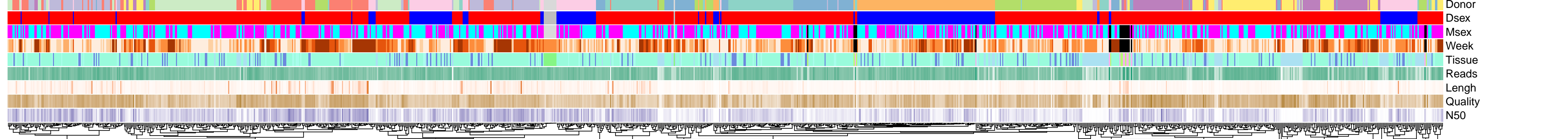


Taxa, N=123

- Segatella copri
- Bacteroides ovatus
- Bacteroides uniformis
- Blautia faecis
- Sellimonas intestinalis
- Akkermansia massiliensis
- Fusicatenibacter saccharivorans
- Ruminococcoides intestinale
- Anthropogastrmicrobium aceti
- Blautia fusiformis
- Phocaeicola dorei
- Ruminococcus intestinalis
- Blautia intestinhominis
- Coprococcus hominis ex Arizal et
- uncultured Selenomonadales bac
- Candidatus Cibiobacter quibialis
- Evtepia gabavorus
- Adlercreutzia rubneri
- Clostridium sp
- Coprococcus aceti
- Phocaeicola plebeius
- Faecalibacterium taiwanense
- Pilosibacter fragilis
- Hominilimicola fabiformis
- Coprococcus eutactus
- uncultured Oscillospiraceae bacte
- Hominicoprocola fusiformis
- Waltera intestinalis
- Neglectibacter timonensis
- Bacteroides sp CAG 443
- uncultured Ruminococcus sp
- Firmicutes bacterium CAG 176
- Dorea longicatena
- Agathobaculum butyriciproducens
- Faecalibacterium duncaniae
- Eubacterium ventriosum
- Ruminococcus sp UNK MGS 30
- uncultured Collinsella sp
- Gemmiger formicilis
- Alistipes communis
- Bacteroidales bacterium
- Oscillibacter sp MSJ 31
- uncultured Eubacteriales bacteri
- uncultured Porphyromonadaceae
- uncultured Coriobacteriaceae bac
- Anaerobutyricum hallii
- Faecalibacterium prausnitzii
- Coprococcus intestinhominis
- Ruminococcus sp AM36 2AA
- Clostridium fessum
- Faecalibacillus intestinalis
- Oliverpabstia intestinalis
- Eubacterium segne
- Fusicatenibacter faechominis
- Blautia faecicola
- Lachnospiraceae bacterium GAM
- Maccoyibacter intestinhominis
- Vescimonas coprocola
- Pseudoruminococcus massiliensis
- uncultured Clostridia bacterium
- Brotaphodocola catenula
- Coprococcus ammoniilyticus
- Eggerthella sp CAG 298
- Candidatus Fusicatenibacter intes
- Megasphaera massiliensis
- uncultured Eggerthella sp
- Clostridium sp CAG 417
- Clostridium sp CAG 302
- Clostridium sp CAG 245
- uncultured Mycoplasmatota bacte
- Mesosutterella multiformis
- uncultured Bacteroides sp
- Eggerthella sp CAG 209
- Oscillospiraceae bacterium
- Dorea formicigenerans
- Firmicutes bacterium OM04 13BH
- Oscillibacter sp CAG 241
- bacterium
- Clostridium sp CAG 138
- Lachnospira eligens
- Bacteroides sp CAG 545
- Slackia isoflavoniconvertens
- uncultured Mollicutes bacterium
- Candidatus Aphodovivens avicola
- Anaerotruncus sp
- Holdemanella sp MSK 7 32
- Butyrivibrio sp CAG 318
- Clostridium sp CAG 567
- Clostridium sp AM49 4BH
- Clostridiales bacterium
- Lachnospira pectinoschiza
- Mediterranea massiliensis
- Clostridium sp AM22 11AC
- Butyrivibrio intestini
- Lachnospira rogosae ex Hitch et
- uncultured Dialister sp
- Agathobaculum hominis
- Hominisplanchneneus faecis
- Firmicutes bacterium CAG 341
- Dialister sp CAG 486
- Roseburia amylophila
- Hominenteromicrobium mulieris
- Eubacterium sp CAG 180
- Clostridium sp 27_14
- Faecalibacterium sp CAG 74
- Prevotella sp
- Candidatus Aphodomorpha intest
- Anaerostipes amylophilus
- Faecalibacillus faecis
- Clostridium saudiense
- Clostridium sp CAG 343
- Lachnospiraceae bacterium
- Romboutsia timonensis
- Gallintestinimicrobium propionicu
- Candidatus Parasutterella galliste
- Dorea sp CAG 317
- Roseburia faecis
- Clostridium sp AF37 5
- Ruminococcus sp CAG 254
- Hominimerdicola aceti
- Klebsiella pneumoniae
- uncultured Clostridium sp
- Bacteroides eggertii



Relative abundance, capped at 0.5

