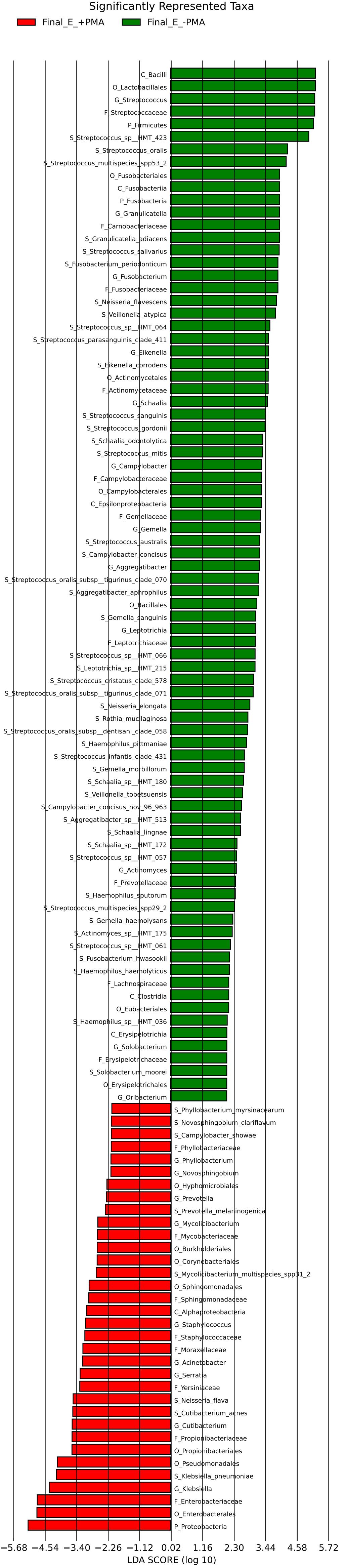
Significantly Represented Taxa
Final_E_+PMA
Final_E_-PMA
C_Bacilli
O_Lactobacillales
G_Streptococcus
F_Streptococcaceae
P_Firmicutes
S_Streptococcus_sp__HMT_423
S_Streptococcus_oralis
S_Streptococcus_multispecies_spp53_2
O_Fusobacteriales
C_Fusobacteriia
P_Fusobacteria
G_Granulicatella
F_Carnobacteriaceae
S_Granulicatella_adiacens
S_Streptococcus_salivarius
S_Fusobacterium_periodonticum
G_Fusobacterium
F_Fusobacteriaceae
S_Neisseria_flavescens
S_Veillonella_atypica
S_Streptococcus_sp__HMT_064
S_Streptococcus_parasanguinis_clade_411
G_Eikenella
S_Eikenella_corrodens
O_Actinomycetales
F_Actinomycetaceae
G_Schaalia
S_Streptococcus_sanguinis
S_Streptococcus_gordonii
S_Schaalia_odontolytica
S_Streptococcus_mitis
G_Campylobacter
F_Campylobacteraceae
O_Campylobacterales
C_Epsilonproteobacteria
F_Gemellaceae
G_Gemella
S_Streptococcus_australis
S_Campylobacter_concisus
G_Aggregatibacter
S_Streptococcus_oralis_subsp__tigurinus_clade_070
S_Aggregatibacter_aphrophilus
O_Bacillales
S_Gemella_sanguinis
G_Leptotrichia
F_Leptotrichiaceae
S_Streptococcus_sp__HMT_066
S_Leptotrichia_sp__HMT_215
S_Streptococcus_cristatus_clade_578
S_Streptococcus_oralis_subsp__tigurinus_clade_071
S_Neisseria_elongata
S_Rothia_mucilaginosa
S_Streptococcus_oralis_subsp__dentisani_clade_058
S_Haemophilus_pittmaniae
S_Streptococcus_infantis_clade_431
S_Gemella_morbillorum
S_Schaalia_sp__HMT_180
S_Veillonella_tobetsuensis
S_Campylobacter_concisus_nov_96_963
S_Aggregatibacter_sp__HMT_513
S_Schaalia_lingnae
S_Schaalia_sp__HMT_172
S_Streptococcus_sp__HMT_057
G_Actinomyces
F_Prevotellaceae
S_Haemophilus_sputorum
S_Streptococcus_multispecies_spp29_2
S_Gemella_haemolysans
S_Actinomyces_sp__HMT_175
S_Streptococcus_sp__HMT_061
S_Fusobacterium_hwasookii
S_Haemophilus_haemolyticus
F_Lachnospiraceae
C_Clostridia
O_Eubacteriales
S_Haemophilus_sp__HMT_036
C_Erysipelotrichia
G_Solobacterium
F_Erysipelotrichaceae
S_Solobacterium_moorei
O_Erysipelotrichales
G_Oribacterium
S_Phyllobacterium_myrsinacearum
S_Novosphingobium_clariflavum
S_Campylobacter_showae
F_Phyllobacteriaceae
G_Phyllobacterium
G_Novosphingobium
O_Hyphomicrobiales
G_Prevotella
S_Prevotella_melaninogenica
G_Mycolicibacterium
F_Mycobacteriaceae
O_Burkholderiales
O_Corynebacteriales
S_Mycolicibacterium_multispecies_spp31_2
O_Sphingomonadales
F_Sphingomonadaceae
C_Alphaproteobacteria
G_Staphylococcus
F_Staphylococcaceae
F_Moraxellaceae
G_Acinetobacter
G_Serratia
F_Yersiniaceae
S_Neisseria_flava
S_Cutibacterium_acnes
G_Cutibacterium
F_Propionibacteriaceae
O_Propionibacteriales
O_Pseudomonadales
S_Klebsiella_pneumoniae
G_Klebsiella
F_Enterobacteriaceae
O_Enterobacterales
P_Proteobacteria
−5.68
−4.54
−3.40
−2.26
−1.12
0.02
1.16
2.30
3.44
4.58
5.72
LDA SCORE (log 10)