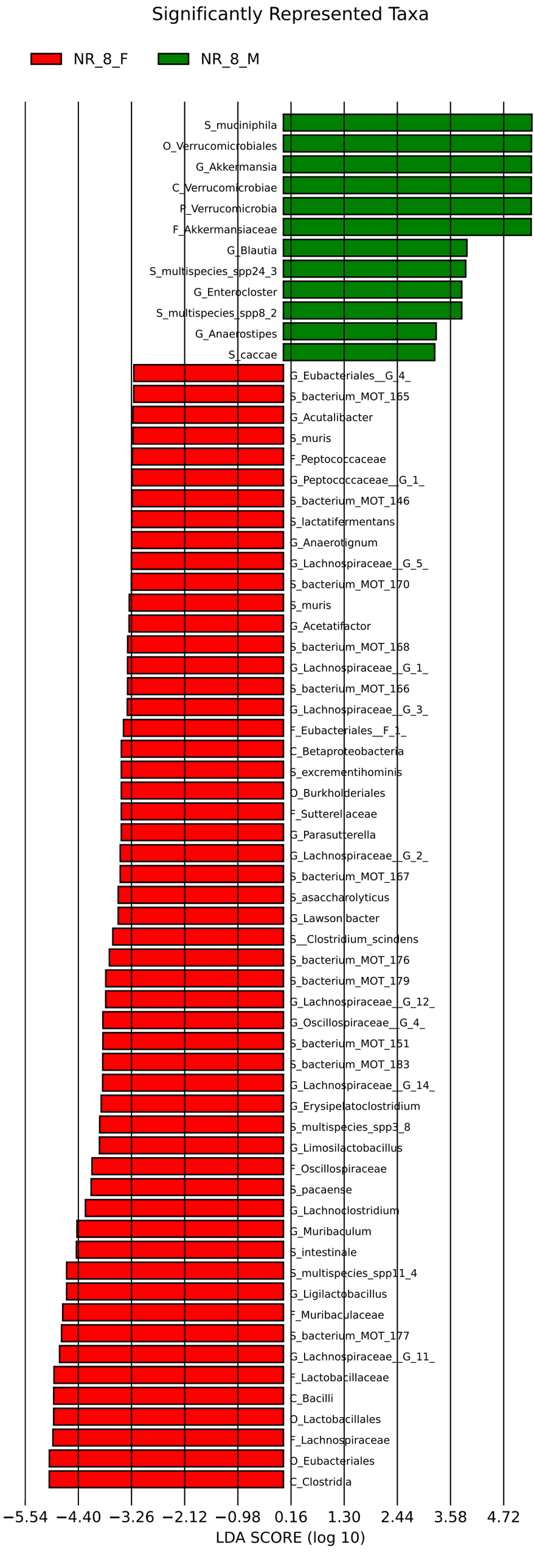
Significantly Represented Taxa
NR_8_F
NR_8_M
S_mucinipbila
O_Verrucomicrobiales
G_Akkermansia
C_Verrucomicrobiae
P_Verrucomicrobia
F_Akkermansiaceae
G_Blautia
S_multispecies_spp24_3
G_Enterocloster
S_multispecies_spp8_2
G_Anaerostipes
S_caccae
G_Eubacteriales__G_4_
S_bacterium_MOT_165
G_Acutalibacter
S_muris
F_Peptococcaceae
G_Peptococcaceae__G_1_
S_bacterium_MOT_146
S_lactatifermentans
G_Anaerotignum
G_Lachnospiraceae__G_5_
S_bacterium_MOT_170
S_muris
G_Acetatifactor
S_bacterium_MOT_168
G_Lachnospiraceae__G_1_
S_bacterium_MOT_166
G_Lachnospiraceae__G_3_
F_Eubacteriales__F_1_
C_Betaproteobacteria
S_excrementihominis
O_Burkholderiales
F_Sutterellaceae
G_Parasutterella
G_Lachnospiraceae__G_2_
S_bacterium_MOT_167
S_asaccharolyticus
G_Lawsonibacter
S__Clostridium_scindens
S_bacterium_MOT_176
S_bacterium_MOT_179
G_Lachnospiraceae__G_12_
G_Oscillospiraceae__G_4_
S_bacterium_MOT_151
S_bacterium_MOT_183
G_Lachnospiraceae__G_14_
G_Erysipelatoclostridium
S_multispecies_spp3_8
G_Limosilactobacillus
F_Oscillospiraceae
S_pacaense
G_Lachnoclostridium
G_Muribaculum
S_intestinale
S_multispecies_spp11_4
G_Ligilactobacillus
F_Muribaculaceae
S_bacterium_MOT_177
G_Lachnospiraceae__G_11_
F_Lactobacillaceae
C_Bacilli
O_Lactobacillales
F_Lachnospiraceae
O_Eubacteriales
C_Clostridia
−5.54
−4.40
−3.26
−2.12
−0.98
0.16
1.30
2.44
3.58
4.72
LDA SCORE (log 10)