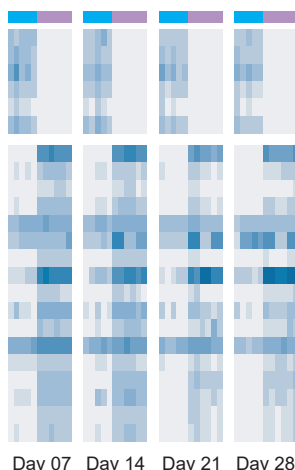


D

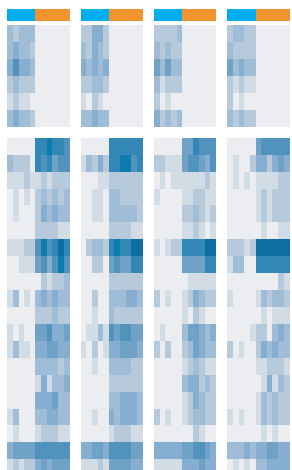
The differentially abundant metagenomic species compared to the control group at each time point

Probiotic+GOS (Continuous)



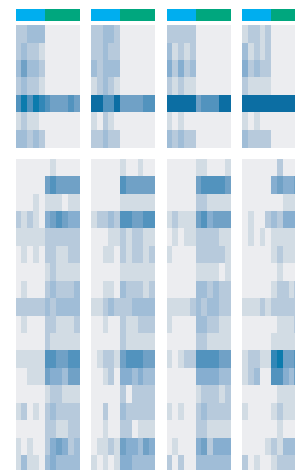
Alloprevotella sp. E39
Clostridium hylemonae
Flintibacter sp. KGMB00164
Lachnospiraceae bacterium
Pseudobutyrvibrio xylanivorans
Ruminococcus gnavus
Acutalibacter muris
Bacillus cereus
Bacillus subtilis
Bacillus thuringiensis
Bacteroides salanitronis
Bacteroides xylanisolvens
Clostridium sporogenes
Duncaniella sp.
Enterobacter hormaechei
Intestinimonas butyriciproducens
Klebsiella pneumoniae
Parabacteroides distasonis
Pseudomonas fluorescens
Ruthenibacterium lactatiformans
Salmonella enterica
Streptococcus gallolyticus
Streptococcus pyogenes

Probiotic+GOS (Pulsed)



Alloprevotella sp. E39
Clostridium hylemonae
Flintibacter sp. KGMB00164
Lachnospiraceae bacterium
Pseudobutyrvibrio xylanivorans
Ruminococcus gnavus
Acutalibacter muris
Alcanivorax sp. N3-2A
Alistipes sp. 5CBH24
Bacillus cereus
Bacillus thuringiensis
Clostridium sporogenes
Duncaniella sp. B8
Duncaniella sp. C9
Enterobacter hormaechei
Enterococcus faecium
Erysipelotrichaceae bacterium
Halomonas sp. N3-2A
Intestinimonas butyriciproducens
Klebsiella pneumoniae
Lactobacillus plantarum
Longibaculum sp.
Oscillibacter sp. PEA192
Paenibacillus polymyxa
Parabacteroides distasonis
Parabacteroides sp. CT06
Pseudomonas aeruginosa
Ruthenibacterium lactatiformans
Salmonella enterica
Streptococcus gallolyticus
Streptococcus pyogenes

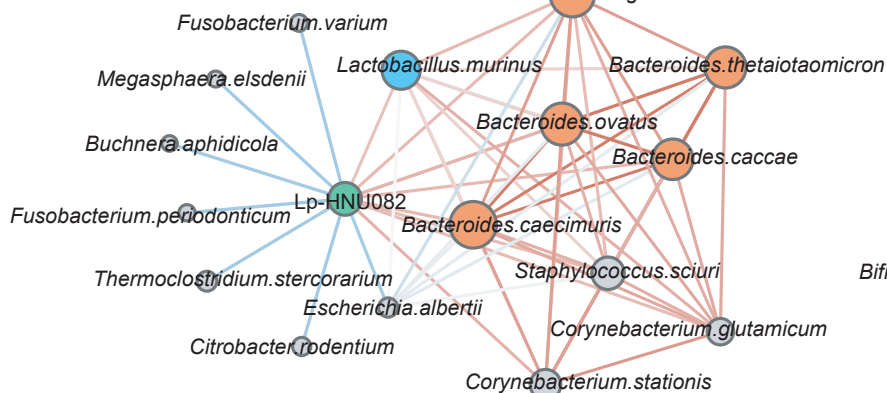
Probiotic



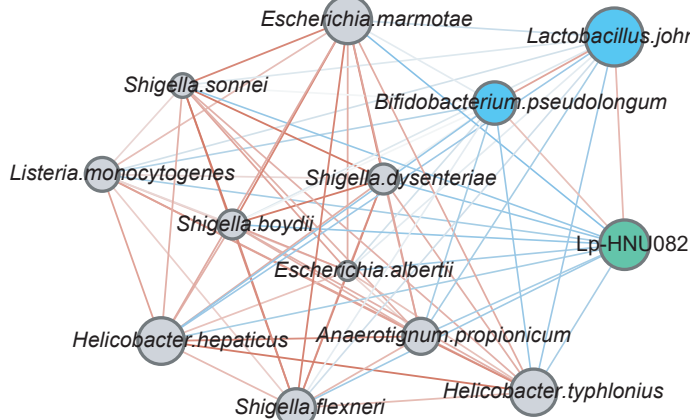
Alloprevotella sp. E39
Clostridium hylemonae
Flintibacter sp. KGMB00164
Lachnospiraceae bacterium
Muribaculum sp. TLL-A4
Pseudobutyrvibrio xylanivorans
Ruminococcus gnavus
Acinetobacter baumannii
Acutalibacter muris
Aeromonas hydrophila
Alcanivorax sp. N3-2A
Alistipes sp. 5CBH24
Bacillus cereus
Bacillus subtilis
Bacillus thuringiensis
Bacteroides sp. A1C1
Campylobacter jejuni
Clostridium sporogenes
Duncaniella sp. B8
Duncaniella sp. C9
Enterobacter hormaechei
Enterococcus faecium
Erysipelotrichaceae bacterium
Halomonas sp. N3-2A
Intestinimonas butyriciproducens
Klebsiella pneumoniae
Lactobacillus plantarum
Longibaculum sp. KGMB06250
Oscillibacter sp. PEA192
Paenibacillus polymyxa
Parabacteroides distasonis
Parabacteroides sp. CT06
Pseudomonas aeruginosa
Pseudomonas fluorescens
Ruthenibacterium lactatiformans
Salmonella enterica
Streptococcus gallolyticus
Streptococcus pyogenes

E

Probiotic+GOS (Continuous)



Probiotic+GOS (Pulsed)



Lp HNU082 and its significantly correlated indigenous intestinal microbes among the 3 groups

Probiotic

