Supplementary Information

Host association and intracellularity evolved multiple times independently in the *Rickettsiales*

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This file contains the following:

Supplementary Note 1. Taxonomic descriptions of novel species and families discovered in this study.

Supplementary Note 2. General comparative description of metabolic and functional features.

Supplementary Note 3. Detailed description of the genome sequencing and assembly procedures (with embedded Supplementary Figures 1-17 and Supplementary Tables 1-8)

Supplementary Note 4. Detailed description of the phylogenomic analyses.

Supplementary Note 5. Detailed description of the gene content analyses.

Supplementary Figures 1-32. (Supplementary Figures 1-17 are embedded within Supplementary Note 3; Supplementary Figures 18-32 are individually and consecutively presented at the end of this file, with each respective legend preceding the corresponding Supplementary Figure)

Supplementary Note 1: taxonomic descriptions

Description of "*Candidatus* Vederia obscura" gen. nov. sp. nov.

"Candidatus Ve.de'ri.a ob.scu'ra". (Ve.de'ri.a: N.L. fem. n., light as a feather, due to the small genome size, from the Dutch veder, and resembling a character's name in George Lucas' Star Wars saga; ob.scu'ra. L. fem. adj. obscura, hidden, unseen, as the bacterium was not directly observed). This bacterium was found in association with the ciliate *Plagiopyla frontata* strain IBS-3, and belongs to the family "*Candidatus* Midichloriaceae". Uncultured so far. Basis of the assignment, genome sequence.

Description of "*Candidatus* Diomedesia obscura" gen. nov. sp. nov.

"*Candidatus* Di.o.me.de'si.a ob.scu'ra". (Di.o.me.de'si.a: N.L. fem. n., dedicated to Diomedes, in reference to mythological Thracian king Diomedes, owner of mares stolen by Heracles in one of his labours; ob.scu'ra. L. fem. adj. obscura, hidden, unseen, as the bacterium was not directly observed). The genome sequence of this bacterium was obtained from an environmental water sample collected from Black Sea, next to Varna, Bulgaria. Uncultured so far. Basis of the assignment, genome sequence (GCA_016780625.1).

Description of "*Candidatus* Diomedesiaceae" fam. nov.

"*Candidatus* Diomedesiaceae" (Di.o.me.de.si.a'ce.ae, N.L. fem. n. "*Candidatus* Diomedesia" type genus of the family; suff. -aceae ending to denote a family; N.L. fem. pl. n. "*Candidatus* Diomedesiaceae" the family of genus "*Candidatus* Diomedesia").

The family "*Candidatus* Diomedesiaceae" is defined based on phylogenetic analyses of concatenated orthologous genes of uncultured representatives from various marine environments.

The family belongs to the order *Rickettsiales*, and currently contains one genus, "*Candidatus* Diomedesia".

Description of "*Candidatus* Jistubacter obscurus" gen. nov. sp. nov.

"*Candidatus* Jis.tu.bac'ter ob.scu'rus". (Jis.tu.bac'ter: N.L. Jistu, the Native American mythological trickster rabbit, a light-hearted character prone to humorously inappropriate behaviour; N. L. masc. n. bacter, rod; N. L. masc. n. Jistubacter, Jistu rod [also intended as an ironic compliment to one of the authors]; ob.scu'rus. L. adj. obscurus, hidden, unseen, as the bacterium was not directly observed). The genome sequence of this bacterium was obtained from environmental freshwater sample collected from the Chattahoochee river, USA. Uncultured so far. Basis of the assignment, genome sequence (GCA_010031735.1).

Description of "Candidatus Jistubacteraceae" fam. nov.

"*Candidatus* Jistubacteraceae" (Jis.tu.bac.te.ra'ce.ae, N.L. fem. n. "*Candidatus* Jistubacter" type genus of the family; suff. -aceae ending to denote a family; N.L. fem. pl. n. "*Candidatus* Jistubacteraceae" the family of genus "*Candidatus* Jistubacter").

The family "*Candidatus* Jistubacteraceae" is defined based on phylogenetic analyses of concatenated orthologous genes of uncultured representatives from various freshwater and terrestrial environments. The family belongs to the order *Rickettsiales*, and currently contains one genus, "*Candidatus* Jistubacter".

Description of "*Candidatus* Arkhamia obscura" gen. nov. sp. nov.

"*Candidatus* Ar.kha'mi.a ob.scu'ra". (Ar.kha'mi.a: N.L. fem. n., dedicated to Arkham, fictional town in Massachussets created by Howard Phillips Lovecraft; ob.scu'ra. L. fem. adj. obscura, hidden, unseen, as the bacterium was not directly observed). The genome sequence of this

bacterium was found in an environmental soil sample from Massachussets, USA. Basis of the assignment, genome sequence (GCA_013288575.1).

Description of "Candidatus Arkhamiaceae" fam. nov.

"*Candidatus* Arkhamiaceae" (Ar.kha.mi.a'ce.ae, N.L. fem. n. "*Candidatus* Arkhamia" type genus of the family; suff. -aceae ending to denote a family; N.L. fem. pl. n. "*Candidatus* Arkhamiaceae" the family of genus "*Candidatus* Arkhamia").

The family "*Candidatus* Arkhamiaceae" is defined based on phylogenetic analyses of concatenated orthologous genes of uncultured representatives from freshwater and terrestrial environments. The family belongs to the order *Rickettsiales*, and currently contains one genus, "*Candidatus* Arkhamia".

Supplementary Note 2: detailed comparative description of additional metabolic and functional features of *Rickettsiales*

A number of relevant traits/functions for the interaction with eukaryotic cells were selected for detailed analyses, described in the main text, in particular biosynthesis and uptake of metabolic precursors (i.e. amino acids and nucleotides), secretion/adhesion/motility apparatuses and putative effector molecules. A general overview of gene content variation and evolution in *Rickettsiales*, with a special focus on general "family-level" trends, as well as on the single newly characterised genomes, is presented below.

Housekeeping functions and DNA repair

Central housekeeping functions (DNA replication. cell division, general transcription, translation, chaperones) are conserved in all families and their representatives. The main DNA repair systems, namely mismatch repair (rare in *Gamibacteraceae* and *Deianiraeaceae*), nucleotide-excision repair, single- and double-strand break homologous repair/recombination, are present and overall common in all families. The most notable peculiarities in the novel genomes include the lack of nucleotide-excision and single-strand break repair systems in *Lyticum* and *Vederia*, and the split into two ORFs of *mutS* in *Bandiella*, possibly non-functional. Moreover, as previously observed in other unrelated *Rickettsiales* symbionts of ciliates [1-3], only the 5'-3' exonuclease domain of DNA polymerase I is present in *Fokinia cryptica* and *Lyticum*.

Carbohydrate and energy metabolism

The repertoire for carbohydrate and energy metabolism is overall rich in *Rickettsiales*, but quite variable between and within families (especially in crown families). The "canonical" repertoire composed by central reversible core of gluconeogenesis and glycolysis (linking fructose 1-6-bisphosphate and phosphoenolpyruvate) plus some gluconeogenesis-specific enzymes (malate dehydrogenase, fructose 1-6 bisphosphatase, phosphoenolpyruvate synthase), alongside with non-oxidative pentose-phosphate pathway, pyruvate dehydrogenase, Krebs cycle, electron transport chain (including NADH-quinone oxidoreductase, qor type NADPH-quinone oxidoreductase, alternatively followed by ubiquinol-cytochrome c oxidoreductase+cytochrome c oxidase, and/or by the bd-cytochrome ubiquinol terminal oxidase), and ATP synthase are present in all families.

The lineage-specific and possible convergent streamlining of the glycolysis/gluconeogenesis is quite frequent, up to retaining only the initial steps (leading to phosphoenolpyruvate), as in many "classical" *Rickettsiaceae* (namely the monophyletic lineage comprising all characterised organisms, thereby with the exclusion of "basal *Rickettsiaceae*", as previously defined [3]), including the novel genomes obtained in this study, but also occurring in other families, e.g. among *Midichloriaceae, Vederia* has the same subpathway, plus triose-phosphate isomerase. Pentose-phosphate pathway is missing in *Cyrtobacter*, and composed only by ribose-5-phosphate isomerase in *F. cryptica* and *Lyticum*. Moreover, genes belonging to the oxidative branch were found in basal *Rickettsiales*, in particular in *Mitibacteracae*.

Noteworthy is the case of cytochrome c oxidase, of which two distinct alternative forms are available, Cco or cbb3, the latter considered advantageous in anaerobic conditions [4]. Basal *Rickettsiales* present both forms, while in each crown family in general just one alternative is present, namely Cco in *Rickettsiaceae*, *Anaplasmataceae*, *Diomedesiaceae*, and cbb3 in *Midichloriaceae*, *Gamibacteraceae*, and neither in most *Deianiraceaeae* (lacking also ubiquinol-cytochrome c oxidoreductase, thus likely exploiting only their bd alternative oxidase). Such a pattern is clearly not consistent with phylogenetic relationships.

Multiple, probably independent, instances of combined reduction of Krebs cycle and electron transport chain were found. Besides some previously known cases [1, 3, 5], among the newly sequenced *Midichloriaceae*, *Bandiella* lacks the bd oxidase, conversely *Cyrtobacter* lacks c reductase and oxidase, while both *F. cryptica* and *Lyticum* miss the (almost) entire Krebs cycle and possess only NADH-quinone and bd terminal oxidases. The latter two organisms probably exploit NADH from other sources for ATP synthesis [1], or only in case of *Lyticum*, the succinyl-CoA synthase. *Vederia* and the *Midichloriaceae* symbiont of *Reticulomyxa* are fully devoid of Krebs and electron transport, and possibly take ATP directly from their hosts or exploit alternative paths, such as a peculiar protein homologous to the glycolytic enzyme pyruvate kinase in *Vederia*.

As previously observed [6], glyoxylate cycle is present in basal *Rickettsiales*, in particular *Mitibacteraceae*. Additionally, the phosphoenolpyruvate carboxylase, which forms oxaloacetate, thus potentially fuelling both Krebs and glyoxylate cycle, was found in basal *Rickettsiales* and in few crown *Rickettsiales* that are early diverging in the respective families, e.g. *Jidaibacter* and the *Rickettsiaceae* endosymbiont of *Amblyomma* Ac37b, while the nitrate reductase, which may enable the use of this compound as terminal electron acceptor [7], was found in *Mitibacteraceae*, *Jistubacteraceae*, and *Gamibacteraceae*.

The main biosynthetic pathways overall mostly follow comparable presence/absence patterns among *Rickettsiales*. They are present in all families, and experienced multiple, probably independent, reductions or even full losses in single organisms/lineages in crown *Rickettsiales* families, as a possible consequence of the ability to obtain intermediates or final products directly from their hosts.

Lipids and membranes

The biosynthesis of lipids and phospholipids is well conserved among *Rickettsiales*, with exceptions including the pathway holes (lack of plsX and plsY) in *Rickettsia* [8] and many classical *Rickettsiaceae* (including the newly sequenced genomes), but not in basal *Rickettsiaceae*. Concerning isoprenoid precursor biosynthesis, a previously proposed evolutionary scenario appears confirmed [3], proposing an ancestral and widespread methylerythritol pathway, and a replacement by a horizontally-acquired mevalonate pathway in few representatives of *Deianiraeaceae* and classical *Rickettsiaceae*, which include *Trichorickettsia* and the two symbionts of Apicomplexa [9, 10], possibly indicating some link with Alveolata hosts.

Peptidoglycan biosynthesis likely experienced an independent reduction in different *Rickettsiales* sublineages for transpeptidase and transglycosylase activities, in particular *mrcB* gene is absent in *Deianiraeaceae*, *Anaplasmatacae* and many *Rickettsiaceae* (except basal members). Different further steps of streamlining can be observed in lineages such as *Orientia* [11] and multiple *Anaplasmataceae*, up to the condition of *Ehrlichia*, lacking multiple genes related to such activities (e.g. *fstI*, *mrdA*, *mrcA*). Lipopolysaccharide (LPS) biosynthesis is globally absent in *Anaplasmataceae*, and in some members of other crown families, such as *Orientia* and *Fokinia solitaria* [1, 11], as well as *F. cryptica* and *Cyrtobacter*, while *Lyticum* is equipped with most LPS biosynthetic steps, with the exclusion of those producing deoxy-manno-octulosonate.

An interesting pattern is found for the synthesis of N-acetylglucosamine, precursor of both peptidoglycan and LPS in the classical *Rickettsiaceae.* The full pathway from fructose was present in the ancestor, with the last two steps catalysed by distinct polypeptides, due to a split of *glmU* gene, a situation conserved in *Megaira polyxenophila* and *Tisiphia*. Then, most of the pathway was lost independently in *Rickettsia* [8] and *Megaira venefica*, both retaining only the N-terminus of *glmU*, catalysing the very last step.

The synthesis of polyhydroxyalkanoate (PHA) granules as storage compounds, present in all four basal families, is quite common in *Rickettsiaceae*, and found also in several *Midichloriaceae* (including all the novel genomes except *Bandiella*) and in few *Anaplasmataceae* from aquatic environments such as *Xenolissoclinum*.

Cofactors/vitamins

Biosynthetic pathways for cofactors/vitamins are quite common in *Rickettsiales*, differently from those for aminoacids and nucleotides (see below), though some lineages present reduction or complete absence of the pathways for one or more cofactors, with some degree of consistence with the lack of enzymes requiring them. Very common in all families are the synthesis of lipoate, ubiquinone (notable the exception of *Vederia*), and NADP from NAD (with *Lyticum* among few exceptions). Other quite frequent pathways are those for folate and heme (the latter absent in *Cyrtobacter*, *F. cryptica*, *Vederia* and endosymbiont of *Reticulomyxa*, consistently with the lack of cytochrome c reductase and oxidase).

The case of biotin is noteworthy, also considering a beneficial role hypothesised for this vitamin in some invertebrate hosts of *Rickettsiales*, and the multiple previous reports of putative horizontal-gene-transfer events involving genes of this biosynthetic pathway [12-14]. The presence/absence of this pathway in *Rickettsiales* somehow inversely correlates with the one of the bioY biotin transporter, conversely present in representatives of genus *Wolbachia*, the *Midichloriaceae* endosymbiont of *Reticulomyxa*, as well as a group of closely related *Rickettsiaceae* (*Rickettsia*, *Tisiphia*, *Trichorickettsia*, *Megaira*, and symbiont of *Cardiosporidium cionae*). Some exceptions exist, e.g. *Trichorickettsia* and *Rickettsia* endosymbiont of *Ixodes scapularis* have both, while many other classical *Rickettsiaceae* have neither (e.g. *Orientia*, *Sarmatiella*, the latter possibly

representing a recent loss of the biosynthesis [3]). Similarly, a single and short gene (*bioA*) is a possible sign of recent loss of the pathway also in *Bandiella*.

NAD synthesis is quite rare in *Rickettsiaceae* (exceptions include *Sarmatiella* and *Megaira venefica*), while in *Midichloriacae*, if present, it is represented only by the final two steps (among the novel genomes only in the *Reticulomyxa* endosymbiont). Similarly, FAD synthesis is quite rare among *Rickettsiaceae*, being found only in the basal representatives (such as endosymbionts of *Stachyamoeba* and of *Amblyomma* Ac37b), while in the novel *Midichloriaceae* genomes, except for *F. cryptica*, at least the last step is present. For what concerns pantothenate and CoA, the pathway is overall present in all families at variable levels of completeness, starting from the minimal final steps (coaDE), found in most representatives (among the novel genomes, the exception is *Lyticum*, while the richest is *F. cryptica*, from the bifunctional dfp on), up to including also the initial steps from 3-methyl-2-oxobutanoate, common only in the basal families and in *Gamibacteraceae*. Pyridoxal phosphate synthesis is quite rare in crown families, with earlier steps of the pathway being more common in *Rickettsiaceae* and *Midichloriaceae*, while differences can be seen through the order for the final steps, with most *Rickettsiales* (including *Anaplasmataceae*) displaying pdxJ and pdxH, while *Midichloriaceae* display mostly the alternative pdxT and pdxS, as well as the salvage pathway. The latter pathway is the only one present in *F. cryptica*, while *Vederia* is fully devoid of pathways for pyridoxal production/recycling. The presence of biosynthetic pathways for thiamine follows a comparable pattern, with initial steps (thiH) only present in *Mitibacteraceae*, successive steps found also in the other basal families, *Anaplasmataceae* and DDG clade (*Gamibacteraceae* and *Diomedesiaceae* in particular), and the final steps (thiD, thiE and thiL) rather common in all families, though rare in classical *Rickettsiaceae*. This pathway is uncommon in the novel genomes, and only its final step is present solely in *Vederia* and *Bandiella*. Additional cofactor biosynthetic pathways, such as molybdopterin and cobalamin are quite rare in *Rickettsiales*

and found mostly/exclusively in basal families, namely both cofactors in *Mitibacteraceae*, and the former also in *Gamibacteraceae*.

Additional functions

Multiple *Rickettsiales* bear signs of the presence of different kinds of mobile elements, including plasmids (among which identified plasmidic contigs in published [5, 15] and in novel genomes, or plasmidic-like genes such as parA and toxin-antitoxins in other assemblies including e.g. *Vederia*, *Cyrtobacter* and *M. venefica*), phages (e.g. *Cyrtobacter*, the two *Megaira*, *Vederia*, and *Trichorickettsia*, the latter consistent with previous observations [16]), transposons (e.g. *Cyrtobacter*, the two *Megaira*, *Bandiella*), and retrotransposons (e.g *Bandiella* and *M. polyxenophila*).

Another noteworthy feature is the presence of cytoskeletal bactofilin proteins, such as the one previously described in *Deianiraea* [2], in members of the three DDG-clade families, as well as in the basal *Rickettsiales*.

Interestingly, some detoxification and inorganic nutrient uptake proteins, previously found only in basal *Rickettsiales* [6], were also found in some crown lineages. Namely, KatG catalase/peroxidase and arsenic resistance mechanisms (efflux pump and/or reductase) were found in several *Gamibacteraceae* and even in *Diomedesiacae*, whereas ammonium transporters were found in *Diomedesiaceae*, *Gamibacteracaeae*, and a basal *Rickettsiaceae* MAG.

Supplementary Note 3: genome assembly procedures

In this work, the novel genome sequences of 9 *Rickettsiales* bacteria were assembled. This was obtained starting from 7 ciliate strains/populations (with *Euplotes woodruffi* NDG2 harbouring 2 different *Rickettsiales* bacteria) and from one sample derived from a previous study [17] on the foraminiferan *Reticulomyxa filosa*.

Sample origin and maintenance

Among, the seven ciliate strains/populations employed in this study, five were obtained and described in previous studies [16, 18-23]. The origin and laboratory maintenance of the other two strains is reported below.

The population of *Plagiopyla frontata* IBS-3 was obtained from a brackish water sample collected in May 2018 from the Baltic Sea in Inkoo (Finland), following a previously described protocol for the laboratory propagation of anaerobic ciliates [24].

The monoclonal strain *Euplotes woodruffi* NDG2 was isolated from a water sample collected on 15th March 2013 at Naval Dockyard Gate in Visakhapatnam (Andhra Pradesh, India). It was maintained in the laboratory by regular feeding (every 1-2 weeks) with *Dunaliella tertiolecta*, grown in artificial water at 5‰ salinity as previously described (e.g. [23]).

Sample preparation and Illumina sequencing

Four ciliates (*Paramecium biaurelia* US_Bl 11III1, *Paramecium nephridiatum* Sr 2-6, *Euplotes woodruffi* NDG2, *Plagiopyla frontata* IBS-3) were subjected to whole-genome amplification (WGA) with the REPLI-g Single Cell Kit (Qiagen), starting from a limited number of cells (see Supplementary Data 1), and following the protocol for live cells (as in [3]). This procedure allows to obtain a sufficient amount of DNA for Illumina sequencing even for samples (*Plagiopyla*

frontata IBS-3) that are not easily propagated in the laboratory, as well as to minimise the presence of food bacteria contamination thanks to the manual washing procedure, which in any case would not be amenable for larger amounts of host cells. For the sample *Euplotes harpa* BOD18,which was not available as live material, WGA was performed from a DNA extract obtained in a previous study [23], following the dedicated protocol of the Repli-G kit.

For the sample *Paramecium biaurelia* USBL-36I1, 1.2 liters of laboratory culture (ca. 1,500-2,000 *Paramecium* cells/ml) were processed and DNA was extracted for sequencing using a modified CTAB protocol, as previously described [1].

For sample *Paramecium multimicronucleatum* Kr154-4, 400 ml of laboratory culture (ca. 600 *Paramecium* cells/ml) were process and DNA extraction was performed following a phenol-chloroform protocol [25].

Each of the seven DNA samples from ciliates was processed through a Nextera XT library, and sequenced by Admera Health (South Plainfield, NJ, USA) on a Illumina HiSeq X machine producing 2x150 bp paired-end reads (Supplementary Data 1).

The reads from the *Reticulomyxa filosa* sample [17], were kindly provided by Gernot Gloeckner and Marco Groth (University of Koeln, Germany).

Sample preparation and Oxford Nanopore sequencing

In order to perform Nanopore sequencing, a large enough amount of DNA extract was obtained from *Euplotes woodruffii* NDG2 as follows. A total of 3 liters of NDG2 culture were obtained (~ 300,000 *Euplotes* cells). The culture was passed through a sieve with 20 µm-sized pores, so that cells were retained by the filter, resulting concentrated in the final 12 ml of unfiltered liquid, which was then centrifuged at 5000 g for 5 min. The pellet was resuspended in 2 ml of distilled water, and centrifuged again. The final pellet was fixed in ethanol and stored until DNA extraction, performed

with the NucleoSpin™ Tissue Kit (Macherey-Nagel™). The DNA extract was processed through a SQK-LSK109 ligation-sequencing library, following the manufacturer's instructions. Afterwards, library was loaded onto a FLO-MIN106 flowcell and sequenced on a Minion device using the MinKNOW software 18.12.9, for 72 total hours.

Basecalling was then performed with the guppy 5.0.11 software by Oxford Nanopore. Then, reads were processed with Porechop 0.2.4 [26] with default options. Quality of the reads was assessed with NanoPlot 1.23.0 [27]. The following steps are described in the detailed report on the selective assembly of the sample NDG2 below.

Selective assembly of the *Rickettsiales* bacterial genomes from shotgun sequencing of their host samples

In this section a general account of the procedures is presented. Subsequently, a detailed report for each sample is available.

For each sample, after a quality assessment with FastQC [28], the reads were assembled using SPAdes 3.6 [29] with default settings (except for the *Reticulomyxa filosa* sample, which was assembled with Unicycler 0.4.8 [30]), obtaining a "preliminary assembly".

Then, a multi-step procedure was applied, in order to select only those contigs belonging to the symbiont of interest and discard those belonging to the host and to additional organisms present in the sample (e.g. residual food, additional associated bacteria), as described previously (e.g. [2]).

For this purpose, the blobology pipeline was applied [31]. Briefly, the contigs of the "preliminary assembly" were classified according to their length, GC% content, sequencing coverage based on reads mapped with Bowtie2 [32], and NCBI taxonomy of the best megablast hit on NCBI nucleotide. Results were visualised by the R package ggplot2 [33]. Accordingly, a set of contigs was selected, considering also ribosomal RNA genes identified with barrnap [34], using default options for *Bacteria*. Thus, reads mapping on the selected contigs were reassembled separately with

SPAdes. Results were manually revised prior and after reassembly, by examining blastp results on NCBI nr protein database after annotation with Prokka [35], as well as taking advantage of Bandage [36] for visualisation of assembly graphs to identify connections between contigs. The "contigs.fasta", "contigs.fastg", "scaffolds.fasta", and "scaffolds.fastg" SPAdes output files were considered, and, unless specified, reported results refer to the "contigs" files. Only for the sample *E. woodruffi* NDG2, for which Nanopore reads were produced, re-assembly was directly performed as hybrid (Illumina+Nanopore) with Unicycler 0.4.8-beta (see details below).

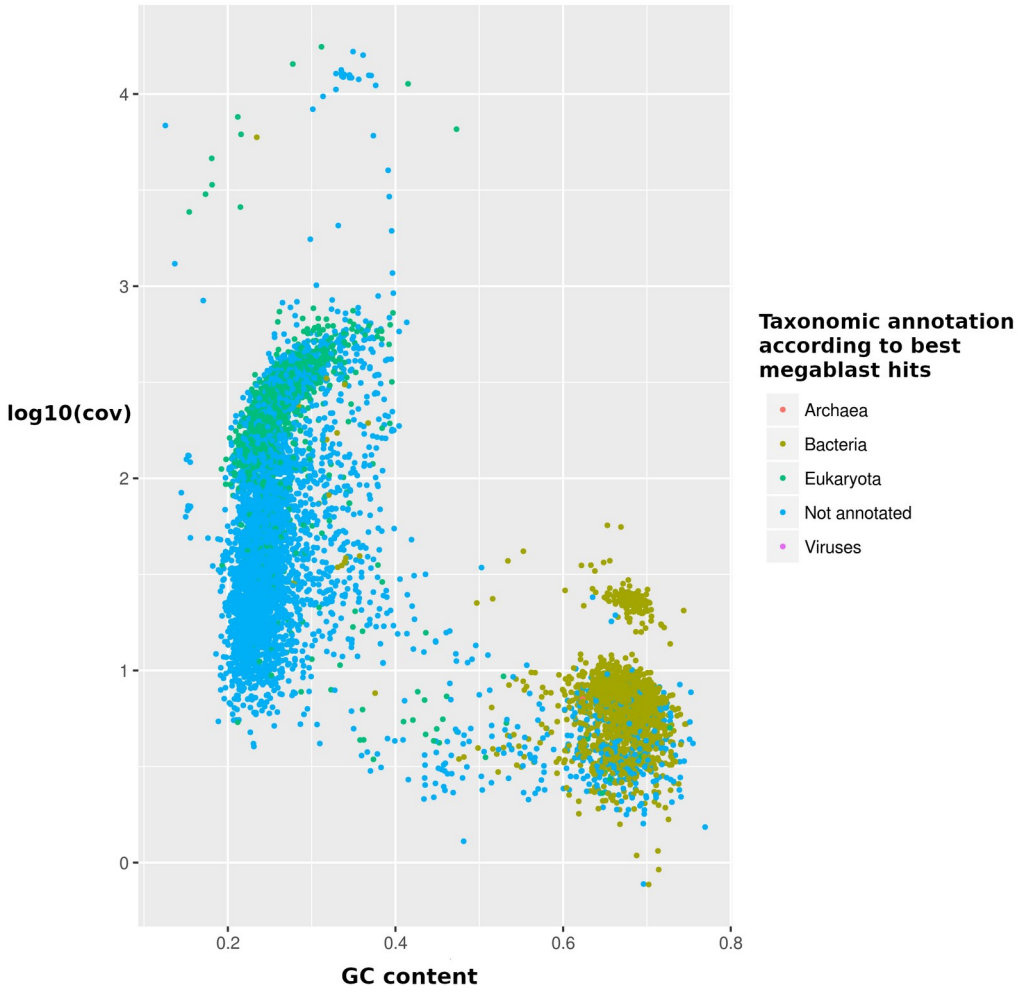
Moreover, an additional round of screening was performed in order to account for potential sequences belonging to *Rickettsiales* symbiont(s) in contigs falling outside the selected sets of contigs, especially considering possible "hybrid" contigs between host and symbiont, which may otherwise have been discarded in case of best hit on host sequences. In detail, all the respectively annotated ORFs [37] where queried on NCBI nr protein database with DIAMOND [38], applying an e-value threshold of 1e-5. Contigs with at least one ORF with a best hit on *Bacteria* were inspected manually (by their blast and DIAMOND hits), and, in case, further contigs selections and/or refinements of the previous ones were made, followed by re-assemblies and manual revision, as described above.

Genome closing by PCR and Sanger sequencing

After selecting the *Rickettsiales* genome sequences from SPAdes assemblies, two samples (*P. multimicronucleatum* 12 and *P. biaurelia* US_Bl 11III1) were selected, based on assembly quality, for molecular biology based finishing. PCR primers were designed next to the ends of larger contigs, and PCR reactions were performed in order to test their connections and join them into larger contigs/scaffolds. PCRs were performed with TaKaRa Ex Taq and reagents (Takara Bio, Japan), following manufacturer's instructions (each primer with final concentration 0.5 μM). Successful PCR results were confirmed by bidirectional Sanger sequencing (after purification with

the EuroGOLD Cycle-Pure kit - EuroClone, Italy) performed by GATC Biotech (Germany) with amplification primers and/or internal primers (see sections below for details on each sample) .

***Paramecium multimicronucleatum* Kr154-4 hosting "*Ca.* Trichorickettsia mobilis"**



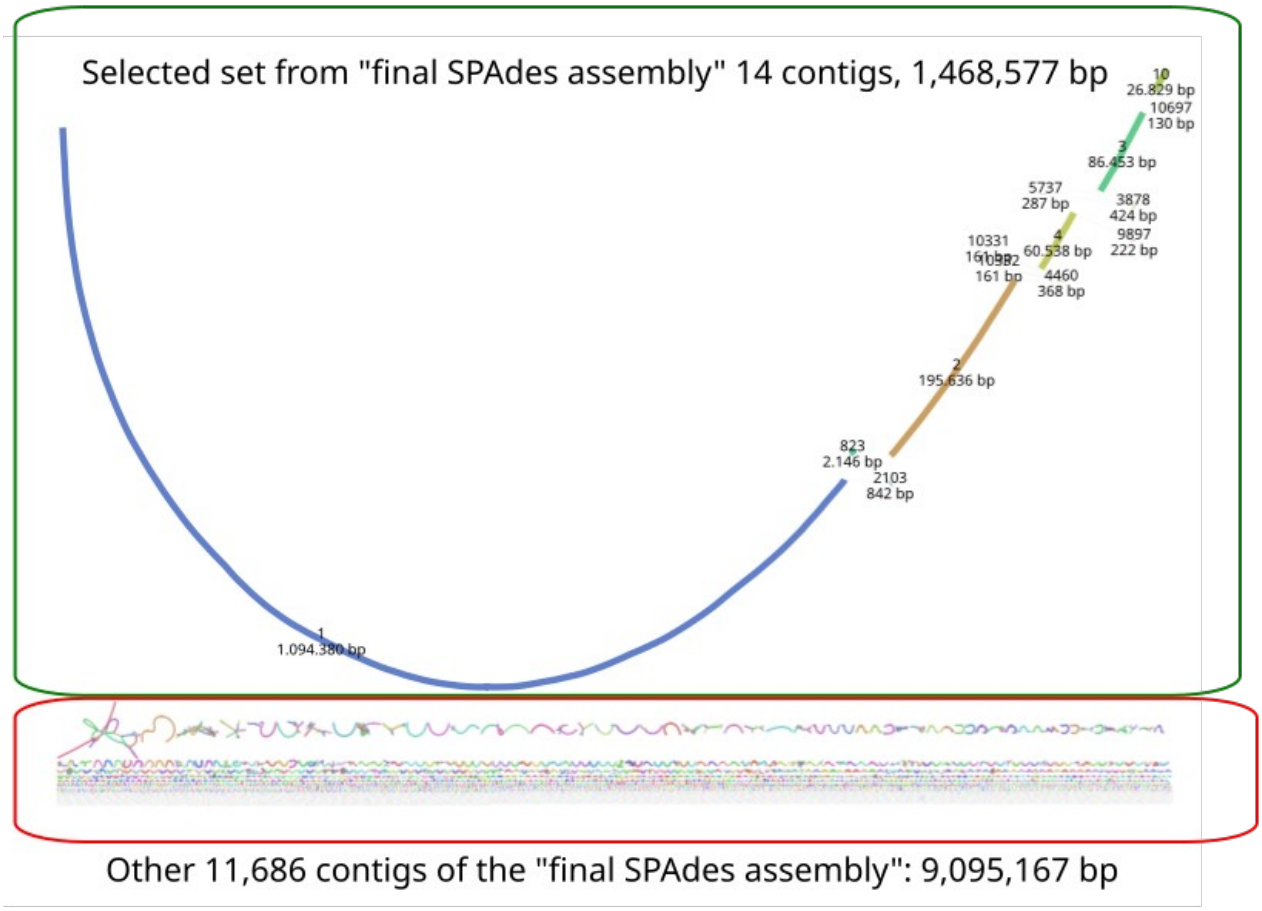
Supplementary Figure 1 Plot of the preliminary assembly contigs according to their GC content and $\log_{10}$ of sequencing coverage, coloured according to the respective best megablast hit. Only contigs with length higher than or equal to 1000 bp are shown for viewers' clarity.

In total, 24 full-length or partial rRNA genes were identified in the "preliminary assembly" (Supplementary Figure 1; Supplementary Data 4):

- 13 complete or partial rRNA genes had best megablast hits on nuclear or mitochondrial *Paramecium* spp., and were thus assigned to the host. The respective contigs ranged from 18.59 to 17607.88 in sequencing coverage
- 3 rRNA genes (16S, 23S and 5S) were identified as belonging to the symbiont, based on their best megablast hits on "*Ca*. Trichorickettsia" (16S) or *Rickettsia* (23S), or for being in the same contig as the 23S (5S). The respective contigs ranged from 36.57 to 38.55 in sequencing coverage, and ~0.34 GC content
- 8 remaining complete or partial rRNA gene sequences had megablast hits on other organisms. The respective contigs ranged from 3.85 to 356.00 sequencing coverage, having generally a higher GC content than the those assigned to "*Ca*. Trichorickettsia" (>0.44), with just one exception (0.26 GC)

Taking into account the plot and the rRNA gene features, we designed a "selection from preliminary assembly" for "*Ca*. Trichorickettsia", including all contigs with $\log_{10}$ of coverage lower than 2.5 and GC content between 0.25 and 0.4, with the exclusion of those having best megablast hit on members of order Peniculida (to with the *Paramecium* host belongs).

The reads mapping to "selection from preliminary assembly" were extracted and reassembled separately with SPAdes default settings: "final SPAdes assembly" (10,563,744 bp, 11700 contigs, N50=2,955 bp; L50=570). In this assembly, a selection was made of contigs belonging to "*Ca*. Trichorickettsia (14 contigs, 1,468,577 bp; N50=1,094,380 bp; L50=1; Supplementary Figure 2).



Supplementary Figure 2 Visual representation of the 11700 contigs of the "final SPAdes assembly" and the relative connections in the assembly graph, obtained with the Bandage software. The green square highlights the selected set of contigs. The red square highlights the remaining contigs of the assembly.

Then, primers were designed next to the ends of the 6 larger contigs in the selected set, and PCR reactions were performed in order to identify/confirm junctions among those contigs. The combinations of primers used for amplification and sequencing, primer sequences, and the reaction protocols used are reported below (Supplementary Table 1, 2, 3, 4).

Supplementary Table 1: primer combinations for closing "*Ca*. Trichorickettsia mobilis" genome

Reaction	Amplification primer 1	Amplification primer 2	Sequencing primer 1	Sequencing primer 2	Protocol
1	Tricho_10Fa	Tricho_3Ra	Tricho_10Fb	Tricho_3Rb	A
2	Tricho_3F	Tricho_4R	Tricho_3F	Tricho_4R	A

3	Tricho_4Fa	Tricho_2Ra	Tricho_4Fb	Tricho_2Rb	A
4	Tricho_2F	Tricho_823F	Tricho_2F	Tricho_823F	B
5	Tricho_823Ra	Tricho_1Fa	Tricho_823Rb	Tricho_1Fb	A
6	Tricho_1Ra	Tricho_10R	Tricho_1Rb	Tricho_10R	A

Supplementary Table 2: primer sequences for closing "*Ca*. Trichorickettsia mobilis" genome

Primer	**Sequence (F: forward; R: reverse)**
Tricho_1Fa	5'-TTGGCAGAAGCACTAATTGAG-3'
Tricho_1Fb	5'-TAACTGGTAATGATCTCCACG-3'
Tricho_1Ra	5'-AGCGAAGCAGTGACATTGG-3'
Tricho_1Rb	5'-TACAGTGACCACAGTTCGG-3'
Tricho_2F	5'-CCCTCATATCTAGGTTGAGC-3'
Tricho_2Ra	5'-TGATAACATACGAGTAGCAGC-3'
Tricho_2Rb	5'-TTAACGCAGGCACTACTCC-3'
Tricho_3F	5'-TCAACGCTCTTTCCTGTGG-3'
Tricho_3Ra	5'-AACCTGCCGTGAGGTGC-3'
Tricho_3Rb	5'-ATCAGTAGCAGCGCCTAC-3'
Tricho_4Fa	5'-AACAGCAGCATGCACTGAG-3'
Tricho_4Fb	5'-CTACCCTCATAGGGTATCC-3'
Tricho_4R	5'-CGACTCAAGGCTCGTGG-3'
Tricho_10Fa	5'-CCAGAGTCCGTTAGAATAGG-3'
Tricho_10Fb	5'-GCCCCAGGCCTTAACATC-3'
Tricho_10R	5'-GTAATTGGAGCCTTAGAGTTC-3'
Tricho_823F	5'-CTTGATTAGGTCTTGCTTCC-3'
Tricho_823Ra	5'-ACTTATCTCGATAGGCTGAAC-3'
Tricho_823Rb	5'-CTGACCTCCTCTATCAAGC-3'

Supplementary Table 3: PCR protocol A (standard) for closing "*Ca*. Trichorickettsia mobilis" genome

94°C	3 min	
94°C	30 s	40 cycles
50°C	30 s	
72°C	4 min	
72°C	10 min	

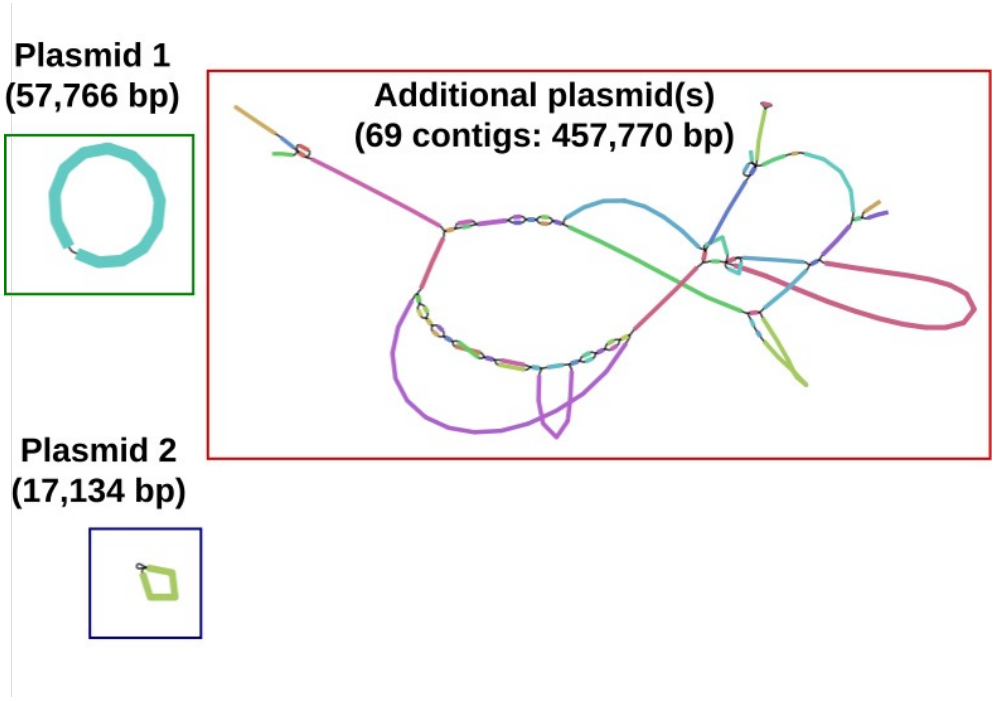
Supplementary Table 4: PCR protocol B (touchdown) for closing "*Ca*. Trichorickettsia mobilis" genome

94°C	3 min	
94°C	30 s	5 cycles
56°C	30 s	
72°C	4 min	
94°C	30 s	10 cycles
53°C	30 s	
72°C	4 min	
94°C	30 s	30 cycles
50°C	30 s	
72°C	4 min	
72°C	10 min	

Thanks to these PCR experiments, it was possible to close the "*Ca*. Trichorickettsia mobilis" genome into a single circular scaffold (1,470,091 bp).

In addition, the DIAMOND hit-based inspection of contigs of the "preliminary assembly" outside the "selection from preliminary assembly" evidenced the presence of putative bacterial/*Rickettsia*-like sequences in higher coverage contigs, which were assigned to putative "*Ca*. Trichorickettsia" plasmid(s). Thus, we designed an additional "selection for plasmids" from the "preliminary assembly", including all contigs with $\log_{10}$ of coverage higher than 1.5.

The reads mapping to "selection for plasmids" were extracted and reassembled separately with SPAdes (based on different attempts, the option -k 21,33,55,77,99 was chosen): "plasmid re-assembly" (39,539,931 bp, 4182 contigs, N50=82,014 bp; L50=128). In this assembly, at least 3 plasmids were identified. Two plasmids were assembled in single circular contigs, 57,766 bp and 17,134 bp long, respectively. The other plasmidic sequences were assembled into 69 contigs (457,770 bp), and may even constitute one or more additional plasmids: "additional plasmid(s)" (Supplementary Figure 3).



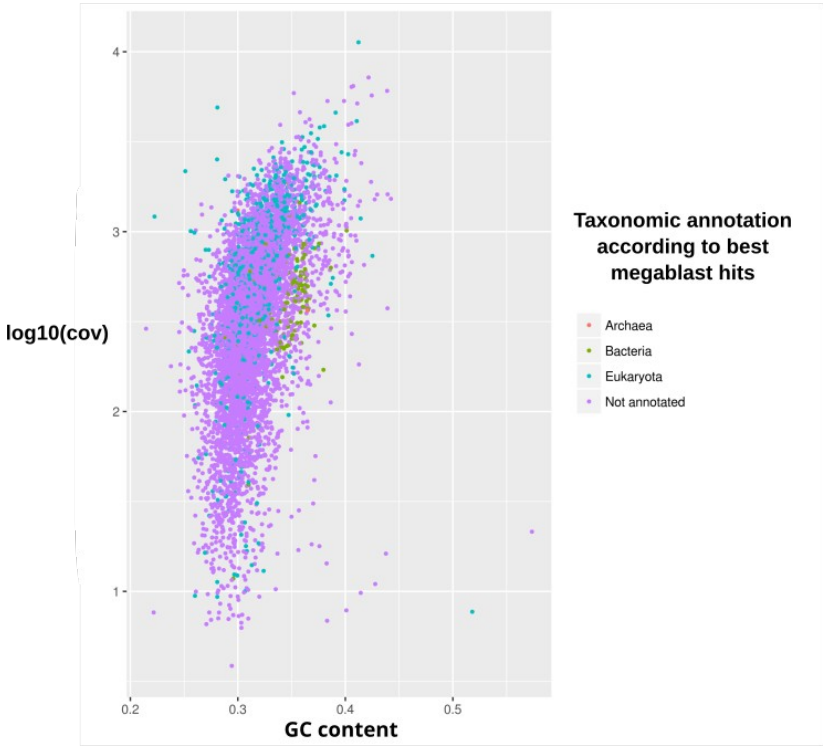
Supplementary Figure 3 Visual representation of the selected 71 contigs of the "plasmid re-assembly" and the relative connections in the assembly graph, obtained with the Bandage software. The green square highlights the plasmid 1, the blue square highlights plasmid 2, and the red square highlights the "additional plasmid(s)"

Finally, the assembly of "additional plasmid(s)" was refined by removing all contigs <5000bp containing no validated ORF (i.e. with no hits on NCBI nr or with hits only on hypothetical proteins, transposases, phages). Thus, the "final assembly" of the "additional plasmid(s)" included 36 contigs (420,184 bp; N50=28,079 bp; L50=26).

In total, the assembly of "*Ca*. Trichorickettsia", including chromosome and all plasmids, consisted of 39 contigs (1,965,805 bp).

***Paramecium nephridiatum* Sr 2-6 hosting "*Ca.* Megaira venefica"**

The "preliminary assembly" was constituted by 21,901 contigs (21,515,176 bp; N50 = 2,009 bp; L50 = 2817)

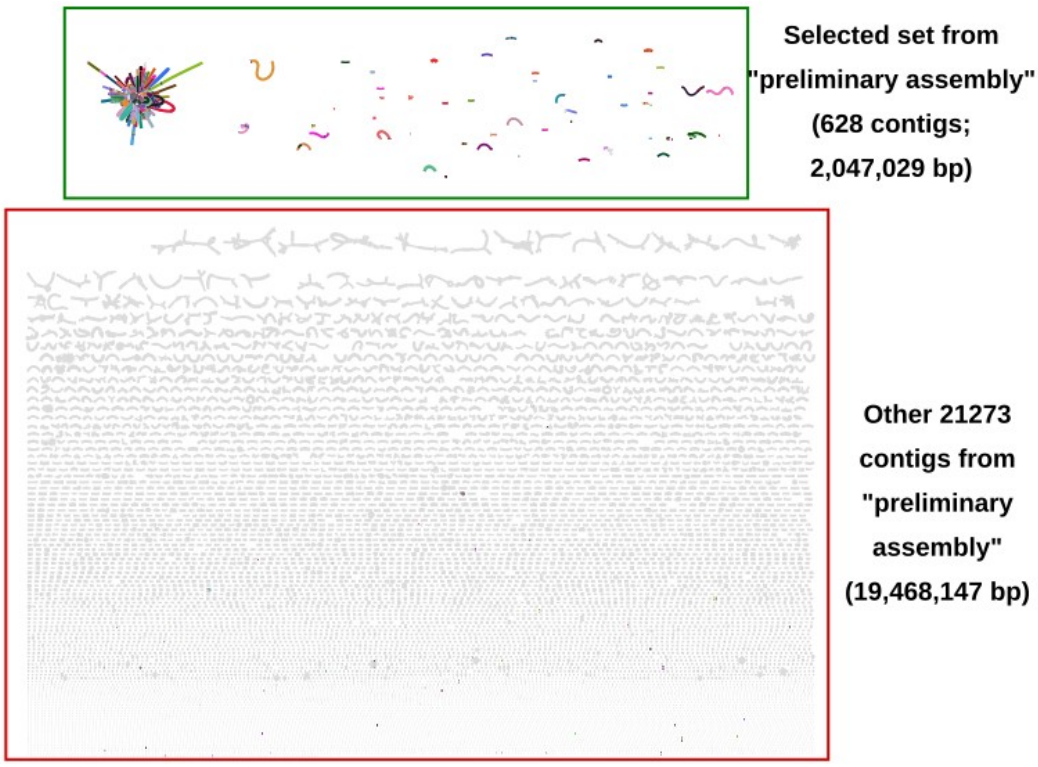


Supplementary Figure 4 Plot of the preliminary contigs of the sample Sr 2-6 according to their GC content and $\log_{10}$ of sequencing coverage, coloured according to the respective best megablast hit. Only contigs with length higher than or equal to 1000 bp are shown for viewers' clarity.

In total, 36 full-length or partial rRNA genes were identified in the "preliminary assembly" (Suppelementary Figure 4; Supplementary Data 4):

- 34 complete rRNA genes had best megablast hits on nuclear *Paramecium* sequences, and were thus assigned to the host. The respective contigs displayed 7.28 and 11285.11 sequencing coverage
- 2 rRNA gene sequences (16S and 5S) were identified as belonging to "*Ca*. Megaira venefica", based on their respective megablast hits. Namely the 16S rRNA gene had high identity (>99%) with "*Ca*. Megaira spp.", while 5S rRNA gene had no "informative" hit (low identity hits ~80% with several other proteobacterial sequences), but its full-length contig had best hit on *Rickettsia japonica*. The two respective contigs displayed 595.70 and 569.53 sequencing coverage, and ~0.36 GC content.

As done for the other samples, we selected contigs based on sequencing coverage, GC content, and best megablast hits. Then, we reassembled the reads mapping on these contigs. However, no significant improvement of the assembly of "*Ca*. Megaira venefica" genome was observed (not shown). Therefore, selection of "*Ca*. Megaira venefica" sequences was performed directly on the "preliminary assembly", counting 628 contigs (2,047,029 bp).



Supplementary Figure 5 Visual representation of the 21,901 contigs of the "preliminary assembly" and the relative connections in the assembly graph, obtained with the Bandage software. The green square highlights the selected set of contigs, the red square highlights the remaining contigs of the assembly.

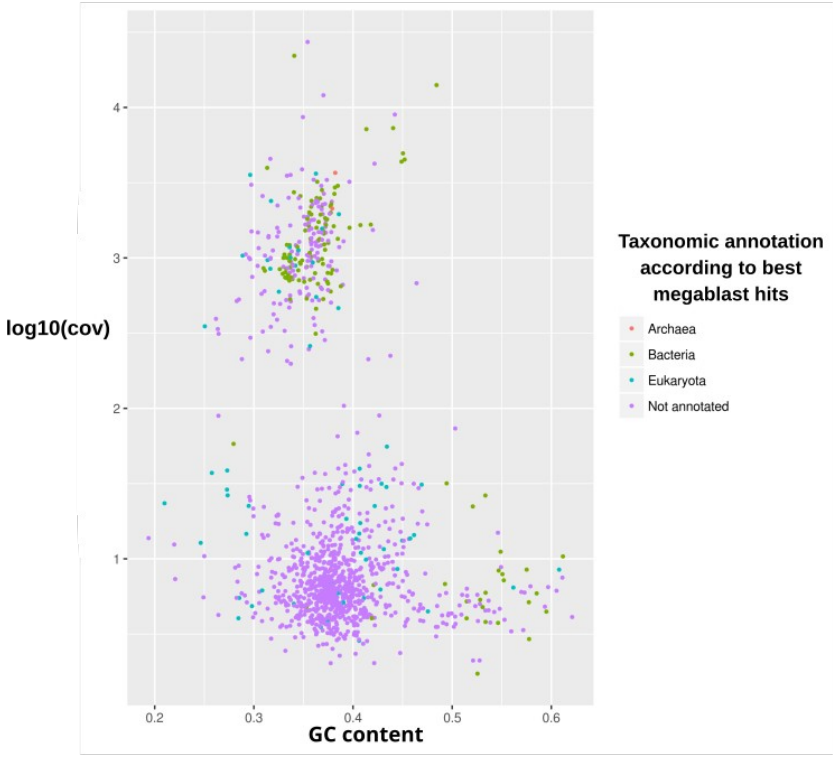
The relatively high fragmentation degree and the presence of several small contigs in the selection from "preliminary assembly" were interpreted as due to the presence of many repeated elements in the genome of "*Ca*. Megaira venefica", considering the high connection degree (Supplementary Figure 5) and the presence of multiple transposase genes. Accordingly, and accounting both for the careful manual revision applied and for the comparative BUSCO results with other *Rickettsiales*

(Supplementary Data 2), we concluded that this assembly likely contains the whole genome sequence (in terms of gene sequences) of "*Ca*. Megaira venefica".

Finally, the assembly was refined by removing all contigs <3000bp containing no validated ORF (i.e. with no hits on NCBI nr or with hits only on hypothetical proteins, transposases, phages). Thus, the "final assembly" of "*Ca*. Megaira venefica" counted 281 contigs (1,862,567 bp; N50=10,544 bp; L50=58).

***Euplotes woodruffi* NDG2 hosting "*Ca*. Megaira polyxenophila" and "*Ca*. Bandiella woodruffii"**

The "preliminary assembly" was constituted by 26,682 contigs (15,101,154 bp; N50 = 772 bp; L50 = 1633)



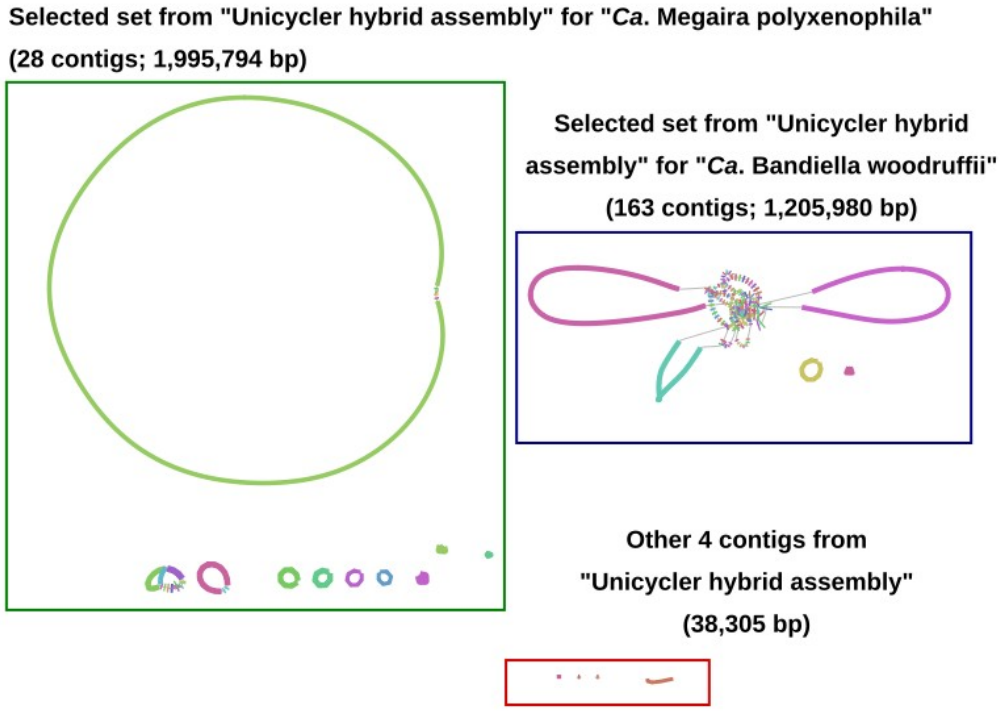
Supplementary Figure 6 Plot of the preliminary contigs of the sample NDG2 according to their GC content and $\log_{10}$ of sequencing coverage, coloured according to the respective best megablast hit. Only contigs with length higher than or equal to 1000 bp are shown for viewers' clarity.

In total, 17 full-length or partial rRNA genes were identified in the "preliminary assembly" (Supplementary Figure 6; Supplementary Data 4):

- 3 partial rRNA genes had best megablast hits on nuclear *Euplotes* sequences, and were thus assigned to the host. The two respective contigs displayed quite lower sequencing coverage (31.12 and 37.25)
- 3 rRNA genes (5S, 16S, 23S) formed a putative operon on a single contig. Based on megablast hits, they were identified as belonging to *Polynucleobacter necessarius*, a betaproteobacterial obligate symbiont of many *Euplotes spp.*, including *E. woodruffi* (e.g. [39]). This contig displayed 4363.69 sequencing coverage
- 3 rRNA genes (5S, 16S, 23S) were identified as belonging to a "*Ca*. Bandiella woodruffii" symbiont, based on their respective best megablast hits on "*Ca*. Midichloriaceae" bacteria. The precise species assignment was due to the 99.70% identity of the 16S rRNA gene with the type "*Ca*. Bandiella woodruffii" endosymbiont of *E. woodruffi* Sq1 [39], though not representing the best hit due to the relatively short length of this sequence. The two respective contigs displayed 648.22 and 1664.01 sequencing coverage
- 3 rRNA gene sequences (16S, 23S and 5S) were identified as belonging to a "*Ca*. Megaira polyxenophila" symbiont, based on their respective megablast hits, including for the 16S rRNA gene hits with high identity (>99%) on "*Ca*. Megaira polyxenophila" sequences (including symbiont of *Carteria cerasiformis* [40]), and for the 23S rRNA hits on *Rickettsia japonica*. The two respective contigs displayed 899.13 and 914.37 sequencing coverage
- 5 remaining complete or partial rRNA gene sequences had megablast hits on other organisms. The respective contigs had comparably much lower coverage (<26.42) than the ones assigned to the two *Rickettsiales* bacteria

Taking into account the plot and the rRNA gene features, we designed a “selection from preliminary assembly” targeting the two *Rickettsiales*, including all contigs with $\log_{10}$ of coverage higher than 1.5, and excluding those with best megablast hit on *Polynucleobacter*.

The reads mapping to this “selection from preliminary assembly” were extracted. In parallel, the corresponding Nanopore reads were extracted by performing a blastn search of the total reads as queries againts the contigs of the same “selection from preliminary assembly” (default megablast options) and keeping all reads with hits. The hybrid assembly of these two sets of reads “Unicycler hybrid re-assembly” included 195 contigs (3,240,079 bp, N50=503,502 bp; L50=2). In this assembly, two selection were made for sequences belonging respectively to “*Ca*. Megaira polyxenophila” (28 contigs, 1,995,794 bp), and to “*Ca*. Bandiella woodruffii” (163 contigs; 1,205,980 bp; Supplementary Figure 7). Each selection contained multiple putative plasmids (at least 9 for “*Ca*. Megaira”, 2 for “*Ca*. Bandiella”), which were assigned to each organism based on the connection in the Illumina assembly graphs, as well as on the sequence similarity of the annotated genes among them and with published sequences (e.g. published plasmidic sequences in *Rickettsia* for sequences assigned to “*Ca*. Megaira”).

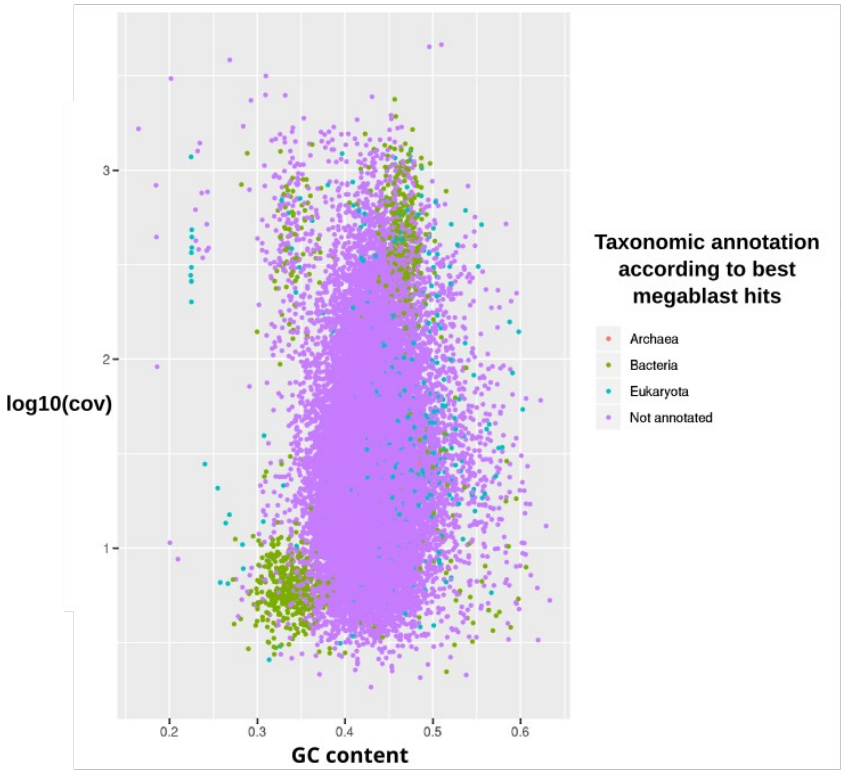


Supplementary Figure 7 Visual representation of the 195 contigs of the "Unicycler hybrid assembly" and the relative connections in the assembly graph, obtained with the Bandage software. The green square highlights the selected set of contigs for "*Ca*. Megaira polyxenophila", the blue square highlights the selected set of contigs for "*Ca*. Bandiella woodruffii", and red square highlights the remaining contigs of the assembly.

For what concerns the putative "*Ca*. Megaira polyxenophila" and "*Ca*. Bandiella woodruffii" chromosomes, a further manual step was performed in order to improve the assembly. Namely, all selected Nanopore reads were employed as queries in a blastn search (default megablast options) against the contig ends (1000 bp, only for contigs larger than 1000 bp), and those with hits were manually inspected, in order to identify potentially bridging reads between contigs. Accordingly, it was possible to close each genome into a single circular contig ("*Ca*. Megaira polyxenophila": 1,508,753 bp; "*Ca*. Bandiella woodruffii": 1,129,747 bp). Moreover, the assembly of plasmids was further refined by removing all contigs ≤1000bp containing no validated ORF (i.e. with no hits on NCBI nr or with hits only on hypothetical proteins or transposases). Thus, the two "final assemblies", including chromosome and plasmids, counted respectively 14 contigs (1,994,314 bp) for "*Ca*. Megaira polyxenophila", and 3 contigs (1,225,299 bp) for "*Ca*. Bandiella woodruffii" (see Supplementary Data 1 for details on the length of each plasmid).

***Euplotes harpa* BOD18 hosting "*Ca*. Cyrtobacter comes"**

The "preliminary assembly" was constituted by 135,782 contigs (99,489,754 bp; N50 = 1,566 bp; L50 = 16270)



Supplementary Figure 8 Plot of the preliminary contigs of the sample BOD18 according to their GC content and $\log_{10}$ of sequencing coverage, coloured according to the respective best megablast hit. Only contigs with length higher than or equal to 1000 bp are shown for viewers' clarity.

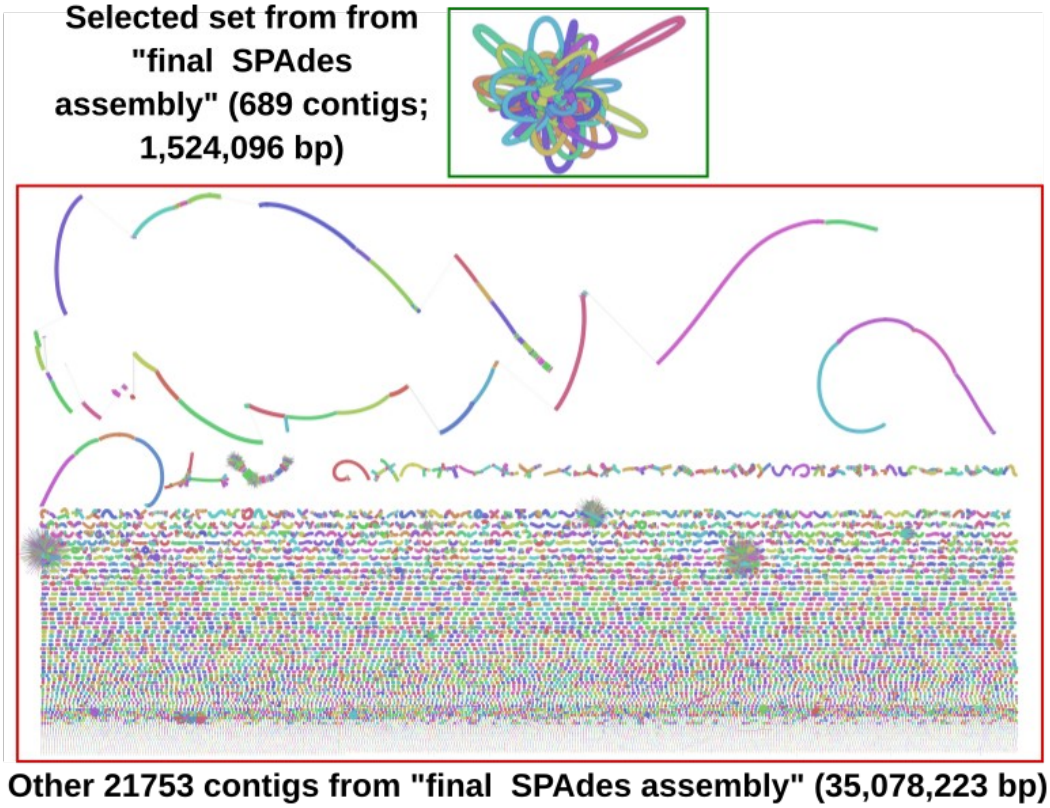
In total, 15 full-length or partial rRNA genes were identified in the "preliminary assembly" (Supplementary Figure 8; Supplementary Data 4):

- 2 complete rRNA genes had best megablast hits on nuclear *Euplotes* sequences, and were thus assigned to the host. The respective contigs displayed 50.00 and 61.05 sequencing coverage
- one 16 rRNA gene sequence was identified as belonging to "*Ca*. Cyrtobacter comes", based on its best megablast hit on this organism with 100% identity. The respective contig displayed 668.69 sequencing coverage, and 0.36 GC content
- one complete and one partial rRNA gene sequences were identified based on their megablast hits as belonging to the *Polynucleobacter necessarius* (*Betaproteobacteria*) symbiont previously characterised in the BOD18 strain (Vannini et al. 2010). The respective contigs

had relatively comparable coverage (330.76 and 557.69) to the "*Ca*. Cyrtobacter" one, but significantly higher GC content (0.48 and 0.52).

- 10 remaining complete or partial rRNA gene sequences had megablast hits on other organisms (9) or no hit (1). The respective contigs had a clearly lower coverage (<37.57) than the one assigned to "*Ca*. Cyrtobacter"

Taking into account the plot and the rRNA gene features, we designed a "selection from preliminary assembly" targeting "*Ca*. Cyrtobacter", including all contigs with $\log_{10}$ of coverage higher then 1.5. The reads mapping to this "selection from preliminary assembly" were extracted and reassembled separately with SPAdes (based on different attempts, the option -k 21,33,55,77,99 was chosen). This "SPAdes re-assembly" included 22442 contigs (36,602,319 bp, N50=3,630 bp; L50=2747). In this assembly, a selection was made of sequences belonging to "*Ca*. Cyrtobacter" (689 contigs, 1,524,096 bp; Supplementary Figure 9).



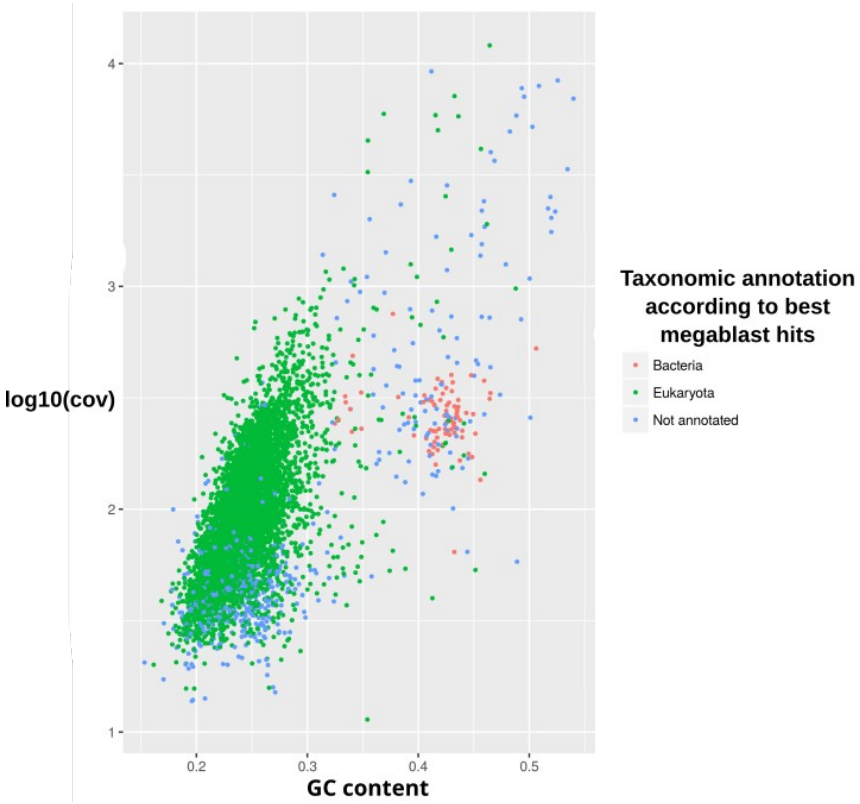
Supplementary Figure 9 Visual representation of the 22442 contigs of the "final SPAdes assembly" and the relative connections in the assembly graph, obtained with the Bandage software. The green square highlights the selected set of contigs, the red square highlights the remaining contigs of the assembly.

The relatively high fragmentation degree and the presence of several small contigs in "final SPAdes assembly" were interpreted as due to the presence of many repeated elements in the genome of "*Ca*. Cyrtobacter", considering the high level of connection between the contigs (Supplementary Figure 9) and the presence of multiple transposase genes (data not shown). Accordingly, and accounting both for the careful manual revision applied and for the comparative BUSCO results with other *Rickettsiales* (Supplementary Data 2):, we concluded that this assembly likely contains the whole genome sequence (in terms of gene sequences) of "*Ca*. Cyrtobacter comes".

Finally, the assembly was refined by removing all contigs <2000bp containing no validated ORF (i.e. with no hits on NCBI nr or with hits only on hypothetical proteins or transposases). Thus, the "final assembly" of the "*Ca*. Cyrtobacter comes" counted 141 contigs (1,308,703 bp; N50=14,445 bp; L50=28).

***Paramecium biaurelia* US_Bl 11III1 hosting "*Ca*. Fokinia cryptica"**

The "preliminary assembly" was constituted by 115,057 contigs (136,752,753 bp; N50 = 10,679 bp; L50 = 2209)



Supplementary Figure 10 Plot of the preliminary contigs of the sample US_BI 11III1 according to their GC content and $\log_{10}$ of sequencing coverage, coloured according to the respective best megablast hit. Only contigs with length higher than or equal to 1000 bp are shown for viewers' clarity.

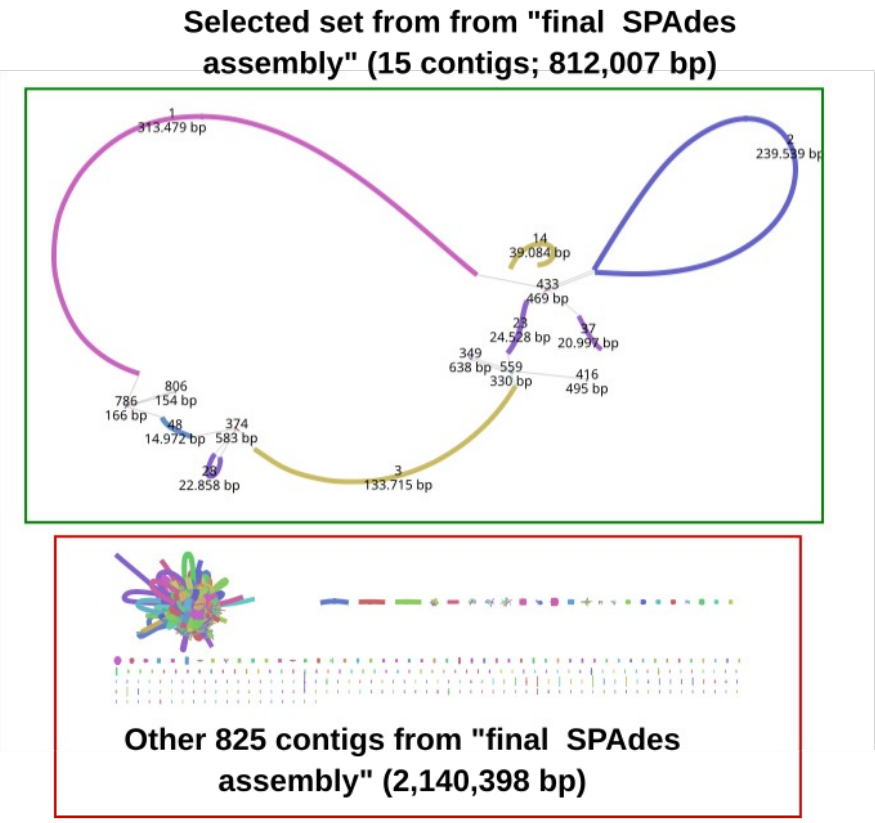
In total, 31 full-length or partial rRNA genes were identified in the "preliminary assembly" (Supplementary Figure 10; Supplementary Data 4):

- 25 complete or partial rRNA genes had best megablast hits on nuclear or mitochondrial *Paramecium* spp., and were thus assigned to the host (in one case, the partial gene sequence had no hit and the assignment was based on the megablast hit of the whole respective contig). The respective contigs ranged from 6.34 to 5944.93 in sequencing coverage
- 3 rRNA gene sequences (16S, 23S, 5S) were identified as belonging to "*Ca*. Fokinia cryptica", based on their best megablast hits on "*Ca*. Fokinia spp.". The two respective contigs displayed 281.37 and 301.99 sequencing coverage, and ~0.34 GC content
- 3 rRNA genes (5S, 16S, 23S) formed a putative operon on a single contig. Based on megablast hits, they were identified as belonging to the "*Ca*. Bealeia paramacronuclearis"

(*Holosporales*) symbiont previously characterised in the US_Bl 11III1 strain [21]. The contig had comparable coverage (312.91) to the "*Ca*. Fokinia" ones, but significantly higher GC content (0.46).

Taking into account the plot and the rRNA gene features, we designed a "selection from preliminary assembly" for "*Ca.* Fokinia cryptica" , including all contigs with $\log_{10}$ of coverage higher than 1.6, and GC content higher than 0.3, with the exception of those having best megablast hit on members of order Peniculida (to with the *Paramecium* host belongs).

The reads mapping to this "selection from preliminary assembly" were extracted and reassembled separately with SPAdes (based on different attempts, the option -k 21,33,55,77,99,127 was chosen). This "SPAdes re-assembly" included 840 contigs (2,952,405 bp, N50=23,802 bp; L50=25). In this assembly, a selection was made of sequences belonging to "*Ca.* Fokinia cryptica" (15 contigs, 812,007 bp; Supplementary Figure 11).



Supplementary Figure 11 Visual representation of the 7695 contigs of the "final SPAdes assembly" and the relative connections in the assembly graph, obtained with the Bandage software. The green square highlights the selected set of contigs, the red square highlights the remaining contigs of the assembly.

Then, primers were designed next to the ends of the 8 larger contigs in the selected set, and PCR reactions were performed in order to identify/confirm junctions among those contigs. The combinations of primers used for amplification and sequencing, primer sequences, and the reaction protocols used are reported below (Supplementary Table 5, 6, 7, 8).

Supplementary Table 5: primer combinations for closing "*Ca*. Fokinia cryptica" genome

Reaction	Amplification primer 1	Amplification primer 2	Sequencing primer 1	Sequencing primer 2	Protocol
1	Fcry_1F	Fcry_48R_a	Fcry_1F	Fcry_48R_b	B
2	Fcry_48F_a	Fcry_28F_a	Fcry_48F_b	Fcry_28F_b	A
3	Fcry_28R_a	Fcry_3F_a	Fcry_28R_b	Fcry_3F_b	B
4	Fcry_3R	Fcry_23F	Fcry_3R	Fcry_23F	A
5	Fcry_23R_a	Fcry_14R_a	Fcry_23R_b	Fcry_14R_b	A
6	Fcry_37F_a	Fcry_2F_a	Fcry_37F_b	Fcry_2F_b	B
7	Fcry_2R_a	Fcry_1R	Fcry_2R_b	Fcry_1R	B

Supplementary Table 6: primer sequences for closing "*Ca*. Fokinia cryptica" genome

Primer	Sequence (F: forward; R: reverse)
Fcry_1F	5'-GACACATCAACCGGAACG-3'
Fcry_48R_a	5'-GTTATACATCAGAGAGAAGCAC-3'
Fcry_48R_b	5'-TGATATGTTACGAGAGTGTGC-3'
Fcry_48F_a	5'-TCTTTAGACTACCACAGAGTG-3'
Fcry_48F_b	5'-AGCAGTTTGCTCAGCCTC-3'
Fcry_28F_a	5'-GGTATCTTACGGGTCAAGC-3'
Fcry_28F_b	5'-ATTGTGAAGCCGTAGTTGTAG-3'
Fcry_28R_a	5'-ACATTATGATACGCTCAACGC-3'
Fcry_28R_b	5'-TGGAGCATACGGAGTGAG-3'
Fcry_3F_a	5'-AGATGTGCCAAGGATTCGC-3'
Fcry_3F_b	5'-CCATTTCCGCCTTATTACCC-3'
Fcry_3R_b	5'-TTATGACGAACGATACAACTAG-3'
Fcry_23F	5'-CGATGTACGTTGTTCTCCC-3'
Fcry_23R_a	5'-GAAATGGGAAGGCAGTAGC-3'

Fcry_23R_b	5'-AGAAGTACTAGGAGCCCAC-3'
Fcry_14R_a	5'-CATGAAAGACGTGTAACGGC-3'
Fcry_14R_b	5'-GTTACTATAATGCCGCGAGG-3'
Fcry_14F_a	5'-ATGTTAAGAGCAGCATCGTAC-3'
Fcry_14F_b	5'-AAGAGGAACAAGAGACGAAC-3'
Fcry_37R_a	5'-GTAGATGTATGGTGGCTTGC-3'
Fcry_37R_b	5'-TTGGAGCAGTGAAGGGATG-3'
Fcry_37F_a	5'-AACATCGCTATTGCCGGTG-3'
Fcry_37F_b	5'-GAGTTACCACAATACCGATG-3'
Fcry_2F_a	5'-AGGTGGTGACTCCTGTTG-3'
Fcry_2F_b	5'-CTAAATAGCAGACGCGGTAG-3'
Fcry_2R_a	5'-TCGCATAACACTGCATTACC-3'
Fcry_2R_b	5'-ATCAAGTAGTGAAGCATCAGG-3'
Fcry_1R	5'-CACAACAGAAGGAATCGCG-3'

Supplementary Table 7: PCR protocol A (standard) for closing "*Ca*. Fokinia cryptica" genome

94°C	3 min	
94°C	30 s	40 cycles
50°C	30 s	
72°C	4 min	
72°C	10 min	

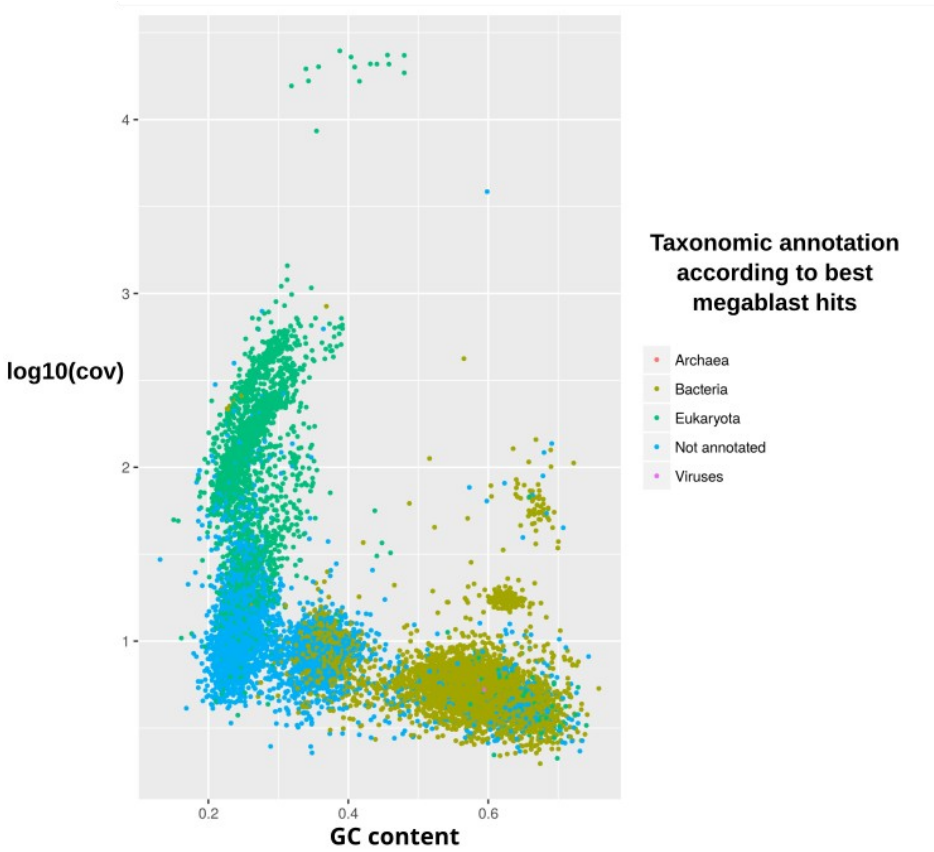
Supplementary Table 8: PCR protocol B (touchdown) for closing "*Ca*. Fokinia cryptica" genome

94°C	3 min	
94°C	30 s	5 cycles
56°C	30 s	
72°C	4 min	
94°C	30 s	10 cycles
53°C	30 s	
72°C	4 min	
94°C	30 s	30 cycles
50°C	30 s	
72°C	4 min	
72°C	10 min	

Thanks to such PCR experiments, it was possible to close the "*Ca*. Fokinia cryptica" genome into a single scaffold (815,586 bp).

Paramecium biaurelia* USBL-36I1 hosting *Lyticum linuosum

The "preliminary assembly" was constituted by 115,057 contigs (136,752,753 bp; N50 = 10,679 bp; L50 = 2209)



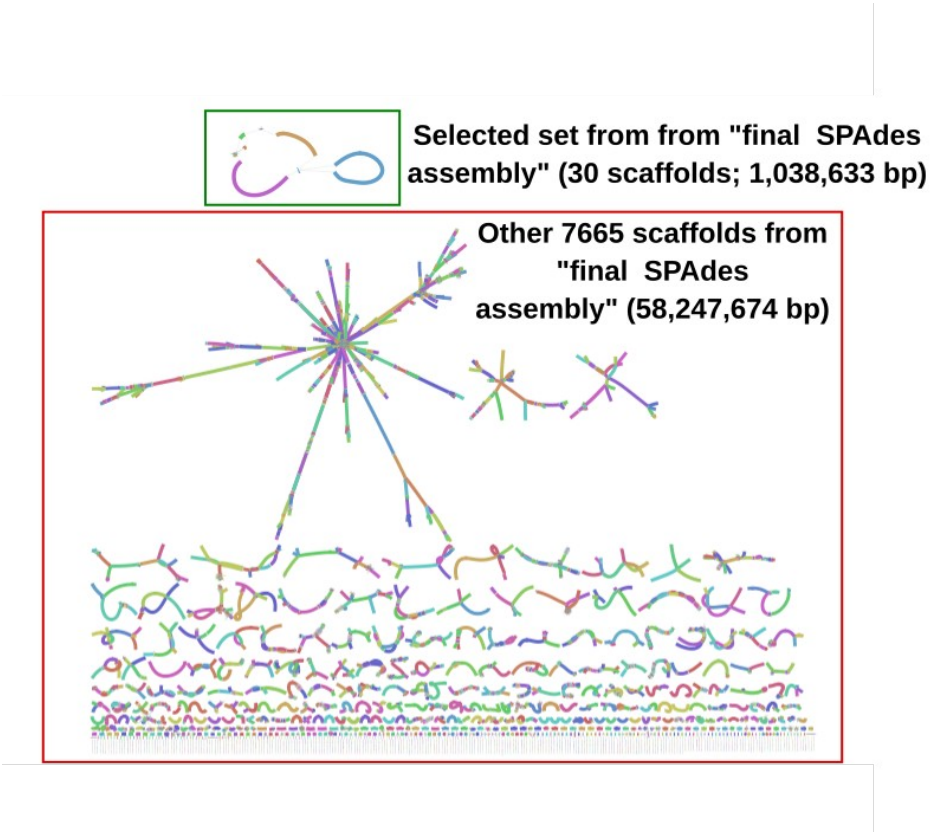
Supplementary Figure 12 Plot of the preliminary contigs of the sample USBL-36I1 according to their GC content and $\log_{10}$ of sequencing coverage, coloured according to the respective best megablast hit. Only contigs with length higher than or equal to 1000 bp are shown for viewers' clarity.

In total, 52 full-length or partial rRNA genes were identified in the "preliminary assembly" (Supplementary Figure 12; Supplementary Data 4):

- 27 complete or partial rRNA genes had best megablast hits on nuclear or mitochondrial *Paramecium* spp., and were thus assigned to the host. The respective contigs ranged from 71.83 to 20140.69 in sequencing coverage
- 2 rRNA gene sequences (16S, 23S) were identified as belonging to *Lyticum*, based on their best megablast hits on *L. sinuosum* (16S), and on the "*Ca*. Midichloriaceae" endosymbiont of *Acanthamoeba* sp. UWC8 (23S). The respective contigs displayed 258.45 and 843.75 sequencing coverage, and 0.37 and 0.25 GC content
- 23 remaining complete or partial rRNA gene sequences had megablast hits on other organisms (22) or no hit (1). The respective contigs had comparably lower coverage and/or clearly higher GC content (≥0.42) than those with *Lyticum* genes

Taking into account the plot and the rRNA gene features, we designed a "selection from preliminary assembly" for *Lyticum,* including all those contigs with $\log_{10}$ of coverage between 2 and 3, and GC content lower than 0.4.

The reads mapping to this "selection from preliminary assembly" were extracted and reassembled separately with SPAdes (based on different attempts, the option -k 21,33,55,77,99 was chosen). This "SPAdes re-assembly" included 7695 scaffolds (59,286,337 bp, N50=41,667 bp; L50=396). In this assembly, a selection was made of sequences belonging to *Lyticum* (30 scaffolds, 1,038,633 bp; Supplementary Figure 13).

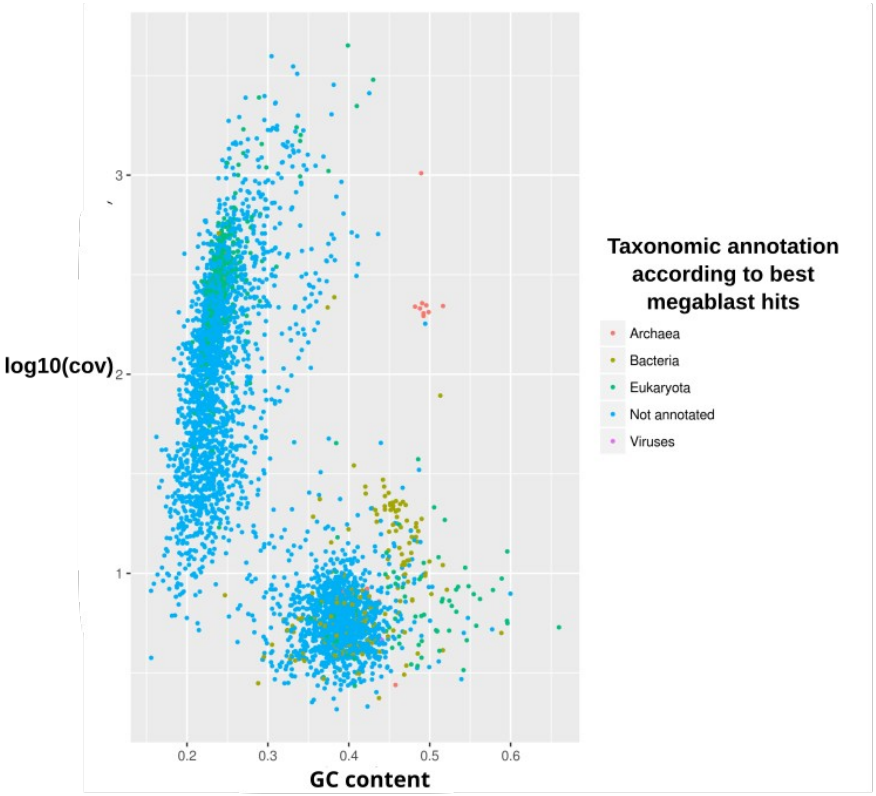


Supplementary Figure 13 Visual representation of the 7695 scaffolds of the "final SPAdes assembly" and the relative connections in the assembly graph, obtained with the Bandage software. The green square highlights the selected set of scaffolds, the red square highlights the remaining scaffolds of the assembly.

Finally, the assembly was refined by removing all scaffolds <5000 bp containing no validated ORF (i.e. with no hits on NCBI nr or with hits only on hypothetical proteins). Thus, the "final assembly" of *Lyticum* counted 6 scaffolds (1,018,517 bp; N50=336,044 bp; L50=2).

***Plagiopyla frontata* IBS-3 hosting the novel "*Ca*. Midichloriaceae" bacterium "*Ca*. Vederia obscura"**

The "preliminary assembly" counted 49,376 contigs (66,833,832 bp; N50 = 33,240 bp; L50 = 443).



Supplementary Figure 14 Plot of the preliminary contigs of the sample IBS-3 according to their GC content and $\log_{10}$ of sequencing coverage, coloured according to the respective best megablast hit. Only contigs with length higher than or equal to 1000 bp are shown for viewers' clarity.

In total, 21 full-length or partial rRNA genes were identified in the "preliminary assembly" (Supplementary Figure 14; Supplementary Data 4):

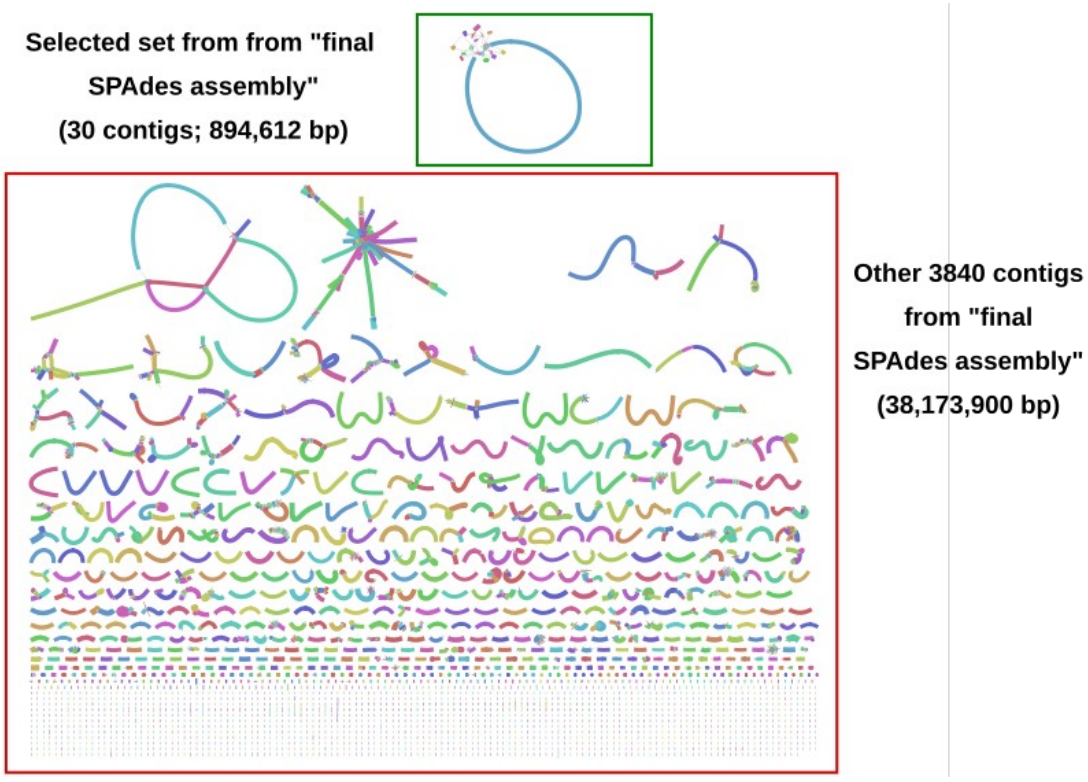
- 1 partial LSU rRNA gene had best megablast hit on the ciliate *Cryptocaryon irritans*. This sequence was assigned to the host, considering the absence of LSU rRNA genes of *Plagiopyla* spp. on NCBI nucleotide. The respective contig had 3014.34 sequencing coverage
- 3 rRNA genes (5S, 16S, 23S) formed a putative operon on a single contig. They had best hits on *Methanocorpospulum* spp., and were thus assigned to a putative archaeal symbiont of *Plagiopyla*. The contig displayed 1022.82 sequencing coverage and 0.49 GC content
- 2 rRNA genes (16S, 23S) were identified as belonging to a novel "*Ca*. Midichloriaceae" bacterium from a new genus, based on their best megablast hits (with <90% identity) on the

"*Ca*. Midichloriaceae" endosymbiont of *Acanthamoeba* sp. UWC8. The respective contigs displayed 243.72 and 216.54 sequencing coverage, and 0.38 and 0.37 GC content

- 15 remaining complete or partial rRNA gene sequences had megablast hits on other organisms. The respective contigs had comparably lower coverage (≤78.10) and higher GC (>0.40) than the ones assigned to the "*Ca*. Midichloriaceae" bacterium

Taking into account the plot and the rRNA gene features, we designed a "selection from preliminary assembly" for this "*Ca.* Midichloriaceae" bacterium (from now on, "*Ca*. Vederia obscura"), including all contigs with $\log_{10}$ of coverage higher than 1.5, excluding those having best megablast hits on ciliate (Ciliophora) sequences.

The reads mapping to "selection from preliminary assembly" were extracted and reassembled separately with SPAdes (based on different attempts, the option -k 21,33,55,77,99 was chosen). This "SPAdes re-assembly" included 3875 contigs (39,068,512 bp, N50=55,917 bp; L50=188). In this assembly, a selection was made of contigs belonging to *"Ca.* Vederia obscura" (35 contigs, 894,612 bp; Supplementary Figure 15).

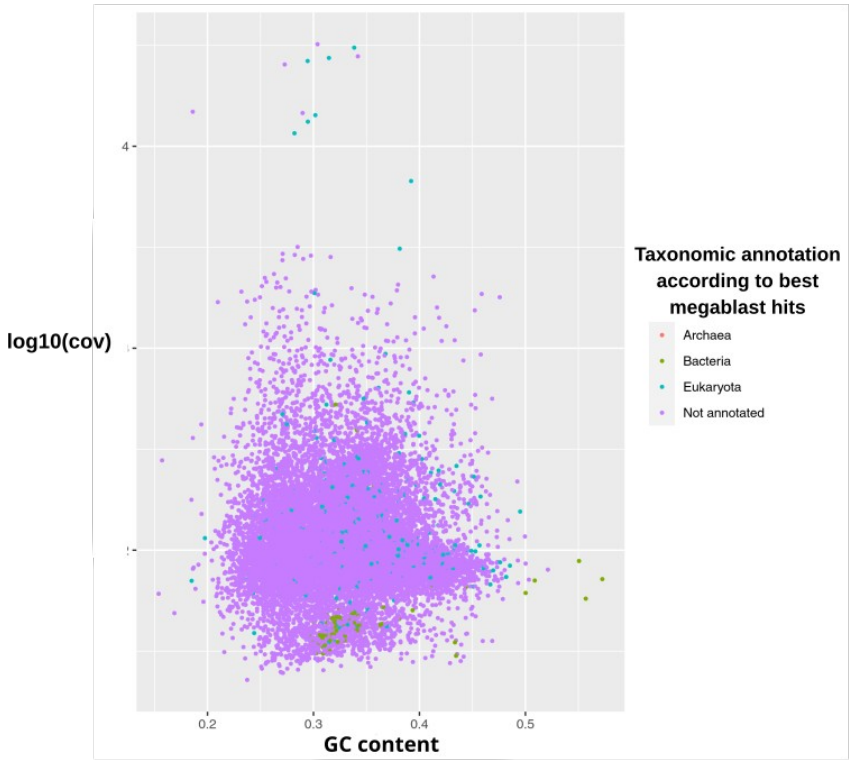


Supplementary Figure 15 Visual representation of the 3875 contigs of the "final SPAdes assembly" and the relative connections in the assembly graph, obtained with the Bandage software. The green square highlights the selected set of contigs, the red square highlights the remaining contigs of the assembly.

Finally, the assembly was refined by removing all contigs <5000 bp containing no validated ORF (i.e. with no hits on NCBI nr or with hits only on hypothetical proteins. Thus, the "final assembly" of "*Ca*. Vederia obscura" counted 19 contigs (886,222 bp; N50=785,721 bp; L50=1).

Reticulomyxa filosa hosting a novel "*Ca*. Midichloriaceae" bacterium

The "preliminary assembly" counted 25064 contigs (85,838,763 bp; N50 = 5,657 bp; L50 = 4263).



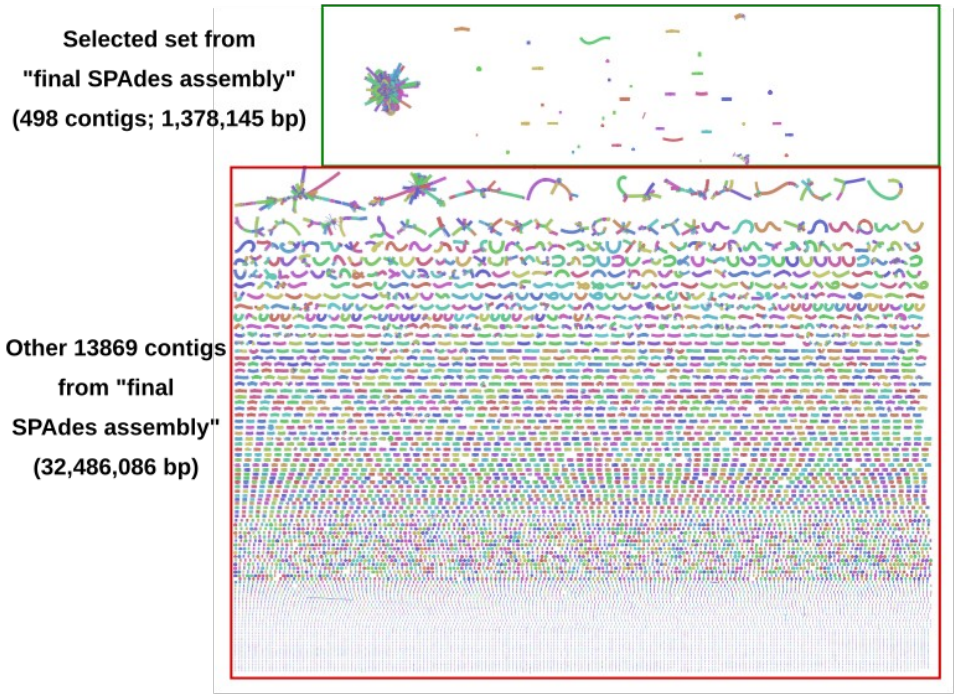
Supplementary Figure 16 Plot of the preliminary contigs of the sample *Reticulomyxa filosa* according to their GC content and $\log_{10}$ of sequencing coverage, coloured according to the respective best megablast hit. Only contigs with length higher than or equal to 1000 bp are shown for viewers' clarity.

In total, 11 full-length or partial rRNA genes were identified in the "preliminary assembly" (Supplementary Figure 16; Supplementary Data 4):

- 3 rRNA genes (16S, 23S, 5S) were identified as belonging to a novel "*Ca*. Midichloriaceae" bacterium from a new genus, based on their best megablast hits (with <94% identity) on the "*Ca*. Midichloriaceae" endosymbiont of *Acanthamoeba* sp. UWC8 and on "*Candidatus* Fokinia solitaria". The respective contigs displayed 89.09 and 101.35 sequencing coverage, and 0.26 and 0.34 GC content
- 8 remaining complete or partial rRNA gene sequences had megablast hits on other organisms (7) or no hit (1). The respective contigs had comparable coverage (78.23-133.15) and GC (0.23-0.31) with the ones assigned to the "*Ca*. Midichloriaceae" bacterium

Taking into account the plot and the rRNA gene features, we designed a "selection from preliminary assembly" for this "*Ca.* Midichloriaceae" bacterium, including all contigs with $\log_{10}$ of coverage lower than 1.5. Moreover, the careful inspection of the DIAMOND hits of contigs with higher coverage revealed the presence of 61 additional contigs putatively belonging to the "*Ca.* Midichloriaceae" bacterium, which were thus individually added to the "selection from preliminary assembly".

The reads mapping to such "selection from preliminary assembly" were extracted and reassembled separately with SPAdes (based on different attempts, the option -k 21,33,55,63 was chosen). This "SPAdes re-assembly" included 14367 contigs (33,864,241 bp, N50=6,105 bp; L50=1629). In this assembly, a selection was made of contigs belonging to the *"Ca. Midichloriaceae"* bacterium (498 contigs, 1,378,145 bp; Supplementary Figure 17).



Supplementary Figure 17 Visual representation of the 14367 contigs of the "final SPAdes assembly" and the relative connections in the assembly graph, obtained with the Bandage software. The green square highlights the selected set of contigs, the red square highlights the remaining contigs of the assembly.

Finally, the assembly was refined by removing all contigs <1000 bp containing no validated ORF (i.e. with no hits on NCBI nr or with hits only on hypothetical proteins or transposases) Thus, the "final assembly" of the "*Ca*. Midichloriaceae bacterium" counted 242 contigs (1,305,893 bp; N50=7,721 bp; L50=53).

Supplementary Note 4: Phylogenomics methods

Phylogenomic analyses were aimed to get a comprehensive view on the evolution and diversity of *Rickettsiales*. To do so, we collected a representative dataset of *Rickettsiales*, including at least one representative per genus. We considered all available genomes and MAGs (metagenome-assembled genomes) belonging to "core" described *Rickettsiales* lineages as of February 2021 (i.e. the four families *Rickettsiaceae*, *Anaplasmataceae*, "*Ca*. Midichloriaceae", "*Ca*. Deianiraeaceae"), and looked also for additional *Rickettsiales*-related organisms, namely any lineage forming a supported monophyletic group with *Rickettsiales* with the exclusion of other (alpha)proteobacterial orders. GenBank assemblies for the phylogenomics were downloaded from NCBI ftp (ftp.ncbi.nlm.nih.gov/genomes/all/GCA) initially in February 2021, and later updated in July 2021 (see below for details).

To reach such objective, the final species dataset for the phylogenomic analyses was built with a progressive refining procedure, described in detail below. The main steps were the following:

1. Collection of the initial dataset including *Rickettsiales* genomes, putative *Rickettsiales* MAGs, other *Alphaproteobacteria* and outgroup organisms (February 2021)
2. Expansion of the set of putative *Rickettsiales* MAGs, and 1st filtering by assembly quality
3. Selection of orthologs for phylogenomics from *Rickettsiales* genomes, *Alphaproteobacteria*, and outgroup
4. Phylogeny-based identification of main MAG clades, and 2nd filtering by phylogenetic relatedness
5. Phylogeny-based tests for the affiliation of each MAG clade to *Rickettsiales*
6. Creation of the final dataset composed by *Rickettsiales* genomes, confirmed *Rickettsiales* MAGs, other *Alphaproteobacteria,* and outgroup organisms, including newly available assemblies (July 2021)

7. Phylogenomic analyses on the final dataset to reconstruct the inner relationships among *Rickettsiales*

Step 1: Collection of the initial dataset including *Rickettsiales* genomes, putative *Rickettsiales* MAGs, other *Alphaproteobacteria* and outgroup organisms (February 2021)

The sequences of other 89 representative non-*Rickettsiales Alphaproteobacteria* (including *Magnetococcia sensu* Parks et al. 2018 [41]) as well as 8 *Gammaproteobacteria* and *Betaproteobacteria* as outgroup were downloaded, taking inspiration from the selection by Muñoz-Gómez and co-authors [42].

All assemblies assigned by NCBI taxid to *Rickettsiales* (as of February 2021) were downloaded in the latest version, excluding anomalous assemblies. This set was manually edited to remove "*Ca*. Hepatobacter penaei" (GCA_000742475.1), actually belonging to *Holosporales*, and conversely to add the endosymbiont of *Acanthamoeba* UWC8 [43], which, though labelled as member of *Holosporales*, is actually a close relative of the "*Ca*. Midichloriaceae" bacterium "*Ca*. Jidaibacter acanthamoeba" UWC36 [44], thus ending up with 1679 assemblies. Out of those, 1164 were obtained in a large-scale study screening *Wolbachia* sequences from host genome sequencing projects [45]. We considered those *Wolbachia* assemblies as phylogenetically redundant for the divergence scale of the present phylogenomic dataset, and thus they were excluded from our analyses. The other assemblies were inspected in detail, and 401 of them, which were found to be derived from genome sequencing studies (in particular, though not exclusively, those labelled as described species or described genera), were treated as "*Rickettsiales* genome assemblies", while the other 114 were treated as "putative *Rickettsiales* MAGs". A manual selection was applied to the 401 "*Rickettsiales* genome assemblies", to obtain a set accounting for at least one representative for

each described genus, and in few cases (highly represented/diversified genera, e.g. *Rickettsia*, *Wolbachia*) more than one, resulting in 35 "selected *Rickettsiales* genomes".

Step 2: Expansion of the set of putative *Rickettsiales* MAGs and 1st filtering by assembly quality

The set of "putative *Rickettsiales* MAGs" was expanded in two ways. On one side, aiming to account for other deep-branching alphaproteobacterial MAGs (which might be potentially related to *Rickettsiales*), those identified in a previous study [46], i.e. "MarineAlpha", were downloaded. On the other side, in order to collect other potentially overlooked (e.g. due to mislabelling) lineages related to *Rickettsiales* or to "MarineAlpha", the respective taxonomy of all previously identified assemblies was collected from gtdb r95 [47], and all other additional MAGs belonging to the same lineages (as well as closely related lineages forming monophyletic clades in the gtdb reference tree) were downloaded as well and added up to the previously selected ones, ending up with 294 total "extended putative *Rickettsiales* MAGs". The quality of the extended MAG set was assessed with BUSCO 5.0.0 [48] with a search on 219 proteobacterial orthologs ("proteobacteria_odb10") (Supplementary Data 2). Based on a comparison with the "selected *Rickettsiales* genomes", MAGs were retained only if having ≥50% single-copy orthologs and <5% duplicated orthologs, thereby discarding potentially poor quality/contaminated assemblies, obtaining 219 "BUSCO-filtered putative *Rickettsiales* MAGs".

Step 3: Selection of orthologs for phylogenomics from *Rickettsiales* genomes, *Alphaproteobacteria*, and outgroup

For all "non-MAG genomes", whenever available, protein sequences were taken directly from the NCBI annotation included in the assembly. In all other cases, i.e. non-annotated genomes (including newly obtained ones) and MAGs, genome sequences were annotated with Prokka 1.10 [35].

For all assemblies (including *Rickettsiales* genomes downloaded from NCBI and newly sequenced ones, MAGs, *Alphaproteobacteria* and outgroup) the eggNOG v5 assignments [49] were then predicted on the annotated proteins with eggnog-mapper 2.0.6 [50] with a taxonomic scope on *Alphaproteobacteria* (options: --tax_scope 28211 --go_evidence non-electronic --target_orthologs all --seed_ortholog_evalue 0.001 --seed_ortholog_score 60 --query_cover 20 --subject_cover 50). Taking into account all assemblies except MAGs, proteins were grouped based on the assigned orthogroup, and each resulting orthogroup was aligned with MAFFT 7.475 L-INS-i [51] and trimmed with BMGE 1.12 [52] with BLOSUM30 matrix. Single gene phylogenies were then performed with FastTree 2.1 [53], and individually examined to remove paralogs and short/poorly aligned sequences. After this "polishing" step, orthogroups were kept only if present in single copy in at least 85% of the genomes of the "*Rickettsiales* genome set for phylogeny" (which, taking together "selected *Rickettsiales* genomes" and newly sequenced genomes, totals 44 organisms), in at least 85% of other *Alphaproteobacteria*, and in at least 50% of outgroup. Thus, by this procedure 179 orthogroups were selected, which were employed for all following phylogenetic analyses (Supplementary Data 5).

Step 4: Phylogeny-based identification of main MAG clades, and 2nd filtering of MAGs by phylogenetic relatedness

The genes assigned to the 179 selected orthogroups in the "BUSCO-filtered putative *Rickettsiales* MAGs" were added to those of the previous selection of organisms, each orthogroup was re-aligned and trimmed with MAFFT and BMGE, and single-gene phylogenies were inferred as described above. Each tree was manually inspected, for removing paralogs and short/poorly aligned sequences derived from the MAGs, ending up with the final sequence selection for those MAGs (Supplementary Data 5). By this procedures 8 MAG were found to harbour <10

alphaproteobacterial orthogroups. Via online blastp searches on NCBI nr, it was found that (a significant part of) their proteome had much higher identities with non-alphaproteobacterial sequences, and were thus deemed as taxonomically mislabelled and removed from successive analyses, leaving 211 "BUSCO+eggNOG-filtered putative *Rickettsiales* MAGs" (Supplementary Data 5).

Then, a first phylogenomic tree was inferred, with the aim to get a general view on the phylogenetic diversity of included MAGs, and on their relationships with *Rickettsiales* and other *Alphaproteobacteria*. Thus, the 179 orthogroup sequences of all the "BUSCO+eggNOG-filtered putative *Rickettsiales* MAGs" were used, together with a "Genome assembly set for MAG classification", namely the other *Alphaproteobacteria*, outgroup organisms and, to speed up phylogenetic computations, a small and phylogenetically-balanced selection of 13 *Rickettsiales* genome assemblies ("*Ca*. Deianiraea vastatrix" for "*Ca*. Deianiraeaceae" and 4 for each other family). Each orthogroup was *de novo* aligned with MAFFT, and trimmed with BMGE, as described above, and all orthogroups were concatenated using AMAS [54]. Then, in order to avoid artefacts due to compositional heterogeneity in the datasets (in particular potential "erroneous" phylogenetic proximity of MAG lineages to "core" *Rickettsiales* due GC/AT biases in the respective genomes), the approach by Muñoz-Gómez and co-authors [42] was applied, and the concatenated alignment was trimmed removing 10%, 20%, 30%, 40% or 50% of most heterogeneous sites. For each of these six alignments (the original and the five trimmed ones), maximum likelihood phylogenetic trees were inferred with IQ-TREE 1.6.12 [55] employing ModelFinder [56] for model selection, performing 1000 ultrafast bootstraps [57] and SH-aLRT with 1000 replicates.

In all the resulting trees, 35 MAGs were found consistently branching within "core" *Rickettsiales* with full support, and thus were directly treated as "confirmed *Rickettsiales* MAGs" (Supplementary Figure 29). Other 2 MAGs were found consistently branching with high support within other alphaproteobacterial lineages (respectively, *Holosporales* and *Rhodospirillales*), and

thus were considered as non-*Rickettsiales* and directly discarded. The other 174 MAGs were grouped into 13 groups (named A,B,C,D,E,F,G,H,I,J,K,L,M), based on monophyly observed across the obtained trees, with the aim to verify the position of each group with a dedicated phylogenomic dataset (see below, Step 5). Moreover, in order to speed up all the following analyses, phylogenetically-redundant MAGs (both within the 13 groups and within the already "confirmed *Rickettsiales* MAGs") were removed as follows. Clusters of MAGs were defined based on supported monophyly and reciprocal AAI (Average Amino acid Identity) >0.85 [58]; Supplementary Figure 30), and for each cluster only the single MAG with best BUSCO scores (in terms of higher single-copy orthologs, or, secondarily, lower duplicated orthologs) (Supplementary Data 2) was kept, thus resulting in 21 "confirmed *Rickettsiales* MAGs" and collectively 106 MAGs in the 13 groups.

Step 5: Phylogeny-based tests for the affiliation of each MAG clade to *Rickettsiales*

The MAGs belonging to each of the 13 previously identified groups were tested separately for the potential relatedness to "core" *Rickettsiales*, with a separate dataset. This was done in order to remove phylogenetic "noise" and potential artefacts caused by the contemporary addition of multiple deep-branching and fast-evolving lineages, and to get the "cleanest" phylogenetic position for the members of each group (such an approach has been previously utilized for similar problematic datasets, e.g. [59]). Accordingly, for each group, the 179 ortholog sequences of the respective organisms were *de novo* aligned with those of the "Genome assembly set for MAG classification" using MAFFT, trimmed with BMGE, and all ortholgs were concatenated with AMAS, as described above. Each concatenated alignment was trimmed removing 10%, 20%, 30%, 40% or 50% of most heterogeneous sites, as described above. For each resulting alignment,

maximum likelihood phylogeny was inferred with IQ-TREE and the LG+C60+F+R6 model, performing 1000 ultrafast bootstraps and SH-aLRT with 1000 replicates (Supplementary Figure 31). All the resulting trees were inspected, allowing the classification of 14 MAGs belonging to groups F, G, and H as additional, deep-branching "confirmed *Rickettsiales* MAGs", based on strongly supported monophyly with "core" *Rickettsiales* on the original concatenated alignment and on all the five alignments with removal of heterogeneous sites. On the other side, none of the MAGs from the other 10 groups was found as monophyletic with *Rickettsiales* with high support in the respective trees, and were thus deemed as non-*Rickettsiales*, and not considered for the following analyses.

Step 6: Creation of the final dataset composed by *Rickettsiales* genomes, confirmed *Rickettsiales* MAGs, other *Alphaproteobacteria*, and outgroup organisms, including newly available assemblies (July 2021)

Then, the assembly and MAG selection was updated according to the latest NCBI version (July 2021), employing the same selection criteria as described above. Namely, the newly published genome of "*Ca*. Echinorickettsia raffii" [60] was directly added to the "*Rickettsiales* genome set for phylogeny", while 100 "new putative *Rickettsiales* MAGs" were processed as described above and 95 of them passed the BUSCO-based filtering by assembly quality (Supplementary Data 2). In order to test the evolutionary relatedness of these novel MAGs to *Rickettsiales*, similarly to what described above, after assignment of their genes to the 179 orthogroups, the respective sequences were newly aligned together with those of the "Genome assembly set for MAG classification" and of the previously identified deep-branching *Rickettiales* lineages (now treated as ascertained *Rickettsiales*, similarly to the "core" lineages). Aligned genes were trimmed and concatenated, and the concatenated alignment was trimmed to remove more compositionally heterogeneous sites, as

described above. For each resulting concatenated alignment, maximum-likelihood phylogeny was inferred with IQ-TREE employing ModelFinder for model selection, as described above (Supplementary Figure 32). In all the resulting trees, 77 MAGs were found consistently branching within "core" or "deep-branching" *Rickettsiales* with full support, and thus were directly added to the previously identified "confirmed *Rickettsiales* MAGs". The other 18 MAGs were found consistently and with high support branching within other alphaproteobacterial lineages (respectively, 1 *Sphingomonadales*, 2 *Rhizobiales*, and 15 *Holosporales*), and thus were considered as non-*Rickettsiales* and discarded. No MAG fell outside previously identified lineages, so no additional phylogeny-based test was required.

In order to remove phylogenetically redundant genomes, among all "confirmed *Rickettsiales* MAGs", including those derived from the July 2021, updated clusters were again defined based on monophyly and reciprocal AAI >0.85 (Supplementary Figure 30) As described above, for each cluster just the MAG with the best BUSCO scores was kept (Supplementary Data 2).

Moreover, few MAGs were found to be closely related to some representatives "*Rickettsiales* genome set for phylogeny". Thus, based on the monophyly and AAI criteria described above, among those the additional "phylogenetically-redundant" MAGs were removed (Supplementary Figure 30).

Therefore, the final "*Rickettsiales* selection for phylogeny" comprised 45 genome assemblies and 68 MAGs, and, together with the 89 other representative *Alphaproteobacteria* and 8 outgroup organisms, formed the "final species selection for phylogeny" (210 total organisms).

Step 7: Phylogenomic analyses on the final dataset to reconstruct the inner relationships among *Rickettsiales*

The gene sequences of the 179 orthogroups for the 210 taxa of the final "*Rickettsiales* selection for phylogeny" were aligned, trimmed, and concatenated as described above. The phylogeny on this final dataset was aimed to reconstruct accurately the inner relationships among core and deep-branching *Rickettsiales* organisms, and at the same time, the relationship of *Rickettsiales* with other *Alphaproteobacteria*, building up the basis for the following gene-content analyses.

Accordingly, we inferred phylogenies on the full "untreated" alignment, as well as after removing 10%, 20%, 30%, 40% or 50% of most heterogeneous sites as described above, with IQ-TREE and the same options as above (LG+C60+F+R6 model, 1000 ultrafast bootstraps and SH-aLRT with 1000 replicates) (Fig. 1; Supplementary Figure 18).

Supplementary Note 5: gene content analyses

Annotation

The newly obtained genomes were all annotated with Prokka 1.10 [35], using the --rfam option. Afterwards, annotation of the genomes of ciliate symbionts was manually curated by a detailed inspection of blastp hits on NCBI nr and on *Rickettsiales* proteins as described previously [2].

Creation of a set of "homology groups" for gene content comparisons

In order to perform gene content comparisons and reconstruct its variation along the inferred species tree, a set of "homology groups" was obtained for the 210 total organisms in the final phylogeny, starting from the previously obtained eggNOGs (see Supplementary Note 4).

The eggNOG [49] database is organised by taxonomy, namely a dedicated set of eggNOG is identified for each lineage from the domain to the order/family level (domain, phylum, class, order, family), and eggNOGs are hierarchically linked. For example 2TSRZ@28211 (DNA sliding clamp in *Alphaproteobacteria* – NCBI taxid 28211) is linked to corresponding eggNOGs in higher taxonomic ranks, such as 1MVD9@1224 (same function in *Proteobacteria* – NCBI taxid 1224) and COG0592@2 (same function in *Bacteria* – NCBI taxid 2). Such hierarchical organisation allows to take advantage of lineage-specific annotations, such as labelling of lineage-specific paralogs, and at the same time gives the possibility to compare eggNOGs identified in different lineages.

In this work, we aimed to obtained "clustered" homology groups of homologous genes, to be inspected and analysed later (see below) for their evolutionary history across *Rickettsiales*, including potential duplication, loss and transfer events, leading to paralogies as well as xenologies,

For the dataset of this study, the raw eggNOG assignments were not directly suitable for the intended approach. First, we considered that any pre-computed orthologs, tailored on already described organisms and sublineages, are inherently not fully suitable to discriminate ortholog/paralog (or xenolog) on novel lineages such as the multiple ones herein treated.. Some eggNOG assignments may also be "impractical" under the desired perspective of homologous groups described above. Extreme observed examples are thaose of some ribosomal protein genes in "*Candidatus* Aquarickettsia rohweri" [61], namely S10 (RST68169.1), L3 (RST68170.1), L10 (RST68925.1), L14 (RST68179.1), L24 (RST68180.1), which have their best hits in eggNOGs assigned to lineages as distant as Metazoa (3C1KH@33208, 3BT1X@33208, 3C01C@33208), *Acyclobacillaceae* (*Firmicutes*) (278I9@186823), and *Sphingomonadales* (2K3XB@204457). While these results might be seen as suggestive of horizontal gene transfer, multiple other reasons are plausible, and it is not possible to discriminate among those a priori, For example, there could be a mis-assignment as a consequence of the high sequence evolution rates in *Rickettsiales*, which may result in extremely high sequence divergence with respect to any other organism (including other *Rickettsiales*), so that hits can be almost equivalently distant from closely related and unrelated lineages [2], even for housekeeping genes. Alternatively, taxonomically mislabelled reference sequences in the eggNOG database could mislead the assignment as well. Contamination of the *Rickettsiales* assemblies is in principle another possibility, which seems overall rather unlikely/rare, as we included in our dataset only closed high-quality genomes, or quality-filtered MAGs. Therefore, aiming at reconstructing the largest "meaningful" homology groups starting from eggNOG assignments, and at the same time retaining as much lineage specific information as possible from the eggNOG database, we designed the following two-step "telescopic" approach, taking advantage of the hierarchical structure of the eggNOG database:

- We started from the eggNOG taxonomic path leading to *Rickettsiales* (root; *Bacteria*; *Proteobacteria*; *Alphaproteobacteria*; *Rickettsiales*), and we considered the "eggNOG OGs"

matches for each gene. When a gene was assigned to an eggNOG belonging to a taxon outside such path, it was moved "upwards" to the respectively proximate higher rank. Such passage was applied recursively until a taxon along the *Rickettsiales* path was met. This allowed also the "connection" of eggNOGs in the non-*Rickettsiales* organisms of the dataset. For example, if a gene was assigned to the 2JQAW@204441 eggNOG (DNA clamp in *Rhodospirillales* – NCBI taxid 204441), it was labelled as the corresponding alphaproteobacterial eggNOG 2TSRZ@28211

- The second step was intended to "connect" the information between different eggNOGs, Namely, whenever appropriate,taxonomically-linked eggNOGs were joined at the respectively highest taxonomic rank. In detail, for each eggNOGs assigned at the "root" level after the previous step, all genes assigned to eggNOGs of lower taxonomic ranks (*Bacteria*; *Proteobacteria*; *Alphaproteobacteria*; *Rickettsiales*) that were linked by the eggNOG hierarchy to the given root eggNOG were moved "upwards" to such root eggNOG. For example, if a gene was assigned to the root DNA clamp COG0592@1, any other gene assigned to the linked 2TSRZ@28211 (*Alphaproteobacteria*) or 1MVD9@1224 (*Proteobacteria*) was moved "upwards" to the COG0592@1. This passage was performed progressively for remaining eggNOGs of lower ranks. It was thus possible to "merge" genes into the desired larger and meaningful "homology groups", while still keeping as much as possible lineage-specific refined annotation.

Applying such "telescopic" approach, a total of 444,226 genes were assigned to 20,041 "homology groups". Only 4009 of such "homology groups" were present in at least one member of *Rickettsiales* ("core" or "deep-branching"), and only 2990 of those were present in 4 or more organisms of the total dataset, and were thus considered for following gene content and phylogenetic analyses.

We thus carefully manually inspected the presence/absence and copy numbers of "homology groups" in the *Rickettsiales*, in comparison with the other *Alphaproteobacteria*, to get a comprehensive overview of their functional repertoire. This allowed us to get some preliminary evolutionary insight, and select traits and functions for further in-depth and more refined analyses, as described in the following sections.

Phylogenetic analyses on biosynthetic pathways for amino acids and nucleotides

We aimed at phylogenetic inferences for the genes involved biosynthetic pathways for amino acids and nucleotides. To this purpose, reference biosynthetic pathways were obtained from the Biocyc database [62]. In order to get more robust and reliable phylogenetic inferences, we aimed to concatenate together sequences of the proteins involved in the same pathway, thus obtaining more phylogenetically informative datasets. For the same purpose, pathways sharing common reactions (e.g. purines, pyrimidines, branched-chain amino acids, aromatic amino acids) were considered together (Supplementary Data 6). Under similar assumptions, single (or two) gene pathways, namely those for glycine, aspartate, asparagine, glutamate, glutamine, and alanine, were not considered phylogenetically informative enough, and were thus not employed in the analyses.

For each gene involved in a chosen pathway performed a blastp search with the selected Biocyc reference sequence as query against the protein sequences from all the 210 selected taxa as database, and manually inspecting the results, in order to selected the corresponding "homology groups". Then, the composition of each group was manually refined, by visual inspection of the respective alignment and of a maximum-likelihood tree obtained with IQ-TREE 1.6.12 [55] employing ModelFinder [56] for model selection, and performing 1000 ultrafast bootstraps [57] and SH-aLRT with 1000 replicates. In particular, short and/or poorly aligned sequences and distant

paralogs were manually removed, especially among non-*Rickettsiales* organisms, and, in some cases (e.g. biosynthetic genes for histidine) single domains from alternative fusions of multi-domain proteins were selected and analysed separately. NCBI conserved domain search [63] was also used to identify such distant paralogs, based on distinct domain annotation. Each manually refined orthogroup was then re-aligned with MAFFT 7.475 L-INS-i and trimmed with BMGE 1.12 with the BLOSUM30 matrix. Phylogeny on each single manually refined was performed as above (Supplementary Figure 25).

Then, based on inspection of such "final" single-gene phylogenies, suspected non-orthologs were removed, and orthogroups belonging to the same pathway (or same group of related pathways) were concatenated together using AMAS [54].

Then, in order to account for compositional heterogeneity (see Supplementary Note 4), each of the concatenated alignments was processed for removing 10%, 20%, 30%, 40% or 50% of the most compositionally heterogeneous sites, following the approach by Muñoz-Gómez and co-authors (2019). On each resulting alignment, phylogeny was inferred with IQ-TREE and the LG+C60+F+R6 model, performing 1000 ultrafast bootstraps and SH-aLRT with 1000 replicates (Supplementary Figure 26).

Identification of amino acid transporters

Amino acids transporters were identified from the TCDB database [64]. The transporter families in TCDB were queried by keywords such as "amino acid(s)" and the name of each of the twenty proteinogenic amino acids. The single database entries (i.e. proteins) belonging to each member of the retrieved families were individually examined, in particular information on the kind of substrate (if known) were collected, and those members with ascertained substrate(s) that did not include

amino acids were discarded, ending up with a list of trusted and substrate-labelled entries of putative amino acid transporters from the TCDB database. We then performed a blastp search with all the *Rickettsiales* proteins of our dataset as queries against the full TCDB. Then, for each *Rickettsiales* genome, only the proteins having a best significant hit (e-value threshold of 1e-5) on each trusted entry were selected, and counted (Supplementary Figure 28).

Identification and phylogenetic analysis of the tlc nucleotide translocasaes

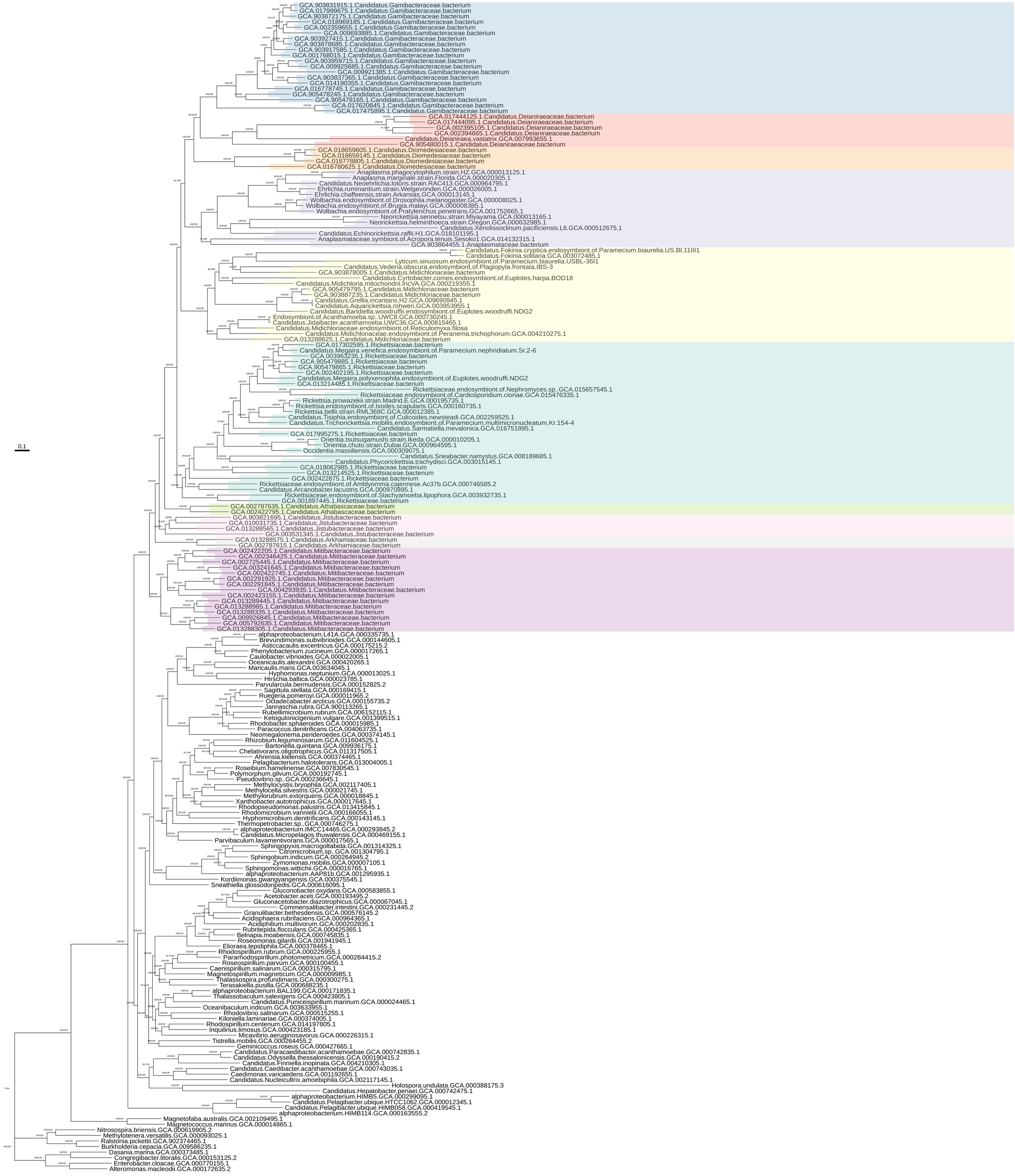
Analyses on nucleotide transporters were focused on the tlc nucleotide translocase transporters, common in *Rickettsiales* and in other host-associated lineages [65]. Starting from the eggNOG classification, a blastp-based inspection using the protein sequences from the paper by Major and co-authors [65] as queries led to the identification of the corresponding homology group assigned to tlc translocases (COG3202@1), which allowed to count the number of genes present for each organism of our dataset. Then, the phylogenetic dataset of tlc translocases by Major and co-authors (2017) was downloaded. Considering the large size of this dataset, a subset was selected, corresponding to a clade of sequences consisting only of the nucleotide transport protein domain and belonging to multiple bacteria (including *Chlamydiae* and several *Proteobacteria* such as *Rickettsiales* and *Holosporales*), as well as to eukaryotes such as Microsporidia, Stramenopiles, and Viridiplantae. The selected sequences from the published dataset and those identified in our dataset (COG3202@1) were all aligned together with MAFFT 7.475 L-INS-i and trimmed with BMGE 1.12 with the BLOSUM30 matrix, and phylogeny was inferred as in [65], namely with IQ-TREE with the LG+C60 model, performing 1000 ultrafast bootstraps and SH-aLRT with 1000 replicates (Supplementary Figure 27).

Identification of genes involved in the interaction with host cells

For getting information on the presence and multiplicity of genes involved in multiple features of the interaction of *Rickettsiales* with host cells, such as secretion systems, putative toxins and other secreted effectors, flagella, adhesion and invasion molecules, the VFDB core reference database was employed [66] (downloaded on 6th May 2022). The VFDB is organised in order to have a separate focus on single pathogens, which implies a significant redundancy of entries of orthologous genes (e.g. flagellar genes) identified in each pathogen. This organisation would not be suitable for the analyses of our large dataset composed almost exclusively by non-model bacteria. Therefore, orthologs were identified within the database with the following approach. Sequences were divided by organism (i.e. single strain) and by VFC (VF Classes). Then, within each selected VFC ("Adherence", "Biofilm", "Effector delivery system", "Exotoxin", "Exoenzyme", "Invasion", "Motility") orthogroups were identified with OrthoFinder 2.5.4 [67], employing blastp as sequence search program. The composition of orthogroups produced by OrthoFinder was then manually inspected and curated. Then, all proteins of our dataset of *Rickettsiales* were employed as queries in a blastp search against the full VFDB core database. Similarly to the previous TCDB blastp search, the whole VFDB set of sequences was employed as database in order to minimise both false negatives and false positive hits. Then, for each *Rickettsiales* genome, proteins were "assigned" to each curated orthogroup as follows: a protein was counted if displaying a significant (evalue 1e-5) best hit on any sequence belonging to the orthogroup, and the total number of proteins having such hits were summed over each orthogroup (Supplementary Figure 20, 21, 22, 23).

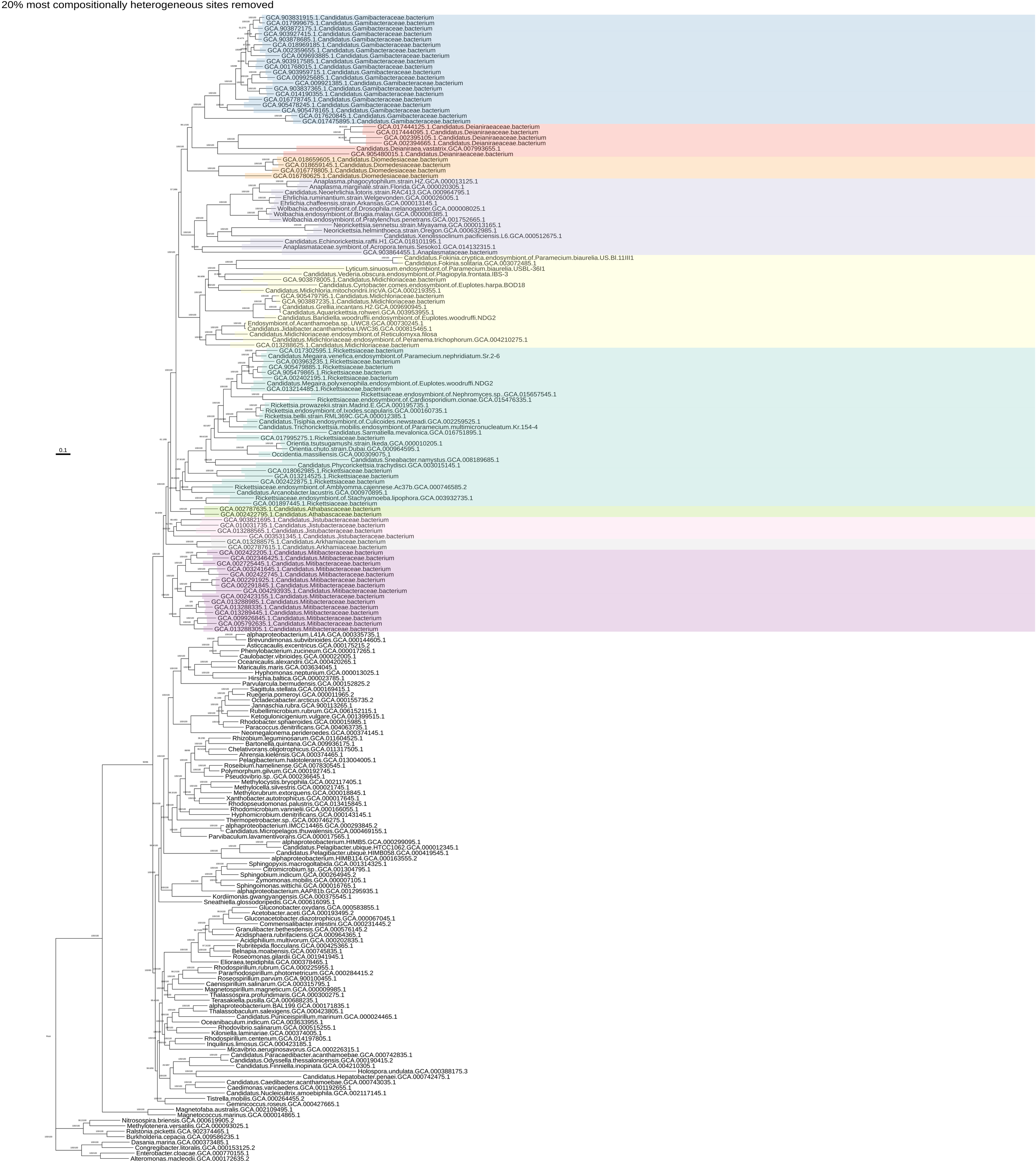
Supplementary Figure 18: phylogenomic trees of the final dataset. These include the "untreated" and the "compositionally trimmed" alignments (namely, with the 10%, 20%, 30%, 40%, or 50% most compositionally heterogeneous sites removed). On each branch, support values by SH-aLRT with 1000 replicates and by 1000 ultrafast bootstraps are reported.

original alignment



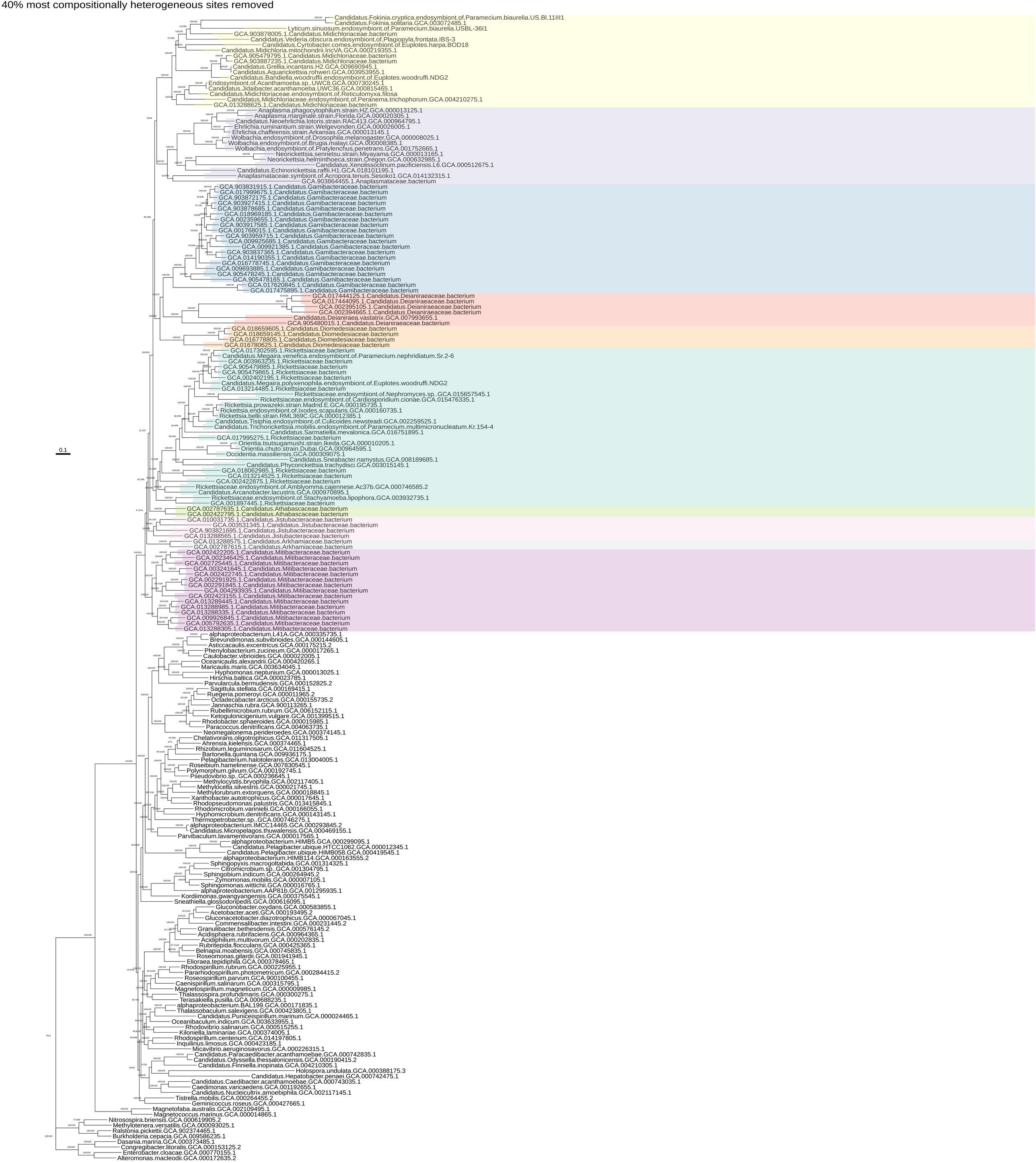
10% most compositionally heterogeneous sites removed

20% most compositionally heterogeneous sites removed



30% most compositionally heterogeneous sites removed

40% most compositionally heterogeneous sites removed



50% most compositionally heterogeneous sites removed

Supplementary Figure 19: copy numbers of "homology groups" in the analysed *Rickettsiales*.

Each column represents total values, or subdivided by functional category.

	Total	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	S	T	U	V	W	Z
Candidatus_Midichloria_mitochondrii_IricVA_GCA_000219355.1	706	0	0	69	19	34	25	26	40	25	122	23	68	59	27	38	23	4	36	12	38	10	0	0
Candidatus_Cyrtobacter_comes_endosymbiont_of_Euplotes_harpa_BOD18	681	0	0	61	21	32	26	19	33	28	119	34	71	40	24	34	21	3	34	9	42	11	0	0
Lyticum_sinuosum_endosymbiont_of_Paramecium_biaurelia_USBL-36I1	554	0	0	44	17	26	25	19	33	27	113	16	38	46	26	30	13	5	22	9	40	8	0	0
Candidatus_Fokinia_solitaria_GCA_003072485.1	518	0	0	49	13	16	25	19	27	27	112	18	57	29	6	25	16	4	22	10	35	9	0	0
Candidatus_Fokinia_cryptica_endosymbiont_of_Paramecium_biaurelia_US_BI_11III1	514	0	0	49	15	16	26	20	28	28	112	17	51	31	6	26	15	3	20	10	34	9	0	0
GCA_903878005.1_Candidatus_Midichloriaceae_bacterium	738	0	0	60	19	49	25	26	47	28	106	34	66	53	31	36	21	8	48	27	35	17	0	0
Candidatus_Vederia_obscura_endosymbiont_of_Plagiopyla_frontata_IBS-3	566	0	0	26	23	27	24	18	17	29	112	17	50	53	29	28	10	5	27	6	41	11	0	0
Candidatus_Bandiella_woodruffii_endosymbiont_of_Euplotes_woodruffi_NDG2	969	0	0	67	27	33	29	19	40	26	128	26	264	59	5	37	22	4	38	12	32	9	0	0
GCA_905479795.1_Candidatus_Midichloriaceae_bacterium	769	0	0	67	19	37	30	28	40	21	117	30	75	64	28	41	27	11	54	13	39	12	0	0
GCA_903887235.1_Candidatus_Midichloriaceae_bacterium	959	0	0	73	30	48	33	30	51	28	127	41	119	64	34	50	29	11	66	20	52	17	0	0
Candidatus_Grellia_incantans_H2_GCA_009690945.1	982	0	0	75	34	61	33	30	63	27	131	35	113	62	33	54	35	11	77	18	50	20	0	0
Candidatus_Aquarickettsia_rohweri_GCA_003953955.1	884	0	0	72	20	44	30	29	53	26	132	33	82	63	29	48	26	8	54	19	44	15	0	0
Candidatus_Jidaibacter_acanthamoeba_UWC36_GCA_000815465.1	1145	0	0	76	30	54	28	34	47	33	138	62	122	92	44	48	29	12	121	26	73	22	0	0
Endosymbiont_of_Acanthamoeba_sp._UWC8_GCA_000730245.1	1033	0	0	78	26	49	33	34	50	36	139	42	88	89	44	53	26	7	113	27	60	18	0	0
Candidatus_Midichloriaceae_endosymbiont_of_Reticulomyxa_filosa	897	0	0	73	31	44	28	29	38	35	134	32	110	85	11	43	37	7	58	18	42	22	0	0
Candidatus_Midichloriaceae_endosymbiont_of_Peranema_trichophorum_GCA_004210275.1	766	0	0	31	23	55	25	18	37	30	128	22	85	80	9	33	18	8	58	17	52	9	0	0
GCA_013288625.1_Candidatus_Midichloriaceae_bacterium	784	0	0	50	28	44	27	32	32	27	87	42	56	97	11	41	37	10	70	18	44	29	0	0
Anaplasma_phagocytophilum_strain_HZ_GCA_000013125.1	737	0	0	80	22	25	47	27	63	26	137	24	71	18	7	47	35	6	38	11	41	4	0	0
Anaplasma_marginale_strain_Florida_GCA_000020305.1	718	0	0	73	21	34	42	26	58	27	126	21	63	30	6	45	33	6	42	11	40	4	0	0
Candidatus_Neoehrlichia_lotoris_strain_RAC413_GCA_000964795.1	711	0	0	70	21	36	41	25	55	27	123	23	63	33	6	43	33	7	42	9	38	4	0	0
Ehrlichia_ruminantium_strain_Welgevonden_GCA_000026005.1	685	0	0	70	17	37	40	24	54	26	123	23	65	18	5	43	34	7	39	9	36	4	0	0
Ehrlichia_chaffeensis_strain_Arkansas_GCA_000013145.1	707	0	0	71	17	38	43	24	56	27	127	22	69	18	6	47	35	7	39	9	37	4	0	0
Wolbachia_endosymbiont_of_Brugia_malayi_GCA_000008385.1	632	0	0	68	20	29	42	20	33	26	120	14	61	31	4	37	32	7	26	7	36	5	0	0
Wolbachia_endosymbiont_of_Drosophila_melanogaster_GCA_000008025.1	814	0	0	76	27	32	44	24	40	27	121	31	98	55	8	46	35	8	57	11	40	9	0	0
Wolbachia_endosymbiont_of_Pratylenchus_penetrans_GCA_001752665.1	610	0	0	66	18	33	38	19	31	27	113	14	59	28	6	39	31	7	29	5	36	7	0	0
Neorickettsia_sennetsu_strain_Miyayama_GCA_000013165.1	620	0	0	67	12	23	39	21	51	25	119	21	54	23	5	37	28	5	28	9	39	5	0	0
Neorickettsia_helminthoeca_strain_Oregon_GCA_000632985.1	623	0	0	67	15	28	41	22	53	25	113	20	49	32	4	35	28	4	27	9	40	5	0	0
Candidatus_Xenolissoclinum_pacificiensis_L6_GCA_000512675.1	525	0	0	54	14	16	32	18	29	25	91	15	54	28	22	27	24	4	21	5	35	9	0	0
Candidatus_Echinorickettsia_raffii_H1_GCA_018101195.1	743	0	0	71	20	43	45	24	53	24	122	24	64	41	23	42	41	6	42	8	41	7	0	0
Anaplasmataceae_symbiont_of_Acropora_tenuis_Sesoko1_GCA_014132315.1	593	0	0	57	12	31	37	22	32	27	107	17	58	18	8	36	29	2	42	13	36	8	0	0
GCA_903864455.1_Anaplasmataceae_bacterium	580	0	0	61	15	33	37	19	43	26	101	17	52	35	4	35	22	4	23	7	35	15	0	0
Candidatus_Deianiraea_vastatrix_GCA_007993655.1	704	0	0	64	17	76	24	24	39	28	110	23	75	70	5	28	17	4	32	9	34	21	0	0
GCA_017444125.1_Candidatus_Deianiraeaceae_bacterium	462	0	0	26	12	35	18	9	13	23	108	20	47	46	6	18	14	4	18	6	29	6	0	0
GCA_017444095.1_Candidatus_Deianiraeaceae_bacterium	467	1	0	24	14	31	19	4	17	19	113	19	61	29	7	22	10	4	20	6	31	11	0	0
GCA_002395105.1_Candidatus_Deianiraeaceae_bacterium	402	0	0	22	10	21	13	5	13	19	103	15	49	35	7	20	7	3	21	5	26	6	0	0
GCA_002394665.1_Candidatus_Deianiraeaceae_bacterium	528	1	0	28	13	58	23	11	12	23	114	20	55	48	8	23	9	4	27	9	33	10	0	0
GCA_905480015.1_Candidatus_Deianiraeaceae_bacterium	754	0	0	69	15	88	46	21	59	28	105	16	82	60	11	29	23	3	42	8	37	16	0	0
GCA_018969185.1_Candidatus_Gamibacteraceae_bacterium	1037	0	0	70	24	106	46	33	66	38	134	34	107	82	9	54	50	6	71	18	50	27	0	0
GCA_002359655.1_Candidatus_Gamibacteraceae_bacterium	1214	1	0	80	29	115	55	40	71	39	141	38	135	87	10	61	57	10	121	28	56	27	0	0
GCA_009693885.1_Candidatus_Gamibacteraceae_bacterium	603	0	0	51	14	72	32	14	41	24	88	17	43	40	10	28	38	7	34	9	40	5	0	0
GCA_903872175.1_Candidatus_Gamibacteraceae_bacterium	1280	0	0	90	32	115	59	49	78	39	144	41	148	92	13	63	61	9	129	22	63	39	0	0
GCA_903831915.1_Candidatus_Gamibacteraceae_bacterium	1109	0	0	87	28	115	53	33	75	38	143	42	99	83	11	62	60	8	77	21	51	24	0	0
GCA_017999675.1_Candidatus_Gamibacteraceae_bacterium	1014	0	0	85	24	104	52	33	79	35	133	30	89	74	10	51	60	4	75	16	45	15	0	0
GCA_903927415.1_Candidatus_Gamibacteraceae_bacterium	1065	1	0	81	27	110	52	40	79	32	135	35	90	85	11	50	53	8	86	17	48	20	0	0
GCA_903878685.1_Candidatus_Gamibacteraceae_bacterium	1108	1	0	87	32	106	52	37	81	35	140	43	101	87	10	50	56	6	93	20	51	19	1	0
GCA_903917585.1_Candidatus_Gamibacteraceae_bacterium	950	2	0	76	22	103	49	31	67	29	130	24	77	74	10	50	48	7	60	19	43	26	0	0
GCA_001768015.1_Candidatus_Gamibacteraceae_bacterium	1029	0	0	85	30	110	49	30	78	34	138	34	93	76	9	55	57	5	58	13	46	25	0	0
GCA_903837365.1_Candidatus_Gamibacteraceae_bacterium	843	0	0	68	19	93	49	32	59	31	119	24	65	65	7	47	43	4	46	14	42	16	0	0
GCA_014190355.1_Candidatus_Gamibacteraceae_bacterium	975	1	0	75	23	110	53	33	72	34	137	26	80	76	9	50	51	5	62	13	48	19	0	0
GCA_903959715.1_Candidatus_Gamibacteraceae_bacterium	918	0	0	74	29	100	49	28	66	34	125	29	76	69	10	39	41	3	56	16	48	25	0	0
GCA_009925685.1_Candidatus_Gamibacteraceae_bacterium	933	0	0	75	22	108	49	33	68	36	125	30	82	72	10	44	50	5	50	14	43	14	0	0
GCA_009921385.1_Candidatus_Gamibacteraceae_bacterium	879	0	0	76	21	99	54	29	68	33	137	21	68	64	10	40	41	7	45	11	44	20	0	0
GCA_016778745.1_Candidatus_Gamibacteraceae_bacterium	829	0	0	69	16	83	41	29	61	33	125	20	76	66	10	42	47	6	45	13	38	15	0	0
GCA_905478245.1_Candidatus_Gamibacteraceae_bacterium	936	0	0	73	24	97	51	31	66	31	131	30	79	70	10	51	48	5	55	12	44	20	0	0
GCA_905478165.1_Candidatus_Gamibacteraceae_bacterium	852	0	0	72	21	98	49	32	66	32	129	22	75	77	9	46	36	5	41	7	40	13	0	0
GCA_017620845.1_Candidatus_Gamibacteraceae_bacterium	602	0	0	23	15	21	27	24	20	20	118	23	78	68	10	27	12	10	34	7	42	19	0	0
GCA_017475895.1_Candidatus_Gamibacteraceae_bacterium	587	1	0	32	11	23	25	20	21	22	122	22	71	61	9	27	8	10	35	8	39	18	0	0
GCA_016780625.1_Candidatus_Diomedesiaceae_bacterium	740	0	0	67	19	83	42	24	59	27	102	14	64	49	7	40	47	3	41	10	35	7	0	0
GCA_018659605.1_Candidatus_Diomedesiaceae_bacterium	851	1	0	69	19	97	44	26	61	29	116	28	71	63	10	38	48	4	54	19	43	14	0	0
GCA_018659145.1_Candidatus_Diomedesiaceae_bacterium	1067	1	0	80	29	112	49	39	76	35	132	35	93	80	12	53	54	9	74	24	50	25	0	0
GCA_016778805.1_Candidatus_Diomedesiaceae_bacterium	865	1	0	71	19	97	46	32	62	29	111	25	74	68	12	48	49	3	57	14	42	12	0	0
Rickettsia_prowazekii_strain_Madrid_E_GCA_000195735.1	733	1	0	79	25	29	23	18	28	29	130	21	65	63	5	42	32	5	58	13	45	11	0	0
Rickettsia_endosymbiont_of_Ixodes_scapularis_GCA_000160735.1	1187	1	0	78	31	45	25	23	38	22	126	53	200	88	4	42	41	10	159	28	54	22	0	0
Rickettsia_bellii_strain_RML369C_GCA_000012385.1	1074	1	0	85	29	43	24	31	34	31	138	51	120	97	10	44	44	8	134	25	58	35	0	0
Candidatus_Tisiphia_endosymbiont_of_Culicoides_newsteadi_GCA_002259525.1	907	0	0	76	29	29	20	25	34	24	132	54	95	86	3	45	37	9	79	28	51	25	0	0
Candidatus_Trichorickettsia_mobilis_endosymbiont_of_Paramecium_multimicronucleatum_Kr_154-4	1207	0	0	91	38	63	33	39	41	37	143	54	128	102	34	54	53	14	130	34	59	30	0	0
Candidatus_Megaira_polyxenophila_endosymbiont_of_Euplotes_woodruffi_NDG2	1206	1	0	86	40	53	23	33	34	34	142	77	166	105	11	56	52	17	124	41	66	28	0	0
GCA_017302595.1_Rickettsiaceae_bacterium	918	0	0	83	26	46	22	33	33	34	140	33	76	71	30	47	47	5	82	27	49	18	0	0
Candidatus_Megaira_venefica_endosymbiont_of_Paramecium_nephridiatum_Sr_2-6	1117	0	0	91	36	50	27	38	30	33	147	53	123	93	33	58	46	12	116	34	56	26	0	0
GCA_003963235.1_Rickettsiaceae_bacterium	809	0	0	71	23	43	16	33	28	25	121	31	92	67	26	43	32	6	67	25	43	13	0	0
GCA_905479885.1_Rickettsiaceae_bacterium	851	0	0	84	26	38	22	30	32	28	110	30	76	75	30	49	36	8	79	25	50	17	0	0
GCA_905479865.1_Rickettsiaceae_bacterium	871	0	0	81	31	43	19	30	34	26	133	31	87	71	6	49	37	6	76	23	52	21	0	0
GCA_002402195.1_Rickettsiaceae_bacterium	955	0	0	78	31	46	26	26	38	23	129	47	106	78	29	49	36	9	83	28	39	24	0	0
GCA_013214485.1_Rickettsiaceae_bacterium	1029	0	0	91	34	54	25	33	47	37	138	37	95	97	27	51	39	12	104	23	55	23	0	0
Rickettsiaceae_endosymbiont_of_Nephromyces_sp._GCA_015657545.1	588	0	0	66	20	34	15	11	17	23	117	22	61	33	24	38	21	5	31	5	39	6	0	0
Rickettsiaceae_endosymbiont_of_Cardiosporidium_cionae_GCA_015476335.1	702	0	0	72	28	38	18	17	20	26	119	22	67	49	26	45	29	7	51	12	47	7	0	3
Candidatus_Sarmatiella_mevalonica_GCA_016751895.1	688	0	0	48	24	27	18	14	26	32	123	19	81	48	23	29	23	4	34	13	44	15	0	0
GCA_017995275.1_Rickettsiaceae_bacterium	646	0	0	60	24	32	19	21	21	26	117	12	61	62	4	36	25	7	52	14	33	15	0	0
Orientia_tsutsugamushi_strain_Ikeda_GCA_000010205.1	1263	1	0	66	22	40	18	13	24	18	121	77	221	65	4	38	28	9	239	66	88	10	0	0
Orientia_chuto_strain_Dubai_GCA_000964595.1	651	1	0	64	22	27	17	13	20	18	125	29	69	31	4	39	28	7	65	15	55	7	0	0
Occidentia_massiliensis_GCA_000309075.1	840	0	0	86	27	56	24	27	34	25	132	28	86	77	6	50	32	5	63	17	48	17	0	0
Candidatus_Sneabacter_namystus_GCA_008189685.1	438	0	0	24	19	23	13	6	6	15	112	25	55	20	21	28	9	1	26	10	22	8	0	0
Candidatus_Phycorickettsia_trachydisci_GCA_003015145.1	737	0	0	60	26	41	22	20	19	30	128	25	85	68	6	34	26	9	42	8	47	22	0	0
GCA_018062985.1_Rickettsiaceae_bacterium	553	0	0	44	13	28	18	27	35	21	98	14	49	50	6	32	29	1	33	11	27	12	0	0
GCA_013214525.1_Rickettsiaceae_bacterium	805	1	0	35	21	56	35	31	36	28	130	28	91	78	5	33	32	8	58	17	49	25	0	0
GCA_002422875.1_Rickettsiaceae_bacterium	738	0	0	64	22	30	25	29	37	29	120	29	69	57	15	35	35	5	62	23	38	11	0	0
Rickettsiaceae_endosymbiont_of_Amblyomma_cajennese_Ac37b_GCA_000746585.2	1213	0	0	86	26	48	52	42	58	39	137	40	85	86	47	56	54	8	102	38	64	15	0	0
Candidatus_Arcanobacter_lacustris_GCA_000970895.1	530	0	0	30	20	22	12	18	17	23	73	25	55	34	31	23	18	4	37	23	26	8	0	0
Rickettsiaceae_endosymbiont_of_Stachyamoeba_lipophora_GCA_003932735.1	987	0	0	81	23	55	35	39	53	36	141	32	84	80	42	52	46	9	70	30	51	22	0	0
GCA_001897445.1_Rickettsiaceae_bacterium	1054	0	0	84	30	51	36	39	51	40	137	38	89	85	53	52	55	8	86	46	52	27	0	0
GCA_002787635.1_Candidatus_Athabascaceae_bacterium	1452	0	0	102	28	126	64	42	82	47	143	50	122	100	72	76	76	20	139	62	83	21	4	0
GCA_002422795.1_Candidatus_Athabascaceae_bacterium	1456	0	0	93	31	116	50	42	86	50	145	65	123	94	30	88	88	21	155	52	67	25	0	0
GCA_013288565.1_Candidatus_Jistubacteraceae_bacterium	955	0	1	63	22	98	31	29	62	41	101	35	65	91	39	64	51	19	70	25	40	11	0	0
GCA_903821695.1_Candidatus_Jistubacteraceae_bacterium	1443	0	0	101	32	116	60	47	85	48	139	52	123	111	61	74	88	17	163	46	62	23	0	0
GCA_010031735.1_Candidatus_Jistubacteraceae_bacterium	1414	0	0	95	25	123	55	40	91	45	143	48	116	109	70	87	78	22	139	59	65	23	0	0
GCA_003531345.1_Candidatus_Jistubacteraceae_bacterium	890	0	0	78	19	87	39	25	47	32	105	23	62	75	57	48	41	10	69	38	47	11	0	0
GCA_013288575.1_Candidatus_Arkhamiaceae_bacterium	662	0	0	55	14	65	32	20	44	28	78	24	52	54	34	39	22	6	51	20	27	11	0	1
GCA_002787615.1_Candidatus_Arkhamiaceae_bacterium	1027	0	0	83	18	91	45	33	71	35	115	28	75	76	52	52	49	15	94	39	62	7	0	0
GCA_013289445.1_Candidatus_Mitibacteraceae_bacterium	859	0	1	58	23	83	36	35	44	32	95	18	46	71	32	61	42	16	72	29	47	13	0	1
GCA_013288985.1_Candidatus_Mitibacteraceae_bacterium	845	1	0	65	17	76	41	25	43	33	94	23	53	56	32	50	47	15	77	33	47	11	0	0
GCA_013288335.1_Candidatus_Mitibacteraceae_bacterium	971	1	1	59	23	80	42	38	55	31	102	25	69	79	39	50	43	18	84	45	58	15	0	2
GCA_013288305.1_Candidatus_Mitibacteraceae_bacterium	752	0	0	65	20	60	25	18	48	31	91	28	40	54	40	34	41	9	54	32	35	9	0	0
GCA_009926845.1_Candidatus_Mitibacteraceae_bacterium	1273	0	0	96	30	113	47	36	77	46	138	49	86	89	62	68	68	11	128	53	63	15	0	0
GCA_005792635.1_Candidatus_Mitibacteraceae_bacterium	1442	0	0	90	35	117	55	48	99	48	142	77	105	87	77	68	68	13	133	60	73	15	0	0
GCA_003241645.1_Candidatus_Mitibacteraceae_bacterium	1380	0	0	91	33	119	57	42	77	49	139	45	108	100	52	82	73	19	142	49	79	24	0	0
GCA_002422745.1_Candidatus_Mitibacteraceae_bacterium	1184	0	0	55	29	109	53	36	74	36	120	40	87	90	65	66	52	16	123	51	74	15	0	0
GCA_002725445.1_Candidatus_Mitibacteraceae_bacterium	1117	1	0	76	23	102	42	45	55	31	121	36	81	79	45	56	67	12	120	53	60	15	0	0
GCA_002422205.1_Candidatus_Mitibacteraceae_bacterium	1491	0	0	95	40	128	57	49	80	44	148	51	108	105	79	90	84	13	146	70	80	23	0	1
GCA_002346425.1_Candidatus_Mitibacteraceae_bacterium	1458	0	0	92	36	122	57	63	77	46	145	53	116	101	74	77	69	16	154	67	65	21	0	0
GCA_002423155.1_Candidatus_Mitibacteraceae_bacterium	1407	0	0	93	42	118	54	43	76	41	144	67	111	87	80	68	63	10	138	63	66	25	0	0
GCA_004293935.1_Candidatus_Mitibacteraceae_bacterium	1128	0	0	79	26	113	49	38	63	38	126	35	96	82	54	58	45	14	97	41	62	18	1	0
GCA_002291925.1_Candidatus_Mitibacteraceae_bacterium	1466	1	0	94	34	135	57	62	78	49	154	43	111	104	71	82	63	21	131	72	75	21	1	2
GCA_002291845.1_Candidatus_Mitibacteraceae_bacterium	1262	0	0	81	30	108	50	55	80	44	132	38	99	91	69	74	56	19	103	56	63	23	0	0

Supplementary Figure 20: components of type IV and type VI secretion systems in the *Rickettsiales.* Heat-map showing the numbers of orthologs identified for each component of type IV and type VI secretion systems in the *Rickettsiales* of the final dataset, ordered by their phylogenetic relationships (Supplementary Figure 18), with families highlighted by different colours on the left. The bar plots on the right indicate the percentage of proteobacterial BUSCO single-copy orthogroups identified in each assembly.

	T4SS											T6SS											
	VirB1	VirB2	VirB3	VirB4	VirB6	VirB7	VirB8	VirB9	VirB10	VirB11	VirD4	clpV	dotU	tssA/impA	tssB/vipA	tssC/vipB	tssE	tssF	tssG	tssK/vasE	tssM/icmF	vrgG	Busco_s_copy
Rickettsia_prowazekii_strain_Madrid_E_GCA_000195735.1	0	1	0	2	5	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	76.7
Rickettsia_endosymbiont_of_Ixodes_scapularis_GCA_000160735.1	0	1	1	6	3	0	2	2	0	0	7	0	0	0	0	0	0	0	0	0	0	0	74
Rickettsia_bellii_strain_RML369C_GCA_000012385.1	0	1	1	3	5	0	2	2	1	1	2	1	0	0	0	0	0	0	0	0	0	0	78.5
Tisiphia_endosymbiont_of_Culicoides_newsteadi_GCA_002259525.1	0	2	1	3	5	0	2	2	1	1	2	1	0	0	0	0	0	0	0	0	0	0	80.4
Trichorickettsia_mobilis_endosymbiont_of_Paramecium_multimicronucleatum_Kr_154-4	0	1	1	2	5	0	2	2	1	1	3	0	1	1	1	2	0	1	1	1	1	1	81.7
Megaira_polyxenophila_endosymbiont_of_Euplotes_woodruffi_NDG2	0	1	1	4	6	0	2	2	1	1	3	0	0	0	0	0	0	0	0	0	0	0	82.2
GCA_017302595.1_Rickettsiaceae_bacterium	0	1	1	2	5	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	80.8
Megaira_venefica_endosymbiont_of_Paramecium_nephridiatum_Sr_2-6	0	1	0	1	0	0	2	2	1	1	3	0	0	0	0	0	0	0	0	0	0	0	77.6
GCA_003963235.1_Rickettsiaceae_bacterium	0	1	1	1	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	70.8
GCA_905479885.1_Rickettsiaceae_bacterium	0	1	1	3	3	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	61.2
GCA_905479865.1_Rickettsiaceae_bacterium	0	1	1	2	6	0	2	2	1	1	3	0	0	0	0	0	0	0	0	0	0	0	74.9
GCA_002402195.1_Rickettsiaceae_bacterium	0	1	0	1	2	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	73.5
GCA_013214485.1_Rickettsiaceae_bacterium	0	1	1	2	6	0	2	2	1	1	4	1	0	0	0	0	0	0	0	0	0	0	77.2
Rickettsiaceae_endosymbiont_of_Nephromyces_sp._GCA_015657545.1	0	1	1	2	5	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	64.8
Rickettsiaceae_endosymbiont_of_Cardiosporidium_cionae_GCA_015476335.1	0	2	1	2	5	0	2	2	1	1	2	0	0	0	0	0	0	0	0	0	0	0	70.8
Sarmatiella_mevalonica_GCA_016751895.1	0	1	1	2	5	0	2	2	1	1	2	0	0	0	0	0	0	0	0	0	0	0	66.7
GCA_017995275.1_Rickettsiaceae_bacterium	0	2	1	1	4	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.9
Orientia_tsutsugamushi_strain_Ikeda_GCA_000010205.1	0	2	1	9	5	0	2	2	1	1	11	0	0	0	0	0	0	0	0	0	0	0	68.9
Orientia_chuto_strain_Dubai_GCA_000964595.1	0	3	1	3	6	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	66.2
Occidentia_massiliensis_GCA_000309075.1	0	1	1	4	6	0	3	2	1	1	2	0	0	0	0	0	0	0	0	0	0	0	74.4
Sneabacter_namystus_GCA_008189685.1	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	2	1	1	1	1	1	0	62.6
Phycorickettsia_trachydisci_GCA_003015145.1	0	3	1	2	5	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	72.6
GCA_018062985.1_Rickettsiaceae_bacterium	0	0	1	1	3	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58
GCA_013214525.1_Rickettsiaceae_bacterium	0	1	1	3	5	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	79.5
GCA_002422875.1_Rickettsiaceae_bacterium	0	0	1	2	4	0	2	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	78.5
Rickettsiaceae_endosymbiont_of_Amblyomma_cajennese_Ac37b_GCA_000746585.2	0	4	1	3	5	0	2	3	2	1	1	0	0	0	0	0	0	0	0	0	0	0	93.6
Arcanobacter_lacustris_GCA_000970895.1	0	1	0	1	0	0	2	1	1	1	3	0	0	0	0	0	0	0	0	0	0	0	40.2
Rickettsiaceae_endosymbiont_of_Stachyamoeba_lipophora_GCA_003932735.1	0	1	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	89
GCA_001897445.1_Rickettsiaceae_bacterium	0	1	1	3	4	0	3	3	2	2	2	0	0	0	0	0	0	0	0	0	0	0	86.3
Midichloria_mitochondrii_IricVA_GCA_000219355.1	0	1	0	1	3	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	77.6
Cyrtobacter_comes_endosymbiont_of_Euplotes_harpa_BOD18	0	0	1	2	6	0	2	3	1	1	3	0	0	0	0	0	0	0	0	0	0	0	76.3
Lyticum_sinuosum_endosymbiont_of_Paramecium_biaurelia_USBL-36I1	0	1	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	64.8
Fokinia_solitaria_GCA_003072485.1	0	1	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	66.7
Fokinia_cryptica_endosymbiont_of_Paramecium_biaurelia_US_BI_11III1	0	1	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	65.8
GCA_903878005.1_Midichloriaceae_bacterium	0	1	1	1	3	0	2	2	0	0	3	0	0	0	0	0	0	0	0	0	0	0	64.4
Vederia_obscura_endosymbiont_of_Plagiopyla_frontata_IBS-3	0	1	1	2	5	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	70.8
Bandiella_woodruffii_endosymbiont_of_Euplotes_woodruffi_NDG2	0	1	1	1	1	0	0	1	0	1	2	0	0	0	0	0	0	0	0	0	0	0	83.1
GCA_905479795.1_Midichloriaceae_bacterium	0	2	1	4	4	0	2	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	74.9
GCA_903887235.1_Midichloriaceae_bacterium	0	1	1	4	4	0	2	2	1	1	5	0	0	0	0	0	0	0	0	0	0	0	86.3
Grellia_incantans_H2_GCA_009690945.1	0	2	1	3	4	0	1	2	1	1	2	0	0	0	0	0	0	0	0	0	0	0	85.4
Aquarickettsia_rohweri_GCA_003953955.1	0	2	1	3	4	0	1	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	83.6
Jidaibacter_acanthamoeba_UWC36_GCA_000815465.1	1	1	1	3	5	0	2	3	2	1	2	0	0	0	0	0	0	0	0	0	0	0	85.4
Endosymbiont_of_Acanthamoeba_sp._UWC8_GCA_000730245.1	0	1	1	2	5	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	86.8
Midichloriaceae_endosymbiont_of_Reticulomyxa_filosa	0	1	0	2	4	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.4
Midichloriaceae_endosymbiont_of_Peranema_trichophorum_GCA_004210275.1	0	1	1	3	4	0	2	2	1	1	2	0	0	0	0	0	0	0	0	0	0	0	82.2
GCA_013288625.1_Midichloriaceae_bacterium	0	0	0	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	50.7
Anaplasma_phagocytophilum_strain_HZ_GCA_000013125.1	0	8	1	4	5	1	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	79
Anaplasma_marginale_strain_Florida_GCA_000020305.1	0	22	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	84
Neoehrlichia_lotoris_strain_RAC413_GCA_000964795.1	0	7	1	2	4	1	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	84.5
Ehrlichia_ruminantium_strain_Welgevonden_GCA_000026005.1	0	4	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	81.3
Ehrlichia_chaffeensis_strain_Arkansas_GCA_000013145.1	0	4	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	83.6
Wolbachia_endosymbiont_of_Brugia_malayi_GCA_000008385.1	0	0	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	80.8
Wolbachia_endosymbiont_of_Drosophila_melanogaster_GCA_000008025.1	0	6	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	84
Wolbachia_endosymbiont_of_Pratylenchus_penetrans_GCA_001752665.1	0	1	1	1	4	0	2	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	78.1
Neorickettsia_sennetsu_strain_Miyayama_GCA_000013165.1	0	0	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	73.1
Neorickettsia_helminthoeca_strain_Oregon_GCA_000632985.1	0	0	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	69.4
Xenolissoclinum_pacificiensis_L6_GCA_000512675.1	0	0	1	2	5	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	60.3
Echinorickettsia_raffii_H1_GCA_018101195.1	0	3	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	80.4
Anaplasmataceae_symbiont_of_Acropora_tenuis_Sesoko1_GCA_014132315.1	0	0	1	2	2	0	1	2	1	1	1	0	1	0	0	0	0	0	0	0	0	0	71.7
GCA_903864455.1_Anaplasmataceae_bacterium	0	1	1	1	5	0	1	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	62.1
Deianiraea_vastatrix_GCA_007993655.1	0	1	1	2	2	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	65.8
GCA_017444125.1_Deianiraeaceae_bacterium	0	0	1	1	1	0	1	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	60.3
GCA_017444095.1_Deianiraeaceae_bacterium	0	0	0	2	2	0	1	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	58
GCA_002395105.1_Deianiraeaceae_bacterium	0	0	1	2	2	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	54.3
GCA_002394665.1_Deianiraeaceae_bacterium	0	1	1	2	1	0	1	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	63.9
GCA_905480015.1_Deianiraeaceae_bacterium	0	1	1	2	2	0	1	2	0	1	2	0	0	0	0	0	0	0	0	0	0	0	70.3
GCA_018969185.1_Gamibacteraceae_bacterium	0	1	1	2	3	0	2	2	1	1	2	0	0	0	0	0	0	0	0	0	0	0	89.5
GCA_002359655.1_Gamibacteraceae_bacterium	0	2	1	3	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	92.7
GCA_009693885.1_Gamibacteraceae_bacterium	0	1	0	3	0	0	2	2	1	1	2	0	0	0	0	0	0	0	0	0	0	0	59.8
GCA_903872175.1_Gamibacteraceae_bacterium	0	1	1	2	3	0	2	2	1	1	3	0	0	0	0	0	0	0	0	0	0	0	94.5
GCA_903831915.1_Gamibacteraceae_bacterium	0	2	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	93.6
GCA_017999675.1_Gamibacteraceae_bacterium	0	1	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	90.9
GCA_903927415.1_Gamibacteraceae_bacterium	0	1	1	3	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	85.8
GCA_903878685.1_Gamibacteraceae_bacterium	0	1	1	2	4	0	2	2	1	1	2	0	0	0	0	0	0	0	0	0	0	0	92.2
GCA_903917585.1_Gamibacteraceae_bacterium	0	0	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	84.5
GCA_001768015.1_Gamibacteraceae_bacterium	0	1	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	91.8
GCA_903837365.1_Gamibacteraceae_bacterium	0	2	1	2	2	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	79.5
GCA_014190355.1_Gamibacteraceae_bacterium	0	3	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	91.3
GCA_903959715.1_Gamibacteraceae_bacterium	0	1	1	3	5	0	1	2	1	1	2	0	0	0	0	0	0	0	0	0	0	0	80.8
GCA_009925685.1_Gamibacteraceae_bacterium	0	0	1	2	2	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	86.8
GCA_009921385.1_Gamibacteraceae_bacterium	0	0	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	73.1
GCA_016778745.1_Gamibacteraceae_bacterium	0	1	0	2	4	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	79.9
GCA_905478245.1_Gamibacteraceae_bacterium	0	0	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	91.8
GCA_905478165.1_Gamibacteraceae_bacterium	0	1	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	87.7
GCA_017620845.1_Gamibacteraceae_bacterium	0	0	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	68
GCA_017475895.1_Gamibacteraceae_bacterium	0	0	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	72.1
GCA_016780625.1_Diomedesiaceae_bacterium	0	2	1	2	5	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	72.1
GCA_018659605.1_Diomedesiaceae_bacterium	0	1	1	3	5	0	1	3	2	2	2	0	0	0	0	0	0	0	0	0	0	0	78.1
GCA_018659145.1_Diomedesiaceae_bacterium	0	1	1	3	4	0	1	2	1	1	2	0	0	0	0	0	0	0	0	0	0	0	90.4
GCA_016778805.1_Diomedesiaceae_bacterium	0	1	1	2	2	0	1	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	77.6
GCA_002787635.1_Athabascaceae_bacterium	0	1	1	2	5	0	3	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	97.7
GCA_002422795.1_Athabascaceae_bacterium	0	2	0	2	0	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	91.8
GCA_013288565.1_Jistubacteraceae_bacterium	0	1	0	1	1	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	72.1
GCA_903821695.1_Jistubacteraceae_bacterium	0	1	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	96.8
GCA_010031735.1_Jistubacteraceae_bacterium	0	2	0	1	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	94.1
GCA_003531345.1_Jistubacteraceae_bacterium	0	3	1	2	3	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	64.4
GCA_013288575.1_Arkhamiaceae_bacterium	0	0	0	0	0	0	0	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	55.3
GCA_002787615.1_Arkhamiaceae_bacterium	0	2	1	2	2	0	1	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	76.7
GCA_013289445.1_Mitibacteraceae_bacterium	0	1	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	1	56.2
GCA_013288985.1_Mitibacteraceae_bacterium	0	2	1	2	1	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	55.7
GCA_013288335.1_Mitibacteraceae_bacterium	0	1	0	2	3	0	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	65.3
GCA_013288305.1_Mitibacteraceae_bacterium	0	1	0	1	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	53
GCA_009926845.1_Mitibacteraceae_bacterium	0	2	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	80.4
GCA_005792635.1_Mitibacteraceae_bacterium	0	5	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	89
GCA_003241645.1_Mitibacteraceae_bacterium	0	1	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	92.2
GCA_002422745.1_Mitibacteraceae_bacterium	0	1	1	2	4	0	2	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0	58.4
GCA_002725445.1_Mitibacteraceae_bacterium	0	0	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	71.7
GCA_002422205.1_Mitibacteraceae_bacterium	0	1	2	3	9	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	2	92.2
GCA_002346425.1_Mitibacteraceae_bacterium	0	1	1	2	4	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	93.2
GCA_002423155.1_Mitibacteraceae_bacterium	0	1	1	2	5	0	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	96.3
GCA_004293935.1_Mitibacteraceae_bacterium	0	1	1	2	4	0	2	2	2	2	2	0	0	0	0	0	0	0	0	0	0	0	86.8
GCA_002291925.1_Mitibacteraceae_bacterium	0	1	1	2	4	0	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	94.5
GCA_002291845.1_Mitibacteraceae_bacterium	0	0	1	2	4	0	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0	1	83.1

Gene copies: 20, 15, 10, 5, 0

Supplementary Figure 21: putative effector protein in the *Rickettsiales*. Heat-map showing the numbers of orthologs identified for each putative effector protein in the *Rickettsiales* of the final dataset, ordered by their phylogenetic relationships (Supplementary Figure 18), with families highlighted by different colours on the left. The bar plots on the right indicate the percentage of proteobacterial BUSCO single-copy orthogroups identified in each assembly.

Effectors

	ankyrin_repeats	Leucine-rich_repeats	Pentapeptide-repeats	TPR_repeats	RTX	haemolysin_C	haemolysin_D	phospholipase_C	phospholipase_D	patatin-like_phospholipase	Ats-1	non-ribosomal_peptide/polyketide_synthase	HipA-like_type_II_toxin-antitoxin_system_toxin	guanine_nucleotide_exchange_effector_RalF	SET_superfamily	Thiol-activated_cytolysin	17_kDa_surface_antigen-like	Alpha-tubulin_suppressor-like_RCC1_domain	Fic/Doc_family	Busco_s_copy
Rickettsia_prowazekii_strain_Madrid_E_GCA_000195735.1	1	0	1	0	0	0	1	0	1	2	0	0	0	1	0	0	1	0	0	76.7
Rickettsia_endosymbiont_of_Ixodes_scapularis_GCA_000160735.1	2	3	2	0	0	0	1	0	2	4	0	1	0	0	0	0	1	0	1	74
Rickettsia_bellii_strain_RML369C_GCA_000012385.1	11	1	1	0	0	0	1	0	1	3	0	0	0	1	0	0	1	0	4	78.5
Tisiphia_endosymbiont_of_Culicoides_newsteadi_GCA_002259525.1	3	2	2	0	0	0	1	0	1	3	0	0	0	0	0	0	1	0	0	80.4
Trichorickettsia_mobilis_endosymbiont_of_Paramecium_multimicronucleatum_Kr_154-4	2	7	2	0	0	0	2	0	1	1	0	0	0	0	0	0	1	0	1	81.7
Megaira_polyxenophila_endosymbiont_of_Euplotes_woodruffi_NDG2	2	2	1	1	0	0	2	0	2	2	0	0	0	0	0	0	1	0	1	82.2
GCA_017302595.1_Rickettsiaceae_bacterium	3	0	3	0	0	0	2	0	1	1	0	0	0	1	0	0	1	0	0	80.8
Megaira_venefica_endosymbiont_of_Paramecium_nephridiatum_Sr_2-6	8	0	2	1	0	0	2	0	3	1	0	0	0	0	0	0	1	0	3	77.6
GCA_003963235.1_Rickettsiaceae_bacterium	7	2	1	0	0	0	1	0	1	1	0	0	0	1	0	0	1	0	0	70.8
GCA_905479885.1_Rickettsiaceae_bacterium	2	3	3	0	0	0	1	0	1	1	0	0	0	0	0	0	1	0	0	61.2
GCA_905479865.1_Rickettsiaceae_bacterium	2	1	2	2	1	0	2	0	0	0	0	0	0	0	0	0	1	0	2	74.9
GCA_002402195.1_Rickettsiaceae_bacterium	8	2	2	7	2	0	2	0	1	1	0	0	1	0	0	0	1	0	5	73.5
GCA_013214485.1_Rickettsiaceae_bacterium	0	1	2	3	1	0	4	0	0	0	0	1	0	2	0	0	0	0	1	77.2
Rickettsiaceae_endosymbiont_of_Nephromyces_sp._GCA_015657545.1	12	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	1	64.8
Rickettsiaceae_endosymbiont_of_Cardiosporidium_cionae_GCA_015476335.1	8	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	3	0	70.8
Sarmatiella_mevalonica_GCA_016751895.1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	66.7
GCA_017995275.1_Rickettsiaceae_bacterium	18	0	0	0	1	0	1	0	0	1	0	0	0	0	0	0	0	0	1	63.9
Orientia_tsutsugamushi_strain_Ikeda_GCA_000010205.1	39	0	2	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	68.9
Orientia_chuto_strain_Dubai_GCA_000964595.1	18	0	2	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	66.2
Occidentia_massiliensis_GCA_000309075.1	25	1	2	0	0	0	2	0	1	1	0	0	0	0	0	0	1	0	1	74.4
Sneabacter_namystus_GCA_008189685.1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	62.6
Phycorickettsia_trachydisci_GCA_003015145.1	99	0	1	0	0	0	1	0	1	1	0	0	0	0	0	0	1	0	1	72.6
GCA_018062985.1_Rickettsiaceae_bacterium	4	0	2	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	58
GCA_013214525.1_Rickettsiaceae_bacterium	4	0	5	5	0	0	1	0	0	2	0	0	0	0	0	0	1	0	3	79.5
GCA_002422875.1_Rickettsiaceae_bacterium	6	0	0	1	0	0	1	0	0	1	0	0	0	0	0	0	1	0	0	78.5
Rickettsiaceae_endosymbiont_of_Amblyomma_cajennese_Ac37b_GCA_000746585.2	35	1	3	0	3	0	1	0	1	0	0	0	0	0	0	0	1	0	0	93.6
Arcanobacter_lacustris_GCA_000970895.1	4	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	1	0	2	40.2
Rickettsiaceae_endosymbiont_of_Stachyamoeba_lipophora_GCA_003932735.1	27	11	1	0	0	0	1	0	1	1	0	0	0	0	0	0	1	0	0	89
GCA_001897445.1_Rickettsiaceae_bacterium	35	0	2	0	0	0	1	0	1	0	0	1	0	0	0	0	2	0	4	86.3
Midichloria_mitochondrii_IricVA_GCA_000219355.1	4	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	1	0	0	77.6
Cyrtobacter_comes_endosymbiont_of_Euplotes_harpa_BOD18	4	0	2	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	76.3
Lyticum_sinuosum_endosymbiont_of_Paramecium_biaurelia_USBL-36I1	1	0	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	64.8
Fokinia_solitaria_GCA_003072485.1	1	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	66.7
Fokinia_cryptica_endosymbiont_of_Paramecium_biaurelia_US_BI_11III1	1	0	2	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	65.8
GCA_903878005.1_Midichloriaceae_bacterium	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	1	0	1	64.4
Vederia_obscura_endosymbiont_of_Plagiopyla_frontata_IBS-3	2	0	1	0	0	0	1	0	0	0	0	0	1	0	0	0	1	0	2	70.8
Bandiella_woodruffii_endosymbiont_of_Euplotes_woodruffi_NDG2	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	83.1
GCA_905479795.1_Midichloriaceae_bacterium	1	0	1	4	0	0	1	0	0	2	0	0	0	0	0	0	1	0	0	74.9
GCA_903887235.1_Midichloriaceae_bacterium	3	1	2	2	2	0	1	0	0	1	0	0	0	0	0	0	1	0	3	86.3
Grellia_incantans_H2_GCA_009690945.1	5	0	2	7	1	0	1	0	0	4	0	0	0	1	0	0	0	0	6	85.4
Aquarickettsia_rohweri_GCA_003953955.1	2	1	2	2	1	0	1	0	0	2	0	0	0	1	0	0	0	0	0	83.6
Jidaibacter_acanthamoeba_UWC36_GCA_000815465.1	85	6	3	1	2	0	2	0	0	4	0	0	0	0	0	0	1	0	1	85.4
Endosymbiont_of_Acanthamoeba_sp._UWC8_GCA_000730245.1	27	3	3	0	1	0	1	0	0	1	0	0	0	0	0	0	1	0	1	86.8
Midichloriaceae_endosymbiont_of_Reticulomyxa_filosa	0	0	2	1	1	0	1	0	0	1	0	0	1	0	0	0	1	0	0	85.4
Midichloriaceae_endosymbiont_of_Peranema_trichophorum_GCA_004210275.1	13	2	2	0	6	0	1	0	0	0	0	0	0	0	0	0	1	0	1	82.2
GCA_013288625.1_Midichloriaceae_bacterium	21	0	1	1	0	0	1	0	0	3	0	0	0	0	0	0	1	0	4	50.7
Anaplasma_phagocytophilum_strain_HZ_GCA_000013125.1	3	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	79
Anaplasma_marginale_strain_Florida_GCA_000020305.1	2	0	1	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	84
Neoehrlichia_lotoris_strain_RAC413_GCA_000964795.1	1	0	1	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	84.5
Ehrlichia_ruminantium_strain_Welgevonden_GCA_000026005.1	2	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	81.3
Ehrlichia_chaffeensis_strain_Arkansas_GCA_000013145.1	3	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	83.6
Wolbachia_endosymbiont_of_Brugia_malayi_GCA_000008385.1	4	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	80.8
Wolbachia_endosymbiont_of_Drosophila_melanogaster_GCA_000008025.1	18	0	1	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	3	84
Wolbachia_endosymbiont_of_Pratylenchus_penetrans_GCA_001752665.1	19	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	78.1
Neorickettsia_sennetsu_strain_Miyayama_GCA_000013165.1	1	0	1	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	73.1
Neorickettsia_helminthoeca_strain_Oregon_GCA_000632985.1	2	0	1	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	69.4
Xenolissoclinum_pacificiensis_L6_GCA_000512675.1	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	1	0	0	0	60.3
Echinorickettsia_raffii_H1_GCA_018101195.1	20	0	1	0	0	0	1	1	0	5	0	0	0	0	0	0	0	0	0	80.4
Anaplasmataceae_symbiont_of_Acropora_tenuis_Sesoko1_GCA_014132315.1	2	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	71.7
GCA_903864455.1_Anaplasmataceae_bacterium	2	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	62.1
Deianiraea_vastatrix_GCA_007993655.1	2	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	65.8
GCA_017444125.1_Deianiraeaceae_bacterium	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.3
GCA_017444095.1_Deianiraeaceae_bacterium	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	58
GCA_002395105.1_Deianiraeaceae_bacterium	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.3
GCA_002394665.1_Deianiraeaceae_bacterium	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.9
GCA_905480015.1_Deianiraeaceae_bacterium	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	70.3
GCA_018969185.1_Gamibacteraceae_bacterium	6	1	0	0	4	1	1	0	0	0	0	0	1	0	0	0	0	0	2	89.5
GCA_002359655.1_Gamibacteraceae_bacterium	5	1	0	0	1	0	1	0	0	0	0	1	3	0	0	0	0	0	4	92.7
GCA_009693885.1_Gamibacteraceae_bacterium	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	59.8
GCA_903872175.1_Gamibacteraceae_bacterium	3	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	7	94.5
GCA_903831915.1_Gamibacteraceae_bacterium	14	1	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	7	93.6
GCA_017999675.1_Gamibacteraceae_bacterium	11	1	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	3	90.9
GCA_903927415.1_Gamibacteraceae_bacterium	5	0	0	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	5	85.8
GCA_903878685.1_Gamibacteraceae_bacterium	6	1	0	0	1	0	1	0	0	0	0	0	2	0	0	0	0	0	8	92.2
GCA_903917585.1_Gamibacteraceae_bacterium	5	0	0	0	2	0	2	0	0	0	0	1	0	0	0	0	0	0	3	84.5
GCA_001768015.1_Gamibacteraceae_bacterium	3	0	0	0	5	1	3	0	0	0	0	0	1	0	0	0	0	0	6	91.8
GCA_903837365.1_Gamibacteraceae_bacterium	10	2	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	1	79.5
GCA_014190355.1_Gamibacteraceae_bacterium	7	2	1	0	4	0	1	0	0	0	0	1	0	0	0	0	0	0	0	91.3
GCA_903959715.1_Gamibacteraceae_bacterium	6	0	1	0	1	1	1	0	0	0	0	1	1	0	0	0	0	0	2	80.8
GCA_009925685.1_Gamibacteraceae_bacterium	6	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	86.8
GCA_009921385.1_Gamibacteraceae_bacterium	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	73.1
GCA_016778745.1_Gamibacteraceae_bacterium	4	0	0	0	2	1	1	0	0	0	0	1	1	0	0	0	0	0	0	79.9
GCA_905478245.1_Gamibacteraceae_bacterium	2	0	0	7	3	0	1	0	0	0	0	1	0	0	0	0	0	0	3	91.8
GCA_905478165.1_Gamibacteraceae_bacterium	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.7
GCA_017620845.1_Gamibacteraceae_bacterium	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68
GCA_017475895.1_Gamibacteraceae_bacterium	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.1
GCA_016780625.1_Diomedesiaceae_bacterium	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.1
GCA_018659605.1_Diomedesiaceae_bacterium	4	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	78.1
GCA_018659145.1_Diomedesiaceae_bacterium	6	1	0	0	2	0	1	0	0	0	0	1	1	0	0	0	0	0	5	90.4
GCA_016778805.1_Diomedesiaceae_bacterium	6	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	77.6
GCA_002787635.1_Athabascaceae_bacterium	8	0	2	2	11	0	2	0	0	0	0	0	3	0	0	0	1	0	0	97.7
GCA_002422795.1_Athabascaceae_bacterium	6	1	2	1	9	0	2	0	1	0	0	0	1	0	0	0	1	0	0	91.8
GCA_013288565.1_Jistubacteraceae_bacterium	1	0	0	2	1	0	1	0	2	0	0	2	0	0	0	0	1	0	0	72.1
GCA_903821695.1_Jistubacteraceae_bacterium	3	0	0	4	14	0	1	0	1	2	0	0	0	0	0	0	2	0	3	96.8
GCA_010031735.1_Jistubacteraceae_bacterium	2	0	0	5	5	0	1	0	0	0	0	0	0	0	0	0	2	0	0	94.1
GCA_003531345.1_Jistubacteraceae_bacterium	1	0	0	1	1	0	0	0	0	0	0	0	1	0	0	0	2	0	2	64.4
GCA_013288575.1_Arkhamiaceae_bacterium	1	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	55.3
GCA_002787615.1_Arkhamiaceae_bacterium	3	0	0	1	2	0	0	0	0	1	0	0	0	0	0	0	3	0	2	76.7
GCA_013289445.1_Mitibacteraceae_bacterium	2	0	0	4	0	0	0	0	1	1	0	0	0	0	0	0	1	0	0	56.2
GCA_013288985.1_Mitibacteraceae_bacterium	3	0	0	2	0	0	0	0	1	1	0	0	0	0	0	0	1	0	0	55.7
GCA_013288335.1_Mitibacteraceae_bacterium	1	0	0	2	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	65.3
GCA_013288305.1_Mitibacteraceae_bacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	53
GCA_009926845.1_Mitibacteraceae_bacterium	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	2	80.4
GCA_005792635.1_Mitibacteraceae_bacterium	2	0	1	0	0	0	0	0	0	1	0	0	1	0	0	0	1	0	1	89
GCA_003241645.1_Mitibacteraceae_bacterium	1	0	0	0	5	2	3	0	0	0	0	1	1	0	0	0	2	1	0	92.2
GCA_002422745.1_Mitibacteraceae_bacterium	1	0	1	1	4	0	2	0	0	0	0	0	0	0	0	0	1	0	0	58.4
GCA_002725445.1_Mitibacteraceae_bacterium	3	0	2	1	8	0	2	0	0	0	0	0	0	0	0	0	1	0	0	71.7
GCA_002422205.1_Mitibacteraceae_bacterium	1	0	1	0	16	0	2	0	1	1	0	0	0	0	0	0	2	0	0	92.2
GCA_002346425.1_Mitibacteraceae_bacterium	1	0	1	0	15	0	2	0	1	0	0	0	0	0	0	0	1	0	1	93.2
GCA_002423155.1_Mitibacteraceae_bacterium	1	0	1	0	6	0	1	0	0	1	0	0	2	0	0	0	3	0	6	96.3
GCA_004293935.1_Mitibacteraceae_bacterium	0	0	1	0	7	0	1	0	0	1	0	0	1	0	0	0	1	0	0	86.8
GCA_002291925.1_Mitibacteraceae_bacterium	1	0	1	3	9	0	2	0	1	1	0	0	0	0	0	0	1	2	0	94.5
GCA_002291845.1_Mitibacteraceae_bacterium	0	0	1	0	6	0	2	0	0	1	0	0	0	0	0	0	1	0	0	83.1

Gene copies: 0, 20, 40, 60

Supplementary Figure 22: component of flagellum and chemotaxis apparatuses in the *Rickettsiales.* Heat-map showing the numbers of orthologs identified for each component of flagellum and chemotaxis apparatuses in the *Rickettsiales* of the final dataset, ordered by their phylogenetic relationships (Supplementary Figure 18), with families highlighted by different colours on the left. The bar plots on the right indicate the percentage of proteobacterial BUSCO single-copy orthogroups identified in each assembly.

flagellum | chemotaxis | Busco_s_copy

Rickettsia_prowazekii_strain_Madrid_E_GCA_000195735.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 76.7
Rickettsia_endosymbiont_of_Ixodes_scapularis_GCA_000160735.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 74
Rickettsia_bellii_strain_RML369C_GCA_000012385.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 78.5
Tisiphia_endosymbiont_of_Culicoides_newsteadi_GCA_002259525.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 80.4
Trichorickettsia_mobilis_endosymbiont_of_Paramecium_multimicronucleatum_Kr_154-4 1 1 1 0 1 1 1 1 0 0 0 0 1 1 0 0 0 1 0 1 1 0 1 0 1 1 0 1 1 1 0 1 1 1 0 0 0 0 0 0 81.7
Megaira_polyxenophila_endosymbiont_of_Euplotes_woodruffi_NDG2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 82.2
GCA_017302595.1_Rickettsiaceae_bacterium 1 1 1 0 1 1 1 1 0 1 0 0 1 1 0 0 0 1 0 1 1 0 0 0 1 1 0 1 1 1 0 1 1 1 0 0 0 0 0 0 80.8
Megaira_venefica_endosymbiont_of_Paramecium_nephridiatum_Sr_2-6 1 1 1 0 1 1 1 1 0 0 0 0 1 1 0 0 0 1 0 1 1 0 0 0 1 1 0 1 1 1 0 1 1 1 1 0 0 0 0 0 77.6
GCA_003963235.1_Rickettsiaceae_bacterium 1 1 1 0 1 1 1 0 0 0 0 0 1 1 0 0 0 0 0 1 1 0 1 0 1 1 0 1 1 1 0 1 1 1 1 0 0 0 0 0 70.8
GCA_905479885.1_Rickettsiaceae_bacterium 1 1 1 0 1 1 1 1 0 0 0 0 1 1 0 0 0 0 0 1 1 0 0 0 1 1 0 1 1 1 0 1 1 1 0 0 0 0 0 0 61.2
GCA_905479865.1_Rickettsiaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 74.9
GCA_002402195.1_Rickettsiaceae_bacterium 1 1 1 0 1 1 1 1 0 1 0 0 0 0 0 0 0 0 0 1 1 0 0 1 1 1 0 1 1 1 0 1 1 0 0 0 0 0 0 0 73.5
GCA_013214485.1_Rickettsiaceae_bacterium 1 1 1 0 0 2 1 1 0 0 0 0 1 1 0 0 0 0 0 1 1 0 1 0 1 1 0 1 1 1 0 1 1 1 1 0 0 0 0 0 77.2
Rickettsiaceae_endosymbiont_of_Nephromyces_sp._GCA_015657545.1 1 1 1 0 1 1 1 1 0 0 0 0 1 1 0 0 0 0 0 1 1 0 0 0 1 1 0 1 1 1 0 1 1 0 0 0 0 0 0 0 64.8
Rickettsiaceae_endosymbiont_of_Cardiosporidium_cionae_GCA_015476335.1 1 1 1 0 1 1 2 1 0 0 0 0 1 1 0 0 0 0 0 1 1 0 1 0 1 1 0 1 1 1 0 1 1 0 0 0 0 0 0 0 70.8
Sarmatiella_mevalonica_GCA_016751895.1 1 0 1 0 1 1 1 1 0 0 0 0 1 1 0 0 0 0 0 1 1 0 1 0 1 1 0 1 1 1 0 1 1 0 0 0 0 0 0 0 66.7
GCA_017995275.1_Rickettsiaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 63.9
Orientia_tsutsugamushi_strain_Ikeda_GCA_000010205.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 68.9
Orientia_chuto_strain_Dubai_GCA_000964595.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 66.2
Occidentia_massiliensis_GCA_000309075.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 74.4
Sneabacter_namystus_GCA_008189685.1 1 0 1 0 1 1 1 1 0 0 0 0 1 1 0 0 0 0 0 1 1 0 0 0 0 1 0 1 1 1 0 1 1 0 0 0 0 0 0 0 62.6
Phycorickettsia_trachydisci_GCA_003015145.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 72.6
GCA_018062985.1_Rickettsiaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 58
GCA_013214525.1_Rickettsiaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 79.5
GCA_002422875.1_Rickettsiaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 3 1 1 0 78.5
Rickettsiaceae_endosymbiont_of_Amblyomma_cajennese_Ac37b_GCA_000746585.2 1 1 1 1 1 1 1 1 0 1 0 0 1 1 0 0 1 1 1 1 1 0 1 1 1 1 0 1 1 1 1 1 1 0 1 1 2 1 1 0 93.6
Arcanobacter_lacustris_GCA_000970895.1 0 0 0 1 1 1 1 1 0 1 0 0 0 1 0 1 1 1 0 1 0 0 0 0 1 0 1 1 0 1 1 1 1 0 1 1 1 1 1 1 40.2
Rickettsiaceae_endosymbiont_of_Stachyamoeba_lipophora_GCA_003932735.1 1 0 1 1 0 2 1 1 0 1 0 0 1 1 0 1 1 1 0 1 1 0 1 1 1 1 0 1 1 1 1 2 1 0 0 0 0 0 0 0 89
GCA_001897445.1_Rickettsiaceae_bacterium 1 1 1 1 1 1 1 1 0 1 0 0 1 1 0 1 1 1 1 1 1 0 1 1 1 1 0 1 1 1 1 2 1 1 2 2 1 2 2 1 86.3

Midichloria_mitochondrii_IricVA_GCA_000219355.1 1 1 1 0 0 2 1 1 0 0 0 0 1 1 0 0 1 0 1 1 1 0 1 1 1 1 0 1 0 1 0 2 1 0 0 0 0 0 0 0 77.6
Cyrtobacter_comes_endosymbiont_of_Euplotes_harpa_BOD18 0 1 1 0 0 0 0 1 0 0 0 0 2 1 0 0 0 0 0 1 1 0 1 0 1 1 0 1 1 1 0 1 1 0 0 0 0 0 0 0 76.3
Lyticum_sinuosum_endosymbiont_of_Paramecium_biaurelia_USBL-36I1 0 1 1 0 1 1 1 1 0 1 0 0 1 1 0 0 0 0 0 1 1 0 1 0 1 1 0 1 1 1 0 1 1 0 0 0 0 0 0 0 64.8
Fokinia_solitaria_GCA_003072485.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 66.7
Fokinia_cryptica_endosymbiont_of_Paramecium_biaurelia_US_BI_11III1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 65.8
GCA_903878005.1_Midichloriaceae_bacterium 1 1 1 1 1 1 0 1 0 1 0 0 1 1 0 0 0 1 1 1 1 0 0 0 1 0 0 1 1 1 0 3 1 1 1 0 0 0 0 0 64.4
Vederia_obscura_endosymbiont_of_Plagiopyla_frontata_IBS-3 1 1 1 0 1 1 1 1 0 1 0 0 1 1 0 0 1 0 1 1 1 0 1 0 1 1 0 1 1 1 0 1 1 0 0 0 0 0 0 0 70.8
Bandiella_woodruffii_endosymbiont_of_Euplotes_woodruffi_NDG2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 83.1
GCA_905479795.1_Midichloriaceae_bacterium 1 1 1 1 1 1 1 1 0 0 0 0 0 1 0 0 1 0 1 1 1 0 1 0 1 0 0 1 1 1 0 1 1 0 0 0 0 0 0 0 74.9
GCA_903887235.1_Midichloriaceae_bacterium 1 0 1 1 1 1 1 1 0 0 0 0 1 1 0 0 1 0 1 1 1 0 1 0 1 1 0 1 1 1 0 1 1 0 0 0 0 0 0 0 86.3
Grellia_incantans_H2_GCA_009690945.1 1 0 1 1 2 1 1 1 0 0 0 0 1 1 0 0 1 0 1 1 1 0 1 0 1 1 0 1 1 1 0 1 1 0 0 0 0 0 0 0 85.4
Aquarickettsia_rohweri_GCA_003953955.1 1 0 1 1 1 2 1 1 0 1 0 0 1 1 0 0 1 0 1 1 1 0 1 0 0 1 0 0 1 1 0 1 1 0 0 0 0 0 0 0 83.6
Jidaibacter_acanthamoeba_UWC36_GCA_000815465.1 1 1 1 1 1 1 1 1 0 1 0 0 1 1 0 0 1 1 1 1 1 0 1 1 1 1 0 1 1 1 0 2 1 1 1 0 0 0 0 0 85.4
Endosymbiont_of_Acanthamoeba_sp._UWC8_GCA_000730245.1 1 1 1 1 1 1 1 1 0 1 0 0 1 1 0 0 1 1 1 1 1 0 1 1 1 1 0 1 1 1 0 2 1 1 1 0 0 0 0 0 86.8
Midichloriaceae_endosymbiont_of_Reticulomyxa_filosa 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 85.4
Midichloriaceae_endosymbiont_of_Peranema_trichophorum_GCA_004210275.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 82.2
GCA_013288625.1_Midichloriaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 50.7

Anaplasma_phagocytophilum_strain_HZ_GCA_000013125.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 79
Anaplasma_marginale_strain_Florida_GCA_000020305.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 84
Neoehrlichia_lotoris_strain_RAC413_GCA_000964795.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 84.5
Ehrlichia_ruminantium_strain_Welgevonden_GCA_000026005.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 81.3
Ehrlichia_chaffeensis_strain_Arkansas_GCA_000013145.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 83.6
Wolbachia_endosymbiont_of_Brugia_malayi_GCA_000008385.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 80.8
Wolbachia_endosymbiont_of_Drosophila_melanogaster_GCA_000008025.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 84
Wolbachia_endosymbiont_of_Pratylenchus_penetrans_GCA_001752665.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 78.1
Neorickettsia_sennetsu_strain_Miyayama_GCA_000013165.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 73.1
Neorickettsia_helminthoeca_strain_Oregon_GCA_000632985.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 69.4
Xenolissoclinum_pacificiensis_L6_GCA_000512675.1 0 0 1 1 1 1 1 1 0 1 0 0 1 0 0 0 0 0 0 1 1 0 1 1 0 0 0 0 1 1 0 1 1 0 0 0 0 0 0 0 60.3
Echinorickettsia_raffii_H1_GCA_018101195.1 1 1 0 1 1 1 1 1 0 1 0 0 0 1 0 0 1 1 0 1 1 0 1 0 0 1 0 1 1 1 0 1 0 0 0 0 0 0 0 0 80.4
Anaplasmataceae_symbiont_of_Acropora_tenuis_Sesoko1_GCA_014132315.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 71.7
GCA_903864455.1_Anaplasmataceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 62.1

Deianiraea_vastatrix_GCA_007993655.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 65.8
GCA_017444125.1_Deianiraeaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 60.3
GCA_017444095.1_Deianiraeaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 58
GCA_002395105.1_Deianiraeaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 54.3
GCA_002394665.1_Deianiraeaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 63.9
GCA_905480015.1_Deianiraeaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 70.3

GCA_018969185.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 89.5
GCA_002359655.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 92.7
GCA_009693885.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 59.8
GCA_903872175.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 94.5
GCA_903831915.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 93.6
GCA_017999675.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 90.9
GCA_903927415.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 85.8
GCA_903878685.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 92.2
GCA_903917585.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 84.5
GCA_001768015.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 91.8
GCA_903837365.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 79.5
GCA_014190355.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 91.3
GCA_903959715.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 80.8
GCA_009925685.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 86.8
GCA_009921385.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 73.1
GCA_016778745.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 79.9
GCA_905478245.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 91.8
GCA_905478165.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 87.7
GCA_017620845.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 68
GCA_017475895.1_Gamibacteraceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 72.1

GCA_016780625.1_Diomedesiaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 72.1
GCA_018659605.1_Diomedesiaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 78.1
GCA_018659145.1_Diomedesiaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 90.4
GCA_016778805.1_Diomedesiaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 77.6

GCA_002787635.1_Athabascaceae_bacterium 1 1 1 1 1 1 1 1 0 1 1 0 1 1 0 0 2 1 1 1 1 0 0 1 1 1 0 1 1 1 2 2 2 0 4 2 1 2 3 0 97.7
GCA_002422795.1_Athabascaceae_bacterium 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 1 1 1 2 1 0 91.8

GCA_013288565.1_Jistubacteraceae_bacterium 0 1 1 1 0 1 1 1 0 1 1 0 0 0 0 1 1 1 1 1 1 0 0 1 0 1 1 0 1 1 1 1 0 1 0 0 0 0 0 0 72.1
GCA_903821695.1_Jistubacteraceae_bacterium 1 1 1 1 1 1 1 1 0 1 0 0 1 1 0 0 1 1 1 1 1 0 1 1 1 1 1 1 1 1 1 2 3 1 3 1 1 1 2 1 96.8
GCA_010031735.1_Jistubacteraceae_bacterium 1 1 1 1 0 2 1 1 0 1 0 0 1 1 0 1 1 1 0 1 2 1 0 1 1 1 2 2 1 1 1 2 2 1 3 2 3 2 2 1 94.1
GCA_003531345.1_Jistubacteraceae_bacterium 1 0 1 1 1 1 1 1 0 1 0 0 1 1 0 0 0 1 1 1 1 0 0 1 1 2 0 1 1 1 1 2 1 1 1 2 2 2 1 0 64.4

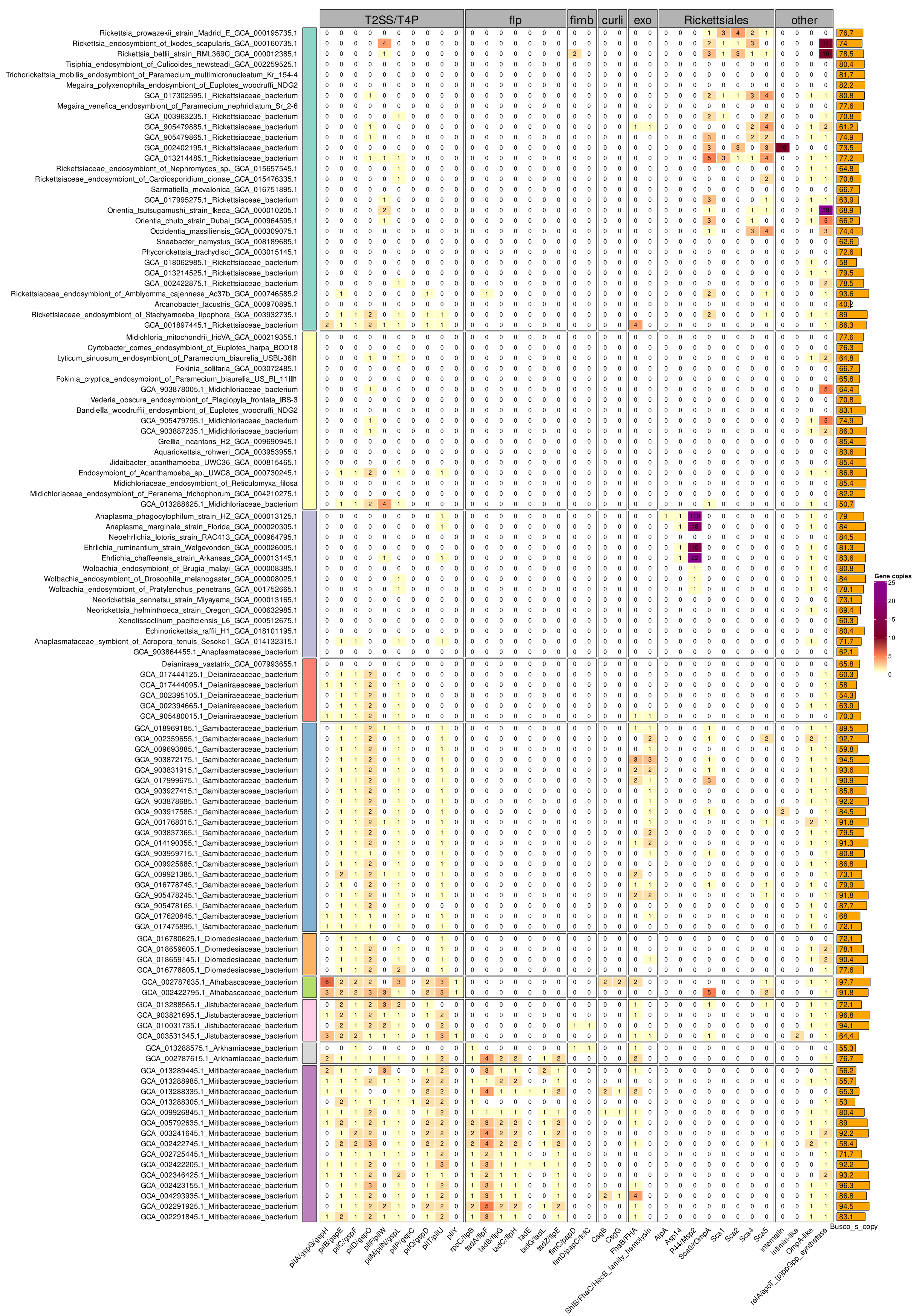
GCA_013288575.1_Arkhamiaceae_bacterium 1 1 1 1 1 1 1 1 1 0 1 0 0 0 1 0 0 1 1 1 1 0 0 0 1 1 0 0 1 1 0 2 1 0 0 0 0 0 0 0 55.3
GCA_002787615.1_Arkhamiaceae_bacterium 1 1 1 1 0 1 1 1 1 1 1 0 1 1 0 1 1 1 1 1 1 0 0 0 0 1 0 1 1 1 0 1 1 1 4 1 1 1 1 0 76.7

GCA_013289445.1_Mitibacteraceae_bacterium 1 1 2 1 0 2 1 1 0 1 0 0 1 0 0 1 2 1 0 1 1 0 1 0 0 1 0 1 0 0 1 0 0 1 0 0 0 0 0 0 56.2
GCA_013288985.1_Mitibacteraceae_bacterium 0 0 0 0 0 0 0 1 1 1 1 0 1 0 0 1 1 0 0 1 1 0 0 0 1 1 0 0 0 0 0 0 0 0 1 1 0 1 1 0 55.7
GCA_013288335.1_Mitibacteraceae_bacterium 0 1 1 1 0 0 0 0 0 0 0 0 1 1 0 0 1 1 1 1 1 0 0 0 0 1 1 1 1 1 1 0 0 1 1 1 0 1 1 1 65.3
GCA_013288305.1_Mitibacteraceae_bacterium 1 0 0 1 1 1 1 1 1 1 1 0 0 0 0 1 3 1 0 0 0 0 0 1 1 0 0 0 0 0 1 1 2 0 1 1 0 1 0 0 53
GCA_009926845.1_Mitibacteraceae_bacterium 1 1 2 1 1 1 1 1 1 0 0 0 1 1 0 1 3 1 1 1 0 0 0 1 1 1 1 0 1 1 1 1 2 1 1 3 4 1 1 1 80.4
GCA_005792635.1_Mitibacteraceae_bacterium 1 0 2 1 1 1 1 1 1 1 0 0 1 1 0 1 2 1 1 1 1 0 0 1 1 1 0 1 1 1 1 3 3 1 2 2 1 2 2 1 89
GCA_003241645.1_Mitibacteraceae_bacterium 0 1 2 1 0 2 0 1 0 1 0 0 1 1 1 1 1 1 1 1 1 0 1 0 0 1 1 1 1 1 1 2 2 1 1 1 1 1 1 0 92.2
GCA_002422745.1_Mitibacteraceae_bacterium 1 1 1 1 2 1 1 1 1 1 1 0 1 1 1 1 1 1 0 1 1 0 1 1 2 1 1 1 1 1 1 2 3 1 1 2 2 2 1 1 58.4
GCA_002725445.1_Mitibacteraceae_bacterium 1 0 0 1 1 1 1 1 2 1 1 1 0 1 0 1 2 1 0 1 1 0 0 0 1 1 0 0 0 0 1 0 2 0 3 1 3 1 1 1 71.7
GCA_002422205.1_Mitibacteraceae_bacterium 1 0 1 1 1 1 1 1 0 1 0 0 1 1 0 0 3 1 1 1 1 0 0 1 1 1 1 1 1 1 1 2 2 1 3 2 2 2 2 1 92.2
GCA_002346425.1_Mitibacteraceae_bacterium 1 1 2 1 1 1 1 1 1 1 0 0 1 1 0 1 2 1 0 1 1 0 0 1 1 1 1 1 1 1 1 2 2 1 2 3 2 3 2 0 93.2
GCA_002423155.1_Mitibacteraceae_bacterium 1 1 2 1 0 2 1 1 1 1 1 0 1 1 0 1 3 1 1 1 1 0 1 0 1 1 0 1 1 1 1 2 2 1 2 2 2 2 2 1 96.3
GCA_004293935.1_Mitibacteraceae_bacterium 1 1 1 0 0 2 1 1 0 1 1 0 1 1 0 1 5 1 1 1 1 0 0 1 1 1 0 0 1 1 1 1 1 0 2 1 1 1 2 0 86.8
GCA_002291925.1_Mitibacteraceae_bacterium 1 1 2 1 1 1 1 1 1 1 0 0 1 2 1 1 2 1 1 1 1 1 0 1 1 1 0 1 1 1 1 2 2 0 3 3 5 2 2 0 94.5
GCA_002291845.1_Mitibacteraceae_bacterium 1 0 2 1 1 1 1 1 1 1 1 0 1 1 0 1 2 1 1 1 1 0 0 1 1 1 0 1 1 1 1 1 2 1 2 3 2 2 2 1 83.1

flgA flgB flgC flgD flgF flgG flgH flgI flgJ flgK flgL flgT flhA flhB flhG fliB/lafV fliC fliD fliE fliF fliG fliH fliI fliL fliM fliN fliO fliP fliQ fliR fliS motA motB ylqH/flhB-like cheA cheB cheM-like cheR cheW cheZ

Gene copies
6
4
2
0

Supplementary Figure 23: possible proteins proteins involved in the interaction with host cells in the *Rickettsiales*. Heat-map showing the numbers of orthologs identified for each component of multiple proteins possibly involved in the interaction with host cells in the *Rickettsiales* of the final dataset. Genes are ordered by functional groups (namely, components of type IV pilus/type II secretion, tight adherence pilus, fimbriae, curli, as well as exoproteins homologous to the FhaBC two-partner secretion system, previously characterised effectors in some *Rickettsiales* bacteria, and further other proteins). Organisms are ordered by their phylogenetic relationships (Supplementary Figure 18), with families highlighted by different colours on the left. The bar plots on the right indicate the percentage of proteobacterial BUSCO single-copy orthogroups identified in each assembly.


T2SS/T4P
flp
fimb
curli
exo
Rickettsiales
other
Rickettsia_prowazekii_strain_Madrid_E_GCA_000195735.1
Rickettsia_endosymbiont_of_Ixodes_scapularis_GCA_000160735.1
Rickettsia_bellii_strain_RML369C_GCA_000012385.1
Tisiphia_endosymbiont_of_Culicoides_newsteadi_GCA_002259525.1
Trichorickettsia_mobilis_endosymbiont_of_Paramecium_multimicronucleatum_Kr_154-4
Megaira_polyxenophila_endosymbiont_of_Euplotes_woodruffi_NDG2
GCA_017302595.1_Rickettsiaceae_bacterium
Megaira_venefica_endosymbiont_of_Paramecium_nephridiatum_Sr_2-6
GCA_003963235.1_Rickettsiaceae_bacterium
GCA_905479885.1_Rickettsiaceae_bacterium
GCA_905479865.1_Rickettsiaceae_bacterium
GCA_002402195.1_Rickettsiaceae_bacterium
GCA_013214485.1_Rickettsiaceae_bacterium
Rickettsiaceae_endosymbiont_of_Nephromyces_sp._GCA_015657545.1
Rickettsiaceae_endosymbiont_of_Cardiosporidium_cionae_GCA_015476335.1
Sarmatiella_mevalonica_GCA_016751895.1
GCA_017995275.1_Rickettsiaceae_bacterium
Orientia_tsutsugamushi_strain_Ikeda_GCA_000010205.1
Orientia_chuto_strain_Dubai_GCA_000964595.1
Occidentia_massiliensis_GCA_000309075.1
Sneabacter_namystus_GCA_008189685.1
Phycorickettsia_trachydisci_GCA_003015145.1
GCA_018062985.1_Rickettsiaceae_bacterium
GCA_013214525.1_Rickettsiaceae_bacterium
GCA_002422875.1_Rickettsiaceae_bacterium
Rickettsiaceae_endosymbiont_of_Amblyomma_cajennese_Ac37b_GCA_000746585.2
Arcanobacter_lacustris_GCA_000970895.1
Rickettsiaceae_endosymbiont_of_Stachyamoeba_lipophora_GCA_003932735.1
GCA_001897445.1_Rickettsiaceae_bacterium
Midichloria_mitochondrii_IricVA_GCA_000219355.1
Cyrtobacter_comes_endosymbiont_of_Euplotes_harpa_BOD18
Lyticum_sinuosum_endosymbiont_of_Paramecium_biaurelia_USBL-36I1
Fokinia_solitaria_GCA_003072485.1
Fokinia_cryptica_endosymbiont_of_Paramecium_biaurelia_US_BI_11III1
GCA_903878005.1_Midichloriaceae_bacterium
Vederia_obscura_endosymbiont_of_Plagiopyla_frontata_IBS-3
Bandiella_woodruffii_endosymbiont_of_Euplotes_woodruffi_NDG2
GCA_905479795.1_Midichloriaceae_bacterium
GCA_903887235.1_Midichloriaceae_bacterium
Grellia_incantans_H2_GCA_009690945.1
Aquarickettsia_rohweri_GCA_003953955.1
Jidaibacter_acanthamoeba_UWC36_GCA_000815465.1
Endosymbiont_of_Acanthamoeba_sp._UWC8_GCA_000730245.1
Midichloriaceae_endosymbiont_of_Reticulomyxa_filosa
Midichloriaceae_endosymbiont_of_Peranema_trichophorum_GCA_004210275.1
GCA_013288625.1_Midichloriaceae_bacterium
Anaplasma_phagocytophilum_strain_HZ_GCA_000013125.1
Anaplasma_marginale_strain_Florida_GCA_000020305.1
Neoehrlichia_lotoris_strain_RAC413_GCA_000964795.1
Ehrlichia_ruminantium_strain_Welgevonden_GCA_000026005.1
Ehrlichia_chaffeensis_strain_Arkansas_GCA_000013145.1
Wolbachia_endosymbiont_of_Brugia_malayi_GCA_000008385.1
Wolbachia_endosymbiont_of_Drosophila_melanogaster_GCA_000008025.1
Wolbachia_endosymbiont_of_Pratylenchus_penetrans_GCA_001752665.1
Neorickettsia_sennetsu_strain_Miyayama_GCA_000013165.1
Neorickettsia_helminthoeca_strain_Oregon_GCA_000632985.1
Xenolissoclinum_pacificiensis_L6_GCA_000512675.1
Echinorickettsia_raffii_H1_GCA_018101195.1
Anaplasmataceae_symbiont_of_Acropora_tenuis_Sesoko1_GCA_014132315.1
GCA_903864455.1_Anaplasmataceae_bacterium
Deianiraea_vastatrix_GCA_007993655.1
GCA_017444125.1_Deianiraeaceae_bacterium
GCA_017444095.1_Deianiraeaceae_bacterium
GCA_002395105.1_Deianiraeaceae_bacterium
GCA_002394665.1_Deianiraeaceae_bacterium
GCA_905480015.1_Deianiraeaceae_bacterium
GCA_018969185.1_Gamibacteraceae_bacterium
GCA_002359655.1_Gamibacteraceae_bacterium
GCA_009693885.1_Gamibacteraceae_bacterium
GCA_903872175.1_Gamibacteraceae_bacterium
GCA_903831915.1_Gamibacteraceae_bacterium
GCA_017999675.1_Gamibacteraceae_bacterium
GCA_903927415.1_Gamibacteraceae_bacterium
GCA_903878685.1_Gamibacteraceae_bacterium
GCA_903917585.1_Gamibacteraceae_bacterium
GCA_001768015.1_Gamibacteraceae_bacterium
GCA_903837365.1_Gamibacteraceae_bacterium
GCA_014190355.1_Gamibacteraceae_bacterium
GCA_903959715.1_Gamibacteraceae_bacterium
GCA_009925685.1_Gamibacteraceae_bacterium
GCA_009921385.1_Gamibacteraceae_bacterium
GCA_016778745.1_Gamibacteraceae_bacterium
GCA_905478245.1_Gamibacteraceae_bacterium
GCA_905478165.1_Gamibacteraceae_bacterium
GCA_017620845.1_Gamibacteraceae_bacterium
GCA_017475895.1_Gamibacteraceae_bacterium
GCA_016780625.1_Diomedesiaceae_bacterium
GCA_018659605.1_Diomedesiaceae_bacterium
GCA_018659145.1_Diomedesiaceae_bacterium
GCA_016778805.1_Diomedesiaceae_bacterium
GCA_002787635.1_Athabascaceae_bacterium
GCA_002422795.1_Athabascaceae_bacterium
GCA_013288565.1_Jistubacteraceae_bacterium
GCA_903821695.1_Jistubacteraceae_bacterium
GCA_010031735.1_Jistubacteraceae_bacterium
GCA_003531345.1_Jistubacteraceae_bacterium
GCA_013288575.1_Arkhamiaceae_bacterium
GCA_002787615.1_Arkhamiaceae_bacterium
GCA_013289445.1_Mitibacteraceae_bacterium
GCA_013288985.1_Mitibacteraceae_bacterium
GCA_013288335.1_Mitibacteraceae_bacterium
GCA_013288305.1_Mitibacteraceae_bacterium
GCA_009926845.1_Mitibacteraceae_bacterium
GCA_005792635.1_Mitibacteraceae_bacterium
GCA_003241645.1_Mitibacteraceae_bacterium
GCA_002422745.1_Mitibacteraceae_bacterium
GCA_002725445.1_Mitibacteraceae_bacterium
GCA_002422205.1_Mitibacteraceae_bacterium
GCA_002346425.1_Mitibacteraceae_bacterium
GCA_002423155.1_Mitibacteraceae_bacterium
GCA_004293935.1_Mitibacteraceae_bacterium
GCA_002291925.1_Mitibacteraceae_bacterium
GCA_002291845.1_Mitibacteraceae_bacterium
Gene copies
25
20
15
10
5
0
Busco_s_copy
pilA/gspG/gspH
pilB/gspE
pilC/gspF
pilD/gspO
pilF/pilW
pilM/pilN/gspL
pilP/gspC
pilQ/gspD
pilT/pilU
pilY
rpcC/flpB
tadA/flpF
tadB/flpG
tadC/flpH
tadE
tadG/tadL
tadZ/flpE
fimC/papD
fimD/papC/tcfC
CsgB
CsgG
FhaB/FHA
ShlB/FhaC/HecB_family_hemolysin
AipA
Asp14
P44/Msp2
Sca0/rOmpA
Sca1
Sca2
Sca4
Sca5
internalin
intimin-like
OmpA-like
relA/spoT_(p)ppGpp_synthetase

Supplementary Figure 24: biosynthetic pathways and transporters for nucleotides. Heat-map showing the presence and abundance of biosynthetic pathways of nucleotides (purines and pyrimidines; blue) and their tlc transporters (red) in *Rickettsiales*. For biosynthesis, the proportion of the total genes of the pathway is shown (Supplementary Data 7), while for transporters, the number of genes is reported. Organisms are ordered by their phylogenetic relationships (Supplementary Figure 18), with families highlighted by different colours on the right. The bar plots on the right indicate the percentage of proteobacterial BUSCO single-copy orthogroups identified in each assembly.

Nucleotide transport and biosynthesis

	Synthesis		Transport	
Rickettsia_prowazekii_strain_Madrid_E_GCA_000195735.1	0.2	0.53	5	76.7
Rickettsia_endosymbiont_of_Ixodes_scapularis_GCA_000160735.1	0.2	0.53	7	74
Rickettsia_bellii_strain_RML369C_GCA_000012385.1	0.2	0.53	5	78.5
Tisiphia_endosymbiont_of_Culicoides_newsteadi_GCA_002259525.1	0.2	0.47	5	80.4
Trichorickettsia_mobilis_endosymbiont_of_Paramecium_multimicronucleatum_Kr_154-4	0.2	0.53	4	81.7
Megaira_polyxenophila_endosymbiont_of_Euplotes_woodruffi_NDG2	0.2	0.47	5	82.2
GCA_017302595.1_Rickettsiaceae_bacterium	0.2	0.47	5	80.8
Megaira_venefica_endosymbiont_of_Paramecium_nephridiatum_Sr_2-6	0.2	0.47	5	77.6
GCA_003963235.1_Rickettsiaceae_bacterium	0.13	0.33	5	70.8
GCA_905479885.1_Rickettsiaceae_bacterium	0.2	0.47	4	61.2
GCA_905479865.1_Rickettsiaceae_bacterium	0.2	0.47	5	74.9
GCA_002402195.1_Rickettsiaceae_bacterium	0.2	0.33	4	73.5
GCA_013214485.1_Rickettsiaceae_bacterium	0.2	0.53	5	77.2
Rickettsiaceae_endosymbiont_of_Nephromyces_sp._GCA_015657545.1	0.07	0.53	5	64.8
Rickettsiaceae_endosymbiont_of_Cardiosporidium_cionae_GCA_015476335.1	0.13	0.53	5	70.8
Sarmatiella_mevalonica_GCA_016751895.1	0.13	0.47	4	66.7
GCA_017995275.1_Rickettsiaceae_bacterium	0.07	0.47	5	63.9
Orientia_tsutsugamushi_strain_Ikeda_GCA_000010205.1	0.2	0.47	5	68.9
Orientia_chuto_strain_Dubai_GCA_000964595.1	0.13	0.47	5	66.2
Occidentia_massiliensis_GCA_000309075.1	0.2	0.47	5	74.4
Sneabacter_namystus_GCA_008189685.1	0.13	0.4	4	62.6
Phycorickettsia_trachydisci_GCA_003015145.1	0.13	0.53	5	72.6
GCA_018062985.1_Rickettsiaceae_bacterium	0.13	0.27	4	58
GCA_013214525.1_Rickettsiaceae_bacterium	0.27	0.53	3	79.5
GCA_002422875.1_Rickettsiaceae_bacterium	0.2	0.53	4	78.5
Rickettsiaceae_endosymbiont_of_Amblyomma_cajennese_Ac37b_GCA_000746585.2	1	0.93	0	93.6
Arcanobacter_lacustris_GCA_000970895.1	0.13	0.2	2	40.2
Rickettsiaceae_endosymbiont_of_Stachyamoeba_lipophora_GCA_003932735.1	0.13	1	3	89
GCA_001897445.1_Rickettsiaceae_bacterium	0.2	1	2	86.3
Midichloria_mitochondrii_IricVA_GCA_000219355.1	0.13	0.53	2	77.6
Cyrtobacter_comes_endosymbiont_of_Euplotes_harpa_BOD18	0.27	0.53	1	76.3
Lyticum_sinuosum_endosymbiont_of_Paramecium_biaurelia_USBL-36I1	0.13	0.47	1	64.8
Fokinia_solitaria_GCA_003072485.1	0.13	0.53	3	66.7
Fokinia_cryptica_endosymbiont_of_Paramecium_biaurelia_US_BI_11III1	0.13	0.53	2	65.8
GCA_903878005.1_Midichloriaceae_bacterium	0.13	0.53	1	64.4
Vederia_obscura_endosymbiont_of_Plagiopyla_frontata_IBS-3	0.27	0.4	1	70.8
Bandiella_woodruffii_endosymbiont_of_Euplotes_woodruffi_NDG2	0.27	0.53	2	83.1
GCA_905479795.1_Midichloriaceae_bacterium	0.27	0.67	1	74.9
GCA_903887235.1_Midichloriaceae_bacterium	0.27	0.67	1	86.3
Grellia_incantans_H2_GCA_009690945.1	0.27	0.67	1	85.4
Aquarickettsia_rohweri_GCA_003953955.1	0.27	0.67	1	83.6
Jidaibacter_acanthamoeba_UWC36_GCA_000815465.1	0.13	0.53	2	85.4
Endosymbiont_of_Acanthamoeba_sp._UWC8_GCA_000730245.1	0.13	0.53	2	86.8
Midichloriaceae_endosymbiont_of_Reticulomyxa_filosa	0.13	0.6	1	85.4
Midichloriaceae_endosymbiont_of_Peranema_trichophorum_GCA_004210275.1	0.13	0.53	2	82.2
GCA_013288625.1_Midichloriaceae_bacterium	0.13	0.33	0	50.7
Anaplasma_phagocytophilum_strain_HZ_GCA_000013125.1	0.93	1	0	79
Anaplasma_marginale_strain_Florida_GCA_000020305.1	0.93	1	0	84
Neoehrlichia_lotoris_strain_RAC413_GCA_000964795.1	0.93	1	0	84.5
Ehrlichia_ruminantium_strain_Welgevonden_GCA_000026005.1	0.93	1	0	81.3
Ehrlichia_chaffeensis_strain_Arkansas_GCA_000013145.1	0.93	1	0	83.6
Wolbachia_endosymbiont_of_Brugia_malayi_GCA_000008385.1	0.93	1	0	80.8
Wolbachia_endosymbiont_of_Drosophila_melanogaster_GCA_000008025.1	0.93	1	0	84
Wolbachia_endosymbiont_of_Pratylenchus_penetrans_GCA_001752665.1	0.93	0.93	1	78.1
Neorickettsia_sennetsu_strain_Miyayama_GCA_000013165.1	0.87	1	0	73.1
Neorickettsia_helminthoeca_strain_Oregon_GCA_000632985.1	0.87	1	0	69.4
Xenolissoclinum_pacificiensis_L6_GCA_000512675.1	0.93	0.47	0	60.3
Echinorickettsia_raffii_H1_GCA_018101195.1	0.93	1	0	80.4
Anaplasmataceae_symbiont_of_Acropora_tenuis_Sesoko1_GCA_014132315.1	0.93	0.93	0	71.7
GCA_903864455.1_Anaplasmataceae_bacterium	0.87	0.93	0	62.1
Deianiraea_vastatrix_GCA_007993655.1	0.13	0.53	1	65.8
GCA_017444125.1_Deianiraeaceae_bacterium	0.13	0.2	1	60.3
GCA_017444095.1_Deianiraeaceae_bacterium	0.13	0.27	1	58
GCA_002395105.1_Deianiraeaceae_bacterium	0.13	0.13	1	54.3
GCA_002394665.1_Deianiraeaceae_bacterium	0.13	0.27	1	63.9
GCA_905480015.1_Deianiraeaceae_bacterium	1	0.87	0	70.3
GCA_018969185.1_Gamibacteraceae_bacterium	1	0.8	0	89.5
GCA_002359655.1_Gamibacteraceae_bacterium	1	1	0	92.7
GCA_009693885.1_Gamibacteraceae_bacterium	0.67	0.67	0	59.8
GCA_903872175.1_Gamibacteraceae_bacterium	1	1	0	94.5
GCA_903831915.1_Gamibacteraceae_bacterium	1	1	0	93.6
GCA_017999675.1_Gamibacteraceae_bacterium	1	0.93	0	90.9
GCA_903927415.1_Gamibacteraceae_bacterium	1	1	0	85.8
GCA_903878685.1_Gamibacteraceae_bacterium	1	1	0	92.2
GCA_903917585.1_Gamibacteraceae_bacterium	0.93	1	0	84.5
GCA_001768015.1_Gamibacteraceae_bacterium	1	0.93	0	91.8
GCA_903837365.1_Gamibacteraceae_bacterium	1	0.93	0	79.5
GCA_014190355.1_Gamibacteraceae_bacterium	1	1	0	91.3
GCA_903959715.1_Gamibacteraceae_bacterium	1	1	0	80.8
GCA_009925685.1_Gamibacteraceae_bacterium	1	1	0	86.8
GCA_009921385.1_Gamibacteraceae_bacterium	0.93	1	0	73.1
GCA_016778745.1_Gamibacteraceae_bacterium	0.87	0.8	0	79.9
GCA_905478245.1_Gamibacteraceae_bacterium	1	1	0	91.8
GCA_905478165.1_Gamibacteraceae_bacterium	1	1	0	87.7
GCA_017620845.1_Gamibacteraceae_bacterium	0.13	0.33	0	68
GCA_017475895.1_Gamibacteraceae_bacterium	0.2	0.33	0	72.1
GCA_016780625.1_Diomedesiaceae_bacterium	0.93	0.8	0	72.1
GCA_018659605.1_Diomedesiaceae_bacterium	0.73	1	0	78.1
GCA_018659145.1_Diomedesiaceae_bacterium	1	0.93	0	90.4
GCA_016778805.1_Diomedesiaceae_bacterium	0.93	0.93	0	77.6
GCA_002787635.1_Athabascaceae_bacterium	1	1	0	97.7
GCA_002422795.1_Athabascaceae_bacterium	1	0.87	0	91.8
GCA_013288565.1_Jistubacteraceae_bacterium	0.6	0.6	0	72.1
GCA_903821695.1_Jistubacteraceae_bacterium	1	1	0	96.8
GCA_010031735.1_Jistubacteraceae_bacterium	1	1	0	94.1
GCA_003531345.1_Jistubacteraceae_bacterium	0.67	0.8	0	64.4
GCA_013288575.1_Arkhamiaceae_bacterium	0.67	0.6	0	55.3
GCA_002787615.1_Arkhamiaceae_bacterium	0.8	0.87	0	76.7
GCA_013289445.1_Mitibacteraceae_bacterium	0.73	0.4	0	56.2
GCA_013288985.1_Mitibacteraceae_bacterium	0.6	0.73	0	55.7
GCA_013288335.1_Mitibacteraceae_bacterium	0.87	0.87	0	65.3
GCA_013288305.1_Mitibacteraceae_bacterium	0.4	0.4	0	53
GCA_009926845.1_Mitibacteraceae_bacterium	0.87	0.8	0	80.4
GCA_005792635.1_Mitibacteraceae_bacterium	1	0.87	0	89
GCA_003241645.1_Mitibacteraceae_bacterium	0.93	1	1	92.2
GCA_002422745.1_Mitibacteraceae_bacterium	0.93	0.87	0	58.4
GCA_002725445.1_Mitibacteraceae_bacterium	0.67	0.6	0	71.7
GCA_002422205.1_Mitibacteraceae_bacterium	1	1	0	92.2
GCA_002346425.1_Mitibacteraceae_bacterium	1	0.93	0	93.2
GCA_002423155.1_Mitibacteraceae_bacterium	1	0.93	0	96.3
GCA_004293935.1_Mitibacteraceae_bacterium	0.87	1	0	86.8
GCA_002291925.1_Mitibacteraceae_bacterium	1	1	0	94.5
GCA_002291845.1_Mitibacteraceae_bacterium	0.87	1	0	83.1

Nucleotide synthesis
1
0.5
0

Nucleotide transporters
8
6
4
2
0

purines
pyrimidines
tlc_nucleotide_translocase
Busco_s_copy

Supplementary Figure 25: single-gene phylogenies for nucleotide and amino acid biosynthesis. Phylogenetic trees of the singles genes of biosynthetic pathways for nucleotides and amino acids (Supplementary Data 7). On each tree, the members of each *Rickettsiales* family are highlighted by different background colours. On each branch, support values by SH-aLRT with 1000 replicates and by 1000 ultrafast bootstraps are reported. The tree scales stand for estimated sequence divergences.

pyrimidine/01_carA_1MUB9@1224

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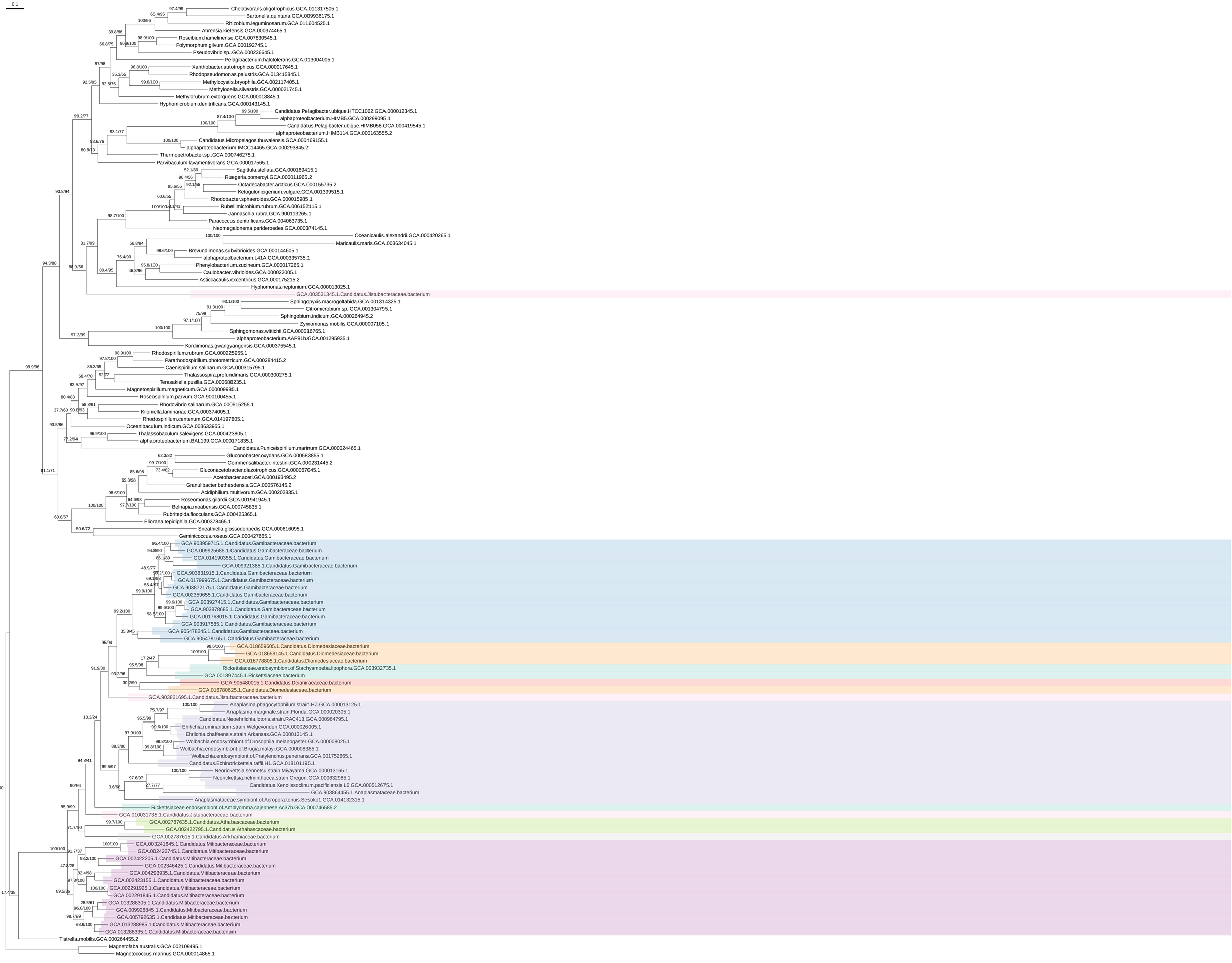

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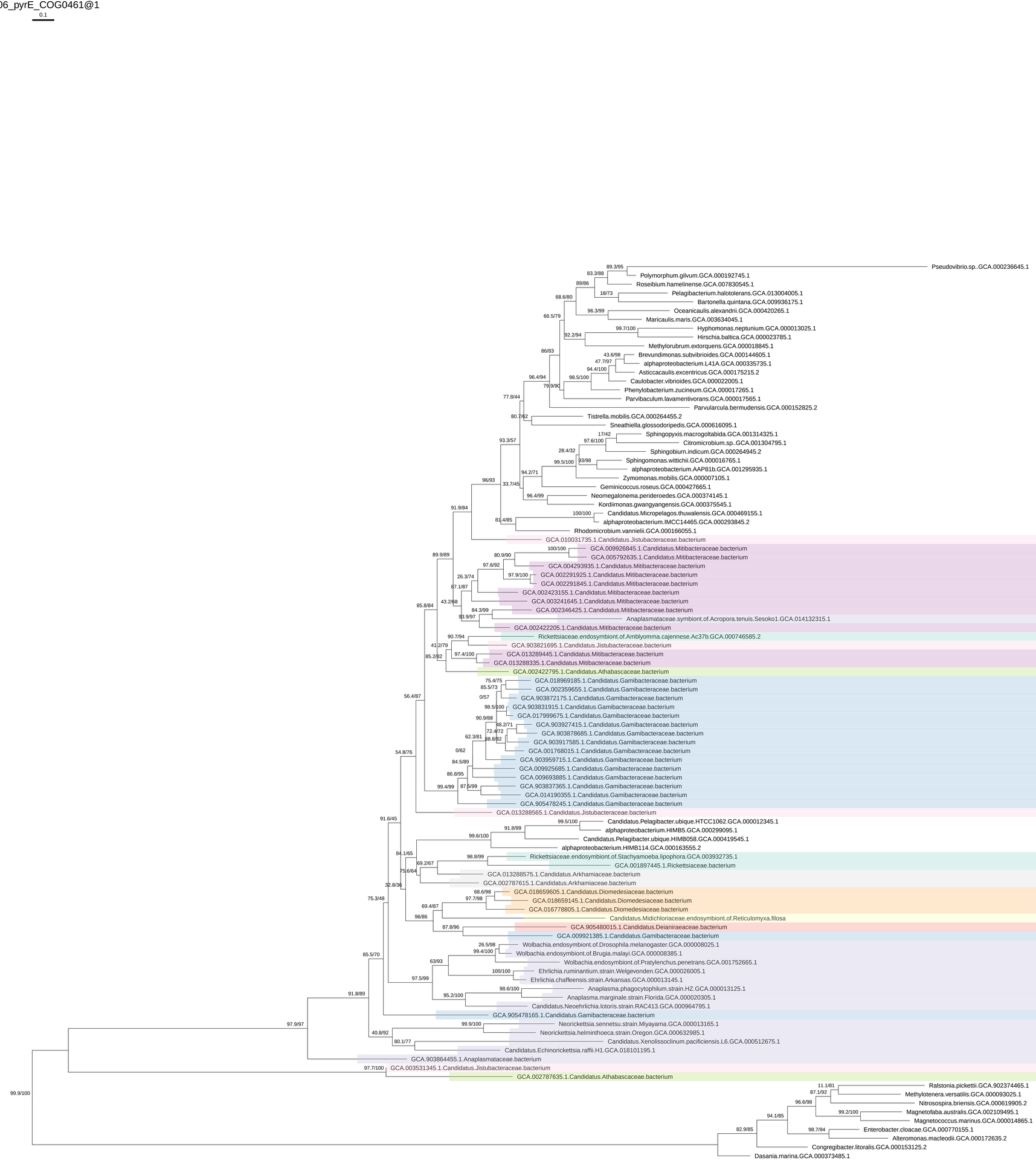

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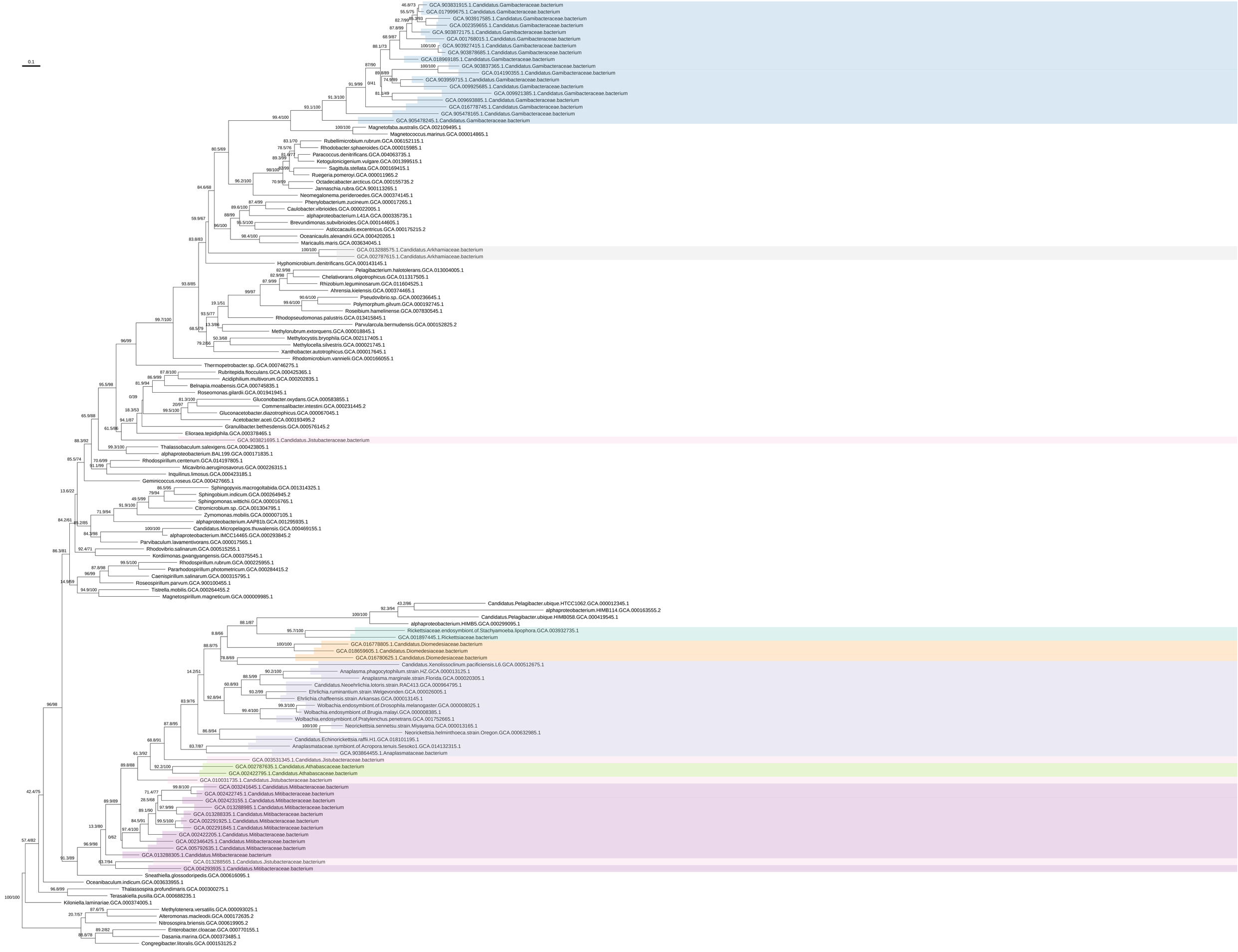

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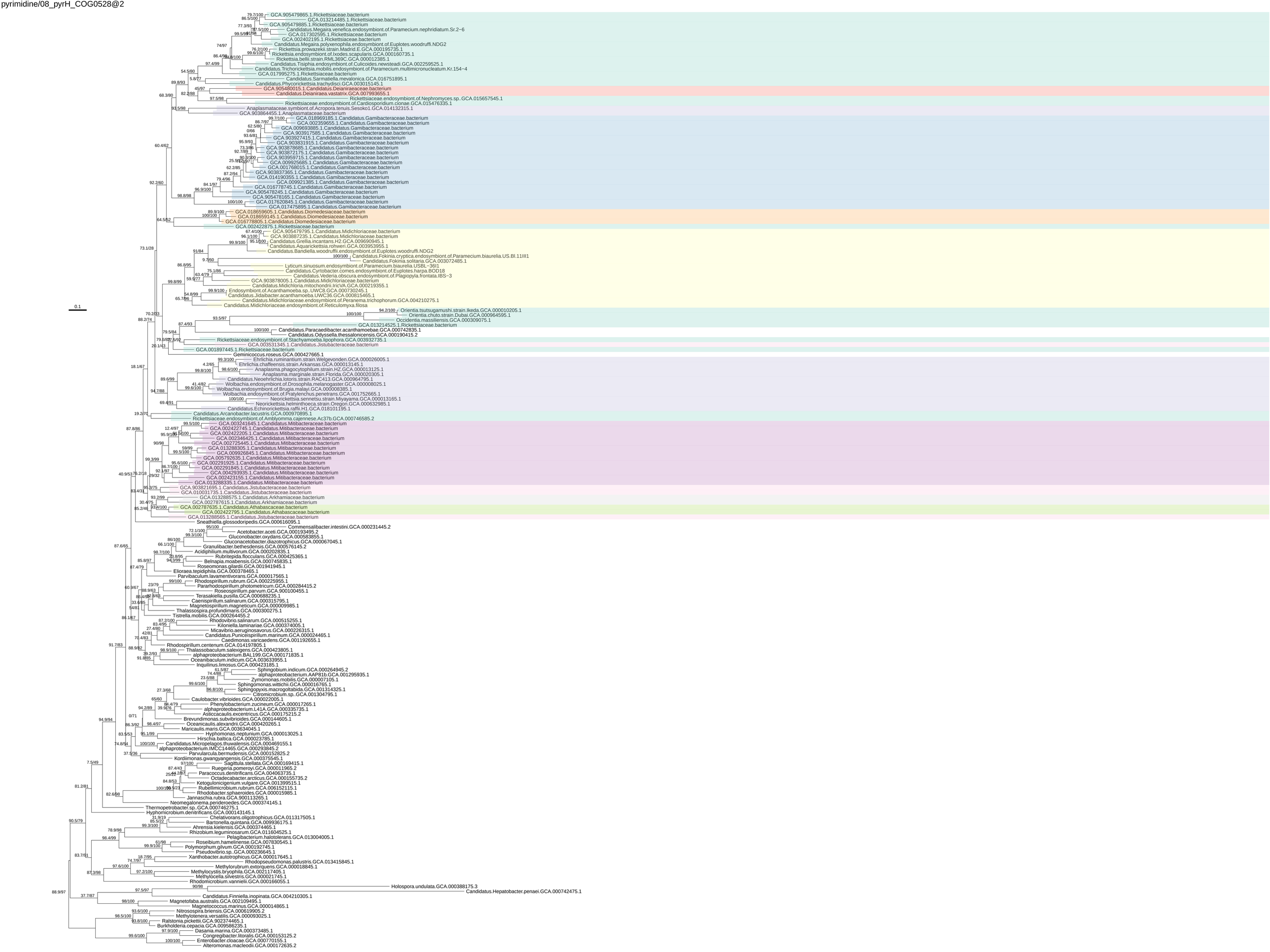

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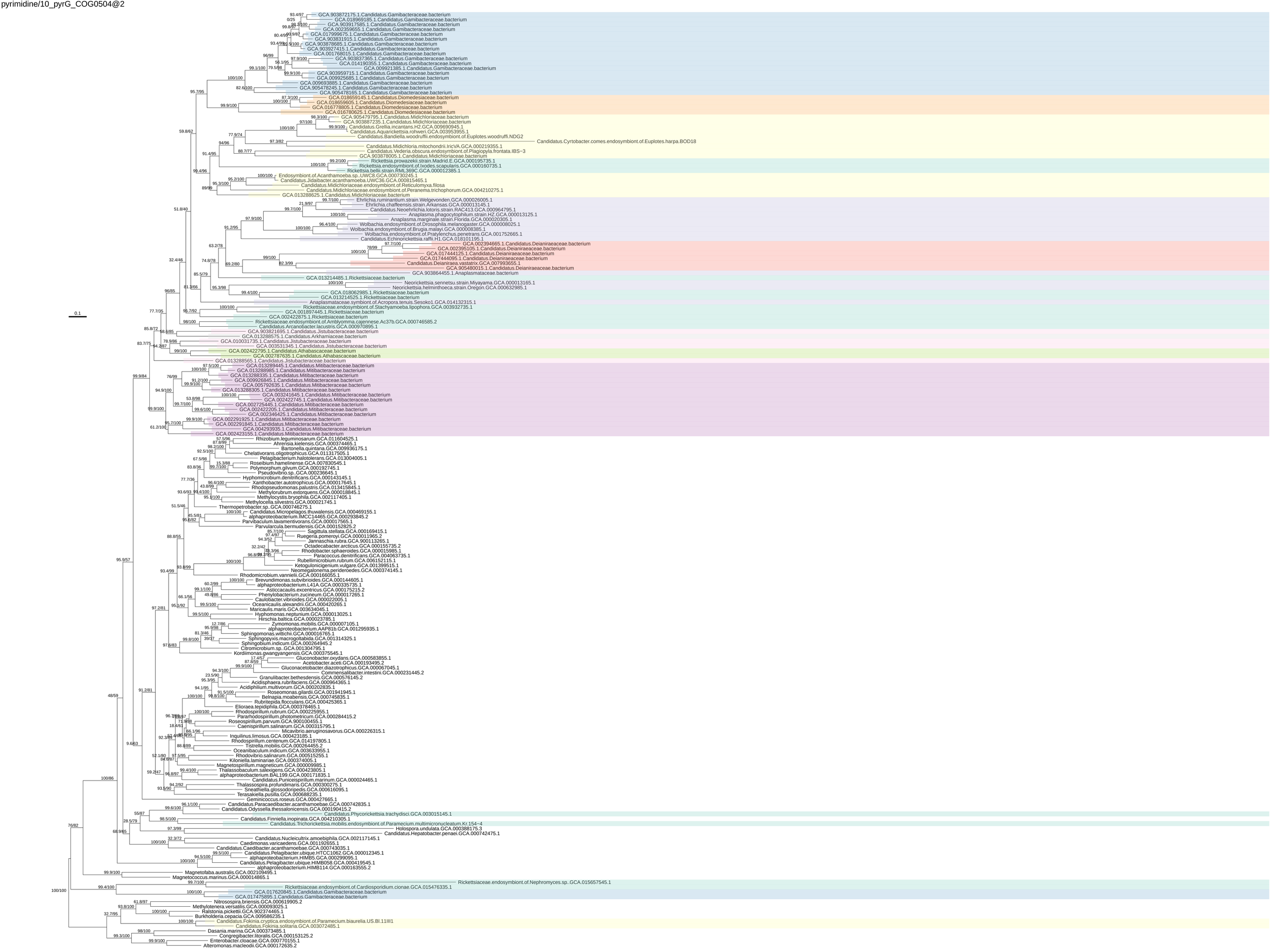

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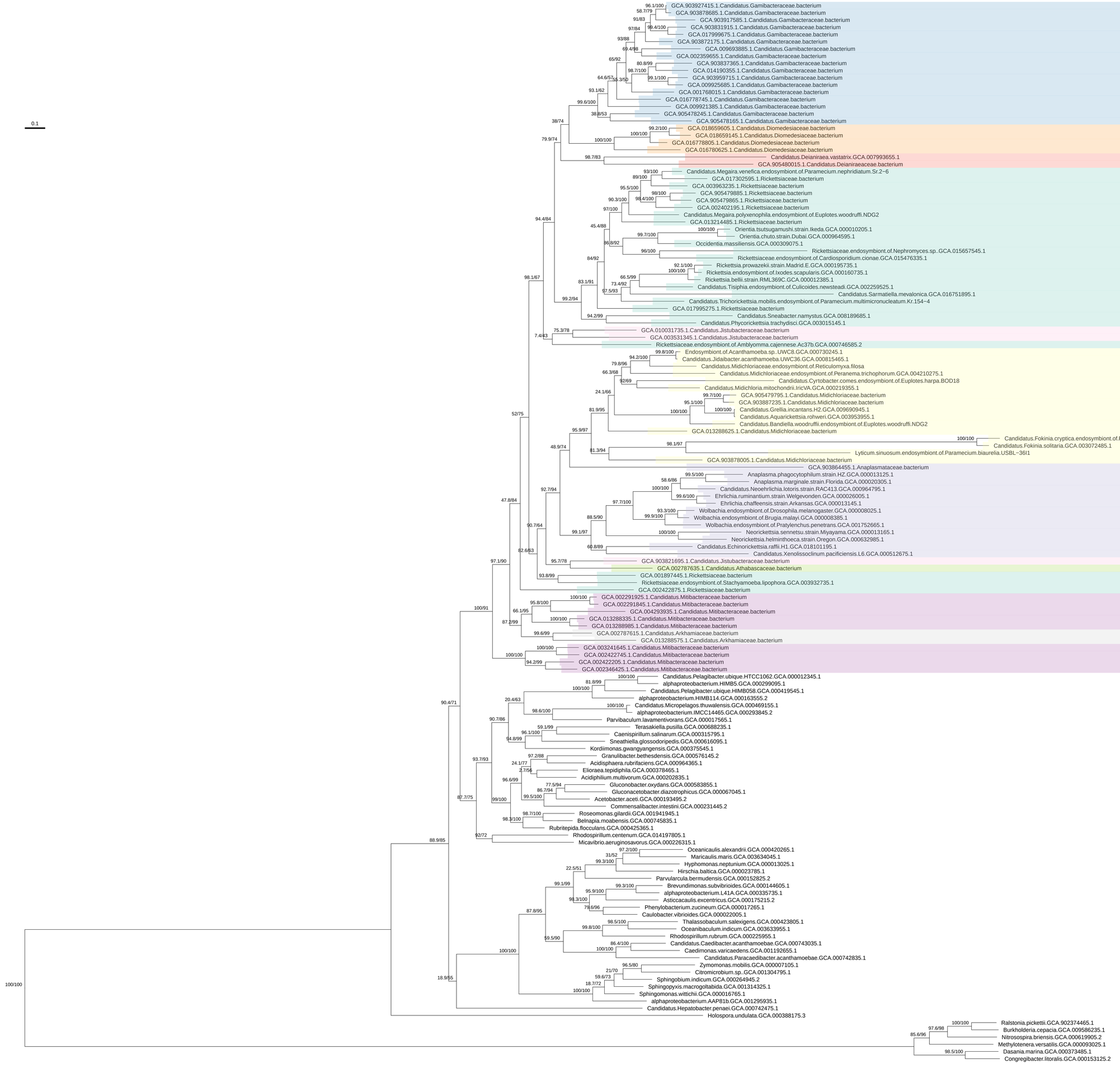

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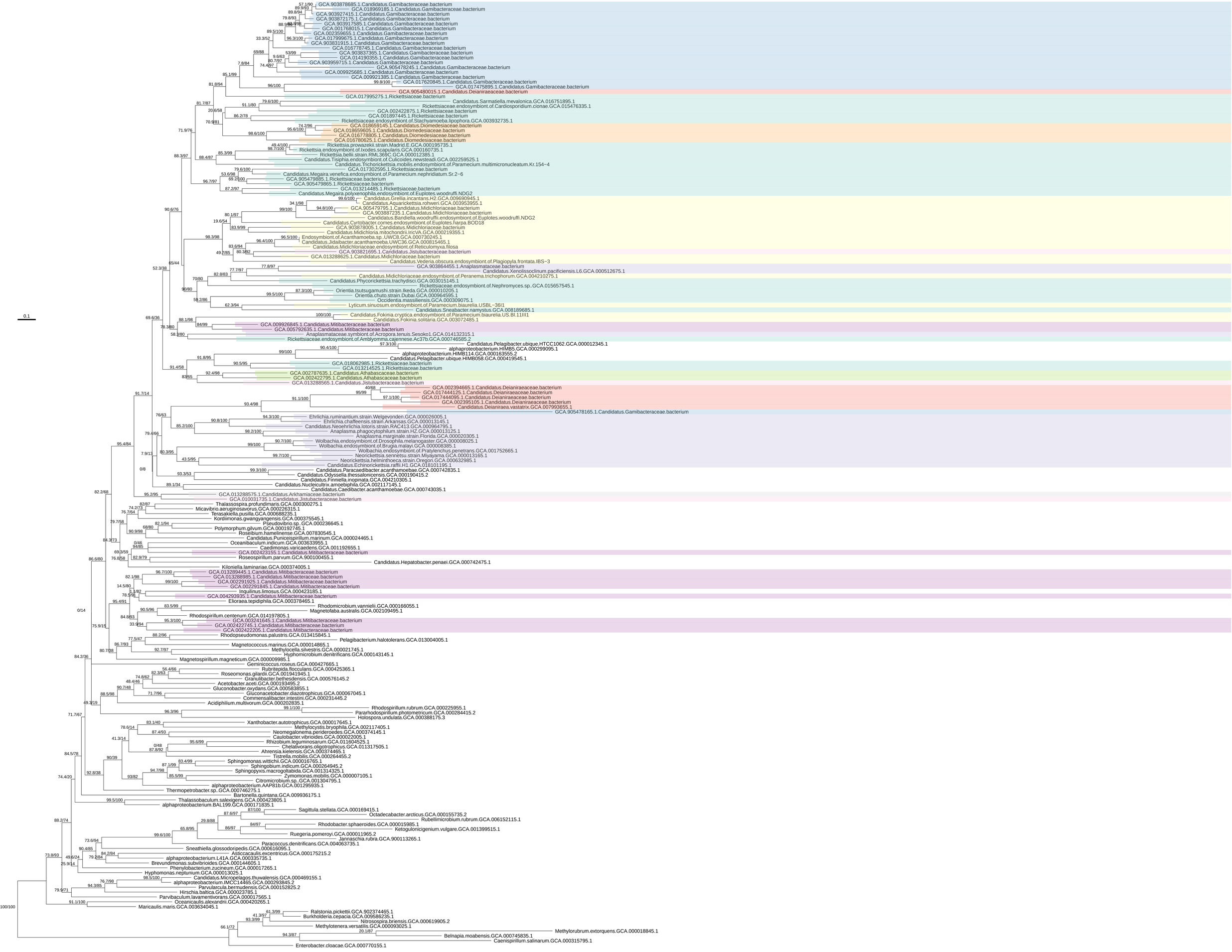
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Wolbachia.endosymbiont.of.Pratylenchus.penetrans.GCA.001752665.1
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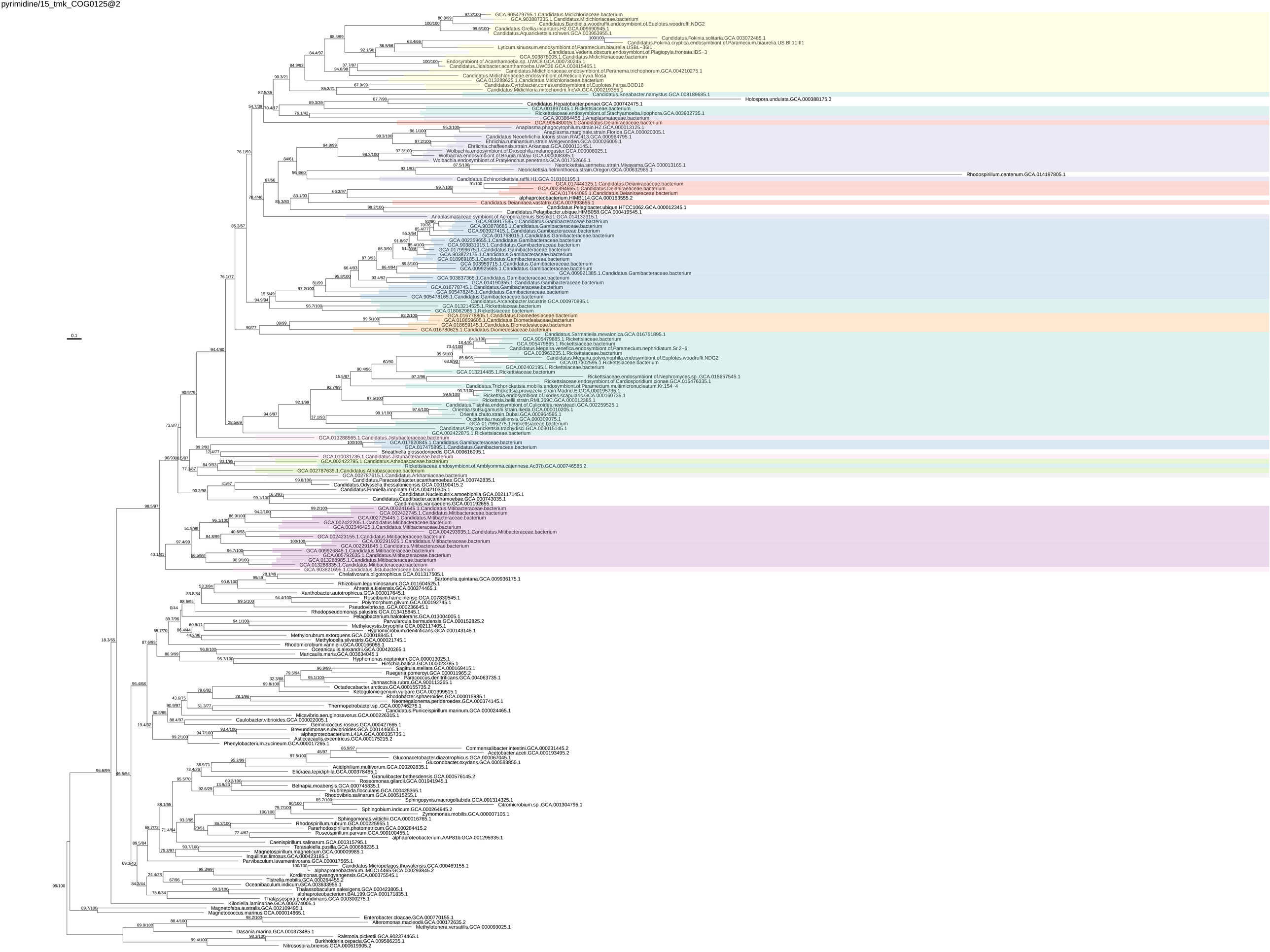

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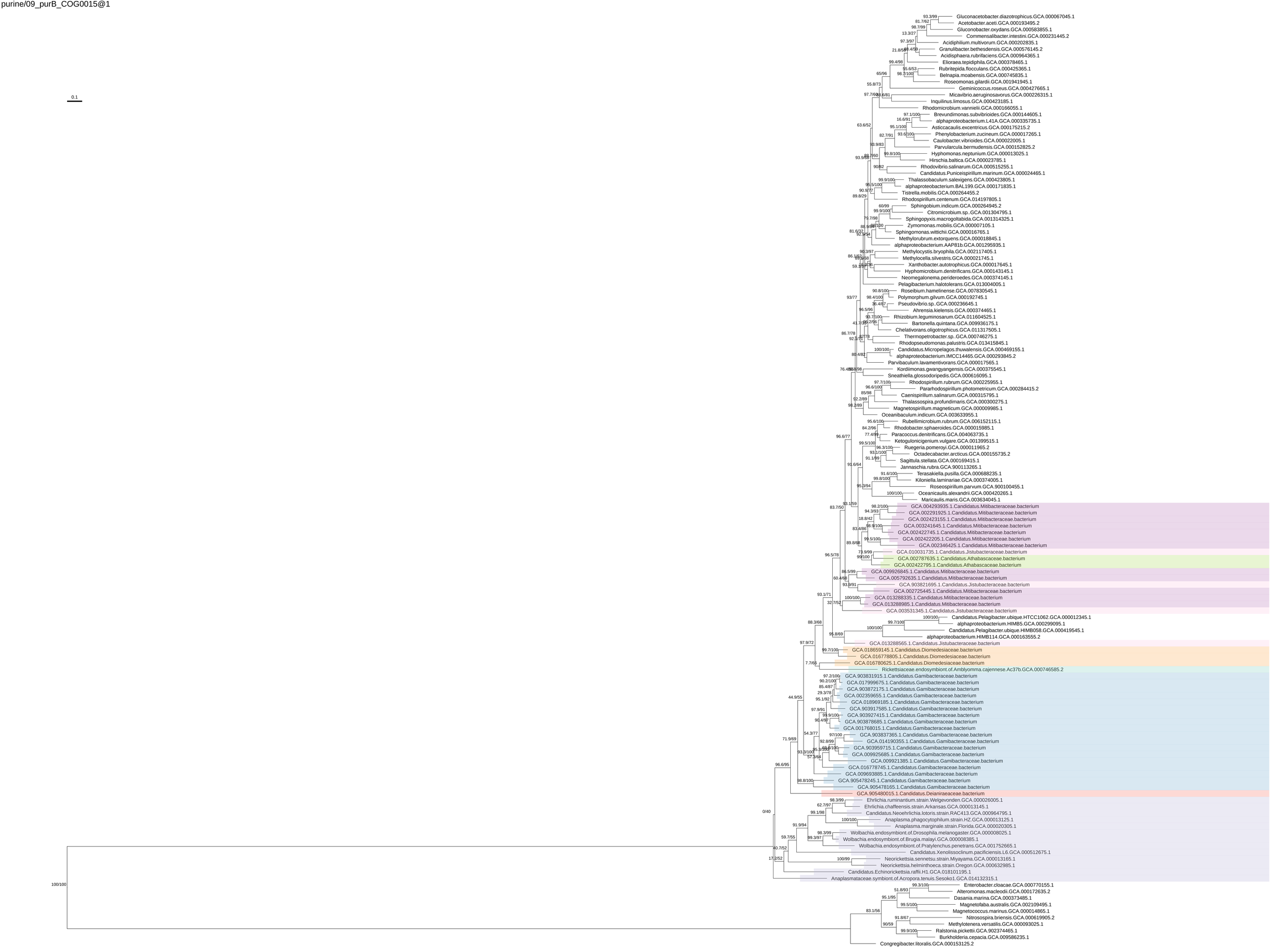

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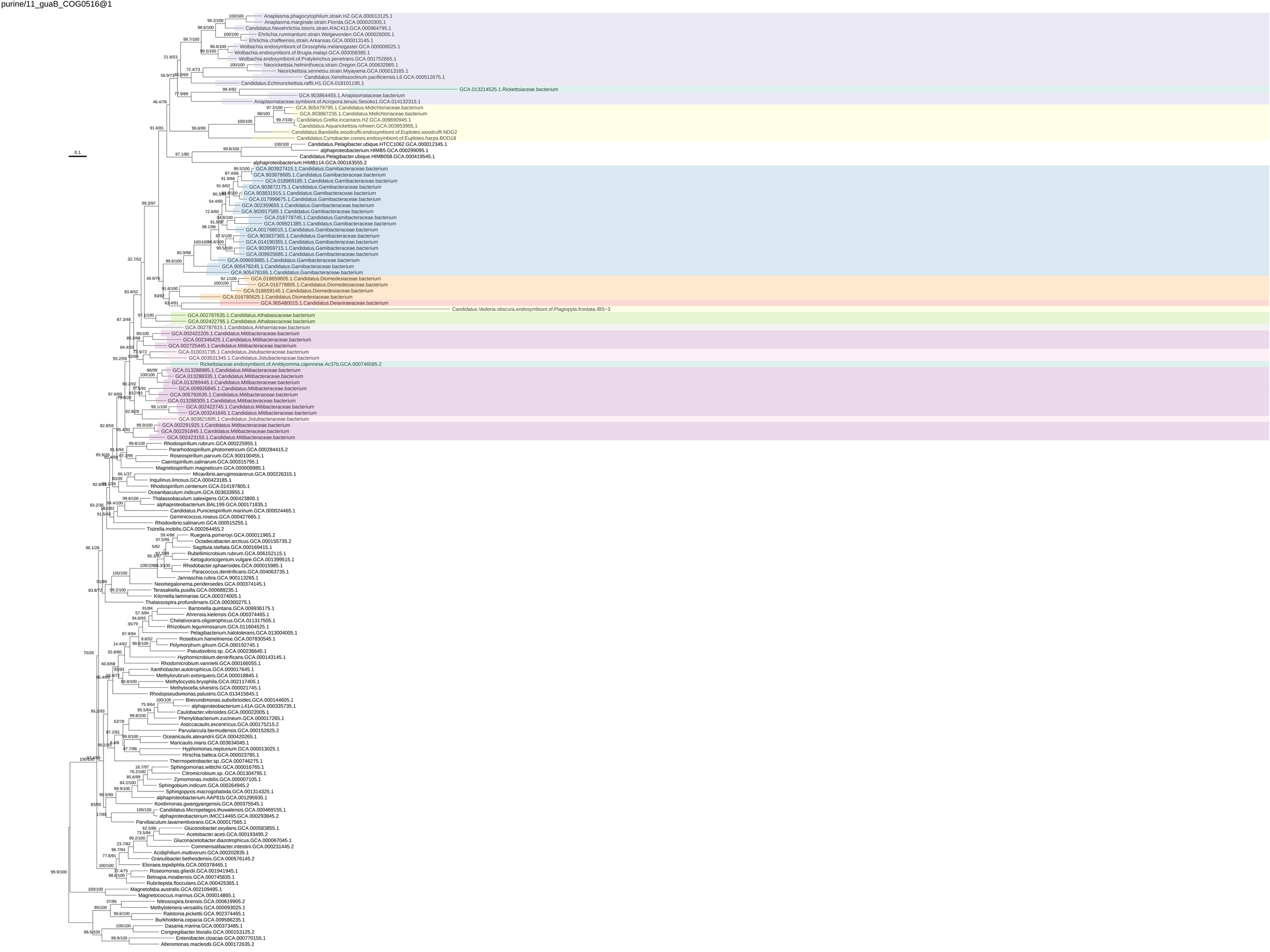
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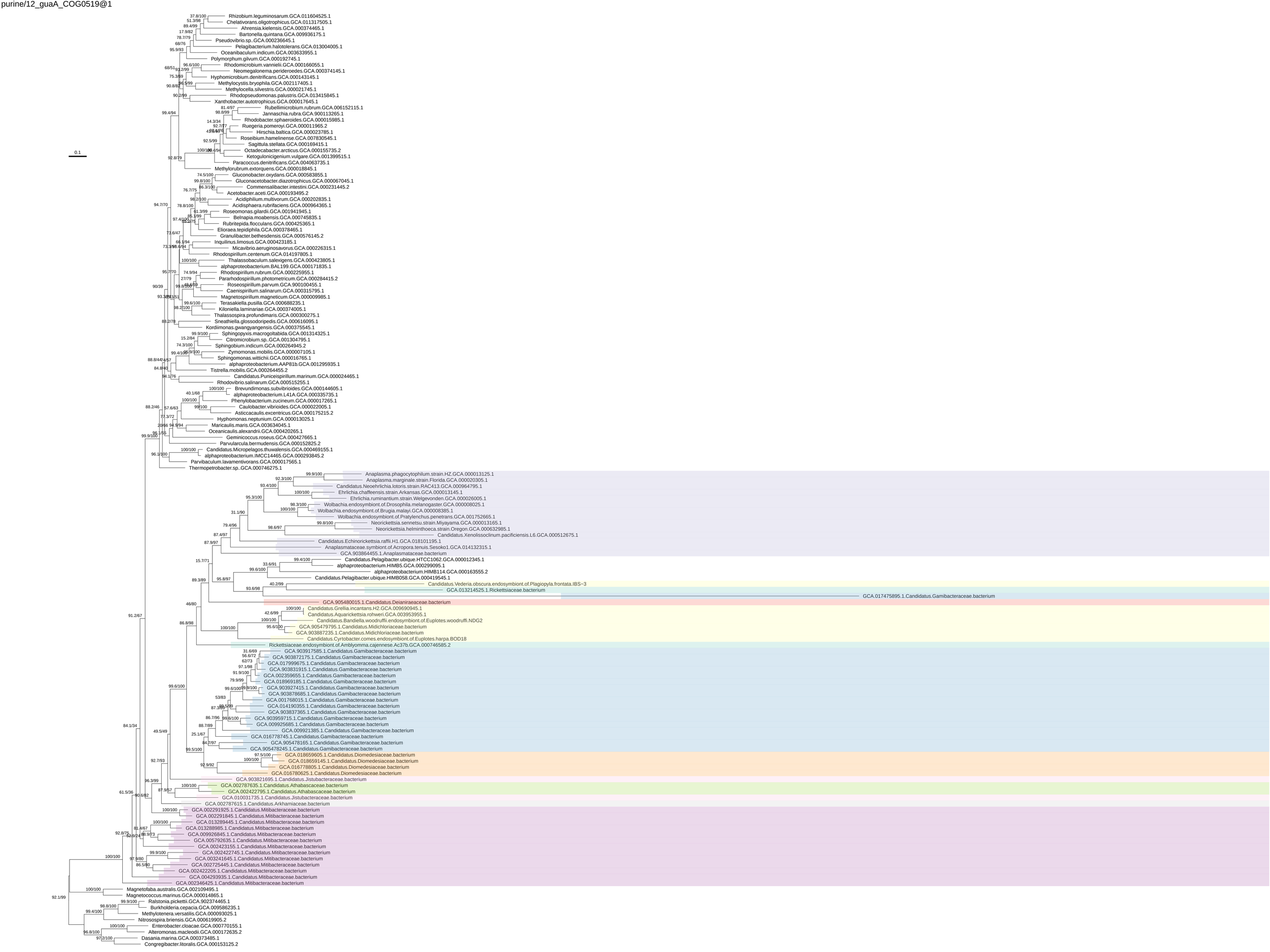

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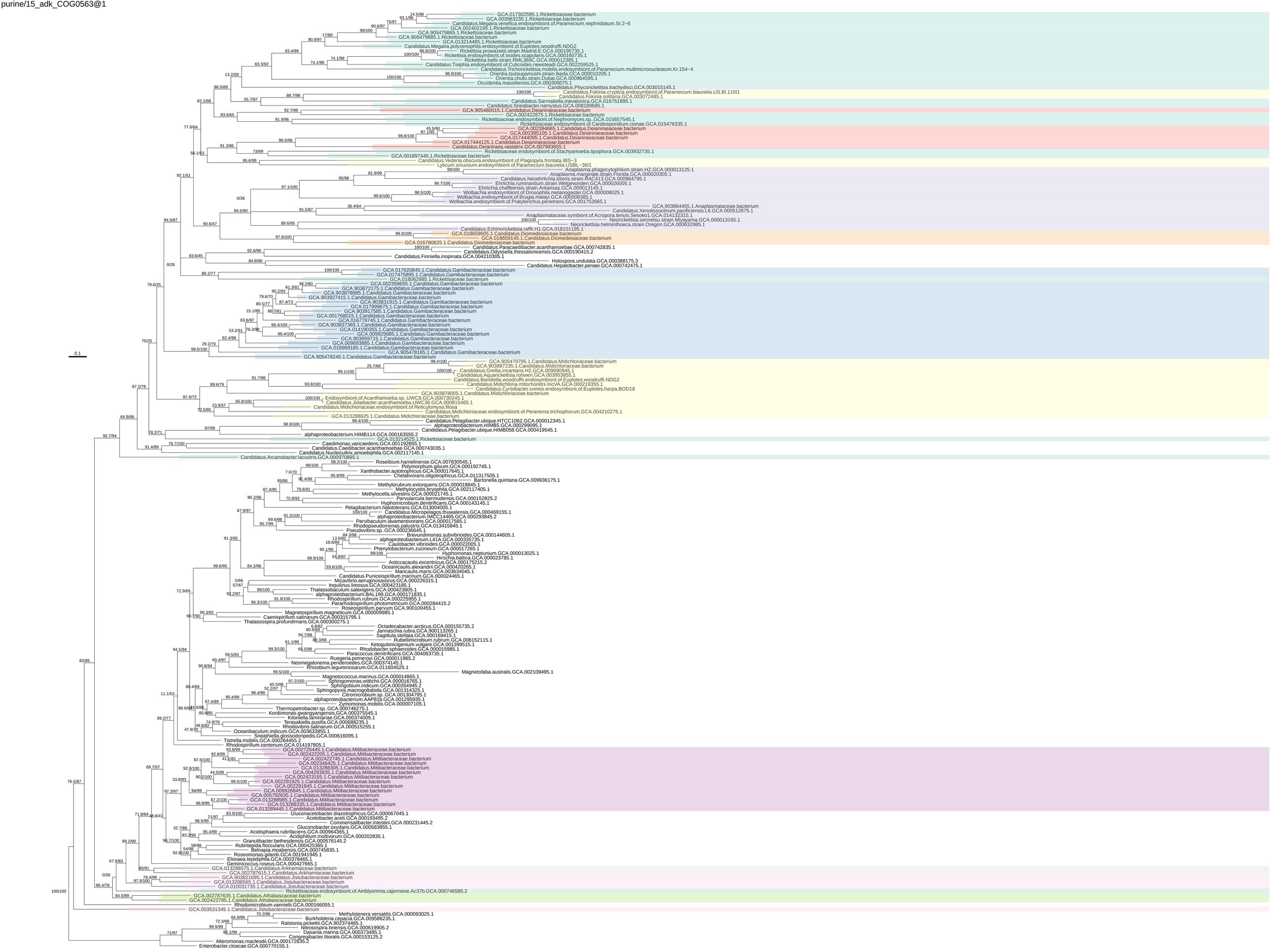

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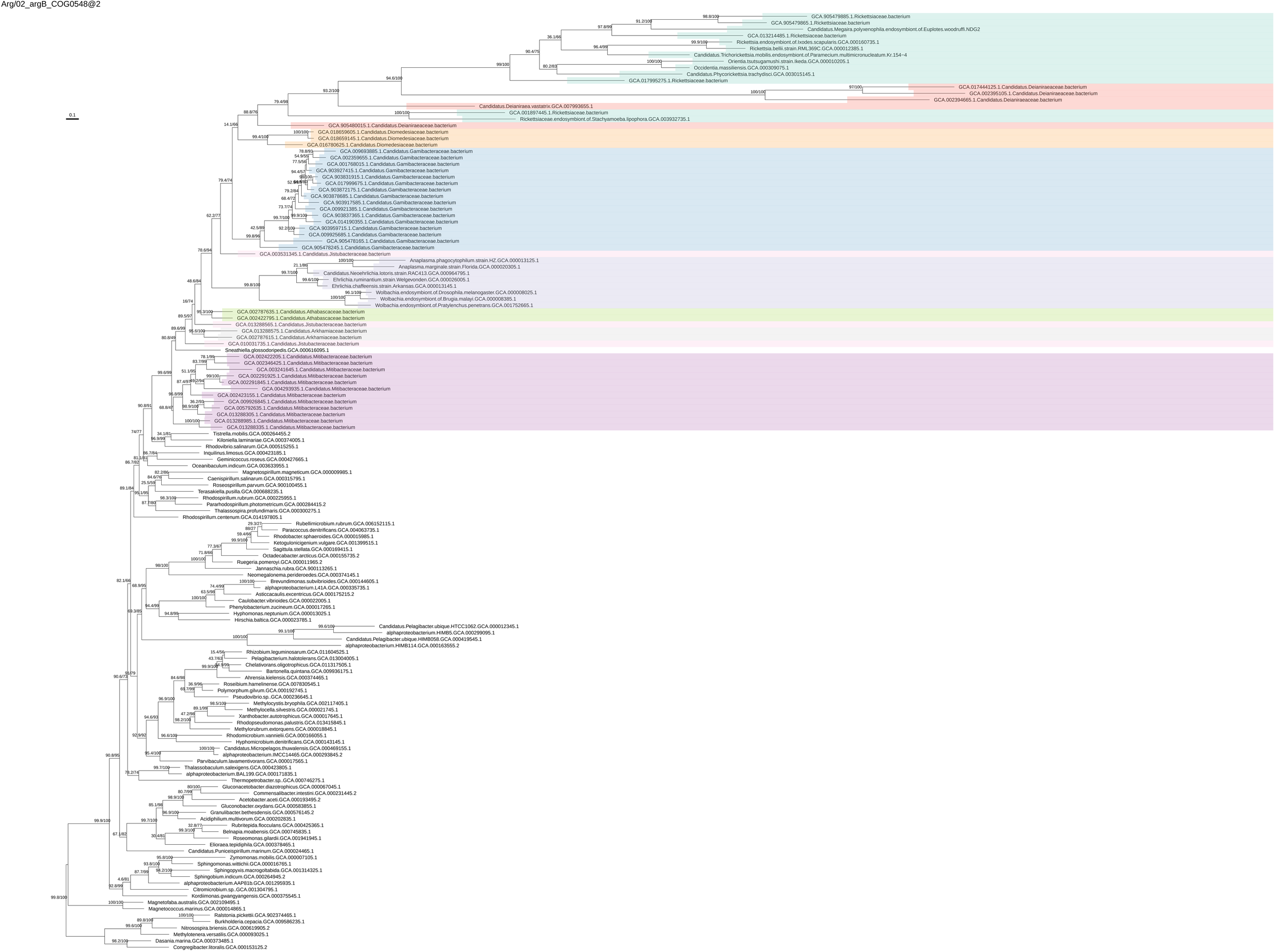

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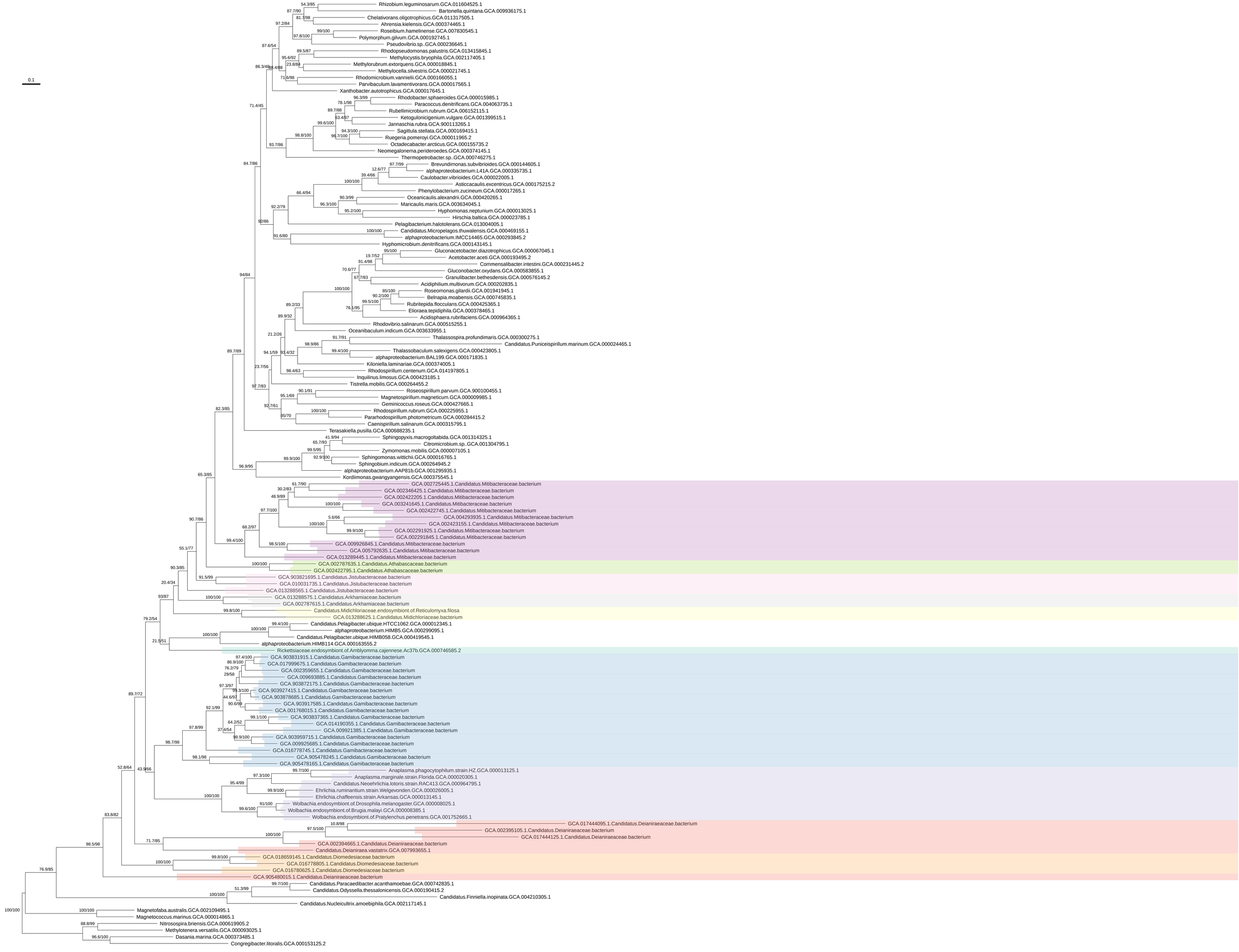

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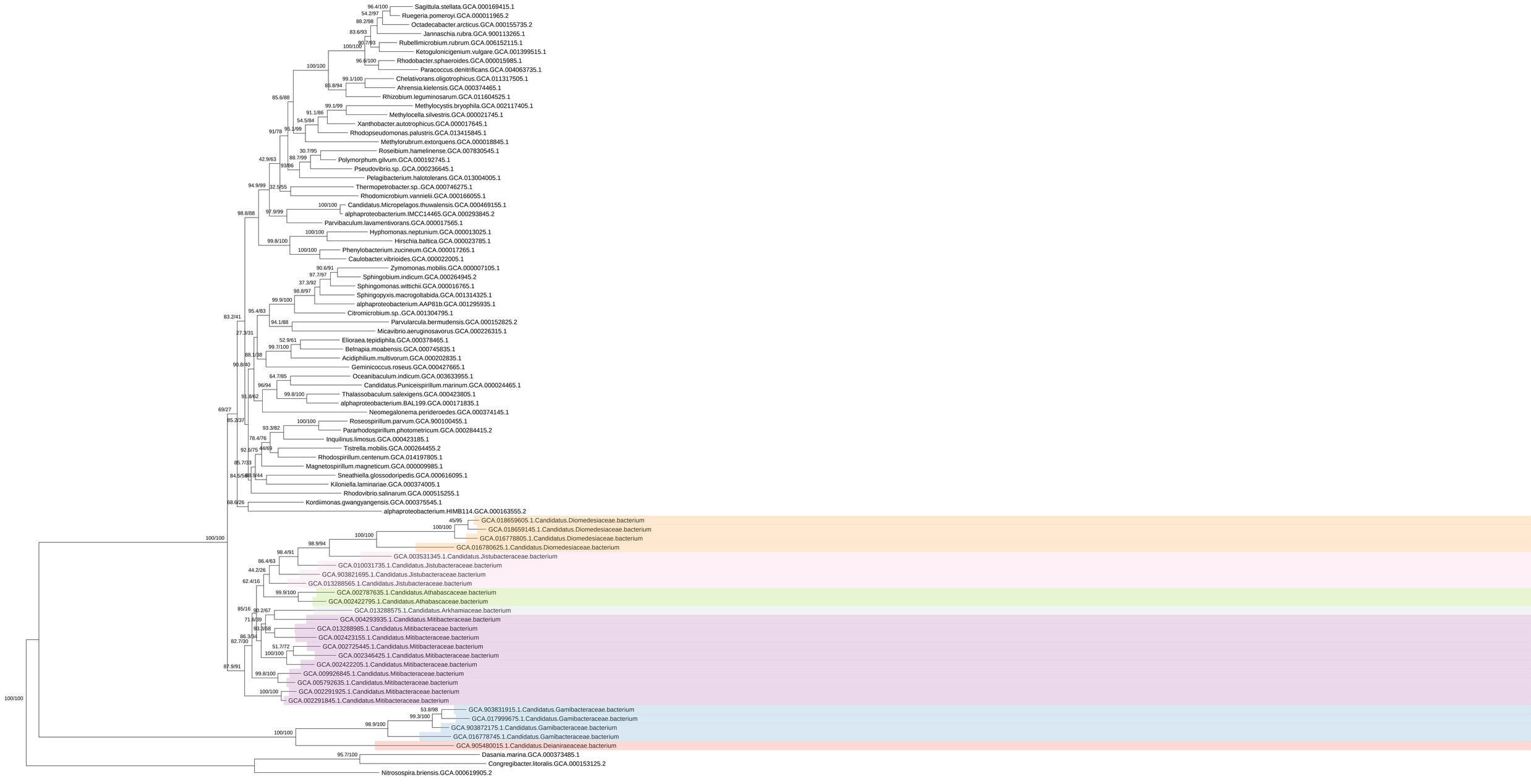

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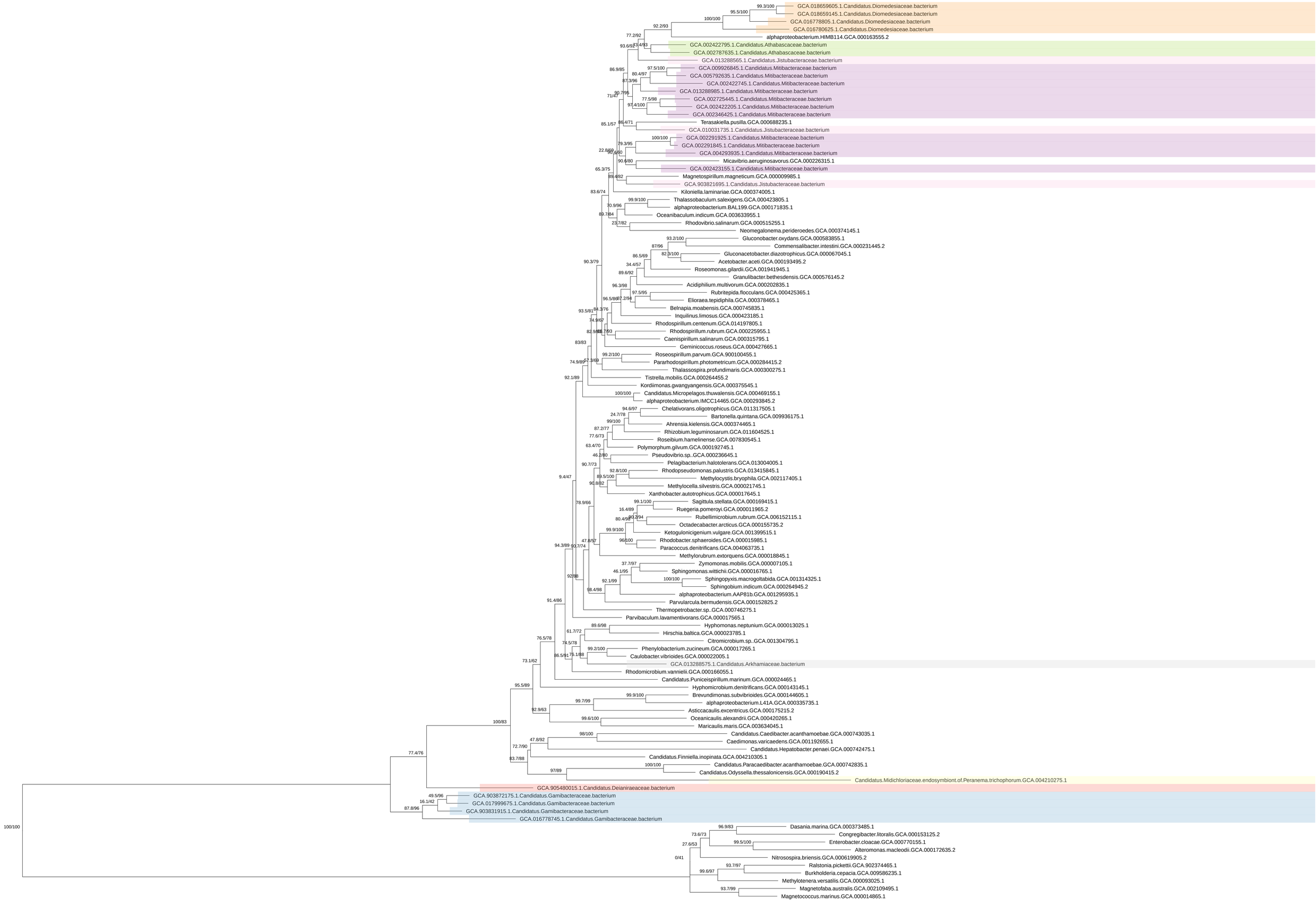

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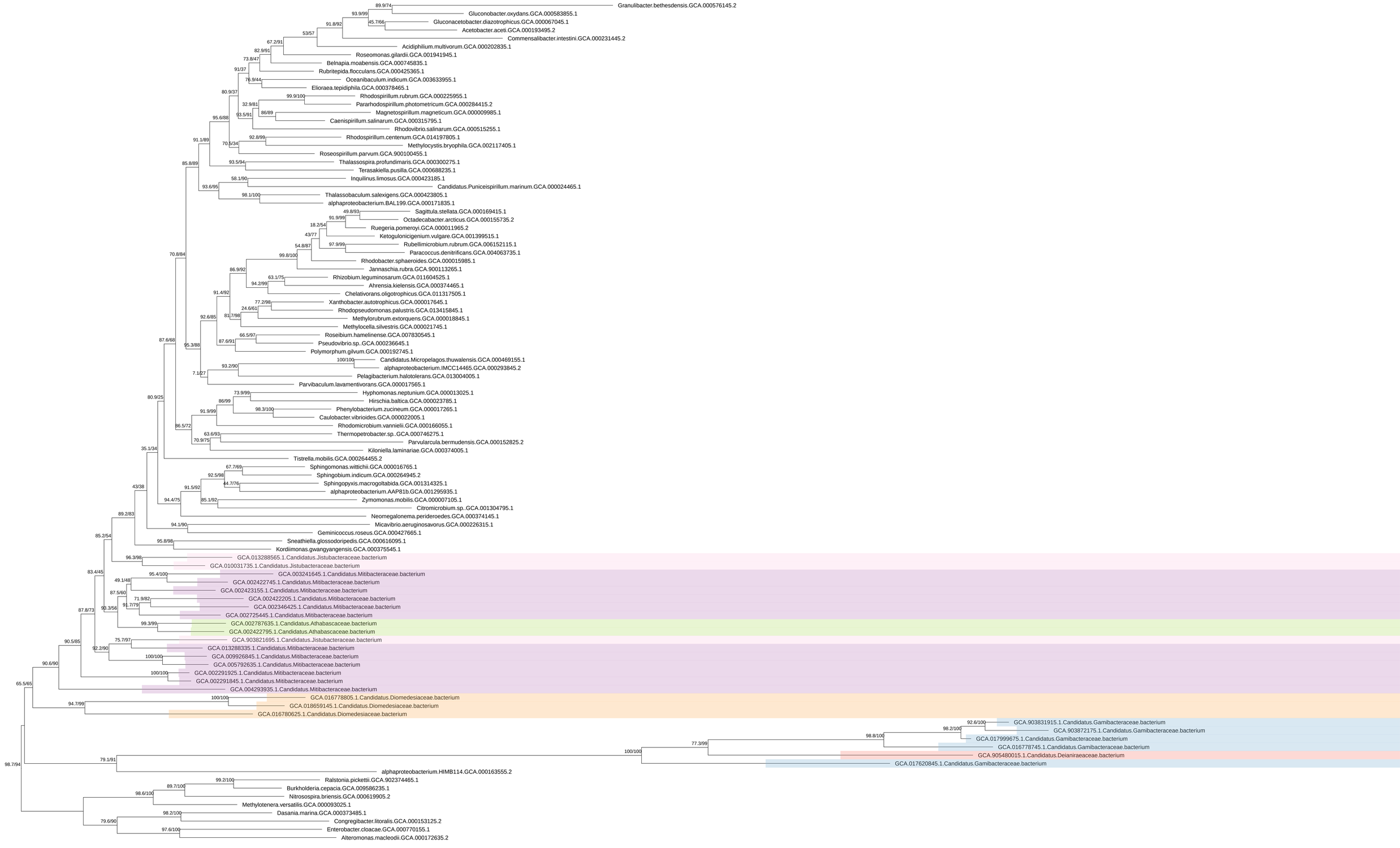

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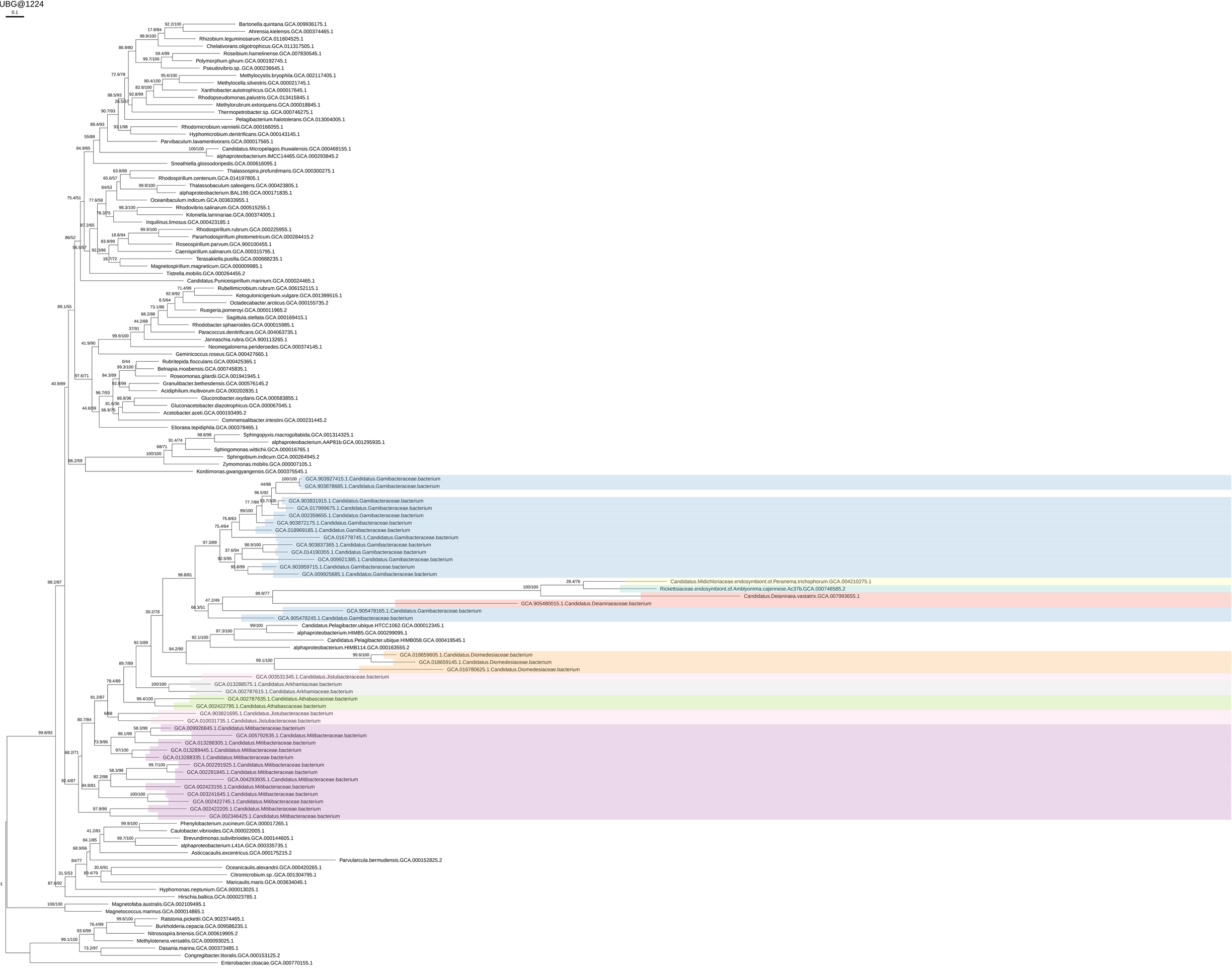

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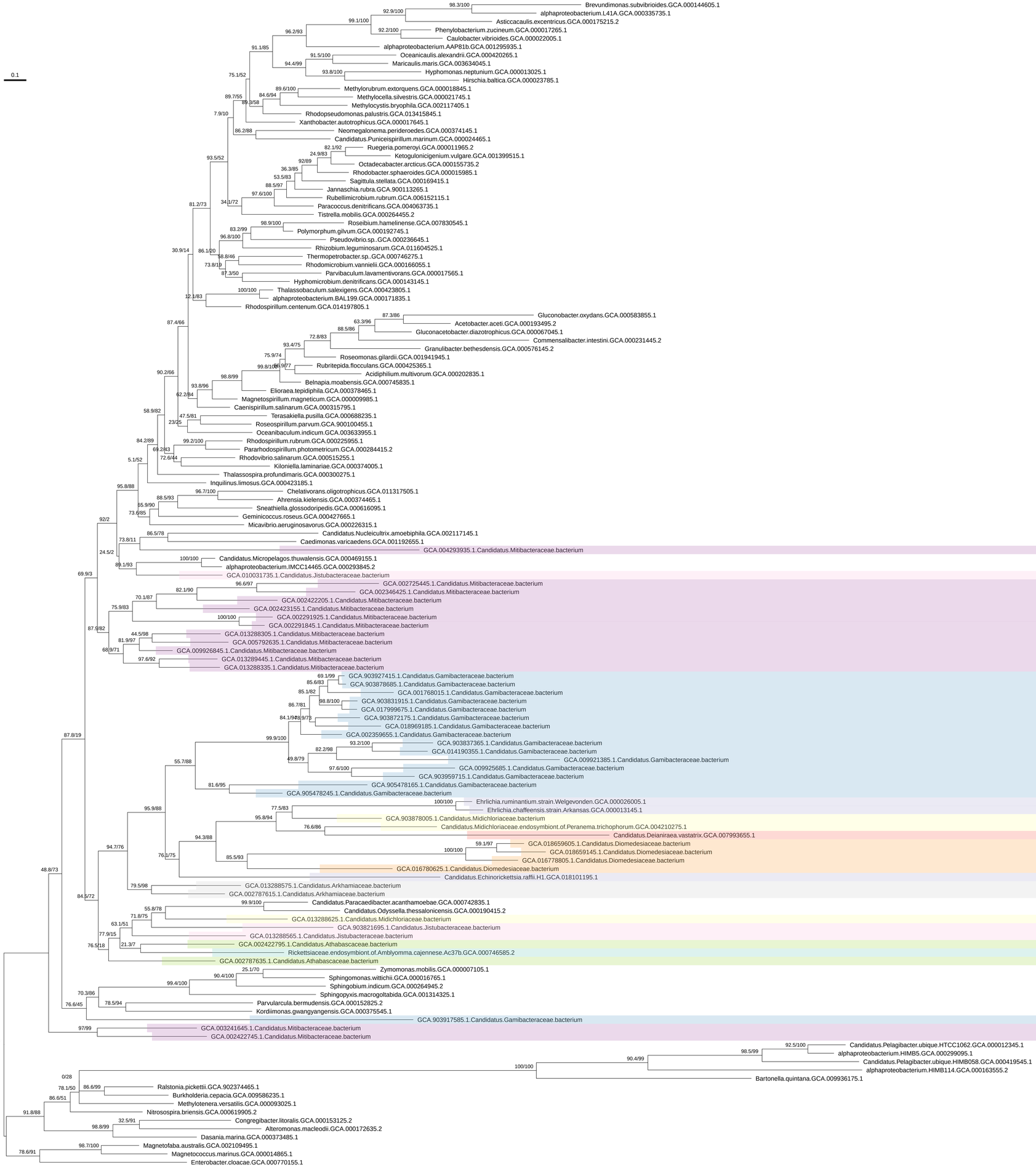

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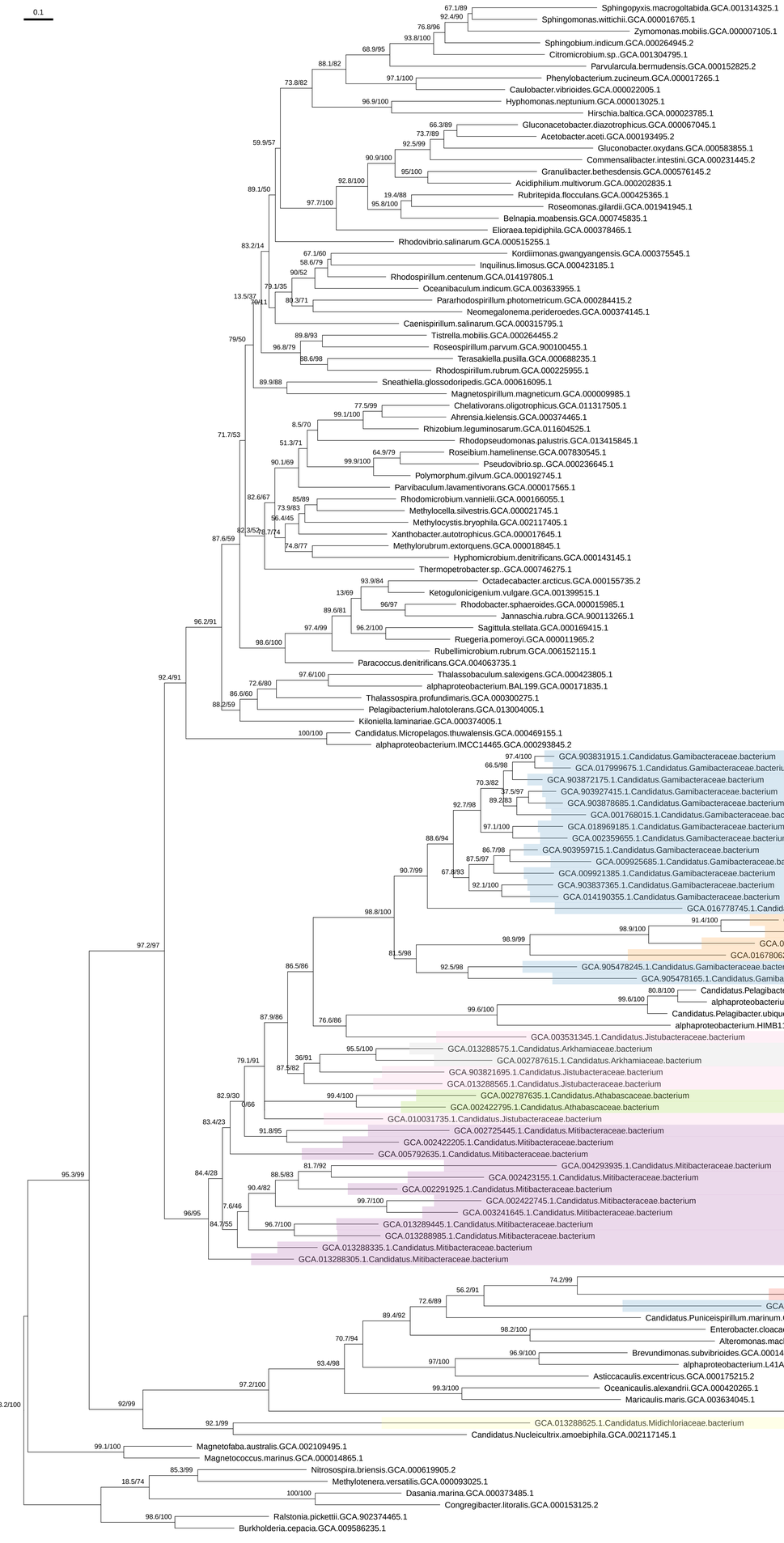

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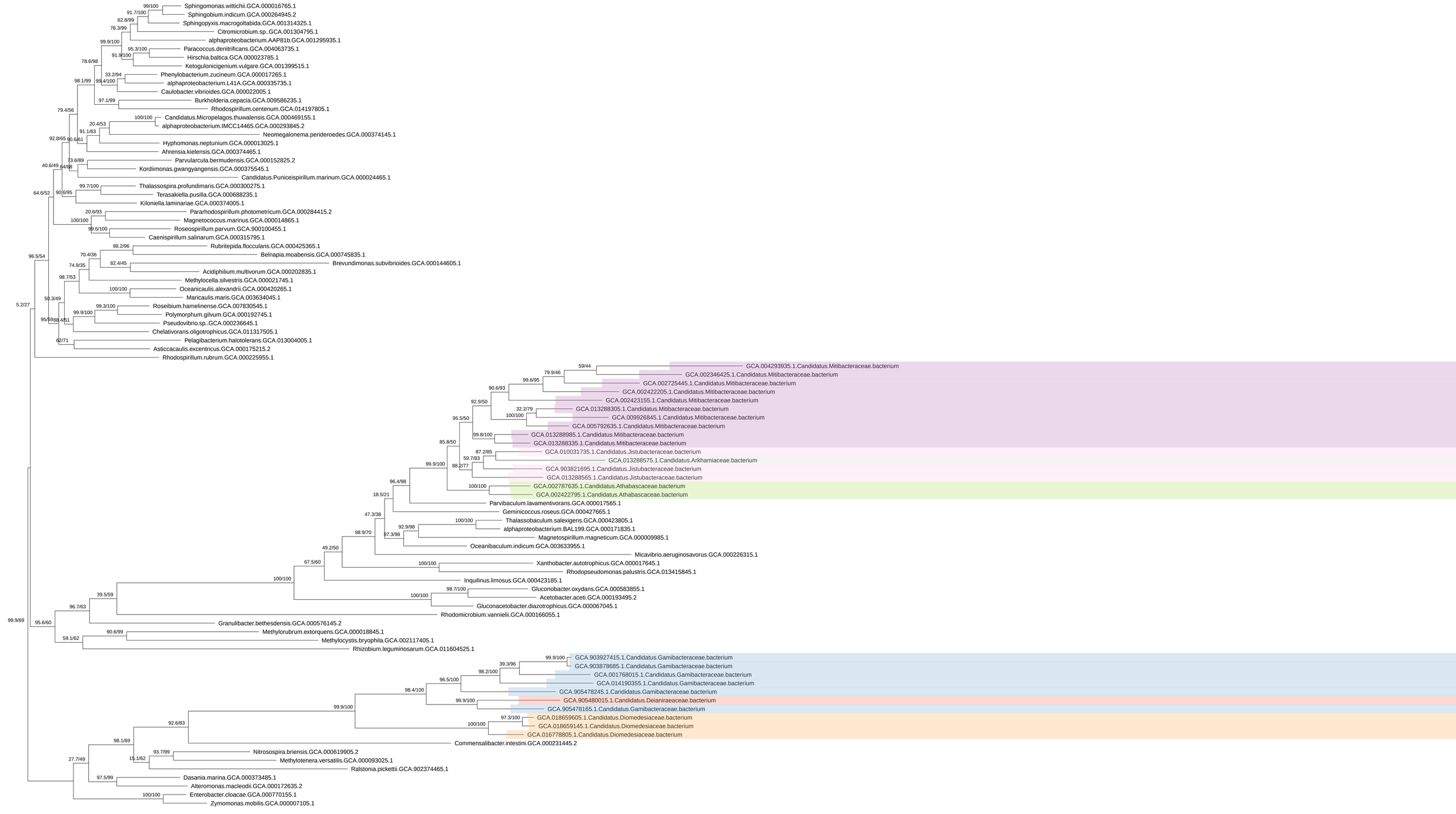

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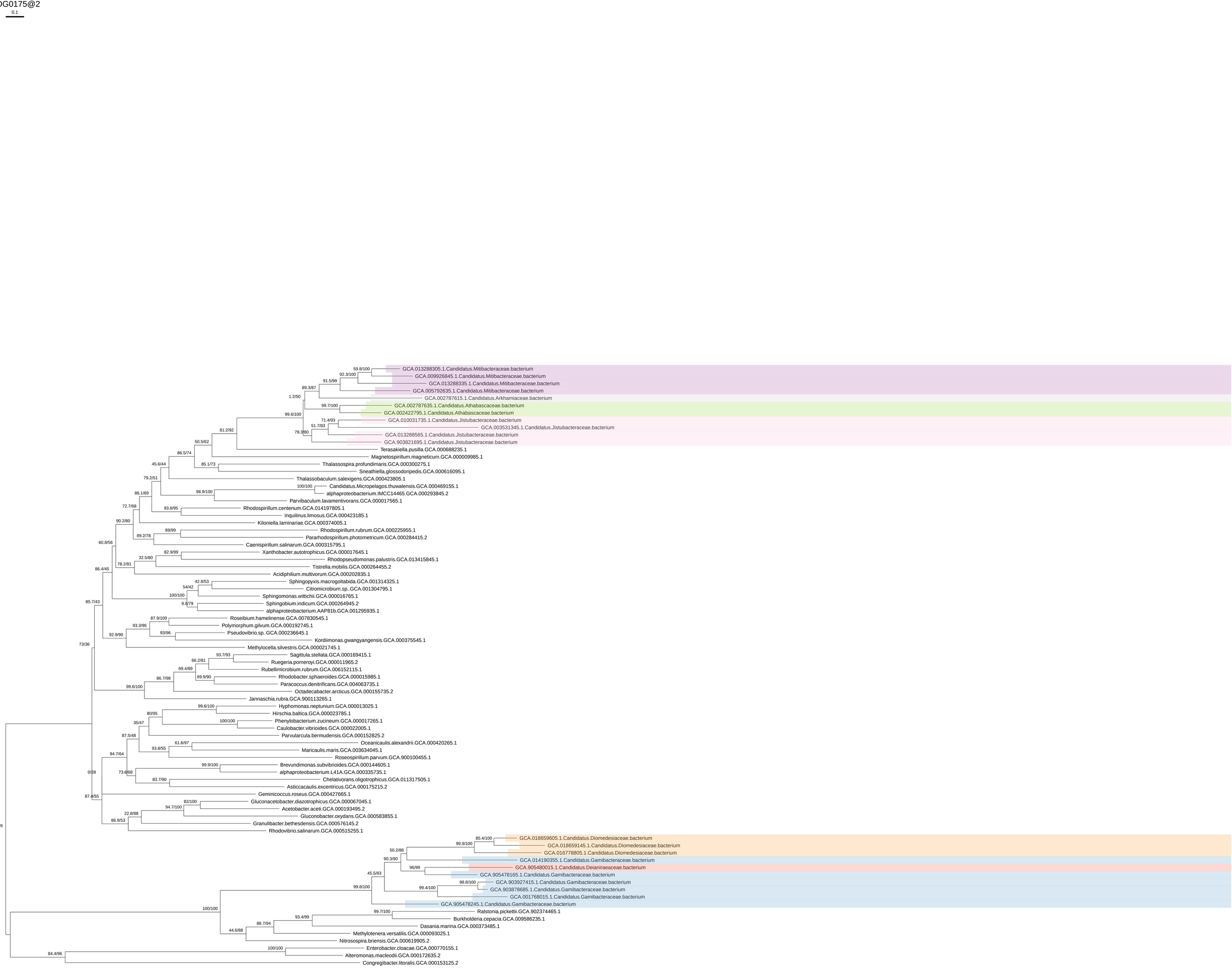

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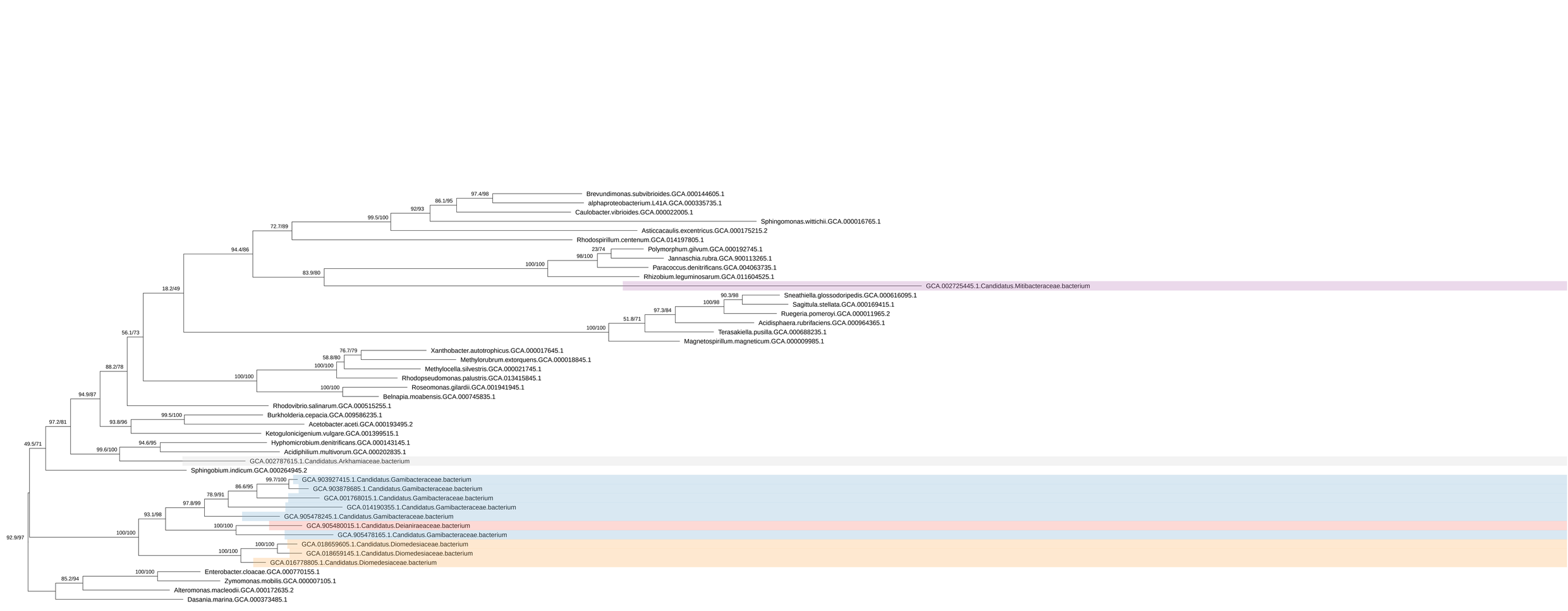

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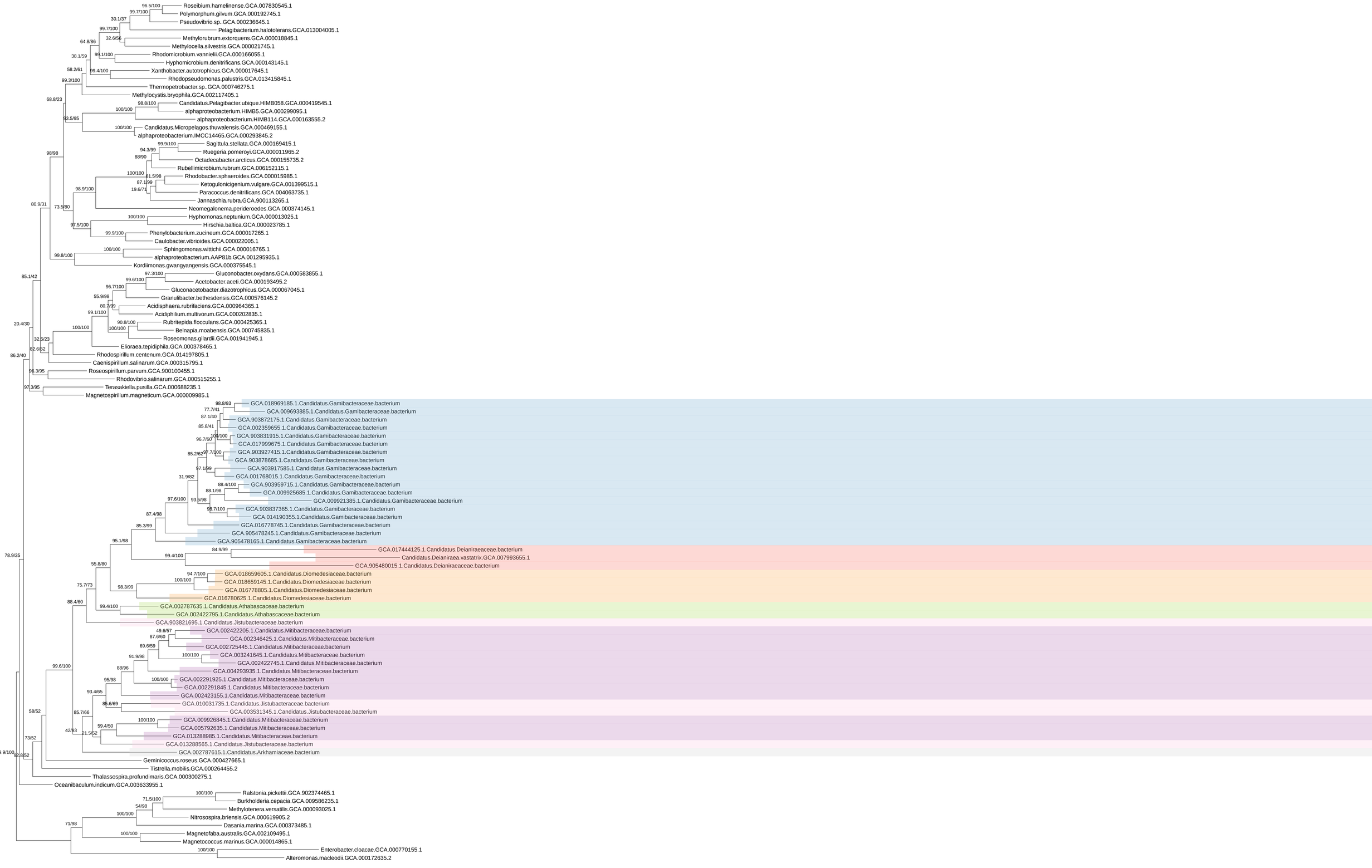

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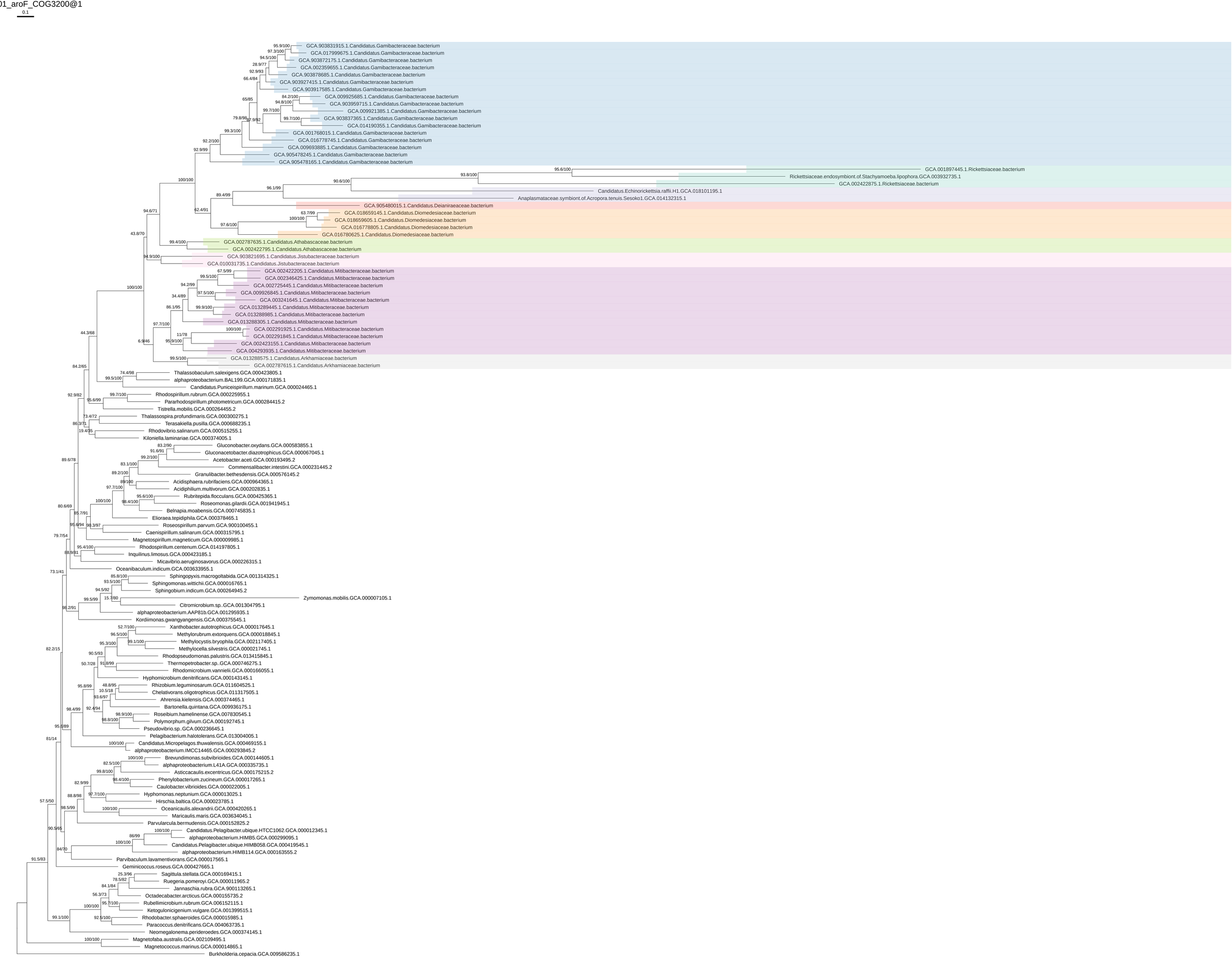

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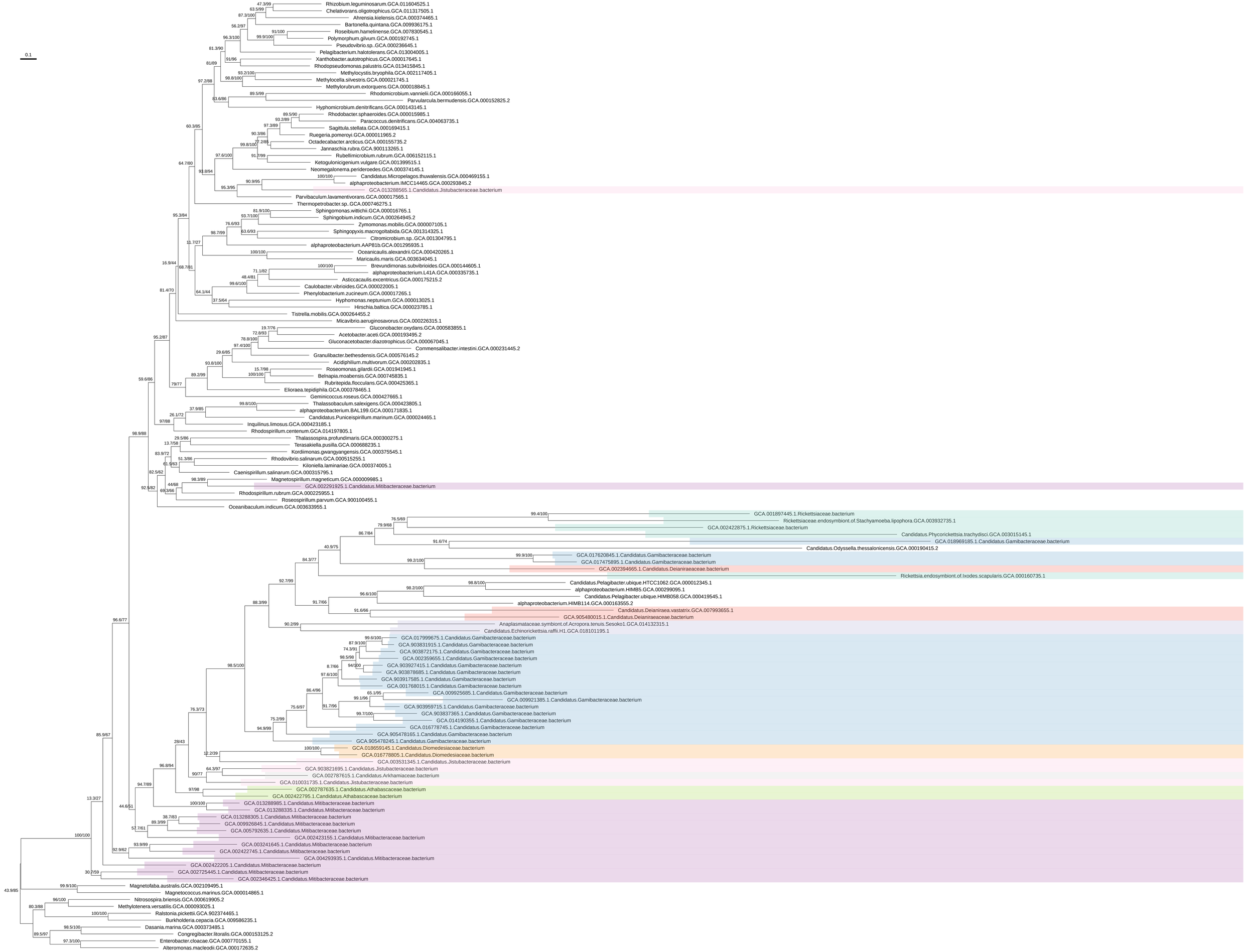

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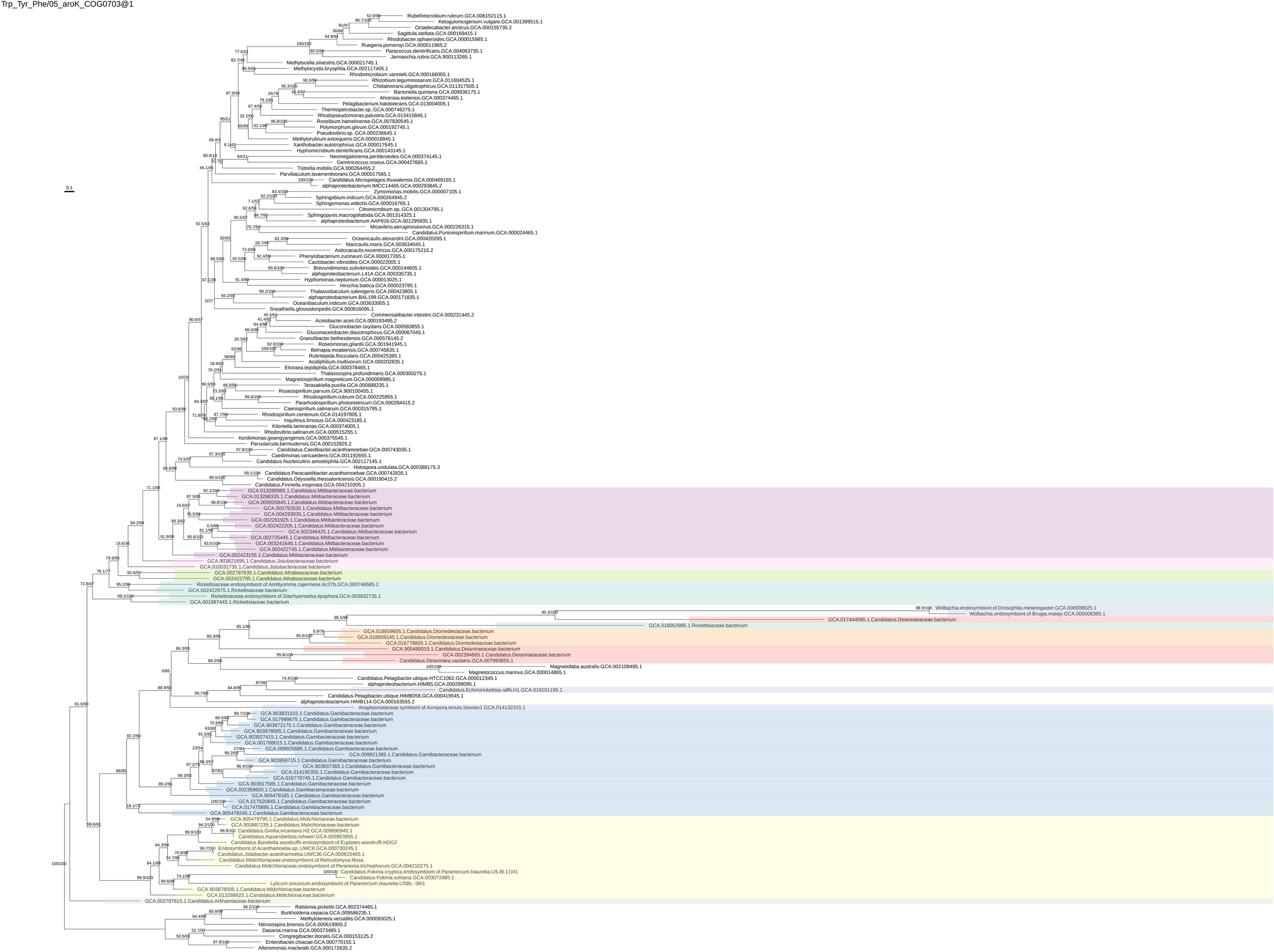

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Acetobacter.aceti.GCA.000193495.2
Granulibacter.bethesdensis.GCA.000576145.2
Acidiphilium.multivorum.GCA.000202835.1
Rubritepida.flocculans.GCA.000425365.1
Belnapia.moabensis.GCA.000745835.1
Elioraea.tepidiphila.GCA.000378465.1
Magnetofaba.australis.GCA.002109495.1
Magnetococcus.marinus.GCA.000014865.1
Nitrosospira.briensis.GCA.000619905.2
Methylotenera.versatilis.GCA.000093025.1
Ralstonia.pickettii.GCA.902374465.1
Burkholderia.cepacia.GCA.009586235.1
Congregibacter.litoralis.GCA.000153125.2

Trp_Tyr_Phe/09_trpD_COG0547@2

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78.1/99 Rubritepida.flocculans.GCA.000425365.1
92.3/100 BeInapia.moabensis.GCA.000745835.1
97.4/73 Roseomonas.gilardii.GCA.001941945.1
94.4/74 Acidiphilium.multivorum.GCA.000202835.1
58.5/62 Granulibacter.bethesdensis.GCA.000576145.2
Elioraea.tepidiphila.GCA.000378465.1
78.7/89 81.8/98 Gluconacetobacter.diazotrophicus.GCA.000067045.1
Acetobacter.aceti.GCA.000193495.2
3.2/42 Gluconobacter.oxydans.GCA.000583855.1
99.6/100 Commensalibacter.intestini.GCA.000231445.2
74.4/99 Sagittula.stellata.GCA.000169415.1
7.5/93 Ruegeria.pomeroyi.GCA.000011965.2
77.9/88 89.9/95 Octadecabacter.arcticus.GCA.000155735.2
77.9/95 Rhodobacter.sphaeroides.GCA.000015985.1
65.7/90 Rubellimicrobium.rubrum.GCA.006152115.1
89.9/96 Ketogulonicigenium.vulgare.GCA.001399515.1
98.2/99 Jannaschia.rubra.GCA.900113265.1
99.4/100 Paracoccus.denitrificans.GCA.004063735.1
Neomegalonema.perideroedes.GCA.000374145.1
97.7/91 88.1/100 Sphingopyxis.macrogoltabida.GCA.001314325.1
94.3/100 Sphingobium.indicum.GCA.000264945.2
99.1/100 Citromicrobium.sp..GCA.001304795.1
85.9/100 Zymomonas.mobilis.GCA.000007105.1
81.1/97 Sphingomonas.wittichii.GCA.000016765.1
28.4/88 alphaproteobacterium.AAP81b.GCA.001295935.1
19.5/82 100/100 GCA.003241645.1.Candidatus.Mitibacteraceae.bacterium
GCA.002422745.1.Candidatus.Mitibacteraceae.bacterium
88.7/89 100/100 Enterobacter.cloacae.GCA.000770155.1
19.6/64 Alteromonas.macleodii.GCA.000172635.2
93/92 Parvularcula.bermudensis.GCA.000152825.2
87.5/99 GCA.002725445.1.Candidatus.Mitibacteraceae.bacterium
86/98 GCA.002422205.1.Candidatus.Mitibacteraceae.bacterium
GCA.002346425.1.Candidatus.Mitibacteraceae.bacterium
93.9/100 Caulobacter.vibrioides.GCA.000022005.1
87.5/30 99.7/100 Asticcacaulis.excentricus.GCA.000175215.2
100/100 Phenylobacterium.zucineum.GCA.000017265.1
99.2/100 Brevundimonas.subvibrioides.GCA.000144605.1
58.4/79 alphaproteobacterium.L41A.GCA.000335735.1
92.3/94 100/100 Oceanicaulis.alexandrii.GCA.000420265.1
Maricaulis.maris.GCA.003634045.1
Inquilinus.limosus.GCA.000423185.1
Candidatus.Puniceispirillum.marinum.GCA.000024465.1
82.1/96 Rhizobium.leguminosarum.GCA.011604525.1
87.1/96 Chelativorans.oligotrophicus.GCA.011317505.1
8.7/40 Ahrensia.kielensis.GCA.000374465.1
Thermopetrobacter.sp..GCA.000746275.1
90.1/92 94/98 Roseibium.hamelinense.GCA.007830545.1
85.3/95 99.3/100 Pseudovibrio.sp..GCA.000236645.1
Polymorphum.gilvum.GCA.000192745.1
85.5/28 97.3/100 Xanthobacter.autotrophicus.GCA.000017645.1
22.1/79 Rhodopseudomonas.palustris.GCA.013415845.1
70.4/99 Methylocystis.bryophila.GCA.002117405.1
99.5/53 99.2/100 Methylocella.silvestris.GCA.000021745.1
Methylorubrum.extorquens.GCA.000018845.1
42/32 93.9/77 Rhodomicrobium.vannielii.GCA.000166055.1
Pelagibacterium.halotolerans.GCA.013004005.1
42.6/30 Rhodospirillum.centenum.GCA.014197805.1
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91/28 Kiloniella.laminariae.GCA.000374005.1
99.8/100 Thalassobaculum.salexigens.GCA.000423805.1
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Oceanibaculum.indicum.GCA.003633955.1
99.8/100 Rhodospirillum.rubrum.GCA.000225955.1
95.7/31 89.5/93 Pararhodospirillum.photometricum.GCA.000284415.2
86.8/90 Magnetospirillum.magneticum.GCA.000009985.1
20.5/71 Roseospirillum.parvum.GCA.900100455.1
31.9/83 Geminicoccus.roseus.GCA.000427665.1
93.5/99 Thalassospira.profundimaris.GCA.000300275.1
83.2/84 87.3/94 Kordiimonas.gwangyangensis.GCA.000375545.1
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89.1/95 GCA.903831915.1.Candidatus.Gamibacteraceae.bacterium
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81.7/92 GCA.009693885.1.Candidatus.Gamibacteraceae.bacterium
6.5/59 98.1/100 GCA.903927415.1.Candidatus.Gamibacteraceae.bacterium
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88.2/82 GCA.014190355.1.Candidatus.Gamibacteraceae.bacterium
19.8/63 GCA.009921385.1.Candidatus.Gamibacteraceae.bacterium
97.9/98 100/100 GCA.903959715.1.Candidatus.Gamibacteraceae.bacterium
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55.6/85 GCA.016778805.1.Candidatus.Diomedesiaceae.bacterium
87.6/90 GCA.905480015.1.Candidatus.Deianiraeaceae.bacterium
39.6/47 GCA.016780625.1.Candidatus.Diomedesiaceae.bacterium
99.7/100 Candidatus.Pelagibacter.ubique.HTCC1062.GCA.000012345.1
99.4/100 alphaproteobacterium.HIMB5.GCA.000299095.1
95.3/92 99.1/100 Candidatus.Pelagibacter.ubique.HIMB058.GCA.000419545.1
65.6/60 alphaproteobacterium.HIMB114.GCA.000163555.2
GCA.903821695.1.Candidatus.Jistubacteraceae.bacterium
92.9/91 9.5/18 77/89 GCA.013288575.1.Candidatus.Arkhamiaceae.bacterium
Candidatus.Midichloriaceae.endosymbiont.of.Peranema.trichophorum.GCA.004210275.1
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27.8/16 GCA.002787635.1.Candidatus.Athabascaceae.bacterium
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87.9/98 GCA.013288335.1.Candidatus.Mitibacteraceae.bacterium
99.6/95 65.2/98 GCA.004293935.1.Candidatus.Mitibacteraceae.bacterium
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24.5/93 GCA.002423155.1.Candidatus.Mitibacteraceae.bacterium
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94.7/99 90/95 Terasakiella.pusilla.GCA.000688235.1
51.2/82 Hyphomicrobium.denitrificans.GCA.000143145.1
77/31 Parvibaculum.lavamentivorans.GCA.000017565.1
Sneathiella.glossodoripedis.GCA.000616095.1
86.5/29 100/100 Candidatus.Micropelagos.thuwalensis.GCA.000469155.1
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99.6/100 Hyphomonas.neptunium.GCA.000013025.1
Hirschia.baltica.GCA.000023785.1
98.6/100 99.8/100 Magnetofaba.australis.GCA.002109495.1
Magnetococcus.marinus.GCA.000014865.1
100/100 Ralstonia.pickettii.GCA.902374465.1
99.6/100 Burkholderia.cepacia.GCA.009586235.1
97.9/100 Nitrosospira.briensis.GCA.000619905.2
Methylotenera.versatilis.GCA.000093025.1
97.3/100 Dasania.marina.GCA.000373485.1
Congregibacter.litoralis.GCA.000153125.2

Trp_Tyr_Phe/10_trpF_COG0135@2

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Candidatus.Pelagibacter.ubique.HIMB058.GCA.000419545.1
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Phenylobacterium.zucineum.GCA.000017265.1
Caulobacter.vibrioides.GCA.000022005.1
Asticcacaulis.excentricus.GCA.000175215.2
Oceanicaulis.alexandrii.GCA.000420265.1
Maricaulis.maris.GCA.003634045.1
Brevundimonas.subvibrioides.GCA.000144605.1
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Chelativorans.oligotrophicus.GCA.011317505.1
Ahrensia.kielensis.GCA.000374465.1
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Roseibium.hamelinense.GCA.007830545.1
Polymorphum.gilvum.GCA.000192745.1
Pseudovibrio.sp..GCA.000236645.1
Rhodomicrobium.vannielii.GCA.000166055.1
Hyphomicrobium.denitrificans.GCA.000143145.1
Thalassobaculum.salexigens.GCA.000423805.1
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Parvibaculum.lavamentivorans.GCA.000017565.1
Oceanibaculum.indicum.GCA.003633955.1
Tistrella.mobilis.GCA.000264455.2
Pelagibacterium.halotolerans.GCA.013004005.1
Methylocella.silvestris.GCA.000021745.1
Rhodopseudomonas.palustris.GCA.013415845.1
Methylocystis.bryophila.GCA.002117405.1
Xanthobacter.autotrophicus.GCA.000017645.1
Methylorubrum.extorquens.GCA.000018845.1
Zymomonas.mobilis.GCA.000007105.1
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Pararhodospirillum.photometricum.GCA.000284415.2
Magnetospirillum.magneticum.GCA.000009985.1
Thalassospira.profundimaris.GCA.000300275.1
Sagittula.stellata.GCA.000169415.1
Rhodobacter.sphaeroides.GCA.000015985.1
Rubellimicrobium.rubrum.GCA.006152115.1
Jannaschia.rubra.GCA.900113265.1
Ruegeria.pomeroyi.GCA.000011965.2
Octadecabacter.arcticus.GCA.000155735.2
Ketogulonicigenium.vulgare.GCA.001399515.1
Paracoccus.denitrificans.GCA.004063735.1
Neomegalonema.perideroedes.GCA.000374145.1
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Kiloniella.laminariae.GCA.000374005.1
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Rhodovibrio.salinarum.GCA.000515255.1
Kordiimonas.gwangyangensis.GCA.000375545.1
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Commensalibacter.intestini.GCA.000231445.2
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Acetobacter.aceti.GCA.000193495.2
Acidisphaera.rubrifaciens.GCA.000964365.1
Acidiphilium.multivorum.GCA.000202835.1
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Rubritepida.flocculans.GCA.000425365.1
Elioraea.tepidiphila.GCA.000378465.1
Roseomonas.gilardii.GCA.001941945.1
Belnapia.moabensis.GCA.000745835.1
Geminicoccus.roseus.GCA.000427665.1
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Ralstonia.pickettii.GCA.902374465.1
Burkholderia.cepacia.GCA.009586235.1
Dasania.marina.GCA.000373485.1
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Magnetococcus.marinus.GCA.000014865.1
Enterobacter.cloacae.GCA.000770155.1
Alteromonas.macleodii.GCA.000172635.2
Parvularcula.bermudensis.GCA.000152825.2

Trp_Tyr_Phe/11_trpC_1MW5K@1224

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Candidatus.Pelagibacter.ubique.HIMB058.GCA.000419545.1
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Tistrella.mobilis.GCA.000264455.2
Rhodovibrio.salinarum.GCA.000515255.1
Oceanibaculum.indicum.GCA.003633955.1
Kiloniella.laminariae.GCA.000374005.1
Terasakiella.pusilla.GCA.000688235.1
Sneathiella.glossodoripedis.GCA.000616095.1
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Thalassospira.profundimaris.GCA.000300275.1
Kordiimonas.gwangyangensis.GCA.000375545.1
Inquilinus.limosus.GCA.000423185.1
Rhodospirillum.centenum.GCA.014197805.1
Geminicoccus.roseus.GCA.000427665.1
Gluconobacter.oxydans.GCA.000583855.1
Gluconacetobacter.diazotrophicus.GCA.000067045.1
Acetobacter.aceti.GCA.000193495.2
Commensalibacter.intestini.GCA.000231445.2
Granulibacter.bethesdensis.GCA.000576145.2
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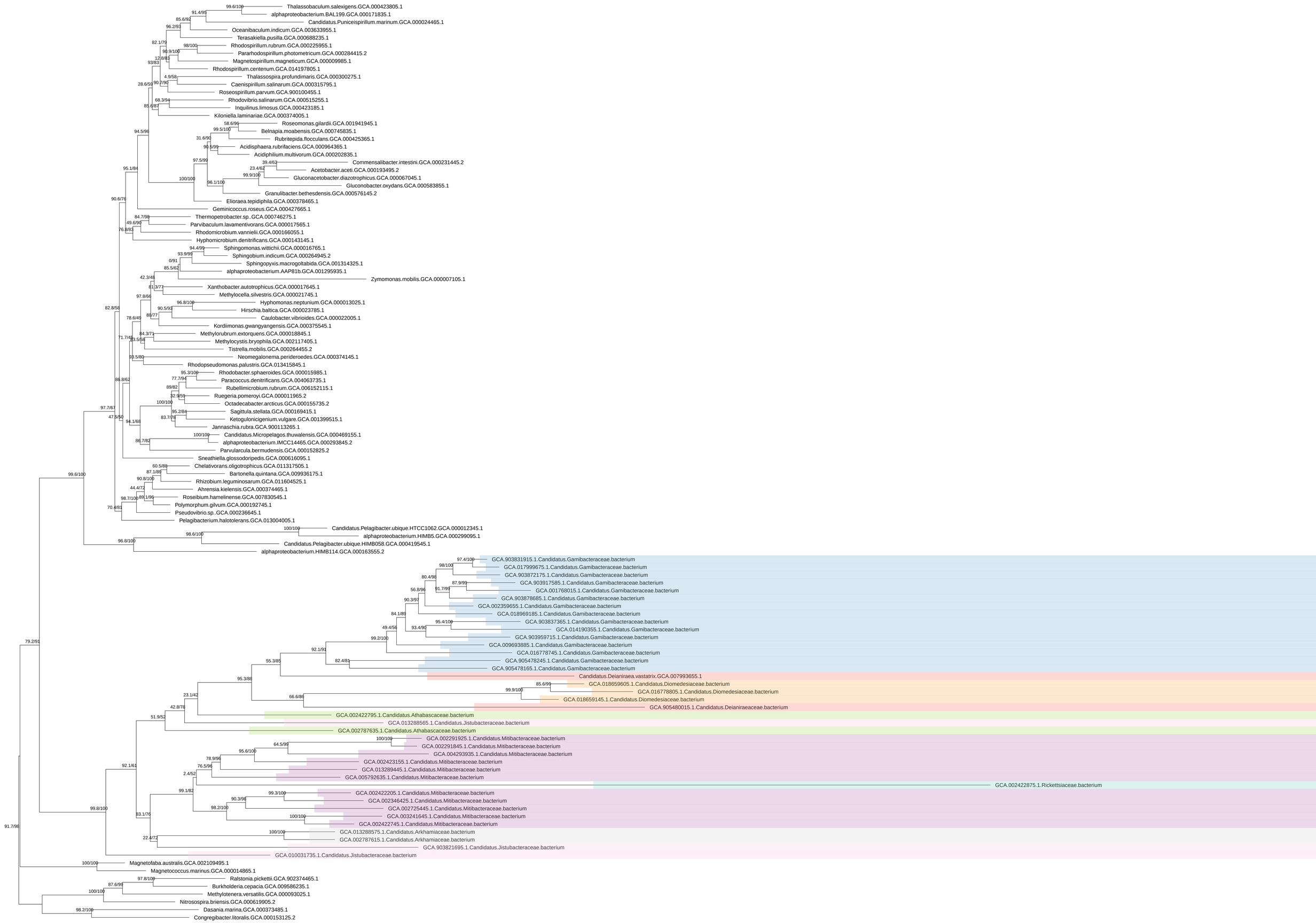

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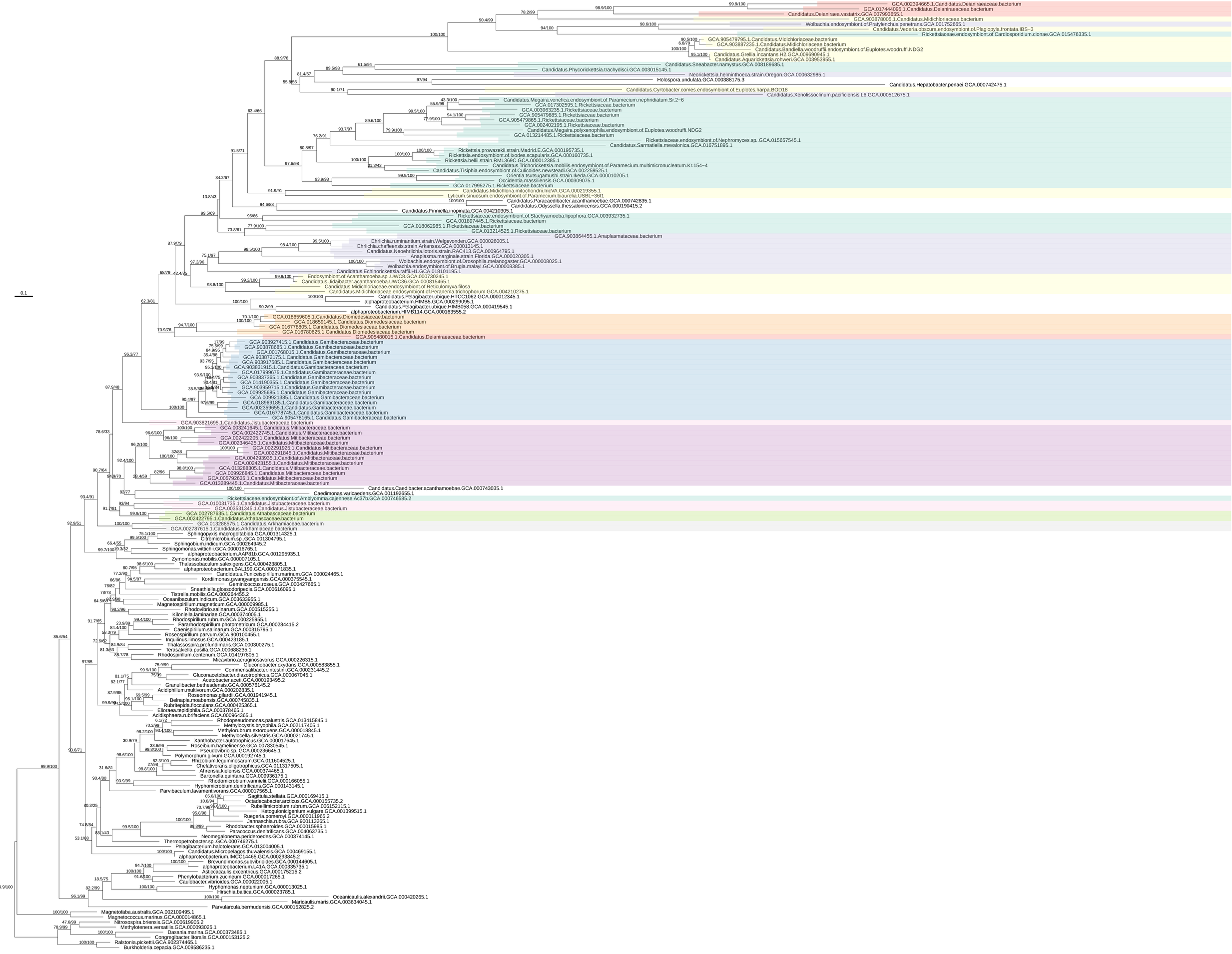

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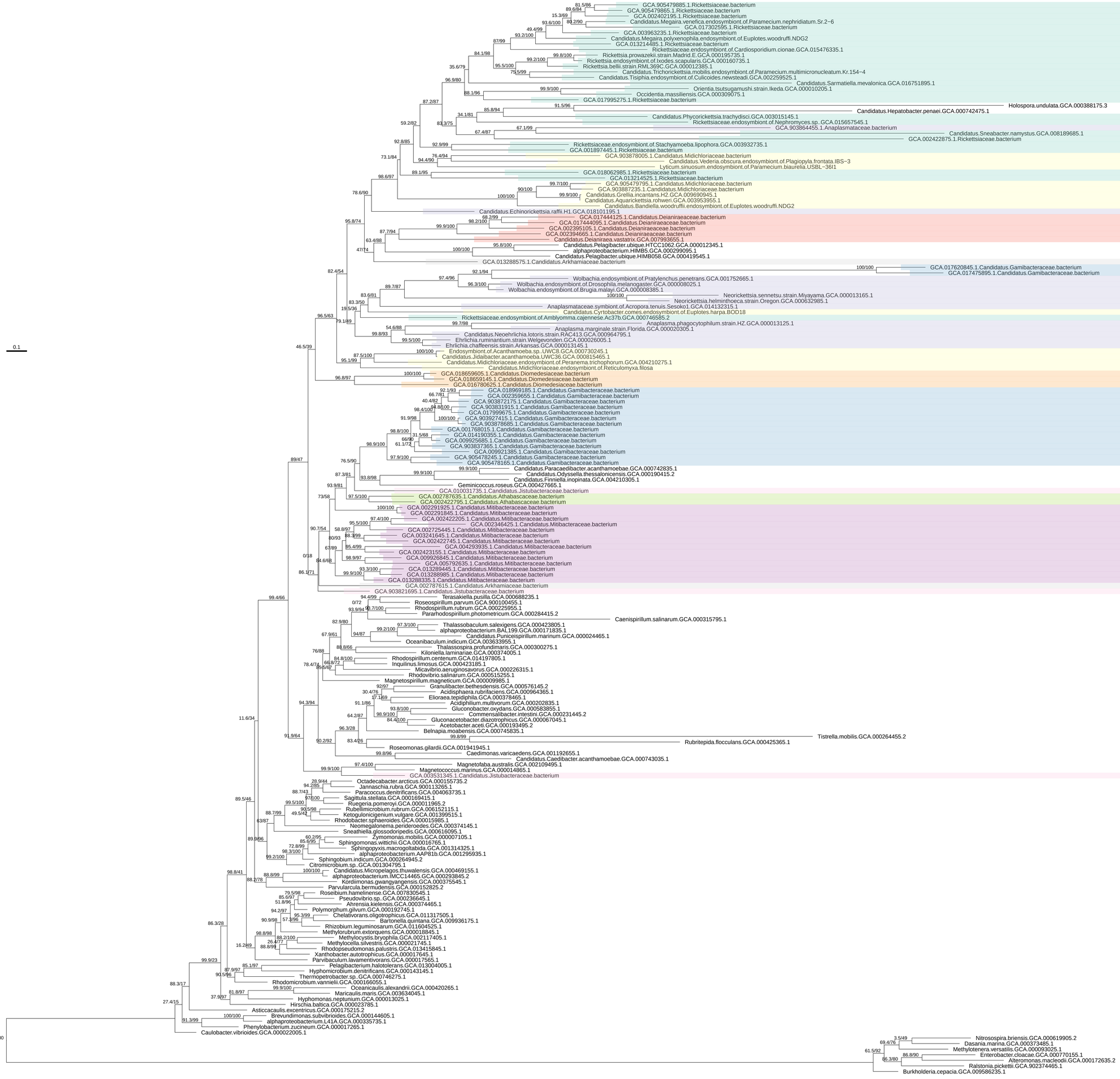

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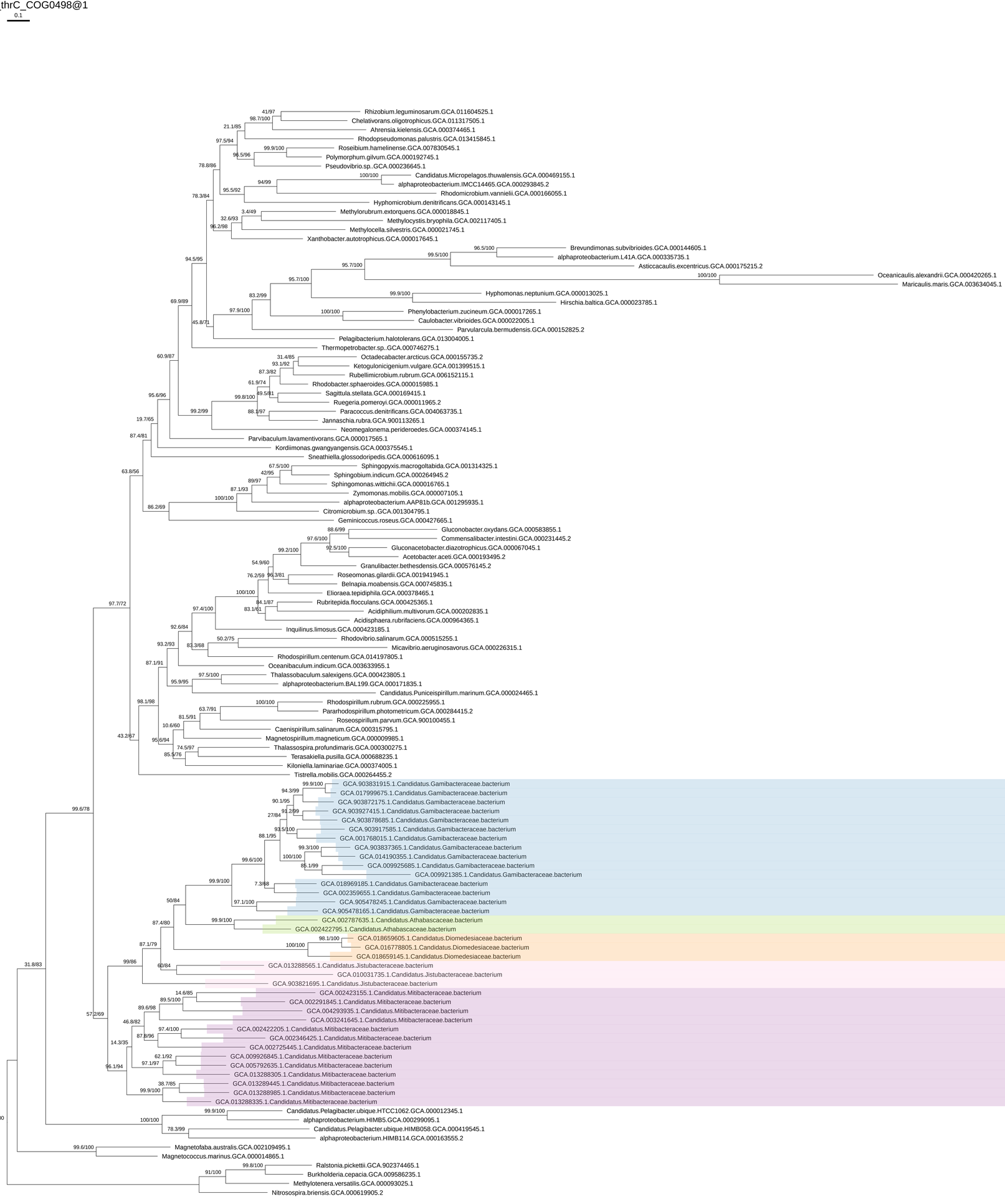

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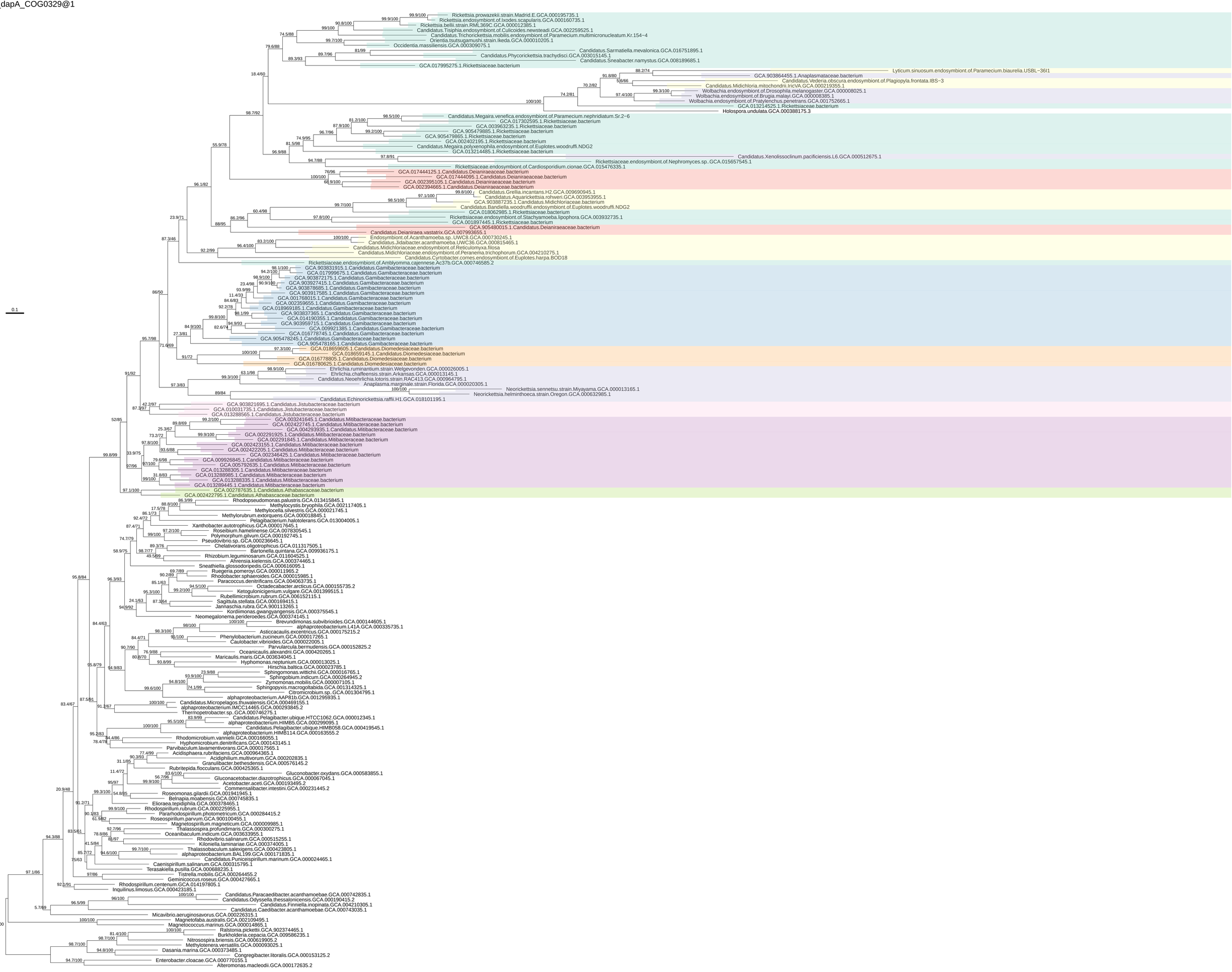

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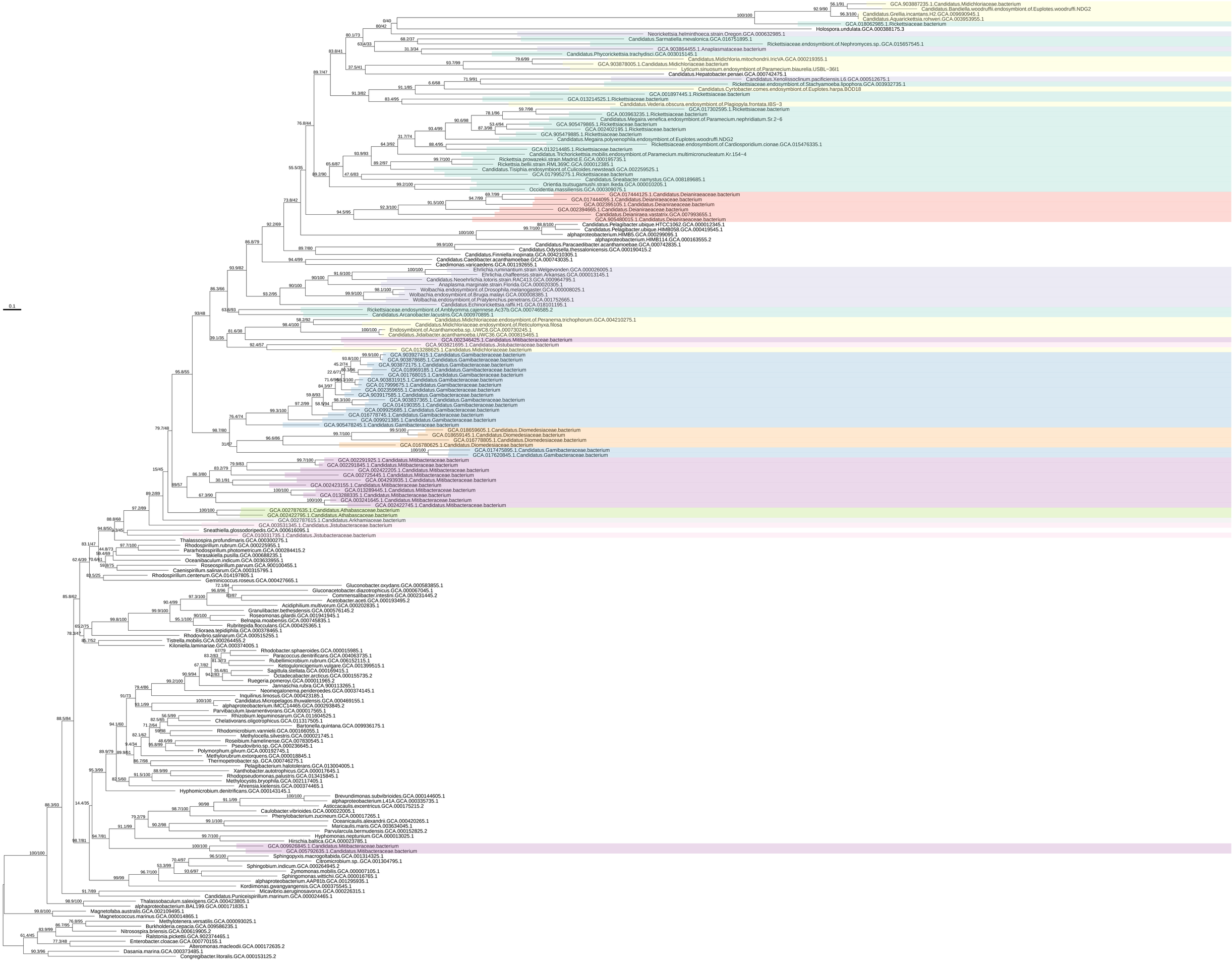

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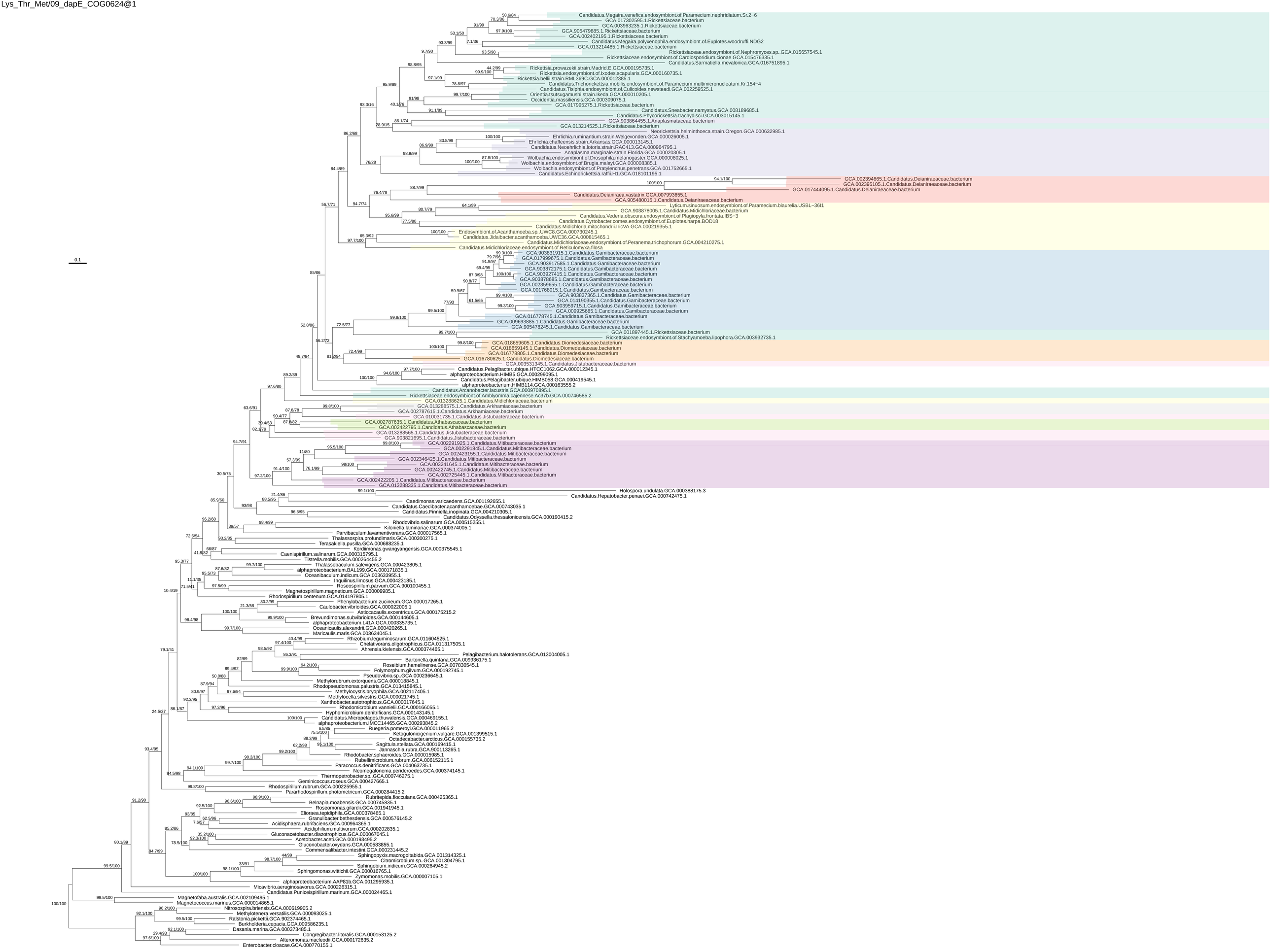

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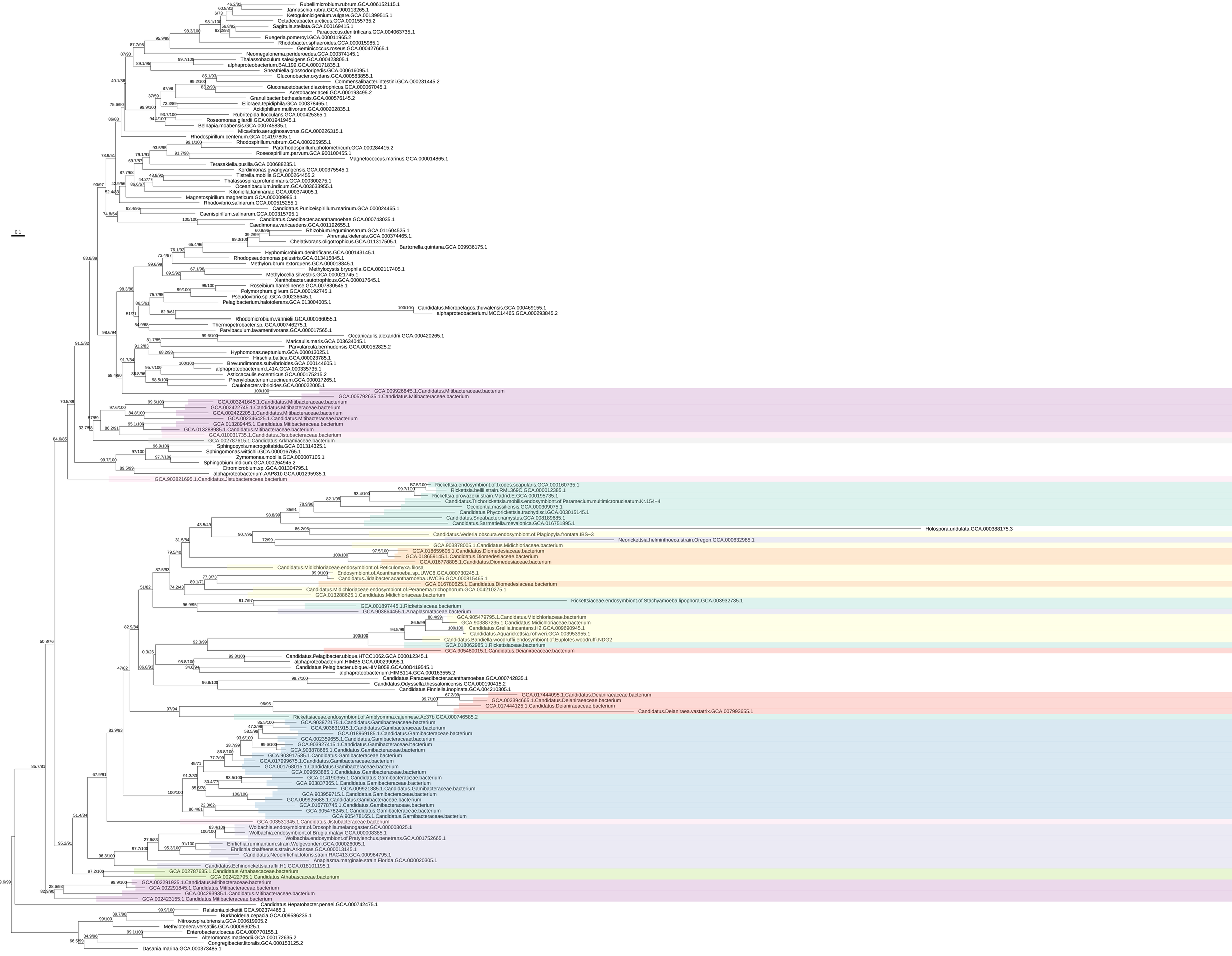

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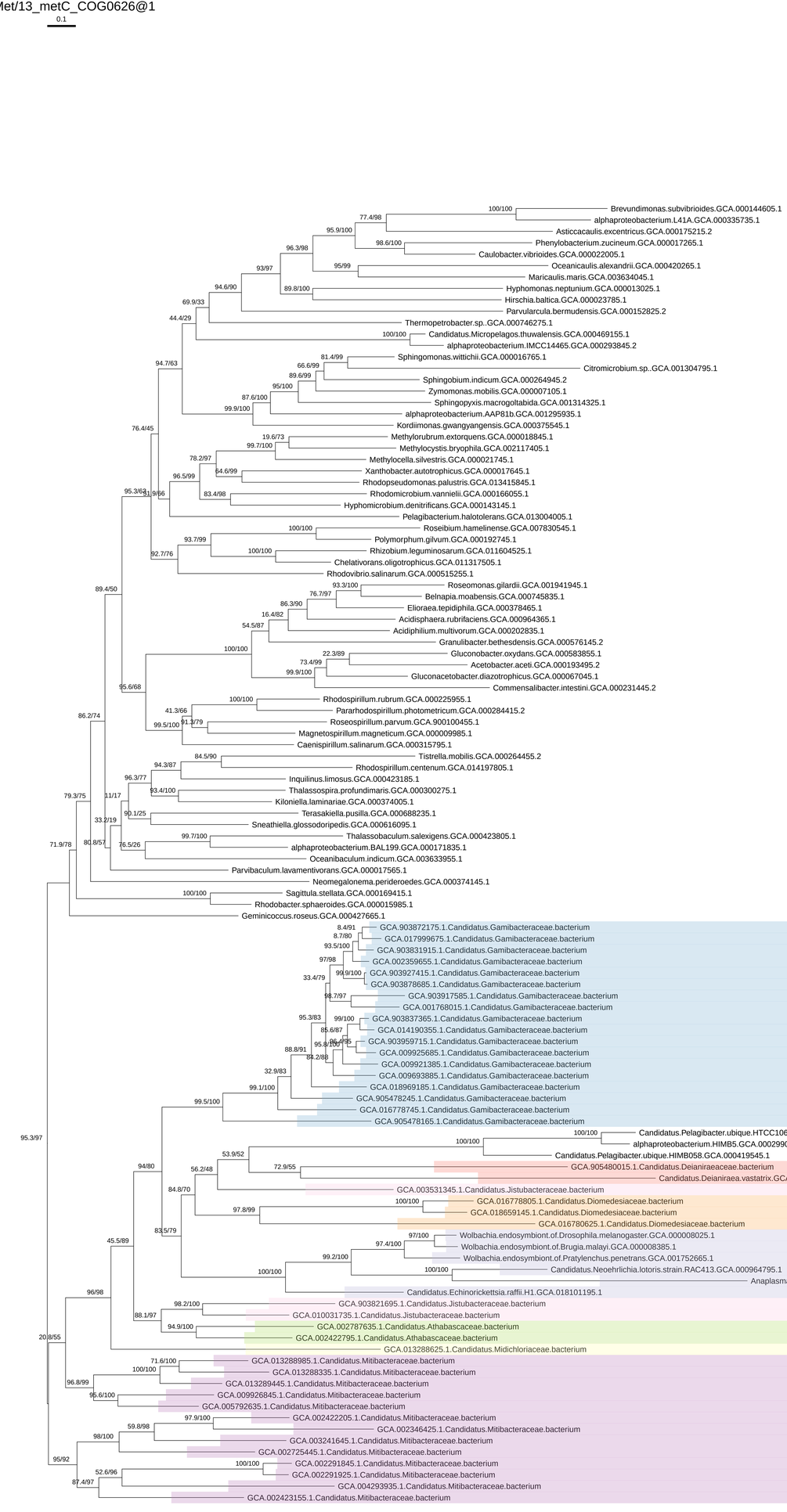

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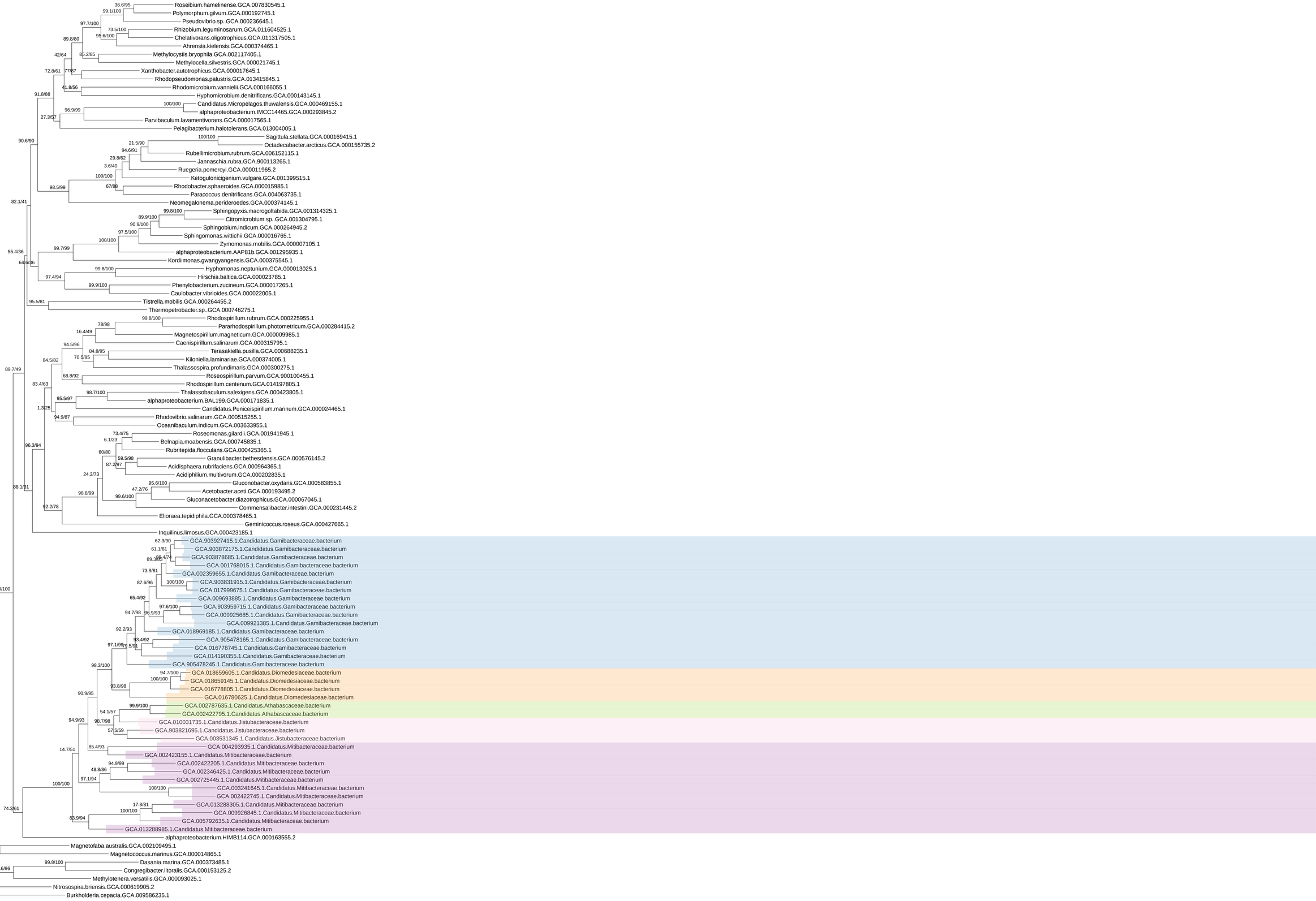

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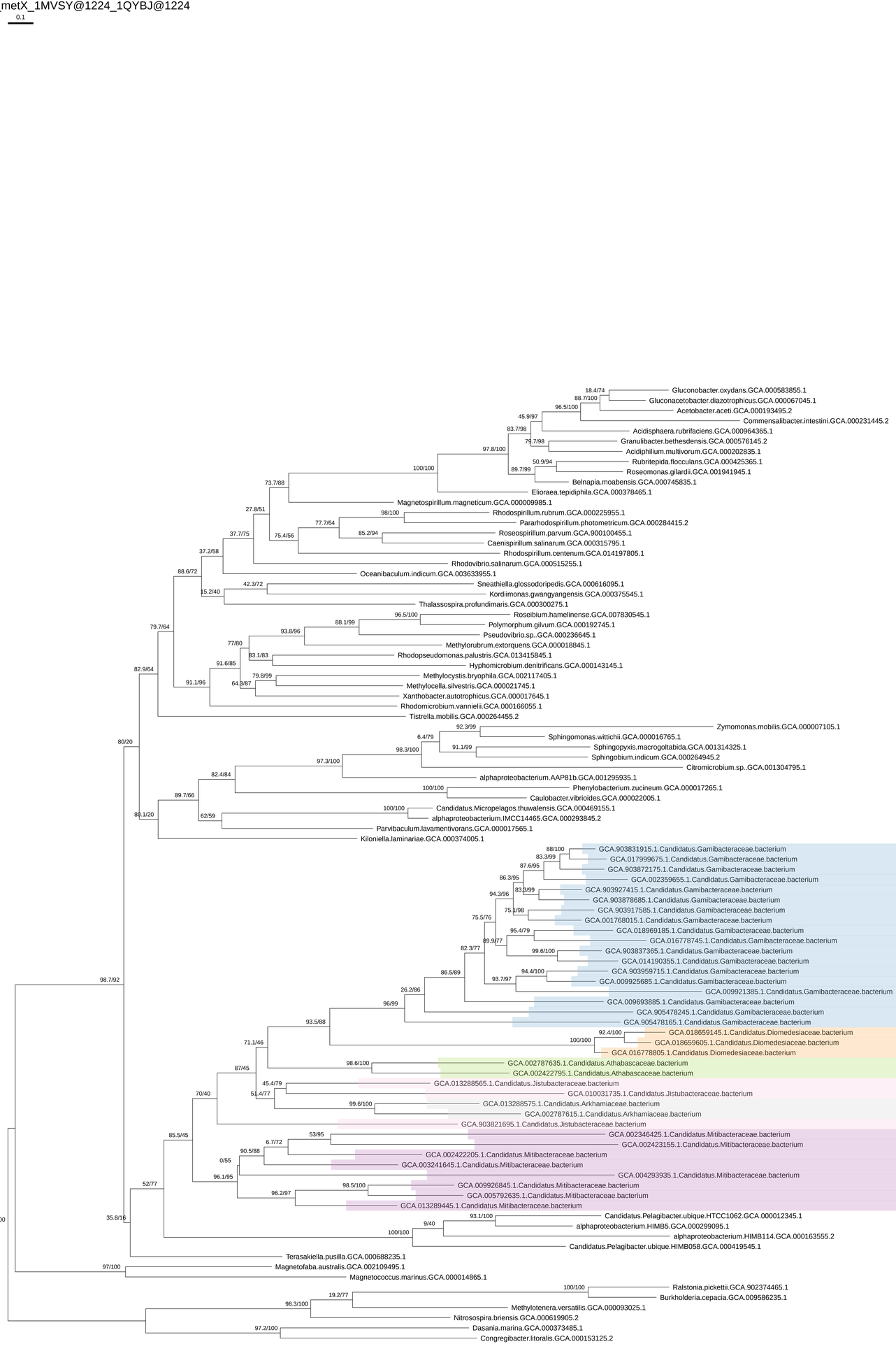
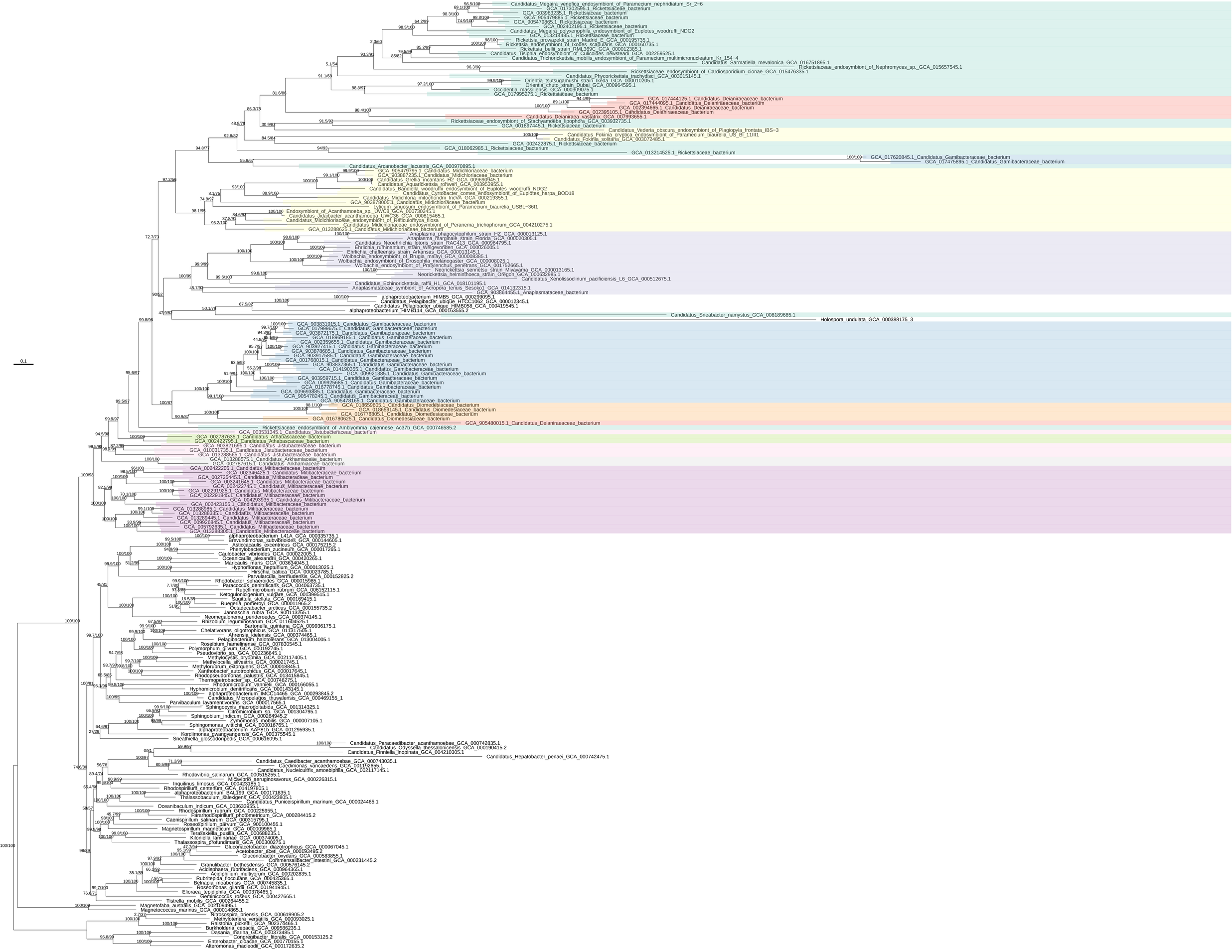


Supplementary Figure 26: concatenated phylogenies for nucleotide and amino acid biosynthesis. Phylogenetic trees of the concatenated genes of biosynthetic pathways for nucleotides and amino acids. For each pathway, the phylogenies are presented for untrimmed alignment and for the alignment with the 10%, 20%, 30%, 40%, or 50% most compositionally heterogeneous sites removed. On each tree, the members of each *Rickettsiales* family are highlighted by different background colours. On each branch, support values by SH-aLRT with 1000 replicates and by 1000 ultrafast bootstraps are reported. The tree scales stand for estimated sequence divergences.

Purine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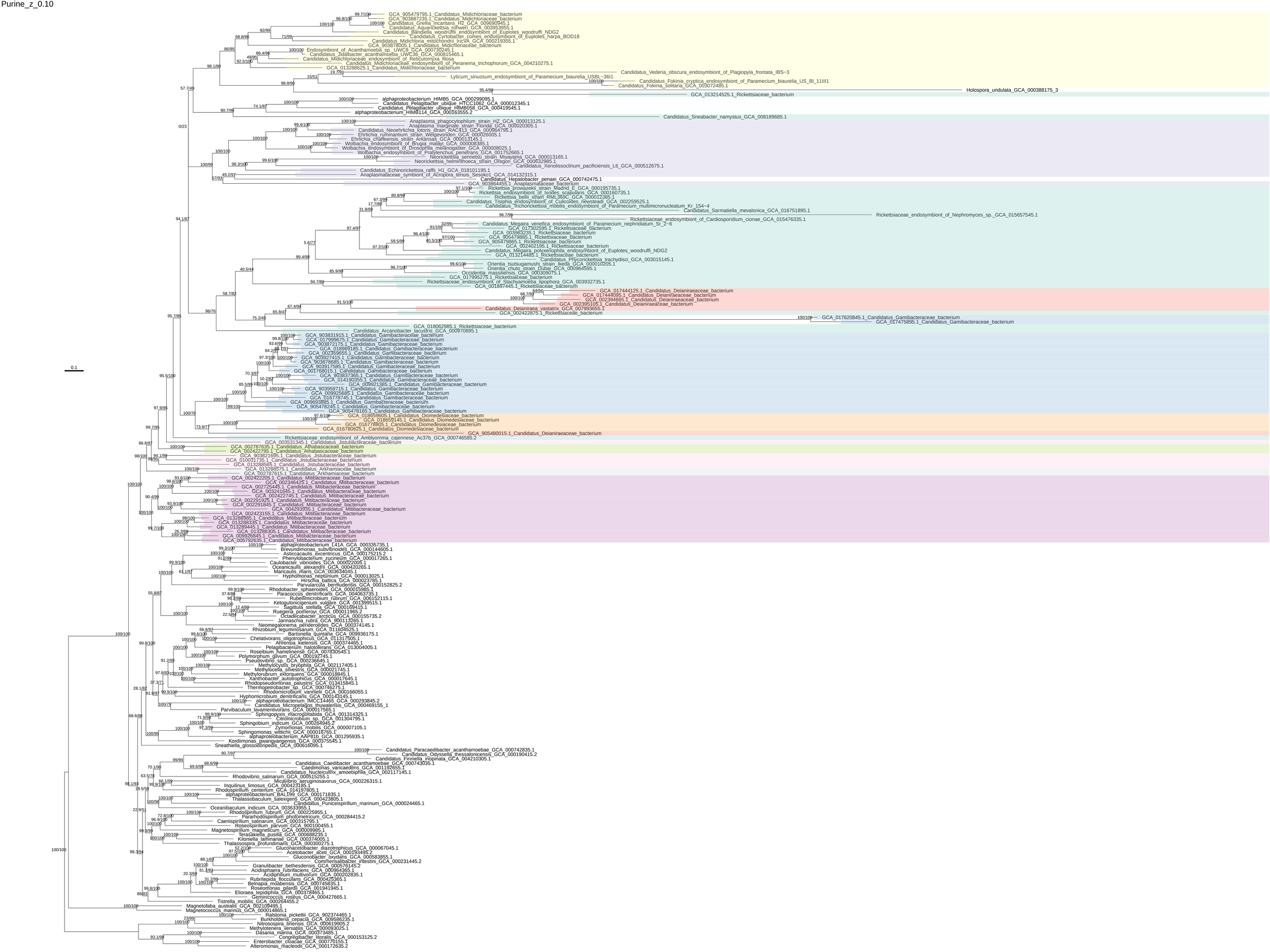
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Wolbachia_endosymbiont_of_Pratylenchus_penetrans_GCA_001752665.1
100/100
Neorickettsia_sennetsu_strain_Miyayama_GCA_000013165.1
99.6/100
Neorickettsia_helminthoeca_strain_Oregon_GCA_000632985.1
100/99
98.3/100
Candidatus_Xenolissoclinum_pacificiensis_L6_GCA_000512675.1
Candidatus_Echinorickettsia_raffii_H1_GCA_018101195.1
49.2/97
Anaplasmataceae_symbiont_of_Acropora_tenuis_Sesoko1_GCA_014132315.1
57/93
Candidatus_Hepatobacter_penaei_GCA_000742475.1
GCA_903864455.1_Anaplasmataceae_bacterium
97.1/100
Rickettsia_prowazekii_strain_Madrid_E_GCA_000195735.1
100/100
Rickettsia_endosymbiont_of_Ixodes_scapularis_GCA_000160735.1
80.8/99
Rickettsia_bellii_strain_RML369C_GCA_000012385.1
67.3/99
Candidatus_Tisiphia_endosymbiont_of_Culicoides_newsteadi_GCA_002259525.1
17.7/86
Candidatus_Trichorickettsia_mobilis_endosymbiont_of_Paramecium_multimicronucleatum_Kr_154−4
31.8/89
Candidatus_Sarmatiella_mevalonica_GCA_016751895.1
96.7/99
Rickettsiaceae_endosymbiont_of_Nephromyces_sp._GCA_015657545.1
94.1/67
Rickettsiaceae_endosymbiont_of_Cardiosporidium_cionae_GCA_015476335.1
32/99
Candidatus_Megaira_venefica_endosymbiont_of_Paramecium_nephridiatum_Sr_2−6
91/100
GCA_017302595.1_Rickettsiaceae_bacterium
97.4/97
96.4/100
GCA_003963235.1_Rickettsiaceae_bacterium
97/100
GCA_905479885.1_Rickettsiaceae_bacterium
40.5/100
59.5/99
GCA_905479865.1_Rickettsiaceae_bacterium
5.6/77
97.2/100
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Candidatus_Megaira_polyxenophila_endosymbiont_of_Euplotes_woodruffi_NDG2
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99.4/98
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Orientia_tsutsugamushi_strain_Ikeda_GCA_000010205.1
40.5/44
96.7/100
Orientia_chuto_strain_Dubai_GCA_000964595.1
85.9/99
Occidentia_massiliensis_GCA_000309075.1
GCA_017995275.1_Rickettsiaceae_bacterium
94.7/89
Rickettsiaceae_endosymbiont_of_Stachyamoeba_lipophora_GCA_003932735.1
GCA_001897445.1_Rickettsiaceae_bacterium
58.7/82
64/94
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66.7/93
GCA_017444095.1_Candidatus_Deianiraeaceae_bacterium
100/100
GCA_002394665.1_Candidatus_Deianiraeaceae_bacterium
91.5/100
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67.4/94
Candidatus_Deianiraea_vastatrix_GCA_007993655.1
96/76
65.8/47
GCA_002422875.1_Rickettsiaceae_bacterium
95.7/95
75.2/45
100/100
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GCA_017475895.1_Candidatus_Gamibacteraceae_bacterium
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Candidatus_Arcanobacter_lacustris_GCA_000970895.1
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93.6/99
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88.7/97
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84.2/97
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97.3/100
100/100
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GCA_001768015.1_Candidatus_Gamibacteraceae_bacterium
70.3/97
100/100
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10.2/87
GCA_014190355.1_Candidatus_Gamibacteraceae_bacterium
95.5/100
85.5/99
100/100
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GCA_905478245.1_Candidatus_Gamibacteraceae_bacterium
97.9/95
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100/78
97.6/100
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73.9/77
100/100
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99.7/95
Rickettsiaceae_endosymbiont_of_Amblyomma_cajennese_Ac37b_GCA_000746585.2
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100/100
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98/100
94.1/99
GCA_903821695.1_Candidatus_Jistubacteraceae_bacterium
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93.6/100
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90.4/99
100/100
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93.9/100
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26.3/89
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Asticcacaulis_excentricus_GCA_000175215.2
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Caulobacter_vibrioides_GCA_000022005.1
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Maricaulis_maris_GCA_003634045.1
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Hirschia_baltica_GCA_000023785.1
Parvularcula_bermudensis_GCA_000152825.2
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Rhodobacter_sphaeroides_GCA_000015985.1
55.8/87
37.8/88
Paracoccus_denitrificans_GCA_004063735.1
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Rubellimicrobium_rubrum_GCA_006152115.1
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Ruegeria_pomeroyi_GCA_000011965.2
100/100
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Octadecabacter_arcticus_GCA_000155735.2
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Rhizobium_leguminosarum_GCA_011609525.1
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Bartonella_quintana_GCA_009936175.1
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100/100
100/100
Chelativorans_oligotrophicus_GCA_011317505.1
Afifensia_kielensis_GCA_000374465.1
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Pelagibacterium_halotolerans_GCA_013004005.1
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Polymorphum_gilvum_GCA_000192745.1
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Pseudovibrio_sp._GCA_000236645.1
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97.8/83
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Methylorubrum_extorquens_GCA_000018845.1
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Xanthobacter_autotrophicus_GCA_000017645.1
37.3/71
Rhodopseudomonas_palustris_GCA_013415845.1
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Parvibaculum_lavamentivorans_GCA_000017565.1
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Sphingopyxis_macrogoltabida_GCA_001314325.1
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Citromicrobium_sp._GCA_001304795.1
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Zymomonas_mobilis_GCA_000007105.1
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Sneathiella_glossodoripedis_GCA_000610095.1
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Candidatus_Paracaedibacter_acanthamoebae_GCA_000742835.1
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Candidatus_Odyssella_thessalonicensis_GCA_000190415.2
99/99
Candidatus_Finniella_inopinata_GCA_004210305.1
Candidatus_Caedibacter_acanthamoebae_GCA_000743035.1
68.6/98
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69.6/95
Caedimonas_varicaedens_GCA_001192655.1
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63.5/78
Rhodovibrio_salinarum_GCA_000515255.1
66.1/99
Micavibrio_aeruginosavorus_GCA_000226315.1
98.1/93
99.9/100
Inquilinus_limosus_GCA_000423185.1
19.5/58
Rhodospirillum_centenum_GCA_014197805.1
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alphaproteobacterium_BAL199_GCA_000171835.1
100/100
Thalassobaculum_Salexigens_GCA_000423805.1
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Candidatus_Puniceispirillum_marinum_GCA_000024465.1
Oceanibaculum_indicum_GCA_003633955.1
22.9/51
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Rhodospirillum_rubrum_GCA_000225955.1
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Parahodospirillum_photometricum_GCA_000284415.2
96.9/100
Caenispirillum_salinarum_GCA_000315795.1
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Roseospirillum_parvum_GCA_900100455.1
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Magnetospirillum_magneticum_GCA_000009985.1
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52.2/100
Gluconacetobacter_diazotrophicus_GCA_000067045.1
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Gluconobacter_oxydans_GCA_000583855.1
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Commensalibacter_intestini_GCA_000231445.2
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81.2/82
Acidisphaera_rubrifaciens_GCA_000964365.1
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Acidiphilium_multivorum_GCA_000202835.1
31.2/85
Rubritepida_flocculans_GCA_000425365.1
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Roseomonas_gilardii_GCA_001941945.1
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Tistrella_mobilis_GCA_000264455.2
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Magnetofaba_australis_GCA_002109495.1
Magnetococcus_marinus_GCA_000014865.1
100/100
Ralstonia_pickettii_GCA_902374465.1
23/99
Burkholderia_cepacia_GCA_009586235.1
100/100
Nitrosospira_briensis_GCA_000619905.2
Methylotenera_versatilis_GCA_000093025.1
100/100
Dasania_marina_GCA_000373485.1
93.1/96
Congregibacter_litoralis_GCA_000153125.2
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Enterobacter_cloacae_GCA_000770155.1
Alteromonas_macleodii_GCA_000172635.2
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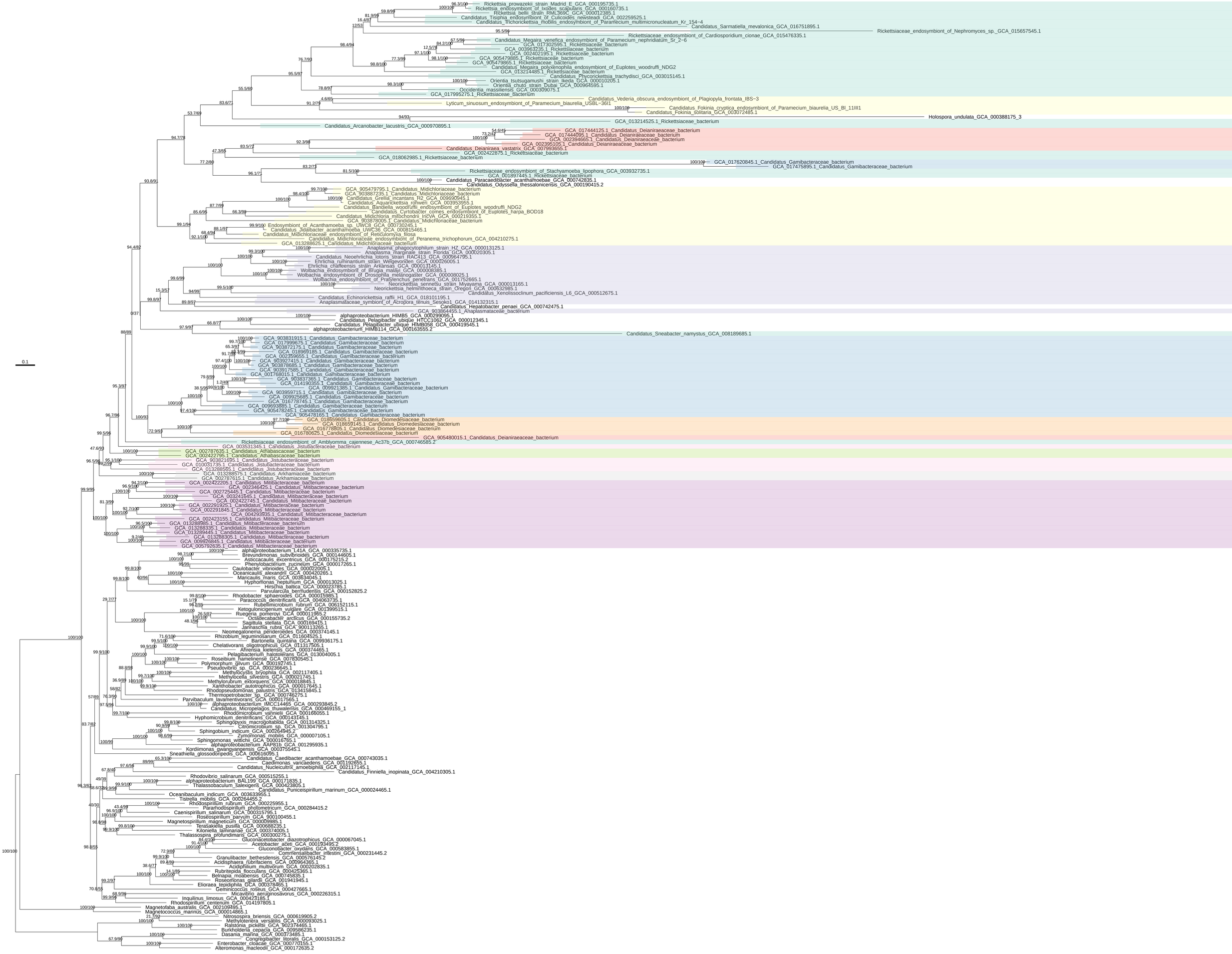
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Rickettsia_bellii_strain_RML369C_GCA_000012385.1
Candidatus_Tisiphia_endosymbiont_of_Culicoides_newsteadi_GCA_002259525.1
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Candidatus_Sarmatiella_mevalonica_GCA_016751895.1
Rickettsiaceae_endosymbiont_of_Nephromyces_sp._GCA_015657545.1
Rickettsiaceae_endosymbiont_of_Cardiosporidium_cionae_GCA_015476335.1
Candidatus_Megaira_venefica_endosymbiont_of_Paramecium_nephridiatum_Sr_2−6
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GCA_002402195.1_Rickettsiaceae_bacterium
GCA_905479885.1_Rickettsiaceae_bacterium
GCA_905479865.1_Rickettsiaceae_bacterium
Candidatus_Megaira_polyxenophila_endosymbiont_of_Euplotes_woodruffi_NDG2
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Candidatus_Phycorickettsia_trachydisci_GCA_003015145.1
Orientia_tsutsugamushi_strain_Ikeda_GCA_000010205.1
Orientia_chuto_strain_Dubai_GCA_000964595.1
Occidentia_massiliensis_GCA_000309075.1
GCA_017995275.1_Rickettsiaceae_bacterium
Candidatus_Vederia_obscura_endosymbiont_of_Plagiopyla_frontata_IBS−3
Lyticum_sinuosum_endosymbiont_of_Paramecium_biaurelia_USBL−36I1
Candidatus_Fokinia_cryptica_endosymbiont_of_Paramecium_biaurelia_US_BI_11III1
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Candidatus_Arcanobacter_lacustris_GCA_000970895.1
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Rickettsiaceae_endosymbiont_of_Stachyamoeba_lipophora_GCA_003932735.1
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Candidatus_Paracaedibacter_acanthamoebae_GCA_000742835.1
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Candidatus_Grellia_incantans_R2_GCA_009690945.1
Candidatus_Aquarickettsia_rohweri_GCA_003953955.1
Candidatus_Bandiella_woodruffii_endosymbiont_of_Euplotes_woodruffi_NDG2
Candidatus_Cyrtobacter_comes_endosymbiont_of_Euplotes_harpa_BOD18
Candidatus_Midichloria_mitochondrii_IricVA_GCA_000219355.1
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Endosymbiont_of_Acanthamoeba_sp._UWC8_GCA_000720245.1
Candidatus_Jidaibacter_acanthamoeba_UWC36_GCA_000815465.1
Candidatus_Midichloriaceae_endosymbiont_of_Reticulomyxa_filosa
Candidatus_Midichloriaceae_endosymbiont_of_Peranema_trichophorum_GCA_004210275.1
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Anaplasma_phagocytophilum_strain_HZ_GCA_000013125.1
Anaplasma_marginale_strain_Florida_GCA_000020305.1
Candidatus_Neoehrlichia_lotoris_strain_RAC413_GCA_000964795.1
Ehrlichia_ruminantium_strain_Welgevonden_GCA_000026005.1
Ehrlichia_chaffeensis_strain_Arkansas_GCA_000013145.1
Wolbachia_endosymbiont_of_Brugia_malayi_GCA_000008385.1
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Neorickettsia_helminthoeca_strain_Oregon_GCA_000832985.1
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Candidatus_Echinorickettsia_raffii_H1_GCA_018101195.1
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Rickettsiaceae_endosymbiont_of_Amblyomma_cajennese_Ac37b_GCA_000746585.2
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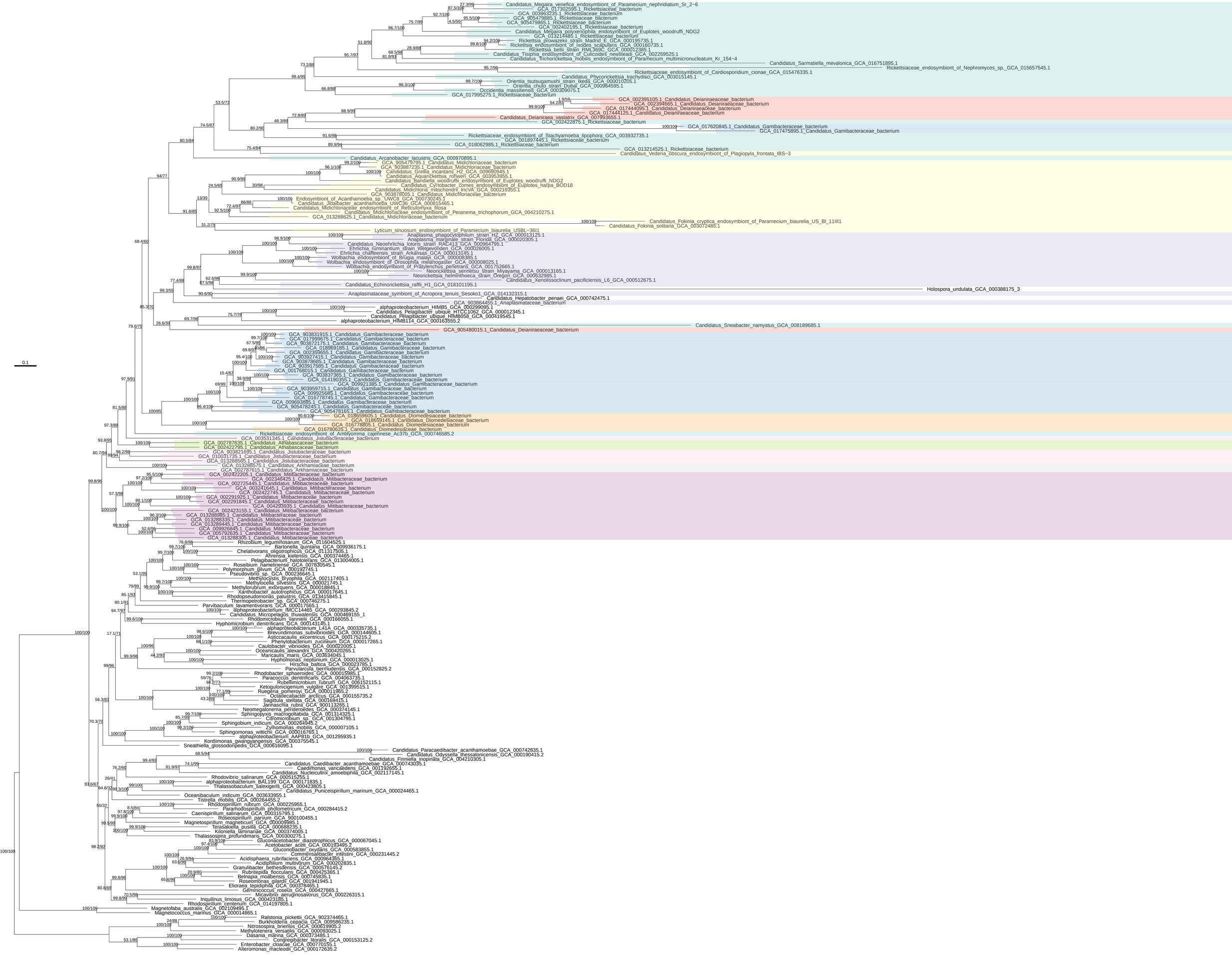
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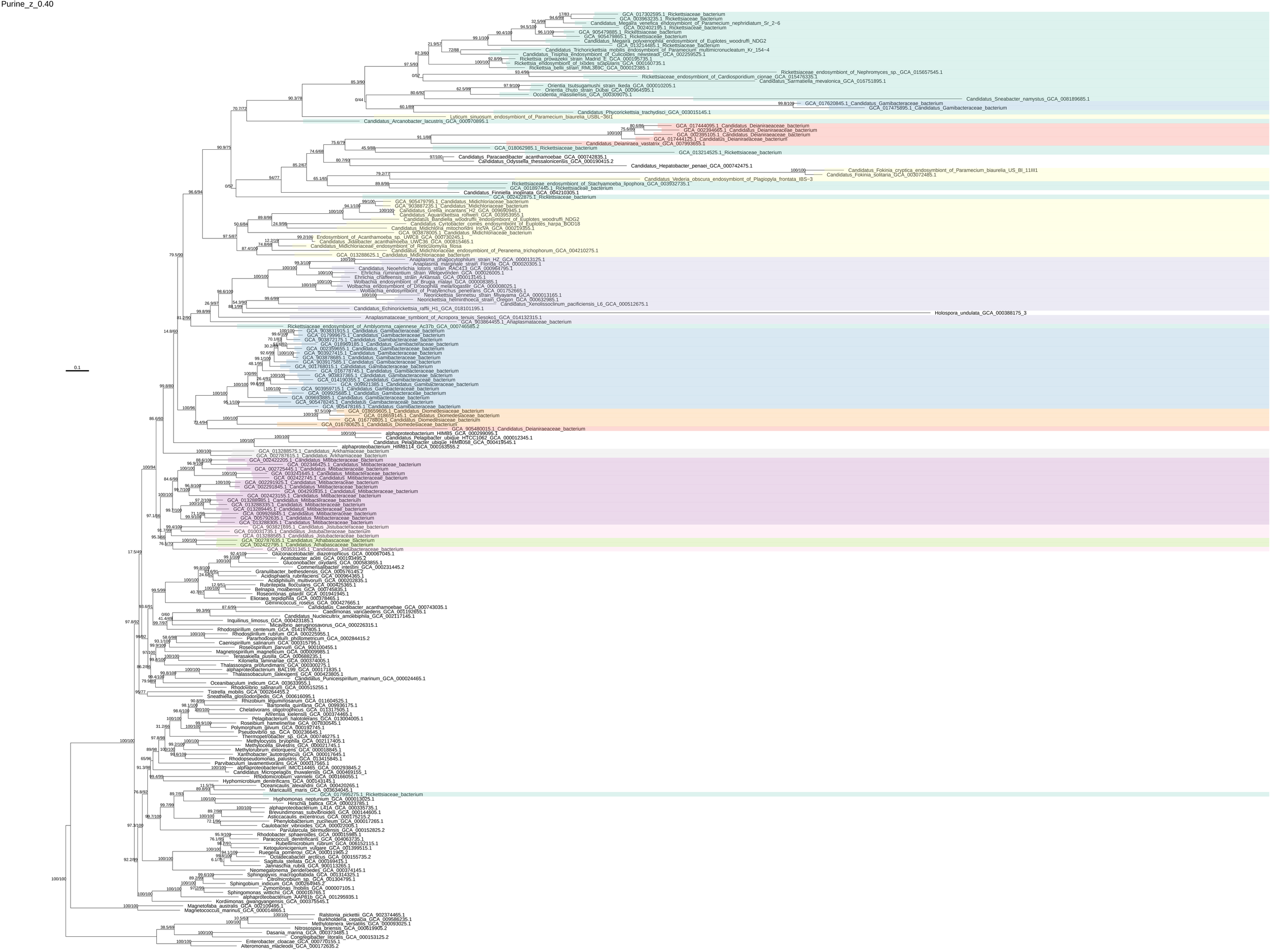
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Ehrlichia_chaffeensis_strain_Arkansas_GCA_000013145.1
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Bartonella_quintana_GCA_009936175.1
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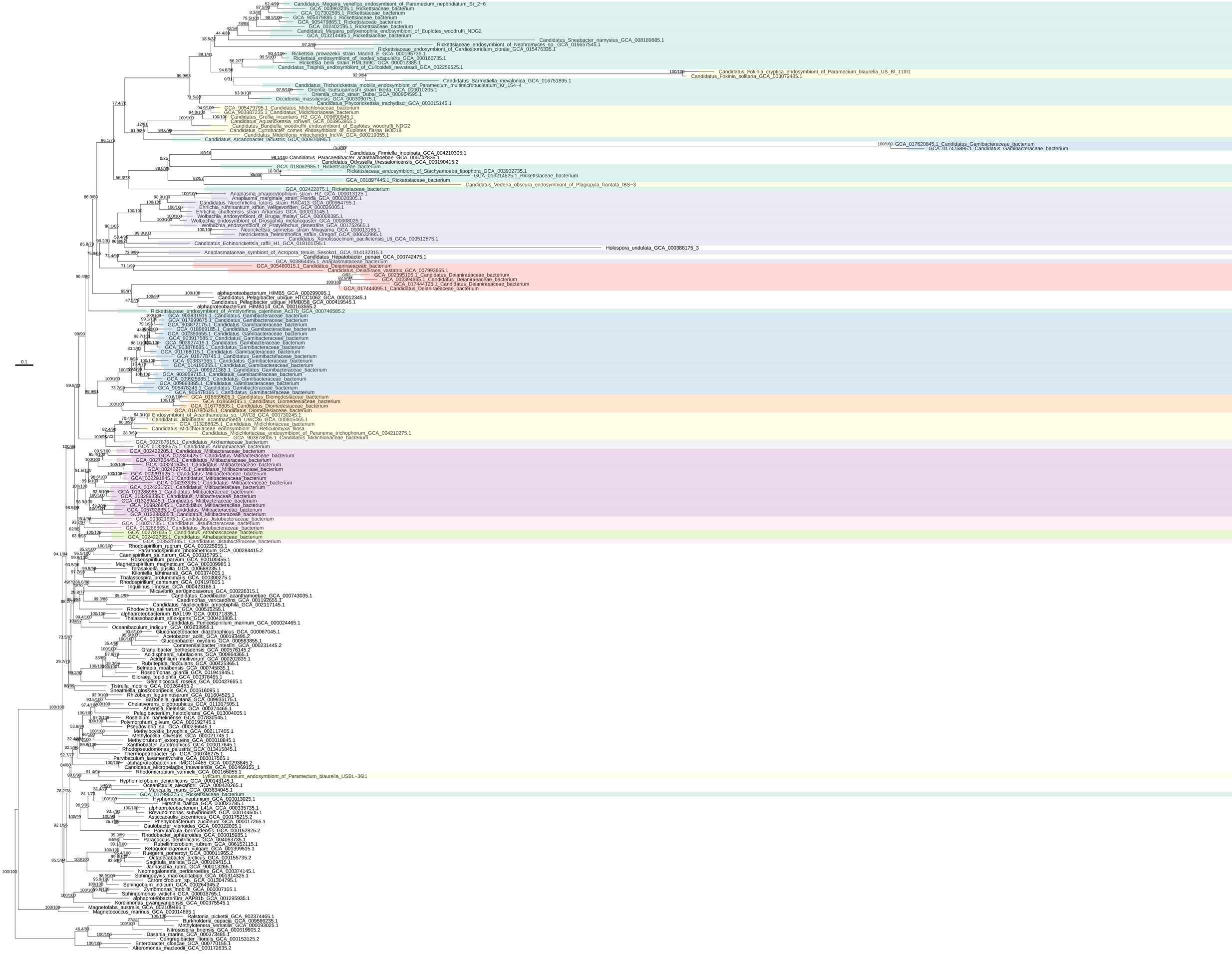
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Xanthobacter_autotrophicus_GCA_000017645.1
Rhodopseudomonas_palustris_GCA_013415845.1
Thermopetrobacter_sp._GCA_000746275.1
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Rhodomicrobium_vannielii_GCA_000165055.1
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Oceaniicaulis_alexandrii_GCA_000420265.1
Maricaulis_maris_GCA_003634045.1
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Hirschia_baltica_GCA_000023785.1
alphaproteobacterium_L41A_GCA_000335735.1
Brevundimonas_subvibrioides_GCA_000144605.1
Asticcacaulis_excentricus_GCA_000175215.2
Phenylobacterium_zucineum_GCA_000017265.1
Caulobacter_vibrioides_GCA_000022005.1
Parvularcula_bermudensis_GCA_000152825.2
Rhodobacter_sphaeroides_GCA_000015985.1
Paracoccus_denitrificans_GCA_004063735.1
Rubellimicrobium_rubrum_GCA_006152115.1
Ketogulonicigenium_vulgare_GCA_001399515.1
Ruegeria_pomeroyi_GCA_000011965.2
Octadecabacter_arcticus_GCA_000155735.2
Sagittula_stellata_GCA_000169415.1
Jannaschia_rubra_GCA_900113265.1
Neomegalonema_perideroedes_GCA_000374145.1
Sphingopyxis_macrogoltabida_GCA_001314325.1
Citromicrobium_sp._GCA_001304795.1
Sphingobium_indicum_GCA_000264945.2
Zymomonas_mobilis_GCA_000007105.1
Sphingomonas_wittichii_GCA_000016765.1
alphaproteobacterium_AAP81b_GCA_001295935.1
Kordiimonas_gwangyangensis_GCA_000375545.1
Magnetofaba_australis_GCA_002109495.1
Magnetococcus_marinus_GCA_000014865.1
Ralstonia_pickettii_GCA_902374465.1
Burkholderia_cepacia_GCA_009586235.1
Methylotenera_versatilis_GCA_000093025.1
Nitrosospira_briensis_GCA_000619905.2
Dasania_marina_GCA_000373485.1
Congregibacter_litoralis_GCA_000153125.2
Enterobacter_cloacae_GCA_000770155.1
Alteromonas_macleodii_GCA_000172635.2
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Pirimidine

0.1

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GCA_903872175.1_Candidatus_Gamibacteraceae_bacterium
GCA_018659185.1_Candidatus_Gamibacteraceae_bacterium
GCA_002359655.1_Candidatus_Gamibacteraceae_bacterium
GCA_903927415.1_Candidatus_Gamibacteraceae_bacterium
GCA_903878685.1_Candidatus_Gamibacteraceae_bacterium
GCA_001768015.1_Candidatus_Gamibacteraceae_bacterium
GCA_903917585.1_Candidatus_Gamibacteraceae_bacterium
GCA_009593885.1_Candidatus_Gamibacteraceae_bacterium
GCA_903837365.1_Candidatus_Gamibacteraceae_bacterium
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GCA_009921385.1_Candidatus_Gamibacteraceae_bacterium
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Occidentia_massiliensis_GCA_000309075.1
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Candidatus_Midichloria_mitochondrii_IricVA_GCA_000219355.1
Endosymbiont_of_Acanthamoeba_sp._UWC8_GCA_000730245.1
Candidatus_Jidaibacter_acanthamoebae_UWC36_GCA_000815465.1
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Candidatus_Midichloriaceae_endosymbiont_of_Perenema_trichophorum_GCA_004210275.1
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GCA_903864455.1_Anaplasmataceae_bacterium
Anaplasma_phagocytophilum_strain_HZ_GCA_000013125.1
Anaplasma_marginale_strain_Florida_GCA_000020305.1
Candidatus_Neoehrlichia_lotoris_strain_RAC413_GCA_000964795.1
Ehrlichia_ruminantium_strain_Welgevonden_GCA_000026005.1
Ehrlichia_chaffeensis_strain_Arkansas_GCA_000013145.1
Wolbachia_endosymbiont_of_Brugia_malayi_GCA_000008385.1
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Wolbachia_endosymbiont_of_Pratylenchus_penetrans_GCA_001752665.1
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Neorickettsia_helminthoeca_strain_Oregon_GCA_000632985.1
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Candidatus_Echinorickettsia_raffii_H1_GCA_018101195.1
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Jannaschia_rubra_GCA_900113265.1
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Ketogulonicigenium_vulgare_GCA_001399515.1
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Neomegalonema_perideroedes_GCA_003741145.1
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Ahrensia_kielensis_GCA_000374465.1
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Rhodopseudomonas_palustris_GCA_013415845.1
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Hyphomicrobium_denitrificans_GCA_000143145.1
Thermopetrobacter_sp._GCA_000746275.1
Sphingopyxis_macrogoltabida_GCA_001314325.1
Citromicrobium_sp._GCA_001304795.1
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Sphingomonas_wittichii_GCA_000016765.1
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Micavibrio_aeruginosavorus_GCA_000226315.1
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Ralstonia_pickettii_GCA_902374465.1
Burkholderia_cepacia_GCA_009586235.1
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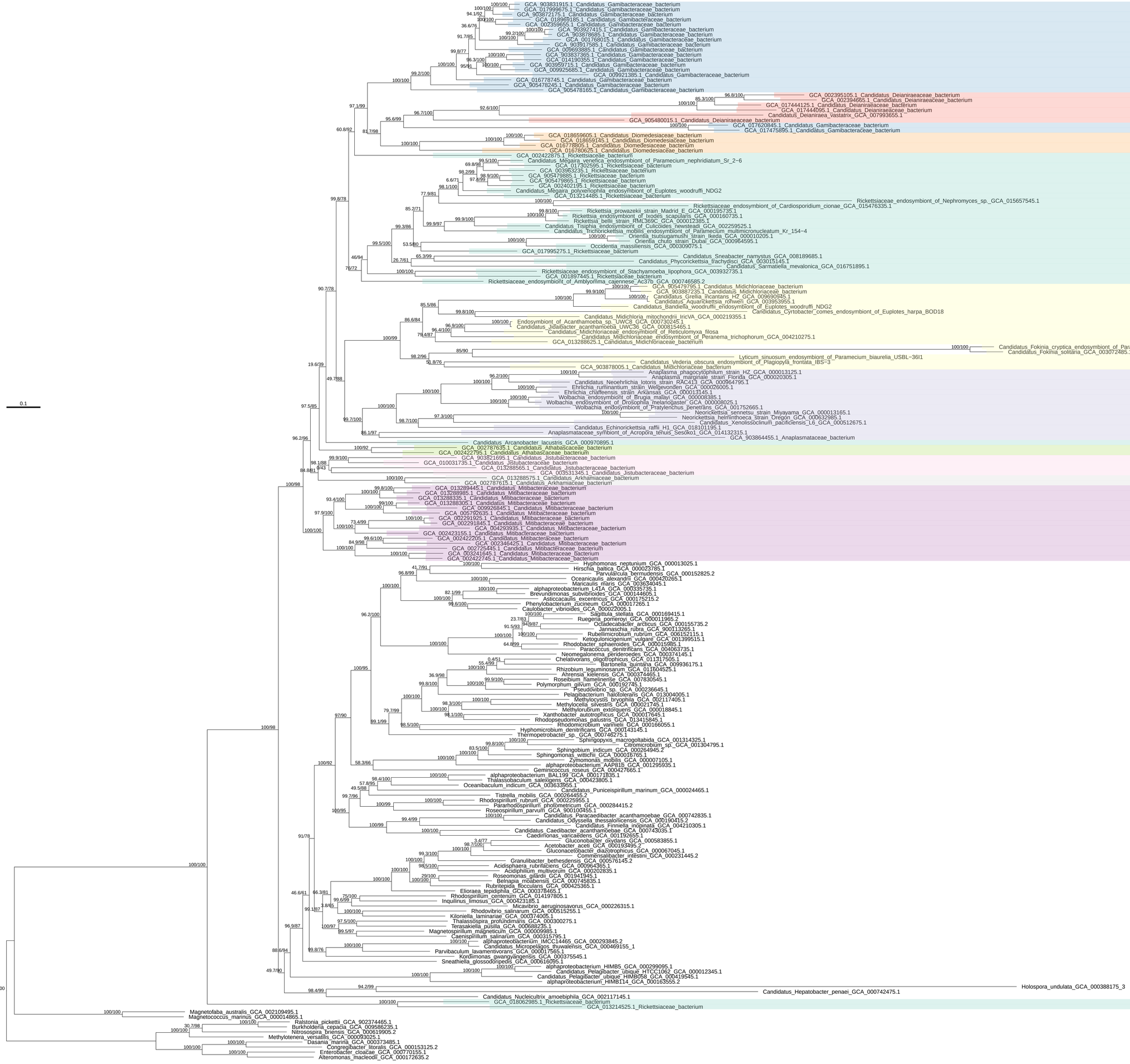

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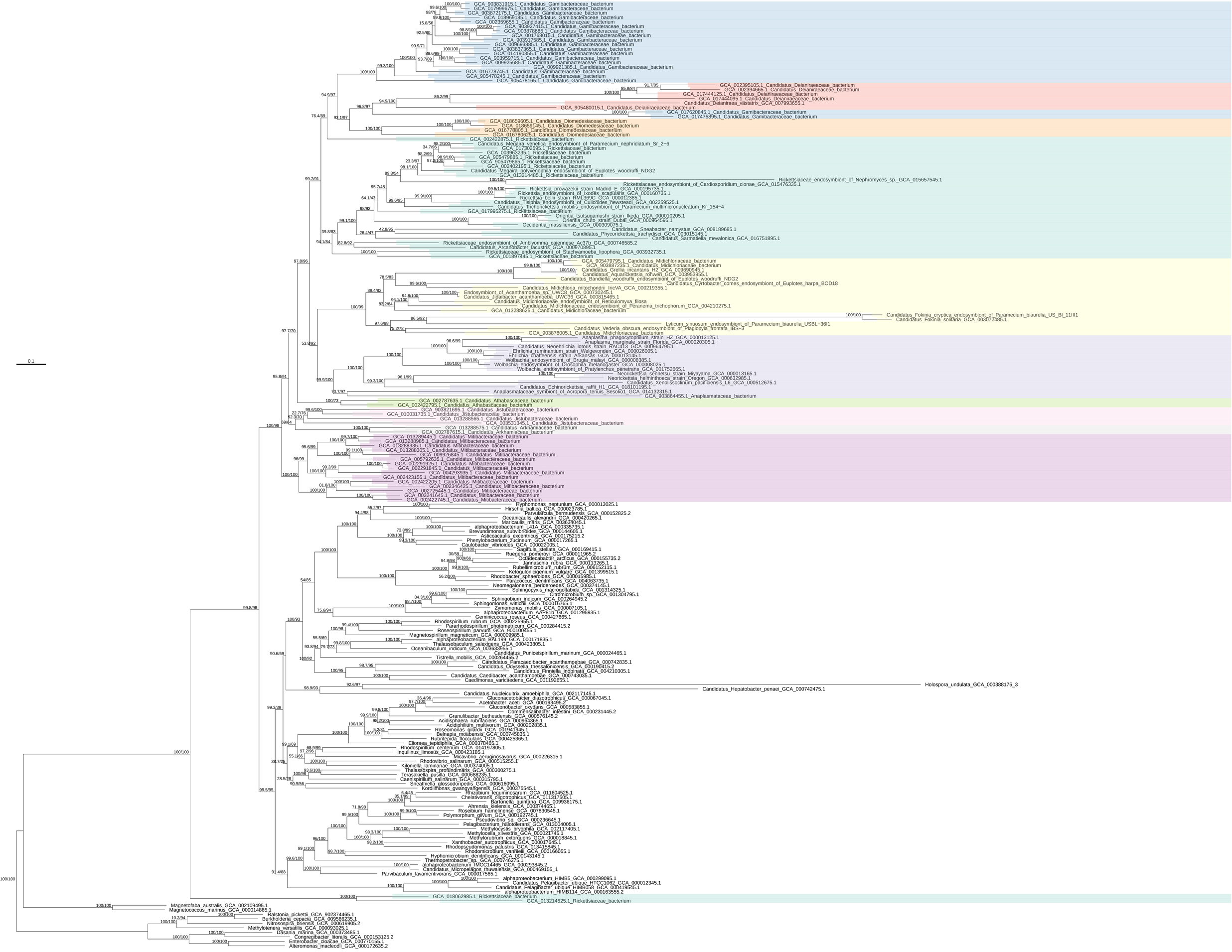

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GCA_903917585.1_Candidatus_Gamibacteraceae_bacterium
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Orientia_tsutsugamushi_strain_Ikeda_GCA_000010205.1
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Occidentia_massiliensis_GCA_000309075.1
GCA_017995275.1_Rickettsiaceae_bacterium
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Anaplasma_phagocytophilum_strain_HZ_GCA_000013125.1
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Ehrlichia_ruminantium_strain_Welgevonden_GCA_000026005.1
Ehrlichia_chaffeensis_strain_Arkansas_GCA_000013145.1
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Candidatus_Vederia_obscura_endosymbiont_of_Plagiopyla_frontata_IBS−3
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Candidatus_Grellia_incantans_H2_GCA_009690945.1
Candidatus_Aquarickettsia_rohweri_GCA_003953955.1
Candidatus_Bandiella_woodruffi_endosymbiont_of_Euplotes_woodruffi_NDG2
Endosymbiont_of_Acanthamoeba_sp._UWC8_GCA_000730245.1
Candidatus_Jidaibacter_acanthamoebae_UWC36_GCA_000815465.1
Candidatus_Midichloriaceae_endosymbiont_of_Reticulomyxa_filosa
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GCA_013288575.1_Candidatus_Arkhamiaceae_bacterium
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GCA_903821695.1_Candidatus_Jidaibacteraceae_bacterium
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Sagittula_stellata_GCA_000169415.1
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Burkholderia_cepacia_GCA_009586235.1
Methylotenera_versatilis_GCA_000093025.1
Nitrosospira_briensis_GCA_000619905.2
Dasania_marina_GCA_000373485.1
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Alteromonas_macleodii_GCA_000172635.2

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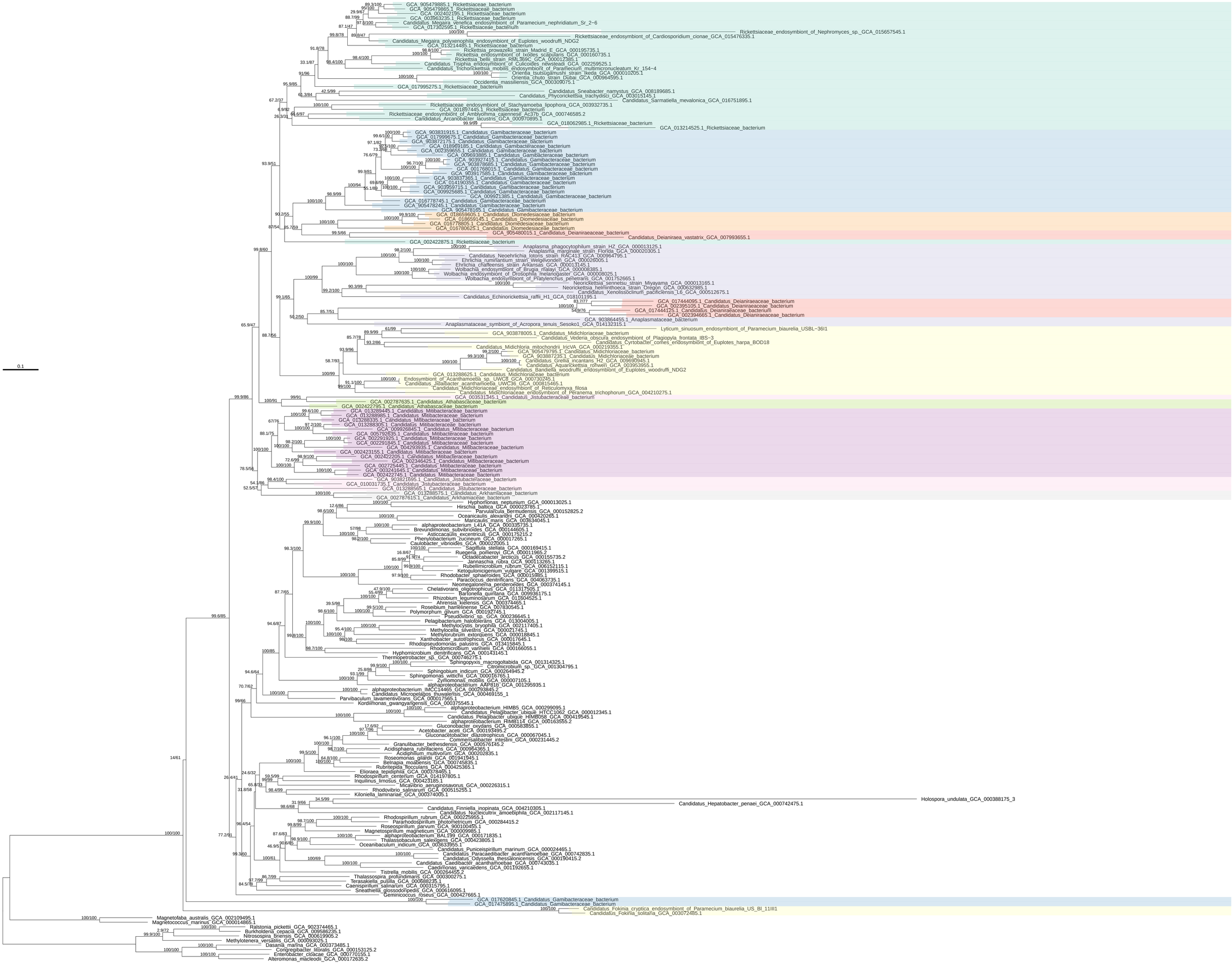

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Orientia_chuto_strain_Dubai_GCA_000964595.1
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Phenylobacterium_zucineum_GCA_000017265.1
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Citromicrobium_sp._GCA_001304795.1
Sphingobium_indicum_GCA_000264945.2
Zymomonas_mobilis_GCA_000007105.1
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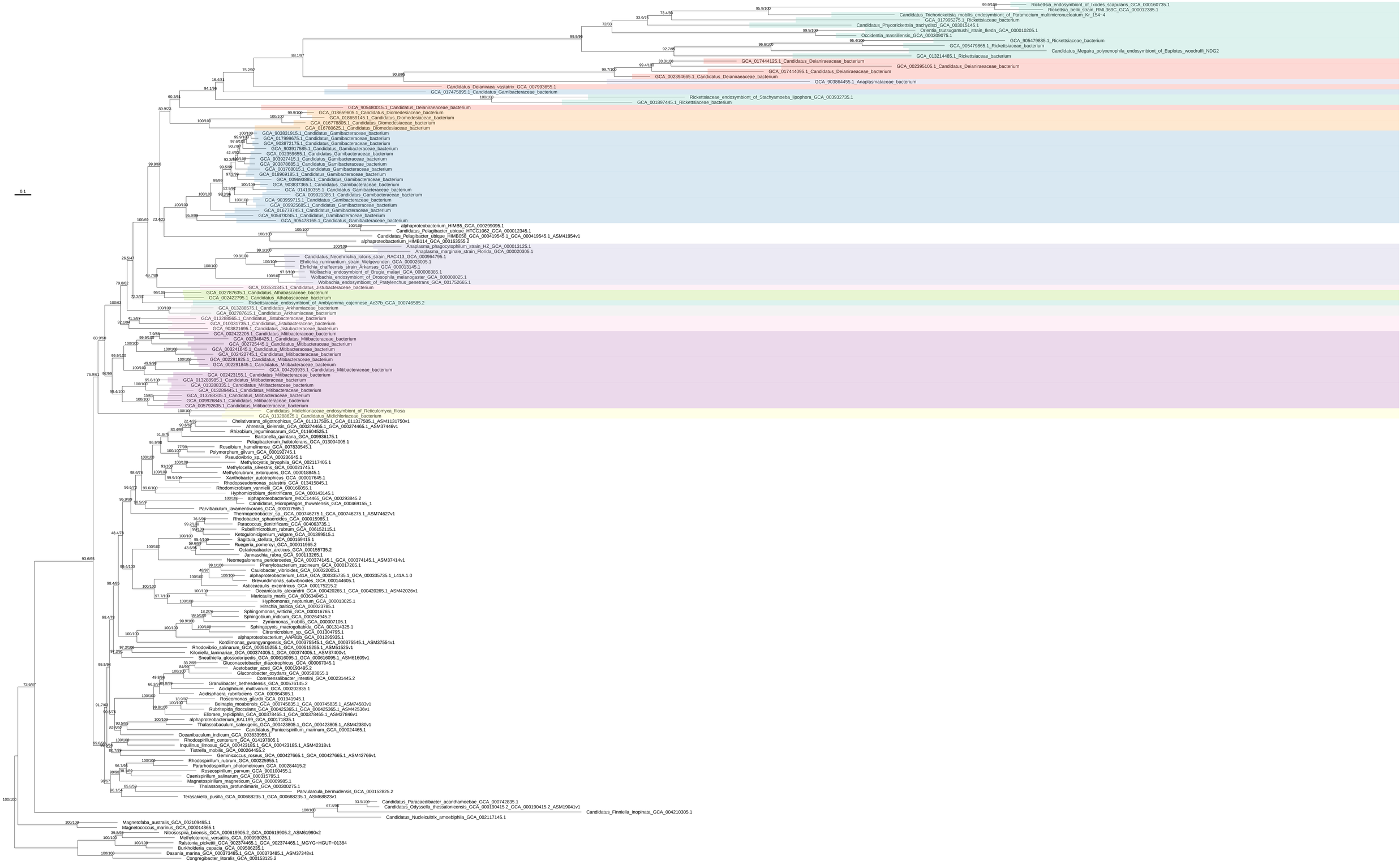
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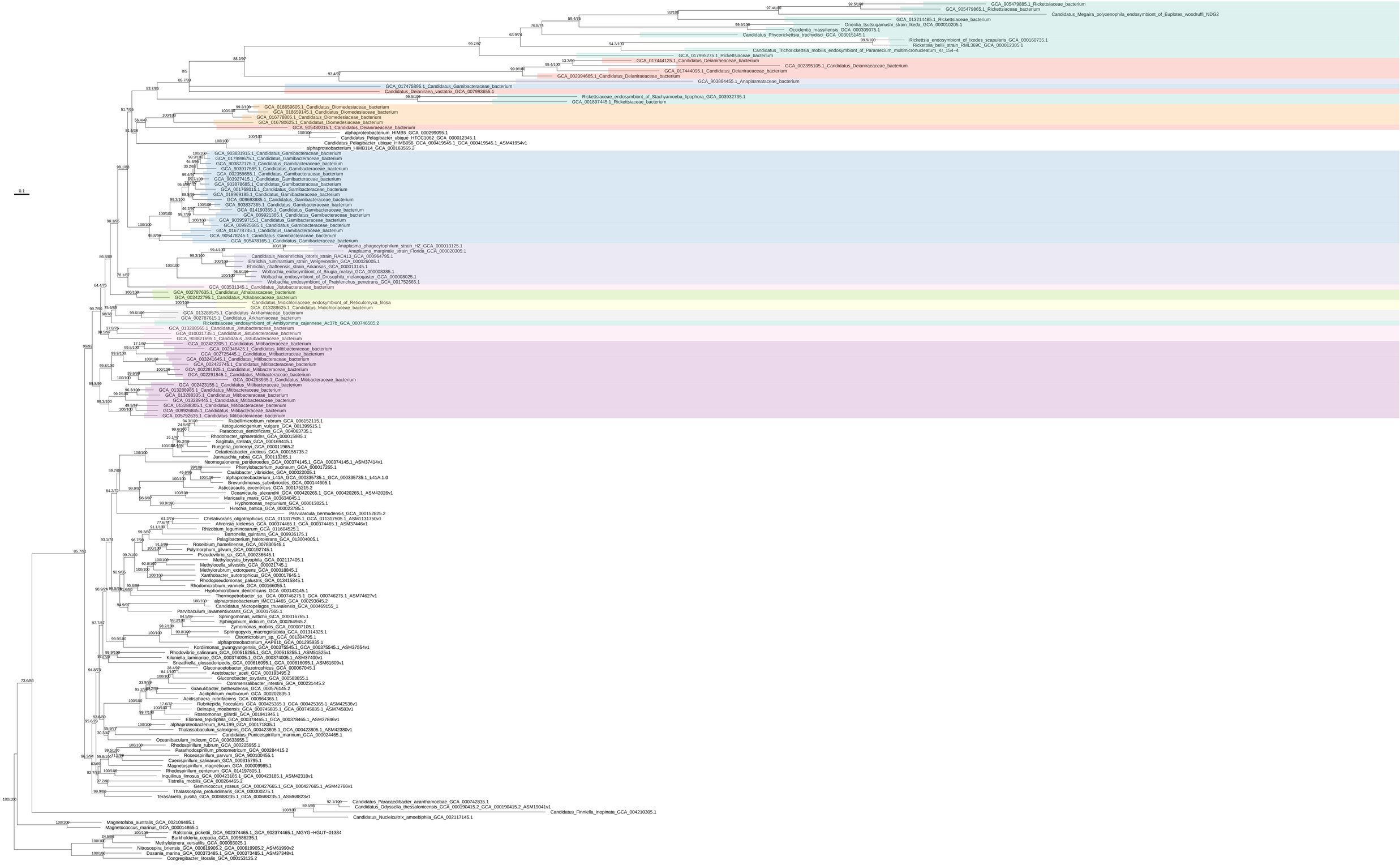
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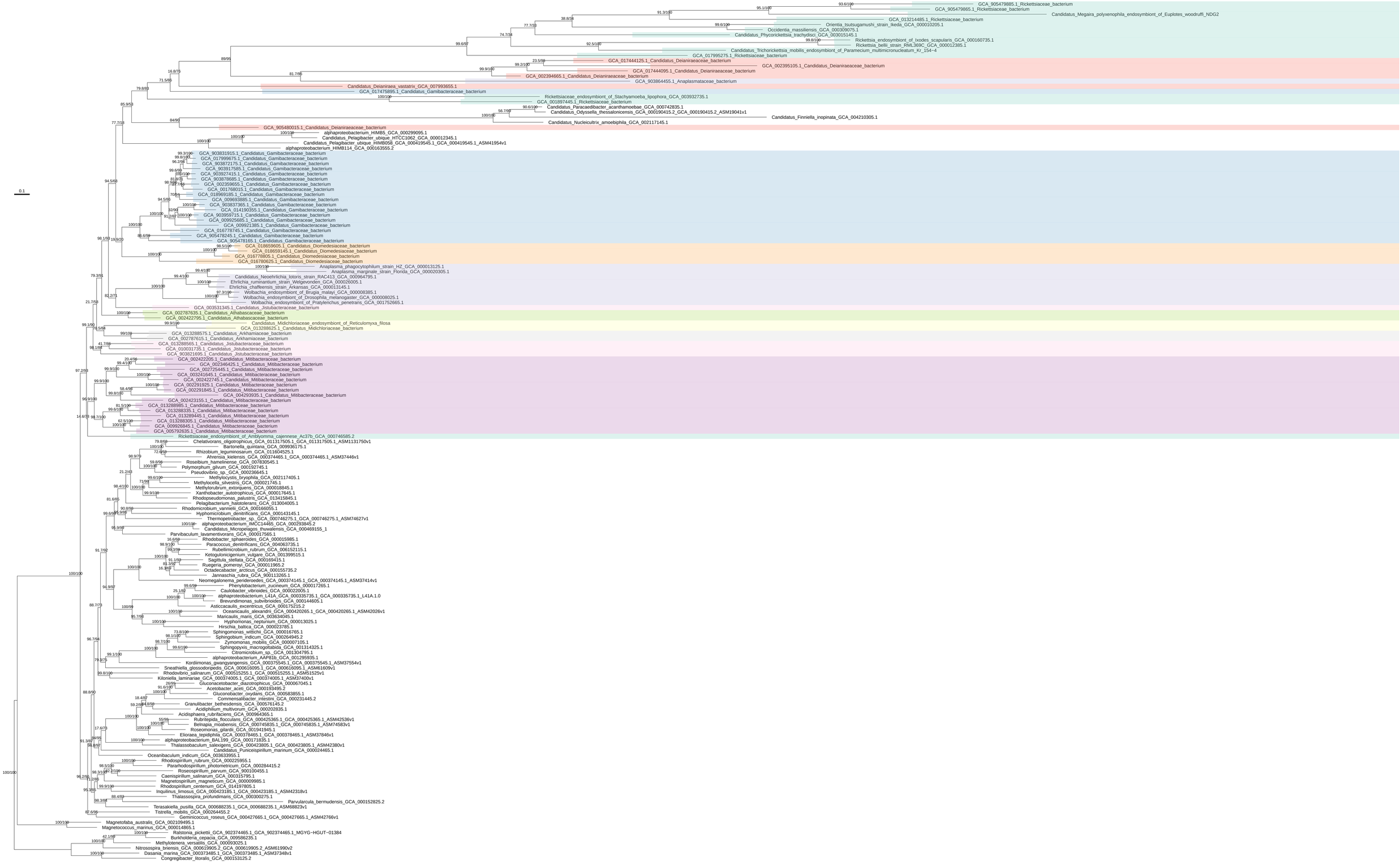
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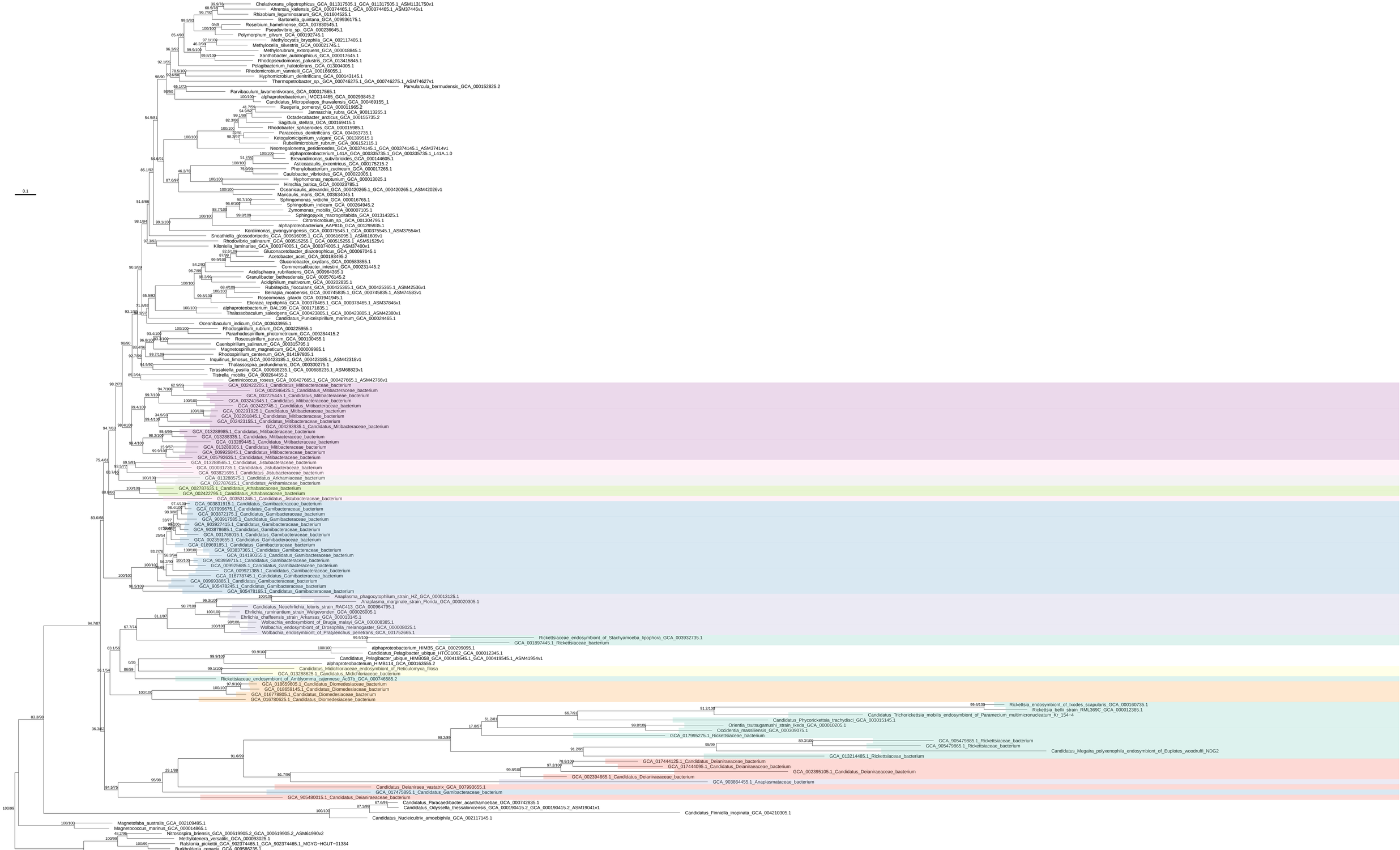
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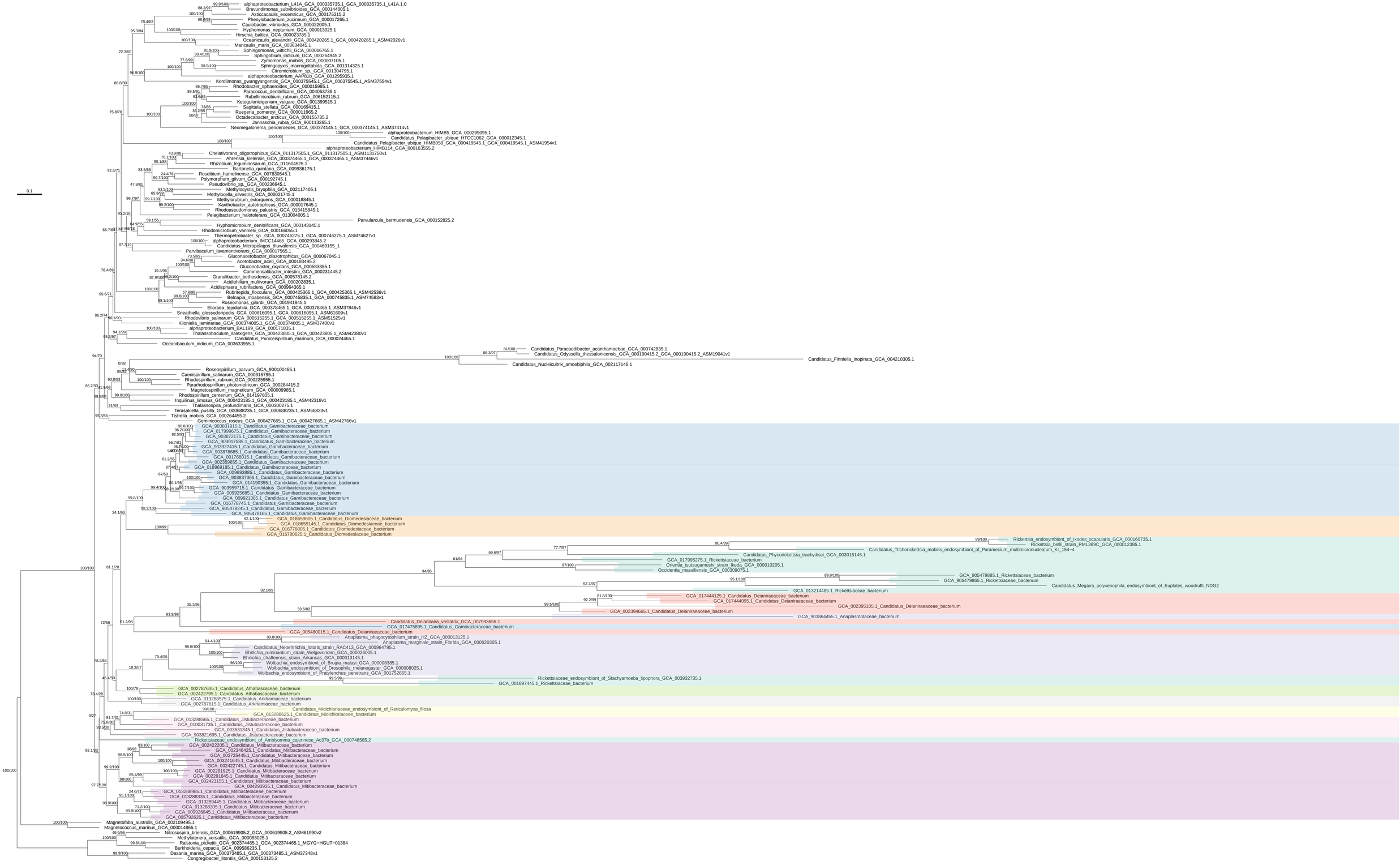
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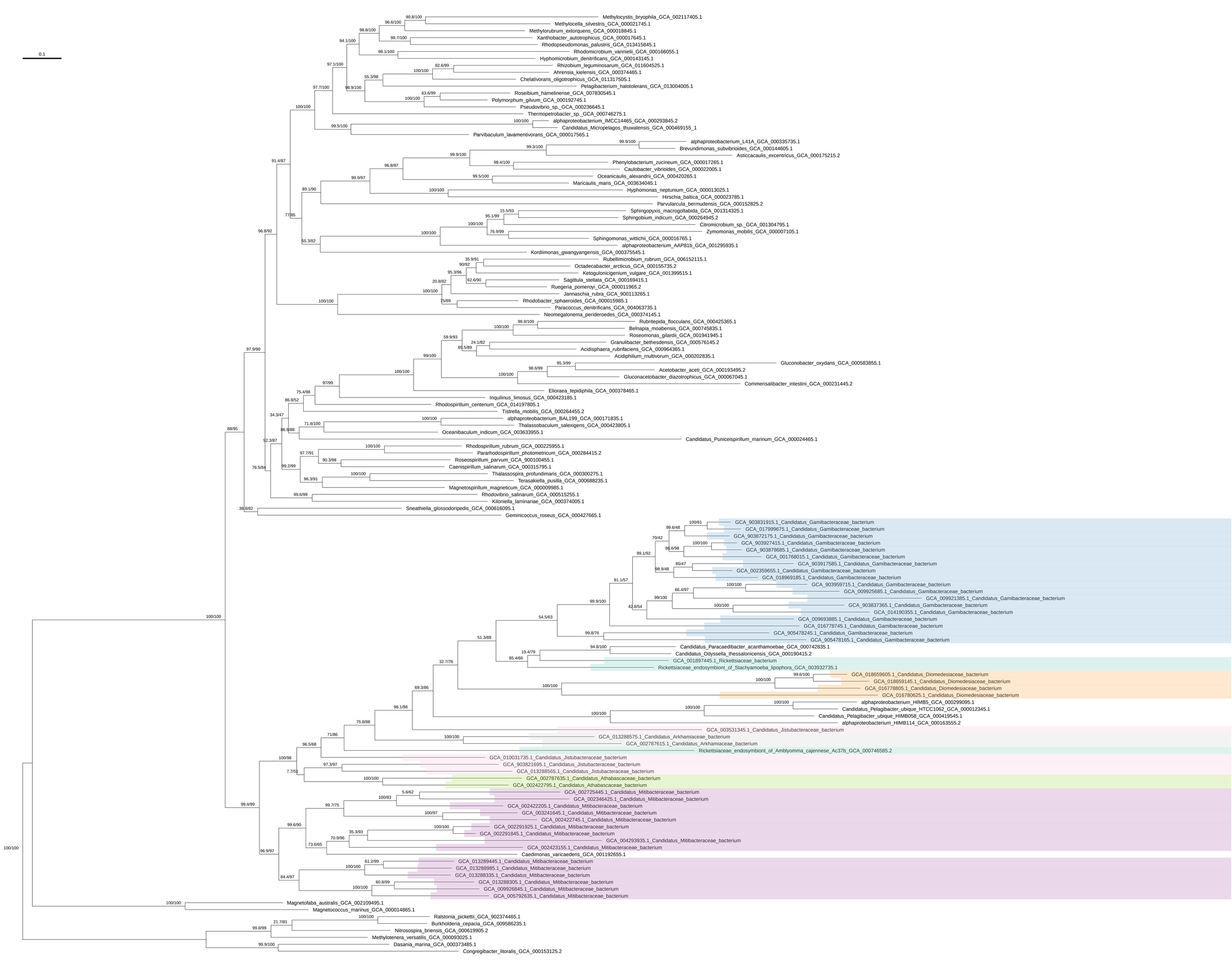
Histidine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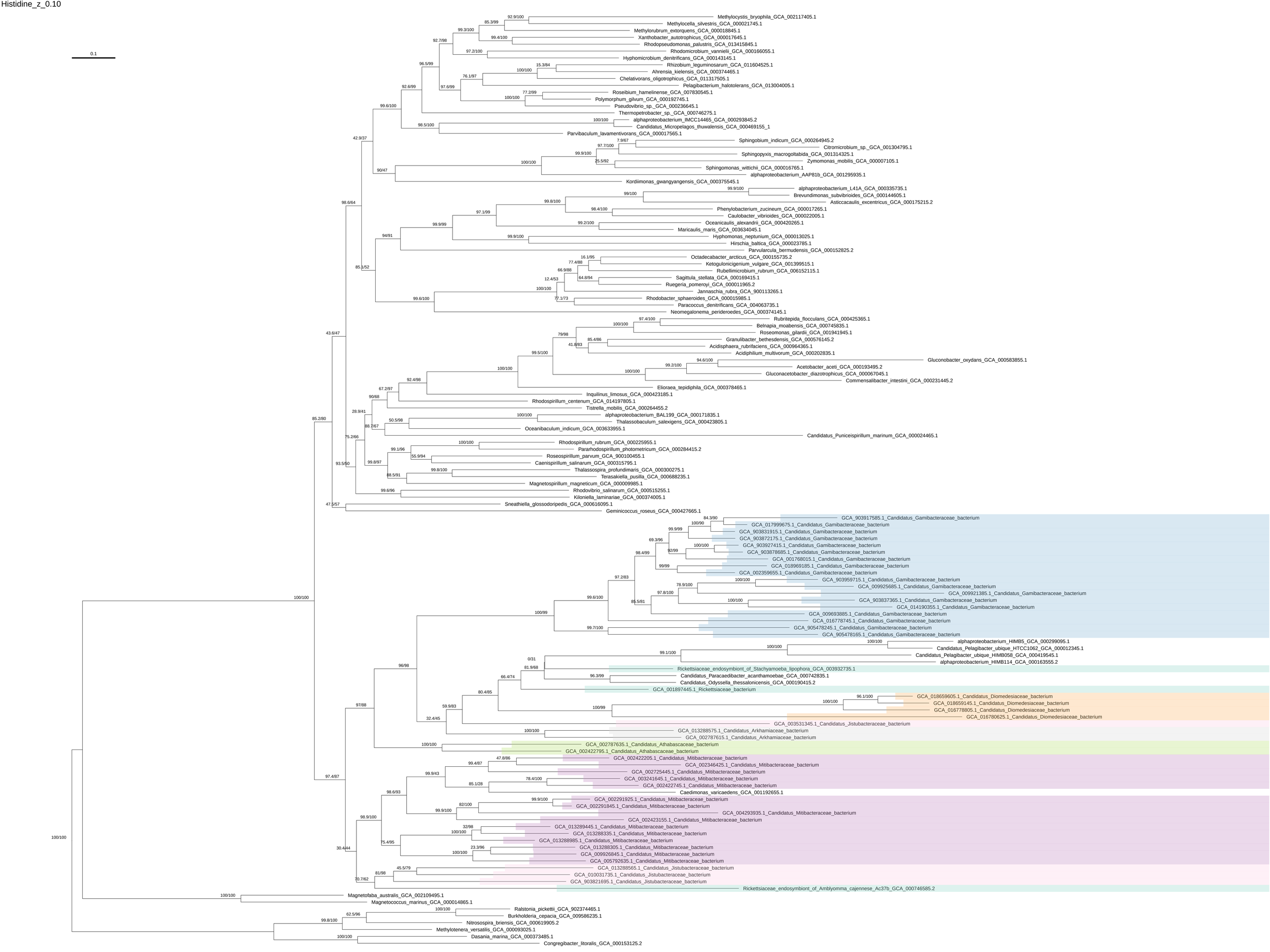
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Rhodobacter_sphaeroides_GCA_000015985.1
Paracoccus_denitrificans_GCA_004063735.1
Jannaschia_rubra_GCA_900113265.1
Neomegalonema_perideroedes_GCA_000374145.1
Geminicoccus_roseus_GCA_000427665.1
Rhodovibrio_salinarum_GCA_000515255.1
Kiloniella_laminariae_GCA_000374005.1
Tistrella_mobilis_GCA_000264455.2
Rubritepida_flocculans_GCA_000425365.1
Belnapia_moabensis_GCA_000745835.1
Roseomonas_gilardii_GCA_001941945.1
Acidisphaera_rubrifaciens_GCA_000964365.1
Acidiphilium_multivorum_GCA_000202835.1
Granulibacter_bethesdensis_GCA_000576145.2
Gluconobacter_oxydans_GCA_000583855.1
Acetobacter_aceti_GCA_000193495.2
Gluconacetobacter_diazotrophicus_GCA_000067045.1
Commensalibacter_intestini_GCA_000231445.2
Elioraea_tepidiphila_GCA_000378465.1
Inquilinus_limosus_GCA_000423185.1
Rhodospirillum_centenum_GCA_014197805.1
alphaproteobacterium_BAL199_GCA_000171835.1
Thalassobaculum_salexigens_GCA_000423805.1
Candidatus_Puniceispirillum_marinum_GCA_000024465.1
Oceanibaculum_indicum_GCA_003633955.1
Rhodospirillum_rubrum_GCA_000225955.1
Pararhodospirillum_photometricum_GCA_000284415.2
Roseospirillum_parvum_GCA_900100455.1
Caenispirillum_salinarum_GCA_000315795.1
Thalassospira_profundimaris_GCA_000300275.1
Terasakiella_pusilla_GCA_000688235.1
Magnetospirillum_magneticum_GCA_000009985.1
Sneathiella_glossodoripedis_GCA_000616095.1
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GCA_017999675.1_Candidatus_Gamibacteraceae_bacterium
GCA_903831915.1_Candidatus_Gamibacteraceae_bacterium
GCA_903872175.1_Candidatus_Gamibacteraceae_bacterium
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Candidatus_Paracaedibacter_acanthamoebae_GCA_000742835.1
Candidatus_Odyssella_thessalonicensis_GCA_000190415.2
Rickettsiaceae_endosymbiont_of_Stachyamoeba_lipophora_GCA_003932735.1
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GCA_905478165.1_Candidatus_Gamibacteraceae_bacterium
GCA_018659605.1_Candidatus_Diomedesiaceae_bacterium
GCA_018659145.1_Candidatus_Diomedesiaceae_bacterium
GCA_016778805.1_Candidatus_Diomedesiaceae_bacterium
GCA_016780625.1_Candidatus_Diomedesiaceae_bacterium
alphaproteobacterium_HIMB5_GCA_000299095.1
Candidatus_Pelagibacter_ubique_HTCC1062_GCA_000012345.1
Candidatus_Pelagibacter_ubique_HIMB058_GCA_000419545.1
alphaproteobacterium_HIMB114_GCA_000163555.2
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GCA_002787635.1_Candidatus_Athabascaceae_bacterium
GCA_002422795.1_Candidatus_Athabascaceae_bacterium
GCA_002422205.1_Candidatus_Mitibacteraceae_bacterium
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GCA_002423155.1_Candidatus_Mitibacteraceae_bacterium
Caedimonas_varicaedens_GCA_001192655.1
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GCA_005792635.1_Candidatus_Mitibacteraceae_bacterium
GCA_013288305.1_Candidatus_Mitibacteraceae_bacterium
GCA_013288565.1_Candidatus_Jistubacteraceae_bacterium
GCA_010031735.1_Candidatus_Jistubacteraceae_bacterium
GCA_903821695.1_Candidatus_Jistubacteraceae_bacterium
Rickettsiaceae_endosymbiont_of_Amblyomma_cajennese_Ac37b_GCA_000746585.2
Magnetofaba_australis_GCA_002109495.1
Magnetococcus_marinus_GCA_000014865.1
Ralstonia_pickettii_GCA_902374465.1
Burkholderia_cepacia_GCA_009586235.1
Nitrosospira_briensis_GCA_000619905.2
Methylotenera_versatilis_GCA_000093025.1
Dasania_marina_GCA_000373485.1
Congregibacter_litoralis_GCA_000153125.2

Histidine_z_0.30

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GCA_017999675.1_Candidatus_Gamibacteraceae_bacterium
GCA_018969185.1_Candidatus_Gamibacteraceae_bacterium
GCA_002359655.1_Candidatus_Gamibacteraceae_bacterium
GCA_903927415.1_Candidatus_Gamibacteraceae_bacterium
GCA_903878685.1_Candidatus_Gamibacteraceae_bacterium
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GCA_905478165.1_Candidatus_Gamibacteraceae_bacterium
Candidatus_Paracaedibacter_acanthamoebae_GCA_000742835.1
Candidatus_Odyssella_thessalonicensis_GCA_000190415.2
GCA_001897445.1_Rickettsiaceae_bacterium
Rickettsiaceae_endosymbiont_of_Stachyamoeba_lipophora_GCA_003932735.1
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Candidatus_Pelagibacter_ubique_HIMB058_GCA_000419545.1
alphaproteobacterium_HIMB114_GCA_000163555.2
alphaproteobacterium_L41A_GCA_000335735.1
Brevundimonas_subvibrioides_GCA_000144605.1
Asticcacaulis_excentricus_GCA_000175215.2
Phenylobacterium_zucineum_GCA_000017265.1
Caulobacter_vibrioides_GCA_000022005.1
Oceanicaulis_alexandrii_GCA_000420265.1
Maricaulis_maris_GCA_003634045.1
Hyphomonas_neptunium_GCA_000013025.1
Hirschia_baltica_GCA_000023785.1
Sphingobium_indicum_GCA_000264945.2
Citromicrobium_sp._GCA_001304795.1
Sphingopyxis_macrogoltabida_GCA_001314325.1
Sphingomonas_wittichii_GCA_000016765.1
Zymomonas_mobilis_GCA_000007105.1
alphaproteobacterium_AAP81b_GCA_001295935.1
Kordiimonas_gwangyangensis_GCA_000375545.1
Roseibium_hamelinense_GCA_007830545.1
Polymorphum_gilvum_GCA_000192745.1
Pseudovibrio_sp._GCA_000236645.1
Rhizobium_leguminosarum_GCA_011604525.1
Ahrensia_kielensis_GCA_000374465.1
Chelativorans_oligotrophicus_GCA_011317505.1
Pelagibacterium_halotolerans_GCA_013004005.1
Xanthobacter_autotrophicus_GCA_000017645.1
Rhodopseudomonas_palustris_GCA_013415845.1
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Methylocella_silvestris_GCA_000021745.1
Rhodomicrobium_vannielii_GCA_000166055.1
Hyphomicrobium_denitrificans_GCA_000143145.1
Thermopetrobacter_sp._GCA_000746275.1
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Candidatus_Micropelagos_thuwalensis_GCA_000469155_1
Parvibaculum_lavamentivorans_GCA_000017565.1
Rubellimicrobium_rubrum_GCA_006152115.1
Octadecabacter_arcticus_GCA_000155735.2
Ketogulonicigenium_vulgare_GCA_001399515.1
Sagittula_stellata_GCA_000169415.1
Ruegeria_pomeroyi_GCA_000011965.2
Jannaschia_rubra_GCA_900113265.1
Rhodobacter_sphaeroides_GCA_000015985.1
Paracoccus_denitrificans_GCA_004063735.1
Neomegalonema_perideroedes_GCA_000374145.1
Geminicoccus_roseus_GCA_000427665.1
Parvularcula_bermudensis_GCA_000152825.2
Rubritepida_flocculans_GCA_000425365.1
Roseomonas_gilardii_GCA_001941945.1
Belnapia_moabensis_GCA_000745835.1
Acidisphaera_rubrifaciens_GCA_000964365.1
Acidiphilium_multivorum_GCA_000202835.1
Granulibacter_bethesdensis_GCA_000576145.2
Gluconobacter_oxydans_GCA_000583855.1
Acetobacter_aceti_GCA_000193495.2
Gluconacetobacter_diazotrophicus_GCA_000067045.1
Commensalibacter_intestini_GCA_000231445.2
Elioraea_tepidiphila_GCA_000378465.1
Inquilinus_limosus_GCA_000423185.1
Rickettsiaceae_endosymbiont_of_Amblyomma_cajennese_Ac37b_GCA_000746585.2
Kiloniella_laminariae_GCA_000374005.1
Rhodovibrio_salinarum_GCA_000515255.1
Rhodospirillum_rubrum_GCA_000225955.1
Pararhodospirillum_photometricum_GCA_000284415.2
Magnetospirillum_magneticum_GCA_000009985.1
Tistrella_mobilis_GCA_000264455.2
Thalassospira_profundimaris_GCA_000300275.1
Terasakiella_pusilla_GCA_000688235.1
Roseospirillum_parvum_GCA_900100455.1
Caenispirillum_salinarum_GCA_000315795.1
alphaproteobacterium_BAL199_GCA_000171835.1
Thalassobaculum_salexigens_GCA_000423805.1
Candidatus_Puniceispirillum_marinum_GCA_000024465.1
Oceanibaculum_indicum_GCA_003633955.1
Rhodospirillum_centenum_GCA_014197805.1
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Caedimonas_varicaedens_GCA_001192655.1
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Sneathiella_glossodoripedis_GCA_000616095.1
Magnetofaba_australis_GCA_002109495.1
Magnetococcus_marinus_GCA_000014865.1
Ralstonia_pickettii_GCA_902374465.1
Burkholderia_cepacia_GCA_009586235.1
Nitrosospira_briensis_GCA_000619905.2
Methylotenera_versatilis_GCA_000093025.1
Dasania_marina_GCA_000373485.1
Congregibacter_litoralis_GCA_000153125.2

Histidine_z_0.40

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GCA_903872175.1_Candidatus_Gamibacteraceae_bacterium
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GCA_018969185.1_Candidatus_Gamibacteraceae_bacterium
GCA_002359655.1_Candidatus_Gamibacteraceae_bacterium
GCA_903927415.1_Candidatus_Gamibacteraceae_bacterium
GCA_903878685.1_Candidatus_Gamibacteraceae_bacterium
GCA_001768015.1_Candidatus_Gamibacteraceae_bacterium
GCA_903837365.1_Candidatus_Gamibacteraceae_bacterium
GCA_014190355.1_Candidatus_Gamibacteraceae_bacterium
GCA_903959715.1_Candidatus_Gamibacteraceae_bacterium
GCA_009925685.1_Candidatus_Gamibacteraceae_bacterium
GCA_009921385.1_Candidatus_Gamibacteraceae_bacterium
GCA_009693885.1_Candidatus_Gamibacteraceae_bacterium
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Candidatus_Paracaedibacter_acanthamoebae_GCA_000742835.1
Candidatus_Odyssella_thessalonicensis_GCA_000190415.2
Rickettsiaceae_endosymbiont_of_Stachyamoeba_lipophora_GCA_003932735.1
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GCA_905478165.1_Candidatus_Gamibacteraceae_bacterium
GCA_001897445.1_Rickettsiaceae_bacterium
GCA_018659605.1_Candidatus_Diomedesiaceae_bacterium
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Roseibium_hamelinense_GCA_007830545.1
Polymorphum_gilvum_GCA_000192745.1
Pseudovibrio_sp._GCA_000236645.1
Rhizobium_leguminosarum_GCA_011604525.1
Ahrensia_kielensis_GCA_000374465.1
Chelativorans_oligotrophicus_GCA_011317505.1
Pelagibacterium_halotolerans_GCA_013004005.1
Xanthobacter_autotrophicus_GCA_000017645.1
Methylorubrum_extorquens_GCA_000018845.1
Rhodopseudomonas_palustris_GCA_013415845.1
Methylocystis_bryophila_GCA_002117405.1
Methylocella_silvestris_GCA_000021745.1
Rhodomicrobium_vannielii_GCA_000166055.1
Hyphomicrobium_denitrificans_GCA_000143145.1
Thermopetrobacter_sp._GCA_000746275.1
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Candidatus_Pelagibacter_ubique_HTCC1062_GCA_000012345.1
Candidatus_Pelagibacter_ubique_HIMB058_GCA_000419545.1
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alphaproteobacterium_IMCC14465_GCA_000293845.2
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Parvibaculum_lavamentivorans_GCA_000017565.1
Kordiimonas_gwangyangensis_GCA_000375545.1
alphaproteobacterium_L41A_GCA_000335735.1
Brevundimonas_subvibrioides_GCA_000144605.1
Asticcacaulis_excentricus_GCA_000175215.2
Phenylobacterium_zucineum_GCA_000017265.1
Caulobacter_vibrioides_GCA_000022005.1
Oceanicaulis_alexandrii_GCA_000420265.1
Maricaulis_maris_GCA_003634045.1
Hyphomonas_neptunium_GCA_000013025.1
Hirschia_baltica_GCA_000023785.1
Sphingobium_indicum_GCA_000264945.2
Citromicrobium_sp._GCA_001304795.1
Sphingopyxis_macrogoltabida_GCA_001314325.1
Sphingomonas_wittichii_GCA_000016765.1
Zymomonas_mobilis_GCA_000007105.1
alphaproteobacterium_AAP81b_GCA_001295935.1
Sagittula_stellata_GCA_000169415.1
Ruegeria_pomeroyi_GCA_000011965.2
Octadecabacter_arcticus_GCA_000155735.2
Jannaschia_rubra_GCA_900113265.1
Rubellimicrobium_rubrum_GCA_006152115.1
Ketogulonicigenium_vulgare_GCA_001399515.1
Rhodobacter_sphaeroides_GCA_000015985.1
Paracoccus_denitrificans_GCA_004063735.1
Neomegalonema_perideroedes_GCA_000374145.1
Geminicoccus_roseus_GCA_000427665.1
Parvularcula_bermudensis_GCA_000152825.2
Rubritepida_flocculans_GCA_000425365.1
Belnapia_moabensis_GCA_000745835.1
Roseomonas_gilardii_GCA_001941945.1
Acidisphaera_rubrifaciens_GCA_000964365.1
Granulibacter_bethesdensis_GCA_000576145.2
Acidiphilium_multivorum_GCA_000202835.1
Gluconobacter_oxydans_GCA_000583855.1
Acetobacter_aceti_GCA_000193495.2
Gluconacetobacter_diazotrophicus_GCA_000067045.1
Commensalibacter_intestini_GCA_000231445.2
Elioraea_tepidiphila_GCA_000378465.1
Inquilinus_limosus_GCA_000423185.1
Rhodovibrio_salinarum_GCA_000515255.1
Kiloniella_laminariae_GCA_000374005.1
Rhodospirillum_rubrum_GCA_000225955.1
Pararhodospirillum_photometricum_GCA_000284415.2
Magnetospirillum_magneticum_GCA_000009985.1
Tistrella_mobilis_GCA_000264455.2
Thalassospira_profundimaris_GCA_000300275.1
Terasakiella_pusilla_GCA_000688235.1
Rickettsiaceae_endosymbiont_of_Amblyomma_cajennese_Ac37b_GCA_000746585.2
Roseospirillum_parvum_GCA_900100455.1
Caenispirillum_salinarum_GCA_000315795.1
alphaproteobacterium_BAL199_GCA_000171835.1
Thalassobaculum_salexigens_GCA_000423805.1
Oceanibaculum_indicum_GCA_003633955.1
Candidatus_Puniceispirillum_marinum_GCA_000024465.1
Rhodospirillum_centenum_GCA_014197805.1
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Caedimonas_varicaedens_GCA_001192655.1
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Sneathiella_glossodoripedis_GCA_000616095.1
Magnetofaba_australis_GCA_002109495.1
Magnetococcus_marinus_GCA_000014865.1
Ralstonia_pickettii_GCA_902374465.1
Burkholderia_cepacia_GCA_009586235.1
Nitrosospira_briensis_GCA_000619905.2
Methylotenera_versatilis_GCA_000093025.1
Dasania_marina_GCA_000373485.1
Congregibacter_litoralis_GCA_000153125.2

Histidine_z_0.50

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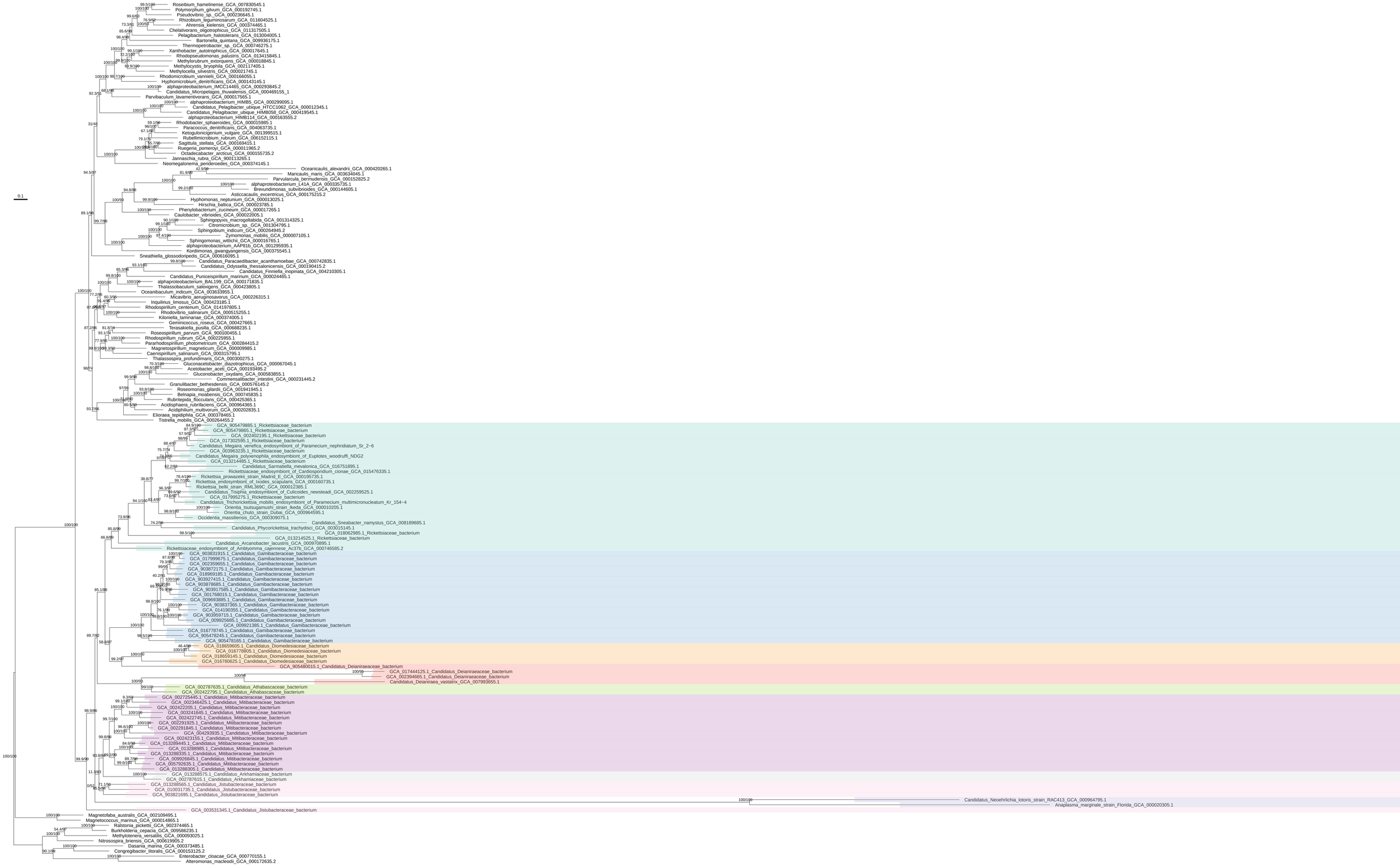
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Kiloniella_laminariae_GCA_000374005.1
Geminicoccus_roseus_GCA_000427665.1
Terasakiella_pusilla_GCA_000688235.1
Roseospirillum_parvum_GCA_900100455.1
Rhodospirillum_rubrum_GCA_000225955.1
Pararhodospirillum_photometricum_GCA_000284415.2
Magnetospirillum_magneticum_GCA_000009985.1
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Acetobacter_aceti_GCA_000193495.2
Gluconobacter_oxydans_GCA_000583855.1
Commensalibacter_intestini_GCA_000231445.2
Granulibacter_bethesdensis_GCA_000576145.2
Roseomonas_gilardii_GCA_001941945.1
Belnapia_moabensis_GCA_000745835.1
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Acidiphilium_multivorum_GCA_000202835.1
Elioraea_tepidiphila_GCA_000378465.1
Tistrella_mobilis_GCA_000264455.2
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Candidatus_Phycorickettsia_trachydisci_GCA_003015145.1
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Rickettsia_prowazekii_strain_Madrid_E_GCA_000195735.1
Rickettsia_endosymbiont_of_Ixodes_scapularis_GCA_000160735.1
Rickettsia_bellii_strain_RML369C_GCA_000012385.1
Candidatus_Tisiphia_endosymbiont_of_Culicoides_newsteadi_GCA_002259525.1
Orientia_tsutsugamushi_strain_Ikeda_GCA_000010205.1
Orientia_chuto_strain_Dubai_GCA_000964595.1
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Magnetococcus_marinus_GCA_000014865.1
Ralstonia_pickettii_GCA_902374465.1
Burkholderia_cepacia_GCA_009586235.1
Methylotenera_versatilis_GCA_000093025.1
Nitrosospira_briensis_GCA_000619905.2
Dasania_marina_GCA_000373485.1
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Chelativorans_oligotrophicus_GCA_011317505.1
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Bartonella_quintana_GCA_009936175.1
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Xanthobacter_autotrophicus_GCA_000017645.1
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Sagittula_stellata_GCA_000169415.1
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Rickettsia_endosymbiont_of_Ixodes_scapularis_GCA_000160735.1
Rickettsia_bellii_strain_RML369C_GCA_000012385.1
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Orientia_chuto_strain_Dubai_GCA_000964595.1
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Burkholderia_cepacia_GCA_009586235.1
Methylotenera_versatilis_GCA_000093025.1
Nitrosospira_briensis_GCA_000619905.2
Dasania_marina_GCA_000373485.1
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Sagittula_stellata_GCA_000169415.1
Ruegeria_pomeroyi_GCA_000011965.2
Octadecabacter_arcticus_GCA_000155735.2
Rubellimicrobium_rubrum_GCA_006152115.1
Paracoccus_denitrificans_GCA_004063735.1
Ketogulonicigenium_vulgare_GCA_001399515.1
Rhodobacter_sphaeroides_GCA_000015985.1
Jannaschia_rubra_GCA_900113265.1
Neomegalonema_perideroedes_GCA_000374145.1
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Maricaulis_maris_GCA_003634045.1
Parvularcula_bermudensis_GCA_000152825.2
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Brevundimonas_subvibrioides_GCA_000144605.1
Asticcacaulis_excentricus_GCA_000175215.2
Hyphomonas_neptunium_GCA_000013025.1
Hirschia_baltica_GCA_000023785.1
Phenylobacterium_zucineum_GCA_000017265.1
Caulobacter_vibrioides_GCA_000022005.1
Sphingopyxis_macrogoltabida_GCA_001314325.1
Citromicrobium_sp._GCA_001304795.1
Sphingobium_indicum_GCA_000264945.2
Zymomonas_mobilis_GCA_000007105.1
Sphingomonas_wittichii_GCA_000016765.1
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Kordiimonas_gwangyangensis_GCA_000375545.1
Sneathiella_glossodoripedis_GCA_000616095.1
Gluconacetobacter_diazotrophicus_GCA_000067045.1
Acetobacter_aceti_GCA_000193495.2
Gluconobacter_oxydans_GCA_000583855.1
Commensalibacter_intestini_GCA_000231445.2
Granulibacter_bethesdensis_GCA_000576145.2
Roseomonas_gilardii_GCA_001941945.1
Belnapia_moabensis_GCA_000745835.1
Rubritepida_flocculans_GCA_000425365.1
Acidisphaera_rubrifaciens_GCA_000964365.1
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Elioraea_tepidiphila_GCA_000378465.1
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Geminicoccus_roseus_GCA_000427665.1
Terasakiella_pusilla_GCA_000688235.1
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Magnetospirillum_magneticum_GCA_000009985.1
Caenispirillum_salinarum_GCA_000315795.1
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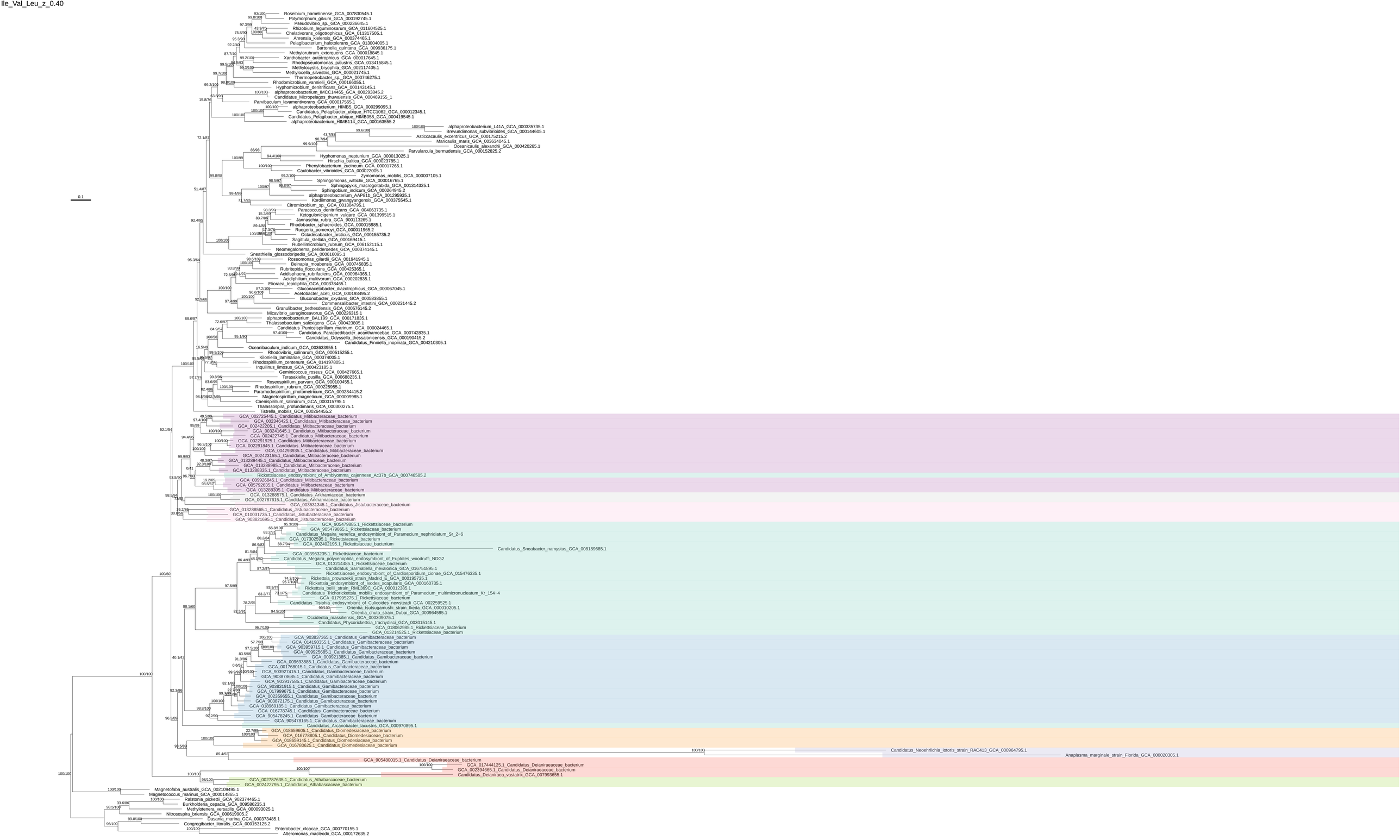
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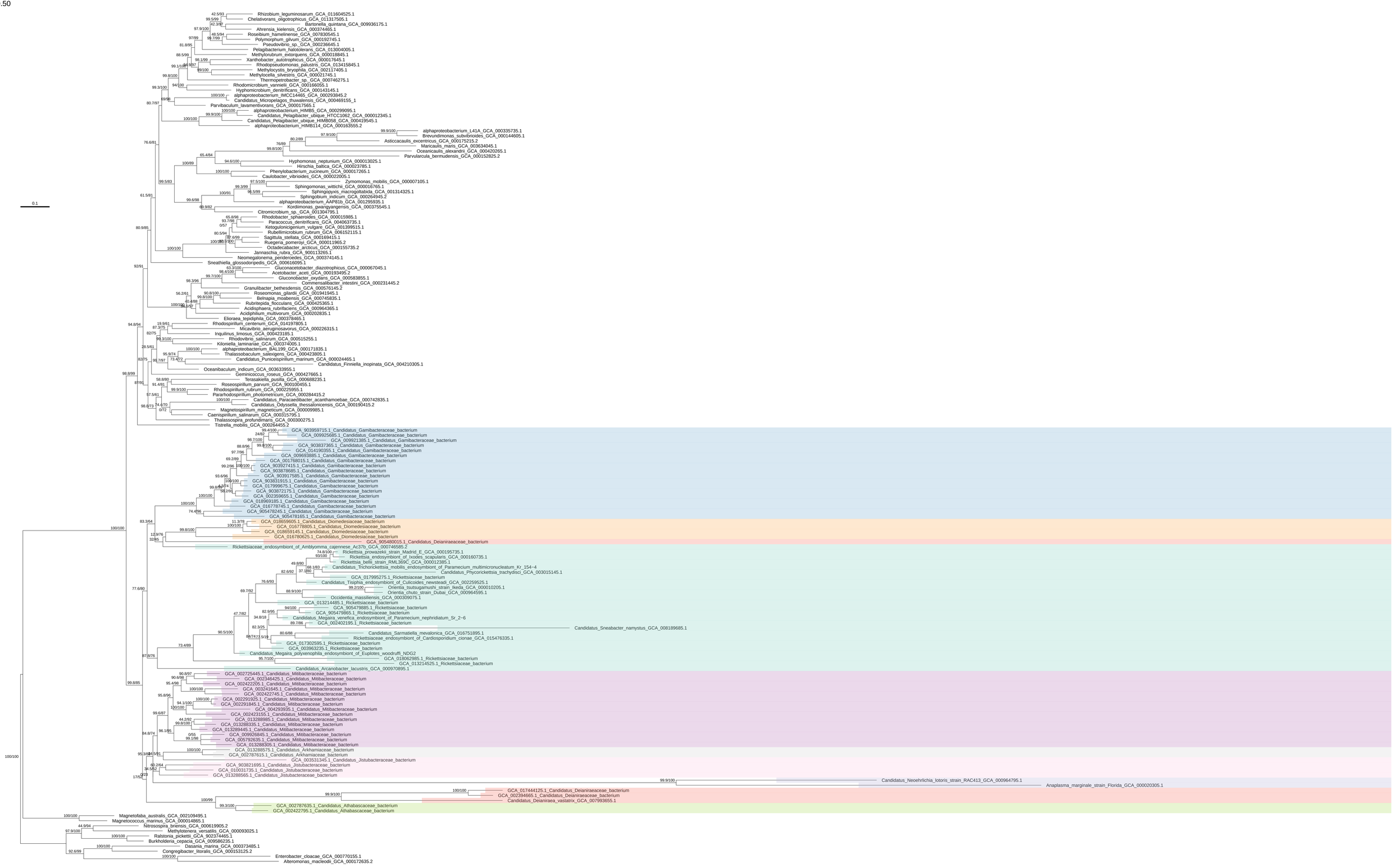

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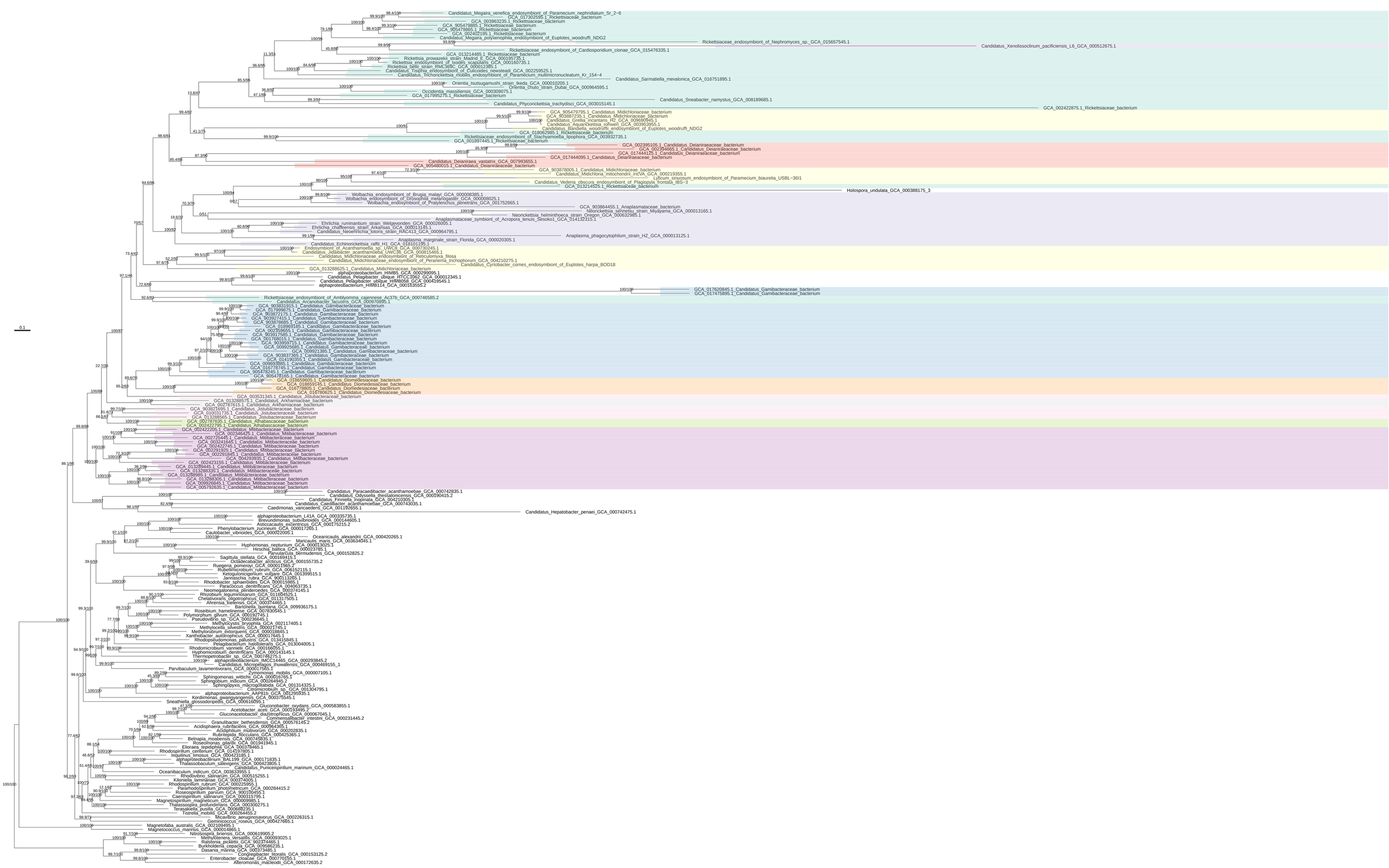
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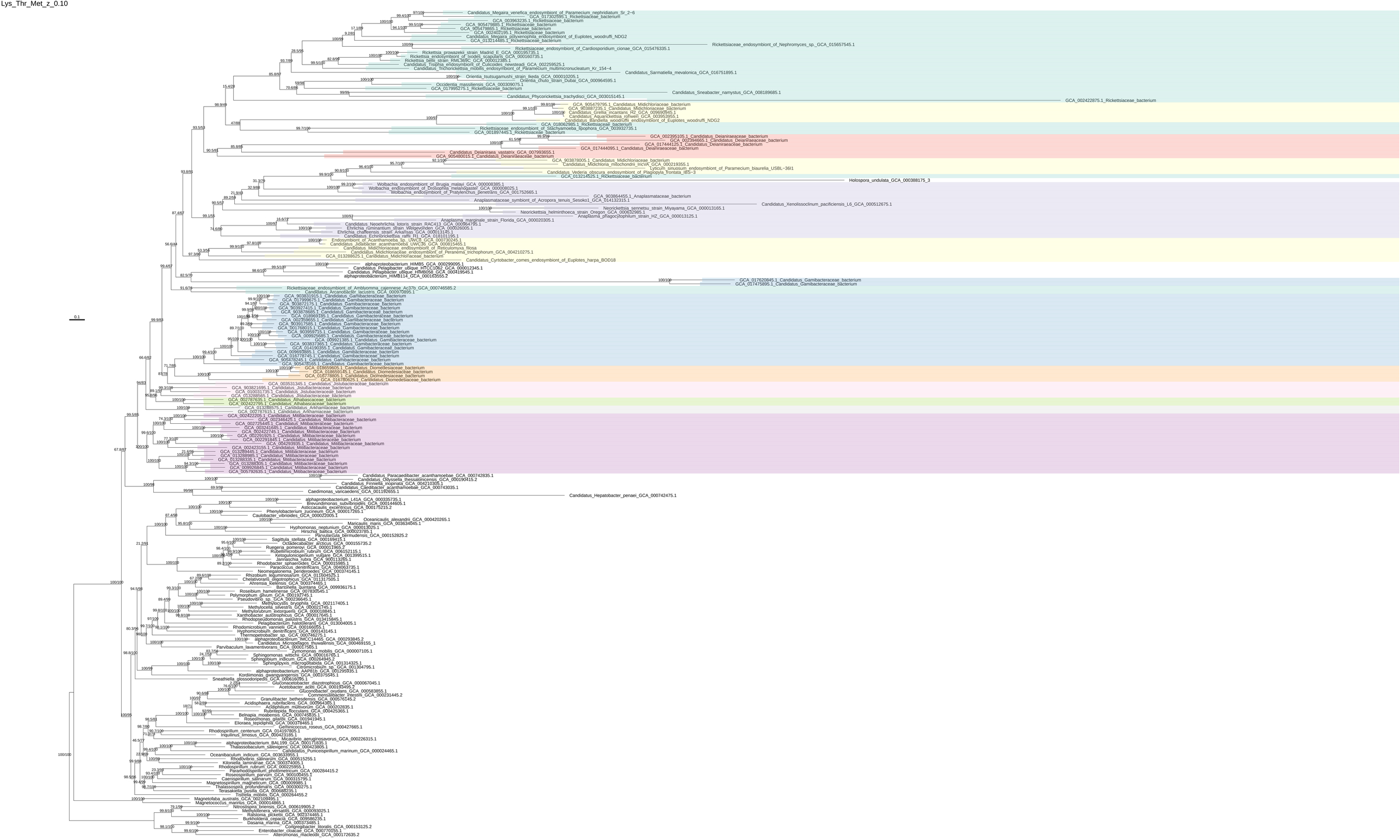
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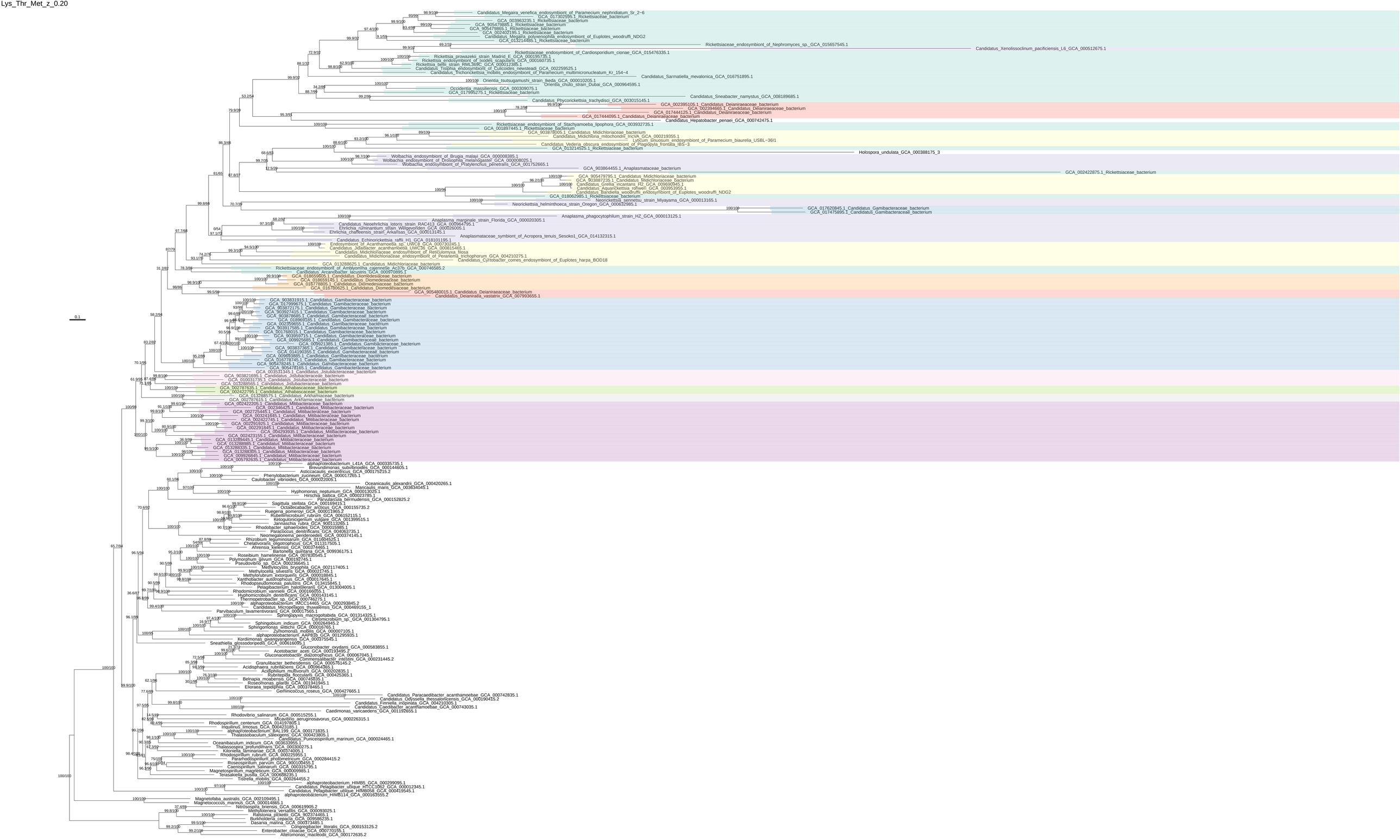
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GCA_013214485.1_Rickettsiaceae_bacterium
Rickettsiaceae_endosymbiont_of_Nephromyces_sp._GCA_015657545.1
Candidatus_Xenolissoclinum_pacificiensis_L6_GCA_000512675.1
Rickettsiaceae_endosymbiont_of_Cardiosporidium_cionae_GCA_015476335.1
Rickettsia_prowazekii_strain_Madrid_E_GCA_000195735.1
Rickettsia_endosymbiont_of_Ixodes_scapularis_GCA_000160735.1
Rickettsia_bellii_strain_RML369C_GCA_000012385.1
Candidatus_Tisiphia_endosymbiont_of_Culicoides_newsteadi_GCA_002259525.1
Candidatus_Trichorickettsia_mobilis_endosymbiont_of_Paramecium_multimicronucleatum_Kr_154~4
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Orientia_tsutsugamushi_strain_Ikeda_GCA_000010205.1
Orientia_chuto_strain_Dubai_GCA_000964595.1
Occidentia_massiliensis_GCA_000309075.1
GCA_017995275.1_Rickettsiaceae_bacterium
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Candidatus_Phycorickettsia_trachydisci_GCA_003015145.1
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GCA_017440095.1_Candidatus_Deianiraeaceae_bacterium
Candidatus_Hepatobacter_penaei_GCA_000742475.1
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GCA_001897445.1_Rickettsiaceae_bacterium
GCA_903878005.1_Candidatus_Midichloriaceae_bacterium
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Lyticum_sinuosum_endosymbiont_of_Paramecium_biaurelia_USBL~36I1
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Wolbachia_endosymbiont_of_Pratylenchus_penetrans_GCA_001752665.1
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Candidatus_Grellia_incantans_R2_GCA_009690945.1
Candidatus_Aquarickettsia_rohweri_GCA_003953955.1
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Anaplasma_marginale_strain_Florida_GCA_000020305.1
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Ehrlichia_ruminantium_strain_Welgevonden_GCA_000026005.1
Ehrlichia_chaffeensis_strain_Arkansas_GCA_000013145.1
Anaplasmataceae_symbiont_of_Acropora_tenuis_Sesoko1_GCA_014132315.1
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Candidatus_Jidaibacter_acanthamoebae_UWC36_GCA_000815465.1
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Phenylobacterium_zucineum_GCA_000017265.1
Caulobacter_vibrioides_GCA_000022005.1
Oceanicaulis_alexandrii_GCA_000420265.1
Maricaulis_maris_GCA_000634045.1
Hyphomonas_neptunium_GCA_000013025.1
Hirschia_baltica_GCA_000023785.1
Parvularcula_bermudensis_GCA_000152825.2
Sagittula_stellata_GCA_000169415.1
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Jannaschia_rubra_GCA_900113285.1
Rhodobacter_sphaeroides_GCA_000015985.1
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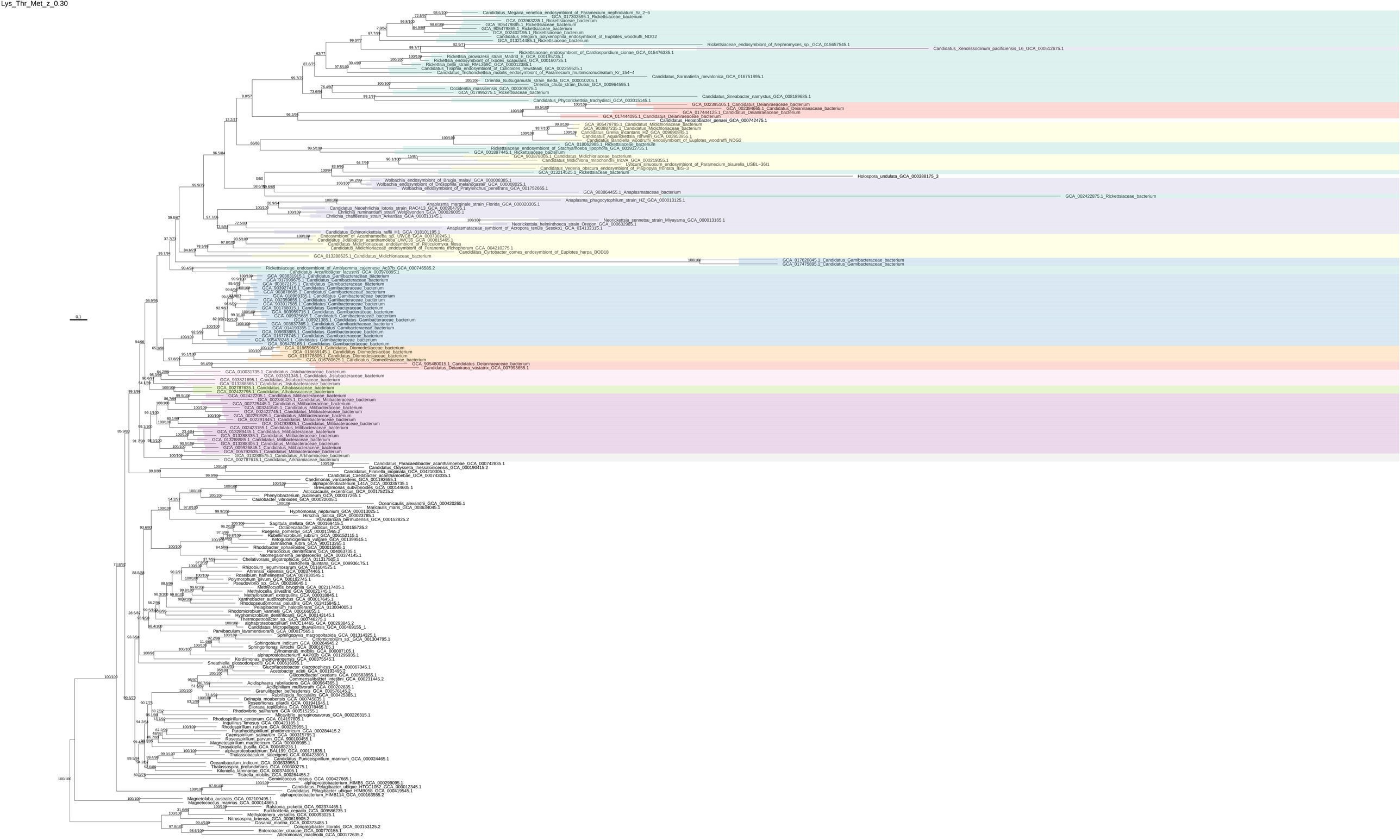
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Candidatus_Sarmatiella_mevalonica_GCA_016751895.1
Orientia_tsutsugamushi_strain_Ikeda_GCA_000010205.1
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Occidentia_massiliensis_GCA_000309075.1
GCA_017995275.1_RickettsiaceaeBacterium
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Wolbachia_endosymbiont_of_Brugia_malayi_GCA_000008385.1
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Ruegeria_pomeroyi_GCA_000017965.2
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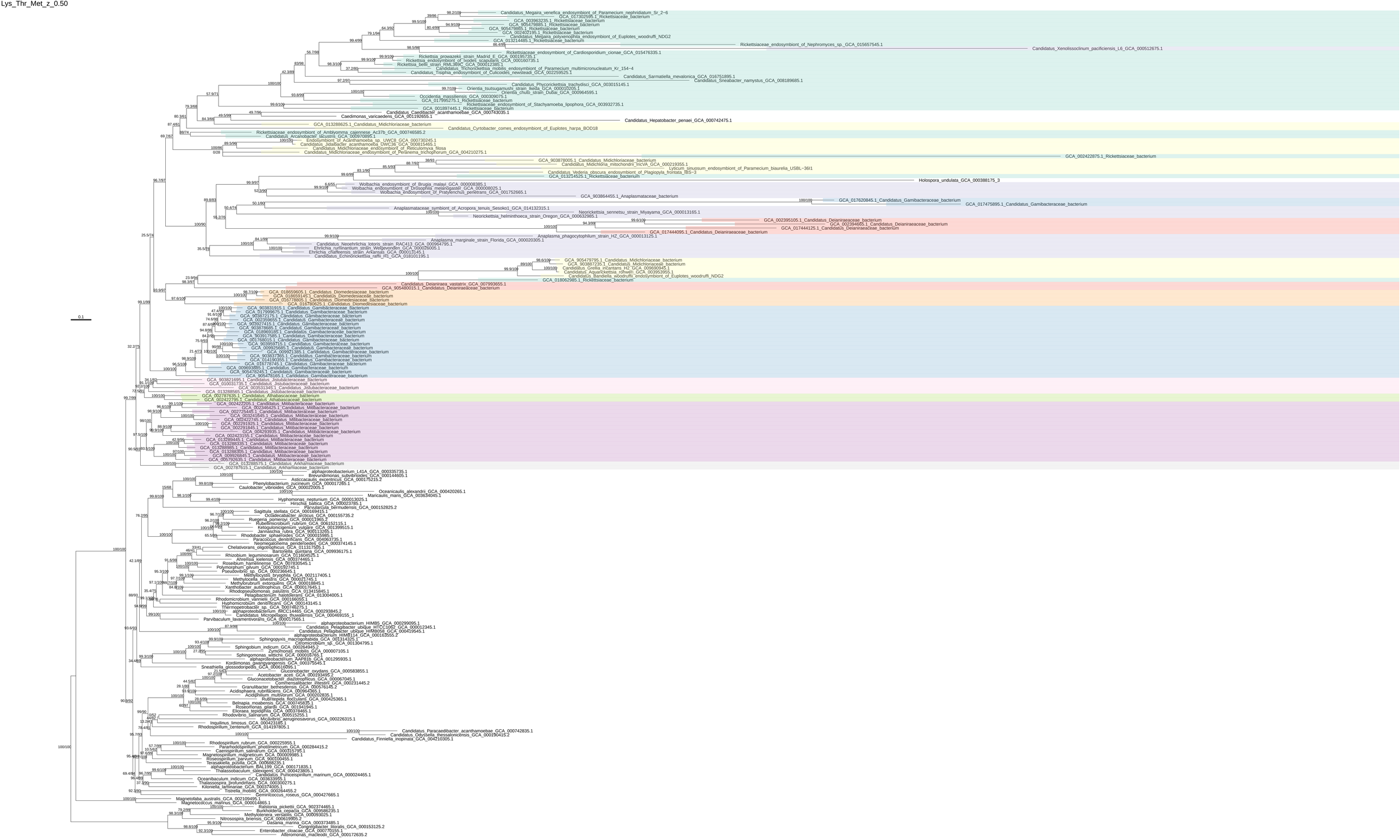
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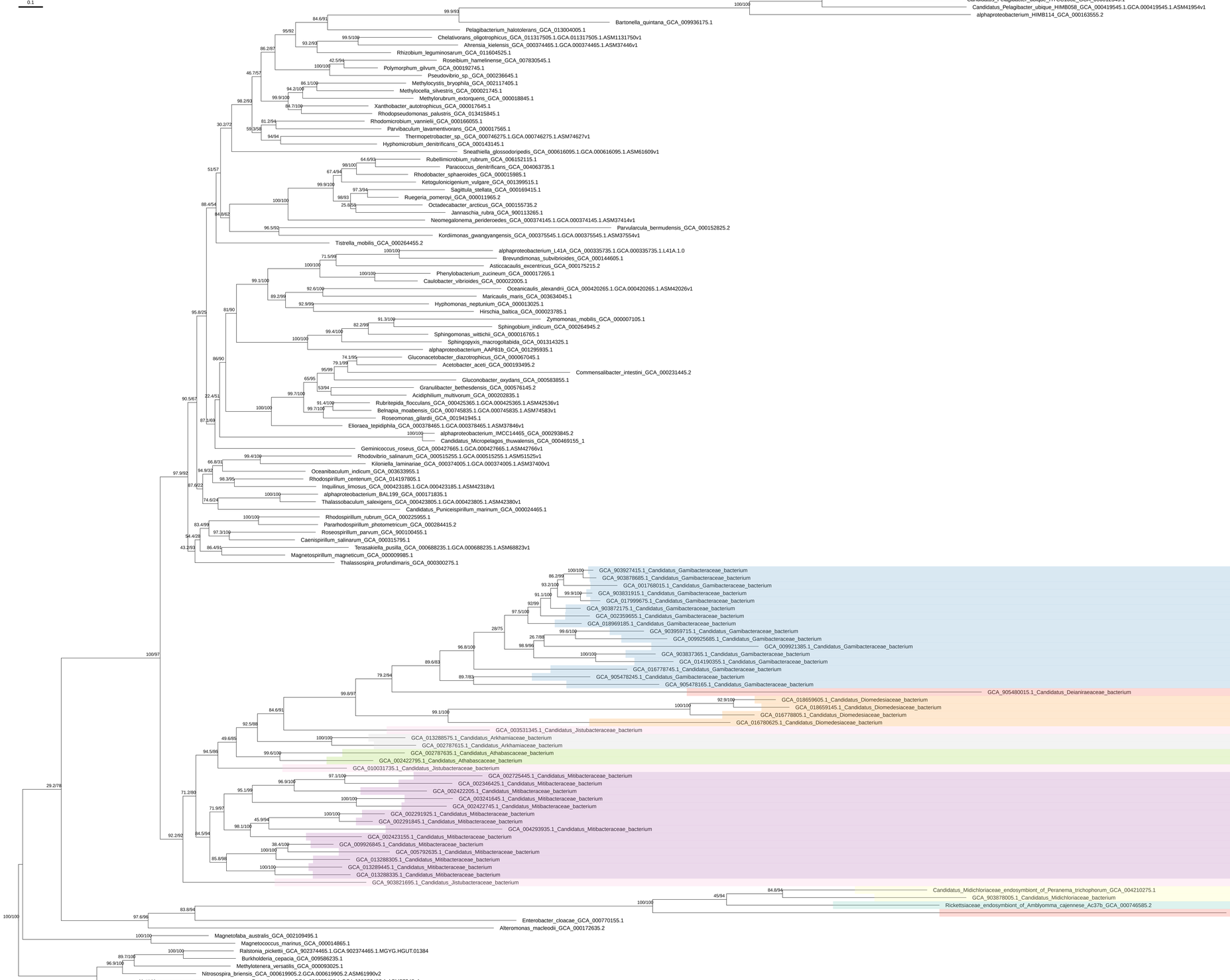
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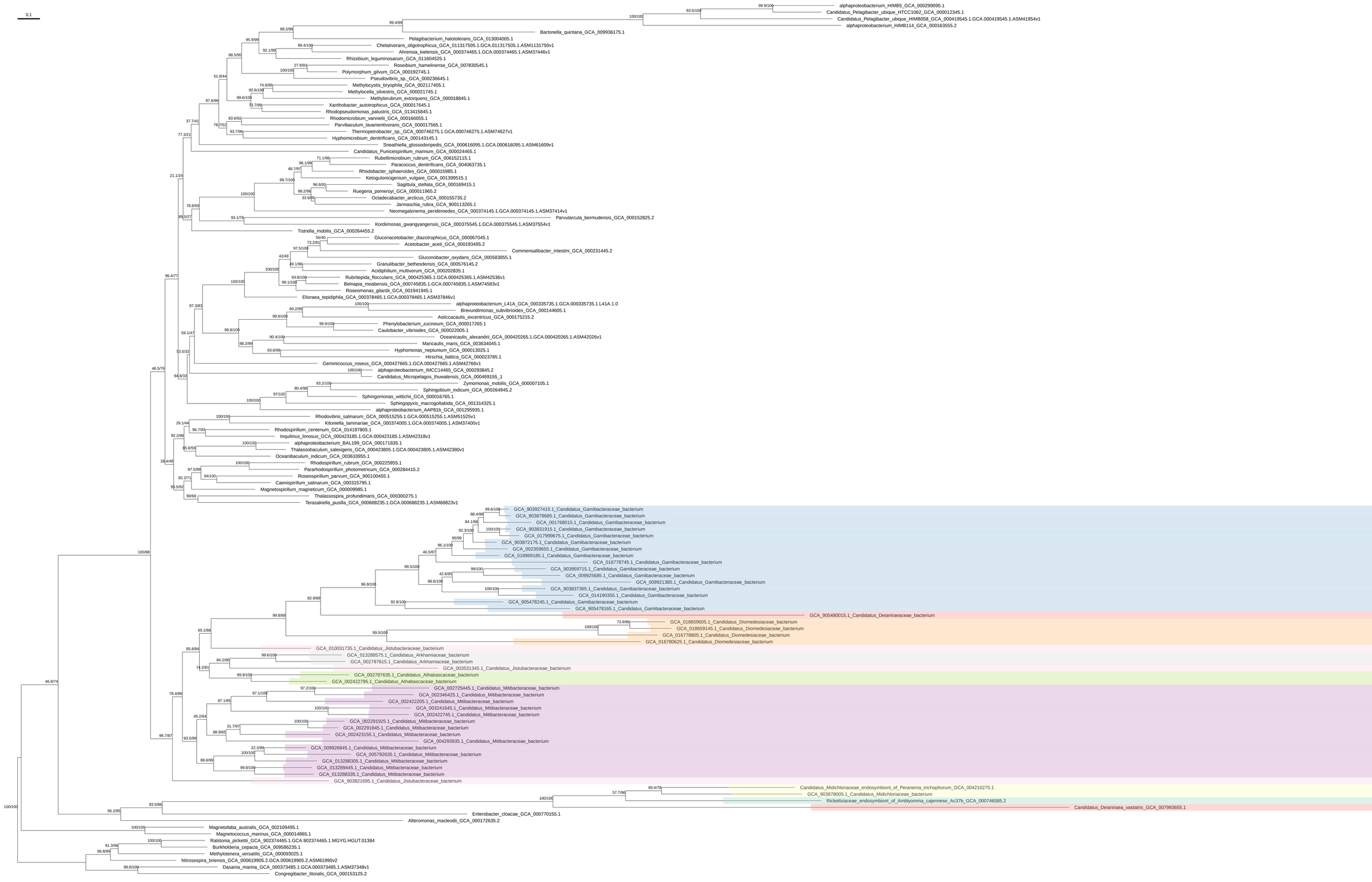
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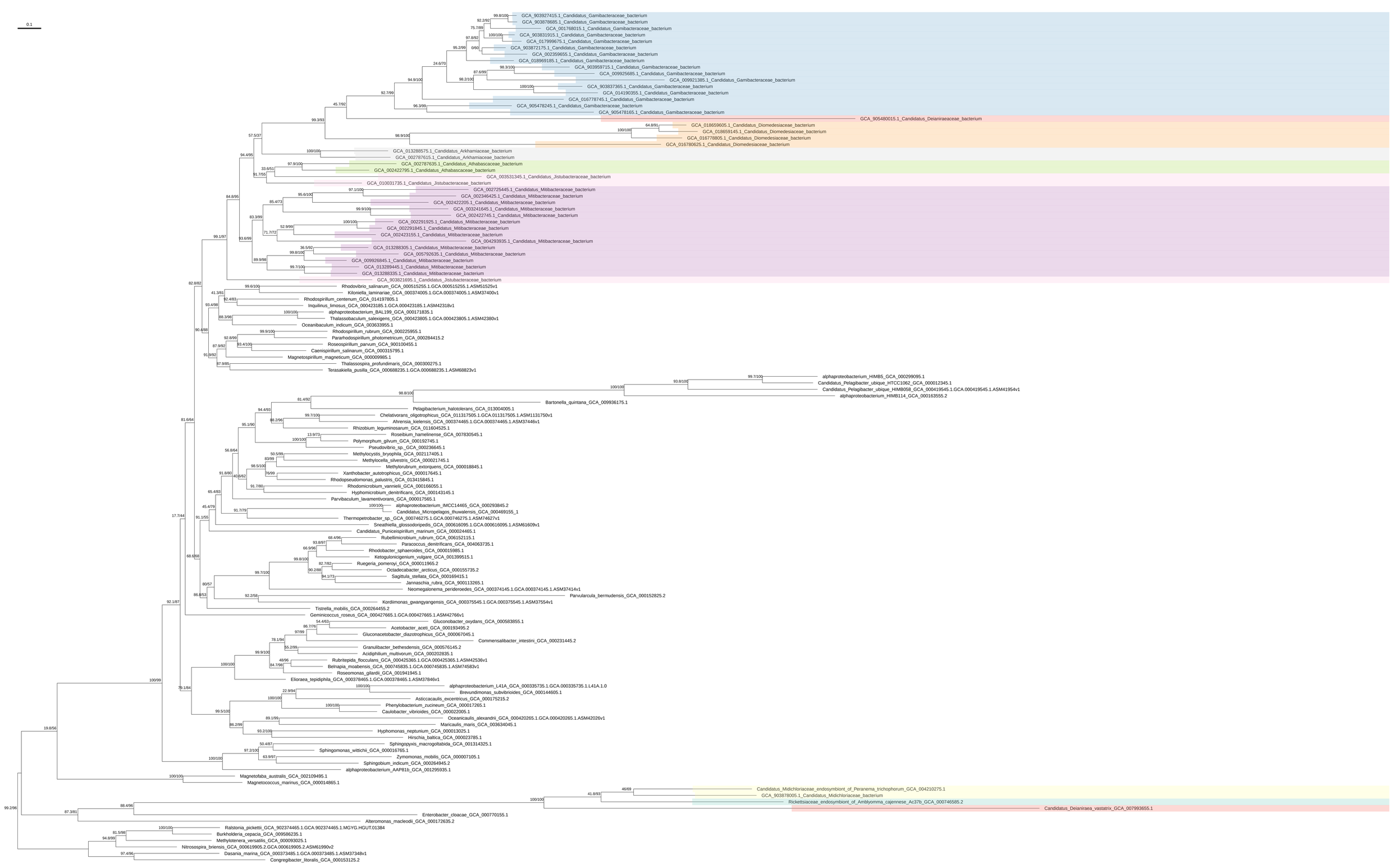
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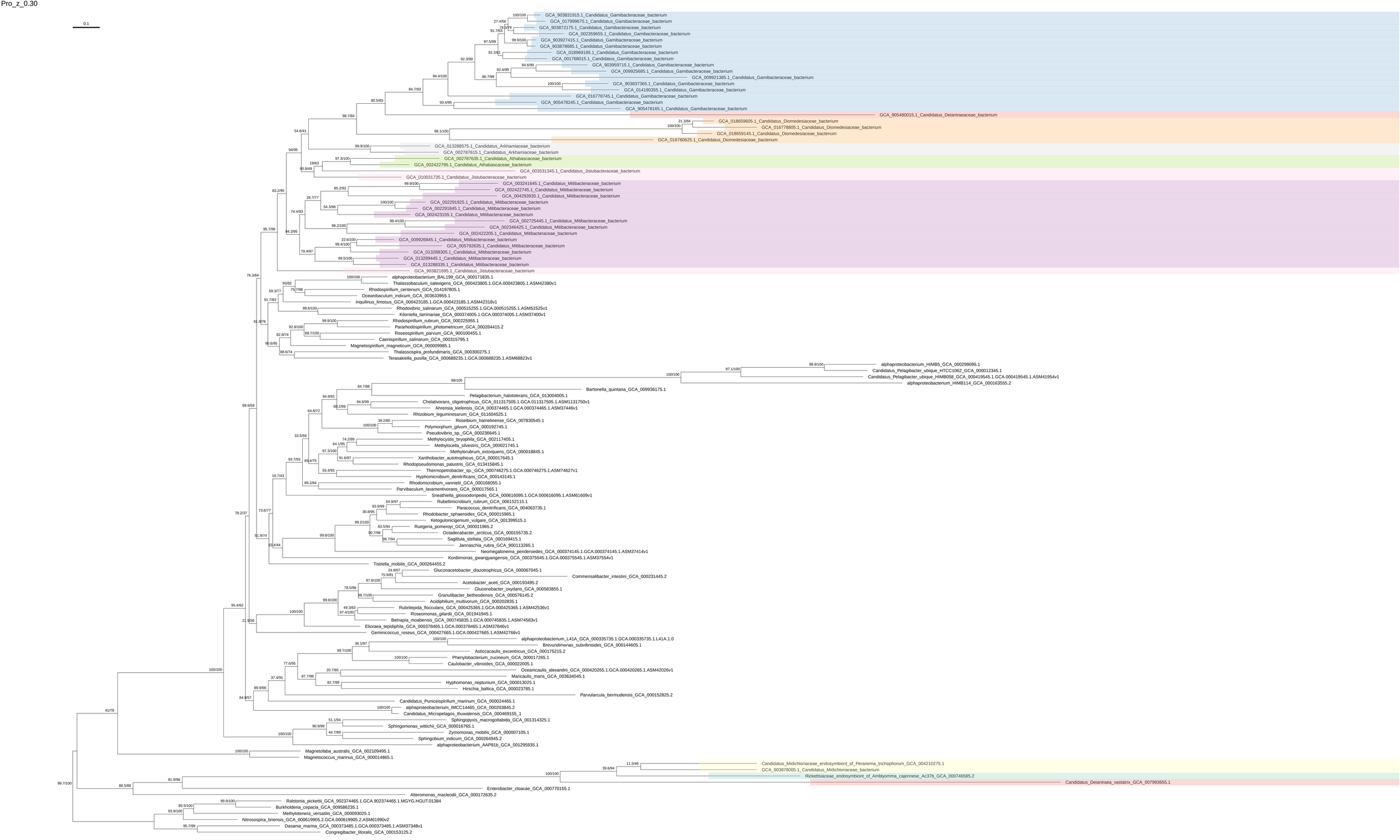
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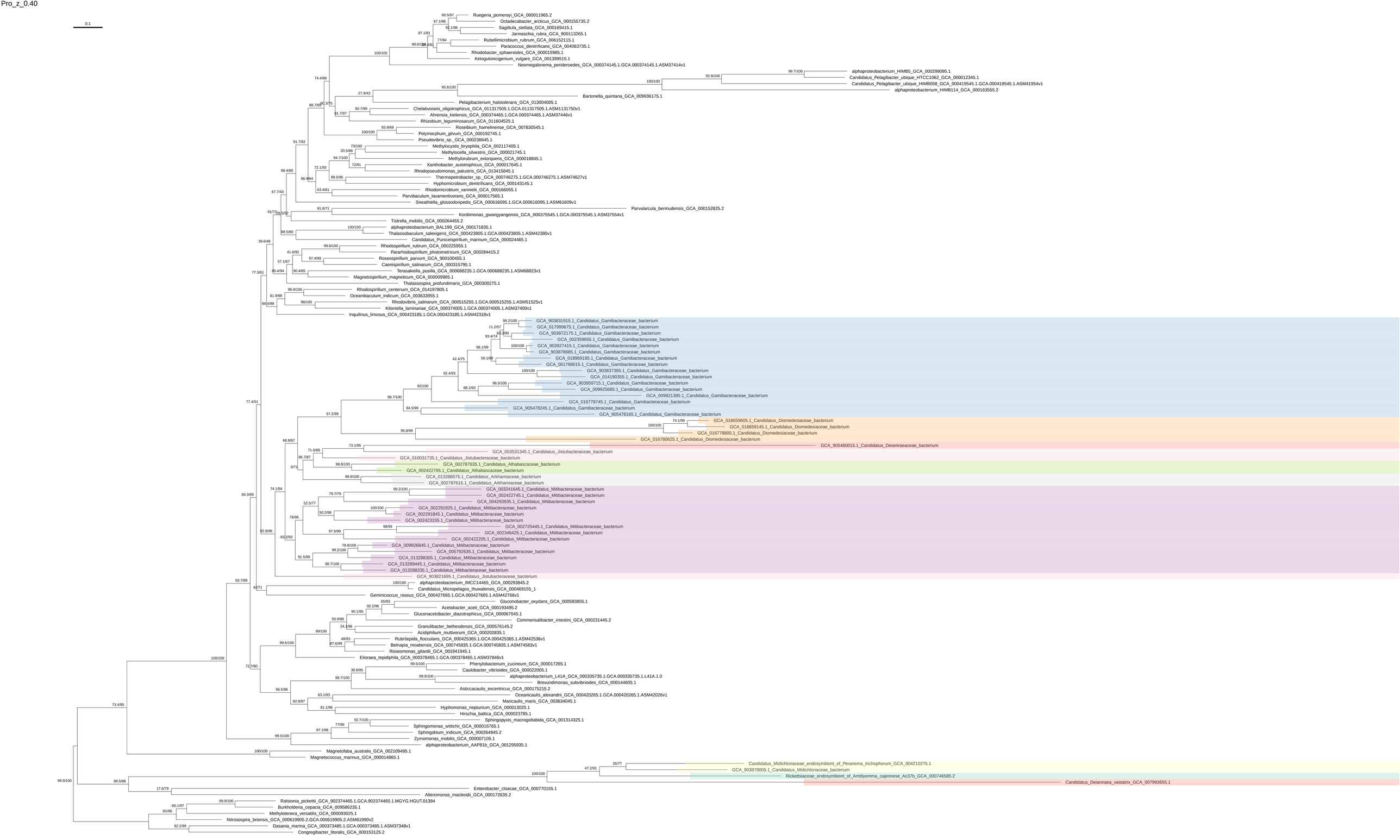
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Nitrosospira_briensis_GCA_000619905.2
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Dasania_marina_GCA_000373485.1
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Geminicoccus_roseus_GCA_000427665.1
alphaproteobacterium_HIMB114_GCA_000163555.2
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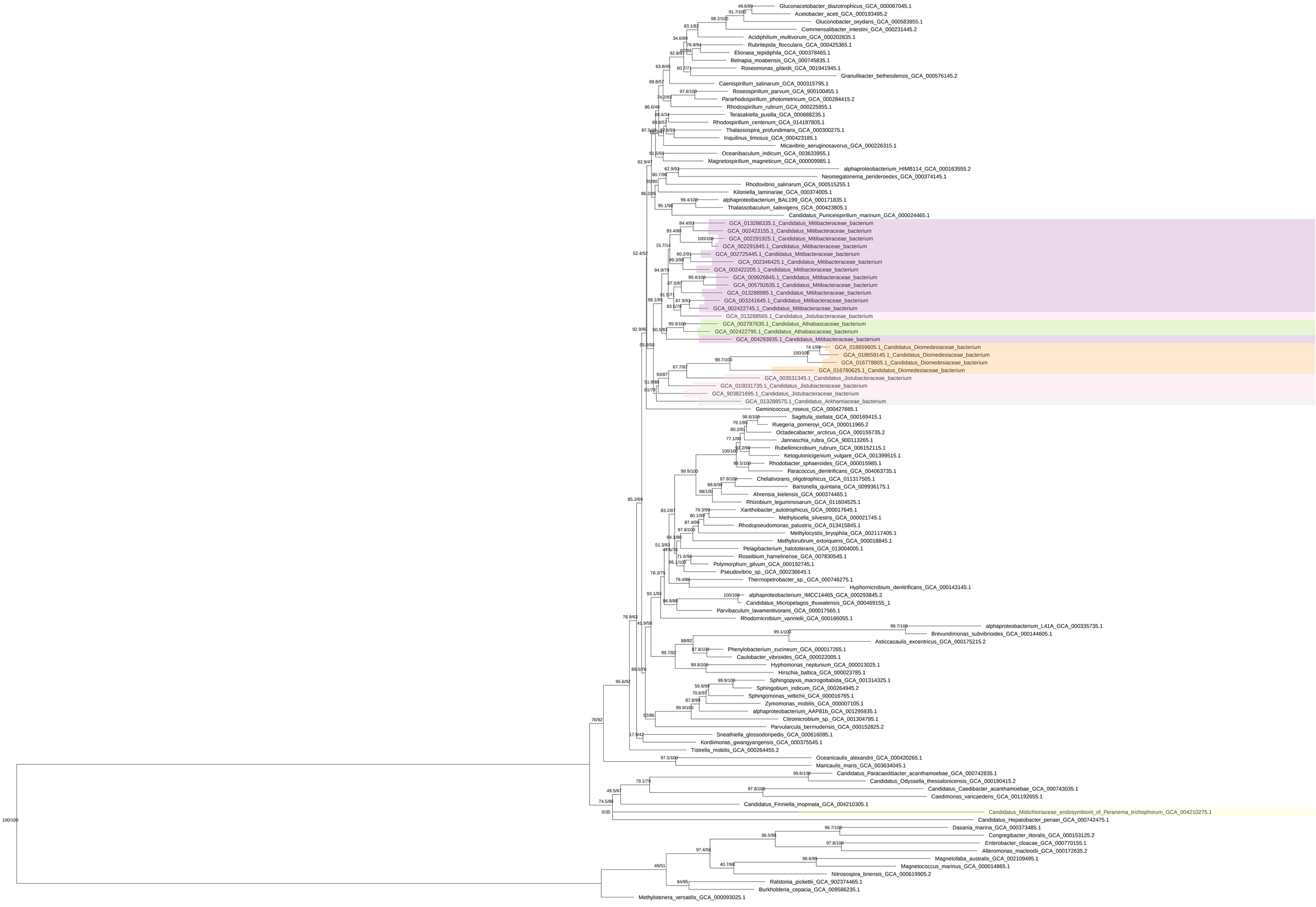

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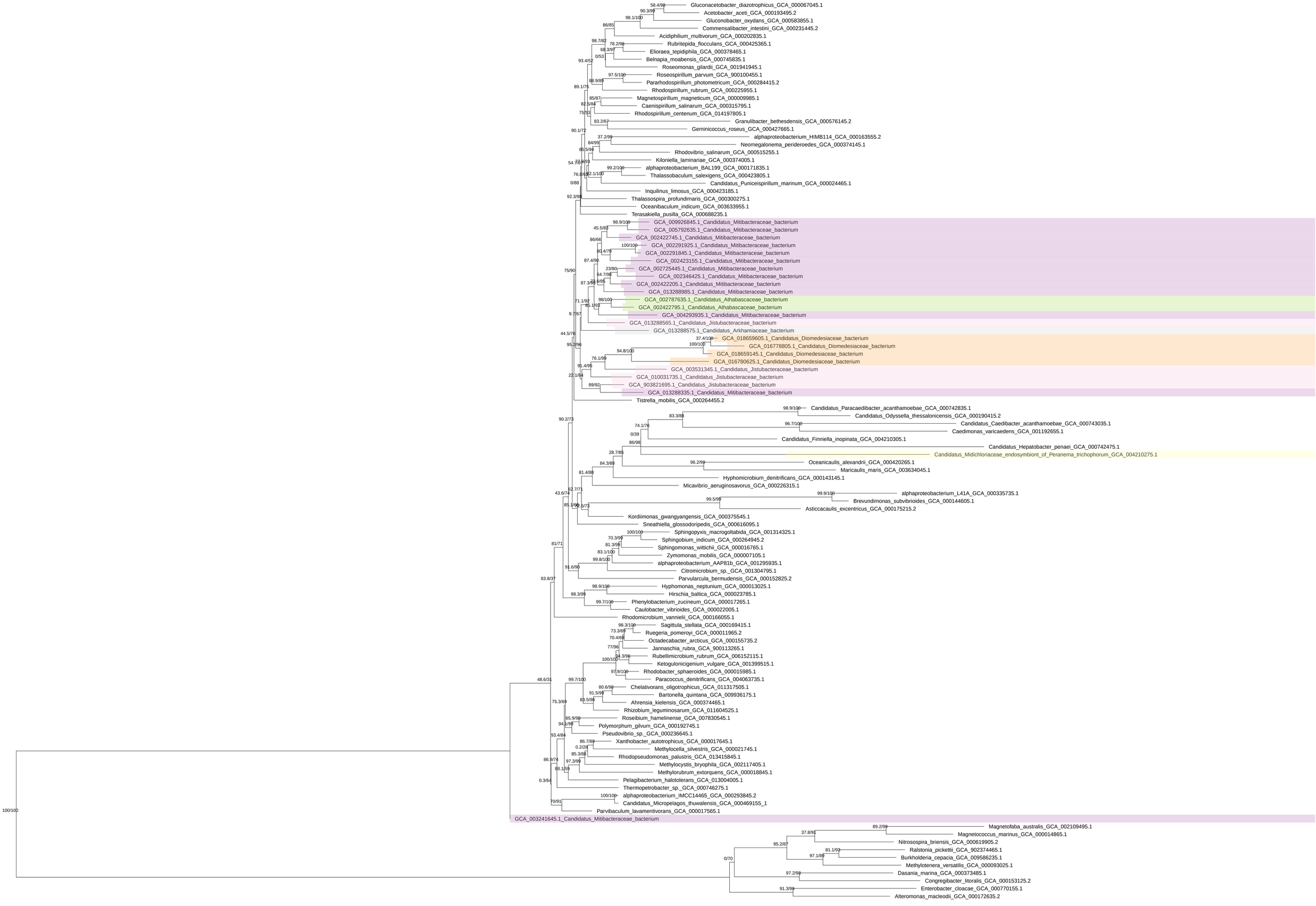

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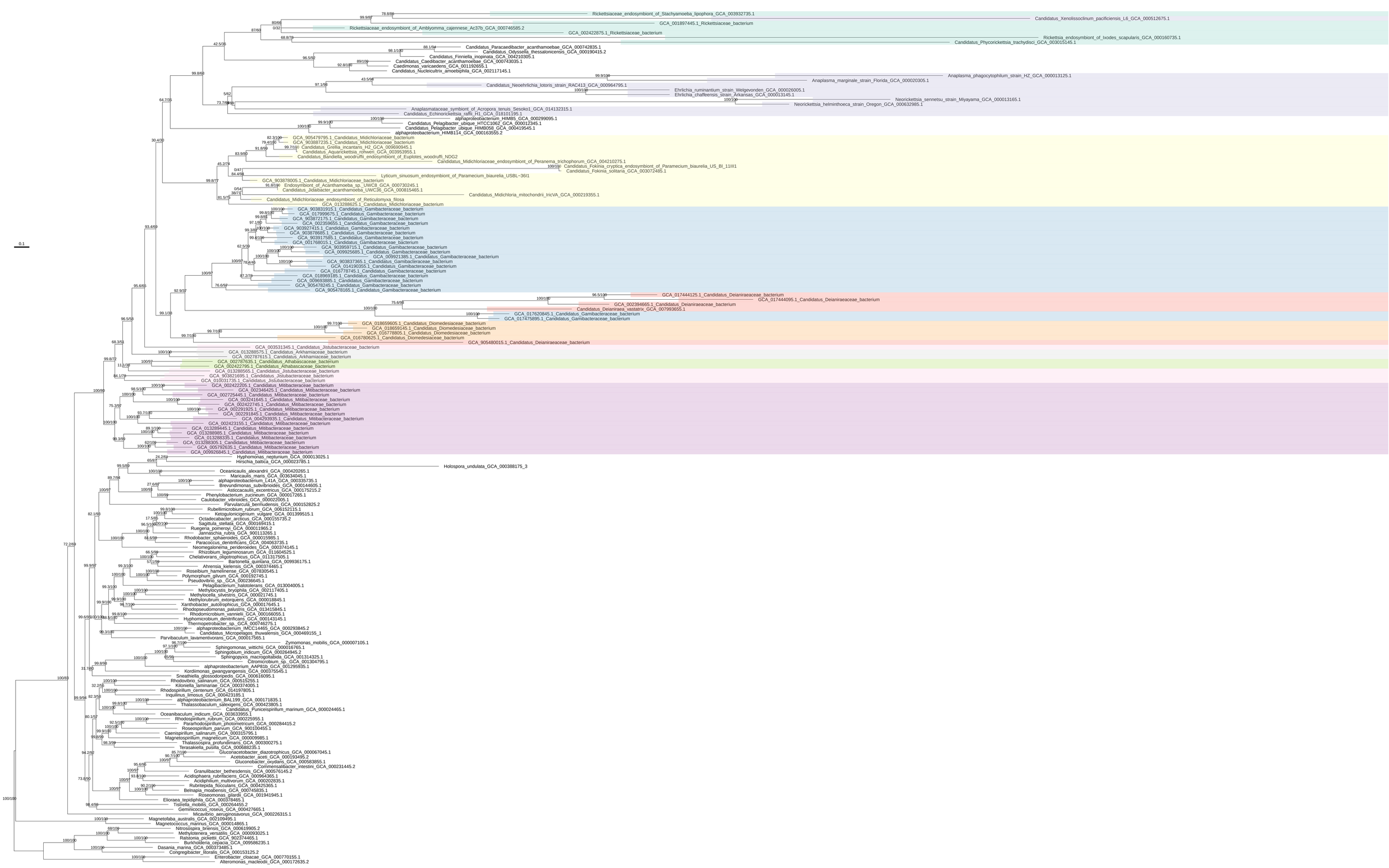
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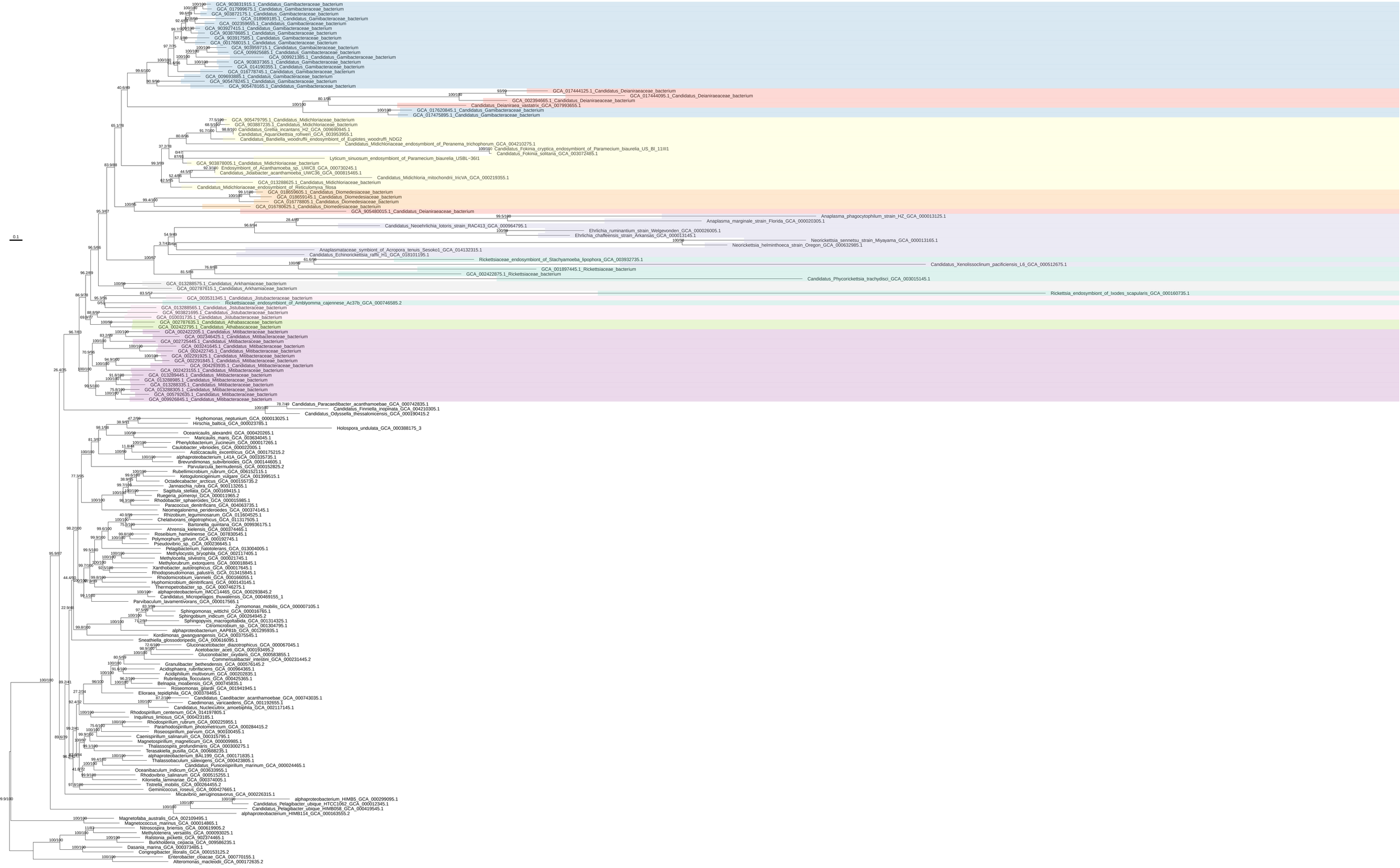

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GCA_009926845.1_Candidatus_Mitibacteraceae_bacterium
alphaproteobacterium_L41A_GCA_000335735.1
Brevundimonas_subvibrioides_GCA_000144605.1
Asticcacaulis_excentricus_GCA_000175215.2
Phenylobacterium_zucineum_GCA_000017265.1
Caulobacter_vibrioides_GCA_000022205.1
Oceanicaulis_alexandrii_GCA_000420265.1
Maricaulis_maris_GCA_003634045.1
Hyphomonas_neptunium_GCA_000013025.1
Hirschia_baltica_GCA_000023785.1
Parvularcula_bermudensis_GCA_000152825.2
Rubellimicrobium_rubrum_GCA_006152115.1
Ketogulonicigenium_vulgare_GCA_001399515.1
Octadecabacter_arcticus_GCA_000155735.2
Sagittula_stellata_GCA_000169415.1
Ruegeria_pomeroyi_GCA_000011965.2
Jannaschia_rubra_GCA_900113265.1
Rhodobacter_sphaeroides_GCA_000015985.1
Paracoccus_denitrificans_GCA_004063735.1
Neomegalonema_perideroedes_GCA_000374145.1
Rhizobium_leguminosarum_GCA_011604525.1
Bartonella_quintana_GCA_009936175.1
Ahrensia_kielensis_GCA_000374465.1
Roseibium_hamelinense_GCA_007830545.1
Polymorphum_gilvum_GCA_000192745.1
Pseudovibrio_sp._GCA_000236645.1
Pelagibacterium_halotolerans_GCA_013004005.1
Methylocystis_bryophila_GCA_002117405.1
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Methylorubrum_extorquens_GCA_000018845.1
Xanthobacter_autotrophicus_GCA_000017645.1
Rhodopseudomonas_palustris_GCA_013415845.1
Rhodomicrobium_vannielii_GCA_000160055.1
Hyphomicrobium_denitrificans_GCA_000143145.1
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Sphingomonas_wittichii_GCA_000016765.1
Sphingobium_indicum_GCA_000264945.2
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Acetobacter_aceti_GCA_000193495.2
Gluconobacter_oxydans_GCA_000583855.1
Commensalibacter_intestini_GCA_000231445.2
Granulibacter_bethesdensis_GCA_000576145.2
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Rubritepida_flocculans_GCA_000425365.1
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Elioraea_tepidiphila_GCA_000378465.1
Candidatus_Caedibacter_acanthamoebae_GCA_000743035.1
Caedimonas_varicaedens_GCA_001192655.1
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Rhodospirillum_centenum_GCA_014197805.1
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Holospora_undulata_GCA_000388175_3
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Magnetococcus_marinus_GCA_000014865.1
Nitrosospira_briensis_GCA_000619905.2
Methylotenera_versatilis_GCA_000093025.1
Ralstonia_pickettii_GCA_902374465.1
Burkholderia_cepacia_GCA_009586235.1
Dasania_marina_GCA_000373485.1
Congregibacter_litoralis_GCA_000153125.2
Enterobacter_cloacae_GCA_000770155.1
Alteromonas_macleodii_GCA_000172635.2

Trp_Tyr_Phe_z_0.30
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90.8/100 GCA_903887235.1_Candidatus_Midichloriaceae_bacterium
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58.7/67 Candidatus_Midichloriaceae_endosymbiont_of_Peranema_trichophorum_GCA_004210275.1
Candidatus_Midichloriaceae_endosymbiont_of_Reticulomyxa_filosa
80.1/75 94/100 Endosymbiont_of_Acanthamoeba_sp._UWC8_GCA_000730245.1
46.2/95 Candidatus_Jidaibacter_acanthamoeba_UWC36_GCA_000815465.1
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Lyticum_sinuosum_endosymbiont_of_Paramecium_biaurelia_USBL-36I1
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96.1/82 83.9/98 GCA_017444125.1_Candidatus_Deiniraeaceae_bacterium
100/99 GCA_017444095.1_Candidatus_Deiniraeaceae_bacterium
65.7/82 GCA_002394665.1_Candidatus_Deiniraeaceae_bacterium
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98.7/90 GCA_903872175.1_Candidatus_Gamibacteraceae_bacterium
88/100 GCA_018969185.1_Candidatus_Gamibacteraceae_bacterium
96.7/82 GCA_002359655.1_Candidatus_Gamibacteraceae_bacterium
98.3/99 99.8/100 GCA_903927415.1_Candidatus_Gamibacteraceae_bacterium
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99.9/100 GCA_009921385.1_Candidatus_Gamibacteraceae_bacterium
64.3/94 100/100 82.1/63 100/100 GCA_903837365.1_Candidatus_Gamibacteraceae_bacterium
GCA_014190355.1_Candidatus_Gamibacteraceae_bacterium
100/95 GCA_016778745.1_Candidatus_Gamibacteraceae_bacterium
GCA_009693885.1_Candidatus_Gamibacteraceae_bacterium
63.1/92 GCA_905478245.1_Candidatus_Gamibacteraceae_bacterium
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95.4/100 GCA_018659605.1_Candidatus_Diomedesiaceae_bacterium
100/100 GCA_018659145.1_Candidatus_Diomedesiaceae_bacterium
97/100 99.1/99 GCA_016778805.1_Candidatus_Diomedesiaceae_bacterium
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GCA_905480015.1_Candidatus_Deiniraeaceae_bacterium
93.2/96 99/97 Anaplasma_phagocytophilum_strain_HZ_GCA_000013125.1
Anaplasma_marginale_strain_Florida_GCA_000020305.1
98.9/95 Candidatus_Neoehrlichia_lotoris_strain_RAC413_GCA_000964795.1
100/97 Ehrlichia_ruminantium_strain_Welgevonden_GCA_000026005.1
Ehrlichia_chaffeensis_strain_Arkansas_GCA_000013145.1
73/71 33.3/65 Candidatus_Paracaedibacter_acanthamoebae_GCA_000742835.1
99.9/100 Candidatus_Odyssella_thessalonicensis_GCA_000190415.2
97.6/96 73.4/88 Candidatus_Finniella_inopinata_GCA_004210305.1
77.3/100 Rickettsiaceae_endosymbiont_of_Stachyamoeba_lipophora_GCA_003932735.1
99.6/100 Candidatus_Xenolissoclinum_pacificiensis_L6_GCA_000512675.1
100/97 77.5/92 GCA_001897445.1_Rickettsiaceae_bacterium
82.3/78 GCA_002422875.1_Rickettsiaceae_bacterium
Candidatus_Phycorickettsia_trachydisci_GCA_003015145.1
92.2/66 75.4/97 Anaplasmataceae_symbiont_of_Acropora_tenuis_Sesoko1_GCA_014132315.1
Candidatus_Echinorickettsia_raffii_H1_GCA_018I01195.1
100/100 GCA_013288575.1_Candidatus_Arkhamiaceae_bacterium
GCA_002787615.1_Candidatus_Arkhamiaceae_bacterium
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3.3/39 GCA_903821695.1_Candidatus_Jidaibacteraceae_bacterium
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100/98 100/100 GCA_002422205.1_Candidatus_Mitibacteraceae_bacterium
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100/100 GCA_004293935.1_Candidatus_Mitibacteraceae_bacterium
100/100 GCA_002423155.1_Candidatus_Mitibacteraceae_bacterium
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37.8/90 Hyphomonas_neptunium_GCA_000013025.1
41.4/85 Hirschia_baltica_GCA_000023785.1
97.3/97 Holospora_undulata_GCA_000388175_3
100/98 Oceanicaulis_alexandrii_GCA_000420265.1
78.5/96 Maricaulis_maris_GCA_003634045.1
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99.8/100 87/99 Brevundimonas_subvibrioides_GCA_000144605.1
100/100 Asticcacaulis_excentricus_GCA_000175215.2
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Caulobacter_vibrioides_GCA_000022005.1
99/100 Parvularcula_bermudensis_GCA_000152825.2
99.3/97 Rubellimicrobium_rubrum_GCA_006152715.1
44.4/91 25/95 Ketogulonicigenium_vulgare_GCA_001399515.1
98.5/97 Octadecabacter_arcticus_GCA_000155735.2
100/100 Jannaschia_rubra_GCA_900113265.1
100/100 Sagittula_stellata_GCA_000169415.1
100/100 95.5/100 Ruegeria_pomeroyi_GCA_000011965.2
Rhodobacter_sphaeroides_GCA_000015985.1
Paracoccus_denitrificans_GCA_004063735.1
Neomegalonema_perideroedes_GCA_003374145.1
93.1/100 Bartonella_quintana_GCA_009936175.1
24.6/86 Ahrensia_kielensis_GCA_000374465.1
72.7/76 100/100 Chelativorans_oligotrophicus_GCA_011317505.1
96.4/100 99.5/100 Rhizobium_leguminosarum_GCA_011604525.1
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96.4/100 100/100 Polymorphum_gilvum_GCA_000192745.1
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Pelagibacterium_halotolerans_GCA_013004005.1
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99.9/100 Methylocella_silvestris_GCA_000021745.1
100/100 99.7/100 Methylorubrum_extorquens_GCA_000018845.1
68.3/56 78.9/99 Xanthobacter_autotrophicus_GCA_000017645.1
Rhodopseudomonas_palustris_GCA_013415845.1
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53.8/95 Zymomonas_mobilis_GCA_000007105.1
98.3/97 Sphingomonas_wittichii_GCA_000016765.1
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100/100 82.4/99 Sphingopyxis_macrogoltabida_GCA_001314325.1
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74.1/56 alphaproteobacterium_AAP81b_GCA_001295935.1
Kordiimonas_gwangyangensis_GCA_003375545.1
Sneathiella_glossodoripedis_GCA_000616095.1
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24.8/84 Commensalibacter_intestini_GCA_000231445.2
100/100 Granulibacter_bethesdensis_GCA_000576145.2
79/77 99.8/100 93.6/100 Acidisphaera_rubrifaciens_GCA_000964365.1
Acidiphilium_multivorum_GCA_000202835.1
77.8/99 Rubritepida_flocculans_GCA_000425365.1
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17.9/78 Roseomonas_gilardii_GCA_001941945.1
Elioraea_tepidiphila_GCA_000378465.1
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33.8/43 Inquilinus_limosus_GCA_000423185.1
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80.7/86 100/100 Rhodospirillum_rubrum_GCA_000225955.1
74/98 Pararhodospirillum_photometricum_GCA_000284415.2
100/100 99.8/100 Roseospirillum_parvum_GCA_900100455.1
Caenispirillum_salinarum_GCA_000315795.1
99.2/99 Magnetospirillum_magneticum_GCA_000009985.1
0/78 89.5/99 Thalassospira_profundimaris_GCA_000300275.1
Terasakiella_pusilla_GCA_000688235.1
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98.1/95 Kiloniella_laminariae_GCA_000374005.1
89.8/100 Candidatus_Caedibacter_acanthamoebae_GCA_000743035.1
99.9/100 99.6/100 Caedimonas_varicaedens_GCA_001192655.1
Candidatus_Nucleicultrix_amoebiphila_GCA_002117145.1
91.2/94 Tistrella_mobilis_GCA_000284455.2
Geminicoccus_roseus_GCA_000427665.1
Micavibrio_aeruginosavorus_GCA_000226315.1
100/100 Magnetofaba_australis_GCA_002109495.1
Magnetococcus_marinus_GCA_000014865.1
11.9/77 100/100 Ralstonia_pickettii_GCA_902374465.1
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Nitrosospira_briensis_GCA_000619905.2
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Congregibacter_litoralis_GCA_000153125.2
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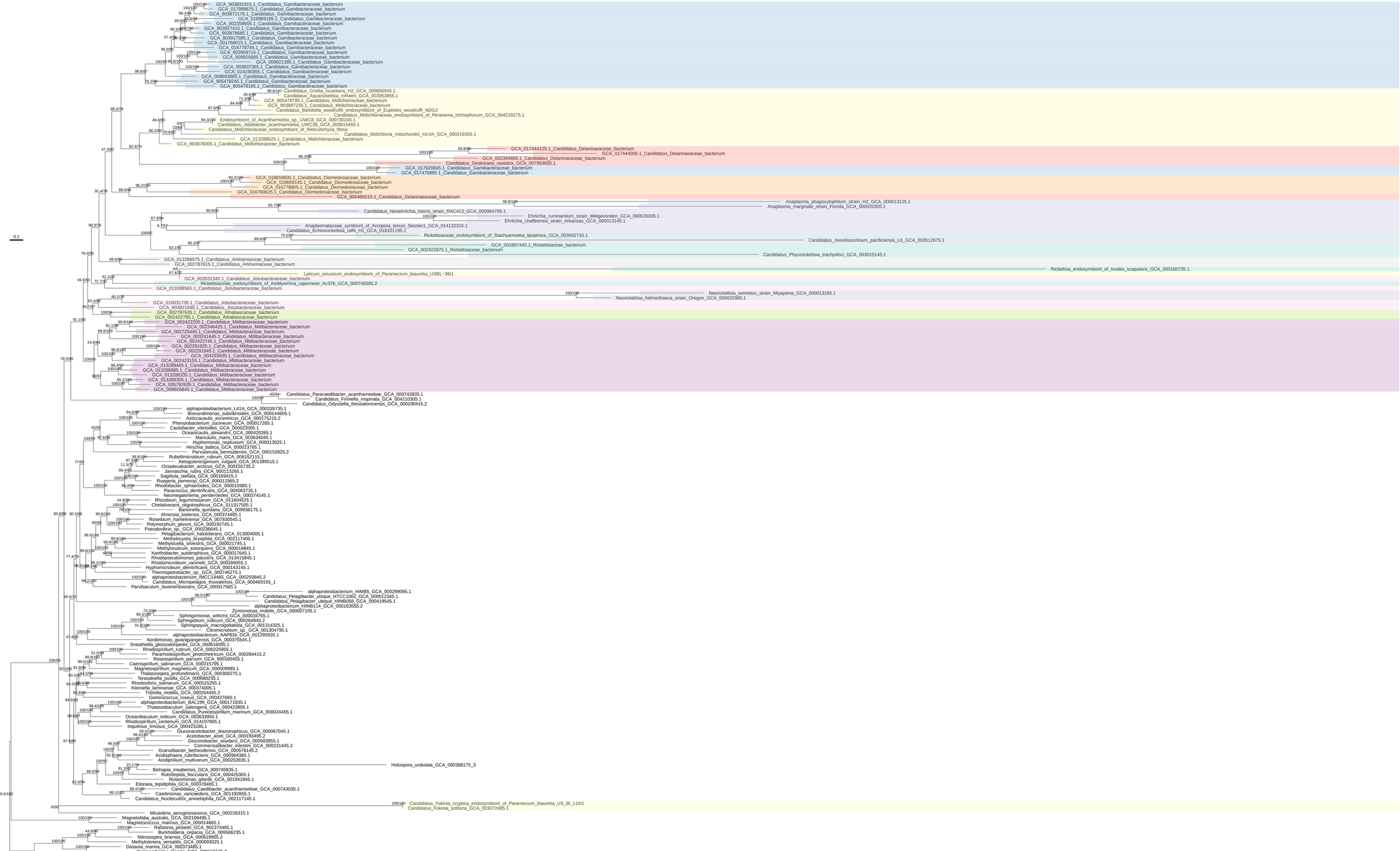
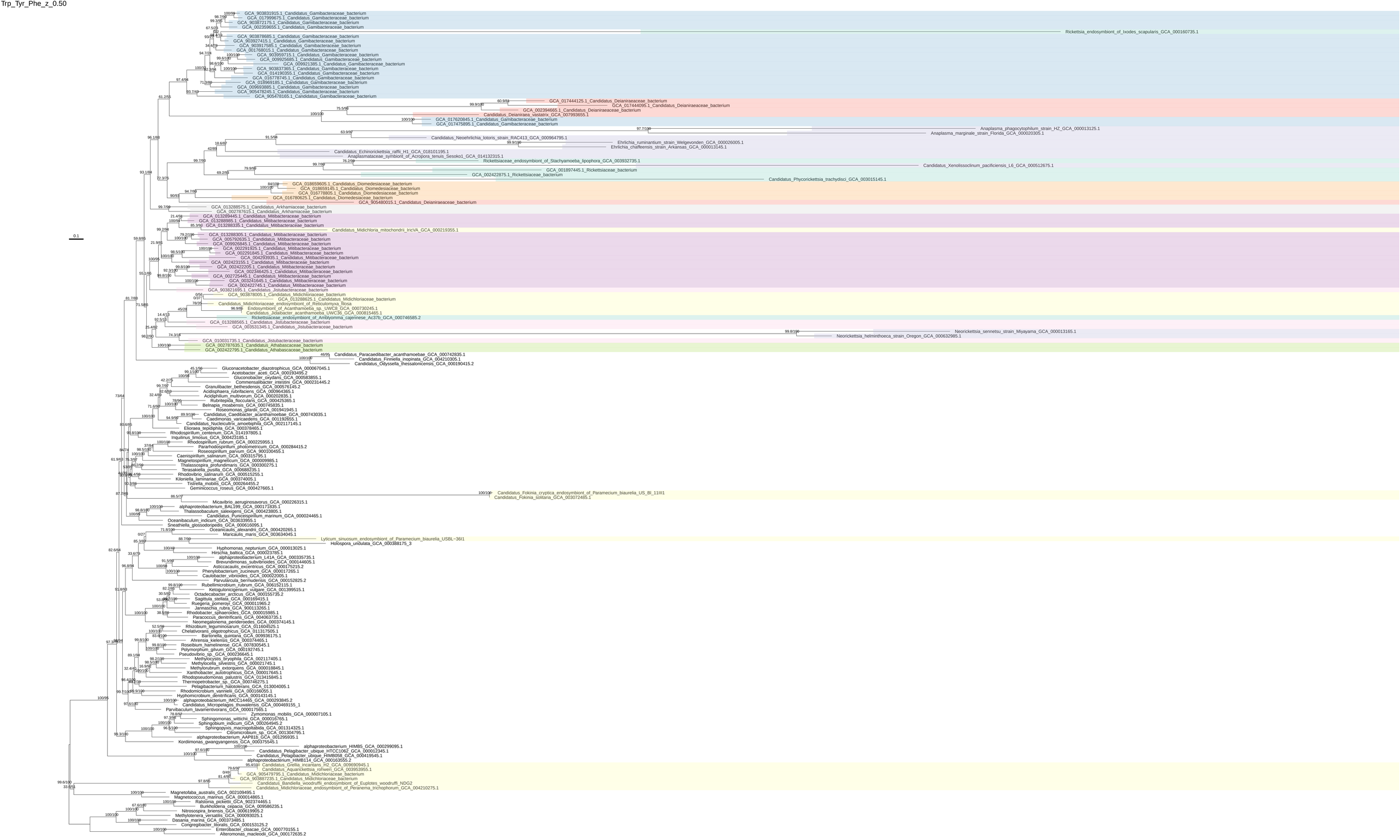
Alteromonas_macleodii_GCA_000172635.2

Trp_Tyr_Phe_z_0.40

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Rickettsia_endosymbiont_of_Ixodes_scapularis_GCA_000160735.1
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GCA_905478165.1_Candidatus_Gamibacteraceae_bacterium
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Candidatus_Xenolissoclinum_pacificiensis_L6_GCA_000512675.1
GCA_001897445.1_Rickettsiaceae_bacterium
GCA_002422875.1_Rickettsiaceae_bacterium
Candidatus_Phycorickettsia_trachydisci_GCA_003015145.1
GCA_018659605.1_Candidatus_Diomedesiaceae_bacterium
GCA_018659145.1_Candidatus_Diomedesiaceae_bacterium
GCA_016778805.1_Candidatus_Diomedesiaceae_bacterium
GCA_016780625.1_Candidatus_Diomedesiaceae_bacterium
GCA_905480015.1_Candidatus_Deiniraeaceae_bacterium
GCA_013288575.1_Candidatus_Arkhamiaceae_bacterium
GCA_002787615.1_Candidatus_Arkhamiaceae_bacterium
GCA_013289445.1_Candidatus_Mitibacteraceae_bacterium
GCA_013288985.1_Candidatus_Mitibacteraceae_bacterium
GCA_013288335.1_Candidatus_Mitibacteraceae_bacterium
Candidatus_Midichloria_mitochondrii_IricVA_GCA_000219355.1
GCA_013288305.1_Candidatus_Mitibacteraceae_bacterium
GCA_005792635.1_Candidatus_Mitibacteraceae_bacterium
GCA_009926845.1_Candidatus_Mitibacteraceae_bacterium
GCA_002291925.1_Candidatus_Mitibacteraceae_bacterium
GCA_002291845.1_Candidatus_Mitibacteraceae_bacterium
GCA_004293935.1_Candidatus_Mitibacteraceae_bacterium
GCA_002423155.1_Candidatus_Mitibacteraceae_bacterium
GCA_002422205.1_Candidatus_Mitibacteraceae_bacterium
GCA_002346425.1_Candidatus_Mitibacteraceae_bacterium
GCA_002725445.1_Candidatus_Mitibacteraceae_bacterium
GCA_003241645.1_Candidatus_Mitibacteraceae_bacterium
GCA_002422745.1_Candidatus_Mitibacteraceae_bacterium
GCA_903821695.1_Candidatus_Jistubacteraceae_bacterium
GCA_903878005.1_Candidatus_Midichloriaceae_bacterium
GCA_013288625.1_Candidatus_Midichloriaceae_bacterium
Candidatus_Midichloriaceae_endosymbiont_of_Reticulomyxa_filosa
Endosymbiont_of_Acanthamoeba_sp._UWC8_GCA_000730245.1
Candidatus_Jidaibacter_acanthamoeba_UWC36_GCA_000815465.1
Rickettsiaceae_endosymbiont_of_Amblyomma_cajennese_Ac37b_GCA_000746585.2
GCA_013288565.1_Candidatus_Jistubacteraceae_bacterium
GCA_003531345.1_Candidatus_Jistubacteraceae_bacterium
Neorickettsia_sennetsu_strain_Miyayama_GCA_000013165.1
Neorickettsia_helminthoeca_strain_Oregon_GCA_000632985.1
GCA_010031735.1_Candidatus_Jistubacteraceae_bacterium
GCA_002787635.1_Candidatus_Athabascaceae_bacterium
GCA_002422795.1_Candidatus_Athabascaceae_bacterium
Candidatus_Paracaedibacter_acanthamoebae_GCA_000742835.1
Candidatus_Finniella_inopinata_GCA_004210305.1
Candidatus_Odyssella_thessalonicensis_GCA_000190415.2
Gluconacetobacter_diazotrophicus_GCA_000067045.1
Acetobacter_aceti_GCA_000193495.2
Gluconobacter_oxydans_GCA_000583855.1
Commensalibacter_intestini_GCA_000231445.2
Granulibacter_bethesdensis_GCA_000576145.2
Acidisphaera_rubrifaciens_GCA_000964365.1
Acidiphilium_multivorum_GCA_000202835.1
Rubritepida_flocculans_GCA_000425365.1
Belnapia_moabensis_GCA_000745835.1
Roseomonas_gilardi_GCA_001941945.1
Candidatus_Caedibacter_acanthamoebae_GCA_000743035.1
Caedimonas_varicaedens_GCA_001192655.1
Candidatus_Nucleicultrix_amoebiphila_GCA_002117145.1
Elioraea_tepidiphila_GCA_000378465.1
Rhodospirillum_centenum_GCA_014197805.1
Inquilinus_limosus_GCA_000423185.1
Rhodospirillum_rubrum_GCA_000225955.1
Pararhodospirillum_photometricum_GCA_000284415.2
Roseospirillum_parvum_GCA_900100455.1
Caenispirillum_salinarum_GCA_000315795.1
Magnetospirillum_magneticum_GCA_000009985.1
Thalassospira_profundimaris_GCA_000300275.1
Terasakiella_pusilla_GCA_000688235.1
Rhodovibrio_salinarum_GCA_000515255.1
Kiloniella_laminariae_GCA_000374005.1
Tistrella_mobilis_GCA_000264455.2
Geminicoccus_roseus_GCA_000427665.1
Candidatus_Fokinia_cryptica_endosymbiont_of_Paramecium_biaurelia_US_BI_11III1
Candidatus_Fokinia_solitaria_GCA_003072485.1
Micavibrio_aeruginosavorus_GCA_000226315.1
alphaproteobacterium_BAL199_GCA_000171835.1
Thalassobaculum_salexigens_GCA_000423805.1
Candidatus_Puniceispirillum_marinum_GCA_000024465.1
Oceanibaculum_indicum_GCA_003633955.1
Sneathiella_glossodoripedis_GCA_000616095.1
Oceanicaulis_alexandrii_GCA_000420265.1
Maricaulis_maris_GCA_003634045.1
Lyticum_sinuosum_endosymbiont_of_Paramecium_biaurelia_USBL~36I1
Holospora_undulata_GCA_000388175_3
Hyphomonas_neptunium_GCA_000013025.1
Hirschia_baltica_GCA_000023785.1
alphaproteobacterium_L41A_GCA_000335735.1
Brevundimonas_subvibrioides_GCA_000144605.1
Asticcacaulis_excentricus_GCA_000175215.2
Phenylobacterium_zucineum_GCA_000017265.1
Caulobacter_vibrioides_GCA_000022005.1
Parvularcula_bermudensis_GCA_000152825.2
Rubellimicrobium_rubrum_GCA_006152115.1
Ketogulonicigenium_vulgare_GCA_001399515.1
Octadecabacter_arcticus_GCA_000155735.2
Sagittula_stellata_GCA_000169415.1
Ruegeria_pomeroyi_GCA_000011965.2
Jannaschia_rubra_GCA_900113265.1
Rhodobacter_sphaeroides_GCA_000015985.1
Paracoccus_denitrificans_GCA_004063735.1
Neomegalonema_perideroedes_GCA_003374145.1
Rhizobium_leguminosarum_GCA_011604525.1
Chelativorans_oligotrophicus_GCA_011317505.1
Bartonella_quintana_GCA_009936175.1
Ahrensia_kielensis_GCA_000374465.1
Roseibium_hamelinense_GCA_007830545.1
Polymorphum_gilvum_GCA_000192745.1
Pseudovibrio_sp._GCA_000236645.1
Methylocystis_bryophila_GCA_002117405.1
Methylocella_silvestris_GCA_000021745.1
Methylorubrum_extorquens_GCA_000018845.1
Xanthobacter_autotrophicus_GCA_000017645.1
Rhodopseudomonas_palustris_GCA_013415845.1
Thermopetrobacter_sp._GCA_000746275.1
Pelagibacterium_halotolerans_GCA_013004005.1
Rhodomicrobium_vannielii_GCA_000166055.1
Hyphomicrobium_denitrificans_GCA_000143145.1
alphaproteobacterium_IMCC14465_GCA_000293845.2
Candidatus_Micropelagos_thuwalensis_GCA_000469155_1
Parvibaculum_lavamentivorans_GCA_000017565.1
Zymomonas_mobilis_GCA_000007105.1
Sphingomonas_wittichii_GCA_000016765.1
Sphingobium_indicum_GCA_000264945.2
Sphingopyxis_macrogoltabida_GCA_001314325.1
Citromicrobium_sp._GCA_001304795.1
alphaproteobacterium_AAP81b_GCA_001295935.1
Kordiimonas_gwangyangensis_GCA_000375545.1
alphaproteobacterium_HIMB5_GCA_000299095.1
Candidatus_Pelagibacter_ubique_HTCC1062_GCA_000012345.1
Candidatus_Pelagibacter_ubique_HIMB058_GCA_000419545.1
alphaproteobacterium_HIMB114_GCA_000163555.2
Candidatus_Grellia_incantans_H2_GCA_009690945.1
Candidatus_Aquarickettsia_rohweri_GCA_003953955.1
GCA_905479795.1_Candidatus_Midichloriaceae_bacterium
GCA_903887235.1_Candidatus_Midichloriaceae_bacterium
Candidatus_Bandiella_woodruffii_endosymbiont_of_Euplotes_woodruffi_NDG2
Candidatus_Midichloriaceae_endosymbiont_of_Peranema_trichophorum_GCA_004210275.1
Magnetofaba_australis_GCA_002109495.1
Magnetococcus_marinus_GCA_000014865.1
Ralstonia_pickettii_GCA_902374465.1
Burkholderia_cepacia_GCA_009586235.1
Nitrosospira_briensis_GCA_000619905.2
Methylotenera_versatilis_GCA_000093025.1
Dasania_marina_GCA_003273485.1
Congregibacter_litoralis_GCA_000153125.2
Enterobacter_cloacae_GCA_000770155.1
Alteromonas_macleodii_GCA_000172635.2

Supplementary Figure 27: phylogenetic tree of the tlc gene family. The members of each *Rickettsiales* family from the dataset of this study are highlighted by different background colours. On each branch, support values by SH-aLRT with 1000 replicates and by 1000 ultrafast bootstraps are reported. The tree scale stands for estimated sequence divergence. The branches on which the ten maximal number of predicted events of HGT with some *Rickettsiales* as recipients are coloured in red.

ADP/ATP translocase

Supplementary Figure 28: biosynthetic pathways and transporters for amino acids. Heat-map showing the presence and abundance of biosynthetic pathways of amino acids (grouped by to their mutually shared enzymatic steps according to BioCyc; blue) and their respective transporters (red) in *Rickettsiales*. Transporters are divided into "characterised" and "uncharacterised" hits, based on whether the corresponding TCDB entry have an experimentally characterised specificity for the given amino acids, or are representatives of a transporter family including amino acid transporters, but their own specificity was not ascertained. For biosynthesis, the proportion of the total genes of the pathway is shown (Supplementary Data 7), while for transporters, the number of genes is reported. Organisms are ordered by their phylogenetic relationships (Supplementary Figure 18), with families highlighted by different colours on the right. The bar plots on the right indicate the percentage of proteobacterial BUSCO single-copy orthogroups identified in each assembly.

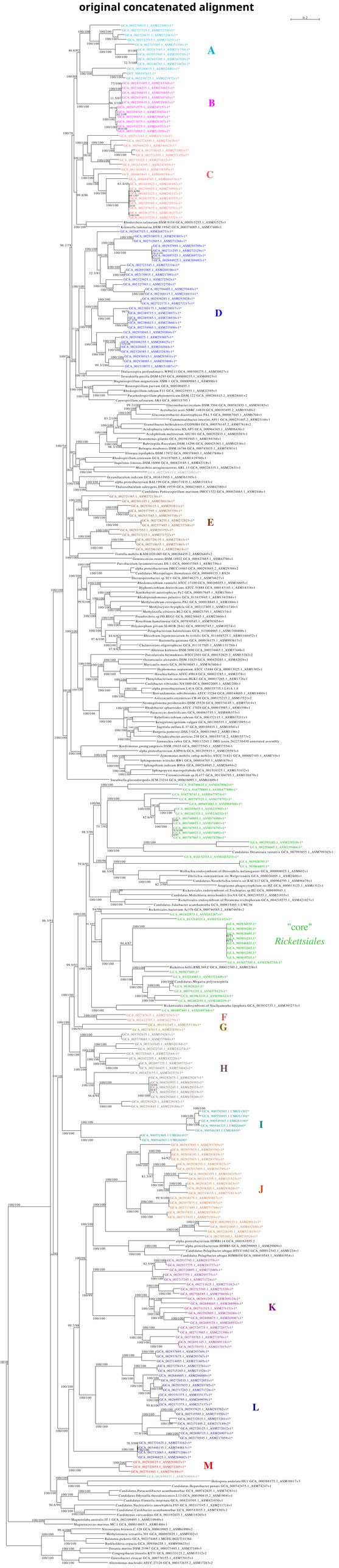
Amino Acids transport and biosynthesis

Synthesis | AA characterised transporters | AA uncharacterised transporters

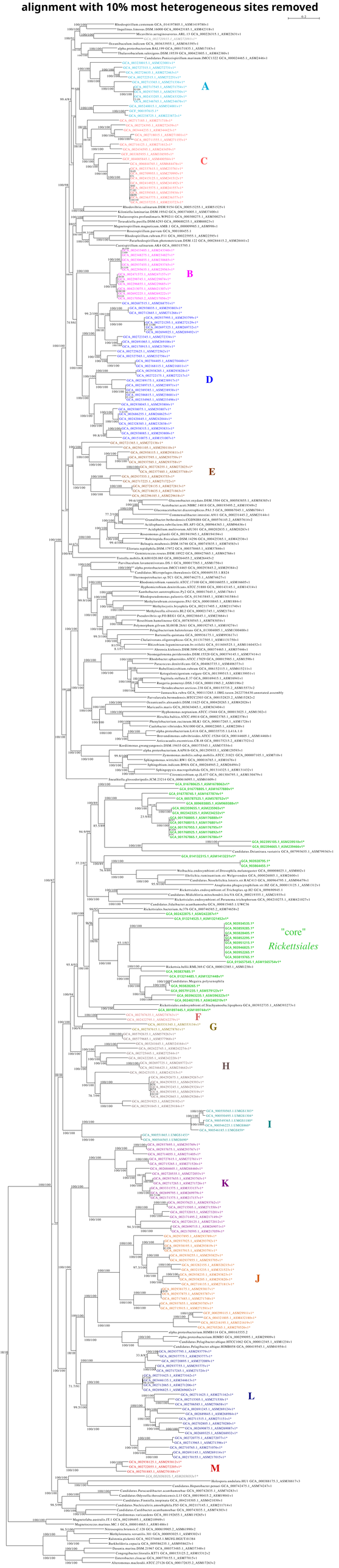
Rickettsia_prowazekii_strain_Madrid_E_GCA_000195735.1 0 0 0 0.1 0.44 0 0 0 | 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 76.7
Rickettsia_endosymbiont_of_Ixodes_scapularis_GCA_000160735.1 0.14 0 0 0.1 0.38 0 0 0.07 | 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 74
Rickettsia_bellii_strain_RML369C_GCA_000012385.1 0.14 0 0 0.1 0.44 0 0 0 | 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 1 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 78.5
Tisiphia_endosymbiont_of_Culicoides_newsteadi_GCA_002259525.1 0 0 0 0.1 0.38 0 0 0 | 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 80.4
Trichorickettsia_mobilis_endosymbiont_of_Paramecium_multimicronucleatum_Kr_154-4 0.14 0 0 0.1 0.44 0 0 0 | 0 0 0 0 0 0 1 0 0 0 0 0 0 1 2 0 0 1 0 1 0 0 0 0 0 1 0 0 0 0 1 0 0 0 0 0 0 | 0 3 0 0 0 1 0 0 0 0 0 0 0 | 81.7
Megaira_polyxenophila_endosymbiont_of_Euplotes_woodruffi_NDG2 0.14 0 0 0.1 0.38 0 0 0 | 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 82.2
GCA_017302595.1_Rickettsiaceae_bacterium 0 0 0 0.1 0.38 0 0 0 | 0 0 0 0 0 1 1 0 0 0 0 0 0 0 1 0 0 1 0 0 1 0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 1 0 0 0 0 0 0 0 | 80.8
Megaira_venefica_endosymbiont_of_Paramecium_nephridiatum_Sr_2-6 0 0 0 0.1 0.38 0 0 0 | 0 0 0 0 0 1 1 0 0 0 0 0 0 0 1 0 0 2 0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 77.6
GCA_003963235.1_Rickettsiaceae_bacterium 0 0 0 0.1 0.38 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 1 | 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 | 70.8
GCA_905479885.1_Rickettsiaceae_bacterium 0.14 0 0 0.1 0.38 0 0 0 | 1 0 0 0 0 1 0 0 0 0 0 0 0 0 1 1 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 61.2
GCA_905479865.1_Rickettsiaceae_bacterium 0.14 0 0 0.1 0.31 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 74.9
GCA_002402195.1_Rickettsiaceae_bacterium 0 0 0 0.1 0.31 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 73.5
GCA_013214485.1_Rickettsiaceae_bacterium 0.14 0 0 0.1 0.38 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 1 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 77.2
Rickettsiaceae_endosymbiont_of_Nephromyces_sp._GCA_015657545.1 0 0 0 0 0.38 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 | 64.8
Rickettsiaceae_endosymbiont_of_Cardiosporidium_cionae_GCA_015476335.1 0 0 0 0.1 0.38 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 2 | 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 | 70.8
Sarmatiella_mevalonica_GCA_016751895.1 0 0 0 0.1 0.44 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 | 0 1 0 0 0 1 0 0 0 0 0 0 0 | 66.7
GCA_017995275.1_Rickettsiaceae_bacterium 0.14 0 0 0.1 0.31 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 63.9
Orientia_tsutsugamushi_strain_Ikeda_GCA_000010205.1 0.14 0 0 0.1 0.38 0 0 0 | 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 68.9
Orientia_chuto_strain_Dubai_GCA_000964595.1 0 0 0 0.1 0.06 0 0 0 | 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 66.2
Occidentia_massiliensis_GCA_000309075.1 0.14 0 0 0.2 0.44 0 0 0 | 0 0 0 0 0 0 2 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 74.4
Sneabacter_namystus_GCA_008189685.1 0 0 0 0.1 0.44 0 0 0 | 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 62.6
Phycorickettsia_trachydisci_GCA_003015145.1 0.14 0 0 0.1 0.44 0 0 0.07 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 72.6
GCA_018062985.1_Rickettsiaceae_bacterium 0 0 0 0.1 0.38 0 0 0.07 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 | 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 | 58
GCA_013214525.1_Rickettsiaceae_bacterium 0 0.12 0 0.1 0.38 0 0 0 | 0 0 0 0 0 0 0 0 1 0 1 0 2 0 0 0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 1 2 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 79.5
GCA_002422875.1_Rickettsiaceae_bacterium 0 0 0 0 0.06 0 0 0.53 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 78.5
Rickettsiaceae_endosymbiont_of_Amblyomma_cajennese_Ac37b_GCA_000746585.2 0.14 0 0.11 0.1 0.5 1 0 0.13 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 2 0 1 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 | 93.6
Arcanobacter_lacustris_GCA_000970895.1 0 0 0 0.1 0.19 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 40.2
Rickettsiaceae_endosymbiont_of_Stachyamoeba_lipophora_GCA_003932735.1 0.14 0.12 0.11 0 0.44 0 0 0.47 | 0 0 0 0 0 0 0 0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 | 0 2 0 0 0 0 0 0 0 0 0 0 0 2 0 | 89
GCA_001897445.1_Rickettsiaceae_bacterium 0.14 0.12 0.11 0 0.44 0 0 0.53 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 2 | 0 2 0 0 0 1 0 0 0 0 0 0 0 | 86.3
Midichloria_mitochondrii_IricVA_GCA_000219355.1 0 0 0 0 0.31 0 0 0.07 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 3 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 1 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 77.6
Cyrtobacter_comes_endosymbiont_of_Euplotes_harpa_BOD18 0 0 0 0 0.38 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 2 1 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 76.3
Lyticum_sinuosum_endosymbiont_of_Paramecium_biaurelia_USBL-36I1 0 0 0 0 0.31 0 0 0.07 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 64.8
Fokinia_solitaria_GCA_003072485.1 0 0 0 0 0 0 0 0.07 | 1 0 0 0 1 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 66.7
Fokinia_cryptica_endosymbiont_of_Paramecium_biaurelia_US_BI_11III1 0 0 0 0 0 0 0 0.07 | 1 0 0 0 1 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 65.8
GCA_903878005.1_Midichloriaceae_bacterium 0 0 0 0.2 0.31 0.67 0 0.07 | 0 0 0 0 2 0 0 0 0 0 0 0 0 0 2 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 2 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 64.4
Vederia_obscura_endosymbiont_of_Plagiopyla_frontata_IBS-3 0 0 0 0 0.44 0 0 0 | 1 0 0 0 0 0 0 0 0 0 0 1 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 70.8
Bandiella_woodruffii_endosymbiont_of_Euplotes_woodruffi_NDG2 0 0 0 0 0.38 0 0 0.07 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 2 0 0 0 0 0 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 1 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 83.1
GCA_905479795.1_Midichloriaceae_bacterium 0 0 0 0 0.25 0 0 0.07 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 1 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 74.9
GCA_903887235.1_Midichloriaceae_bacterium 0 0 0 0 0.38 0 0 0.07 | 0 0 0 0 0 1 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 2 1 0 0 0 0 0 1 0 0 0 1 0 0 0 1 | 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 | 86.3
Grellia_incantans_H2_GCA_009690945.1 0 0 0 0 0.38 0 0 0.07 | 0 0 0 0 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 1 | 0 2 0 0 1 0 0 0 0 0 0 0 0 | 85.4
Aquarickettsia_rohweri_GCA_003953955.1 0 0 0 0 0.38 0 0 0.07 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 1 | 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 | 83.6
Jidaibacter_acanthamoeba_UWC36_GCA_000815465.1 0 0 0 0 0.44 0 0 0.13 | 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 85.4
Endosymbiont_of_Acanthamoeba_sp._UWC8_GCA_000730245.1 0 0 0 0 0.44 0 0 0.13 | 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 86.8
Midichloriaceae_endosymbiont_of_Reticulomyxa_filosa 0.14 0 0 0 0.5 0 0 0.07 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 1 0 0 0 0 0 0 0 | 85.4
Midichloriaceae_endosymbiont_of_Peranema_trichophorum_GCA_004210275.1 0 0 0 0 0.5 1 0.33 0.4 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 1 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 82.2
GCA_013288625.1_Midichloriaceae_bacterium 0.14 0 0.22 0 0.31 0 0 0.13 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 2 0 | 1 0 0 0 0 1 0 0 0 0 0 0 0 | 50.7
Anaplasma_phagocytophilum_strain_HZ_GCA_000013125.1 0.29 0 0 0 0.06 0 0 0.07 | 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 79
Anaplasma_marginale_strain_Florida_GCA_000020305.1 0.43 0 0 0.1 0.5 0 0 0.07 | 0 0 1 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 84
Neoehrlichia_lotoris_strain_RAC413_GCA_000964795.1 1 0 0 0.1 0.56 0 0 0.07 | 0 0 1 0 0 0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 84.5
Ehrlichia_ruminantium_strain_Welgevonden_GCA_000026005.1 1 0 0 0 0.5 0 0 0.07 | 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 81.3
Ehrlichia_chaffeensis_strain_Arkansas_GCA_000013145.1 1 0 0 0 0.5 0 0 0.07 | 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 83.6
Wolbachia_endosymbiont_of_Brugia_malayi_GCA_000008385.1 0.29 0 0 0 0.5 0 0 0.07 | 1 0 1 0 0 0 2 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 80.8
Wolbachia_endosymbiont_of_Drosophila_melanogaster_GCA_000008025.1 0.29 0 0 0 0.5 0 0 0.07 | 2 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 84
Wolbachia_endosymbiont_of_Pratylenchus_penetrans_GCA_001752665.1 0.29 0 0 0 0.5 0 0 0 | 1 0 1 0 0 0 1 0 0 0 0 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 78.1
Neorickettsia_sennetsu_strain_Miyayama_GCA_000013165.1 0 0 0 0 0.12 0 0 0.07 | 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 73.1
Neorickettsia_helminthoeca_strain_Oregon_GCA_000632985.1 0 0 0 0 0.44 0 0 0.07 | 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 69.4
Xenolissoclinum_pacificiensis_L6_GCA_000512675.1 0 0 0 0 0.19 0 0 0.07 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 60.3
Echinorickettsia_raffii_H1_GCA_018101195.1 0 0 0 0 0.56 0 0 0.47 | 0 1 1 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 80.4
Anaplasmataceae_symbiont_of_Acropora_tenuis_Sesoko1_GCA_014132315.1 0 0 0 0 0.06 0 0 0.4 | 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 71.7
GCA_903864455.1_Anaplasmataceae_bacterium 0.29 0 0 0 0.44 0 0 0 | 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 62.1
Deianiraea_vastatrix_GCA_007993655.1 0.29 0.12 1 0.8 0.62 1 0 0.47 | 3 0 0 1 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 1 0 0 1 0 0 0 0 0 | 0 0 0 0 1 1 0 1 0 0 0 0 0 0 0 | 65.8
GCA_017444125.1_Deianiraeaceae_bacterium 0.57 0.25 0.11 0.4 0.38 0 0 0.07 | 0 0 0 1 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 60.3
GCA_017444095.1_Deianiraeaceae_bacterium 0.29 0 0 0 0.56 0 0 0.13 | 1 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 58
GCA_002395105.1_Deianiraeaceae_bacterium 0.29 0 0 0 0.38 0 0 0 | 1 1 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 54.3
GCA_002394665.1_Deianiraeaceae_bacterium 0.71 0.12 0.89 0.3 0.56 0 0 0.47 | 0 0 0 1 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 1 0 0 0 0 0 0 0 0 0 | 63.9
GCA_905480015.1_Deianiraeaceae_bacterium 0.86 0.75 0.78 0.7 0.56 0.67 1 1 | 1 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 70.3
GCA_018969185.1_Gamibacteraceae_bacterium 0.71 0 0.78 1 0.94 1 0 0.87 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 1 0 0 0 0 1 0 0 0 0 | 89.5
GCA_002359655.1_Gamibacteraceae_bacterium 1 0.25 1 1 1 1 0 0.93 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 2 0 0 0 0 1 0 0 0 1 0 0 0 0 | 92.7
GCA_009693885.1_Gamibacteraceae_bacterium 0.86 0.25 0.44 0.6 0.5 0 0 0.67 | 0 0 0 0 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 | 0 2 0 0 0 0 0 0 0 0 1 0 0 0 0 | 59.8
GCA_903872175.1_Gamibacteraceae_bacterium 1 0 0.89 1 1 1 1 1 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 3 0 0 0 0 0 0 0 0 1 0 0 0 0 | 94.5
GCA_903831915.1_Gamibacteraceae_bacterium 1 0 0.89 1 1 1 1 1 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 2 0 0 0 2 0 0 0 0 1 0 0 0 0 | 93.6
GCA_017999675.1_Gamibacteraceae_bacterium 1 0 0.89 1 1 1 1 1 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 2 0 0 0 1 0 0 0 0 1 0 0 0 0 | 90.9
GCA_903927415.1_Gamibacteraceae_bacterium 1 0.88 1 1 1 1 0 0.87 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 2 0 1 0 0 0 0 0 0 1 0 0 0 0 | 85.8
GCA_903878685.1_Gamibacteraceae_bacterium 1 0.88 0.89 0.9 1 1 0 1 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 2 0 0 0 1 0 0 0 0 1 0 0 0 0 | 92.2
GCA_903917585.1_Gamibacteraceae_bacterium 1 0.25 0.78 1 0.81 0 0 1 | 0 0 0 0 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 | 0 2 0 0 0 1 0 0 0 0 0 0 0 0 0 | 84.5
GCA_001768015.1_Gamibacteraceae_bacterium 1 1 1 1 1 1 0 1 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 2 0 1 0 0 0 0 0 0 1 0 0 0 0 | 91.8
GCA_903837365.1_Gamibacteraceae_bacterium 0.71 0 0.89 0.9 0.94 1 0 0.8 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 2 0 0 0 0 0 0 0 0 1 0 0 0 0 | 79.5
GCA_014190355.1_Gamibacteraceae_bacterium 1 0.88 0.89 1 1 1 0 1 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 2 0 0 0 0 0 0 0 0 1 0 0 0 0 | 91.3
GCA_903959715.1_Gamibacteraceae_bacterium 0.86 0.12 0.89 0.9 0.81 1 0 0.93 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 1 0 0 0 0 | 80.8
GCA_009925685.1_Gamibacteraceae_bacterium 1 0.25 0.89 1 0.94 1 0 0.93 | 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 2 0 0 0 0 0 0 0 0 1 0 0 0 0 | 86.8
GCA_009921385.1_Gamibacteraceae_bacterium 0.86 0.12 0.78 1 0.94 1 0 0.93 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 2 0 0 0 0 0 0 0 0 1 0 0 0 0 | 73.1
GCA_016778745.1_Gamibacteraceae_bacterium 0.43 0 0.56 0.8 0.88 0.67 1 0.8 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 79.9
GCA_905478245.1_Gamibacteraceae_bacterium 1 0.88 0.89 1 0.94 1 0 0.93 | 1 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 91.8
GCA_905478165.1_Gamibacteraceae_bacterium 1 0.88 0.89 1 0.88 1 0 1 | 1 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 87.7
GCA_017620845.1_Gamibacteraceae_bacterium 0 0 0 0.1 0.12 0 0.33 0.33 | 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 68
GCA_017475895.1_Gamibacteraceae_bacterium 0.29 0.12 0 0.1 0.12 0 0 0.33 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 72.1
GCA_016780625.1_Diomedesiaceae_bacterium 1 0 0.78 0.9 0.81 1 1 0.73 | 1 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 72.1
GCA_018659605.1_Diomedesiaceae_bacterium 0.86 1 1 0.8 0.88 1 0.67 0.87 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 78.1
GCA_018659145.1_Diomedesiaceae_bacterium 1 0.88 1 0.9 0.94 1 1 1 | 1 0 0 0 0 0 0 0 0 0 0 0 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 90.4
GCA_016778805.1_Diomedesiaceae_bacterium 0.71 1 1 0.9 0.81 0.67 1 1 | 1 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 77.6
GCA_002787635.1_Athabascaceae_bacterium 1 0.75 0.89 0.9 1 1 1 1 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 97.7
GCA_002422795.1_Athabascaceae_bacterium 1 0.75 0.78 1 1 1 1 1 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 1 | 91.8
GCA_013288565.1_Jistubacteraceae_bacterium 0.86 0.75 0.78 0.9 0.56 0 1 0.67 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 | 72.1
GCA_903821695.1_Jistubacteraceae_bacterium 0.86 0.88 0.89 1 1 1 1 1 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 1 0 0 0 0 | 96.8
GCA_010031735.1_Jistubacteraceae_bacterium 1 0.88 1 1 1 1 1 0.93 | 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 1 0 0 0 0 1 0 0 0 0 | 94.1
GCA_003531345.1_Jistubacteraceae_bacterium 0.71 0.62 0.67 0.8 0.69 0.67 0.33 0.6 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 64.4
GCA_013288575.1_Arkhamiaceae_bacterium 0.86 0.12 0.44 0.3 0.44 1 0.67 0.4 | 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 | 55.3
GCA_002787615.1_Arkhamiaceae_bacterium 0.86 0.62

Supplementary Figure 29: "step 4" phylogenomic trees. Phylogenomic trees of *Rickettsiales* and other *Alphaproteobacteria*, for testing the affiliation to *Rickettsiales* of 211 "BUSCO+eggNOG-filtered putative *Rickettsiales* MAGs" (Step 4 in Supplementary Note 4). The phylogeny on the untrimmed concatenated gene alignment, as well as on alignments with the 10%, 20%, 30%, 40%, or 50% most compositionally heterogeneous sites removed are consecutively presented in each panel of this figure. In each tree, the ascertained "core" *Rickettsiales* MAGs are highlighted in green, the ascertained non-*Rickettsiales* MAGs in gray and italics, and the members of each of 13 additional groups (labelled from A to M) in a different colour. On each branch, support values by SH-aLRT with 1000 replicates and by 1000 ultrafast bootstraps are reported. The tree scales stand for estimated sequence divergence.

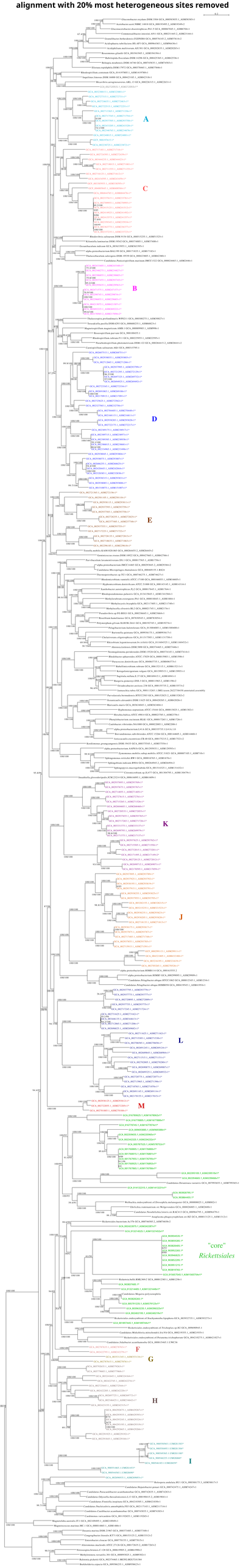
original concatenated alignment



alignment with 10% most heterogeneous sites removed



alignment with 20% most heterogeneous sites removed


0.2
Gloeomargarita cryohalinа DSM 3504 GCA_000935455.1_ASM93545v1
Acaryochloris sp. CCMEE 5410 GCA_002300495.1_ASM230049v1
Gloeomargaritaceae diversispirillum PALCY GCA_000983765.1_ASM98376v1
Cyanosarcina cherrieae strain ATCC BAA-1613 GCA_000317665.2_ASM31766v2
Geminicoccus roseus DSM 18922 GCA_000427065.1_ASM42706v1
Pleurocapsa sp. PCC 7327 GCA_000317125.1_ASM31712v1
Chroococcidiopsis sp. TS-821 GCA_000317145.1_ASM31714v1
Cyanobacterium aponinum PCC 10605 GCA_000317185.1_ASM31718v1
Synechococcus sp. PCC 7502 GCA_000317205.1_ASM31720v1
Synechococcus sp. PCC 7335 GCA_000317225.1_ASM31722v1
Cyanobium gracile PCC 6307 GCA_000317245.1_ASM31724v1
Prochlorococcus marinus str. MIT 9515 GCA_000317265.1_ASM31726v1
Prochlorococcus marinus str. MIT 9301 GCA_000317285.1_ASM31728v1
Prochlorococcus marinus str. MIT 9312 GCA_000317305.1_ASM31730v1
Prochlorococcus marinus str. MIT 9303 GCA_000317325.1_ASM31732v1
Prochlorococcus marinus str. MIT 9211 GCA_000317345.1_ASM31734v1
Prochlorococcus marinus str. MIT 9215 GCA_000317365.1_ASM31736v1
Prochlorococcus marinus str. MIT 9313 GCA_000317385.1_ASM31738v1
Prochlorococcus marinus str. MIT 9302 GCA_000317405.1_ASM31740v1
Prochlorococcus marinus str. MIT 9116 GCA_000317425.1_ASM31742v1
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Prochlorococcus marinus str. MIT 9515 GCA_000317845.1_ASM31784v1
Prochlorococcus marinus str. MIT 9314 GCA_000317865.1_ASM31786v1
Prochlorococcus marinus str. MIT 9211 GCA_000317885.1_ASM31788v1
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Prochlorococcus marinus str. MIT 9312 GCA_000317925.1_ASM31792v1
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Prochlorococcus marinus str. MIT 9211 GCA_000318005.1_ASM31800v1
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Prochlorococcus marinus str. MIT 9321 GCA_000318085.1_ASM31808v1
Prochlorococcus marinus str. MIT 9515 GCA_000318105.1_ASM31810v1
Prochlorococcus marinus str. MIT 9314 GCA_000318125.1_ASM31812v1
Prochlorococcus marinus str. MIT 9211 GCA_000318145.1_ASM31814v1
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Prochlorococcus marinus str. MIT 9312 GCA_000318185.1_ASM31818v1
Prochlorococcus marinus str. MIT 9303 GCA_000318205.1_ASM31820v1
Prochlorococcus marinus str. MIT 9301 GCA_000318225.1_ASM31822v1
Prochlorococcus marinus str. MIT 9313 GCA_000318245.1_ASM31824v1
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Prochlorococcus marinus str. MIT 9202 GCA_000318285.1_ASM31828v1
Prochlorococcus marinus str. MIT 9201 GCA_000318305.1_ASM31830v1
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Prochlorococcus marinus str. MIT 9321 GCA_000318345.1_ASM31834v1
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Prochlorococcus marinus str. MIT 9314 GCA_000318385.1_ASM31838v1
Prochlorococcus marinus str. MIT 9211 GCA_000318405.1_ASM31840v1
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Prochlorococcus marinus str. MIT 9312 GCA_000318445.1_ASM31844v1
Prochlorococcus marinus str. MIT 9303 GCA_000318465.1_ASM31846v1
Prochlorococcus marinus str. MIT 9301 GCA_000318485.1_ASM31848v1
Prochlorococcus marinus str. MIT 9313 GCA_000318505.1_ASM31850v1
Prochlorococcus marinus str. MIT 9211 GCA_000318525.1_ASM31852v1
Prochlorococcus marinus str. MIT 9202 GCA_000318545.1_ASM31854v1
Prochlorococcus marinus str. MIT 9201 GCA_000318565.1_ASM31856v1
Prochlorococcus marinus str. MIT 9214 GCA_000318585.1_ASM31858v1
Prochlorococcus marinus str. MIT 9321 GCA_000318605.1_ASM31860v1
Prochlorococcus marinus str. MIT 9515 GCA_000318625.1_ASM31862v1
Prochlorococcus marinus str. MIT 9314 GCA_000318645.1_ASM31864v1
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Prochlorococcus marinus str. MIT 9312 GCA_000318705.1_ASM31870v1
Prochlorococcus marinus str. MIT 9303 GCA_000318725.1_ASM31872v1
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Prochlorococcus marinus str. MIT 9202 GCA_000318805.1_ASM31880v1
Prochlorococcus marinus str. MIT 9201 GCA_000318825.1_ASM31882v1
Prochlorococcus marinus str. MIT 9214 GCA_000318845.1_ASM31884v1
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Prochlorococcus marinus str. MIT 9515 GCA_000318885.1_ASM31888v1
Prochlorococcus marinus str. MIT 9314 GCA_000318905.1_ASM31890v1
Prochlorococcus marinus str. MIT 9211 GCA_000318925.1_ASM31892v1
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Prochlorococcus marinus str. MIT 9303 GCA_000318985.1_ASM31898v1
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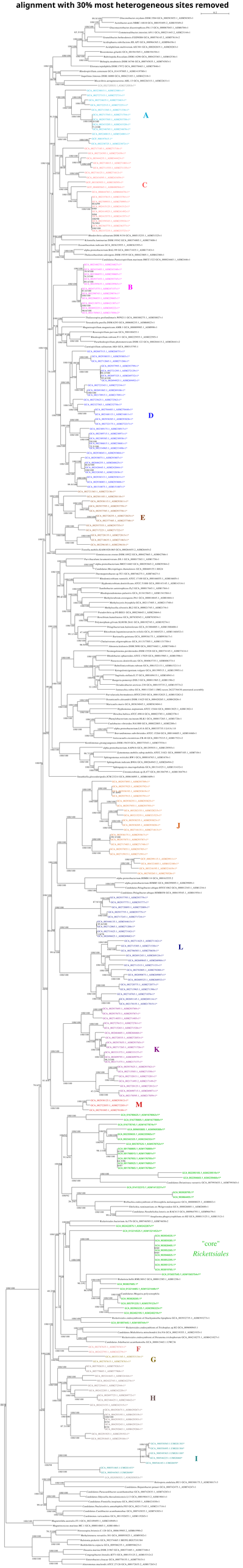
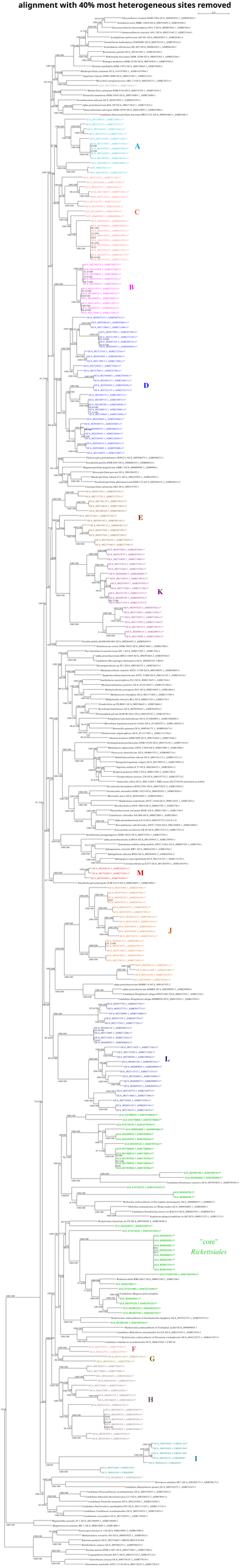
Prochlorococcus marinus str

alignment with 30% most heterogeneous sites removed

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"core"
Rickettsiales
A
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D
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I
J
M
L

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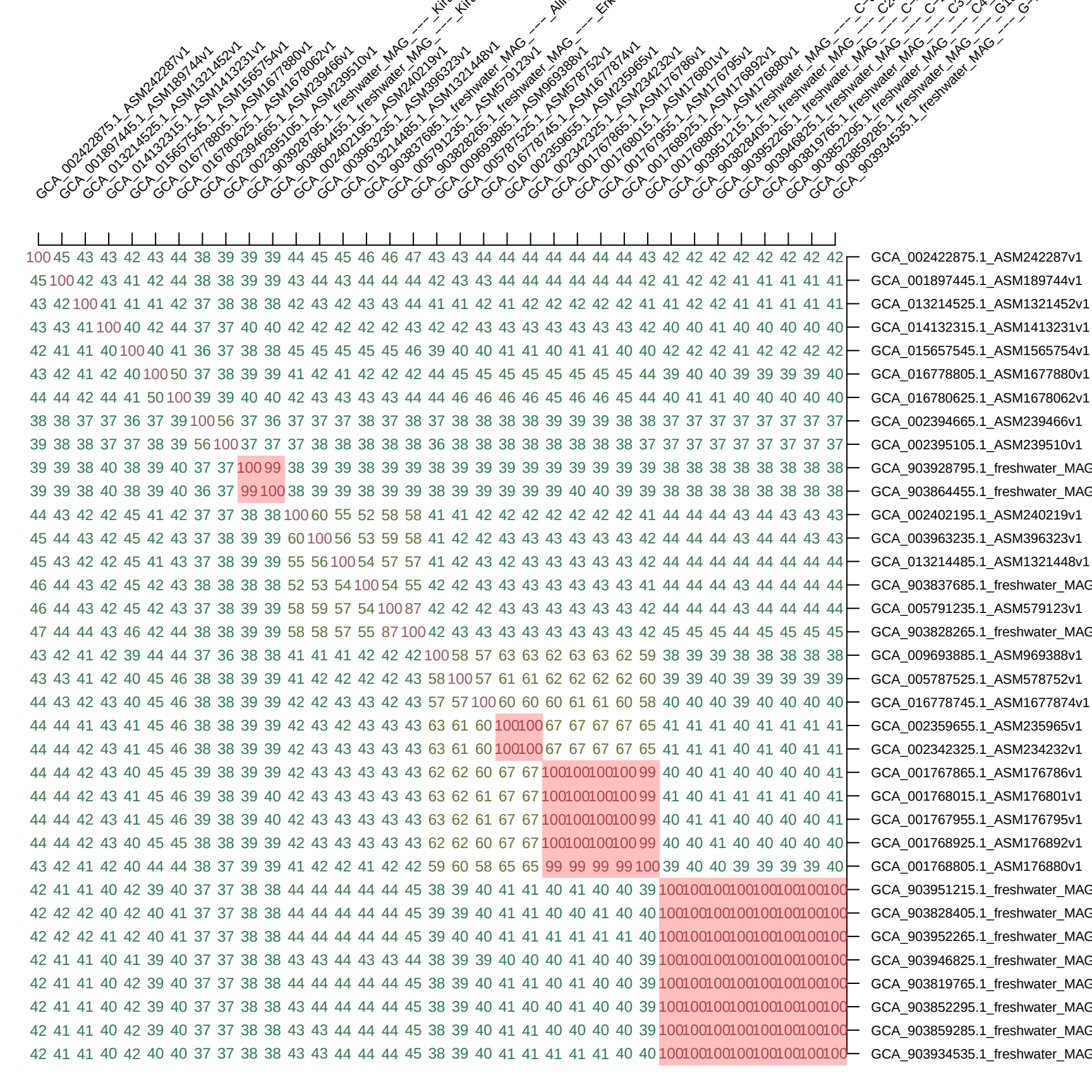
Supplementary Figure 30: identity values. AAI (Average Amino acid Identity) values within each examined clade of MAGs and *Rickettsiales* genomes. Specifically, in the order, “core *Rickettsiales*”, groups A-M, five combinations of “new putative *Rickettsiales* MAGs” with “BUSCO+eggNOG-filtered putative *Rickettsiales* MAGs”, and finally a combination of *Rickettsiales* genomes and closely related MAGs.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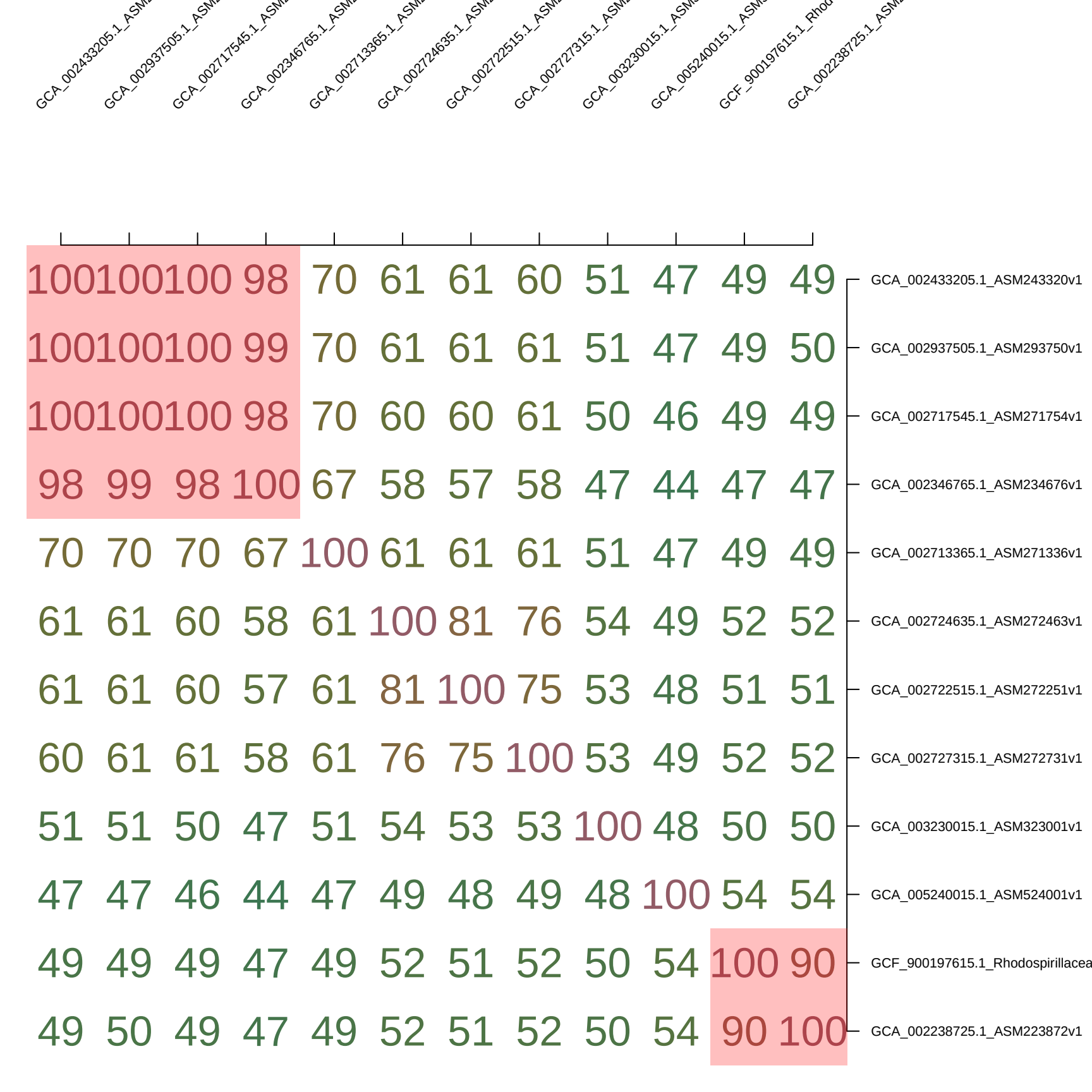
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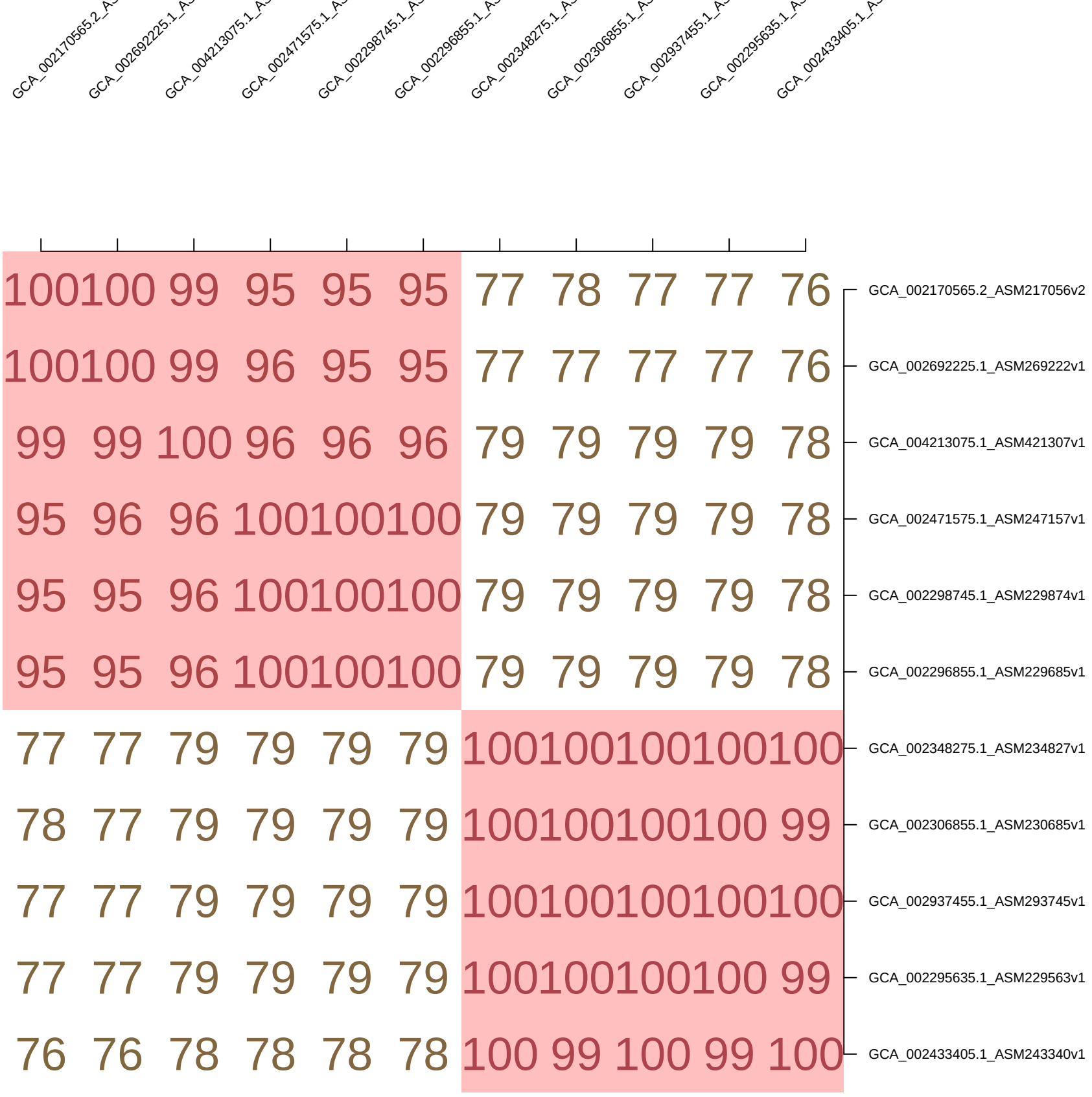
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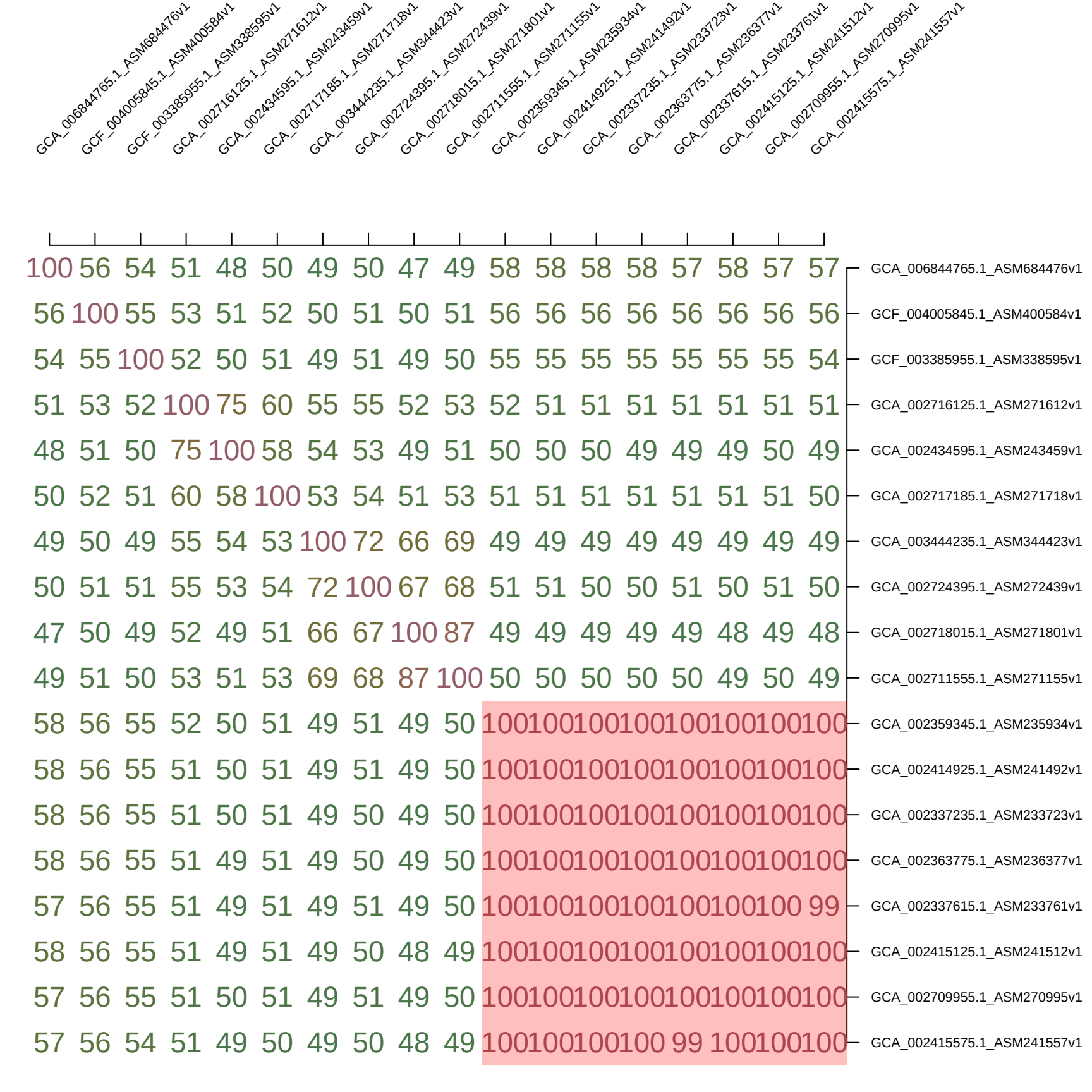
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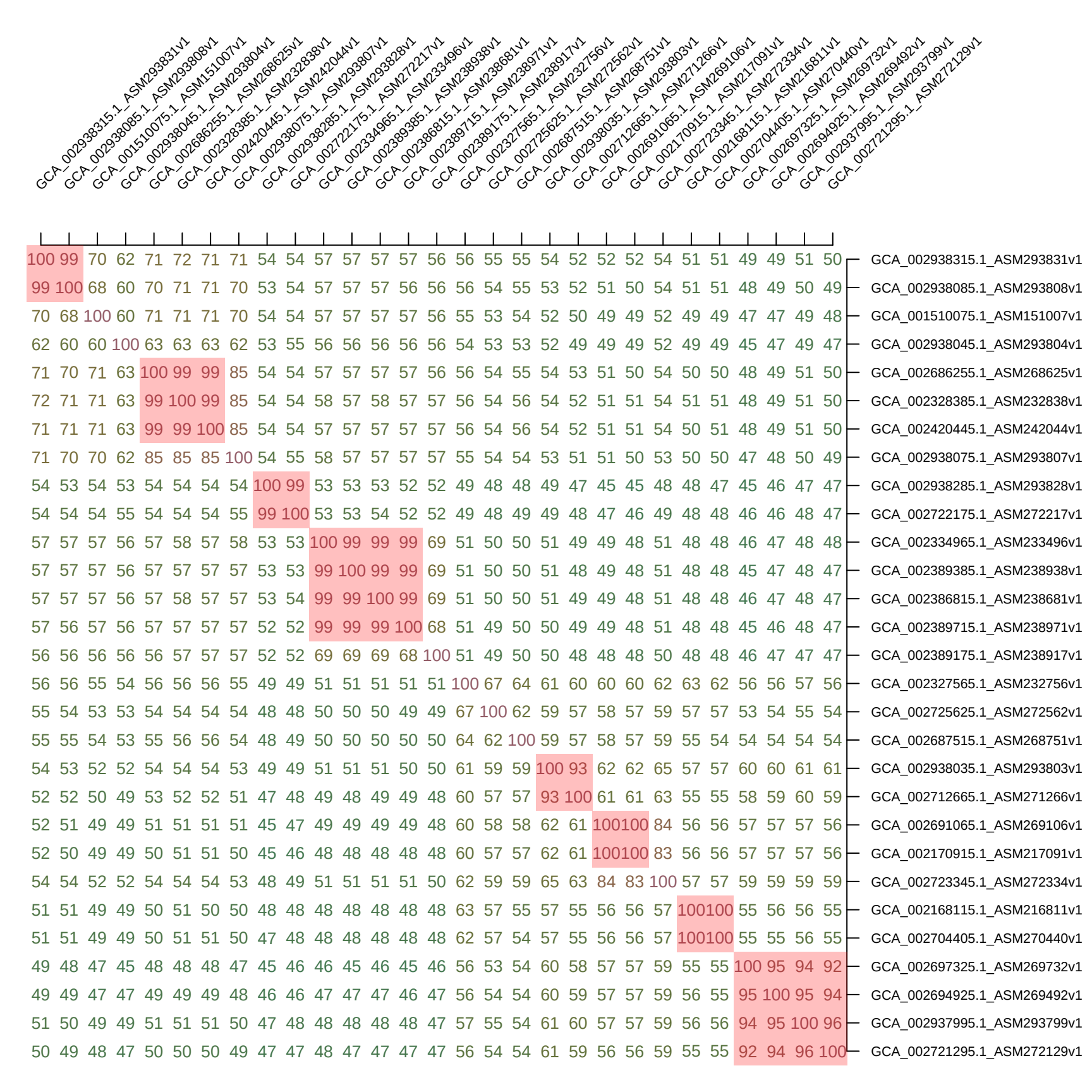
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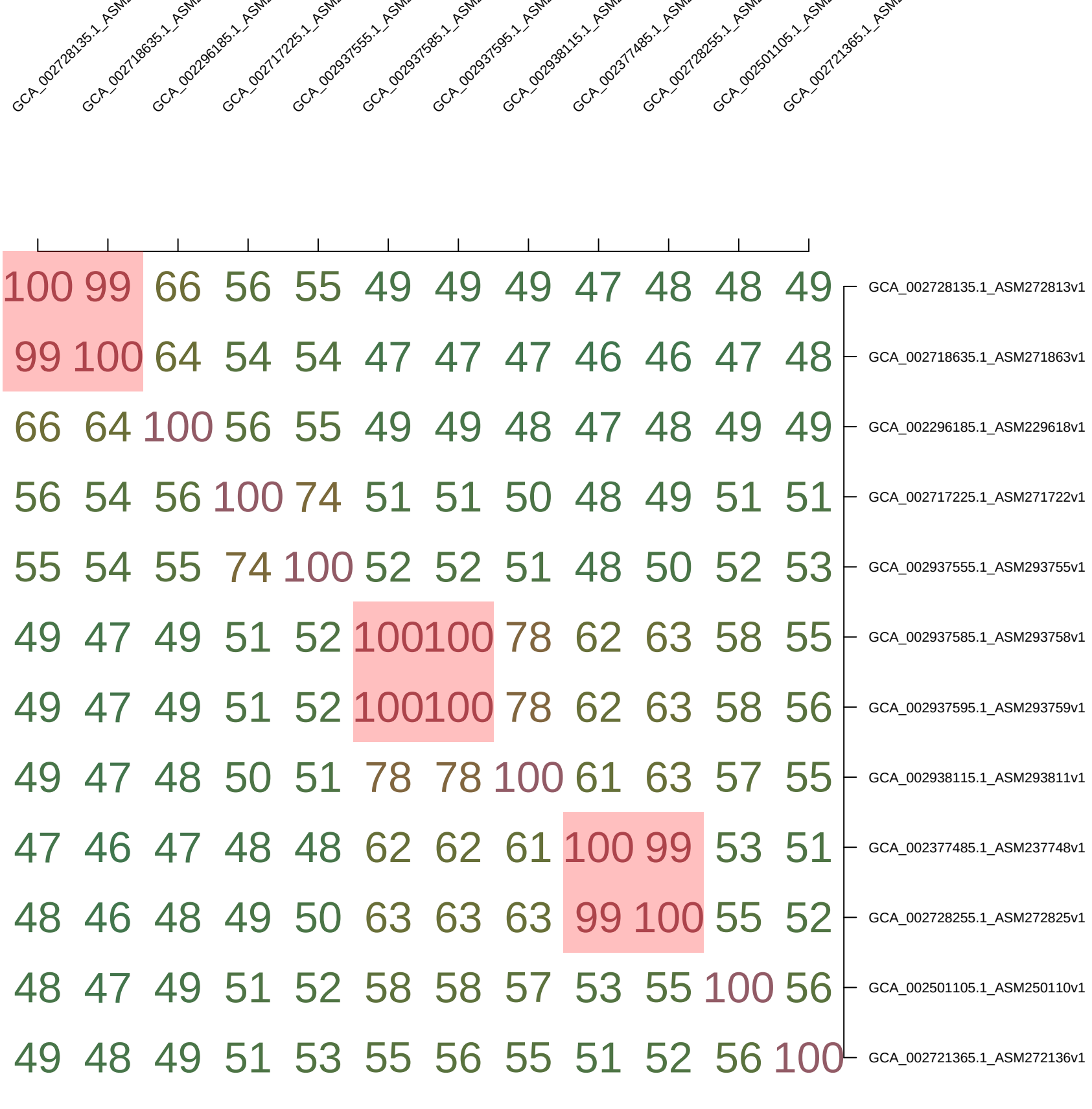
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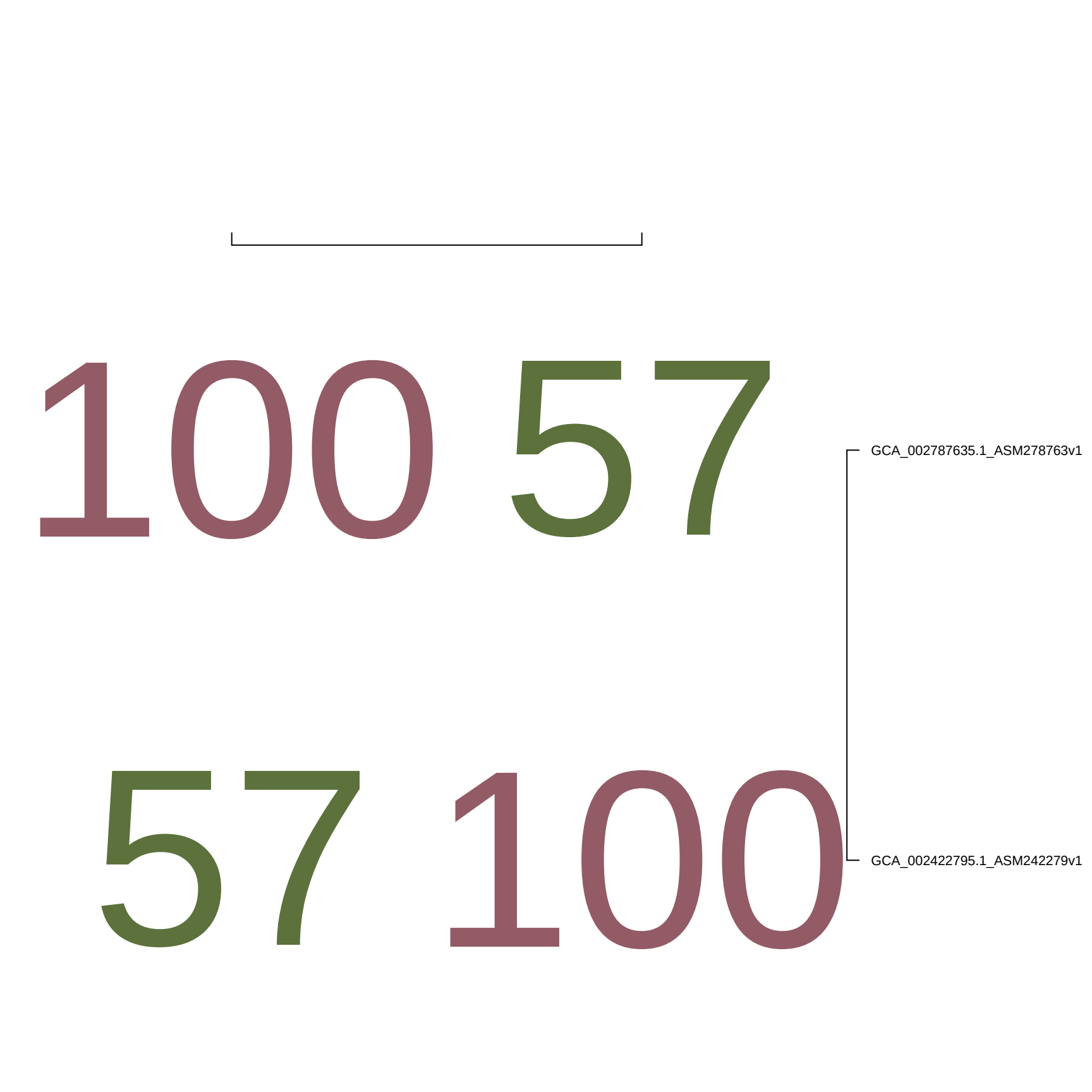
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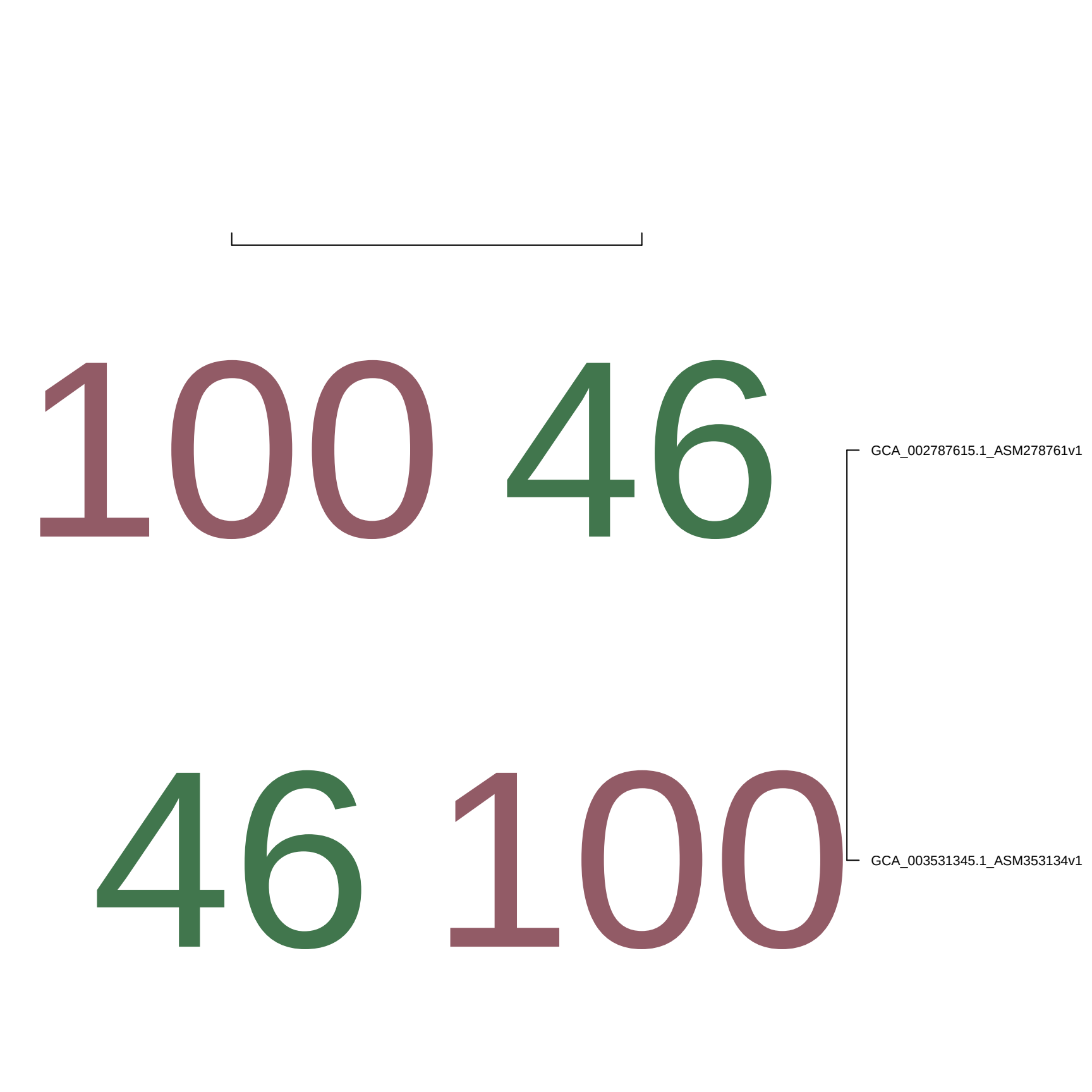
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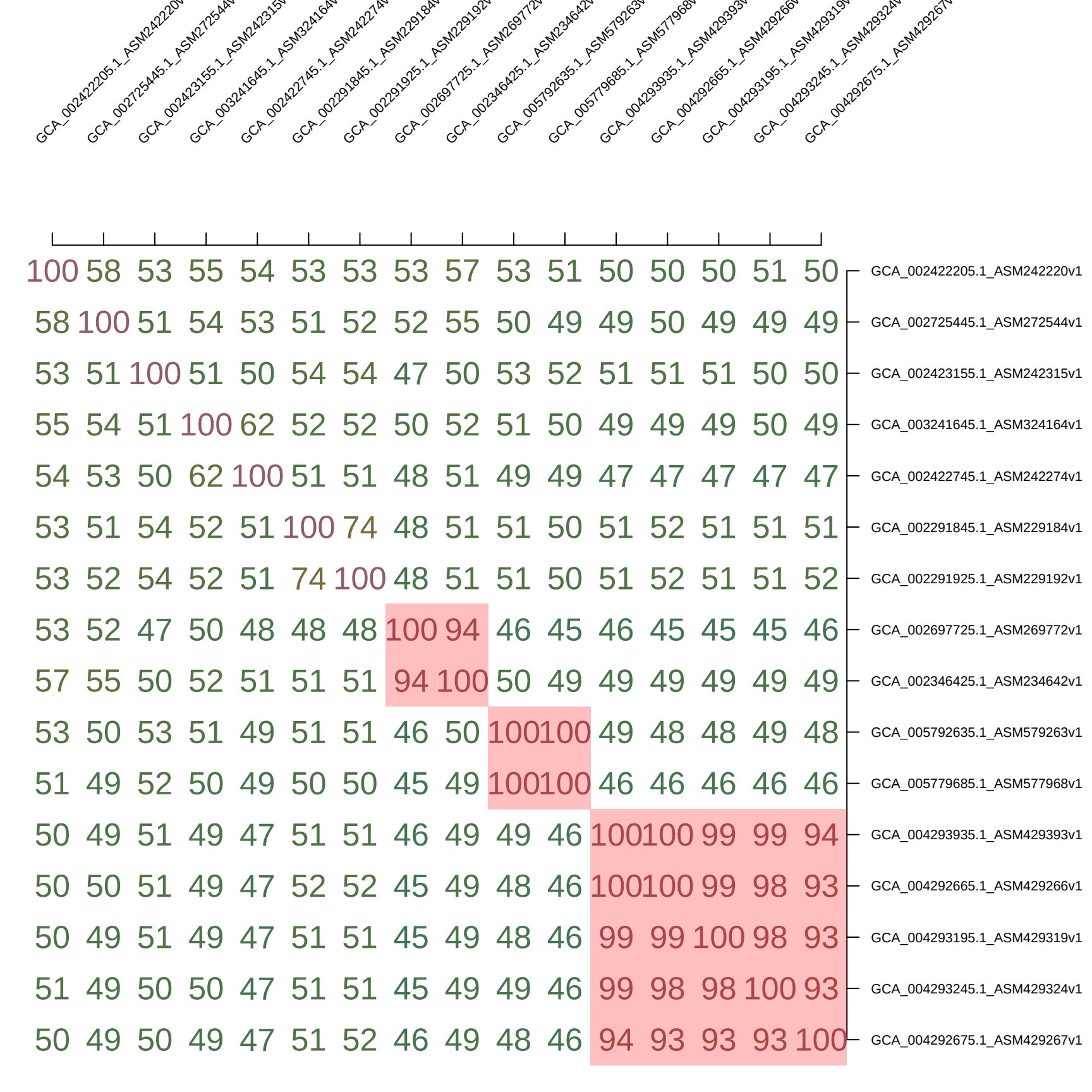
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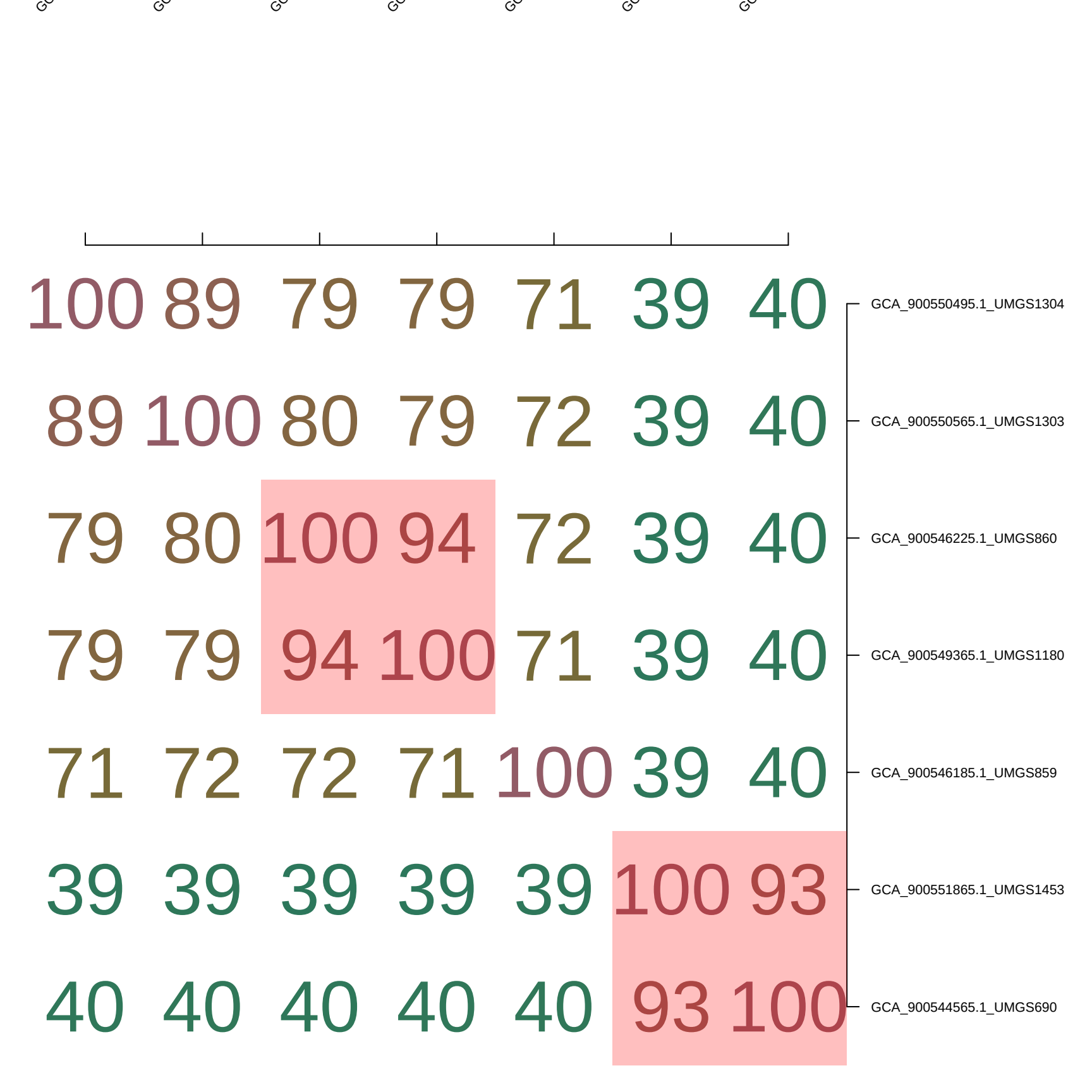
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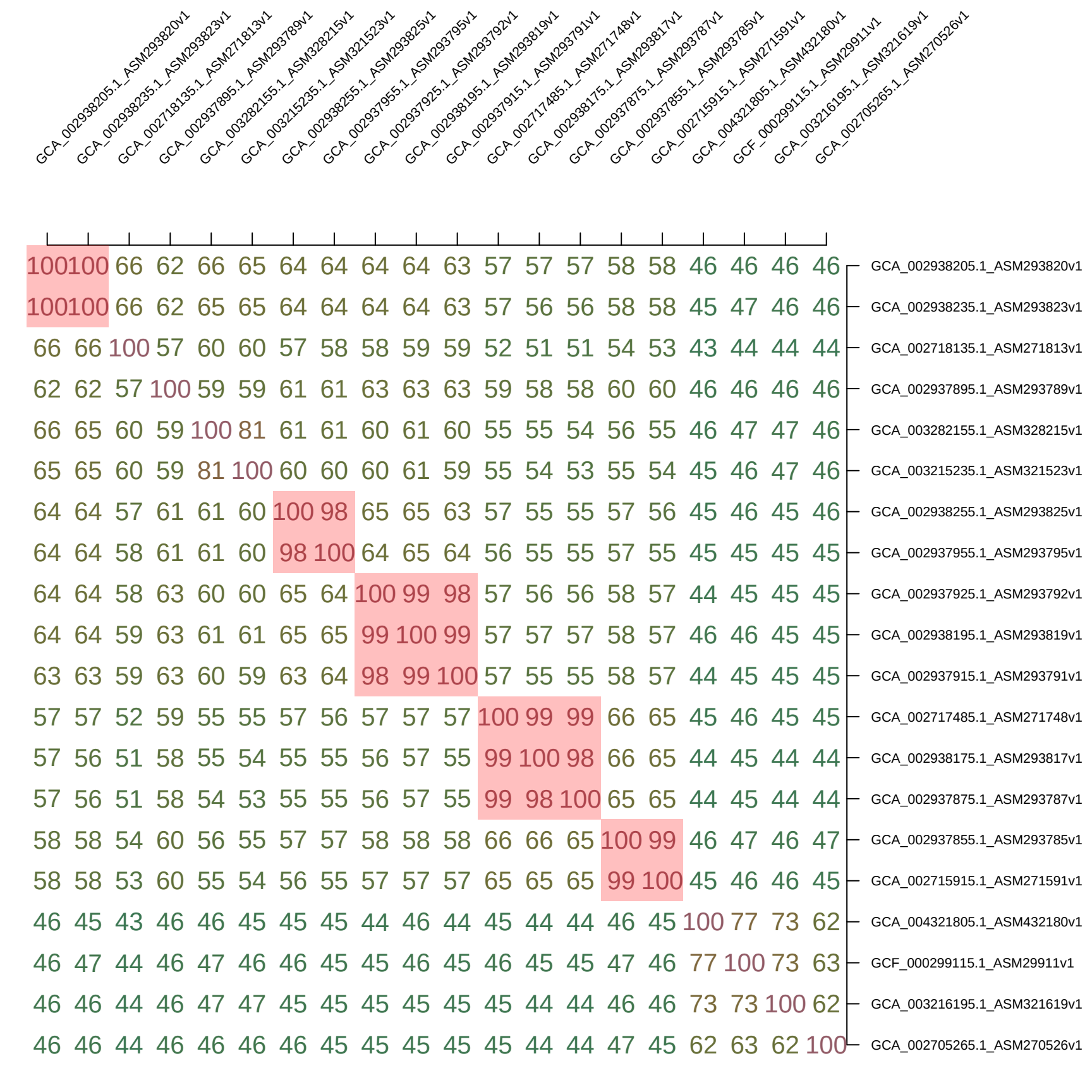
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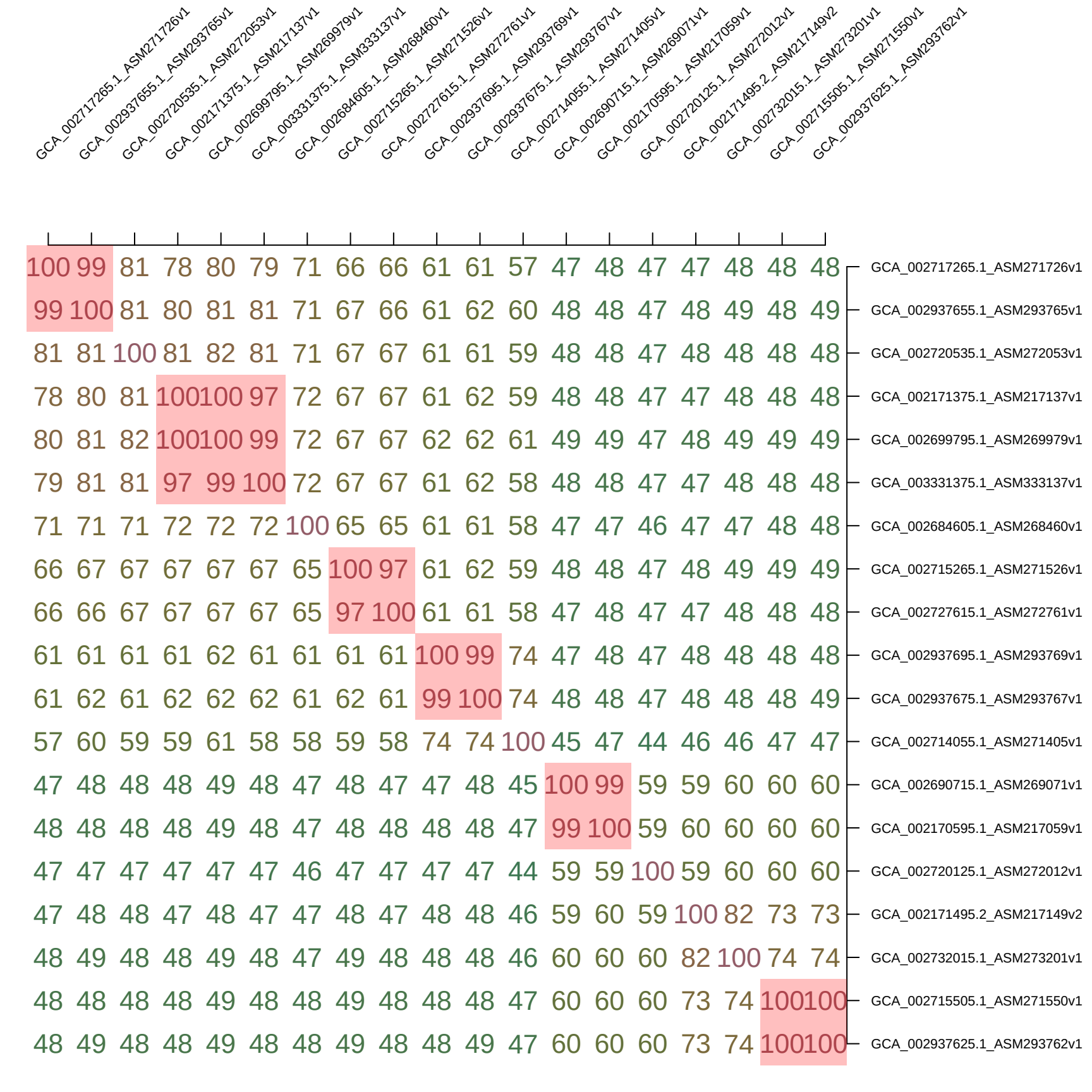
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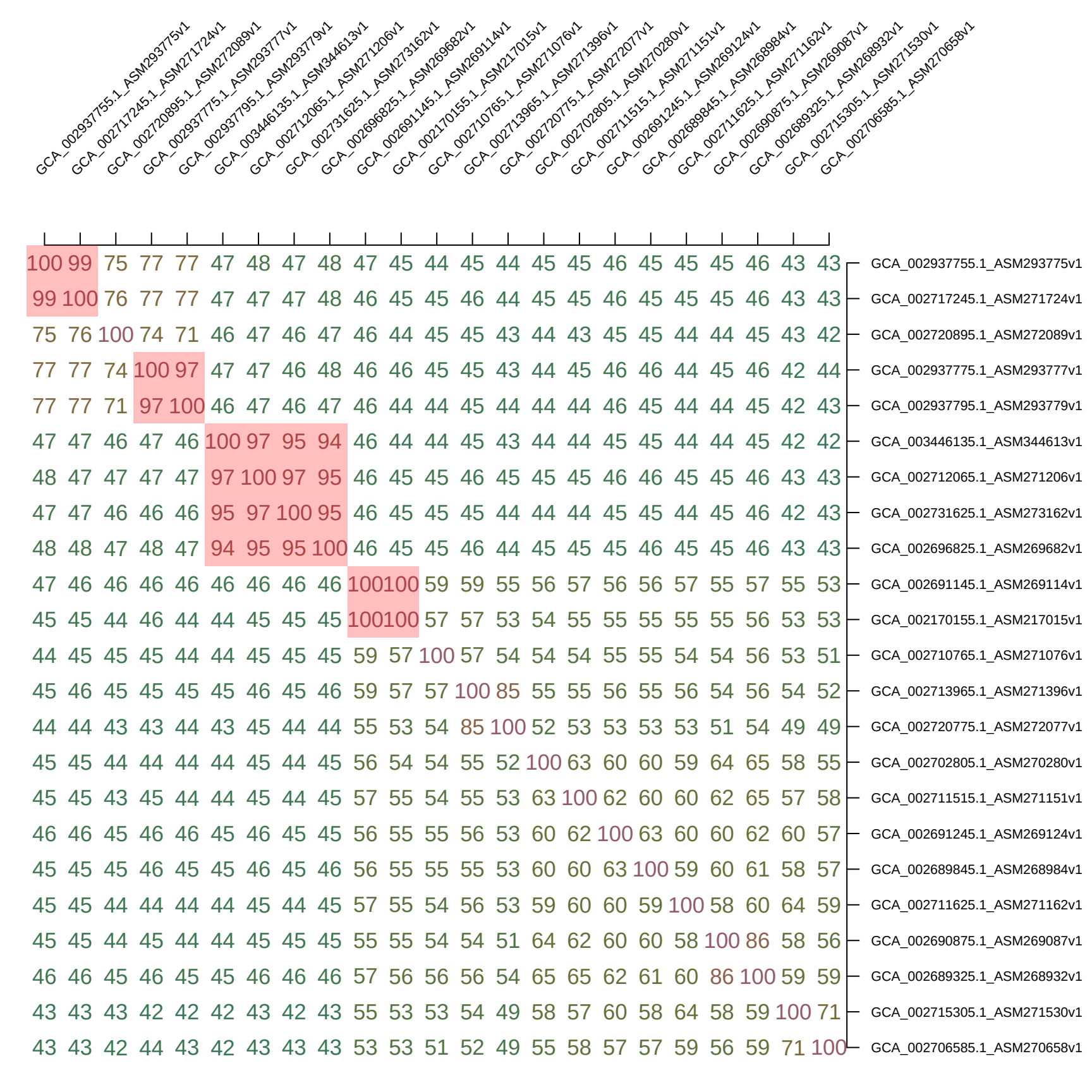
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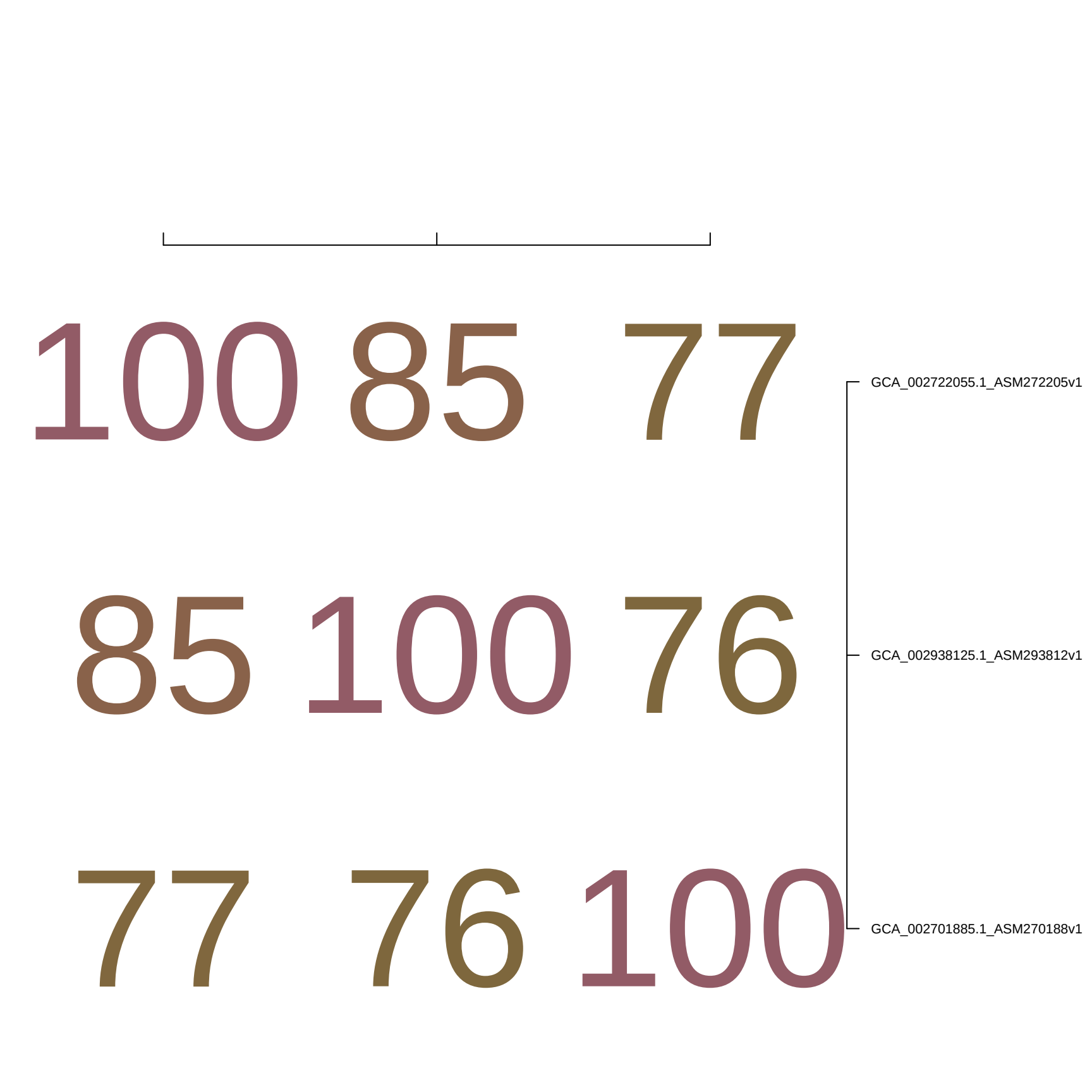
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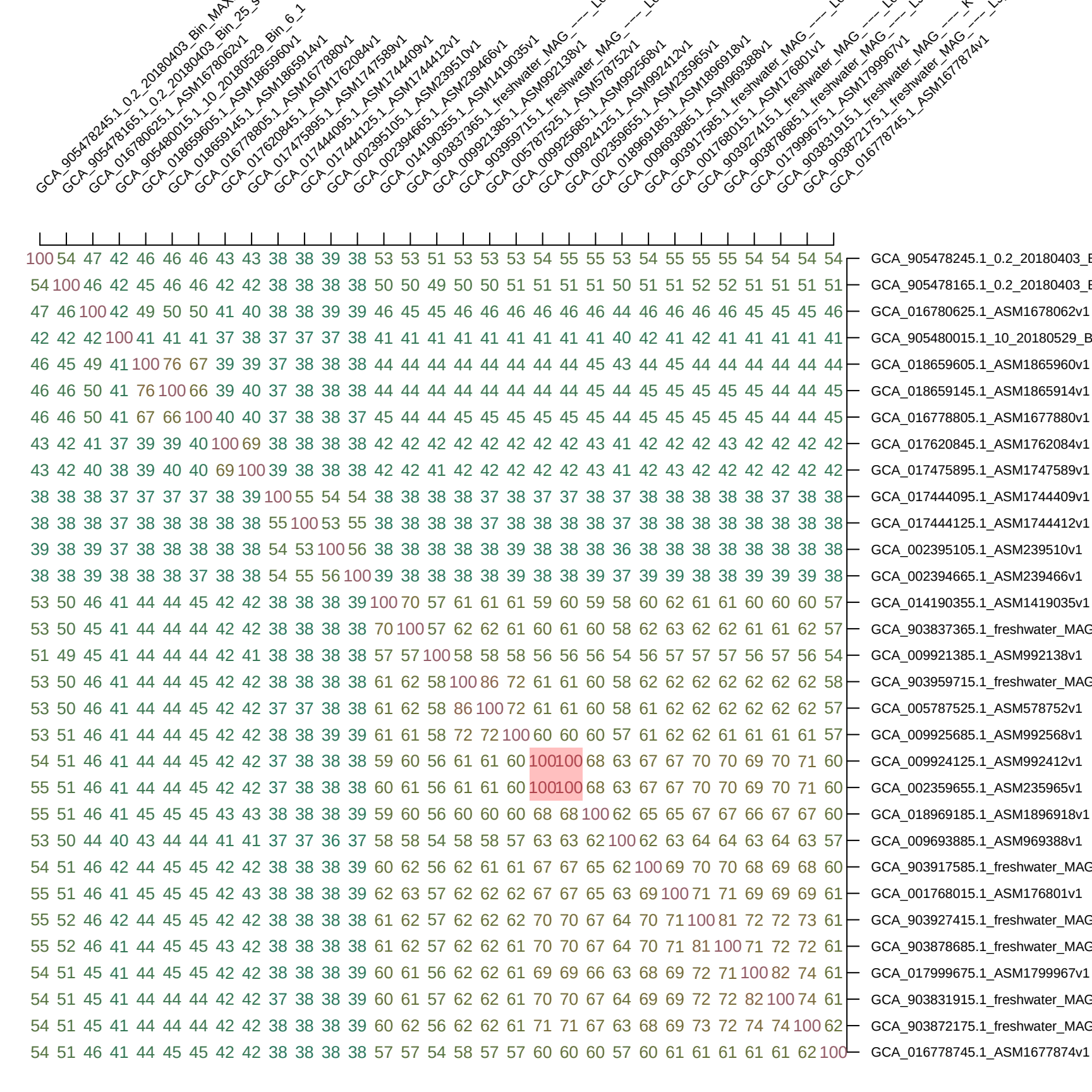
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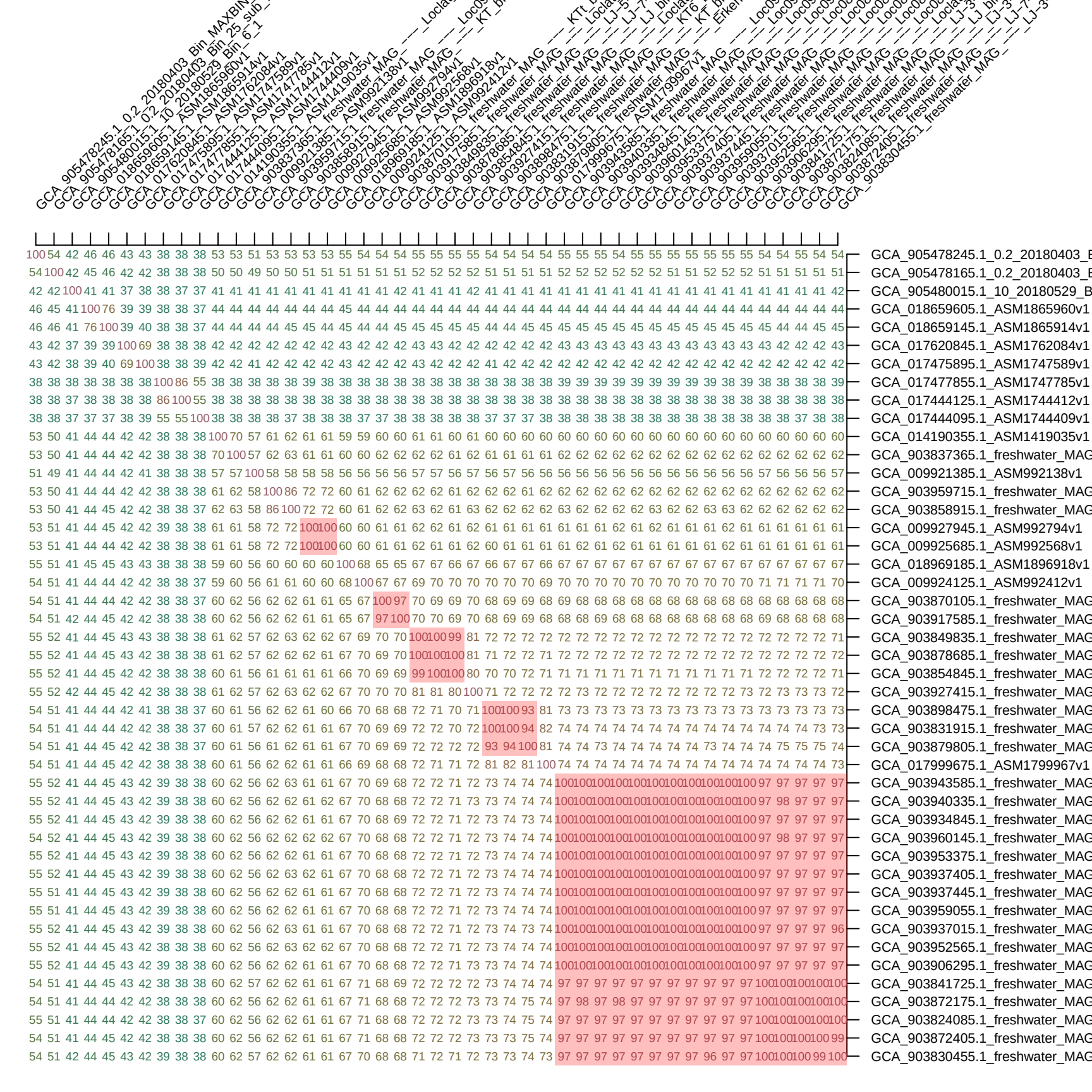

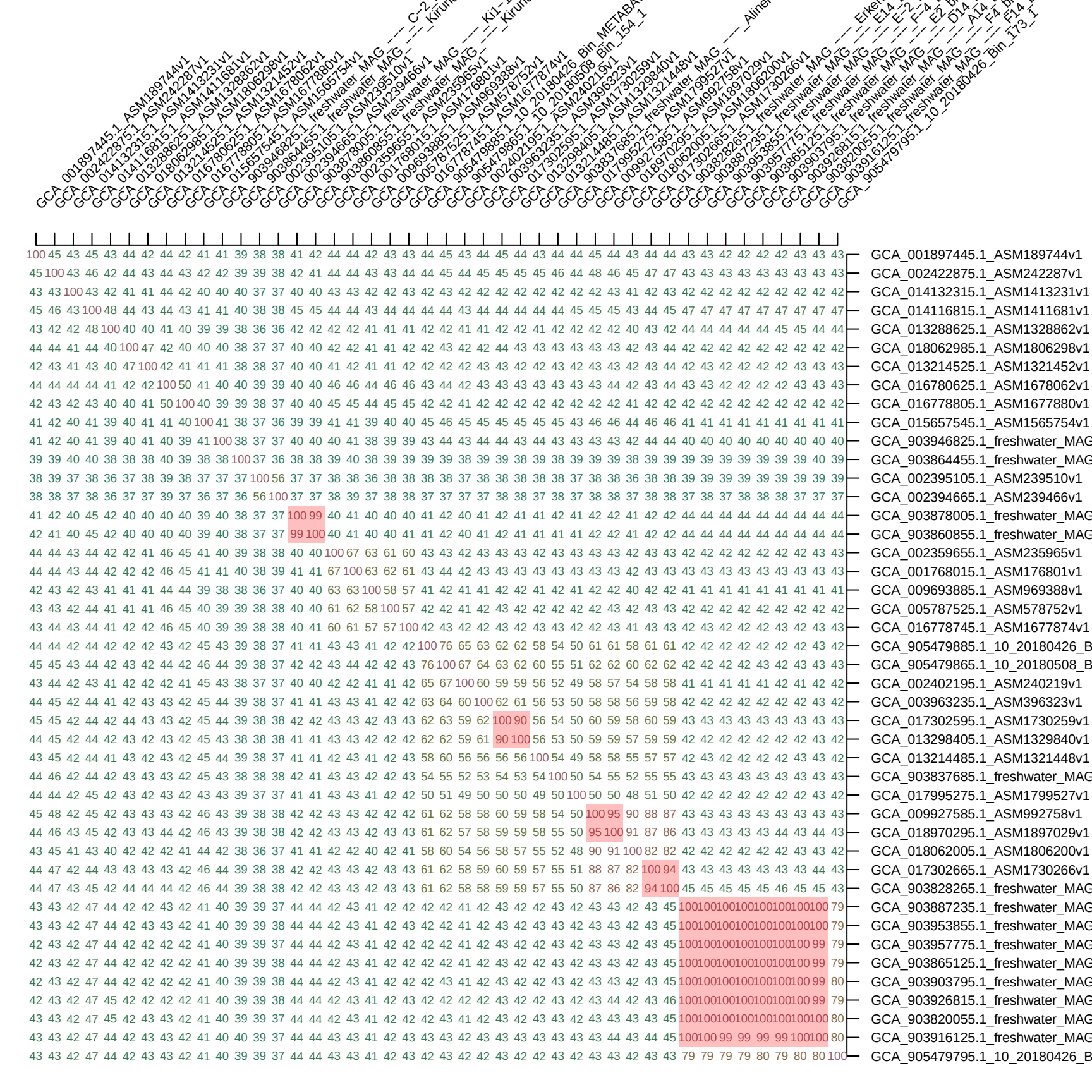
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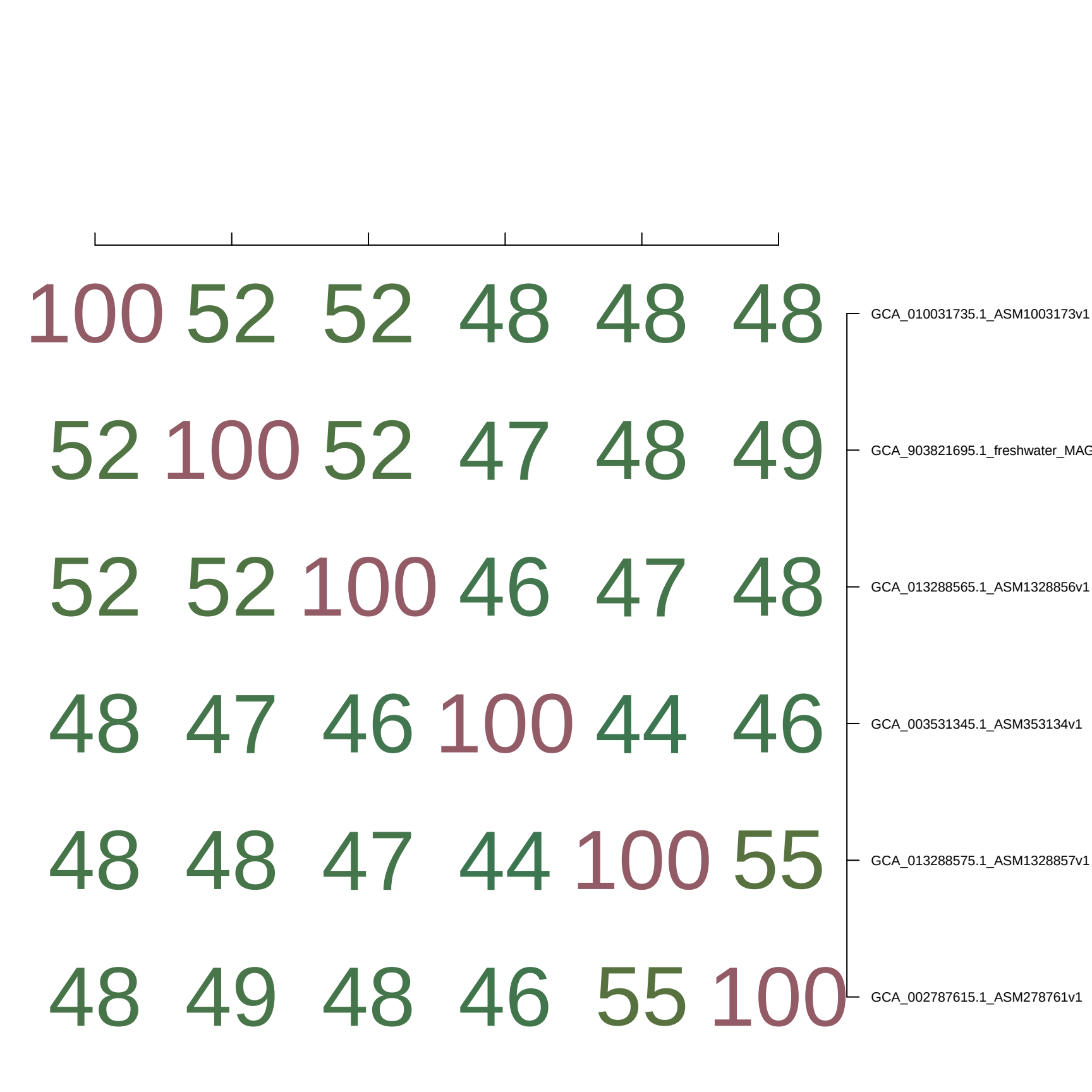
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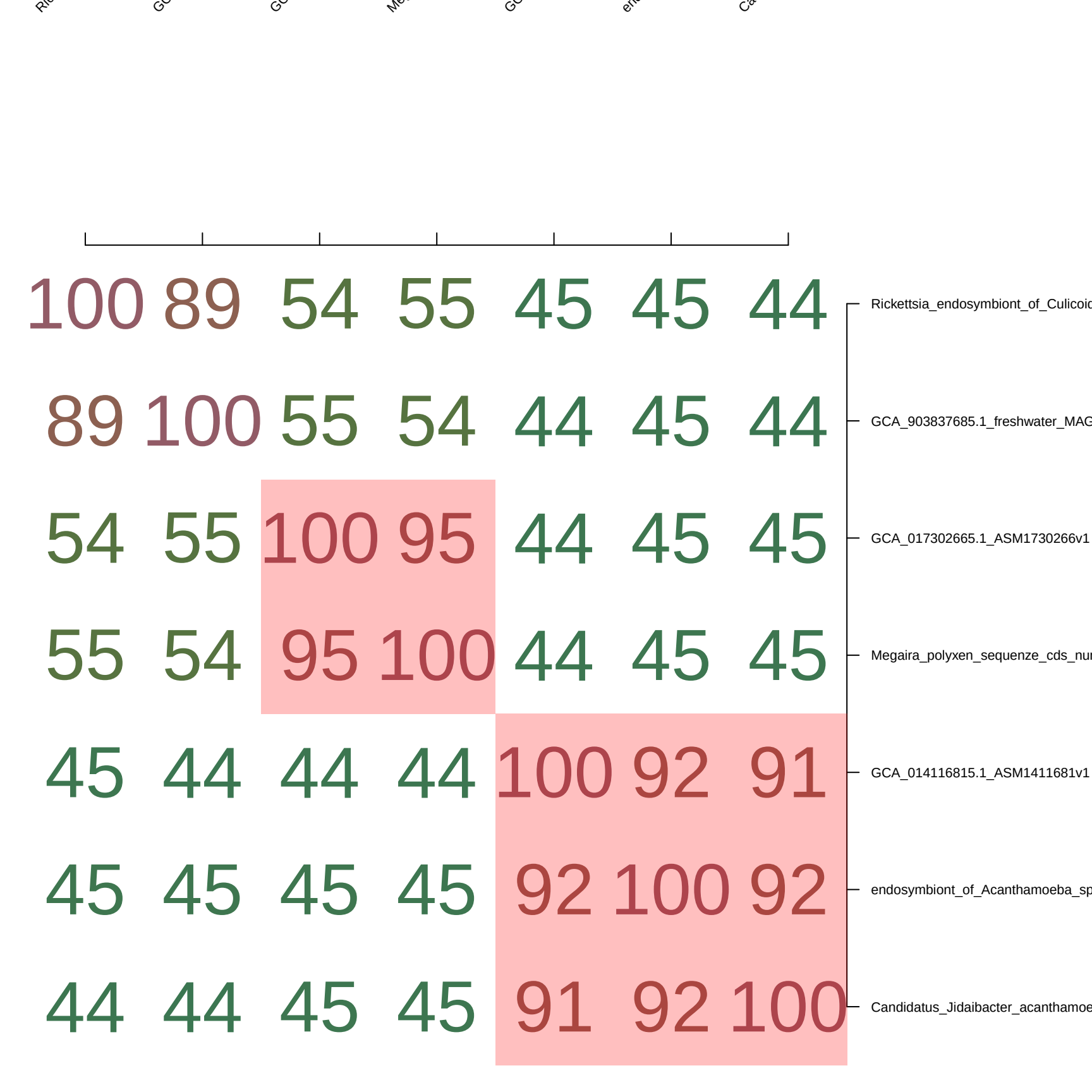
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Supplementary Figure 31: "step 5" phylogenomic trees. Phylogenomic trees of *Rickettsiales* and other *Alphaproteobacteria*, for testing the affiliation to *Rickettsiales* of the members of each previously identified MAG groups (Groups A-M; Step 5 in Supplementary Note 4). For each clade, the phylogenies on the respective untrimmed concatenated gene alignment, as well as on alignments with the 10%, 20%, 30%, 40%, or 50% most compositionally heterogeneous sites removed, are reported in order. In each tree, the investigated MAGs are highlighted in blue. On each branch, support values by SH-aLRT with 1000 replicates and by 1000 ultrafast bootstraps are reported.

Group A

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Caulobacter.vibrioides.NA1000 GCA_000022005.1_ASM2200v1
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100/100
Maricaulis.maris GCA_003634045.1_ASM363404v1
100/100
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Hirschia.baltica.ATCC.49814 GCA_000023785.1_ASM2378v1
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Sagittula.stellata.E.37 GCA_000169415.1_ASM16941v1
100/100
Ruegeria.pomeroyi.DSS.3 GCA_000011965.2_ASM1196v2
99.9/100
Octadecabacter.arcticus.238 GCA_000155735.2_ASM15573v2
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100/100
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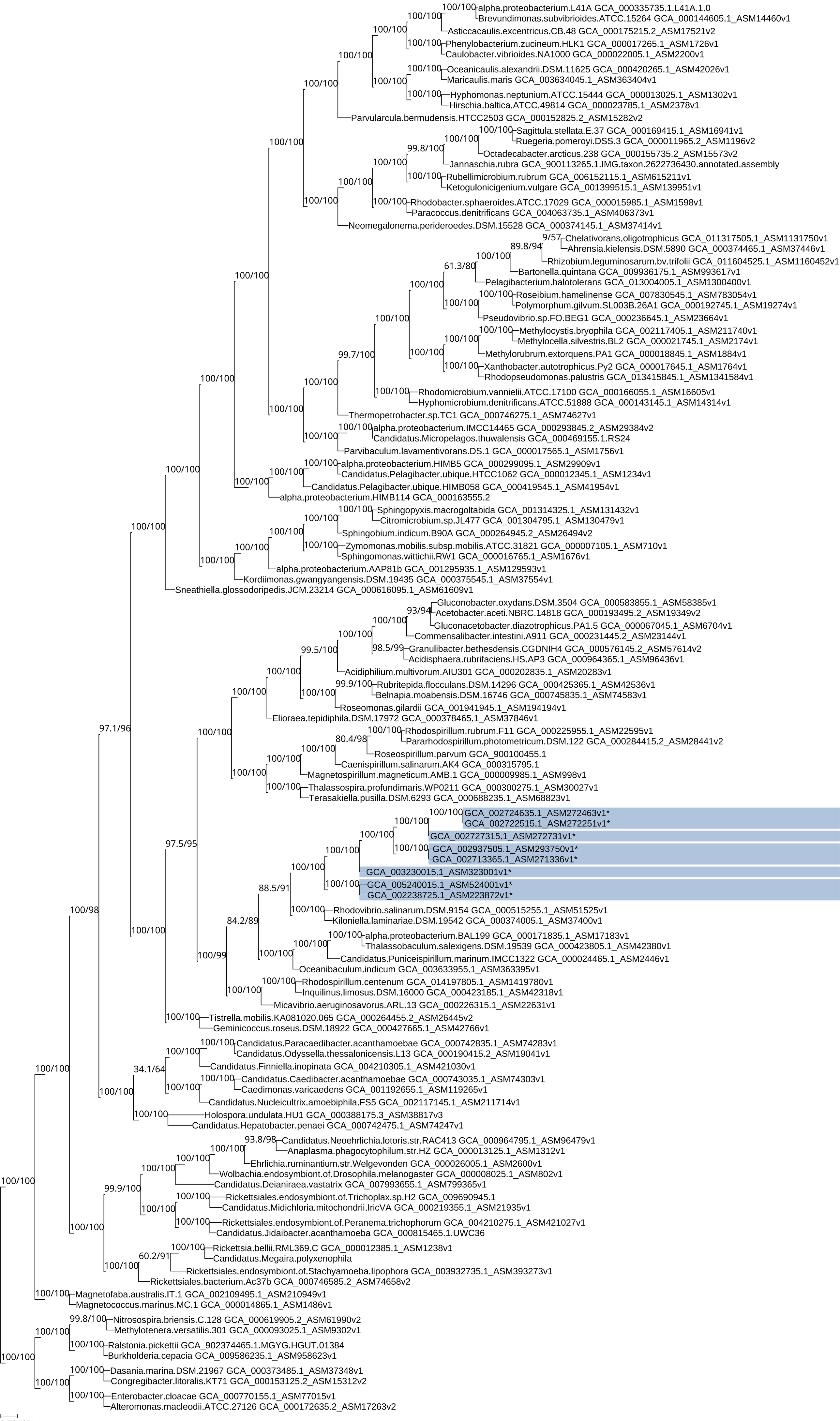
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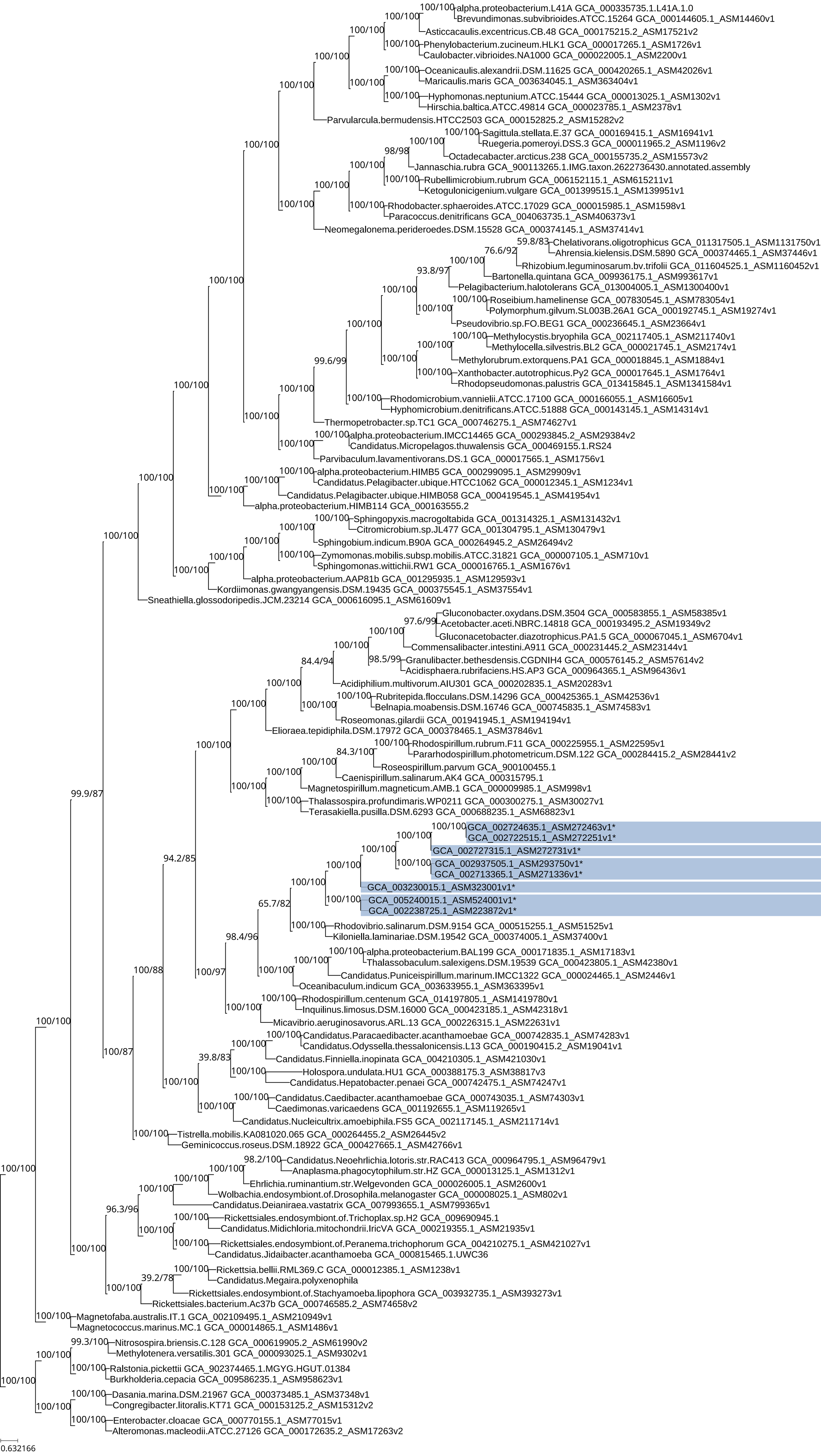
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Granulibacter.bethesdensis.CGDNIH4 GCA_000576145.2_ASM57614v2
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Acidiphilium.multivorum.AIU301 GCA_000202835.1_ASM20283v1
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Belnapia.moabensis.DSM.16746 GCA_000745835.1_ASM74583v1
Roseomonas.gilardii GCA_001941945.1_ASM194194v1
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Rhodospirillum.rubrum.F11 GCA_000225955.1_ASM22595v1
84.3/100
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Kiloniella.laminariae.DSM.19542 GCA_000374005.1_ASM37400v1
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Oceanibaculum.indicum GCA_003633955.1_ASM363395v1
Rhodospirillum.centenum GCA_014197805.1_ASM1419780v1
Inquilinus.limosus.DSM.16000 GCA_000423185.1_ASM42318v1
Micavibrio.aeruginosavorus.ARL.13 GCA_000226315.1_ASM22631v1
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Caulobacter.vibrioides.NA1000 GCA_000022005.1_ASM2200v1
Oceanicaulis.alexandrii.DSM.11625 GCA_000420265.1_ASM42026v1
Maricaulis.maris GCA_003634045.1_ASM363404v1
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Hirschia.baltica.ATCC.49814 GCA_000023785.1_ASM2378v1
Parvularcula.bermudensis.HTCC2503 GCA_000152825.2_ASM15282v2
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Ruegeria.pomeroyi.DSS.3 GCA_000011965.2_ASM1196v2
95.7/98
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69.9/89 Ahrensia.kielensis.DSM.5890 GCA_000374465.1_ASM37446v1
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Methylocystis.bryophila GCA_002117405.1_ASM211740v1
Methylocella.silvestris.BL2 GCA_000021745.1_ASM2174v1
98.8/99 Methylorubrum.extorquens.PA1 GCA_000018845.1_ASM1884v1
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86.9/92
Rhodovibrio.salinarum.DSM.9154 GCA_000515255.1_ASM51525v1
Kiloniella.laminariae.DSM.19542 GCA_000374005.1_ASM37400v1
97.2/97
alpha.proteobacterium.BAL199 GCA_000171835.1_ASM17183v1
Thalassobaculum.salexigens.DSM.19539 GCA_000423805.1_ASM42380v1
99.7/98
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Micavibrio.aeruginosavorus.ARL.13 GCA_000226315.1_ASM22631v1
100/73
Rhodospirillum.rubrum.F11 GCA_000225955.1_ASM22595v1
90.6/98 Pararhodospirillum.photometricum.DSM.122 GCA_000284415.2_ASM28441v2
Roseospirillum.parvum GCA_900100455.1
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Thalassospira.profundimaris.WP0211 GCA_000300275.1_ASM30027v1
Terasakiella.pusilla.DSM.6293 GCA_000688235.1_ASM68823v1
Gluconobacter.oxydans.DSM.3504 GCA_000583855.1_ASM58385v1
94.7/98 Acetobacter.aceti.NBRC.14818 GCA_000193495.2_ASM19349v2
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96.9/73
Commensalibacter.intestini.A911 GCA_000231445.2_ASM23144v1
72/91 Granulibacter.bethesdensis.CGDNIH4 GCA_000576145.2_ASM57614v2
Acidisphaera.rubrifaciens.HS.AP3 GCA_000964365.1_ASM96436v1
93.5/96
Acidiphilium.multivorum.AIU301 GCA_000202835.1_ASM20283v1
Rubritepida.flocculans.DSM.14296 GCA_000425365.1_ASM42536v1
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Candidatus.Odyssella.thessalonicensis.L13 GCA_000190415.2_ASM19041v1
68.6/88 Candidatus.Finniella.inopinata GCA_004210305.1_ASM421030v1
Holospora.undulata.HU1 GCA_000388175.3_ASM38817v3
Candidatus.Hepatobacter.penaei GCA_000742475.1_ASM74247v1
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Candidatus.Nucleicultrix.amoebiphila.FS5 GCA_002117145.1_ASM211714v1
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Geminicoccus.roseus.DSM.18922 GCA_000427665.1_ASM42766v1
99.8/100 Candidatus.Neoehrlichia.lotoris.str.RAC413 GCA_000964795.1_ASM96479v1
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75.9/86
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Rickettsia.bellii.RML369.C GCA_000012385.1_ASM1238v1
21.2/72 Candidatus.Megaira.polyxenophila
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Magnetococcus.marinus.MC.1 GCA_000014865.1_ASM1486v1
98.4/99 Nitrosospira.briensis.C.128 GCA_000619905.2_ASM61990v2
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Burkholderia.cepacia GCA_009586235.1_ASM958623v1
Dasania.marina.DSM.21967 GCA_000373485.1_ASM37348v1
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Phenylobacterium.zucineum.HLK1 GCA_000017265.1_ASM1726v1
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Caulobacter.vibrioides.NA1000 GCA_000022005.1_ASM2200v1
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Ruegeria.pomeroyi.DSS.3 GCA_000011965.2_ASM1196v2
85.2/89
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Kiloniella.laminariae.DSM.19542 GCA_000374005.1_ASM37400v1
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Roseospirillum.parvum GCA_900100455.1
Caenispirillum.salinarum.AK4 GCA_000315795.1
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Thalassospira.profundimaris.WP0211 GCA_000300275.1_ASM30027v1
Terasakiella.pusilla.DSM.6293 GCA_000688235.1_ASM68823v1
Gluconobacter.oxydans.DSM.3504 GCA_000583855.1_ASM58385v1
Acetobacter.aceti.NBRC.14818 GCA_000193495.2_ASM19349v2
Gluconacetobacter.diazotrophicus.PA1.5 GCA_000067045.1_ASM6704v1
Commensalibacter.intestini.A911 GCA_000231445.2_ASM23144v1
Granulibacter.bethesdensis.CGDNIH4 GCA_000576145.2_ASM57614v2
Acidisphaera.rubrifaciens.HS.AP3 GCA_000964365.1_ASM96436v1
Acidiphilium.multivorum.AIU301 GCA_000202835.1_ASM20283v1
Rubritepida.flocculans.DSM.14296 GCA_000425365.1_ASM42536v1
Belnapia.moabensis.DSM.16746 GCA_000745835.1_ASM74583v1
Roseomonas.gilardii GCA_001941945.1_ASM194194v1
Elioraea.tepidiphila.DSM.17972 GCA_000378465.1_ASM37846v1
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Candidatus.Finniella.inopinata GCA_004210305.1_ASM421030v1
Holospora.undulata.HU1 GCA_000388175.3_ASM38817v3
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Caedimonas.varicaedens GCA_001192655.1_ASM119265v1
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Tistrella.mobilis.KA081020.065 GCA_000264455.2_ASM26445v2
Geminicoccus.roseus.DSM.18922 GCA_000427665.1_ASM42766v1
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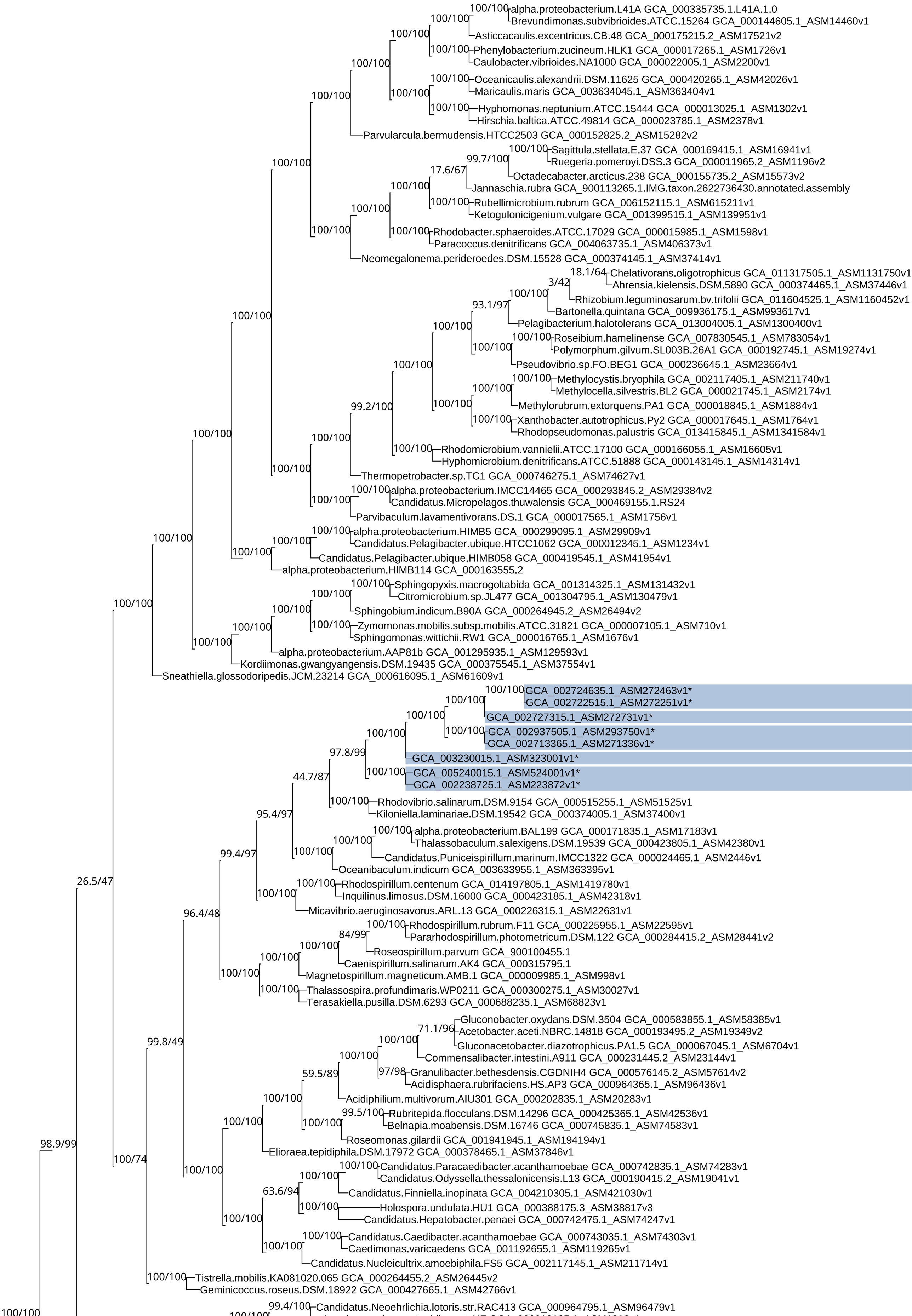
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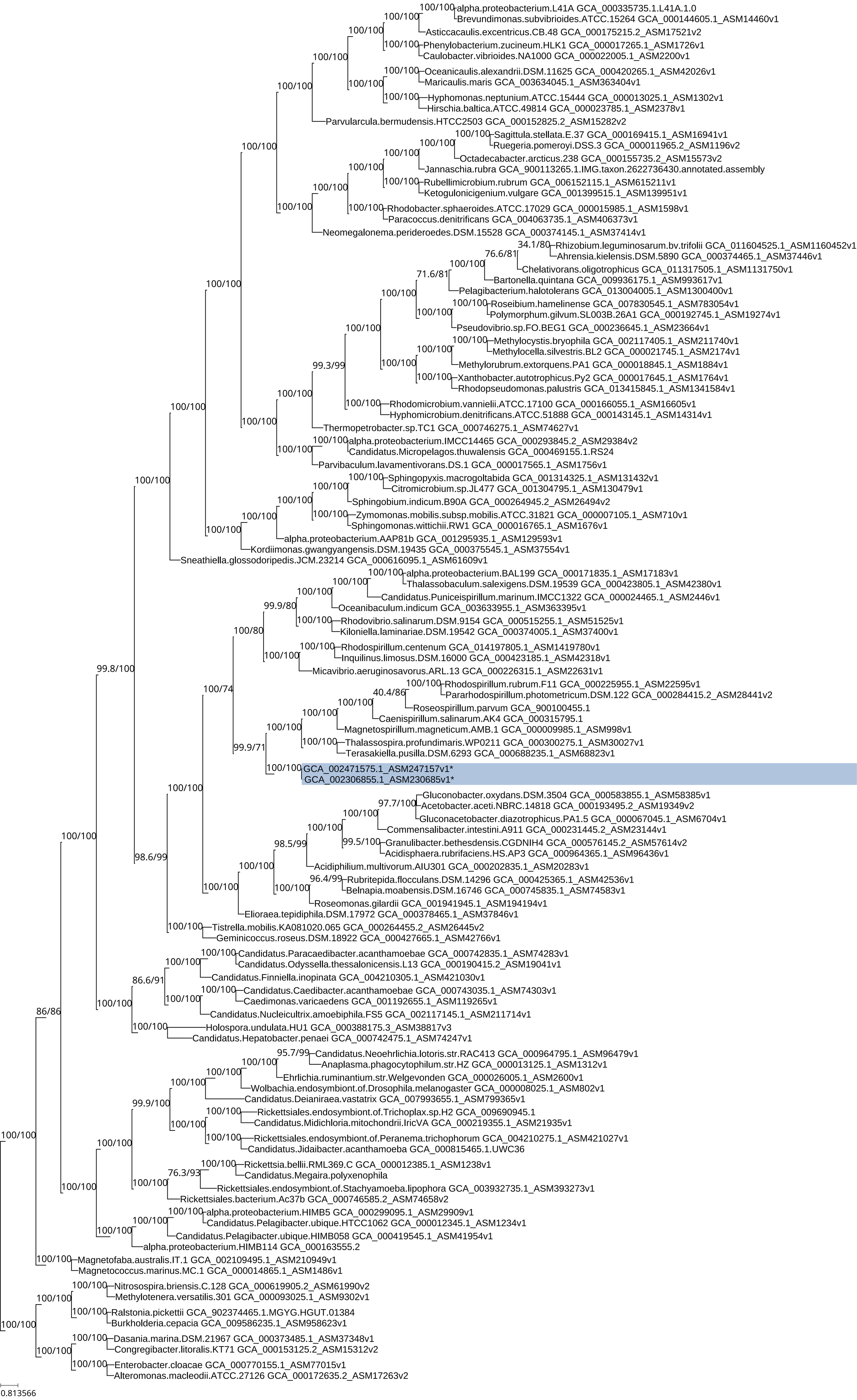
Group B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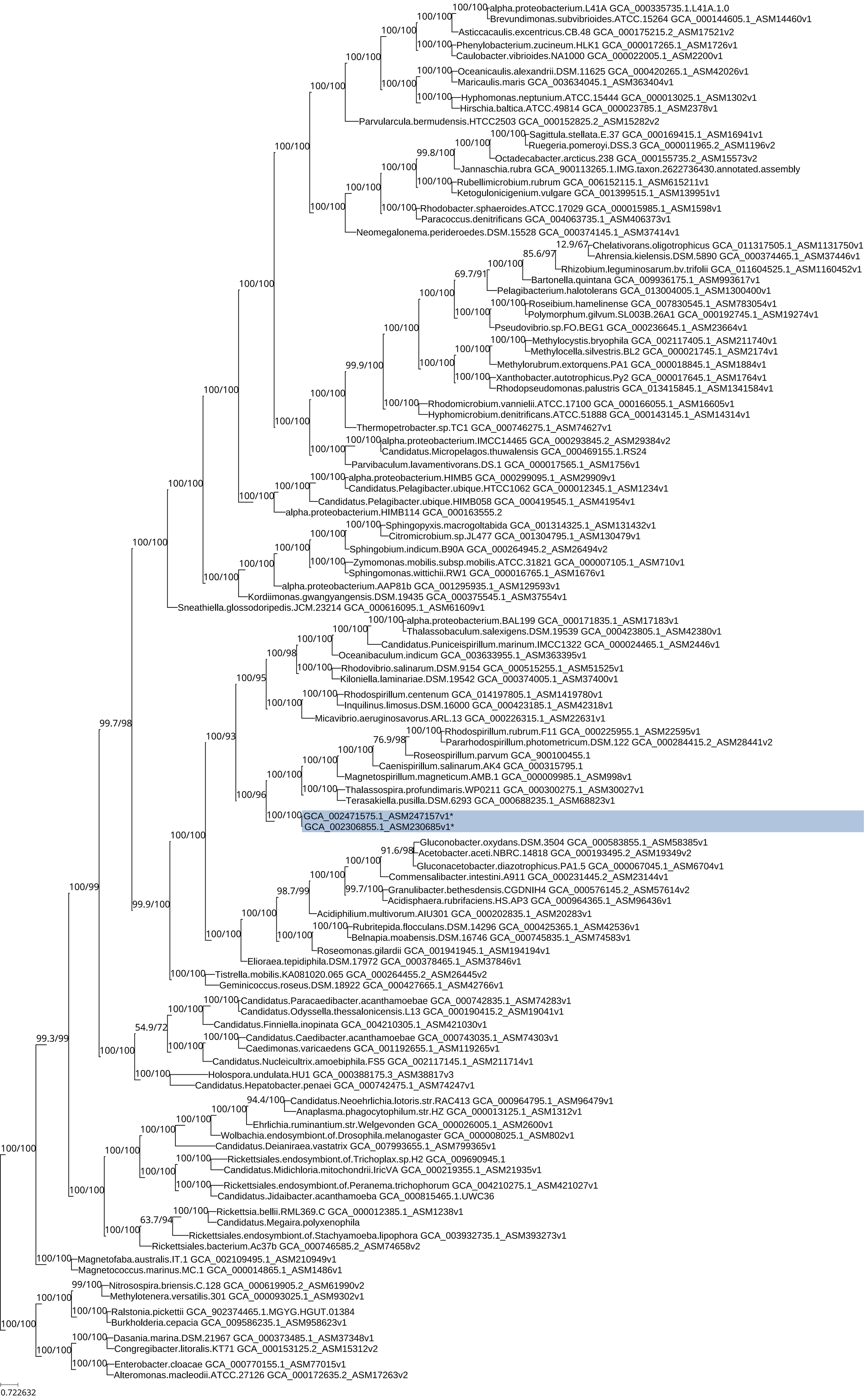
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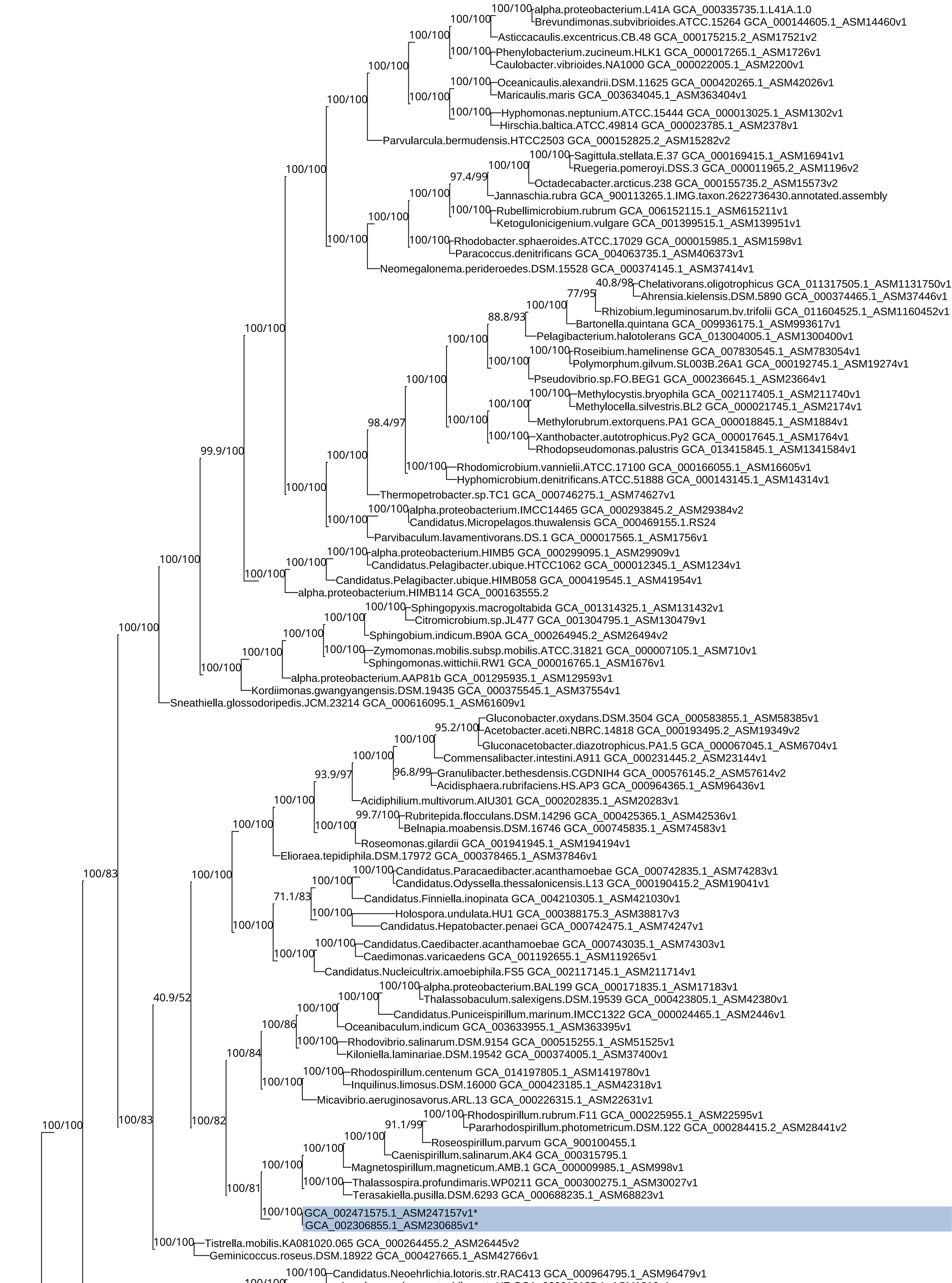
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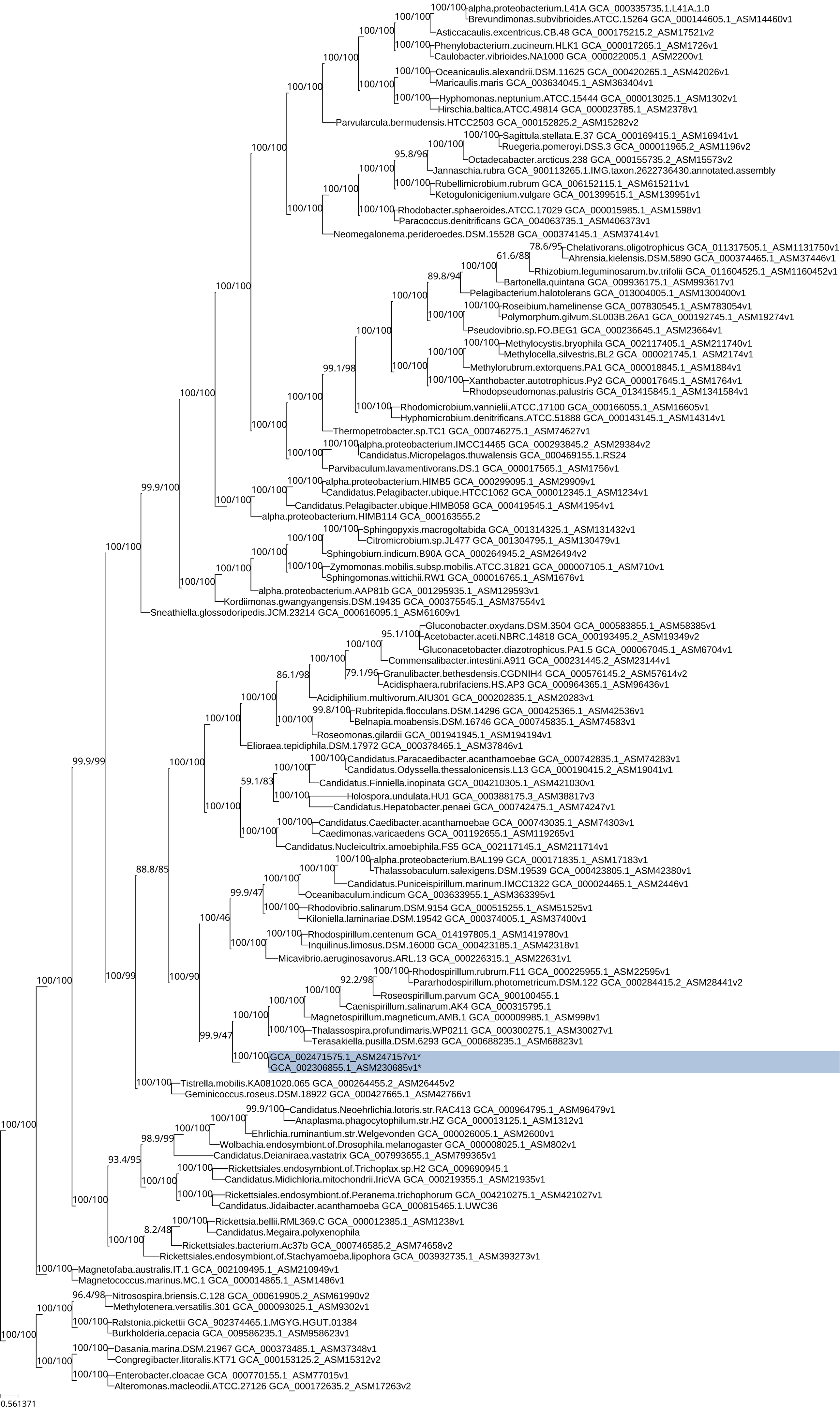
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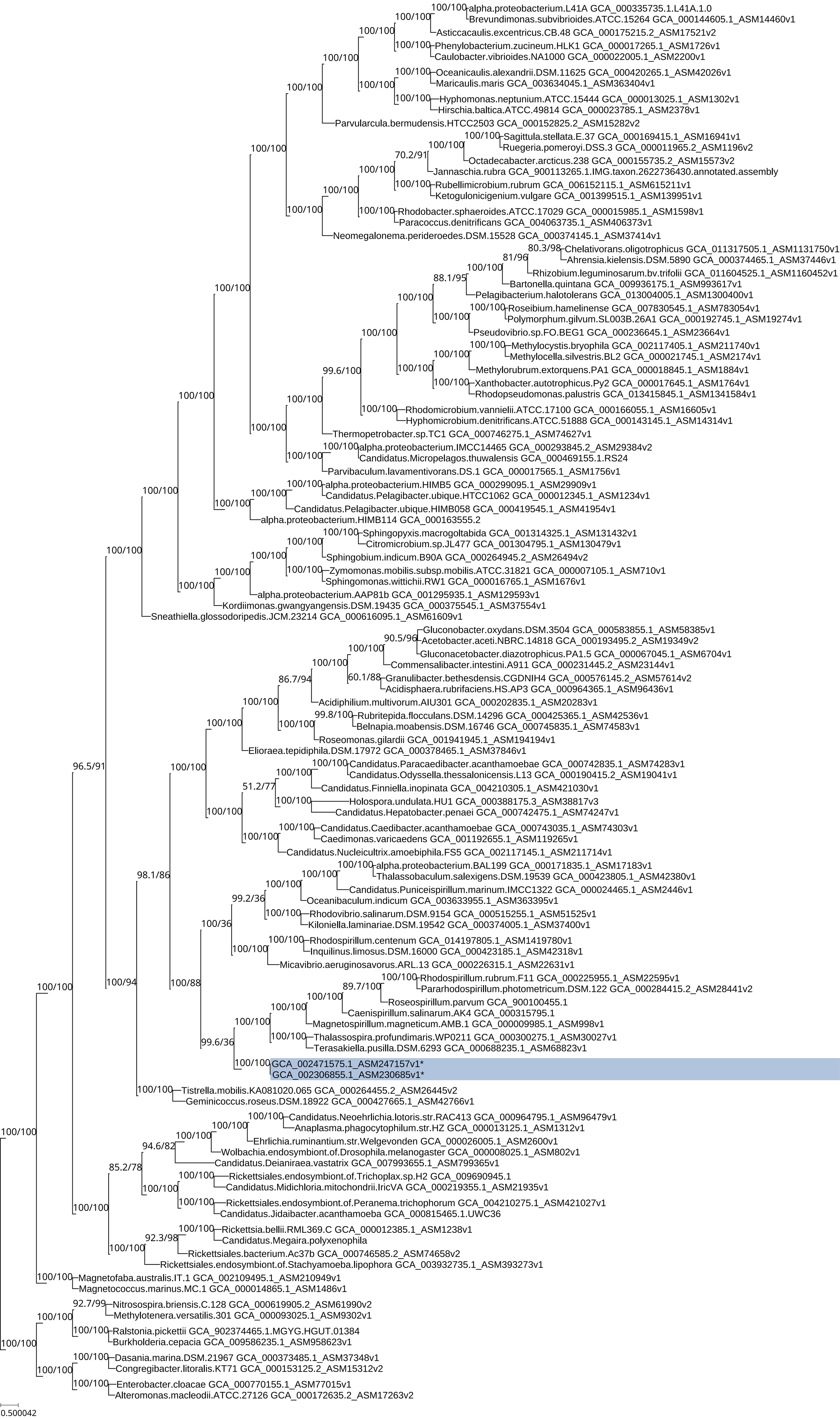
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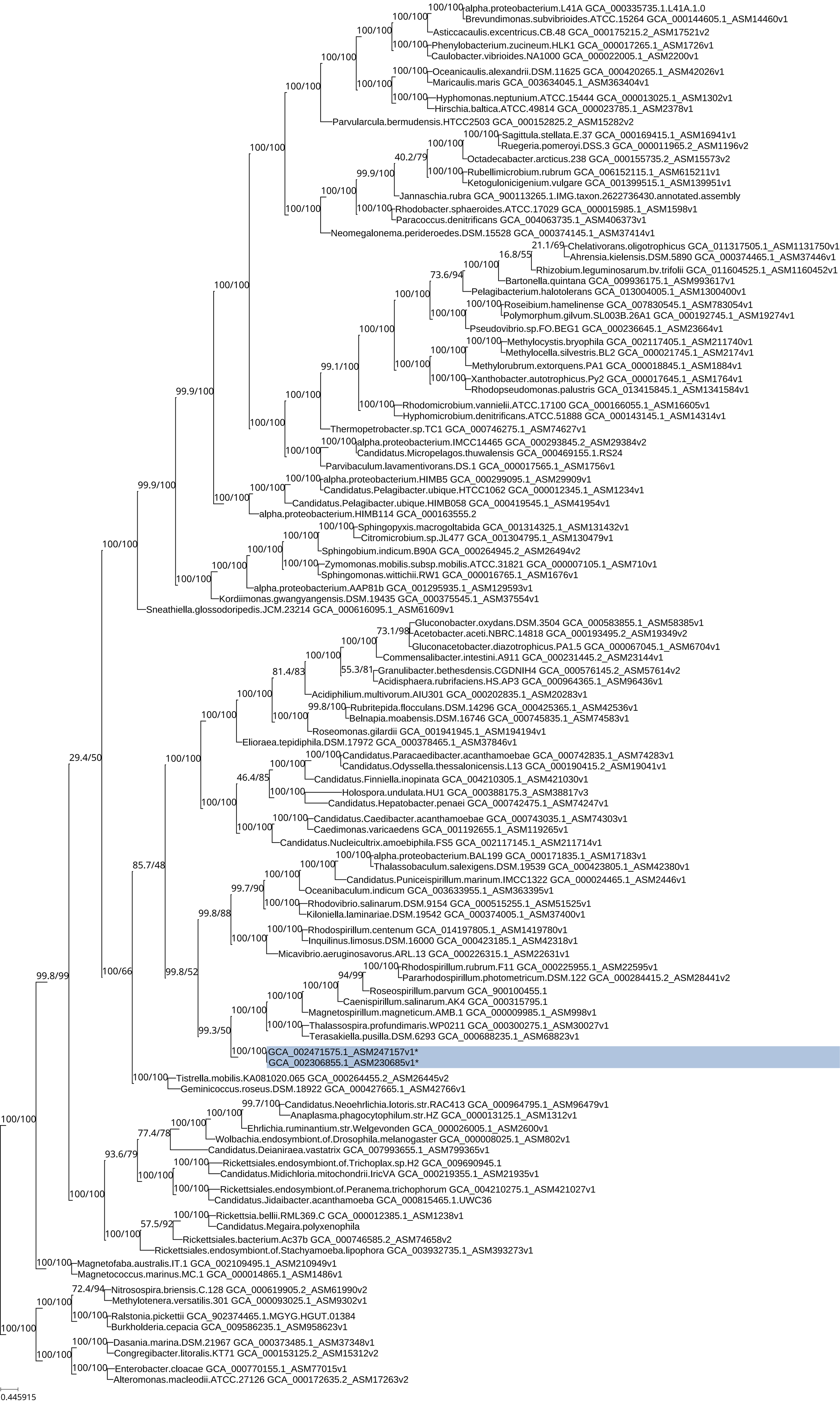
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Wolbachia.endosymbiont.of.Drosophila.melanogaster GCA_000008025.1_ASM802v1
Candidatus.Deianiraea.vastatrix GCA_007993655.1_ASM799365v1
93.6/79
100/100
Rickettsiales.endosymbiont.of.Trichoplax.sp.H2 GCA_009690945.1
Candidatus.Midichloria.mitochondrii.IricVA GCA_000219355.1_ASM21935v1
100/100
Rickettsiales.endosymbiont.of.Peranema.trichophorum GCA_004210275.1_ASM421027v1
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Rickettsia.bellii.RML369.C GCA_000012385.1_ASM1238v1
57.5/92
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100/100
Magnetofaba.australis.IT.1 GCA_002109495.1_ASM210949v1
Magnetococcus.marinus.MC.1 GCA_000014865.1_ASM1486v1
72.4/94
Nitrosospira.briensis.C.128 GCA_000619905.2_ASM61990v2
Methylotenera.versatilis.301 GCA_000093025.1_ASM9302v1
100/100
Ralstonia.pickettii GCA_902374465.1.MGYG.HGUT.01384
Burkholderia.cepacia GCA_009586235.1_ASM958623v1
100/100
Dasania.marina.DSM.21967 GCA_000373485.1_ASM37348v1
Congregibacter.litoralis.KT71 GCA_000153125.2_ASM15312v2
100/100
Enterobacter.cloacae GCA_000770155.1_ASM77015v1
Alteromonas.macleodii.ATCC.27126 GCA_000172635.2_ASM17263v2
0.445915

Group C

100/100
alpha.proteobacterium.L41A GCA_000335735.1.L41A.1.0
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Asticcacaulis.excentricus.CB.48 GCA_000175215.2_ASM17521v2
Phenylobacterium.zucineum.HLK1 GCA_000017265.1_ASM1726v1
Caulobacter.vibrioides.NA1000 GCA_000022005.1_ASM2200v1
Oceanicaulis.alexandrii.DSM.11625 GCA_000420265.1_ASM42026v1
Maricaulis.maris GCA_003634045.1_ASM363404v1
Hyphomonas.neptunium.ATCC.15444 GCA_000013025.1_ASM1302v1
Hirschia.baltica.ATCC.49814 GCA_000023785.1_ASM2378v1
Parvularcula.bermudensis.HTCC2503 GCA_000152825.2_ASM15282v2
Sagittula.stellata.E.37 GCA_000169415.1_ASM16941v1
Ruegeria.pomeroyi.DSS.3 GCA_000011965.2_ASM1196v2
Octadecabacter.arcticus.238 GCA_000155735.2_ASM15573v2
Jannaschia.rubra GCA_900113265.1.IMG.taxon.2622736430.annotated.assembly
Rubellimicrobium.rubrum GCA_006152115.1_ASM615211v1
Ketogulonicigenium.vulgare GCA_001399515.1_ASM139951v1
Rhodobacter.sphaeroides.ATCC.17029 GCA_000015985.1_ASM1598v1
Paracoccus.denitrificans GCA_004063735.1_ASM406373v1
Neomegalonema.perideroedes.DSM.15528 GCA_000374145.1_ASM37414v1
11.2/68
Rhizobium.leguminosarum.bv.trifolii GCA_011604525.1_ASM1160452v1
56.3/88
Ahrensia.kielensis.DSM.5890 GCA_000374465.1_ASM37446v1
Chelativorans.oligotrophicus GCA_011317505.1_ASM1131750v1
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Bartonella.quintana GCA_009936175.1_ASM993617v1
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Pseudovibrio.sp.FO.BEG1 GCA_000236645.1_ASM23664v1
Methylocystis.bryophila GCA_002117405.1_ASM211740v1
Methylocella.silvestris.BL2 GCA_000021745.1_ASM2174v1
Methylorubrum.extorquens.PA1 GCA_000018845.1_ASM1884v1
Xanthobacter.autotrophicus.Py2 GCA_000017645.1_ASM1764v1
Rhodopseudomonas.palustris GCA_013415845.1_ASM1341584v1
99.5/99
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Zymomonas.mobilis.subsp.mobilis.ATCC.31821 GCA_000007105.1_ASM710v1
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98.2/99
63.2/82
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52.5/74
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Granulibacter.bethesdensis.CGDNIH4 GCA_000576145.2_ASM57614v2
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Acidisphaera.rubrifaciens.HS.AP3 GCA_000964365.1_ASM96436v1
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87.4/88
97.6/92
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Burkholderia.cepacia GCA_009586235.1_ASM958623v1
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Congregibacter.litoralis.KT71 GCA_000153125.2_ASM15312v2
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Alteromonas.macleodii.ATCC.27126 GCA_000172635.2_ASM17263v2
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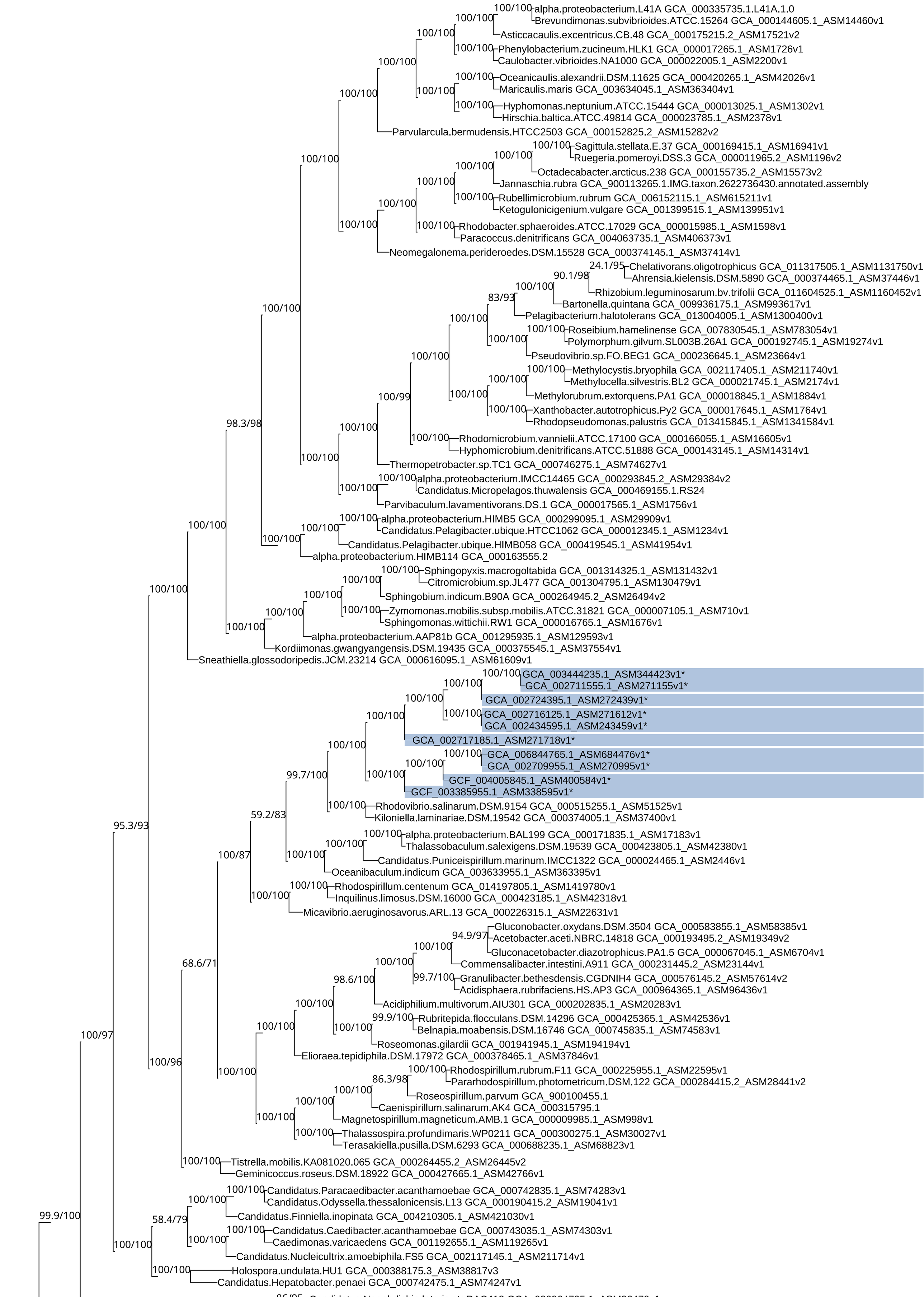
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100/100 Caulobacter.vibrioides.NA1000 GCA_000022005.1_ASM2200v1
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100/100 Sagittula.stellata.E.37 GCA_000169415.1_ASM16941v1
100/100 Ruegeria.pomeroyi.DSS.3 GCA_000011965.2_ASM1196v2
100/100 Octadecabacter.arcticus.238 GCA_000155735.2_ASM15573v2
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Paracoccus.denitrificans GCA_004063735.1_ASM406373v1
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24.1/95 Chelativorans.oligotrophicus GCA_011317505.1_ASM1131750v1
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Methylorubrum.extorquens.PA1 GCA_000018845.1_ASM1884v1
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100/100 alpha.proteobacterium.HIMB5 GCA_000299095.1_ASM29909v1
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100/100 Zymomonas.mobilis.subsp.mobilis.ATCC.31821 GCA_000007105.1_ASM710v1
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Rickettsia.bellii.RML369.C GCA_000012385.1_ASM1238v1
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98.8/100 Nitrosospira.briensis.C.128 GCA_000619905.2_ASM61990v2
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Burkholderia.cepacia GCA_009586235.1_ASM958623v1
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Congregibacter.litoralis.KT71 GCA_000153125.2_ASM15312v2
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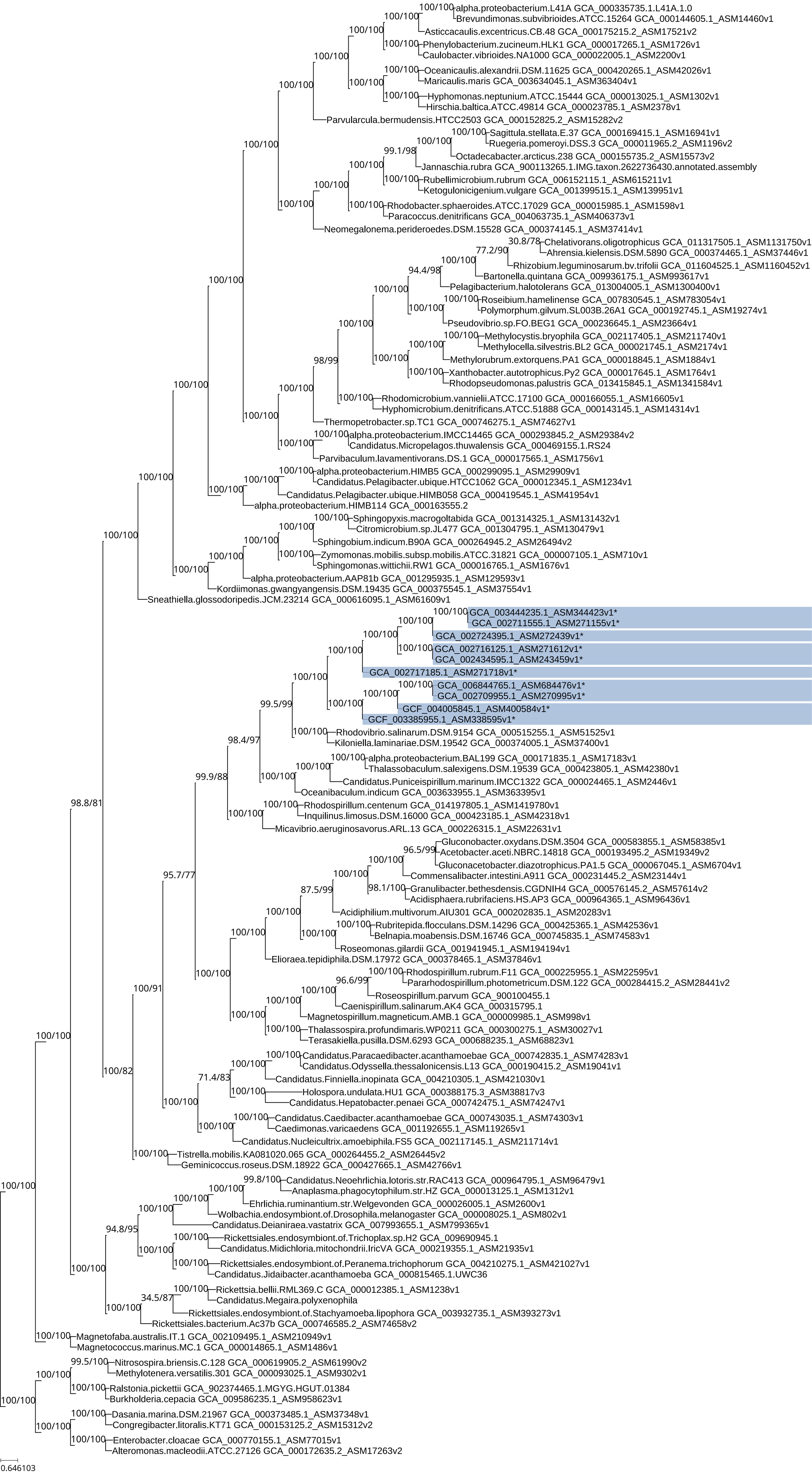
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Hirschia.baltica.ATCC.49814 GCA_000023785.1_ASM2378v1
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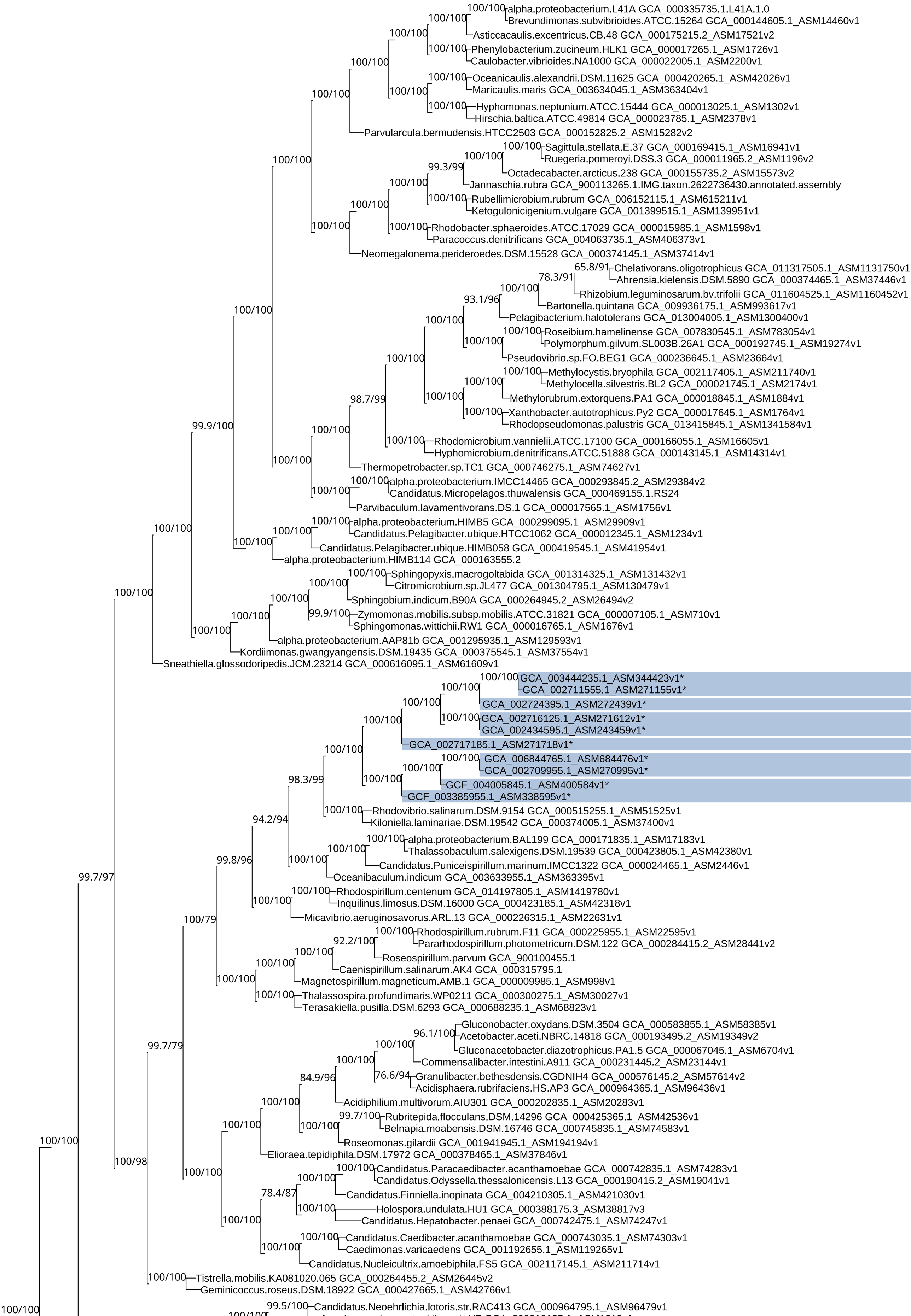
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Zymomonas.mobilis.subsp.mobilis.ATCC.31821 GCA_000007105.1_ASM710v1
Sphingomonas.wittichii.RW1 GCA_000016765.1_ASM1676v1
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99.9/70
Rhodospirillum.rubrum.F11 GCA_000225955.1_ASM22595v1
86.9/96 Pararhodospirillum.photometricum.DSM.122 GCA_000284415.2_ASM28441v2
Roseospirillum.parvum GCA_900100455.1
Caenispirillum.salinarum.AK4 GCA_000315795.1
Magnetospirillum.magneticum.AMB.1 GCA_000009985.1_ASM998v1
Thalassospira.profundimaris.WP0211 GCA_000300275.1_ASM30027v1
Terasakiella.pusilla.DSM.6293 GCA_000688235.1_ASM68823v1
Gluconobacter.oxydans.DSM.3504 GCA_000583855.1_ASM58385v1
79.1/96 Acetobacter.aceti.NBRC.14818 GCA_000193495.2_ASM19349v2
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Gluconacetobacter.diazotrophicus.PA1.5 GCA_000067045.1_ASM6704v1
Commensalibacter.intestini.A911 GCA_000231445.2_ASM23144v1
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Acidisphaera.rubrifaciens.HS.AP3 GCA_000964365.1_ASM96436v1
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94.3/99 Nitrosospira.briensis.C.128 GCA_000619905.2_ASM61990v2
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Gluconacetobacter.diazotrophicus.PA1.5 GCA_000067045.1_ASM6704v1
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88.9/99 Granulibacter.bethesdensis.CGDNIH4 GCA_000576145.2_ASM57614v2
Acidisphaera.rubrifaciens.HS.AP3 GCA_000964365.1_ASM96436v1
Acidiphilium.multivorum.AIU301 GCA_000202835.1_ASM20283v1
99.1/100 Rubritepida.flocculans.DSM.14296 GCA_000425365.1_ASM42536v1
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Elioraea.tepidiphila.DSM.17972 GCA_000378465.1_ASM37846v1
100/100 Rhodospirillum.rubrum.F11 GCA_000225955.1_ASM22595v1
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Roseospirillum.parvum GCA_900100455.1
Caenispirillum.salinarum.AK4 GCA_000315795.1
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Anaplasma.phagocytophilum.str.HZ GCA_000013125.1_ASM1312v1
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68.1/96 Nitrosospira.briensis.C.128 GCA_000619905.2_ASM61990v2
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Burkholderia.cepacia GCA_009586235.1_ASM958623v1
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Congregibacter.litoralis.KT71 GCA_000153125.2_ASM15312v2
Enterobacter.cloacae GCA_000770155.1_ASM77015v1
Alteromonas.macleodii.ATCC.27126 GCA_000172635.2_ASM17263v2
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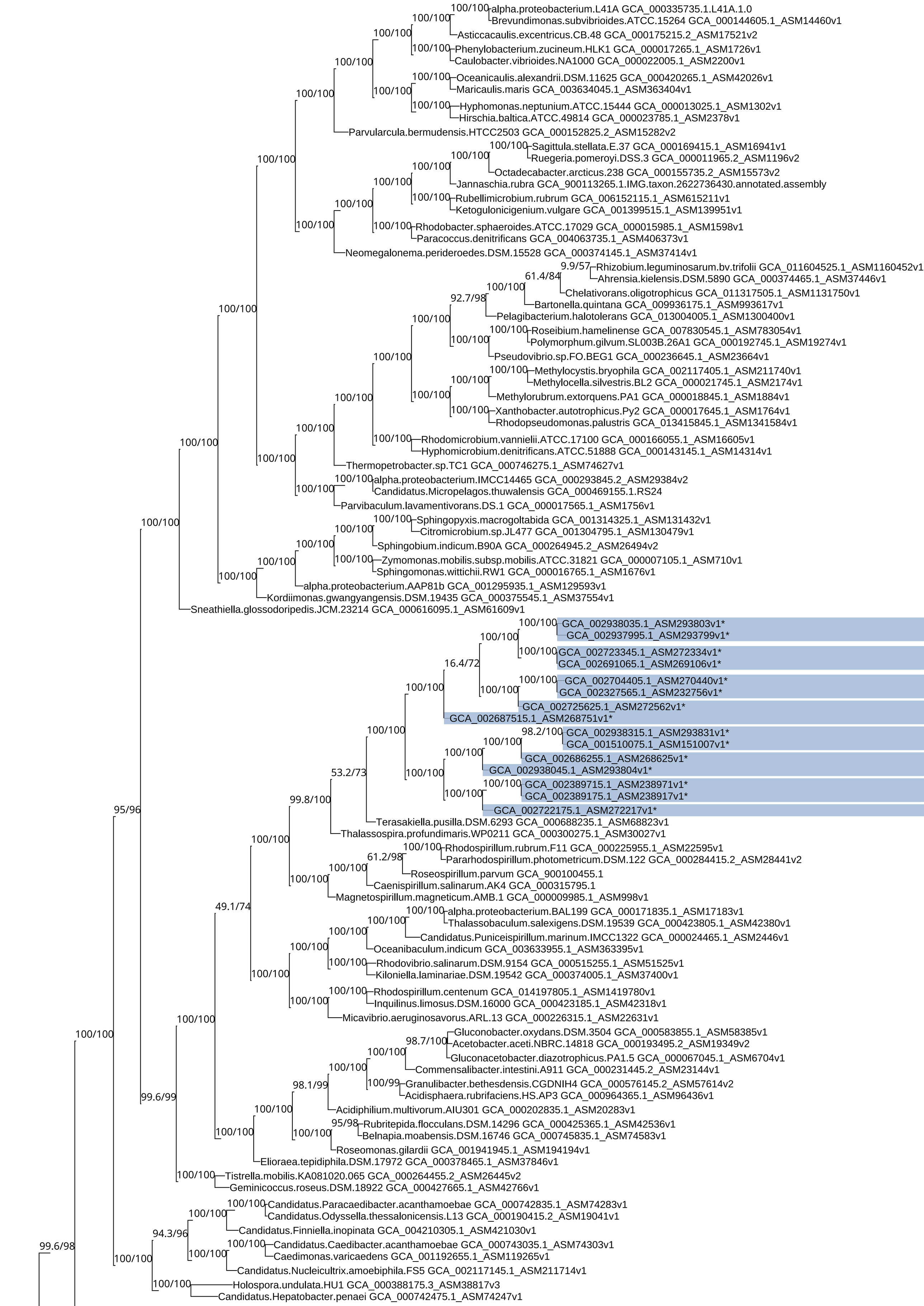
Group D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Ahrensia.kielensis.DSM.5890 GCA_000374465.1_ASM37446v1
61.4/84 Chelativorans.oligotrophicus GCA_011317505.1_ASM1131750v1
Bartonella.quintana GCA_009936175.1_ASM993617v1
92.7/98 Pelagibacterium.halotolerans GCA_013004005.1_ASM1300400v1
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Methylorubrum.extorquens.PA1 GCA_000018845.1_ASM1884v1
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Roseospirillum.parvum GCA_900100455.1
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Kiloniella.laminariae.DSM.19542 GCA_000374005.1_ASM37400v1
Rhodospirillum.centenum GCA_014197805.1_ASM1419780v1
Inquilinus.limosus.DSM.16000 GCA_000423185.1_ASM42318v1
Micavibrio.aeruginosavorus.ARL.13 GCA_000226315.1_ASM22631v1
Gluconobacter.oxydans.DSM.3504 GCA_000583855.1_ASM58385v1
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97.6/99
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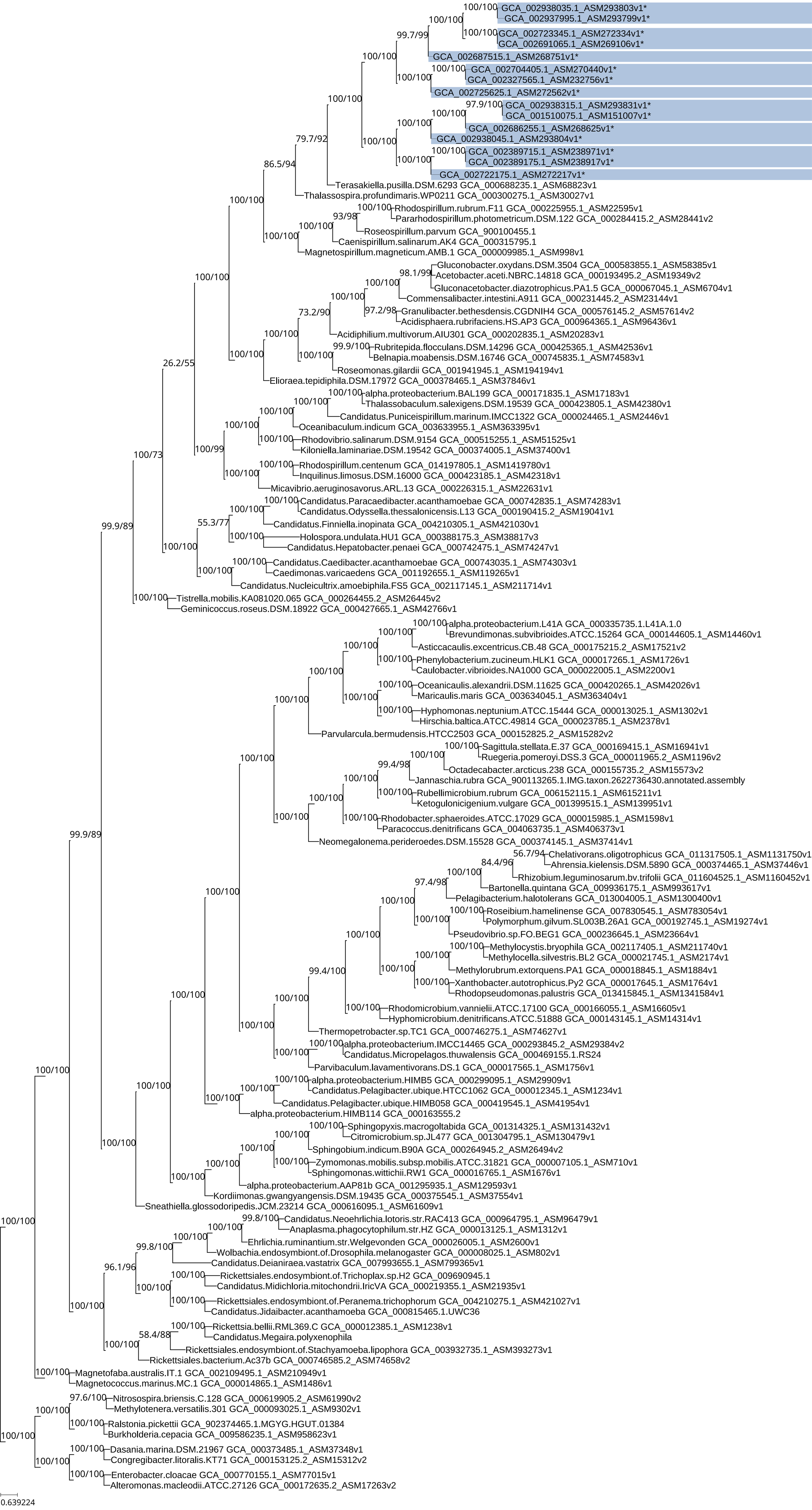
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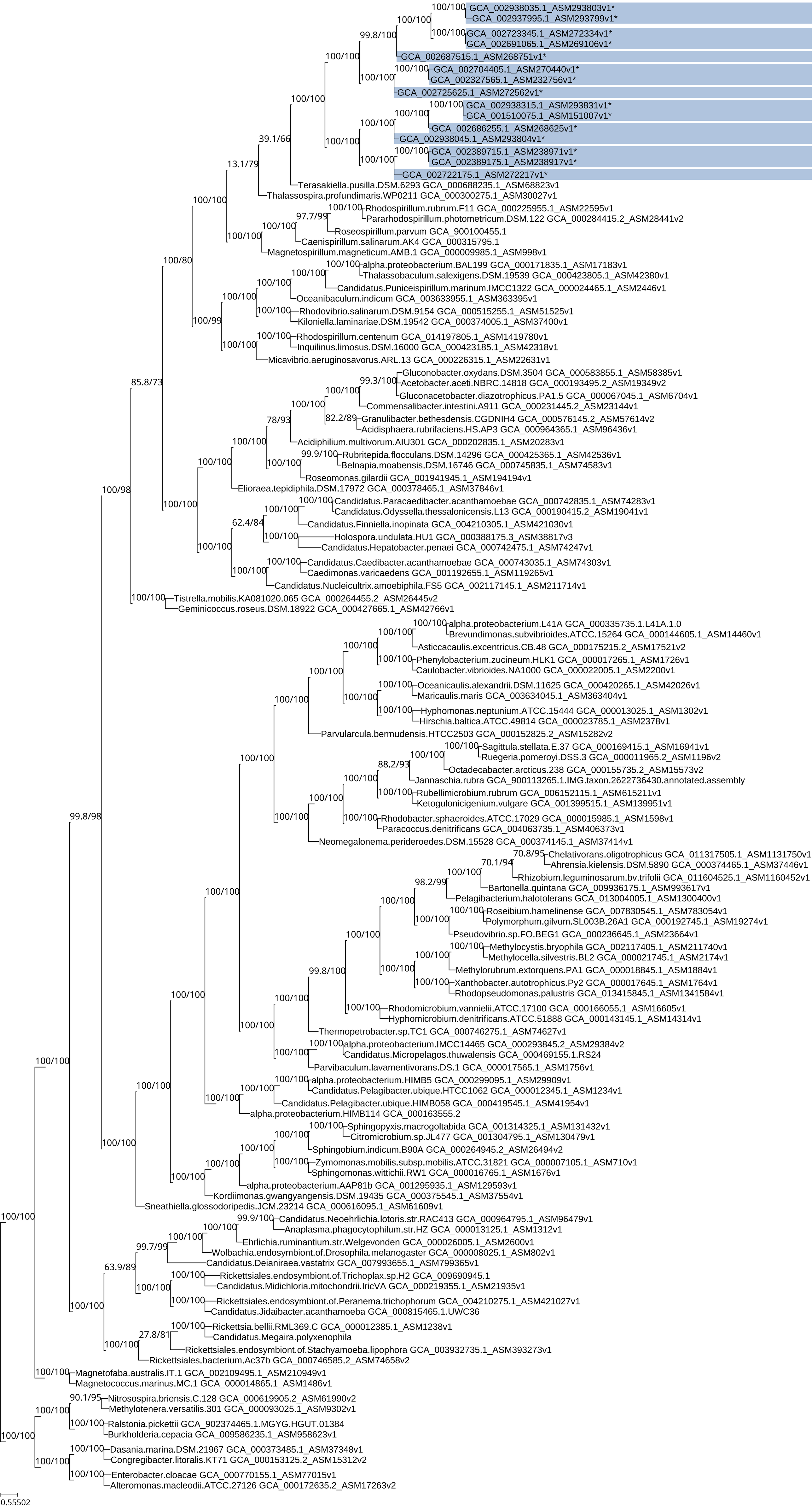
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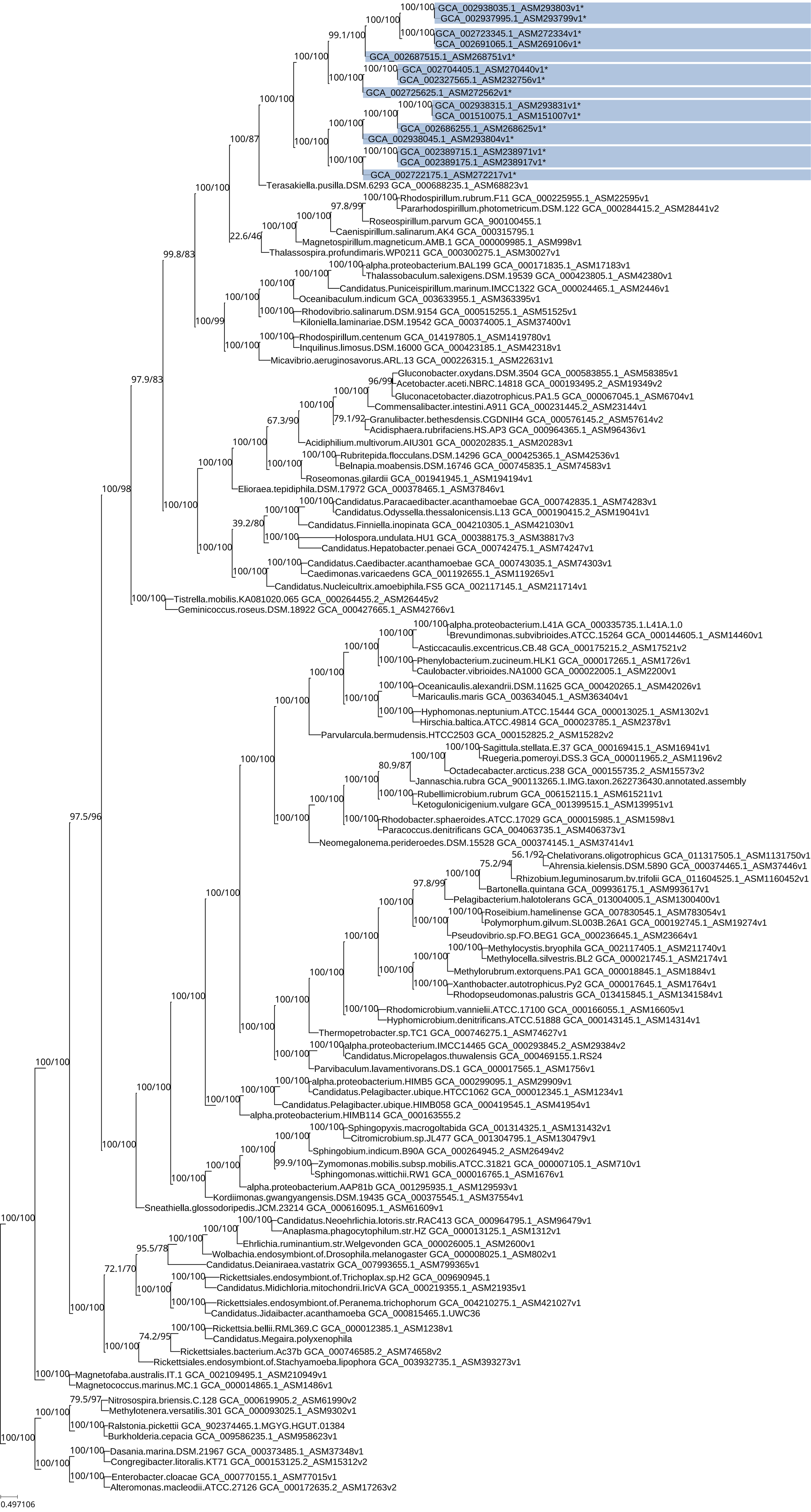
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100/100
alpha.proteobacterium.IMCC14465 GCA_000293845.2_ASM29384v2
Candidatus.Micropelagos.thuwalensis GCA_000469155.1.RS24
Parvibaculum.lavamentivorans.DS.1 GCA_000017565.1_ASM1756v1
100/100
100/100
100/100
alpha.proteobacterium.HIMB5 GCA_000299095.1_ASM29909v1
100/100
Candidatus.Pelagibacter.ubique.HTCC1062 GCA_000012345.1_ASM1234v1
100/100
Candidatus.Pelagibacter.ubique.HIMB058 GCA_000419545.1_ASM41954v1
alpha.proteobacterium.HIMB114 GCA_000163555.2
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100/100
Sphingopyxis.macrogoltabida GCA_001314325.1_ASM131432v1
Citromicrobium.sp.JL477 GCA_001304795.1_ASM130479v1
100/100
100/100
Sphingobium.indicum.B90A GCA_000264945.2_ASM26494v2
100/100
99.9/100
Zymomonas.mobilis.subsp.mobilis.ATCC.31821 GCA_000007105.1_ASM710v1
Sphingomonas.wittichii.RW1 GCA_000016765.1_ASM1676v1
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100/100
alpha.proteobacterium.AAP81b GCA_001295935.1_ASM129593v1
Kordiimonas.gwangyangensis.DSM.19435 GCA_000375545.1_ASM37554v1
Sneathiella.glossodoripedis.JCM.23214 GCA_000616095.1_ASM61609v1
100/100
100/100
Candidatus.Neoehrlichia.lotoris.str.RAC413 GCA_000964795.1_ASM96479v1
100/100
Anaplasma.phagocytophilum.str.HZ GCA_000013125.1_ASM1312v1
100/100
Ehrlichia.ruminantium.str.Welgevonden GCA_000026005.1_ASM2600v1
95.5/78
Wolbachia.endosymbiont.of.Drosophila.melanogaster GCA_000008025.1_ASM802v1
Candidatus.Deianiraea.vastatrix GCA_007993655.1_ASM799365v1
72.1/70
100/100
Rickettsiales.endosymbiont.of.Trichoplax.sp.H2 GCA_009690945.1
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Candidatus.Midichloria.mitochondrii.IricVA GCA_000219355.1_ASM21935v1
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Rickettsiales.endosymbiont.of.Peranema.trichophorum GCA_004210275.1_ASM421027v1
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Candidatus.Jidaibacter.acanthamoeba GCA_000815465.1.UWC36
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Rickettsia.bellii.RML369.C GCA_000012385.1_ASM1238v1
Candidatus.Megaira.polyxenophila
74.2/95
Rickettsiales.bacterium.Ac37b GCA_000746585.2_ASM74658v2
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Rickettsiales.endosymbiont.of.Stachyamoeba.lipophora GCA_003932735.1_ASM393273v1
100/100
100/100
Magnetofaba.australis.IT.1 GCA_002109495.1_ASM210949v1
Magnetococcus.marinus.MC.1 GCA_000014865.1_ASM1486v1
100/100
79.5/97
Nitrosospira.briensis.C.128 GCA_000619905.2_ASM61990v2
Methylotenera.versatilis.301 GCA_000093025.1_ASM9302v1
100/100
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Ralstonia.pickettii GCA_902374465.1.MGYG.HGUT.01384
Burkholderia.cepacia GCA_009586235.1_ASM958623v1
100/100
100/100
Dasania.marina.DSM.21967 GCA_000373485.1_ASM37348v1
100/100
Congregibacter.litoralis.KT71 GCA_000153125.2_ASM15312v2
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Enterobacter.cloacae GCA_000770155.1_ASM77015v1
Alteromonas.macleodii.ATCC.27126 GCA_000172635.2_ASM17263v2
0.497106

Group E

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alpha.proteobacterium.L41A GCA_000335735.1.L41A.1.0
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Brevundimonas.subvibrioides.ATCC.15264 GCA_000144605.1_ASM14460v1
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Asticcacaulis.excentricus.CB.48 GCA_000175215.2_ASM17521v2
100/100
Phenylobacterium.zucineum.HLK1 GCA_000017265.1_ASM1726v1
100/100
Caulobacter.vibrioides.NA1000 GCA_000022005.1_ASM2200v1
100/100
100/100
Oceanicaulis.alexandrii.DSM.11625 GCA_000420265.1_ASM42026v1
100/100
Maricaulis.maris GCA_003634045.1_ASM363404v1
100/100
Hyphomonas.neptunium.ATCC.15444 GCA_000013025.1_ASM1302v1
Hirschia.baltica.ATCC.49814 GCA_000023785.1_ASM2378v1
Parvularcula.bermudensis.HTCC2503 GCA_000152825.2_ASM15282v2
100/100
100/100
Sagittula.stellata.E.37 GCA_000169415.1_ASM16941v1
100/100
Ruegeria.pomeroyi.DSS.3 GCA_000011965.2_ASM1196v2
99.9/100
Octadecabacter.arcticus.238 GCA_000155735.2_ASM15573v2
Jannaschia.rubra GCA_900113265.1.IMG.taxon.2622736430.annotated.assembly
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Rubellimicrobium.rubrum GCA_006152115.1_ASM615211v1
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Ketogulonicigenium.vulgare GCA_001399515.1_ASM139951v1
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Rhodobacter.sphaeroides.ATCC.17029 GCA_000015985.1_ASM1598v1
Paracoccus.denitrificans GCA_004063735.1_ASM406373v1
Neomegalonema.perideroedes.DSM.15528 GCA_000374145.1_ASM37414v1
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Rhizobium.leguminosarum.bv.trifolii GCA_011604525.1_ASM1160452v1
75.5/91
Ahrensia.kielensis.DSM.5890 GCA_000374465.1_ASM37446v1
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Chelativorans.oligotrophicus GCA_011317505.1_ASM1131750v1
91.9/100
Bartonella.quintana GCA_009936175.1_ASM993617v1
100/100
Pelagibacterium.halotolerans GCA_013004005.1_ASM1300400v1
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Roseibium.hamelinense GCA_007830545.1_ASM783054v1
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Polymorphum.gilvum.SL003B.26A1 GCA_000192745.1_ASM19274v1
100/100
Pseudovibrio.sp.FO.BEG1 GCA_000236645.1_ASM23664v1
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Methylocystis.bryophila GCA_002117405.1_ASM211740v1
100/100
Methylocella.silvestris.BL2 GCA_000021745.1_ASM2174v1
99.7/100
100/100
Methylorubrum.extorquens.PA1 GCA_000018845.1_ASM1884v1
100/100
Xanthobacter.autotrophicus.Py2 GCA_000017645.1_ASM1764v1
Rhodopseudomonas.palustris GCA_013415845.1_ASM1341584v1
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Rhodomicrobium.vannielii.ATCC.17100 GCA_000166055.1_ASM16605v1
Hyphomicrobium.denitrificans.ATCC.51888 GCA_000143145.1_ASM14314v1
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Thermopetrobacter.sp.TC1 GCA_000746275.1_ASM74627v1
100/100
alpha.proteobacterium.IMCC14465 GCA_000293845.2_ASM29384v2
100/100
Candidatus.Micropelagos.thuwalensis GCA_000469155.1.RS24
Parvibaculum.lavamentivorans.DS.1 GCA_000017565.1_ASM1756v1
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100/100
Sphingopyxis.macrogoltabida GCA_001314325.1_ASM131432v1
100/100
Citromicrobium.sp.JL477 GCA_001304795.1_ASM130479v1
100/100
Sphingobium.indicum.B90A GCA_000264945.2_ASM26494v2
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100/100
Zymomonas.mobilis.subsp.mobilis.ATCC.31821 GCA_000007105.1_ASM710v1
Sphingomonas.wittichii.RW1 GCA_000016765.1_ASM1676v1
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alpha.proteobacterium.AAP81b GCA_001295935.1_ASM129593v1
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Kordiimonas.gwangyangensis.DSM.19435 GCA_000375545.1_ASM37554v1
Sneathiella.glossodoripedis.JCM.23214 GCA_000616095.1_ASM61609v1
Gluconobacter.oxydans.DSM.3504 GCA_000583855.1_ASM58385v1
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Acetobacter.aceti.NBRC.14818 GCA_000193495.2_ASM19349v2
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Gluconacetobacter.diazotrophicus.PA1.5 GCA_000067045.1_ASM6704v1
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Commensalibacter.intestini.A911 GCA_000231445.2_ASM23144v1
98.5/100
99.6/100
Granulibacter.bethesdensis.CGDNIH4 GCA_000576145.2_ASM57614v2
Acidisphaera.rubrifaciens.HS.AP3 GCA_000964365.1_ASM96436v1
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Acidiphilium.multivorum.AIU301 GCA_000202835.1_ASM20283v1
97.8/100
Rubritepida.flocculans.DSM.14296 GCA_000425365.1_ASM42536v1
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Belnapia.moabensis.DSM.16746 GCA_000745835.1_ASM74583v1
Roseomonas.gilardii GCA_001941945.1_ASM194194v1
Elioraea.tepidiphila.DSM.17972 GCA_000378465.1_ASM37846v1
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47.9/85
Pararhodospirillum.photometricum.DSM.122 GCA_000284415.2_ASM28441v2
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Roseospirillum.parvum GCA_900100455.1
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Caenispirillum.salinarum.AK4 GCA_000315795.1
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Thalassospira.profundimaris.WP0211 GCA_000300275.1_ASM30027v1
Terasakiella.pusilla.DSM.6293 GCA_000688235.1_ASM68823v1
80.4/87
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alpha.proteobacterium.BAL199 GCA_000171835.1_ASM17183v1
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Rhodovibrio.salinarum.DSM.9154 GCA_000515255.1_ASM51525v1
Kiloniella.laminariae.DSM.19542 GCA_000374005.1_ASM37400v1
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Rhodospirillum.centenum GCA_014197805.1_ASM1419780v1
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Inquilinus.limosus.DSM.16000 GCA_000423185.1_ASM42318v1
Micavibrio.aeruginosavorus.ARL.13 GCA_000226315.1_ASM22631v1
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Geminicoccus.roseus.DSM.18922 GCA_000427665.1_ASM42766v1
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Candidatus.Paracaedibacter.acanthamoebae GCA_000742835.1_ASM74283v1
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Candidatus.Odyssella.thessalonicensis.L13 GCA_000190415.2_ASM19041v1
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Candidatus.Finniella.inopinata GCA_004210305.1_ASM421030v1
100/100
Candidatus.Caedibacter.acanthamoebae GCA_000743035.1_ASM74303v1
100/100
Caedimonas.varicaedens GCA_001192655.1_ASM119265v1
Candidatus.Nucleicultrix.amoebiphila.FS5 GCA_002117145.1_ASM211714v1
100/100
Holospora.undulata.HU1 GCA_000388175.3_ASM38817v3
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92.8/100
Candidatus.Neoehrlichia.lotoris.str.RAC413 GCA_000964795.1_ASM96479v1
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100/100
Ehrlichia.ruminantium.str.Welgevonden GCA_000026005.1_ASM2600v1
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Wolbachia.endosymbiont.of.Drosophila.melanogaster GCA_000008025.1_ASM802v1
Candidatus.Deianiraea.vastatrix GCA_007993655.1_ASM799365v1
100/100
100/100
Rickettsiales.endosymbiont.of.Trichoplax.sp.H2 GCA_009690945.1
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Candidatus.Midichloria.mitochondrii.IricVA GCA_000219355.1_ASM21935v1
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Rickettsiales.endosymbiont.of.Peranema.trichophorum GCA_004210275.1_ASM421027v1
Candidatus.Jidaibacter.acanthamoeba GCA_000815465.1.UWC36
100/100
100/100
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84.7/100
Candidatus.Megaira.polyxenophila
100/100
Rickettsiales.endosymbiont.of.Stachyamoeba.lipophora GCA_003932735.1_ASM393273v1
Rickettsiales.bacterium.Ac37b GCA_000746585.2_ASM74658v2
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Candidatus.Pelagibacter.ubique.HTCC1062 GCA_000012345.1_ASM1234v1
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Candidatus.Pelagibacter.ubique.HIMB058 GCA_000419545.1_ASM41954v1
alpha.proteobacterium.HIMB114 GCA_000163555.2
99.1/100
100/100
Magnetofaba.australis.IT.1 GCA_002109495.1_ASM210949v1
Magnetococcus.marinus.MC.1 GCA_000014865.1_ASM1486v1
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Nitrosospira.briensis.C.128 GCA_000619905.2_ASM61990v2
Methylotenera.versatilis.301 GCA_000093025.1_ASM9302v1
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100/100
Ralstonia.pickettii GCA_902374465.1.MGYG.HGUT.01384
Burkholderia.cepacia GCA_009586235.1_ASM958623v1
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100/100
Dasania.marina.DSM.21967 GCA_000373485.1_ASM37348v1
100/100
Congregibacter.litoralis.KT71 GCA_000153125.2_ASM15312v2
100/100
Enterobacter.cloacae GCA_000770155.1_ASM77015v1
Alteromonas.macleodii.ATCC.27126 GCA_000172635.2_ASM17263v2
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100/100 Brevundimonas.subvibrioides.ATCC.15264 GCA_000144605.1_ASM14460v1
100/100 Asticcacaulis.excentricus.CB.48 GCA_000175215.2_ASM17521v2
100/100 Phenylobacterium.zucineum.HLK1 GCA_000017265.1_ASM1726v1
100/100 Caulobacter.vibrioides.NA1000 GCA_000022005.1_ASM2200v1
100/100 Oceanicaulis.alexandrii.DSM.11625 GCA_000420265.1_ASM42026v1
100/100 Maricaulis.maris GCA_003634045.1_ASM363404v1
100/100 Hyphomonas.neptunium.ATCC.15444 GCA_000013025.1_ASM1302v1
Hirschia.baltica.ATCC.49814 GCA_000023785.1_ASM2378v1
Parvularcula.bermudensis.HTCC2503 GCA_000152825.2_ASM15282v2
100/100 Sagittula.stellata.E.37 GCA_000169415.1_ASM16941v1
100/100 Ruegeria.pomeroyi.DSS.3 GCA_000011965.2_ASM1196v2
99.8/99 Octadecabacter.arcticus.238 GCA_000155735.2_ASM15573v2
Jannaschia.rubra GCA_900113265.1.IMG.taxon.2622736430.annotated.assembly
100/100 Rubellimicrobium.rubrum GCA_006152115.1_ASM615211v1
Ketogulonicigenium.vulgare GCA_001399515.1_ASM139951v1
100/100 Rhodobacter.sphaeroides.ATCC.17029 GCA_000015985.1_ASM1598v1
Paracoccus.denitrificans GCA_004063735.1_ASM406373v1
Neomegalonema.perideroedes.DSM.15528 GCA_000374145.1_ASM37414v1
3.2/54 Chelativorans.oligotrophicus GCA_011317505.1_ASM1131750v1
85.9/92 Ahrensia.kielensis.DSM.5890 GCA_000374465.1_ASM37446v1
100/100 Rhizobium.leguminosarum.bv.trifolii GCA_011604525.1_ASM1160452v1
86/90 Bartonella.quintana GCA_009936175.1_ASM993617v1
Pelagibacterium.halotolerans GCA_013004005.1_ASM1300400v1
100/100 Roseibium.hamelinense GCA_007830545.1_ASM783054v1
Polymorphum.gilvum.SL003B.26A1 GCA_000192745.1_ASM19274v1
Pseudovibrio.sp.FO.BEG1 GCA_000236645.1_ASM23664v1
100/100 Methylocystis.bryophila GCA_002117405.1_ASM211740v1
Methylocella.silvestris.BL2 GCA_000021745.1_ASM2174v1
Methylorubrum.extorquens.PA1 GCA_000018845.1_ASM1884v1
Xanthobacter.autotrophicus.Py2 GCA_000017645.1_ASM1764v1
Rhodopseudomonas.palustris GCA_013415845.1_ASM1341584v1
Rhodomicrobium.vannielii.ATCC.17100 GCA_000166055.1_ASM16605v1
Hyphomicrobium.denitrificans.ATCC.51888 GCA_000143145.1_ASM14314v1
Thermopetrobacter.sp.TC1 GCA_000746275.1_ASM74627v1
alpha.proteobacterium.IMCC14465 GCA_000293845.2_ASM29384v2
Candidatus.Micropelagos.thuwalensis GCA_000469155.1.RS24
Parvibaculum.lavamentivorans.DS.1 GCA_000017565.1_ASM1756v1
alpha.proteobacterium.HIMB5 GCA_000299095.1_ASM29909v1
Candidatus.Pelagibacter.ubique.HTCC1062 GCA_000012345.1_ASM1234v1
Candidatus.Pelagibacter.ubique.HIMB058 GCA_000419545.1_ASM41954v1
alpha.proteobacterium.HIMB114 GCA_000163555.2
Sphingopyxis.macrogoltabida GCA_001314325.1_ASM131432v1
Citromicrobium.sp.JL477 GCA_001304795.1_ASM130479v1
Sphingobium.indicum.B90A GCA_000264945.2_ASM26494v2
Zymomonas.mobilis.subsp.mobilis.ATCC.31821 GCA_000007105.1_ASM710v1
Sphingomonas.wittichii.RW1 GCA_000016765.1_ASM1676v1
alpha.proteobacterium.AAP81b GCA_001295935.1_ASM129593v1
Kordiimonas.gwangyangensis.DSM.19435 GCA_000375545.1_ASM37554v1
Sneathiella.glossodoripedis.JCM.23214 GCA_000616095.1_ASM61609v1
Gluconobacter.oxydans.DSM.3504 GCA_000583855.1_ASM58385v1
97.3/100 Acetobacter.aceti.NBRC.14818 GCA_000193495.2_ASM19349v2
Gluconacetobacter.diazotrophicus.PA1.5 GCA_000067045.1_ASM6704v1
Commensalibacter.intestini.A911 GCA_000231445.2_ASM23144v1
98.3/99 99.5/100 Granulibacter.bethesdensis.CGDNIH4 GCA_000576145.2_ASM57614v2
Acidisphaera.rubrifaciens.HS.AP3 GCA_000964365.1_ASM96436v1
Acidiphilium.multivorum.AIU301 GCA_000202835.1_ASM20283v1
Rubritepida.flocculans.DSM.14296 GCA_000425365.1_ASM42536v1
Belnapia.moabensis.DSM.16746 GCA_000745835.1_ASM74583v1
Roseomonas.gilardii GCA_001941945.1_ASM194194v1
Elioraea.tepidiphila.DSM.17972 GCA_000378465.1_ASM37846v1
Rhodospirillum.rubrum.F11 GCA_000225955.1_ASM22595v1
78.9/90 Pararhodospirillum.photometricum.DSM.122 GCA_000284415.2_ASM28441v2
Roseospirillum.parvum GCA_900100455.1
Caenispirillum.salinarum.AK4 GCA_000315795.1
Magnetospirillum.magneticum.AMB.1 GCA_000009985.1_ASM998v1
Thalassospira.profundimaris.WP0211 GCA_000300275.1_ASM30027v1
Terasakiella.pusilla.DSM.6293 GCA_000688235.1_ASM68823v1
94.6/96
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Thalassobaculum.salexigens.DSM.19539 GCA_000423805.1_ASM42380v1
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Oceanibaculum.indicum GCA_003633955.1_ASM363395v1
Rhodovibrio.salinarum.DSM.9154 GCA_000515255.1_ASM51525v1
Kiloniella.laminariae.DSM.19542 GCA_000374005.1_ASM37400v1
Rhodospirillum.centenum GCA_014197805.1_ASM1419780v1
Inquilinus.limosus.DSM.16000 GCA_000423185.1_ASM42318v1
Micavibrio.aeruginosavorus.ARL.13 GCA_000226315.1_ASM22631v1
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Geminicoccus.roseus.DSM.18922 GCA_000427665.1_ASM42766v1
Candidatus.Paracaedibacter.acanthamoebae GCA_000742835.1_ASM74283v1
Candidatus.Odyssella.thessalonicensis.L13 GCA_000190415.2_ASM19041v1
Candidatus.Finniella.inopinata GCA_004210305.1_ASM421030v1
54/65
Candidatus.Caedibacter.acanthamoebae GCA_000743035.1_ASM74303v1
Caedimonas.varicaedens GCA_001192655.1_ASM119265v1
Candidatus.Nucleicultrix.amoebiphila.FS5 GCA_002117145.1_ASM211714v1
Holospora.undulata.HU1 GCA_000388175.3_ASM38817v3
Candidatus.Hepatobacter.penaei GCA_000742475.1_ASM74247v1
89.6/94 Candidatus.Neoehrlichia.lotoris.str.RAC413 GCA_000964795.1_ASM96479v1
Anaplasma.phagocytophilum.str.HZ GCA_000013125.1_ASM1312v1
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Wolbachia.endosymbiont.of.Drosophila.melanogaster GCA_000008025.1_ASM802v1
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82.8/88 Octadecabacter.arcticus.238 GCA_000155735.2_ASM15573v2
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Paracoccus.denitrificans GCA_004063735.1_ASM406373v1
Neomegalonema.perideroedes.DSM.15528 GCA_000374145.1_ASM37414v1
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83.1/93 Ahrensia.kielensis.DSM.5890 GCA_000374465.1_ASM37446v1
Rhizobium.leguminosarum.bv.trifolii GCA_011604525.1_ASM1160452v1
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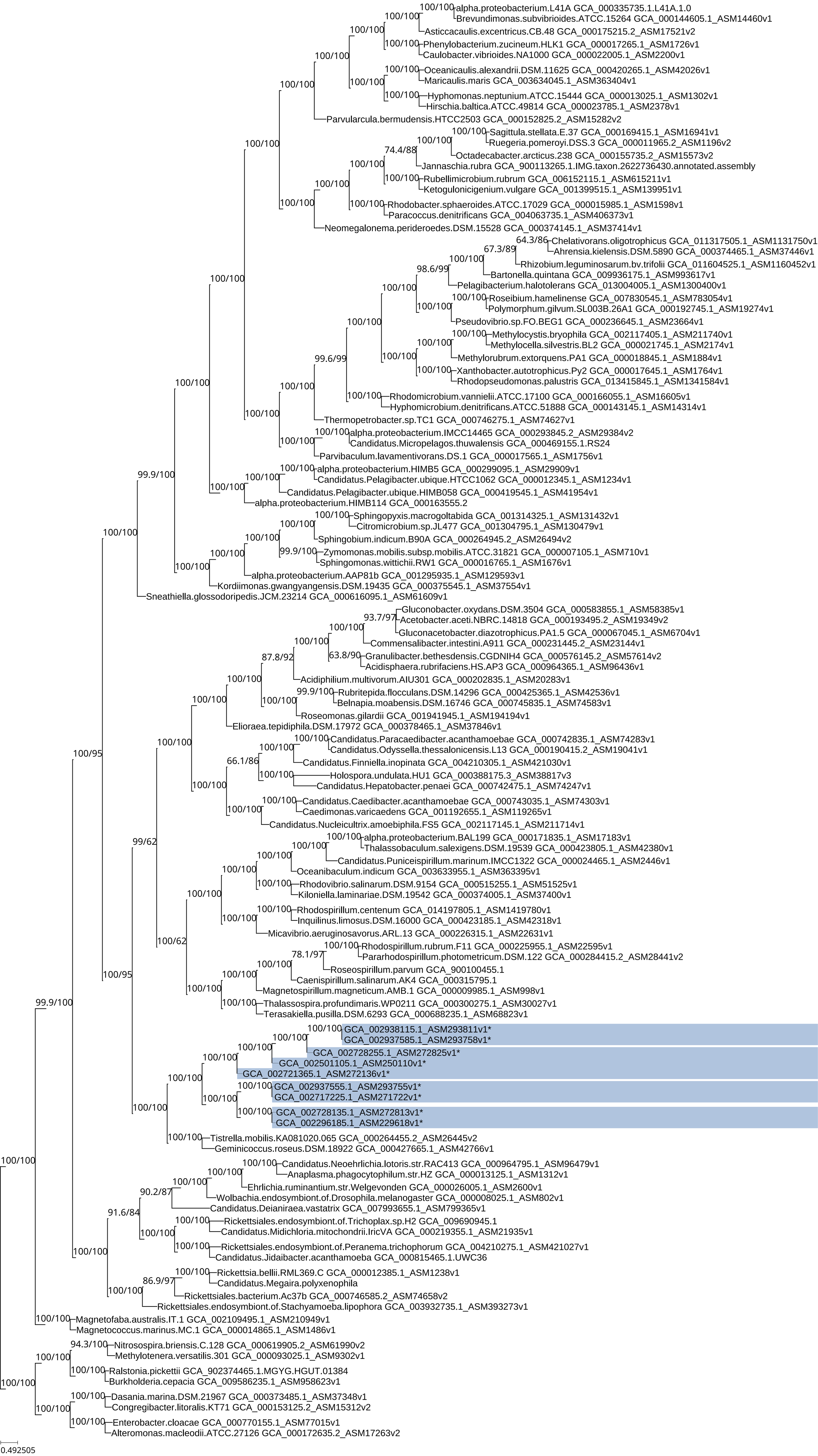
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Maricaulis.maris GCA_003634045.1_ASM363404v1
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Hyphomonas.neptunium.ATCC.15444 GCA_000013025.1_ASM1302v1
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Sagittula.stellata.E.37 GCA_000169415.1_ASM16941v1
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Ruegeria.pomeroyi.DSS.3 GCA_000011965.2_ASM1196v2
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64.3/86
Chelativorans.oligotrophicus GCA_011317505.1_ASM1131750v1
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Methylocystis.bryophila GCA_002117405.1_ASM211740v1
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100/100
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Candidatus.Micropelagos.thuwalensis GCA_000469155.1.RS24
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99.9/100
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78.6/94
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74.9/91
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94.4/79
99.6/76
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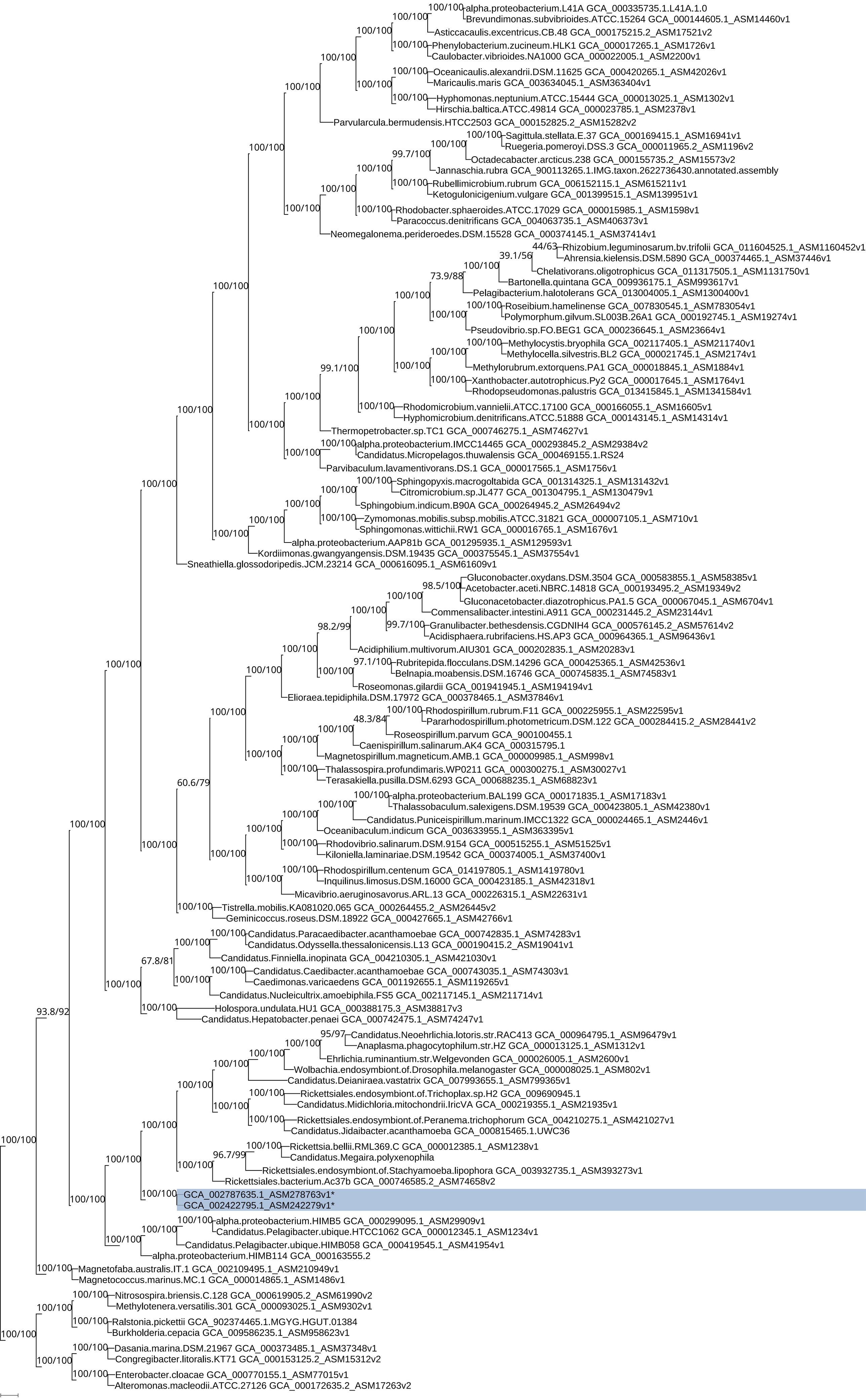
Group F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Octadecabacter.arcticus.238 GCA_000155735.2_ASM15573v2
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Pseudovibrio.sp.FO.BEG1 GCA_000236645.1_ASM23664v1
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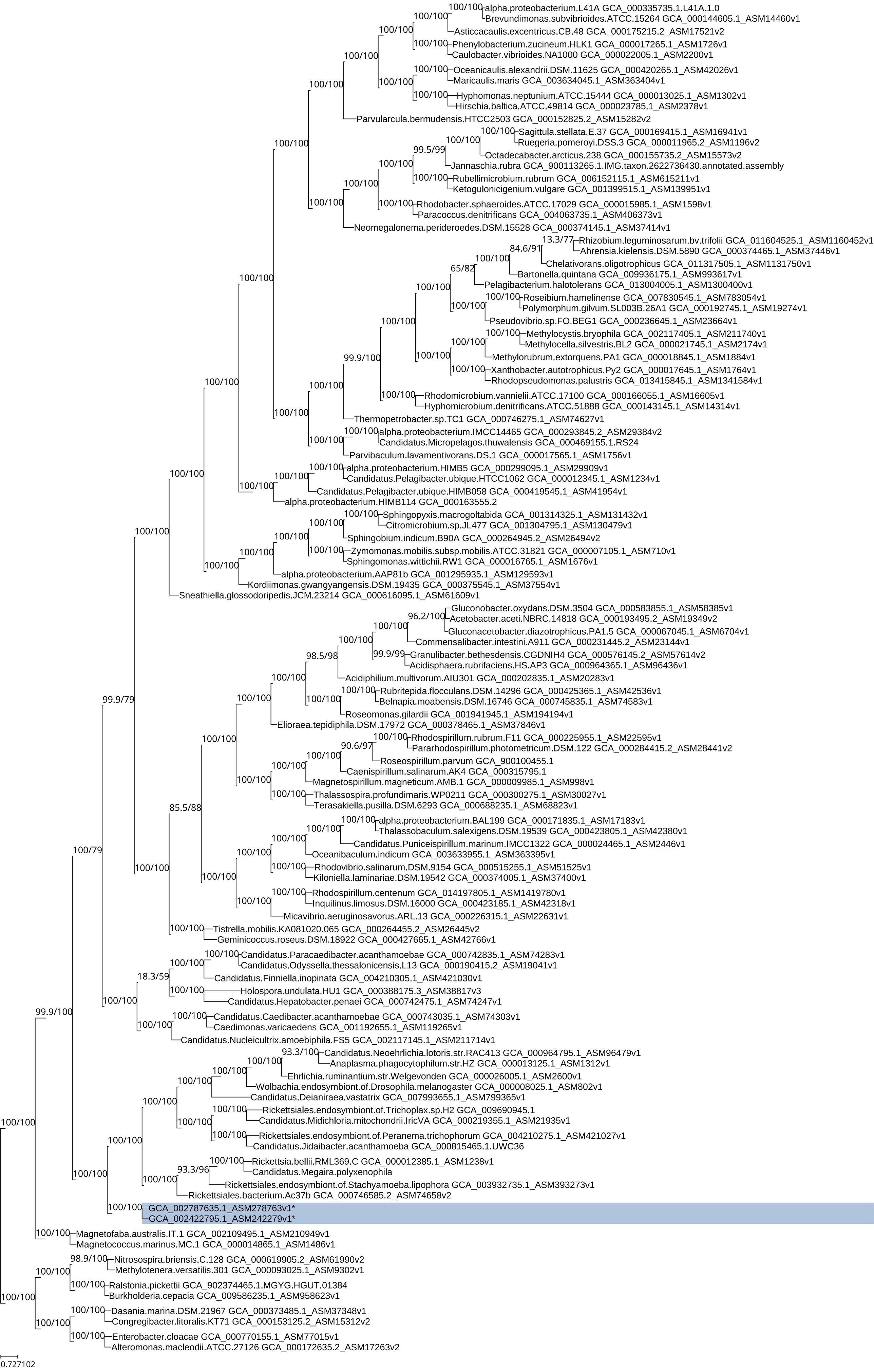
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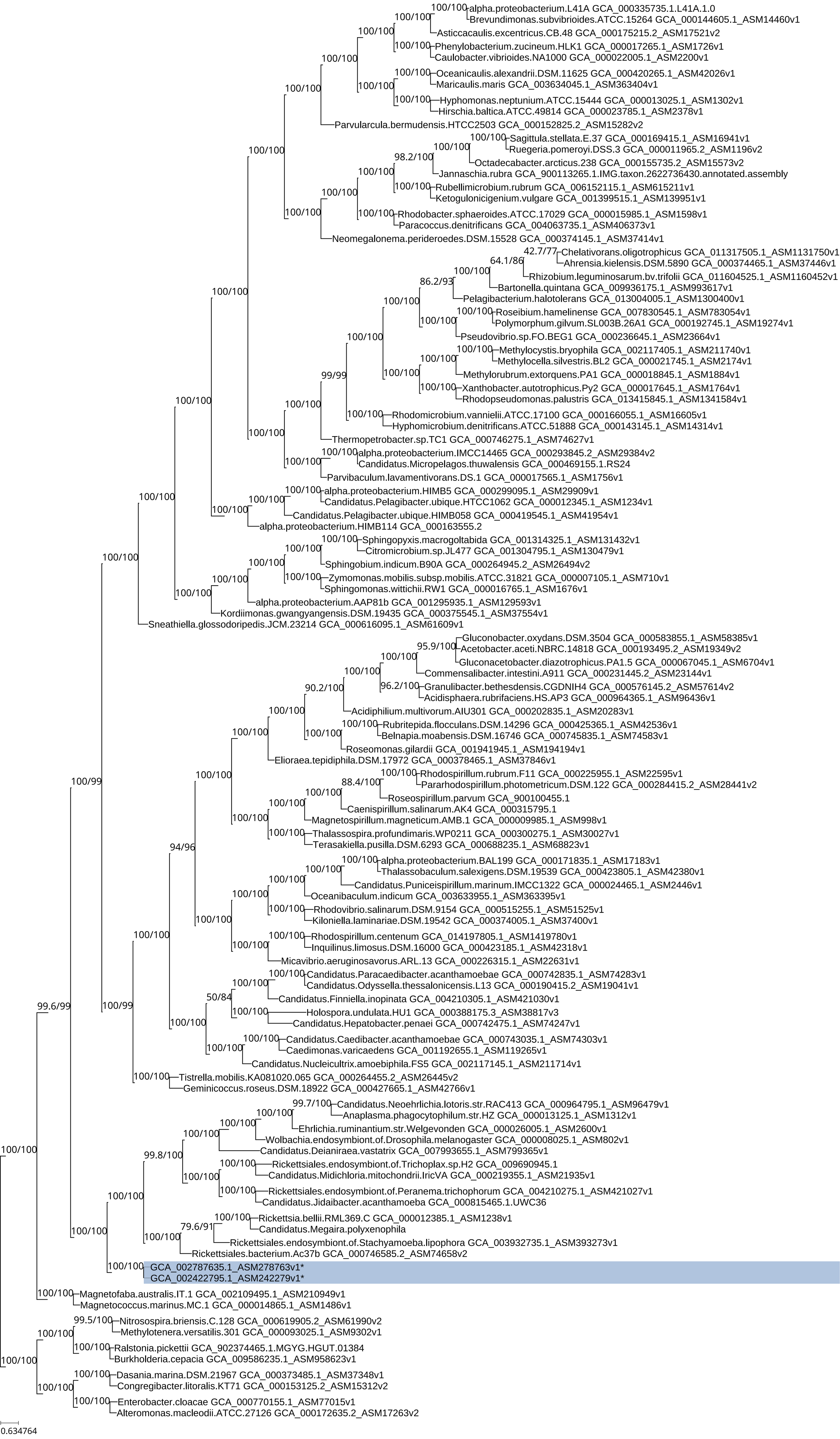
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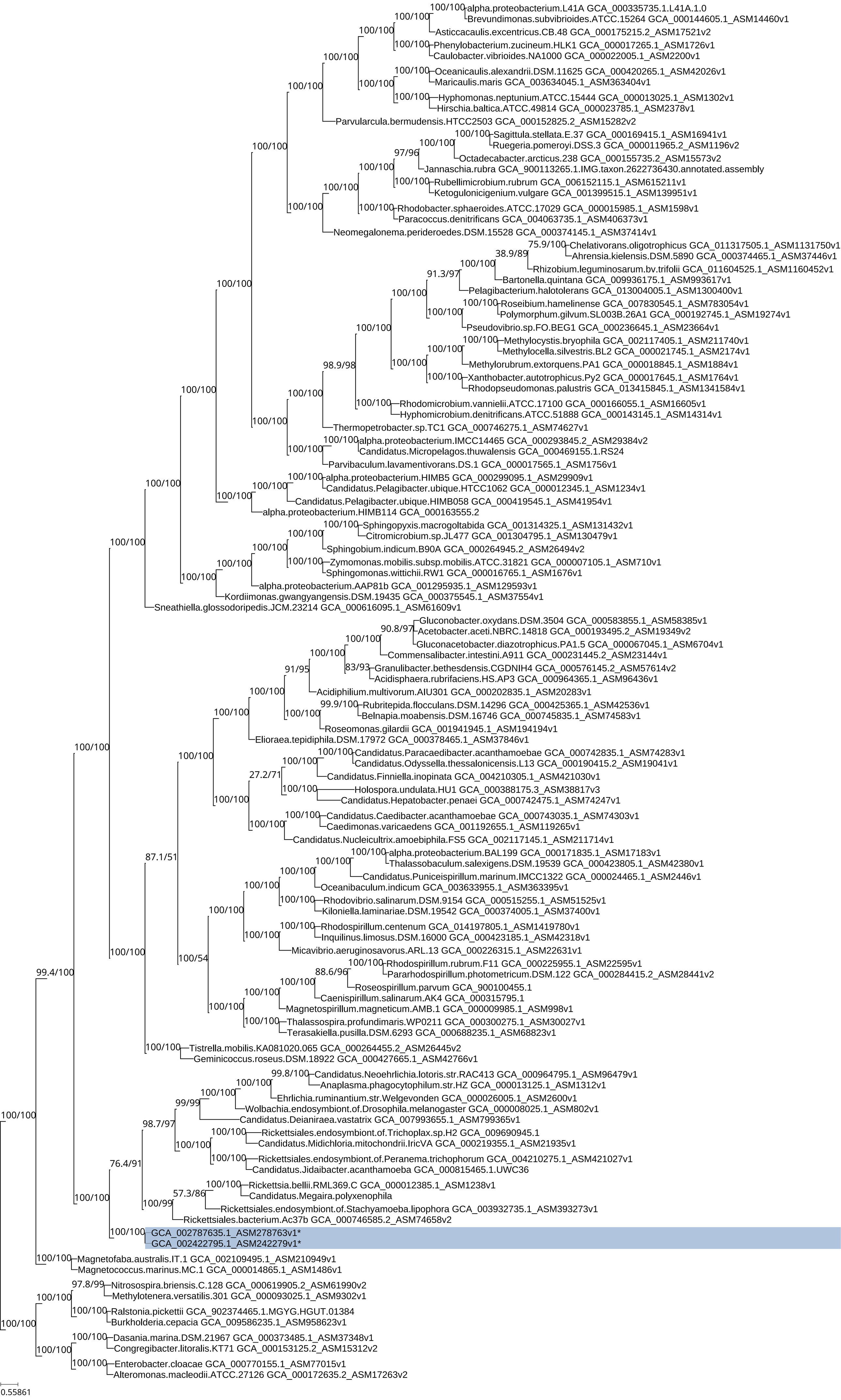
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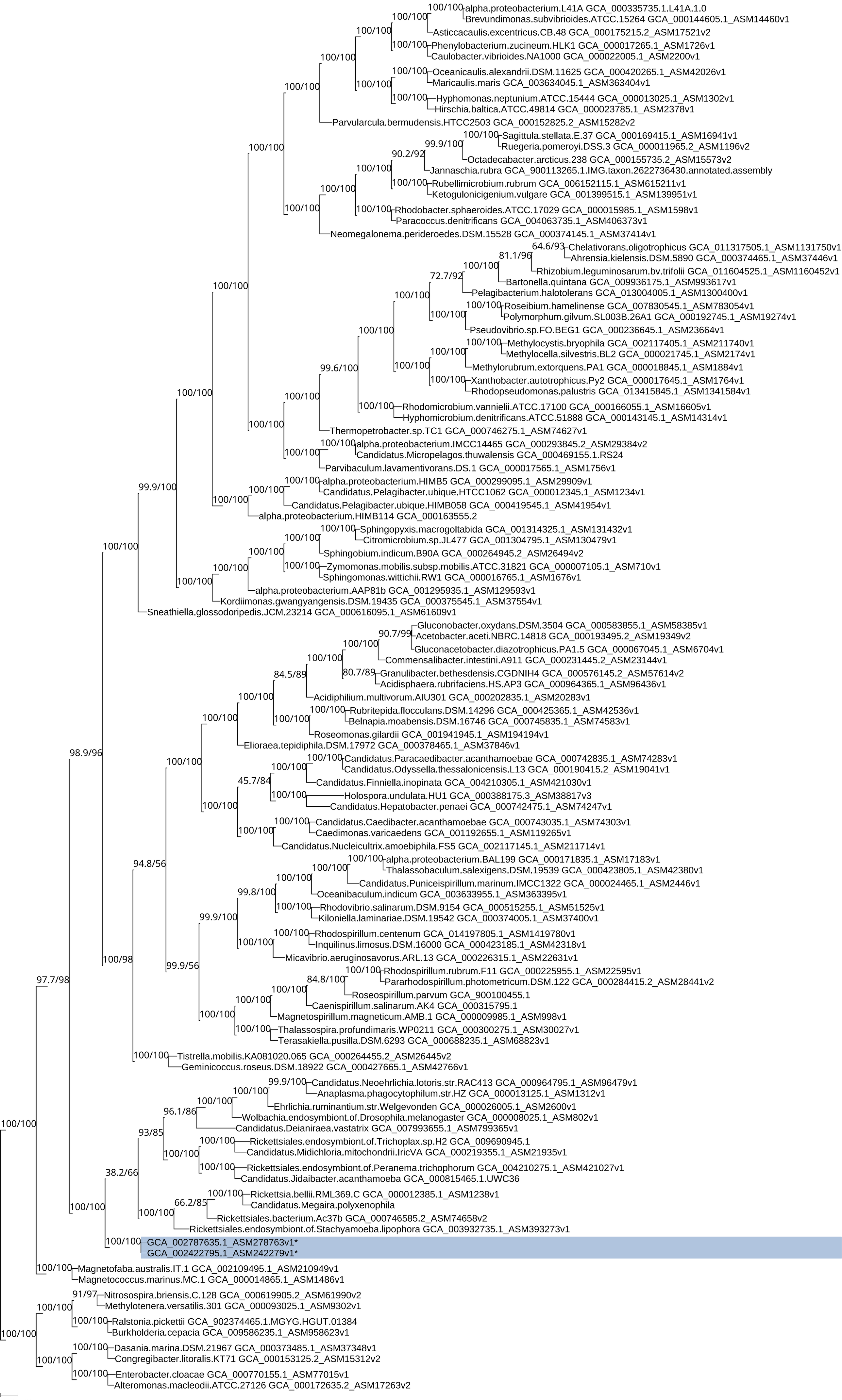
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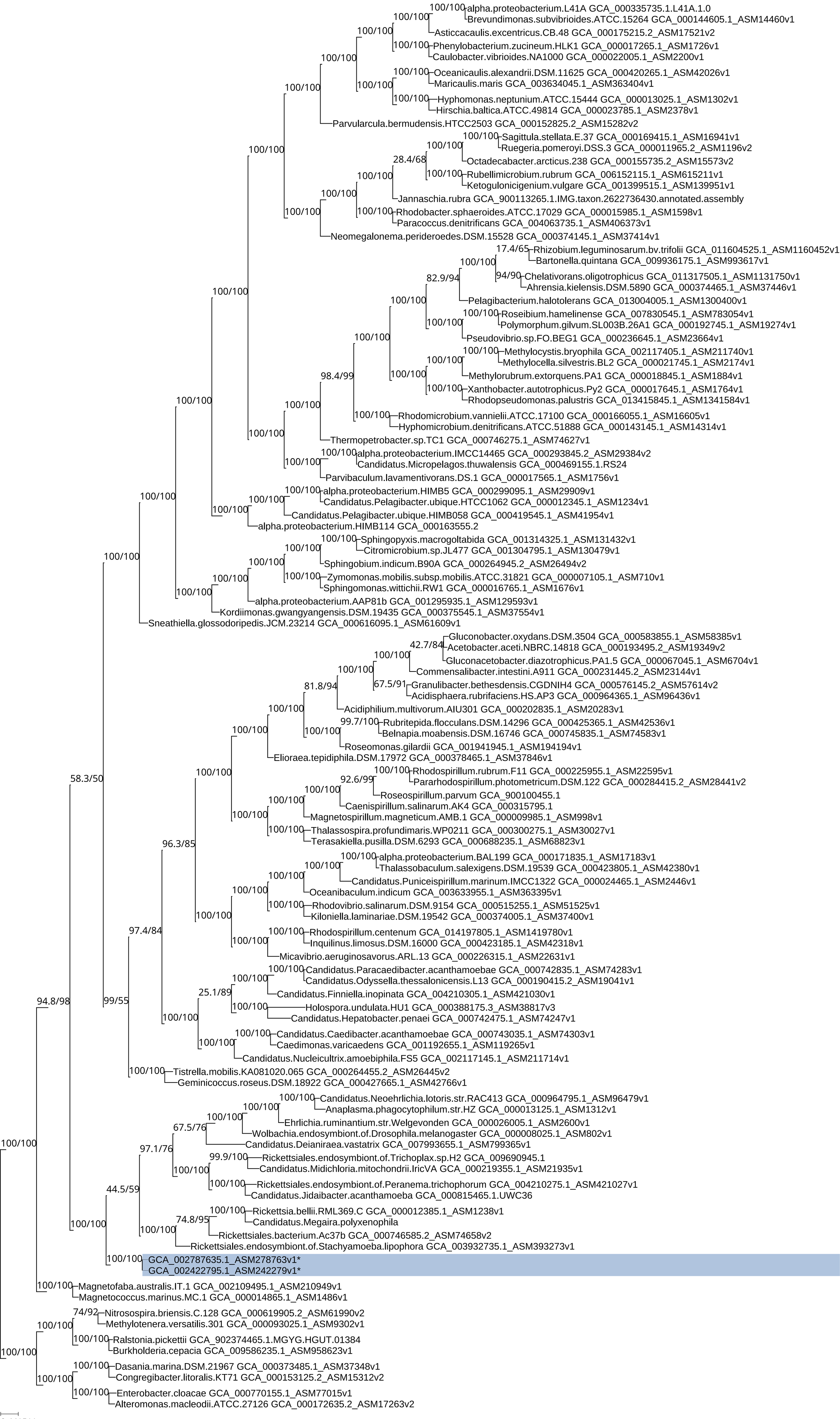
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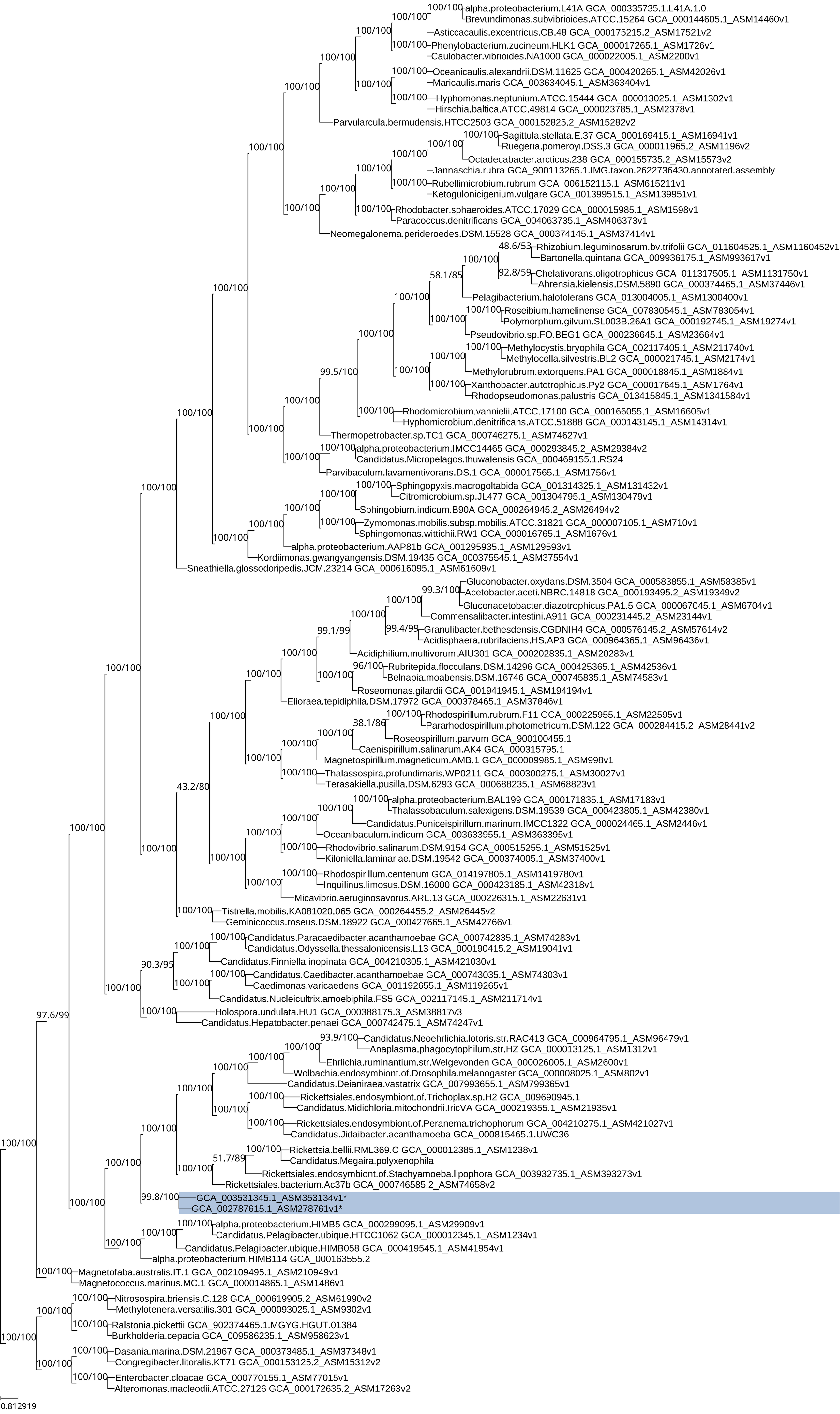
Group G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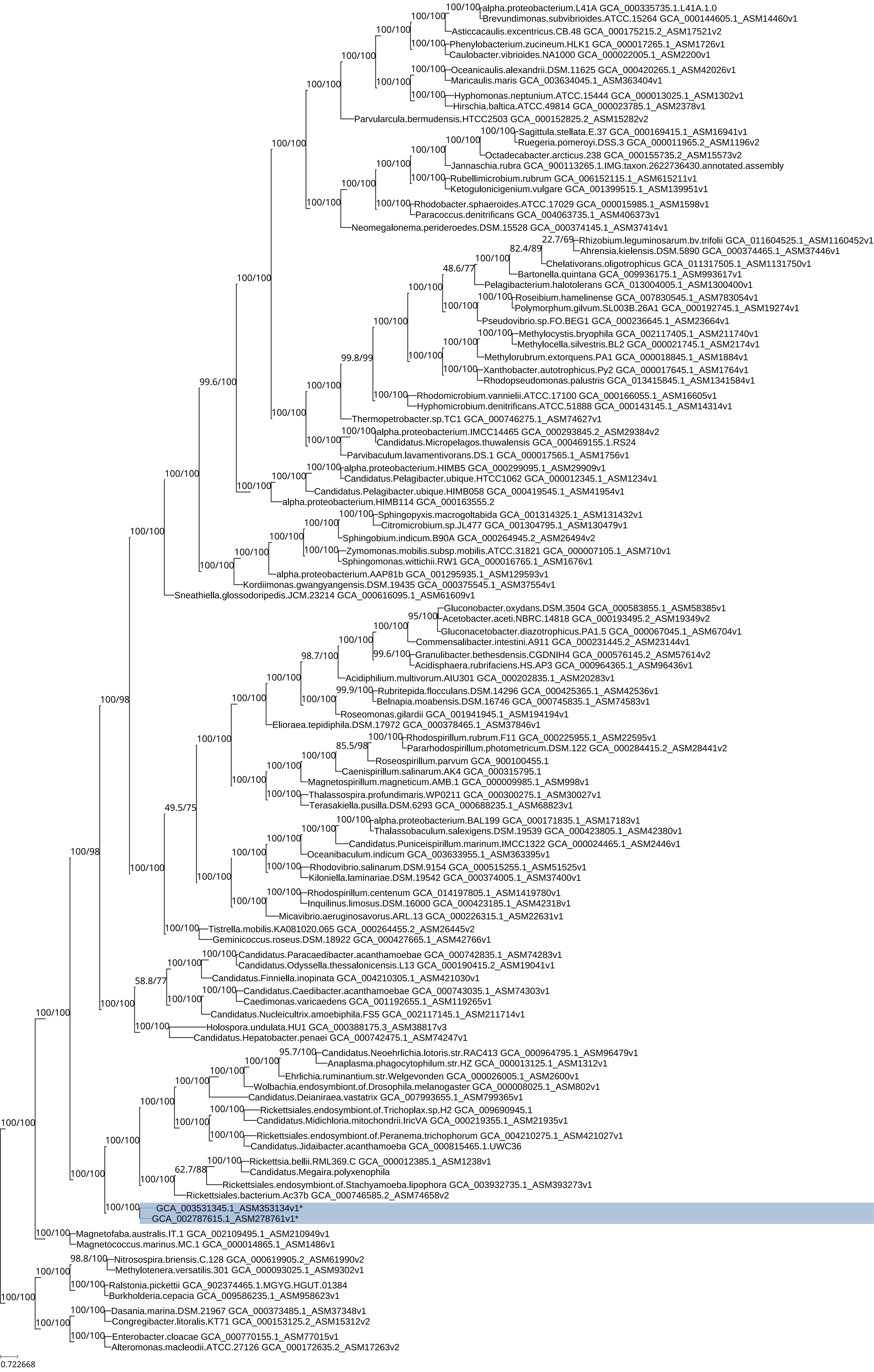
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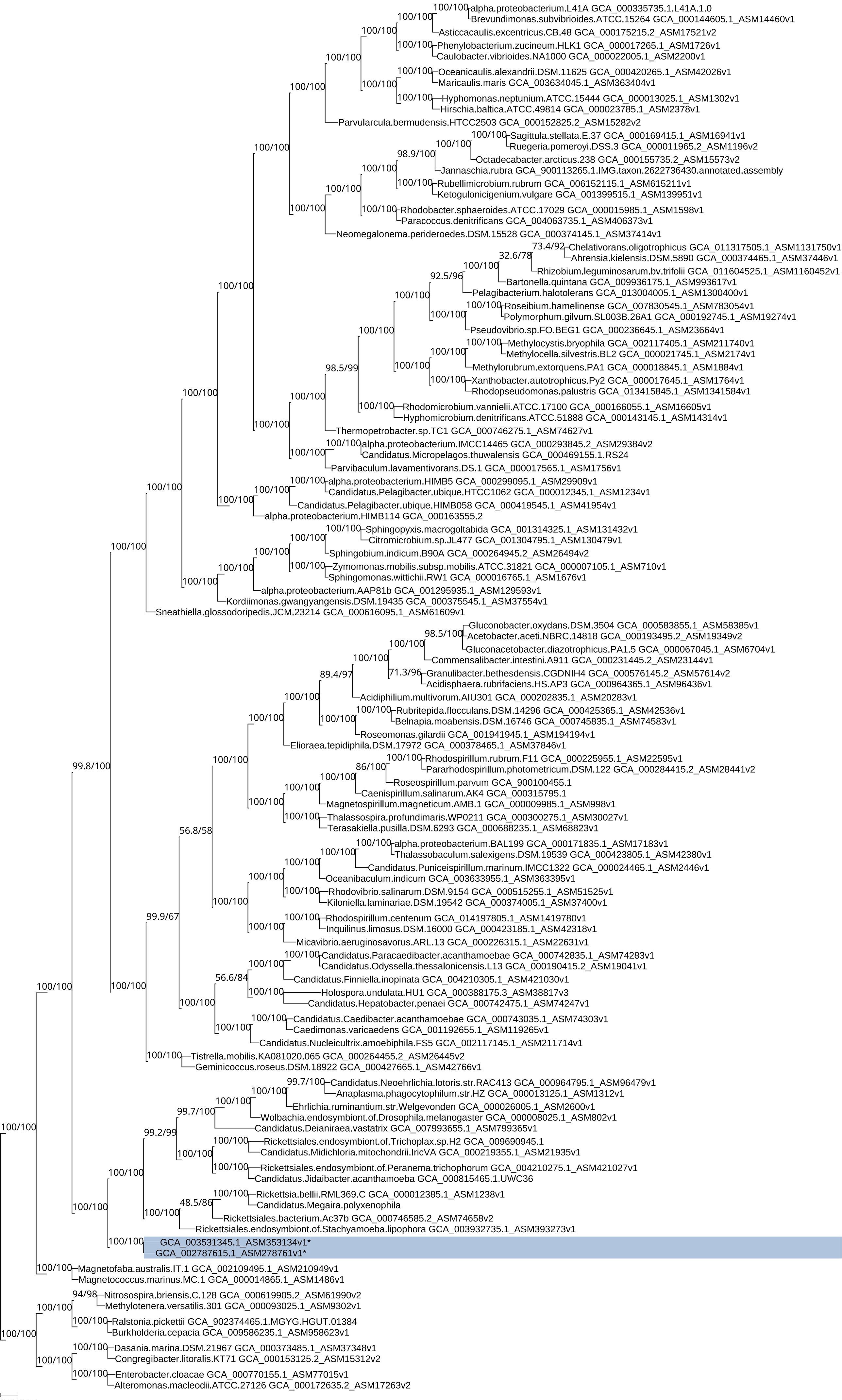
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Pseudovibrio.sp.FO.BEG1 GCA_000236645.1_ASM23664v1
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Methylocystis.bryophila GCA_002117405.1_ASM211740v1
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Methylocella.silvestris.BL2 GCA_000021745.1_ASM2174v1
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Methylorubrum.extorquens.PA1 GCA_000018845.1_ASM1884v1
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Xanthobacter.autotrophicus.Py2 GCA_000017645.1_ASM1764v1
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Rhodopseudomonas.palustris GCA_013415845.1_ASM1341584v1
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Hyphomicrobium.denitrificans.ATCC.51888 GCA_000143145.1_ASM14314v1
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Sphingomonas.wittichii.RW1 GCA_000016765.1_ASM1676v1
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Kordiimonas.gwangyangensis.DSM.19435 GCA_000375545.1_ASM37554v1
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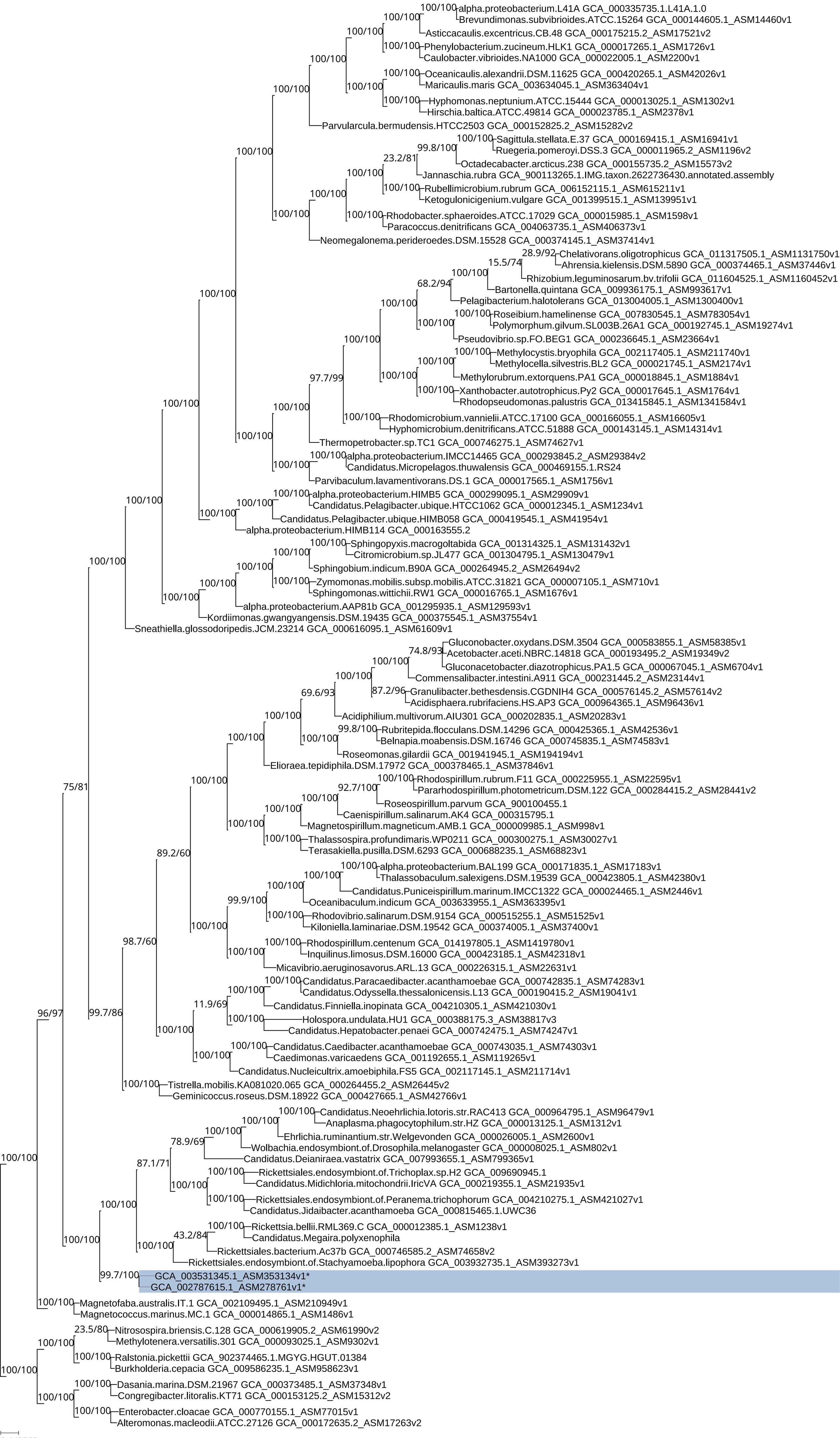
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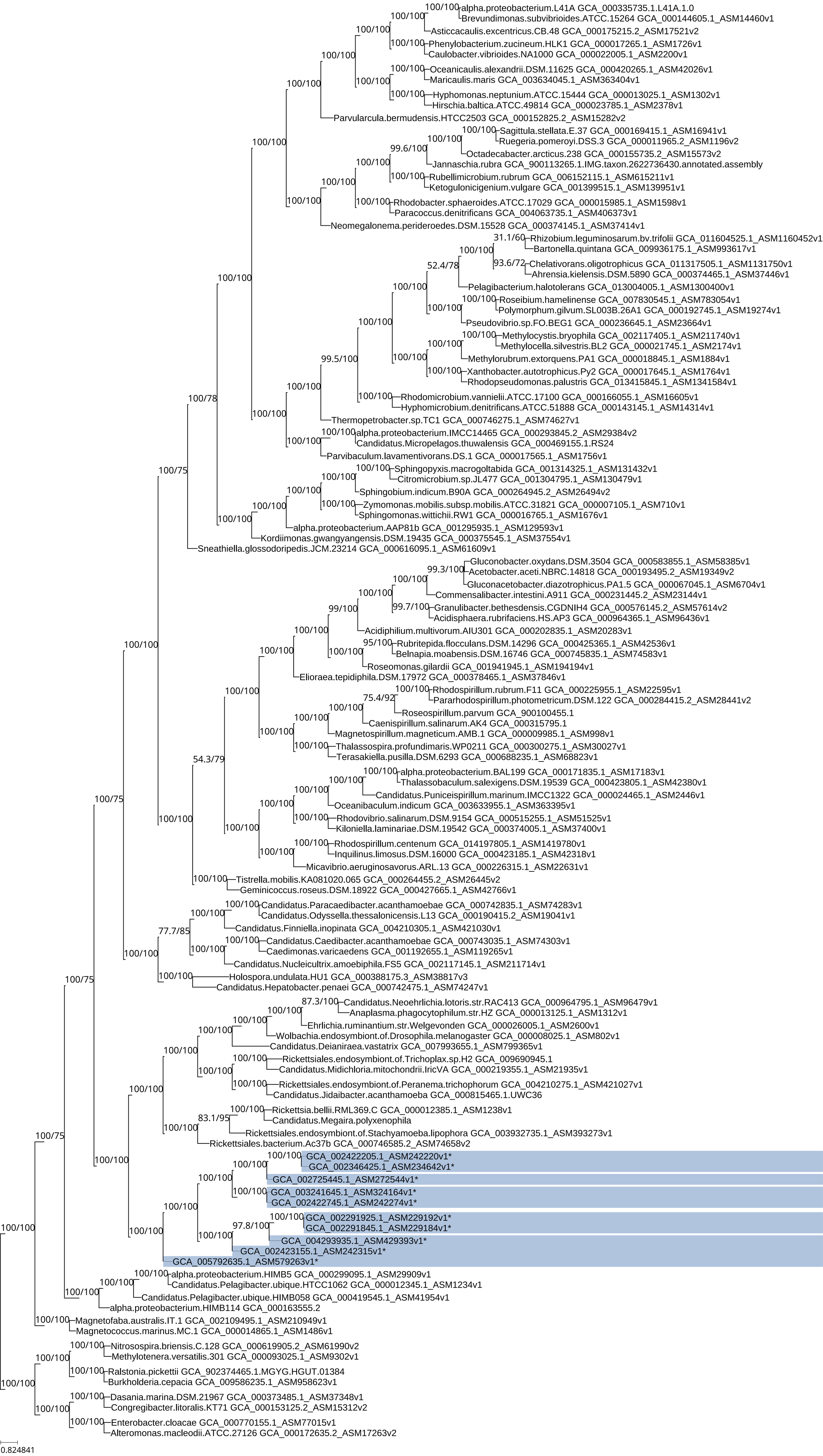
Group H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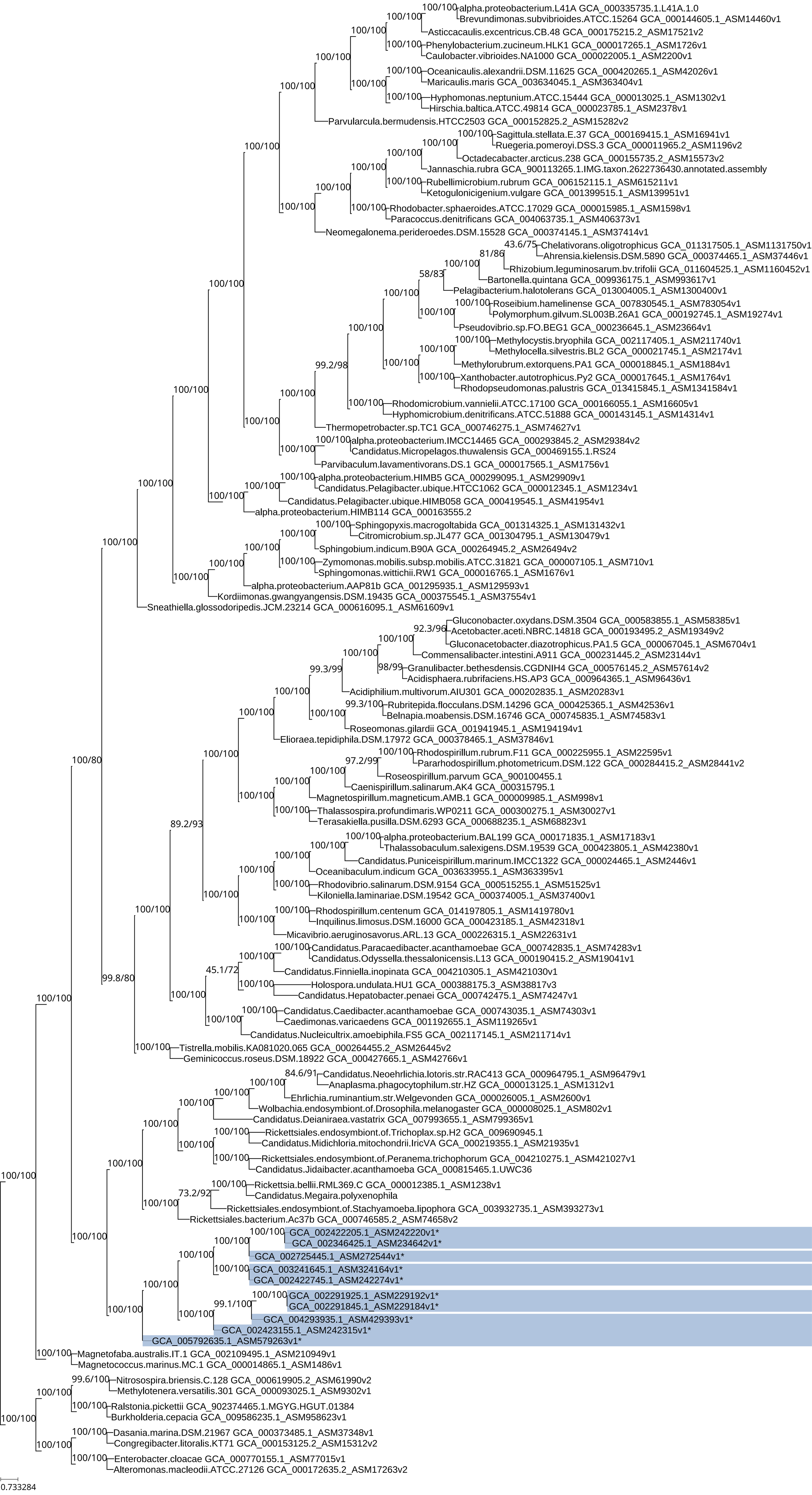
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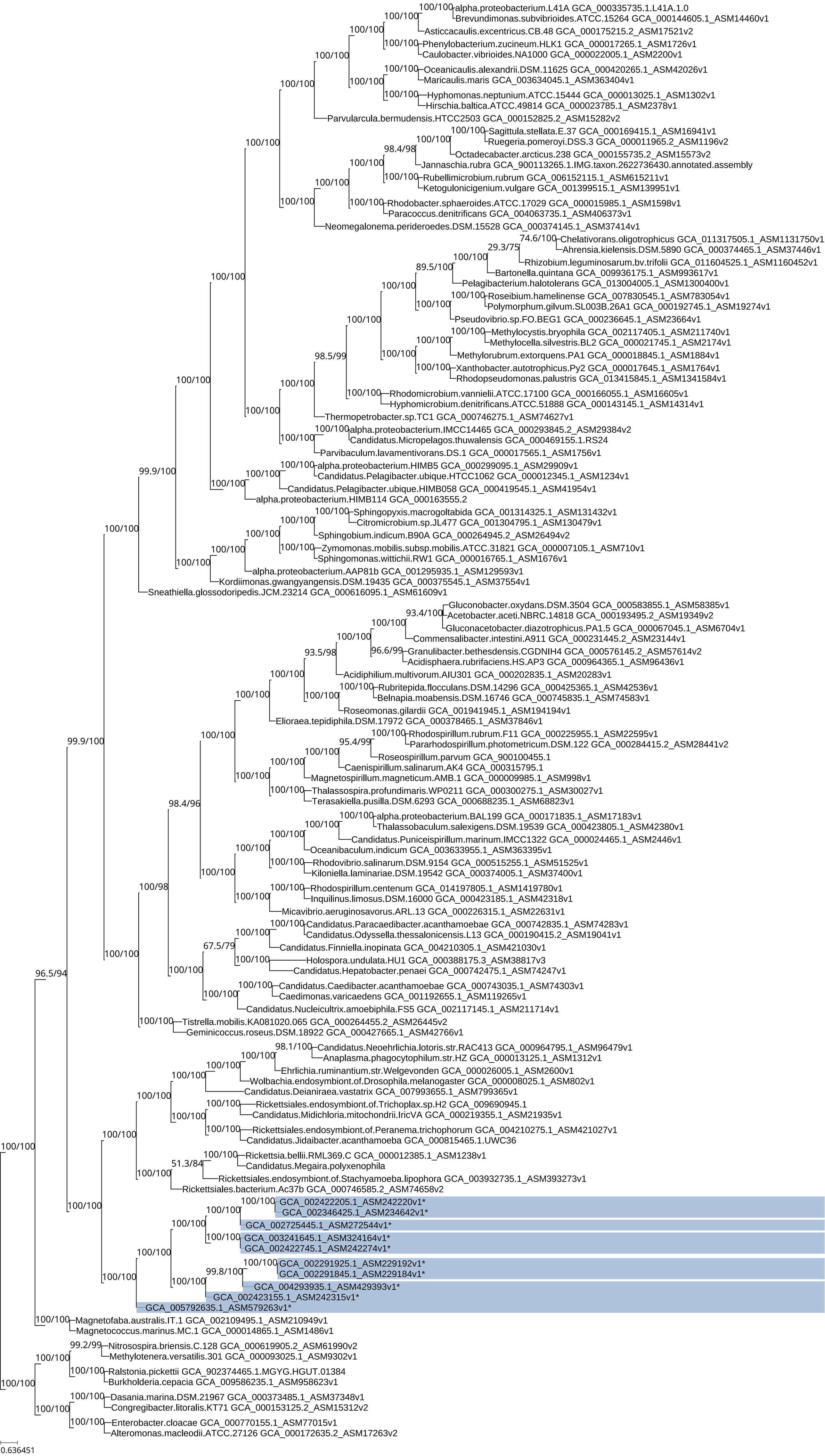
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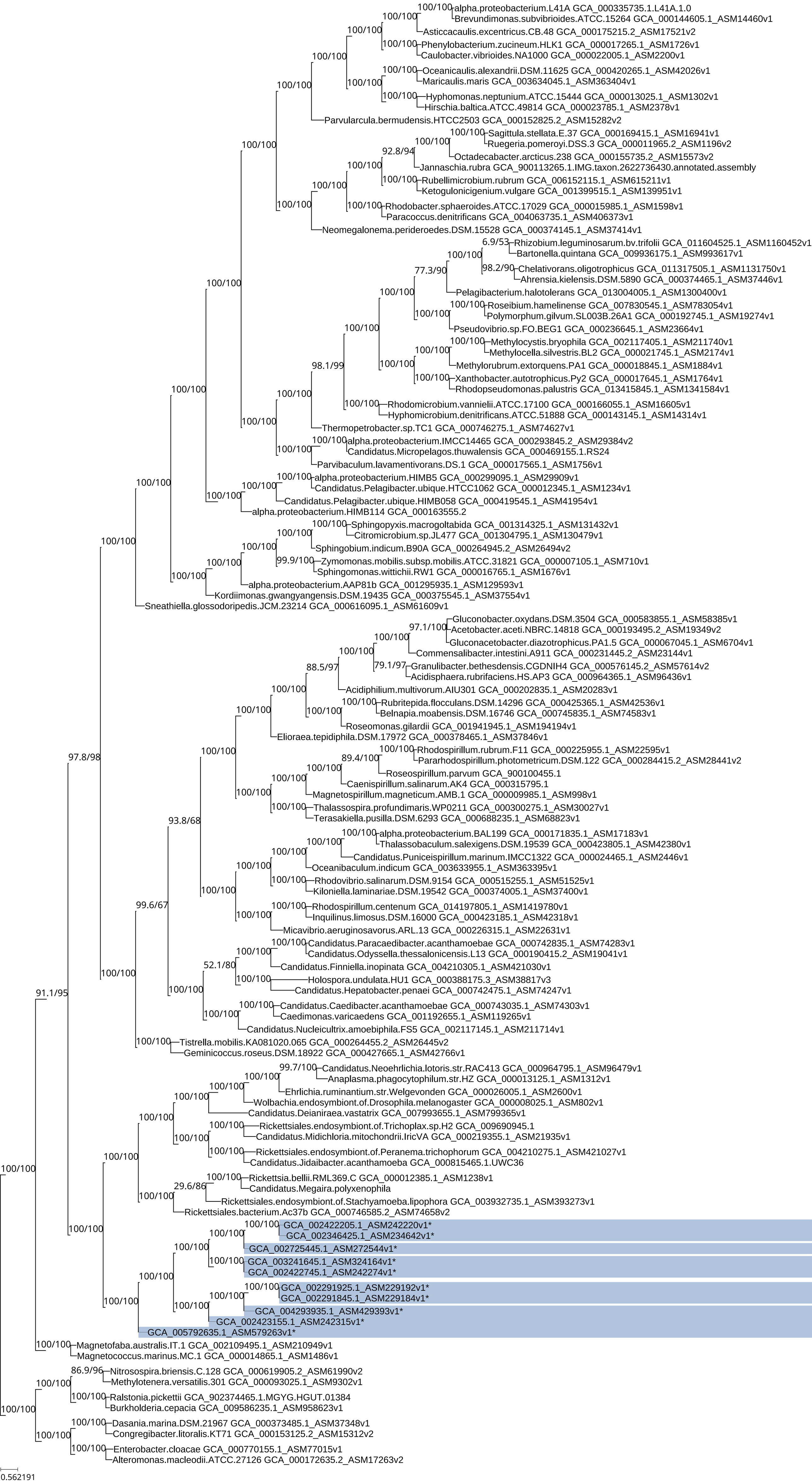
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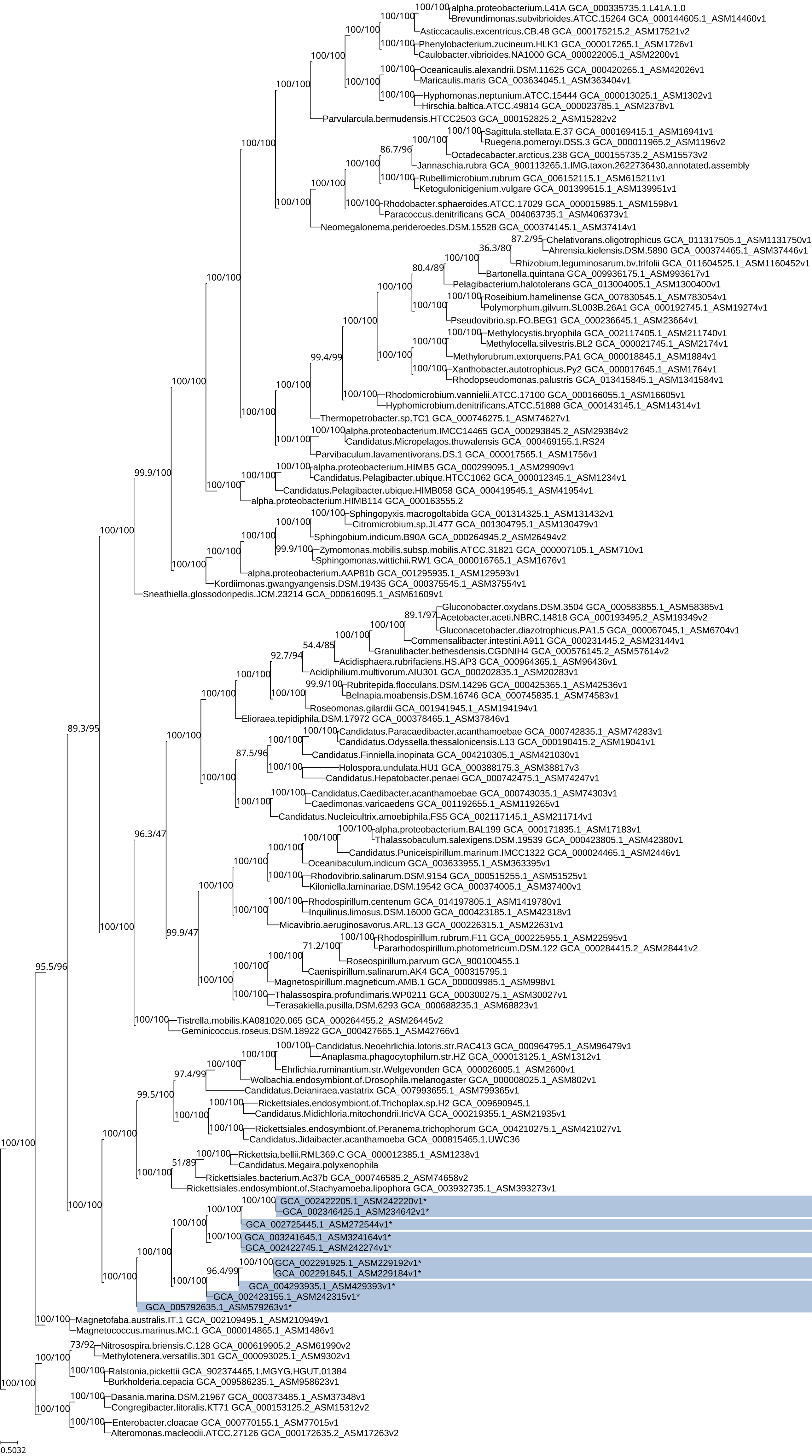
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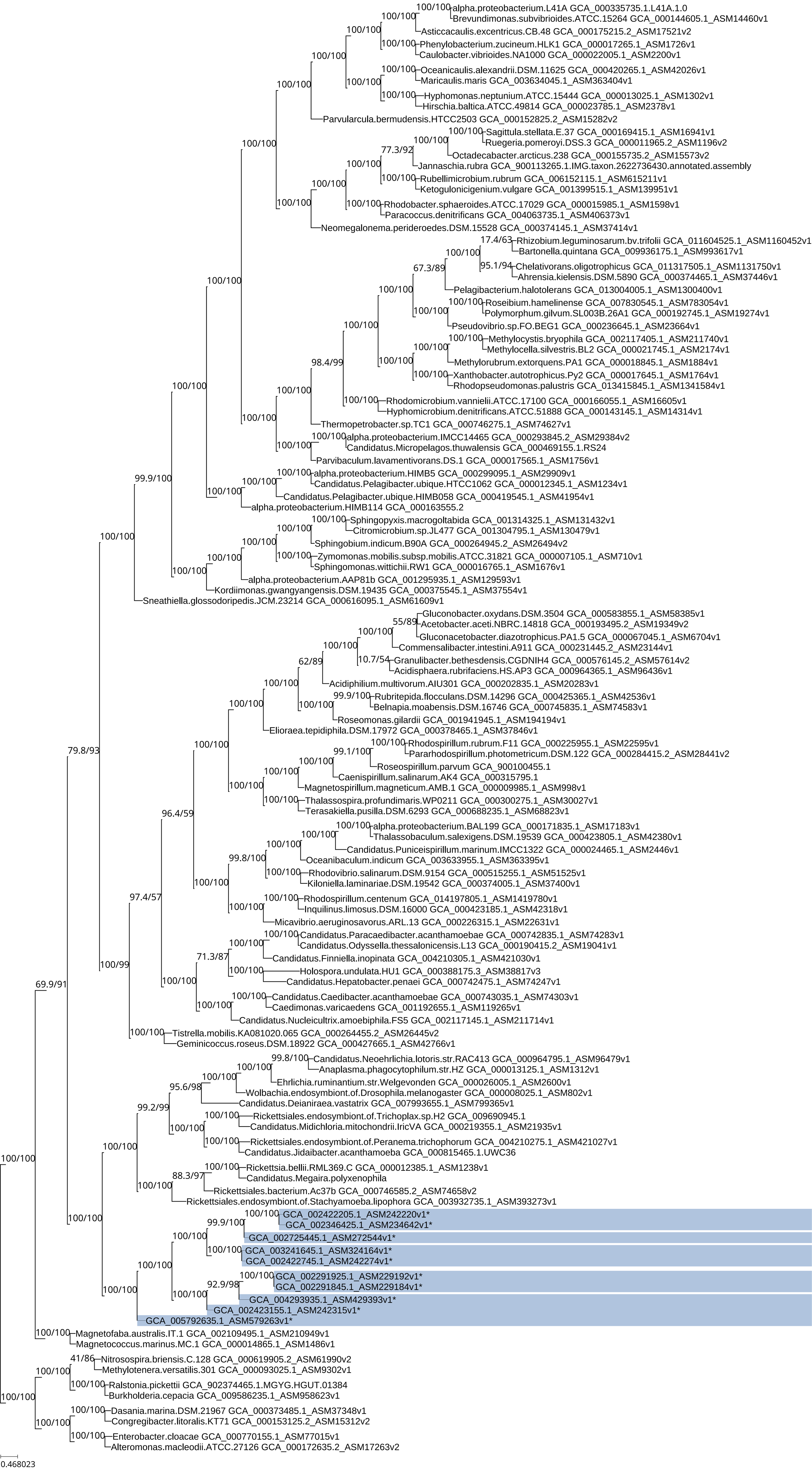
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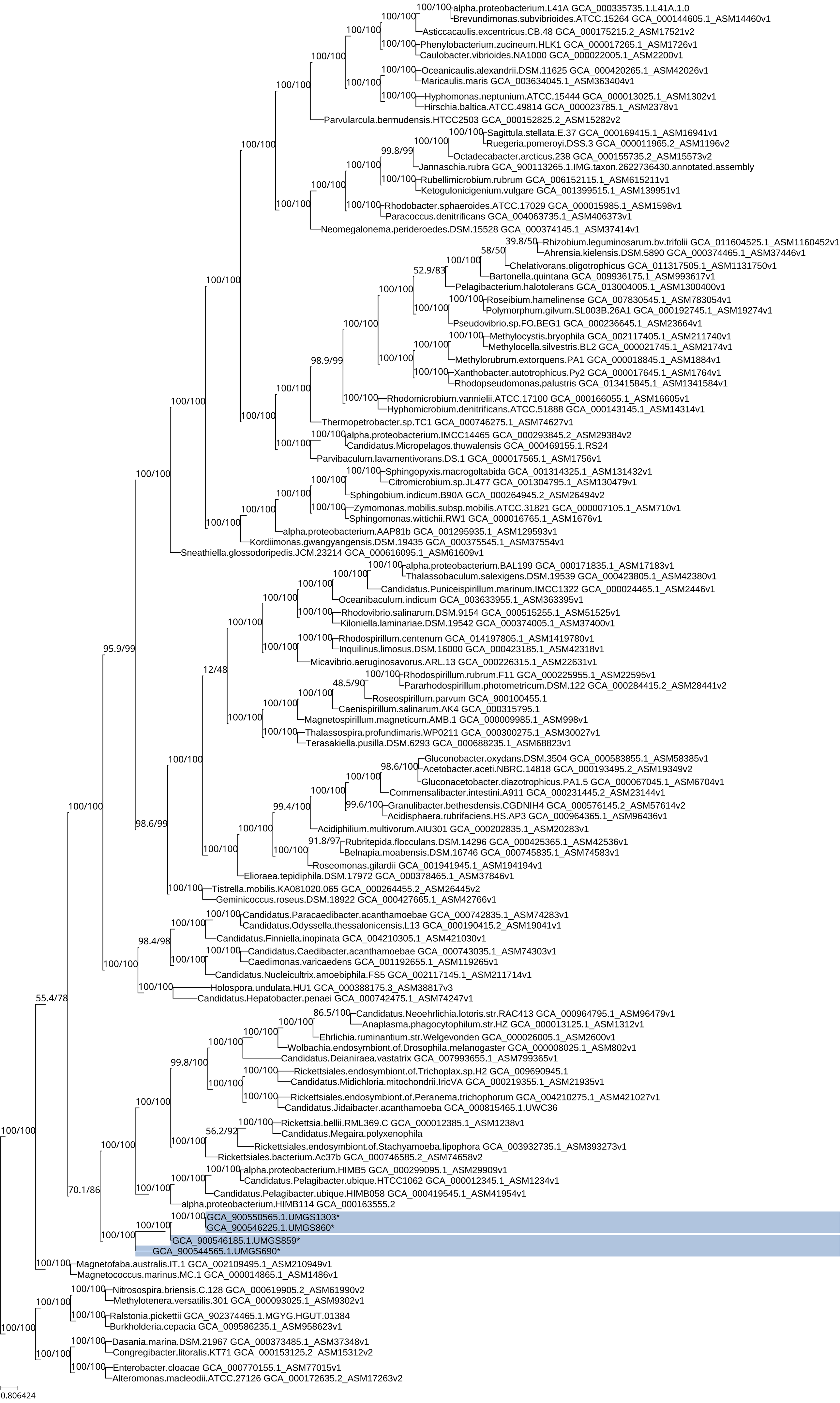
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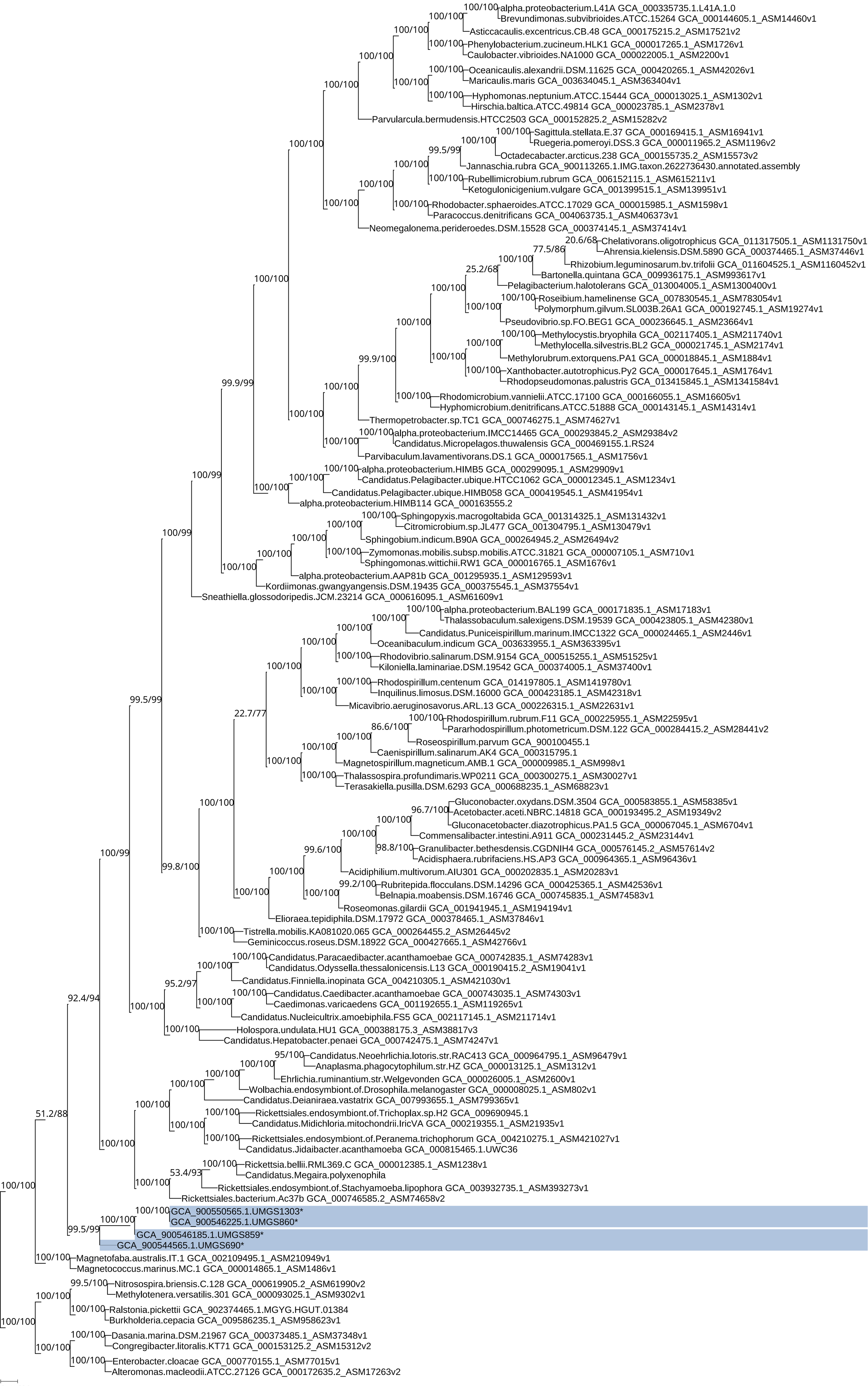
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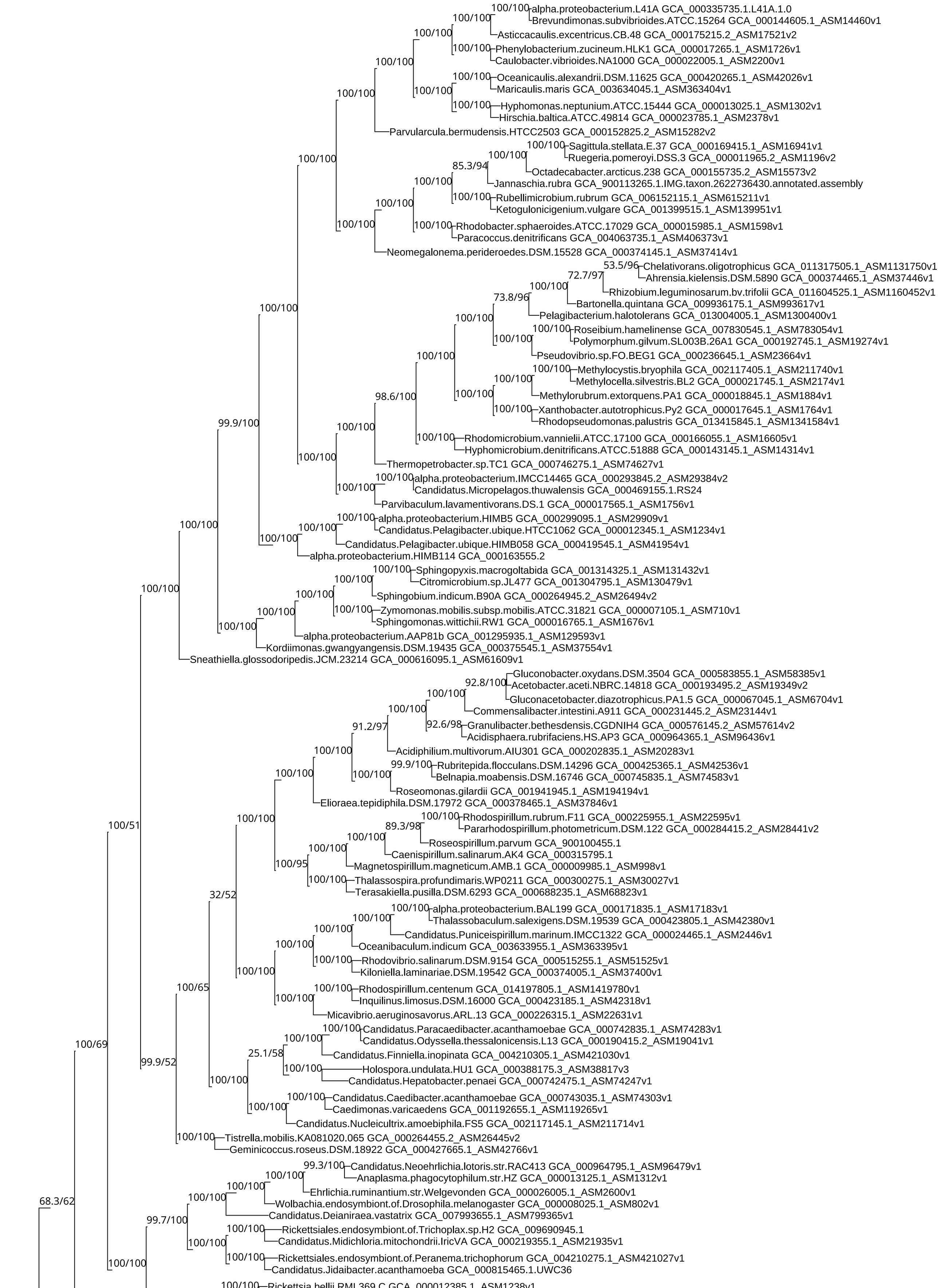
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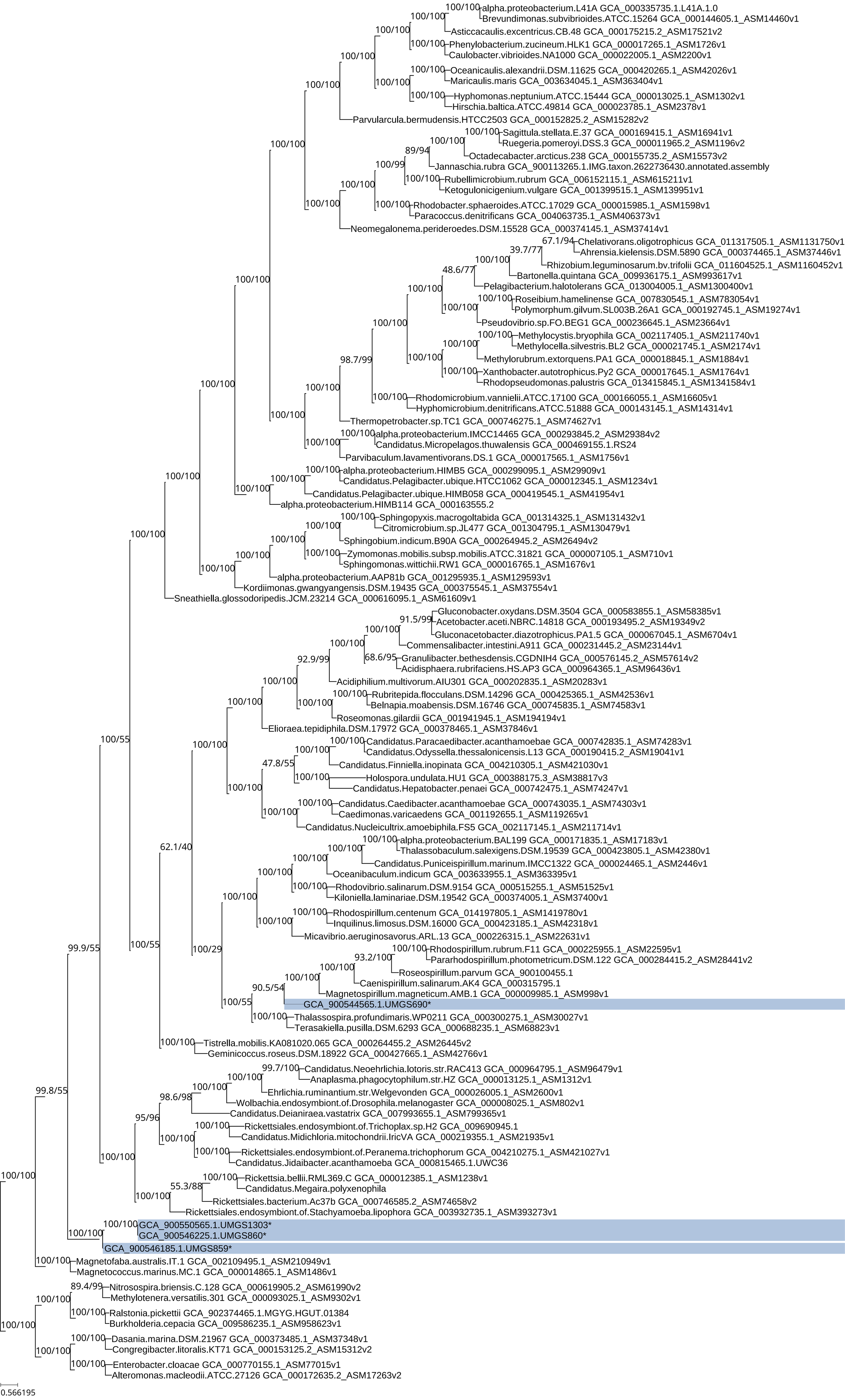
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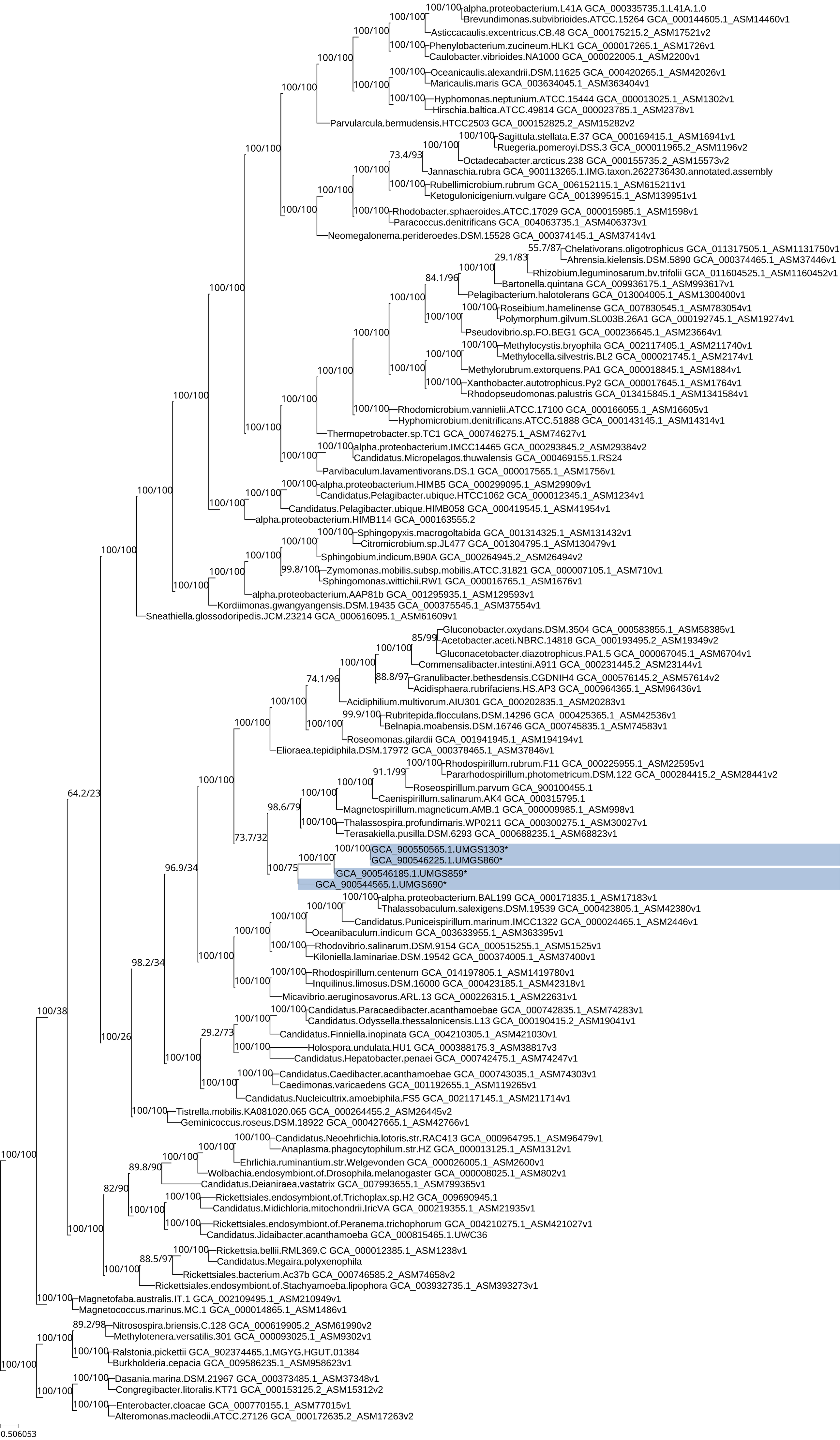
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Sphingopyxis.macrogoltabida GCA_001314325.1_ASM131432v1
Citromicrobium.sp.JL477 GCA_001304795.1_ASM130479v1
Sphingobium.indicum.B90A GCA_000264945.2_ASM26494v2
99.8/100
Zymomonas.mobilis.subsp.mobilis.ATCC.31821 GCA_000007105.1_ASM710v1
Sphingomonas.wittichii.RW1 GCA_000016765.1_ASM1676v1
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Kordiimonas.gwangyangensis.DSM.19435 GCA_000375545.1_ASM37554v1
Sneathiella.glossodoripedis.JCM.23214 GCA_000616095.1_ASM61609v1
Gluconobacter.oxydans.DSM.3504 GCA_000583855.1_ASM58385v1
85/99
Acetobacter.aceti.NBRC.14818 GCA_000193495.2_ASM19349v2
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Commensalibacter.intestini.A911 GCA_000231445.2_ASM23144v1
88.8/97
Granulibacter.bethesdensis.CGDNIH4 GCA_000576145.2_ASM57614v2
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74.1/96
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99.9/100
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Belnapia.moabensis.DSM.16746 GCA_000745835.1_ASM74583v1
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Elioraea.tepidiphila.DSM.17972 GCA_000378465.1_ASM37846v1
64.2/23
100/100
Rhodospirillum.rubrum.F11 GCA_000225955.1_ASM22595v1
91.1/99
Pararhodospirillum.photometricum.DSM.122 GCA_000284415.2_ASM28441v2
Roseospirillum.parvum GCA_900100455.1
Caenispirillum.salinarum.AK4 GCA_000315795.1
98.6/79
Magnetospirillum.magneticum.AMB.1 GCA_000009985.1_ASM998v1
Thalassospira.profundimaris.WP0211 GCA_000300275.1_ASM30027v1
Terasakiella.pusilla.DSM.6293 GCA_000688235.1_ASM68823v1
73.7/32
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96.9/34
100/75
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Oceanibaculum.indicum GCA_003633955.1_ASM363395v1
Rhodovibrio.salinarum.DSM.9154 GCA_000515255.1_ASM51525v1
Kiloniella.laminariae.DSM.19542 GCA_000374005.1_ASM37400v1
98.2/34
Rhodospirillum.centenum GCA_014197805.1_ASM1419780v1
Inquilinus.limosus.DSM.16000 GCA_000423185.1_ASM42318v1
Micavibrio.aeruginosavorus.ARL.13 GCA_000226315.1_ASM22631v1
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Candidatus.Paracaedibacter.acanthamoebae GCA_000742835.1_ASM74283v1
Candidatus.Odyssella.thessalonicensis.L13 GCA_000190415.2_ASM19041v1
29.2/73
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Holospora.undulata.HU1 GCA_000388175.3_ASM38817v3
Candidatus.Hepatobacter.penaei GCA_000742475.1_ASM74247v1
Candidatus.Caedibacter.acanthamoebae GCA_000743035.1_ASM74303v1
Caedimonas.varicaedens GCA_001192655.1_ASM119265v1
Candidatus.Nucleicultrix.amoebiphila.FS5 GCA_002117145.1_ASM211714v1
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Ehrlichia.ruminantium.str.Welgevonden GCA_000026005.1_ASM2600v1
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88.5/97
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Burkholderia.cepacia GCA_009586235.1_ASM958623v1
Dasania.marina.DSM.21967 GCA_000373485.1_ASM37348v1
Congregibacter.litoralis.KT71 GCA_000153125.2_ASM15312v2
Enterobacter.cloacae GCA_000770155.1_ASM77015v1
Alteromonas.macleodii.ATCC.27126 GCA_000172635.2_ASM17263v2
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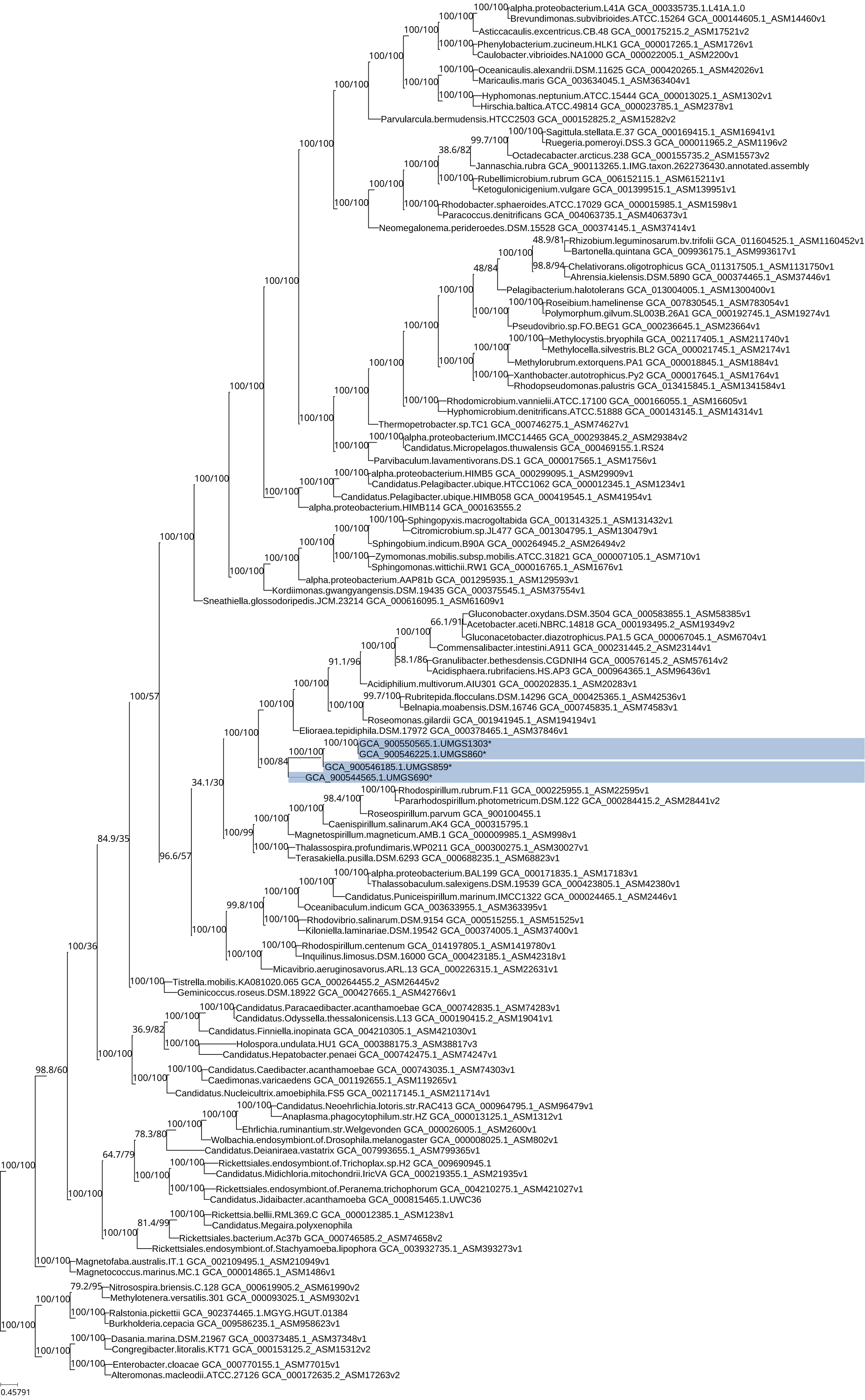
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100/100
Phenylobacterium.zucineum.HLK1 GCA_000017265.1_ASM1726v1
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Caulobacter.vibrioides.NA1000 GCA_000022005.1_ASM2200v1
100/100
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100/100
Maricaulis.maris GCA_003634045.1_ASM363404v1
100/100
Hyphomonas.neptunium.ATCC.15444 GCA_000013025.1_ASM1302v1
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Parvularcula.bermudensis.HTCC2503 GCA_000152825.2_ASM15282v2
100/100
Sagittula.stellata.E.37 GCA_000169415.1_ASM16941v1
99.7/100
Ruegeria.pomeroyi.DSS.3 GCA_000011965.2_ASM1196v2
38.6/82
Octadecabacter.arcticus.238 GCA_000155735.2_ASM15573v2
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Rhodobacter.sphaeroides.ATCC.17029 GCA_000015985.1_ASM1598v1
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Neomegalonema.perideroedes.DSM.15528 GCA_000374145.1_ASM37414v1
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98.8/94
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Pelagibacterium.halotolerans GCA_013004005.1_ASM1300400v1
Roseibium.hamelinense GCA_007830545.1_ASM783054v1
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Methylocella.silvestris.BL2 GCA_000021745.1_ASM2174v1
Methylorubrum.extorquens.PA1 GCA_000018845.1_ASM1884v1
Xanthobacter.autotrophicus.Py2 GCA_000017645.1_ASM1764v1
Rhodopseudomonas.palustris GCA_013415845.1_ASM1341584v1
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Hyphomicrobium.denitrificans.ATCC.51888 GCA_000143145.1_ASM14314v1
Thermopetrobacter.sp.TC1 GCA_000746275.1_ASM74627v1
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Candidatus.Micropelagos.thuwalensis GCA_000469155.1.RS24
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Candidatus.Pelagibacter.ubique.HIMB058 GCA_000419545.1_ASM41954v1
alpha.proteobacterium.HIMB114 GCA_000163555.2
Sphingopyxis.macrogoltabida GCA_001314325.1_ASM131432v1
Citromicrobium.sp.JL477 GCA_001304795.1_ASM130479v1
Sphingobium.indicum.B90A GCA_000264945.2_ASM26494v2
Zymomonas.mobilis.subsp.mobilis.ATCC.31821 GCA_000007105.1_ASM710v1
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Kordiimonas.gwangyangensis.DSM.19435 GCA_000375545.1_ASM37554v1
Sneathiella.glossodoripedis.JCM.23214 GCA_000616095.1_ASM61609v1
Gluconobacter.oxydans.DSM.3504 GCA_000583855.1_ASM58385v1
66.1/91
Acetobacter.aceti.NBRC.14818 GCA_000193495.2_ASM19349v2
Gluconacetobacter.diazotrophicus.PA1.5 GCA_000067045.1_ASM6704v1
Commensalibacter.intestini.A911 GCA_000231445.2_ASM23144v1
58.1/86
Granulibacter.bethesdensis.CGDNIH4 GCA_000576145.2_ASM57614v2
Acidisphaera.rubrifaciens.HS.AP3 GCA_000964365.1_ASM96436v1
91.1/96
Acidiphilium.multivorum.AIU301 GCA_000202835.1_ASM20283v1
99.7/100
Rubritepida.flocculans.DSM.14296 GCA_000425365.1_ASM42536v1
Belnapia.moabensis.DSM.16746 GCA_000745835.1_ASM74583v1
Roseomonas.gilardii GCA_001941945.1_ASM194194v1
Elioraea.tepidiphila.DSM.17972 GCA_000378465.1_ASM37846v1
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GCA_900546225.1.UMGS860*
GCA_900546185.1.UMGS859*
GCA_900544565.1.UMGS690*
Rhodospirillum.rubrum.F11 GCA_000225955.1_ASM22595v1
98.4/100
Pararhodospirillum.photometricum.DSM.122 GCA_000284415.2_ASM28441v2
Roseospirillum.parvum GCA_900100455.1
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Magnetospirillum.magneticum.AMB.1 GCA_000009985.1_ASM998v1
Thalassospira.profundimaris.WP0211 GCA_000300275.1_ASM30027v1
Terasakiella.pusilla.DSM.6293 GCA_000688235.1_ASM68823v1
alpha.proteobacterium.BAL199 GCA_000171835.1_ASM17183v1
Thalassobaculum.salexigens.DSM.19539 GCA_000423805.1_ASM42380v1
Candidatus.Puniceispirillum.marinum.IMCC1322 GCA_000024465.1_ASM2446v1
Oceanibaculum.indicum GCA_003633955.1_ASM363395v1
Rhodovibrio.salinarum.DSM.9154 GCA_000515255.1_ASM51525v1
Kiloniella.laminariae.DSM.19542 GCA_000374005.1_ASM37400v1
Rhodospirillum.centenum GCA_014197805.1_ASM1419780v1
Inquilinus.limosus.DSM.16000 GCA_000423185.1_ASM42318v1
Micavibrio.aeruginosavorus.ARL.13 GCA_000226315.1_ASM22631v1
Tistrella.mobilis.KA081020.065 GCA_000264455.2_ASM26445v2
Geminicoccus.roseus.DSM.18922 GCA_000427665.1_ASM42766v1
Candidatus.Paracaedibacter.acanthamoebae GCA_000742835.1_ASM74283v1
Candidatus.Odyssella.thessalonicensis.L13 GCA_000190415.2_ASM19041v1
Candidatus.Finniella.inopinata GCA_004210305.1_ASM421030v1
Holospora.undulata.HU1 GCA_000388175.3_ASM38817v3
Candidatus.Hepatobacter.penaei GCA_000742475.1_ASM74247v1
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Caedimonas.varicaedens GCA_001192655.1_ASM119265v1
Candidatus.Nucleicultrix.amoebiphila.FS5 GCA_002117145.1_ASM211714v1
Candidatus.Neoehrlichia.lotoris.str.RAC413 GCA_000964795.1_ASM96479v1
Anaplasma.phagocytophilum.str.HZ GCA_000013125.1_ASM1312v1
Ehrlichia.ruminantium.str.Welgevonden GCA_000026005.1_ASM2600v1
Wolbachia.endosymbiont.of.Drosophila.melanogaster GCA_000008025.1_ASM802v1
Candidatus.Deianiraea.vastatrix GCA_007993655.1_ASM799365v1
Rickettsiales.endosymbiont.of.Trichoplax.sp.H2 GCA_009690945.1
Candidatus.Midichloria.mitochondrii.IricVA GCA_000219355.1_ASM21935v1
Rickettsiales.endosymbiont.of.Peranema.trichophorum GCA_004210275.1_ASM421027v1
Candidatus.Jidaibacter.acanthamoeba GCA_000815465.1.UWC36
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Rickettsiales.bacterium.Ac37b GCA_000746585.2_ASM74658v2
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Magnetofaba.australis.IT.1 GCA_002109495.1_ASM210949v1
Magnetococcus.marinus.MC.1 GCA_000014865.1_ASM1486v1
79.2/95
Nitrosospira.briensis.C.128 GCA_000619905.2_ASM61990v2
Methylotenera.versatilis.301 GCA_000093025.1_ASM9302v1
Ralstonia.pickettii GCA_902374465.1.MGYG.HGUT.01384
Burkholderia.cepacia GCA_009586235.1_ASM958623v1
Dasania.marina.DSM.21967 GCA_000373485.1_ASM37348v1
Congregibacter.litoralis.KT71 GCA_000153125.2_ASM15312v2
Enterobacter.cloacae GCA_000770155.1_ASM77015v1
Alteromonas.macleodii.ATCC.27126 GCA_000172635.2_ASM17263v2
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Group J

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Asticcacaulis.excentricus.CB.48 GCA_000175215.2_ASM17521v2
Phenylobacterium.zucineum.HLK1 GCA_000017265.1_ASM1726v1
Caulobacter.vibrioides.NA1000 GCA_000022005.1_ASM2200v1
Oceanicaulis.alexandrii.DSM.11625 GCA_000420265.1_ASM42026v1
Maricaulis.maris GCA_003634045.1_ASM363404v1
Hyphomonas.neptunium.ATCC.15444 GCA_000013025.1_ASM1302v1
Hirschia.baltica.ATCC.49814 GCA_000023785.1_ASM2378v1
Parvularcula.bermudensis.HTCC2503 GCA_000152825.2_ASM15282v2
Sagittula.stellata.E.37 GCA_000169415.1_ASM16941v1
Ruegeria.pomeroyi.DSS.3 GCA_000011965.2_ASM1196v2
Octadecabacter.arcticus.238 GCA_000155735.2_ASM15573v2
Jannaschia.rubra GCA_900113265.1.IMG.taxon.2622736430.annotated.assembly
Rubellimicrobium.rubrum GCA_006152115.1_ASM615211v1
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Rhodobacter.sphaeroides.ATCC.17029 GCA_000015985.1_ASM1598v1
Paracoccus.denitrificans GCA_004063735.1_ASM406373v1
Neomegalonema.perideroedes.DSM.15528 GCA_000374145.1_ASM37414v1
30.3/50 Rhizobium.leguminosarum.bv.trifolii GCA_011604525.1_ASM1160452v1
Bartonella.quintana GCA_009936175.1_ASM993617v1
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Pelagibacterium.halotolerans GCA_013004005.1_ASM1300400v1
Roseibium.hamelinense GCA_007830545.1_ASM783054v1
Polymorphum.gilvum.SL003B.26A1 GCA_000192745.1_ASM19274v1
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Sphingomonas.wittichii.RW1 GCA_000016765.1_ASM1676v1
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Kordiimonas.gwangyangensis.DSM.19435 GCA_000375545.1_ASM37554v1
Sneathiella.glossodoripedis.JCM.23214 GCA_000616095.1_ASM61609v1
Gluconobacter.oxydans.DSM.3504 GCA_000583855.1_ASM58385v1
Acetobacter.aceti.NBRC.14818 GCA_000193495.2_ASM19349v2
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Commensalibacter.intestini.A911 GCA_000231445.2_ASM23144v1
Granulibacter.bethesdensis.CGDNIH4 GCA_000576145.2_ASM57614v2
Acidisphaera.rubrifaciens.HS.AP3 GCA_000964365.1_ASM96436v1
Acidiphilium.multivorum.AIU301 GCA_000202835.1_ASM20283v1
Rubritepida.flocculans.DSM.14296 GCA_000425365.1_ASM42536v1
Belnapia.moabensis.DSM.16746 GCA_000745835.1_ASM74583v1
Roseomonas.gilardii GCA_001941945.1_ASM194194v1
Elioraea.tepidiphila.DSM.17972 GCA_000378465.1_ASM37846v1
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Pararhodospirillum.photometricum.DSM.122 GCA_000284415.2_ASM28441v2
Roseospirillum.parvum GCA_900100455.1
Caenispirillum.salinarum.AK4 GCA_000315795.1
Magnetospirillum.magneticum.AMB.1 GCA_000009985.1_ASM998v1
Thalassospira.profundimaris.WP0211 GCA_000300275.1_ASM30027v1
Terasakiella.pusilla.DSM.6293 GCA_000688235.1_ASM68823v1
alpha.proteobacterium.BAL199 GCA_000171835.1_ASM17183v1
Thalassobaculum.salexigens.DSM.19539 GCA_000423805.1_ASM42380v1
Candidatus.Puniceispirillum.marinum.IMCC1322 GCA_000024465.1_ASM2446v1
Oceanibaculum.indicum GCA_003633955.1_ASM363395v1
Rhodovibrio.salinarum.DSM.9154 GCA_000515255.1_ASM51525v1
Kiloniella.laminariae.DSM.19542 GCA_000374005.1_ASM37400v1
Rhodospirillum.centenum GCA_014197805.1_ASM1419780v1
Inquilinus.limosus.DSM.16000 GCA_000423185.1_ASM42318v1
Micavibrio.aeruginosavorus.ARL.13 GCA_000226315.1_ASM22631v1
Tistrella.mobilis.KA081020.065 GCA_000264455.2_ASM26445v2
Geminicoccus.roseus.DSM.18922 GCA_000427665.1_ASM42766v1
Candidatus.Paracaedibacter.acanthamoebae GCA_000742835.1_ASM74283v1
Candidatus.Odyssella.thessalonicensis.L13 GCA_000190415.2_ASM19041v1
Candidatus.Finniella.inopinata GCA_004210305.1_ASM421030v1
Candidatus.Caedibacter.acanthamoebae GCA_000743035.1_ASM74303v1
Caedimonas.varicaedens GCA_001192655.1_ASM119265v1
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100/100
Roseibium.hamelinense GCA_007830545.1_ASM783054v1
100/100
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99.4/100
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69.5/86
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30.3/86
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Nitrosospira.briensis.C.128 GCA_000619905.2_ASM61990v2
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Methylorubrum.extorquens.PA1 GCA_000018845.1_ASM1884v1
Xanthobacter.autotrophicus.Py2 GCA_000017645.1_ASM1764v1
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Roseomonas.gilardii GCA_001941945.1_ASM194194v1
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Ehrlichia.ruminantium.str.Welgevonden GCA_000026005.1_ASM2600v1
Wolbachia.endosymbiont.of.Drosophila.melanogaster GCA_000008025.1_ASM802v1
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Rickettsiales.endosymbiont.of.Trichoplax.sp.H2 GCA_009690945.1
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Rickettsia.bellii.RML369.C GCA_000012385.1_ASM1238v1
Candidatus.Megaira.polyxenophila
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Magnetofaba.australis.IT.1 GCA_002109495.1_ASM210949v1
Magnetococcus.marinus.MC.1 GCA_000014865.1_ASM1486v1
Nitrosospira.briensis.C.128 GCA_000619905.2_ASM61990v2
Methylotenera.versatilis.301 GCA_000093025.1_ASM9302v1
Ralstonia.pickettii GCA_902374465.1.MGYG.HGUT.01384
Burkholderia.cepacia GCA_009586235.1_ASM958623v1
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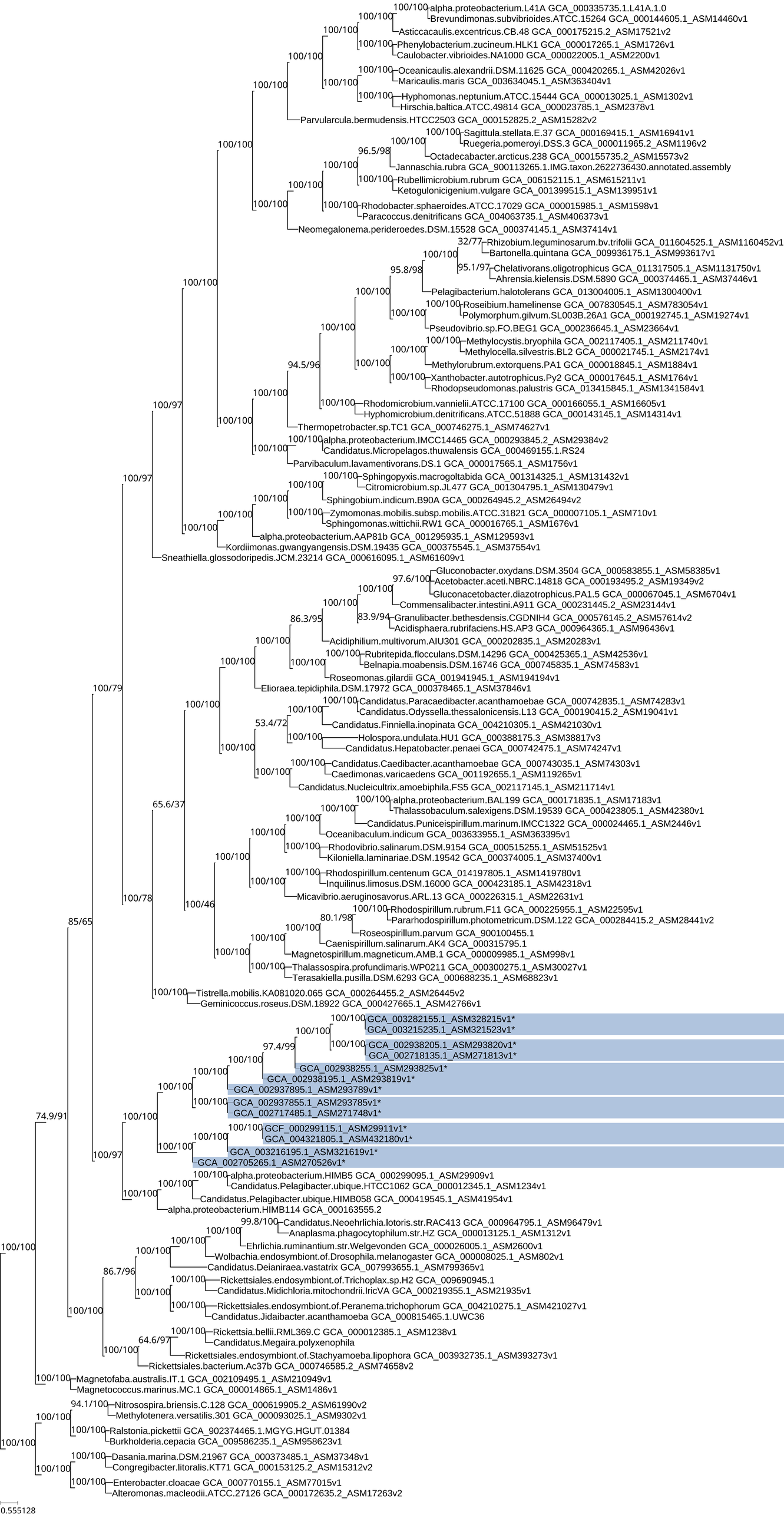
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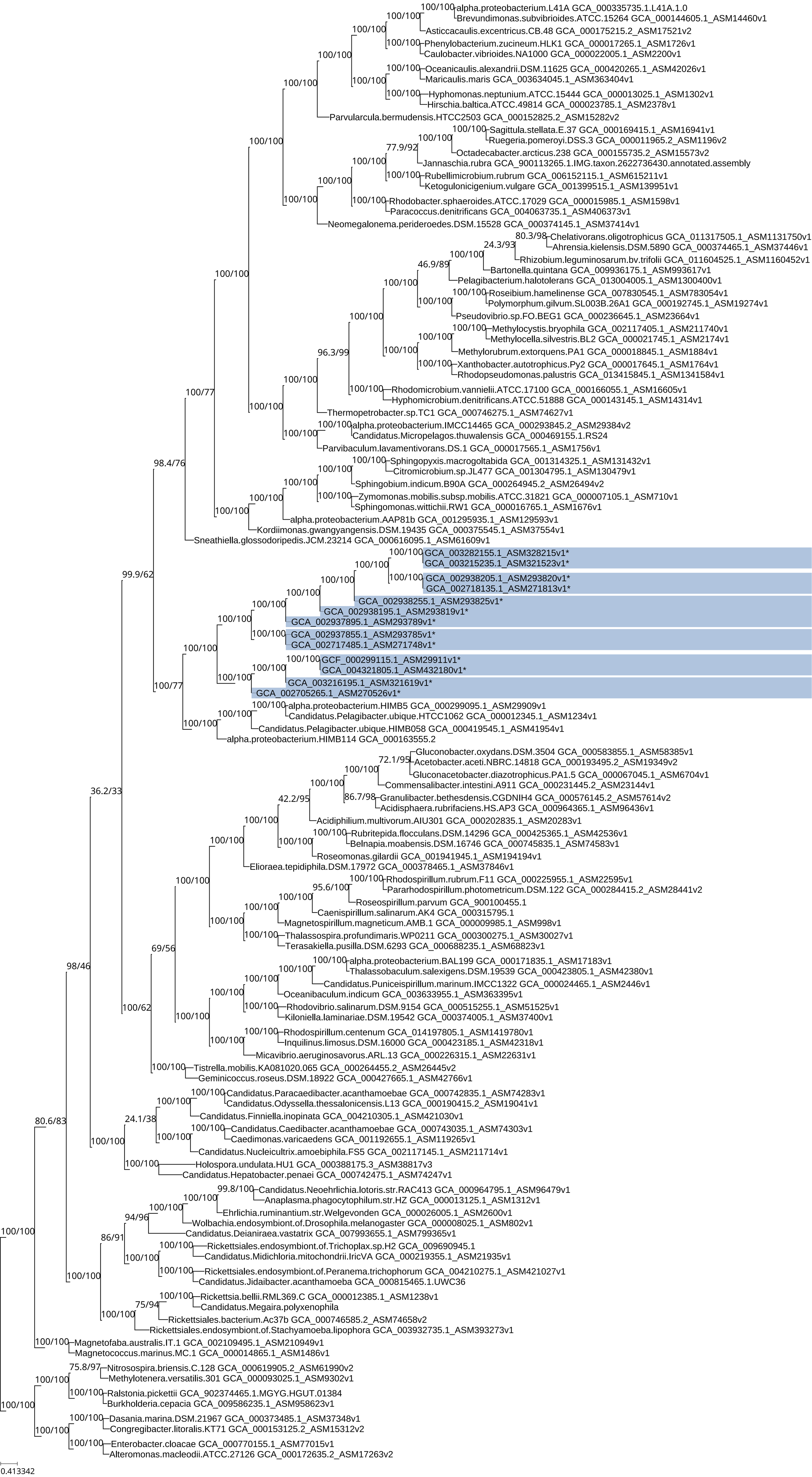
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Bartonella.quintana GCA_009936175.1_ASM993617v1
Pelagibacterium.halotolerans GCA_013004005.1_ASM1300400v1
100/100
100/100
Roseibium.hamelinense GCA_007830545.1_ASM783054v1
100/100
Polymorphum.gilvum.SL003B.26A1 GCA_000192745.1_ASM19274v1
100/100
Pseudovibrio.sp.FO.BEG1 GCA_000236645.1_ASM23664v1
100/100
Methylocystis.bryophila GCA_002117405.1_ASM211740v1
100/100
Methylocella.silvestris.BL2 GCA_000021745.1_ASM2174v1
100/100
96.3/99
Methylorubrum.extorquens.PA1 GCA_000018845.1_ASM1884v1
100/100
Xanthobacter.autotrophicus.Py2 GCA_000017645.1_ASM1764v1
Rhodopseudomonas.palustris GCA_013415845.1_ASM1341584v1
100/100
100/100
Rhodomicrobium.vannielii.ATCC.17100 GCA_000166055.1_ASM16605v1
Hyphomicrobium.denitrificans.ATCC.51888 GCA_000143145.1_ASM14314v1
100/100
100/77
Thermopetrobacter.sp.TC1 GCA_000746275.1_ASM74627v1
100/100
alpha.proteobacterium.IMCC14465 GCA_000293845.2_ASM29384v2
100/100
Candidatus.Micropelagos.thuwalensis GCA_000469155.1.RS24
Parvibaculum.lavamentivorans.DS.1 GCA_000017565.1_ASM1756v1
98.4/76
100/100
Sphingopyxis.macrogoltabida GCA_001314325.1_ASM131432v1
100/100
Citromicrobium.sp.JL477 GCA_001304795.1_ASM130479v1
100/100
Sphingobium.indicum.B90A GCA_000264945.2_ASM26494v2
100/100
100/100
Zymomonas.mobilis.subsp.mobilis.ATCC.31821 GCA_000007105.1_ASM710v1
100/100
Sphingomonas.wittichii.RW1 GCA_000016765.1_ASM1676v1
alpha.proteobacterium.AAP81b GCA_001295935.1_ASM129593v1
Kordiimonas.gwangyangensis.DSM.19435 GCA_000375545.1_ASM37554v1
Sneathiella.glossodoripedis.JCM.23214 GCA_000616095.1_ASM61609v1
100/100
GCA_003282155.1_ASM328215v1*
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GCA_003215235.1_ASM321523v1*
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100/100
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99.9/62
100/100
GCA_002938255.1_ASM293825v1*
100/100
GCA_002938195.1_ASM293819v1*
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100/100
100/100
GCA_002937855.1_ASM293785v1*
GCA_002717485.1_ASM271748v1*
100/100
100/100
GCF_000299115.1_ASM29911v1*
GCA_004321805.1_ASM432180v1*
100/100
100/100
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GCA_002705265.1_ASM270526v1*
100/77
100/100
alpha.proteobacterium.HIMB5 GCA_000299095.1_ASM29909v1
100/100
Candidatus.Pelagibacter.ubique.HTCC1062 GCA_000012345.1_ASM1234v1
100/100
Candidatus.Pelagibacter.ubique.HIMB058 GCA_000419545.1_ASM41954v1
alpha.proteobacterium.HIMB114 GCA_000163555.2
72.1/95
Gluconobacter.oxydans.DSM.3504 GCA_000583855.1_ASM58385v1
Acetobacter.aceti.NBRC.14818 GCA_000193495.2_ASM19349v2
100/100
Gluconacetobacter.diazotrophicus.PA1.5 GCA_000067045.1_ASM6704v1
100/100
Commensalibacter.intestini.A911 GCA_000231445.2_ASM23144v1
36.2/33
86.7/98
Granulibacter.bethesdensis.CGDNIH4 GCA_000576145.2_ASM57614v2
42.2/95
Acidisphaera.rubrifaciens.HS.AP3 GCA_000964365.1_ASM96436v1
100/100
Acidiphilium.multivorum.AIU301 GCA_000202835.1_ASM20283v1
100/100
100/100
Rubritepida.flocculans.DSM.14296 GCA_000425365.1_ASM42536v1
100/100
Belnapia.moabensis.DSM.16746 GCA_000745835.1_ASM74583v1
Roseomonas.gilardii GCA_001941945.1_ASM194194v1
Elioraea.tepidiphila.DSM.17972 GCA_000378465.1_ASM37846v1
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100/100
Rhodospirillum.rubrum.F11 GCA_000225955.1_ASM22595v1
95.6/100
Pararhodospirillum.photometricum.DSM.122 GCA_000284415.2_ASM28441v2
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Roseospirillum.parvum GCA_900100455.1
100/100
Caenispirillum.salinarum.AK4 GCA_000315795.1
100/100
Magnetospirillum.magneticum.AMB.1 GCA_000009985.1_ASM998v1
100/100
Thalassospira.profundimaris.WP0211 GCA_000300275.1_ASM30027v1
Terasakiella.pusilla.DSM.6293 GCA_000688235.1_ASM68823v1
69/56
98/46
100/100
alpha.proteobacterium.BAL199 GCA_000171835.1_ASM17183v1
100/100
Thalassobaculum.salexigens.DSM.19539 GCA_000423805.1_ASM42380v1
100/100
Candidatus.Puniceispirillum.marinum.IMCC1322 GCA_000024465.1_ASM2446v1
100/100
Oceanibaculum.indicum GCA_003633955.1_ASM363395v1
100/62
100/100
Rhodovibrio.salinarum.DSM.9154 GCA_000515255.1_ASM51525v1
Kiloniella.laminariae.DSM.19542 GCA_000374005.1_ASM37400v1
100/100
Rhodospirillum.centenum GCA_014197805.1_ASM1419780v1
100/100
Inquilinus.limosus.DSM.16000 GCA_000423185.1_ASM42318v1
Micavibrio.aeruginosavorus.ARL.13 GCA_000226315.1_ASM22631v1
100/100
Tistrella.mobilis.KA081020.065 GCA_000264455.2_ASM26445v2
Geminicoccus.roseus.DSM.18922 GCA_000427665.1_ASM42766v1
100/100
Candidatus.Paracaedibacter.acanthamoebae GCA_000742835.1_ASM74283v1
100/100
Candidatus.Odyssella.thessalonicensis.L13 GCA_000190415.2_ASM19041v1
80.6/83
24.1/38
Candidatus.Finniella.inopinata GCA_004210305.1_ASM421030v1
100/100
Candidatus.Caedibacter.acanthamoebae GCA_000743035.1_ASM74303v1
100/100
Caedimonas.varicaedens GCA_001192655.1_ASM119265v1
100/100
Candidatus.Nucleicultrix.amoebiphila.FS5 GCA_002117145.1_ASM211714v1
100/100
Holospora.undulata.HU1 GCA_000388175.3_ASM38817v3
Candidatus.Hepatobacter.penaei GCA_000742475.1_ASM74247v1
99.8/100
Candidatus.Neoehrlichia.lotoris.str.RAC413 GCA_000964795.1_ASM96479v1
100/100
Anaplasma.phagocytophilum.str.HZ GCA_000013125.1_ASM1312v1
100/100
Ehrlichia.ruminantium.str.Welgevonden GCA_000026005.1_ASM2600v1
94/96
Wolbachia.endosymbiont.of.Drosophila.melanogaster GCA_000008025.1_ASM802v1
100/100
Candidatus.Deianiraea.vastatrix GCA_007993655.1_ASM799365v1
86/91
100/100
Rickettsiales.endosymbiont.of.Trichoplax.sp.H2 GCA_009690945.1
100/100
Candidatus.Midichloria.mitochondrii.IricVA GCA_000219355.1_ASM21935v1
100/100
Rickettsiales.endosymbiont.of.Peranema.trichophorum GCA_004210275.1_ASM421027v1
100/100
Candidatus.Jidaibacter.acanthamoeba GCA_000815465.1.UWC36
100/100
Rickettsia.bellii.RML369.C GCA_000012385.1_ASM1238v1
75/94
Candidatus.Megaira.polyxenophila
100/100
Rickettsiales.bacterium.Ac37b GCA_000746585.2_ASM74658v2
Rickettsiales.endosymbiont.of.Stachyamoeba.lipophora GCA_003932735.1_ASM393273v1
100/100
Magnetofaba.australis.IT.1 GCA_002109495.1_ASM210949v1
Magnetococcus.marinus.MC.1 GCA_000014865.1_ASM1486v1
75.8/97
Nitrosospira.briensis.C.128 GCA_000619905.2_ASM61990v2
100/100
Methylotenera.versatilis.301 GCA_000093025.1_ASM9302v1
100/100
Ralstonia.pickettii GCA_902374465.1.MGYG.HGUT.01384
100/100
Burkholderia.cepacia GCA_009586235.1_ASM958623v1
100/100
100/100
Dasania.marina.DSM.21967 GCA_000373485.1_ASM37348v1
100/100
Congregibacter.litoralis.KT71 GCA_000153125.2_ASM15312v2
100/100
Enterobacter.cloacae GCA_000770155.1_ASM77015v1
Alteromonas.macleodii.ATCC.27126 GCA_000172635.2_ASM17263v2
0.413342

Group K

100/100 alpha.proteobacterium.L41A GCA_000335735.1.L41A.1.0
100/100 Brevundimonas.subvibrioides.ATCC.15264 GCA_000144605.1_ASM14460v1
100/100 Asticcacaulis.excentricus.CB.48 GCA_000175215.2_ASM17521v2
100/100 Phenylobacterium.zucineum.HLK1 GCA_000017265.1_ASM1726v1
Caulobacter.vibrioides.NA1000 GCA_000022005.1_ASM2200v1
100/100 Oceanicaulis.alexandrii.DSM.11625 GCA_000420265.1_ASM42026v1
100/100 Maricaulis.maris GCA_003634045.1_ASM363404v1
100/100 Hyphomonas.neptunium.ATCC.15444 GCA_000013025.1_ASM1302v1
Hirschia.baltica.ATCC.49814 GCA_000023785.1_ASM2378v1
Parvularcula.bermudensis.HTCC2503 GCA_000152825.2_ASM15282v2
100/100 Sagittula.stellata.E.37 GCA_000169415.1_ASM16941v1
100/100 Ruegeria.pomeroyi.DSS.3 GCA_000011965.2_ASM1196v2
99.9/100 Octadecabacter.arcticus.238 GCA_000155735.2_ASM15573v2
Jannaschia.rubra GCA_900113265.1.IMG.taxon.2622736430.annotated.assembly
100/100 Rubellimicrobium.rubrum GCA_006152115.1_ASM615211v1
Ketogulonicigenium.vulgare GCA_001399515.1_ASM139951v1
100/100 Rhodobacter.sphaeroides.ATCC.17029 GCA_000015985.1_ASM1598v1
Paracoccus.denitrificans GCA_004063735.1_ASM406373v1
Neomegalonema.perideroedes.DSM.15528 GCA_000374145.1_ASM37414v1
33.1/50 Rhizobium.leguminosarum.bv.trifolii GCA_011604525.1_ASM1160452v1
100/100 Bartonella.quintana GCA_009936175.1_ASM993617v1
71.7/89 94.8/55 Chelativorans.oligotrophicus GCA_011317505.1_ASM1131750v1
Ahrensia.kielensis.DSM.5890 GCA_000374465.1_ASM37446v1
Pelagibacterium.halotolerans GCA_013004005.1_ASM1300400v1
100/100 Roseibium.hamelinense GCA_007830545.1_ASM783054v1
100/100 Polymorphum.gilvum.SL003B.26A1 GCA_000192745.1_ASM19274v1
Pseudovibrio.sp.FO.BEG1 GCA_000236645.1_ASM23664v1
100/100 Methylocystis.bryophila GCA_002117405.1_ASM211740v1
Methylocella.silvestris.BL2 GCA_000021745.1_ASM2174v1
Methylorubrum.extorquens.PA1 GCA_000018845.1_ASM1884v1
98.7/98
100/100 Xanthobacter.autotrophicus.Py2 GCA_000017645.1_ASM1764v1
Rhodopseudomonas.palustris GCA_013415845.1_ASM1341584v1
100/100 Rhodomicrobium.vannielii.ATCC.17100 GCA_000166055.1_ASM16605v1
Hyphomicrobium.denitrificans.ATCC.51888 GCA_000143145.1_ASM14314v1
Thermopetrobacter.sp.TC1 GCA_000746275.1_ASM74627v1
100/100 alpha.proteobacterium.IMCC14465 GCA_000293845.2_ASM29384v2
100/100 Candidatus.Micropelagos.thuwalensis GCA_000469155.1.RS24
Parvibaculum.lavamentivorans.DS.1 GCA_000017565.1_ASM1756v1
100/100 Sphingopyxis.macrogoltabida GCA_001314325.1_ASM131432v1
Citromicrobium.sp.JL477 GCA_001304795.1_ASM130479v1
Sphingobium.indicum.B90A GCA_000264945.2_ASM26494v2
100/100 Zymomonas.mobilis.subsp.mobilis.ATCC.31821 GCA_000007105.1_ASM710v1
Sphingomonas.wittichii.RW1 GCA_000016765.1_ASM1676v1
alpha.proteobacterium.AAP81b GCA_001295935.1_ASM129593v1
Kordiimonas.gwangyangensis.DSM.19435 GCA_000375545.1_ASM37554v1
Sneathiella.glossodoripedis.JCM.23214 GCA_000616095.1_ASM61609v1
100/100 alpha.proteobacterium.BAL199 GCA_000171835.1_ASM17183v1
Thalassobaculum.salexigens.DSM.19539 GCA_000423805.1_ASM42380v1
Candidatus.Puniceispirillum.marinum.IMCC1322 GCA_000024465.1_ASM2446v1
Oceanibaculum.indicum GCA_003633955.1_ASM363395v1
Rhodovibrio.salinarum.DSM.9154 GCA_000515255.1_ASM51525v1
Kiloniella.laminariae.DSM.19542 GCA_000374005.1_ASM37400v1
Rhodospirillum.centenum GCA_014197805.1_ASM1419780v1
Inquilinus.limosus.DSM.16000 GCA_000423185.1_ASM42318v1
Micavibrio.aeruginosavorus.ARL.13 GCA_000226315.1_ASM22631v1
5.5/35
100/100 Rhodospirillum.rubrum.F11 GCA_000225955.1_ASM22595v1
57.2/94 Pararhodospirillum.photometricum.DSM.122 GCA_000284415.2_ASM28441v2
Roseospirillum.parvum GCA_900100455.1
Caenispirillum.salinarum.AK4 GCA_000315795.1
Magnetospirillum.magneticum.AMB.1 GCA_000009985.1_ASM998v1
Thalassospira.profundimaris.WP0211 GCA_000300275.1_ASM30027v1
Terasakiella.pusilla.DSM.6293 GCA_000688235.1_ASM68823v1
Gluconobacter.oxydans.DSM.3504 GCA_000583855.1_ASM58385v1
98.8/100 Acetobacter.aceti.NBRC.14818 GCA_000193495.2_ASM19349v2
Gluconacetobacter.diazotrophicus.PA1.5 GCA_000067045.1_ASM6704v1
Commensalibacter.intestini.A911 GCA_000231445.2_ASM23144v1
97.3/99 99.7/99 Granulibacter.bethesdensis.CGDNIH4 GCA_000576145.2_ASM57614v2
Acidisphaera.rubrifaciens.HS.AP3 GCA_000964365.1_ASM96436v1
Acidiphilium.multivorum.AIU301 GCA_000202835.1_ASM20283v1
87.6/97 Rubritepida.flocculans.DSM.14296 GCA_000425365.1_ASM42536v1
Belnapia.moabensis.DSM.16746 GCA_000745835.1_ASM74583v1
Roseomonas.gilardii GCA_001941945.1_ASM194194v1
Elioraea.tepidiphila.DSM.17972 GCA_000378465.1_ASM37846v1
Tistrella.mobilis.KA081020.065 GCA_000264455.2_ASM26445v2
Geminicoccus.roseus.DSM.18922 GCA_000427665.1_ASM42766v1
GCA_002937655.1_ASM293765v1*
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51.4/88
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GCA_002170595.1_ASM217059v1*
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Candidatus.Pelagibacter.ubique.HTCC1062 GCA_000012345.1_ASM1234v1
Candidatus.Pelagibacter.ubique.HIMB058 GCA_000419545.1_ASM41954v1
alpha.proteobacterium.HIMB114 GCA_000163555.2
95.8/100 Candidatus.Neoehrlichia.lotoris.str.RAC413 GCA_000964795.1_ASM96479v1
Anaplasma.phagocytophilum.str.HZ GCA_000013125.1_ASM1312v1
Ehrlichia.ruminantium.str.Welgevonden GCA_000026005.1_ASM2600v1
Wolbachia.endosymbiont.of.Drosophila.melanogaster GCA_000008025.1_ASM802v1
Candidatus.Deianiraea.vastatrix GCA_007993655.1_ASM799365v1
99.1/100
Rickettsiales.endosymbiont.of.Trichoplax.sp.H2 GCA_009690945.1
Candidatus.Midichloria.mitochondrii.IricVA GCA_000219355.1_ASM21935v1
Rickettsiales.endosymbiont.of.Peranema.trichophorum GCA_004210275.1_ASM421027v1
Candidatus.Jidaibacter.acanthamoeba GCA_000815465.1.UWC36
Rickettsia.bellii.RML369.C GCA_000012385.1_ASM1238v1
Candidatus.Megaira.polyxenophila
66.2/89
Rickettsiales.endosymbiont.of.Stachyamoeba.lipophora GCA_003932735.1_ASM393273v1
Rickettsiales.bacterium.Ac37b GCA_000746585.2_ASM74658v2
Candidatus.Paracaedibacter.acanthamoebae GCA_000742835.1_ASM74283v1
Candidatus.Odyssella.thessalonicensis.L13 GCA_000190415.2_ASM19041v1
Candidatus.Finniella.inopinata GCA_004210305.1_ASM421030v1
98.9/97
Candidatus.Caedibacter.acanthamoebae GCA_000743035.1_ASM74303v1
Caedimonas.varicaedens GCA_001192655.1_ASM119265v1
Candidatus.Nucleicultrix.amoebiphila.FS5 GCA_002117145.1_ASM211714v1
Holospora.undulata.HU1 GCA_000388175.3_ASM38817v3
Candidatus.Hepatobacter.penaei GCA_000742475.1_ASM74247v1
68/49
Magnetofaba.australis.IT.1 GCA_002109495.1_ASM210949v1
Magnetococcus.marinus.MC.1 GCA_000014865.1_ASM1486v1
Nitrosospira.briensis.C.128 GCA_000619905.2_ASM61990v2
Methylotenera.versatilis.301 GCA_000093025.1_ASM9302v1
Ralstonia.pickettii GCA_902374465.1.MGYG.HGUT.01384
Burkholderia.cepacia GCA_009586235.1_ASM958623v1
Dasania.marina.DSM.21967 GCA_000373485.1_ASM37348v1
Congregibacter.litoralis.KT71 GCA_000153125.2_ASM15312v2
Enterobacter.cloacae GCA_000770155.1_ASM77015v1
Alteromonas.macleodii.ATCC.27126 GCA_000172635.2_ASM17263v2
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Brevundimonas.subvibrioides.ATCC.15264 GCA_000144605.1_ASM14460v1
100/100
Asticcacaulis.excentricus.CB.48 GCA_000175215.2_ASM17521v2
100/100
Phenylobacterium.zucineum.HLK1 GCA_000017265.1_ASM1726v1
100/100
Caulobacter.vibrioides.NA1000 GCA_000022005.1_ASM2200v1
100/100
Oceanicaulis.alexandrii.DSM.11625 GCA_000420265.1_ASM42026v1
100/100
Maricaulis.maris GCA_003634045.1_ASM363404v1
100/100
Hyphomonas.neptunium.ATCC.15444 GCA_000013025.1_ASM1302v1
100/100
Hirschia.baltica.ATCC.49814 GCA_000023785.1_ASM2378v1
100/100
Parvularcula.bermudensis.HTCC2503 GCA_000152825.2_ASM15282v2
100/100
Sagittula.stellata.E.37 GCA_000169415.1_ASM16941v1
100/100
Ruegeria.pomeroyi.DSS.3 GCA_000011965.2_ASM1196v2
99.8/100
Octadecabacter.arcticus.238 GCA_000155735.2_ASM15573v2
100/100
Jannaschia.rubra GCA_900113265.1.IMG.taxon.2622736430.annotated.assembly
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Rubellimicrobium.rubrum GCA_006152115.1_ASM615211v1
100/100
Ketogulonicigenium.vulgare GCA_001399515.1_ASM139951v1
100/100
Rhodobacter.sphaeroides.ATCC.17029 GCA_000015985.1_ASM1598v1
100/100
Paracoccus.denitrificans GCA_004063735.1_ASM406373v1
100/100
Neomegalonema.perideroedes.DSM.15528 GCA_000374145.1_ASM37414v1
10.4/59
Chelativorans.oligotrophicus GCA_011317505.1_ASM1131750v1
81.4/93
Ahrensia.kielensis.DSM.5890 GCA_000374465.1_ASM37446v1
100/100
Rhizobium.leguminosarum.bv.trifolii GCA_011604525.1_ASM1160452v1
90.8/94
Bartonella.quintana GCA_009936175.1_ASM993617v1
100/100
Pelagibacterium.halotolerans GCA_013004005.1_ASM1300400v1
100/100
Roseibium.hamelinense GCA_007830545.1_ASM783054v1
100/100
Polymorphum.gilvum.SL003B.26A1 GCA_000192745.1_ASM19274v1
100/100
Pseudovibrio.sp.FO.BEG1 GCA_000236645.1_ASM23664v1
100/100
Methylocystis.bryophila GCA_002117405.1_ASM211740v1
100/100
Methylocella.silvestris.BL2 GCA_000021745.1_ASM2174v1
100/100
Methylorubrum.extorquens.PA1 GCA_000018845.1_ASM1884v1
99.4/100
100/100
Xanthobacter.autotrophicus.Py2 GCA_000017645.1_ASM1764v1
100/100
Rhodopseudomonas.palustris GCA_013415845.1_ASM1341584v1
100/100
Rhodomicrobium.vannielii.ATCC.17100 GCA_000166055.1_ASM16605v1
100/100
Hyphomicrobium.denitrificans.ATCC.51888 GCA_000143145.1_ASM14314v1
100/100
Thermopetrobacter.sp.TC1 GCA_000746275.1_ASM74627v1
100/100
alpha.proteobacterium.IMCC14465 GCA_000293845.2_ASM29384v2
100/100
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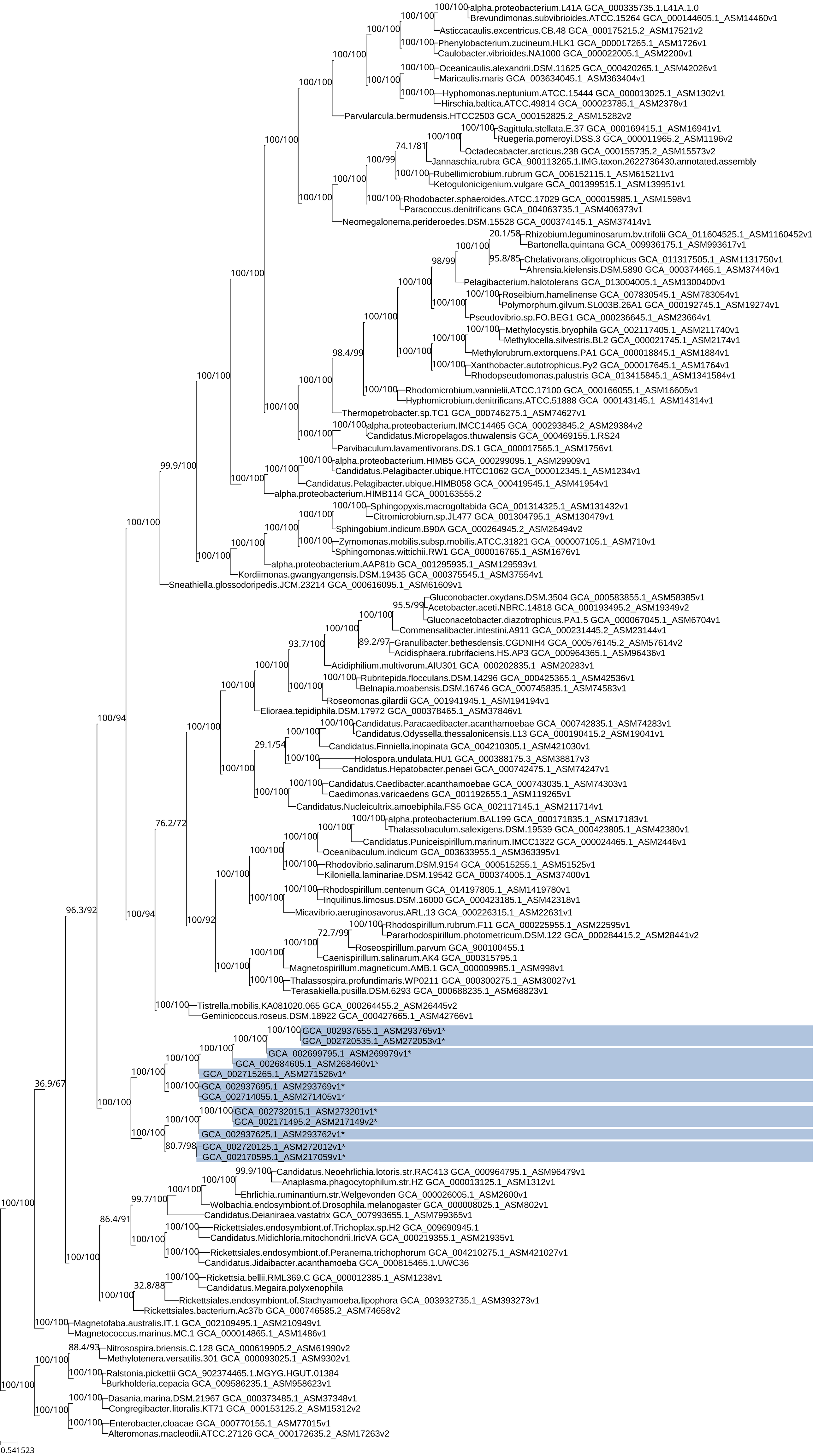
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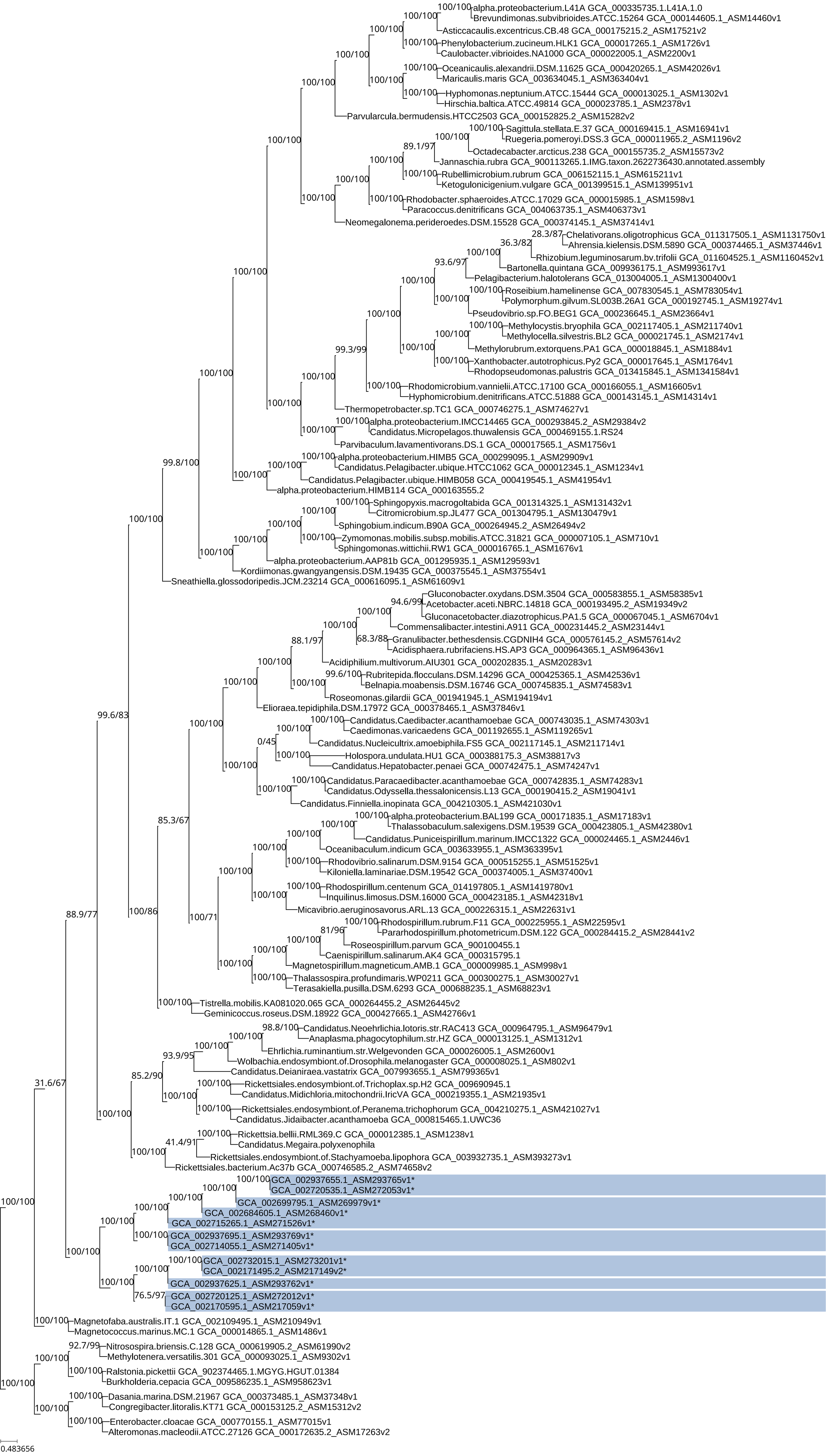
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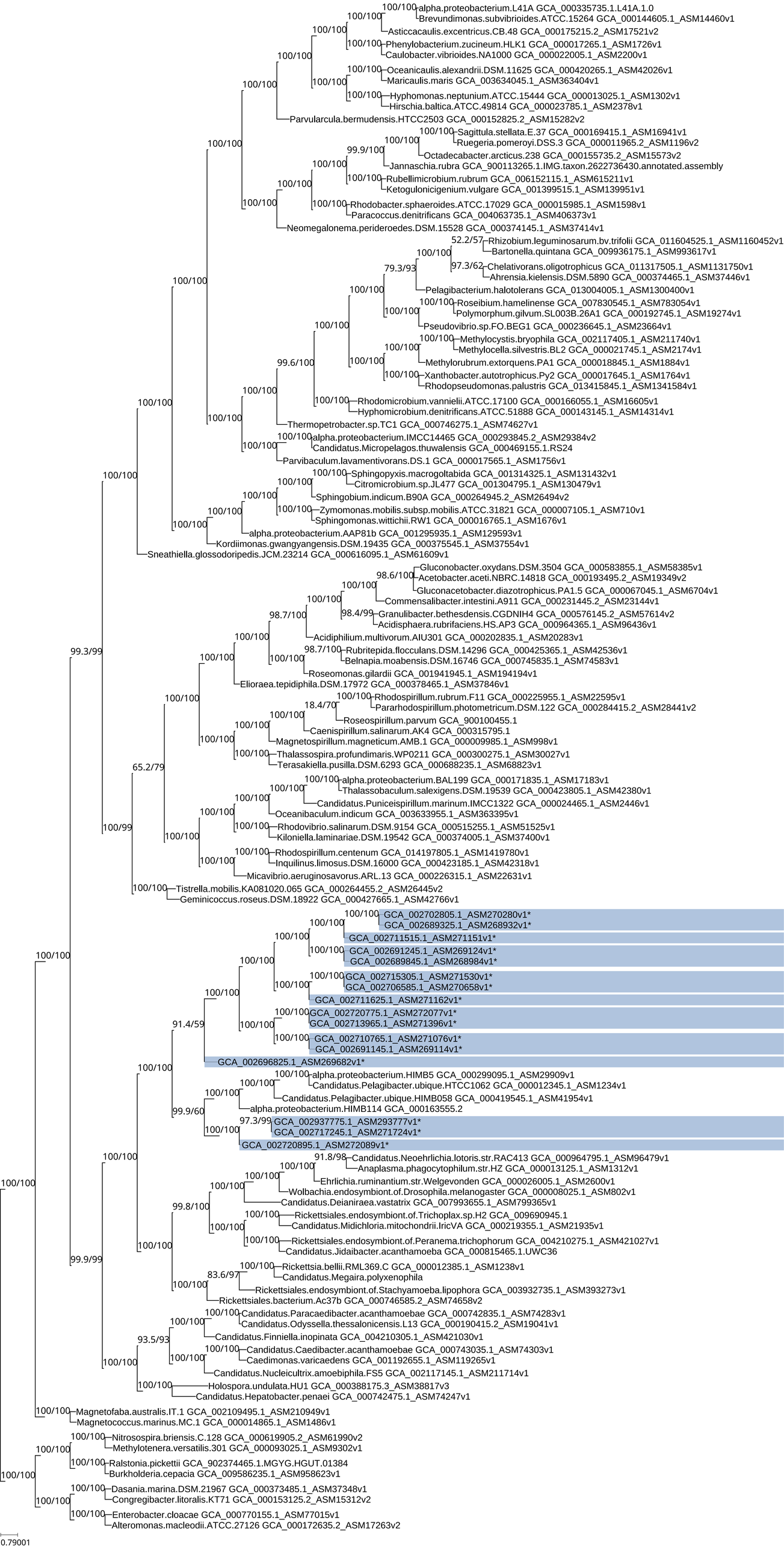
Group L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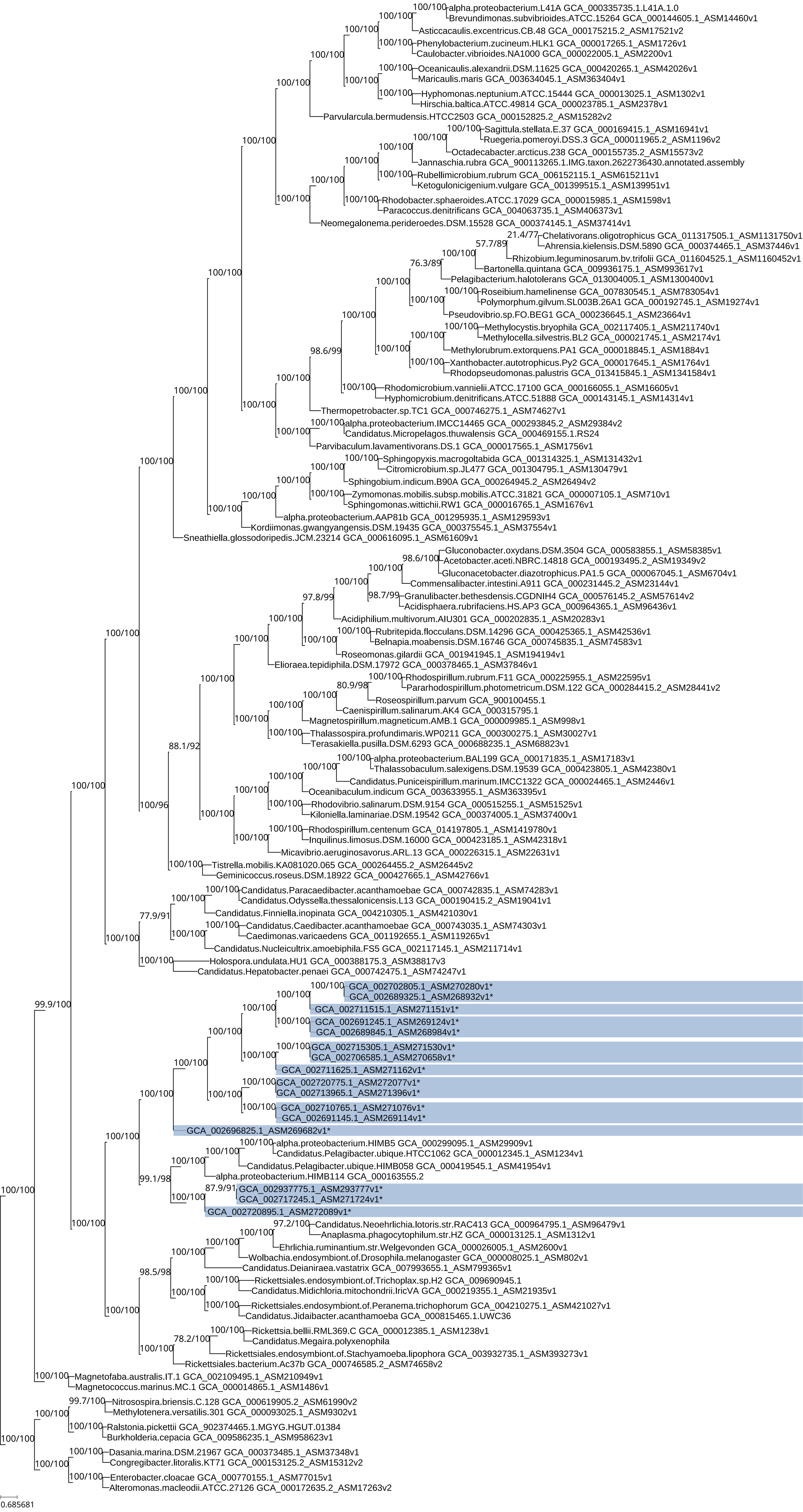
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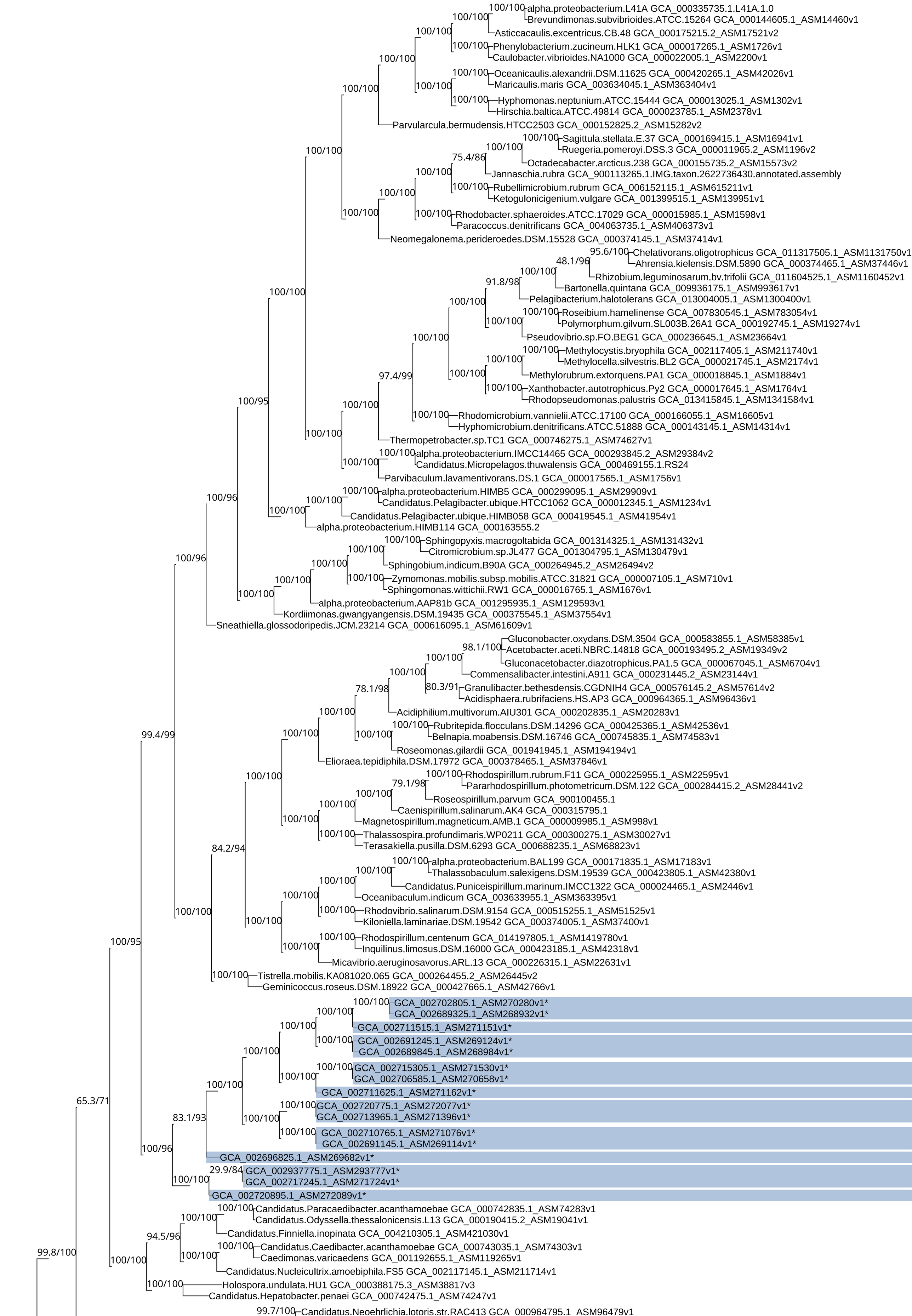
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59.5/88 Candidatus.Megaira.polyxenophila
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Caedimonas.varicaedens GCA_001192655.1_ASM119265v1
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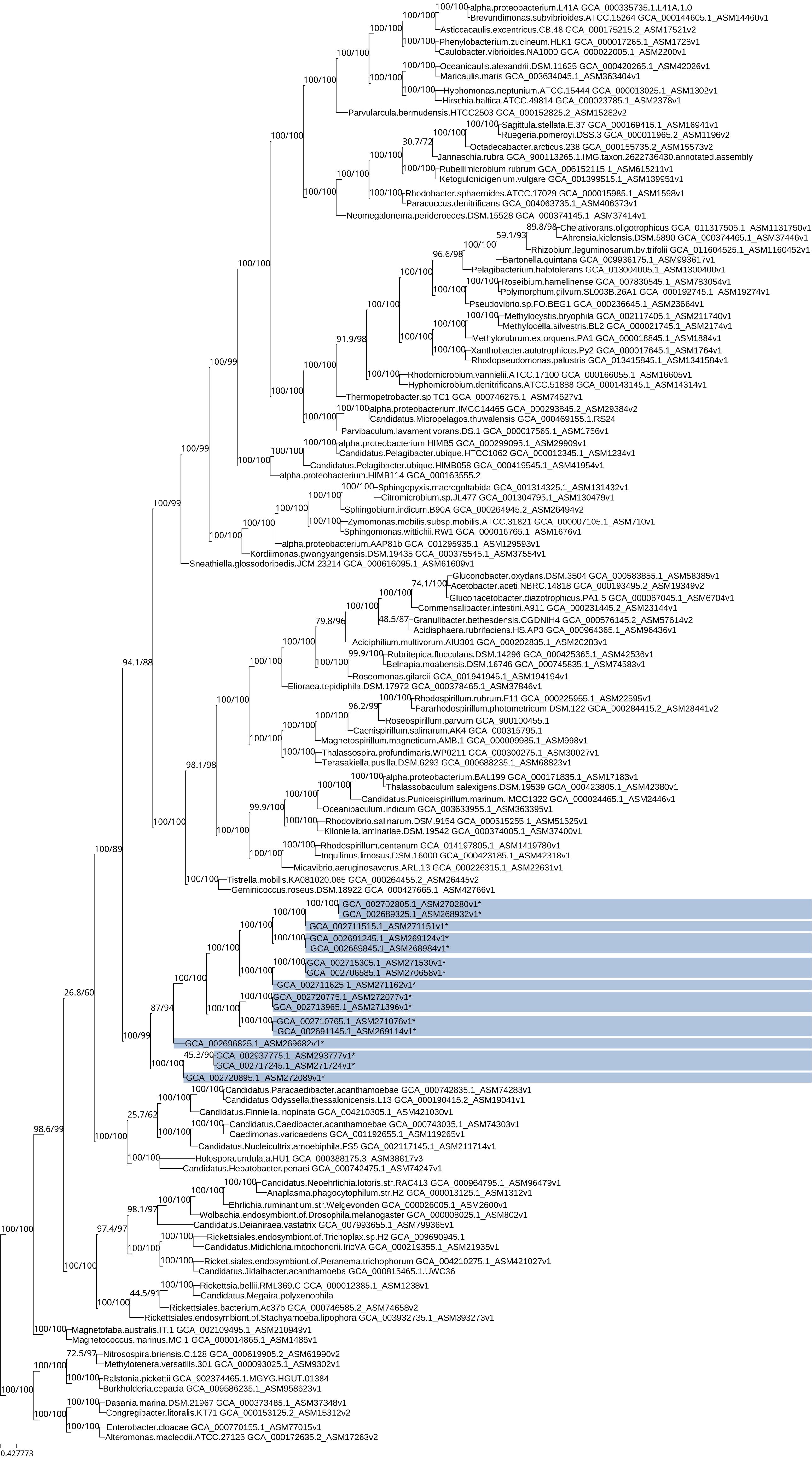
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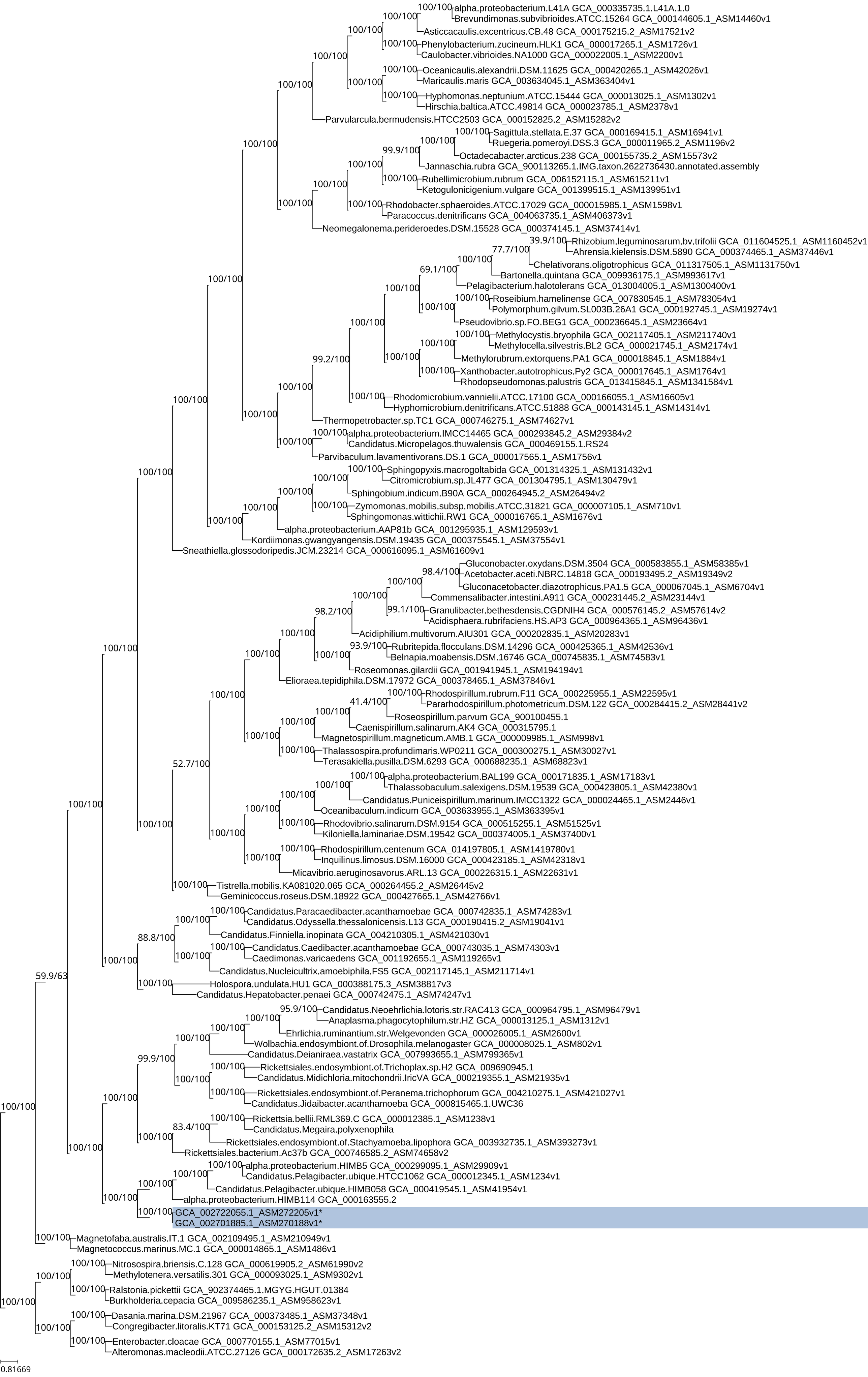
Group M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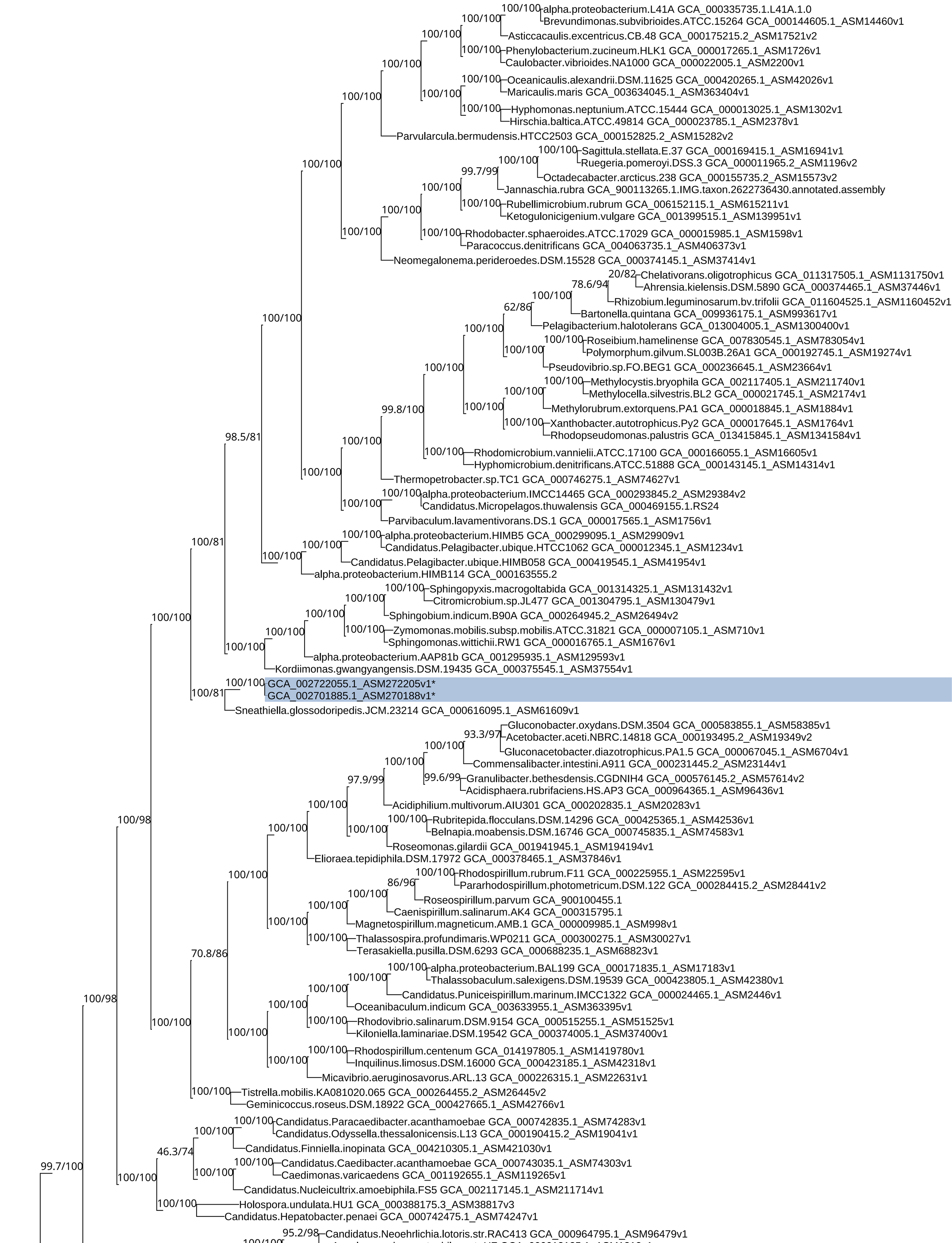
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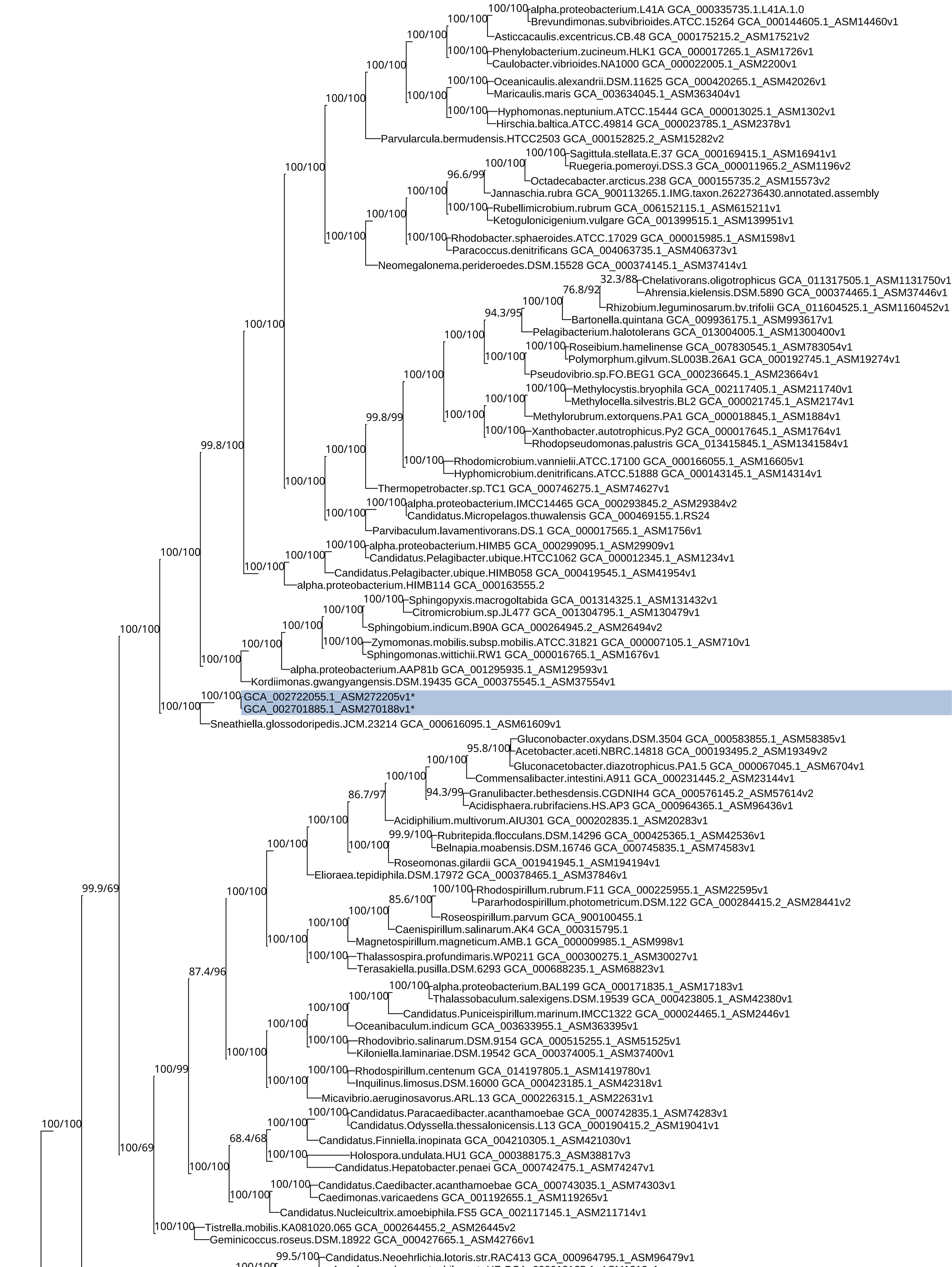
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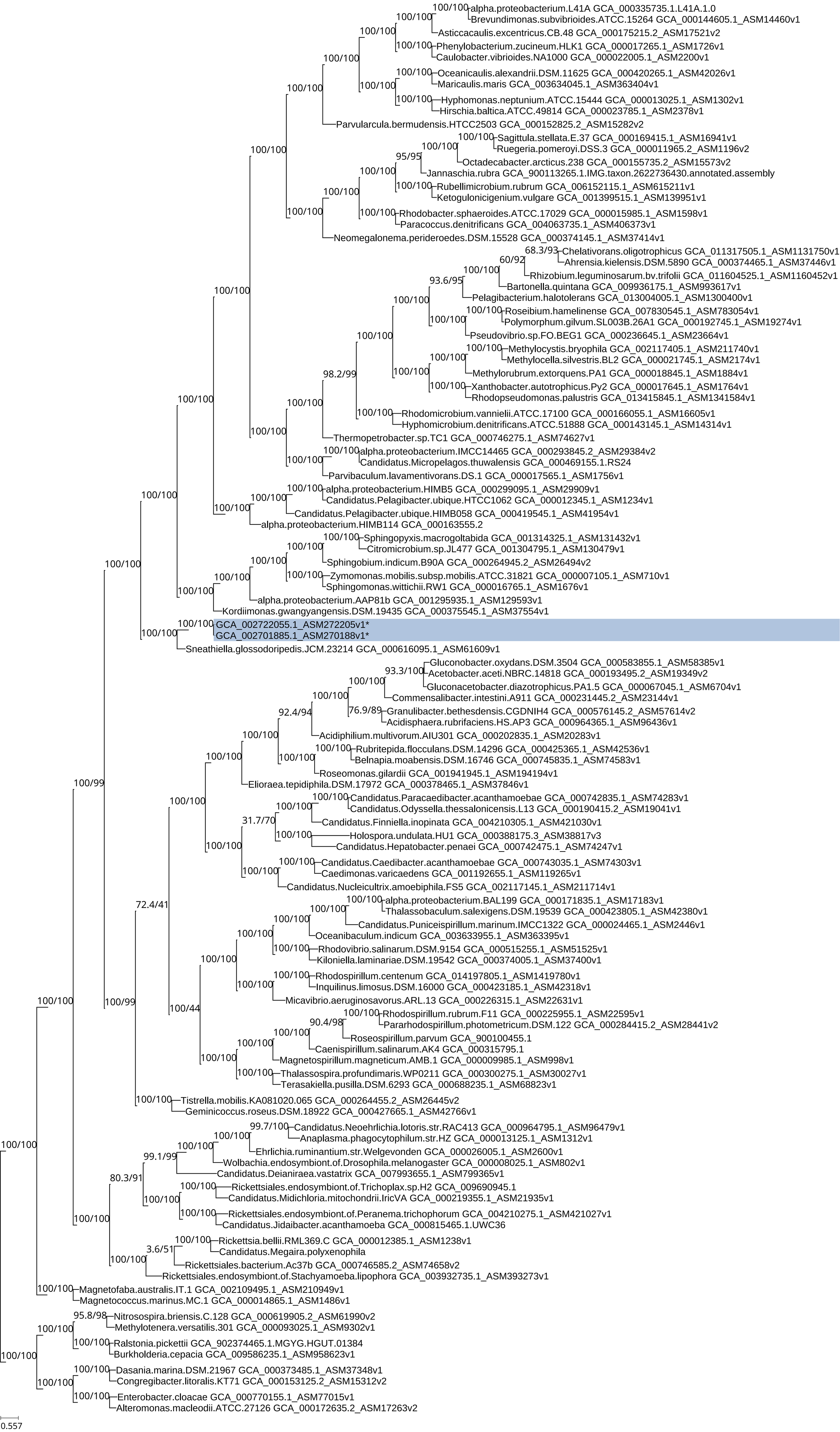
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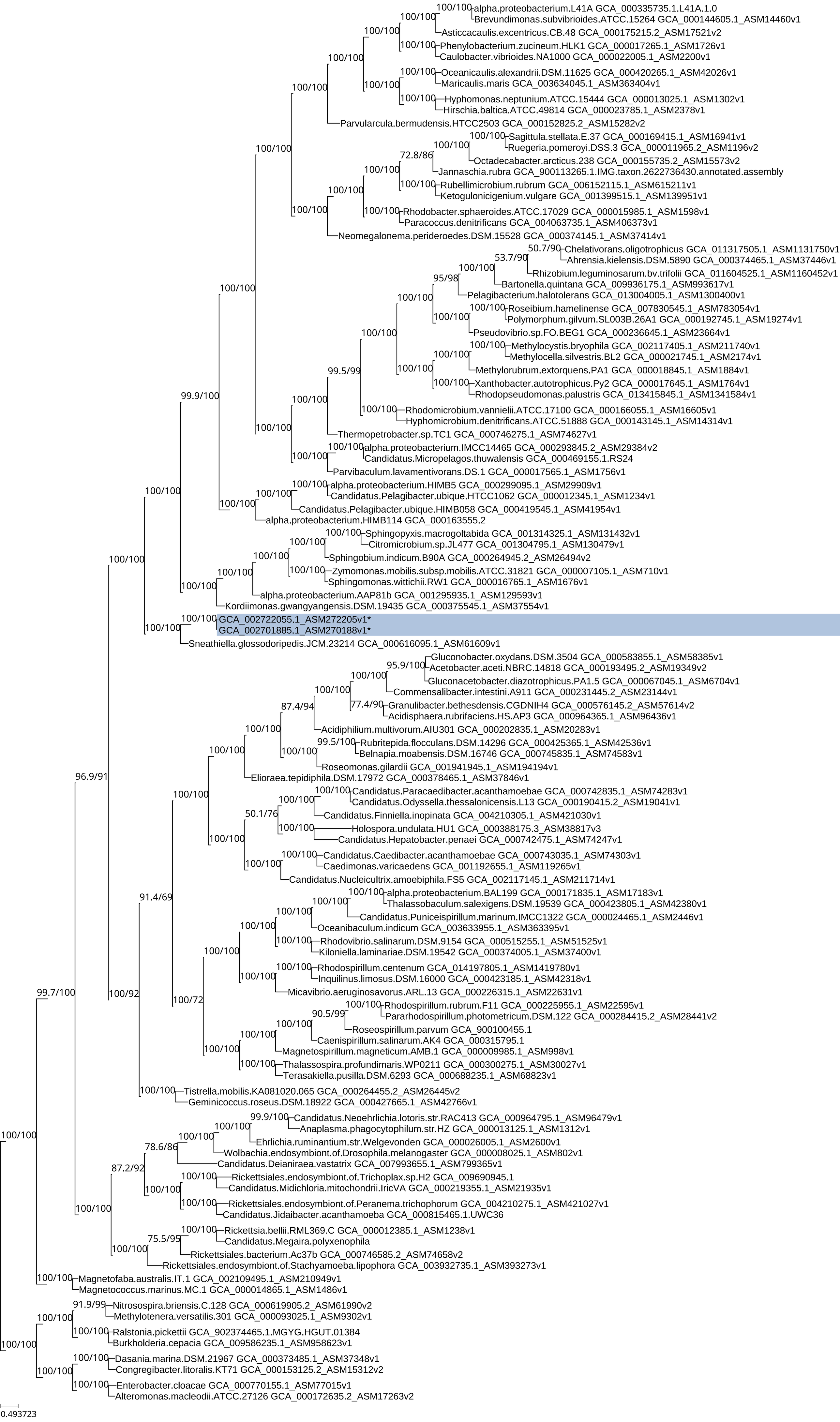
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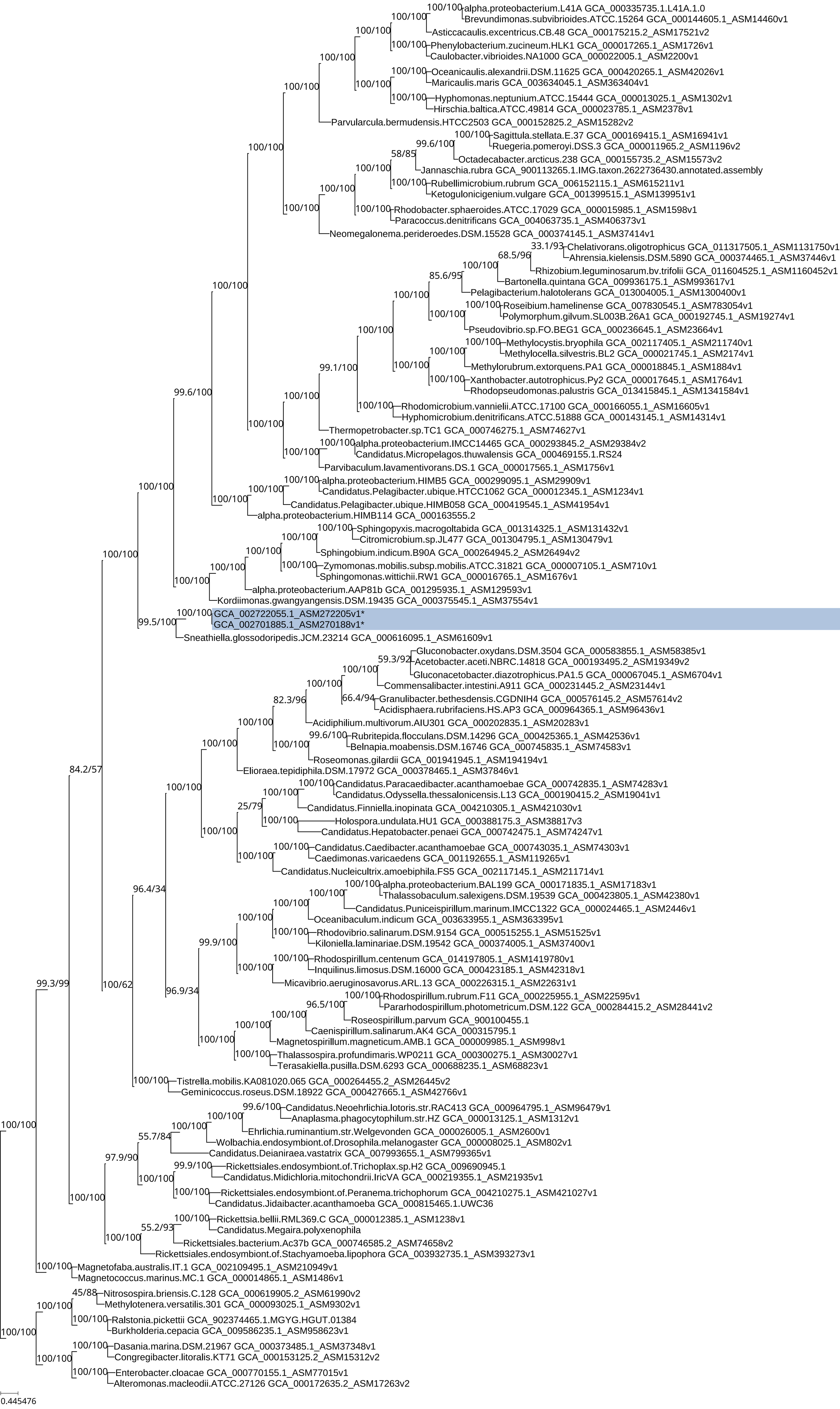
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Rubritepida.flocculans.DSM.14296 GCA_000425365.1_ASM42536v1
Belnapia.moabensis.DSM.16746 GCA_000745835.1_ASM74583v1
Roseomonas.gilardii GCA_001941945.1_ASM194194v1
84.2/57
Elioraea.tepidiphila.DSM.17972 GCA_000378465.1_ASM37846v1
Candidatus.Paracaedibacter.acanthamoebae GCA_000742835.1_ASM74283v1
Candidatus.Odyssella.thessalonicensis.L13 GCA_000190415.2_ASM19041v1
25/79
Candidatus.Finniella.inopinata GCA_004210305.1_ASM421030v1
Holospora.undulata.HU1 GCA_000388175.3_ASM38817v3
Candidatus.Hepatobacter.penaei GCA_000742475.1_ASM74247v1
Candidatus.Caedibacter.acanthamoebae GCA_000743035.1_ASM74303v1
Caedimonas.varicaedens GCA_001192655.1_ASM119265v1
Candidatus.Nucleicultrix.amoebiphila.FS5 GCA_002117145.1_ASM211714v1
96.4/34
100/62
96.9/34
100/100
alpha.proteobacterium.BAL199 GCA_000171835.1_ASM17183v1
Thalassobaculum.salexigens.DSM.19539 GCA_000423805.1_ASM42380v1
Candidatus.Puniceispirillum.marinum.IMCC1322 GCA_000024465.1_ASM2446v1
Oceanibaculum.indicum GCA_003633955.1_ASM363395v1
Rhodovibrio.salinarum.DSM.9154 GCA_000515255.1_ASM51525v1
Kiloniella.laminariae.DSM.19542 GCA_000374005.1_ASM37400v1
99.9/100
Rhodospirillum.centenum GCA_014197805.1_ASM1419780v1
Inquilinus.limosus.DSM.16000 GCA_000423185.1_ASM42318v1
Micavibrio.aeruginosavorus.ARL.13 GCA_000226315.1_ASM22631v1
99.3/99
Rhodospirillum.rubrum.F11 GCA_000225955.1_ASM22595v1
96.5/100
Pararhodospirillum.photometricum.DSM.122 GCA_000284415.2_ASM28441v2
Roseospirillum.parvum GCA_900100455.1
Caenispirillum.salinarum.AK4 GCA_000315795.1
Magnetospirillum.magneticum.AMB.1 GCA_000009985.1_ASM998v1
Thalassospira.profundimaris.WP0211 GCA_000300275.1_ASM30027v1
Terasakiella.pusilla.DSM.6293 GCA_000688235.1_ASM68823v1
Tistrella.mobilis.KA081020.065 GCA_000264455.2_ASM26445v2
Geminicoccus.roseus.DSM.18922 GCA_000427665.1_ASM42766v1
99.6/100
Candidatus.Neoehrlichia.lotoris.str.RAC413 GCA_000964795.1_ASM96479v1
Anaplasma.phagocytophilum.str.HZ GCA_000013125.1_ASM1312v1
Ehrlichia.ruminantium.str.Welgevonden GCA_000026005.1_ASM2600v1
55.7/84
Wolbachia.endosymbiont.of.Drosophila.melanogaster GCA_000008025.1_ASM802v1
Candidatus.Deianiraea.vastatrix GCA_007993655.1_ASM799365v1
97.9/90
99.9/100
Rickettsiales.endosymbiont.of.Trichoplax.sp.H2 GCA_009690945.1
Candidatus.Midichloria.mitochondrii.IricVA GCA_000219355.1_ASM21935v1
Rickettsiales.endosymbiont.of.Peranema.trichophorum GCA_004210275.1_ASM421027v1
Candidatus.Jidaibacter.acanthamoeba GCA_000815465.1.UWC36
Rickettsia.bellii.RML369.C GCA_000012385.1_ASM1238v1
55.2/93
Candidatus.Megaira.polyxenophila
Rickettsiales.bacterium.Ac37b GCA_000746585.2_ASM74658v2
Rickettsiales.endosymbiont.of.Stachyamoeba.lipophora GCA_003932735.1_ASM393273v1
Magnetofaba.australis.IT.1 GCA_002109495.1_ASM210949v1
Magnetococcus.marinus.MC.1 GCA_000014865.1_ASM1486v1
45/88
Nitrosospira.briensis.C.128 GCA_000619905.2_ASM61990v2
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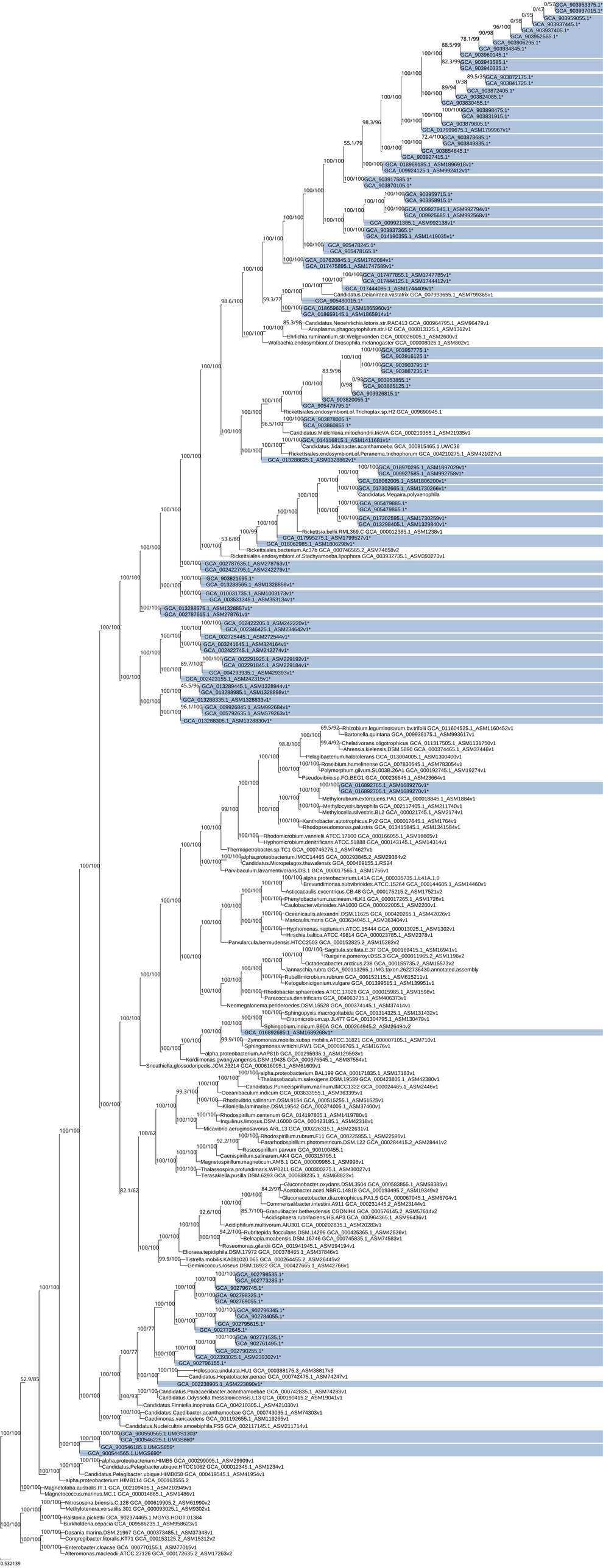
Ralstonia.pickettii GCA_902374465.1.MGYG.HGUT.01384
Burkholderia.cepacia GCA_009586235.1_ASM958623v1
Dasania.marina.DSM.21967 GCA_000373485.1_ASM37348v1
Congregibacter.litoralis.KT71 GCA_000153125.2_ASM15312v2
Enterobacter.cloacae GCA_000770155.1_ASM77015v1
Alteromonas.macleodii.ATCC.27126 GCA_000172635.2_ASM17263v2
0.445476

Supplementary Figure 32: "step 6" phylogenomic trees. Phylogenomic trees of *Rickettsiales* and other *Alphaproteobacteria*, for testing the affiliation to *Rickettsiales* of 95 BUSCO-filtered "new putative *Rickettsiales* MAGs" (Step 6 in Supplementary Note 4). The phylogenies on the untrimmed concatenated gene alignment, as well as on alignments with the 10%, 20%, 30%, 40%, or 50% most compositionally heterogeneous sites removed are reported in order. In each tree, the "new putative *Rickettsiales* MAGs" are highlighted in blue. On each branch, support values by SH-aLRT with 1000 replicates and by 1000 ultrafast bootstraps are reported.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GCA_903952565.1*
78.1/99 GCA_903906295.1*
90/98 GCA_903934845.1*
88.5/99 GCA_903960145.1*
100/100 GCA_903943585.1*
82.3/99 GCA_903940335.1*
100/100 89.5/39 GCA_903872175.1*
GCA_903841725.1*
0/38 89/94 GCA_903872405.1*
100/100 GCA_903824085.1*
GCA_903830455.1*
100/100 GCA_903898475.1*
100/100 GCA_903831915.1*
100/100 GCA_903879805.1*
GCA_017999675.1_ASM1799967v1*
98.3/96 72.4/100 GCA_903878685.1*
GCA_903849835.1*
100/100 GCA_903854845.1*
55.1/79 100/100 GCA_903927415.1*
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GCA_009924125.1_ASM992412v1*
100/100 GCA_903917585.1*
GCA_903870105.1*
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GCA_009925685.1_ASM992568v1*
100/100 GCA_009921385.1_ASM992138v1*
100/100 GCA_903837365.1*
GCA_014190355.1_ASM1419035v1*
100/100 GCA_905478245.1*
GCA_905478165.1*
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100/100 GCA_017477855.1_ASM1747785v1*
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100/100 GCA_017444095.1_ASM1744409v1*
Candidatus.Deianiraea.vastatrix GCA_007993655.1_ASM799365v1
GCA_905480015.1*
100/100 GCA_018659605.1_ASM1865960v1*
GCA_018659145.1_ASM1865914v1*
98.6/100 59.3/77 100/100 85.3/98 Candidatus.Neoehrlichia.lotoris.str.RAC413 GCA_000964795.1_ASM96479v1
Anaplasma.phagocytophilum.str.HZ GCA_000013125.1_ASM312v1
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100/100 GCA_903903795.1*
GCA_903887235.1*
83.9/96 100/100 0/98 GCA_903953855.1*
0/98 GCA_903865125.1*
GCA_903926815.1*
100/100 GCA_903820055.1*
GCA_905479795.1*
Rickettsiales.endosymbiont.of.Tricholax.sp.H2 GCA_009690945.1
100/100 GCA_903878005.1*
96.5/100 GCA_903860855.1*
Candidatus.Midichloria.mitochondrii.IricVA GCA_000219355.1_ASM21935v1
100/100 GCA_014116815.1_ASM1411681v1*
Candidatus.Jidaibacter.acanthamoeba GCA_000815465.1.UWC36
Rickettsiales.endosymbiont.of.Peranema.trichophorum GCA_004210275.1_ASM421027v1
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100/100 Rickettsia.bellii.RML369.C GCA_000012385.1_ASM1238v1
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Pseudovibrio.sp.FO.BEG1 GCA_000236645.1_ASM23664v1
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Kiloniella.laminariae.DSM.19542 GCA_000374005.1_ASM37400v1
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Inquilinus.limosus.DSM.16000 GCA_000423185.1_ASM42318v1
Micavibrio.aeruginosavorus.ARL.13 GCA_000226315.1_ASM22631v1
100/100 Rhodospirillum.rubrum.F11 GCA_000225955.1_ASM22595v1
92.2/100 Parahodospirillum.photometricum.DSM.122 GCA_000284415.2_ASM28441v2
100/100 Roseospirillum.parvum GCA_900100455.1
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Terasakiella.pusilla.DSM.6293 GCA_000688235.1_ASM68823v1
100/100 Gluconobacter.oxydans.DSM.3504 GCA_000583855.1_ASM58385v1
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100/100 100/100 GCA_902796345.1*
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100/77 100/100 GCA_902771535.1*
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Candidatus.Nucleicultrix.amoebiphila.FS5 GCA_002117145.1_ASM211714v1
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100/100 100/100 Ralstonia.pickettii GCA_902374465.1.MGYG.HGUT.01384
Burkholderia.cepacia GCA_009586235.1_ASM958623v1
100/100 100/100 Dasania.marina.DSM.21967 GCA_000373485.1_ASM37348v1
Congregibacter.litoralis.KT71 GCA_000153125.2_ASM15312v2
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Alteromonas.macleodii.ATCC.27126 GCA_000172635.2_ASM17263v2
0.0532139

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87.7/86 GCA_903934845.1*
100/100 GCA_903960145.1*
71.2/88 GCA_903943585.1*
GCA_903940335.1*
100/100 71.6/94 GCA_903872405.1*
GCA_903824085.1*
34.9/92 93/94 GCA_903841725.1*
100/100 GCA_903872175.1*
GCA_903830455.1*
100/100 GCA_903898475.1*
100/100 GCA_903831915.1*
95.7/92 100/100 GCA_903879805.1*
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57.1/100 GCA_903878685.1*
23.5/51 100/100 GCA_903849835.1*
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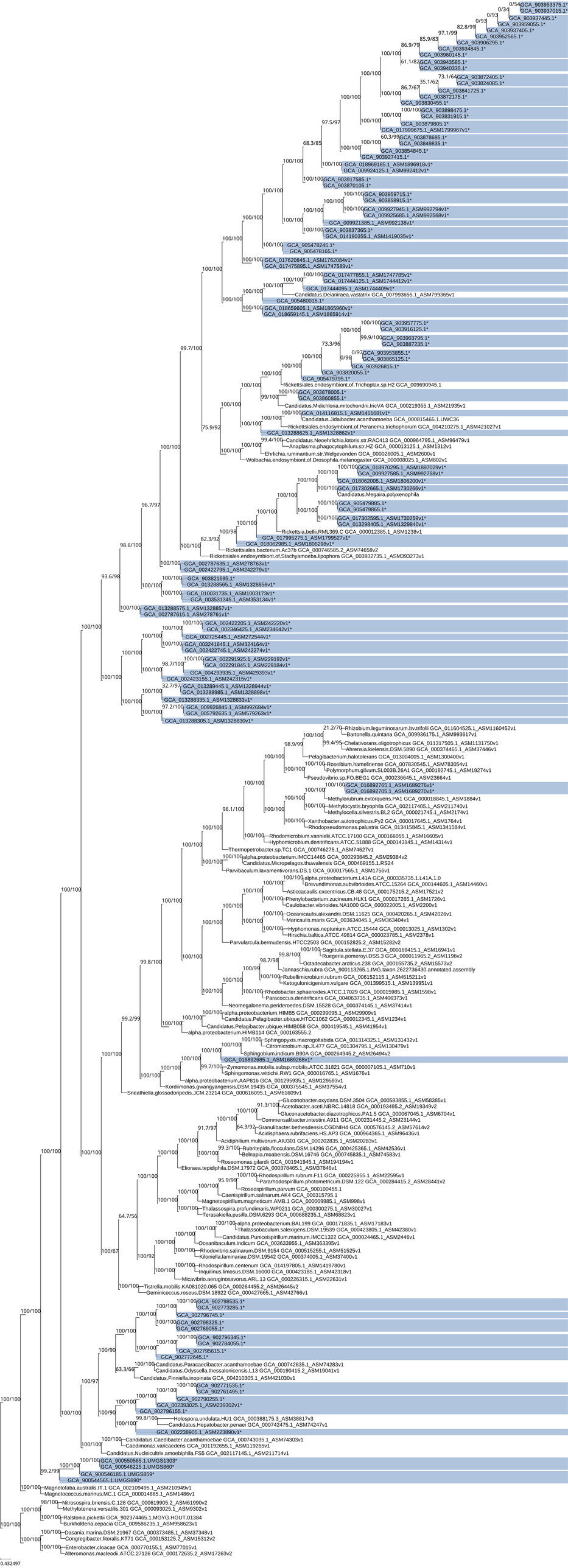
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Acidisphaera.rubrifaciens.HS.AP3 GCA_000964365.1_ASM96436v1
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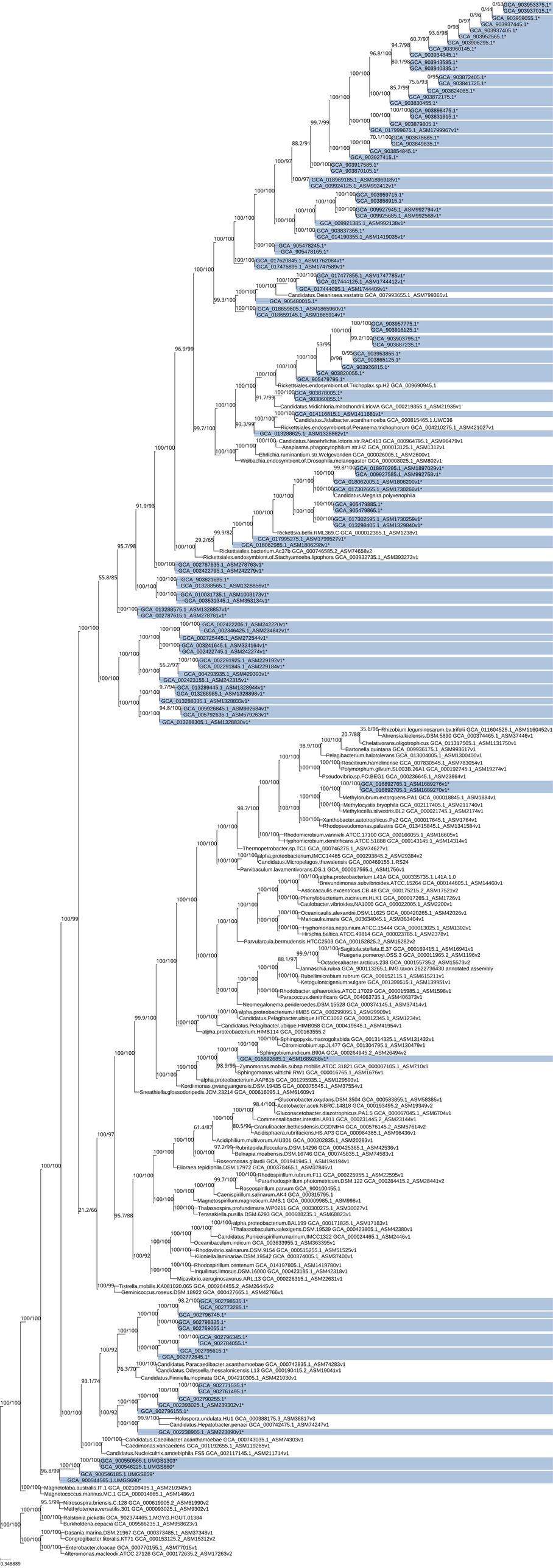
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Sagittula.stellata.E.37 GCA_000169415.1_ASM16941v1
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88.1/97
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99.9/100
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Enterobacter.cloacae GCA_000770155.1_ASM770155v1
Alteromonas.macleodii.ATCC.27126 GCA_000172635.2_ASM17263v2
0.348889

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