CLAIMS:

1. A composition comprising:

(a) a consortium comprising

(i) *Clostridium citroniae*, *Bacteroides salyersiae*, *Blautia obeum*, *Parabacteroides merdae*, *Parabacteroides distasonis*, *Anaerostipes hadrus*, *Lachnospiraceae sp. FBI00033*, *Eubacterium eligens*, *Bifidobacterium dentium*, *Blautia wexlerae*, *Fusicatenibacter saccharivorans*, *Bacteroides nordii*, *Dorea formicigenerans*, *Dorea longicatena*, *Bacteroides stercorirosoris*, *Bifidobacterium longum*, *Bacteroides kribbi*, *Lachnospiraceae sp. FBI00071*, *Bacteroides thetaiotaomicron*, *Clostridium clostridioforme*, *Clostridium scindens*, *Roseburia hominis*, *Clostridium fessum*, *Coprococcus comes*, *Blautia faecis*, *Hungatella hathewayi*, *Bacteroides stercoris*, *Collinsella aerofaciens*, *Hungatella effluvii*, *Bifidobacterium adolescentis*, *Bifidobacterium catenulatum*, *Lactobacillus rogosae*, *Bacteroides faecis*, *Bacteroides finegoldii*, *Clostridiaceae sp. FBI00191*, *Ruminococcus faecis*, *Lachnoclostridium pacaense*, *Clostridium bolteae*, *Longicatena caecimuris*, *Eggerthella lenta*, *Blautia massiliensis*, *Bacteroides xylanisolvens*, *Bacteroides vulgatus*, *Megasphaera massiliensis*, *Butyricimonas faecihominis*, *Eisenbergiella tayi*, *Acidaminococcus intestini*, *Emergencia timonensis*, *Bifidobacterium pseudocatenulatum*, *Eubacterium hallii*, *Anaerofustis stercorihominis*, *Eubacterium ventriosum*, *Blautia hydrogenotrophica*, *Lachnospiraceae sp. FBI00290*, or a functional equivalent thereof; or

(ii) FBI00001, FBI00002, FBI00010, FBI00013, FBI00029, FBI00032, FBI00033, FBI00034, FBI00043, FBI00044, FBI00048, FBI00050, FBI00051, FBI00057, FBI00059, FBI00060, FBI00070, FBI00071, FBI00076, FBI00079, FBI00087, FBI00093, FBI00102, FBI00109, FBI00117, FBI00120, FBI00125, FBI00127, FBI00128, FBI00145, FBI00162, FBI00174, FBI00184, FBI00190, FBI00191, FBI00194, FBI00198, FBI00199, FBI00200, FBI00201, FBI00205, FBI00206, FBI00211, FBI00220, FBI00221, FBI00236, FBI00245, FBI00248, FBI00251, FBI00254, FBI00267, FBI00278, FBI00288, and FBI00290, or a functional equivalent thereof;

(b) a consortium comprising

(i) *Acutalibacter timonensis*, *Alistipes onderdonkii*, *Bacteroides uniformis*, *Eubacterium rectale*, *Alistipes timonensis*, *Bacteroides kribbi*, *Coprococcus eutactus*, *Bilophila wadsworthia*, *Bacteroides caccae*, *Alistipes shahii*, *Parasutterella excrementihominis*, *Paraprevotella clara*, *Sutterella wadsworthensis*, *Sutterella massiliensis*, *Porphyromonas asaccharolytica*, *Ruminococcus bromii*, *Monoglobus pectinilyticus*, *Ruminococcaceae sp. FBI00097*, *Gordonibacter pamelaeae*, *Bacteroides uniformis*, *Gordonibacter pamelaeae*, *Bacteroides fragilis*, *Phascolarctobacterium faecium*, *Monoglobus pectinilyticus*, *Clostridium aldenense*, *Ruthenibacterium lactatiformans*, *Bacteroides ovatus*, *Bifidobacterium bifidum*, *Anaerotruncus massiliensis*, *Clostridium aldenense*, *Sutterella wadsworthensis*, *Catabacter hongkongensis*, *Alistipes senegalensis*, *Ruminococcaceae sp. FBI00233*, *Alistipes shahii*, *Dielma fastidiosa*, *Eubacterium siraeum*, *Faecalibacterium prausnitzii*, *Turicibacter sanguinis*, *Eubacterium rectale*, *Bacteroides caccae*, *Methanobrevibacter smithii*, *Barnesiella intestinihominis*, *Alistipes onderdonkii*, *Methanobrevibacter smithii*, or a functional equivalent thereof; or

(ii) FBI00004, FBI00012, FBI00015, FBI00018, FBI00019, FBI00021, FBI00038, FBI00040, FBI00046, FBI00061, FBI00066, FBI00075, FBI00077, FBI00080, FBI00081, FBI00085, FBI00092, FBI00097, FBI00099, FBI00112, FBI00132, FBI00137, FBI00140, FBI00149, FBI00151, FBI00176, FBI00189, FBI00197, FBI00208, FBI00212, FBI00224, FBI00226, FBI00229, FBI00233, FBI00235, FBI00237, FBI00243, FBI00244, FBI00258, FBI00260, FBI00263, FBI00270, FBI00273, FBI00277, and FBI00292, or a functional equivalent thereof;

(c) a consortium comprising

(i) *Bifidobacterium adolescentis*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bacteroides thetaiotaomicron*, *Coprococcus comes*, *Fusicatenibacter saccharivorans*, *Eggerthella lenta*, *Eubacterium eligens*, *Bacteroides xylanisolvens*, *Lactobacillus rogosae*, *Clostridium citroniae*, *Collinsella aerofaciens*, *Blautia obeum*, *Eggerthella lenta*, *Blautia wexlerae*, *Lachnoclostridium pacaense*, *Bacteroides vulgatus*, *Parabacteroides merdae*, *Dorea formicigenerans*, *Ruminococcus faecis*, *Roseburia hominis*, *Anaerostipes hadrus*, *Bifidobacterium adolescentis*, *Bifidobacterium pseudocatenulatum*, *Clostridium bolteae*, *Eisenbergiella tayi*, *Dorea*

longicatena, *Eggerthella lenta*, *Bacteroides stercoris*, *Hungatella hathewayi*, *Bacteroides xylanisolvens*, or a functional equivalent thereof; or

(ii) FBI00009, FBI00011, FBI00016, FBI00020, FBI00025, FBI00027, FBI00030, FBI00047, FBI00052, FBI00053, FBI00056, FBI00062, FBI00078, FBI00096, FBI00104, FBI00110, FBI00111, FBI00113, FBI00115, FBI00116, FBI00123, FBI00124, FBI00126, FBI00135, FBI00147, FBI00159, FBI00167, FBI00170, FBI00232, FBI00255, and FBI00271, or a functional equivalent thereof;

(d) a consortium comprising

(i) *Alistipes putredinis, Dialister succinatiphilus, Akkermansia muciniphila, Ruminococcus bromii, Dialister invisus, Bacteroides massiliensis, Bilophila wadsworthia, Holdemanella biformis, Parasutterella excrementihominis, Alistipes sp. FBI00180, Bacteroides coprocola, Alistipes sp. FBI00238, Alistipes putredinis, Eubacterium xylanophilum, Senegalimassilia anaerobia*, or a functional equivalent thereof; or

(ii) FBI00022, FBI00049, FBI00068, FBI00069, FBI00152, FBI00165, FBI00171, FBI00175, FBI00177, FBI00180, FBI00182, FBI00238, FBI00269, FBI00274, and FBI00281, or a functional equivalent thereof; or

(e) a combination thereof.

2. The composition of claim 1, wherein

(a) each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147;

(b) each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148;

(c) each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139;

(d) each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144; or

(e) a combination thereof.

3. The composition of claim 1 or 2, wherein the composition further comprises at least 1 oxalate-metabolizing microbial strain, wherein the at least one strain expresses an enzyme selected from a formyl-CoA transferase, an oxalate-formate antiporter, and an oxalyl-CoA decarboxylase, optionally wherein the at least 1 oxalate-metabolizing microbial strain is from the *Oxalobacter* genus.

4. The composition of claim 3, said composition comprising at least 3 oxalate-metabolizing microbial strains, wherein the at least 3 oxalate-metabolizing microbial strains are different strains of the same species.

5. The composition of claim 3 or 4, wherein each oxalate-metabolizing microbial strain is selected from

(a) a first *O. formigenes* strain, FBI00067, or a functional equivalent thereof;

(b) a second *O. formigenes* strain, FBI00133, or a functional equivalent thereof; and/or

(c) a third *O. formigenes* strain, FBI00289, or a functional equivalent thereof.

6. The composition of claim 5, wherein each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146.

7. The composition of any one of claims 1-6, which is a pharmaceutical composition, optionally wherein the composition comprises from about 5×10^{10} to about 5×10^{11} viable cells, from about 5×10^{9} to about 5×10^{10} viable cells, from about 5×10^{11} to about 5×10^{12} viable cells, up to about 5×10^{12} viable cells.

8. A microbial consortium comprising microbial strains set forth in Table 1, Table 2, Table 3, Table 4, Table 5, Table 6, Table 7, Table 8, Table 9, Table 10, Table 11, Table 12, Table 13, Table 14, Table 15, Table 16, Table 17, Table 18, Table 19, Table 22, or a functional equivalent thereof, optionally wherein each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148.

9. A method of manufacturing the composition of any one of claims 1-6, the method comprising:

(a) obtaining a first consortium comprising

(i) *Clostridium citroniae*, *Bacteroides salyersiae*, *Blautia obeum*, *Parabacteroides merdae*, *Parabacteroides distasonis*, *Anaerostipes hadrus*, *Lachnospiraceae sp. FBI00033*, *Eubacterium eligens*, *Bifidobacterium dentium*, *Blautia wexlerae*, *Fusicatenibacter saccharivorans*, *Bacteroides nordii*, *Dorea*

formicigenerans, *Dorea longicatena*, *Bacteroides stercorirosoris*, *Bifidobacterium longum*, *Bacteroides kribbi*, *Lachnospiraceae sp. FBI00071*, *Bacteroides thetaiotaomicron*, *Clostridium clostridioforme*, *Clostridium scindens*, *Roseburia hominis*, *Clostridium fessum*, *Coprococcus comes*, *Blautia faecis*, *Hungatella hathewayi*, *Bacteroides stercoris*, *Collinsella aerofaciens*, *Hungatella effluvii*, *Bifidobacterium adolescentis*, *Bifidobacterium catenulatum*, *Lactobacillus rogosae*, *Bacteroides faecis*, *Bacteroides finegoldii*, *Clostridiaceae sp. FBI00191*, *Ruminococcus faecis*, *Lachnoclostridium pacaense*, *Clostridium bolteae*, *Longicatena caecimuris*, *Eggerthella lenta*, *Blautia massiliensis*, *Bacteroides xylanisolvens*, *Bacteroides vulgatus*, *Megasphaera massiliensis*, *Butyricimonas faecihominis*, *Eisenbergiella tayi*, *Acidaminococcus intestini*, *Emergencia timonensis*, *Bifidobacterium pseudocatenulatum*, *Eubacterium hallii*, *Anaerofustis stercorihominis*, *Eubacterium ventriosum*, *Blautia hydrogenotrophica*, *Lachnospiraceae sp. FBI00290*, or a functional equivalent thereof; or

(ii) FBI00001, FBI00002, FBI00010, FBI00013, FBI00029, FBI00032, FBI00033, FBI00034, FBI00043, FBI00044, FBI00048, FBI00050, FBI00051, FBI00057, FBI00059, FBI00060, FBI00070, FBI00071, FBI00076, FBI00079, FBI00087, FBI00093, FBI00102, FBI00109, FBI00117, FBI00120, FBI00125, FBI00127, FBI00128, FBI00145, FBI00162, FBI00174, FBI00184, FBI00190, FBI00191, FBI00194, FBI00198, FBI00199, FBI00200, FBI00201, FBI00205, FBI00206, FBI00211, FBI00220, FBI00221, FBI00236, FBI00245, FBI00248, FBI00251, FBI00254, FBI00267, FBI00278, FBI00288, and FBI00290, or a functional equivalent thereof;

(b) obtaining a second consortium comprising

(i) *Acutalibacter timonensis*, *Alistipes onderdonkii*, *Bacteroides uniformis*, *Eubacterium rectale*, *Alistipes timonensis*, *Bacteroides kribbi*, *Coprococcus eutactus*, *Bilophila wadsworthia*, *Bacteroides caccae*, *Alistipes shahii*, *Parasutterella excrementihominis*, *Paraprevotella clara*, *Sutterella wadsworthensis*, *Sutterella massiliensis*, *Porphyromonas asaccharolytica*, *Ruminococcus bromii*, *Monoglobus pectinilyticus*, *Ruminococcaceae sp. FBI00097*, *Gordonibacter pamelaeae*, *Bacteroides uniformis*, *Gordonibacter pamelaeae*, *Bacteroides fragilis*, *Phascolarctobacterium faecium*, *Monoglobus pectinilyticus*, *Clostridium aldenense*, *Ruthenibacterium*

lactatiformans, *Bacteroides ovatus*, *Bifidobacterium bifidum*, *Anaerotruncus massiliensis*, *Clostridium aldenense*, *Sutterella wadsworthensis*, *Catabacter hongkongensis*, *Alistipes senegalensis*, *Ruminococcaceae sp. FBI00233*, *Alistipes shahii*, *Dielma fastidiosa*, *Eubacterium siraeum*, *Faecalibacterium prausnitzii*, *Turicibacter sanguinis*, *Eubacterium rectale*, *Bacteroides caccae*, *Methanobrevibacter smithii*, *Barnesiella intestinihominis*, *Alistipes onderdonkii*, *Methanobrevibacter smithii*, or a functional equivalent thereof; or

(ii) FBI00004, FBI00012, FBI00015, FBI00018, FBI00019, FBI00021, FBI00038, FBI00040, FBI00046, FBI00061, FBI00066, FBI00075, FBI00077, FBI00080, FBI00081, FBI00085, FBI00092, FBI00097, FBI00099, FBI00112, FBI00132, FBI00137, FBI00140, FBI00149, FBI00151, FBI00176, FBI00189, FBI00197, FBI00208, FBI00212, FBI00224, FBI00226, FBI00229, FBI00233, FBI00235, FBI00237, FBI00243, FBI00244, FBI00258, FBI00260, FBI00263, FBI00270, FBI00273, FBI00277, and FBI00292, or a functional equivalent thereof;

(c) obtaining a third consortium comprising

(i) *Bifidobacterium adolescentis*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bacteroides thetaiotaomicron*, *Coprococcus comes*, *Fusicatenibacter saccharivorans*, *Eggerthella lenta*, *Eubacterium eligens*, *Bacteroides xylanisolvens*, *Lactobacillus rogosae*, *Clostridium citroniae*, *Collinsella aerofaciens*, *Blautia obeum*, *Eggerthella lenta*, *Blautia wexlerae*, *Lachnoclostridium pacaense*, *Bacteroides vulgatus*, *Parabacteroides merdae*, *Dorea formicigenerans*, *Ruminococcus faecis*, *Roseburia hominis*, *Anaerostipes hadrus*, *Bifidobacterium adolescentis*, *Bifidobacterium pseudocatenulatum*, *Clostridium bolteae*, *Eisenbergiella tayi*, *Dorea longicatena*, *Eggerthella lenta*, *Bacteroides stercoris*, *Hungatella hathewayi*, *Bacteroides xylanisolvens*, or a functional equivalent thereof; or

(ii) FBI00009, FBI00011, FBI00016, FBI00020, FBI00025, FBI00027, FBI00030, FBI00047, FBI00052, FBI00053, FBI00056, FBI00062, FBI00078, FBI00096, FBI00104, FBI00110, FBI00111, FBI00113, FBI00115, FBI00116, FBI00123, FBI00124, FBI00126, FBI00135, FBI00147, FBI00159, FBI00167, FBI00170, FBI00232, FBI00255, and FBI00271, or a functional equivalent thereof

(d) obtaining a fourth consortium comprising

(i) *Alistipes putredinis*, *Dialister succinatiphilus*, *Akkermansia muciniphila*, *Ruminococcus bromii*, *Dialister invisus*, *Bacteroides massiliensis*, *Bilophila wadsworthia*, *Holdemanella biformis*, *Parasutterella excrementihominis*, *Alistipes sp. FBI00180*, *Bacteroides coprocola*, *Alistipes sp. FBI00238*, *Alistipes putredinis*, *Eubacterium xylanophilum*, *Senegalimassilia anaerobia*, or a functional equivalent thereof; or

(ii) FBI00022, FBI00049, FBI00068, FBI00069, FBI00152, FBI00165, FBI00171, FBI00175, FBI00177, FBI00180, FBI00182, FBI00238, FBI00269, FBI00274, and FBI00281, or a functional equivalent thereof; and

(e) blending the first consortium, the second consortium, the third consortium, and the fourth to thereby obtain the composition.

10. The method of claim 9, further comprising

(a) obtaining a fifth consortium comprising a first *O. formigenes* strain, FBI00067, or a functional equivalent thereof;

(b) obtaining a sixth consortium comprising a second *O. formigenes* strain, FBI00133, or a functional equivalent thereof;

(c) obtaining a seventh consortium comprising a third *O. formigenes* strain, FBI00289, or a functional equivalent thereof; and

(d) blending the fifth consortium, the sixth consortium, and the seventh consortium with the composition.

11. The method of claim 9 or 10, wherein the fourth composition is obtained by growing microbes in presence of threonine.

12. The method of any one of claims 9-11, wherein the composition comprises a lyoprotectant, maltodextrin, inulin, or a combination thereof.

13. The method of any one of claims 9-12, wherein (a) each consortium is separately lyophilized before blending; (b) each consortium is prepared using inoculation density adjustment; (c) each consortium is cultured or has been cultured in presence of gas overlay; and/or (d) each consortium is cultured or has been cultured in absence of gas sparging.

14. The composition of any one of claims 3-7 for use in treating hyperoxaluria, reducing the risk of developing hyperoxaluria, and/or reducing urinary oxalate in a subject in need thereof.

15. Use of the composition of any one of claims 3-7 in the manufacture of a medicament for treating hyperoxaluria, reducing the risk of developing hyperoxaluria, and/or reducing urinary oxalate in a subject in need thereof, wherein a first dose of the composition of any one of claims 3-7 is to be administered.

16. The use of claim 15, wherein a second dose of the composition is to be further administered.

17. The use of claim 15, wherein the hyperoxaluria is a primary hyperoxaluria, a secondary hyperoxaluria, or an enteric hyperoxaluria.

18. A kit comprising the composition of any one of claims 1-7.

19. A method of culturing a microbial strain from the *Akkermansia* genus comprising contacting the strain with N-Acetylgalactosamine (GalNAc).