



Relative abundance, capped at 1

0 0.5 1

Donor F0 F2 M4 F6 F8 OMM12 F1 F3 M5 F7 F9

Donor sex Male Female

Mouse sex Male Female

Week 1 2 3 4 6

Tissue Colon Ileum Cecum

Reads, log10 3 4 5 6 7

Length, median 500 1000 1500 21

Quality, median 22 23 24 25

Read N50 2000 4000 6000

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