



- Eubacteriales_[G-4] bacterium_MOT-164
- Ligilactobacillus animalis
- Streptomyces aculeolatus
- Secundilactobacillus paracollinoides
- Mollicutes_[G-1] bacterium_MOT-186
- Staphylococcus ureilyticus
- Atopostipes sp._MOT-201
- Actinidia eriantha
- Ralstonia sp._HMT_406
- Cutibacterium granulosum
- Mammaliococcus lentus
- Clostridium disporicum
- Staphylococcus equorum
- Moraxella osloensis
- Corynebacterium stationis
- Limosilactobacillus reuteri
- Ligilactobacillus murinus
- Leptothrix sp._HMT_025
- Streptococcus thermophilus
- Jeotgalicoccus halotolerans
- Stenotrophomonas maltophilia
- Enterococcus gallinarum
- Delftia acidovorans
- Lachnospiraceae_[G-11] bacterium_MOT-177
- Massilia aurea
- Dubosiella newyorkensis
- Eubacteriales_[G-2] bacterium_MOT-162
- Staphylococcus saprophyticus
- Anaerococcus sp._HMT_290
- Cutibacterium acnes
- Stenotrophomonas [Pseudomonas] hibiscicola
- Psychrobacter alimentarius
- Akkermansia muciniphila
- Bradyrhizobium pachyrhizi
- Pelomonas saccharophila
- Corynebacterium ammoniagenes
- Lachnospiraceae_[G-14] bacterium_MOT-185
- Pseudomonas helleri
- Bifidobacterium pseudolongum
- Enterococcus faecalis
- Triticum aestivum
- Lactobacillus johnsonii
- Fusobacterium varium_nov_96.696%
- Duncaniella freteri_nov_93.293%
- Muribaculaceae_[G-2] bacterium_MOT-104_nov_88.867%
- Enterococcus faecalis_nov_95.825%
- Duncaniella freteri_nov_89.775%
- Fusicatenibacter saccharivorans_nov_90.526%
- Alistipes senegalensis_nov_93.443%
- Peptococcus sp._HMT_168_nov_84.866%
- Duncaniella freteri_nov_89.718%
- Oscillospiraceae_[G-6] bacterium_MOT-153_nov_91.631%
- Muribaculaceae_[G-2] bacterium_MOT-104_nov_89.000%
- Lachnospiraceae_[G-14] bacterium_MOT-185_nov_92.719%
- Fusobacterium perfoetens_nov_91.126%
- Actinidia eriantha_nov_97.011%
- Muribaculaceae_[G-2] bacterium_MOT-104_nov_88.423%
- Duncaniella freteri_nov_88.934%
- Yaniella halotolerans_nov_97.040%
- Oscillospiraceae_[G-1] bacterium_MOT-147_nov_96.674%
- Lachnoclostridium [Clostridium] aminophilum_nov_89.792%
- Duncaniella freteri_nov_93.699%
- Oscillospiraceae_[G-3] bacterium_MOT-150_nov_92.917%
- Muribaculaceae_[G-1] bacterium_MOT-129_nov_85.887%
- Muribaculaceae_[G-1] bacterium_MOT-129_nov_88.105%
- Parafannyhessea umbonata_nov_92.161%
- Turicibacter sanguinis_nov_95.923%
- Oscillospiraceae_[G-2] bacterium_MOT-149_nov_95.198%
- Oribacterium parvum_nov_89.770%
- Staphylococcus saprophyticus_xylosus
- Sphingomonas aquatilis_melonis
- Lactacaseibacillus_Lactobacillus casei_rhamnosus
- Faecalicatena multispecies_sppn3_2_nov_92.067%

F17722.S01

F17722.S02

F17722.S03

F17722.S04

F17722.S05

F17722.S11

F17722.S12

F17722.S13

F17722.S14

F17722.S15

Samples

Species