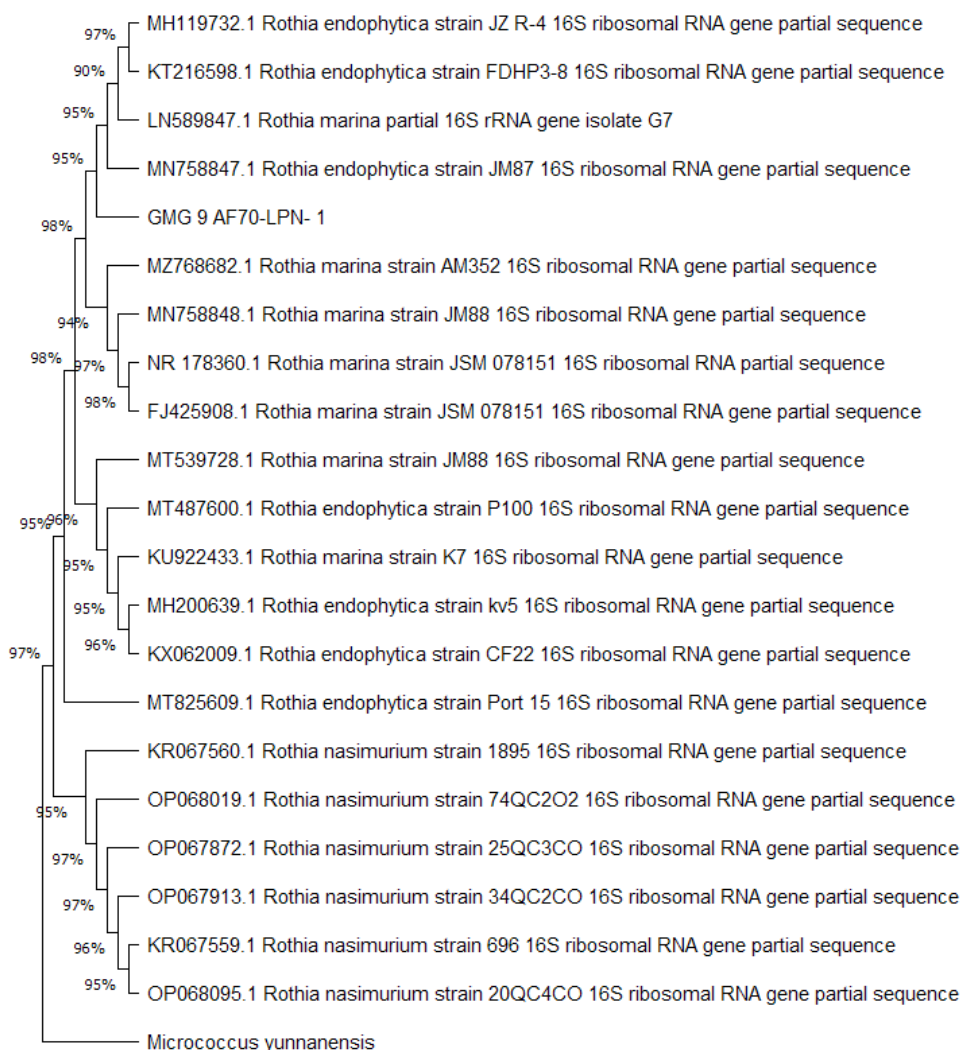
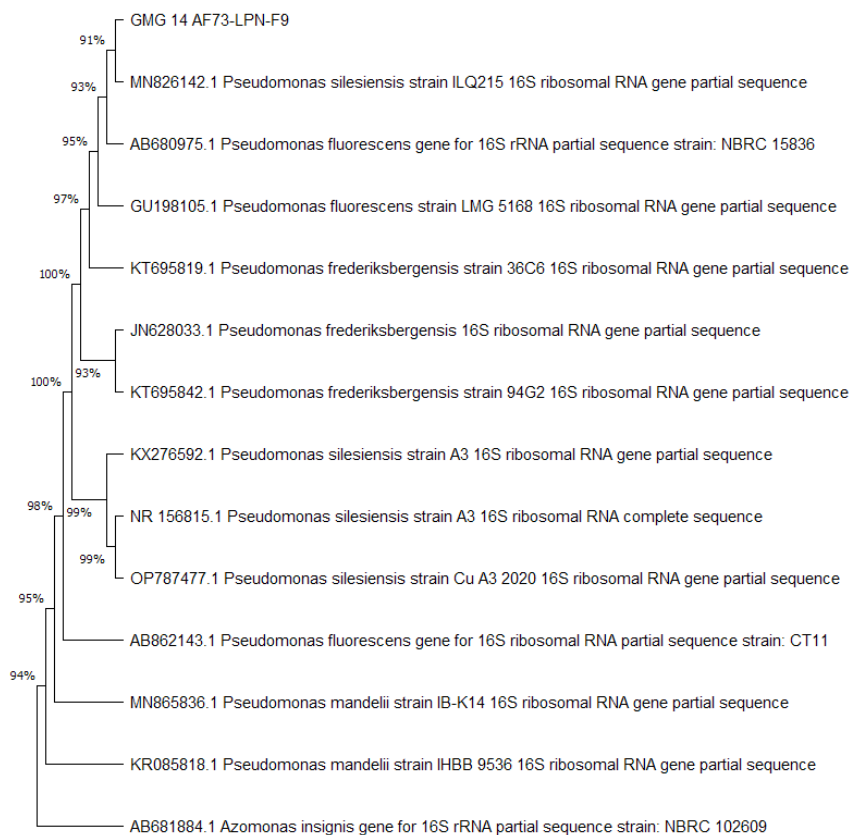


Table S1. Description of soil samples, morphology of colonies and bacteria, phylogenetic trees for 17 strains participating in the experiment on the effect on plant growth.

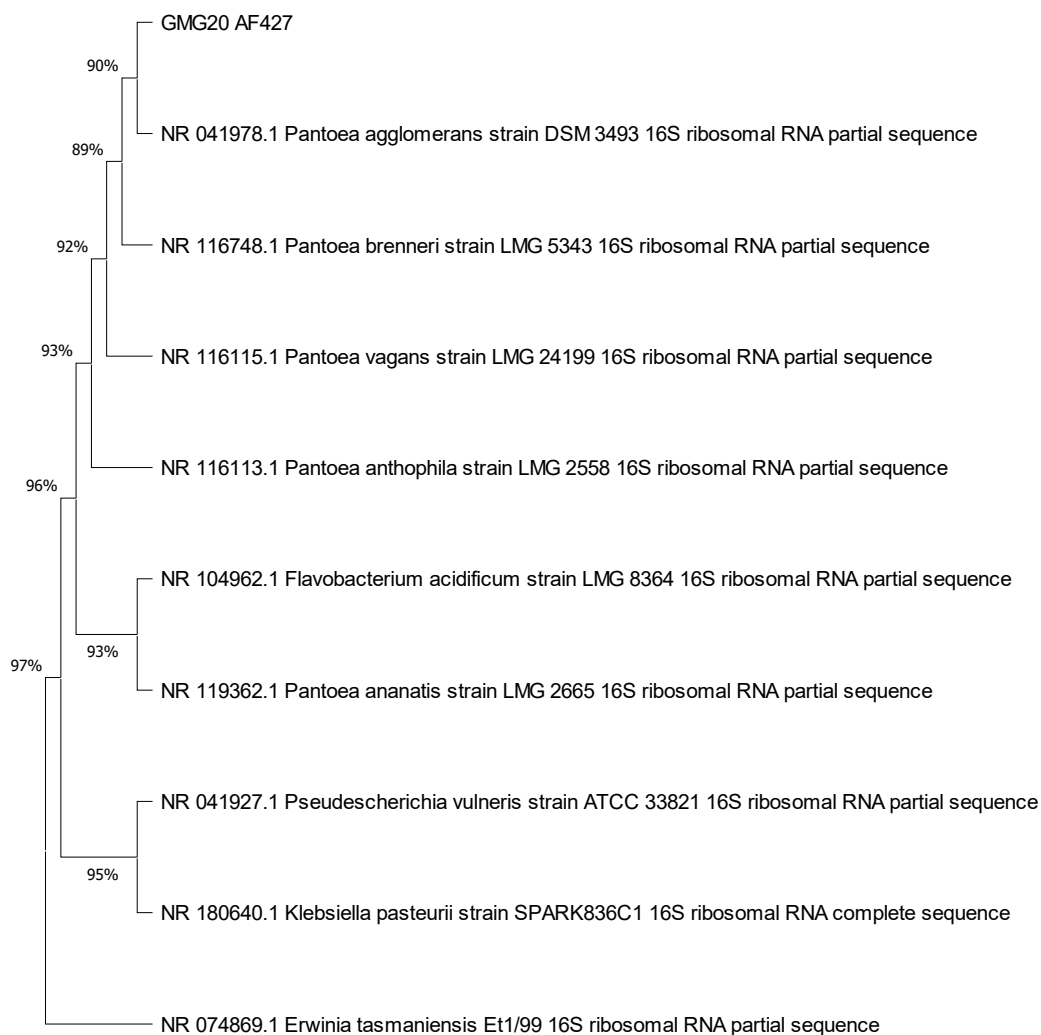
No	16S rRNA Identification	GenBank Accession No.	Coordinates of the Terrain for Obtaining Soil	Date of Obtaining the Soil	Colony Color	Colony Morphology	Gram Staining	Form Bacteria
GMG_9	<i>Rothia endophytica</i>	OR497741	44.680935, 33.615939	10.2021	white with a lilac shade	the colony is concentric in shape, the profile is flat, dull	Gram-positive	coccus



GMG_11	<i>Pseudomonas koreensis</i>	OR49774 2	54.879 886, 83.111 747	10.202 1	beige	colony of irregular shape, creeping, shiny	Gram- negati ve	rod bacteriu m
<p>Phylogenetic tree showing the relationship between GMG11-AF70-LPN-H2 and other <i>Pseudomonas</i> strains. The tree is rooted with AB681884.1 <i>Azomonas insignis</i> gene for 16S rRNA partial sequence strain: NBRC 102609. The main cluster of <i>Pseudomonas</i> strains is supported by a 97% bootstrap value. Within this cluster, GMG11-AF70-LPN-H2 is closely related to MH144336.1 <i>Pseudomonas koreensis</i> strain PgBE266 16S ribosomal RNA gene partial sequence (91% bootstrap) and MH211310.1 <i>Pseudomonas koreensis</i> strain PgBe221 16S ribosomal RNA gene partial sequence (93% bootstrap). Other strains include KJ819580.1 <i>Pseudomonas putida</i> strain NBFPALD RAS137 16S ribosomal RNA gene partial sequence (94% bootstrap), MW471622.1 <i>Pseudomonas koreensis</i> 16S ribosomal RNA gene partial sequence (96% bootstrap), and OQ733323.1 <i>Pseudomonas atacamensis</i> strain KSS-6 16S ribosomal RNA gene partial sequence (94% bootstrap). The KT695840.1 <i>Pseudomonas fluorescens</i> strain 90F12-2 16S ribosomal RNA gene partial sequence and KT695838.1 <i>Pseudomonas fluorescens</i> strain 90D7A 16S ribosomal RNA gene partial sequence are sister taxa with 100% bootstrap support.</p>								
GMG_14	<i>Pseudomonas silesiensis</i>	OR49774 3	54.879 886, 83.111 747	10.202 1	colorle ss	the colony is round in shape, the surface is smooth, the profile is convex	Gram- negati ve	rod- shaped bacteriu m.

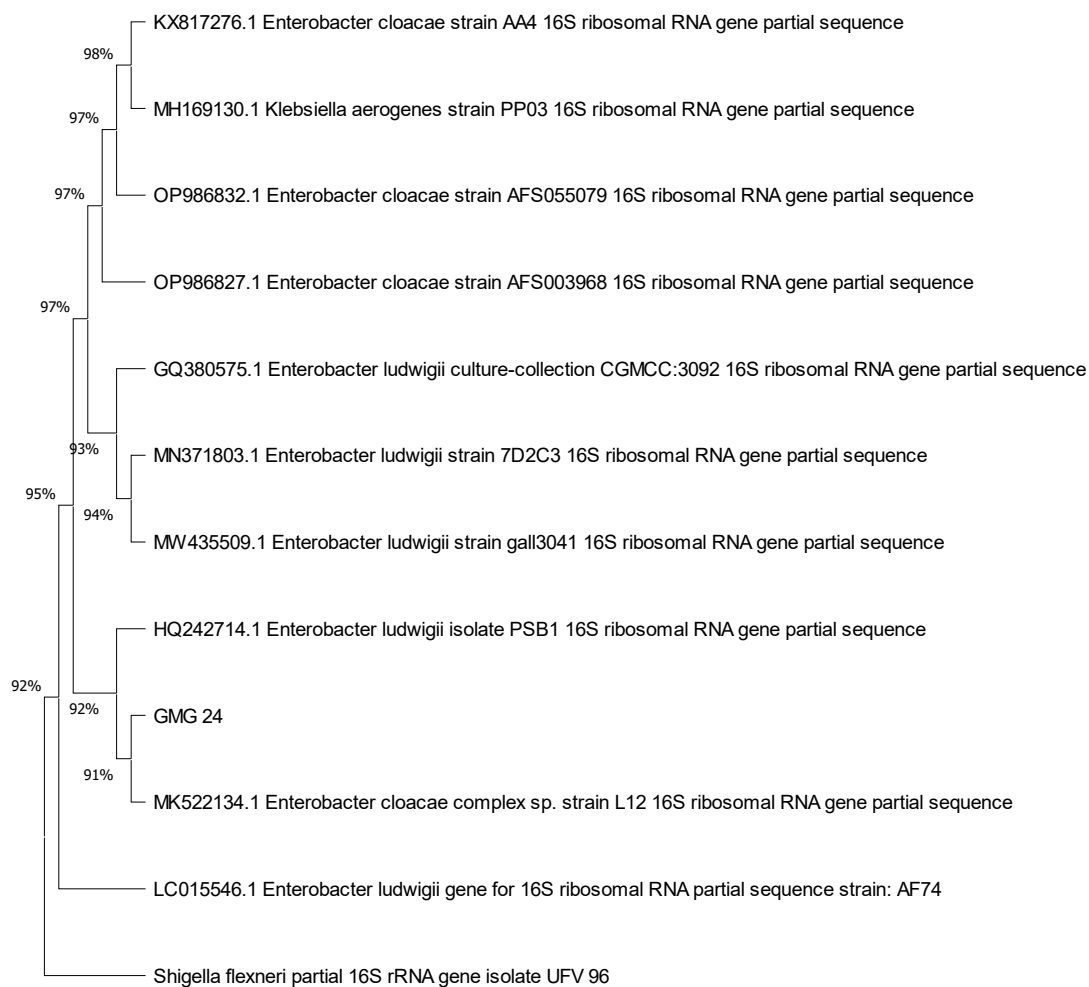


GMG_20	<i>Pantoea agglomerans</i>	OR49778 3	54.879 886, 83.111 747	10.202 1	orange	the colony is round in shape, the surface is smooth, the profile is convex, shiny	Gram- negati ve	rod bacteriu m
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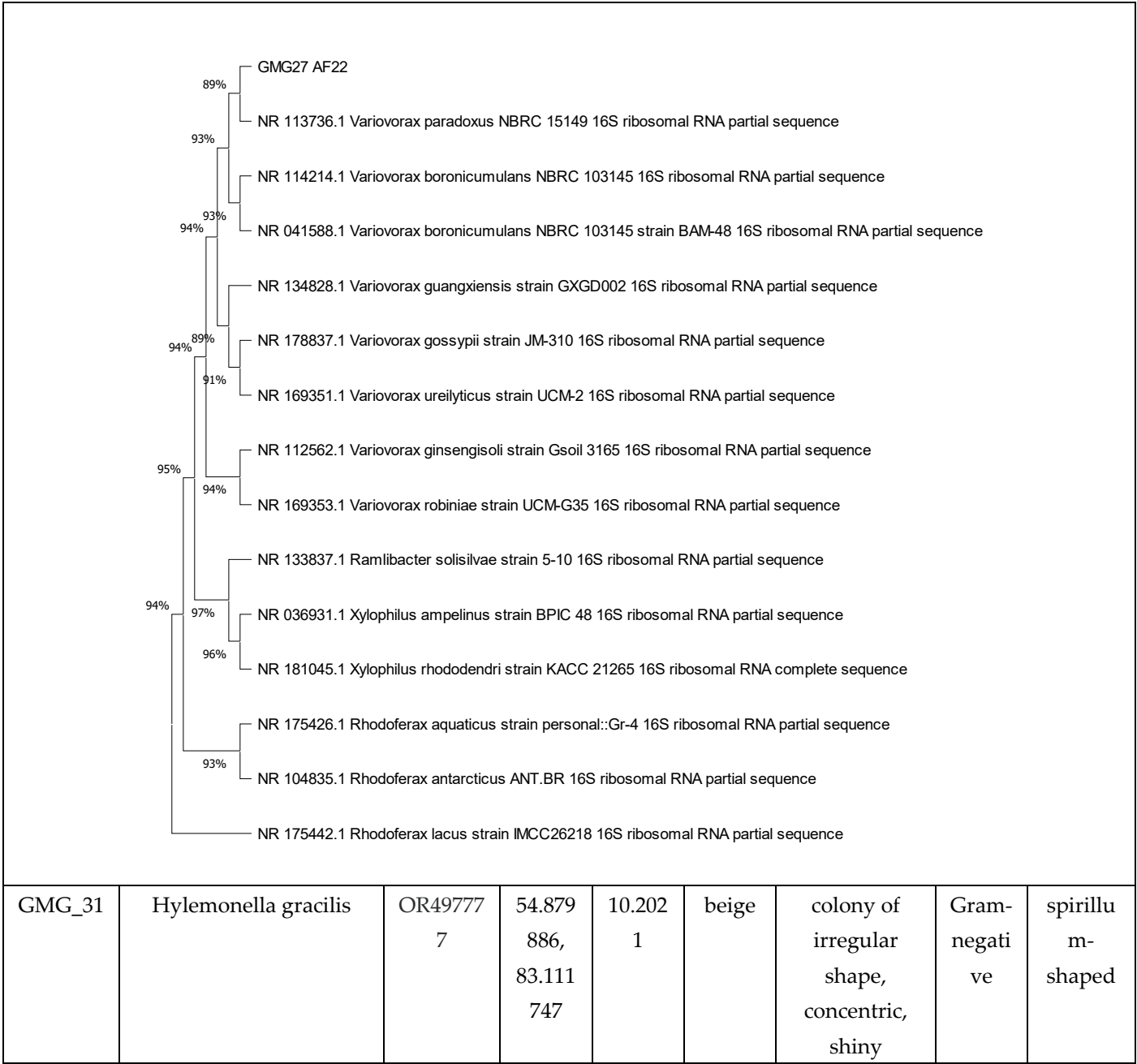


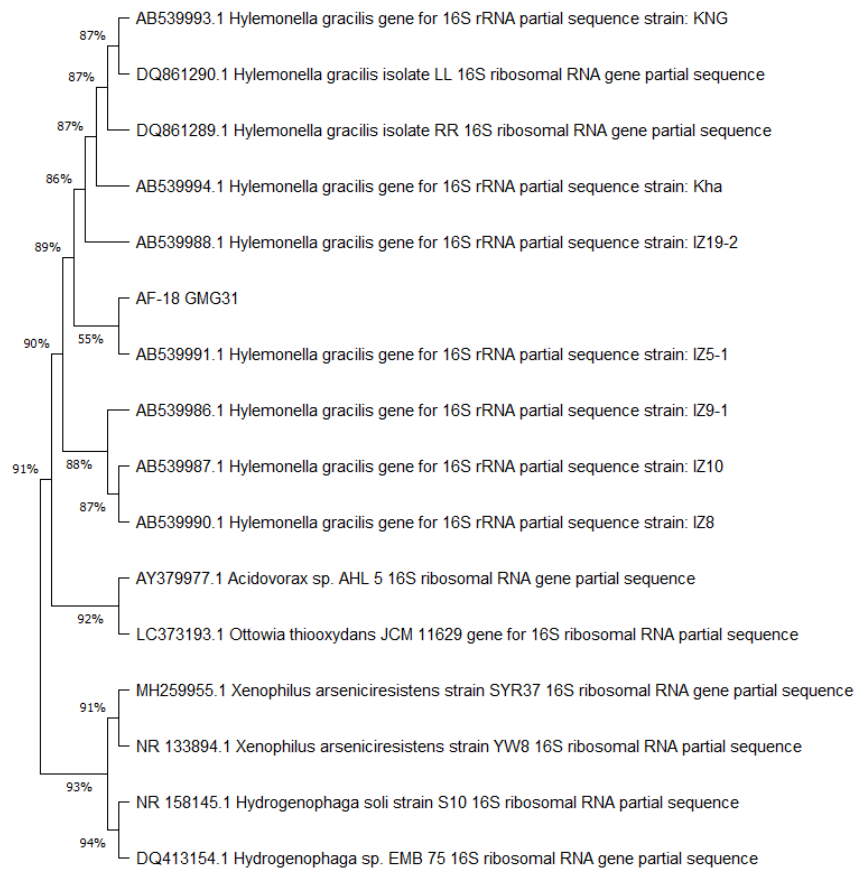
GMG_21	<i>Rhodococcus erythropolis</i>	OR49774 4	54,879 886, 83,111 747	10,202 1	white with an orange tint	the colony is irregular in shape, the surface is smooth, the profile is convex, shiny	Gram- positiv e	coccus- shaped
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<p>NR 104776.1 <i>Nocardia coeliaca</i> strain DSM 44595 16S ribosomal RNA partial sequence</p> <p>96%</p> <p>94%</p> <p>92%</p> <p>91%</p> <p>90%</p> <p>90%</p> <p>92%</p> <p>LC020106.1 <i>Rhodococcus erythropolis</i> gene for 16S ribosomal RNA partial sequence strain: LA73-1</p> <p>AJ131637.1 <i>Rhodococcus erythropolis</i> 16S rRNA gene strain DCL14 partial</p> <p>KF976880.1 <i>Rhodococcus erythropolis</i> strain K85 16S ribosomal RNA gene partial sequence</p> <p>FJ164059.1 <i>Actinobacterium</i> CH21i 16S ribosomal RNA gene partial sequence</p> <p>GMG21 AF72-NN-G6</p> <p>KX035054.1 <i>Rhodococcus erythropolis</i> strain ISE 16 16S ribosomal RNA gene partial sequence</p> <p>MT406572.1 <i>Nocardia coeliaca</i> strain Hal180 16S ribosomal RNA gene partial sequence</p> <p>AF532870.1 <i>Rhodococcus erythropolis</i> 16S ribosomal RNA gene partial sequence</p>								
GMG_24	<i>Enterobacter cloacae</i>	OR497780	54,879,886,83.111747	10.2021	colorless	the colony is round in shape, the surface is smooth, the profile is teardrop-shaped	Gram-negative	rod-shaped bacterium.

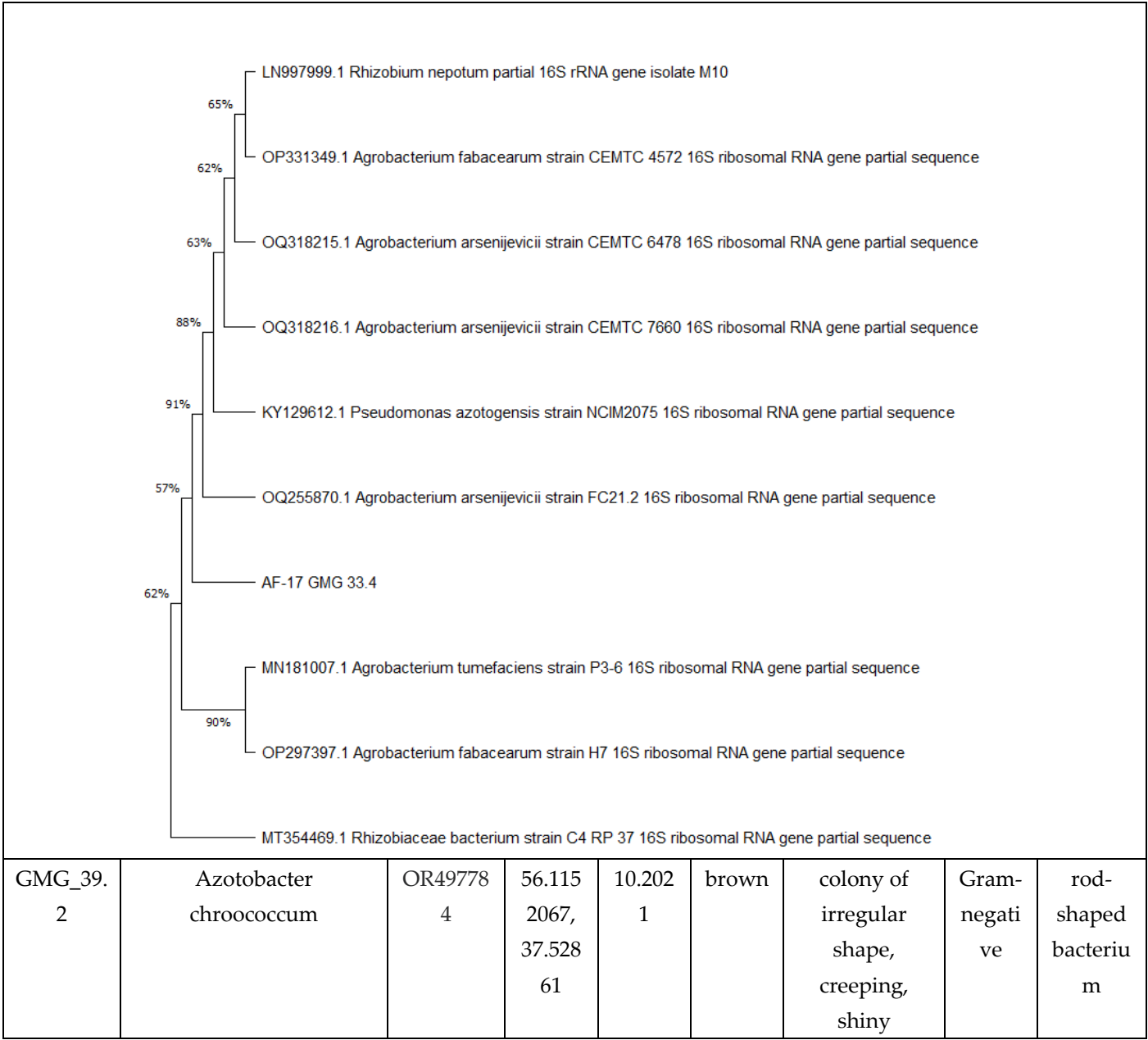


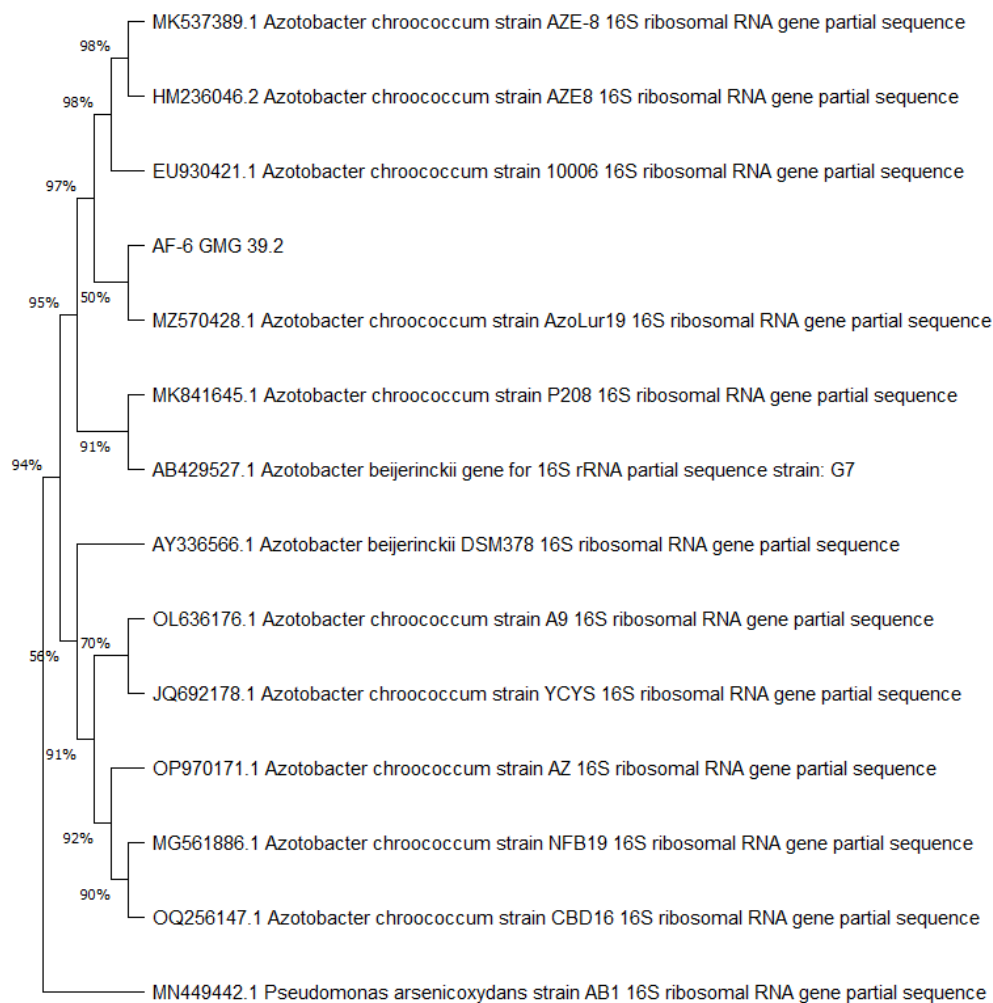
GMG_27	Variovorax paradoxus	OR49777 8	44.680 935, 33.615 939	10.202 1	brown	the colony is round in shape, the surface is smooth, shiny	Gram- negati ve	rod- shaped bacteriu m
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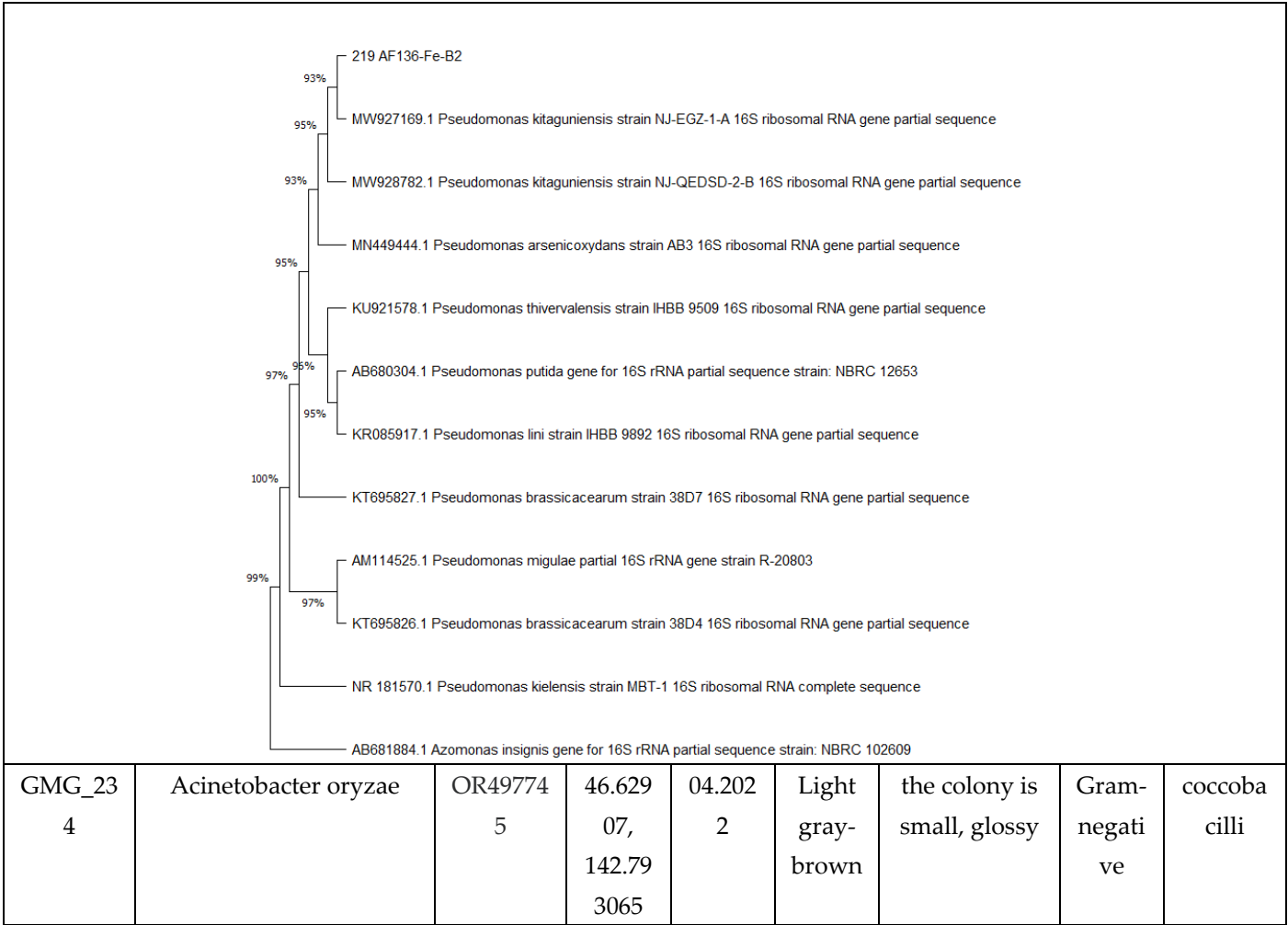


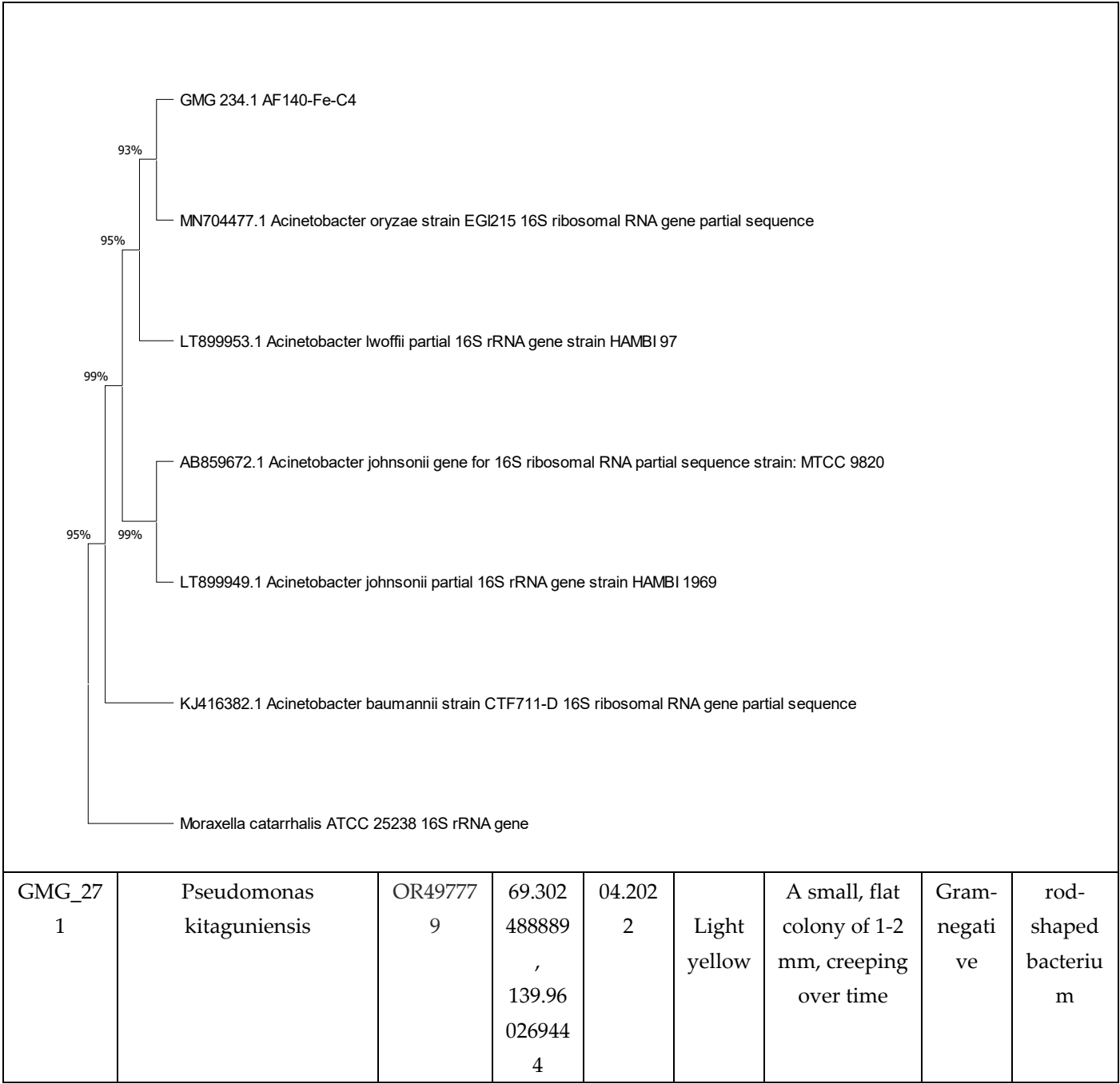
GMG_33. 4	Agrobacterium arsenijevicii	OR49778 2	56.115 2067, 37.528 61	10.202 1	Light yellow	the colony is round, convex, shiny	Gram- negati ve	rod- shaped bacteriu m
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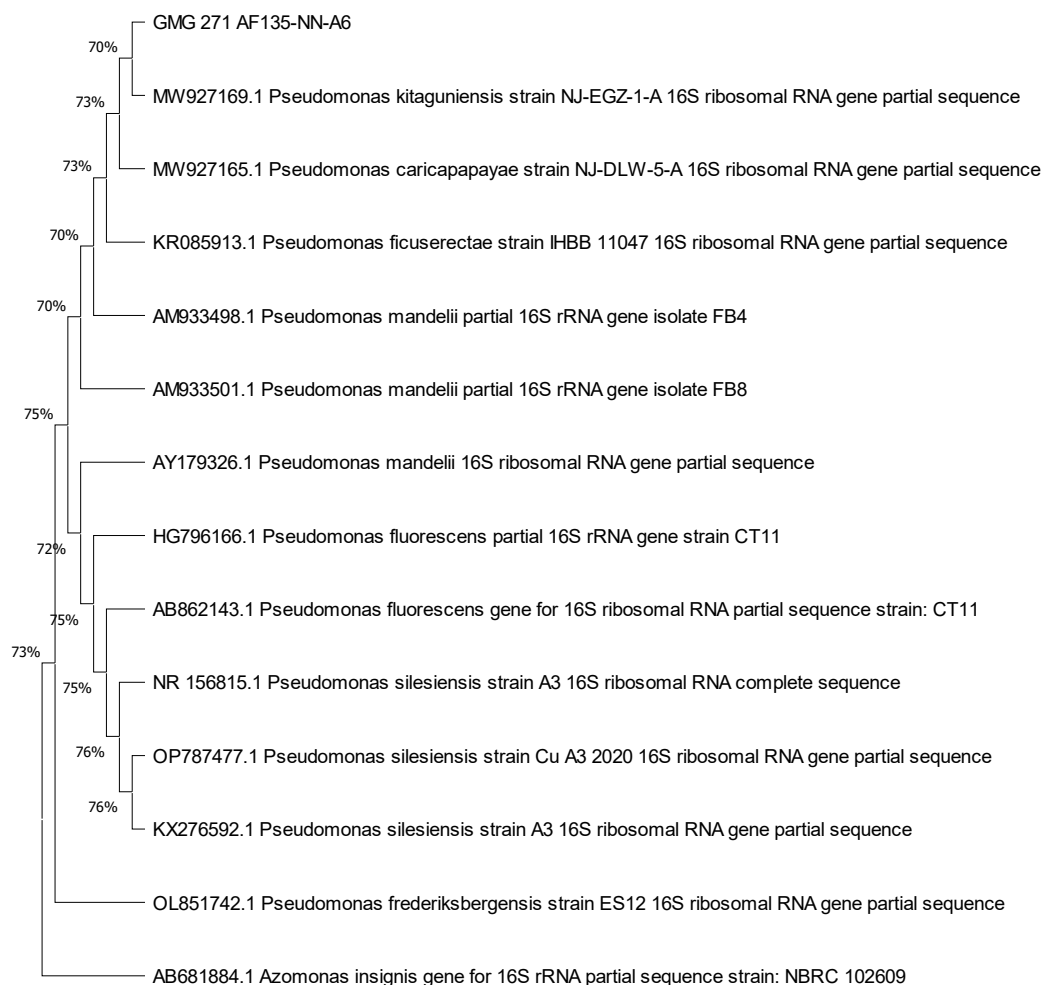




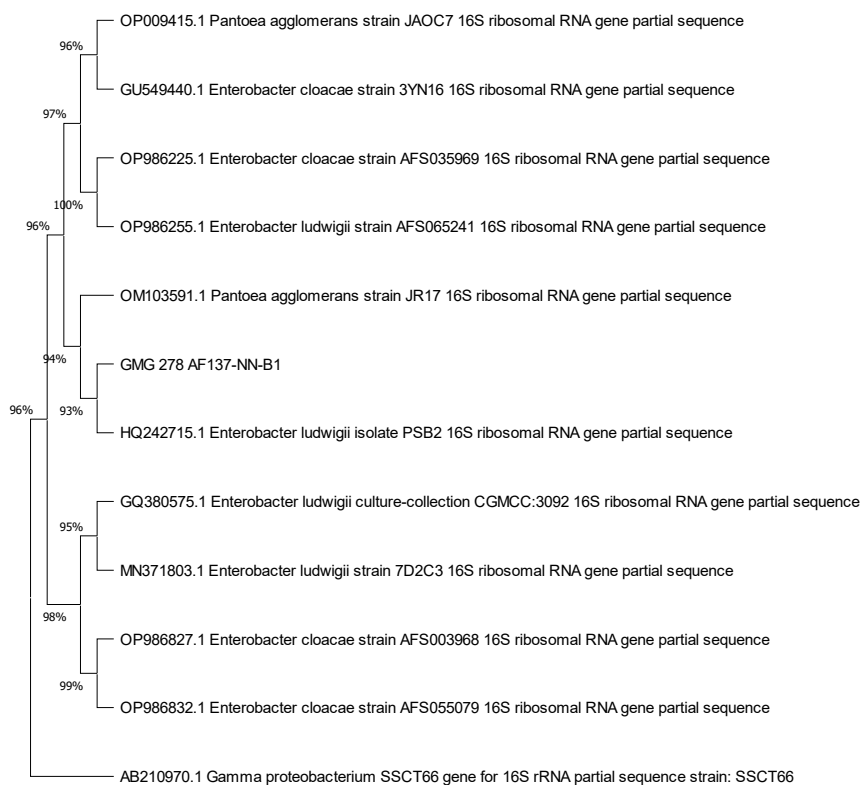
GMG_21 9	<i>Pseudomonas</i> <i>kitaguniensis</i>	OR49778 0	69.302 488889 , 139.96 026944 4	04.202 2	Light yellow	A small, flat colony of 1-2 mm, creeping over time	Gram- negati ve	rod- shaped bacteriu m
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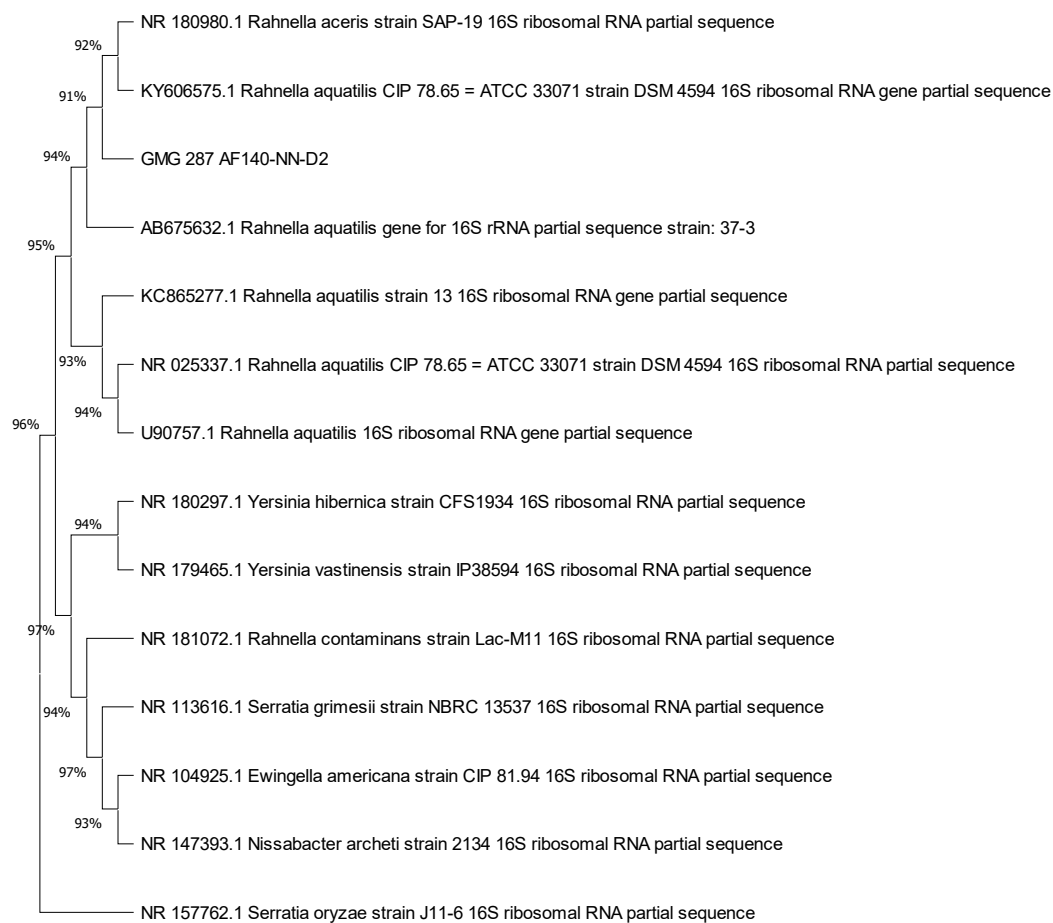




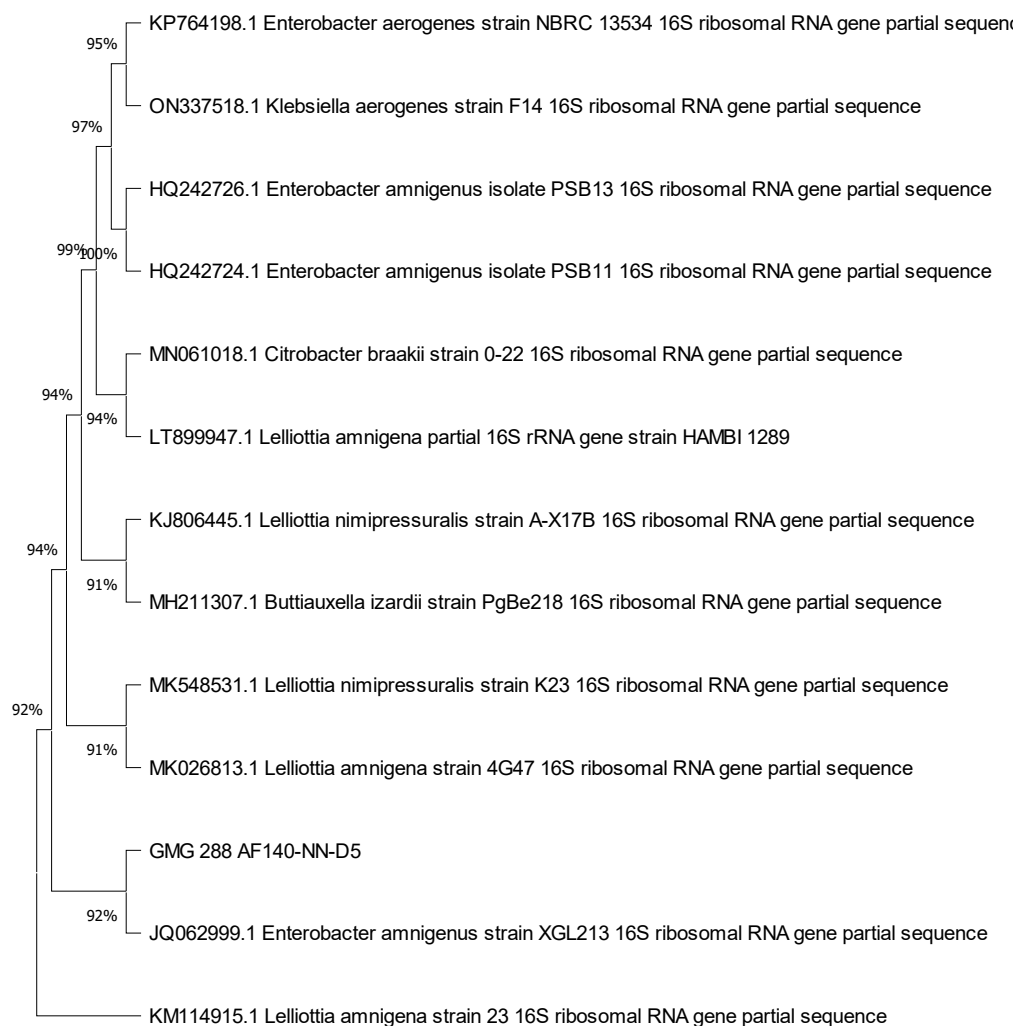
GMG_27 8	<i>Enterobacter ludwigii</i>	OQ72737 6	46.962 08, 142.75 7798	04.202 2	beige	The colony is convex with a smooth edge, glossy	Gram- negati ve	rod- shaped bacteriu m
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GMG_28 7	Rahnella aquatilis	OR49774 6	46.629 07, 142.79 3065	04.202 2	beige	The average colony is 3-4 mm, glossy, with time a creeping transparent rhizoid edge is formed	Gram-negative	rod bacterium
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GMG_28 8	<i>Enterobacter amnigenus</i>	OR49774 7	46.629 07, 142.79 3065	04.202 2	Light yellow	Convex colony with smooth edges, glossy	Gram- negati ve	rod bacteriu m
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GMG_29 4	Rahnella aceris	OR49774 8	46.629 07, 142.79 3065	04.202 2	beige	The average colony is 3-4 mm, glossy, with time a creeping transparent rhizoid edge is formed	Gram-negative	rod-shaped bacterium
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