

Supplementary Data S6 – Phylogenetic trees

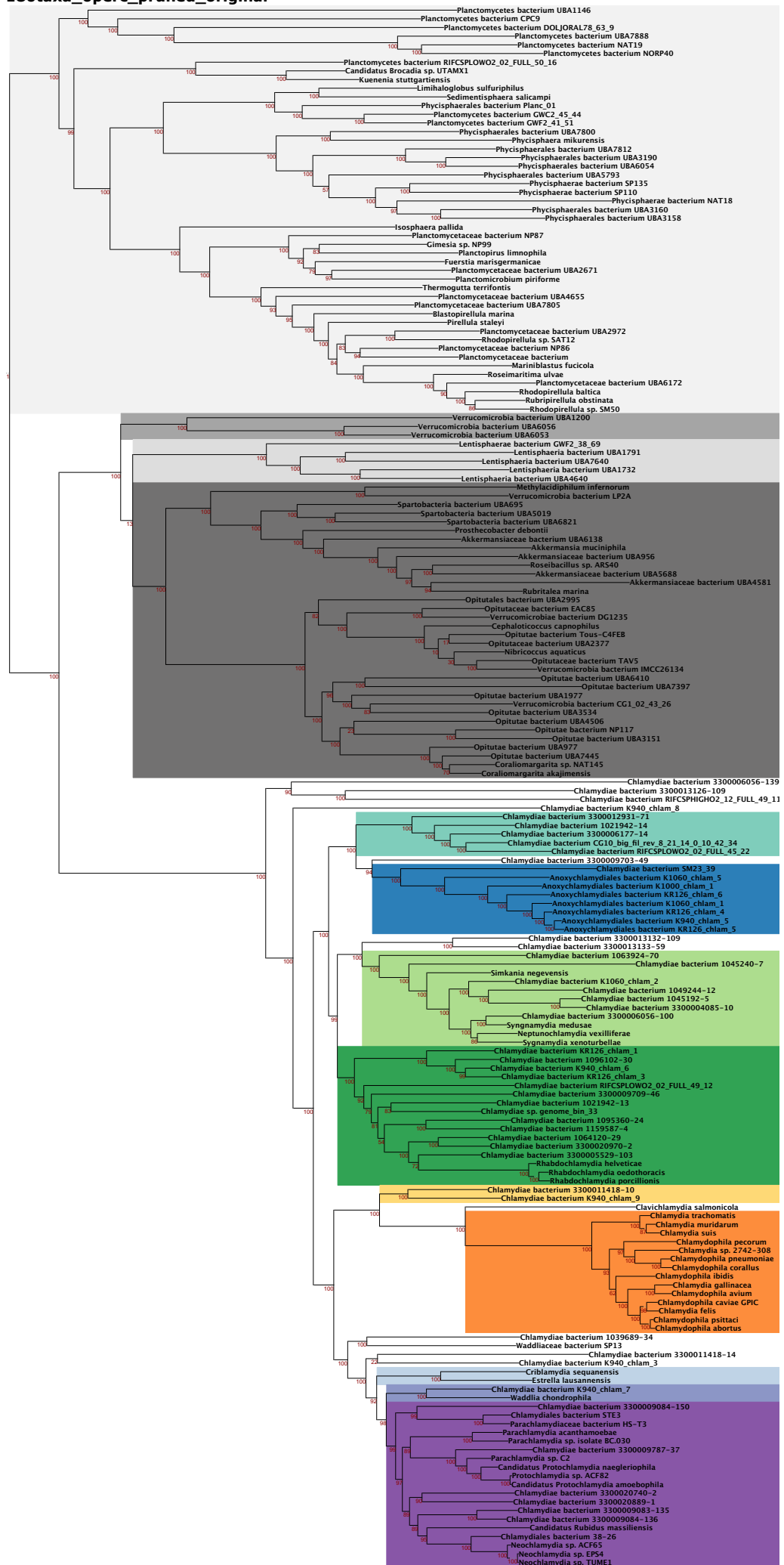
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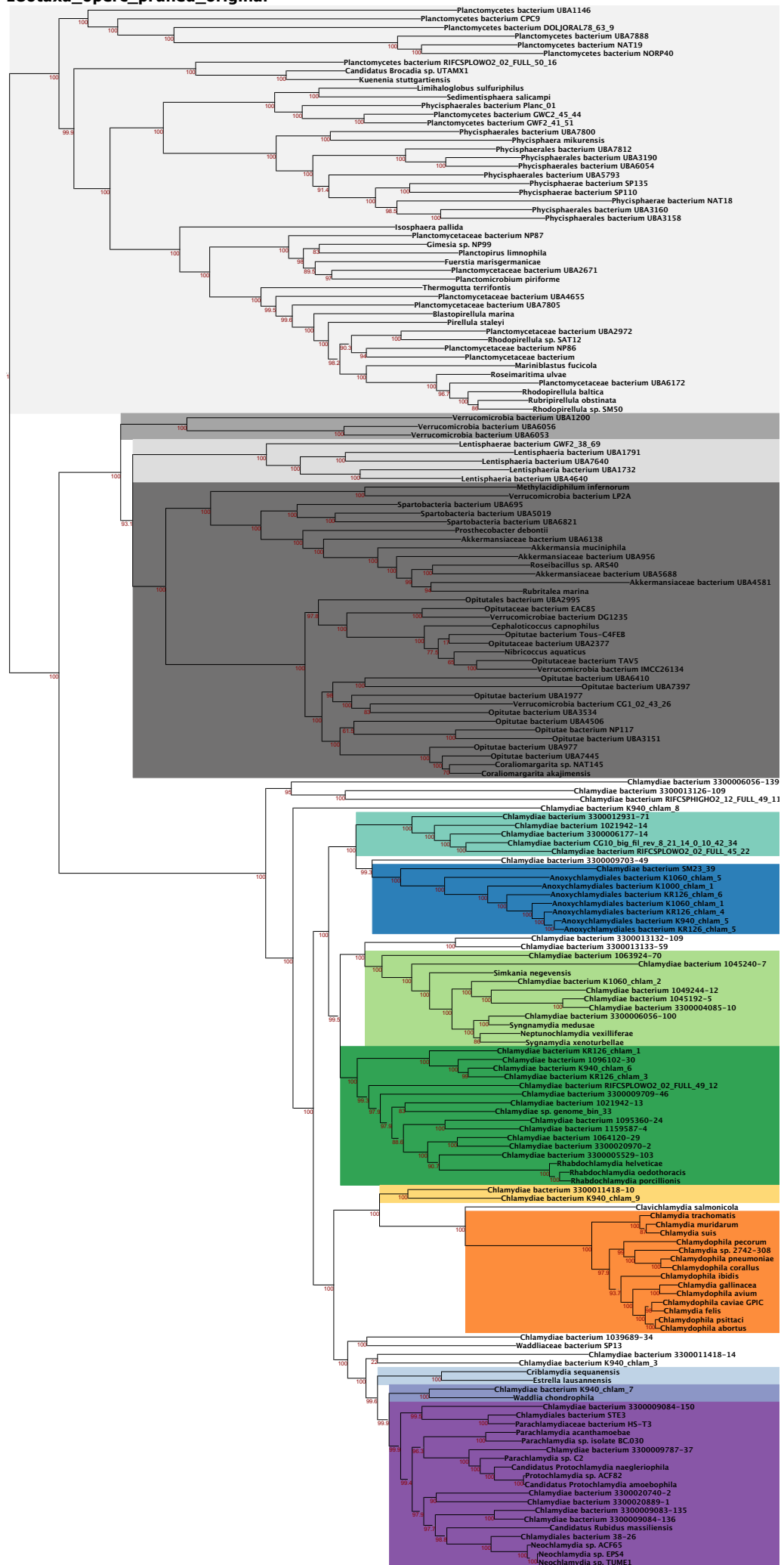
*NOG includes additional paralogous chlamydial sequences that form distinct clusters. Only the tree encoding the functional paralog of interest is shown, which in all cases here is the largest cluster of chlamydial sequences. Trees of other NOG clusters are in the repository.

**Based on Pfam domains, chlamydial sequences mapped to the NOG including AtpG (COG0224) are a different paralog.

180taxa_0perc_pruned_original

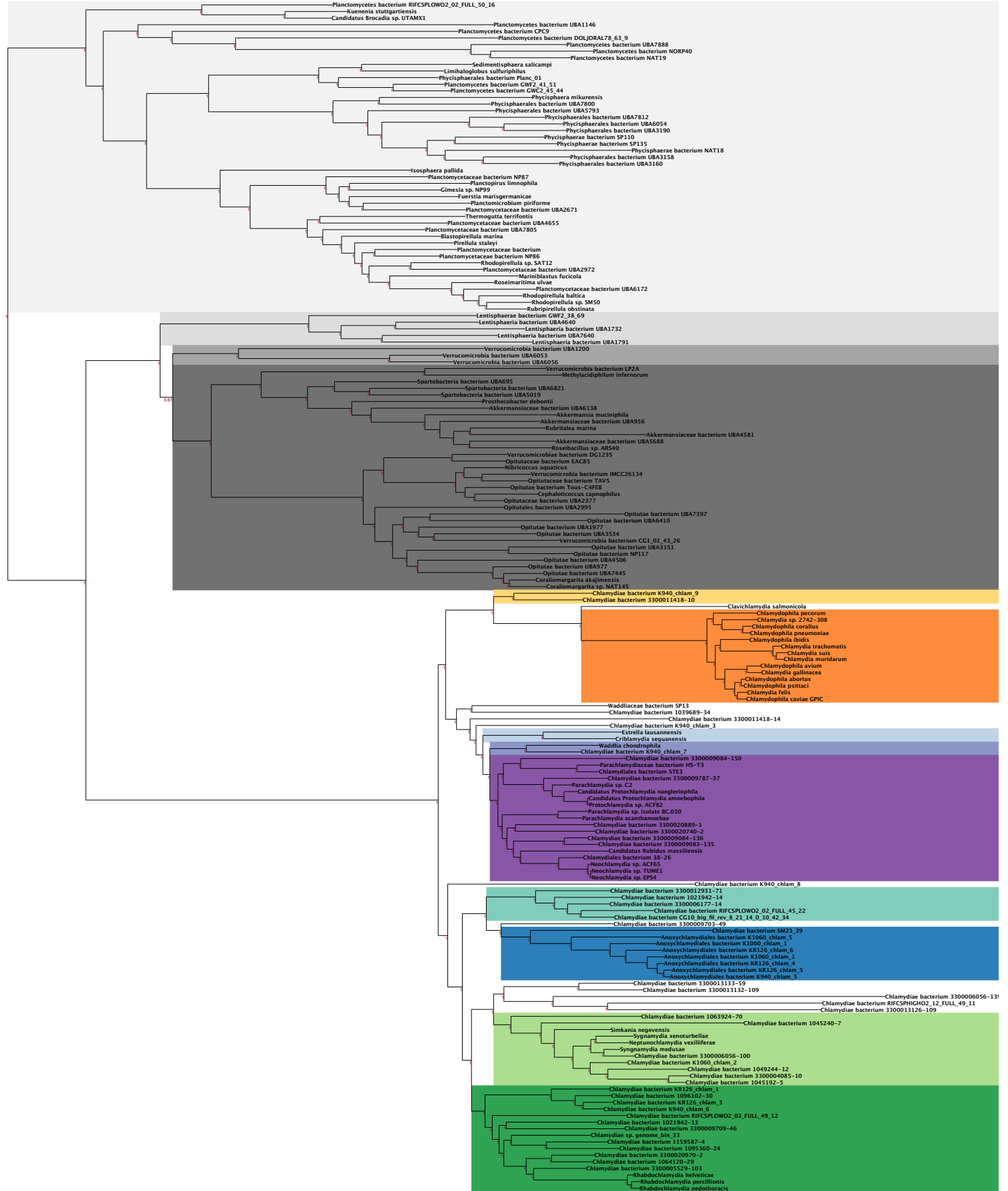


180taxa_0perc_pruned_original



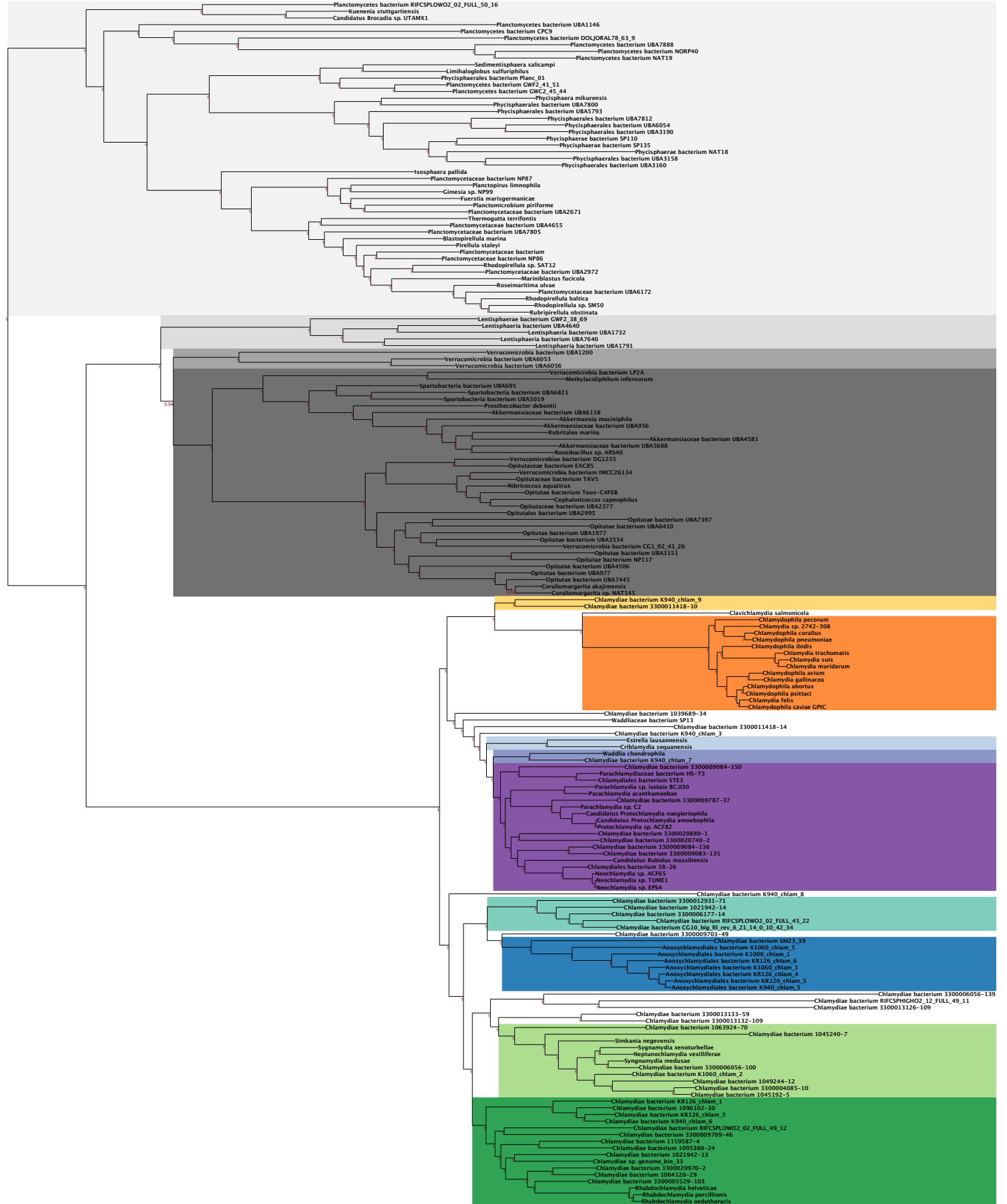
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chain1



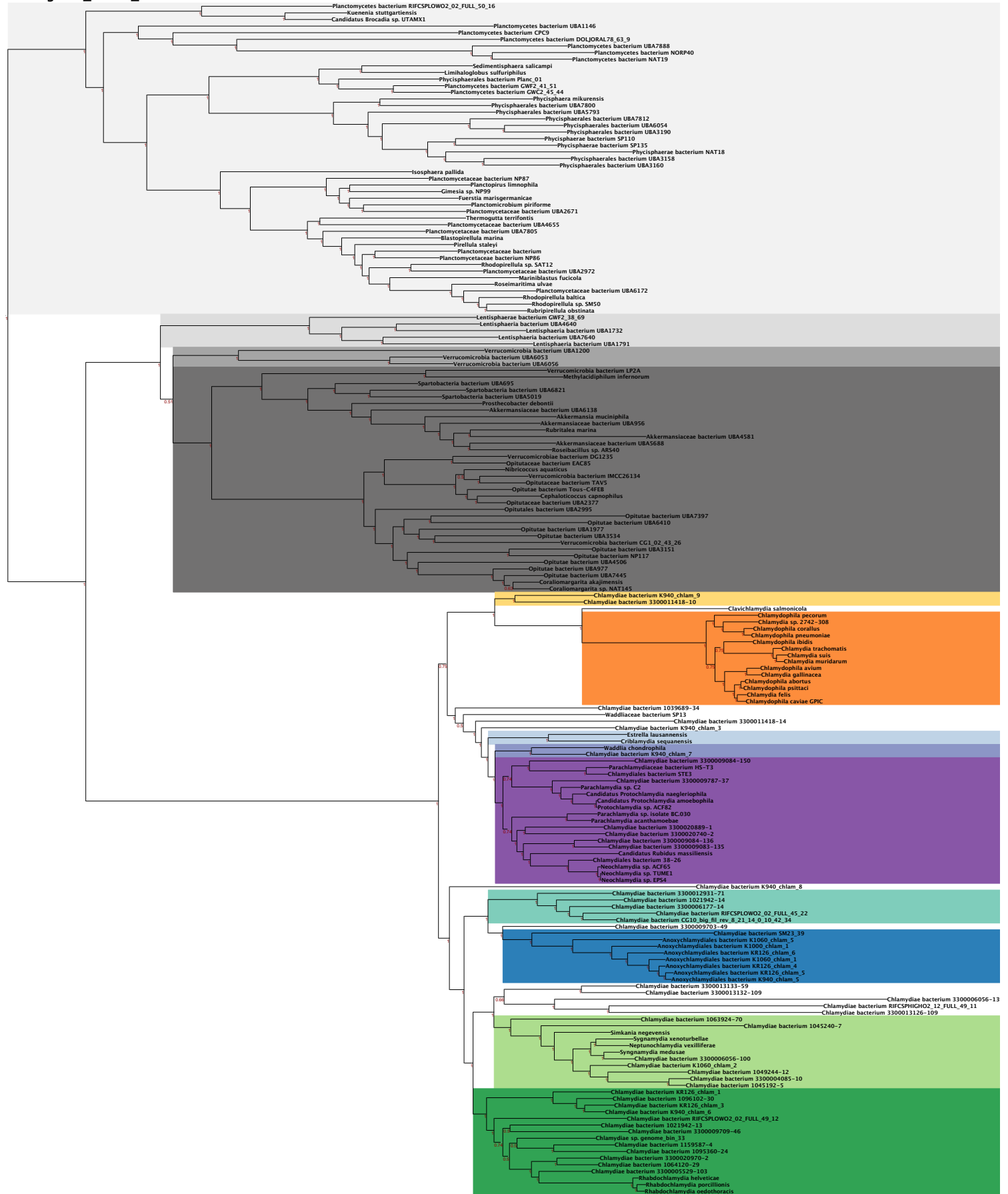
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chain2

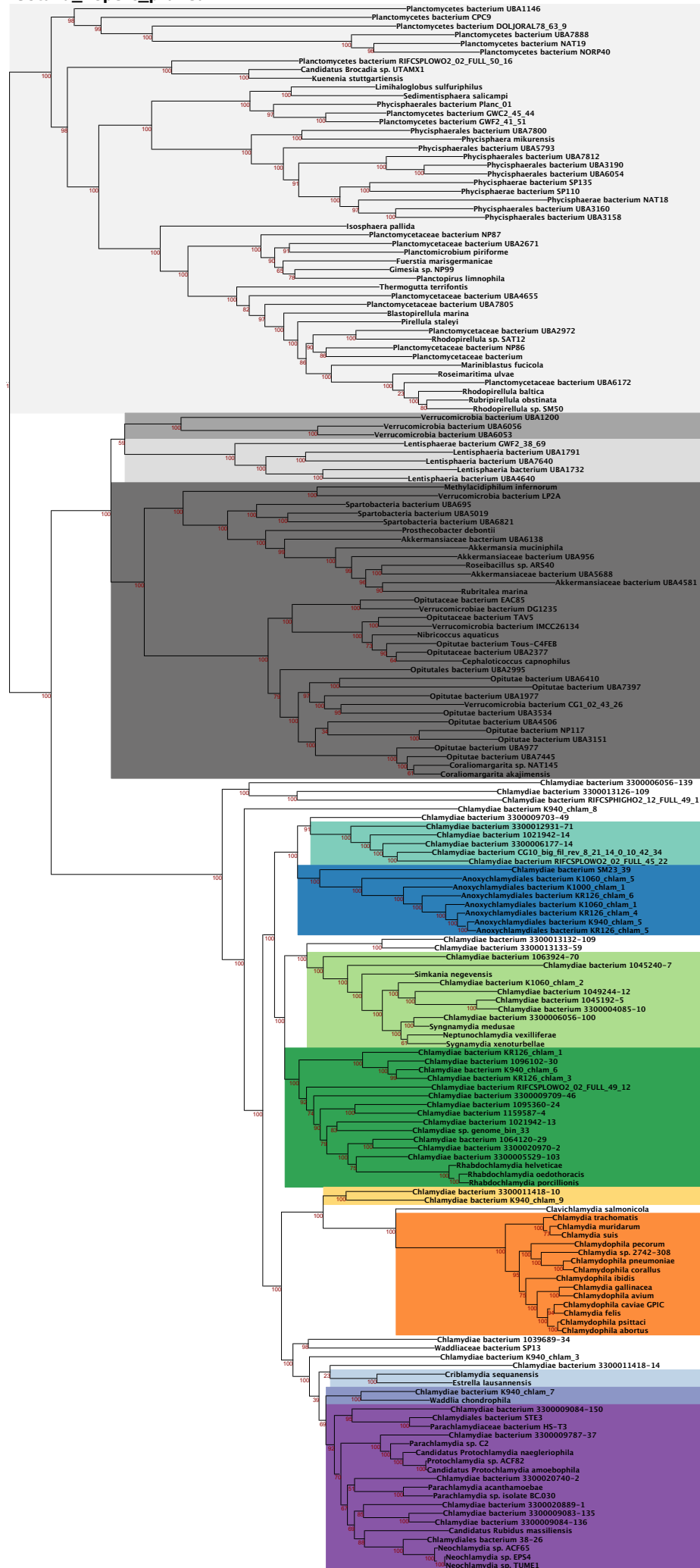


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convergence_chains_1234

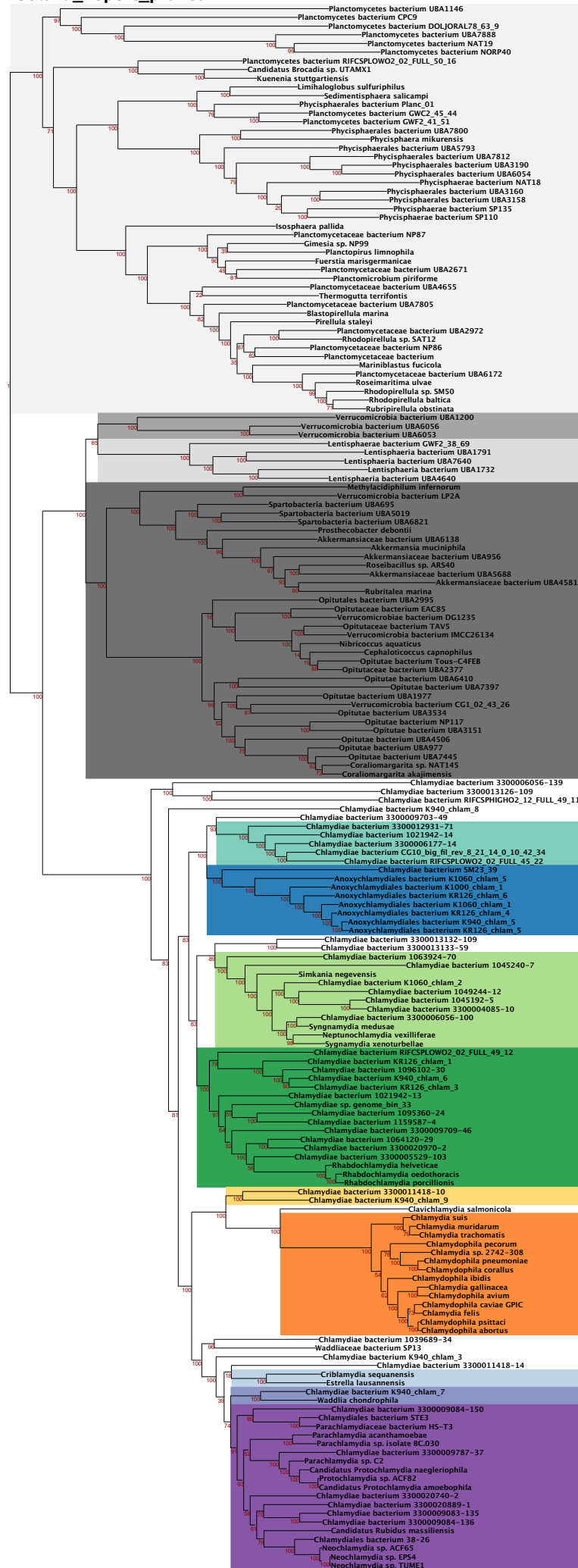


180taxa_20perc_pruned



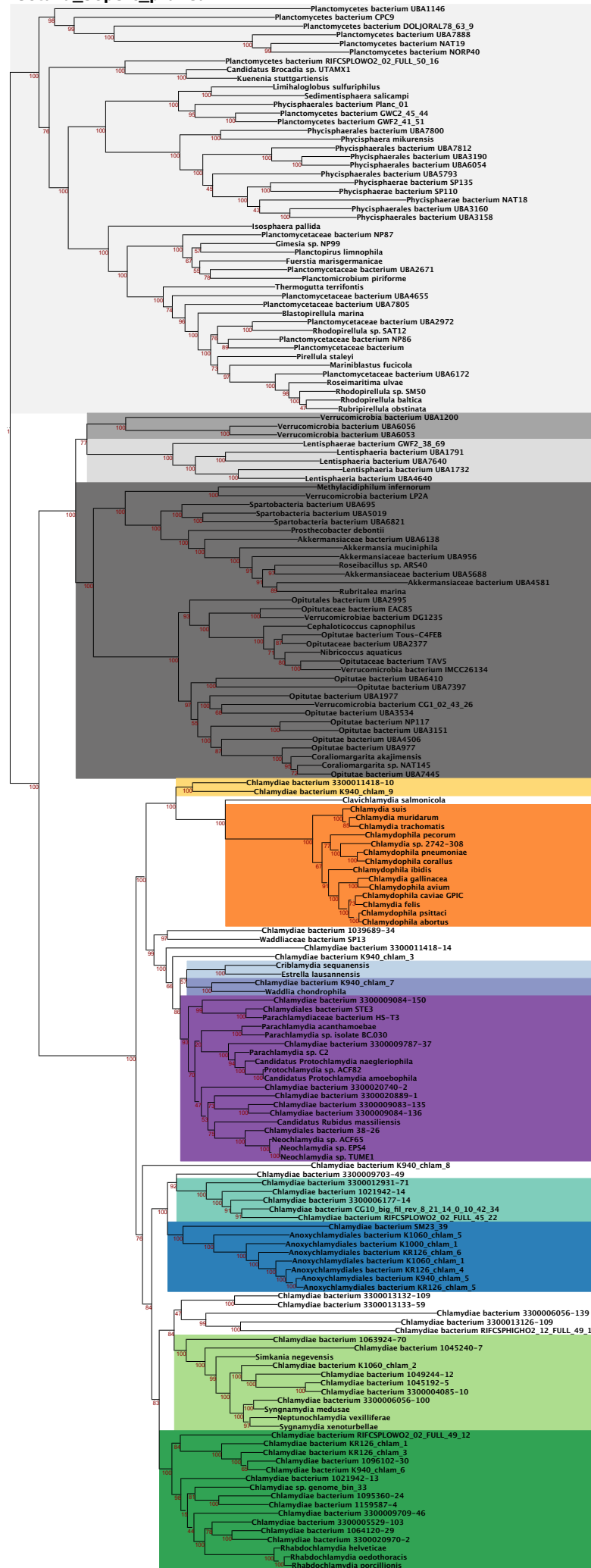
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180taxa_40perc_pruned



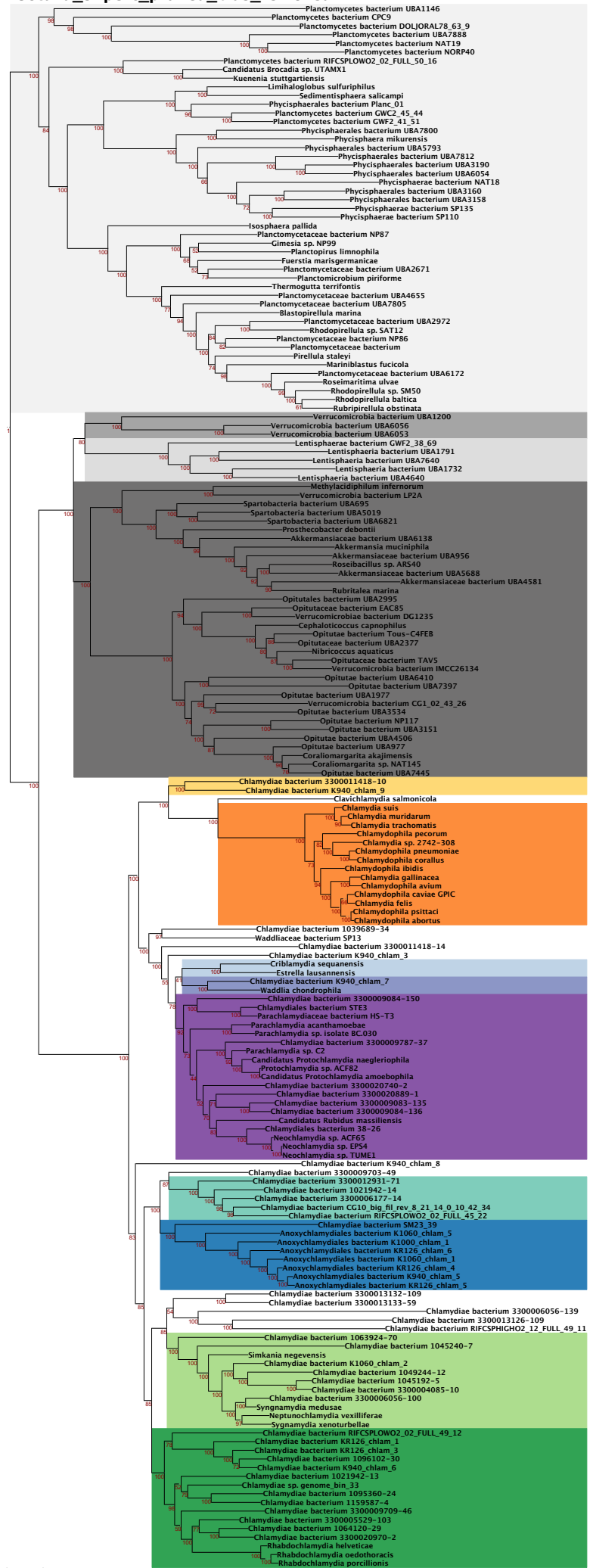
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180taxa_50perc_pruned

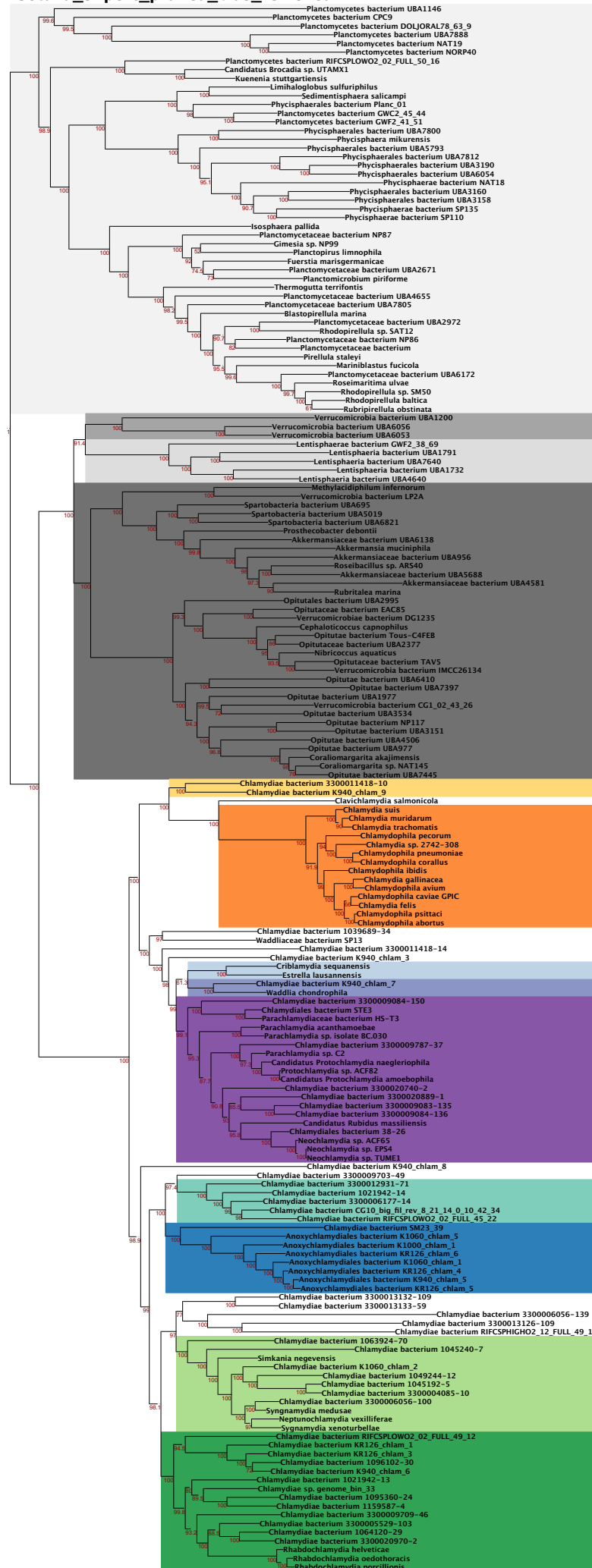


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180taxa_51perc_pruned_bias_removed

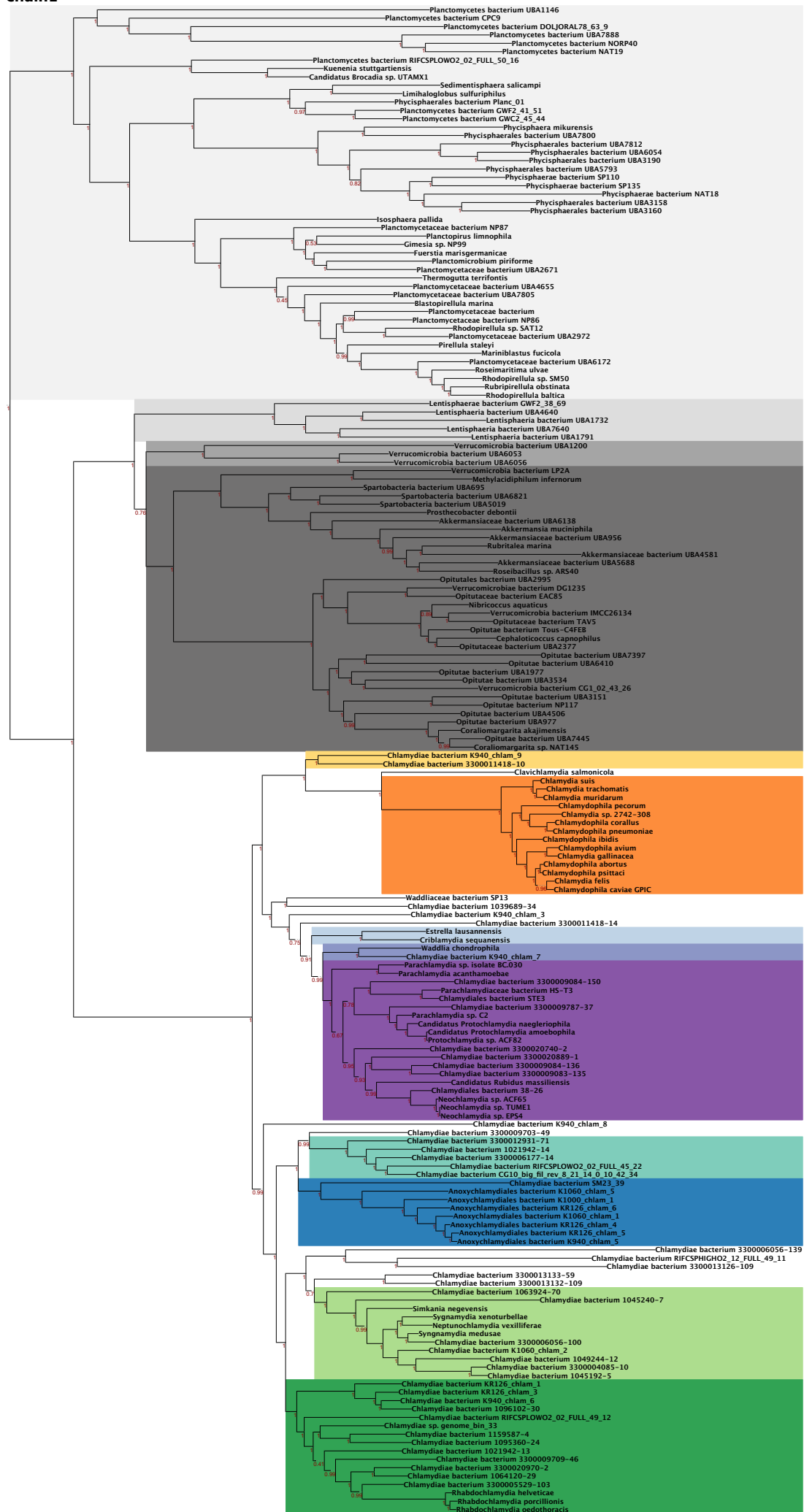


180taxa_51perc_pruned_bias_removed

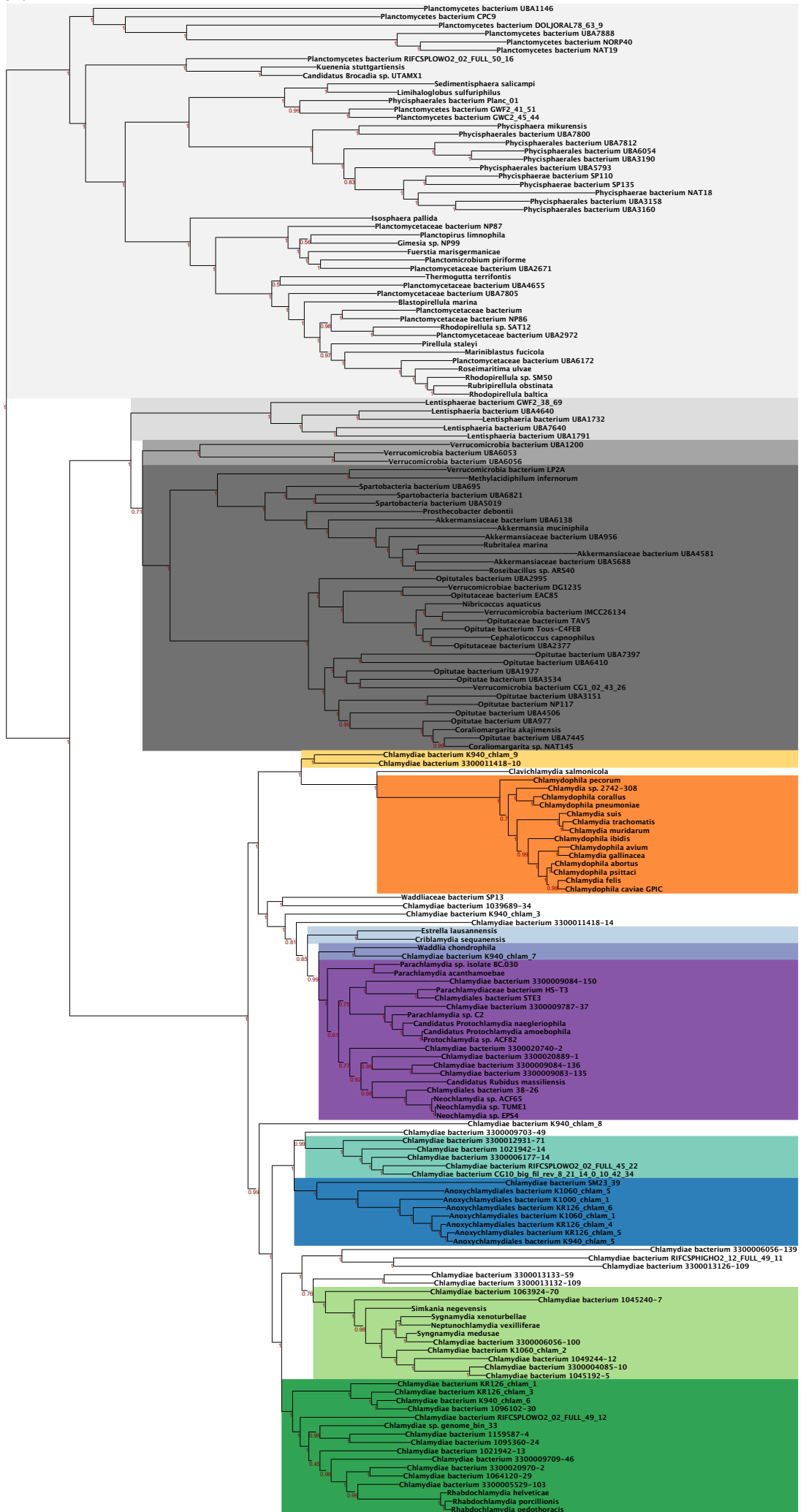


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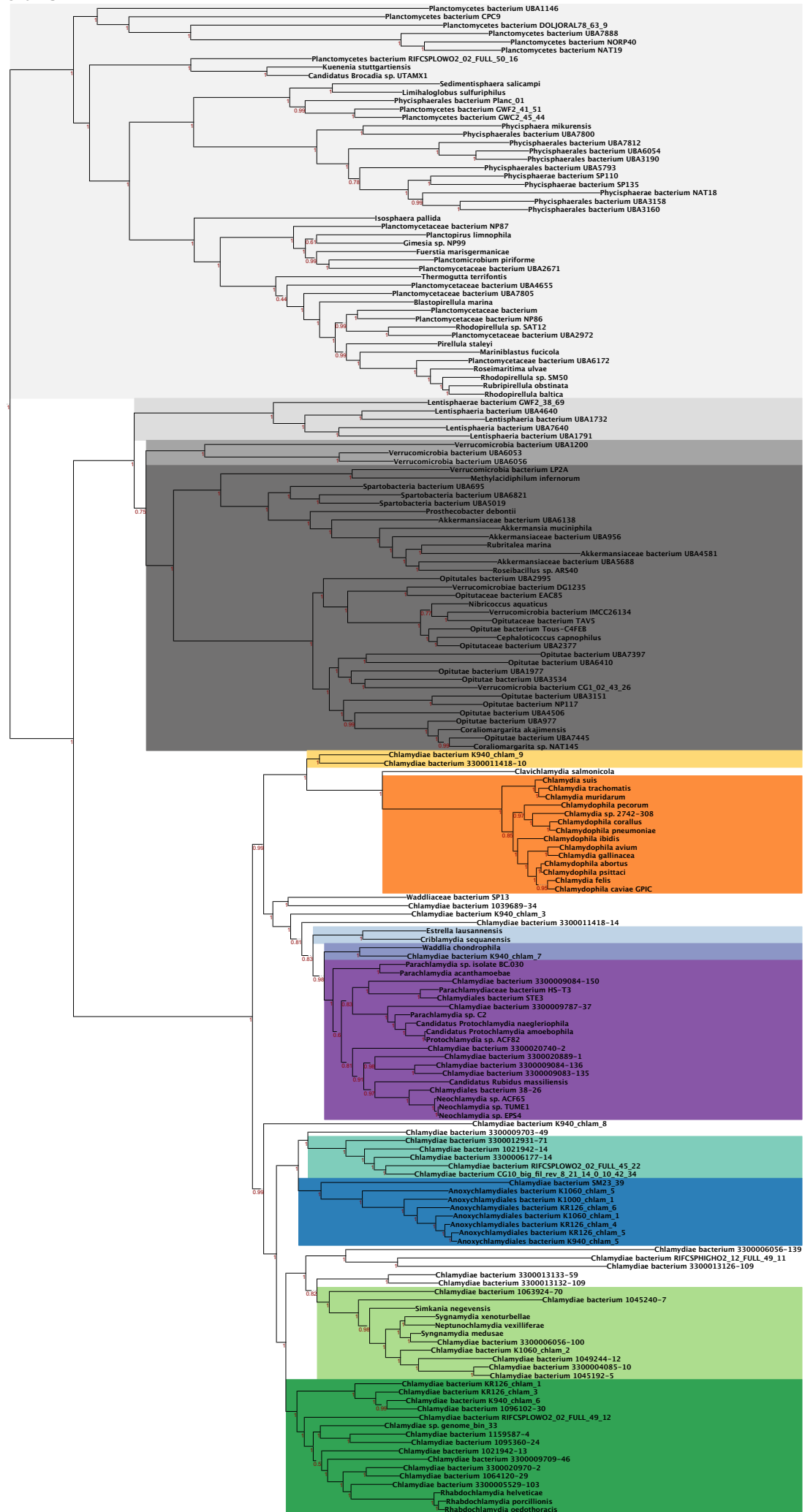
chain1



chain2

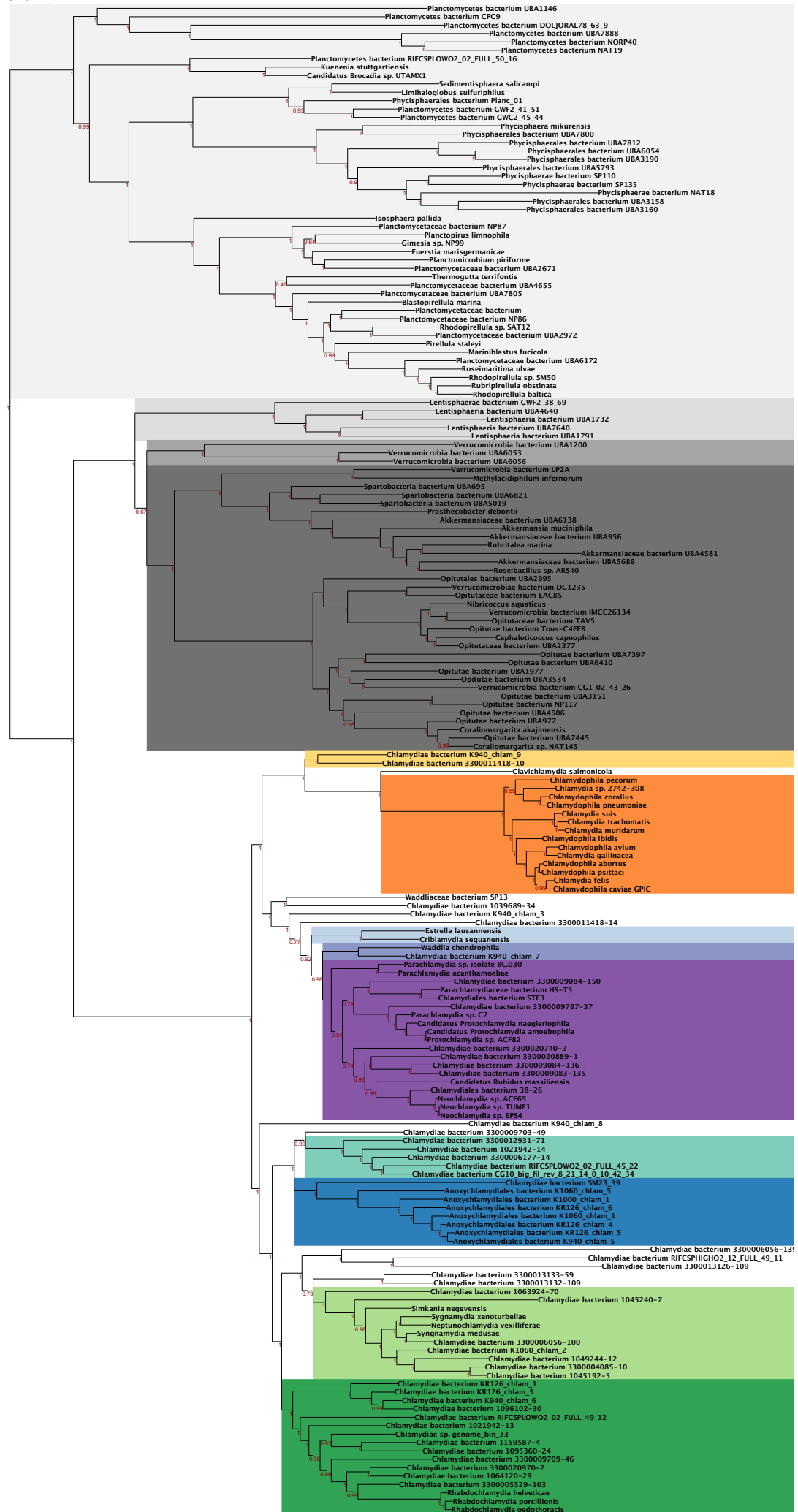


chain3



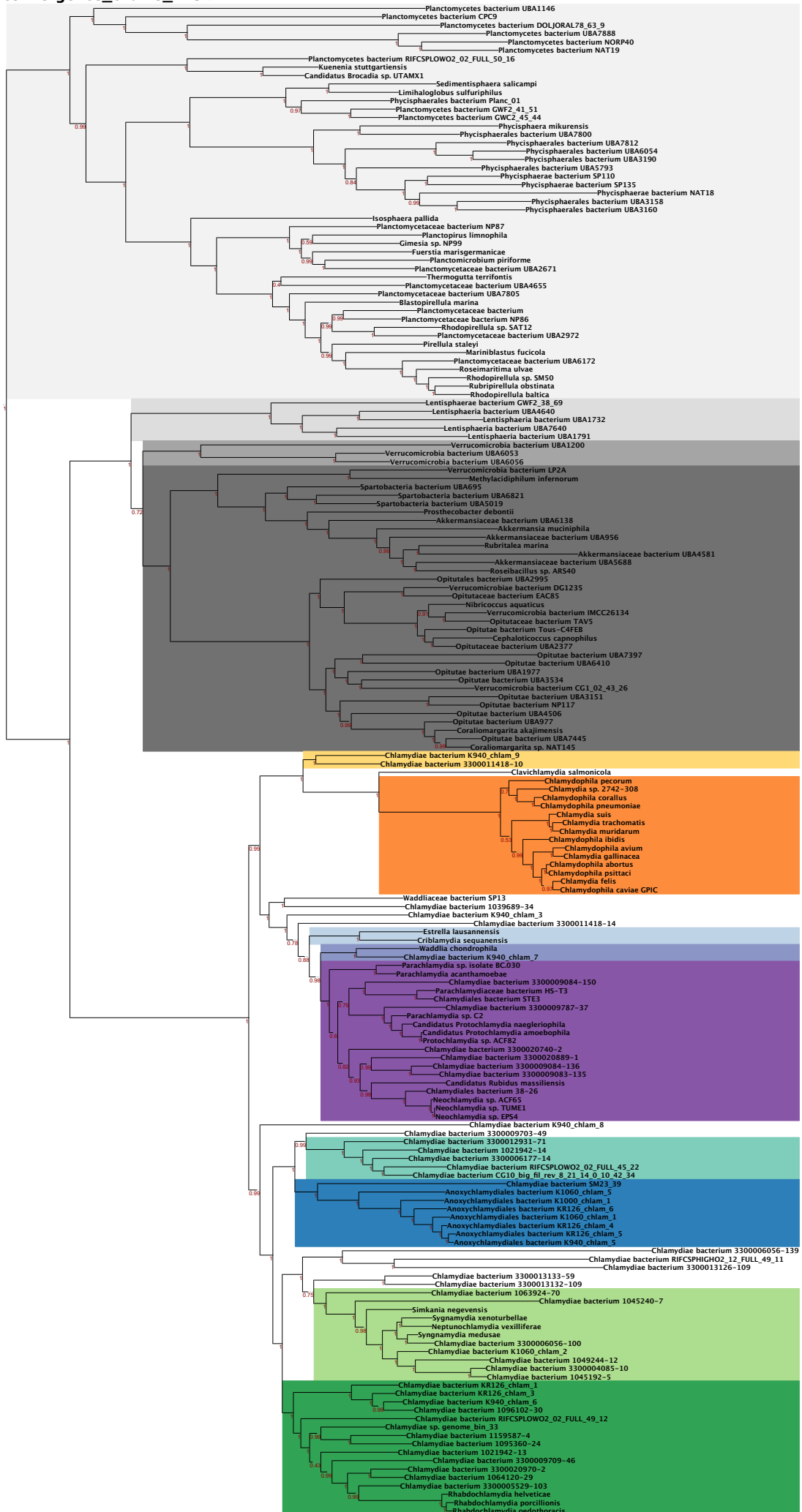
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chain4

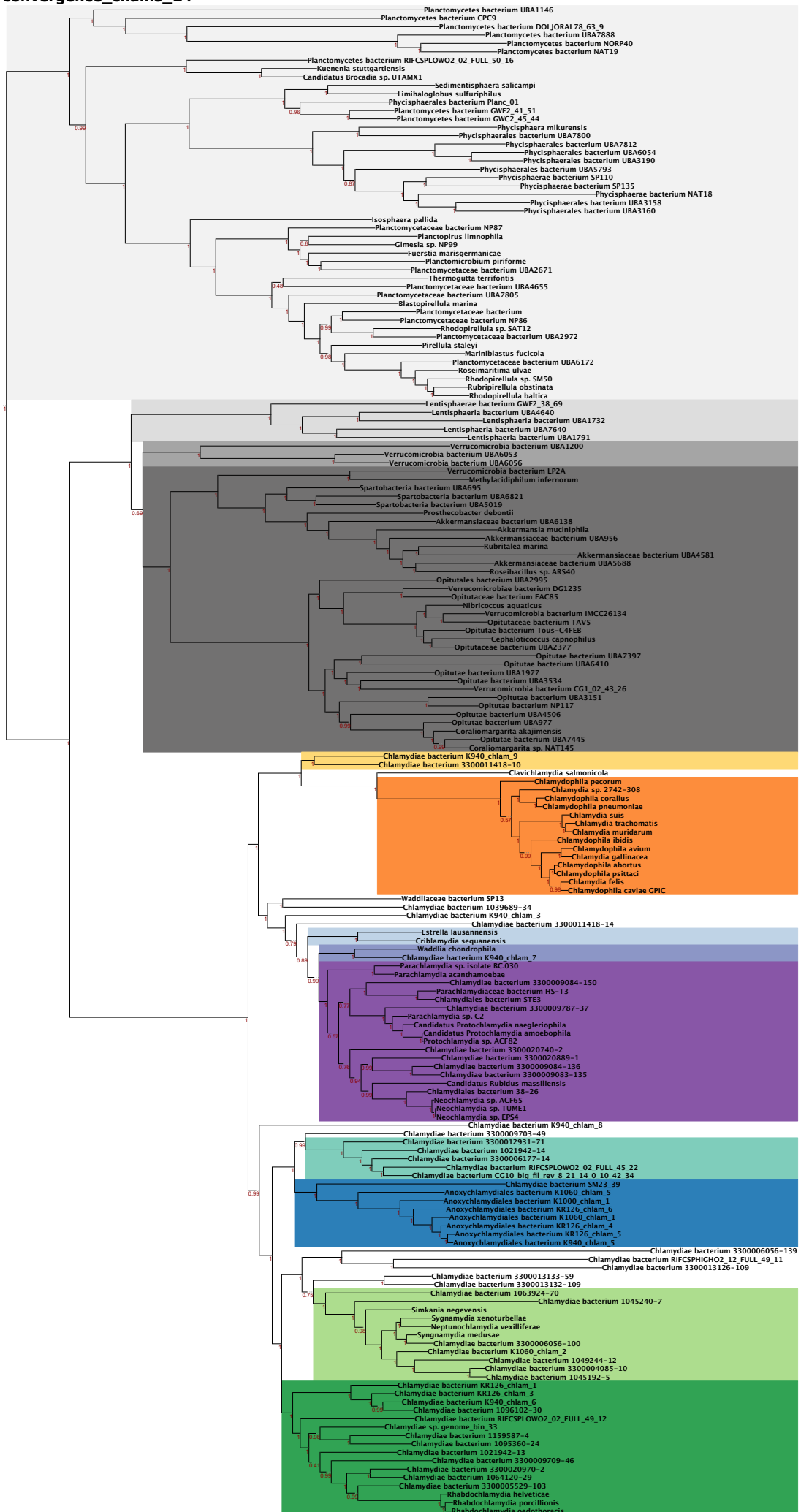


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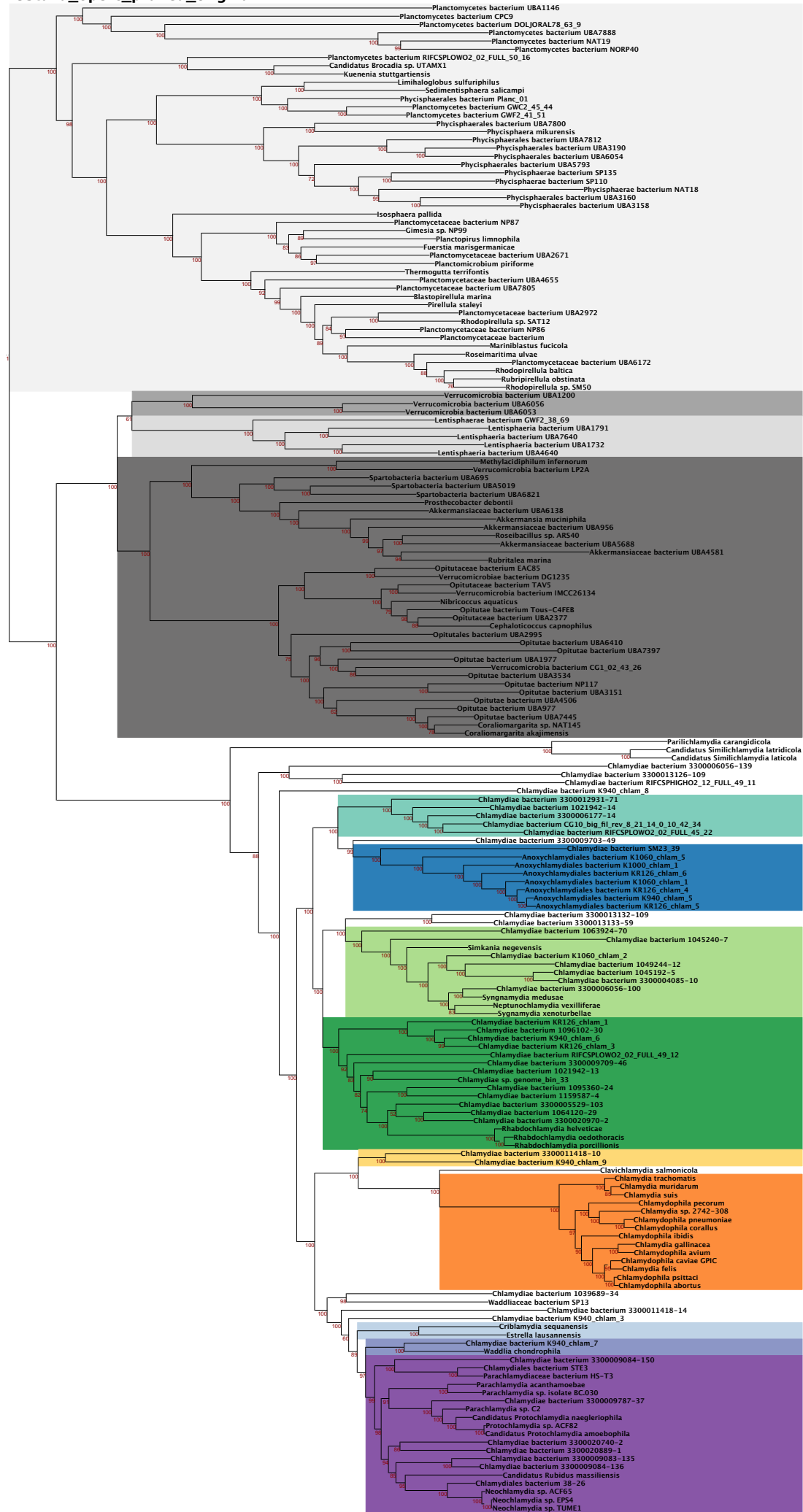
convergence_chains_1234



convergence_chains_24

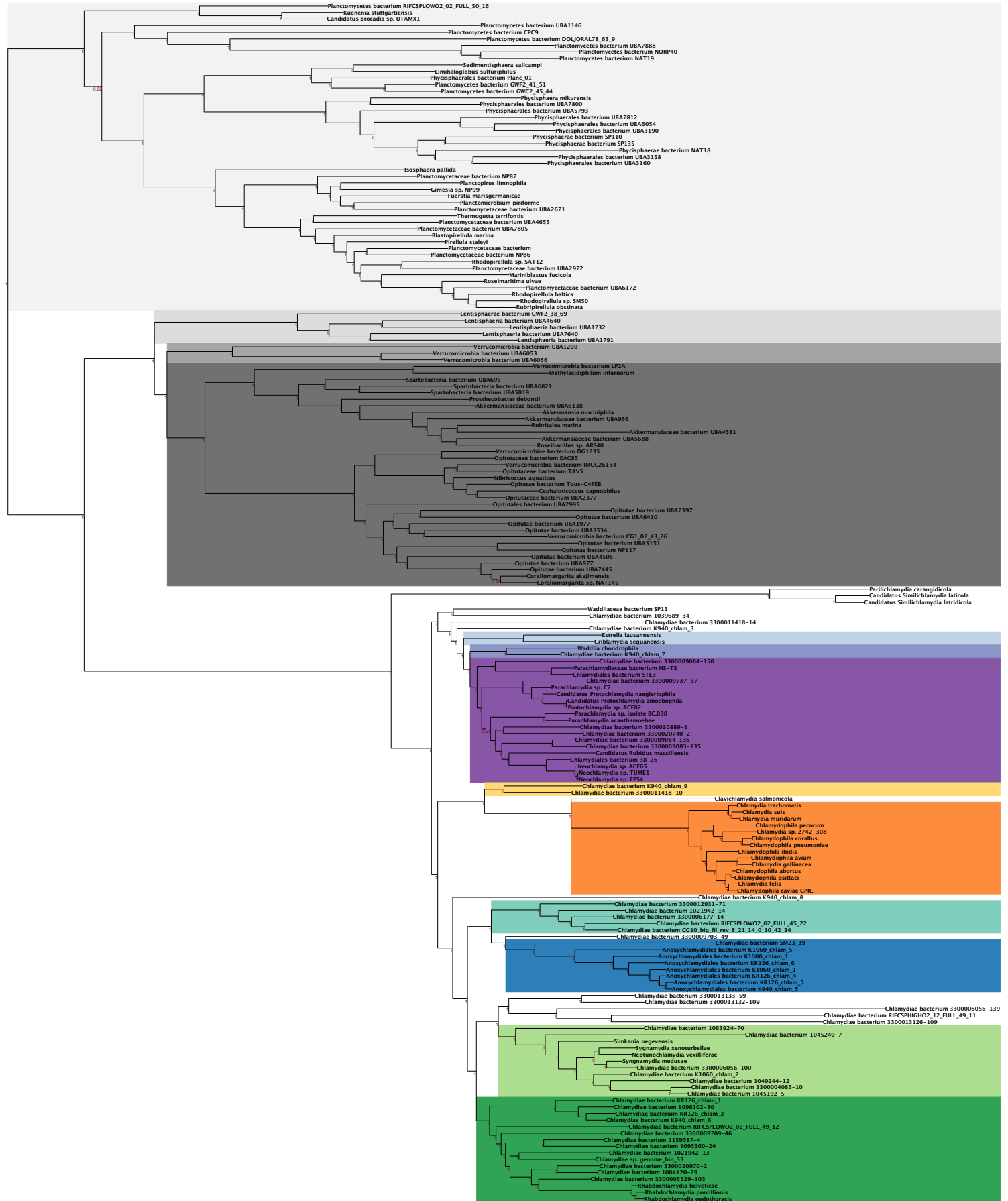


183taxa_0perc_pruned_original



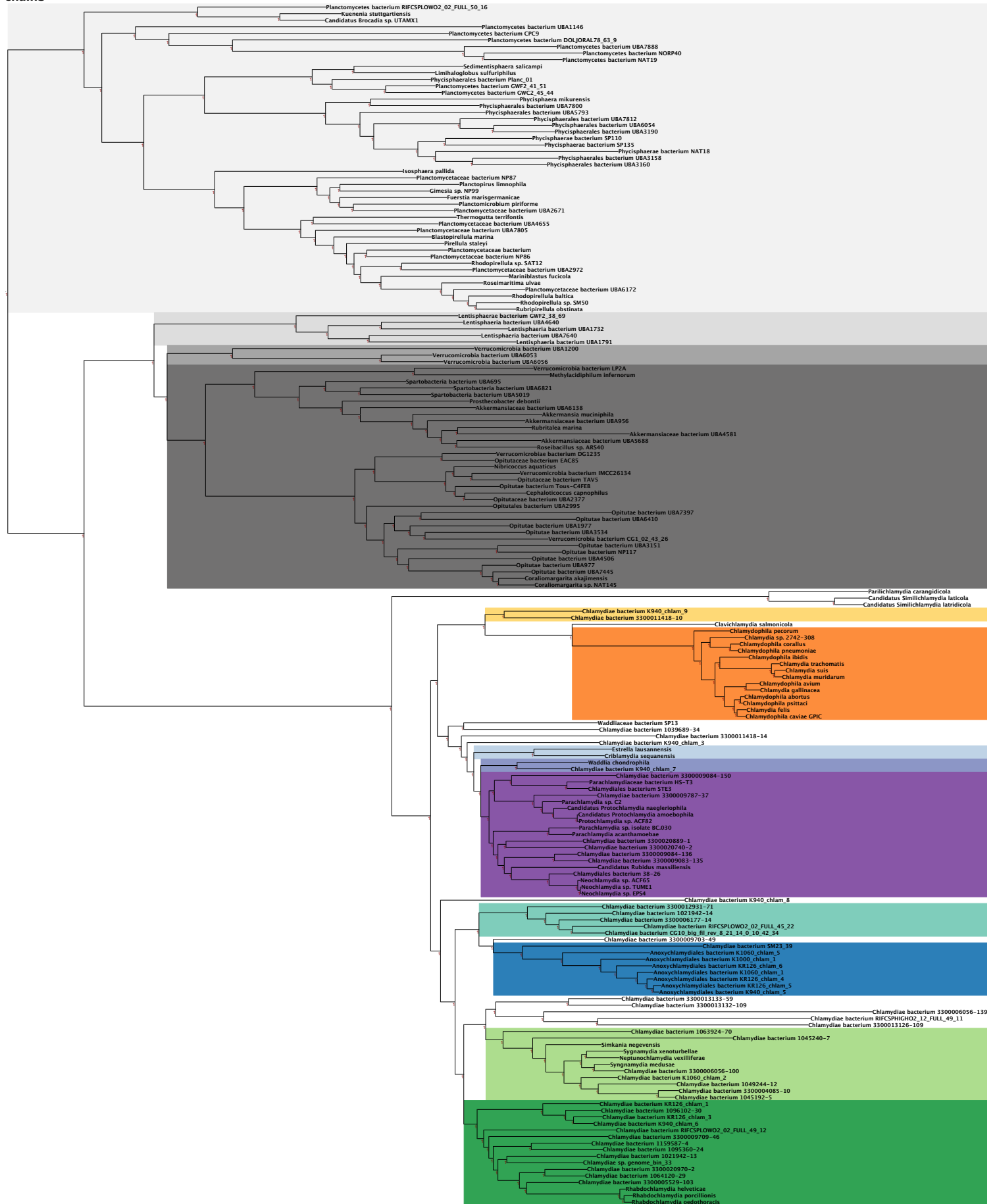
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chain2



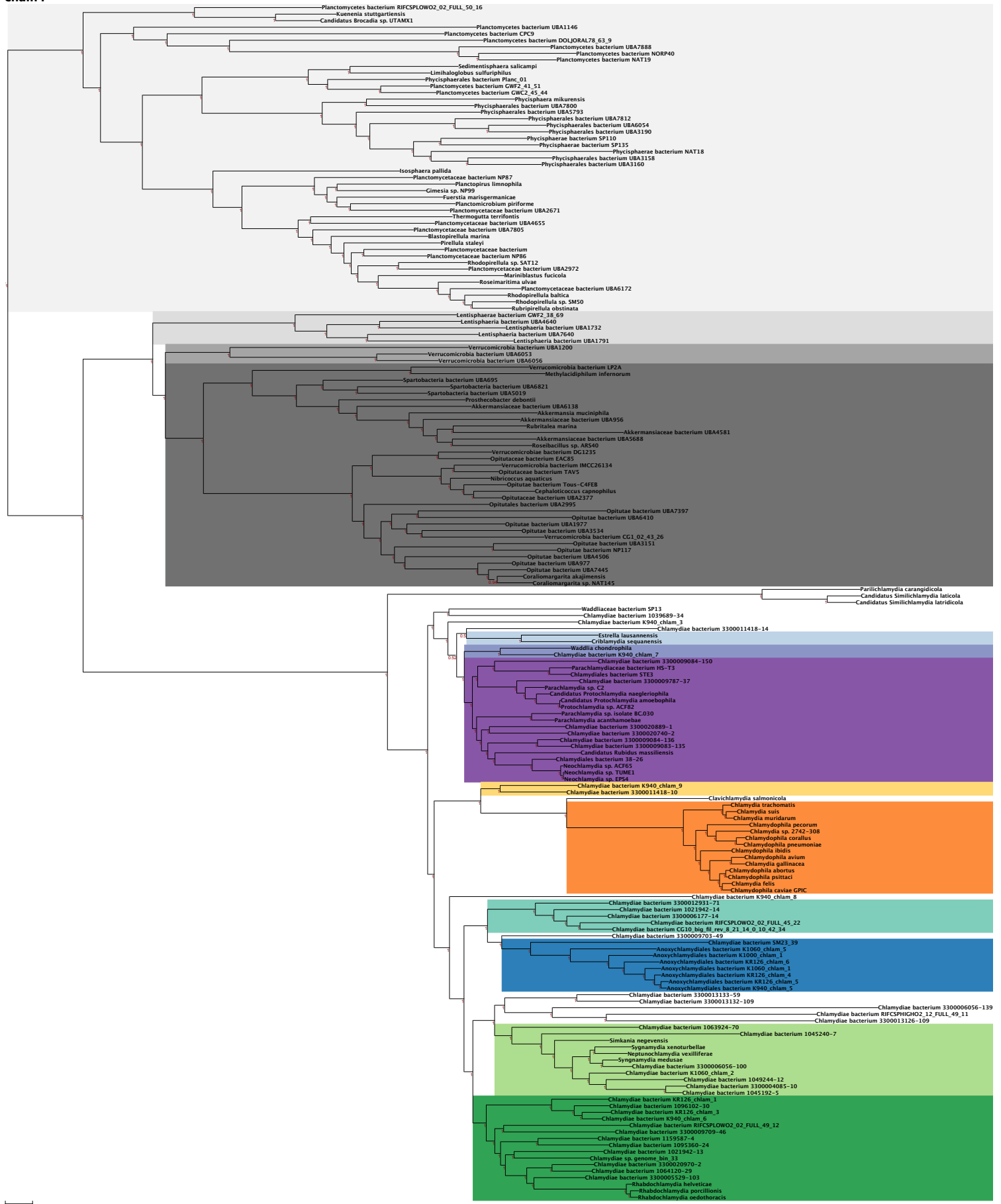
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chain3



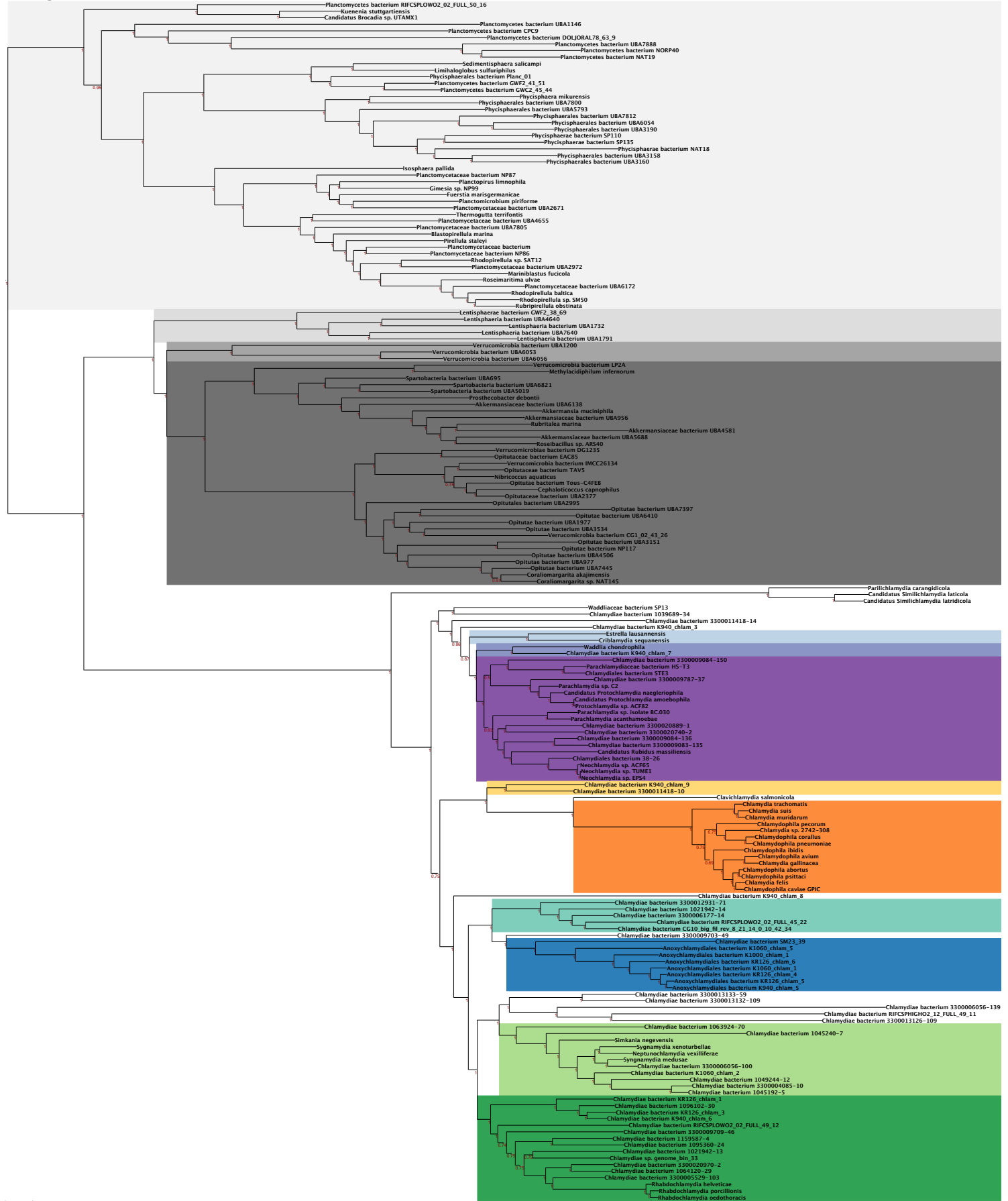
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chain4



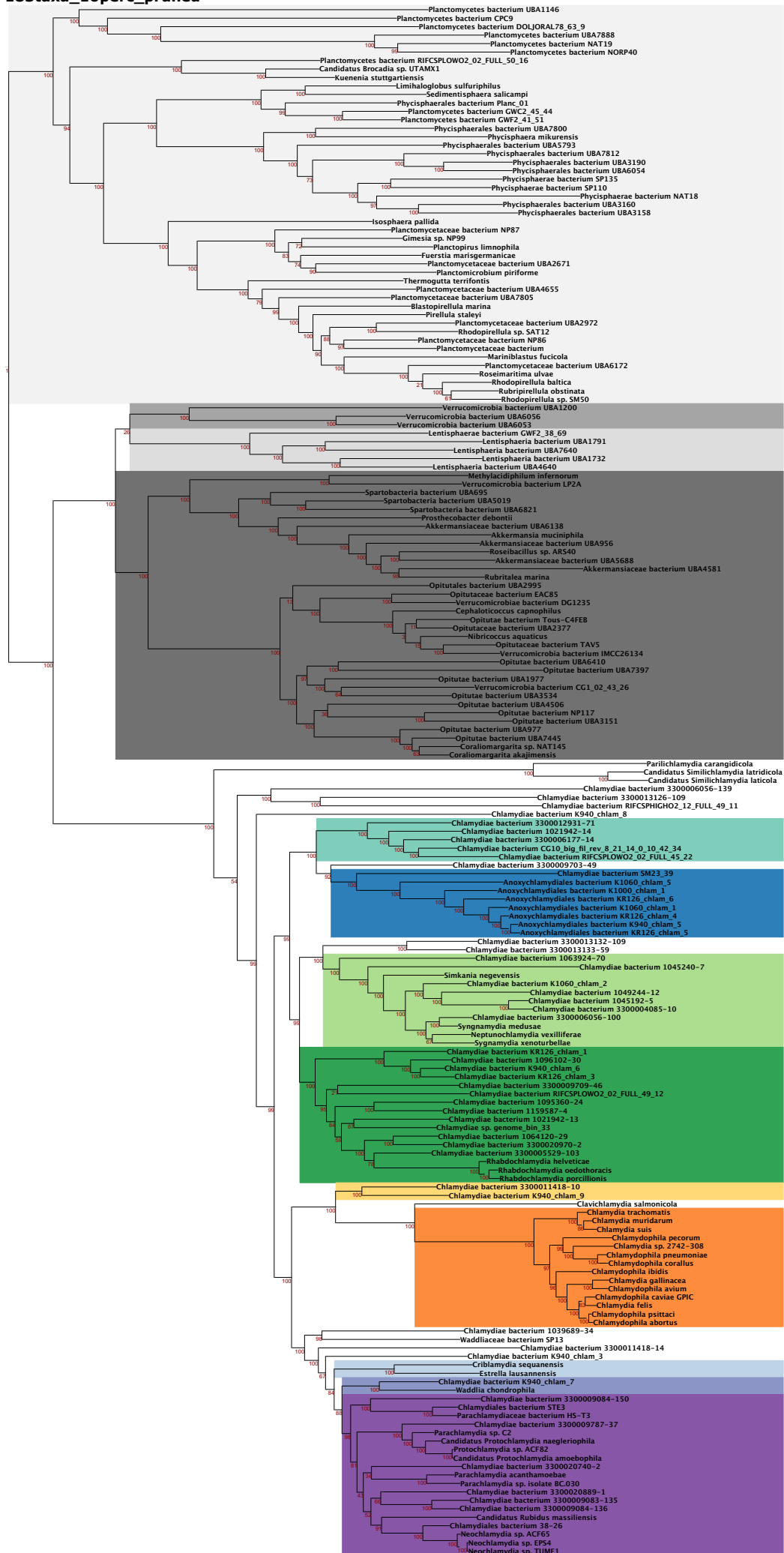
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convergence_chains_1234



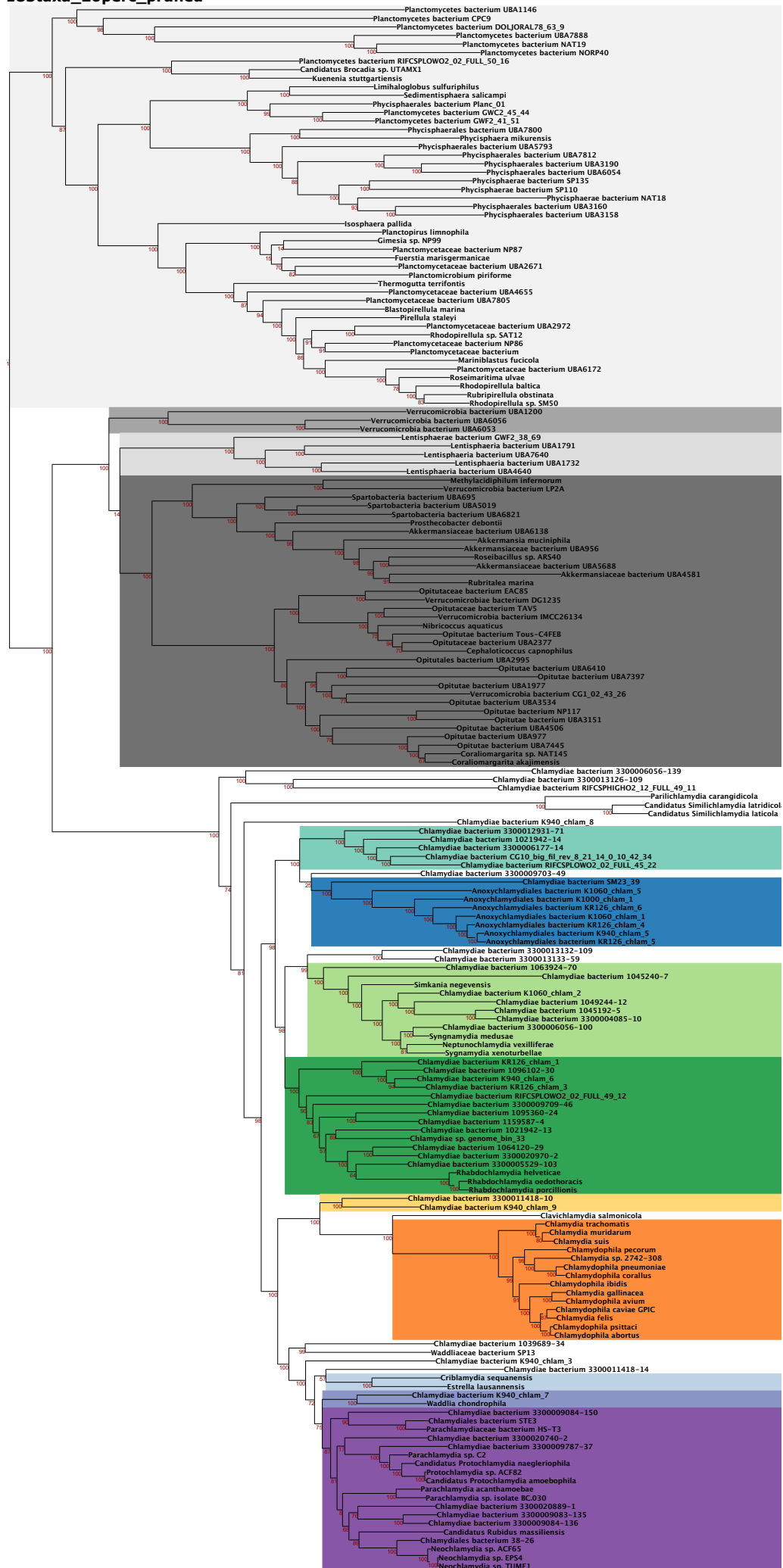
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183taxa_10perc_pruned



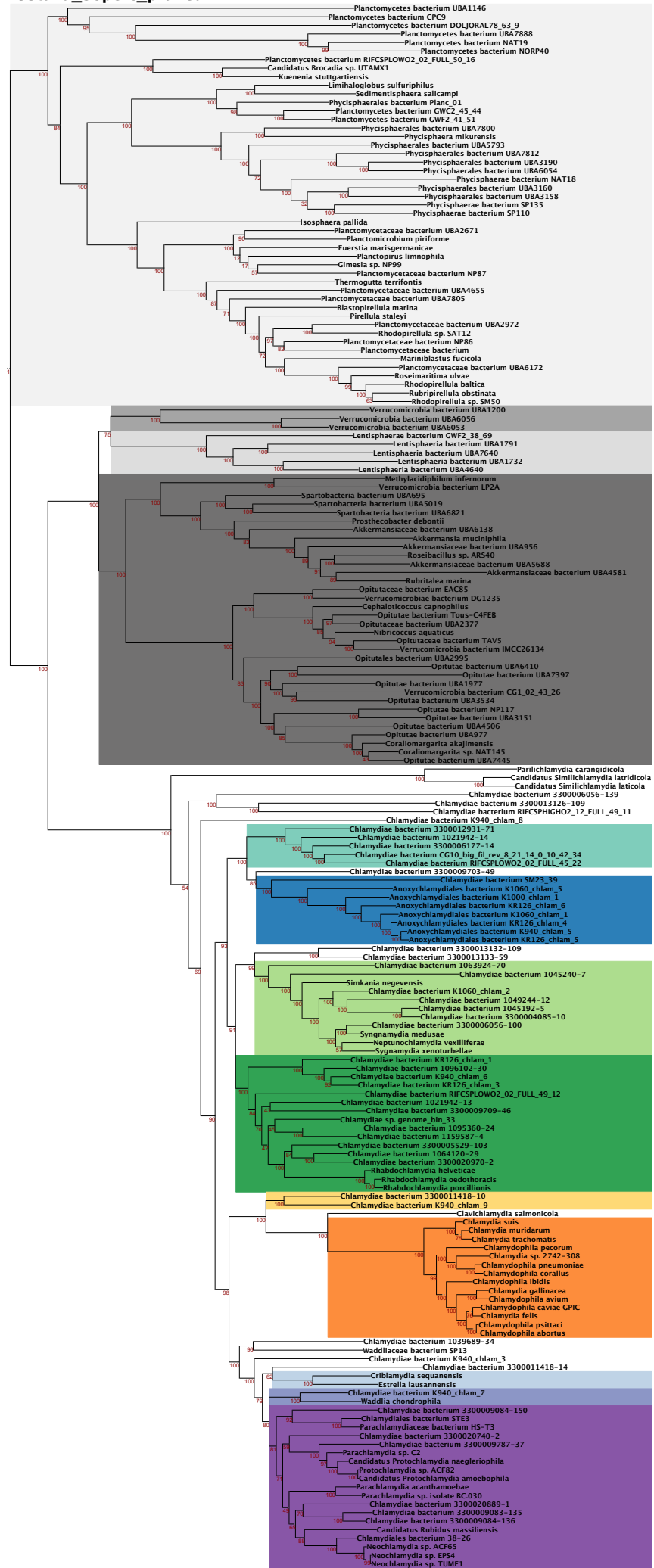
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183taxa_20perc_pruned



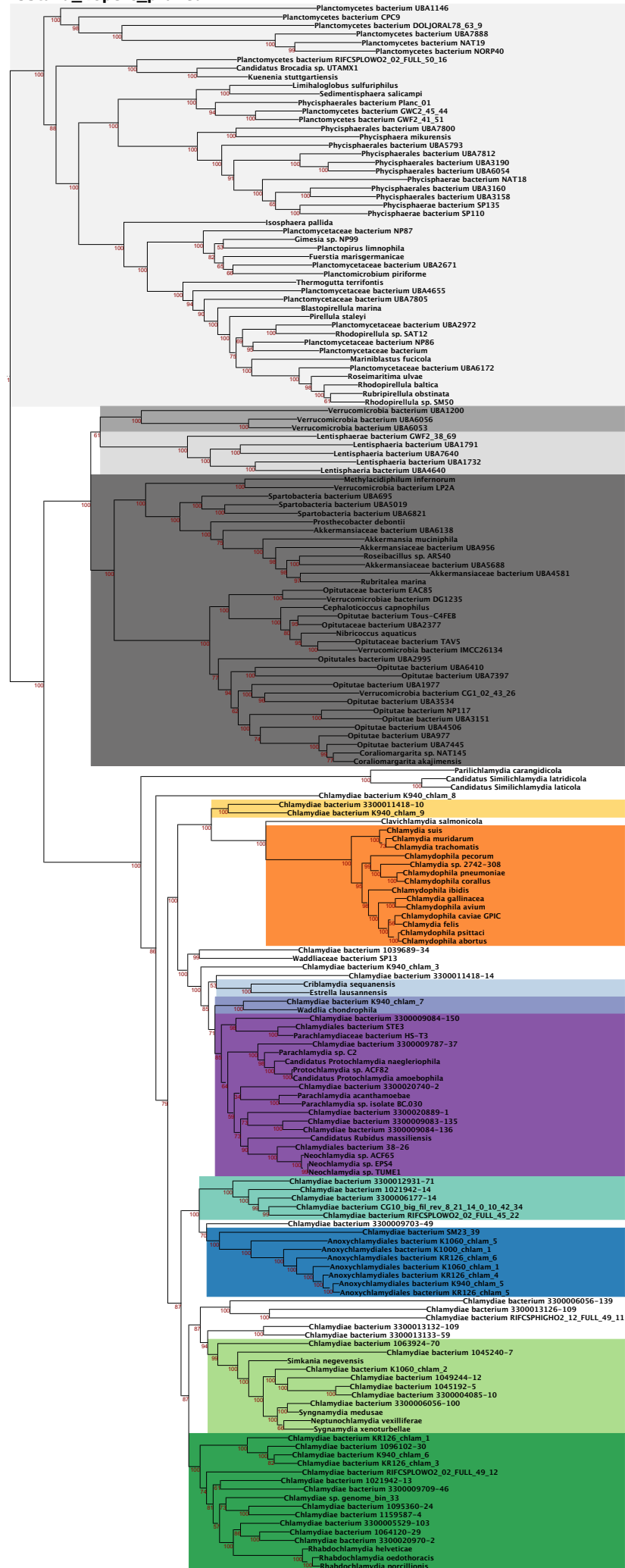
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183taxa_30perc_pruned



0.1

183taxa_40perc_pruned



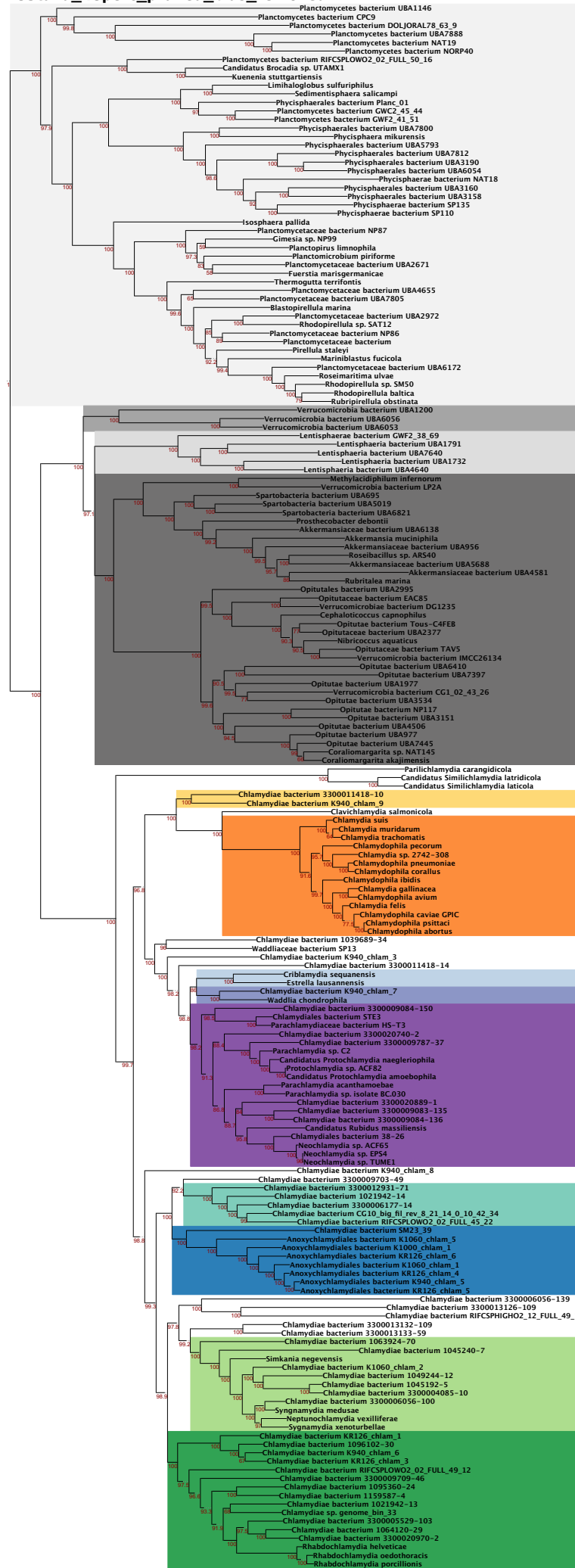
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183taxa_48perc_pruned_bias_removed

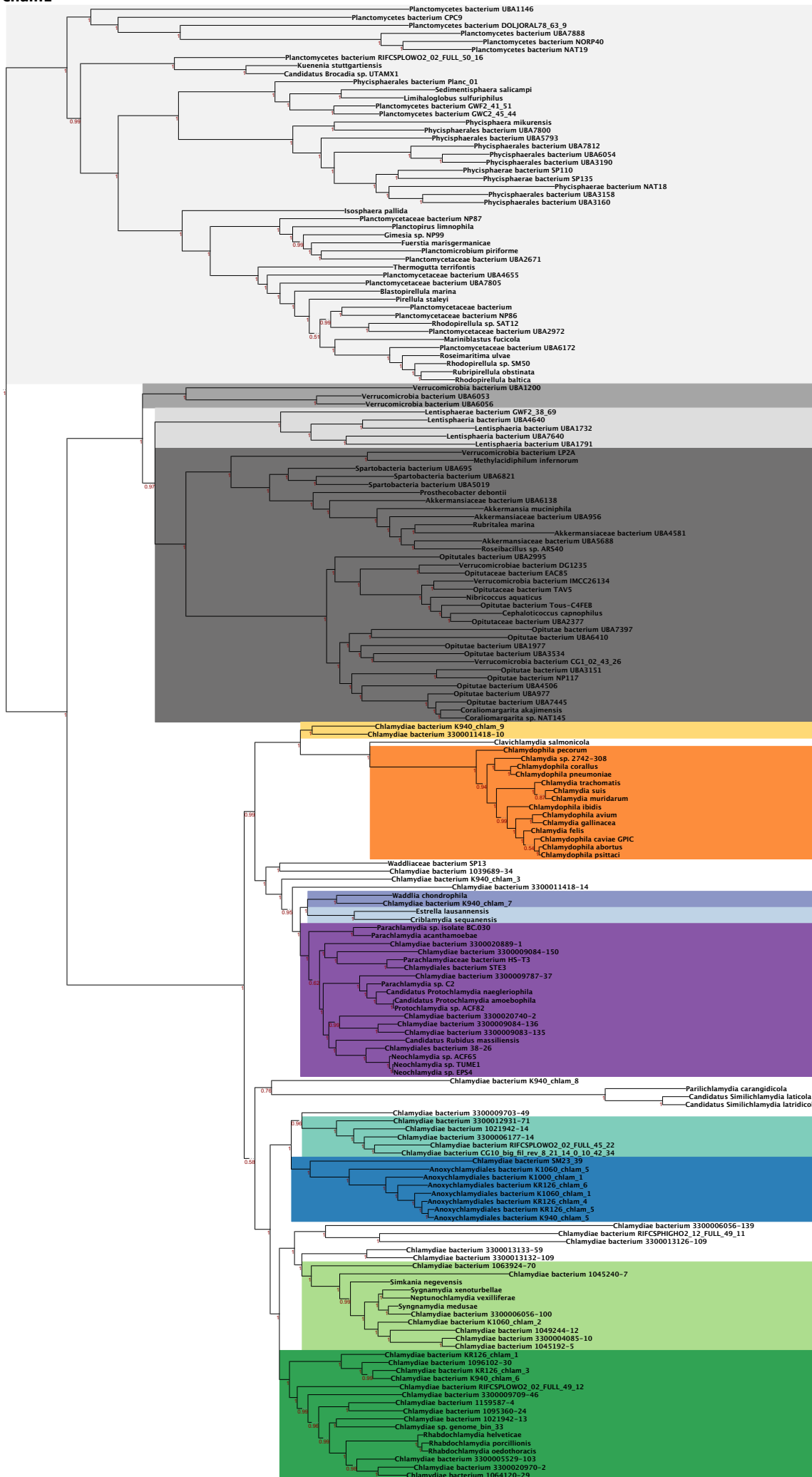


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183taxa_48perc_pruned_bias_removed

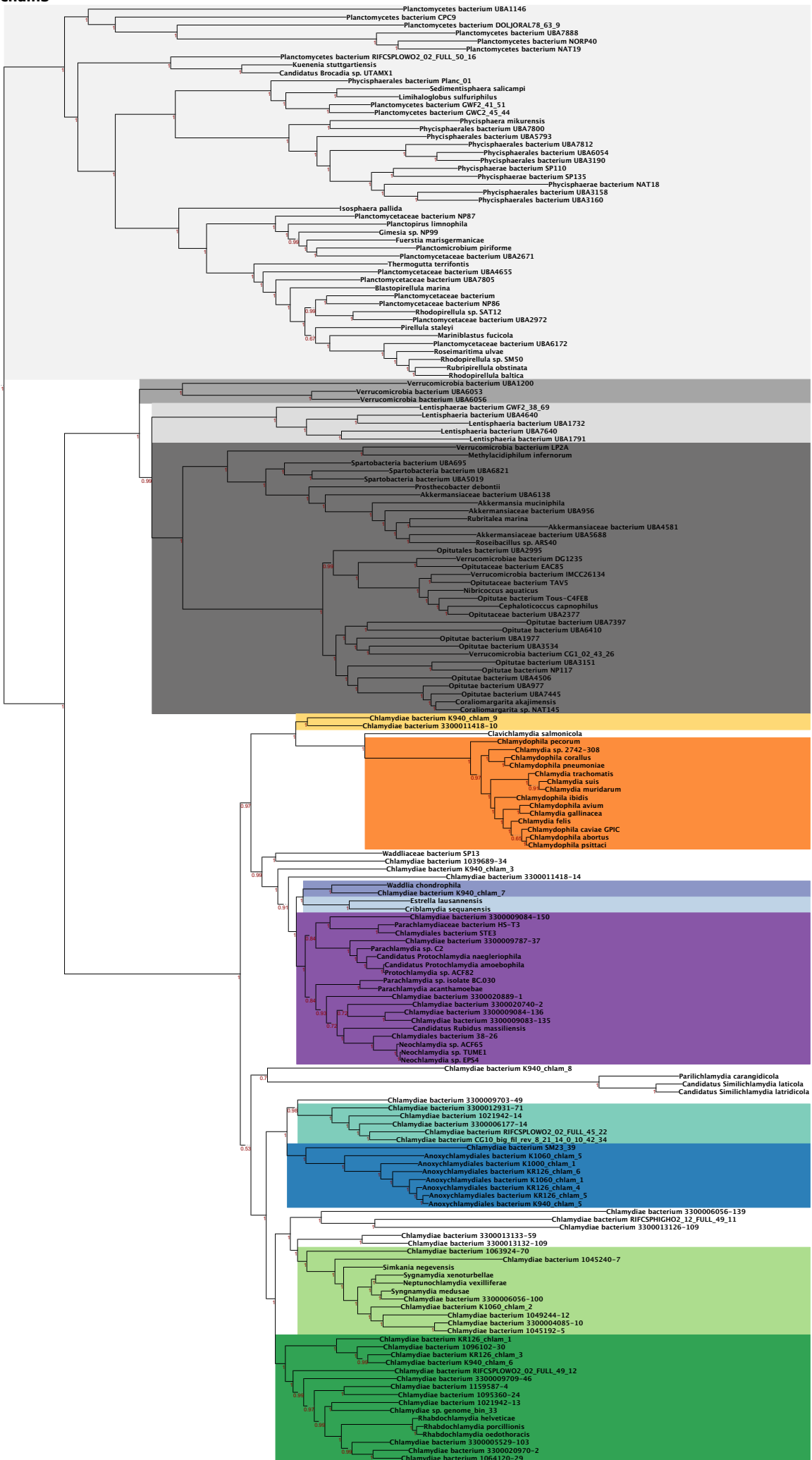


chain1



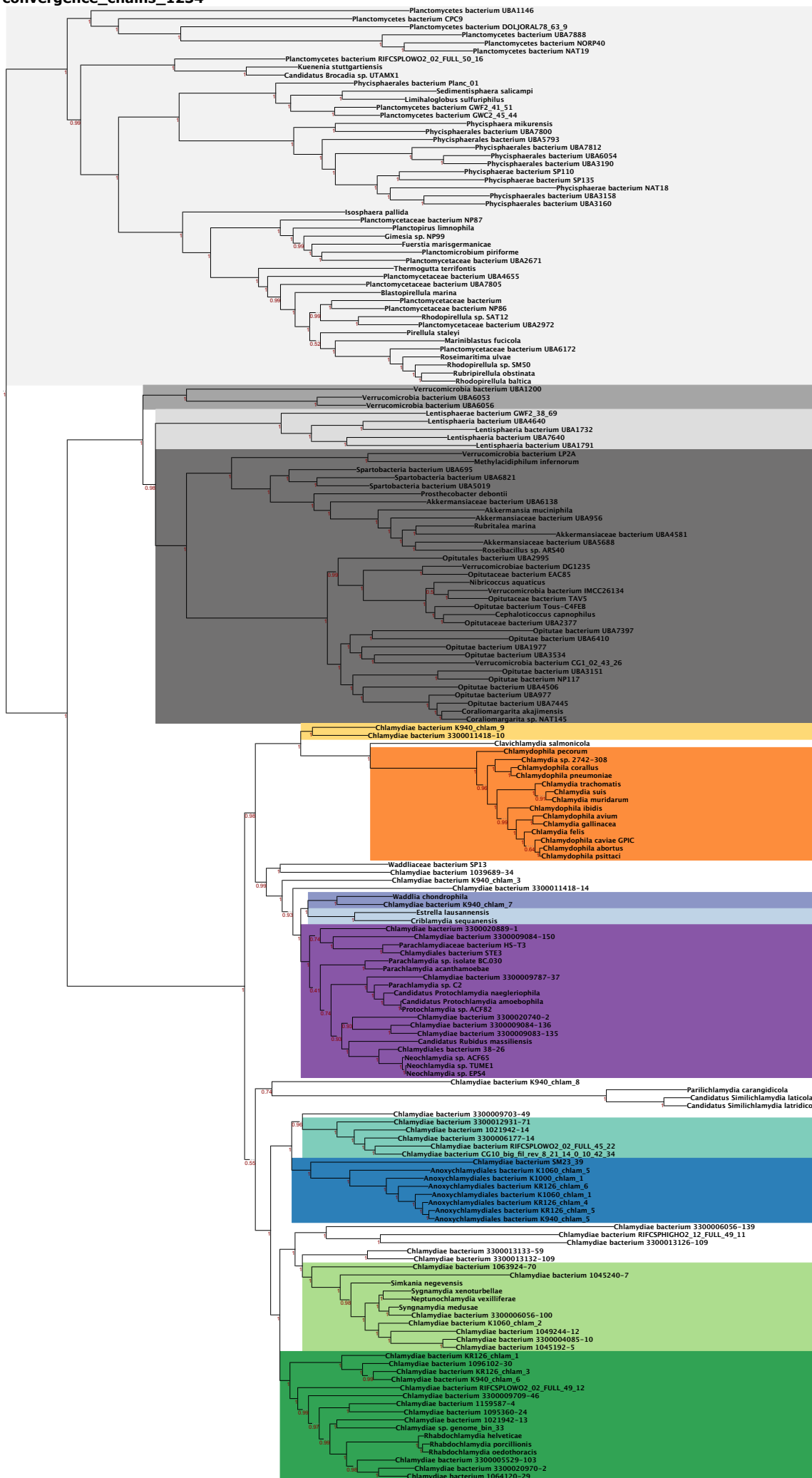
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chain3

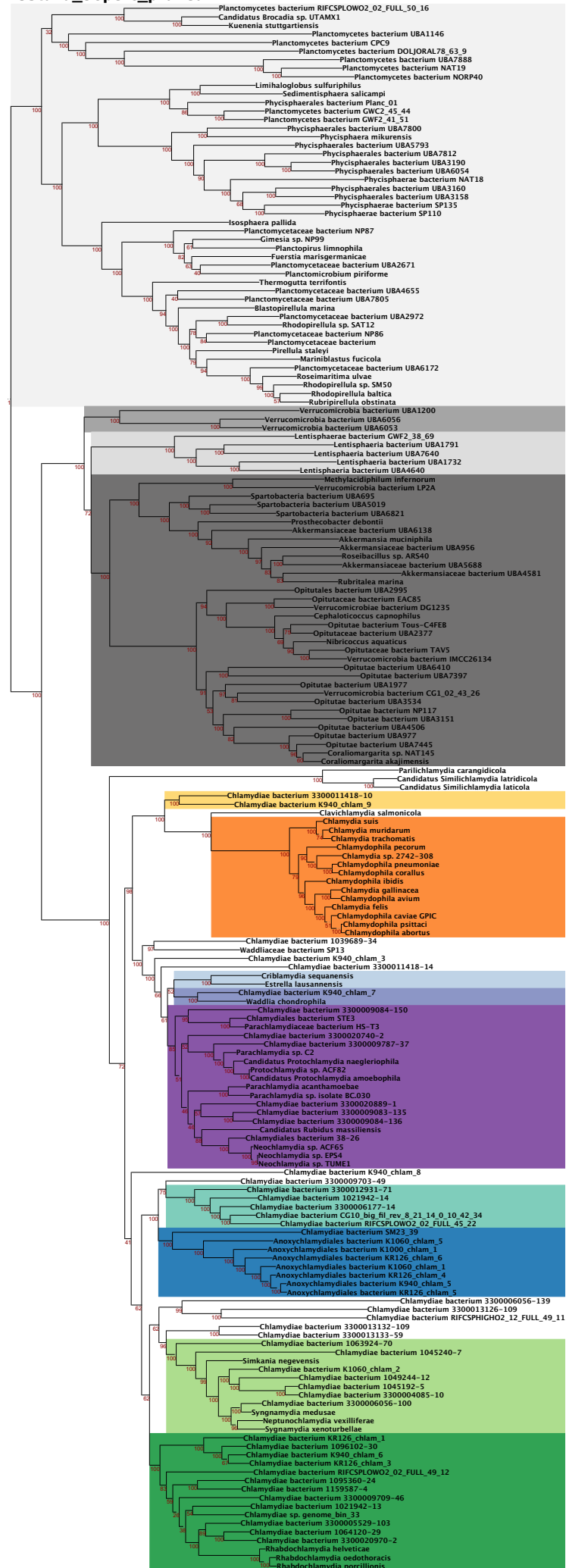


0.1

convergence_chains_1234

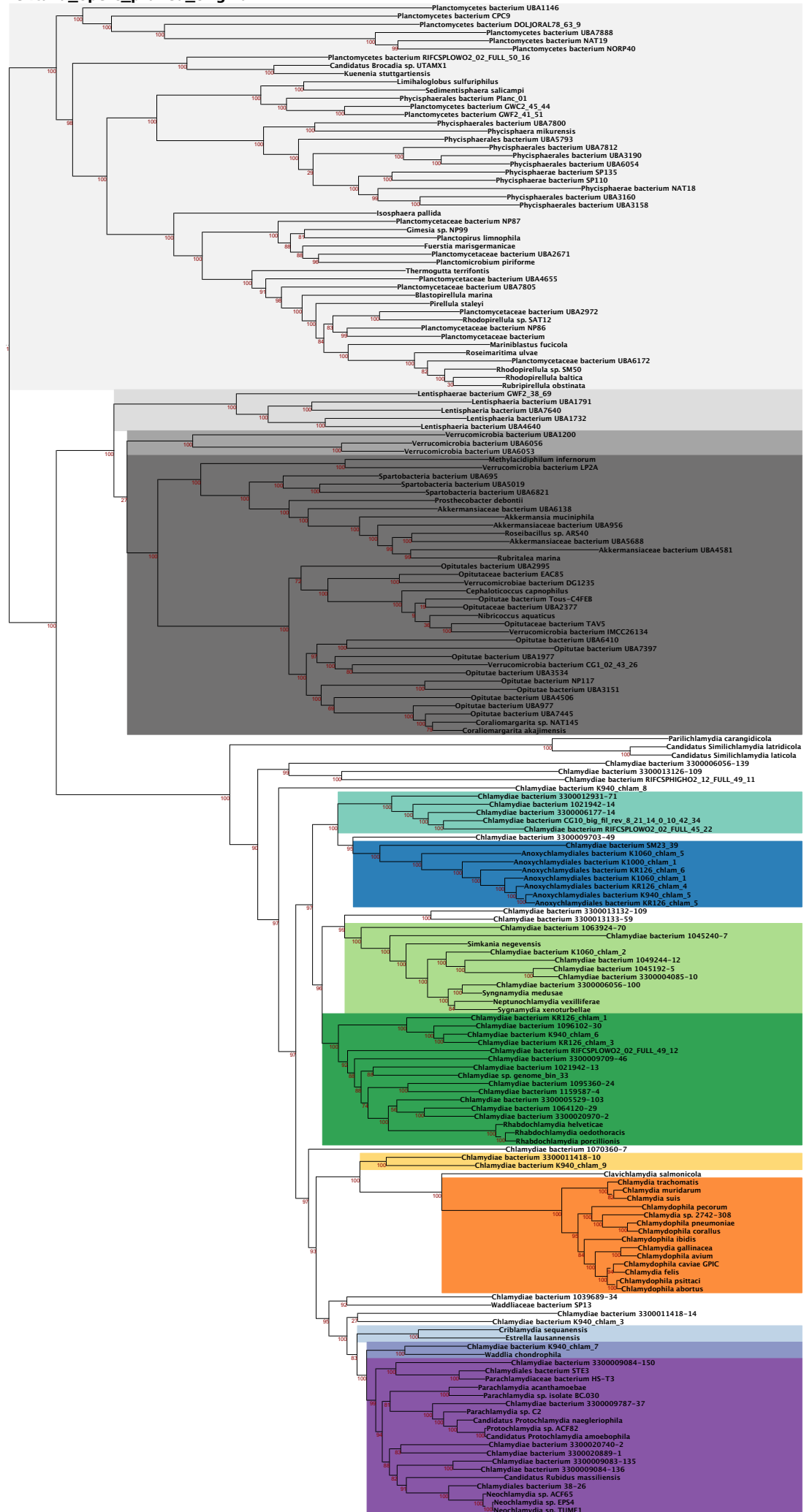


183taxa_50perc_pruned

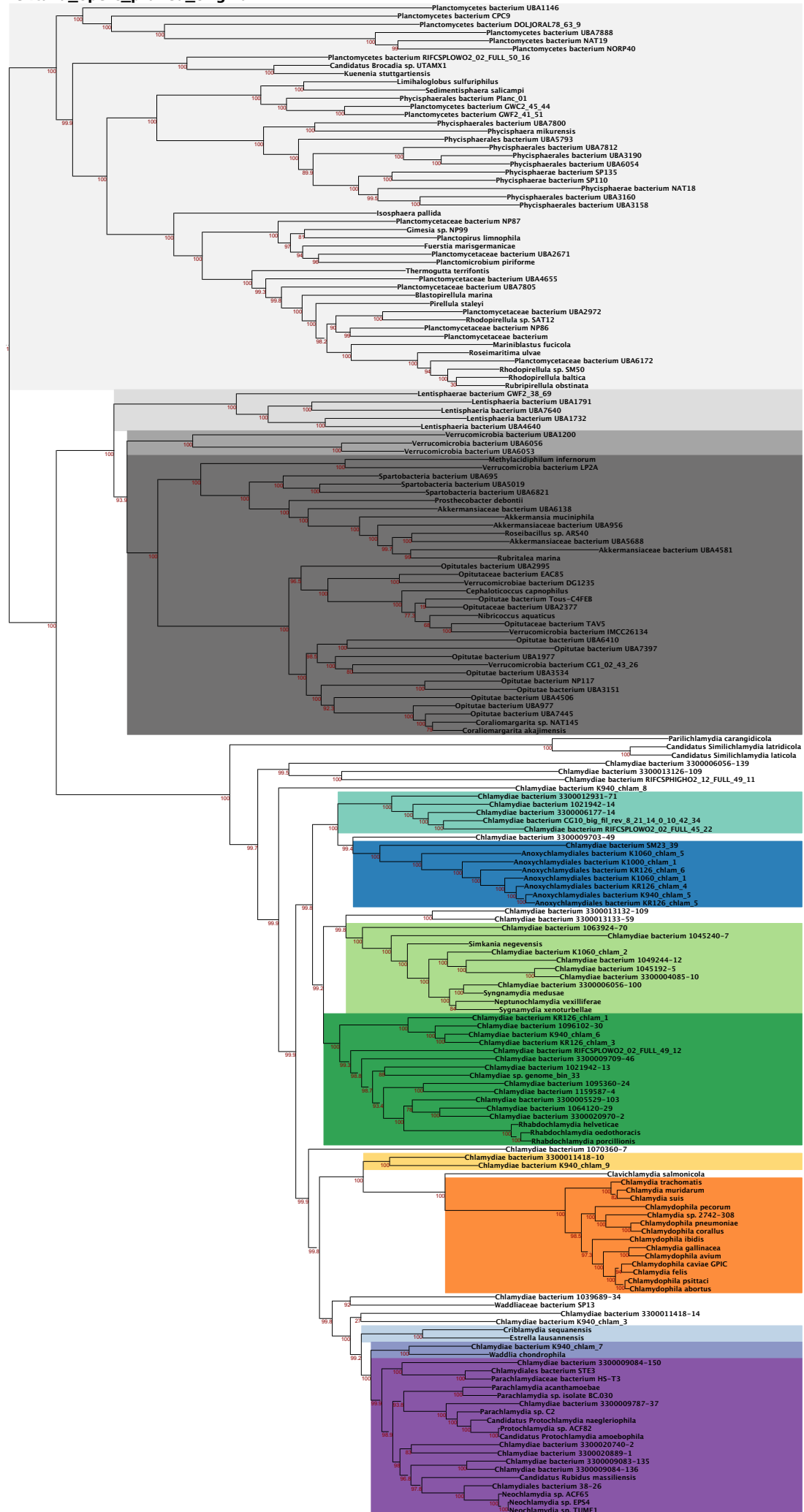


0.1

184taxa_0perc_pruned_original

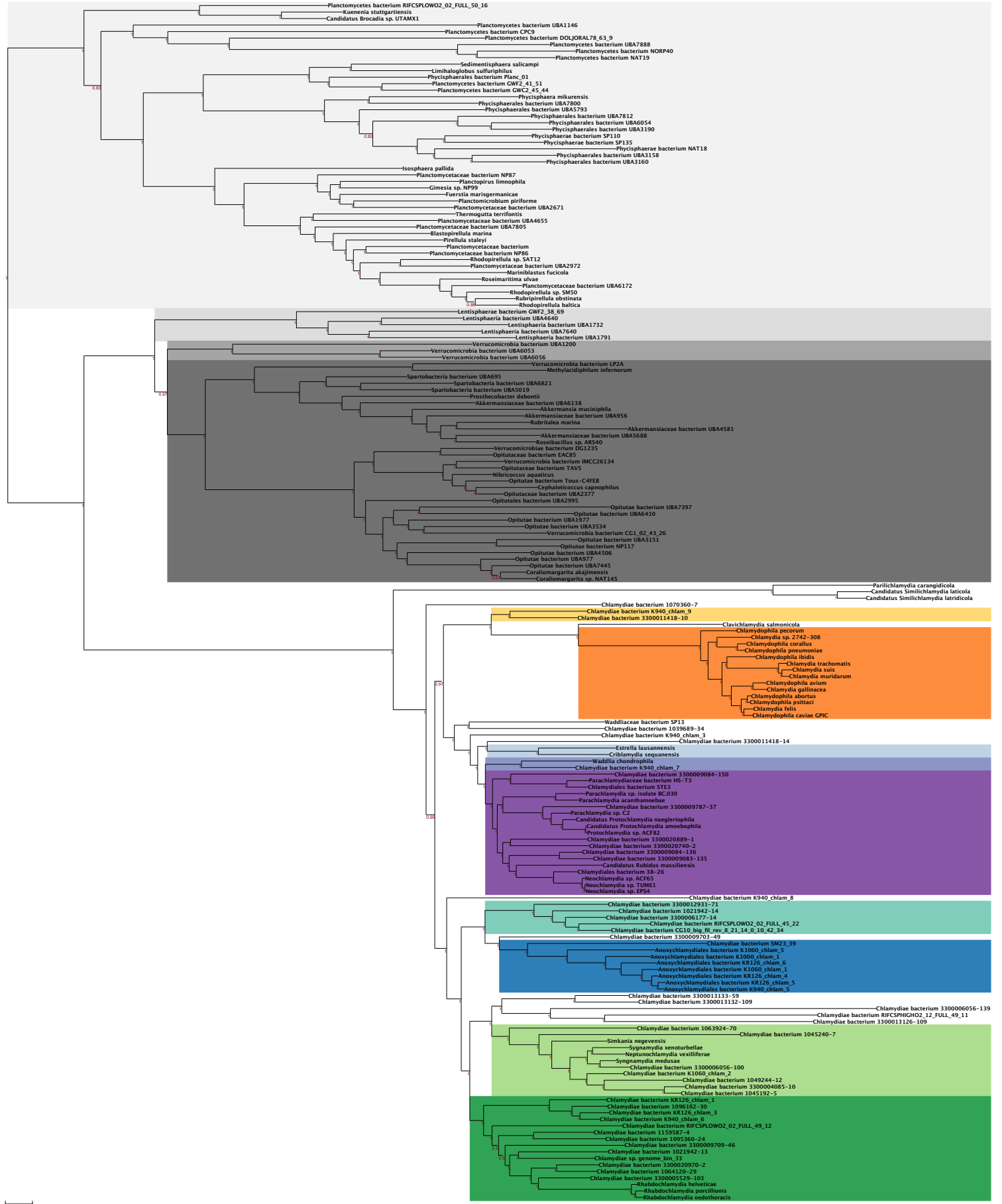


184taxa_0perc_pruned_original



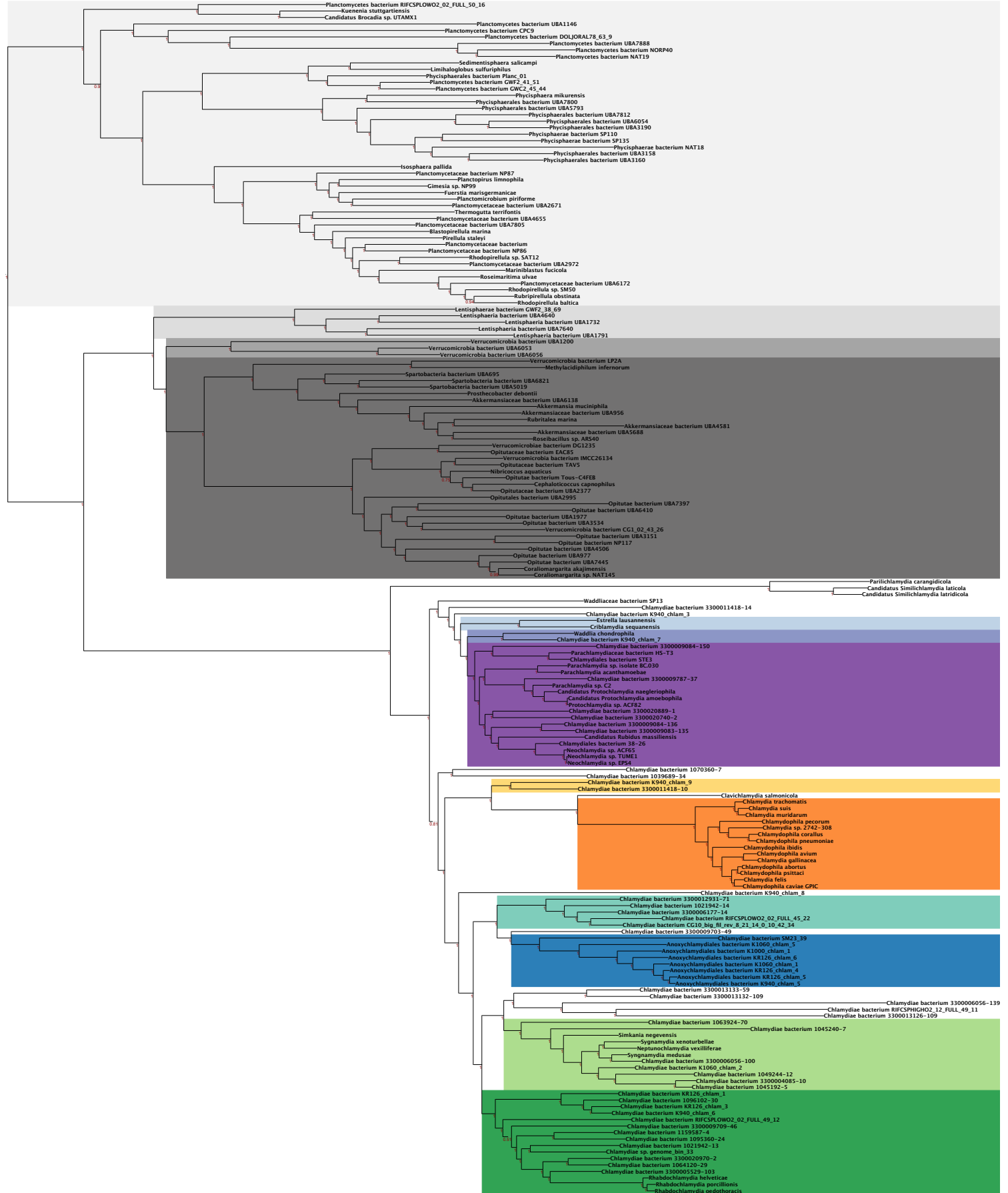
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chain1



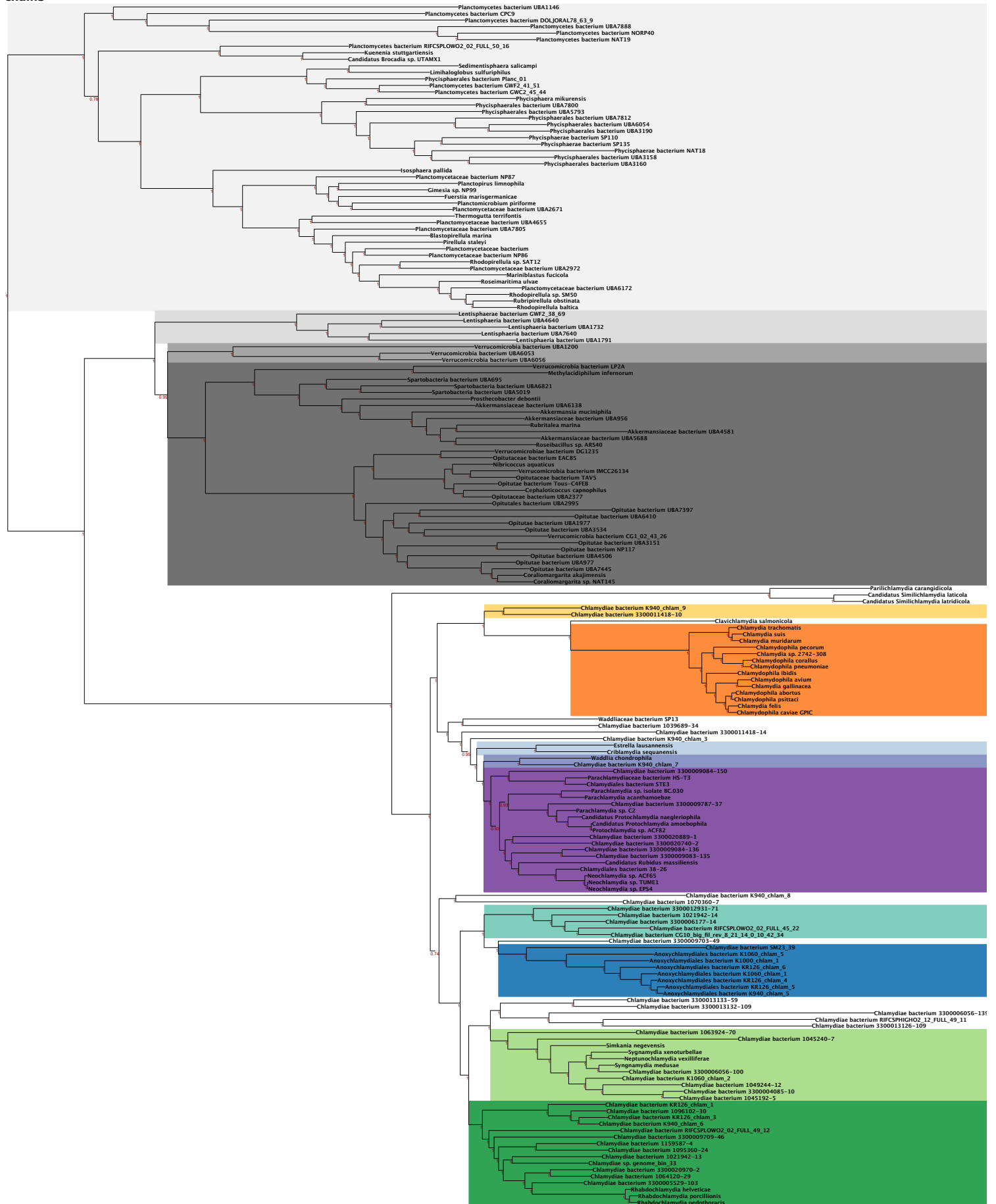
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chain2

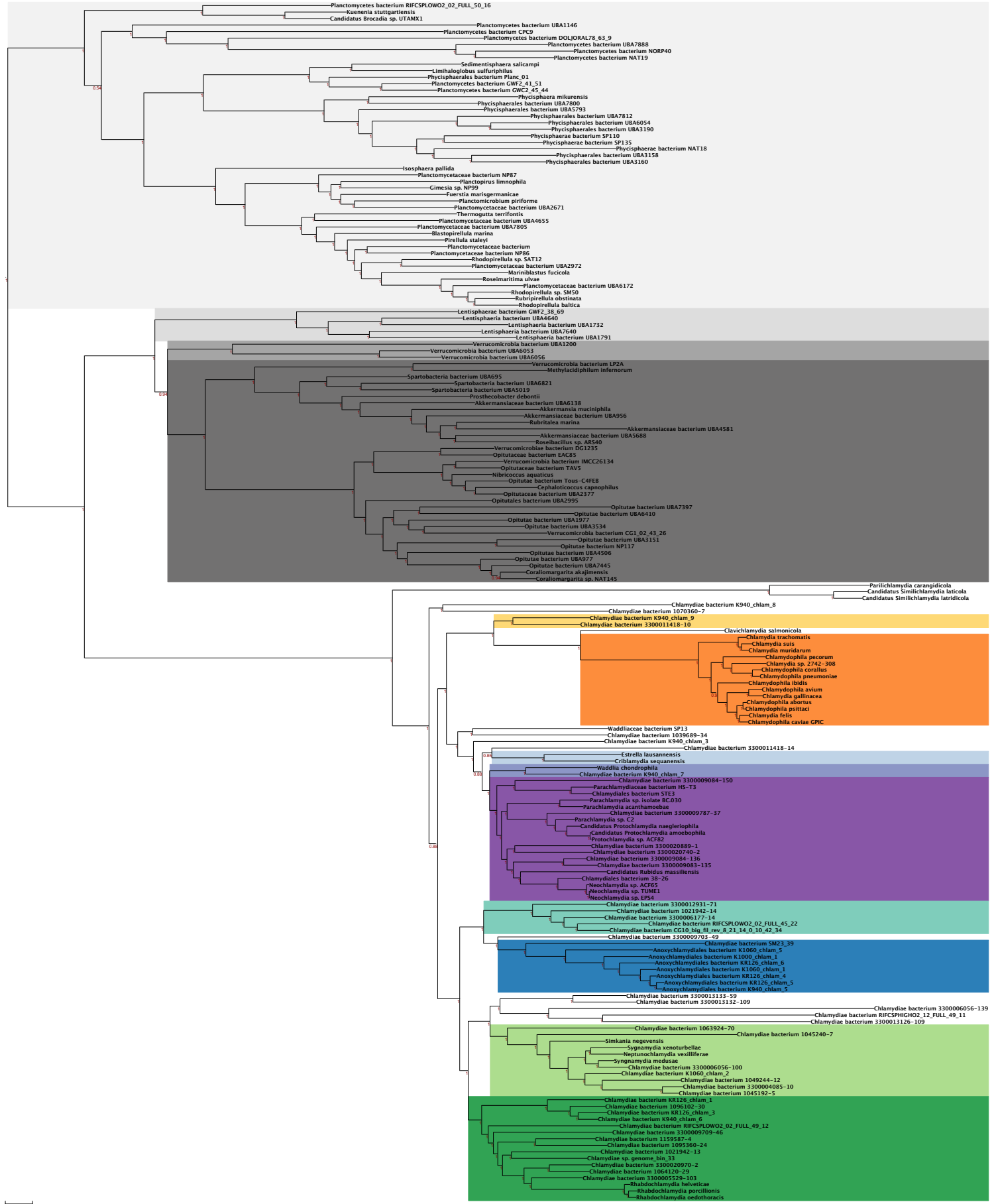


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chain3

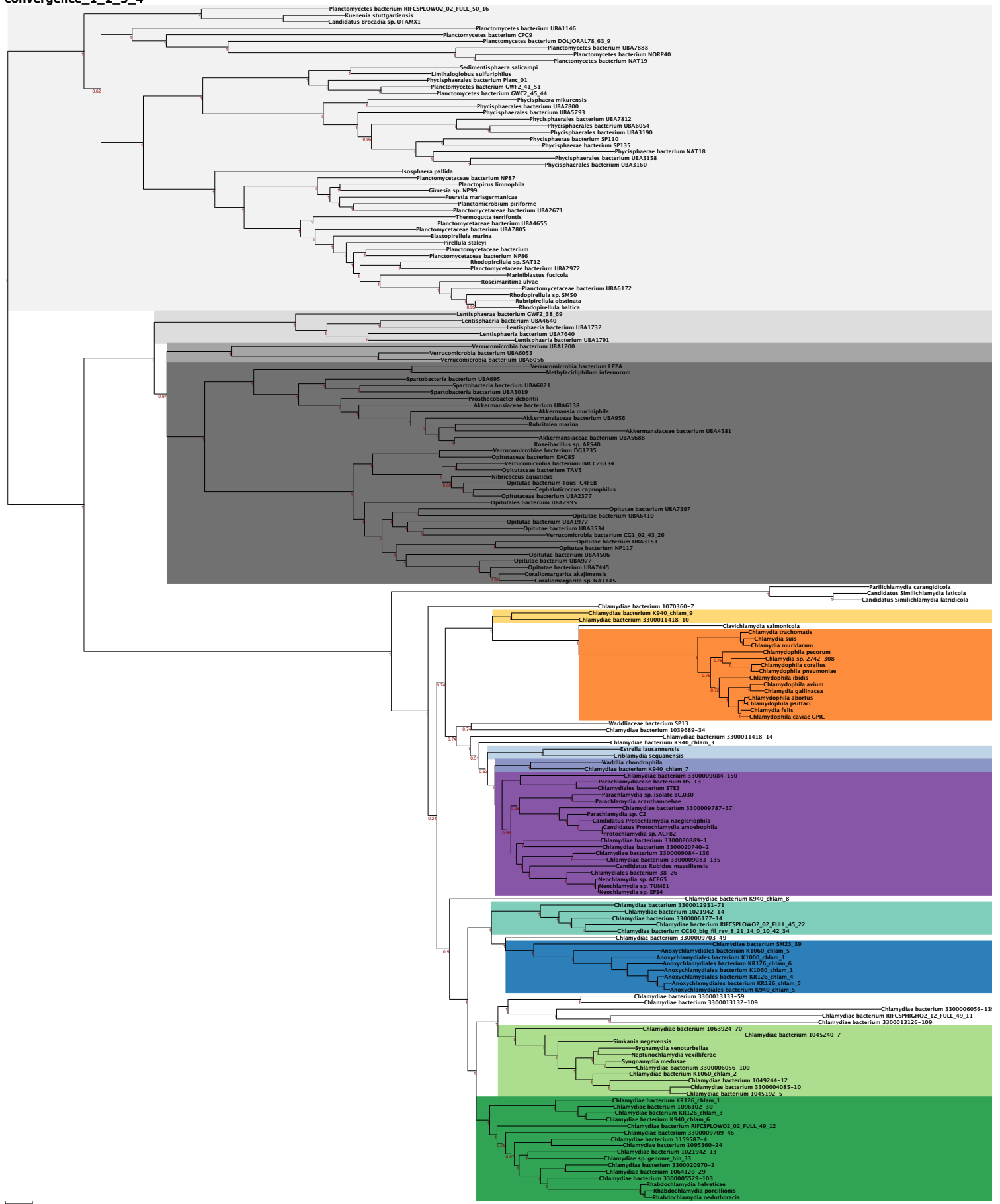


chain4

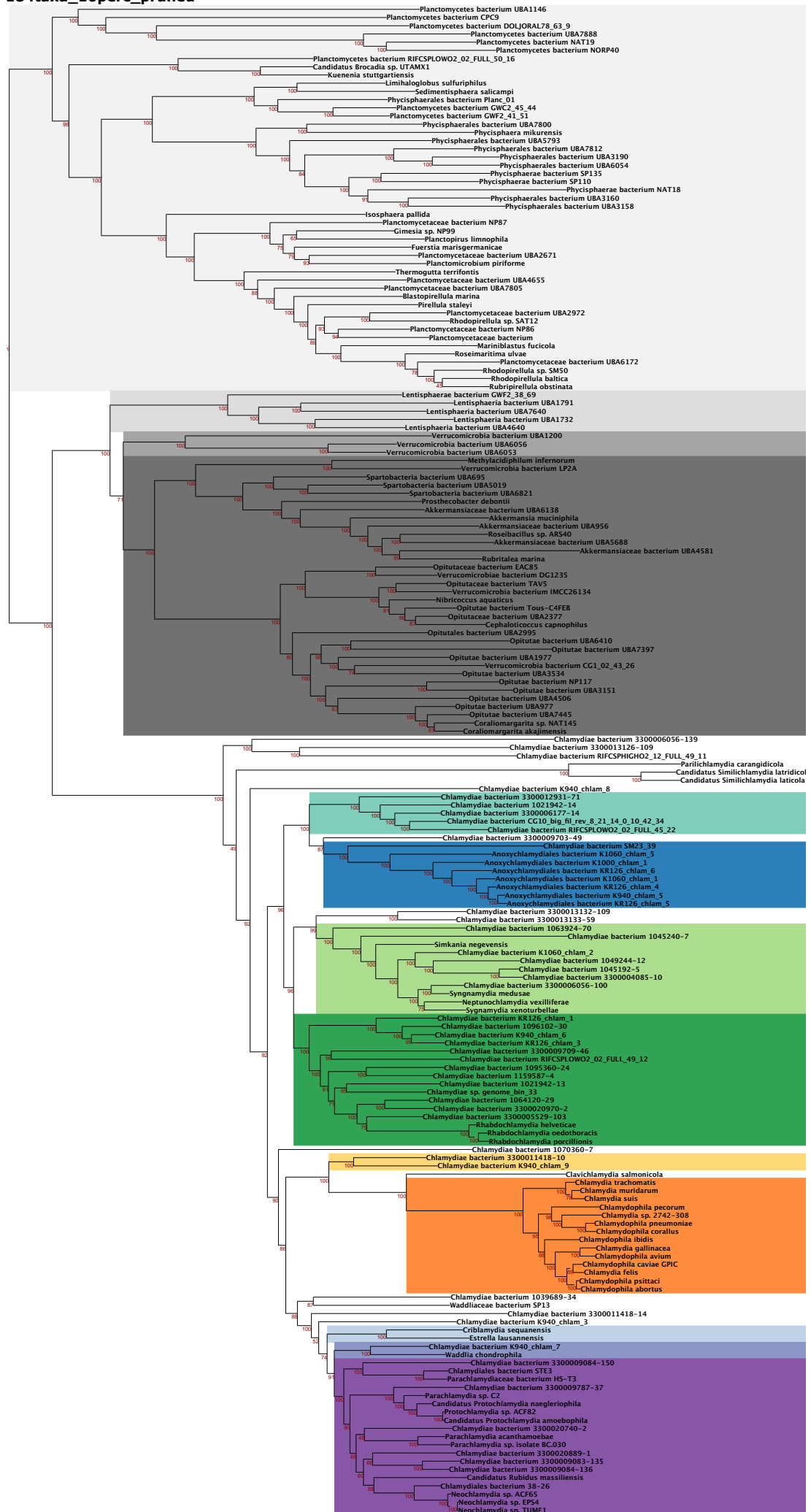


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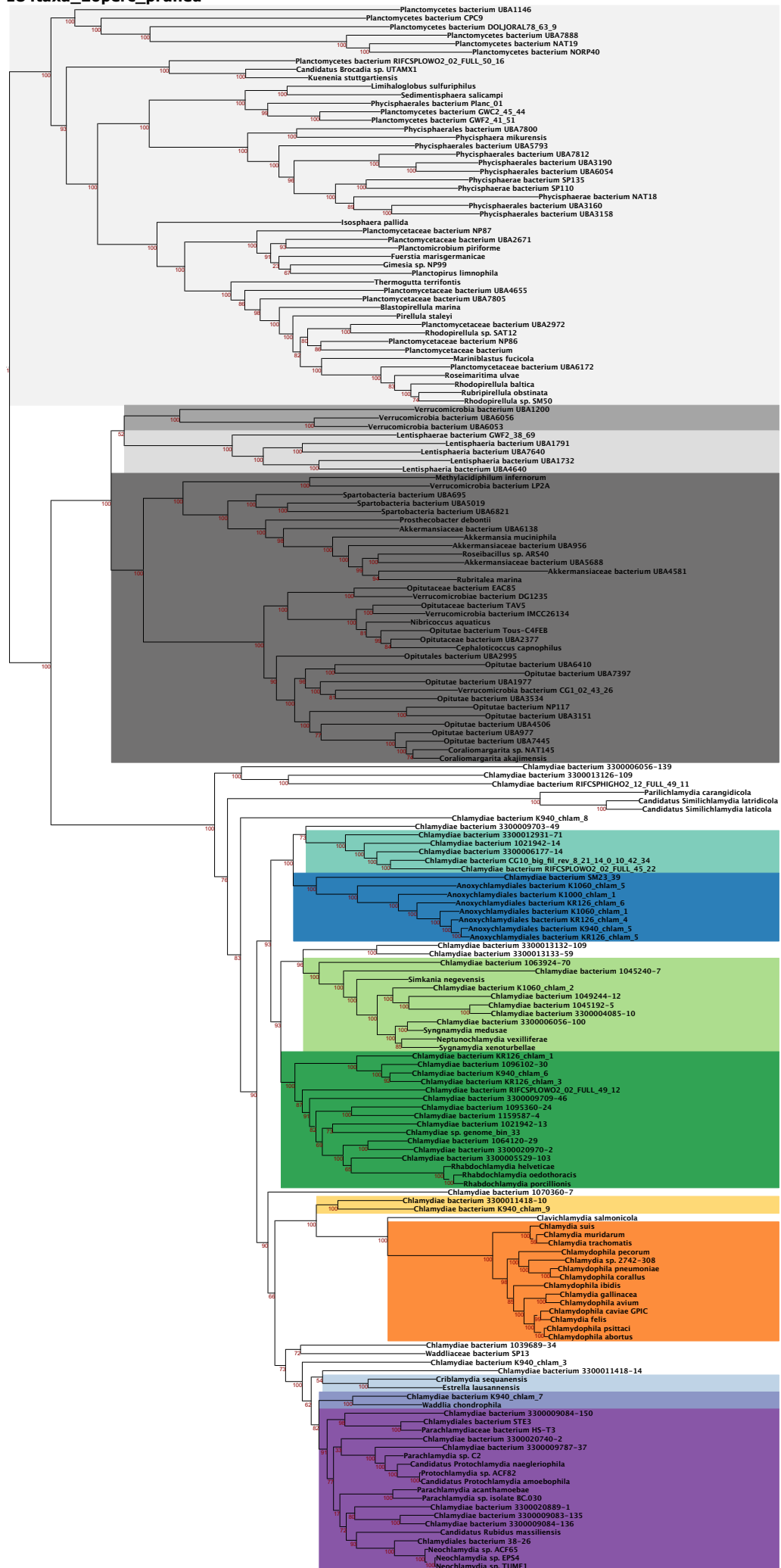
convergence_1_2_3_4



184taxa_10perc_pruned

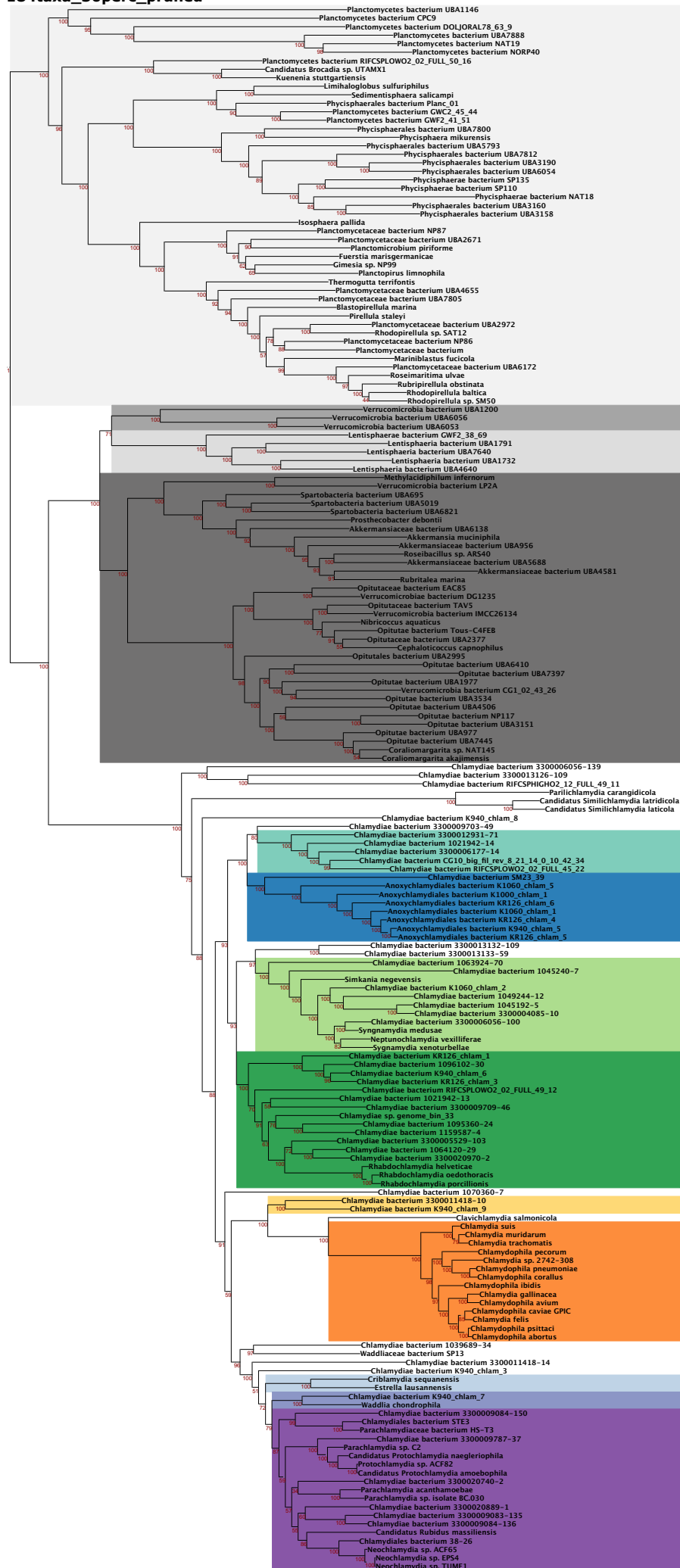


184taxa_20perc_pruned



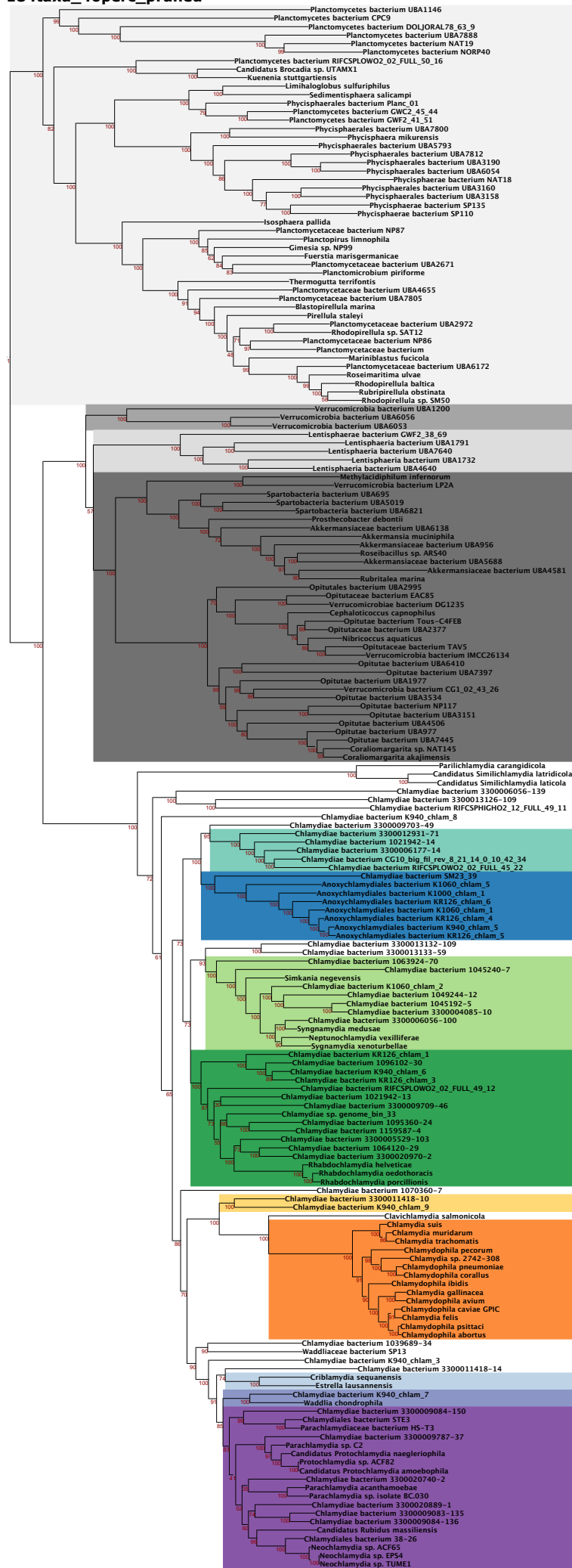
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184taxa_30perc_pruned



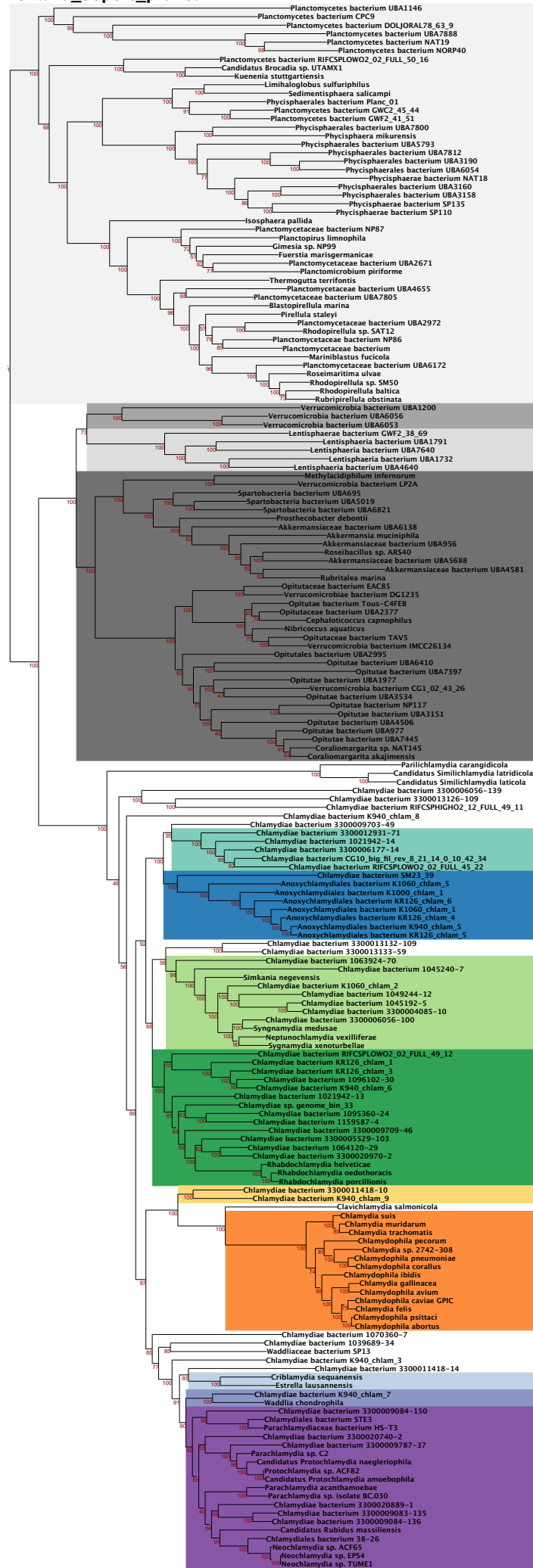
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184taxa_40perc_pruned



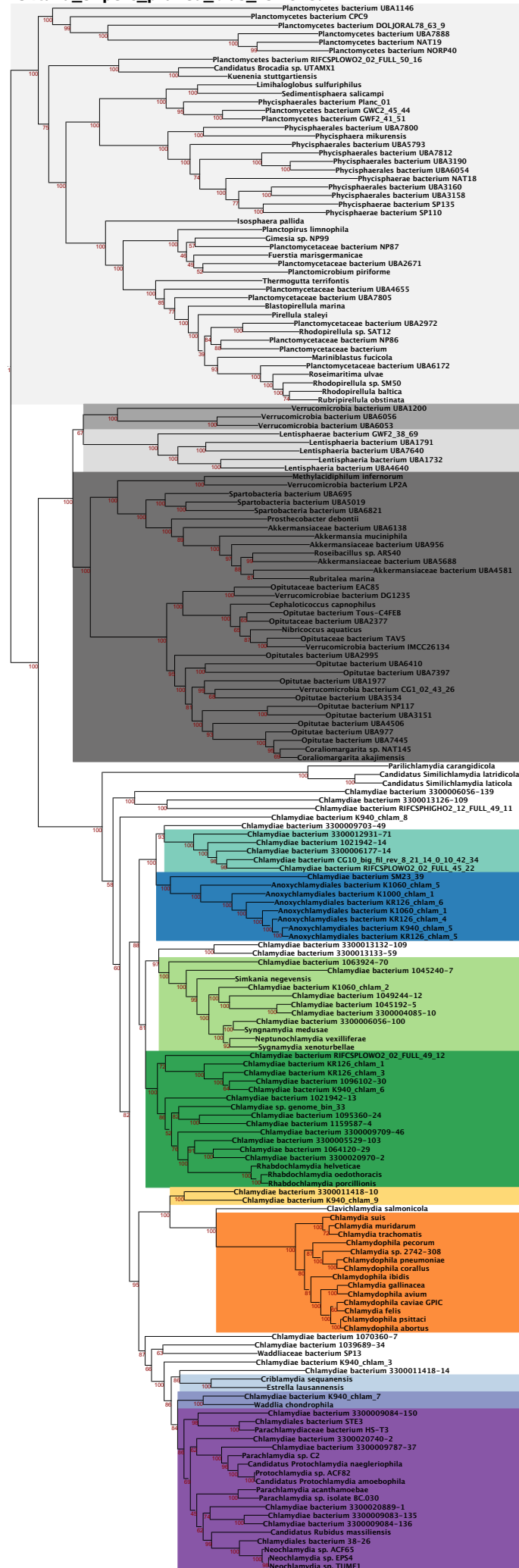
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184taxa_50perc_pruned



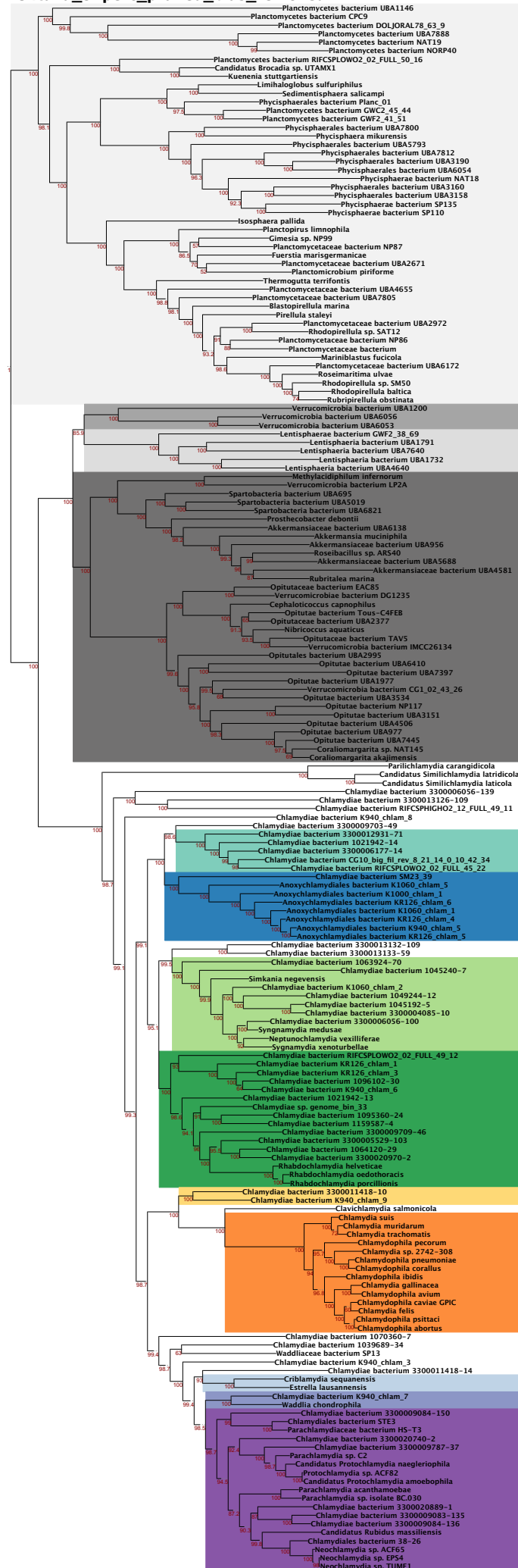
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184taxa_51perc_pruned_bias_removed



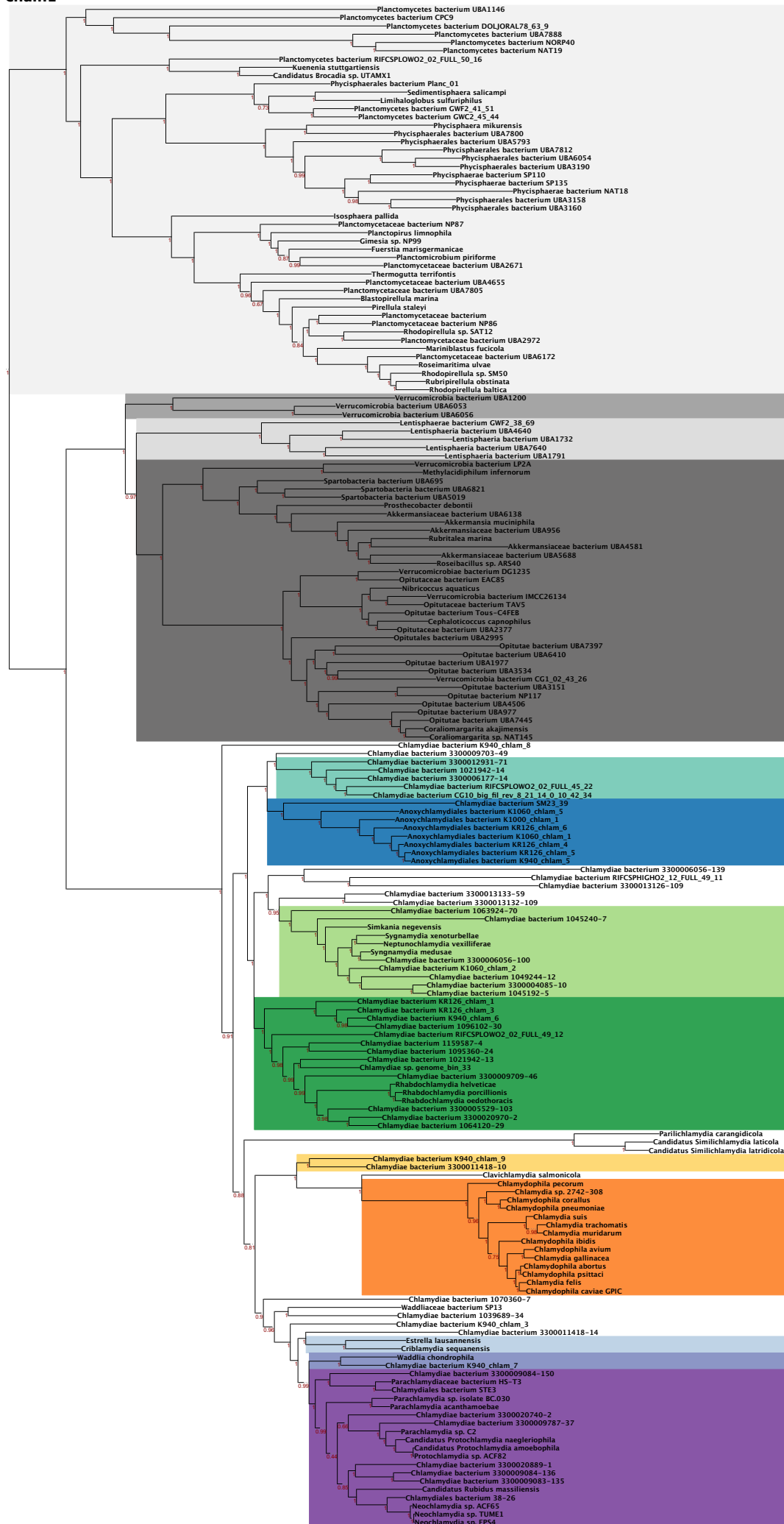
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184taxa_51perc_pruned_bias_removed



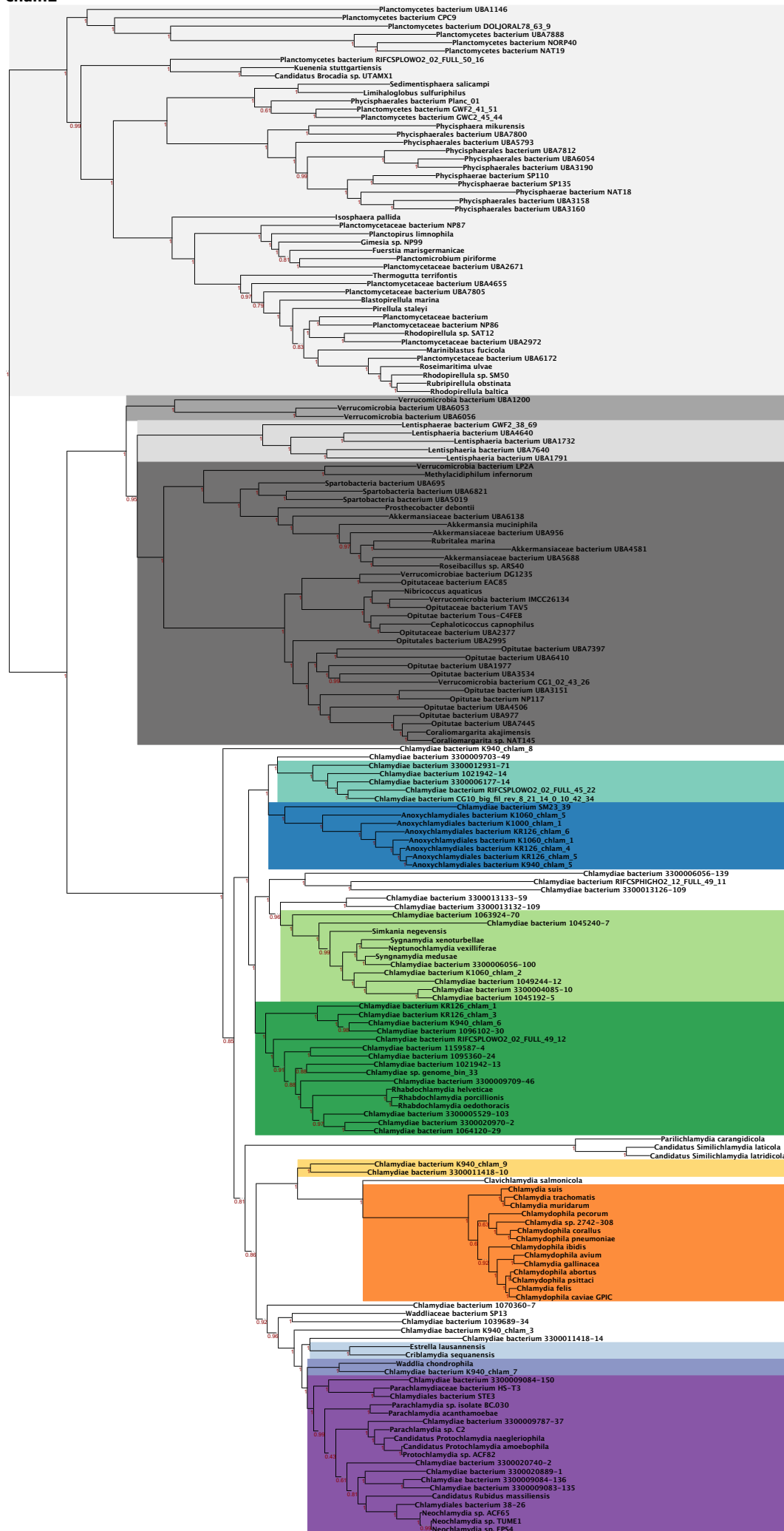
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chain1



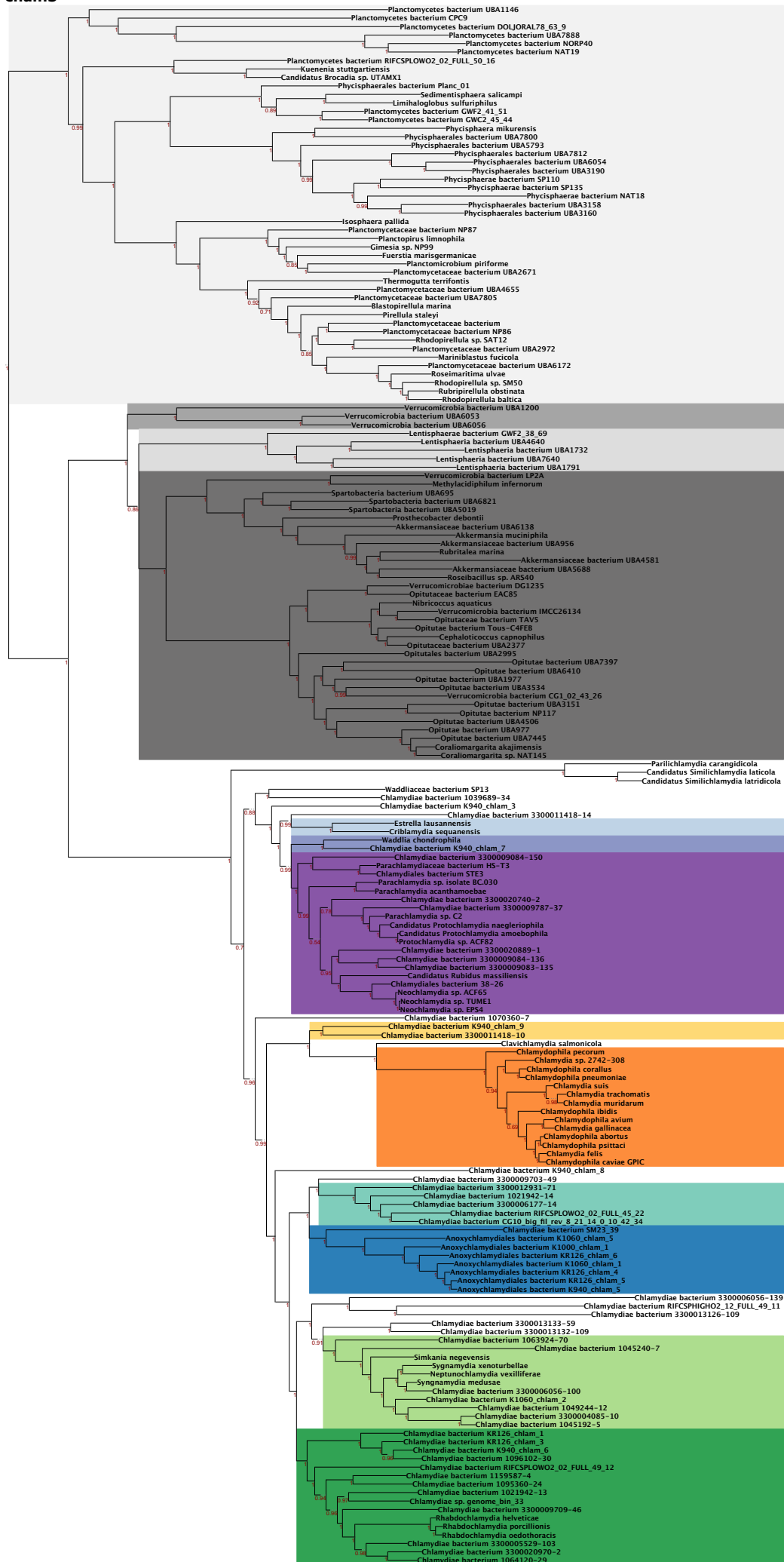
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chain2

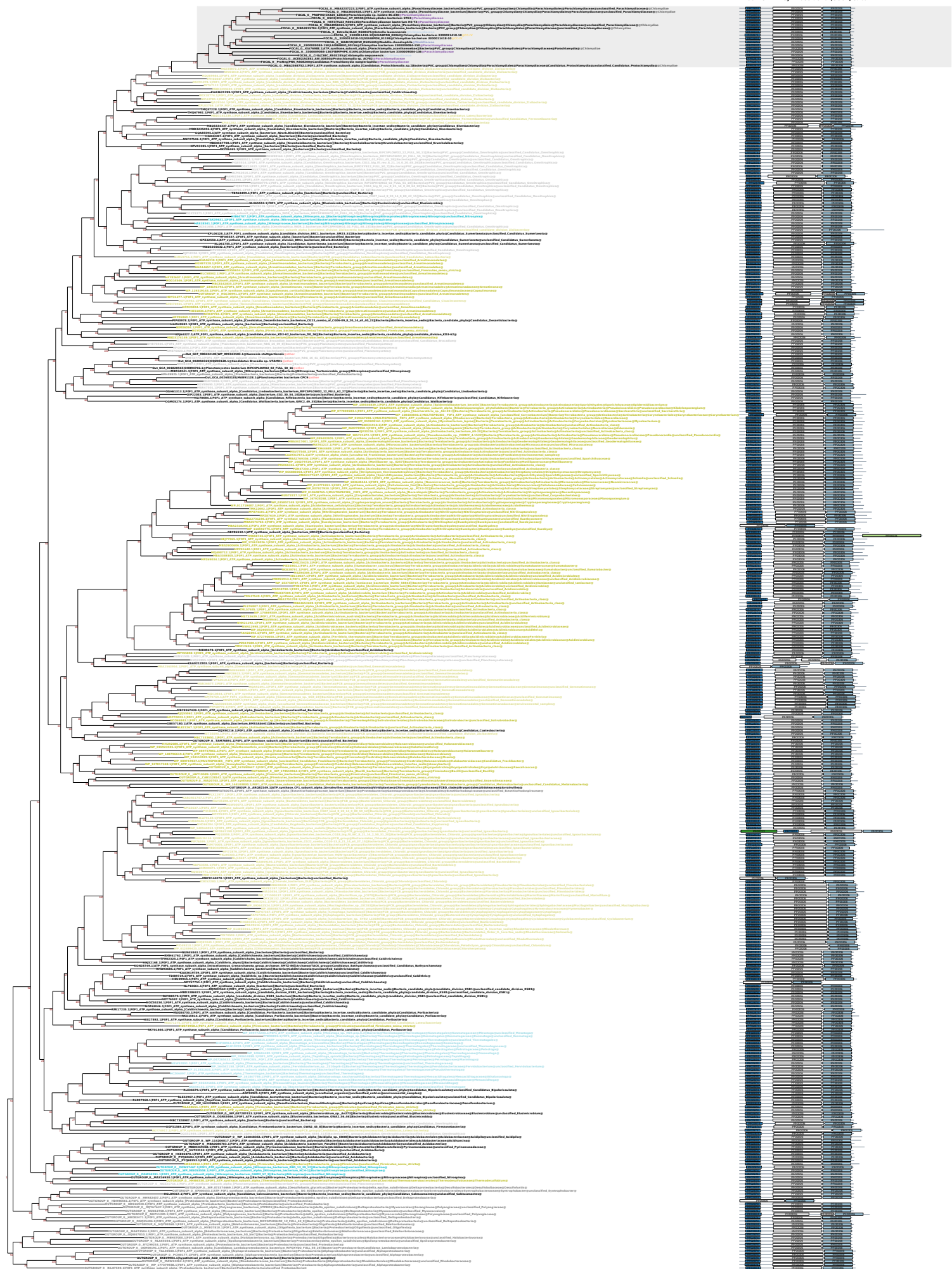


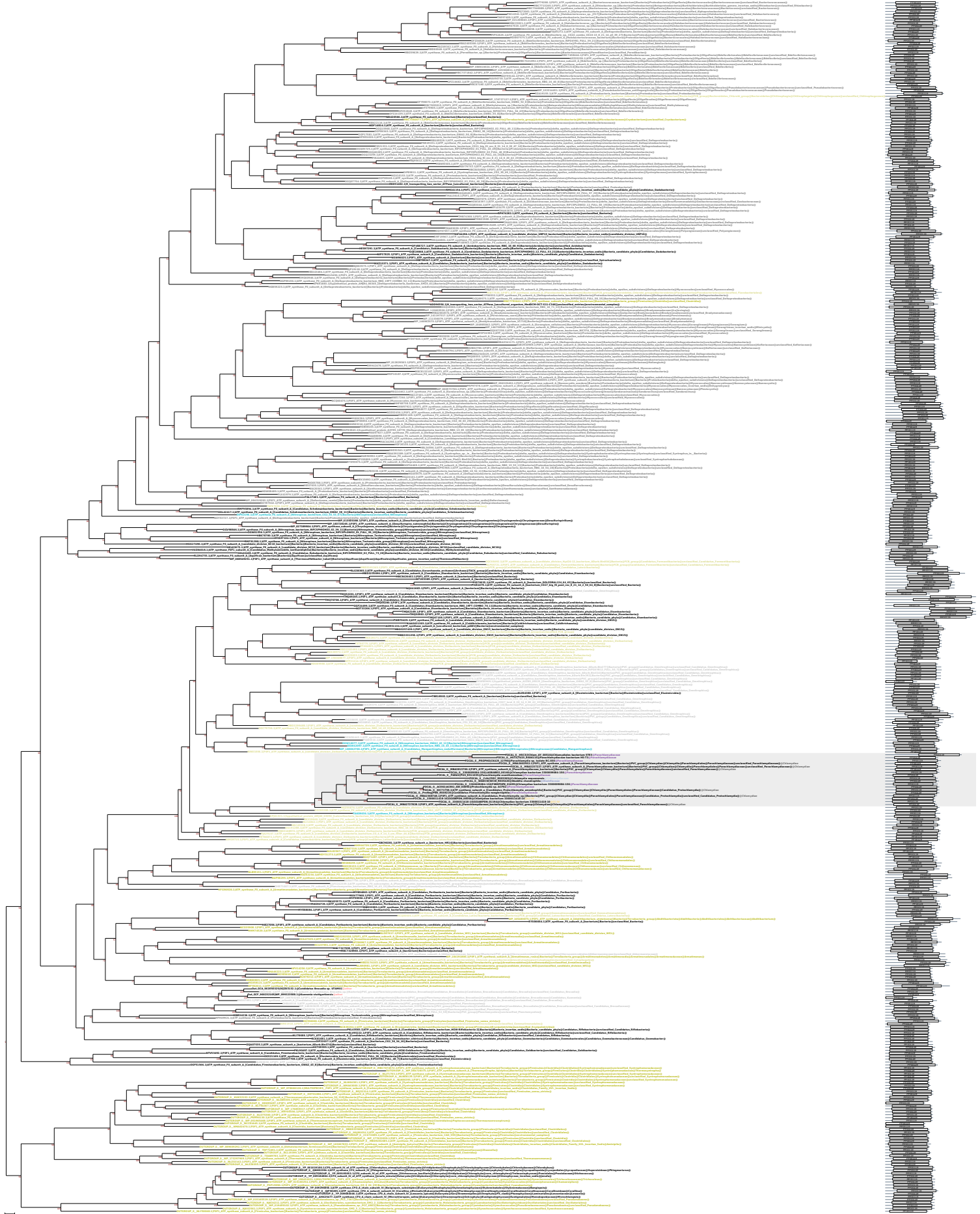
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chain3

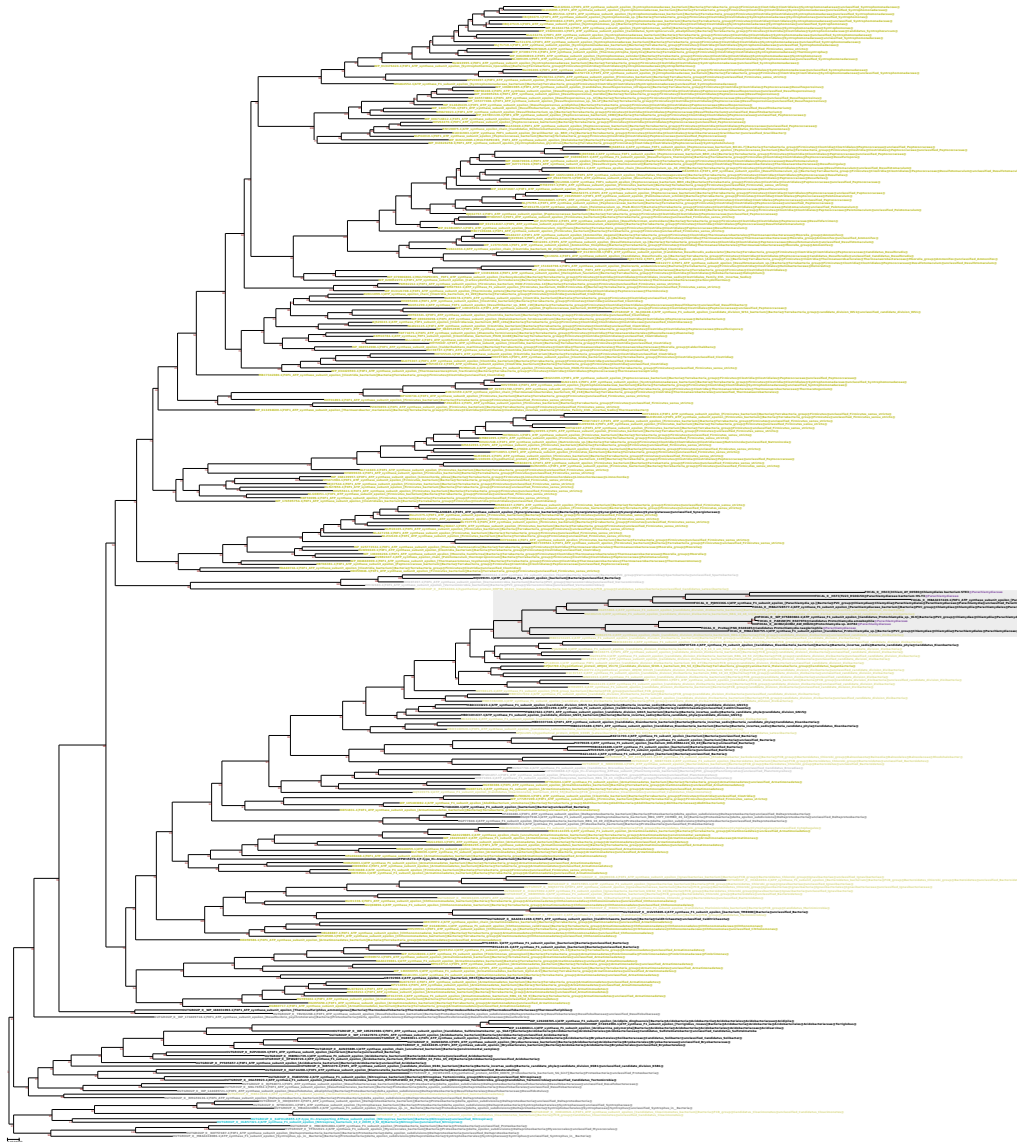


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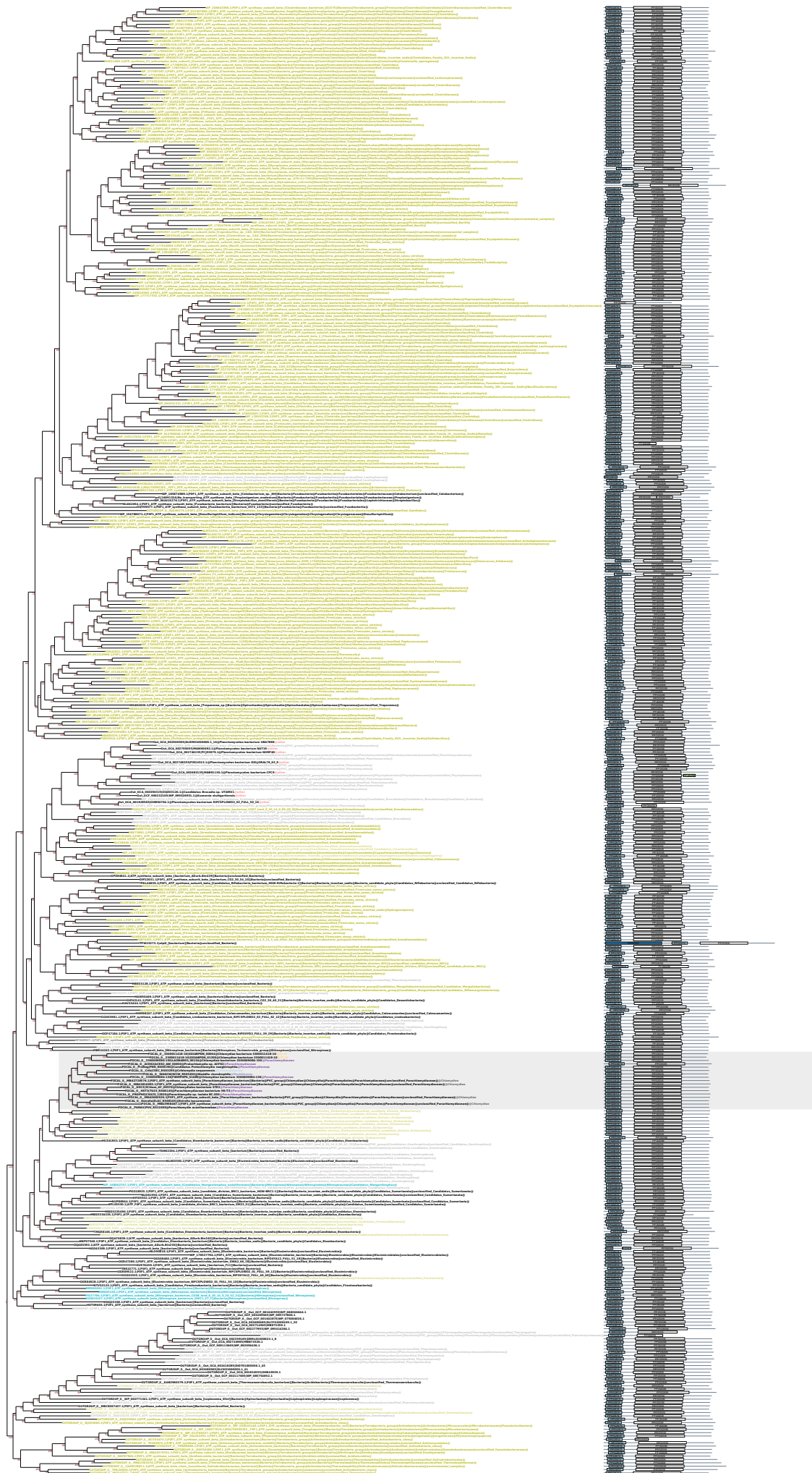


11Y2G
49C
402114
F-type H⁺-transporting ATPase subunit epsilon



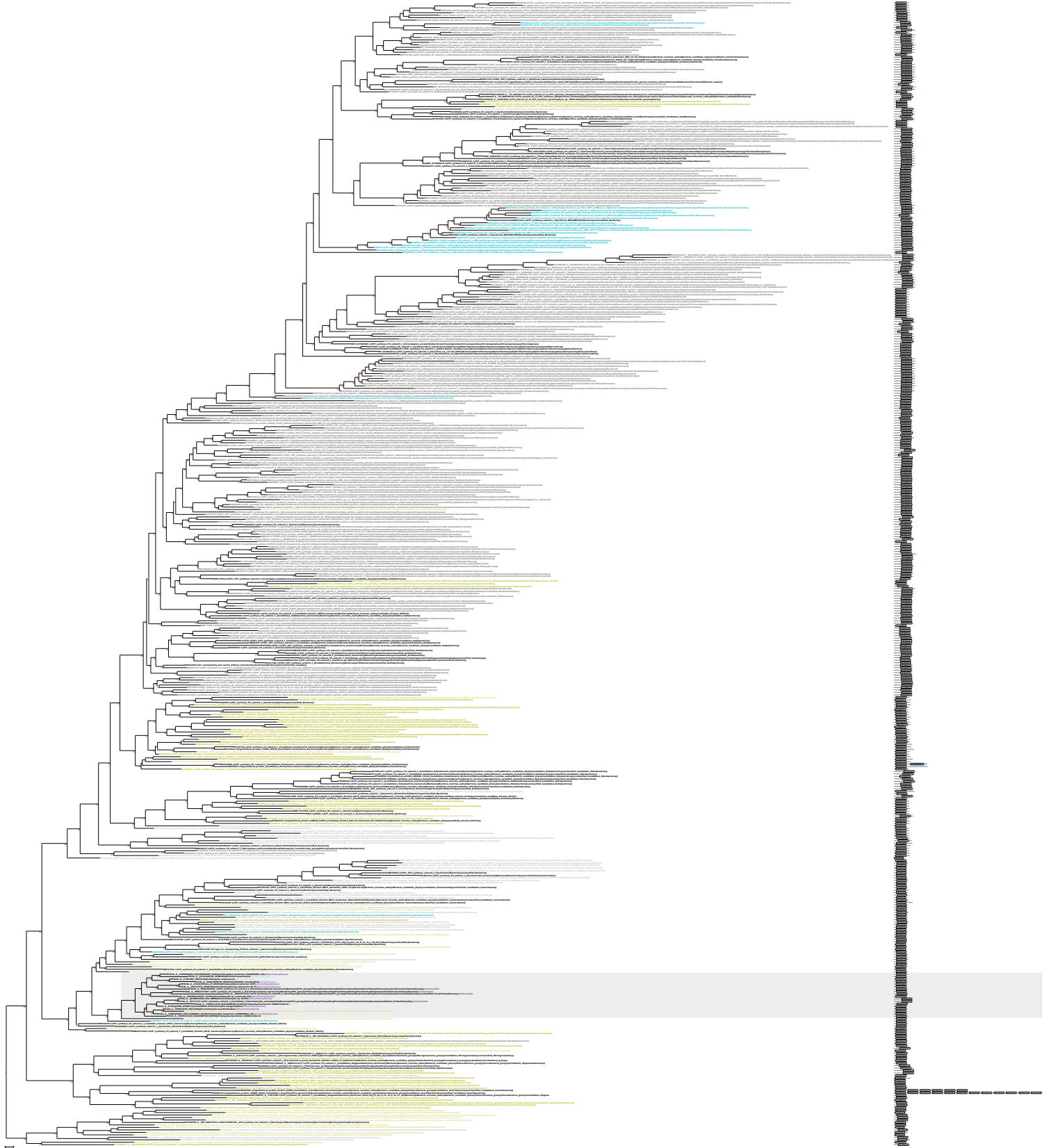
PF08621: ATP synthase, Delta/Epsilon chain, long alpha-helic domain
PF02822: ATP synthase, Delta/Epsilon chain, beta sandwich domain





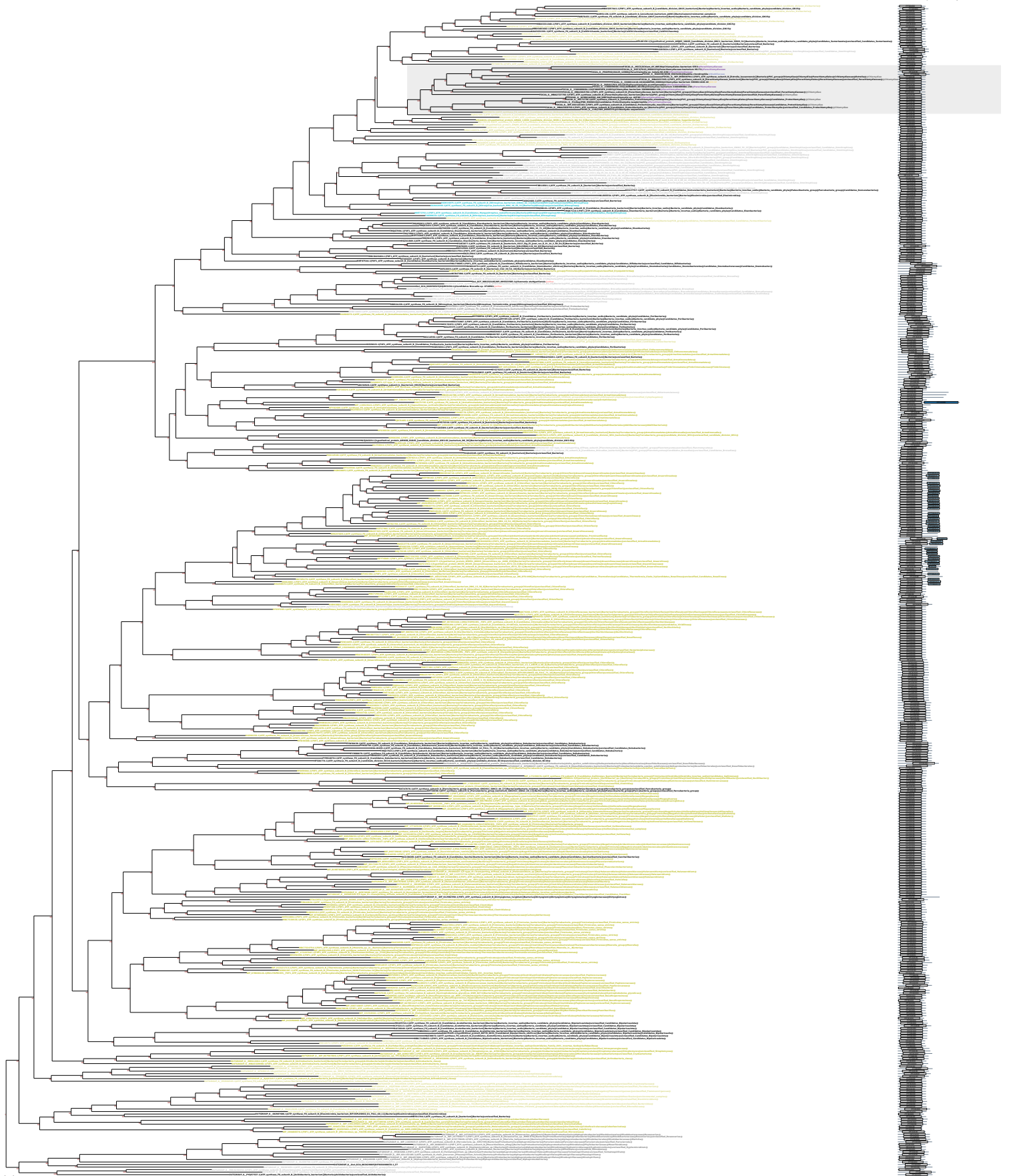
0246
atp
002110
F-type H⁺-transporting ATPase subunit c

PF00117: ATP synthase subunit C
PF00118: Intrins, domain 3

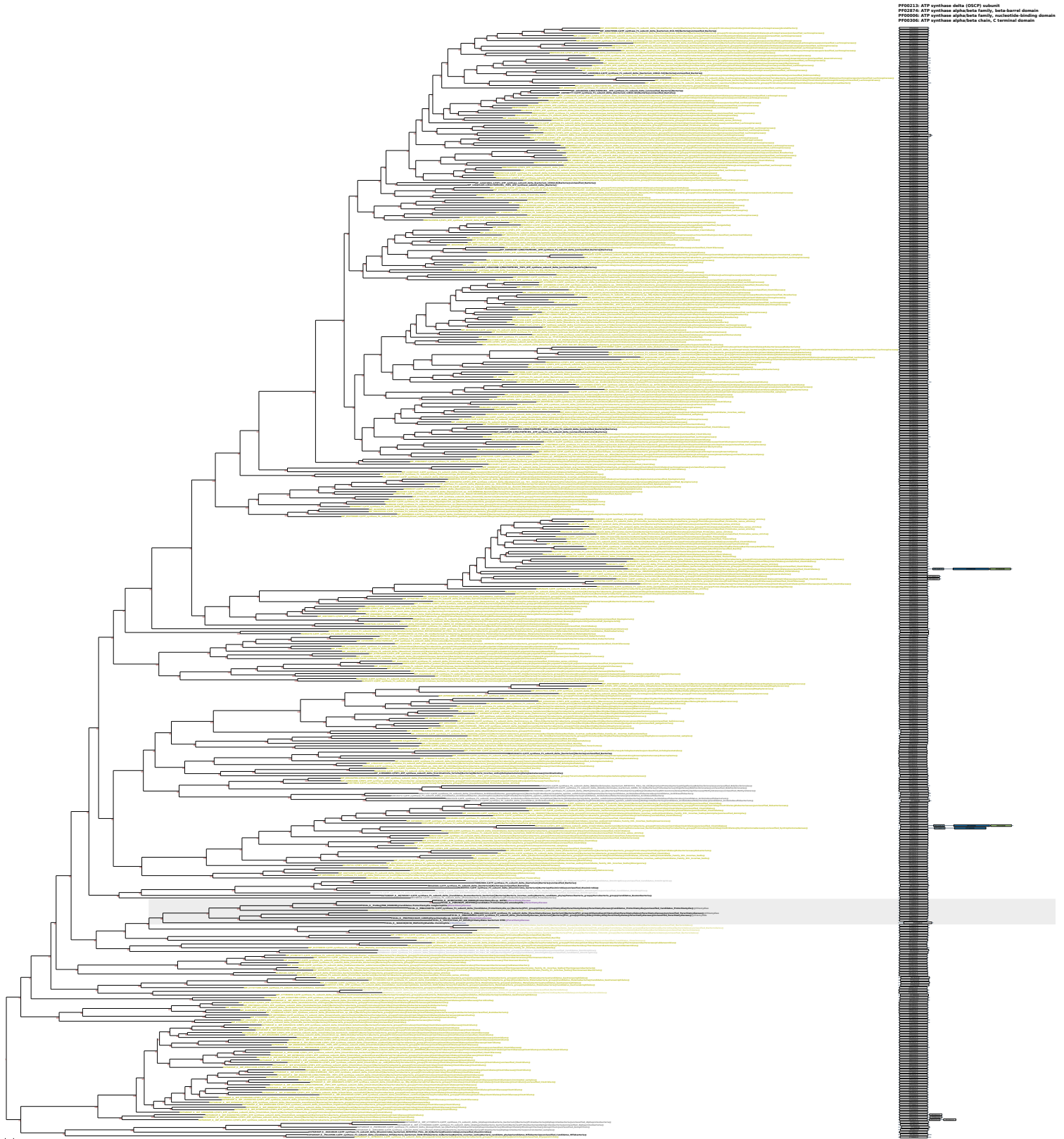


CG0711
atpF
K02109
F-type H⁺-transporting ATPase subunit b

PF00430: ATP synthase B/B' CF0
PF02115: ATP synthase delta (OSCF1) subunit
PF04380: Papillase family M28



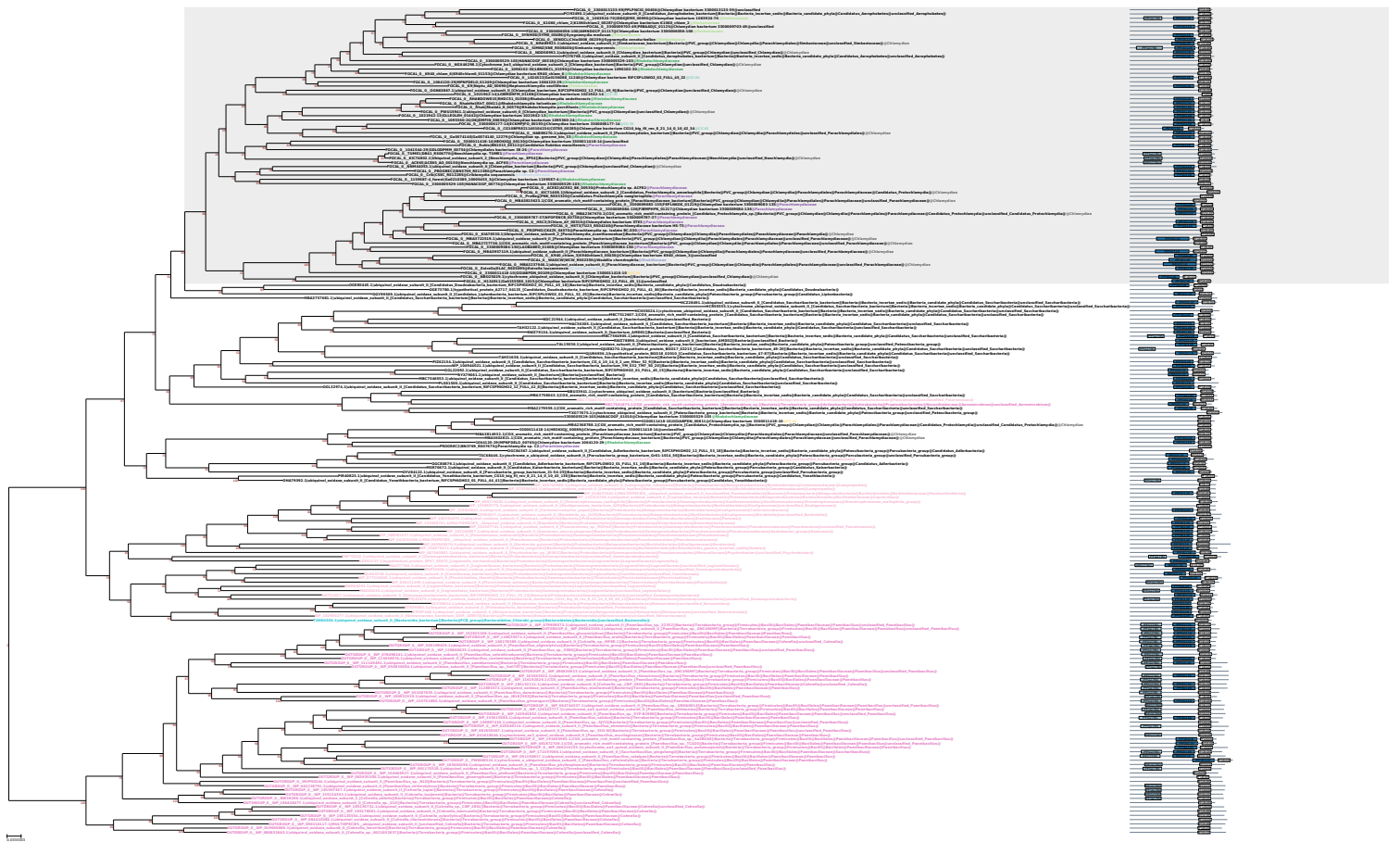
COG0712
atpH
F-type H⁺-transporting ATPase subunit delta



PF00213: ATP synthase delta (OSCP) subunit
PF02376: ATP synthase alpha/beta family, beta-barrel domain
PF00006: ATP synthase alpha/beta family, nucleotide-binding domain
PF00206: ATP synthase alpha/beta chain, C-terminal domain

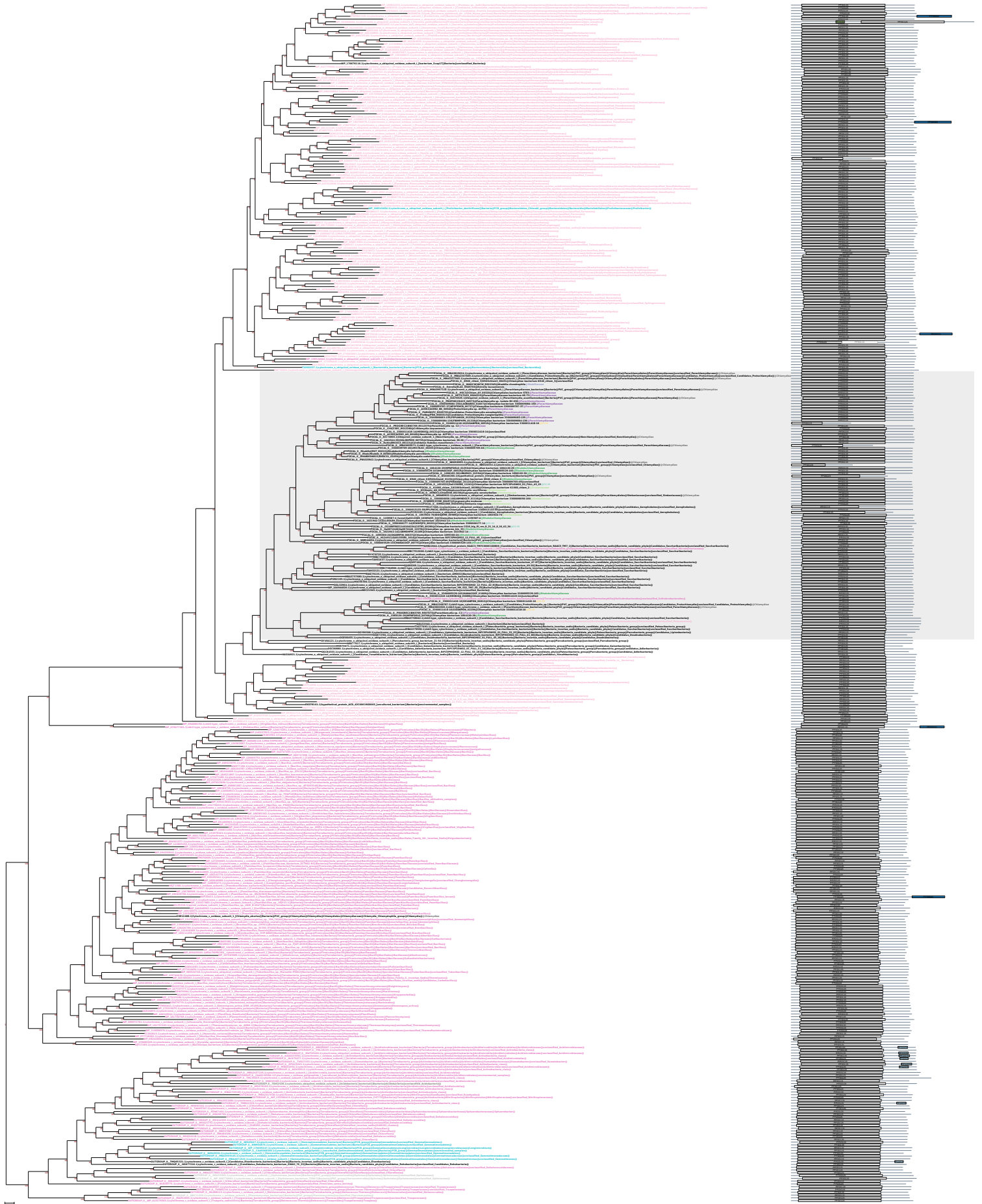
COG1622
cyaA
K02297
cytochrome o ubiquinol oxidase subunit II

PF06481: COX Aromatic Rich Motif
PF02790: Cytochrome C oxidase subunit II, transmembrane domain
PF00116: Cytochrome C oxidase subunit II, periplasmic domain



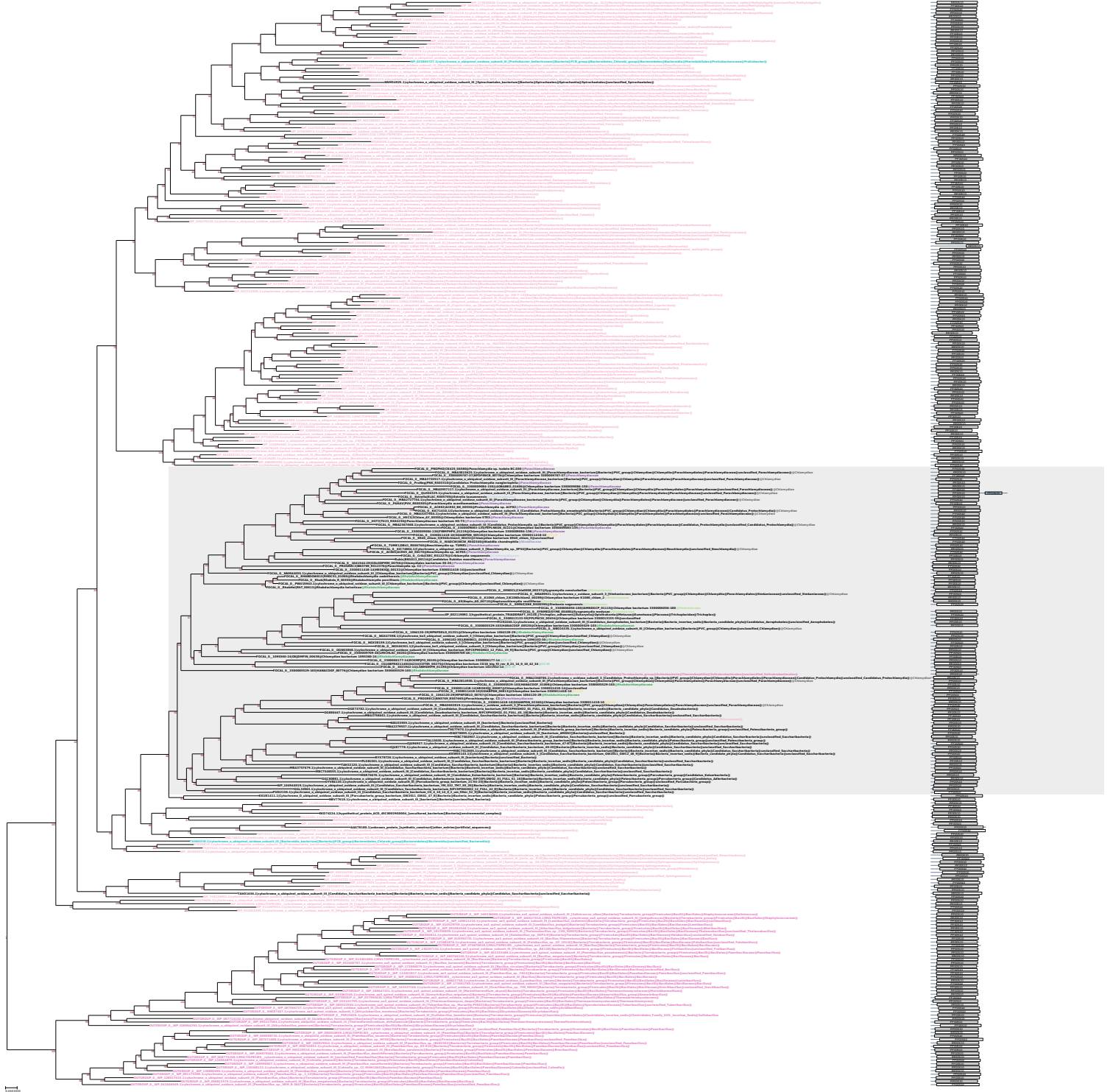
COG0843
cyb
K02298
cytochrome o ubiquinol oxidase subunit I

PF00115: Cytochrome C and Quinol oxidase polypeptide I
PF12270: Cytochrome c oxidase subunit IV
PF00510: Cytochrome c oxidase subunit III
PF08491: COX Aromatic Rich Motif



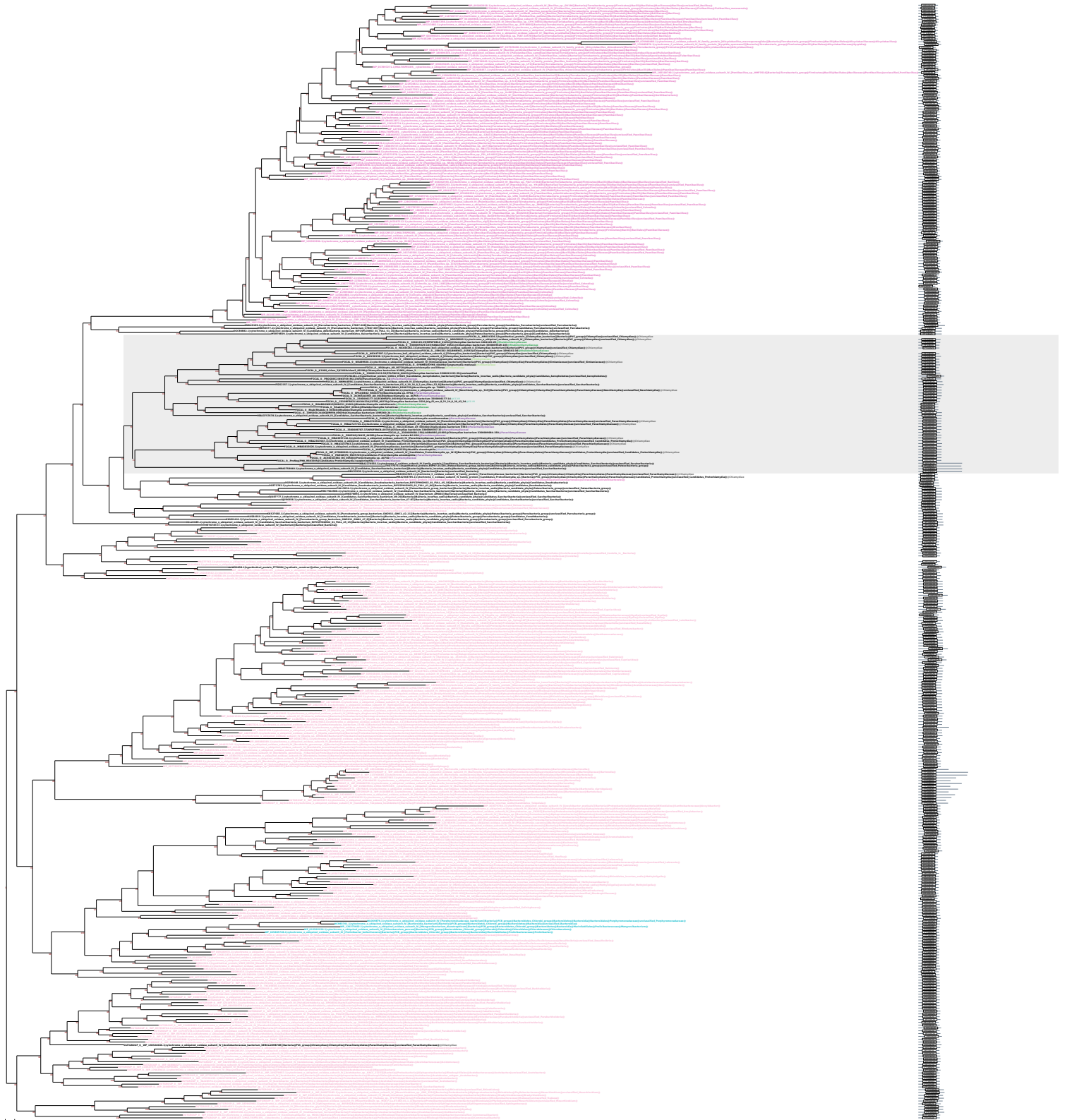
COG1845
cyoC
K02239
cytochrome o ubiquinol oxidase subunit III

PF00510: Cytochrome c oxidase subunit III
PF03626: Prokaryotic Cytochrome C oxidase subunit IV



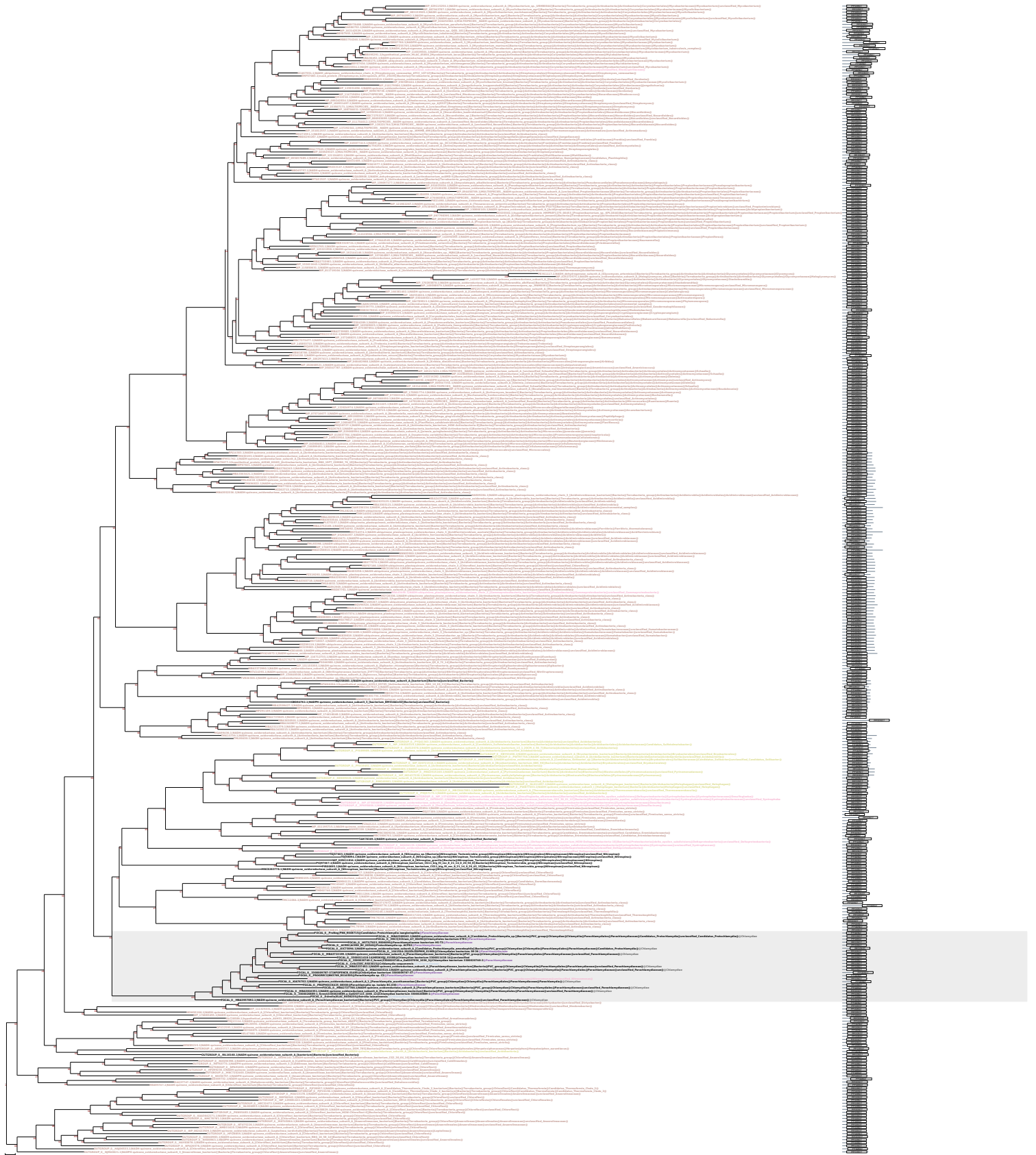
COG3125
cyd
K02390
cytochrome o ubiquinol oxidase subunit IV

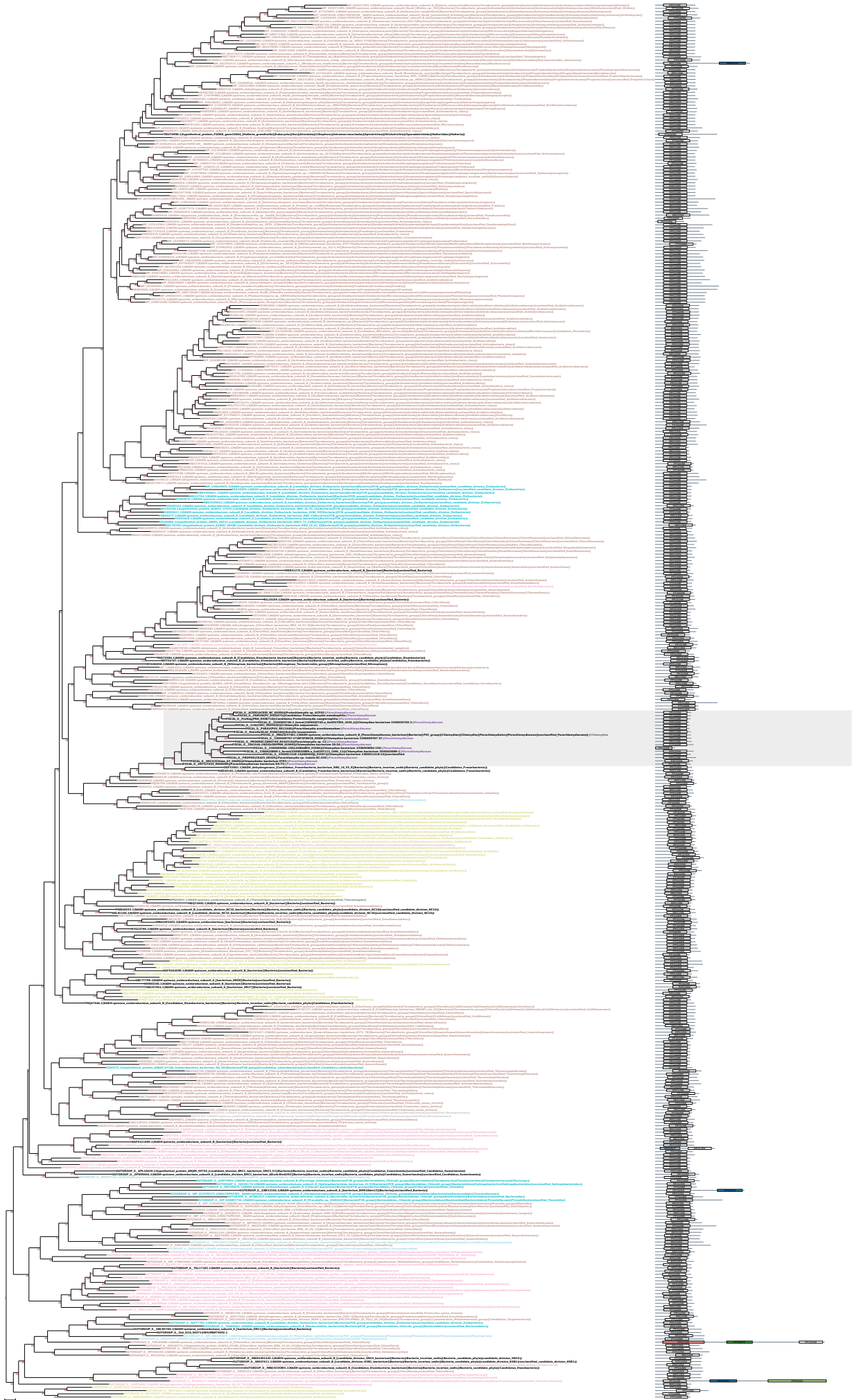
PF03626: Prokaryotic Cytochrome C oxidase subunit IV



COG0838
ruoA
K00330
NADH-quinone oxidoreductase subunit A

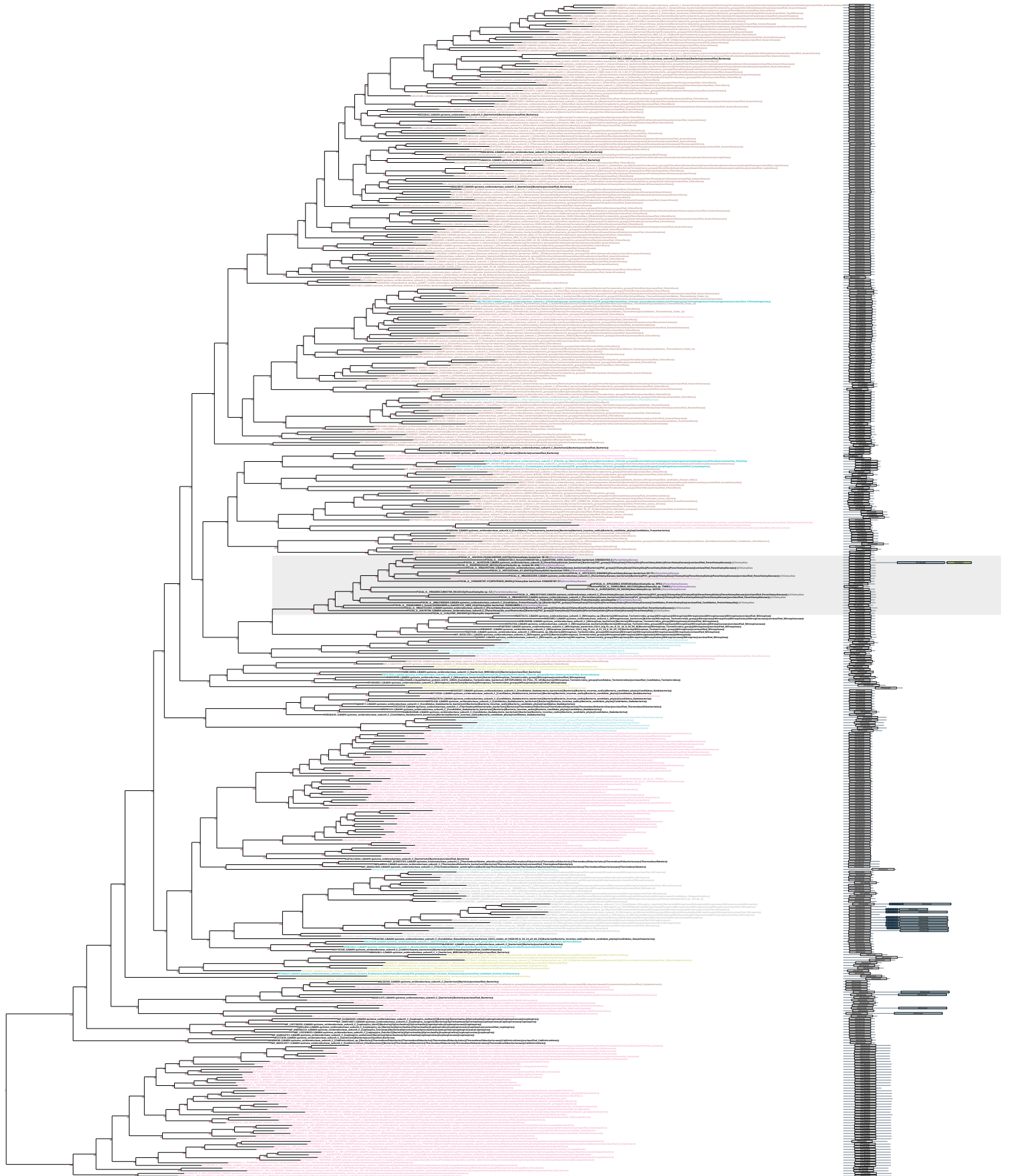
PF00507: NADH-ubiquinone/plastoquinone oxidoreductase, chain 3



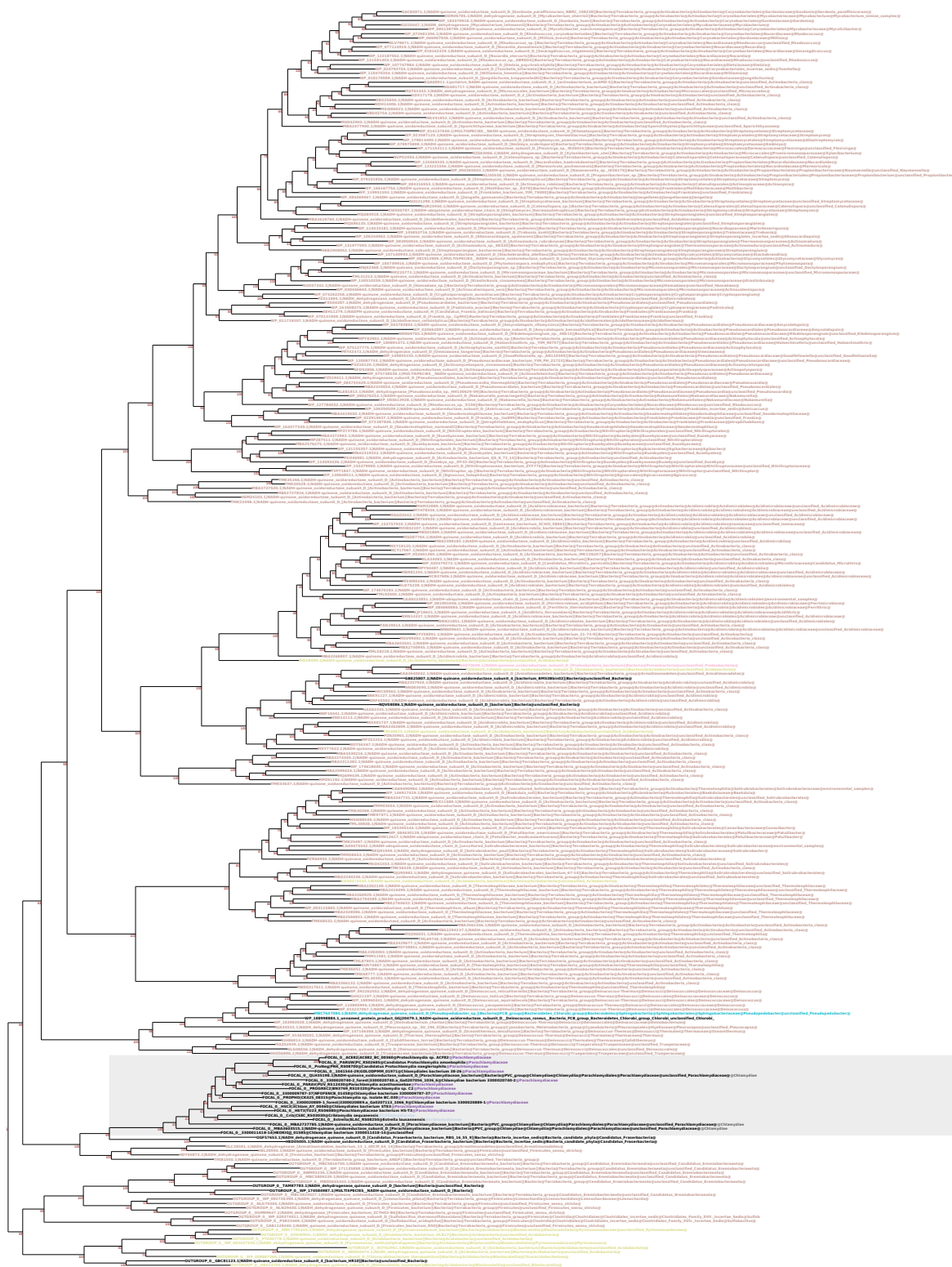


COG0852
RuqC
K00332
NADH-quinone oxidoreductase subunit C

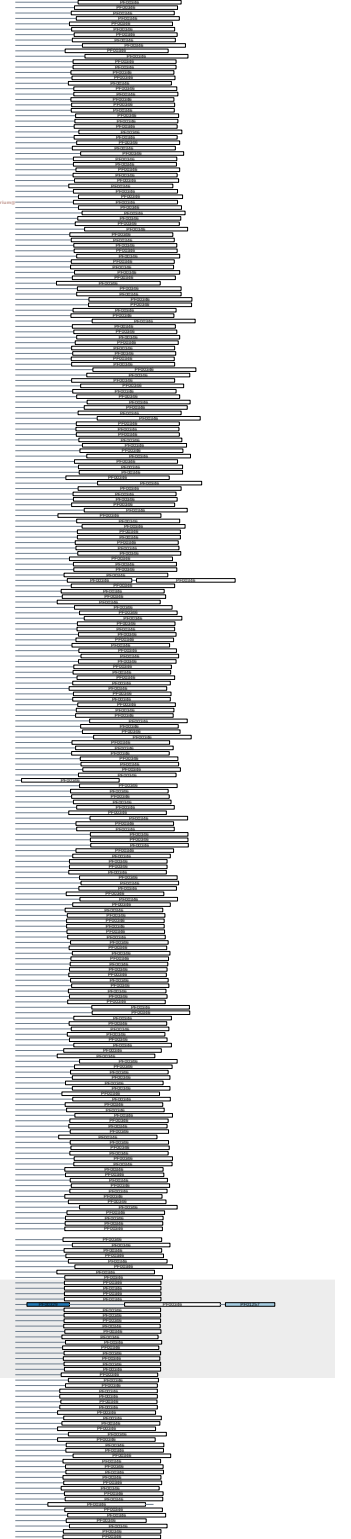
PF00229: Respiratory-chain NADH dehydrogenase, 30 kD subunit
PF00344: Respiratory-chain NADH dehydrogenase, 49 kD subunit
PF02774: NiS4-dependent hydrogenase
PF01257: Thioesterase-like [2Fe-2S] ferredoxin

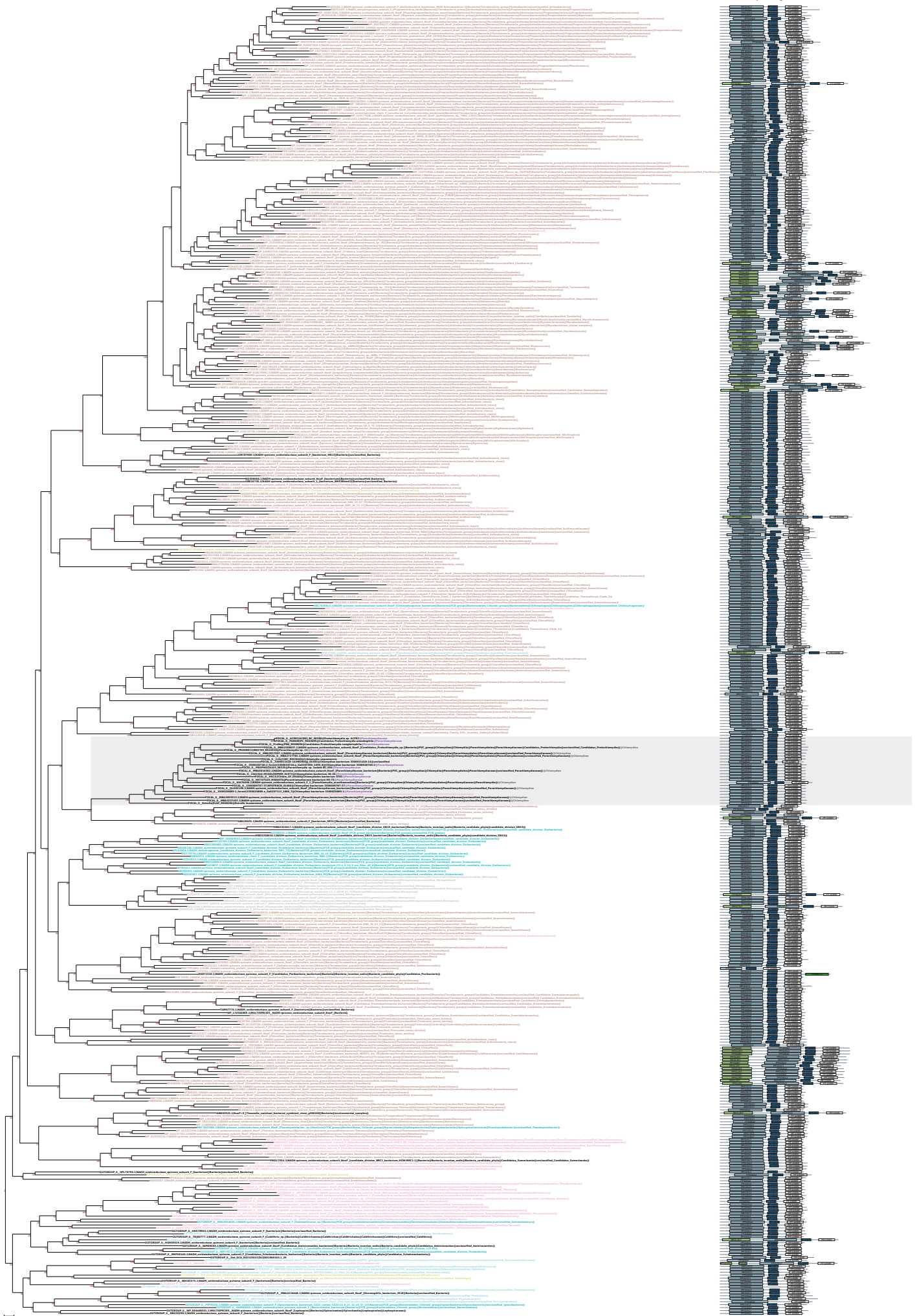


COG0649
nuoD
K00333
NADH-quinone oxidoreductase subunit D

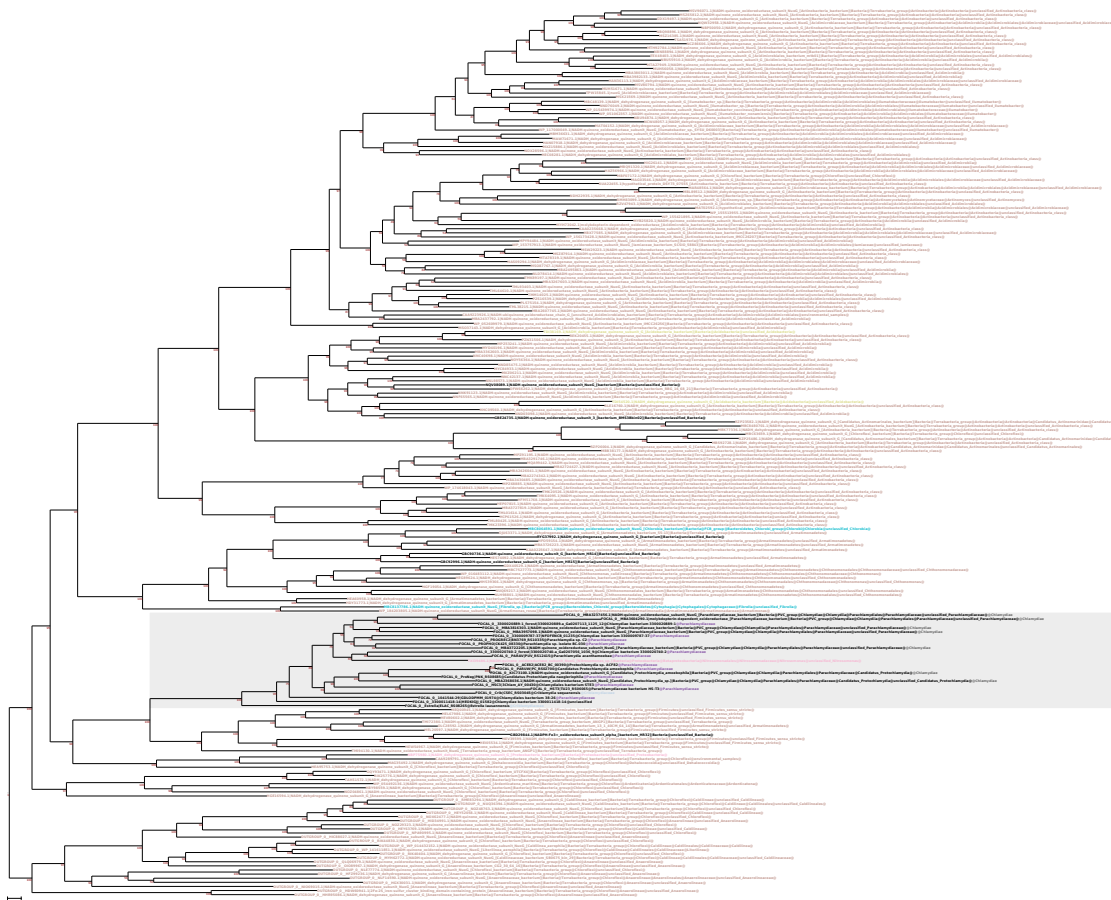


PF00346: Respiratory-chain NADH dehydrogenase, 49 Kd subunit
PF01257: Thioredoxin-like [Fe-S] ferredoxin
PF00329: Respiratory-chain NADH dehydrogenase, 30 Kd subunit

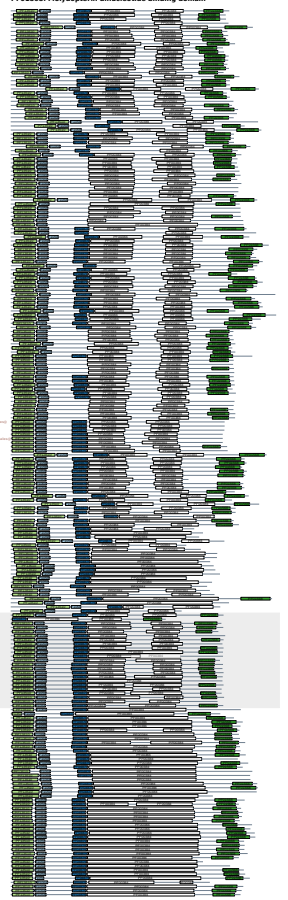




COG3383
nuoG
K00336
NADH-quinone oxidoreductase subunit G

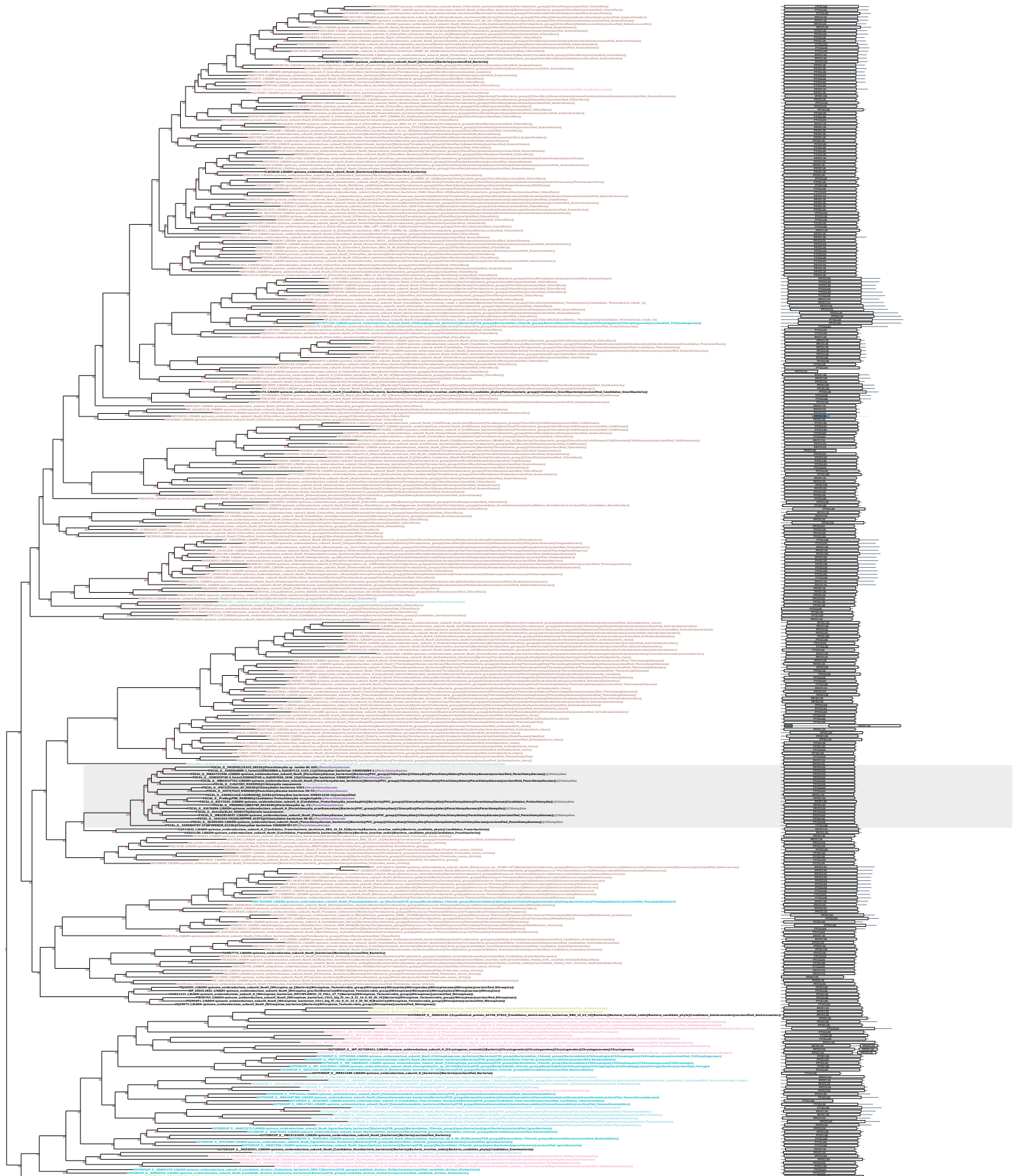


PF03284: Molybdopterin oxidoreductase
PF10588: NADH-ubiquinone oxidoreductase-G iron-sulfur binding region
PF04879: Molybdopterin oxidoreductase Fe-S4 domain
PF13510: 2Fe-2S iron-sulfur cluster binding domain
PF01560: Molybdopterin dinucleotide binding domain



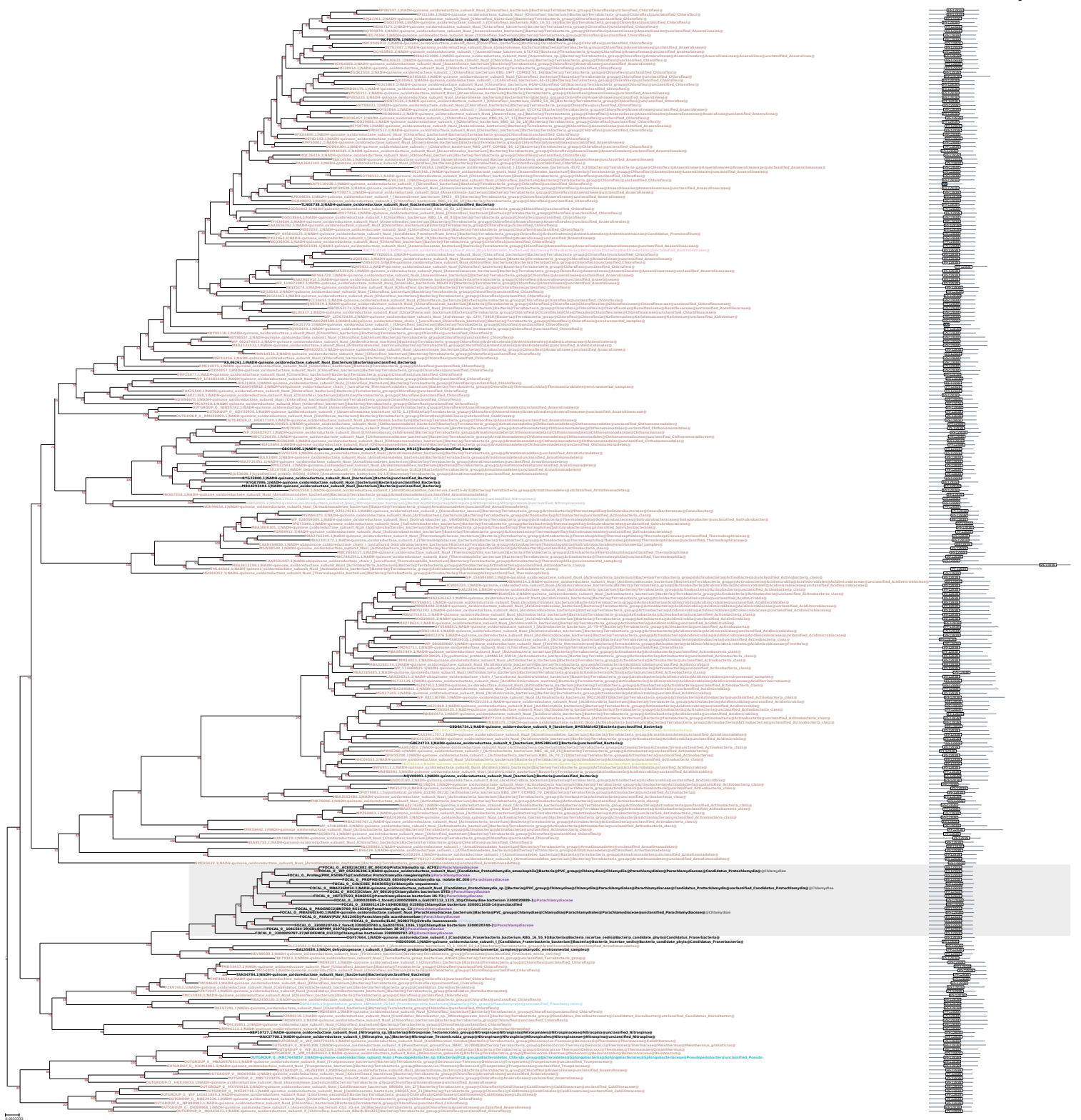
COG1005
nuoH
K00337
NADH-quinone oxidoreductase subunit H

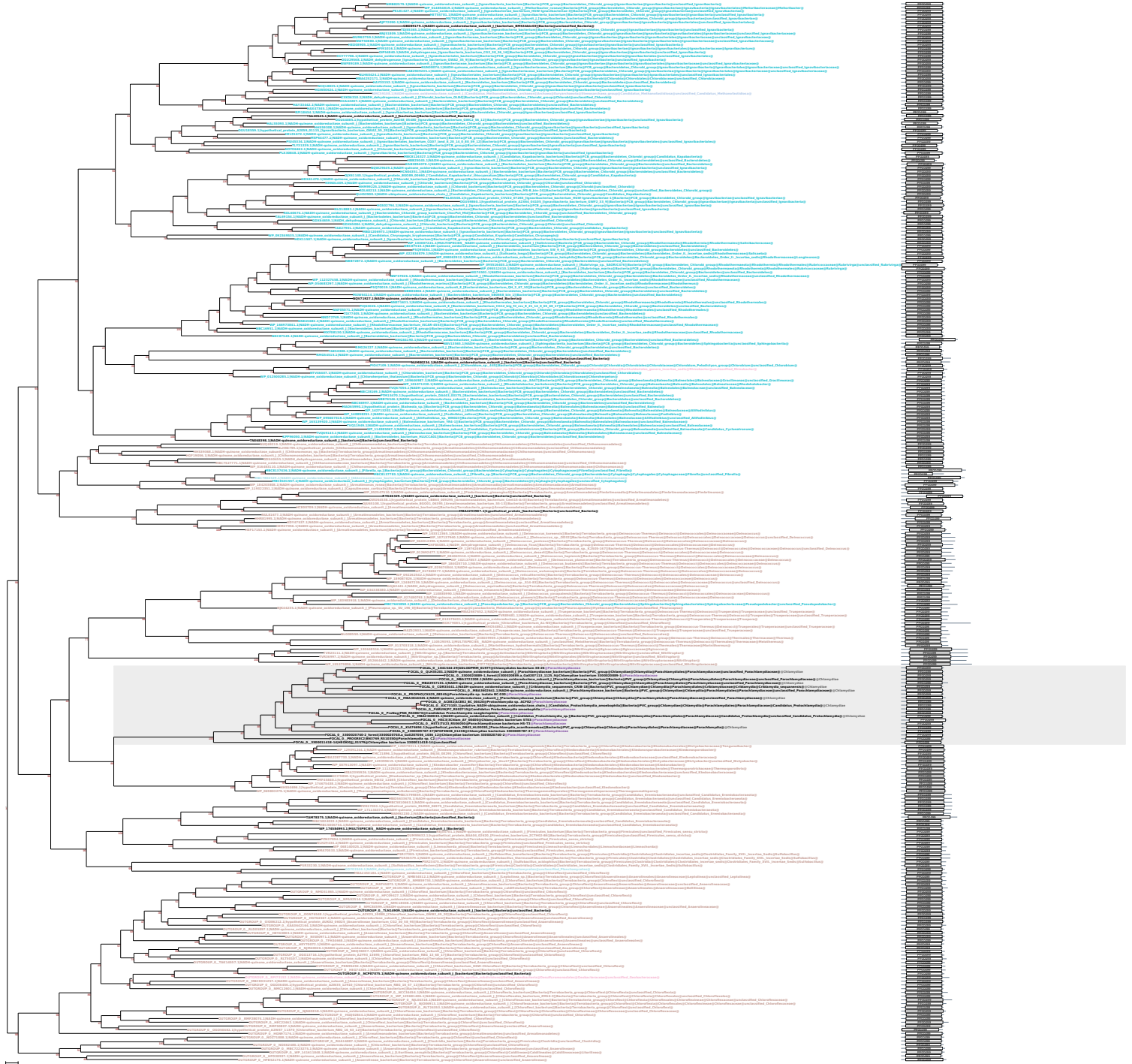
PF00146: NADH dehydrogenase
PF00384: Molybdopterin oxidoreductase
PF05745: Chlamydia 15 kDa cysteine-rich outer membrane protein (CRPA)



COG1143
nuoL
K00338
NADH-quinone oxidoreductase subunit I

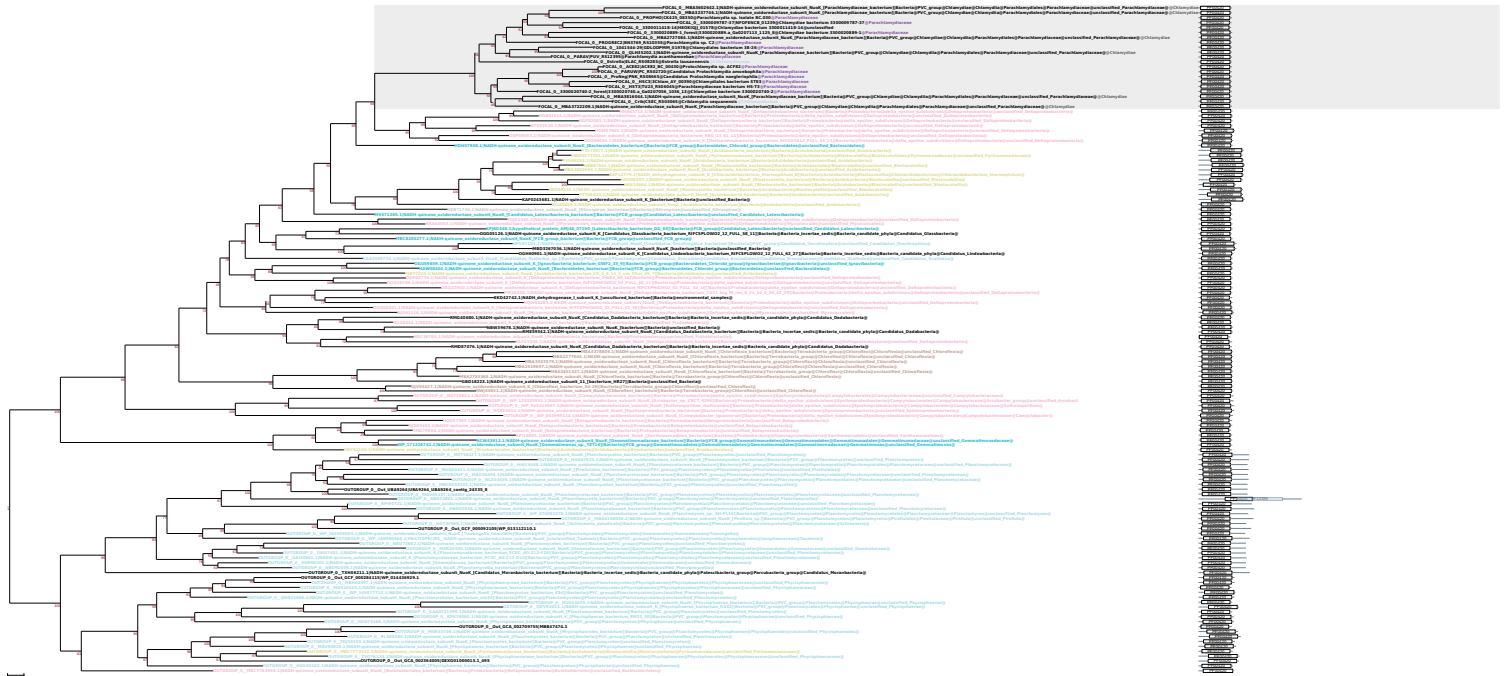
PF12838: 4Fe-4S dicluster domain
PF00037: 4Fe-4S binding domain



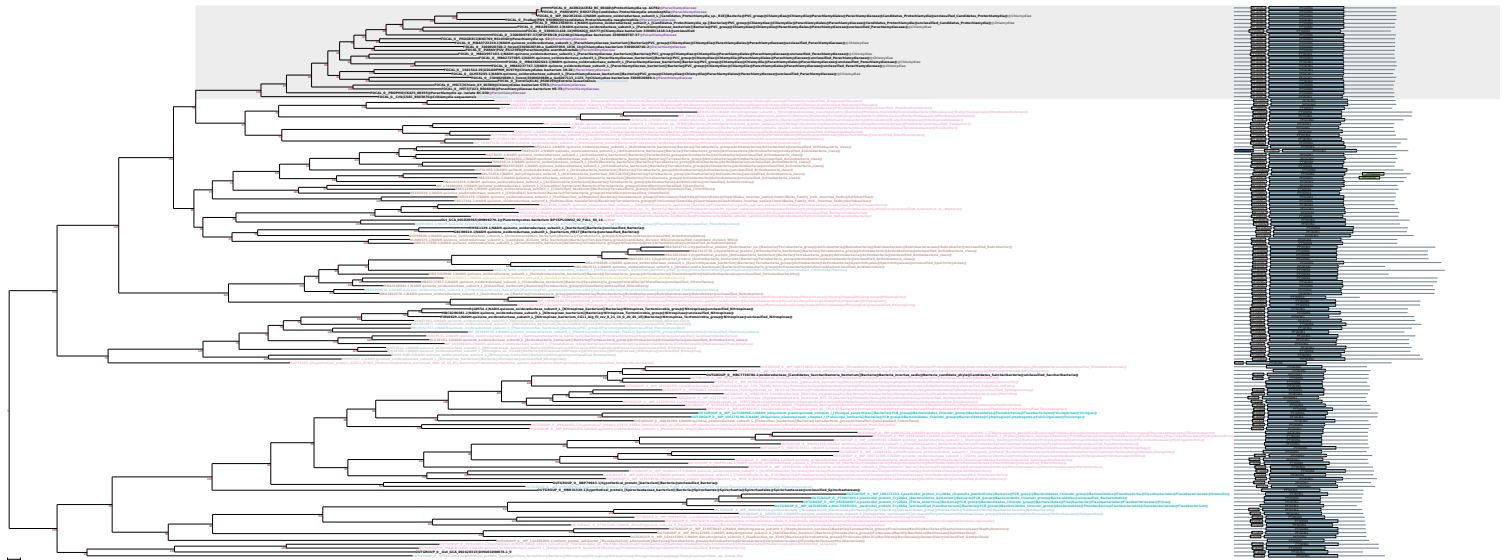


COG0713
nuoK
K00340
NADH-quinone oxidoreductase subunit K

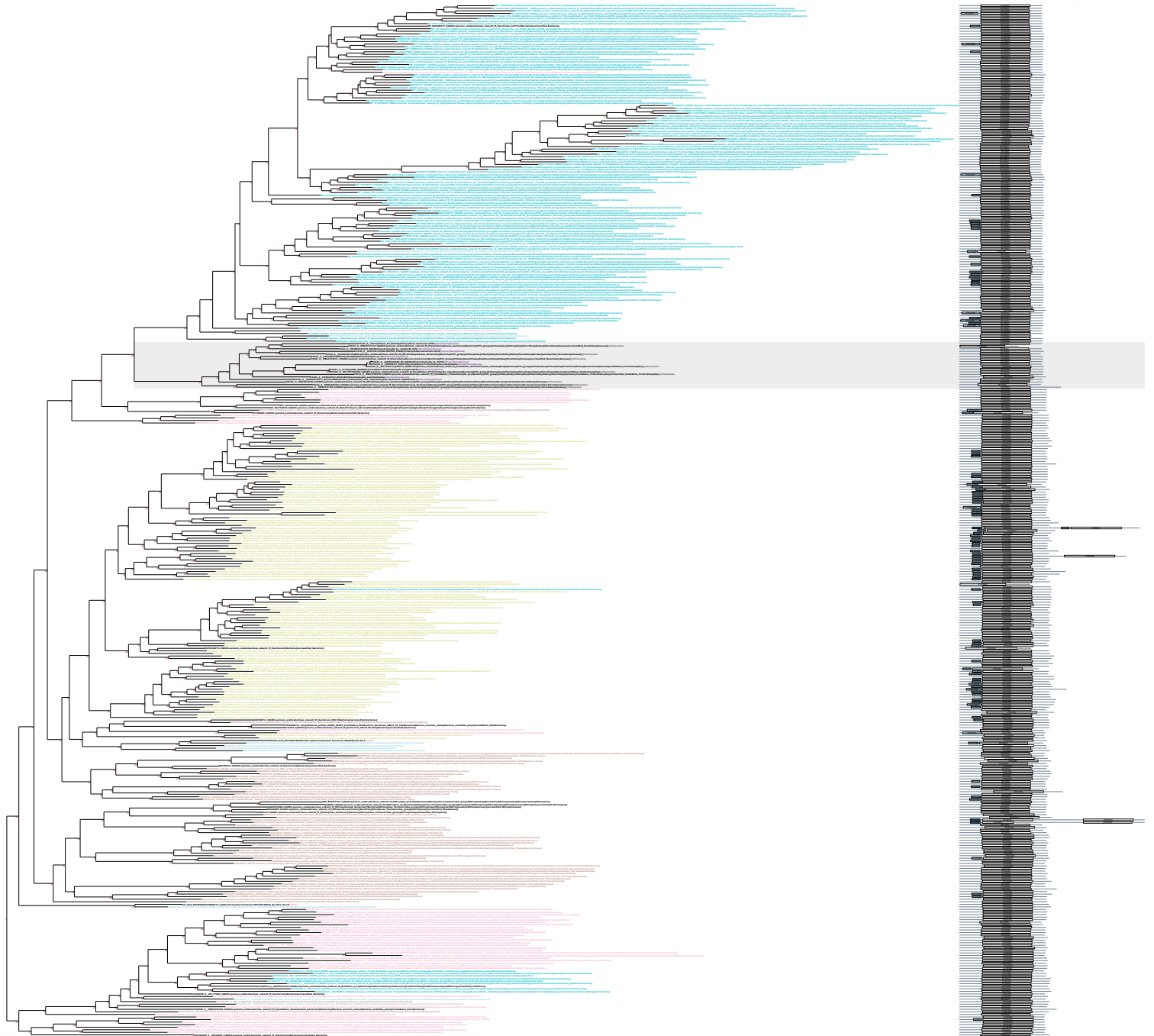
PF00420: NADH-ubiquinone/plastoquinone oxidoreductase chain 4L
PF13385: Concanavalin A-like lectin/glucanases superfamily



CG1009
nucl.
K00341
NADH-quinone oxidoreductase subunit L



COG1009
nuoM
K02342
NADH-quinone oxidoreductase subunit M



PF00261: Proton-conducting membrane transporter
PF01029: NADH-ubiquinone oxidoreductase chain 4, amino terminal
PF00262: NADH-ubiquinone oxidoreductase complex I, chain 2, N-terminal

COG1007
nuoH
K00343
NADH-quinone oxidoreductase subunit N

PF00361: Proton-conducting membrane transporter

