Significantly Represented Taxa

Legend: ■ negative ■ positive

Taxa	LDA Score (log 10)
P_Firmicutes	positive
C_Clostridia	positive
O_Clostridiales	positive
G_Rothia	positive
F_Micrococcaceae	positive
O_Micrococcales	positive
S_mucilaginosa	positive
F_Peptostreptococcaceae__XI_	positive
F_Lachnospiraceae__XIV_	positive
S_adiacens	positive
S_multispecies_spp162_4	positive
S_multispecies_spp123_7	positive
O_Negativicutes	positive
F_Veillonellaceae	positive
G_Veillonella	positive
S_multispecies_spp91_3	positive
S_multispecies_spp88_4	positive
S_multispecies_spp81_2	positive
G_Oribacterium	positive
G_Schaalia	positive
F_Actinomycetaceae	positive
O_Actinomycetales	positive
C_Actinobacteria	positive
S_sinus	positive
S_stomatis	positive
G_Peptostreptococcus	positive
G_Stomatobaculum	positive
F_Peptoniphilaceae	positive
S_micra	positive
G_Parvimonas	positive
S_sp__HMT_172	positive
S_timonensis	positive
G_Romboutsia	positive
S_sp__HMT_097	positive
C_Coriobacteriia	positive
O_Eubacteriales	positive
O_Coriobacteriales	positive
S_dispar	positive
G_Lachnoanaerobaculum	positive
F_multifamily	positive
S_multispecies_spp21_2	positive
G_multigenus	positive
G_Mogibacterium	positive
S_difficile	positive
G_Clostridioides	positive
O_Erysipelotrichales	positive
C_Erysipelotrichia	positive
F_Erysipelotrichaceae	positive
S_graevenitzii	positive
S_multispecies_spp82_4	positive
S_moorei	positive
G_Solobacterium	positive
F_Peptostreptococcaceae	positive
S_multispecies_spp145_3	positive
S_Eubacterium__brachy	positive
G_Peptostreptococcaceae__XI_G_9_	positive
G_Peptostreptococcaceae__XI_G_1_	positive
S_multispecies_spp16_2	positive
S_Eubacterium__sulci	positive
S_asaccharolyticum	positive
S_lingnae_Not_Validly_Published_	positive
G_Fretibacterium	positive
F_Synergistaceae	positive
O_Synergistales	positive
C_Synergistia	positive
P_Synergistetes	positive
S_anginosus	positive
S_sp__HMT_078	positive
S_sp__HMT_360	positive
S_timidum	positive
S_sp__HMT_894	positive
G_Ottowia	positive
F_Comamonadaceae	positive
G_Pseudoramibacter	positive
S_alactolyticus	positive
S_morbi	positive
F_Eubacteriaceae	positive
G_Veillonellaceae__G_1_	positive
S_bacterium_HMT_155	positive
S_parvum	positive
G_Johnsonella	positive
G_Peptidiphaga	positive
S_sp__HMT_044	positive
G_Catonella	positive
S_sp__HMT_166	positive
S_sp__HMT_455	positive
S_gingivicola	positive
S_sp__HMT_183	positive
G_Peptostreptococcaceae__XI_G_2_	positive
S_bacterium_HMT_091	positive
S_satelles	positive
G_Shuttleworthia	positive
S_sp_HMT_102	negative
S_bacterium_HMT_505	negative
S_amylovorum	negative
S_sp__HMT_246	negative
S_bacterium_HMT_507	negative
S_sp__HMT_012	negative
S_fusca	negative
S_multispecies_spp141_2	negative
S_mutans	negative
S_sp__HMT_907	negative
S_actinomycetemcomitans	negative
S_multispecies_spp159_7	negative
F_Enterobacteriaceae	negative
G_multigenus	negative
O_Enterobacterales	negative
G_Kocuria	negative
S_multispecies_spp42_2	negative
S_multispecies_spp129_2	negative
S_denticola	negative
S_multispecies_spp59_2	negative
S_sp__HMT_930	negative

X-axis: LDA SCORE (log 10), ranging from -4 to 5