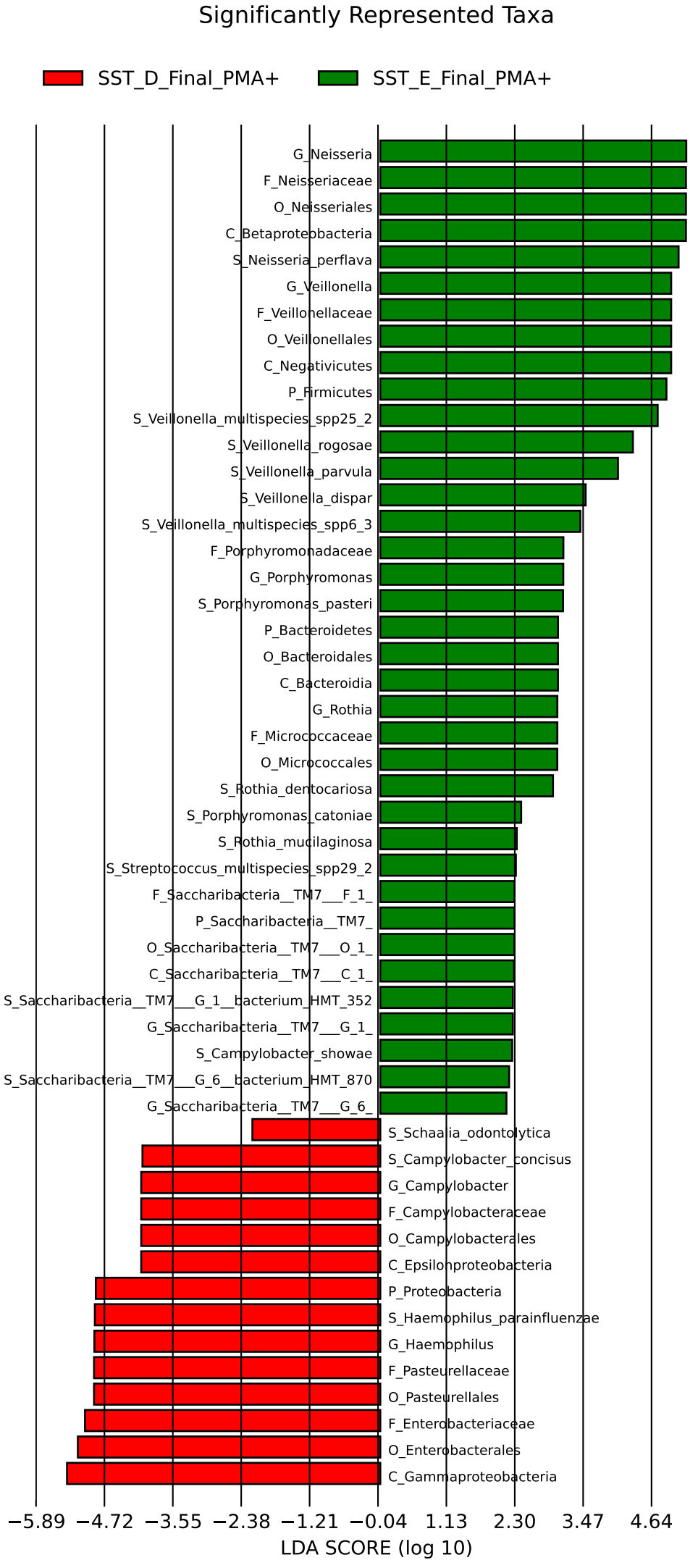
Significantly Represented Taxa
SST_D_Final_PMA+
SST_E_Final_PMA+
G_Neisseria
F_Neisseriaceae
O_Neisseriales
C_Betaproteobacteria
S_Neisseria_perflava
G_Veillonella
F_Veillonellaceae
O_Veillonellales
C_Negativicutes
P_Firmicutes
S_Veillonella_multispecies_spp25_2
S_Veillonella_rogosae
S_Veillonella_parvula
S_Veillonella_dispar
S_Veillonella_multispecies_spp6_3
F_Porphyromonadaceae
G_Porphyromonas
S_Porphyromonas_pasteri
P_Bacteroidetes
O_Bacteroidales
C_Bacteroidia
G_Rothia
F_Micrococcaceae
O_Micrococcales
S_Rothia_dentocariosa
S_Porphyromonas_catoniae
S_Rothia_mucilaginosa
S_Streptococcus_multispecies_spp29_2
F_Saccharibacteria__TM7___F_1_
P_Saccharibacteria__TM7_
O_Saccharibacteria__TM7___O_1_
C_Saccharibacteria__TM7___C_1_
S_Saccharibacteria__TM7___G_1__bacterium_HMT_352
G_Saccharibacteria__TM7___G_1_
S_Campylobacter_showae
S_Saccharibacteria__TM7___G_6__bacterium_HMT_870
G_Saccharibacteria__TM7___G_6_
S_Schaalia_odontolytica
S_Campylobacter_concisus
G_Campylobacter
F_Campylobacteraceae
O_Campylobacterales
C_Epsilonproteobacteria
P_Proteobacteria
S_Haemophilus_parainfluenzae
G_Haemophilus
F_Pasteurellaceae
O_Pasteurellales
F_Enterobacteriaceae
O_Enterobacterales
C_Gammaproteobacteria
−5.89
−4.72
−3.55
−2.38
−1.21
−0.04
1.13
2.30
3.47
4.64
LDA SCORE (log 10)