

Species

- SP1 Eubacteriales [G-4] bacterium_MOT-164
- SP10 Ligilactobacillus animalis
- SP12 Streptomyces aculeolatus
- SP14 Secundilactobacillus paracollinoides
- SP15 Mollicutes [G-1] bacterium_MOT-186
- SP18 Staphylococcus ureilyticus
- SP19 Atopostipes sp._MOT-201
- SP2 Actinidia eriantha
- SP20 Ralstonia sp._HMT_406
- SP23 Cutibacterium granulosum
- SP26 Mammaliicoccus lentus
- SP27 Clostridium disporicum
- SP28 Staphylococcus equorum
- SP29 Moraxella osloensis
- SP3 Corynebacterium stationis
- SP30 Limosilactobacillus reuteri
- SP31 Ligilactobacillus murinus
- SP34 Leptothrix sp._HMT_025
- SP38 Streptococcus thermophilus
- SP4 Jeotgalicoccus halotolerans
- SP42 Stenotrophomonas maltophilia
- SP44 Enterococcus gallinarum
- SP49 Delftia acidovorans
- SP52 Lachnospiraceae [G-11] bacterium_MOT-177
- SP54 Massilia aurea
- SP57 Dubosiella newyorkensis
- SP58 Eubacteriales [G-2] bacterium_MOT-162
- SP6 Staphylococcus saprophyticus
- SP61 Anaerococcus sp._HMT_290
- SP7 Cutibacterium acnes
- SP72 Stenotrophomonas [Pseudomonas] hibiscicola
- SP73 Psychrobacter alimentarius
- SP76 Akkermansia muciniphila
- SP77 Bradyrhizobium pachyrhizi
- SP79 Pelomonas saccharophila
- SP8 Corynebacterium ammoniagenes
- SP80 Lachnospiraceae [G-14] bacterium_MOT-185
- SP81 Pseudomonas helleri
- SP88 Bifidobacterium pseudolongum
- SP89 Enterococcus faecalis
- SP9 Triticum aestivum
- SP90 Lactobacillus johnsonii
- SPN101 Fusobacterium varium_nov_96.696%
- SPN106 Duncaniella freteri_nov_93.293%
- SPN116 Muribaculaceae [G-2] bacterium_MOT-104_nov_88.867%
- SPN117 Enterococcus faecalis_nov_95.825%
- SPN148 Duncaniella freteri_nov_89.775%
- SPN16 Fusicatenibacter saccharivorans_nov_90.526%
- SPN170 Alistipes senegalensis_nov_93.443%
- SPN177 Peptococcus sp._HMT_168_nov_84.866%
- SPN181 Duncaniella freteri_nov_89.718%
- SPN187 Oscillospiraceae [G-6] bacterium_MOT-153_nov_91.631%
- SPN192 Muribaculaceae [G-2] bacterium_MOT-104_nov_89.000%
- SPN204 Lachnospiraceae [G-14] bacterium_MOT-185_nov_92.719%
- SPN216 Fusobacterium perfoetens_nov_91.126%
- SPN218 Actinidia eriantha_nov_97.011%
- SPN29 Muribaculaceae [G-2] bacterium_MOT-104_nov_88.423%
- SPN33 Duncaniella freteri_nov_88.934%
- SPN35 Yaniella halotolerans_nov_97.040%
- SPN39 Oscillospiraceae [G-1] bacterium_MOT-147_nov_96.674%
- SPN43 Lachnoclostridium [Clostridium] aminophilum_nov_89.792%
- SPN49 Duncaniella freteri_nov_93.699%
- SPN50 Oscillospiraceae [G-3] bacterium_MOT-150_nov_92.917%
- SPN59 Muribaculaceae [G-1] bacterium_MOT-129_nov_85.887%
- SPN65 Muribaculaceae [G-1] bacterium_MOT-129_nov_88.105%
- SPN66 Parafannyhessea umbonata_nov_92.161%
- SPN81 Turicibacter sanguinis_nov_95.923%
- SPN82 Oscillospiraceae [G-2] bacterium_MOT-149_nov_95.198%
- SPN9 Oribacterium parvum_nov_89.770%
- SPP1 Staphylococcus saprophyticus_xylosus
- SPP3 Sphingomonas aquatilis_melonis
- SPP4 Lactacaseibacillus_Lactobacillus casei_rhamnosus
- SPPN3 Faecalicatena multispecies_sppn3_2_nov_92.067%