

Species

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| SP1 Lachnospiraceae_[G-14] bacterium_MOT-164 | SP60 Feijuniphilus lacydionis | SPN314 Muribaculaceae_[G-2] bacterium_MOT-104_nov_86.340% | SPN526 Anaerotaenia torta_nov_88.773% |
| SP10 Limosilactobacillus fermentum | SP82 Eubacteriales_[G-1] bacterium_MOT-159 | SPN538 Muricomes intestini_nov_89.648% | SPN539 Lachnospiraceae_[G-3] bacterium_MOT-168_nov_92.946% |
| SP100 Clostridium chromiireducens | SP83 Anaerotignum sp._strain_[1XD42-85] | SPN550 Streptococcus danieliae_nov_96.787% | SPN551 Duncaniella freteri_nov_87.976% |
| SP109 Anaerobium sp._strain_[C-37] | SP84 Achromobacter pulmonis | SPN562 Duncaniella freteri_nov_87.976% | SPN574 Duncaniella freteri_nov_94.898% |
| SP11 Shigella sonnei | SP86 Acidipropionibacterium theonii | SPN586 Lachnospiraceae_[G-11] bacterium_MOT-178_nov_95.562% | SPN598 Lachnospiraceae_[G-11] bacterium_MOT-177_nov_95.679% |
| SP111 Coprococcus sp._strain_[1XD21-23] | SP89 Alistipes sp._MOT-127 | SPN610 Eubacterium coprostanoligenes_nov_91.489% | SPN621 Lachnospiraceae_[G-3] bacterium_MOT-168_nov_94.606% |
| SP112 Pseudomonas aestus | SP9 Ligilactobacillus murinus | SPN624 Lachnospiraceae_[G-3] bacterium_MOT-168_nov_93.776% | SPN633 Phocaea massiliensis_nov_89.787% |
| SP116 Finegoldia magna | SP95 Erysipelatoclostridium [Clostridium] cocleatum | SPN643 Anaeromassilibacillus senegalensis_nov_93.008% | SPN655 Anaerotignum sp._strain_[D2-1X-45]_nov_96.205% |
| SP118 Robinsoniella sp._strain_[D2-1X-13] | SP96 Actinidia eriantha | SPN667 Duncaniella freteri_nov_91.952% | SPN668 Eubacteriales_[G-1] bacterium_MOT-161_nov_97.881% |
| SP12 Enterococcus gallinarum | SP99 Enterobacter sp._MOT-050 | SPN679 Lachnospiraceae_[G-11] bacterium_MOT-178_nov_95.344% | SPN691 Adlercreutzia equolifaciens_nov_89.530% |
| SP120 Ruminococcus sp._strain_[C-28] | SPN1010 Duncaniella freteri_nov_89.463% | SPN70 Prevetella shahii_nov_87.903% | SPN703 Clostridium disporicum_nov_97.849% |
| SP121 Duncaniella freteri | SPN1028 Streptococcus danieliae_nov_97.379% | SPN715 Faecalicatena fissicatena_nov_94.824% | SPN72 Streptococcus danieliae_nov_93.387% |
| SP127 Stenotrophomonas maltophilia | SPN1053 Actinomyces polynesiensis_nov_97.183% | SPN727 Lachnospiraceae_[G-14] bacterium_MOT-185_nov_92.537% | SPN738 Lachnospiraceae_[G-6] bacterium_MOT-171_nov_95.218% |
| SP129 Eubacteriales_[G-4] bacterium_MOT-164 | SPN109 Alistipes senegalensis_nov_93.483% | SPN741 Muribaculaceae_[G-2] bacterium_MOT-104_nov_89.264% | SPN750 Cutibacterium acnes_nov_96.815% |
| SP131 Eubacteriales_[G-2] bacterium_MOT-162 | SPN1093 Actinomyces polynesiensis_nov_94.153% | SPN763 Lachnospiraceae_[G-11] bacterium_MOT-178_nov_95.344% | SPN775 Fusicatenibacter saccharivorans_nov_88.912% |
| SP139 Paracoccus mangrovi | SPN1137 Streptococcus danieliae_nov_93.952% | SPN787 Muribaculaceae_[G-2] bacterium_MOT-104_nov_89.703% | SPN788 Adlercreutzia equolifaciens_nov_96.983% |
| SP149 Adlercreutzia muris | SPN1167 Duncaniella freteri_nov_88.577% | SPN799 Lachnospiraceae_[G-14] bacterium_MOT-185_nov_92.766% | SPN811 Lachnospiraceae_[G-14] bacterium_MOT-183_nov_97.868% |
| SP15 Escherichia coli | SPN121 Muribaculaceae_[G-2] bacterium_MOT-104_nov_88.911% | SPN822 Adlercreutzia caecimuris_nov_89.270% | SPN834 Streptococcus danieliae_nov_96.774% |
| SP16 Phyllobacterium myrsinacearum | SPN1211 Cutibacterium granulosum_nov_96.788% | SPN834 Streptococcus danieliae_nov_96.774% | SPN84 Lachnospiraceae_[G-14] bacterium_MOT-183_nov_94.670% |
| SP163 Oscillospiraceae_[G-3] bacterium_MOT-150 | SPN1242 Lachnospiraceae_[G-7] bacterium_MOT-172_nov_91.770% | SPN855 Eubacterium coprostanoligenes_nov_90.213% | SPN857 Lachnospiraceae_[G-11] bacterium_MOT-177_nov_95.679% |
| SP169 Trichococcus pasteurii | SPN1283 Duncaniella freteri_nov_89.780% | SPN868 Anaerocolumna cellulositytica_nov_91.909% | SPN891 Marinisporobacter balticus_nov_82.839% |
| SP17 Enterococcus camelliae | SPN1323 Wolinella succinogenes_nov_80.044% | SPN902 Duncaniella freteri_nov_88.668% | SPN903 Murimonas sp._strain_[WYJ26-X68]_nov_94.105% |
| SP18 Streptococcus sp._MOT-012 | SPN133 Lachnospiraceae_[G-6] bacterium_MOT-171_nov_94.179% | SPN913 Eisenbergiella sp._strain_[1XD8-92]_nov_92.841% | SPN925 Anaerocolumna cellulositytica_nov_90.683% |
| SP182 Streptococcus chosunense | SPN1396 Salinibacillus xinjiangensis_nov_86.160% | SPN937 Beduini massiliensis_nov_86.708% | SPN937 Beduini massiliensis_nov_86.708% |
| SP185 Cutibacterium granulosum | SPN1437 Lachnospiraceae_[G-12] bacterium_MOT-180_nov_89.676% | SPN949 Phocaea massiliensis_nov_89.787% | SPN96 Lachnospiraceae_[G-14] bacterium_MOT-185_nov_97.015% |
| SP19 Escherichia fergusonii | SPN145 Duncaniella freteri_nov_95.510% | SPN974 Duncaniella freteri_nov_93.750% | SPN961 Pliibacter termitis_nov_90.581% |
| SP193 Lachnospiraceae_[G-11] bacterium_MOT-177 | SPN149 Streptococcus danieliae_nov_95.582% | SPN975 Lachnospiraceae_[G-11] bacterium_MOT-177_nov_92.608% | SPN974 Duncaniella freteri_nov_93.750% |
| SP199 Mesorhizobium huakuii | SPN1509 Duncaniella freteri_nov_86.373% | SPN986 Anaerocolumna xylanovorans_nov_88.212% | SPN986 Anaerocolumna xylanovorans_nov_88.212% |
| SP2 Streptococcus danieliae | SPN1555 Alkalibacterium olivapovilticus_nov_97.595% | SPN998 Lachnospiraceae_[G-7] bacterium_MOT-172_nov_94.617% | SPN998 Lachnospiraceae_[G-7] bacterium_MOT-172_nov_94.617% |
| SP202 Oscillibacter sp._strain_[128x] | SPN157 Glucerbacter canis_nov_93.542% | SPP109 Staphylococcus capitis_epidermidis | SPP14 Escherichia_Shigella_albertii_sonnei |
| SP21 Clostridium disporicum | SPN160 Eisenbergiella massiliensis_nov_85.744% | SPP18 Enterococcus casseliflavus_gallinarum | SPP22 Staphylococcus saprophyticus_xylosum |
| SP22 Lactobacillus johnsonii | SPN1628 Muribaculaceae_[G-1] bacterium_MOT-129_nov_88.200% | SPP27 Agrobacterium_Rhizobium_lusitanum_rhizogenes | SPP4 Streptococcus mitis_pneumoniae_pseudopneumoniae |
| SP222 Lachnospiraceae_[G-1] bacterium_MOT-166 | SPN1674 Lacrimispora xylanolytica_nov_94.398% | SPP45 Lactobacillus johnsonii_taiwanensis | SPP55 Achromobacter aegrifaciens_insuavis |
| SP23 Alkalibacterium pelagium | SPN169 Duncaniella freteri_nov_92.121% | SPP59 Burkholderia_Caenibaculum_aenigmatica_baiyandianus_cepacia_contaminans_diffu_...(8 species) | SPP66 Burkholderia_aenigmatica_cepacia_contaminans_lata_multivorans |
| SP24 Shigella boydii | SPN1744 Duncaniella freteri_nov_91.515% | SPP69 Burkholderia contaminans_lata_multivorans | SPP85 Bacillus_haltolerans_spizizenii |
| SP25 Lachnospiraceae_[G-14] bacterium_MOT-185 | SPN1791 Lachnospiraceae_[G-14] bacterium_MOT-185_nov_97.228% | SPP89 Staphylococcus argenteus_aureus_rotterdamii | SPPN10 Faecalicatena multispecies_sppn10_2_nov_93.568% |
| SP26 Lachnospiraceae_[G-11] bacterium_MOT-177 | SPN181 Acetivibrio sp._strain_[D16-59]_nov_90.812% | SPPN31 Faecalicatena multispecies_sppn31_2_nov_93.802% | |
| SP27 Anaerotignum sp._strain_[D2-1X-72] | SPN1858 Duncaniella freteri_nov_86.922% | | |
| SP3 Faecalibaculum rodentium | SPN194 Muribaculaceae_[G-1] bacterium_MOT-129_nov_85.972% | | |
| SP30 Limosilactobacillus reuteri | SPN195 Oscillospiraceae_[G-6] bacterium_MOT-153_nov_91.684% | | |
| SP31 Enterococcus faecalis | SPN206 Duncaniella freteri_nov_90.982% | | |
| SP312 Tessaracoccus aquimaris | SPN218 Phocaeicola massiliensis_nov_93.509% | | |
| SP4 Cutibacterium acnes | SPN229 Lachnospiraceae_[G-14] bacterium_MOT-185_nov_95.745% | | |
| SP40 Mammaliococcus lentus | SPN241 Muribaculaceae_[G-1] bacterium_MOT-129_nov_86.720% | | |
| SP41 Acutalibacter muris | SPN253 Bariatricus massiliensis_nov_89.506% | | |
| SP42 Staphylococcus ureilyticus | SPN274 Lachnospiraceae_[G-14] bacterium_MOT-185_nov_97.228% | | |
| SP43 Corynebacterium tuberculostearicum | SPN277 Eubacteriales_[G-1] bacterium_MOT-159_nov_81.420% | | |
| SP44 Listeria monocytogenes | SPN284 Pseudoflavonifractor sp._strain_[136x]_nov_93.407% | | |
| SP46 Kineothrix sp._strain_[1XD8-87] | SPN295 Muribaculaceae_[G-2] bacterium_MOT-104_nov_87.873% | | |
| SP47 Enterococcus olivae | SPN308 Muribaculaceae_[G-1] bacterium_MOT-129_nov_91.870% | | |
| SP5 Mammaliococcus sciuri | SPN309 Blautia hominis_nov_89.583% | | |
| SP50 Actinomyces polynesiensis | SPN31 Anaerotignum sp._strain_[1XD42-85]_nov_97.098% | | |
| SP53 Mucispirillum schaedleri | SPN321 Kineothrix alysoides_nov_89.855% | | |
| SP59 Eisenbergiella sp._strain_[1XD8-92] | SPN332 Coprococcus sp._strain_[1XD21-23]_nov_95.595% | | |
| SP6 Marvimbryantia sp._strain_[D2-1X-79] | SPN344 Murimonas sp._strain_[WYJ26-X68]_nov_93.873% | | |
| SP60 Mordavella sp._strain_[D2-1X-71] | SPN356 Duncaniella freteri_nov_87.298% | | |
| SP61 Streptococcus mitis | SPN368 Lachnospiraceae_[G-6] bacterium_MOT-171_nov_92.931% | | |
| SP62 Shigella flexneri | SPN380 Lachnospiraceae_[G-7] bacterium_MOT-172_nov_93.320% | | |
| SP63 Triticum aestivum | SPN383 Cellulomonas bogoriensis_nov_97.872% | | |
| SP64 Corynebacterium pilbarensis | SPN392 Anaerocolumna cellulositytica_nov_86.071% | | |
| SP67 Lactobacillus intestinalis | SPN404 Eisenbergiella sp._strain_[1XD8-92]_nov_97.309% | | |
| SP69 Oscillospiraceae_[G-7] bacterium_MOT-154 | SPN417 Eubacterium coprostanoligenes_nov_91.667% | | |
| SP7 Salmonella enterica | SPN430 Turicibacter sanguinis_nov_95.949% | | |
| SP70 Romboutsia ilealis | SPN431 Alistipes senegalensis_nov_93.522% | | |
| SP71 Paracoccus laevigulosivorans | SPN442 Magnetovibrio blakemorei_nov_83.259% | | |
| SP72 Staphylococcus hominis | SPN454 Muribaculaceae_[G-1] bacterium_MOT-129_nov_85.111% | | |
| SP73 Corynebacterium mucifaciens | SPN466 Duncaniella freteri_nov_87.273% | | |
| SP74 Absiella sp._strain_[1XD42-72] | SPN478 Fusicatenibacter saccharivorans_nov_90.586% | | |
| SP75 Roseburia sp._strain_[MGB-1] | SPN490 Streptococcus danieliae_nov_96.976% | | |
| SP79 Parasutterella excrementihominis | SPN502 Duncaniella freteri_nov_87.149% | | |
| SP8 Akkermansia muciniphila | SPN502 Duncaniella freteri_nov_87.149% | | |
| SP81 Akkermansia muciniphila | SPN502 Duncaniella freteri_nov_87.149% | | |