[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 one aspect, the present disclosure provides 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 upon administration 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).

[0007a] In another aspect, the present disclosure provides a pharmaceutical composition comprising the microbial consortium as described herein and a pharmaceutically acceptable carrier or excipient. In another aspect, the present disclosure provides a use of the pharmaceutical composition as described herein in the manufacture of a medicament for 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. In another aspect, the present disclosure provides the pharmaceutical composition as described herein for use in therapy

[0007b] In another aspect, the present disclosure provides 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 upon administration 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).

[0007c] In some ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, the supportive community of microbes comprises one or more of the subclades Bacteroidales, Clostridiales, Erysipelotrichales. Negativicutes, Coriobacteriia, Bifidobacteriales, or Methanobacteriales.

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

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

[0015] In some ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, the supportive community of microbes comprises between 20 and 200 microbial strains. In some ~~embodiment~~examples, the supportive community comprises at least 4 phyla selected from the group consisting of Bacteroidetes, Firmicutes, Actinobacteria, and Proteobacteria. In some ~~embodiment~~examples, the supportive community comprises a *Ruminococcus*, *Clostridium*, *Bacteroides*, *Neglecta*, *Bifidobacterium*, *Egerthella*, *Clostridiaceae, Parabacteroides*, *Bilophila*, *Dorea*, *Collinsella*, and *Faecalibacterium*.

[0019] In some ~~embodiment~~examples, 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 ~~embodiment~~examples, 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*.

[0021] In some ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, the supportive community of microbes comprises between 100 and 150 microbial strains.

[0026] In some ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples the lower pH is at 4.5 ± 0.5.

[0030] In some ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, the higher pH is at 7.5 ± 0.5.

[0031] In some ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, the microbial consortium of the present ~~invention~~disclosure comprises a plurality of active microbes comprising 2 to 200 microbial strains. In certain ~~embodiment~~examples, the plurality of active microbes comprises 2 to 20 microbial strains.

[0035] In some ~~embodiment~~examples of the present ~~invention~~disclosure, the first metabolic substrate is oxalate. In some ~~embodiment~~examples, the one or more than one metabolite is selected from the group consisting of formate and carbon dioxide (CO_2). In some ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, the microbial consortium of the present ~~invention~~disclosure 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 ~~embodiment~~examples 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 ~~embodiment~~examples 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 ~~embodiment~~examples 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 ~~embodiment~~examples, 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 ~~embodiment~~examples 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, the plurality of active microbes comprises 3 microbial strains. In some ~~embodiment~~examples, the plurality of active microbes comprises 3 Proteobacteria strains. In some ~~embodiment~~examples, the plurality of active microbes comprises 3 *Oxalobacter formigenes* strains.

[0043] In some ~~embodiment~~examples, the first metabolic substrate is a bile acid. For example, in some ~~embodiment~~examples, the bile acid is lithocholic acid (LCA) or deoxycholic acid (DCA). In In some ~~embodiment~~examples, the one or more than one metabolite produced by the plurality of active microbes is a secondary bile acid. For example, in some ~~embodiment~~examples, the secondary bile acid is selected from the group consisting of iso-lithocholic acid (iso-LCA), or iso-deoxycholic acid (iso-DCA). In some ~~embodiment~~examples, 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 ~~embodiment~~examples, the supportive community of microbes enhances the conversion of CA to 7-beta-cholic acid (7betaCA). In other ~~embodiment~~examples, the supportive community of microbes enhances the conversion of CDCA to ursodeoxycholic acid (UDCA).

[0044] In some ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, 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 ~~embodiment~~examples, the plurality of active microbes comprises one or more microbial phyla selected from Firmicutes and Actinobacteria. In some ~~embodiment~~examples, the plurality of active microbes comprises one or more microbial strain selected from *Eggerthella lenta* and *Clostridium scindens.*

[0047] In some ~~embodiment~~examples, the microbial consortium of the present ~~invention~~disclosure 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 ~~embodiment~~examples, the microbial consortium, when administered to the animal, decreases a concentration of the first metabolic substrate in the animal.

[0049] In some ~~embodiment~~examples 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~~disclosure.

[0052] In some ~~embodiment~~examples, 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 ~~embodiment~~examples, the first metabolic substrate is oxalate. In other ~~embodiment~~examples, the first metabolic substrate is DCA or LCA. In some ~~embodiment~~examples the level of first metabolic substrate is determined from a blood, serum, stool, or urine sample.

CLAIMS

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~~ upon ~~administered~~ administration 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 upon administration ~~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 upon administration ~~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 upon administration ~~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 upon administration ~~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 upon administration ~~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 upon administration ~~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 upon administration ~~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

a. at least three phyla selected from the group consisting of Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia, and Euryarchaeota;

~~14.~~b. ~~.~~

~~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;

~~15.~~c. ~~.~~

~~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;

~~16.~~d. ~~.~~

~~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,

~~17.~~e. ~~.~~

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

~~18.~~f. ~~.~~

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

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

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

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

~~23.~~j. ~~The microbial consortium according to any one of claims 14 to 22, wherein the supportive community of microorganisms comprises~~ the subclade Bifidobacteriales; and/or~~.~~

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

~~25.~~15. The microbial consortium of claim 1, wherein the first metabolic substrate is oxalate.

~~26.~~16. The microbial consortium of claim ~~25~~15, wherein the metabolite is formate, and the supportive community of microbes catalyzes synthesis of methane from formate and H_2.

~~27.~~17. The microbial consortium of claim ~~26~~16, wherein the plurality of active microbes comprises *Oxalobacter formigenes*.

18. The microbial consortium of claim 17~~27~~, wherein the supportive community of microbes comprises

~~28.~~a. a Bacteroidetes and a Euryarchaeota;~~.~~

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

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

~~31.~~19. The microbial consortium of claim ~~25~~18, wherein the supportive community of microbes comprises between 20 and 200 microbial strains.

~~32.~~20. The microbial consortium of claim ~~31~~19, wherein the supportive community comprises at least 4 phyla selected from the group consisting of Bacteroidetes, Firmicutes, Actinobacteria, and Proteobacteria.

21. The microbial consortium of claim 20~~32~~, wherein the supportive community comprises

~~33.~~a. a *Ruminococcus*, *Clostridium*, *Bacteroides*, *Neglecta*, *Bifidobacterium*, *Egerthella*, *Clostridiaceae, Parabacteroides*, *Bilophila*, *Dorea*, *Collinsella*, and *Faecalibacterium*;~~.~~

~~34.~~b. ~~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.~~c. ~~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 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*; or~~.~~

~~36.~~d. ~~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.~~22. The microbial consortium of claim 21~~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.~~*23.* The microbial consortium of claim 20~~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.~~24. The microbial consortium of claim 23~~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.~~25. The microbial consortium of claim 23~~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*.

26. The microbial consortium of claim ~~25~~15, wherein the microbial consortium or the supportive community of microbes comprises

~~41.~~a. 20 to 200 microbial strains.

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

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

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

~~45.~~e. ~~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.~~27. The microbial consortium according to any one of claims 1 to 14~~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.

28. The microbial consortium of claim 27~~61~~, wherein at least one of the plurality of active microbes has

~~62.~~a. 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; or ~~.~~

b. ~~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;

~~63.~~ optionally, ~~.~~

~~64. The microbial consortium of claim 62 or 63,~~ wherein the lower pH is at 4.5 ± 0.5 or the higher pH is at 7.5 ± 0.5.

29. The microbial consortium according to ~~any one of~~ claim~~s 61 to 64~~28, wherein

~~65.~~a. 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; or ~~.~~

~~66.~~b. ~~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; optionally, ~~.~~

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

~~68.~~30. The microbial consortium according to ~~any one of~~ claim~~s 61 to 67~~28, 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.~~31. The microbial consortium according to ~~any one of~~ claim~~s 63, 64, 66, or 67~~28 or 29, 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.

32. The microbial consortium according to any one of claims 27~~61~~ to 31~~69~~, wherein

~~70.~~a. 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.~~b. ~~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.~~c. ~~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.~~d. ~~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; or~~.~~

~~74.~~e. ~~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.~~33. The microbial consortium according to ~~any one of~~ claim~~s 71, 73, or~~ 32~~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.~~34. The microbial consortium according to any one of claims 27~~61~~ to 33~~75~~, wherein the first metabolic substrate is oxalate.

~~77.~~35. The microbial consortium according to claim 34~~76~~, wherein the one or more than one metabolite is selected from the group consisting of formate and carbon dioxide.

36. The microbial consortium of claim 34~~76~~ or 35~~77~~, wherein

~~78.~~a. 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.~~b. ~~The microbial consortium according to any one of claims 76 to 78, wherein~~ at least 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.~~c. ~~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.~~d. ~~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;~~.~~ or

~~82.~~e. ~~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.

37. The microbial consortium according to any one of claims 34~~76~~ to 36~~82~~, wherein

~~83.~~a. 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;~~.~~ or

~~84.~~b. ~~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.~~38. The microbial consortium according to any one of claims 34~~76~~ to 37~~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.~~39. The microbial consortium of claim 38~~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.~~40. The microbial consortium according to claim 38~~85~~ or claim 39~~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.

41. The microbial consortium according to any one of claims claim 38 ~~85~~ to 40~~87~~, wherein

~~88.~~a. 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;~~,~~ or

~~89.~~b. ~~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.~~42. The microbial consortium according to any one of claims 38~~85~~ to 41~~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.~~43. The microbial consortium according to any one of claims 38~~85~~ to 42~~90~~, wherein the microbial consortium, upon administration ~~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.~~44. The microbial consortium according to any one of claims 32~~71~~ to 43~~91~~, wherein the plurality of active microbes comprises 3 microbial strains; optionally

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

~~94.~~45. The microbial consortium of claim ~~93~~44, wherein the plurality of active microbes comprises 3 *Oxalobacter formigenes* strains.

46. The microbial consortium according to any one of claim 34~~76~~ to ~~94~~45, wherein the microbial consortium or the supportive community of microbes comprises

~~95.~~a. 20 to 200 microbial strains;~~.~~

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

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

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

~~99.~~e. ~~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.~~47. The microbial consortium according to any one of claims 1 to 14~~23~~, wherein the first metabolic substrate is a primary bile acid, optionally ~~.~~

~~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.~~48. The microbial consortium of claim 47~~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).

49. The microbial consortium according to any one of claims 47~~115~~ to ~~117~~48, wherein the supportive community of microbes enhances the conversion of

~~118.~~a. 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);~~.~~

~~The microbial consortium according to any one of claims 115 to 118, wherein the supportive community of microbes enhances the conversion of~~

~~119.~~b. CA to 7-beta-cholic acid (7betaCA); and/or ~~.~~

~~120.~~c. ~~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).

50. The microbial consortium according to any one of claims 47~~115~~ to ~~120~~49, wherein

~~121.~~a. 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.~~b. ~~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.~~c. ~~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.~~d. ~~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; ~~and/or~~

~~125.~~e. ~~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.~~51. The microbial consortium according to any one of claims 47~~115~~ to 50~~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.~~52. The microbial consortium according to any one of claims 47~~115~~ to 51~~126~~, wherein the plurality of active microbes comprises one or more microbial phyla selected from Firmicutes and Actinobacteria.

~~128.~~53. The microbial consortium of claim ~~127~~52, wherein the plurality of active microbes comprises one or more microbial strain selected from *Eggerthella lenta* and *Clostridium scindens.*

54. The microbial consortium according to any one of claim 47~~115~~ to ~~128~~53, wherein the microbial consortium or the supportive community of microbes comprises

~~129.~~a. 20 to 200 microbial strains.

~~130.~~b. ~~The microbial consortium of claim 129, wherein the microbial consortium or the supportive community of microbes comprises~~ 70 to 80 microbial strains;~~.~~

~~131.~~c. ~~The microbial consortium of claim 129, wherein the microbial consortium or the supportive community of microbes comprises~~ 80 to 90 microbial strains;~~.~~

~~132.~~d. ~~The microbial consortium of claim 129, wherein the microbial consortium or the supportive community of microbes comprises~~ 100 to 110 microbial strains~~;~~. or

~~133.~~e. ~~The microbial consortium of claim 129, wherein the microbial consortium or the supportive community of microbes comprises~~ 150 to 160 microbial strains.

~~134.~~55. The microbial consortium according to any one of claims 1 to 54~~133~~, wherein the microbial consortium is to be 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.~~56. A pharmaceutical composition comprising the microbial consortium according to any one of claims 1 to 55~~136~~ and a pharmaceutically acceptable carrier or excipient.

~~138.~~57. Use of the pharmaceutical composition of claim 56 in the manufacture of a medicament for ~~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~~.

58. The ~~method~~ use of claim 57~~138~~, wherein administration of the pharmaceutical composition reduces levels of the first metabolic substrate in the subject by

~~139.~~a. 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.~~b. ~~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.~~c. ~~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; ~~.~~or

~~142.~~d. ~~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.~~59. The ~~method~~ use according to ~~any one of~~ claim~~s 138 to~~ 58.d, wherein the first metabolic substrate is oxalate or ~~.~~

~~144. The method according to any one of claims 138 to 142, wherein the first metabolic substrate is~~ DCA or LCA.

~~145.~~60. The ~~method~~ use according to ~~any one of~~ claim~~s~~ 58~~139 to 142~~, wherein the level of first metabolic substrate is determined from a blood, serum, stool, or urine sample.

~~146.~~61. 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~~upon administration 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.~~62. The supportive community of claim 61~~146~~, wherein the supportive community comprises between 20 and 200 microbial strains.

~~148.~~63. The supportive community of claim ~~147~~62, wherein the supportive community comprises at least 4 phyla selected from the group consisting of Bacteroidetes, Firmicutes, Actinobacteria, and Proteobacteria.

64. The supportive community of claim 63~~148~~ , wherein the supportive community comprises

~~149.~~a. a *Ruminococcus*, *Clostridium*, *Bacteroides*, *Neglecta*, *Bifidobacterium*, *Egerthella*, *Clostridiaceae, Parabacteroides*, *Bilophila*, *Dorea*, *Collinsella*, and *Faecalibacterium*;~~.~~

~~150.~~b. ~~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.~~c. ~~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*; or.

152.d. 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.~~65. The supportive community of claim ~~64~~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.~~66. The supportive community of claim ~~148~~63, 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.~~67. The supportive community of claim 66~~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.~~68. The supportive community of claim 66~~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*.

69. The pharmaceutical composition of claim 56 for use in therapy.