What is claimed is:

1. A non-naturally occurring microbial organism, comprising a microbial organism having a 1,4-butanediol (BDO) pathway comprising at least one exogenous nucleic acid encoding a BDO pathway enzyme expressed in a sufficient amount to produce BDO, wherein said microbial organism is genetically modified to express exogenous succinyl-CoA synthetase, to express exogenous alpha-ketoglutarate decarboxylase; to express exogenous succinate semialdehyde dehydrogenase and 4-hydroxybutyrate dehydrogenase and optionally 4-hydroxybutyryl-CoA/acetyl-CoA transferase; to express exogenous butyrate kinase and phosphotransbutyrylase; to express exogenous 4-hydroxybutyryl-CoA reductase; and to express exogenous 4-hydroxybutanal reductase; to express exogenous pyruvate dehydrogenase; to disrupt a gene encoding an aerobic respiratory control regulatory system; to express an exogenous NADH insensitive citrate synthase; to express exogenous phosphoenolpyruvate carboxykinase.

2. The non-naturally occurring microbial organism of claim 1, wherein the succinyl-CoA synthetase is encoded by the *Escherichia coli sucCD* genes.

3. The non-naturally occurring microbial organism of claim 1, wherein said alpha-ketoglutarate decarboxylase is encoded by the *Mycobacterium bovis sucA* gene.

4. The non-naturally occurring microbial organism of claim 1, wherein the succinate semialdehyde dehydrogenase (CoA-dependent), 4-hydroxybutyrate dehydrogenase and 4-hydroxybutyryl-CoA/acetyl-CoA transferase are encoded by *Porphyromonas gingivalis* W83 genes.

5. The non-naturally occurring microbial organism of claim 1, wherein the butyrate kinase and phosphotransbutyrylase are encoded by *Clostridium acetobutilicum buk1* and *ptb* genes.

6. The non-naturally occurring microbial organism of claim 1, wherein the 4-hydroxybutyryl-CoA reductase is encoded by *Clostridium beijerinckii ald* gene.

7. The non-naturally occurring microbial organism of claim 1, wherein the 4-hydroxybutanal reductase is encoded by *Geobacillus thermoglucosidasius adh1* gene.

8. The non-naturally occurring microbial organism of claim 1, wherein said exogenous pyruvate dehydrogenase is NADH insensitive.

9. The non-naturally occurring microbial organism of claim 1, wherein said exogenous pyruvate dehydrogenase is encoded by the *Klebsiella pneumonia lpdA* gene.

10. The non-naturally occurring microbial organism of claim 1, wherein one or more of the pyruvate dehydrogenase subunit genes of said microbial organism is under the control of a pyruvate formate lyase promoter.

11. The non-naturally occurring microbial organism of claim 1, wherein the disruption of said anaerobic respiratory control regulatory system is disruption of the *arcA* gene.

12. The non-naturally occurring microbial organism of claim 1, further comprising disruption of a gene encoding malate dehydrogenase.

13. The non-naturally occurring microbial organism of claim 1, wherein NADH insensitive citrate synthase is encoded by *gltA*.

14. The non-naturally occurring microbial organism of claim 1, wherein said NADH insensitive citrate synthase is encoded by an R163L mutant of *gltA*.

15. The non-naturally occurring microbial organism of claim 1, wherein said phosphoenolpyruvate carboxykinase is encoded by an *Haemophilus influenza* phosphoenolpyruvate carboxykinase gene.

16. The non-naturally occurring microbial organism of claim 1, wherein one or more genes encoding said exogenously expressed enzymes are integrated into the *fimD* locus of the host organism.

17. The non-naturally occurring microbial organism of claim 1, wherein said organism expresses a non-phosphotransferase sucrose uptake system.

18. The non-naturaly occurring microbial organism of claim 1, wherein said organism further comprises disruption of endogenous lactate dehydrogenase, alcohol dehydrogenase and pyruvate formate lyase.

19. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises 4-hydroxybutanoate dehydrogenase, succinyl-CoA synthetase, CoA-dependent succinic semialdehyde dehydrogenase, 4-hydroxybutyrate:CoA transferase, 4-butyrate kinase, phosphotransbutyrylase, alpha-ketoglutarate decarboxylase, aldehyde dehydrogenase, alcohol dehydrogenase or an aldehyde/alcohol dehydrogenase.

20. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises 4-aminobutyrate CoA transferase, 4-aminobutyryl-CoA hydrolase, 4-aminobutyrate-CoA ligase, 4-aminobutyryl-CoA oxidoreductase (deaminating), 4-aminobutyryl-CoA transaminase, or 4-hydroxybutyryl-CoA dehydrogenase.

21. The non-naturally occurring microbial organism of claim 20, wherein said BDO pathway further comprises 4-hydroxybutyryl-CoA reductase (alcohol forming), 4-hydroxybutyryl-CoA reductase, or 1,4-butanediol dehydrogenase

22. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises 4-aminobutyrate CoA transferase, 4-aminobutyryl-CoA hydrolase, 4-aminobutyrate-CoA ligase, 4-aminobutyryl-CoA reductase (alcohol forming), 4-aminobutyryl-CoA reductase, 4-aminobutan-1-ol dehydrogenase, 4-aminobutan-1-ol oxidoreductase (deaminating) or 4-aminobutan-1-ol transaminase.

23. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises 4-aminobutyrate kinase, 4-aminobutyraldehyde dehydrogenase (phosphorylating), 4-aminobutan-1-ol dehydrogenase, 4-aminobutan-1-ol oxidoreductase (deaminating), 4-aminobutan-1-ol transaminase, [(4-aminobutanolyl)oxy]phosphonic acid oxidoreductase (deaminating), [(4-aminobutanolyl)oxy]phosphonic acid transaminase, 4-hydroxybutyryl-phosphate dehydrogenase, or 4-hydroxybutyraldehyde dehydrogenase (phosphorylating).

24. The non-naturally occurring microbial organism of claim 23, wherein said BDO pathway further comprises 1,4-butanediol dehydrogenase.

25. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises alpha-ketoglutarate 5-kinase, 2,5-dioxopentanoic semialdehyde dehydrogenase (phosphorylating), 2,5-dioxopentanoic acid reductase, alpha-ketoglutarate CoA transferase, alpha-ketoglutaryl-CoA hydrolase, alpha-ketoglutaryl-CoA ligase, alpha-ketoglutaryl-CoA reductase, 5-hydroxy-2-oxopentanoic acid dehydrogenase, alpha-ketoglutaryl-CoA reductase (alcohol forming), 5-hydroxy-2-oxopentanoic acid decarboxylase, or 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation).

26. The non-naturally occurring microbial organism of claim 25, wherein said BDO pathway further comprises 4-hydroxybutyryl-CoA reductase (alcohol forming), 4-hydroxybutyryl-CoA reductase, or 1,4-butanediol dehydrogenase.

27. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises glutamate CoA transferase, glutamyl-CoA hydrolase, glutamyl-CoA ligase, glutamate 5-kinase, glutamate-5-semialdehyde dehydrogenase (phosphorylating), glutamyl-CoA reductase, glutamate-5-semialdehyde reductase, glutamyl-CoA reductase (alcohol forming), 2-amino-5-hydroxypentanoic acid oxidoreductase (deaminating), 2-amino-5-hydroxypentanoic acid transaminase, 5-hydroxy-2-oxopentanoic acid decarboxylase, 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation).

28. The non-naturally occurring microbial organism of claim 27, wherein said BDO pathway further comprises 4-hydroxybutyryl-CoA reductase (alcohol forming), 4-hydroxybutyryl-CoA reductase, or 1,4-butanediol dehydrogenase.

29. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprising 3-hydroxybutyryl-CoA dehydrogenase, 3-hydroxybutyryl-CoA dehydratase, vinylacetyl-CoA Δ-isomerase, or 4-hydroxybutyryl-CoA dehydratase.

30. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises homoserine deaminase, homoserine CoA transferase, homoserine-CoA hydrolase, homoserine-CoA ligase, homoserine-CoA deaminase, 4-hydroxybut-2-enoyl-CoA transferase, 4-hydroxybut-2-enoyl-CoA hydrolase, 4-hydroxybut-2-enoyl-CoA ligase, 4-hydroxybut-2-enoate reductase, 4-hydroxybutyryl-CoA transferase, 4-hydroxybutyryl-CoA hydrolase, 4-hydroxybutyryl-CoA ligase, or 4-hydroxybut-2-enoyl-CoA reductase.

31. The non-naturally occurring microbial organism of claim 30, wherein said BDO pathway further comprises 4-hydroxybutyryl-CoA reductase (alcohol forming), 4-hydroxybutyryl-CoA reductase, or 1,4-butanediol dehydrogenase.

32. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises succinyl-CoA reductase (alcohol forming), 4-hydroxybutyryl-CoA hydrolase, 4-hydroxybutyryl-CoA ligase, or 4-hydroxybutanal dehydrogenase (phosphorylating).

33. The non-naturally occurring microbial organism of claim 32, wherein said BDO pathway further comprises succinyl-CoA reductase, 4-hydroxybutyrate dehydrogenase, 4-hydroxybutyryl-CoA transferase, 4-hydroxybutyrate kinase, phosphotrans-4-hydroxybutyrylase, 4-hydroxybutyryl-CoA reductase, 4-hydroxybutyryl-CoA reductase (alcohol forming), or 1,4-butanediol dehydrogenase.

34. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises glutamate dehydrogenase, 4-aminobutyrate oxidoreductase (deaminating), 4-aminobutyrate transaminase, glutamate decarboxylase, 4-hydroxybutyryl-CoA hydrolase, 4-hydroxybutyryl-CoA ligase, or 4-hydroxybutanal dehydrogenase (phosphorylating).

35. The non-naturally occurring microbial organism of claim 34, wherein said BDO pathway further comprises alpha-ketoglutarate decarboxylase, 4-hydroxybutyrate dehydrogenase, 4-hydroxybutyryl-CoA transferase, 4-hydroxybutyrate kinase, phosphotrans-4-hydroxybutyrylase, 4-hydroxybutyryl-CoA reductase, 4-hydroxybutyryl-CoA reductase (alcohol forming), or 1,4-butanediol dehydrogenase.

36. A non-naturally occurring microbial organism, comprising a microbial organism having a 1,4-butanediol (BDO) pathway comprising at least one exogenous nucleic acid encoding a BDO pathway enzyme expressed in a sufficient amount to produce BDO, wherein said microbial organism is genetically modified as in any of strains 3-20 of Table 28.

37. A method for producing 1,4-butanediol (BDO), comprising culturing the non-naturally occurring microbial organism of any of claims 1-36 under conditions and for a sufficient period of time to produce BDO.

What is claimed is:

1. A non-naturally occurring microbial organism having a 1,4-butanediol (BDO) pathway comprising BDO pathway enzymes expressed in a sufficient amount to produce BDO, wherein said microbial organism is genetically modified, and wherein said microbial organism:

(A) comprises a BDO pathway selected from:

(i) a BDO pathway comprising:

(a) alpha-ketoglutarate decarboxylase; and/or

succinyl-CoA synthetase and CoA-dependent succinate semialdehyde dehydrogenase;

(b) 4-hydroxybutyrate dehydrogenase;

(c) 4-hydroxybutyryl-CoA transferase; and/or

4-hydroxybutyrate kinase and phosphotrans-4-hydroxybutyrylase; and

(d) aldehyde dehydrogenase and alcohol dehydrogenase; and/or

aldehyde/alcohol dehydrogenase;

(ii) a BDO pathway comprising:

(a) alpha-ketoglutarate decarboxylase;

alpha-ketoglutarate dehydrogenase and CoA-dependent succinate semialdehyde dehydrogenase; and/or

glutamate:succinate semialdehyde transaminase and glutamate decarboxylase;

(b) 4-hydroxybutyrate dehydrogenase;

(c) 4-hydroxybutyryl-CoA/acetyl-CoA transferase; and/or

butyrate kinase and phosphotransbutyrylase;

(d) 4-hydroxybutyryl-CoA reductase and 4-hydroxybutanal reductase; and/or aldehyde/alcohol dehydrogenase;

(iii) a BDO pathway comprising:

(a) alpha-ketoglutarate decarboxylase;

glutamate dehydrogenase; glutamate decarboxylase; and deaminating 4-aminobutyrate oxidoreductase or 4-aminobutyrate transaminase; and/or

alpha-ketoglutarate dehydrogenase and CoA-dependent succinate semialdehyde dehydrogenase;

(b) 4-hydroxybutyrate dehydrogenase; and

(c) 4-hydroxybutyrate kinase; phosphotrans-4-hydroxybutyrylase; 4-hydroxybutyryl-CoA reductase; and 4-hydroxybutyraldehyde reductase;

4-hydroxybutyrate kinase; phosphorylating 4-hydroxybutanal dehydrogenase; and 4-hydroxybutyraldehyde reductase;

4-hydroxybutyrate kinase; phosphotrans-4-hydroxybutyrylase; and alcohol forming 4-hydroxybutyryl-CoA reductase;

4-hydroxybutyryl-CoA transferase or 4-hydroxybutyryl-CoA hydrolase or 4-hydroxybutyryl-CoA ligase; 4-hydroxybutyryl-CoA reductase; and 4-hydroxybutyraldehyde reductase; and/or

4-hydroxybutyryl-CoA transferase or 4-hydroxybutyryl-CoA hydrolase or 4-hydroxybutyryl-CoA ligase; and alcohol forming 4-hydroxybutyryl-CoA reductase;

(iv) a BDO pathway comprising:

(a) glutamate CoA transferase or glutamyl-CoA hydrolase or glutamyl-CoA ligase; glutamyl-CoA reductase; and glutamate-5-semialdehyde reductase;

glutamate CoA transferase or glutamyl-CoA hydrolase or glutamyl-CoA ligase; and alcohol forming glutamyl-CoA reductase; and/or

glutamate 5-kinase; phosphorylating glutamate-5-semialdehyde dehydrogenase; and glutamate-5-semialdehyde reductase;

(b) deaminating 2-amino-5-hydroxypentanoic acid oxidoreductase or 2-amino-5-hydroxypentanoic acid transaminase; and

(c) 5-hydroxy-2-oxopentanoic acid decarboxylase; and 4-hydroxybutyraldehyde reductase;

decarboxylating 5-hydroxy-2-oxopentanoic acid dehydrogenase; 4-hydroxybutyryl-CoA reductase; and 4-hydroxybutyraldehyde reductase; and/or

decarboxylating 5-hydroxy-2-oxopentanoic acid dehydrogenase and alcohol forming 4-hydroxybutyryl-CoA reductase;

(v) a BDO pathway comprising 4-hydroxybutanoate dehydrogenase, succinyl-CoA synthetase, CoA-dependent succinic semialdehyde dehydrogenase, 4-hydroxybutyrate:CoA transferase, 4-butyrate kinase, phosphotransbutyrylase, alpha-ketoglutarate decarboxylase, aldehyde dehydrogenase, alcohol dehydrogenase or an aldehyde/alcohol dehydrogenase;

(vi) a BDO pathway comprising 4-aminobutyrate CoA transferase, 4-aminobutyryl-CoA hydrolase, 4-aminobutyrate-CoA ligase, 4-aminobutyryl-CoA oxidoreductase (deaminating), 4-aminobutyryl-CoA transaminase, or 4-hydroxybutyryl-CoA dehydrogenase;

(vii) a BDO pathway comprising 4-aminobutyrate CoA transferase, 4-aminobutyryl-CoA hydrolase, 4-aminobutyrate-CoA ligase, 4-aminobutyryl-CoA reductase (alcohol forming), 4-aminobutyryl-CoA reductase, 4-aminobutan-1-ol dehydrogenase, 4-aminobutan-1-ol oxidoreductase (deaminating) or 4-aminobutan-1-ol transaminase;

(viii) a BDO pathway comprising 4-aminobutyrate kinase, 4-aminobutyraldehyde dehydrogenase (phosphorylating), 4-aminobutan-1-ol dehydrogenase, 4-aminobutan-1-ol oxidoreductase (deaminating), 4-aminobutan-1-ol transaminase, [(4-aminobutanolyl)oxy]phosphonic acid oxidoreductase (deaminating), [(4-

aminobutanolyl)oxy]phosphonic acid transaminase, 4-hydroxybutyryl-phosphate dehydrogenase, or 4-hydroxybutyraldehyde dehydrogenase (phosphorylating);

(ix) a BDO pathway comprising alpha-ketoglutarate 5-kinase, 2,5-dioxopentanoic semialdehyde dehydrogenase (phosphorylating), 2,5-dioxopentanoic acid reductase, alpha-ketoglutarate CoA transferase, alpha-ketoglutaryl-CoA hydrolase, alpha-ketoglutaryl-CoA ligase, alpha-ketoglutaryl-CoA reductase, 5-hydroxy-2-oxopentanoic acid dehydrogenase, alpha-ketoglutaryl-CoA reductase (alcohol forming), 5-hydroxy-2-oxopentanoic acid decarboxylase, or 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation);

(x) a BDO pathway comprising glutamate CoA transferase, glutamyl-CoA hydrolase, glutamyl-CoA ligase, glutamate 5-kinase, glutamate-5-semialdehyde dehydrogenase (phosphorylating), glutamyl-CoA reductase, glutamate-5-semialdehyde reductase, glutamyl-CoA reductase (alcohol forming), 2-amino-5-hydroxypentanoic acid oxidoreductase (deaminating), 2-amino-5-hydroxypentanoic acid transaminase, 5-hydroxy-2-oxopentanoic acid decarboxylase, 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation);

(xi) a BDO pathway comprising 3-hydroxybutyryl-CoA dehydrogenase, 3-hydroxybutyryl-CoA dehydratase, vinylacetyl-CoA Δ-isomerase, or 4-hydroxybutyryl-CoA dehydratase;

(xii) a BDO pathway comprising homoserine deaminase, homoserine CoA transferase, homoserine-CoA hydrolase, homoserine-CoA ligase, homoserine-CoA deaminase, 4-hydroxybut-2-enoyl-CoA transferase, 4-hydroxybut-2-enoyl-CoA hydrolase, 4-hydroxybut-2-enoyl-CoA ligase, 4-hydroxybut-2-enoate reductase, 4-hydroxybutyryl-CoA transferase, 4-hydroxybutyryl-CoA hydrolase, 4-hydroxybutyryl-CoA ligase, or 4-hydroxybut-2-enoyl-CoA reductase;

(xiii) a BDO pathway comprising succinyl-CoA reductase (alcohol forming), 4-hydroxybutyryl-CoA hydrolase, 4-hydroxybutyryl-CoA ligase, or 4-hydroxybutanal dehydrogenase (phosphorylating); and

(xiv) a BDO pathway comprising glutamate dehydrogenase, 4-aminobutyrate oxidoreductase (deaminating), 4-aminobutyrate transaminase, glutamate decarboxylase, 4-hydroxybutyryl-CoA hydrolase, 4-hydroxybutyryl-CoA ligase, or 4-hydroxybutanal dehydrogenase (phosphorylating); and

(B) comprises disruption of a gene encoding an aerobic respiratory control regulatory system; or expresses an exogenous NADH insensitive citrate synthase.

2. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises:

(a) alpha-ketoglutarate decarboxylase; and/or

succinyl-CoA synthetase and CoA-dependent succinate semialdehyde dehydrogenase;

(b) 4-hydroxybutyrate dehydrogenase;

(c) 4-hydroxybutyryl-CoA transferase; and/or

4-hydroxybutyrate kinase and phosphotrans-4-hydroxybutyrylase; and

(d) aldehyde dehydrogenase and alcohol dehydrogenase; and/or

aldehyde/alcohol dehydrogenase.

3. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises:

(a) alpha-ketoglutarate decarboxylase;

alpha-ketoglutarate dehydrogenase and CoA-dependent succinate semialdehyde dehydrogenase; and/or

glutamate:succinate semialdehyde transaminase and glutamate decarboxylase;

(b) 4-hydroxybutyrate dehydrogenase;

(c) 4-hydroxybutyryl-CoA/acetyl-CoA transferase; and/or

butyrate kinase and phosphotransbutyrylase;

(d) 4-hydroxybutyryl-CoA reductase and 4-hydroxybutanal reductase; and/or

aldehyde/alcohol dehydrogenase.

4. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises:

(a) alpha-ketoglutarate decarboxylase;

glutamate dehydrogenase; glutamate decarboxylase; and deaminating 4-aminobutyrate oxidoreductase or 4-aminobutyrate transaminase; and/or

alpha-ketoglutarate dehydrogenase and CoA-dependent succinate semialdehyde dehydrogenase;

(b) 4-hydroxybutyrate dehydrogenase; and

(c) 4-hydroxybutyrate kinase; phosphotrans-4-hydroxybutyrylase; 4-hydroxybutyryl-CoA reductase; and 4-hydroxybutyraldehyde reductase;

4-hydroxybutyrate kinase; phosphorylating 4-hydroxybutanal dehydrogenase; and 4-hydroxybutyraldehyde reductase;

4-hydroxybutyrate kinase; phosphotrans-4-hydroxybutyrylase; and alcohol forming 4-hydroxybutyryl-CoA reductase;

4-hydroxybutyryl-CoA transferase or 4-hydroxybutyryl-CoA hydrolase or 4-hydroxybutyryl-CoA ligase; 4-hydroxybutyryl-CoA reductase; and 4-hydroxybutyraldehyde reductase; and/or

4-hydroxybutyryl-CoA transferase or 4-hydroxybutyryl-CoA hydrolase or 4-hydroxybutyryl-CoA ligase; and alcohol forming 4-hydroxybutyryl-CoA reductase.

5. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises:

(a) glutamate CoA transferase or glutamyl-CoA hydrolase or glutamyl-CoA ligase; glutamyl-CoA reductase; and glutamate-5-semialdehyde reductase;

glutamate CoA transferase or glutamyl-CoA hydrolase or glutamyl-CoA ligase; and alcohol forming glutamyl-CoA reductase; and/or

glutamate 5-kinase; phosphorylating glutamate-5-semialdehyde dehydrogenase; and glutamate-5-semialdehyde reductase;

(b) deaminating 2-amino-5-hydroxypentanoic acid oxidoreductase or 2-amino-5-hydroxypentanoic acid transaminase; and

(c) 5-hydroxy-2-oxopentanoic acid decarboxylase; and 4-hydroxybutyraldehyde reductase;

decarboxylating 5-hydroxy-2-oxopentanoic acid dehydrogenase; 4-hydroxybutyryl-CoA reductase; and 4-hydroxybutyraldehyde reductase; and/or

decarboxylating 5-hydroxy-2-oxopentanoic acid dehydrogenase and alcohol forming 4-hydroxybutyryl-CoA reductase.

6. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises 4-hydroxybutanoate dehydrogenase, succinyl-CoA synthetase, CoA-dependent succinic semialdehyde dehydrogenase, 4-hydroxybutyrate:CoA transferase, 4-butyrate kinase, phosphotransbutyrylase, alpha-ketoglutarate decarboxylase, aldehyde dehydrogenase, alcohol dehydrogenase or an aldehyde/alcohol dehydrogenase.

7. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises 4-aminobutyrate CoA transferase, 4-aminobutyryl-CoA hydrolase, 4-aminobutyrate-CoA ligase, 4-aminobutyryl-CoA oxidoreductase (deaminating), 4-aminobutyryl-CoA transaminase, or 4-hydroxybutyryl-CoA dehydrogenase.

8. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises 4-aminobutyrate CoA transferase, 4-aminobutyryl-CoA hydrolase, 4-aminobutyrate-CoA ligase, 4-aminobutyryl-CoA reductase (alcohol forming), 4-aminobutyryl-CoA reductase, 4-aminobutan-1-ol dehydrogenase, 4-aminobutan-1-ol oxidoreductase (deaminating) or 4-aminobutan-1-ol transaminase.

9. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises 4-aminobutyrate kinase, 4-aminobutyraldehyde dehydrogenase (phosphorylating), 4-aminobutan-1-ol dehydrogenase, 4-aminobutan-1-ol oxidoreductase (deaminating), 4-aminobutan-1-ol transaminase, [(4-aminobutanolyl)oxy]phosphonic acid oxidoreductase (deaminating), [(4-aminobutanolyl)oxy]phosphonic acid transaminase, 4-hydroxybutyryl-phosphate dehydrogenase, or 4-hydroxybutyraldehyde dehydrogenase (phosphorylating).

10. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises alpha-ketoglutarate 5-kinase, 2,5-dioxopentanoic semialdehyde dehydrogenase (phosphorylating), 2,5-dioxopentanoic acid reductase, alpha-ketoglutarate CoA transferase, alpha-ketoglutaryl-CoA hydrolase, alpha-ketoglutaryl-CoA ligase, alpha-ketoglutaryl-CoA reductase, 5-hydroxy-2-oxopentanoic acid dehydrogenase, alpha-ketoglutaryl-CoA reductase (alcohol forming), 5-hydroxy-2-oxopentanoic acid decarboxylase, or 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation).

11. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises glutamate CoA transferase, glutamyl-CoA hydrolase, glutamyl-CoA ligase, glutamate 5-kinase, glutamate-5-semialdehyde dehydrogenase (phosphorylating), glutamyl-CoA reductase, glutamate-5-semialdehyde reductase, glutamyl-CoA reductase (alcohol forming), 2-amino-5-hydroxypentanoic acid oxidoreductase (deaminating), 2-amino-5-hydroxypentanoic acid transaminase, 5-hydroxy-2-oxopentanoic acid decarboxylase, 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation).

12. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprising 3-hydroxybutyryl-CoA dehydrogenase, 3-hydroxybutyryl-CoA dehydratase, vinylacetyl-CoA Δ-isomerase, or 4-hydroxybutyryl-CoA dehydratase.

13. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises homoserine deaminase, homoserine CoA transferase, homoserine-CoA hydrolase, homoserine-CoA ligase, homoserine-CoA deaminase, 4-hydroxybut-2-enoyl-CoA transferase, 4-hydroxybut-2-enoyl-CoA hydrolase, 4-hydroxybut-2-enoyl-CoA ligase, 4-hydroxybut-2-enoate reductase, 4-hydroxybutyryl-CoA transferase, 4-hydroxybutyryl-CoA hydrolase, 4-hydroxybutyryl-CoA ligase, or 4-hydroxybut-2-enoyl-CoA reductase.

14. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises succinyl-CoA reductase (alcohol forming), 4-hydroxybutyryl-CoA hydrolase, 4-hydroxybutyryl-CoA ligase, or 4-hydroxybutanal dehydrogenase (phosphorylating).

15. The non-naturally occurring microbial organism of claim 1, wherein said BDO pathway comprises glutamate dehydrogenase, 4-aminobutyrate oxidoreductase (deaminating), 4-aminobutyrate transaminase, glutamate decarboxylase, 4-hydroxybutyryl-CoA hydrolase, 4-hydroxybutyryl-CoA ligase, or 4-hydroxybutanal dehydrogenase (phosphorylating).

16. The non-naturally occurring microbial organism of claim 1, wherein the succinyl-CoA synthetase is encoded by the *Escherichia coli sucCD* genes.

17. The non-naturally occurring microbial organism of claim 1, wherein said alpha-ketoglutarate decarboxylase is encoded by the *Mycobacterium bovis sucA* gene.

18. The non-naturally occurring microbial organism of claim 1, wherein the succinate semialdehyde dehydrogenase (CoA-dependent), 4-hydroxybutyrate dehydrogenase and 4-hydroxybutyryl-CoA/acetyl-CoA transferase are encoded by *Porphyromonas gingivalis* W83 genes.

19. The non-naturally occurring microbial organism of claim 1, wherein the butyrate kinase and phosphotransbutyrylase are encoded by *Clostridium acetobutilicum buk1* and *ptb* genes.

20. The non-naturally occurring microbial organism of claim 1, wherein the 4-hydroxybutyryl-CoA reductase is encoded by *Clostridium beijerinckii ald* gene.

21. The non-naturally occurring microbial organism of claim 1, wherein the 4-hydroxybutanal reductase is encoded by *Geobacillus thermoglucosidasius adh1* gene.

22. The non-naturally occurring bacterial organism of claim 1, wherein said microbial organism is genetically modified to express exogenous pyruvate dehydrogenase.

23. The non-naturally occurring microbial organism of claim 1, wherein said exogenous pyruvate dehydrogenase is NADH insensitive.

24. The non-naturally occurring microbial organism of claim 1, wherein said exogenous pyruvate dehydrogenase is encoded by the *Klebsiella pneumonia lpdA* gene.

25. The non-naturally occurring microbial organism of claim 1, wherein one or more of the pyruvate dehydrogenase subunit genes of said microbial organism is under the control of a pyruvate formate lyase promoter.

26. The non-naturally occurring microbial organism of claim 1, wherein the disruption of said anaerobic respiratory control regulatory system is disruption of the *arcA* gene.

27. The non-naturally occurring microbial organism of claim 1, further comprising disruption of a gene encoding malate dehydrogenase.

28. The non-naturally occurring microbial organism of claim 1, wherein NADH insensitive citrate synthase is encoded by *gltA*.

29. The non-naturally occurring microbial organism of claim 1, wherein said NADH insensitive citrate synthase is encoded by an R163L mutant of *gltA*.

30. The non-naturally occurring microbial organism of claim 1, wherein said microbial organism is genetically modified to express exogenous phosphoenolpyruvate carboxykinase.

31. The non-naturally occurring microbial organism of claim 30, wherein said phosphoenolpyruvate carboxykinase is encoded by an *Haemophilus influenza* phosphoenolpyruvate carboxykinase gene.

32. The non-naturally occurring microbial organism of claim 1, wherein one or more genes encoding said exogenously expressed enzymes are integrated into the *fimD* locus of the host organism.

33. The non-naturally occurring microbial organism of claim 1, wherein said organism expresses a non-phosphotransferase sucrose uptake system.

34. The non-naturaly occurring microbial organism of claim 1, wherein said organism further comprises disruption of endogenous lactate dehydrogenase, alcohol dehydrogenase and pyruvate formate lyase.

35. The non-naturally occurring microbial organism of any one of claims 7, 10, 11 or 13, wherein said BDO pathway further comprises 4-hydroxybutyryl-CoA reductase (alcohol forming), 4-hydroxybutyryl-CoA reductase, or 1,4-butanediol dehydrogenase.

36. The non-naturally occurring microbial organism of claim 9, wherein said BDO pathway further comprises 1,4-butanediol dehydrogenase.

37. The non-naturally occurring microbial organism of claim 14, wherein said BDO pathway further comprises succinyl-CoA reductase, 4-hydroxybutyrate dehydrogenase, 4-hydroxybutyryl-CoA transferase, 4-hydroxybutyrate kinase, phosphotrans-4-hydroxybutyrylase, 4-hydroxybutyryl-CoA reductase, 4-hydroxybutyryl-CoA reductase (alcohol forming), or 1,4-butanediol dehydrogenase.

38. The non-naturally occurring microbial organism of claim 15, wherein said BDO pathway further comprises alpha-ketoglutarate decarboxylase, 4-hydroxybutyrate dehydrogenase, 4-hydroxybutyryl-CoA transferase, 4-hydroxybutyrate kinase, phosphotrans-4-hydroxybutyrylase, 4-hydroxybutyryl-CoA reductase, 4-hydroxybutyryl-CoA reductase (alcohol forming), or 1,4-butanediol dehydrogenase.

39. A method for producing 1,4-butanediol (BDO), comprising culturing the non-naturally occurring microbial organism of any of claims 1-38 under conditions and for a sufficient period of time to produce BDO.

40. The method of claim 39, further comprising the step of isolating the 1,4-BDO.

41. The method of claim 40, wherein the 1,4-BDO is isolated by distillation.