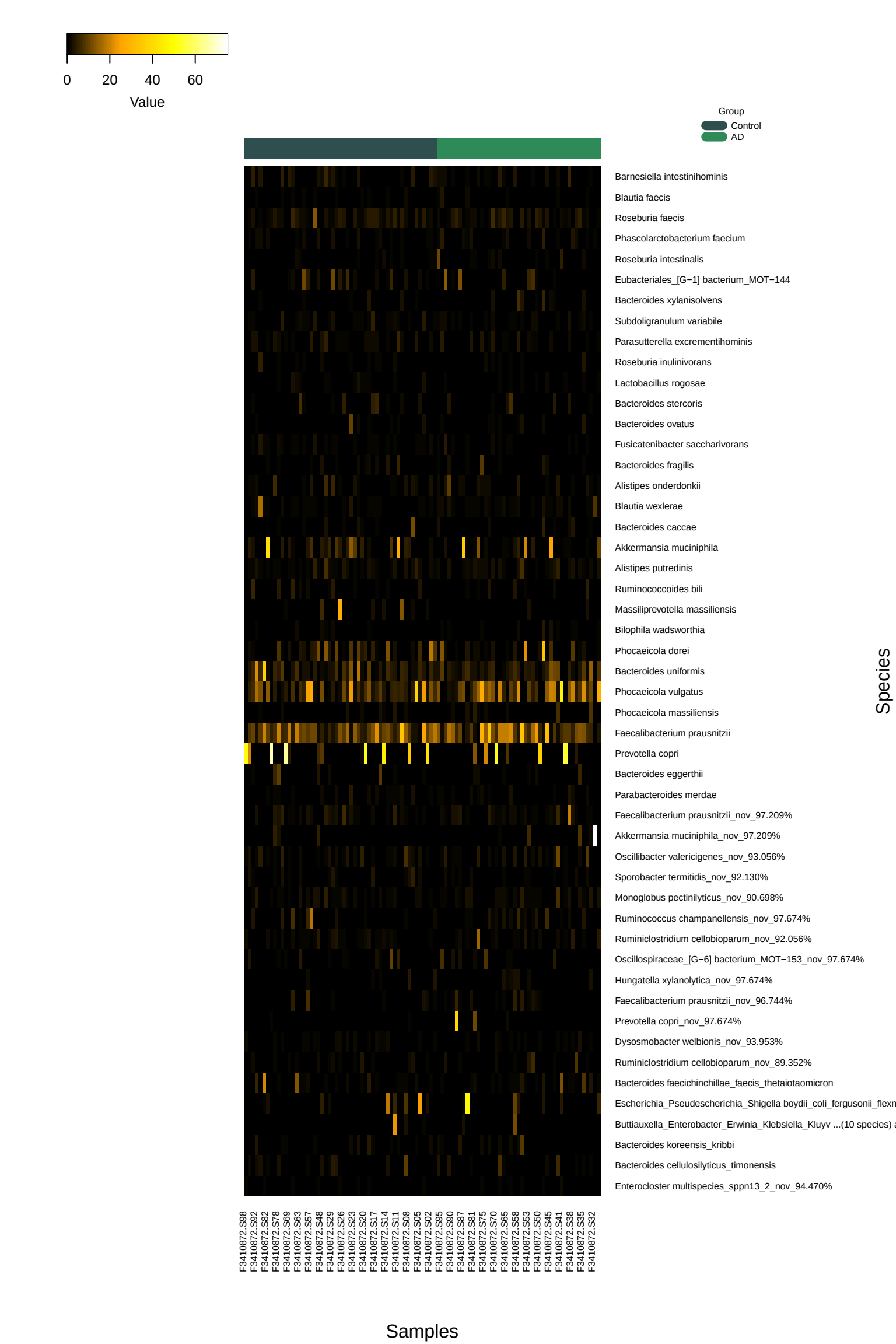
0
20
40
60
Value
Group
Control
AD
Barnesiella intestinihominis
Blautia faecis
Roseburia faecis
Phascolarctobacterium faecium
Roseburia intestinalis
Eubacteriales_[G−1] bacterium_MOT−144
Bacteroides xylanisolvens
Subdoligranulum variabile
Parasutterella excrementihominis
Roseburia inulinivorans
Lactobacillus rogosae
Bacteroides stercoris
Bacteroides ovatus
Fusicatenibacter saccharivorans
Bacteroides fragilis
Alistipes onderdonkii
Blautia wexlerae
Bacteroides caccae
Akkermansia muciniphila
Alistipes putredinis
Ruminococcoides bili
Massiliprevotella massiliensis
Bilophila wadsworthia
Phocaeicola dorei
Bacteroides uniformis
Phocaeicola vulgatus
Phocaeicola massiliensis
Faecalibacterium prausnitzii
Prevotella copri
Bacteroides eggerthii
Parabacteroides merdae
Faecalibacterium prausnitzii_nov_97.209%
Akkermansia muciniphila_nov_97.209%
Oscillibacter valericigenes_nov_93.056%
Sporobacter termitidis_nov_92.130%
Monoglobus pectinilyticus_nov_90.698%
Ruminococcus champanellensis_nov_97.674%
Ruminiclostridium cellobioparum_nov_92.056%
Oscillospiraceae_[G−6] bacterium_MOT−153_nov_97.674%
Hungatella xylanolytica_nov_97.674%
Faecalibacterium prausnitzii_nov_96.744%
Prevotella copri_nov_97.674%
Dysosmobacter welbionis_nov_93.953%
Ruminiclostridium cellobioparum_nov_89.352%
Bacteroides faecichinchillae_faecis_thetaiotaomicron
Escherichia_Pseudescherichia_Shigella boydii_coli_fergusonii_flexn
Buttiauxella_Enterobacter_Erwinia_Klebsiella_Kluyv ...(10 species) a
Bacteroides koreensis_kribbi
Bacteroides cellulosilyticus_timonensis
Enterocloster multispecies_sppn13_2_nov_94.470%
Species
F3410872.S98
F3410872.S92
F3410872.S82
F3410872.S78
F3410872.S69
F3410872.S63
F3410872.S57
F3410872.S48
F3410872.S29
F3410872.S26
F3410872.S23
F3410872.S20
F3410872.S17
F3410872.S14
F3410872.S11
F3410872.S08
F3410872.S05
F3410872.S02
F3410872.S95
F3410872.S90
F3410872.S87
F3410872.S81
F3410872.S75
F3410872.S70
F3410872.S65
F3410872.S58
F3410872.S53
F3410872.S50
F3410872.S45
F3410872.S41
F3410872.S38
F3410872.S35
F3410872.S32
Samples