

Source/incubation	GTDB classification	Closest placement reference	Closest placement taxonomy	Closest placement (ANI)	Classification Method	Completeness (%)	Contamination (%)
sub muros	d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Chitinophagales; f__Chitinophagaceae; g__Puia; s__	-	-	-	taxonomic classification fully defined by topology	98.28	0.74
sub muros	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Undibacterium; s__	-	-	-	taxonomic classification defined by topology and ANI	99.45	1.1
sub muros	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__Rhodanobacteraceae; g__Rhodanobacter; s__	-	-	-	taxonomic classification defined by topology and ANI	99.66	1.03
sub muros	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Paraburkholderia; s__Paraburkholderia fungorum	GCF_902833645.1	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Paraburkholderia; s__Paraburkholderia fungorum	95.25	taxonomic classification defined by topology and ANI	86.83	4.31
sub muros	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__Mesorhizobium; s__	-	-	-	taxonomic classification defined by topology and ANI	98.88	5.21
sub muros	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__DSM-16500; f__DSM-16500; g__UBA5158; s__	-	-	-	taxonomic classification fully defined by topology	91.28	1.94
sub muros	d__Bacteria; p__Acidobacteriota; c__Acidobacteriae; o__Acidobacteriales; f__Acidobacteriaceae; g__Edaphobacter; s__	-	-	-	ANI	96.59	1.72
sub muros	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Variovorax; s__Variovorax sp001899795	GCA_001899795.1	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Variovorax; s__Variovorax sp001899795	98.29	taxonomic classification defined by topology and ANI	97.28	0.68
sub muros	d__Bacteria; p__Acidobacteriota; c__Acidobacteriae; o__Acidobacteriales; f__Acidobacteriaceae; g__Edaphobacter; s__	GCF_000381605.1	d__Bacteria; p__Acidobacteriota; c__Acidobacteriae; o__Acidobacteriales; f__Acidobacteriaceae; g__Edaphobacter; s__Edaphobacter sp000381605	81.12	taxonomic classification defined by topology and ANI	81.48	4.55
sub muros	d__Bacteria; p__Chlamydiota; c__Chlamydiia; o__Chlamydiales; f__Parachlamydiaceae; g__JABDDC01; s__	-	-	-	taxonomic novelty determined using RED	97.97	1.35
sub muros	d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Sphingobacteriales; f__Sphingobacteriaceae; g__Mucilaginibacter; s__	GCA_013286565.1	d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Sphingobacteriales; f__Sphingobacteriaceae; g__Mucilaginibacter; s__Mucilaginibacter sp013286565	79.04	taxonomic classification defined by topology and ANI	97.62	0.71
sub muros	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales_A; f__Rhizobiaceae_A; g__Phyllobacterium; s__Phyllobacterium sp900539805	GCA_900539805.1	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales_A; f__Rhizobiaceae_A; g__Phyllobacterium; s__Phyllobacterium sp900539805	96.87	taxonomic classification defined by topology and ANI	94.13	0.0
sub muros	d__Bacteria; p__Acidobacteriota; c__Acidobacteriae; o__Acidobacteriales; f__Acidobacteriaceae; g__Granulicella_C; s__	GCA_903970285.1	d__Bacteria; p__Acidobacteriota; c__Acidobacteriae; o__Acidobacteriales; f__Acidobacteriaceae; g__Granulicella_C; s__Granulicella_C sp903970285	77.92	taxonomic classification defined by topology and ANI	94.02	0.0

sub muros	d__Bacteria; p__Actinobacteriota; c__Actinomycetia; o__Actinomycetales; f__Micrococcaceae; g__MA-N2; s__MA-N2 sp002009585	GCF_002009585.1	d__Bacteria; p__Actinobacteriota; c__Actinomycetia; o__Actinomycetales; f__Micrococcaceae; g__MA-N2; s__MA-N2 sp002009585	95.76	taxonomic classification defined by topology and ANI	94.78	0.29
sub muros	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Steroidobacterales; f__Steroidobacteraceae; g__Bog-1198; s__	GCA_003165495.1	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Steroidobacterales; f__Steroidobacteraceae; g__Bog-1198; s__Bog-1198 sp003165495	84.08	taxonomic classification defined by topology and ANI	93.98	5.78
sub muros	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Azospirillales_A; f__BOG-932; g__BOG-932; s__	GCA_003165335.1	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Azospirillales_A; f__BOG-932; g__BOG-932; s__BOG-932 sp003165335	80.01	taxonomic classification defined by topology and ANI	94.2	2.55
sub muros	d__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Acidimicrobiales; f__RAAP-2; g__Bog-756; s__	GCA_003153575.1	d__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Acidimicrobiales; f__RAAP-2; g__Bog-756; s__Bog-756 sp003153575	82.73	taxonomic classification defined by topology and ANI	93.94	0.43
anoxic	d__Bacteria; p__Firmicutes_D; c__Proteinivoracia; o__UBA4975; f__UBA4975; g__; s__	-	-	-	taxonomic novelty determined using RED	81.92	0.0
anoxic	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Hyphomicrobiaceae; g__Hyphomicrobium; s__	-	-	-	ANI	91.67	1.42
anoxic	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Beijerinckiaceae; g__Microvirga; s__	GCF_011777495.1	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Beijerinckiaceae; g__Microvirga; s__Microvirga sp011777495	87.18	taxonomic classification defined by topology and ANI	97.54	1.52
anoxic	d__Bacteria; p__Firmicutes_B; c__Thermincolia; o__Thermincolales; f__UBA2595; g__; s__	-	-	-	taxonomic novelty determined using RED	98.85	3.18
anoxic	d__Bacteria; p__Acidobacteriota; c__Acidobacteriae; o__Bryobacterales; f__Bryobacteraceae; g__Solibacter; s__	-	-	-	taxonomic novelty determined using RED	96.3	0.88
anoxic	d__Bacteria; p__Acidobacteriota; c__Acidobacteriae; o__Bryobacterales; f__Bryobacteraceae; g__; s__	-	-	-	taxonomic novelty determined using RED	99.12	1.75
anoxic	d__Bacteria; p__Firmicutes_A; c__Clostridia_A; o__Christensenellales; f__; g__; s__	-	-	-	taxonomic novelty determined using RED	91.93	2.92
anoxic	d__Bacteria; p__Firmicutes_E; c__DTU015; o__UBA9673; f__UBA9673; g__; s__	GCA_003599345.1	d__Bacteria; p__Firmicutes_E; c__DTU015; o__UBA9673; f__UBA9673; g__SURF-36; s__SURF-36 sp003599345	77.36	taxonomic classification defined by topology and ANI	87.62	3.8
anoxic	d__Bacteria; p__Firmicutes_B; c__Thermincolia; o__Carboxydocellales; f__; g__; s__	-	-	-	taxonomic novelty determined using RED	98.34	1.19
anoxic	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__Tardiphaga; s__	GCA_004173095.1	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__Tardiphaga; s__Tardiphaga sp004173095	85.46	taxonomic classification defined by topology and ANI	95.27	0.93
anoxic	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhizobiaceae; g__DUSC01; s__	-	-	-	taxonomic novelty determined using RED	82.9	5.51
anoxic	d__Bacteria; p__Firmicutes_B; c__Desulfitobacteriia; o__Desulfitobacterales; f__; g__; s__	-	-	-	taxonomic novelty determined using RED	90.26	4.59
anoxic	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__; s__	-	-	-	taxonomic classification fully defined by topology	96.52	1.53

anoxic	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas; s__	GCA_903884945.1	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas; s__Sphingomonas sp903884945	83.1	taxonomic classification defined by topology and ANI	99.66	2.29
anoxic	d__Bacteria; p__Firmicutes_B; c__Thermincolia; o__Thermincolales; f__ ; g__ ; s__	-	-	-	taxonomic novelty determined using RED	99.74	1.11
anoxic	d__Bacteria; p__Firmicutes; c__Bacilli; o__Paenibacillales; f__Paenibacillaceae; g__Paenibacillus_G; s__	GCF_007786445.1	d__Bacteria; p__Firmicutes; c__Bacilli; o__Paenibacillales; f__Paenibacillaceae; g__Paenibacillus_G; s__Paenibacillus_G sp007786445	77.94	taxonomic classification defined by topology and ANI	86.14	0.45
anoxic	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__PALSA-894; s__	-	-	-	taxonomic novelty determined using RED	99.6	2.82
anoxic	d__Bacteria; p__Actinobacteriota; c__Thermoleophilia; o__Solirubrobacterales; f__Solirubrobacteraceae; g__Conexibacter; s__	GCF_014199525.1	d__Bacteria; p__Actinobacteriota; c__Thermoleophilia; o__Solirubrobacterales; f__Solirubrobacteraceae; g__Conexibacter; s__Conexibacter arvalis	86.9	taxonomic classification defined by topology and ANI	96.15	3.42
anoxic	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__VAZQ01; s__	GCA_009377695.1	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__VAZQ01; s__VAZQ01 sp009377695	83.42	taxonomic classification defined by topology and ANI	86.46	1.69
anoxic	d__Bacteria; p__Firmicutes_B; c__Thermincolia; o__Thermincolales; f__UBA2595; g__GW- Firmicutes-8; s__	GCA_002840165.1	d__Bacteria; p__Firmicutes_B; c__Thermincolia; o__Thermincolales; f__UBA2595; g__GW- Firmicutes-8; s__GW-Firmicutes-8 sp002840165	92.8	taxonomic classification defined by topology and ANI	99.49	1.15
oxic	d__Bacteria; p__Firmicutes_B; c__Thermincolia; o__Carboxydocellales; f__ ; g__ ; s__	-	-	-	taxonomic novelty determined using RED	94.82	8.49
oxic	d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Sphingobacteriales; f__Sphingobacteriaceae; g__Mucilaginibacter; s__	GCA_013286565.1	d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Sphingobacteriales; f__Sphingobacteriaceae; g__Mucilaginibacter; s__Mucilaginibacter sp013286565	78.96	taxonomic classification defined by topology and ANI	89.24	3.65