

## Species

- SP10 Erysipelotrichaceae\_[G-1] bacterium\_MOT-189
- SP11 Streptococcus danieliae
- SP12 Enterococcus faecalis
- SP13 Ileibacterium valens
- SP15 Shigella sonnei
- SP17 Streptococcus thoraltensis
- SP18 Bifidobacterium pseudolongum
- SP19 Erysipelatoclostridium [Clostridium] innocuum
- SP2 Shigella dysenteriae
- SP23 Escherichia coli
- SP24 Enterobacter hormaechei
- SP26 Dubosiella newyorkensis
- SP27 Faecalibaculum rodentium
- SP3 Enterococcus gallinarum
- SP39 Cutibacterium acnes
- SP4 Bifidobacterium animalis
- SP42 Bacteroides acidifaciens
- SP43 Akkermansia muciniphila
- SP46 Lactobacillus johnsonii
- SP49 Mammaliococcus lentus
- SP53 Streptococcus sp.\_MOT-012
- SP54 Streptococcus acidominimus
- SP55 Corynebacterium mastitidis
- SP6 Limosilactobacillus reuteri
- SP8 Clostridium disporicum
- SP9 Ligilactobacillus murinus
- SPN1 Parafannyhessea umbonata\_nov\_92.161%
- SPN11 Faecalibaculum rodentium\_nov\_97.125%
- SPN23 Parasutterella excrementihominis\_nov\_94.578%
- SPN45 Bacteroides uniformis\_nov\_96.099%
- SPN72 Eggerthella timonensis\_nov\_90.929%
- SPP2 Escherichia\_Shigella fergusonii\_flexneri
- SPP3 Staphylococcus saprophyticus\_xylosus
- SPPN1 Olsenella multispecies\_sppn1\_2\_nov\_91.966%