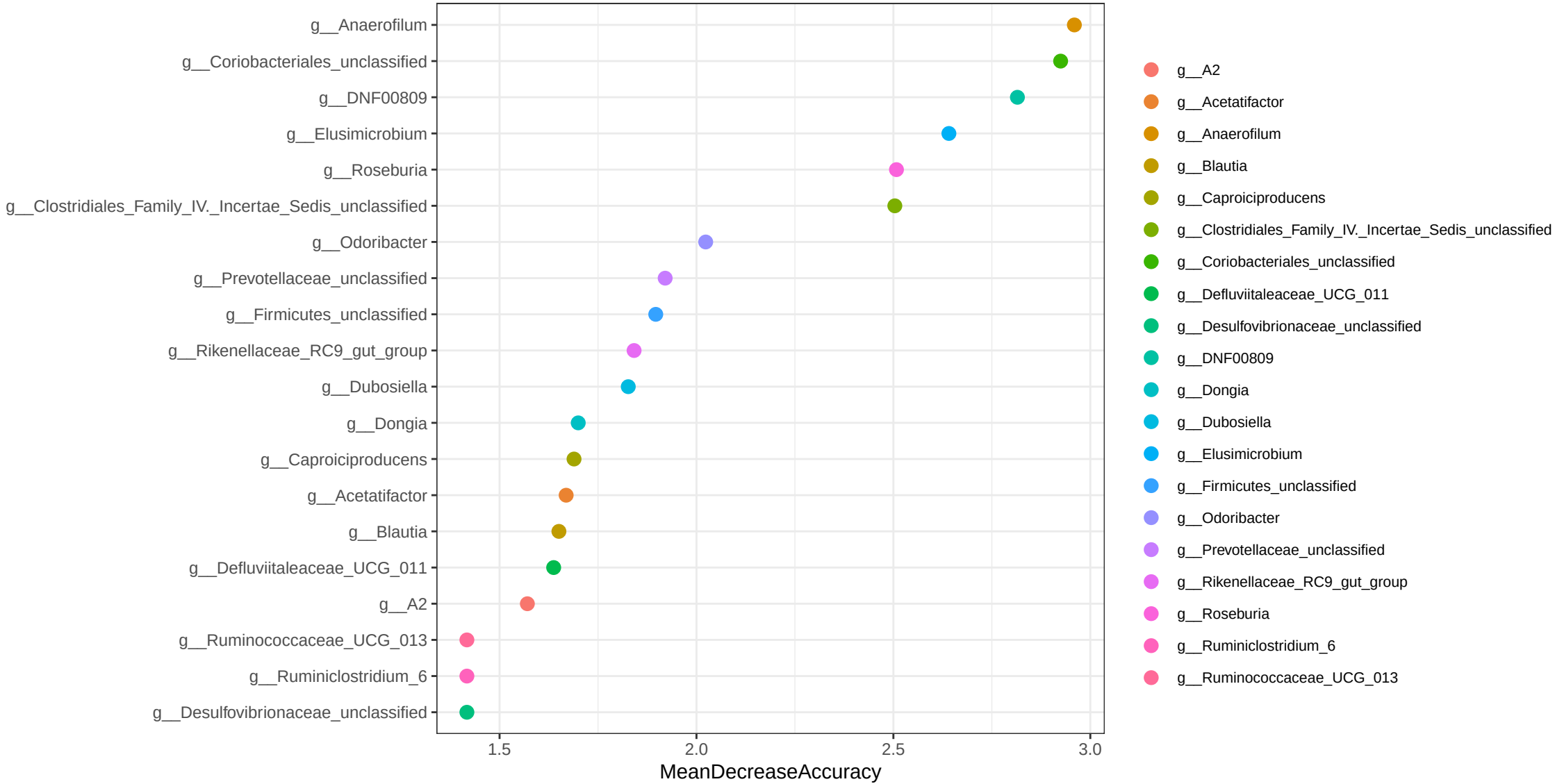
g__Anaerofilum
g__Coriobacteriales_unclassified
g__DNF00809
g__Elusimicrobium
g__Roseburia
g__Clostridiales_Family_IV._Incertae_Sedis_unclassified
g__Odoribacter
g__Prevotellaceae_unclassified
g__Firmicutes_unclassified
g__Rikenellaceae_RC9_gut_group
g__Dubosiella
g__Dongia
g__Caproiciproducens
g__Acetatifactor
g__Blautia
g__Defluviitaleaceae_UCG_011
g__A2
g__Ruminococcaceae_UCG_013
g__Ruminiclostridium_6
g__Desulfovibrionaceae_unclassified
1.5
2.0
2.5
3.0
MeanDecreaseAccuracy
g__A2
g__Acetatifactor
g__Anaerofilum
g__Blautia
g__Caproiciproducens
g__Clostridiales_Family_IV._Incertae_Sedis_unclassified
g__Coriobacteriales_unclassified
g__Defluviitaleaceae_UCG_011
g__Desulfovibrionaceae_unclassified
g__DNF00809
g__Dongia
g__Dubosiella
g__Elusimicrobium
g__Firmicutes_unclassified
g__Odoribacter
g__Prevotellaceae_unclassified
g__Rikenellaceae_RC9_gut_group
g__Roseburia
g__Ruminiclostridium_6
g__Ruminococcaceae_UCG_013