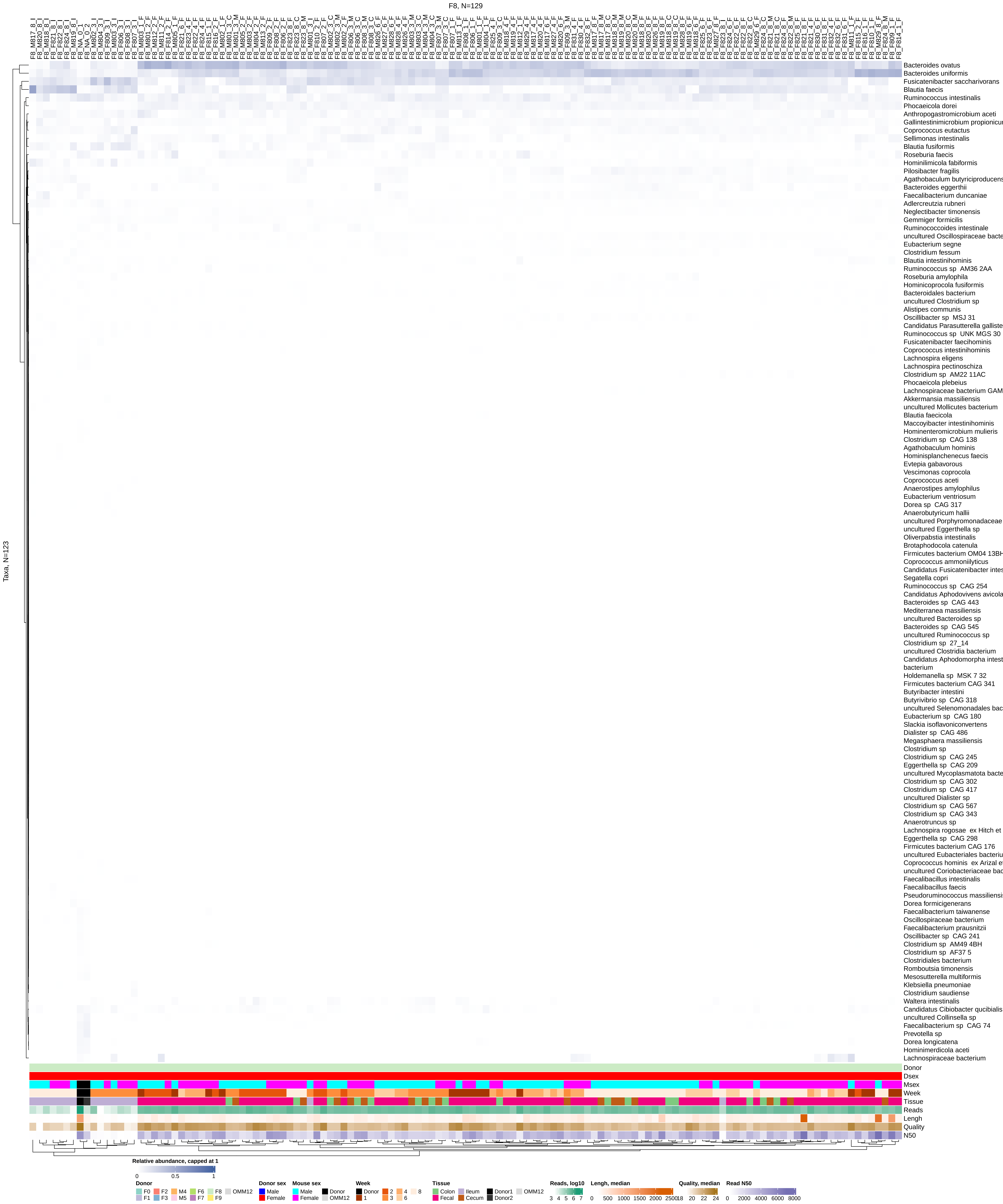
F8, N=129
F8_M817_8_I
F8_M820_8_I
F8_M818_8_I
F8_F821_8_I
F8_F822_8_I
F8_F824_8_I
F8_M819_8_I
F8_NA_0_1
F8_NA_0_2
F8_M802_3_I
F8_M804_3_I
F8_F809_3_I
F8_M803_3_I
F8_F806_3_I
F8_F808_3_I
F8_F807_3_I
F8_M803_1_F
F8_M801_2_F
F8_M812_2_F
F8_M811_2_F
F8_F814_2_F
F8_M805_1_F
F8_F821_6_F
F8_F823_4_F
F8_F822_4_F
F8_F824_4_F
F8_F815_1_F
F8_F816_2_F
F8_M802_1_F
F8_M801_3_C
F8_M801_3_M
F8_M805_2_F
F8_M803_2_F
F8_M804_2_F
F8_M813_2_F
F8_F809_2_F
F8_F808_2_F
F8_F806_2_F
F8_F823_8_F
F8_F823_8_C
F8_F823_8_M
F8_M801_3_I
F8_F810_2_F
F8_F807_2_F
F8_M802_3_C
F8_M802_3_M
F8_M802_2_F
F8_F806_3_M
F8_F806_3_C
F8_F808_3_M
F8_F808_3_C
F8_M826_6_F
F8_M827_6_F
F8_M828_6_F
F8_M828_4_F
F8_M826_4_F
F8_M803_3_M
F8_M803_3_C
F8_M804_3_M
F8_M804_3_C
F8_F807_3_M
F8_F807_3_C
F8_F807_1_F
F8_M813_1_F
F8_F808_1_F
F8_F806_1_F
F8_M801_1_F
F8_M804_1_F
F8_F825_4_F
F8_F809_3_C
F8_M818_4_F
F8_M819_4_F
F8_M812_1_F
F8_M829_4_F
F8_M817_4_F
F8_M820_4_F
F8_M817_6_F
F8_M827_4_F
F8_M820_6_F
F8_F809_3_M
F8_F831_4_F
F8_F830_4_F
F8_F832_8_F
F8_M817_8_F
F8_M817_8_M
F8_M817_8_C
F8_M818_8_M
F8_M819_8_M
F8_M820_8_C
F8_M820_8_M
F8_M818_8_F
F8_M820_8_F
F8_M826_8_F
F8_M819_8_F
F8_M818_8_C
F8_M819_8_C
F8_M828_8_F
F8_M819_6_F
F8_M818_6_F
F8_F825_6_F
F8_F823_6_F
F8_M827_8_F
F8_F823_8_I
F8_F824_6_F
F8_F822_6_F
F8_F822_8_F
F8_F822_8_C
F8_M829_6_F
F8_F824_8_C
F8_F821_8_M
F8_F821_8_C
F8_F824_8_F
F8_F822_8_M
F8_F825_8_F
F8_F821_8_F
F8_F821_4_F
F8_F830_6_F
F8_F831_8_F
F8_F832_4_F
F8_F832_6_F
F8_F831_6_F
F8_M811_1_F
F8_F815_2_F
F8_F816_1_F
F8_F810_1_F
F8_M829_8_F
F8_F824_8_M
F8_F809_1_F
F8_F814_1_F
Taxa, N=123
Bacteroides ovatus
Bacteroides uniformis
Fusicatenibacter saccharivorans
Blautia faecis
Ruminococcus intestinalis
Phocaeicola dorei
Anthropogastromicrobium aceti
Gallintestinimicrobium propionicu
Coprococcus eutactus
Sellimonas intestinalis
Blautia fusiformis
Roseburia faecis
Hominilimicola fabiformis
Pilosibacter fragilis
Agathobaculum butyriciproducens
Bacteroides eggerthii
Faecalibacterium duncaniae
Adlercreutzia rubneri
Neglectibacter timonensis
Gemmiger formicilis
Ruminococcoides intestinale
uncultured Oscillospiraceae bacte
Eubacterium segne
Clostridium fessum
Blautia intestinihominis
Ruminococcus sp AM36 2AA
Roseburia amylophila
Hominicoprocola fusiformis
Bacteroidales bacterium
uncultured Clostridium sp
Alistipes communis
Oscillibacter sp MSJ 31
Candidatus Parasutterella galliste
Ruminococcus sp UNK MGS 30
Fusicatenibacter faecihominis
Coprococcus intestinihominis
Lachnospira eligens
Lachnospira pectinoschiza
Clostridium sp AM22 11AC
Phocaeicola plebeius
Lachnospiraceae bacterium GAM
Akkermansia massiliensis
uncultured Mollicutes bacterium
Blautia faecicola
Maccoyibacter intestinihominis
Hominenteromicrobium mulieris
Clostridium sp CAG 138
Agathobaculum hominis
Hominisplanchenecus faecis
Evtepia gabavorous
Vescimonas coprocola
Coprococcus aceti
Anaerostipes amylophilus
Eubacterium ventriosum
Dorea sp CAG 317
Anaerobutyricum hallii
uncultured Porphyromonadaceae
uncultured Eggerthella sp
Oliverpabstia intestinalis
Brotaphodocola catenula
Firmicutes bacterium OM04 13BH
Coprococcus ammoniilyticus
Candidatus Fusicatenibacter intes
Segatella copri
Ruminococcus sp CAG 254
Candidatus Aphodovivens avicola
Bacteroides sp CAG 443
Mediterranea massiliensis
uncultured Bacteroides sp
Bacteroides sp CAG 545
uncultured Ruminococcus sp
Clostridium sp 27_14
uncultured Clostridia bacterium
Candidatus Aphodomorpha intest
bacterium
Holdemanella sp MSK 7 32
Firmicutes bacterium CAG 341
Butyribacter intestini
Butyrivibrio sp CAG 318
uncultured Selenomonadales bac
Eubacterium sp CAG 180
Slackia isoflavoniconvertens
Dialister sp CAG 486
Megasphaera massiliensis
Clostridium sp
Clostridium sp CAG 245
Eggerthella sp CAG 209
uncultured Mycoplasmatota bacte
Clostridium sp CAG 302
Clostridium sp CAG 417
uncultured Dialister sp
Clostridium sp CAG 567
Clostridium sp CAG 343
Anaerotruncus sp
Lachnospira rogosae ex Hitch et
Eggerthella sp CAG 298
Firmicutes bacterium CAG 176
uncultured Eubacteriales bacteriu
Coprococcus hominis ex Arizal e
uncultured Coriobacteriaceae bac
Faecalibacillus intestinalis
Faecalibacillus faecis
Pseudoruminococcus massiliensis
Dorea formicigenerans
Faecalibacterium taiwanense
Oscillospiraceae bacterium
Faecalibacterium prausnitzii
Oscillibacter sp CAG 241
Clostridium sp AM49 4BH
Clostridium sp AF37 5
Clostridiales bacterium
Romboutsia timonensis
Mesosutterella multiformis
Klebsiella pneumoniae
Clostridium saudiense
Waltera intestinalis
Candidatus Cibiobacter qucibialis
uncultured Collinsella sp
Faecalibacterium sp CAG 74
Prevotella sp
Dorea longicatena
Hominimerdicola aceti
Lachnospiraceae bacterium
Donor
Dsex
Msex
Week
Tissue
Reads
Lengh
Quality
N50
Relative abundance, capped at 1
0
0.5
1
Donor
F0
F1
F2
F3
M4
M5
F6
F7
F8
F9
OMM12
Donor sex
Male
Female
Mouse sex
Male
Female
Donor
OMM12
Week
Donor
1
2
3
4
6
8
Tissue
Colon
Fecal
Ileum
Cecum
Donor1
Donor2
OMM12
Reads, log10
3
4
5
6
7
Lengh, median
0
500
1000
1500
2000
2500
Quality, median
18
20
22
24
Read N50
0
2000
4000
6000
8000