M4, N=130
Taxa, N=123
Segatella copri
Bacteroides uniformis
Blautia faecis
Fusicatenibacter saccharivorans
Anthropogastromicrobium aceti
Adlercreutzia rubneri
Evtepia gabavorous
Bacteroides ovatus
Blautia fusiformis
uncultured Ruminococcus sp
Sellimonas intestinalis
Hominilimicola fabiformis
Eubacterium ventriosum
Oliverpabstia intestinalis
Dorea longicatena
uncultured Collinsella sp
Phocaeicola dorei
Bacteroidales bacterium
Alistipes communis
Coprococcus intestinihominis
Phocaeicola plebeius
Hominisplanchenecus faecis
Hominenteromicrobium mulieris
Dorea sp CAG 317
Faecalibacterium duncaniae
Clostridium sp AM22 11AC
Faecalibacterium taiwanense
Lachnospira eligens
Bacteroides sp CAG 443
Firmicutes bacterium OM04 13BH
Megasphaera massiliensis
Slackia isoflavoniconvertens
Eggerthella sp CAG 298
Faecalibacterium prausnitzii
Candidatus Cibiobacter qucibialis
Oscillospiraceae bacterium
Clostridium sp AM49 4BH
Clostridium sp 27_14
Blautia faecicola
Clostridium fessum
Agathobaculum butyriciproducens
Pilosibacter fragilis
Bacteroides eggerthii
Hominicoprocola fusiformis
Ruminococcus sp UNK MGS 30
Klebsiella pneumoniae
Anaerostipes amylophilus
Blautia intestinihominis
Fusicatenibacter faecihominis
Ruminococcus sp AM36 2AA
Eubacterium segne
Lachnospiraceae bacterium GAM
Clostridiales bacterium
Lachnospira pectinoschiza
Candidatus Parasutterella galliste
Dorea formicigenerans
Clostridium sp
Faecalibacillus intestinalis
Holdemanella sp MSK 7 32
Roseburia amylophila
Agathobaculum hominis
Lachnospiraceae bacterium
Faecalibacillus faecis
Coprococcus hominis ex Arizal et
Coprococcus eutactus
Gemmiger formicilis
Maccoyibacter intestinihominis
Waltera intestinalis
Prevotella sp
Vescimonas coprocola
uncultured Oscillospiraceae bacte
Roseburia faecis
uncultured Bacteroides sp
uncultured Clostridium sp
Brotaphodocola catenula
Oscillibacter sp CAG 241
Oscillibacter sp MSJ 31
Firmicutes bacterium CAG 176
Ruminococcoides intestinale
Clostridium sp CAG 245
Clostridium sp AF37 5
Candidatus Fusicatenibacter intes
uncultured Selenomonadales bac
Ruminococcus intestinalis
Anaerotruncus sp
Clostridium sp CAG 343
uncultured Eggerthella sp
Mediterranea massiliensis
bacterium
Coprococcus aceti
uncultured Eubacteriales bacteriu
Clostridium sp CAG 567
Candidatus Aphodomorpha intest
Faecalibacterium sp CAG 74
Eubacterium sp CAG 180
Pseudoruminococcus massiliensis
Clostridium sp CAG 138
Butyrivibrio sp CAG 318
uncultured Clostridia bacterium
Butyribacter intestini
Bacteroides sp CAG 545
Ruminococcus sp CAG 254
Mesosutterella multiformis
Firmicutes bacterium CAG 341
Eggerthella sp CAG 209
Clostridium sp CAG 417
uncultured Coriobacteriaceae bac
Dialister sp CAG 486
Clostridium sp CAG 302
uncultured Mycoplasmatota bacte
uncultured Mollicutes bacterium
Coprococcus ammoniilyticus
Hominimerdicola aceti
Candidatus Aphodovivens avicola
Neglectibacter timonensis
uncultured Porphyromonadaceae
Gallintestinimicrobium propionicum
Romboutsia timonensis
Anaerobutyricum hallii
Akkermansia massiliensis
Lachnospira rogosae ex Hitch et
uncultured Dialister sp
Clostridium saudiense
Donor
Dsex
Msex
Week
Tissue
Reads
Lengh
Quality
N50
Relative abundance, capped at 0.5
0 0.2 0.4 0.6
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
3 4 5 6 7
Lengh, median
100 200 300 400 500 600
Quality, median
18 20 22 24
Read N50
0 2000 4000 6000 8000