0 20 40 60 80 100
Value
Group
Saliva Group 8
Saliva Group 9
Rothia nasimurium_nov_97.228%
Streptococcus sp._MOT−045_nov_97.764%
Streptococcus mutans
Eubacteriales_[G−1] bacterium_MOT−159_nov_92.797%
Lachnospiraceae_[G−6] bacterium_MOT−171_nov_94.549%
Agathobaculum desmolans_nov_86.345%
Eubacteriales_[G−1] bacterium_MOT−161_nov_92.308%
Bacteroides xylanisolvens
Gluceribacter canis_nov_93.946%
Oscillospiraceae_[G−3] bacterium_MOT−150_nov_96.458%
Drancourtella massiliensis_nov_92.276%
Parabacteroides goldsteinii
Oscillospiraceae_[G−2] bacterium_MOT−149_nov_87.885%
Eubacteriales_[G−1] bacterium_MOT−158_nov_91.507%
Oscillospiraceae_[G−4] bacterium_MOT−151_nov_95.417%
Dysosmobacter welbionis_nov_86.902%
Oscillospiraceae_[G−4] bacterium_MOT−151_nov_96.042%
Parasutterella excrementihominis
Erysipelatoclostridium [Clostridium] saccharogumia_nov_96.042%
Lachnospiraceae_[G−3] bacterium_MOT−168_nov_93.946%
Clostridium disporicum
Blautia producta_nov_96.226%
Blautia luti_nov_96.429%
Blautia glucerasea
Gluceribacter canis_nov_94.561%
Longicatena caecimuris
Raoultibacter timonensis_nov_90.476%
Erysipelatoclostridium [Clostridium] innocuum_nov_87.078%
Oscillospiraceae_[G−1] bacterium_MOT−147_nov_92.975%
Bacteroides thetaiotaomicron
Ruminococcus albus_nov_91.045%
Staphylococcus pettenkoferi_pseudolugdunensis
Staphylococcus caprae
Eubacterium coprostanoligenes_nov_90.129%
Muribaculaceae_[G−2] bacterium_MOT−104_nov_86.228%
Lachnospiraceae_[G−14] bacterium_MOT−185_nov_91.121%
Oscillospiraceae_[G−4] bacterium_MOT−151_nov_93.971%
Cuneatibacter caecimuris_nov_92.308%
Anaerocolumna cellulosilytica_nov_88.655%
Oscillospiraceae_[G−1] bacterium_MOT−147_nov_93.595%
Kineothrix alysoides_nov_91.441%
Mediterraneibacter [Ruminococcus] torques_nov_93.515%
Lawsonibacter asaccharolyticus_nov_90.909%
Lachnoclostridium [Clostridium] polysaccharolyticum_nov_90.437%
Lachnospiraceae_[G−3] bacterium_MOT−168_nov_93.737%
Oscillospiraceae_[G−6] bacterium_MOT−153
Faecalicatena fissicatena_nov_93.946%
Blautia producta_nov_89.834%
Blautia schinkii_nov_94.340%
Lachnospiraceae_[G−3] bacterium_MOT−168
Fusicatenibacter saccharivorans_nov_89.263%
Oribacterium parvum_nov_89.770%
Mediterraneibacter [Ruminococcus] torques_nov_92.693%
Lachnospiraceae_[G−14] bacterium_MOT−183_nov_92.060%
Blautia multispecies_sppn28_2_nov_95.198%
Turicibacter sanguinis_nov_96.137%
Bacteroides uniformis
Eubacterium coprostanoligenes_nov_91.379%
Bacteroides intestinalis
Lachnoclostridium [Clostridium] herbivorans_nov_92.917%
Eubacterium coprostanoligenes_nov_91.379%
Akkermansia muciniphila
Chryseobacterium culicis_nov_97.280%
Duncaniella freteri_nov_89.024%
Eubacterium xylanophilum_nov_91.313%
Blautia faecicola_nov_93.111%
Oscillospiraceae_[G−1] bacterium_MOT−147_nov_90.760%
Lacrimispora saccharolytica_nov_90.625%
Collinsella aerofaciens
Staphylococcus haemolyticus
Corynebacterium amycolatum
Granulicatella adiacens
Ruminococcus champanellensis_nov_91.810%
Oscillospiraceae_[G−6] bacterium_MOT−153_nov_97.831%
Romboutsia ilealis
Lactiplantibacillus plantarum
Lactiplantibacillus_Lactobacillus pentosus_plantarum
Lactobacillus intestinalis
Streptococcus sp._HMT_064
Staphylococcus saprophyticus_xylosus
Enterococcus gallinarum
Phocaeicola vulgatus
Enterococcus avium
Shigella sonnei
Shigella flexneri
Streptococcus agalactiae
Staphylococcus argenteus_aureus_roterodami
Enterococcus faecalis
Escherichia coli
Shigella dysenteriae
Salmonella enterica
Veillonella dispar_parvula
Bifidobacterium pseudolongum
Veillonella parvula
Streptococcus parasanguinis_parasanguinis_clade_721
Mammaliicoccus sciuri
Staphylococcus ureilyticus
Citrobacter koseri
Haemophilus parainfluenzae
Ligilactobacillus murinus
Species
F18249.S12
F18249.S14
F18249.S11
F18249.S13
F18249.S15
F18249.S16
F18249.S10
F18249.S09
F18249.S05
F18249.S06
F18249.S08
F18249.S02
F18249.S07
F18249.S04
F18249.S01
F18249.S03
Samples