MUN MUO MUN MUO Modularity 0.76 0.737 Natural connectivity 0.008 Number of components 71 89 Positive edge percentage 82.667 85.185 Shuttleworthia **Edge density** 0.009 0.006 Clustering coefficient 0.351 Methanobrevibacter [Eubacterium] brachy group Rikenellaceae RC9 gut group [Clostridium] inholaim ganjfractor [Clostridium] inholaim on ifractor Lachnospiraceae NK4B4 group [Eubacterium] fissicatena group [Eubacterium] fissicatena group Lachnospiraceae ND3007 group Lachnospiraceae ND3007 group Lachnospira UCG-003 Akkermansia Akkermansia [Eubacterium] ventriosum group Phascolarctobacterium Phascolarctobacterium Coprococcus Bacteroides [Bacteroides] pectinophilus group [Bacteroides] pectinophilus group Odoribacter Lachnospiraceae UCG-007 Odoribacter Lachnospiraceae UCG-007 Lachnospiraceae NK3A20 group Lachnospiraceae NK3A20 group Parabacteroides Erysipelotrichaceae UCG-003 Parabacteroides Erysipelotrichaceae UCG-003 Lachnospiraceae UCG-010 Lachnospiraceae UCG-010 Fusicatenibacter CAG-56 [Ruminococcus] torques group [Ruminococcus] torques group Lachnospiraceae FCS020 groupRoseburia Lachnospiraceae FCS020 groupRoseburia Lachnospiraceae NK4A136 group Holdemanella Megasphaera Candidatus Soleaferrea Mitsuokella Bilophila UCG-009 Coriobacteriaceae UCG-003 Coriobacteriaceae UCG-003 Olsenella Peptococcus