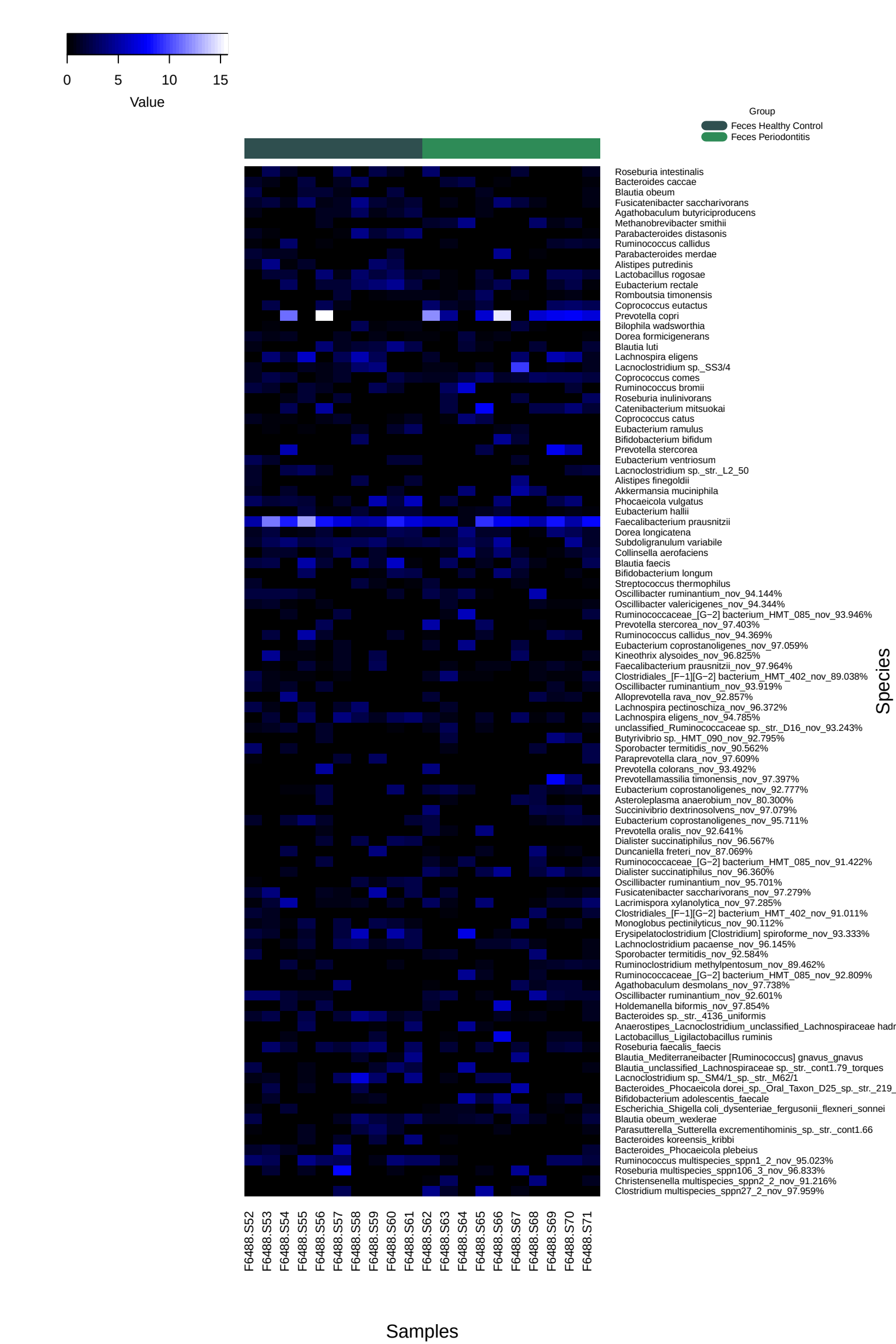
0
5
10
15
Value
Group
Feces Healthy Control
Feces Periodontitis
Roseburia intestinalis
Bacteroides caccae
Blautia obeum
Fusicatenibacter saccharivorans
Agathobaculum butyriciproducens
Methanobrevibacter smithii
Parabacteroides distasonis
Ruminococcus callidus
Parabacteroides merdae
Alistipes putredinis
Lactobacillus rogosae
Eubacterium rectale
Romboutsia timonensis
Coprococcus eutactus
Prevotella copri
Bilophila wadsworthia
Dorea formicigenerans
Blautia luti
Lachnospira eligens
Lacnoclostridium sp._SS3/4
Coprococcus comes
Ruminococcus bromii
Roseburia inulinivorans
Catenibacterium mitsuokai
Coprococcus catus
Eubacterium ramulus
Bifidobacterium bifidum
Prevotella stercorea
Eubacterium ventriosum
Lacnoclostridium sp._str._L2_50
Alistipes finegoldii
Akkermansia muciniphila
Phocaeicola vulgatus
Eubacterium hallii
Faecalibacterium prausnitzii
Dorea longicatena
Subdoligranulum variabile
Collinsella aerofaciens
Blautia faecis
Bifidobacterium longum
Streptococcus thermophilus
Oscillibacter ruminantium_nov_94.144%
Oscillibacter valericigenes_nov_94.344%
Ruminococcaceae_[G−2] bacterium_HMT_085_nov_93.946%
Prevotella stercorea_nov_97.403%
Ruminococcus callidus_nov_94.369%
Eubacterium coprostanoligenes_nov_97.059%
Kineothrix alysoides_nov_96.825%
Faecalibacterium prausnitzii_nov_97.964%
Clostridiales_[F−1][G−2] bacterium_HMT_402_nov_89.038%
Oscillibacter ruminantium_nov_93.919%
Alloprevotella rava_nov_92.857%
Lachnospira pectinoschiza_nov_96.372%
Lachnospira eligens_nov_94.785%
unclassified_Ruminococcaceae sp._str._D16_nov_93.243%
Butyrivibrio sp._HMT_090_nov_92.795%
Sporobacter termitidis_nov_90.562%
Paraprevotella clara_nov_97.609%
Prevotella colorans_nov_93.492%
Prevotellamassilia timonensis_nov_97.397%
Eubacterium coprostanoligenes_nov_92.777%
Asteroleplasma anaerobium_nov_80.300%
Succinivibrio dextrinosolvens_nov_97.079%
Eubacterium coprostanoligenes_nov_95.711%
Prevotella oralis_nov_92.641%
Dialister succinatiphilus_nov_96.567%
Duncaniella freteri_nov_87.069%
Ruminococcaceae_[G−2] bacterium_HMT_085_nov_91.422%
Dialister succinatiphilus_nov_96.360%
Oscillibacter ruminantium_nov_95.701%
Fusicatenibacter saccharivorans_nov_97.279%
Lacrimispora xylanolytica_nov_97.285%
Clostridiales_[F−1][G−2] bacterium_HMT_402_nov_91.011%
Monoglobus pectinilyticus_nov_90.112%
Erysipelatoclostridium [Clostridium] spiroforme_nov_93.333%
Lachnoclostridium pacaense_nov_96.145%
Sporobacter termitidis_nov_92.584%
Ruminoclostridium methylpentosum_nov_89.462%
Ruminococcaceae_[G−2] bacterium_HMT_085_nov_92.809%
Agathobaculum desmolans_nov_97.738%
Oscillibacter ruminantium_nov_92.601%
Holdemanella biformis_nov_97.854%
Bacteroides sp._str._4136_uniformis
Anaerostipes_Lacnoclostridium_unclassified_Lachnospiraceae hadr
Lactobacillus_Ligilactobacillus ruminis
Roseburia faecalis_faecis
Blautia_Mediterraneibacter [Ruminococcus] gnavus_gnavus
Blautia_unclassified_Lachnospiraceae sp._str._cont1.79_torques
Lacnoclostridium sp._SM4/1_sp._str._M62/1
Bacteroides_Phocaeicola dorei_sp._Oral_Taxon_D25_sp._str._219_
Bifidobacterium adolescentis_faecale
Escherichia_Shigella coli_dysenteriae_fergusonii_flexneri_sonnei
Blautia obeum_wexlerae
Parasutterella_Sutterella excrementihominis_sp._str._cont1.66
Bacteroides koreensis_kribbi
Bacteroides_Phocaeicola plebeius
Ruminococcus multispecies_sppn1_2_nov_95.023%
Roseburia multispecies_sppn106_3_nov_96.833%
Christensenella multispecies_sppn2_2_nov_91.216%
Clostridium multispecies_sppn27_2_nov_97.959%
Species
F6488.S52
F6488.S53
F6488.S54
F6488.S55
F6488.S56
F6488.S57
F6488.S58
F6488.S59
F6488.S60
F6488.S61
F6488.S62
F6488.S63
F6488.S64
F6488.S65
F6488.S66
F6488.S67
F6488.S68
F6488.S69
F6488.S70
F6488.S71
Samples