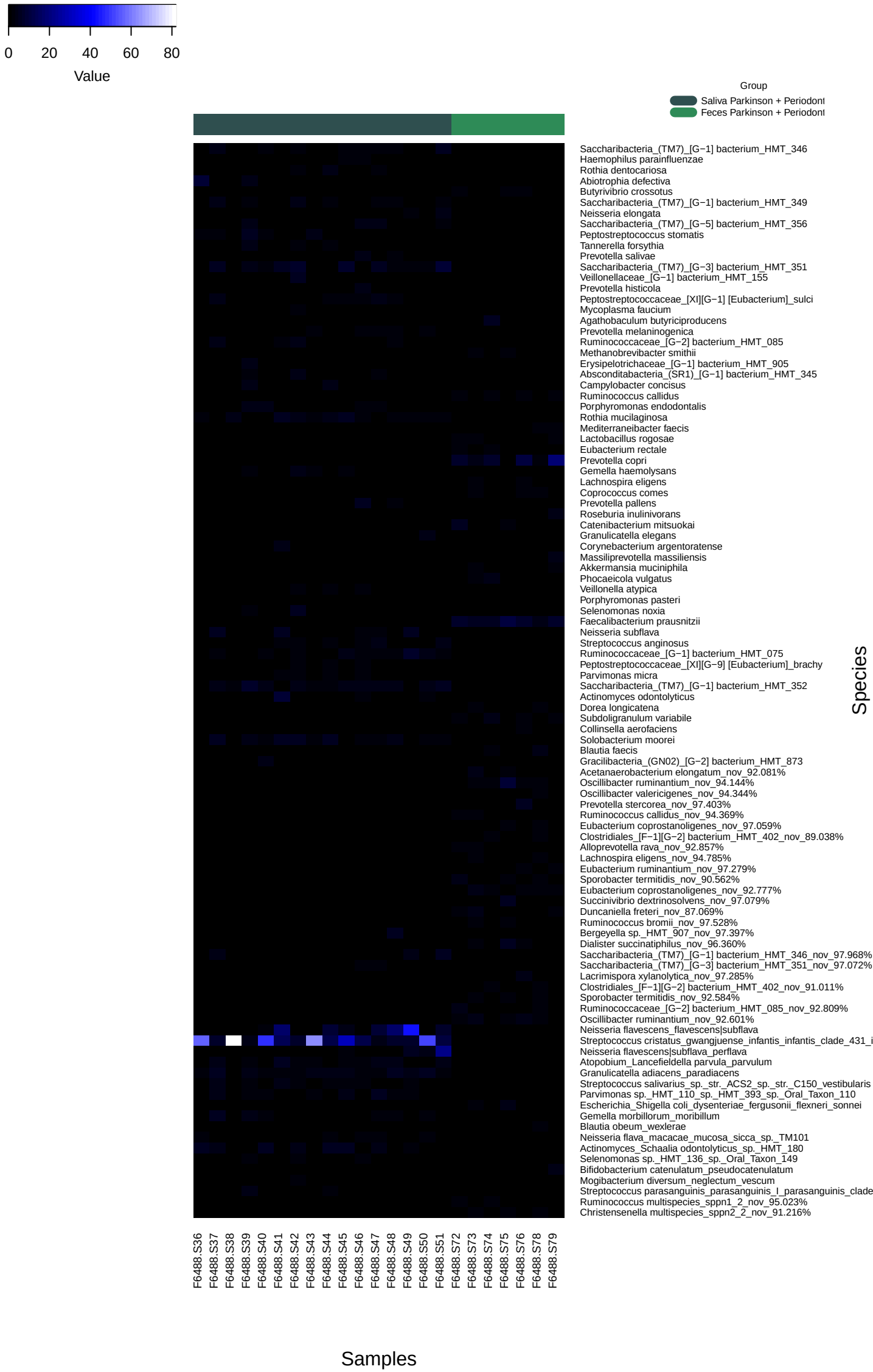
0
20
40
60
80
Value
Group
Saliva Parkinson + Periodont
Feces Parkinson + Periodont
Saccharibacteria_(TM7)_[G−1] bacterium_HMT_346
Haemophilus parainfluenzae
Rothia dentocariosa
Abiotrophia defectiva
Butyrivibrio crossotus
Saccharibacteria_(TM7)_[G−1] bacterium_HMT_349
Neisseria elongata
Saccharibacteria_(TM7)_[G−5] bacterium_HMT_356
Peptostreptococcus stomatis
Tannerella forsythia
Prevotella salivae
Saccharibacteria_(TM7)_[G−3] bacterium_HMT_351
Veillonellaceae_[G−1] bacterium_HMT_155
Prevotella histicola
Peptostreptococcaceae_[XI][G−1] [Eubacterium]_sulci
Mycoplasma faucium
Agathobaculum butyriciproducens
Prevotella melaninogenica
Ruminococcaceae_[G−2] bacterium_HMT_085
Methanobrevibacter smithii
Erysipelotrichaceae_[G−1] bacterium_HMT_905
Absconditabacteria_(SR1)_[G−1] bacterium_HMT_345
Campylobacter concisus
Ruminococcus callidus
Porphyromonas endodontalis
Rothia mucilaginosa
Mediterraneibacter faecis
Lactobacillus rogosae
Eubacterium rectale
Prevotella copri
Gemella haemolysans
Lachnospira eligens
Coprococcus comes
Prevotella pallens
Roseburia inulinivorans
Catenibacterium mitsuokai
Granulicatella elegans
Corynebacterium argentoratense
Massiliprevotella massiliensis
Akkermansia muciniphila
Phocaeicola vulgatus
Veillonella atypica
Porphyromonas pasteri
Selenomonas noxia
Faecalibacterium prausnitzii
Neisseria subflava
Streptococcus anginosus
Ruminococcaceae_[G−1] bacterium_HMT_075
Peptostreptococcaceae_[XI][G−9] [Eubacterium]_brachy
Parvimonas micra
Saccharibacteria_(TM7)_[G−1] bacterium_HMT_352
Actinomyces odontolyticus
Dorea longicatena
Subdoligranulum variabile
Collinsella aerofaciens
Solobacterium moorei
Blautia faecis
Gracilibacteria_(GN02)_[G−2] bacterium_HMT_873
Acetanaerobacterium elongatum_nov_92.081%
Oscillibacter ruminantium_nov_94.144%
Oscillibacter valericigenes_nov_94.344%
Prevotella stercorea_nov_97.403%
Ruminococcus callidus_nov_94.369%
Eubacterium coprostanoligenes_nov_97.059%
Clostridiales_[F−1][G−2] bacterium_HMT_402_nov_89.038%
Alloprevotella rava_nov_92.857%
Lachnospira eligens_nov_94.785%
Eubacterium ruminantium_nov_97.279%
Sporobacter termitidis_nov_90.562%
Eubacterium coprostanoligenes_nov_92.777%
Succinivibrio dextrinosolvens_nov_97.079%
Duncaniella freteri_nov_87.069%
Ruminococcus bromii_nov_97.528%
Bergeyella sp._HMT_907_nov_97.397%
Dialister succinatiphilus_nov_96.360%
Saccharibacteria_(TM7)_[G−1] bacterium_HMT_346_nov_97.968%
Saccharibacteria_(TM7)_[G−3] bacterium_HMT_351_nov_97.072%
Lacrimispora xylanolytica_nov_97.285%
Clostridiales_[F−1][G−2] bacterium_HMT_402_nov_91.011%
Sporobacter termitidis_nov_92.584%
Ruminococcaceae_[G−2] bacterium_HMT_085_nov_92.809%
Oscillibacter ruminantium_nov_92.601%
Neisseria flavescens_flavescens|subflava
Streptococcus cristatus_gwangjuense_infantis_infantis_clade_431_i
Neisseria flavescens|subflava_perflava
Atopobium_Lancefieldella parvula_parvulum
Granulicatella adiacens_paradiacens
Streptococcus salivarius_sp._str._ACS2_sp._str._C150_vestibularis
Parvimonas sp._HMT_110_sp._HMT_393_sp._Oral_Taxon_110
Escherichia_Shigella coli_dysenteriae_fergusonii_flexneri_sonnei
Gemella morbillorum_moribillum
Blautia obeum_wexlerae
Neisseria flava_macacae_mucosa_sicca_sp._TM101
Actinomyces_Schaalia odontolyticus_sp._HMT_180
Selenomonas sp._HMT_136_sp._Oral_Taxon_149
Bifidobacterium catenulatum_pseudocatenulatum
Mogibacterium diversum_neglectum_vescum
Streptococcus parasanguinis_parasanguinis_I_parasanguinis_clade
Ruminococcus multispecies_sppn1_2_nov_95.023%
Christensenella multispecies_sppn2_2_nov_91.216%
Species
F6488.S36
F6488.S37
F6488.S38
F6488.S39
F6488.S40
F6488.S41
F6488.S42
F6488.S43
F6488.S44
F6488.S45
F6488.S46
F6488.S47
F6488.S48
F6488.S49
F6488.S50
F6488.S51
F6488.S72
F6488.S73
F6488.S74
F6488.S75
F6488.S76
F6488.S78
F6488.S79
Samples