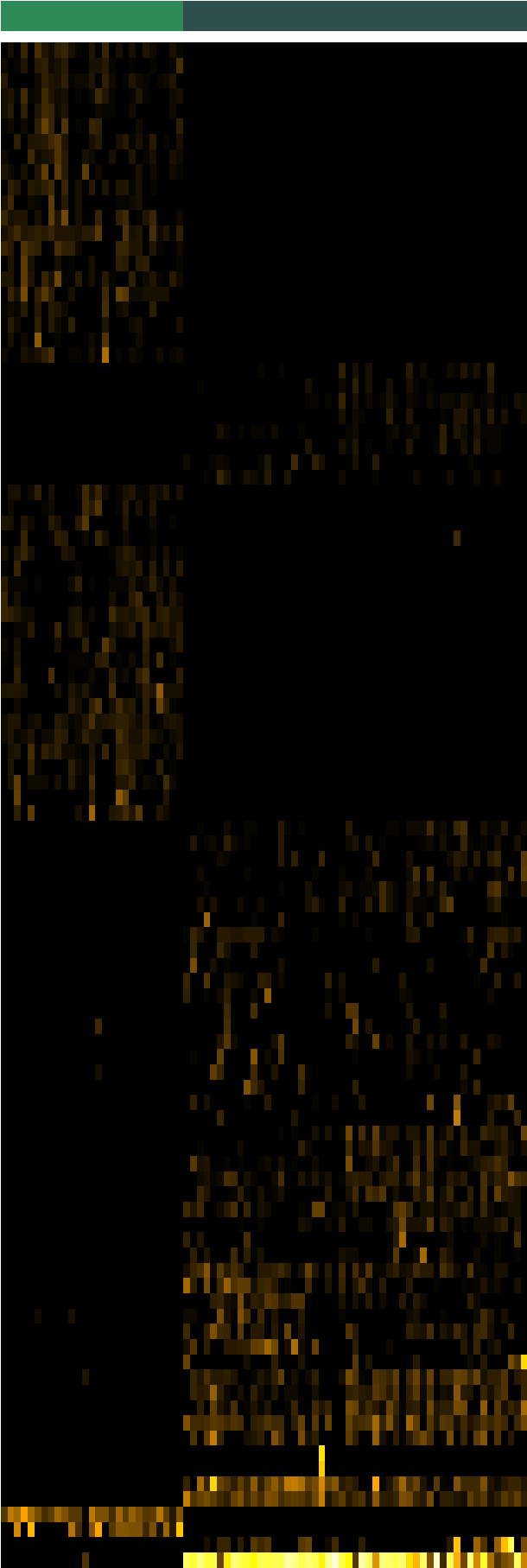
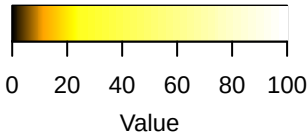




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F6488_S140
F6488_S142
F6488_S144
F6488_S146
F6488_S148
F6488_S150

- Source
- Saliva
 - Feces
- Species
- Lachnospira eligens_nov_94.785%
 - Lachnoclostridium pacaense_nov_96.145%
 - Blautia obeum_wexlerae
 - Fusicatenibacter saccharivorans
 - Bacteroides sp._str_4136_uniformis
 - Lachnoclostridium sp._SM4/1_sp._str_M62/1
 - Eubacterium rectale
 - Blautia luti
 - Erysipelatoclostridium [Clostridium] spiroforme_nov_93.333%
 - Roseburia faecalis_faecis
 - Fusicatenibacter saccharivorans_nov_97.279%
 - Phocaeicola vulgatus
 - Subdoligranulum variabile
 - Ruminococcus multispecies_sppn1_2_nov_95.023%
 - Ruminococcus callidus_nov_94.369%
 - Blautia faecis
 - Lachnospira eligens
 - Monoglobus pectinilyticus_nov_90.112%
 - Roseburia intestinalis
 - Roseburia multispecies_sppn106_3_nov_96.833%
 - Lachnoclostridium sp._SS3/4
 - Peptostreptococcaceae_[XII][G-9] [Eubacterium]_brachy
 - Peptostreptococcaceae_[XII][G-4] bacterium_HMT_369
 - Mycoplasma faucium
 - Parvimonas micra
 - Streptococcus parasanguinis_parasanguinis_I_parasanguinis_clade
 - Tannerella forsythia
 - Streptococcus sanguinis_sp._HMT_074
 - Oribacterium sinus
 - Collinsella aerofaciens
 - Bifidobacterium adolescentis_faecale
 - Ruminococcus bromii
 - Bifidobacterium longum
 - Eubacterium coprostanoligenes_nov_95.711%
 - Ruminococcus callidus
 - Clostridiales_[F-1][G-2] bacterium_HMT_402_nov_89.038%
 - Sporobacter termitidis_nov_90.562%
 - Oscillibacter ruminantium_nov_92.601%
 - Eubacterium coprostanoligenes_nov_92.777%
 - Akkermansia muciniphila
 - Escherichia_Shigella coli_dysenteriae_fergusonii_flexneri_sonnei
 - Duncaniella freteri_nov_87.069%
 - Oscillibacter ruminantium_nov_94.144%
 - Dialister succinatiphilus_nov_96.360%
 - Coprococcus comes
 - Dorea longicatena
 - Lactobacillus rogosae
 - Coprococcus eutactus
 - Lacrimispora xylanolytica_nov_97.285%
 - Prevotella stercorea
 - Catenibacterium mitsuokai
 - Ruminococcaceae_[G-2] bacterium_HMT_085
 - Absconditabacteria_(SR1)_[G-1] bacterium_HMT_345
 - Streptococcus anginosus
 - Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346_nov_97.968%
 - Saccharibacteria_(TM7)_[G-5] bacterium_HMT_356
 - Porphyromonas endodontalis
 - Schaalia sp._HMT_180
 - Prevotella melaninogenica
 - Prevotella pallens
 - Mobiluncus multispecies_sppn34_2_nov_97.817%
 - Bergeyella sp._HMT_322
 - Capnocytophaga gingivalis
 - Schaalia sp._HMT_172
 - Veillonella parvula_tobetsuensis
 - Selenomonas sp._HMT_136_sp._Oral_Taxon_149
 - Actinomyces graevenitzi
 - Veillonella dispar_parvula
 - Actinomyces sp._HMT_169_sp._str_ChDCB197
 - Neisseria subflava
 - Actinomyces odontolyticus
 - Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346
 - Saccharibacteria_(TM7)_[G-1] bacterium_HMT_349
 - Peptostreptococcaceae_[XII][G-1] [Eubacterium]_sulci
 - Ruminococcaceae_[G-1] bacterium_HMT_075
 - Parvimonas sp._HMT_110_sp._HMT_393_sp._Oral_Taxon_110
 - Gemella haemolysans
 - Gemella morbillorum_moribillum
 - Granulicatella elegans
 - Abiotrophia defectiva
 - Peptostreptococcus stomatis
 - Porphyromonas pasteri
 - Gemella sanguinis
 - Haemophilus parainfluenzae
 - Streptococcus salivarius_sp._str_ACS2_sp._str_C150_vestibularis
 - Rothia dentocariosa
 - Neisseria flavescens|subflava_perflava
 - Solobacterium moorei
 - Atopobium_Lancefieldella parvula_parvulum
 - Saccharibacteria_(TM7)_[G-3] bacterium_HMT_351
 - Saccharibacteria_(TM7)_[G-1] bacterium_HMT_352
 - Actinomyces_Schaalia odontolyticus_sp._HMT_180
 - Enterobacter mori
 - Enterobacter cloacae
 - Rothia mucilaginosa
 - Granulicatella adiacens_paradiacens
 - Faecalibacterium prausnitzii
 - Prevotella copri
 - Neisseria flavescens_flavescens|subflava
 - Streptococcus cristatus_gwangjuense_infantis_infantis_clade_431_i

Samples