

Additional File 6. Potential eukaryote-to-eukaryote LGTs

See legend of Additional File 5 for details, including the taxa color key. These trees recovered one or more eukaryote taxa in a polytomy or as part of the same well-supported clan supporting, or which cannot reject, potential LGT between eukaryotes. (trees numbered EEXXX). Taxon sampling suggests, for several cases, at least one initial LGT from a prokaryote donor to a eukaryote followed by potential eukaryote to eukaryote LGT.

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21 September, 2012

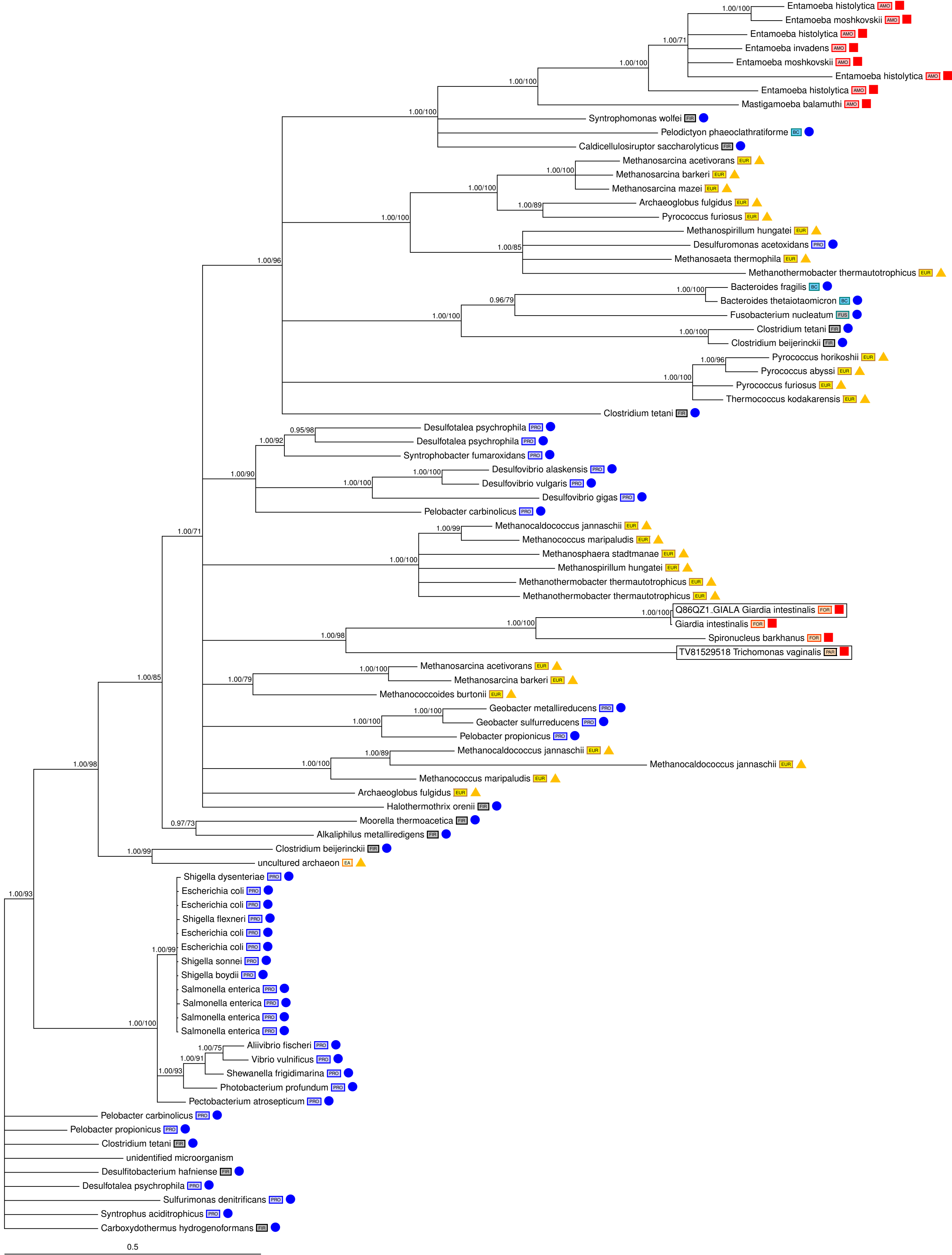
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EE001

Candy accession: TV81529518
RefSeq accession: XP_001583562.1
Uniprot accession: Q6XKE2_TRIVA
Comments: LGT - E-E LGT OR DEAP LGT INTO
METAMONADA (DIMPLONADS+PARABASALA)?
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Hydrogenosomal oxygen reductase
Name of enzyme/protein: Protein containing metallo-beta-lactamase/flavodoxin domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

Candy accession: Q86QZ1_GIALA
RefSeq accession: XP_001707670.1
Uniprot accession: Q86QZ1_GIAIN
Comments: LGT - E-E LGT OR DEAP LGT INTO
METAMONADA (DIMPLONADS+PARABASALA)?
Species affected: GI,SB,TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: A-type flavoprotein lateral transfer candidate
Name of enzyme/protein: Protein containing metallo-beta-lactamase/flavodoxin domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



EE002

Candy accession: TV92066132
RefSeq accession: XP_001319096.1
Uniprot accession: A2EKG5_TRIVA
Comments: LGT - POSSIBLE LGT BETWEEN APICOMPLEXA AND PARABASALA

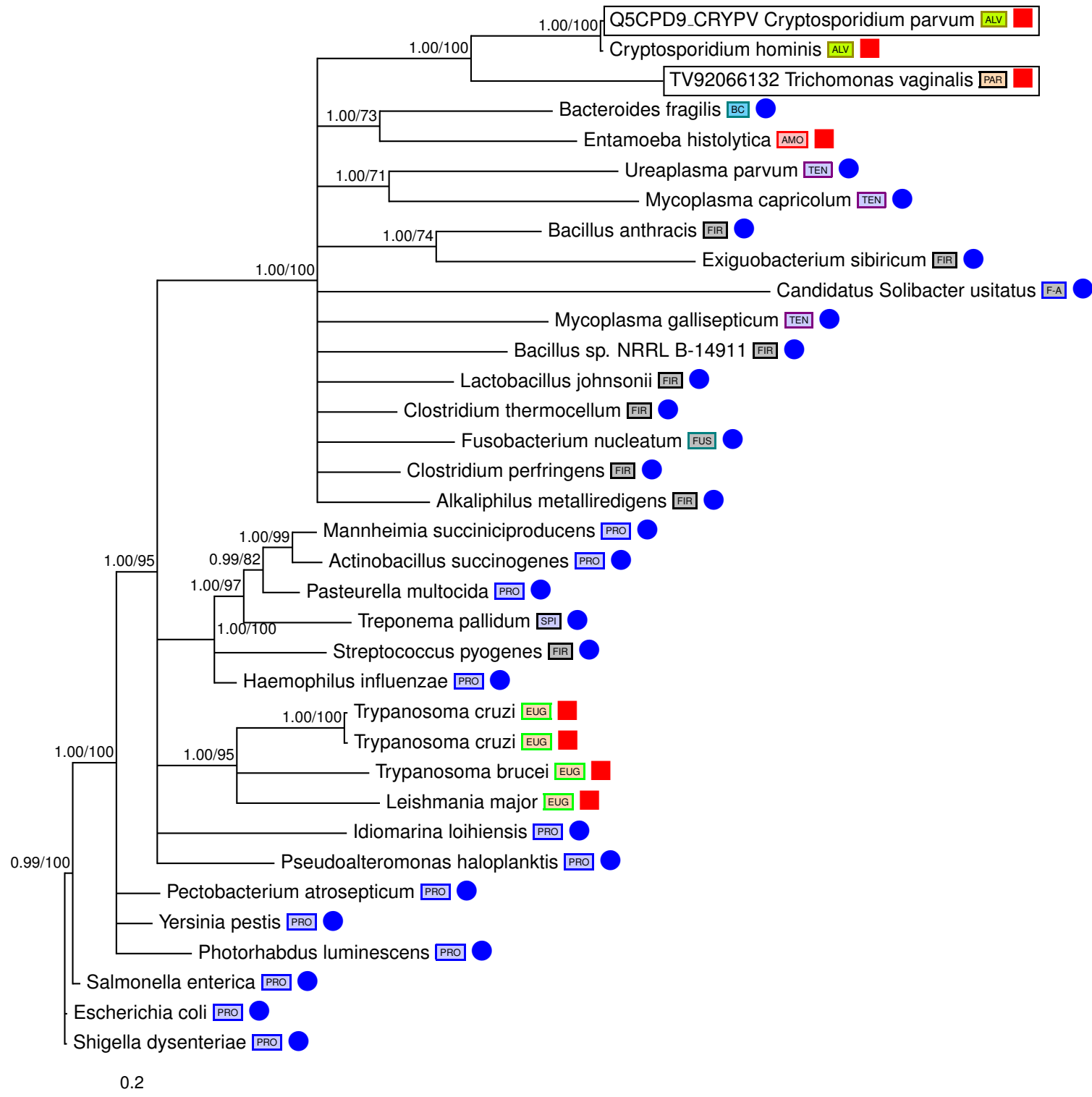
Species affected: TV
Adjacent taxa in tree: Apicomplexa

EC annotation - (Blast/Profile): EC:6.3.1.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
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: Q5CPD9_CRYPV
RefSeq accession: XP_625302.1
Uniprot accession: Q5CPD9_CRYPV
Comments: LGT - POSSIBLE LGT BETWEEN APICOMPLEXA AND PARABASALA

Species affected: CP,CH
Adjacent taxa in tree: Parabasala

EC annotation - (Blast/Profile): EC:6.3.1.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: asparagine synthetase A (AsnA) like protein
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



EE003

Candy accession: Q95WU5_GIALA
RefSeq accession: XP_001707929.1
Uniprot accession: Q95WU5_GIAIN
Comments: LGT - POSSIBLE LGT BETWEEN DIPLOMONAD
AND AMOEBOZOA

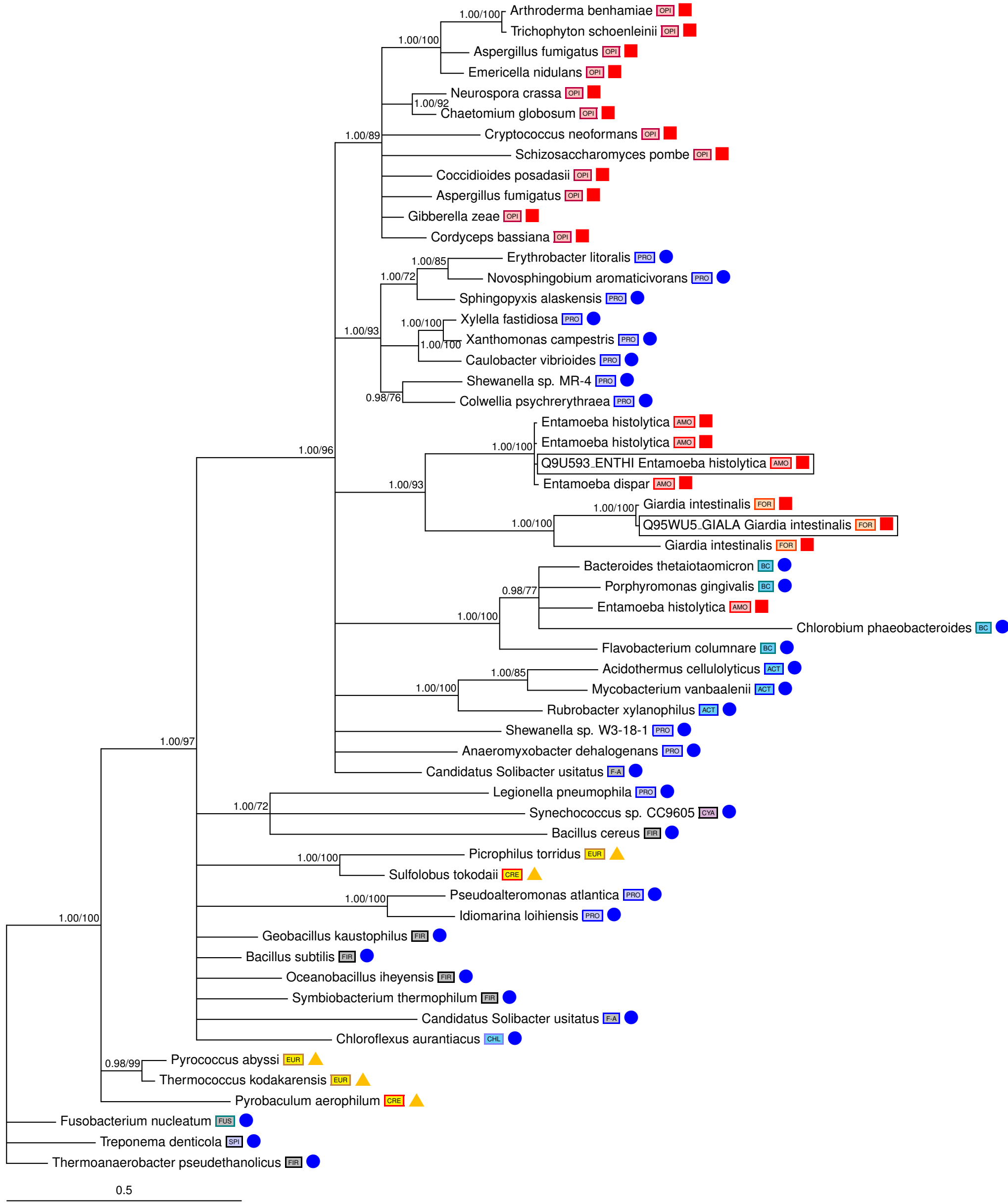
Species affected: EH
Adjacent taxa in tree: Diplomonads

EC annotation - (Blast/Profile): EC:3.4.19.1
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: Alanyl dipeptidyl peptidase
Name of enzyme/protein: acylaminoacyl-peptidase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction

Candy accession: Q9U593_ENTHI
RefSeq accession: XP_655222.1
Uniprot accession: Q9U593_ENTHI
Comments: LGT - POSSIBLE LGT BETWEEN DIPLOMONAD
AND AMOEBOZOA

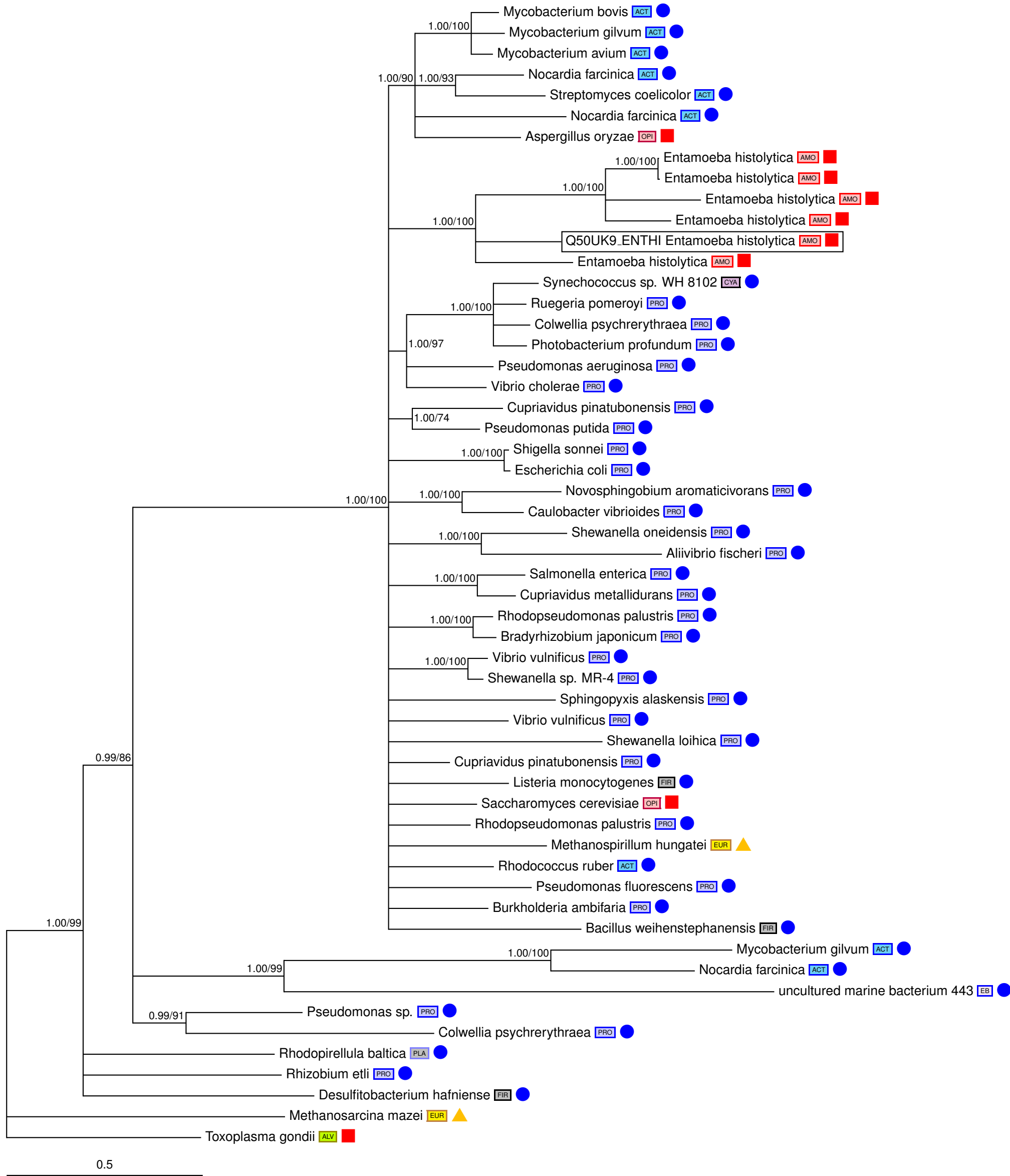
Species affected: GI
Adjacent taxa in tree: Amoebozoa

EC annotation - (Blast/Profile): EC:3.4.19.1
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: dipeptidyl-peptidase
Name of enzyme/protein: acylaminoacyl-peptidase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



EE004

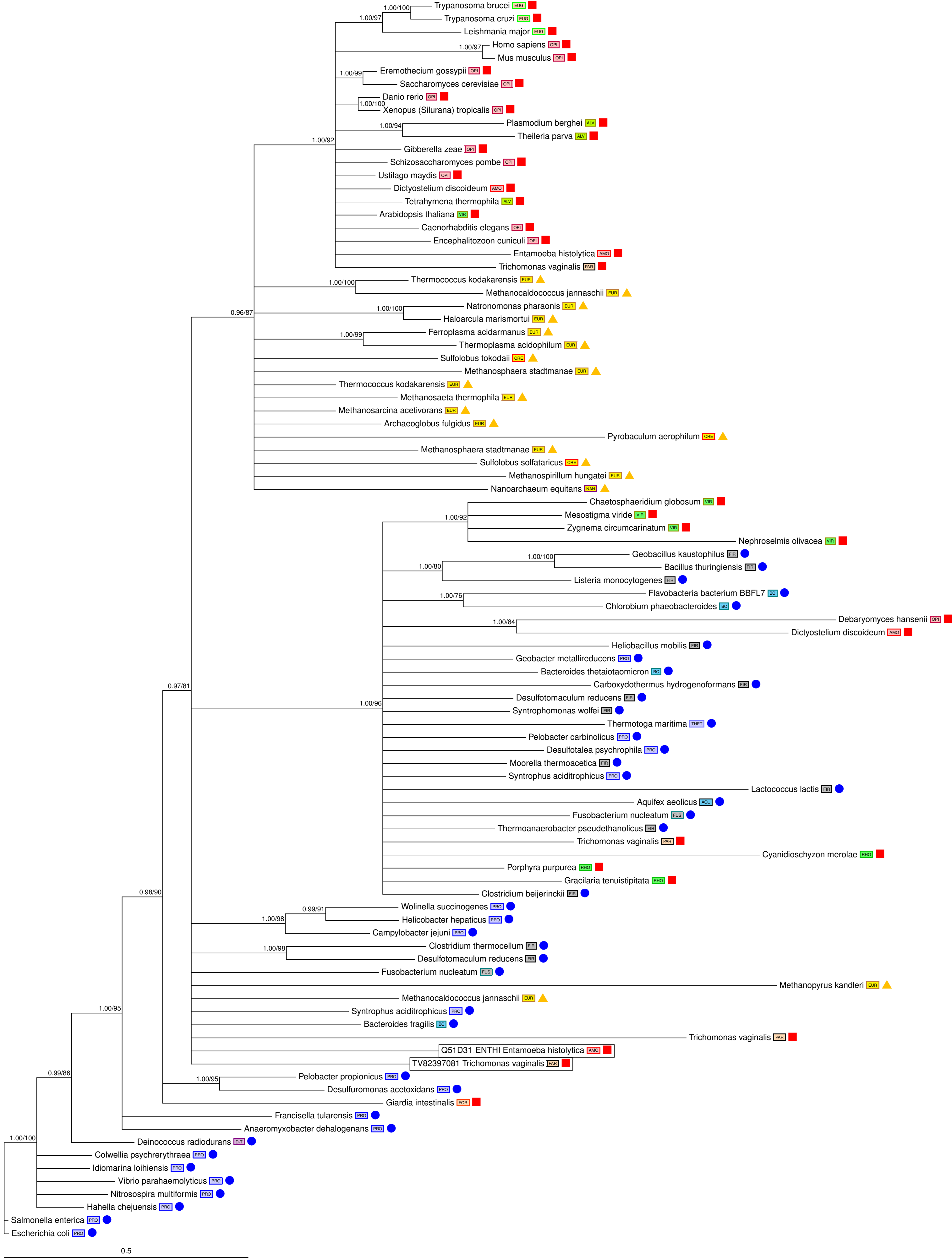
Candy accession: Q50UK9_ENTHI
RefSeq accession: XP_650664.1
Uniprot accession: C4M148_ENTHI
Comments: LGT? - EH POLYTOMY WITH SC
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: metallo-beta-lactamase superfamily protein
Name of enzyme/protein: Predicted metallo-beta-lactamase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



EE005

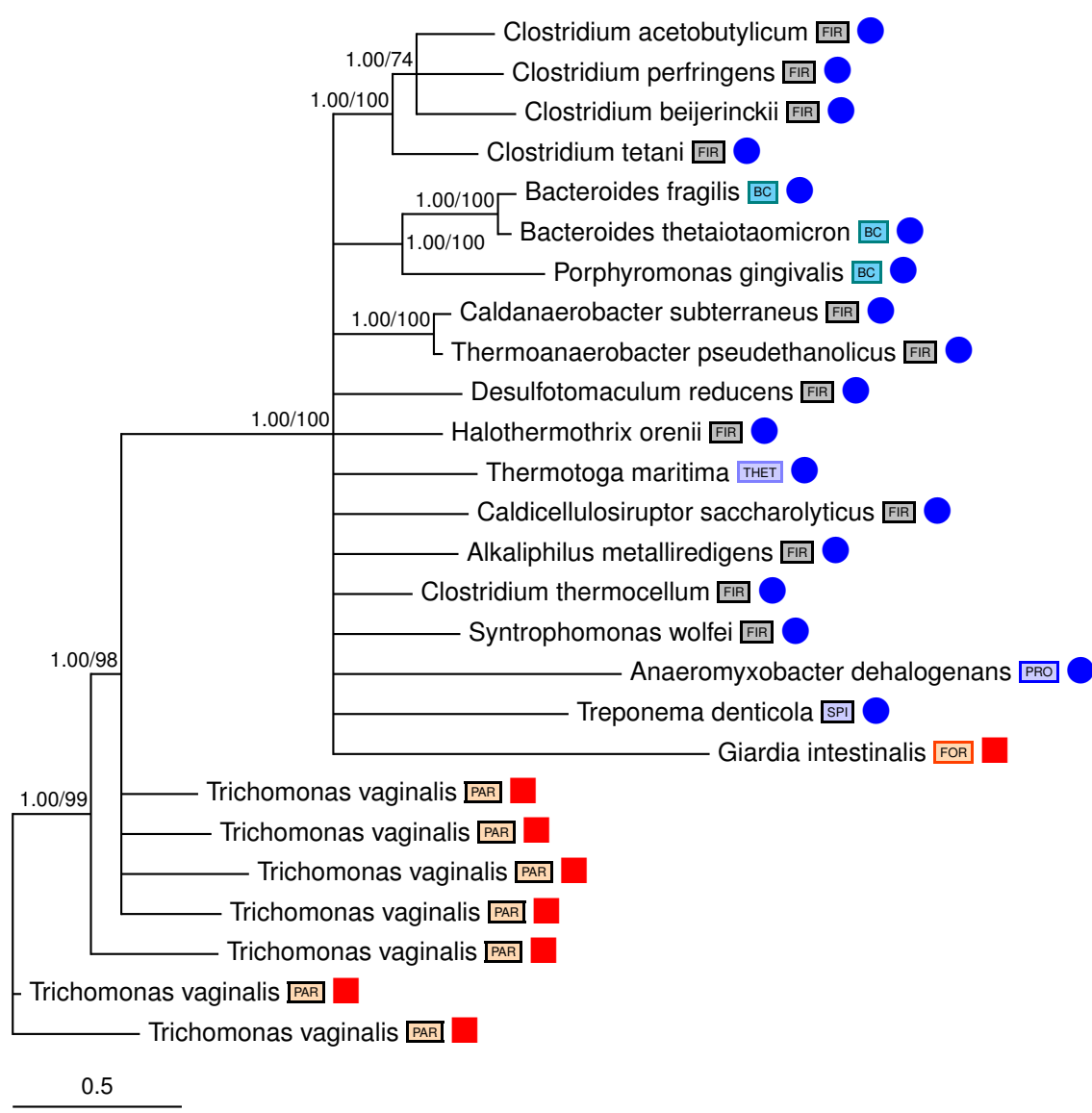
Candy accession: TV82397081
RefSeq accession: XP_001310516.1
Uniprot accession: A2FBY7_TRIVA
Comments: LGT? - TV-EH POLYTOMY
Species affected: TV
Adjacent taxa in tree: Polytomy
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted tRNA(Ile)-lysidine synthase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

Candy accession: Q51D31_ENTHI
RefSeq accession: XP_656114.1
Uniprot accession: C4LXX3_ENTHI
Comments: LGT? - EH-TV POLYTOMY
Species affected: EH
Adjacent taxa in tree: Polytomy
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted tRNA(Ile)-lysidine synthase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



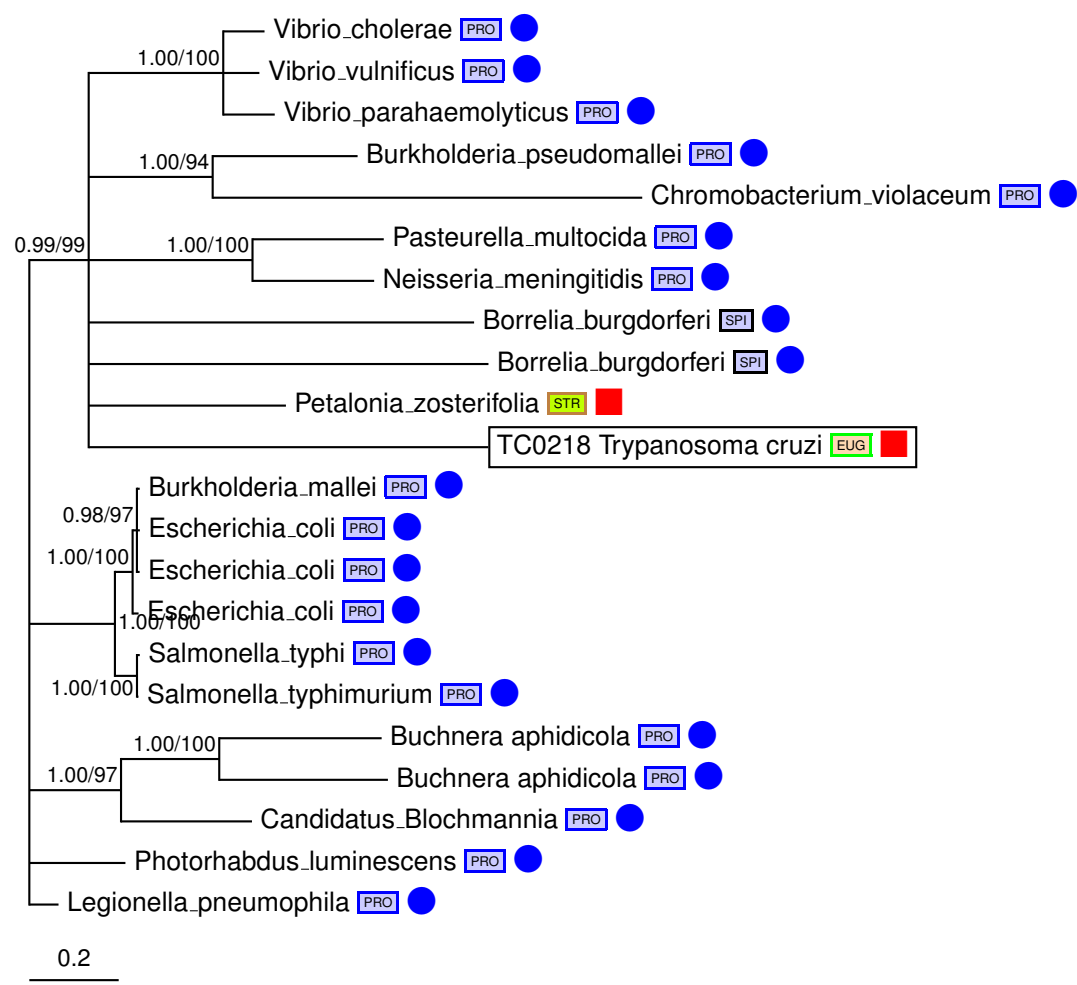
EE006

Candy accession: A2FLL8_TRIVA
 RefSeq accession: XP_001307121.1
 Uniprot accession: A2FLL8_TRIVA
 Comments: LGT? - GI-TV POLYTOMY
 Species affected: GI, TV
 Adjacent taxa in tree: Polytomy
 EC annotation - (Blast/Profile): EC:6.1.1.3
 RefSeq annotation: Phosphoribulokinase family protein-
 related protein
 Name of enzyme/protein: Phosphoribulokinase family protein-
 related protein
 KEGG PATHWAY - level 1: Translation - Genetic Information
 Processing
 KEGG PATHWAY - level 2: Translation - Genetic Information
 Processing



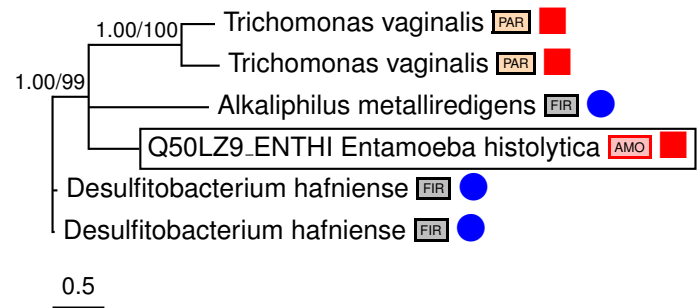
EE007

Candy accession: TC0218
RefSeq accession: XP_813761.1
Uniprot accession: Q4DHC1_TRYCR
Comments: LGT? - TC - POLYTONY WITH A BROWN ALGEA?
Species affected: TC,PZ
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.1.3.18
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: haloacid dehalogenase hydrolase
Name of enzyme/protein: phosphoglycolate phosphatase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Glyoxylate and dicarboxylate metabolism



EE008

Candy accession: Q50LZ9_ENTHI
RefSeq accession: XP_648004.1
Uniprot accession: C4MBF0_ENTHI
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED ANAEROBIC PROTISTS - TV AND
EH
Species affected: EH,TV
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 nitroreductase domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



EE009

Candy accession: Q9GQI5_GIAIN
RefSeq accession: XP_001704452.1
Uniprot accession: Q9GQI5_GIAIN
Comments: LGT - LIKELY LGT BETWEEN DIPLOMONAD AND AMOEBOZOA

Species affected: GI
Adjacent taxa in tree: Entamoeba

EC annotation - (Blast/Profile): EC:6.1.1.7
PHOBIUS SP: 0
PHOBIUS TMD: 0

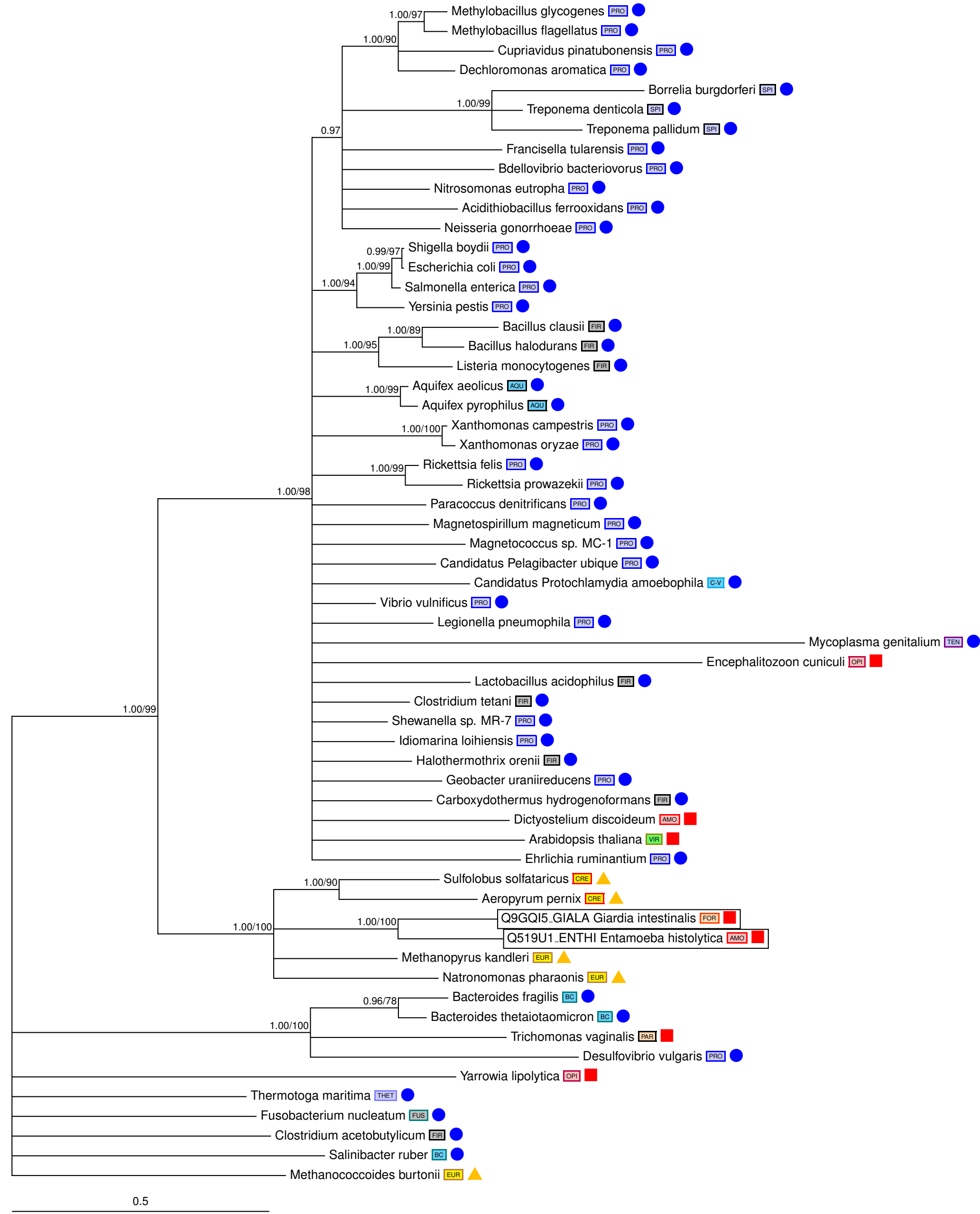
RefSeq annotation: Alanyl-tRNA synthetase
Name of enzyme/protein: alanine-tRNA ligase
KEGG PATHWAY - level 1: Translation - Genetic Information Processing
KEGG PATHWAY - level 2: Aminoacyl-tRNA biosynthesis

Candy accession: Q519U1_ENTHI
RefSeq accession: XP_654998.1
Uniprot accession: Q519U1_ENTHI
Comments: LGT - LIKELY LGT BETWEEN DIPLOMONAD AND AMOEBOZOA

Species affected: EH
Adjacent taxa in tree: Giardia

EC annotation - (Blast/Profile): EC:6.1.1.7
PHOBIUS SP: 0
PHOBIUS TMD: 0

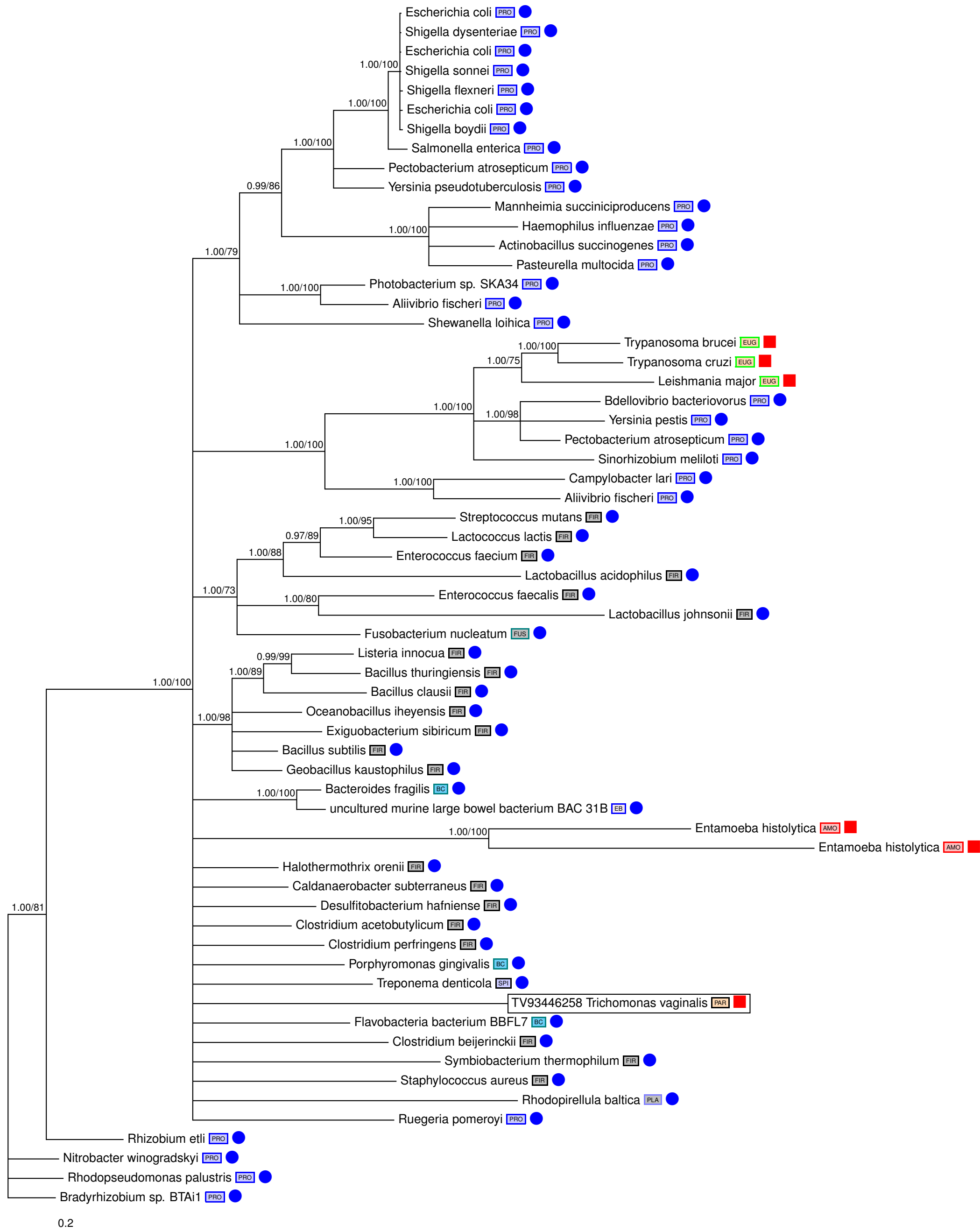
RefSeq annotation: alanyl-tRNA synthetase
Name of enzyme/protein: alanine-tRNA ligase
KEGG PATHWAY - level 1: Translation - Genetic Information Processing
KEGG PATHWAY - level 2: Translation - Genetic Information Processing



EE010

Candy accession: TV93446258
RefSeq accession: XP_001327107.1
Uniprot accession: A2DXD2_TRIVA
Comments: LGT?- POLYTOMY OF ANIMAL HOST ASSOCIATED ANAEROBIC PROTISTS - TV AND EH
Species affected: EH,TV
Adjacent taxa in tree: Polytomy
EC annotation - (Blast/Profile): EC:3.4.11.4
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Clan MH, family M20, peptidase T-like metallopeptidase
Name of enzyme/protein: tripeptide aminopeptidase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction

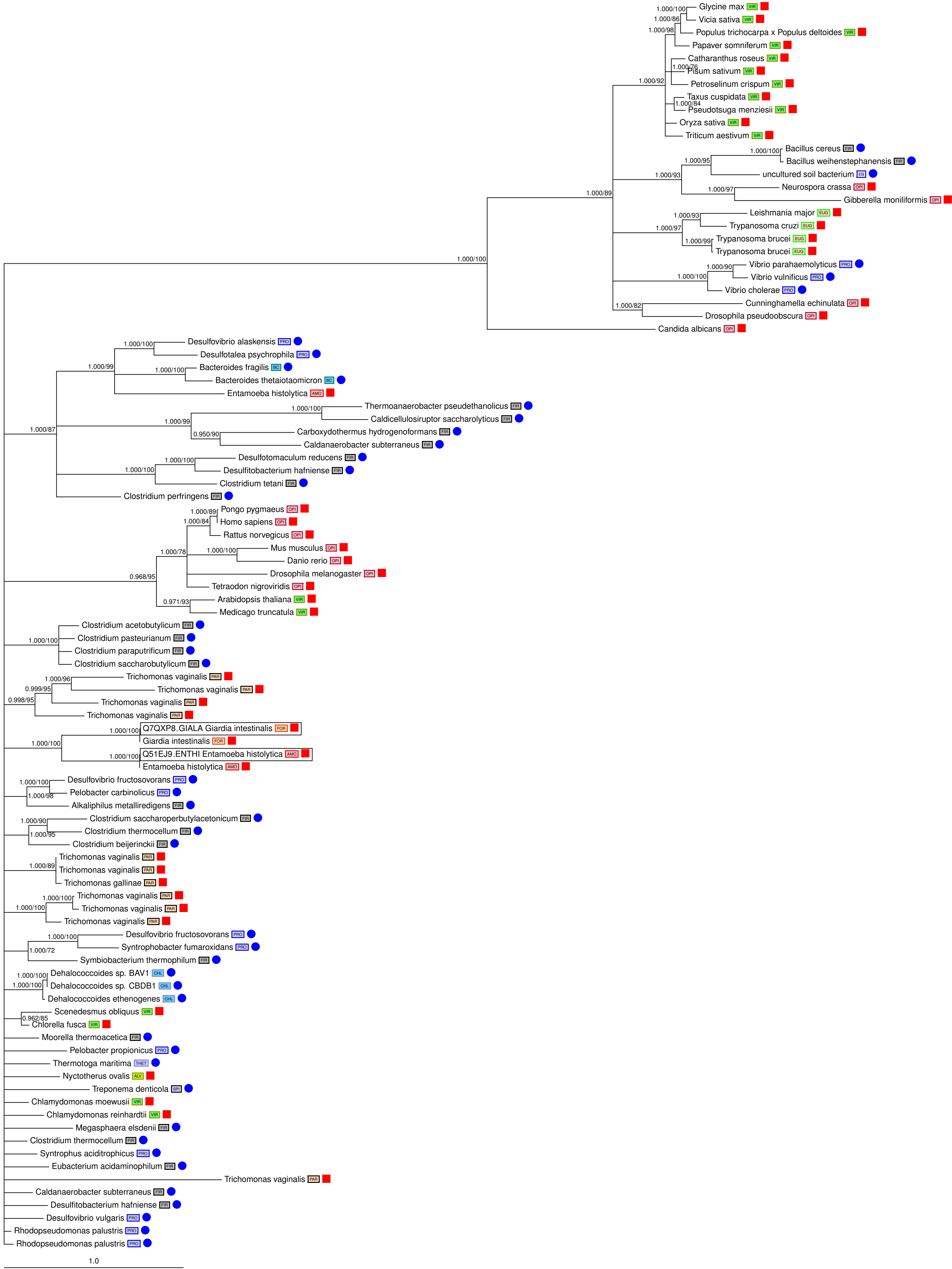
Candy accession: C4M2F1_ENTHI
RefSeq accession: XP_650152
Uniprot accession: C4M2F1_ENTHI
Comments: LGT?- POLYTOMY OF ANIMAL HOST ASSOCIATED ANAEROBIC PROTISTS - TV AND EH
Species affected: EH,TV
Adjacent taxa in tree: Polytomy
EC annotation - (Blast/Profile): EC:3.4.11.14
RefSeq annotation: peptidase T
Name of enzyme/protein: peptidase T
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



EE011

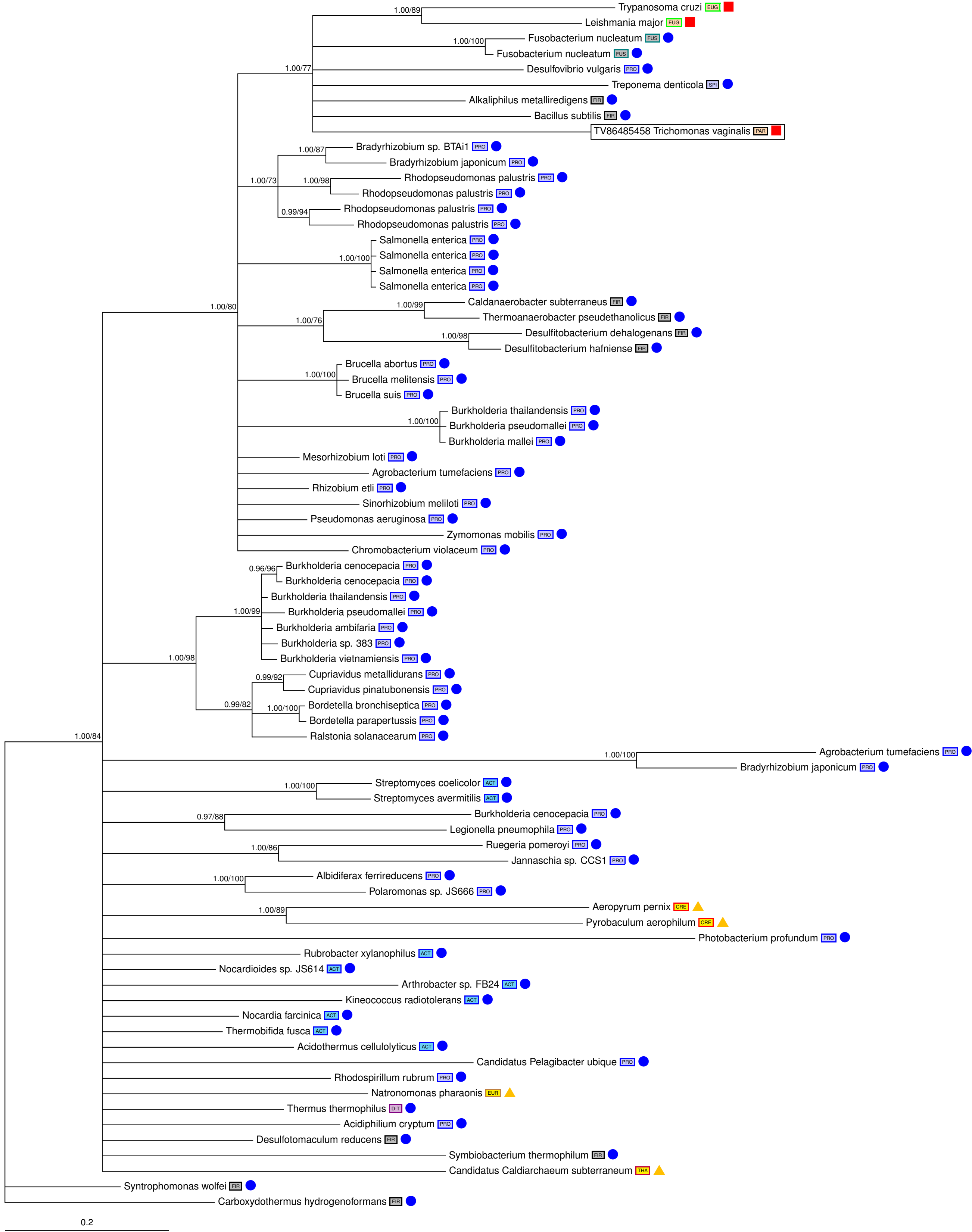
Candy accession: Q7QXP8_GIALA
RefSeq accession: XP_001709915.1
Uniprot accession: Q7QXP8_GIALA
Comments: LGT - POSSIBLE LGT BETWEEN DIPLOMONAD
AND AMOEBOZOA
Species affected: GL,EH
Adjacent taxa in tree: Entamoeba
EC annotation - (Blast/Profile): EC:1.12.7.2
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Fe-hydrogenase-1
Name of enzyme/protein: Iron hydrogenase
KEGG PATHWAY - level 1: Energy Metabolism
KEGG PATHWAY - level 2: Methane metabolism

Candy accession: Q51EJ9_ENTHI
RefSeq accession: XP_656685.1
Uniprot accession: Q51EJ9_ENTHI
Comments: LGT - POSSIBLE LGT BETWEEN DIPLOMONAD
AND AMOEBOZOA
Species affected: GL,EH
Adjacent taxa in tree: Giardia
EC annotation - (Blast/Profile): EC:1.12.7.2
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Fe-hydrogenase
Name of enzyme/protein: Iron hydrogenase
KEGG PATHWAY - level 1: Energy Metabolism
KEGG PATHWAY - level 2: Methane metabolism



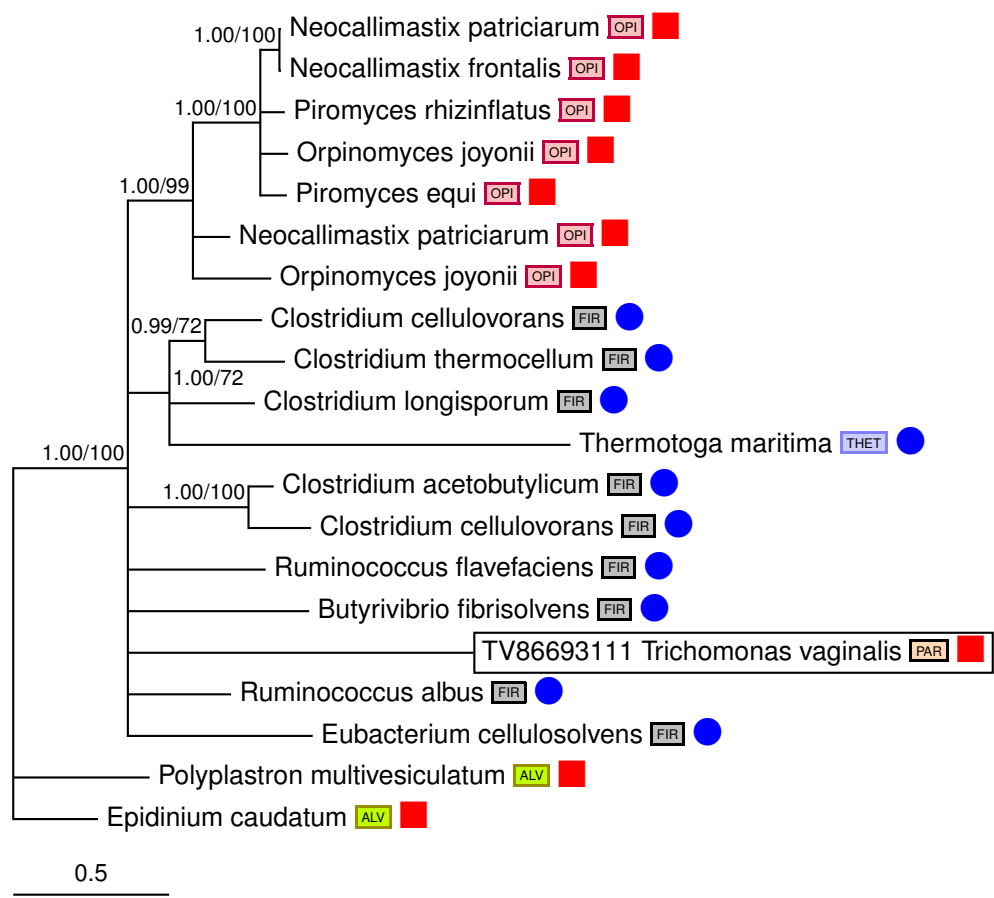
EE012

Candy accession: TV86485458
RefSeq accession: XP_001584037.1
Uniprot accession: A2D925_TRIVA
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED PROTISTS - TV AND KINETOPLASTIDS
Species affected: TV,LM,TC
Adjacent taxa in tree: Bacterial
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: YbaK / prolyl-tRNA synthetases associated domain containing protein
Name of enzyme/protein: Predicted cysteinyl-tRNA(Pro) deacylases
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



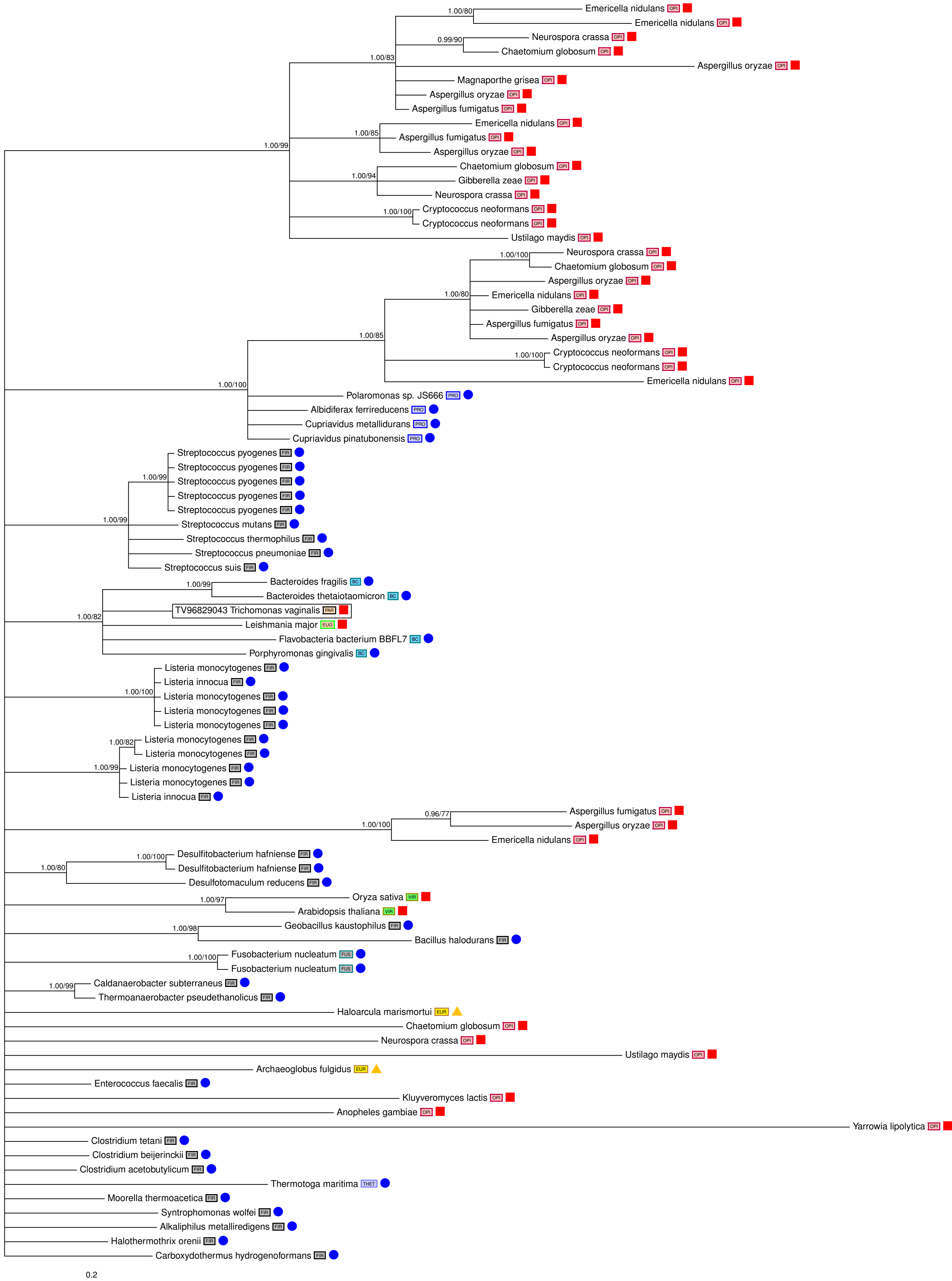
EE013

Candy accession: TV86693111
RefSeq accession: XP_001316689.1
Uniprot accession: A2ESA2_TRIVA
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED ANAEROBIC MICROBIAL
EUKARYOTES - RUMEN CILIATES, RUMEN FUNGI
AND TV
Species affected: TV
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): EC:3.2.1.4
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: cellulase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Starch and sucrose metabolism



EE014

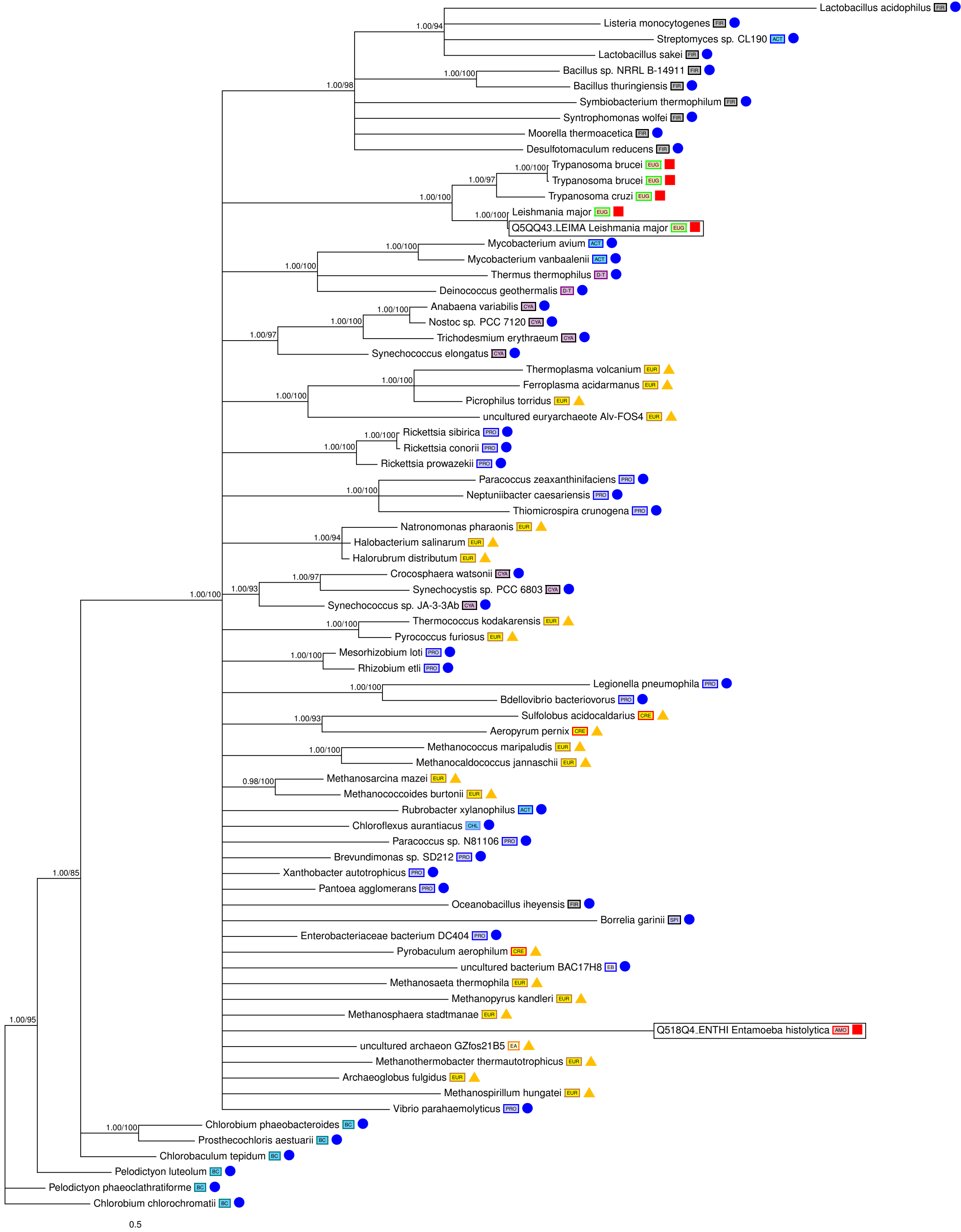
Candy accession: TV96829043
RefSeq accession: XP_001307133.1
Uniprot accession: A2FLNO_TRIVA
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED PROTISTS TV AND LM WITH
BACTERIA IN SAME CLAN
Species affected: n
Adjacent taxa in tree: Bacteroidetes
EC annotation - (Blast/Profile): EC:1.3.1.9
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: oxidoreductase, 2-nitropropane
dioxygenase family protein
Name of enzyme/protein: enoyl-[acyl-carrier-protein] reductase
(NADH)
KEGG PATHWAY - level 1: Lipid Metabolism
KEGG PATHWAY - level 2: Fatty acid biosynthesis



EE015

Candy accession: Q518Q4_ENTHI
RefSeq accession: XP_654698.1
Uniprot accession: C4LZV4_ENTHI
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED PROTISTS - LM,TC,TB AND EH
Species affected: EH, LM,TB,TC
Adjacent taxa in tree: Polytomy
EC annotation - (Blast/Profile): EC:5.3.3.2
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: isopentenyl-diphosphate delta-isomerase
Name of enzyme/protein: isopentenyl-diphosphate Delta-isomerase
KEGG PATHWAY - level 1: Metabolism of Terpenoids and Polyketides
KEGG PATHWAY - level 2: Terpenoid backbone biosynthesis

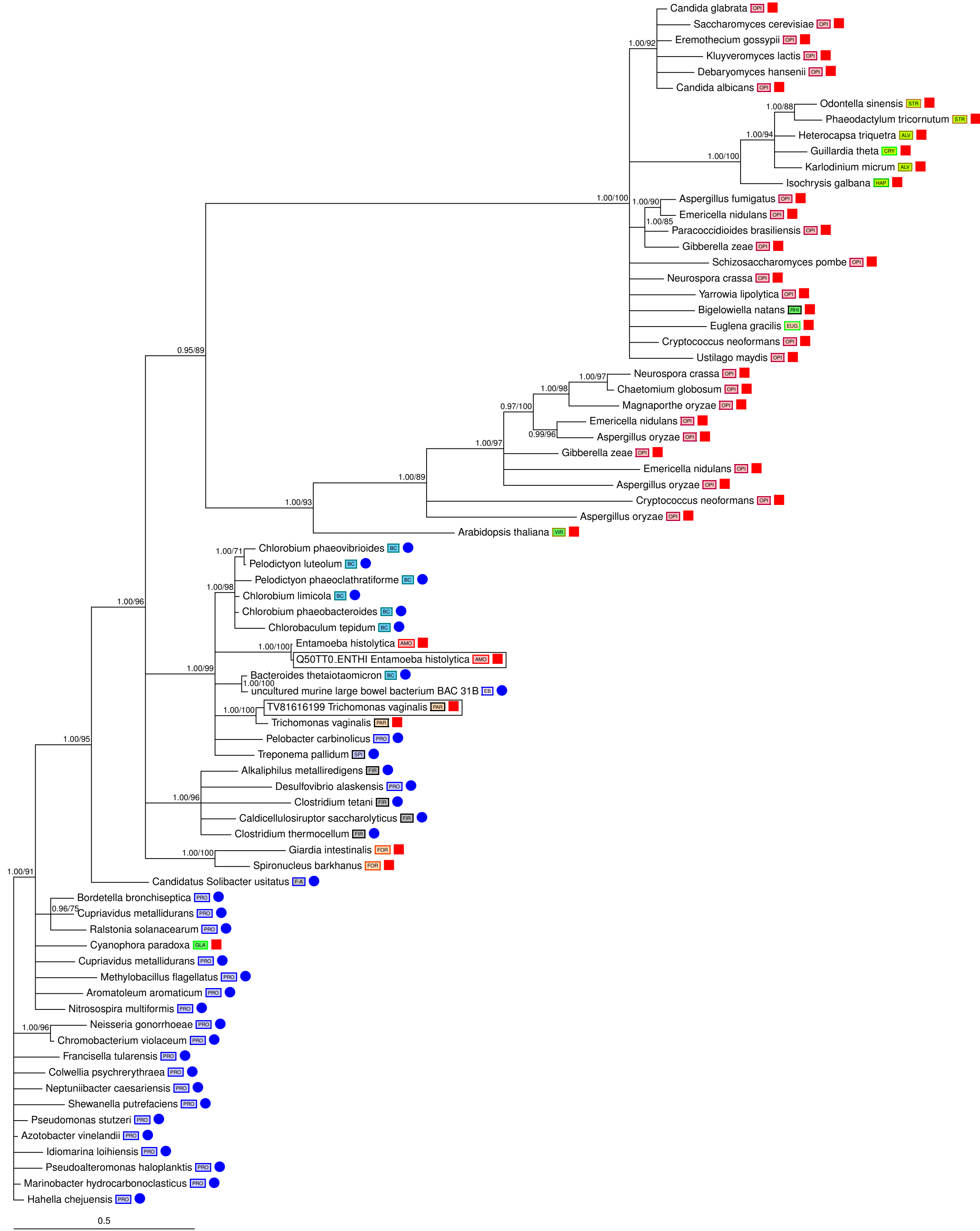
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RefSeq accession: XP_843634.1
Uniprot accession: Q5QQ43_LEIMA
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED PROTISTS - LM,TC,TB AND EH
Species affected: EH, LM,TB,TC
Adjacent taxa in tree: Polytomy
EC annotation - (Blast/Profile): EC:5.3.3.2
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: isomerase
Name of enzyme/protein: isopentenyl-diphosphate Delta-isomerase
KEGG PATHWAY - level 1: Metabolism of Terpenoids and Polyketides
KEGG PATHWAY - level 2: Terpenoid backbone biosynthesis



EE016

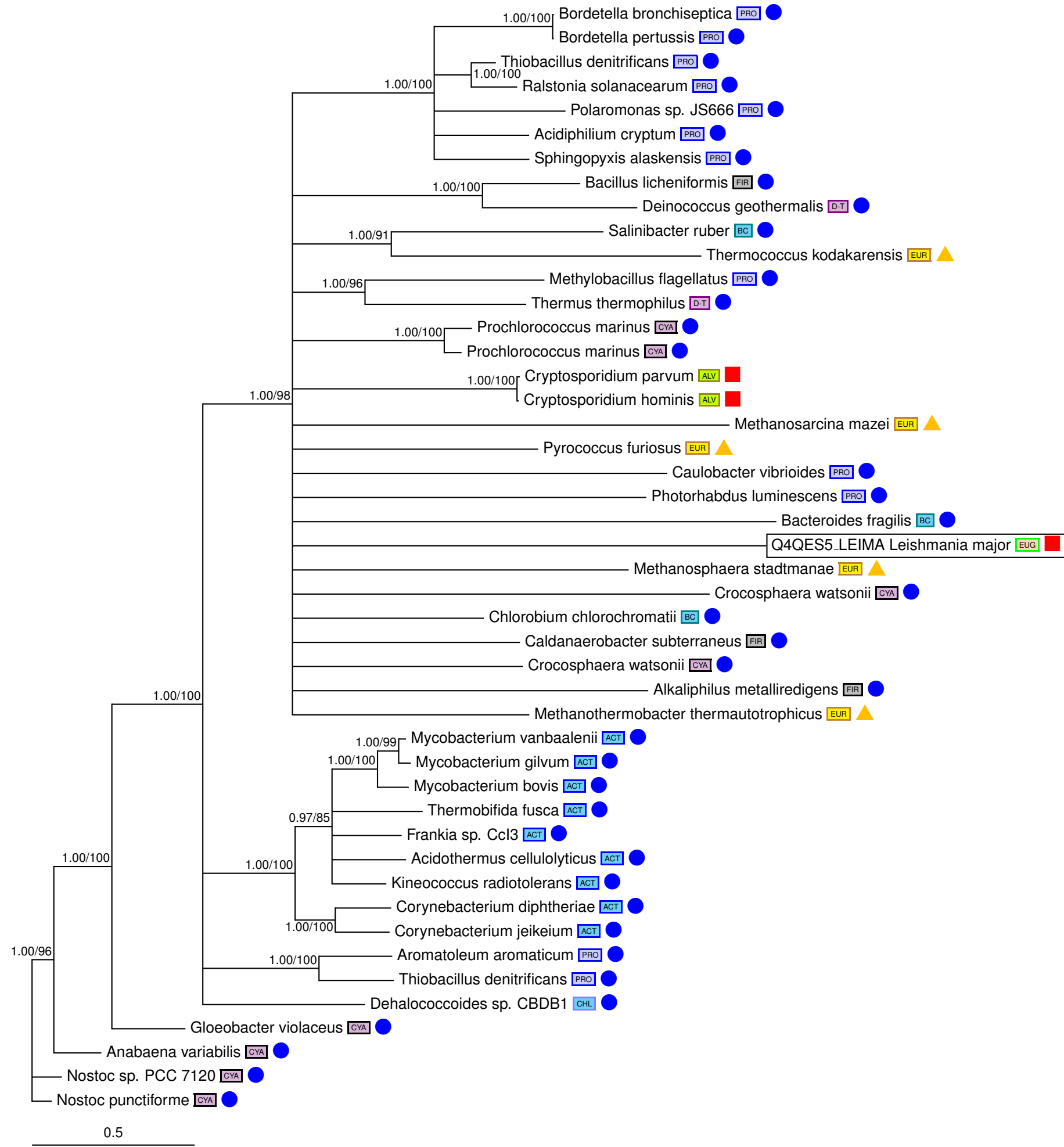
Candy accession: TV81616199
RefSeq accession: XP_001326960.1
Uniprot accession: A2DY01_TRIVA
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED ANAEROBIC PROTISTS - TV AND
EH ONE NODE
Species affected: EH, TV
Adjacent taxa in tree: Bacterial
EC annotation - (Blast/Profile): EC:4.1.2.13
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: fructose-1,6-bisphosphate aldolase
Name of enzyme/protein: fructose-bisphosphate aldolase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Glycolysis / Gluconeogenesis, Pentose phosphate pathway, Fructose and mannose metabolism

Candy accession: Q50TT0_ENTHI
RefSeq accession: XP_650373.1
Uniprot accession: C4LXD7_ENTHI
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED ANAEROBIC PROTISTS - TV AND
EH ONE NODE
Species affected: EH, TV
Adjacent taxa in tree: Bacterial
EC annotation - (Blast/Profile): EC:4.1.2.13
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: fructose-1,6-bisphosphate aldolase
Name of enzyme/protein: fructose-bisphosphate aldolase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Glycolysis / Gluconeogenesis / Fructose and mannose metabolism



EE017

Candy accession: Q4QES5_LEIMA
RefSeq accession: XP_001682173.1
Uniprot accession: Q4QES5_LEIMA
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED PARASITC PROTISTS - LM+CP+CH
Species affected: LM, CP
Adjacent taxa in tree: Polytomy
EC annotation - (Blast/Profile): EC:2.4.1.14
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: sucrose-phosphate synthase-like protein
Name of enzyme/protein: sucrose-phosphate synthase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Starch and sucrose metabolism

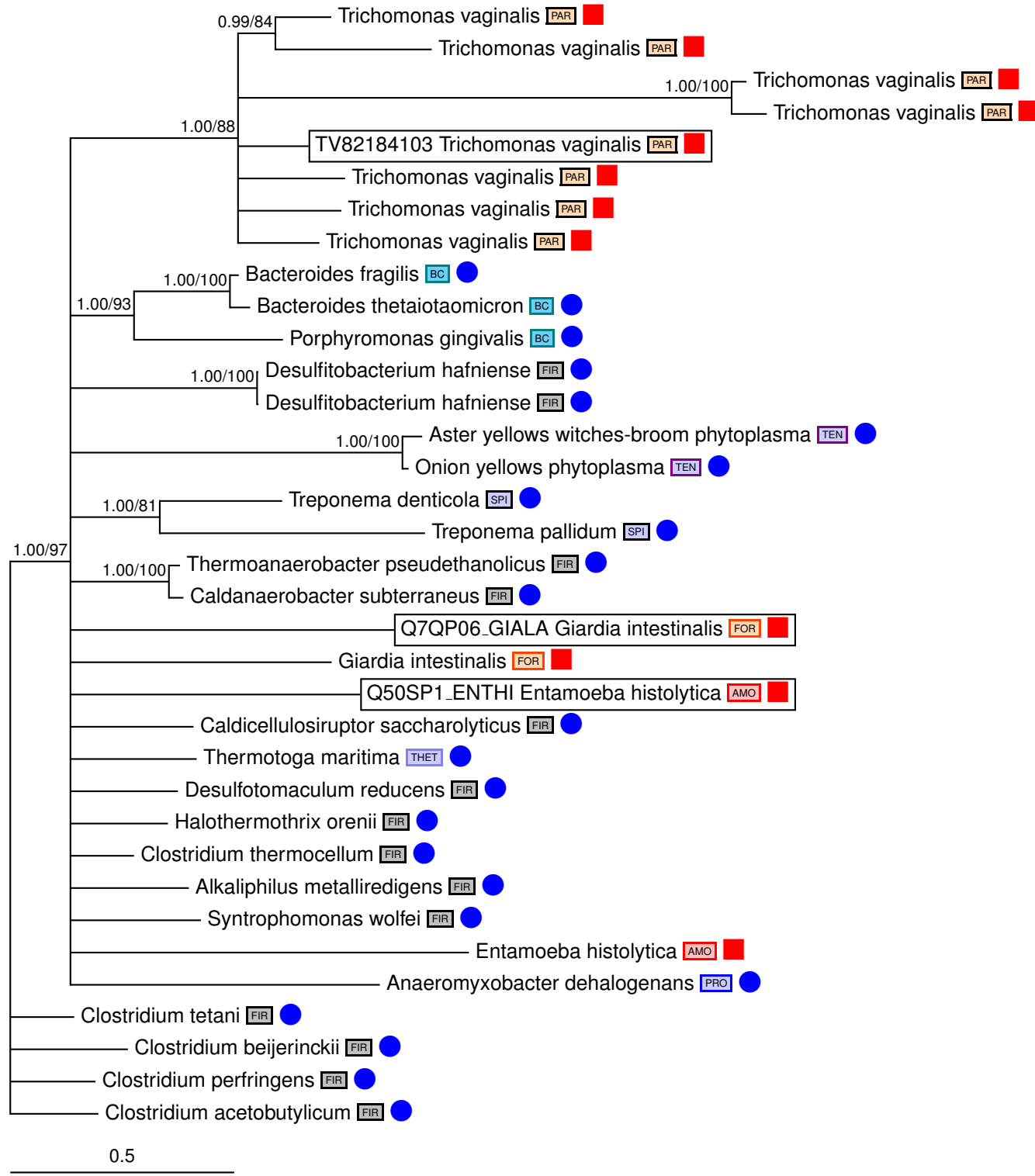


EE018

Candy accession: TV82184103
RefSeq accession: XP_001311676.1
Uniprot accession: A2F8L4_TRIVA
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED ANAEROBIC PROTISTS - TV, EH, GI
Species affected: EH,GI,TV
Adjacent taxa in tree: Polytoomy
EC annotation - (Blast/Profile): EC:2.7.1.48
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Phosphoribulokinase / Uridine kinase family protein
Name of enzyme/protein: uridine kinase
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Pyrimidine metabolism

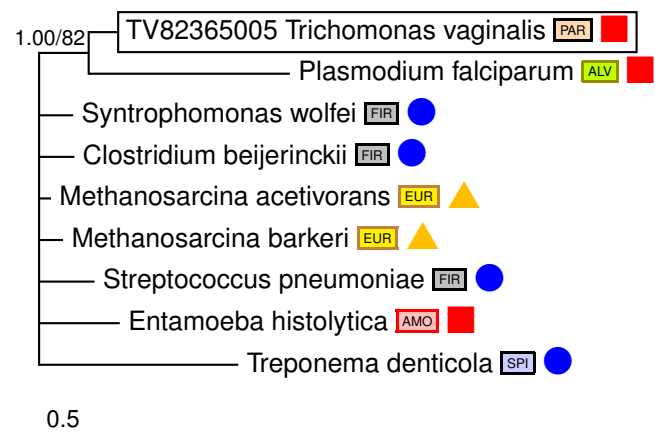
Candy accession: Q7QP06_GIALA
RefSeq accession: XF_001704181.1
Uniprot accession: A8BYJ2_GIALA
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED ANAEROBIC PROTISTS - TV, EH, GI
Species affected: EH,GI,TV
Adjacent taxa in tree: Polytoomy
EC annotation - (Blast/Profile): EC:2.7.1.48
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Uridine kinase
Name of enzyme/protein: uridine kinase
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Pyrimidine metabolism

Candy accession: Q50SP1_ENTHI
RefSeq accession: XP_656795.1
Uniprot accession: C4LYS1_ENTHI
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED ANAEROBIC PROTISTS - TV, EH, GI
Species affected: EH,GI,TV
Adjacent taxa in tree: Polytoomy
EC annotation - (Blast/Profile): EC:2.7.1.48
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: phosphoribulokinase /uridine kinase family protein
Name of enzyme/protein: uridine kinase
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Pyrimidine metabolism



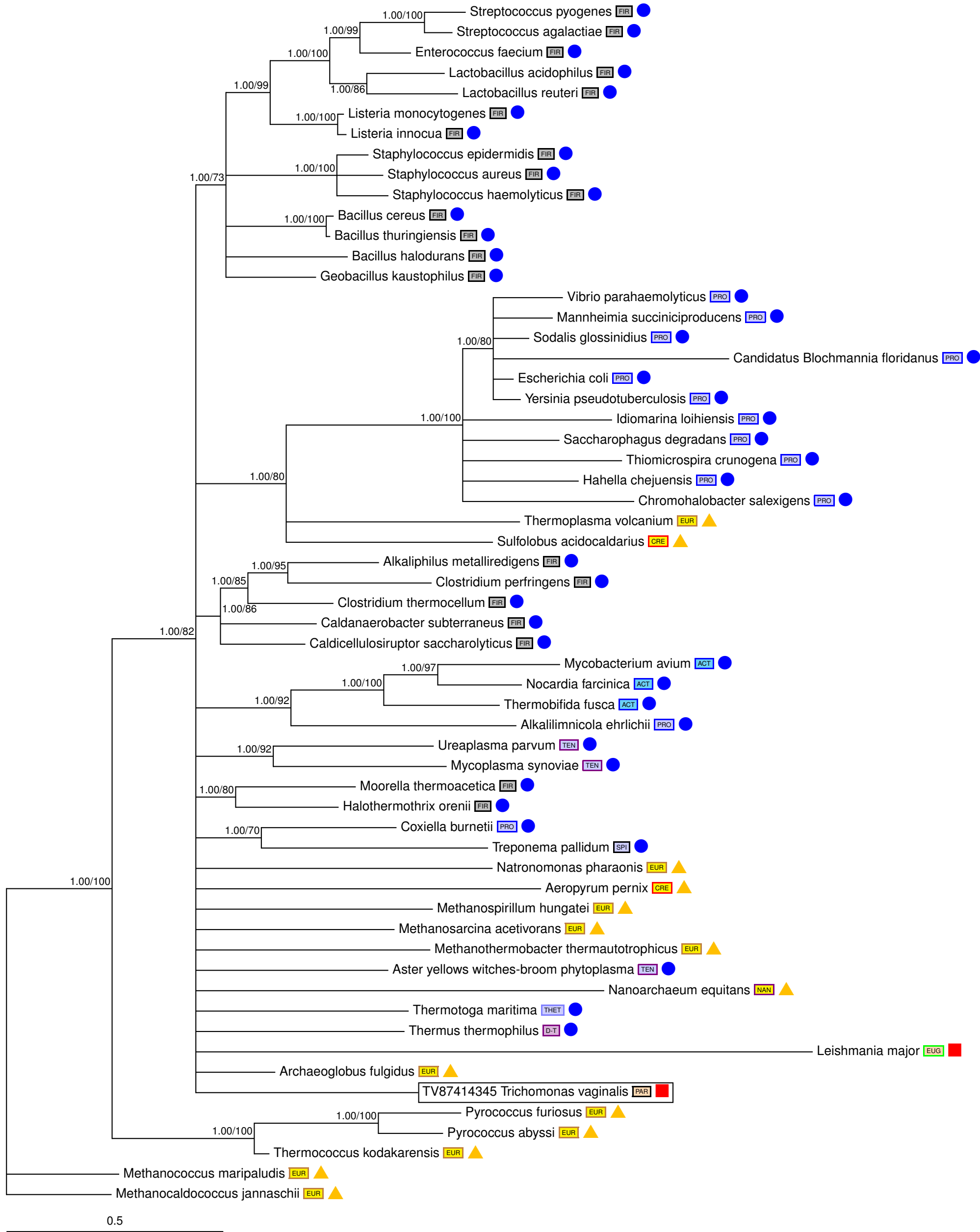
EE019

Candy accession: TV82365005
RefSeq accession: XP_001295233.1
Uniprot accession: A2GKL5_TRIVA
 Comments: LGT? - POLYTOMY OF ANIMAL HOST
 ASSOCIATED ANAEROBIC PROTISTS - TV, EH
Species affected: PF,TV,EH
Adjacent taxa in tree: Prokaryote
EC annotation - (Blast/Profile): na
 PHOBIOUS SP: 0
 PHOBIOUS TMD: 0
RefSeq annotation: choline binding protein
Name of enzyme/protein: Protein containing LRR domains
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na



EE020

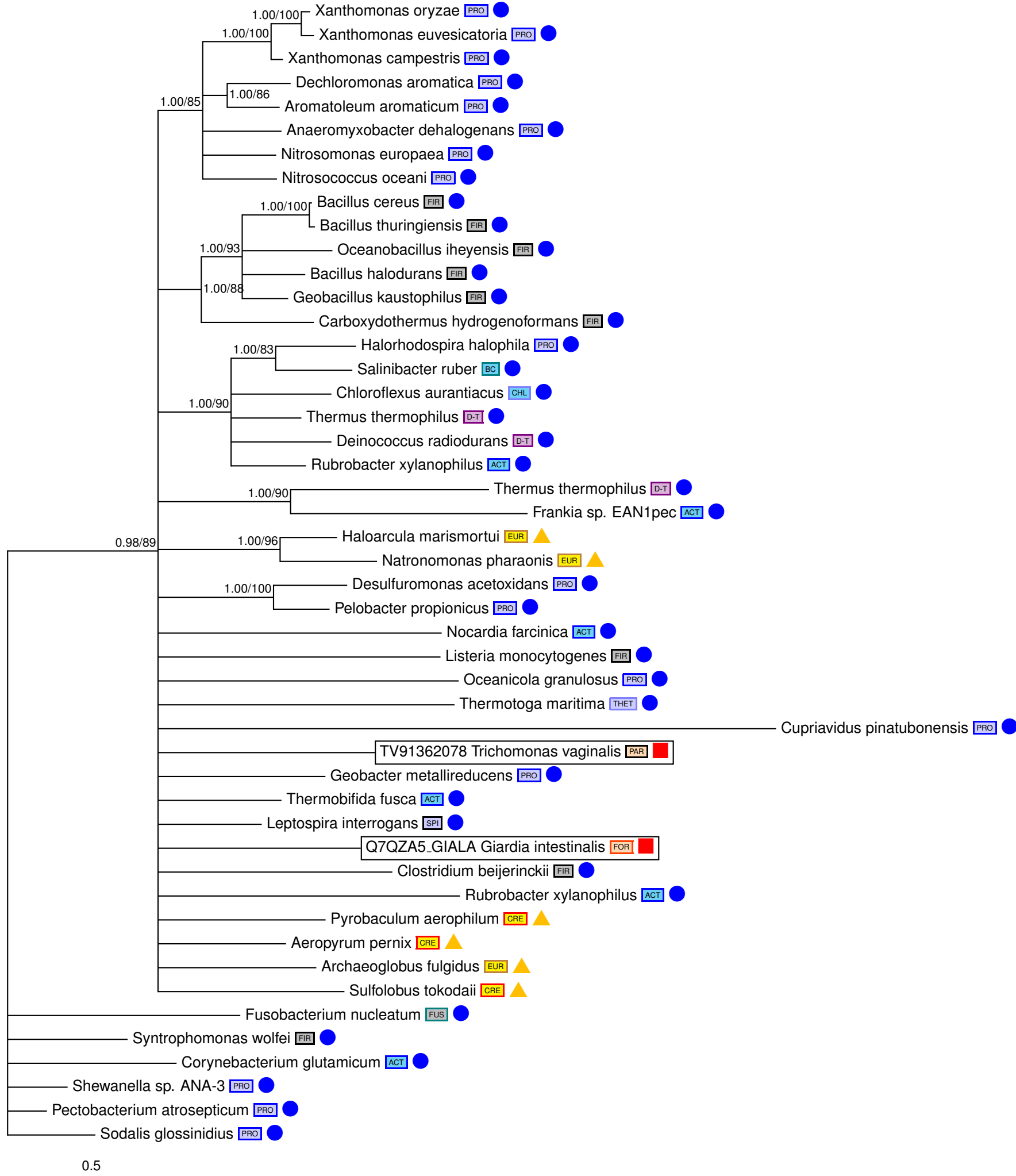
Candy accession: TV87414345
RefSeq accession: XP_001580194.1
Uniprot accession: A2DK37_TRIVA
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED PROTISTS - TV, LM
Species affected: TV,LM
Adjacent taxa in tree: Prokaryote
EC annotation - (Blast/Profile): na
PHOBIOUS SP: 0
PHOBIOUS TMD: 0
RefSeq annotation: thiamine biosynthesis protein ThiI
Name of enzyme/protein: Predicted thiamine biosynthesis protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na



EE021

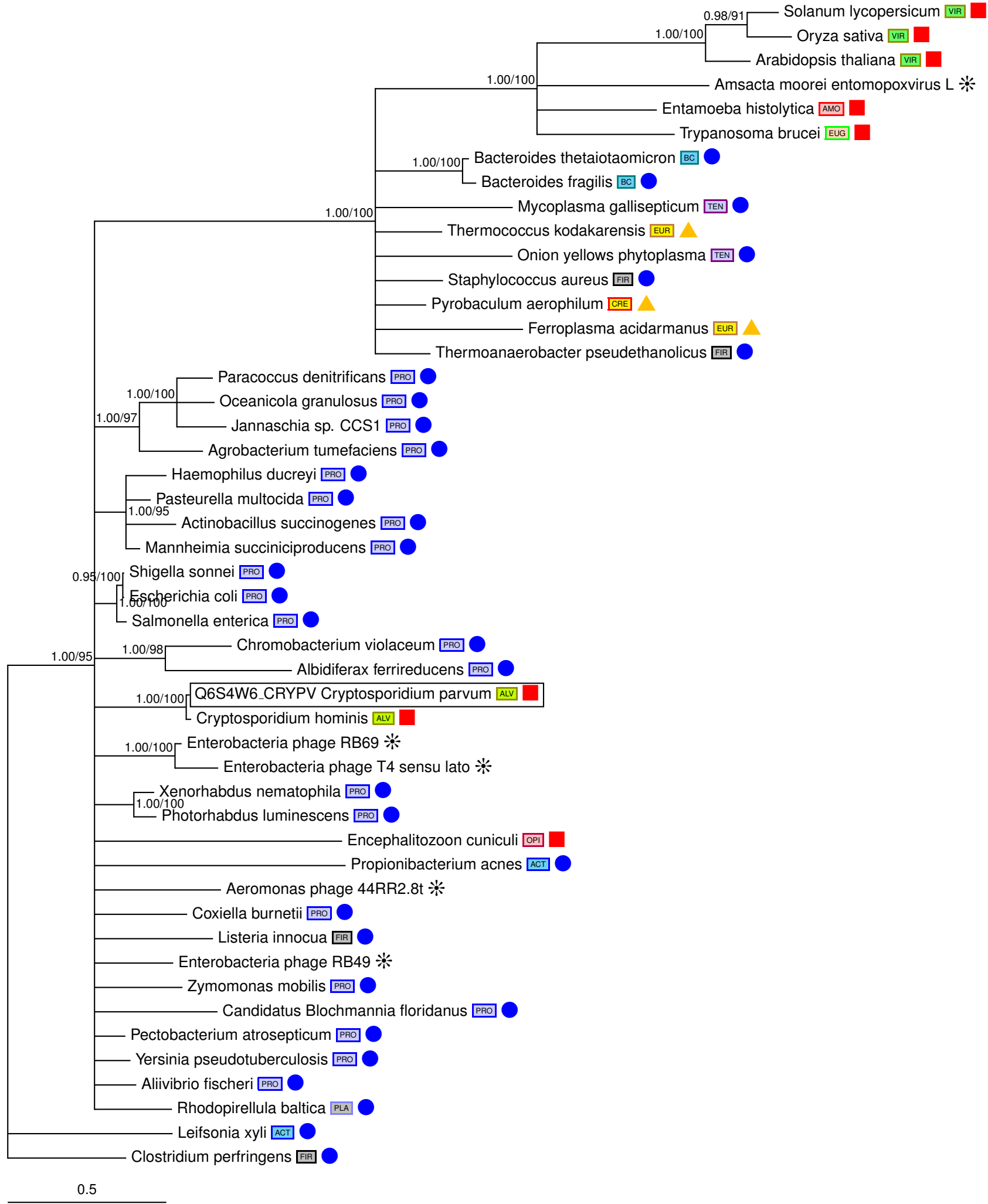
Candy accession: TV91362078
RefSeq accession: XP_001330242.1
Uniprot accession: A2F143_TRIVA
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED ANAEROBIC PROTISTS - TV, GI
Species affected: TV
Adjacent taxa in tree: GI?
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: metallo-beta-lactamase superfamily
protein
Name of enzyme/protein: Predicted Metallo-beta-lactamase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

Candy accession: Q7QZA5_GIALA
RefSeq accession: XP_001708073.1
Uniprot accession: A8BBV2_GIATC
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED ANAEROBIC PROTISTS - TV, GI
Species affected: GI
Adjacent taxa in tree: TV?
EC annotation - (Blast/Profile): EC:3.1.2.6
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Metallo-beta-lactamase superfamily
protein
Name of enzyme/protein: Predicted Metallo-beta-lactamase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction



EE022

Candy accession: Q6S4W6_CRYPV
RefSeq accession: XP_625605.1
Uniprot accession: Q6S4W6_CRYPV
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED INTRACELLULAR PARASITIC
PROTISTS - CP, CH, EC
Species affected: CP,CH,EC
Adjacent taxa in tree: Polytoomy
EC annotation - (Blast/Profile): EC:2.7.1.21
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: thymidine kinase of likely bacterial origin
Name of enzyme/protein: Thymidine kinase
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Pyrimidine metabolism



EE023

Candy accession: Q50TU7_ENTHI
RefSeq accession: XP_650419.1
Uniprot accession: C4LVY0_ENTHI
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED ANAEROBIC PROTISTS - TV, EH

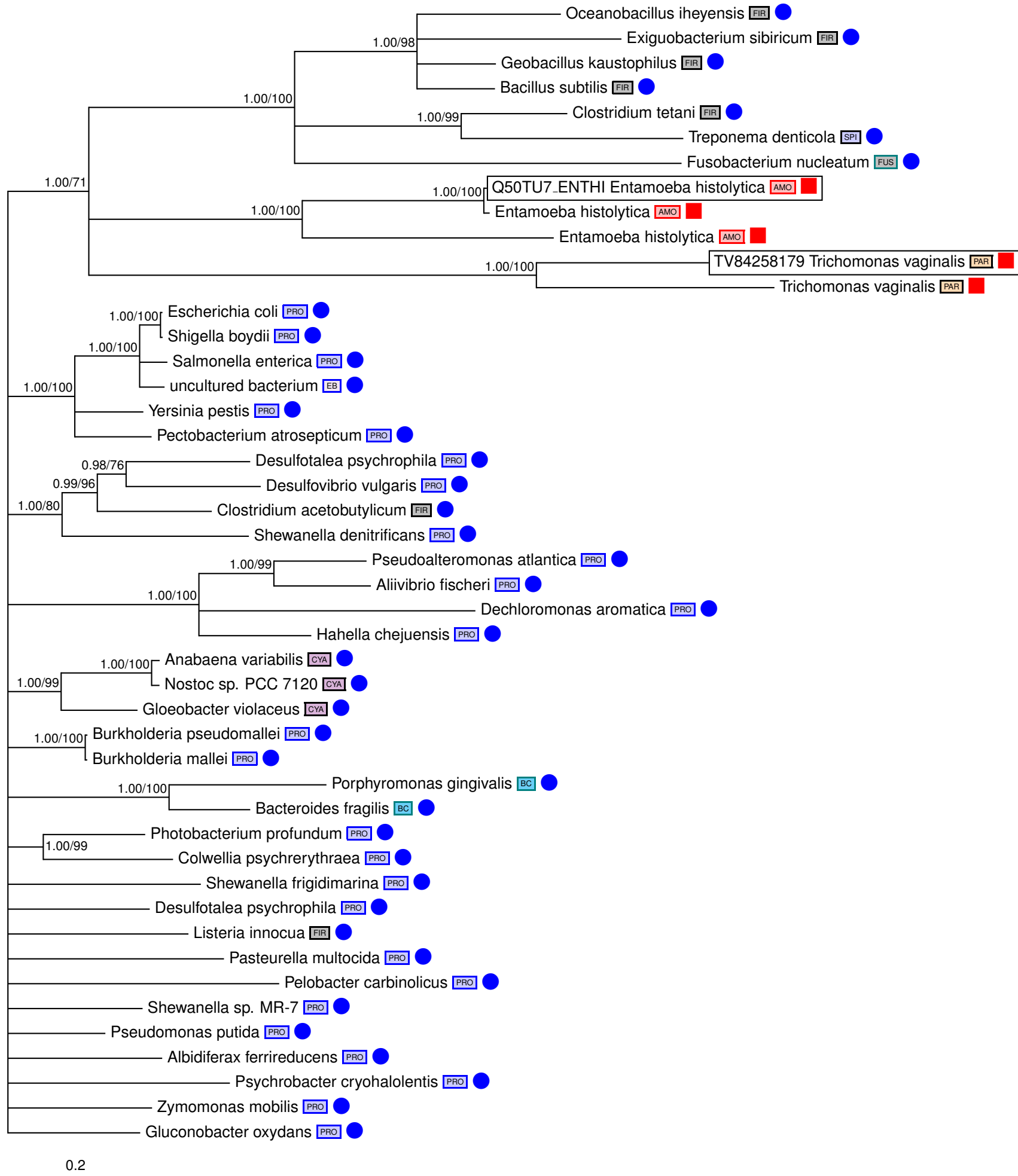
Species affected: EH
Adjacent taxa in tree: Polytoomy

EC annotation - (Blast/Profile): EC 1.1.1.2
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Bacterial
Name of enzyme/protein: Alcohol dehydrogenase
KEGG PATHWAY - level 1: Carbohydrate Metabolism, Lipid Metabolism
KEGG PATHWAY - level 2: Glycolysis / Gluconeogenesis / Glycerolipid metabolism

Candy accession: TV84258179
RefSeq accession: XF_001319933.1
Uniprot accession: A2EHX8_TRIVA
Comments: LGT? - POLYTOMY OF ANIMAL HOST
ASSOCIATED ANAEROBIC PROTISTS - TV, EH

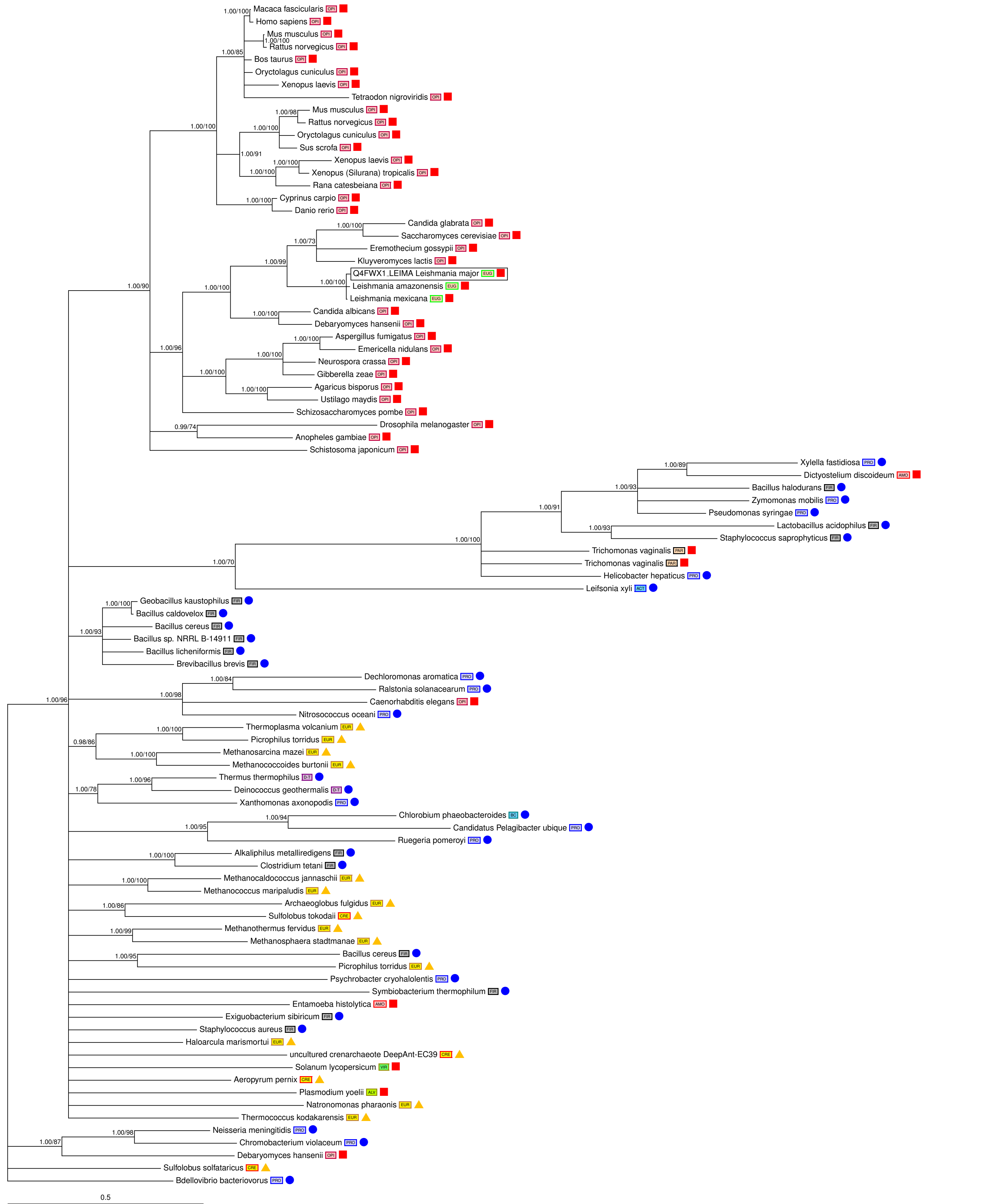
Species affected: TV
Adjacent taxa in tree: Polytoomy

EC annotation - (Blast/Profile): EC 1.1.1.2
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Bacterial
Name of enzyme/protein: Alcohol dehydrogenase
KEGG PATHWAY - level 1: Carbohydrate Metabolism, Lipid Metabolism
KEGG PATHWAY - level 2: Glycolysis / Gluconeogenesis / Glycerolipid metabolism



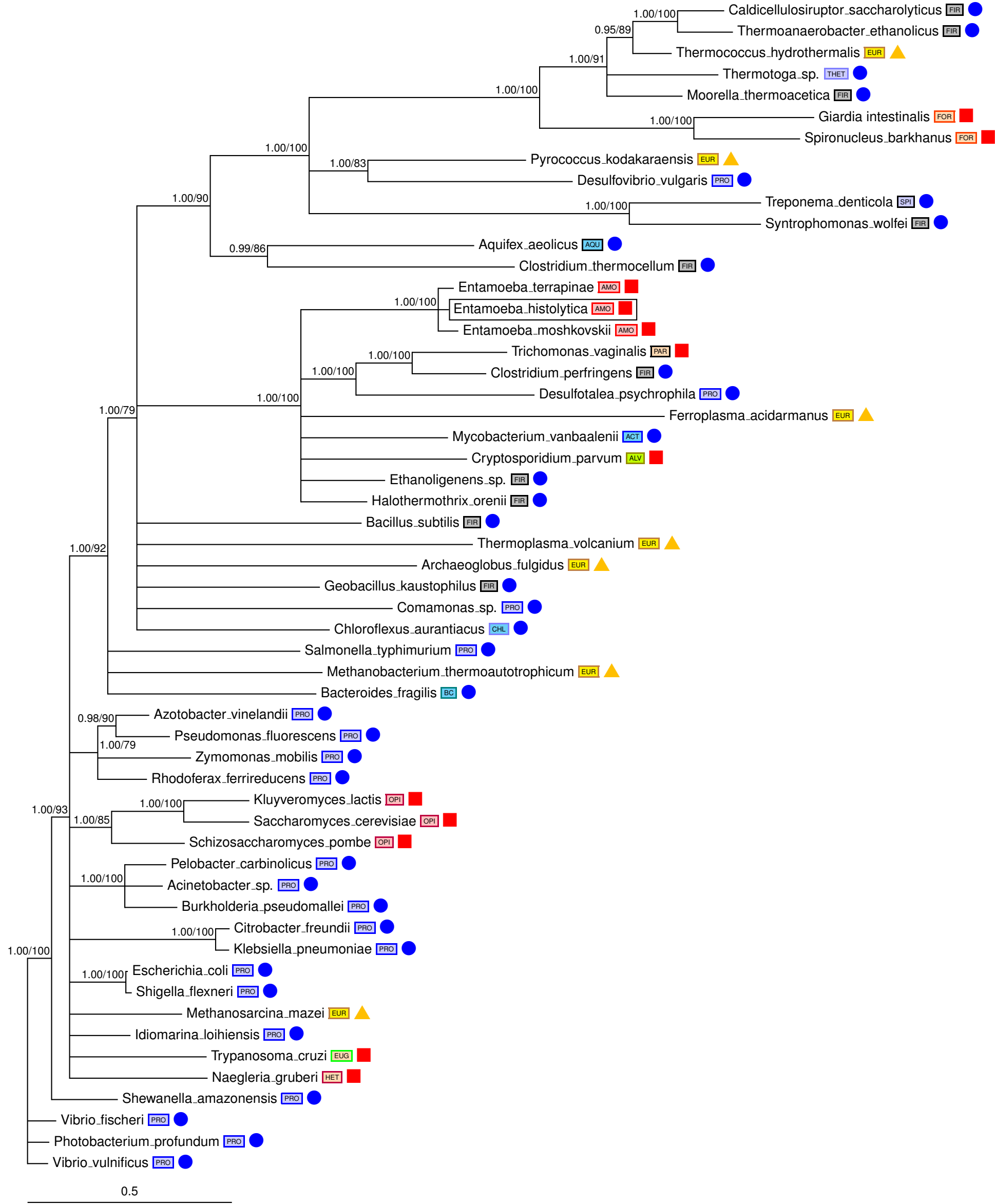
EE024

Candy accession: Q4FWX1_LEIMA
RefSeq accession: XP_843254
Uniprot accession: A2FNL2_TRIVA
Comments: LGT - FUNGI TO LM
Species affected: LM, FUNGI
Adjacent taxa in tree: Fungi
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



EE025

Candy accession: Q51C70_ENTHI
RefSeq accession: XP_652300.1
Uniprot accession: C4M230_ENTHI
Comments: LGT? - POLYTOMY EH AND CP
Species affected: EH,HT,HM
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:1.1.1.1
PHOBIUS SP: 0
PHOBIUS 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



EE026

Candy accession: B1N387_ENTHI
RefSeq accession: XP_001913653
Uniprot accession: B1N387_ENTHI
Comments: LGT - DEEP LGT INTO AMOEBOZOEA -> CP AND FUNGI, ALL HOST ASSOCIATED
Species affected: Amoebozoa, CP, PIROMYCETES
Adjacent taxa in tree: Prokaryotes
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

