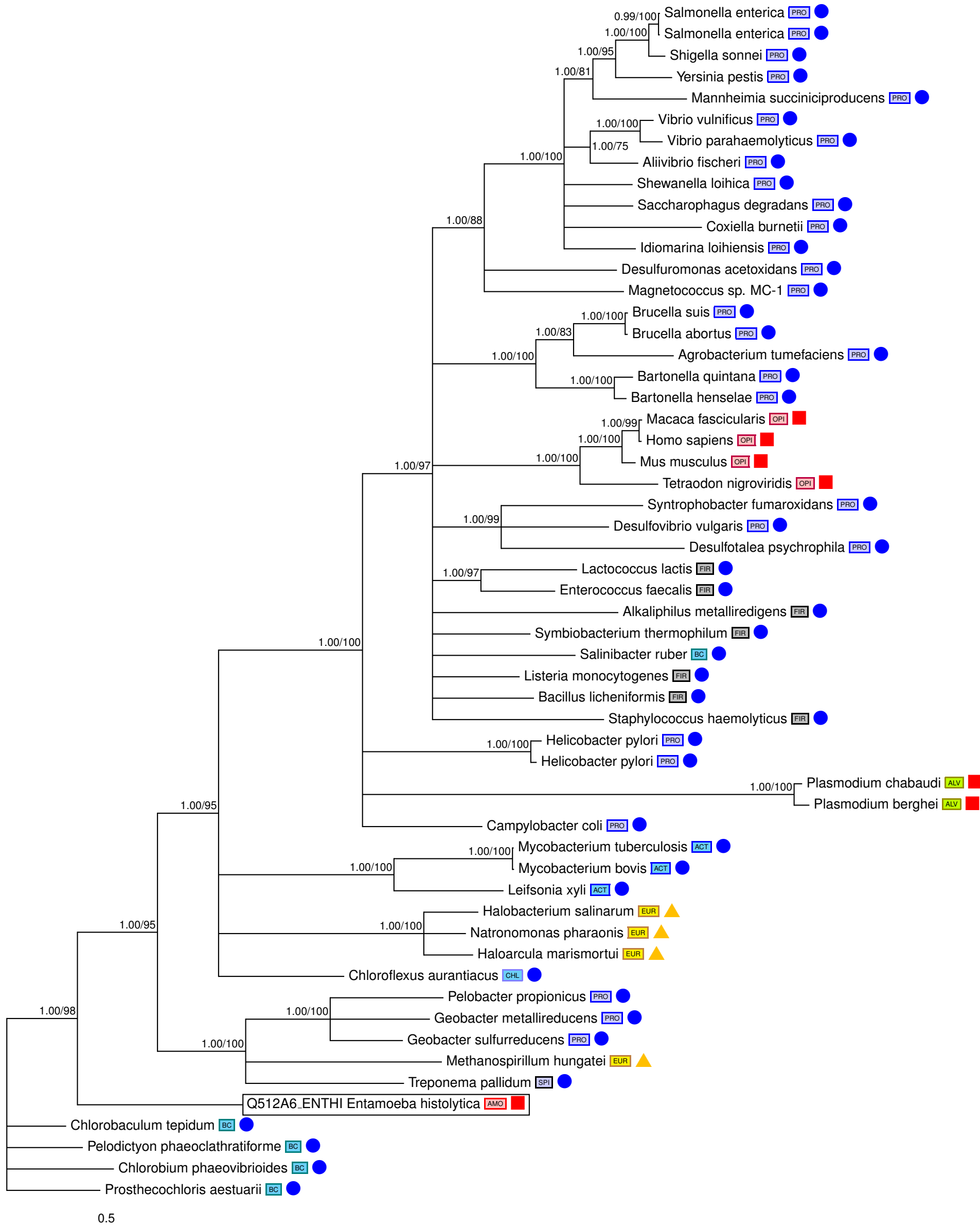
TN136

Candy accession: Q387A0_9TRYP
RefSeq accession: XP_828243.1
Uniprot accession: Q387A0_9TRYP
Comments: LGT - KINETOPLASTIDS
Species affected: LM,TB,TC
Adjacent taxa in tree: Spirochaetes - Leptospira
EC annotation - (Blast/Profile): EC:1.3.99.10
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: isovaleryl-coA dehydrogenase
Name of enzyme/protein: Isovaleryl-coA dehydrogenase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Valine, leucine and isoleucine degradation



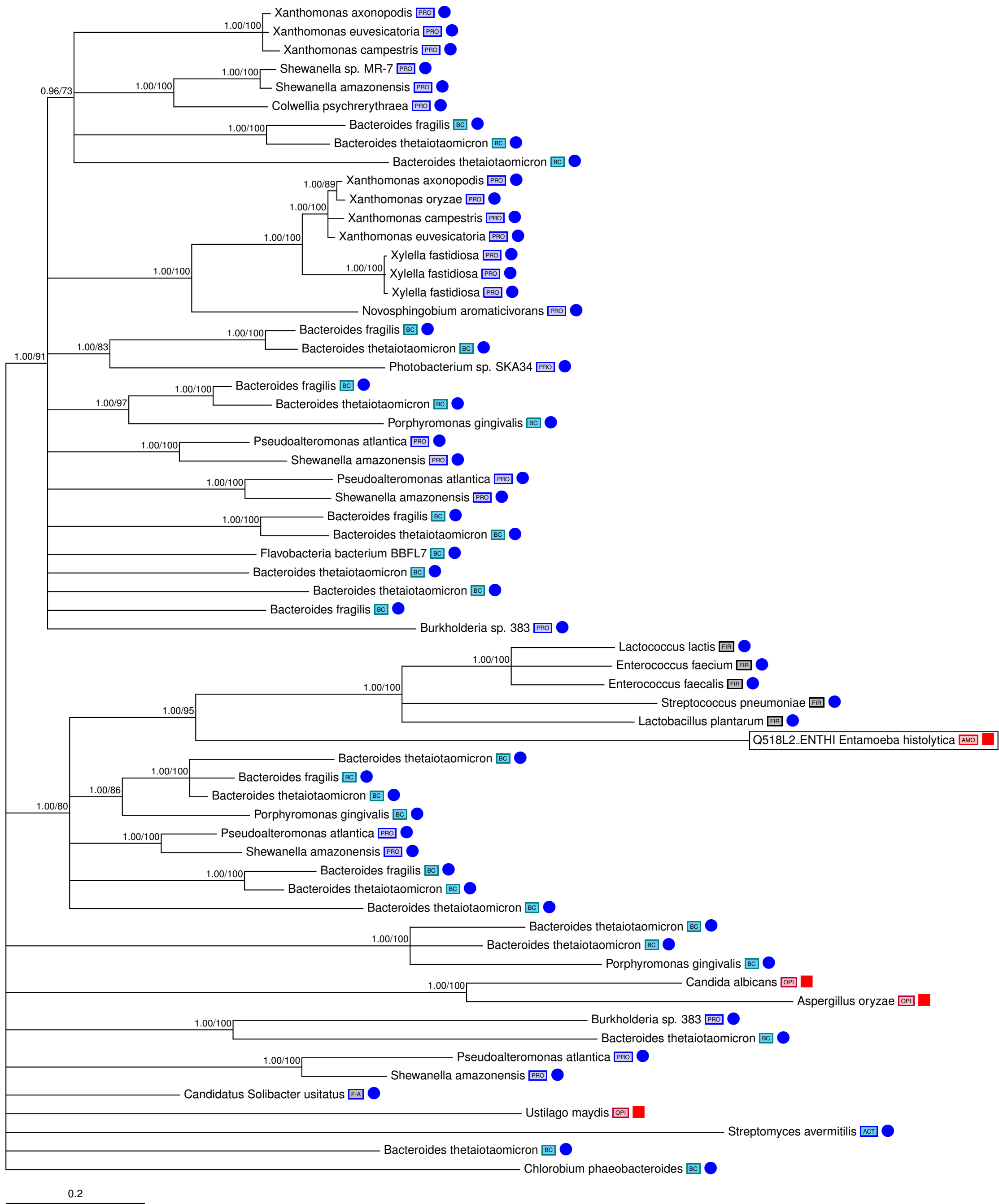
TN137

Candy accession: Q512A6_ENTHI
RefSeq accession: XP_653060.1
Uniprot accession: C4LYV7_ENTHI
Comments: LGT - EH TWO NODES
Species affected: EH
Adjacent taxa in tree: Bacteroidetes/Chlorobi group
EC annotation - (Blast/Profile): EC:3.2.2.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: A/G-specific adenine glycosylase
Name of enzyme/protein: A/G-specific adenine glycosylase
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Purine metabolism



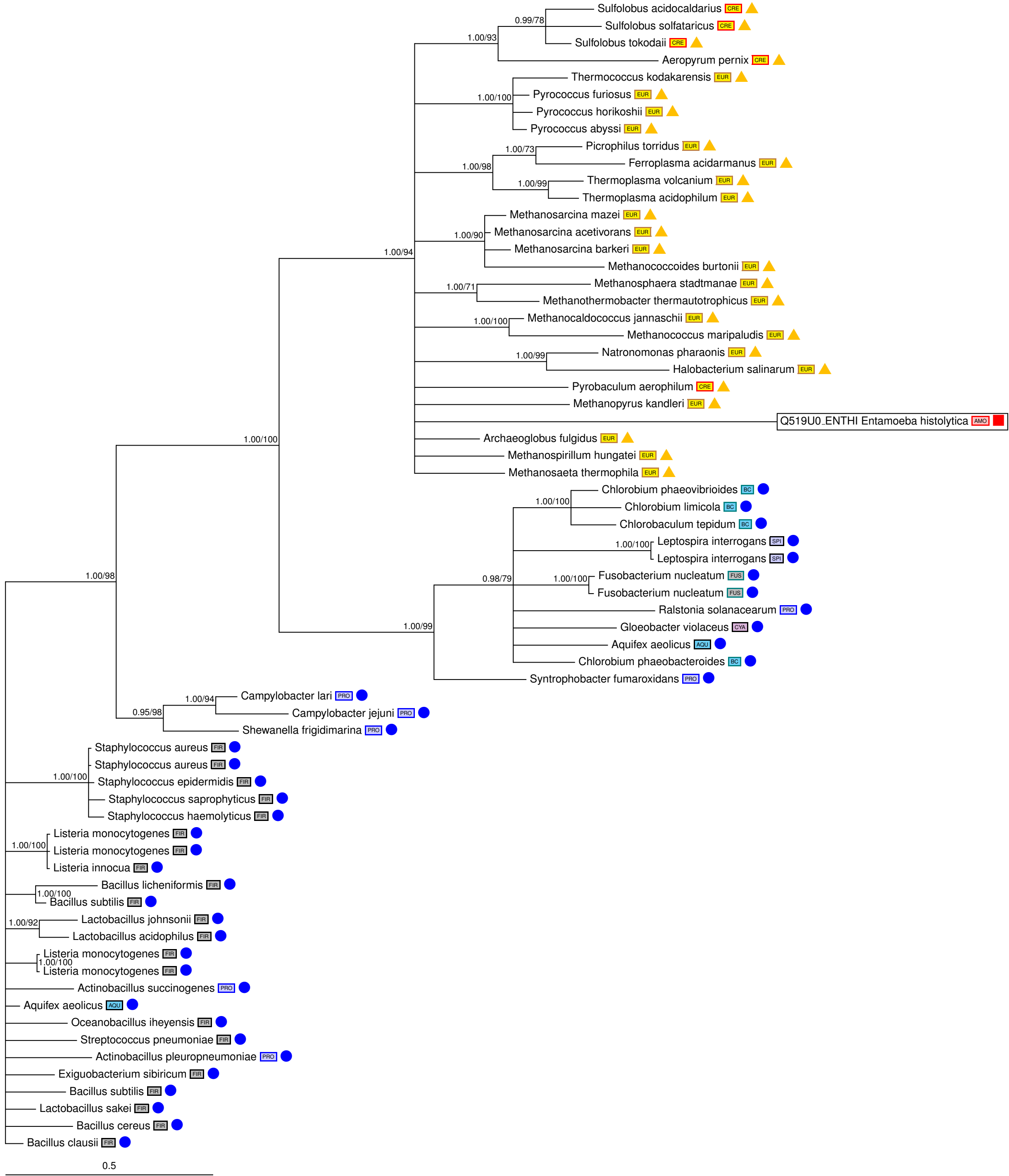
TN138

Candy accession: Q518L2_ENTHI
RefSeq accession: XP_654665.1
Uniprot accession: C4LZ28_ENTHI
Comments: LGT - EH TWO NODES + FUNGI
Species affected: EH
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): EC:3.2.1.113
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: alpha-1,2-mannosidase
Name of enzyme/protein: Protein containing alpha-1,2-mannosidase domain (Glycosyl hydrolase family 92)
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism
KEGG PATHWAY - level 2: Glycan biosynthesis and metabolism



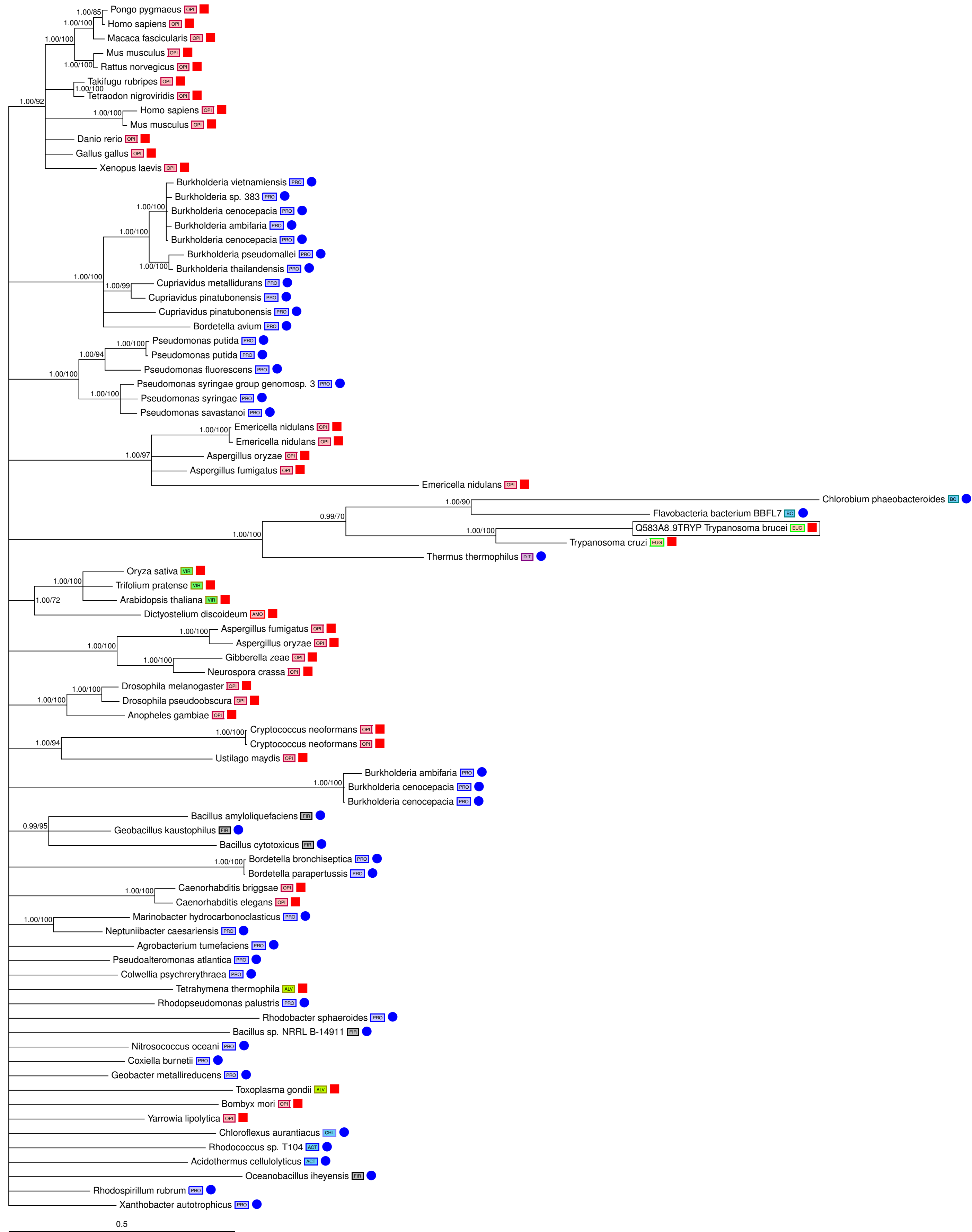
TN139

Candy accession: Q519U0_ENTHI
RefSeq accession: XP_654999.1
Uniprot accession: C4LWS6_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Archaea
EC annotation - (Blast/Profile): EC:2.7.7.39
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: cytidylyltransferase
Name of enzyme/protein: glycerol-3-phosphate
 cytidylyltransferase
KEGG PATHWAY - level 1: Lipid Metabolism
KEGG PATHWAY - level 2: Glycerophospholipid metabolism



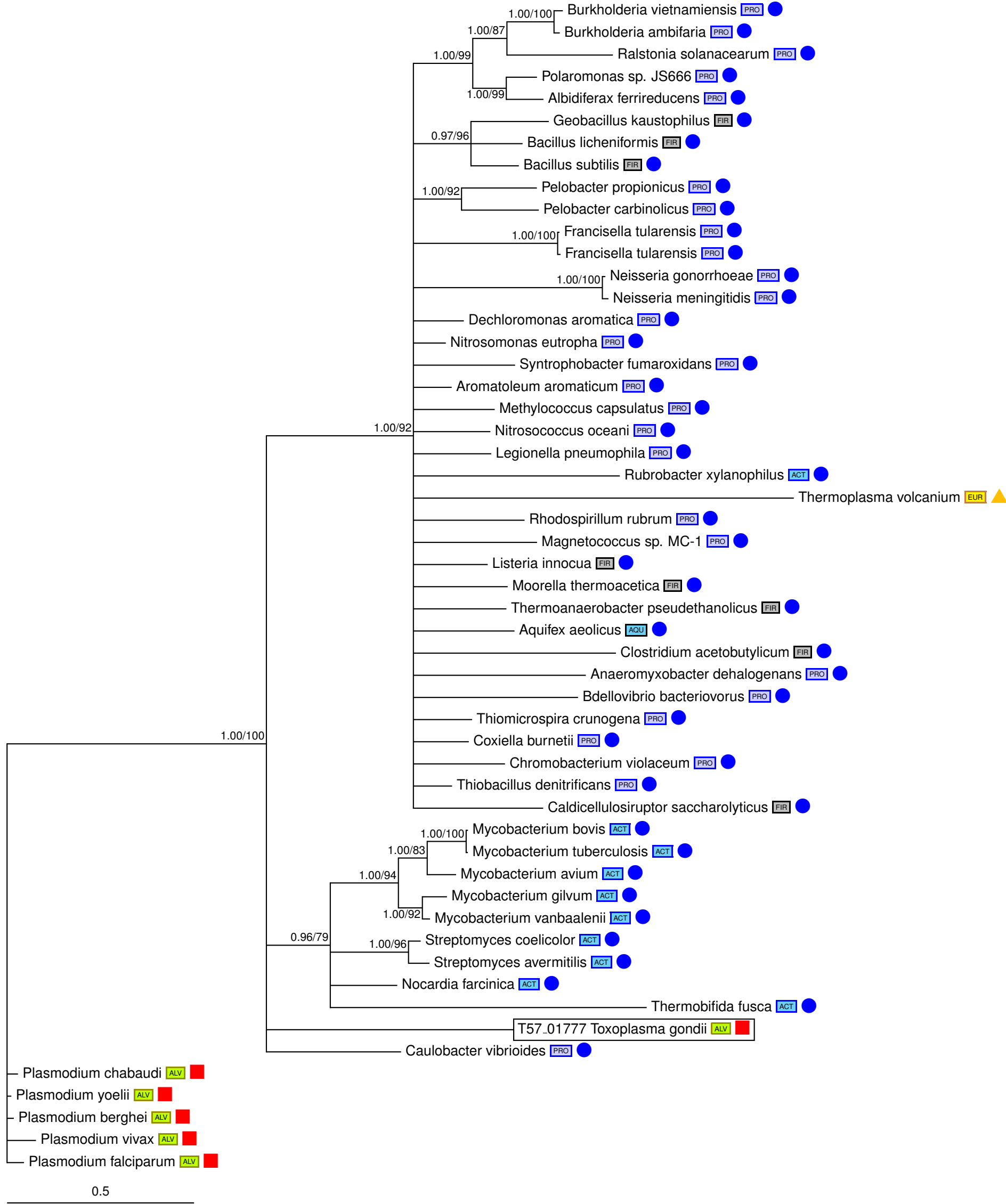
TN140

Candy accession: Q583A8.9TRYP
RefSeq accession: XP_844420.1
Uniprot accession: Q583A8.9TRYP
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: TB, TC
Adjacent taxa in tree: Bacteroidetes/Chlorobi
EC annotation - (Blast/Profile): EC:4.1.3.4
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hydroxymethylglutaryl-CoA lyase
Name of enzyme/protein: 3-hydroxy-3-methylglutaryl-CoA lyase
KEGG PATHWAY - level 1: Lipid Metabolism, Amino Acid Metabolism
KEGG PATHWAY - level 2: Synthesis and degradation of ketone
bodies, Valine, leucine and isoleucine
degradation



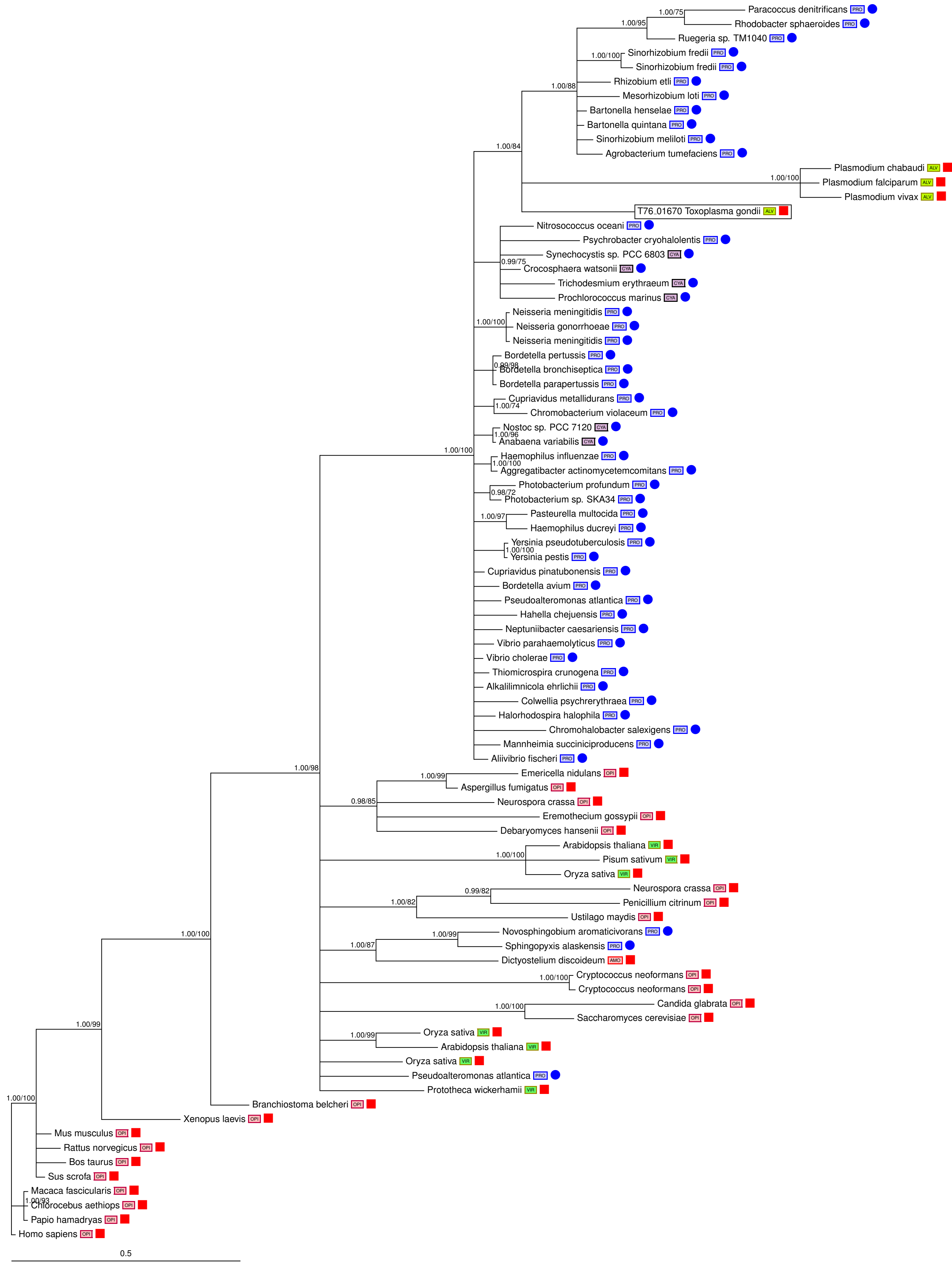
TN141

Candy accession: T57_01777
RefSeq accession: XP_002368713.1
Uniprot accession: B6KLW3_TOXGO
Comments: LGT - APICOMPLEXA ONLY
Species affected: TG,PF,PV,PY
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.4.24.-
PHOBIUS SP: 0
PHOBIUS TMD: 6
RefSeq annotation: sterol-regulatory element binding
protein site 2 protease, putative
Name of enzyme/protein: Predicted sterol regulatory element-
binding protein/ peptidase M50 family
protein
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



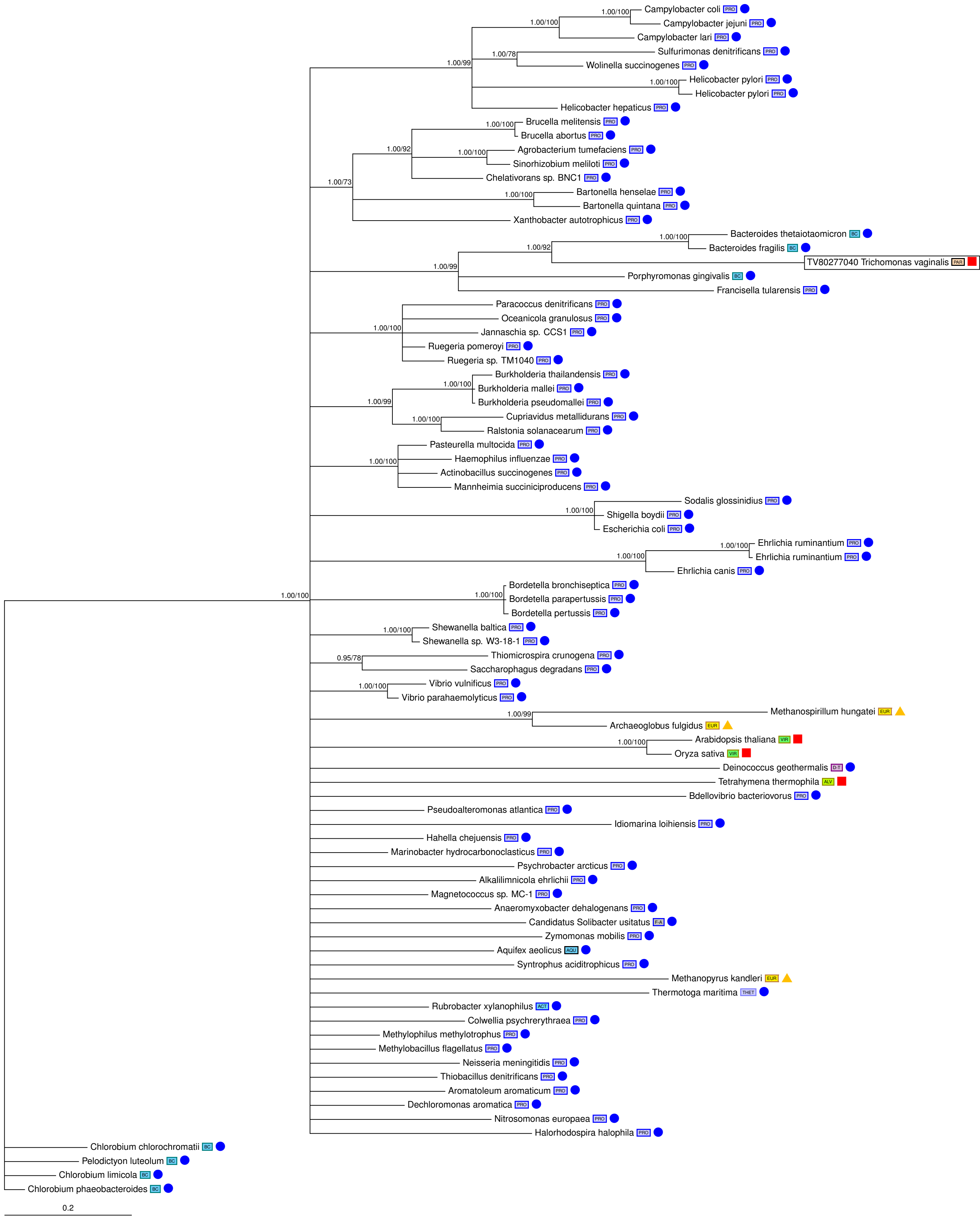
TN142

Candy accession: T76_01670
RefSeq accession: XP_002369289.1
Uniprot accession: B6KN66_TOXGO
Comments: LGT - APICOMPLEXA + TWO LIKELY CASES OF E->B LGT CASES
Species affected: PF,PC,PV,TG
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:1.11.1.15
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: peroxiredoxin family protein/glutaredoxin, putative
Name of enzyme/protein: peroxiredoxin
KEGG PATHWAY - level 1: Metabolism of Other Amino Acids
KEGG PATHWAY - level 2: Glutathione metabolism



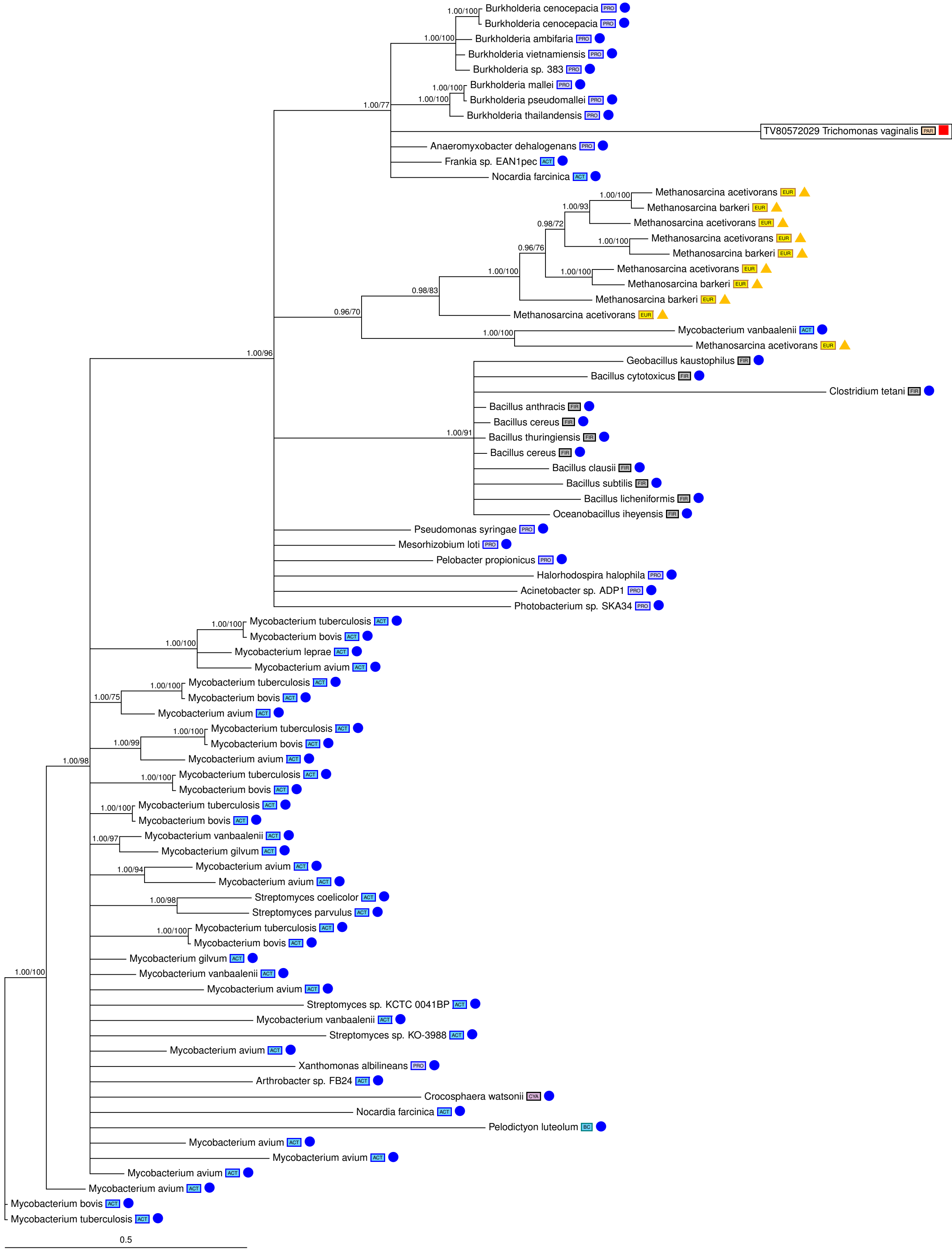
TN143

Candy accession: TV80277040
RefSeq accession: XP_001304924.1
Uniprot accession: A2FSX2_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:4.1.1.20
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Pyridoxal-dependent decarboxylase, C-terminal sheet domain containing protein
Name of enzyme/protein: diaminopimelate decarboxylase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Lysine biosynthesis



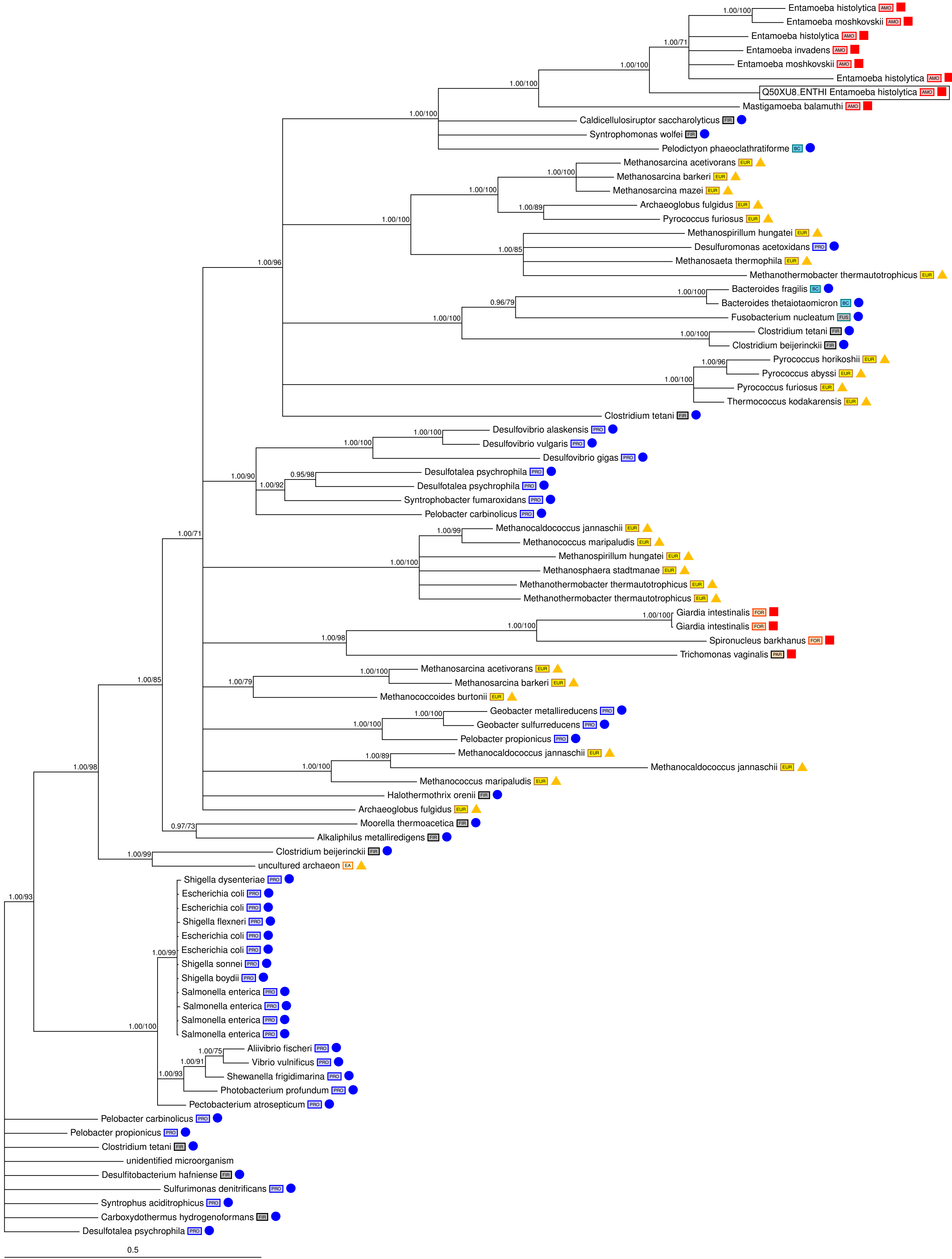
TN144

Candy accession: TV80572029
RefSeq accession: XP_001302043.1
Uniprot accession: A2G151_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: methyltransferase, TIGR00027 family protein
Name of enzyme/protein: Predicted methyltransferase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



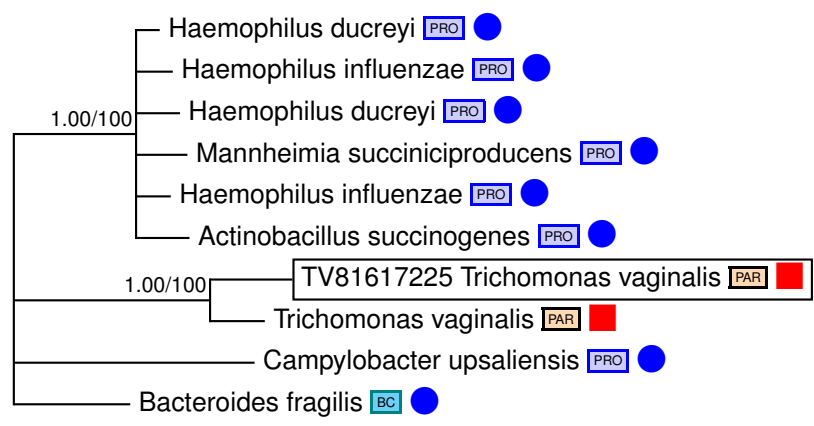
TN145

Candy accession: Q50XU8_ENTHI
RefSeq accession: XP_651815.1
Uniprot accession: Q50XU8_ENTHI
Comments: LGT - AMOEBOZOA TWO NODES - DEAP LGT
 INTO AMOEBOZOA
Species affected: EH,EI,EM,MB
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
 PHOBIUS SP: 0
 PHOBIUS TMD: 0
RefSeq annotation: type A flavoprotein
Name of enzyme/protein: Uncharacterised flavoproteins
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



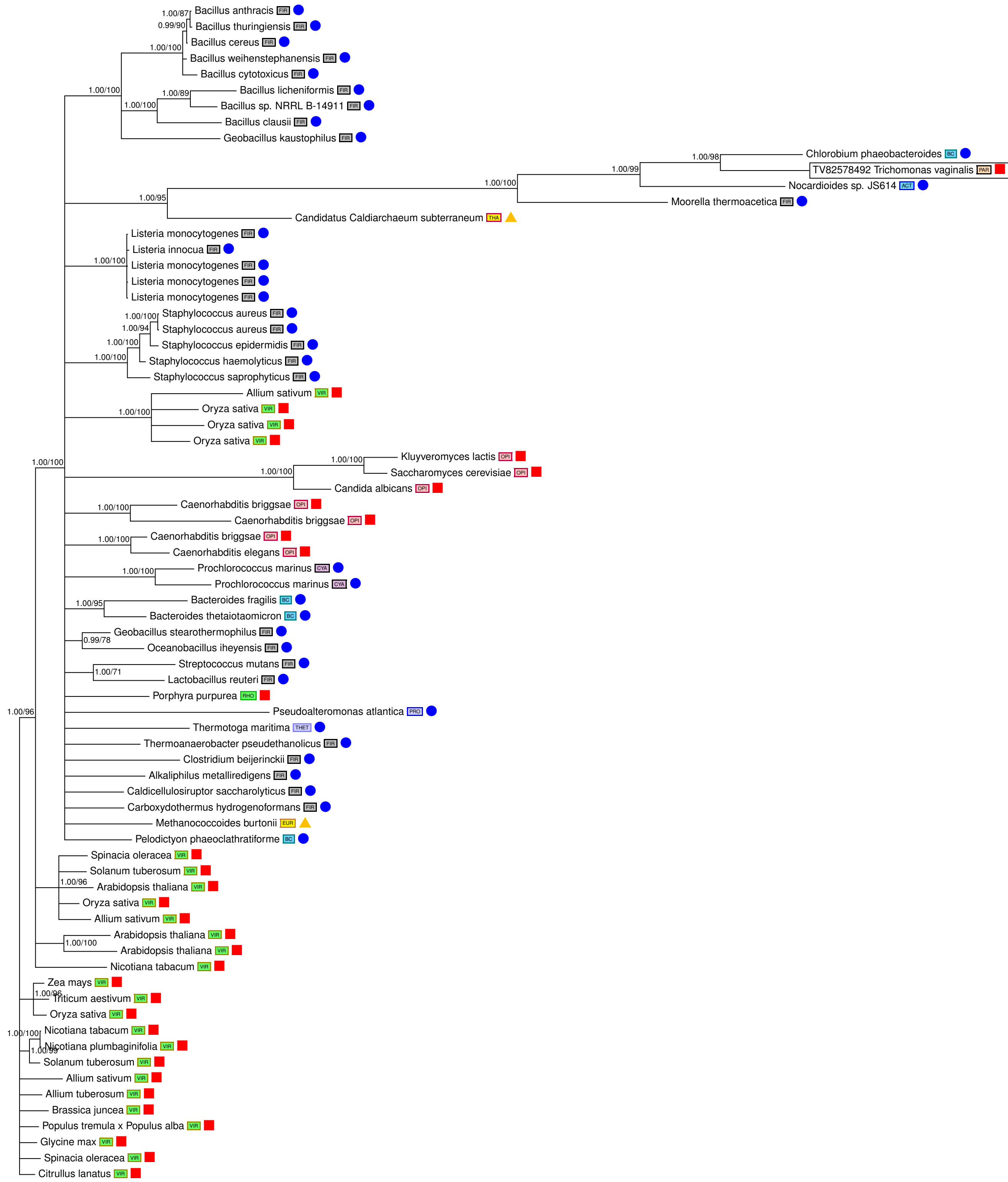
TN146

Candy accession: TV81617225
RefSeq accession: XP_001324287.1
Uniprot accession: A2E5M3_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted D12 class N6 adenine-specific
DNA methyltransferase
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na



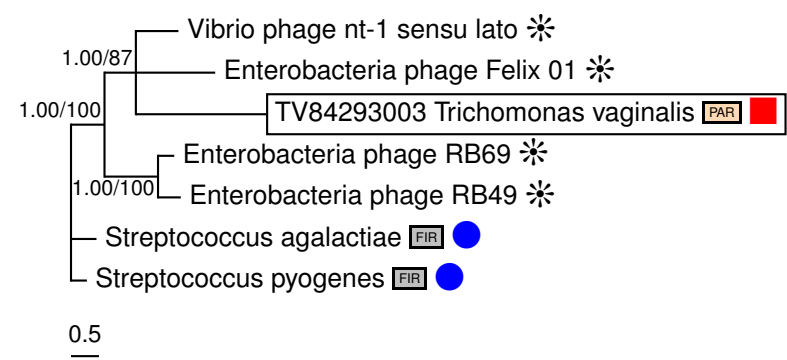
TN147

Candy accession: TV82578492
RefSeq accession: XP_001584430.1
Uniprot accession: A2D811_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Chlorobium
EC annotation - (Blast/Profile): EC:2.5.1.47
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Pyridoxal-phosphate dependent enzyme family protein
Name of enzyme/protein: cysteine synthase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Energy Metabolism
KEGG PATHWAY - level 2: Cysteine and methionine metabolism, Sulfur metabolism



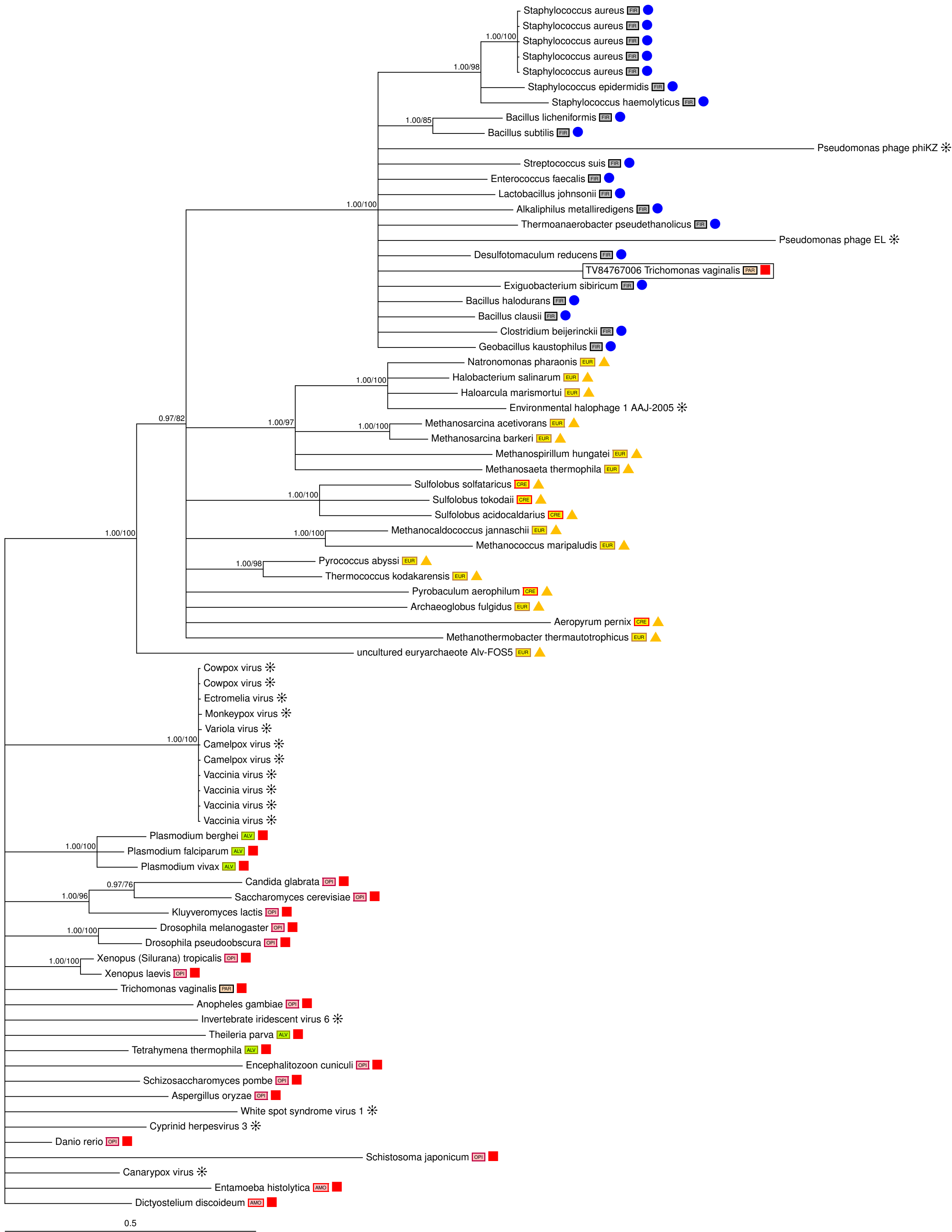
TN148

Candy accession: TV84293003
RefSeq accession: XP_001321311.1
Uniprot accession: A2EDX6_TRIVA
Comments: LGT - TV ONLY - PHAGES AND BACTERIA
Species affected: TV
Adjacent taxa in tree: Bacteria/phage
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing phage tail repeat like domain
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



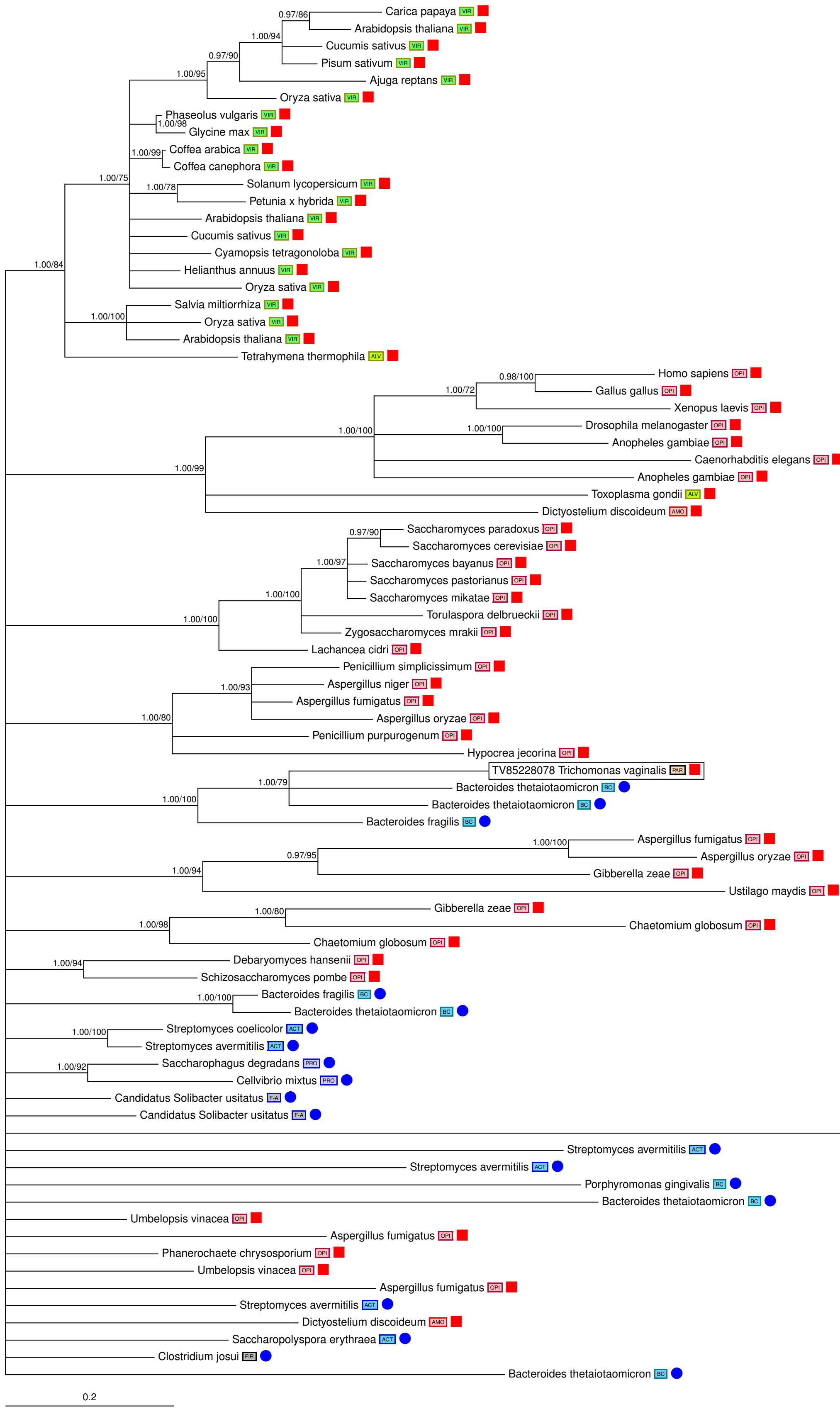
TN149

Candy accession: TV84767006
RefSeq accession: XP_001295357.1
Uniprot accession: A2GK91_TRIVA
Comments: LGT - TWO NODES + PHAGES AND VIRUSES - 3
DOMAIN ToL
Species affected: TV
Adjacent taxa in tree: Bacteria/phage
EC annotation - (Blast/Profile): EC:2.7.4.9
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: thymidylate kinase family protein
Name of enzyme/protein: Thymidylate kinase family protein
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Pyrimidine metabolism



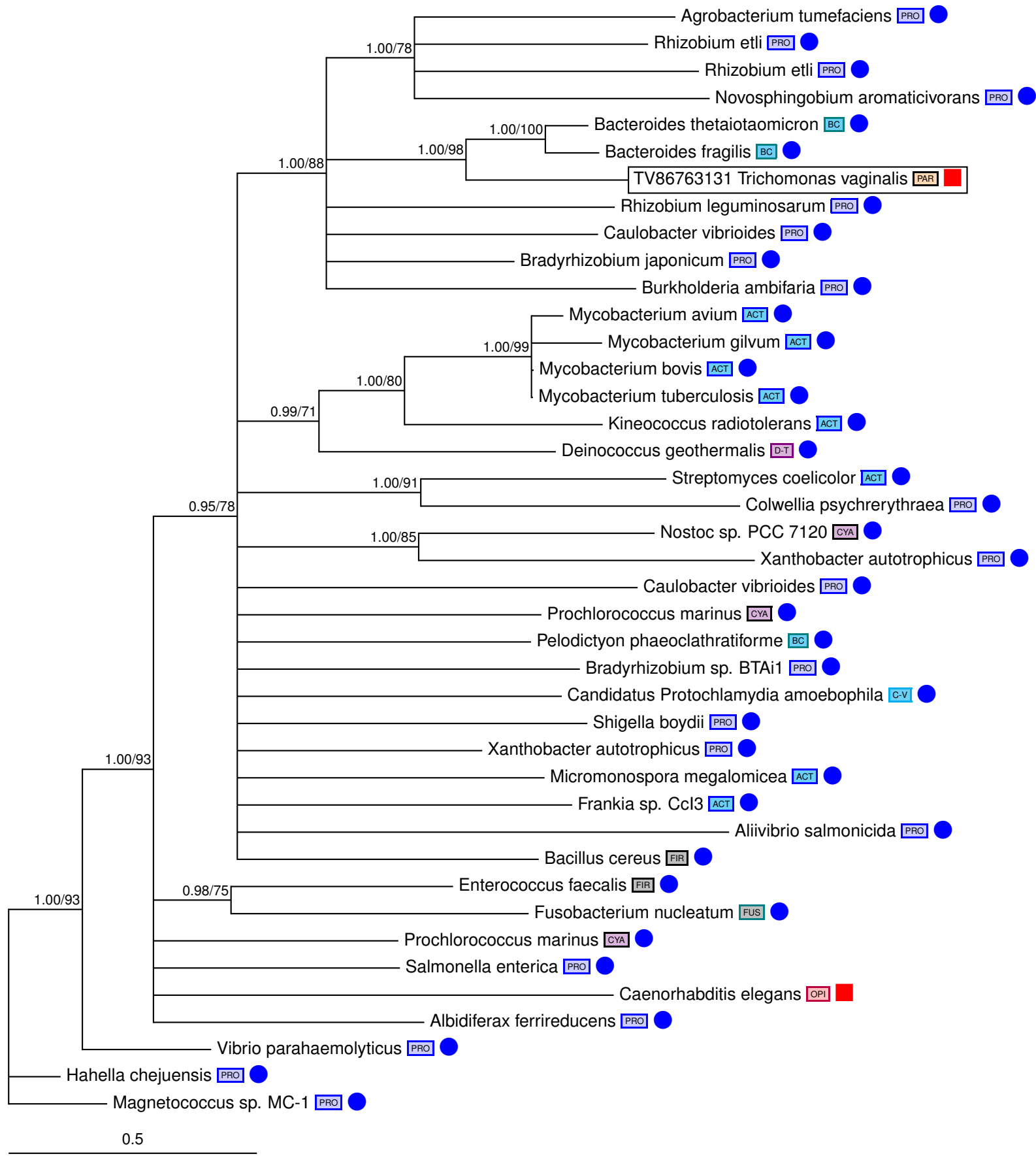
TN150

Candy accession: TV85228078
RefSeq accession: XP_001315888.1
Uniprot accession: A2EUL6_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:3.2.1.22
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Melibiase family protein
Name of enzyme/protein: alpha-galactosidase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Galactose metabolism, Glycerolipid metabolism, Sphingolipid metabolism, Glycosphingolipid biosynthesis



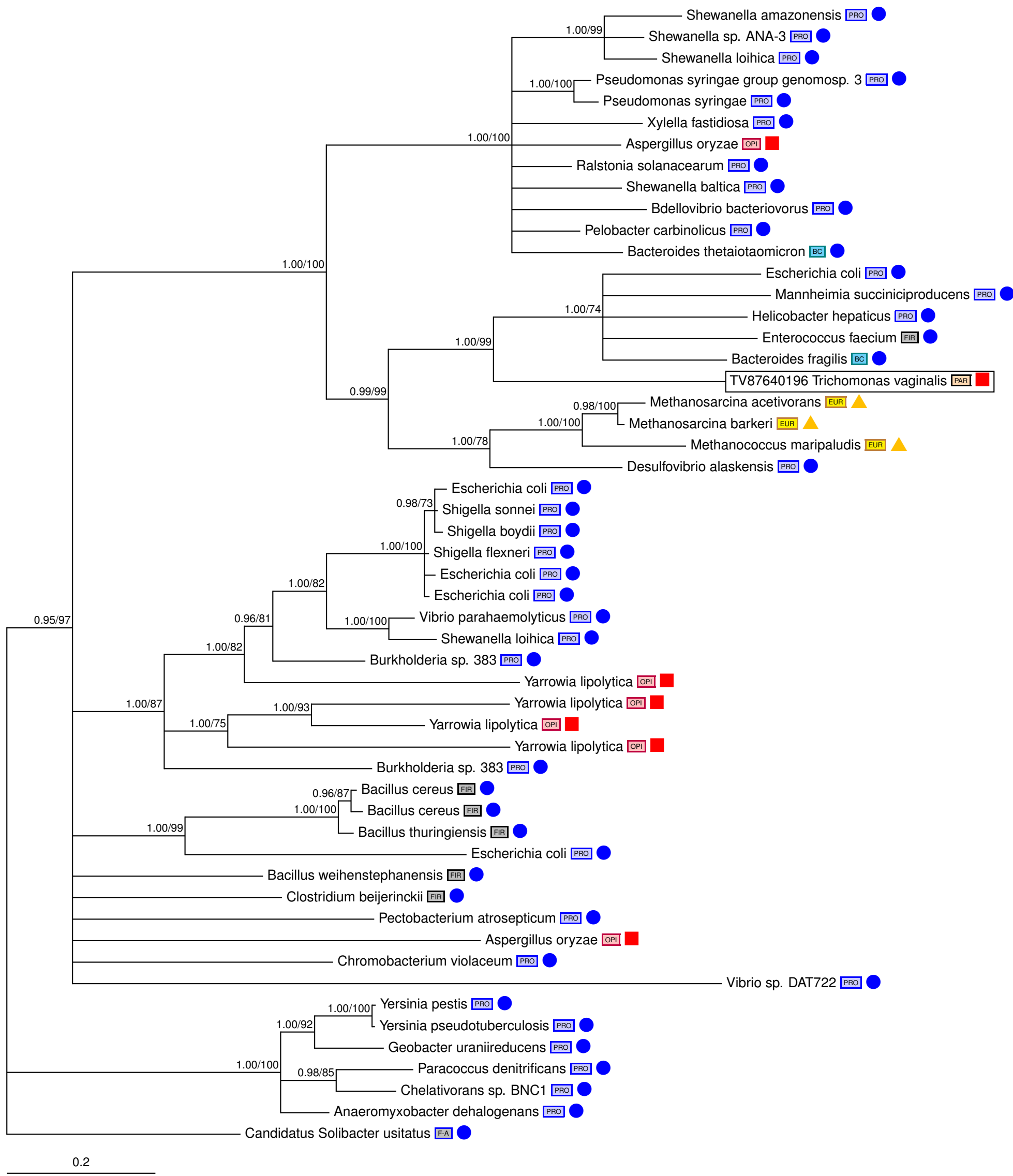
TN151

Candy accession: TV86763131
RefSeq accession: XP_001316224.1
Uniprot accession: A2ETN3_TRIVA
Comments: LGT - TV TWO NODES + C.ELEGANS
Species affected: TV,CE
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 11
RefSeq annotation: Acyltransferase family protein
Name of enzyme/protein: Acyltransferase family protein
KEGG PATHWAY - level 1: Other function - Membrane transport
KEGG PATHWAY - level 2: na



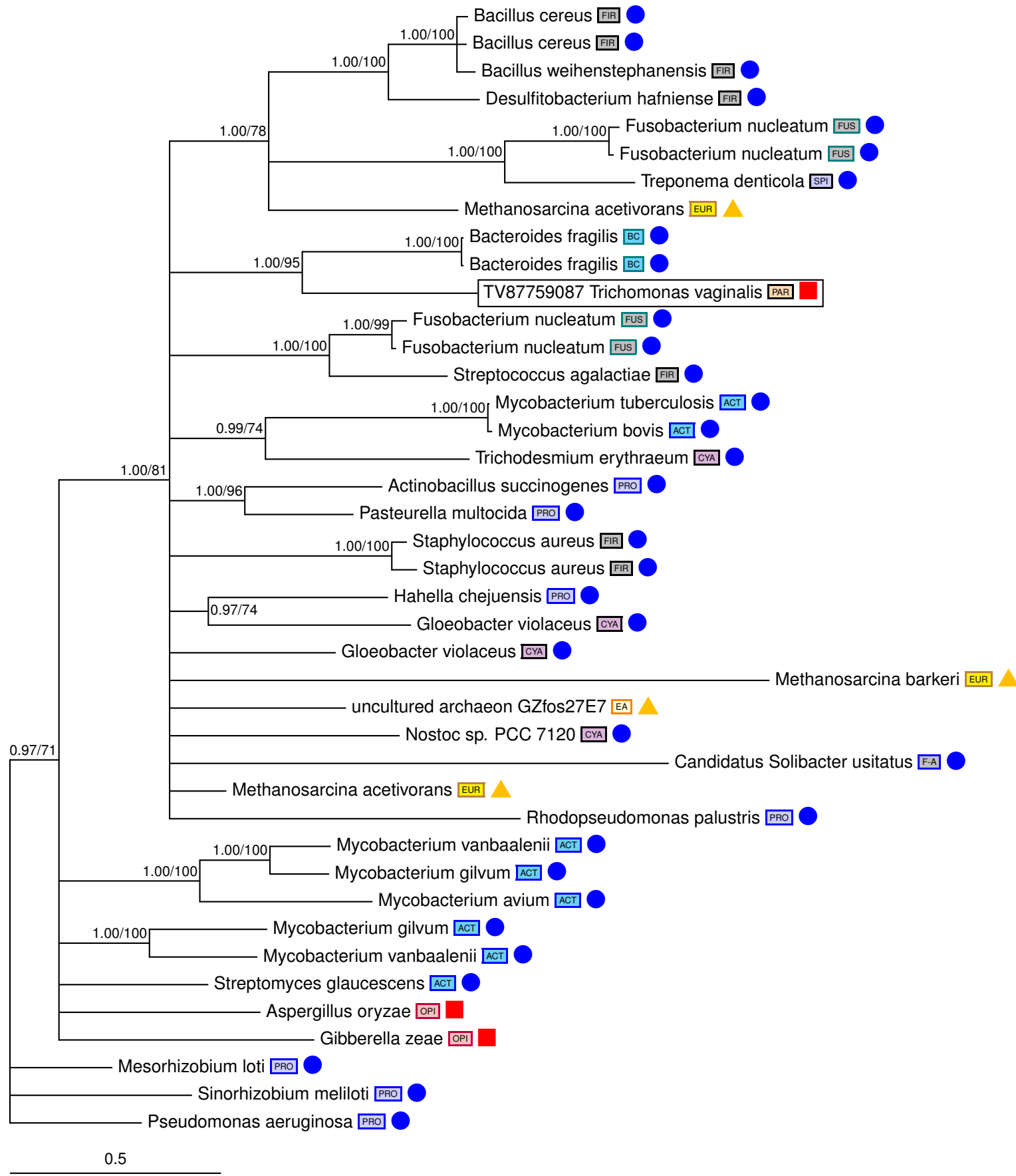
TN152

Candy accession: TV87640196
RefSeq accession: XP_001327002.1
Uniprot accession: A2DXR9_TRIVA
Comments: LGT - TV TWO NODES + LGT INTO FUNGI
Species affected: TV,FUNGI
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: opdE downstream ORF 2
Name of enzyme/protein: Predicted hydrolases of the alpha/beta superfamily
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



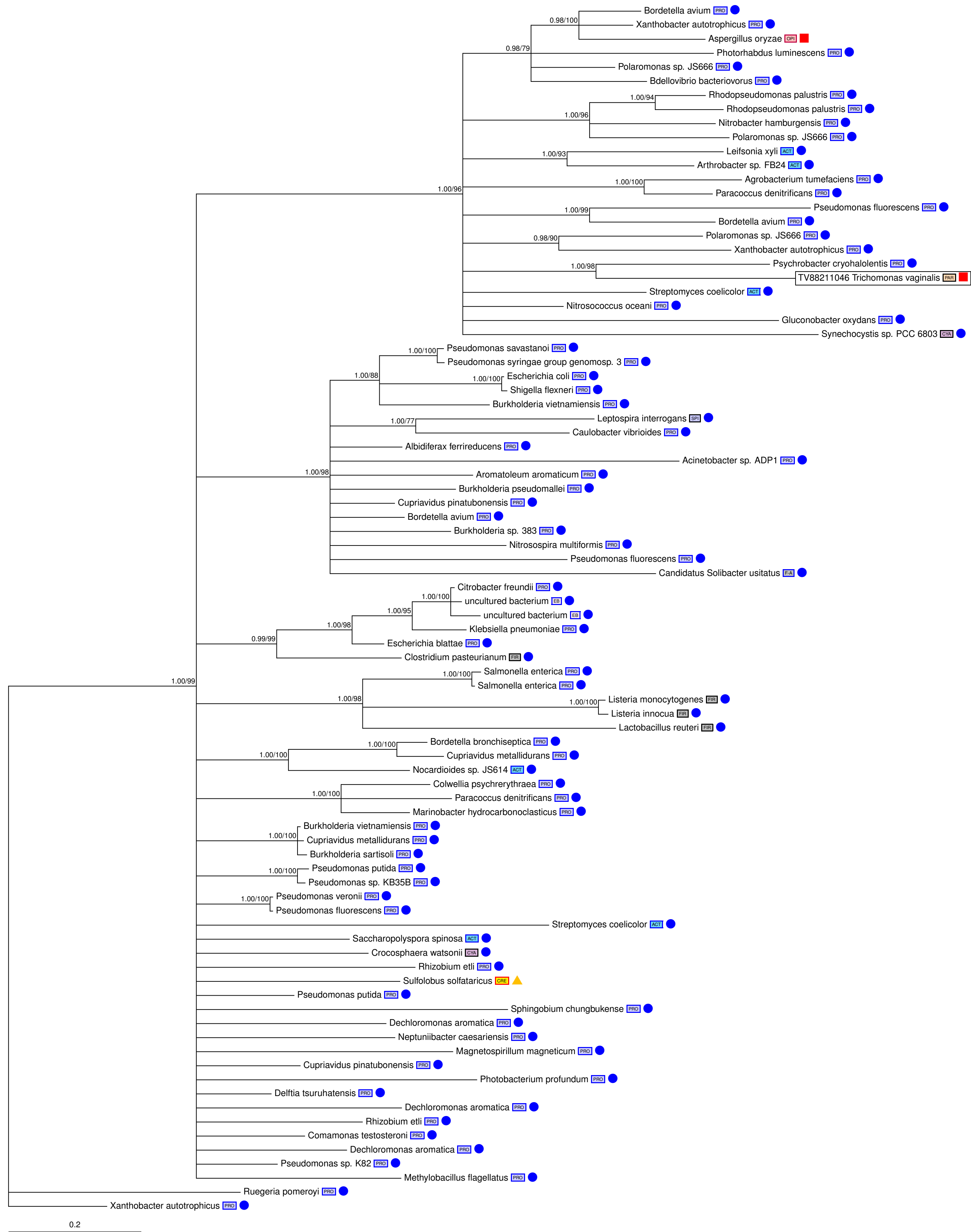
TN153

Candy accession: TV87759087
RefSeq accession: XP_001312818.1
Uniprot accession: A2F5C5_TRIVA
Comments: LGT - TV TWO NODES + LGT INTO FUNGI
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:2.1.1.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: 0-methyltransferase N-terminus family protein
Name of enzyme/protein: transferase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



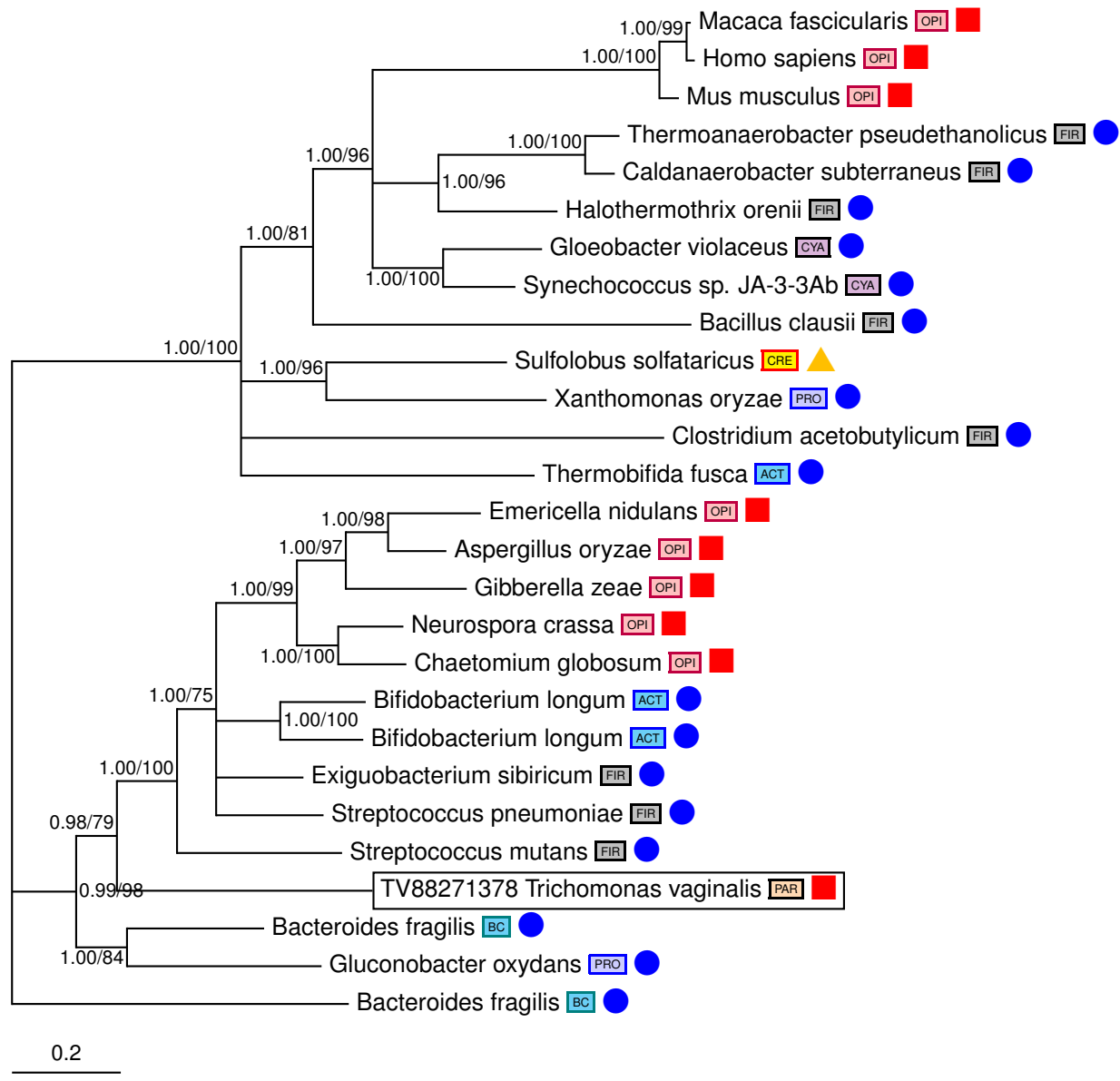
TN154

Candy accession: TV8211046
RefSeq accession: XP_001310705.1
Uniprot accession: A2FBE1.TRIVA
Comments: LGT - TV TWO NODES + FUNGI
Species affected: TV
Adjacent taxa in tree: Proteobacteria - Psychrobacter
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF336
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



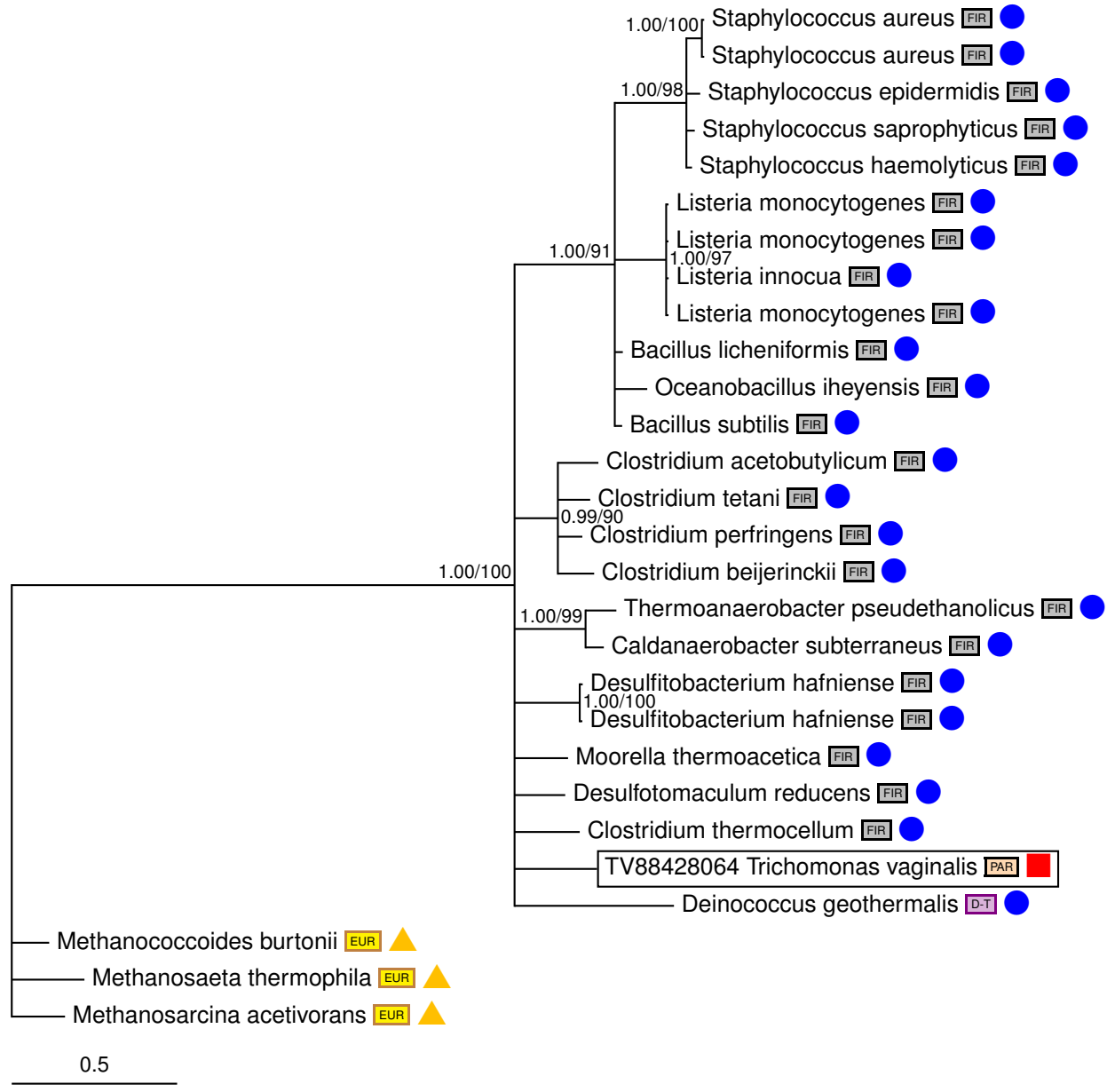
TN155

Candy accession: TV88271378
RefSeq accession: XP_001582671.1
Uniprot accession: A2DCR1_TRIVA
Comments: LGT - TV TWO NODES + FUNGI + MAMMALS
Species affected: TV,FUNGI
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.2.1.20
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glycosyl hydrolase
Name of enzyme/protein: alpha-glucosidase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Galactose metabolism, Starch and sucrose metabolism



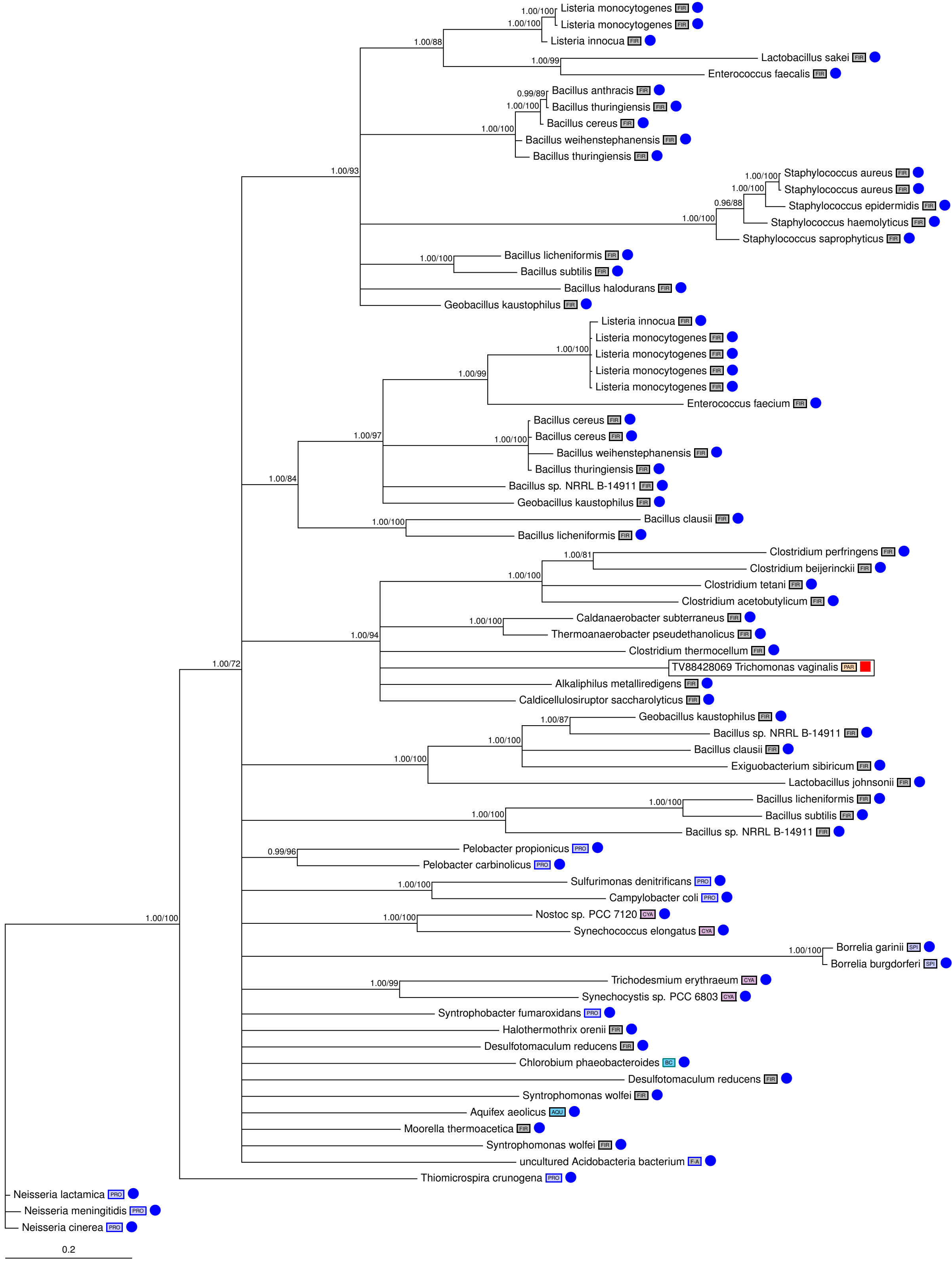
TN156

Candy accession: TV88428064
RefSeq accession: XP_001307952.1
Uniprot accession: A2FJA8_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.7.7.8
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: S1 RNA binding domain containing protein
Name of enzyme/protein: polyribonucleotide
nucleotidyltransferase
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Purine metabolism, Pyrimidine metabolism



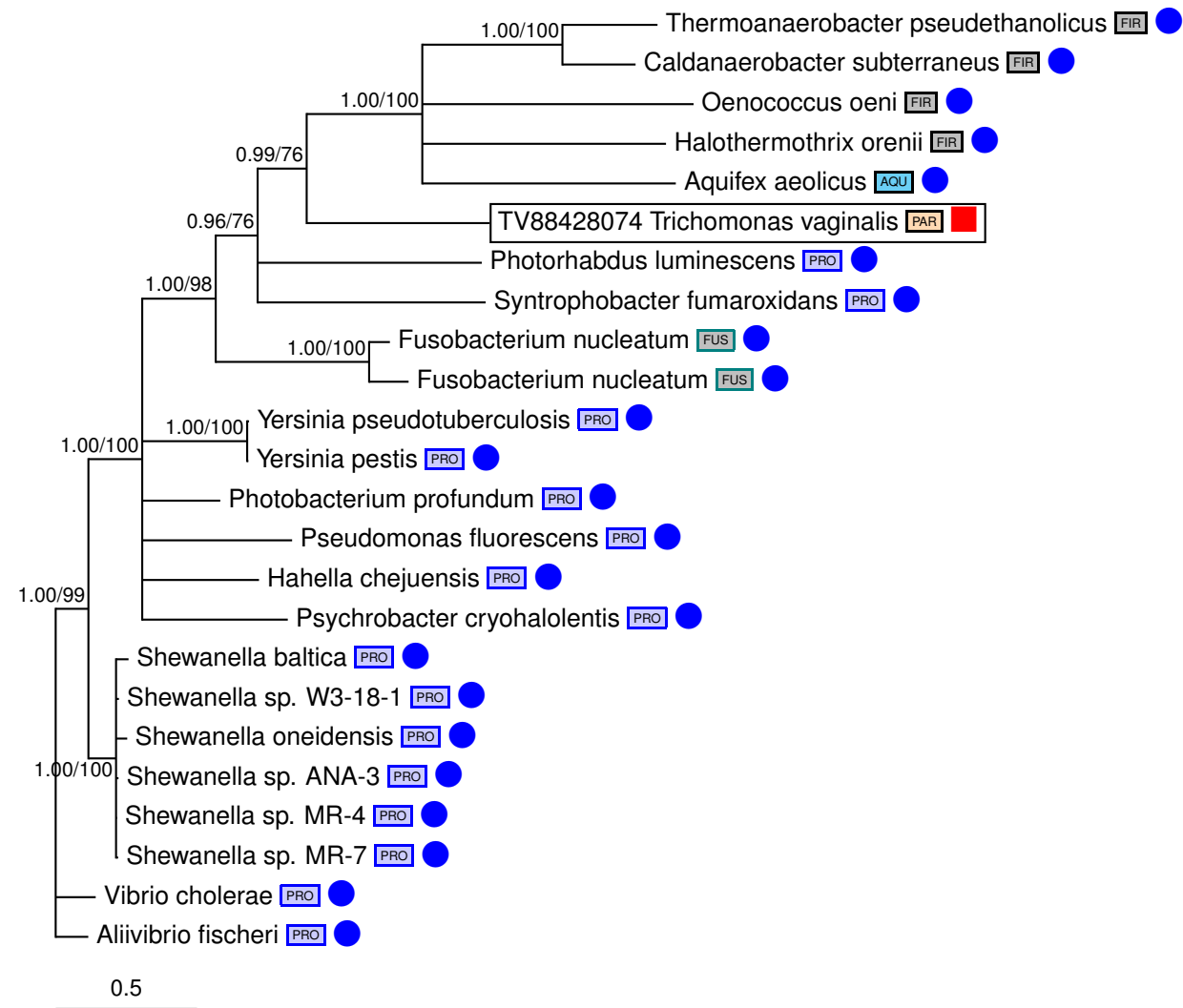
TN157

Candy accession: TV88428069
RefSeq accession: XP_001307956.1
Uniprot accession: A2FJB2_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): EC:2.4.1.129
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: penicillin binding protein
transpeptidase
Name of enzyme/protein: peptidoglycan glycosyltransferase
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism
KEGG PATHWAY - level 2: Peptidoglycan biosynthesis



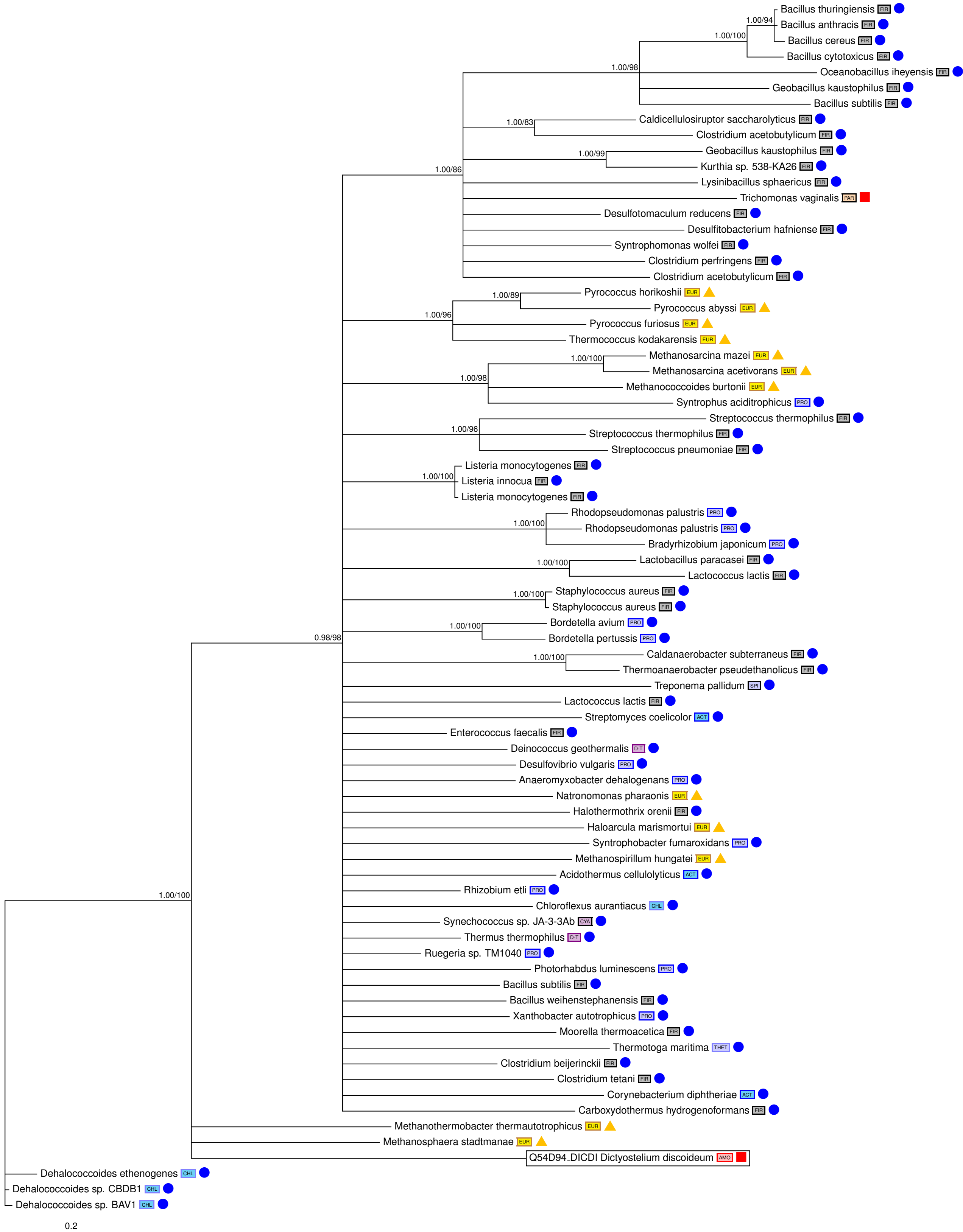
TN158

Candy accession: TV88428074
RefSeq accession: XP_001307946.1
Uniprot accession: A2FJA2_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 8
RefSeq annotation: Auxin Efflux Carrier family protein
Name of enzyme/protein: Auxin Efflux Carrier family protein
KEGG PATHWAY - level 1: Other function - Membrane transport
KEGG PATHWAY - level 2: na



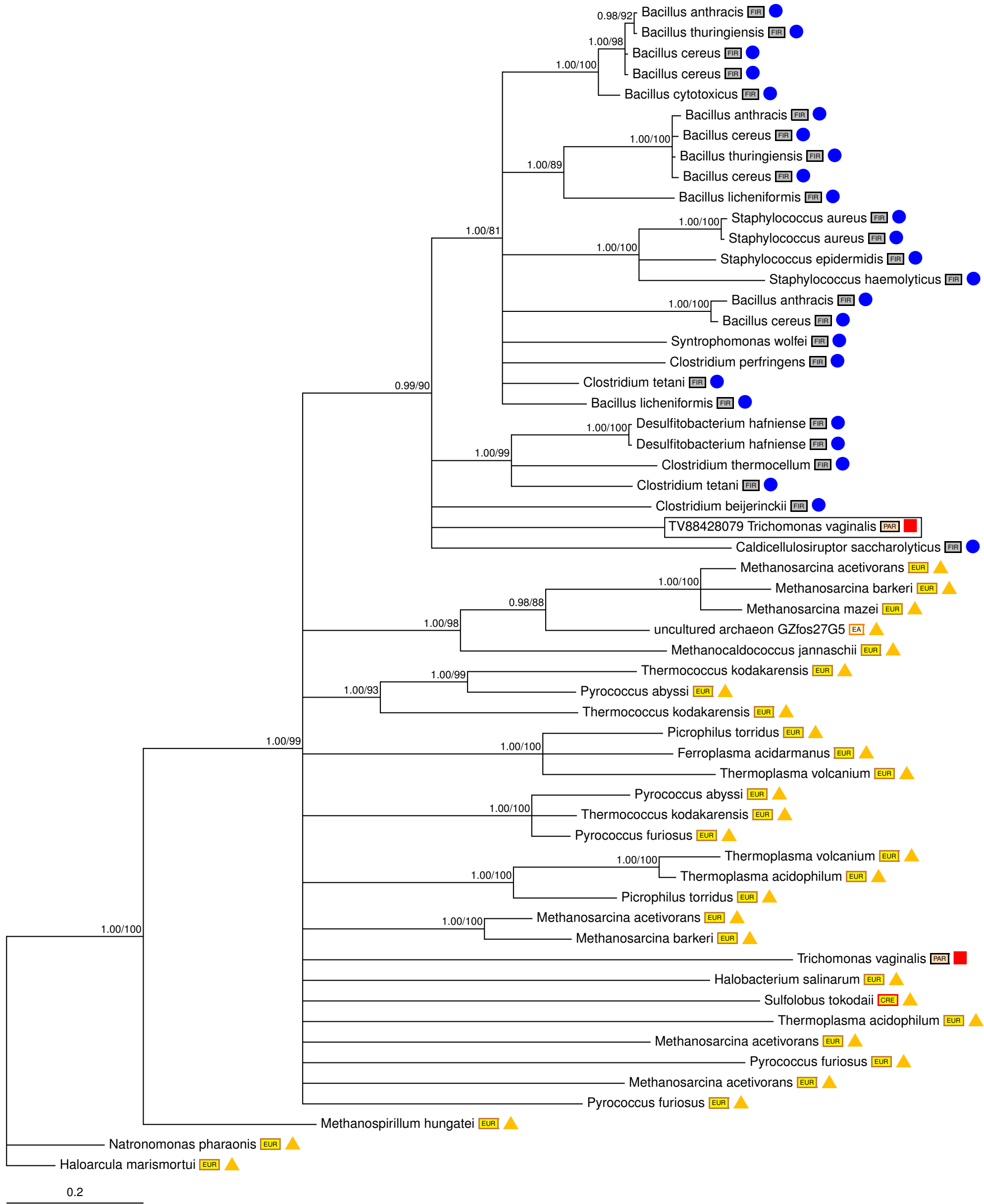
TN159

Candy accession: Q54D94_DICDI
RefSeq accession: XP_629602.1
Uniprot accession: Q54D94_DICDI
Comments: LGT - DD TWO NODES
Species affected: DD
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 6
RefSeq annotation: hypothetical protein DDB_G0292424
Name of enzyme/protein: Predicted BioY family
KEGG PATHWAY - level 1: Other function - Membrane transport
KEGG PATHWAY - level 2: na



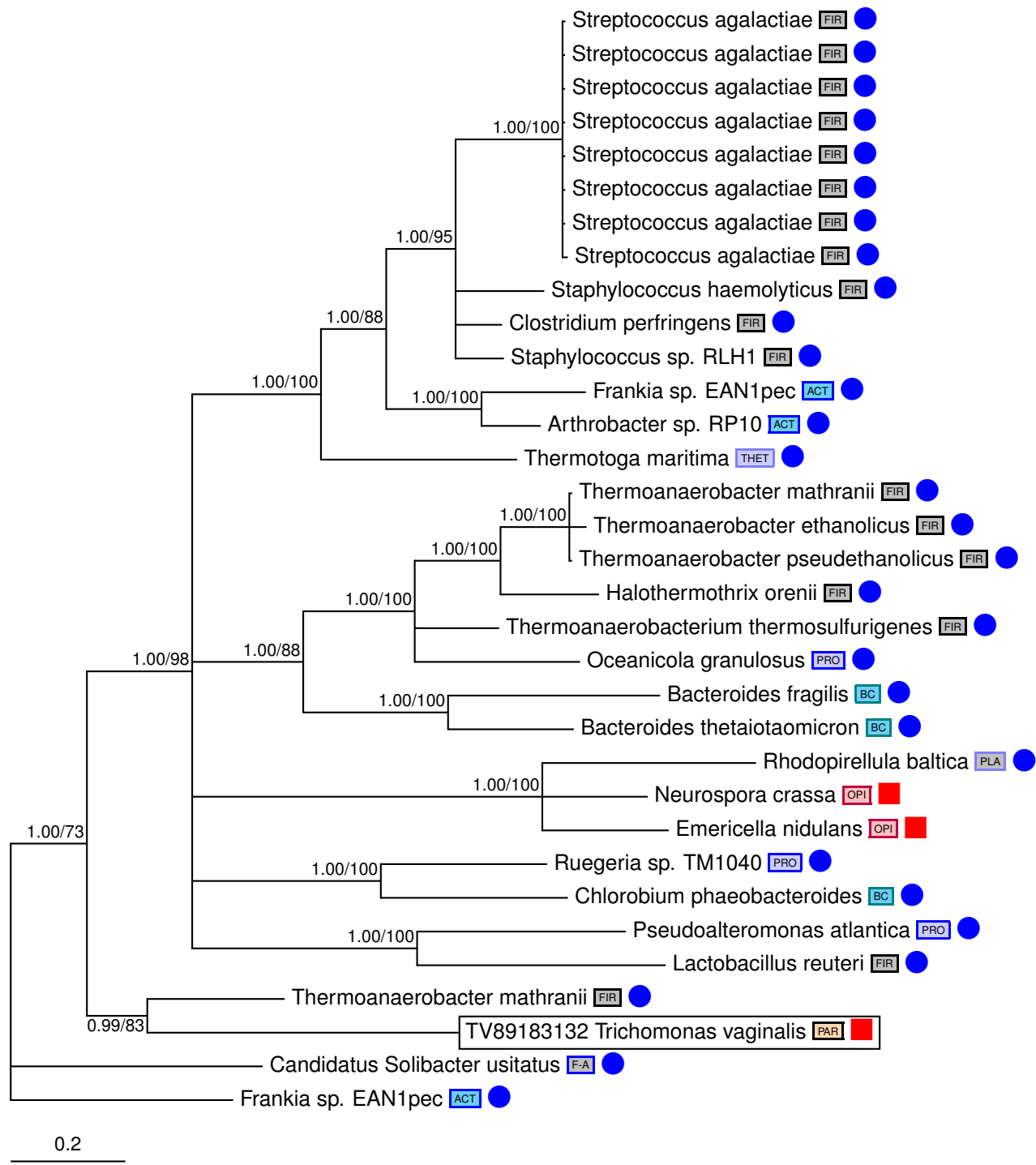
TN160

Candy accession: TV88428079
RefSeq accession: XP_001307937.1
Uniprot accession: A2FJ93_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): EC:3.6.3.25
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: transporter
Name of enzyme/protein: sulfate-transporting ATPase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



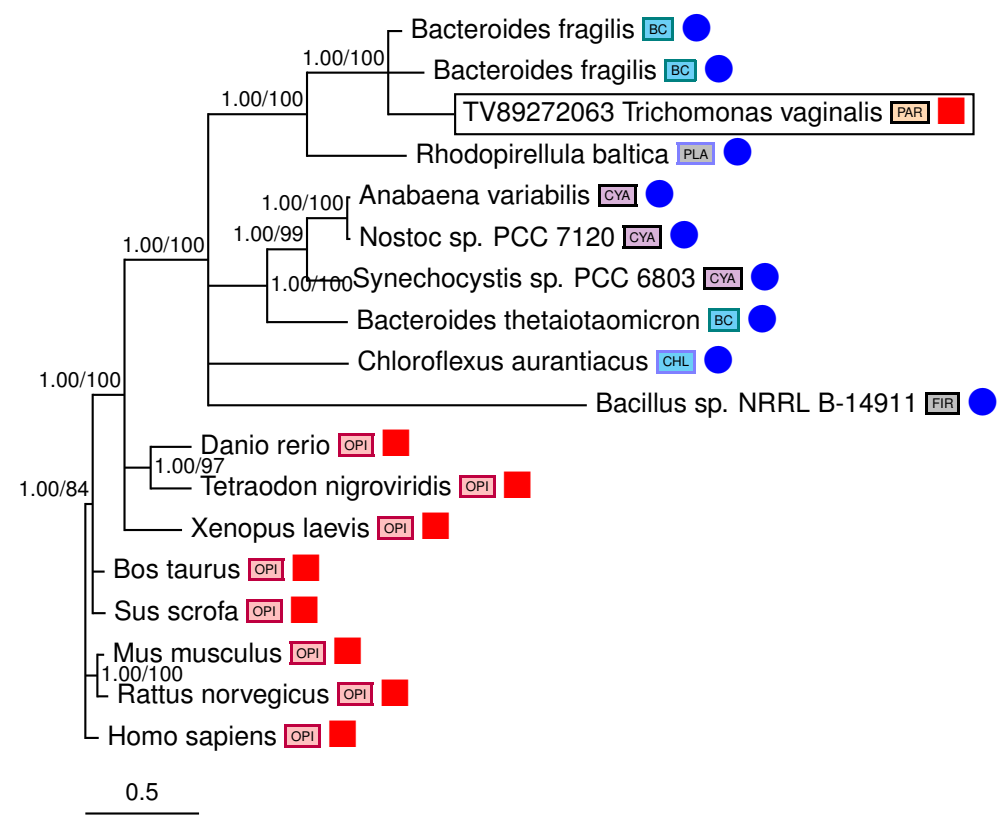
TN161

Candy accession: TV89183132
RefSeq accession: XP_001320621.1
Uniprot accession: A2EG37_TRIVA
Comments: LGT - TV TWO NODES + FUNGI
Species affected: TV,FUNGI
Adjacent taxa in tree: Firmicutes - Thermoanaerobacter
EC annotation - (Blast/Profile): EC:3.2.1.23
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glycosyl hydrolase
Name of enzyme/protein: beta-galactosidase
KEGG PATHWAY - level 1: Carbohydrate Metabolism, Glycan Biosynthesis and Metabolism, Lipid Metabolism
KEGG PATHWAY - level 2: Galactose metabolism, Other glycan degradation, Glycosaminoglycan degradation, Sphingolipid metabolism



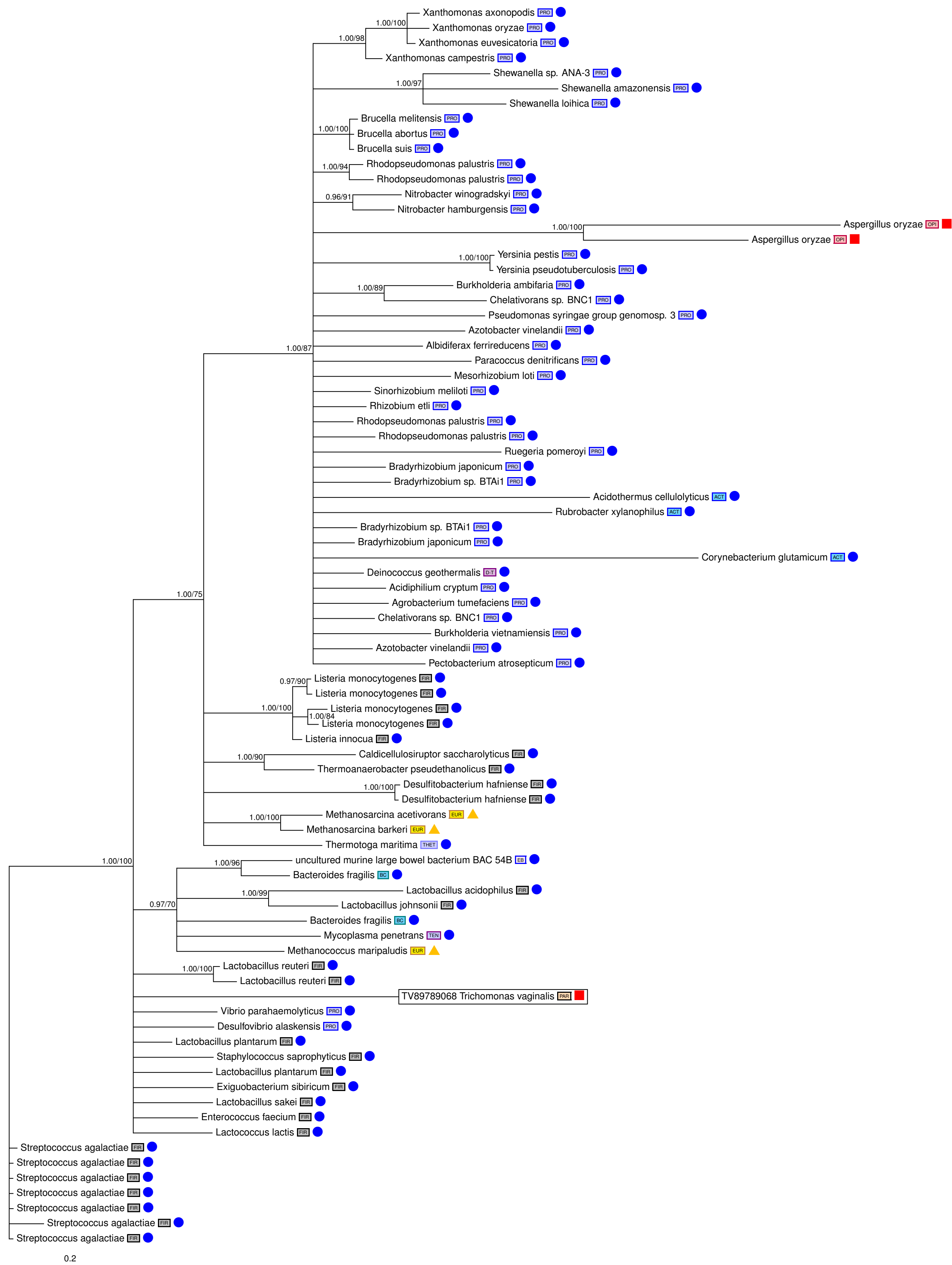
TN162

Candy accession: TV89272063
RefSeq accession: XP_001308218.1
Uniprot accession: A2FIH1_TRIVA
Comments: LGT - TV TWO NODES + ANIMALS
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:5.1.3.8
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: renin binding protein
Name of enzyme/protein: N-acylglucosamine 2-epimerase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Amino sugar and nucleotide sugar metabolism



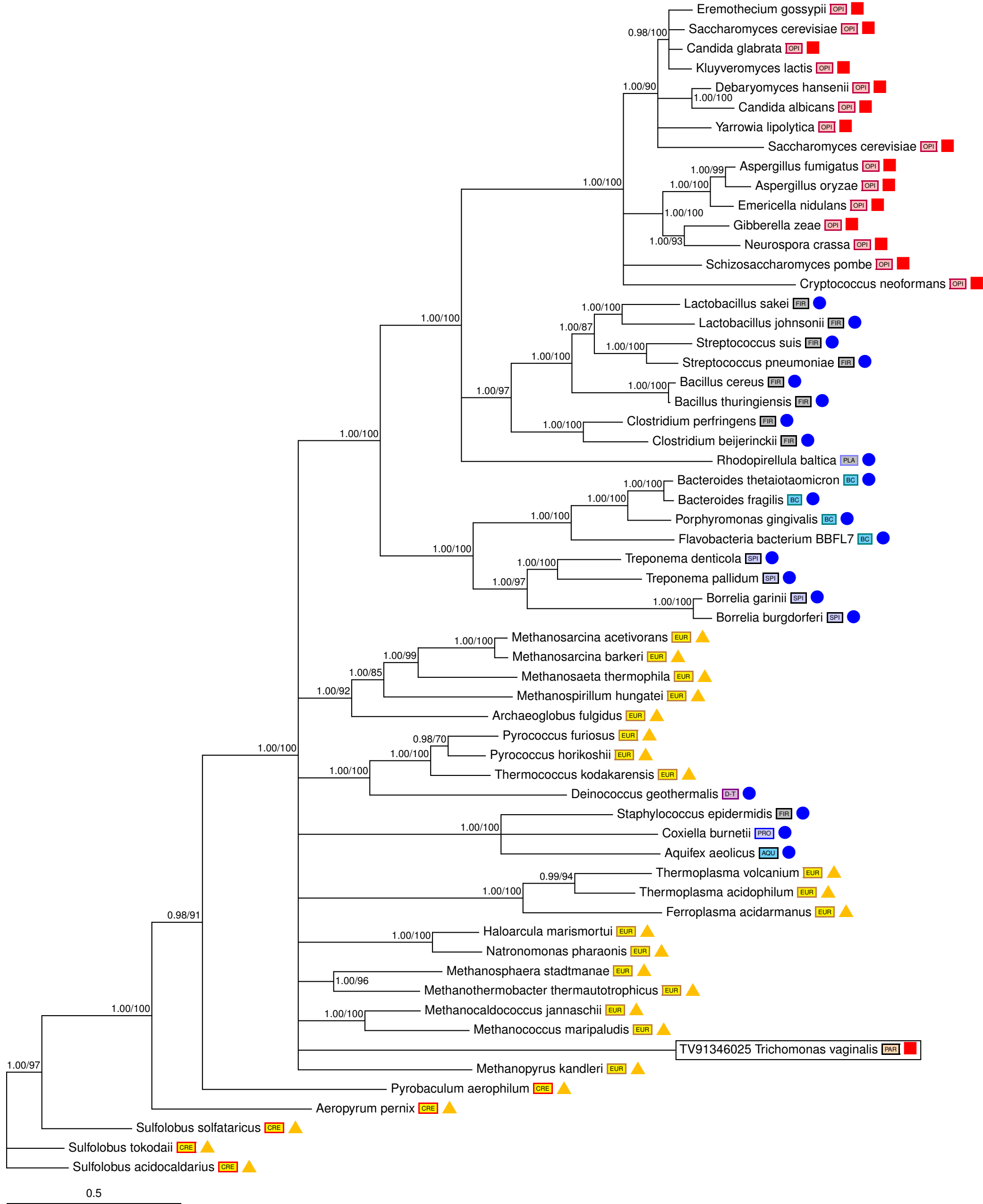
TN163

Candy accession: TV89789068
RefSeq accession: XP_001306707.1
Uniprot accession: A2FMW0_TR1VA
Comments: LGT - TV TWO NODES + 2 FUNGI
Species affected: TV_FUNGI
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:4.1.1.44
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: 4-carboxymuconolactone decarboxylase
KEGG PATHWAY - level 1: Xenobiotics Biodegradation and Metabolism
KEGG PATHWAY - level 2: Benzoate degradation



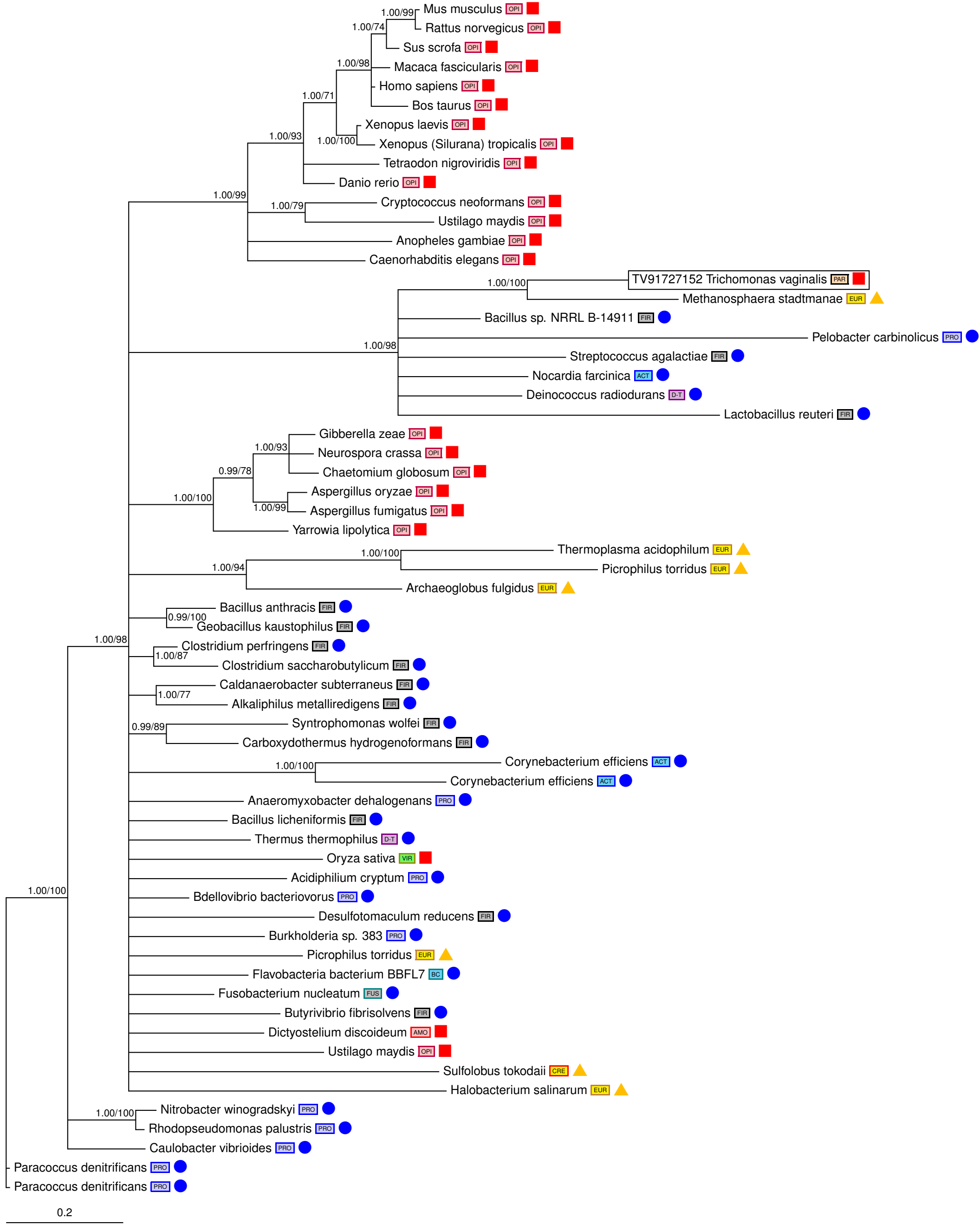
TN164

Candy accession: TV91346025
RefSeq accession: XP_001299401.1
Uniprot accession: A2G8P4_TRIVA
Comments: LGT - TV TWO NODES + FUNGI
Species affected: TV,FUNGI
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:6.1.1.19
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: DALR anticodon binding domain containing protein
Name of enzyme/protein: arginyl-tRNA synthetase
KEGG PATHWAY - level 1: Translation - Genetic Information Processing
KEGG PATHWAY - level 2: Aminoacyl-tRNA biosynthesis



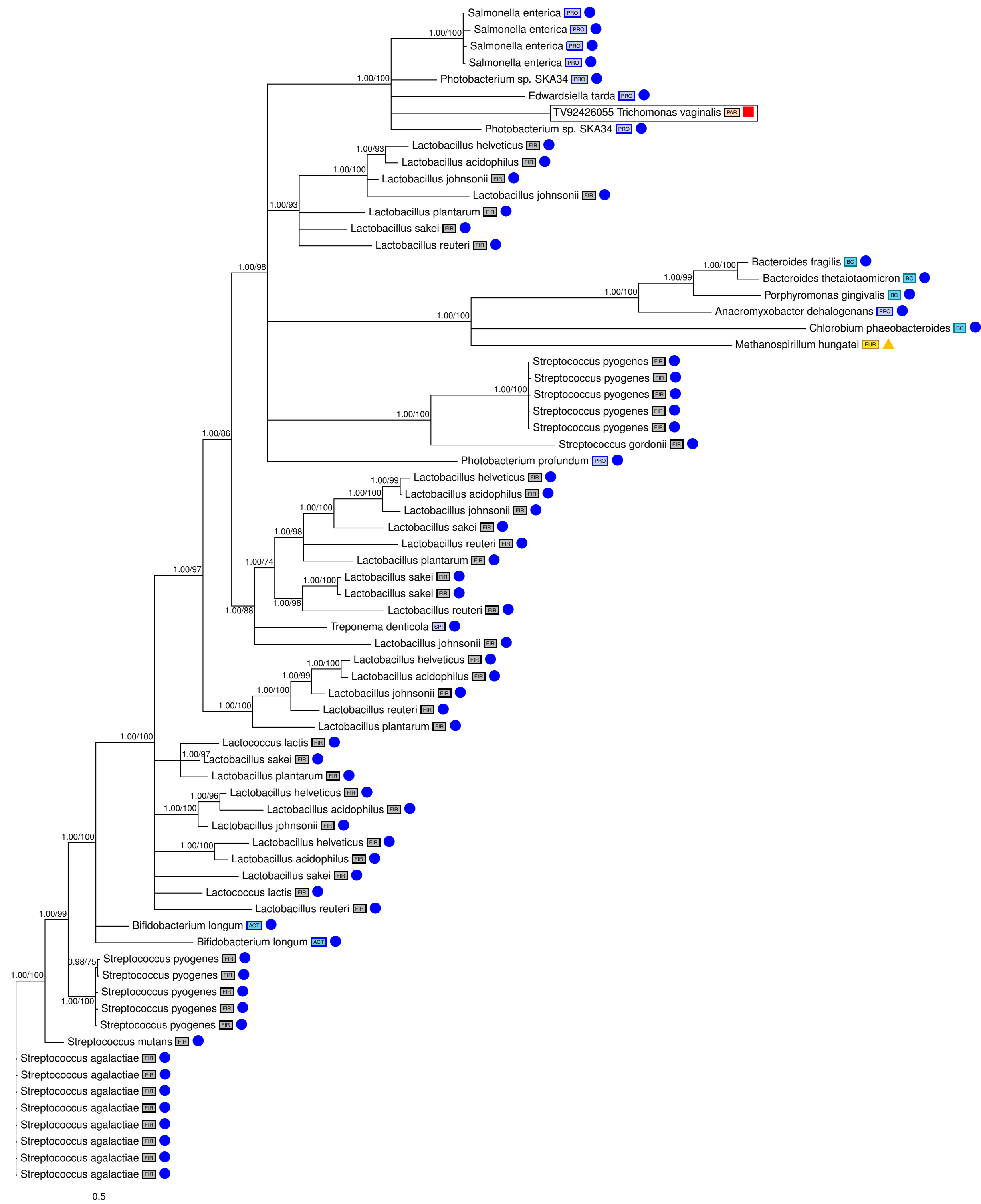
TN165

Candy accession: TV91727152
RefSeq accession: XP_001320207.1
Uniprot accession: A2EHA5_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Archaea - Methanosphaera
EC annotation - (Blast/Profile): EC:1.1.1.157
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: 3-hydroxyacyl-CoA dehydrogenase,
C-terminal domain containing protein
Name of enzyme/protein: 3-hydroxyacyl-CoA dehydrogenase
KEGG PATHWAY - level 1: Xenobiotics Biodegradation and
Metabolism, Carbohydrate Metabolism
KEGG PATHWAY - level 2: Benzoate degradation, Butanoate
metabolism



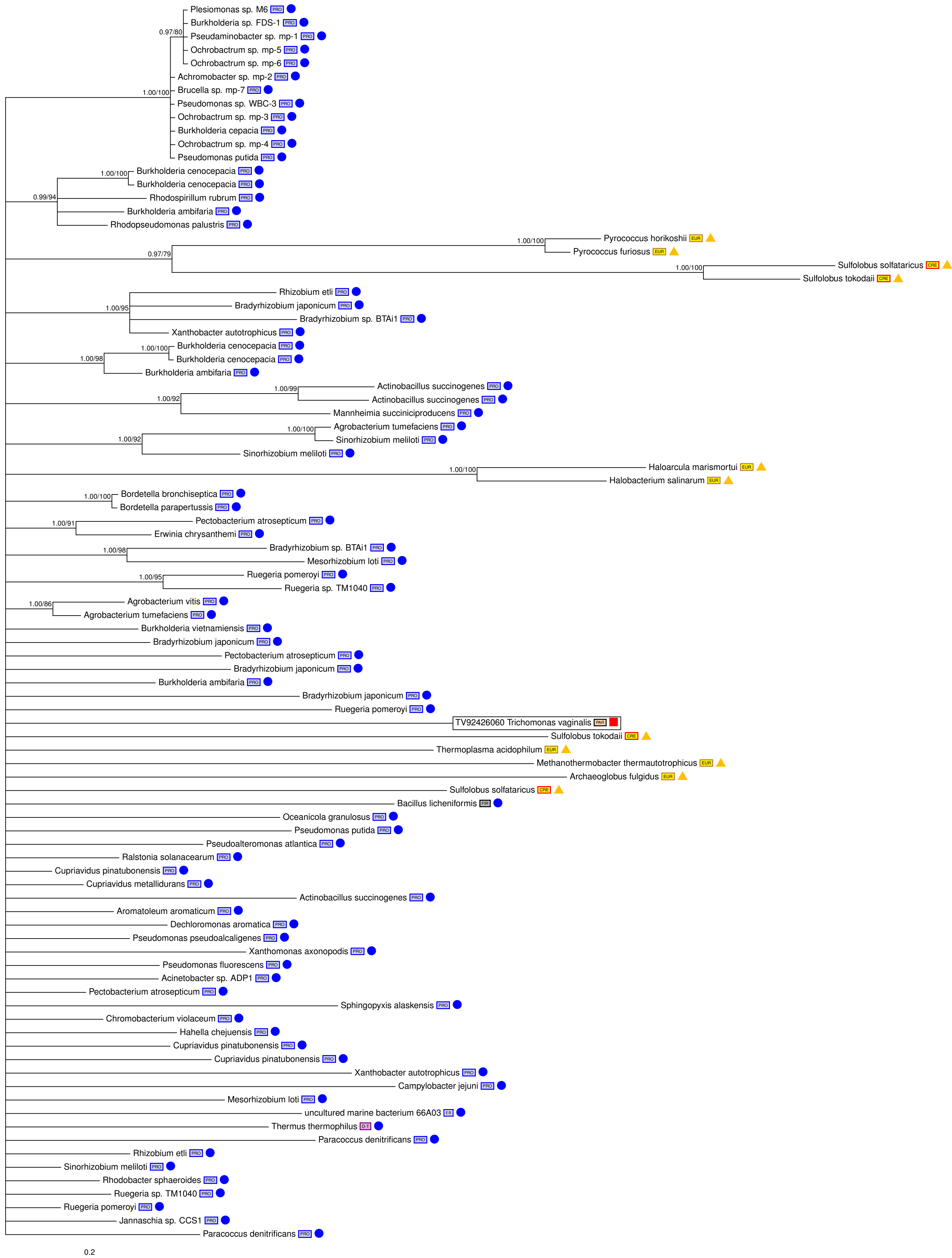
TN166

Candi accession: TV92426055
 RefSeq accession: XP_001313452.1
 Uniprot accession: A2F3K0_TRIVA
 Comments: LGT - TV ONLY
 Species affected: TV
 Adjacent taxa in tree: Protobacteria
 EC annotation - (Blast/Profile): EC:3.4.13.18
 PHOBIUS SP: 0
 PHOBIUS TMD: 0
 RefSeq annotation: Clan PB, family C69, PipD-like cysteine
 peptidase
 Name of enzyme/protein: Cytosolic nonspecific dipeptidase
 KEGG PATHWAY - level 1: Amino Acid Metabolism, Metabolism of
 Other Amino Acids
 KEGG PATHWAY - level 2: Arginine and proline metabolism,
 Histidine metabolism, beta-Alanine
 metabolism



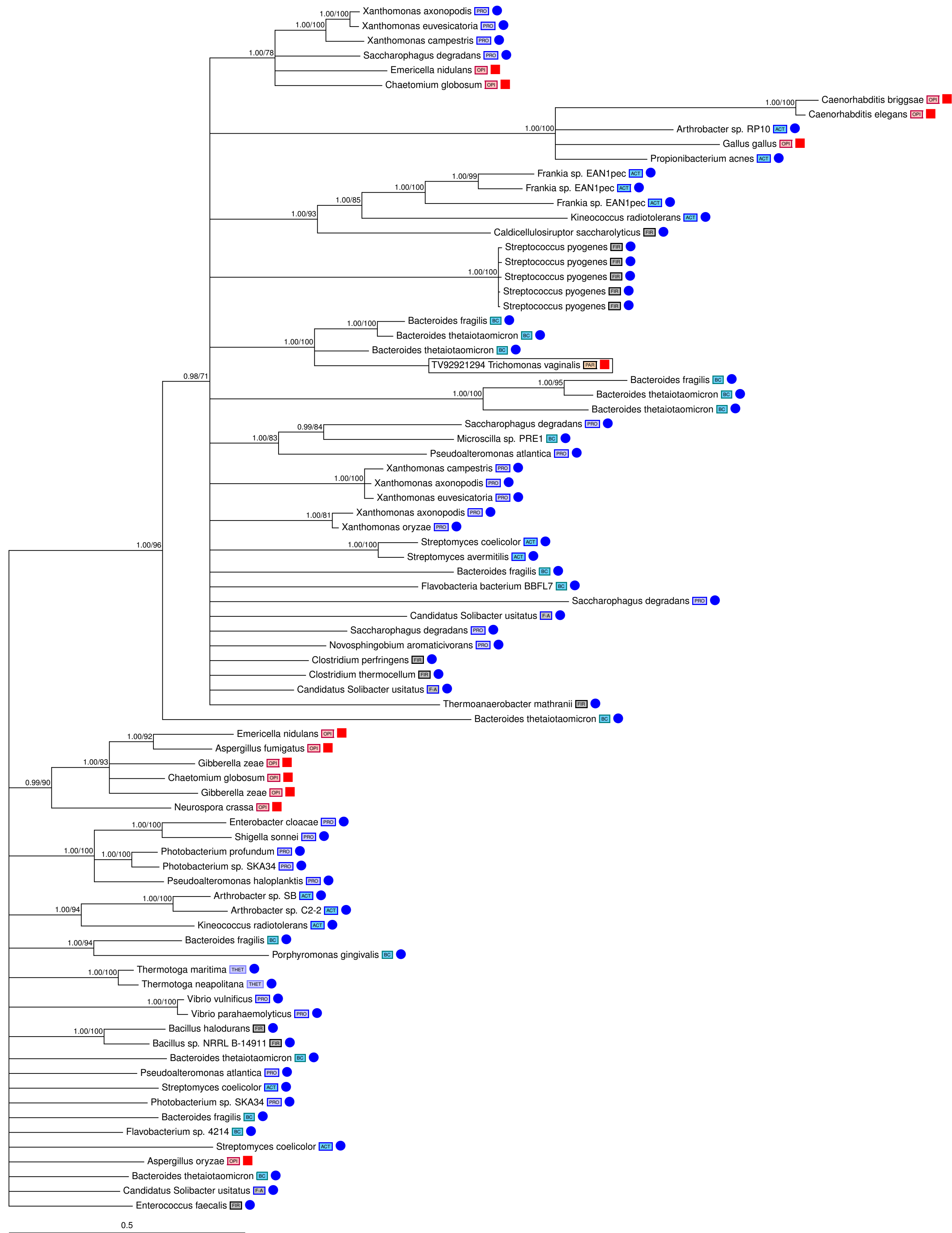
TN167

Candy accession: TV92426060
RefSeq accession: XP_001313458.1
Uniprot accession: A2F3K6_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:3.1.-.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: metallo-beta-lactamase superfamily
protein
Name of enzyme/protein: Predicted Zn-dependent hydrolase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



TN168

Candy accession: TV92921294
RefSeq accession: XP_001581038.1
Uniprot accession: A2DHK4_TRIVA
Comments: LGT - TV TWO NODES + FUNGI
Species affected: TV, FUNGI
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:3.2.1.23
PHOBIOUS SP: Y
PHOBIOUS TMD: 0
RefSeq annotation: beta-galactosidase
Name of enzyme/protein: Beta-galactosidase
KEGG PATHWAY - level 1: Carbohydrate Metabolism, Glycan
Biosynthesis and Metabolism, Lipid
Metabolism
KEGG PATHWAY - level 2: Galactose metabolism, Other glycan
degradation, Glycosaminoglycan
degradation, Sphingolipid metabolism

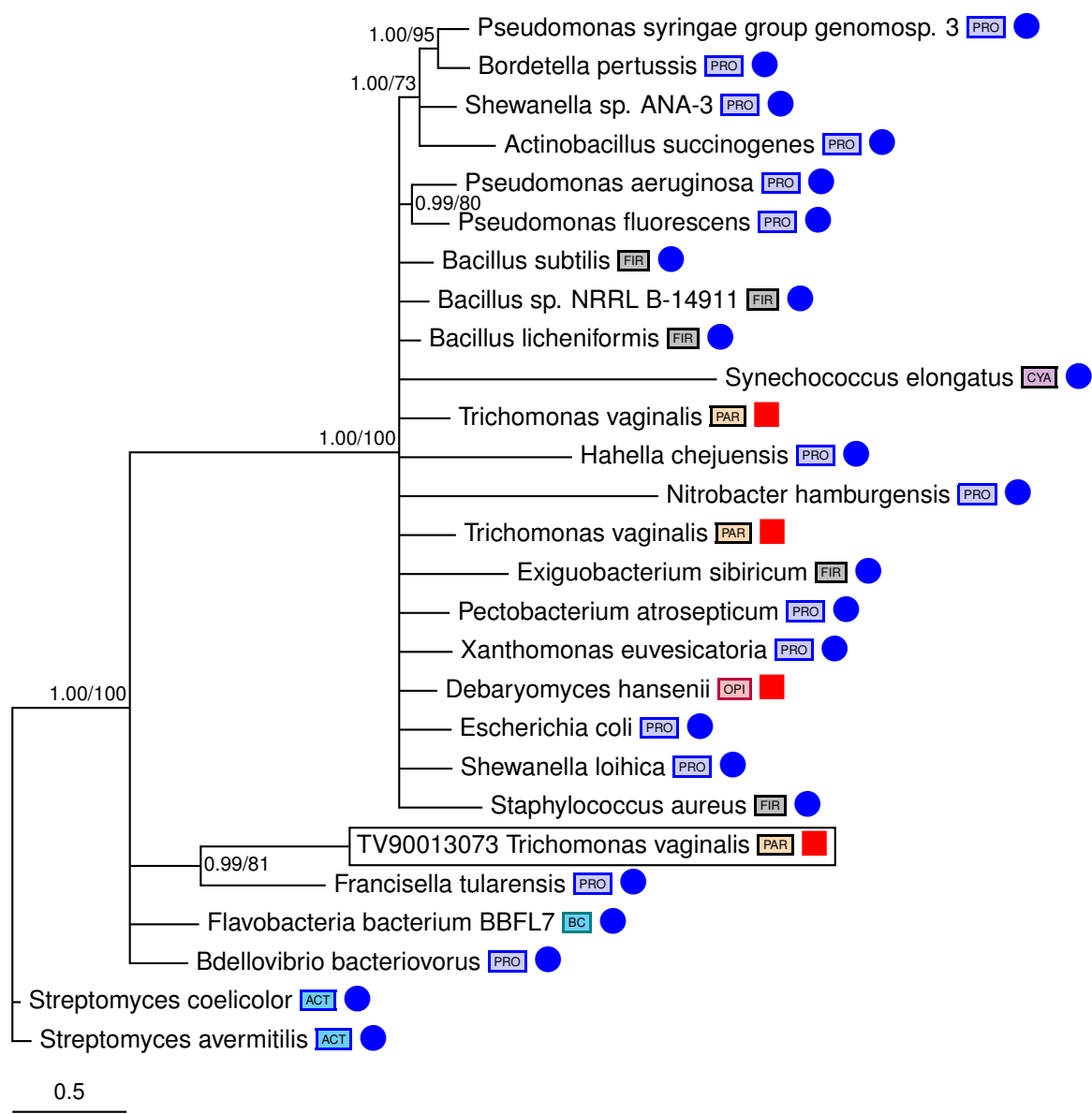


TN169

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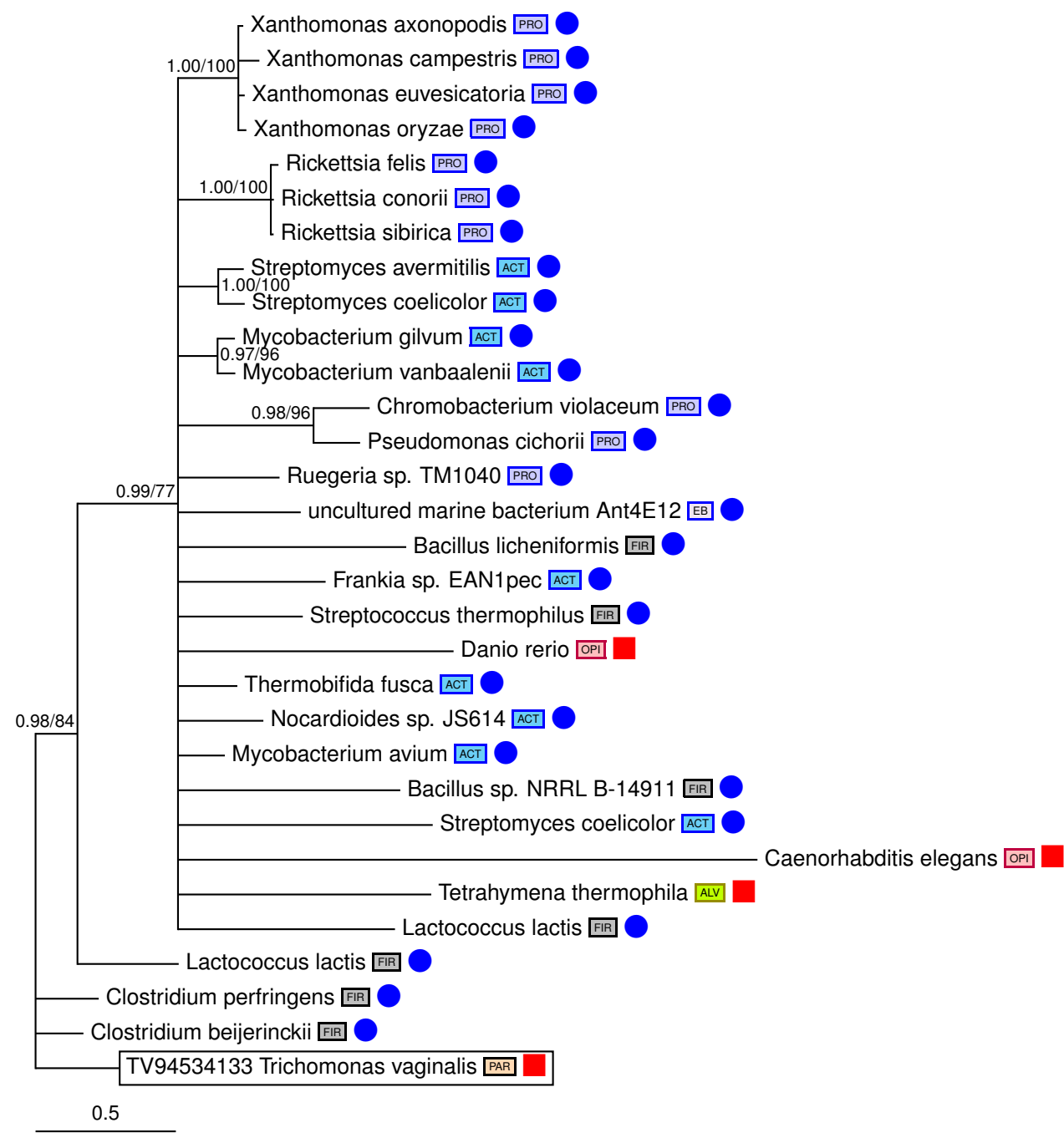
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      RefSeq accession: XP_001313313.1
      Uniprot accession: A2F3W8_TRIIVA
      Comments: LGT - TV TWO NODES + FUNGI
      Species affected: TV, FUNGI
      Adjacent taxa in tree: Proteobacteria - Francisella
EC annotation - (Blast/Profile): na
      PHOBIUS SP: 0
      PHOBIUS TMD: 0
      RefSeq annotation: beta lactamase
      Name of enzyme/protein: Predicted Zn-dependent hydrolases of the
                           beta-lactamase
      KEGG PATHWAY - level 1: Other function
      KEGG PATHWAY - level 2: na

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TN170

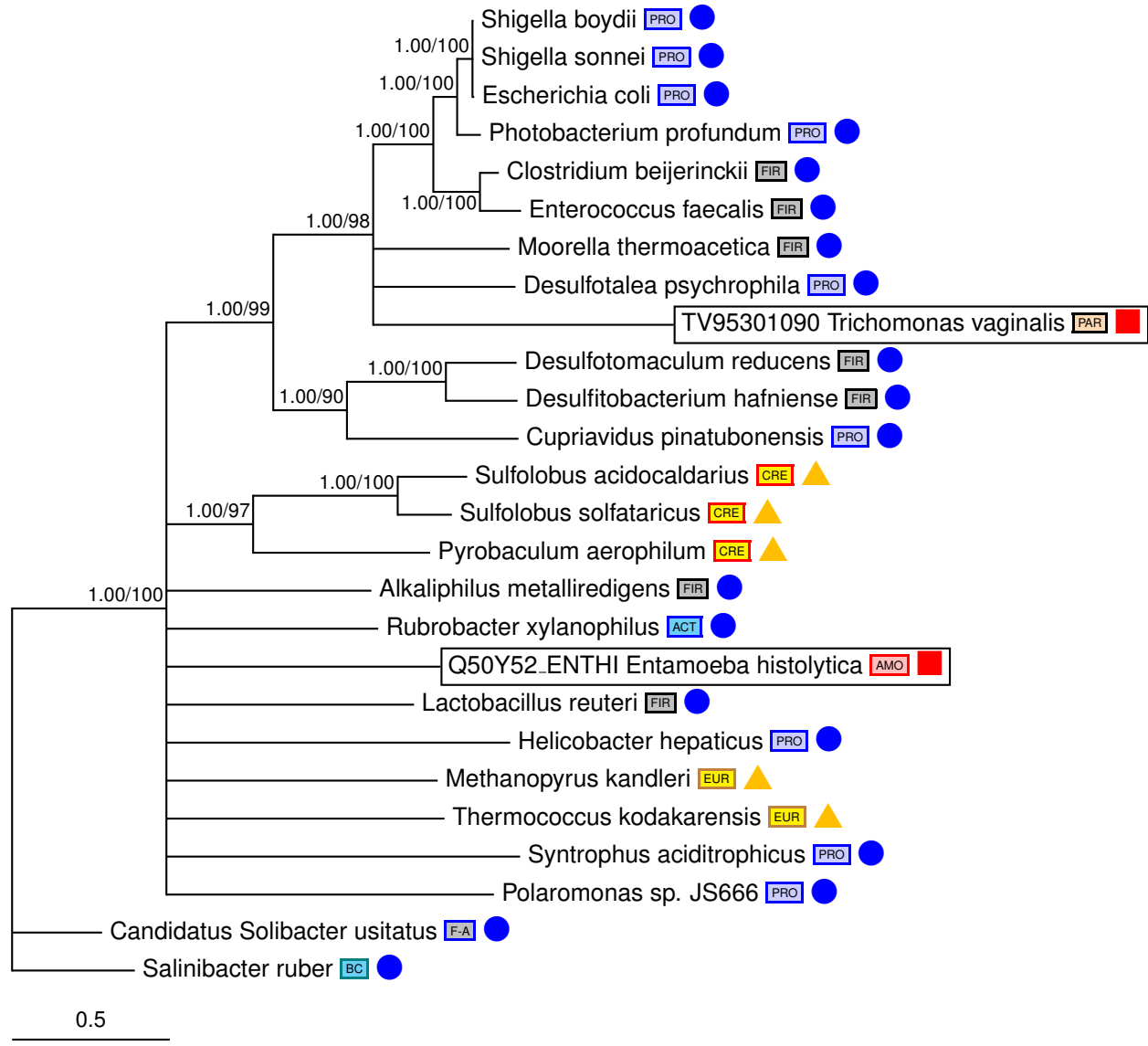
Candy accession: TV94534133
RefSeq accession: XP_001321964.1
Uniprot accession: A2EC64_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Firmicutes - Clostridia
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hydrolase, NUDIX family protein
Name of enzyme/protein: Predicted hydrolase, NUDIX family protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



TN171

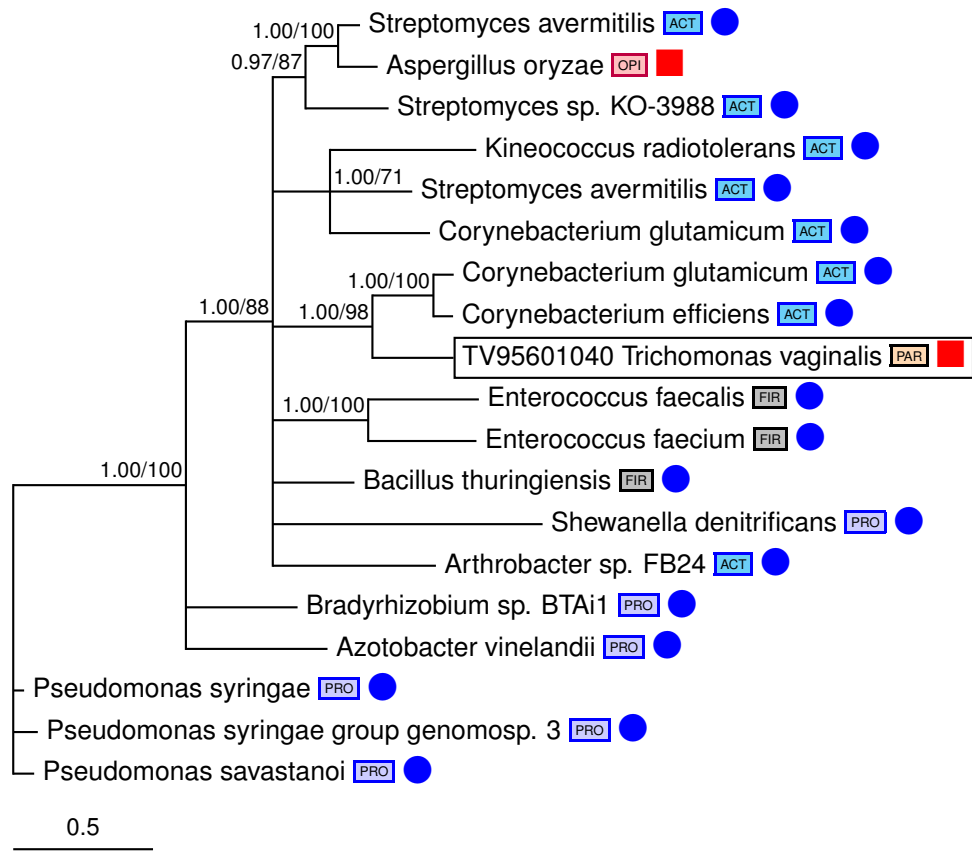
Candy accession: TV95301090
RefSeq accession: XP_001311981.1
Uniprot accession: A2F7S4_TRIVA
Comments: LGT - TV NICE TREE
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.5.1.18
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Clan MH, family M20, peptidase T-like metallopeptidase
Name of enzyme/protein: succinyl-diaminopimelate desuccinylase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Lysine biosynthesis

Candy accession: Q50Y52_ENTHI
RefSeq accession: XP_651923.2
Uniprot accession: Q50Y52_ENTHI
Comments: LGT - EH NICE TREE
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:3.5.1.18
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: succinyl-diaminopimelate desuccinylase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Lysine biosynthesis



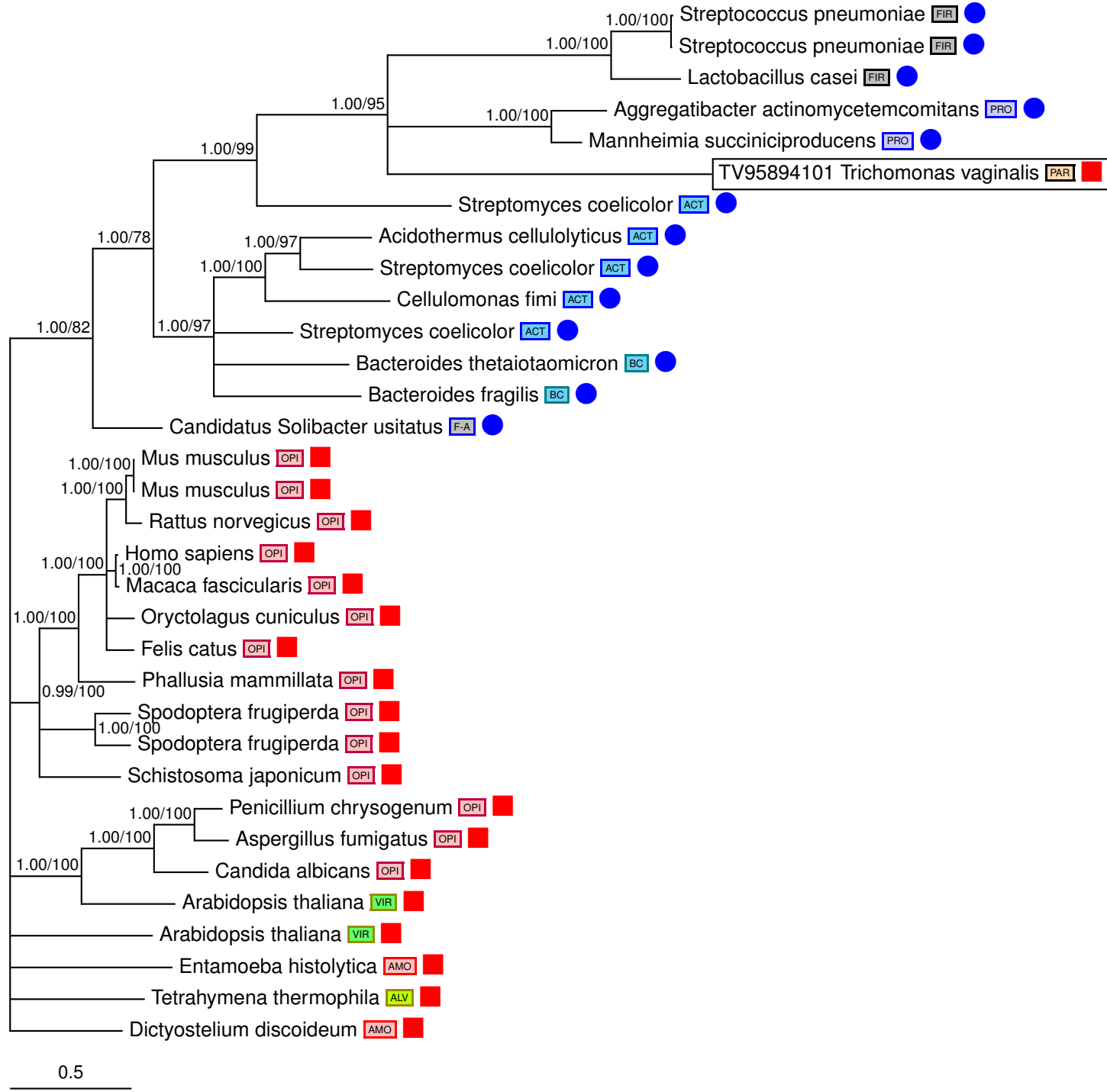
TN172

Candy accession: TV95601040
RefSeq accession: XP_001302065.1
Uniprot accession: A2G132_TRIVA
Comments: LGT - TV TWO NODES + FUNGI
Species affected: TV,FUNGI
Adjacent taxa in tree: Actinobacteria - Corynebacterium
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Hypothetical protein
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



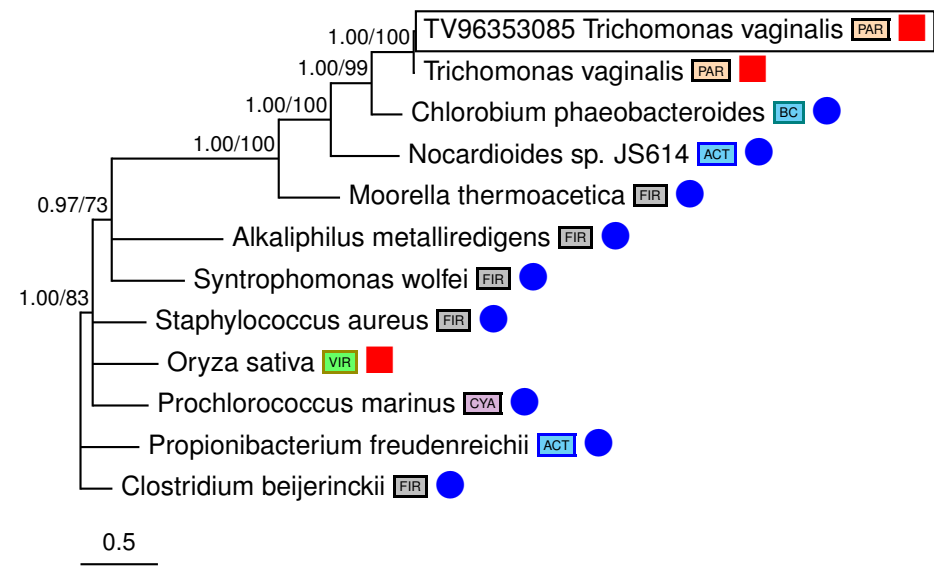
TN173

Candy accession: TV95894101
RefSeq accession: XP_001310032.1
Uniprot accession: A2FDA0_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.2.1.52
PHOBIUS SP: 0
PHOBIUS TMD: 1
RefSeq annotation: glycosyl hydrolase
Name of enzyme/protein: beta-N-acetylhexosaminidase
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism, Carbohydrate Metabolism
KEGG PATHWAY - level 2: Other glycan degradation, Various types of N-glycan biosynthesis, Glycosaminoglycan degradation, Amino sugar and nucleotide sugar metabolism



TN174

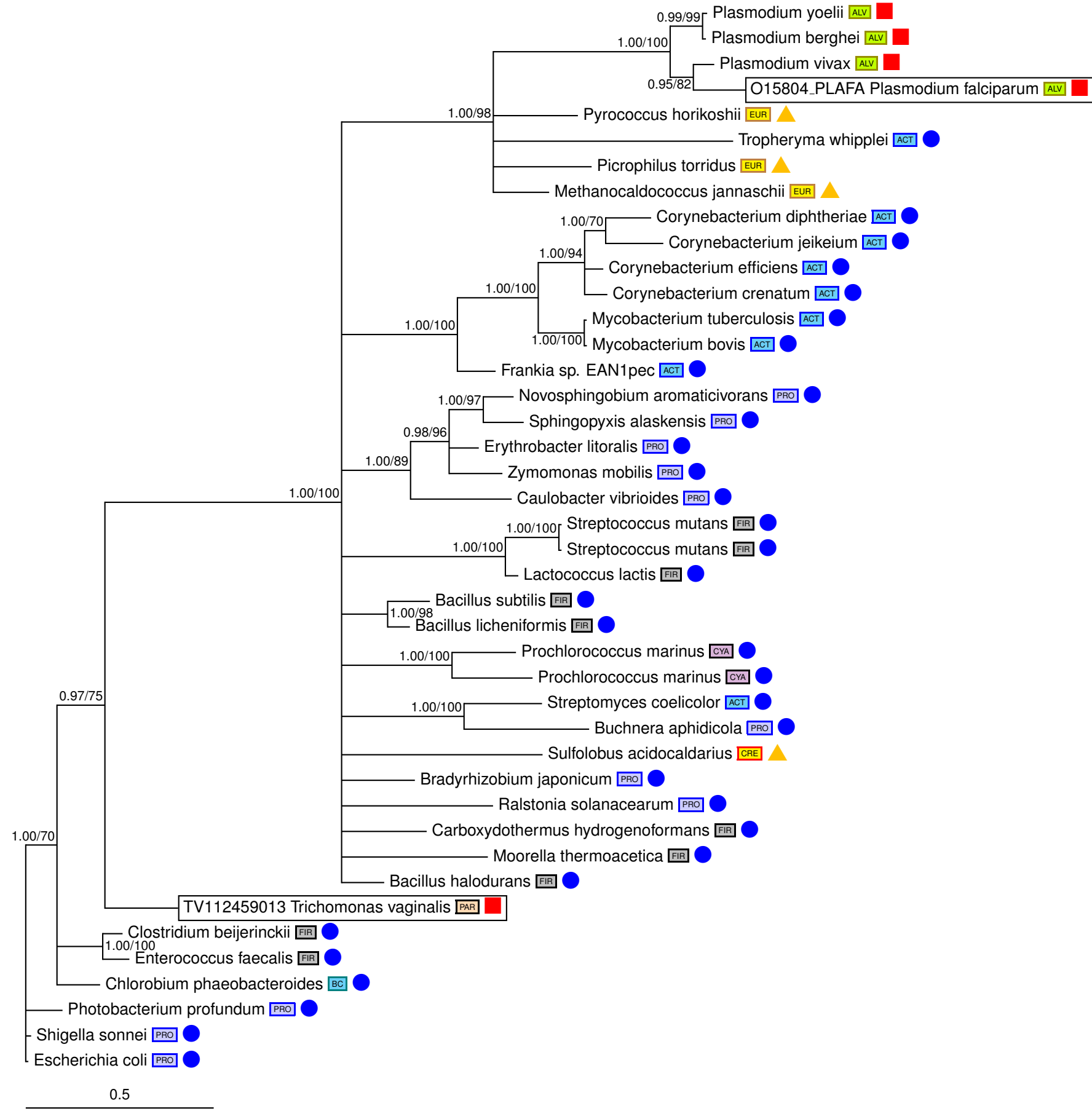
Candy accession: TV96353085
RefSeq accession: XP_001307242.1
Uniprot accession: A2FL96_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Chlorobium
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing cysteine synthase domain
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



TN175

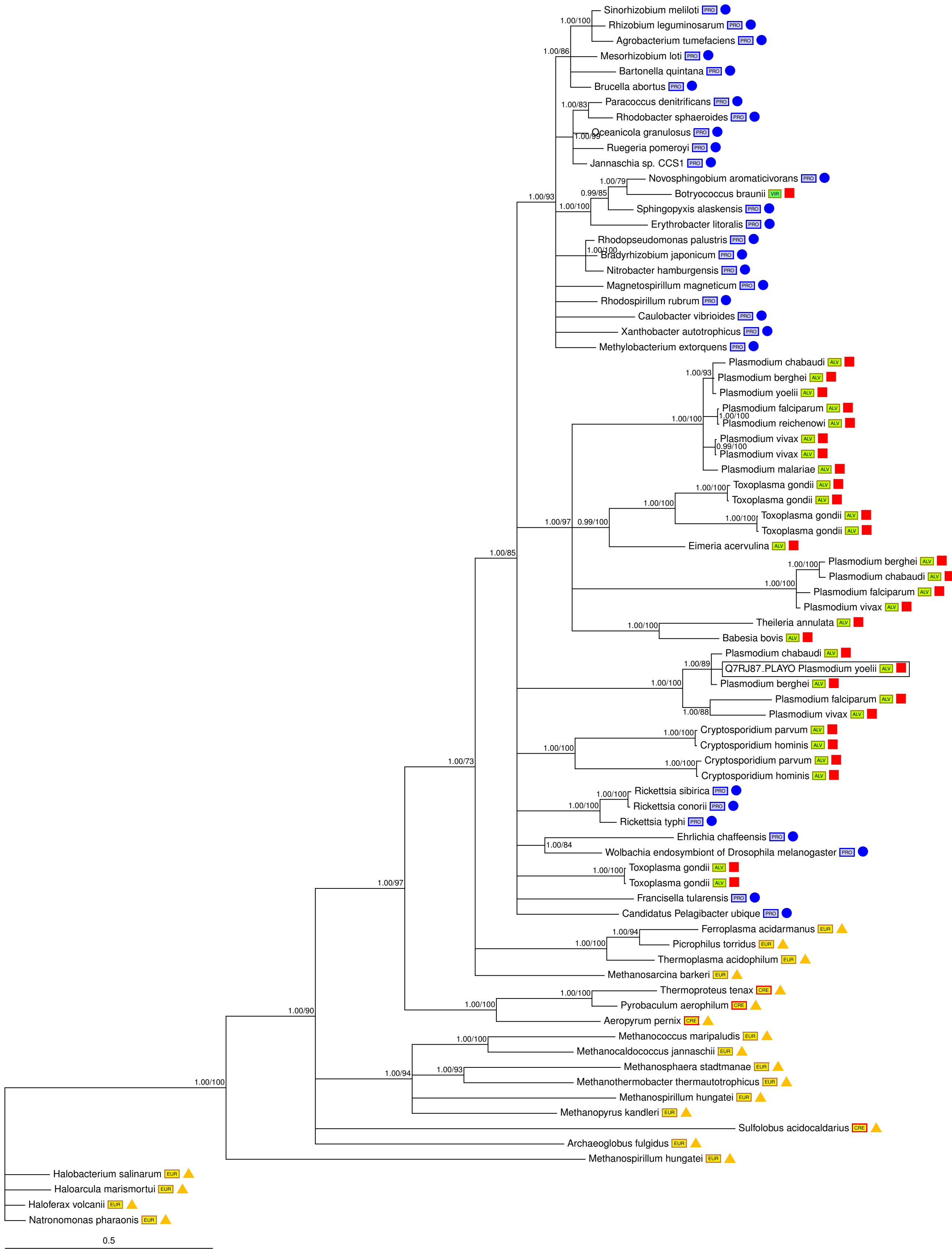
Candy accession: O15804_PLAFA
RefSeq accession: XP_001350162.1
Uniprot accession: O15804_PLAFA
Comments: LGT - PLASMODIUM
Species affected: PF,PV,PY
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:2.1.3.3
PHOBIUS SP: 0
PHOBIUS TMD: 1
RefSeq annotation: aspartate carbamoyltransferase
Name of enzyme/protein: ornithine carbamoyltransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism

Candy accession: TV112459013
RefSeq accession: XP_001298740.1
Uniprot accession: A2GAK6_TRIVA
Comments: LGT - TV
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.1.3.3
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Aspartate/ornithine carbamoyltransferase, carbamoyl-P binding domain containing protein
Name of enzyme/protein: ornithine carbamoyltransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism



TN176

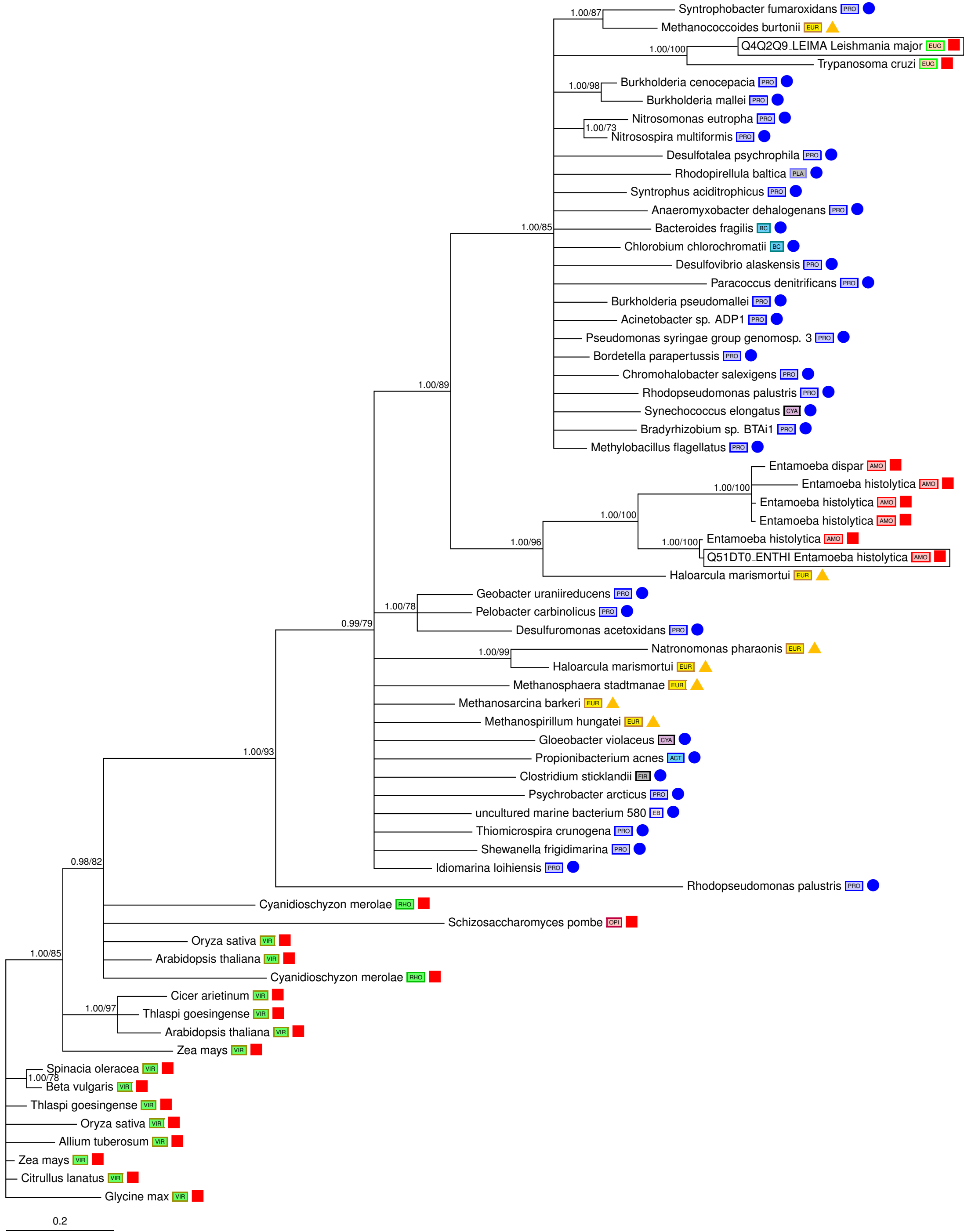
Candy accession: Q7RJ87_PLAYO
RefSeq accession: XP_731378.1
Uniprot accession: Q7RJ87_PLAYO
Comments: LGT - DEAP APICOMPLEXA LGT+DUPLICATIONS
+ A GREEN ALGAE
Species affected: PF, PV,PY,TG,CP
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:1.1.1.37
PHOBIUS SP: 0
PHOBIUS TMD: 1
RefSeq annotation: malate dehydrogenase
Name of enzyme/protein: malate dehydrogenase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Citrate cycle (TCA cycle), Pyruvate metabolism, Glyoxylate and dicarboxylate metabolism



TN177

Candy accession: Q4Q2Q9_LEIMA
RefSeq accession: XP_001686389.1
Uniprot accession: Q4Q2Q9_LEIMA
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM,TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.3.1.30
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: serine acetyltransferase
Name of enzyme/protein: Serine O-acetyltransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Energy Metabolism
KEGG PATHWAY - level 2: Cysteine and methionine metabolism, Sulfur metabolism

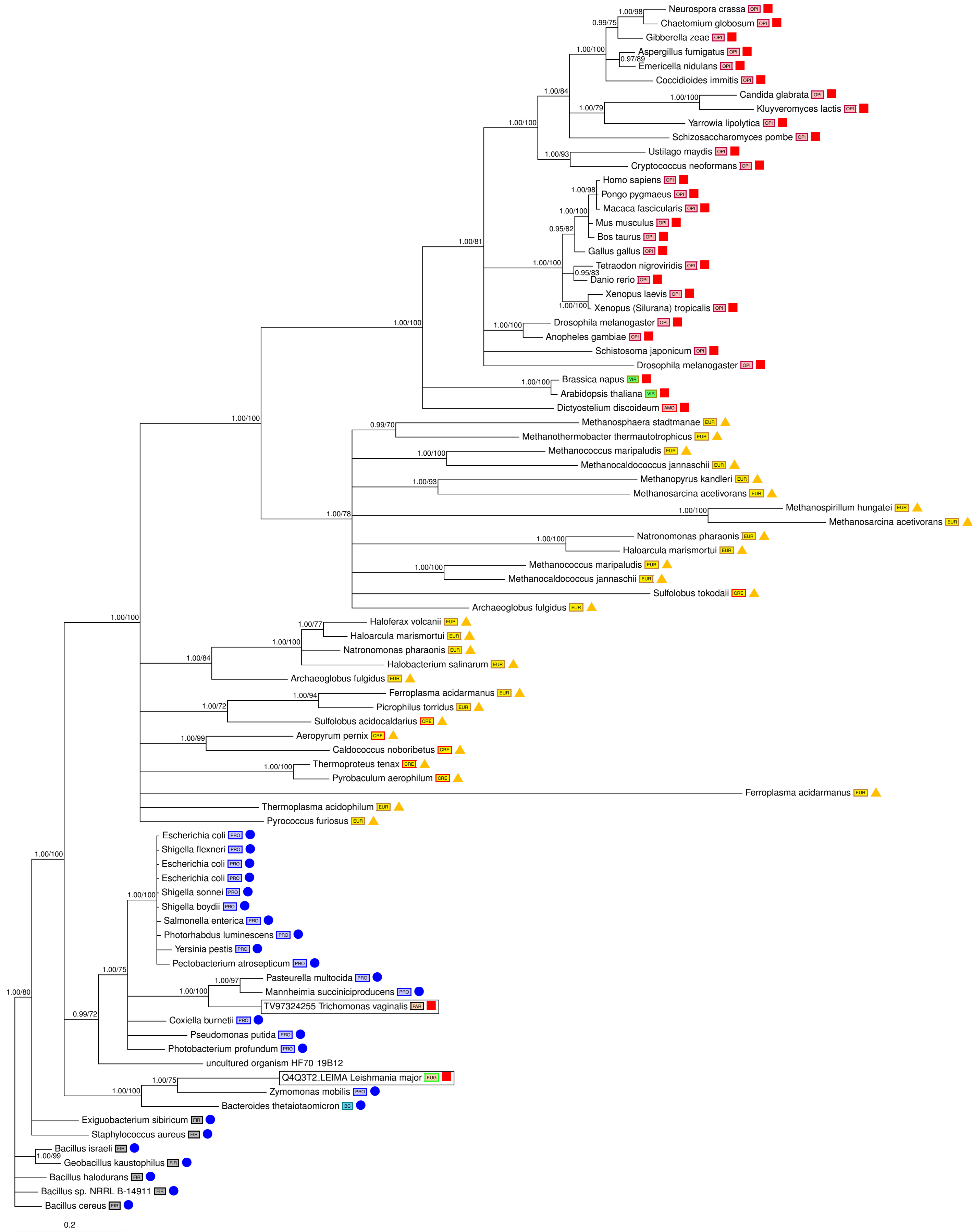
Candy accession: Q51DT0_ENTHI
RefSeq accession: XP_656373.1
Uniprot accession: Q401L4_ENTHI
Comments: LGT - EH,ED TWO NODES
Species affected: EH,ED
Adjacent taxa in tree: Archaea - Haloarcula
EC annotation - (Blast/Profile): EC:2.3.1.30
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: serine acetyltransferase 1
Name of enzyme/protein: Serine O-acetyltransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Energy Metabolism
KEGG PATHWAY - level 2: Cysteine and methionine metabolism, Sulfur metabolism



TN178

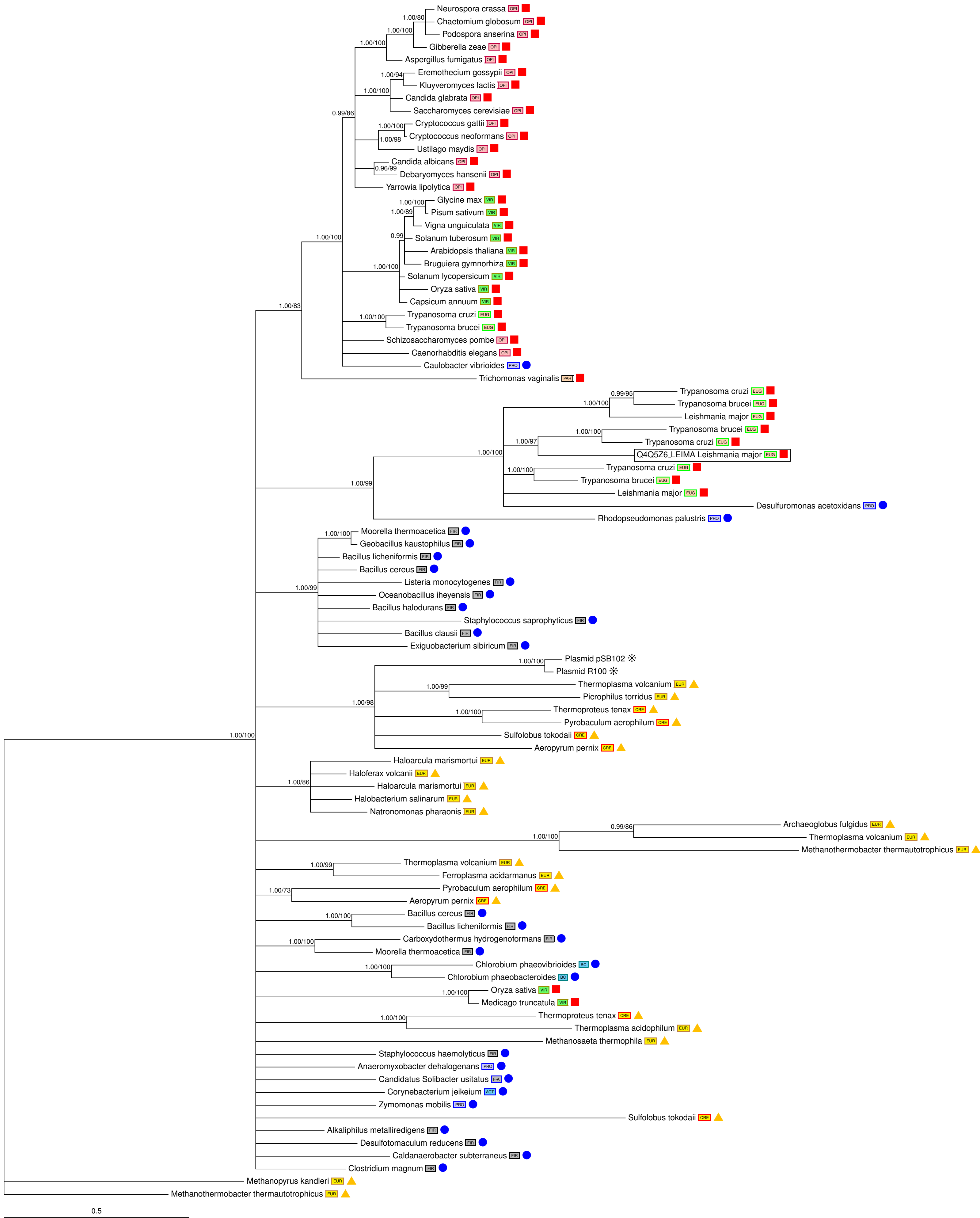
Candy accession: TV97324255
RefSeq accession: XP_001329597.1
Uniprot accession: A2DQ35_TRIVA
Comments: LGT - TV TWO NODES - 3 DOMAIN ToL
Species affected: TV
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:1.1.1.42
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: isocitrate dehydrogenase
Name of enzyme/protein: Isocitrate dehydrogenase [NADP]
KEGG PATHWAY - level 1: Carbohydrate Metabolism, Amino Acid metabolism
KEGG PATHWAY - level 2: Citrate cycle (TCA cycle), Glutathione metabolism

Candy accession: Q4Q3T2_LEIMA
RefSeq accession: XP_001686016.1
Uniprot accession: Q4Q3T2_LEIMA
Comments: LGT - TV TWO NODES - 3 DOMAIN ToL
Species affected: LM
Adjacent taxa in tree: Proteobacteria - Zymomonas
EC annotation - (Blast/Profile): EC:1.1.1.42
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: isocitrate dehydrogenase
Name of enzyme/protein: Isocitrate dehydrogenase [NADP]
KEGG PATHWAY - level 1: Carbohydrate Metabolism, Amino Acid metabolism
KEGG PATHWAY - level 2: Citrate cycle (TCA cycle), Glutathione metabolism



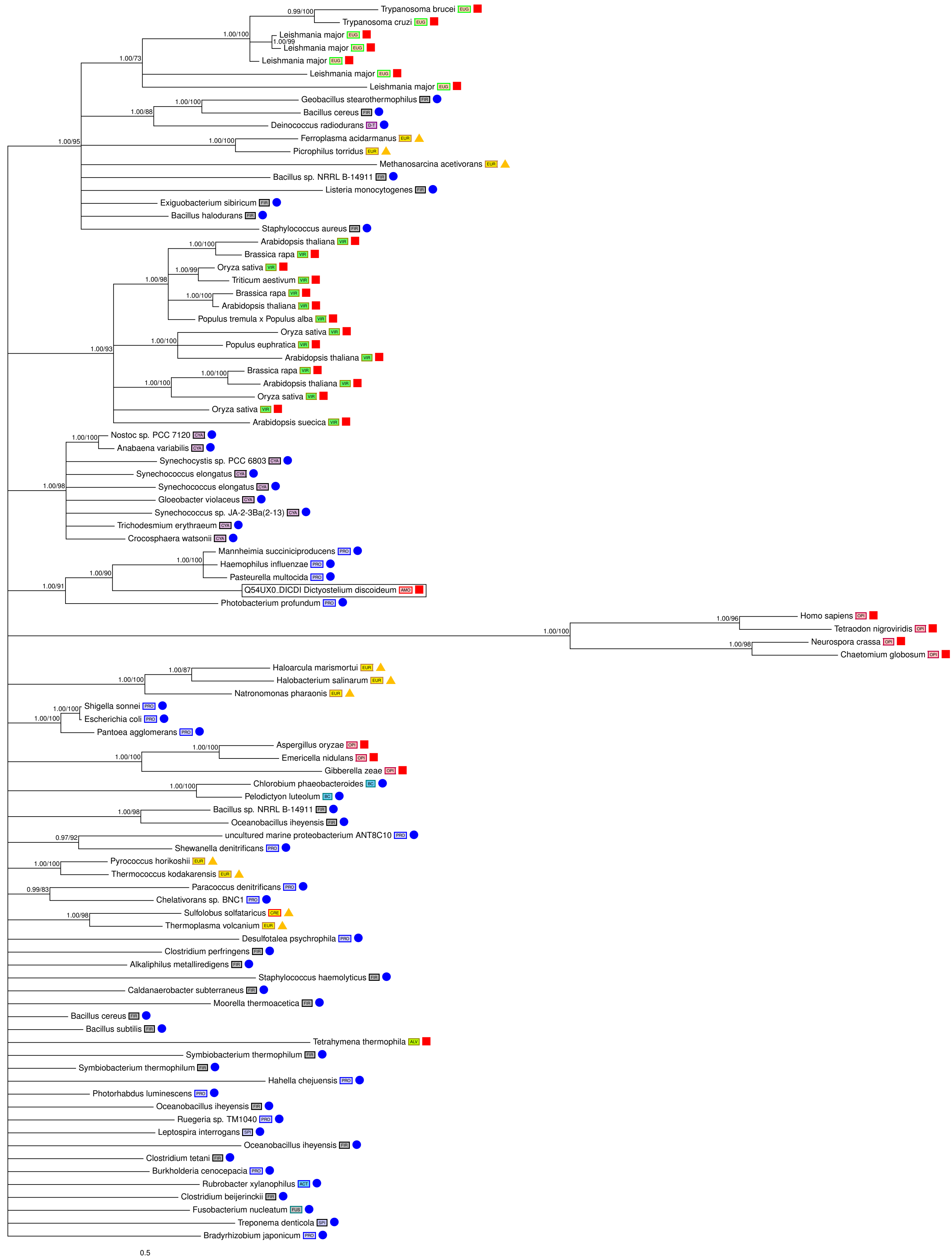
TN179

Candy accession: Q4Q5Z6_LEIMA
RefSeq accession: XP_001685252.1
Uniprot accession: Q4Q5Z6_LEIMA
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM,TB,TC
Adjacent taxa in tree: Proteobacteria - Desulfuromonas
EC annotation - (Blast/Profile): EC:1.8.1.4
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: acetoin dehydrogenase e3 component-like protein
Name of enzyme/protein: dihydrolipoyl dehydrogenase
KEGG PATHWAY - level 1: Carbohydrate Metabolism, Amino Acid metabolism
KEGG PATHWAY - level 2: Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Pyruvate metabolism, Glycine, serine and threonine metabolism, Valine, leucine and isoleucine degradation

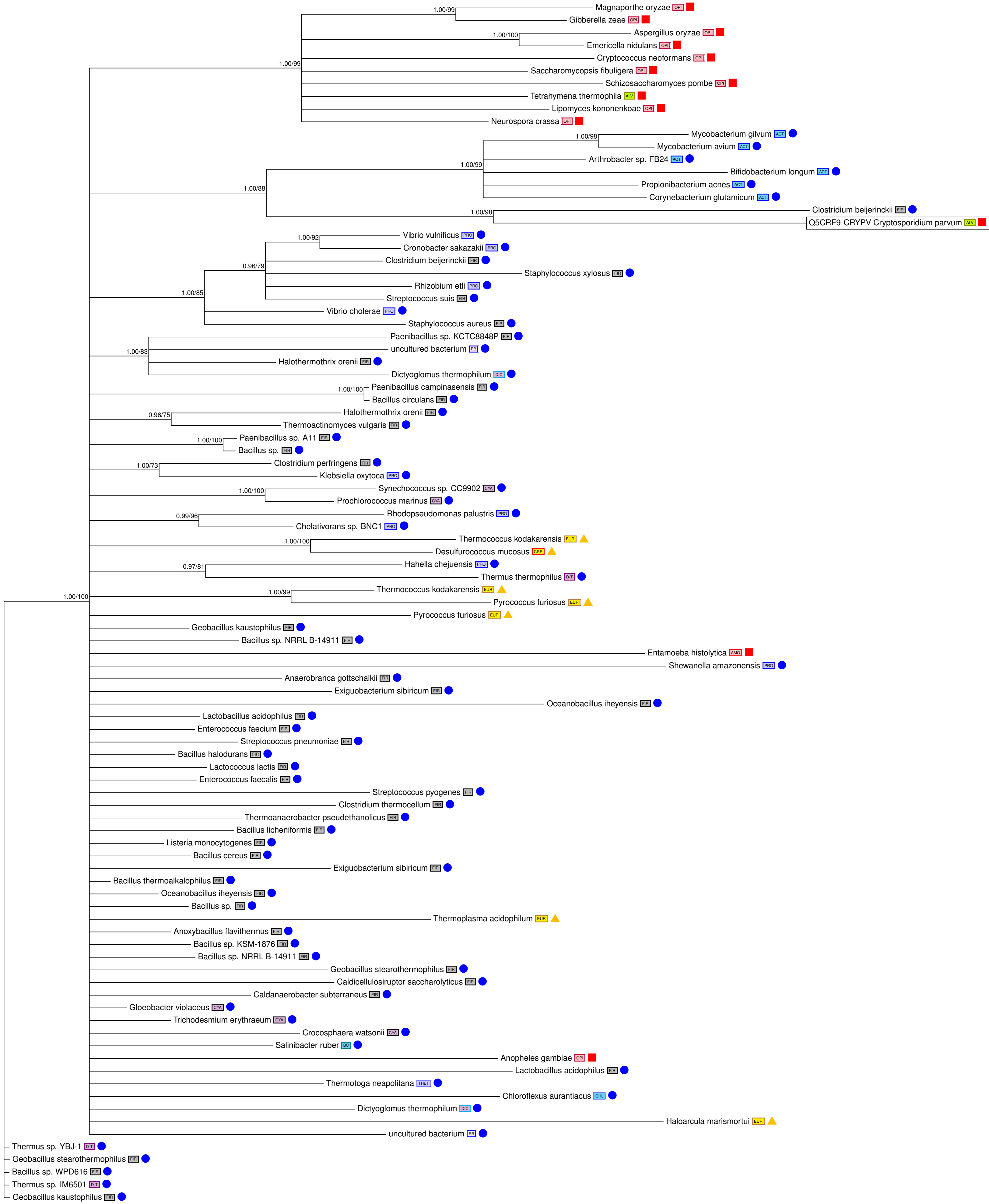


TN180

Candy accession: Q54UX0_DICDI
RefSeq accession: XP_641017.1
Uniprot accession: Q54UX0_DICDI
Comments: LGT - DD TWO NODES
Species affected: DD
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:3.5.1.14
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0280767
Name of enzyme/protein: aminooacylase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism



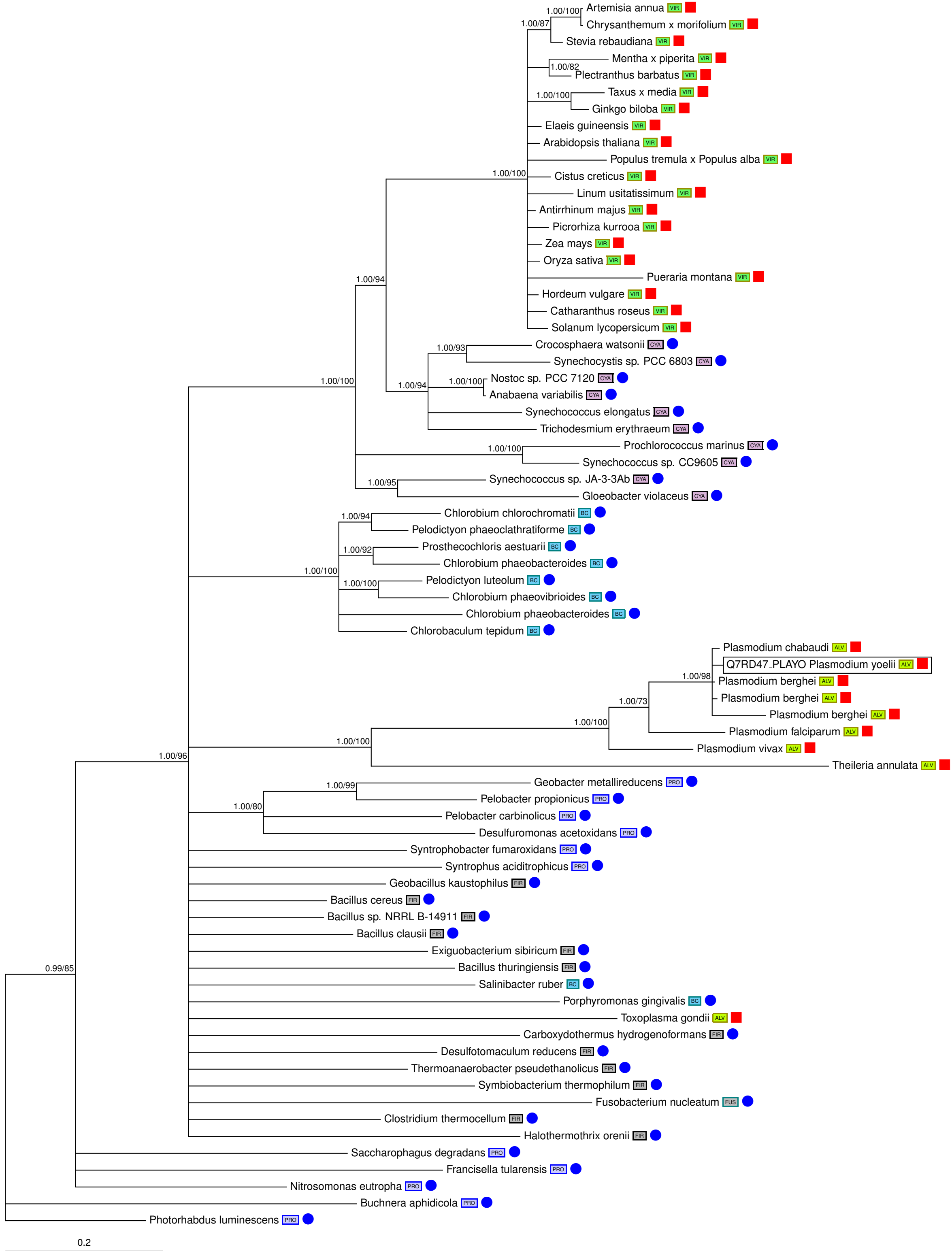
Candy accession: Q5CRF9 CRYPV
RefSeq accession: XP_652044.1
Uniprot accession: Q5CRF9 CRYPV
Comments: LGT - CP TWO NODES
Species affected: CP
Adjacent taxa in tree: Firmicutes - Clostridia
EC annotation - (Blast/Profile): EC:3.2.1.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: alpha-amylase family protein
Name of enzyme/protein: Alpha-amylase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Starch and sucrose metabolism



0.2

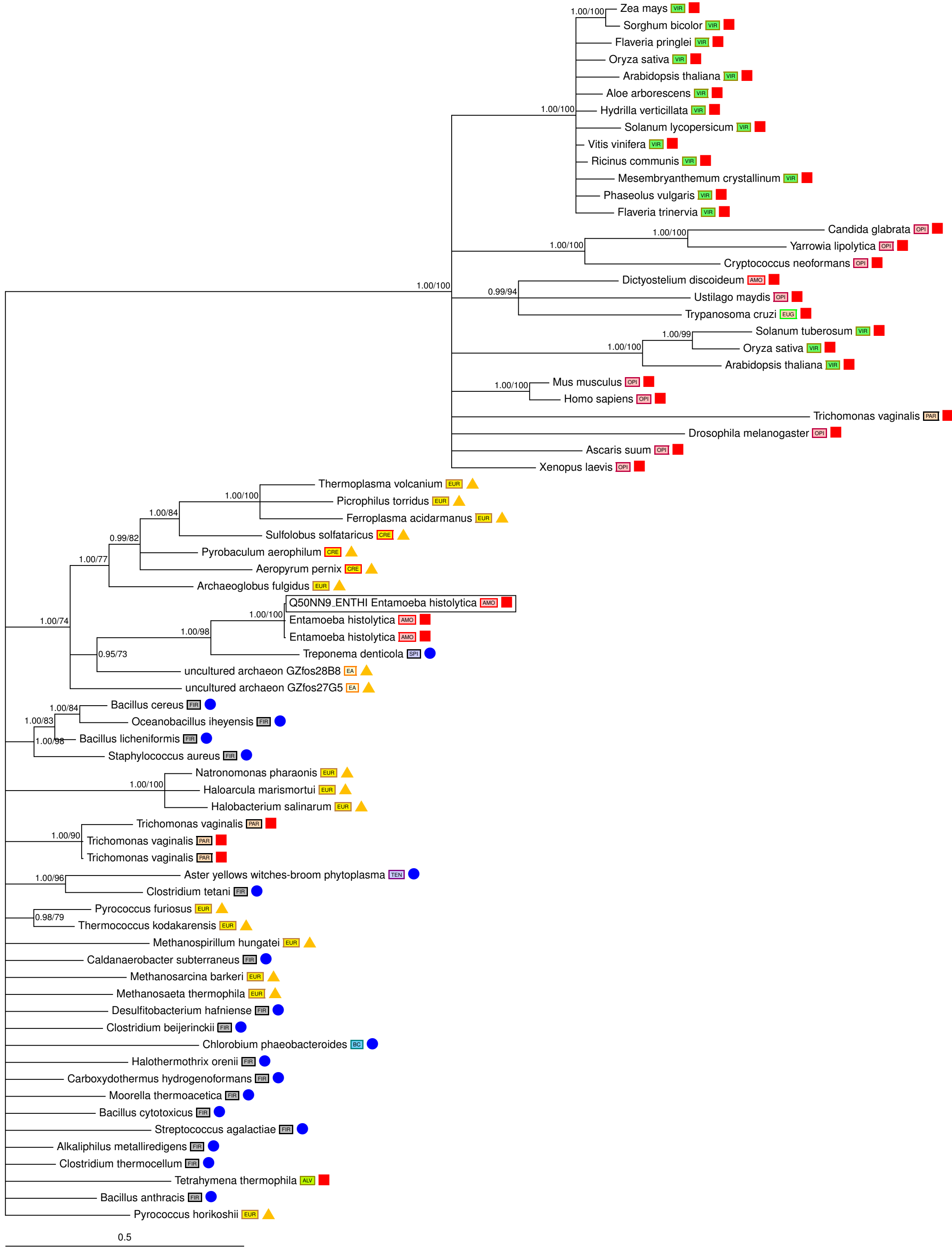
TN182

Candy accession: Q7RD47_PLAYO
RefSeq accession: XP_726051.1
Uniprot accession: Q7RD47_PLAYO
Comments: LGT - APICOMPLEXA TWO NODES
(+CYANOBACTERIA EGT INTO PLANTS)
Species affected: PF,PV,PY,PB,PC,TA,TG
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:1.1.1.267
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: 1-deoxy-D-xylulose 5-phosphate reductoisomerase
Name of enzyme/protein: 1-deoxy-D-xylulose 5-phosphate reductoisomerase
KEGG PATHWAY - level 1: Metabolism of Terpenoids and Polyketides
KEGG PATHWAY - level 2: Terpenoid backbone biosynthesis



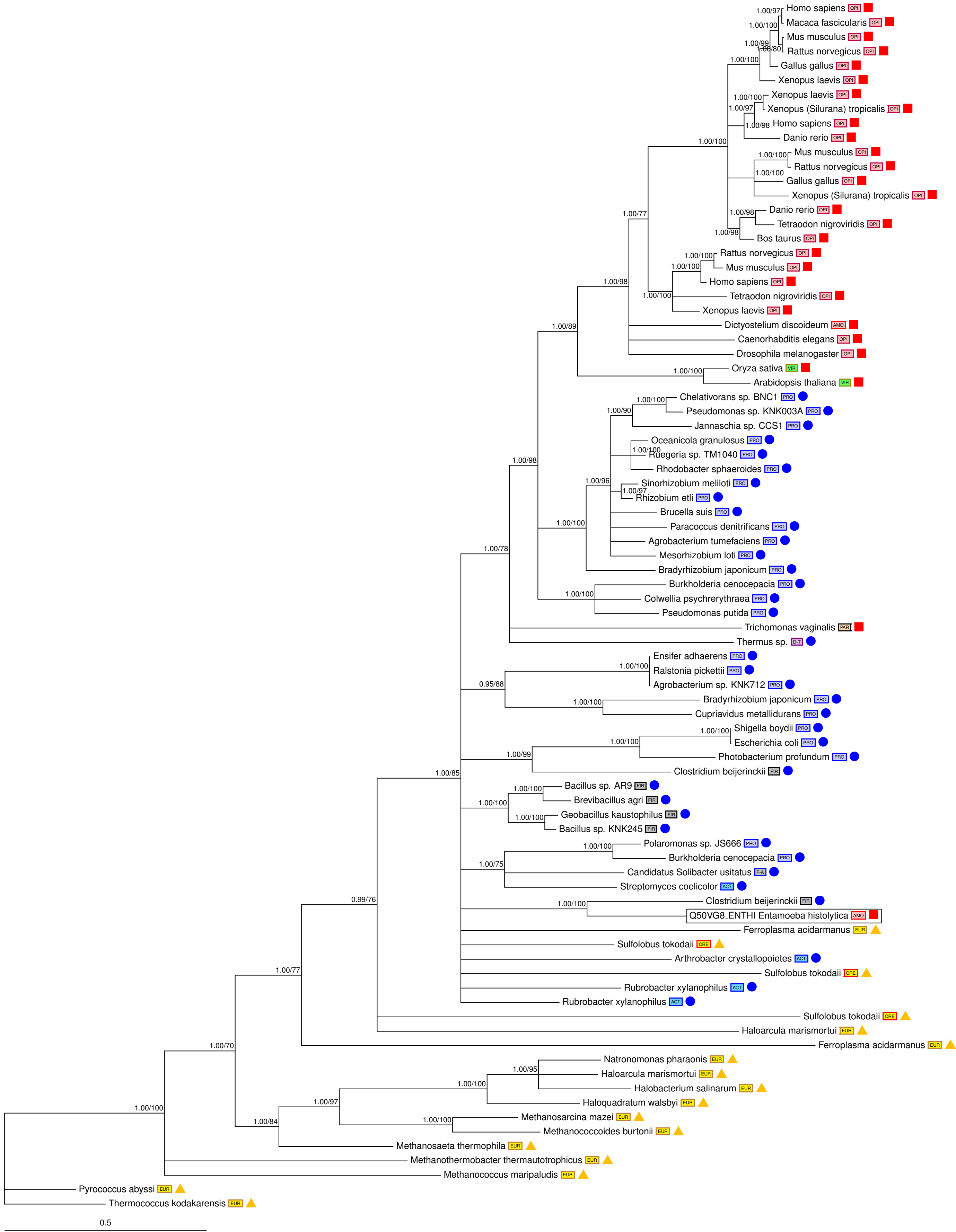
TN183

Candy accession: Q50NN9_ENTHI
RefSeq accession: XP_648590.1
Uniprot accession: Q9NH04_ENTHI
Comments: LGT - EH TWO NODES
Species affected: EH
Adjacent taxa in tree: Spirochaetes - Treponema
EC annotation - (Blast/Profile): EC:1.1.1.38
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: malic enzyme
Name of enzyme/protein: malate dehydrogenase (oxaloacetate-decarboxylating)
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pyruvate metabolism



TN184

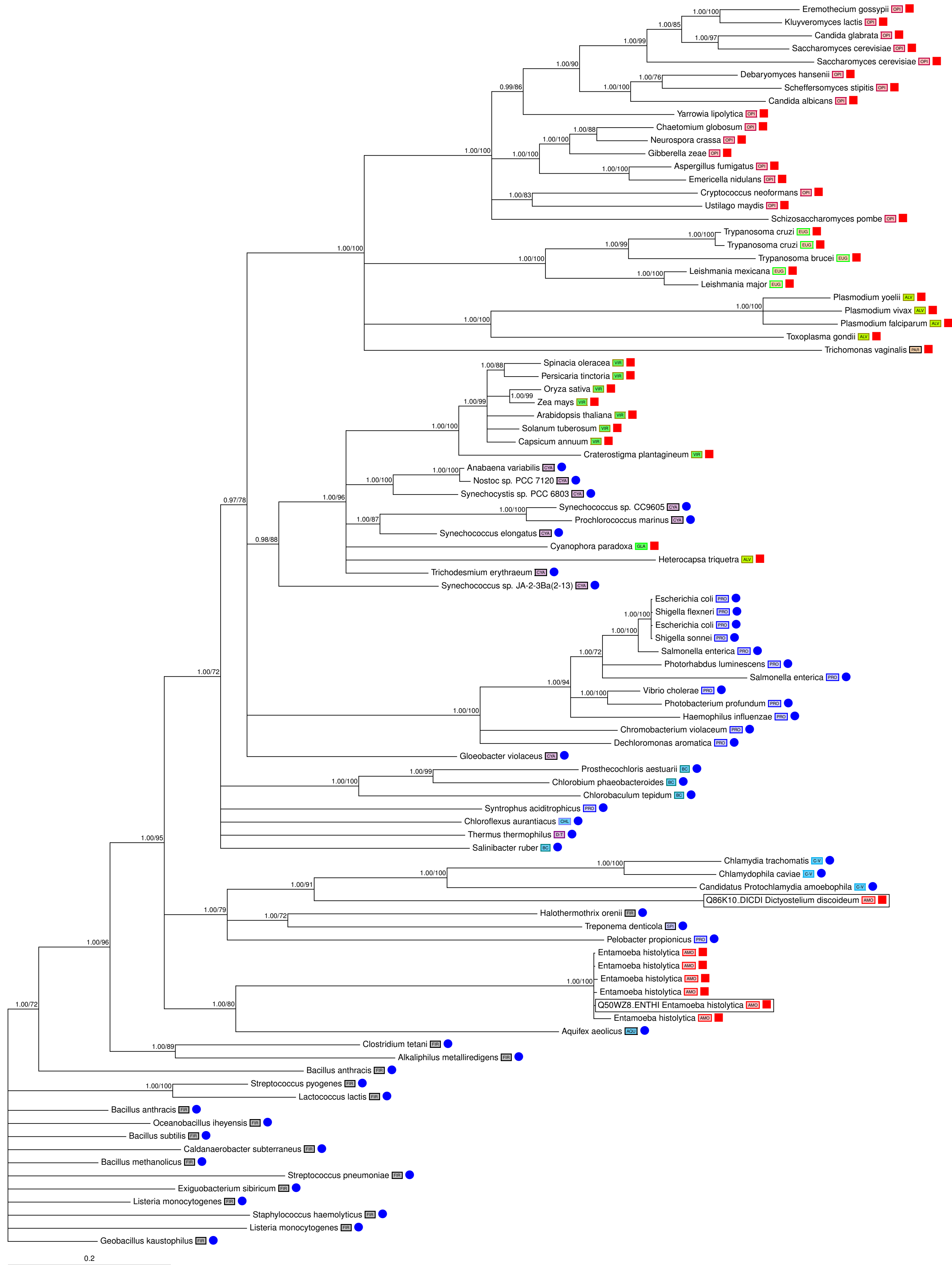
Candy accession: Q50VG8_ENTHI
RefSeq accession: XP_650972.1
Uniprot accession: C4M0I4_ENTHI
Comments: LGT - EH TWO NODES
Species affected: EH
Adjacent taxa in tree: Firmicutes - Clostridia
EC annotation - (Blast/Profile): EC:3.5.2.3
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: D-hydantoinase
Name of enzyme/protein: dihydroorotase
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Pyrimidine metabolism



TN185

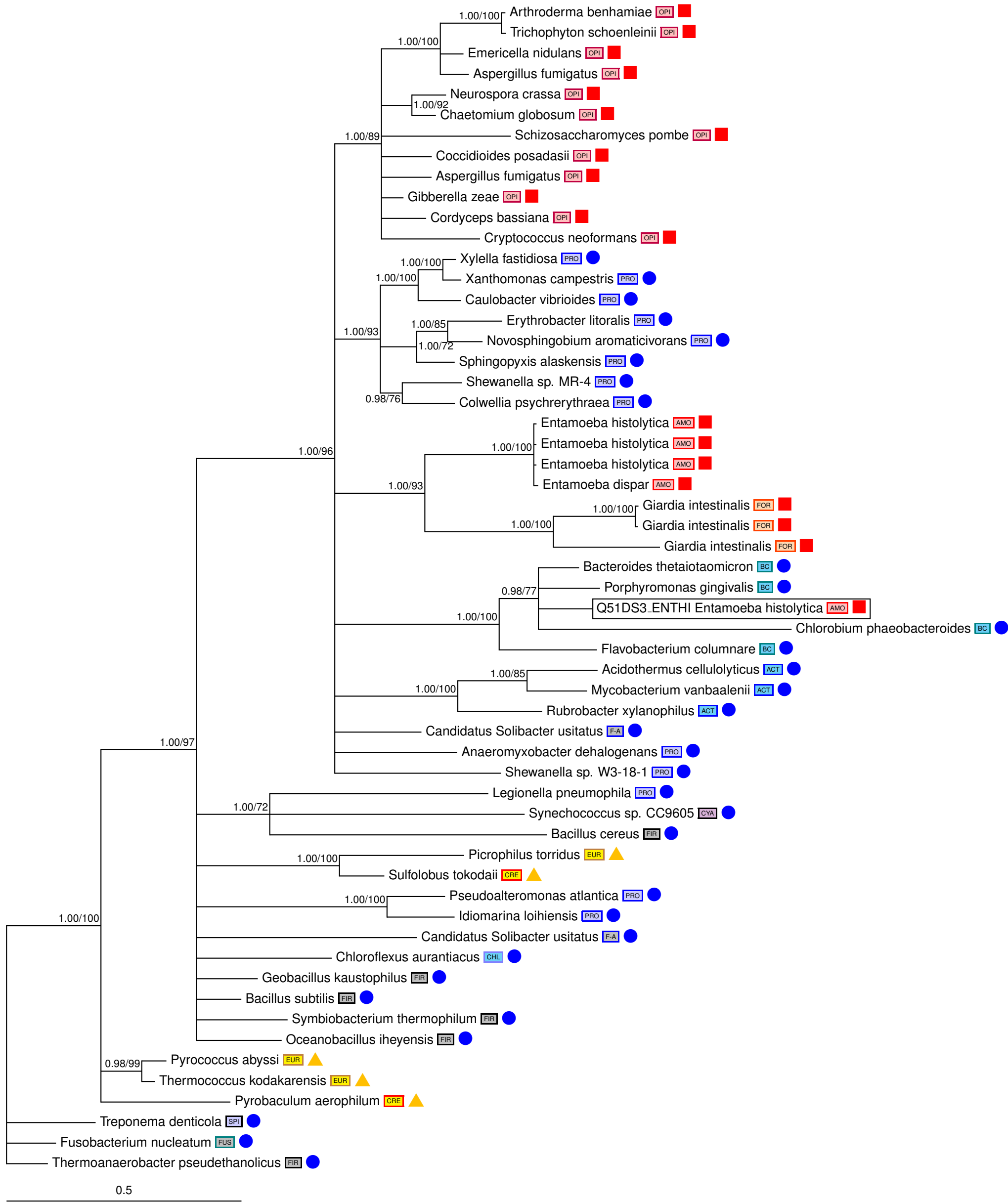
Candy accession: Q86K10.DICDI
RefSeq accession: XP_645046.1
Uniprot accession: TKT_DICDI
Comments: LGT - DD TWO NODES
Species affected: DD
Adjacent taxa in tree: Chlamydiae/Verrucomicrobia
EC annotation - (Blast/Profile): EC:2.2.1.1
PHOBius SP: 0
PHOBius TMD: 0
RefSeq annotation: hypothetical protein DDB_G0272618
Name of enzyme/protein: Transketolase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pentose phosphate pathway

Candy accession: Q50WZ8_ENTHI
RefSeq accession: XP_650850.1
Uniprot accession: Q50WZ8_ENTHI
Comments: LGT - EH TWO NODES
Species affected: EH
Adjacent taxa in tree: Aquificae - Aquifex
EC annotation - (Blast/Profile): EC:2.2.1.1
PHOBUS SP: 0
PHOBUS TMD: 0
RefSeq annotation: transketolase
Name of enzyme/protein: Transketolase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pentose phosphate pathway



TN186

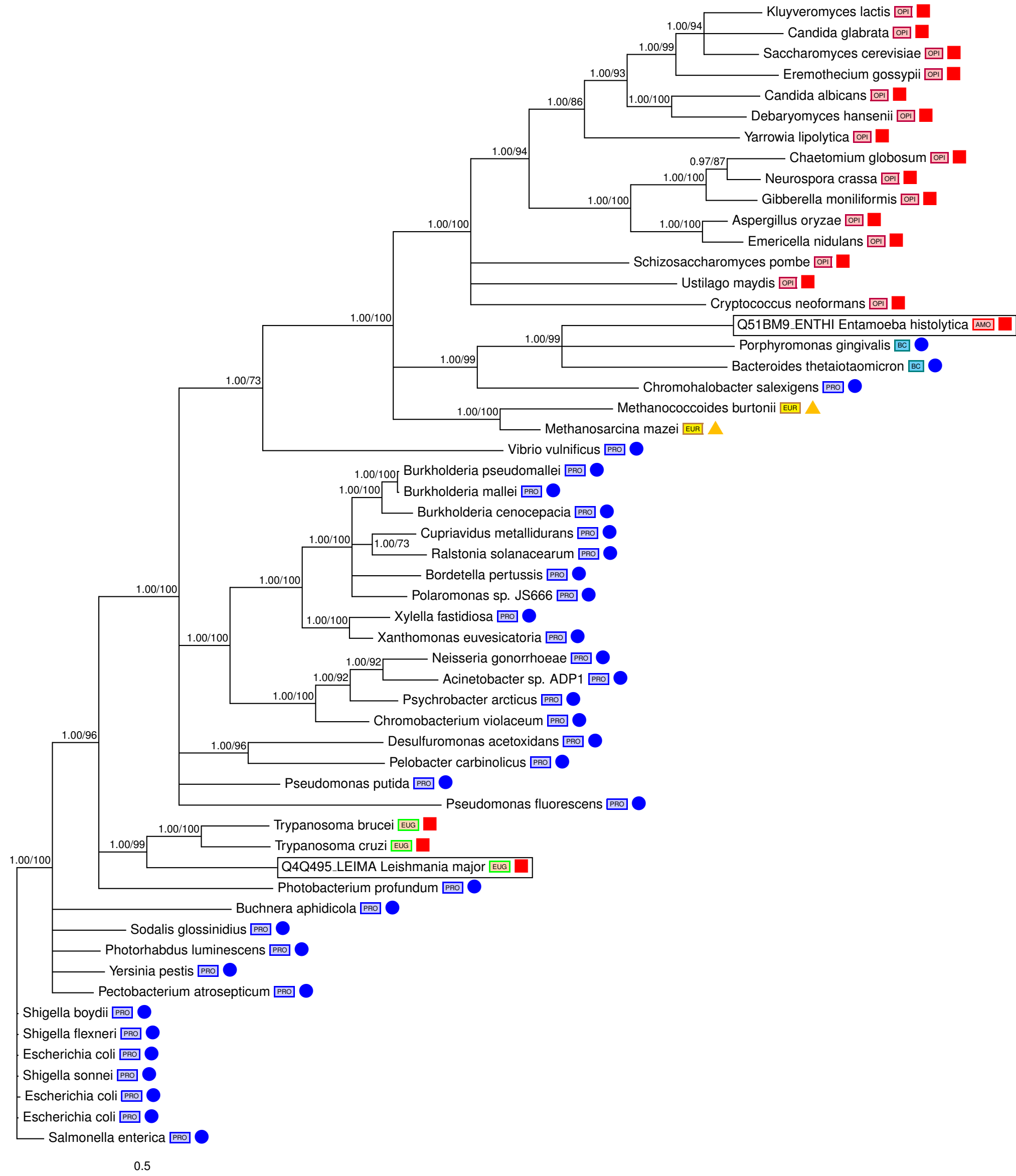
Candy accession: Q51DS3_ENTHI
RefSeq accession: XP_656380.2
Uniprot accession: C4LSC6_ENTHI
Comments: LGT - EH TWO NODES
Species affected: EH
Adjacent taxa in tree: Bacteroidetes/Chlorobi
EC annotation - (Blast/Profile): EC:3.4.19.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: prolyl oligopeptidase family protein
Name of enzyme/protein: acylaminoacyl-peptidase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



TN187

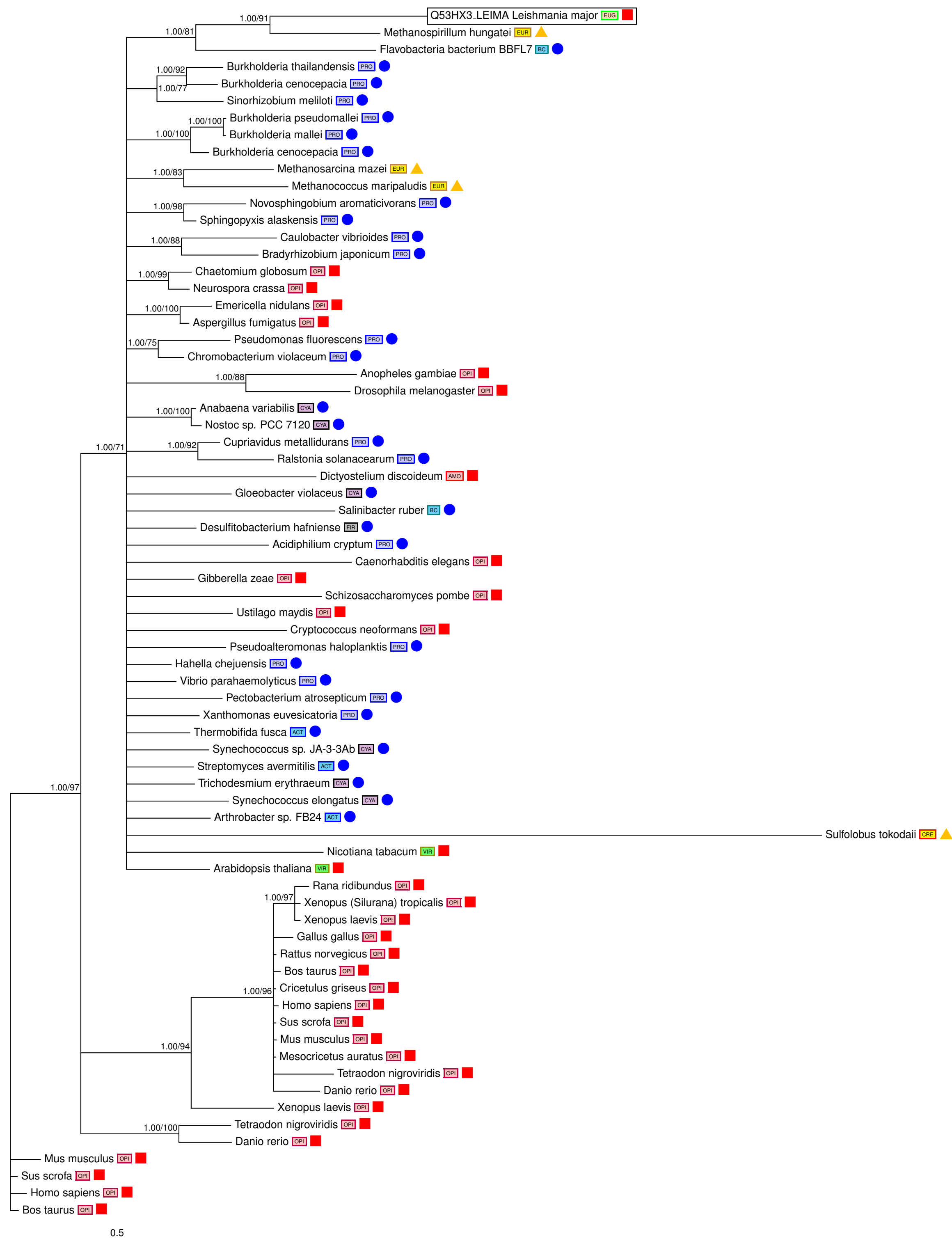
Candy accession: Q4Q495_LEIMA
RefSeq accession: XP_001685853.1
Uniprot accession: Q4Q495_LEIMA
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM, TB,TC
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:2.4.2.11
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: nicotinate phosphoribosyltransferase
Name of enzyme/protein: Nicotinate phosphoribosyltransferase
KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Nicotinate and nicotinamide metabolism

Candy accession: Q51BM9_ENTHI
RefSeq accession: XP_655646.1
Uniprot accession: C4LUN7_ENTHI
Comments: LGT - EH TWO NODES
Species affected: EH
Adjacent taxa in tree: Bacteroidetes/Chlorobi
EC annotation - (Blast/Profile): EC:2.4.2.11
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: nicotinate phosphoribosyltransferase
Name of enzyme/protein: Nicotinate phosphoribosyltransferase
KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Nicotinate and nicotinamide metabolism



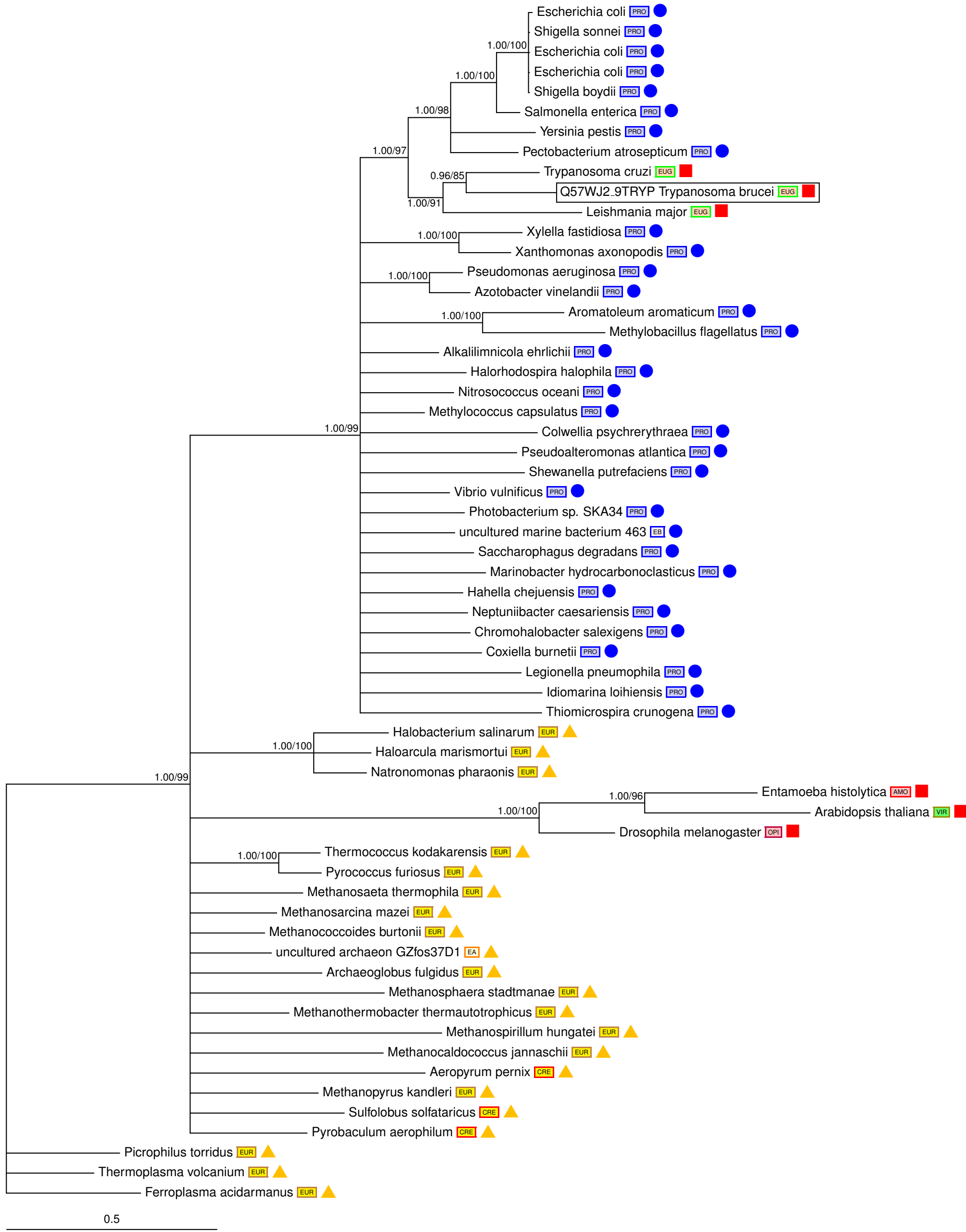
TN188

Candy accession: Q53HX3_LEIMA
RefSeq accession: XP_001686853.1
Uniprot accession: Q53HX3_LEIMA
Comments: LGT - LM TWO NODES
Species affected: LM
Adjacent taxa in tree: Archaea - Methanospirillum
EC annotation - (Blast/Profile): EC.2.3.1.57
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: acetyltransferase-like protein
Name of enzyme/protein: diamine N-acetyltransferase
KEGG PATHWAY - level 1: Amino Acid metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism



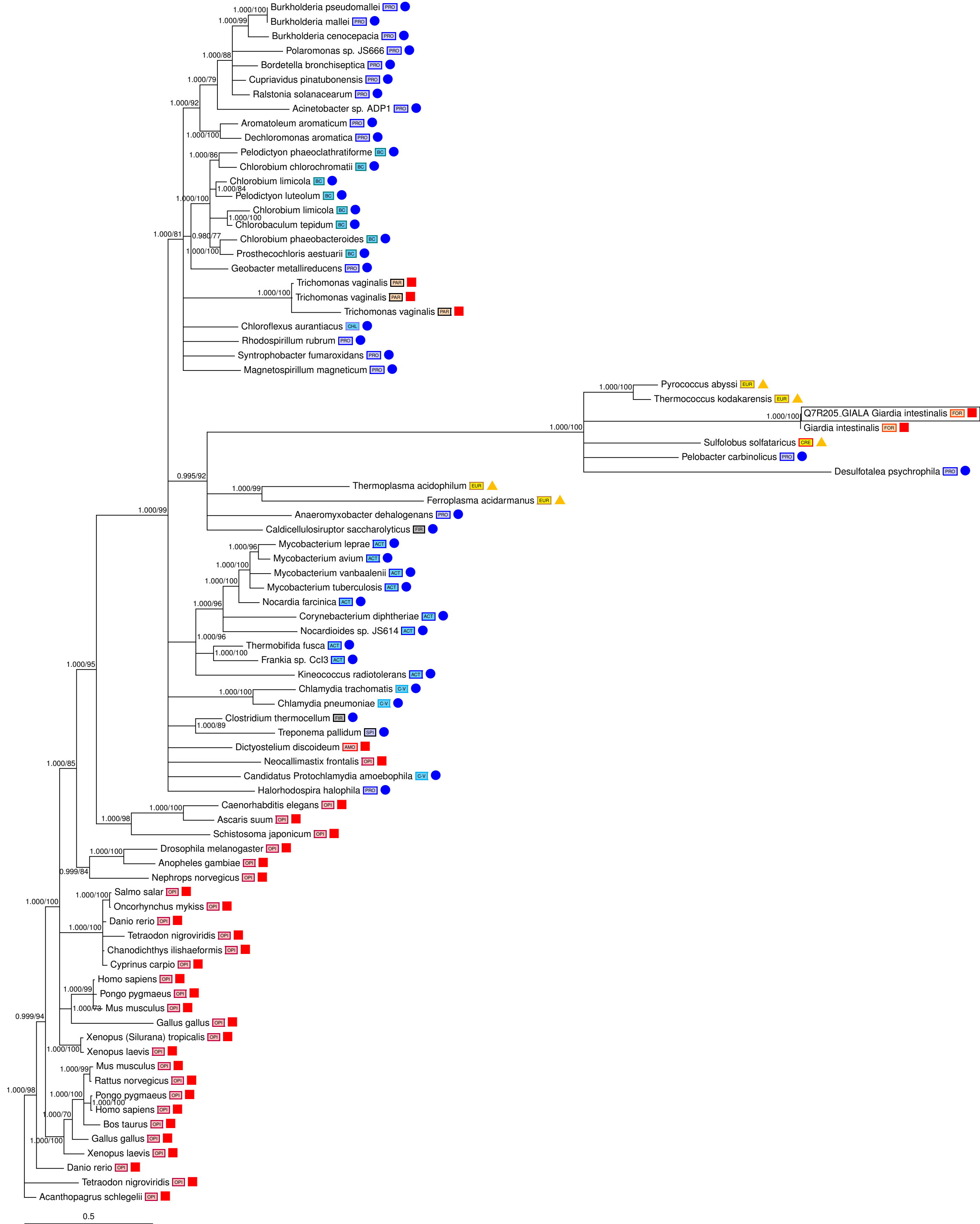
TN189

Candy accession: Q57WJ2_9TRYP
RefSeq accession: XP_846000.1
Uniprot accession: Q57WJ2_9TRYP
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM,TC,TE
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: putative carbohydrate kinase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



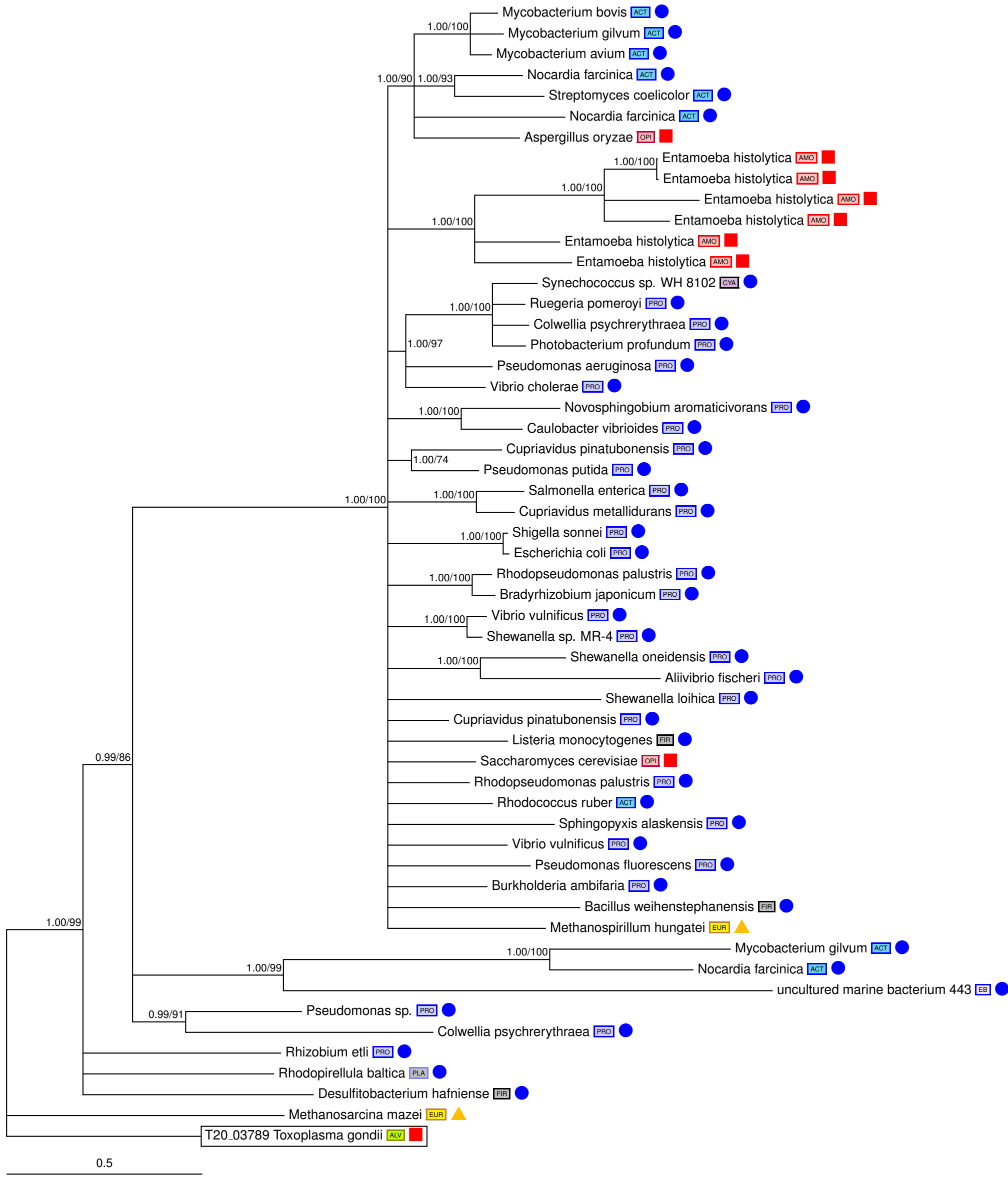
TN190

Candy accession: Q7R205_GIALA
RefSeq accession: XP_001709869.1
Uniprot accession: A8B1Z3_GIALA
Comments: LGT - GI TWO NODES
Species affected: GI
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:4.1.1.32
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Phosphoenolpyruvate carboxykinase
Name of enzyme/protein: Phosphoenolpyruvate carboxykinase (GTP)
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Pyruvate metabolism



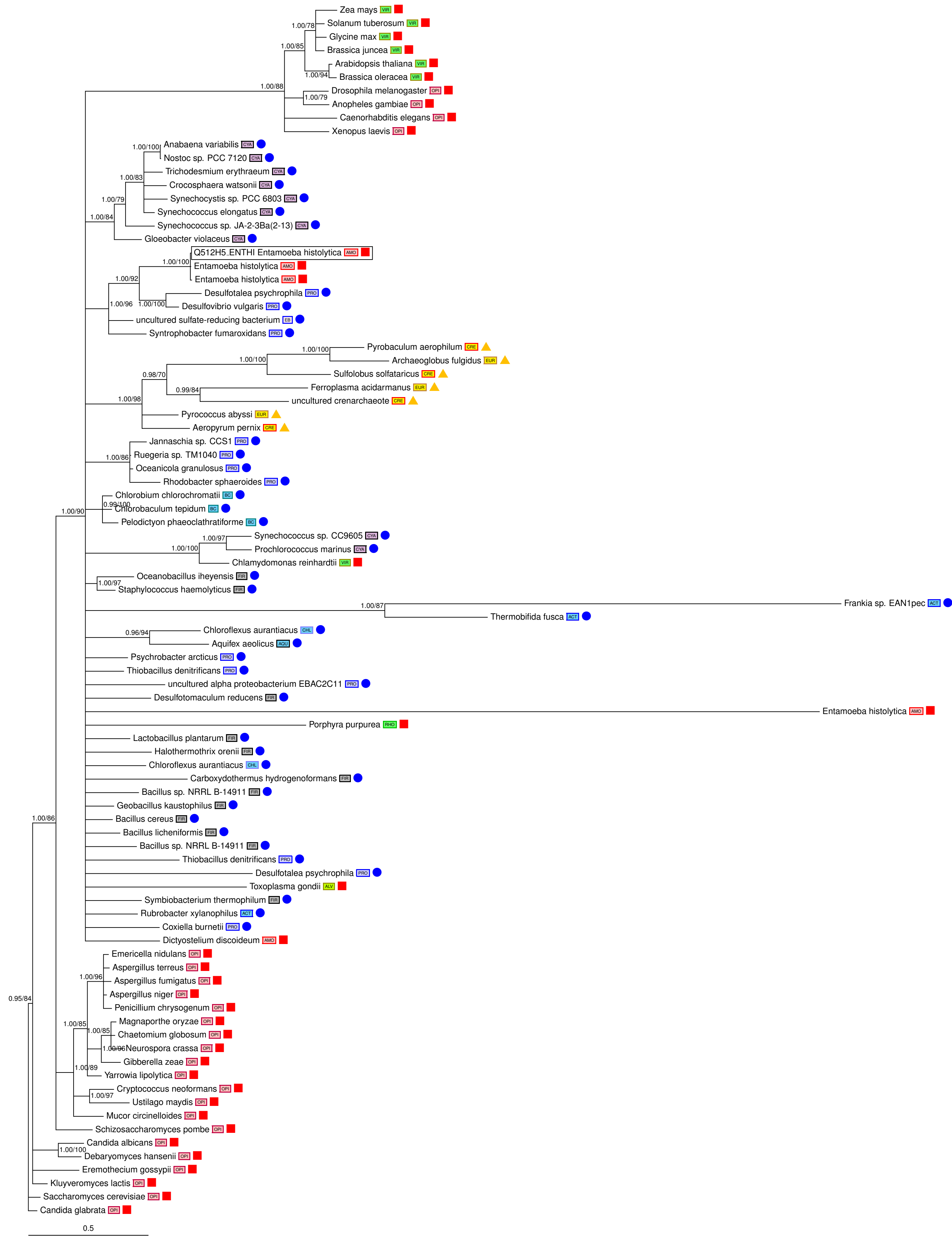
TN191

Candy accession: T20_03789
RefSeq accession: XP_002367616.1
Uniprot accession: B6KHX1_TOXGO
Comments: LGT - TG TWO NODES - ONE NODE FOR FUNGI
LGT
Species affected: TG,FUNGI
Adjacent taxa in tree: Archaea - Methanosarcina
EC annotation - (Blast/Profile): EC:3.5.2.6
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: alkyl sulfatase, putative
Name of enzyme/protein: beta-lactam hydrolase
KEGG PATHWAY - level 1: Biosynthesis of Other Secondary Metabolites
KEGG PATHWAY - level 2: Penicillin and cephalosporin biosynthesis, beta-Lactam resistance



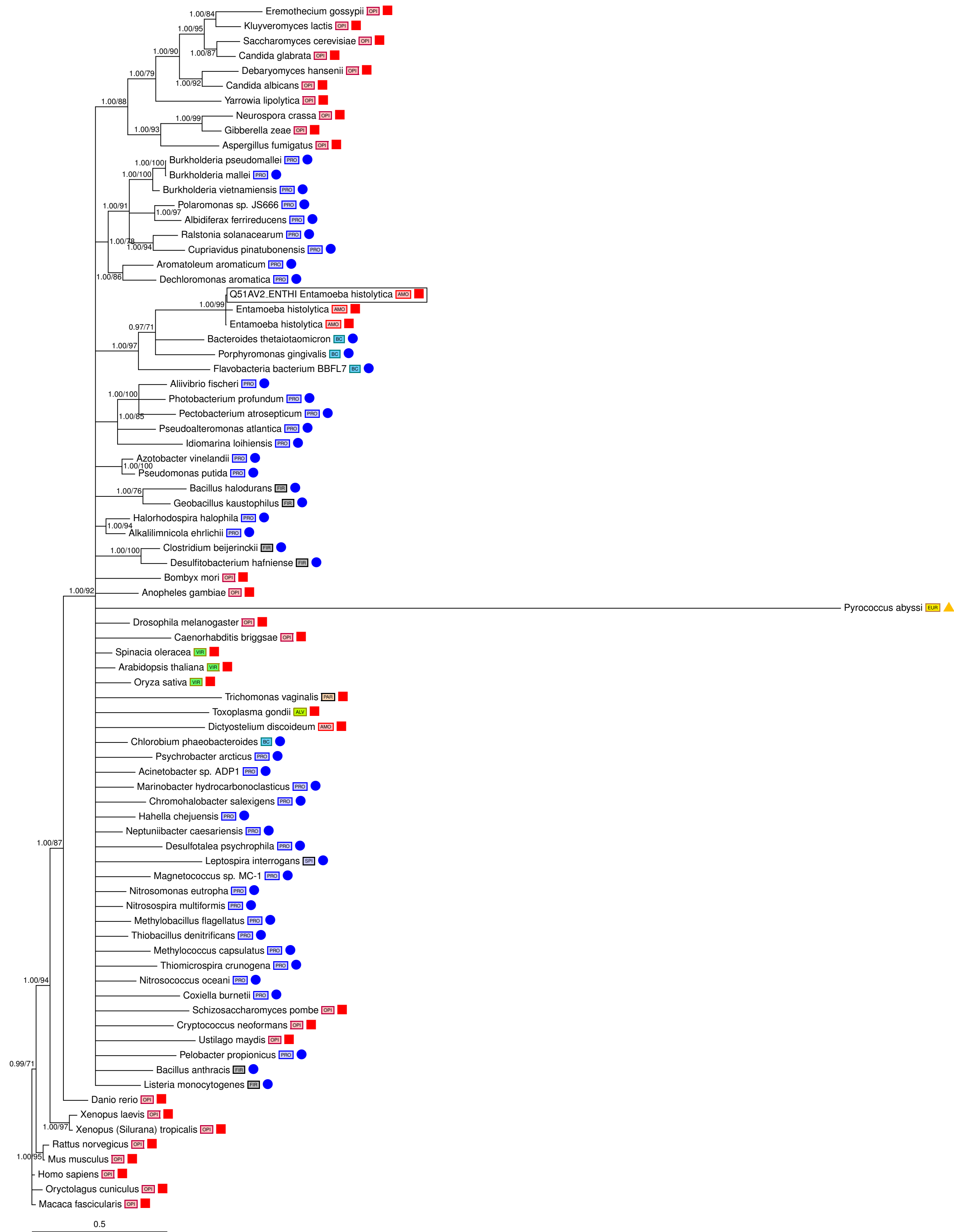
TN192

Candy accession: Q512H5 ENTHI
RefSeq accession: XP_653570.1
Uniprot accession: C4LV03.ENTHI
Comments: LGT - EH TWO NODES + LGT FROM
CYANOBACTERIA INTO CHLAMYDOMONAS - EGT?
Species affected: EH, GREEN ALGAE
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:2.7.7.4
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: sulfatase adenylyltransferase
Name of enzyme/protein: Sulfate adenylyltransferase
KEGG PATHWAY - level 1: Nucleotide Metabolism, Metabolism of
Other Amino Acids, Energy metabolism
KEGG PATHWAY - level 2: Purine metabolism, Selenocompound
metabolism, Sulfur metabolism



TN193

Candy accession: Q51AV2_ENTHI
RefSeq accession: XP_655383.1
Uniprot accession: Q60138_ENTHI
Comments: LGT - EH TWO NODES
Species affected: EH
Adjacent taxa in tree: Bacteroidetes/Chlorobi
EC annotation - (Blast/Profile): EC:2.6.1.52
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: phosphoserine aminotransferase
Name of enzyme/protein: phosphoserine transaminase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Metabolism of
Cofactors and Vitamins
KEGG PATHWAY - level 2: Glycine, serine and threonine
metabolism, Vitamin B6 metabolism



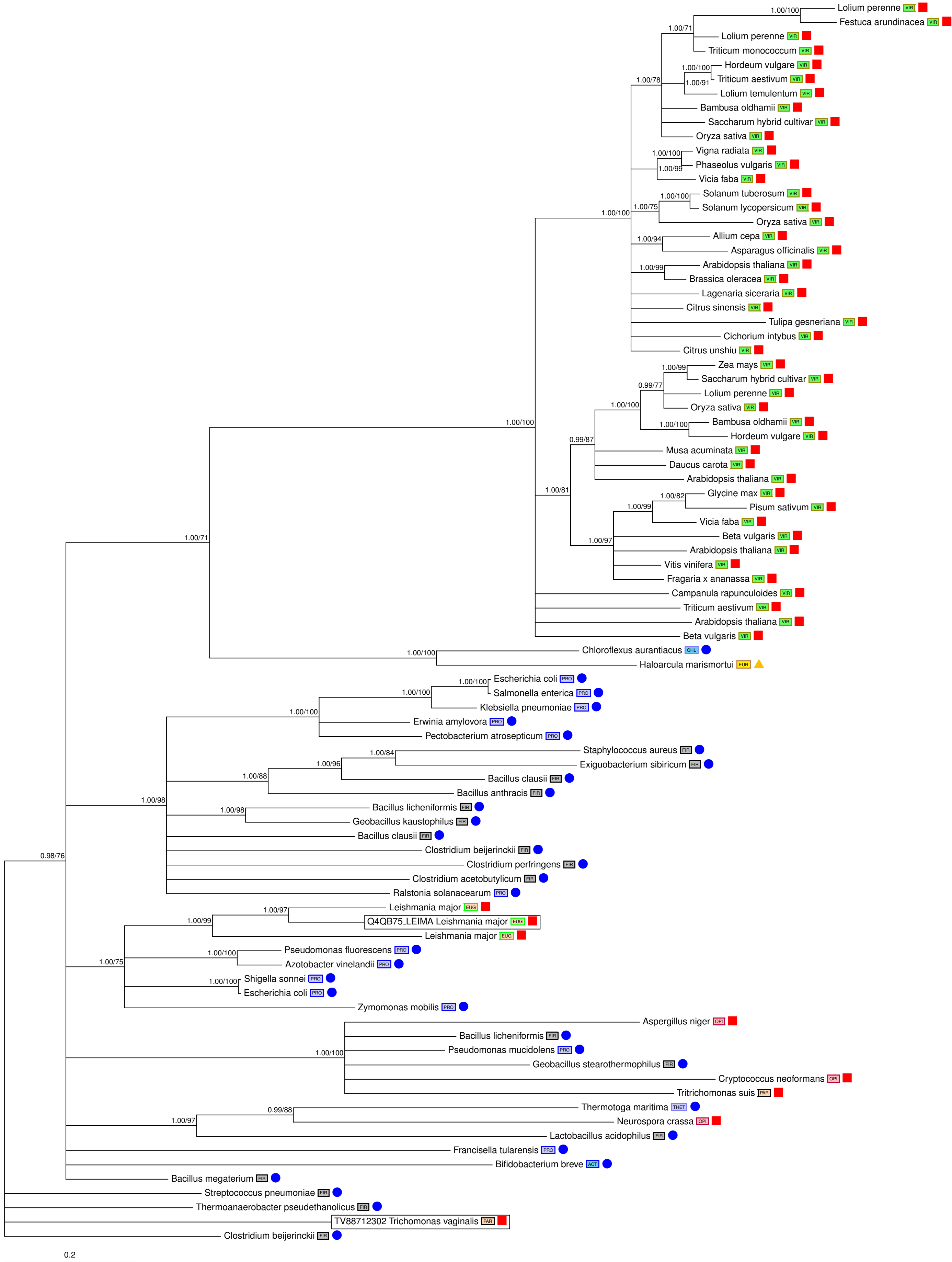
TN194

Candy accession: TV88712302
RefSeq accession: XP_001579287.1
Uniprot accession: A2DMTO_TRIVA
Comments: LGT - TV TWO NODES - LGT INTO TRITRICHOMONAS AND FUNGI?

Species affected: TV
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): EC:3.2.1.26
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glycosyl hydrolase
Name of enzyme/protein: Beta-fructosidase-like protein
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Galactose metabolism, Starch and sucrose metabolism

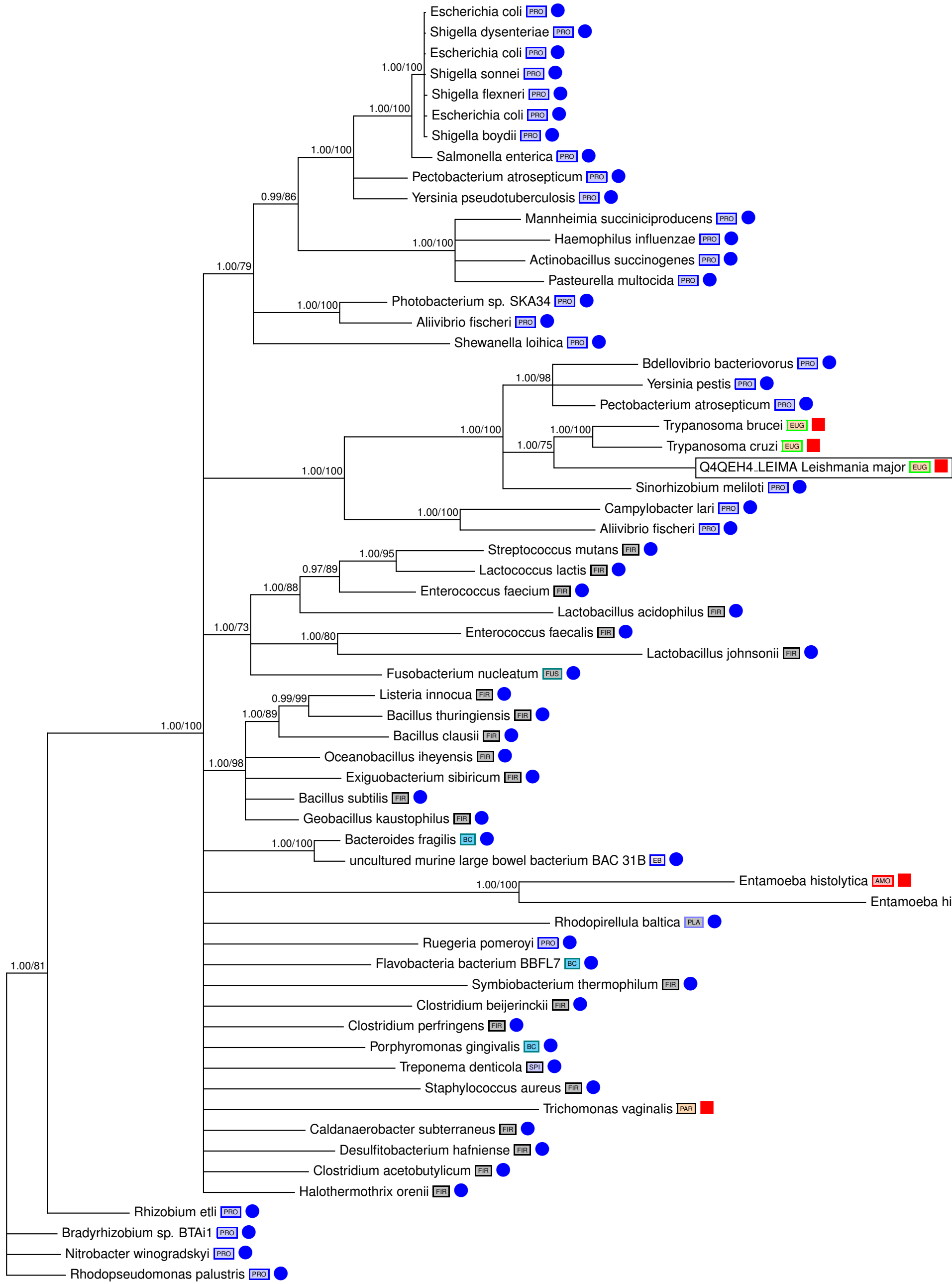
Candy accession: Q4QB75_LEIMA
RefSeq accession: XP_001683423.1
Uniprot accession: Q4QB75_LEIMA
Comments: LGT - LM TWO NODES - LGT INTO TRITRICHOMONAS AND FUNGI?

Species affected: LM
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:3.2.1.26
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: beta-fructosidase-like protein; invertase-like protein; sucrose hydrolase-like protein
Name of enzyme/protein: Beta-fructosidase-like protein
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Galactose metabolism, Starch and sucrose metabolism



TN195

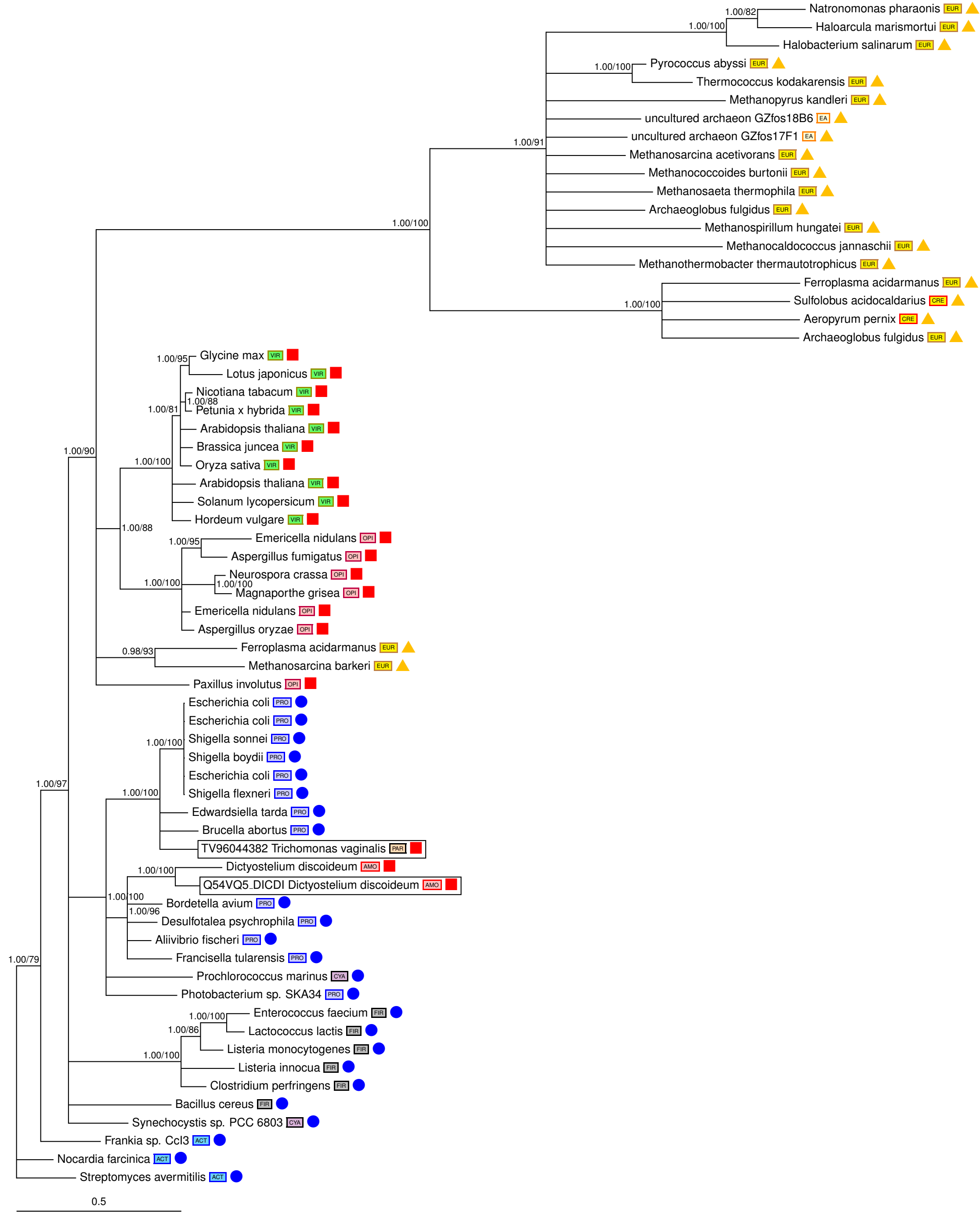
Candy accession: Q4QEH4_LEIMA
RefSeq accession: XP_001682274.1
Uniprot accession: Q4QEH4_LEIMA
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM,TB,TC,
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:3.4.11.14
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: peptidase T; peptidase T, metallo-
peptidase, ClanMH, family M20B
Name of enzyme/protein: cytosol alanyl aminopeptidase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



TN196

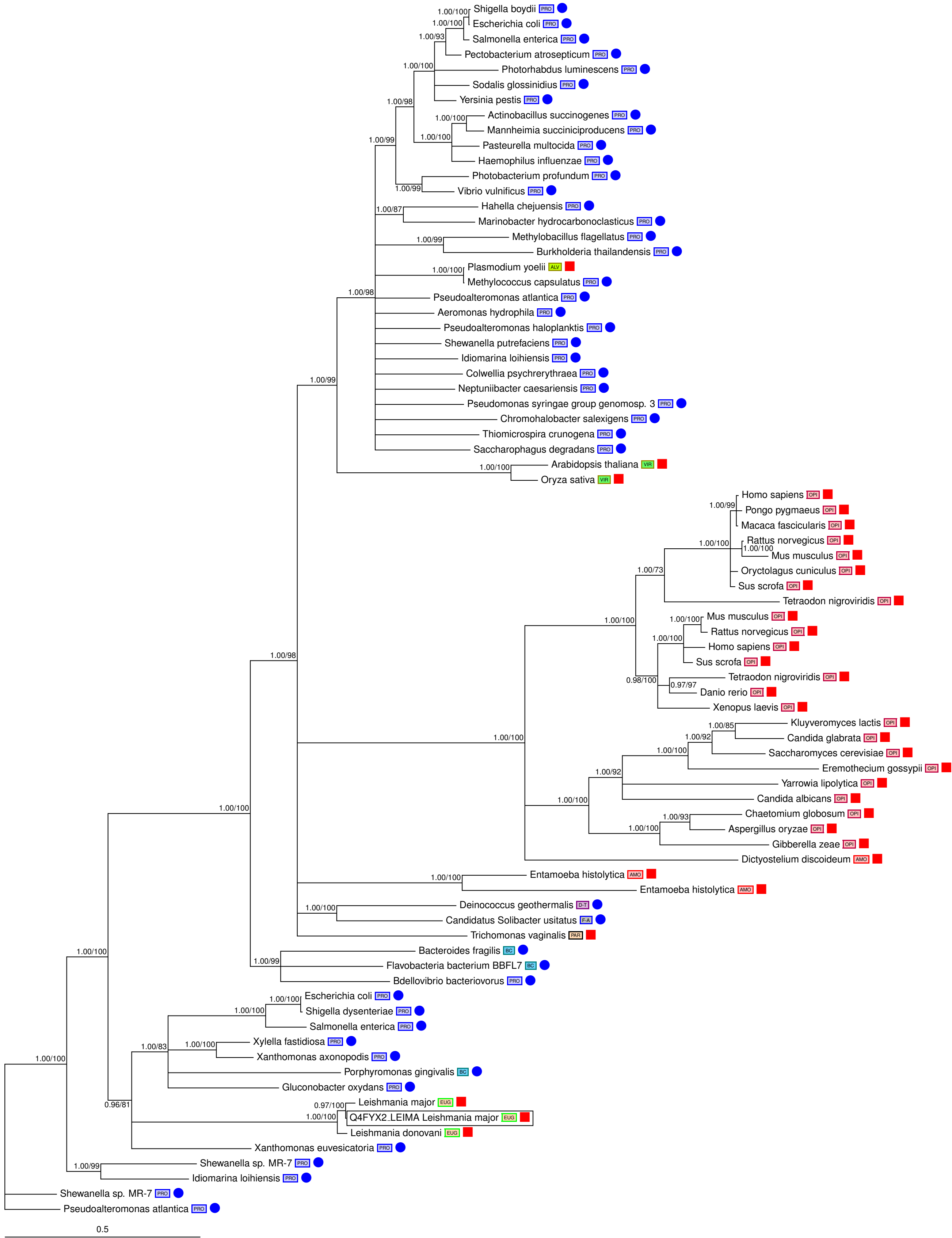
Candy accession: TV96044382
RefSeq accession: XP_001583076.1
Uniprot accession: A2DC49_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:4.1.1.15
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glutamate decarboxylase beta
Name of enzyme/protein: Glutamate decarboxylase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Metabolism of Other Amino Acids, Carbohydrate Metabolism
KEGG PATHWAY - level 2: Alanine, aspartate and glutamate metabolism, Beta-Alanine metabolism, Taurine and hypotaurine metabolism, Butanoate metabolism

Candy accession: Q54VQ5_DICDI
RefSeq accession: XP_641300.1
Uniprot accession: GADA_DICDI
Comments: LGT - DD TWO NODES
Species affected: DD
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:4.1.1.15
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glutamate decarboxylase
Name of enzyme/protein: Glutamate decarboxylase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Metabolism of Other Amino Acids, Carbohydrate Metabolism
KEGG PATHWAY - level 2: Alanine, aspartate and glutamate metabolism, Beta-Alanine metabolism, Taurine and hypotaurine metabolism, Butanoate metabolism



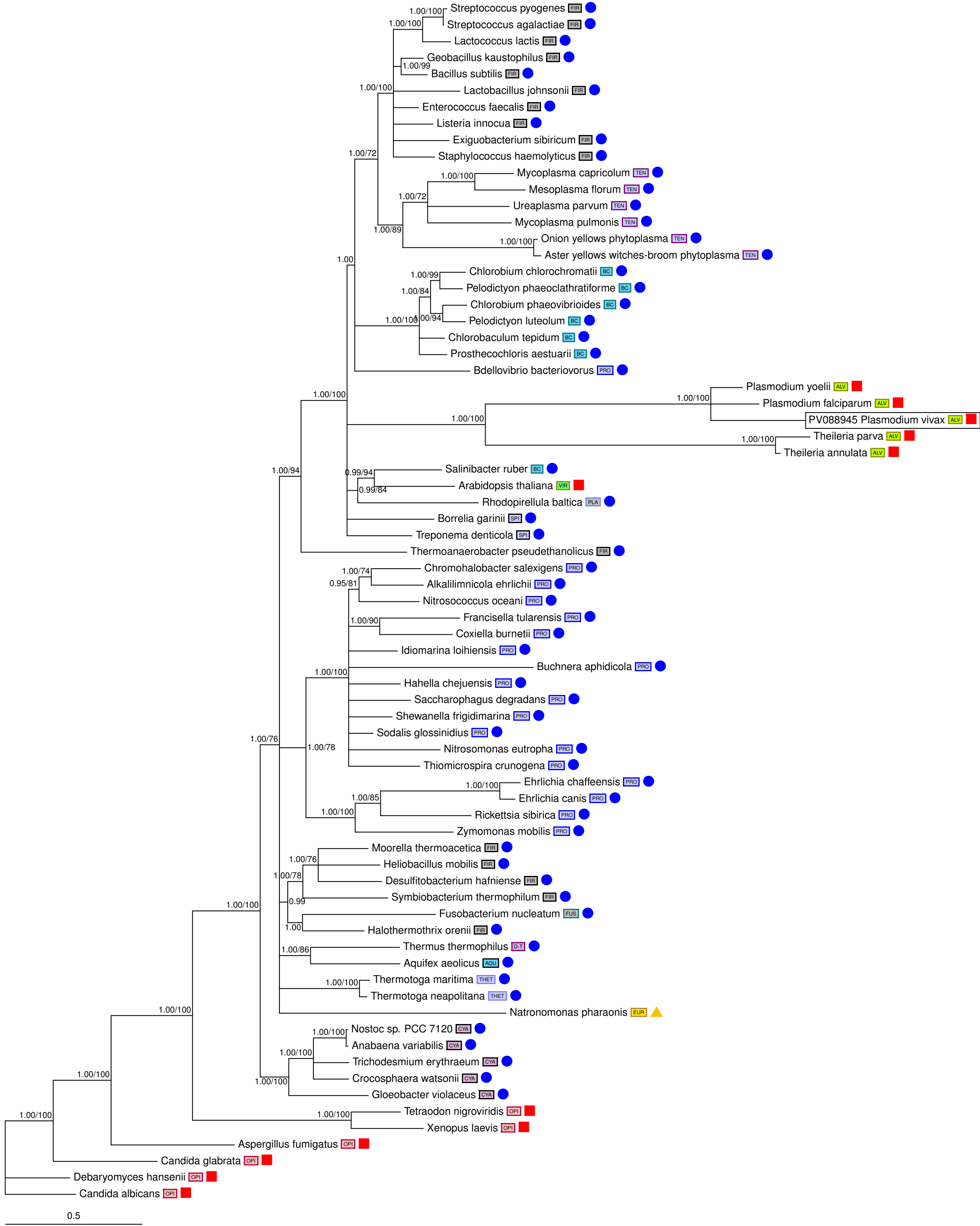
TN197

Candy accession: Q4FYX2 LEIMA
RefSeq accession: XP_822272.1
Uniprot accession: Q4FYX2_LEIMA
Comments: LGT - LM,LD TWO NODES
Species affected: LM
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:3.4.24.70
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: metallo-peptidase, Clan MA(E), Family M3
Name of enzyme/protein: oligopeptidase A
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



TN198

Candy accession: PV088945
RefSeq accession: XP_001614881.1
Uniprot accession: A5K5G9_PLAVS
Comments: LGT - APICOMPLEXA TWO NODES
Species affected: PF,PV,PY,PB, TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:6.1.1.4
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: leucyl-tRNA synthetase
Name of enzyme/protein: Leucyl-tRNA synthetase
KEGG PATHWAY - level 1: Translation - Genetic Information Processing
KEGG PATHWAY - level 2: Aminoacyl-tRNA biosynthesis

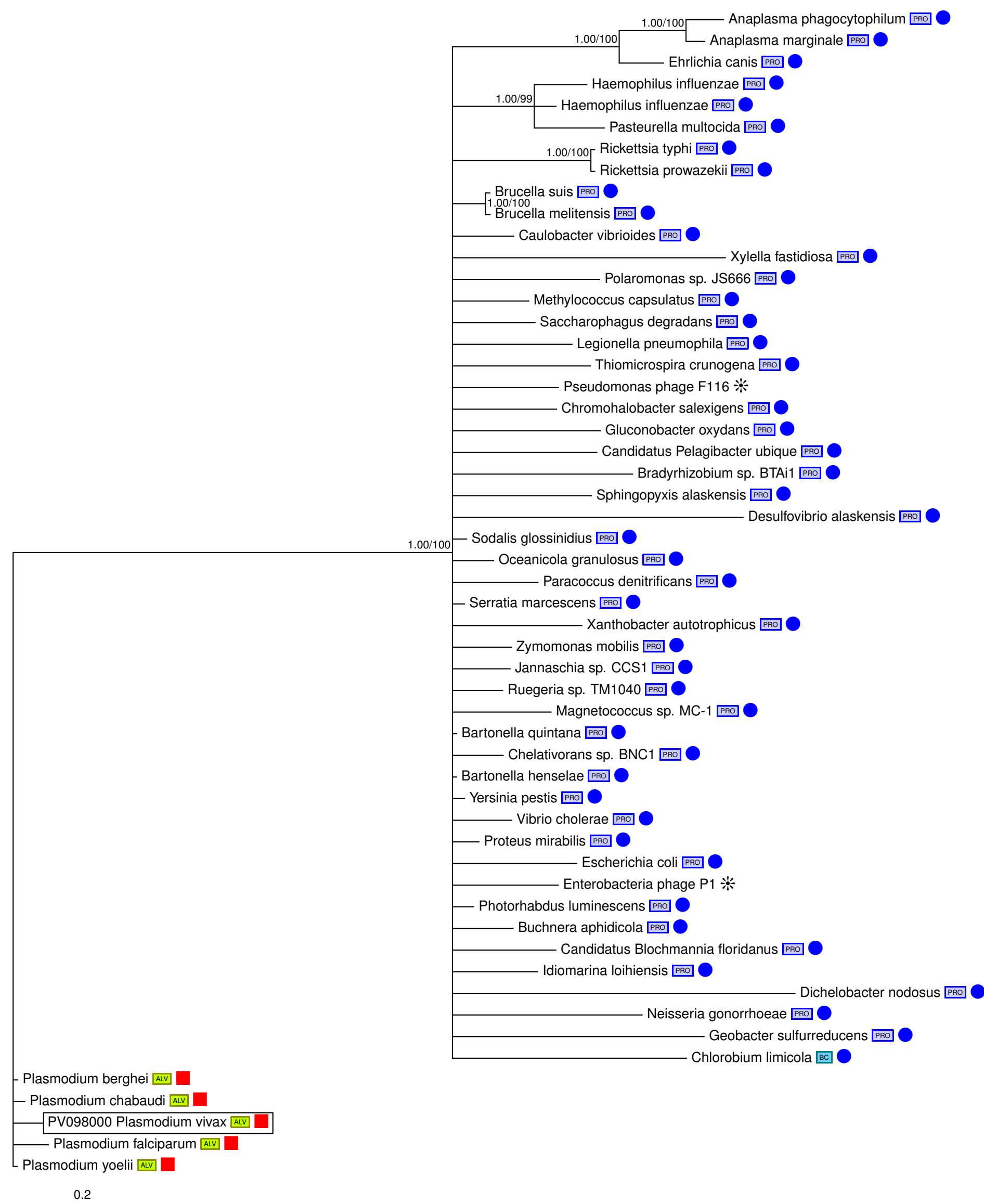


TN199

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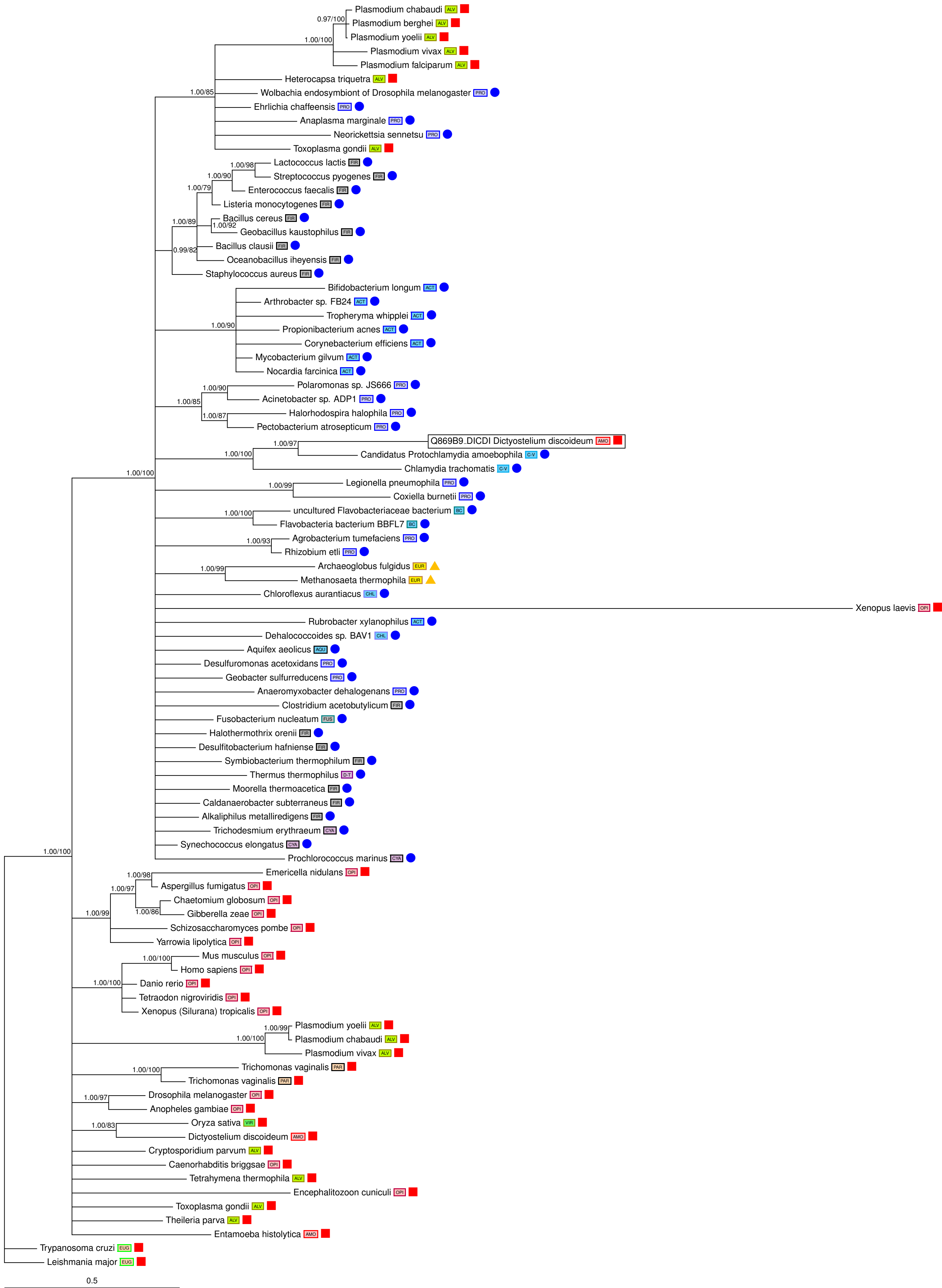
      Candy accession: PVO98000
      RefSeq accession: XP_001613260.1
      Uniprot accession: A5KB16_PLAUVI
      Comments: LGT - APCOMPLEXA ONLY + PHAGES
      Species affected: PF,PV,PP,PS,PC
      Adjacent taxa in tree: Bacteria/phage
EC annotation - (Blast/Profile): na
      PHOBIUS SP: Y
      PHOBIUS TMD: 0
      RefSeq annotation: single-strand binding protein
      Name of enzyme/protein: Predicted single stranded DNA binding
                             protein
      KEGG PATHWAY - level 1: Other function
      KEGG PATHWAY - level 2: na

```



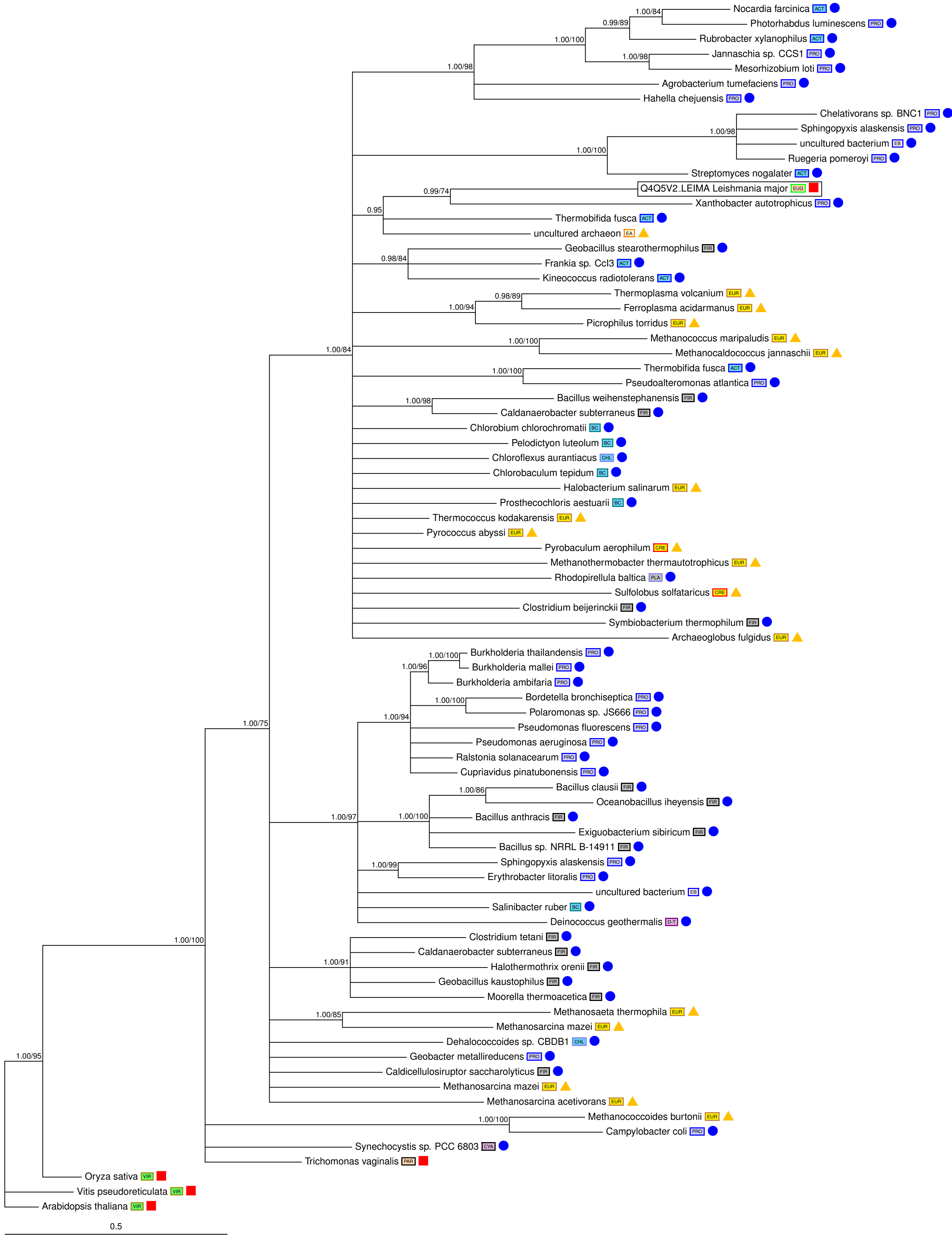
TN200

Candy accession: Q869B9_DICDI
RefSeq accession: XP_643448.1
Uniprot accession: Q869B9_DICDI
Comments: LGT - DD TWO NODES - INTRACELLULAR
BACTERIA
Species affected: DD
Adjacent taxa in tree: Chlamydiae/Verrucomicrobia -
Protochlamydia
EC annotation - (Blast/Profile): EC:2.4.2.29
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0275613
Name of enzyme/protein: tRNA-guanine transglycosylase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



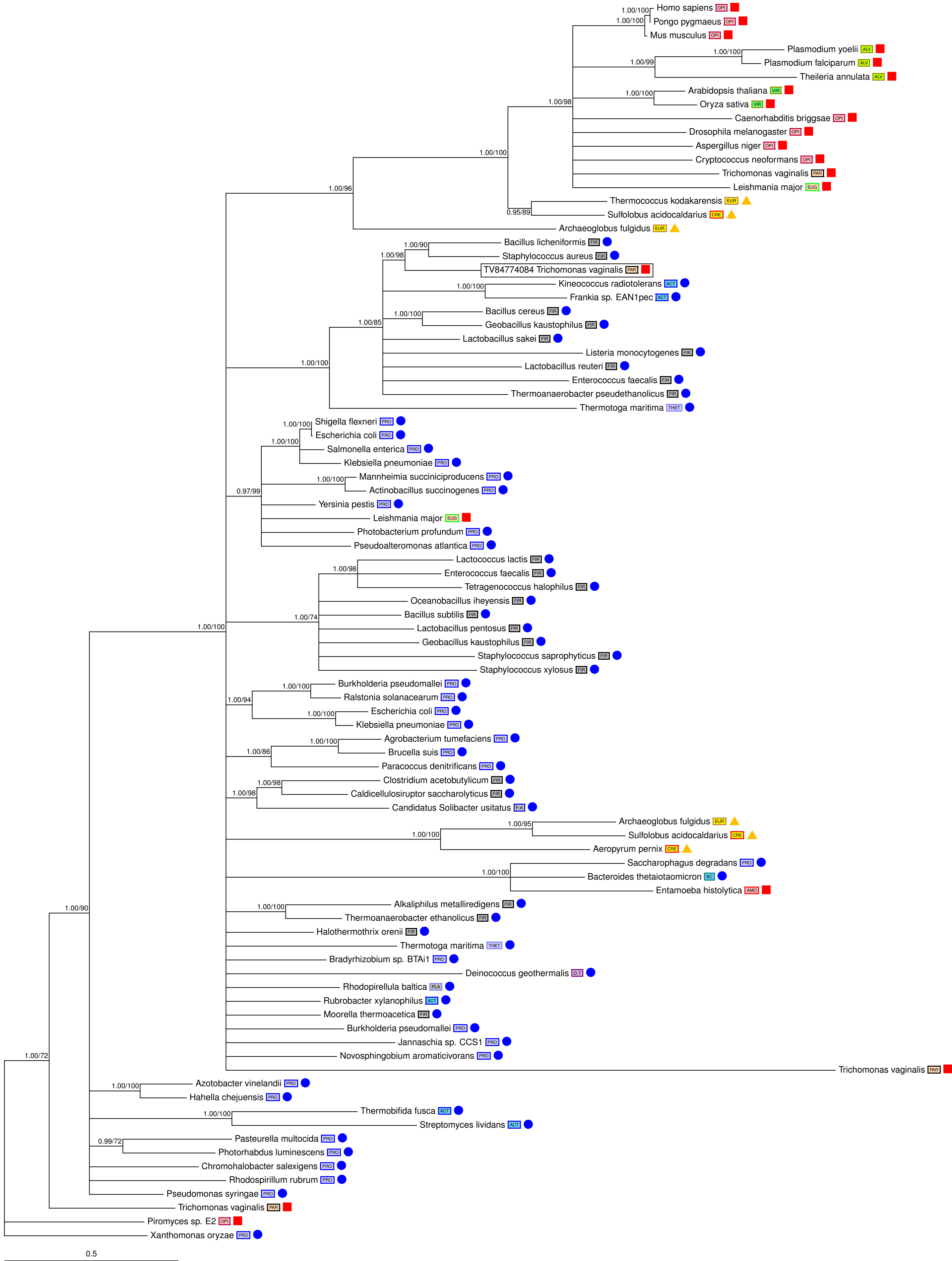
TN201

Candy accession: Q4Q5V2_LEIMA
RefSeq accession: XP_001685296.1
Uniprot accession: Q4Q5V2_LEIMA
Comments: LGT - LM TWO NODES
Species affected: LM
Adjacent taxa in tree: Proteobacteria - Xanthobacter
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing cyclase domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

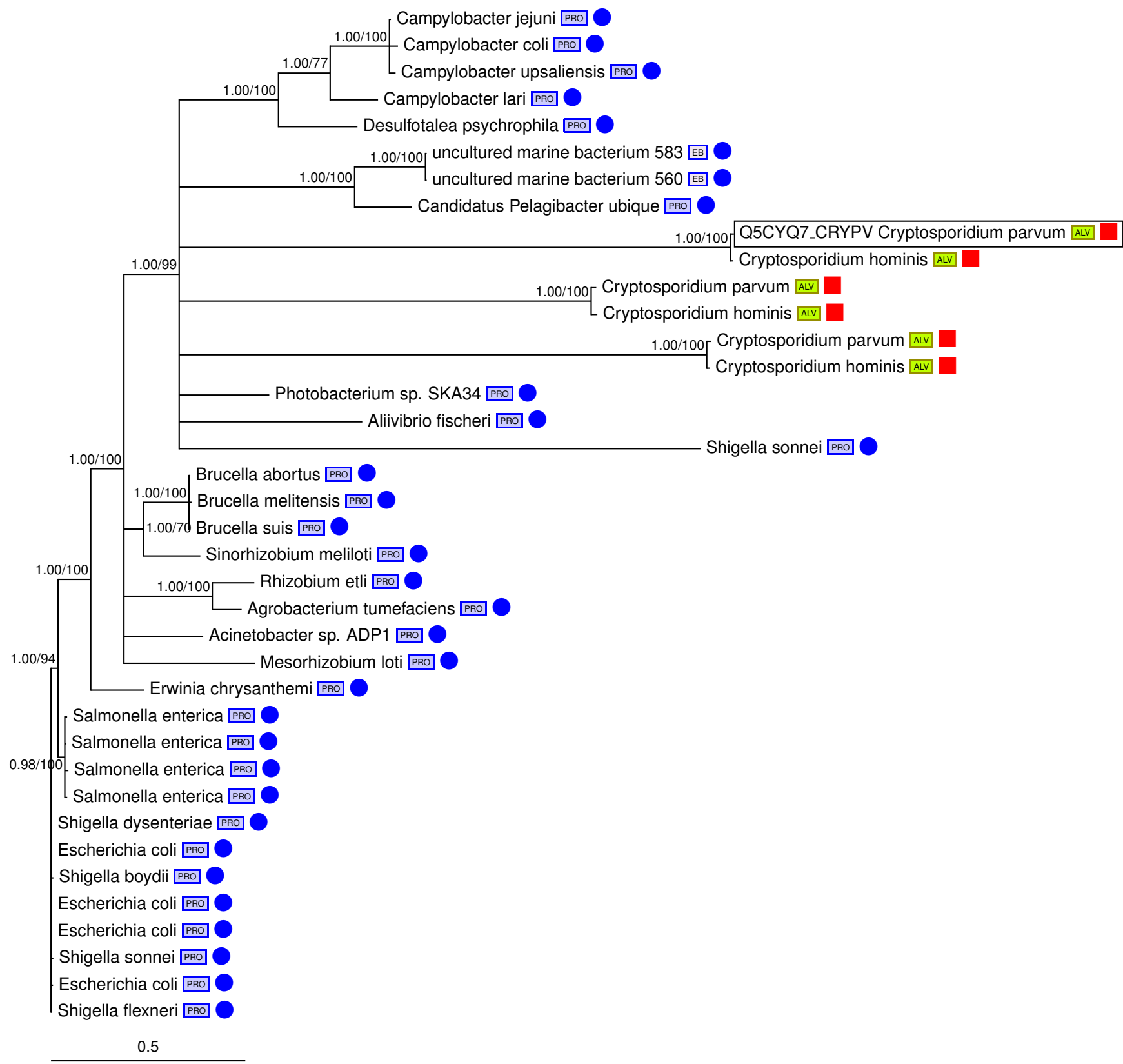


TN202

Candy accession: TV84774084
RefSeq accession: XP_001310401.1
Uniprot accession: A2FCA8_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): EC:2.7.1.12
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: sugar kinase
Name of enzyme/protein: gluconokinase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pentose phosphate pathway

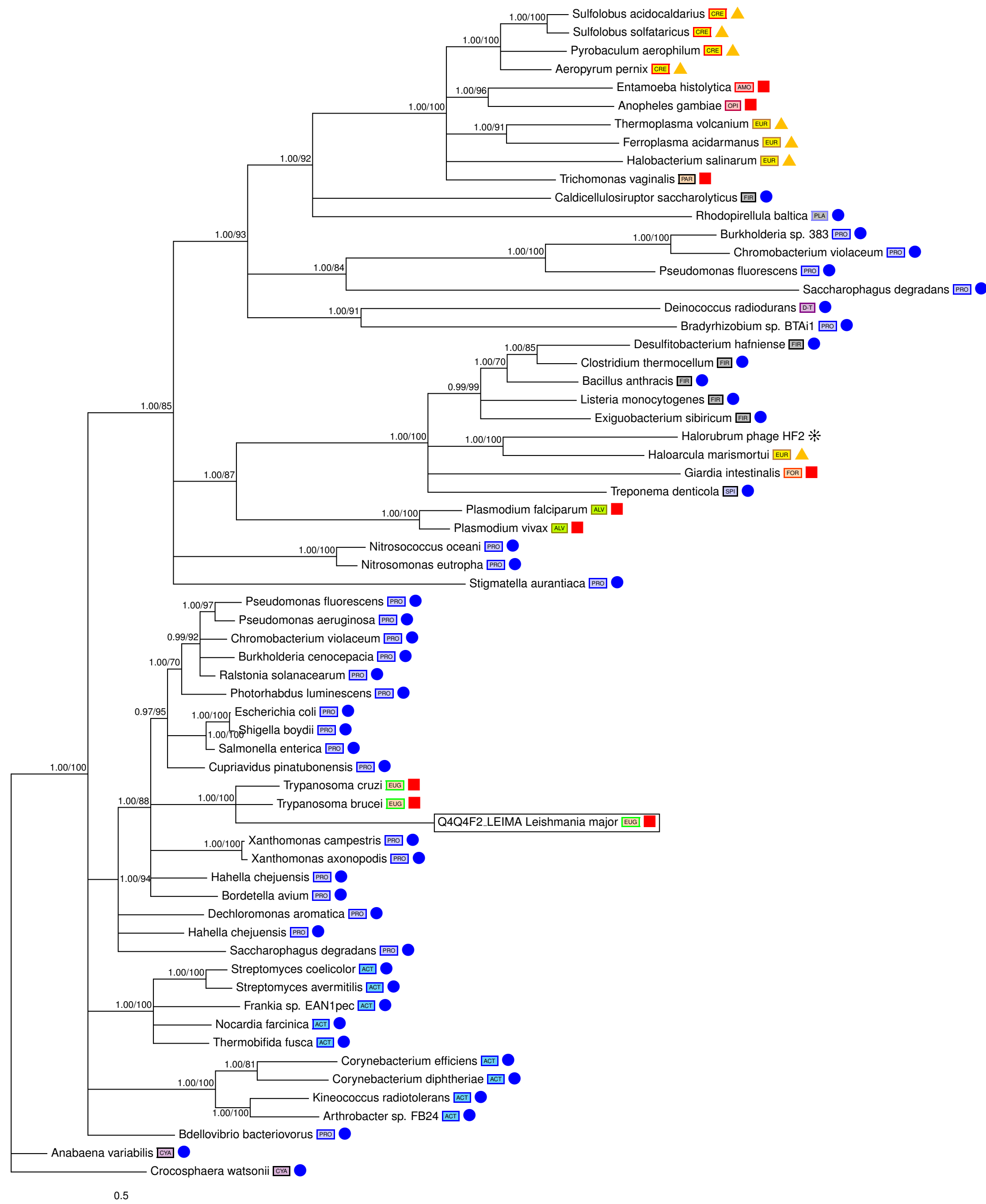


Candy accession: Q5CYQ7_CRYPV
RefSeq accession: XP_628323.1
Uniprot accession: Q5CYQ7_CRYPV
Comments: LGT - CRYPTOSPORIDIUM ONLY - 3 PAIRS OF
CP+CH PARALOGUES
Species affected: CP,CH
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 6
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Putative ABC-type long-chain fatty acid
transport system
KEGG PATHWAY - level 1: Other function - Membrane transport
KEGG PATHWAY - level 2: na



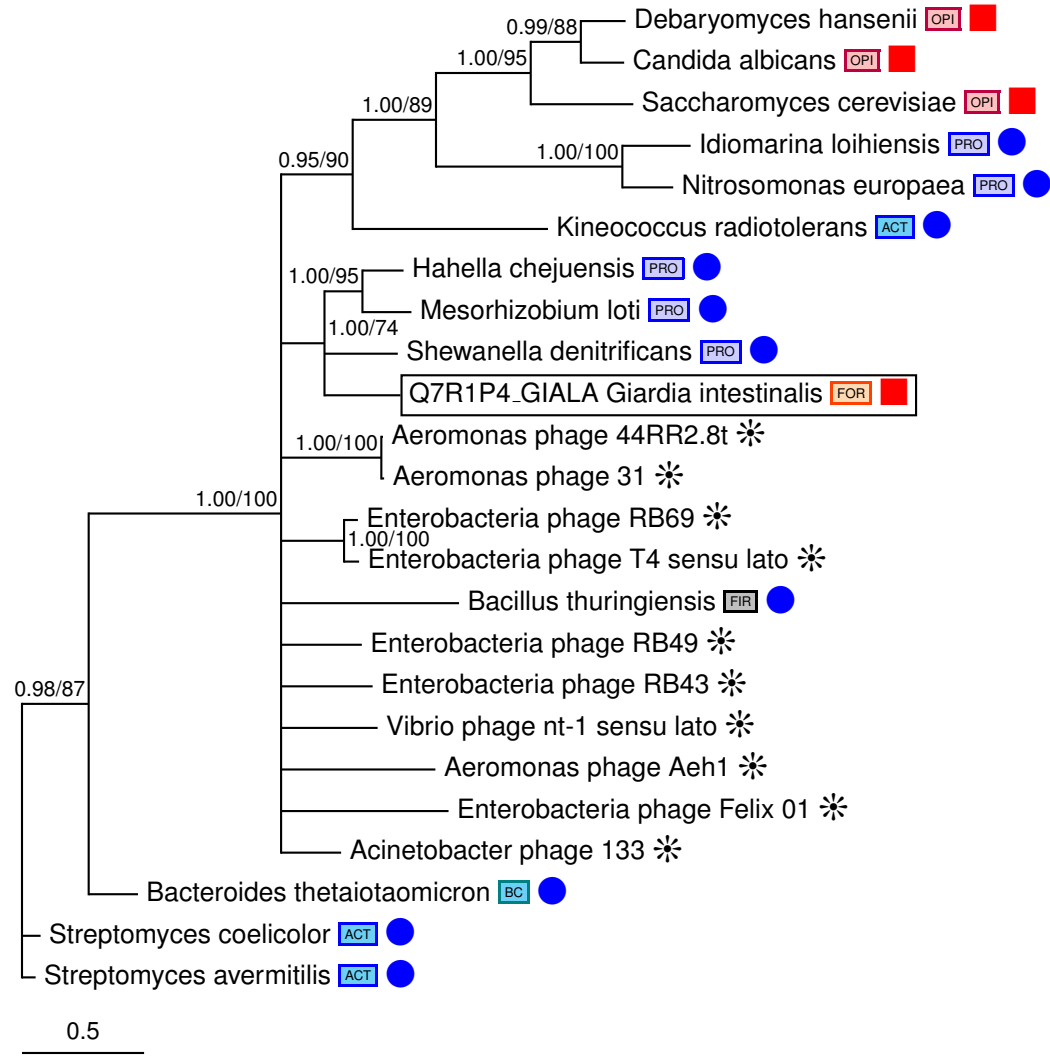
TN204

Candy accession: Q4Q4F2.LEIMA
RefSeq accession: XP_001685796.1
Uniprot accession: Q4Q4F2.LEIMA
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM,TB,TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Uncharacterized protein family UPF0027
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



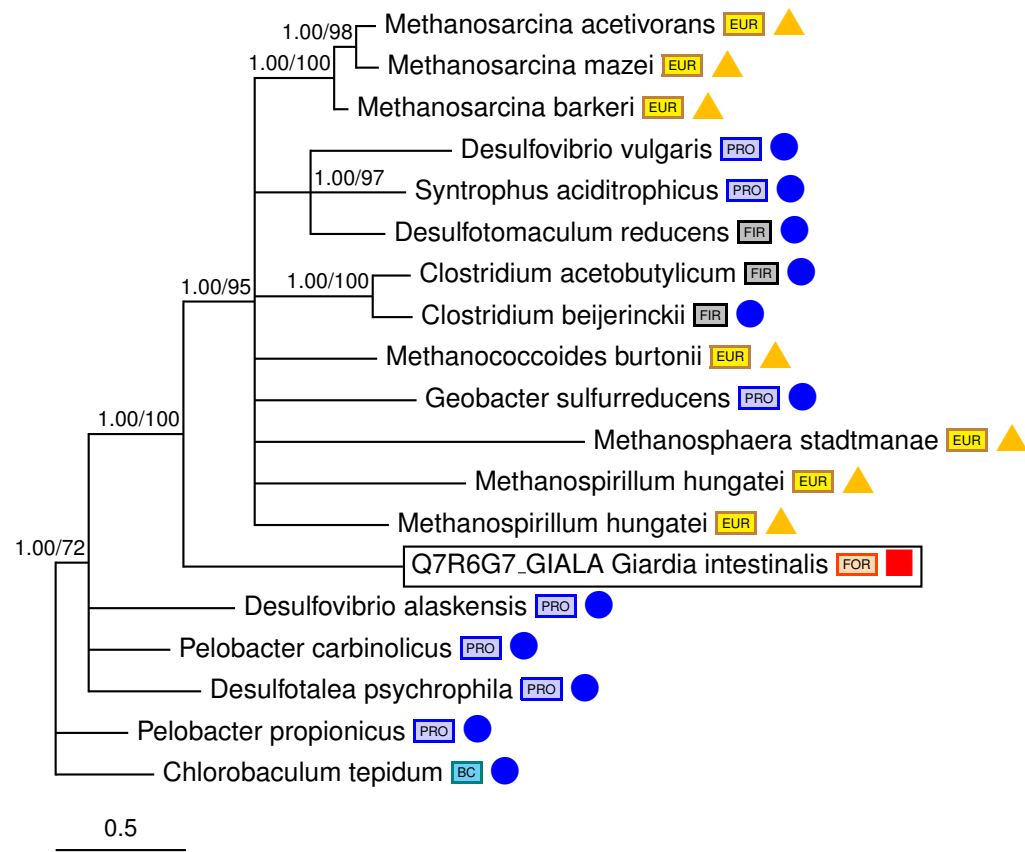
TN205

Candy accession: Q7R1P4_GIALA
RefSeq accession: XP_001706109.1
Uniprot accession: A8BMJ3_GIALA
Comments: LGT - GI TWO NODES - PHAGES - DEAP LGT INTO FUNGI
Species affected: GI,FUNGI
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Phosphatase similar to the C-terminal domain of histone macroH2A1
Name of enzyme/protein: Predicted Macro domain, Poalp-like family
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



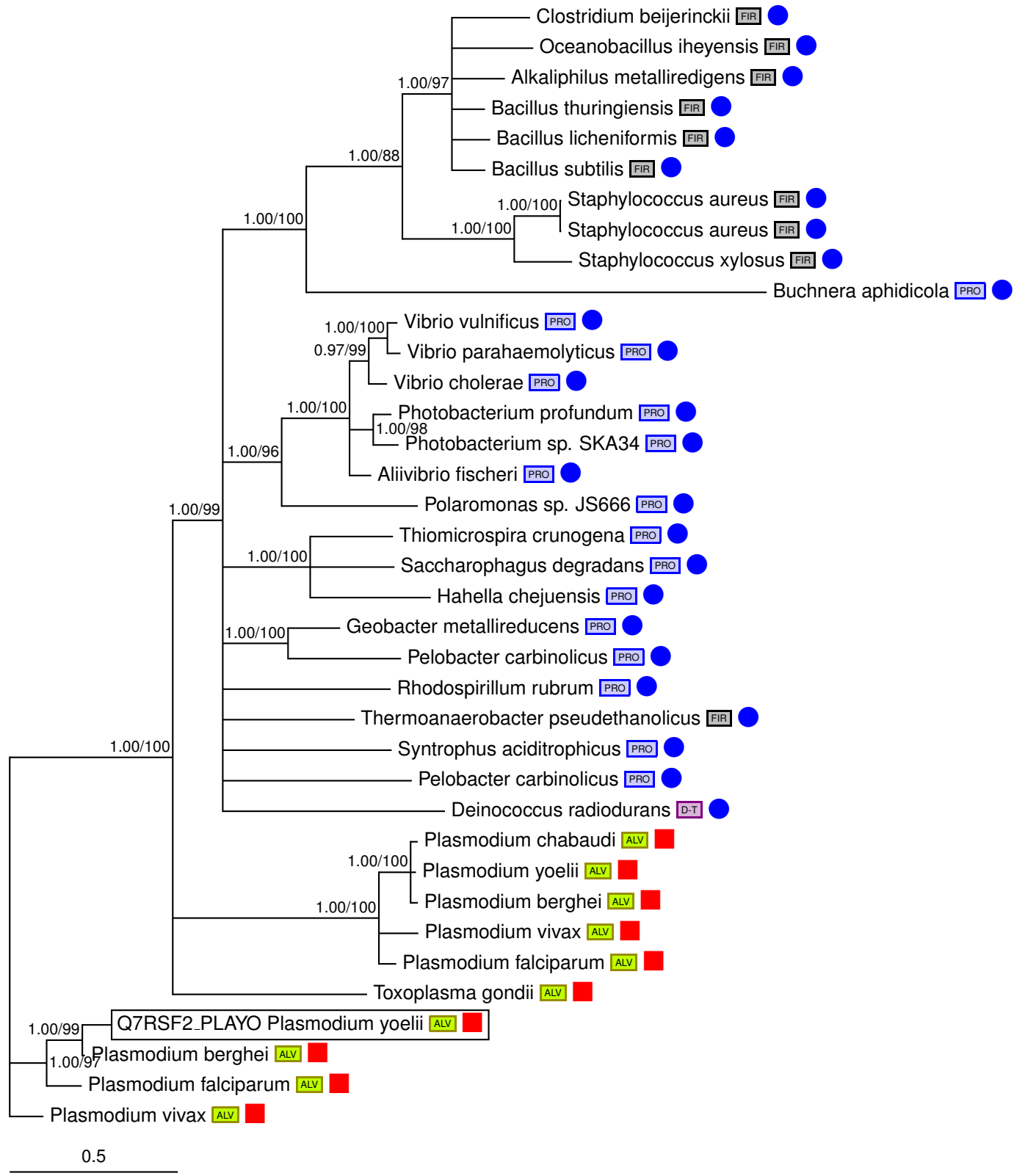
TN206

Candy accession: Q7R6G7_GIALA
RefSeq accession: XP_001707931.1
Uniprot accession: A8BCL1_GIALA
Comments: LGT - GI ONLY
Species affected: GI
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: Nitroreductase Fd-NR2
Name of enzyme/protein: Predicted oxidoreductase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



TN207

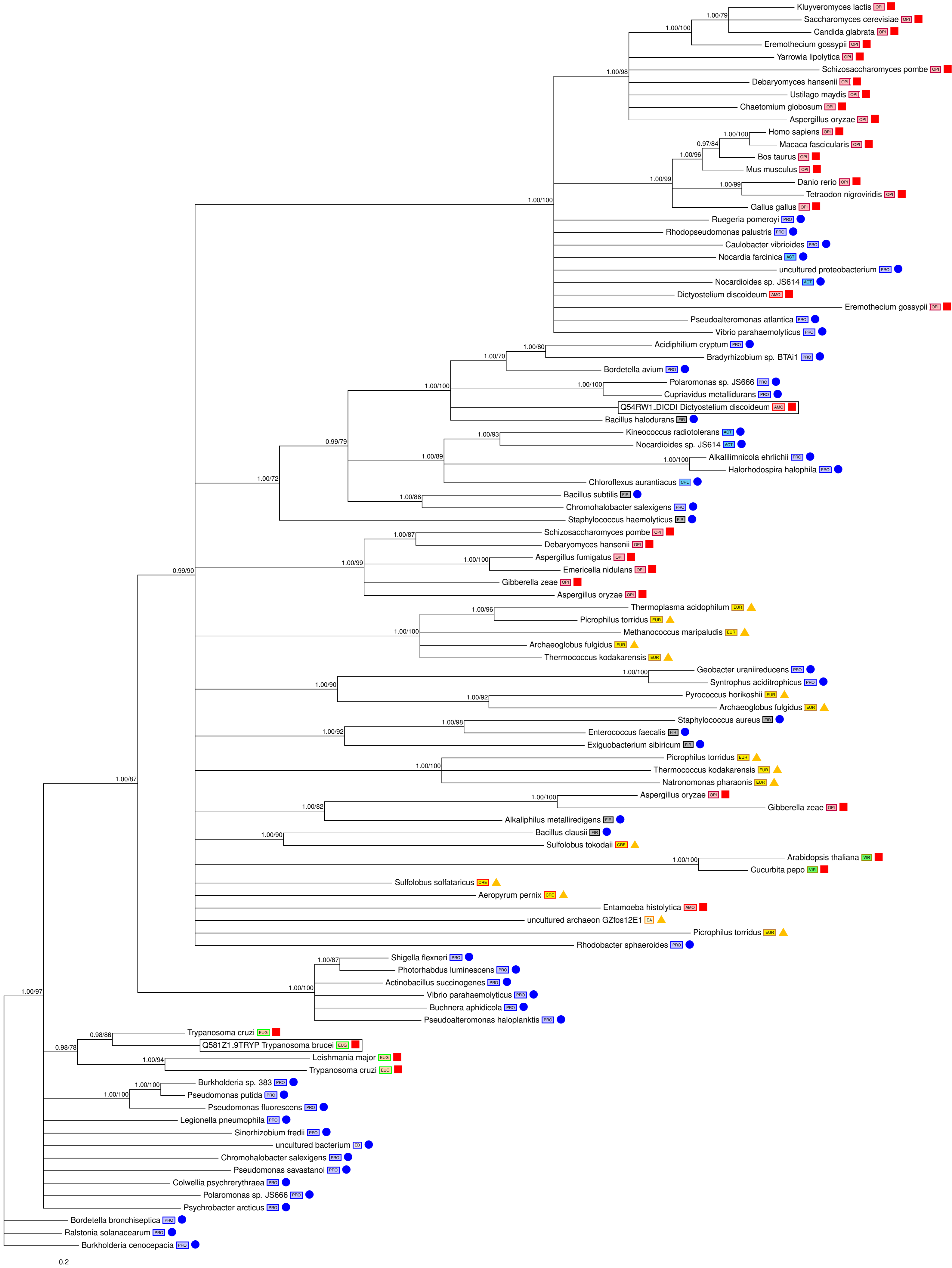
Candy accession: Q7RSF2_PLAYO
RefSeq accession: XP_724075.1
Uniprot accession: Q7RSF2_PLAYO
Comments: LGT - APICOMPLEXA ONLY
Species affected: PF,PV,PY,TG
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted SAM-dependent
methyltransferases; 23S rRNA m(5)C1962
methyltransferase;
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



TN208

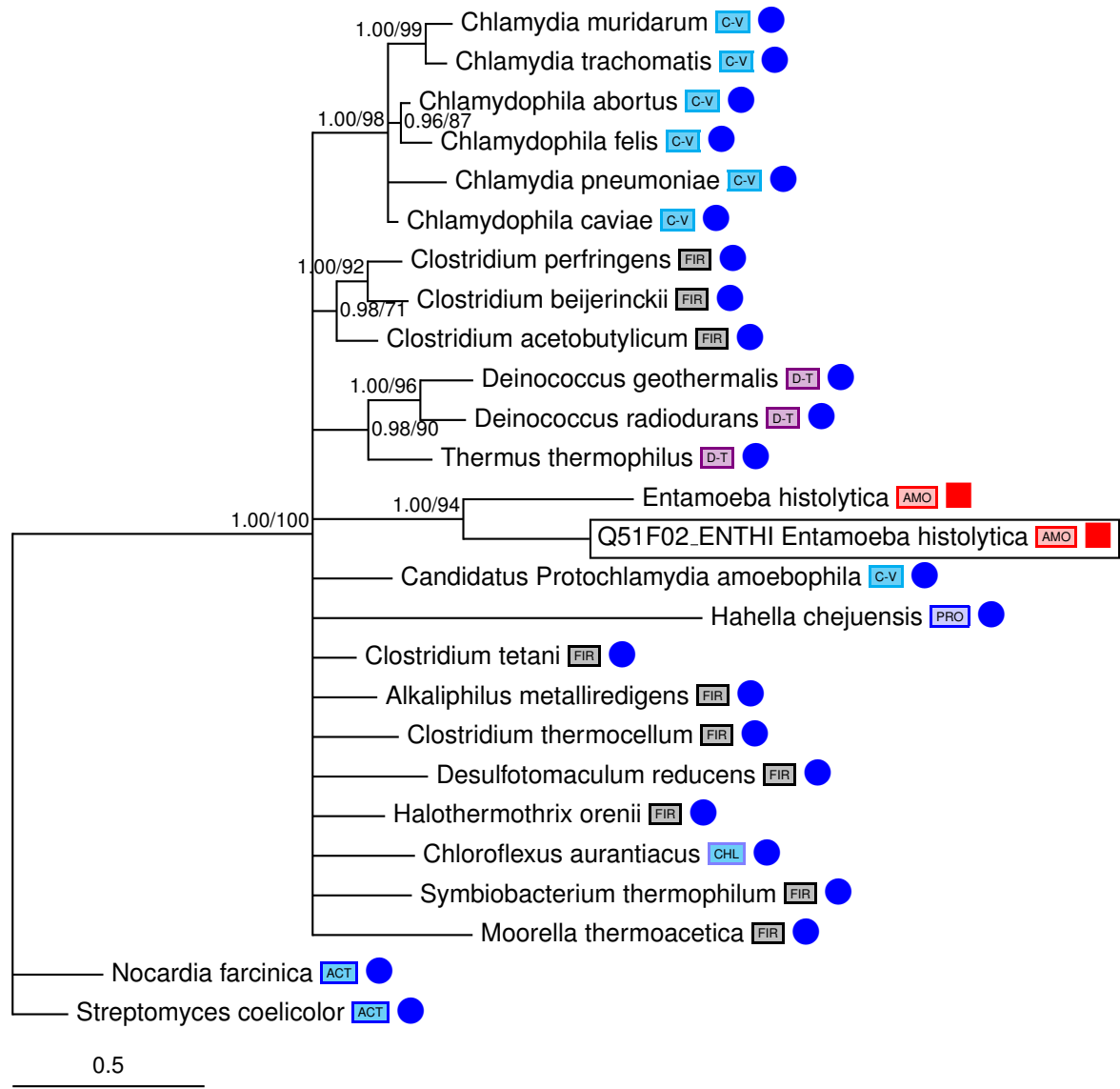
Candy accession: Q54RW1_DICDI
RefSeq accession: XP_639376.1
Uniprot accession: Q54RW1_DICDI
Comments: LGT - DD TWO NODES
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.5.1.16
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0282881
Name of enzyme/protein: acetylornithine deacetylase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism

Candy accession: Q581Z1_9TRYP
RefSeq accession: XP_847024.1
Uniprot accession: Q581Z1_9TRYP
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: TB,TC,LM
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:3.5.1.16
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: acetylornithine deacetylase
Name of enzyme/protein: acetylornithine deacetylase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism



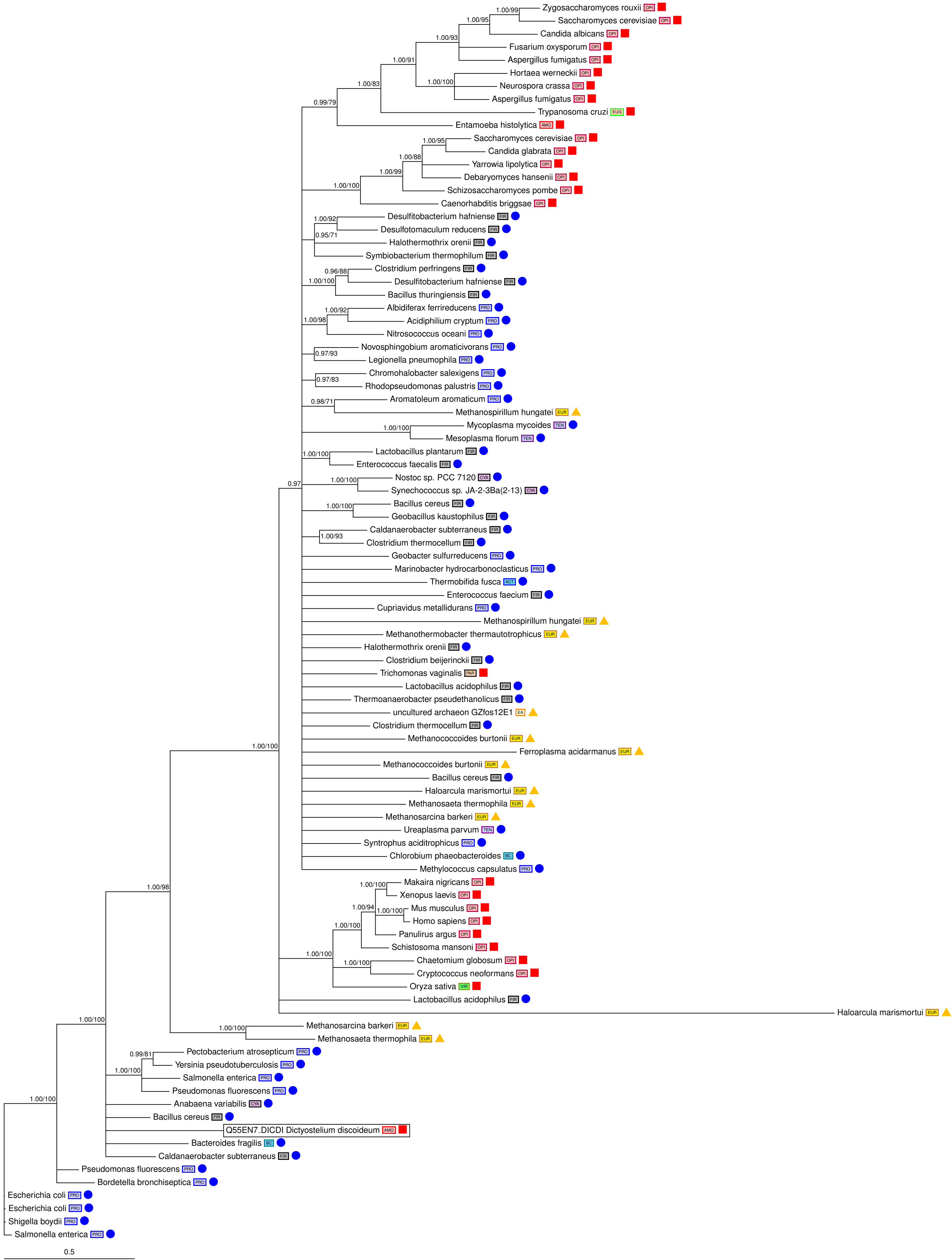
TN209

Candy accession: Q51F02_ENTHI
RefSeq accession: XP_656821.2
Uniprot accession: C4M5A2_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: ser/thr protein phosphatase family protein
Name of enzyme/protein: Predicted phosphohydrolase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



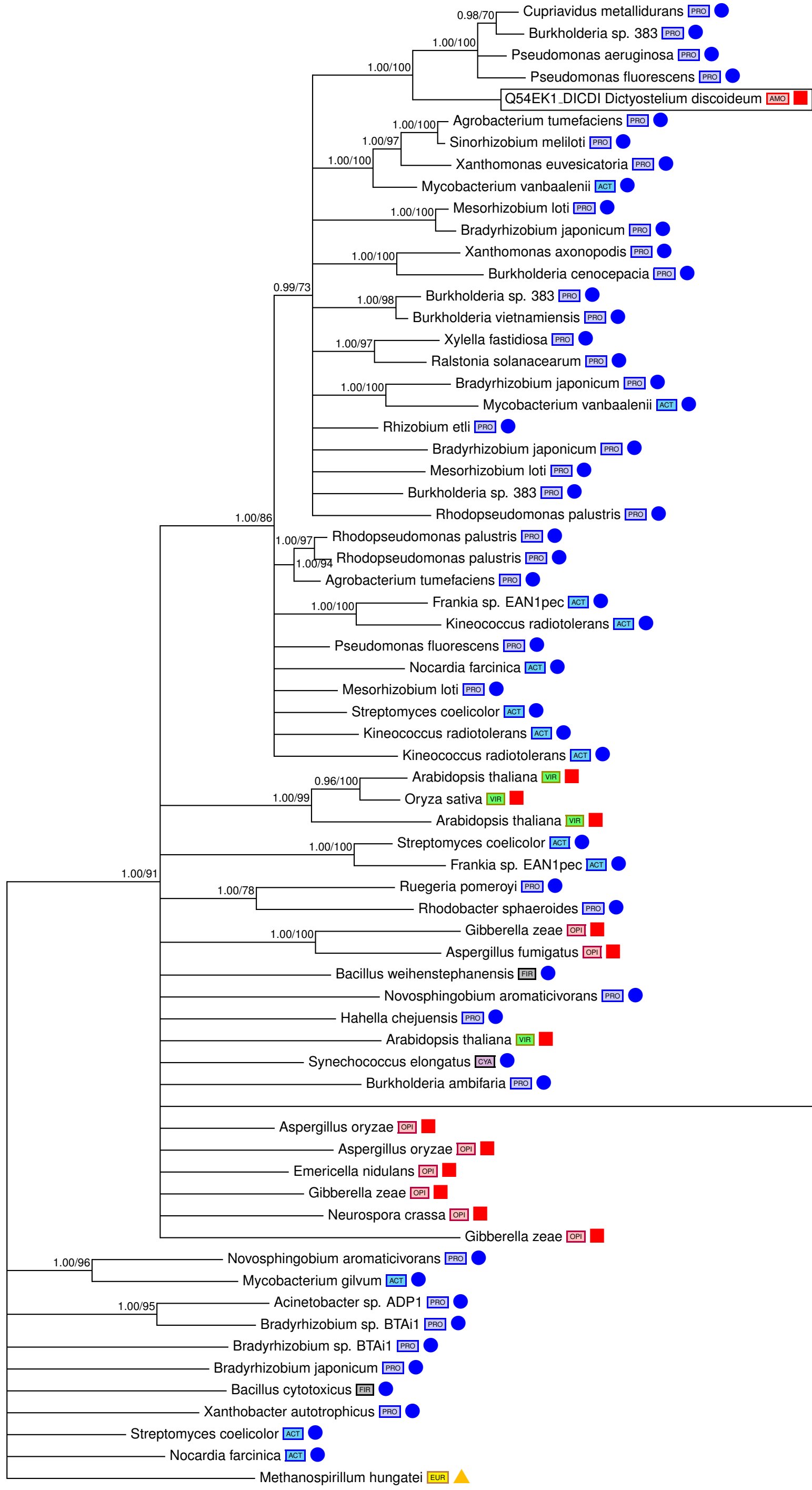
TN210

Candy accession: Q55EN7_DICDI
RefSeq accession: XP_646983.1
Uniprot accession: Q55EN7_DICDI
Comments: LGT - DD TWO NODES
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.6.3.2
PHOBIUS SP: 0
PHOBIUS TMD: 8
RefSeq annotation: transmembrane protein
Name of enzyme/protein: Mg2+-importing ATPase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



TN211

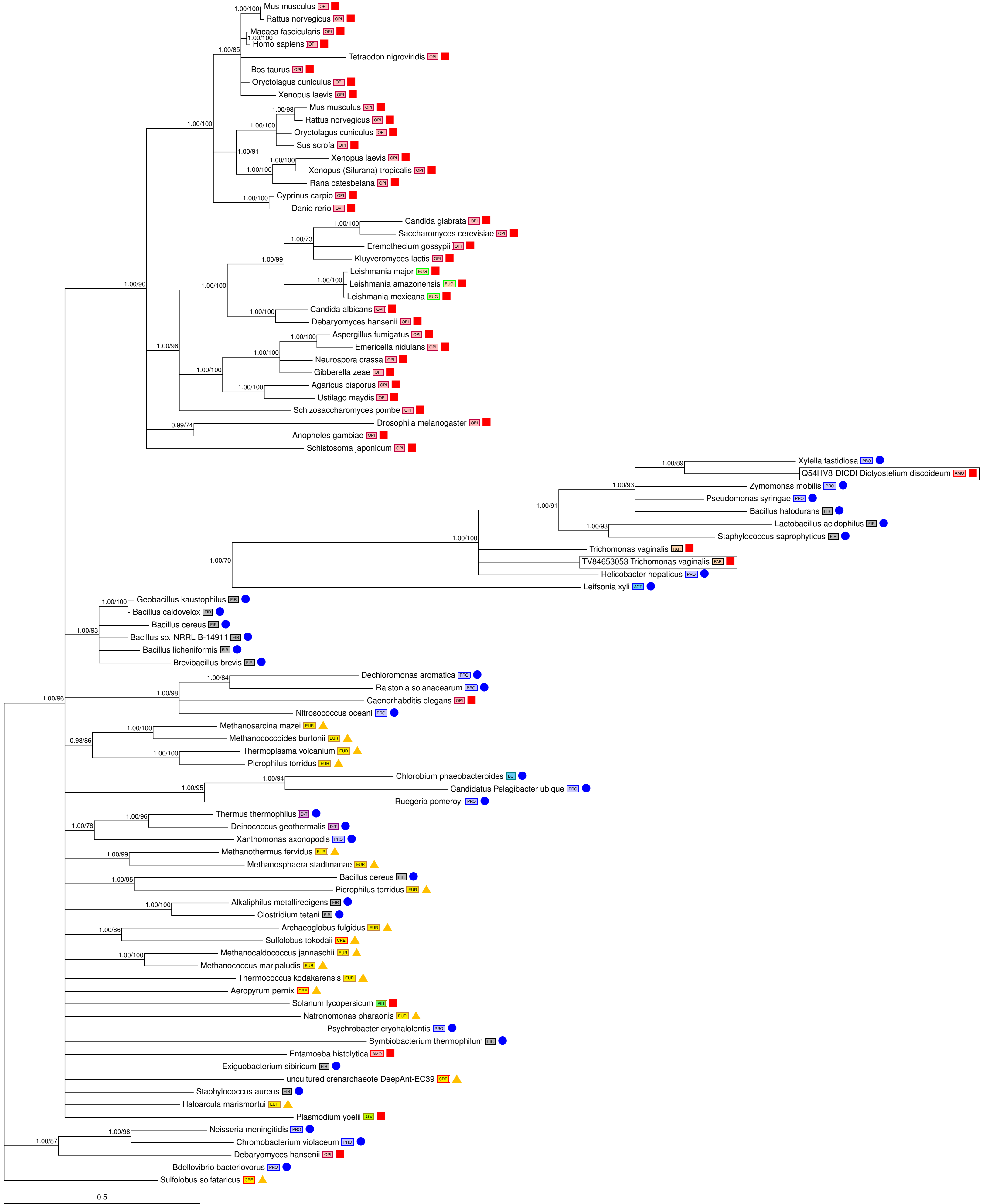
Candy accession: Q54EK1_DICDI
RefSeq accession: XP_635239.1
Uniprot accession: Q54EK1_DICDI
Comments: LGT - DD TWO NODES
Species affected: DD
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: esterase/lipase/thioesterase domain-containing protein
Name of enzyme/protein: Protein contianing alpha/beta hydrolase domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



TN212

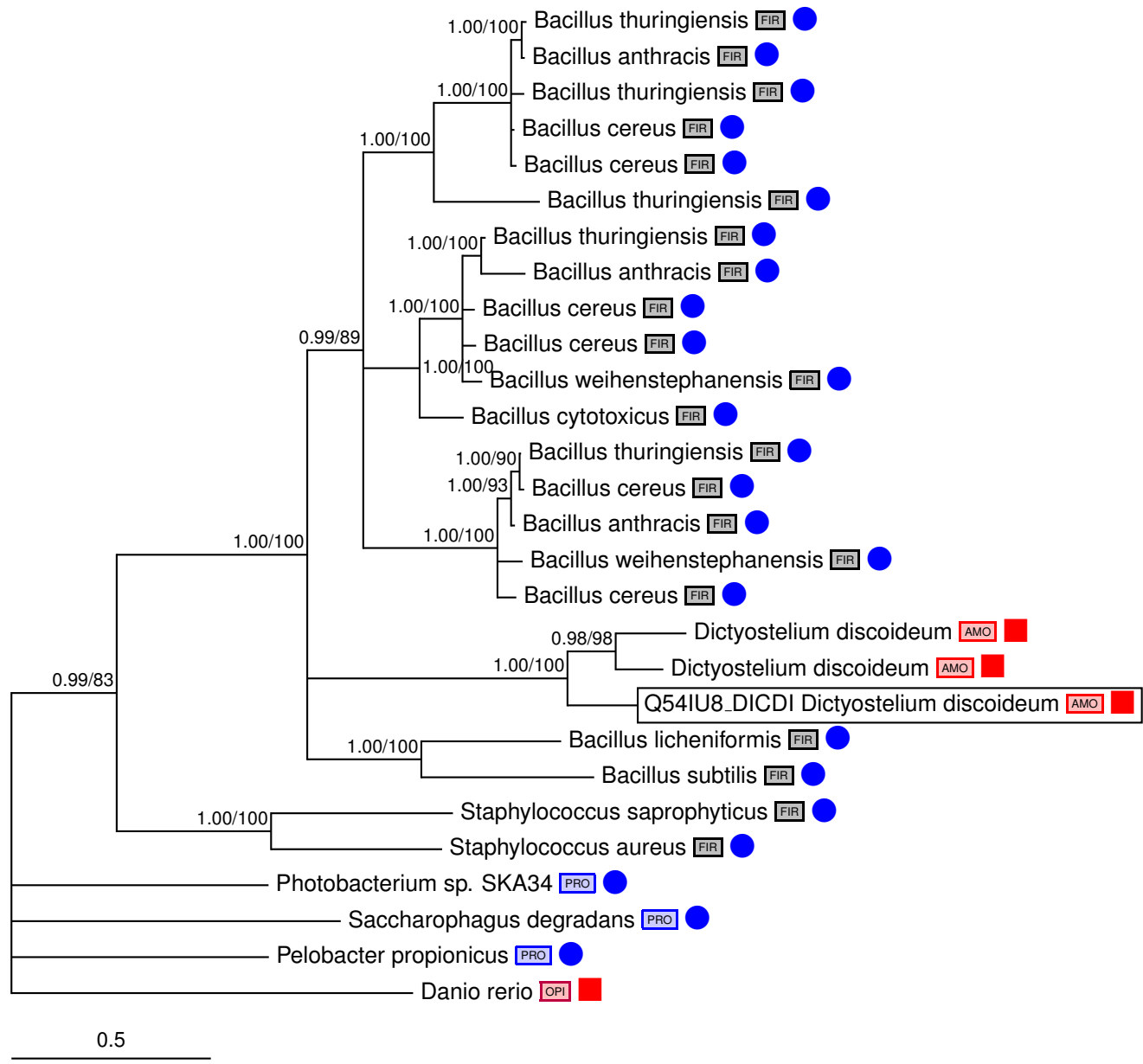
Candy accession: TV84653053
RefSeq accession: XP_001306442.1
Uniprot accession: A2FNL2_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.5.3.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Arginase family protein
Name of enzyme/protein: Arginase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism

Candy accession: Q54HV8_DICDI
RefSeq accession: XP_636331.1
Uniprot accession: Q54HV8_DICDI
Comments: LGT - DD TWO NODES
Species affected: DD
Adjacent taxa in tree: Proteobacteria - Xylella
EC annotation - (Blast/Profile): EC:3.5.3.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: arginase/agmatinase/formiminoglutamase family protein
Name of enzyme/protein: Arginase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism



TN213

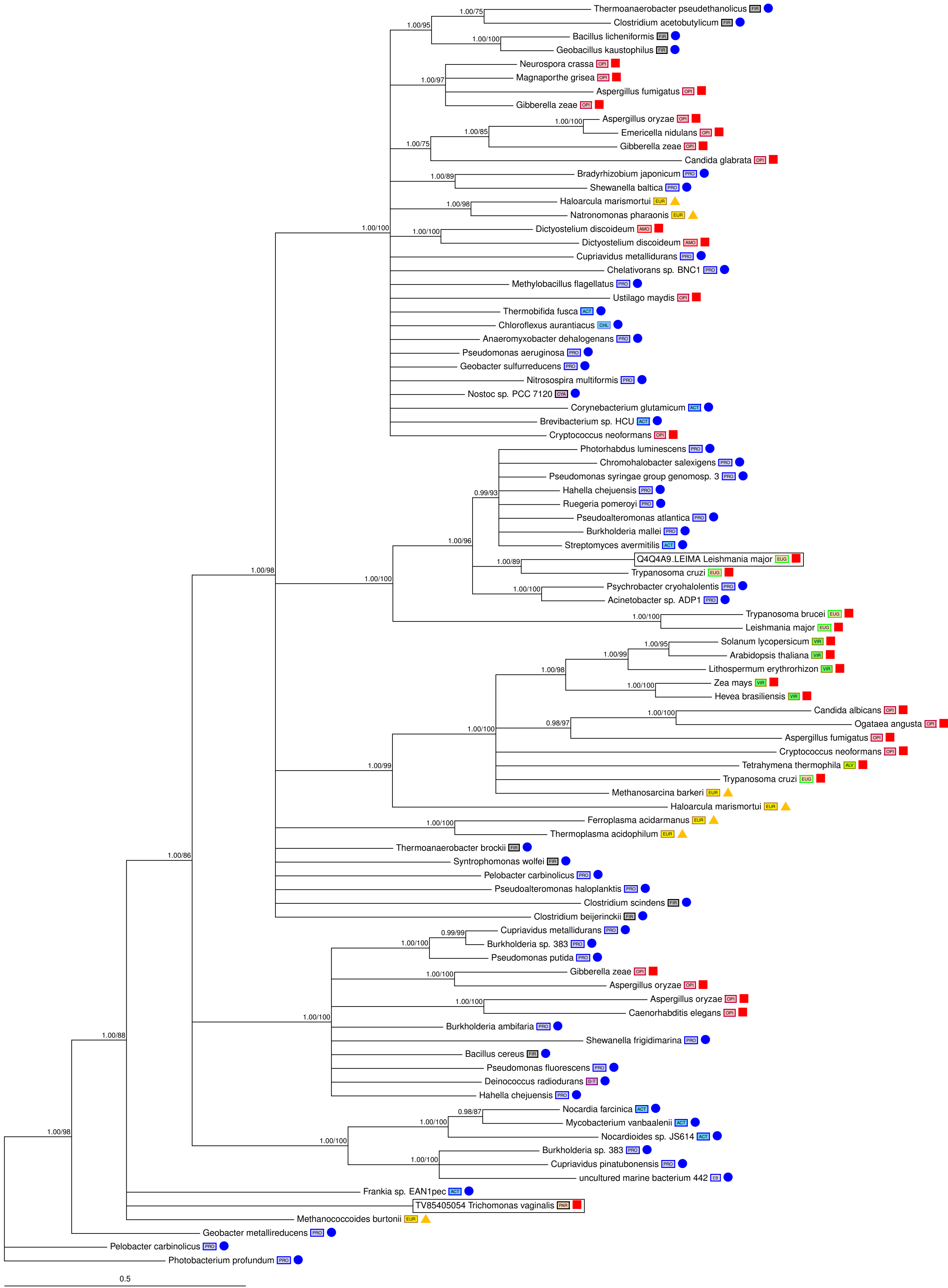
Candy accession: Q54IU8_DICDI
RefSeq accession: XP_636690.1
Uniprot accession: ARY2_DICDI
Comments: LGT - DD TWO NODES
Species affected: DD
Adjacent taxa in tree: Firmicutes - Bacillus
EC annotation - (Blast/Profile): EC:2.3.1.5
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: arylamine N-acetyltransferase family protein
Name of enzyme/protein: arylamine N-acetyltransferase
KEGG PATHWAY - level 1: Biosynthesis of Other Secondary Metabolites, Xenobiotics Biodegradation and Metabolism,
KEGG PATHWAY - level 2: Caffeine metabolism, Nitrotoluene degradation, Drug metabolism - other enzymes



TN214

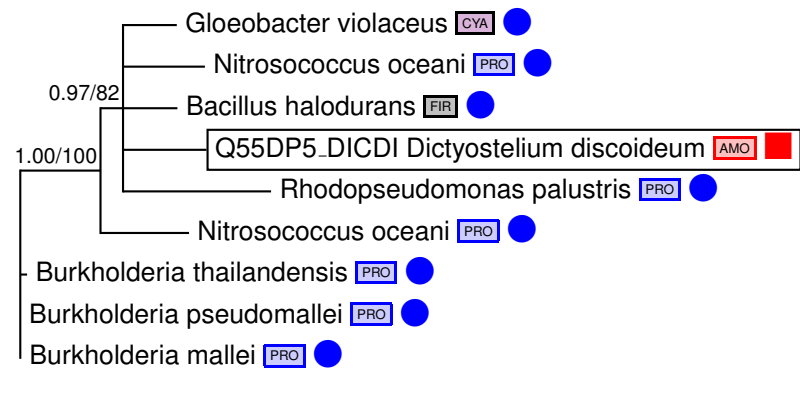
Candy accession: Q4Q4A9_LEIMA
RefSeq accession: XP_001685839.1
Uniprot accession: Q4Q4A9_LEIMA
Comments: LGT - TV TWO NODES
Species affected: LM, TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:1.3.1.34
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: oxidoreductase, FAD/FMN-binding family protein
Name of enzyme/protein: NADPH dehydrogenase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction

Candy accession: TV85405054
RefSeq accession: XP_001303632.1
Uniprot accession: A2FWL7_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:1.6.99.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: oxidoreductase, FAD/FMN-binding family protein
Name of enzyme/protein: NADPH dehydrogenase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



TN215

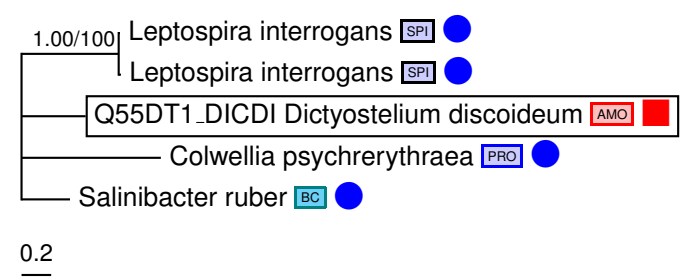
Candy accession: Q55DP5_DICDI
RefSeq accession: XP_646086.1
Uniprot accession: Q55DP5_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 1
RefSeq annotation: hypothetical protein DDB_G0270564
Name of enzyme/protein: Predicted RNA methyltransferase
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na



0.5

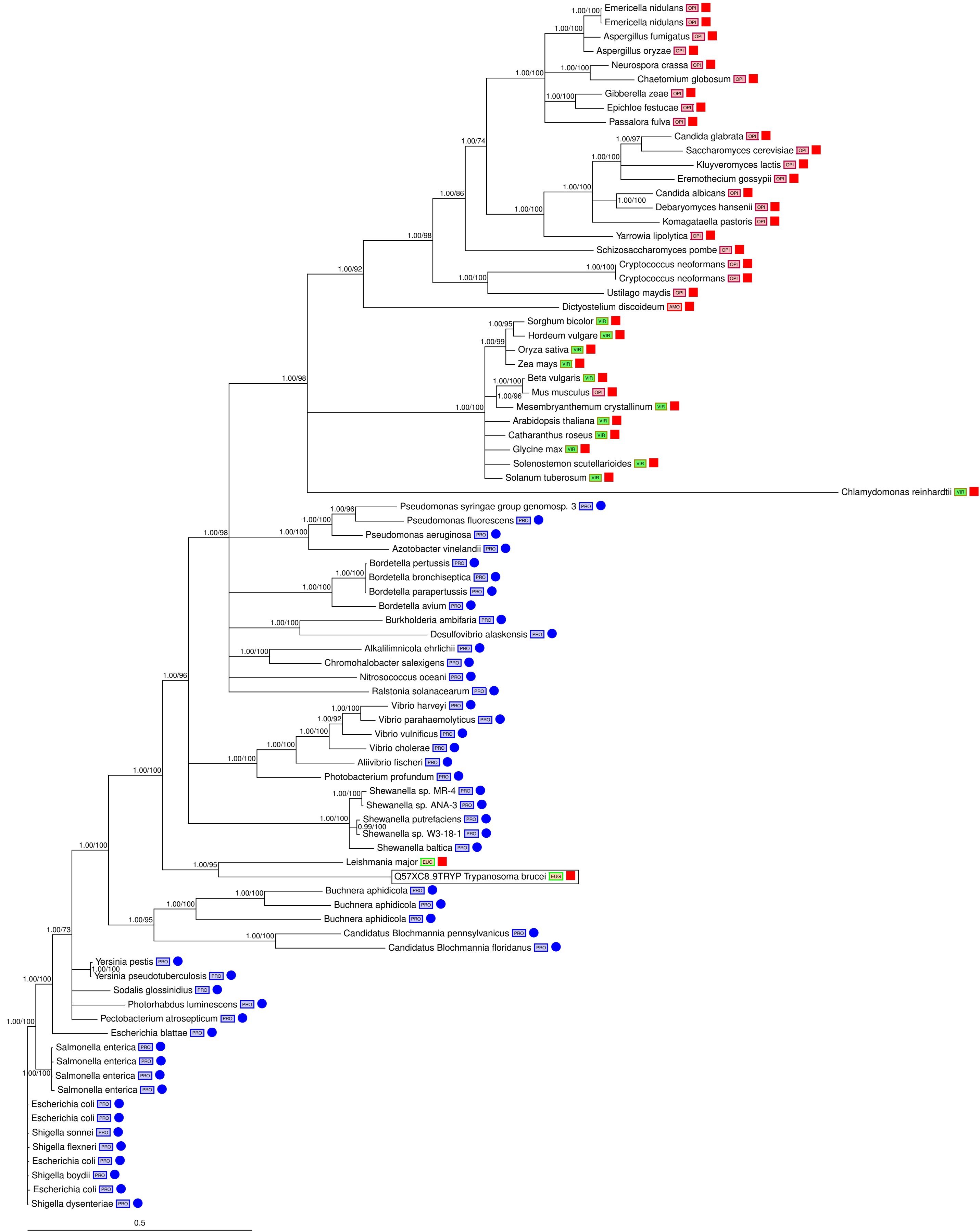
TN216

Candy accession: Q55DT1_DICDI
RefSeq accession: XP_646050.1
Uniprot accession: Q55DT1_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0269538
Name of enzyme/protein: Predicted NTF2-like protein
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



TN217

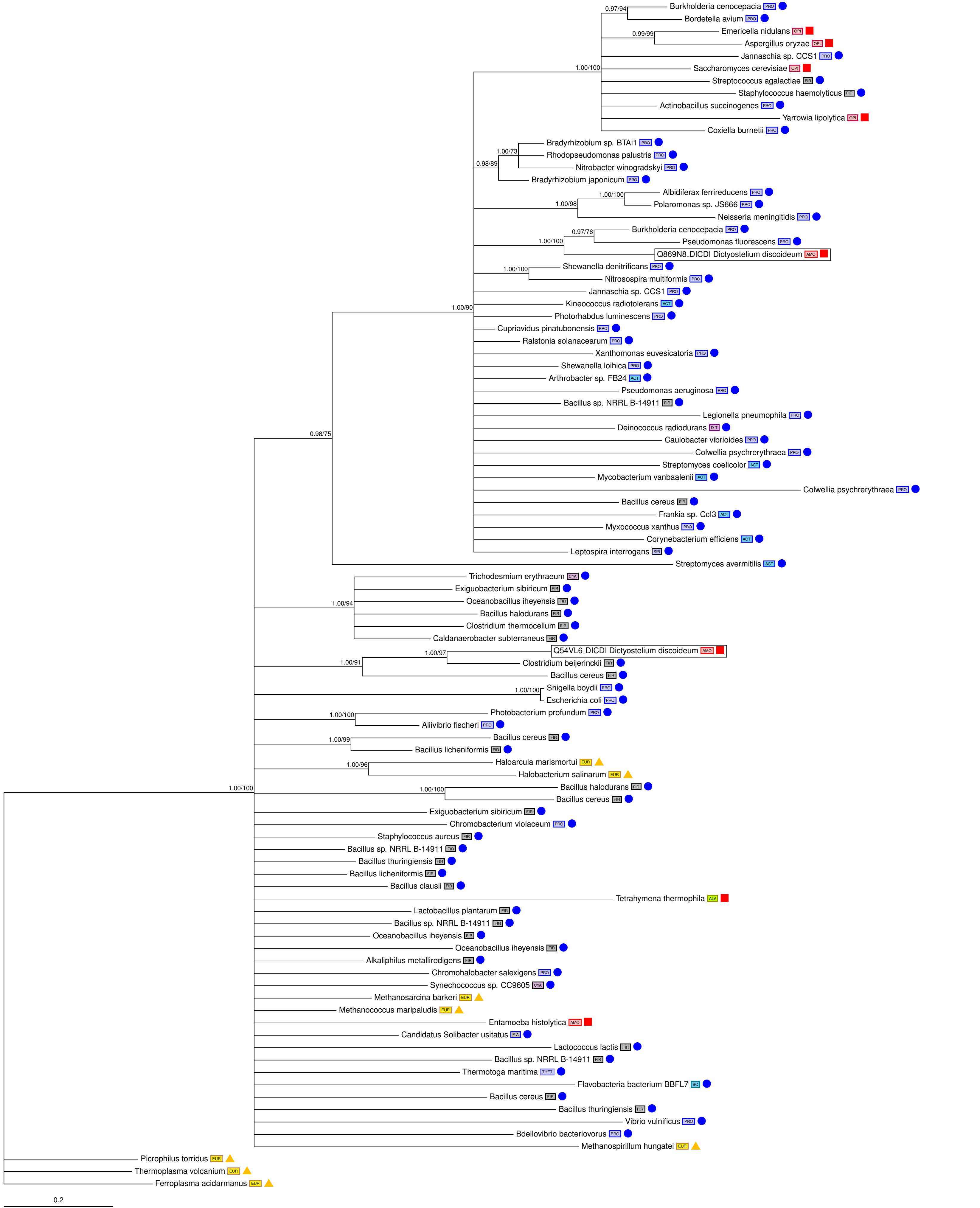
Candy accession: Q57XC8_9TRYP
RefSeq accession: XP_847094.1
Uniprot accession: Q57XC8_9TRYP
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM,TB
Adjacent taxa in tree: Protobacteria
EC annotation - (Blast/Profile): EC:2.1.1.14
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase
Name of enzyme/protein: 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Metabolism of Other Amino Acids
KEGG PATHWAY - level 2: Cysteine and methionine metabolism, Selenocompound metabolism



TN218

Candy accession: Q54VL6_DICDI
RefSeq accession: XP_641339.1
Uniprot accession: Q54VL6_DICDI
Comments: LGT - DD TWO NODES
Species affected: DD
Adjacent taxa in tree: Firmicutes - Clostridium
EC annotation - (Blast/Profile): EC:2.3.1.128
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0280265
Name of enzyme/protein: ribosomal-protein-alanine
N-acetyltransferase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction

Candy accession: Q869N8_DICDI
RefSeq accession: XP_645442.1
Uniprot accession: Q869N8_DICDI
Comments: LGT - DD TWO NODES
Species affected: DD
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:2.3.1.128
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0271854
Name of enzyme/protein: ribosomal-protein-alanine
N-acetyltransferase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction

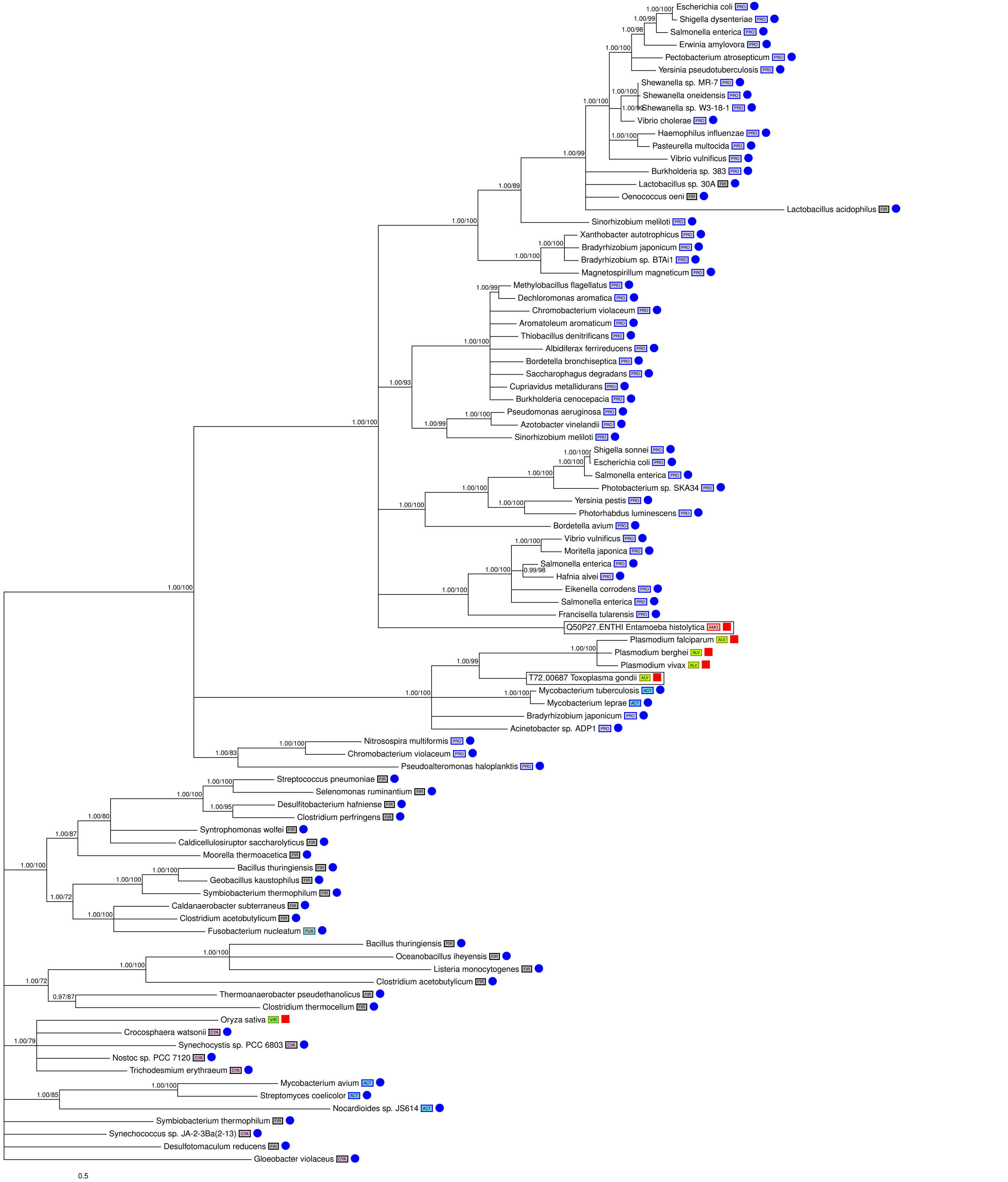


0.2

TN219

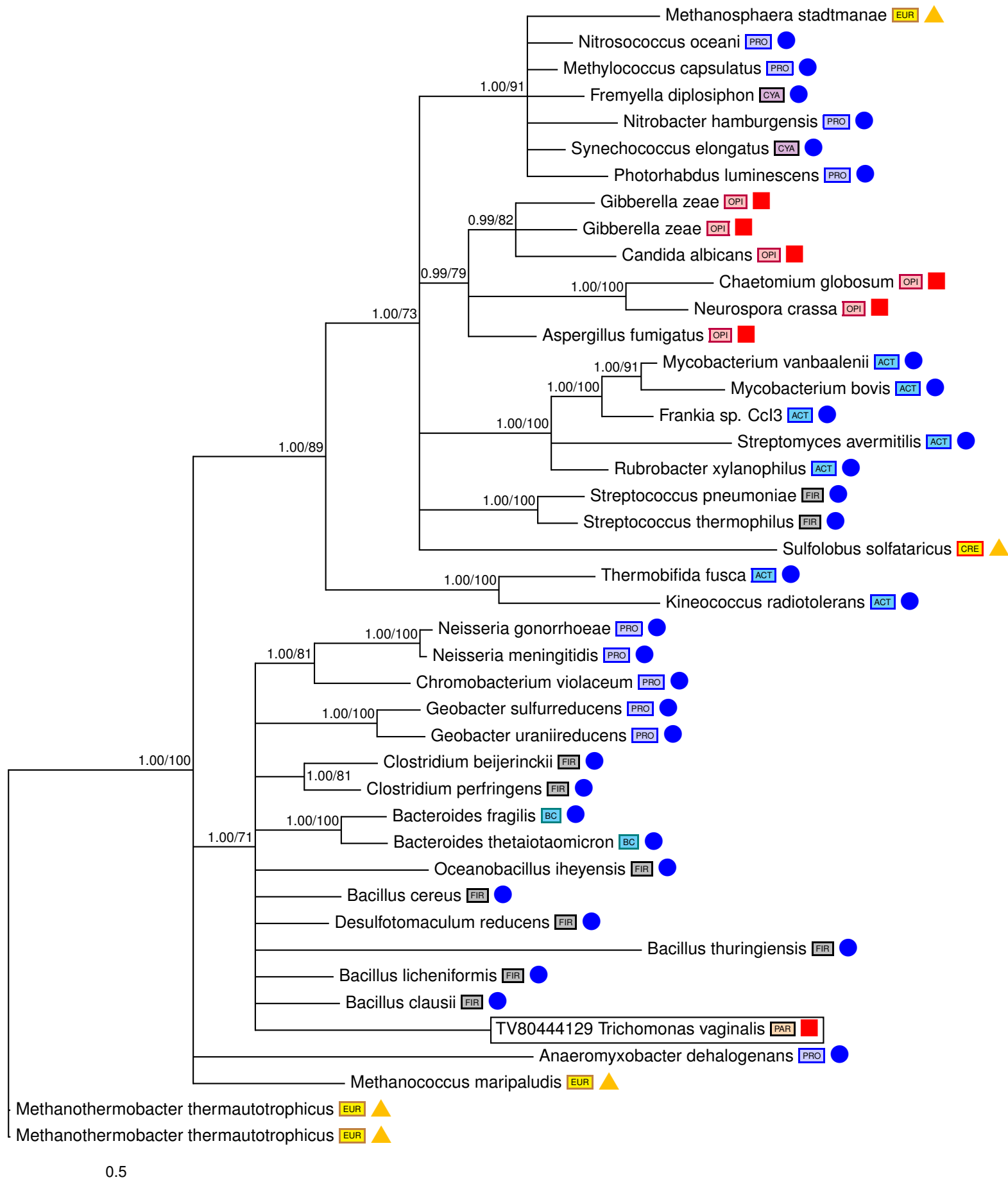
Candy accession: T72_00687
RefSeq accession: XP_002371464.1
Uniprot accession: B6KUE1_TOXGO
Comments: LGT - TG,PLASMODIUM TWO NODES, DEAP LGT INTO APICOMPLEXA
Species affected: PF,PV,TG
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:4.1.1.18
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: lysine decarboxylase, putative
Name of enzyme/protein: Lysine decarboxylase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Biosynthesis of Other Secondary Metabolites
KEGG PATHWAY - level 2: Lysine degradation, Tropane, piperidine and pyridine alkaloid biosynthesis

Candy accession: Q50P27_ENTHI
RefSeq accession: XP_648734.2
Uniprot accession: C4LXC0_ENTHI
Comments: LGT - TG,PLASMODIUM TWO NODES, DEAP LGT INTO APICOMPLEXA
Species affected: EH
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:4.1.1.18
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Orn/Arg/Lys decarboxylase
Name of enzyme/protein: Lysine decarboxylase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Biosynthesis of Other Secondary Metabolites
KEGG PATHWAY - level 2: Lysine degradation, Tropane, piperidine and pyridine alkaloid biosynthesis



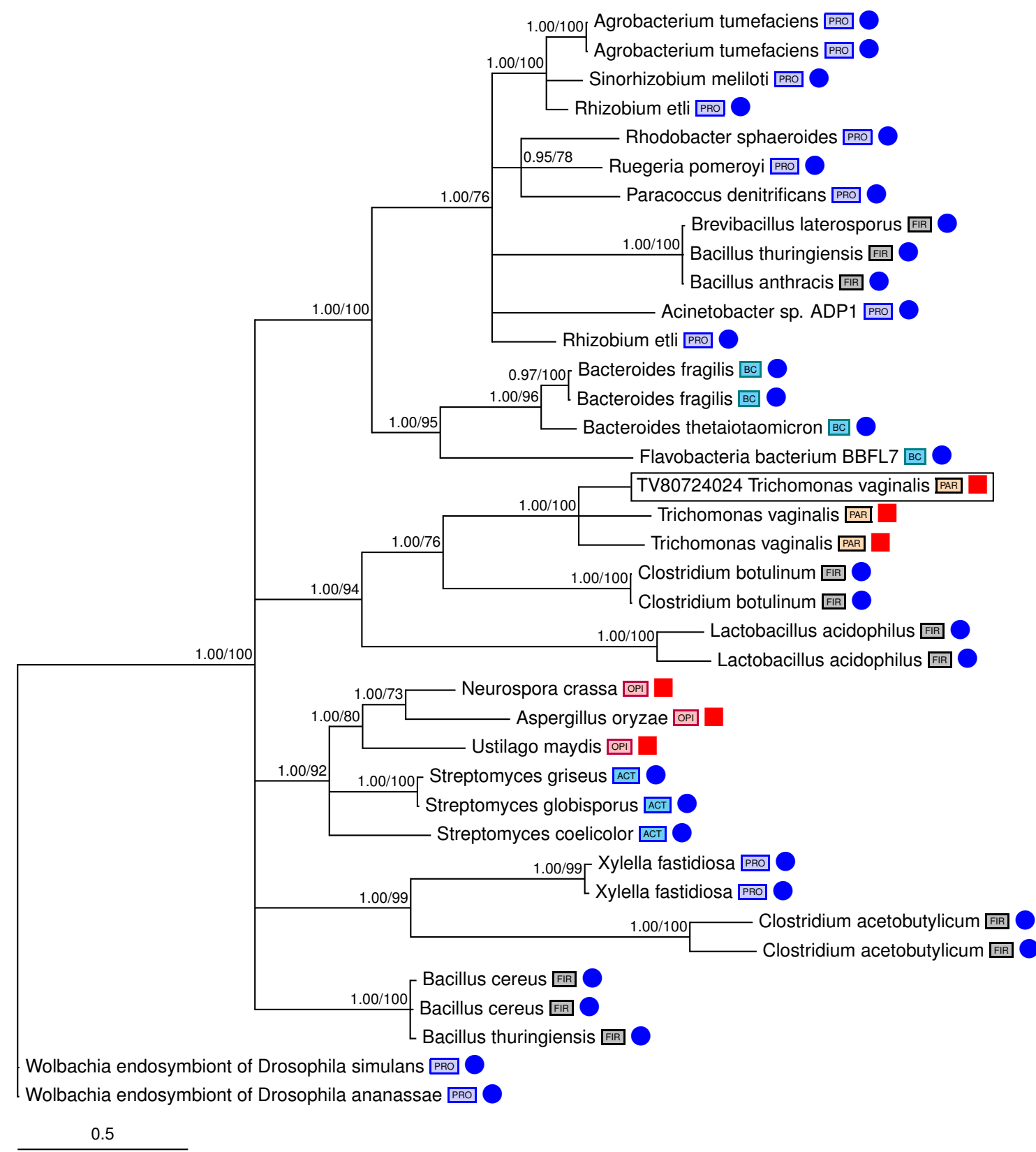
TN220

Candy accession: TV80444129
RefSeq accession: XP_001317907.1
Uniprot accession: A2ENQ8_TRIVA
Comments: LGT - TV TWO NODES + LGT INTO FUNGI
Species affected: TV, FUNGI
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:4.2.1.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Carbonic anhydrase family protein
Name of enzyme/protein: Carbonic anhydrase
KEGG PATHWAY - level 1: Energy Metabolism
KEGG PATHWAY - level 2: Nitrogen metabolism



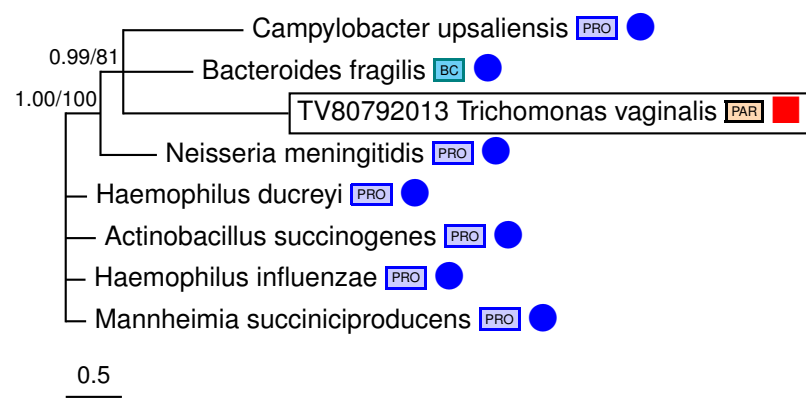
TN221

Candy accession: TV80724024
RefSeq accession: XP_001300299.1
Uniprot accession: A2G653-TRIVA
Comments: LGT - TV TWO NODES + LGT INTO FUNGI
Species affected: TV, FUNGI
Adjacent taxa in tree: Firmicutes - Clostridium
EC annotation - (Blast/Profile): EC:3.2.1.17
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glycosyl hydrolase
Name of enzyme/protein: lysozyme
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



TN222

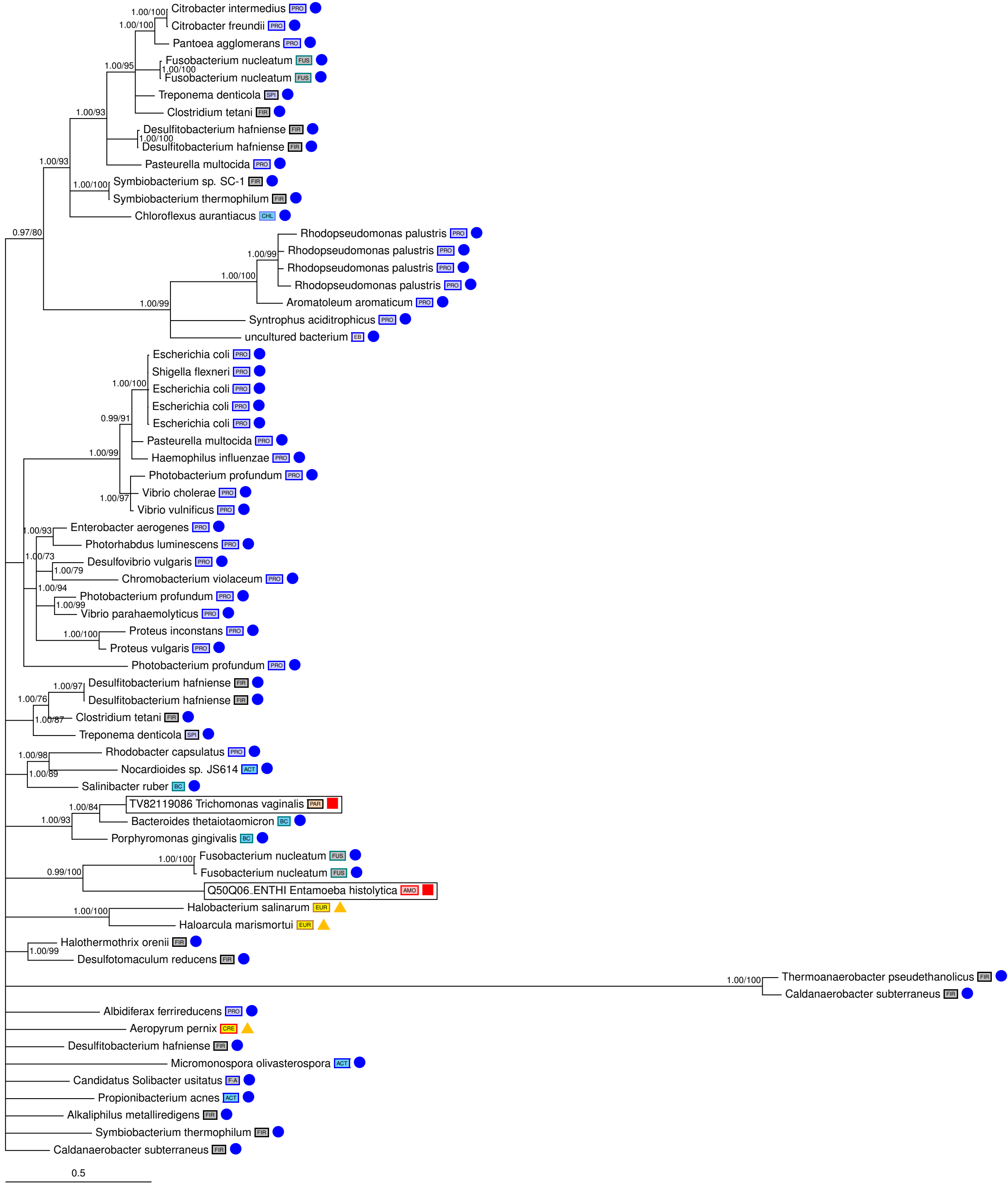
Candy accession: TV80792013
RefSeq accession: XP_001579050.1
Uniprot accession: A2DN76_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted DNA polymerase
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na



TN224

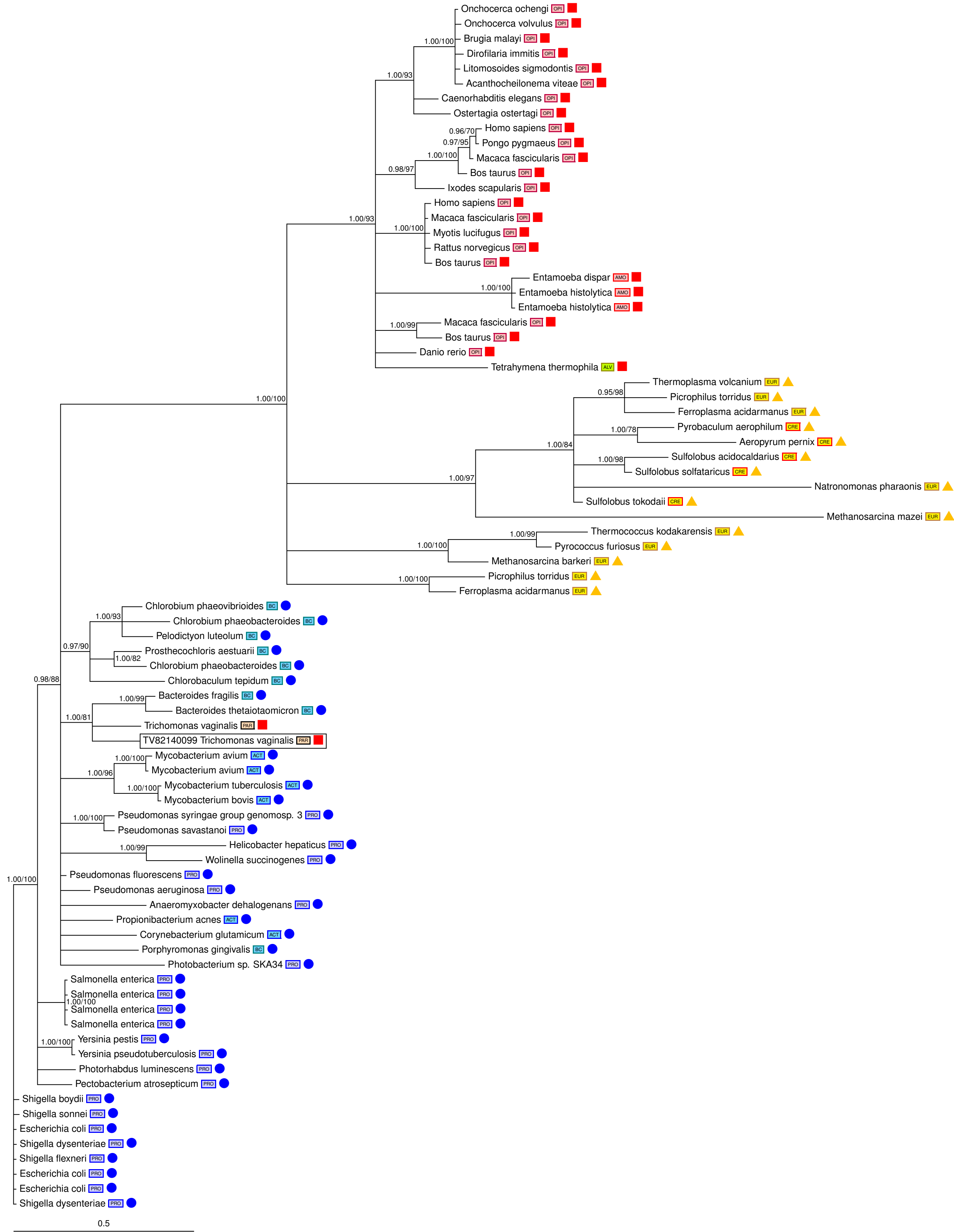
Candy accession: TV82119086
RefSeq accession: XP_001330618.1
Uniprot accession: BELY_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:4.1.99.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: beta-eliminating lyase
Name of enzyme/protein: tryptophanase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Energy metabolism
KEGG PATHWAY - level 2: Tryptophan metabolism, Nitrogen metabolism

Candy accession: Q50Q06_ENTHI
RefSeq accession: XP_649067.1
Uniprot accession: C4M571_ENTHI
Comments: LGT - EH TWO NODES
Species affected: EH
Adjacent taxa in tree: Fusobacteria - Fusobacterium
EC annotation - (Blast/Profile): EC:4.1.99.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: tryptophanase
Name of enzyme/protein: tryptophanase
KEGG PATHWAY - level 1: Amino Acid Metabolism, Energy metabolism
KEGG PATHWAY - level 2: Tryptophan metabolism, Nitrogen metabolism



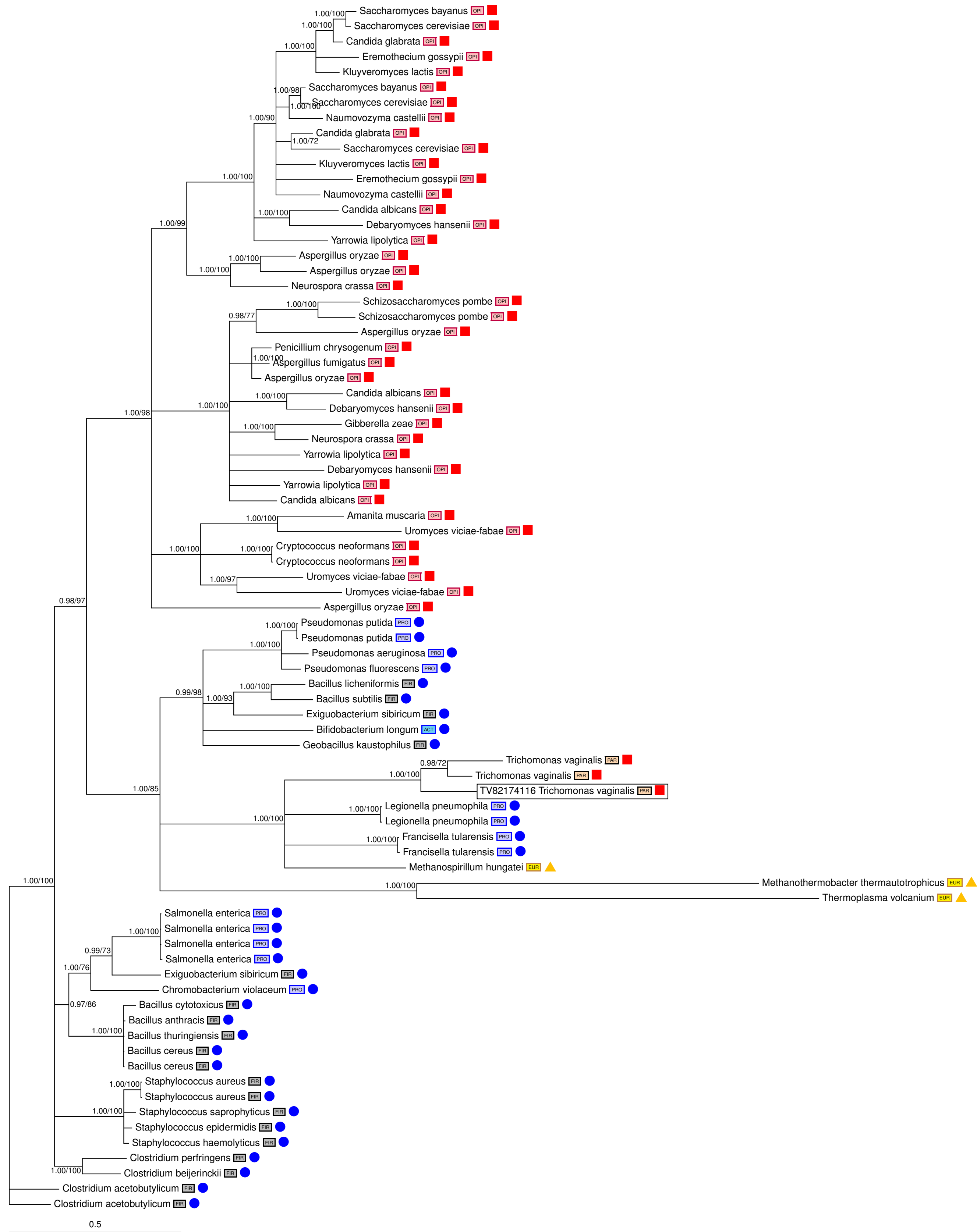
TN225

Candy accession: TV82140099
RefSeq accession: XP_001316257.1
Uniprot accession: A2ETI8_TRIVA
Comments: LGT - TV TWO NODES - 3 DOMAIN ToL
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:1.11.1.15
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: thiol peroxidase
Name of enzyme/protein: Thiol peroxidase
KEGG PATHWAY - level 1: Metabolism of Other Amino Acids
KEGG PATHWAY - level 2: Glutathione metabolism



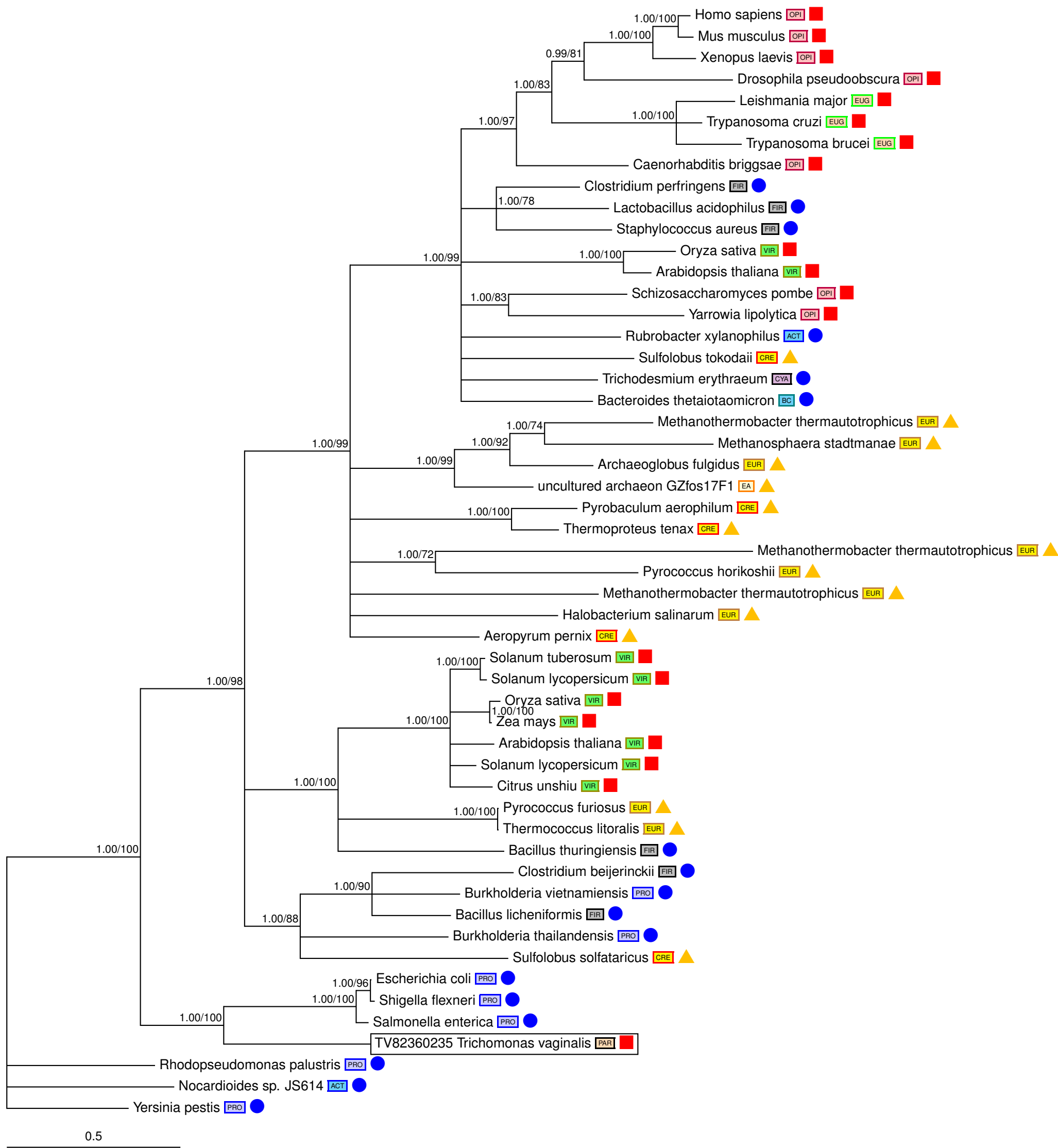
TN226

Candy accession: TV82174116
 RefSeq accession: XP_001318849.1
 Uniprot accession: A2EL73_TR1VA
 Comments: LGT - TV TWO NODES - DEAP LGT INTO FUNGI?
 Species affected: TV
 Adjacent taxa in tree: Prokaryotes
 EC annotation - (Blast/Profile): na
 PHOBIUS SP: 0
 PHOBIUS TMD: 12
 RefSeq annotation: Amino acid permease family protein
 Name of enzyme/protein: Amino acid permease family protein
 KEGG PATHWAY - level 1: Other function - Membrane transport
 KEGG PATHWAY - level 2: na



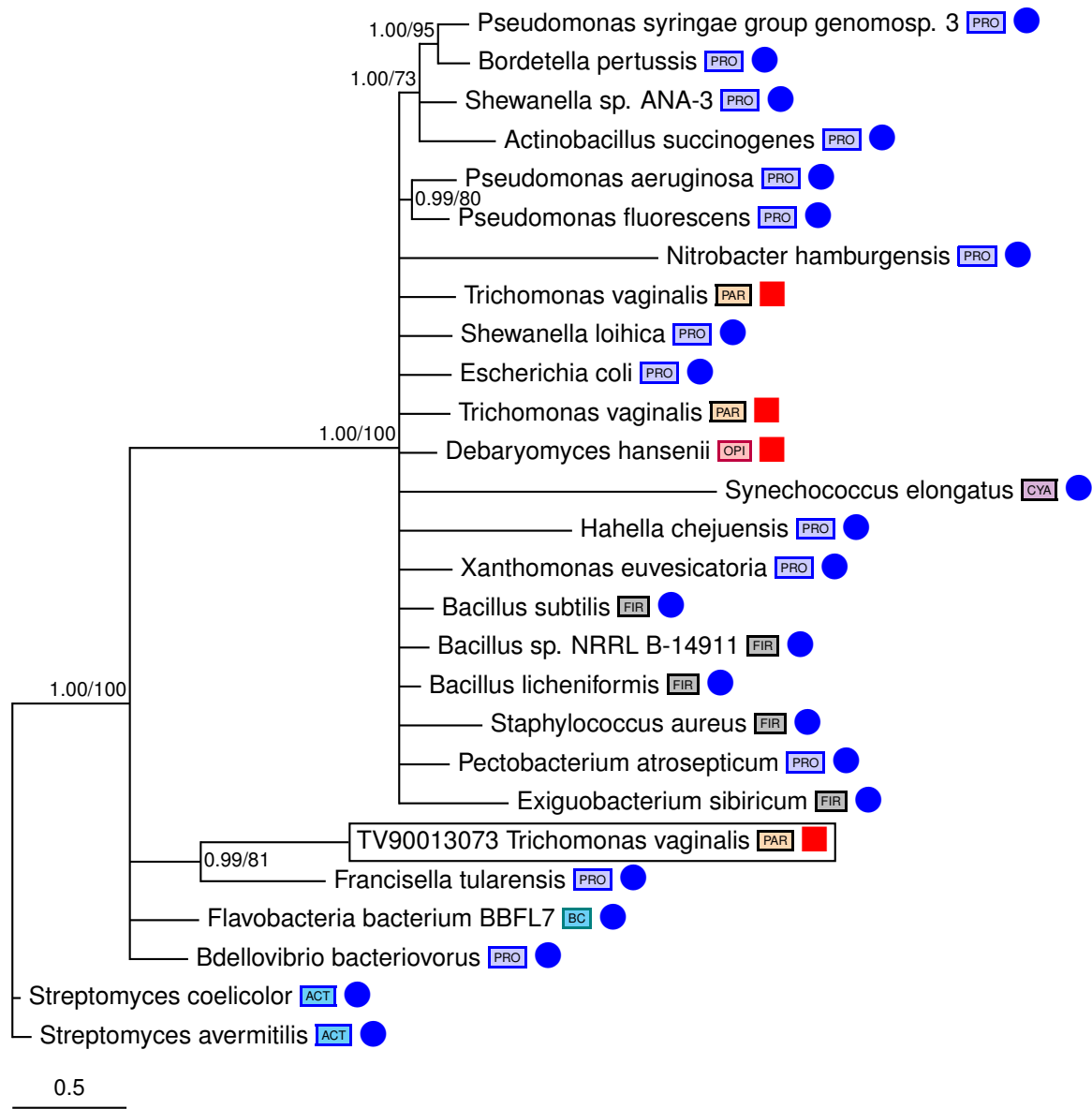
TN227

Candy accession: TV82360235
 RefSeq accession: XP_001579672.1
 Uniprot accession: A2DLQ3_TRIVA
 Comments: LGT - TV TWO NODES
 Species affected: TV
 Adjacent taxa in tree: *Proteobacteria*
 EC annotation - (Blast/Profile): EC:2.7.1.15
 PHOBUS SP: 0
 PHOBUS TMD: 0
 RefSeq annotation: kinase, pfkB family protein
 Name of enzyme/protein: ribokinase
 KEGG PATHWAY - level 1: Carbohydrate Metabolism
 KEGG PATHWAY - level 2: Pentose phosphate pathway



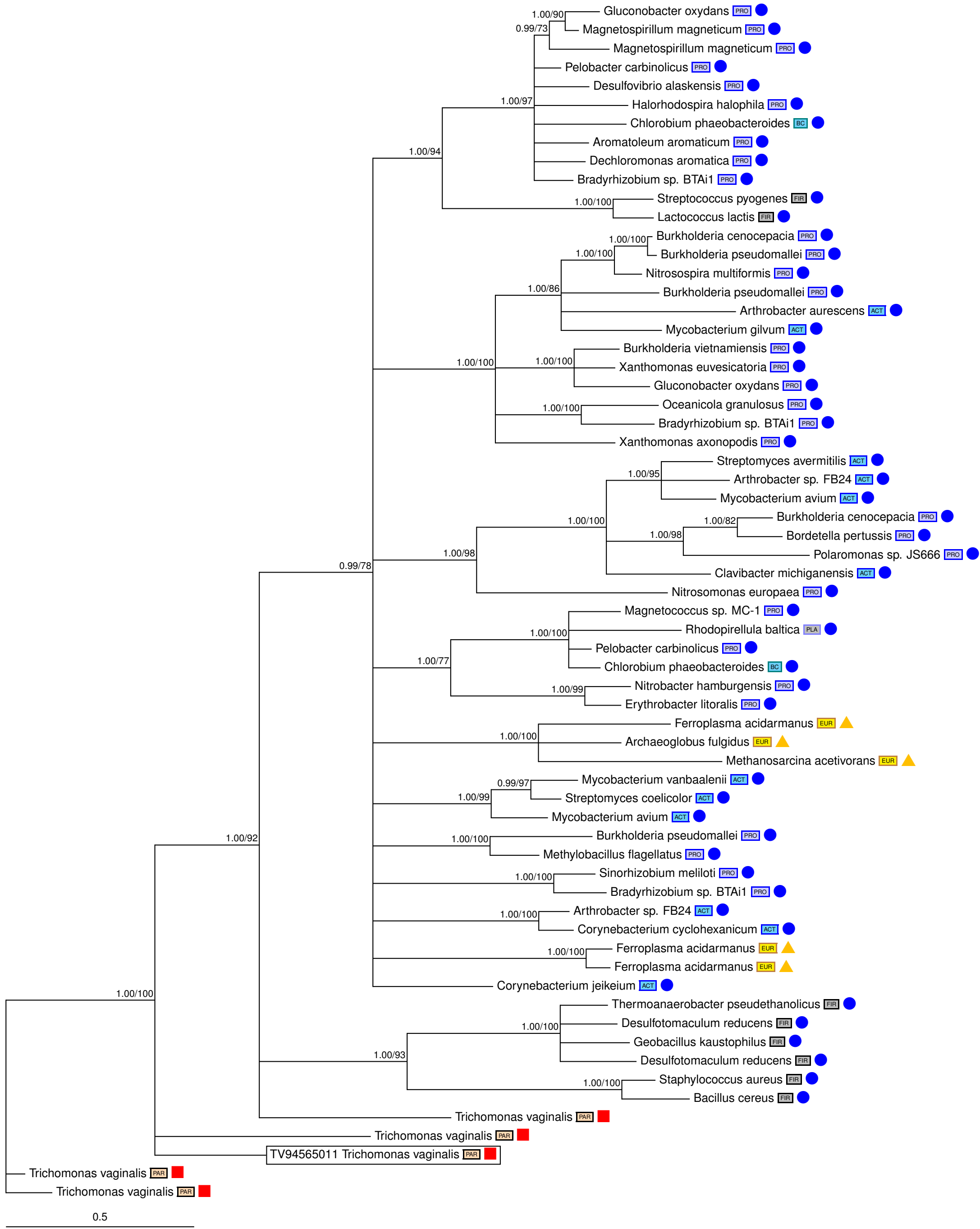
TN228

Candy accession: TV90013073
RefSeq accession: XP_001313313.1
Uniprot accession: A2F3W8_TRIVA
Comments: LGT - TV TWO NODES + ONE FUNGI
Species affected: TV
Adjacent taxa in tree: Proteobacteria - Francisella
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Zn-dependent hydrolase of beta-lactamase
Name of enzyme/protein: Zn-dependent hydrolase of beta-lactamase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



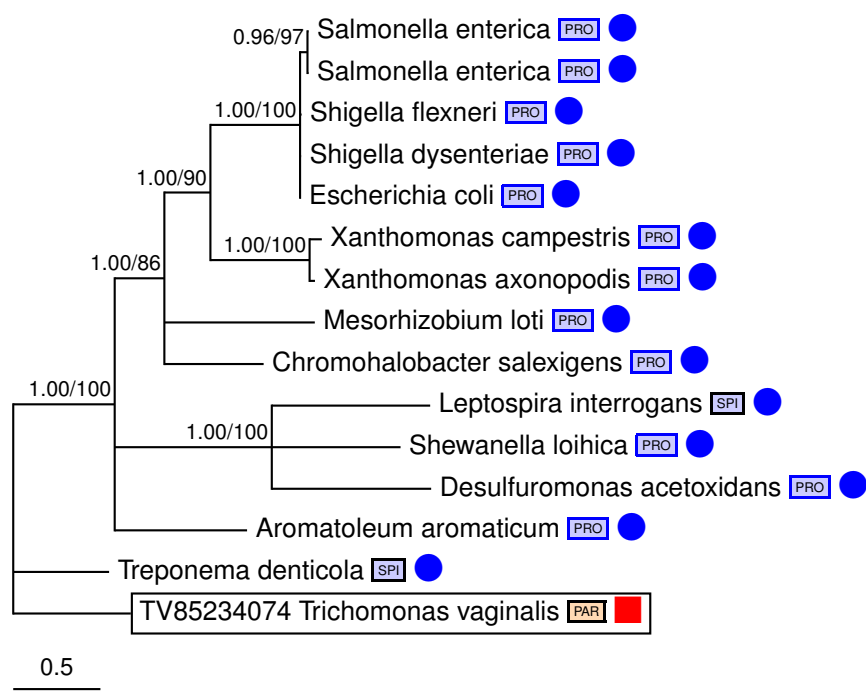
TN229

Candy accession: TV94565011
RefSeq accession: XP_001301668.1
Uniprot accession: A2G280_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Integrase core domain containing protein
Name of enzyme/protein: Putative transposase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



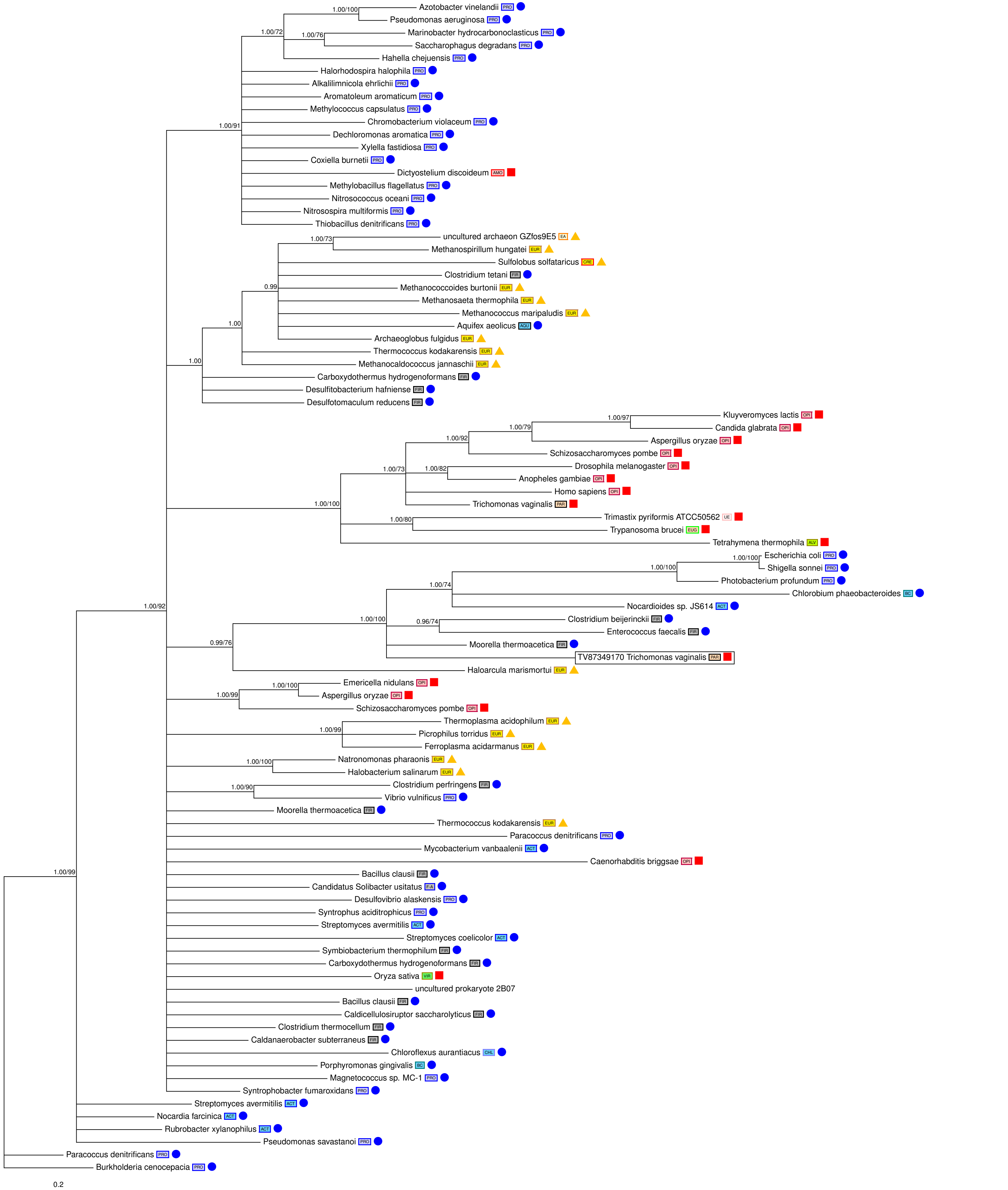
TN230

Candy accession: TV85234074
RefSeq accession: XP_001311801.1
Uniprot accession: A2F8B1_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Spirochaetes - Treponema
EC annotation - (Blast/Profile): EC:2.7.8.20
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Phosphoglycerol transferase I
KEGG PATHWAY - level 1: Lipid Metabolism
KEGG PATHWAY - level 2: Glycerolipid metabolism



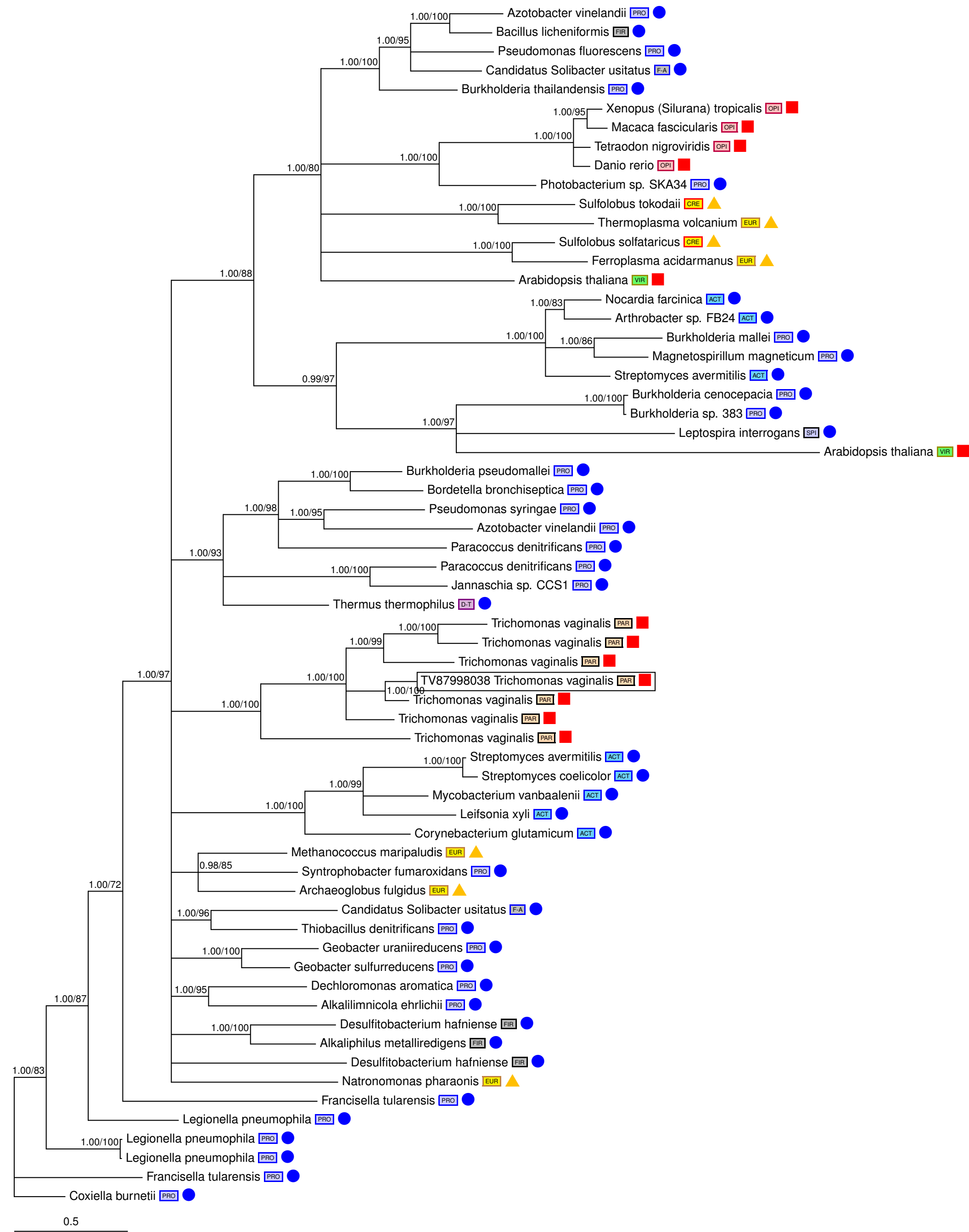
TN232

Candy accession: TV87349170
RefSeq accession: XP_001318930.1
Uniprot accession: A2EKZ9_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.8.1.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Amidohydrolase family protein
Name of enzyme/protein: Hydrolases (Putative
chlorohydrolase/aminohydrolase)
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



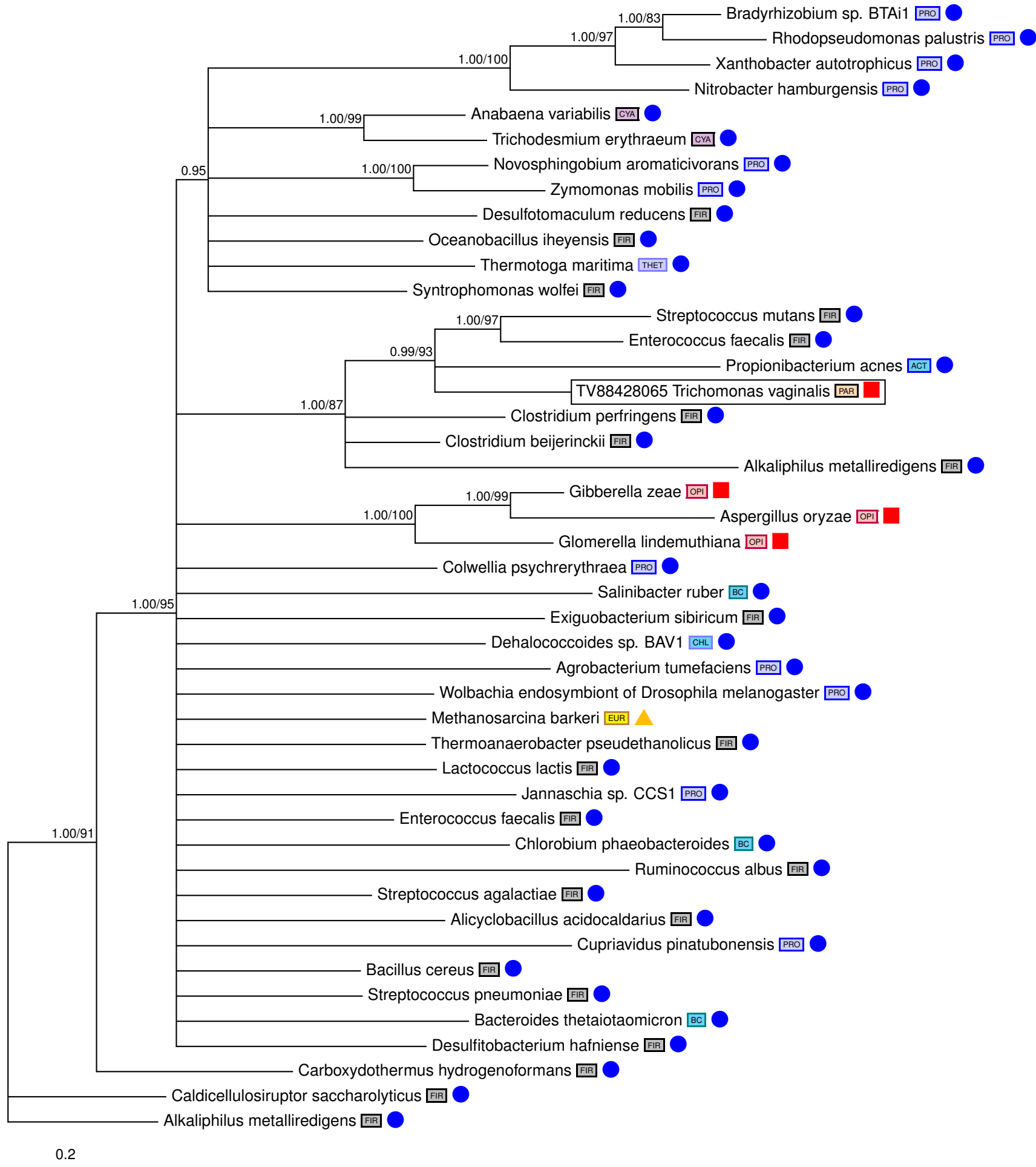
TN233

Candy accession: TV87998038
RefSeq accession: XP_001302090.1
Uniprot accession: A2G102.TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 11
RefSeq annotation: major facilitator superfamily
transporter
Name of enzyme/protein: major facilitator superfamily
transporter
KEGG PATHWAY - level 1: Other function - Membrane transport
KEGG PATHWAY - level 2: na



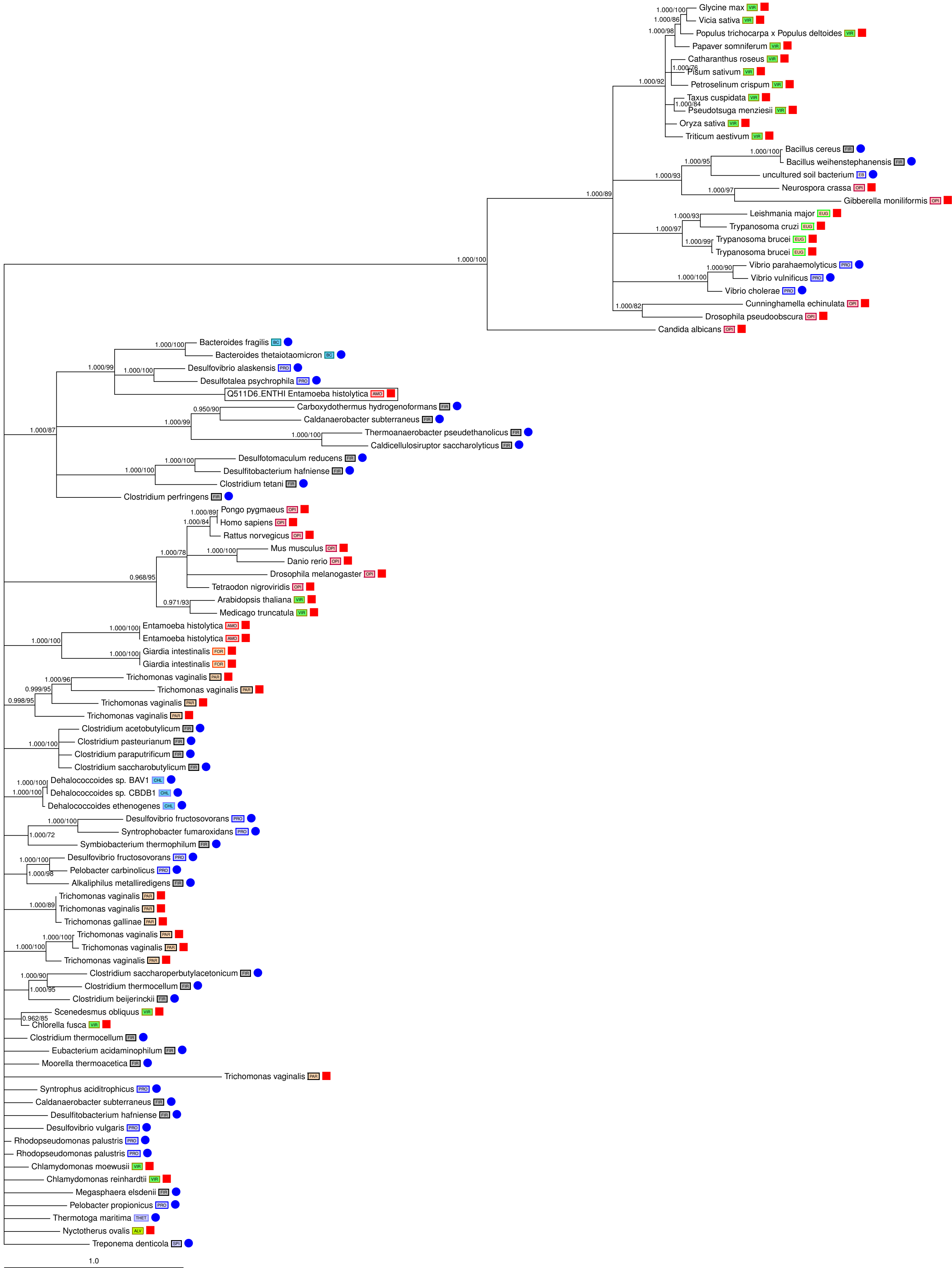
TN234

Candy accession: TV88428065
RefSeq accession: XP_001307943.1
Uniprot accession: A2FJ99_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV, FUNGI
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.5.1.41
PHOBIUS SP: 0
PHOBIUS TMD: 1
RefSeq annotation: Polysaccharide deacetylase family protein
Name of enzyme/protein: Chitin deacetylase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Amino sugar and nucleotide sugar metabolism

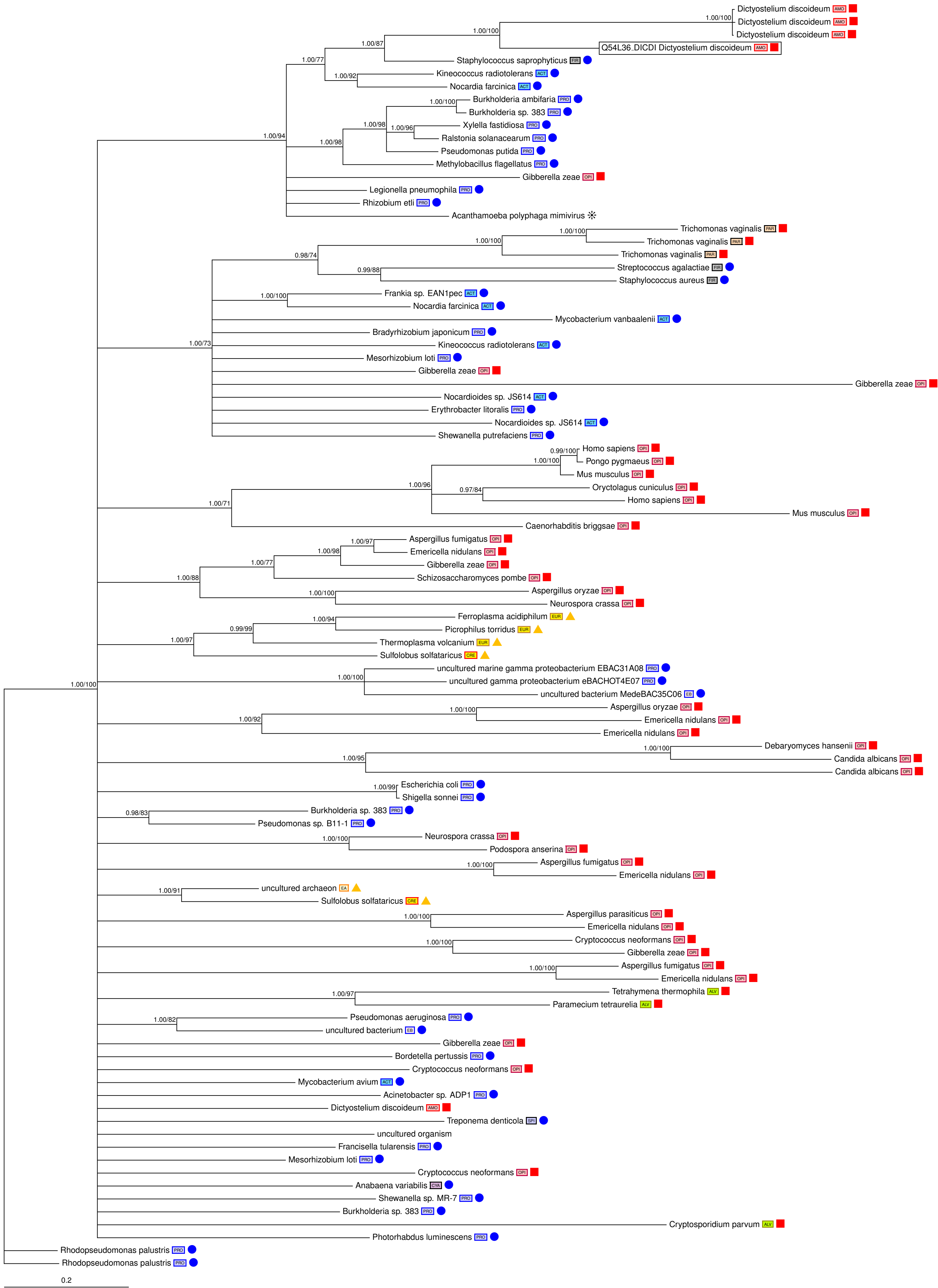


TN235

Candy accession: Q511D6_ENTHI
RefSeq accession: XP_652839.1
Uniprot accession: Q869B1_ENTHI
Comments: LGT - EH TWO NODES
Species affected: EH
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:1.12.7.2
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Fe-hydrogenase
Name of enzyme/protein: ferredoxin hydrogenase
KEGG PATHWAY - level 1: Energy Metabolism
KEGG PATHWAY - level 2: Methane metabolism



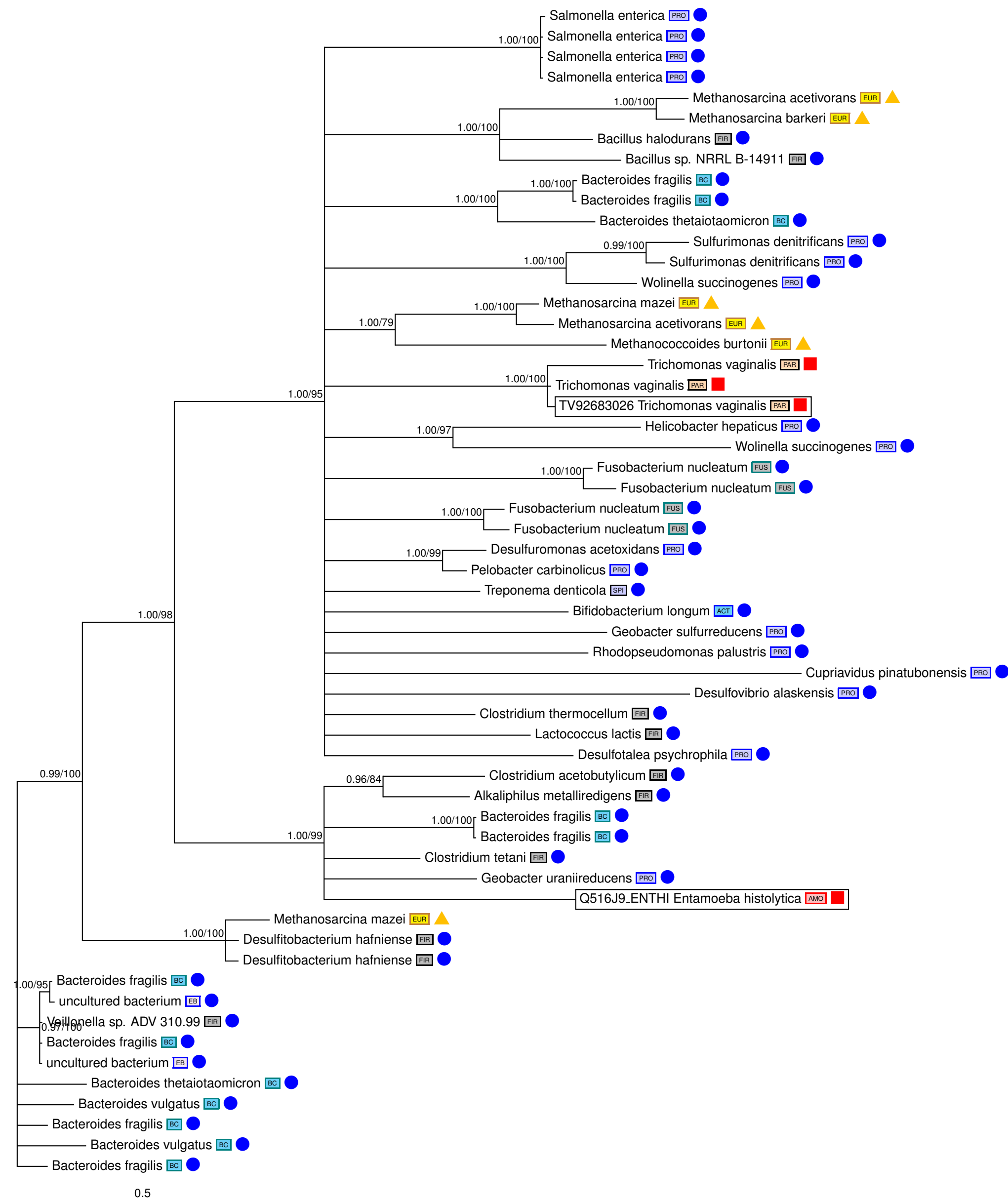
Candy accession: Q54L36_DICDI
RefSeq accession: XP_637467.1
Uniprot accession: Q54L36_DICDI
Comments: LGT - DD TWO NODES
Species affected: DD
Adjacent taxa in tree: Firmicutes - Staphylococcus
EC annotation - (Blast/Profile): EC:3.1.1.3
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: esterase/lipase/thioesterase domain-containing protein
Name of enzyme/protein: triacylglycerol lipase
KEGG PATHWAY - level 1: Lipid Metabolism
KEGG PATHWAY - level 2: Glycerolipid metabolism



TN237

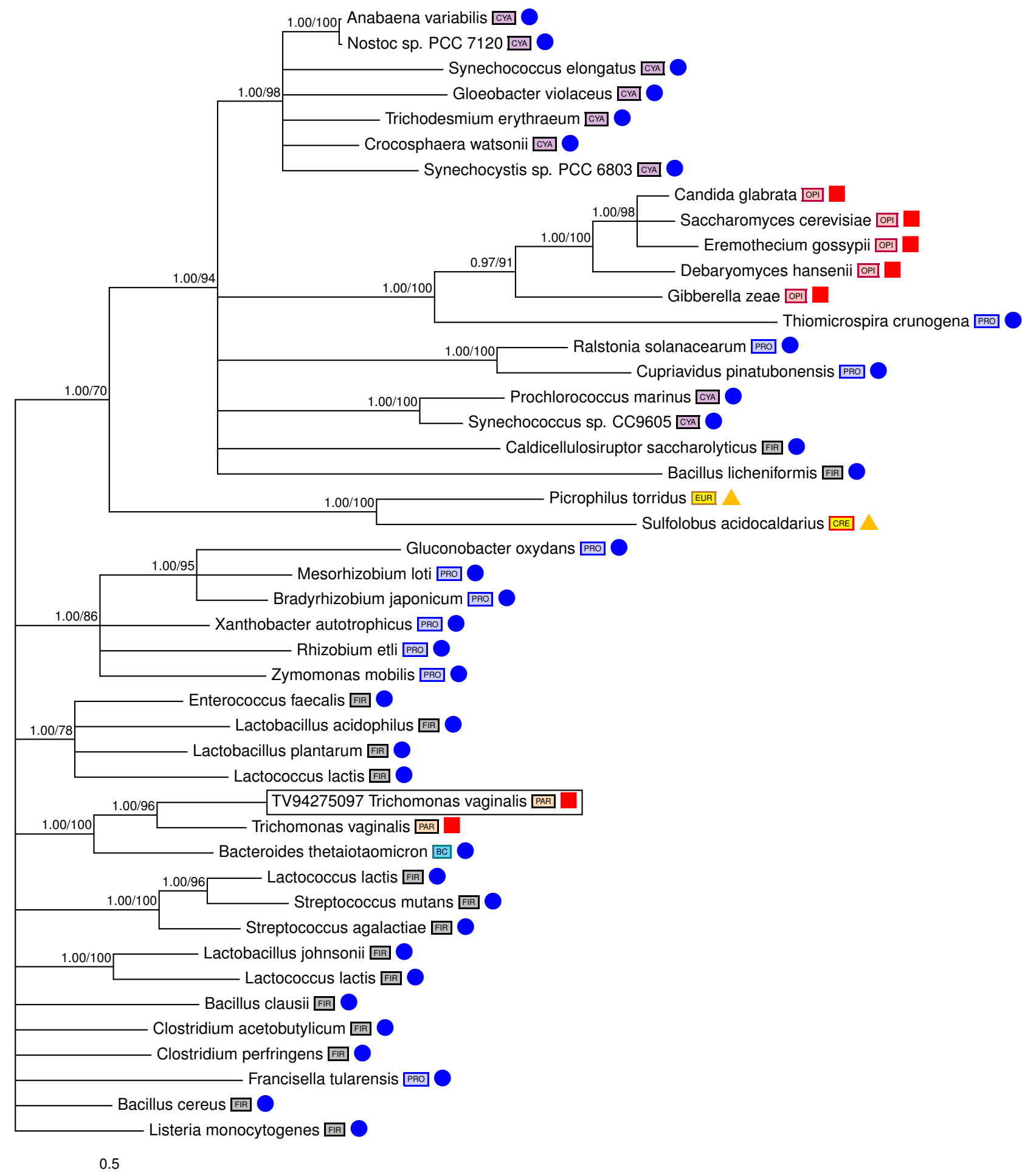
Candy accession: TV92683026
RefSeq accession: XP_001302496.1
Uniprot accession: A2FZU4_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: nitroimidazole resistance protein
Name of enzyme/protein: Predicted flavin-nucleotide-binding protein/5-nitroimidazole antibiotic resistance protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

Candy accession: Q516J9_ENTHI
RefSeq accession: XP_654156.2
Uniprot accession: C4LU35_ENTHI
Comments: LGT - EH TWO NODES
Species affected: EH
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: 5-nitroimidazole antibiotic resistance protein
Name of enzyme/protein: Predicted flavin-nucleotide-binding protein/5-nitroimidazole antibiotic resistance protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



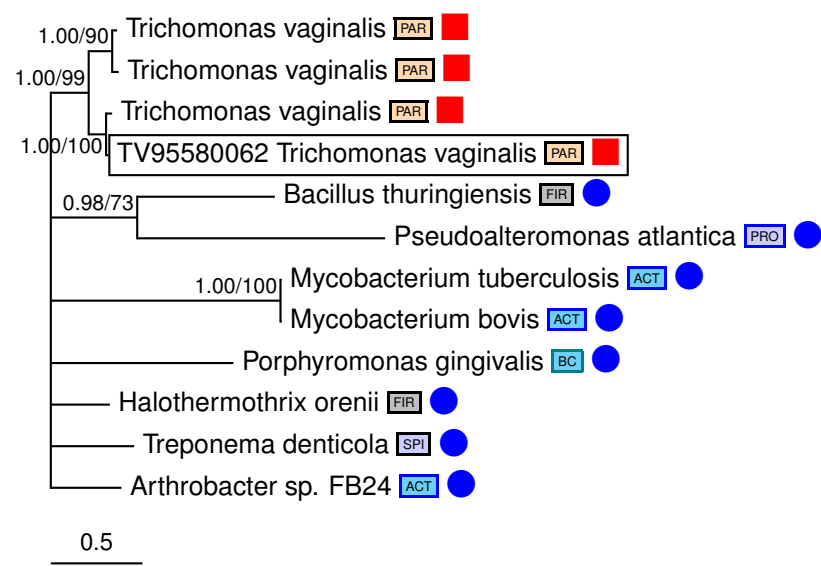
TN238

Candy accession: TV94275097
RefSeq accession: XP_001313279.1
Uniprot accession: A2F3Z6_TRIVA
Comments: LGT - TV TWO NODES + LGT INTO FUNGI
Species affected: TV,FUNGI
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:5.1.3.3
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: Aldose 1-epimerase family protein
Name of enzyme/protein: Aldose 1-epimerase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Glycolysis / Gluconeogenesis



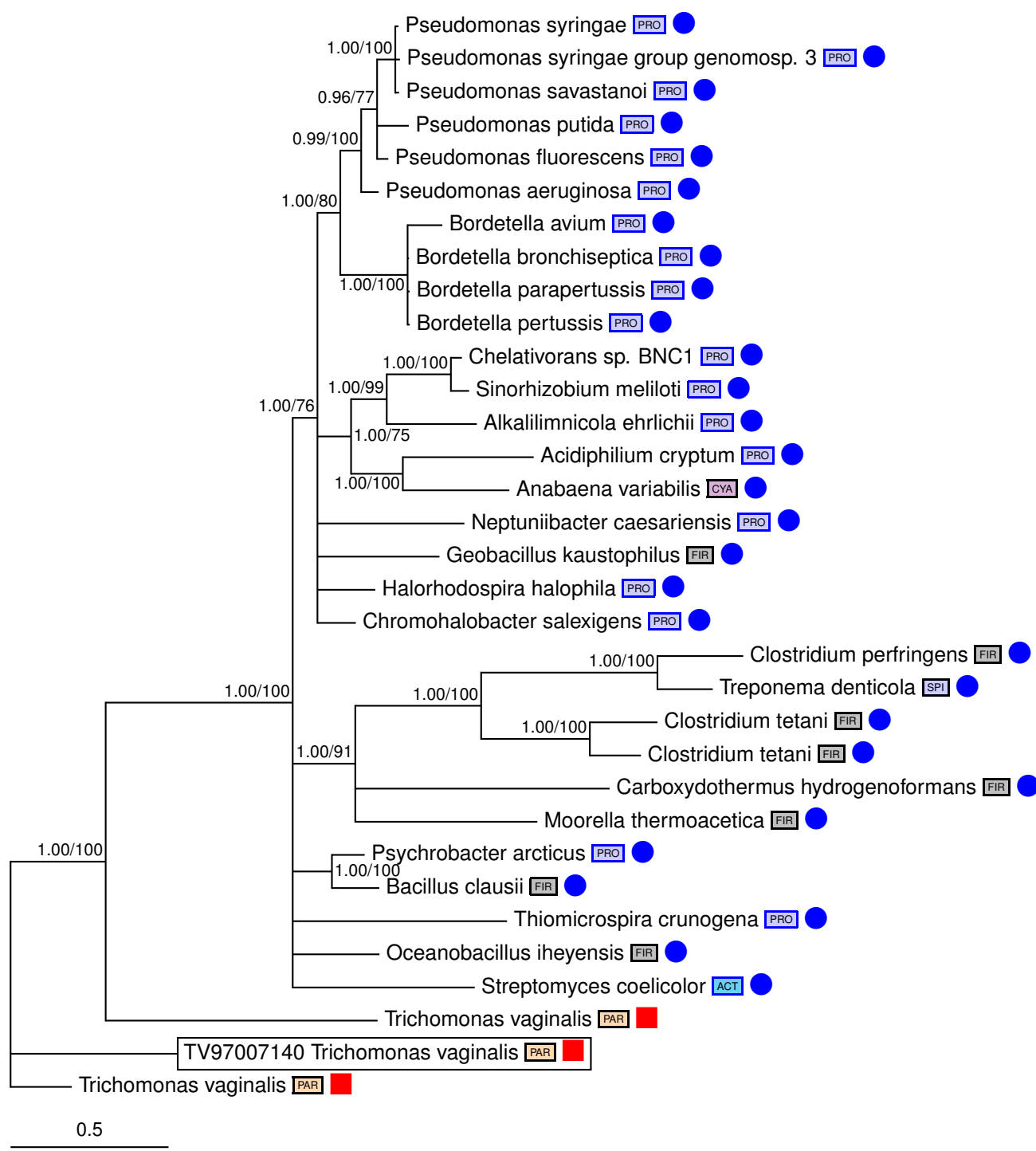
TN239

Candy accession: TV95580062
RefSeq accession: XP_001305004.1
Uniprot accession: A2FSP3_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:5.1.3.2
PHOBIUS SP: 0
PHOBIUS TMD: 1
RefSeq annotation: hypothetical protein
Name of enzyme/protein: UDP-glucose 4-epimerase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Galactose metabolism, Amino sugar and nucleotide sugar metabolism



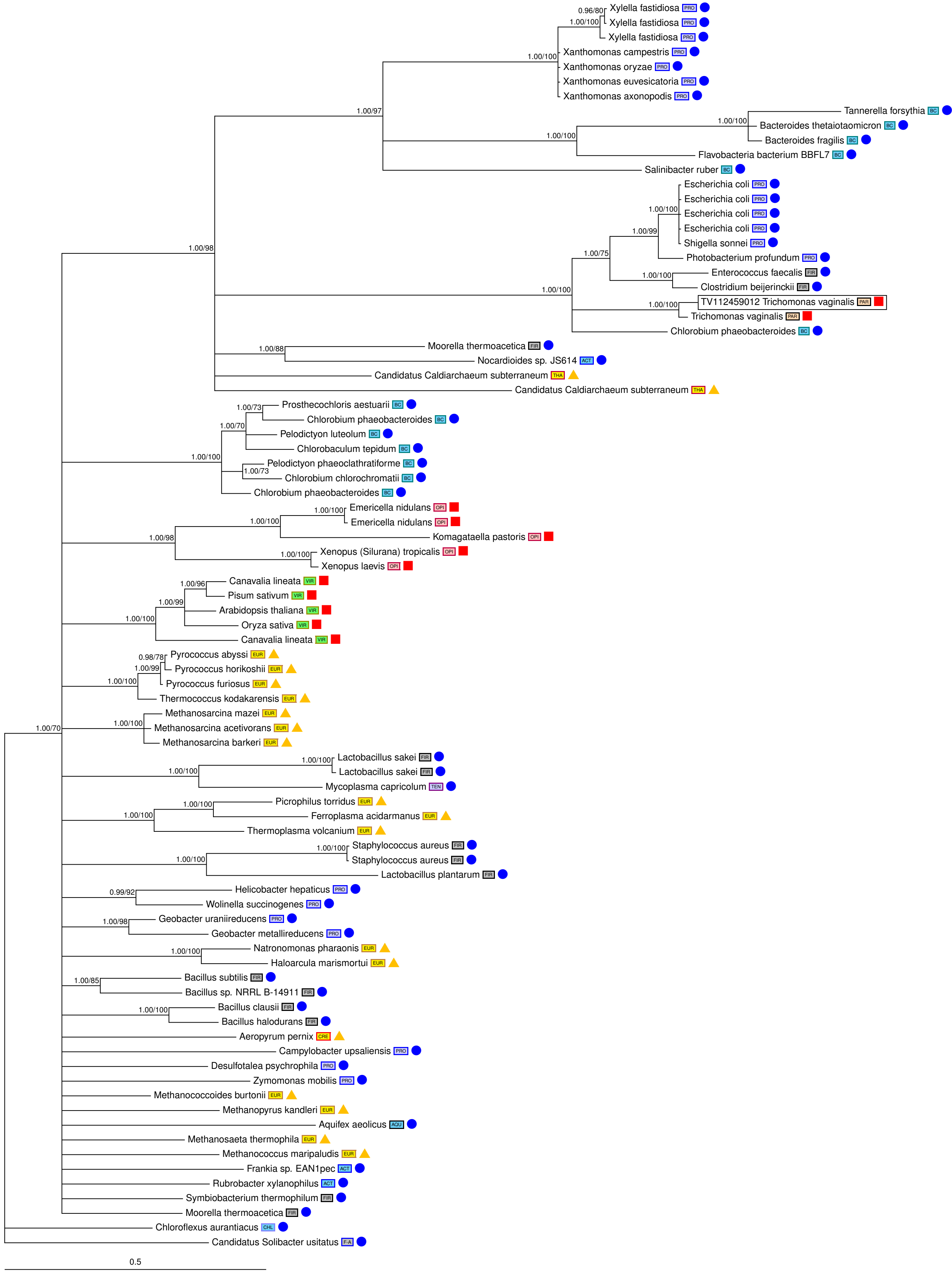
TN240

Candy accession: TV97007140
RefSeq accession: XP_001322711.1
Uniprot accession: A2EA42_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 10
RefSeq annotation: YeeE/YedE family protein
Name of enzyme/protein: YeeE/YedE family protein
KEGG PATHWAY - level 1: Other function - Membrane transport
KEGG PATHWAY - level 2: na



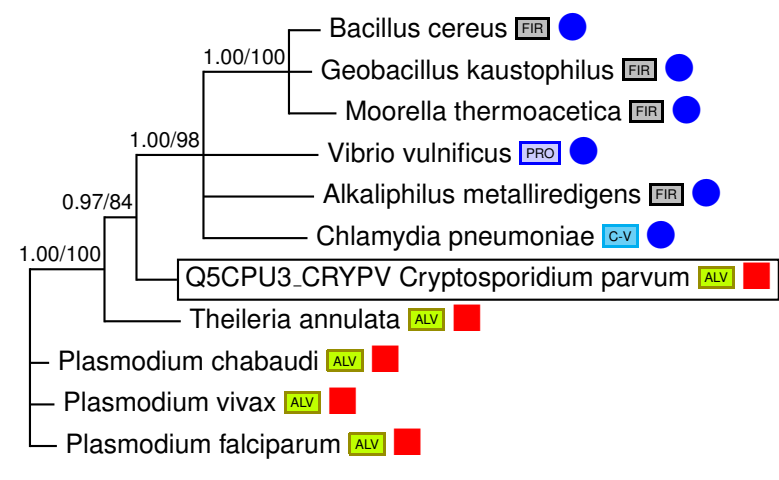
TN241

Candy accession: TV112459012
RefSeq accession: XP_001298741.1
Uniprot accession: A2GAK7_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.1.3.9
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: N-acetylornithine carbamoyltransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism



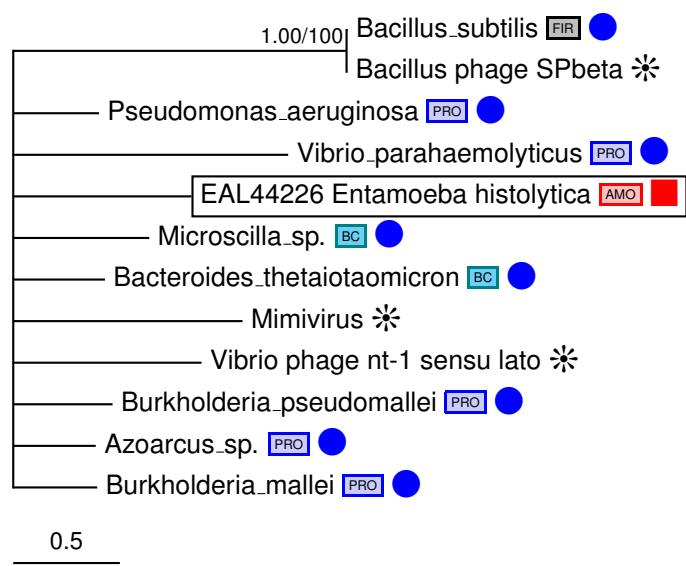
TN242

Candy accession: Q5CPU3_CRYPV
RefSeq accession: XP_625421.1
Uniprot accession: Q5CPU3_CRYPV
Comments: LGT - DEEP LGT INTO APICOMPLEXA
Species affected: CP,TA,PF,PC,PV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.3.1.88
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: possible ribosomal-protein-alanine
acetyltransferase
Name of enzyme/protein: Predicted acetyltransferase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



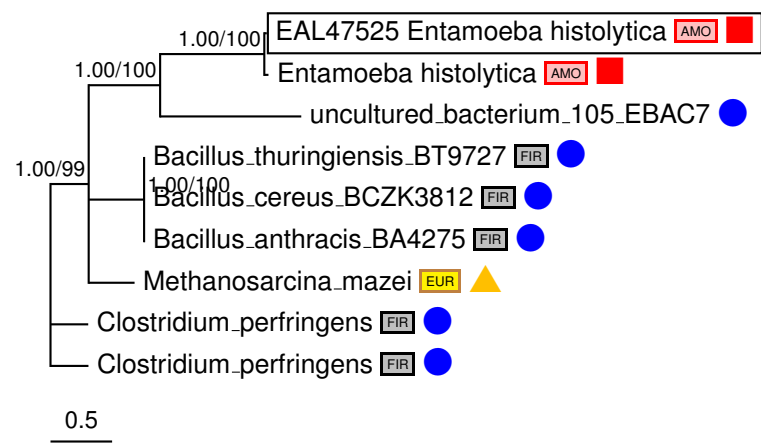
TN243

Candy accession: EAL44226
RefSeq accession: XP_649612.1
Uniprot accession: C4M2R8_ENTHI
Comments: LGT - EH ONLY + MINIVIRUS + PHAGES
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: ser/thr protein phosphatase family protein
Name of enzyme/protein: Protein containing metallophosphatase domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



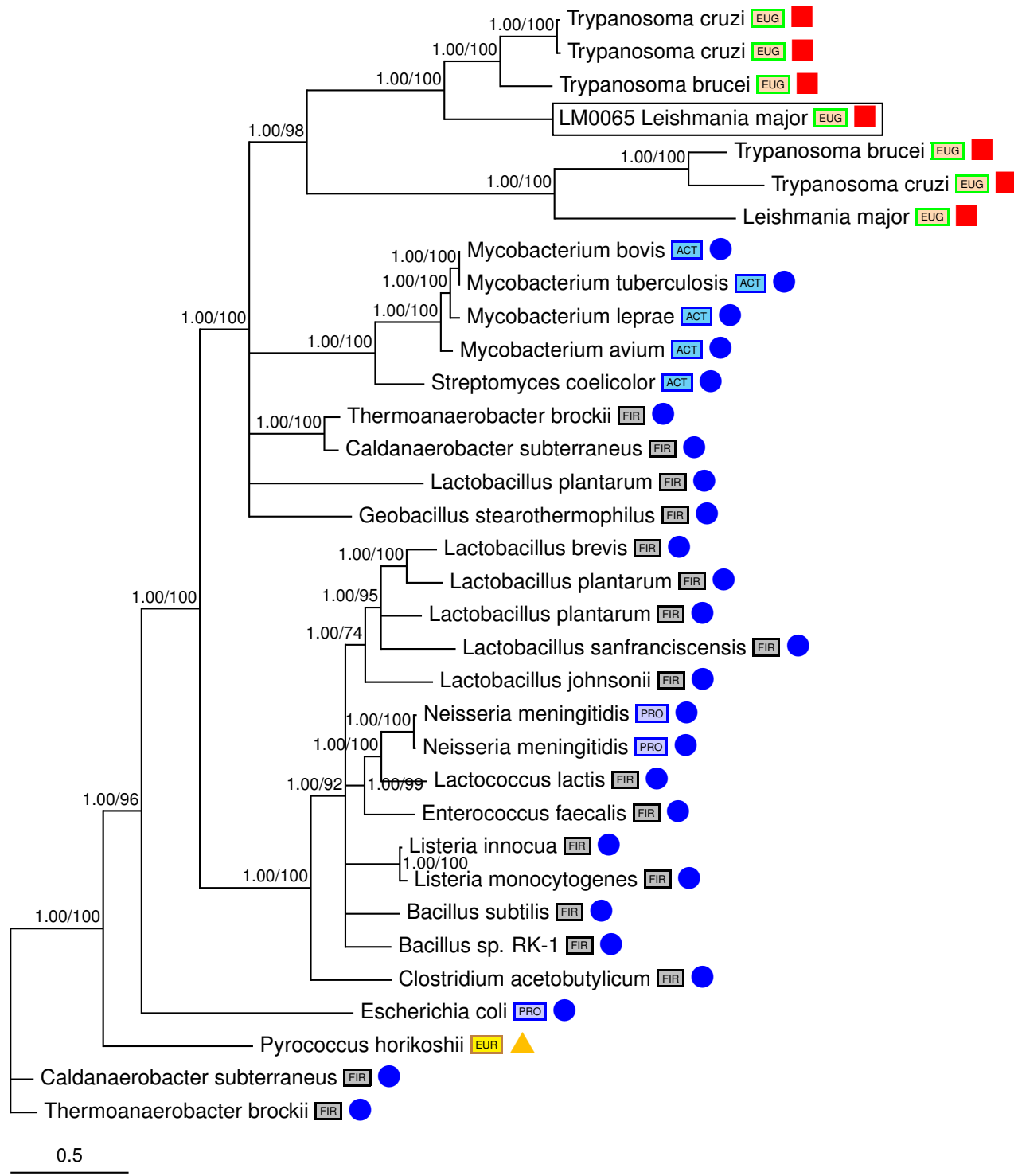
TN244

Candy accession: EAL47525
RefSeq accession: XP_652912.1
Uniprot accession: C4M4C4_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: competence protein ComEC
Name of enzyme/protein: Predicted lactamase B superafamily
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



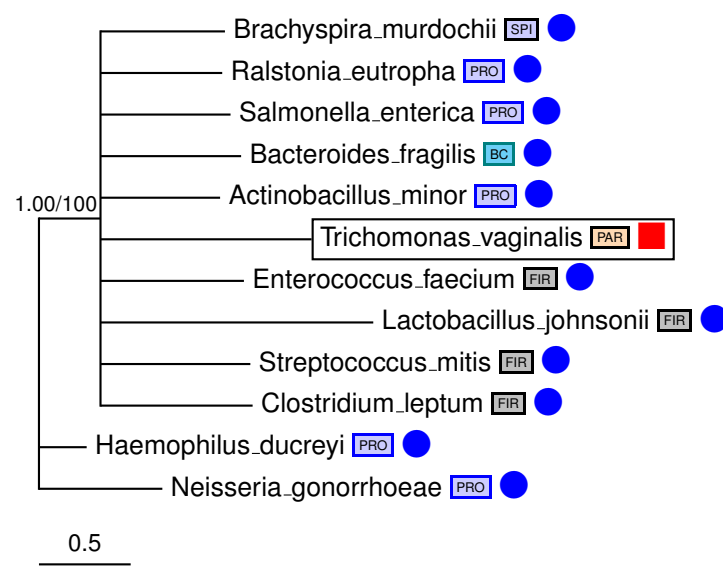
TN245

Candy accession: LM0065
RefSeq accession: XP_001687110.1
Uniprot accession: Q4Q0N8_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY - WITH DEAP
DUPLICATION
Species affected: LM,TB,TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.2.1.28
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glycosyl hydrolase
Name of enzyme/protein: alpha,alpha-trehalase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Starch and sucrose metabolism



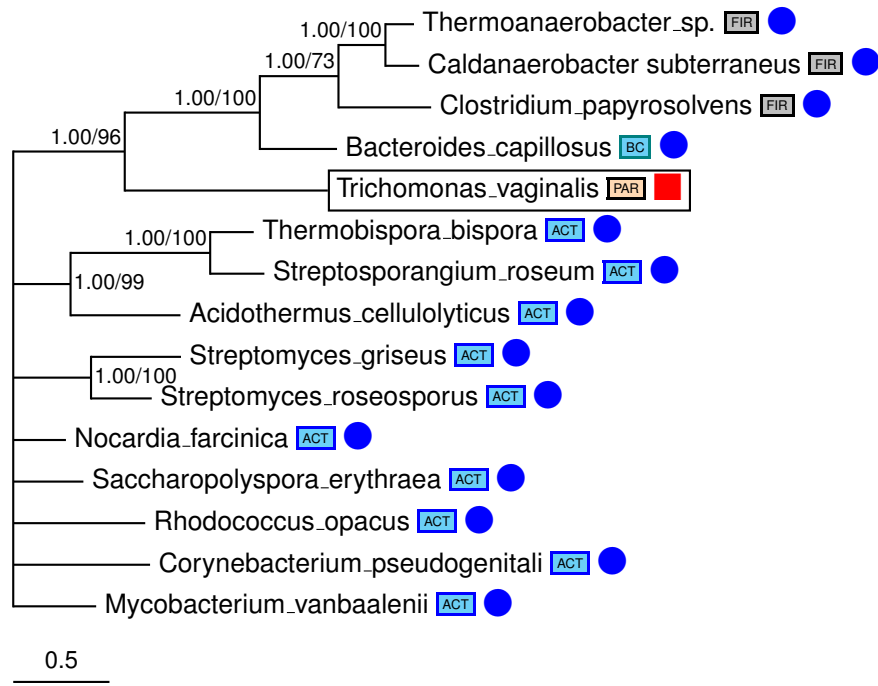
TN246

Candy accession: TV143798005
RefSeq accession: XP_001294330.1
Uniprot accession: A2GN67_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.4.1.58
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glycosyl transferase
Name of enzyme/protein: lipopolysaccharide glucosyltransferase I
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism
KEGG PATHWAY - level 2: Lipopolysaccharide biosynthesis



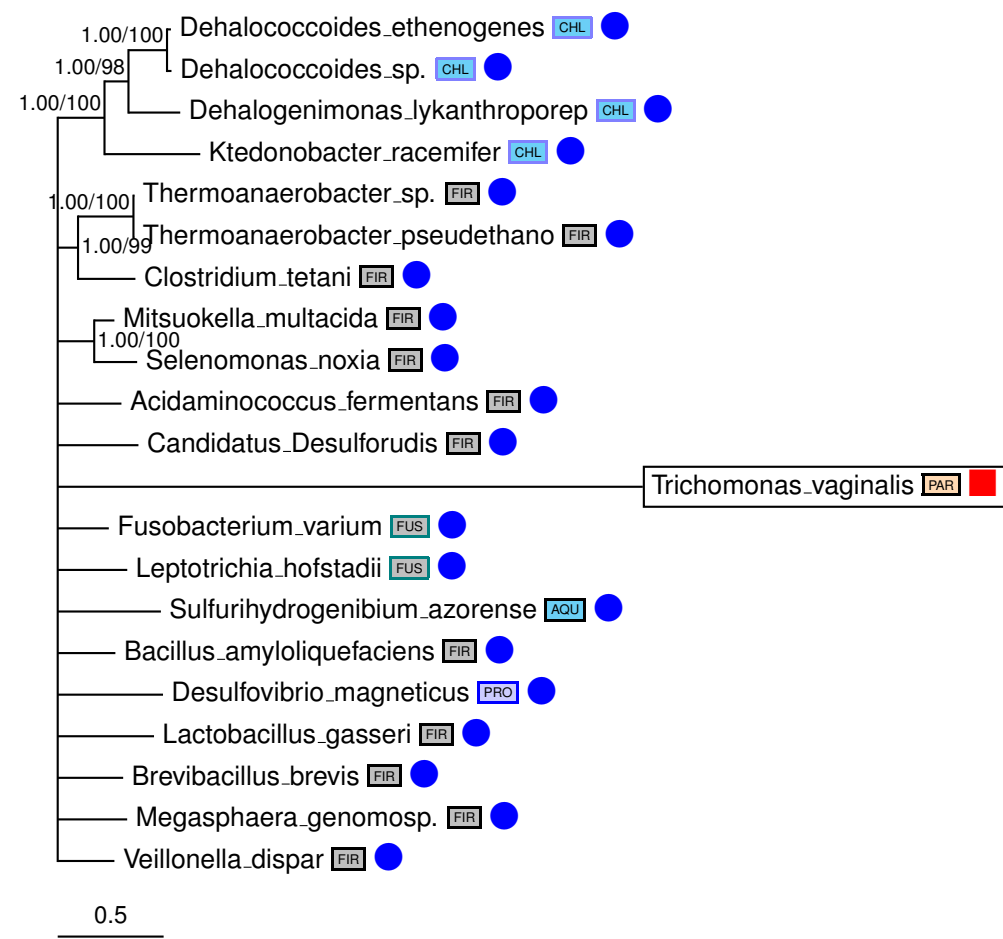
TN247

Candy accession: TV84270673
RefSeq accession: XP_001276902.1
Uniprot accession: A2D7D7_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.4.-.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Clan CA, family C40, NlpC/P60
superfamily cysteine peptidase
Name of enzyme/protein: Peptidase family C40
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



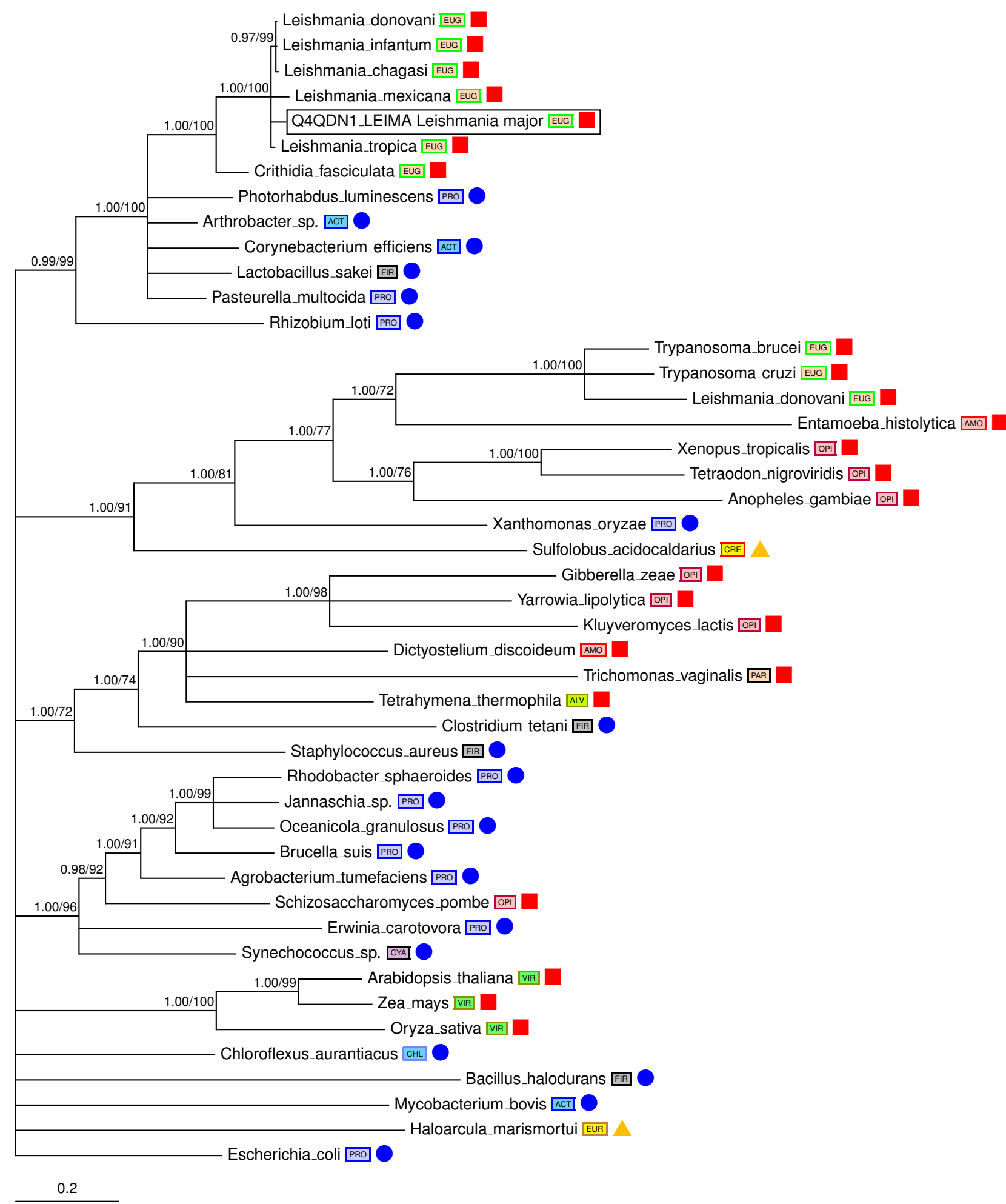
TN248

Candy accession: TV90380186
RefSeq accession: XP_001324349.1
Uniprot accession: A2E5G5_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:6.1.1.15
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: YbaK / prolyl-tRNA synthetases associated domain containing protein
Name of enzyme/protein: prolyl-tRNA synthetase (fragment)
KEGG PATHWAY - level 1: Translation - Genetic Information Processing
KEGG PATHWAY - level 2: Aminoacyl-tRNA biosynthesis



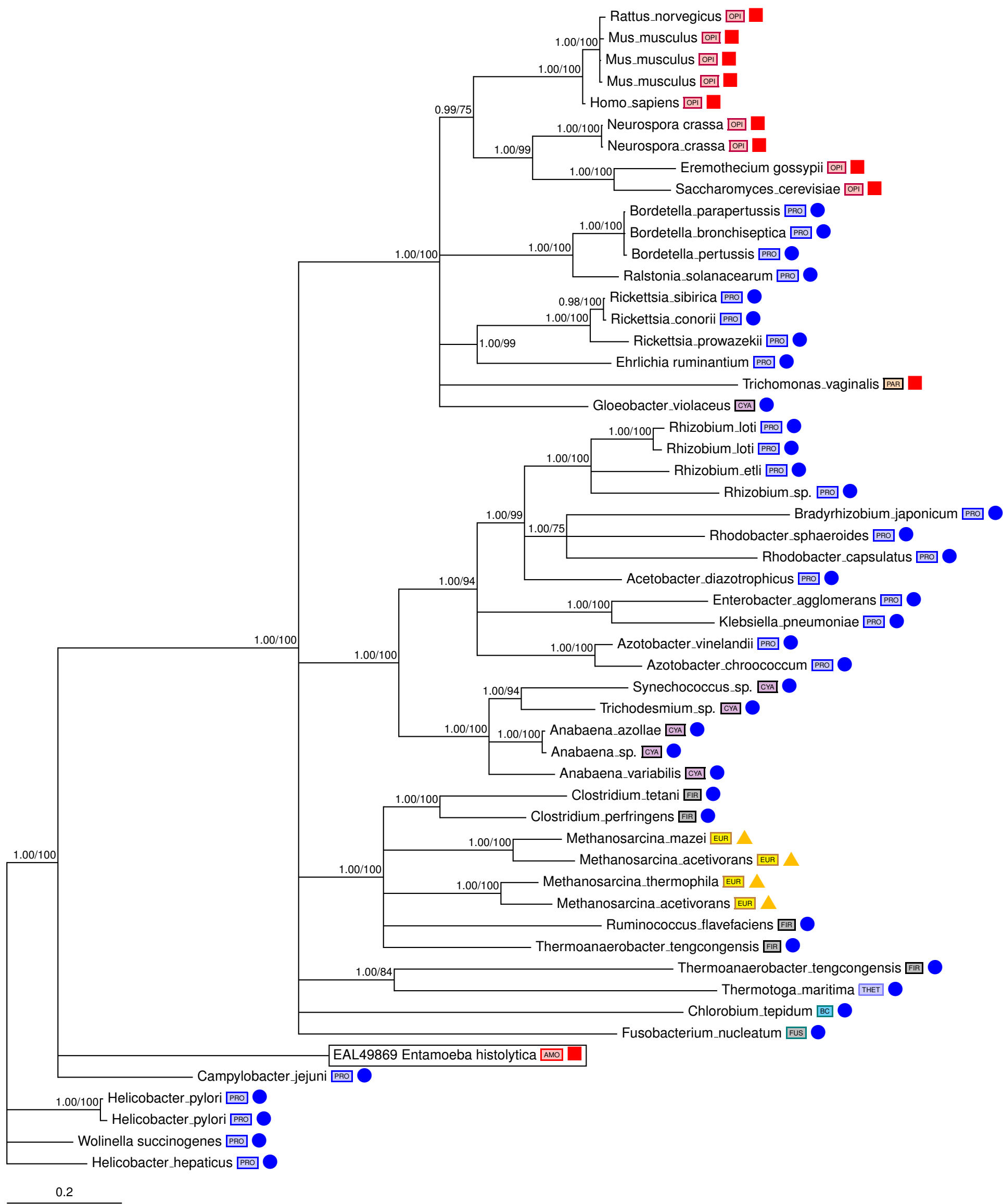
TN249

Candy accession: Q4QDN1_LEIMA
RefSeq accession: XP_001682567.1
Uniprot accession: Q4QDN1_LEIMA
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM,LD,LI,LC,LT,CF
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.2.2.1, EC:3.2.2.3
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: nonspecific nucleoside hydrolase
Name of enzyme/protein: purine nucleosidase, uridine nucleosidase
KEGG PATHWAY - level 1: Nucleotide Metabolism, Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Purine metabolism, Nicotinate and nicotinamide metabolism



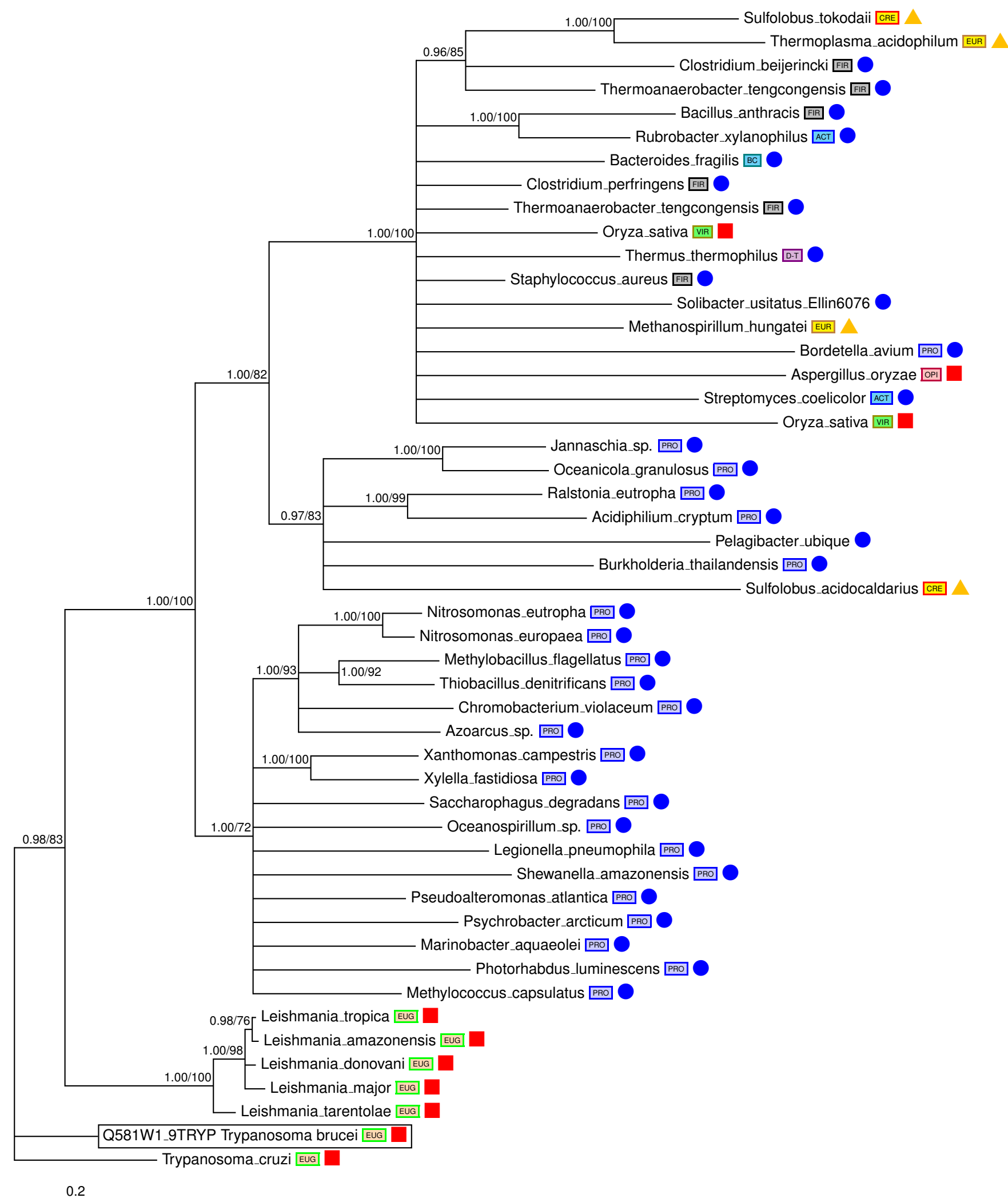
TN250

Candy accession: EAL49869
 RefSeq accession: XP_655257.1
 Uniprot accession: Q76917_ENTHI
 Comments: LCT - EH TWO NODES
 Species affected: EH
 Adjacent taxa in tree: Proteobacteria
 EC annotation - (Blast/Profile): EC:2.8.1.7
 PHOBIOUS SP: 0
 PHOBIOUS TMD: 0
 RefSeq annotation: cysteine desulfurase
 Name of enzyme/protein: Cysteine desulfurase
 KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins
 KEGG PATHWAY - level 2: Thiamine metabolism



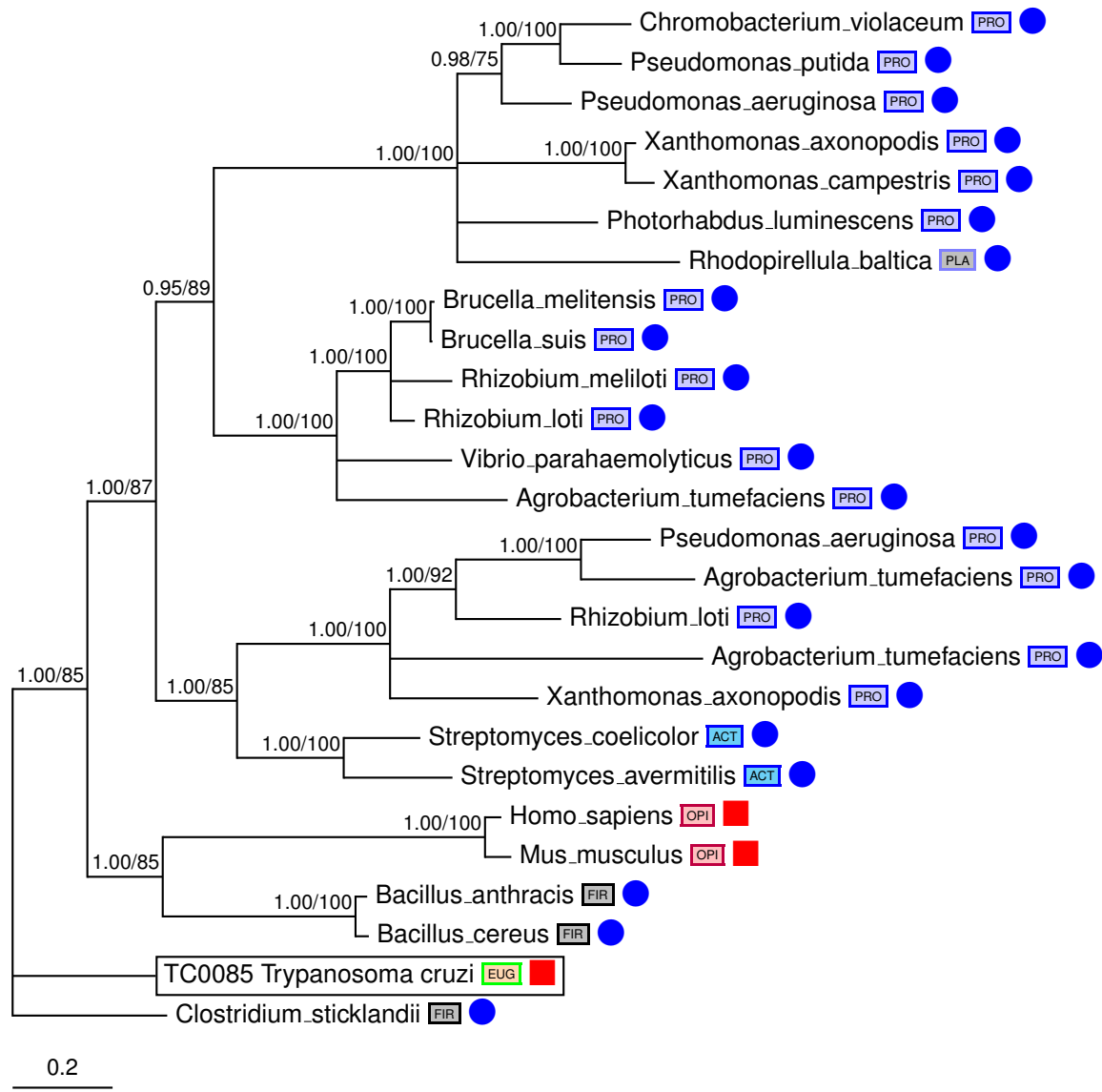
TN251

Candy accession: Q581W1_9TRYPLmtc
RefSeq accession: XP_047054.1
Uniprot accession: Q581W1_9TRYVP
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM,LT,LA,LD,LT2,TB,TC
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:1.5.1.33
PHOBUS SP: 0
PHOBUS TMD: 0
RefSeq annotation: pteridine reductase
Name of enzyme/protein: Pteridine reductase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



TN252

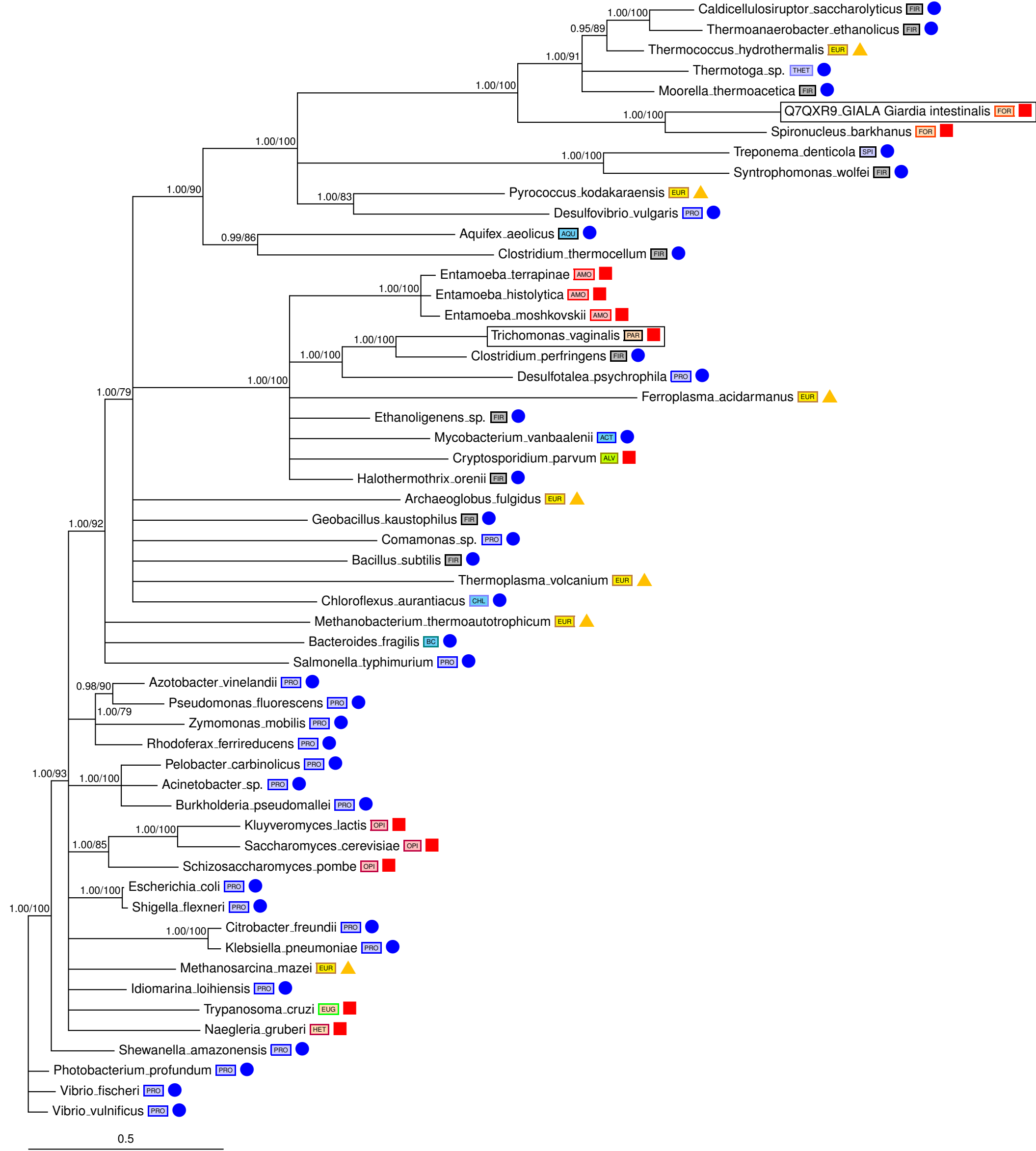
Candy accession: TC0085
RefSeq accession: XP_803162.1
Uniprot accession: PRCMB_TRYCR
Comments: LGT - TC TWO NODES
Species affected: TC
Adjacent taxa in tree: Firmicutes - Clostridium
EC annotation - (Blast/Profile): EC:5.1.1.4
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: proline racemase
Name of enzyme/protein: Proline racemase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism



TN253

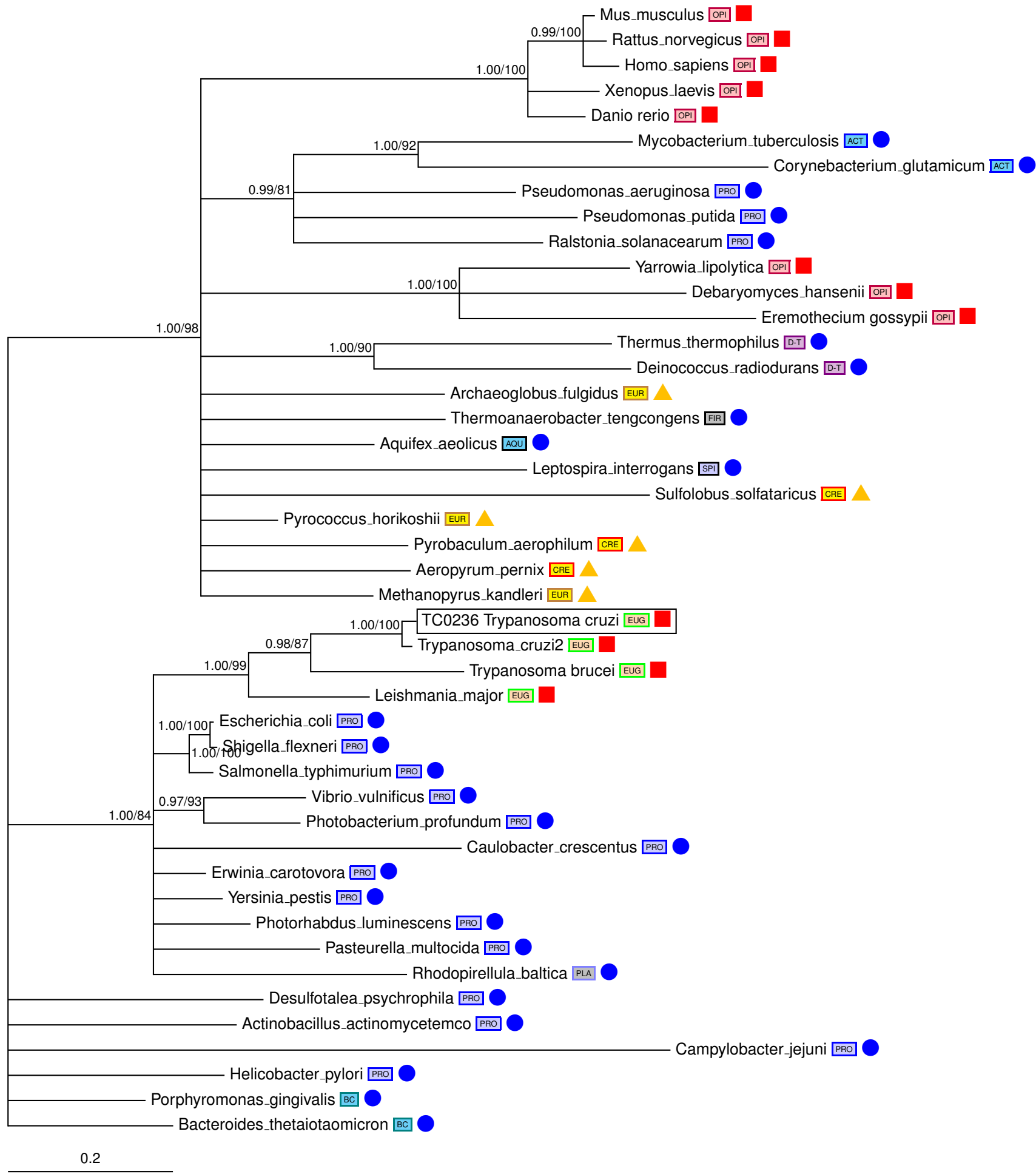
Candy accession: TV94939050
RefSeq accession: XP_001307535.1
Uniprot accession: Q86S09_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Firmicutes - Clostridium
EC annotation - (Blast/Profile): EC:1.1.1.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: alcohol dehydrogensae
Name of enzyme/protein: Oxidoreductases
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction

Candy accession: Q7QXR9_GIALA
RefSeq accession: XP_001706932.1
Uniprot accession: Q7QXR9_GIALA
Comments: LGT - GI,SB TWO NODES
Species affected: GI,SB
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:1.1.1.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Alcohol dehydrogenase 3 lateral transfer candidate
Name of enzyme/protein: alcohol dehydrogenase
KEGG PATHWAY - level 1: Carbohydrate Metabolism, Lipid Metabolism, Amino Acid Metabolism
KEGG PATHWAY - level 2: Glycolysis / Gluconeogenesis, Fatty acid metabolism, Glycine, serine and threonine metabolism



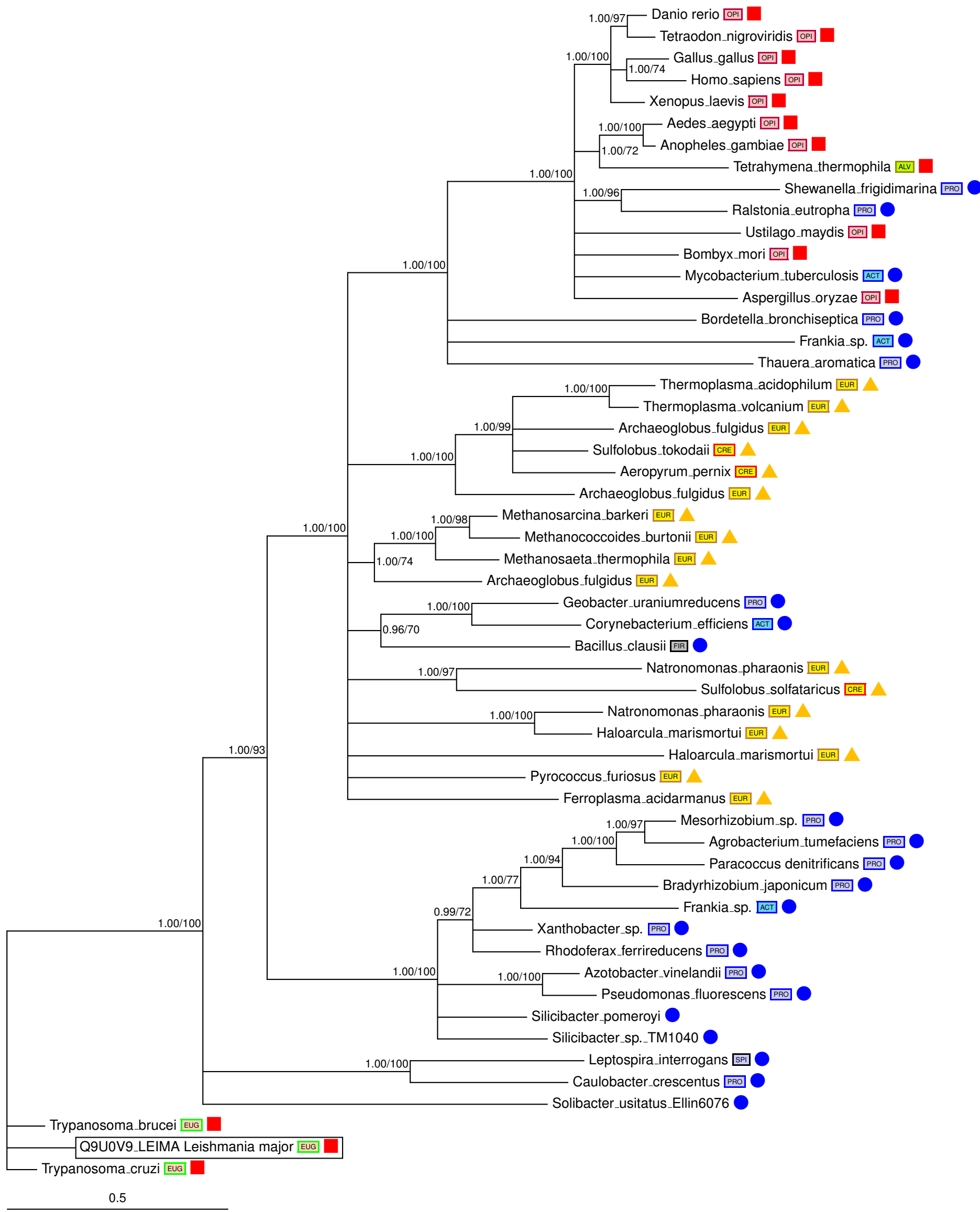
TN254

Candy accession: TC0236
RefSeq accession: XP_821790.1
Uniprot accession: Q4E5B9_TRYCR
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM,TB,TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.5.1.-
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: NAD-dependent deacetylase
Name of enzyme/protein: Hydrolases (NAD-dependent deacetylase)
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



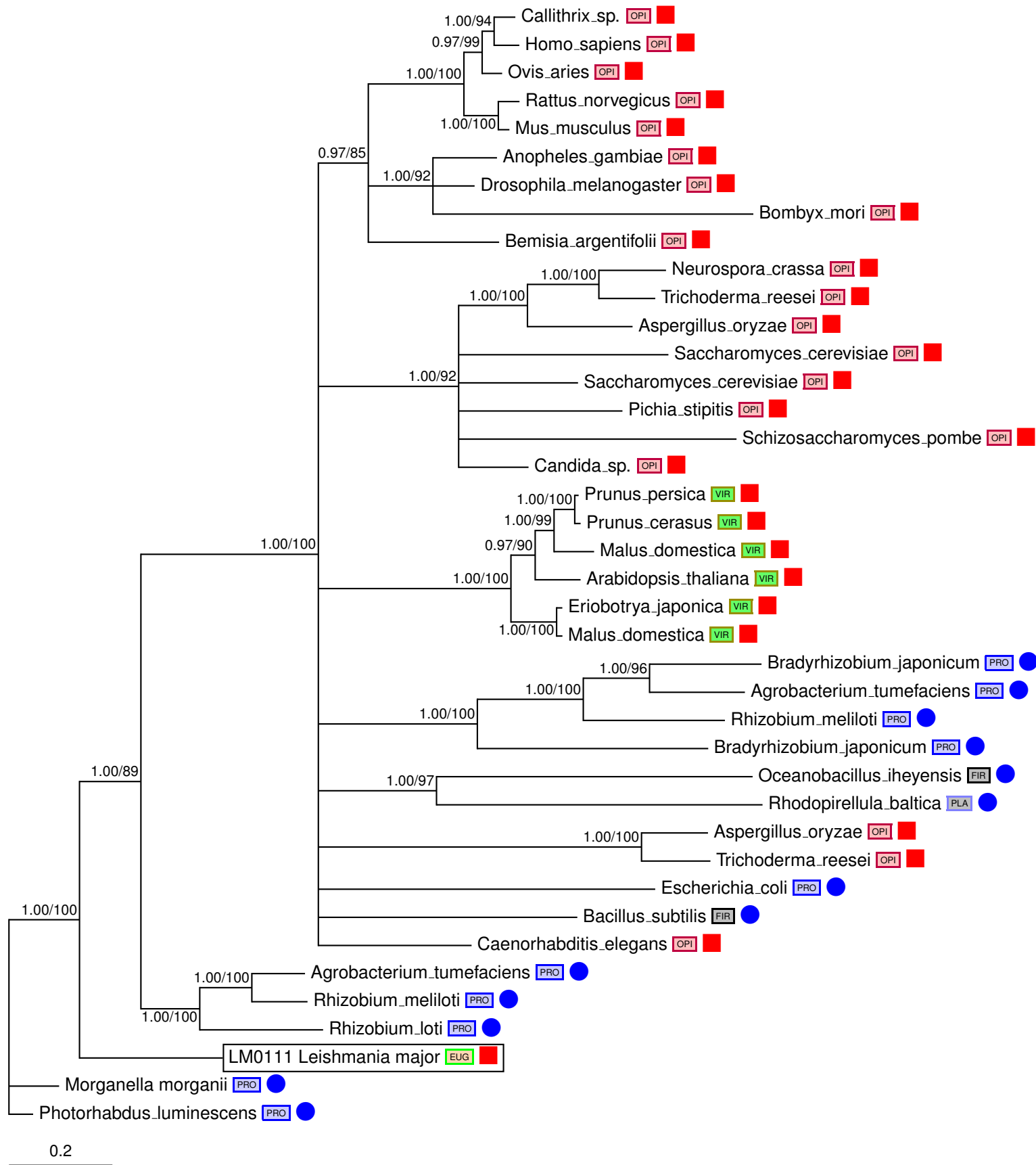
TN255

Candy accession: Q9U0V9_LEIMA
RefSeq accession: XP_001683404.1
Uniprot accession: Q9U0V9_LEIMA
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM, TB,TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.3.1.16
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: 3-ketoacyl-coa thiolase-like protein
Name of enzyme/protein: acetyl-CoA C-acyltransferase
KEGG PATHWAY - level 1: Lipid Metabolism, Amino Acid Metabolism
KEGG PATHWAY - level 2: Fatty acid elongation, Fatty acid metabolism, Valine, leucine and isoleucine degradation



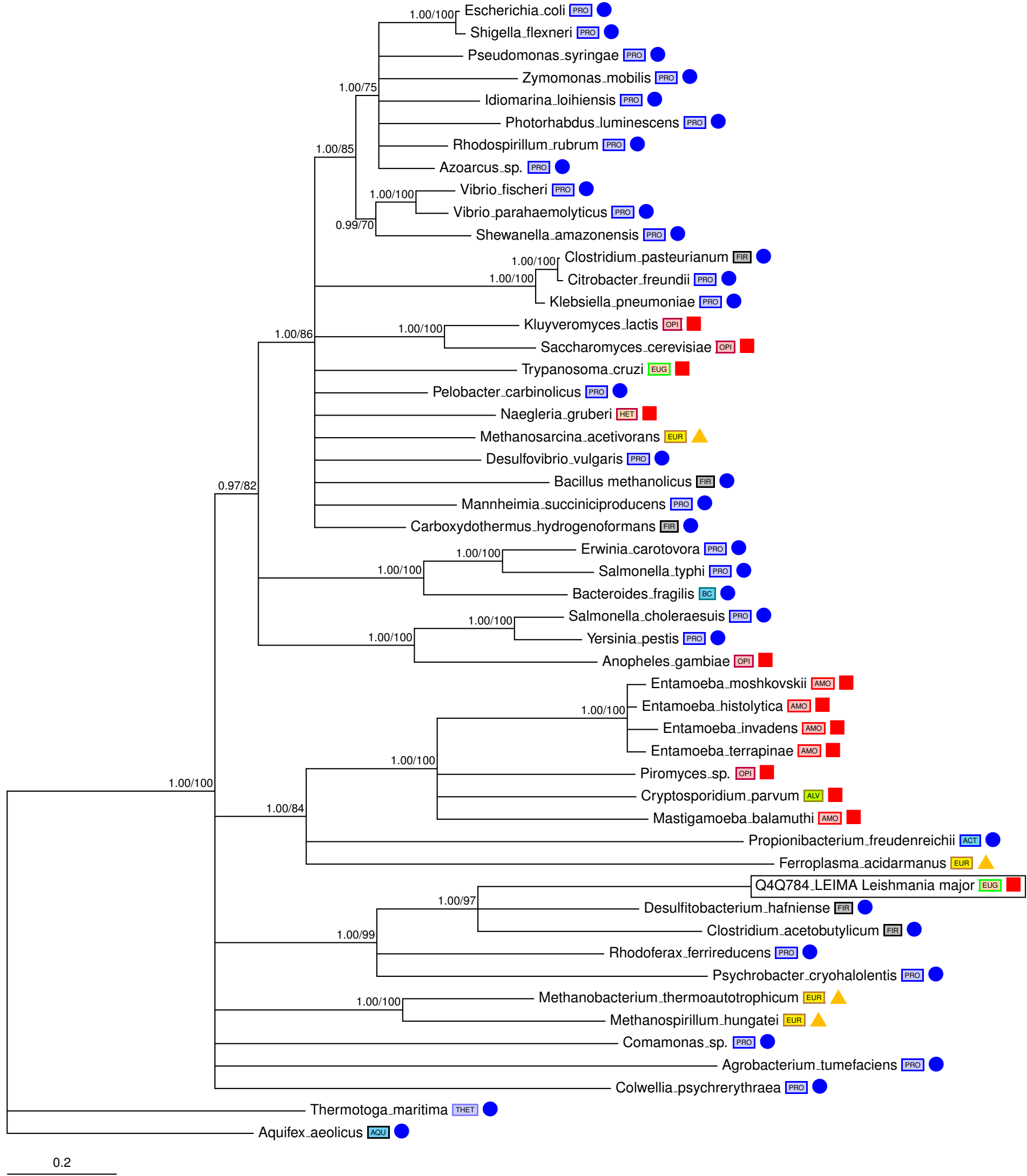
TN256

Candy accession: LM0111
RefSeq accession: XP_001685791.1
Uniprot accession: Q4Q4F7_LEIMA
Comments: LGT - LM TWO NODES
Species affected: LM
Adjacent taxa in tree: Protobacteria
EC annotation - (Blast/Profile): EC:1.1.1.9
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: d-xylulose reductase
Name of enzyme/protein: D-xylulose reductase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pentose and glucuronate interconversions



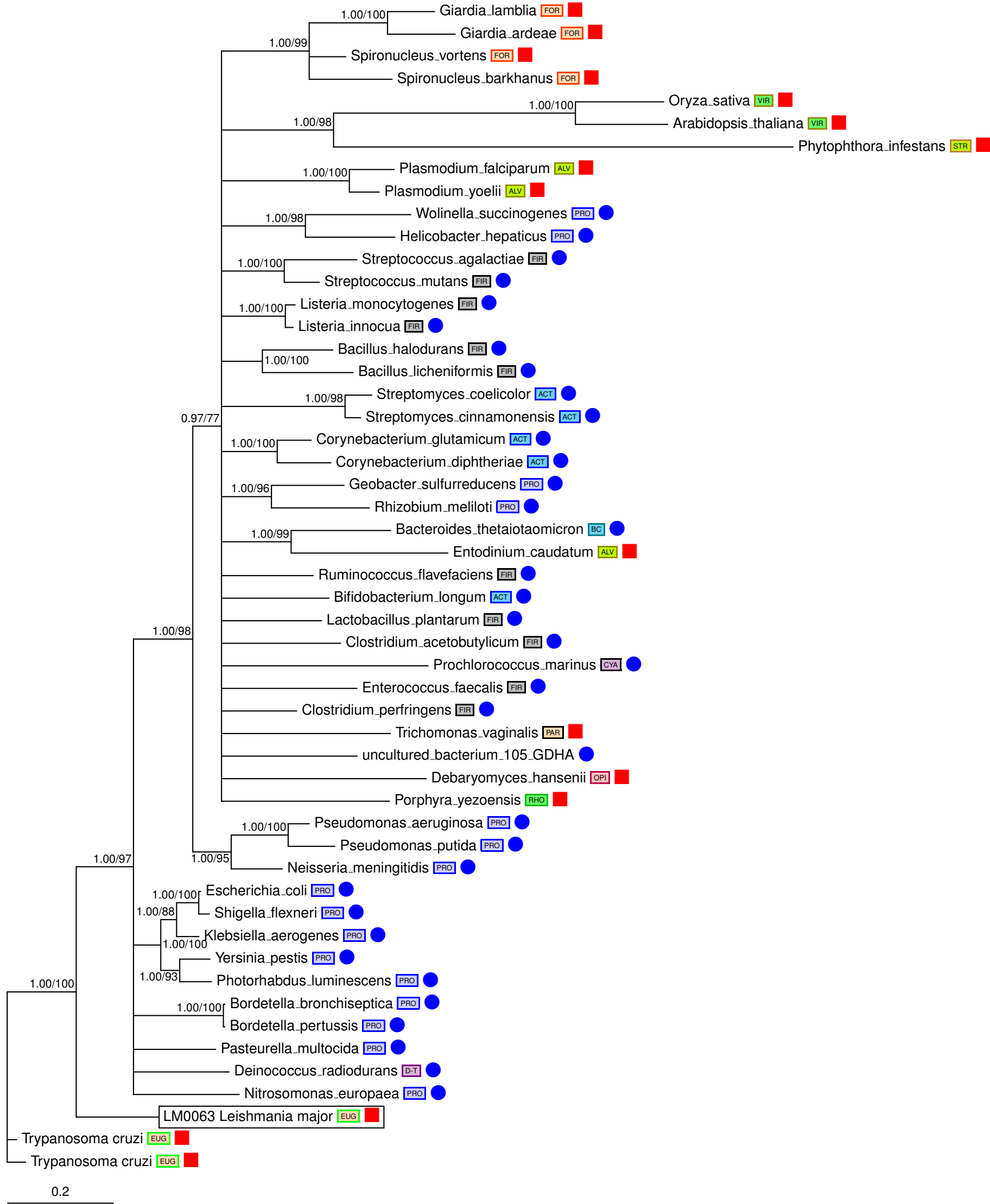
TN257

Candy accession: Q4Q784_LEIMAtc
RefSeq accession: XP_001684814.1
Uniprot accession: Q4Q784_LEIMA
Comments: LGT - LM TWO NODES
Species affected: LM
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): EC:1.1.1.1
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: alcohol dehydrogenase
Name of enzyme/protein: alcohol dehydrogenase
KEGG PATHWAY - level 1: Carbohydrate Metabolism, Lipid Metabolism, Amino Acid Metabolism
KEGG PATHWAY - level 2: Glycolysis / Gluconeogenesis, Fatty acid metabolism, Glycine, serine and threonine metabolism



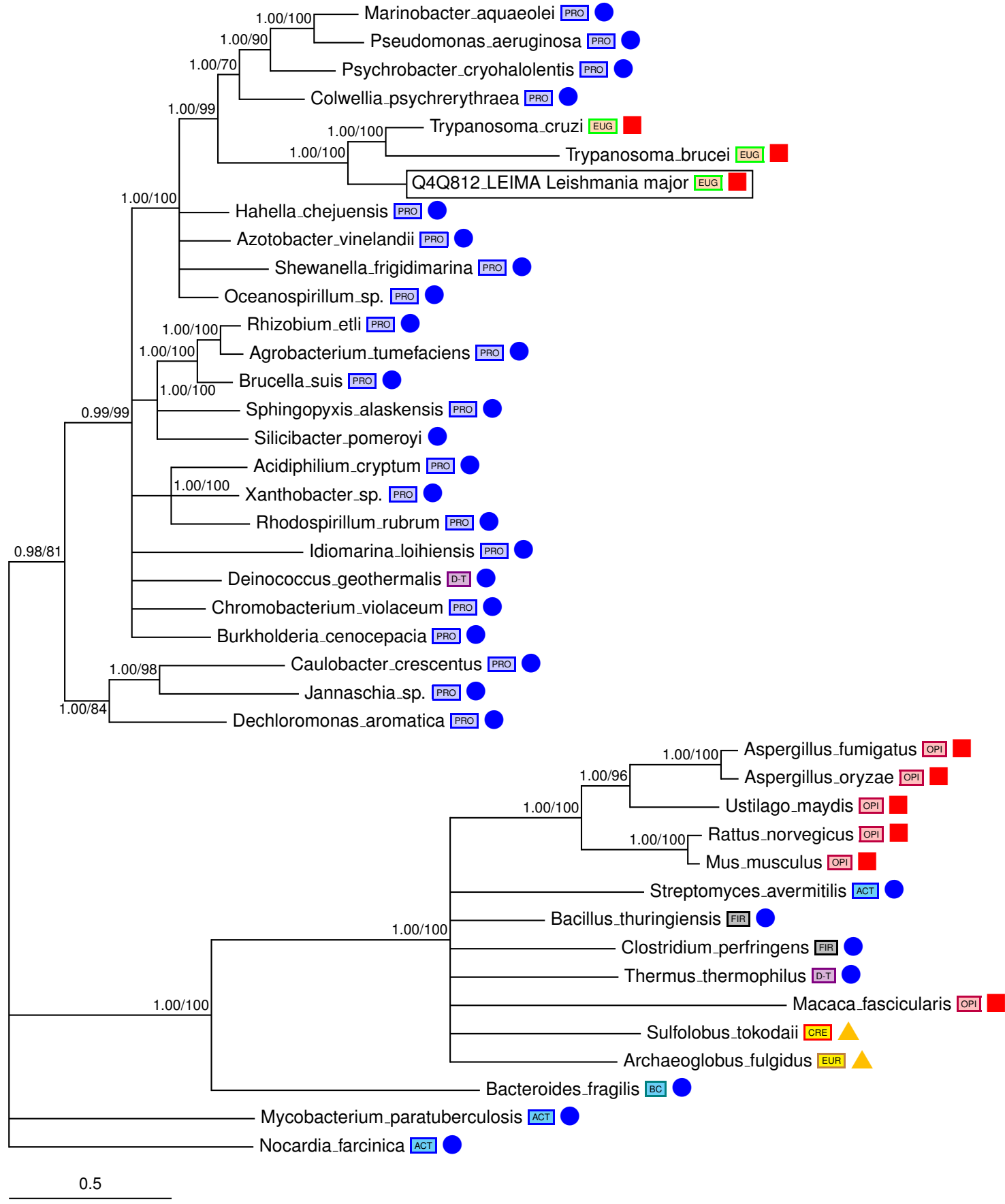
TN258

Candy accession: LM0063tc
RefSeq accession: XP_001684577.1
Uniprot accession: Q4Q7X1_LEIMA
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM,TC
Adjacent taxa in tree: Bacteria/phage
EC annotation - (Blast/Profile): EC:1.4.1.4
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glutamate dehydrogenase
Name of enzyme/protein: Glutamate dehydrogenase (NADP+)
KEGG PATHWAY - level 1: Amino Acid Metabolism, Energy Metabolism
KEGG PATHWAY - level 2: Alanine, aspartate and glutamate metabolism, Arginine and proline metabolism, Nitrogen metabolism



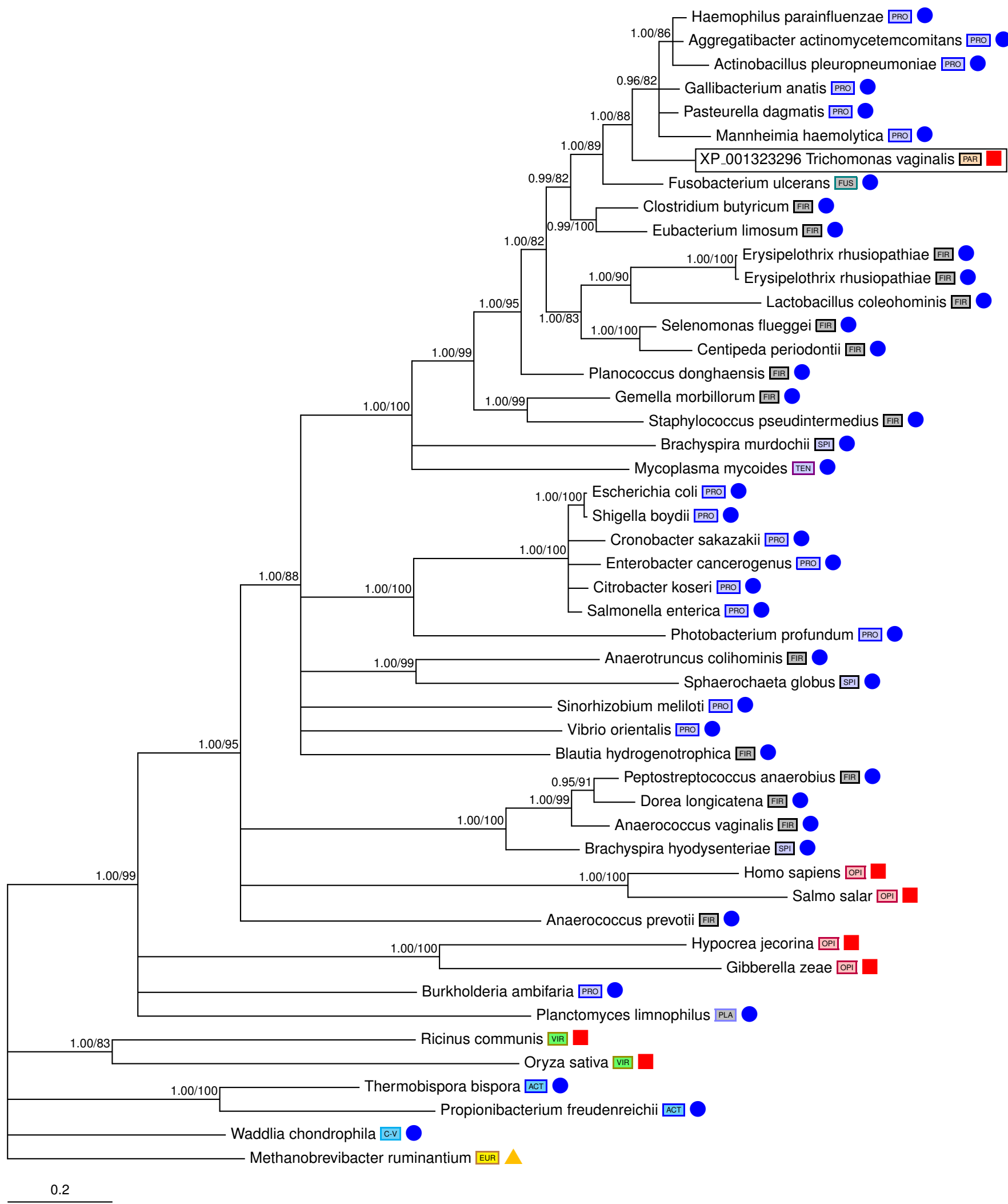
TN259

Candy accession: Q4Q812_LEIMAtbtc
RefSeq accession: XP_001684536.1
Uniprot accession: Q4Q812_LEIMA
Comments: LGT - KINETOPLASTIDS TWO NODES
Species affected: LM, TB,TC
Adjacent taxa in tree: Protobacteria
EC annotation - (Blast/Profile): EC:1.3.8.7
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: acyl-coa dehydrogenase
Name of enzyme/protein: Acyl-coa dehydrogenase
KEGG PATHWAY - level 1: Lipid Metabolism, Amino Acid Metabolism, Metabolism of Other Amino Acids
KEGG PATHWAY - level 2: Fatty acid metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism



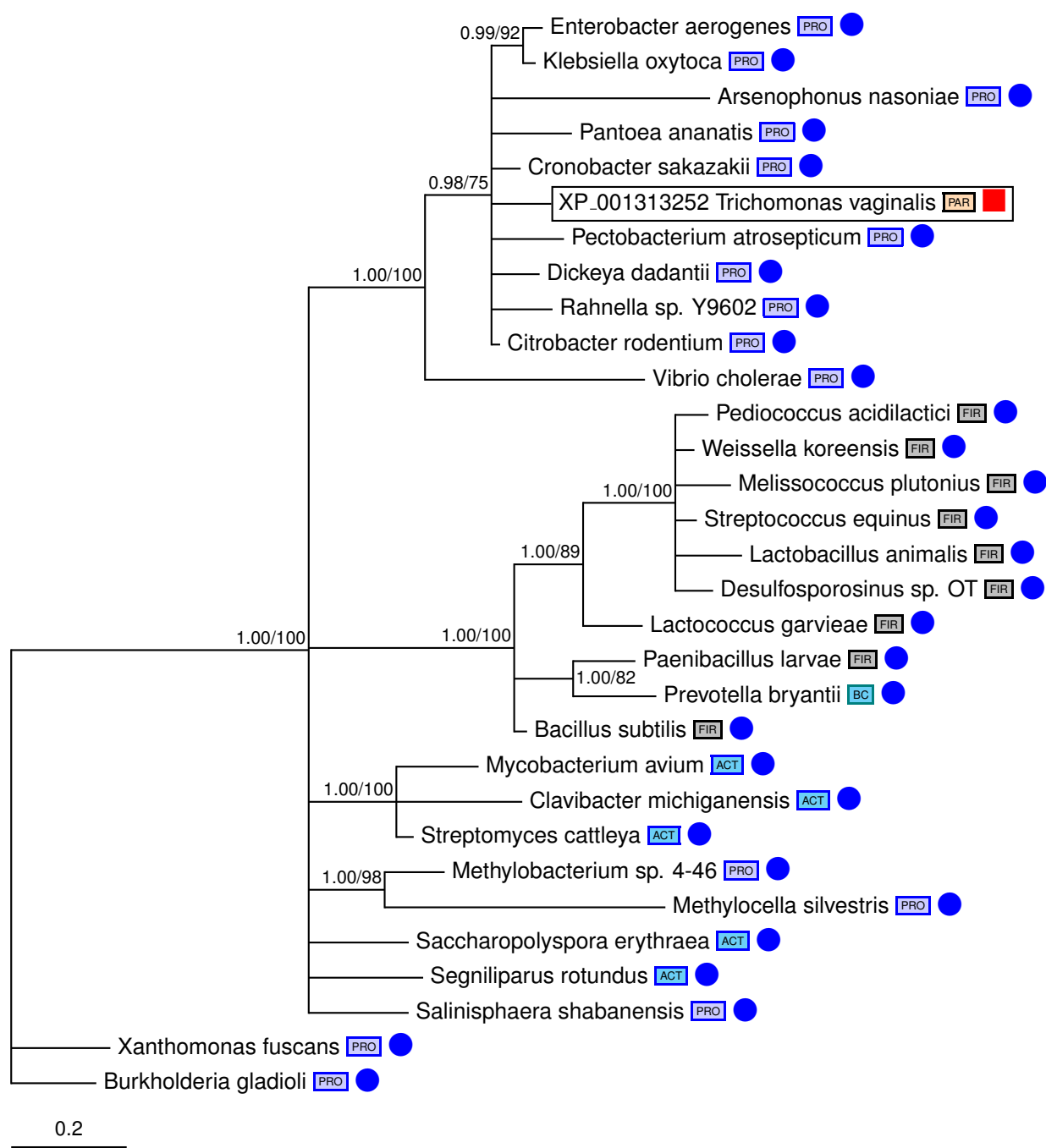
TN260

Candy accession: XP_001323296
RefSeq accession: XP_001323296
Uniprot accession: A2E8E5_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Protobacteria
EC annotation - (Blast/Profile): EC:4.1.3.3
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: N-acetylneuraminate lyase
Name of enzyme/protein: N-acetylneuraminate lyase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Amino sugar and nucleotide sugar metabolism



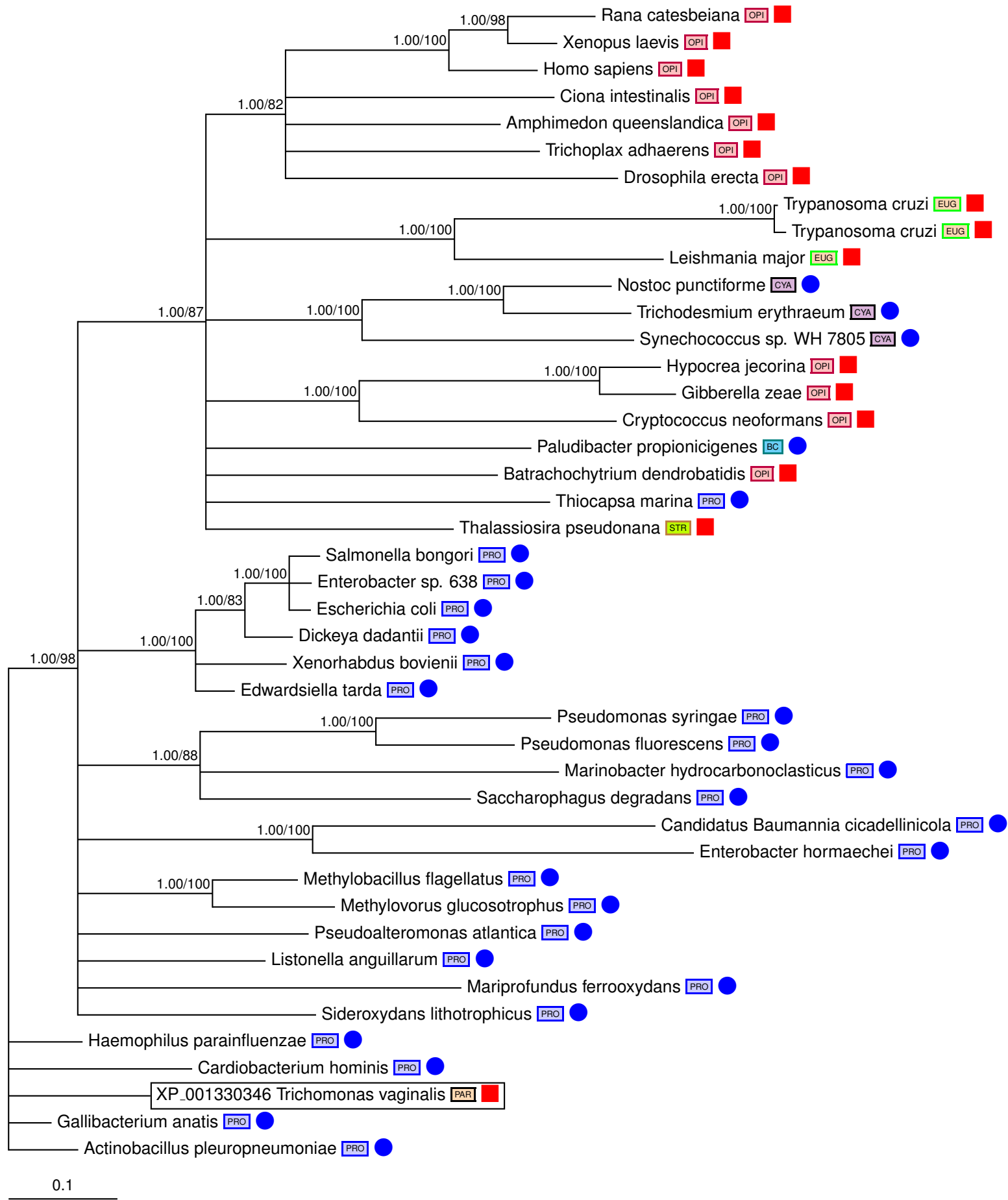
TN261

Candy accession: XP_001313252
RefSeq accession: XP_001313252
Uniprot accession: A2F476_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Protobacteria
EC annotation - (Blast/Profile): EC:4.1.1.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: ferulate decarboxylase
Name of enzyme/protein: Phenolic acid decarboxylase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



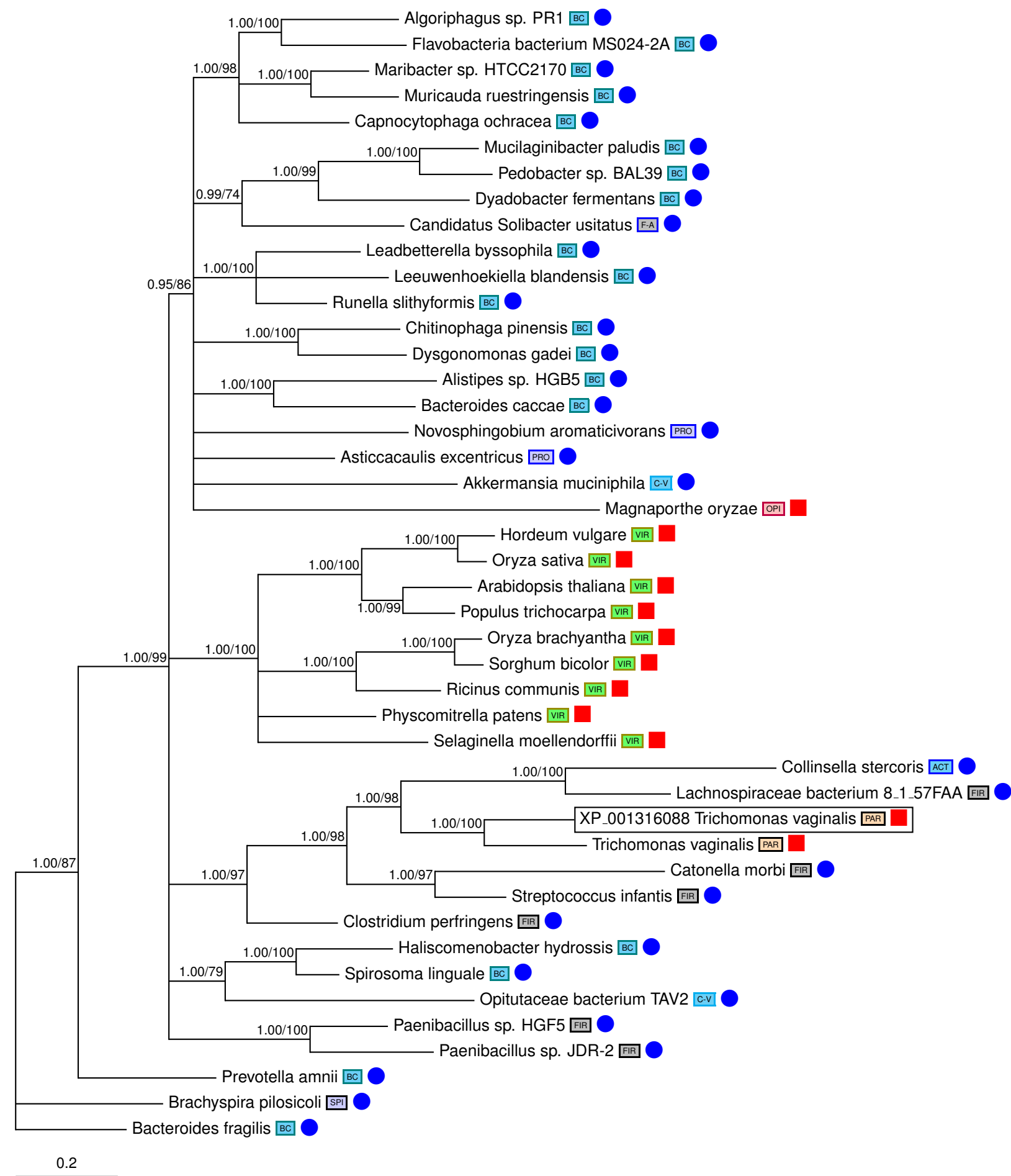
TN262

Candy accession: XP_001330346
RefSeq accession: XP_001330346
Uniprot accession: A2FOHO_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Protobacteria
EC annotation - (Blast/Profile): EC:2.2.1.2
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Transaldolase A
Name of enzyme/protein: Transaldolase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pentose phosphate pathway



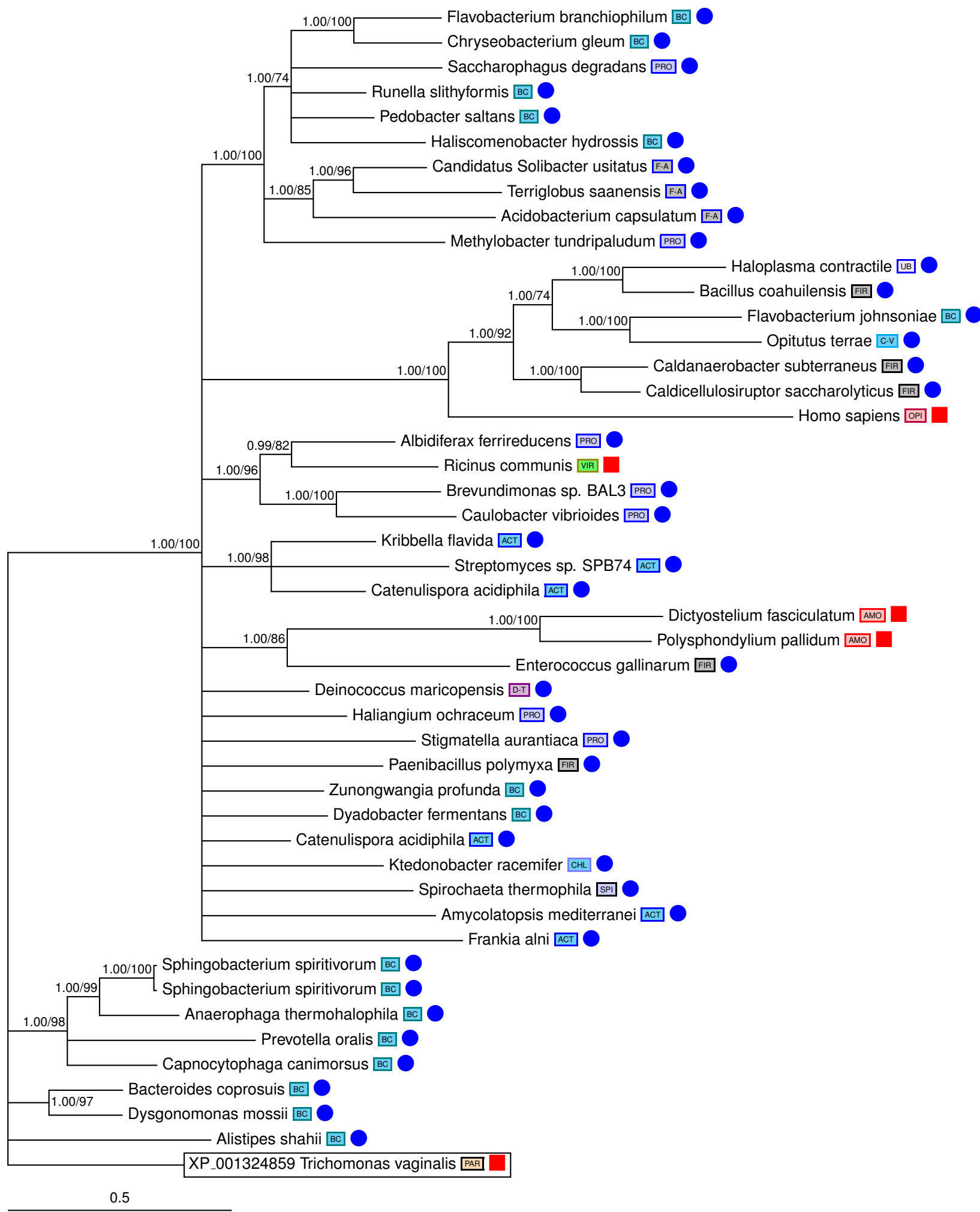
TN263

Candy accession: XP_001316088
RefSeq accession: XP_001316088
Uniprot accession: A2ETX7_TR1VA
Comments: LGT - TV TWO NODES
Species affected: TV,FUNGI
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.2.1.51
PHOBIUS SP: 0
PHOBIUS TMD: 1
RefSeq annotation: Calx-beta domain containing protein
Name of enzyme/protein: alpha-L-fucosidase
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism
KEGG PATHWAY - level 2: Other glycan degradation



TN264

Candy accession: XP_001324859
RefSeq accession: XP_001324859
Uniprot accession: A2E3Y1_TR1VA
Comments: LGT - TV TW NODES
Species affected: TV_AMOEBOZOA
Adjacent taxa in tree: Bacteroidetes/Chlorobi
EC annotation - (Blast/Profile): EC:3.2.1.45
PHOBUS SP: 0
PHOBUS TMD: 0
RefSeq annotation: O-Glycosyl hydrolase family 30 protein
Name of enzyme/protein: glucosylceramidase
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism,
Lipid Metabolism
KEGG PATHWAY - level 2: Other glycan degradation, Sphingolipid
metabolism



TN265

Candy accession: XP_001319692
RefSeq accession: XP_001319692
Uniprot accession: A2EIP2_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV,FUNGI
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Maribacter
EC annotation - (Blast/Profile): EC:3.2.1.18
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: BNR/Asp-box repeat family protein
Name of enzyme/protein: exo-alpha-sialidase
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism,
Lipid Metabolism
KEGG PATHWAY - level 2: Other glycan degradation, Sphingolipid
metabolism

