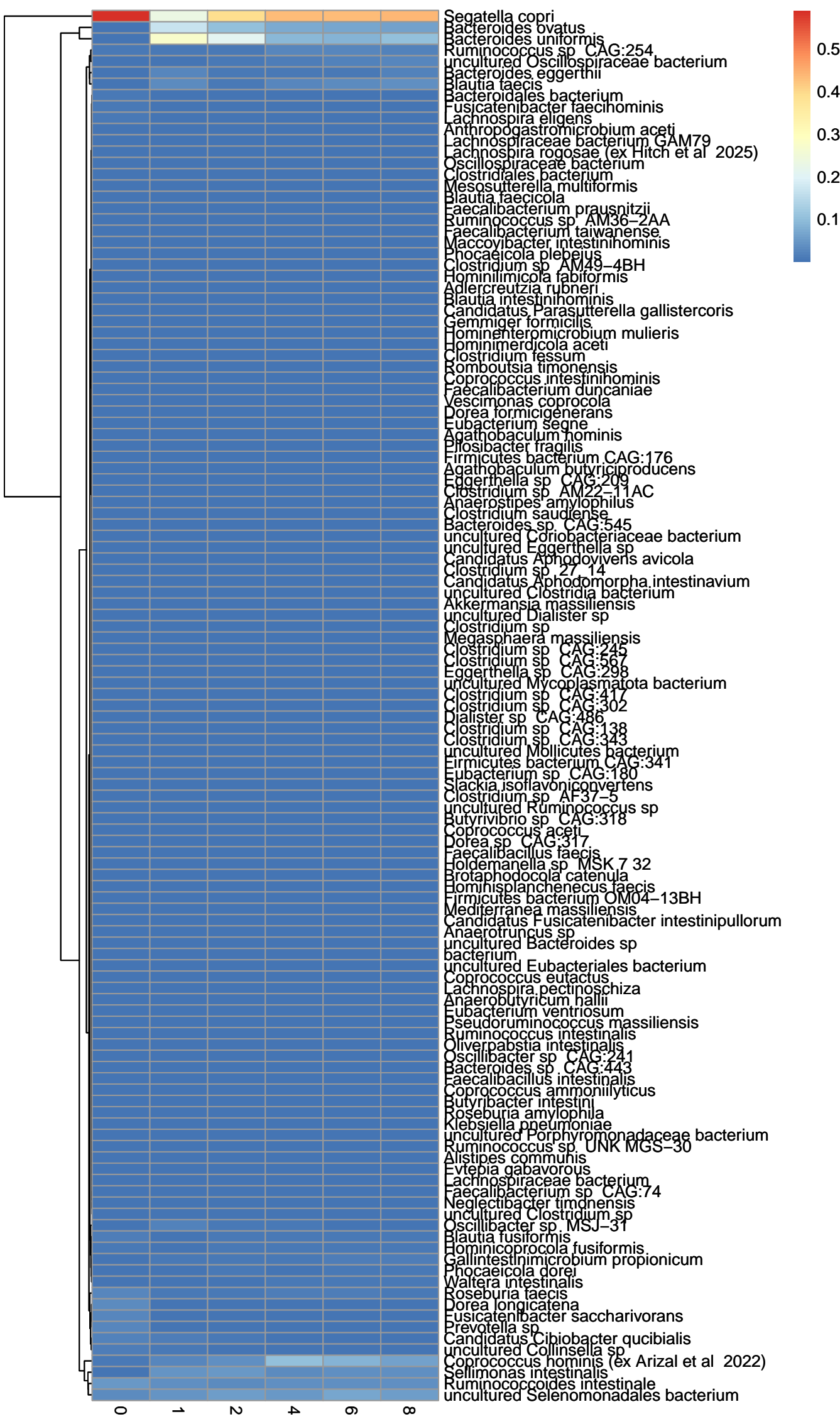
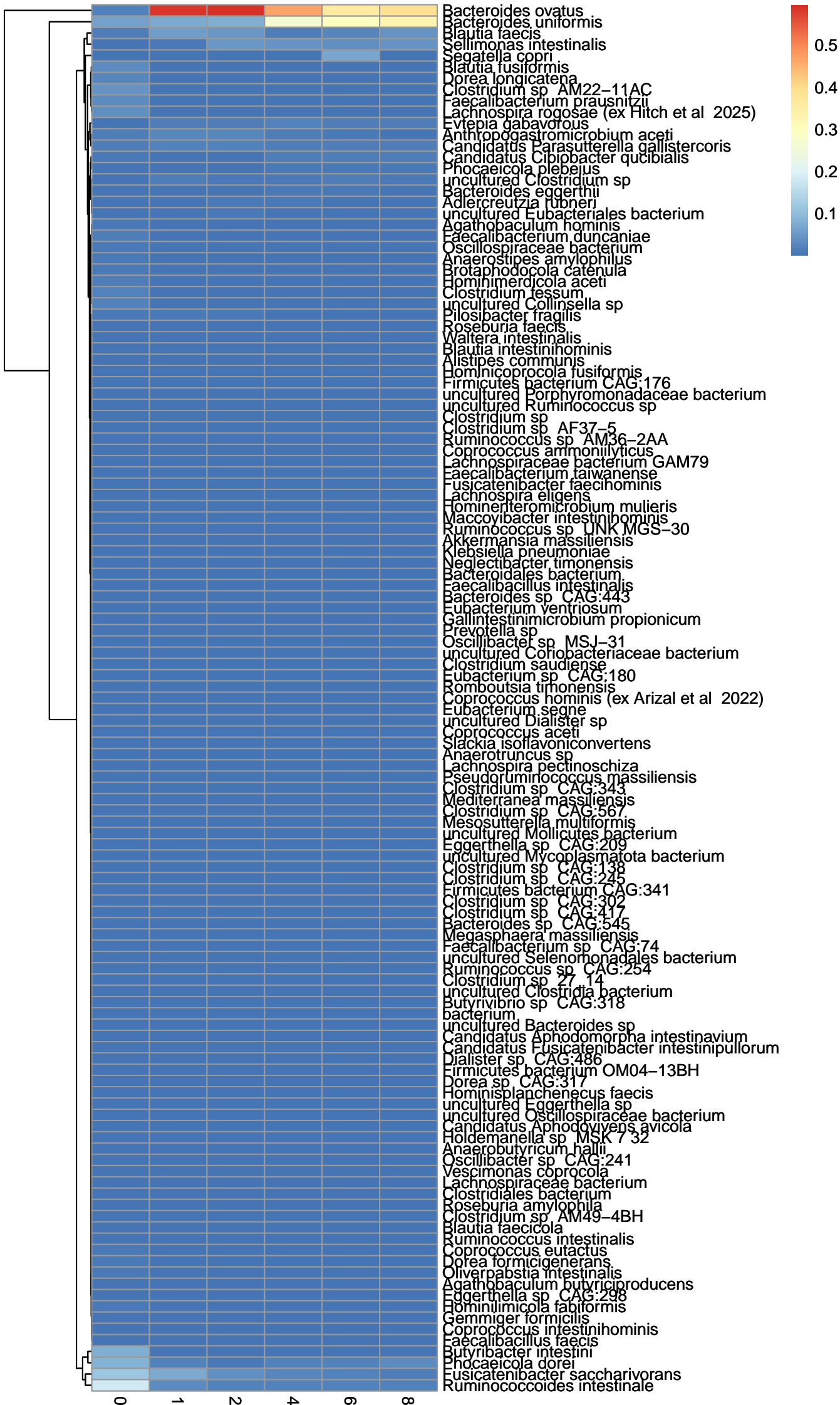


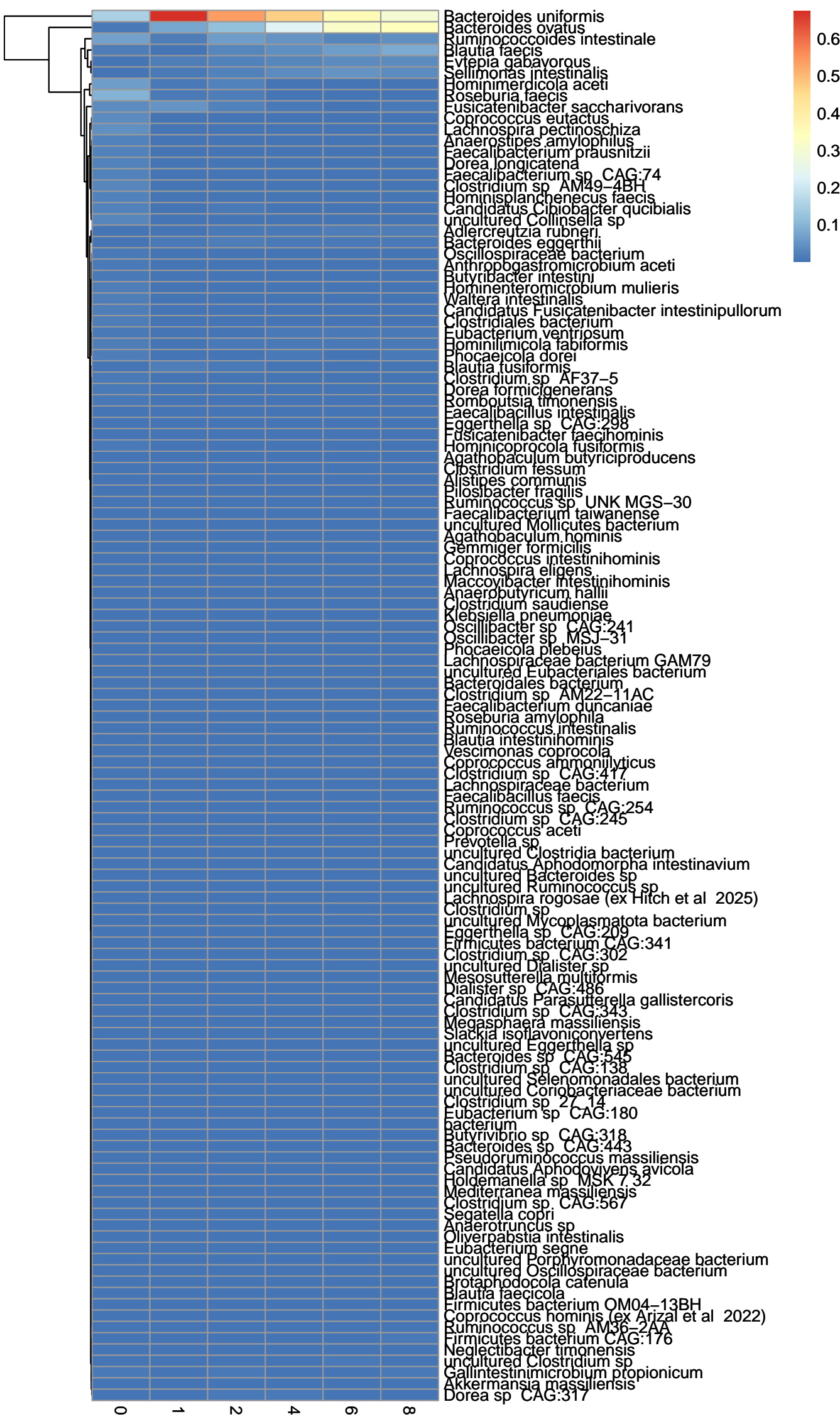
F0



F1



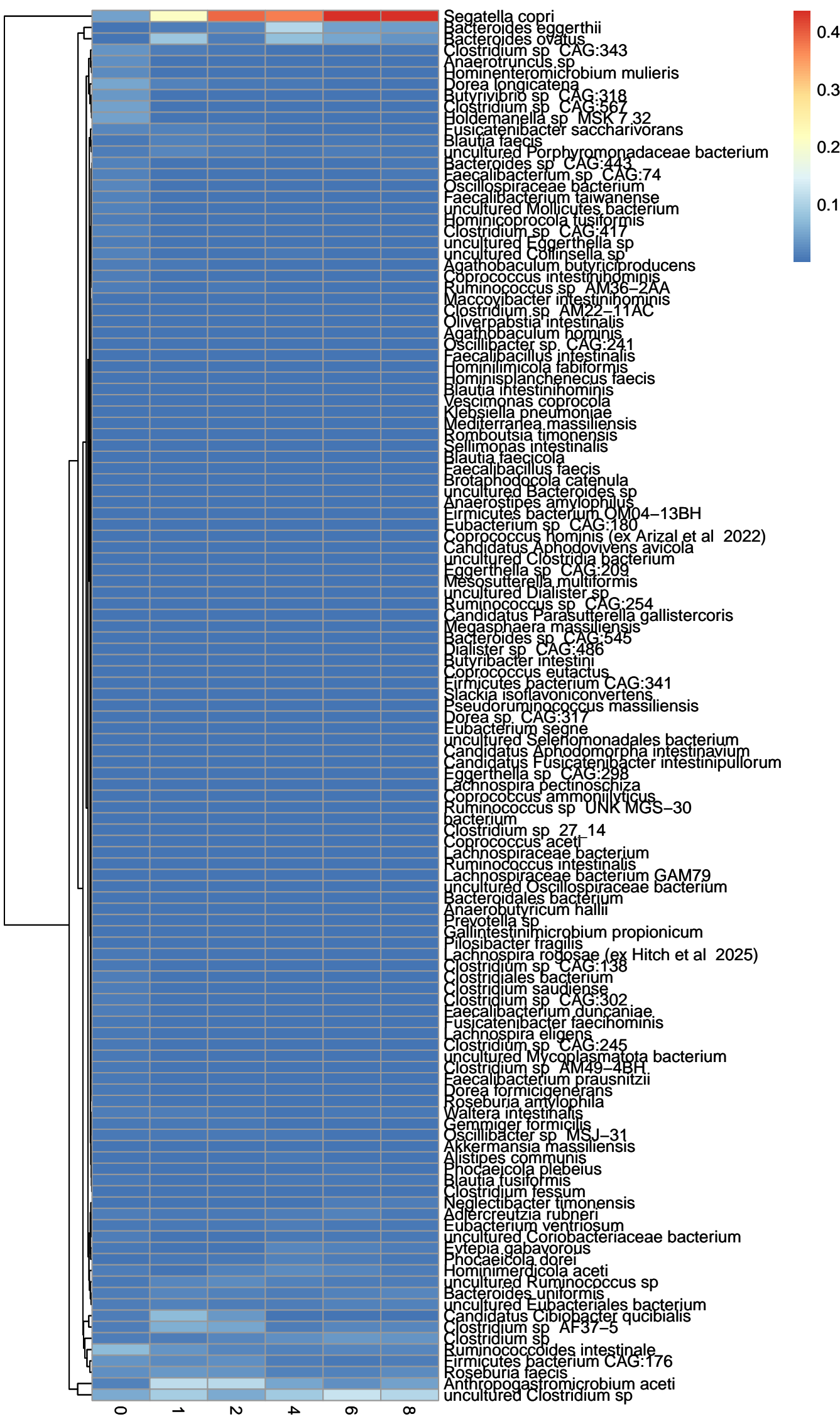
F2



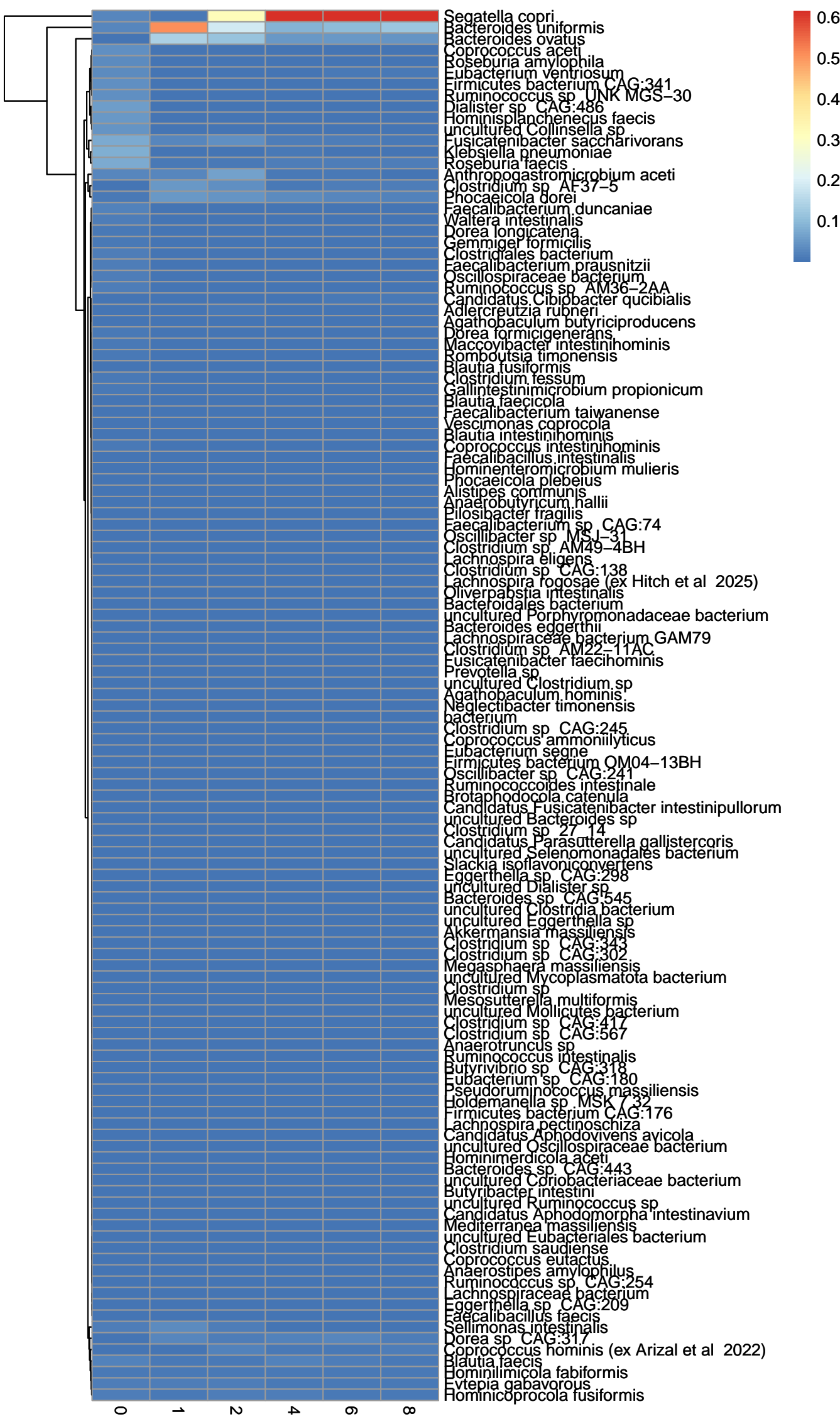
- Bacteroides uniformis
- Bacteroides ovatus
- Ruminococcus intestinale
- Blautia faecis
- Eviepia gabavorous
- Sellimonas intestinalis
- Hominimerdicola aceti
- Roseburia faecis
- Fusicatenibacter saccharivorans
- Coprococcus eutactus
- Lachnospira pectinoschiza
- Anaerostipes amylophilus
- Faecalibacterium prausnitzii
- Dorea longicatena
- Faecalibacterium sp. CAG:74
- Clostridium sp. AM49-4BH
- Hominisplancheneucus faecis
- Candidatus Cibiobacter qucibialis
- uncultured Collinsella sp
- Adlercreutzia rubneri
- Bacteroides eggertii
- Oscillospiraceae bacterium
- Anthropogastromicrobium aceti
- Butyrivibrio intestini
- Hominenteromicrobium mulieris
- Walteria intestinalis
- Candidatus Fusicatenibacter intestinipullorum
- Clostridiales bacterium
- Eubacterium ventriosum
- Hominilimicola fabiformis
- Phocaeicola dorei
- Blautia fusiformis
- Clostridium sp. AF37-5
- Dorea formicigenans
- Romboutsia timonensis
- Faecalibacillus intestinalis
- Eggerthella sp. CAG:298
- Fusicatenibacter faecihominis
- Hominicoprocola fusiformis
- Agathobaculum butyriciproducens
- Clostridium fessum
- Alistipes communis
- Bifidobacter fragilis
- Ruminococcus sp. UNK MGS-30
- Faecalibacterium taiwanense
- uncultured Mollicutes bacterium
- Agathobaculum hominis
- Gemmiger formicilis
- Coprococcus intestinihominis
- Lachnospira eligens
- Maccovibacter intestinihominis
- Anaerobutyricum hallii
- Clostridium saudienae
- Klebsiella pneumoniae
- Oscillibacter sp. CAG:241
- Oscillibacter sp. MSJ-31
- Phocaeicola plebeius
- Lachnospiraceae bacterium GAM79
- uncultured Eubacteriales bacterium
- Bacteroidales bacterium
- Clostridium sp. AM22-11AC
- Faecalibacterium duncaniae
- Roseburia amylophila
- Ruminococcus intestinalis
- Blautia intestinihominis
- Vescimonas coprocola
- Coprococcus ammoniolyticus
- Clostridium sp. CAG:417
- Lachnospiraceae bacterium
- Faecalibacillus faecis
- Ruminococcus sp. CAG:254
- Clostridium sp. CAG:245
- Coprococcus aceti
- Prevotella sp
- uncultured Clostridia bacterium
- Candidatus Aphodomorpha intestinavium
- uncultured Bacteroides sp
- uncultured Ruminococcus sp
- Lachnospira rogosae (ex Hitch et al 2025)
- Clostridium sp
- uncultured Mycoplasmatota bacterium
- Eggerthella sp. CAG:209
- Firmicutes bacterium CAG:341
- Clostridium sp. CAG:302
- uncultured Dialister sp
- Mesosutterella multiformis
- Dialister sp. CAG:486
- Candidatus Parasutterella gallistercoris
- Clostridium sp. CAG:343
- Megasphaera massiliensis
- Slackia isoflavoniconvertens
- uncultured Eggerthella sp
- Bacteroides sp. CAG:545
- Clostridium sp. CAG:138
- uncultured Selenomonadales bacterium
- uncultured Coriobacteriaceae bacterium
- Clostridium sp. 27_14
- Eubacterium sp. CAG:180
- bacterium
- Butyrivibrio sp. CAG:318
- Bacteroides sp. CAG:443
- Pseudoruminococcus massiliensis
- Candidatus Aphodovivens avicola
- Holdemanella sp. MSK 7.32
- Mediterranea massiliensis
- Clostridium sp. CAG:567
- Segatella copri
- Anaerotruncus sp
- Oliverpabstia intestinalis
- Eubacterium segne
- uncultured Porphyromonadaceae bacterium
- uncultured Oscillospiraceae bacterium
- Brotaphodocola catenula
- Blautia faecicola
- Firmicutes bacterium OM04-13BH
- Coprococcus hominis (ex Arizal et al 2022)
- Ruminococcus sp. AM36-2AA
- Firmicutes bacterium CAG:176
- Neglectibacter timonensis
- uncultured Clostridium sp
- Gallintestinimicrobium propionicum
- Akkermansia massiliensis
- Dorea sp. CAG:317

0 1 2 4 6 8

F3



F6



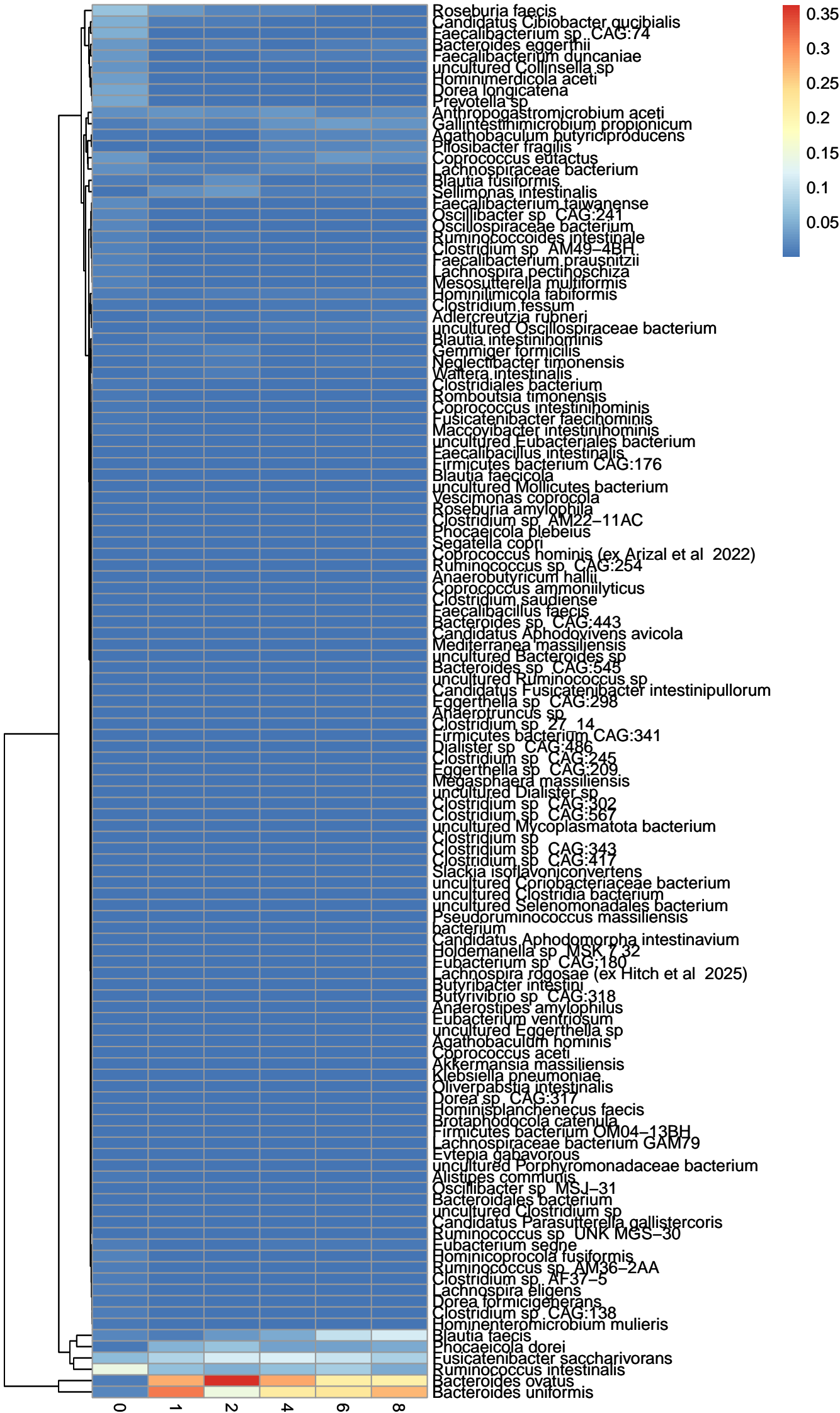
- Segatella copri
- Bacteroides uniformis
- Bacteroides ovatus
- Coprococcus acetii
- Roseburia amylophila
- Eubacterium ventriosum
- Firmicutes bacterium CAG:341
- Ruminococcus sp. UNK MGS-30
- Dialister sp. CAG:486
- Hominisplanchenecus faecis
- uncultured Collinsella sp.
- Fusicatenibacter saccharivorans
- Klebsiella pneumoniae
- Roseburia faecis
- Anthropogastronmicrobium acetii
- Clostridium sp. AF-37-5
- Phocaeicola dorei
- Faecalibacterium duncaniae
- Walteria intestinalis
- Dorea longicatena
- Gemmiger formicilis
- Clostridiales bacterium
- Faecalibacterium prausnitzii
- Oscillospiraceae bacterium
- Ruminococcus sp. AM36-2AA
- Candidatus Cibibacter qucibialis
- Adlercreutzia rubneri
- Agathobaculum butyriciproducens
- Dorea formicigenerans
- Maccovibacter intestinalihominis
- Romboutsia timonensis
- Blautia fusiformis
- Clostridium fessum
- Gallintestinimicrobium propionicum
- Blautia faecicola
- Faecalibacterium taiwanense
- Vescimonas coprocola
- Blautia intestinalihominis
- Coprococcus intestinalihominis
- Faecalibacillus intestinalis
- Hominenteromicrobium mulieris
- Phocaeicola plebeius
- Alistipes communis
- Anaerobutyricum hallii
- Filosibacter fragilis
- Faecalibacterium sp. CAG:74
- Oscillibacter sp. MSJ-31
- Clostridium sp. AM49-4BH
- Lachnospira eligens
- Clostridium sp. CAG:138
- Lachnospira fogosae (ex Hitch et al 2025)
- Oliverpabstia intestinalis
- Bacteroidales bacterium
- uncultured Porphyromonadaceae bacterium
- Bacteroides edgerthii
- Lachnospiraceae bacterium GAM79
- Clostridium sp. AM22-11AC
- Fusicatenibacter faecihominis
- Prevotella sp.
- uncultured Clostridium sp.
- Agathobaculum hominis
- Neglectibacter timonensis
- bacterium
- Clostridium sp. CAG:245
- Coprococcus ammoniilyticus
- Eubacterium segne
- Firmicutes bacterium OM04-13BH
- Oscillibacter sp. CAG:241
- Ruminococcoides intestinale
- Brotaphodocola catenula
- Candidatus Fusicatenibacter intestinipullorum
- uncultured Bacteroides sp.
- Clostridium sp. 27_14
- Candidatus Parasutterella gallistercoris
- uncultured Selenomonadales bacterium
- Slackia isoflavoniconvertens
- Eggerthella sp. CAG:298
- uncultured Dialister sp.
- Bacteroides sp. CAG:545
- uncultured Clostridia bacterium
- uncultured Eggerthella sp.
- Akkermansia massiliensis
- Clostridium sp. CAG:343
- Clostridium sp. CAG:302
- Megasphaera massiliensis
- uncultured Mycoplasmatota bacterium
- Clostridium sp.
- Mesosutterella multiformis
- uncultured Mollicutes bacterium
- Clostridium sp. CAG:417
- Clostridium sp. CAG:567
- Anaerotruncus sp.
- Ruminococcus intestinalis
- Butyrivibrio sp. CAG:318
- Eubacterium sp. CAG:180
- Pseudoruminococcus massiliensis
- Holdemanella sp. MSK 7_32
- Firmicutes bacterium CAG:176
- Lachnospira pectinoschiza
- Candidatus Aphodovivens avicola
- uncultured Oscillospiraceae bacterium
- Hominimerdicola acetii
- Bacteroides sp. CAG:443
- uncultured Coriobacteriaceae bacterium
- Butyribacter intestini
- uncultured Ruminococcus sp.
- Candidatus Aphodomorpha intestinavium
- Mediterranea massiliensis
- uncultured Eubacteriales bacterium
- Clostridium saudiense
- Coprococcus eutactus
- Anaerostipes amylophilus
- Ruminococcus sp. CAG:254
- Lachnospiraceae bacterium
- Eggerthella sp. CAG:209
- Faecalibacillus faecis
- Sellimonas intestinalis
- Dorea sp. CAG:317
- Coprococcus hominis (ex Arizal et al 2022)
- Blautia faecis
- Hominilimicola fabiformis
- Eutepia gabavorous
- Hominicoprocola fusiformis

0 1 2 4 6 8

F7



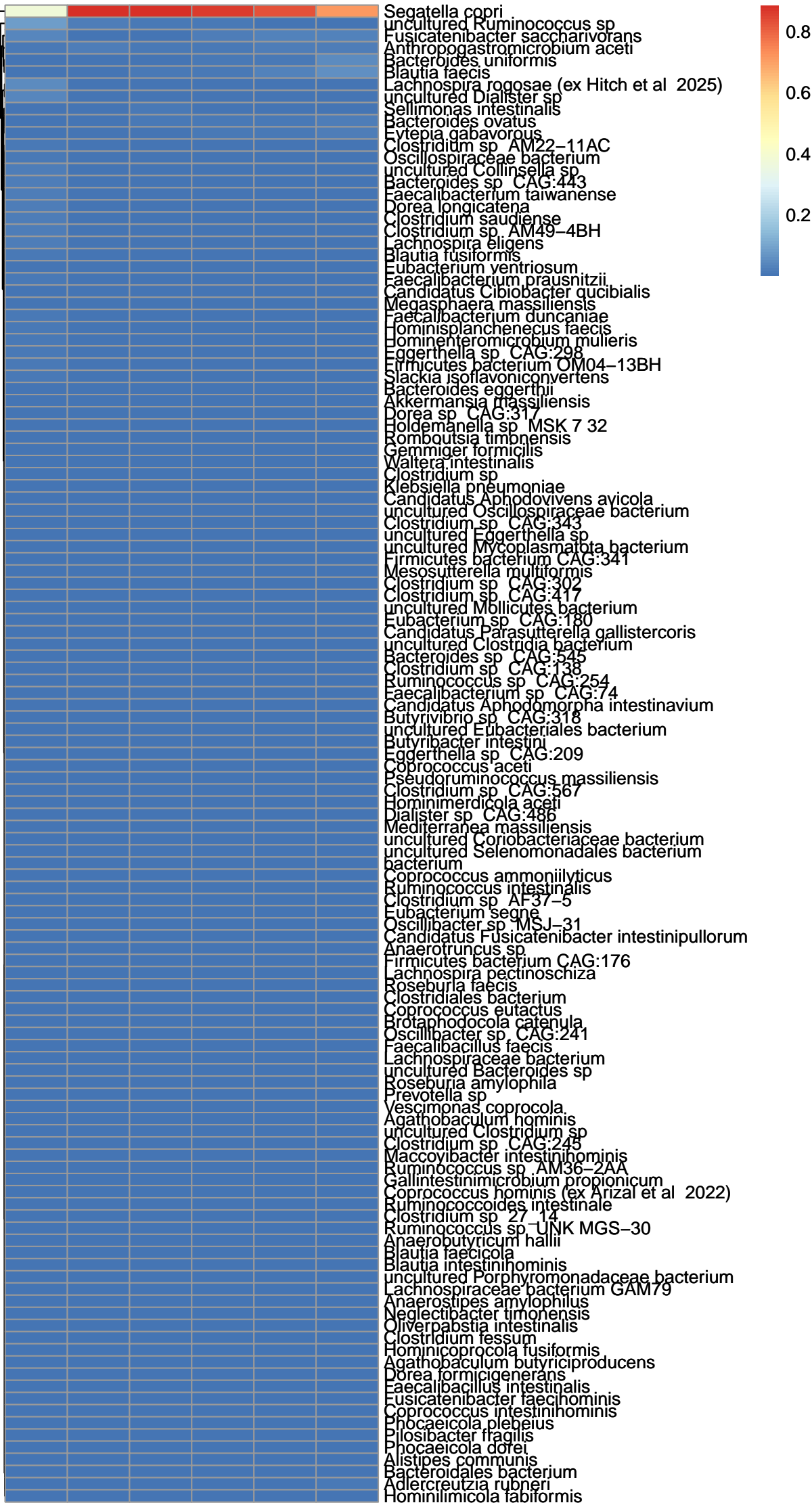
F8



F9



M4



M5

