



- Segatella copri
- Bacteroides uniformis
- Bacteroides ovatus
- Coprococcus hominis ex Arizal et
- uncultured Selenomonadales bac
- Sellimonas intestinalis
- Ruminococcoides intestinale
- Blautia faecis
- Ruminococcus sp CAG 254
- Blautia fusiformis
- Bacteroides eggerthii
- Roseburia faecis
- uncultured Oscillospiraceae bacte
- Gallintestinimicrobium propionicu
- Adlercreutzia rubneri
- Candidatus Cibiobacter quicubialis
- Oscillibacter sp MSJ 31
- Hominicoprocola fusiformis
- Phocaeicola dorei
- Waltera intestinalis
- Hominilimicola fabiformis
- Ruminococcus sp AM36 2AA
- uncultured Collinsella sp
- Clostridium sp AM49 4BH
- Blautia intestinihominis
- Bacteroidales bacterium
- Gemmiger formicilis
- Faecalibacterium sp CAG 74
- Faecalibacterium taiwanense
- Candidatus Parasutterella galliste
- Neglectibacter timonensis
- uncultured Clostridium sp
- Phocaeicola plebeius
- Maccoyibacter intestinihominis
- Faecalibacterium duncaniae
- Clostridiales bacterium
- Lachnospira rogosae ex Hitch et
- Eubacterium segne
- Vescimonas coprocola
- Hominenteromicrobium mulieris
- Clostridium fessum
- Pilosibacter fragilis
- Agathobaculum hominis
- Coprococcus intestinihominis
- Dorea formicigenerans
- Oscillospiraceae bacterium
- Faecalibacterium prausnitzii
- Anthropogastromicrobium aceti
- Lachnospiraceae bacterium GAM
- Mesosutterella multiformis
- Fusicatenibacter faecihominis
- Blautia faecicola
- Ruminococcus sp UNK MGS 30
- uncultured Porphyromonadaceae
- Firmicutes bacterium CAG 176
- Evtepia gabavorous
- Alistipes communis
- Clostridium sp AM22 11AC
- Lachnospiraceae bacterium
- Oscillibacter sp CAG 241
- Faecalibacillus intestinalis
- Brotaphodocola catenula
- Firmicutes bacterium OM04 13BH
- Ruminococcus intestinalis
- Anaerobutyricum hallii
- Bacteroides sp CAG 443
- Mediterranea massiliensis
- Oliverpabstia intestinalis
- Coprococcus ammoniilyticus
- Anaerotruncus sp
- Eubacterium ventriosum
- Faecalibacillus faecis
- Dorea sp CAG 317
- Clostridium sp AF37 5
- Butyrivibrio sp CAG 318
- uncultured Bacteroides sp
- Bacteroides sp CAG 545
- Butyribacter intestini
- Roseburia amylophila
- Holdemanella sp MSK 7 32
- Coprococcus aceti
- uncultured Coriobacteriaceae bac
- Candidatus Aphodomorpha intest
- uncultured Ruminococcus sp
- Candidatus Aphodovivens avicola
- bacterium
- uncultured Eggerthella sp
- uncultured Clostridia bacterium
- Coprococcus eutactus
- uncultured Eubacteriales bacteriu
- Clostridium sp 27\_14
- Slackia isoflavoniconvertens
- Clostridium sp CAG 138
- uncultured Dialister sp
- uncultured Mollicutes bacterium
- Firmicutes bacterium CAG 341
- Clostridium sp CAG 417
- uncultured Mycoplasmatota bacte
- Eggerthella sp CAG 298
- Dialister sp CAG 486
- Candidatus Fusicatenibacter intes
- Clostridium sp
- Clostridium sp CAG 302
- Megasphaera massiliensis
- Clostridium sp CAG 343
- Clostridium sp CAG 245
- Clostridium sp CAG 567
- Eubacterium sp CAG 180
- Pseudoruminococcus massiliensis
- Lachnospira pectinoschiza
- Agathobaculum butyriciproducens
- Eggerthella sp CAG 209
- Hominimerdicola aceti
- Clostridium saudiense
- Anaerostipes amylophilus
- Akkermansia massiliensis
- Hominiplancheneus faecis
- Lachnospira eligens
- Romboutsia timonensis
- Dorea longicatena
- Fusicatenibacter saccharivorans
- Prevotella sp
- Klebsiella pneumoniae
- Donor
- Dsex
- Msex
- Week
- Tissue
- Reads
- Length
- Quality
- N50

Relative abundance, capped at 0.5



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

Donor sex: Male, Female

Mouse sex: Male, Female

Week: 1, 2, 4, 8

Tissue: Colon, Cecum

Reads, log10: 4, 5, 6, 7

Length, median: 0, 500, 1000, 1500, 2000, 2500

Quality, median: 20, 21, 22, 23, 24

Read N50: 2000, 4000, 6000, 8000