human gut metagenome Clostridiaceae bacterium DJF LS40 Clostridium sp. Culture Jar-8 [Eubacterium] siraeum V10Sc8auman gut metagenome Ruminiclostridium 5 [Eubacterium] coprostanoligenes group Ruminicoccaceae 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-0124 y sipelotrichaceae 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 **Verrucomi**crobiae 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
TyzzerellaLachnospiraceae bacterium G11 Bacteroidia Enterobac **Nodes** Lachnospiraceae bacterium A2Hungatella Lachnospiraceae bacterium G11 Bacteroidia Enterobacteriaceae

A2 Lachnospiraceae NK4A136 group Bacteroidales Escherichia-Shigella

Shuttleworthia Lachnospiraceae bacterium AJ110941

Triticum aestivum (bread wheat) -5.000.00 Shuttleworthia Lachnospiraceae bacterium AJ110941 Oscillospiraceae bacterium dagsethnospiraceae
Clostridiales bacterium CIEAF 012 nospiraceae gut metagenome Tannerellaceae 3.31 -3.33Parabacteroides Marvinbryantilachnospiracedebl@Gsp@ceae @CGridiOth] symbiosum ATCC 14940 ratio 13.20 Clostridium sp. ASF502UC5-1-2E3 Clostridium sp. M62/1 -1.67human gut metagenome metagenome metagenome Acetatifactor metagenome Eisenbergiella Lachnospiraceae bacterium 5 1 57FAA [Eubacterium] fissicatena group 0.00 29.80 Salmonella enterica subsostridieribacterium UC511a250clostridium Eubacteriaceae bacterium DSY8 Blautia Clostridium fusifor Pois stridium 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