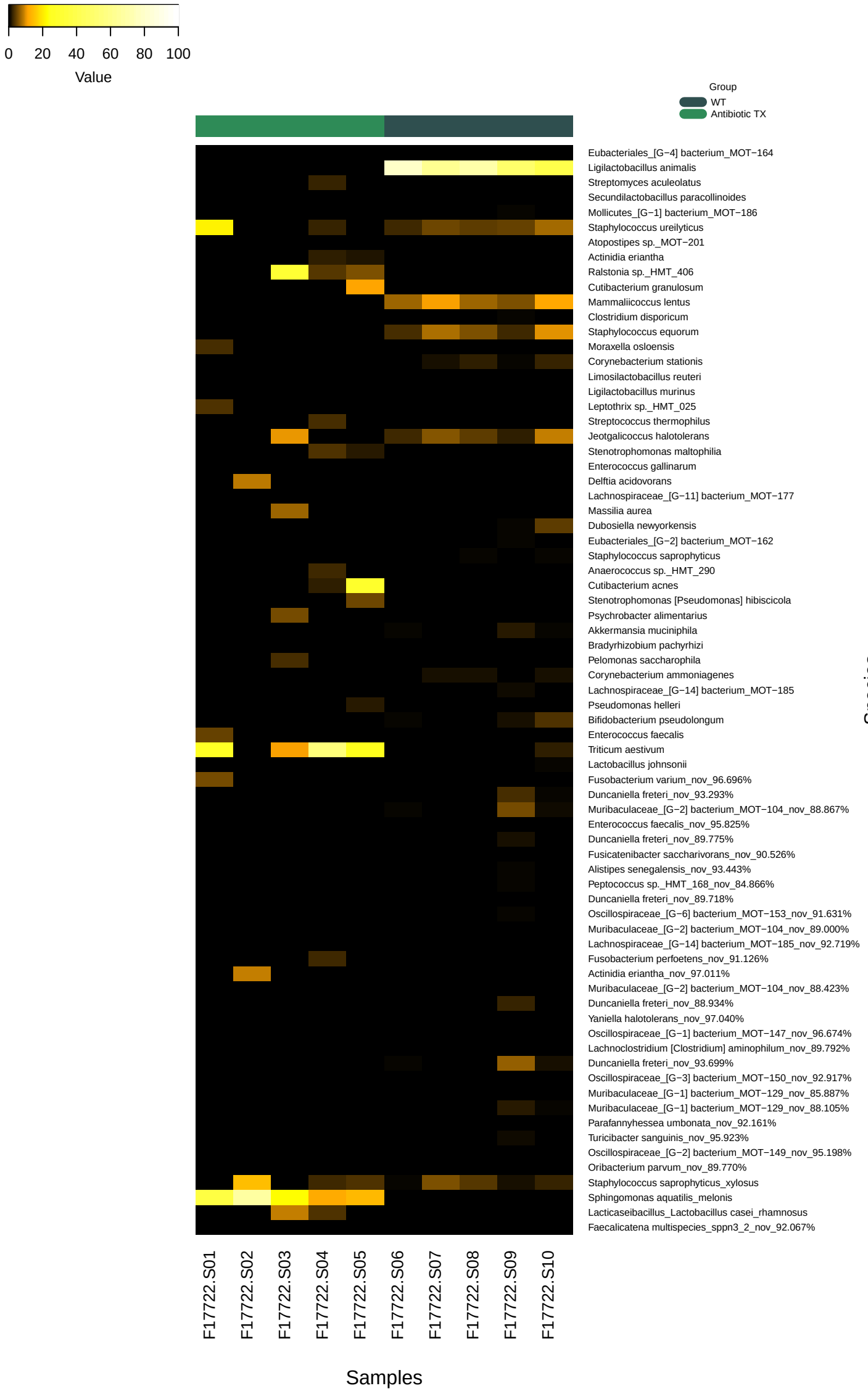
0
20
40
60
80
100
Value
Group
WT
Antibiotic TX
Eubacteriales_[G−4] bacterium_MOT−164
Ligilactobacillus animalis
Streptomyces aculeolatus
Secundilactobacillus paracollinoides
Mollicutes_[G−1] bacterium_MOT−186
Staphylococcus ureilyticus
Atopostipes sp._MOT−201
Actinidia eriantha
Ralstonia sp._HMT_406
Cutibacterium granulosum
Mammaliicoccus lentus
Clostridium disporicum
Staphylococcus equorum
Moraxella osloensis
Corynebacterium stationis
Limosilactobacillus reuteri
Ligilactobacillus murinus
Leptothrix sp._HMT_025
Streptococcus thermophilus
Jeotgalicoccus halotolerans
Stenotrophomonas maltophilia
Enterococcus gallinarum
Delftia acidovorans
Lachnospiraceae_[G−11] bacterium_MOT−177
Massilia aurea
Dubosiella newyorkensis
Eubacteriales_[G−2] bacterium_MOT−162
Staphylococcus saprophyticus
Anaerococcus sp._HMT_290
Cutibacterium acnes
Stenotrophomonas [Pseudomonas] hibiscicola
Psychrobacter alimentarius
Akkermansia muciniphila
Bradyrhizobium pachyrhizi
Pelomonas saccharophila
Corynebacterium ammoniagenes
Lachnospiraceae_[G−14] bacterium_MOT−185
Pseudomonas helleri
Bifidobacterium pseudolongum
Enterococcus faecalis
Triticum aestivum
Lactobacillus johnsonii
Fusobacterium varium_nov_96.696%
Duncaniella freteri_nov_93.293%
Muribaculaceae_[G−2] bacterium_MOT−104_nov_88.867%
Enterococcus faecalis_nov_95.825%
Duncaniella freteri_nov_89.775%
Fusicatenibacter saccharivorans_nov_90.526%
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%
Turicibacter sanguinis_nov_95.923%
Oscillospiraceae_[G−2] bacterium_MOT−149_nov_95.198%
Oribacterium parvum_nov_89.770%
Staphylococcus saprophyticus_xylosus
Sphingomonas aquatilis_melonis
Lacticaseibacillus_Lactobacillus casei_rhamnosus
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