2. SUMMARY

[0004] Provided herein are non-naturally occurring eukaryotic organisms that can be engineered to produce and increase the availability of cytosolic acetyl-CoA. Such organisms would advantageously allow for the production of cytosolic acetyl-CoA, which can then be used by the organism to produce compounds of interest, such as 1,3-BDO, using a cytosolic production pathway. Also provided herein are non-naturally occurring eukaryotic organisms having a 1,3-BDO pathway. and methods of using such organisms to produce 1,3-BDO. Thus, the present invention is directed to subject matter as defined in the claims.

[0005] In ~~a first aspect~~one example, provided herein is a non-naturally occurring eukaryotic organism comprising an acetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to (i) transport acetyl-CoA from a mitochondrion and/or peroxisome of said organism to the cytosol of said organism, (ii) produce acetyl-CoA in the cytoplasm of said organism, and/or (iii) increase acetyl-CoA in the cytosol of said organism. In certain ~~embodiments~~examples, the acetyl-CoA pathway comprises one or more enzymes selected from the group consisting of a citrate synthase; a citrate transporter; a citrate/oxaloacetate transporter; a citrate/malate transporter; an ATP citrate lyase; a citrate lyase; an acetyl-CoA synthetase; an oxaloacetate transporter; a cytosolic malate dehydrogenase; a malate transporter; a mitochondrial malate dehydrogenase; a pyruvate oxidase (acetate forming); an acetyl-CoA ligase or transferase; an acetate kinase; a phosphotransacetylase; a pyruvate decarboxylase; an acetaldehyde dehydrogenase; a pyruvate oxidase (acetyl-phosphate forming); a pyruvate dehydrogenase, a pyruvate:ferredoxin oxidoreductase or pyruvate formate lyase; a acetaldehyde dehydrogenase (acylating); a threonine aldolase; a mitochondrial acetylcarnitine transferase; a peroxisomal acetylcarnitine transferase; a cytosolic acetylcarnitine transferase; a mitochondrial acetylcarnitine translocase; a peroxisomal acetylcarnitine translocase; a phosphoenolpyruvate (PEP) carboxylase; a PEP carboxykinase; an oxaloacetate decarboxylase; a malonate semialdehyde dehydrogenase (acetylating); an acetyl-CoA carboxylase; a malonyl-CoA decarboxylase; an oxaloacetate dehydrogenase; an oxaloacetate oxidoreductase; a malonyl-CoA reductase; a pyruvate carboxylase; a malonate semialdehyde dehydrogenase; a malonyl-CoA synthetase; a

malonyl-CoA transferase; a malic enzyme; a malate dehydrogenase; a malate oxidoreductase; a pyruvate kinase; and a PEP phosphatase.

[0006] In another ~~aspect~~example, provided herein is a method for transporting acetyl-CoA from a mitochondrion and/or peroxisome to a cytosol of a non-naturally occurring eukaryotic organism, comprising culturing a non-naturally occurring eukaryotic organism comprising an acetyl-CoA pathway under conditions and for a sufficient period of time to transport the acetyl-CoA from a mitochondrion and/or peroxisome to a cytosol of the non-naturally occurring eukaryotic organism. In some ~~embodiments~~examples, provided herein is a method for transporting acetyl-CoA from a mitochondrion to a cytosol of said non-naturally occurring eukaryotic organism. In other ~~embodiments~~examples, provided herein is a method for transporting acetyl-CoA from a peroxisome to a cytosol of said non-naturally occurring eukaryotic organism. In some ~~embodiments~~examples culturing a non-naturally occurring eukaryotic organism comprising an acetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to transport acetyl-CoA from a mitochondrion and/or peroxisome of said organism to the cytosol of said organism. In certain ~~embodiments~~examples, the acetyl-CoA pathway comprises one or more enzymes selected from the group consisting of a citrate synthase; a citrate transporter; a citrate/oxaloacetate transporter; a citrate/malate transporter; an ATP citrate lyase; a citrate lyase; an acetyl-CoA synthetase; an oxaloacetate transporter; a cytosolic malate dehydrogenase; a malate transporter; a mitochondrial malate dehydrogenase; a pyruvate oxidase (acetate forming); an acetyl-CoA ligase or transferase; an acetate kinase; a phosphotransacetylase; a pyruvate decarboxylase; an acetaldehyde dehydrogenase; a pyruvate oxidase (acetyl-phosphate forming); a pyruvate dehydrogenase, a pyruvate:ferredoxin oxidoreductase or pyruvate formate lyase; a acetaldehyde dehydrogenase (acylating); a threonine aldolase; a mitochondrial acetylcarnitine transferase; a peroxisomal acetylcarnitine transferase; a cytosolic acetylcarnitine transferase; a mitochondrial acetylcarnitine translocase; and a peroxisomal acetylcarnitine translocase; a PEP carboxylase; a PEP carboxykinase; an oxaloacetate decarboxylase; a malonate semialdehyde dehydrogenase (acetylating); an acetyl-CoA carboxylase; a malonyl-CoA decarboxylase; an oxaloacetate dehydrogenase; an oxaloacetate oxidoreductase; a malonyl-CoA reductase; a pyruvate carboxylase; a malonate semialdehyde dehydrogenase; a malonyl-CoA synthetase; a malonyl-CoA transferase; a malic

enzyme; a malate dehydrogenase; a malate oxidoreductase; a pyruvate kinase; and a PEP phosphatase.

[0007] In another ~~aspect~~example, provided herein is a method for producing cytosolic acetyl-CoA, comprising culturing a non-naturally occurring eukaryotic organism comprising an acetyl-CoA pathway under conditions and for a sufficient period of time to produce cytosolic acetyl-CoA. In one ~~embodiment~~example, provided herein is a method for producing cytosolic acetyl-CoA, comprising culturing a non-naturally occurring eukaryotic organism comprising an acetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to produce cytosolic acetyl-CoA in said organism. In certain ~~embodiments~~examples, the acetyl-CoA pathway comprises one or more enzymes selected from the group consisting of a citrate synthase; a citrate transporter; a citrate/oxaloacetate transporter; a citrate/malate transporter; an ATP citrate lyase; a citrate lyase; an acetyl-CoA synthetase; an oxaloacetate transporter; a cytosolic malate dehydrogenase; a malate transporter; a mitochondrial malate dehydrogenase; a pyruvate oxidase (acetate forming); an acetyl-CoA ligase or transferase; an acetate kinase; a phosphotransacetylase; a pyruvate decarboxylase; an acetaldehyde dehydrogenase; a pyruvate oxidase (acetyl-phosphate forming); a pyruvate dehydrogenase, a pyruvate:ferredoxin oxidoreductase or pyruvate formate lyase; a acetaldehyde dehydrogenase (acylating); a threonine aldolase; a mitochondrial acetylcarnitine transferase; a peroxisomal acetylcarnitine transferase; a cytosolic acetylcarnitine transferase; a mitochondrial acetylcarnitine translocase; and a peroxisomal acetylcarnitine translocase; a PEP carboxylase; a PEP carboxykinase; an oxaloacetate decarboxylase; a malonate semialdehyde dehydrogenase (acetylating); an acetyl-CoA carboxylase; a malonyl-CoA decarboxylase; an oxaloacetate dehydrogenase; an oxaloacetate oxidoreductase; a malonyl-CoA reductase; a pyruvate carboxylase; a malonate semialdehyde dehydrogenase; a malonyl-CoA synthetase; a malonyl-CoA transferase; a malic enzyme; a malate dehydrogenase; a malate oxidoreductase; a pyruvate kinase; and a PEP phosphatase.

[0008] In another ~~aspect~~example, provided herein is a method for increasing acetyl-CoA in the cytosol of a non-naturally occurring eukaryotic organism, comprising culturing a non-naturally occurring eukaryotic organism comprising an acetyl-CoA pathway under conditions and for a sufficient period of time to increase the acetyl-CoA in the cytosol of the organism. In some ~~embodiments~~examples, provided herein is a method for increasing acetyl-CoA in the

cytosol of a non-naturally occurring eukaryotic organism, comprising culturing a non-naturally occurring eukaryotic organism

comprising an acetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to increase acetyl-CoA in the cytosol of said non-naturally occurring eukaryotic organism. In certain ~~embodiments~~examples, the acetyl-CoA pathway comprises one or more enzymes selected from the group consisting of a citrate synthase; a citrate transporter; a citrate/oxaloacetate transporter; a citrate/malate transporter; an ATP citrate lyase; a citrate lyase; an acetyl-CoA synthetase; an oxaloacetate transporter; a cytosolic malate dehydrogenase; a malate transporter; a mitochondrial malate dehydrogenase; a pyruvate oxidase (acetate forming); an acetyl-CoA ligase or transferase; an acetate kinase; a phosphotransacetylase; a pyruvate decarboxylase; an acetaldehyde dehydrogenase; a pyruvate oxidase (acetyl-phosphate forming); a pyruvate dehydrogenase, a pyruvate:ferredoxin oxidoreductase or pyruvate formate lyase; a acetaldehyde dehydrogenase (acylating); a threonine aldolase; a mitochondrial acetylcarnitine transferase; a peroxisomal acetylcarnitine transferase; a cytosolic acetylcarnitine transferase; a mitochondrial acetylcarnitine translocase; and a peroxisomal acetylcarnitine translocase; a PEP carboxylase; a PEP carboxykinase; an oxaloacetate decarboxylase; a malonate semialdehyde dehydrogenase (acetylating); an acetyl-CoA carboxylase; a malonyl-CoA decarboxylase; an oxaloacetate dehydrogenase; an oxaloacetate oxidoreductase; a malonyl-CoA reductase; a pyruvate carboxylase; a malonate semialdehyde dehydrogenase; a malonyl-CoA synthetase; a malonyl-CoA transferase; a malic enzyme; a malate dehydrogenase; a malate oxidoreductase; a pyruvate kinase; and a PEP phosphatase.

[0009] ~~Provided~~Disclosed herein are non-naturally occurring eukaryotic organisms and methods thereof to produce and increase the availability of cytosolic acetyl-CoA in the eukaryotic organisms thereof. Also ~~provided~~disclosed herein are non-naturally occurring eukaryotic organisms and methods thereof to produce optimal yields of certain commodity chemicals, such as 1,3-BDO, or other compounds of interest.

[0010] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism, comprising (1) an acetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient

amount to (i) transport acetyl-CoA from a mitochondrion and/or peroxisome of said organism to the cytosol of

said organism, (ii) produce acetyl-CoA in the cytoplasm of said organism, and/or (iii) increase acetyl-CoA in the cytosol of said organism, and (2) a 1,3-BDO pathway, comprising at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO. In certain ~~embodiments~~examples, (1) the acetyl-CoA pathway comprises one or more enzymes selected from the group consisting of a citrate synthase; a citrate transporter; a citrate/oxaloacetate transporter; a citrate/malate transporter; an ATP citrate lyase; a citrate lyase; an acetyl-CoA synthetase; an oxaloacetate transporter; a cytosolic malate dehydrogenase; a malate transporter; a mitochondrial malate dehydrogenase; a pyruvate oxidase (acetate forming); an acetyl-CoA ligase or transferase; an acetate kinase; a phosphotransacetylase; a pyruvate decarboxylase; an acetaldehyde dehydrogenase; a pyruvate oxidase (acetyl-phosphate forming); a pyruvate dehydrogenase, a pyruvate:ferredoxin oxidoreductase or pyruvate formate lyase; a acetaldehyde dehydrogenase (acylating); a threonine aldolase; a mitochondrial acetylcarnitine transferase; a peroxisomal acetylcarnitine transferase; a cytosolic acetylcarnitine transferase; a mitochondrial acetylcarnitine translocase; a peroxisomal acetylcarnitine translocase; a PEP carboxylase; a PEP carboxykinase; an oxaloacetate decarboxylase; a malonate semialdehyde dehydrogenase (acetylating); an acetyl-CoA carboxylase; a malonyl-CoA decarboxylase; an oxaloacetate dehydrogenase; an oxaloacetate oxidoreductase; a malonyl-CoA reductase; a pyruvate carboxylase; a malonate semialdehyde dehydrogenase; a malonyl-CoA synthetase; a malonyl-CoA transferase; a malic enzyme; a malate dehydrogenase; a malate oxidoreductase; a pyruvate kinase; and a PEP phosphatase; and/or (2) the 1,3-BDO pathway comprises one or more enzymes selected from the group consisting of an acetoacetyl-CoA thiolase; an acetyl-CoA carboxylase; an acetoacetyl-CoA synthase; an acetoacetyl-CoA reductase (CoA-dependent, alcohol forming); 3-oxobutyraldehyde reductase (aldehyde reducing); 4-hydroxy,2-butanone reductase; an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming); a 3-oxobutyraldehyde reductase (ketone reducing); 3-hydroxybutyraldehyde reductase; an acetoacetyl-CoA reductase (ketone reducing); a 3-hydroxybutyryl-CoA reductase (aldehyde forming); a 3-hydroxybutyryl-CoA reductase (alcohol forming); an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA synthetase, or a phosphotransacetoacetylase and acetoacetate kinase; an acetoacetate reductase; a 3-hydroxybutyryl-CoA transferase,

hydrolase, or synthetase; a 3-hydroxybutyrate reductase; and a 3-hydroxybutyrate dehydrogenase.

[0011] In another ~~aspect~~example, provided herein is a method for producing 1,3-BDO, comprising culturing a non-naturally occurring eukaryotic organism under conditions and for a sufficient period of time to produce the 1,3-BDO, wherein the non-naturally occurring eukaryotic organism comprises (1) an acetyl-CoA pathway, and (2) a 1,3-BDO pathway. In certain ~~embodiments~~examples, provided herein is a method for producing 1,3-BDO, comprising culturing a non-naturally occurring eukaryotic organism, comprising an acetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to (i) transport acetyl-CoA from a mitochondrion and/or peroxisome of said organism to the cytosol of said organism, (ii) produce acetyl-CoA in the cytoplasm of said organism, and/or (iii) increase acetyl-CoA in the cytosol of said organism; and/or (2) a 1,3-BDO pathway, comprising at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO. In certain ~~embodiments~~examples, the acetyl-CoA pathway comprises one or more enzymes selected from the group consisting of a citrate synthase; a citrate transporter; a citrate/oxaloacetate transporter; a citrate/malate transporter; an ATP citrate lyase; a citrate lyase; an acetyl-CoA synthetase; an oxaloacetate transporter; a cytosolic malate dehydrogenase; a malate transporter; a mitochondrial malate dehydrogenase; a pyruvate oxidase (acetate forming); an acetyl-CoA ligase or transferase; an acetate kinase; a phosphotransacetylase; a pyruvate decarboxylase; an acetaldehyde dehydrogenase; a pyruvate oxidase (acetyl-phosphate forming); a pyruvate dehydrogenase, a pyruvate:ferredoxin oxidoreductase or pyruvate formate lyase; a acetaldehyde dehydrogenase (acylating); a threonine aldolase; a mitochondrial acetylcarnitine transferase; a peroxisomal acetylcarnitine transferase; a cytosolic acetylcarnitine transferase; a mitochondrial acetylcarnitine translocase; a peroxisomal acetylcarnitine translocase; a PEP carboxylase; a PEP carboxykinase; an oxaloacetate decarboxylase; a malonate semialdehyde dehydrogenase (acetylating); an acetyl-CoA carboxylase; a malonyl-CoA decarboxylase; an oxaloacetate dehydrogenase; an oxaloacetate oxidoreductase; a malonyl-CoA reductase; a pyruvate carboxylase; a malonate semialdehyde dehydrogenase; a malonyl-CoA synthetase; a malonyl-

CoA transferase; a malic enzyme; a malate dehydrogenase; a malate oxidoreductase; a pyruvate kinase; and a PEP

phosphatase; and (2) the 1,3-BDO pathway comprises one or more enzymes selected from the group consisting of an acetoacetyl-CoA thiolase; an acetyl-CoA carboxylase; an acetoacetyl-CoA synthase; an acetoacetyl-CoA reductase (CoA-dependent, alcohol forming); 3-oxobutyraldehyde reductase (aldehyde reducing); 4-hydroxy,2-butanone reductase; an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming); a 3-oxobutyraldehyde reductase (ketone reducing); 3-hydroxybutyraldehyde reductase; an acetoacetyl-CoA reductase (ketone reducing); a 3-hydroxybutyryl-CoA reductase (aldehyde forming); a 3-hydroxybutyryl-CoA reductase (alcohol forming); an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA synthetase, or a phosphotransacetoacetylase and acetoacetate kinase; an acetoacetate reductase; a 3-hydroxybutyryl-CoA transferase, hydrolase, or synthetase; a 3-hydroxybutyrate reductase; and a 3-hydroxybutyrate dehydrogenase.

[0012] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising (1) a 1,3-BDO pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO and (2) a deletion or attenuation of one or more enzymes or pathways that utilize one or more precursors and/or intermediates of a 1,3-BDO pathway. In a specific ~~embodiment~~example, the non-naturally occurring eukaryotic organism comprises a deletion or attenuation of a competing pathway that utilizes acetyl-CoA. In a specific ~~embodiment~~example, the non-naturally occurring eukaryotic organism comprises a deletion or attenuation of a 1,3-BDO intermediate byproduct pathway.

[0013] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising (1) a 1,3-BDO pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO and (2) a deletion or attenuation of one or more enzymes or pathways that utilize one or more cofactors of a 1,3-BDO pathway.

[0014] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises one or more endogenous and/or exogenous nucleic acids encoding an attenuated 1,3-BDO pathway enzyme

selected from the group consisting of an acetoacetyl-CoA reductase (CoA-dependent, alcohol forming), a 3-oxobutyraldehyde reductase (aldehyde reducing), a 4-hydroxy-2-butanone reductase, an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming), a 3-

oxobutyraldehyde reductase (ketone reducing), a 3-hydroxybutyraldehyde reductase, an acetoacetyl-CoA reductase (ketone reducing), a 3-hydroxybutyryl-CoA reductase (aldehyde forming), a 3-hydroxybutyryl-CoA reductase (alcohol forming), an acetoacetate reductase, 3-hydroxybutyrate reductase, a 3-hydroxybutyrate dehydrogenase and a 3-hydroxybutyraldehyde reductase; and wherein the attenuated 1,3-BDO pathway enzyme is NAPDH-dependent and has lower enzymatic activity as compared to the 1,3-BDO pathway enzyme encoded by an unaltered or wild-type nucleic acid.

[0015] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism one or more endogenous and/or exogenous nucleic acids encoding a 1,3-BDO pathway enzyme selected from the group consisting of an acetoacetyl-CoA reductase (CoA-dependent, alcohol forming), a 3-oxobutyraldehyde reductase (aldehyde reducing), a 4-hydroxy-2-butanone reductase, an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming), a 3-oxobutyraldehyde reductase (ketone reducing), a 3-hydroxybutyraldehyde reductase, an acetoacetyl-CoA reductase (ketone reducing), a 3-hydroxybutyryl-CoA reductase (aldehyde forming), a 3-hydroxybutyryl-CoA reductase (alcohol forming), an acetoacetate reductase, 3-hydroxybutyrate reductase, a 3-hydroxybutyrate dehydrogenase and a 3-hydroxybutyraldehyde reductase; wherein at least one nucleic acid has been altered such that the 1,3-BDO pathway enzyme encoded by the nucleic acid has a greater affinity for NADH than the 1,3-BDO pathway enzyme encoded by an unaltered or wild-type nucleic acid.

[0016] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises one or more endogenous and/or exogenous nucleic acids encoding a 1,3-BDO pathway enzyme selected from the group consisting of an acetoacetyl-CoA reductase (CoA-dependent, alcohol forming), a 3-oxobutyraldehyde reductase (aldehyde reducing), a 4-hydroxy-2-butanone reductase, an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming), a 3-oxobutyraldehyde reductase (ketone reducing), a 3-hydroxybutyraldehyde reductase, an acetoacetyl-CoA reductase (ketone reducing), a 3-hydroxybutyryl-CoA reductase (aldehyde forming), a 3-hydroxybutyryl-CoA

reductase (alcohol forming), an acetoacetate reductase, 3-hydroxybutyrate reductase, a 3-hydroxybutyrate dehydrogenase and a 3-hydroxybutyraldehyde reductase, wherein at least one nucleic acid has been altered such that the 1,3-BDO pathway enzyme encoded by the nucleic acid has a lesser affinity for NADPH than the 1,3-BDO pathway enzyme encoded by an unaltered or wild-type nucleic acid.

[0017] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising: (1) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and (2) an acetyl-CoA pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to increase NADH in the organism; wherein the acetyl-CoA pathway comprises (i.) an NAD-dependent pyruvate dehydrogenase; (ii.) a pyruvate formate lyase and an NAD-dependent formate dehydrogenase; (iii.) a pyruvate:ferredoxin oxidoreductase and an NADH:ferredoxin oxidoreductase; (iv.) a pyruvate decarboxylase and an NAD-dependent acylating acetylaldehyde dehydrogenase; (v.) a pyruvate decarboxylase, a NAD-dependent acylating acetaldehyde dehydrogenase, an acetate kinase, and a phosphotransacetylase; or (vi.) a pyruvate decarboxylase, an NAD-dependent acylating acetaldehyde dehydrogenase, and an acetyl-CoA synthetase.

[0018] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising: (1) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and (2) a pentose phosphate pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a pentose phosphate pathway enzyme selected from the group consisting of glucose-6-phosphate dehydrogenase, 6-phosphogluconolactonase, and 6-phosphogluconate dehydrogenase (decarboxylating).

[0019] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising: (1) a 1,3-BDO pathway, wherein said organism comprises at least one

endogenous and/or exogenous nucleic acid encoding an NADPH-dependent 1,3-BDO pathway enzyme

expressed in a sufficient amount to produce 1,3-BDO; and (2) an Entner Doudoroff pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an Entner Doudoroff pathway enzyme selected from the group consisting of glucose-6-phosphate dehydrogenase, 6-phosphogluconolactonase, phosphogluconate dehydratase, and 2-keto-3-deoxygluconate 6-phosphate aldolase.

[0020] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising: (1) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and (2) an endogenous and/or exogenous nucleic acid encoding a soluble or membrane-bound transhydrogenase, wherein the transhydrogenase is expressed in a sufficient amount to convert NADH to NADPH.

[0021] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising: (1) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and (2) an endogenous and/or exogenous nucleic acid encoding an NADP-dependent phosphorylating or non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase.

[0022] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising: (1) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and (2) an acetyl-CoA pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to increase NADPH in the organism; wherein the acetyl-CoA pathway comprises (i) an NADP-dependent pyruvate dehydrogenase; (ii) a pyruvate formate lyase and an NADP-dependent formate dehydrogenase; (iii) a pyruvate:ferredoxin oxidoreductase and an NADPH:ferredoxin oxidoreductase; (iv) a pyruvate decarboxylase and an NADP-dependent acylating acetylaldehyde dehydrogenase; (v) a pyruvate decarboxylase, a NADP-dependent acylating acetaldehyde dehydrogenase, an acetate

kinase, and a phosphotransacetylase; or (vi) a pyruvate decarboxylase, an NADP-dependent acylating acetaldehyde dehydrogenase, and an acetyl-CoA synthetase.

[0023] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising: (1) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and (2) one or more endogenous and/or exogenous nucleic acids encoding a NAD(P)H cofactor enzyme selected from the group consisting of phosphorylating or non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase; pyruvate dehydrogenase; formate dehydrogenase; and acylating acetylaldehyde dehydrogenase; wherein the one or more nucleic acids encoding a NAD(P)H cofactor enzyme has been altered such that the NAD(P)H cofactor enzyme encoded by the nucleic acid has a greater affinity for NADPH than the NAD(P)H cofactor enzyme encoded by an unaltered or wild-type nucleic acid.

[0024] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising: (1) a 1,3-BDO pathway, comprising at least one endogenous and/or exogenous nucleic acid encoding a NADPH dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and (2) one or more endogenous and/or exogenous nucleic acids encoding a NAD(P)H cofactor enzyme selected from the group consisting of a phosphorylating or non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase; a pyruvate dehydrogenase; a formate dehydrogenase; and an acylating acetylaldehyde dehydrogenase; wherein the one or more nucleic acids encoding NAD(P)H cofactor enzyme nucleic acid has been altered such that the NAD(P)H cofactor enzyme that it encodes for has a lesser affinity for NADH than the NAD(P)H cofactor enzyme encoded by an unaltered or wild-type nucleic acid.

[0025] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism, and wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the organism: (i) comprises a disruption in a endogenous and/or exogenous nucleic acid encoding a NADH

dehydrogenase; (ii) expresses an attenuated NADH dehydrogenase; and/or (iii) has lower or no NADH dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism.

[0026] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the organism: (i) comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a cytochrome oxidase; (ii) expresses an attenuated cytochrome oxidase; and/or (iii) has lower or no cytochrome oxidase enzymatic activity as compared to a wild-type version of the eukaryotic organism.

[0027] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the organism: (i) comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a glycerol-3-phosphate (G3P) dehydrogenase; (ii) expresses an attenuated G3P dehydrogenase; (iii) has lower or no G3P dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism; and/or (iv) produces lower levels of glycerol as compared to a wild-type version of the eukaryotic organism.

[0028] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the organism: (i) comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a G3P phosphatase; (ii) expresses an attenuated G3P phosphatase; (iii) has lower or no G3P phosphatase enzymatic activity as compared to a wild-type version of the eukaryotic organism; and/or (iv) produces lower levels of glycerol as compared to a wild-type version of the eukaryotic organism.

[0029] In another ~~aspect~~example, provided herein is a non-naturally eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous

nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the organism: (i) comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a pyruvate decarboxylase; (ii) expresses an attenuated pyruvate decarboxylase; (iii) has lower or no pyruvate decarboxylase enzymatic activity as compared to a wild-type version of the eukaryotic organism; and/or (iv) produces lower levels of ethanol from pyruvate as compared to a wild-type version of the eukaryotic organism.

[0030] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the organism: (i) comprises a disruption in an endogenous and/or exogenous nucleic acid encoding an ethanol dehydrogenase; (ii) expresses an attenuated ethanol dehydrogenase; (iii) has lower or no ethanol dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism; and/or (iv) produces lower levels of ethanol as compared to a wild-type version of the eukaryotic organism.

[0031] In another ~~aspect~~example, provided herein is a non-naturally eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the organism: (i) comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a malate dehydrogenase; (ii) expresses an attenuated malate dehydrogenase; (iii) has lower or no malate dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism; and/or (iv) has an attenuation or blocking of a malate-asparate shuttle, a malate oxaloacetate shuttle, and/or a malate-pyruvate shuttle.

[0032] In another ~~aspect~~example, provided herein is a non-naturally eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the organism: (i) comprises a disruption in an endogenous and/or exogenous nucleic acid encoding an acetoacetyl-CoA hydrolase or

transferase; (ii) expresses an attenuated acetoacetyl-CoA hydrolase or transferase; and/or (iii) has lower or no acetoacetyl-

CoA hydrolase or transferase enzymatic activity as compared to a wild-type version of the eukaryotic organism.

[0033] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the organism: (i) comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a 3-hydroxybutyryl-CoA hydrolase or transferase; (ii) expresses an attenuated 3-hydroxybutyryl-CoA hydrolase or transferase; and/or (iii) has lower or no 3-hydroxybutyryl-CoA hydrolase or transferase enzymatic activity as compared to a wild-type version of the eukaryotic organism

[0034] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and wherein the organism: (i) comprises a disruption in an endogenous and/or exogenous nucleic acid encoding an acetaldehyde dehydrogenase (acylating); (ii) expresses an attenuated acetaldehyde dehydrogenase (acylating); and/or (iii) has lower or no acetaldehyde dehydrogenase (acylating) enzymatic activity as compared to a wild-type version of the eukaryotic organism.

[0035] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the organism: (i) comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a 3-hydroxybutyraldehyde dehydrogenase; (ii) expresses an attenuated 3-hydroxybutyraldehyde dehydrogenase; and/or (iii) has lower or no 3-hydroxybutyraldehyde dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism.

[0036] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic

organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous

and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the organism: (i) comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a 3-oxobutyraldehyde dehydrogenase; (ii) expresses an attenuated 3-oxobutyraldehyde dehydrogenase; and/or (iii) has lower or no 3-oxobutyraldehyde dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism.

[0037] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the organism: (i) comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a 1,3-butanediol dehydrogenase; (ii) expresses an attenuated 1,3-butanediol dehydrogenase; and/or (iii) has lower or no 1,3-butanediol dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism

[0038] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the organism: (i) comprises a disruption in an endogenous and/or exogenous nucleic acid encoding an acetoacetyl-CoA thiolase; (ii) expresses an attenuated acetoacetyl-CoA thiolase; and/or (iii) has lower or no acetoacetyl-CoA thiolase enzymatic activity as compared to a wild-type version of the eukaryotic organism

[0039] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and wherein said organism further comprises an endogenous and/or exogenous nucleic acid encoding a 1,3-BDO transporter, wherein the nucleic acid encoding the 1,3-BDO transporter is expressed in a sufficient amount for the exportation of 1,3-BDO from the eukaryotic organism.

[0040] In another ~~aspect~~example, provided herein is a non-naturally occurring eukaryotic organism comprising a combined mitochondrial/cytosolic 1,3-BDO pathway, wherein said organism comprises at least endogenous and/or exogenous nucleic acid encoding a combined mitochondrial/cytosolic 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO. In certain ~~embodiments~~examples, the combined mitochondrial/cytosolic 1,3-BDO pathway comprises one or more enzymes selected from the group consisting of a mitochondrial acetoacetyl-CoA thiolase; an acetyl-CoA carboxylase; an acetoacetyl-CoA synthase; a mitochondrial acetoacetyl-CoA reductase; a mitochondrial acetoacetyl-CoA hydrolase, transferase or synthetase; a mitochondrial 3-hydroxybutyryl-CoA hydrolase, transferase or synthetase; a mitochondrial. 3-hydroxybutyrate dehydrogenase; an acetoacetate transporter; a 3-hydroxybutyrate transporter; a 3-hydroxybutyryl-CoA transferase or synthetase, a cytosolic acetoacetyl-CoA transferase or synthetase; an acetoacetyl-CoA reductase (CoA-dependent, alcohol forming); a 3-oxobutyraldehyde reductase (aldehyde reducing); a 4-hydroxy-2-butanone reductase; an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming); a 3-oxobutyraldehyde reductase (ketone reducing); a 3-hydroxybutyraldehyde reductase; an acetoacetyl-CoA reductase (ketone reducing); a 3-hydroxybutyryl-CoA reductase (aldehyde forming); a 3-hydroxybutyryl-CoA reductase (alcohol forming); an acetoacetate reductase; a 3-hydroxybutyryl-CoA transferase, hydrolase, or synthetase; a 3-hydroxybutyrate reductase; and a 3-hydroxybutyrate dehydrogenase.

[0041] In another ~~aspect~~example, provided herein is a method for producing 1,3-BDO, comprising culturing any one of the non-naturally occurring eukaryotic organisms comprising a 1,3-BDO pathway provided herein under conditions and for a sufficient period of time to produce 1,3-BDO. In certain ~~embodiments~~examples, the eukaryotic organism is cultured in a substantially anaerobic culture medium. In other ~~embodiments~~examples, the eukaryotic organism is a Crabtree positive organism.

[0042] In another ~~aspect~~example, provided herein is a method for selecting an exogenous 1,3-BDO pathway enzyme to be introduced into a non-naturally occurring eukaryotic organism, wherein the exogenous 1,3-BDO pathway enzyme is expressed in a sufficient amount in the organism to produce 1,3-BDO, said method comprising (i.) measuring the activity of at least one

1,3-BDO pathway enzyme that uses NADH as a cofactor; (ii.) measuring the activity of at least 1,3-BDO pathway enzyme that uses NADPH as a cofactor; and (iii.) introducing into the organism at least one 1,3-BDO

pathway enzyme that has a greater preference for NADH than NADPH as a cofactor as determined in steps 1 and 2.

3. BRIEF DESCRIPTIONS OF THE DRAWINGS

[0043] **FIG. 1** shows an exemplary pathway for the production of acetyl-CoA in the cytosol of a eukaryotic organism.

[0044] **FIG. 2** shows pathways for the production of cytosolic acetyl-CoA from mitochondrial acetyl-CoA using citrate and oxaloacetate transporters. Enzymes are: A) citrate synthase; B) citrate transporter; C) citrate/oxaloacetate transporter; D) ATP citrate lyase; E) citrate lyase; F) acetyl-CoA synthetase or transferase, or acetate kinase and phosphotransacetylase; G) oxaloacetate transporter; K) acetate kinase; and L) phosphotransacetylase.

[0045] **FIG. 3** shows pathways for the production of cytosolic acetyl-CoA from mitochondrial acetyl-CoA using citrate and malate transporters. Enzymes are A) citrate synthase; B) citrate transporter; C) citrate/malate transporter; D) ATP citrate lyase; E) citrate lyase; F) acetyl-CoA synthetase or transferase, or acetate kinase and phosphotransacetylase; H) cytosolic malate dehydrogenase; I) malate transporter; J) mitochondrial malate dehydrogenase; K) acetate kinase; and L) phosphotransacetylase.

[0046] **FIG. 4** shows pathways for the biosynthesis of 1,3-BDO from acetyl-CoA. The enzymatic transformations shown are carried out by the following enzymes: A) Acetoacetyl-CoA thiolase, B) Acetoacetyl-CoA reductase (CoA-dependent, alcohol forming), C) 3-oxobutyraldehyde reductase (aldehyde reducing), D) 4-hydroxy-2-butanone reductase, E) Acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming), F) 3-oxobutyraldehyde reductase (ketone reducing), G) 3-hydroxybutyraldehyde reductase, H) Acetoacetyl-CoA reductase (ketone reducing), I) 3-hydroxybutyryl-CoA reductase (aldehyde forming), J) 3-hydroxybutyryl-CoA reductase (alcohol forming), K) an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA synthetase, or a phosphotransacetoacetylase and acetoacetate kinase, L) acetoacetate reductase, M) 3-hydroxybutyryl-CoA transferase, hydrolase,

or synthetase, N) 3-hydroxybutyrate reductase, and O) 3-hydroxybutyrate dehydrogenase. An alternative to the conversion of acetyl-CoA to acetoacetyl-CoA by acetoacetyl-CoA thiolase (step A) in the 1,3-BDO pathways depicted in FIG. 4 involves the conversion of acetyl-CoA to malonyl-CoA by acetyl-CoA carboxylase, and the conversion of an acetyl-CoA and the malonyl-CoA to acetoacetyl-CoA by acetoacetyl-CoA synthetase (not shown; refer to FIG. 7, steps E and F, or FIG. 9).

What is claimed is:

1. A non-naturally occurring eukaryotic organism comprising an acetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to transport acetyl-CoA from a mitochondrion of said organism to the cytosol of said organism and/or increase acetyl-CoA in the cytosol of said organism, wherein said acetyl-CoA pathway comprises a pathway selected from the group consisting of:

   i. 2A, 2B and 2D;

   ii. 2A, 2C and 2D;

   iii. 2A, 2B, 2E and 2F;

   iv. 2A, 2C, 2E and 2F;

   v. 2A, 2B, 2E, 2K and 2L; and

   vi. 2A, 2C, 2E, 2K and 2L;

   wherein 2A is a citrate synthase; 2B is a citrate transporter; 2C is a citrate/oxaloacetate transporter or a citrate/malate transporter; 2D is an ATP citrate lyase; 2E is a citrate lyase; 2F is an acetyl-CoA synthetase; 2K is an acetate kinase; and 2L is a phosphotransacetylase.

2. The organism of claim 1, wherein said acetyl-CoA pathway further comprises 2G, 3I and/or 3J, wherein 2G is an oxaloacetate transporter, 3H is a cytosolic malate dehydrogenase, 3I is a malate transporter, and 3J is a mitochondrial malate dehydrogenase.

3. A non-naturally occurring eukaryotic organism comprising an acetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to increase acetyl-CoA in the cytosol of said organism, wherein said acetyl-CoA pathway comprises a pathway selected from the group consisting of:

   i. 5A and 5B;

ii. 5A, 5C and 5D;

iii. 5E, 5F, 5C and 5D; and

iv. 5G and 5D;

wherein 5A is a pyruvate oxidase (acetate forming); 5B is an acetyl-CoA synthetase, ligase or transferase; 5C is an acetate kinase; 5D is a phosphotransacetylase; 5E is a pyruvate decarboxylase, 5F is an acetaldehyde dehydrogenase; and 5G is pyruvate oxidase (acetyl-phosphate forming).

4. A non-naturally occurring eukaryotic organism comprising an acetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to transport acetyl-CoA from a mitochondrion and/or peroxisome of said organism to the cytosol of said organism and/or increase acetyl-CoA in the cytosol of said organism, wherein said acetyl-CoA pathway comprises a pathway selected from the group consisting of:

i. 6A, 6D and 6C; and

ii. 6B, 6E and 6C;

wherein 6A is mitochondrial acetylcarnitine transferase; 6B is a peroxisomal acetylcarnitine transferase; 6C is a cytosolic acetylcarnitine transferase; 6D is a mitochondrial acetylcarnitine translocase; and 6E is a peroxisomal acetylcarnitine translocase.

5. A non-naturally occurring eukaryotic organism comprising an acetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to increase acetyl-CoA in the cytosol of said organism, wherein said acetyl-CoA pathway comprises a pathway selected from the group consisting of:

i. 10A, 10B and 10C;

ii. 10N, 10H, 10B and 10C;

iii. 10N, 10L, 10M, 10B and 10C;

iv. 10A, 10B, 10G and 10D;

v. 10N, 10H, 10B, 10G and 10D;

vi. 10N, 10L, 10M, 10B, 10G and 10D;

vii. 10A, 10B, 10J, 10K and 10D;

viii. 10N, 10H, 10B, 10J, 10K and 10D;

ix. 10N, 10L, 10M, 10B, 10J, 10K and 10D;

x. 10A, 10F and 10D;

xi. 10N, 10H, 10F and 10D; and

xii. 10N, 10L, 10M, 10F and 10D;

wherein 10A is a PEP carboxylase or PEP carboxykinase; 10B is an oxaloacetate decarboxylase; 10C is a malonate semialdehyde dehydrogenase (acetylating); 10D is a malonyl-CoA decarboxylase; 10F is an oxaloacetate dehydrogenase or oxaloacetate oxidoreductase; 10G is a malonyl-CoA reductase; 10H is a pyruvate carboxylase; 10J is a malonate semialdehyde dehydrogenase; 10K is a malonyl-CoA synthetase or transferase; 10L is a malic enzyme; 10M is a malate dehydrogenase or oxidoreductase; and 10N is a pyruvate kinase or PEP phosphatase.

6. The organism of any one of claims 1 to 5, wherein said eukaryotic organism comprises two, three, four, five, six, seven, eight, nine or ten exogenous nucleic acids each encoding an acetyl-CoA pathway enzyme.

7. The organism of any one of claims 1 to 6, further comprising a 1,3-butanediol (1,3-BDO) pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the 1,3-BDO pathway comprises a pathway selected from the group consisting of:

i. 4A, 4E, 4F and 4G;

ii. 4A, 4B and 4D;

iii. 4A, 4E, 4C and 4D;

iv. 4A, 4H and 4J;

v. 4A, 4H, 4I and 4G;

vi. 4A, 4H, 4M, 4N and 4G;

vii. 4A, 4K, 4O, 4N and 4G;

viii. 4A, 4K, 4L, 4F and 4G;

ix. 7E, 7F, 4E, 4F and 4G;

x. 7E, 7F, 4B and 4D;

xi. 7E, 7F, 4E, 4C and 4D;

xii. 7E, 7F, 4H and 4J;

xiii. 7E, 7F, 4H, 4I and 4G;

xiv. 7E, 7F, 4H, 4M, 4N and 4G;

xv. 7E, 7F, 4K, 4O, 4N and 4G; and

xvi. 7E, 7F, 4K, 4L, 4F and 4G;

wherein 4A is an acetoacetyl-CoA thiolase; 4B is an acetoacetyl-CoA reductase (CoA-dependent, alcohol forming); 4C is a 3-oxobutyraldehyde reductase (aldehyde reducing); 4D is a 4-hydroxy,2-butanone reductase; 4E is an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming); 4F is a 3-oxobutyraldehyde reductase (ketone reducing); 4G is a 3-hydroxybutyraldehyde reductase; 4H is an acetoacetyl-CoA reductase (ketone reducing); 4I is a 3-hydroxybutyryl-CoA reductase (aldehyde forming); 4J is a 3-hydroxybutyryl-CoA reductase (alcohol forming); 4K is an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA synthetase, or a phosphotransacetoacetylase and acetoacetate kinase; 4L is an acetoacetate reductase; 4M is a 3-hydroxybutyryl-CoA transferase, hydrolase, or synthetase; 4N is a 3-hydroxybutyrate reductase; 4O is a 3-hydroxybutyrate dehydrogenase; 7E is an acetyl-CoA carboxylase; and 7F is an acetoacetyl-CoA synthase.

8. The organism of claim 7, wherein:

i. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

ii. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises (ii) 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

iii. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

iv. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

v. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

vi. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

vii. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

viii. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

ix. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

x. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xi. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xii. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xiii. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xiv. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xv. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xvi. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xvii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xviii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xix. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xx. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xxi. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;;

xxii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xxiii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N or 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xxiv. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xxv. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xxvi. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xxvii. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xxviii. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xxix. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xxx. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xxxi. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xxxii. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xxxiii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xxxiv. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises (ii) 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xxxv. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xxxvi. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xxxvii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xxxviii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xxxix. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xl. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xli. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xlii. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises (ii) 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xliii. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xliv. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xlv. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xlvi. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xlvii. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xlviii. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xlix. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

l. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

li. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

lii. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

liii. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

liv. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

lv. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

lvi. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

lvii. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

lviii. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

lix. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

lx. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

lxi. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

lxii. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

lxiii. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

lxiv. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

lxv. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

lxvi. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

lxvii. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

lxviii. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

lxix. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

lxx. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

lxxi. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

lxxii. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

lxxiii. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

lxxiv. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

lxxv. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

lxxvi. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

lxxvii. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

lxxviii. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

lxxix. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G; or

lxxx. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

lxxxi. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

lxxxii. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

lxxxiii. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

lxxxiv. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

lxxxv. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

lxxxvi. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

lxxxvii. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

lxxxviii. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

lxxxix. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xc. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xci. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xcii. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xciii. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xciv. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xcv. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xcvi. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xcvii. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xcviii. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xcix. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

c. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

ci. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cii. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

ciii. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

civ. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cv. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cvi. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

cvii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

cviii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

cix. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cx. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cxi. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

cxii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cxiii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cxiv. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

cxv. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

cxvi. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

cxvii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cxviii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cxix. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

cxx. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cxxi. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cxxii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

cxxiii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

cxxiv. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

cxxv. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cxxvi. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cxxvii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

cxxviii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cxxix. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cxxx. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

cxxxi. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

cxxxii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

cxxxiii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cxxxiv. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cxxxv. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

cxxxvi. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cxxxvii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cxxxviii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

cxxxix. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

cxl. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

cxli. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cxlii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cxliii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

cxliv. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cxlv. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cxlvi. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

cxlvii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

cxlviii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

cxlix. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cl. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cli. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

cliii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cliii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cliv. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

clv. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

clvi. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

clvii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

clviii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

clix. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

clx. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

clxi. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

clxii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

clxiii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

clxiv. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

clxv. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

clxvi. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

clxvii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

clxviii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

clxix. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

clxx. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

clxxi. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

clxxii. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

clxxiii. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

clxxiv. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

clxxv. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

clxxvi. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

clxxvii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

clxxviii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

clxxix. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

clxxx. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

clxxxi. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

clxxxii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

clxxxiii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

clxxxiv. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

clxxxv. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

clxxxvi. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

clxxxvii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

clxxxviii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

clxxxix. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cxc. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cxci. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G; or

cxcii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G.

9. A non-naturally occurring eukaryotic organism comprising:

(1) an acetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to increase acetyl-CoA in the cytosol of said organism, wherein said acetyl-CoA pathway comprises a pathway selected from the group consisting of:

i. 5J and 5I;

ii. 5J, 5F and 5B; and

iii. 5H;

wherein 5B is an acetyl-CoA synthetase, ligase or transferase; 5F is an acetaldehyde dehydrogenase; 5H is a pyruvate dehydrogenase, pyruvate:ferredoxin oxidoreductase or pyruvate formate lyase; 5I is a acetaldehyde dehydrogenase (acylating); and 5J is a threonine aldolase; and

(2) a 1,3-BDO pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the 1,3-BDO pathway comprises a pathway selected from the group consisting of:

i. 4A, 4E, 4F and 4G;

ii. 4A, 4B and 4D;

iii. 4A, 4E, 4C and 4D;

iv. 4A, 4H and 4J;

v. 4A, 4H, 4I and 4G;

vi. 4A, 4H, 4M, 4N and 4G;

vii. 4A, 4K, 4O, 4N and 4G;

viii. 4A, 4K, 4L, 4F and 4G;

ix. 7E, 7F, 4E, 4F and 4G;

x. 7E, 7F, 4B and 4D;

xi. 7E, 7F, 4E, 4C and 4D;

xii. 7E, 7F, 4H and 4J;

xiii. 7E, 7F, 4H, 4I and 4G;

xiv. 7E, 7F, 4H, 4M, 4N and 4G;

xv. 7E, 7F, 4K, 4O, 4N and 4G; and

xvi. 7E, 7F, 4K, 4L, 4F and 4G;

wherein 4A is an acetoacetyl-CoA thiolase; 4B is an acetoacetyl-CoA reductase (CoA-dependent, alcohol forming); 4C is a 3-oxobutyraldehyde reductase (aldehyde reducing), wherein 4D is a 4-hydroxy,2-butanone reductase; 4E is an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming); 4F is a 3-oxobutyraldehyde reductase (ketone reducing); 4G is a 3-hydroxybutyraldehyde reductase or a 3-hydroxybutyraldehyde reductase; 4H is an acetoacetyl-CoA reductase (ketone reducing); 4I is a 3-hydroxybutyryl-CoA reductase (aldehyde forming); 4J is a 3-hydroxybutyryl-CoA reductase (alcohol forming); 4K is an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA synthetase, or a phosphotransacetoacetylase and acetoacetate kinase; 4L is an acetoacetate reductase; 4M is a 3-hydroxybutyryl-CoA transferase, hydrolase, or synthetase; 4N is a 3-hydroxybutyrate reductase; 4O is a 3-hydroxybutyrate dehydrogenase; 7E is an acetyl-CoA carboxylase; and 7F is an acetoacetyl-CoA synthase.

10. The organism of claim 9, wherein

i. (1) the acetyl-CoA pathway comprises (1) 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

ii. (1) the acetyl-CoA pathway comprises 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

iii. (1) the acetyl-CoA pathway comprises 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

iv. (1) the acetyl-CoA pathway comprises 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

v. (1) the acetyl-CoA pathway comprises 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

vi. (1) the acetyl-CoA pathway comprises 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

vii. (1) the acetyl-CoA pathway comprises 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

viii. wherein the acetyl-CoA pathway comprises (1) 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

ix. wherein the acetyl-CoA pathway comprises (1) 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

x. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xi. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xii. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xiii. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xiv. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xv. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xvi. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xvii. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xviii. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xix. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xx. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xxi. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xxii. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xxiii. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G; or

xxiv. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G.

11. A non-naturally occurring eukaryotic organism comprising:

(1) an acetoacetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetoacetyl-CoA pathway enzyme expressed in a sufficient amount to increase acetoacetyl-CoA in the cytosol of said organism, wherein said acetoacetyl-CoA pathway comprises:

i. 8A, 8C, 8F and 8I, wherein 8A is a mitochondrial acetoacetyl-CoA thiolase; 8C is a mitochondrial acetoacetyl-CoA hydrolase, transferase or synthetase; 8F is an acetoacetate transporter; and 8I is a cytosolic acetoacetyl-CoA transferase or synthetase; or

ii. 8J, 8K, 8C, 8F and 8I; wherein 8J is a mitochondrial acetyl-CoA carboxylase; 8K is a mitochondrial acetoacetyl-CoA synthase; 8C is a mitochondrial acetoacetyl-CoA hydrolase, transferase or synthetase; 8F is an acetoacetate transporter; and 8I is a cytosolic acetoacetyl-CoA transferase or synthetase; and

(2) a 1,3-BDO pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO in the cytosol of said organism, and wherein the 1,3-BDO pathway comprises a pathway selected from:

i. 4E, 4F and 4G;

ii. 4B and 4D;

iii. 4E, 4C and 4D;

iv. 4H and 4J;

v. 4H, 4I and 4G; and

vi. 4H, 4M, 4N and 4G;

wherein 4B is an acetoacetyl-CoA reductase (CoA-dependent, alcohol forming); 4C is a 3-oxobutyraldehyde reductase (aldehyde reducing); 4D is a 4-hydroxy,2-butanone reductase; 4E is an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming); 4F is

a 3-oxobutyraldehyde reductase (ketone reducing); 4G is a 3-hydroxybutyraldehyde reductase; 4H is an acetoacetyl-CoA reductase (ketone reducing); 4I is a 3-hydroxybutyryl-CoA reductase (aldehyde forming); 4J is a 3-hydroxybutyryl-CoA reductase (alcohol forming); 4L is an acetoacetate reductase; 4M is a 3-hydroxybutyryl-CoA transferase, hydrolase, or synthetase; and 4N is a 3-hydroxybutyrate reductase.

12. The organism of claim 11, wherein

i. (1) the acetoacetyl-CoA pathway comprises 8A, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4E, 4F and 4G;

ii. (1) the acetoacetyl-CoA pathway comprises 8A, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4B and 4D;

iii. (1) the acetoacetyl-CoA pathway comprises 8A, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4E, 4C and 4D;

iv. (1) the acetoacetyl-CoA pathway comprises 8A, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4H and 4J;

v. (1) the acetoacetyl-CoA pathway comprises 8A, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4H, 4I and 4G;

vi. (1) the acetoacetyl-CoA pathway comprises 8A, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4H, 4M, 4N and 4G;

vii. (1) the acetoacetyl-CoA pathway comprises 8J, 8K, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4E, 4F and 4G;

viii. (1) the acetoacetyl-CoA pathway comprises 8J, 8K, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4B and 4D;

ix. (1) the acetoacetyl-CoA pathway comprises 8J, 8K, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4E, 4C and 4D;

x. (1) the acetoacetyl-CoA pathway comprises 8J, 8K, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4H and 4J;

xi. (1) the acetoacetyl-CoA pathway comprises 8J, 8K, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4H, 4I and 4G; or

xii. (1) the acetoacetyl-CoA pathway comprises 8J, 8K, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4H, 4M, 4N and 4G.

13. The organism of any one of claims 1 to 12, wherein said organism comprises two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen or fifteen exogenous nucleic acids each encoding a 1,3-BDO pathway enzyme.

14. The organism of any one of claims 1 to 13, wherein said at least one exogenous nucleic acid is a heterologous nucleic acid.

15. The organism of any one of claims 1 to 14, wherein said organism is in a substantially anaerobic culture medium.

16. The organism of anyone of claims 1 to 15, further comprising an attenuation or deletion of one or more byproduct pathways.

17. The organism of claim 16, wherein the one or more byproduct pathways are one or more byproduct pathways depicted in FIG. 7, 3-oxobutyraldehyde dehydrogenase or acetoacetyl-CoA thiolase.

18. The organism of claim 16 or 19, wherein the byproduct pathway comprises

i. a glycerol-3-phosphate (G3P) dehydrogenase that converts dihydroxyacetone to G3P;

ii. a G3P phosphatase that converts G3P to glycerol;

iii. a pyruvate decarboxylase that converts pyruvate to acetaldehyde;

iv. an ethanol dehydrogenase that converts acetaldehyde to ethanol;

v. an acetaldehyde dehydrogenase (acylating) that converts acetyl-CoA to acetaldehyde;

vi. an acetoacetyl-CoA hydrolase or transferase that converts acetoacetyl-CoA to acetoacetate;

vii. a 3-hydroxybutyryl-CoA hydrolase or transferase that converts 3-hydroxybutyryl-CoA (3-HBCoA) to 3-hydroxybutyrate;

viii. a 3-hydroxybutyraldehyde dehydrogenase that converts 3-hydroxybutyraldehyde to 3-hydroxybutyrate;

ix. a 1,3-butanediol dehydrogenase that converts 1,3-butanediol to 3-oxobutanol;

x. a mitochondrial pyruvate dehydrogenase that converts pyruvate to acetyl-CoA;

xi. a 3-oxobutyraldehyde dehydrogenase that converts 3-oxobutyraldehyde to acetoacetate; and/or

xii. an acetoacetyl-CoA thiolase that converts acetoacetyl-CoA to acetyl-CoA.

19. A method for transporting acetyl-CoA from a mitochondrion to a cytosol of a non-naturally occurring eukaryotic organism, comprising culturing the organism of any one of claims 1 to 18 under conditions and for a sufficient period of time to transport the acetyl-CoA from a mitochondrion to a cytosol of the non-naturally occurring eukaryotic organism.

20. A method for increasing acetyl-CoA in the cytosol of a non-naturally occurring eukaryotic organism, comprising culturing the organism of any one of claims 1 to 18 under conditions and for a sufficient period of time to increase the acetyl-CoA in the cytosol of the organism.

21. A method for transporting acetyl-CoA from a peroxisome to a cytosol of a non-naturally occurring eukaryotic organism, comprising culturing the organism of any one of claims 4 or 6 to 19 under conditions and for a sufficient period of time to transport the acetyl-CoA from a perioxisome to a cytosol of the non-naturally occurring eukaryotic organism.

22. A non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism further comprises one or more endogenous and/or exogenous nucleic acids encoding:

i. a 1,3-BDO pathway enzyme selected from the group consisting of 4A, 4B, 4C, 4D, 4E, 4F, 4G, 4H, 4I, 4J, 4L, 4N, 4O, 7E and 7F; wherein at least

one nucleic acid has been altered such that the 1,3-BDO pathway enzyme encoded by the nucleic acid has a greater affinity for NADH than the 1,3-BDO pathway enzyme encoded by an unaltered or wild-type nucleic acid;

ii. an attenuated 1,3-BDO pathway enzyme selected from the group consisting of 4A, 4B, 4C, 4D, 4E, 4F, 4G, 4H, 4I, 4J, 4L, 4N, 4O, 7E and 7F; wherein the attenuated 1,3-BDO pathway enzyme is NAPDH-dependent and has lower enzymatic activity as compared to the 1,3-BDO pathway enzyme encoded by an unaltered or wild-type nucleic acid;

iii. a 1,3-BDO pathway enzyme selected from the group consisting of 4A, 4B, 4C, 4D, 4E, 4F, 4G, 4H, 4I, 4J, 4L, 4N, 4O, 7E and 7F; wherein the eukaryotic organism comprises one or more gene disruptions that attenuate the activity of an endogenous NADPH-dependent 1,3-BDO pathway enzyme; or

iv. a 1,3-BDO pathway enzyme selected from the group consisting of 4A, 4B, 4C, 4D, 4E, 4F, 4G, 4H, 4I, 4J, 4L, 4N, 4O, 7E and 7F; wherein at least one nucleic acid has been altered such that the 1,3-BDO pathway enzyme encoded by the nucleic acid has a lesser affinity for NADPH than the 1,3-BDO pathway enzyme encoded by an unaltered or wild-type nucleic acid.

23. A non-naturally occurring eukaryotic organism comprising:

(1) (a) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(b) an acetyl-CoA pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to increase NADH in the organism; wherein the acetyl-CoA pathway comprises:

i. a NAD-dependent pyruvate dehydrogenase;

ii. a pyruvate formate lyase and an NAD-dependent formate dehydrogenase;

iii. a pyruvate:ferredoxin oxidoreductase and an NADH:ferredoxin oxidoreductase;

iv. a pyruvate decarboxylase and an NAD-dependent acylating acetylaldehyde dehydrogenase;

v. a pyruvate decarboxylase, a NAD-dependent acylating acetaldehyde dehydrogenase, an acetate kinase, and a phosphotransacetylase; or

vi. a pyruvate decarboxylase, an NAD-dependent acylating acetaldehyde dehydrogenase, and an acetyl-CoA synthetase;

(2) (a) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(b) an endogenous and/or exogenous nucleic acid encoding a soluble or membrane-bound transhydrogenase, wherein the transhydrogenase is expressed in a sufficient amount to convert NADH to NADPH;

(3) (a) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(b) an endogenous and/or exogenous nucleic acid encoding an NADP-dependent phosphorylating or non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase;

(4) (a) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(b) one or more endogenous and/or exogenous nucleic acids encoding a NAD(P)H cofactor enzyme selected from the group consisting of phosphorylating

or non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase; pyruvate dehydrogenase; formate dehydrogenase; and acylating acetylaldehyde dehydrogenase; wherein the one or more nucleic acids encoding a NAD(P)H cofactor enzyme has been altered such that the NAD(P)H cofactor enzyme encoded by the nucleic acid has a greater affinity for NADPH than the NAD(P)H cofactor enzyme encoded by an unaltered or wild-type nucleic acid; or

(5) (a) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(b) one or more endogenous and/or exogenous nucleic acids encoding a NAD(P)H cofactor enzyme selected from the group consisting of a phosphorylating or non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase; a pyruvate dehydrogenase; a formate dehydrogenase; and an acylating acetylaldehyde dehydrogenase; wherein the one or more nucleic acids encoding NAD(P)H cofactor enzyme nucleic acid has been altered such that the NAD(P)H cofactor enzyme that it encodes for has a lesser affinity for NADH than the NAD(P)H cofactor enzyme encoded by an unaltered or wild-type nucleic acid.

24. A non-naturally occurring eukaryotic organism comprising:

(1) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(2) a pentose phosphate pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a pentose phosphate pathway enzyme selected from the group consisting of glucose-6-phosphate dehydrogenase, 6-phosphogluconolactonase, and 6 phosphogluconate dehydrogenase (decarboxylating).

25. The eukaryotic organism of claim 24, further comprising a genetic alteration that increases metabolic flux into the pentose phosphate pathway.

26. A non-naturally occurring eukaryotic organism comprising:

(1) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(2) an Entner Doudoroff pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an Entner Doudoroff pathway enzyme selected from the group consisting of glucose-6-phosphate dehydrogenase, 6-phosphogluconolactonase, phosphogluconate dehydratase, and 2-keto-3-deoxygluconate 6-phosphate aldolase.

27. The eukaryotic organism of claim 26 further comprising a genetic alteration that increases metabolic flux into the Entner Doudoroff pathway.

28. A non-naturally occurring eukaryotic organism comprising:

(1) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(2) an acetyl-CoA pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to increase NADPH in the organism; wherein the acetyl-CoA pathway comprises

i. an NADP-dependent pyruvate dehydrogenase;

ii. a pyruvate formate lyase and an NADP-dependent formate dehydrogenase;

iii. a pyruvate:ferredoxin oxidoreductase and an NADPH:ferredoxin oxidoreductase;

iv. a pyruvate decarboxylase and an NADP-dependent acylating acetylaldehyde dehydrogenase;

v. a pyruvate decarboxylase, a NADP-dependent acylating acetaldehyde dehydrogenase, an acetate kinase, and a phosphotransacetylase; or

vi. a pyruvate decarboxylase, an NADP-dependent acylating acetaldehyde dehydrogenase, and an acetyl-CoA synthetase.

29. A non-naturally occurring eukaryotic organism of claim 28, further comprising one or more gene disruptions that attenuate the activity of an endogenous NAD-dependant pyruvate dehydrogenase, NAD-dependent formate dehydrogenase, NADH:ferredoxin oxidoreductase, NAD-dependent acylating acetylaldehyde dehydrogenase, or NAD-dependent acylating acetaldehyde dehydrogenase.

30. A non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and:

(1) wherein the organism:

i. comprises a disruption in a endogenous and/or exogenous nucleic acid encoding a NADH dehydrogenase;

ii. expresses an attenuated NADH dehydrogenase;

iii. has lower or no NADH dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(2) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a cytochrome oxidase;

ii. expresses an attenuated cytochrome oxidase;

iii. has lower or no cytochrome oxidase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(3) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a pyruvate decarboxylase;

ii. expresses an attenuated pyruvate decarboxylase;

iii. has lower or no pyruvate decarboxylase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. produces lower levels of ethanol from pyruvate as compared to a wild-type version of the eukaryotic organism;

v. (i.) and (ii.);

vi. (i.) and (iii.);

vii. (i.) and (iv.);

viii. (ii.) and (iii.);

ix. (ii.) and (iv.);

x. (iii.) and (iv.);

xi. (i.), (ii.) and (iii.);

xii. (i.), (iii.) and (iv.);

xiii. (ii.), (iii.) and (iv.); or

xiv. (i.), (ii.), (iii.) and (iv.);

(4) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding an ethanol dehydrogenase;

ii. expresses an attenuated ethanol dehydrogenase;

iii. has lower or no ethanol dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. produces lower levels of ethanol as compared to a wild-type version of the eukaryotic organism;

v. (i.) and (ii.);

vi. (i.) and (iii.);

vii. (i.) and (iv.);

viii. (ii.) and (iii.);

ix. (ii.) and (iv.);

x. (iii.) and (iv.);

xi. (i.), (ii.) and (iii.);

xii. (i.), (iii.) and (iv.);

xiii. (ii.), (iii.) and (iv.); or

xiv. (i.), (ii.), (iii.) and (iv.);

(5) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a malate dehydrogenase;

ii. expresses an attenuated malate dehydrogenase;

iii. has lower or no malate dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. has an attenuation or blocking of a malate-asparate shuttle, a malate oxaloacetate shuttle, and/or a malate-pyruvate shuttle;

v. (i.) and (ii.);

vi. (i.) and (iii.);

vii. (i.) and (iv.);

viii. (ii.) and (iii.);

ix. (ii.) and (iv.);

x. (iii.) and (iv.);

xi. (i.), (ii.) and (iii.);

xii. (i.), (iii.) and (iv.);

xiii. (ii.), (iii.) and (iv.); or

xiv. (i.), (ii.), (iii.) and (iv.);

(6) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding an acetoacetyl-CoA hydrolase or transferase;

ii. expresses an attenuated acetoacetyl-CoA hydrolase or transferase;

iii. has lower or no acetoacetyl-CoA hydrolase or transferase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(7) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a 3-hydroxybutyryl-CoA hydrolase or transferase;

ii. expresses an attenuated 3-hydroxybutyryl-CoA hydrolase or transferase;

iii. has lower or no 3-hydroxybutyryl-CoA hydrolase or transferase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(8) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding an acetaldehyde dehydrogenase (acylating);

ii. expresses an attenuated acetaldehyde dehydrogenase (acylating);

iii. has lower or no acetaldehyde dehydrogenase (acylating) enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(9) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a 3-hydroxybutyraldehyde dehydrogenase;

ii. expresses an attenuated 3-hydroxybutyraldehyde dehydrogenase;

iii. has lower or no 3-hydroxybutyraldehyde dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(10) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a 3-oxobutyraldehyde dehydrogenase;

ii. expresses an attenuated 3-oxobutyraldehyde dehydrogenase;

iii. has lower or no 3-oxobutyraldehyde dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(11) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a 1,3-butanediol dehydrogenase;

ii. expresses an attenuated 1,3-butanediol dehydrogenase;

iii. has lower or no 1,3-butanediol dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.); or

(12) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding an acetoacetyl-CoA thiolase

ii. expresses an attenuated acetoacetyl-CoA thiolase

iii. has lower or no acetoacetyl-CoA thiolase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii).

31. The organism of any one of claims 1 to 6, wherein said organism further comprises a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and

(l) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a G3P dehydrogenase;

ii. expresses an attenuated G3P dehydrogenase;

iii. has lower or no G3P dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. produces lower levels of glycerol as compared to a wild-type version of the eukaryotic organism;

v. (i.) and (ii.);

vi. (i.) and (iii.);

vii. (i.) and (iv.);

viii. (ii.) and (iii.);

ix. (ii.) and (iv.);

x. (iii.) and (iv.);

xi. (i.), (ii.) and (iii.);

xii. (i.), (iii.) and (iv.);

xiii. (ii.), (iii.) and (iv.); or

xiv. (i.), (ii.), (iii.) and (iv.); or

(2) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a G3P phosphatase;

ii. expresses an attenuated G3P phosphatase;

iii. has lower or no G3P phosphatase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. produces lower levels of glycerol as compared to a wild-type version of the eukaryotic organism;

v. (i.) and (ii.);

vi. (i.) and (iii.);

vii. (i.) and (iv.);

viii. (ii.) and (iii.);

ix. (ii.) and (iv.);

x. (iii.) and (iv.);

xi. (i.), (ii.) and (iii.);

xii. (i.), (iii.) and (iv.);

xiii. (ii.), (iii.) and (iv.); or

xiv. (i.), (ii.), (iii.) and (iv.).

32. A non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acids encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and wherein said organism further comprises an endogenous and/or exogenous

nucleic acid encoding a 1,3-BDO transporter, wherein the nucleic acid encoding the 1,3-BDO transporter is expressed in a sufficient amount for the exportation of 1,3-BDO from the eukaryotic organism.

33. The organism of any one of claims 24 to 32, wherein the 1,3-BDO pathway enzyme is selected from the group consisting of 4B, 4C, 4D, 4E, 4F, 4G, 4H, 4I, 4J, 4L, 4N, and 4O.

34. The organism of any one of claims 23 to 33, wherein the 1,3-BDO pathway comprises a pathway selected from the group consisting of:

i. 4A, 4E, 4F and 4G;

ii. 4A, 4B and 4D;

iii. 4A, 4E, 4C and 4D;

iv. 4A, 4H and 4J;

v. 4A, 4H, 4I and 4G;

vi. 4A, 4H, 4M, 4N and 4G;

vii. 4A, 4K, 4O, 4N and 4G;

viii. 4A, 4K, 4L, 4F and 4G

ix. 7E, 7F, 4E, 4F and 4G;

x. 7E, 7F, 4B and 4D;

xi. 7E, 7F, 4E, 4C and 4D;

xii. 7E, 7F, 4H and 4J;

xiii. 7E, 7F, 4H, 4I and 4G;

xiv. 7E, 7F, 4H, 4M, 4N and 4G;

xv. 7E, 7F, 4K, 4O, 4N and 4G; and

xvi. 7E, 7F, 4K, 4L, 4F and 4G.

35. The organism of claim 34, wherein the organism comprises an acetyl-CoA pathway selected from the group consisting of:

i. 2A, 2B and 2D;

ii. 2A, 2C and 2D;

iii. 2A, 2B, 2E and 2F;

iv. 2A, 2C, 2E and 2F;

v. 2A, 2B, 2E, 2K and 2L;

vi. 2A, 2C, 2E, 2K and 2L;

vii. 5A and 5B;

viii. 5A, 5C and 5D;

ix. 5E, 5F, 5C and 5D;

x. 5G and 5D;

xi. 6A, 6D and 6C;

xii. 6B, 6E and 6C;

xiii. 10A, 10B and 10C;

xiv. 10N, 10H, 10B and 10C;

xv. 10N, 10L, 10M, 10B and 10C;

xvi. 10A, 10B, 10G and 10D;

xvii. 10N, 10H, 10B, 10G and 10D;

xviii. 10N, 10L, 10M, 10B, 10G and 10D;

xix. 10A, 10B, 10J, 10K and 10D;

xx. 10N, 10H, 10B, 10J, 10K and 10D;

xxi. 10N, 10L, 10M, 10B, 10J, 10K and 10D;

xxii. 10A, 10F and 10D;

xxiii. 10N, 10H, 10F and 10D; and

xxiv. 10N, 10L, 10M, 10F and 10D.

36. The organism of any one of claims 22 to 35; wherein the endogenous and/or exogenous nucleic acid is an endogenous nucleic acid.

37. The organism of any one of claims 22 to 35, wherein the endogenous and/or exogenous nucleic acid is an exogenous nucleic acid.

38. A non-naturally occurring eukaryotic organism comprising:

(1) an acetoacetate pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetoacetate pathway enzyme expressed in a sufficient amount to increase acetoacetate in the cytosol of said organism, wherein said acetoacetate pathway comprises 8A, 8C, and 8F, wherein 8A is a mitochondrial acetoacetyl-CoA thiolase; 8C is a mitochondrial acetoacetyl-CoA hydrolase, transferase or synthetase; and 8F is an acetoacetate transporter; and

(2) a 1,3-BDO pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO in the cytosol of said organism, and wherein the 1,3-BDO pathway comprises a pathway selected from:

i. 4O, 4N, and 4G; and

ii. 4L, 4F, and 4G;

wherein 4F is a 3-oxobutyraldehyde reductase (ketone reducing); 4G is a 3-hydroxybutyraldehyde reductase; 4L is an acetoacetate reductase; 4N is a 3-hydroxybutyrate reductase; and 4O is a 3-hydroxybutyrate dehydrogenase.

39. A non-naturally occurring eukaryotic organism comprising:

(1) a 3-hydroxybutyrate pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 3-hydroxybutyrate pathway enzyme expressed in a sufficient amount to increase 3-hydroxybutyrate in the cytosol of said organism, wherein said 3-hydroxybutyrate pathway comprises a pathway selected from the group consisting of:

i. 8A, 8B, 8D and 8G;

ii. 8A, 8C, 8E and 8G;

iii. 8J, 8K, 8D and 8G; and

iv. 8J, 8K, 8E and 8G;

wherein 8A is a mitochondrial acetoacetyl-CoA thiolase; 8B is a mitochondrial acetoacetyl-CoA reductase; 8C is a mitochondrial acetoacetyl-CoA hydrolase, transferase or synthetase; 8D is a mitochondrial 3-hydroxybutyryl-CoA hydrolase, transferase or synthetase; 8E is a mitochondrial 3-hydroxybutyrate dehydrogenase; and 8G is a 3-hydroxybutyrate transporter; 8J is a mitochondrial acetyl-CoA carboxylase; 8K is a mitochondrial acetoacetyl-CoA synthase; and

(2) a 1,3-BDO pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO in the cytosol of said organism, and wherein the 1,3-BDO pathway comprises 4N and 4G, wherein 4G is a 3-hydroxybutyraldehyde reductase; and 4N is a 3-hydroxybutyrate reductase.

40. A non-naturally occurring eukaryotic organism comprising:

(1) a 3-hydroxybutyryl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 3-hydroxybutyryl-CoA pathway enzyme expressed in a sufficient amount to increase 3-hydroxybutyryl-CoA in the cytosol of said organism, wherein said 3-hydroxybutyryl-CoA pathway comprises a pathway selected from the group consisting of:

i. 8A, 8B, 8D, 8G and 8H;

ii. 8A, 8C, 8E, 8G and 8H;

iii. 8J, 8K, 8B, 8D, 8G, 8H; and

iv. 8J, 8K, 8C, 8E, 8G, 8H;

wherein 8A is a mitochondrial acetoacetyl-CoA thiolase; 8B is a mitochondrial acetoacetyl-CoA reductase; 8C is a mitochondrial acetoacetyl-CoA hydrolase, transferase or synthetase; 8D is a mitochondrial 3-hydroxybutyryl-CoA hydrolase,

transferase or synthetase; 8E is a mitochondrial 3-hydroxybutyrate dehydrogenase; 8G is a 3-hydroxybutyrate transporter; and 8H is a 3-hydroxybutyryl-CoA transferase or synthetase; 8J is a mitochondrial acetyl-CoA carboxylase; 8K is a mitochondrial acetoacetyl-CoA synthase; and

(2) a 1,3-BDO pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO in the cytosol of said organism, and wherein the 1,3-BDO pathway comprises a pathway selected from the group consisting of:

i. 4I and 4G; and

ii. 4J;

wherein 4I is a 3-hydroxybutyryl-CoA reductase (aldehyde forming); wherein 4G is a 3-hydroxybutyraldehyde reductase; and 4J is a 3-hydroxybutyryl-CoA reductase (alcohol forming).

41. The organism of claim 40, wherein

i. (1) the 3-hydroxybutyryl-CoA pathway comprises 8A, 8B, 8D, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4I and 4G;

ii. (1) the 3-hydroxybutyryl-CoA pathway comprises 8A, 8C, 8E, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4I and 4G;

iii. (1) the 3-hydroxybutyryl-CoA pathway comprises 8J, 8K, 8B, 8D, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4I and 4G;

iv. (1) 3-hydroxybutyryl-CoA pathway comprises 8J, 8K, 8C, 8E, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4I and 4G;

v. (1) the 3-hydroxybutyryl-CoA pathway comprises 8A, 8B, 8D, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4J;

vi. (1) the 3-hydroxybutyryl-CoA pathway comprises 8A, 8C, 8E, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4J;

vii. (1) the 3-hydroxybutyryl-CoA pathway comprises 8J, 8K, 8B, 8D, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4J; or

viii. (1) 3-hydroxybutyryl-CoA pathway comprises 8J, 8K, 8C, 8E, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4J.

42. The organism of any one of claims 22 to 41; wherein said organism is in a substantially anaerobic culture medium.

43. A method for producing 1,3-BDO, comprising culturing the organism of any one of claims 7 to 17 or 21 to 42 under conditions and for a sufficient period of time to produce 1,3-BDO.

44. The method of claim 43, wherein the organism is a Crabtree positive organism, and wherein eukaryotic organism is in a culture medium comprising excess glucose.

45. A method for selecting an exogenous 1,3-BDO pathway enzyme to be introduced into a non-naturally occurring eukaryotic organism, wherein the exogenous 1,3-BDO pathway enzyme is expressed in a sufficient amount in the organism to produce 1,3-BDO, said method comprising the steps of:

(i) measuring the activity of at least one 1,3-BDO pathway enzyme that uses NADH as a cofactor;

(ii) measuring the activity of at least one 1,3-BDO pathway enzyme that uses NADPH as a cofactor; and

(iii) introducing into the organism at least one 1,3-BDO pathway enzyme that has a greater preference for NADH than NADPH as a cofactor as determined in steps (i) and (ii).

What is claimed is:

1. A non-naturally occurring eukaryotic organism comprising:

(1) an acetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to increase acetyl-CoA in the cytosol of said organism, wherein said acetyl-CoA pathway comprises a pathway selected from the group consisting of:

i. 5H;

ii. 5J and 5I; and

iii. 5J, 5F and 5B;

wherein 5B is an acetyl-CoA synthetase, ligase or transferase; 5F is an acetaldehyde dehydrogenase; 5H is a pyruvate dehydrogenase, pyruvate:ferredoxin oxidoreductase or pyruvate formate lyase; 5I is a acetaldehyde dehydrogenase (acylating); and 5J is a threonine aldolase; and

(2) a 1,3-BDO pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the 1,3-BDO pathway comprises a pathway selected from the group consisting of:

i. 4A, 4H, 4I and 4G;

ii. 4A, 4E, 4F and 4G;

iii. 4A, 4B and 4D;

iv. 4A, 4E, 4C and 4D;

v. 4A, 4H and 4J;

vi. 4A, 4H, 4M, 4N and 4G;

vii. 4A, 4K, 4O, 4N and 4G;

viii. 4A, 4K, 4L, 4F and 4G;

ix. 7E, 7F, 4E, 4F and 4G;

x. 7E, 7F, 4B and 4D;

xi. 7E, 7F, 4E, 4C and 4D;

xii. 7E, 7F, 4H and 4J;

xiii. 7E, 7F, 4H, 4I and 4G;

xiv. 7E, 7F, 4H, 4M, 4N and 4G;

xv. 7E, 7F, 4K, 4O, 4N and 4G; and

xvi. 7E, 7F, 4K, 4L, 4F and 4G;

wherein 4A is an acetoacetyl-CoA thiolase; 4B is an acetoacetyl-CoA reductase (CoA-dependent, alcohol forming); 4C is a 3-oxobutyraldehyde reductase (aldehyde reducing), wherein 4D is a 4-hydroxy,2-butanone reductase; 4E is an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming); 4F is a 3-oxobutyraldehyde reductase (ketone reducing); 4G is a 3-hydroxybutyraldehyde reductase or a 3-hydroxybutyraldehyde reductase; 4H is an acetoacetyl-CoA reductase (ketone reducing); 4I is a 3-hydroxybutyryl-CoA reductase (aldehyde forming); 4J is a 3-hydroxybutyryl-CoA reductase (alcohol forming); 4K is an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA synthetase, or a phosphotransacetoacetylase and acetoacetate kinase; 4L is an acetoacetate reductase; 4M is a 3-hydroxybutyryl-CoA transferase, hydrolase, or synthetase; 4N is a 3-hydroxybutyrate reductase; 4O is a 3-hydroxybutyrate dehydrogenase; 7E is an acetyl-CoA carboxylase; and 7F is an acetoacetyl-CoA synthase;

wherein optionally

i. (1) the acetyl-CoA pathway comprises (1) 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

ii. (1) the acetyl-CoA pathway comprises 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

iii. (1) the acetyl-CoA pathway comprises 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

iv. (1) the acetyl-CoA pathway comprises 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

v. (1) the acetyl-CoA pathway comprises 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

vi. (1) the acetyl-CoA pathway comprises 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

vii. (1) the acetyl-CoA pathway comprises 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

viii. wherein the acetyl-CoA pathway comprises (1) 5J and 5I; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

ix. wherein the acetyl-CoA pathway comprises (1) 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

x. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xi. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xii. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xiii. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xiv. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xv. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xvi. wherein (1) the acetyl-CoA pathway comprises 5J, 5F and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xvii. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xviii. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xix. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xx. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xxi. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xxii. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xxiii. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G; or

xxiv. wherein (1) the acetyl-CoA pathway comprises 5H; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G.

2. A non-naturally occurring eukaryotic organism comprising an acetyl-CoA pathway, wherein:

(A) said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to transport acetyl-CoA from a mitochondrion of said organism to the cytosol of said organism and/or increase acetyl-CoA in the cytosol of said organism, wherein said acetyl-CoA pathway comprises a pathway selected from the group consisting of:

i. 2A, 2B and 2D;

ii. 2A, 2C and 2D;

iii. 2A, 2B, 2E and 2F;

iv. 2A, 2C, 2E and 2F;

v. 2A, 2B, 2E, 2K and 2L; and

vi. 2A, 2C, 2E, 2K and 2L;

wherein 2A is a citrate synthase; 2B is a citrate transporter; 2C is a citrate/oxaloacetate transporter or a citrate/malate transporter; 2D is an ATP citrate lyase; 2E is a citrate lyase; 2F is an acetyl-CoA synthetase; 2K is an acetate kinase; and 2L is a phosphotransacetylase;

wherein optionally said acetyl-CoA pathway further comprises 2G, 3I and/or 3J, wherein 2G is an oxaloacetate transporter, 3H is a cytosolic malate dehydrogenase, 3I is a malate transporter, and 3J is a mitochondrial malate dehydrogenase;

(B) said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to increase acetyl-CoA in the cytosol of said organism, wherein said acetyl-CoA pathway comprises a pathway selected from the group consisting of:

i. 5A and 5B;

ii. 5A, 5C and 5D;

iii. 5E, 5F, 5C and 5D; and

iv. 5G and 5D;

wherein 5A is a pyruvate oxidase (acetate forming); 5B is an acetyl-CoA synthetase, ligase or transferase; 5C is an acetate kinase; 5D is a phosphotransacetylase; 5E is a pyruvate decarboxylase, 5F is an acetaldehyde dehydrogenase; and 5G is pyruvate oxidase (acetyl-phosphate forming);

(C) said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to transport acetyl-CoA from a mitochondrion and/or peroxisome of said organism to the cytosol of said organism and/or increase acetyl-CoA in the cytosol of said organism, wherein said acetyl-CoA pathway comprises a pathway selected from the group consisting of:

i. 6A, 6D and 6C; and

ii. 6B, 6E and 6C;

wherein 6A is mitochondrial acetylcarnitine transferase; 6B is a peroxisomal acetylcarnitine transferase; 6C is a cytosolic acetylcarnitine transferase; 6D is a mitochondrial acetylcarnitine translocase; and 6E is a peroxisomal acetylcarnitine translocase; or

(D) said organism comprises at least one exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to increase acetyl-CoA in the cytosol of said organism, wherein said acetyl-CoA pathway comprises a pathway selected from the group consisting of:

i. 10A, 10B and 10C;

ii. 10N, 10H, 10B and 10C;

iii. 10N, 10L, 10M, 10B and 10C;

iv. 10A, 10B, 10G and 10D;

v. 10N, 10H, 10B, 10G and 10D;

vi. 10N, 10L, 10M, 10B, 10G and 10D;

vii. 10A, 10B, 10J, 10K and 10D;

viii. 10N, 10H, 10B, 10J, 10K and 10D;

ix. 10N, 10L, 10M, 10B, 10J, 10K and 10D;

x. 10A, 10F and 10D;

xi. 10N, 10H, 10F and 10D; and

xii. 10N, 10L, 10M, 10F and 10D;

wherein 10A is a PEP carboxylase or PEP carboxykinase; 10B is an oxaloacetate decarboxylase; 10C is a malonate semialdehyde dehydrogenase (acetylating); 10D is a malonyl-CoA decarboxylase; 10F is an oxaloacetate dehydrogenase or oxaloacetate oxidoreductase; 10G is a malonyl-CoA reductase; 10H is a pyruvate carboxylase; 10J is a malonate semialdehyde dehydrogenase; 10K is a malonyl-CoA synthetase or transferase; 10L is a malic enzyme; 10M is a malate dehydrogenase or oxidoreductase; and 10N is a pyruvate kinase or PEP phosphatase;

wherein optionally said eukaryotic organism comprises two, three, four, five, six, seven, eight, nine or ten exogenous nucleic acids each encoding an acetyl-CoA pathway enzyme.

3. The organism of claim 2, wherein said organism further comprises a 1,3-butanediol (1,3-BDO) pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and wherein the 1,3-BDO pathway comprises a pathway selected from the group consisting of:

i. 4A, 4E, 4F and 4G;

ii. 4A, 4B and 4D;

iii. 4A, 4E, 4C and 4D;

iv. 4A, 4H and 4J;

v. 4A, 4H, 4I and 4G;

vi. 4A, 4H, 4M, 4N and 4G;

vii. 4A, 4K, 4O, 4N and 4G;

viii. 4A, 4K, 4L, 4F and 4G;

ix. 7E, 7F, 4E, 4F and 4G;

x. 7E, 7F, 4B and 4D;

xi. 7E, 7F, 4E, 4C and 4D;

xii. 7E, 7F, 4H and 4J;

xiii. 7E, 7F, 4H, 4I and 4G;

xiv. 7E, 7F, 4H, 4M, 4N and 4G;

xv. 7E, 7F, 4K, 4O, 4N and 4G; and

xvi. 7E, 7F, 4K, 4L, 4F and 4G;

wherein 4A is an acetoacetyl-CoA thiolase; 4B is an acetoacetyl-CoA reductase (CoA-dependent, alcohol forming); 4C is a 3-oxobutyraldehyde reductase (aldehyde reducing); 4D is a 4-hydroxy,2-butanone reductase; 4E is an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming); 4F is a 3-oxobutyraldehyde reductase (ketone reducing); 4G is a 3-hydroxybutyraldehyde reductase; 4H is an acetoacetyl-CoA reductase (ketone reducing); 4I is a 3-hydroxybutyryl-CoA reductase (aldehyde forming); 4J is a 3-hydroxybutyryl-CoA reductase (alcohol forming); 4K is an acetoacetyl-CoA transferase, an acetoacetyl-CoA hydrolase, an acetoacetyl-CoA synthetase, or a phosphotransacetoacetylase and acetoacetate kinase; 4L is an acetoacetate reductase; 4M is a 3-hydroxybutyryl-CoA transferase, hydrolase, or synthetase; 4N is a 3-hydroxybutyrate reductase; 4O is a 3-hydroxybutyrate dehydrogenase; 7E is an acetyl-CoA carboxylase; and 7F is an acetoacetyl-CoA synthase;

wherein optionally:

i. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

ii. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises (ii) 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

iii. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

iv. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

v. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

vi. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

vii. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

viii. (1) the acetyl-CoA pathway comprises 2A, 2B and 2D and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

ix. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

x. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xi. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xii. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xiii. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xiv. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xv. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xvi. (1) the acetyl-CoA pathway comprises 2A, 2C and 2D and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xvii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xviii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xix. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xx. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xxi. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;;

xxii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xxiii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N or 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xxiv. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xxv. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xxvi. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xxvii. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xxviii. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xxix. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xxx. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xxxi. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xxxii. (1) 2A, 2C, 2E and 2F and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xxxiii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xxxiv. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises (ii) 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xxxv. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xxxvi. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xxxvii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xxxviii. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xxxix. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xl. (1) the acetyl-CoA pathway comprises 2A, 2B, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xli. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xlii. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises (ii) 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xliii. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xliv. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xlv. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xlvi. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xlvii. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xlviii. (1) the acetyl-CoA pathway comprises 2A, 2C, 2E, 2K and 2L and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xlix. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

l. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

li. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

lii. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

liii. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

liv. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

lv. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

lvi. (1) the acetyl-CoA pathway comprises 5A and 5B; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

lvii. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

lviii. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

lix. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

lx. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

lxi. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

lxii. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

lxiii. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

lxiv. (1) the acetyl-CoA pathway comprises 5A, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

lxv. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

lxvi. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

lxvii. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

lxviii. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

lxix. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

lxx. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

lxxi. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

lxxii. (1) the acetyl-CoA pathway comprises 5E, 5F, 5C and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

lxxiii. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

lxxiv. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

lxxv. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

lxxvi. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

lxxvii. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

lxxviii. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

lxxix. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G; or

lxxx. (1) the acetyl-CoA pathway comprises 5G and 5D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

lxxxi. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

lxxxii. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

lxxxiii. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

lxxxiv. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

lxxxv. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

lxxxvi. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

lxxxvii. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

lxxxviii. (1) the acetyl-CoA pathway comprises 6A, 6D and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

lxxxix. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xc. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xci. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

xcii. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

xciii. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

xciv. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

xcv. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

xcvi. (1) the acetyl-CoA pathway comprises 6B, 6E and 6C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

xcvii. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

xcviii. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

xcix. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

c. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

ci. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cii. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

ciii. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

civ. (1) the acetyl-CoA pathway comprises 10A, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cv. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cvi. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

cvii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

cviii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

cix. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cx. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cxi. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

cxii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cxiii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cxiv. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

cxv. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

cxvi. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

cxvii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cxviii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cxix. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

cxx. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B and 10C; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cxxi. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cxxii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

cxxiii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

cxxiv. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

cxxv. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cxxvi. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cxxvii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

cxxviii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cxxix. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cxxx. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

cxxxi. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

cxxxii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

cxxxiii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cxxxiv. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cxxxv. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

cxxxvi. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cxxxvii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cxxxviii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

cxxxix. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

cxl. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

cxli. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cxlii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cxliii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

cxliv. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10G and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cxlv. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cxlvi. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

cxlvii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

cxlviii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

cxlix. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cl. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cli. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

clii. (1) the acetyl-CoA pathway comprises 10A, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

cliii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

cliv. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

clv. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

clvi. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

clvii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

clviii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

clix. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

clx. (1) the acetyl-CoA pathway comprises 10N, 10H, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

clxi. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

clxii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

clxiii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

clxiv. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

clxv. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

clxvi. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

clxvii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

clxviii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10B, 10J, 10K and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

clxix. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

clxx. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

clxxi. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

clxxii. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

clxxiii. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

clxxiv. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

clxxv. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

clxxvi. (1) the acetyl-CoA pathway comprises 10A, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

clxxvii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

clxxviii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

clxxix. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

clxxx. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

clxxxi. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

clxxxii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

clxxxiii. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G;

clxxxiv. (1) the acetyl-CoA pathway comprises 10N, 10H, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G;

clxxxv. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4F and 4G; or 7E, 7F, 4E, 4F and 4G;

clxxxvi. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4B and 4D; or 7E, 7F, 4B and 4D;

clxxxvii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4E, 4C and 4D; or 7E, 7F, 4E, 4C and 4D;

clxxxviii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H and 4J; or 7E, 7F, 4H and 4J;

clxxxix. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4I and 4G; or 7E, 7F, 4H, 4I and 4G;

cxc. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4H, 4M, 4N and 4G; or 7E, 7F, 4H, 4M, 4N and 4G;

cxci. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4O, 4N and 4G; or 7E, 7F, 4K, 4O, 4N and 4G; or

cxcii. (1) the acetyl-CoA pathway comprises 10N, 10L, 10M, 10F and 10D; and (2) the 1,3-BDO pathway comprises 4A, 4K, 4L, 4F and 4G; or 7E, 7F, 4K, 4L, 4F and 4G.

4. A non-naturally occurring eukaryotic organism comprising:

(1) an acetoacetyl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetoacetyl-CoA pathway enzyme expressed in a sufficient amount to increase acetoacetyl-CoA in the cytosol of said organism, wherein said acetoacetyl-CoA pathway comprises:

i. 8A, 8C, 8F and 8I, wherein 8A is a mitochondrial acetoacetyl-CoA thiolase; 8C is a mitochondrial acetoacetyl-CoA hydrolase, transferase or synthetase; 8F is an acetoacetate transporter; and 8I is a cytosolic acetoacetyl-CoA transferase or synthetase; or

ii. 8J, 8K, 8C, 8F and 8I; wherein 8J is a mitochondrial acetyl-CoA carboxylase; 8K is a mitochondrial acetoacetyl-CoA synthase; 8C is a mitochondrial acetoacetyl-CoA hydrolase, transferase or synthetase; 8F is an acetoacetate transporter; and 8I is a cytosolic acetoacetyl-CoA transferase or synthetase; and

(2) a 1,3-BDO pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO in the cytosol of said organism, and wherein the 1,3-BDO pathway comprises a pathway selected from:

i. 4E, 4F and 4G;

ii. 4B and 4D;

iii. 4E, 4C and 4D;

iv. 4H and 4J;

v. 4H, 4I and 4G; and

vi. 4H, 4M, 4N and 4G;

wherein 4B is an acetoacetyl-CoA reductase (CoA-dependent, alcohol forming); 4C is a 3-oxobutyraldehyde reductase (aldehyde reducing); 4D is a 4-hydroxy,2-butanone reductase; 4E is an acetoacetyl-CoA reductase (CoA-dependent, aldehyde forming); 4F is a 3-oxobutyraldehyde reductase (ketone reducing); 4G is a 3-hydroxybutyraldehyde reductase; 4H is an acetoacetyl-CoA reductase (ketone reducing); 4I is a 3-hydroxybutyryl-CoA reductase (aldehyde forming); 4J is a 3-hydroxybutyryl-CoA reductase (alcohol forming); 4L is an acetoacetate reductase; 4M is a 3-hydroxybutyryl-CoA transferase, hydrolase, or synthetase; and 4N is a 3-hydroxybutyrate reductase;

wherein optionally

i. (1) the acetoacetyl-CoA pathway comprises 8A, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4E, 4F and 4G;

ii. (1) the acetoacetyl-CoA pathway comprises 8A, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4B and 4D;

iii. (1) the acetoacetyl-CoA pathway comprises 8A, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4E, 4C and 4D;

iv. (1) the acetoacetyl-CoA pathway comprises 8A, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4H and 4J;

v. (1) the acetoacetyl-CoA pathway comprises 8A, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4H, 4I and 4G;

vi. (1) the acetoacetyl-CoA pathway comprises 8A, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4H, 4M, 4N and 4G;

vii. (1) the acetoacetyl-CoA pathway comprises 8J, 8K, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4E, 4F and 4G;

viii. (1) the acetoacetyl-CoA pathway comprises 8J, 8K, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4B and 4D;

ix. (1) the acetoacetyl-CoA pathway comprises 8J, 8K, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4E, 4C and 4D;

x. (1) the acetoacetyl-CoA pathway comprises 8J, 8K, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4H and 4J;

xi. (1) the acetoacetyl-CoA pathway comprises 8J, 8K, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4H, 4I and 4G; or

xii. (1) the acetoacetyl-CoA pathway comprises 8J, 8K, 8C, 8F and 8I; and (2) the 1,3-BDO pathway comprises 4H, 4M, 4N and 4G.

5. The organism of any one of claims 1 to 4, wherein

(a) said organism comprises two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen or fifteen exogenous nucleic acids each encoding a 1,3-BDO pathway enzyme;

(b) said at least one exogenous nucleic acid is a heterologous nucleic acid;

(c) said organism is in a substantially anaerobic culture medium; and/or

(d) said organism further comprises an attenuation or deletion of one or more byproduct pathways;

wherein optionally the one or more byproduct pathways are one or more byproduct pathways depicted in FIG. 7, 3-oxobutyraldehyde dehydrogenase or acetoacetyl-CoA thiolase; and/or

wherein optionally the byproduct pathway comprises

i. a glycerol-3-phosphate (G3P) dehydrogenase that converts dihydroxyacetone to G3P;

ii. a G3P phosphatase that converts G3P to glycerol;

iii. a pyruvate decarboxylase that converts pyruvate to acetaldehyde;

iv. an ethanol dehydrogenase that converts acetaldehyde to ethanol;

v. an acetaldehyde dehydrogenase (acylating) that converts acetyl-CoA to acetaldehyde;

vi. an acetoacetyl-CoA hydrolase or transferase that converts acetoacetyl-CoA to acetoacetate;

vii. a 3-hydroxybutyryl-CoA hydrolase or transferase that converts 3-hydroxybutyryl-CoA (3-HBCoA) to 3-hydroxybutyrate;

viii. a 3-hydroxybutyraldehyde dehydrogenase that converts 3-hydroxybutyraldehyde to 3-hydroxybutyrate;

ix. a 1,3-butanediol dehydrogenase that converts 1,3-butanediol to 3-oxobutanol;

x. a mitochondrial pyruvate dehydrogenase that converts pyruvate to acetyl-CoA;

xi. a 3-oxobutyraldehyde dehydrogenase that converts 3-oxobutyraldehyde to acetoacetate; and/or

xii. an acetoacetyl-CoA thiolase that converts acetoacetyl-CoA to acetyl-CoA.

6. A method for transporting acetyl-CoA from a mitochondrion to a cytosol of a non-naturally occurring eukaryotic organism, comprising culturing the organism of any one of claims 1 to 5 under conditions and for a sufficient period of time to transport the acetyl-CoA from a mitochondrion to a cytosol of the non-naturally occurring eukaryotic organism.

7. A method for increasing acetyl-CoA in the cytosol of a non-naturally occurring eukaryotic organism, comprising culturing the organism of any one of claims 1 to 5 under conditions and for a sufficient period of time to increase the acetyl-CoA in the cytosol of the organism.

8. A method for transporting acetyl-CoA from a peroxisome to a cytosol of a non-naturally occurring eukaryotic organism, comprising culturing the organism of claim 2, part (C) or any one of claims 1, and 3 to 5 under conditions and for a sufficient period of time to transport the acetyl-CoA from a perioxisome to a cytosol of the non-naturally occurring eukaryotic organism.

9. A non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism further comprises one or more endogenous and/or exogenous nucleic acids encoding:

i. a 1,3-BDO pathway enzyme selected from the group consisting of 4A, 4B, 4C, 4D, 4E, 4F, 4G, 4H, 4I, 4J, 4L, 4N, 4O, 7E and 7F; wherein at least one nucleic acid has been altered such that the 1,3-BDO pathway enzyme encoded by the nucleic acid has a greater affinity for NADH than the 1,3-BDO pathway enzyme encoded by an unaltered or wild-type nucleic acid;

ii. an attenuated 1,3-BDO pathway enzyme selected from the group consisting of 4A, 4B, 4C, 4D, 4E, 4F, 4G, 4H, 4I, 4J, 4L, 4N, 4O, 7E and 7F; wherein the attenuated 1,3-BDO pathway enzyme is NAPDH-dependent and has lower enzymatic activity as compared to the 1,3-BDO pathway enzyme encoded by an unaltered or wild-type nucleic acid;

iii. a 1,3-BDO pathway enzyme selected from the group consisting of 4A, 4B, 4C, 4D, 4E, 4F, 4G, 4H, 4I, 4J, 4L, 4N, 4O, 7E and 7F; wherein the eukaryotic organism comprises one or more gene disruptions that attenuate the activity of an endogenous NADPH-dependent 1,3-BDO pathway enzyme; or

iv. a 1,3-BDO pathway enzyme selected from the group consisting of 4A, 4B, 4C, 4D, 4E, 4F, 4G, 4H, 4I, 4J, 4L, 4N, 4O, 7E and 7F; wherein at least one nucleic acid has been altered such that the 1,3-BDO pathway enzyme encoded by the nucleic acid has a lesser affinity for NADPH than the 1,3-BDO pathway enzyme encoded by an unaltered or wild-type nucleic acid.

10. A non-naturally occurring eukaryotic organism comprising:

(1) (a) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(b) an acetyl-CoA pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to increase NADH in the organism; wherein the acetyl-CoA pathway comprises:

i. a NAD-dependent pyruvate dehydrogenase;

ii. a pyruvate formate lyase and an NAD-dependent formate dehydrogenase;

iii. a pyruvate:ferredoxin oxidoreductase and an NADH:ferredoxin oxidoreductase;

iv. a pyruvate decarboxylase and an NAD-dependent acylating acetylaldehyde dehydrogenase;

v. a pyruvate decarboxylase, a NAD-dependent acylating acetaldehyde dehydrogenase, an acetate kinase, and a phosphotransacetylase; or

vi. a pyruvate decarboxylase, an NAD-dependent acylating acetaldehyde dehydrogenase, and an acetyl-CoA synthetase;

(2) (a) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(b) an endogenous and/or exogenous nucleic acid encoding a soluble or membrane-bound transhydrogenase, wherein the transhydrogenase is expressed in a sufficient amount to convert NADH to NADPH;

(3) (a) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(b) an endogenous and/or exogenous nucleic acid encoding an NADP-dependent phosphorylating or non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase;

(4) (a) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(b) one or more endogenous and/or exogenous nucleic acids encoding a NAD(P)H cofactor enzyme selected from the group consisting of phosphorylating or non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase; pyruvate dehydrogenase; formate dehydrogenase; and acylating acetylaldehyde dehydrogenase; wherein the one or more nucleic acids encoding a NAD(P)H

cofactor enzyme has been altered such that the NAD(P)H cofactor enzyme encoded by the nucleic acid has a greater affinity for NADPH than the NAD(P)H cofactor enzyme encoded by an unaltered or wild-type nucleic acid; or

(5) (a) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(b) one or more endogenous and/or exogenous nucleic acids encoding a NAD(P)H cofactor enzyme selected from the group consisting of a phosphorylating or non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase; a pyruvate dehydrogenase; a formate dehydrogenase; and an acylating acetylaldehyde dehydrogenase; wherein the one or more nucleic acids encoding NAD(P)H cofactor enzyme nucleic acid has been altered such that the NAD(P)H cofactor enzyme that it encodes for has a lesser affinity for NADH than the NAD(P)H cofactor enzyme encoded by an unaltered or wild-type nucleic acid.

11. A non-naturally occurring eukaryotic organism comprising:

(A) (1) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(2) a pentose phosphate pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a pentose phosphate pathway enzyme selected from the group consisting of glucose-6-phosphate dehydrogenase, 6-phosphogluconolactonase, and 6 phosphogluconate dehydrogenase (decarboxylating);

wherein optionally the organism comprises a genetic alteration that increases metabolic flux into the pentose phosphate pathway;

(B) (1) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(2) an Entner Doudoroff pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an Entner Doudoroff pathway enzyme selected from the group consisting of glucose-6-phosphate dehydrogenase, 6-phosphogluconolactonase, phosphogluconate dehydratase, and 2-keto-3-deoxygluconate 6-phosphate aldolase;

wherein optionally the organism further comprises a genetic alteration that increases metabolic flux into the Entner Doudoroff pathway;

(C) (1) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a NADPH-dependent 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and

(2) an acetyl-CoA pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding an acetyl-CoA pathway enzyme expressed in a sufficient amount to increase NADPH in the organism; wherein the acetyl-CoA pathway comprises

i. an NADP-dependent pyruvate dehydrogenase;

ii. a pyruvate formate lyase and an NADP-dependent formate dehydrogenase;

iii. a pyruvate:ferredoxin oxidoreductase and an NADPH:ferredoxin oxidoreductase;

iv. a pyruvate decarboxylase and an NADP-dependent acylating acetylaldehyde dehydrogenase;

v. a pyruvate decarboxylase, a NADP-dependent acylating acetaldehyde dehydrogenase, an acetate kinase, and a phosphotransacetylase; or

vi. a pyruvate decarboxylase, an NADP-dependent acylating acetaldehyde dehydrogenase, and an acetyl-CoA synthetase;

wherein optionally the organism comprises one or more gene disruptions that attenuate the activity of an endogenous NAD-dependant pyruvate dehydrogenase,

NAD-dependent formate dehydrogenase, NADH:ferredoxin oxidoreductase, NAD-dependent acylating acetylaldehyde dehydrogenase, or NAD-dependent acylating acetaldehyde dehydrogenase; or

(D) a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and:

(1) wherein the organism:

i. comprises a disruption in a endogenous and/or exogenous nucleic acid encoding a NADH dehydrogenase;

ii. expresses an attenuated NADH dehydrogenase;

iii. has lower or no NADH dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(2) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a cytochrome oxidase;

ii. expresses an attenuated cytochrome oxidase;

iii. has lower or no cytochrome oxidase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(3) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a pyruvate decarboxylase;

ii. expresses an attenuated pyruvate decarboxylase;

iii. has lower or no pyruvate decarboxylase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. produces lower levels of ethanol from pyruvate as compared to a wild-type version of the eukaryotic organism;

v. (i.) and (ii.);

vi. (i.) and (iii.);

vii. (i.) and (iv.);

viii. (ii.) and (iii.);

ix. (ii.) and (iv.);

x. (iii.) and (iv.);

xi. (i.), (ii.) and (iii.);

xii. (i.), (iii.) and (iv.);

xiii. (ii.), (iii.) and (iv.); or

xiv. (i.), (ii.), (iii.) and (iv.);

(4) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding an ethanol dehydrogenase;

ii. expresses an attenuated ethanol dehydrogenase;

iii. has lower or no ethanol dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. produces lower levels of ethanol as compared to a wild-type version of the eukaryotic organism;

v. (i.) and (ii.);

vi. (i.) and (iii.);

vii. (i.) and (iv.);

viii. (ii.) and (iii.);

ix. (ii.) and (iv.);

x. (iii.) and (iv.);

xi. (i.), (ii.) and (iii.);

xii. (i.), (iii.) and (iv.);

xiii. (ii.), (iii.) and (iv.); or

xiv. (i.), (ii.), (iii.) and (iv.);

(5) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a malate dehydrogenase;

ii. expresses an attenuated malate dehydrogenase;

iii. has lower or no malate dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. has an attenuation or blocking of a malate-asparate shuttle, a malate oxaloacetate shuttle, and/or a malate-pyruvate shuttle;

v. (i.) and (ii.);

vi. (i.) and (iii.);

vii. (i.) and (iv.);

viii. (ii.) and (iii.);

ix. (ii.) and (iv.);

x. (iii.) and (iv.);

xi. (i.), (ii.) and (iii.);

xii. (i.), (iii.) and (iv.);

xiii. (ii.), (iii.) and (iv.); or

xiv. (i.), (ii.), (iii.) and (iv.);

(6) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding an acetoacetyl-CoA hydrolase or transferase;

ii. expresses an attenuated acetoacetyl-CoA hydrolase or transferase;

iii. has lower or no acetoacetyl-CoA hydrolase or transferase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(7) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a 3-hydroxybutyryl-CoA hydrolase or transferase;

ii. expresses an attenuated 3-hydroxybutyryl-CoA hydrolase or transferase;

iii. has lower or no 3-hydroxybutyryl-CoA hydrolase or transferase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(8) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding an acetaldehyde dehydrogenase (acylating);

ii. expresses an attenuated acetaldehyde dehydrogenase (acylating);

iii. has lower or no acetaldehyde dehydrogenase (acylating) enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(9) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a 3-hydroxybutyraldehyde dehydrogenase;

ii. expresses an attenuated 3-hydroxybutyraldehyde dehydrogenase;

iii. has lower or no 3-hydroxybutyraldehyde dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(10) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a 3-oxobutyraldehyde dehydrogenase;

ii. expresses an attenuated 3-oxobutyraldehyde dehydrogenase;

iii. has lower or no 3-oxobutyraldehyde dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.);

(11) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a 1,3-butanediol dehydrogenase;

ii. expresses an attenuated 1,3-butanediol dehydrogenase;

iii. has lower or no 1,3-butanediol dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii.); or

(12) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding an acetoacetyl-CoA thiolase

ii. expresses an attenuated acetoacetyl-CoA thiolase

iii. has lower or no acetoacetyl-CoA thiolase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. (i.) and (ii.);

v. (i.) and (iii.);

vi. (ii.) and (iii.); or

vii. (i.), (ii.) and (iii).

12. The organism of any one of claim 2, wherein said organism further comprises a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO, and

(1) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a G3P dehydrogenase;

ii. expresses an attenuated G3P dehydrogenase;

iii. has lower or no G3P dehydrogenase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. produces lower levels of glycerol as compared to a wild-type version of the eukaryotic organism;

v. (i.) and (ii.);

vi. (i.) and (iii.);

vii. (i.) and (iv.);

viii. (ii.) and (iii.);

ix. (ii.) and (iv.);

x. (iii.) and (iv.);

xi. (i.), (ii.) and (iii.);

xii. (i.), (iii.) and (iv.);

xiii. (ii.), (iii.) and (iv.); or

xiv. (i.), (ii.), (iii.) and (iv.); or

(2) wherein the organism:

i. comprises a disruption in an endogenous and/or exogenous nucleic acid encoding a G3P phosphatase;

ii. expresses an attenuated G3P phosphatase;

iii. has lower or no G3P phosphatase enzymatic activity as compared to a wild-type version of the eukaryotic organism;

iv. produces lower levels of glycerol as compared to a wild-type version of the eukaryotic organism;

v. (i.) and (ii.);

vi. (i.) and (iii.);

vii. (i.) and (iv.);

viii. (ii.) and (iii.);

ix. (ii.) and (iv.);

x. (iii.) and (iv.);

xi. (i.), (ii.) and (iii.);

xii. (i.), (iii.) and (iv.);

xiii. (ii.), (iii.) and (iv.); or

xiv. (i.), (ii.), (iii.) and (iv.).

13. A non-naturally occurring eukaryotic organism comprising a 1,3-BDO pathway, wherein said organism comprises at least one endogenous and/or exogenous nucleic acids encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO; and wherein said organism further comprises an endogenous and/or exogenous nucleic acid encoding a 1,3-BDO transporter, wherein the nucleic acid encoding the 1,3-BDO transporter is expressed in a sufficient amount for the exportation of 1,3-BDO from the eukaryotic organism.

14. The organism of any one of claims 11 to 13, wherein the 1,3-BDO pathway enzyme is selected from the group consisting of 4B, 4C, 4D, 4E, 4F, 4G, 4H, 4I, 4J, 4L, 4N, and 4O.

15. The organism of any one of claims 10 to 14, wherein the 1,3-BDO pathway comprises a pathway selected from the group consisting of:

i. 4A, 4E, 4F and 4G;

ii. 4A, 4B and 4D;

iii. 4A, 4E, 4C and 4D;

iv. 4A, 4H and 4J;

v. 4A, 4H, 4I and 4G;

vi. 4A, 4H, 4M, 4N and 4G;

vii. 4A, 4K, 4O, 4N and 4G;

viii. 4A, 4K, 4L, 4F and 4G

ix. 7E, 7F, 4E, 4F and 4G;

x. 7E, 7F, 4B and 4D;

xi. 7E, 7F, 4E, 4C and 4D;

xii. 7E, 7F, 4H and 4J;

xiii. 7E, 7F, 4H, 4I and 4G;

xiv. 7E, 7F, 4H, 4M, 4N and 4G;

xv. 7E, 7F, 4K, 4O, 4N and 4G; and

xvi. 7E, 7F, 4K, 4L, 4F and 4G;

wherein optionally the organism comprises an acetyl-CoA pathway selected from the group consisting of:

i. 2A, 2B and 2D;

ii. 2A, 2C and 2D;

iii. 2A, 2B, 2E and 2F;

iv. 2A, 2C, 2E and 2F;

v. 2A, 2B, 2E, 2K and 2L;

vi. 2A, 2C, 2E, 2K and 2L;

vii. 5A and 5B;

viii. 5A, 5C and 5D;

ix. 5E, 5F, 5C and 5D;

x. 5G and 5D;

xi. 6A, 6D and 6C;

xii. 6B, 6E and 6C;

xiii. 10A, 10B and 10C;

xiv. 10N, 10H, 10B and 10C;

xv. 10N, 10L, 10M, 10B and 10C;

xvi. 10A, 10B, 10G and 10D;

xvii. 10N, 10H, 10B, 10G and 10D;

xviii. 10N, 10L, 10M, 10B, 10G and 10D;

xix. 10A, 10B, 10J, 10K and 10D;

xx. 10N, 10H, 10B, 10J, 10K and 10D;

xxi. 10N, 10L, 10M, 10B, 10J, 10K and 10D;

xxii. 10A, 10F and 10D;

xxiii. 10N, 10H, 10F and 10D; and

xxiv. 10N, 10L, 10M, 10F and 10D.

16. The organism of any one of claims 9 to 15; wherein the endogenous and/or exogenous nucleic acid is an endogenous nucleic acid.

17. The organism of any one of claims 9 to 15, wherein the endogenous and/or exogenous nucleic acid is an exogenous nucleic acid.

18. A non-naturally occurring eukaryotic organism comprising:

(A) (1) an acetoacetate pathway, wherein said organism comprises at least one exogenous nucleic acid encoding an acetoacetate pathway enzyme expressed in a sufficient amount to increase acetoacetate in the cytosol of said organism, wherein

said acetoacetate pathway comprises 8A, 8C, and 8F, wherein 8A is a mitochondrial acetoacetyl-CoA thiolase; 8C is a mitochondrial acetoacetyl-CoA hydrolase, transferase or synthetase; and 8F is an acetoacetate transporter; and

(2) a 1,3-BDO pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO in the cytosol of said organism, and wherein the 1,3-BDO pathway comprises a pathway selected from:

i. 4O, 4N, and 4G; and

ii. 4L, 4F, and 4G;

wherein 4F is a 3-oxobutyraldehyde reductase (ketone reducing); 4G is a 3-hydroxybutyraldehyde reductase; 4L is an acetoacetate reductase; 4N is a 3-hydroxybutyrate reductase; and 4O is a 3-hydroxybutyrate dehydrogenase;

(B) (1) a 3-hydroxybutyrate pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 3-hydroxybutyrate pathway enzyme expressed in a sufficient amount to increase 3-hydroxybutyrate in the cytosol of said organism, wherein said 3-hydroxybutyrate pathway comprises a pathway selected from the group consisting of:

i. 8A, 8B, 8D and 8G;

ii. 8A, 8C, 8E and 8G;

iii. 8J, 8K, 8D and 8G; and

iv. 8J, 8K, 8E and 8G;

wherein 8A is a mitochondrial acetoacetyl-CoA thiolase; 8B is a mitochondrial acetoacetyl-CoA reductase; 8C is a mitochondrial acetoacetyl-CoA hydrolase, transferase or synthetase; 8D is a mitochondrial 3-hydroxybutyryl-CoA hydrolase, transferase or synthetase; 8E is a mitochondrial 3-hydroxybutyrate dehydrogenase; and 8G is a 3-hydroxybutyrate transporter; 8J is a mitochondrial acetyl-CoA carboxylase; 8K is a mitochondrial acetoacetyl-CoA synthase; and

(2) a 1,3-BDO pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO in the cytosol of said organism, and wherein the 1,3-BDO pathway comprises 4N and 4G, wherein 4G is a 3-hydroxybutyraldehyde reductase; and 4N is a 3-hydroxybutyrate reductase; or

(C) (1) a 3-hydroxybutyryl-CoA pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 3-hydroxybutyryl-CoA pathway enzyme expressed in a sufficient amount to increase 3-hydroxybutyryl-CoA in the cytosol of said organism, wherein said 3-hydroxybutyryl-CoA pathway comprises a pathway selected from the group consisting of:

i. 8A, 8B, 8D, 8G and 8H;

ii. 8A, 8C, 8E, 8G and 8H;

iii. 8J, 8K, 8B, 8D, 8G, 8H; and

iv. 8J, 8K, 8C, 8E, 8G, 8H;

wherein 8A is a mitochondrial acetoacetyl-CoA thiolase; 8B is a mitochondrial acetoacetyl-CoA reductase; 8C is a mitochondrial acetoacetyl-CoA hydrolase, transferase or synthetase; 8D is a mitochondrial 3-hydroxybutyryl-CoA hydrolase, transferase or synthetase; 8E is a mitochondrial 3-hydroxybutyrate dehydrogenase; 8G is a 3-hydroxybutyrate transporter; and 8H is a 3-hydroxybutyryl-CoA transferase or synthetase; 8J is a mitochondrial acetyl-CoA carboxylase; 8K is a mitochondrial acetoacetyl-CoA synthase; and

(2) a 1,3-BDO pathway, wherein said organism comprises at least one exogenous nucleic acid encoding a 1,3-BDO pathway enzyme expressed in a sufficient amount to produce 1,3-BDO in the cytosol of said organism, and wherein the 1,3-BDO pathway comprises a pathway selected from the group consisting of:

i. 4I and 4G; and

ii. 4J;

wherein 4I is a 3-hydroxybutyryl-CoA reductase (aldehyde forming); wherein 4G is a 3-hydroxybutyraldehyde reductase; and 4J is a 3-hydroxybutyryl-CoA reductase (alcohol forming);

wherein optionally

i. (1) the 3-hydroxybutyryl-CoA pathway comprises 8A, 8B, 8D, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4I and 4G;

ii. (1) the 3-hydroxybutyryl-CoA pathway comprises 8A, 8C, 8E, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4I and 4G;

iii. (1) the 3-hydroxybutyryl-CoA pathway comprises 8J, 8K, 8B, 8D, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4I and 4G;

iv. (1) 3-hydroxybutyryl-CoA pathway comprises 8J, 8K, 8C, 8E, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4I and 4G;

v. (1) the 3-hydroxybutyryl-CoA pathway comprises 8A, 8B, 8D, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4J;

vi. (1) the 3-hydroxybutyryl-CoA pathway comprises 8A, 8C, 8E, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4J;

vii. (1) the 3-hydroxybutyryl-CoA pathway comprises 8J, 8K, 8B, 8D, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4J; or

viii. (1) 3-hydroxybutyryl-CoA pathway comprises 8J, 8K, 8C, 8E, 8G, and 8H, and (2) the 1,3-BDO pathway comprises 4J.

19. The organism of any one of claims 9 to 18; wherein said organism is in a substantially anaerobic culture medium.

20. A method for producing 1,3-BDO, comprising culturing the organism of any one of claims 1, 3 to 5, and 8 to 19 under conditions and for a sufficient period of time to produce 1,3-BDO;

wherein optionally the organism is a Crabtree positive organism, and wherein eukaryotic organism is in a culture medium comprising excess glucose.

21. A method for selecting an exogenous 1,3-BDO pathway enzyme to be introduced into a non-naturally occurring eukaryotic organism, wherein the exogenous 1,3-BDO pathway enzyme is expressed in a sufficient amount in the organism to produce 1,3-BDO, said method comprising the steps of:

(i) measuring the activity of at least one 1,3-BDO pathway enzyme that uses NADH as a cofactor;

(ii) measuring the activity of at least one 1,3-BDO pathway enzyme that uses NADPH as a cofactor; and

(iii) introducing into the organism at least one 1,3-BDO pathway enzyme that has a greater preference for NADH than NADPH as a cofactor as determined in steps (i) and (ii).