What is claimed is:

1. A genetically modified microorganism comprising:

(a) at least one genetic modification to produce 3-hydroxypropionic acid ("3-HP"); ~~and~~

(b) a disruption of aldA; ~~and~~

(c) a disruption of puuC.

2. The genetically modified microorganism of claim 1, wherein (a) increases microbial synthesis of 3-HP above a rate or titer of a control microorganism lacking (a) .

3. The genetically modified microorganism of claim 1, further comprising a genetic modification effective to increase the 3-HP tolerance of the genetically modified microorganism by at least about 5 percent, at least about 10 percent, at least about 20 percent, at least about 30 percent, or at least about 50 percent above the 3-HP tolerance of a control microorganism.

4. The genetically modified microorganism of claim 3, wherein the genetic modification comprises a modification of one or more ~~3HPTGC~~ 3-hydroxypropionic toleragenic complex genes selected from a group consisting of: tyrR, trpR, metJ, purR, lysR, nrdR, equivalent genes, and any combination thereof.

5. The genetically modified microorganism of claim 4, wherein the modification comprises a disruption.

6. The genetically modified microorganism of any one of the preceding claims, wherein the genetic modification is selected from a group consisting of: increasing expression of an endogenous genetic element; decreasing functionality of a gene; altering or modifying feedback inhibition; introducing a heterologous genetic element; increasing copy number of a nucleic acid sequence encoding a polypeptide catalyzing an enzymatic conversion of the ~~3HPTGC~~ 3-hydroxypropionic toleragenic complex; mutating a genetic element to provide a mutated protein to increase specific enzymatic activity; random mutagenesis, and any combination thereof.

7. The genetically modified microorganism of any one of the preceding claims, wherein at least one of the genetic modification(s) encodes at least one polypeptide catalyzing at least one enzymatic conversion of the ~~3HPTGC~~ 3-hydroxypropionic toleragenic complex.

8. The genetically modified microorganism of any one of the preceding claims, further comprising increasing the expression of SEQ ID NO:129.

9. The genetically modified microorganism of any one of the preceding claims wherein the genetically modified microorganism has an increase in one or more enzymatic conversions of the ~~3HPTGC~~ 3-hydroxypropionic toleragenic complex compared to a control microorganism lacking the genetic modification(s).

10. The genetically modified microorganism of any one of the preceding claims comprising increased carbonic anhydrase activity.

11. The genetically modified microorganism of claim 8, wherein the genetically modified microorganism is *E. coli* or *Cupriavidus necator*.

12. The genetically modified microorganism of any one of the preceding claims, that is a gram-negative bacterium.

13. The genetically modified microorganism of claim 12, that is selected from a group consisting of: *Zymomonas*, *Escherichia*, *Pseudomonas*, *Alcaligenes*, *Salmonella*, *Shigella*, *Burkholderia*, *Oligotropha*, and *Klebsiella*.

14. The genetically modified microorganism of claim 12,that is selected from a group consisting of: *Escherichia coli*, *Cupriavidus necator*, *Oligotropha carboxidovorans*, and *Pseudomonas putida*.

15. The genetically modified microorganism of claim 12, that is *E. coli*.

16. The genetically modified microorganism of any one of claims 1-3, 4-7, 8-9, or 10, that is a gram-positive bacterium.

17. The genetically modified microorganism of claim 16, that is selected from a group consisting of: *Clostridium*, *Rhodococcus*, *Bacillus*, *Lactobacillus*, *Enterococcus*, *Paenibacillus*, *Arthrobacter*, *Corynebacterium*, and *Brevibacterium*.

18. The genetically modified microorganism of claim 16, that is selected from a group consisting of: *Bacillus licheniformis*, *Paenibacillus macerans*, *Rhodococcus erythropolis*, *Lactobacillus plantarum*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus faecalis*, and *Bacillus subtilis*.

19. The genetically modified microorganism of claim 16, that is *B. subtilis*.

20. The genetically modified microorganism of any one of claims 1-3, 4-7, 8-9, or 10, that is a fungus.

21. The genetically modified microorganism of claim 20, that is a yeast.

22. The genetically modified microorganism of claim 21, that is selected from a group consisting of: *Pichia*, *Candida*, *Hansenula* and *Saccharomyces*.

23. The genetically modified microorganism of claim 21, that is *Saccharomyces cerevisiae*.

24. A culture system comprising:

(a) the genetically modified microorganism of any of the above claims; and

(b) medium comprising at least about 1 g/L of 3-HP.

25. The culture system of claim 24, wherein the medium comprises at least about 5 g/L of 3-HP.

26. The culture system of claim 24, wherein the medium comprises at least about 10 g/L of 3-HP.

27. The culture system of claim 24, wherein the medium comprises at least about 20 g/L of 3-HP.

28. The culture system of claim 24, wherein the medium comprises at least about 50 g/L of 3-HP.

29. The culture system of claim 24, further comprising at least one supplementthat comprises at least one reactant of an enzymatic conversion of the ~~3HPTGC~~ 3-hydroxypropionic toleragenic complex.

30. The culture system of claim 29, wherein the at least one supplement is selected from Table 3.

31. The culture system of claim 24, wherein the genetically modified microorganism has increased 3-HP tolerance compared to a control microorganism.

32. The culture system of claim 31, wherein the genetically modified microorganism has increased 3-HP tolerance of at least about 5 percent greater, at least about 10 percent greater, at least about 20 percent greater, at least about 30 percent greater, or at least about 50 percent greater than the control microorganism.

33. The culture system of claim 24, wherein the medium is a minimal medium .

34. A method of making a genetically modified microorganism comprising:

(a) introducing into a microorganism at least one or more genes of the 3-HP production pathway to increase microbial synthesis of 3-HP above the rate of a control microorganism lacking the at least one or more genes; ~~and~~

(b) disrupting aldA; ~~and.~~

(c) disrupting puuC.

35. The method of claim 34, wherein two or more genes of the 3-HP production pathway are introduced into the microorganism.

36. The method of claim 34, wherein the control microorganism does not produce 3-HP.

37. A genetically modified microorganism made by the method of claim 34, 35, or 36.

38. The genetically modified microorganism of or employed by any of claims 1-33, or 37, further comprising a heterologous malonyl-CoA reductase gene.

39. The method of any of claims 34-36, further comprising introducing into the microorganism a heterologous malonyl-CoA reductase gene.

40. The genetically modified microorganism of claim 1, further comprising at least one genetic modification of one or more ~~3HPTGC~~ 3-hydroxypropionic toleragenic complex genes selected from a group consisting of: aceA, aceB, aceE, aceF, ackA, argB, argH, aroB, aroE, cysM, folA, folD, gcvH, gcvP, gcvT, gdhA, gltA, ilvA, ldhA, 1pd, pfkA, pfkB, pflB, poxB, pta, ~~puuC,~~ pyrC, and any combination thereof.

~~41. The genetically modified microorganism of claim 40, wherein the at least one genetic modification is to puuC.~~

~~42.~~41. The genetically modified microorganism of claims 40 ~~or 41~~, wherein the least one genetic modification comprises a disruption.

~~43.~~42. The method of claim 34, further comprising introducing to the microorganism at least one genetic modification of one or more ~~3HPTGC~~ 3-hydroxypropionic toleragenic complex genes selected from a group consisting of: aceA, aceB, aceE, aceF, ackA, argB, argH, aroB, aroE, cysM, folA, folD, gcvH, gcvP, gcvT, gdhA, gltA, ilvA, ldhA, 1pd, pfkA, pfkB, pflB, poxB, pta, ~~puuC,~~ pyrC, and any combination thereof.

~~44. The method of claim 43, wherein the at least one genetic modification is to puuC.~~

~~45.~~43. The method of claims 4243 ~~or 44~~, wherein the modification comprises a disruption.

~~46.~~44. The genetically modified microorganism of or employed by any of claims 1, 5, 34, 4142, and 4345, wherein the disruption is a deletion.

~~47. A genetically modified microorganism comprising:~~

~~(a) at least one genetic modification to produce 3-HP; and~~

~~(b) a disruption of puuC.~~

48. The genetically modified microorganism of claim 47, wherein (a) increases microbial synthesis of 3-HP above a rate or titer of a control microorganism lacking (a).

49. The genetically modified microorganism of claim 47, further comprising a genetic modification effective to increase the 3-HP tolerance of the genetically modified microorganism by at least about 5 percent, at least about 10 percent, at least about 20 percent, at least about 30 percent, or at least about 50 percent above the 3-HP tolerance of a control microorganism.

50. The genetically modified microorganism of claim 49, wherein the genetic modification comprises a modification of one or more 3HPTGC genes selected from a group consisting of: aceA, aceB, aceE, aceF, ackA, aldA, argB, argH, aroB, aroE, cysM, folA, folD, gcvH, gcvP, gcvT, gdhA, gltA, ilvA, ldhA, lpd, lysR, metJ, nrdR, pfkA, pfkB, pflB, poxB, pta, purR, pyrC, tyrR, trpR, equivalent genes, and any combination thereof.

51. The genetically modified microorganism of claim 50, wherein the modification comprises a disruption.

52. The genetically modified microorganism of claim 51, wherein the disruption is a deletion.

53. The genetically modified microorganism of any one of claims 47-52, wherein the genetic modification is selected from a group consisting of: increasing expression of an endogenous genetic element; decreasing functionality of a gene; altering or modifying feedback inhibition; introducing a heterologous genetic element; increasing copy number of a nucleic acid sequence encoding a polypeptide catalyzing an enzymatic conversion of the 3HPTGC; mutating a genetic element to provide a mutated protein to increase specific enzymatic activity; random mutagenesis, and any combination thereof.

54. The genetically modified microorganism of any one of claims 47-53, wherein at least one of the genetic modification(s) encodes at least one polypeptide catalyzing at least one enzymatic conversion of the 3HPTGC.

55. The genetically modified microorganism of any one of claims 47-54, further comprising increasing the expression of SEQ ID NO:129.

56. The genetically modified microorganism of any one of claims 47-55, wherein the genetically modified microorganism has an increase in one or more enzymatic conversions of the 3HPTGC compared to a control microorganism lacking the genetic modification(s).

57. The genetically modified microorganism of any one of claims 47-56, comprising increased carbonic anhydrase activity.

58. The genetically modified microorganism of claim 55, wherein the genetically modified microorganism is *E. coli* or *Cupriavidus necator*.

59. The genetically modified microorganism of any one of claims 47-58, that is a gram-negative bacterium.

60. The genetically modified microorganism of claim 59, that is selected from a group consisting of: *Zymomonas*, *Escherichia*, *Pseudomonas*, *Alcaligenes*, *Salmonella*, *Shigella*, *Burkholderia*, *Oligotropha*, and *Klebsiella*.

61. The genetically modified microorganism of claim 59, that is selected from a group consisting of: *Escherichia coli*, *Cupriavidus necator*, *Oligotropha carboxidovorans*, and *Pseudomonas putida*.

62. The genetically modified microorganism of claim 59, that is *E. coli*.

63. The genetically modified microorganism of any one of claims 47-49, 51-54, 55-56, or 57, that is a gram-positive bacterium.

64. The genetically modified microorganism of claim 63, that is selected from a group consisting of: *Clostridium*, *Rhodococcus*, *Bacillus*, *Lactobacillus*, *Enterococcus*, *Paenibacillus*, *Arthrobacter*, *Corynebacterium*, and *Brevibacterium*.

65. The genetically modified microorganism of claim 63, that is selected from a group consisting of: *Bacillus licheniformis*, *Paenibacillus macerans*, *Rhodococcus erythropolis*, *Lactobacillus plantarum*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus faecalis*, and *Bacillus subtilis*.

66. The genetically modified microorganism of claim 63, wherein that is *B. subtilis*.

67. The genetically modified microorganism of any one of claims 47-49, 51-54, or 55-57, that is a fungus.

68. The genetically modified microorganism of claim 67, that is a yeast.

69. The genetically modified microorganism of claim 68, that is selected from a group consisting of: *Pichia*, *Candida*, *Hansenula* and *Saccharomyces*.

70. The genetically modified microorganism of claim 68, that is *Saccharomyces cerevisiae*.

71. A method of making a genetically modified microorganism comprising:

(a) introducing into a microorganism at least one or more genes of the 3-HP production pathway to increase microbial synthesis of 3-HP above the rate of a control microorganism lacking the at least one or more genes; and

(b) disrupting puuC.

72. The method of claim 71, wherein two or more genes of the 3-HP production pathway are introduced into the microorganism.

73. The method of claim 71, wherein the control microorganism does not produce 3-HP.

74. A genetically modified microorganism, made by the method of claim 71, 72, or 73.

75. The genetically modified microorganism of claims 1-70, further comprising a heterologous malonyl-CoA reductase gene.

76. The method of any of claims 71-73, further comprising introducing into the microorganism a heterologous malonyl-CoA reductase gene.

77. The method of claim 71, wherein the disruption is a deletion.