



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

Relative abundance, capped at 1

