CLAIMS

The following is claimed:

1. A modified microorganism capable of butyl acetate (BA) production, the microorganism capable of expressing an alcohol acyl transferase (AAT); and comprising a butanol synthesis pathway.
2. The modified microorganism of claim 1, wherein the AAT is selected from one or more of: Vaat, Saat, Atf1, Eht1, and a functional homolog of any of the foregoing.
3. The modified microorganism of claim 1 or 2, comprising an acetyl CoA synthesis pathway.
4. The modified microorganism of any one of claims 1-3, comprising multiple nucleic acid sequences each encoding Atf1 or a functional homolog of Atf1.
5. The modified microorganism of any one of claims 1-4, wherein the microorganism is selected from *Clostridium saccharoperbutylacetonicum, Clostridium beijerinckii, Clostridium pasteurianum,* and *Clostridium tyrobutyricum.*
6. The modified microorganism of any one of claims 1-5, capable of expressing Lipase B or a functional homolog of Lipase B.
7. The modified microorganism of any one of claims 1-6, having reduced or eliminated NuoG activity.
8. The modified microorganism of any one of claims 1-7, capable of expressing a heterologous Sadh or a functional homolog thereof.
9. The modified microorganism of any one of claims 1-8, comprising an exogenous AAT gene operatively linked to promoter $P_{adh.}$
10. The modified microorganism of any one of claims 1-9 wherein the AAT is localized at the cell membrane.
11. The modified microorganism of any one of claims 1-10, wherein the microorganism has been cured of all native prophages.
12. The modified microorganism of any one of claims 1-11, wherein the microorganism is a bacterium of genus *Clostridium,* and wherein the microorganism has been cured of one or more of prophages P1, P2, P3, P4, and P5.
13. The modified microorganism of any one of claims 1-12, wherein said microorganism does not express a functional redox-sensing transcriptional repressor Rex.

14. The modified microorganism of any one of claims 1-13, capable of expressing soluble pyridine nucleotide transhydrogenase (SthA) or a functional homolog thereof.
15. The modified microorganism of any one of claims 1-14, wherein said microorganism does not express a functional *cftA1-ctfB1* gene cluster.
16. A modified microorganism that is a *Clostridium saccharoperbutylacetonicum* having improved BA production and designated YM028P, having NCMA designation number 202012116, deposited on 16 December 2020 at the National Center for Marine Algae and Microbiota at Bigelow Laboratory for Ocean Sciences, 60 Bigelow Drive, East Boothbay, ME 04544 USA.
17. A modified microorganism that is a *Clostridium saccharoperbutylacetonicum* having improved BA production and designated FJ-1301, having NCMA designation number 202012114, deposited on 16 December 2020 at the National Center for Marine Algae and Microbiota at Bigelow Laboratory for Ocean Sciences, 60 Bigelow Drive, East Boothbay, ME 04544 USA.
18. A method of BA production, comprising culturing the modified microorganism of any one of claims 1-17 under conditions suitable to produce BA.
19. The method of claim 18, comprising culturing the modified microorganism in a medium containing a biomass hydrolysate.
20. The method of claim 18 or 19, producing at least 1.5 g BA/L of culture.