0
20
40
60
80
100
Value
Group
Feces Group 8
Feces Group 9
Sporobacter termitidis_nov_87.124%
Raoultibacter timonensis_nov_90.476%
Eubacterium ventriosum_nov_93.320%
Oscillospiraceae_[G−2] bacterium_MOT−149_nov_87.885%
Oscillospiraceae_[G−4] bacterium_MOT−151_nov_93.347%
Faecalicatena fissicatena_nov_93.946%
Lawsonibacter asaccharolyticus_nov_90.083%
Lachnospiraceae_[G−12] bacterium_MOT−180_nov_90.184%
Oscillospiraceae_[G−4] bacterium_MOT−151_nov_90.496%
Rothia nasimurium_nov_97.228%
Streptococcus sp._MOT−045_nov_97.764%
Frisingicoccus caecimuris_nov_96.451%
Lachnospira multipara_nov_84.298%
Lachnoclostridium [Clostridium] polysaccharolyticum_nov_90.437%
Cuneatibacter caecimuris_nov_92.308%
Anaerocolumna cellulosilytica_nov_88.655%
Lawsonibacter asaccharolyticus_nov_90.909%
Pseudoflavonifractor phocaeensis_nov_91.511%
Gluceribacter canis_nov_93.946%
Longibaculum muris_nov_89.506%
Blautia faecicola_nov_93.319%
Sporobacter termitidis_nov_88.223%
Blautia multispecies_sppn28_2_nov_95.198%
Adlercreutzia equolifaciens
Erysipelatoclostridium [Clostridium] saccharogumia_nov_96.042%
Roseburia faecis_nov_97.917%
Lactobacillus rogosae_nov_94.990%
Kineothrix alysoides_nov_91.441%
Spongiibacter marinus_nov_80.142%
Eubacterium xylanophilum_nov_90.505%
Gluceribacter canis_nov_95.388%
Mediterraneibacter [Ruminococcus] gnavus_nov_95.188%
Eisenbergiella massiliensis
Blautia schinkii_nov_94.130%
Coprococcus eutactus_nov_92.704%
Butyricicoccus pullicaecorum_nov_87.216%
Eubacterium coprostanoligenes_nov_91.379%
Oscillospiraceae_[G−6] bacterium_MOT−153
Clostridium disporicum_nov_97.619%
Paludicola psychrotolerans_nov_88.115%
Oscillospiraceae_[G−7] bacterium_MOT−154_nov_92.918%
Oscillospiraceae_[G−1] bacterium_MOT−147_nov_90.760%
Eubacterium xylanophilum_nov_91.313%
Eubacterium coprostanoligenes_nov_91.379%
Mediterraneibacter [Ruminococcus] torques_nov_93.515%
Oscillospiraceae_[G−1] bacterium_MOT−147_nov_93.595%
Eubacteriales_[G−1] bacterium_MOT−158
Alistipes finegoldii
Barnesiella viscericola_nov_90.447%
Eubacteriales_[G−1] bacterium_MOT−158_nov_91.507%
Kiloniella majae_nov_85.144%
Gluceribacter canis_nov_94.561%
Odoribacter laneus
Erysipelatoclostridium [Clostridium] saccharogumia
Dysosmobacter welbionis_nov_86.902%
Lachnoclostridium [Clostridium] herbivorans_nov_92.723%
Ruminococcus champanellensis_nov_90.713%
Oscillospiraceae_[G−2] bacterium_MOT−149_nov_93.555%
Lachnospiraceae_[G−11] bacterium_MOT−177_nov_95.851%
Lachnoclostridium [Clostridium] herbivorans_nov_92.917%
Eisenbergiella massiliensis_nov_86.486%
Lachnospiraceae_[G−14] bacterium_MOT−183_nov_92.060%
Lacrimispora saccharolytica_nov_90.625%
Blautia schinkii_nov_94.340%
Agathobaculum desmolans_nov_86.345%
Ruminococcus albus_nov_91.045%
Blautia producta_nov_95.178%
Coprococcus eutactus_nov_95.085%
Ruminococcus flavefaciens_nov_94.760%
Eubacterium coprostanoligenes_nov_90.129%
Blautia luti
Blautia luti_nov_97.899%
Bacteroides thetaiotaomicron
Bacteroides xylanisolvens
Alistipes finegoldii_nov_94.835%
Parabacteroides goldsteinii
Bacteroides uniformis
Muribaculaceae_[G−2] bacterium_MOT−104_nov_86.228%
Parasutterella excrementihominis
Fusicatenibacter saccharivorans_nov_97.689%
Lachnospiraceae_[G−4] bacterium_MOT−169_nov_97.484%
Fusicatenibacter saccharivorans
Blautia glucerasea
Blautia producta_nov_96.226%
Longicatena caecimuris
Akkermansia muciniphila
Bacteroides intestinalis
Ruminococcus champanellensis_nov_91.810%
Oscillospiraceae_[G−6] bacterium_MOT−153_nov_97.831%
Blautia faecicola_nov_93.111%
Clostridium disporicum
Turicibacter sanguinis_nov_96.137%
Collinsella aerofaciens
Blautia luti_nov_96.429%
Romboutsia ilealis
Duncaniella freteri_nov_89.024%
Phocaeicola vulgatus
Ligilactobacillus murinus
Lactobacillus intestinalis
Bifidobacterium pseudolongum
Species
F18249.S33
F18249.S34
F18249.S35
F18249.S36
F18249.S37
F18249.S38
F18249.S39
F18249.S40
F18249.S41
F18249.S42
F18249.S43
F18249.S44
F18249.S45
F18249.S46
F18249.S47
F18249.S48
Samples