



Relative abundance, capped at 0.1

0 0.05 0.1

Donor	Donor sex	Mouse sex	Week	Tissue	Reads, log10	Length, median	Quality, median	Read N50
F0 F1	Male Female	Male Female	Donor OMM12	Colon Ileum Cecum	3 4 5 6 7	0 1000 2000 3000 4000	22 23 24 25	0 2000 4000 6000 8000 10000

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