D_0_Archaea;D_1_Bathyarchaeota;D_2_uncultured archaeon;D_3_uncultured archaeon D_0_Archaea;D_1_Diapherotrites;D_2_Diapherotrites Incertae Sedis;D_3_Unknown Order D_0_Archaea;D_1_Euryarchaeota;D_2_Methanobacteria;D_3_Methanobacteriales D_0_Archaea;D_1_Euryarchaeota;D_2_Methanomicrobia;D_3_Methanocellales D_0_Archaea;D_1_Euryarchaeota;D_2_Methanomicrobia;D_3_Methanosarcinales D_0_Archaea;D_1_Euryarchaeota;D_2_Thermoplasmata;D_3_Thermoplasmatales D_0_Archaea;D_1_Miscellaneous Euryarchaeotic Group(MEG);D_2_uncultured archaeon;D_3_uncultured archaeon D_0_Archaea;D_1_Parvarchaeota;D_2_uncultured archaeon;D_3_uncultured archaeon D_0_Archaea;D_1_Thaumarchaeota;D_2_FHMa11 terrestrial group;Ambiguous_taxa D_0_Archaea;D_1_Thaumarchaeota;D_2_FHMa11 terrestrial group;D_3_uncultured archaeon D_0_Archaea;D_1_Thaumarchaeota;D_2_FHMa11 terrestrial group;D_3_uncultured crenarchaeote D_0_Archaea;D_1_Thaumarchaeota;D_2_Soil Crenarchaeotic Group(SCG);Ambiguous_taxa D_0_Archaea;D_1_Thaumarchaeota;D_2_Soil Crenarchaeotic Group(SCG);D_3_Unknown Order D_0_Archaea;D_1_Thaumarchaeota;D_2_Soil Crenarchaeotic Group(SCG);D_3_uncultured archaeon D_0_Archaea;D_1_Thaumarchaeota;D_2_Soil Crenarchaeotic Group(SCG);D_3_uncultured crenarchaeote D_0_Archaea;D_1_Thaumarchaeota;D_2_Soil Crenarchaeotic Group(SCG);Other D_0_Archaea;D_1_Thaumarchaeota;D_2_South African Gold Mine Gp 1(SAGMCG-1);D_3_uncultured archaeon D_0_Archaea;D_1_Woesearchaeota (DHVEG-6);D_2_uncultured archaeon;D_3_uncultured archaeon D_0_Archaea;D_1_Woesearchaeota (DHVEG-6);D_2_uncultured euryarchaeote;D_3_uncultured euryarchaeote D_0_Bacteria;D_1_Acidobacteria;D_2_AT-s3-28;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_AT-s3-28;D_3_unidentified D_0_Bacteria;D_1_Acidobacteria;D_2_Acidobacteria;D_3_Acidobacteriales D_0_Bacteria;D_1_Acidobacteria;D_2_Blastocatellia;D_3_Blastocatellales D_0_Bacteria;D_1_Acidobacteria;D_2_Holophagae;D_3_Holophagales D_0_Bacteria;D_1_Acidobacteria;D_2_Holophagae;D_3_Subgroup 10 D_0_Bacteria;D_1_Acidobacteria;D_2_Holophagae;D_3_Subgroup 7 D_0_Bacteria;D_1_Acidobacteria;D_2_Holophagae;D_3_TPD-58 D_0_Bacteria;D_1_Acidobacteria;D_2_Holophagae;Other D_0_Bacteria;D_1_Acidobacteria;D_2_Solibacteres;D_3_Solibacterales D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 11;Ambiguous_taxa D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 11;D_3_uncultured Acidobacteria bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 11;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 11;Other D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 12;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 13;Ambiguous_taxa D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 13;D_3_uncultured Holophaga sp. D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 13;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 13;Other D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 15;D_3_uncultured Acidobacteria bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 15;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 17;Ambiguous_taxa D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 17;D_3_uncultured Acidobacteria bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 17;D_3_uncultured Acidobacteriales bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 17;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 17;Other D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 18;Ambiguous_taxa D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 18;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 18;Other D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 19;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 2;Ambiguous_taxa D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 2;D_3_uncultured Acidobacteria bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 2;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 2;Other D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 20;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 21;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 22;Ambiguous_taxa D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 22;D_3_uncultured Acidobacteria bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 22;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 22;Other D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 25;D_3_uncultured Acidobacteria bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 25;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 25;Other D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 5;Ambiguous_taxa D 0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 5;D_3_uncultured Acidobacteria bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 5;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 5;Other D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 6;Ambiguous_taxa D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 6;D_3_Unknown Order D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 6;D_3_uncultured Acidobacteria bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 6;D_3_uncultured Acidobacteriales bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 6;D_3_uncultured Thermoanaerobaculum sp. D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 6;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 6;D_3_unidentified D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 6;Other D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 9;Ambiguous_taxa D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 9;D_3_uncultured bacterium D_0_Bacteria;D_1_Acidobacteria;D_2_uncultured Acidobacteria bacterium;D_3_uncultured Acidobacteria bacterium D_0_Bacteria;D_1_Acidobacteria;Other;Other D_0_Bacteria;D_1_Actinobacteria;D_2_Acidimicrobiia;D_3_Acidimicrobiales D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Actinomycetales D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Bifidobacteriales D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Catenulisporales D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Corynebacteriales D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Frankiales D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Glycomycetales D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Kineosporiales D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Micrococcales D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Micromonosporales D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_PeM15 D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Propionibacteriales D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Streptomycetales D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Streptosporangiales D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;Other D_0_Bacteria;D_1_Actinobacteria;D_2_KIST-JJY010;D_3_uncultured bacterium D_0_Bacteria;D_1_Actinobacteria;D_2_MB-A2-108;Ambiguous_taxa D_0_Bacteria;D_1_Actinobacteria;D_2_MB-A2-108;D_3_uncultured Catenulispora sp. D_0_Bacteria;D_1_Actinobacteria;D_2_MB-A2-108;D_3_uncultured Micromonospora sp. D_0_Bacteria;D_1_Actinobacteria;D_2_MB-A2-108;D_3_uncultured bacterium D_0_Bacteria;D_1_Actinobacteria;D_2_MB-A2-108;Other D_0_Bacteria;D_1_Actinobacteria;D_2_Nitriliruptoria;D_3_Euzebyales D_0_Bacteria;D_1_Actinobacteria;D_2_Rubrobacteria;D_3_Rubrobacterales D_0_Bacteria;D_1_Actinobacteria;D_2_TakashiAC-B11;D_3_uncultured bacterium D_0_Bacteria;D_1_Actinobacteria;D_2_TakashiAC-B11;Other D_0_Bacteria;D_1_Actinobacteria;D_2_Thermoleophilia;D_3_Gaiellales D_0_Bacteria;D_1_Actinobacteria;D_2_Thermoleophilia;D_3_Solirubrobacterales D_0_Bacteria;D_1_Actinobacteria;D_2_Thermoleophilia;Other D_0_Bacteria;D_1_Actinobacteria;Other;Other D_0_Bacteria;D_1_Aminicenantes;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Armatimonadetes;D_2_Armatimonadia;D_3_Armatimonadales D_0_Bacteria;D_1_Armatimonadetes;D_2_Fimbriimonadia;D_3_Fimbriimonadales D_0_Bacteria;D_1_Armatimonadetes;D_2_uncultured;Ambiguous_taxa D_0_Bacteria;D_1_Armatimonadetes;D_2_uncultured;D_3_uncultured bacterium D_0_Bacteria;D_1_Armatimonadetes;D_2_uncultured;Other D_0_Bacteria;D_1_BJ-169;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_BRC1;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_BRC1;D_2_uncultured organism;D_3_uncultured organism D_0_Bacteria;D_1_BRC1;Other;Other D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidetes BD2-2;Other D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidetes Incertae Sedis;D_3_Order II D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidetes VC2.1 Bac22;D_3_uncultured bacterium D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidetes vadinHA17;Ambiguous_taxa D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidetes vadinHA17;D_3_uncultured Bacteroidales bacterium D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidetes vadinHA17;D_3_uncultured bacterium D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidetes vadinHA17;Other D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales D_0_Bacteria;D_1_Bacteroidetes;D_2_Cytophagia;D_3_Cytophagales D_0_Bacteria;D_1_Bacteroidetes;D_2_Flavobacteriia;D_3_Flavobacteriales D_0_Bacteria;D_1_Bacteroidetes;D_2_SB-5;D_3_uncultured bacterium D_0_Bacteria;D_1_Bacteroidetes;D_2_SB-5;Other D_0_Bacteria;D_1_Bacteroidetes;D_2_SM1A07;D_3_uncultured bacterium D_0_Bacteria;D_1_Bacteroidetes;D_2_WCHB1-32;Ambiguous_taxa D_0_Bacteria;D_1_Bacteroidetes;D_2_WCHB1-32;D_3_uncultured bacterium D_0_Bacteria;D_1_Bacteroidetes;D_2_WCHB1-32;Other D_0_Bacteria;D_1_Bacteroidetes;Other;Other D_0_Bacteria;D_1_Candidatus Berkelbacteria;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Candidatus Berkelbacteria;D_2_uncultured soil bacterium;D_3_uncultured soil bacterium D_0_Bacteria;D_1_Candidatus Berkelbacteria;Other;Other D_0_Bacteria;D_1_Chlamydiae;D_2_Chlamydiae;D_3_Chlamydiales D_0_Bacteria;D_1_Chlamydiae;D_2_LD1-PA32;D_3_uncultured bacterium D_0_Bacteria;D_1_Chlorobi;D_2_Chlorobia;D_3_Chlorobiales D_0_Bacteria;D_1_Chloroflexi;D_2_1-20;Ambiguous_taxa D_0_Bacteria;D_1_Chloroflexi;D_2_Anaerolineae;D_3_Anaerolineales D_0_Bacteria;D_1_Chloroflexi;D_2_Ardenticatenia;D_3_Ardenticatenales D_0_Bacteria;D_1_Chloroflexi;D_2_Ardenticatenia;D_3_uncultured D_0_Bacteria;D_1_Chloroflexi;D_2_Caldilineae;D_3_Caldilineales D_0_Bacteria;D_1_Chloroflexi;D_2_Chloroflexia;D_3_Chloroflexales D_0_Bacteria;D_1_Chloroflexi;D_2_Chloroflexia;D_3_Herpetosiphonales D_0_Bacteria;D_1_Chloroflexi;D_2_Chloroflexia;D_3_Kallotenuales D_0_Bacteria;D_1_Chloroflexi;D_2_Elev-1554;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_Gitt-GS-136;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_Gitt-GS-136;Other D 0 Bacteria;D_1_Chloroflexi;D_2_JG30-KF-CM66;Ambiguous_taxa D_0_Bacteria;D_1_Chloroflexi;D_2_JG30-KF-CM66;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_JG30-KF-CM66;Other D_0_Bacteria;D_1_Chloroflexi;D_2_JG37-AG-4;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_KD4-96;Ambiguous_taxa D_0_Bacteria;D_1_Chloroflexi;D_2_KD4-96;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_KD4-96;Other D_0_Bacteria;D_1_Chloroflexi;D_2_Ktedonobacteria;D_3_B10-SB3A D_0_Bacteria;D_1_Chloroflexi;D_2_Ktedonobacteria;D_3_B12-WMSP1 D_0_Bacteria;D_1_Chloroflexi;D_2_Ktedonobacteria;D_3_C0119 D_0_Bacteria;D_1_Chloroflexi;D_2_Ktedonobacteria;D_3_JG30-KF-AS9 D_0_Bacteria;D_1_Chloroflexi;D_2_Ktedonobacteria;D_3_Ktedonobacterales D_0_Bacteria;D_1_Chloroflexi;D_2_MSB-5E12;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_NLS2-31;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_P2-11E;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_S085;Ambiguous_taxa D_0_Bacteria;D_1_Chloroflexi;D_2_S085;D_3_uncultured Chloroflexi bacterium D 0_Bacteria;D_1_Chloroflexi;D_2_S085;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_S085;Other D_0_Bacteria;D_1_Chloroflexi;D_2_SAR202 clade;Ambiguous_taxa D_0_Bacteria;D_1_Chloroflexi;D_2_SAR202 clade;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_SAR202 clade;D_3_uncultured eubacterium H1.2.f D_0_Bacteria;D_1_Chloroflexi;D_2_SBR2076;Ambiguous_taxa D_0_Bacteria;D_1_Chloroflexi;D_2_SBR2076;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_SBR2076;D_3_uncultured soil bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_SBR2076;Other D_0_Bacteria;D_1_Chloroflexi;D_2_SHA-26;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_SHA-26;Other D_0_Bacteria;D_1_Chloroflexi;D_2_SJA-15;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_SJA-15;Other D_0_Bacteria;D_1_Chloroflexi;D_2_TK10;Ambiguous_taxa D_0_Bacteria;D_1_Chloroflexi;D_2_TK10;D_3_uncultured Chloroflexi bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_TK10;D_3_uncultured bacterium D_0_Bacteria;D_1_Chloroflexi;D_2_TK10;Other D_0_Bacteria;D_1_Chloroflexi;D_2_Thermomicrobia;D_3_AKYG1722 D_0_Bacteria;D_1_Chloroflexi;D_2_Thermomicrobia;D_3_JG30-KF-CM45 D_0_Bacteria;D_1_Chloroflexi;D_2_Thermomicrobia;D_3_Sphaerobacterales D_0_Bacteria;D_1_Chloroflexi;D_2_uncultured Bellilinea sp.;D_3_uncultured Bellilinea sp. D_0_Bacteria;D_1_Chloroflexi;Other;Other D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;Ambiguous_taxa D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;D_3_Bryum argenteum var. argenteum D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;D_3_Camellia sinensis var. sinensis D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;D_3_Lolium perenne D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;D_3_Solanum melongena (eggplant) D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;D_3_uncultured bacterium D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;D_3_uncultured diatom D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;D_3_uncultured organism D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;Other D_0_Bacteria;D_1_Cyanobacteria;D_2_Cyanobacteria;D_3_SubsectionII D_0_Bacteria;D_1_Cyanobacteria;D_2_Cyanobacteria;D_3_SubsectionIII D_0_Bacteria;D_1_Cyanobacteria;D_2_Cyanobacteria;D_3_SubsectionIV D_0_Bacteria;D_1_Cyanobacteria;D_2_ML635J-21;Ambiguous_taxa D_0_Bacteria;D_1_Cyanobacteria;D_2_ML635J-21;D_3_Hyaloperonospora arabidopsidis D_0_Bacteria;D_1_Cyanobacteria;D_2_ML635J-21;D_3_uncultured bacterium D_0_Bacteria;D_1_Cyanobacteria;D_2_ML635J-21;D_3_uncultured cyanobacterium D_0_Bacteria;D_1_Cyanobacteria;D_2_ML635J-21;Other D_0_Bacteria;D_1_Cyanobacteria;D_2_Melainabacteria;D_3_Caenarcaniphilales D_0_Bacteria;D_1_Cyanobacteria;D_2_Melainabacteria;D_3_Obscuribacterales D_0_Bacteria;D_1_Cyanobacteria;D_2_Melainabacteria;D_3_Vampirovibrionales D_0_Bacteria;D_1_Deferribacteres;D_2_Deferribacteres Incertae Sedis;D_3_Unknown Order D_0_Bacteria;D_1_Deinococcus-Thermus;D_2_Deinococci;D_3_Deinococcales D_0_Bacteria;D_1_Deinococcus-Thermus;D_2_Deinococci;D_3_KD3-62 D_0_Bacteria;D_1_Elusimicrobia;D_2_Elusimicrobia;D_3_4-29 D 0 Bacteria:D 1 Flusimicrobia:D 2 Flusimicrobia:D 3 FCPU45 D_0_Bacteria;D_1_Elusimicrobia;D_2_Elusimicrobia;D_3_Lineage Ila D_0_Bacteria;D_1_Elusimicrobia;D_2_Elusimicrobia;D_3_Lineage IIb D_0_Bacteria;D_1_Elusimicrobia;D_2_Elusimicrobia;D_3_Lineage IIc D_0_Bacteria;D_1_Elusimicrobia;D_2_Elusimicrobia;D_3_Lineage IV D_0_Bacteria;D_1_Elusimicrobia;D_2_Elusimicrobia;D_3_MVP-88 D_0_Bacteria;D_1_FBP;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_FBP;D_2_uncultured soil bacterium;D_3_uncultured soil bacterium D_0_Bacteria;D_1_FBP;Other;Other D_0_Bacteria;D_1_FCPU426;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Fibrobacteres;D_2_Chitinivibrionia;D_3_uncultured D_0_Bacteria;D_1_Fibrobacteres;D_2_Fibrobacteria;D_3_Fibrobacterales D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_C178B D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_SHBZ1548 D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_TSCOR001-H18 D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_uncultured D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;Other D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridia Incertae Sedis D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_D8A-2 D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Halanaerobiales D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_M55-D21 D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_MBA03 D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Thermoanaerobacterales D_0_Bacteria;D_1_Firmicutes;D_2_Erysipelotrichia;D_3_Erysipelotrichales D_0_Bacteria;D_1_Firmicutes;D_2_Limnochordia;D_3_Limnochordales D_0_Bacteria;D_1_Firmicutes;D_2_Negativicutes;D_3_Selenomonadales D_0_Bacteria;D_1_Fusobacteria;D_2_Fusobacteriia;D_3_Fusobacteriales D_0_Bacteria;D_1_GAL15;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Gemmatimonadetes;D_2_AKAU4049;D_3_uncultured bacterium D_0_Bacteria;D_1_Gemmatimonadetes;D_2_BD2-11 terrestrial group;D_3_uncultured bacterium D_0_Bacteria;D_1_Gemmatimonadetes;D_2_BD2-11 terrestrial group;Other D_0_Bacteria;D_1_Gemmatimonadetes;D_2_Gemmatimonadetes;D_3_Gemmatimonadales D_0_Bacteria;D_1_Gemmatimonadetes;D_2_Longimicrobia;D_3_Longimicrobiales D 0 Bacteria; D 1 Gemmatimonadetes; D 2 S0134 terrestrial group; Ambiguous taxa D_0_Bacteria;D_1_Gemmatimonadetes;D_2_S0134 terrestrial group;D_3_uncultured bacterium D_0_Bacteria;D_1_Gemmatimonadetes;D_2_S0134 terrestrial group;D_3_uncultured soil bacterium D_0_Bacteria;D_1_Gemmatimonadetes;D_2_S0134 terrestrial group;Other D_0_Bacteria;D_1_Gracilibacteria;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Gracilibacteria;Other;Other D_0_Bacteria;D_1_Hydrogenedentes;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Hydrogenedentes;D_2_uncultured organism;D_3_uncultured organism D_0_Bacteria;D_1_Hydrogenedentes;Other;Other D_0_Bacteria;D_1_Ignavibacteriae;D_2_Ignavibacteria;D_3_Ignavibacteriales D_0_Bacteria;D_1_Latescibacteria;Ambiguous_taxa;Ambiguous_taxa D_0_Bacteria;D_1_Latescibacteria;D_2_Latescibacteria Incertae Sedis;D_3_Unknown Order D_0_Bacteria;D_1_Latescibacteria;D_2_uncultured Latescibacteria bacterium;D_3_uncultured Latescibacteria bacterium D_0_Bacteria;D_1_Latescibacteria;D_2_uncultured Pelobacter sp.;D_3_uncultured Pelobacter sp. D_0_Bacteria;D_1_Latescibacteria;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Latescibacteria;Other;Other D_0_Bacteria;D_1_Lentisphaerae;D_2_Oligosphaeria;D_3_SS1-B-02-17 D_0_Bacteria;D_1_Microgenomates;D_2_Candidatus Curtissbacteria;D_3_uncultured bacterium D_0_Bacteria;D_1_Microgenomates;D_2_Candidatus Daviesbacteria;D_3_uncultured bacterium D_0_Bacteria;D_1_Microgenomates;D_2_Candidatus Pacebacteria;D_3_uncultured bacterium D_0_Bacteria;D_1_Microgenomates;D_2_Candidatus Woesebacteria;Ambiguous_taxa D_0_Bacteria;D_1_Microgenomates;D_2_Candidatus Woesebacteria;D_3_uncultured Microgenomates group bacterium D_0_Bacteria;D_1_Microgenomates;D_2_Candidatus Woesebacteria;D_3_uncultured bacterium D_0_Bacteria;D_1_Microgenomates;D_2_Candidatus Woesebacteria;Other D_0_Bacteria;D_1_Microgenomates;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Microgenomates;D_2_uncultured candidate division WS6 bacterium;D_3_uncultured candidate division WS6 bacterium D_0_Bacteria;D_1_Microgenomates;D_2_uncultured soil bacterium;D_3_uncultured soil bacterium D_0_Bacteria;D_1_Microgenomates;Other;Other D_0_Bacteria;D_1_Nitrospirae;D_2_Nitrospira;D_3_Nitrospirales D_0_Bacteria;D_1_Omnitrophica;D_2_Omnitrophica Incertae Sedis;D_3_Unknown Order D_0_Bacteria;D_1_Omnitrophica;D_2_uncultured Firmicutes bacterium;D_3_uncultured Firmicutes bacterium D_0_Bacteria;D_1_Omnitrophica;D_2_uncultured Omnitrophica bacterium;D_3_uncultured Omnitrophica bacterium D_0_Bacteria;D_1_Omnitrophica;D_2_uncultured Verrucomicrobia bacterium;D_3_uncultured Verrucomicrobia bacterium D_0_Bacteria;D_1_Omnitrophica;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Omnitrophica;Other;Other D_0_Bacteria;D_1_PAUC34f;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Adlerbacteria;Other D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Azambacteria;D_3_Candidatus Azambacteria bacterium GW2011_GWF2_42_22 D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Azambacteria;D_3_uncultured Parcubacteria group bacterium D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Azambacteria;D_3_uncultured bacterium D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Azambacteria;Other D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Campbellbacteria;Ambiguous_taxa D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Giovannonibacteria;D_3_Candidatus Giovannonibacteria bacterium GW2011_GWF2_42_19 D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Giovannonibacteria;Other D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Magasanikbacteria;D_3_uncultured bacterium D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Magasanikbacteria;Other D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Moranbacteria;Other D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Nomurabacteria;D_3_uncultured bacterium D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Nomurabacteria;D_3_uncultured soil bacterium D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Nomurabacteria;Other D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Uhrbacteria;D_3_uncultured bacterium D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Uhrbacteria;D_3_uncultured soil bacterium D_0_Bacteria;D_1_Parcubacteria;D_2_Candidatus Uhrbacteria;Other D_0_Bacteria;D_1_Parcubacteria;D_2_uncultured Parcubacteria group bacterium;D_3_uncultured Parcubacteria group bacterium D_0_Bacteria;D_1_Parcubacteria;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Parcubacteria;Other;Other D_0_Bacteria;D_1_Peregrinibacteria;D_2_Candidatus Peribacteria;D_3_groundwater metagenome D_0_Bacteria;D_1_Peregrinibacteria;D_2_Candidatus Peribacteria;D_3_uncultured bacterium D_0_Bacteria;D_1_Peregrinibacteria;D_2_Candidatus Peribacteria;D_3_uncultured bacterium GKS2-174 D_0_Bacteria;D_1_Peregrinibacteria;D_2_Candidatus Peribacteria;D_3_uncultured sludge bacterium D_0_Bacteria;D_1_Peregrinibacteria;D_2_Candidatus Peribacteria;D_3_uncultured soil bacterium D_0_Bacteria;D_1_Peregrinibacteria;D_2_Candidatus Peribacteria;Other D_0_Bacteria;D_1_Peregrinibacteria;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Peregrinibacteria;Other;Other D_0_Bacteria;D_1_Planctomycetes;D_2_028H05-P-BN-P5;D_3_uncultured bacterium D_0_Bacteria;D_1_Planctomycetes;D_2_BD7-11;Ambiguous_taxa D_0_Bacteria;D_1_Planctomycetes;D_2_BD7-11;D_3_uncultured bacterium D_0_Bacteria;D_1_Planctomycetes;D_2_BD7-11;D_3_uncultured planctomycete D_0_Bacteria;D_1_Planctomycetes;D_2_BD7-11;Other D_0_Bacteria;D_1_Planctomycetes;D_2_OM190;Ambiguous_taxa D_0_Bacteria;D_1_Planctomycetes;D_2_OM190;D_3_uncultured Planctomyces sp. D_0_Bacteria;D_1_Planctomycetes;D_2_OM190;D_3_uncultured Planctomycetaceae bacterium D_0_Bacteria;D_1_Planctomycetes;D_2_OM190;D_3_uncultured bacterium D_0_Bacteria;D_1_Planctomycetes;D_2_OM190;D_3_uncultured microorganism D_0_Bacteria;D_1_Planctomycetes;D_2_OM190;D_3_uncultured planctomycete D_0_Bacteria;D_1_Planctomycetes;D_2_OM190;Other D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae;D_3_C86 D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae;D_3_CCM11a D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae;D_3_CPla-3 termite group D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae;D_3_MSB-3A7 sediment group D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae;D_3_MSBL9 D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae;D_3_Phycisphaerales D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae;D_3_Pla1 lineage D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae;D_3_S-70 D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae;D_3_S15A-MN16 D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae;D_3_SHA-43 D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae;D_3_Tepidisphaerales D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae;D_3_mle1-8 D_0_Bacteria;D_1_Planctomycetes;D_2_Pla3 lineage;D_3_uncultured bacterium D_0_Bacteria;D_1_Planctomycetes;D_2_Pla3 lineage;Other D_0_Bacteria;D_1_Planctomycetes;D_2_Pla4 lineage;D_3_uncultured bacterium D_0_Bacteria;D_1_Planctomycetes;D_2_Pla4 lineage;D_3_uncultured planctomycete D_0_Bacteria;D_1_Planctomycetes;D_2_Pla4 lineage;D_3_uncultured prokaryote D_0_Bacteria;D_1_Planctomycetes;D_2_Pla4 lineage;Other D_0_Bacteria;D_1_Planctomycetes;D_2_Planctomycetacia;D_3_Planctomycetales D_0_Bacteria;D_1_Planctomycetes;D_2_vadinHA49;Ambiguous_taxa D_0_Bacteria;D_1_Planctomycetes;D_2_vadinHA49;D_3_uncultured bacterium D_0_Bacteria;D_1_Planctomycetes;D_2_vadinHA49;Other D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_4-Org1-14 D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Alphaproteobacteria Incertae Sedis D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Caulobacterales D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Parvularculales D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhizobiales D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhodobacterales D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhodospirillales D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rickettsiales D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Sneathiellales D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Sphingomonadales D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;Other D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_B1-7BS D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Burkholderiales D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Hot Creek 32 D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Hydrogenophilales D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Methylophilales D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Neisseriales D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Nitrosomonadales D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Procabacteriales D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Rhodocyclales D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_SC-I-84 D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_TRA3-20 D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_UCT N117 D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_uncultured D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;Other D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_43F-1404R D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Bdellovibrionales D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Bradymonadales D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Deltaproteobacteria Incertae Sedis D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Desulfarculales D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Desulfobacterales D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Desulfovibrionales D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Desulfurellales D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Desulfuromonadales D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Myxococcales D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_NB1-j D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Oligoflexales D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_SAR324 clade(Marine group B) D 0 Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Syntrophobacterales D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;Other D_0_Bacteria;D_1_Proteobacteria;D_2_Elev-16S-509;D_3_uncultured bacterium D_0_Bacteria;D_1_Proteobacteria;D_2_Epsilonproteobacteria;D_3_Campylobacterales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;Ambiguous_taxa D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_1013-28-CG33 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_34P16 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Acidiferrobacterales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Acidithiobacillales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Aeromonadales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Alteromonadales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_BD72BR169 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Cellvibrionales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Chromatiales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_EC3 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_F9P41300-M23 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Gammaproteobacteria Incertae Sedis D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_HTA4 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_KI89A clade D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Legionellales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Methylococcales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Oceanospirillales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_PYR10d3 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pasteurellales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pseudomonadales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Salinisphaerales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Thiotrichales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Vibrionales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_WN-HWB-116 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_X35 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Xanthomonadales D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_eub62A3 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_uncultured D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;Other D_0_Bacteria;D_1_Proteobacteria;D_2_JTB23;D_3_uncultured bacterium D_0_Bacteria;D_1_Proteobacteria;D_2_Proteobacteria Incertae Sedis;D_3_Unknown Order D_0_Bacteria;D_1_Proteobacteria;D_2_SPOTSOCT00m83;D_3_uncultured bacterium D_0_Bacteria;D_1_Proteobacteria;D_2_SPOTSOCT00m83;Other D_0_Bacteria;D_1_Proteobacteria;Other;Other D_0_Bacteria;D_1_RBG-1 (Zixibacteria);Ambiguous_taxa;Ambiguous_taxa D_0_Bacteria;D_1_RBG-1 (Zixibacteria);D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_RsaHf231;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_SBR1093;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_SR1 (Absconditabacteria);Ambiguous_taxa;Ambiguous_taxa D_0_Bacteria;D_1_SR1 (Absconditabacteria);D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_SR1 (Absconditabacteria);D_2_uncultured candidate division SR1 bacterium;D_3_uncultured candidate division SR1 bacterium D_0_Bacteria;D_1_SR1 (Absconditabacteria);Other;Other D_0_Bacteria;D_1_Saccharibacteria;D_2_uncultured Candidatus Saccharibacteria bacterium;D_3_uncultured Candidatus Saccharibacteria bacterium D_0_Bacteria;D_1_Saccharibacteria;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Saccharibacteria;D_2_uncultured soil bacterium;D_3_uncultured soil bacterium D_0_Bacteria;D_1_Saccharibacteria;Other;Other D_0_Bacteria;D_1_Spirochaetae;D_2_Spirochaetes;D_3_Spirochaetales D_0_Bacteria;D_1_Synergistetes;D_2_Synergistia;D_3_Synergistales D_0_Bacteria;D_1_TM6 (Dependentiae);Ambiguous_taxa;Ambiguous_taxa D_0_Bacteria;D_1_TM6 (Dependentiae);D_2_uncultured Acidobacteria bacterium;D_3_uncultured Acidobacteria bacterium D_0_Bacteria;D_1_TM6 (Dependentiae);D_2_uncultured Candidatus Dependentiae bacterium;D_3_uncultured Candidatus Dependentiae bacterium D_0_Bacteria;D_1_TM6 (Dependentiae);D_2_uncultured Nautiliales bacterium;D_3_uncultured Nautiliales bacterium D_0_Bacteria;D_1_TM6 (Dependentiae);D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_TM6 (Dependentiae);D_2_uncultured deep-sea bacterium;D_3_uncultured deep-sea bacterium D_0_Bacteria;D_1_TM6 (Dependentiae);D_2_uncultured organism;D_3_uncultured organism D_0_Bacteria;D_1_TM6 (Dependentiae);D_2_uncultured proteobacterium;D_3_uncultured proteobacterium D_0_Bacteria;D_1_TM6 (Dependentiae);Other;Other D_0_Bacteria;D_1_Tectomicrobia;D_2_Tectomicrobia Incertae Sedis;D_3_Unknown Order D_0_Bacteria;D_1_Tectomicrobia;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_Tenericutes;D_2_Mollicutes;D_3_Entomoplasmatales D_0_Bacteria;D_1_Tenericutes;D_2_Mollicutes;D_3_Haloplasmatales D_0_Bacteria;D_1_Tenericutes;D_2_Mollicutes;D_3_Mollicutes RF9 D_0_Bacteria;D_1_Tenericutes;D_2_Mollicutes;D_3_Mycoplasmatales D_0_Bacteria;D_1_Tenericutes;D_2_Mollicutes;D_3_NB1-n D_0_Bacteria;D_1_Verrucomicrobia;D_2_OPB35 soil group;Ambiguous_taxa D_0_Bacteria;D_1_Verrucomicrobia;D_2_OPB35 soil group;D_3_Unknown Order D_0_Bacteria;D_1_Verrucomicrobia;D_2_OPB35 soil group;D_3_uncultured Verrucomicrobia bacterium D_0_Bacteria;D_1_Verrucomicrobia;D_2_OPB35 soil group;D_3_uncultured bacterium D_0_Bacteria;D_1_Verrucomicrobia;D_2_OPB35 soil group;D_3_uncultured soil bacterium D_0_Bacteria;D_1_Verrucomicrobia;D_2_OPB35 soil group;Other D_0_Bacteria;D_1_Verrucomicrobia;D_2_Opitutae;D_3_Opitutae vadinHA64 D_0_Bacteria;D_1_Verrucomicrobia;D_2_Opitutae;D_3_Opitutales D_0_Bacteria;D_1_Verrucomicrobia;D_2_Opitutae;D_3_Puniceicoccales D_0_Bacteria;D_1__Verrucomicrobia;D_2__Opitutae;Other D_0_Bacteria;D_1_Verrucomicrobia;D_2_S-BQ2-57 soil group;D_3_uncultured Verrucomicrobia bacterium D_0_Bacteria;D_1_Verrucomicrobia;D_2_S-BQ2-57 soil group;D_3_uncultured bacterium D_0_Bacteria;D_1_Verrucomicrobia;D_2_S-BQ2-57 soil group;Other D 0 Bacteria;D 1 Verrucomicrobia;D 2 UA11;D 3 uncultured bacterium D_0_Bacteria;D_1_Verrucomicrobia;D_2_Verrucomicrobia Incertae Sedis;D_3_Unknown Order D_0_Bacteria;D_1_Verrucomicrobia;D_2_Verrucomicrobiae;D_3_Verrucomicrobiales D_0_Bacteria;D_1_Verrucomicrobia;D_2_WCHB1-41;D_3_uncultured bacterium D_0_Bacteria;D_1_Verrucomicrobia;D_2_WCHB1-41;D_3_uncultured organism D_0_Bacteria;D_1_Verrucomicrobia;D_2_WCHB1-41;Other D_0_Bacteria;D_1_Verrucomicrobia;Other;Other D_0_Bacteria;D_1_WS1;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_WS2;D_2_uncultured organism;D_3_uncultured organism D_0_Bacteria;D_1_WS2;Other;Other D_0_Bacteria;D_1_WWE3;Ambiguous_taxa;Ambiguous_taxa D_0_Bacteria;D_1_WWE3;D_2_uncultured bacterium;D_3_uncultured bacterium D_0_Bacteria;D_1_WWE3;Other;Other D_0_Bacteria;Other;Other;Other Unassigned;Other;Other;Other