WHAT IS CLAIMED IS:

1. A recombinant microorganism comprising a biosynthetic pathway which uses a 3-keto acid as an intermediate, wherein said recombinant microorganism is engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of said 3-keto acid to a 3-hydroxyacid by-product.

2. The recombinant microorganism of claim 1, wherein said 3-keto acid intermediate is acetolactate and said 3-hydroxyacid by-product is 2,3-dihydroxy-2-methylbutanoic acid (DH2MB).

3. The recombinant microorganism of claim 2, wherein the DH2MB carbon yield from acetolactate is reduced by at least about 50% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of acetolactate to DH2MB.

4. The recombinant microorganism of claim 2, wherein the DH2MB carbon yield from acetolactate is reduced by at least about 75% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of acetolactate to DH2MB.

5. The recombinant microorganism of claim 2, wherein the DH2MB carbon yield from acetolactate is reduced by at least about 95% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of acetolactate to DH2MB.

6. The recombinant microorganism of claim 2, wherein said recombinant microorganism produces an acetolactate-derived product.

7. The recombinant microorganism of claim 6, wherein said acetolactate-derived product is selected from isobutanol, 2-butanol, 1-butanol, 2-butanone, 2,3-

butanediol, acetoin, diacetyl, valine, leucine, pantothenic acid, isobutylene, 3-methyl-1-butanol, 4-methyl-1-pentanol, and coenzyme A.

8. The recombinant microorganism of claim 1, wherein said 3-keto acid intermediate is 2-aceto-2-hydroxybutyrate and said 3-hydroxyacid by-product is 2-ethyl-2,3-dihydroyxbutanoate.

9. The recombinant microorganism of claim 8, wherein the 2-ethyl-2,3-dihydroyxbutanoate carbon yield from 2-aceto-2-hydroxybutyrate is reduced by at least about 50% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of 2-aceto-2-hydroxybutyrate to 2-ethyl-2,3-dihydroyxbutanoate.

10. The recombinant microorganism of claim 8, wherein the 2-ethyl-2,3-dihydroyxbutanoate carbon yield from 2-aceto-2-hydroxybutyrate is reduced by at least about 75% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of 2-aceto-2-hydroxybutyrate to 2-ethyl-2,3-dihydroyxbutanoate.

11. The recombinant microorganism of claim 8, wherein the 2-ethyl-2,3-dihydroyxbutanoate carbon yield from 2-aceto-2-hydroxybutyrate is reduced by at least about 95% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of 2-aceto-2-hydroxybutyrate to 2-ethyl-2,3-dihydroyxbutanoate .

12. The recombinant microorganism of claim 8, wherein said recombinant microorganism produces a 2-aceto-2-hydroxybutyrate-derived product.

13. The recombinant microorganism of claim 12, wherein said 2-aceto-2-hydroxybutyrate-derived product is selected from 2-methyl-1-butanol, isoleucine, 3-methyl-1-pentanol, 4-methyl-1-hexanol, and 5-methyl-1-heptanol.

14. The recombinant microorganism of any of the preceding claims, wherein said enzyme catalyzing the conversion of a 3-keto acid to a 3-hydroxyacid by-product is a 3-keto acid reductase.

15. The recombinant microorganism of claim 14, wherein said 3-keto acid reductase is the *S. cerevisiae* YMR226 (SEQ ID NO: 1) or a homolog or variant thereof.

16. The recombinant microorganism of claim 14, wherein said 3-keto acid reductase is selected from SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, and SEQ ID NO: 23, or homologs or variants thereof.

17. A recombinant microorganism comprising a biosynthetic pathway which uses an aldehyde as an intermediate, wherein said recombinant microorganism is engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of said aldehyde to an acid by-product.

18. The recombinant microorganism of claim 17, wherein the acid by-product carbon yield from the aldehyde intermediate is reduced by at least 35% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one more enzymes involved in catalyzing the conversion of an aldehyde to acid by-product.

19. The recombinant microorganism of claim 17, wherein the acid by-product carbon yield from the aldehyde intermediate is reduced by at least 75% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one more enzymes involved in catalyzing the conversion of an aldehyde to acid by-product.

20. The recombinant microorganism of claim 17, wherein the acid by-product carbon yield from the aldehyde intermediate is reduced by at least 95% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one more enzymes involved in catalyzing the conversion of an aldehyde to acid by-product.

21. The recombinant microorganism of claim 17, wherein said biosynthetic pathway which uses an aldehyde as intermediate is selected from a pathway for the biosynthesis of isobutanol, 1-butanol, 2-methyl-1-butanol, 3-methyl-1-butanol, 1-propanol, 1-pentanol, 1-hexanol, 3-methyl-1-pentanol, 4-methyl-1-pentanol, 4-methyl-1-hexanol, and 5-methyl-1-heptanol.

22. The recombinant microorganism of any of claims 17-21, wherein said enzyme catalyzing the conversion of an aldehyde to an acid by-product is an aldehyde dehydrogenase.

23. The recombinant microorganism of claim 22, wherein said aldehyde dehydrogenase is the *S. cerevisiae* ALD6 (SEQ ID NO: 25) or a homolog or variant thereof.

24. The recombinant microorganism of claim 22, wherein said aldehyde dehydrogenase is selected from SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, and SEQ ID NO: 41, or homologs or variants thereof.

25. A recombinant microorganism comprising a biosynthetic pathway which uses a 3-keto acid and an aldehyde as an intermediate, wherein said recombinant microorganism is:

(i) engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of said 3-keto acid to a 3-hydroxyacid by-product; and

(ii) engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of said aldehyde to an acid by-product.

26. The recombinant microorganism of claim 25, wherein said 3-keto acid intermediate is acetolactate and said 3-hydroxyacid by-product is 2,3-dihydroxy-2-methylbutanoic acid (DH2MB).

27. The recombinant microorganism of claim 26, wherein the DH2MB carbon yield from acetolactate is reduced by at least about 50% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of acetolactate to DH2MB.

28. The recombinant microorganism of claim 26, wherein the DH2MB carbon yield from acetolactate is reduced by at least about 75% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of acetolactate to DH2MB.

29. The recombinant microorganism of claim 26, wherein the DH2MB carbon yield from acetolactate is reduced by at least about 95% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of acetolactate to DH2MB.

30. The recombinant microorganism of claim 26, wherein said recombinant microorganism produces an acetolactate-derived product.

31. The recombinant microorganism of claim 30, wherein said acetolactate derived product is selected from isobutanol, 1-butanol, and 3-methyl-1-butanol.

32. The recombinant microorganism of claim 25, wherein said 3-keto acid intermediate is 2-aceto-2-hydroxybutyrate and said 3-hydroxyacid by-product is 2-ethyl-2,3-dihydroyxbutanoate.

33. The recombinant microorganism of claim 32, wherein the 2-ethyl-2,3-dihydroyxbutanoate carbon yield from 2-aceto-2-hydroxybutyrate is reduced by at least about 50% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of 2-aceto-2-hydroxybutyrate to 2-ethyl-2,3-dihydroyxbutanoate.

34. The recombinant microorganism of claim 32, wherein the 2-ethyl-2,3-dihydroyxbutanoate carbon yield from 2-aceto-2-hydroxybutyrate is reduced by at least about 75% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of 2-aceto-2-hydroxybutyrate to 2-ethyl-2,3-dihydroyxbutanoate.

35. The recombinant microorganism of claim 32, wherein the 2-ethyl-2,3-dihydroyxbutanoate carbon yield from 2-aceto-2-hydroxybutyrate is reduced by at least about 95% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of 2-aceto-2-hydroxybutyrate to 2-ethyl-2,3-dihydroyxbutanoate .

36. The recombinant microorganism of claim 32, wherein said recombinant microorganism produces a 2-aceto-2-hydroxybutyrate-derived product.

37. The recombinant microorganism of claim 36, wherein said 2-aceto-2-hydroxybutyrate-derived product is selected from 2-methyl-1-butanol, 3-methyl-1-pentanol, 4-methyl-1-hexanol, and 5-methyl-1-heptanol.

38. The recombinant microorganism of any of claims 25-37, wherein said enzyme catalyzing the conversion of a 3-keto acid to a 3-hydroxyacid by-product is a 3-keto acid reductase.

39. The recombinant microorganism of claim 38, wherein said 3-keto acid reductase is the *S. cerevisiae* YMR226 (SEQ ID NO: 1) or a homolog or variant thereof.

40. The recombinant microorganism of claim 38, wherein said 3-keto acid reductase is selected from SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, and SEQ ID NO: 23, or homologs or variants thereof.

41. The recombinant microorganism of any of claims 25-40, wherein the acid by-product carbon yield from the aldehyde intermediate is reduced by at least 35% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one more enzymes involved in catalyzing the conversion of an aldehyde to acid by-product.

42. The recombinant microorganism of any of claims 25-40, wherein the acid by-product carbon yield from the aldehyde intermediate is reduced by at least 75% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one more enzymes involved in catalyzing the conversion of an aldehyde to acid by-product.

43. The recombinant microorganism any of claims 25-40, wherein the acid by-product carbon yield from the aldehyde intermediate is reduced by at least 95% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one more enzymes involved in catalyzing the conversion of an aldehyde to acid by-product.

44. The recombinant microorganism of any of claims 25-43, wherein said enzyme catalyzing the conversion of an aldehyde to an acid by-product is an aldehyde dehydrogenase.

45. The recombinant microorganism of claim 44, wherein said aldehyde dehydrogenase is the *S. cerevisiae* ALD6 (SEQ ID NO: 25) or a homolog or variant thereof.

46. The recombinant microorganism of claim 44, wherein said aldehyde dehydrogenase is selected from SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, and SEQ ID NO: 41, or homologs or variants thereof.

47. The recombinant microorganism of any of the preceding claims, wherein said recombinant microorganism is engineered to reduce or eliminate pyruvate decarboxylase (PDC) activity.

48. The recombinant microorganism of any of the preceding claims, wherein said recombinant microorganism is engineered to reduce or eliminate glycerol-3-phosphate dehydrogenase (GPD) activity.

49. The recombinant microorganism of any of the preceding claims, wherein said recombinant microorganism is a yeast microorganism.

50. The recombinant microorganism of claim 49, wherein said recombinant microorganism is a yeast microorganism of the Saccharomyces clade.

51. The recombinant microorganism of claim 49, wherein said recombinant microorganism is a *Saccharomyces sensu stricto* microorganism.

52. The recombinant microorganism of claim 51, wherein said *Saccharomyces sensu stricto* microorganism is selected from the group consisting of *S. cerevisiae, S. kudriavzevii, S. mikatae, S. bayanus, S. uvarum, S. carocanis* and hybrids thereof.

53. The recombinant microorganism of claim 49, wherein said recombinant microorganism is a Crabtree-negative yeast microorganism.

54. The recombinant microorganism of claim 53, wherein said Crabtree-negative yeast microorganism is classified into a genus selected from a group consisting of *Saccharomyces, Kluyveromyces, Pichia, Hansenula*, *Issatchenkia* and *Candida*.

55. The recombinant microorganism of claim 54, wherein said Crabtree-negative yeast microorganism is selected from the group consisting of *Saccharomyces kluyveri, Kluyveromyces lactis, Kluyveromyces marxianus, Pichia anomala, Pichia stipitis, Pichia kudriavzevii, Issatchenkia orientalis, Hansenula anomala, Candida utilis* and *Kluyveromyces waltii.*

56. The recombinant microorganism of claim 49, wherein said recombinant microorganism is a Crabtree-positive yeast microorganism.

57. The recombinant microorganism of claim 56, wherein said Crabtree-positive yeast microorganism is classified into a genus selected from a group consisting of *Saccharomyces, Kluyveromyces, Zygosaccharomyces, Debaryomyces, Pichia, Candida*, and *Schizosaccharomyces*.

58. The recombinant microorganism of claim 57, wherein said Crabtree-positive yeast microorganism is selected from the group consisting of *Saccharomyces cerevisiae, Saccharomyces uvarum, Saccharomyces bayanus, Saccharomyces paradoxus, Saccharomyces castelli, Kluyveromyces thermotolerans, Candida glabrata, Zygosaccharomyces bailli, Zygosaccharomyces rouxii, Debaryomyces hansenii, Pichia pastorius, Schizosaccharomyces pombe,* and *Saccharomyces uvarum.*

59. The recombinant microorganism of claim 49, wherein said recombinant microorganism is a post-WGD (whole genome duplication) yeast microorganism.

60. The recombinant microorganism of claim 59, wherein said post-WGD yeast microorganism is classified into a genus selected from a group consisting of *Saccharomyces* or *Candida*.

61. The recombinant microorganism of claim 60, wherein said post-WGD yeast microorganism is selected from the group consisting of *Saccharomyces cerevisiae, Saccharomyces uvarum, Saccharomyces bayanus, Saccharomyces paradoxus, Saccharomyces castelli,* and *Candida glabrata.*

62. The recombinant microorganism of claim 49, wherein said recombinant microorganism is a pre-WGD (whole genome duplication) yeast microorganism.

63. The recombinant microorganism of claim 62, wherein said pre-WGD yeast microorganism is classified into a genus selected from a group consisting of *Saccharomyces, Kluyveromyces, Candida, Pichia, Debaryomyces, Hansenula, Issatchenkia, Pachysolen, Yarrowia* and *Schizosaccharomyces.*

64. The recombinant microorganism of claim 63, wherein said pre-WGD yeast microorganism is selected from the group consisting of *Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces marxianus, Kluyveromyces waltii, Kluyveromyces lactis, Candida tropicalis, Pichia pastoris, Pichia anomala, Pichia stipitis, Pichia kudriavzevii, Issatchenkia orientalis, Debaryomyces hansenii, Hansenula anomala, Pachysolen tannophilis, Yarrowia lipolytica,* and *Schizosaccharomyces pombe.*

65. A method of producing a beneficial metabolite derived from a 3-keto acid intermediate, comprising:

(a) providing a recombinant microorganism according to any of claims 1-16 and 25-64;

(b) cultivating the recombinant microorganism in a culture medium containing a feedstock providing the carbon source, until a recoverable quantity of the beneficial metabolite is produced; and

(c) recovering the beneficial metabolite.

66. The method of claim 65, wherein said 3-keto acid intermediate is acetolactate and the beneficial metabolite is selected from isobutanol, 2-butanol, 1-butanol, 2-butanone, 2,3-butanediol, acetoin, diacetyl, valine, leucine, pantothenic acid, isobutylene, 3-methyl-1-butanol, 4-methyl-1-pentanol, and coenzyme A.

67. The method of claim 65, wherein said 3-keto acid intermediate is 2-aceto-2-hydroxybutyrate and the beneficial metabolite is selected from 2-methyl-1-butanol, isoleucine, 3-methyl-1-pentanol, 4-methyl-1-hexanol, and 5-methyl-1-heptanol.

68. A method of producing a beneficial metabolite derived from an aldehyde intermediate, comprising:

(a) providing a recombinant microorganism according to any of claims 17-64;

(b) cultivating the recombinant microorganism in a culture medium containing a feedstock providing the carbon source, until a recoverable quantity of the beneficial metabolite is produced; and

(c) recovering the beneficial metabolite.

69. The method of claim 68, wherein said aldehyde intermediate is selected from isobutyraldehyde, 1-butanal, 2-methyl-1-butanal, 3-methyl-1-butanal, 1-propanal, 1-pentanal, 1-hexanal, 3-methyl-1-pentanal, 4-methyl-1-pentanal, 4-methyl-1-hexanal, and 5-methyl-1-heptanal.

70. The method of claim 69, wherein said beneficial metabolite is selected from isobutanol, 1-butanol, 2-methyl-1-butanol, 3-methyl-1-butanol, 1-propanol, 1-pentanol, 1-hexanol, 3-methyl-1-pentanol, 4-methyl-1-pentanol, 4-methyl-1-hexanol, and 5-methyl-1-heptanol.

71. A method of producing a beneficial metabolite derived from a 3-keto acid and an aldehyde intermediate, comprising:

(a) providing a recombinant microorganism according to any of claims 25-64;

(b) cultivating the recombinant microorganism in a culture medium containing a feedstock providing the carbon source, until a recoverable quantity of the beneficial metabolite is produced; and

(c) recovering the beneficial metabolite.

72. The method of claim 71, wherein said 3-keto acid intermediate is acetolactate and the beneficial metabolite is selected from isobutanol, 1-butanol, and 3-methyl-1-butanol.

73. The method of claim 71, wherein said 3-keto acid intermediate is 2-aceto-2-hydroxybutyrate and the beneficial metabolite is selected from 2-methyl-1-butanol, 3-methyl-1-pentanol, 4-methyl-1-hexanol, and 5-methyl-1-heptanol.

74. A recombinant microorganism comprising an isobutanol producing metabolic pathway, wherein said recombinant microorganism is engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of acetolactate to 2,3-dihydroxy-2-methylbutanoic acid (DH2MB).

75. The recombinant microorganism of claim 74, wherein the DH2MB carbon yield from acetolactate is reduced by at least about 50% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of acetolactate to DH2MB.

76. The recombinant microorganism of claim 74, wherein the DH2MB carbon yield from acetolactate is reduced by at least about 75% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of acetolactate to DH2MB.

77. The recombinant microorganism of claim 74, wherein the DH2MB carbon yield from acetolactate is reduced by at least about 95% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of acetolactate to DH2MB.

78. The recombinant microorganism of any of claims 74-77, wherein said enzyme catalyzing the conversion of acetolactate to DH2MB is a 3-keto acid reductase.

79. The recombinant microorganism of claim 78, wherein said 3-keto acid reductase is the *S. cerevisiae* YMR226 (SEQ ID NO: 1) or a homolog or variant thereof.

80. The recombinant microorganism of claim 78, wherein said 3-keto acid reductase is selected from SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, and SEQ ID NO: 23, or homologs or variants thereof.

81. A recombinant microorganism comprising an isobutanol producing metabolic pathway, wherein said recombinant microorganism is engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of isobutyraldehyde to isobutyrate.

82. The recombinant microorganism of claim 81, wherein the isobutyrate carbon yield from isobutyraldehyde is reduced by at least 35% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one more enzymes involved in catalyzing the conversion of isobutyraldehyde to isobutyrate.

83. The recombinant microorganism of claim 81, wherein the isobutyrate carbon yield from isobutyraldehyde is reduced by at least 75% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one more enzymes involved in catalyzing the conversion of isobutyraldehyde to isobutyrate.

84. The recombinant microorganism of claim 81, wherein the isobutyrate carbon yield from isobutyraldehyde is reduced by at least 95% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one more enzymes involved in catalyzing the conversion of isobutyraldehyde to isobutyrate.

85. The recombinant microorganism of any of claims 81-84, wherein said enzyme catalyzing the conversion of isobutyraldehyde to isobutyrate is an aldehyde dehydrogenase.

86. The recombinant microorganism of claim 85, wherein said aldehyde dehydrogenase is the *S. cerevisiae* ALD6 (SEQ ID NO: 25) or a homolog or variant thereof.

87. The recombinant microorganism of claim 86, wherein said aldehyde dehydrogenase is selected from SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, and SEQ ID NO: 41, or homologs or variants thereof.

88. A recombinant microorganism comprising an isobutanol producing metabolic pathway, wherein said recombinant microorganism is
(i) engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of acetolactate to 2,3-dihydroxy-2-methylbutanoic acid (DH2MB); and
(ii) engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of isobutyraldehyde to isobutyrate.

89. The recombinant microorganism of claim 88, wherein the DH2MB carbon yield from acetolactate is reduced by at least about 50% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of acetolactate to DH2MB.

90. The recombinant microorganism of claim 88, wherein the DH2MB carbon yield from acetolactate is reduced by at least about 75% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or

activity of one or more enzymes involved in catalyzing the conversion of acetolactate to DH2MB.

91. The recombinant microorganism of claim 88, wherein the DH2MB carbon yield from acetolactate is reduced by at least about 95% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one or more enzymes involved in catalyzing the conversion of acetolactate to DH2MB.

92. The recombinant microorganism of any of claims 88-91, wherein said enzyme catalyzing the conversion of acetolactate to DH2MB is a 3-keto acid reductase.

93. The recombinant microorganism of claim 92, wherein said 3-keto acid reductase is the *S. cerevisiae* YMR226 (SEQ ID NO: 1) or a homolog or variant thereof.

94. The recombinant microorganism of claim 92, wherein said 3-keto acid reductase is selected from SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, and SEQ ID NO: 23, or homologs or variants thereof.

95. The recombinant microorganism of claim 88, wherein the isobutyrate carbon yield from isobutyraldehyde is reduced by at least 35% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one more enzymes involved in catalyzing the conversion of isobutyraldehyde to isobutyrate.

96. The recombinant microorganism of claim 88, wherein the isobutyrate carbon yield from isobutyraldehyde is reduced by at least 75% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or

activity of one more enzymes involved in catalyzing the conversion of isobutyraldehyde to isobutyrate.

97. The recombinant microorganism of claim 88, wherein the isobutyrate carbon yield from isobutyraldehyde is reduced by at least 95% as compared to a parental microorganism that does not comprise a reduction or elimination of the expression or activity of one more enzymes involved in catalyzing the conversion of isobutyraldehyde to isobutyrate.

98. The recombinant microorganism of any of claims 88-97, wherein said enzyme catalyzing the conversion of isobutyraldehyde to isobutyrate is an aldehyde dehydrogenase.

99. The recombinant microorganism of claim 98, wherein said aldehyde dehydrogenase is the *S. cerevisiae* ALD6 (SEQ ID NO: 25) or a homolog or variant thereof.

100. The recombinant microorganism of claim 98, wherein said aldehyde dehydrogenase is selected from SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, and SEQ ID NO: 41, or homologs or variants thereof.

101. The recombinant microorganism of any of claims 88-100, wherein said recombinant microorganism is engineered to reduce or eliminate pyruvate decarboxylase (PDC) activity.

102. The recombinant microorganism of any of claims 88-101, wherein said recombinant microorganism is engineered to reduce or eliminate glycerol-3-phosphate dehydrogenase (GPD) activity.

103. The recombinant microorganism of any of claims 88-102, wherein said recombinant microorganism is a yeast microorganism.

104. The recombinant microorganism of claim 103, wherein said recombinant microorganism is a yeast microorganism of the Saccharomyces clade.

105. The recombinant microorganism of claim 103, wherein said recombinant microorganism is a *Saccharomyces sensu stricto* microorganism.

106. The recombinant microorganism of claim 105, wherein said *Saccharomyces sensu stricto* microorganism is selected from the group consisting of *S. cerevisiae, S. kudriavzevii, S. mikatae, S. bayanus, S. uvarum, S. carocanis* and hybrids thereof.

107. The recombinant microorganism of claim 103, wherein said recombinant microorganism is a Crabtree-negative yeast microorganism.

108. The recombinant microorganism of claim 107, wherein said Crabtree-negative yeast microorganism is classified into a genus selected from a group consisting of *Saccharomyces, Kluyveromyces, Pichia, Hansenula*, *Issatchenkia* and *Candida*.

109. The recombinant microorganism of claim 108, wherein said Crabtree-negative yeast microorganism is selected from the group consisting of *Saccharomyces kluyveri, Kluyveromyces lactis, Kluyveromyces marxianus, Pichia anomala, Pichia stipitis, Pichia kudriavzevii, Issatchenkia orientalis, Hansenula anomala, Candida utilis* and *Kluyveromyces waltii.*

110. The recombinant microorganism of claim 103, wherein said recombinant microorganism is a Crabtree-positive yeast microorganism.

111. The recombinant microorganism of claim 110, wherein said Crabtree-positive yeast microorganism is classified into a genus selected from a group consisting of *Saccharomyces, Kluyveromyces, Zygosaccharomyces, Debaryomyces, Pichia*, *Candida*, and *Schizosaccharomyces*.

112. The recombinant microorganism of claim 111, wherein said Crabtree-positive yeast microorganism is selected from the group consisting of *Saccharomyces*

cerevisiae, Saccharomyces uvarum, Saccharomyces bayanus, Saccharomyces paradoxus, Saccharomyces castelli, Kluyveromyces thermotolerans, Candida glabrata, Zygosaccharomyces bailli, Zygosaccharomyces rouxii, Debaryomyces hansenii, Pichia pastorius, Schizosaccharomyces pombe, and *Saccharomyces uvarum.*

113. The recombinant microorganism of claim 103, wherein said recombinant microorganism is a post-WGD (whole genome duplication) yeast microorganism.

114. The recombinant microorganism of claim 113, wherein said post-WGD yeast microorganism is classified into a genus selected from a group consisting of *Saccharomyces* or *Candida.*

115. The recombinant microorganism of claim 114, wherein said post-WGD yeast microorganism is selected from the group consisting of *Saccharomyces cerevisiae, Saccharomyces uvarum, Saccharomyces bayanus, Saccharomyces paradoxus, Saccharomyces castelli,* and *Candida glabrata.*

116. The recombinant microorganism of claim 103, wherein said recombinant microorganism is a pre-WGD (whole genome duplication) yeast microorganism.

117. The recombinant microorganism of claim 116, wherein said pre-WGD yeast microorganism is classified into a genus selected from a group consisting of *Saccharomyces, Kluyveromyces, Candida, Pichia, Debaryomyces, Hansenula, Issatchenkia, Pachysolen, Yarrowia* and *Schizosaccharomyces.*

118. The recombinant microorganism of claim 117, wherein said pre-WGD yeast microorganism is selected from the group consisting of *Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces marxianus, Kluyveromyces waltii, Kluyveromyces lactis, Candida tropicalis, Pichia pastoris, Pichia anomala, Pichia stipitis, Pichia kudriavzevii, Issatchenkia orientalis, Debaryomyces hansenii, Hansenula anomala, Pachysolen tannophilis, Yarrowia lipolytica,* and *Schizosaccharomyces pombe.*

119. A method of producing isobutanol, comprising:

(a) providing a recombinant microorganism according to any of claims 74-118;

(b) cultivating the recombinant microorganism in a culture medium containing a feedstock providing the carbon source, until a recoverable quantity of isobutanol is produced; and

(c) recovering the isobutanol.

120. A recombinant microorganism comprising a biosynthetic pathway which uses a 3-keto acid as an intermediate, wherein said recombinant microorganism is:

(a) engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of said 3-keto acid to a 3-hydroxyacid by-product; and/or is

(b) substantially free of an enzyme catalyzing the conversion of a 3-keto acid to a 3-hydroxyacid by-product.

121. A recombinant microorganism comprising a biosynthetic pathway which uses an aldehyde as an intermediate, wherein said recombinant microorganism is:

(a) engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of said aldehyde intermediate to an acid by-product; and/or is

(b) substantially free of an enzyme catalyzing the conversion of an aldehyde intermediate to an acid by-product.

122. A recombinant microorganism comprising a biosynthetic pathway which uses a 3-keto acid and an aldehyde as an intermediate, wherein said recombinant microorganism is:

(a) engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of said 3-keto acid to a 3-hydroxyacid by-product; and/or is

(b) substantially free of an enzyme catalyzing the conversion of a 3-keto acid to a 3-hydroxyacid by-product; and

(c) engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of said aldehyde intermediate to an acid by-product; and/or is

(d) substantially free of an enzyme catalyzing the conversion of an aldehyde intermediate to an acid by-product.

123. A recombinant microorganism comprising an isobutanol producing metabolic pathway, wherein said recombinant microorganism is:
(a) engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of acetolactate to 2,3-dihydroxy-2-methylbutanoic acid (DH2MB); and/or is

(b) substantially free of an enzyme catalyzing the conversion of acetolactate to 2,3-dihydroxy-2-methylbutanoic acid (DH2MB).

124. A recombinant microorganism comprising an isobutanol producing metabolic pathway, wherein said recombinant microorganism is:
(a) engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of isobutyraldehyde to isobutyrate; and/or is

(b) substantially free of an enzyme catalyzing the conversion of isobutyraldehyde to isobutyrate.

125. A recombinant microorganism comprising an isobutanol producing metabolic pathway, wherein said recombinant microorganism is:
(a) engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of acetolactate to 2,3-dihydroxy-2-methylbutanoic acid (DH2MB); and/or is

(b) substantially free of an enzyme catalyzing the conversion of acetolactate to 2,3-dihydroxy-2-methylbutanoic acid (DH2MB); and
(c) engineered to reduce or eliminate the expression or activity of one or more enzymes catalyzing the conversion of isobutyraldehyde to isobutyrate; and/or is

(d) substantially free of an enzyme catalyzing the conversion of isobutyraldehyde to isobutyrate.

126. A recombinant microorganism comprising,

(a) a gene encoding a cytosolically localized polypeptide having acetolactate synthase activity and wherein the cell converts pyruvate to acetolactate; and

(b) an overexpressed ketol-acid reductoisomerase, wherein said KARI has been engineered to exhibit a reduced K_M for acetolactate and/or an increased k_{cat} for acetolactate as compared to a wild-type or parental KARI.

127. A recombinant microorganism comprising,

(a) a gene encoding a cytosolically localized polypeptide having at least 0.5U/mg lysate acetolactate synthase activity and wherein the cell converts pyruvate to acetolactate; and

(b) an overexpressed ketol-acid reductoisomerase (KARI), wherein said KARI has at least 0.03U/mg lysate KARI activity.

128. A recombinant microorganism comprising,

(a) a gene encoding a cytosolically localized polypeptide having at least 0.5U/mg lysate acetolactate synthase activity and wherein the cell converts pyruvate to acetolactate; and

(b) an overexpressed dihydroxyacid dehydratase (DHAD), wherein said DHAD has at least 0.03U/mg lysate DHAD activity.

129. A recombinant microorganism comprising,

(a) a gene encoding a cytosolically localized polypeptide having acetolactate synthase activity and wherein the cell converts pyruvate to acetolactate;

(b) a reduction or deletion of the activity or expression of one or more endogenous proteins involved in catalyzing the conversion of acetolactate to 2,3-dihydroxy-2-methylbutanoic acid (DH2MB); and

(c) an overexpressed ketol-acid reductoisomerase.

130. A recombinant microorganism comprising an isobutanol producing metabolic pathway, wherein said recombinant microorganism overexpresses an endogenous or heterologous protein capable of converting 2,3-dihydroxy-2-methylbutanoic acid (DH2MB) into acetolactate.

131. A recombinant microorganism comprising an isobutanol producing metabolic pathway, wherein said recombinant microorganism overexpresses an endogenous

or heterologous protein capable of converting 2,3-dihydroxy-2-methylbutanoic acid (DH2MB) into 2,3-dihydroxyisovalerate (DHIV).

132. A recombinant microorganism for the production of 2,3-dihydroxy-2-methylbutanoic acid (DH2MB), wherein said recombinant microorganism overexpresses one or more enzymes capable of converting acetolactate to 2,3-dihydroxy-2-methylbutanoic acid (DH2MB).

133. The recombinant microorganism of claim 132, wherein said enzyme capable of converting acetolactate to 2,3-dihydroxy-2-methylbutanoic acid (DH2MB) is a 3-keto acid reductase.

134. The recombinant microorganism of claim 133, wherein said 3-keto acid reductase is the *S. cerevisiae* YMR226 (SEQ ID NO: 1) or a homolog or variant thereof.

135. The recombinant microorganism of claim 133, wherein said 3-keto acid reductase is selected from SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, and SEQ ID NO: 23, or homologs or variants thereof.

136. A method for the production of 2,3-dihydroxy-2-methylbutanoic acid (DH2MB), comprising:

(a) providing a recombinant microorganism according to any of claims 132-135;

(b) cultivating the recombinant microorganism in a culture medium containing a feedstock providing the carbon source, until a recoverable quantity of DH2MB is produced; and

(c) recovering the DH2MB.

137. A recombinant microorganism for the production of 2-ethyl-2,3-dihydroyxbutanoate, wherein said recombinant microorganism overexpresses one or more enzymes capable of converting 2-aceto-2-hydroxybutyrate to 2-ethyl-2,3-dihydroyxbutanoate.

138. The recombinant microorganism of claim 137, wherein said enzyme capable of converting 2-aceto-2-hydroxybutyrate to 2-ethyl-2,3-dihydroyxbutanoate is a 3-keto acid reductase.

139. The recombinant microorganism of claim 138, wherein said 3-keto acid reductase is the *S. cerevisiae* YMR226 (SEQ ID NO: 1) or a homolog or variant thereof.

140. The recombinant microorganism of claim 138, wherein said 3-keto acid reductase is selected from SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, and SEQ ID NO: 23, or homologs or variants thereof.

141. A method for the production of 2-ethyl-2,3-dihydroyxbutanoate, comprising:

(a) providing a recombinant microorganism according to any of claims 137-140;

(b) cultivating the recombinant microorganism in a culture medium containing a feedstock providing the carbon source, until a recoverable quantity of 2-ethyl-2,3-dihydroyxbutanoate is produced; and

(c) recovering the 2-ethyl-2,3-dihydroyxbutanoate.

142. A recombinant microorganism for the production of an acid product, wherein said recombinant microorganism overexpresses one or more enzymes capable of converting an aldehyde to acid by-product.

143. The recombinant microorganism of claim 142, wherein said enzyme catalyzing the conversion of an aldehyde to acid product is an aldehyde dehydrogenase.

144. The recombinant microorganism of claim 143, wherein said aldehyde dehydrogenase is the *S. cerevisiae* ALD6 (SEQ ID NO: 25) or a homolog or variant thereof.

145. The recombinant microorganism of claim 143, wherein said aldehyde dehydrogenase is selected from SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, and SEQ ID NO: 41, or homologs or variants thereof.

146. A method for the production of an acid product, comprising:

(a) providing a recombinant microorganism according to any of claims 142-145;

(b) cultivating the recombinant microorganism in a culture medium containing a feedstock providing the carbon source, until a recoverable quantity of the acid product is produced; and

(c) recovering the acid product.

147. The method of claim 146, wherein said acid by-product is selected from isobutyrate, butyrate, 2-methyl-1-butyrate, 3-methyl-1-butyrate, propionate, pentanoate, hexanoate, 3-methyl-1-pentanoate, 4-methyl-1-pentanoate, 4-methyl-1-hexanoate, and 5-methyl-1-heptanoate.

148. A modified alcohol dehydrogenase (ADH) comprising one or more modifications at positions corresponding to amino acids selected from the group consisting of: (a) tyrosine 50 of the wild-type *L. lactis* AdhA (SEQ ID NO: 2); (b) glutamine 77 of the wild-type *L. lactis* AdhA; (c) valine 108 of the wild-type *L. lactis* AdhA; (d) tyrosine 113 of the wild-type *L. lactis* AdhA; (e) isoleucine 212 of the wild-type *L. lactis* AdhA; and (f) leucine 264 of the wild-type *L. lactis* AdhA.

149. The modified alcohol dehydrogenase (ADH) of claim 148, wherein said tyrosine 50 residue is replaced with a phenylalanine or tryptophan residue.

150. The modified alcohol dehydrogenase (ADH) of claim 148, wherein said glutamine 77 residue is replaced with an arginine or serine residue.

151. The modified alcohol dehydrogenase (ADH) of claim 148, wherein said valine 108 residue is replaced with a serine or alanine residue.

152. The modified alcohol dehydrogenase (ADH) of claim 148, wherein said tyrosine 113 residue is replaced with a phenylalanine or glycine residue.

153. The modified alcohol dehydrogenase (ADH) of claim 148, wherein said isoleucine 212 residue is replaced with a threonine, alanine, or valine residue.

154. The modified alcohol dehydrogenase (ADH) of claim 148, wherein said leucine 264 residue is replaced with a valine residue.

155. The modified alcohol dehydrogenase (ADH) of claim 148, wherein the catalytic efficiency for the conversion of isobutyraldehyde to isobutanol of the modified ADH is enhanced by at least about 50% as compared to the wild-type ADH.

156. The modified alcohol dehydrogenase (ADH) of claim 148, wherein the catalytic efficiency for the conversion of isobutyraldehyde to isobutanol of the modified ADH is enhanced by at least about 100% as compared to the wild-type ADH.

157. The modified alcohol dehydrogenase (ADH) of claim 148, wherein the catalytic efficiency for the conversion of isobutyraldehyde to isobutanol of the modified ADH is enhanced by at least about 200% as compared to the wild-type ADH.

158. The modified alcohol dehydrogenase (ADH) of claim 148, wherein the ADH is derived from a genus selected from *Lactococcus, Lactobacillus, Pediococcus, Bacillus, Leptotrichia, Actinobacillus, Streptococcus, Streptobacillus, Staphylococcus, Eikenella, Weissella, Kingella, Rothia,* and *Exiguobacterium*..

159. The modified alcohol dehydrogenase (ADH) of claim 158, wherein the ADH is codon optimized for expression in a host cell.

160. The modified alcohol dehydrogenase (ADH) of claim 159, wherein said host cell is yeast.

161. The modified alcohol dehydrogenase (ADH) of claim 159, wherein said host cell is *E. coli*.

162. A recombinant microorganism transformed with a nucleic acid construct encoding a modified alcohol dehydrogenase (ADH) according to any of claims 148-161.

163. The recombinant microorganism of claim 15, wherein said recombinant microorganism comprises an isobutanol producing metabolic pathway comprising one or more isobutanol metabolic pathway enzymes selected from acetolactate synthase (ALS), ketol-acid reductoisomerase (KARI), dihydroxy acid dehydratase (DHAD), and 2-keto-acid decarboxylase (KIVD).

164. The recombinant microorganism of claim 163, wherein said recombinant microorganism is a yeast microorganism.

165. A method of producing isobutanol, comprising:

(a) providing a recombinant microorganism according to any one of claims 148-164; and

(b) cultivating said recombinant microorganism in a culture medium containing a feedstock providing the carbon source, until a recoverable quantity of the isobutanol is produced.

CLAIMS:

1. A recombinant microorganism comprising:

a) an isobutanol producing metabolic pathway, wherein said isobutanol producing metabolic pathway comprises at least one exogenous gene or at least one overexpressed endogenous gene encoding an enzyme that catalyzes a pathway step in the conversion of pyruvate to isobutanol; and

b) at least one modification which disrupts the expression or activity of an endogenous enzyme having 3-keto acid reductase activity, wherein said modification is selected from the group consisting of:

I. a mutation of an endogenous gene encoding said endogenous enzyme having 3-keto acid reductase activity; and

II. a mutation of a regulatory element associated with an endogenous gene encoding said endogenous enzyme having 3-keto acid reductase activity;

wherein said endogenous enzyme having 3-keto acid reductase activity catalyzes the conversion of acetolactate to 2,3-dihydroxy-2-methylbutanoic acid (DH2MB).

2. The recombinant microorganism of claim 1, wherein said endogenous enzyme having 3-keto acid reductase activity is the *S. cerevisiae* YMR226C (SEQ ID NO: 1).

3. The recombinant microorganism of claim 1, wherein said endogenous enzyme having 3-keto acid reductase activity is selected from SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, and SEQ ID NO: 23.

4. The recombinant microorganism of claim 1, wherein said recombinant microorganism is engineered to reduce or eliminate pyruvate decarboxylase (PDC) activity.

5. The recombinant microorganism of claim 1, wherein said recombinant microorganism is engineered to reduce or eliminate glycerol-3-phosphate dehydrogenase (GPD) activity.

6. The recombinant microorganism of claim 1, wherein said recombinant microorganism is a yeast microorganism.

7. The recombinant microorganism of claim 6, wherein said recombinant microorganism is a yeast microorganism of the *Saccharomyces* clade.

8. The recombinant microorganism of claim 6, wherein said recombinant microorganism is a *Saccharomyces* sensu stricto microorganism.

9. The recombinant microorganism of claim 6, wherein said recombinant microorganism is a Crabtree-negative yeast microorganism.

10. The recombinant microorganism of claim 9, wherein said Crabtree-negative yeast microorganism is classified into a genus selected from a group consisting of *Saccharomyces, Kluyveromyces, Pichia, Hansenula, Issatchenkia* and *Candida.*

11. The recombinant microorganism of claim 6, wherein said recombinant microorganism is a Crabtree-positive yeast microorganism.

12. The recombinant microorganism of claim 11, wherein said Crabtree-positive yeast microorganism is classified into a genus selected from a group consisting of *Saccharomyces, Kluyveromyces, Zygosaccharomyces, Debaryomyces, Pichia, Candida*, and *Schizosaccharomyces.*

13. The recombinant microorganism of claim 12, wherein said Crabtree-positive yeast microorganism is selected from the group consisting of *Saccharomyces cerevisiae, Saccharomyces uvarum, Saccharomyces bayanus, Saccharomyces paradoxus, Saccharomyces castelli, Kluyveromyces thermotolerans, Candida*

glabrata, Zygosaccharomyces bailli, Zygosaccharomyces rouxii, Debaryomyces hansenii, Pichia pastorius, and *Schizosaccharomyces pombe*.

14. The recombinant microorganism of claim 6, wherein said recombinant microorganism is a post-WGD (whole genome duplication) yeast microorganism.

15. The recombinant microorganism of claim 14, wherein said post-WGD yeast microorganism is classified into a genus selected from a group consisting of *Saccharomyces* or *Candida*.

16. The recombinant microorganism of claim 6, wherein said recombinant microorganism is a pre-WGD (whole genome duplication) yeast microorganism.

17. The recombinant microorganism of claim 16, wherein said pre-WGD yeast microorganism is classified into a genus selected from a group consisting of *Saccharomyces, Kluyveromyces, Candida, Pichia, Debaryomyces, Hansenula, Issatchenkia, Pachysolen, Yarrowia,* and *Schizosaccharomyces*.

18. A method of producing isobutanol, comprising:

(a) providing a recombinant microorganism according to claim 1; and

(b) cultivating the recombinant microorganism in a culture medium containing a feedstock providing a carbon source, until a recoverable quantity of isobutanol is produced.

19. The recombinant microorganism of claim 1, wherein said mutation results in the alteration of one or more amino acids, the insertion of one or more amino acids, the deletion of one more amino acids, a gene disruption, the introduction of a regulated promoter, the introduction of a weak constitutive promoter, or combinations thereof.