Significantly Represented Taxa

Legend: Control_Endo_Before (red), Control_Perio_Before (green)

LDA SCORE (log 10)

Control_Perio_Before (green bars):
- F_Streptococcaceae
- G_Streptococcus
- O_Lactobacillales
- S_sanguinis
- C_Epsilonproteobacteria
- O_Campylobacterales
- F_Campylobacteraceae
- G_Campylobacter
- S_multispecies_spp77_17
- O_Negativicutes
- G_Veillonella
- F_Veillonellaceae
- S_gracilis
- C_Betaproteobacteria
- O_Neisseriales
- F_Neisseriaceae
- G_Neisseria
- S_dispar
- P_Spirochaetes
- O_Spirochaetales
- C_Spirochaetia
- G_Treponema
- F_Treponemataceae
- S_intermedius
- S_haemolyticus
- S_multispecies_spp53_2
- G_Filifactor
- S_alocis
- S_nucleatum_subsp__vincentii
- O_Actinomycetales
- G_Actinomyces
- F_Actinomycetaceae
- S_multispecies_spp164_4
- S__Eubacterium__brachy
- G_Peptostreptococcaceae__XI__G_9_
- S_multispecies_spp248_2
- S_socranskii
- G_Aggregatibacter
- S_lactarius
- G_Bacteroidales__G_2_
- F_Bacteroidales__F_2_
- S_bacterium_HMT_274
- F_Prevotellaceae
- G_Prevotella
- S_oris
- S_sp__HMT_237
- S_multispecies_spp174_2
- S_gordonii
- F_Carnobacteriaceae
- F_Aerococcaceae
- S_multispecies_spp16_2
- O_Actinomycetales
- F_Actinomycetaceae
- S_adiacens
- G_Granulicatella
- G_Catonella
- S_gerencseriae
- S_nucleatum
- F_Moraxellaceae
- F_Selenomonadaceae
- G_Selenomonas
- O_Moraxellales
- G_Acinetobacter
- F_Burkholderiaceae
- O_Selenomonadales
- G_Lachnoanaerobaculum
- F_multifamily
- O_multiorder
- G_Lautropia
- S_mirabilis
- S_multispecies_spp142_2
- S_multispecies_spp184_2
- S_denticariosi
- G_multigenus
- S_haemolysans
- G_Eikenella
- S_aphrophilus
- S_pleuritidis
- O_Flavobacteriales
- G_Capnocytophaga
- C_Flavobacteriia
- F_Flavobacteriaceae
- S_noxia
- S_parvula
- G_Comamonas
- S_faecalis_nov_97_674
- S_corrodens
- S_multispecies_spp49_4

Control_Endo_Before (red bars):
- F_Gemellaceae
- G_Gemella
- S_multispecies_spp187_2
- S_faecalis
- S_bacterium_HMT_383
- O_Corynebacteriales
- F_Corynebacteriaceae
- G_Corynebacterium
- G_Bacteroidaceae__G_1_
- F_Bacteroidaceae
- S_bacterium_HMT_272
- F_Enterococcaceae
- G_Enterococcus
- S__Eubacterium__infirmum
- G_Pseudoramibacter
- S_alactolyticus
- F_Eubacteriaceae
- S_sinensis
- G_Peptostreptococcaceae__XI__G_1_
- F_Sphingomonadaceae
- O_Sphingomonadales
- G_Sphingomonas
- S_multispecies_spp216_6

X-axis: LDA SCORE (log 10), values from -6.0 to 6.0