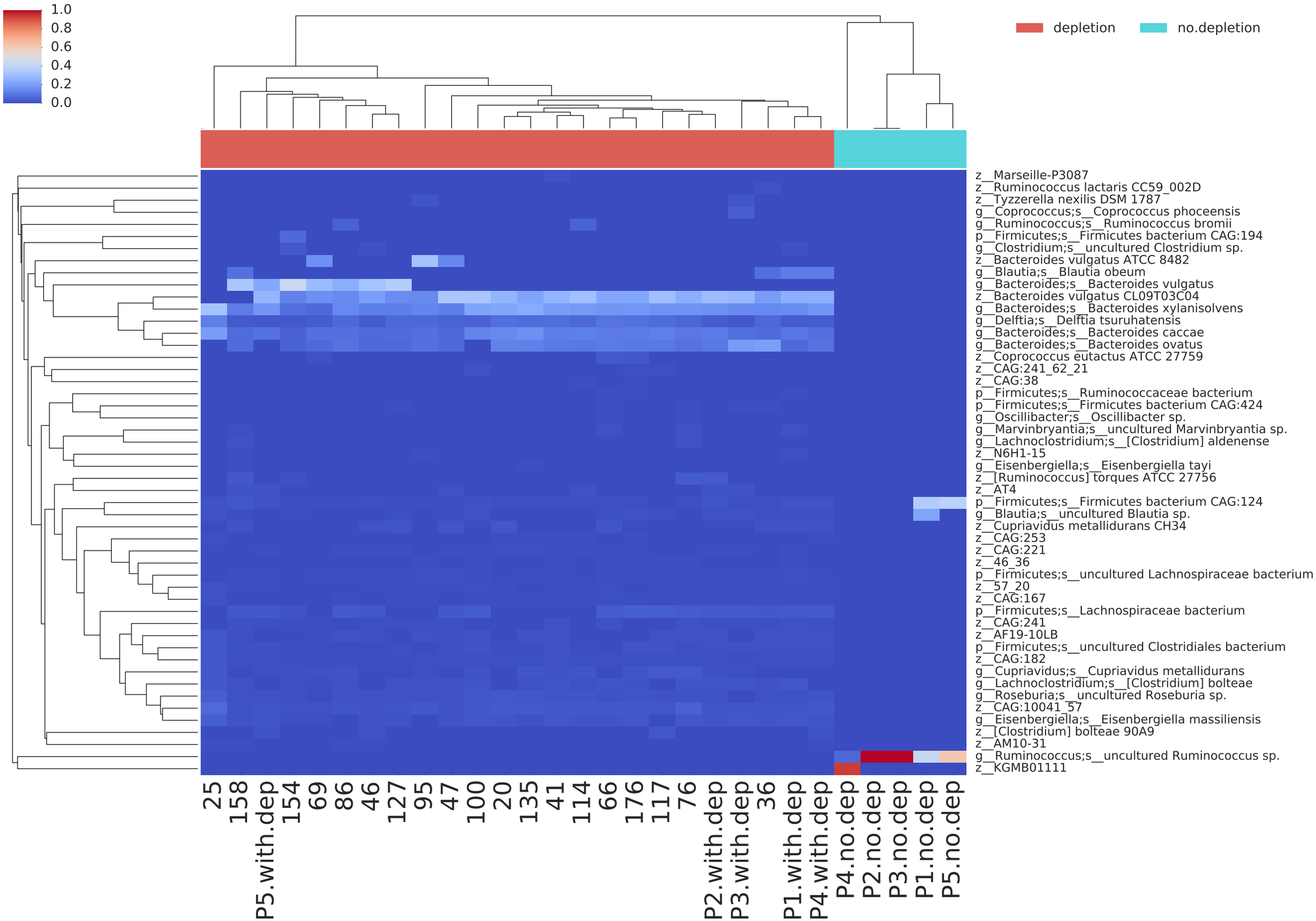
1.0
0.8
0.6
0.4
0.2
0.0
depletion
no.depletion
z__Marseille-P3087
z__Ruminococcus lactaris CC59_002D
z__Tyzzerella nexilis DSM 1787
g__Coprococcus;s__Coprococcus phoceensis
g__Ruminococcus;s__Ruminococcus bromii
p__Firmicutes;s__Firmicutes bacterium CAG:194
g__Clostridium;s__uncultured Clostridium sp.
z__Bacteroides vulgatus ATCC 8482
g__Blautia;s__Blautia obeum
g__Bacteroides;s__Bacteroides vulgatus
z__Bacteroides vulgatus CL09T03C04
g__Bacteroides;s__Bacteroides xylanisolvens
g__Delftia;s__Delftia tsuruhatensis
g__Bacteroides;s__Bacteroides caccae
g__Bacteroides;s__Bacteroides ovatus
z__Coprococcus eutactus ATCC 27759
z__CAG:241_62_21
z__CAG:38
p__Firmicutes;s__Ruminococcaceae bacterium
p__Firmicutes;s__Firmicutes bacterium CAG:424
g__Oscillibacter;s__Oscillibacter sp.
g__Marvinbryantia;s__uncultured Marvinbryantia sp.
g__Lachnoclostridium;s__[Clostridium] aldenense
z__N6H1-15
g__Eisenbergiella;s__Eisenbergiella tayi
z__[Ruminococcus] torques ATCC 27756
z__AT4
p__Firmicutes;s__Firmicutes bacterium CAG:124
g__Blautia;s__uncultured Blautia sp.
z__Cupriavidus metallidurans CH34
z__CAG:253
z__CAG:221
z__46_36
p__Firmicutes;s__uncultured Lachnospiraceae bacterium
z__57_20
z__CAG:167
p__Firmicutes;s__Lachnospiraceae bacterium
z__CAG:241
z__AF19-10LB
p__Firmicutes;s__uncultured Clostridiales bacterium
z__CAG:182
g__Cupriavidus;s__Cupriavidus metallidurans
g__Lachnoclostridium;s__[Clostridium] bolteae
g__Roseburia;s__uncultured Roseburia sp.
z__CAG:10041_57
g__Eisenbergiella;s__Eisenbergiella massiliensis
z__[Clostridium] bolteae 90A9
z__AM10-31
g__Ruminococcus;s__uncultured Ruminococcus sp.
z__KGMB01111
Taxon
25
158
P5.with.dep
154
69
86
46
127
95
47
100
20
135
41
114
66
176
117
76
P2.with.dep
P3.with.dep
36
P1.with.dep
P4.with.dep
P4.no.dep
P2.no.dep
P3.no.dep
P1.no.dep
P5.no.dep