crotyl alcohol or 3-buten-1-ol. The present invention satisfies this need and provides related advantages as well.

SUMMARY OF INVENTION

Disclosed herein are non-naturally occurring microbial organisms containing 2,4-pentadienoate, butadiene, propylene, 1,3-butanediol, crotyl alcohol or 3-buten-1-ol pathways having at least one exogenous nucleic acid encoding a butadiene pathway enzyme expressed in a sufficient amount to produce 2,4-pentadienoate, butadiene, propylene, 1,3-butanediol, crotyl alcohol or 3-buten-1-ol. Also disclosed herein are methods of using such microbial organisms to produce 2,4-pentadienoate, butadiene, propylene, 1,3-butanediol, crotyl alcohol or 3-buten-1-ol, by culturing a non-naturally occurring microbial organism containing 2,4-pentadienoate, butadiene, propylene, 1,3-butanediol, crotyl alcohol or 3-buten-1-ol pathways as described herein under conditions and for a sufficient period of time to produce 2,4-pentadienoate, butadiene, propylene, 1,3-butanediol, crotyl alcohol or 3-buten-1-ol.

Thus, the present invention refers to non-naturally occurring microbial organisms, methods and processes as defined in any one of claims 1~~, 10, 11, 23, 24, 36, 37, 46, 47, 48, 57, 58, 67 and 68~~to 50.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows exemplary pathways to 3-buten-1-ol, 2,4-pentadienoate and butadiene from 2-oxoadipate, 2-aminoadipate, 5-aminopentanoate and glutaryl-CoA. Enzymes are: A. 2-aminoadipate decarboxylase, B. 5-aminopentanoate reductase, C. 5-aminopent-2-enoate aminotransferase, dehydrogenase or amine oxidase, D. 2-oxoadipate decarboxylase, E. glutarate semialdehyde reductase, F. 5-hydroxyvalerate dehydrogenase, G. 5-hydroxypent-2-enoate dehydratase, H. 2-aminoadipate aminotransferase, dehydrogenase or amine oxidase, I. 5-aminopentanoate aminotransferase, dehydrogenase or amine oxidase, J. 5-aminopent-2-enoate deaminase, K. 5-hydroxypent-2-enoate reductase, L. 5-hydroxyvaleryl-CoA transferase and/or synthetase, M. 5-hydroxypentanoyl-CoA dehydrogenase, N. 5-hydroxypent-2-enoyl-CoA

What is claimed is:

1. A non-naturally occurring microbial organism, comprising a microbial organism having a 1,3-butanediol pathway comprising exogenous nucleic acids each encoding a 1,3-butanediol pathway enzyme expressed in a sufficient amount to produce 1,3-butanediol, wherein said 1,3-butanediol pathway comprises a pathway selected from:

(33) 7AS, 7P, 7N and 7AA;
(1) 4A, 4B, 4C and 4D;
(2) 5A, 5H, 5J, 5K and 5G;
(3) 5A, 5H, 5I and 5G;
(4) 5A, 5H and 5L;
(5) 5A, 5F and 5G;
(6) 7A, 7D, 7E, 7F, 7G and 7S;
(7) 7A, 7D, 7I, 7G and 7S;
(8) 7A, 7D, 7K and 7S;
(9) 7A, 7H, 7F, 7G and 7S;
(10) 7A, 7J, 7G and 7S;
(11) 7A, 7J, 7R and 7AA;
(12) 7A, 7H, 7F, 7R and 7AA;
(13) 7A, 7H, 7Q, 7Z and 7AA;
(14) 7A, 7D, 7I, 7R and 7AA;
(15) 7A, 7D, 7E, 7F, 7R and 7AA;
(16) 7A, 7D, 7E, 7Q, 7Z and 7AA;
(17) 7A, 7D, 7P, 7N and 7AA;
(18) 7A, 7D, 7P, 7Y, 7Z and 7AA;
(19) 7A, 7B, 7M and 7AA;
(20) 7A, 7B, 7L, 7Z and 7AA;
(21) 7A, 7B, 7X, 7N and 7AA;
(22) 7A, 7B, 7X, 7Y, 7Z and 7AA;
(23) 7A, 7D, 7P and 7O;
(24) 7A, 7B, 7X and 7O;
(25) 7A, 7D, 7E, 7F, 7R and 7AA;
(26) 7A, 7D, 7E, 7F, 7G and 7S;
(27) 7AS, 7E, 7F, 7G and 7S;
(28) 7AS, 7I, 7G and 7S;
(29) 7AS, 7K and 7S;

(30) 7AS, 7I, 7R and 7AA;

(31) 7AS, 7E, 7F, 7R and 7AA;

(32) 7AS, 7E, 7Q, 7Z and 7AA;

(34) 7AS, 7P, 7Y, 7Z and 7AA;

(35) 7AS, 7P and 7O;

(36) 7AS, 7E, 7F, 7R and 7AA; and

(37) 7AS, 7E, 7F, 7G and 7S,

wherein 4A is a 3-oxo-5-hydroxypentanoyl-CoA thiolase or a 3-oxo-5-hydroxypentanoyl-CoA synthase, wherein 4B is a 3-oxo-5-hydroxypentanoyl-CoA hydrolase, 3-oxo-5-hydroxypentanoyl-CoA transferase or 3-oxo-5-hydroxypentanoyl-CoA synthetase, wherein 4C is a 3-oxo-5-hydroxypentanoate decarboxylase, wherein 4D is a 3-oxobutanol reductase, wherein in 5A is a 4-hydroxy-2-oxovalerate aldolase, wherein 5F is a 4-hydroxy-2-oxovalerate decarboxylase, wherin 5G is a 3-hydroxybutanal reductase, wherein 5H is a 4-hydroxy-2-oxopentanoate dehydrogenase, a 4-hydroxy-2-oxopentanoate:ferredoxin oxidoreductase or a 4-hydroxy-2-oxopentanoate formate lyase, wherein 5I is a 3-hydroxybutyryl-CoA reductase (aldehyde forming), wherein 5J is a 3-hydroxybutyryl-CoA hydrolase, a 3-hydroxybutyryl-CoA transferase or a 3-hydroxybutyryl-CoA synthetase, wherein 5K is a 3-hydroxybutyrate reductase, wherein 5L is a 3-hydroxybutyryl-CoA reductase (alcohol forming), wherein 7A is a 3-ketoacyl-ACP synthase, wherein 7B is an acetoacetyl-ACP reductase, wherein 7D is an acetoacetyl-CoA:ACP transferase, wherein 7E is an acetoacetyl-CoA hydrolase, acetoacetyl-CoA transferase or acetoacetyl-CoA synthetase, wherein 7F is an acetoacetate reductase (acid reducing), wherein 7G is a 3-oxobutyraldehyde reductase (aldehyde reducing), wherein 7H is an acetoacetyl-ACP thioesterase, wherein 7I is an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming), wherein 7J is an acetoacetyl-ACP reductase (aldehyde forming), wherein 7K is an acetoacetyl-CoA reductase (alcohol forming), wherein 7L is a 3-hydroxybutyryl-ACP thioesterase, wherein 7M is a 3-hydroxybutyryl-ACP reductase (aldehyde forming), wherein 7N is a 3-hydroxybutyryl-CoA reductase (aldehyde forming), wherein 7O is a 3-hydroxybutyryl-CoA reductase (alcohol forming), wherein 7P is an acetoacetyl-CoA reductase (ketone reducing), wherein 7Q is an acetoacetate reductase (ketone reducing), wherein 7R is a 3-oxobutyraldehyde reductase (ketone reducing), wherein 7S is a 4-hydroxy-2-butanone reductase, wherein 7X is a 3-hydroxybutyryl-CoA:ACP transferase, wherein 7Y is a 3-hydroxybutyryl-CoA hydrolase, a 3-hydroxybutyryl-CoA transferase or a 3-hydroxybutyryl-CoA synthetase, wherein 7Z is a 3-hydroxybutyrate reductase, wherein 7AA is a 3-hydroxybutyraldehyde reductase, wherein 7AS is an acetoacetyl-CoA synthase, and

wherein said exogenous nucleic acids encode each of the enzymes of at least one of the pathways selected from (1)-(37).

2. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (1) 4A, 4B, 4C and 4D.

3. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (2) 5A, 5H, 5J, 5K and 5G.

4. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (3) 5A, 5H, 5I and 5G.

5. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (4) 5A, 5H and 5L.

6. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (5) 5A, 5F and 5G.

7. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (6) 7A, 7D, 7E, 7F, 7G and 7S.

8. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (7) 7A, 7D, 7I, 7G and 7S.

9. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (8) 7A, 7D, 7K and 7S.

10. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (9) 7A, 7H, 7F, 7G and 7S.

11. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (10) 7A, 7J, 7G and 7S.

12. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (11) 7A, 7J, 7R and 7AA.

13. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (12) 7A, 7H, 7F, 7R and 7AA.

14. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (13) 7A, 7H, 7Q, 7Z and 7AA.

15. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (14)7A, 7D, 7I, 7R and 7AA.

16. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (15)7A, 7D, 7E, 7F, 7R and 7AA.

17. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (16)7A, 7D, 7E, 7Q, 7Z and 7AA.

18. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (17)7A, 7D, 7P, 7N and 7AA.

19. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (18)7A, 7D, 7P, 7Y, 7Z and 7AA.

20. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (19)7A, 7B, 7M and 7AA.

21. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (20)7A, 7B, 7L, 7Z and 7AA.

22. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (21)7A, 7B, 7X, 7N and 7AA.

23. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (22)7A, 7B, 7X, 7Y, 7Z and 7AA.

24. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (23)7A, 7D, 7P and 7O.

25. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (24)7A, 7B, 7X and 7O.

26. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (25)7A, 7D, 7E, 7F, 7R and 7AA.

27. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (26)7A, 7D, 7E, 7F, 7G and 7S.

28. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (27)7AS, 7E, 7F, 7G and 7S.

29. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (28) 7AS, 7I, 7G and 7S.

30. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (29) 7AS, 7K and 7S.

31. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (30) 7AS, 7I, 7R and 7AA.

32. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (31) 7AS, 7E, 7F, 7R and 7AA.

33. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (32) 7AS, 7E, 7Q, 7Z and 7AA.

34. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (33) 7AS, 7P, 7N and 7AA.

35. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (34) 7AS, 7P, 7Y, 7Z and 7AA.

36. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (35) 7AS, 7P and 7O.

37. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (36) 7AS, 7E, 7F, 7R and 7AA.

38. The non-naturally occurring microbial organism of claim 1, wherein said 1,3-butanediol pathway comprises pathway (37) 7AS, 7E, 7F, 7G and 7S.

39. The non-naturally occurring microbial organism of any one of claims 1-38, wherein at least one, two, three, four, five or six exogenous nucleic acids are heterologous nucleic acids.

40. The non-naturally occurring microbial organism of any one of claims 1-39, wherein said non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

41. The non-naturally occurring microbial organism of any one of claims 1-40, further comprising:

(i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, a citrate lyase, a citryl-CoA synthetase, a citryl-CoA lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

(ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

(iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof.

42. The non-naturally occurring microbial organism of claim 41, wherein said microbial organism comprising (i) further comprises an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, ferredoxin, and combinations thereof.

43. The non-naturally occurring microbial organism of claim 41, wherein said microbial organism comprising (ii) further comprises an exogenous nucleic acid encoding an enzyme selected from an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, and combinations thereof.

44. The non-naturally occurring microbial orgnaism of claim 41, wherein said microbial organism comprising (i) comprises three exogenous nucleic acids encoding an ATP-citrate lyase or a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

wherein said microbial organism comprising (ii) comprises four exogenous nucleic acids encoding a pyruvate:ferredoxin oxidoreductase; a phosphoenolpyruvate carboxylase or a phosphoenolpyruvate carboxykinase; a CO dehydrogenase; and an H_2 hydrogenase; or

wherein said microbial organism comprising (iii) comprises two exogenous nucleic acids encoding a CO dehydrogenase and an H_2 hydrogenase.

45. The non-naturally occurring microbial organism of any one of claims 1-44, wherein said microbial organism is a species of bacteria, yeast, or fungus.

46. The non-naturally occurring microbial organism of claim 45, wherein the bacteria is selected from the group consisting of *Escherichia coli, Klebsiella oxytoca, Anaerobiospirillum succiniciproducens, Actinobacillus succinogenes, Mannheimia succiniciproducens, Rhizobium etli, Bacillus subtilis, Corynebacterium glutamicum, Cupriavidus necator, Gluconobacter oxydans, Zymomonas mobilis, Lactococcus lactis, Lactobacillus plantarum, Streptomyces coelicolor, Clostridium acetobutylicum, Pseudomonas fluorescens,* and *Pseudomonas putida*.

47. The non-naturally occurring microbial organism of claim 45, wherein the yeast or fungus is selected from the group consisting of *Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces lactis, Kluyveromyces marxianus, Aspergillus terreus, Aspergillus niger, Pichia pastoris, Rhizopus arrhizus, Rhizobus oryzae, Yarrowia lipolytica*, and *Candida albicans*.

48. A method for producing 1,3-butanediol, comprising culturing the non-naturally occurring microbial organism of any one of claims 1-47 under conditions and for a sufficient period of time to produce 1,3-butanediol.

49. The method of claim 48, wherein said method further comprises separating the 1,3-butanediol from other components in the culture.

50. The method of claim 49, 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.

What is claimed is:

1. A non-naturally occurring microbial organism, comprising a microbial organism having a 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, wherein said 1,3-butanediol pathway comprises a pathway selected from:

(33) 7AS, 7P, 7N and 7AA;
(1) 4A, 4B, 4C and 4D;
(2) 5A, 5H, 5J, 5K and 5G;
(3) 5A, 5H, 5I and 5G;
(4) 5A, 5H and 5L;
(5) 5A, 5F and 5G;
(6) 7A, 7D, 7E, 7F, 7G and 7S;
(7) 7A, 7D, 7I, 7G and 7S;
(8) 7A, 7D, 7K, and 7S;
(9) 7A, 7H, 7F, 7G and 7S;
(10) 7A, 7J, 7G and 7S;
(11) 7A, 7J, 7R and 7AA;
(12) 7A, 7H, 7F, 7R and 7AA;
(13) 7A, 7H, 7Q, 7Z and 7AA;
(14) 7A, 7D, 7I, 7R and 7AA;
(15) 7A, 7D, 7E, 7F, 7R and 7AA;
(16) 7A, 7D, 7E, 7Q, 7Z and 7AA;
(17) 7A, 7D, 7P, 7N and 7AA;
(18) 7A, 7D, 7P, 7Y, 7Z and 7AA;
(19) 7A, 7B, 7M and 7AA;
(20) 7A, 7B, 7L, 7Z and 7AA;
(21) 7A, 7B, 7X, 7N and 7AA;
(22) 7A, 7B, 7X, 7Y, 7Z and 7AA;
(23) 7A, 7D, 7P and 7O;
(24) 7A, 7B, 7X and 7O;
(25) 7A, 7D, 7E, 7F, 7R, 7AA;
(26) 7A, 7D, 7E, 7F, 7G, 7S;
(27) 7AS, 7E, 7F, 7G and 7S;

(28) 7AS, 7I, 7G and 7S;

(29) 7AS, 7K, and 7S;

(30) 7AS, 7I, 7R and 7AA;

(31) 7AS, 7E, 7F, 7R and 7AA;

(32) 7AS, 7E, 7Q, 7Z and 7AA;

(34) 7AS, 7P, 7Y, 7Z and 7AA;

(35) 7AS, 7P and 7O;

(36) 7AS, 7E, 7F, 7R, and 7AA; and

(37) 7AS, 7E, 7F, 7G, and 7S,

wherein 4A is a 3-oxo-5-hydroxypentanoyl-CoA thiolase or a 3-oxo-5-hydroxypentanoyl-CoA synthase, wherein 4B is a 3-oxo-5-hydroxypentanoyl-CoA hydrolase, 3-oxo-5-hydroxypentanoyl-CoA transferase or 3-oxo-5-hydroxypentanoyl-CoA synthetase, wherein 4C is a 3-oxo-5-hydroxypentanoate decarboxylase, wherein 4D is a 3-oxobutanol reductase, wherein in 5A is a 4-hydroxy-2-oxovalerate aldolase, wherein 5F is a 4-hydroxy-2-oxovalerate decarboxylase, wherin 5G is a 3-hydroxybutanal reductase, wherein 5H is a 4-hydroxy-2-oxopentanoate dehydrogenase, a 4-hydroxy-2-oxopentanoate:ferredoxin oxidoreductase or a 4-hydroxy-2-oxopentanoate formate lyase, wherein 5I is a 3-hydroxybutyryl-CoA reductase (aldehyde forming), wherein 5J is a 3-hydroxybutyryl-CoA hydrolase, a 3-hydroxybutyryl-CoA transferase or a 3-hydroxybutyryl-CoA synthetase, wherein 5K is a 3-hydroxybutyrate reductase, wherein 5L is a 3-hydroxybutyryl-CoA reductase (alcohol forming), wherein 7A is a 3-ketoacyl-ACP synthase, wherein 7B is an acetoacetyl-ACP reductase, wherein 7D is an acetoacetyl-CoA:ACP transferase, wherein 7E is an acetoacetyl-CoA hydrolase, acetoacetyl-CoA transferase or acetoacetyl-CoA synthetase, wherein 7F is an acetoacetate reductase (acid reducing), wherein 7G is a 3-oxobutyraldehyde reductase (aldehyde reducing), wherein 7H is an acetoacetyl-ACP thioesterase, wherein 7I is an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming), wherein 7J is an acetoacetyl-ACP reductase (aldehyde forming), wherein 7K is an acetoacetyl-CoA reductase (alcohol forming), wherein 7L is a 3-hydroxybutyryl-ACP thioesterase, wherein 7M is a 3-hydroxybutyryl-ACP reductase (aldehyde forming), wherein 7N is a 3-hydroxybutyryl-CoA reductase (aldehyde forming), wherein 7O is a 3-hydroxybutyryl-CoA reductase (alcohol forming), wherein 7P is an acetoacetyl-CoA reductase (ketone reducing), wherein 7Q is an acetoacetate reductase (ketone reducing), wherein 7R is a 3-oxobutyraldehyde reductase (ketone reducing), wherein 7S is a 4-hydroxy-2-butanone reductase, wherein 7X is a 3-hydroxybutyryl-

CoA:ACP transferase, wherein 7Y is a 3-hydroxybutyryl-CoA hydrolase, a 3-hydroxybutyryl-CoA transferase or a 3-hydroxybutyryl-CoA synthetase, wherein 7Z is a 3-hydroxybutyrate reductase, wherein 7AA is a 3-hydroxybutyraldehyde reductase and wherein 7AS is an acetoacetyl-CoA synthase.

2. The non-naturally occurring microbial organism of claim 1, wherein said microbial organism comprises two, three, four or five exogenous nucleic acids each encoding a 1,3-butanediol pathway enzyme.

3 The non-naturally occurring microbial organism of claim 2, wherein said microbial organism comprises exogenous nucleic acids encoding each of the enzymes of at least one of the pathways selected from (1)-(37).

4. The non-naturally occurring microbial organism of claim 1, wherein said at least one exogenous nucleic acid is a heterologous nucleic acid.

5. The non-naturally occurring microbial organism of claim 1, wherein said non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

6. The non-naturally occurring microbial organism of claim 1, further comprising:

(i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, a citrate lyase, a citryl-CoA synthetase, a citryl-CoA lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

(ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

(iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof.

7. The non-naturally occurring microbial organism of claim 6, wherein said microbial organism comprising (i) further comprises an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate

dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, ferredoxin, and combinations thereof.

8. The non-naturally occurring microbial organism of claim 6, wherein said microbial organism comprising (ii) further comprises an exogenous nucleic acid encoding an enzyme selected from an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, and combinations thereof.

9. The non-naturally occurring microbial orgnaism of claim 6, wherein said microbial organism comprising (i) comprises three exogenous nucleic acids encoding an ATP-citrate lyase or a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

wherein said microbial organism comprising (ii) comprises four exogenous nucleic acids encoding a pyruvate:ferredoxin oxidoreductase; a phosphoenolpyruvate carboxylase or a phosphoenolpyruvate carboxykinase; a CO dehydrogenase; and an H_2 hydrogenase; or

wherein said microbial organism comprising (iii) comprises two exogenous nucleic acids encoding a CO dehydrogenase and an H_2 hydrogenase.

10. A method for producing 1,3-butanediol, comprising culturing the non-naturally occurring microbial organism of any one of claims 1-9 under conditions and for a sufficient period of time to produce 1,3-butanediol.

11. A non-naturally occurring microbial organism, comprising a microbial organism having a 2,4-pentadienoate pathway comprising at least one exogenous nucleic acid encoding a 2,4-pentadienoate pathway enzyme expressed in a sufficient amount to produce 2,4-pentadienoate, wherein said 2,4-pentadienoate pathway comprises a pathway selected from:

(1) 1D, 1I, 1B, 1C, 1K and 1G;
(2) 1D, 1E, 1F and 1G;
(3) 1D, 1E, 1L, 1M, 1P and 1G;
(4) 1D, 1I, 1B and 1J;
(5) 1D, 1I, 1B, 1C, 1K, 1P, 1N and 1O;

(6) 1D, 1E, 1F, 1P, 1N and 1O;

(7) 1D, 1E, 1L, 1M, 1N and 1O;

(8) 1D, 1E, 1L, 1Q and 1O;

(9) 1S, 1I, 1B, 1C, 1K and 1G;

(10) 1S, 1E, 1F and 1G;

(11) 1S, 1I, 1B and 1J;

(12) 1S, 1I, 1B, 1C, 1K, 1P, 1N and 1O;

(13) 1S, 1E, 1F, 1P, 1N and 1O;

(14) 1S, 1E, 1L, 1M, 1N and 1O;

(15) 1S, 1E, 1L, 1Q and 1O;

(16) 1B, 1C, 1K and 1G;

(17) 1I, 1E, 1F and 1G;

(18) 1I, 1E, 1L, 1M, 1P and 1G;

(19) 1B and 1J;

(20) 1I, 1E, 1F, 1P, 1N and 1O;

(21) 1I, 1E, 1L, 1M, 1N and 1O;

(22) 1I, 1E, 1L, 1Q and 1O;

(23) 3A, 3B, 3C, 3D, 3E and 3F; and

(24) 3A, 3B, 3C, 3G and 3F,

wherein 1B is a 5-aminopentanoate reductase, wherein 1C is a 5-aminopent-2-enoate aminotransferase, a 5-aminopent-2-enoate dehydrogenase or an amine oxidase, wherein 1D is a 2-oxoadipate decarboxylase, wherein 1E is a glutarate semialdehyde reductase, wherein 1F is a 5-hydroxyvalerate dehydrogenase, wherein 1G is a 5-hydroxypent-2-enoate dehydratase, wherein 1I is a 5-aminopentanoate aminotransferase, a 5-aminopentanoate dehydrogenase or a 5-aminopentanoate amine oxidase, wherein 1J is a 5-aminopent-2-enoate deaminase, wherin 1K is a 5-hydroxypent-2-enoate reductase, wherein 1L is a 5-hydroxyvaleryl-CoA transferase or a 5-hydroxyvaleryl-CoA synthetase, wherein 1M is a 5-hydroxypentanoyl-CoA dehydrogenase, wherein 1N is a 5-hydroxypent-2-enoyl-CoA dehydratase, wherein 1O is a 2,4-pentadienoyl-CoA transferase, a 2,4-pentadienoyl-CoA synthetase or a 2,4-pentadienoyl-CoA hydrolase, wherein 1P is a 5-hydroxypent-2-enoyl-CoA transferase or a 5-hydroxypent-2-enoyl-CoA synthetase, wherein 1Q is a 5-hydroxyvaleryl-CoA dehydratase/dehydrogenase, wherein 1S a glutaryl-CoA reductase, wherein 3A is a 3-oxopentanoyl-CoA thiolase or a 3-oxopentanoyl-CoA synthase, wherein 3B is a 3-oxopentanoyl-CoA reductase, wherein 3C

is a 3-hydroxypentanoyl-CoA dehydratase, wherein 3D is a pent-2-enoyl-CoA isomerase, wherein 3E is a pent-3-enoyl-CoA dehydrogenase, wherein 3F is a 2,4-pentadienoyl-CoA hydrolase, a 2,4-pentadienoyl-CoA transferase or a 2,4-pentadienoyl-CoA synthetase, wherein 3G is a pent-2-enoyl-CoA dehydrogenase.

12. The non-naturally occurring microbial organism of claim 11, wherein said microbial organism comprises two, three, four, five, six, seven, eight, nine or ten exogenous nucleic acids each encoding a 2,4-pentadienoate pathway enzyme.

13. The non-naturally occurring microbial organism of claim 12, wherein said microbial organism comprises exogenous nucleic acids encoding each of the enzymes of at least one of the pathways selected from (1)-(24).

14. The non-naturally occurring microbial organism of claim 11, wherein said at least one exogenous nucleic acid is a heterologous nucleic acid.

15. The non-naturally occurring microbial organism of claim 11, wherein said non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

16. The non-naturally occurring microbial organism of claim 11, wherein said non-naturally occuring microbial organism comprising a 2,4-pentadienoate pathway selected from (9)-(15) further comprises a glutaryl-CoA pathway comprising at least one exogenous nucleic acid encoding a glutaryl-CoA pathway enzyme expressed in a sufficient amount to produce glutaryl-CoA, said glutaryl-CoA pathway comprising a pathway selected from:

an acetoacetyl-CoA thiolase or an acetoacetyl-CoA synthase; an acetoacetyl-CoA reductase; a 3-hydroxybutyryl-CoA dehydratase; and a glutaryl-CoA dehydrogenase; or

a 2-aminoadipate aminotransferase, a 2-aminoadipate dehydrogenase or a 2-aminoadipate amine oxidase; and a 2-oxoadipate dehydrogenase, a 2-oxoadipate:ferridoxin oxidoreductase or a 2-oxoadipate formate lyase.

17. The non-naturally occurring microbial organism of claim 11, wherein said non-naturally occuring microbial organism comprising a 2,4-pentadienoate pathway selected from (16)-(22) further comprises a 5-aminopentanoate pathway comprising at least one exogenous nucleic acid encoding a 5-aminopentanoate pathway enzyme expressed in a sufficient amount to produce 5-aminopentanoate, said 5-aminopentanoate

pathway comprising a 2-aminoadipate decarboxylase; or a 2-aminoadipate decarboxylase and a 2-aminoadipate aminotransferase, a 2-aminoadipate dehydrogenase or a 2-aminoadipate amine oxidase.

18. The non-naturally occurring microbial organism of claim 11, wherein said non-naturally occuring microbial organism comprising a 2,4-pentadienoate pathway selected from (1)-(8) further comprises a 2-oxoadipate pathway comprising an exogenous nucleic acid encoding a 2-oxoadipate pathway enzyme expressed in a sufficient amount to produce a 2-oxoadipate, said 2-oxoadipate pathway comprising a 2-aminoadipate aminotransferase, a 2-aminoadipate dehydrogenase or a 2-aminoadipate amine oxidase.

19. The non-naturally occurring microbial organism of claim 11, further comprising:

(i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, a citrate lyase, a citryl-CoA synthetase, a citryl-CoA lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

(ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

(iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof.

20. The non-naturally occurring microbial organism of claim 19, wherein said microbial organism comprising (i) further comprises an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, ferredoxin, and combinations thereof.

21. The non-naturally occurring microbial organism of claim 19, wherein said microbial organism comprising (ii) further comprises an exogenous nucleic acid encoding

an enzyme selected from an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, and combinations thereof.

22. The non-naturally occurring microbial orgnaism of claim 19, wherein said microbial organism comprising (i) comprises three exogenous nucleic acids encoding an ATP-citrate lyase or a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

wherein said microbial organism comprising (ii) comprises four exogenous nucleic acids encoding a pyruvate:ferredoxin oxidoreductase; a phosphoenolpyruvate carboxylase or a phosphoenolpyruvate carboxykinase; a CO dehydrogenase; and an H_2 hydrogenase; or

wherein said microbial organism comprising (iii) comprises two exogenous nucleic acids encoding a CO dehydrogenase and an H_2 hydrogenase.

23. A method for producing 2,4-pentadienoate, comprising culturing the non-naturally occurring microbial organism of any one of claims 11-22 under conditions and for a sufficient period of time to produce 2,4-pentadienoate.

24. A non-naturally occurring microbial organism, comprising a microbial organism having a butadiene pathway comprising at least one exogenous nucleic acid encoding a butadiene pathway enzyme expressed in a sufficient amount to produce butadiene, wherein said butadiene pathway comprises a pathway selected from:

(1) 1D, 1I, 1B, 1C, 1K, 1G and 1T;
(2) 1D, 1E, 1F, 1G and 1T;
(3) 1D, 1E, 1L, 1M, 1P, 1G and 1T;
(4) 1D, 1I, 1B, 1J and 1T;
(5) 1D, 1I, 1B, 1C, 1K, 1P, 1N, 1O and 1T;
(6) 1D, 1E, 1F, 1P, 1N, 1O and 1T;
(7) 1D, 1E, 1L, 1M, 1N, 1O and 1T;
(8) 1D, 1E, 1L, 1Q, 1O and 1T;
(9) 1D, 1E, 1F, 1U and 1V;
(10) 1D, 1I, 1B, 1C, 1K, 1U and 1V;
(11) 1D, 1E, 1L, 1M, 1P, 1U and 1V;
(12) 1D, 1E, 1W and 1V;

(13) 1D, 1I, 1B, 1C, 1K, 1G, 6A and 6B;

(14) 1D, 1E, 1F, 1G, 6A and 6B;

(15) 1D, 1E, 1L, 1M, 1P, 1G, 6A and 6B;

(16) 1D, 1I, 1B, 1J, 6A and 6B;

(17) 1D, 1I, 1B, 1C, 1K, 1P, 1N, 1O, 6A and 6B;

(18) 1D, 1E, 1F, 1P, 1N, 1O, 6A and 6B;

(19) 1D, 1E, 1L, 1M, 1N, 1O, 6A and 6B;

(20) 1D, 1E, 1L, 1Q, 1O, 6A and 6B;

(21) 1D, 1I, 1B, 1C, 1K, 1G, 6H, 6E and 6B;

(22) 1D, 1E, 1F, 1G, 6H, 6E and 6B;

(23) 1D, 1E, 1L, 1M, 1P, 1G, 6H, 6E and 6B;

(24) 1D, 1I, 1B, 1J, 6H, 6E and 6B;

(25) 1D, 1I, 1B, 1C, 1K, 1P, 1N, 1O, 6H, 6E and 6B;

(26) 1D, 1E, 1F, 1P, 1N, 1O, 6H, 6E and 6B;

(27) 1D, 1E, 1L, 1M, 1N, 1O, 6H, 6E and 6B;

(28) 1D, 1E, 1L, 1Q, 1O, 6H, 6E and 6B;

(29) 1D, 1I, 1B, 1C, 1K, 1P, 1N, 6C and 6B;

(30) 1D, 1E, 1F, 1P, 1N, 6C and 6B;

(31) 1D, 1E, 1L, 1M, 1N, 6C and 6B;

(32) 1D, 1E, 1L, 1Q, 6C and 6B;

(33) 1D, 1I, 1B, 1C, 1K, 1P, 1N, 6D, 6E and 6B;

(34) 1D, 1E, 1F, 1P, 1N, 6D, 6E and 6B;

(35) 1D, 1E, 1L, 1M, 1N, 6D, 6E and 6B;

(36) 1D, 1E, 1L, 1Q, 6D, 6E and 6B;

(37) 1D, 1I, 1B, 1C, 1K, 1G, 6F, 6C and 6B;

(38) 1D, 1E, 1F, 1G, 6F, 6C and 6B;

(39) 1D, 1E, 1L, 1M, 1P, 1G, 6F, 6C and 6B;

(40) 1D, 1I, 1B, 1C, 1K, 1G, 6F, 6D, 6E and 6B;

(41) 1D, 1E, 1F, 1G, 6F, 6D, 6E and 6B;

(42) 1D, 1E, 1L, 1M, 1P, 1G, 6F, 6D, 6E and 6B;

(43) 1S, 1I, 1B, 1C, 1K, 1G and 1T;

(44) 1S, 1E, 1F, 1G and 1T;

(45) 1S, 1I, 1B, 1J and 1T;

(46) 1S, 1I, 1B, 1C, 1K, 1P, 1N, 1O and 1T;

(47) 1S, 1E, 1F, 1P, 1N, 1O and 1T;

(48) 1S, 1E, 1L, 1M, 1N, 1O and 1T;

(49) 1S, 1E, 1L, 1Q, 1O and 1T;

(50) 1S, 1E, 1F, 1U and 1V;

(51) 1S, 1I, 1B, 1C, 1K, 1U and 1V;

(52) 1S, 1E, 1L, 1M, 1P, 1U and 1V;

(53) 1S, 1E, 1W and 1V;

(54) 1S, 1I, 1B, 1C, 1K, 1G, 6A and 6B;

(55) 1S, 1E, 1F, 1G, 6A and 6B;

(56) 1S, 1I, 1B, 1J, 6A and 6B;

(57) 1S, 1I, 1B, 1C, 1K, 1P, 1N, 1O, 6A and 6B;

(58) 1S, 1E, 1F, 1P, 1N, 1O, 6A and 6B;

(59) 1S, 1E, 1L, 1M, 1N, 1O, 6A and 6B;

(60) 1S, 1E, 1L, 1Q, 1O, 6A and 6B;

(61) 1S, 1I, 1B, 1C, 1K, 1G, 6H, 6E and 6B;

(62) 1S, 1E, 1F, 1G, 6H, 6E and 6B;

(63) 1S, 1I, 1B, 1J, 6H, 6E and 6B;

(64) 1S, 1I, 1B, 1C, 1K, 1P, 1N, 1O, 6H, 6E and 6B;

(65) 1S, 1E, 1F, 1P, 1N, 1O, 6H, 6E and 6B;

(66) 1S, 1E, 1L, 1M, 1N, 1O, 6H, 6E and 6B;

(67) 1S, 1E, 1L, 1Q, 1O, 6H, 6E and 6B;

(68) 1S, 1I, 1B, 1C, 1K, 1P, 1N, 6C and 6B;

(69) 1S, 1E, 1F, 1P, 1N, 6C and 6B;

(70) 1S, 1E, 1L, 1M, 1N, 6C and 6B;

(71) 1S, 1E, 1L, 1Q, 6C and 6B;

(72) 1S, 1I, 1B, 1C, 1K, 1P, 1N, 6D, 6E and 6B;

(73) 1S, 1E, 1F, 1P, 1N, 6D, 6E and 6B;

(74) 1S, 1E, 1L, 1M, 1N, 6D, 6E and 6B;

(75) 1S, 1E, 1L, 1Q, 6D, 6E and 6B;

(76) 1S, 1I, 1B, 1C, 1K, 1G, 6F, 6C and 6B;

(77) 1S, 1E, 1F, 1G, 6F, 6C and 6B;

(78) 1S, 1I, 1B, 1C, 1K, 1G, 6F, 6D, 6E and 6B;

(79) 1S, 1E, 1F, 1G, 6F, 6D, 6E and 6B;

(80) 1B, 1C, 1K, 1G and 1T;

(81) 1I, 1E, 1F, 1G and 1T;

(82) 1I, 1E, 1L, 1M, 1P, 1G and 1T;

(83) 1B, 1J and 1T;

(84) 1I, 1E, 1F, 1P, 1N, 1O and 1T;

(85) 1I, 1E, 1L, 1M, 1N, 1O and 1T;

(86) 1I, 1E, 1L, 1Q, 1O and 1T;

(87) 1B, 1C, 1K, 1U and 1V;

(88) 1I, 1E, 1F, 1U and 1V;

(89) 1I, 1E, 1L, 1M, 1P, 1U and 1V;

(90) 1I, 1E, 1W and 1V;

(91) 1B, 1C, 1K, 1G, 6A and 6B;

(92) 1I, 1E, 1F, 1G, 6A and 6B;

(93) 1I, 1E, 1L, 1M, 1P, 1G, 6A and 6B;

(94) 1B, 1J, 6A and 6B;

(95) 1I, 1E, 1F, 1P, 1N, 1O, 6A and 6B;

(96) 1I, 1E, 1L, 1M, 1N, 1O, 6A and 6B;

(97) 1I, 1E, 1L, 1Q, 1O, 6A and 6B;

(98) 1B, 1C, 1K, 1G, 6H, 6E and 6B;

(99) 1I, 1E, 1F, 1G, 6H, 6E and 6B;

(100) 1I, 1E, 1L, 1M, 1P, 1G, 6H, 6E and 6B;

(101) 1B, 1J, 6H, 6E and 6B;

(102) 1I, 1E, 1F, 1P, 1N, 1O, 6H, 6E and 6B;

(103) 1I, 1E, 1L, 1M, 1N, 1O, 6H, 6E and 6B;

(104) 1I, 1E, 1L, 1Q, 1O, 6H, 6E and 6B;

(105) 1I, 1E, 1F, 1P, 1N, 6C and 6B;

(106) 1I, 1E, 1L, 1M, 1N, 6C and 6B;

(107) 1I, 1E, 1L, 1Q, 6C and 6B;

(108) 1I, 1E, 1F, 1P, 1N, 6D, 6E and 6B;

(109) 1I, 1E, 1L, 1M, 1N, 6D, 6E and 6B;

(110) 1I, 1E, 1L, 1Q, 6D, 6E and 6B;

(111) 1B, 1C, 1K, 1G, 6F, 6C and 6B;

(112) 1I, 1E, 1F, 1G, 6F, 6C and 6B;

(113) 1I, 1E, 1L, 1M, 1P, 1G, 6F, 6C and 6B;

(114) 1B, 1C, 1K, 1G, 6F, 6D, 6E and 6B;

(115) 1I, 1E, 1F, 1G, 6F, 6D, 6E and 6B;

(116) 1I, 1E, 1L, 1M, 1P, 1G, 6F, 6D, 6E and 6B;

(117) 3A, 3B, 3C, 3D, 3E, 3F and 1T;

(118) 3A, 3B, 3C, 3D, 3E, 3F, 6A and 6B;

(119) 3A, 3B, 3C, 3D, 3E, 3F, 6H, 6E and 6B;

(120) 3A, 3B, 3C, 3D, 3E, 6C and 6B;

(121) 3A, 3B, 3C, 3D, 3E, 6D, 6E and 6B; and

(122) 3A, 3B, 3C, 3G, 3F and 1T;

(123) 3A, 3B, 3C, 3G, 3F, 6A and 6B;

(124) 3A, 3B, 3C, 3G, 3F, 6H, 6E and 6B;

(125) 3A, 3B, 3C, 3G, 6C and 6B;

(126) 3A, 3B, 3C, 3G, 6D, 6E and 6B;

(127) 5A, 5B, 5C, 5D and 5E;

(128) 7A, 7J, 7R, 7AD, 7AH, 12A, 12B and 12C;

(129) 7A, 7H, 7F, 7R, 7AD, 7AH, 12A, 12B and 12C;

(130) 7A, 7H, 7Q, 7Z, 7AD, 7AH, 12A, 12B and 12C;

(131) 7A, 7H, 7Q, 7AC, 7AG, 7AH, 12A, 12B and 12C;

(132) 7A, 7D, 7I, 7R, 7AD, 7AH, 12A, 12B and 12C;

(133) 7A, 7D, 7E, 7F, 7R, 7AD, 7AH, 12A, 12B and 12C;

(134) 7A, 7D, 7E, 7Q, 7Z, 7AD, 7AH, 12A, 12B and 12C;

(135) 7A, 7D, 7E, 7Q, 7AC, 7AG, 7AH, 12A, 12B and 12C;

(136) 7A, 7D, 7P, 7N, 7AD, 7AH, 12A, 12B and 12C;

(137) 7A, 7D, 7P, 7Y, 7Z, 7AD, 7AH, 12A, 12B and 12C;

(138) 7A, 7D, 7P, 7Y, 7AC, 7AG, 7AH, 12A, 12B and 12C;

(139) 7A, 7D, 7P, 7AB, 7V, 7AH, 12A, 12B and 12C;

(140) 7A, 7D, 7P, 7AB, 7AF, 7AG, 7AH, 12A, 12B and 12C;

(141) 7A, 7B, 7M, 7AD, 7AH, 12A, 12B and 12C;

(142) 7A, 7B, 7L, 7Z, 7AD, 7AH, 12A, 12B and 12C;

(143) 7A, 7B, 7L, 7AC, 7AG, 7AH, 12A, 12B and 12C;

(144) 7A, 7B, 7X, 7Y, 7Z, 7AD, 7AH, 12A, 12B and 12C;

(145) 7A, 7B, 7X, 7Y, 7AC, 7AG, 7AH, 12A, 12B and 12C;

(146) 7A, 7B, 7X, 7AB, 7V, 7AH, 12A, 12B and 12C;

(147) 7A, 7B, 7X, 7AB, 7AF, 7AG, 7AH, 12A, 12B and 12C;

(148) 7A, 7B, 7C, 7U, 7AH, 12A, 12B and 12C;

(149) 7A, 7B, 7C, 7T, 7AG, 7AH, 12A, 12B and 12C;

(150) 7A, 7B, 7C, 7AE, 7AF, 7AG, 7AH, 12A, 12B and 12C;

(151) 7A, 7D, 7P, 7AB, 7W, 12A, 12B and 12C;

(152) 7A, 7B, 7X, 7AB, 7W, 12A, 12B and 12C;

(153) 7A, 7B, 7C, 7AE, 7W, 12A, 12B and 12C;

(154) 7A, 7B, 7C, 7AE, 7V, 7AH; , 12A, 12B and 12C

(155) 7A, 7J, 7R, 7AD, 7AH, 12D and 12C;

(156) 7A, 7H, 7F, 7R, 7AD, 7AH, 12D and 12C;

(157) 7A, 7H, 7Q, 7Z, 7AD, 7AH, 12D and 12C;

(158) 7A, 7H, 7Q, 7AC, 7AG, 7AH, 12D and 12C;

(159) 7A, 7D, 7I, 7R, 7AD, 7AH, 12D and 12C;

(160) 7A, 7D, 7E, 7F, 7R, 7AD, 7AH, 12D and 12C;

(161) 7A, 7D, 7E, 7Q, 7Z, 7AD, 7AH, 12D and 12C;

(164) 7A, 7D, 7E, 7Q, 7AC, 7AG, 7AH, 12D and 12C;

(163) 7A, 7D, 7P, 7N, 7AD, 7AH, 12D and 12C;

(164) 7A, 7D, 7P, 7Y, 7Z, 7AD, 7AH, 12D and 12C;

(165) 7A, 7D, 7P, 7Y, 7AC, 7AG, 7AH, 12D and 12C;

(166) 7A, 7D, 7P, 7AB, 7V, 7AH, 12D and 12C;

(167) 7A, 7D, 7P, 7AB, 7AF, 7AG, 7AH, 12D and 12C;

(168) 7A, 7B, 7M, 7AD, 7AH, 12D and 12C;

(169) 7A, 7B, 7L, 7Z, 7AD, 7AH, 12D and 12C;

(170) 7A, 7B, 7L, 7AC, 7AG, 7AH, 12D and 12C;

(171) 7A, 7B, 7X, 7Y, 7Z, 7AD, 7AH, 12D and 12C;

(172) 7A, 7B, 7X, 7Y, 7AC, 7AG, 7AH, 12D and 12C;

(173) 7A, 7B, 7X, 7AB, 7V, 7AH, 12D and 12C;

(174) 7A, 7B, 7X, 7AB, 7AF, 7AG, 7AH, 12D and 12C;

(175) 7A, 7B, 7C, 7U, 7AH, 12D and 12C;

(176) 7A, 7B, 7C, 7T, 7AG, 7AH, 12D and 12C;

(177) 7A, 7B, 7C, 7AE, 7AF, 7AG, 7AH, 12D and 12C;

(178) 7A, 7D, 7P, 7AB, 7W, 12D and 12C;

(179) 7A, 7B, 7X, 7AB, 7W, 12D and 12C;

(180) 7A, 7B, 7C, 7AE, 7W, 12D and 12C;

(181) 7A, 7B, 7C, 7AE, 7V, 7AH, 12D and 12C;

(182) 7I, 7R, 7AD, 7AH, 12A, 12B and 12C;

(183) 7E, 7F, 7R, 7AD, 7AH, 12A, 12B and 12C;

(184) 7E, 7Q, 7Z, 7AD, 7AH, 12A, 12B and 12C;

(185) 7E, 7Q, 7AC, 7AG, 7AH, 12A, 12B and 12C;

(186) 7P, 7N, 7AD, 7AH, 12A, 12B and 12C;

(187) 7P, 7Y, 7Z, 7AD, 7AH, 12A, 12B and 12C;

(188) 7P, 7Y, 7AC, 7AG, 7AH, 12A, 12B and 12C;

(189) 7P, 7AB, 7V, 7AH, 12A, 12B and 12C;

(190) 7P, 7AB, 7AF, 7AG, 7AH, 12A, 12B and 12C;

(191) 7P, 7AB, 7W, 12A, 12B and 12C;

(192) 7I, 7R, 7AD, 7AH, 12D and 12C;

(193) 7E, 7F, 7R, 7AD, 7AH, 12D and 12C;

(194) 7E, 7Q, 7Z, 7AD, 7AH, 12D and 12C;

(195) 7E, 7Q, 7AC, 7AG, 7AH, 12D and 12C;

(196) 7P, 7N, 7AD, 7AH, 12D and 12C;

(197) 7P, 7Y, 7Z, 7AD, 7AH, 12D and 12C;

(198) 7P, 7Y, 7AC, 7AG, 7AH, 12D and 12C;

(199) 7P, 7AB, 7V, 7AH, 12D and 12C;

(200) 7P, 7AB, 7AF, 7AG, 7AH, 12D and 12C;

(201) 7P, 7AB, 7W, 12D and 12C;

(202) 7AS, 7I, 7R, 7AD, 7AH, 12A, 12B and 12C;

(203) 7AS, 7E, 7F, 7R, 7AD, 7AH, 12A, 12B and 12C;

(204) 7AS, 7E, 7Q, 7Z, 7AD, 7AH, 12A, 12B and 12C;

(205) 7AS, 7E, 7Q, 7AC, 7AG, 7AH, 12A, 12B and 12C;

(206) 7AS, 7P, 7N, 7AD, 7AH, 12A, 12B and 12C;

(207) 7AS, 7P, 7Y, 7Z, 7AD, 7AH, 12A, 12B and 12C;

(208) 7AS, 7P, 7Y, 7AC, 7AG, 7AH, 12A, 12B and 12C;

(209) 7AS, 7P, 7AB, 7V, 7AH, 12A, 12B and 12C;

(210) 7AS, 7P, 7AB, 7AF, 7AG, 7AH, 12A, 12B and 12C;

(211) 7AS, 7P, 7AB, 7W, 12A, 12B and 12C;

(212) 7AS, 7I, 7R, 7AD, 7AH, 12D and 12C;

(213) 7AS, 7E, 7F, 7R, 7AD, 7AH, 12D and 12C;

(214) 7AS, 7E, 7Q, 7Z, 7AD, 7AH, 12D and 12C;

(215) 7AS, 7E, 7Q, 7AC, 7AG, 7AH, 12D and 12C;

(216) 7AS, 7P, 7N, 7AD, 7AH, 12D and 12C;

(217) 7AS, 7P, 7Y, 7Z, 7AD, 7AH, 12D and 12C;

(218) 7AS, 7P, 7Y, 7AC, 7AG, 7AH, 12D and 12C;

(219) 7AS, 7P, 7AB, 7V, 7AH, 12D and 12C;

(220) 7AS, 7P, 7AB, 7AF, 7AG, 7AH, 12D and 12C; and

(221) 7AS, 7P, 7AB, 7W, 12D and 12C,

wherein 1B is a 5-aminopentanoate reductase, a 5-aminopent-2-enoate aminotransferase, a 5-aminopent-2-enoate dehydrogenase or 5-aminopent-2-enoate amine oxidase, wherein 1D is a 2-oxoadipate decarboxylase, wherein 1E is a glutarate semialdehyde reductase, wherein 1F is a 5-hydroxyvalerate reductase, wherein 1G is a 5-hydroxypent-2-enoate dehydratase, wherein 1I is a 5-aminopentanoate aminotransferase, a 5-aminopentanoate dehydrogenase or a 5-aminopentanoate amine oxidase, wherein 1J is a 5-aminopent-4-enoate deaminase, wherein 1K is a 5-hydroxypent-2-enoate reductase, wherein 1L is a 5-hydroxyvaleryl-CoA transferase or a 5-hydroxyvaleryl-CoA synthetase, wherein 1M is a 5-hydroxypentanoyl-CoA dehydrogenase, wherin 1N is a 5-hydroxypent-2-enoyl-CoA dehydratase, wherein 1O is a 2,4-pentadienoyl-CoA transferase, a 2,4-pentadienoyl-CoA synthetase or a 2,4-pentadienoyl-CoA hydrolase, wherein 1P is a 5-hydroxypent-2-enoyl-CoA transferase or a 5-hydroxypent-2-enoyl-CoA synthetase, wherein in 1Q is a 5-hydroxyvaleryl-CoA dehydratase/dehydrogenase, wherein 1S is a glutaryl-CoA reductase, wherein 1T is a 2,4-pentadienoate decarboxylase, wherein 1U is a 5-hydroxypent-2-enoate decarboxylase, wherein 1V is a 3-buten-1-ol dehydratase, wherein 1W is a 5-hydroxyvalerate decarboxylase, wherein 3A is a 3-oxopentanoyl-CoA thiolase or a 3-oxopentanoyl-CoA synthase, wherein 3B is a 3-oxopentanoyl-CoA reductase, wherein 3C is a 3-hydroxypentanoyl-CoA dehydratase, wherein 3D is a pent-2-enoyl-CoA isomerase, wherein 3E is a pent-3-enoyl-CoA dehydrogenase, wherein 3F is a 2,4-pentadienoyl-CoA hydrolase, a 2,4-pentadienoyl-CoA transferase or a 2,4-pentadienoyl-CoA synthetase, wherein 3G is a pent-2-enoyl-CoA dehydrogenase, wherein 5A is a 4-hydroxy-2-oxovalerate aldolase, wherein 5B is a 4-hydroxy-2-oxovalerate dehydratase, wherein 5C is a 2-oxopentenoate decarboxylase, wherein 5D is a 3-buten-1-al reductase, wherein 5E is a 3-buten-1-ol dehydratase, wherein 6A is a 2,4-pentadienoate reductase (acid reducing), wherein 6B is a penta-2,4-dienal decarbonylase, wherein 6C is a 2,4-pentadienoyl-CoA reductase (acid reducing), wherein 6D is a 2,4-pentadienoyl-CoA phosphotransferase, wherein 6E is a 2,4-pentadienoyl-phosphate reductase, wherein 6F is a 2,4-pentadienoyl-CoA hydrolase, a 2,4-pentadienoyl-CoA transferase or a 2,4-pentadienoyl-CoA synthetase, wherein 6H is a 2,4-pentadienoate kinase, wherein 7A is a

3-ketoacyl-ACP synthase, wherein 7B is an acetoacetyl-ACP reductase, wherein 7C is a 3-hydroxybutyryl-ACP dehydratase, wherein 7D is an acetoacetyl-CoA:ACP transferase, wherein 7E is an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA transferase or an acetoacetyl-CoA synthetase, wherein 7F is an acetoacetate reductase (acid reducing), wherein 7H is an acetoacetyl-ACP thioesterase, wherein 7I is an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming), wherein 7J is an acetoacetyl-ACP reductase (aldehyde forming), wherein 7K is an acetoacetyl-CoA reductase (alcohol forming), wherein 7L is an 3-hydroxybutyryl-ACP thioesterase, wherein 7M is an 3-hydroxybutyryl-ACP reductase (aldehyde forming), wherein 7N is an 3-hydroxybutyryl-CoA reductase (aldehyde forming), wherein 7O is an 3-hydroxybutyryl-CoA reductase (alcohol forming), wherein 7P is an acetoacetyl-CoA reductase (ketone reducing), wherein 7Q is an acetoacetate reductase (ketone reducing), wherein 7R is a 3-oxobutyraldehyde reductase (ketone reducing), wherein 7T is a crotonyl-ACP thioesterase, wherein 7U is a crotonyl-ACP reductase (aldehyde forming), wherein 7V is a crotonyl-CoA reductase (aldehyde forming), wherein 7W is a crotonyl-CoA (alcohol forming), wherein 7X is a 3-hydroxybutyryl-CoA:ACP transferase, wherein 7Y is a 3-hydroxybutyryl-CoA hydrolase, a 3-hydroxybutyryl-CoA transferase or a 3-hydroxybutyryl-CoA synthetase, wherein 7Z is a 3-hydroxybutyrate reductase, wherein 7AB is a 3-hydroxybutyryl-CoA dehydratase, wherein 7AC is a 3-hydroxybutyrate dehydratase, wherein 7AD is a 3-hydroxybutyraldehyde dehydratase, wherein 7AE is a crotonyl-CoA:ACP transferase, wherein 7AF is a crotonyl-CoA hydrolase, a crotonyl-CoA transferase or a crotonyl-CoA synthetase, wherein 7AG is a crotonate reductase, wherein 7AH is a crotonaldehyde reductase, wherein 7AS is an acetoacetyl-CoA synthase, wherein 12A is a crotyl alcohol kinase, wherein 12B is a 2-butenyl-4-phosphate kinase, wherein 12C is a butadiene synthase, and wherein 12D is a crotyl alcohol diphosphokinase.

25. The non-naturally occurring microbial organism of claim 24, wherein said microbial organism comprises two, three, four, five, six, seven, eight, nine, ten or eleven exogenous nucleic acids each encoding a butadiene pathway enzyme.

26. The non-naturally occurring microbial organism of claim 25, wherein said microbial organism comprises exogenous nucleic acids encoding each of the enzymes of at least one of the pathways selected from (1)-(221).

27. The non-naturally occurring microbial organism of claim 24, wherein said at least one exogenous nucleic acid is a heterologous nucleic acid.

28. The non-naturally occurring microbial organism of claim 24, wherein said non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

29. The non-naturally occurring microbial organism of claim 24, wherein said non-naturally occuring microbial organism comprising a butadiene pathway selected from (43)-(79) further comprises a glutaryl-CoA pathway comprising at least one exogenous nucleic acid encoding a glutaryl-CoA pathway enzyme expressed in a sufficient amount to produce glutaryl-CoA, said glutaryl-CoA pathway comprising a pathway selected from:

an acetoacetyl-CoA thiolase or acetoacetyl-CoA synthase; an acetoacetyl-CoA reductase; a 3-hydroxybutyryl-CoA dehydratase; and a glutaryl-CoA dehydrogenase; or

a 2-aminoadipate aminotransferase, a 2-aminoadipate dehydrogenase or a 2-amininoadipate amine oxidase; and a 2-oxoadipate dehydrogenase, a 2-oxoadipate:ferridoxin oxidoreductase or a 2-oxoadipate formate lyase.

30. The non-naturally occurring microbial organism of claim 24, wherein said non-naturally occuring microbial organism comprising a butadiene pathway selected from (80)-(116) further comprises a 5-aminopentanoate pathway comprising at least one exogenous nucleic acid encoding a 5-aminopentanoate pathway enzyme expressed in a sufficient amount to produce 5-aminopentanoate, said 5-aminopentanoate pathway comprising a 2-aminoadipate decarboxylase; or a 2-aminoadipate decarboxylase and a 2-aminoadipate aminotransferase, a 2-aminoadipate dehydrogenase or a 2-aminoadipate amine oxidase.

31. The non-naturally occurring microbial organism of claim 24, wherein said non-naturally occuring microbial organism comprising a butadiene pathway selected from (1)-(42) further comprises a 2-oxoadipate pathway comprising an exogenous nucleic acid encoding a 2-oxoadipate pathway enzyme expressed in a sufficient amount to produce a 2-oxoadipate, said 2-oxoadipate pathway comprising a 2-aminoadipate aminotransferase, a 2-aminoadipate dehydrogenase or a 2-aminoadipate amine oxidase.

32. The non-naturally occurring microbial organism of claim 24, further comprising:

(i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic

acid is selected from an ATP-citrate lyase, a citrate lyase, a citryl-CoA synthetase, a citryl-CoA lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

(ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

(iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof.

33. The non-naturally occurring microbial organism of claim 32, wherein said microbial organism comprising (i) further comprises an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, ferredoxin, and combinations thereof.

34. The non-naturally occurring microbial organism of claim 32, wherein said microbial organism comprising (ii) further comprises an exogenous nucleic acid encoding an enzyme selected from an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, and combinations thereof.

35. The non-naturally occurring microbial orgnaism of claim 32, wherein said microbial organism comprising (i) comprises three exogenous nucleic acids encoding an ATP-citrate lyase or a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

wherein said microbial organism comprising (ii) comprises four exogenous nucleic acids encoding a pyruvate:ferredoxin oxidoreductase; a phosphoenolpyruvate carboxylase or a phosphoenolpyruvate carboxykinase; a CO dehydrogenase; and an H_2 hydrogenase; or

wherein said microbial organism comprising (iii) comprises two exogenous nucleic acids encoding a CO dehydrogenase and an H_2 hydrogenase.

36. A method for producing butadiene, comprising culturing the non-naturally occurring microbial organism of any one of claims 24-35 under conditions and for a sufficient period of time to produce butadiene.

37. A non-naturally occurring microbial organism, comprising a microbial organism having a 3-buten-1-ol pathway comprising at least one exogenous nucleic acid encoding a 3-buten-1-ol pathway enzyme expressed in a sufficient amount to produce 3-buten-1-ol, wherein said 3-buten-1-ol pathway comprises a pathway selected from:

(1) 1D, 1E, 1F and 1U;
(2) 1D, 1I, 1B, 1C, 1K and 1U;
(3) 1D, 1E, 1L, 1M, 1P and 1U;
(4) 1D, 1E and 1W;
(5) 1S, 1E, 1F and 1U;
(6) 1S, 1I, 1B, 1C, 1K and 1U;
(7) 1S, 1E, 1L, 1M, 1P and 1U;
(8) 1S, 1E and 1W;
(9) 1B, 1C, 1K and 1U;
(10) 1I, 1E, 1F and 1U;
(11) 1I, 1E, 1L, 1M, 1P and 1U;
(12) 1I, 1E and 1W; and
(13) 5A, 5B, 5C and 5D;

wherein 1B is a 5-aminopentanoate reductase, wherein 1C is a 5-aminopent-2-enoate aminotransferase, a 5-aminopent-2-enoate dehydrogenase or an amine oxidase, wherein 1D is a 2-oxoadipate decarboxylase, wherein 1E is a glutarate semialdehyde reductase, wherein 1F is a 5-hydroxyvalerate dehydrogenase, wherein 1I is a 5-aminopentanoate aminotransferase, a 5-aminopentanoate dehydrogenase or a 5-aminopentanoate amine oxidase, wherein 1K is a 5-hydroxypent-2-enoate reductase, wherein 1L is a 5-hydroxyvaleryl-CoA transferase or a 5-hydroxyvaleryl-CoA synthetase, wherein 1M is a 5-hydroxypentanoyl-CoA dehydrogenase, wherein 1P is a 5-hydroxypent-2-enoyl-CoA transferase or a 5-hydroxypent-2-enoyl-CoA synthetase, wherein 1S is a glutaryl-CoA reductase, wherein 1U is a 5-hydroxypent-2-enoate decarboxylase, wherein 1W is a 5-hydroxyvalerate decarboxylase, wherein 5A is a 4-hydroxy-2-oxovalerate aldolase, wherein 5B is a 4-hydroxy-2-oxovalerate dehydratase, wherein 5C is a 2-oxopentenoate decarboxylase, wherein 5D is a 3-buten-1-al reductase.

38. The non-naturally occurring microbial organism of claim 37, wherein said microbial organism comprises two, three, four, five or six exogenous nucleic acids each encoding a 3-buten-1-ol pathway enzyme.

39. The non-naturally occurring microbial organism of claim 38, wherein said microbial organism comprises exogenous nucleic acids encoding each of the enzymes of at least one of the pathways selected from (1)-(13).

40. The non-naturally occurring microbial organism of claim 37, wherein said at least one exogenous nucleic acid is a heterologous nucleic acid.

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

42. The non-naturally occurring microbial organism of claim 37, further comprising:

(i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

(ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

(iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof.

43. The non-naturally occurring microbial organism of claim 42, wherein said microbial organism comprising (i) further comprises an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, ferredoxin, and combinations thereof.

44. The non-naturally occurring microbial organism of claim 42, wherein said microbial organism comprising (ii) further comprises an exogenous nucleic acid encoding an enzyme selected from an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, and combinations thereof.

45. The non-naturally occurring microbial orgnaism of claim 42, wherein said microbial organism comprising (i) comprises three exogenous nucleic acids encoding an ATP-citrate lyase or a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

wherein said microbial organism comprising (ii) comprises four exogenous nucleic acids encoding a pyruvate:ferredoxin oxidoreductase; a phosphoenolpyruvate carboxylase or a phosphoenolpyruvate carboxykinase; a CO dehydrogenase; and an H_2 hydrogenase; or

wherein said microbial organism comprising (iii) comprises two exogenous nucleic acids encoding a CO dehydrogenase and an H_2 hydrogenase.

46. A method for producing 3-buten-1-ol, comprising culturing the non-naturally occurring microbial organism of any one of claims 37-45 under conditions and for a sufficient period of time to produce 3-buten-1-ol.

47. A method for producing butadiene, comprising culturing the non-naturally occurring microbial organism of any one of claims 37-45 under conditions and for a sufficient to produce 3-buten-1-ol, and chemically dehydrating said 3-buten-1-ol to produce butadiene.

48. A non-naturally occurring microbial organism, comprising a microbial organism having a crotyl alcohol pathway comprising at least one exogenous nucleic acid encoding a crotyl alcohol pathway enzyme expressed in a sufficient amount to produce crotyl alcohol, wherein said crotyl alcohol pathway comprises a pathway selected from:

(1) 7A, 7J, 7R, 7AD and 7AH;
(2) 7A, 7H, 7F, 7R, 7AD and 7AH;
(3) 7A, 7H, 7Q, 7Z, 7AD and 7AH;
(4) 7A, 7H, 7Q, 7AC, 7AG and 7AH;
(5) 7A, 7D, 7I, 7R, 7AD and 7AH;

(6) 7A, 7D, 7E, 7F, 7R, 7AD and 7AH;

(7) 7A, 7D, 7E, 7Q, 7Z, 7AD and 7AH;

(8) 7A, 7D, 7E, 7Q, 7AC, 7AG and 7AH;

(9) 7A, 7D, 7P, 7N, 7AD and 7AH;

(10) 7A, 7D, 7P, 7Y, 7Z, 7AD and 7AH;

(11) 7A, 7D, 7P, 7Y, 7AC, 7AG and 7AH;

(12) 7A, 7D, 7P, 7AB, 7V and 7AH;

(13) 7A, 7D, 7P, 7AB, 7AF, 7AG and 7AH;

(14) 7A, 7B, 7M, 7AD and 7AH;

(15) 7A, 7B, 7L, 7Z, 7AD and 7AH;

(16) 7A, 7B, 7L, 7AC, 7AG and 7AH;

(17) 7A, 7B, 7X, 7Y, 7Z, 7AD and 7AH;

(18) 7A, 7B, 7X, 7Y, 7AC, 7AG and 7AH;

(19) 7A, 7B, 7X, 7AB, 7V and 7AH;

(20) 7A, 7B, 7X, 7AB, 7AF, 7AG and 7AH;

(21) 7A, 7B, 7C, 7U and 7AH;

(22) 7A, 7B, 7C, 7T, 7AG and 7AH;

(23) 7A, 7B, 7C, 7AE, 7AF, 7AG and 7AH;

(24) 7A, 7D, 7P, 7AB and 7W;

(25) 7A, 7B, 7X, 7AB and 7W;

(26) 7A, 7B, 7C, 7AE and 7W;

(27) 7A, 7B, 7C, 7AE, 7V and 7AH;

(28) 7I, 7R, 7AD and 7AH;

(29) 7E, 7F, 7R, 7AD and 7AH;

(30) 7E, 7Q, 7Z, 7AD and 7AH;

(31) 7E, 7Q, 7AC, 7AG and 7AH;

(32) 7P, 7N, 7AD and 7AH;

(33) 7P, 7Y, 7Z, 7AD and 7AH;

(34) 7P, 7Y, 7AC, 7AG and 7AH;

(35) 7P, 7AB, 7V and 7AH;

(36) 7P, 7AB, 7AF, 7AG and 7AH;

(37) 7P, 7AB and 7W;

(38) 7AS, 7I, 7R, 7AD and 7AH;

(39) 7AS, 7E, 7F, 7R, 7AD and 7AH;

(40) 7AS, 7E, 7Q, 7Z, 7AD and 7AH;

(41) 7AS, 7E, 7Q, 7AC, 7AG and 7AH;

(42) 7AS, 7P, 7N, 7AD and 7AH;

(43) 7AS, 7P, 7Y, 7Z, 7AD and 7AH;

(44) 7AS, 7P, 7Y, 7AC, 7AG and 7AH;

(45) 7AS, 7P, 7AB, 7V and 7AH;

(46) 7AS, 7P, 7AB, 7AF, 7AG and 7AH; and

(47) 7AS, 7P, 7AB and 7W,

wherein 7A is a 3-ketoacyl-ACP synthase, wherein 7B is an acetoacetyl-ACP reductase, wherein 7C is a 3-hydroxybutyryl-ACP dehydratase, wherein 7D is an acetoacetyl-CoA:ACP transferase, wherein 7E is an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA transferase or an acetoacetyl-CoA synthetase, wherein 7F is an acetoacetate reductase (acid reducing), wherein 7H is an acetoacetyl-ACP thioesterase, wherein 7I is an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming), wherein 7J is an acetoacetyl-ACP reductase (aldehyde forming), wherein 7K is an acetoacetyl-CoA reductase (alcohol forming), wherein 7L is an 3-hydroxybutyryl-ACP thioesterase, wherein 7M is an 3-hydroxybutyryl-ACP reductase (aldehyde forming), wherein 7N is an 3-hydroxybutyryl-CoA reductase (aldehyde forming), wherein 7O is an 3-hydroxybutyryl-CoA reductase (alcohol forming), wherein 7P is an acetoacetyl-CoA reductase (ketone reducing), wherein 7Q is an acetoacetate reductase (ketone reducing), wherein 7R is a 3-oxobutyraldehyde reductase (ketone reducing), wherein 7T is a crotonyl-ACP thioesterase, wherein 7U is a crotonyl-ACP reductase (aldehyde forming), wherein 7V is a crotonyl-CoA reductase (aldehyde forming), wherein 7W is a crotonyl-CoA (alcohol forming), wherein 7X is a 3-hydroxybutyryl-CoA:ACP transferase, wherein 7Y is a 3-hydroxybutyryl-CoA hydrolase, a 3-hydroxybutyryl-CoA transferase or a 3-hydroxybutyryl-CoA synthetase, wherein 7Z is a 3-hydroxybutyrate reductase, wherein 7AB is a 3-hydroxybutyryl-CoA dehydratase, wherein 7AC is a 3-hydroxybutyrate dehydratase, wherein 7AD is a 3-hydroxybutyraldehyde dehydratase, wherein 7AE is a crotonyl-CoA:ACP transferase, wherein 7AF is a crotonyl-CoA hydrolase, a crotonyl-CoA transferase or a crotonyl-CoA synthetase, wherein 7AG is a crotonate reductase, wherein 7AH is a crotonaldehyde reductase and wherein 7AS is an acetoacetyl-CoA synthase.

49. The non-naturally occurring microbial organism of claim 1, wherein said microbial organism comprises two, three, four, five, six or seven exogenous nucleic acids each encoding a crotyl alcohol pathway enzyme.

50. The non-naturally occurring microbial organism of claim 1A, wherein said microbial organism comprises exogenous nucleic acids encoding each of the enzymes of at least one of the pathways selected from (1)-(47).

51. The non-naturally occurring microbial organism of claim 1, wherein said at least one exogenous nucleic acid is a heterologous nucleic acid.

52. The non-naturally occurring microbial organism of claim 1, wherein said non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

53. The non-naturally occurring microbial organism of claim 48, further comprising:

(i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, a citrate lyase, a citryl-CoA synthetase, a citryl-CoA lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

(ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

(iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof.

54. The non-naturally occurring microbial organism of claim 53, wherein said microbial organism comprising (i) further comprises an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, ferredoxin, and combinations thereof.

55. The non-naturally occurring microbial organism of claim 53, wherein said microbial organism comprising (ii) further comprises an exogenous nucleic acid encoding an enzyme selected from an aconitase, an isocitrate dehydrogenase, a succinyl-CoA

synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, and combinations thereof.

56. The non-naturally occurring microbial orgnaism of claim 53, wherein said microbial organism comprising (i) comprises three exogenous nucleic acids encoding an ATP-citrate lyase or a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

wherein said microbial organism comprising (ii) comprises four exogenous nucleic acids encoding a pyruvate:ferredoxin oxidoreductase; a phosphoenolpyruvate carboxylase or a phosphoenolpyruvate carboxykinase; a CO dehydrogenase; and an H_2 hydrogenase; or

wherein said microbial organism comprising (iii) comprises two exogenous nucleic acids encoding a CO dehydrogenase and an H_2 hydrogenase.

57. A method for producing crotyl alcohol, comprising culturing the non-naturally occurring microbial organism of any one of claims 48-56 under conditions and for a sufficient period of time to produce crotyl alcohol.

58. A non-naturally occurring microbial organism, comprising a microbial organism having a propylene pathway comprising at least one exogenous nucleic acid encoding a propylene pathway enzyme expressed in a sufficient amount to produce propylene, wherein said propylene pathway comprises a pathway selected from:

(1) 7A, 7J, 7R, 7AD and 7AO;
(2) 7A, 7H, 7F, 7R, 7AD and 7AO;
(3) 7A, 7D, 7L, 7R, 7AD and 7AO;
(4) 7A, 7D, 7E, 7F, 7R, 7AD and 7AO;
(5) 7A, 7H, 7Q, 7Z, 7AD and 7AO;
(6) 7A, 7D, 7E, 7Q, 7AD and 7AO;
(7) 7A, 7D, 7P, 7Y, 7Z, 7AD and 7AO;
(8) 7A, 7D, 7P, 7N, 7AD and 7AO;
(9) 7A, 7B, 7X, 7N, 7AD and 7AO;
(10) 7A, 7B, 7X, 7Y, 7Z, 7AD and 7AO;
(11) 7A, 7H, 7Q, 7V, 7AG and 7AO;
(12) 7A, 7D, 7E, 7Q, 7AC, 7AG and 7AO;
(13) 7A, 7D, 7P, 7Y, 7AC, 7AG and 7AO;

(14) 7A, 7D, 7P, 7AB, 7AF, 7AG and 7AO;

(15) 7A, 7P, 7AB, 7V and 7AO;

(16) 7A, 7B, 7M, 7AD and 7AO;

(17) 7A, 7B, 7L, 7Z, 7AD and 7AO;

(18) 7A, 7B, 7X, 7N, 7AD and 7AO;

(19) 7A, 7B, 7X, 7Y, 7Z, 7AD and 7AO;

(20) 7A, 7B, 7C, 7U and 7AO;

(21) 7A, 7B, 7C, 7T, 7AG and 7AO;

(22) 7A, 7B, 7C, 7AE, 7V and 7AO;

(23) 7A, 7B, 7C, 7AE, 7AF, 7AG and 7AO;

(24) 7A, 7H, 7Q and 7AR;

(25) 7A, 7D, 7E, 7Q and 7AR;

(26) 7A, 7D, 7P, 7Y and 7AR;

(27) 7A, 7B, 7X, 7Y and 7AR;

(28) 7A, 7B, 7L and 7AR;

(29) 7A, 7H, 7Q, 7AC and 7AQ;

(30) 7A, 7D, 7E, 7Q, 7AC and 7AQ;

(31) 7A, 7D, 7P, 7Y, 7AC and 7AQ;

(32) 7A, 7D, 7P, 7AB, 7AF and 7AQ;

(33) 7A, 7B, 7L, 7AC and 7AQ;

(34) 7A, 7B, 7X, 7Y, 7AC and 7AQ;

(35) 7A, 7B, 7X, 7AB, 7AF and 7AQ;

(36) 7A, 7B, 7C, 7AE, 7AF and 7AQ;

(37) 7A, 7B, 7C, 7T and 7AQ;

(38) 7A, 7H, 7Q, 7AC, 7AN and 7AK

(39) 7A, 7D, 7E, 7Q, 7AC, 7AN and 7AK;

(40) 7A, 7D, 7P, 7Y, 7AC, 7AN and 7AK;

(41) 7A, 7D, 7P, 7AB, 7AF, 7AN and 7AK;

(42) 7A, 7D, 7P, 7AB, 7AM, 7AJ and 7AK;

(43) 7A, 7B, 7L, 7AC, 7AN and 7AK;

(44) 7A, 7B, 7X, 7Y, 7AC, 7AN and 7AK;

(45) 7A, 7B, 7X, 7AB, 7AF, 7AN and 7AK;

(46) 7A, 7B, 7X, 7AB, 7AM, 7AJ and 7AK;

(47) 7A, 7B, 7C, 7T, 7AN and 7AK;

(48) 7A, 7B, 7C, 7AE, 7AF, 7AN and 7AK;

(49) 7A, 7B, 7C, 7AE, 7AM, 7AJ and 7AK;

(50) 7A, 7B, 7C, 7AL, 7AP and 7AK;

(51) 7A, 7B, 7C, 7AL, 7AI, 7AJ and 7AK;

(52) 7A, 7B, 7X, 7AB, 7V and 7AO;

(53) 7A 7B, 7L, 7AC, 7AG and 7AO;

(54) 7A, 7B, 7X, 7Y, 7AC, 7AC, 7AG and 7AO;

(55) 7A, 7B, 7X, 7AB, 7AF, 7AG and 7AO;

(56) 7A, 7H, 7Q, 7AC, 7AG and 7AO;

(57) 7I, 7R, 7AD and 7AO;

(58) 7E, 7F, 7R, 7AD and 7AO;

(59) 7E, 7Q, 7Z, 7AD and 7AO;

(60) 7P, 7Y, 7Z, 7AD and 7AO;

(61) 7P, 7N, 7AD and 7AO;

(62) 7E, 7Q, 7AC, 7AG and 7AO;

(63) 7P, 7Y, 7AC, 7AG and 7AO;

(64) 7P, 7AB, 7AF, 7AG and 7AO;

(65) 7P, 7AB, 7V and 7AO;

(66) 7E, 7Q and 7AR;

(67) 7P, 7Y and 7AR;

(68) 7E, 7Q, 7AC and 7AQ;

(69) 7P, 7Y, 7AC and 7AQ;

(70) 7P, 7AB, 7AF and 7AQ;

(71) 7E, 7Q, 7AC, 7AN and 7AK;

(72) 7P, 7Y, 7AC, 7AN and 7AK;

(73) 7P, 7AB, 7AF, 7AN and 7AK;

(74) 7P, 7AB, 7AM, 7AJ and 7AK;

(75) 7AS, 7I, 7R, 7AD and 7AO;

(76) 7AS, 7E, 7F, 7R, 7AD and 7AO;

(77) 7AS, 7E, 7Q, 7AD and 7AO;

(78) 7AS, 7P, 7Y, 7Z, 7AD and 7AO;

(79) 7AS, 7P, 7N, 7AD and 7AO;

(80) 7AS, 7E, 7Q, 7AC, 7AG and 7AO;

(81) 7AS, 7P, 7Y, 7AC, 7AG and 7AO;

(82) 7AS, 7P, 7AB, 7AF, 7AG and 7AO;

(83) 7AS, 7E, 7Q and 7AR;

(84) 7AS, 7P, 7Y and 7AR;

(85) 7AS, 7E, 7Q, 7AC and 7AQ;

(86) 7AS, 7P, 7Y, 7AC and 7AQ;

(87) 7AS, 7P, 7AB, 7AF and 7AQ;

(88) 7AS, 7E, 7Q, 7AC, 7AN and 7AK;

(89) 7AS, 7P, 7Y, 7AC, 7AN and 7AK;

(90) 7AS, 7P, 7AB, 7AF, 7AN and 7AK; and

(91) 7AS, 7P, 7AB, 7AM, 7AJ and 7AK,

wherein 7A is a 3-ketoacyl-ACP synthase, wherein 7B is an acetoacetyl-ACP reductase, wherein 7C is a 3-hydroxybutyryl-ACP dehydratase, wherein 7D is an acetoacetyl-CoA:ACP transferase, wherein 7E is an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA transferase or an acetoacetyl-CoA synthetase, wherein 7F is an acetoacetate reductase (acid reducing), wherein 7H is an acetoacetyl-ACP thioesterase, wherein 7I is an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming), wherein 7J is an acetoacetyl-ACP reductase (aldehyde forming), wherein 7L is a 3-hydroxybutyryl-ACP thioesterase, wherein 7M is a 3-hydroxybutyryl-ACP reductase (aldehyde forming), wherein 7N is a 3-hydroxybutyryl-CoA reductase (aldehyde forming), wherein 7P is an acetoacetyl-CoA reductase (ketone reducing), wherein 7Q is an acetoacetate reductase (ketone reducing), wherein 7R is a 3-oxobutyraldehyde reductase (ketone reducing), wherein 7S is a 4-hydroxy-2-butanone reductase, wherein 7T is a crotonyl-ACP thioesterase, wherein 7U is a crotonyl-ACP reductase (aldehyde forming), wherein 7V is a crotonyl-CoA reductase (aldehyde forming), wherein 7X is a 3-hydroxybutyryl-CoA:ACP transferase, wherein 7Y is a 3-hydroxybutyryl-CoA hydrolase, a 3-hydroxybutyryl-CoA transferase or a 3-hydroxybutyryl-CoA synthetase, wherein 7Z is a 3-hydroxybutyrate reductase, wherein 7AB is a 3-hydroxybutyryl-CoA dehydratase, wherein 7AC is a 3-hydroxybutyrate dehydratase, wherein 7AD is a 3-hydroxybutyraldehyde dehydratase, wherein 7AE is a crotonyl-CoA:ACP transferase, wherein 7AF is a crotonyl-CoA hydrolase, a crotonyl-CoA transferase or a crotonyl-CoA synthetase, wherein 7AG is a crotonate reductase, wherein 7AI is a butryl-CoA:ACP transferase, wherein 7AJ is a butyryl-CoA transferase, a butyryl-CoA hydrolase or a butyryl-CoA synthetase, wherein 7AK is a butyrate decarboxylase, wherein 7AL is a crotonyl-ACP reductase, wherein 7AM is a crotonyl-CoA reductase, wherein 7AN is a crotonate reductase, wherein 7AO is

a crotonaldehyde decarbonylase, wherein 7AP is a butyryl-ACP thioesterase, wherein 7AQ is a crotonate decarboxylase, wherein 7AR is a 3-hydroxybutyrate decarboxylase and wherein 7AS is an acetoacetyl-CoA synthase.

59. The non-naturally occurring microbial organism of claim 58, wherein said microbial organism comprises two, three, four, five, six, seven or eight exogenous nucleic acids each encoding a propylene pathway enzyme.

60. The non-naturally occurring microbial organism of claim 59, wherein said microbial organism comprises exogenous nucleic acids encoding each of the enzymes of at least one of the pathways selected from (1)-(91).

61. The non-naturally occurring microbial organism of claim 58, wherein said at least one exogenous nucleic acid is a heterologous nucleic acid.

62. The non-naturally occurring microbial organism of claim 58, wherein said non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

63. The non-naturally occurring microbial organism of claim 58, further comprising:

(i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, a citrate lyase, a citryl-CoA synthetase, a citryl-CoA lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

(ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

(iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof.

64. The non-naturally occurring microbial organism of claim 63, wherein said microbial organism comprising (i) further comprises an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate

dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, ferredoxin, and combinations thereof.

65. The non-naturally occurring microbial organism of claim 63, wherein said microbial organism comprising (ii) further comprises an exogenous nucleic acid encoding an enzyme selected from an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, and combinations thereof.

66. The non-naturally occurring microbial orgnaism of claim 63, wherein said microbial organism comprising (i) comprises three exogenous nucleic acids encoding an ATP-citrate lyase or a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

wherein said microbial organism comprising (ii) comprises four exogenous nucleic acids encoding a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase or a phosphoenolpyruvate carboxykinase; a CO dehydrogenase; and an H_2 hydrogenase; or

wherein said microbial organism comprising (iii) comprises two exogenous nucleic acids encoding a CO dehydrogenase and an H_2 hydrogenase.

67. A method for producing propylene, comprising culturing the non-naturally occurring microbial organism of any one of claims 58-66 under conditions and for a sufficient period of time to produce propylene.

68. A process for the production of butadiene comprising:

(a) culturing by fermentation in a sufficient amount of nutrients and media the non-naturally occurring microbial organism of any one of claims 48-56 to produce crotyl alcohol; and

(b) converting crotyl alcohol produced by culturing said non-naturally occurring microbial organism to butadiene.

69. The process of claim 68, wherein step (b) is performed by chemical dehydration in the presence of a catalyst.