



- Bacteroides uniformis
- Bacteroides ovatus
- Blautia faecis
- Ruminococcoides intestinale
- Sellimonas intestinalis
- Eteplia gabavorous
- Adlercreutzia rubneri
- Hominimerdicola aceti
- Fusicatenibacter saccharivorans
- Hominilimicola fabiformis
- Bacteroides eggerthii
- Phocaeicola dorei
- Eubacterium ventriosum
- Dorea sp CAG 317
- Akkermansia massiliensis
- Neglectibacter timonensis
- Gallintestinimicrobium propionicum
- Firmicutes bacterium CAG 176
- uncultured Collinsella sp
- Blautia fusiformis
- uncultured Clostridium sp
- Faecalibacterium prausnitzii
- Ruminococcus sp UNK MGS 30
- Pilosobacter fragilis
- uncultured Mollicutes bacterium
- Alistipes communis
- Hominicoprocola fusiformis
- Bacteroidales bacterium
- Faecalibacterium taiwanense
- Clostridium sp AM22 11AC
- Hominenteromicrobium mulieris
- Anthropogastromicrobium aceti
- Waltera intestinalis
- Hominisplanchneneucus 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
- 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 intestinhominis
- 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 al
- bacterium
- uncultured Selenomonadales bacterium
- Slackia isoflavoniconvertens
- 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 multiformis
- 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 faechomnis
- Dorea formicigenerans
- Lachnospira eligens
- Romboutsia timonensis
- Eggerthella sp CAG 298
- Anaerobutyricum hallii
- Coprococcus intestinhominis
- Clostridium saudiense
- Oscillospiraceae bacterium
- Candidatus Fusicatenibacter intestinhominis
- Butyrivibrio sp
- Faecalibacillus intestinalis
- Blautia intestinhominis
- Ruminococcus sp AM36 2AA
- Firmicutes bacterium OM04 13BH
- Coprococcus hominis ex Arizal et al
- Coprococcus eutactus
- Faecalibacterium sp CAG 74
- Lachnospira pectinoschiza
- Anaerostipes amylophilus
- Klebsiella pneumoniae
- Candidatus Cibiobacter qucibialis
- Clostridium sp AF37 5
- Roseburia faecis
- Segatella copri

Taxa, N=123

Relative abundance, capped at 0.5

