F6, N=114
Taxa, N=123
Segatella copri
Bacteroides uniformis
Bacteroides ovatus
Phocaeicola dorei
Fusicatenibacter saccharivorans
Dorea sp CAG 317
Clostridium sp AF37 5
Coprococcus hominis ex Arizal et
Blautia faecis
Hominilimicola fabiformis
Candidatus Cibiobacter qucibialis
Adlercreutzia rubneri
Roseburia faecis
Evtepia gabavorous
Hominicoprocola fusiformis
Sellimonas intestinalis
Ruminococcus sp UNK MGS 30
Agathobaculum butyriciproducens
Eubacterium ventriosum
Firmicutes bacterium CAG 341
Faecalibacterium duncaniae
Hominenteromicrobium mulieris
Blautia fusiformis
Anaerobutyricum hallii
Gallintestinimicrobium propionicu
Waltera intestinalis
Alistipes communis
Phocaeicola plebeius
Blautia faecicola
Oliverpabstia intestinalis
Blautia intestinihominis
Clostridium fessum
Pilosibacter fragilis
Bacteroidales bacterium
Bacteroides eggerthii
uncultured Porphyromonadaceae
Lachnospiraceae bacterium GAM
Fusicatenibacter faecihominis
uncultured Clostridium sp
Prevotella sp
uncultured Eubacteriales bacteriu
Agathobaculum hominis
Clostridium sp AM22 11AC
Neglectibacter timonensis
Anaerostipes amylophilus
Firmicutes bacterium OM04 13BH
Coprococcus eutactus
Lachnospiraceae bacterium
Eggerthella sp CAG 209
uncultured Bacteroides sp
Eubacterium segne
Candidatus Fusicatenibacter intes
Anaerotruncus sp
Hominimerdicola aceti
Coprococcus ammoniilyticus
Eubacterium sp CAG 180
uncultured Coriobacteriaceae bac
Candidatus Aphodovivens avicola
uncultured Eggerthella sp
Firmicutes bacterium CAG 176
Bacteroides sp CAG 443
Mediterranea massiliensis
Candidatus Aphodomorpha intest
uncultured Oscillospiraceae bacte
Pseudoruminococcus massiliensis
Butyribacter intestini
uncultured Ruminococcus sp
Butyrivibrio sp CAG 318
Candidatus Parasutterella galliste
uncultured Selenomonadales bac
uncultured Clostridia bacterium
Bacteroides sp CAG 545
Akkermansia massiliensis
Slackia isoflavoniconvertens
uncultured Mollicutes bacterium
Clostridium sp CAG 567
Clostridium sp CAG 417
Clostridium sp
Clostridium sp CAG 343
Mesosutterella multiformis
uncultured Dialister sp
Clostridium sp CAG 302
Clostridium sp CAG 245
Megasphaera massiliensis
uncultured Mycoplasmatota bacte
Eggerthella sp CAG 298
Clostridium sp 27_14
Clostridium saudiense
Oscillibacter sp CAG 241
Brotaphodocola catenula
bacterium
Lachnospira pectinoschiza
Holdemanella sp MSK 7 32
Ruminococcus sp CAG 254
Faecalibacillus faecis
Ruminococcoides intestinale
Ruminococcus intestinalis
Oscillibacter sp MSJ 31
Faecalibacterium taiwanense
Clostridium sp AM49 4BH
Faecalibacterium sp CAG 74
Vescimonas coprocola
Coprococcus intestinihominis
Lachnospira eligens
Lachnospira rogosae ex Hitch et
Faecalibacillus intestinalis
Gemmiger formicilis
Dorea longicatena
Ruminococcus sp AM36 2AA
Oscillospiraceae bacterium
Faecalibacterium prausnitzii
Maccoyibacter intestinihominis
Dorea formicigenerans
Romboutsia timonensis
Clostridiales bacterium
Clostridium sp CAG 138
Coprococcus aceti
Hominisplanchenecus faecis
Roseburia amylophila
uncultured Collinsella sp
Dialister sp CAG 486
Anthropogastromicrobium aceti
Klebsiella pneumoniae
Donor
Dsex
Msex
Week
Tissue
Reads
Lengh
Quality
N50
Relative abundance, capped at 0.5
0 0.2 0.4 0.6
Donor
F0 F2 M4 F6 F8 OMM12
F1 F3 M5 F7 F9
Donor sex
Male
Female
Mouse sex
Male
Female
Donor
OMM12
Week
Donor 2 4 8
1 3 6
Tissue
Colon Ileum Donor1 OMM12
Fecal Cecum Donor2
Reads, log10
3 4 5 6 7
Lengh, median
0 200 400 600 800
Quality, median
18 20 22 24 26
Read N50
0 2000 4000 6000