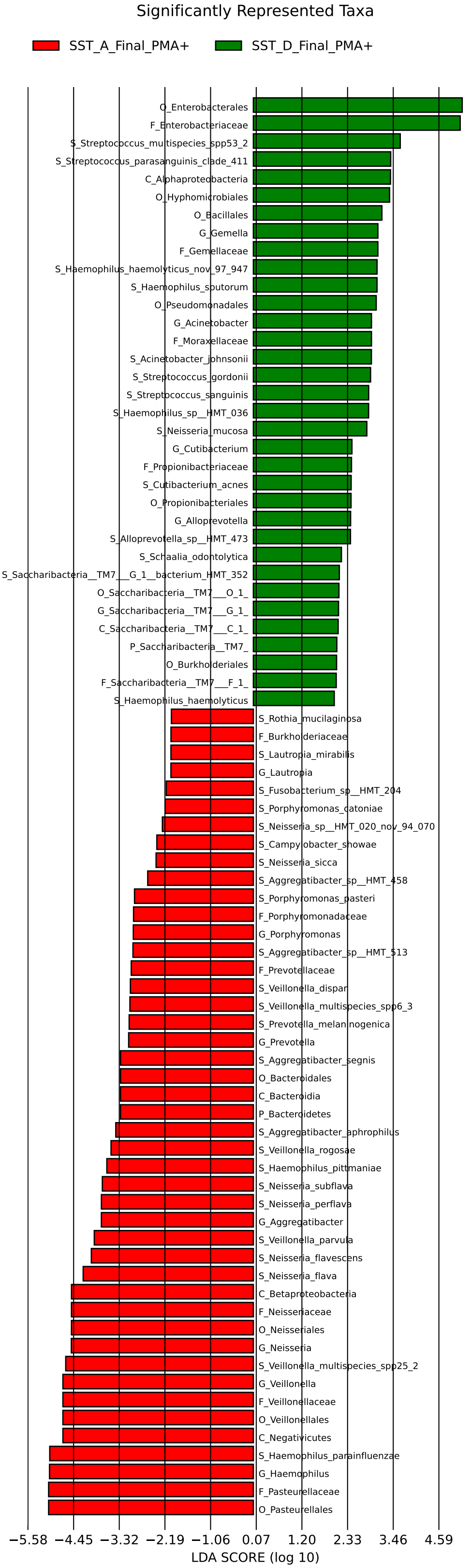
Significantly Represented Taxa
SST_A_Final_PMA+
SST_D_Final_PMA+
O_Enterobacterales
F_Enterobacteriaceae
S_Streptococcus_multispecies_spp53_2
S_Streptococcus_parasanguinis_clade_411
C_Alphaproteobacteria
O_Hyphomicrobiales
O_Bacillales
G_Gemella
F_Gemellaceae
S_Haemophilus_haemolyticus_nov_97_947
S_Haemophilus_sputorum
O_Pseudomonadales
G_Acinetobacter
F_Moraxellaceae
S_Acinetobacter_johnsonii
S_Streptococcus_gordonii
S_Streptococcus_sanguinis
S_Haemophilus_sp__HMT_036
S_Neisseria_mucosa
G_Cutibacterium
F_Propionibacteriaceae
S_Cutibacterium_acnes
O_Propionibacteriales
G_Alloprevotella
S_Alloprevotella_sp__HMT_473
S_Schaalia_odontolytica
S_Saccharibacteria__TM7___G_1__bacterium_HMT_352
O_Saccharibacteria__TM7___O_1_
G_Saccharibacteria__TM7___G_1_
C_Saccharibacteria__TM7___C_1_
P_Saccharibacteria__TM7_
O_Burkholderiales
F_Saccharibacteria__TM7___F_1_
S_Haemophilus_haemolyticus
S_Rothia_mucilaginosa
F_Burkholderiaceae
S_Lautropia_mirabilis
G_Lautropia
S_Fusobacterium_sp__HMT_204
S_Porphyromonas_catoniae
S_Neisseria_sp__HMT_020_nov_94_070
S_Campylobacter_showae
S_Neisseria_sicca
S_Aggregatibacter_sp__HMT_458
S_Porphyromonas_pasteri
F_Porphyromonadaceae
G_Porphyromonas
S_Aggregatibacter_sp__HMT_513
F_Prevotellaceae
S_Veillonella_dispar
S_Veillonella_multispecies_spp6_3
S_Prevotella_melaninogenica
G_Prevotella
S_Aggregatibacter_segnis
O_Bacteroidales
C_Bacteroidia
P_Bacteroidetes
S_Aggregatibacter_aphrophilus
S_Veillonella_rogosae
S_Haemophilus_pittmaniae
S_Neisseria_subflava
S_Neisseria_perflava
G_Aggregatibacter
S_Veillonella_parvula
S_Neisseria_flavescens
S_Neisseria_flava
C_Betaproteobacteria
F_Neisseriaceae
O_Neisseriales
G_Neisseria
S_Veillonella_multispecies_spp25_2
G_Veillonella
F_Veillonellaceae
O_Veillonellales
C_Negativicutes
S_Haemophilus_parainfluenzae
G_Haemophilus
F_Pasteurellaceae
O_Pasteurellales
−5.58
−4.45
−3.32
−2.19
−1.06
0.07
1.20
2.33
3.46
4.59
LDA SCORE (log 10)