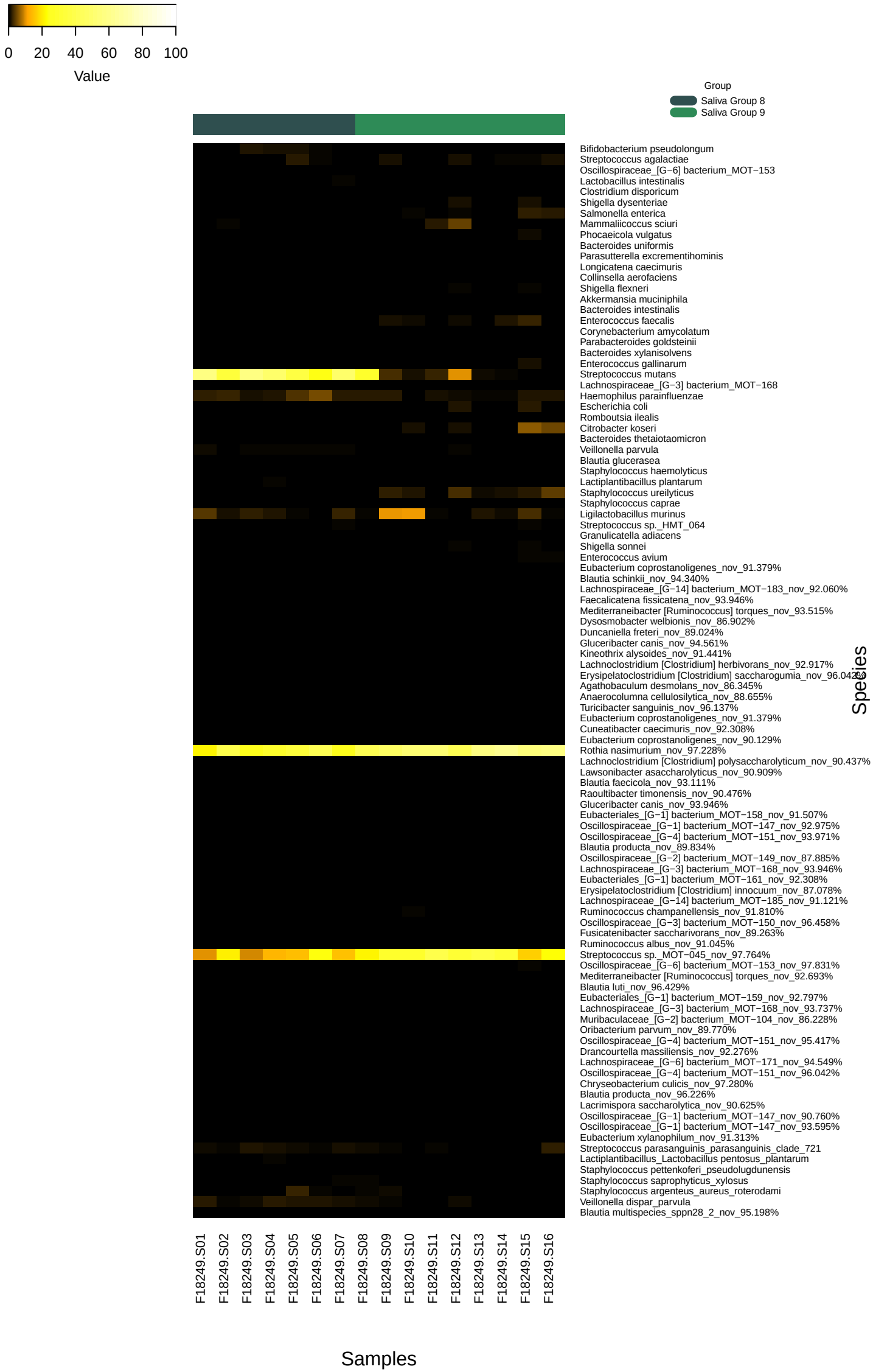
0
20
40
60
80
100
Value
Group
Saliva Group 8
Saliva Group 9
Bifidobacterium pseudolongum
Streptococcus agalactiae
Oscillospiraceae_[G−6] bacterium_MOT−153
Lactobacillus intestinalis
Clostridium disporicum
Shigella dysenteriae
Salmonella enterica
Mammaliicoccus sciuri
Phocaeicola vulgatus
Bacteroides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