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:

(a) 4-aminobutyrate CoA transferase;

4-aminobutyryl-CoA hydrolase; or

4-aminobutyrate-CoA ligase;

(b) 4-aminobutyryl-CoA oxidoreductase (deaminating); or

4-aminobutyryl-CoA transaminase;

(c) 4-hydroxybutyryl-CoA dehydrogenase; and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase;

(vi) a BDO pathway comprising:

(a) 4-aminobutyrate CoA transferase;

4-aminobutyryl-CoA hydrolase; or

4-aminobutyrate-CoA ligase;

(b) 4-aminobutyryl-CoA reductase (alcohol forming); or

4-aminobutyryl-CoA reductase and 4-aminobutan-1-ol dehydrogenase;

(c) 4-aminobutan-1-ol oxidoreductase (deaminating) or 4-aminobutan-1-ol transaminase; and

(d) 1,4-butanediol dehydrogenase;

(vii) a BDO pathway comprising;

(a) 4-aminobutyrate kinase;

(b) 4-aminobutyraldehyde dehydrogenase (phosphorylating);

(c) 4-aminobutan-1-ol dehydrogenase;

(d) 4-aminobutan-1-ol oxidoreductase (deaminating); or

4-aminobutan-1-ol transaminase; and

(e) 1,4-butandiol dehydrogenase;

(viii) a BDO pathway comprising;

(a) 4-aminobutyrate kinase;

(b) [(4-aminobutanolyl)oxy]phosphonic acid oxidoreductase (deaminating); or [(4-aminobutanolyl)oxy]phosphonic acid transaminase;

(c) 4-hydroxybutyryl-phosphate dehydrogenase;

(d) 4-hydroxybutyraldehyde dehydrogenase (phosphorylating); and

(e) 1,4-butandiol dehydrogenase;

(ix) a BDO pathway comprising:

(a) alpha-ketoglutarate 5-kinase;

(b) 2,5-dioxopentanoic semialdehyde dehydrogenase (phosphorylating);

(c) 2,5-dioxopentanoic acid reductase;

(d) 5-hydroxy-2-oxopentanoic acid decarboxylase; and

(e) 1,4-butanediol dehydrogenase;

(x) a BDO pathway comprising:

(a) alpha-ketoglutarate CoA transferase;

alpha-ketoglutaryl-CoA hydrolase; or

alpha-ketoglutaryl-CoA ligase;

(b) alpha-ketoglutaryl-CoA reductase and 5-hydroxy-2-oxopentanoic acid dehydrogenase; or

alpha-ketoglutaryl-CoA reductase (alcohol forming);

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

(d) 1,4-butanediol dehydrogenase;

(xi) a BDO pathway comprising:

(a) alpha-ketoglutarate 5-kinase;

(b) 2,5-dioxopentanoic semialdehyde dehydrogenase (phosphorylating);

(c) 2,5-dioxopentanoic acid reductase;

(d) 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation); and

(e) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase;

(xii) a BDO pathway comprising:

(a) alpha-ketoglutarate CoA transferase;

alpha-ketoglutaryl-CoA hydrolase; or

alpha-ketoglutaryl-CoA ligase;

(b) alpha-ketoglutaryl-CoA reductase and 5-hydroxy-2-oxopentanoic acid dehydrogenase; or

alpha-ketoglutaryl-CoA reductase (alcohol forming);

(c) 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation); and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase;

(xiii) a BDO pathway comprising:

(a) glutamate CoA transferase;

glutamyl-CoA hydrolase; or

glutamyl-CoA ligase;

(b) glutamyl-CoA reductase and glutamate-5-semialdehyde reductase; or

glutamyl-CoA reductase (alcohol forming);

(c) 2-amino-5-hydroxypentanoic acid oxidoreductase (deaminating); or

2-amino-5-hydroxypentanoic acid transaminase;

(d) 5-hydroxy-2-oxopentanoic acid decarboxylase; and

(e) 1,4-butanediol dehydrogenase;

(xiv) a BDO pathway comprising:

(a) glutamate 5-kinase;

(b) glutamate-5-semialdehyde dehydrogenase (phosphorylating);

(c) glutamate-5-semialdehyde reductase;

(d) 2-amino-5-hydroxypentanoic acid oxidoreductase (deaminating); or

2-amino-5-hydroxypentanoic acid transaminase;

(e) 5-hydroxy-2-oxopentanoic acid decarboxylase; and

(f) 1,4-butanediol dehydrogenase;

(xv) a BDO pathway comprising:

(a) glutamate CoA transferase;

glutamyl-CoA hydrolase;

glutamyl-CoA ligase;

(b) glutamyl-CoA reductase and glutamate-5-semialdehyde reductase; or

glutamyl-CoA reductase (alcohol forming);

(c) 2-amino-5-hydroxypentanoic acid oxidoreductase (deaminating); or

2-amino-5-hydroxypentanoic acid transaminase;

(d) 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation); and

(e) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase;

(xvi) a BDO pathway comprising:

(a) glutamate 5-kinase;

(b) glutamate-5-semialdehyde dehydrogenase (phosphorylating);

(c) glutamate-5-semialdehyde reductase;

(d) 2-amino-5-hydroxypentanoic acid oxidoreductase (deaminating); or

2-amino-5-hydroxypentanoic acid transaminase;

(e) 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation); and

(f) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase;

(xvii) a BDO pathway comprising:

(a) 3-hydroxybutyryl-CoA dehydrogenase;

(b) 3-hydroxybutyryl-CoA dehydratase;

(c) vinylacetyl-CoA Δ-isomerase; and

(d) 4-hydroxybutyryl-CoA dehydratase;

(xviii) a BDO pathway comprising:

(a) homoserine deaminase;

(b) 4-hydroxybut-2-enoyl-CoA transferase;

4-hydroxybut-2-enoyl-CoA hydrolase; or

4-hydroxybut-2-enoyl-CoA ligase;

(c) 4-hydroxybut-2-enoyl-CoA reductase; and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase;

(xix) a BDO pathway comprising:

(a) homoserine deaminase;

(b) 4-hydroxybut-2-enoate reductase;

(c) 4-hydroxybutyryl-CoA transferase;

4-hydroxybutyryl-CoA hydrolase; or

4-hydroxybutyryl-CoA ligase; and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase;

(xx) a BDO pathway comprising:

(a) homoserine CoA transferase;

homoserine-CoA hydrolase; or

homoserine-CoA ligase;

(b) homoserine-CoA deaminase;

(c) 4-hydroxybut-2-enoyl-CoA reductase; and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase;

(xxi) a BDO pathway comprising:

(a) succinyl-CoA reductase and 4-hydroxybutyrate dehydrogenase; or

succinyl-CoA reductase (alcohol forming);

(b) 4-hydroxybutyryl-CoA transferase;

4-hydroxybutyryl-CoA hydrolase; or

4-hydroxybutyryl-CoA ligase; and

(c) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase;

(xxii) a BDO pathway comprising:

(a) succinyl-CoA reductase and 4-hydroxybutyrate dehydrogenase; or

succinyl-CoA reductase (alcohol forming);

(b) 4-hydroxybutyrate kinase;

(c) phosphotrans-4-hydroxybutyrylase; and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase;

(xxiii) a BDO pathway comprising:

(a) succinyl-CoA reductase and 4-hydroxybutyrate dehydrogenase; or

succinyl-CoA reductase (alcohol forming);

(b) 4-hydroxybutyrate kinase;

(c) 4-hydroxybutanal dehydrogenase (phosphorylating); and

(d) 1,4-butanediol dehydrogenase;

(xxiv) a BDO pathway comprising:

(a) glutamate dehydrogenase;

(b) glutamate decarboxylase;

(c) 4-aminobutyrate oxidoreductase (deaminating); or

4-aminobutyrate transaminase;

(d) 4-hydroxybutyrate dehydogenase;

(e) 4-hydroxybutyryl-CoA transferase;

4-hydroxybutyryl-CoA hydrolase; or

4-hydroxybutyryl-CoA ligase; and

(f) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase;

(xxv) a BDO pathway comprising:

(a) alpha-ketoglutarate decarboxylase;

(b) 4-hydroxybutyrate dehydogenase;

(c) 4-hydroxybutyryl-CoA transferase;

4-hydroxybutyryl-CoA hydrolase;

4-hydroxybutyryl-CoA ligase; and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase;

(xxvi) a BDO pathway comprising:

(a) glutamate dehydrogenase;

(b) glutamate decarboxylase;

(c) 4-aminobutyrate oxidoreductase (deaminating); or

4-aminobutyrate transaminase;

(d) 4-hydroxybutyrate dehydogenase;

(e) 4-hydroxybutyrate kinase;

(f) phosphotrans-4-hydroxybutyrylase; and

(g) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase;

(xxvii) a BDO pathway comprising:

(a) alpha-ketoglutarate decarboxylase;

(b) 4-hydroxybutyrate dehydogenase;

(c) 4-hydroxybutyrate kinase;

(d) 4-hydroxybutanal dehydrogenase (phosphorylating); and

(e) 1,4-butanediol dehydrogenase; 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;

(a) 4-aminobutyrate CoA transferase;

4-aminobutyryl-CoA hydrolase; or

4-aminobutyrate-CoA ligase;

(b) 4-aminobutyryl-CoA oxidoreductase (deaminating); or

4-aminobutyryl-CoA transaminase;

(c) 4-hydroxybutyryl-CoA dehydrogenase; and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase.

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

(a) 4-aminobutyrate CoA transferase;

4-aminobutyryl-CoA hydrolase; or

4-aminobutyrate-CoA ligase;

(b) 4-aminobutyryl-CoA reductase (alcohol forming); or

4-aminobutyryl-CoA reductase and , 4-aminobutan-1-ol dehydrogenase;

(c) 4-aminobutan-1-ol oxidoreductase (deaminating) or 4-aminobutan-1-ol transaminase; and

(d) 1,4-butanediol dehydrogenase.

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

(a) 4-aminobutyrate kinase;

(b) 4-aminobutyraldehyde dehydrogenase (phosphorylating);

(c) 4-aminobutan-1-ol dehydrogenase;

(d) 4-aminobutan-1-ol oxidoreductase (deaminating); or

4-aminobutan-1-ol transaminase; and

(e) 1,4-butandiol dehydrogenase.

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

(a) 4-aminobutyrate kinase;

(b) [(4-aminobutanolyl)oxy]phosphonic acid oxidoreductase (deaminating); or

[(4-aminobutanolyl)oxy]phosphonic acid transaminase;

(c) 4-hydroxybutyryl-phosphate dehydrogenase;

(d) 4-hydroxybutyraldehyde dehydrogenase (phosphorylating); and

(e) 1,4-butandiol dehydrogenase.

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

(a) alpha-ketoglutarate 5-kinase;

(b) 2,5-dioxopentanoic semialdehyde dehydrogenase (phosphorylating);

(c) 2,5-dioxopentanoic acid reductase;

(d) 5-hydroxy-2-oxopentanoic acid decarboxylase; and

(e) 1,4-butanediol dehydrogenase.

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

(a) alpha-ketoglutarate CoA transferase;

alpha-ketoglutaryl-CoA hydrolase; or

alpha-ketoglutaryl-CoA ligase;

(b) alpha-ketoglutaryl-CoA reductase and 5-hydroxy-2-oxopentanoic acid dehydrogenase; or

alpha-ketoglutaryl-CoA reductase (alcohol forming);

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

(d) 1,4-butanediol dehydrogenase.

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

(a) alpha-ketoglutarate 5-kinase;

(b) 2,5-dioxopentanoic semialdehyde dehydrogenase (phosphorylating);

(c) 2,5-dioxopentanoic acid reductase;

(d) 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation); and

(e) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase.

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

(a) alpha-ketoglutarate CoA transferase;

alpha-ketoglutaryl-CoA hydrolase;

alpha-ketoglutaryl-CoA ligase;

(b) alpha-ketoglutaryl-CoA reductase and 5-hydroxy-2-oxopentanoic acid dehydrogenase; or

alpha-ketoglutaryl-CoA reductase (alcohol forming);

(c) 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation); and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase.

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

(a) glutamate CoA transferase;

glutamyl-CoA hydrolase; or

glutamyl-CoA ligase;

(b) glutamyl-CoA reductase and glutamate-5-semialdehyde reductase; or

glutamyl-CoA reductase (alcohol forming);

(c) 2-amino-5-hydroxypentanoic acid oxidoreductase (deaminating); or

2-amino-5-hydroxypentanoic acid transaminase;

(d) 5-hydroxy-2-oxopentanoic acid decarboxylase; and

(e) 1,4-butanediol dehydrogenase.

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

(a) glutamate 5-kinase;

(b) glutamate-5-semialdehyde dehydrogenase (phosphorylating);

(c) glutamate-5-semialdehyde reductase;

(d) 2-amino-5-hydroxypentanoic acid oxidoreductase (deaminating); or

2-amino-5-hydroxypentanoic acid transaminase;

(e) 5-hydroxy-2-oxopentanoic acid decarboxylase; and

(f) 1,4-butanediol dehydrogenase.

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

(a) glutamate CoA transferase;

glutamyl-CoA hydrolase;

glutamyl-CoA ligase;

(b) glutamyl-CoA reductase and glutamate-5-semialdehyde reductase; or

glutamyl-CoA reductase (alcohol forming);

(c) 2-amino-5-hydroxypentanoic acid oxidoreductase (deaminating); or

2-amino-5-hydroxypentanoic acid transaminase;

(d) 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation); and

(e) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase.

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

(a) glutamate 5-kinase;

(b) glutamate-5-semialdehyde dehydrogenase (phosphorylating);

(c) glutamate-5-semialdehyde reductase;

(d) 2-amino-5-hydroxypentanoic acid oxidoreductase (deaminating); or

2-amino-5-hydroxypentanoic acid transaminase;

(e) 5-hydroxy-2-oxopentanoic acid dehydrogenase (decarboxylation); and

(f) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase.

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

(a) 3-hydroxybutyryl-CoA dehydrogenase;

(b) 3-hydroxybutyryl-CoA dehydratase;

(c) vinylacetyl-CoA Δ-isomerase; and

(d) 4-hydroxybutyryl-CoA dehydratase.

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

(a) homoserine deaminase;

(b) 4-hydroxybut-2-enoyl-CoA transferase;

4-hydroxybut-2-enoyl-CoA hydrolase; or

4-hydroxybut-2-enoyl-CoA ligase;

(c) 4-hydroxybut-2-enoyl-CoA reductase; and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase.

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

(a) homoserine deaminase;

(b) 4-hydroxybut-2-enoate reductase;

(c) 4-hydroxybutyryl-CoA transferase;

4-hydroxybutyryl-CoA hydrolase; or

4-hydroxybutyryl-CoA ligase; and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase.

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

(a) homoserine CoA transferase;

homoserine-CoA hydrolase; or

homoserine-CoA ligase;

(b) homoserine-CoA deaminase;

(c) 4-hydroxybut-2-enoyl-CoA reductase; and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase.

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

(a) succinyl-CoA reductase and 4-hydroxybutyrate dehydrogenase; or

succinyl-CoA reductase (alcohol forming);

(b) 4-hydroxybutyryl-CoA transferase;

4-hydroxybutyryl-CoA hydrolase; or

4-hydroxybutyryl-CoA ligase; and

(c) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase.

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

(a) succinyl-CoA reductase and 4-hydroxybutyrate dehydrogenase; or

succinyl-CoA reductase (alcohol forming);

(b) 4-hydroxybutyrate kinase;

(c) phosphotrans-4-hydroxybutyrylase; and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase.

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

(a) succinyl-CoA reductase and 4-hydroxybutyrate dehydrogenase; or

succinyl-CoA reductase (alcohol forming);

(b) 4-hydroxybutyrate kinase;

(c) 4-hydroxybutanal dehydrogenase (phosphorylating); and

(d) 1,4-butanediol dehydrogenase.

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

(a) glutamate dehydrogenase;

(b) glutamate decarboxylase;

(c) 4-aminobutyrate oxidoreductase (deaminating); or

4-aminobutyrate transaminase;

(d) 4-hydroxybutyrate dehydogenase;

(e) 4-hydroxybutyryl-CoA transferase;

4-hydroxybutyryl-CoA hydrolase; or

4-hydroxybutyryl-CoA ligase; and

(f) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase.

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

(a) alpha-ketoglutarate decarboxylase;

(b) 4-hydroxybutyrate dehydogenase;

(c) 4-hydroxybutyryl-CoA transferase;

4-hydroxybutyryl-CoA hydrolase;

4-hydroxybutyryl-CoA ligase; and

(d) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase.

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

(a) glutamate dehydrogenase;

(b) glutamate decarboxylase;

(c) 4-aminobutyrate oxidoreductase (deaminating); or

4-aminobutyrate transaminase;

(d) 4-hydroxybutyrate dehydogenase;

(e) 4-hydroxybutyrate kinase;

(f) phosphotrans-4-hydroxybutyrylase; and

(g) 4-hydroxybutyryl-CoA reductase (alcohol forming); or

4-hydroxybutyryl-CoA reductase and 1,4-butanediol dehydrogenase.

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

(a) alpha-ketoglutarate decarboxylase;

(b) 4-hydroxybutyrate dehydogenase;

(c) 4-hydroxybutyrate kinase;

(d) 4-hydroxybutanal dehydrogenase (phosphorylating); and

(e) 1,4-butanediol dehydrogenase.

29. The non-naturally occurring microbial organism of any one of claims 1 to 28, wherein said microbial organism comprises disruption of a gene encoding a protein in an aerobic respiratory control regulatory system and expresses an exogenous NADH insensitive citrate synthase.

30. The non-naturally occurring microbial organism of any one of claims 1 to 28, wherein said microbial organism is genetically modified to express exogenous phosphoenolpyruvate carboxykinase.

31. The non-naturally occurring microbial organism of claim 30, wherein said microbial organism comprises comprises disruption of a gene encoding a protein in an aerobic respiratory control regulatory system and expresses exogenous phosphoenolpyruvate carboxykinase.

32. The non-naturally occurring microbial organism of claim 30, wherein said microbial organism expresses an exogenous NADH insensitive citrate synthase and expresses exogenous phosphoenolpyruvate carboxykinase.

33. The non-naturally occurring microbial organism of claim 30, wherein said microbial organism comprises comprises disruption of a gene encoding a protein in an aerobic respiratory control regulatory system, expresses an exogenous NADH insensitive citrate synthase, and expresses exogenous phosphoenolpyruvate carboxykinase.

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

35. The non-naturally occurring microbial organism of any one of claims 1 to 4, 26 or 28, wherein said alpha-ketoglutarate decarboxylase is encoded by the *Mycobacterium bovis sucA* gene.

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

37. The non-naturally occurring microbial organism of any one of claims 1 to 4, 23, 24, 27 or 28, wherein the butyrate kinase or 4-hydroxybutyrate kinase is encoded by the *Clostridium acetobutilicum buk1* gene or phosphotransbutyrylase or phosphotrans-4-hydroxybutyrylase is encoded by *Clostridium acetobutilicum ptb* gene.

38. The non-naturally occurring microbial organism of any one of claims 1 to 6, 12, 13, 16, 17, 19 to 23 or 25 to 27, wherein the 4-hydroxybutyryl-CoA reductase or aldehyde dehydrogenase is encoded by *Clostridium beijerinckii ald* gene.

39. The non-naturally occurring microbial organism of any one of claims 1 to 6, 12, 13, 16, 17, 19 to 23 or 25 to 27, wherein the 4-hydroxybutanal reductase or 4-hydroxybutyraldehyde reductase or alcohol dehydrogenase is encoded by *Geobacillus thermoglucosidasius adh1* gene.

40. The non-naturally occurring bacterial organism of any one of claims 1 to 39, wherein said microbial organism is genetically modified to express exogenous pyruvate dehydrogenase.

41. The non-naturally occurring microbial organism of claim 40, wherein said exogenous pyruvate dehydrogenase is NADH insensitive.

42. The non-naturally occurring microbial organism of claim 40, wherein said exogenous pyruvate dehydrogenase is encoded by the *Klebsiella pneumonia lpdA* gene.

43. The non-naturally occurring microbial organism of any one of claims 1 to 42, wherein one or more of the pyruvate dehydrogenase subunit genes of said microbial organism is under the control of a pyruvate formate lyase promoter.

44. The non-naturally occurring microbial organism of any one of claims 1 to 31 or 33 to 43, wherein the disruption of said anaerobic respiratory control regulatory system is disruption of the *arcA* gene.

45. The non-naturally occurring microbial organism of any one of claims 1 to 44, further comprising disruption of a gene encoding malate dehydrogenase.

46. The non-naturally occurring microbial organism of any one of claims 1 to 30 or 32 to 45, wherein NADH insensitive citrate synthase is encoded by *gltA*.

47. The non-naturally occurring microbial organism of any one of claims 1 to 30 or 32 to 45, wherein said NADH insensitive citrate synthase is encoded by an R163L mutant of *gltA*.

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

49. The non-naturally occurring microbial organism of any one of claims 1 to 48, wherein one or more genes encoding said exogenously expressed enzymes are integrated into the *fimD* locus of the host organism.

50. The non-naturally occurring microbial organism of any one of claims 1 to 49, wherein said organism expresses a non-phosphotransferase sucrose uptake system.

51. The non-naturaly occurring microbial organism of any one of claims 1 to 50, wherein said organism further comprises disruption of endogenous lactate dehydrogenase, alcohol dehydrogenase and pyruvate formate lyase.

52. A method for producing 1,4-butanediol (BDO), comprising culturing the non-naturally occurring microbial organism of any of claims 1 to 51 under conditions and for a sufficient period of time to produce BDO.

53. The method of claim 52, further comprising the step of isolating the 1,4-BDO.

54. The method of claim 53, wherein the 1,4-BDO is isolated by distillation.

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.