0
20
40
60
80
100
Value
Group
KO0Dfec
KO3Hlig
Adlercreutzia mucosicola
Povalibacter uvarum_nov_91.702%
Paraburkholderia hospita_nov_91.083%
Aminipila butyrica_nov_91.910%
Bacteroides acidifaciens
Oscillospiraceae_[G−7] bacterium_MOT−154
Lachnoclostridium [Clostridium] scindens
Coprococcus catus_nov_94.357%
Eubacterium ventriosum_nov_96.154%
Faecalibaculum rodentium
Kineothrix alysoides_nov_97.517%
Eubacteriales_[G−2] bacterium_MOT−162_nov_95.260%
Lachnospiraceae_[G−6] bacterium_MOT−171_nov_94.570%
Butyricicoccus pullicaecorum_nov_94.407%
Desulfovibrio fairfieldensis_nov_94.647%
Muribaculaceae_[G−1] bacterium_MOT−129
Alistipes sp._MOT−127
Lactobacillus johnsonii
Helicobacter ganmani
Muribaculaceae_[G−2] bacterium_MOT−104_nov_92.857%
Carnobacteriaceae_[G−1] bacterium_MOT−198
Odoribacter splanchnicus_nov_93.521%
Muribaculaceae_[G−2] bacterium_MOT−104_nov_92.457%
Lachnospiraceae_[G−10] bacterium_MOT−175_nov_95.034%
Devosia insulae
Duncaniella freteri_nov_92.903%
Kineothrix alysoides_nov_95.485%
Povalibacter uvarum_nov_90.618%
multigenus multispecies_sppn292_3_nov_87.368%
Eubacteriales_[G−1] bacterium_MOT−159_nov_94.118%
Muribaculaceae_[G−2] bacterium_MOT−104_nov_92.625%
Bacteroides acidifaciens_acidofaciens
Harryflintia acetispora_nov_88.889%
Gemella sp._MOT−043
Phocaeicola sartorii
Sphingomonas limnosediminicola
Bifidobacterium pseudolongum
Lactobacillus_Limosilactobacillus reuteri_reuteri_clade_938
Alistipes senegalensis_nov_95.680%
Lactobacillus intestinalis
Erysipelatoclostridium [Clostridium] innocuum
Paraeggerthella hongkongensis_nov_92.793%
Faecalicatena multispecies_sppn189_2_nov_97.279%
Desulfovibrio fairfieldensis_nov_94.421%
Lachnospiraceae_[G−9] bacterium_MOT−174_nov_95.485%
Muribaculaceae_[G−1] bacterium_MOT−129_nov_91.757%
Muribaculum intestinale_nov_92.424%
Saccharibacteria_(TM7)_[G−3] bacterium_HMT_351_nov_96.60%
Kineothrix alysoides_nov_93.275%
Muribaculaceae_[G−1] bacterium_MOT−129_nov_91.304%
Muribaculaceae_[G−2] bacterium_MOT−104_nov_91.810%
Muribaculaceae_[G−2] bacterium_MOT−104_nov_91.991%
Muribaculaceae_[G−2] bacterium_MOT−104_nov_92.704%
Mailhella massiliensis_nov_92.111%
Eubacteriales_[G−4] bacterium_MOT−164_nov_97.743%
Anaerostipes caccae
Lachnospiraceae_[G−11] bacterium_MOT−178
Muribaculum intestinale
Muribaculaceae_[G−2] bacterium_MOT−104_nov_93.521%
Eubacteriales_[G−1] bacterium_MOT−160
Muribaculaceae_[G−1] bacterium_MOT−129_nov_91.540%
Staphylococcus saprophyticus_xylosus
Ramlibacter monticola
Afipia_Bradyrhizobium archetypum_australiense_broomeae_elkanii
Oscillospiraceae_[G−3] bacterium_MOT−150
Ileibacterium valens
Arthrobacter_Paeniglutamicibacter_Pseudarthrobacter cryotolerans
Eubacteriales_[G−2] bacterium_MOT−162
Lachnospiraceae_[G−12] bacterium_MOT−179
Kineothrix alysoides_nov_96.840%
Parabacteroides merdae_nov_95.032%
Anaerotaenia torta_nov_97.059%
Holdemania massiliensis_nov_92.060%
Prevotella sp._MOT−128
Eubacteriales_[G−4] bacterium_MOT−165
Muribaculaceae_[G−2] bacterium_MOT−104_nov_92.441%
Muribaculum intestinale_nov_89.744%
Muribaculaceae_[G−2] bacterium_MOT−104_nov_93.074%
Ruminococcus bromii
Turicimonas muris
Blautia hansenii_hominis_marasmi
Muribaculaceae_[G−1] bacterium_MOT−129_nov_91.323%
Corynebacterium mastitidis
Muribaculaceae_[G−1] bacterium_MOT−129_nov_91.087%
Eubacteriales_[G−4] bacterium_MOT−164
Lactobacillus taiwanensis
Muribaculaceae_[G−1] bacterium_MOT−129_nov_91.087%
Eubacteriales_[G−1] bacterium_MOT−159
Clostridium disporicum_saudiense
Helicobacter typhlonius
Parabacteroides goldsteinii
Escherichia_Shigella coli_fergusonii_flexneri_sonnei
Ligilactobacillus animalis_apodemi_murinus
Streptococcus acidominimus_sp._MOT−012
Pasteurella_Rodentibacter caecimuris_heylii
Erysipelatoclostridium [Clostridium] cocleatum
Akkermansia muciniphila
Erysipelotrichaceae_[G−1] bacterium_MOT−189
Streptococcus danieliae
Rodentibacter pneumotropicus
Species
F0000.S069
F0000.S067
F0000.S068
F0000.S070
F0000.S065
F0000.S066
F0000.S064
F0000.S063
F0000.S006
F0000.S001
F0000.S009
F0000.S007
F0000.S010
F0000.S008
F0000.S004
F0000.S005
F0000.S002
F0000.S003
Samples