```
D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Micrococcales;D_4_Bogoriellaceae;D_5_Georgenia
   D_0_Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Cellulomonadaceae;D_5__Actinotalea
D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Micrococcales;D_4_Cellulomonadaceae;D_5_Cellulomonas
D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Micrococcales;D_4_Demequinaceae;Other
D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Micrococcales;D_4_Microbacteriaceae;Ambiguous_taxa
D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Micrococcales;D_4_Microbacteriaceae;D_5_Pseudoclavibacter
D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Micrococcales;D_4_Micrococcaceae;D_5_Nesterenkonia
D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Pseudonocardiales;D_4_Pseudonocardiaceae;D_5_Pseudonocardia
D_0_Bacteria;D_1_Actinobacteria;D_2_Coriobacteriia;D_3_Coriobacteriales;D_4_Coriobacteriaceae;D_5_Enterorhabdus
D_0_Bacteria;D_1_Actinobacteria;D_2_Coriobacteriia;D_3_Coriobacteriales;D_4_Coriobacteriaceae;D_5_Parvibacter
D_0_Bacteria;D_1_Actinobacteria;D_2_Coriobacteriia;D_3_Coriobacteriales;D_4_Coriobacteriaceae;D_5_uncultured
D_0_Bacteria;D_1_Actinobacteria;D_2_Coriobacteriia;D_3_Coriobacteriales;D_4_Coriobacteriaceae;Other
D_0_Bacteria;D_1_Actinobacteria;D_2_Thermoleophilia;D_3_Gaiellales;D_4_uncultured;D_5_uncultured bacterium
   D_0_Bacteria;D_1_Actinobacteria;D_2_Thermoleophilia;D_3_Solirubrobacterales;D_4_Elev-16S-1332;D_5_uncultured microorganism
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Bacteroidaceae;D_5_Bacteroides
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Bacteroidales S24-7 group;D_5_mouse gut metagenome
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Bacteroidales S24-7 group;D_5_uncultured bacterium
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Bacteroidales S24-7 group;Other
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Porphyromonadaceae;D_5_Dysgonomonas
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Porphyromonadaceae;D_5_Parabacteroides
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Porphyromonadaceae;D_5_uncultured
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Prevotellaceae;D_5_Prevotella 9
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Prevotellaceae;D_5_Prevotellaceae UCG-001
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Rikenellaceae;D_5_Alistipes
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;Other;Other
D_0_Bacteria;D_1_Bacteroidetes;D_2_Cytophagia;D_3_Cytophagales;D_4_Cytophagaceae;D_5_Chryseolinea
D_0_Bacteria;D_1_Bacteroidetes;D_2_Cytophagia;D_3_Cytophagales;D_4_Cytophagaceae;D_5_Spirosoma
D_0_Bacteria;D_1_Bacteroidetes;D_2_Flavobacteriia;D_3_Flavobacteriales;D_4_Flavobacteriaceae;D_5_Flavobacterium
D_0_Bacteria;D_1_Chlamydiae;D_2_Chlamydiae;D_3_Chlamydiales;D_4_Parachlamydiaceae;D_5_Candidatus Protochlamydia
  D_0_Bacteria;D_1_Chloroflexi;D_2_Anaerolineae;D_3_Anaerolineales;D_4_Anaerolineaceae;D_5_Ornatilinea
D_0_Bacteria;D_1_Chloroflexi;D_2_TK10;D_3_uncultured bacterium;D_4_;D_5_
D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;Ambiguous_taxa;D_4__;D_5_
D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;Other;Other;Other
D_0_Bacteria;D_1_Cyanobacteria;D_2_Melainabacteria;D_3_Gastranaerophilales;Ambiguous_taxa;D_5_
D_0_Bacteria;D_1_Cyanobacteria;D_2_Melainabacteria;D_3_Gastranaerophilales;D_4_uncultured bacterium;D_5_
D 0 Bacteria;D 1 Cyanobacteria;D 2 Melainabacteria;D 3 Gastranaerophilales;Other;Other
D_0_Bacteria;D_1_Cyanobacteria;D_2_Melainabacteria;D_3_Vampirovibrionales;Ambiguous_taxa;D_5_
D_0_Bacteria;D_1_Deferribacteres;D_2_Deferribacteres;D_3_Deferribacterales;D_4_Deferribacteraceae;D_5_Mucispirillum
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Alicyclobacillaceae;D_5_Tumebacillus
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Bacillaceae;D_5_Bacillus
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Family XII;D_5_Exiguobacterium
  D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Paenibacillaceae;D_5_Paenibacillus
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Planococcaceae;Ambiguous_taxa
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Planococcaceae;D_5_Bhargavaea
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Planococcaceae;D_5_Domibacillus
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Planococcaceae;D_5_Kurthia
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Planococcaceae;D_5_Lysinibacillus
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Planococcaceae;D_5_Rummeliibacillus
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Planococcaceae;D_5_Solibacillus
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Planococcaceae;D_5_Sporosarcina
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Planococcaceae;Other
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Staphylococcaceae;D_5_Staphylococcus
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Aerococcaceae;D_5_Aerococcus
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Carnobacteriaceae;D_5_Granulicatella
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Carnobacteriaceae;D_5_Trichococcus
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Enterococcaceae;D_5_Enterococcus
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Enterococcaceae;Other
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Lactobacillaceae;D_5_Lactobacillus
 D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Leuconostocaceae;D_5_Leuconostoc
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Leuconostocaceae;D_5_Weissella
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Rs-D42;D_5_uncultured bacterium
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Streptococcaceae;D_5_Streptococcus
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;Other;Other
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Christensenellaceae;D_5_Christensenellaceae R-7 group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Christensenellaceae;D_5_uncultured
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Christensenellaceae;Other
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Clostridiaceae 1;D_5_Candidatus Arthromitus
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Clostridiaceae 1;D_5_Clostridium sensu stricto 1
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Clostridiaceae 1;D_5_Clostridium sensu stricto 8
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Clostridiaceae 1;Other
  D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Clostridiales vadinBB60 group;Ambiguous_taxa
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Clostridiales vadinBB60 group;D_5_uncultured bacterium
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Clostridiales vadinBB60 group;Other
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Defluviitaleaceae;D_5_Defluviitaleaceae UCG-011
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Eubacteriaceae;D_5_Anaerofustis
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Family XIII;D_5_Anaerovorax
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Family XIII;D_5_Family XIII AD3011 group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Family XIII;D_5_Family XIII UCG-001
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Family XIII;D_5_[Eubacterium] brachy group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Family XIII;D_5_[Eubacterium] nodatum group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Family XIII;Other
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Gracilibacteraceae;D_5_uncultured
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Acetatifactor
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Acetitomaculum
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Anaerosporobacter
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Anaerostipes
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Blautia
  D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Coprococcus 1
  D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Coprococcus 2
D 0 Bacteria;D 1 Firmicutes;D 2 Clostridia;D 3 Clostridiales;D 4 Lachnospiraceae;D 5 Dorea
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Eisenbergiella
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Fusicatenibacter
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnoclostridium
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnoclostridium 5
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnospiraceae AC2044 group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnospiraceae FCS020 group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnospiraceae NK4A136 group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnospiraceae NK4B4 group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnospiraceae UCG-001
   D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnospiraceae UCG-004
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnospiraceae UCG-006
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnospiraceae UCG-008
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnospiraceae UCG-009
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnospiraceae UCG-010
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Marvinbryantia
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Mobilitalea
D 0 Bacteria:D 1 Firmicutes:D 2 Clostridia:D 3 Clostridiales:D 4 Lachnospiraceae:D 5 Moryella
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Oribacterium
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Roseburia
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Shuttleworthia
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Syntrophococcus
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Tyzzerella
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Tyzzerella 3
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_[Eubacterium] hallii group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_[Eubacterium] oxidoreducens group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_[Eubacterium] rectale group
 D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_[Eubacterium] ruminantium group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_[Eubacterium] ventriosum group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_[Eubacterium] xylanophilum group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_[Ruminococcus] torques group
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_uncultured
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;Other
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Peptococcaceae;D_5_Peptococcus
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Peptococcaceae;D_5_uncultured
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Peptostreptococcaceae;D_5_Peptoclostridium
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Peptostreptococcaceae;D_5_uncultured
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Peptostreptococcaceae;Other
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;Ambiguous_taxa
     D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Anaerofilum
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Anaerotruncus
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Butyricicoccus
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Candidatus Soleaferrea
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Caproiciproducens
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Faecalibacterium
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Flavonifractor
D 0 Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Hydrogenoanaerobacterium
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Intestinimonas
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Oscillibacter
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Oscillospira
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Papillibacter
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminiclostridium
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminiclostridium 1
D 0 Bacteria; D 1 Firmicutes; D 2 Clostridia; D 3 Clostridiales; D 4 Ruminococcaceae; D 5 Ruminiclostridium 5
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminiclostridium 6
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminiclostridium 9
 D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminococcaceae NK4A214 group
  D 0 Bacteria;D 1 Firmicutes;D 2 Clostridia;D 3 Clostridiales;D 4 Ruminococcaceae;D 5 Ruminococcaceae UCG-002
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminococcaceae UCG-003
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminococcaceae UCG-004
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminococcaceae UCG-005
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminococcaceae UCG-009
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminococcaceae UCG-010
D 0 Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminococcaceae UCG-011
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminococcaceae UCG-013
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminococcaceae UCG-014
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Ruminococcus 1
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Subdoligranulum
     \label{local_prop_def} $D_0_Bacteria; D_1_Firmicutes; D_2\_Clostridia; D_3\_Clostridiales; D_4\_Ruminococcaceae; D_5\_[Eubacterium] coprostanoligenes group to the property of t
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_uncultured
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;Other
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;Other;Other
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Thermoanaerobacterales;D_4_Thermoanaerobacteraceae;D_5_Gelria
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Thermoanaerobacterales;D_4_Thermoanaerobacteraceae;D_5_uncultured Thermoanaerobacterales bacterium
D_0_Bacteria;D_1_Firmicutes;D_2_Erysipelotrichia;D_3_Erysipelotrichales;D_4_Erysipelotrichaceae;D_5_Erysipelatoclostridium
D_0_Bacteria;D_1_Firmicutes;D_2_Erysipelotrichia;D_3_Erysipelotrichales;D_4_Erysipelotrichaceae;D_5_Erysipelotrichaceae UCG-003
D_0_Bacteria;D_1_Firmicutes;D_2_Erysipelotrichia;D_3_Erysipelotrichales;D_4_Erysipelotrichaceae;D_5_Faecalibaculum
D_0_Bacteria;D_1_Firmicutes;D_2_Erysipelotrichia;D_3_Erysipelotrichales;D_4_Erysipelotrichaceae;D_5_Turicibacter
D_0_Bacteria;D_1_Firmicutes;D_2_Erysipelotrichia;D_3_Erysipelotrichales;D_4_Erysipelotrichaceae;D_5_uncultured
D_0_Bacteria;D_1_Firmicutes;D_2_Erysipelotrichia;D_3_Erysipelotrichales;D_4_Erysipelotrichaceae;Other
D 0 Bacteria;D_1_ Proteobacteria;D_2_ARKICE-90;D_3_Mesorhizobium sp. enrichment culture clone SA_NR7_1;D_4__;D_5__
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhizobiales;D_4_Bradyrhizobiaceae;D_5_Bosea
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhizobiales;D_4_Bradyrhizobiaceae;D_5_Bradyrhizobium
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhizobiales;D_4_Hyphomicrobiaceae;D_5_Devosia
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhizobiales;D_4_Hyphomicrobiaceae;D_5_Hyphomicrobium
  D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhizobiales;D_4_Methylobacteriaceae;D_5_Methylobacterium
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhizobiales;D_4_Methylocystaceae;D_5_Methylosinus
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhizobiales;D_4_Phyllobacteriaceae;D_5_Mesorhizobium
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhizobiales;D_4_Rhizobiaceae;D_5_Rhizobium
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhizobiales;D_4_Rhodobiaceae;D_5_Tepidamorphus
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhizobiales;D_4_Xanthobacteraceae;Ambiguous_taxa
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhizobiales;D_4_Xanthobacteraceae;D_5_Ancylobacter
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhodobacterales;D_4_Rhodobacteraceae;D_5_Sediminimonas
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhodospirillales;D_4_DA111;D_5_uncultured alpha proteobacterium
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhodospirillales;D_4_Rhodospirillaceae;D_5_uncultured
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rickettsiales;D_4_Rickettsiales Incertae Sedis;D_5_Candidatus Odyssella
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rickettsiales;D_4_uncultured;D_5_uncultured bacterium
    \label{localization} $$D_0_Bacteria; D_1_Proteobacteria; D_2_Alphaproteobacteria; D_3_Sphingomonadales; D_4_Sphingomonadaceae; D_5_Sphingobium $$D_0_Bacteria; D_1_Sphingomonadaceae; D_2_Sphingomonadaceae; D_3_Sphingomonadaceae; D_3_Sphingomonadaceae; D_3_Sphingomonadaceae; D_4_Sphingomonadaceae; D_5_Sphingomonadaceae; D
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Sphingomonadales;D_4_Sphingomonadaceae;D_5_Sphingomonas
D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Burkholderiales;D_4_Alcaligenaceae;D_5_Achromobacter
D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Burkholderiales;D_4_Alcaligenaceae;D_5_Parasutterella
D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Burkholderiales;D_4_Burkholderiaceae;D_5_Ralstonia
D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Burkholderiales;D_4_Comamonadaceae;D_5_Comamonas
D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Burkholderiales;D_4_Comamonadaceae;D_5_Delftia
D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Burkholderiales;D_4_Comamonadaceae;D_5_Extensimonas
D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Burkholderiales;D_4_Comamonadaceae;D_5_Hydrogenophaga
D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Burkholderiales;D_4_Comamonadaceae;D_5_Ramlibacter
D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Burkholderiales;D_4_Oxalobacteraceae;D_5_Janthinobacterium
D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Methylophilales;D_4_Methylophilaceae;D_5_uncultured
D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Neisseriales;D_4_Neisseriaceae;D_5_Aquaspirillum
D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Rhodocyclales;D_4_Rhodocyclaceae;D_5_Azospira
D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Desulfurellales;D_4_Desulfurellaceae;D_5_H16
D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Desulfuromonadales;D_4_Desulfuromonadaceae;Other
 D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Desulfuromonadales;D_4_Geobacteraceae;D_5_Geobacter
D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Myxococcales;D_4_KD3-10;D_5_uncultured bacterium
D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Oligoflexales;D_4_Oligoflexaceae;D_5_uncultured bacterium
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Cellvibrionales;D_4_Porticoccaceae;D_5_C1-B045
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Chromatiales;D_4_Chromatiaceae;D_5_Rheinheimera
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;Ambiguous_taxa
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Enterobacter
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Escherichia-Shigella
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Proteus
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Legionellales;D_4_Legionellaceae;D_5_Legionella
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Methylococcales;D_4_Methylococcaceae;D_5_Methylocaldum
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pseudomonadales;D_4_Moraxellaceae;D_5_Acinetobacter
   D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pseudomonadales;D_4_Moraxellaceae;D_5_Enhydrobacter
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pseudomonadales;D_4_Pseudomonadaceae;D_5_Pseudomonas
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Vibrionales;D_4_Vibrionaceae;D_5_Vibrio
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Xanthomonadales;D_4_Xanthomonadaceae;D_5_Stenotrophomonas
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;Other;Other
D_0_Bacteria;D_1_Saccharibacteria;D_2_Unknown Class;D_3_Unknown Order;D_4_Unknown Family;D_5_Candidatus Saccharimonas
D_0_Bacteria;D_1_Tenericutes;D_2_Mollicutes;D_3_Anaeroplasmatales;D_4_Anaeroplasmataceae;D_5_Anaeroplasma
D_0_Bacteria;D_1_Tenericutes;D_2_Mollicutes;D_3_Entomoplasmatales;D_4_Spiroplasmataceae;D_5_Spiroplasma
D_0_Bacteria;D_1_Tenericutes;D_2_Mollicutes;D_3_Mollicutes RF9;Ambiguous_taxa;D_5_
D_0_Bacteria;D_1_Tenericutes;D_2_Mollicutes;D_3_Mollicutes RF9;D_4_uncultured bacterium;D_5_
D_0_Bacteria;D_1_Tenericutes;D_2_Mollicutes;D_3_Mollicutes RF9;D_4_uncultured rumen bacterium;D_5_
D_0_Bacteria;D_1_Tenericutes;D_2_Mollicutes;D_3_Mollicutes RF9;Other;Other
D_0_Bacteria;D_1_Verrucomicrobia;D_2_Verrucomicrobiae;D_3_Verrucomicrobiales;D_4_Verrucomicrobiaceae;D_5_Akkermansia
D_0_Bacteria;Other;Other;Other;Other
Unassigned;Other;Other;Other;Other
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D_0_Archaea;D_1_Euryarchaeota;D_2_Methanobacteria;D_3_Methanobacteriales;D_4_Methanobacteriaceae;D_5_Methanobacterium

D_0_Archaea;D_1_Euryarchaeota;D_2_Methanobacteria;D_3_Methanobacteriales;D_4_Methanobacteriaceae;D_5_Methanothermobacter

D_0_Bacteria;D_1_Acidobacteria;D_2_Solibacteres;D_3_Solibacterales;D_4_Solibacteraceae (Subgroup 3);D_5_Candidatus Solibacter

D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Corynebacteriales;D_4_Corynebacteriaceae;D_5_Corynebacterium 1