CLAIMS

1. A non-naturally occurring bacterium having decreased or eliminated activity of an enzyme belonging to EC 1.2.7.5 compared to a parental bacterium, wherein the non-naturally occurring bacterium comprises at least one disruptive mutation in a gene encoding the enzyme that belongs to EC 1.2.7.5.

2. The non-naturally occurring bacterium of claim 1, wherein the enzyme belonging to EC 1.2.7.5 is aldehyde:ferredoxin oxidoreductase.

3. The non-naturally occurring bacterium of claim 1, wherein the non-naturally occurring bacterium further has decreased or eliminated activity of at least one enzyme belonging to EC 1.2.1.10 and/or EC 1.1.1.1 compared to the parental bacterium, wherein the non-naturally occurring bacterium comprises at least one disruptive mutation in a gene encoding the enzyme that belongs to EC 1.2.1.10 and/or EC 1.1.1.1.

4. The non-naturally occurring bacterium of claim 3, wherein the enzyme belonging to EC 1.2.1.10 and/or EC 1.1.1.1 is selected from the group consisting of bifunctional aldehyde/alcohol dehydrogenase, aldehyde dehydrogenase, and alcohol dehydrogenase.

5. The non-naturally occurring bacterium of claim 1, wherein the non-naturally occurring bacterium produces a product selected from the group consisting of acetyl-CoA, acetoacetyl-CoA, acetoacetate, acetone, isopropanol, 3-hydroxyisovaleryl-CoA, 3-hydroxyisovalerate, isobutylene, isoprene, 3-hydroxybutyryl-CoA, 3-hydroxybutyrate, 3-hydroxybutyrylaldehyde, 1,3-butanediol, 2-hydroxyisobutyryl-CoA, 2-hydroxyisobutyrate, pyruvate, acetolactate, acetoin, 2,3-butanediol and lactate.

6. The non-naturally occurring bacterium of claim 1, wherein the non-naturally occurring bacterium consumes a gaseous substrate comprising one or more of CO, CO_2, and H_2.

7. The non-naturally occurring bacterium of claim 1, wherein the parental bacterium is selected from the group consisting of *Alkalibaculum bacchi, Blautia product, Butyribacterium methylotrophicum, Chloroflexus aurantiacus, Clostridium aceticum, Clostridium acetobutylicum, Clostridium autoethanogenum, Clostridium botulinum, Clostridium carboxidivorans, Clostridium coskatii, Clostridium drakei, Clostridium formicoaceticum, Clostridium ljungdahlii, Clostridium ragsdalei, Desulfovibrio vulgaris, Eubacterium limosum, Geobacter sulfurreducens, Methylomicrobium alcaliphilum, Moorella*

thermoautrophica, Moorella thermoacetica, Rhodospirillum rubrum, Sporomusa ovata, Sporomusa silvacetica, Sporomusa sphaeroides, Thermanaerovibrio acidaminovorans, Thermanaerovibrio acidaminovorans, Thermoanaerobacter wiegelii, Thermodesulfovibrio yellowstonii, Thermodesulfovibrio yellowstonii, and *Thermus thermophilus.*

8. A method of producing a product by culturing the non-naturally occurring bacterium of claim 1 in the presence of a gaseous substrate comprising one or more of CO, CO_2, and H_2.

9. The method of claim 8, wherein the enzyme belonging to EC 1.2.7.5 is aldehyde:ferredoxin oxidoreductase.

10. The method of claim 8, wherein the non-naturally occurring bacterium further has decreased or eliminated activity of at least one enzyme belonging to EC 1.2.1.10 and/or EC 1.1.1.1 compared to the parental bacterium, wherein the non-naturally occurring bacterium comprises at least one disruptive mutation in a gene encoding the enzyme that belongs to EC 1.2.1.10 and/or EC 1.1.1.1.

11. The method of claim 10, wherein the enzyme belonging to EC 1.2.1.10 and/or EC 1.1.1.1 is selected from the group consisting of bifunctional aldehyde/alcohol dehydrogenase, aldehyde dehydrogenase, and alcohol dehydrogenase.

12. The method of claim 8, wherein the product is an acetyl-CoA-derived product selected from the group consisting of acetyl-CoA, acetoacetyl-CoA, acetoacetate, acetone, isopropanol, 3-hydroxyisovaleryl-CoA, 3-hydroxyisovalerate, isobutylene, isoprene, 3-hydroxybutyryl-CoA, 3-hydroxybutyrate, 3-hydroxybutyrylaldehyde, 1,3-butanediol, 2-hydroxyisobutyryl-CoA, 2-hydroxyisobutyrate, pyruvate, acetolactate, acetoin, 2,3-butanediol and lactate.

13. The method of claim 8, wherein the parental bacterium is selected from the group consisting of *Alkalibaculum bacchi, Blautia product, Butyribacterium methylotrophicum, Chloroflexus aurantiacus, Clostridium aceticum, Clostridium acetobutylicum, Clostridium autoethanogenum, Clostridium botulinum, Clostridium carboxidivorans, Clostridium coskatii, Clostridium drakei, Clostridium formicoaceticum, Clostridium ljungdahlii, Clostridium ragsdalei, Desulfovibrio vulgaris, Eubacterium limosum, Geobacter sulfurreducens, Methylomicrobium alcaliphilum, Moorella thermoautrophica, Moorella thermoacetica, Rhodospirillum rubrum, Sporomusa ovata, Sporomusa silvacetica, Sporomusa sphaeroides, Thermanaerovibrio acidaminovorans, Thermanaerovibrio acidaminovorans, Thermoanaerobacter wiegelii, Thermodesulfovibrio yellowstonii, Thermodesulfovibrio yellowstonii,* and *Thermus thermophilus.*