



OTU 1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter radioresistens DSM 6976 = NBRC 102413 = CIP 103788
OTU 2	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flaviramulus; s__marine bacterium J20-17
OTU 3	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Robiginitomaculum; s__uncultured alpha proteobacterium
OTU 4	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionIII; f__FamilyI; g__Phormidium; s__uncultured bacterium
OTU 5	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__uncultured; s__uncultured bacterium
OTU 6	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus; s__uncultured bacterium AD12-E7
OTU 7	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Aquibacter; s__uncultured bacterium
OTU 8	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Mesoflavibacter; s__Mesoflavibacter sp. NBRC 110217
OTU 9	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Loktanela; s__uncultured alpha proteobacterium
OTU 10	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Erythrobacteraceae; g__Erythrobacter; s__uncultured bacterium
OTU 11	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae; g__Pseudahrensia; s__uncultured marine bacterium
OTU 12	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Ruegeria; s__uncultured Ruegeria sp.
OTU 13	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Alphaproteobacteria Incertae Sedis; f__Unknown Family; g__uncultured; s__uncultured bacterium
OTU 14	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Phyllobacteriaceae; g__Hoeflea; s__uncultured bacterium
OTU 15	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Aestuariicella; s__Proteobacteria
OTU 16	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__uncultured; s__uncultured bacterium
OTU 17	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__OM1 clade; g__Candidatus Actinomarina; s__uncultured bacterium
OTU 18	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__SAR11 clade; f__Surface 1; g__uncultured bacterium
OTU 19	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Pseudofulvibacter;

	s__Pseudovulvibacter geojedonensis
OTU 20	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Arenicellales; f__Arenicellaceae; g__Arenicella; s__uncultured proteobacterium
OTU 21	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus; s__Oleiphilus sp. HI0081
OTU 22	k__Bacteria; p__Cyanobacteria; c__Cyanobacteria; o__SubsectionI; f__FamilyI; g__Synechococcus; s__uncultured bacterium
OTU 23	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__uncultured cyanobacterium
OTU 24	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Rhodobiaceae; g__uncultured; s__uncultured bacterium
OTU 25	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Simiduia; s__uncultured bacterium
OTU 26	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__uncultured; s__uncultured bacterium
OTU 27	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum; s__Tenacibaculum aiptasiae
OTU 28	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__uncultured bacterium
OTU 29	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__Spongiispira; s__Spongiispira norvegica
OTU 30	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Leptobacterium; s__uncultured bacterium
OTU 31	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Myxococcales; f__Nannocystaceae; g__uncultured; s__uncultured proteobacterium
OTU 32	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Oleiphilaceae; g__Oleiphilus; s__uncultured Oleiphilus sp.
OTU 33	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__SS1-B-06-26; g__uncultured bacterium
OTU 34	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Alteromonadaceae; g__Alteromonas; s__uncultured bacterium
OTU 35	k__Bacteria; p__Cyanobacteria; c__Chloroplast; o__Virgulinema fragilis
OTU 36	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Pseudophaeobacter; s__Phaeobacter sp. 11ANDIMAR09
OTU 37	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter 4; s__uncultured bacterium
OTU 38	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphin