Significantly Represented Taxa
O_Clostridiales
C_Clostridia
F_Peptostreptococcaceae_XI_
P_Firmicutes
F_Peptoniphilaceae
G_Paviminas
S_micra
G_Peptostreptococcaceae_XI_G_4_
S_bacterium_HMT_369
G_Peptostreptococcaceae_XI_G_9
S__Eubacterium__brachy
G_Peptostreptococcaceae_XI_G_6_
S__Eubacterium__nodatum
S_bacterium_HMT_103
S__Eubacterium__saphenum
G_Peptostreptococcaceae_XI_G_5_
S_sp__HMT_110
S_Japonicum_nov_86_848
G_Desulfoglaranum
S_timidum
G_Mogibacterium
S_micra_nov_93_971
S__Eubacterium_brachy_nov_96_050
S_micra_nov_95_426
S__Eubacterium__nodatum_nov_95_218
S_spelunceae
O_Rhodobacterales
G_Paracoccus
F_Rhodobacteraceae
S_sp__HMT_237
S_hominis
G_Peptococcus
F_Methylobacteriaceae
S_aphrophilus
S_sp__HMT_169
S_saprophyticus
O_Phyphomicrobiales
S_putida
S_stomalis
S_nucleatum
G_Dialister
S_sp__HMT_167
G_Peptostreptococcus
S_mvilusi
S_socranskii
S_intermedius
F_Comamonadaceae
G_Schaalia
S_nucleatum_subsp__animalis
C_Actinobacteria
S_endodontalis
O_Enterobacterales
F_Peptococcaceae
F_Actinomycetaceae
O_Actinomycetales
S_fluenggei
S_sp__HMT_417
S_meyeri
F_Bacteroidales__F_2_
S_bacterium_HMT_346
G_Bacteroidales__G_2_
S_oris
F_Enterobacteriaceae
S_bacterium_HMT_274
G_Enterobacter
S_sp__HMT_212
S_fastidiosum
S_adhaerens
S_elongata
S_sinensis
S_morbillorum
S_multispecies_spp8_18
G_Tannerella
S_multispecies_spp10_20
G_Fretibacterium
S_multispecies_spp47_2
S_multispecies_spp114_3
P_Synergistetes
F_Synergistaceae
C_Synergistia
S_granulosa
C_Spirochaetia
S_saccharii
G_Treponema
F_Treponemataceae
F_Moraxellaceae
S_multispecies_spp22_3
G_Psychrobacter
O_Moraxellales
O_Synergistales
C_Flavobacteriia
F_Flavobacteriaceae
O_Spirochaetales
G_Catonella
S_concisus
O_Flavobacteriales
G_Peptostreptococcaceae_XI_G_2_
P_Spirochaetes
G_Lachnoanaerobaculum
G_Capnocytophaga
G_Lachnospiraceae__G_3_
S_lactarius
S_multispecies_spp2_2
F_Actinomycetaceae
G_Actinomyces
G_Absiitrophia
S_sp__HMT_146
O_Actinomycetales
S_multispecies_spp40_3
S_sp__HMT_134
S_defectiva
S_bacterium_HMT_100
S_multispecies_spp72_3
G_Eikenella
F_Aerococcaceae
S_hongkongensis
S_salivarium
S_cornodens
S_parvula
S_multispecies_spp36_3
G_Filifactor
F_multifamily
S_alocis
S_multispecies_spp94_2
G_multigenus
F_Lachnospiraceae
S_nucleatum_subsp__vincentii
S_multispecies_spp81_6
F_Bacillaceae
G_Cardiobacterium
O_Cardiobacteriales
F_Cardiobacteriaceae
F_Saccharibacteria__TM7___F_1_
S_multispecies_spp7_2
G_parahaemolyticus
O_Saccharibacteria__TM7___O_1_
G_Gemella
F_Gemellaceae
G_Saccharibacteria__TM7___G_1_
C_Saccharibacteria__TM7___C_1_
P_Saccharibacteria__TM7_
S_multispecies_spp39_2
G_Haemophilus
O_Sphingomonadales
F_Sphingomonadaceae
G_Sphingomonas
F_Staphylococcaceae
G_Staphylococcus
G_Porphyromonas
S_aeria
G_Rothia
F_Micrococcaceae
O_Micrococcales
S_bacterium_HMT_155
S_buccalis
G_Neisseria
G_Granulicatella
S_saburreum
F_Porphyromonadaceae
F_Carnobacteriaceae
G_Prevotella
S_multispecies_spp104_3
F_Prevotellaceae
G_Veillonellaceae__G_1_
S_gordonii_nov_95_814
S_acines
F_Propionibacteriaceae
S_noxia
C_Actinomycetia
C_Cutibacterium
P_Actinobacteria
F_Neisseriaceae
O_Neisseriales
O_Veillonellales
F_Veillonellaceae
S_shuzenii
S_sanguinis
G_Stutzerimonas
F_multifamily
S_warneri
S_multispecies_spp122_2
G_Lautropia
S_mirabilis
F_Burkholderiaceae
S_sp__HMT_498
G_Aggregatibacter
S_multispecies_spp34_17_nov_95_592
G_multigenus
O_multiorder
C_multiclass
S_pseudoporcinus_nov_93_488
S_sputigena
S_dispar
S_multispecies_spp118_2
O_Bacillales
S_multispecies_spp62_3
G_Pelomonas
G_Pseudomonas
F_Pseudomonadaceae
S_aquatica
S_faecalis
F_Enterococcaceae
G_Enterococcus
F_Pasteurellaceae
O_Pasteurellales
C_Bacteroidia
O_Bacteroidales
O_Pseudomonadales
O_Negativicutes
F_Veillonellaceae
G_Veillonella
S_gordonii
P_Bacteroidetes
S_multispecies_spp23_2_nov_96_512
O_Fusobacteriales
F_Leptotrichiaceae
C_Fusobacteria
G_Leptotrichia
F_Selenomonadaceae
G_Selenomonas
O_Selenomonadales
S_nanshinii
S_sp__HMT_203
F_Lachnospiraceae_XIV_
C_Negativicutes
O_Desulfobulbus
C_Gammaproteobacteria
S_sp__HMT_041
S_multispecies_spp53_3
G_Janthinobacterium
F_Oxalobacteraceae
G_Fusobacterium
C_Fusobacteria
F_Fusobacteriaceae
O_Fusobacteriales
O_Burkholderiales
C_Betaproteobacteria
P_Fusobacteria
S_gracilis
O_Campylobacterales
C_Epsilonproteobacteria
F_Campylobacteraceae
G_Campylobacter
S_multispecies_spp12_17
G_Streptococcus
F_Streptococcaceae
O_Lactobacillales
C_Bacilli
P_Proteobacteria
−6.0
−4.8
−3.6
−2.4
−1.2
0.0
1.2
2.4
3.6
4.8
6.0
LDA SCORE (log 10)