

Phylogenetic group	Mo(0)	Mo(28)	Mo(56)	Mo(84)	Mo(112)	Mo(140)	Wk(0)	Wk(28)	Wk(56)	Wk(84)	Wk(112)	Wk(140)	Fd(0)	Fd(140)
Bacilli-Bacillales-Paenibacillaceae-unclassified	0.20	-	-	-	-	-	0.09	-	-	-	-	-	-	0.02
Bacilli-Bacillales-Paenibacillaceae- <i>Cohnella</i>	0.16	0.09	-	-	-	-	0.06	0.03	-	0.01	0.03	-	0.01	0.01
Bacilli-Bacillales-Paenibacillaceae- <i>Brevibacillus</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.01	0.02
Bacilli-Bacillales-Paenibacillaceae- <i>Paenibacillus</i>	-	0.02	-	0.04	-	-	-	-	-	-	-	-	0.02	0.03
Bacilli-Bacillales-Baciliaceae-unclassified	-	0.02	-	-	0.02	-	0.02	-	-	-	-	-	-	0.01
Bacilli-Bacillales-Baciliaceae- <i>Bacillus</i>	0.02	0.02	-	0.02	-	-	0.01	-	-	-	-	0.01	0.11	0.11
Bacilli-Bacillales-Thermoactinomycetaceae- <i>Laceyella</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01
Bacilli-Bacillales-Thermoactinomycetaceae- <i>Shimazuella</i>	-	0.02	-	-	-	-	0.01	-	-	-	-	0.01	0.01	-
Bacilli-Bacillales-Thermoactinomycetaceae- <i>Thermoactinomyces</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01
Bacilli-Bacillales-Planococcaceae- <i>Paenisporosarcina</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.02	-
Bacilli-Bacillales-Planococcaceae- <i>Sporosarcina</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.01	-
Clostridia-unclassified	-	0.02	-	0.02	-	-	-	-	-	0.01	-	-	0.07	0.04
Clostridia-Clostridiales-unclassified	-	-	-	-	0.05	0.02	0.02	0.01	-	0.02	-	-	0.09	0.17
Clostridia-Clostridiales-Syntrophomonadaceae-unclassified	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01
Clostridia-Clostridiales-Incertae Sedis XVIII- <i>Symbiobacterium</i>	0.02	-	-	-	-	-	-	-	0.01	-	-	-	0.01	-
Clostridia-Clostridiales-Peptococcaceae-Peptococcaceae 1- <i>Desulfosporosinus</i>	-	-	0.03	-	-	-	-	-	-	-	-	-	0.02	0.05
Clostridia-Clostridiales-Peptococcaceae-Peptococcaceae 2- <i>Pelotomaculum</i>	-	-	-	-	0.05	-	-	0.01	-	-	-	-	0.01	-
Clostridia-Clostridiales-Peptococcaceae-Peptococcaceae 2- <i>Cryptanaerobacter</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01
Clostridia-Clostridiales-Peptococcaceae-Peptococcaceae 2- <i>Thermincola</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.01	-
Clostridia-Clostridiales-Ruminococcaceae-unclassified	-	-	-	-	-	-	-	-	-	-	0.01	-	0.01	0.01
Clostridia-Clostridiales-Ruminococcaceae- <i>Acetivibrio</i>	0.02	-	-	-	-	-	-	0.02	-	0.01	-	-	0.01	0.12
Clostridia-Clostridiales-Ruminococcaceae- <i>Sporobacter</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.01	-
Clostridia-Clostridiales-Lachnospiraceae-unclassified	-	-	-	-	-	-	-	-	-	-	-	-	0.01	-
Clostridia-Clostridiales-Veillonellaceae-unclassified	-	-	-	-	-	-	-	-	-	-	-	-	0.05	0.02
Clostridia-Clostridiales-Veillonellaceae- <i>Sporotalea</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01
Clostridia-Clostridiales-Veillonellaceae- <i>Sporomusa</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.03	-
Clostridia-Clostridiales-Clostridiaceae-unclassified	-	-	-	-	-	-	-	-	-	-	-	-	0.01	-
Clostridia-Clostridiales-Clostridiaceae-Clostridiaceae 1-unclassified	-	-	-	0.04	-	-	-	-	-	-	-	-	0.02	-
Clostridia-Clostridiales-Clostridiaceae-Clostridiaceae 1- <i>Clostridium</i>	-	-	-	0.04	-	-	-	-	-	-	-	-	-	0.05
Clostridia-Clostridiales-Clostridiaceae-Clostridiaceae 1- <i>Oxybacter</i>	-	-	-	-	-	-	-	-	-	-	-	0.01	-	-
Clostridia-Clostridiales-Gracilibacteraceae- <i>Gracilibacter</i>	-	0.02	-	-	-	-	-	-	-	-	-	-	0.04	0.01
Clostridia-Thermoanaerobacterales-Thermoanaerobacteraceae- <i>Mahella</i>	-	-	-	-	-	-	-	-	-	-	-	0.01	0.03	-
Clostridia-Thermoanaerobacterales-Thermoanaerobacteraceae- <i>Moorella</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.02	-
TM7-TM7_genera_incertae_sedis	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01
Bacteroidetes-														
unclassified	8.66	17.47	9.74	9.28	15.84	4.67	4.49	3.81	1.29	1.50	3.26	1.26	0.01	0.03
Sphingobacteria-Sphingobacteriales-unclassified	0.40	0.31	0.07	0.02	0.45	0.22	0.10	0.23	0.07	0.07	0.09	0.05	-	-
Sphingobacteria-Sphingobacteriales-Chitinophagaceae-unclassified	2.99	2.17	2.50	2.25	1.98	1.00	2.65	1.24	0.85	0.68	0.48	0.16	0.01	-
Sphingobacteria-Sphingobacteriales-Chitinophagaceae- <i>Sediminibacterium</i>	0.33	0.03	0.04	0.33	4.41	12.53	0.36	1.77	2.16	1.60	1.05	0.54	-	-
Sphingobacteria-Sphingobacteriales-Chitinophagaceae- <i>Flavisolibacter</i>	0.20	0.09	0.05	0.07	0.02	-	0.10	0.03	0.02	0.03	0.01	-	-	-
Sphingobacteria-Sphingobacteriales-Chitinophagaceae- <i>Niastella</i>	0.02	-	-	-	-	-	0.03	-	-	-	-	-	-	-
Sphingobacteria-Sphingobacteriales-Chitinophagaceae- <i>Terrimonas</i>	7.22	2.93	2.45	1.32	0.37	0.09	7.12	0.94	0.28	0.14	0.15	0.20	-	-
Sphingobacteria-Sphingobacteriales-Cytophagaceae- <i>Dyadobacter</i>	0.07	0.09	0.12	0.26	0.07	0.04	0.02	0.01	0.01	-	-	0.01	0.55	0.22
Sphingobacteria-Sphingobacteriales-Sphingobacteriaceae- <i>Olivibacter</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.01	0.02
Sphingobacteria-Sphingobacteriales-Sphingobacteriaceae- <i>Pedobacter</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	0.12
Sphingobacteria-Sphingobacteriales-Sphingobacteriaceae- <i>Muciliaginibacter</i>	-	-	-	-	-	-	-	-	-	-	0.02	-	-	-
Flavobacteria-Flavobacteriales-unclassified	0.02	0.02	-	0.04	-	-	0.01	-	-	0.01	-	-	-	-
Flavobacteria-Flavobacteriales-Flavobacteriaceae-unclassified	0.24	0.06	0.17	0.28	0.05	0.02	0.36	-	0.01	0.02	-	0.01	-	0.01
Flavobacteria-Flavobacteriales-Flavobacteriaceae- <i>Flavobacterium</i>	0.84	0.06	0.03	0.15	-	-	0.38	0.02	-	-	-	-	-	0.12
Flavobacteria-Flavobacteriales-Flavobacteriaceae- <i>Chryseobacterium</i>	0.82	0.20	0.29	0.47	0.02	-	0.57	0.04	-	-	-	-	-	0.01
Proteobacteria-														
unclassified	5.03	5.60	4.77	4.86	7.85	4.59	5.30	4.64	3.25	3.73	3.50	3.68	2.02	1.59

Phylogenetic group	Mo(0)	Mo(28)	Mo(56)	Mo(84)	Mo(112)	Mo(140)	Wk(0)	Wk(28)	Wk(56)	Wk(84)	Wk(112)	Wk(140)	Fd(0)	Fd(140)
Epsilonproteobacteria-Campylobacteriales-Helicobacteraceae-unclassified	-	0.02	-	-	-	-	-	-	-	-	-	-	0.01	-
Deltaproteobacteria-unclassified	0.02	0.09	0.08	0.02	-	-	-	-	0.03	-	0.05	0.01	0.07	0.05
Deltaproteobacteria-Syntrophobacteriales-Syntrophaceae-unclassified	-	-	-	-	-	-	-	-	-	-	-	-	0.01	0.01
Deltaproteobacteria-Syntrophobacteriales-Syntrophaceae- <i>Desulfomonile</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.01	-
Deltaproteobacteria-Bdellovibrionales-Bacteriovoraceae- <i>Peredibacter</i>	-	-	-	-	-	-	0.01	-	-	-	-	-	-	-
Deltaproteobacteria-Desulfuromonadales-Desulfuromonadaceae-unclassified	-	-	-	-	-	-	-	-	-	-	-	-	0.01	-
Deltaproteobacteria-Desulfuromonadales-Geobacteraceae- <i>Geobacter</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01
Deltaproteobacteria-Desulfobacteriales-Desulfobulbaceae-unclassified	-	-	-	-	-	-	-	0.01	-	-	-	-	-	0.01
Deltaproteobacteria-Myxococcales-unclassified	-	0.02	0.09	0.09	0.02	0.11	-	-	0.01	-	0.01	0.03	0.01	0.01
Deltaproteobacteria-Myxococcales-Cystobacterineae-Cystobacteraceae-unclassified	-	-	0.01	-	-	-	-	-	-	-	-	-	-	-
Deltaproteobacteria-Myxococcales-Sorangineae-unclassified	-	-	-	-	-	-	0.01	-	-	-	-	-	-	0.01
Deltaproteobacteria-Myxococcales-Sorangineae-Polyangiaceae-unclassified	-	-	-	-	-	-	-	-	0.03	0.02	0.01	-	-	-
Deltaproteobacteria-Myxococcales-Sorangineae-Polyangiaceae- <i>Byssovorax</i>	-	-	-	-	-	-	-	-	0.02	-	-	-	-	0.02
Betaproteobacteria-unclassified	4.36	2.82	2.14	1.95	1.56	2.19	4.56	2.21	1.98	2.04	2.47	1.87	1.00	0.72
Betaproteobacteria-Nitrosomonadales-Nitrosomonadaceae-unclassified	0.09	0.46	0.19	0.20	0.30	0.04	0.10	0.12	-	0.01	0.05	0.04	-	-
Betaproteobacteria-Nitrosomonadales-Nitrosomonadaceae- <i>Nitrosomonas</i>	0.02	0.20	0.04	0.06	0.12	0.04	0.02	0.04	-	0.03	-	0.01	-	-
Betaproteobacteria-Nitrosomonadales-Nitrosomonadaceae- <i>Nitrospira</i>	0.16	-	-	-	0.03	0.02	0.06	0.01	-	-	-	-	-	-
Betaproteobacteria-Burkholderiales-unclassified	0.84	0.54	0.49	0.47	0.22	0.61	0.87	0.87	0.68	0.59	0.62	0.48	0.41	0.70
Betaproteobacteria-Burkholderiales-Burkholderiales_incertae_sedis-unclassified	0.13	0.17	0.17	0.13	0.03	0.11	0.12	0.07	0.03	0.02	0.04	0.04	1.10	1.23
Betaproteobacteria-Burkholderiales-Burkholderiales_incertae_sedis- <i>Methylibium</i>	0.31	0.19	0.40	0.60	0.03	0.26	0.18	0.06	0.07	0.06	0.01	0.02	0.02	0.03
Betaproteobacteria-Burkholderiales-Burkholderiales_incertae_sedis- <i>Aquabacterium</i>	-	-	-	-	-	-	0.01	0.01	-	-	-	-	0.01	0.07
Betaproteobacteria-Burkholderiales-Burkholderiales_incertae_sedis- <i>Xylophilus</i>	-	-	0.03	-	-	-	-	-	-	-	-	-	-	-
Betaproteobacteria-Burkholderiales-Burkholderiaceae-unclassified	0.04	0.02	0.01	0.04	-	-	0.03	-	0.02	-	0.02	0.01	0.16	0.01
Betaproteobacteria-Burkholderiales-Burkholderiaceae- <i>Cupriavidus</i>	0.13	0.05	0.04	0.11	0.13	0.04	0.15	0.07	0.01	-	0.01	-	1.35	1.14
Betaproteobacteria-Burkholderiales-Burkholderiaceae- <i>Wautersia</i>	-	-	-	-	-	-	-	-	-	0.03	-	-	-	-
Betaproteobacteria-Burkholderiales-Burkholderiaceae- <i>Ralstonia</i>	-	-	-	-	-	0.02	-	0.04	-	0.05	0.02	-	0.29	0.18
Betaproteobacteria-Burkholderiales-Burkholderiaceae- <i>Burkholderia</i>	0.04	-	-	0.02	-	-	0.03	-	0.03	0.01	0.01	-	0.55	0.36
Betaproteobacteria-Burkholderiales-Alcaligenaceae-unclassified	0.02	-	-	0.02	-	-	0.01	-	-	-	-	0.01	0.02	0.01
Betaproteobacteria-Burkholderiales-Alcaligenaceae- <i>Pigmentiphaga</i>	0.02	0.03	0.04	0.02	-	0.02	0.06	-	-	-	-	-	0.07	0.08
Betaproteobacteria-Burkholderiales-Alcaligenaceae- <i>Achromobacter</i>	0.04	0.05	-	-	-	-	0.07	0.01	0.01	-	-	-	0.15	0.12
Betaproteobacteria-Burkholderiales-Oxalobacteraceae-unclassified	0.24	0.13	0.24	0.13	0.08	0.17	0.21	0.02	0.03	0.04	0.01	-	0.33	0.30
Betaproteobacteria-Burkholderiales-Oxalobacteraceae- <i>Hermiimonas</i>	0.89	0.08	0.09	0.02	-	0.04	0.80	0.14	0.03	0.07	0.02	0.02	2.94	1.90
Betaproteobacteria-Burkholderiales-Oxalobacteraceae- <i>Massilia</i>	-	0.06	-	-	-	-	-	-	-	-	-	-	0.02	-
Betaproteobacteria-Burkholderiales-Oxalobacteraceae- <i>Janthinobacterium</i>	-	-	-	-	-	-	0.01	-	-	-	-	-	-	-
Betaproteobacteria-Burkholderiales-Oxalobacteraceae- <i>Naxibacter</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.01	-
Betaproteobacteria-Burkholderiales-Oxalobacteraceae- <i>Herbaspirillum</i>	0.04	0.02	0.03	0.02	-	-	0.01	0.02	-	-	-	-	0.21	0.11
Betaproteobacteria-Burkholderiales-Comamonadaceae-unclassified	1.66	2.44	3.05	2.49	1.50	1.99	2.73	2.48	2.48	2.89	2.45	2.38	0.92	1.51
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Simplicispira</i>	-	0.03	-	-	-	0.02	-	-	-	0.01	-	-	-	-
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Ranlibacter</i>	0.07	0.02	0.01	0.02	-	0.02	0.02	-	0.02	0.01	0.02	-	-	-
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Comamonas</i>	0.20	0.20	0.20	0.09	0.17	0.22	0.15	0.35	0.40	0.26	0.13	0.15	8.31	9.46
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Caenimonas</i>	-	0.02	-	-	-	-	0.02	-	0.01	0.03	0.01	-	-	-
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Delftia</i>	0.02	-	-	-	-	-	-	-	-	-	-	-	-	0.03
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Pseudorhodoferax</i>	0.22	-	-	-	-	-	0.11	-	-	-	-	-	-	-
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Curvibacter</i>	-	-	-	-	-	-	-	-	-	-	0.01	-	-	0.01
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Diaphorobacter</i>	0.09	0.02	0.03	0.04	-	0.02	0.05	0.05	0.01	0.04	0.05	0.03	1.02	1.37
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Ottovia</i>	-	-	-	-	-	-	-	-	-	-	0.01	-	-	-
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Acidovorax</i>	5.56	12.30	19.85	15.93	3.51	24.97	5.38	17.35	22.08	19.18	16.48	14.36	10.39	9.55
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Rhodoferax</i>	0.02	-	0.01	0.02	0.02	-	0.03	-	-	-	-	-	-	-
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Hydrogenophaga</i>	-	-	0.03	-	-	-	-	-	-	-	-	-	0.04	0.04
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Variovorax</i>	0.42	0.20	0.13	0.15	0.02	0.11	0.20	0.07	0.09	0.05	0.01	-	0.37	0.94
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Polaromonas</i>	0.20	0.02	0.08	-	0.08	-	0.32	0.26	0.11	0.20	0.10	0.05	-	-
Betaproteobacteria-Burkholderiales-Comamonadaceae- <i>Alicyclophilus</i>	-	-	-	0.02	-	-	0.01	-	0.01	-	-	0.01	0.01	0.02

Phylogenetic group	Mo(0)	Mo(28)	Mo(56)	Mo(84)	Mo(112)	Mo(140)	Wk(0)	Wk(28)	Wk(56)	Wk(84)	Wk(112)	Wk(140)	Fd(0)	Fd(140)
Betaproteobacteria-Hydrogenophilales-Hydrogenophilaceae- <i>Thiobacillus</i>	4.92	4.83	7.03	6.73	3.79	6.99	4.52	7.19	6.72	6.25	6.71	4.94	0.15	0.19
Betaproteobacteria-Methylphilales-Methylphilaceae-unclassified	0.02	0.02	-	-	-	-	-	-	-	-	-	-	-	-
Betaproteobacteria-Methylphilales-Methylphilaceae- <i>Methylorvorous</i>	-	-	-	-	-	-	-	0.03	-	-	-	-	0.23	0.11
Betaproteobacteria-Neisseriales-Neisseriaceae-unclassified	-	-	0.01	0.04	0.02	-	0.01	0.02	0.03	0.03	0.05	-	-	-
Betaproteobacteria-Neisseriales-Neisseriaceae- <i>Pseudogulbenkiana</i>	-	-	-	-	-	-	-	0.01	-	0.02	-	-	0.01	-
Betaproteobacteria-Neisseriales-Neisseriaceae- <i>Vogesella</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.03	-
Betaproteobacteria-Rhodocyclales-Rhodocyclaceae-unclassified	-	0.02	-	-	-	-	0.03	-	-	-	-	-	-	-
Betaproteobacteria-Rhodocyclales-Rhodocyclaceae- <i>Shinella</i>	-	-	-	-	-	-	0.01	0.01	0.01	-	-	-	-	-
Betaproteobacteria-Rhodocyclales-Rhodocyclaceae- <i>Thaueria</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.01	-
Betaproteobacteria-Rhodocyclales-Rhodocyclaceae- <i>Propionivibrio</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01
Betaproteobacteria-Rhodocyclales-Rhodocyclaceae- <i>Denitratisoma</i>	-	-	-	0.02	-	-	-	-	0.01	-	-	-	-	-
Betaproteobacteria-Rhodocyclales-Rhodocyclaceae- <i>Azocarus</i>	0.02	-	-	0.04	-	0.09	-	-	-	-	-	-	0.06	0.19
Betaproteobacteria-Rhodocyclales-Rhodocyclaceae- <i>Azospira</i>	-	0.02	-	-	-	-	-	-	-	-	-	-	0.03	0.03
Alphaproteobacteria-unclassified	5.87	2.96	3.71	4.06	3.38	3.96	6.64	4.56	3.90	3.76	3.40	4.12	0.31	0.42
Alphaproteobacteria-Rhizobiales-unclassified	4.03	3.01	2.45	2.73	1.15	2.62	4.30	2.76	2.52	2.37	2.10	2.58	0.30	0.39
Alphaproteobacteria-Rhizobiales-Bradyrhizobiaceae-unclassified	5.69	2.09	1.54	1.21	0.52	0.76	4.75	1.25	0.43	0.46	0.41	0.52	1.64	2.12
Alphaproteobacteria-Rhizobiales-Bradyrhizobiaceae- <i>Balneimonas</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01
Alphaproteobacteria-Rhizobiales-Bradyrhizobiaceae- <i>Rhodopseudomonas</i>	-	-	-	0.06	-	-	0.01	-	-	-	-	-	-	-
Alphaproteobacteria-Rhizobiales-Bradyrhizobiaceae- <i>Bradyrhizobium</i>	0.33	0.20	0.28	0.41	0.15	0.37	0.30	0.32	0.16	0.11	0.10	0.05	-	0.02
Alphaproteobacteria-Rhizobiales-Bradyrhizobiaceae- <i>Afipia</i>	-	-	-	-	-	-	0.02	0.01	-	-	-	-	-	-
Alphaproteobacteria-Rhizobiales-Bradyrhizobiaceae- <i>Nitrobacter</i>	0.20	0.22	0.09	0.13	0.07	0.06	0.13	0.09	0.04	0.04	0.03	0.08	-	-
Alphaproteobacteria-Rhizobiales-Bradyrhizobiaceae- <i>Bosea</i>	0.07	0.11	0.08	0.15	0.07	0.02	0.06	0.12	0.12	0.09	0.08	0.09	0.01	0.03
Alphaproteobacteria-Rhizobiales-Bradyrhizobiaceae- <i>Agromonas</i>	0.02	-	-	-	-	0.02	0.01	0.02	0.01	-	-	0.01	0.01	-
Alphaproteobacteria-Rhizobiales-Rhizobiaceae-unclassified	0.04	0.02	-	-	-	-	-	0.02	-	0.01	-	0.02	-	-
Alphaproteobacteria-Rhizobiales-Rhizobiaceae- <i>Kaistia</i>	0.33	0.22	0.05	0.07	0.05	0.06	0.26	0.02	0.02	-	-	-	-	0.12
Alphaproteobacteria-Rhizobiales-Rhizobiaceae- <i>Rhizobium</i>	0.35	0.11	0.25	0.32	0.05	0.32	0.15	0.17	0.11	0.08	0.11	0.32	0.09	0.10
Alphaproteobacteria-Rhizobiales-Methylocystaceae-unclassified	-	-	0.03	-	-	-	0.01	-	-	-	0.01	-	0.07	0.17
Alphaproteobacteria-Rhizobiales-Methylocystaceae- <i>Methylocystis</i>	-	-	-	-	0.02	0.02	-	-	-	-	-	-	-	-
Alphaproteobacteria-Rhizobiales-Methylocystaceae- <i>Pleomorhomonas</i>	-	-	-	-	-	-	-	-	-	-	-	0.01	-	-
Alphaproteobacteria-Rhizobiales-Methylocystaceae- <i>Methylophila</i>	-	-	-	-	-	-	0.02	-	-	-	-	-	0.02	0.18
Alphaproteobacteria-Rhizobiales-Phyllobacteriaceae-unclassified	0.02	-	0.04	0.17	0.15	0.13	0.01	0.07	0.03	0.01	0.01	0.01	-	0.02
Alphaproteobacteria-Rhizobiales-Phyllobacteriaceae- <i>Mesorhizobium</i>	0.18	0.25	0.25	0.32	0.27	0.24	0.11	0.30	0.25	0.28	0.12	0.15	-	0.19
Alphaproteobacteria-Rhizobiales-Rhodobiaceae-unclassified	-	0.02	0.04	-	-	0.02	0.01	0.01	-	0.01	-	-	-	-
Alphaproteobacteria-Rhizobiales-Rhodobiaceae- <i>Parvibaculum</i>	1.95	3.29	4.01	1.19	1.03	1.54	2.64	0.42	0.07	0.04	-	0.02	-	0.03
Alphaproteobacteria-Rhizobiales-Brucellaceae- <i>Mycoplana</i>	0.02	0.02	-	0.02	-	-	0.03	0.06	0.03	0.04	-	0.04	-	-
Alphaproteobacteria-Rhizobiales-Xanthobacteraceae-unclassified	-	0.02	-	-	-	-	-	-	-	-	-	-	-	-
Alphaproteobacteria-Rhizobiales-Xanthobacteraceae- <i>Ancylobacter</i>	-	0.02	-	-	-	-	0.07	-	-	-	-	-	-	0.01
Alphaproteobacteria-Rhizobiales-Xanthobacteraceae- <i>Xanthobacter</i>	-	-	-	-	-	-	-	0.02	-	-	-	-	-	-
Alphaproteobacteria-Rhizobiales-Xanthobacteraceae- <i>Pseudolabrys</i>	0.07	0.02	0.04	0.02	-	-	0.07	0.01	-	-	-	-	-	-
Alphaproteobacteria-Rhizobiales-Xanthobacteraceae- <i>Starkeya</i>	0.02	-	-	-	-	-	0.01	-	-	-	-	-	0.01	0.01
Alphaproteobacteria-Rhizobiales-Hyphomicrobiaceae-unclassified	0.60	0.33	0.20	0.37	0.17	0.28	0.48	0.50	0.25	0.36	0.31	0.55	-	0.02
Alphaproteobacteria-Rhizobiales-Hyphomicrobiaceae- <i>Angulomicrobium</i>	-	-	-	-	0.03	-	-	-	-	-	-	-	-	-
Alphaproteobacteria-Rhizobiales-Hyphomicrobiaceae- <i>Prosthecomicrobium</i>	-	-	-	0.02	-	-	-	-	-	-	-	-	0.01	-
Alphaproteobacteria-Rhizobiales-Hyphomicrobiaceae- <i>Devosia</i>	0.66	0.13	-	0.07	-	-	0.62	0.16	0.05	0.03	0.04	0.05	-	-
Alphaproteobacteria-Rhizobiales-Hyphomicrobiaceae- <i>Blastochloris</i>	0.02	-	-	-	-	-	-	0.02	0.01	0.03	0.01	0.02	-	-
Alphaproteobacteria-Rhizobiales-Hyphomicrobiaceae- <i>Pedomicrobium</i>	-	-	-	-	-	-	-	-	0.01	-	-	-	-	-
Alphaproteobacteria-Rhizobiales-Hyphomicrobiaceae- <i>Hyphomicrobium</i>	0.11	0.08	0.08	0.07	-	0.04	0.19	0.08	0.11	0.17	0.03	0.11	0.01	0.01
Alphaproteobacteria-Rhizobiales-Hyphomicrobiaceae- <i>Rhodoplanes</i>	0.07	0.03	0.01	0.04	0.08	0.13	0.10	0.14	0.06	0.08	0.04	0.06	-	0.01
Alphaproteobacteria-Rhizobiales-Methylbacteriaceae- <i>Methylbacterium</i>	-	-	-	-	-	-	0.01	-	-	-	-	0.01	-	-
Alphaproteobacteria-Caulobacterales-unclassified	-	-	-	-	-	-	0.03	0.02	0.01	-	-	-	0.01	-
Alphaproteobacteria-Caulobacterales-Caulobacteraceae-unclassified	0.20	0.25	0.20	0.15	0.02	0.06	0.20	0.37	0.41	0.49	0.28	0.46	-	0.01
Alphaproteobacteria-Caulobacterales-Caulobacteraceae- <i>Caulobacter</i>	0.84	0.60	0.82	0.24	0.18	0.32	1.84	0.36	0.10	0.05	0.02	0.01	0.01	-

Phylogenetic group	Mo(0)	Mo(28)	Mo(56)	Mo(84)	Mo(112)	Mo(140)	Wk(0)	Wk(28)	Wk(56)	Wk(84)	Wk(112)	Wk(140)	Fd(0)	Fd(140)
Alphaproteobacteria-Caulobacterales-Caulobacteraceae- <i>Brevundimonas</i>	3.52	0.60	1.76	1.10	0.40	0.43	4.02	7.02	10.90	12.08	5.39	7.56	-	0.01
Alphaproteobacteria-Caulobacterales-Caulobacteraceae- <i>Phenylobacterium</i>	1.82	1.12	0.61	0.58	0.33	1.04	2.83	2.44	1.69	1.63	1.31	1.46	0.05	0.05
Alphaproteobacteria-Rhodospirillales-unclassified	-	-	-	-	-	-	-	-	-	-	-	-	0.01	0.01
Alphaproteobacteria-Rhodospirillales-Rhodospirillaceae-unclassified	-	-	-	-	-	-	-	-	-	-	-	-	0.01	-
Alphaproteobacteria-Rhodospirillales-Rhodospirillaceae- <i>Skermanella</i>	0.11	-	0.01	-	-	-	0.04	0.01	0.01	-	-	-	0.20	0.08
Alphaproteobacteria-Rhodospirillales-Acetobacteraceae-unclassified	0.04	0.03	0.04	-	0.02	0.02	0.04	0.02	-	-	-	-	-	0.03
Alphaproteobacteria-Rhodospirillales-Acetobacteraceae- <i>Belnapia</i>	0.18	-	-	0.02	-	0.02	0.07	-	-	0.01	-	-	0.05	0.04
Alphaproteobacteria-Rhodospirillales-Acetobacteraceae- <i>Roseomonas</i>	0.24	0.03	0.01	0.02	-	-	0.06	0.02	0.02	0.01	0.01	0.01	0.23	0.38
Alphaproteobacteria-Sphingomonadales-unclassified	0.38	0.41	0.45	0.63	0.18	0.93	0.55	0.39	0.42	0.60	0.53	0.53	1.61	4.05
Alphaproteobacteria-Sphingomonadales-Sphingomonadaceae-unclassified	3.28	3.26	4.50	5.97	1.76	5.19	3.53	3.36	3.11	3.19	3.64	4.43	6.36	4.91
Alphaproteobacteria-Sphingomonadales-Sphingomonadaceae- <i>Sphingomonas</i>	0.60	1.07	3.35	5.38	2.53	4.28	1.12	1.40	1.67	1.33	2.10	2.56	0.24	0.30
Alphaproteobacteria-Sphingomonadales-Sphingomonadaceae- <i>Sphingopyxis</i>	0.04	-	0.03	0.04	0.05	0.13	0.01	0.01	0.02	-	-	0.01	-	-
Alphaproteobacteria-Sphingomonadales-Sphingomonadaceae- <i>Novosphingobium</i>	0.38	0.22	0.50	0.86	0.07	0.26	0.29	0.26	0.27	0.46	0.86	0.46	0.65	0.50
Alphaproteobacteria-Sphingomonadales-Sphingomonadaceae- <i>Sphingosinicella</i>	3.61	1.75	0.61	0.28	0.03	0.15	4.86	5.14	3.11	3.14	1.64	1.19	-	0.01
Alphaproteobacteria-Sphingomonadales-Sphingomonadaceae- <i>Sphingobium</i>	1.71	1.61	1.56	2.51	0.60	1.73	1.97	1.30	0.38	0.29	0.22	0.27	7.63	6.27
Alphaproteobacteria-Sphingomonadales-Erythrobacteraceae-unclassified	0.24	0.35	0.25	0.33	0.17	0.76	0.80	0.37	0.20	0.17	0.15	0.21	2.62	6.25
Alphaproteobacteria-Sphingomonadales-Erythrobacteraceae- <i>Porphyrobacter</i>	0.04	0.02	0.05	0.02	0.03	0.04	0.11	0.02	0.04	0.03	0.01	0.04	0.02	0.07
Alphaproteobacteria-Sphingomonadales-Erythrobacteraceae- <i>Altererythrobacter</i>	-	-	-	-	-	-	0.01	-	-	-	-	-	-	-
Alphaproteobacteria-Sphingomonadales-Erythrobacteraceae- <i>Erythrobacter</i>	-	-	-	-	-	-	0.01	-	-	-	-	-	-	-
Alphaproteobacteria-Rhodobacteriales-Rhodobacteraceae-unclassified	0.33	0.27	0.36	0.22	0.07	0.26	0.27	0.22	0.13	0.06	0.10	0.04	0.07	0.19
Alphaproteobacteria-Rhodobacteriales-Rhodobacteraceae- <i>Rhodobacter</i>	-	-	0.04	0.02	-	-	0.01	-	-	-	-	-	0.02	-
Alphaproteobacteria-Rhodobacteriales-Rhodobacteraceae- <i>Haematobacter</i>	-	-	-	-	-	-	-	0.01	-	-	-	-	0.03	0.02
Alphaproteobacteria-Rhodobacteriales-Rhodobacteraceae- <i>Rubellimicrobium</i>	-	-	-	-	-	-	-	-	-	-	-	0.02	-	0.01
Gammaproteobacteria-unclassified	6.82	15.26	8.12	6.14	34.13	7.73	6.15	12.62	11.05	8.86	9.12	8.55	0.42	0.46
Gammaproteobacteria-Gammaproteobacteria_incertae_sedis- <i>Solimonas</i>	-	-	-	-	-	0.02	0.01	-	-	0.02	-	-	-	-
Gammaproteobacteria-Pseudomonadales-unclassified	0.07	0.08	0.11	-	0.02	0.02	0.05	0.06	0.09	0.02	0.07	0.04	-	0.01
Gammaproteobacteria-Pseudomonadales-Moraxellaceae- <i>Acintebacter</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01
Gammaproteobacteria-Pseudomonadales-Pseudomonadaceae-unclassified	0.04	0.02	0.01	-	-	-	-	0.09	0.01	0.01	0.02	0.02	0.15	0.20
Gammaproteobacteria-Pseudomonadales-Pseudomonadaceae- <i>Cellvibrio</i>	-	-	-	-	-	-	0.01	0.02	0.02	-	-	0.01	-	-
Gammaproteobacteria-Pseudomonadales-Pseudomonadaceae- <i>Pseudomonas</i>	0.18	0.08	0.09	0.06	0.13	0.22	0.07	0.46	0.28	0.08	0.06	0.04	5.51	5.89
Gammaproteobacteria-Pseudomonadales-Pseudomonadaceae- <i>Azotobacter</i>	-	-	-	-	-	-	-	0.01	-	0.02	-	-	-	-
Gammaproteobacteria-Chromatiales-unclassified	0.07	-	-	-	0.05	-	0.03	-	-	-	0.01	-	-	-
Gammaproteobacteria-Ectothiorhodospiraceae-unclassified	-	-	-	-	0.02	0.04	0.01	0.01	-	-	-	0.02	-	-
Gammaproteobacteria-Legionellales-Legionellaceae- <i>Legionella</i>	-	-	-	-	-	-	0.02	-	-	-	-	-	-	0.01
Gammaproteobacteria-Legionellales-Coxiellaceae- <i>Aquicella</i>	-	-	-	-	-	-	0.03	-	-	-	-	0.02	-	-
Gammaproteobacteria-Enterobacteriales-Enterobacteriaceae-unclassified	-	-	-	-	-	-	-	-	-	-	-	-	0.01	0.02
Gammaproteobacteria-Enterobacteriales-Enterobacteriaceae- <i>Enterobacter</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.02	0.03
Gammaproteobacteria-Xanthomonadales-unclassified	-	0.05	-	-	-	-	-	-	0.01	0.01	0.01	-	0.01	0.01
Gammaproteobacteria-Xanthomonadales-Sinobacteraceae-unclassified	0.02	-	0.01	-	-	-	-	0.01	0.03	-	-	-	0.17	0.18
Gammaproteobacteria-Xanthomonadales-Sinobacteraceae- <i>Alkanibacter</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.03	-
Gammaproteobacteria-Xanthomonadales-Sinobacteraceae- <i>Steroidobacter</i>	0.24	0.16	-	0.02	0.03	-	0.32	0.09	0.03	0.06	0.02	-	0.01	-
Gammaproteobacteria-Xanthomonadales-Sinobacteraceae- <i>Nevskia</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.01	-
Gammaproteobacteria-Xanthomonadales-Xanthomonadaceae-unclassified	0.27	0.14	0.75	1.62	2.68	0.32	0.28	0.27	0.19	0.44	0.09	0.23	2.82	2.37
Gammaproteobacteria-Xanthomonadales-Xanthomonadaceae- <i>Luteimonas</i>	0.24	0.60	0.70	2.75	3.28	0.19	0.44	0.15	0.05	0.18	0.08	0.05	-	-
Gammaproteobacteria-Xanthomonadales-Xanthomonadaceae- <i>Rhodanobacter</i>	0.02	-	-	-	-	-	0.01	-	-	-	-	0.10	-	-
Gammaproteobacteria-Xanthomonadales-Xanthomonadaceae- <i>Lysobacter</i>	-	-	-	-	-	-	-	-	-	-	0.02	0.02	-	-
Gammaproteobacteria-Xanthomonadales-Xanthomonadaceae- <i>Thermomonas</i>	-	-	0.01	-	-	-	-	-	0.03	0.05	0.06	0.16	-	-
Gammaproteobacteria-Xanthomonadales-Xanthomonadaceae- <i>Stenotrophomonas</i>	-	-	0.03	-	-	-	-	-	-	-	-	-	-	-
Gammaproteobacteria-Xanthomonadales-Xanthomonadaceae- <i>Pseudoxanthomonas</i>	1.20	0.38	0.50	0.35	0.17	0.71	1.31	0.81	0.62	0.71	0.31	0.42	33.53	28.30
Gammaproteobacteria-Methylococcales-Methylococcaceae- <i>Methylococcus</i>	0.04	-	-	-	-	-	-	0.01	-	-	-	-	-	-
Nitrospira-Nitrospira-Nitrospirales-Nitrospiraceae- <i>Nitrospira</i>	-	-	-	-	-	0.02	-	-	-	0.08	0.07	0.05	0.01	-
Gemmatimonadetes-Gemmatimonadetes-Gemmatimonadales-Gemmatimonadaceae- <i>Gemmatimonas</i>	0.07	-	-	-	-	-	0.32	0.35	0.40	0.39	0.37	0.12	-	-

Phylogenetic group	Mo(0)	Mo(28)	Mo(56)	Mo(84)	Mo(112)	Mo(140)	Wk(0)	Wk(28)	Wk(56)	Wk(84)	Wk(112)	Wk(140)	Fd(0)	Fd(140)
Acidobacteria-														
Acidobacteria-unclassified	-	0.02	-	-	-	0.02	0.06	0.16	0.25	0.25	0.21	0.25	-	0.01
Acidobacteria-Group 4	0.18	0.57	3.28	6.92	0.35	0.48	0.12	1.40	8.18	13.01	23.04	25.44	0.01	0.06
Acidobacteria-Group 3	0.58	0.46	0.49	0.19	0.23	0.43	0.46	0.74	0.67	0.46	0.49	0.57	0.01	0.01
Acidobacteria-Group 2	-	-	-	-	-	-	-	-	-	-	-	-	0.01	0.01
Acidobacteria-Group 1	-	-	-	0.04	0.02	0.02	0.04	0.02	0.04	0.01	0.07	0.03	0.31	0.06
Acidobacteria-Group 7	-	-	-	-	-	-	-	-	0.01	0.03	0.09	0.16	-	-
Acidobacteria-Group 6	0.27	0.14	0.11	0.07	-	0.09	0.23	0.51	0.53	0.50	0.44	0.41	0.02	0.02
Acidobacteria-Group 15	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01
Acidobacteria-Group 16	0.02	0.03	0.01	-	-	0.04	0.02	0.02	0.01	0.03	-	-	0.02	-
Deinococcus-Thermus-Deinococci-Deinococcales-Deinococcaceae- <i>Deinococcus</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01
Verrucomicrobia-														
Opiritae-Opiritales-Opiritaceae- <i>Opiritus</i>	-	0.03	0.09	0.13	0.03	0.06	-	-	0.01	-	0.01	-	-	-
Verrucomicrobiae-Verrucomicrobiales-Verrucomicrobiaceae- <i>Luteobacter</i>	-	0.11	0.01	-	-	-	-	-	0.01	-	-	-	-	-
Verrucomicrobiae-Verrucomicrobiales-Verrucomicrobiaceae- <i>Verrucomicrobium</i>	0.02	-	-	-	-	-	-	-	0.03	-	0.01	-	-	-
Subdivision 3-Subdivision 3_genera_incertae_sedis	-	-	-	-	-	-	-	-	0.02	-	-	-	-	-
Plantomycetes-														
Planctomycetacia-Planctomycetacia-Planctomycetales-Planctomycetaceae-unclassified	-	-	-	-	-	-	-	0.02	-	0.01	0.01	-	-	-
Planctomycetacia-Planctomycetacia-Planctomycetales-Planctomycetaceae- <i>Singulisphaera</i>	-	-	-	-	-	-	0.04	-	-	-	-	-	-	-
Chloroflexia-Thermomicrobia-unclassified	-	-	-	-	-	-	-	-	-	-	-	-	0.01	-
Bacteria_incertae_sedis-Ktedonobacteria-Ktedonobacteria-Ktedonobacteraceae- <i>Ktedonobacter</i>	-	-	0.01	-	-	-	-	-	-	-	-	-	0.03	-

^a Abbreviations as defined in Table 1.

^b As user-defined phylogenetic groups (e.g., Pyrene Group 2, Anthracene Group 1) are not recognized by RDP-II, they do not appear in this table.