[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

[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 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 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 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 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 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 examples, the supportive community of microbes comprises one or more of the subclades Bacteroidales, Clostridiales, Erysipelotrichales. Negativicutes, Coriobacteriia, Bifidobacteriales, or Methanobacteriales.

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

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

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

[0019] In some 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 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 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 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 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 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 examples, the supportive community of microbes comprises between 100 and 150 microbial strains.

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

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

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

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

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

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

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

[0049] In some 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 disclosure.

[0052] In some 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 examples, the first metabolic substrate is oxalate. In other examples, the first metabolic substrate is DCA or LCA. In some 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 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).

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 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 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 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 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 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 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 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;
    b. at least four phyla selected from the group consisting of Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia, and Euryarchaeota;
    c. at least five phyla selected from the group consisting of Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia, and Euryarchaeota;
    d. at least six phyla selected from the group consisting of Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, Verrucomicrobia, and Euryarchaeota,
    e. the subclade Bacteroidales;
    f. the subclade Clostridiales;
    g. the subclade Erysipelotrichales;
    h. the subclade Negativicutes;
    i. the subclade Coriobacteriia;
    j. the subclade Bifidobacteriales; and/or
    k. the subclade Methanobacteriales.

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

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

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

18. The microbial consortium of claim 17, wherein the supportive community of microbes comprises
    a. a Bacteroidetes and a Euryarchaeota;
    b. a *Bacteroides* and *Methanobrevibacter*; or
    c. a *Bacteroides thetaiotaomicron* and/or *Bacteroides vulgatus*, and *Methanobrevibacter smithii*.

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

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

d. *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*.

22. The microbial consortium of claim 21, 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*.

23. The microbial consortium of claim 20, 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.*

24. The microbial consortium of claim 23, 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*.

25. The microbial consortium of claim 23, 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 15, wherein the microbial consortium or the supportive community of microbes comprises
    a. 20 to 200 microbial strains.
    b. 70 to 80 microbial strains;
    c. 80 to 90 microbial strains;
    d. 100 to 110 microbial strains; or
    e. 150 to 160 microbial strains.

27. The microbial consortium according to any one of claims 1 to 14, 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, wherein at least one of the plurality of active microbes has
    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. 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; optionally,

    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 claim 28, wherein
    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
    b. 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,

    wherein the higher pH is at 7.5 ± 0.5.

30. The microbial consortium according to claim 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.

31. The microbial consortium according to claim 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 to 31, wherein

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;

b. 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;

c. 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;

d. 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

e. 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.

33. The microbial consortium according to claim 32, 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.

34. The microbial consortium according to any one of claims 27 to 33, wherein the first metabolic substrate is oxalate.

35. The microbial consortium according to claim 34, 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 or 35, wherein

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.
b. 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.
c. 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;
d. 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
e. 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 to 36, wherein

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

b. 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.

38. The microbial consortium according to any one of claims 34 to 37, 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.

39. The microbial consortium of claim 38, 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.

40. The microbial consortium according to claim 38 or claim 39, 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 to 40, wherein
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
b. 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.

42. The microbial consortium according to any one of claims 38 to 41, 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.

43. The microbial consortium according to any one of claims 38 to 42, wherein the microbial consortium, upon administration 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.

44. The microbial consortium according to any one of claims 32 to 43, wherein the plurality of active microbes comprises 3 microbial strains; optionally
wherein the plurality of active microbes comprises 3 Proteobacteria strains.

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

46. The microbial consortium according to any one of claim 34 to 45, wherein the microbial consortium or the supportive community of microbes comprises
    a. 20 to 200 microbial strains;
    b. 70 to 80 microbial strains;
    c. 80 to 90 microbial strains;
    d. 100 to 110 microbial strains; or
    e. 150 to 160 microbial strains.

47. The microbial consortium according to any one of claims 1 to 14, wherein the first metabolic substrate is a primary bile acid, optionally
wherein the bile acid is selected from the group consisting of lithocholic acid (LCA), and deoxycholic acid (DCA).

48. The microbial consortium of claim 47, 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 to 48, wherein the supportive community of microbes enhances the conversion of
    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);
    b. CA to 7-beta-cholic acid (7betaCA); and/or
    c. CDCA to ursodeoxycholic acid (UDCA).

50. The microbial consortium according to any one of claims 47 to 49.c, wherein
    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;
    b. 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;
    c. 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;

d. 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
e. 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.

51. The microbial consortium according to any one of claims 47 to 50, 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.

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

53. The microbial consortium of claim 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 to 53, wherein the microbial consortium or the supportive community of microbes comprises
    a. 20 to 200 microbial strains.
    b. 70 to 80 microbial strains;
    c. 80 to 90 microbial strains;
    d. 100 to 110 microbial strains; or
    e. 150 to 160 microbial strains.

55. The microbial consortium according to any one of claims 1 to 54, 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.

56. A pharmaceutical composition comprising the microbial consortium according to any one of claims 1 to 55 and a pharmaceutically acceptable carrier or excipient.

57. Use of the pharmaceutical composition of claim 56 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.

58. The use of claim 57, wherein administration of the pharmaceutical composition reduces levels of the first metabolic substrate in the subject by
    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;
    b. 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;
    c. 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
    d. 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.

59. The use according to claim 58, wherein the first metabolic substrate is oxalate or DCA or LCA.

60. The use according to claim 58, wherein the level of first metabolic substrate is determined from a blood, serum, stool, or urine sample.

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 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).

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

63. The supportive community of claim 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, wherein the supportive community comprises

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

b. *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;*

c. 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

d. *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*.

65. The supportive community of claim 64, 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*.

66. The supportive community of claim 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.*

67. The supportive community of claim 66, 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*.

68. The supportive community of claim 66, 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.