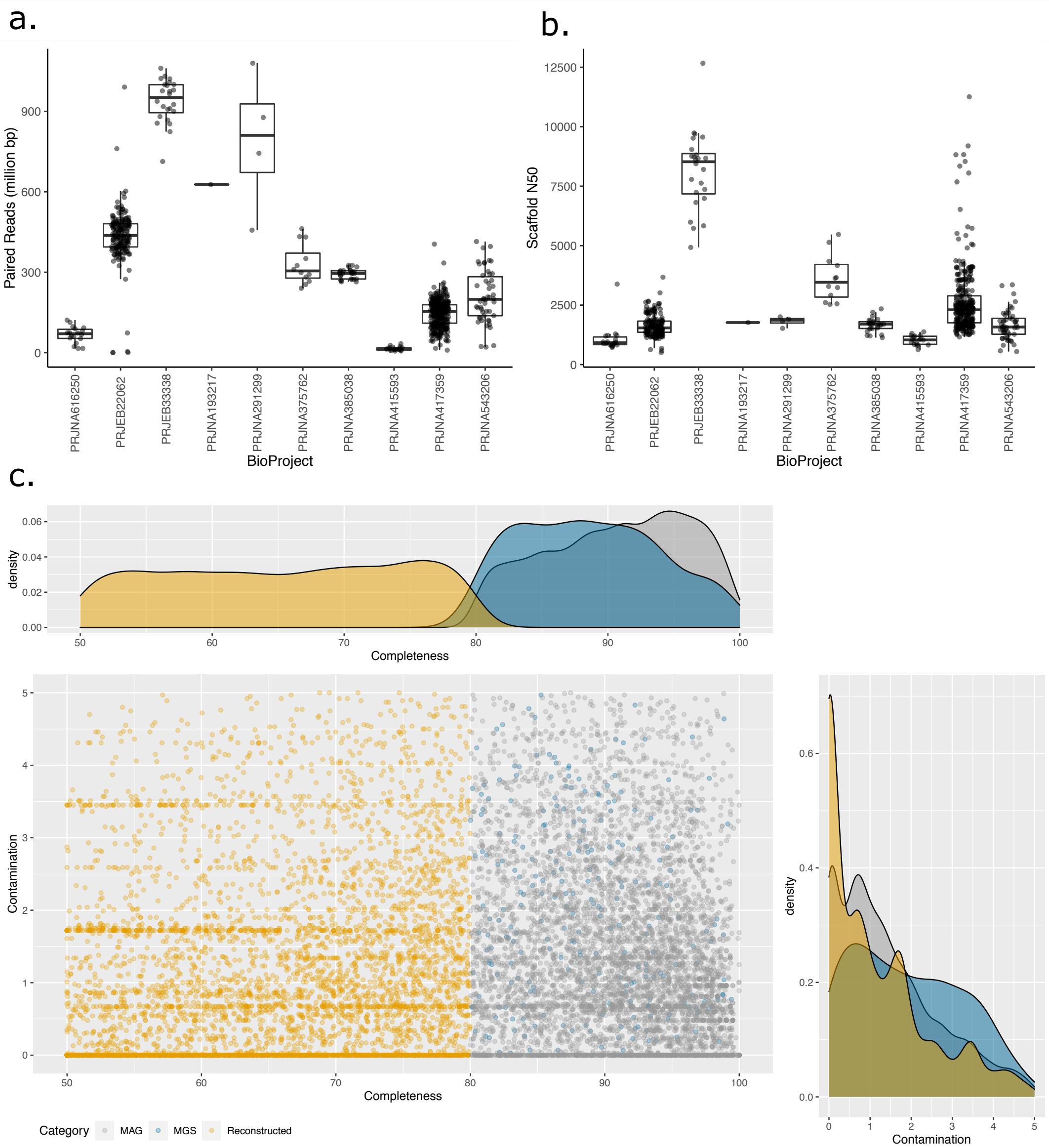
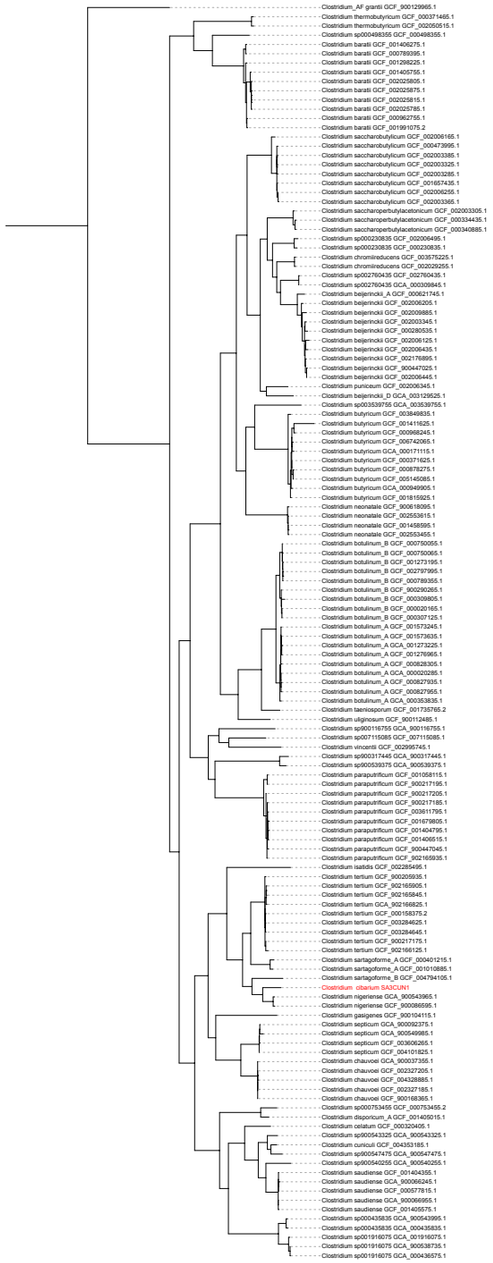


Figure S1. Comparisons between metagenomic samples according to BioProject from which they were sourced with regard to **a.** Number of paired reads input and **b.** Assembled scaffold N50. **c.** Completeness and contamination of MAGs and MGS derived from single assembly or co-assembly of all metagenomic samples. Quality estimates were estimated by CheckM and are reported for all Low Quality (designated Reconstructed) (≥50% completion, <5% contamination) Medium Quality (≥80% - ≤90% completion, <5% contamination) and High Quality (>90% completion, <5% contamination) MAGs, with MAGs clustered to form MGS being shown in blue.

Tree scale: 1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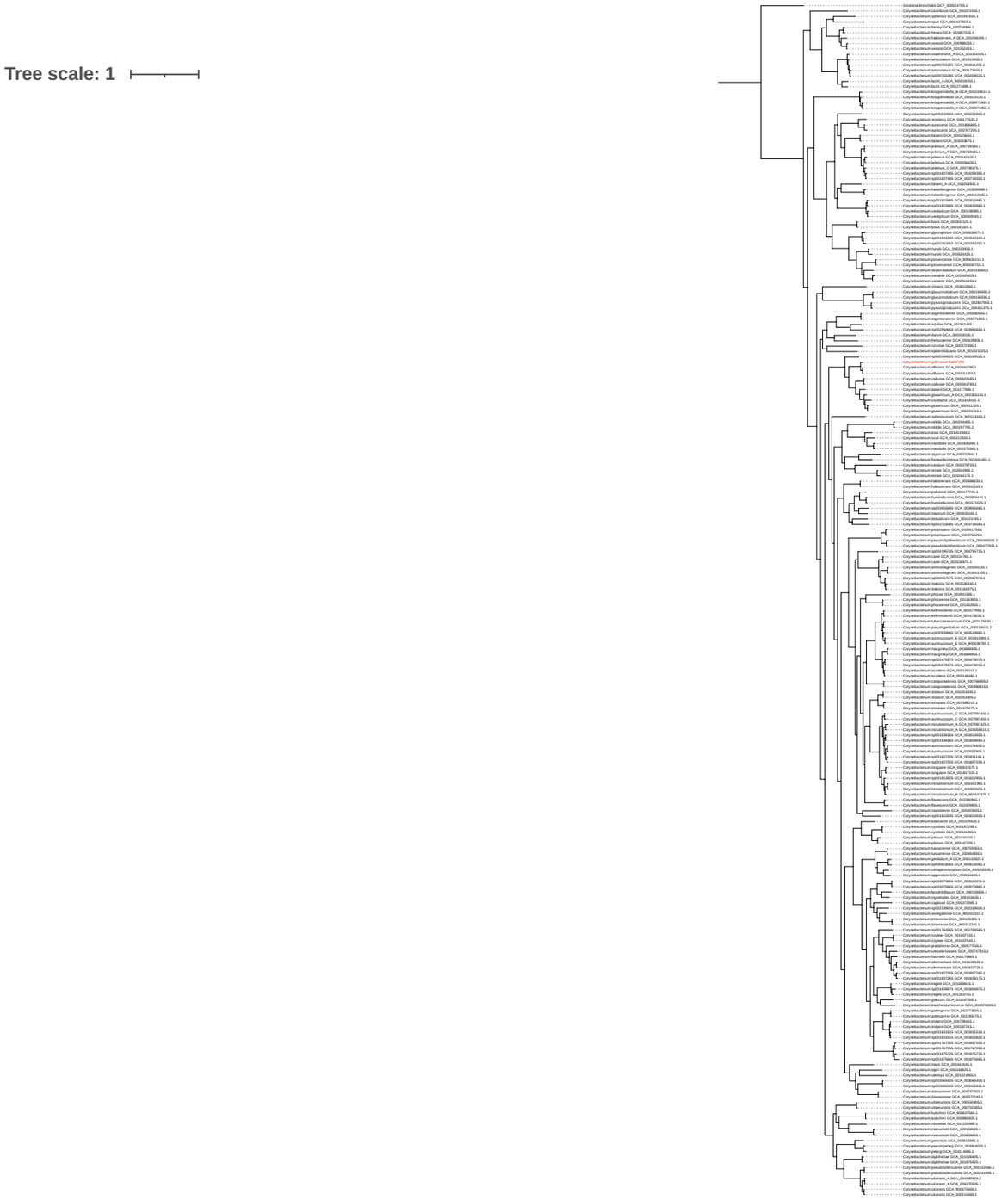
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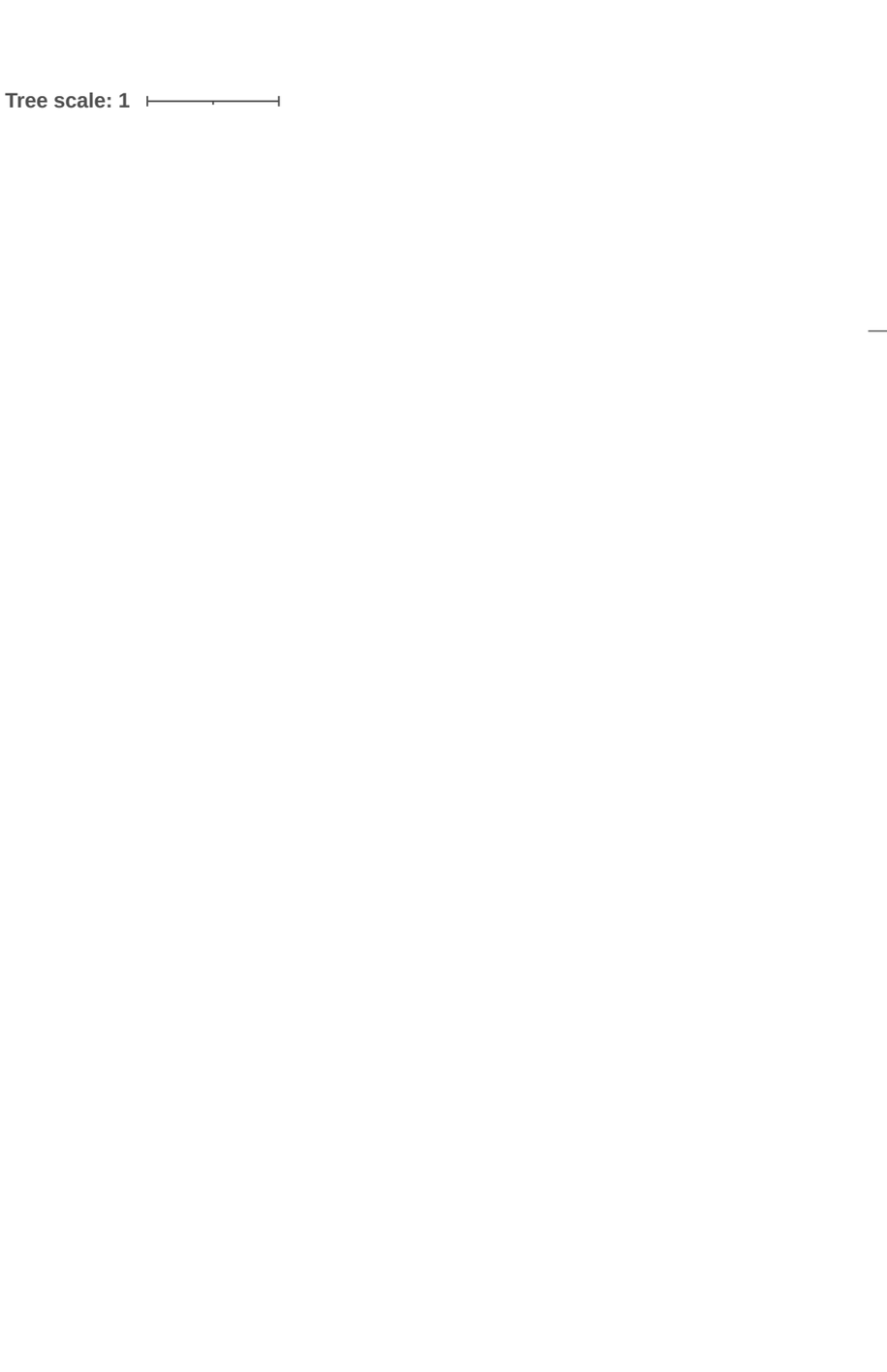
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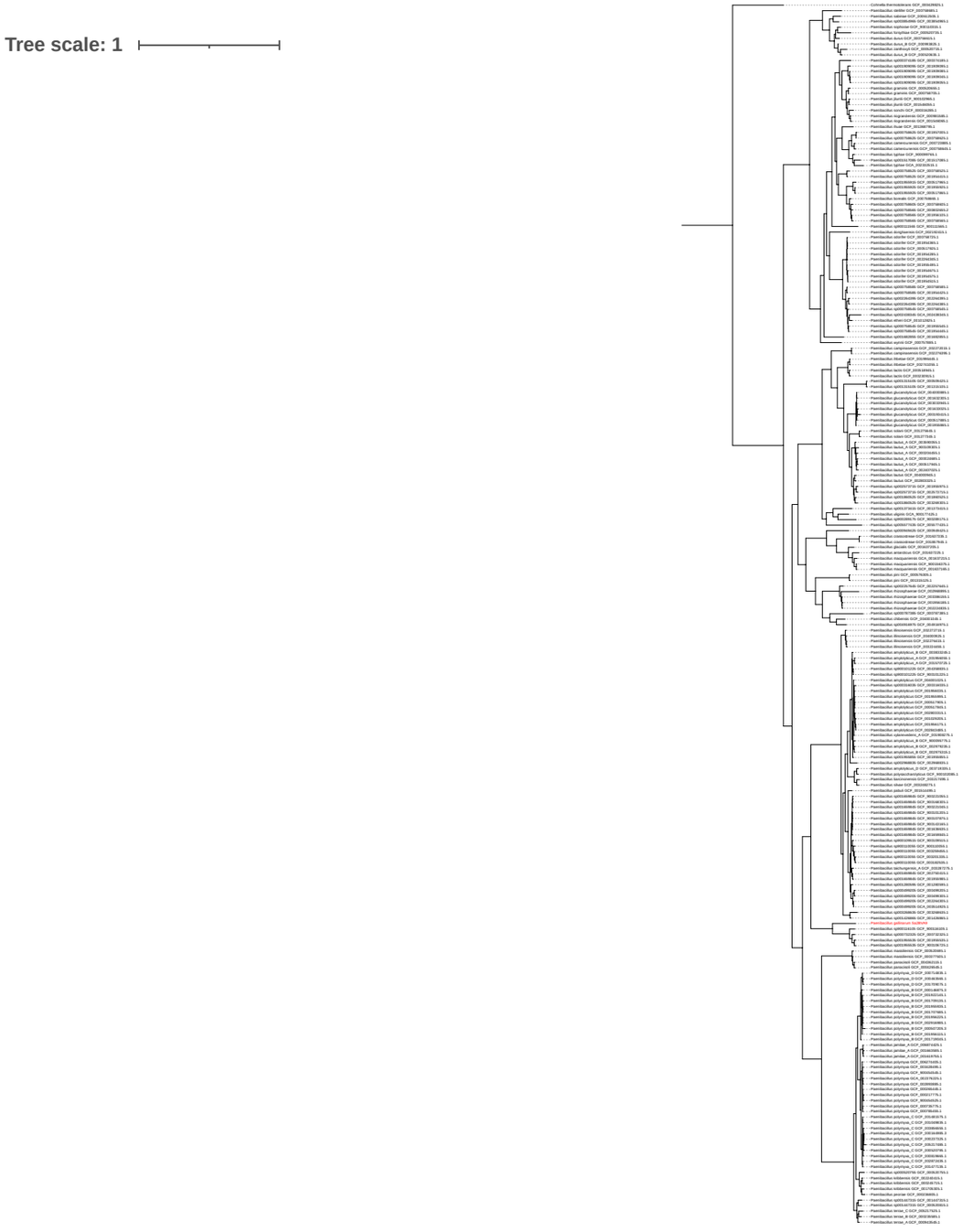
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Tree scale: 1
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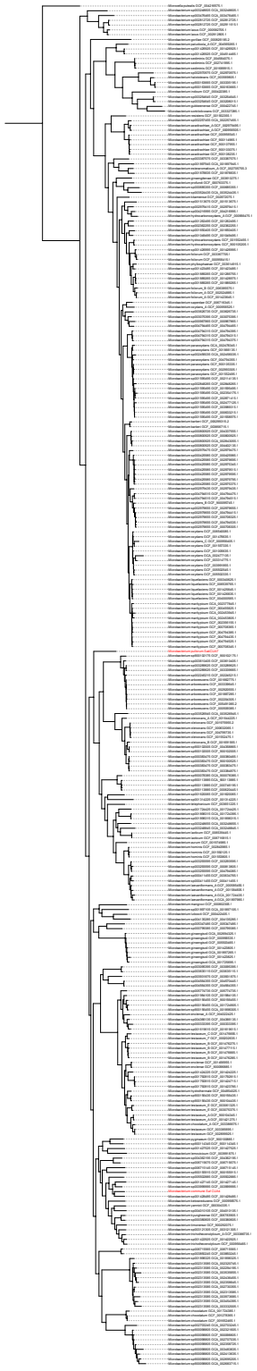
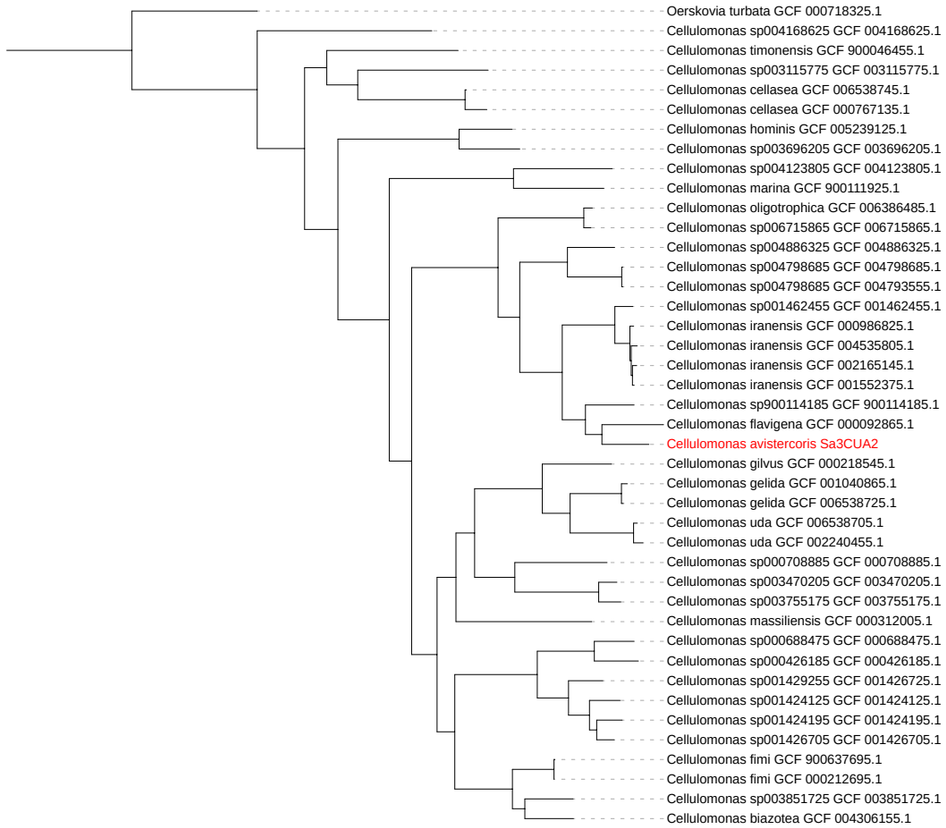
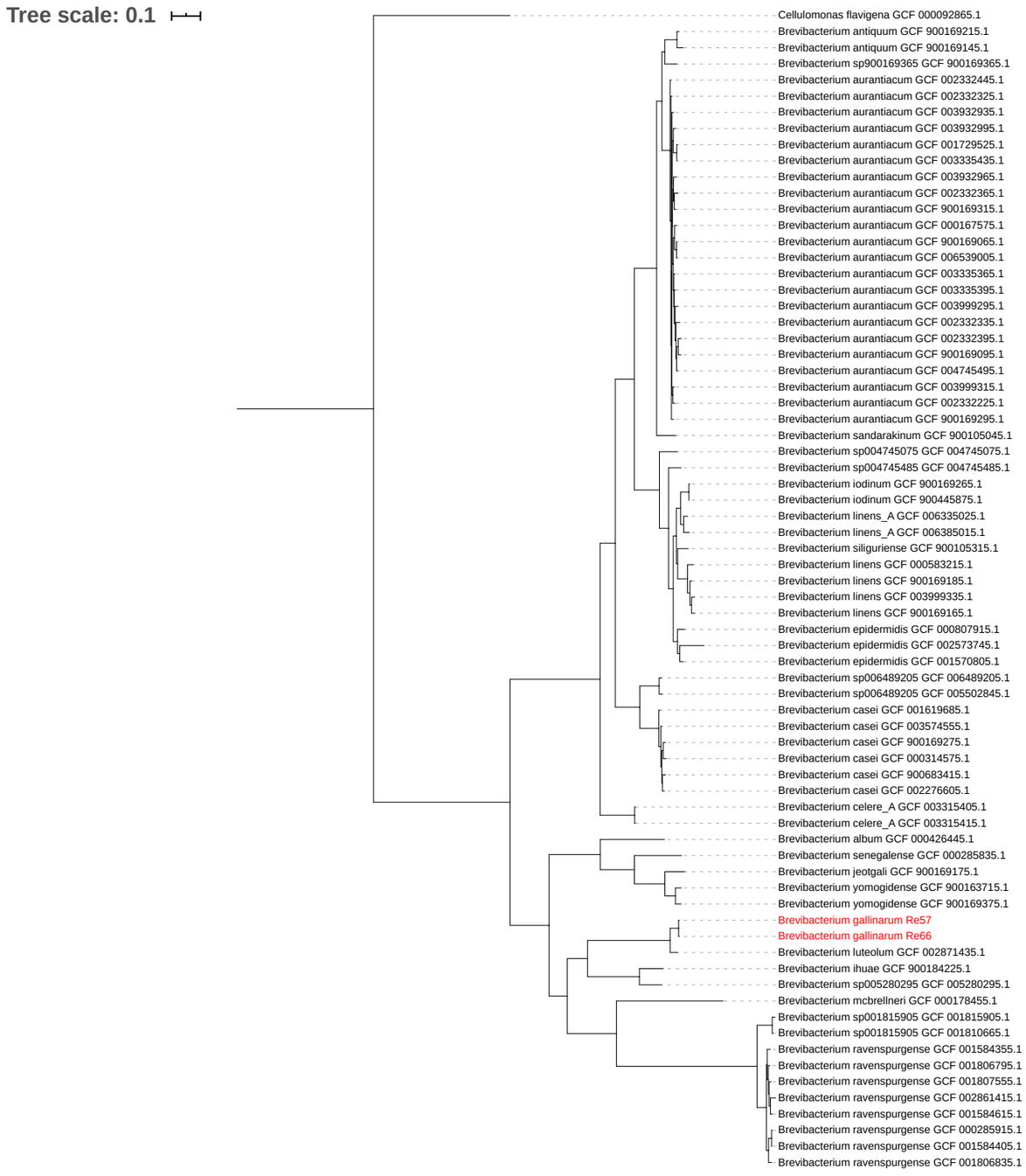


Tree scale: 0.1

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Brevibacterium aurantiacum GCF 002332445.1
Brevibacterium aurantiacum GCF 002332325.1
Brevibacterium aurantiacum GCF 003932935.1
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Brevibacterium aurantiacum GCF 002332365.1
Brevibacterium aurantiacum GCF 900169315.1
Brevibacterium aurantiacum GCF 000167575.1
Brevibacterium aurantiacum GCF 900169065.1
Brevibacterium aurantiacum GCF 006539005.1
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Brevibacterium aurantiacum GCF 003335395.1
Brevibacterium aurantiacum GCF 003999295.1
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Brevibacterium sp004745485 GCF 004745485.1
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Brevibacterium linens_A GCF 006385015.1
Brevibacterium siliguriense GCF 900105315.1
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Brevibacterium album GCF 000426445.1
Brevibacterium senegalense GCF 000285835.1
Brevibacterium jeotgali GCF 900169175.1
Brevibacterium yomogidense GCF 900163715.1
Brevibacterium yomogidense GCF 900169375.1
Brevibacterium gallinarum Re57
Brevibacterium gallinarum Re66
Brevibacterium luteolum GCF 002871435.1
Brevibacterium ihuae GCF 900184225.1
Brevibacterium sp005280295 GCF 005280295.1
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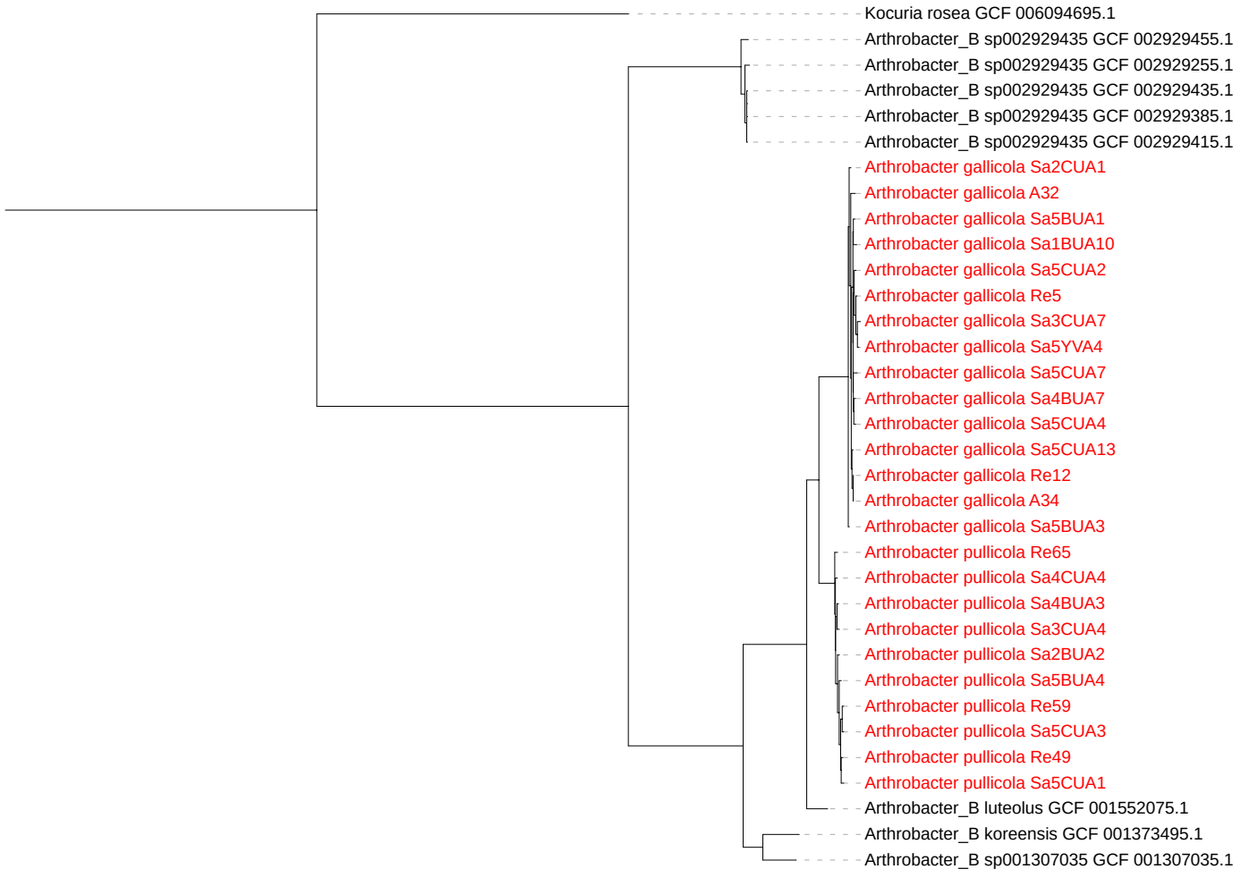
Tree scale: 0.1



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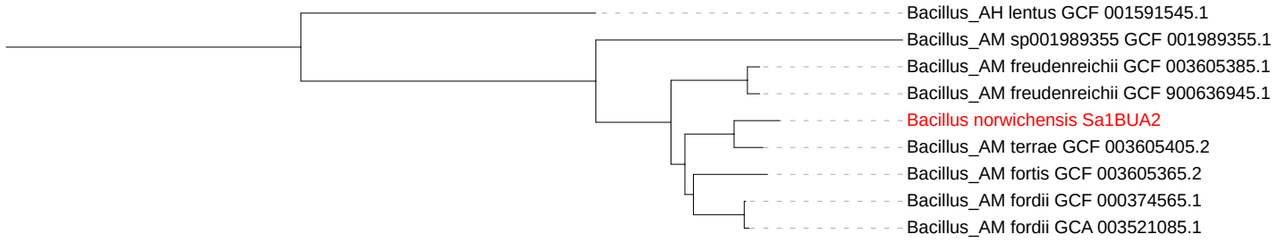

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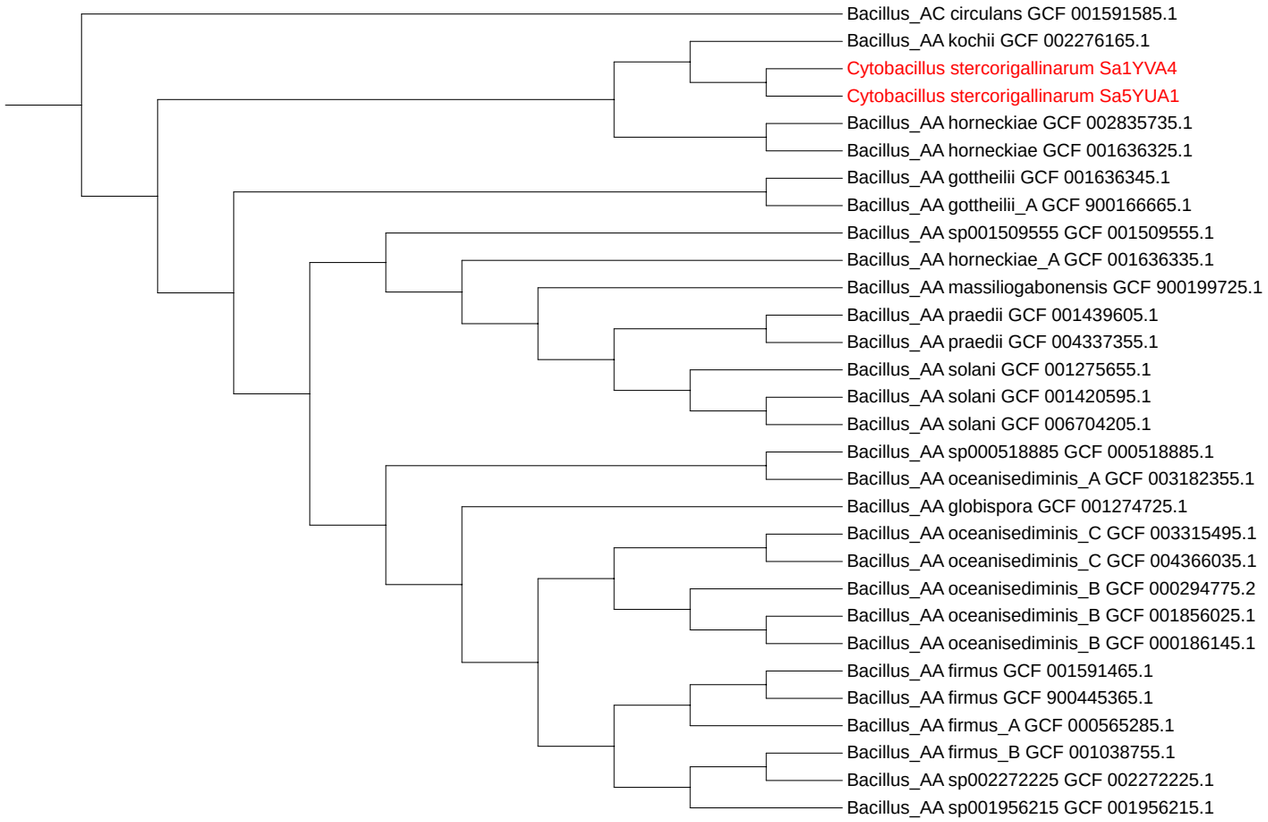
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Bacillus_AA horneckiae GCF 002835735.1
Bacillus_AA horneckiae GCF 001636325.1
Bacillus_AA gottheilii GCF 001636345.1
Bacillus_AA gottheilii_A GCF 900166665.1
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Bacillus_AA sp000518885 GCF 000518885.1
Bacillus_AA oceanisediminis_A GCF 003182355.1
Bacillus_AA globispora GCF 001274725.1
Bacillus_AA oceanisediminis_C GCF 003315495.1
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Bacillus_AA firmus GCF 001591465.1
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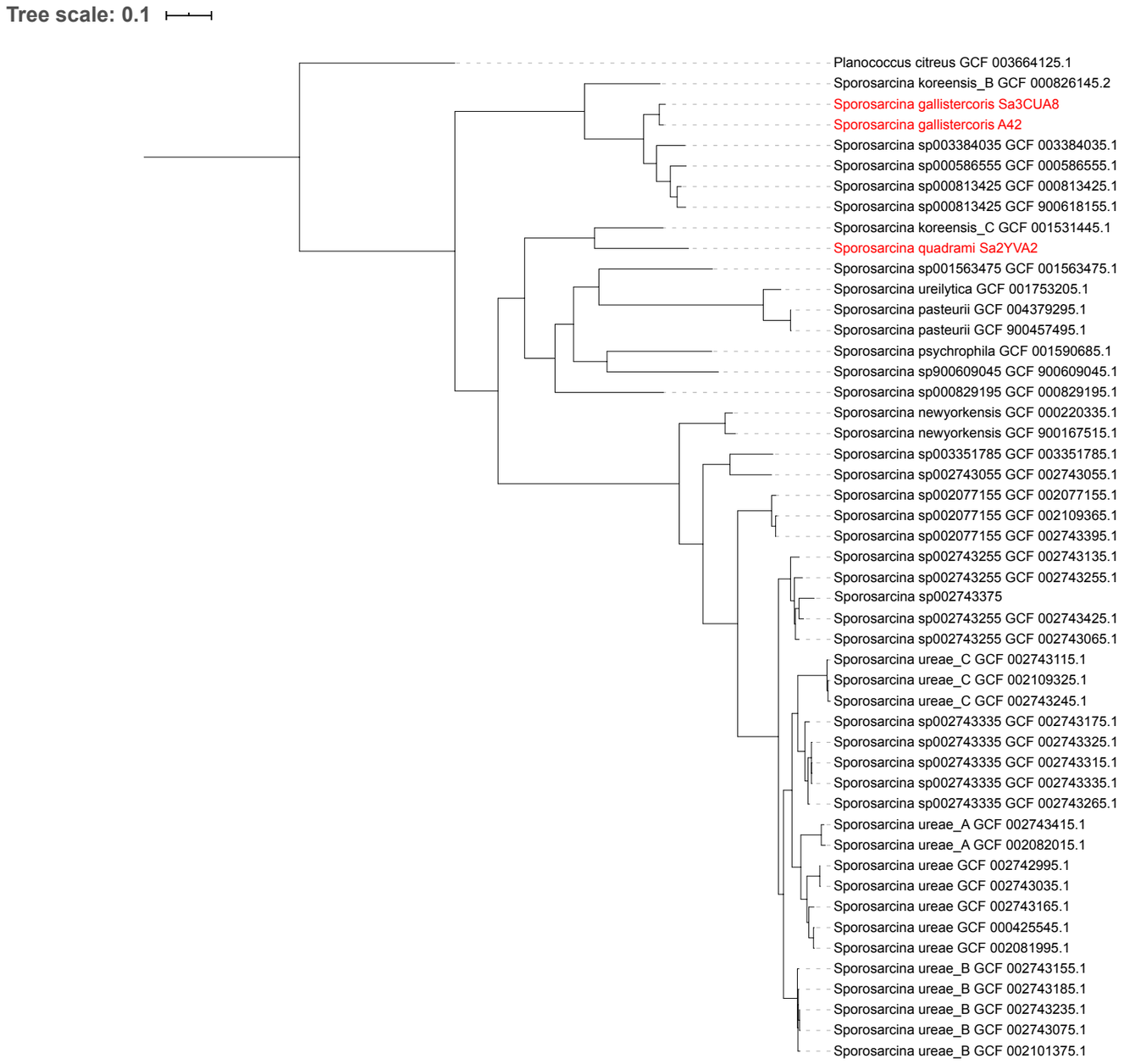
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Sporosarcina sp003384035 GCF 003384035.1
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Sporosarcina koreensis_C GCF 001531445.1
Sporosarcina quadrami Sa2YVA2
Sporosarcina sp001563475 GCF 001563475.1
Sporosarcina ureilytica GCF 001753205.1
Sporosarcina pasteurii GCF 004379295.1
Sporosarcina pasteurii GCF 900457495.1
Sporosarcina psychrophila GCF 001590685.1
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Sporosarcina ureae GCF 000425545.1
Sporosarcina ureae GCF 002081995.1
Sporosarcina ureae_B GCF 002743155.1
Sporosarcina ureae_B GCF 002743185.1
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Sporosarcina ureae_B GCF 002743075.1
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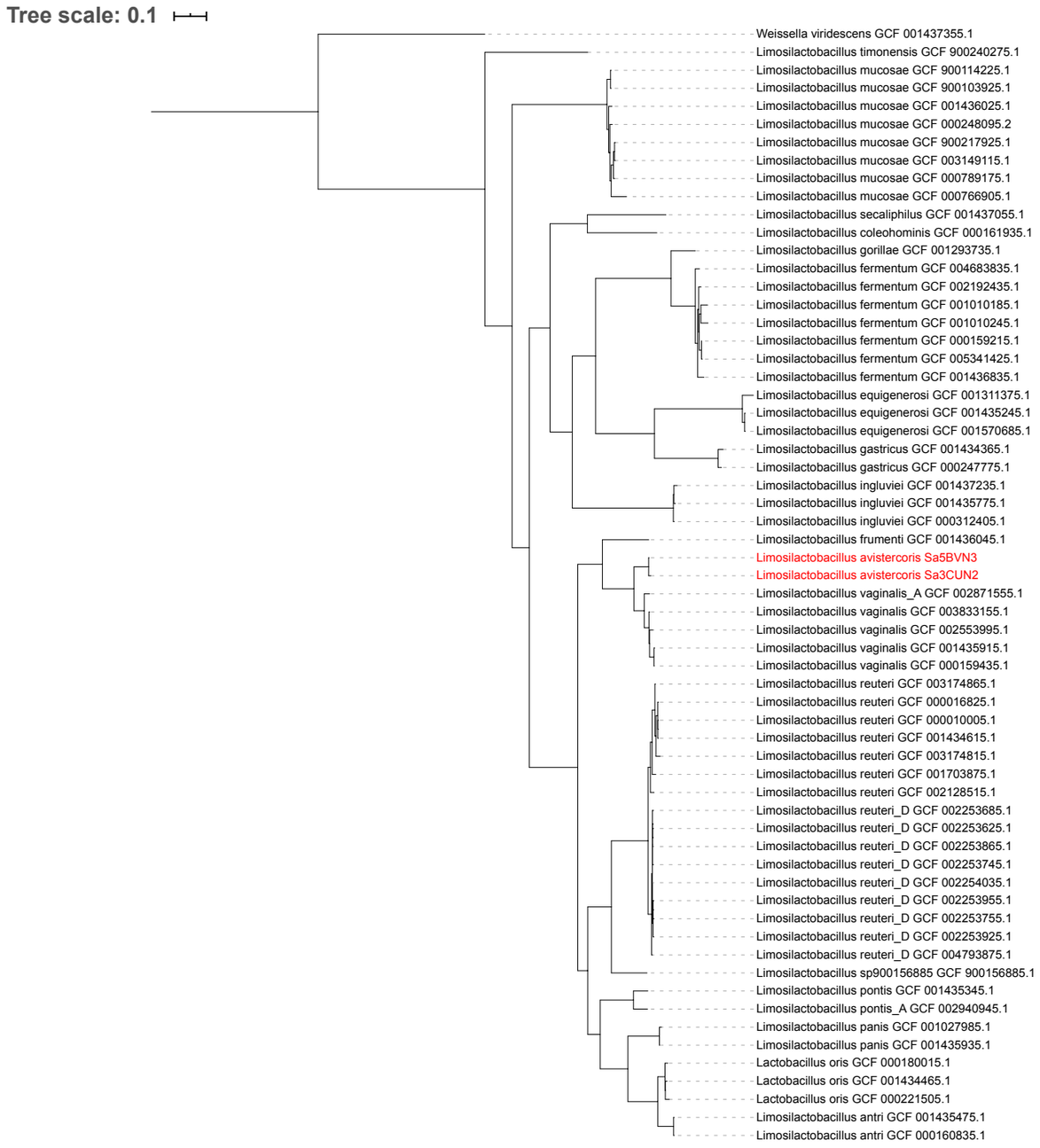
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Limosilactobacillus mucosae GCF 900103925.1
Limosilactobacillus mucosae GCF 001436025.1
Limosilactobacillus mucosae GCF 000248095.2
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Limosilactobacillus mucosae GCF 000789175.1
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Limosilactobacillus secaliphilus GCF 001437055.1
Limosilactobacillus coleohominis GCF 000161935.1
Limosilactobacillus gorillae GCF 001293735.1
Limosilactobacillus fermentum GCF 004683835.1
Limosilactobacillus fermentum GCF 002192435.1
Limosilactobacillus fermentum GCF 001010185.1
Limosilactobacillus fermentum GCF 001010245.1
Limosilactobacillus fermentum GCF 000159215.1
Limosilactobacillus fermentum GCF 005341425.1
Limosilactobacillus fermentum GCF 001436835.1
Limosilactobacillus equigenerosi GCF 001311375.1
Limosilactobacillus equigenerosi GCF 001435245.1
Limosilactobacillus equigenerosi GCF 001570685.1
Limosilactobacillus gastricus GCF 001434365.1
Limosilactobacillus gastricus GCF 000247775.1
Limosilactobacillus ingluviei GCF 001437235.1
Limosilactobacillus ingluviei GCF 001435775.1
Limosilactobacillus ingluviei GCF 000312405.1
Limosilactobacillus frumenti GCF 001436045.1
Limosilactobacillus avistercoris Sa5BVN3
Limosilactobacillus avistercoris Sa3CUN2
Limosilactobacillus vaginalis_A GCF 002871555.1
Limosilactobacillus vaginalis GCF 003833155.1
Limosilactobacillus vaginalis GCF 002553995.1
Limosilactobacillus vaginalis GCF 001435915.1
Limosilactobacillus vaginalis GCF 000159435.1
Limosilactobacillus reuteri GCF 003174865.1
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Limosilactobacillus reuteri GCF 000010005.1
Limosilactobacillus reuteri GCF 001434615.1
Limosilactobacillus reuteri GCF 003174815.1
Limosilactobacillus reuteri GCF 001703875.1
Limosilactobacillus reuteri GCF 002128515.1
Limosilactobacillus reuteri_D GCF 002253685.1
Limosilactobacillus reuteri_D GCF 002253625.1
Limosilactobacillus reuteri_D GCF 002253865.1
Limosilactobacillus reuteri_D GCF 002253745.1
Limosilactobacillus reuteri_D GCF 002254035.1
Limosilactobacillus reuteri_D GCF 002253955.1
Limosilactobacillus reuteri_D GCF 002253755.1
Limosilactobacillus reuteri_D GCF 002253925.1
Limosilactobacillus reuteri_D GCF 004793875.1
Limosilactobacillus sp900156885 GCF 900156885.1
Limosilactobacillus pontis GCF 001435345.1
Limosilactobacillus pontis_A GCF 002940945.1
Limosilactobacillus panis GCF 001027985.1
Limosilactobacillus panis GCF 001435935.1
Lactobacillus oris GCF 000180015.1
Lactobacillus oris GCF 001434465.1
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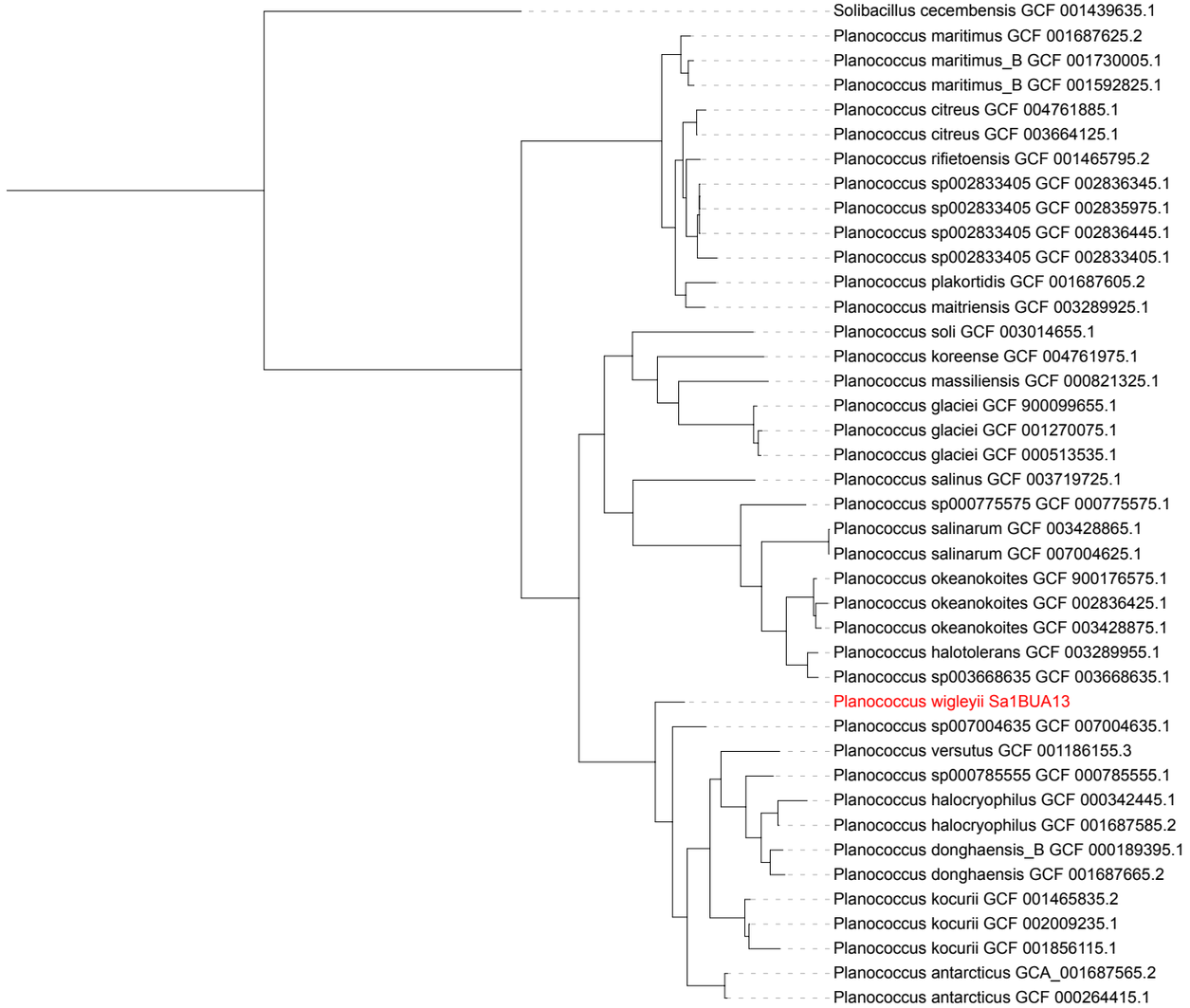

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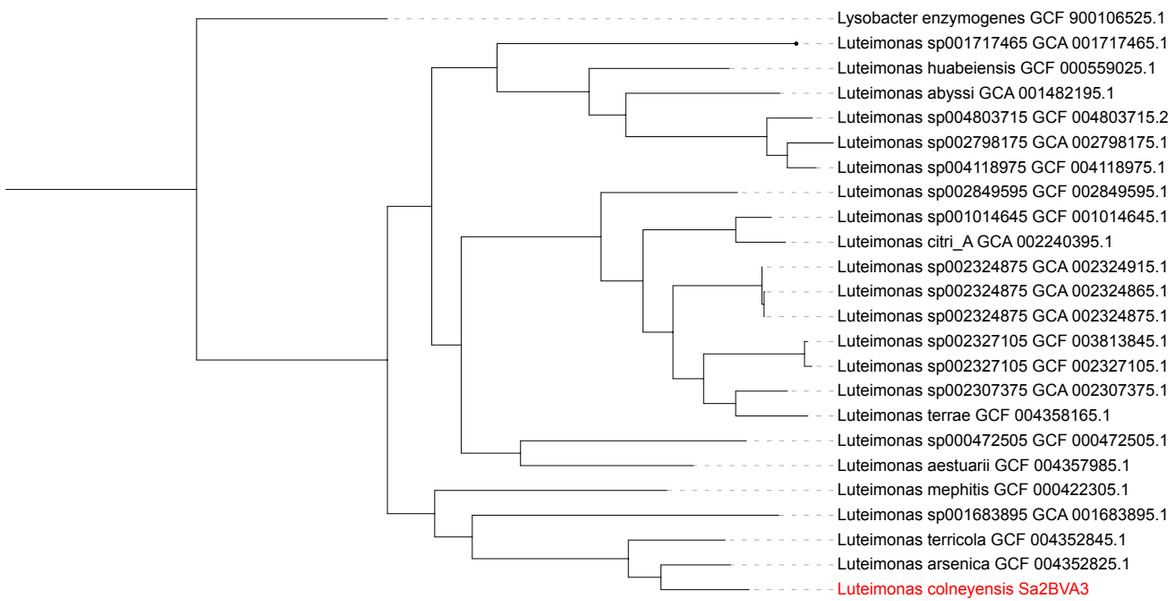

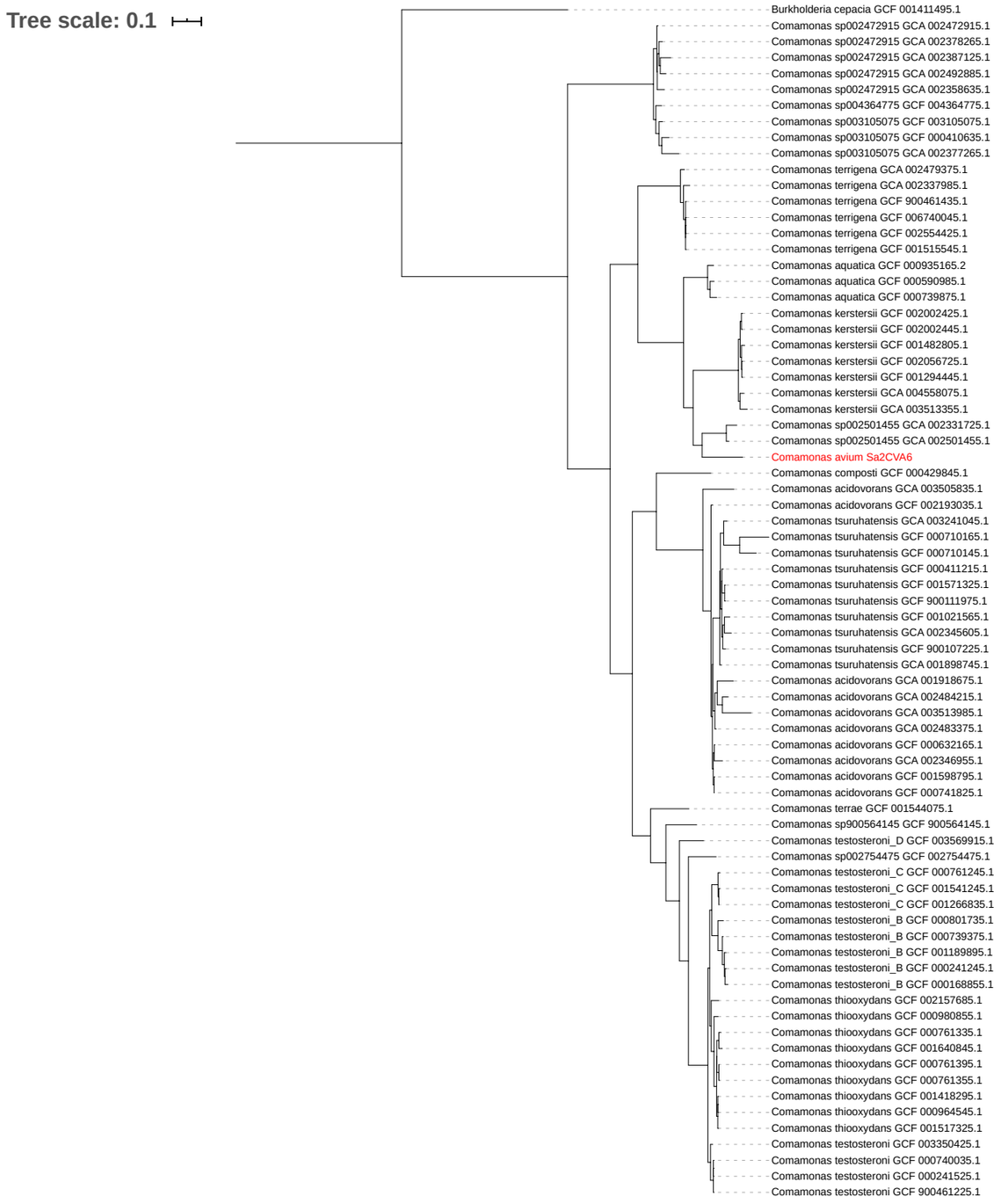
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Comamonas sp002472915 GCA 002358635.1
Comamonas sp004364775 GCF 004364775.1
Comamonas sp003105075 GCF 003105075.1
Comamonas sp003105075 GCF 000410635.1
Comamonas sp003105075 GCA 002377265.1
Comamonas terrigena GCA 002479375.1
Comamonas terrigena GCA 002337985.1
Comamonas terrigena GCF 900461435.1
Comamonas terrigena GCF 006740045.1
Comamonas terrigena GCF 002554425.1
Comamonas terrigena GCF 001515545.1
Comamonas aquatica GCF 000935165.2
Comamonas aquatica GCF 000590985.1
Comamonas aquatica GCF 000739875.1
Comamonas kerstersii GCF 002002425.1
Comamonas kerstersii GCF 002002445.1
Comamonas kerstersii GCF 001482805.1
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Comamonas kerstersii GCA 004558075.1
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Comamonas sp002501455 GCA 002331725.1
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Comamonas avium Sa2CVA6
Comamonas composti GCF 000429845.1
Comamonas acidovorans GCA 003505835.1
Comamonas acidovorans GCF 002193035.1
Comamonas tsuruhatensis GCA 003241045.1
Comamonas tsuruhatensis GCF 000710165.1
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Comamonas terrae GCF 001544075.1
Comamonas sp900564145 GCF 900564145.1
Comamonas testosteroni_D GCF 003569915.1
Comamonas sp002754475 GCF 002754475.1
Comamonas testosteroni_C GCF 000761245.1
Comamonas testosteroni_C GCF 001541245.1
Comamonas testosteroni_C GCF 001266835.1
Comamonas testosteroni_B GCF 000801735.1
Comamonas testosteroni_B GCF 000739375.1
Comamonas testosteroni_B GCF 001189895.1
Comamonas testosteroni_B GCF 000241245.1
Comamonas testosteroni_B GCF 000168855.1
Comamonas thiooxydans GCF 002157685.1
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Comamonas testosteroni GCF 003350425.1
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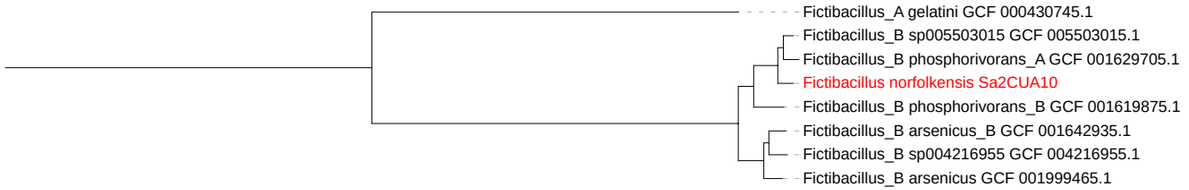

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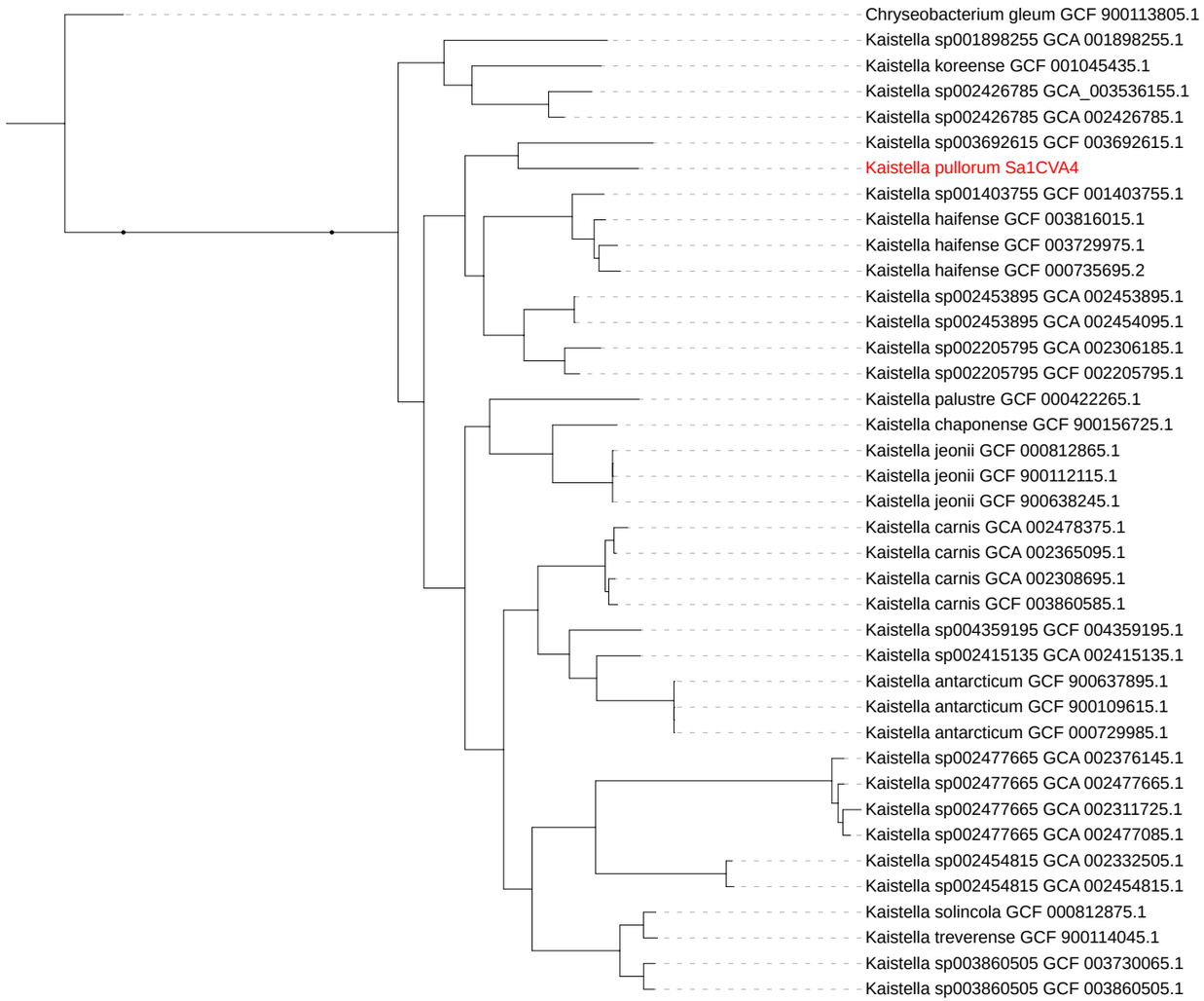

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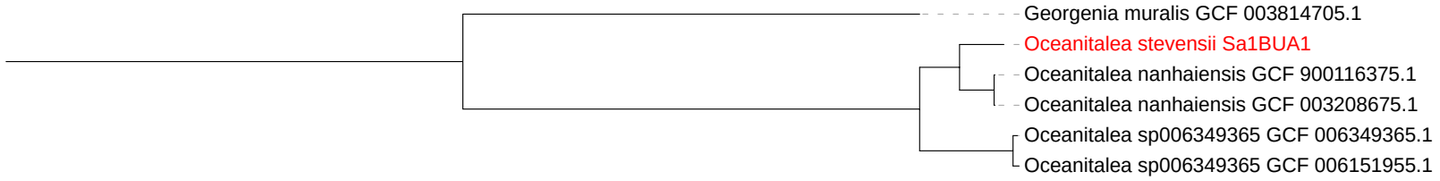

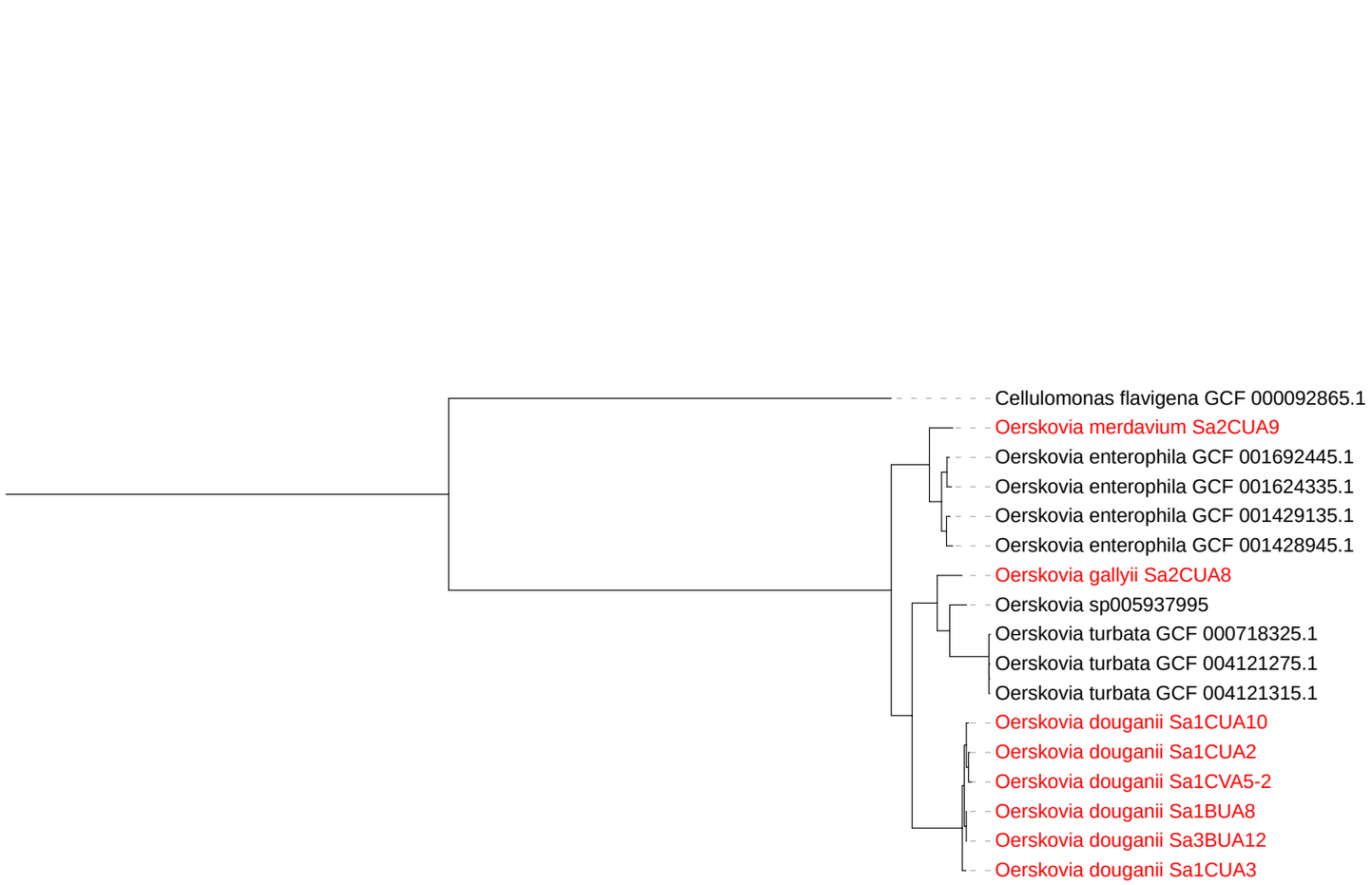
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Oerskovia enterophila GCF 001692445.1
Oerskovia enterophila GCF 001624335.1
Oerskovia enterophila GCF 001429135.1
Oerskovia enterophila GCF 001428945.1
Oerskovia gallyii Sa2CUA8
Oerskovia sp005937995
Oerskovia turbata GCF 000718325.1
Oerskovia turbata GCF 004121275.1
Oerskovia turbata GCF 004121315.1
Oerskovia douganii Sa1CUA10
Oerskovia douganii Sa1CUA2
Oerskovia douganii Sa1CVA5-2
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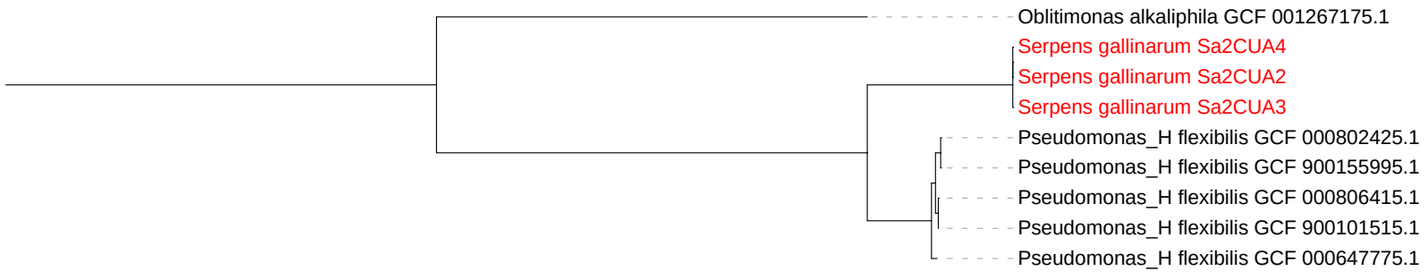
Tree scale: 0.1



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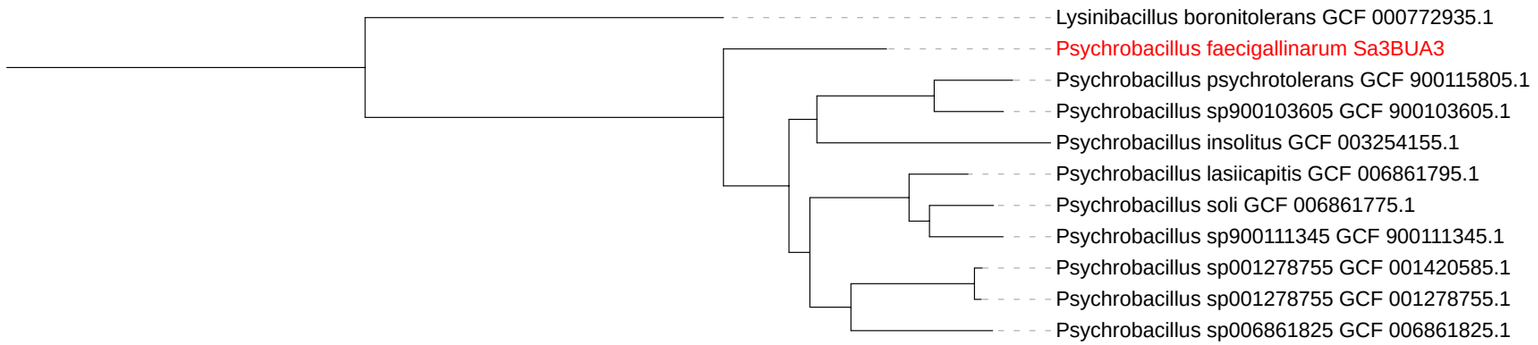

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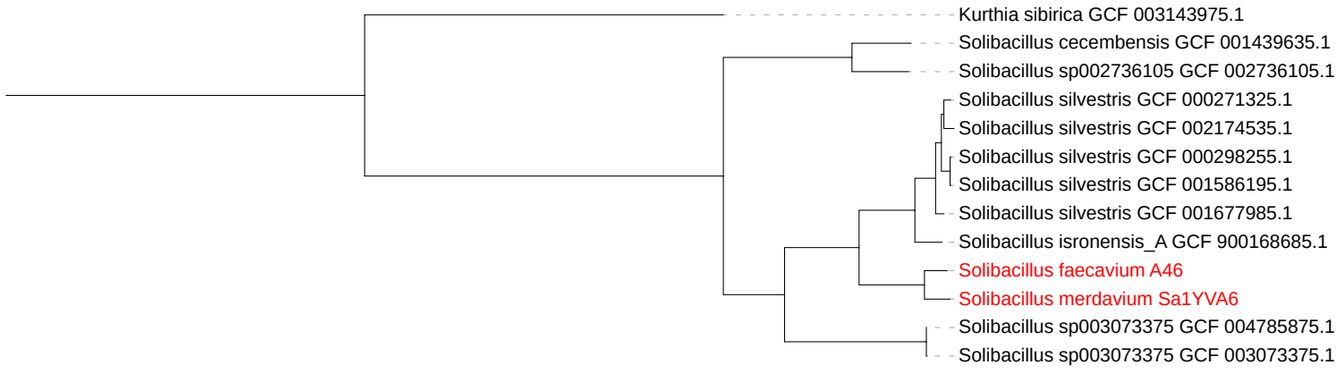


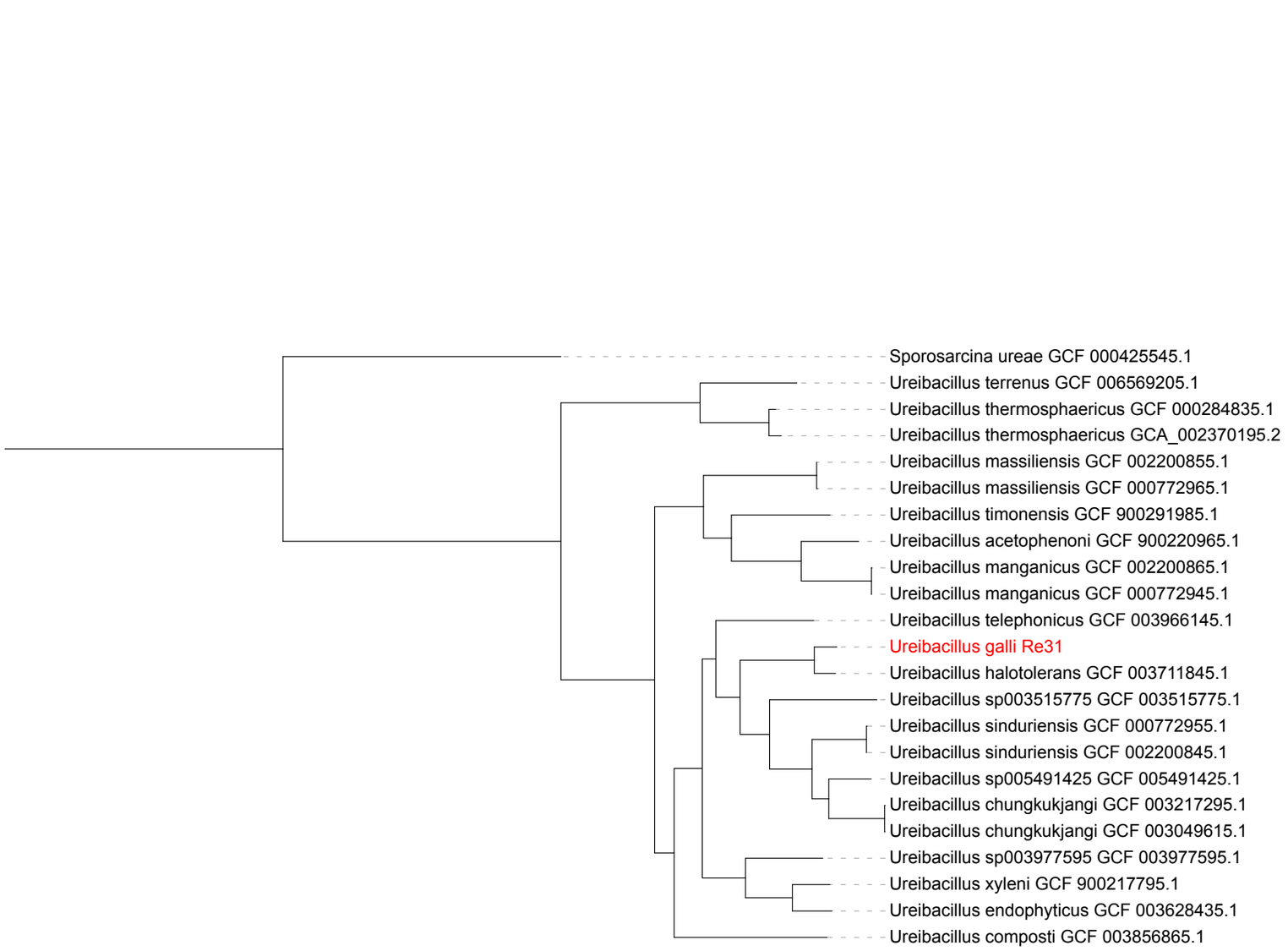
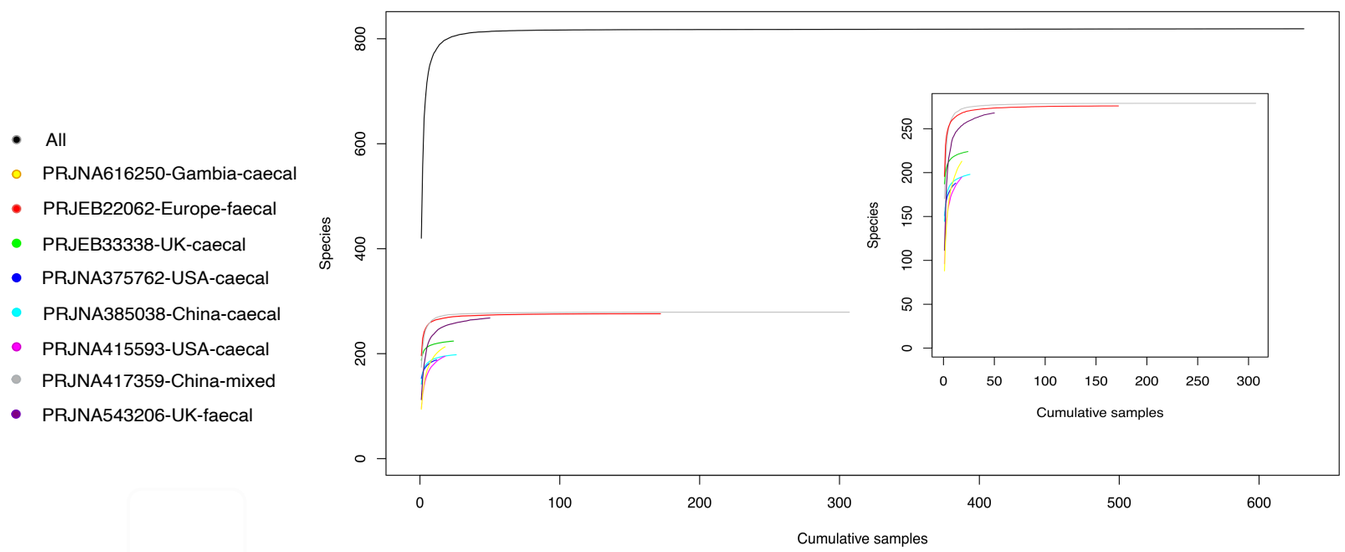
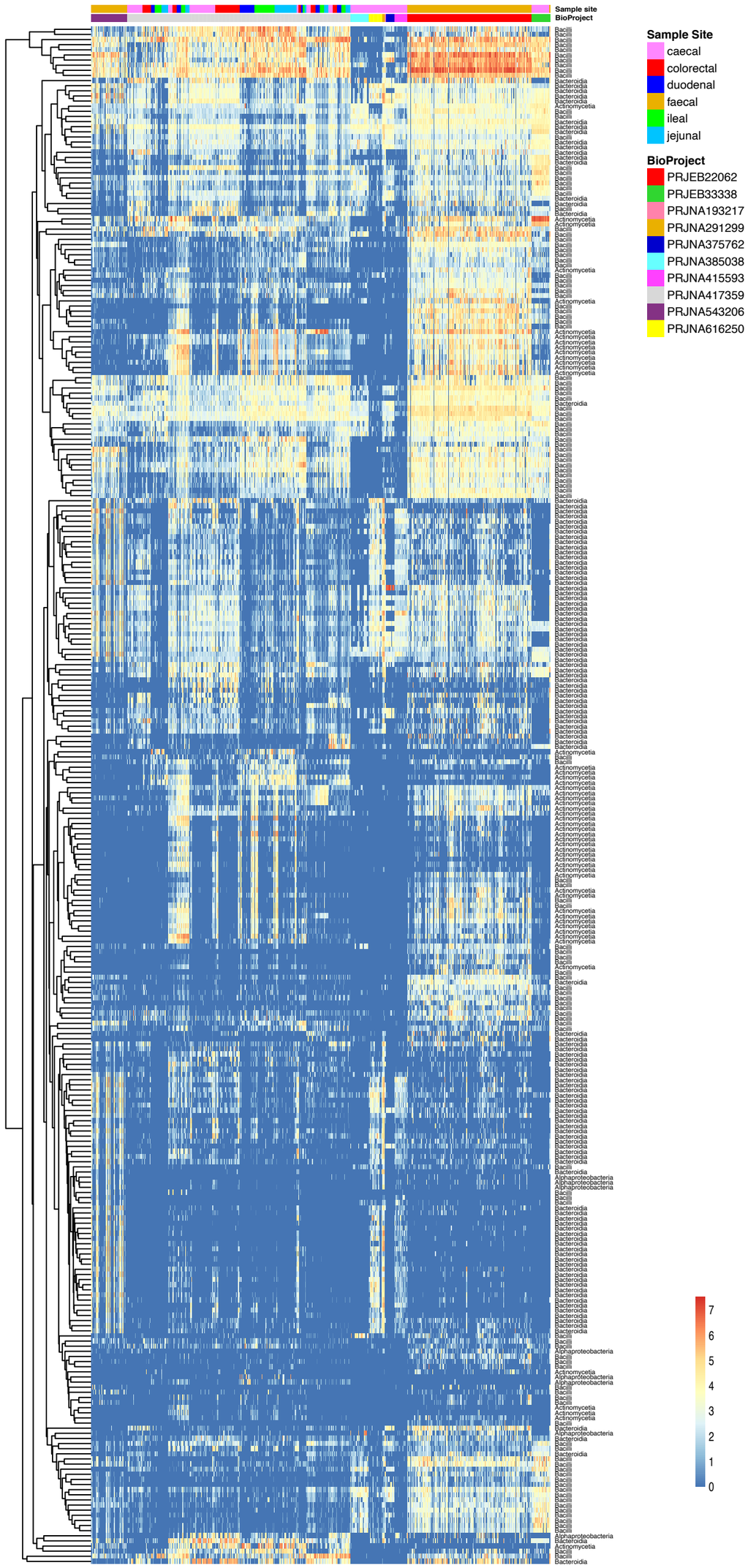


Figure S2. Phylogenetic trees reconstructed for genomes of each novel cultured isolate against all available reference genomes of the respective genus obtained from NCBI. Trees were reconstructed using PhyloPhlAn 3.0.58 against 400 marker genes before reconstruction using FastTree and RAxML of a MAFFT sequence alignment. Genomes of isolates cultured in this study have been highlighted in red and detailed with their respective strain identifier.

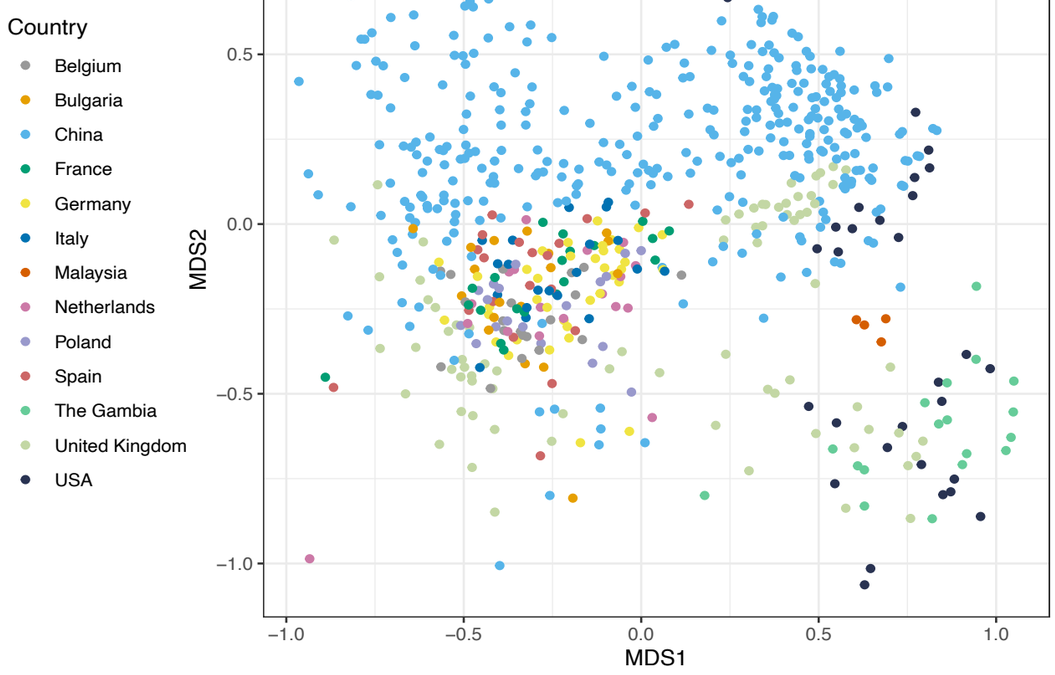
a.



b.



c.



d.

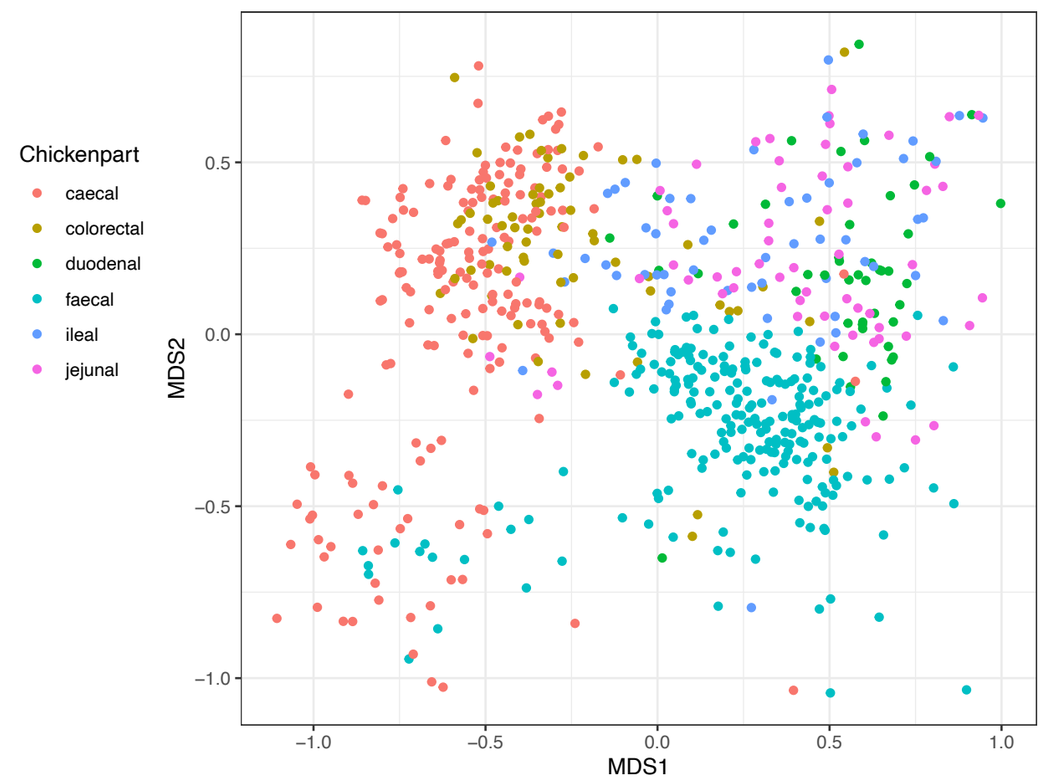


Figure S4a Species accumulation curve for 632 samples over 10 publicly available BioProjects accounting for 820 MGS. Only studies with > 1 sample are included in this plot. A further curve has been plotted to depict species accumulation for all metagenomic samples from all BioProjects (.pdf format).**b**. A heatmap depicting the abundance of the top 300 MGS, ordered by maximum sample abundance, across 632 samples derived from 10 BioProjects. Rows (MGS) were ordered by correlation clustering while columns (metagenomic sample) were ordered by source BioProject. Metagenomic species have been annotated with their taxonomic class. All data were Log10 transformed with Blue colour depicting species of low abundance and Red showing high abundance.**c**. Principle component analysis (PCA) based on Bray Curtis dissimilarity matrices between country of origin for MGS relative abundance. d. and for GIT sample site