

What is claimed is:

1. A non-naturally occurring microbial organism comprising at least one exogenous nucleic acid encoding an enzyme expressed in a sufficient amount to produce reducing equivalents from carbon monoxide or hydrogen, thereby fixing CO₂ via a reductive tricarboxylic acid (rTCA) cycle, wherein said at least one exogenous nucleic acid is selected from a carbon monoxide dehydrogenase, a hydrogenase, and an NAD(P)H:ferredoxin oxidoreductase, wherein said microbial organism further comprises a 1,4-butanediol pathway, wherein said pathway comprises an enzyme selected from the group consisting of a 4-hydroxybutyraldehyde reductase, a 4-hydroxybutyryl-CoA reductase (aldehyde forming), a succinyl-CoA transferase, a succinyl-CoA synthetase, a succinyl-CoA reductase (aldehyde forming), a 4-hydroxybutyrate dehydrogenase, a 4-hydroxybutyrate kinase, a phosphotrans-4-hydroxybutyrylase, a succinate reductase, a 4-hydroxybutyryl-CoA transferase, a 4-hydroxybutyryl-CoA synthetase, a 4-hydroxybutyrate reductase, a 4-hydroxybutyryl-phosphate reductase and a 4-hydroxybutyryl-CoA reductase (alcohol forming).
2. The non-naturally occurring microbial organism of claim 1, wherein said microbial organism further comprises a ferredoxin.
3. A non-naturally occurring microbial organism comprising a microbial organism having carbon monoxide dehydrogenase or hydrogenase activity and a reductive tricarboxylic acid (rTCA) pathway comprising at least one exogenous nucleic acid encoding a rTCA pathway enzyme expressed in a sufficient amount to convert CO, CO₂ or H₂ to acetyl-CoA, wherein said rTCA pathway enzyme is selected from the group consisting of an ATP citrate-lyase, a citrate lyase, an aconitase, an isocitrate dehydrogenase, an alpha-ketoglutarate:ferredoxin oxidoreductase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarate reductase, a fumarase and a malate dehydrogenase, wherein said microbial organism further comprises a 1,4-butanediol pathway, wherein said 1,4-butanediol pathway comprises an enzyme selected from the group consisting of a 4-hydroxybutyryl-CoA reductase (alcohol forming), a 4-hydroxybutyryl-CoA reductase (aldehyde forming), a 4-hydroxybutyraldehyde reductase, and a 4-hydroxybutyrate reductase.
4. The non-naturally occurring microbial organism of claim 3, wherein said microbial organism comprising a 4-hydroxybutyrate reductase further comprises a 4-hydroxybutyryl-CoA

transferase; a 4-hydroxybutyryl-CoA synthetase; or a phosphotrans-4-hydroxybutyrylase and a 4-hydroxybutyrate kinase.

5. The non-naturally occurring microbial organism of claim 3, wherein said microbial organism further comprises an acetoacetyl-CoA thiolase or a crotonase.

6. The non-naturally occurring microbial organism of claim 3, wherein said rTCA pathway enzyme is selected from the group consisting of an ATP citrate-lyase, a citrate lyase, an alpha-ketoglutarate:ferredoxin oxidoreductase, and a fumarate reductase.

7. The non-naturally occurring microbial organism of claim 3, wherein said rTCA pathway enzyme is selected from an aconitase or an isocitrate dehydrogenase.

8. A non-naturally occurring microbial organism, comprising a microbial organism having an n-propanol pathway and an isopropanol pathway, said n-propanol pathway comprising at least one exogenous nucleic acid encoding an n-propanol pathway enzyme expressed in a sufficient amount to produce n-propanol, said n-propanol pathway comprising:

a propanol dehydrogenase, a propionaldehyde dehydrogenase, a propionyl-CoA:phosphate propanoyltransferase, a propionyl-CoA hydrolase, a propionyl-CoA transferase, a propionyl-CoA synthetase, a propionate kinase, a propionate reductase or a propionyl phosphate reductase,

said isopropanol pathway comprising at least one exogenous nucleic acid encoding an isopropanol pathway enzyme expressed in a sufficient amount to produce isopropanol, said isopropanol pathway comprising:

an isopropanol dehydrogenase, an acetyl-CoA acetyl thiolase, an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA synthetase, or an acetoacetate decarboxylase.

9. The non-naturally occurring microbial organism of claim 8, further comprising an acetyl-CoA pathway comprising at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to produce acetyl-CoA, said acetyl-CoA pathway comprising:

a pyruvate kinase, a pyruvate dehydrogenase, a pyruvate ferredoxin oxidoreductase, a pyruvate formate lyase, a pyruvate formate lyase activating enzyme, or a formate dehydrogenase.

10. The non-naturally occurring microbial organism of claim 8, further comprising a propionyl-CoA pathway comprising at least one exogenous nucleic acid encoding a propionyl-CoA pathway enzyme expressed in a sufficient amount to produce propionyl-CoA, said propionyl-CoA pathway comprising:

a PEP carboxykinase, a PEP carboxylase, a malate dehydrogenase, a fumarase, a fumarate reductase, a succinyl-CoA transferase, a succinyl-CoA synthetase, a methylmalonyl-CoA mutase, a methylmalonyl-CoA epimerase or a methylmalonyl-CoA decarboxylase.

11. The non-naturally occurring microbial organism of claim 10, wherein said propionyl-CoA pathway further comprises a pyruvate carboxylase or a methylmalonyl-CoA carboxytransferase.

12. The non-naturally occurring microbial organism of claim 8, further comprising a propionyl-CoA pathway comprising at least one exogenous nucleic acid encoding a propionyl-CoA pathway enzyme expressed in a sufficient amount to produce propionyl-CoA, said propionyl-CoA pathway comprising:

a PEP carboxykinase, a PEP carboxylase, a threonine deaminase, or a 2-oxobutanoate dehydrogenase.

13. The non-naturally occurring microbial organism of claim 12, wherein said n-propanol pathway further comprises 2-oxobutanoate decarboxylase.

14. The non-naturally occurring microbial organism of claim 8, further comprising a propionyl-CoA pathway comprising at least one exogenous nucleic acid encoding a propionyl-CoA pathway enzyme expressed in a sufficient amount to produce propionyl-CoA, said propionyl-CoA pathway comprising:

an acetyl-CoA carboxylase, a malonyl-CoA reductase, a malonate semialdehyde reductase or propionyl-CoA synthase.

15. The non-naturally occurring microbial organism of claim 8, further comprising a propionyl-CoA pathway comprising at least one exogenous nucleic acid encoding a propionyl-CoA pathway enzyme expressed in a sufficient amount to produce propionyl-CoA, said propionyl-CoA pathway comprising:

a lactate dehydrogenase, a lactate-CoA transferase, a lactyl-CoA dehydratase or acryloyl CoA reductase.

16. A non-naturally occurring microbial organism, comprising a microbial organism having an n-propanol pathway and an isopropanol pathway, said n-propanol pathway comprising a first set of exogenous nucleic acids encoding n-propanol pathway enzymes expressed in a sufficient amount to produce n-propanol, said first set of exogenous nucleic acids encoding:

a propionaldehyde dehydrogenase and a propanol dehydrogenase; or

a propionyl-CoA:phosphate propanoyltransferase, a propionyl phosphate reductase and a propanol dehydrogenase; or

a propionyl-CoA hydrolase or a propionyl-CoA transferase or a propionyl-CoA synthetase, a propionate kinase, a propionyl phosphate reductase and a propanol dehydrogenase; or

a propionyl-CoA hydrolase or a propionyl-CoA transferase or a propionyl-CoA synthetase, a propionate reductase and a propanol dehydrogenase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

17. The non-naturally occurring microbial organism of claim 16, further comprising an acetyl-CoA pathway comprising a third set of exogenous nucleic acids encoding acetyl-CoA pathway enzymes expressed in a sufficient amount to produce acetyl-CoA, said third set of exogenous nucleic acids encoding:

a pyruvate kinase; and a pyruvate dehydrogenase or a pyruvate ferredoxin oxidoreductase; or a pyruvate formate lyase, a pyruvate formate lyase activating enzyme and a formate dehydrogenase.

18. The non-naturally occurring microbial organism of claim 16, further comprising a propionyl-CoA pathway comprising a third set of exogenous nucleic acids encoding propionyl-CoA pathway enzymes expressed in a sufficient amount to produce propionyl-CoA, said third set of exogenous nucleic acids encoding:

a PEP carboxykinase or a PEP carboxylase; a malate dehydrogenase; a fumarase; a fumarate reductase; a succinyl-CoA transferase or a succinyl-CoA synthetase; a methylmalonyl-CoA mutase; and a methylmalonyl-CoA decarboxylase.

19. The non-naturally occurring microbial organism of claim 18, wherein said third set of exogenous nucleic acids further encodes a methylmalonyl-CoA epimerase, a pyruvate carboxylase or a methylmalonyl-CoA carboxytransferase.

20. The non-naturally occurring microbial organism of claim 16, further comprising a propionyl-CoA pathway comprising a third set of exogenous nucleic acids encoding propionyl-CoA pathway enzymes expressed in a sufficient amount to produce propionyl-CoA, said third set of exogenous nucleic acids encoding:

a PEP carboxykinase or a PEP carboxylase; a threonine deaminase; and a 2-oxobutanoate dehydrogenase.

21. The non-naturally occurring microbial organism of claim 20, wherein said third set of exogenous nucleic acids further encodes a or a methylmalonyl-CoA carboxytransferase or a pyruvate carboxylase.

22. The non-naturally occurring microbial organism of claim 20, wherein said second set of exogenous nucleic acids further encode a 2-oxobutanoate decarboxylase.

23. The non-naturally occurring microbial organism of claim 16, further comprising a propionyl-CoA pathway comprising a third set of exogenous nucleic acids encoding propionyl-CoA pathway enzymes expressed in a sufficient amount to produce propionyl-CoA, said third set of exogenous nucleic acids encoding:

an acetyl-CoA carboxylase; a malonyl-CoA reductase; a malonate semialdehyde reductase; and propionyl-CoA synthase.

24. The non-naturally occurring microbial organism of claim 16, further comprising a propionyl-CoA pathway comprising a third set of exogenous nucleic acids encoding propionyl-CoA pathway enzymes expressed in a sufficient amount to produce propionyl-CoA, said third set of exogenous nucleic acids encoding:

a lactate dehydrogenase; a lactate-CoA transferase; a lactyl-CoA dehydratase; and acetyl CoA reductase.

25. A non-naturally occurring microbial organism, comprising a microbial organism having an n-propanol pathway and an isopropanol pathway, said n-propanol pathway comprising a first set of exogenous nucleic acids encoding n-propanol pathway enzymes expressed in a sufficient amount to produce n-propanol, said first set of exogenous nucleic acids encoding:

a PEP carboxykinase or a PEP carboxylase; a malate dehydrogenase; a fumarase; a fumarate reductase; a succinyl-CoA transferase or a succinyl-CoA synthetase; a methylmalonyl-CoA mutase; a methylmalonyl-CoA decarboxylase; and a propionaldehyde dehydrogenase and a propanol dehydrogenase; or a propionyl-CoA:phosphate propanoyltransferase and a propionyl phosphate reductase; or a propionyl-CoA hydrolase or a propionyl-CoA transferase or a propionyl-CoA synthetase, a propionate kinase, a propionyl phosphate reductase and a propanol dehydrogenase; or a propionyl-CoA hydrolase or a propionyl-CoA transferase or a propionyl-CoA synthetase, a propionate reductase and a propanol dehydrogenase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

a pyruvate kinase; a pyruvate dehydrogenase or a pyruvate ferredoxin oxidoreductase; or a pyruvate formate lyase, a pyruvate formate lyase activating enzyme and a formate dehydrogenase; an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

26. The non-naturally occurring microbial organism of claim 25, wherein said first set of exogenous nucleic acids further encodes a methylmalonyl-CoA epimerase, a pyruvate carboxylase or a methylmalonyl-CoA carboxytransferase.

27. A non-naturally occurring microbial organism, comprising a microbial organism having an n-propanol pathway and an isopropanol pathway, said n-propanol pathway comprising a first set of exogenous nucleic acids encoding n-propanol pathway enzymes expressed in a sufficient amount to produce n-propanol, said first set of exogenous nucleic acids encoding:

a PEP carboxykinase or a PEP carboxylase; a threonine deaminase; and a 2-oxobutanoate decarboxylase and a propanol dehydrogenase; or a 2-oxobutanoate dehydrogenase, a propionaldehyde dehydrogenase and a propanol dehydrogenase; or a 2-oxobutanoate dehydrogenase, a propionyl-CoA:phosphate propanoyltransferase, a propionyl phosphate reductase and a propanol dehydrogenase; or a 2-oxobutanoate dehydrogenase, a propionyl-CoA hydrolase or a propionyl-CoA transferase or a propionyl-CoA synthetase, a propionate kinase, a propionyl phosphate reductase and a propanol dehydrogenase; or a 2-oxobutanoate dehydrogenase, a propionyl-CoA hydrolase or a propionyl-CoA transferase or a propionyl-CoA synthetase, a propionate reductase and a propanol dehydrogenase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

a pyruvate kinase; a pyruvate dehydrogenase or a pyruvate ferredoxin oxidoreductase; or a pyruvate formate lyase, a pyruvate formate lyase activating enzyme and a formate dehydrogenase; an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

28. The non-naturally occurring microbial organism of claim 27, wherein said second set of exogenous nucleic acids further encodes a methylmalonyl-CoA decarboxylase or a pyruvate carboxylase.

29. A non-naturally occurring microbial organism, comprising a microbial organism having an n-propanol pathway and an isopropanol pathway, said n-propanol pathway comprising a first set of

exogenous nucleic acids encoding n-propanol pathway enzymes expressed in a sufficient amount to produce n-propanol, said first set of exogenous nucleic acids encoding:

a pyruvate kinase; a pyruvate dehydrogenase or a pyruvate ferredoxin oxidoreductase; or a pyruvate formate lyase, a pyruvate formate lyase activating enzyme and a formate dehydrogenase; an acetyl-CoA carboxylase; a malonyl-CoA reductase; a malonate semialdehyde reductase; propionyl-CoA synthase; and a propionaldehyde dehydrogenase and a propanol dehydrogenase; or a propionyl-CoA:phosphate propanoyltransferase, a propionyl phosphate reductase and propanol dehydrogenase; or a propionyl-CoA hydrolase or a propionyl-CoA transferase or a propionyl-CoA synthetase, a propionate kinase, a propionyl phosphate reductase and a propanol dehydrogenase; or a propionyl-CoA hydrolase or a propionyl-CoA transferase or a propionyl-CoA synthetase, a propionate reductase and a propanol dehydrogenase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

30. A non-naturally occurring microbial organism, comprising a microbial organism having an n-propanol pathway and an isopropanol pathway, said n-propanol pathway comprising a first set of exogenous nucleic acids encoding n-propanol pathway enzymes expressed in a sufficient amount to produce n-propanol, said first set of exogenous nucleic acids encoding:

a lactate dehydrogenase; a lactate-CoA transferase; a lactyl-CoA dehydratase; acryloyl CoA reductase; and a propionaldehyde dehydrogenase and a propanol dehydrogenase; or a propionyl-CoA:phosphate propanoyltransferase, a propionyl phosphate reductase and a propanol dehydrogenase; or a propionyl-CoA hydrolase or a propionyl-CoA transferase or a propionyl-CoA synthetase, a propionate kinase, a propionyl phosphate reductase and a propanol dehydrogenase; or a propionyl-CoA hydrolase or a propionyl-CoA transferase or a propionyl-CoA synthetase, a propionate reductase and a propanol dehydrogenase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

a pyruvate dehydrogenase or a pyruvate ferredoxin oxidoreductase; or a pyruvate formate lyase, a pyruvate formate lyase activating enzyme and a formate dehydrogenase; an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

31. The non-naturally occurring microbial organism of any one of claims 8-30, wherein said exogenous nucleic acid is a heterologous nucleic acid.

32. The non-naturally occurring microbial organism of any one of claims 8-30, wherein said non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

33. A method for producing n-propanol and isopropanol, comprising culturing a non-naturally occurring microbial organism of any one of claims 8-30 under conditions and for a sufficient period of time to produce n-propanol and isopropanol.

34. The method of claim 33, wherein said conditions comprise substantially anaerobic culture conditions.

35. The method of claim 33, wherein said exogenous nucleic acid is a heterologous nucleic acid.

36. A non-naturally occurring microbial organism, comprising a microbial organism having an n-propanol pathway, said n-propanol pathway comprising at least one exogenous nucleic acid encoding an n-propanol pathway enzyme expressed in a sufficient amount to produce n-propanol, said n-propanol pathway comprising:

a propanol dehydrogenase, a propionaldehyde dehydrogenase, a propionyl-CoA:phosphate propanoyltransferase, a propionyl-CoA hydrolase, a propionyl-CoA transferase, a propionyl-CoA synthetase, a propionate kinase, a propionate reductase, or a propionyl phosphate reductase.

37. A non-naturally occurring microbial organism, comprising a microbial organism having an n-propanol pathway, said n-propanol pathway comprising a set of exogenous nucleic acids encoding

n-propanol pathway enzymes expressed in a sufficient amount to produce n-propanol, said set of exogenous nucleic acids encoding:

a propionaldehyde dehydrogenase and a propanol dehydrogenase; or a propionyl-CoA:phosphate propanoyltransferase, a propionyl phosphate reductase and a propanol dehydrogenase; or a propionyl-CoA hydrolase or a propionyl-CoA transferase or a propionyl-CoA synthetase, a propionate kinase, a propionyl phosphate reductase and a propanol dehydrogenase; or a propionyl-CoA hydrolase or a propionyl-CoA transferase or a propionyl-CoA synthetase, a propionate reductase and a propanol dehydrogenase.

38. The non-naturally occurring microbial organism of claim 36 or 37, wherein said exogenous nucleic acid is a heterologous nucleic acid.

39. The non-naturally occurring microbial organism of claim 36 or 37, wherein said non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

40. A method for producing n-propanol, comprising culturing a non-naturally occurring microbial organism of claim 36 or 37 under conditions and for a sufficient period of time to produce n-propanol.

41. The method of claim 40, wherein said conditions comprise substantially anaerobic culture conditions.

42. The method of claim 40, wherein said exogenous nucleic acid is a heterologous nucleic acid.

43. A non-naturally occurring microbial organism, comprising a microbial organism having a 1,4-butanediol pathway and an isopropanol pathway, said 1,4-butanediol pathway comprising at least one exogenous nucleic acid encoding a 1,4-butanediol pathway enzyme expressed in a sufficient amount to produce 1,4-butanediol, said 1,4-butanediol pathway comprising:

a 4-hydroxybutyraldehyde reductase, a succinyl-CoA reductase, a succinate reductase, a 4-hydroxybutyrate dehydrogenase, a 4-hydroxybutyryl-CoA transferase, a 4-hydroxybutyryl-CoA synthetase, a 4-hydroxybutyryl-CoA reductase (aldehyde-forming), 4-hydroxybutyryl-phosphate reductase, a 4-hydroxybutyrate reductase; a 4-hydroxybutyrate kinase, a phosphotrans-4-hydroxybutyrylase, or a 4-hydroxybutyryl-CoA reductase (alcohol-forming);

said isopropanol pathway comprising at least one exogenous nucleic acid encoding an isopropanol pathway enzyme expressed in a sufficient amount to produce isopropanol, said isopropanol pathway comprising:

an isopropanol dehydrogenase, an acetyl-CoA acetyl thiolase, an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA synthetase, or an acetoacetate decarboxylase.

44. A non-naturally occurring microbial organism, comprising a microbial organism having a 1,3-butanediol pathway and an isopropanol pathway, said 1,3-butanediol pathway comprising at least one exogenous nucleic acid encoding a 1,3-butanediol pathway enzyme expressed in a sufficient amount to produce 1,3-butanediol, said 1,3-butanediol pathway comprising:

a 3-hydroxybutyraldehyde reductase, a succinyl-CoA reductase, a succinate reductase, a 4-hydroxybutyrate dehydrogenase, a 4-hydroxybutyryl-CoA transferase, a 4-hydroxybutyryl-CoA synthetase, a 4-hydroxybutyrate kinase, a phosphotrans-4-hydroxybutyrylase, a 4-hydroxybutyryl-CoA dehydratase, a crotonase, a 3-hydroxybutyryl-CoA transferase, a 3-hydroxybutyryl-CoA synthetase, a 3-hydroxybutyryl-CoA hydrolase, a 3-hydroxybutyrate reductase, a 3-hydroxybutyryl-CoA reductase (aldehyde forming), or a 3-hydroxybutyryl-CoA reductase (alcohol-forming);

said isopropanol pathway comprising at least one exogenous nucleic acid encoding an isopropanol pathway enzyme expressed in a sufficient amount to produce isopropanol, said isopropanol pathway comprising:

an isopropanol dehydrogenase, an acetyl-CoA acetyl thiolase, an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA synthetase, or an acetoacetate decarboxylase.

45. A non-naturally occurring microbial organism, comprising a microbial organism having a methylacrylic acid pathway and an isopropanol pathway, said methylacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methylacrylic acid pathway enzyme expressed in a sufficient amount to produce methylacrylic acid, said methylacrylic acid pathway comprising:

a 4-hydroxybutyryl-CoA mutase, a succinyl-CoA reductase, a succinate reductase, a 4-hydroxybutyrate dehydrogenase, a 4-hydroxybutyryl-CoA transferase, a 4-hydroxybutyryl-CoA

synthetase, a 4-hydroxybutyrate kinase, a phosphotrans-4-hydroxybutyrylase, a 3-hydroxyisobutyryl-CoA dehydratase, a methacrylyl-CoA transferase, a methacrylyl-CoA synthetase, a methacrylyl-CoA hydrolase, a 3-hydroxyisobutyryl-CoA transferase, a 3-hydroxyisobutyryl-CoA synthetase, a 3-hydroxyisobutyryl-CoA hydrolase, a 3-hydroxyisobutyrate dehydratase, a methylmalonyl-CoA mutase, a methylmalonyl-CoA epimerase, a methylmalonyl-CoA transferase, a methylmalonyl-CoA synthetase, a methylmalonyl-CoA hydrolase, a methylmalonate reductase, a methylmalonyl-CoA reductase (aldehyde forming), a 3-hydroxyisobutyrate dehydrogenase, a methylmalonyl-CoA reductase (alcohol forming), or a 3-hydroxyisobutyrate dehydratase;

said isopropanol pathway comprising at least one exogenous nucleic acid encoding an isopropanol pathway enzyme expressed in a sufficient amount to produce isopropanol, said isopropanol pathway comprising:

an isopropanol dehydrogenase, an acetyl-CoA acetyl thiolase, an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA synthetase, or an acetoacetate decarboxylase.

46. The non-naturally occurring microbial organism of any one of claims 43-45, further comprising an acetyl-CoA pathway comprising at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to produce acetyl-CoA, said acetyl-CoA pathway comprising:

a pyruvate kinase, a pyruvate dehydrogenase, a pyruvate ferredoxin oxidoreductase, a pyruvate formate lyase, a pyruvate formate lyase activating enzyme, or a formate dehydrogenase.

47. The non-naturally occurring microbial organism of any one of claims 43-45, further comprising a succinyl-CoA pathway comprising at least one exogenous nucleic acid encoding a succinyl-CoA pathway enzyme expressed in a sufficient amount to produce succinyl-CoA, said succinyl-CoA pathway comprising:

a PEP carboxykinase, a PEP carboxylase, a malate dehydrogenase, a fumarase, a fumarate reductase, a succinyl-CoA transferase or a succinyl-CoA synthetase.

48. The non-naturally occurring microbial organism of claim 47, wherein said succinyl-CoA pathway further comprises a pyruvate carboxylase or a methylmalonyl-CoA carboxytransferase.

49. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,4-butanediol pathway and an isopropanol pathway, said 1,4-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,4-butanediol pathway enzymes expressed in a sufficient amount to produce 1,4-butanediol, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; a 4-hydroxybutyryl-CoA reductase (aldehyde-forming); and a 4-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

50. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,4-butanediol pathway and an isopropanol pathway, said 1,4-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,4-butanediol pathway enzymes expressed in a sufficient amount to produce 1,4-butanediol, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate reductase; and a 4-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

51. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,4-butanediol pathway and an isopropanol pathway, said 1,4-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,4-butanediol pathway enzymes expressed in a sufficient amount to produce 1,4-butanediol, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; a 4-hydroxybutyryl-CoA reductase (aldehyde-forming), and a 4-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

52. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,4-butanediol pathway and an isopropanol pathway, said 1,4-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,4-butanediol pathway enzymes expressed in a sufficient amount to produce 1,4-butanediol, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a 4-hydroxybutyryl-phosphate reductase; and a 4-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

53. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,4-butanediol pathway and an isopropanol pathway, said 1,4-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,4-butanediol pathway enzymes expressed in a sufficient amount to produce 1,4-butanediol, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; and a 4-hydroxybutyryl-CoA reductase (alcohol-forming),

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

54. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,4-butanediol pathway and an isopropanol pathway, said 1,4-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,4-butanediol pathway enzymes expressed in a sufficient amount to produce 1,4-butanediol, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; and a 4-hydroxybutyryl-CoA reductase (alcohol-forming),

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

55. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,4-butanediol pathway and an isopropanol pathway, said 1,4-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,4-butanediol pathway enzymes expressed in a sufficient amount to produce 1,4-butanediol, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; a 4-hydroxybutyryl-CoA reductase (aldehyde-forming); and a 4-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

56. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,4-butanediol pathway and an isopropanol pathway, said 1,4-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,4-butanediol pathway enzymes expressed in a sufficient amount to produce 1,4-butanediol, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate reductase; and a 4-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

57. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,4-butanediol pathway and an isopropanol pathway, said 1,4-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,4-butanediol pathway enzymes expressed in a sufficient amount to produce 1,4-butanediol, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; a 4-hydroxybutyryl-CoA reductase (aldehyde-forming); and a 4-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

58. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,4-butanediol pathway and an isopropanol pathway, said 1,4-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,4-butanediol pathway enzymes expressed in a sufficient amount to produce 1,4-butanediol, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a 4-hydroxybutyryl-phosphate reductase; and a 4-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

59. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,4-butanediol pathway and an isopropanol pathway, said 1,4-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,4-butanediol pathway enzymes expressed in a sufficient amount to produce 1,4-butanediol, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; and a 4-hydroxybutyryl-CoA reductase (alcohol-forming),

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

60. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,4-butanediol pathway and an isopropanol pathway, said 1,4-butanediol pathway comprising a first

set of exogenous nucleic acids encoding 1,4-butanediol pathway enzymes expressed in a sufficient amount to produce 1,4-butanediol, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; and a 4-hydroxybutyryl-CoA reductase (alcohol-forming),

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

61. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,3-butanediol pathway and an isopropanol pathway, said 1,3-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,3-butanediol pathway enzymes expressed in a sufficient amount to produce 1,3-butanediol, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; a 4-hydroxybutyryl-CoA dehydratase; a crotonase; a 3-hydroxybutyryl-CoA reductase (aldehyde forming); and a 3-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

62. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,3-butanediol pathway and an isopropanol pathway, said 1,3-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,3-butanediol pathway enzymes expressed in a sufficient amount to produce 1,3-butanediol, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; a 4-hydroxybutyryl-CoA dehydratase; a crotonase; a 3-hydroxybutyryl-CoA transferase or a 3-hydroxybutyryl-CoA synthetase or a 3-hydroxybutyryl-CoA hydrolase; a 3-hydroxybutyrate reductase; and a 3-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

63. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,3-butanediol pathway and an isopropanol pathway, said 1,3-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,3-butanediol pathway enzymes expressed in a sufficient amount to produce 1,3-butanediol, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; a 4-hydroxybutyryl-CoA dehydratase; a crotonase; a 3-hydroxybutyryl-CoA reductase (aldehyde forming); and a 3-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

64. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,3-butanediol pathway and an isopropanol pathway, said 1,3-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,3-butanediol pathway enzymes expressed in a sufficient amount to produce 1,3-butanediol, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; a 4-hydroxybutyryl-CoA dehydratase; a crotonase; a 3-hydroxybutyryl-CoA transferase or a 3-hydroxybutyryl-CoA synthetase or a 3-hydroxybutyryl-CoA hydrolase; a 3-hydroxybutyrate reductase; and a 3-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

65. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,3-butanediol pathway and an isopropanol pathway, said 1,3-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,3-butanediol pathway enzymes expressed in a sufficient amount to produce 1,3-butanediol, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; a 4-hydroxybutyryl-CoA dehydratase; a crotonase; and a 3-hydroxybutyryl-CoA reductase (alcohol-forming),

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

66. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,3-butanediol pathway and an isopropanol pathway, said 1,3-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,3-butanediol pathway enzymes expressed in a sufficient amount to produce 1,3-butanediol, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; a 4-hydroxybutyryl-CoA dehydratase; a crotonase; and a 3-hydroxybutyryl-CoA reductase (alcohol-forming),

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

67. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,3-butanediol pathway and an isopropanol pathway, said 1,3-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,3-butanediol pathway enzymes expressed in a sufficient amount to produce 1,3-butanediol, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; a 4-hydroxybutyryl-CoA dehydratase; a crotonase; a 3-hydroxybutyryl-CoA reductase (aldehyde forming); and a 3-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

68. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,3-butanediol pathway and an isopropanol pathway, said 1,3-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,3-butanediol pathway enzymes expressed in a sufficient amount to produce 1,3-butanediol, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; a 4-hydroxybutyryl-CoA dehydratase; a crotonase; a 3-

hydroxybutyryl-CoA transferase or a 3-hydroxybutyryl-CoA synthetase or a 3-hydroxybutyryl-CoA hydrolase; a 3-hydroxybutyrate reductase; and a 3-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

69. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,3-butanediol pathway and an isopropanol pathway, said 1,3-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,3-butanediol pathway enzymes expressed in a sufficient amount to produce 1,3-butanediol, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; a 4-hydroxybutyryl-CoA dehydratase; a crotonase; a 3-hydroxybutyryl-CoA reductase (aldehyde forming); and a 3-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

70. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,3-butanediol pathway and an isopropanol pathway, said 1,3-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,3-butanediol pathway enzymes expressed in a sufficient amount to produce 1,3-butanediol, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; a 4-hydroxybutyryl-CoA dehydratase; a crotonase; a 3-hydroxybutyryl-CoA transferase or a 3-hydroxybutyryl-CoA synthetase or a 3-hydroxybutyryl-CoA hydrolase; a 3-hydroxybutyrate reductase; and a 3-hydroxybutyraldehyde reductase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

71. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,3-butanediol pathway and an isopropanol pathway, said 1,3-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,3-butanediol pathway enzymes expressed in a sufficient amount to produce 1,3-butanediol, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; a crotonase; and a 3-hydroxybutyryl-CoA reductase (alcohol-forming),

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

72. A non-naturally occurring microbial organism, comprising a microbial organism having an 1,3-butanediol pathway and an isopropanol pathway, said 1,3-butanediol pathway comprising a first set of exogenous nucleic acids encoding 1,3-butanediol pathway enzymes expressed in a sufficient amount to produce 1,3-butanediol, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; a 4-hydroxybutyryl-CoA dehydratase; a crotonase; and a 3-hydroxybutyryl-CoA reductase (alcohol-forming),

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

73. A non-naturally occurring microbial organism, comprising a microbial organism having a methylacrylic acid pathway and an isopropanol pathway, said methylacrylic acid pathway comprising a first set of exogenous nucleic acids encoding methylacrylic acid pathway enzymes expressed in a sufficient amount to produce methylacrylic acid, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; a 4-hydroxybutyryl-CoA mutase; a 3-hydroxyisobutyryl-CoA transferase, a 3-hydroxyisobutyryl-CoA synthetase or a 3-hydroxyisobutyryl-CoA hydrolase; and a 3-hydroxyisobutyrate dehydratase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

74. A non-naturally occurring microbial organism, comprising a microbial organism having a methylacrylic acid pathway and an isopropanol pathway, said methylacrylic acid pathway comprising a first set of exogenous nucleic acids encoding methylacrylic acid pathway enzymes expressed in a sufficient amount to produce methylacrylic acid, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; a 4-hydroxybutyryl-CoA mutase; a 3-hydroxyisobutyryl-CoA dehydratase; and a methacrylyl-CoA transferase, a methacrylyl-CoA synthetase or a methacrylyl-CoA hydrolase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

75. A non-naturally occurring microbial organism, comprising a microbial organism having a methylacrylic acid pathway and an isopropanol pathway, said methylacrylic acid pathway comprising a first set of exogenous nucleic acids encoding methylacrylic acid pathway enzymes expressed in a sufficient amount to produce methylacrylic acid, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; a 4-hydroxybutyryl-CoA mutase; a 3-hydroxyisobutyryl-CoA transferase, a 3-hydroxyisobutyryl-CoA synthetase or a 3-hydroxyisobutyryl-CoA hydrolase; and a 3-hydroxyisobutyrate dehydratase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

76. A non-naturally occurring microbial organism, comprising a microbial organism having a methylacrylic acid pathway and an isopropanol pathway, said methylacrylic acid pathway comprising a first set of exogenous nucleic acids encoding methylacrylic acid pathway enzymes expressed in a sufficient amount to produce methylacrylic acid, said first set of exogenous nucleic acids encoding:

a succinyl-CoA reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; a 4-hydroxybutyryl-CoA mutase; a 3-hydroxyisobutyryl-CoA

dehydratase; and a methacrylyl-CoA transferase, a methacrylyl-CoA synthetase or a methacrylyl-CoA hydrolase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

77. A non-naturally occurring microbial organism, comprising a microbial organism having a methylacrylic acid pathway and an isopropanol pathway, said methylacrylic acid pathway comprising a first set of exogenous nucleic acids encoding methylacrylic acid pathway enzymes expressed in a sufficient amount to produce methylacrylic acid, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; a 4-hydroxybutyryl-CoA mutase; a 3-hydroxyisobutyryl-CoA transferase, a 3-hydroxyisobutyryl-CoA synthetase or a 3-hydroxyisobutyryl-CoA hydrolase; and a 3-hydroxyisobutyrate dehydratase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

78. A non-naturally occurring microbial organism, comprising a microbial organism having a methylacrylic acid pathway and an isopropanol pathway, said methylacrylic acid pathway comprising a first set of exogenous nucleic acids encoding methylacrylic acid pathway enzymes expressed in a sufficient amount to produce methylacrylic acid, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase; a 4-hydroxybutyryl-CoA mutase; a 3-hydroxyisobutyryl-CoA dehydratase; and a methacrylyl-CoA transferase, a methacrylyl-CoA synthetase or a methacrylyl-CoA hydrolase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

79. A non-naturally occurring microbial organism, comprising a microbial organism having a methylacrylic acid pathway and an isopropanol pathway, said methylacrylic acid pathway comprising a first set of exogenous nucleic acids encoding methylacrylic acid pathway enzymes expressed in a sufficient amount to produce methylacrylic acid, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; a 4-hydroxybutyryl-CoA mutase; a 3-hydroxyisobutyryl-CoA transferase, a 3-hydroxyisobutyryl-CoA synthetase or a 3-hydroxyisobutyryl-CoA hydrolase; and a 3-hydroxyisobutyrate dehydratase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

80. A non-naturally occurring microbial organism, comprising a microbial organism having a methylacrylic acid pathway and an isopropanol pathway, said methylacrylic acid pathway comprising a first set of exogenous nucleic acids encoding methylacrylic acid pathway enzymes

expressed in a sufficient amount to produce methylacrylic acid, said first set of exogenous nucleic acids encoding:

a succinate reductase; a 4-hydroxybutyrate dehydrogenase; a 4-hydroxybutyrate kinase; a phosphotrans-4-hydroxybutyrylase; a 4-hydroxybutyryl-CoA mutase; a 3-hydroxyisobutyryl-CoA dehydratase; and a methacrylyl-CoA transferase, a methacrylyl-CoA synthetase or a methacrylyl-CoA hydrolase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

81. A non-naturally occurring microbial organism, comprising a microbial organism having a methylacrylic acid pathway and an isopropanol pathway, said methylacrylic acid pathway comprising a first set of exogenous nucleic acids encoding methylacrylic acid pathway enzymes expressed in a sufficient amount to produce methylacrylic acid, said first set of exogenous nucleic acids encoding:

a methylmalonyl-CoA mutase; a methylmalonyl-CoA reductase (aldehyde forming); a 3-hydroxyisobutyrate dehydrogenase; and a 3-hydroxyisobutyrate dehydratase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

82. A non-naturally occurring microbial organism, comprising a microbial organism having a methylacrylic acid pathway and an isopropanol pathway, said methylacrylic acid pathway comprising a first set of exogenous nucleic acids encoding methylacrylic acid pathway enzymes

expressed in a sufficient amount to produce methylacrylic acid, said first set of exogenous nucleic acids encoding:

a methylmalonyl-CoA mutase; a methylmalonyl-CoA epimerase; a methylmalonyl-CoA transferase; a methylmalonyl-CoA synthetase or a methylmalonyl-CoA hydrolase; a methylmalonate reductase; a 3-hydroxyisobutyrate dehydrogenase; and a 3-hydroxyisobutyrate dehydratase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

83. A non-naturally occurring microbial organism, comprising a microbial organism having a methylacrylic acid pathway and an isopropanol pathway, said methylacrylic acid pathway comprising a first set of exogenous nucleic acids encoding methylacrylic acid pathway enzymes expressed in a sufficient amount to produce methylacrylic acid, said first set of exogenous nucleic acids encoding:

a methylmalonyl-CoA mutase; a methylmalonyl-CoA transferase, a methylmalonyl-CoA synthetase or a methylmalonyl-CoA hydrolase; a methylmalonate reductase; a 3-hydroxyisobutyrate dehydrogenase; and a 3-hydroxyisobutyrate dehydratase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

84. A non-naturally occurring microbial organism, comprising a microbial organism having a methylacrylic acid pathway and an isopropanol pathway, said methylacrylic acid pathway comprising a first set of exogenous nucleic acids encoding methylacrylic acid pathway enzymes

expressed in a sufficient amount to produce methylacrylic acid, said first set of exogenous nucleic acids encoding:

a methylmalonyl-CoA mutase; a methylmalonyl-CoA reductase (alcohol forming); and a 3-hydroxyisobutyrate dehydratase,

said isopropanol pathway comprising a second set of exogenous nucleic acids encoding isopropanol pathway enzymes expressed in a sufficient amount to produce isopropanol, said second set of exogenous nucleic acids encoding:

an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase or an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

85. The non-naturally occurring microbial organism of any one of claims 49-84, further comprising an acetyl-CoA pathway comprising a third set of exogenous nucleic acids encoding acetyl-CoA pathway enzymes expressed in a sufficient amount to produce acetyl-CoA, said third set of exogenous nucleic acids encoding:

a pyruvate kinase; and a pyruvate dehydrogenase or a pyruvate ferredoxin oxidoreductase; or a pyruvate formate lyase, a pyruvate formate lyase activating enzyme and a formate dehydrogenase.

86. The non-naturally occurring microbial organism of any one of claims 49-84, further comprising a succinyl-CoA pathway comprising a third set of exogenous nucleic acids encoding succinyl-CoA pathway enzymes expressed in a sufficient amount to produce succinyl-CoA, said third set of exogenous nucleic acids encoding:

a PEP carboxykinase, a PEP carboxylase, a malate dehydrogenase, a fumarase, a fumarate reductase, a succinyl-CoA transferase and a succinyl-CoA synthetase.

87. The non-naturally occurring microbial organism of claim 86, wherein said third set of exogenous nucleic acids further encodes a pyruvate carboxylase or a methylmalonyl-CoA carboxytransferase.

88. The non-naturally occurring microbial organism of any one of claims 43-45 or 49-84, wherein said exogenous nucleic acid is a heterologous nucleic acid.

89. The non-naturally occurring microbial organism of any one of claims 43-45 or 49-84, wherein said non-naturally occurring microbial organism is in a substantially anaerobic culture medium.
90. A method for producing 1,4-butanediol and isopropanol, comprising culturing a non-naturally occurring microbial organism of any one of claims 43, or 49-60 under conditions and for a sufficient period of time to produce 1,4-butanediol and isopropanol.
91. The method of claim 90, wherein said conditions comprise substantially anaerobic culture conditions.
92. The method of claim 90, wherein said exogenous nucleic acid is a heterologous nucleic acid.
93. A method for producing 1,3-butanediol and isopropanol, comprising culturing a non-naturally occurring microbial organism of any one of claims 44 or 61-72 under conditions and for a sufficient period of time to produce 1,3-butanediol and isopropanol.
94. The method of claim 93, wherein said conditions comprise substantially anaerobic culture conditions.
95. The method of claim 93, wherein said exogenous nucleic acid is a heterologous nucleic acid.
96. A method for producing methylacrylic acid and isopropanol, comprising culturing a non-naturally occurring microbial organism of any one of claims 45, or 74-84 under conditions and for a sufficient period of time to produce methylacrylic acid and isopropanol.
97. The method of claim 96, wherein said conditions comprise substantially anaerobic culture conditions.
98. The method of claim 96, wherein said exogenous nucleic acid is a heterologous nucleic acid.
99. A non-naturally occurring microbial organism comprising a microbial organism having carbon monoxide dehydrogenase or hydrogenase activity and a reductive tricarboxylic acid (rTCA) pathway comprising at least one exogenous nucleic acid encoding a rTCA pathway enzyme expressed in a sufficient amount to convert CO, CO₂ or H₂ to acetyl-CoA, wherein said rTCA

pathway enzyme is selected from the group consisting of an ATP citrate-lyase, a citrate lyase, an aconitase, an isocitrate dehydrogenase, an alpha-ketoglutarate:ferredoxin oxidoreductase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarate reductase, a fumarase and a malate dehydrogenase, wherein said microbial organism further comprises an isopropanol pathway, said isopropanol pathway converting acetyl-CoA to isopropanol, wherein said isopropanol pathway comprises an enzyme selected from the group consisting of an acetoacetyl-CoA thiolase, an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA synthetase, an acetoacetate decarboxylase and an isopropanol dehydrogenase.

100. The non-naturally occurring microbial organism of claim 99, wherein said rTCA pathway enzyme is selected from the group consisting of an ATP citrate-lyase, a citrate lyase, an alpha-ketoglutarate:ferredoxin oxidoreductase, and a fumarate reductase.

101. The non-naturally occurring microbial organism of claim 99, wherein said rTCA pathway enzyme is selected from an aconitase or an isocitrate dehydrogenase.

102. A non-naturally occurring microbial organism comprising a microbial organism having carbon monoxide dehydrogenase or hydrogenase activity and a reductive tricarboxylic acid (rTCA) pathway comprising at least one exogenous nucleic acid encoding a rTCA pathway enzyme expressed in a sufficient amount to convert CO, CO₂ or H₂ to acetyl-CoA, wherein said rTCA pathway enzyme is selected from the group consisting of an ATP citrate-lyase, a citrate lyase, an aconitase, an isocitrate dehydrogenase, an alpha-ketoglutarate:ferredoxin oxidoreductase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarate reductase, a fumarase and a malate dehydrogenase, wherein said microbial organism comprises a 1,3-butanediol pathway, wherein said 1,3-butanediol pathway comprises an enzyme selected from the group consisting of a 3-hydroxybutyraldehyde reductase and a 3-hydroxybutyryl-CoA reductase (aldehyde forming), a 3-hydroxybutyryl-CoA reductase (alcohol forming), a 3-hydroxybutyryl-CoA transferase, a 3-hydroxybutyryl-CoA hydrolase, a 3-hydroxybutyryl-CoA synthetase, and a 3-hydroxybutyrate reductase.

103. A non-naturally occurring microbial organism of claim 102, wherein said microbial organism further comprises at least one enzyme selected from an acetoacetyl-CoA thiolase; an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase.

104. The non-naturally occurring microbial organism of claim 102, wherein said rTCA pathway enzyme is selected from the group consisting of an ATP citrate-lyase, a citrate lyase, an alpha-ketoglutarate:ferredoxin oxidoreductase, and a fumarate reductase.

105. The non-naturally occurring microbial organism of claim 102, wherein said rTCA pathway enzyme is selected from an aconitase or an isocitrate dehydrogenase.

106. A non-naturally occurring microbial organism comprising at least one exogenous nucleic acid encoding an enzyme expressed in a sufficient amount to produce reducing equivalents from carbon monoxide or hydrogen, thereby fixing CO₂ via a reductive tricarboxylic acid (rTCA) cycle, wherein said at least one exogenous nucleic acid is selected from a carbon monoxide dehydrogenase, a hydrogenase, and an NAD(P)H:ferredoxin oxidoreductase, wherein said microbial organism further comprises a 1,3-butanediol pathway, wherein said 1,3-butanediol pathway comprises an enzyme selected from the group consisting of a succinyl-CoA transferase, a succinyl-CoA synthetase, a succinyl-CoA reductase (aldehyde forming), a 4-hydroxybutyrate dehydrogenase, a 4-hydroxybutyrate kinase, a phosphotrans-4-hydroxybutyrylase, a 4-hydroxybutyryl-CoA dehydratase, a crotonase, a 3-hydroxybutyryl-CoA reductase (aldehyde forming), a 3-hydroxybutyraldehyde reductase, a succinate reductase, a succinyl-CoA reductase (alcohol forming), a 4-hydroxybutyryl-CoA transferase, a 4-hydroxybutyryl-CoA synthetase, a 3-hydroxybutyryl-CoA reductase (alcohol forming), a 3-hydroxybutyryl-CoA hydrolase, a 3-hydroxybutyryl-CoA synthetase, a 3-hydroxybutyryl-CoA transferase, and a 3-hydroxybutyrate reductase.

107. The non-naturally occurring microbial organism of claim 106, wherein said microbial organism further comprises a ferredoxin.

108. A non-naturally occurring microbial organism comprising a microbial organism having a reductive tricarboxylic acid (rTCA) pathway comprising at least one exogenous nucleic acid encoding a rTCA pathway enzyme expressed in a sufficient amount to convert 1) CO, 2) CO₂ and H₂, 3) CO and CO₂, 4) synthesis gas comprising CO and H₂, or 5) synthesis gas comprising CO, CO₂, and H₂, to acetyl-CoA; wherein said rTCA pathway enzyme is selected from an ATP citrate-lyase, a citrate lyase, an aconitase, an isocitrate dehydrogenase, an alpha-ketoglutarate:ferredoxin oxidoreductase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarate reductase, a

fumarase and a malate dehydrogenase; and a reducing equivalent producing pathway comprising at least one exogenous nucleic acid encoding a reducing equivalent producing enzyme selected from a carbon monoxide dehydrogenase, a hydrogenase and a NAD(P)H:ferredoxin oxidoreductase, wherein said microbial organism further comprises a isopropanol pathway, said isopropanol pathway converting acetyl-CoA to isopropanol, wherein said isopropanol pathway comprises an enzyme selected from the group consisting of an acetoacetyl-CoA thiolase, an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA synthetase, an acetoacetate decarboxylase and an isopropanol dehydrogenase.

109. The non-naturally occurring microbial organism of claim 108, wherein said microbial organism further comprises a ferredoxin.

110. The non-naturally occurring microbial organism of claim 108, wherein said rTCA pathway enzyme is selected from the group consisting of an ATP citrate-lyase, a citrate lyase, an alpha-ketoglutarate:ferredoxin oxidoreductase, and a fumarate reductase.

111. The non-naturally occurring microbial organism of claim 108, wherein said rTCA pathway enzyme is selected from an aconitase or an isocitrate dehydrogenase.

112. A non-naturally occurring microbial organism comprising a microbial organism having a reductive tricarboxylic acid (rTCA) pathway comprising at least one exogenous nucleic acid encoding a rTCA pathway enzyme expressed in a sufficient amount to convert 1) CO, 2) CO₂ and H₂, 3) CO and CO₂, 4) synthesis gas comprising CO and H₂, or 5) synthesis gas comprising CO, CO₂, and H₂, to acetyl-CoA; wherein said rTCA pathway enzyme is selected from an ATP citrate-lyase, a citrate lyase, an aconitase, an isocitrate dehydrogenase, an alpha-ketoglutarate:ferredoxin oxidoreductase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarate reductase, a fumarase and a malate dehydrogenase; and a reducing equivalent producing pathway comprising at least one exogenous nucleic acid encoding a reducing equivalent producing enzyme selected from a carbon monoxide dehydrogenase, a hydrogenase and a NAD(P)H:ferredoxin oxidoreductase, wherein said microbial organism comprises a 1,3-butanediol pathway, wherein said 1,3-butanediol pathway comprises an enzyme selected from the group consisting of a 3-hydroxybutyraldehyde reductase and a 3-hydroxybutyryl-CoA reductase (aldehyde forming), a 3-hydroxybutyryl-CoA

reductase (alcohol forming), a 3-hydroxybutyryl-CoA transferase, a 3-hydroxybutyryl-CoA hydrolase, a 3-hydroxybutyryl-CoA synthetase, and a 3-hydroxybutyrate reductase.

113. The non-naturally occurring microbial organism of claim 112, wherein said microbial organism further comprises a ferredoxin.

114. The non-naturally occurring microbial organism of claim 112, wherein said rTCA pathway enzyme is selected from the group consisting of an ATP citrate-lyase, a citrate lyase, an alpha-ketoglutarate:ferredoxin oxidoreductase, and a fumarate reductase.

115. The non-naturally occurring microbial organism of claim 112, wherein said rTCA pathway enzyme is selected from an aconitase or an isocitrate dehydrogenase.

116. A non-naturally occurring microbial organism comprising a microbial organism having a reductive tricarboxylic acid (rTCA) pathway comprising at least one exogenous nucleic acid encoding a rTCA pathway enzyme expressed in a sufficient amount to convert 1) CO, 2) CO₂ and H₂, 3) CO and CO₂, 4) synthesis gas comprising CO and H₂, or 5) synthesis gas comprising CO, CO₂, and H₂, to acetyl-CoA; wherein said rTCA pathway enzyme is selected from an ATP citrate-lyase, a citrate lyase, an aconitase, an isocitrate dehydrogenase, an alpha-ketoglutarate:ferredoxin oxidoreductase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarate reductase, a fumarase and a malate dehydrogenase; and a reducing equivalent producing pathway comprising at least one exogenous nucleic acid encoding a reducing equivalent producing enzyme selected from a carbon monoxide dehydrogenase, a hydrogenase and a NAD(P)H:ferredoxin oxidoreductase, wherein said microbial organism further comprises a 1,4-butanediol pathway, wherein said 1,4-butanediol pathway comprises an enzyme selected from the group consisting of a 4-hydroxybutyryl-CoA reductase (alcohol forming), a 4-hydroxybutyryl-CoA reductase (aldehyde forming), a 4-hydroxybutyraldehyde reductase, and a 4-hydroxybutyrate reductase.

117. The non-naturally occurring microbial organism of claim 116, wherein said microbial organism comprising a 4-hydroxybutyrate reductase further comprises a 4-hydroxybutyryl-CoA transferase; a 4-hydroxybutyryl-CoA synthetase; or a phosphotrans-4-hydroxybutyrylase and a 4-hydroxybutyrate kinase.

118. The non-naturally occurring microbial organism of claim 116, wherein said microbial organism further comprises an acetoacetyl-CoA thiolase or a crotonase.

119. The non-naturally occurring microbial organism of claim 116, wherein said microbial organism further comprises a ferredoxin.

120. The non-naturally occurring microbial organism of claim 116, wherein said rTCA pathway enzyme is selected from the group consisting of an ATP citrate-lyase, a citrate lyase, an alpha-ketoglutarate:ferredoxin oxidoreductase, and a fumarate reductase.

121. The non-naturally occurring microbial organism of claim 116, wherein said rTCA pathway enzyme is selected from an aconitase or an isocitrate dehydrogenase.

What is claimed is:

1. A non-naturally occurring microbial organism comprising an exogenous nucleic acid encoding a carbon monoxide dehydrogenase and an exogenous nucleic acid encoding an rTCA enzyme or protein selected from the group consisting of ATP citrate-lyase, citrate lyase, aconitase, isocitrate dehydrogenase, alpha-ketoglutarate:ferredoxin oxidoreductase, fumarate reductase, fumarase and malate dehydrogenase, wherein said carbon monoxide dehydrogenase extracts reducing equivalents from CO, wherein said microbial organism further comprises a 1,4-butanediol (14-BDO) pathway, wherein said pathway comprises:

(a) a succinyl-CoA reductase (aldehyde forming) or succinate reductase (aldehyde forming);

(b) a 4-hydroxybutyrate dehydrogenase;

(c) a 4-hydroxybutyryl-CoA transferase or a 4-hydroxybutyryl-CoA synthetase;

(d) a 4-hydroxybutyryl-CoA reductase (aldehyde-forming); and

(e) a 4-hydroxybutyraldehyde reductase.

2. The non-naturally occurring microbial organism of claim 1, wherein said microbial organism further comprises a ferredoxin.

3. The non-naturally occurring microbial organism of claim 1 or 2, wherein said microbial organism further comprises an exogenous nucleic acid encoding a hydrogenase, wherein said hydrogenase extracts reducing equivalents from H₂.

4. The non-naturally occurring microbial organism of any one of claims 1-3, wherein said microbial organism further comprises an exogenous nucleic acid encoding an NAD(P)H:ferredoxin oxidoreductase.

5. The non-naturally occurring microbial organism of any one of claims 1-4, wherein said microbial organism further comprises an exogenous nucleic acid encoding an rTCA enzyme or protein selected from the group consisting of ATP citrate-lyase, citrate lyase, alpha-ketoglutarate:ferredoxin oxidoreductase, and fumarate reductase.

6. The non-naturally occurring microbial organism of claim 5, wherein said microbial organism comprises three exogenous nucleic acids encoding ATP-citrate lyase or citrate lyase; alpha-ketoglutarate:ferredoxin oxidoreductase; and fumarate reductase.
7. The non-naturally occurring microbial organism of any one of claims 1-4, wherein said microbial organism further comprises a succinyl-CoA pathway comprising at least one exogenous nucleic acid encoding a succinyl-CoA pathway enzyme expressed in a sufficient amount to produce succinyl-CoA, wherein said succinyl-CoA pathway comprises a phosphoenolpyruvate carboxykinase, a phosphoenolpyruvate carboxylase, a malate dehydrogenase, a fumarase, a fumarate reductase, a succinyl-CoA transferase or a succinyl-CoA synthetase.
8. The non-naturally occurring microbial organism of any one of claims 1-7, wherein said microbial organism further comprises an acetyl-CoA pathway having at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to produce acetyl-CoA, wherein said acetyl-CoA pathway comprises a pyruvate kinase, a pyruvate dehydrogenase, a pyruvate ferredoxin oxidoreductase, a pyruvate formate lyase, a pyruvate formate lyase activating enzyme, or a formate dehydrogenase.
9. The non-naturally occurring microbial organism of any one of claims 1-8, wherein at least one, two, three, four, or five enzymes of said 14-BDO pathway are encoded by exogenous nucleic acids.
10. The non-naturally occurring microbial organism of any one of claims 1-9, wherein said exogenous nucleic acids are heterologous nucleic acids.
11. The non-naturally occurring microbial organism of any one of claims 1-10, wherein said non-naturally occurring microbial organism is in a substantially anaerobic culture medium.
12. The non-naturally occurring microbial organism of any one of claims 1-11, wherein said microbial organism is a species of bacteria, yeast, or fungus.
13. The non-naturally occurring microbial organism of any one of claims 1-12, wherein said microbial organism further comprises an isopropanol pathway comprising at least one exogenous nucleic acid encoding an isopropanol pathway enzyme expressed in a sufficient

amount to produce isopropanol, said isopropanol pathway comprising: an acetyl-CoA acetyl thiolase; an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase or an acetoacetyl-CoA synthetase; an acetoacetate decarboxylase; and an isopropanol dehydrogenase.

14. A method for producing 1,4-butanediol (14-BDO) comprising culturing the non-naturally occurring microbial organism of any one of claims 1-13 under conditions and for a sufficient period of time to produce 14-BDO.

15. The method of claim 14 further comprising culturing the non-naturally occurring microbial organism of claim 13 under conditions and for a sufficient period of time to produce 14-BDO and isopropanol.

16. The method of claim 14 or 15, wherein said method further comprises separating the 14-BDO or 14-BDO and isopropanol from other components in the culture.

17. The method of claim 16, wherein the separating comprises extraction, continuous liquid-liquid extraction, pervaporation, membrane filtration, membrane separation, reverse osmosis, electrodialysis, distillation, crystallization, centrifugation, extractive filtration, ion exchange chromatography, absorption chromatography, or ultrafiltration.

18. Culture medium comprising 1,4-butanediol (14-BDO) produced by the microbial organism of any one of claims 1-13.

19. The culture medium of claim 18, further comprising isopropanol produced by the microbial organism of claim 13.

20. The culture medium of claim 18 or 19, wherein said culture medium is separated from the microbial organism.