human gut metagenome Clostridiaceae bacterium DJF LS40 Clostridium sp. Culture Jar-8 [Eubacterium] siraeum V10Sc8auman gut metagenome Ruminiclostridium 5 [Eubacterium] coprostanoligenes group Ruminiclostridium 6 Ruminococcaceae UCG-004 [Clostridium] cocleatum Angelakisella massiliensis Clostridiales bacterium 30-4c Angelakisella Flavonifractor Ervsipelatoclostridium Anaerotruncus sp. G3(2012) Ruminococcaceae bacterium enrichment culture Lactobacillus apodemi DSM 16634 = JCM 16172 Anaerotruncus Ruminococcaceae UCG-0124ysipelotrichaceae Ruminiclostridium@ostridium saudiense Lactobacillus Ruminococcaceae UCG-010 gut metagenome Lactobacillaceae Ruminiclostridium Clostridium sensu stricto 1 Oscillibacter metagenome Erysipelotrichales Lactobacillales [Clostridium] leptum Clostridiaceae 1 Erysipelotrichia Akkermansia sp. UNK.MGS-1 Romboutsia ilealis Bacilli Akkermansia Peptostreptococcaceae Romboutsia Akkermansiaceae Mucispirillum schaedleri ASF457 Clostridiales Firmicutes Verrucomicrobiales Mucispirillum Clostridia Verrucomicrobia Verrucomicrobiae Deferribacteraceae **Deferribacterales** Deferribacteres Deferribacteres metagenome Lachnospiraceae bacterium DW67 Clostridium sp. Clone-44 Clostridiaceae bacterium SH021 Bacteria Roseburia GCA-900066575
Clostridiales bacterium CIEAF 017 human gut metagenome Bacteroidetes Gammaproteobacteria
TyzzerellaLachnospiraceae bacterium DW17 Enterobacteriales **Nodes** Lachnospiraceae bacterium A2Hungatella Lachnospiraceae bacterium G11 Bacteroidia Enterobacteriaceae
Lachnospiraceae NK4A136 group Bacteroidales Escherichia-Shigella
Lachnospiraceae bacterium AJ110941

Shuttleworthia -5.000.00 Shuttleworthia Lachnospiraceae bacterium AJ110941 Oscillospiraceae bacterium Pagethnospiraceae
Clostridiales bacterium CIEAF 012 nospiraceae gut metagenome Tannerellaceae 3.31 -3.33Parabacteroides Marvinbryantibachnospiracealcabl@Gsp@Gceae @GGridloth] symbiosum ATCC 14940 ratio Clostridium sp. ASF502UC5-1-2E3 Clostridium sp. M62/1 13.20 -1.67human gut metagenome metagenome Acetatifactor metagenome metagenome [Eubacterium] fissicatena group Eisenbergiella Lachnospiraceae bacterium 5_1_57FAA 0.00 29.80 Salmonella enterica sul spoteritieribacterium UC511a@Enoclostridium Eubacteriaceae bacterium DSY8 Blautia Clostridium fusifo [Pilostridium asparagiforme] DSM 15981 1.67 52.90 Eisenbergiella tayi mouse gut metagenome 3.33 82.60 Lachnospiraceae bacterium DW3 Lachnospiraceae bacterium 28–4 Clostridiales bacterium VE202-06 5.00 119.00