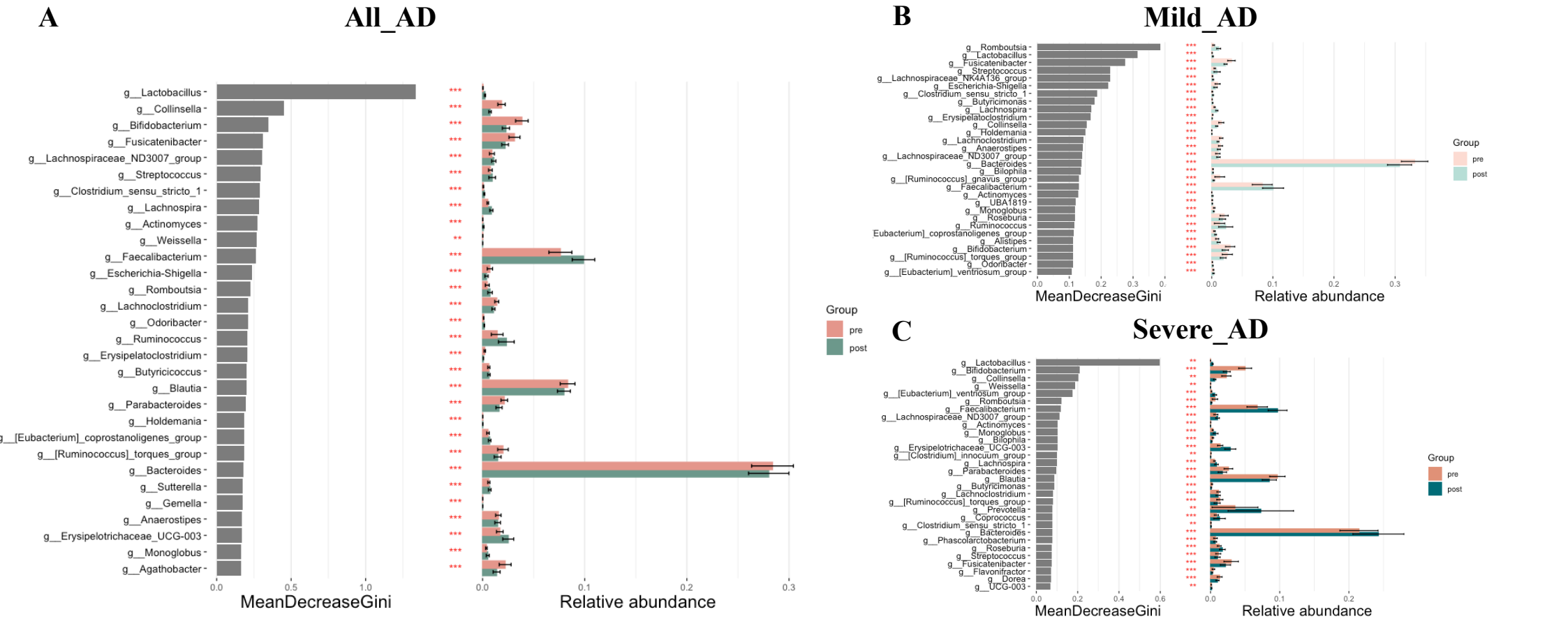
A
All_AD
g__Lactobacillus
g__Collinsella
g__Bifidobacterium
g__Fusicatenibacter
g__Lachnospiraceae_ND3007_group
g__Streptococcus
g__Clostridium_sensu_stricto_1
g__Lachnospira
g__Actinomyces
g__Weissella
g__Faecalibacterium
g__Escherichia-Shigella
g__Romboutsia
g__Lachnoclostridium
g__Odoribacter
g__Ruminococcus
g__Erysipelatoclostridium
g__Butyricicoccus
g__Blautia
g__Parabacteroides
g__Holdemania
g__[Eubacterium]_coprostanoligenes_group
g__[Ruminococcus]_torques_group
g__Bacteroides
g__Sutterella
g__Gemella
g__Anaerostipes
g__Erysipelotrichaceae_UCG-003
g__Monoglobus
g__Agathobacter
0.0
0.5
1.0
MeanDecreaseGini
0.0
0.1
0.2
0.3
Relative abundance
Group
pre
post
B
Mild_AD
g__Romboutsia
g__Lactobacillus
g__Fusicatenibacter
g__Streptococcus
g__Lachnospiraceae_NK4A136_group
g__Escherichia-Shigella
g__Clostridium_sensu_stricto_1
g__Butyricimonas
g__Lachnospira
g__Erysipelatoclostridium
g__Collinsella
g__Holdemania
g__Lachnoclostridium
g__Anaerostipes
g__Lachnospiraceae_ND3007_group
g__Bacteroides
g__Bilophila
g__[Ruminococcus]_gnavus_group
g__Faecalibacterium
g__Actinomyces
g__UBA1819
g__Monoglobus
g__Roseburia
g__Ruminococcus
[Eubacterium]_coprostanoligenes_group
g__Alistipes
g__Bifidobacterium
g__[Ruminococcus]_torques_group
g__Odoribacter
g__[Eubacterium]_ventriosum_group
0.0
0.1
0.2
0.3
MeanDecreaseGini
0.0
0.1
0.2
0.3
Relative abundance
Group
pre
post
C
Severe_AD
g__Lactobacillus
g__Bifidobacterium
g__Collinsella
g__Weissella
g__[Eubacterium]_ventriosum_group
g__Romboutsia
g__Faecalibacterium
g__Lachnospiraceae_ND3007_group
g__Actinomyces
g__Monoglobus
g__Bilophila
g__Erysipelotrichaceae_UCG-003
g__[Clostridium]_innocuum_group
g__Lachnospira
g__Parabacteroides
g__Blautia
g__Butyricimonas
g__Lachnoclostridium
g__[Ruminococcus]_torques_group
g__Prevotella
g__Coprococcus
g__Clostridium_sensu_stricto_1
g__Bacteroides
g__Phascolarctobacterium
g__Roseburia
g__Streptococcus
g__Fusicatenibacter
g__Flavonifractor
g__Dorea
g__UCG-003
0.0
0.2
0.4
0.6
MeanDecreaseGini
0.0
0.1
0.2
Relative abundance
Group
pre
post