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F6488.S134
F6488.S136
F6488.S138
F6488.S140
F6488.S142
F6488.S144
F6488.S146
F6488.S148
F6488.S150

Source
Saliva
Feces

- Roseburia intestinalis
- Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346
- Schaalia sp._HMT_180
- Haemophilus parainfluenzae
- Rothia dentocariosa
- Abiotrophia defectiva
- Saccharibacteria_(TM7)_[G-1] bacterium_HMT_349
- Schaalia sp._HMT_172
- Saccharibacteria_(TM7)_[G-5] bacterium_HMT_356
- Peptostreptococcus stomatis
- Tannerella forsythia
- Saccharibacteria_(TM7)_[G-3] bacterium_HMT_351
- Bergeyella sp._HMT_322
- Fusicatenibacter saccharivorans
- Peptostreptococcaceae_[XII][G-1] [Eubacterium]_sulci
- Mycoplasma faucium
- Agathobaculum butyriciproducens
- Oribacterium sinus
- Prevotella melaninogenica
- Ruminococcaceae_[G-2] bacterium_HMT_085
- Methanobrevibacter smithii
- Gemella sanguinis
- Absconditabacteria_(SR1)_[G-1] bacterium_HMT_345
- Ruminococcus callidus
- Actinomyces graevenitzi
- Porphyromonas endodontalis
- Rothia mucilaginosa
- Lactobacillus rogosae
- Eubacterium rectale
- Coprococcus eutactus
- Capnocytophaga gingivalis
- Prevotella copri
- Gemella haemolysans
- Blautia luti
- Lachnospira eligens
- Lacnospirillum sp._SS3/4
- Coprococcus comes
- Prevotella pallens
- Ruminococcus bromii
- Catenibacterium mitsuokai
- Granulicatella elegans
- Prevotella stercora
- Akkermansia muciniphila
- Phocaeicola vulgatus
- Porphyromonas pasteri
- Faecalibacterium prausnitzii
- Neisseria subflava
- Streptococcus anginosus
- Ruminococcaceae_[G-1] bacterium_HMT_075
- Peptostreptococcaceae_[XII][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
- Bifidobacterium longum
- Oscillibacter ruminantium_nov_94.144%
- Ruminococcus callidus_nov_94.369%
- Clostridiales_[F-1][G-2] bacterium_HMT_402_nov_89.038%
- Lachnospira eligens_nov_94.785%
- Sporobacter termitidis_nov_90.562%
- Eubacterium coprostanoligenes_nov_92.777%
- Succinivibrio dextrinosolvens_nov_97.079%
- Eubacterium coprostanoligenes_nov_95.711%
- Duncaniella freteri_nov_87.069%
- Dialister succinatiphilus_nov_96.360%
- Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346_nov_97.968%
- Fusicatenibacter saccharivorans_nov_97.279%
- Lacrimispora xylanolytica_nov_97.285%
- Monoglobus pectinilyticus_nov_90.112%
- Erysipelatoclostridium [Clostridium]_spiroforme_nov_93.333%
- Lachnoclostridium pacaense_nov_96.145%
- Sporobacter termitidis_nov_92.584%
- Oscillibacter ruminantium_nov_92.601%
- Bacteroides sp._str_4136_uniformis
- Neisseria flavescens_flavescens[subflava
- Streptococcus cristatus_gwangjuense_infantis_infantis_clade_431_i
- Neisseria flavescens[subflava_perflava
- Streptococcus sanguinis_sp_HMT_074
- Atopobium_Lancefieldella parvula_parvulum
- Roseburia faecalis_faecis
- Granulicatella adiacens_padiaciens
- Lacnospirillum sp._SM4/1_sp._str_M62/1
- Streptococcus salivarius_sp._str_ACS2_sp._str_C150_vestibularis
- Parvimonas sp._HMT_110_sp._HMT_393_sp._Oral_Taxon_110
- Bifidobacterium adolescentis_faecale
- Escherichia_Shigella coli_dysenteriae_fergusonii_flexneri_sonnei
- Gemella morbillorum_moribillum
- Blautia obeum_wexlerae
- Actinomyces_Schaalia odontolyticus_sp_HMT_180
- Selenomonas sp._HMT_136_sp._Oral_Taxon_149
- Veillonella dispar_parvula
- Veillonella parvula_tobetsuensis
- Actinomyces sp._HMT_169_sp._str_ChDCB197
- Streptococcus parasanguinis_parasanguinis_l_parasanguinis_clade
- Ruminococcus multispecies_sppn1_2_nov_95.023%
- Roseburia multispecies_sppn106_3_nov_96.833%

Species

Samples