
F7, N=111
F7_F712_2_F
F7_F713_1_F
F7_F712_1_F
F7_F719_8_F
F7_M711_1_F
F7_F707_1_F
F7_F706_1_F
F7_M710_1_F
F7_M701_3_I
F7_M703_2_F
F7_M704_3_I
F7_F705_3_I
F7_M715_4_F
F7_F719_8_I
F7_M710_2_F
F7_F719_4_F
F7_F721_8_C
F7_F721_8_M
F7_F726_4_F
F7_M714_4_F
F7_M716_4_F
F7_F719_8_C
F7_F719_6_F
F7_M702_3_I
F7_M704_3_M
F7_M704_3_C
F7_M704_2_F
F7_M702_2_F
F7_M702_3_C
F7_M702_3_M
F7_M703_3_M
F7_M703_3_C
F7_F713_2_F
F7_F706_2_F
F7_M702_1_F
F7_M704_1_F
F7_M703_1_F
F7_F708_2_F
F7_F707_2_F
F7_F708_3_I
F7_F707_3_I
F7_M703_3_I
F7_M714_8_I
F7_M716_8_I
F7_F708_3_C
F7_M715_8_I
F7_F721_4_F
F7_F721_6_F
F7_M716_6_F
F7_F718_6_F
F7_M716_8_M
F7_F718_8_C
F7_F722_4_F
F7_M701_3_C
F7_F720_8_I
F7_M717_4_F
F7_F720_4_F
F7_M723_4_F
F7_M725_6_F
F7_F727_6_F
F7_M723_6_F
F7_F727_8_F
F7_M701_1_F
F7_F706_3_C
F7_F706_3_M
F7_M701_2_F
F7_M717_8_I
F7_F706_3_I
F7_M717_6_F
F7_M717_8_C
F7_F718_8_M
F7_M717_8_F
F7_F722_8_F
F7_F726_6_F
F7_M725_8_F
F7_F727_4_F
F7_F722_6_F
F7_F720_8_M
F7_F720_8_C
F7_F721_8_F
F7_F720_6_F
F7_M724_8_F
F7_M724_6_F
F7_M725_4_F
F7_F718_4_F
F7_M714_8_M
F7_F707_3_C
F7_M716_8_C
F7_M717_8_M
F7_F726_8_F
F7_M714_8_F
F7_M716_8_F
F7_M715_8_C
F7_M715_8_F
F7_M715_8_M
F7_M715_6_F
F7_M723_8_F
F7_NA_0_2
F7_NA_0_1
F7_F709_1_F
F7_F708_1_F
F7_F705_1_F
F7_F705_2_F
F7_F705_3_C
F7_F705_3_M
F7_F708_3_M
F7_M714_8_C
F7_M711_2_F
F7_F718_8_I
F7_M701_3_M
F7_F721_8_I
Taxa, N=123
Akkermansia massiliensis
Blautia faecis
Bacteroides ovatus
Bacteroides uniformis
Sellimonas intestinalis
Ruminococcoides intestinale
Ruminococcus sp CAG 254
Anthropogastromicrobium aceti
Evtepia gabavorous
Candidatus Cibiobacter qucibialis
Fusicatenibacter saccharivorans
Roseburia faecis
Blautia fusiformis
Phocaeicola dorei
Clostridium sp
Adlercreutzia rubneri
Faecalibacillus faecis
Anaerostipes amylophilus
Clostridium sp CAG 343
Gemmiger formicilis
Eubacterium sp CAG 180
uncultured Coriobacteriaceae bac
Eubacterium ventriosum
Hominilimicola fabiformis
Neglectibacter timonensis
Agathobaculum hominis
uncultured Collinsella sp
Homineteromicrobium mulieris
Faecalibacterium prausnitzii
Bacteroides eggerthii
Hominicoprocola fusiformis
Alistipes communis
Hominisplanchenecus faecis
Coprococcus intestinihominis
Blautia intestinihominis
Klebsiella pneumoniae
Agathobaculum butyriciproducens
Ruminococcus sp AM36 2AA
Faecalibacterium taiwanense
Oliverpabstia intestinalis
Pilosibacter fragilis
Anaerobutyricum hallii
Ruminococcus sp UNK MGS 30
Clostridium sp AM22 11AC
Bacteroidales bacterium
uncultured Mollicutes bacterium
Faecalibacillus intestinalis
Waltera intestinalis
Maccoyibacter intestinihominis
Fusicatenibacter faecihominis
Phocaeicola plebeius
Lachnospiraceae bacterium GAM
Blautia faecicola
Firmicutes bacterium OM04 13BH
uncultured Clostridium sp
Coprococcus eutactus
Vescimonas coprocola
uncultured Eubacteriales bacteriu
Oscillibacter sp MSJ 31
Eggerthella sp CAG 298
Dorea sp CAG 317
uncultured Porphyromonadaceae
Oscillibacter sp CAG 241
Coprococcus hominis ex Arizal e
Ruminococcus intestinalis
Holdemanella sp MSK 7 32
uncultured Oscillospiraceae bacte
Butyribacter intestini
Lachnospiraceae bacterium
Brotaphodocola catenula
Firmicutes bacterium CAG 176
Anaerotruncus sp
Candidatus Fusicatenibacter intes
Bacteroides sp CAG 443
Segatella copri
Faecalibacterium sp CAG 74
Eubacterium segne
uncultured Ruminococcus sp
Candidatus Aphodomorpha intest
Pseudoruminococcus massiliensis
Clostridium sp 27_14
Butyrivibrio sp CAG 318
uncultured Clostridia bacterium
bacterium
Lachnospira rogosae ex Hitch et
Firmicutes bacterium CAG 341
uncultured Eggerthella sp
Candidatus Parasutterella galliste
Clostridium sp CAG 138
Bacteroides sp CAG 545
Megasphaera massiliensis
Mesosutterella multiformis
Clostridium sp CAG 567
uncultured Mycoplasmatota bacte
Clostridium sp CAG 302
uncultured Dialister sp
Slackia isoflavoniconvertens
Candidatus Aphodovivens avicola
uncultured Selenomonadales bac
Dialister sp CAG 486
Oscillospiraceae bacterium
Lachnospira eligens
Coprococcus ammoniilyticus
Clostridium fessum
Dorea formicigenerans
Clostridium sp AF37 5
Clostridium sp CAG 245
Clostridium sp CAG 417
Clostridium saudiense
Faecalibacterium duncaniae
Eggerthella sp CAG 209
Romboutsia timonensis
Roseburia amylophila
Gallintestinimicrobium propionicu
Dorea longicatena
Mediterranea massiliensis
Prevotella sp
Clostridiales bacterium
uncultured Bacteroides sp
Clostridium sp AM49 4BH
Lachnospira pectinoschiza
Coprococcus aceti
Hominimerdicola aceti
Donor
Dsex
Msex
Week
Tissue
Reads
Lengh
Quality
N50
Relative abundance, capped at 1
0
0.5
1
Donor
F0
F1
F2
F3
M4
M5
F6
F7
F8
F9
OMM12
Donor sex
Male
Female
Mouse sex
Male
Female
Donor
OMM12
Week
Donor
1
2
3
4
6
8
Tissue
Colon
Fecal
Ileum
Cecum
Donor1
Donor2
OMM12
Reads, log10
4
5
6
7
Lengh, median
0
200
400
600
800
1000
Quality, median
20
22
24
26
Read N50
0
5000
10000