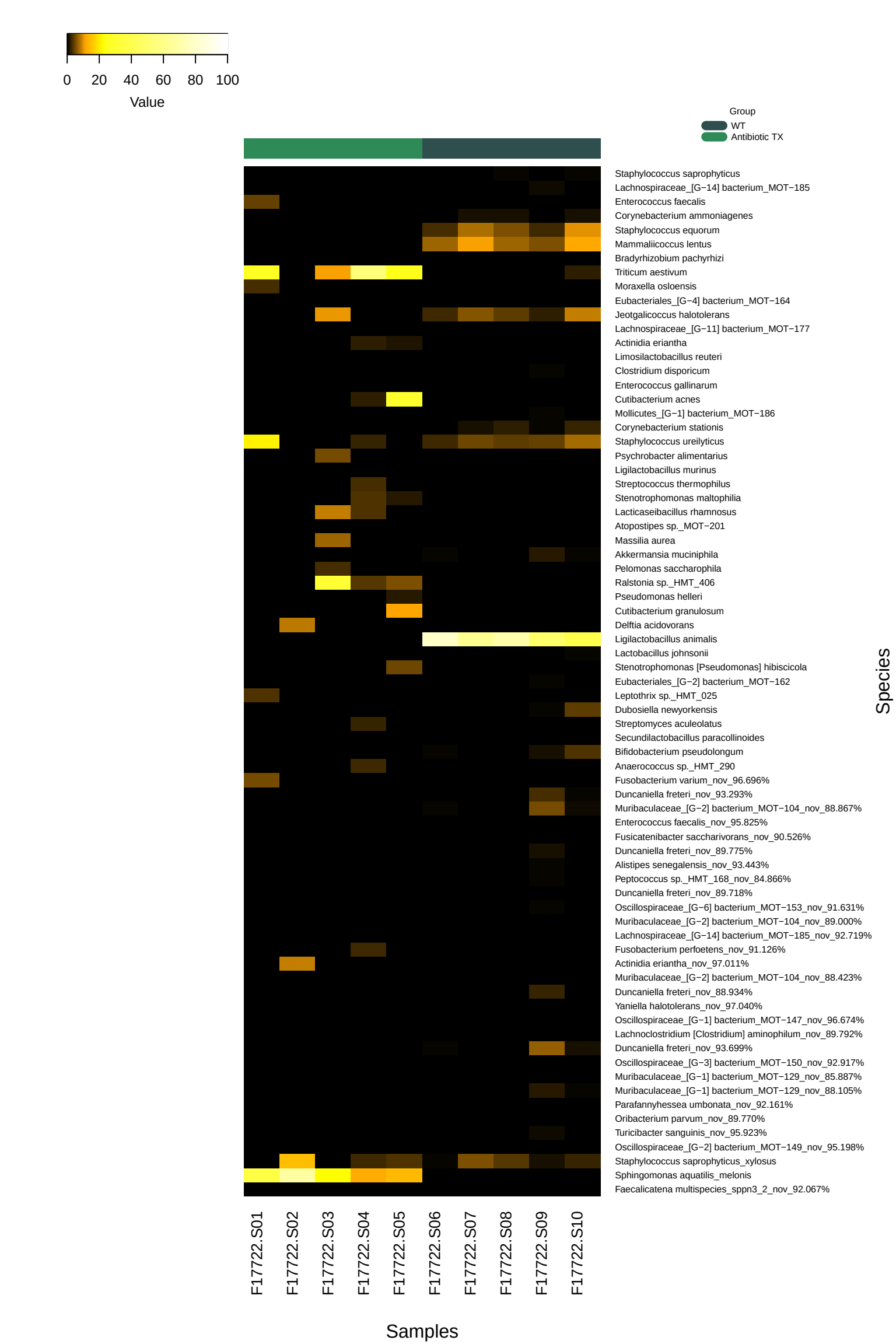
0
20
40
60
80
100
Value
Group
WT
Antibiotic TX
Staphylococcus saprophyticus
Lachnospiraceae_[G−14] bacterium_MOT−185
Enterococcus faecalis
Corynebacterium ammoniagenes
Staphylococcus equorum
Mammaliicoccus lentus
Bradyrhizobium pachyrhizi
Triticum aestivum
Moraxella osloensis
Eubacteriales_[G−4] bacterium_MOT−164
Jeotgalicoccus halotolerans
Lachnospiraceae_[G−11] bacterium_MOT−177
Actinidia eriantha
Limosilactobacillus reuteri
Clostridium disporicum
Enterococcus gallinarum
Cutibacterium acnes
Mollicutes_[G−1] bacterium_MOT−186
Corynebacterium stationis
Staphylococcus ureilyticus
Psychrobacter alimentarius
Ligilactobacillus murinus
Streptococcus thermophilus
Stenotrophomonas maltophilia
Lacticaseibacillus rhamnosus
Atopostipes sp._MOT−201
Massilia aurea
Akkermansia muciniphila
Pelomonas saccharophila
Ralstonia sp._HMT_406
Pseudomonas helleri
Cutibacterium granulosum
Delftia acidovorans
Ligilactobacillus animalis
Lactobacillus johnsonii
Stenotrophomonas [Pseudomonas] hibiscicola
Eubacteriales_[G−2] bacterium_MOT−162
Leptothrix sp._HMT_025
Dubosiella newyorkensis
Streptomyces aculeolatus
Secundilactobacillus paracollinoides
Bifidobacterium pseudolongum
Anaerococcus sp._HMT_290
Fusobacterium varium_nov_96.696%
Duncaniella freteri_nov_93.293%
Muribaculaceae_[G−2] bacterium_MOT−104_nov_88.867%
Enterococcus faecalis_nov_95.825%
Fusicatenibacter saccharivorans_nov_90.526%
Duncaniella freteri_nov_89.775%
Alistipes senegalensis_nov_93.443%
Peptococcus sp._HMT_168_nov_84.866%
Duncaniella freteri_nov_89.718%
Oscillospiraceae_[G−6] bacterium_MOT−153_nov_91.631%
Muribaculaceae_[G−2] bacterium_MOT−104_nov_89.000%
Lachnospiraceae_[G−14] bacterium_MOT−185_nov_92.719%
Fusobacterium perfoetens_nov_91.126%
Actinidia eriantha_nov_97.011%
Muribaculaceae_[G−2] bacterium_MOT−104_nov_88.423%
Duncaniella freteri_nov_88.934%
Yaniella halotolerans_nov_97.040%
Oscillospiraceae_[G−1] bacterium_MOT−147_nov_96.674%
Lachnoclostridium [Clostridium] aminophilum_nov_89.792%
Duncaniella freteri_nov_93.699%
Oscillospiraceae_[G−3] bacterium_MOT−150_nov_92.917%
Muribaculaceae_[G−1] bacterium_MOT−129_nov_85.887%
Muribaculaceae_[G−1] bacterium_MOT−129_nov_88.105%
Parafannyhessea umbonata_nov_92.161%
Oribacterium parvum_nov_89.770%
Turicibacter sanguinis_nov_95.923%
Oscillospiraceae_[G−2] bacterium_MOT−149_nov_95.198%
Staphylococcus saprophyticus_xylosus
Sphingomonas aquatilis_melonis
Faecalicatena multispecies_sppn3_2_nov_92.067%
Species
F17722.S01
F17722.S02
F17722.S03
F17722.S04
F17722.S05
F17722.S06
F17722.S07
F17722.S08
F17722.S09
F17722.S10
Samples