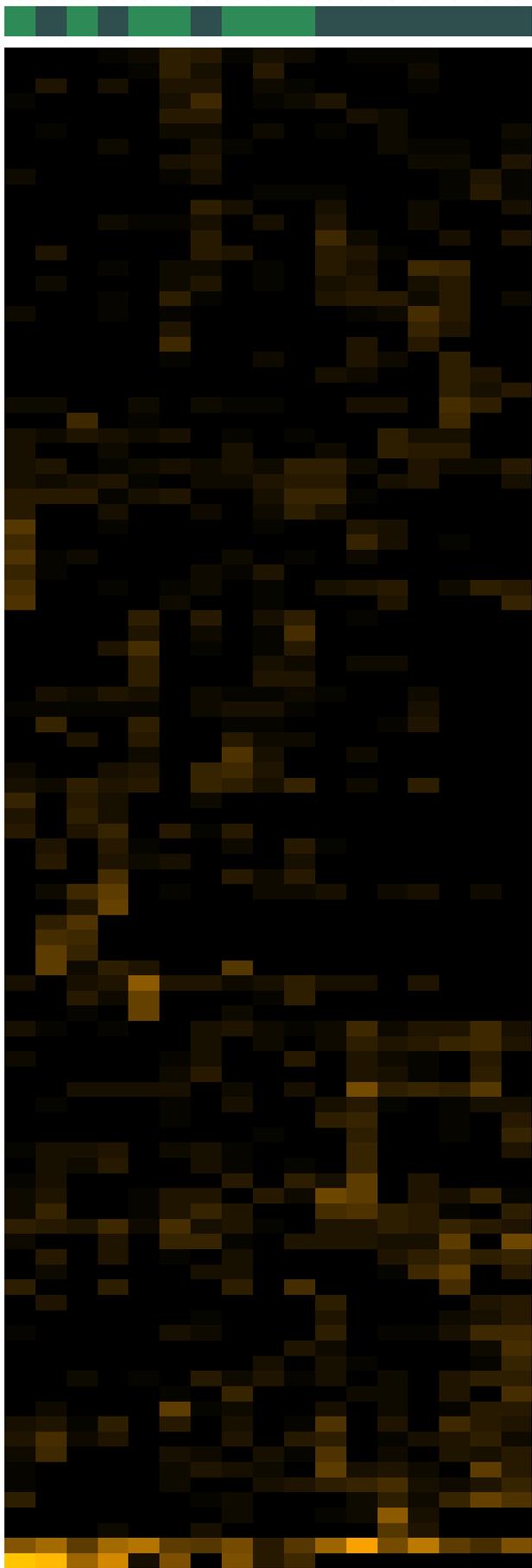


Group
 Feces Healthy Control
 Feces Parkinson + Periodont



- Clostridiales_[F-1][G-2] bacterium_HMT_402_nov_89.038%
- Clostridiales_[F-1][G-2] bacterium_HMT_402_nov_91.011%
- Oscillibacter ruminantium_nov_93.919%
- Sporobacter termitidis_nov_93.243%
- Phascolarctobacterium faecium
- Coprococcus catus
- Dorea formicigenerans
- Barnesiella intestinihominis
- Streptococcus thermophilus
- Bilophila wadsworthia
- Eubacterium ventriosum
- Parabacteroides merdae
- Blautia_unclassified_Lachnospiraceae_sp_str_cont1.79_torques
- Blautia obeum
- Alistipes putredinis
- Ruminococcus bromii
- Monoglobus pectinilyticus_nov_90.112%
- Kineothrix alysoides_nov_96.825%
- Bacteroides stercoris
- Roseburia multispecies_sppn52_2_nov_97.072%
- Faecalibacterium prausnitzii_nov_97.964%
- Parasutterella_Sutterella excrementihominis_sp_str_cont1.66
- Alistipes onderdonkii
- Lacnospirillum sp._SS3/4
- Megasphaera elsdenii
- Collinsella aerofaciens
- Roseburia intestinalis
- Dorea longicatena
- Coprococcus comes
- Eubacterium coprostanoligenes_nov_92.777%
- Akkermansia muciniphila
- Roseburia inulinivorans
- Blautia_Mediterraneibacter [Ruminococcus] lactaris_lactaris
- Massiliprevotella massiliensis
- Mediterraneibacter faecis
- Lacnospirillum pacaense_nov_96.145%
- Bifidobacterium catenulatum_pseudocatenulatum
- Sporobacter termitidis_nov_92.584%
- Acetanaerobacterium elongatum_nov_92.081%
- Escherichia_Shigella coli_dysenteriae_fergusonii_flexneri_sonnei
- Eubacterium coprostanoligenes_nov_97.059%
- Christensenella multispecies_sppn2_2_nov_91.216%
- unclassified_Ruminococcaceae_sp_str_D16_nov_93.243%
- Oscillibacter valericigenes_nov_94.344%
- Coprococcus eutactus
- Butyrivibrio crossotus
- Ruminococcaceae_[G-2] bacterium_HMT_085_nov_92.809%
- Sporobacter termitidis_nov_90.562%
- Oscillibacter ruminantium_nov_92.601%
- Eubacterium ruminantium_nov_97.279%
- Prevotella copri_nov_97.397%
- Ruminococcus callidus
- Ruminoclostridium methylpentosum_nov_89.462%
- Holdemania biformis_nov_97.854%
- Alloprevotella rava_nov_92.857%
- Lacrimispora xylanolytica_nov_97.285%
- Prevotella stercorea
- Prevotella stercorea_nov_97.403%
- Prevotella copri_nov_96.537%
- Prevotella colorans_nov_93.492%
- Catenibacterium mitsuokai
- Oscillibacter ruminantium_nov_94.144%
- Dialister succinatiphilus_nov_96.360%
- Succinivibrio dextrinosolvens_nov_97.079%
- Fusicatenibacter saccharivorans
- Bacteroides sp._str_4136_uniformis
- Bacteroides caccae
- Lachnospira pectinoschiza_nov_96.372%
- Lachnospira eligens
- Eubacterium hallii
- Bifidobacterium longum
- Anaerostipes_Lacnospirillum_unclassified_Lachnospiraceae_hadr
- Eubacterium coprostanoligenes_nov_95.711%
- Lacnospirillum sp._str_L2_50
- Ruminococcus callidus_nov_94.369%
- Blautia faecis
- Ruminococcus multispecies_sppn1_2_nov_95.023%
- Subdoligranulum variabile
- Phocaeicola vulgatus
- Roseburia faecalis_faecis
- Fusicatenibacter saccharivorans_nov_97.279%
- Duncaniella freteri_nov_87.069%
- Dialister succinatiphilus_nov_96.567%
- Oscillibacter ruminantium_nov_95.701%
- Parabacteroides distasonis
- Blautia_Mediterraneibacter [Ruminococcus] gnavus_gnavus
- Eubacterium ramulus
- Blautia obeum_wexlerae
- Bacteroides koreensis_kribbi
- Agathobaculum butyriciproducens
- Eubacterium rectale
- Lactobacillus rogosae
- Blautia luti
- Erysipelatoclostridium [Clostridium] spiroforme_nov_93.333%
- Lachnospira eligens_nov_94.785%
- Lacnospirillum sp._SM4/1_sp_str_M62/1
- Roseburia multispecies_sppn106_3_nov_96.833%
- Bacteroides_Phocaeicola plebeius
- Faecalibacterium prausnitzii
- Prevotella copri

Species

F6488.S79
 F6488.S56
 F6488.S76
 F6488.S54
 F6488.S75
 F6488.S74
 F6488.S52
 F6488.S72
 F6488.S78
 F6488.S73
 F6488.S60
 F6488.S55
 F6488.S57
 F6488.S53
 F6488.S59
 F6488.S58
 F6488.S61

Samples