

Species

- SP1 *Triticum aestivum*
- SP10 *Delftia acidovorans*
- SP11 *Enterococcus gallinarum*
- SP13 *Staphylococcus saprophyticus*
- SP15 *Ligilactobacillus murinus*
- SP17 *Pseudomonas helleri*
- SP18 Eubacteriales_[G-4] bacterium_MOT-164
- SP19 *Stenotrophomonas maltophilia*
- SP2 *Psychrobacter alimentarius*
- SP24 Eubacteriales_[G-2] bacterium_MOT-162
- SP26 *Clostridium disporicum*
- SP27 *Stenotrophomonas* [*Pseudomonas*] *hibiscicola*
- SP29 *Cutibacterium acnes*
- SP33 Lachnospiraceae_[G-11] bacterium_MOT-177
- SP34 *Cutibacterium granulosum*
- SP35 *Corynebacterium stationis*
- SP36 *Streptococcus thermophilus*
- SP39 *Staphylococcus equorum*
- SP4 *Massilia aurea*
- SP41 *Jeotgalicoccus halotolerans*
- SP42 *Mammaliicoccus lentus*
- SP44 Lachnospiraceae_[G-14] bacterium_MOT-185
- SP50 *Dubosiella newyorkensis*
- SP51 *Corynebacterium ammoniagenes*
- SP53 *Enterococcus faecalis*
- SP56 *Actinidia eriantha*
- SP57 *Atopostipes* sp._MOT-201
- SP59 Mollicutes_[G-1] bacterium_MOT-186
- SP6 *Ralstonia* sp._HMT_406
- SP63 *Anaerococcus* sp._HMT_290
- SP65 *Streptomyces aculeolatus*
- SP66 *Lactobacillus johnsonii*
- SP67 *Bifidobacterium pseudolongum*
- SP7 *Staphylococcus ureilyticus*
- SP70 *Lactocaseibacillus rhamnosus*
- SP72 *Akkermansia muciniphila*
- SP75 *Leptothrix* sp._HMT_025
- SP8 *Limosilactobacillus reuteri*
- SP80 *Moraxella osloensis*
- SP81 *Secundilactobacillus paracollinoides*
- SP88 *Pelomonas saccharophila*
- SP9 *Ligilactobacillus animalis*
- SP94 *Bradyrhizobium pachyrhizi*
- SPN102 *Fusobacterium varium*_nov_96.696%
- SPN107 *Duncaniella freteri*_nov_93.293%
- SPN116 Muribaculaceae_[G-2] bacterium_MOT-104_nov_88.867%
- SPN117 *Enterococcus faecalis*_nov_95.825%
- SPN15 *Fusicatenibacter saccharivorans*_nov_90.526%
- SPN150 *Duncaniella freteri*_nov_89.775%
- SPN173 *Alistipes senegalensis*_nov_93.443%
- SPN179 *Peptococcus* sp._HMT_168_nov_84.866%
- SPN183 *Duncaniella freteri*_nov_89.718%
- SPN190 Oscillospiraceae_[G-6] bacterium_MOT-153_nov_91.631%
- SPN194 Muribaculaceae_[G-2] bacterium_MOT-104_nov_89.000%
- SPN208 Lachnospiraceae_[G-14] bacterium_MOT-185_nov_92.719%
- SPN218 *Fusobacterium perfoetens*_nov_91.126%
- SPN220 *Actinidia eriantha*_nov_97.011%
- SPN28 Muribaculaceae_[G-2] bacterium_MOT-104_nov_88.423%
- SPN32 *Yaniella halotolerans*_nov_97.040%
- SPN33 *Duncaniella freteri*_nov_88.934%
- SPN39 Oscillospiraceae_[G-1] bacterium_MOT-147_nov_96.674%
- SPN45 *Lachnoclostridium* [*Clostridium*] *aminophilum*_nov_89.792%
- SPN49 *Duncaniella freteri*_nov_93.699%
- SPN50 Oscillospiraceae_[G-3] bacterium_MOT-150_nov_92.917%
- SPN55 Muribaculaceae_[G-1] bacterium_MOT-129_nov_88.105%
- SPN60 Muribaculaceae_[G-1] bacterium_MOT-129_nov_85.887%
- 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
- SPPN3 *Faecalicatena multispecies_sppn3_2_nov_92.067%*