Microbial Consortia for the Treatment of Disease

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of and priority to U.S. Provisional Patent Application No. 62/987,757, filed March 10, 2020, the disclosure of which is hereby incorporated by reference in its entirety for all purposes.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on March 10, 2021, is named FBI-002WO_SL.txt and is 878,406 bytes in size.

FIELD OF THE INVENTION

[0003] The invention generally relates to microbial consortia for administration to an animal for degradation of a disease-associated metabolic substrate.

BACKGROUND

[0004] The gastrointestinal tract comprises various biological niches along its longitudinal length having different physical, chemical, and nutrient compositions. As a consequence of these diverse conditions, specific microbial communities are established within a particular biological niche. The microbial species comprising a specific microbial community are highly responsive to their local environment and produce an array of bioactive molecules that facilitate host engraftment, inter-microbial communication, nutrient metabolism, and inclusion or exclusion of competing microbial species. Adding further complexity, there is substantial diversity of microbial species and strains in the human GI tract between individuals, which is attributed to a number of factors including genetics, diet, antibiotic and antifungal use, surgical intervention (*e.g.*, gastric by-pass/bowel resection), presence of inflammatory bowel disease and/or irritable bowel syndrome, and other environmental influences. However, despite this interindividual diversity, the functional attributes of the varying human gut microbiota are relatively consistent among healthy adults and comprise core metabolic pathways involved in carbohydrate metabolism, amino acid metabolism, fermentation, and oxidative phosphorylation.

[0005] Modulation of microbial species in the GI tract through the use of antibiotics, antifungals, and more recently, fecal microbial transplantation ("FMT"), have been approaches clinically investigated for the treatment and/or prevention of certain diseases and disorders. For example, Dodd *et al.* (*Nature*, 2007, 551: 648-652) have proposed FMT as a therapeutic to modulate the levels of aromatic amino acid metabolites in the serum of gnotobiotic mice, which affect intestinal permeability and systemic immunity. In further examples, administration of bacterial compositions has also been proposed as a method for treating *Clostridium difficile* infection, ulcerative colitis, cholestatic disease, and hyperoxaluria (*see e.g.,* US 2018/0353554, WO 2019/036510, US RE39,585).

[0006] As a modality for treating various diseases and/or conditions, there is a need for microbial compositions comprising a plurality of microbial species having improved therapeutic efficacy and an ability to efficiently engraft in a host, grow, and metabolize pathogenic substrates to non-pathogenic metabolic products within the various biological niches of the GI tract and within the diverse GI environments of different individuals.

SUMMARY OF THE INVENTION

[0007] Disclosed here is a microbial consortium for administration to an animal comprising a plurality of active microbes and an effective amount of a supportive community of microbes. In some embodiments, the plurality of active microbes metabolize a first metabolic substrate to produce one or more than one metabolite, wherein the first metabolic substrate causes or contributes to disease in an animal.

[0008] In some embodiments, the supportive community of microbes comprises between 1 and 300 microbial strains and meets one, two, three, or four of the following conditions:

1) the supportive community of microbes metabolizes one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the first metabolic substrate by one or more of the plurality of active microbes,

2) the supportive community of microbes increases the flux of a precursor of the first metabolic substrate into a biochemical pathway that converts said precursor into a metabolite that is not the first metabolic substrate,

3) the supportive community of microbes enhances one or more than one characteristic of the plurality of active microbes when administered to an animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c)

first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes, and

4) the supportive community of microbes catalyzes one or more than one reaction selected from the group consisting of: fermentation of polysaccharides to one or more than one of the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2, fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2, synthesis of one or more than one of the group consisting of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

[0009] In some embodiments, the first metabolic substrate metabolizing activity of at least one of the plurality of active microbes is significantly different when measured in a standardized substrate metabolization assay at two pH values within a range of 4 to 8, and wherein the difference between the two pH values is at least one pH unit.

[0010] In some embodiments, the first metabolic substrate metabolizing activity of at least one of the plurality of active microbes is significantly different when measured in a standardized substrate metabolization assay at two first metabolic substrate concentrations within a 100 fold range, and wherein the difference between the two first metabolic substrate concentrations is at least 1.2-fold.

[0011] In some embodiments, the supportive community of microbes comprises at least three, at least four, at least five, or six phyla selected from Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia, and Euryarchaeota.

[0012] In some embodiments, the supportive community of microbes comprises one or more of the subclades Bacteroidales, Clostridiales, Erysipelotrichales. Negativicutes, Coriobacteriia, Bifidobacteriales, or Methanobacteriales.

[0013] In some embodiments, the first metabolic substrate is oxalate. In some embodiments, the supportive community of microbes catalyzes synthesis of methane from formate and H_2.

[0014] In some embodiments, the plurality of active microbes comprises *Oxalobacter formigenes*. In some embodiments the supportive community of microbes comprises a Bacteroidetes and a Euryarchaeota. In some embodiments, the supportive community of microbes comprises a Bateroides and Methanobrevibacter. In further embodiments, the supportive community of microbes comprises *Bacteroides thetaiotaomicron* and/or *Bacteroides vulgatus*, and *Methanobrevibacter smithii*.

[0015] In some embodiments, the supportive community of microbes metabolizes one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the plurality of active microbes.

[0016] In some embodiments, the supportive community of microbes enhances one or more than one characteristic of the plurality of active microbes when administered to an animal selected from the group consisting of gastrointestinal engraftment, biomass, first metabolic substrate metabolism, and longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes.

[0017] In some embodiments, the supportive community catalyzes one or more than one reaction selected from the group consisting of:

fermentation of polysaccharides to one or more than one of the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2,

fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2,

synthesis of one or more than one of the group consisting of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate

and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate, and

deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

[0018] In some embodiments, the supportive community of microbes comprises between 20 and 200 microbial strains. In some embodiments, the supportive community comprises at least 4 phyla selected from the group consisting of Bacteroidetes, Firmicutes, Actinobacteria, and Proteobacteria. In some embodiments, the supportive community comprises a *Ruminococcus*, *Clostridium*, *Bacteroides*, *Neglecta*, *Bifidobacterium*, *Egerthella*, *Clostridiaceae, Parabacteroides*, *Bilophila*, *Dorea*, *Collinsella*, and *Faecalibacterium*.

[0019] In some embodiments, the supportive community comprises *Ruminococcus bromii*, *Clostridium citroniae*, *Bacteroides salyersiae*, *Neglecta timonensis*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bacteroides thetaiotaomicron*, *Eggerthella lenta*, *Clostridiaceae sp.*, *Bifidobacterium dentium*, *Parabacteroides merdae*, *Bilophila wadsworthia*, *Bacteroides caccae*, *Dorea longicatena*, *Collinsella aerofaciens*, *Clostridium scindens*, *Faecalibacterium prausnitzii*, *Clostridium symbiosum*, and *Bacteroides vulgatus*.

[0020] In some embodiments, the supportive community comprises an *Acidaminococcus*, an *Akkermansia*, an *Alistipes*, an *Anaerofustis*, an *Anaerostipes*, an *Anaerotruncus*, a *Bacteroides*, a *Barnesiella*, a *Bifidobacterium*, a *Bilophila*, a *Blautia*, a *Butyricimonas*, a *Catabacter hongkongensis*, a *Clostridiaceae*, a *Clostridiales*, a *Clostridium*, a *Collinsella*, a *Coprococcus*, a *Dialister*, a *Dielma, a Dorea*, an *Eggerthella*, an *Eisenbergiella*, a *Eubacterium*, a *Faecalibacterium*, a *Fusicatenibacter saccharivorans*, a *Gordonibacter pamelaeae*, a *Holdemanella*, a *Hungatella*, a *Lachnoclostridium*, *Lachnospiraceae*, a *Lactobacillus*, a *Longicatena*, a *Megasphaera*, a *Methanobrevibacter*, a *Monoglobus*, a *Neglecta*, a *Parabacteroides*, a *Paraprevotella*, a *Parasutterella*, a *Phascolarctobacterium*, a *Porphyromonas*, a *Roseburia hominis*, a *Ruminococcaceae*, a *Ruminococcus*, a *Ruthenibacterium*, a *Senegalimassilia*, a *Sutterella*, and a *Turicibacter*.

[0021] In some embodiments, the supportive community comprises or consists of *Acidaminococcus intestine*, *Akkermansia muciniphila*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Alistipes senegalensis*, *Alistipes shahii*, *Alistipes sp.*, *Alistipes timonensis*,

Anaerofustis stercorihominis, *Anaerostipes hadrus*, *Anaerotruncus massiliensis*, *Bacteroides caccae*, *Bacteroides coprocola*, *Bacteroides faecis*, *Bacteroides finegoldii*, *Bacteroides fragilis*, *Bacteroides kribbi*, *Bacteroides massiliensis*, *Bacteroides nordii*, *Bacteroides ovatus*, *Bacteroides salyersiae*, *Bacteroides stercorirosoris*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvens*, *Barnesiella intestinihominis*, *Bifidobacterium adolescentis*, *Bifidobacterium bifidum*, *Bifidobacterium catenulatum*, *Bifidobacterium dentium*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bilophila wadsworthia*, *Blautia faecis*, *Blautia hydrogenotrophica*, *Blautia massiliensis*, *Blautia obeum*, *Blautia wexlerae*, *Butyricimonas faecihominis*, *Catabacter hongkongensis*, *Clostridiaceae sp.*, *Clostridiales sp.*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium citroniae*, *Clostridium clostridioforme*, *Clostridium fessum*, *Clostridium scindens*, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dialister succinatiphilus*, *Dielma fastidiosa*, *Dorea formicigenerans*, *Dorea longicatena*, *Eggerthella lenta*, *Eisenbergiella tayi*, *Eubacterium eligens*, *Eubacterium hallii*, *Eubacterium rectale*, *Eubacterium siraeum*, *Eubacterium ventriosum*, *Eubacterium xylanophilum*, *Faecalibacterium prausnitzii*, *Fusicatenibacter saccharivorans*, *Gordonibacter pamelaeae*, *Holdemanella biformis*, *Hungatella effluvia*, *Lachnoclostridium pacaense*, *Lachnospiraceae sp.*, *Lactobacillus rogosae*, *Longicatena caecimuris*, *Megasphaera massiliensis*, *Methanobrevibacter smithii*, *Monoglobus pectinilyticus*, *Neglecta timonensis*, *Parabacteroides distasonis*, *Parabacteroides merdae*, *Paraprevotella clara*, *Parasutterella excrementihominis*, *Phascolarctobacterium faecium*, *Porphyromonas asaccharolytica*, *Roseburia hominis*, *Ruminococcaceae sp.*, *Ruminococcus bromii*, *Ruminococcus faecis*, *Ruthenibacterium lactatiformans*, *Senegalimassilia anaerobia*, *Sutterella massiliensis*, *Sutterella wadsworthensis*, and *Turicibacter sanguinis*.

[0022] In some embodiments, the supportive community of microbes comprises an *Akkermansia*, an *Alistipes*, an *Anaerostipes*, a *Bacteroides*, a *Bifidobacterium*, a *Bilophila*, a *Blautia*, a *Clostridium*, a *Collinsella aerofaciens*, a *Coprococcus*, *Dialister*, a *Dorea*, an *Eggerthella*, an *Eisenbergiella*, a *Eubacterium*, a *Faecalibacterium*, a *Fusicatenibacter*, a *Gordonibacter*, a *Holdemanella*, a *Hungatella*, a *Lachnoclostridium*, a *Lachnospiraceae*, a *Lactobacillus*, a *Monoglobus*, a *Neglecta*, a *Parabacteroides*, a *Paraprevotella*, a *Parasutterella*, a *Phascolarctobacterium*, a *Porphyromonas*, a *Roseburia*, a *Ruminococcaceae*, a *Ruminococcus*, a *Ruthenibacterium*, and a *Sutterella*.

[0023] In some embodiments, the supportive community of microbes comprises or consists of *Akkermansia muciniphila*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Alistipes*

shahii, *Alistipes timonensis*, *Anaerostipes hadrus*, *Bacteroides caccae*, *Bacteroides fragilis*, *Bacteroides kribbi*, *Bacteroides koreensis*, *Bacteroides massiliensis*, *Bacteroides nordii*, *Bacteroides salyersiae*, *Bacteroides stercorirosoris*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvens*, *Bifidobacterium adolescentis*, *Bifidobacterium catenulatum*, *Bifidobacterium dentium*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bilophila wadsworthia*, *Bilophila wadsworthia*, *Blautia faecis*, *Blautia obeum*, *Blautia wexlerae*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium citroniae*, *Clostridium clostridioforme*, *Clostridium fessum*, *Clostridium scindens*, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dialister succinatiphilus*, *Dorea formicigenerans*, *Dorea longicatena*, *Eggerthella lenta*, *Eisenbergiella tayi*, *Eubacterium eligens*, *Eubacterium rectale*, *Faecalibacterium prausnitzii*, *Fusicatenibacter saccharivorans*, *Gordonibacter pamelaeae*, *Holdemanella biformis*, *Hungatella effluvia*, *Lachnoclostridium pacaense*, *Lachnospiraceae sp.*, *Lactobacillus rogosae*, *Monoglobus pectinilyticus*, *Neglecta timonensis*, *Parabacteroides distasonis*, *Parabacteroides merdae*, *Paraprevotella clara*, *Parasutterella excrementihominis*, *Phascolarctobacterium faecium*, *Porphyromonas asaccharolytica*, *Roseburia hominis*, *Ruminococcaceae sp.*, *Ruminococcus bromii*, *Ruminococcus faecis*, *Ruthenibacterium lactatiformans*, *Sutterella massiliensis*, and *Sutterella wadsworthensis*.

[0024] In some embodiments, the microbial consortium or the supportive community of microbes comprises 20 to 200, 70 to 80, 80 to 90, 100 to 110, or 150 to 160 microbial strains.

[0025] In some embodiments, the supportive community of microbes comprises between 100 and 150 microbial strains.

[0026] In some embodiments, the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 80% identical, at least 90% identical, or at least 97% identical to any one of the microbes listed in Table 4, 22, 23, 20, 16, 17, 18 or 19.

[0027] In some embodiments, the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 80% identical, at least 90% identical, or at least 97% identical to any one of the microbes listed in Table 22, 23, 20, 16, 17, 18 or 19.

[0028] In some embodiments, the first metabolic substrate metabolizing activity of one of the plurality of active microbes is significantly different compared to the first metabolic substrate activity of at least one other of the plurality of active microbes when measured in a standardized substrate metabolization assay under the same conditions.

[0029] In some embodiments, one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower pH compared to at least one other of the plurality of active microbes at the same lower pH. In some embodiments, one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower pH compared to a first metabolic substrate metabolizing activity of the same active microbe at a higher pH. In some embodiments the lower pH is at 4.5 ± 0.5.

[0030] In some embodiments, one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a higher pH compared to at least one other of the plurality of active microbes at the same higher pH. In some embodiments, one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a higher pH compared to a first metabolic substrate activity of the same active microbe at a lower pH. In some embodiments, the higher pH is at 7.5 ± 0.5.

[0031] In some embodiments, one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower pH and one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a higher pH. In some embodiments, the difference between the two pH values is at least 1.5, 2.0, 2.5, 3.0, 3.5, or 4.0 pH units.

[0032] In some embodiments, one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower concentration of first metabolic substrate compared to the first metabolic substrate activity of at least one other of the plurality of active microbes when measured in a standardized substrate metabolization assay under the same conditions. In some embodiments, one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower concentration of first metabolic substrate compared to a first metabolic substrate metabolizing activity of the same active microbe at a higher concentration of first metabolic substrate. In some embodiments, one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a higher concentration of first metabolic substrate compared to the first metabolic substrate activity of at least one other of the plurality of active microbes when measured in a standardized substrate metabolization assay under the same conditions. In some embodiments, one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower concentration of first metabolic substrate compared to a first metabolic substrate metabolizing activity of the same active microbe at a higher concentration of first metabolic substrate.

[0033] In some embodiments one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower first metabolic substrate concentration and one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a higher first metabolic substrate concentration. In some embodiments, the difference between the two first metabolic substrate concentrations is at least 1.2 fold, 2.0 fold, 3.0 fold, 4.0 fold, 5.0 fold, 6.0 fold, 7.0 fold, 8.0 fold, 9.0 fold, 10 fold, 20 fold, 30 fold, 40 fold, 50 fold, 60 fold, 70 fold, 80 fold, 90 fold, 100 fold, or greater than 100 fold.

[0034] In some embodiments, the microbial consortium of the present invention comprises a plurality of active microbes comprising 2 to 200 microbial strains. In certain embodiments, the plurality of active microbes comprises 2 to 20 microbial strains.

[0035] In some embodiments of the present invention, the first metabolic substrate is oxalate. In some embodiments, the one or more than one metabolite is selected from the group consisting of formate and carbon dioxide (CO_2). In some embodiments, at least one of the plurality of active microbes has a higher oxalate metabolizing activity at 0.75 mM of oxalate compared to the oxalate metabolizing activity of at least one other of the plurality of active microbes when measured in a standardized oxalate metabolization assay under the same conditions. In some embodiments, one of the plurality of active microbes has a higher oxalate metabolizing activity at 0.75 mM of oxalate compared to an oxalate metabolizing activity of the same active microbe at a higher concentration of oxalate. In some embodiments, at least one of the plurality of active microbes has a higher oxalate metabolizing activity at 40 mM of oxalate compared to the oxalate metabolizing activity of at least one other of the plurality of active microbes when measured in a standardized oxalate metabolization assay under the same conditions. In some embodiments, one of the plurality of active microbes has a higher oxalate metabolizing activity at 40 mM of oxalate compared to an oxalate metabolizing activity of the same active microbe at a lower concentration of oxalate. In some embodiments, one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at 0.75 mM of oxalate and another one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at 40 mM of oxalate.

[0036] In some embodiments, the standardized substrate metabolization assay comprises analysis of sample microbial cultures using a colorimetric enzyme assay that measures the activity of oxalate oxidase in a culture sample comprising the microbial consortium, wherein the culture sample comprises three or more microbial strains in an appropriate culture medium incubated for 1 hour to 120 hours in the presence of oxalate at a

concentration of 0.5 mM to 50 mM, at a pH of 3.5 to 8.0, and at a temperature of 35 °C to 40 °C.

[0037] In some embodiments, the standardized substrate metabolization assay comprises liquid chromatography – mass spectrometry, wherein the culture sample comprises three or more microbial strains in an appropriate culture medium incubated for 1 hour to 120 hours in the presence of oxalate at a concentration of 0.5 mM to 50 mM, at a pH of 3.5 to 8.0, and at a temperature of 35 °C to 40 °C.

[0038] In some embodiments, the microbial consortium of the present invention further comprises: a fermenting microbe that metabolizes a fermentation substrate to one or more than one fermentation product; and a synthesizing microbe that catalyzes a synthesis reaction that combines the one or more than one metabolite and the one or more than one fermentation product to generate one or more than one synthesis product.

[0039] In some embodiments the one or more than one fermentation product is a second metabolic substrate for the plurality of active microbes or a third metabolic substrate for the synthesizing microbe. In some embodiments the one or more than one synthesis product is a second metabolic substrate for the plurality of active microbes or a fourth metabolic substrate for the fermenting microbe. In some embodiments the fermentation substrate is a polysaccharide and the one or more than one fermentation product is selected from the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2. In some embodiments, the fermentation substrate is an amino acid and the one or more than one fermentation product is selected from the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2.

[0040] In some embodiments the reaction catalyzed by the synthesizing microbe is selected from the group consisting of: synthesis of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate.

[0041] In some embodiments, the microbial consortium, when administered to an animal on a high oxalate diet, significantly reduces oxalate concentration in a sample selected from the group consisting of blood, serum, stool, or urine, as compared to a sample collected

from a corresponding control animal on a high oxalate diet that has not been administered with the microbial consortium.

[0042] In some embodiments, the plurality of active microbes comprises 3 microbial strains. In some embodiments, the plurality of active microbes comprises 3 Proteobacteria strains. In some embodiments, the plurality of active microbes comprises 3 *Oxalobacter formigenes* strains.

[0043] In some embodiments, the first metabolic substrate is a bile acid. For example, in some embodiments, the bile acid is lithocholic acid (LCA) or deoxycholic acid (DCA). In In some embodiments, the one or more than one metabolite produced by the plurality of active microbes is a secondary bile acid. For example, in some embodiments, the secondary bile acid is selected from the group consisting of iso-lithocholic acid (iso-LCA), or iso-deoxycholic acid (iso-DCA). In some embodiments, the the supportive community of microbes enhances the conversion of one or more conjugated bile acids selected from the group consisting of taurochenodeoxycholic acid (TCDCA), glycochenodeoxycholic acid (GCDCA), taurocholic acid (TCA), and glycocholic acid (GCA), to cholic acid (CA) or chenodeoxycholic acid (CDCA). In some embodiments, the supportive community of microbes enhances the conversion of CA to 7-beta-cholic acid (7betaCA). In other embodiments, the supportive community of microbes enhances the conversion of CDCA to ursodeoxycholic acid (UDCA).

[0044] In some embodiments, at least one of the plurality of active microbes has a higher bile acid metabolization activity at a bile acid concentration of 0.1 mM compared to the bile acid metabolization activity of at least one other of the plurality of active microbes when measured in a standardized bile acid metabolization assay under the same conditions. In some embodiments, at least one of the plurality of active microbes has a higher bile acid metabolizing activity at a bile acid concentration of 0.1 mM compared to a bile acid metabolizing activity of the same active microbe at a higher bile acid concentration. In some embodiments, at least one of the plurality of active microbes has a higher bile acid metabolization activity at a bile acid concentration of 10 mM compared to the bile acid metabolization activity of at least one other of the plurality of active microbes when measured in a standardized bile acid metabolization assay under the same conditions. In some embodiments, at least one of the plurality of active microbes has a higher bile acid metabolizing activity at a bile acid concentration of 10 mM compared to a bile acid metabolizing activity of the same active microbe at a lower bile acid concentration. In some embodiments, one of the plurality of active microbes has a higher bile acid metabolization

activity at 0.1 mM of bile acid and another one of the plurality of active microbes has a higher bile acid metabolization activity at 10 mM of bile acid.

[0045] In some embodiments, the standardized substrate metabolization assay comprises using liquid chromatography – mass spectrometry to determine the bile acid profile in a culture sample comprising the microbial consortium, wherein the culture sample comprises three or more microbial strains in an appropriate culture media incubated for 1 hour to 96 hours in the presence of bile acids at a concentration of 0.1 mM to 10 mM, at a pH of 3.5 to 8.0, and at a temperature of 35 °C to 40 °C.

[0046] In some embodiments, the plurality of active microbes comprises one or more microbial phyla selected from Firmicutes and Actinobacteria. In some embodiments, the plurality of active microbes comprises one or more microbial strain selected from *Eggerthella lenta* and *Clostridium scindens*.

[0047] In some embodiments, the microbial consortium of the present invention is administered as a pre-determined dose ranging from 1 X 10^6 to 1 X 10^{13} total colony forming units (CFU)/kg.

[0048] In some embodiments, the microbial consortium, when administered to the animal, decreases a concentration of the first metabolic substrate in the animal.

[0049] In some embodiments the animal provides an experimental model of the disease.

[0050] The present disclosure also provides a pharmaceutical composition comprising a microbial consortium and a pharmaceutically acceptable carrier or excipient.

[0051] Also provided in the present disclosure is a method of treating a subject diagnosed with or at risk for a metabolic disease or condition selected from the group consisting of primary hyperoxaluria, secondary hyperoxaluria, cholestatic diseases (*e.g.* primary sclerosing cholangitis, primary biliary cholangitis, progressive familial intrahepatic cholestasis, or nonalcoholic steatohepatitis), and multiple sclerosis with a microbial consortium of the present invention.

[0052] In some embodiments, administration of the pharmaceutical composition disclosed herein reduces levels of the first metabolic substrate in a subject by at least 20%, at least 40%, at least 60%, or at least 80% as compared to an untreated control subject or as compared to pre-administration levels of the first metabolic substrate in the subject. In some embodiments, the first metabolic substrate is oxalate. In other embodiments, the first metabolic substrate is DCA or LCA. In some embodiments the level of first metabolic substrate is determined from a blood, serum, stool, or urine sample.

BRIEF DESCRIPTION OF THE DRAWINGS

[0053] **FIG. 1** shows a bar graph of % *in vitro* growth inhibition of supportive community strains in the presence of 0.5% oxalate (closed bars) or 0.125% oxalate (open bars) in culture media.

[0054] **FIG. 2A** shows a bar graph of *in vitro* oxalate-metabolizing activities of active microbial strains cultured for 72 hours in Mega Media, pH 7.5, containing 7.5 mM oxalate (closed bars) or 750 μM oxalate (open bars). **FIG. 2B** shows a bar graph of *in vitro* oxalate-metabolizing activities of active microbial strains cultured for 72 hours in Chopped Meat Media, pH 7.5, containing 7.5 mM oxalate (closed bars) or 750 μM oxalate (open bars).

[0055] **FIG. 3A** shows a bar graph of *in vitro* oxalate-metabolizing activities of active microbial strains cultured for 72 hours in Mega Media, at pH 4.5 (closed bars) or 7.2 (open bars), containing 7.5 mM oxalate. **FIG. 3B** shows a bar graph of *in vitro* oxalate-metabolizing activities of active microbial strains cultured for 72 hours in Chopped Meat Media, at pH 4.5 (closed bars) or 7.2 (open bars), containing 7.5 mM oxalate.

[0056] **FIG. 4A** shows a bar graph of *in vitro* oxalate levels (as measured by $Absorbance_{595}$) in microbial cultures comprising *Oxalobacter formigenes* only, active strains only, supportive strains only, or both active and supportive strains in Mega Medium. **FIG. 4B** shows a bar graph of *in vitro* oxalate levels (as measured by $Absorbance_{595}$) in microbial cultures comprising *Oxalobacter formigenes* only, active strains only, supportive strains only, or both active and supportive strains in Chopped Meat Medium at pH 7.2. $Absorbance_{595}$ was measured at the start of microbial culture incubation with 7.5 mM oxalate (t = 0 hours, closed bars) and after 72 hours incubation with 7.5 mM oxalate (t = 72 hours, open bars).

[0057] **FIG. 5** shows the percent body weight gain (**FIG. 5A**), and food consumption (**FIG. 5B**) of gnotobiotic Balb/c mice on a normal or high oxalate diet, uncolonized or treated by gavage with *Oxalobacter formigenes* only, active strains only (actives), supportive strains only (supportives), or both active and supportive strains (full community).

[0058] **FIG. 6** shows urinary oxalate concentrations of gnotobiotic Balb/c mice on a normal (no-oxalate) (**FIG. 6A**) or high oxalate (oxalate-supplemented) (**FIG. 6B**) diet, uncolonized (control) or treated by gavage with *Oxalobacter formigenes* only (formigenes), active strains only (Active), supportive strains only (Support), or both active and supportive strains (Active + Support).

[0059] **FIG. 7** shows serum liver enzyme/function levels in gnotobiotic Balb/c mice on a normal (non-bold) or high oxalate diet (**bold**), treated by gavage with *Oxalobacter*

formigenes only (*O. formigenes*), active strains only (Active), supportive strains only (Supportive), both active and supportive strains (Active + Supportive), or saline vehicle control (Saline). ALT = Alanine transaminase (**FIG. 7A**), AST = Aspartate transaminase (**FIG. 7B**), ALB = Albumin (**FIG. 7C**), ALP = Alanine phosphatase (**FIG. 7D**), A/G Ratio = Albumin/Globulin Ratio (**FIG. 7E**), TBIL = Total Bilirubin (**FIG. 7F**), GGT = Gamma-glutamyl transferase (**FIG. 7G**), TP = Prothrombin Time (**FIG. 7H**).

[0060] **FIG. 8** shows serum kidney enzyme/function levels in gnotobiotic Balb/c mice on a normal (non-bold) or high oxalate diet (**bold**), treated by gavage with *Oxalobacter formigenes* only (*O. formigenes*), active strains only (Active), supportive strains only (Supportive), both active and supportive strains (Active + Supportive), or saline vehicle control (Saline). UREA = Urea (**FIG. 8A**), CREA = Creatinine (**FIG. 8B**), PHOS = Phosphorus (**FIG 8C**), CA = Calcium (**FIG. 8D**), CL = Chloride **FIG. 8E**), NA = Sodium (**FIG. 8F**), K = Potassium (**FIG. 8G**), GLOB = Globulin (**FIG. 8H**).

[0061] **FIG. 9** shows serum triglyceride (TRIG, **FIG. 9A**), cholesterol (CHOL, **FIG. 9B),** glucose (GLUC, **FIG. 9C**), and creatine kinase (CK, **FIG. 9D**) levels in gnotobiotic Balb/c mice on a normal (non-bold) or high oxalate diet (**bold**), treated by gavage with *Oxalobacter formigenes* only (*O. formigenes*), active strains only (Active), supportive strains only (Supportive), both active and supportive strains (Active + Supportive), or saline vehicle control.

[0062] **FIG. 10** shows microbial species in fecal samples collected at the time of gavage or 2 weeks post-gavage from gnotobiotic Balb/c mice on a normal (Control; **FIG. 10A**, **FIG. 10B**, and **FIG. 10C**) or high oxalate (High-Ox; **FIG. 10D**, **FIG 10E**, and **FIG 10F**) diet, treated with active strains only (Actives; **FIG. 10A** and **FIG. 10D**), supportive strains only (Supportives; **FIG. 10B** and **FIG. 10E**), or active and supportive strains (Actives + Supportives; **FIG. 10C** and **FIG. 10F**).

[0063] **FIG. 11** shows a bar graph of *in vitro* oxalate levels (as measured by LC-MS) in microbial cultures comprising a donor-derived strain grown in YCFAC base medium for 120 h at either pH 7.0 (white bars), pH 6.0 (grey bars), or pH 5.0 (black bars). % oxalate remaining is calculated relative to the amount of oxalate present at the start of the assay (2 mM). Oxalate levels in the pH 6.0 and pH 7.0 *O. formigenes* cultures (FBI00067) were below the limit of detection at the conclusion of the assay (< 1.9% and < 1.7% oxalate remaining, respectively).

[0064] **FIG. 12** shows growth of cultures of donor-derived *O. formigenes* strains grown in YCFAC base medium supplemented with the indicated concentration of oxalate (0 mM, 2

mM, 40 mM, 80 mM, 120 mM, 160 mM) and grown for 144 hours (x-axis). Cultures are monitored by turbidity (OD600; y-axis). **FIG. 12A-C** show culture growth at pH 7.0 for the indicated strains, **FIG. 12D-F** show culture growth at pH 6.0 for the indicated strains, and **FIG. 12G-I** show culture growth at pH 5.0 for the indicated strains.

[0065] **FIG. 13** shows urinary oxalate levels in germ-free C57Bl/6NTac mice (n = 4 per condition) fed a low-complexity high-oxalate diet, uncolonized (-) or treated by gavage with one of 5 candidate microbial consortia (I to V) or a proof-of-concept consortium (+).

[0066] **FIG. 14** shows urinary oxalate levels in germ-free C57Bl/6NTac mice (n = 4 per condition) fed a high-complexity diet and given oxalate-supplemented drinking water, uncolonized (-) or treated by gavage with one of 5 candidate microbial consortia (I to V) or a positive-control consortium (+).

[0067] **FIG. 15** shows urinary oxalate levels in germ-free C57Bl/6NTac mice (n = 4 per condition) which were colonized with a non-oxalate-controlling human microbiome prior to the study. Mice were fed a high-complexity diet and given oxalate-supplemented drinking water, cleared of the human microbiome by antibiotic treatment, and were either left uncolonized (-) or were recolonized by gavage with one of 5 candidate microbial consortia (I to V), a positive-control consortium containing commercial strains (+), or a collection of donor-derived strains ("Putative Oxalate Degraders Only") comprising 3 *O. formigenes* strains and a set of additional strains which had been preliminarily classified as oxalate-degrading.

[0068] **FIG. 16** shows the diversity of microbial strains in fecal samples from the mice of **FIG. 15** (measured by metagenomic sequencing).

[0069] **FIG. 17** shows the relative abundance (**FIG. 17A**) and absolute abundance (**FIG. 17B**) of *O. formigenes* in feces of germ-free mice treated with a candidate microbial consortium (I to V) or a supportive community alone that lacks *O. formigenes*.

[0070] **FIG. 18** shows the concentration of various bile acid compounds (including TCA, CA, and DCA) in cultures of commercial strains that were spiked with 100 μM TCA and incubated for 24 h at 37 °C.

DETAILED DESCRIPTION

[0071] Disclosed herein are microbial consortia for administration to an animal comprising a plurality of active microbes which metabolize a first metabolic substrate which causes or contributes to disease in the animal. The microbial consortia disclosed herein further comprise an effective amount of a supportive community of microbes that metabolize

one or more than one metabolite produced by the plurality of active microbes, and wherein the one or more than one metabolite inhibits metabolism of the plurality of active microbes. These microbial consortia are advantageous in having enhanced characteristics when administered to an animal as compared to administration of the plurality of active microbes alone. Enhanced characteristics of the microbial consortia include one or more of improved gastrointestinal engraftment, increased biomass, increased metabolism of the first metabolic substrate, and improved longitudinal stability.

[0072] To facilitate an understanding of the present invention, a number of terms and phrases are defined below.

[0073] The term "a" and "an" as used herein mean "one or more" and include the plural unless the context is appropriate

[0074] As used herein, the term "active microbes" refers to microbes that express sufficient amounts of one or more than one metabolic enzyme to metabolize a substrate that causes or contributes to disease in an animal.

[0075] As used herein, the term "biomass," refers to the total mass of one or more than one microbe, or consortium in a given area or volume.

[0076] As used herein, the term "microbial consortium," refers to a mixture of two or more microbial strains wherein one microbial strain in the mixture has a beneficial or desired effect on another microbial strain in the mixture.

[0077] As used herein, the term "gastrointestinal engraftment" refers to the establishment of one or more than one microbe, or microbial consortium, in one or more than one niche of the gastrointestinal tract that, prior to administration of the one or more than one microbe, or microbial consortium, is absent in the one or more than one microbe, or microbial consortium. Gastrointestinal engraftment may be transient, or may be persistent.

[0078] As used herein, the term "effective amount" refers to an amount sufficient to achieve a beneficial or desired result. In some embodiments, an effective amount can be improved gastrointestinal engraftment of one or more than one of the plurality of active microbes, increased biomass of one or more than one of the plurality of active microbes, increased metabolism of the first metabolic substrate, or improved longitudinal stability).

[0079] As used herein, the term "fermenting microbe" refers to a microbe that expresses sufficient amounts of one or more than one enzyme to catalyze a fermentation reaction in a gastrointestinal niche.

[0080] As used herein, the term "longitudinal stability" refers to the ability of one or more than one microbe, or microbial consortium to remain engrafted and metabolically active

in one of more than one niche of the gastrointestinal tract despite transient or long-term environmental changes to the gastrointestinal niche.

[0081] As used herein, the term "metabolism," "metabolize," "metabolization," or variants thereof refers to the biochemical conversion of a metabolic substrate to a metabolic product. In some embodiments, metabolization includes isomerization.

[0082] As used herein, the term "microbe" refers to a microbial organism including, but not limited to, bacteria, archaea, protozoa, and unicellular fungi.

[0083] As used herein, the term "microbial consortium" refers to a preparation of two or more microbes wherein the metabolic product of one of the two or more microbes is the metabolic substrate for one other microbe comprising the consortium.

[0084] As used herein, the term "pharmaceutical composition" refers to the combination of an active agent with a carrier, inert or active, making the composition especially suitable for therapeutic use *in vivo* or *ex vivo*.

[0085] As used herein, the term "pharmaceutically acceptable carrier" refers to any of the standard pharmaceutical carriers, such as phosphate buffered saline solution, water, emulsions (*e.g.*, such as oil/water or water/oil emulsions), and various types of wetting agents. The compositions also can include stabilizers and preservatives. For examples of carriers, stabilizers, and adjuvants, *see e.g.,* Martin, Remington's Pharmaceutical Sciences, 15th Ed. Mack Publ. Co., Easton, PA [1975].

[0086] As used herein, "significantly" or "significant" refers to a change or alteration in a measurable parameter to a statistically significant degree as determined in accordance with an appropriate statistically relevant test. For example, in some embodiments, a change or alteration is significant if it is statistically significant in accordance with, *e.g.*, a Student's t-test, chi-square, or Mann Whitney test.

[0087] As used herein, the term "standardized substrate metabolization assay" refers to an experimental assay known to persons of ordinary skill in the art used to quantify the amount of substrate converted to a metabolic product.

[0088] As used herein, the term "subject" refers to an organism to be treated by the microbial consortium and compositions described herein. Such organisms preferably include, but are not limited to, mammals (*e.g.*, murines, simians, equines, bovines, porcines, canines, felines, and the like), and more preferably include humans.

[0089] As used herein, the term "supportive community" refers to one or more than one microbial strain that, when administered with an active microbe, enhances one or more than

one characteristic of the active microbe selected from the group consisting of gastrointestinal engraftment, biomass, metabolic substrate metabolism, and longitudinal stability.

[0090] As used herein, the term "synthesizing microbe" refers to a microbe that expresses sufficient amounts of one or more than one enzyme to catalyze the combination of one or more than one metabolite produced by an active microbe, and one or more than one fermentation product produced by a fermenting microbe in a gastrointestinal niche.

[0091] The term percent "identity" or "sequence identity," in the context of two or more nucleic acid or polypeptide sequences, refer to two or more sequences or subsequences that have a specified percentage of nucleotides or amino acid residues that are the same, when compared and aligned for maximum correspondence, as measured using one of the sequence comparison algorithms described below (*e.g.*, BLASTP and BLASTN or other algorithms available to persons of skill) or by visual inspection. Depending on the application, the percent "identity" can exist over a region of the sequence being compared, *e.g.*, over a functional domain, or, alternatively, exist over the full length of the two sequences to be compared.

[0092] For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

[0093] Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by visual inspection (see generally Ausubel et al., infra).

[0094] One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al., J. Mol. Biol. 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov/).

[0095] When used in reference to 16S rRNA sequences, a "sequence identity" of at least 97% indicates that two microbial strains are likely to belong to the same species, whereas 16S rRNA sequences having less than 97% sequence identity indicate that two microbial strains likely belong to different species, and 16S rRNA sequences having less than 95% sequence identity indicates that two microbial strains likely belong to distinct genera (Stackebrandt E., and Goebel, B.M., Int J Syst Bact, 44 (1994) 846-849.).

[0096] Throughout the description, where compositions are described as having, including, or comprising specific components, or where processes and methods are described as having, including, or comprising specific steps, it is contemplated that, additionally, there are compositions of the present invention that consist essentially of, or consist of, the recited components, and that there are processes and methods according to the present invention that consist essentially of, or consist of, the recited processing steps.

[0097] As a general matter, compositions specifying a percentage are by weight unless otherwise specified. Further, if a variable is not accompanied by a definition, then the previous definition of the variable controls.

Biological Niches

[0098] The present invention provides microbial consortia capable of engrafting into one or more than one niche of a gastrointestinal tract where it is capable of metabolizing a substrate that causes or contributes to disease in an animal. These niches comprise specific microbial communities whose composition varies according to a number of environmental factors including, but not limited to, the particular physical compartment of the gastrointestinal tract inhabited by a microbial community, the chemical and physicochemical properties of the environment inhabited, the metabolic substrate composition of the environment inhabited, and other co-inhabiting microbial species.

Physical Compartments

[0099] A gastrointestinal tract comprises a number of physical compartments. For example, the human gastrointestinal tract includes the oral cavity, pharynx, esophagus, stomach, small intestine (duodenum, jejunum, ileum), cecum, large intestine (ascending colon, transverse colon, descending colon), and rectum. The pancreas, liver, gallbladder, and associated ducts, additionally comprise compartments of the human gastrointestinal tract.

Each of these compartments has, for example, variable anatomical shape and dimension, aeration, water content, levels of mucus secretion, luminal presence of antimicrobial peptides, and presence or absence of peristaltic motility. Furthermore, the different gastrointestinal compartments vary in their pH. In humans, the pH of the oral cavity, upper stomach, lower stomach, duodenum, jejunum, ileum, and colon range from 6.5-7.5, 4.0-6.5, 1.5-4.0, 7.0-8.5, 4.0-7.0, and 4.0-7.0, respectively. Compartments of the gastrointestinal tract also differ in their levels of oxygenation which are subject to large degrees of fluctuation. For example, the luminal partial pressure of oxygen in the stomach of mice has been measured to be approximately 58 mm Hg, while the luminal partial pressure of oxygen in the distal sigmoid colon has been measured to be approximately 3 mm Hg (He *et al.*, 1999). Oxygen levels of the gastrointestinal tract are highly determinative of the biochemical pathways utilized by commensal microbes. For example, commensal bacteria utilize aerobic respiration at oxygen concentrations above 5 mbar of O_2, anaerobic respiration between 1-5 mbar of O_2, and fermentation at O_2 concentrations below 1 mbar. The sensitivity of microbes to O_2 levels and their ability to carry out metabolic reactions under aerobic and/or anaerobic conditions influences which microbial species engraft in a particular gastrointestinal compartment.

Metabolic Compartments

[0100] In addition to the various physical and chemical environments contributing to a gastrointestinal niche, different niches comprise different metabolic substrates.

[0101] Metabolic substrates that may be present in a gastrointestinal niche may include, but are not limited to, oxalate, fructan, inulin, glucuronoxylan, arabinoxylan, glucomannan, β-mannan, dextran, starch, arabinan, xyloglucan, galacturonan, β-glucan, galactomannan, rhamnogalacturonan I, rhamnogalacturonan II, arabinogalactan, mucin O-linked glycans, yeast α-mannan, yeast β-glucan, chitin, alginate, porphyrin, laminarin, carrageenan, agarose, alternan, levan, xanthan gum, galactooligosaccharides, hyaluronan, chondrointin sulfate, dermatan sulfate, heparin sulfate, keratan sulfate, phenylalanine, tyrosine, tryptophan, leucine, valine, isoleucine, glycine, proline, asparagine, glutamine, aspartate, glutamate, cysteine, lysine, arginine, serine, methionine, alanine, arginine, histidine, ornithine, citrulline, carnitine, hydroxyproline, cholic acid, chenodeoxycholic acid, taurochenodeoxycholic acid, glycochenodeoxycholic acid, cholesterol, cinnamic acid, coumaric acid, sinapinic acid, ferulic acid, caffeic acid, quinic acid, chlorogenic acid, catechin, epicatechin, gallic acid,

pyrogallol, catechol, quercetin, myricetin, campherol, luteolin, apigenin, naringenin, and hesperidin.

Microbial Consortia

[0102] The present invention provides microbial consortia comprising a plurality of active microbes and an effective amount of a supportive community of microbes. In some embodiments, a microbial consortium comprises 3 to 500 microbial strains. For example, in some embodiments, a microbial consortium comprises 3 to 500, 4 to 500, 5 to 500, 6 to 500, 7 to 500, 8 to 500, 9 to 500, 10 to 500, 11 to 500, 12 to 500, 13 to 500, 14 to 500, 15 to 500, 16 to 500, 17 to 500, 18 to 500, 19 to 500, 20 to 500, 21 to 500, 22 to 500, 23 to 500, 24 to 500, 25 to 500, 30 to 500, 35 to 500, 40 to 500, 45 to 500, 50 to 500, 60 to 500, 70 to 500, 80 to 500, 90 to 500, 100 to 500, 110 to 500, 120 to 500, 130 to 500, 140 to 500, 150 to 500, 160 to 500, 170 to 500, 180 to 500, 190 to 500, 200 to 500, 210 to 500, 220 to 500, 230 to 500, 240 to 500, 250 to 500, 260 to 500, 270 to 500, 280 to 500, 290 to 500, 300 to 500, 400 to 500, 3 to 300, 4 to 300, 5 to 300, 6 to 300, 7 to 300, 8 to 300, 9 to 300, 10 to 300, 11 to 300, 12 to 300, 13 to 300, 14 to 300, 15 to 300, 16 to 300, 17 to 300, 18 to 300, 19 to 300, 20 to 300, 21 to 300, 22 to 300, 23 to 300, 24 to 300, 25 to 300, 30 to 300, 35 to 300, 40 to 300, 45 to 300, 50 to 300, 60 to 300, 70 to 300, 80 to 300, 90 to 300, 100 to 300, 110 to 300, 120 to 300, 130 to 300, 140 to 300, 150 to 300, 160 to 300, 170 to 300, 180 to 300, 190 to 300, 200 to 300, 210 to 300, 220 to 300, 230 to 300, 240 to 300, 250 to 300, 260 to 300, 270 to 300, 280 to 300, 290 to 300, 3 to 250, 4 to 250, 5 to 250, 6 to 250, 7 to 250, 8 to 250, 9 to 250, 10 to 250, 11 to 250, 12 to 250, 13 to 250, 14 to 250, 15 to 250, 16 to 250, 17 to 250, 18 to 250, 19 to 250, 20 to 250, 21 to 250, 22 to 250, 23 to 250, 24 to 250, 25 to 250, 30 to 250, 35 to 250, 40 to 250, 45 to 250, 50 to 250, 60 to 250, 70 to 250, 80 to 250, 90 to 250, 100 to 250, 110 to 250, 120 to 250, 130 to 250, 140 to 250, 150 to 250, 160 to 250, 170 to 250, 180 to 250, 190 to 250, 200 to 250, 210 to 250, 220 to 250, 230 to 250, 240 to 250, 3 to 200, 4 to 200, 5 to 200, 6 to 200, 7 to 200, 8 to 200, 9 to 200, 10 to 200, 11 to 200, 12 to 200, 13 to 200, 14 to 200, 15 to 200, 16 to 200, 17 to 200, 18 to 200, 19 to 200, 20 to 200, 21 to 200, 22 to 200, 23 to 200, 24 to 200, 25 to 200, 30 to 200, 35 to 200, 40 to 200, 45 to 200, 50 to 200, 60 to 200, 70 to 200, 80 to 200, 90 to 200, 100 to 200, 110 to 200, 120 to 200, 130 to 200, 140 to 200, 150 to 200, 160 to 200, 170 to 200, 180 to 200, 190 to 200, 3 to 150, 4 to 150, 5 to 150, 6 to 150, 7 to 150, 8 to 150, 9 to 150, 10 to 150, 11 to 150, 12 to 150, 13 to 150, 14 to 150, 15 to 150, 16 to 150, 17 to 150, 18 to 150, 19 to 150, 20 to 150, 21 to 150, 22 to 150, 23

to 150, 24 to 150, 25 to 150, 30 to 150, 35 to 150, 40 to 150, 45 to 150, 50 to 150, 60 to 150, 70 to 150, 80 to 150, 90 to 150, 100 to 150, 110 to 150, 120 to 150, 130 to 150, 140 to 150, 3 to 100, 4 to 100, 5 to 100, 6 to 100, 7 to 100, 8 to 100, 9 to 100, 10 to 100, 11 to 100, 12 to 100, 13 to 100, 14 to 100, 15 to 100, 16 to 100, 17 to 100, 18 to 100, 19 to 100, 20 to 100, 21 to 100, 22 to 100, 23 to 100, 24 to 100, 25 to 100, 30 to 100, 35 to 100, 40 to 100, 45 to 100, 50 to 100, 60 to 100, 70 to 100, 80 to 100, 90 to 100, 3 to 75, 4 to 75, 5 to 75, 6 to 75, 7 to 75, 8 to 75, 9 to 75, 10 to 75, 11 to 75, 12 to 75, 13 to 75, 14 to 75, 15 to 75, 16 to 75, 17 to 75, 18 to 75, 19 to 75, 20 to 75, 21 to 75, 22 to 75, 23 to 75, 24 to 75, 25 to 75, 30 to 75, 35 to 75, 40 to 75, 45 to 75, 50 to 75, 60 to 75, 70 to 75, 3 to 50, 4 to 50, 5 to 50, 6 to 50, 7 to 50, 8 to 50, 9 to 50, 10 to 50, 11 to 50, 12 to 50, 13 to 50, 14 to 50, 15 to 50, 16 to 50, 17 to 50, 18 to 50, 19 to 50, 20 to 50, 21 to 50, 22 to 50, 23 to 50, 24 to 50, 25 to 50, 30 to 50, 35 to 50, 40 to 50, 45 to 50, 3 to 25, 4 to 25, 5 to 25, 6 to 25, 7 to 25, 8 to 25, 9 to 25, 10 to 25, 11 to 25, 12 to 25, 13 to 25, 14 to 25, 15 to 25, 16 to 25, 17 to 25, 18 to 25, 19 to 25, 20 to 25, 21 to 25, 22 to 25, 23 to 25, or 24 to 25 microbial strains. For example, in some embodiments, a microbial consortium comprises about 20 to about 200, about 70 to about 80, about 80 to about 90, about 100 to about 110, or about 150 to about 160 microbial strains.

[0103] In some embodiments, a microbial consortium described herein comprises a microbial strain having a relative abundance of approximately 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, 10%, 5%, 1%, 0.1%, 0.01%, 0.001%, 0.0001%, 0.00001%, or 0.000001% of the total microbial consortium. In some embodiments, the relative abundance of a microbial strain is determined by metagenomic sequencing and calculated as the percentage of reads that are classified as an identified microbial strain, divided by the genome size. For example, in some embodiments, the relative abundance of a microbial strain of the invention is determined by metagenomic shotgun sequencing.

Active Microbes

[0104] The microbial consortia of the present invention comprise a plurality of active microbes capable of metabolizing a first metabolic substrate that causes or contributes to disease in an animal. In some embodiments, the current invention provides a microbial consortium capable of metabolizing the first metabolic substrate at a pH within a range of 4 to 8. For example, in some embodiments, one or more than one of the plurality of active microbes is capable of metabolizing a first metabolic substrate at a pH within a range of 4 to 8, 4.2 to 8, 4.4 to 8, 4.6 to 8, 4.8 to 8, 5 to 8, 5.2 to 8, 5.4 to 8, 5.6 to 8, 5.8 to 8, 6 to 8, 6.2 to

8, 6.4 to 8, 6.6 to 8, 6.8 to 8, 7 to 8, 7.2 to 8, 7.4 to 8, 7.6 to 8, 7.8 to 8, 4 to 7, 4.2 to 7, 4.4 to 7, 4.6 to 7, 4.8 to 7, 5 to 7, 5.2 to 7, 5.4 to 7, 5.6 to 7, 5.8 to 7, 6 to 7, 6.2 to 7, 6.4 to 7, 6.6 to 7, 6.8 to 7, 4 to 6, 4.2 to 6, 4.4 to 6, 4.6 to 6, 4.8 to 6, 5 to 6, 5.2 to 6, 5.4 to 6, 5.6 to 6, 5.8 to 6, 4 to 6, 4.2 to 6, 4.4 to 6, 4.6 to 6, 4.8 to 6, 5 to 6, 5.2 to 6, 5.4 to 6, 5.6 to 6, or 5.8 to 6.

[0105] In some embodiments, the plurality of active microbes comprises one microbial strain having a significantly different first metabolic substrate-metabolizing activity in a standard substrate-metabolizing assay conducted at two pH values differing by 1 pH unit and within a pH range of 4 to 8. In some embodiments, the difference between the two pH values is 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3.0, 3.2, 3.2, 3.3, 3.4., 3.5, 3.6, 3.7, 3.8, 3.9, or 4.0 pH units. For example, in some embodiments, one microbial strain has significantly different first metabolic substrate-metabolizing activities in a standard substrate metabolizing assay at pH 4 and pH 8, pH 5 and pH 8, pH 6 and pH 8, pH 7 and pH 8, pH 4 and pH 7, pH 5 and pH 7, pH 6 and pH 7, pH 4 and pH 6, pH 5 and pH 6, or pH 4 and pH 5.

[0106] As used herein, "lower pH" refers to a pH in a standardized substrate metabolization assay that is lower in value as compared to another pH value. For example, a standardized substrate metabolization assay performed at pH 4.5 has a lower pH as compared to a standardized substrate metabolization assay preformed at a pH of 7.5. "Higher pH," as used herein, refers to a pH in a standardized substrate metabolization assay that is higher in value as compared to another pH value. For example a standardized substrate metabolization assay preformed at pH 7.5 has a higher pH as compared to a standardized substrate metabolization assay performed at a pH of 4.5.

[0107] As used herein, "higher first metabolic substrate-metabolizing activity" means either a first metabolic substrate-metabolizing activity of a microbial strain that is higher as compared to a first metabolic substrate-metabolizing activity of the same microbial strain under different conditions, and/or a first metabolic substrate-metabolizing activity of a microbial strain that is higher as compared to a first metabolic substrate-metabolizing activity of a different microbial strain under the same conditions.

[0108] In some embodiments, the plurality of active microbes comprises two microbial strains having significantly different first metabolic substrate-metabolizing activities. For example, in some embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a lower pH as compared to the first metabolic substrate-metabolizing activity of another microbial strain in the plurality of active microbes at the same lower pH. In some embodiments, one of the plurality of active

microbes has a significantly higher first metabolic substrate-metabolizing activity at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5 as compared to the first metabolic substrate-metabolizing activity of another microbial strain in the plurality of active microbes at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5, respectively. In some embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a higher pH as compared to the first metabolic substrate-metabolizing activity of another microbial strain in the plurality of active microbes at the same higher pH. In some embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at pH 7.5, 7.6. 7.7, 7.8, 7.9, or 8.0 as compared to the first metabolic substrate-metabolizing activity of another microbial strain in the plurality of active microbes at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0, respectively.

[0109] In some embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a lower pH as compared to its first metabolic substrate-metabolizing activity at a higher pH. For example, in some embodiments one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5 than it does at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0. In some embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a higher pH as compared to its first metabolic substrate-metabolizing activity at a lower pH. For example, in some embodiments one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at pH 7.5, 7.6. 7.7, 7.8, 7.9, or 8.0 than it does at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5.

[0110] In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at a lower pH and another microbe having a higher first metabolic substrate-metabolizing activity at a higher pH. For example, in some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.5. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.6. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.7. In some embodiments, the plurality of active microbes

comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.8. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.9. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 8.0. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.5. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.6. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.7. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.8. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.9. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 8.0. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 5.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.5. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 5.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.6. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 5.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.7. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at

pH 5.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.8. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 5.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.9. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 5.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 8.0. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 5.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.5. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 5.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.6. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 5.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.7. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 5.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.8. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 5.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.9. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 5.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 8.0. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 6.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.5. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 6.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.6. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 6.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.7. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 6.0 and another microbe having a higher first metabolic substrate-metabolizing activity at

pH 7.8. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 6.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.9. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 6.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 8.0. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 6.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.5. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 6.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.6. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 6.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.7. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 6.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.8. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 6.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.9. In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 6.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 8.0.

[0111] In some embodiments, the plurality of active microbes comprises one microbial strain having a significantly different first metabolic substrate-metabolizing activity in a standard substrate-metabolizing assay conducted at a first metabolic substrate concentration as compared to its first metabolic substrate-metabolizing activity in a standard substrate-metabolizing assay conducted at a different first metabolic substrate concentration, wherein the difference between the two first metabolic substrate concentrations is within a 100 fold range. In some embodiments, the difference between the two first metabolic concentrations is 1.2 fold. For example, in some embodiments, the difference between the two first metabolic substrate concentrations is at least 1.2 fold, 1.4 fold, 1.6 fold, 1.8 fold, 2.0 fold, 4 fold, 6 fold, 8 fold, 10 fold, 20 fold, 30 fold, 40 fold, 50 fold, 60 fold, 70 fold, 80 fold, 90 fold, or 100 fold or greater.

[0112] As used herein, "lower concentration of first metabolic substrate" refers to a substrate concentration in a standardized substrate metabolization assay that is lower in value as compared to another substrate concentration. "Higher concentration of first metabolic substrate," as used herein, refers to a substrate concentration in a standardized substrate metabolization assay that is higher in value as compared to another substrate concentration.

[0113] In some embodiments, the plurality of active microbes comprises two microbial strains having significantly different first metabolic substrate-metabolizing activities. For example, in some embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a lower concentration of first metabolic substrate as compared to the first metabolic substrate-metabolizing activity of another microbial strain in the plurality of active microbes at the same lower concentration of first metabolic substrate. In some embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a higher concentration of first metabolic substrate as compared to the first metabolic substrate-metabolizing activity of another microbial strain in the plurality of active microbes at the same higher concentration of first metabolic substrate.

[0114] In some embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a lower concentration of first metabolic substrate as compared to its first metabolic substrate-metabolizing activity at a higher concentration of first metabolic substrate. In some embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a higher concentration of first metabolic substrate as compared to its first metabolic substrate-metabolizing activity at a lower concentration of first metabolic substrate.

[0115] In some embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at a lower concentration of first metabolic substrate and another microbe having a higher first metabolic substrate-metabolizing activity at a higher concentration of first metabolic substrate. For example, in some embodiments, the difference between the lower concentration of first metabolic substrate and the higher concentration of first metabolic substrate is at least 1.2 fold, 1.4 fold, 1.6 fold, 1.8 fold, 2.0 fold, 4 fold, 6 fold, 8 fold, 10 fold, 20 fold, 30 fold, 40 fold, 50 fold, 60 fold, 70 fold, 80 fold, 90 fold, or 100 fold or greater.

[0116] In some embodiments, the plurality of active microbes comprises two microbial strains having significantly different growth rates. For example, in some embodiments, one of the plurality of active microbes has a significantly higher growth rate at a lower pH as

compared to the growth rate of another microbial strain in the plurality of active microbes at the same lower pH. In some embodiments, one of the plurality of active microbes has a significantly higher growth rate at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5 as compared to the growth rate of another microbial strain in the plurality of active microbes at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5, respectively. In some embodiments, one of the plurality of active microbes has a significantly higher growth rate at a higher pH as compared to the growth rate of another microbial strain in the plurality of active microbes at the same higher pH. In some embodiments, one of the plurality of active microbes has a significantly higher growth rate at pH 7.5, 7.6. 7.7, 7.8, 7.9, or 8.0 as compared to the growth rate of another microbial strain in the plurality of active microbes at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0, respectively.

[0117] In some embodiments, one of the plurality of active microbes has a significantly higher growth rate at a lower pH as compared to its growth rate at a higher pH. For example, in some embodiments one of the plurality of active microbes has a significantly higher growth rate at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5 than it does at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0. In some embodiments, one of the plurality of active microbes has a significantly higher growth rate at a higher pH as compared to its growth rate at a lower pH. For example, in some embodiments one of the plurality of active microbes has a significantly higher growth rate at pH 7.5, 7.6. 7.7, 7.8, 7.9, or 8.0 than it does at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5.

[0118] In some embodiments, the plurality of active microbes comprises one microbial strain having a significantly higher growth rate when cultured in media containing a certain concentration of first metabolic substrate concentration as compared to the growth rate of another microbial strain in the plurality of active microbes cultured in the same media containing the same concentration of the first metabolic substrate. In some embodiments, the difference between the two growth rates is at least 0.2 fold, at least 0.4 fold, at least 0.6 fold, at least 0.8 fold, at least 1.0 fold, at least 1.2 fold, at least 1.4 fold, at least 1.6 fold, at least 1.8 fold, or at least 2.0 fold.

[0119] In some embodiments, the first metabolic substrate may be selected from, but not limited to, oxalate and a bile acid (*e.g.*, lithocholic acid (LCA), deoxycholic acid (DCA)).

[0120] In some embodiments, the current disclosure provides a microbial consortium comprising a plurality of active microbes capable of metabolizing a first metabolic substrate to one or more than one metabolite. For example, in some embodiments, the one or more than one metabolite may be selected from, but not limited to, formate, CO_2, and a secondary bile acid (*e.g.*, 3-oxo-deoxycholic acid (3 oxoDCA), 3-oxo-lithocholic acid (3oxoLCA), iso-lithocholic acid (iso- LCA), or iso-deoxycholic acid (iso- DCA)). In some embodiments, the

plurality of active microbes can comprise 2 to 200 microbial strains. For example, in some embodiments, a microbial consortium comprises 2 to 10, 2 to 15, 2 to 20, 2 to 25, 2 to 30, 2 to 35, 2 to 40, 2 to 45, 2 to 50, 2 to 75, 2 to 100, 2 to 125, 2 to 150, 2 to 175, or 2 to 200 active microbial strains. In certain embodiments, the plurality of active microbes can comprise 2 to 20 microbial strains.

Oxalate-Metabolizing Active Microbes

[0121] In one aspect, the current disclosure provides a microbial consortium comprising a plurality of active microbes that metabolize oxalate. In some embodiments, each of the plurality of active microbes that metabolize oxalate express sufficient amounts of one or more than one enzyme involved in oxalate metabolism. For example, in some embodiments, one or more than one active microbe expresses formyl-CoA transferase (*Frc*), an oxalate-formate antiporter (*e.g.*, *OxIT*), and oxalyl-CoA decarboxylase (*e.g.*, *OxC*), and/or oxalate decarboxylase (*e.g.*, *OxD*).

[0122] In some embodiments, the plurality of active microbes that metabolize oxalate comprise 2 to 20 oxalate-metabolizing microbial strains. For example, in some embodiments, a microbial consortium comprises 2 to 20, 3 to 20, 4 to 20, 5 to 20, 6 to 20, 7 to 20, 8 to 20, 9 to 20, 10 to 20, 11 to 20, 12 to 20, 13 to 20, 14 to 20, 15 to 20, 16 to 20, 17 to 20, 18 to 20, 19 to 20, 2 to 18, 3 to 18, 4 to 18, 5 to 18, 6 to 18, 7 to 18, 8 to 18, 9 to 18, 10 to 18, 11 to 18, 12 to 18, 13 to 18, 14 to 18, 15 to 18, 16 to 18, 17 to 18, 2 to 16, 3 to 16, 4 to 16, 5 to 16, 6 to 16, 7 to 16, 8 to 16, 9 to 16, 10 to 16, 11 to 16, 12 to 16, 13 to 16, 14 to 16, 15 to 16, 2 to 14, 3 to 14, 4 to 14, 5 to 14, 6 to 14, 7 to 14, 8 to 14, 9 to 14, 10 to 14, 11 to 14, 12 to 14, 13 to 14, 2 to 13, 3 to 13, 4 to 13, 5 to 13, 6 to 13, 7 to 13, 8 to 13, 9 to 13, 10 to 13, 11 to 13, 12 to 13, 2 to 12, 3 to 12, 4 to 12, 5 to 12, 6 to 12, 7 to 12, 8 to 12, 9 to 12, 10 to 12, 11 to 12, 2 to 12, 3 to 12, 4 to 12, 5 to 12, 6 to 12, 7 to 12, 8 to 12, 9 to 12, 10 to 12, 11 to 12, 2 to 10, 3 to 10, 4 to 10, 5 to 10, 6 to 10, 7 to 10, 8 to 10, 9 to 10, 2 to 10, 3 to 10, 4 to 10, 5 to 10, 6 to 10, 7 to 10, 8 to 10, 9 to 10, 2 to 8, 3 to 8, 4 to 8, 5 to 8, 6 to 8, 7 to 8, 2 to 6, 3 to 6, 4 to 6, 5 to 6, 2 to 4, or 3 to 4 oxalate-metabolizing strains of microbes. In some embodiments, the plurality of active microbes comprises 3 strains of oxalate-metabolizing microbes. In some embodiments the plurality of active microbes consists of 3 strains of oxalate-metabolizing microbes.

[0123] In some embodiments, the plurality of active microbes that metabolize oxalate may comprise one or more microbial species selected from, but not limited to *Oxalobacter*

formigenes, *Bifidobacterium sp.*, *Bifidobacterium dentium*, *Dialister invisus*, *Lactobacillus acidophilus*, *Lactobacillus gasseri*, *Lactobacillus helveticus*, *Lactobacillus reuteri*, *Eggerthella lenta*, *Lactobacillus rhamnosus*, *Enterococcus faecalis*, *Enterococcus gallinarum*, *Enterococcus faecium*, *Providencia rettgeri*, *Streptococcus thermophilus*, *Lactobacillus plantarum*, *Lactobacillus casei*, *Lactobacillus salivarius*, *Lactobacillus johnsii*, *Bifidobacterium infantis*, *Bifidobacterium animalis*, *Clostridium sporogenes*, *Leuconostoc lactis*, *Leuconostoc mesenteroides*.

[0124] In some embodiments the plurality of active microbes that metabolize oxalate may comprise two or more microbial species selected from, but not limited to, *Bifidobacterium dentium* ATCC 27678, *Enterococcus faecalis* HM-432, *Lactobacillus helveticus* DSM 20075, *Bifidobacterium dentium* ATCC 27680, *Lactobacillus acidophilus* ATCC 4357, *Lactobacillus reuteri* HM-102, *Bifidobacterium dentium* DSM 20221, *Lactobacillus acidophilus* DSM 20079, *Lactobacillus rhamnosus* ATCC 53103, *Bifidobacterium dentium* DSM 20436, *Lactobacillus acidophilus* DSM 20242, *Lactobacillus rhamnosus* DSM 20245, *Bifidobacterium* sp. HM-868, *Lactobacillus gasseri* ATCC 33323, *Lactobacillus rhamnosus* DSM 8746, *Dialister invisus* DSM 15470, *Lactobacillus gasseri* DSMZ 107525, *Lactobacillus rhamnosus* HM-106, *Eggerthella lenta* ATCC 43055, *Lactobacillus gasseri* DSMZ 20077, *Oxalobacter formigenes* ATCC 35274, *Eggerthella lenta* DSM 2243, *Lactobacillus gasseri* HM-104, *Oxalobacter formigenes* DSM 4420, *Enterococcus faecalis* HM-202, *Lactobacillus gasseri* HM-644, and *Oxalobacter formigenes* HM-1.

[0125] In some embodiments, the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to SEQ ID NO: 67, SEQ ID NO: 133, or SEQ ID NO:289. In some embodiments, the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 67, SEQ ID NO: 133, or SEQ ID NO:289.

[0126] In some embodiments the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to SEQ ID NO: 67 and an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to SEQ ID NO: 133. In some embodiments, the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%,

identical to SEQ ID NO: 67 and an *Oxalobacter formigenes* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 133.

[0127] In some embodiments the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to SEQ ID NO: 133 and an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to SEQ ID NO: 289. In some embodiments, the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 133 and an *Oxalobacter formigenes* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 289.

[0128] In some embodiments the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to SEQ ID NO: 67 and an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to SEQ ID NO: 289. In some embodiments, the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 67 and an *Oxalobacter formigenes* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 289.

[0129] In some embodiments the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to SEQ ID NO: 67, an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to SEQ ID NO: 133, and an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to SEQ ID NO: 289. In some embodiments the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 67, an *Oxalobacter formigenes* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 133, and an *Oxalobacter formigenes* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 289.

[0130] In some embodiments the plurality of active microbes consists of an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to SEQ ID NO: 67, an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to SEQ ID NO: 133, and an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to SEQ ID NO: 289. In some embodiments the plurality of active microbes consists of an *Oxalobacter formigenes* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 67, an *Oxalobacter formigenes* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 133, and an *Oxalobacter formigenes* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 289.

[0131] As used herein, "substantially metabolizing oxalate," "substantial metabolization of oxalate," and variants thereof, refer to a statistically significant reduction in the amount of oxalate in an *in vitro* assay (for example, as described in Example 3). In some embodiments, one or more than one of the plurality of active microbes is capable of substantially metabolizing oxalate at a pH within a range of 4 to 8. For example, in some embodiments, one or more than one of the plurality of active microbes is capable of metabolizing oxalate at a pH within a range of 4 to 8, 4.2 to 8, 4.4 to 8, 4.6 to 8, 4.8 to 8, 5 to 8, 5.2 to 8, 5.4 to 8, 5.6 to 8, 5.8 to 8, 6 to 8, 6.2 to 8, 6.4 to 8, 6.6 to 8, 6.8 to 8, 7 to 8, 7.2 to 8, 7.4 to 8, 7.6 to 8, 7.8 to 8, 4 to 7, 4.2 to 7, 4.4 to 7, 4.6 to 7, 4.8 to 7, 5 to 7, 5.2 to 7, 5.4 to 7, 5.6 to 7, 5.8 to 7, 6 to 7, 6.2 to 7, 6.4 to 7, 6.6 to 7, 6.8 to 7, 4 to 6, 4.2 to 6, 4.4 to 6, 4.6 to 6, 4.8 to 6, 5 to 6, 5.2 to 6, 5.4 to 6, 5.6 to 6, 5.8 to 6, 4 to 6, 4.2 to 6, 4.4 to 6, 4.6 to 6, 4.8 to 6, 5 to 6, 5.2 to 6, 5.4 to 6, 5.6 to 6, or 5.8 to 6.

[0132] In some embodiments, the plurality of active microbes comprises one microbial strain having a significantly different oxalate-metabolizing activity in a standard oxalate metabolizing assay conducted at two pH values differing by at least 1 pH unit and within a pH range of 4 to 8. For example, in some embodiments, one microbial strain has significantly different oxalate-metabolizing activities in a standard oxalate metabolizing assay at pH 4 and pH 8, pH 5 and pH 8, pH 6 and pH 8, pH 7 and pH 8, pH 4 and pH 7, pH 5 and pH 7, pH 6 and pH 7, pH 4 and pH 6, pH 5 and pH 6, or pH 4 and pH 5.

[0133] In some embodiments, oxalate-metabolizing activity is detected using a standard oxalate metabolization assay. For example, in some embodiments, oxalate-metabolizing

activity is detected using a colorimetric enzyme assay that measures the activity of oxalate oxidase. In certain embodiments, relative changes in oxalate abundance in culture media inoculated with microbial strains are measured using a commercial oxalate assay kit (*e.g.*, Sigma-Aldrich, Catalog# MAK315). In some embodiments, oxalate-metabolizing activity is detected using liquid chromatography–mass spectrometry (LC-MS/MS). In some embodiments, relative changes in oxalate abundance is compared between the abundance of oxalate at the beginning of incubation (*i.e.* t=0), and after 2 hours, 4 hours, 6 hours, 8, hours, 10 hours, 12 hours, 14 hours, 16 hours, 18 hours, 24 hours, 30 hours, 36 hours, 48 hours, 60, hours, 72 hours, 84 hours, 96 hours, 120 hours, or 144 hours incubation.

[0134] As used herein, "higher oxalate metabolizing activity" means either an oxalate metabolizing activity of a microbial strain that is higher as compared to an oxalate metabolizing activity of the same microbial strain under different conditions, and/or an oxalate metabolizing activity of a microbial strain that is higher as compared to an oxalate metabolizing activity of a different microbial strain under the same conditions.

[0135] In some embodiments, the plurality of active microbes comprises two microbial strains having significantly different oxalate metabolizing activities. For example, in some embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a lower pH as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at the same lower pH. In some embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5 as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5, respectively. In some embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a higher pH as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at the same higher pH. In some embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at pH 7.5, 7.6. 7.7, 7.8, 7.9, or 8.0 as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at pH 7.5, 7.6. 7.7, 7.8, 7.9, or 8.0, respectively.

[0136] In some embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a lower pH as compared to its oxalate metabolizing activity at a higher pH. For example, in some embodiments one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5 than it does at pH 7.5, 7.6. 7.7, 7.8, 7.9, or 8.0. In some embodiments, one of the

plurality of active microbes has a significantly higher oxalate metabolizing activity at a higher pH as compared to its oxalate metabolizing activity at a lower pH. For example, in some embodiments one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at pH 7.5, 7.6. 7.7, 7.8, 7.9, or 8.0 than it does at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5.

[0137] In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at a lower pH and another microbe having a higher oxalate metabolizing activity at a higher pH. For example, in some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 4.0 and another microbe having a higher oxalate metabolizing activity at pH 7.5. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 4.0 and another microbe having a higher oxalate metabolizing activity at pH 7.6. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 4.0 and another microbe having a higher oxalate metabolizing activity at pH 7.7. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 4.0 and another microbe having a higher oxalate metabolizing activity at pH 7.8. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 4.0 and another microbe having a higher oxalate metabolizing activity at pH 7.9. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 4.0 and another microbe having a higher oxalate metabolizing activity at pH 8.0. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 4.5 and another microbe having a higher oxalate metabolizing activity at pH 7.5. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 4.5 and another microbe having a higher oxalate metabolizing activity at pH 7.6. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 4.5 and another microbe having a higher oxalate metabolizing activity at pH 7.7. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 4.5 and another microbe having a higher oxalate metabolizing activity at pH 7.8. In some embodiments, the plurality of active microbes comprises an active microbe having a higher

oxalate metabolizing activity at pH 4.5 and another microbe having a higher oxalate metabolizing activity at pH 7.9. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 4.5 and another microbe having a higher oxalate metabolizing activity at pH 8.0. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 5.0 and another microbe having a higher oxalate metabolizing activity at pH 7.5. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 5.0 and another microbe having a higher oxalate metabolizing activity at pH 7.6. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 5.0 and another microbe having a higher oxalate metabolizing activity at pH 7.7. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 5.0 and another microbe having a higher oxalate metabolizing activity at pH 7.8. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 5.0 and another microbe having a higher oxalate metabolizing activity at pH 7.9. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 5.0 and another microbe having a higher oxalate metabolizing activity at pH 8.0. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 5.5 and another microbe having a higher oxalate metabolizing activity at pH 7.5. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 5.5 and another microbe having a higher oxalate metabolizing activity at pH 7.6. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 5.5 and another microbe having a higher oxalate metabolizing activity at pH 7.7. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 5.5 and another microbe having a higher oxalate metabolizing activity at pH 7.8. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 5.5 and another microbe having a higher oxalate metabolizing activity at pH 7.9. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 5.5 and another microbe having a higher oxalate metabolizing activity at pH 8.0. In some

embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.0 and another microbe having a higher oxalate metabolizing activity at pH 7.5. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.0 and another microbe having a higher oxalate metabolizing activity at pH 7.6. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.0 and another microbe having a higher oxalate metabolizing activity at pH 7.7. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.0 and another microbe having a higher oxalate metabolizing activity at pH 7.8. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.0 and another microbe having a higher oxalate metabolizing activity at pH 7.9. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.0 and another microbe having a higher oxalate metabolizing activity at pH 8.0. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.5 and another microbe having a higher oxalate metabolizing activity at pH 7.5. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.5 and another microbe having a higher oxalate metabolizing activity at pH 7.6. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.5 and another microbe having a higher oxalate metabolizing activity at pH 7.7. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.5 and another microbe having a higher oxalate metabolizing activity at pH 7.8. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.5 and another microbe having a higher oxalate metabolizing activity at pH 7.9. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.5 and another microbe having a higher oxalate metabolizing activity at pH 8.0.

[0138] In some embodiments, one or more than one of the plurality of active microbes is capable of substantially metabolizing oxalate at an oxalate concentration of about 0.75 mM to about 40 mM of oxalate. For example, in some embodiments, one or more than one of the plurality of active microbes is capable of substantially metabolizing oxalate at an oxalate

concentration within a range of about 0.75 mM to about 40 mM, of about 1 mM to about 40 mM, of about 2.5 mM to about 40 mM, of about 5 mM to about 40 mM, of about 7.5 mM to about 40 mM, of about 10 mM to about 40 mM, of about 15 mM to about 40 mM, of about 20 mM to about 40 mM, of about 25 mM to about 40 mM, of about 30 mM to about 40 mM, of about 0.75 mM to about 30 mM, of about 1 mM to about 30 mM, of about 2.5 mM to about 30 mM, of about 5 mM to about 30 mM, of about 7.5 mM to about 30 mM, of about 10 mM to about 30 mM, of about 15 mM to about 30 mM, of about 20 mM to about 30 mM, of about 25 mM to about 30 mM, of about 0.75 mM to about 25 mM, of about 1 mM to about 25 mM, of about 2.5 mM to about 25 mM, of about 5 mM to about 25 mM, of about 7.5 mM to about 25 mM, of about 10 mM to about 25 mM, of about 15 mM to about 25 mM, of about 20 mM to about 25 mM, of about 0.75 mM to about 20 mM, of about 1 mM to about 20 mM, of about 2.5 mM to about 20 mM, of about 5 mM to about 20 mM, of about 7.5 mM to about 20 mM, of about 10 mM to about 20 mM, of about 15 mM to about 20 mM, of about 0.75 mM to about 15 mM, of about 1 mM to about 15 mM, of about 2.5 mM to about 15 mM, of about 5 mM to about 15 mM, of about 7.5 mM to about 15 mM, of about 10 mM to about 15 mM, of about 0.75 mM to about 10 mM, of about 1 mM to about 10 mM, of about 2.5 mM to about 10 mM, of about 5 mM to about 10 mM, of about 7.5 mM to about 10 mM, of about 0.75 mM to about 5 mM, of about 1 mM to about 5 mM, of about 2.5 mM to about 5 mM, or of about 0.75 mM to about 1 mM.

[0139] In some embodiments, the plurality of active microbes comprises one microbial strain having a significantly different oxalate-metabolizing activity in a standard *in vitro* oxalate metabolizing assay (for example, as described in Example 3) at an oxalate concentration as compared to its oxalate-metabolizing activity in a standard *in* vitro oxalate metabolizing assay conducted at a different oxalate concentration, wherein the difference between the two oxalate concentrations is within 100 fold. For example, in some embodiments, one microbial strain has significantly different oxalate-metabolizing activities in a standard oxalate metabolizing assay conducted at about 0.75 mM oxalate and about 40 mM oxalate, about 1 mM and about 40 mM, about 2.5 mM and about 40 mM, about 5 mM and about 40 mM, about 7.5 mM and about 40 mM, about 10 mM and about 40 mM, about 15 mM and about 40 mM, about 20 mM and about 40 mM, about 25 mM and about 40 mM, about 30 mM and about 40 mM, about 0.75 mM and about 30 mM, about 1 mM and about 30 mM, about 2.5 mM and about 30 mM, about 5 mM and about 30 mM, about 7.5 mM and about 30 mM, about 10 mM and about 30 mM, about 15 mM and about 30 mM, about 20

mM and about 30 mM, about 25 mM and about 30 mM, about 0.75 mM and about 25 mM, about 1 mM and about 25 mM, about 2.5 mM and about 25 mM, about 5 mM and about 25 mM, about 7.5 mM and about 25 mM, about 10 mM and about 25 mM, about 15 mM and about 25 mM, about 20 mM and about 25 mM, about 0.75 mM and about 20 mM, about 1 mM and about 20 mM, about 2.5 mM and about 20 mM, about 5 mM and about 20 mM, about 7.5 mM and about 20 mM, about 10 mM and about 20 mM, about 15 mM and about 20 mM, about 0.75 mM and about 15 mM, about 1 mM and about 15 mM, about 2.5 mM and about 15 mM, about 5 mM and about 15 mM, about 7.5 mM and about 15 mM, about 10 mM and about 15 mM, about 0.75 mM and about 10 mM, about 1 mM and about 10 mM, about 2.5 mM and about 10 mM, about 5 mM and about 10 mM, about 7.5 mM and about 10 mM, about 0.75 mM and about 5 mM, about 1 mM and about 5 mM, about 2.5 mM and about 5 mM, or about 0.75 mM and about 1 mM.

[0140] In some embodiments, the plurality of active microbes comprises two microbial strains having significantly different oxalate metabolizing activities. For example, in some embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a lower concentration of oxalate as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at the same lower concentration of oxalate. In some embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at an oxalate concentration of 0.75 mM, 1 mM, 2.5 mM, 5 mM, or 7.5 mM, as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at an oxalate concentration of 0.75 mM, 1 mM, 2.5 mM, 5 mM, or 7.5 mM, respectively. In some embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a higher concentration of oxalate as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at the same higher concentration of oxalate. In some embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at an oxalate concentration of 15 mM, 20 mM, 25 mM 30 mM, or 40 mM as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at an oxalate concentration of 15 mM, 20 mM, 25 mM 30 mM, or 40 mM, respectively.

[0141] In some embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a lower oxalate concentration as compared to its oxalate metabolizing activity at a higher oxalate concentration. For example, in some

embodiments one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at 0.75 mM, 1 mM, 2.5 mM, 5 mM, or 7.5 mM of oxalate than it does at 15 mM, 20 mM, 25 mM 30 mM, or 40 mM of oxalate. In some embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a higher oxalate concentration as compared to its oxalate metabolizing activity at a lower oxalate concentration. For example, in some embodiments one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at 15 mM, 20 mM, 25 mM 30 mM, or 40 mM of oxalate than it does at 0.75 mM, 1 mM, 2.5 mM, 5 mM, or 7.5 mM of oxalate.

[0142] In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at a lower concentration of oxalate and another microbe having a higher oxalate metabolizing activity at a higher concentration of oxalate. For example, in some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at about 0.75 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 40 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 1 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 40 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 2.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 40 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 40 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 7.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 40 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 0.75 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 30 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 1 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 30 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 2.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 30 mM oxalate. In

some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 30 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 7.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 30 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 0.75 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 25 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 1 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 25 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 2.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 25 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 25 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 7.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 25 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 0.75 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 20 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 1 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 20 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 2.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 20 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 20 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 7.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 20 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher

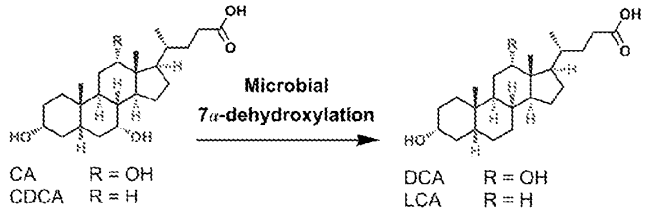
oxalate metabolizing activity at 0.75 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 15 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 1 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 15 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 2.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 15 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 15 mM oxalate. In some embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at 7.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 15 mM oxalate.

[0143] In some embodiments, when tested in an *in vitro* oxalate metabolization assay (e.g., as described in Example 3 below), a plurality of active microbes of the present invention significantly reduces the concentration of oxalate present in a sample by at least 20%, by at least 30%, by at least 40%, by at least 50%, by at least 60%, by at least 70%, or by at least 80%.

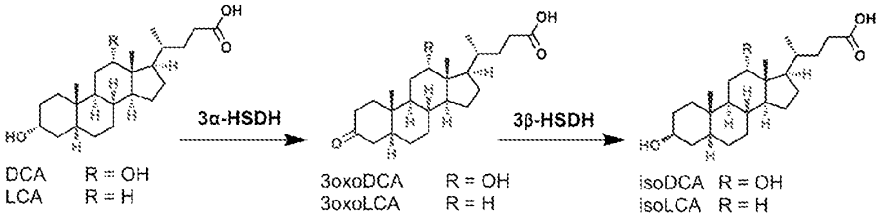
[0144] In some embodiments, a plurality of active microbes of the present invention significantly reduces the concentration of oxalate present in a sample of blood, serum, bile, stool, or urine when administered to a subject by at least 20%, by at least 30%, by at least 40%, by at least 50%, by at least 60%, by at least 70%, or by at least 80% as compared to an untreated control subject or pre-administration levels. Concentrations of oxalate in a blood, serum, bile, stool or urine sample can be measured using a liquid chromatography–mass spectrometry (LC-MS), method as described in Example 4, below.

Bile Salt-Modifying Active Microbes

[0145] Unconjugated primary bile acids, cholic acid (CA) and chenodeoxycholic acid (CDCA), are substrates for 7α-dehydroxylation by select members of the gut microbiota. As shown below, 7α-dehydroxylation converts CA and CDCA to lithocholic acid (LCA) and deoxycholic acid (DCA), respectively. LCA and DCA are secondary bile acids that have been implicated in adverse health outcomes.



[0146] In some embodiments, a microbial consortium disclosed herein comprises microbial strains having robust 3α-hydroxysteroid dehydrogenase (3α-HSDH) and 3β-hydroxysteroid dehydrogenase (3β-HSDH) activity. As shown below, 3α-HSDH and 3β-HSDH convert DCA and LCA into alternative secondary bile acids isoDCA and isoLCA, respectively.



[0147] In some embodiments, microbial consortia provided herein comprise a plurality of active microbes expressing 3α-HSDH selected from one or more of *Eggerthella lenta*, *Ruminococcus gnavus*, *Clostridium perfringens, Peptostreptococcus productus, and Clostridium scindens*. In some embodiments, microbial consortia provided herein comprise a plurality of active microbes expressing 3β-HSDH selected from one or more of *Peptostreptococcus productus*, *Clostridium innocuum*, and *Clostridium scindens.*

[0148] In some embodiments, the plurality of active microbes comprises one or more than one microbial strain selected from: an *Eggethella lenta* strain having a 16S sequence at least 80% identical to SEQ ID NO: 30, an *Eggethella lenta* strain having a 16S sequence at least 80% identical to SEQ ID NO: 96, an *Eggethella lenta* strain having a 16S sequence at

least 80% identical to SEQ ID NO: 170, an *Eggethella lenta* strain having a 16S sequence at least 80% identical to SEQ ID NO: 201, or a *Clostridum scindens* strain having a 16S sequence at least 80% identical to SEQ ID NO: 87.

[0149] In some embodiments, the plurality of active microbes comprises one or more than one microbial strain selected from: an *Eggethella lenta* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 30, an *Eggethella lenta* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 96, an *Eggethella lenta* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 170, an *Eggethella lenta* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 201, or a *Clostridum scindens* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 87.

[0150] In some embodiments, the plurality of active microbes comprises two microbial strains having significantly different bile acid-metabolizing activities. For example, in some embodiments, one of the plurality of active microbes has a significantly higher bile acid-metabolizing activity at a lower concentration of bile acid as compared to the bile acid-metabolizing activity of another microbial strain in the plurality of active microbes at the same lower concentration of bile acid. In some embodiments, one of the plurality of active microbes has a significantly higher bile acid-metabolizing activity at a bile acid concentration of 0.1 mM, 0.2 mM, 0.3 mM, 0.4 mM, 0.5 mM, 0.6 mM, 0.7 mM, 0.8 mM, 0.9 mM, 1.0 mM, as compared to the bile acid-metabolizing activity of another microbial strain in the plurality of active microbes at an oxalate concentration of 0.1 mM, 0.2 mM, 0.3 mM, 0.4 mM, 0.5 mM, 0.6 mM, 0.7 mM, 0.8 mM, 0.9 mM, or 1.0 mM, respectively. In some embodiments, one of the plurality of active microbes has a significantly higher bile acid-metabolizing activity at a higher concentration of bile acid as compared to the bile acid-metabolizing activity of another microbial strain in the plurality of active microbes at the same higher concentration of bile acid. In some embodiments, one of the plurality of active microbes has a significantly higher bile acid metabolizing activity at a bile acid concentration of 5.0 mM, 5.5 mM, 6.0 mM, 6.5 mM, 7.0 mM, 7.5 mM, 8.0 mM, 8.5 mM, 9.0 mM, 9.5 mM, or 10.0

mM as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at an oxalate concentration of 5.0 mM, 5.5 mM, 6.0 mM, 6.5 mM, 7.0 mM, 7.5 mM, 8.0 mM, 8.5 mM, 9.0 mM, 9.5 mM, or 10.0 mM, respectively.

[0151] In some embodiments, one of the plurality of active microbes has a significantly higher bile acid-metabolizing activity at a lower bile acid concentration as compared to its bile acid-metabolizing activity at a higher bile acid concentration. For example, in some embodiments one of the plurality of active microbes has a significantly higher bile acid-metabolizing activity at 0.1 mM, 0.2 mM, 0.3 mM, 0.4 mM, 0.5 mM, 0.6 mM, 0.7 mM, 0.8 mM, 0.9 mM, or 1.0 mM of bile acid than it does at. 5.0 mM, 5.5 mM, 6.0 mM, 6.5 mM, 7.0 mM, 7.5 mM, 8.0 mM, 8.5 mM, 9.0 mM, 9.5 mM, or 10.0 mM of bile acid. In some embodiments, one of the plurality of active microbes has a significantly higher bile acid-metabolizing activity at a higher bile acid concentration as compared to its bile acid metabolizing activity at a lower bile acid concentration. For example, in some embodiments one of the plurality of active microbes has a significantly higher bile acid-metabolizing activity at 5.0 mM, 5.5 mM, 6.0 mM, 6.5 mM, 7.0 mM, 7.5 mM, 8.0 mM, 8.5 mM, 9.0 mM, 9.5 mM, or 10.0 mM of bile acid than it does at 0.1 mM, 0.2 mM, 0.3 mM, 0.4 mM, 0.5 mM, 0.6 mM, 0.7 mM, 0.8 mM, 0.9 mM, or 1.0 mM of bile acid.

[0152] In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid-metabolizing activity at a lower concentration of bile acid and another microbe having a higher bile acid-metabolizing activity at a higher concentration of bile acid. For example, in some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.1 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 10 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.2 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 10 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.3 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 10 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.4 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 10 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.5 mM bile acid and another active microbe having a higher

bile acid-metabolizing activity at about 10 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.1 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 7.5 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.2 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 7.5 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.3 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 5.0 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.4 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 7.5 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.5 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 7.5 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.1 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 5.0 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.2 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 5.0 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.3 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 5.0 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.4 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 5.0 mM bile acid. In some embodiments, the plurality of active microbes comprises an active microbe having a higher bile acid metabolizing activity at about 0.5 mM bile acid and another active microbe having a higher bile acid-metabolizing activity at about 5.0 mM bile acid.

[0153] In some embodiments, when tested in a standard *in vitro* bile acid metabolization assay, a plurality of active microbes of the present invention significantly reduces the concentration of lithoholic acid (LCA) and or deoxycholic acid (DCA) present in a sample by

at least 20%, by at least 30%, by at least 40%, by at least 50%, by at least 60%, by at least 70%, or by at least 80%.

[0154] In some embodiments, a plurality of active microbes of the present invention significantly reduces the concentration of LCA and/or DCA present in a sample of blood, serum, bile, stool, or urine when administered to a subject by at least 20%, by at least 30%, by at least 40%, by at least 50%, by at least 60%, by at least 70%, or by at least 80% as comparted to an untreated control subject or pre-administration levels.

Supportive Community of Microbes

[0155] The microbial consortia of the present invention further comprise a supportive community of microbes that enhances one or more than one characteristic of the plurality of active microbes. For example, in some embodiments, the supportive community of microbes enhances gastrointestinal engraftment of the plurality of active microbes. In other embodiments, the supportive community of microbes enhances biomass of the plurality of active microbes. In other embodiments, the supportive community of microbes enhances metabolism of the first metabolic substrate by the plurality of active microbes. In other embodiments, the supportive community of microbes enhances longitudinal stability of the plurality of active microbes.

[0156] The supportive community of microbes disclosed herein metabolize one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the plurality of active microbes. For example, in some embodiments, the supportive community of microbes metabolizes formate produced by the plurality of active microbes, wherein the presence of formate inhibits the metabolism of oxalate by the plurality of active microbes. In some embodiments, the supportive community of microbes of the current invention catalyzes the fermentation of polysaccharides to one or more than one of the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2. In some embodiments, the supportive community of microbes catalyzes the fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2, In some embodiments, the supportive community catalyzes the synthesis of one or more than one of the group consisting of methane from H_2 and CO_2, methane from formate

and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate. In some embodiments, the supportive community of microbes of the current invention catalyzes the deconjugation of conjugated bile acids to produce primary bile acids, the conversion of cholic acid (CA) to 7-oxocholic acid, the conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), the conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and/or the conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

[0157] The supportive community of microbes of the current invention comprises between one and 300 microbial strains. For example, in some embodiments, the supportive community of microbes comprises between 1 and 300, 5 and 300, 10 and 300, 15 and 300, 20 and 300, 30 and 300, 40 and 300, 50 and 300, 60 and 300, 70 and 300, 80 and 300, 90 and 300, 100 and 300, 110 and 300, 120 and 300, 130 and 300, 140 and 300, 150 and 300, 160 and 300, 170 and 300, 180 and 300, 190 and 300, 200 and 300, 210 and 300, 220 and 300, 230 and 300, 240 and 300, 250 and 300, 260 and 300, 270 and 300, 280 and 300, 290 and 300, 1 and 250, 5 and 250, 10 and 250, 15 and 250, 20 and 250, 30 and 250, 40 and 250, 50 and 250, 60 and 250, 70 and 250, 80 and 250, 90 and 250, 100 and 250, 110 and 250, 120 and 250, 130 and 250, 140 and 250, 150 and 250, 160 and 250, 170 and 250, 180 and 250, 190 and 250, 200 and 250, 210 and 250, 220 and 250, 230 and 250, 240 and 250, 1 and 200, 5 and 200, 10 and 200, 15 and 200, 20 and 200, 30 and 200, 40 and 200, 50 and 200, 60 and 200, 70 and 200, 80 and 200, 90 and 200, 100 and 200, 110 and 200, 120 and 200, 130 and 200, 140 and 200, 150 and 200, 160 and 200, 170 and 200, 180 and 200, 190 and 200, 1 and 150, 5 and 150, 10 and 150, 15 and 150, 20 and 150, 30 and 150, 40 and 150, 50 and 150, 60 and 150, 70 and 150, 80 and 150, 90 and 150, 100 and 150, 110 and 150, 120 and 150, 130 and 150, 140 and 150, 1 and 100, 5 and 100, 10 and 100, 15 and 100, 20 and 100, 30 and 100, 40 and 100, 50 and 100, 60 and 100, 70 and 100, 80 and 100, 90 and 100, 1 and 50, 5 and 50, 10 and 50, 15 and 50, 20 and 50, 30 and 50, or 40 and 50 microbial strains. For example, in some embodiments, the supportive community of microbes comprises about 20 to about 200, about 70 to about 80, about 80 to about 90, about 100 to about 110, or about 150 to about 160 microbial strains.

[0158] In some embodiments, the supportive community of microbes comprises species of at least one, at least two, at least three, at least four, or at least five of the following phyla: Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia, and

Euryarchaeota. In some embodiments, the supportive community of microbes comprises species of at least one, at least two, at least three, at least four, or at least five of the following subclades: Bacteroidales, Clostridiales, Erysipelotrichales, Negativicutes, Coriobacteriia, Bifidobacteriales, and Methanobacteriales.

[0159] In some embodiments, the supportive community of microbes of the current invention consumes one or more metabolites derived from an animal diet. For example, in some embodiments, the supportive community of microbes of the current invention consumes one or more than one of the following metabolites: a-mannan, acetate, agarose, alanine, arabinan, arabinogalactan, arabinoxylan, arginine, asparagine, aspartate, b-glucans, benzoic acids, carrageenan, catechol, chlorogenic acids, chondroitin sulfate, cysteine, dextran, enterodiol, flavan-3-ols, flavanones, flavones, flavonols, folate, formate, galactomannan, galacturonan, galacturonate, glucomannan, glutamine, glycine, hyaluronan, hydrogen, hydroxyproline, inulin, isoflavones, lactate, laminarin, leucine, levan, methionine, mucin O-linked glycans, phenylalanine, proline, rhamnogalacturonan I, rhamnogalacturonan II, secoisolariciresinol diglucoside, serine, starch, tyrosine, valine, xyloglucan, and xylooligosaccharides. In some embodiments, the supportive community of microbes is designed to maximize the number of metabolites derived from the host diet that the supportive community can consume.

[0160] In some embodiments, the supportive community of microbes of the current invention consumes one or more of the following dietary, host-derived, or microbial metabolites: thiamine, methanol, indole-3-acetate, L-glutamate, L-ornithine, niacin, 2-oxobutyrate, betaine, D-fructuronate, D-gluconate, D-tagaturonate, D-turanose, inosine, glycine, histidine, L-idonate, isoleucine, serine, N-acetyl-D-mannosamine, nitrate, thymidine, uridine, butyrate, propanoate, indole, glutamine, inositol, arginine, aspartate, malate, oxalate, phenol, succinate, ethanol, hydrogen, formate, lactate, aminobenzoate, lyxose, isomaltose, phenylalanine, tyrosine, pyruvate, mannitol, sorbitol, D-tagatose, glycerol, leucine, N-acetylgalactosamine, isovalerate, biotin, isobutyrate, 2-methylbutyrate, D-galactosamine, glycolithocholate, valine, melibiose, taurolithocholate, menaquinone, chenodeoxycholic acid, cholic acid, glycochenodeoxycholate, glycocholate, glycodeoxycholate, thiosulfate, pyridoxal, bicarbonate, N-acetyl-D-glucosamine, sulfate, riboflavin, methionine, N-acetylneuraminic acid, ribose, D-galacturonate, taurochenodeoxycholate, taurocholate, arabinose, rhamnose, pantothenic acid, xylooligosaccharide, acetate, D-glucuronic acid, cysteine, adenosylcobalamin, sucrose, trehalose, urea, xylose, cellobiose, mannose, L-fucose,

D-galactose, D-glucosamine, D-psicose, fructooligosaccharide, carbon dioxide, maltose, ammonia, raffinose, dextrin, lactose, glucose, and fructose.

[0161] In some embodiments, the supportive community of microbes of the current invention produces one or more of the following metabolites: dimethylamine, folic acid, butylamine, phenylethylamine, 1,2-propanediol, acetone, trimethylamine, putrescine, tyramine, 4-aminobutyrate, valerate, 1,2-ethanediol, methylamine, phenylacetate, spermidine, hydrogen sulfide, linoleic acid, formaldehyde, trimethylamine N-oxide, cadaverine, alanine, threonine, methane, and pentanol.

[0162] In some embodiments of the invention, an original dosage form of the disclosed microbial consortium comprises active microbes and supportive microbes in a colony forming unit (CFU) ratio of about 5:1, 4:1, 3:1, 2:1, 1:1, 1:2, 1:3, 1:4, 1:5. In some embodiments, an original dosage form of the disclosed microbial consortium comprises active microbes and supportive microbes in total CFU amounts within about one order of magnitude, about two orders of magnitude, about three orders of magnitude, about four orders of magnitude, about 5 orders of magnitude, about 6 orders of magnitude, about 7 orders of magnitude, about 8 orders of magnitude, about 9 orders of magnitude, or about 10 orders of magnitude of each other.

[0163] In some embodiments, the supportive community of microbes may comprise one or more than one microbial strains selected from, but not limited to, *Absiella dolichum, Bacteroides uniformis, Eubacterium siraeum, Acidaminococcus fermentans, Bacteroides vulgatus, Eubacterium ventriosum, Acidaminococcus sp., Bacteroides xylanisolvens, Faecalibacterium prausnitzii, Adlercreutzia equolifaciens, Bifidobacterium breve, Granulicatella adiacens, Akkermansia muciniphila, Bifidobacterium catenulatum, Holdemanella biformis, Alistipes finegoldii, Bifidobacterium pseudocatenulatum, Holdemania filiformis, Alistipes indistinctus, Bilophila wadsworthia, Hungatella hathewayi, Alistipes onderdonkii, Blautia hansenii, Intestinibacter bartlettii, Alistipes putredinis, Blautia hydrogenotrophica, Intestinimonas butyriciproducens, Alistipes senegalensis, Blautia obeum, Lactobacillus ruminis, Alistipes shahii, Blautia sp., Marvinbryantia formatexigens, Anaerobutyricum hallii, Blautia wexlerae, Megasphaera, Anaerofustis stercorihominis, Butyricimonas virosa, Methanobrevibacter smithii, Anaerostipes caccae, Butyrivibrio crossotus, Anaerotruncus colihominis, Catenibacterium mitsuokai, Bacteroides caccae, Clostridium asparagiforme, Bacteroides cellulosilyticus, Clostridium bolteae, Mitsuokella multacida, Bacteroides coprocola, Clostridium hiranonis, Odoribacter splanchnicus,*

Bacteroides coprophilus, Clostridium hylemonae, Olsenella uli, Bacteroides dorei, Clostridium leptum, Oscillibacter sp., Bacteroides dorei, Clostridium methylpentosum, Parabacteroides distasonis, Bacteroides eggerthii, Clostridium orbiscindens, Parabacteroides johnsonii, Bacteroides finegoldii, Clostridium saccharolyticum, Parabacteroides merdae, Bacteroides fragilis, Clostridium scindens, Parabacteroides sp., Bacteroides intestinalis, Clostridium sp., Prevotella buccalis, Bacteroides ovatus, Prevotella copri, Bacteroides pectinophilus, Roseburia inulinivorans, Bacteroides plebeius, Clostridium spiroforme, Ruminococcus gauvreauii, Bacteroides rodentium, Collinsella aerofaciens, Ruminococcus gnavus, Collinsella stercoris, Ruminococcus lactaris, Coprococcus comes, Ruminococcus torques, Coprococcus eutactus, Slackia exigua, Desulfovibrio piger, Slackia heliotrinireducens, Dorea formicigenerans, Solobacterium moorei, Dorea longicatena, Streptococcus salivarius subsp. Thermophilus, Bacteroides stercoris, Ethanoligenens harbinense, Subdoligranulum variabile, Bacteroides thetaiotaomicron, Eubacterium rectale, Turicibacter sanguinis, and *Tyzzerella nexilis.*

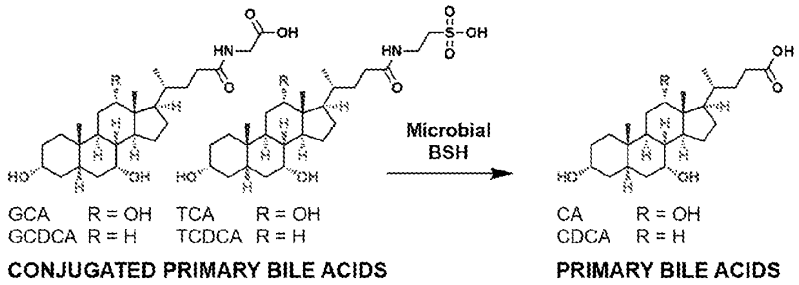
[0164] In some embodiments the supportive community of microbes may comprise one or more than one microbial strains selected from, but not limited to, *Absiella dolichum* DSM 3991, *Bilophila wadsworthia* ATCC 49260, *Intestinibacter bartlettii* DSM 16795, *Acidaminococcus fermentans* DSM 20731, *Bilophila wadsworthia* DSM 11045, *Intestinimonas butyriciproducens* DSM 26588, *Acidaminococcus* sp. HM-81, *Blautia hansenii* DSM 20583, *Lactobacillus amylovorus* DSM 20552, *Adlercreutzia equolifaciens* DSM 19450, *Blautia hydrogenotrophica* DSM 10507, *Lactobacillus casei* subsp. casei ATCC 393, *Akkermansia muciniphila* ATCC BAA-835, *Blautia obeum* DSMZ 25238, *Lactobacillus casei* subsp. *casei* ATCC 39539, *Alistipes finegoldii* DSM 17242, *Blautia* sp. HM-1032, *Lactobacillus crispatus* HM-370, *Alistipes indistinctus* DSM 22520, *Blautia wexlerae* DSM 19850, *Lactobacillus johnsonii* HM-643, *Alistipes onderdonkii* DSM 19147, *Butyricimonas virosa* DSM 23226, *Lactobacillus parafarraginis* HM-478, *Alistipes putredinis* DSM 17216, *Butyrivibrio crossotus* DSM 2876, *Lactobacillus plantarum* ATCC 14917, *Alistipes senegalensis* DSM 25460, *Catenibacterium mitsuokai* DSM 15897, *Lactobacillus plantarum* ATCC 202195, *Alistipes shahii* DSM 19121, *Cetobacterium somerae* DSM 23941, *Lactobacillus ruminis* ATCC 25644, *Anaerobutyricum hallii* DSM 3353, *Clostridium asparagiforme* DSM 15981, *Lactobacillus ruminis* DSM 20404, *Anaerococcus lactolyticus* DSM 7456, *Clostridium bolteae* DSM 15670, *Lactobacillus ultunensis* DSM 16048, *Anaerofustis stercorihominis* DSM 17244, *Clostridium bolteae* HM-1038, *Lactococcus lactis* Berridge DSM 20729, *Anaerostipes caccae* DSM 14662,

Clostridium bolteae HM-318, *Marvinbryantia formatexigens* DSM 14469, *Anaerotruncus colihominis* DSM 17241, *Clostridium cadaveris* HM-1040, *Megasphaera indica* DSM 25562, *Bacteroides caccae* ATCC 43185, *Clostridium citroniae* HM-315, *Megasphaera* sp. DSM 102144, *Bacteroides caccae* HM-728, *Clostridium hiranonis* DSM 13275, *Methanobrevibacter smithii* DSM 11975, *Bacteroides cellulosilyticus* DSM 14838, *Clostridium hylemonae* DSM 15053, *Methanobrevibacter smithii* DSM 2374, *Bacteroides cellulosilyticus* HM-726, *Clostridium innocuum* HM-173, *Methanobrevibacter smithii* DSM 2375, *Bacteroides coprocola* DSM 17136, *Clostridium leptum* DSM 753, *Methanobrevibacter smithii* DSM 861, *Bacteroides coprophilus* DSM 18228, *Clostridium methylpentosum* DSM 5476, *Methanomassiliicoccus luminyensis* DSM 25720, *Bacteroides dorei* DSM 17855, *Clostridium saccharolyticum* DSM 2544, *Methanosphaera stadtmanae* DSMZ 3091, *Bacteroides dorei* HM-29, *Clostridium scindens* DSM 5676, *Mitsuokella multacida* DSM 20544, *Bacteroides dorei* HM-718, *Clostridium scindens* VPI 12708, *Odoribacter splanchnicus* DSM 20712, *Bacteroides eggerthii* DSM 20697, *Clostridium* sp. ATCC 29733, *Olsenella uli* DSM 7084, *Bacteroides eggerthii* HM-210, *Clostridium* sp. DSM 4029, *Oscillibacter* sp. HM-1030, *Bacteroides finegoldii* DSM 17565, *Clostridium* sp. HM-634, *Parabacteroides distasonis* ATCC 8503, *Bacteroides finegoldii* HM-727, *Clostridium* sp. HM-635, *Parabacteroides goldsteinii* HM-1050, *Bacteroides fragilis* HM-20, *Clostridium spiroforme* DSM 1552, *Parabacteroides johnsonii* DSM 18315, *Bacteroides fragilis* HM-709, *Clostridium sporogenes* ATCC 15579, *Parabacteroides johnsonii* HM-731, *Bacteroides fragilis* HM-710, *Clostridium sporogenes* ATCC 17889, *Parabacteroides merdae* DSM 19495, *Bacteroides intestinalis* DSM 17393, *Clostridium sporogenes* DSM 767, *Parabacteroides merdae* HM-729, *Bacteroides ovatus* ATCC 8483, *Clostridium symbiosum* HM-309, *Parabacteroides merdae* HM-730, *Bacteroides ovatus* HM-222, *Clostridium symbiosum* HM-319, *Parabacteroides* sp. HM-77, *Bacteroides pectinophilus* ATCC 43243, *Collinsella aerofaciens* ATCC 25986, *Peptostreptococcus anaerobius* DSM 2949, *Bacteroides plebeius* DSM 17135, *Collinsella stercoris* DSM 13279, *Prevotella buccae* HM-45, *Bacteroides rodentium* DSM 26882, *Coprococcus catus* ATCC 27761, *Prevotella buccalis* DSM 20616, *Bacteroides salyersiae* HM-725, *Coprococcus comes* ATCC 27758, *Prevotella copri* DSM 18205, *Bacteroides* sp. HM-18, *Coprococcus eutactus* ATCC 27759, *Proteocatella sphenisci* DSM 23131, *Bacteroides* sp. HM-19, *Coprococcus eutactus* ATCC 51897, *Providencia rettgeri* ATCC BAA-2525, *Bacteroides* sp. HM-23, *Coprococcus* sp. DSM 21649, *Roseburia intestinalis* DSM 14610, *Bacteroides* sp. HM-27, *Desulfovibrio piger* ATCC 29098, *Roseburia inulinivorans* DSM 16841, *Bacteroides* sp. HM-28, *Dialister*

pneumosintes ATCC 51894, *Ruminococcaceae* sp. HM-79, *Bacteroides* sp. HM-58, *Dorea formicigenerans* ATCC 27755, *Ruminococcus albus* ATCC 27210, *Bacteroides stercoris* DSM 19555, *Dorea longicatena* DSM 13814, *Ruminococcus bromii* ATCC 27255, *Bacteroides stercoris* HM-1036, *Eggerthella* sp. DSM 11767, *Ruminococcus bromii* ATCC 51896, *Bacteroides thetaiotaomicron* ATCC 29148, *Eggerthella* sp. DSM 11863, *Ruminococcus gauvreauii* DSM 19829, *Bacteroides uniformis* ATCC 8492, *Eggerthella* sp. HM-1099, *Ruminococcus gnavus* ATCC 29149, *Bacteroides vulgatus* ATCC 8482, *Ethanoligenens harbinense* DSM 18485, *Ruminococcus gnavus* DSM 108212, *Bacteroides vulgatus* HM-720, *Eubacterium eligens* ATCC 27750, *Ruminococcus gnavus* HM-1056, *Bacteroides xylanisolvens* DSM 18836, *Eubacterium rectale* ATCC 33656, *Ruminococcus lactaris* ATCC 29176, *Bifidobacterium adolescentis* HM-633, *Eubacterium siraeum* DSM 15702, *Ruminococcus lactaris* HM-1057, *Bifidobacterium angulatum* HM-1189, *Eubacterium ventriosum* ATCC 27560, *Ruminococcus torques* ATCC 27756, *Bifidobacterium animalis* DSM 20104, *Faecalibacterium prausnitzii* ATCC 27766, *Slackia exigua* DSM 15923, *Bifidobacterium animalis* subsp. *Lactis* DSMZ 10140, *Faecalibacterium prausnitzii* ATCC 27768, *Slackia heliotrinireducens* DSM 20476, *Bifidobacterium bifidum* ATCC 11863, *Faecalibacterium prausnitzii* DSM 17677, *Solobacterium moorei* DSM 22971, *Bifidobacterium breve* DSM 20213, *Faecalibacterium prausnitzii* HM-473, *Streptococcus salivarius* subsp. *thermophilus* ATCC BAA-491, *Bifidobacterium catenulatum* DSM 16992, *Flavonifractor plautii* HM-1044, *Streptococcus thermophilus* ATCC 14485, *Bifidobacterium longum infantis* ATCC 55813, *Flavonifractor plautii* HM-303, *Subdoligranulum variabile* DSM 15176, *Bifidobacterium longum* subsp. *longum* HM-845, *Gramulicatella adiacens* ATCC 49175, *Turicibacter sanguinis* DSM 14220, *Bifidobacterium longum* subsp. *longum* HM-846, *Holdemanella biformis* DSM 3989, *Tyzzerella nexilis* DSM 1787, *Bifidobacterium longum* subsp. *longum* HM-847, *Holdemania filiformis* DSM 12042, *Veillonella dispar* ATCC 17748, *Bifidobacterium longum* subsp. *longum* HM-848, *Hungatella* (prev. *Clostridium*) *hathewayi* HM-308, *Veillonella* sp. HM-49, *Bifidobacterium pseudocatenulatum* DSM 20438, *Hungatella hathewayi* DSM 13479, and *Veillonella* sp. HM-64.

[0165] Conjugated primary bile acids are synthesized in the liver from cholesterol, concentrated and stored in the gallbladder, and secreted into the duodenum to facilitate the solubilization and absorption of dietary lipids. Most bile acids are reabsorbed and recycled back to the liver through enterohepatic recirculation, but a sizable fraction (5%) escapes recycling, enters the large intestine, and is heavily metabolized into secondary bile acids by

resident colonic microbes. Through microbial metabolism, four conjugated primary bile acids produced in the liver: taurochenoxycholic acid (TCDCA), glycochenodeoxycholic acid (GCDCA), taurocholic acid (TCA), and glycocholic acid (GCA), can be converted into over 100 molecules that have profound effects on host physiology. The unique profile of molecules produced is dependent on the metabolic capabilities of the resident colonic microbial community. As shown below, the first metabolic step upstream of secondary bile acid production is the deconjugation of conjugated primary bile acids by microbial bile salt hydrolases (BSH).

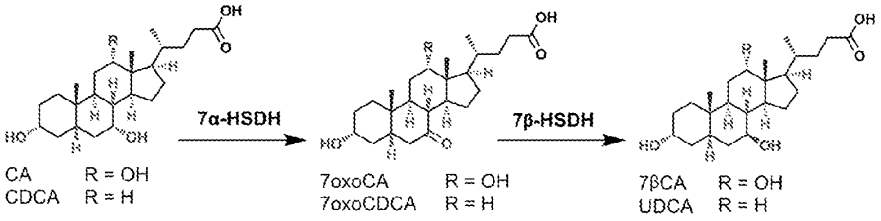


[0166] In some embodiments, the supportive community of microbes may comprise one or more microbial strains having robust and/or redundant BSH activity, so that deconjugation of primary bile acids can occur despite differences in host physiology, diet, plurality of active microbes present in the microbial consortium, or the pre-existing composition of the conjugated bile acid pool.

[0167] In some embodiments, the supportive community of microbes may comprise one or more than one microbial strains selected from, *Alistipes indistinctus*, *Bacteroides ovatus, Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvens*, *Bifidobacterium angulatum*, *Bifidobacterium bifidum*, *Bifidobacterium breve*, *Bifidobacterium longum infantis*, *Bifidobacterium pseudocatenulatum*, *Blautia obeum*, *Clostridium hylemonae*, *Enterococcus faecalis*, *Hungatella hathewayi*, *Lactobacillus acidophilus*, *Methanobrevibacter smithii, Parabacteroides distasonis*, *Parabacteroides goldsteini*, *Providencia rettgeri, Roseburia inulinivorans*, *Ruminococcus bromii*, *Ruminococcus gnavus*, and *Turicibacter sanguinis*.

[0168] In some embodiments, the current disclosure provides a microbial consortium comprising a plurality of active microbes that convert CA and CDCA into alternative

secondary bile acids, thereby shifting the bile acid pool away from 7α-dehydroxylation products, LCA and DCA. For example, in some embodiments, a microbial consortium disclosed herein comprises microbial strains having robust 7α-hydroxysteroid dehydrogenase (7α-HSDH) and 7β-hydroxysteroid dehydrogenase (7β-HSDH) activity. As shown below, 7α-HSDH creates 7oxoCA and 7oxoCDCA intermediates, and 7β-HSDH converts CA and CDCA to 7βCA and ursodeoxycholic acid (UDCA).



[0169] In some embodiments, microbial consortia provided herein comprise a plurality of active microbes expressing 7α-HSDH selected from one or more of *Acinetobacter calcoaceticusi, Bacteroides thetaiotaomicron, Bacteroides intestinalis, Bacteroides fragilis, Eggerthella lenta, Ruminococcus sp.*. In some embodiments, microbial consortia provided herein comprises a plurality of active microbes expressing 7β-HSDH selected from one or both of *Ruminococcus torques* and *Peptostreptococcus productus*.

Fermenting and Synthesizing Microbes

[0170] In some embodiments, the microbial consortium of the current invention further comprises a fermenting microbe that metabolizes a fermentation substrate to generate one or more than one fermentation product. For example, in some embodiments, the fermentation product is a second metabolic substrate for one or more of the plurality of active microbes. In some embodiments, the fermentation product is a metabolic substrate for one or more of the supportive microbes. In some embodiments, the fermentation substrate is a polysaccharide and the generated fermentation product is one or more than one of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2. In some embodiments, the fermentation substrate is an amino acid and the generated fermentation product is one or more than one of

acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2.

[0171] In some embodiments, the microbial consortium of the current invention further comprises a synthesizing microbe that catalyzes a synthesis reaction that combines the one or more than one metabolite generated by the plurality of active microbes and the one or more than one fermentation product generated by the fermenting microbe to produce one or more than one synthesis product. In some embodiments the fermentation product generated by the fermenting microbe is a third metabolic substrate for the synthesizing microbe. In some embodiments, the one or more than one synthesis product is a second metabolic substrate for the plurality of active microbes. In some embodiments, the one or more than one synthesis product is a fourth metabolic substrate for the fermenting microbe.

[0172] In some embodiments, the synthesizing microbe catalyzes the synthesis of one or more than one of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate.

[0173] In some embodiments, a fermenting microbe may be for example, but not limited to, *Bacteroides thetaiotaomicron* or *Bactorides vulgatus*. In some embodiments, a synthesizing microbe may be for example, but not limited to, *Methanobrevibacter smithii* or *Methanomassiliicoccus luminyensis.*

[0174] In some embodiments, the fermenting microbe is selected from a *Bacteroides thetaiotaomicron* strain having a 16S sequence at least 80% identical to SEQ ID NO: 20, SEQ ID NO: 76, SEQ ID NO: 139, or SEQ ID NO: 280. In some embodiments, the fermenting microbe is selected from a *Bacteroides vulgatus* strain having a 16S sequence at least 80% identical to SEQ ID NO: 39, SEQ ID NO: 111, SEQ ID NO: 121, SEQ ID NO: 173, SEQ ID NO: 211, SEQ ID NO: 308, SEQ ID NO: 321, or SEQ ID NO: 326. In some embodiments, the synthesizing microbe is selected from a *Methanobrevibacter smithii* strain having a 16S sequence at least 80% identical to SEQ ID NO: 292.

[0175] In some embodiments, the fermenting microbe is selected from a *Bacteroides thetaiotaomicron* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 20, SEQ ID NO: 76, SEQ ID NO: 139, or SEQ ID NO: 280. In some embodiments, the fermenting microbe is selected from a *Bacteroides vulgatus* strain

having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 39, SEQ ID NO: 111, SEQ ID NO: 121, SEQ ID NO: 173, SEQ ID NO: 211, SEQ ID NO: 308, SEQ ID NO: 321, or SEQ ID NO: 326. In some embodiments, the synthesizing microbe is selected from a *Methanobrevibacter smithii* strain having a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 292.

[0176] In some embodiments, the microbial consortium disclosed herein comprises active microbes, fermenting microbes and synthesizing microbes in a colony forming unit (CFU) ratio selected from 1:1:1, 1:2:1, 1:1:2, 2:1:1, 2:1:2, 1:3:1, 1:1:3, 3:1:1, 3:1:3, 2:3:2, 2:2:3, 3:2:2, 3:2:3, 1:5:1, 1:1:5, 5:1:1, 5:1:5, 2:5:2, 2:2:5, 5:2:2, 5:2:5, 3:5:3, 3:3:5, 5:3:3, 5:3:5, 4:5:4, 4:4:5, 5:4:4, and 5:4:5. In some embodiments, an original dosage form of the disclosed microbial consortium comprises active microbes, fermenting microbes and synthesizing microbes in total CFU amounts within about one order of magnitude, about two orders of magnitude, about three orders of magnitude, about four orders of magnitude, about 5 orders of magnitude, about 6 orders of magnitude, about 7 orders of magnitude, about 8 orders of magnitude, about 9 orders of magnitude, or about 10 orders of magnitude of each other. In other embodiments, an original dosage form of the disclosed microbial consortium comprises active microbes, fermenting microbes and synthesizing microbes in CFU amounts within about two orders of magnitude of each other. In some embodiments, an original dosage form of the disclosed microbial consortium comprises active microbes and fermenting microbes in total CFU amounts within one order of magnitude, about two orders of magnitude, about three orders of magnitude, about four orders of magnitude, about 5 orders of magnitude, about 6 orders of magnitude, about 7 orders of magnitude, about 8 orders of magnitude, about 9 orders of magnitude, or about 10 orders of magnitude of each other. In some embodiments, an original dosage form of the disclosed microbial consortium comprises active microbes and synthesizing microbes in total CFU amounts within one order of magnitude, about two orders of magnitude, about three orders of magnitude, about four orders of magnitude, about 5 orders of magnitude, about 6 orders of magnitude, about 7 orders of magnitude, about 8 orders of magnitude, about 9 orders of magnitude, or about 10 orders of magnitude of each other. In some embodiments, an original dosage form of the disclosed microbial consortium comprises fermenting microbes and synthesizing microbes in total CFU amounts within one order of magnitude, about two orders of magnitude, about three orders of magnitude, about four orders of magnitude, about 5 orders of magnitude,

about 6 orders of magnitude, about 7 orders of magnitude, about 8 orders of magnitude, about 9 orders of magnitude, or about 10 orders of magnitude of each other.

Microbial Consortia Design

[0177] In some embodiments, microbial consortia disclosed herein are designed to meet one or more than one of the following criteria:

(i) an ability to eliminate or reduce levels of a first metabolic substrate causing or contributing to a disease in an animal;

(ii) an ability to metabolize or convert one or more than one metabolite produced by the metabolism of the first metabolic substrate;

(iii) an ability to metabolize one or more than one nutrient typically found in the human diet;

(iv) an ability to fulfill unique and potentially beneficial biological functions in the gastrointestinal (GI) tract (e.g., bile salt hydrolase activity or butyrate production);

(v) an ability to engraft in various biological niches and physical and metabolic compartments of the GI tract of an animal;

(vi) an ability to increase biomass upon engraftment in the GI tract;

(vii) an ability to have longitudinal stability in the GI tract of an animal;

(viii) an ability to increase the flux of a precursor of the first metabolic substrate into a biochemical pathway that converts said precursor into a metabolite that is not the first metabolic substrate;

(ix) diversity of component microbial species across one or more than one taxonomic phyla; and

(x) natural prevalence of component microbial species in the GI tract of healthy adults.

[0178] In some embodiments, the microbial consortia of the present invention are designed to comprise a plurality of active microbes capable of metabolizing a first metabolic substrate that causes or contributes to disease in an animal. For example, in some embodiments, the first metabolic substrate may be selected from, but not limited to, oxalate and a bile acid (e.g., lithocholic acid (LCA), deoxycholic acid (DCA)). In some embodiments, the microbial consortium is designed to be capable of metabolizing the first metabolic substrate across a variety of pH ranges found within the GI tract (e.g., pH 4 to 8). In some embodiments, the microbial consortium is designed to be capable of metabolizing

the first metabolic substrate in the presence of various concentrations of first metabolic substrate as they exist in different regions of the GI tract.

[0179] For example, in designing which active microbes to include in a microbial consortium for the treatment of primary or secondary hyperoxaluria, an *in vitro* colorimetric assay (e.g., as described in Example 3 below) can be used to measure the capacity of a candidate microbe to metabolize oxalate in a sample. Microbes capable of reducing the concentration of oxalate present in a sample by at least 20%, by at least 30%, by at least 40%, by at least 50%, by at least 60%, by at least 70%, or by at least 80% can be included in a microbial consortium disclosed herein.

[0180] In other embodiments, an *in vivo* mouse assay can be used to measure the efficacy of a designed microbial consortium of the present invention in reducing the concentration of oxalate present in a sample of blood, serum, bile, stool, or urine when administered to a subject. Concentrations of oxalate in a blood, serum, bile, stool or urine sample can be measured using a liquid chromatography–mass spectrometry (LC-MS) method as described in Example 4, below. Microbial consortia capable of reducing blood, serum, bile, stool, or urine oxalate levels by at least 20%, by at least 30%, by at least 40%, by at least 50%, by at least 60%, by at least 70%, or by at least 80% as compared to levels in untreated controls or pre-administration levels can be candidates for further evaluation for the treatment of primary or secondary hyperoxaluria.

[0181] In some embodiments, a microbial consortium disclosed herein is designed to metabolize one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the plurality of active microbes. In some embodiments, the microbial consortia are designed to maximize consumption and/or production of a defined set of metabolites using a minimal number of strains. For example, in some embodiments, a microbial consortium is designed to include a microbe that metabolizes formate produced by the plurality of active microbes, wherein the presence of formate inhibits the metabolism of oxalate by the plurality of active microbes, e.g., in a negative feedback loop. In some embodiments, a microbial consortium is designed to include microbes that catalyze the fermentation of polysaccharides to one or more than one of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2. In some embodiments, a microbial consortium is designed to catalyze the fermentation of amino acids to one or more than one of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate,

isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2. In some embodiments, the microbial consortium is designed to catalyze the synthesis of one or more than one of the group consisting of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate. In some embodiments, the microbial consortium is designed to catalyze the deconjugation of conjugated bile acids to produce primary bile acids, the conversion of cholic acid (CA) to 7-oxocholic acid, the conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), the conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and/or the conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

[0182] In some embodiments, a microbial consortium disclosed herein is designed to metabolize one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the plurality of active microbes. In some embodiments, the microbial consortia are designed to maximize consumption and/or production of a defined set of metabolites using a minimal number of strains. For example, in some embodiments, a microbial consortium is designed to include a microbe that metabolizes formate produced by the plurality of active microbes, wherein the presence of formate inhibits the metabolism of oxalate by the plurality of active microbes, e.g., in a negative feedback loop. In some embodiments, a microbial consortium is designed to include microbes that catalyze the fermentation of polysaccharides to one or more than one of acetate, propionate, succinate, lactate, butyrate, formate, H_2, and CO_2. In some embodiments, a microbial consortium is designed to catalyze the fermentation of amino acids to one or more than one of acetate, propionate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, H_2, H_2S, and CO_2. In other embodiments, a microbial consortium is designed to include microbes that catalyze the synthesis of one or more than one of methane from formate and H_2; acetate from H_2 and CO_2; acetate from formate and H_2; acetate and sulfide from H_2, CO_2, and sulfate; propionate and CO_2 from succinate; succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate and butyrate, acetate, H_2, and CO_2 from lactate.

[0183] In some embodiments, microbial consortia are designed to include microbes capable of metabolizing one or more nutrient typically found in a broad spectrum of human diets. For example, in some embodiments, microbial consortia are designed include microbes

capable of metabolizing one or more than one of oxalate, fructan, inulin, glucuronoxylan, arabinoxylan, glucomannan, β-mannan, dextran, starch, arabinan, xyloglucan, galacturonan, β-glucan, galactomannan, rhamnogalacturonan I, rhamnogalacturonan II, arabinogalactan, mucin O-linked glycans, yeast α-mannan, yeast β-glucan, chitin, alginate, porphyrin, laminarin, carrageenan, agarose, alternan, levan, xanthan gum, galactooligosaccharides, hyaluronan, chondrointin sulfate, dermatan sulfate, heparin sulfate, keratan sulfate, phenylalanine, tyrosine, tryptophan, leucine, valine, isoleucine, glycine, proline, asparagine, glutamine, aspartate, glutamate, cysteine, lysine, arginine, serine, methionine, alanine, arginine, histidine, ornithine, citrulline, carnitine, hydroxyproline, cholic acid, chenodeoxycholic acid, taurochenodeoxycholic acid, glycochenodeoxycholic acid, cholesterol, cinnamic acid, coumaric acid, sinapinic acid, ferulic acid, caffeic acid, quinic acid, chlorogenic acid, catechin, epicatechin, gallic acid, pyrogallol, catechol, quercetin, myricetin, campherol, luteolin, apigenin, naringenin, and hesperidin. In some embodiments, microbial consortia are designed to enrich for consumption of dietary carbon and energy sources. In other embodiments, microbial consortia are designed to enrich for the production or consumption of host metabolites, including bile acids, sugars, amino acids, vitamins, short-chain fatty acids, and gasses.

[0184] In some embodiments, microbial consortia are designed to include microbes having potentially beneficial biological functions in the GI tract. For example, microbial consortia are designed to include microbial strains having robust and/or redundant bile salt hydrolase (BSH) activity, so that deconjugation of primary bile acids can occur despite differences in host physiology, diet, plurality of active microbes present in the microbial consortium, or the pre-existing composition of the conjugated bile acid pool. In other embodiments, microbial consortia are designed to include microbial strains capable of producing butyrate from the fermentation of dietary fiber in the GI tract, which contributes to intestinal homeostasis, energy metabolism, anti-inflammatory processes, enhancement of intestinal barrier function, and mucosal immunity.

[0185] In some embodiments, microbial consortia described herein are designed to be able to engraft in various biological niches and physical and metabolic compartments of the GI tract of an animal (e.g., a human).

[0186] As used herein, “engraftment” (and grammatical variants thereof, e.g., "engraft") refers to the ability of a microbial strain or microbial community to establish in one or more niches of the gut of an animal. Operationally, a microbial strain or microbial consortium is

"engrafted" if evidence of its establishment, post-administration, can be obtained. In some embodiments, that evidence is obtained by molecular identification (e.g., Matrix-Assisted Laser Desorption/Ionization Time-Of-Flight Mass Spectrometry (MALDI-TOF MS), 16S rRNA sequencing, or genomic sequencing) of a sample obtained from the animal. In some embodiments, the sample is a stool sample. In some embodiments, the sample is a biopsy sample taken from the gut of the animal (e.g., from a location along the gastrointestinal tract of the animal). Engraftment may be transient or may be persistent. In some embodiments, transient engraftment means that the microbial strain or microbial community can no longer be detected in an animal to which it has been administered after the lapse of about 1 week, about 2 weeks, about three weeks, about 1 month, about 2 months, about 3 months, about 4 months, about 6 months, about 8 month, about 10 months, about 1 year, about 1.5 years, or about 2 years.

[0187] For example, microbial consortia are designed to be capable of engrafting into one or more than one niche of the gastrointestinal tract whose composition varies according to a number of environmental factors including, but not limited to, the particular physical compartment of the gastrointestinal tract, the chemical and physicochemical properties of the niche environment (e.g., gastrointestinal motility, pH), the metabolic substrate composition of the niche environment, and other co-inhabiting commensal microbial species. To analyze engraftment of a designed microbial consortium described herein, an *in vivo* assay can be used as described in Example 8, wherein stool samples from treated mice are analyzed for the presence of specific microbial strains comprising the microbial consortium by whole genome shotgun sequencing of microbial DNA extracted from fecal pellets and sequence reads mapped against a comprehensive database of complete, sequenced genomes of all the defined microbial strains comprising the microbial consortium.

[0188] In some embodiments, a microbial consortium described herein is designed to include microbes that support the growth and increase the biomass of one or more than one other microbe in the consortium when engrafted in the GI tract of an animal (e.g., a human). For example, in some embodiments, microbial consortia are designed to promote co-culturability and/or ecological stability of one or more than one microbial strain of the consortium.

[0189] In some embodiments, a microbial consortium described herein is designed to include one or more than one microbe having longitudinal stability in the GI tract of an animal (e.g., a human) despite transient or long-term changes to the gastrointestinal niche due

to modifications in diet, the presence or absence of disease, or other physiological or environmental factors. In some embodiments, longitudinal stability of a community refers to the ability of a microbial consortium to persist (i.e. remain engrafted) in the GI tract of an animal following microbial challenge. In some embodiments, when given sufficient time to permit colonization of microbial challenge strains in the GI tract of an animal engrafted with a microbial consortium, longitudinal stability can be defined as one where at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% of the defined microbial strains are detectable by metagenomic analysis. For example, in some embodiments, metagenomic analysis comprises whole genome shotgun sequencing analysis.

[0190] In other embodiments, longitudinal stability of a community refers to the characteristic of microbial strains comprising a consortium to maintain a metabolic phenotype over a period of time or following microbial challenge. For example, in some embodiments, defined microbial strains comprising a consortium can maintain a metabolic phenotype for at least 1 week, at least 2 weeks, at least 3 weeks, at least 4 weeks, at least 6 weeks, at least 8 weeks, at least 10 weeks, at least 12 weeks, at least 4 months, at least 6 months at least 8 months, at least 10 months, at least 1 year, at least 1.5 years, or at least 2 years.

[0191] In some embodiments, a longitudinal stability can be defined as one where the defined microbial strains comprising a consortium maintain the one or more metabolic phenotype of mucin degradation, polysaccharide fermentation, hydrogen utilization, succinate metabolism, butyrate production, amino acid metabolism, bile acid metabolism, CO_2 fixation, formate metabolism, methanogenesis, acetogenesis, hydrogen production, or propionate production over a period of time or following microbial challenge.

[0192] In some embodiments, a microbial consortium is designed to include one or more than one microbe capable of increasing the flux of a precursor of the first metabolic substrate into a biochemical pathway that converts said precursor into a metabolite that is not the first metabolic substrate. For example, in some embodiments, a microbial consortium can be designed to include microbial strains having robust 7α-HSDH and 7β- HSDH activity, which direct precursors of DCA and LCA first metabolic substrates (CA and CDCA, respectively) down biochemical pathways producing 7betaCA and UDCA.

[0193] In some embodiments, microbial consortia described herein are designed to include representative microbial strains isolated from a healthy donor fecal sample, with the

exception of species known to be associated with pathogenesis, which represent microbial species belonging to a diverse array of taxonomic phyla including, Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia and Euryarchaeota. In some embodiments, microbial consortia having phylogenetic diversity are less sensitive to perturbations in the GI environment and are more stably engrafted For example, in some embodiments, microbial consortia can be designed to include one or more than one microbial species from Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia, or Euryarchaeota.

[0194] In some embodiments, microbial consortia can be designed to include one or more than one microbial species from Bacteroidetes and Firmicutes, Bacteroidetes and Actinobacteria, Bacteroidetes and Proteobacteria, Bacteroidetes and Verrucomicrobia, Bacteroidetes and Euryarchaeota, Firmicutes and Actinobacteria, Firmicutes and Proteobacteria, Firmicutes and Verrucomicrobia, Firmicutes and Euryarchaeota, Actinobacteria and Proteobacteria, Actinobacteria and Verrucomicrobia, Actinobacteria and Euryarchaeota, Proteobacteria and Verrucomicrobia, Proteobacteria and Euryarchaeota, or Verrucomicrobia and Euryarchaeota.

[0195] In some embodiments, microbial consortia can be designed to include one or more than one microbial species from: Bacteroidetes, Firmicutes, and Actinobacteria; Bacteroidetes, Firmicutes, and Proteobacteria; Bacteroidetes, Firmicutes, and Verrucomicrobia; Bacteroidetes, Firmicutes and Euryarchaeota; Bacteroidetes, Actinobacteria, and Proteobacteria; Bacteroidetes, Actinobacteria, and Verrucomicrobia; Bacteroidetes, Actinobacteria, and Euryarchaeota; Bacteroidetes, Proteobacteria, and Verrucomicrobia; Bacteroidetes, Proteobacteria, and Euryarchaeota; Bacteroidetes, Verrucomicrobia, and Euryarchaeota; Firmicutes, Actinobacteria, and Proteobacteria; Firmicuates, Actinobacteria, andVerrucomicrobia; Firmicuates, Actinobacteria, and Euryarchaeota; Firmicuates, Proteobacteria, and Verrucomicrobia; Firmicuates, Proteobacteria, and Euryarchaeota; Firmicutes, Verrucomicrobia, and Euryarchaeota; Actinobacteria, Proteobacteria, and Verrrucomicrobia; Actinobacteria, Proteobacteria, and Euryarchaeota; or Proteobacteria, Verrucomicrobia, and Euryarchaeota.

[0196] In some embodiments, microbial consortia can be designed to include one or more than one microbial species from: Bacteoidetes, Firmicutes, Actinobacteria, and Proteobacteria; Bacteoidetes, Firmicutes, Actinobacteria and Verrucomicrobia; Bacteoidetes, Firmicutes, Actinobacteria, and Euryarchaeota; Bacteroidetes, Actinobacteria, Proteobacteria, and Verrucomicrobia; Bacteroidetes, Actinobacteria, Proteobacteria, and Euryarchaeota;

Bacteroidetes, Proteobacteria, Verrucomicrobia, and Euryarchaeota; Firmicutes, Actinobacteria, Proteobacteria, and Verrucomicrobia; Firmicutes, Actinobacteria, Proteobacteria, and Euryarchaeota; Firmicuates, Proteobacteria, Verrucomicrobia, and Euryarchaeota; or Actinobacteria, Proteobacteria, Verrucomicrobia, and Euryarchaeota.

[0197] In some embodiments, microbial consortia can be designed to include one or more than one microbial species from: Bacteoidetes, Firmicutes, Actinobacteria, Proteobacteria, and Verrucomicrobia; Bacteoidetes, Firmicutes, Actinobacteria, Proteobacteria, and Euryarchaeota; Bacteroidetes, Firmicutes, Actinobacteria, Verrucomicrobia, and Euryarchaeota; Bacteoidetes, Firmicutes, Proteobacteria, Verrucomicrobia, and Eurarchaeota; Bacteoidetes, Actinobacteria, Proteobacteria, Verrucomicrobia, and Eurarchaeota; or Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia, and Eurarchaeota.

[0198] In some embodiments, microbial consortia can be designed to include one or more than one microbial species from: Bacteoidetes, Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia, and Euryarchaeota.

[0199] For example, in some embodiments, a microbial consortium can be designed to include one or more than one Bacteroidetes strain listed in Table 4. In some embodiments, a microbial consortium can be designed to include a Bacteroidetes strain comprising a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the Bacteroidetes microbes listed in Table 4. In some embodiments, a microbial consortium can be designed to include a Bacteroidetes strain comprising a 16S sequence at least 80% identical to any one of the Bacteroidetes microbes listed in Table 4.

[0200] In some embodiments, a microbial consortium can be designed to include one or more than one Firmicutes strain listed in Table 4. In some embodiments, a microbial consortium can be designed to include a Firmicutes strain comprising a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the Firmicutes microbes listed in Table 4. In some embodiments, a microbial consortium can be designed to include a Firmicutes strain comprising a 16S sequence at least 80% identical to any one of the Firmicutes microbes listed in Table 4.

[0201] In some embodiments, a microbial consortium can be designed to include one or more than one Actinobacteria strain listed in Table 4. In some embodiments, a microbial consortium can be designed to include a Actinobacteria strain comprising a 16S sequence at

least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the Actinobacteria microbes listed in Table 4. In some embodiments, a microbial consortium can be designed to include a Actinobacteria strain comprising a 16S sequence at least 80% identical to any one of the Actinobacteria microbes listed in Table 4.

[0202] In some embodiments, a microbial consortium can be designed to include one or more than one Proteobacteria strain listed in Table 4. In some embodiments, a microbial consortium can be designed to include a Proteobacteria strain comprising a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the Proteobacteria microbes listed in Table 4. In some embodiments, a microbial consortium can be designed to include a Proteobacteria strain comprising a 16S sequence at least 80% identical to any one of the Proteobacteria microbes listed in Table 4.

[0203] In some embodiments, a microbial consortium can be designed to include one or more than one Verrucomicrobia strain listed in Table 4. In some embodiments, a microbial consortium can be designed to include a Verrucomicrobia strain comprising a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the Verrucomicrobia microbes listed in Table 4. In some embodiments, a microbial consortium can be designed to include a Verrucomicrobia strain comprising a 16S sequence at least 80% identical to any one of the Verrucomicrobia microbes listed in Table 4.

[0204] In some embodiments, a microbial consortium can be designed to include *Methonobrevibacter smithii*. In some embodiments, a microbial consortium can be designed to include a *Methonobrevibacter smithii* strain comprising a 16S sequence at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 292. In some embodiments, a microbial consortium can be designed to include a *Methonobrevibacter smithii* strain comprising a 16S sequence at least 80% identical to SEQ ID NO: 292.

[0205] In some embodiments, a microbial consortium is designed such that when administered to a subject the plurality of active microbes and the supportive community of microbes have one or more than one synergistic effect. For example, in some embodiments administration of a microbial consortium comprising the plurality of active microbes in combination with the supportive community of microbes results in an enhanced metabolization of a first metabolic substrate than achieved by administration of either the

plurality of active microbes or supportive community of microbes alone. For example, in some embodiments administration of a microbial consortium results in enhanced oxalate metabolism (e.g., as measured by urinary oxalate levels) in a subject as compared to a subject administered with either a plurality of active microbes or a supportive community of microbes alone. In other embodiments, administration of a microbial consortium results in enhanced conversion of primary bile acids (e.g., DCA and/or LCA) in a subject as compared to a subject administered with either a plurality of active microbes or a supportive community of microbes alone. In some embodiments, a microbial composition comprising the plurality of active microbes in combination with the supportive community of microbes results in enhanced GI engraftment than the engraftment achieved by administration of either the plurality of active microbes or supportive community of microbes alone. In some embodiments, a microbial composition comprising the plurality of active microbes in combination with the supportive community of microbes results in greater biomass in the GI tract than the biomass achieved by administration of either the plurality of active microbes or supportive community of microbes alone. In some embodiments, a microbial composition comprising the plurality of active microbes in combination with the supportive community of microbes results in enhanced longitudinal stability than the stability achieved by administration of either the plurality of active microbes or supportive community of microbes alone. In some embodiments, a microbial composition comprising the plurality of active microbes in combination with the supportive community of microbes results in enhanced clinical efficacy in the treatment of a disease than the efficacy achieved by administration of either the plurality of active microbes or supportive community of microbes alone.

[0206] In some embodiments, a microbial consortium is designed to comprise 20 to 300, 20 to 250, 20 to 200, 20 to 190, 20 to 180, 20 to 170, 20 to 160, 20 to 150, 20 to 140, 20 to 130, 20 to 120, 20 to 110, 20 to 100, 20 to 90, 20 to 80, 20 to 70, 20 to 60, 20 to 50, 50 to 300, 50 to 250, 50 to 200, 50 to 190, 50 to 180, 50 to 170, 50 to 160, 50 to 150, 50 to 140, 50 to 130, 50 to 120, 50 to 110, 50 to 100, 50 to 90, 50 to 80, 50 to 70, 50 to 60, 100 to 300, 100 to 250, 100 to 200, 100 to 190, 100 to 180, 100 to 170, 100 to 160, 100 to 150, 100 to 140, 100 to 130, 100 to 120, 100 to 110, 70 to 80, 80 to 90, or 150 to 160 microbial strains, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 4.

[0207] In some embodiments, a microbial consortium is designed to comprise 20 to 160, 30 to 160, 40 to 160, 50 to 160, 60 to 160, 70 to 160, 80 to 160, 90 to 160, 100 to 160,

110 to 160, 120 to 160, 130 to 160, 140 to 160, 150 to 160, 20 to 140, 30 to 140, 40 to 140, 50 to 140, 60 to 140, 70 to 140, 80 to 140, 90 to 140, 100 to 140, 110 to 140, 120 to 140, 130 to 140, 20 to 120, 30 to 120, 40 to 120, 50 to 120, 60 to 120, 70 to 120, 80 to 120, 90 to 120, 100 to 120, 110 to 120, 20 to 100, 30 to 100, 40 to 100, 50 to 100, 60 to 100, 70 to 100, 80 to 100, 90 to 100, 20 to 80, 30 to 80, 40 to 80, 50 to 80, 60 to 80, or 70 to 80 microbial strains, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 22.

[0208] In some embodiments, a microbial consortium is designed to comprise 20 to 104, 40 to 104, 60 to 104, 80 to 104, 100 to 104, 20 to 80, 40 to 80, 60 to 80, 20 to 60, or 40 to 60 microbial strains, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 23.

[0209] In some embodiments, a microbial consortium is designed to comprise 20 to 104, 40 to 104, 60 to 104, 80 to 104, 100 to 104, 20 to 80, 40 to 80, 60 to 80, 20 to 60, or 40 to 60 microbial strains, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 24.

[0210] In some embodiments, a microbial consortium is designed to comprise 20 to 158, 30 to 158, 40 to 158, 50 to 158, 60 to 158, 70 to 158, 80 to 158, 90 to 158, 100 to 158, 110 to 158, 120 to 158, 130 to 158, 140 to 158, 150 to 158, 20 to 140, 30 to 140, 40 to 140, 50 to 140, 60 to 140, 70 to 140, 80 to 140, 90 to 140, 100 to 140, 110 to 140, 120 to 140, 130 to 140, 20 to 120, 30 to 120, 40 to 120, 50 to 120, 60 to 120, 70 to 120, 80 to 120, 90 to 120, 100 to 120, 110 to 120, 20 to 100, 30 to 100, 40 to 100, 50 to 100, 60 to 100, 70 to 100, 80 to 100, 90 to 100, 20 to 80, 30 to 80, 40 to 80, 50 to 80, 60 to 80, or 70 to 80 microbial strains, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 20.

[0211] In some embodiments, a microbial consortium is designed to comprise 20 to 152, 30 to 152, 40 to 152, 50 to 152, 60 to 152, 70 to 152, 80 to 152, 90 to 152, 100 to 152, 110 to 152, 120 to 152, 130 to 152, 140 to 152, 150 to 152, 20 to 140, 30 to 140, 40 to 140, 50 to 140, 60 to 140, 70 to 140, 80 to 140, 90 to 140, 100 to 140, 110 to 140, 120 to 140, 130 to 140, 20 to 120, 30 to 120, 40 to 120, 50 to 120, 60 to 120, 70 to 120, 80 to 120, 90 to 120, 100 to 120, 110 to 120, 20 to 100, 30 to 100, 40 to 100, 50 to 100, 60 to 100, 70 to 100, 80 to

100, 90 to 100, 20 to 80, 30 to 80, 40 to 80, 50 to 80, 60 to 80, or 70 to 80 microbial strains, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 16.

[0212] In some embodiments, a microbial consortium is designed to comprise 20 to 88, 40 to 88, 60 to 88, 80 to 88, 20 to 80, 40 to 80, 60 to 80, 20 to 60, or 40 to 60 microbial strains, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 17.

[0213] In some embodiments a microbial consortium is designed to comprise 20 to 89, 40 to 89, 60 to 89, 80 to 89, 20 to 80, 40 to 80, 60 to 80, 20 to 60, or 40 to 60 microbial strains, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 18.

[0214] In some embodiments, a microbial consortium is designed to comprise 20 to 75, 40 to 75, 60 to 75, 80 to 75, 20 to 60, or 40 to 60 microbial strains, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 19.

[0215] In some embodiments, a microbial consortium is designed to comprise 2 to 51, 5 to 51, 10 to 51, 20 to 51, 30 to 51, or 40 to 51 Actinobacteria; 10 to 102, 20 to 102, 30 to 102, 40 to 102, 50 to 102, 60 to 102, 70 to 102, 80 to 102, 90 to 102, 10 to 50, 20 to 50, 30 to 50, or 40 to 50 Bacteroidetes; 1 or 2 Euryacrchaeota; 20 to 197, 40 to 197, 60 to 197, 80 to 197, 100 to 197, 120 to 197, 140 to 197, 160 to 197, 180 to 197, 20 to 150, 40 to 150, 60 to 150, 80 to 150, 100 to 150, 120 to 150, 140 to 150, 20 to 100, 40 to 100, 60 to 100, or 80 to 100 Firmicutes; 2 to 24, 8 to 24, 12 to 24, 18 to 24, or 20 to 24 Proteobacteria; and 1 Verrucomicrobia, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 4.

[0216] In some embodiments, a microbial consortium is designed to comprise 2 to 20, 5 to 20, 10 to 20, or 15 to 20 Actinobacteria; 2 to 48, 10 to 48, 20 to 48, 30 to 48, 40 to 48 Bacteroidetes; 2 to 76, 10 to 76, 20 to 76, 30 to 76, 40 to 76, 50 to 76, 60 to 76, 70 to 76, 2 to 50, 10 to 50, 20 to 50, 30 to 50, 40 to 50 Firmicutes; 2 to 7 Proteobacteria; and 1 Verrucomicrobia, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at

least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 16.

[0217] In some embodiments, a microbial consortium is designed to comprise 2 to 22, 10 to 22, or 20 to 22 Actinobacteria; 2 to 27, 10 to 27, or 20 to 27 Bacteroidetes; 2 to 29, 10 to 29, or 20 to 29 Firmicutes; 1 to 9 Proteobacteria; and 1 Verrucomicrobia, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 17.

[0218] In some embodiments, a microbial consortium is designed to comprise 2 to 18 or 10 to 18 Actinobacteria; 2 to 27, 10 to 27, or 20 to 27 Bacteroidetes; 2 to 38, 10 to 38, 20 to 38, 30 to 38 Firmicutes; and 2 to 6 Proteobacteria, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 18.

[0219] In some embodiments, a microbial consortium is designed to comprise 2 to 7 Actinobacteria; 2 to 20 or 10 to 20 Bacteroidetes; 2 to 38, 10 to 38, 20 to 38, or 30 to 38 Firmicutes; 2 to 8 Proteobacteria; and 1 Verrucomicrobia, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 19.

[0220] In some embodiments, a microbial consortium is designed to comprise 2 to 20 or 10 to 20 Actinobacteria; 2 to 42, 10 to 42, 20 to 42, 30 to 42, or 40 to 42 Bacteroidetes; 2 to 84, 10 to 84, 20 to 84, 30 to 84, 40 to 84, 50 to 84, 60 to 84, 70 to 84, 80 to 84, 2 to 50, 10 to 50, 20 to 50, 30 to 50, or 40 to 50 Firmicutes; 2 to 11 Proteobacteria; and 1 Verrucomicrobia, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 20.

[0221] In some embodiments, a microbial consortium is designed to comprise 2 to 20 or 10 to 20 Actinobacteria; 2 to 44, 10 to 44, 20 to 44, 30 to 44, or 40 to 44 Bacteroidetes; 1 or 2 Euryarcheota; 2 to 83, 10 to 83, 20 to 83, 30 to 83, 40 to 83, 50 to 83, 60 to 83, 70 to 83, 80 to 83, 2 to 50, 10 to 50, 20 to 50, 30 to 50, or 40 to 50 Firmicutes; 2 to 10 Proteobacteria; and 1 Verrucomicrobia, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 22.

[0222] In some embodiments, a microbial consortium is designed to comprise 2 to 15 or 10 to 15 Actinobacteria; 2 to 25, 10 to 25, or 20 to 25 Bacteroidetes; 2 to 55, 10 to 55, 20 to 55, 30 to 55, 40 to 55, 50 to 55, 2 to 25, 10 to 25, or 20 to 25 Firmicutes; 2 to 8 Proteobacteria; and 1 Verrucomicrobia, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 23.

[0223] In some embodiments, a microbial consortium is designed to comprise 2 to 11 Actinobacteria; 2 to 28, 10 to 28, or 20 to 28 Bacteroidetes; 1 Euryarchaeota; 2 to 56, 10 to 56, 20 to 56, 30 to 56, 40 to 56, 50 to 56, 2 to 25, 10 to 25, or 20 to 25 Firmicutes; 2 to 7 Proteobacteria; and 1 Verrucomicrobia, each comprising a 16S sequence at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to any one of the microbes listed in Table 24.

Isolation and Propagation of Microbial Strains

[0224] Active and supportive microbial strains can be derived from human donor fecal samples, or purchased from the American Type Culture Collection (ATCC; www.atcc.org), the Leibniz institute DSMZ (www.dsmz.de), or BEI Resources (www.beiresources.org). Microbial strains purchased from a depository can be cultured according to depository instructions and microbial strains derived from human donors can be cultured according to the media conditions described in Table 3, below.

[0225] Fecal donors can be selected based on multiple criteria, including a health and medical history questionnaire, physical exam, and blood and stool tests for assessing pathogen-free status. Upon collection of a stool sample from a donor, stool samples can cultured in an anaerobic chamber (5% CO_2, 5% H_2, 90% N_2) and microbial strains isolated by making serial dilution aliquots of the stool samples and plating said aliquots on a variety of microbial cultivation media suitable for growth of anaerobes. Specific enrichment techniques can be performed for species having particular metabolic capabilities, such as consumption or tolerance of oxalate or bile acids. In order to enrich for strains having oxalate metabolism capabilities, aliquots of the serially-diluted stool samples can be plated on agar growth media supplemented with varying concentrations of potassium oxalate (20 mM, 40 mM, 80 mM, 160 mM, or 200 mM). In order to enrich for species capable of metabolizing bile acids, aliquots of serially diluted stool samples can be plated on growth

media supplemented with 2% bile. Archaea can be isolated by diluting fecal samples and plating on culture media containing a mixture of antibiotics that is lethal to both gram-positive and gram-negative bacteria. Microbial strain identification can be performed either by 16S rRNA gene sequencing or proteomic fingerprinting using high-throughput Matrix-Assisted Laser Desorption/Ionization Time-Of-Flight Mass Spectrometry (MALDI-TOF MS).

[0226] In some embodiments, methods of producing a microbial consortium described herein comprise individually culturing each of a plurality of active microbes and supportive microbes prior to combining the microbes to form the consortium. In other embodiments, methods of producing a microbial consortium described herein comprise culturing all of a plurality of active microbes and supportive microbes together. In still other embodiments, methods of producing a microbial consortium comprise individually culturing one or more than one microbial strain and co-culturing two or more microbial strains having compatible culture growth conditions, then combining together the individually-cultured microbial strains and co-cultured defined microbial strains to form a microbial consortium. In other embodiments, methods of producing a microbial consortium comprise individually culturing one or more than one microbial strain and co-culturing two or more microbial strains having compatible culture growth conditions, then combining together the individually-cultured microbial strains and co-cultured defined microbial strains to form a microbial consortium.

Pharmaceutical Compositions

[0227] The present disclosure also provides pharmaceutical compositions that contain an effective amount of a microbial consortium described herein. The composition can be formulated for use in a variety of delivery systems. One or more physiologically acceptable buffer(s) or carrier(s) can also be included in the composition for proper formulation. Suitable formulations for use in the present disclosure are found in Remington's Pharmaceutical Sciences, Mack Publishing Company, Philadelphia, Pa., 17th ed., 1985. For a brief review of methods for drug delivery, *see, e.g.*, Langer (Science 249:1527-1533, 1990).

[0228] In some embodiments, microbial cells of the present invention are harvested by microfiltration and centrifugation. In some embodiments, microfiltration is done with a membrane comprising a nonreactive polymer. For example, in some embodiments, said membrane comprises Polyvinylidene fluoride, Polysulfones, or nitrocellulose. In some

embodiments, a membrane for microfiltration has a pore size of approximately 0.2 to 0.45 μm. In some embodiments, the cells are centrifuged at approximately 1000 to 30000, 5000 to 30000, 10000 to 30000, 15000 to 30000, 20000 to 30000, 25000 to 30000, 1000 to 25000, 5000 to 25000, 10000 to 25000, 15000 to 25000, 20000 to 25000, 1000 to 20000, 5000 to 20000, 10000 to 20000, 15000 to 20000, 1000 to 15000, 5000 to 15000, 10000 to 15000, 1000 to 10000, 5000 to 10000, 1000 to 5000 g force. In some embodiments, the cells are concentrated to approximately $1x10^6$ to $1x10^{12}$, $1x10^7$ to $1x10^{12}$, $1x10^8$ to $1x10^{12}$, $1x10^9$ to $1x10^{12}$, $1x10^{10}$ to $1x10^{12}$, $1x10^{11}$ to $1x10^{12}$, $1x10^6$ to $1x10^{11}$, $1x10^7$ to $1x10^{11}$, $1x10^8$ to $1x10^{11}$, $1x10^9$ to $1x10^{11}$, $1x10^{10}$ to $1x10^{11}$, $1x10^6$ to $1x10^{10}$, $1x10^7$ to $1x10^{10}$, $1x10^8$ to $1x10^{10}$, $1x10^9$ to $1x10^{10}$, $1x10^6$ to $1x10^9$, $1x10^7$ to $1x10^9$, $1x10^8$ to $1x10^9$, $1x10^6$ to $1x10^8$, $1x10^7$ to $1x10^8$ $1x10^6$ to $1x10^7$ CFUs per milliliter.

[0229] In some embodiments, microbial cells of the present invention are frozen. In some embodiments, the microbial cells of the present invention are mixed with one or more cryoprotective agents (CPAs) before freezing. In some embodiments, the ratio of cells to CPA is approximately 25:1, 10:1, 5:1, 4:1, 3:1, 2:1, 1:1, 1:2, 1:3, 1:4, 1:5, 1:10, or 1:25. In some embodiments, a CPA comprises one or more of glycerol, maltodextrin, sucrose, inulin, trehalose, and alginate. In some embodiments, a CPA further comprises one or more antioxidants. In some embodiments, an antioxidant is selected from the list of cysteine, ascorbic acid, and riboflavin.

[0230] In some embodiments, the microbial cells of the present invention are lyophilized. In some embodiments, the lyophilized cells are used to make an orally-administered dose of the invention. In some embodiments, primary drying is conducted below approximately -20 °C. In some embodiments, primary drying is followed by a secondary drying at a higher temperature, *e.g.* greater than 0 °C, greater than 5 °C, or greater than 10 °C.

[0231] In some embodiments a pharmaceutical composition disclosed herein may comprise a microbial consortium of the present invention and one or more than one agent selected from, but not limited to: carbohydrates (*e.g.*, glucose, sucrose, galactose, mannose, ribose, arabinose, xylose, fructose, maltose, cellobiose, lactose, deoxyribose, hexose); lipids (*e.g.* lauric acid (12:0) myristic acid (14:0), palmitic acid (16:0), palmitoleic acid (16: 1), margaric acid (17:0), heptadecenoic acid (17: 1), stearic acid (18:0), oleic acid (18: 1), linoleic acid (18:2), linolenic acid (1 8:3), octadecatetraenoic acid (18:4), arachidic acid (20:0), eicosenoic acid (20: 1), eicosadienoic acid (20:2), eicosatetraenoic acid (20:4),

eicosapentaenoic acid (20:5) (EPA), docosanoic acid (22:0), docosenoic acid (22: 1), docosapentaenoic acid (22:5), docosahexaenoic acid (22:6) (DHA), and tetracosanoic acid (24:0)); minerals (*e.g.*, chloride, sodium, calcium, iron, chromium, copper, iodine, zinc, magnesium, manganese, molybdenum, phosphorus, potassium, and selenium); vitamins (*e.g.*, vitamin C, vitamin A, vitamin E, vitamin B 12, vitamin K, riboflavin, niacin, vitamin D, vitamin B6, folic acid, pyridoxine, thiamine, pantothenic acid, and biotin); buffering agents (*e.g.* sodium citrate, magnesium carbonate, magnesium bicarbonate, calcium carbonate, and calcium bicarbonate); preservatives (*e.g.*, alpha-tocopherol, ascorbate, parabens, chlorobutanol, and phenol); binders (*e.g.*, starches, pregelatinized starches, gelatin, polyvinylpyrolidone, cellulose, methylcellulose, sodium carboxymethylcellulose, ethylcellulose, polyacrylamides, polyvinyloxoazolidone, polyvinylalcohols, C_{12}-C_{18} fatty acid alcohol, polyethylene glycol, polyols, saccharides, oligosaccharides); lubricants (*e.g.* magnesium stearate, calcium stearate, zinc stearate, hydrogenated vegetable oils, sterotex, polyoxyethylene monostearate, talc, polyethyleneglycol, sodium benzoate, sodium lauryl sulfate, magnesium lauryl sulfate, and light mineral oil); dispersants (*e.g.*, starch, alginic acid, polyvinylpyrrolidones, guar gum, kaolin, bentonite, purified wood cellulose, sodium starch glycolate, isoamorphous silicate, and microcrystalline cellulose); disintegrants (*e.g.*, com starch, potato starch, pregelatinized and modified starches thereof, sweeteners, clays, such as bentonite, micro-crystalline cellulose, alginates, sodium starch glycolate, gums such as agar, guar, locust bean, karaya, pecitin, tragacanth, sodium bicarbonate in combination with citric acid, and sodium bicarbonate in combination with tartaric acid); flavoring agents; sweeteners; and coloring agents. In some embodiments, additional nutrients such as oxalate or formate are added to support robust revival of specific strains from the capsule.

[0232] In certain embodiments, a microbial consortium of the present invention is administered orally as a lyophilized powder, capsule, tablet, troche, lozenge, granule, gel or liquid. In some embodiments, a microbial consortium of the present invention is administered as a tablet or pill and can be compressed, multiply compressed, multiply layered, and/or coated. For example, in some embodiments, a lyophilized powder is filled in "0", "00", or "000" size capsules to accommodate various strengths. In some embodiments the tablet or pill comprises an enteric coating.

Therapeutic Applications

[0233] The present invention provides microbial consortia capable of engrafting into one or more than one niche of a gastrointestinal tract where it is capable of metabolizing a first metabolic substrate that causes or contributes to disease in an animal. In some embodiments, the animal is a mouse. In some embodiments, the animal is a germ-free mouse. In some embodiments, the animal is a mouse engrafted with a human microbiome. In some embodiments, the animal is a human.

[0234] In some embodiments of the invention, when administered to an animal, the animal is pre-treated with one or more antibiotics prior to administration of the microbial consortium. In some embodiments, the one or more antibiotics is selected from ampicillin, enrofloxacin, clarithromycin, and metronidazole. In some embodiments, the animal is pre-treated with a polyethylene glycol bowel-preparation procedure.

[0235] In some embodiments, when administered to an animal, the microbial consortium of the present invention significantly reduces the concentration of a first metabolic substrate present in the blood, serum, bile, stool or urine as compared to samples collected pretreatment from the same animal or from corresponding control animal that have not been administered with the microbial consortium. For example, in some embodiments, when administered to an animal on a high oxalate diet, the microbial consortium of the present invention significantly reduces the concentration of oxalate present in a sample of blood, serum, bile, stool or urine as compared to samples collected pretreatment from the same animal or from a corresponding control animal that has not been administered with the microbial consortium. As used herein, a "high oxalate diet" refers to a diet that induces a hyperoxaluria phenotype in an animal. For example, in some embodiments, an animal may be maintained on a high oxalate diet for 7 days to 1 month. In some embodiments, an animal may be maintained on a high oxalate diet for 7 days, 14 days, 21 days, or 1 month. In some embodiments, a high oxalate diet can have a calcium to oxalate molar ratio of less than 2.0. For example, in some embodiments, a high oxalate diet can have a calcium to oxalate molar ratio of about 0.1 to about 0.8. In some embodiments, an animal may be maintained on a grain-based diet that is rich in complex polysaccharides and nutritionally complete and given *ad libitum* drinking water supplemented with about 0.5% to 1% oxalate. In some embodiments, a control animal may be maintained on a diet as shown in Table 1 or an animal may be maintained on a high oxalate diet as shown in Table 2.

TABLE 1

Control Diet	
Casein	200 mg/g
DL-Methionine	3.0 mg/g
Sucrose	302.8 mg/g
Corn Starch	280.0 mg/g
Corn Oil	50.0 mg/g
Inulin	35.0 mg/g
Pectin	35.0 mg/g
Cellulose	25.0 mg/g
Mineral Mix, Ca-P Deficient (79055)	13.37 mg/g
Potassium phosphate, monobasic	11.4 mg/g
Calcium chloride	14.94 mg/g
Sodium chloride	19.48 mg/g
Vitamin Mix, Teklad (40060)	10.0 mg/g
Ethoxyquin, antioxidant	0.01 mg/g

TABLE 2

Oxalate Diet	
Casein	200 mg/g
DL-Methionine	3.0 mg/g
Sucrose	316.2 mg/g
Corn Starch	280.0 mg/g
Corn Oil	50.0 mg/g
Inulin	35.0 mg/g
Pectin	35.0 mg/g

Cellulose	25.0 mg/g
Mineral Mix, Ca-P Deficient (79055)	13.37 mg/g
Potassium phosphate, monobasic	11.4 mg/g
Calcium chloride	1.05 mg/g
Sodium chloride	16.23 mg/g
Vitamin Mix, Teklad (40060)	10.0 mg/g
Ethoxyquin, antioxidant	0.01 mg/g
Sodium oxalate	3.72 mg/g

[0236] In some embodiments, a microbial consortium of the present invention is administered to an animal on a diet supplemented with one or more bile acids. In some embodiments, the diet is supplemented with one or more of TCDCA, GCDCA, TCA, GCA, CA, CDCA, LCA, or DCA. For example, in some embodiments, an animal may be maintained on a diet supplemented with one or more bile acids for 7 days to 1 month. In some embodiments, an animal may be maintained on a diet supplemented with bile acids for 7 days, 14 days, 21 days, or 1 month.

[0237] In some embodiments, a microbial consortium of the present invention is used to treat a subject having or at risk of developing a metabolic disease or condition. For example, in some embodiments, the metabolic disease is primary hyperoxaluria. In some embodiments, the metabolic disease is secondary hyperoxaluria. In some embodiments, the metabolic disease is secondary hyperoxaluria associated with bowel resection surgery or IBD. In some embodiments, a microbial consortium of the present invention significantly reduces the concentration of oxalate present in a sample of blood, serum, bile, stool, or urine when administered to a subject by at least 20%, by at least 30%, by at least 40%, by at least 50%, by at least 60%, by at least 70%, or by at least 80% as compared to untreated subjects or pre-administration concentrations.

[0238] In some embodiments, a microbial consortium of the present invention significantly alters the profile and/or concentration of bile acids present in an animal. For example, in some embodiments, a microbial consortium of the present invention significantly alters the profile and/or concentration of Tβ-MCA, Tα-MCA, TUDCA, THDCA, TCA, 7β-

CA, 7-oxo-CA, TCDCA, Tω-MCA, TDCA, α-MCA, β-MCA, ω-MCA, Muro-CA, d4-CA, CA, TLCA, UDCA, HDCA, CDCA, DCA, and LCA in an animal.

[0239] In some embodiments, a high-complexity defined gut microbial community of the present invention can be used to treat an animal having a cholestatic disease, such as, for example, primary sclerosing cholangitis, primary biliary cholangitis, progressive familial intrahepatic cholestasis, or nonalcoholic steatohepatitis. For example in some embodiments, the animal may be a mammal, and more particularly a human.

[0240] In some embodiments, a microbial consortium of the present invention can be administered via an enteric route. For example, in some embodiments, a microbial consortium is administered orally, rectally (e.g., by enema, suppository, or colonoscope), or by oral or nasal tube.

[0241] In some embodiments, a microbial consortium of the present invention can be administered to a specific location along the gastrointestinal tract. For example, in some embodiments, a microbial consortium can be administered into one or more than one gastrointestinal location including the mouth, esophagus, stomach, small intestine (duodenum, jejunum, ileum), large intestine (cecum, ascending colon, transverse colon, descending colon), or rectum. In some embodiments, a microbial consortium can be administered in all regions of the gastrointestinal tract.

Dosages

[0242] In some embodiments, a microbial consortium of the present invention is administered in a dosage form having a total amount of microbial consortium of at least 1 x 10^6 colony forming units (CFU) or above, at least 2 x 10^6 CFU or above, at least 3 x 10^6 CFU or above, at least 4 x 10^6 CFU or above, at least 5 x 10^6 CFU or above, at least 6 x 10^6 CFU or above, at least 7 x 10^6 CFU or above, at least 8 x 10^6 CFU or above, at least 9 x 10^6 CFU or above, at least 1 x 10^7 CFU or above, at least 2 x 10^7 CFU or above, at least 3 x 10^7 CFU or above, at least 4 x 10^7 CFU or above, at least 5 x 10^7 CFU or above, at least 6 x 10^7 CFU or above, at least 7 x 10^7 CFU or above, at least 8 x 10^7 CFU or above, at least 9 x 10^7 CFU or above, 1 x 10^8 CFU or above, at least 2 x 10^8 CFU or above, at least 3 x 10^8 CFU or above, at least 4 x 10^8 CFU or above, at least 5 x 10^8 CFU or above, at least 6 x 10^8 CFU or above, at least 7 x 10^8 CFU or above, at least 8 x 10^8 CFU or above, at least 9 x 10^8 CFU or above, 1 x 10^9 CFU or above, at least 2 x 10^9 CFU or above, at least 3 x 10^9 CFU or above, at least 4 x 10^9 CFU or above, at least 5 x 10^9 CFU or above, at least 6 x 10^9 CFU or above, at least 7 x

10^9 CFU or above, at least 8 x 10^9 CFU or above, at least 9 x 10^9 CFU or above, 1 x 10^{10} CFU or above, at least 2 x 10^{10} CFU or above, at least 3 x 10^{10} CFU or above, at least 4 x 10^{10} CFU or above, at least 5 x 10^{10} CFU or above, at least 6 x 10^{10} CFU or above, at least 7 x 10^{10} CFU or above, at least 8 x 10^{10} CFU or above, at least 9 x 10^{10} CFU or above, 1 x 10^{11} CFU or above, at least 2 x 10^{11} CFU or above, at least 3 x 10^{11} CFU or above, at least 4 x 10^{11} CFU or above, at least 5 x 10^{11} CFU or above, at least 6 x 10^{11} CFU or above, at least 7 x 10^{11} CFU or above, at least 8 x 10^{11} CFU or above, at least 9 x 10^{11} CFU or above, 1 x 10^{12} CFU or above, at least 2 x 10^{12} CFU or above, at least 3 x 10^{12} CFU or above, at least 4 x 10^{12} CFU or above, at least 5 x 10^{12} CFU or above, at least 6 x 10^{12} CFU or above, at least 7 x 10^{12} CFU or above, at least 8 x 10^{12} CFU or above, or at least 9 x 10^{12} CFU or above.

[0243] In some embodiments, a microbial consortium of the present invention is administered in a dosage form having a total amount of microbial consortium of 0.1 ng to 500 mg, 0.5 ng to 500 mg, 1 ng to 500 mg, 5 ng to 500 mg, 10 ng to 500 mg, 50 ng to 500 mg, 100 ng to 500 mg, 500 ng to 500 mg, 1 μg to 500 mg, 5 μg to 500 mg, 10 μg to 500 mg, 50 μg to 500 mg, 100 μg to 500 mg, 500 μg to 500 mg, 1 mg to 500 mg, 5 mg to 500 mg, 10 mg to 500 mg, 50 mg to 500 mg, 100 mg to 500 mg, 0.1 ng to 100 mg, 0.5 ng to 100 mg, 1 ng to 100 mg, 5 ng to 100 mg, 10 ng to 100 mg, 50 ng to 100 mg, 100 ng to 100 mg, 500 ng to 500 mg, 1 μg to 100 mg, 5 μg to 100 mg, 10 μg to 100 mg, 50 μg to 100 mg, 100 μg to 100 mg, 500 μg to 100 mg, 1 mg to 500 mg, 5 mg to 100 mg, 10 mg to 100 mg, 50 mg to 100 mg, 0.1 ng to 50 mg, 0.5 ng to 50 mg, 1 ng to 50 mg, 5 ng to 50 mg, 10 ng to 50 mg, 50 ng to 50 mg, 100 ng to 50 mg, 500 ng to 500 mg, 1 μg to 50 mg, 5 μg to 50 mg, 10 μg to 50 mg, 50 μg to 50 mg, 100 μg to 50 mg, 500 μg to 50 mg, 1 mg to 500 mg, 5 mg to 50 mg, 10 mg to 50 mg, 0.1 ng to 10 mg, 0.5 ng to 10 mg, 1 ng to 10 mg, 5 ng to 10 mg, 10 ng to 10 mg, 50 ng to 10 mg, 100 ng to 10 mg, 500 ng to 500 mg, 1 μg to 10 mg, 5 μg to 10 mg, 10 μg to 10 mg, 50 μg to 10 mg, 100 μg to 10 mg, 500 μg to 10 mg, 1 mg to 500 mg, 5 mg to 10 mg, 0.1 ng to 5 mg, 0.5 ng to 5 mg, 1 ng to 5 mg, 5 ng to 5 mg, 10 ng to 5 mg, 50 ng to 5 mg, 100 ng to 5 mg, 500 ng to 500 mg, 1 μg to 5 mg, 5 μg to 5 mg, 10 μg to 5 mg, 50 μg to 5 mg, 100 μg to 5 mg, 500 μg to 5 mg, 1 mg to 500 mg, 0.1 ng to 1 mg, 0.5 ng to 1 mg, 1 ng to 1 mg, 5 ng to 1 mg, 10 ng to 1 mg, 50 ng to 1 mg, 100 ng to 1 mg, 500 ng to 500 mg, 1 μg to 1 mg, 5 μg to 1 mg, 10 μg to 1 mg, 50 μg to 1 mg, 100 μg to 1 mg, 500 μg to 1 mg, 0.1 ng to 500 μg, 0.5 ng to 500 μg, 1 ng to 500 μg, 5 ng to 500 μg, 10 ng to 500 μg, 50 ng to 500 μg, 100 ng to 500 μg, 500 ng to 500 μg, 1 μg to 500 μg, 5 μg to 500 μg, 10 μg to 500 μg, 50 μg to 500 μg, 100 μg to 500 μg, 0.1 ng to 100 μg, 0.5 ng to 100 μg, 1 ng to 100 μg, 5 ng to 100 μg, 10 ng to

100 μg, 50 ng to 100 μg, 100 ng to 100 μg, 500 ng to 100 μg, 1 μg to 100 μg, 5 μg to 100 μg, 10 μg to 100 μg, 50 μg to 100 μg, 0.1 ng to 50 μg, 0.5 ng to 50 μg, 1 ng to 50 μg, 5 ng to 50 μg, 10 ng to 50 μg, 50 ng to 50 μg, 100 ng to 50 μg, 500 ng to 50 μg, 1 μg to 50 μg, 5 μg to 50 μg, 10 μg to 50 μg, 0.1 ng to 10 μg, 0.5 ng to 10 μg, 1 ng to 10 μg, 5 ng to 10 μg, 10 ng to 10 μg, 50 ng to 10 μg, 100 ng to 10 μg, 500 ng to 10 μg, 1 μg to 10 μg, 5 μg to 10 μg, 0.1 ng to 5 μg, 0.5 ng to 5 μg, 1 ng to 5 μg, 5 ng to 5 μg, 10 ng to 5 μg, 50 ng to 5 μg, 100 ng to 5 μg, 500 ng to 5 μg, 1 μg to 5 μg, 0.1 ng to 1 μg, 0.5 ng to 1 μg, 1 ng to 1 μg, 5 ng to 1 μg, 10 ng to 1 μg, 50 ng to 1 μg, 100 ng to 1 μg, 500 ng to 1 μg, 0.1 ng to 500 ng, 0.5 ng to 500 ng, 1 ng to 500 ng, 5 ng to 500 ng, 10 ng to 500 ng, 50 ng to 500 ng, 100 ng to 500 ng, 0.1 ng to 100 ng, 0.5 ng to 100 ng, 1 ng to 100 ng, 5 ng to 100 ng, 10 ng to 100 ng, 50 ng to 100 ng, 0.1 ng to 50 ng, 0.5 ng to 50 ng, 1 ng to 50 ng, 5 ng to 50 ng, 10 ng to 50 ng, 0.1 ng to 10 ng, 0.5 ng to 10 ng, 1 ng to 10 ng, 5 ng to 10 ng, 0.1 ng to 5 ng, 0.5 ng to 5 ng, 1 ng to 5 ng, 0.1 ng to 1 ng, 0.1 ng to 1 ng, or 0.1 ng to 0.5 ng total dry weight.

[0244] In other embodiments, a microbial consortium of the present invention is consumed at a rate of 0.1 ng to 500 mg a day, 0.5 ng to 500 mg a day, 1 ng to 500 mg a day, 5 ng to 500 mg a day, 10 ng to 500 mg a day, 50 ng to 500 mg a day, 100 ng to 500 mg a day, 500 ng to 500 mg a day, 1 μg to 500 mg a day, 5 μg to 500 mg a day, 10 μg to 500 mg a day, 50 μg to 500 mg a day, 100 μg to 500 mg a day, 500 μg to 500 mg a day, 1 mg to 500 mg a day, 5 mg to 500 mg a day, 10 mg to 500 mg a day, 50 mg to 500 mg a day, 100 mg to 500 mg a day, 0.1 ng to 100 mg a day, 0.5 ng to 100 mg a day, 1 ng to 100 mg a day, 5 ng to 100 mg a day, 10 ng to 100 mg a day, 50 ng to 100 mg a day, 100 ng to 100 mg a day, 500 ng to 500 mg a day, 1 μg to 100 mg a day, 5 μg to 100 mg a day, 10 μg to 100 mg a day, 50 μg to 100 mg a day, 100 μg to 100 mg a day, 500 μg to 100 mg a day, 1 mg to 500 mg a day, 5 mg to 100 mg a day, 10 mg to 100 mg a day, 50 mg to 100 mg a day, 0.1 ng to 50 mg a day, 0.5 ng to 50 mg a day, 1 ng to 50 mg a day, 5 ng to 50 mg a day, 10 ng to 50 mg a day, 50 ng to 50 mg a day, 100 ng to 50 mg a day, 500 ng to 500 mg a day, 1 μg to 50 mg a day, 5 μg to 50 mg a day, 10 μg to 50 mg a day, 50 μg to 50 mg a day, 100 μg to 50 mg a day, 500 μg to 50 mg a day, 1 mg to 500 mg a day, 5 mg to 50 mg a day, 10 mg to 50 mg a day, 0.1 ng to 10 mg a day, 0.5 ng to 10 mg a day, 1 ng to 10 mg a day, 5 ng to 10 mg a day, 10 ng to 10 mg a day, 50 ng to 10 mg a day, 100 ng to 10 mg a day, 500 ng to 500 mg a day, 1 μg to 10 mg a day, 5 μg to 10 mg a day, 10 μg to 10 mg a day, 50 μg to 10 mg a day, 100 μg to 10 mg a day, 500 μg to 10 mg a day, 1 mg to 500 mg a day, 5 mg to 10 mg a day, 0.1 ng to 5 mg a day, 0.5 ng to 5 mg a day, 1 ng to 5 mg a day, 5 ng to 5 mg a day, 10 ng to 5 mg a day, 50 ng

to 5 mg a day, 100 ng to 5 mg a day, 500 ng to 500 mg a day, 1 μg to 5 mg a day, 5 μg to 5 mg a day, 10 μg to 5 mg a day, 50 μg to 5 mg a day, 100 μg to 5 mg a day, 500 μg to 5 mg a day, 1 mg to 500 mg a day, 0.1 ng to 1 mg a day, 0.5 ng to 1 mg a day, 1 ng to 1 mg a day, 5 ng to 1 mg a day, 10 ng to 1 mg a day, 50 ng to 1 mg a day, 100 ng to 1 mg a day, 500 ng to 500 mg a day, 1 μg to 1 mg a day, 5 μg to 1 mg a day, 10 μg to 1 mg a day, 50 μg to 1 mg a day, 100 μg to 1 mg a day, 500 μg to 1 mg a day, 0.1 ng to 500 μg a day, 0.5 ng to 500 μg a day, 1 ng to 500 μg a day, 5 ng to 500 μg a day, 10 ng to 500 μg a day, 50 ng to 500 μg a day, 100 ng to 500 μg a day, 500 ng to 500 μg a day, 1 μg to 500 μg a day, 5 μg to 500 μg a day, 10 μg to 500 μg a day, 50 μg to 500 μg a day, 100 μg to 500 μg a day, 0.1 ng to 100 μg a day, 0.5 ng to 100 μg a day, 1 ng to 100 μg a day, 5 ng to 100 μg a day, 10 ng to 100 μg a day, 50 ng to 100 μg a day, 100 ng to 100 μg a day, 500 ng to 100 μg a day, 1 μg to 100 μg a day, 5 μg to 100 μg a day, 10 μg to 100 μg a day, 50 μg to 100 μg a day, 0.1 ng to 50 μg a day, 0.5 ng to 50 μg a day, 1 ng to 50 μg a day, 5 ng to 50 μg a day, 10 ng to 50 μg a day, 50 ng to 50 μg a day, 100 ng to 50 μg a day, 500 ng to 50 μg a day, 1 μg to 50 μg a day, 5 μg to 50 μg a day, 10 μg to 50 μg a day, 0.1 ng to 10 μg a day, 0.5 ng to 10 μg a day, 1 ng to 10 μg a day, 5 ng to 10 μg a day, 10 ng to 10 μg a day, 50 ng to 10 μg a day, 100 ng to 10 μg a day, 500 ng to 10 μg a day, 1 μg to 10 μg a day, 5 μg to 10 μg a day, 0.1 ng to 5 μg a day, 0.5 ng to 5 μg a day, 1 ng to 5 μg a day, 5 ng to 5 μg a day, 10 ng to 5 μg a day, 50 ng to 5 μg a day, 100 ng to 5 μg a day, 500 ng to 5 μg a day, 1 μg to 5 μg a day, 0.1 ng to 1 μg a day, 0.5 ng to 1 μg a day, 1 ng to 1 μg a day, 5 ng to 1 μg a day, 10 ng to 1 μg a day, 50 ng to 1 μg a day, 100 ng to 1 μg a day, 500 ng to 1 μg a day, 0.1 ng to 500 ng a day, 0.5 ng to 500 ng a day, 1 ng to 500 ng a day, 5 ng to 500 ng a day, 10 ng to 500 ng a day, 50 ng to 500 ng a day, 100 ng to 500 ng a day, 0.1 ng to 100 ng a day, 0.5 ng to 100 ng a day, 1 ng to 100 ng a day, 5 ng to 100 ng a day, 10 ng to 100 ng a day, 50 ng to 100 ng a day, 0.1 ng to 50 ng a day, 0.5 ng to 50 ng a day, 1 ng to 50 ng a day, 5 ng to 50 ng a day, 10 ng to 50 ng a day, 50 ng to 50 ng a day, 0.1 ng to 10 ng a day, 0.5 ng to 10 ng a day, 1 ng to 10 ng a day, 5 ng to 10 ng a day, 0.1 ng to 5 ng a day, 0.5 ng to 5 ng a day, 1 ng to 5 ng a day, 0.1 ng to 1 ng a day, 0.1 ng to 1 ng a day, or 0.1 ng to 0.5 ng a day.

[0245] In some embodiments, the microbial composition of the present invention is administered for a period of at least 1 day to 1 week, 1 week to 1 month, 1 month to 3 months, 3 months to 6 months, 6 months to 1 year, or more than 1 year. For example, in some embodiments, the microbial composition of the present invention is administered for a period of at least 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, or 1 year.

[0246] In some embodiments, a microbial consortium of the present invention is administered as a single dose or as multiple doses. For example, in some embodiments, a microbial consortium of the present invention is administered once a day for 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 2 weeks 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, or 1 year. In some embodiments, a microbial consortium of the present invention is administered multiple times daily. For example, in some embodiments, a microbial consortium of the present invention is administered twice daily, three times daily, 4 times daily, or 5 times daily. In some embodiments, a microbial consortium of the present invention is administered intermittently. For example, in some embodiments, a microbial consortium of the present invention is administered once weekly, once monthly, or when a subject is in need thereof.

Combination Therapy

[0247] In some embodiments, a microbial consortium of the present invention can be administered in combination with other agents. For example, in some embodiments, a microbial consortium of the present invention can be administered with an antimicrobial agent, an antifungal agent, an antiviral agent, an antiparasitic agent or a prebiotic. In some embodiments, a microbial consortium of the present invention can be administered subsequent to administration of an antimicrobial agent, an antifungal agent, an antiviral agent, an antiparasitic agent or a prebiotic. In some embodiments, administration may be sequential over a period of hours or days, or simultaneously.

[0248] For example, in some embodiments, a microbial consortium can be administered with, or pre-administered with, one or more than one antibacterial agent selected from fluoroquinolone antibiotics (ciprofloxacin, Levaquin, floxin, tequin, avelox, and norflox); cephalosporin antibiotics (cephalexin, cefuroxime, cefadroxil, cefazolin, cephalothin, cefaclor, cefamandole, cefoxitin, cefprozil, and ceftobiprole);penicillin antibiotics (amoxicillin, ampicillin, penicillin V, dicloxacillin, carbenicillin, vancomycin, and methicillin); tetracycline antibiotics (tetracycline, minocycline, oxytetracycline, and doxycycline); and carbapenem antibiotics (ertapenem, doripenem, imipenem/cilastatin, and meropenem).

[0249] For example, in some embodiments, a microbial consortium can be administered with one or more than one antiviral agent selected from Abacavir, Acyclovir, Adefovir, Amprenavir, Atazanavir, Cidofovir, Darunavir, Delavirdine, Didanosine, Docosanol,

Efavirenz, Elvitegravir, Emtricitabine, Enfuvi1tide, Etravirine, Famciclovir, Foscamet, Fomivirsen, Ganciclovir, Indinavir, Idoxuridine, Lamivudine, Lopinavir Maraviroc, MK-2048, Nelfinavir, Nevirapine, Penciclovir, Raltegravir, Rilpivirine, Ritonavir, Saquinavir, Stavudine, Tenofovir Trifluridine, Valaciclovir, Valganciclovir, Vidarabine, Ibacitabine, Amantadine, Oseltamivir, Rimantidine, Tipranavir, Zalcitabine, Zanamivir, and Zidovudine.

[0250] In some embodiments, a microbial consortium can be administered with one or more than one antifungal agent selected from miconazole, ketoconazole, clotrimazole, econazole, omoconazole, bifonazole, butoconazole, fenticonazole, isoconazole, oxiconazole, sertaconazole, sulconazole, and tioconazole; triazole antifungals such as fluconazole, itraconazole, isavuconazole, ravuconazole, posaconazole, voriconazok, terconazole, and albaconazole; thiazole antifungals such as abafungin; allylamine antifungals such as terbinafine, naftifine, and butenafine; and echinocandin antifungals such as anidulafungin, caspofungin, and micafungin; polygodial; benzoic acid; ciclopirox; tolnaftate; undecylenic acid; flucytosine or 5-fluorocytosine; griseofulvin; and haloprogin.

[0251] In some embodiments, a microbial consortium can be administered with one or more than one anti-inflammatory and/or immunosuppressive agent selected from cyclophosphamide, mycophenolate mofetil, corticosteroids, mesalazine, mesalamine, sulfasalazine, sulfasalazine derivatives, cyclosporin A, mercaptopurine, azathiopurine, prednisone, methotrexate, antihistamines, glucocorticoids, epinephrine, theophylline, cromolyn sodium, anti-leukotrienes, anticholinergics, monoclonal anti-IgE, immunomodulatory peptides, immunomodulatory small molecules, immunomodulatory cytokines, immunomodulatory antibodies, and vaccines.

[0252] In some embodiments, a microbial consortium of the present invention can be administered with one or more than one prebiotic selected from, but not limited to, amino acids, biotin, fructooligosaccharides, galactooligosaccharides, inulin, lactulose, mannan oligosaccharides, oligofructose-enriched inulin, oligofructose, oligodextrose, tagatose, trans-galactooligosaccharide, and xylooligosaccharides.

EXAMPLES

[0253] The disclosure now being generally described, will be more readily understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present disclosure, and are not intended to limit the scope of the disclosure in any way.

Example 1: Sourcing and identification of active and supportive microbial strains

[0254] Active and supportive microbial strains were derived from human donor fecal samples, or were purchased from one of three depositories: the American Type Culture Collection (ATCC; www.atcc.org), the Leibniz institute DSMZ (www.dsmz.de), or BEI Resources (www.beiresources.org).

[0255] Microbial strains purchased from a depository were cultured according to depository instructions.

Isolation of donor-derived active and supportive microbial strains

[0256] Fecal donors were selected based on multiple criteria, including a health and medical history questionnaire, physical exam, and blood and stool tests for assessing pathogen-free status. Stool samples from donors who did not meet the inclusion criteria based on any of the above-mentioned assessment were discarded from quarantine.

[0257] Donors provided a stool sample sealed in a plastic container. Upon collection, stool samples were immediately transferred to an anaerobic chamber (5% CO_2, 5% H_2, 90% N_2) within 15 minutes of collection.

[0258] Once transferred to the anaerobic chamber, the fresh stool sample was labeled, weighed, evaluated for anomalies (presence of urine, toilet paper, etc.), and scored according to the Bristol scale. A stool sample weighing less than 45 g, or that failed to conform to a Bristol Stool Scale type 2, 3, 4 or 5, was rejected. Stool samples that met the acceptance criteria were processed and aliquoted. 45 g of the stool sample was transferred into a sterile container for specific pathogen testing. The remainder of the sample was mixed with cryopresertative, homogenized, and aliquoted into cryovials (approximately 2 g of sample per vial; 6 vials per stool sample). These vials were transferred from the anaerobic chamber to a -80 °C freezer for storage until shipping on dry ice.

[0259] Microbial strain isolation was performed by making serial dilution aliquots of the stool samples and plating said aliquots on a variety of microbial cultivation media suitable for growth of anaerobes. All cultures were grown under anaerobic conditions for the duration of culturing. Approximately 20 different media/culture conditions were used to isolate a variety of gut microbial species. Specific enrichment techniques were performed for species having particular metabolic capabilities, such as consumption or tolerance of oxalate or bile acids. In order to enrich for strains having oxalate metabolism capabilities, aliquots of the serially-diluted stool samples were plated on agar growth media supplemented with varying concentrations of potassium oxalate (20 mM, 40 mM, 80 mM, 160 mM, or 200 mM).

In order to enrich for species capable of metabolizing bile acids, aliquots of serially diluted stool samples were plated on growth media supplemented with 2% bile. In order to isolate archaea, diluted fecal samples were plated on culture media containing a mixture of antibiotics that is lethal to both gram-positive and gram-negative bacteria. This archaeal isolation plate was co-incubated in a small enclosed container together with a separate plate containing a heterogenous population of microbes derived from a fecal sample; the heterogenous population contained hydrogen-producing microbes, thereby providing hydrogen (through diffusion within the small container) to allow archaea on the archaeal isolation plate to grow.

[0260] Single colonies from isolation or enrichment plates were picked for further isolation on appropriate microbial cultivation agar media plates (passage 2). After incubation at 37 °C, if the single colony plating resulted in uniformly isolated colony morphology, the culture was further investigated for strain identification. Preliminary strain identification was performed either by 16S rRNA gene sequencing or by creating and analyzing proteomic fingerprinting using high-throughput Matrix-Assisted Laser Desorption/Ionization Time-Of-Flight Mass Spectrometry (MALDI-TOF MS). If the single-colony plating resulted in multiple colony morphologies, each unique colony type was picked for further isolation on an appropriate cultivation agar plate until uniform colony morphology was achieved (passage 3 or more). Monoculture identity was confirmed by 16S rRNA gene sequencing.

[0261] Isolated colonies of strains purified to monocultures for species of interest, as well as novel strains of unknown species, were inoculated into culture tubes containing appropriate broth media and incubated under anaerobic conditions at 37 °C. For most strains, sufficient growth was visualized during this first broth passaging as indicated by turbidity. However, some strains required more than one broth passaging to achieve sufficient growth. Sterile glycerol solution was added to the microbial culture to achieve a final glycerol concentration of 25% prior to mixing and aliquoting into cryovials. The cryovials were removed from the anaerobic gas chambers and were promptly transferred to -80°C.

[0262] After at least 10 hours of freezing, one vial of each purified frozen strain isolate was retrieved from the freezer and thawed under anaerobic conditions followed by plating on agar plates containing appropriate growth media. The plates were incubated under anaerobic conditions at 37 °C. Growth on the plate was observed to confirm revival and uniform morphology for each purified isolate. Individual colonies of the isolates were subsequently analyzed by 16S rRNA gene sequencing to confirm the identity and colony purity of each

frozen strain against the National Center for Biotechnology Information (NCBI) 16S rRNA gene databases.

[0263] A list of donor-derived isolates and a summary of their corresponding isolation media and growth/banking media is reported in Table 3. Additional identifying information for the isolates is reported in Table 4.

[0264] *in vitro* activity-based assays, bioinformatic screens to identify strains with the genetic capability to metabolize oxalate, and identification of target species with known oxalate metabolizing activity based on scientific literature, were utilized to identify candidate active strains. Active oxalate-metabolizing strains obtained from depositories ("commercial strains") include those listed in Table 5. Supportive commercial strains include those listed in Table 6. Strains in Table 5 and Table 6 are identified by their genus/species and by the depository catalog number. "ATCC" strains were obtained from ATCC, "DSM" strains were obtained from the Liebniz Institute DSMZ, and "HM" strains were obtained from BEI Resources.

MALDI-TOF MS

[0265] MALDI-TOF mass spectrometry was used for preliminary identification of bacterial strains (genus and/or species) using a BD Bruker MALDI Biotyper. Briefly, an α-cyano-4-hydroxycinnamic acid (HCCA) matrix was prepared in Bruker standard solvent (acetonitrile 50%, water 47.5% and trifluoroacetic acid 2.5%). A disposable MALDI Biotyper Biotarget plate was loaded with a smear of the sample bacterial colony, overlaid with HCCA matrix and allowed to dry. For strains that required extended extraction, 70% formic acid was added to the sample smear prior to adding HCCA matrix. Bruker Bacterial Testing Standards (BTS) were also loaded onto the Biotarget for quality control analysis. The Biotarget as then loaded into a Biotyper MALDI-TOF machine, and the sample was analyzed. The machine was configured to perform the quality control analysis of the BTS quality control samples first and aborted the run if the BTS quality control analysis failed. The generated spectrum of the test sample was then compared to a database of the reference proteomics spectra containing strains belonging to species which were previously characterized by their proteomic fingerprinting.

DNA Extraction

[0266] DNA was extracted from fecal samples using a Qiagen DNeasy Power Soil Kit (Qiagen, Germantown, MD) in accordance with the manufacturer's instructions. Alternative methods for extracting DNA from fecal samples are well-known and routinely practiced in

the art (*e.g.*, described by Sambrook and Russell, *Molecular Cloning: A Laboratory Manual*, 3d ed., 2001).

Whole Genome Shotgun Sequencing

[0267] Sequencing of DNA samples was carried out using the TruSeq Nano DNA Library Preparation kit (Illumina, San Diego, CA, US) and a NextSeq platform (Illumina, San Diego, CA, US). In brief, sequencing libraries were prepared from DNA extracted from each sample. DNA was mechanically fragmented using an ultrasonicator. The fragmented DNA was subjected to end repair and size selection of fragments, adenylation of 3' ends, linked with adaptors, and DNA fragments enriched according to the TruSeq Nano DNA Library Preparation kit manual (Illumina, San Diego, CA, US). Samples were sequenced to generate more than 50 million paired-end reads of 150. 250, or 300 bp length.

16S rRNA Gene Sequencing and Species Identification

[0268] Microbial species identification was performed by full-length Sanger sequencing of the 16S rRNA gene using the 27F and 1492 primers (PMID 18296538). Species were identified by performing a bidirectional best-BLAST search against a database of curated 16S rRNA gene sequences of type species. To refine species identities, 16S rRNA gene sequences were inserted into a phylogenetic tree of curated 16S rRNA gene sequences of type species. If the sequence formed a monophyletic cluster with a known species, the strain was assigned to that species. Otherwise, the strain was assigned to a novel species. Optionally, isolates were additionally characterized by whole-genome sequencing. Genome assemblies were inserted into a phylogenetic tree of curated genomes of type species. If the sequence formed a monophyletic cluster with a known species, the strain was assigned to that species. Otherwise, the strain was assigned to a novel species.

TABLE 3: Summary of Isolation/Growth Media for Donor-Derived Isolates

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00001	Clostridium citroniae	Bifidobacterium Selective agar (Anaerobe Systems, AS-6423)	40 mM Potassium oxalate	40 mM	NO	YCFAC + 40 mM oxalate
FBI00002	Bacteroides salyersiae	Bifidobacterium Selective agar (Anaerobe Systems, AS-6423)	40 mM Potassium oxalate	40 mM	NO	YCFAC + 40 mM oxalate
FBI00003	Enterococcus faecalis	Bifidobacterium Selective agar (Anaerobe Systems, AS-6423)	40 mM Potassium oxalate	40 mM	NO	YCFAC + 40 mM oxalate
FBI00004	Neglecta timonensis	YCFAC-B (Anaerobe Systems, AS-677)	80 mM Potassium oxalate	80 mM	NO	YCFAC + 80 mM oxalate
FBI00005	Enterococcus casseliflavus	YCFAC-B (Anaerobe Systems, AS-677)	80 mM Potassium oxalate	80 mM	NO	YCFAC + 80 mM oxalate
FBI00006	Enterobacter himalayensis	YCFAC-B (Anaerobe Systems, AS-677)	80 mM Potassium oxalate	80 mM	NO	YCFAC + 80 mM oxalate
FBI00007	Enterococcus casseliflavus	YCFAC-B (Anaerobe Systems, AS-677)	80 mM Potassium oxalate	80 mM	NO	YCFAC + 80 mM oxalate

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00008	Blautia luti	YCFAC-B (Anaerobe Systems, AS-677)	20 mM Potassium oxalate	20 mM	NO	YCFAC + 20 mM oxalate
FBI00009	Bifidobacterium adolescentis	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00010	Blautia obeum	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00011	Bifidobacterium longum	Bifidobacterium Selective agar (Anaerobe Systems, AS-6423)		NO	NO	YCFAC
FBI00012	Alistipes onderdonkii	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC
FBI00013	Parabacteroides merdae	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00014	Blautia luti	YCFAC-B (Anaerobe Systems, AS-677)	20 mM Potassium oxalate	20 mM	NO	YCFAC + 20 mM oxalate
FBI00015	Bacteroides uniformis	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00016	Bifidobacterium pseudocatenulatum	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00017	Blautia obeum	YCFAC-B (Anaerobe Systems, AS-677)	20 mM Potassium oxalate	20 mM	NO	YCFAC + 20 mM oxalate
FBI00018	Eubacterium rectale	Bifidobacterium Selective agar (Anaerobe Systems, AS-6423)		NO	NO	YCFAC
FBI00019	Alistipes timonensis	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC
FBI00020	Bacteroides thetaiotaomicron	Bifidobacterium Selective agar (Anaerobe Systems, AS-6423)	40 mM Potassium oxalate	40 mM	NO	YCFAC + 40 mM oxalate
FBI00021	Bacteroides kribbi / Bacteroides koreensis species cluster	YCFAC-B (Anaerobe Systems, AS-677)	80 mM Potassium oxalate	80 mM	NO	YCFAC + 80 mM oxalate
FBI00022	Alistipes putredinis	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC
FBI00023	Enterococcus casseliflavus	Strain Isolation Media 1 (SL1)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00024	Bacteroides kribbi / Bacteroides koreensis species cluster	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00025	Coprococcus comes	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00026	Enterobacter hormaechei	YCFAC-BO 200 mM (Anaerobe Systems, AS-7529)		200 mM	NO	YCFAC + 80 mM oxalate
FBI00027	Fusicatenibacter saccharivorans	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00028	Oscillibacter sp. FBI00028	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00029	Parabacteroides distasonis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00030	Eggerthella lenta	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00031	Enterobacter hormaechei	YCFAC-BO 200 mM (Anaerobe Systems, AS-7529)		200 mM	NO	YCFAC + 80 mM oxalate
FBI00032	Anaerostipes hadrus	Bifidobacterium Selective agar (Anaerobe Systems, AS-6423)		NO	NO	YCFAC
FBI00033	Lachnospiraceae sp. FBI00033	YCFAC-B (Anaerobe Systems, AS-677)	20 mM Potassium oxalate	20 mM	NO	YCFAC + 20 mM oxalate
FBI00034	Eubacterium eligens	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00035	Enterococcus casseliflavus	YCFAC-BO 200 mM (Anaerobe Systems, AS-7529)		200 mM	NO	YCFAC + 80 mM oxalate
FBI00036	Blautia faecis	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00037	Enterococcus casseliflavus	YCFAC-BO 200 mM (Anaerobe Systems, AS-7529)		200 mM	NO	YCFAC + 80 mM oxalate
FBI00038	Coprococcus eutactus	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00039	Bacteroides vulgatus	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00040	Bilophila wadsworthia	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC
FBI00041	Phascolarctobacterium faecium	YCFAC-B (Anaerobe Systems, AS-677)	80 mM Potassium oxalate	80 mM	NO	YCFAC + 80 mM oxalate
FBI00042	Bacteroides xylanisolvens	Strain Isolation Media 1 (SL1)		NO	NO	YCFAC
FBI00043	Bifidobacterium dentium	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00044	Blautia wexlerae	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00045	Bifidobacterium adolescentis	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00046	Bacteroides caccae	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00047	Eubacterium eligens	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00048	Fusicatenibacter saccharivorans	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00049	Dialister succinatiphilus	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00050	Bacteroides nordii	Bifidobacterium Selective agar (Anaerobe Systems, AS-6423)	40 mM Potassium oxalate	40 mM	NO	YCFAC + 40 mM oxalate
FBI00051	Dorea formicigenerans	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00052	Bacteroides xylanisolvens	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC + 40 mM oxalate
FBI00053	Lactobacillus rogosae	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC + 40 mM oxalate
FBI00054	Escherichia flexneri	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC + 80 mM oxalate
FBI00055	Bacteroides kribbi / Bacteroides koreensis species cluster	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC + 80 mM oxalate
FBI00056	Clostridium citroniae	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC + 80 mM oxalate

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00057	Dorea longicatena	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00058	Eubacterium rectale	Lactobacillus MRS (Anaerobe Systems, AS-6429)	40 mM Potassium oxalate	40 mM	NO	YCFAC
FBI00059	Bacteroides stercorirosoris	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00060	Bifidobacterium longum	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00061	Alistipes shahii	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC
FBI00062	Collinsella aerofaciens	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00063	Lachnospira sp. FBI00063 FBI00285 FBI00364	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00064	Dorea sp. FBI00064	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00065	Sutterellaceae sp. FBI00065	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00066	Parasutterella excrementihominis	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC
FBI00067	Oxalobacter formigenes	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC + 100 mM oxalate
FBI00068	Akkermansia muciniphila	Strain Isolation Media 1 (SL1)		NO	NO	YCFAC
FBI00069	Ruminococcus bromii	Bifidobacterium Selective agar (Anaerobe Systems, AS-6423)	40 mM Potassium oxalate	40 mM	NO	YCFAC
FBI00070	Bacteroides kribbi / Bacteroides koreensis species cluster	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC + 40 mM oxalate
FBI00071	Lachnospiraceae sp. FBI00071	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00072	Coprococcus eutactus	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00073	Parabacteroides distasonis	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00074	Clostridium fessum	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00075	Paraprevotella clara	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00076	Bacteroides thetaiotaomicron	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00077	Sutterella wadsworthensis	Lactobacillus MRS (Anaerobe Systems, AS-6429)	20 mM Potassium oxalate	20 mM	NO	YCFAC
FBI00078	Blautia obeum	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00079	Clostridium clostridioforme	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00080	Sutterella massiliensis	Lactobacillus MRS (Anaerobe Systems, AS-6429)	40 mM Potassium oxalate	40 mM	NO	YCFAC
FBI00081	Porphyromonas asaccharolytica	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00082	Ruminococcaceae sp. FBI00082 FBI00097	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00083	Alistipes shahii	Columbia agar, 5% sheep blood (BD, 221165)	Antibiotics	NO	NO	YCFAC
FBI00084	Bifidobacterium longum	Bifidobacterium Selective agar (Anaerobe Systems, AS-6423)		NO	NO	YCFAC
FBI00085	Ruminococcus bromii	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00086	Ruminococcus bromii	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00087	Clostridium scindens	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00088	Lactobacillus rogosae	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00089	Bifidobacterium longum	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00090	Eubacterium eligens	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00091	Eubacterium rectale	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00092	Monoglobus pectinilyticus	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00093	Roseburia hominis	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00094	Enterococcus faecium	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00095	Ruminococcus bromii	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00096	Eggerthella lenta	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00097	Ruminococcaceae sp. FBI00082 FBI00097	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00098	Bacteroides dorei	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00099	Gordonibacter pamelaeae	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00100	Lachnospira sp. FBI00063 FBI00285 FBI00364	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00101	Faecalibacterium prausnitzii	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00102	Clostridium fessum	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00103	Bacteroides massiliensis	Bifidobacterium Selective agar (Anaerobe Systems, AS-6423)		NO	NO	YCFAC
FBI00104	Blautia wexlerae	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00105	Ruminococcaceae sp. FBI00105 FBI00160	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00106	Enterococcus durans	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00107	Enterococcus durans	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00108	Ruminococcaceae sp. FBI00108	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00109	Coprococcus comes	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00110	Lachnoclostridium pacaense	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00111	Bacteroides vulgatus	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00112	Bacteroides uniformis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00113	Parabacteroides merdae	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00114	Dorea formicigenerans	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00115	Dorea formicigenerans	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00116	Ruminococcus faecis	Bifidobacterium Selective agar (Anaerobe Systems, AS-6423)	40 mM Potassium oxalate	40 mM	NO	YCFAC
FBI00117	Blautia faecis	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00118	Blautia faecis	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00119	Blautia obeum	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00120	Hungatella effluvii	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00121	Bacteroides vulgatus	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00122	Bacteroides uniformis	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00123	Roseburia hominis	YCFAC-BO 160 mM (Anaerobe Systems, AS-7527)		160 mM	NO	YCFAC
FBI00124	Anaerostipes hadrus	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00125	Bacteroides stercoris	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00126	Bifidobacterium adolescentis	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00127	Collinsella aerofaciens	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00128	Hungatella effluvii	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00129	Escherichia flexneri	YCFAC-BO 200 mM (Anaerobe Systems, AS-7529)		200 mM	NO	YCFAC
FBI00130	Coprococcus comes	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00131	Fusicatenibacter saccharivorans	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00132	Gordonibacter pamelaeae	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00133	Oxalobacter formigenes	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC + 100 mM oxalate
FBI00134	Bifidobacterium adolescentis	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00135	Bifidobacterium pseudocatenulatum	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00136	Eisenbergiella tayi	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00137	Bacteroides fragilis	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00138	Blautia massiliensis	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00139	Bacteroides thetaiotaomicron	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00140	Phascolarctobacterium faecium	YCFAC-BO 160 mM (Anaerobe Systems, AS-7527)		160 mM	NO	YCFAC + 80 mM oxalate
FBI00141	Phascolarctobacterium faecium	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC + 80 mM oxalate
FBI00142	Clostridium fessum	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00143	Parabacteroides merdae	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00144	Holdemanella biformis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC + hemin/vitamin K
FBI00145	Bifidobacterium adolescentis	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00146	Blautia faecis	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00147	Clostridium bolteae	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00148	Oscillibacter sp. FBI00028	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00149	Monoglobus pectinilyticus	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00150	Lachnospiraceae sp. FBI00033	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00151	Clostridium aldenense	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00152	Dialister invisus	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC + hemin/vitamin K
FBI00153	Dialister succinatiphilus	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC + 3mM succinate + 7.3 mM formate
FBI00154	Bacteroides dorei	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00155	Blautia obeum	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00156	Enterococcus durans	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00157	Lachnospiraceae sp. FBI00157	Bifidobacterium Selective agar (Anaerobe Systems, AS-6423)		NO	NO	YCFAC
FBI00158	Butyricimonas sp. FBI00158	Columbia agar, 5% sheep blood (BD, 221165)	Antibiotics	NO	NO	YCFAC
FBI00159	Eisenbergiella tayi	YCFAC-BO 160 mM (Anaerobe Systems, AS-7527)		160 mM	NO	YCFAC
FBI00160	Ruminococcaceae sp. FBI00105 FBI00160	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00161	Bacteroides cellulosilyticus	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00162	Bifidobacterium catenulatum	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00163	Acidaminococcus intestini	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00164	Bacteroides stercoris	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00165	Bacteroides massiliensis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00166	Blautia massiliensis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00167	Dorea longicatena	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00168	Collinsella aerofaciens	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00169	Parabacteroides distasonis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00170	Eggerthella lenta	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00171	Bilophila wadsworthia	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00172	Bifidobacterium longum	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00173	Bacteroides vulgatus	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC
FBI00174	Lactobacillus rogosae	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00175	Holdemanella biformis	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC + hemin/vitamin K
FBI00176	Ruthenibacterium lactatiformans	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00177	Parasutterella excrementihominis	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC
FBI00178	Bifidobacterium adolescentis	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00179	Bifidobacterium adolescentis	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00180	Alistipes sp. FBI00180	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC
FBI00181	Blautia wexlerae	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00182	Bacteroides coprocola	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00183	Bacteroides dorei	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00184	Bacteroides faecis	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00185	Eisenbergiella tayi	YCFAC-BO 160 mM (Anaerobe Systems, AS-7527)		160 mM	NO	YCFAC
FBI00186	Coprococcus comes	OxyPras Plus Brucella Blood Agar (Oxyrase, P-BRU-BA)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00187	Eubacterium rectale	OxyPras Plus Brucella Blood Agar (Oxyrase, P-BRU-BA)		NO	NO	YCFAC
FBI00188	Blautia faecis	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00189	Bacteroides ovatus	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00190	Bacteroides finegoldii	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00191	Clostridiaceae sp. FBI00191	OxyPras Plus Brucella Blood Agar (Oxyrase, P-BRU-BA)		NO	NO	YCFAC + hemin/vitamin K
FBI00192	Sutterella wadsworthensis	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00193	Alistipes onderdonkii	OxyPras Plus Brucella Blood Agar (Oxyrase, P-BRU-BA)		NO	NO	YCFAC
FBI00194	Ruminococcus faecis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00195	Parasutterella excrementihominis	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00196	Blautia obeum	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00197	Bifidobacterium bifidum	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00198	Lachnoclostridium pacaense	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00199	Clostridium bolteae	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00200	Longicatena caecimuris	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00201	Eggerthella lenta	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00202	Erysipelotrichaceae sp. FBI00202	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00203	Bacteroides kribbi / Bacteroides koreensis species cluster	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00204	Escherichia flexneri	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00205	Blautia massiliensis	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00206	Bacteroides xylanisolvens	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00207	Parabacteroides merdae	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00208	Anaerotruncus massiliensis	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00209	Bacteroides salyersiae	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00210	Bifidobacterium bifidum	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00211	Bacteroides vulgatus	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00212	Clostridium aldenense	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00213	Ruminococcus bromii	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00214	Blautia obeum	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00215	Eubacterium rectale	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00216	Blautia faecis	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00217	Alistipes shahii	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC
FBI00218	Bacteroides uniformis	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00219	Roseburia hominis	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00220	Megasphaera massiliensis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00221	Butyricimonas faecihominis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00222	Alistipes onderdonkii	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00223	Alistipes onderdonkii	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00224	Sutterella wadsworthensis	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00225	Phascolarctobacterium faecium	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC + 80 mM oxalate
FBI00226	Catabacter hongkongensis	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC + hemin/vitamin K
FBI00227	Bacteroides cellulosilyticus	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00228	Collinsella aerofaciens	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00229	Alistipes senegalensis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	Thioglycollate with hemin/vitamin K

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00230	Eisenbergiella tayi	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00231	Parabacteroides distasonis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00232	Bacteroides stercoris	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00233	Ruminococcaceae sp. FBI00233	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC + hemin/vitamin K
FBI00234	Faecalicatena contorta	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00235	Alistipes shahii	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00236	Eisenbergiella tayi	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC
FBI00237	Dielma fastidiosa	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00238	Alistipes sp. FBI00238	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00239	Lactonifactor longoviformis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00240	Clostridium citroniae	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00241	Collinsella aerofaciens	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC + hemin/vitamin K
FBI00242	Clostridium aldenense	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00243	Eubacterium siraeum	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC, pH 6
FBI00244	Faecalibacterium prausnitzii	YCFAC-BO 40 mM (Anaerobe Systems, AS-7523)		40 mM	NO	YCFAC, pH 6
FBI00245	Acidaminococcus intestini	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC + hemin/vitamin K
FBI00246	Bifidobacterium longum	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00247	Phascolarctobacterium faecium	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC + 80 mM oxalate
FBI00248	Neglecta timonensis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00249	Citrobacter portucalensis	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00250	Bifidobacterium adolescentis	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00251	Bifidobacterium pseudocatenulatum	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00252	Oscillibacter sp. FBI00028	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	BHI + hemin/vitK
FBI00253	Roseburia hominis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00254	Eubacterium hallii	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00255	Hungatella effluvii	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00256	Blautia faecis	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00257	Eubacterium eligens	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00258	Turicibacter sanguinis	Strain Isolation Media 3 (SL3)		NO	NO	Thioglycollate with hemin/vitamin K
FBI00259	Dorea longicatena	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00260	Eubacterium rectale	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00261	Bacteroides uniformis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00262	Bacteroides massiliensis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00263	Bacteroides caccae	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00264	Bifidobacterium adolescentis	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00265	Bacteroides cellulosilyticus	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00266	Coprococcus eutactus	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00267	Anaerofustis stercorihominis	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00268	Clostridiales sp. FBI00268	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	Thioglycollate with hemin/vitamin K
FBI00269	Alistipes putredinis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00270	Methanobrevibacter smithii	Columbia agar, 5% sheep blood (BD, 221165)	Antibiotics	NO	NO	SAB

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00271	Bacteroides xylanisolvens	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00272	Clostridiales XIII sp. FBI00272	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	Thioglycollate with hemin/vitamin K
FBI00273	Barnesiella intestinihominis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00274	Eubacterium xylanophilum	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC, pH 6
FBI00275	Holdemanella biformis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC + hemin/vitamin K
FBI00276	Dorea formicigenerans	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00277	Alistipes onderdonkii	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00278	Eubacterium ventriosum	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC, pH 6

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00279	Coprococcus comes	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00280	Bacteroides thetaiotaomicron	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC
FBI00281	Senegalimassilia anaerobia	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00282	Porphyromonas asaccharolytica	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00283	Ruminococcus bromii	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00284	Blautia obeum	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00285	Lachnospira sp. FBI00063 FBI00285 FBI00364	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00286	Fusicatenibacter saccharivorans	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00287	Alistipes shahii	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00288	Blautia hydrogenotrophica	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00289	Oxalobacter formigenes	YCFAC-BO 80 mM (Anaerobe Systems, AS-7524)		80 mM	NO	YCFAC + 80 mM oxalate
FBI00290	Lachnospiraceae sp. FBI00290	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00291	Oribacterium sp. FBI00291	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00292	Methanobrevibacter smithii	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	SAB
FBI00293	Bifidobacterium adolescentis	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00294	Bacteroides stercoris	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00295	Bifidobacterium adolescentis	Reinforced Clostridial Agar (RCA) (Teknova, C0205)		NO	NO	YCFAC
FBI00296	Dorea longicatena	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00297	Alistipes obesi	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC + hemin/vitamin K
FBI00298	Faecalibacterium prausnitzii	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00299	Streptococcus pasteurianus	Lactobacillus MRS (Anaerobe Systems, AS-6429)		NO	NO	YCFAC
FBI00300	Collinsella aerofaciens	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00301	Bifidobacterium adolescentis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00302	Blautia faecis	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00303	Parabacteroides merdae	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00304	Dorea longicatena	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00305	Alistipes onderdonkii	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00306	Parasutterella excrementihominis	Strain Isolation Media 3 (SL3)		NO	NO	BHI + hemin/vitK
FBI00307	Parasutterella excrementihominis	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	BHI + hemin/vitK
FBI00308	Bacteroides vulgatus	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00309	Eubacterium rectale	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00310	Butyricimonas faecihominis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00311	Anaerostipes hadrus	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00312	Alistipes shahii	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC
FBI00313	Collinsella aerofaciens	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00314	Anaerotignum lactatifermentans	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00315	Blautia obeum	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00316	Collinsella aerofaciens	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00317	Bifidobacterium longum	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00318	Collinsella aerofaciens	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00319	Collinsella aerofaciens	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00320	Dorea formicigenerans	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00321	Bacteroides vulgatus	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00322	Bifidobacterium adolescentis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00323	Blautia wexlerae	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00324	Bilophila wadsworthia	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00325	Alistipes indistinctus	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC + hemin/vitamin K
FBI00326	Bacteroides vulgatus	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00327	Coprococcus comes	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00328	Blautia luti	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00329	Alistipes indistinctus	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00330	Bifidobacterium longum	Lactobacillus MRS (Anaerobe Systems, AS-6429)		NO	NO	YCFAC
FBI00331	Bacillus circulans	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00332	Clostridium intestinale	YCFAC-B (Anaerobe Systems, AS-677)		NO	NO	YCFAC
FBI00333	Alistipes onderdonkii	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00334	Bacteroides caccae	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00335	Anaerostipes hadrus	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00336	Staphylococcus epidermidis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00337	Coprococcus comes	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00338	Blautia obeum	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00339	Eubacterium rectale	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00340	Lachnospiraceae sp. FBI00033	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00341	Lachnospiraceae sp. FBI00071	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00342	Alistipes indistinctus	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC
FBI00343	Sutterella massiliensis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00344	Alistipes putredinis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00345	Roseburia inulinivorans	Strain Isolation Media 1 (SL1)		NO	NO	YCFAC
FBI00346	Coriobacteriia sp. FBI00346	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00347	Bacteroides uniformis	Strain Isolation Media 1 (SL1)		NO	NO	YCFAC
FBI00348	Parabacteroides merdae	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00349	Holdemanella biformis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	BHI + hemin/vitK
FBI00350	Alistipes putredinis	Bacteroides Bile Esculin (BBE) (Anaerobe Systems, AS-144)		NO	YES	YCFAC
FBI00351	Alistipes obesi	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC
FBI00352	Collinsella aerofaciens	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00353	Bifidobacterium adolescentis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00354	Bifidobacterium adolescentis	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC
FBI00355	Blautia massiliensis	Strain Isolation Media 1 (SL1)		NO	NO	YCFAC
FBI00356	Eubacterium eligens	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00357	Bacteroides kribbi / Bacteroides koreensis species cluster	Strain Isolation Media 1 (SL1)		NO	NO	YCFAC
FBI00358	Eubacterium hallii	Strain Isolation Media 1 (SL1)		NO	NO	YCFAC
FBI00359	Eubacterium rectale	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00360	Bacteroides massiliensis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00361	Bacteroides stercoris	Strain Isolation Media 3 (SL3)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00362	Prevotella copri	Chocolate Agar (Teknova, C4900)		NO	NO	Thioglycollate with hemin/vitamin K
FBI00363	Roseburia intestinalis	Strain Isolation Media 1 (SL1)		NO	NO	YCFAC
FBI00364	Lachnospira sp. FBI00063 FBI00285 FBI00364	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00365	Paraprevotella clara	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00366	Eubacterium eligens	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00367	Phascolarctobacterium faecium	Strain Isolation Media 1 (SL1)		NO	NO	YCFAC
FBI00368	Alistipes putredinis	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00369	Clostridiales sp. FBI00369	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	BHI + hemin/vitK
FBI00370	Bifidobacterium adolescentis	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	YCFAC

Strain #	Species ID	Stool plating agar media type (Vendor, Cat #)	Additives information	Isolated from media containing oxalate	Isolated from media containing 2% Ox bile	Glycerol stock media
FBI00371	Bacteroides stercoris	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	YCFAC
FBI00372	Dorea longicatena	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00373	Coriobacteriaceae sp. FBI00373 FBI00374	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	Thioglycollate with hemin/vitamin K
FBI00374	Coriobacteriaceae sp. FBI00373 FBI00374	Columbia agar, 5% sheep blood (BD, 221165)		NO	NO	Thioglycollate with hemin/vitamin K
FBI00375	Dorea longicatena	Chocolate Agar (Teknova, C4900)		NO	NO	YCFAC
FBI00376	Dialister succinatiphilus	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	BHI + hemin/vitK
FBI00377	Clostridiales sp. FBI00377	Brain Heart Infusion (BHI), hemin, vitamin K (Teknova, B1093)		NO	NO	Thioglycollate with hemin/vitamin K

TABLE 4.

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00001	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.64	1
FBI00002	Bacteroides salyersiae	bacteria	bacteroidetes	291644	Bacteroides salyersiae	99.5	2
FBI00003	Enterococcus faecalis	bacteria	firmicutes	1351	Enterococcus faecalis	99.93	3
FBI00004	Neglecta timonensis	bacteria	firmicutes	1776382	Neglecta timonensis	99.14	4
FBI00005	Enterococcus casseliflavus	bacteria	firmicutes	37734	Enterococcus gallinarum	99.65	5
FBI00006	Enterobacter himalayensis	bacteria	proteobacteria	547	Enterobacter hormaechei	99	6
FBI00007	Enterococcus casseliflavus	bacteria	firmicutes	37734	Enterococcus casseliflavus	99.05	7
FBI00008	Blautia luti	bacteria	firmicutes	89014	Blautia luti	97.02	8
FBI00009	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium faecale	98.6	9
FBI00010	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.12	10
FBI00011	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.28	11
FBI00012	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.71	12
FBI00013	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.5	13
FBI00014	Blautia luti	bacteria	firmicutes	89014	Blautia luti	97.02	14
FBI00015	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	15
FBI00016	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.64	16

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00017	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.34	17
FBI00018	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.71	18
FBI00019	Alistipes timonensis	bacteria	bacteroidetes	1465754	Alistipes timonensis	99.78	19
FBI00020	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.57	20
FBI00021	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides kribbi	99.07	21
FBI00022	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	99.93	22
FBI00023	Enterococcus casseliflavus	bacteria	firmicutes	37734	Enterococcus gallinarum	99.65	23
FBI00024	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides koreensis	99.07	24
FBI00025	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.21	25
FBI00026	Enterobacter hormaechei	bacteria	proteobacteria	158836	Enterobacter hormaechei	99.14	26
FBI00027	Fusicatenibacter saccharivorans	bacteria	firmicutes	1150298	Fusicatenibacter saccharivorans	97.6	27
FBI00028	Oscillibacter sp. FBI00028	bacteria	firmicutes	459786	Oscillibacter valericigenes	93.85	28
FBI00029	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	99.26	29

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00030	Eggerthella lenta	bacteria	firmicutes	84112	Eggerthella lenta	98.47	30
FBI00031	Enterobacter hormaechei	bacteria	proteobacteria	158836	Enterobacter hormaechei	99.43	31
FBI00032	Anaerostipes hadrus	bacteria	firmicutes	649756	Anaerostipes hadrus	99.64	32
FBI00033	Lachnospiraceae sp. FBI00033	bacteria	firmicutes	186803	Clostridium amygdalinum	93.56	33
FBI00034	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.78	34
FBI00035	Enterococcus casseliflavus	bacteria	firmicutes	37734	Enterococcus casseliflavus	98.24	35
FBI00036	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.53	36
FBI00037	Enterococcus casseliflavus	bacteria	firmicutes	37734	Enterococcus gallinarum	99.65	37
FBI00038	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	95.96	38
FBI00039	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.71	39
FBI00040	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.38	40
FBI00041	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.23	41
FBI00042	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.71	42
FBI00043	Bifidobacterium dentium	bacteria	actinobacteria	1689	Bifidobacterium dentium	99.35	43
FBI00044	Blautia wexlerae	bacteria	firmicutes	418240	Blautia wexlerae	98.69	44

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00045	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium faecale	99.56	45
FBI00046	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.71	46
FBI00047	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.79	47
FBI00048	Fusicatenibacter saccharivorans	bacteria	firmicutes	1150298	Fusicatenibacter saccharivorans	97.95	48
FBI00049	Dialister succinatiphilus	bacteria	firmicutes	487173	Dialister succinatiphilus	95.74	49
FBI00050	Bacteroides nordii	bacteria	bacteroidetes	291645	Bacteroides nordii	98.63	50
FBI00051	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	98.07	51
FBI00052	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.14	52
FBI00053	Lactobacillus rogosae	bacteria	firmicutes	706562	Lachnospira pectinoschiza	97.36	53
FBI00054	Escherichia flexneri	bacteria	proteobacteria	623	Escherichia fergusonii	99.71	54
FBI00055	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides kribbi	99.64	55
FBI00056	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.2	56
FBI00057	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.7	57
FBI00058	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.71	58
FBI00059	Bacteroides stercorirosoris	bacteria	bacteroidetes	871324	Bacteroides oleiciplenus	98.81	59

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00060	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.49	60
FBI00061	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	99.19	61
FBI00062	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.48	62
FBI00063	Lachnospira sp. FBI00063 FBI00285 FBI00364	bacteria	firmicutes	28050	Lactobacillus rogosae	95.3	63
FBI00064	Dorea sp. FBI00064	bacteria	firmicutes	189330	Ruminococcus gnavus	95.58	64
FBI00065	Sutterellaceae sp. FBI00065	bacteria	proteobacteria	995019	Turicimonas muris	91.55	65
FBI00066	Parasutterella excrementihominis	bacteria	proteobacteria	487175	Parasutterella excrementihominis	99.13	66
FBI00067	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	98.84	67
FBI00068	Akkermansia muciniphila	bacteria	verrucomicrobia	239935	Akkermansia muciniphila	99.42	68
FBI00069	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.84	69
FBI00070	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides koreensis	99.71	70
FBI00071	Lachnospiraceae sp. FBI00071	bacteria	firmicutes	186803	Roseburia faecis	94.92	71
FBI00072	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	96.17	72
FBI00073	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	98.99	73

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00074	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.03	74
FBI00075	Paraprevotella clara	bacteria	bacteroidetes	454154	Paraprevotella clara	98.85	75
FBI00076	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.78	76
FBI00077	Sutterella wadsworthensis	bacteria	proteobacteria	40545	Sutterella wadsworthensis	99.86	77
FBI00078	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.34	78
FBI00079	Clostridium clostridioforme	bacteria	firmicutes	1531	Clostridium clostridioforme	99.14	79
FBI00080	Sutterella massiliensis	bacteria	proteobacteria	1816689	Sutterella massiliensis	99.78	80
FBI00081	Porphyromonas asaccharolytica	bacteria	bacteroidetes	28123	Porphyromonas asaccharolytica	99.35	81
FBI00082	Ruminococcaceae sp. FBI00082 FBI00097	bacteria	firmicutes	541000	Phocea massiliensis	93.08	82
FBI00083	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	99.64	83
FBI00084	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	98.07	84
FBI00085	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.62	85
FBI00086	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.77	86
FBI00087	Clostridium scindens	bacteria	firmicutes	29347	Clostridium scindens	98.28	87
FBI00088	Lactobacillus rogosae	bacteria	firmicutes	706562	Lactobacillus rogosae	99.64	88

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00089	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	98.49	89
FBI00090	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.71	90
FBI00091	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.86	91
FBI00092	Monoglobus pectinilyticus	bacteria	firmicutes	1981510	Monoglobus pectinilyticus	99.5	92
FBI00093	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	99.71	93
FBI00094	Enterococcus faecium	bacteria	firmicutes	1352	Enterococcus faecium	99.38	94
FBI00095	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.7	95
FBI00096	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.76	96
FBI00097	Ruminococcaceae sp. FBI00082 FBI00097	bacteria	firmicutes	541000	Phocea massiliensis	93.07	97
FBI00098	Bacteroides dorei	bacteria	bacteroidetes	357276	Bacteroides dorei	99.93	98
FBI00099	Gordonibacter pamelaeae	bacteria	actinobacteria	471189	Gordonibacter pamelaeae	99.56	99
FBI00100	Lachnospira sp. FBI00063 FBI00285 FBI00364	bacteria	firmicutes	28050	Lactobacillus rogosae	95.35	100
FBI00101	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	97.97	101
FBI00102	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.31	102
FBI00103	Bacteroides massiliensis	bacteria	bacteroidetes	204516	Bacteroides massiliensis	99.86	103

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00104	Blautia wexlerae	bacteria	firmicutes	418240	Blautia luti	97.18	104
FBI00105	Ruminococcaceae sp. FBI00105 FBI00160	bacteria	firmicutes	541000	Pseudoflavonifractor phocaeensis	95.06	105
FBI00106	Enterococcus durans	bacteria	firmicutes	53345	Enterococcus lactis	96.68	106
FBI00107	Enterococcus durans	bacteria	firmicutes	53345	Enterococcus faecium	98.83	107
FBI00108	Ruminococcaceae sp. FBI00108	bacteria	firmicutes	541000	Gemmiger formicilis	96.96	108
FBI00109	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	98.39	109
FBI00110	Lachnoclostridium pacaense	bacteria	firmicutes	1917870	Lachnoclostridium pacaense	98.92	110
FBI00111	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.43	111
FBI00112	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	112
FBI00113	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.79	113
FBI00114	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	97.83	114
FBI00115	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	97.98	115
FBI00116	Ruminococcus faecis	bacteria	firmicutes	592978	Ruminococcus faecis	99.57	116
FBI00117	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.52	117
FBI00118	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.84	118
FBI00119	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.02	119

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00120	Hungatella effluvii	bacteria	firmicutes	154046	Hungatella hathewayi	98.78	120
FBI00121	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.86	121
FBI00122	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.57	122
FBI00123	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	100	123
FBI00124	Anaerostipes hadrus	bacteria	firmicutes	649756	Anaerostipes hadrus	99.86	124
FBI00125	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	99.64	125
FBI00126	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	98.98	126
FBI00127	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	98.81	127
FBI00128	Hungatella effluvii	bacteria	firmicutes	1096246	Hungatella effluvii	98.71	128
FBI00129	Escherichia flexneri	bacteria	proteobacteria	623	Escherichia fergusonii	99.43	129
FBI00130	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.35	130
FBI00131	Fusicatenibacter saccharivorans	bacteria	firmicutes	1150298	Fusicatenibacter saccharivorans	99.2	131
FBI00132	Gordonibacter pamelaeae	bacteria	actinobacteria	471189	Gordonibacter pamelaeae	99.48	132
FBI00133	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	133
FBI00134	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium faecale	98.92	134
FBI00135	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.57	135

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00136	Eisenbergiella tayi	bacteria	firmicutes	1432052	Eisenbergiella tayi	99.77	136
FBI00137	Bacteroides fragilis	bacteria	bacteroidetes	817	Bacteroides fragilis	99.71	137
FBI00138	Blautia massiliensis	bacteria	firmicutes	1737424	Blautia luti	97.94	138
FBI00139	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.5	139
FBI00140	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.58	140
FBI00141	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.15	141
FBI00142	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.07	142
FBI00143	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.07	143
FBI00144	Holdemanella biformis	bacteria	firmicutes	1735	Holdemanella biformis	97.73	144
FBI00145	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	99.14	145
FBI00146	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.68	146
FBI00147	Clostridium bolteae	bacteria	firmicutes	208479	Clostridium bolteae	99.28	147
FBI00148	Oscillibacter sp. FBI00028	bacteria	firmicutes	459786	Oscillibacter ruminantium	94.28	148
FBI00149	Monoglobus pectinilyticus	bacteria	firmicutes	1981510	Monoglobus pectinilyticus	99.5	149

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00150	Lachnospiraceae sp. FBI00033	bacteria	firmicutes	186803	Clostridium amygdalinum	93.55	150
FBI00151	Clostridium aldenense	bacteria	firmicutes	358742	Clostridium aldenense	98.55	151
FBI00152	Dialister invisus	bacteria	firmicutes	218538	Dialister invisus	99.58	152
FBI00153	Dialister succinatiphilus	bacteria	firmicutes	487173	Dialister succinatiphilus	95.72	153
FBI00154	Bacteroides dorei	bacteria	bacteroidetes	357276	Bacteroides dorei	100	154
FBI00155	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.7	155
FBI00156	Enterococcus durans	bacteria	firmicutes	53345	Enterococcus sp.	96.45	156
FBI00157	Lachnospiraceae sp. FBI00157	bacteria	firmicutes	186803	Cuneatibacter caecimuris	91.24	157
FBI00158	Butyricimonas sp. FBI00158	bacteria	bacteroidetes	574697	Butyricimonas sp.	97.54	158
FBI00159	Eisenbergiella tayi	bacteria	firmicutes	1432052	Eisenbergiella tayi	99.03	159
FBI00160	Ruminococcaceae sp. FBI00105 FBI00160	bacteria	firmicutes	541000	Pseudoflavonifractor capillosus	97.17	160
FBI00161	Bacteroides cellulosilyticus	bacteria	bacteroidetes	246787	Bacteroides cellulosilyticus	99.14	161
FBI00162	Bifidobacterium catenulatum	bacteria	actinobacteria	1686	Bifidobacterium catenulatum	99.14	162
FBI00163	Acidaminococcus intestini	bacteria	firmicutes	187327	Acidaminococcus intestini	99.72	163
FBI00164	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	98.56	164

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00165	Bacteroides massiliensis	bacteria	bacteroidetes	204516	Bacteroides massiliensis	99.71	165
FBI00166	Blautia massiliensis	bacteria	firmicutes	1737424	Blautia luti	97.55	166
FBI00167	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.39	167
FBI00168	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.26	168
FBI00169	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	98.7	169
FBI00170	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.61	170
FBI00171	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.45	171
FBI00172	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.05	172
FBI00173	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	100	173
FBI00174	Lactobacillus rogosae	bacteria	firmicutes	706562	Lachnospira pectinoschiza	97.92	174
FBI00175	Holdemanella biformis	bacteria	firmicutes	1735	Holdemanella biformis	98.19	175
FBI00176	Ruthenibacterium lactatiformans	bacteria	firmicutes	1550024	Ruthenibacterium lactatiformans	99.71	176
FBI00177	Parasutterella excrementihominis	bacteria	proteobacteria	487175	Parasutterella excrementihominis	99.71	177
FBI00178	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium faecale	98.99	178
FBI00179	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium faecale	98.91	179

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00180	Alistipes sp. FBI00180	bacteria	bacteroidetes	239759	Alistipes senegalensis	97.56	180
FBI00181	Blautia wexlerae	bacteria	firmicutes	418240	Blautia wexlerae	97.17	181
FBI00182	Bacteroides coprocola	bacteria	bacteroidetes	310298	Bacteroides coprocola	99.64	182
FBI00183	Bacteroides dorei	bacteria	bacteroidetes	357276	Bacteroides dorei	99.86	183
FBI00184	Bacteroides faecis	bacteria	bacteroidetes	674529	Bacteroides faecis	99.78	184
FBI00185	Eisenbergiella tayi	bacteria	firmicutes	1432052	Eisenbergiella tayi	98.96	185
FBI00186	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.06	186
FBI00187	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.57	187
FBI00188	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.05	188
FBI00189	Bacteroides ovatus	bacteria	bacteroidetes	28116	Bacteroides koreensis	99.93	189
FBI00190	Bacteroides finegoldii	bacteria	bacteroidetes	338188	Bacteroides finegoldii	98.91	190
FBI00191	Clostridiaceae sp. FBI00191	bacteria	firmicutes	31979	Clostridium swellfunianum	96.24	191
FBI00192	Sutterella wadsworthensis	bacteria	proteobacteria	40545	Sutterella wadsworthensis	99.71	192
FBI00193	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.64	193
FBI00194	Ruminococcus faecis	bacteria	firmicutes	592978	Ruminococcus faecis	98.41	194
FBI00195	Parasutterella excrementihominis	bacteria	proteobacteria	487175	Parasutterella excrementihominis	99.06	195

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00196	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.3	196
FBI00197	Bifidobacterium bifidum	bacteria	actinobacteria	1681	Bifidobacterium bifidum	99.85	197
FBI00198	Lachnoclostridium pacaense	bacteria	firmicutes	1917870	Lachnoclostridium pacaense	99.71	198
FBI00199	Clostridium bolteae	bacteria	firmicutes	208479	Clostridium bolteae	99.28	199
FBI00200	Longicatena caecimuris	bacteria	firmicutes	1796635	Longicatena caecimuris	99.71	200
FBI00201	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.83	201
FBI00202	Erysipelotrichaceae sp. FBI00202	bacteria	firmicutes	128827	Longibaculum muris	92.85	202
FBI00203	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides koreensis	100	203
FBI00204	Escherichia flexneri	bacteria	proteobacteria	623	Escherichia fergusonii	98.98	204
FBI00205	Blautia massiliensis	bacteria	firmicutes	1737424	Blautia luti	97.55	205
FBI00206	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.56	206
FBI00207	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.49	207
FBI00208	Anaerotruncus massiliensis	bacteria	firmicutes	1673720	Anaerotruncus colihominis	96.52	208
FBI00209	Bacteroides salyersiae	bacteria	bacteroidetes	291644	Bacteroides salyersiae	99.63	209
FBI00210	Bifidobacterium bifidum	bacteria	actinobacteria	1681	Bifidobacterium bifidum	99.93	210

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00211	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.78	211
FBI00212	Clostridium aldenense	bacteria	firmicutes	358742	Clostridium aldenense	99.1	212
FBI00213	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.99	213
FBI00214	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.67	214
FBI00215	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.78	215
FBI00216	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.76	216
FBI00217	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	98.77	217
FBI00218	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.42	218
FBI00219	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	99.78	219
FBI00220	Megasphaera massiliensis	bacteria	firmicutes	1232428	Megasphaera massiliensis	98.8	220
FBI00221	Butyricimonas faecihominis	bacteria	bacteroidetes	1472416	Butyricimonas faecihominis	98.61	221
FBI00222	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.78	222
FBI00223	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.7	223
FBI00224	Sutterella wadsworthensis	bacteria	proteobacteria	40545	Sutterella wadsworthensis	99.71	224
FBI00225	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.37	225

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00226	Catabacter hongkongensis	bacteria	firmicutes	270498	Catabacter hongkongensis	99.71	226
FBI00227	Bacteroides cellulosilyticus	bacteria	bacteroidetes	246787	Bacteroides cellulosilyticus	99.2	227
FBI00228	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.27	228
FBI00229	Alistipes senegalensis	bacteria	bacteroidetes	1288121	Alistipes senegalensis	99.19	229
FBI00230	Eisenbergiella tayi	bacteria	firmicutes	1432052	Eisenbergiella tayi	99.48	230
FBI00231	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	99.11	231
FBI00232	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	98.84	232
FBI00233	Ruminococcaceae sp. FBI00233	bacteria	firmicutes	474960	Anaerotruncus colihominis	91.63	233
FBI00234	Faecalicatena contorta	bacteria	firmicutes	39482	Faecalicatena contorta	99.21	234
FBI00235	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	99.86	235
FBI00236	Eisenbergiella tayi	bacteria	firmicutes	1432052	Eisenbergiella tayi	99.41	236
FBI00237	Dielma fastidiosa	bacteria	firmicutes	1034346	Dielma fastidiosa	99.78	237
FBI00238	Alistipes sp. FBI00238	bacteria	bacteroidetes	239759	Alistipes finegoldii	95.84	238
FBI00239	Lactonifactor longoviformis	bacteria	firmicutes	341220	Lactonifactor longoviformis	98.99	239
FBI00240	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.57	240

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00241	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.34	241
FBI00242	Clostridium aldenense	bacteria	firmicutes	358742	Clostridium aldenense	99.05	242
FBI00243	Eubacterium siraeum	bacteria	firmicutes	39492	Eubacterium siraeum	98.53	243
FBI00244	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	98.69	244
FBI00245	Acidaminococcus intestini	bacteria	firmicutes	187327	Acidaminococcus intestini	99.72	245
FBI00246	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.7	246
FBI00247	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.79	247
FBI00248	Neglecta timonensis	bacteria	firmicutes	1776382	Emergencia timonensis	99.64	248
FBI00249	Citrobacter portucalensis	bacteria	proteobacteria	1639133	Citrobacter freundii	99.79	249
FBI00250	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium faecale	99.24	250
FBI00251	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.85	251
FBI00252	Oscillibacter sp. FBI00028	bacteria	firmicutes	459786	Oscillibacter ruminantium	95.79	252
FBI00253	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	99.71	253
FBI00254	Eubacterium hallii	bacteria	firmicutes	39488	Eubacterium hallii	99.08	254
FBI00255	Hungatella effluvii	bacteria	firmicutes	1096246	Hungatella hathewayi	98.56	255

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00256	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	97.86	256
FBI00257	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	99.28	257
FBI00258	Turicibacter sanguinis	bacteria	firmicutes	154288	Turicibacter sanguinis	99.93	258
FBI00259	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.7	259
FBI00260	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.64	260
FBI00261	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.21	261
FBI00262	Bacteroides massiliensis	bacteria	bacteroidetes	204516	Bacteroides massiliensis	99.71	262
FBI00263	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.56	263
FBI00264	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium faecale	99.2	264
FBI00265	Bacteroides cellulosilyticus	bacteria	bacteroidetes	246787	Bacteroides cellulosilyticus	99.21	265
FBI00266	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	99.2	266
FBI00267	Anaerofustis stercorihominis	bacteria	firmicutes	214853	Anaerofustis stercorihominis	97.29	267
FBI00268	Clostridiales sp. FBI00268	bacteria	firmicutes	186802	Catabacter hongkongensis	86.05	268
FBI00269	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	100	269
FBI00270	Methanobrevibacter smithii	archaea	euryarchaeota	2173	Methanobrevibacter smithii	99.69	270

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00271	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	98.42	271
FBI00272	Clostridiales XIII sp. FBI00272	bacteria	firmicutes	543314	Anaerovorax odorimutans	93.12	272
FBI00273	Barnesiella intestinihominis	bacteria	bacteroidetes	487174	Barnesiella intestinihominis	99.43	273
FBI00274	Eubacterium xylanophilum	bacteria	firmicutes	39497	Eubacterium xylanophilum	93.5	274
FBI00275	Holdemanella biformis	bacteria	firmicutes	1735	Holdemanella biformis	98.99	275
FBI00276	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	98.19	276
FBI00277	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.63	277
FBI00278	Eubacterium ventriosum	bacteria	firmicutes	39496	Eubacterium ventriosum	94.14	278
FBI00279	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	98.48	279
FBI00280	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	100	280
FBI00281	Senegalimassilia anaerobia	bacteria	actinobacteria	1473216	Senegalimassilia anaerobia	99.45	281
FBI00282	Porphyromonas asaccharolytica	bacteria	bacteroidetes	28123	Porphyromonas asaccharolytica	99.35	282
FBI00283	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	96.02	283
FBI00284	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.67	284

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00285	Lachnospira sp. FBI00063 FBI00285 FBI00364	bacteria	firmicutes	28050	Lactobacillus rogosae	95.3	285
FBI00286	Fusicatenibacter saccharivorans	bacteria	firmicutes	1150298	Fusicatenibacter saccharivorans	96.32	286
FBI00287	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	98.47	287
FBI00288	Blautia hydrogenotrophica	bacteria	firmicutes	53443	Blautia hydrogenotrophica	99.57	288
FBI00289	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	289
FBI00290	Lachnospiraceae sp. FBI00290	bacteria	firmicutes	186803	Eubacterium ruminantium	94.81	290
FBI00291	Oribacterium sp. FBI00291	bacteria	firmicutes	265975	Lactobacillus rogosae	91.63	291
FBI00292	Methanobrevibacter smithii	archaea	euryarchaeota	2173	Methanobrevibacter smithii	99.44	292
FBI00293	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	98.77	293
FBI00294	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	99.35	294
FBI00295	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	98.48	295
FBI00296	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.21	296
FBI00297	Alistipes obesi	bacteria	bacteroidetes	2585118	Alistipes obesi	99.49	297
FBI00298	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	97.24	298

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00299	Streptococcus pasteurianus	bacteria	firmicutes	197614	Streptococcus pasteurianus	100	299
FBI00300	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.49	300
FBI00301	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	98.64	301
FBI00302	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.6	302
FBI00303	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	98.78	303
FBI00304	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.7	304
FBI00305	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.85	305
FBI00306	Parasutterella excrementihominis	bacteria	proteobacteria	487175	Parasutterella excrementihominis	98.53	306
FBI00307	Parasutterella excrementihominis	bacteria	proteobacteria	487175	Parasutterella excrementihominis	98.53	307
FBI00308	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.64	308
FBI00309	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.71	309
FBI00310	Butyricimonas faecihominis	bacteria	bacteroidetes	1472416	Butyricimonas faecihominis	99.13	310
FBI00311	Anaerostipes hadrus	bacteria	firmicutes	649756	Anaerostipes hadrus	99.07	311
FBI00312	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	99.35	312
FBI00313	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.56	313

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00314	Anaerotignum lactatifermentans	bacteria	firmicutes	160404	Anaerotignum lactatifermentans	99.57	314
FBI00315	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.82	315
FBI00316	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.26	316
FBI00317	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.49	317
FBI00318	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.41	318
FBI00319	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.56	319
FBI00320	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	98.13	320
FBI00321	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	97.63	321
FBI00322	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	98.7	322
FBI00323	Blautia wexlerae	bacteria	firmicutes	418240	Blautia wexlerae	99.28	323
FBI00324	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.52	324
FBI00325	Alistipes indistinctus	bacteria	bacteroidetes	626932	Alistipes indistinctus	99.93	325
FBI00326	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	98.63	326
FBI00327	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.34	327
FBI00328	Blautia luti	bacteria	firmicutes	89014	Blautia luti	97.78	328
FBI00329	Alistipes indistinctus	bacteria	bacteroidetes	626932	Alistipes indistinctus	99.93	329

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00330	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.28	330
FBI00331	Bacillus circulans	bacteria	firmicutes	1397	Bacillus circulans	96.84	331
FBI00332	Clostridium intestinale	bacteria	firmicutes	36845	Clostridium intestinale	99.13	332
FBI00333	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.93	333
FBI00334	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.56	334
FBI00335	Anaerostipes hadrus	bacteria	firmicutes	649756	Anaerostipes hadrus	99.64	335
FBI00336	Staphylococcus epidermidis	bacteria	firmicutes	1282	Staphylococcus epidermidis	99.93	336
FBI00337	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.21	337
FBI00338	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	97.75	338
FBI00339	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.86	339
FBI00340	Lachnospiraceae sp. FBI00033	bacteria	firmicutes	186803	Clostridium amygdalinum	93.57	340
FBI00341	Lachnospiraceae sp. FBI00071	bacteria	firmicutes	186803	Roseburia faecis	95.06	341
FBI00342	Alistipes indistinctus	bacteria	bacteroidetes	626932	Alistipes indistinctus	100	342
FBI00343	Sutterella massiliensis	bacteria	proteobacteria	1816689	Sutterella massiliensis	99.86	343
FBI00344	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	99.93	344
FBI00345	Roseburia inulinivorans	bacteria	firmicutes	360807	Roseburia inulinivorans	97.35	345

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00346	Coriobacteriia sp. FBI00346	bacteria	actinobacteria	84998	Paraeggerthella hongkongensis	93.84	346
FBI00347	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.85	347
FBI00348	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.93	348
FBI00349	Holdemanella biformis	bacteria	firmicutes	1735	Holdemanella biformis	98.14	349
FBI00350	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	100	350
FBI00351	Alistipes obesi	bacteria	bacteroidetes	2585118	Alistipes obesi	99.78	351
FBI00352	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.56	352
FBI00353	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	98.85	353
FBI00354	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium stercoris	98.7	354
FBI00355	Blautia massiliensis	bacteria	firmicutes	1737424	Blautia luti	98.09	355
FBI00356	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.5	356
FBI00357	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides koreensis	99.71	357
FBI00358	Eubacterium hallii	bacteria	firmicutes	39488	Eubacterium hallii	98.26	358
FBI00359	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.79	359
FBI00360	Bacteroides massiliensis	bacteria	bacteroidetes	204516	Bacteroides massiliensis	99.93	360

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00361	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	99.36	361
FBI00362	Prevotella copri	bacteria	bacteroidetes	165179	Prevotella copri	98.5	362
FBI00363	Roseburia intestinalis	bacteria	firmicutes	166486	Roseburia intestinalis	99.78	363
FBI00364	Lachnospira sp. FBI00063 FBI00285 FBI00364	bacteria	firmicutes	28050	Lactobacillus rogosae	95.2	364
FBI00365	Paraprevotella clara	bacteria	bacteroidetes	454154	Paraprevotella clara	98.78	365
FBI00366	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	99	366
FBI00367	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.58	367
FBI00368	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	99.86	368
FBI00369	Clostridiales sp. FBI00369	bacteria	firmicutes	186802	Catabacter hongkongensis	86	369
FBI00370	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	97.11	370
FBI00371	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	99.21	371
FBI00372	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.7	372
FBI00373	Coriobacteriaceae sp. FBI00373 FBI00374	bacteria	actinobacteria	84107	Parolsenella catena	96.58	373
FBI00374	Coriobacteriaceae sp. FBI00373 FBI00374	bacteria	actinobacteria	84107	Parolsenella catena	97.11	374
FBI00375	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.62	375

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00376	Dialister succinatiphilus	bacteria	firmicutes	487173	Dialister succinatiphilus	95.82	376
FBI00377	Clostridiales sp. FBI00377	bacteria	firmicutes	186802	Christensenella massiliensis	88.69	377

TABLE 5: Commercial Oxalate-metabolizing strains

Bifidobacterium dentium ATCC 27678	Enterococcus faecalis HM-432	Lactobacillus helveticus DSM 20075
Bifidobacterium dentium ATCC 27680	Lactobacillus acidophilus ATCC 4357	Lactobacillus reuteri HM-102
Bifidobacterium dentium DSM 20221	Lactobacillus acidophilus DSM 20079	Lactobacillus rhamnosus ATCC 53103
Bifidobacterium dentium DSM 20436	Lactobacillus acidophilus DSM 20242	Lactobacillus rhamnosus DSM 20245
Bifidobacterium sp. HM-868	Lactobacillus gasseri ATCC 33323	Lactobacillus rhamnosus DSM 8746
Dialister invisus DSM 15470	Lactobacillus gasseri DSMZ 107525	Lactobacillus rhamnosus HM-106
Eggerthella lenta ATCC 43055	Lactobacillus gasseri DSMZ 20077	Oxalobacter formigenes ATCC 35274
Eggerthella lenta DSM 2243	Lactobacillus gasseri HM-104	Oxalobacter formigenes DSM 4420
Enterococcus faecalis HM-202	Lactobacillus gasseri HM-644	Oxalobacter formigenes HM-1

TABLE 6: Commercial Supportive strains

Absiella dolichum DSM 3991	Bilophila wadsworthia ATCC 49260	Intestinibacter bartlettii DSM 16795
Acidaminococcus fermentans DSM 20731	Bilophila wadsworthia DSM 11045	Intestinimonas butyriciproducens DSM 26588
Acidaminococcus sp. HM-81	Blautia hansenii DSM 20583	Lactobacillus amylovorus DSM 20552
Adlercreutzia equolifaciens DSM 19450	Blautia hydrogenotrophica DSM 10507	Lactobacillus casei subsp. casei ATCC 393
Akkermansia muciniphila ATCC BAA-835	Blautia obeum DSMZ 25238	Lactobacillus casei subsp. casei ATCC 39539
Alistipes finegoldii DSM 17242	Blautia sp. HM-1032	Lactobacillus crispatus HM-370
Alistipes indistinctus DSM 22520	Blautia wexlerae DSM 19850	Lactobacillus johnsonii HM-643

Alistipes onderdonkii DSM 19147	Butyricimonas virosa DSM 23226	Lactobacillus parafarraginis HM-478
Alistipes putredinis DSM 17216	Butyrivibrio crossotus DSM 2876	Lactobacillus plantarum ATCC 14917
Alistipes senegalensis DSM 25460	Catenibacterium mitsuokai DSM 15897	Lactobacillus plantarum ATCC 202195
Alistipes shahii DSM 19121	Cetobacterium somerae DSM 23941	Lactobacillus ruminis ATCC 25644
Anaerobutyricum hallii DSM 3353	Clostridium asparagiforme DSM 15981	Lactobacillus ruminis DSM 20404
Anaerococcus lactolyticus DSM 7456	Clostridium bolteae DSM 15670	Lactobacillus ultunensis DSM 16048
Anaerofustis stercorihominis DSM 17244	Clostridium bolteae HM-1038	Lactococcus lactis Berridge DSM 20729
Anaerostipes caccae DSM 14662	Clostridium bolteae HM-318	Marvinbryantia formatexigens DSM 14469
Anaerotruncus colihominis DSM 17241	Clostridium cadaveris HM-1040	Megasphaera indica DSM 25562
Bacteroides caccae ATCC 43185	Clostridium citroniae HM-315	Megasphaera sp. DSM 102144
Bacteroides caccae HM-728	Clostridium hiranonis DSM 13275	Methanobrevibacter smithii DSM 11975
Bacteroides cellulosilyticus DSM 14838	Clostridium hylemonae DSM 15053	Methanobrevibacter smithii DSM 2374
Bacteroides cellulosilyticus HM-726	Clostridium innocuum HM-173	Methanobrevibacter smithii DSM 2375
Bacteroides coprocola DSM 17136	Clostridium leptum DSM 753	Methanobrevibacter smithii DSM 861
Bacteroides coprophilus DSM 18228	Clostridium methylpentosum DSM 5476	Methanomassiliicoccus luminyensis DSM 25720
Bacteroides dorei DSM 17855	Clostridium saccharolyticum DSM 2544	Methanosphaera stadtmanae DSMZ 3091
Bacteroides dorei HM-29	Clostridium scindens DSM 5676	Mitsuokella multacida DSM 20544
Bacteroides dorei HM-718	Clostridium scindens VPI 12708	Odoribacter splanchnicus DSM 20712

Bacteroides eggerthii DSM 20697	Clostridium sp. ATCC 29733	Olsenella uli DSM 7084
Bacteroides eggerthii HM-210	Clostridium sp. DSM 4029	Oscillibacter sp. HM-1030
Bacteroides finegoldii DSM 17565	Clostridium sp. HM-634	Parabacteroides distasonis ATCC 8503
Bacteroides finegoldii HM-727	Clostridium sp. HM-635	Parabacteroides goldsteinii HM-1050
Bacteroides fragilis HM-20	Clostridium spiroforme DSM 1552	Parabacteroides johnsonii DSM 18315
Bacteroides fragilis HM-709	Clostridium sporogenes ATCC 15579	Parabacteroides johnsonii HM-731
Bacteroides fragilis HM-710	Clostridium sporogenes ATCC 17889	Parabacteroides merdae DSM 19495
Bacteroides intestinalis DSM 17393	Clostridium sporogenes DSM 767	Parabacteroides merdae HM-729
Bacteroides ovatus ATCC 8483	Clostridium symbiosum HM-309	Parabacteroides merdae HM-730
Bacteroides ovatus HM-222	Clostridium symbiosum HM-319	Parabacteroides sp. HM-77
Bacteroides pectinophilus ATCC 43243	Collinsella aerofaciens ATCC 25986	Peptostreptococcus anaerobius DSM 2949
Bacteroides plebeius DSM 17135	Collinsella stercoris DSM 13279	Prevotella buccae HM-45
Bacteroides rodentium DSM 26882	Coprococcus catus ATCC 27761	Prevotella buccalis DSM 20616
Bacteroides salyersiae HM-725	Coprococcus comes ATCC 27758	Prevotella copri DSM 18205
Bacteroides sp. HM-18	Coprococcus eutactus ATCC 27759	Proteocatella sphenisci DSM 23131
Bacteroides sp. HM-19	Coprococcus eutactus ATCC 51897	Providencia rettgeri ATCC BAA-2525
Bacteroides sp. HM-23	Coprococcus sp. DSM 21649	Roseburia intestinalis DSM 14610
Bacteroides sp. HM-27	Desulfovibrio piger ATCC 29098	Roseburia inulinivorans DSM 16841

Bacteroides sp. HM-28	Dialister pneumosintes ATCC 51894	Ruminococcaceae sp. HM-79
Bacteroides sp. HM-58	Dorea formicigenerans ATCC 27755	Ruminococcus albus ATCC 27210
Bacteroides stercoris DSM 19555	Dorea longicatena DSM 13814	Ruminococcus bromii ATCC 27255
Bacteroides stercoris HM-1036	Eggerthella sp. DSM 11767	Ruminococcus bromii ATCC 51896
Bacteroides thetaiotaomicron ATCC 29148	Eggerthella sp. DSM 11863	Ruminococcus gauvreauii DSM 19829
Bacteroides uniformis ATCC 8492	Eggerthella sp. HM-1099	Ruminococcus gnavus ATCC 29149
Bacteroides vulgatus ATCC 8482	Ethanoligenens harbinense DSM 18485	Ruminococcus gnavus DSM 108212
Bacteroides vulgatus HM-720	Eubacterium eligens ATCC 27750	Ruminococcus gnavus HM-1056
Bacteroides xylanisolvens DSM 18836	Eubacterium rectale ATCC 33656	Ruminococcus lactaris ATCC 29176
Bifidobacterium adolescentis HM-633	Eubacterium siraeum DSM 15702	Ruminococcus lactaris HM-1057
Bifidobacterium angulatum HM-1189	Eubacterium ventriosum ATCC 27560	Ruminococcus torques ATCC 27756
Bifidobacterium animalis DSM 20104	Faecalibacterium prausnitzii ATCC 27766	Slackia exigua DSM 15923
Bifidobacterium animalis subsp. Lactis DSMZ 10140	Faecalibacterium prausnitzii ATCC 27768	Slackia heliotrinireducens DSM 20476
Bifidobacterium bifidum ATCC 11863	Faecalibacterium prausnitzii DSM 17677	Solobacterium moorei DSM 22971
Bifidobacterium breve DSM 20213	Faecalibacterium prausnitzii HM-473	Streptococcus salivarius subsp. thermophilus ATCC BAA-491
Bifidobacterium catenulatum DSM 16992	Flavonifractor plautii HM-1044	Streptococcus thermophilus ATCC 14485
Bifidobacterium longum infantis ATCC 55813	Flavonifractor plautii HM-303	Subdoligranulum variabile DSM 15176

Bifidobacterium longum subsp. longum HM-845	Granulicatella adiacens ATCC 49175	Turicibacter sanguinis DSM 14220
Bifidobacterium longum subsp. longum HM-846	Holdemanella biformis DSM 3989	Tyzzerella nexilis DSM 1787
Bifidobacterium longum subsp. longum HM-847	Holdemania filiformis DSM 12042	Veillonella dispar ATCC 17748
Bifidobacterium longum subsp. longum HM-848	Hungatella (prev. Clostridium) hathewayi HM-308	Veillonella sp. HM-49
Bifidobacterium pseudocatenulatum DSM 20438	Hungatella hathewayi DSM 13479	Veillonella sp. HM-64

Example 2: Commercial microbial strain sensitivities to oxalate concentration

[0269] To determine the effect of the presence of oxalate on growth of commercial microbial strains, cultures were grown in their respective banking media (*e.g.*, Mega Media, or Chopped Meat Media) to saturation and back-diluted into the same respective banking media containing no oxalate, 0.5% oxalate, or 0.125% oxalate. FIGURE 1 shows % growth inhibition of microbial strains in the presence of 0.5% oxalate (closed bars) or 0.125% oxalate (open bars). % growth inhibition was calculated by determining the ratio of background-subtracted optical density (O.D.) of a microbial strain in the presence of oxalate to the O.D. of the same microbial strain grown in the absence of oxalate.

Example 3: *in vitro* oxalate metabolization by commercial microbial strains

[0270] 48-well deep well plates were filled with 2.5 mL of banking media per commercial microbial strain, per condition. Potassium oxalate was added to achieve final oxalate concentrations of 7.5 mM or 750 µM. 50 µl of each microbial strain in banking media was added to the appropriate well and mixed by trituration. 1 mL of each sample was transferred to an appropriate well of a 96-well collection plate containing 25 µl of 6N HCl and mixed by trituration. The collection plate was covered and incubated at 37 °C for 0, 24, or 72 hours under anaerobic conditions.

[0271] The oxalate metabolizing activity of the microbial strains was measured using a commercial colorimetric enzyme kit (Sigma Aldrich Oxalate Assay kit, Catalog No. MAK315) in accordance with the manufacturer's instructions.

[0272] In brief, acidified microbial suspensions were centrifuged for 1 minute at >10,000 x g to pellet intact cells and cellular debris. 10 µl of sample supernatant was transferred into each of three separate wells of a multiwell plate designated as a "Sample Blank," "Sample," or "Internal Standard." 10 µl of dH_2O was added to Sample Blank and Sample wells, and 10 µl of oxalate standard was added to the Internal Standard well. Blank reagent was prepared for all Sample Blank wells by mixing 155 µl of Reagent B and 1 µl of Horseradish peroxidase ("HRP") enzyme per Sample Blank well. 157 µl of Working Reagent (155 µl of Reagent B, 1 µl of oxalate oxidase enzyme, and 1 µl of HRP) was prepared for each Sample and Internal Standard well. 150 µl of Blank Reagent was added to each Sample Blank well and 150 µl of Working Reagent was added to each Sample and Internal Standard Well. Solutions were mixed and incubated for 10 minutes at room temperature. Following incubation, optical density was measured for each sample well at 595 nm using a BioTek Epoch 2 plate reader. Sample and Internal Standard values were corrected by subtracting the measured OD_{595} of the Sample Blank well from the measured OD_{595} of the Sample and Internal Standard wells. The proportion of oxalate remaining in each sample after 24 or 72 hour incubation was determined by dividing the corrected OD_{595} value from the Sample well for the initial timepoint (*i.e.*, t = 0 hours).

[0273] FIGURE 2 shows % oxalate remaining in microbial strain cultures in Mega Media (FIGURE 2A) or Chopped Meat Media (FIGURE 2B) seeded with 7.5 mM oxalate (closed bars) or 750 µM oxalate (open bars) after 72 hours incubation at 37 °C under anaerobic conditions.

in vitro oxalate metabolizing activities of microbial strains cultured under different pH

[0274] To determine the effect of pH on oxalate metabolization, the *in vitro* oxalate metabolization assay as described above was performed at an oxalate concentration of 7.5 mM, in culture media at pH 7.2 or adjusted to pH 4.5 with NaOH.

[0275] FIGURE 3 shows % oxalate remaining in microbial strain cultures in Mega Media (FIGURE 3A) or Chopped Meat Media (FIGURE 3B) seeded with 7.5 mM oxalate at pH 4.5 (closed bars) or pH 7.2 (open bars) after 72 hours incubation at 37 °C under anaerobic conditions.

in vitro oxalate-metabolizing activity of microbial consortia

[0276] To determine the oxalate-metabolizing activity of a microbial consortium, the *in vitro* oxalate metabolization assay was performed at an oxalate concentration of 7.5 mM.

[0277] FIGURE 4 shows the Absorbance (595 nm) of cultures comprising *O. formigenes* only, active microbial strains only, supportive microbial strains only, or a complete microbial consortium (*i.e.* both active and supportive microbial strains) in Mega Media (FIGURE 4A) or Chopped Meat Media (FIGURE 4B) at the time of oxalate addition (t = 0, closed bars) or after 72 hours (open bars).

Example 4: Oxalate analysis by liquid chromatography tandem mass spectrometry (LC-MS/MS)

[0278] In order to quantify oxalate levels in incubation medium, an aliquot of medium was transferred to a polypropylene tube containing 60 µL of 6N HCl /ml medium, vortex mixed, snap frozen, and then stored at -70 °C. On the day of analysis, samples were thawed and vortexed to mix, and then 50 µL of media or media diluted with 0.1% formic acid were transferred with mixing to a polypropylene tube containing 20 µL of internal standard (1 mM $^{13}C_2$-oxalate in 0.1% formic acid) and vortex mixed. A 500 µL aliquot of 2% formic acid was added and vortex mixed. The entire sample was passed through a conditioned Strata-X-AW solid phase extraction plate (Phenomenex, 10 mg, 8E-S038-AGB), washed, and then eluted with 5% ammonium hydroxide in methanol. The eluent was then dried under nitrogen gas, re-constituted in 0.1% formic acid, and then placed on an API6500 autosampler and 5 µL were injected into a 2.1x50 mm Waters XBridge HILIC 3.5 µm particle size column. LC-MS/MS parameters were as indicated in Table 7.

[0279] In order to quantify oxalate levels in urine, urine samples were collected and immediately snap frozen and stored at -70 °C. On the day of analysis, samples were thawed and vortexed, and then 50 µL of urine or urine diluted with 0.1% formic acid was transferred with mixing to a polypropylene tube containing 20 µL of internal standard (1 mM $^{13}C_2$-oxalate + 5 mM $^{2}H_3$-creatinine in 0.1% formic acid) and vortex mixed. A 500 µL aliquot of 2% formic acid was added and vortex mixed. The entire sample was passed through a conditioned Strata-X-AW solid phase extraction plate (Phenomenex, 10 mg, 8E-S038-AGB), washed, and then eluted with 5% ammonium hydroxide in methanol. The eluent was then dried under nitrogen gas, re-constituted in 0.1% formic acid, and then placed on an API6500 autosampler and 5 µL were injected into a 2.1x50 mm Waters XBridge HILIC 3.5 µm particle size column. LC-MS/MS parameters were as indicated in Table 7.

TABLE 7.

Time (min)	% Eluent B
Initial	89.5
1	89.5
2.5	0
4.20	0
4.21	89.5
6.69	89.5
6.70	End
Eluent A: 95:5 20mM Ammonium Acetate pH 8:Acetonitrile	
Eluent B: Acetonitrile	
Autosampler Wash: 50% methanol	
Flow rate: 500 µL/min	
Column temperature: 50°C	
Divert output to waste from initial to 1.5 min and after 4.5 min	

Example 5: *in vivo* oxalate metabolization in Balb/c male mice treated with a microbial consortium containing commercial strains of microbes

[0280] This example describes a study testing the ability of a microbial consortium, containing commercial strains of microbes, to degrade oxalate *in vivo* in Balb/c male mice.

[0281] To determine the *in vivo* oxalate degrading activity of a microbial consortium described herein, 30 gnotobiotic (n = 3 per condition) Balb/c male mice were weighed on Day 0 and colonized by oral gavage with either a plurality of active microbes alone, a supportive community alone, *O. formigenes* alone, or a complete microbial consortium (active and supportives). The plurality of active microbes and the supportive community of microbes contained the strains in Table 8 marked with an 'X' in the indicated column. Colonized mice were fed either a defined, low-complexity diet supplemented with excess oxalate in order to induce hyperoxaluria (*see* Table 2 above) or a nutritionally equivalent control diet lacking oxalate (*see* Table 1 above).

[0282] After a two-week period, mice were sacrificed and a variety of samples were collected including terminal urine, feces, serum, kidneys, liver, gall bladder, cecum and spleen.

TABLE 8

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Acidaminococcus fermentans	DSM 20731	Supportive				X
Acidaminococcus intestini	HM-81	Supportive		X		X
Adlercreutzia equolifaciens	DSM 19450	Supportive		X		X
Akkermansia muciniphila	ATCC BAA-835	Supportive		X		X
Alistipes finegoldii	DSM 17242	Supportive		X		X
Alistipes indistinctus	DSM 22520	Supportive		X		X
Alistipes onderdonkii	DSM 19147	Supportive		X		X
Alistipes putredinis	DSM 17216	Supportive				X
Alistipes senegalensis	DSM 25460	Supportive		X		X
Alistipes shahii	DSM 19121	Supportive		X		X
Anaerobutyricum hallii	DSM 3353	Supportive				X
Anaerococcus lactolyticus	DSM 7456	Supportive				
Anaerofustis stercorihominis	DSM 17244	Supportive				X
Anaerostipes caccae	DSM 14662	Supportive		X		X
Anaerotruncus colihominis	DSM 17241	Supportive		X		X

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Bacteroides caccae	ATCC 43185	Supportive		X		X
Bacteroides caccae	HM-728	Supportive				
Bacteroides cellulosilyticus	DSM 14838	Supportive		X		X
Bacteroides cellulosilyticus	HM-726	Supportive				
Bacteroides coprocola	DSM 17136	Supportive		X		X
Bacteroides coprophilus	DSM 18228	Supportive		X		X
Bacteroides dorei	DSM 17855	Supportive		X		X
Bacteroides dorei	HM-27	Supportive		X		X
Bacteroides dorei	HM-29	Supportive		X		X
Bacteroides dorei	HM-718	Supportive				
Bacteroides eggerthii	DSM 20697	Supportive		X		X
Bacteroides eggerthii	HM-210	Supportive				
Bacteroides finegoldii	DSM 17565	Supportive		X		X
Bacteroides finegoldii	HM-727	Supportive				
Bacteroides fragilis	HM-20	Supportive		X		X
Bacteroides fragilis	HM-58	Supportive		X		X
Bacteroides fragilis	HM-709	Supportive				

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Bacteroides fragilis	HM-710	Supportive				
Bacteroides intestinalis	DSM 17393	Supportive		X		X
Bacteroides ovatus	ATCC 8483	Supportive		X		X
Bacteroides ovatus	HM-222	Supportive				
Bacteroides pectinophilus	ATCC 43243	Supportive				X
Bacteroides plebeius	DSM 17135	Supportive				X
Bacteroides rodentium	DSM 26882	Supportive		X		X
Bacteroides salyersiae	HM-725	Supportive				
Bacteroides sp.	HM-28	Supportive		X		X
Bacteroides stercoris	DSM 19555	Supportive		X		X
Bacteroides stercoris	HM-1036	Supportive				
Bacteroides thetaiotaomicron	ATCC 29148	Supportive		X		X
Bacteroides thetaiotaomicron	HM-23	Supportive				X
Bacteroides uniformis	ATCC 8492	Supportive		X		X
Bacteroides vulgatus	ATCC 8482	Supportive		X		X
Bacteroides vulgatus	HM-720	Supportive				

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Bacteroides xylanisolvens	DSM 18836	Supportive		X		X
Bacteroides xylanisolvens	HM-18	Supportive		X		X
Bifidobacterium adolescentis	HM-633	Supportive				
Bifidobacterium angulatum	HM-1189	Supportive				
Bifidobacterium animalis	DSM 20104	Supportive				
Bifidobacterium animalis	DSMZ 10140	Supportive				
Bifidobacterium bifidum	ATCC 11863	Supportive				
Bifidobacterium breve	DSM 20213	Supportive		X		X
Bifidobacterium catenulatum	DSM 16992	Supportive		X		X
Bifidobacterium dentium	ATCC 27678	Active	X		X	
Bifidobacterium dentium	ATCC 27680	Active	X		X	
Bifidobacterium dentium	DSM 20221	Active	X		X	
Bifidobacterium dentium	DSM 20436	Active	X		X	
Bifidobacterium dentium	HM-868	Active	X		X	
Bifidobacterium infantis	ATCC 55813	Supportive				
Bifidobacterium longum	HM-845	Supportive				

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Bifidobacterium longum	HM-846	Supportive				
Bifidobacterium longum	HM-847	Supportive				
Bifidobacterium longum	HM-848	Supportive				
Bifidobacterium pseudocatenulatum	DSM 20438	Supportive		X		X
Bilophila wadsworthia	ATCC 49260	Supportive		X		X
Bilophila wadsworthia	DSM 11045	Supportive				
Bittarella massiliensis	ATCC 29733	Supportive		X		X
Bittarella massiliensis	DSM 4029	Supportive				
Blautia hansenii	DSM 20583	Supportive		X		X
Blautia hydrogenotrophica	DSM 10507	Supportive				X
Blautia massiliensis	HM-1032	Supportive		X		X
Blautia obeum	DSMZ 25238	Supportive		X		X
Blautia wexlerae	DSM 19850	Supportive				X
Butyricimonas virosa	DSM 23226	Supportive		X		X
Butyrivibrio crossotus	DSM 2876	Supportive				X

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Catenibacterium mitsuokai	DSM 15897	Supportive		X		X
Cetobacterium somerae	DSM 23941	Supportive				
Clostridium asparagiforme	DSM 15981	Supportive		X		X
Clostridium bolteae	DSM 15670	Supportive				X
Clostridium bolteae	HM-1038	Supportive				
Clostridium bolteae	HM-318	Supportive				
Clostridium cadaveris	HM-1040	Supportive				
Clostridium citroniae	HM-315	Supportive				
Clostridium hiranonis	DSM 13275	Supportive		X		X
Clostridium hylemonae	DSM 15053	Supportive		X		X
Clostridium innocuum	HM-173	Supportive				
Clostridium leptum	DSM 753	Supportive		X		X
Clostridium methylpentosum	DSM 5476	Supportive				X
Clostridium nexile	DSM 1787	Supportive		X		X
Clostridium orbiscindens	HM-303	Supportive				X
Clostridium orbiscindens	HM-1044	Supportive				

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Clostridium saccharolyticum	DSM 2544	Supportive		X		X
Clostridium saccharolyticum	HM-635	Supportive				X
Clostridium scindens	DSM 5676	Supportive		X		X
Clostridium scindens	VPI 12708	Supportive				
Clostridium sp.	HM-634	Supportive		X		X
Clostridium spiroforme	DSM 1552	Supportive				X
Clostridium sporogenes	ATCC 15579	Supportive				
Clostridium sporogenes	ATCC 17889	Supportive				
Clostridium sporogenes	DSM 767	Supportive				
Clostridium symbiosum	HM-309	Supportive				
Clostridium symbiosum	HM-319	Supportive				
Collinsella aerofaciens	ATCC 25986	Supportive		X		X
Collinsella stercoris	DSM 13279	Supportive		X		X
Coprococcus catus	ATCC 27761	Supportive				
Coprococcus comes	ATCC 27758	Supportive		X		X
Coprococcus eutactus	ATCC 27759	Supportive				X

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Coprococcus eutactus	ATCC 51897	Supportive				
Coprococcus sp.	DSM 21649	Supportive				
Desulfovibrio piger	ATCC 29098	Supportive		X		X
Dialister invisus	DSM 15470	Active	X		X	
Dialister pneumosintes	ATCC 51894	Supportive				
Dorea formicigenerans	ATCC 27755	Supportive		X		X
Dorea longicatena	DSM 13814	Supportive		X		X
Eggerthella lenta	ATCC 43055	Active	X		X	
Eggerthella lenta	DSM 2243	Active	X		X	
Eggerthella lenta	DSM 11767	Supportive				
Eggerthella lenta	DSM 11863	Supportive				
Eggerthella lenta	HM-1099	Supportive				
Enterococcus faecalis	HM-202	Active	X		X	
Enterococcus faecalis	HM-432	Active			X	
Ethanoligenens harbinense	DSM 18485	Supportive				X
Eubacterium dolichum	DSM 3991	Supportive		X		X
Eubacterium eligens	ATCC 27750	Supportive				

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Eubacterium rectale	ATCC 33656	Supportive		X		X
Eubacterium siraeum	DSM 15702	Supportive		X		X
Eubacterium ventriosum	ATCC 27560	Supportive		X		X
Faecalibacterium prausnitzii	DSM 17677	Supportive		X		X
Faecalibacterium prausnitzii	ATCC 27766	Supportive				
Faecalibacterium prausnitzii	ATCC 27768	Supportive				
Faecalibacterium prausnitzii	HM-473	Supportive				
Granulicatella adiacens	ATCC 49175	Supportive		X		X
Holdemanella biformis	DSM 3989	Supportive		X		X
Holdemania filiformis	DSM 12042	Supportive		X		X
Hungatella hathewayi	DSM 13479	Supportive		X		X
Hungatella hathewayi	HM-308	Supportive				
Intestinibacter bartlettii	DSM 16795	Supportive				X
Intestinimonas butyriciproducens	DSM 26588	Supportive				X
Lactobacillus acidophilus	DSM 20079	Active	X		X	
Lactobacillus acidophilus	ATCC 4357	Active				

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Lactobacillus acidophilus	DSM 20242	Active				
Lactobacillus amylovorus	DSM 20552	Supportive				
Lactobacillus casei	ATCC 393	Supportive				
Lactobacillus casei	ATCC 39539	Supportive				
Lactobacillus crispatus	HM-370	Supportive				
Lactobacillus gasseri	ATCC 33323	Active	X		X	
Lactobacillus gasseri	DSMZ 107525	Active				
Lactobacillus gasseri	DSMZ 20077	Active				
Lactobacillus gasseri	HM-104	Active				
Lactobacillus gasseri	HM-644	Active				
Lactobacillus helveticus	DSM 20075	Active	X		X	
Lactobacillus johnsonii	HM-643	Supportive				
Lactobacillus parafarraginis	HM-478	Supportive				
Lactobacillus plantarum	ATCC 14917	Supportive				
Lactobacillus plantarum	ATCC 202195	Supportive				
Lactobacillus reuteri	HM-102	Active	X		X	

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Lactobacillus rhamnosus	DSM 20245	Active	X		X	
Lactobacillus rhamnosus	HM-106	Active	X		X	
Lactobacillus rhamnosus	ATCC 53103	Active				
Lactobacillus rhamnosus	DSM 8746	Active				
Lactobacillus ruminis	ATCC 25644	Supportive		X		X
Lactobacillus ruminis	DSM 20404	Supportive				
Lactobacillus ultunensis	DSM 16048	Supportive				
Lactococcus lactis	DSM 20729	Supportive				
Marvinbryantia formatexigens	DSM 14469	Supportive		X		X
Megasphaera indica	DSM 25562	Supportive				
Megasphaera stantonii	DSM 102144	Supportive		X		X
Methanobrevibacter smithii	DSM 11975	Supportive				
Methanobrevibacter smithii	DSM 2374	Supportive				
Methanobrevibacter smithii	DSM 2375	Supportive				
Methanobrevibacter smithii	DSM 861	Supportive				

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Methanomassiliicoccus luminyensis	DSM 25720	Supportive				
Methanosphaera stadtmanae	DSM 3091	Supportive				
Mitsuokella multacida	DSM 20544	Supportive		X		X
Odoribacter splanchnicus	DSM 20712	Supportive		X		X
Olsenella uli	DSM 7084	Supportive		X		X
Oscillibacter welbionis	HM-1030	Supportive				X
Oxalobacter formigenes	ATCC 35274	Active	X		X	
Oxalobacter formigenes	HM-1	Active	X		X	
Oxalobacter formigenes	DSM 4420	Active				
Oxalobacter vibrioformis	DSM 5502	Supportive				
Oxalophagus oxalicus	ATCC 49686	Supportive				
Parabacteroides distasonis	HM-19	Supportive		X		X
Parabacteroides distasonis	HM-77	Supportive		X		X
Parabacteroides goldsteinii	HM-1050	Supportive				
Parabacteroides johnsonii	DSM 18315	Supportive		X		X

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Parabacteroides johnsonii	HM-731	Supportive				
Parabacteroides merdae	DSM 19495	Supportive				X
Parabacteroides merdae	HM-729	Supportive				
Parabacteroides merdae	HM-730	Supportive				
Peptostreptococcus anaerobius	DSM 2949	Supportive				
Prevotella buccae	HM-45	Supportive				
Prevotella buccalis	DSM 20616	Supportive		X		X
Prevotella copri	DSM 18205	Supportive				X
Prevotella histicola	DSM 26979	Supportive				
Proteocatella sphenisci	DSM 23131	Supportive				
Providencia rettgeri	ATCC BAA-2525	Supportive				
Roseburia intestinalis	DSM 14610	Supportive				
Roseburia inulinivorans	DSM 16841	Supportive		X		X
Ruminococcaceae sp.	HM-79	Supportive				
Ruminococcus albus	ATCC 27210	Supportive				
Ruminococcus bromii	ATCC 27255	Supportive				

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Ruminococcus bromii	ATCC 51896	Supportive				
Ruminococcus gauvreauii	DSM 19829	Supportive		X		X
Ruminococcus gnavus	ATCC 29149	Supportive		X		X
Ruminococcus gnavus	DSM 108212	Supportive				
Ruminococcus gnavus	HM-1056	Supportive				
Ruminococcus lactaris	ATCC 29176	Supportive				X
Ruminococcus lactaris	HM-1057	Supportive				
Ruminococcus torques	ATCC 27756	Supportive		X		X
s__Parabacteroides distasonis	ATCC 8503	Supportive		X		X
Slackia exigua	DSM 15923	Supportive				X
Slackia heliotrinireducens	DSM 20476	Supportive				X
Solobacterium moorei	DSM 22971	Supportive		X		X
Streptococcus thermophilus	ATCC BAA-491	Supportive		X		X
Streptococcus thermophilus	ATCC 14485	Supportive				
Subdoligranulum variabile	DSM 15176	Supportive				X
Turicibacter sanguinis	DSM 14220	Supportive				X

			Examples 5 and 8		Examples 6, 7, 12, 13, 14	
Species	**Catalog Number**	**Active or Supportive**	**Active**	**Support-ive**	**Active**	**Support-ive**
Veillonella dispar	ATCC 17748	Supportive				
Veillonella parvula	HM-49	Supportive				
Veillonella parvula	HM-64	Supportive				

[0283] FIGURE 5A and FIGURE 5B show the % body weight gain and food consumption, respectively, of the uncolonized mice, mice gavaged with either *O. formigenes* alone, active microbes alone, supportive microbes alone, or a complete microbial consortium (active and supportives) as described above.

[0284] Table 9 shows the incidence of diarrhea in the uncolonized mice, mice gavaged with either *O. formigenes* alone, active microbes alone, supportive microbes alone, or a complete microbial consortium (active and supportives) as described above. Mice treated with a complete microbial consortium were observed to have normal stool pellets and a reduced incidence of diarrhea.

TABLE 9

Uncolonized		***O. formigenes***		**Actives**		**Supportives**		**Full Community**	
Control Diet	Oxalate Diet	Control Diet	Oxalate Diet	Control Diet	Oxalate Diet	Control Diet	Oxalate Diet	Control Diet	Oxalate Diet
3/3	3/3	3/3	3/3	3/3	3/3	3/3	3/3	0/3	0/3
Runny stool						Soft stool		Normal stool	

[0285] Table 10 shows the incidence of fatty liver in the uncolonized mice, mice gavaged with either *O. formigenes* alone, active microbes alone, supportive microbes alone, or a complete microbial consortium (active and supportives) as described above.

TABLE 10

Uncolonized		***O. formigenes***		**Actives**		**Supportives**		**Full Community**	
Control Diet	Oxalate Diet	Control Diet	Oxalate Diet	Control Diet	Oxalate Diet	Control Diet	Oxalate Diet	Control Diet	Oxalate Diet
0/3	0/3	1/3	2/3	0/3	1/3	0/3	2/3	0/3	0/3
No Fatty Liver		Fatty Liver observed in 6/18 mice						No Fatty Liver	

Urinary Oxalate Concentrations

[0286] To assess the effect of a microbial consortium described herein on steady-state levels of oxalate in urine, which correlates well with human urolithiasis, urine was terminally collected from all test groups. Each mouse was transferred to the bottom of a standard petri dish, placed into a CO_2 chamber, and administered CO_2 for 90 seconds according to the approved IACUC protocol until the mouse ceased moving and was lying prone on the chamber floor. The CO_2 chamber lid was opened and the anaesthetized mouse was placed on its side on the petri dish. The CO_2 chamber lid was then replaced and terminal urination collected in the petri dish and transferred to a sterile microcentrifuge tube. Urine samples were processed and prepared for solid phase extraction followed by LC/MS-based analysis as described in Example 4 above.

[0287] As shown in Table 11 and FIGURE 6A-B, mice fed with control diet lacking supplemental oxalate predictably exhibited low levels of urinary oxalate (1.2 mM in uncolonized controls) compared with mice fed a diet containing excess oxalate (11.9 mM in uncolonized controls), showing that dietary supplementation with oxalate can induce hyperoxaluria in gnotobiotic mice.

[0288] Regardless of diet, the lowest levels of urinary oxalate were observed in mice colonized with the complete microbial consortium (active and supportives); average oxalate levels in consortium-colonized mice fed the oxalate-free (control) diet were approximately 50% lower than observed in uncolonized mice, and in animals fed the high oxalate diet, steady-state urinary oxalate levels were approximately 66% lower in consortium-colonized mice compared to uncolonized controls (4.5 mM vs. 11.9 mM).

[0289] Mice treated with a complete microbial consortium outperformed mice treated with the plurality of active microbes and supportive community of microbes alone, as well as mice treated with *O. formigenes* alone, with respect to urinary oxalate concentrations. Mice colonized with *O. formigenes* alone or the plurality of active microbes alone and fed the

oxalate-supplemented diet exhibited urinary oxalate concentrations that were not significantly different from those observed in uncolonized mice. Furthermore, mice colonized with the supportive community of microbes alone exhibited significantly higher urinary oxalate levels than uncolonized controls (16.7 mM and 11.9 mM, respectively). Whereas colonization with either the plurality of active microbes alone or the supportive community alone did not reduce levels of urinary oxalate, colonization with the full consortium resulted in a synergistic drop in urinary oxalate concentration.

TABLE 11

Communities	**Urinary Oxalate (mM) n=3 mice/group**	
	Oxalate Diet	**Control Diet**
Control (gnotobiotic)	11.9 ± 1.8	1.2 ± 0.2
Supportive Community only	16.7 ± 3.0	0.6 ± 0.1
O. formigenes only	10.5 ± 2.2	1.2 ± 0.2
Plurality of Active Microbes only	9.5 ± 0.4	1.5 ± 0.2
Full Microbial Consortium (Active + Supportive)	4.5 ± 0.1	0.6 ± 0.1

Serum Liver Enzyme Assay

[0290] Mouse serum samples were analyzed for a standard panel of serum liver enzymes by the Charles River Laboratories. FIGURES 7A, 7B, 7C, 7D, 7E, 7F, 7G, and 7H show serum levels or function of alanine transaminase, aspartate transaminase, albumin, alanine phosphatase, albumin/globulin ratio, total bilirubin, gamma-glutamyl transferase, and prothrombin time, respectively, in gnotobiotic Balb/c mice on a normal (non-bold) or high oxalate diet (**bold**), treated by gavage with *Oxalobacter formigenes* only (*O. formigenes*), active strains only (Active), supportive strains only (Supportive), both active and supportive strains (Active and Supportive), or saline vehicle control (Saline) as described above.

Kidney Function Assay

[0291] Mouse serum samples were analyzed for a standard panel of serum kidney metabolites/electrolytes by the Charles River Laboratories. FIGURES 8A, 8B, 8C, 8D, 8E, 8F, 8G, and 8H show serum levels of urea, creatinine, phosphorus, calcium, chloride, sodium, potassium, and globulin, respectively, in gnotobiotic Balb/c mice on a normal (non-bold) or high oxalate diet **(bold)**, treated by gavage with *Oxalobacter formigenes* only (*O. formigenes*), active strains only (Active), supportive strains only (Supportive), both active and supportive strains (Active + Supportive), or saline vehicle control (Saline) as described above.

Triglyceride, Cholesterol, Glucose and Creatine Kinase Assay

[0292] Mouse serum samples were analyzed for a standard triglyceride, cholesterol, glucose and creatine kinase panel by the Charles River Laboratories. FIGURES 9A, 9B, 9C, and 9D shows serum triglyceride, cholesterol, glucose, and creatine kinase levels, respectively, in gnotobiotic Balb/c mice on a normal (non-bold) or high oxalate diet **(bold)**, treated by gavage with *Oxalobacter formigenes* only (*O. formigenes*), active strains only (Active), supportive strains only (Supportive), both active and supportive strains (Active + Supportive), or saline vehicle control as described above.

Example 6: i*n vivo* oxalate metabolization in C57/B6 female mice treated with a microbial consortium containing commercial strains of microbes

[0293] This example describes a study testing the ability of a microbial consortium, containing commercially-sourced strains of microbes, to degrade oxalate *in vivo* in C57/B6 female mice.

[0294] To test whether the *in vivo* activity of a microbial consortium as presently described was observed in a different sex and strain of study mouse, female C57/B6 mice (n = 3 per condition) were colonized by oral gavage with either a plurality of active microbes alone, a supportive community alone, a supportive community plus *O. formigenes* alone, a supportive community plus a plurality of active microbes lacking *O. formigenes*, a complete microbial consortium (active and supportives), or a fecal sample from a human donor found to be positive for *O. formigenes* DNA. The plurality of active microbes and the supportive community contained the strains in Table 8 marked with an 'X' in the indicated columns. Colonized mice were fed either a defined, low-complexity diet supplemented with excess oxalate in order to induce hyperoxaluria (*see* Table 2 above) or a nutritionally equivalent

control diet lacking oxalate (*see* Table 1 above). After a two-week period, mice were sacrificed and urine, stool, serum and tissue samples were collected for analysis.

Urinary Oxalate Concentrations

[0295] Urine was terminally collected from all groups and processed for solid phase extraction followed by LC-MS-based analysis of oxalate concentrations as described in Example 4. Absolute oxalate concentrations detected in individual urine samples were normalized based on the ratio of oxalate to creatinine.

[0296] As shown in Table 12, urinary oxalate levels were reduced in mice colonized with the complete microbial consortium. Partial reduction was also observed in mice colonized with the supportive community alone, the supportive community plus the plurality of active microbes lacking *O. formigenes*, and the plurality of active microbes alone.

TABLE 12

Communities	**Normalized Urinary Oxalate (mM) n=3 mice/group**	
	Oxalate:Creatinine (μM)	**% of Urinary Oxalate (normalized) in Supportive Only**
Control (gnotobiotic)	4.5 ± 0.73	120.4% ± 19.6
Supportive Community only	3.74 ± 1.27	100.0% ± 34.0
Plurality of Active Microbes only	2.13 ± 1.81	57% ± 48.4
Supportive Community + *O. formigenes*	2.10 ± 0.90	56.1% ± 24.0
Supportive Community + Plurality of Active Microbes (minus *O. formigenes*)	2.82 ± 1.94	75.5% ± 52.0
Full Microbial Consortium (Active + Supportive)	0.91 ± 0.42	24.3% ± 11.3
Human donor fecal sample (*O. formigenes* positive)	1.64 ± 1.49	44.0% ± 40.0

Example 7: in *vivo* oxalate metabolization in C57/B6 female mice treated with frozen stocks of microbial consortium

[0297] To test whether a microbial consortium as presently described maintains *in vivo* activity after freezing, individual live microbial cultures of commercially-sourced strains were pooled in approximately equal proportions to form a supportive community alone, a supportive community plus a plurality of active microbes lacking *O. formigenes,* and an *O. formigenes* community comprising two commercial strains of *O. formigenes,* and frozen as aliquots in 30% glycerol in the vapor phase of a liquid nitrogen dewar for one month prior to administration to mice. The plurality of active microbes and the supportive community contained the strains in Table 8 marked with an 'X' in the indicated column.

[0298] Gnotobiotic, female, C57/B6 mice (n = 3 per condition) were colonized by oral gavage with either a plurality of active microbes alone (including *O. formigenes),* a supportive community alone, or a complete microbial consortium (active and supportives). Hyperoxaluria was induced in colonized mice by providing *ad libitum* drinking water sweetened with sucralose and containing 0.875% oxalate. Control mice were provided with sucralose-sweetened drinking water without oxalate. All mice were maintained on a standard Autoclavable Mouse Breeder Diet (LabDiet®, St. Louis, MO). After a two week period, mice were sacrificed and a variety of samples were collected including urine, stool, serum, and kidneys.

Urinary Oxalate Concentrations

[0299] As in Example 6, urine was terminally collected from all groups and processed for solid phase extraction followed by LC/MS-based analysis of oxalate concentrations. Absolute oxalate concentrations detected in individual urine samples were normalized based on the ratio of oxalate to creatinine.

[0300] As shown in Table 13, mice provided with drinking water containing 0.875% oxalate exhibited significantly elevated levels of urinary oxalate compared with mice given control water *(e.g.,* an approximate 4-fold increase in both the mice administered with the plurality of active microbes alone and the mice administered with the supportive community alone). Consistent with Examples 5 and 6, mice colonized with the complete microbial consortium had significantly lower urinary oxalate levels compared with the mice administered with the plurality of active microbes alone or the mice administered with the supportive community alone. Furthermore, as compared to Examples 5 and 6, the complete

microbial consortium still exhibited significant oxalate metabolizing activity in mice maintained on a markedly different standard dietary formulation

TABLE 13

Communities	Oxalate:Creatinine (μM)	SD
No Oxalate Treatment		
Supportive Community+ Plurality of Active Microbes	0.254	0.021
Supportive Community only	0.246	0.025
Plurality of Active Microbes only	0.279	0.019
0.875% Oxalate Treatment		
Supportive Community+ Plurality of Active Microbes	0.618	0.085
Supportive Community only	0.937	0.111
Plurality of Active Microbes only	2.427	2.284

Example 8: *in vivo* engraftment of oxalate-metabolizing microbial strains

[0301] Stool samples from the treated mice described in Example 5 were analyzed for the presence of oxalate-metabolizing microbial strains by whole genome shotgun sequencing of microbial DNA extracted from fecal pellets. DNA extraction from fecal samples and whole genome shotgun sequencing were performed by methods as previously described in Example 1. Sequence reads were mapped against a comprehensive database of complete, sequenced genomes of all the defined microbial strains comprising the microbial consortium. The results of this experiment are summarized in FIGURES 10A-F.

[0302] Table 14 shows detection of engrafted oxalate-metabolizing active microbial strains in the treated mice described in Example 5. Microbial strains were counted as "detected" if their relative abundance was >0.1% of total sequence reads.

TABLE 14

Active community component	**Actives-only** (Control Diet)	**Actives-only** (Oxalate Diet)	**Actives + Supportives** (Control Diet)	**Actives + Supportives** (Oxalate Diet)
Oxalobacter formigenes	0 %	100 %	0 %	100 %
Bifidobacterium dentium	100 %	100 %	0 %	0 %
Eggerthella lenta	100 %	100 %	0 %	0 %
Enterococcus faecalis	100 %	100 %	0 %	0 %
Lactobacillus rhamnosus	100 %	100 %	0 %	0 %
Dialister invisus	33.3 %	66.6 %	0 %	0 %
Lactobacillus helveticus	33.3 %	0 %	0 %	0 %
Lactobacillus acidophilus	0 %	0 %	0 %	0 %
Lactobacillus gasseri	0 %	0 %	0 %	0 %
Lactobacillus reuteri	0 %	0 %	0 %	0 %

[0303] Table 15 shows detection of engrafted supportive microbial strains in the treated mice described in Example 5. Microbial strains were counted as "detected" if their relative abundance was >0.1% of total sequence reads.

TABLE 15

Supportive Community Component	**Supportives-only** (Control Diet)	**Supportives-only** (Oxalate Diet)	**Actives + Supportives** (Control Diet)	**Actives + Supportives** (Oxalate Diet)
13 species	100 %	100 %	100 %	100 %
Alistipes senegalensis	100 %	0 %	66.6 %	100 %

Catenibacterium mitsuokai	100 %	0 %	66.6 %	10 0%
Bacteroides coprocola	0 %	0 %	0 %	100 %
Clostridium scindens	0 %	0 %	66.6 %	66.6 %
Bacteroides cellulosilyticus	100 %	0 %	66.6 %	0 %
Tyzzerella nexilis	100 %	0 %	66.6 %	0 %
17 species	0 to 100 %	0 to 100 %	0 to 100 %	0 to 100 %
33 species	0 %	0 %	0 %	0 %

Example 9: *in vitro* oxalate metabolization by donor-derived strains

[0304] In order to determine the *in vitro* oxalate-metabolizing activity of three donor-derived *O. formigenes* strains, strains were grown in YFCAC base medium at either pH 7.0, 6.0, or 5.0 in the presence of 80 mM oxalate. Strains were incubated at 37 °C for 72, and at the conclusion of the protocol the amount of oxalate in the medium was quantified by LC-MS as described in Example 4. For all three strains, the amount of oxalate remaining in the culture medium after 72 hours was below the limit of detection when assayed at pH 7.0 or 6.0. No oxalate degradation was detected for cultures of any of the three strains when incubated at pH 5.0.

[0305] To determine the oxalate-metabolizing activity of additional donor-derived microbial strains, strains were grown in anaerobic conditions in YCFAC base medium at either pH 7.0, 6.0, or 5.0 in the presence of 2 mM oxalate. Strains were incubated at 37 °C for 120 hours, and at the conclusion of the protocol the amount of oxalate in the medium was quantified by LC/MS as described in Example 4. A donor-derived strain of *O. formigenes* was included as a positive control. Results are reported as the percentage of oxalate remaining in the media at the conclusion of the assay relative to the starting concentration (FIGURE 11). As expected, the amount of oxalate remaining in a culture of donor-derived *O. formigenes* was below the limit of detection when assayed at pH 6 or pH 7, although no oxalate degradation was detected at pH 5. By contrast, none of the other tested donor-derived isolates were found to reduce oxalate by more than 11% at any pH tested.

Example 10: Growth of donor-derived *O. formigenes* strains at different pHs and oxalate concentrations

[0306] Three *O. formigenes* strains isolated from donor fecal samples were assayed for their ability to grow at different pHs (5.0, 6.0, or 7.0) and at different oxalate concentrations (0 mM, 2 mM, 40 mM, 80 mM, 120 mM, 160 mM). Strains were grown under anaerobic conditions in the appropriate banking medium, and culture turbidity was recorded after 24, 48, 72, and 144 hours. The results of this assay are reported in FIGURES 12A-12C. One *O. formigenes* strain (FBI00067) was observed to grow better at a lower pH; another strain (FBI00133) was observed to be more tolerant of higher oxalate concentrations.

Example 11: Design of supportive communities comprising donor-derived strains

[0307] Supportive communities of microbes were designed using donor-derived strains. Five candidate communities were designed according to different design principles.

[0308] The supportive community of candidate consortium I was designed to incorporate all isolated species that were present in more than 50% of a set of healthy donor fecal samples. The community further included donor-derived strains whose identified species had been represented in the proof-of-concept consortium of commercial strains, or (if no matching species had been isolated) then a strain of the species that was the closest relative within the genus. The final consortium (actives and supportives) contained 152 strains and 70 species in total, listed in Table 16.

[0309] The supportive communities of candidate consortia II and III were designed to maximize consumption and/or production of a defined set of metabolites using a minimal number of strains. In both cases, metabolites of interest were identified by conducting a literature review, as well as by bioinformatic annotation of healthy microbiomes. Next, the genomes of donor-derived strains were bioinformatically analyzed to identify strains capable of producing or consuming said metabolites of interest. A literature review was also conducted to identify donor-derived strains belonging to species known to consume and/or produce each metabolite of interest. Donor-derived strains were scored for their ability to produce or consume said metabolite, and the community was designed to maximize the desired metabolic coverage with the fewest number of species. The supportive community of candidate consortium II was designed to enrich for consumption of 51 dietary carbon and energy sources. The supportive community of candidate consortia III was designed to enrich for the production or consumption of metabolites present in the host, including bile acids, sugars, amino acids, vitamins, SCFAs, and gasses. The strains included in candidate

consortium II are listed in Table 17, and the strains included in candidate consortium III are listed in Table 18.

[0310] The supportive community of candidate consortium IV was constructed using strains isolated exclusively from fecal samples of two healthy donors. Sourcing many supportive strains from one or a small number of donors may have the benefit of enhancing co-culturability and/or ecological stability. The two specific donors selected both had stool that was found to be capable of reducing urinary oxalate *in vivo*, potentially enhancing the use of the community in embodiments of the invention designed to degrade oxalate. The strains included in candidate consortium IV are listed in Table 19.

[0311] The supportive community of candidate consortium V was designed to include all strains isolated from healthy donor fecal samples, with the exception of species known to be associated with pathogenesis. This diverse community incorporated species from all five major phyla that comprise normal gut commensals (Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, and Verrucomicrobia). The final consortium contained 103 species and 158 strains in total, which are listed in Table 20.

TABLE 16

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00001	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.64	1
FBI00002	Bacteroides salyersiae	bacteria	bacteroidetes	291644	Bacteroides salyersiae	99.5	2
FBI00004	Neglecta timonensis	bacteria	firmicutes	1776382	Neglecta timonensis	99.14	4
FBI00008	Blautia luti	bacteria	firmicutes	89014	Blautia luti	97.02	8
FBI00010	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.12	10
FBI00011	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.28	11
FBI00012	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.71	12
FBI00013	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.5	13
FBI00015	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	15
FBI00016	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.64	16
FBI00017	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.34	17
FBI00018	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.71	18
FBI00019	Alistipes timonensis	bacteria	bacteroidetes	1465754	Alistipes timonensis	99.78	19
FBI00020	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.57	20
FBI00022	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	99.93	22

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00025	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.21	25
FBI00029	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	99.26	29
FBI00030	Eggerthella lenta	bacteria	firmicutes	84112	Eggerthella lenta	98.47	30
FBI00032	Anaerostipes hadrus	bacteria	firmicutes	649756	Anaerostipes hadrus	99.64	32
FBI00033	Lachnospiraceae sp. FBI00033	bacteria	firmicutes	186803	Clostridium amygdalinum	93.56	33
FBI00034	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.78	34
FBI00036	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.53	36
FBI00038	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	95.96	38
FBI00039	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.71	39
FBI00040	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.38	40
FBI00042	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.71	42
FBI00043	Bifidobacterium dentium	bacteria	actinobacteria	1689	Bifidobacterium dentium	99.35	43
FBI00044	Blautia wexlerae	bacteria	firmicutes	418240	Blautia wexlerae	98.69	44
FBI00046	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.71	46
FBI00047	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.79	47
FBI00050	Bacteroides nordii	bacteria	bacteroidetes	291645	Bacteroides nordii	98.63	50

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00051	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	98.07	51
FBI00052	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.14	52
FBI00056	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.2	56
FBI00057	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.7	57
FBI00058	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.71	58
FBI00059	Bacteroides stercorirosoris	bacteria	bacteroidetes	871324	Bacteroides oleiciplenus	98.81	59
FBI00060	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.49	60
FBI00061	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	99.19	61
FBI00062	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.48	62
FBI00066	Parasutterella excrementihominis	bacteria	proteobacteria	487175	Parasutterella excrementihominis	99.13	66
FBI00067	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	98.84	67
FBI00068	Akkermansia muciniphila	bacteria	verrucomicrobia	239935	Akkermansia muciniphila	99.42	68
FBI00069	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.84	69
FBI00072	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	96.17	72
FBI00073	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	98.99	73
FBI00074	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.03	74

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00075	Paraprevotella clara	bacteria	bacteroidetes	454154	Paraprevotella clara	98.85	75
FBI00076	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.78	76
FBI00078	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.34	78
FBI00085	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.62	85
FBI00086	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.77	86
FBI00087	Clostridium scindens	bacteria	firmicutes	29347	Clostridium scindens	98.28	87
FBI00090	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.71	90
FBI00091	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.86	91
FBI00093	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	99.71	93
FBI00096	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.76	96
FBI00099	Gordonibacter pamelaeae	bacteria	actinobacteria	471189	Gordonibacter pamelaeae	99.56	99
FBI00101	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	97.97	101
FBI00102	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.31	102
FBI00104	Blautia wexlerae	bacteria	firmicutes	418240	Blautia luti	97.18	104
FBI00109	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	98.39	109
FBI00111	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.43	111

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00112	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	112
FBI00113	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.79	113
FBI00115	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	97.98	115
FBI00116	Ruminococcus faecis	bacteria	firmicutes	592978	Ruminococcus faecis	99.57	116
FBI00117	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.52	117
FBI00118	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.84	118
FBI00120	Hungatella effluvii	bacteria	firmicutes	154046	Hungatella hathewayi	98.78	120
FBI00122	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.57	122
FBI00123	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	100	123
FBI00124	Anaerostipes hadrus	bacteria	firmicutes	649756	Anaerostipes hadrus	99.86	124
FBI00125	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	99.64	125
FBI00126	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	98.98	126
FBI00127	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	98.81	127
FBI00130	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.35	130
FBI00132	Gordonibacter pamelaeae	bacteria	actinobacteria	471189	Gordonibacter pamelaeae	99.48	132
FBI00133	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	133

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00135	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.57	135
FBI00137	Bacteroides fragilis	bacteria	bacteroidetes	817	Bacteroides fragilis	99.71	137
FBI00138	Blautia massiliensis	bacteria	firmicutes	1737424	Blautia luti	97.94	138
FBI00139	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.5	139
FBI00142	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.07	142
FBI00143	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.07	143
FBI00145	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	99.14	145
FBI00147	Clostridium bolteae	bacteria	firmicutes	208479	Clostridium bolteae	99.28	147
FBI00151	Clostridium aldenense	bacteria	firmicutes	358742	Clostridium aldenense	98.55	151
FBI00152	Dialister invisus	bacteria	firmicutes	218538	Dialister invisus	99.58	152
FBI00155	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.7	155
FBI00162	Bifidobacterium catenulatum	bacteria	actinobacteria	1686	Bifidobacterium catenulatum	99.14	162
FBI00164	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	98.56	164
FBI00165	Bacteroides massiliensis	bacteria	bacteroidetes	204516	Bacteroides massiliensis	99.71	165

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00167	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.39	167
FBI00168	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.26	168
FBI00169	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	98.7	169
FBI00170	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.61	170
FBI00171	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.45	171
FBI00172	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.05	172
FBI00173	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	100	173
FBI00175	Holdemanella biformis	bacteria	firmicutes	1735	Holdemanella biformis	98.19	175
FBI00177	Parasutterella excrementihominis	bacteria	proteobacteria	487175	Parasutterella excrementihominis	99.71	177
FBI00180	Alistipes sp. FBI00180	bacteria	bacteroidetes	239759	Alistipes senegalensis	97.56	180
FBI00181	Blautia wexlerae	bacteria	firmicutes	418240	Blautia wexlerae	97.17	181
FBI00182	Bacteroides coprocola	bacteria	bacteroidetes	310298	Bacteroides coprocola	99.64	182
FBI00186	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.06	186
FBI00188	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.05	188
FBI00190	Bacteroides finegoldii	bacteria	bacteroidetes	338188	Bacteroides finegoldii	98.91	190
FBI00193	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.64	193

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00194	Ruminococcus faecis	bacteria	firmicutes	592978	Ruminococcus faecis	98.41	194
FBI00199	Clostridium bolteae	bacteria	firmicutes	208479	Clostridium bolteae	99.28	199
FBI00201	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.83	201
FBI00205	Blautia massiliensis	bacteria	firmicutes	1737424	Blautia luti	97.55	205
FBI00206	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.56	206
FBI00208	Anaerotruncus massiliensis	bacteria	firmicutes	1673720	Anaerotruncus colihominis	96.52	208
FBI00211	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.78	211
FBI00212	Clostridium aldenense	bacteria	firmicutes	358742	Clostridium aldenense	99.1	212
FBI00217	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	98.77	217
FBI00218	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.42	218
FBI00219	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	99.78	219
FBI00229	Alistipes senegalensis	bacteria	bacteroidetes	1288121	Alistipes senegalensis	99.19	229
FBI00232	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	98.84	232
FBI00235	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	99.86	235
FBI00238	Alistipes sp. FBI00238	bacteria	bacteroidetes	239759	Alistipes finegoldii	95.84	238
FBI00241	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.34	241
FBI00243	Eubacterium siraeum	bacteria	firmicutes	39492	Eubacterium siraeum	98.53	243

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00244	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	98.69	244
FBI00245	Acidaminococcus intestini	bacteria	firmicutes	187327	Acidaminococcus intestini	99.72	245
FBI00246	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.7	246
FBI00251	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.85	251
FBI00253	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	99.71	253
FBI00254	Eubacterium hallii	bacteria	firmicutes	39488	Eubacterium hallii	99.08	254
FBI00255	Hungatella effluvii	bacteria	firmicutes	1096246	Hungatella hathewayi	98.56	255
FBI00257	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	99.28	257
FBI00258	Turicibacter sanguinis	bacteria	firmicutes	154288	Turicibacter sanguinis	99.93	258
FBI00259	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.7	259
FBI00260	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.64	260
FBI00262	Bacteroides massiliensis	bacteria	bacteroidetes	204516	Bacteroides massiliensis	99.71	262
FBI00263	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.56	263
FBI00265	Bacteroides cellulosilyticus	bacteria	bacteroidetes	246787	Bacteroides cellulosilyticus	99.21	265

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	%Match (16S)	SEQ ID NO: X
FBI00266	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	99.2	266
FBI00267	Anaerofustis stercorihominis	bacteria	firmicutes	214853	Anaerofustis stercorihominis	97.29	267
FBI00269	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	100	269
FBI00271	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	98.42	271
FBI00274	Eubacterium xylanophilum	bacteria	firmicutes	39497	Eubacterium xylanophilum	93.5	274
FBI00275	Holdemanella biformis	bacteria	firmicutes	1735	Holdemanella biformis	98.99	275
FBI00276	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	98.19	276
FBI00277	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.63	277
FBI00278	Eubacterium ventriosum	bacteria	firmicutes	39496	Eubacterium ventriosum	94.14	278
FBI00283	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	96.02	283
FBI00288	Blautia hydrogenotrophica	bacteria	firmicutes	53443	Blautia hydrogenotrophica	99.57	288
FBI00289	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	289

TABLE 17

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00001	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.64	1
FBI00002	Bacteroides salyersiae	bacteria	bacteroidetes	291644	Bacteroides salyersiae	99.5	2
FBI00004	Neglecta timonensis	bacteria	firmicutes	1776382	Neglecta timonensis	99.14	4
FBI00011	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.28	11
FBI00013	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.5	13
FBI00015	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	15
FBI00016	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.64	16
FBI00018	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.71	18
FBI00020	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.57	20
FBI00029	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	99.26	29
FBI00030	Eggerthella lenta	bacteria	firmicutes	84112	Eggerthella lenta	98.47	30
FBI00033	Lachnospiraceae sp. FBI00033	bacteria	firmicutes	186803	Clostridium amygdalinum	93.56	33
FBI00039	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.71	39

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00040	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.38	40
FBI00043	Bifidobacterium dentium	bacteria	actinobacteria	1689	Bifidobacterium dentium	99.35	43
FBI00046	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.71	46
FBI00056	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.2	56
FBI00057	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.7	57
FBI00058	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.71	58
FBI00060	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.49	60
FBI00062	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.48	62
FBI00064	Dorea sp. FBI00064	bacteria	firmicutes	189330	Ruminococcus gnavus	95.58	64
FBI00067	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	98.84	67
FBI00068	Akkermansia muciniphila	bacteria	verrucomicrobia	239935	Akkermansia muciniphila	99.42	68
FBI00069	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.84	69
FBI00073	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	98.99	73
FBI00074	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.03	74

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00076	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.78	76
FBI00077	Sutterella wadsworthensis	bacteria	proteobacteria	40545	Sutterella wadsworthensis	99.86	77
FBI00085	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.62	85
FBI00086	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.77	86
FBI00087	Clostridium scindens	bacteria	firmicutes	29347	Clostridium scindens	98.28	87
FBI00091	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.86	91
FBI00096	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.76	96
FBI00099	Gordonibacter pamelaeae	bacteria	actinobacteria	471189	Gordonibacter pamelaeae	99.56	99
FBI00101	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	97.97	101
FBI00102	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.31	102
FBI00109	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	98.39	109
FBI00111	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.43	111
FBI00112	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	112
FBI00113	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.79	113
FBI00122	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.57	122
FBI00125	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	99.64	125

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00126	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	98.98	126
FBI00127	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	98.81	127
FBI00130	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.35	130
FBI00132	Gordonibacter pamelaeae	bacteria	actinobacteria	471189	Gordonibacter pamelaeae	99.48	132
FBI00133	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	133
FBI00135	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.57	135
FBI00137	Bacteroides fragilis	bacteria	bacteroidetes	817	Bacteroides fragilis	99.71	137
FBI00139	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.5	139
FBI00142	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.07	142
FBI00143	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.07	143
FBI00145	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	99.14	145
FBI00162	Bifidobacterium catenulatum	bacteria	actinobacteria	1686	Bifidobacterium catenulatum	99.14	162
FBI00164	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	98.56	164

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00165	Bacteroides massiliensis	bacteria	bacteroidetes	204516	Bacteroides massiliensis	99.71	165
FBI00167	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.39	167
FBI00168	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.26	168
FBI00169	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	98.7	169
FBI00170	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.61	170
FBI00171	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.45	171
FBI00172	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.05	172
FBI00173	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	100	173
FBI00186	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.06	186
FBI00192	Sutterella wadsworthensis	bacteria	proteobacteria	40545	Sutterella wadsworthensis	99.71	192
FBI00197	Bifidobacterium bifidum	bacteria	actinobacteria	1681	Bifidobacterium bifidum	99.85	197
FBI00201	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.83	201
FBI00208	Anaerotruncus massiliensis	bacteria	firmicutes	1673720	Anaerotruncus colihominis	96.52	208
FBI00210	Bifidobacterium bifidum	bacteria	actinobacteria	1681	Bifidobacterium bifidum	99.93	210
FBI00211	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.78	211

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00218	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.42	218
FBI00224	Sutterella wadsworthensis	bacteria	proteobacteria	40545	Sutterella wadsworthensis	99.71	224
FBI00232	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	98.84	232
FBI00233	Ruminococcaceae sp. FBI00233	bacteria	firmicutes	474960	Anaerotruncus colihominis	91.63	233
FBI00239	Lactonifactor longoviformis	bacteria	firmicutes	341220	Lactonifactor longoviformis	98.99	239
FBI00241	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.34	241
FBI00243	Eubacterium siraeum	bacteria	firmicutes	39492	Eubacterium siraeum	98.53	243
FBI00246	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.7	246
FBI00249	Citrobacter portucalensis	bacteria	proteobacteria	1639133	Citrobacter freundii	99.79	249
FBI00251	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.85	251
FBI00259	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.7	259
FBI00260	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.64	260
FBI00262	Bacteroides massiliensis	bacteria	bacteroidetes	204516	Bacteroides massiliensis	99.71	262
FBI00263	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.56	263

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00265	Bacteroides cellulosilyticus	bacteria	bacteroidetes	246787	Bacteroides cellulosilyticus	99.21	265
FBI00283	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	96.02	283
FBI00289	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	289

TABLE 18

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00001	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.64	1
FBI00002	Bacteroides salyersiae	bacteria	bacteroidetes	291644	Bacteroides salyersiae	99.5	2
FBI00004	Neglecta timonensis	bacteria	firmicutes	1776382	Neglecta timonensis	99.14	4
FBI00010	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.12	10
FBI00011	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.28	11
FBI00013	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.5	13
FBI00016	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.64	16
FBI00017	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.34	17

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00020	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.57	20
FBI00022	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	99.93	22
FBI00030	Eggerthella lenta	bacteria	firmicutes	84112	Eggerthella lenta	98.47	30
FBI00033	Lachnospiraceae sp. FBI00033	bacteria	firmicutes	186803	Clostridium amygdalinum	93.56	33
FBI00034	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.78	34
FBI00038	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	95.96	38
FBI00039	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.71	39
FBI00040	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.38	40
FBI00042	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.71	42
FBI00043	Bifidobacterium dentium	bacteria	actinobacteria	1689	Bifidobacterium dentium	99.35	43
FBI00046	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.71	46
FBI00047	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.79	47
FBI00052	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.14	52
FBI00056	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.2	56
FBI00057	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.7	57
FBI00060	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.49	60
FBI00062	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.48	62

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00067	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	98.84	67
FBI00069	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.84	69
FBI00072	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	96.17	72
FBI00074	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.03	74
FBI00076	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.78	76
FBI00077	Sutterella wadsworthensis	bacteria	proteobacteria	40545	Sutterella wadsworthensis	99.86	77
FBI00085	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.62	85
FBI00086	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.77	86
FBI00087	Clostridium scindens	bacteria	firmicutes	29347	Clostridium scindens	98.28	87
FBI00090	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.71	90
FBI00096	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.76	96
FBI00101	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	97.97	101
FBI00102	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.31	102
FBI00109	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	98.39	109
FBI00111	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.43	111
FBI00112	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	112
FBI00113	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.79	113
FBI00115	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	97.98	115

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00120	Hungatella effluvii	bacteria	firmicutes	154046	Hungatella hathewayi	98.78	120
FBI00122	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.57	122
FBI00125	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	99.64	125
FBI00127	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	98.81	127
FBI00133	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	133
FBI00135	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.57	135
FBI00137	Bacteroides fragilis	bacteria	bacteroidetes	817	Bacteroides fragilis	99.71	137
FBI00139	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.5	139
FBI00142	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.07	142
FBI00143	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.07	143
FBI00147	Clostridium bolteae	bacteria	firmicutes	208479	Clostridium bolteae	99.28	147
FBI00162	Bifidobacterium catenulatum	bacteria	actinobacteria	1686	Bifidobacterium catenulatum	99.14	162
FBI00164	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	98.56	164
FBI00167	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.39	167
FBI00168	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.26	168
FBI00170	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.61	170
FBI00171	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.45	171

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00172	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.05	172
FBI00173	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	100	173
FBI00182	Bacteroides coprocola	bacteria	bacteroidetes	310298	Bacteroides coprocola	99.64	182
FBI00197	Bifidobacterium bifidum	bacteria	actinobacteria	1681	Bifidobacterium bifidum	99.85	197
FBI00199	Clostridium bolteae	bacteria	firmicutes	208479	Clostridium bolteae	99.28	199
FBI00201	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.83	201
FBI00206	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.56	206
FBI00208	Anaerotruncus massiliensis	bacteria	firmicutes	1673720	Anaerotruncus colihominis	96.52	208
FBI00210	Bifidobacterium bifidum	bacteria	actinobacteria	1681	Bifidobacterium bifidum	99.93	210
FBI00211	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.78	211
FBI00232	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	98.84	232
FBI00238	Alistipes sp. FBI00238	bacteria	bacteroidetes	239759	Alistipes finegoldii	95.84	238
FBI00241	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.34	241
FBI00243	Eubacterium siraeum	bacteria	firmicutes	39492	Eubacterium siraeum	98.53	243
FBI00244	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	98.69	244
FBI00246	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.7	246
FBI00251	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.85	251

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00254	Eubacterium hallii	bacteria	firmicutes	39488	Eubacterium hallii	99.08	254
FBI00255	Hungatella effluvii	bacteria	firmicutes	1096246	Hungatella hathewayi	98.56	255
FBI00257	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	99.28	257
FBI00260	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.64	260
FBI00265	Bacteroides cellulosilyticus	bacteria	bacteroidetes	246787	Bacteroides cellulosilyticus	99.21	265
FBI00266	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	99.2	266
FBI00269	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	100	269
FBI00271	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	98.42	271
FBI00278	Eubacterium ventriosum	bacteria	firmicutes	39496	Eubacterium ventriosum	94.14	278
FBI00283	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	96.02	283
FBI00288	Blautia hydrogenotrophica	bacteria	firmicutes	53443	Blautia hydrogenotrophica	99.57	288
FBI00289	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	289

TABLE 19

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00001	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.64	1
FBI00002	Bacteroides salyersiae	bacteria	bacteroidetes	291644	Bacteroides salyersiae	99.5	2

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00003	Enterococcus faecalis	bacteria	firmicutes	1351	Enterococcus faecalis	99.93	3
FBI00004	Neglecta timonensis	bacteria	firmicutes	1776382	Neglecta timonensis	99.14	4
FBI00005	Enterococcus casseliflavus	bacteria	firmicutes	37734	Enterococcus gallinarum	99.65	5
FBI00006	Enterobacter himalayensis	bacteria	proteobacteria	547	Enterobacter hormaechei	99	6
FBI00009	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium faecale	98.6	9
FBI00010	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.12	10
FBI00011	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.28	11
FBI00012	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.71	12
FBI00013	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.5	13
FBI00015	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	15
FBI00016	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.64	16
FBI00017	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.34	17
FBI00018	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.71	18
FBI00019	Alistipes timonensis	bacteria	bacteroidetes	1465754	Alistipes timonensis	99.78	19
FBI00020	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.57	20
FBI00021	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides kribbi	99.07	21
FBI00022	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	99.93	22
FBI00025	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.21	25
FBI00027	Fusicatenibacter saccharivorans	bacteria	firmicutes	1150298	Fusicatenibacter saccharivorans	97.6	27

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00029	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	99.26	29
FBI00030	Eggerthella lenta	bacteria	firmicutes	84112	Eggerthella lenta	98.47	30
FBI00031	Enterobacter hormaechei	bacteria	proteobacteria	158836	Enterobacter hormaechei	99.43	31
FBI00033	Lachnospiraceae sp. FBI00033	bacteria	firmicutes	186803	Clostridium amygdalinum	93.56	33
FBI00034	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.78	34
FBI00036	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.53	36
FBI00038	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	95.96	38
FBI00040	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.38	40
FBI00041	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.23	41
FBI00043	Bifidobacterium dentium	bacteria	actinobacteria	1689	Bifidobacterium dentium	99.35	43
FBI00044	Blautia wexlerae	bacteria	firmicutes	418240	Blautia wexlerae	98.69	44
FBI00046	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.71	46
FBI00047	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.79	47
FBI00048	Fusicatenibacter saccharivorans	bacteria	firmicutes	1150298	Fusicatenibacter saccharivorans	97.95	48
FBI00049	Dialister succinatiphilus	bacteria	firmicutes	487173	Dialister succinatiphilus	95.74	49
FBI00050	Bacteroides nordii	bacteria	bacteroidetes	291645	Bacteroides nordii	98.63	50
FBI00051	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	98.07	51

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00052	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.14	52
FBI00053	Lactobacillus rogosae	bacteria	firmicutes	706562	Lachnospira pectinoschiza	97.36	53
FBI00055	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides kribbi	99.64	55
FBI00056	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.2	56
FBI00057	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.7	57
FBI00058	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.71	58
FBI00060	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.49	60
FBI00061	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	99.19	61
FBI00062	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.48	62
FBI00066	Parasutterella excrementihominis	bacteria	proteobacteria	487175	Parasutterella excrementihominis	99.13	66
FBI00067	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	98.84	67
FBI00068	Akkermansia muciniphila	bacteria	verrucomicrobia	239935	Akkermansia muciniphila	99.42	68
FBI00069	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.84	69
FBI00070	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides koreensis	99.71	70
FBI00073	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	98.99	73
FBI00075	Paraprevotella clara	bacteria	bacteroidetes	454154	Paraprevotella clara	98.85	75

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00076	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.78	76
FBI00077	Sutterella wadsworthensis	bacteria	proteobacteria	40545	Sutterella wadsworthensis	99.86	77
FBI00080	Sutterella massiliensis	bacteria	proteobacteria	1816689	Sutterella massiliensis	99.78	80
FBI00085	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.62	85
FBI00087	Clostridium scindens	bacteria	firmicutes	29347	Clostridium scindens	98.28	87
FBI00092	Monoglobus pectinilyticus	bacteria	firmicutes	1981510	Monoglobus pectinilyticus	99.5	92
FBI00093	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	99.71	93
FBI00098	Bacteroides dorei	bacteria	bacteroidetes	357276	Bacteroides dorei	99.93	98
FBI00101	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	97.97	101
FBI00102	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.31	102
FBI00104	Blautia wexlerae	bacteria	firmicutes	418240	Blautia luti	97.18	104
FBI00110	Lachnoclostridium pacaense	bacteria	firmicutes	1917870	Lachnoclostridium pacaense	98.92	110
FBI00111	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.43	111
FBI00116	Ruminococcus faecis	bacteria	firmicutes	592978	Ruminococcus faecis	99.57	116
FBI00117	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.52	117
FBI00132	Gordonibacter pamelaeae	bacteria	actinobacteria	471189	Gordonibacter pamelaeae	99.48	132
FBI00133	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	133

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00140	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.58	140
FBI00141	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.15	141
FBI00155	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.7	155
FBI00289	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	289

TABLE 20

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00001	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.64	1
FBI00002	Bacteroides salyersiae	bacteria	bacteroidetes	291644	Bacteroides salyersiae	99.5	2
FBI00004	Neglecta timonensis	bacteria	firmicutes	1776382	Neglecta timonensis	99.14	4
FBI00009	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium faecale	98.6	9
FBI00010	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.12	10
FBI00011	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.28	11
FBI00012	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.71	12
FBI00013	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.5	13
FBI00015	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	15
FBI00016	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.64	16
FBI00018	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.71	18

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00019	Alistipes timonensis	bacteria	bacteroidetes	1465754	Alistipes timonensis	99.78	19
FBI00020	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.57	20
FBI00021	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides kribbi	99.07	21
FBI00022	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	99.93	22
FBI00025	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.21	25
FBI00027	Fusicatenibacter saccharivorans	bacteria	firmicutes	1150298	Fusicatenibacter saccharivorans	97.6	27
FBI00029	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	99.26	29
FBI00030	Eggerthella lenta	bacteria	firmicutes	84112	Eggerthella lenta	98.47	30
FBI00032	Anaerostipes hadrus	bacteria	firmicutes	649756	Anaerostipes hadrus	99.64	32
FBI00033	Lachnospiraceae sp. FBI00033	bacteria	firmicutes	186803	Clostridium amygdalinum	93.56	33
FBI00034	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.78	34
FBI00036	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.53	36
FBI00038	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	95.96	38
FBI00040	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.38	40
FBI00043	Bifidobacterium dentium	bacteria	actinobacteria	1689	Bifidobacterium dentium	99.35	43
FBI00044	Blautia wexlerae	bacteria	firmicutes	418240	Blautia wexlerae	98.69	44
FBI00046	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.71	46
FBI00047	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.79	47

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00048	Fusicatenibacter saccharivorans	bacteria	firmicutes	1150298	Fusicatenibacter saccharivorans	97.95	48
FBI00049	Dialister succinatiphilus	bacteria	firmicutes	487173	Dialister succinatiphilus	95.74	49
FBI00050	Bacteroides nordii	bacteria	bacteroidetes	291645	Bacteroides nordii	98.63	50
FBI00051	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	98.07	51
FBI00052	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.14	52
FBI00053	Lactobacillus rogosae	bacteria	firmicutes	706562	Lachnospira pectinoschiza	97.36	53
FBI00055	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides kribbi	99.64	55
FBI00056	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.2	56
FBI00057	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.7	57
FBI00059	Bacteroides stercorirosoris	bacteria	bacteroidetes	871324	Bacteroides oleiciplenus	98.81	59
FBI00060	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.49	60
FBI00061	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	99.19	61
FBI00062	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.48	62
FBI00066	Parasutterella excrementihominis	bacteria	proteobacteria	487175	Parasutterella excrementihominis	99.13	66
FBI00067	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	98.84	67
FBI00068	Akkermansia muciniphila	bacteria	verrucomicrobia	239935	Akkermansia muciniphila	99.42	68
FBI00069	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.84	69

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00070	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides koreensis	99.71	70
FBI00071	Lachnospiraceae sp. FBI00071	bacteria	firmicutes	186803	Roseburia faecis	94.92	71
FBI00072	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	96.17	72
FBI00074	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.03	74
FBI00075	Paraprevotella clara	bacteria	bacteroidetes	454154	Paraprevotella clara	98.85	75
FBI00076	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.78	76
FBI00077	Sutterella wadsworthensis	bacteria	proteobacteria	40545	Sutterella wadsworthensis	99.86	77
FBI00078	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.34	78
FBI00079	Clostridium clostridioforme	bacteria	firmicutes	1531	Clostridium clostridioforme	99.14	79
FBI00080	Sutterella massiliensis	bacteria	proteobacteria	1816689	Sutterella massiliensis	99.78	80
FBI00081	Porphyromonas asaccharolytica	bacteria	bacteroidetes	28123	Porphyromonas asaccharolytica	99.35	81
FBI00082	Ruminococcaceae sp. FBI00082 FBI00097	bacteria	firmicutes	541000	Phocea massiliensis	93.08	82
FBI00085	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.62	85
FBI00087	Clostridium scindens	bacteria	firmicutes	29347	Clostridium scindens	98.28	87
FBI00092	Monoglobus pectinilyticus	bacteria	firmicutes	1981510	Monoglobus pectinilyticus	99.5	92
FBI00093	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	99.71	93
FBI00096	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.76	96

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00097	Ruminococcaceae sp. FBI00082 FBI00097	bacteria	firmicutes	541000	Phocea massiliensis	93.07	97
FBI00099	Gordonibacter pamelaeae	bacteria	actinobacteria	471189	Gordonibacter pamelaeae	99.56	99
FBI00101	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	97.97	101
FBI00102	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.31	102
FBI00104	Blautia wexlerae	bacteria	firmicutes	418240	Blautia luti	97.18	104
FBI00109	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	98.39	109
FBI00110	Lachnoclostridium pacaense	bacteria	firmicutes	1917870	Lachnoclostridium pacaense	98.92	110
FBI00111	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.43	111
FBI00112	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	112
FBI00113	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.79	113
FBI00115	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	97.98	115
FBI00116	Ruminococcus faecis	bacteria	firmicutes	592978	Ruminococcus faecis	99.57	116
FBI00117	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.52	117
FBI00120	Hungatella effluvii	bacteria	firmicutes	154046	Hungatella hathewayi	98.78	120
FBI00123	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	100	123
FBI00124	Anaerostipes hadrus	bacteria	firmicutes	649756	Anaerostipes hadrus	99.86	124
FBI00125	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	99.64	125
FBI00126	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	98.98	126
FBI00127	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	98.81	127

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00128	Hungatella effluvii	bacteria	firmicutes	1096246	Hungatella effluvii	98.71	128
FBI00132	Gordonibacter pamelaeae	bacteria	actinobacteria	471189	Gordonibacter pamelaeae	99.48	132
FBI00133	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	133
FBI00135	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.57	135
FBI00137	Bacteroides fragilis	bacteria	bacteroidetes	817	Bacteroides fragilis	99.71	137
FBI00140	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.58	140
FBI00141	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.15	141
FBI00145	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	99.14	145
FBI00147	Clostridium bolteae	bacteria	firmicutes	208479	Clostridium bolteae	99.28	147
FBI00149	Monoglobus pectinilyticus	bacteria	firmicutes	1981510	Monoglobus pectinilyticus	99.5	149
FBI00151	Clostridium aldenense	bacteria	firmicutes	358742	Clostridium aldenense	98.55	151
FBI00152	Dialister invisus	bacteria	firmicutes	218538	Dialister invisus	99.58	152
FBI00159	Eisenbergiella tayi	bacteria	firmicutes	1432052	Eisenbergiella tayi	99.03	159
FBI00162	Bifidobacterium catenulatum	bacteria	actinobacteria	1686	Bifidobacterium catenulatum	99.14	162
FBI00165	Bacteroides massiliensis	bacteria	bacteroidetes	204516	Bacteroides massiliensis	99.71	165
FBI00167	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.39	167
FBI00170	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.61	170

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00171	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.45	171
FBI00174	Lactobacillus rogosae	bacteria	firmicutes	706562	Lachnospira pectinoschiza	97.92	174
FBI00175	Holdemanella biformis	bacteria	firmicutes	1735	Holdemanella biformis	98.19	175
FBI00176	Ruthenibacterium lactatiformans	bacteria	firmicutes	1550024	Ruthenibacterium lactatiformans	99.71	176
FBI00177	Parasutterella excrementihominis	bacteria	proteobacteria	487175	Parasutterella excrementihominis	99.71	177
FBI00180	Alistipes sp. FBI00180	bacteria	bacteroidetes	239759	Alistipes senegalensis	97.56	180
FBI00182	Bacteroides coprocola	bacteria	bacteroidetes	310298	Bacteroides coprocola	99.64	182
FBI00184	Bacteroides faecis	bacteria	bacteroidetes	674529	Bacteroides faecis	99.78	184
FBI00189	Bacteroides ovatus	bacteria	bacteroidetes	28116	Bacteroides koreensis	99.93	189
FBI00190	Bacteroides finegoldii	bacteria	bacteroidetes	338188	Bacteroides finegoldii	98.91	190
FBI00191	Clostridiaceae sp. FBI00191	bacteria	firmicutes	31979	Clostridium swellfunianum	96.24	191
FBI00194	Ruminococcus faecis	bacteria	firmicutes	592978	Ruminococcus faecis	98.41	194
FBI00197	Bifidobacterium bifidum	bacteria	actinobacteria	1681	Bifidobacterium bifidum	99.85	197
FBI00198	Lachnoclostridium pacaense	bacteria	firmicutes	1917870	Lachnoclostridium pacaense	99.71	198
FBI00199	Clostridium bolteae	bacteria	firmicutes	208479	Clostridium bolteae	99.28	199
FBI00200	Longicatena caecimuris	bacteria	firmicutes	1796635	Longicatena caecimuris	99.71	200
FBI00201	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.83	201
FBI00205	Blautia massiliensis	bacteria	firmicutes	1737424	Blautia luti	97.55	205

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00206	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.56	206
FBI00208	Anaerotruncus massiliensis	bacteria	firmicutes	1673720	Anaerotruncus colihominis	96.52	208
FBI00210	Bifidobacterium bifidum	bacteria	actinobacteria	1681	Bifidobacterium bifidum	99.93	210
FBI00211	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.78	211
FBI00212	Clostridium aldenense	bacteria	firmicutes	358742	Clostridium aldenense	99.1	212
FBI00220	Megasphaera massiliensis	bacteria	firmicutes	1232428	Megasphaera massiliensis	98.8	220
FBI00221	Butyricimonas faecihominis	bacteria	bacteroidetes	1472416	Butyricimonas faecihominis	98.61	221
FBI00224	Sutterella wadsworthensis	bacteria	proteobacteria	40545	Sutterella wadsworthensis	99.71	224
FBI00226	Catabacter hongkongensis	bacteria	firmicutes	270498	Catabacter hongkongensis	99.71	226
FBI00229	Alistipes senegalensis	bacteria	bacteroidetes	1288121	Alistipes senegalensis	99.19	229
FBI00232	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	98.84	232
FBI00233	Ruminococcaceae sp. FBI00233	bacteria	firmicutes	474960	Anaerotruncus colihominis	91.63	233
FBI00234	Faecalicatena contorta	bacteria	firmicutes	39482	Faecalicatena contorta	99.21	234
FBI00236	Eisenbergiella tayi	bacteria	firmicutes	1432052	Eisenbergiella tayi	99.41	236
FBI00237	Dielma fastidiosa	bacteria	firmicutes	1034346	Dielma fastidiosa	99.78	237
FBI00238	Alistipes sp. FBI00238	bacteria	bacteroidetes	239759	Alistipes finegoldii	95.84	238

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00239	Lactonifactor longoviformis	bacteria	firmicutes	341220	Lactonifactor longoviformis	98.99	239
FBI00243	Eubacterium siraeum	bacteria	firmicutes	39492	Eubacterium siraeum	98.53	243
FBI00244	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	98.69	244
FBI00245	Acidaminococcus intestini	bacteria	firmicutes	187327	Acidaminococcus intestini	99.72	245
FBI00248	Neglecta timonensis	bacteria	firmicutes	1776382	Emergencia timonensis	99.64	248
FBI00249	Citrobacter portucalensis	bacteria	proteobacteria	1639133	Citrobacter freundii	99.79	249
FBI00251	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.85	251
FBI00254	Eubacterium hallii	bacteria	firmicutes	39488	Eubacterium hallii	99.08	254
FBI00255	Hungatella effluvii	bacteria	firmicutes	1096246	Hungatella hathewayi	98.56	255
FBI00258	Turicibacter sanguinis	bacteria	firmicutes	154288	Turicibacter sanguinis	99.93	258
FBI00260	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.64	260
FBI00263	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.56	263
FBI00267	Anaerofustis stercorihominis	bacteria	firmicutes	214853	Anaerofustis stercorihominis	97.29	267
FBI00269	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	100	269
FBI00271	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	98.42	271
FBI00273	Barnesiella intestinihominis	bacteria	bacteroidetes	487174	Barnesiella intestinihominis	99.43	273

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00274	Eubacterium xylanophilum	bacteria	firmicutes	39497	Eubacterium xylanophilum	93.5	274
FBI00275	Holdemanella biformis	bacteria	firmicutes	1735	Holdemanella biformis	98.99	275
FBI00277	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.63	277
FBI00278	Eubacterium ventriosum	bacteria	firmicutes	39496	Eubacterium ventriosum	94.14	278
FBI00281	Senegalimassilia anaerobia	bacteria	actinobacteria	1473216	Senegalimassilia anaerobia	99.45	281
FBI00282	Porphyromonas asaccharolytica	bacteria	bacteroidetes	28123	Porphyromonas asaccharolytica	99.35	282
FBI00288	Blautia hydrogenotrophica	bacteria	firmicutes	53443	Blautia hydrogenotrophica	99.57	288
FBI00289	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	289
FBI00290	Lachnospiraceae sp. FBI00290	bacteria	firmicutes	186803	Eubacterium ruminantium	94.81	290

Example 12: *in vivo* oxalate reduction by candidate consortia in a germ-free mouse model fed a low-complexity diet

[0312] A set of five candidate oxalate-eliminating microbial consortia, comprising active and supportive microbes isolated from human fecal samples as described in Example 1, were tested for the ability to control oxalate levels *in vivo* in germ-free mice fed a limited ingredient, low-complexity diet supplemented with oxalate (*see* Table 1).

[0313] One week prior to colonization, germ-free C57Bl/6NTac mice (n = 4 per condition) were fed a refined diet rich in casein and simple sugars supplemented with oxalate to induce hyperoxaluria (*see* Table 2). One week later, the candidate consortia described in Example 11 (I to V) were introduced to the mice via oral gavage. One group of mice was mock-colonized with PBS alone as a negative control. Another group of mice was colonized with a previously-characterized microbial consortium as a positive control, which contains microbial strains sourced from depositories and was previously shown to reduce oxalate levels *in vivo* (*see* Examples 6 and 7; Table 8). Urine and fecal samples were collected each week for two weeks thereafter, with an endpoint at 14 days following colonization. Terminal urine (collected immediately following euthanasia) was processed by solid-phase extraction and oxalate levels were quantified by LC/MS as described in Example 4.

[0314] Average urinary oxalate concentrations for each study group at study endpoint are reported in FIGURE 13. Mice colonized with the positive control proof-of-concept community containing commercially sourced strains of *O. formigenes* (+) exhibited a 53% average reduction in urinary oxalate relative to the uncolonized negative control (-). The five proprietary candidate communities (I-V), each of which comprised three internally isolated strains of *O. formigenes*, were found to reduce urinary oxalate by 32-70%, demonstrating efficacy on par with the positive control community. The reduction in urinary oxalate for all tested communities was statistically significant relative to the negative control.

Example 13: *in vivo* oxalate reduction by candidate consortia in a germ free mouse fed a high-complexity diet

[0315] The set of five candidate oxalate-eliminating microbial consortia described in Example 10 were further tested for the ability to control oxalate levels *in vivo* in germ free mice fed a complex, nutritionally complete diet.

[0316] One week prior to colonization, germ-free C57Bl/6NTac mice (n = 4 per condition) were fed a complex, grain-based diet and given *ad libitum* drinking water supplemented with 0.875% oxalate to induce hyperoxaluria. One week later, the mice were

colonized with the therapeutic communities via oral gavage. One group of mice was mock-colonized with PBS alone as a negative control. Another group of mice was colonized with a previously-characterized microbial consortium as a positive control, which contained microbial strains sourced from depositories and was previously shown to reduce oxalate levels *in vivo* (*see* Examples 6 and 7; Table 8). Urine and fecal samples were collected each week for two weeks thereafter, with a study endpoint at 8 days following colonization. Terminal urine (collected immediately following euthanasia) was processed by solid-phase extraction and oxalate levels were quantified using LC-MS as described in Example 4.

[0317] Average urinary oxalate concentrations for each study group at study endpoint are presented in FIGURE 14. Mice colonized with the positive control community containing commercially sourced strains of *O. formigenes* (+) exhibited a 54% average reduction in urinary oxalate relative to the uncolonized negative control (-). The five proprietary candidate communities (I-V), each of which comprised three internally isolated strains of *O. formigenes*, were found to reduce urinary oxalate by 49-75%, demonstrating efficacy on par with the positive control community. The reduction in urinary oxalate for all tested communities was statistically significant relative to the negative control.

Example 14: *in vivo* oxalate reduction by candidate consortia in a humanized gnotobiotic mouse

[0318] The set of five candidate oxalate-eliminating microbial consortia described in Example 11 were further tested for the ability to control oxalate levels *in vivo* in humanized, recolonized mice fed a complex, nutritionally complete diet.

[0319] Germ-free C57Bl/6NTac mice (n = 4 per condition) were humanized by introducing a previously characterized human donor fecal sample that lacks *O. formigenes* and does not appreciably degrade urinary oxalate. One week following colonization, the humanized mice were fed a complex, grain-based diet supplemented with oxalate to induce hyperoxaluria. One week later, the mice were given an antibiotic cocktail containing ampicillin (1 mg/ml) and enrofloxacin (0.575 mg/ml) *ad libidum* in drinking water for seven days, after which the antibiotic treatment was ended and the therapeutic communities (I-V) were introduced via oral gavage. One group of mice was mock-colonized with PBS alone as a negative control. Another group of mice was colonized with a previously-characterized microbial consortium as a positive control, which contained microbial strains sourced from depositories and was previously shown to reduce oxalate levels *in vivo* (*see* Examples 6 and 7; Table 8). A final group of mice was colonized with a set of strains ("Putative Oxalate

Degraders") that included three donor-derived strains of *O. formigenes* in addition to other donor-derived strains predicted to have oxalate-degrading activity. This set of strains is listed in Table 21.

TABLE 21

Strain #	Species ID	SEQ ID NO: X
FBI00001	Clostridium citroniae	1
FBI00002	Bacteroides salyersiae	2
FBI00004	Neglecta timonensis	4
FBI00008	Blautia luti	8
FBI00009	Bifidobacterium adolescentis	9
FBI00011	Bifidobacterium longum	11
FBI00016	Bifidobacterium pseudocatenulatum	16
FBI00017	Blautia obeum	17
FBI00020	Bacteroides thetaiotaomicron	20
FBI00021	Bacteroides kribbi / Bacteroides koreensis species cluster	21
FBI00028	Oscillibacter sp. FBI00028	28
FBI00030	Eggerthella lenta	30
FBI00033	Lachnospiraceae sp. FBI00033	33
FBI00041	Phascolarctobacterium faecium	41
FBI00043	Bifidobacterium dentium	43
FBI00045	Bifidobacterium adolescentis	45
FBI00050	Bacteroides nordii	50
FBI00052	Bacteroides xylanisolvens	52
FBI00053	Lactobacillus rogosae	53
FBI00056	Clostridium citroniae	56
FBI00060	Bifidobacterium longum	60
FBI00063	Lachnospira sp. FBI00063 FBI00285 FBI00364	63
FBI00064	Dorea sp. FBI00064	64
FBI00067	Oxalobacter formigenes	67
FBI00069	Ruminococcus bromii	69
FBI00070	Bacteroides kribbi / Bacteroides koreensis species cluster	70

Strain #	Species ID	SEQ ID NO: X
FBI00133	Oxalobacter formigenes	133
FBI00289	Oxalobacter formigenes	289

[0320] Mice were sampled each week for two weeks following recolonization to determine microbiome composition and urinary oxalate levels, with a study endpoint at 14 days following colonization with the experimental communities. Average urinary oxalate concentrations for each study group at study endpoint are presented in FIGURE 15. Re-colonization with the positive control proof-of-concept community containing commercially sourced strains of *O. formigenes* (+) yielded a 52% average reduction in urinary oxalate relevant to the mock-treated negative control (-). The five proprietary candidate communities (I-V), each of which comprises three donor-derived strains of *O. formigenes*, were found to reduce urinary oxalate by 22-65%, demonstrating efficacy on par with the positive control community. The reduction in urinary oxalate for all tested communities was statistically significant for all but one community (IV), with no significant differences observed between the remaining colonized groups. Notably, recolonization with the set of putative oxalate-degrading microbes alone did not result in a reduction in urinary oxalate, demonstrating the enhanced effect of combining a plurality of active oxalate-degrading microbes with a rationally designed supportive community.

[0321] Mouse fecal samples were analyzed by metagenomic sequencing in order to determine the composition of the microbiome. Briefly, genomic DNA was extracted from mouse fecal pellets and sequenced using short-read (Illumina) sequencing. Individual reads were classified against a comprehensive reference database, containing genomes from species throughout the tree of life. The total reads classified to a species were summed and normalized by genome size to obtain estimates of relative abundance. The results of this analysis are summarized in FIGURE 16. Re-colonization with one of the candidate microbial consortia (I-V) resulted in enhanced microbiome species diversity relative to both the proof-of-concept consortium and the collection of Putative Oxalate Degraders.

Example 15: Effect of candidate supportive communities on *in vivo* engraftment of *O. formigenes*

[0322] The set of five candidate oxalate-eliminating microbial consortia described in Example 10 were further tested for the ability to support engraftment of the active oxalate-degrading microbe *O. formigenes* into germ-free mice.

[0323] Germ-free C57Bl/6NTac mice (n = 4 per condition) were colonized with candidate microbial consortia (I to V) via oral gavage. One group of mice was colonized with only a supportive community of microbes as a negative control. At the conclusion of the experiment, fecal samples were analyzed via metagenomic sequencing to measure the relative and absolute abundance of *O. formigenes* in the microbiome. Briefly, genomic DNA was extracted from mouse fecal pellets and sequenced using short-read (Illumina) sequencing. Individual reads were classified against a comprehensive reference database, containing genomes from species throughout the tree of life. The total reads classified to a species were summed and normalized by genome size to obtain estimates of relative abundance. Absolute abundance estimates were obtained by injecting a known quantity of heterologous cells into the fecal sample prior to DNA extraction and sequencing.

[0324] The results of this study are reported in FIGURE 17. *O. formigenes* was detected in all mice colonized with one of the five candidate consortia, and treatment with candidate V resulted in the largest quantity of *O. formigenes* in the fecal sample.

Example 16: Production of an exemplary therapeutic oxalate-degrading consortium

[0325] This example describes the production of an exemplary microbial consortium intended for use in human subjects. In one embodiment of the invention, said exemplary consortium consists of the strains listed in Table 22, including three active oxalate-degrader strains of donor-derived *O. formigenes*. In another embodiment of the invention, said exemplary consortium consists of the strains listed in in Table 23. In another embodiment of the invention, said exemplary consortium consists of the strains listed in Table 24. All strains included in the exemplary consortium meet at least one of five criteria:

a. Has an experimentally confirmed ability to eliminate oxalate *in vitro*
b. Belongs to a species that is known to metabolize formate, a primary byproduct and potential inhibitor of oxalate metabolism in the gut
c. Belongs to a species known to contribute to metabolism of one or more nutrients typically found in the human diet

d. Belongs to species known to fulfill unique and potentially beneficial biological functions in the GI tract (*e.g.*, bile salt hydrolase activity or butyrate production)
e. Belongs to a species found in the GI tract of one or more healthy human adults.

[0326] The final drug product consists of up to 7 drug substances, each comprising at least one characterized bacterial strain. Some drug substances are pure cultures, whereas others are from mixed-culture fermentation of anaerobic and facultative aerobic bacteria. The drug substance culture conditions are determined by one skilled in the art.

[0327] Cells are harvested and concentrated by a combination of microfiltration using 0.2 – 0.45 μm pore size membranes made of nonreactive polymers such as Polyvinylidene fluoride, Polysulfones, and/or nitrocellulose; and centrifugation (10,000 – 20,000 g force) to a final CFU concentration of $1x10^6$ to $1x10^{12}$ CFU/ml. The concentrated biomass is mixed with sterilized cryoprotectant agent (CPA) at a volumetric ratio between 10:1 to 1:10.

[0328] The CPA is composed of a cryoprotectant/carbohydrate/bulking agent/nutrient such as glycerol (0 to 250 g/l), maltodextrin (0 to 100 g/l), sucrose (0 to 100 g/l), inulin (0 to 40 g/l), trehalose (0 to 50 g/l) and/or alginate (0 to 10 g/l). Additionally, antioxidants such as cysteine (0.25 to 0.50 g/l), ascorbic acid (0 to 5 g/l) and/or riboflavin (0 to 0.01 g/l) are added to CPA. The specific concentrations are determined by a person skilled in the art.

[0329] Finally, additional nutrients such as oxalate (0 – 100 mM) or formate (0 – 100 mM) are added to support robust revival of specific strains from the capsule, the specific concentrations being determined by one skilled in the art.

[0330] The cells are either stored frozen in a CPA or combination of CPAs, or are lyophilized to prepare various solid oral dosage forms (*e.g.*, enteric coated capsules or enteric coated tablets). The formulated cells are lyophilized to yield a stable product. Primary drying is conducted below collapse temperature of the chosen formulation (typically below -20 °C), followed by secondary drying at higher temperature (5 °C or higher). Lyophilized powder is filled in "0" to "000" size capsules to accommodate various strengths. To prepare tablets, lyophilized powder is added to a binding agent (*e.g.* sucrose or starch) and pressed into tablets. The tablets are enteric coated to protect the drug product from the low pH gastric environment.

[0331] Composition of the drug product is defined by the Relative Abundance of the various intended strains. The relative abundance of microbial strains in the drug substance or drug product is determined as follows: total bacterial genomic DNA is extracted from a

pelleted aliquot (*e.g.* 1 ml) of the drug substance/product and quantified, normalized by concentration, and prepared into an indexed library for whole-genome shotgun sequencing on an Illumina sequencer (*e.g.* NovaSeq). Following quality trimming, short paired-end Illumina reads (PE-150) are classified using a custom bioinformatics pipeline and taxonomically-structured database built from the genome sequences of strains in the drug product. The taxonomically-structured database links genome nucleotide sequences of a fixed length (k-mers) to a least common ancestor(s) (strain, species … phylum) that contain the same k-mer in the database. 150 base-pair sequencing reads are classified by retrieving the taxa for all k-mers in the read and assigning a classification based on the least common ancestor. Sequences that have no k-mers in the database are discarded. Reads that do not get classified to the strain level are distributed to the strain level using Bayes theorem to estimate true strain-level abundance. The relative abundance of a strain is calculated as the percentage of reads that are classified as that strain, divided by genome size. Absolute abundance is calculated by dividing the total bacterial cell number in the drug product (quantified by Beckman Coulter Counter) by the percent relative abundance.

[0332] A person of ordinary skill in the art shall be able to determine useful ratios of active and supportive microbes that constitute the exemplary consortium, and shall ensure that the relative abundance of supportive microbial strains is at least sufficient to enable function and stable engraftment of the plurality of active microbes.

TABLE 22

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00001	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.64	1
FBI00002	Bacteroides salyersiae	bacteria	bacteroidetes	291644	Bacteroides salyersiae	99.5	2
FBI00004	Neglecta timonensis	bacteria	firmicutes	1776382	Neglecta timonensis	99.14	4
FBI00009	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium faecale	98.6	9
FBI00010	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.12	10
FBI00011	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.28	11
FBI00012	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.71	12
FBI00013	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.5	13
FBI00015	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	15
FBI00016	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.64	16
FBI00018	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.71	18
FBI00019	Alistipes timonensis	bacteria	bacteroidetes	1465754	Alistipes timonensis	99.78	19
FBI00020	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.57	20
FBI00021	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides kribbi	99.07	21
FBI00022	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	99.93	22
FBI00025	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.21	25
FBI00027	Fusicatenibacter saccharivorans	bacteria	firmicutes	1150298	Fusicatenibacter saccharivorans	97.6	27

FBI00029	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	99.26	29
FBI00030	Eggerthella lenta	bacteria	firmicutes	84112	Eggerthella lenta	98.47	30
FBI00032	Anaerostipes hadrus	bacteria	firmicutes	649756	Anaerostipes hadrus	99.64	32
FBI00033	Lachnospiraceae sp. FBI00033	bacteria	firmicutes	186803	Clostridium amygdalinum	93.56	33
FBI00034	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.78	34
FBI00036	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.53	36
FBI00038	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	95.96	38
FBI00040	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.38	40
FBI00043	Bifidobacterium dentium	bacteria	actinobacteria	1689	Bifidobacterium dentium	99.35	43
FBI00044	Blautia wexlerae	bacteria	firmicutes	418240	Blautia wexlerae	98.69	44
FBI00046	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.71	46
FBI00047	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.79	47
FBI00048	Fusicatenibacter saccharivorans	bacteria	firmicutes	1150298	Fusicatenibacter saccharivorans	97.95	48
FBI00049	Dialister succinatiphilus	bacteria	firmicutes	487173	Dialister succinatiphilus	95.74	49
FBI00050	Bacteroides nordii	bacteria	bacteroidetes	291645	Bacteroides nordii	98.63	50
FBI00051	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	98.07	51
FBI00052	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.14	52
FBI00053	Lactobacillus rogosae	bacteria	firmicutes	706562	Lachnospira pectinoschiza	97.36	53
FBI00055	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides kribbi	99.64	55
FBI00056	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.2	56

FBI00057	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.7	57
FBI00059	Bacteroides stercorirosoris	bacteria	bacteroidetes	871324	Bacteroides oleiciplenus	98.81	59
FBI00060	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.49	60
FBI00061	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	99.19	61
FBI00062	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.48	62
FBI00066	Parasutterella excrementihominis	bacteria	proteobacteria	487175	Parasutterella excrementihominis	99.13	66
FBI00067	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	98.84	67
FBI00068	Akkermansia muciniphila	bacteria	verrucomicrobia	239935	Akkermansia muciniphila	99.42	68
FBI00069	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.84	69
FBI00070	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides koreensis	99.71	70
FBI00071	Lachnospiraceae sp. FBI00071	bacteria	firmicutes	186803	Roseburia faecis	94.92	71
FBI00072	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	96.17	72
FBI00074	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.03	74
FBI00075	Paraprevotella clara	bacteria	bacteroidetes	454154	Paraprevotella clara	98.85	75
FBI00076	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.78	76
FBI00077	Sutterella wadsworthensis	bacteria	proteobacteria	40545	Sutterella wadsworthensis	99.86	77
FBI00078	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.34	78
FBI00079	Clostridium clostridioforme	bacteria	firmicutes	1531	Clostridium clostridioforme	99.14	79

FBI00080	Sutterella massiliensis	bacteria	proteobacteria	1816689	Sutterella massiliensis	99.78	80
FBI00081	Porphyromonas asaccharolytica	bacteria	bacteroidetes	28123	Porphyromonas asaccharolytica	99.35	81
FBI00082	Ruminococcaceae sp. FBI00082 FBI00097	bacteria	firmicutes	541000	Phocea massiliensis	93.08	82
FBI00085	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.62	85
FBI00087	Clostridium scindens	bacteria	firmicutes	29347	Clostridium scindens	98.28	87
FBI00092	Monoglobus pectinilyticus	bacteria	firmicutes	1981510	Monoglobus pectinilyticus	99.5	92
FBI00093	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	99.71	93
FBI00096	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.76	96
FBI00097	Ruminococcaceae sp. FBI00082 FBI00097	bacteria	firmicutes	541000	Phocea massiliensis	93.07	97
FBI00099	Gordonibacter pamelaeae	bacteria	actinobacteria	471189	Gordonibacter pamelaeae	99.56	99
FBI00101	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	97.97	101
FBI00102	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.31	102
FBI00104	Blautia wexlerae	bacteria	firmicutes	418240	Blautia luti	97.18	104
FBI00109	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	98.39	109
FBI00110	Lachnoclostridium pacaense	bacteria	firmicutes	1917870	Lachnoclostridium pacaense	98.92	110
FBI00111	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.43	111
FBI00112	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	112
FBI00113	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.79	113
FBI00115	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	97.98	115
FBI00116	Ruminococcus faecis	bacteria	firmicutes	592978	Ruminococcus faecis	99.57	116

FBI00117	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.52	117
FBI00120	Hungatella effluvii	bacteria	firmicutes	154046	Hungatella hathewayi	98.78	120
FBI00123	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	100	123
FBI00124	Anaerostipes hadrus	bacteria	firmicutes	649756	Anaerostipes hadrus	99.86	124
FBI00125	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	99.64	125
FBI00126	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	98.98	126
FBI00127	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	98.81	127
FBI00128	Hungatella effluvii	bacteria	firmicutes	1096246	Hungatella effluvii	98.71	128
FBI00132	Gordonibacter pamelaeae	bacteria	actinobacteria	471189	Gordonibacter pamelaeae	99.48	132
FBI00133	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	133
FBI00135	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.57	135
FBI00137	Bacteroides fragilis	bacteria	bacteroidetes	817	Bacteroides fragilis	99.71	137
FBI00140	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.58	140
FBI00141	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.15	141
FBI00145	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	99.14	145
FBI00147	Clostridium bolteae	bacteria	firmicutes	208479	Clostridium bolteae	99.28	147
FBI00149	Monoglobus pectinilyticus	bacteria	firmicutes	1981510	Monoglobus pectinilyticus	99.5	149
FBI00151	Clostridium aldenense	bacteria	firmicutes	358742	Clostridium aldenense	98.55	151
FBI00152	Dialister invisus	bacteria	firmicutes	218538	Dialister invisus	99.58	152
FBI00159	Eisenbergiella tayi	bacteria	firmicutes	1432052	Eisenbergiella tayi	99.03	159

FBI00162	Bifidobacterium catenulatum	bacteria	actinobacteria	1686	Bifidobacterium catenulatum	99.14	162
FBI00165	Bacteroides massiliensis	bacteria	bacteroidetes	204516	Bacteroides massiliensis	99.71	165
FBI00167	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.39	167
FBI00170	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.61	170
FBI00171	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.45	171
FBI00174	Lactobacillus rogosae	bacteria	firmicutes	706562	Lachnospira pectinoschiza	97.92	174
FBI00175	Holdemanella biformis	bacteria	firmicutes	1735	Holdemanella biformis	98.19	175
FBI00176	Ruthenibacterium lactatiformans	bacteria	firmicutes	1550024	Ruthenibacterium lactatiformans	99.71	176
FBI00177	Parasutterella excrementihominis	bacteria	proteobacteria	487175	Parasutterella excrementihominis	99.71	177
FBI00180	Alistipes sp. FBI00180	bacteria	bacteroidetes	239759	Alistipes senegalensis	97.56	180
FBI00182	Bacteroides coprocola	bacteria	bacteroidetes	310298	Bacteroides coprocola	99.64	182
FBI00184	Bacteroides faecis	bacteria	bacteroidetes	674529	Bacteroides faecis	99.78	184
FBI00189	Bacteroides ovatus	bacteria	bacteroidetes	28116	Bacteroides koreensis	99.93	189
FBI00190	Bacteroides finegoldii	bacteria	bacteroidetes	338188	Bacteroides finegoldii	98.91	190
FBI00191	Clostridiaceae sp. FBI00191	bacteria	firmicutes	31979	Clostridium swellfunianum	96.24	191
FBI00194	Ruminococcus faecis	bacteria	firmicutes	592978	Ruminococcus faecis	98.41	194
FBI00197	Bifidobacterium bifidum	bacteria	actinobacteria	1681	Bifidobacterium bifidum	99.85	197
FBI00198	Lachnoclostridium pacaense	bacteria	firmicutes	1917870	Lachnoclostridium pacaense	99.71	198
FBI00199	Clostridium bolteae	bacteria	firmicutes	208479	Clostridium bolteae	99.28	199
FBI00200	Longicatena caecimuris	bacteria	firmicutes	1796635	Longicatena caecimuris	99.71	200
FBI00201	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.83	201
FBI00205	Blautia massiliensis	bacteria	firmicutes	1737424	Blautia luti	97.55	205

FBI00206	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.56	206
FBI00208	Anaerotruncus massiliensis	bacteria	firmicutes	1673720	Anaerotruncus colihominis	96.52	208
FBI00210	Bifidobacterium bifidum	bacteria	actinobacteria	1681	Bifidobacterium bifidum	99.93	210
FBI00211	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.78	211
FBI00212	Clostridium aldenense	bacteria	firmicutes	358742	Clostridium aldenense	99.1	212
FBI00220	Megasphaera massiliensis	bacteria	firmicutes	1232428	Megasphaera massiliensis	98.8	220
FBI00221	Butyricimonas faecihominis	bacteria	bacteroidetes	1472416	Butyricimonas faecihominis	98.61	221
FBI00224	Sutterella wadsworthensis	bacteria	proteobacteria	40545	Sutterella wadsworthensis	99.71	224
FBI00226	Catabacter hongkongensis	bacteria	firmicutes	270498	Catabacter hongkongensis	99.71	226
FBI00229	Alistipes senegalensis	bacteria	bacteroidetes	1288121	Alistipes senegalensis	99.19	229
FBI00231	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	99.11	231
FBI00232	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	98.84	232
FBI00233	Ruminococcaceae sp. FBI00233	bacteria	firmicutes	474960	Anaerotruncus colihominis	91.63	233
FBI00235	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	99.86	235
FBI00236	Eisenbergiella tayi	bacteria	firmicutes	1432052	Eisenbergiella tayi	99.41	236
FBI00237	Dielma fastidiosa	bacteria	firmicutes	1034346	Dielma fastidiosa	99.78	237
FBI00238	Alistipes sp. FBI00238	bacteria	bacteroidetes	239759	Alistipes finegoldii	95.84	238
FBI00243	Eubacterium siraeum	bacteria	firmicutes	39492	Eubacterium siraeum	98.53	243

FBI00244	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	98.69	244
FBI00245	Acidaminococcus intestini	bacteria	firmicutes	187327	Acidaminococcus intestini	99.72	245
FBI00248	Neglecta timonensis	bacteria	firmicutes	1776382	Emergencia timonensis	99.64	248
FBI00251	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.85	251
FBI00254	Eubacterium hallii	bacteria	firmicutes	39488	Eubacterium hallii	99.08	254
FBI00255	Hungatella effluvii	bacteria	firmicutes	1096246	Hungatella hathewayi	98.56	255
FBI00258	Turicibacter sanguinis	bacteria	firmicutes	154288	Turicibacter sanguinis	99.93	258
FBI00260	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.64	260
FBI00263	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.56	263
FBI00267	Anaerofustis stercorihominis	bacteria	firmicutes	214853	Anaerofustis stercorihominis	97.29	267
FBI00269	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	100	269
FBI00270	Methanobrevibacter smithii	archaea	euryarchaeota	2173	Methanobrevibacter smithii	99.69	270
FBI00271	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	98.42	271
FBI00273	Barnesiella intestinihominis	bacteria	bacteroidetes	487174	Barnesiella intestinihominis	99.43	273
FBI00274	Eubacterium xylanophilum	bacteria	firmicutes	39497	Eubacterium xylanophilum	93.5	274
FBI00275	Holdemanella biformis	bacteria	firmicutes	1735	Holdemanella biformis	98.99	275
FBI00277	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.63	277
FBI00278	Eubacterium ventriosum	bacteria	firmicutes	39496	Eubacterium ventriosum	94.14	278

FBI00281	Senegalimassilia anaerobia	bacteria	actinobacteria	1473216	Senegalimassilia anaerobia	99.45	281
FBI00282	Porphyromonas asaccharolytica	bacteria	bacteroidetes	28123	Porphyromonas asaccharolytica	99.35	282
FBI00288	Blautia hydrogenotrophica	bacteria	firmicutes	53443	Blautia hydrogenotrophica	99.57	288
FBI00289	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	289
FBI00290	Lachnospiraceae sp. FBI00290	bacteria	firmicutes	186803	Eubacterium ruminantium	94.81	290
FBI00292	Methanobrevibacter smithii	archaea	euryarchaeota	2173	Methanobrevibacter smithii	99.44	292
FBI00377	Clostridiales sp. FBI00377	bacteria	firmicutes	186802	Christensenella massiliensis	88.69	377

TABLE 23

Strain #	Species ID	Kingdom	Phylum	NCBI Taxonomy ID	Closest 16S Species	% Match (16S)	SEQ ID NO: X
FBI00001	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.64	1
FBI00002	Bacteroides salyersiae	bacteria	bacteroidetes	291644	Bacteroides salyersiae	99.5	2
FBI00004	Neglecta timonensis	bacteria	firmicutes	1776382	Neglecta timonensis	99.14	4
FBI00009	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium faecale	98.6	9
FBI00010	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.12	10
FBI00011	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.28	11
FBI00012	Alistipes onderdonkii	bacteria	bacteroidetes	328813	Alistipes onderdonkii	99.71	12

FBI00013	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.5	13
FBI00015	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	15
FBI00016	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.64	16
FBI00018	Eubacterium rectale	bacteria	firmicutes	39491	Eubacterium rectale	99.71	18
FBI00019	Alistipes timonensis	bacteria	bacteroidetes	1465754	Alistipes timonensis	99.78	19
FBI00020	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.57	20
FBI00021	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides kribbi	99.07	21
FBI00022	Alistipes putredinis	bacteria	bacteroidetes	28117	Alistipes putredinis	99.93	22
FBI00025	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	99.21	25
FBI00027	Fusicatenibacter saccharivorans	bacteria	firmicutes	1150298	Fusicatenibacter saccharivorans	97.6	27
FBI00029	Parabacteroides distasonis	bacteria	bacteroidetes	823	Parabacteroides distasonis	99.26	29
FBI00030	Eggerthella lenta	bacteria	firmicutes	84112	Eggerthella lenta	98.47	30
FBI00032	Anaerostipes hadrus	bacteria	firmicutes	649756	Anaerostipes hadrus	99.64	32
FBI00033	Lachnospiraceae sp. FBI00033	bacteria	firmicutes	186803	Clostridium amygdalinum	93.56	33
FBI00034	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.78	34
FBI00036	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.53	36
FBI00038	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	95.96	38
FBI00040	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.38	40
FBI00043	Bifidobacterium dentium	bacteria	actinobacteria	1689	Bifidobacterium dentium	99.35	43
FBI00044	Blautia wexlerae	bacteria	firmicutes	418240	Blautia wexlerae	98.69	44

FBI00046	Bacteroides caccae	bacteria	bacteroidetes	47678	Bacteroides caccae	99.71	46
FBI00047	Eubacterium eligens	bacteria	firmicutes	39485	Eubacterium eligens	98.79	47
FBI00048	Fusicatenibacter saccharivorans	bacteria	firmicutes	1150298	Fusicatenibacter saccharivorans	97.95	48
FBI00049	Dialister succinatiphilus	bacteria	firmicutes	487173	Dialister succinatiphilus	95.74	49
FBI00050	Bacteroides nordii	bacteria	bacteroidetes	291645	Bacteroides nordii	98.63	50
FBI00051	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	98.07	51
FBI00052	Bacteroides xylanisolvens	bacteria	bacteroidetes	371601	Bacteroides xylanisolvens	99.14	52
FBI00053	Lactobacillus rogosae	bacteria	firmicutes	706562	Lachnospira pectinoschiza	97.36	53
FBI00055	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides kribbi	99.64	55
FBI00056	Clostridium citroniae	bacteria	firmicutes	358743	Clostridium citroniae	99.2	56
FBI00057	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.7	57
FBI00059	Bacteroides stercorirosoris	bacteria	bacteroidetes	871324	Bacteroides oleiciplenus	98.81	59
FBI00060	Bifidobacterium longum	bacteria	actinobacteria	216816	Bifidobacterium longum	99.49	60
FBI00061	Alistipes shahii	bacteria	bacteroidetes	328814	Alistipes shahii	99.19	61
FBI00062	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	99.48	62
FBI00066	Parasutterella excrementihominis	bacteria	proteobacteria	487175	Parasutterella excrementihominis	99.13	66
FBI00067	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	98.84	67
FBI00068	Akkermansia muciniphila	bacteria	verrucomicrobia	239935	Akkermansia muciniphila	99.42	68
FBI00069	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.84	69

FBI00070	Bacteroides kribbi / Bacteroides koreensis species cluster	bacteria	bacteroidetes	816	Bacteroides koreensis	99.71	70
FBI00071	Lachnospiraceae sp. FBI00071	bacteria	firmicutes	186803	Roseburia faecis	94.92	71
FBI00072	Coprococcus eutactus	bacteria	firmicutes	33043	Coprococcus eutactus	96.17	72
FBI00074	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.03	74
FBI00075	Paraprevotella clara	bacteria	bacteroidetes	454154	Paraprevotella clara	98.85	75
FBI00076	Bacteroides thetaiotaomicron	bacteria	bacteroidetes	818	Bacteroides thetaiotaomicron	99.78	76
FBI00077	Sutterella wadsworthensis	bacteria	proteobacteria	40545	Sutterella wadsworthensis	99.86	77
FBI00078	Blautia obeum	bacteria	firmicutes	40520	Blautia obeum	98.34	78
FBI00079	Clostridium clostridioforme	bacteria	firmicutes	1531	Clostridium clostridioforme	99.14	79
FBI00080	Sutterella massiliensis	bacteria	proteobacteria	1816689	Sutterella massiliensis	99.78	80
FBI00081	Porphyromonas asaccharolytica	bacteria	bacteroidetes	28123	Porphyromonas asaccharolytica	99.35	81
FBI00082	Ruminococcaceae sp. FBI00082 FBI00097	bacteria	firmicutes	541000	Phocea massiliensis	93.08	82
FBI00085	Ruminococcus bromii	bacteria	firmicutes	40518	Ruminococcus bromii	98.62	85
FBI00087	Clostridium scindens	bacteria	firmicutes	29347	Clostridium scindens	98.28	87
FBI00092	Monoglobus pectinilyticus	bacteria	firmicutes	1981510	Monoglobus pectinilyticus	99.5	92
FBI00093	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	99.71	93
FBI00096	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.76	96
FBI00097	Ruminococcaceae sp. FBI00082 FBI00097	bacteria	firmicutes	541000	Phocea massiliensis	93.07	97

FBI00099	Gordonibacter pamelaeae	bacteria	actinobacteria	471189	Gordonibacter pamelaeae	99.56	99
FBI00101	Faecalibacterium prausnitzii	bacteria	firmicutes	853	Faecalibacterium prausnitzii	97.97	101
FBI00102	Clostridium fessum	bacteria	firmicutes	2126740	Clostridium symbiosum	94.31	102
FBI00104	Blautia wexlerae	bacteria	firmicutes	418240	Blautia luti	97.18	104
FBI00109	Coprococcus comes	bacteria	firmicutes	410072	Coprococcus comes	98.39	109
FBI00110	Lachnoclostridium pacaense	bacteria	firmicutes	1917870	Lachnoclostridium pacaense	98.92	110
FBI00111	Bacteroides vulgatus	bacteria	bacteroidetes	821	Bacteroides vulgatus	99.43	111
FBI00112	Bacteroides uniformis	bacteria	bacteroidetes	820	Bacteroides uniformis	99.78	112
FBI00113	Parabacteroides merdae	bacteria	bacteroidetes	46503	Parabacteroides merdae	99.79	113
FBI00115	Dorea formicigenerans	bacteria	firmicutes	39486	Dorea formicigenerans	97.98	115
FBI00116	Ruminococcus faecis	bacteria	firmicutes	592978	Ruminococcus faecis	99.57	116
FBI00117	Blautia faecis	bacteria	firmicutes	871665	Blautia faecis	99.52	117
FBI00120	Hungatella effluvii	bacteria	firmicutes	154046	Hungatella hathewayi	98.78	120
FBI00123	Roseburia hominis	bacteria	firmicutes	301301	Roseburia hominis	100	123
FBI00124	Anaerostipes hadrus	bacteria	firmicutes	649756	Anaerostipes hadrus	99.86	124
FBI00125	Bacteroides stercoris	bacteria	bacteroidetes	46506	Bacteroides stercoris	99.64	125
FBI00126	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	98.98	126
FBI00127	Collinsella aerofaciens	bacteria	actinobacteria	74426	Collinsella aerofaciens	98.81	127
FBI00128	Hungatella effluvii	bacteria	firmicutes	1096246	Hungatella effluvii	98.71	128
FBI00132	Gordonibacter pamelaeae	bacteria	actinobacteria	471189	Gordonibacter pamelaeae	99.48	132
FBI00133	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	133
FBI00135	Bifidobacterium pseudocatenulatum	bacteria	actinobacteria	28026	Bifidobacterium pseudocatenulatum	99.57	135
FBI00137	Bacteroides fragilis	bacteria	bacteroidetes	817	Bacteroides fragilis	99.71	137

FBI00140	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.58	140
FBI00141	Phascolarctobacterium faecium	bacteria	firmicutes	33025	Phascolarctobacterium faecium	99.15	141
FBI00145	Bifidobacterium adolescentis	bacteria	actinobacteria	1680	Bifidobacterium adolescentis	99.14	145
FBI00147	Clostridium bolteae	bacteria	firmicutes	208479	Clostridium bolteae	99.28	147
FBI00149	Monoglobus pectinilyticus	bacteria	firmicutes	1981510	Monoglobus pectinilyticus	99.5	149
FBI00151	Clostridium aldenense	bacteria	firmicutes	358742	Clostridium aldenense	98.55	151
FBI00152	Dialister invisus	bacteria	firmicutes	218538	Dialister invisus	99.58	152
FBI00159	Eisenbergiella tayi	bacteria	firmicutes	1432052	Eisenbergiella tayi	99.03	159
FBI00162	Bifidobacterium catenulatum	bacteria	actinobacteria	1686	Bifidobacterium catenulatum	99.14	162
FBI00165	Bacteroides massiliensis	bacteria	bacteroidetes	204516	Bacteroides massiliensis	99.71	165
FBI00167	Dorea longicatena	bacteria	firmicutes	88431	Dorea longicatena	99.39	167
FBI00170	Eggerthella lenta	bacteria	actinobacteria	84112	Eggerthella lenta	98.61	170
FBI00171	Bilophila wadsworthia	bacteria	proteobacteria	35833	Desulfovibrio desulfuricans	91.45	171
FBI00174	Lactobacillus rogosae	bacteria	firmicutes	706562	Lachnospira pectinoschiza	97.92	174
FBI00175	Holdemanella biformis	bacteria	firmicutes	1735	Holdemanella biformis	98.19	175
FBI00176	Ruthenibacterium lactatiformans	bacteria	firmicutes	1550024	Ruthenibacterium lactatiformans	99.71	176
FBI00289	Oxalobacter formigenes	bacteria	proteobacteria	847	Oxalobacter formigenes	99.21	289

TABLE 24.

Strain #	Species: 16S Best-BLAST	% Match (16S)	Kingdom	Phylum	NCBI Taxonomy ID	SEQ ID NO: X
FBI00002	Bacteroides salyersiae	99.5	bacteria	bacteroidetes	291644	2
FBI00004	Neglecta timonensis	99.14	bacteria	firmicutes	1776382	4
FBI00009	Bifidobacterium faecale	98.6	bacteria	actinobacteria	1454229	9
FBI00010	Blautia obeum	98.12	bacteria	firmicutes	40520	10
FBI00012	Alistipes onderdonkii	99.71	bacteria	bacteroidetes	328813	12
FBI00013	Parabacteroides merdae	99.5	bacteria	bacteroidetes	46503	13
FBI00015	Bacteroides uniformis	99.78	bacteria	bacteroidetes	820	15
FBI00016	Bifidobacterium pseudocatenulatum	99.64	bacteria	actinobacteria	28026	16
FBI00018	Eubacterium rectale	99.71	bacteria	firmicutes	39491	18
FBI00019	Alistipes timonensis	99.78	bacteria	bacteroidetes	1465754	19
FBI00021	Bacteroides kribbi	99.07	bacteria	bacteroidetes	1912894	21
FBI00022	Alistipes putredinis	99.93	bacteria	bacteroidetes	28117	22
FBI00029	Parabacteroides distasonis	99.26	bacteria	bacteroidetes	823	29
FBI00032	Anaerostipes hadrus	99.64	bacteria	firmicutes	649756	32
FBI00033	Clostridium amygdalinum	93.56	bacteria	firmicutes	31979	33
FBI00034	Eubacterium eligens	98.78	bacteria	firmicutes	39485	34
FBI00038	Coprococcus eutactus	95.96	bacteria	firmicutes	33043	38

FBI00043	Bifidobacterium dentium	99.35	bacteria	actinobacteria	1689	43
FBI00044	Blautia wexlerae	98.69	bacteria	firmicutes	418240	44
FBI00046	Bacteroides caccae	99.71	bacteria	bacteroidetes	47678	46
FBI00048	Fusicatenibacter saccharivorans	97.95	bacteria	firmicutes	1150298	48
FBI00049	Dialister succinatiphilus	95.74	bacteria	firmicutes	487173	49
FBI00050	Bacteroides nordii	98.63	bacteria	bacteroidetes	291645	50
FBI00051	Dorea formicigenerans	98.07	bacteria	firmicutes	39486	51
FBI00052	Bacteroides xylanisolvens	99.14	bacteria	bacteroidetes	28116	52
FBI00056	Clostridium citroniae	99.2	bacteria	firmicutes	358743	56
FBI00057	Dorea longicatena	99.7	bacteria	firmicutes	88431	57
FBI00059	Bacteroides oleiciplenus	98.81	bacteria	bacteroidetes	626931	59
FBI00060	Bifidobacterium longum	99.49	bacteria	actinobacteria	216816	60
FBI00061	Alistipes shahii	99.19	bacteria	bacteroidetes	328814	61
FBI00067	Oxalobacter formigenes	98.84	bacteria	proteobacteria	847	67
FBI00068	Akkermansia muciniphila	99.42	bacteria	verrucomicrobia	239935	68
FBI00069	Ruminococcus bromii	98.84	bacteria	firmicutes	40518	69
FBI00070	Bacteroides koreensis	99.71	bacteria	bacteroidetes	1912896	70
FBI00071	Roseburia faecis	94.92	bacteria	firmicutes	1732	71
FBI00075	Paraprevotella clara	98.85	bacteria	bacteroidetes	454154	75
FBI00076	Bacteroides thetaiotaomicron	99.78	bacteria	bacteroidetes	818	76
FBI00079	Clostridium clostridioforme	99.14	bacteria	firmicutes	1531	79

FBI00080	Sutterella massiliensis	99.78	bacteria	proteobacteria	1816689	80
FBI00087	Clostridium scindens	98.28	bacteria	firmicutes	29347	87
FBI00093	Roseburia hominis	99.71	bacteria	firmicutes	301301	93
FBI00097	Phocea massiliensis	93.07	bacteria	firmicutes	1841867	97
FBI00101	Faecalibacterium prausnitzii	97.97	bacteria	firmicutes	853	101
FBI00102	Clostridium symbiosum	94.31	bacteria	firmicutes	1512	102
FBI00104	Blautia luti	97.18	bacteria	firmicutes	418240	104
FBI00109	Coprococcus comes	98.39	bacteria	firmicutes	410072	109
FBI00117	Blautia faecis	99.52	bacteria	firmicutes	871665	117
FBI00120	Hungatella hathewayi	98.78	bacteria	firmicutes	154046	120
FBI00125	Bacteroides stercoris	99.64	bacteria	bacteroidetes	46506	125
FBI00127	Collinsella aerofaciens	98.81	bacteria	actinobacteria	74426	127
FBI00128	Hungatella effluvii	98.71	bacteria	firmicutes	1096246	128
FBI00132	Gordonibacter pamelaeae	99.48	bacteria	actinobacteria	471189	132
FBI00133	Oxalobacter formigenes	99.21	bacteria	proteobacteria	847	133
FBI00137	Bacteroides fragilis	99.71	bacteria	bacteroidetes	817	137
FBI00141	Phascolarctobacterium faecium	99.15	bacteria	firmicutes	33025	141
FBI00145	Bifidobacterium adolescentis	99.14	bacteria	actinobacteria	1680	145
FBI00149	Monoglobus pectinilyticus	99.5	bacteria	firmicutes	1981510	149
FBI00151	Clostridium aldenense	98.55	bacteria	firmicutes	358742	151
FBI00152	Dialister invisus	99.58	bacteria	firmicutes	218538	152

FBI00162	Bifidobacterium catenulatum	99.14	bacteria	actinobacteria	1686	162
FBI00165	Bacteroides massiliensis	99.71	bacteria	bacteroidetes	204516	165
FBI00171	Desulfovibrio desulfuricans	91.45	bacteria	proteobacteria	876	171
FBI00174	Lachnospira pectinoschiza	97.92	bacteria	firmicutes	28052	174
FBI00176	Ruthenibacterium lactatiformans	99.71	bacteria	firmicutes	1550024	176
FBI00177	Parasutterella excrementihominis	99.71	bacteria	proteobacteria	487175	177
FBI00180	Alistipes senegalensis	97.56	bacteria	bacteroidetes	1288121	180
FBI00182	Bacteroides coprocola	99.64	bacteria	bacteroidetes	310298	182
FBI00184	Bacteroides faecis	99.78	bacteria	bacteroidetes	674529	184
FBI00190	Bacteroides finegoldii	98.91	bacteria	bacteroidetes	338188	190
FBI00191	Clostridium swellfunianum	96.24	bacteria	firmicutes	1367462	191
FBI00194	Ruminococcus faecis	98.41	bacteria	firmicutes	592978	194
FBI00197	Bifidobacterium bifidum	99.85	bacteria	actinobacteria	1681	197
FBI00198	Lachnoclostridium pacaense	99.71	bacteria	firmicutes	1917870	198
FBI00199	Clostridium bolteae	99.28	bacteria	firmicutes	208479	199
FBI00200	Longicatena caecimuris	99.71	bacteria	firmicutes	1796635	200
FBI00201	Eggerthella lenta	98.83	bacteria	actinobacteria	84112	201
FBI00205	Blautia luti	97.55	bacteria	firmicutes	89014	205
FBI00208	Anaerotruncus colihominis	96.52	bacteria	firmicutes	169435	208
FBI00211	Bacteroides vulgatus	99.78	bacteria	bacteroidetes	821	211
FBI00220	Megasphaera massiliensis	98.8	bacteria	firmicutes	1232428	220

FBI00221	Butyricimonas faecihominis	98.61	bacteria	bacteroidetes	1472416	221
FBI00224	Sutterella wadsworthensis	99.71	bacteria	proteobacteria	40545	224
FBI00226	Catabacter hongkongensis	99.71	bacteria	firmicutes	270498	226
FBI00233	Anaerotruncus colihominis	91.63	bacteria	firmicutes	474960	233
FBI00236	Eisenbergiella tayi	99.41	bacteria	firmicutes	1432052	236
FBI00237	Dielma fastidiosa	99.78	bacteria	firmicutes	1034346	237
FBI00238	Alistipes finegoldii	95.84	bacteria	bacteroidetes	214856	238
FBI00243	Eubacterium siraeum	98.53	bacteria	firmicutes	39492	243
FBI00245	Acidaminococcus intestini	99.72	bacteria	firmicutes	187327	245
FBI00248	Emergencia timonensis	99.64	bacteria	firmicutes	1776384	248
FBI00254	Eubacterium hallii	99.08	bacteria	firmicutes	39488	254
FBI00258	Turicibacter sanguinis	99.93	bacteria	firmicutes	154288	258
FBI00267	Anaerofustis stercorihominis	97.29	bacteria	firmicutes	214853	267
FBI00273	Barnesiella intestinihominis	99.43	bacteria	bacteroidetes	487174	273
FBI00274	Eubacterium xylanophilum	93.5	bacteria	firmicutes	39497	274
FBI00275	Holdemanella biformis	98.99	bacteria	firmicutes	1735	275
FBI00278	Eubacterium ventriosum	94.14	bacteria	firmicutes	39496	278
FBI00281	Senegalimassilia anaerobia	99.45	bacteria	actinobacteria	1473216	281
FBI00282	Porphyromonas asaccharolytica	99.35	bacteria	bacteroidetes	28123	282
FBI00288	Blautia hydrogenotrophica	99.57	bacteria	firmicutes	53443	288
FBI00289	Oxalobacter formigenes	99.21	bacteria	proteobacteria	847	289

FBI00290	Eubacterium ruminantium	94.81	bacteria	firmicutes	42322	290
FBI00292	Methanobrevibacter smithii	99.44	archaea	euryarchaeota	2173	292
FBI00377	Christensenella massiliensis	88.69	bacteria	firmicutes	186802	377

Example 17: *in vivo* oxalate reduction by a therapeutic microbial consortium in healthy humans treated with a high oxalate / low calcium diet

[0333] This study evaluates the ability of a rationally designed oxalate-degrading microbial consortium to reduce urinary oxalate levels *in vivo* in human subjects.

[0334] Approximately 64 healthy subjects are enrolled for the study. Six days prior to administration of the consortium, subjects are placed on a high oxalate / low calcium (HOLC) diet in order to create a temporary hyperoxaluric state akin to what is seen in enteric hyperoxaluria (Langman *et al.*, 2016, "A double-blind, placebo controlled, randomized phase 1 cross-over study with ALLN-177, an orally administered oxalate degrading enzyme," *Am J Nephrol.* 44(2):150-8). When administered to healthy subjects over 7 days, this diet has been previously shown to increase urinary oxalate from 27.2 ± 9.5 mg/day during screening to 80.8 ± 24.1 mg/day. This is well above the generally accepted upper limit of normal (40 mg/day) and clearly within the range seen in enteric hyperoxaluria.

[0335] Some subjects are additionally pre-treated with a course of broad spectrum antibiotics (a combination of metronidazole and clarithromycin) in order to pre-clear bacteria from the gut and facilitate subsequent engraftment of the heterologous community. This combination is selected based on the complementary coverage of gram-positive as well as gram-negative bacteria, broad coverage of obligate anaerobes (which dominate the microbial population in the GI tract) as well as facultative anaerobes, including enteric pathobionts (i.e. human commensals with pathogenic potential), and the relatively favorable safety and tolerability profiles of the constituent drugs. The goal of antibiotic pretreatment is to reduce pre-existing gastrointestinal bacterial load in an attempt to suppress colonization resistance, a microbially-mediated phenomenon that could limit the engraftment of strains in the consortium.

[0336] On Day 6 of administration of the HOLC diet and (optionally) the antibiotic pretreatment, some subjects are additionally given a polyethylene glycol (PEG) bowel preparation treatment, an approach commonly used in fecal matter transplant administration and that will be familiar to one skilled in the art. This treatment is designed to clear remaining antibiotics from the gastrointestinal tract and further reduce remaining bacterial load from the host.

[0337] Six days following administration of the HOLC diet, subjects are administered the therapeutic microbial consortium. The duration of treatment with the consortium or the placebo is 10 days. Urine oxalate excretion is used as a biomarker for treatment efficacy, and

is monitored by LC-MS as described in Example 4. Stool samples are collected at all stages of the trial (including 1 month post-treatment) and used to monitor the composition of the microbiome by metagenomic sequencing. This facilitates monitoring the level and duration of engraftment of consortium strains.

[0338] Approximately 64 healthy human subjects are randomly assigned to one of the following five regimens in a 1:1:1:1 ratio:

a. Antibiotic pretreatment followed by bowel preparation with PEG followed by the treatment with the consortium.
b. Antibiotic pretreatment followed by treatment with the consortium.
c. Antibiotic placebo treatment followed by bowel preparation with PEG followed by treatment with the consortium.
d. Antibiotic pretreatment followed by treatment with a placebo.

[0339] Subjects are kept in confinement for two periods, separated by an approximately 20 day washout. The first confinement period is approximately 18 days, which includes antibiotic/antibiotic placebo pretreatment, followed by either a bowel preparation with PEG or no bowel preparation, followed by 10-day course of a therapeutic consortium or a placebo. The second confinement period is approximately 6 days. The sample size of this study was chosen to distinguish an approximately 20% change in in urinary oxalate levels between cohorts. This study enables evaluation of the ability of a therapeutic consortium to reduce levels of urine oxalate in a human subject. This study further evaluates the efficacy of the described pretreatment methods (antibiotic pretreatment and PEG preparation).

Example 18: *in vivo* oxalate reduction by a therapeutic microbial consortium in humans patients with enteric hyperoxaluria

[0340] Enteric hyperoxaluria is characterized by excess absorption or consumption of dietary oxalate leading to increased renal oxalate excretion (>40 mg/day), recurrent kidney stones, renal calcium deposition (nephrocalcinosis) and, in severe cases, progressive renal impairment and end-stage renal failure (Liu and Nazzal, 2019, "Enteric hyperoxaluria: role of microbiota and antibiotics," *Curr Opin Nephrol Hypertens*. 28(4):352-359; Ermer *et al.*, 2016, "Oxalate, inflammasome, and progression of kidney disease," *Curr Opin Nephrol Hypertens*. 25(4):363-71). Roux-en-Y Gastric Bypass (RYGB) surgery is a common comorbidity associated with enteric hyperoxaluria (~60% of RYGB patients). This study evaluates the ability of an oxalate-degrading microbial consortium to reduce urinary oxalate

levels *in vivo* in a cohort of up to approximately 16 Roux-en-Y Gastric Bypass (RYGB) patients with enteric hyperoxaluria.

[0341] A cohort of up to approximately 16 subjects is given an antibiotic pretreatment, a PEG bowel preparation treatment, and a 10-day treatment with a therapeutic microbial consortium as described in Example 17. Urine and stool samples are collected at different stages of the treatment to monitor urine oxalate levels and engraftment of consortium strains as described in Example 17. Stool samples are further collected after 30, 60, and 90 days to evaluate long-term engraftment of consortium strains by metagenomic sequencing. This study will demonstrate the ability of the consortium to reduce urinary oxalate levels in the RYGB patients.

Example 19: Screening strains for *in vitro* bile acid compound metabolic activity

[0342] *in vitro* metabolic screening is necessary to definitively characterize the ability of a microbial strain to degrade bile acid compounds. Strains are screened against a panel of bile acid compounds and structural conversion of the bile acids are evaluated as described. Briefly, overnight microbial monocultures are harvested by anaerobic centrifugation and resuspended in fresh pre-reduced growth medium (*e.g.* Mega Medium) spiked with 100 µM of bile acid (e.g. TCA, TCDCA, GCA, GCDCA, CA, CDCA, 3oxoCA, 7oxoCA, 12oxoCA, UDCA, DCA, LCA, 3oxoLCA) and allowed to incubate at 37 °C for 24 h. Cultures are sampled for bile acid analysis at 0, 6 and 24 h post-bile acid spike. For bile acid analysis, 2 ml of culture are sampled and immediately acidified with 50 µl of 6 N HCl to stop all metabolic activity and protonate bile acids to make them more soluble in organic solvent. Acidified cultures are extracted for bile acids and analyzed by LCMS (UPLC-QTOF or UPLC-QQQ).

[0343] Preliminary screening of commercial strains using TCA as the feeder molecule were obtained using this protocol, and the results are illustrated in FIGURE 18.

Example 20: Screening strains for resistance to bile acids

[0344] To determine the effect of the presence of bile acid on microbial strain growth, microbial cultures are grown in their respective banking medium (*e.g.* Mega Media or Chopped Meat Media) to saturation and back-diluted into the same respective banking medium containing a variable concentration of bile acids. % growth inhibition is calculated by determining the ratio of background-subtracted optical density (O.D.) of a microbial strain

grown in the presence of bile acid to the O.D. of the same microbial strain grown in the absence of bile acid.

Example 21: Murine model of chemically-induced primary sclerosing cholangitis and microbiome-induced shift in bile acid composition

[0345] This example describes the establishment of a chemically-induced murine model of primary sclerosing cholangitis (PSC) and demonstrates that alterations to a microbiome can alter the composition of the bile acid pool and affect disease severity.

[0346] On Day 0 of the experiment, germ-free 7-9 week-old germ-free C57B/6N female mice are weighed and colonized by oral gavage with one of two rationally-designed microbial consortia. One cohort of mice is colonized with a full microbial consortium that comprises a plurality of microbes including species having 7α-dehydroxylation activity and species having bile salt hydrolase (BSH) activity. A second cohort of mice is colonized with a partial microbial consortium which is identical in composition to the full consortium except that it lacks species having 7α-dehydroxylation activity. A control cohort of mice is treated with sterile saline.

[0347] The mice are fed for two weeks on a standard laboratory diet while the microbiome stabilizes. Beginning on Day 14 and for the following 14 days, the standard diet is supplemented either with 1% (w/w) hepatotoxic secondary bile acid LCA to induce PSC, or with an equimolar concentration of the conjugated bile acid GCDCA or the primary bile acid CDCA. GCDCA can be metabolized into CDCA by a population of microbes having BSH activity, and CDCA can be metabolized into LCA by a population of microbes having 7α-dehydroxylation activity.

[0348] On Days 0, 7, 14, 21, and 28, mice are monitored for indicators of chemically-induced PSC (*e.g.* reduced body weight, reduced food consumption, elevated liver enzyme levels) and fecal samples are collected. Fecal samples are analyzed by both LC/MS to determine the composition of the bile acid pool and by metagenomic sequencing to monitor microbial strain engraftment. Mice are euthanized on or before Day 28 and terminal samples are collected to enable screening for additional PSC indicators (*e.g.* changes to GI physiology, cecum bile acid composition).

[0349] Mice fed a diet supplemented with hepatotoxic LCA are expected to have elevated levels of fecal LCA and are expected to exhibit signs of PSC, thereby establishing a murine model of the disease. Mice colonized with the full set of microbes and fed a diet supplemented with GCDCA or CDCA are likewise expected to have elevated LCA content,

as the upstream substrates can be metabolized into LCA by the engrafted set of microbes. Mice implanted with the partial set of microbes and fed a diet supplemented with conjugated bile acid are expected to not have LCA in their bile acid pool because the implanted microbial population lacks the activity necessary to metabolize the upstream substrates into LCA; these mice are accordingly expected to exhibit less severe signs of PSC. Taken together, these results will demonstrate that alterations to the microbiome can drive shifts in the bile acid pool in an animal and affect disease severity.

Example 22: *in vivo* reduction of hepatotoxic bile acids in a mouse model of PSC by treatment with a microbial consortium

[0350] This example evaluates the ability of a bile-acid-metabolizing microbial consortium, comprising a plurality of active microbes and a supportive community of microbes, to alter the bile acid pool of an animal and affect disease severity. Said microbial consortium comprises a plurality of active microbes and a supportive community of microbes, wherein said plurality of active microbes comprises strains experimentally verified to have 3α-HSDH and/or 3β-HSDH activity, and said supportive community of microbes comprises strains experimentally verified to have 7α-HSDH activity, 7β-HSDH activity, and/or bile salt hydrolase activity.

[0351] To test the *in vivo* activity of a bile-acid-metabolizing microbial consortium described herein, germ-free C57B/6N female mice are weighed on Day 0 and colonized by oral gavage with either a plurality of active microbes alone, a supportive community alone, or a complete microbial consortium (actives and supportives). The mice are fed for two weeks on a standard laboratory diet while the microbiome stabilizes. Beginning on Day 14 and for the following 14 days, the standard diet is supplemented with the hepatotoxic secondary bile acid LCA (1% w/w) to induce PSC. Body weight, food weight, and fecal bile acid composition are monitored over the course of two weeks. After the two-week period, mice are sacrificed and a variety of terminal samples are collected including the cecum, feces, and serum.

[0352] Mice treated with the complete microbial consortium (actives and supportives) are expected to have reduced levels of hepatotoxic LCA and are expected to exhibit less severe signs of PSC relative to an untreated control (no microbial implantation). The mice treated with the active microbes alone are also expected to have lowered LCA levels relative to the untreated mice, but less so than the mice treated with the full consortium. The mice implanted with the supportive community only are not expected to have substantially lower

LCA levels than the untreated mice. Taken together, these results will demonstrate the ability of a bile-acid-metabolizing microbial consortium to alter the pool of bile acids in an animal and consequently alleviate PSC symptoms.

CLAIMS

WHAT IS CLAIMED IS:

1. A microbial consortium for administration to an animal, comprising:
a plurality of active microbes and an effective amount of a supportive community of microbes, wherein
the plurality of active microbes metabolize a first metabolic substrate to produce one or more than one metabolite, wherein the first metabolic substrate causes or contributes to disease in an animal, and
the supportive community of microbes comprises between 1 and 300 microbial strains,
wherein for the supportive community of microbes, at least one of the following four conditions is met:
1) the supportive community of microbes metabolizes one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the first metabolic substrate by one or more of the plurality of active microbes,
2) the supportive community of microbes increases the flux of a precursor of the first metabolic substrate into a biochemical pathway that converts said precursor into a metabolite that is not the first metabolic substrate,
3) the supportive community of microbes enhances one or more than one characteristic of the plurality of active microbes when administered to an animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes, and
4) the supportive community of microbes catalyzes one or more than one reaction selected from the group consisting of: fermentation of polysaccharides to one or more than one of the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2, fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2, synthesis of one or

more than one of the group consisting of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

2. The microbial consortium of claim 1, wherein the supportive community of microbes:

1) metabolizes one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the first metabolic substrate by one or more of the plurality of active microbes, and

2) increases the flux of a precursor of the first metabolic substrate into a biochemical pathway that converts said precursor into a metabolite that is not the first metabolic substrate.

3. The microbial consortium of claim 1, wherein the supportive community of microbes:

1) metabolizes one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the first metabolic substrate by one or more of the plurality of active microbes, and

2) enhances one or more than one characteristic of the plurality of active microbes when administered to the animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes.

4. The microbial consortium of claim 1, wherein the supportive community of microbes:

1) metabolizes one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the first metabolic substrate by one or more of the plurality of active microbes, and

2) catalyzes one or more than one reaction selected from the group consisting of: fermentation of polysaccharides to one or more than one of the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2, fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2, synthesis of one or more than one of the group consisting of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

5. The microbial consortium of claim 1, wherein the supportive community of microbes:

1) increases the flux of a precursor of the first metabolic substrate into a biochemical pathway that converts said precursor into a metabolite that is not the first metabolic substrate, and

2) enhances one or more than one characteristic of the plurality of active microbes when administered to the animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes.

6. The microbial consortium of claim 1, wherein the supportive community of microbes:

1) increases the flux of a precursor of the first metabolic substrate into a biochemical pathway that converts said precursor into a metabolite that is not the first metabolic substrate, and

2) catalyzes one or more than one reaction selected from the group consisting of: fermentation of polysaccharides to one or more than one of the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2, fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2, synthesis of one or more than one of the group consisting of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

7. The microbial consortium of claim 1, wherein the supportive community of microbes:

1) enhances one or more than one characteristic of the plurality of active microbes when administered to the animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes, and

2) catalyzes one or more than one reaction selected from the group consisting of: fermentation of polysaccharides to one or more than one of the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol,

succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2, fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2, synthesis of one or more than one of the group consisting of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

8. The microbial consortium of claim 1, wherein the supportive community of microbes:

1) metabolizes one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the first metabolic substrate by one or more of the plurality of active microbes,

2) increases the flux of a precursor of the first metabolic substrate into a biochemical pathway that converts said precursor into a metabolite that is not the first metabolic substrate, and

3) enhances one or more than one characteristic of the plurality of active microbes when administered to an animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes.

9. The microbial consortium of claim 1, wherein the supportive community of microbes:

1) increases the flux of a precursor of the first metabolic substrate into a biochemical pathway that converts said precursor into a metabolite that is not the first metabolic substrate, and

2) enhances one or more than one characteristic of the plurality of active microbes when administered to an animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes, and

3) catalyzes one or more than one reaction selected from the group consisting of: fermentation of polysaccharides to one or more than one of the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2, fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2, synthesis of one or more than one of the group consisting of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

10. The microbial consortium of claim 1, wherein the supportive community of microbes:

1) metabolizes one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the first metabolic substrate by one or more of the plurality of active microbes,

2) increases the flux of a precursor of the first metabolic substrate into a biochemical pathway that converts said precursor into a metabolite that is not the first metabolic substrate, and

3) catalyzes one or more than one reaction selected from the group consisting of: fermentation of polysaccharides to one or more than one of the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2, fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2, synthesis of one or more than one of the group consisting of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

11. The microbial consortium of claim 1, wherein the supportive community of microbes:

1) metabolizes one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the first metabolic substrate by one or more of the plurality of active microbes,

2) enhances one or more than one characteristic of the plurality of active microbes when administered to an animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes, and

3) catalyzes one or more than one reaction selected from the group consisting of: fermentation of polysaccharides to one or more than one of the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2, fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2, synthesis of one or more than one of the group consisting of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

12. The microbial consortium of claim 1, wherein the supportive community of microbes:

1) metabolizes one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the first metabolic substrate by one or more of the plurality of active microbes,

2) increases the flux of a precursor of the first metabolic substrate into a biochemical pathway that converts said precursor into a metabolite that is not the first metabolic substrate,

3) enhances one or more than one characteristic of the plurality of active microbes when administered to an animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes, and

4) catalyzes one or more than one reaction selected from the group consisting of: fermentation of polysaccharides to one or more than one of the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2, fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2, synthesis of one or more than one of the group consisting of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

13. The microbial consortium according to any one of claims 1 to 12, wherein at least one of the two following conditions is met:

the first metabolic substrate metabolizing activity of at least one of the plurality of active microbes is significantly different when measured in a standardized substrate metabolization assay at two pH values within a range of 4 to 8, and wherein the difference between the two pH values is at least one pH unit, and

the first metabolic substrate metabolizing activity of at least one of the plurality of active microbes is significantly different when measured in a standardized substrate metabolization assay at two first metabolic substrate concentrations within a 100 fold range, and wherein the difference between the two first metabolic substrate concentrations is at least 1.2-fold.

14. The microbial consortium according to any one of claims 1 to 13, wherein the supportive community of microbes comprises at least three phyla selected from the group consisting

of Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia, and Euryarchaeota.

15. The microbial consortium of claim 14, wherein the supportive community of microbes comprises at least four phyla selected from the group consisting of Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia, and Euryarchaeota.

16. The microbial consortium of claim 15, wherein the supportive community of microbes comprises at least five phyla selected from the group consisting of Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia, and Euryarchaeota.

17. The microbial consortium of claim 16, wherein the supportive community of microbes comprises at least six phyla selected from the group consisting of Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia, and Euryarchaeota.

18. The microbial consortium according to any one of claims 14 to 17, wherein the supportive community of microorganisms comprises the subclade Bacteroidales.

19. The microbial consortium according to any one of claims 14 to 18, wherein the supportive community of microorganisms comprises the subclade Clostridiales.

20. The microbial consortium according to any one of claims 14 to 19, wherein the supportive community of microorganisms comprises the subclade Erysipelotrichales.

21. The microbial consortium according to any one of claims 14 to 20 wherein the supportive community of microorganisms comprises the subclade Negativicutes.

22. The microbial consortium according to any one of claims 14 to 21, wherein the supportive community of microorganisms comprises the subclade Coriobacteriia.

23. The microbial consortium according to any one of claims 14 to 22, wherein the supportive community of microorganisms comprises the subclade Bifidobacteriales.

24. The microbial consortium according to any one of claims 14 to 23, wherein the supportive community of microorganisms comprises the subclade Methanobacteriales.

25. The microbial consortium of claim 1, wherein the first metabolic substrate is oxalate.

26. The microbial consortium of claim 25, the metabolite is formate, and the supportive community of microbes catalyzes synthesis of methane from formate and H_2.

27. The microbial consortium of claim 26, wherein the plurality of active microbes comprises *Oxalobacter formigenes*.

28. The microbial consortium of claim 27, wherein the supportive community of microbes comprises a Bacteroidetes and a Euryarchaeota.

29. The microbial consortium of claim 28, wherein the supportive community of microbes comprises a *Bacteroides* and *Methanobrevibacter*.

30. The microbial consortium of claim 29, wherein the supportive community of microbes comprises *Bacteroides thetaiotaomicron* and/or *Bacteroides vulgatus*, and *Methanobrevibacter smithii*.

31. The microbial consortium of claim 25, wherein the supportive community of microbes comprises between 20 and 200 microbial strains.

32. The microbial consortium of claim 31, wherein the supportive community comprises at least 4 phyla selected from the group consisting of Bacteroidetes, Firmicutes, Actinobacteria, and Proteobacteria.

33. The microbial consortium of claim 32, wherein the supportive community comprises a *Ruminococcus*, *Clostridium*, *Bacteroides*, *Neglecta*, *Bifidobacterium*, *Egerthella*, *Clostridiaceae*, *Parabacteroides*, *Bilophila*, *Dorea*, *Collinsella*, and *Faecalibacterium*.

34. The microbial consortium of claim 33, wherein the supportive community comprises *Ruminococcus bromii*, *Clostridium citroniae*, *Bacteroides salyersiae*, *Neglecta*

timonensis, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bacteroides thetaiotaomicron*, *Eggerthella lenta*, *Clostridiaceae sp.*, *Bifidobacterium dentium*, *Parabacteroides merdae*, *Bilophila wadsworthia*, *Bacteroides caccae*, *Dorea longicatena*, *Collinsella aerofaciens*, *Clostridium scindens*, *Faecalibacterium prausnitzii*, *Clostridium symbiosum*, and *Bacteroides vulgatus*.

35. The microbial consortium of claim 32, wherein the supportive community comprises an *Acidaminococcus*, an *Akkermansia*, an *Alistipes*, an *Anaerofustis*, an *Anaerostipes*, an *Anaerotruncus*, a *Bacteroides*, a *Barnesiella*, a *Bifidobacterium*, a *Bilophila*, a *Blautia*, a *Butyricimonas*, a *Catabacter hongkongensis*, a *Clostridiaceae*, a *Clostridiales*, a *Clostridium*, a *Collinsella*, a *Coprococcus*, a *Dialister*, a *Dielma, a Dorea*, an *Eggerthella*, an *Eisenbergiella*, a *Eubacterium*, a *Faecalibacterium*, a *Fusicatenibacter saccharivorans*, a *Gordonibacter pamelaeae*, a *Holdemanella*, a *Hungatella*, a *Lachnoclostridium*, *Lachnospiraceae*, a *Lactobacillus*, a *Longicatena*, a *Megasphaera*, a *Methanobrevibacter*, a *Monoglobus*, a *Neglecta*, a *Parabacteroides*, a *Paraprevotella*, a *Parasutterella*, a *Phascolarctobacterium*, a *Porphyromonas*, a *Roseburia hominis*, a *Ruminococcaceae*, a *Ruminococcus*, a *Ruthenibacterium*, a *Senegalimassilia*, a *Sutterella*, and a *Turicibacter*.

36. The microbial consortium of claim 35, wherein the supportive community comprises *Acidaminococcus intestine*, *Akkermansia muciniphila*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Alistipes senegalensis*, *Alistipes shahii*, *Alistipes sp.*, *Alistipes timonensis*, *Anaerofustis stercorihominis*, *Anaerostipes hadrus*, *Anaerotruncus massiliensis*, *Bacteroides caccae*, *Bacteroides coprocola*, *Bacteroides faecis*, *Bacteroides finegoldii*, *Bacteroides fragilis*, *Bacteroides kribbi*, *Bacteroides massiliensis*, *Bacteroides nordii*, *Bacteroides ovatus*, *Bacteroides salyersiae*, *Bacteroides stercorirosoris*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvens*, *Barnesiella intestinihominis*, *Bifidobacterium adolescentis*, *Bifidobacterium bifidum*, *Bifidobacterium catenulatum, Bifidobacterium dentium*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bilophila wadsworthia*, *Blautia faecis*, *Blautia hydrogenotrophica*, *Blautia massiliensis*, *Blautia obeum*, *Blautia wexlerae*, *Butyricimonas faecihominis*, *Catabacter hongkongensis*, *Clostridiaceae sp.*, *Clostridiales sp.*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium citroniae*, *Clostridium clostridioforme*, *Clostridium fessum*, *Clostridium scindens*, *Collinsella*

aerofaciens, *Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dialister succinatiphilus*, *Dielma fastidiosa*, *Dorea formicigenerans*, *Dorea longicatena*, *Eggerthella lenta*, *Eisenbergiella tayi*, *Eubacterium eligens*, *Eubacterium hallii*, *Eubacterium rectale*, *Eubacterium siraeum*, *Eubacterium ventriosum*, *Eubacterium xylanophilum*, *Faecalibacterium prausnitzii*, *Fusicatenibacter saccharivorans*, *Gordonibacter pamelaeae*, *Holdemanella biformis*, *Hungatella effluvia*, *Lachnoclostridium pacaense*, *Lachnospiraceae sp.*, *Lactobacillus rogosae*, *Longicatena caecimuris*, *Megasphaera massiliensis*, *Methanobrevibacter smithii*, *Monoglobus pectinilyticus*, *Neglecta timonensis*, *Parabacteroides distasonis*, *Parabacteroides merdae*, *Paraprevotella clara*, *Parasutterella excrementihominis*, *Phascolarctobacterium faecium*, *Porphyromonas asaccharolytica*, *Roseburia hominis*, *Ruminococcaceae sp.*, *Ruminococcus bromii*, *Ruminococcus faecis*, *Ruthenibacterium lactatiformans*, *Senegalimassilia anaerobia*, *Sutterella massiliensis*, *Sutterella wadsworthensis*, and *Turicibacter sanguinis*.

37. The microbial consortium of claim 35, wherein the supportive community consists of *Acidaminococcus intestine*, *Akkermansia muciniphila*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Alistipes senegalensis*, *Alistipes shahii*, *Alistipes sp.*, *Alistipes timonensis*, *Anaerofustis stercorihominis*, *Anaerostipes hadrus*, *Anaerotruncus massiliensis*, *Bacteroides caccae*, *Bacteroides coprocola*, *Bacteroides faecis*, *Bacteroides finegoldii*, *Bacteroides fragilis*, *Bacteroides kribbi*, *Bacteroides massiliensis*, *Bacteroides nordii*, *Bacteroides ovatus*, *Bacteroides salyersiae*, *Bacteroides stercorirosoris*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvens*, *Barnesiella intestinihominis*, *Bifidobacterium adolescentis*, *Bifidobacterium bifidum*, *Bifidobacterium catenulatum*, *Bifidobacterium dentium*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bilophila wadsworthia*, *Blautia faecis*, *Blautia hydrogenotrophica*, *Blautia massiliensis*, *Blautia obeum*, *Blautia wexlerae*, *Butyricimonas faecihominis*, *Catabacter hongkongensis*, *Clostridiaceae sp.*, *Clostridiales sp.*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium citroniae*, *Clostridium clostridioforme*, *Clostridium fessum*, *Clostridium scindens*, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dialister succinatiphilus*, *Dielma fastidiosa*, *Dorea formicigenerans*, *Dorea longicatena*, *Eggerthella lenta*, *Eisenbergiella tayi*, *Eubacterium eligens*, *Eubacterium hallii*, *Eubacterium rectale*, *Eubacterium siraeum*, *Eubacterium ventriosum*, *Eubacterium*

xylanophilum, *Faecalibacterium prausnitzii*, *Fusicatenibacter saccharivorans*, *Gordonibacter pamelaeae*, *Holdemanella biformis*, *Hungatella effluvia*, *Lachnoclostridium pacaense*, *Lachnospiraceae sp.*, *Lactobacillus rogosae*, *Longicatena caecimuris*, *Megasphaera massiliensis*, *Methanobrevibacter smithii*, *Monoglobus pectinilyticus*, *Neglecta timonensis*, *Parabacteroides distasonis*, *Parabacteroides merdae*, *Paraprevotella clara*, *Parasutterella excrementihominis*, *Phascolarctobacterium faecium*, *Porphyromonas asaccharolytica*, *Roseburia hominis*, *Ruminococcaceae sp.*, *Ruminococcus bromii*, *Ruminococcus faecis*, *Ruthenibacterium lactatiformans*, *Senegalimassilia anaerobia*, *Sutterella massiliensis*, *Sutterella wadsworthensis*, and *Turicibacter sanguinis*.

38. The microbial consortium of claim 32, wherein the supportive community comprises an *Akkermansia*, an *Alistipes*, an *Anaerostipes*, a *Bacteroides*, a *Bifidobacterium*, a *Bilophila*, a *Blautia*, a *Clostridium*, a *Collinsella aerofaciens,* a *Coprococcus*, *Dialister*, a *Dorea*, an *Eggerthella*, an *Eisenbergiella*, a *Eubacterium*, a *Faecalibacterium*, a *Fusicatenibacter*, a *Gordonibacter*, a *Holdemanella*, a *Hungatella*, a *Lachnoclostridium*, a *Lachnospiraceae,* a *Lactobacillus*, a *Monoglobus*, a *Neglecta*, a *Parabacteroides*, a *Paraprevotella*, a *Parasutterella*, a *Phascolarctobacterium*, a *Porphyromonas*, a *Roseburia*, a *Ruminococcaceae*, a *Ruminococcus*, a *Ruthenibacterium*, and a *Sutterella.*

39. The microbial consortium of claim 38, wherein the supportive community comprises *Akkermansia muciniphila*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Alistipes shahii*, *Alistipes timonensis*, *Anaerostipes hadrus*, *Bacteroides caccae*, *Bacteroides fragilis*, *Bacteroides kribbi, Bacteroides koreensis, Bacteroides massiliensis*, *Bacteroides nordii*, *Bacteroides salyersiae*, *Bacteroides stercorirosoris*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvens*, *Bifidobacterium adolescentis*, *Bifidobacterium catenulatum*, *Bifidobacterium dentium*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bilophila wadsworthia*, *Bilophila wadsworthia*, *Blautia faecis*, *Blautia obeum*, *Blautia wexlerae*, *Clostridium aldenense, Clostridium bolteae*, *Clostridium citroniae*, *Clostridium clostridioforme*, *Clostridium fessum*, *Clostridium scindens*, *Collinsella aerofaciens,* *Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dialister succinatiphilus*, *Dorea formicigenerans*, *Dorea longicatena*, *Eggerthella lenta*, *Eisenbergiella tayi*, *Eubacterium eligens*, *Eubacterium rectale*, *Faecalibacterium prausnitzii*,

Fusicatenibacter saccharivorans, *Gordonibacter pamelaeae*, *Holdemanella biformis*, *Hungatella effluvia*, *Lachnoclostridium pacaense*, *Lachnospiraceae sp.*, *Lactobacillus rogosae*, *Monoglobus pectinilyticus*, *Neglecta timonensis*, *Parabacteroides distasonis*, *Parabacteroides merdae*, *Paraprevotella clara*, *Parasutterella excrementihominis*, *Phascolarctobacterium faecium*, *Porphyromonas asaccharolytica*, *Roseburia hominis*, *Ruminococcaceae sp.*, *Ruminococcus bromii*, *Ruminococcus faecis*, *Ruthenibacterium lactatiformans*, *Sutterella massiliensis*, and *Sutterella wadsworthensis*.

40. The microbial consortium of claim 38, wherein the supportive community consists of *Akkermansia muciniphila*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Alistipes shahii*, *Alistipes timonensis*, *Anaerostipes hadrus*, *Bacteroides caccae*, *Bacteroides fragilis*, *Bacteroides kribbi*, *Bacteroides koreensis*, *Bacteroides massiliensis*, *Bacteroides nordii*, *Bacteroides salyersiae*, *Bacteroides stercorirosoris*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvens*, *Bifidobacterium adolescentis*, *Bifidobacterium catenulatum*, *Bifidobacterium dentium*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bilophila wadsworthia*, *Bilophila wadsworthia*, *Blautia faecis*, *Blautia obeum*, *Blautia wexlerae*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium citroniae*, *Clostridium clostridioforme*, *Clostridium fessum*, *Clostridium scindens*, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dialister succinatiphilus*, *Dorea formicigenerans*, *Dorea longicatena*, *Eggerthella lenta*, *Eisenbergiella tayi*, *Eubacterium eligens*, *Eubacterium rectale*, *Faecalibacterium prausnitzii*, *Fusicatenibacter saccharivorans*, *Gordonibacter pamelaeae*, *Holdemanella biformis*, *Hungatella effluvia*, *Lachnoclostridium pacaense*, *Lachnospiraceae sp.*, *Lactobacillus rogosae*, *Monoglobus pectinilyticus*, *Neglecta timonensis*, *Parabacteroides distasonis*, *Parabacteroides merdae*, *Paraprevotella clara*, *Parasutterella excrementihominis*, *Phascolarctobacterium faecium*, *Porphyromonas asaccharolytica*, *Roseburia hominis*, *Ruminococcaceae sp.*, *Ruminococcus bromii*, *Ruminococcus faecis*, *Ruthenibacterium lactatiformans*, *Sutterella massiliensis*, and *Sutterella wadsworthensis*.

41. The microbial consortium of claim 25, wherein the microbial consortium or the supportive community of microbes comprises 20 to 200 microbial strains.

42. The microbial consortium of claim 41, wherein the microbial consortium or the supportive community of microbes comprises 70 to 80 microbial strains.

43. The microbial consortium of claim 41, wherein the microbial consortium or the supportive community of microbes comprises 80 to 90 microbial strains.

44. The microbial consortium of claim 41, wherein the microbial consortium or the supportive community of microbes comprises 100 to 110 microbial strains.

45. The microbial consortium of claim 41, wherein the microbial consortium or the supportive community of microbes comprises 150 to 160 microbial strains.

46. The microbial consortium according to any one of claims 41 to 45, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 4.

47. The microbial consortium according to any one of claims 41 to 45, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 22.

48. The microbial consortium according to any one of claims 41 to 45, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 23.

49. The microbial consortium according to any one of claims 41 to 45, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 20.

50. The microbial consortium according to any one of claims 41 to 45, wherein the plurality of active microbes and the supportive community of microbes are selected from a group

of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 16.

51. The microbial consortium according to any one of claims 41 to 45, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 17.

52. The microbial consortium according to any one of claims 41 to 45, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 18.

53. The microbial consortium according to any one of claims 41 to 45, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 19.

54. The microbial consortium of claim 41 or 45, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 22.

55. The microbial consortium of claim 41 or 44, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 23.

56. The microbial consortium of claim 41 or 45, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 20.

57. The microbial consortium of claim 41 or 45, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 16.

58. T The microbial consortium of claim 41 or 43, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 17.

59. The microbial consortium of claim 41 or 43, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 18.

60. The microbial consortium of claim 41 or 42, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 19.

61. The microbial consortium according to any one of claims 1 to 23, wherein the first metabolic substrate metabolizing activity of one of the plurality of active microbes is significantly different compared to the first metabolic substrate activity of at least one other of the plurality of active microbes when measured in a standardized substrate metabolization assay under the same conditions.

62. The microbial consortium of claim 61, wherein at least one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower pH compared to at least one other of the plurality of active microbes at the same lower pH.

63. The microbial consortium of claim 61 or 62, wherein at least one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower pH compared to a first metabolic substrate metabolizing activity of the same active microbe at a higher pH.

64. The microbial consortium of claim 62 or 63, wherein the lower pH is at 4.5 ± 0.5.

65. The microbial consortium according to any one of claims 61 to 64, wherein at least one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a higher pH compared to at least one other of the plurality of active microbes at the same higher pH.

66. The microbial consortium according to any one of claims 61 to 65, wherein at least one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a higher pH compared to a first metabolic substrate activity of the same active microbe at a lower pH.

67. The microbial consortium of claim 65 or 66, wherein the higher pH is at 7.5 ± 0.5.

68. The microbial consortium according to any one of claims 61 to 67, wherein at least one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower pH and one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a higher pH.

69. The microbial consortium according to any one of claims 63, 64, 66, or 67, wherein the difference between the two pH values is at least 1.5, 2.0, 2.5, 3.0, 3.5, or 4.0 pH units.

70. The microbial consortium according to any one of claims 61 to 69, wherein at least one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower concentration of first metabolic substrate compared to the first metabolic substrate activity of at least one other of the plurality of active microbes when measured in a standardized substrate metabolization assay under the same conditions.

71. The microbial consortium according to any one of claims 61 to 70, wherein at least one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower concentration of first metabolic substrate compared to a first metabolic substrate metabolizing activity of the same active microbe at a higher concentration of first metabolic substrate.

72. The microbial consortium according to any one of claims 61 to 71, wherein at least one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a higher concentration of first metabolic substrate compared to the first metabolic substrate activity of at least one other of the plurality of active microbes when measured in a standardized substrate metabolization assay under the same conditions.

73. The microbial consortium according to any one of claims 61 to 72, wherein at least one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower concentration of first metabolic substrate compared to a first metabolic substrate metabolizing activity of the same active microbe at a higher concentration of first metabolic substrate.

74. The microbial consortium according to any one of claims 61 to 73, wherein at least one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a lower first metabolic substrate concentration and one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at a higher first metabolic substrate concentration.

75. The microbial consortium according to any one of claims 71, 73, or 74, wherein the difference between the two first metabolic substrate concentrations is at least 1.2 fold, 2.0 fold, 3.0 fold, 4.0 fold, 5.0 fold, 6.0 fold, 7.0 fold, 8.0 fold, 9.0 fold, 10 fold, 20 fold, 30 fold, 40 fold, 50 fold, 60 fold, 70 fold, 80 fold, 90 fold, or 100 fold.

76. The microbial consortium according to any one of claims 61 to 75, wherein the first metabolic substrate is oxalate.

77. The microbial consortium according to claim 76, wherein the one or more than one metabolite is selected from the group consisting of formate and carbon dioxide.

78. The microbial consortium of claim 76 or 77, wherein at least one of the plurality of active microbes has a higher oxalate metabolizing activity at 0.75 mM of oxalate compared to the oxalate metabolizing activity of at least one other of the plurality of active microbes when measured in a standardized oxalate metabolization assay under the same conditions.

79. The microbial consortium according to any one of claims 76 to 78, wherein one of the plurality of active microbes has a higher oxalate metabolizing activity at 0.75 mM of oxalate compared to an oxalate metabolizing activity of the same active microbe at a higher concentration of oxalate.

80. The microbial consortium according to any one of claims 76 to 79, wherein at least one of the plurality of active microbes has a higher oxalate metabolizing activity at 40 mM of oxalate compared to the oxalate metabolizing activity of at least one other of the plurality of active microbes when measured in a standardized oxalate metabolization assay under the same conditions.

81. The microbial consortium according to any one of claims 76 to 80, wherein at least one of the plurality of active microbes has a higher oxalate metabolizing activity at 40 mM of oxalate compared to an oxalate metabolizing activity of the same active microbe at a lower concentration of oxalate.

82. The microbial consortium according to any one of claims 76 to 81, wherein at least one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at 0.75 mM of oxalate and one of the plurality of active microbes has a higher first metabolic substrate metabolizing activity at 40 mM of oxalate.

83. The microbial consortium according to any one of claims 76 to 82, wherein the standardized substrate metabolization assay comprises using a colorimetric enzyme assay that measures the activity of oxalate oxidase in a culture sample comprising the microbial consortium, wherein the culture sample comprises three or more microbial strains in an appropriate culture media incubated for 1 hour to 96 hours in the presence of oxalate at a concentration of 0.5 mM to 50 mM, at a pH of 3.5 to 8.0, and at a temperature of 35 °C to 40 °C.

84. The microbial consortium according to any one of claims 76 to 82, wherein the standardized substrate metabolization assay comprises using liquid chromatography-tandem mass spectrometry (LC-MS/MS) to measure the amount of oxalate in a culture sample comprising the microbial consortium, wherein the culture sample comprises three or more microbial strains in an appropriate culture media incubated for 1 hour to 96 hours in the presence of oxalate at a concentration of 0.5 mM to 50 mM, at a pH of 3.5 to 8.0, and at a temperature of 35 °C to 40 °C.

85. The microbial consortium according to any one of claims 76 to 84, wherein the consortium further comprises:

a fermenting microbe that metabolizes a fermentation substrate to one or more than one fermentation product; and

a synthesizing microbe that catalyzes a synthesis reaction that combines the one or more than one metabolite and the one or more than one fermentation product to generate one or more than one synthesis product.

86. The microbial consortium of claim 85, wherein the one or more than one fermentation product is a second metabolic substrate for the plurality of active microbes or a third metabolic substrate for the synthesizing microbe.

87. The microbial consortium according to claim 85 or 86, wherein the one or more than one synthesis product is a second metabolic substrate for the plurality of active microbes or a fourth metabolic substrate for the fermenting microbe.

88. The microbial consortium according to any one of claims 85 to 87, wherein the fermentation substrate is a polysaccharide and the one or more than one fermentation product is selected from the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, hydrogen gas, and carbon dioxide.

89. The microbial consortium according to any one of claims 85 to 88, wherein the fermentation substrate is an amino acid and the one or more than one fermentation product is selected from the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, hydrogen gas, hydrogen sulfide, and carbon dioxide.

90. The microbial consortium according to any one of claims 85 to 89, wherein the reaction catalyzed by the synthesizing microbe is selected from the group consisting of: synthesis of methane from carbon dioxide and hydrogen gas; synthesis of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate,

91. The microbial consortium according to any one of claims 85 to 90, wherein the microbial consortium, when administered to an animal on a high oxalate diet, significantly reduces oxalate concentration in a sample selected from the group consisting of blood, serum, stool, or urine, as compared to a sample collected from a corresponding control animal on a high oxalate diet that has not been administered with the microbial consortium.

92. The microbial consortium according to any one of claims 76 to 91, wherein the plurality of active microbes comprises 3 microbial strains

93. The microbial consortium of claim 92, wherein the plurality of active microbes comprises 3 Proteobacteria strains.

94. The microbial consortium of claim 93, wherein the plurality of active microbes comprises 3 *Oxalobacter formigenes* strains.

95. The microbial consortium according to any one of claim 76 to 94, wherein the microbial consortium or the supportive community of microbes comprises 20 to 200 microbial strains.

96. The microbial consortium of claim 95, wherein the microbial consortium or the supportive community of microbes comprises 70 to 80 microbial strains.

97. The microbial consortium of claim 95, wherein the microbial consortium or the supportive community of microbes comprises 80 to 90 microbial strains.

98. The microbial consortium of claim 95, wherein the microbial consortium or the supportive community of microbes comprises 100 to 110 microbial strains.

99. The microbial consortium of claim 95, wherein the microbial consortium or the supportive community of microbes comprises 150 to 160 microbial strains.

100. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each

comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 4.

101. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 22.

102. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 23.

103. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 20.

104. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 16.

105. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 17.

106. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 18.

107. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes are selected from a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 19.

108. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 22.

109. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 23.

110. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 20.

111. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 16.

112. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 17.

113. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 18.

114. The microbial consortium of claim 95, wherein the plurality of active microbes and the supportive community of microbes consist of a group of microbes each comprising a 16S sequence at least 97% identical to any one of the microbes listed in Table 19.

115. The microbial consortium according to any one of claims 1 to 23, wherein the first metabolic substrate is a primary bile acid.

116. The microbial consortium of claim 115, wherein the bile acid is selected from the group consisting of lithocholic acid (LCA), and deoxycholic acid (DCA).

117. The microbial consortium of claim 115 or claim 116, wherein the one or more than one metabolite is selected from the group consisting of iso-lithocholic acid (iso-LCA), or iso-deoxycholic acid (iso-DCA).

118. The microbial consortium according to any one of claims 115 to 117, wherein the supportive community of microbes enhances the conversion of one or more conjugated bile acids selected from the group consisting of taurochenodeoxycholic acid (TCDCA), glycochenodeoxycholic acid (GCDCA), taurocholic acid (TCA), and glycocholic acid (GCA), to cholic acid (CA) or chenodeoxycholic acid (CDCA).

119. The microbial consortium according to any one of claims 115 to 118, wherein the supportive community of microbes enhances the conversion of CA to 7-beta-cholic acid (7betaCA).

120. The microbial consortium according to any one of claims 115 to 119, wherein the supportive community of microbes enhances the conversion of CDCA to ursodeoxycholic acid (UDCA).

121. The microbial consortium according to any one of claims 115 to 120, wherein at least one of the plurality of active microbes has a higher bile acid metabolization activity at a bile acid concentration of 0.1 mM compared to the bile acid metabolization activity of at least one other of the plurality of active microbes when measured in a standardized bile acid metabolization assay under the same conditions.

122. The microbial consortium according to any one of claims 115 to 121, wherein one of the plurality of active microbes has a higher bile acid metabolizing activity at a bile acid concentration of 0.1 mM compared to a bile acid metabolizing activity of the same active microbe at a higher bile acid concentration.

123. The microbial consortium according to any one of claims 115 to 122, wherein at least one of the plurality of active microbes has a higher bile acid metabolization activity at a bile acid concentration of 10 mM compared to the bile acid metabolization activity of at least one other of the plurality of active microbes when measured in a standardized bile acid metabolization assay under the same conditions.

124. The microbial consortium according to any one of claims 115 to 123, wherein one of the plurality of active microbes has a higher bile acid metabolizing activity at a bile acid concentration of 10 mM compared to a bile acid metabolizing activity of the same active microbe at a lower bile acid concentration.

125. The microbial consortium according to any one of claims 115 to 124, wherein one of the plurality of active microbes has a higher bile acid metabolization activity at 0.1 mM of bile acid and one of the plurality of active microbes has a higher bile acid metabolization activity at 10 mM of bile acid.

126. The microbial consortium according to any one of claims 115 to 125, wherein the standardized substrate metabolization assay comprises using liquid chromatography – mass spectrometry to determine the bile acid profile in a culture sample comprising the microbial consortium, wherein the culture sample comprises three or more microbial strains in an appropriate culture media incubated for 1 hour to 96 hours in the presence of bile acids at a concentration of 0.1 mM to 10 mM, at a pH of 3.5 to 8.0, and at a temperature of 35 °C to 40 °C.

127. The microbial consortium according to any one of claims 115 to 126, wherein the plurality of active microbes comprises one or more microbial phyla selected from Firmicutes and Actinobacteria.

128. The microbial consortium of claim 127, wherein the plurality of active microbes comprises one or more microbial strain selected from *Eggerthella lenta* and *Clostridium scindens*.

129. The microbial consortium according to any one of claim 115 to 128, wherein the microbial consortium or the supportive community of microbes comprises 20 to 200 microbial strains.

130. The microbial consortium of claim 129, wherein the microbial consortium or the supportive community of microbes comprises 70 to 80 microbial strains.

131. The microbial consortium of claim 129, wherein the microbial consortium or the supportive community of microbes comprises 80 to 90 microbial strains.

132. The microbial consortium of claim 129, wherein the microbial consortium or the supportive community of microbes comprises 100 to 110 microbial strains.

133. The microbial consortium of claim 129, wherein the microbial consortium or the supportive community of microbes comprises 150 to 160 microbial strains.

134. The microbial consortium according to any one of claims 1 to 133, wherein the microbial consortium is administered as a pre-determined dose in a range from 1 X 10^6 total CFU to 1 X 10^{13} total CFU.

135. The microbial consortium according to any one of claims 1 to 134, wherein the microbial consortium, when administered to the animal, decreases a concentration of the first metabolic substrate in the animal.

136. The microbial consortium according to any one of claims 1 to 135, wherein the animal provides an experimental model of the disease.

137. A pharmaceutical composition comprising the microbial consortium according to any one of claims 1 to 136 and a pharmaceutically acceptable carrier or excipient.

138. A method of treating a subject diagnosed with or at risk for a metabolic disease or condition selected from the group consisting of primary hyperoxaluria, secondary hyperoxaluria, primary sclerosing cholangitis, primary biliary cholangitis, progressive familial intrahepatic cholestasis, nonalcoholic steatohepatitis, and multiple sclerosis, the

method comprising administering to the subject, the pharmaceutical composition of claim 137.

139. The method of claim 138, wherein administration of the pharmaceutical composition reduces levels of the first metabolic substrate in the subject by at least 20% as compared to an untreated control subject or as compared to pre-administration levels of the first metabolic substrate in the subject.

140. The method of claim 139, wherein administration of the pharmaceutical composition reduces levels of the first metabolic substrate in the subject by at least 40% as compared to an untreated control subject or as compared to pre-administration levels of the first metabolic substrate in the subject.

141. The method of claim 140, wherein administration of the pharmaceutical composition reduces levels of the first metabolic substrate in the subject by at least 60% as compared to an untreated control subject or as compared to pre-administration levels of the first metabolic substrate in the subject.

142. The method of claim 141, wherein administration of the pharmaceutical composition reduces levels of the first metabolic substrate in the subject by at least 80% as compared to an untreated control subject or as compared to pre-administration levels of the first metabolic substrate in the subject.

143. The method according to any one of claims 138 to 142, wherein the first metabolic substrate is oxalate.

144. The method according to any one of claims 138 to 142, wherein the first metabolic substrate is DCA or LCA.

145. The method according to any one of claims 139 to 142, wherein the level of first metabolic substrate is determined from a blood, serum, stool, or urine sample.

146. A supportive community of microbes comprising between 1 and 300 microbial strains, wherein at least one of the following four conditions is met:

1) the supportive community of microbes metabolizes one or more than one metabolite produced by a plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of a first metabolic substrate by one or more of the plurality of active microbes, wherein the first metabolic substrate causes or contributes to a disease in an animal,

2) the supportive community of microbes increases the flux of a precursor of the first metabolic substrate into a biochemical pathway that converts said precursor into a metabolite that is not the first metabolic substrate,

3) the supportive community of microbes enhances one or more than one characteristic of the plurality of active microbes when administered to an animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes, and

4) the supportive community of microbes catalyzes one or more than one reaction selected from the group consisting of: fermentation of polysaccharides to one or more than one of the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H_2, and CO_2, fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H_2, H_2S, and CO_2, synthesis of one or more than one of the group consisting of methane from H_2 and CO_2, methane from formate and H_2, acetate from H_2 and CO_2, acetate from formate and H_2, acetate and sulfide from H_2, CO_2, and sulfate, propionate and CO_2 from succinate, succinate from H_2 and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H_2, and CO_2 from lactate, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

147. The supportive community of claim 146, wherein the supportive community comprises between 20 and 200 microbial strains.

148. The supportive community of claim 147 wherein the supportive community comprises at least 4 phyla selected from the group consisting of Bacteroidetes, Firmicutes, Actinobacteria, and Proteobacteria.

149. The supportive community of claim 148, wherein the supportive community comprises a *Ruminococcus*, *Clostridium*, *Bacteroides*, *Neglecta*, *Bifidobacterium*, *Egerthella*, *Clostridiaceae, Parabacteroides*, *Bilophila*, *Dorea*, *Collinsella*, and *Faecalibacterium*.

150. The supportive community of claim 149, wherein the supportive community comprises *Ruminococcus bromii*, *Clostridium citroniae*, *Bacteroides salyersiae*, *Neglecta timonensis*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bacteroides thetaiotaomicron*, *Eggerthella lenta*, *Clostridiaceae sp.*, *Bifidobacterium dentium*, *Parabacteroides merdae*, *Bilophila wadsworthia*, *Bacteroides caccae*, *Dorea longicatena*, *Collinsella aerofaciens*, *Clostridium scindens*, *Faecalibacterium prausnitzii*, *Clostridium symbiosum*, and *Bacteroides vulgatus*.

151. The supportive community of claim 148, wherein the supportive community comprises an *Acidaminococcus*, an *Akkermansia*, an *Alistipes*, an *Anaerofustis*, an *Anaerostipes*, an *Anaerotruncus*, a *Bacteroides*, a *Barnesiella*, a *Bifidobacterium*, a *Bilophila*, a *Blautia*, a *Butyricimonas*, a *Catabacter hongkongensis*, a *Clostridiaceae*, a *Clostridiales*, a *Clostridium*, a *Collinsella*, a *Coprococcus*, a *Dialister*, a *Dielma, a Dorea*, an *Eggerthella*, an *Eisenbergiella*, a *Eubacterium*, a *Faecalibacterium*, a *Fusicatenibacter saccharivorans*, a G*ordonibacter pamelaeae*, a *Holdemanella*, a *Hungatella*, a *Lachnoclostridium*, *Lachnospiraceae*, a *Lactobacillus*, a *Longicatena*, a *Megasphaera*, a *Methanobrevibacter*, a *Monoglobus*, a *Neglecta*, a *Parabacteroides*, a *Paraprevotella*, a *Parasutterella*, a *Phascolarctobacterium*, a *Porphyromonas*, a *Roseburia hominis*, a *Ruminococcaceae*, a *Ruminococcus*, a *Ruthenibacterium*, a *Senegalimassilia*, a *Sutterella*, and a *Turicibacter*.

152. The supportive community of claim 151, wherein the supportive community comprises *Acidaminococcus intestine*, *Akkermansia muciniphila*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Alistipes senegalensis*, *Alistipes shahii*, *Alistipes sp.*, *Alistipes*

timonensis, *Anaerofustis stercorihominis*, *Anaerostipes hadrus*, *Anaerotruncus massiliensis*, *Bacteroides caccae*, *Bacteroides coprocola*, *Bacteroides faecis*, *Bacteroides finegoldii*, *Bacteroides fragilis*, *Bacteroides kribbi*, *Bacteroides massiliensis*, *Bacteroides nordii*, *Bacteroides ovatus*, *Bacteroides salyersiae*, *Bacteroides stercorirosoris*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvens*, *Barnesiella intestinihominis*, *Bifidobacterium adolescentis*, *Bifidobacterium bifidum*, *Bifidobacterium catenulatum*, *Bifidobacterium dentium*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bilophila wadsworthia*, *Blautia faecis*, *Blautia hydrogenotrophica*, *Blautia massiliensis*, *Blautia obeum*, *Blautia wexlerae*, *Butyricimonas faecihominis*, *Catabacter hongkongensis*, *Clostridiaceae sp.*, *Clostridiales sp.*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium citroniae*, *Clostridium clostridioforme*, *Clostridium fessum*, *Clostridium scindens*, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dialister succinatiphilus*, *Dielma fastidiosa*, *Dorea formicigenerans*, *Dorea longicatena*, *Eggerthella lenta*, *Eisenbergiella tayi*, *Eubacterium eligens*, *Eubacterium hallii*, *Eubacterium rectale*, *Eubacterium siraeum*, *Eubacterium ventriosum*, *Eubacterium xylanophilum*, *Faecalibacterium prausnitzii*, *Fusicatenibacter saccharivorans*, *Gordonibacter pamelaeae*, *Holdemanella biformis*, *Hungatella effluvia*, *Lachnoclostridium pacaense*, *Lachnospiraceae sp.*, *Lactobacillus rogosae*, *Longicatena caecimuris*, *Megasphaera massiliensis*, *Methanobrevibacter smithii*, *Monoglobus pectinilyticus*, *Neglecta timonensis*, *Parabacteroides distasonis*, *Parabacteroides merdae*, *Paraprevotella clara*, *Parasutterella excrementihominis*, *Phascolarctobacterium faecium*, *Porphyromonas asaccharolytica*, *Roseburia hominis*, *Ruminococcaceae sp.*, *Ruminococcus bromii*, *Ruminococcus faecis*, *Ruthenibacterium lactatiformans*, *Senegalimassilia anaerobia*, *Sutterella massiliensis*, *Sutterella wadsworthensis*, and *Turicibacter sanguinis*.

153. The supportive community of claim 151, wherein the supportive community consists of *Acidaminococcus intestine*, *Akkermansia muciniphila*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Alistipes senegalensis*, *Alistipes shahii*, *Alistipes sp.*, *Alistipes timonensis*, *Anaerofustis stercorihominis*, *Anaerostipes hadrus*, *Anaerotruncus massiliensis*, *Bacteroides caccae*, *Bacteroides coprocola*, *Bacteroides faecis*, *Bacteroides finegoldii*, *Bacteroides fragilis*, *Bacteroides kribbi*, *Bacteroides massiliensis*, *Bacteroides nordii*, *Bacteroides ovatus*, *Bacteroides salyersiae*, *Bacteroides stercorirosoris*, *Bacteroides*

stercoris, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvens*, *Barnesiella intestinihominis*, *Bifidobacterium adolescentis*, *Bifidobacterium bifidum*, *Bifidobacterium catenulatum*, *Bifidobacterium dentium*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bilophila wadsworthia*, *Blautia faecis*, *Blautia hydrogenotrophica*, *Blautia massiliensis*, *Blautia obeum*, *Blautia wexlerae*, *Butyricimonas faecihominis*, *Catabacter hongkongensis*, *Clostridiaceae sp.*, *Clostridiales sp.*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium citroniae*, *Clostridium clostridioforme*, *Clostridium fessum*, *Clostridium scindens*, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dialister succinatiphilus*, *Dielma fastidiosa*, *Dorea formicigenerans*, *Dorea longicatena*, *Eggerthella lenta*, *Eisenbergiella tayi*, *Eubacterium eligens*, *Eubacterium hallii*, *Eubacterium rectale*, *Eubacterium siraeum*, *Eubacterium ventriosum*, *Eubacterium xylanophilum*, *Faecalibacterium prausnitzii*, *Fusicatenibacter saccharivorans*, *Gordonibacter pamelaeae*, *Holdemanella biformis*, *Hungatella effluvia*, *Lachnoclostridium pacaense*, *Lachnospiraceae sp.*, *Lactobacillus rogosae*, *Longicatena caecimuris*, *Megasphaera massiliensis*, *Methanobrevibacter smithii*, *Monoglobus pectinilyticus*, *Neglecta timonensis*, *Parabacteroides distasonis*, *Parabacteroides merdae*, *Paraprevotella clara*, *Parasutterella excrementihominis*, *Phascolarctobacterium faecium*, *Porphyromonas asaccharolytica*, *Roseburia hominis*, *Ruminococcaceae sp.*, *Ruminococcus bromii*, *Ruminococcus faecis*, *Ruthenibacterium lactatiformans*, *Senegalimassilia anaerobia*, *Sutterella massiliensis*, *Sutterella wadsworthensis*, and *Turicibacter sanguinis*.

154. The supportive community of claim 148, wherein the supportive community comprises an *Akkermansia*, an *Alistipes*, an *Anaerostipes*, a *Bacteroides*, a *Bifidobacterium*, a *Bilophila*, a *Blautia*, a *Clostridium*, a *Collinsella aerofaciens*, a *Coprococcus*, *Dialister*, a *Dorea*, an *Eggerthella*, an *Eisenbergiella*, a *Eubacterium*, a *Faecalibacterium*, a *Fusicatenibacter*, a *Gordonibacter*, a *Holdemanella*, a *Hungatella*, a *Lachnoclostridium*, a *Lachnospiraceae*, a *Lactobacillus*, a *Monoglobus*, a *Neglecta*, a *Parabacteroides*, a *Paraprevotella*, a *Parasutterella*, a *Phascolarctobacterium*, a *Porphyromonas*, a *Roseburia*, a *Ruminococcaceae*, a *Ruminococcus*, a *Ruthenibacterium*, and a *Sutterella*.

155. The supportive community of claim 154, wherein the supportive community comprises *Akkermansia muciniphila*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Alistipes shahii*, *Alistipes timonensis*, *Anaerostipes hadrus*, *Bacteroides caccae*, *Bacteroides fragilis*, *Bacteroides kribbi, Bacteroides koreensis, Bacteroides massiliensis*, *Bacteroides nordii*, *Bacteroides salyersiae*, *Bacteroides stercorirosoris*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvens*, *Bifidobacterium adolescentis*, *Bifidobacterium catenulatum*, *Bifidobacterium dentium*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bilophila wadsworthia*, *Bilophila wadsworthia*, *Blautia faecis*, *Blautia obeum*, *Blautia wexlerae*, *Clostridium aldenense, Clostridium bolteae*, *Clostridium citroniae*, *Clostridium clostridioforme*, *Clostridium fessum*, *Clostridium scindens*, *Collinsella aerofaciens, Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dialister succinatiphilus*, *Dorea formicigenerans*, *Dorea longicatena*, *Eggerthella lenta*, *Eisenbergiella tayi*, *Eubacterium eligens*, *Eubacterium rectale*, *Faecalibacterium prausnitzii*, *Fusicatenibacter saccharivorans*, *Gordonibacter pamelaeae*, *Holdemanella biformis*, *Hungatella effluvia*, *Lachnoclostridium pacaense*, *Lachnospiraceae sp., Lactobacillus rogosae*, *Monoglobus pectinilyticus*, *Neglecta timonensis*, *Parabacteroides distasonis*, *Parabacteroides merdae*, *Paraprevotella clara*, *Parasutterella excrementihominis*, *Phascolarctobacterium faecium*, *Porphyromonas asaccharolytica*, *Roseburia hominis*, *Ruminococcaceae sp., Ruminococcus bromii*, *Ruminococcus faecis*, *Ruthenibacterium lactatiformans*, *Sutterella massiliensis*, and *Sutterella wadsworthensis*.

156. The supportive community of claim 154, wherein the supportive community consists of *Akkermansia muciniphila*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Alistipes shahii*, *Alistipes timonensis*, *Anaerostipes hadrus*, *Bacteroides caccae*, *Bacteroides fragilis*, *Bacteroides kribbi, Bacteroides koreensis, Bacteroides massiliensis*, *Bacteroides nordii*, *Bacteroides salyersiae*, *Bacteroides stercorirosoris*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvens*, *Bifidobacterium adolescentis*, *Bifidobacterium catenulatum*, *Bifidobacterium dentium*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bilophila wadsworthia*, *Bilophila wadsworthia*, *Blautia faecis*, *Blautia obeum*, *Blautia wexlerae*, *Clostridium aldenense, Clostridium bolteae*, *Clostridium citroniae*, *Clostridium clostridioforme*, *Clostridium fessum*, *Clostridium scindens*, *Collinsella aerofaciens, Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dialister succinatiphilus*,

Dorea formicigenerans, *Dorea longicatena*, *Eggerthella lenta*, *Eisenbergiella tayi*, *Eubacterium eligens*, *Eubacterium rectale*, *Faecalibacterium prausnitzii*, *Fusicatenibacter saccharivorans*, *Gordonibacter pamelaeae*, *Holdemanella biformis*, *Hungatella effluvia*, *Lachnoclostridium pacaense*, *Lachnospiraceae sp.*, *Lactobacillus rogosae*, *Monoglobus pectinilyticus*, *Neglecta timonensis*, *Parabacteroides distasonis*, *Parabacteroides merdae*, *Paraprevotella clara*, *Parasutterella excrementihominis*, *Phascolarctobacterium faecium*, *Porphyromonas asaccharolytica*, *Roseburia hominis*, *Ruminococcaceae sp.*, *Ruminococcus bromii*, *Ruminococcus faecis*, *Ruthenibacterium lactatiformans*, *Sutterella massiliensis*, and *Sutterella wadsworthensis*.