We claim:

1. A genetically modified Yarrowia lipoytica yeast comprising (i) an active, modified endogenous acyl-coA oxidase polypeptide or an active, modified endogenous acyl-coA dehydrogenase polypeptide; (ii) a genetic modification that alters a native enoyl co-A isomerase activity; and (iii) a genetic modification that alters a native dieneoyl CoA reductase (DCR) activity, wherein the yeast is capable of producing a diacid from a feedstock comprising one or more components from a vegetable oil.

2. A genetically modified yeast comprising an active, modified endogenous acyl-CoA oxidase polypeptide or an active, modified endogenous acyl-CoA dehydrogenase polypeptide, which yeast is capable of producing a diacid from a feedstock comprising one or more components from a vegetable oil.

3. The genetically modified yeast of claim 2, wherein the yeast is a genetically modified Candida spp. yeast.

4. The genetically modified yeast of claim 3, wherein the Candida spp. yeast is selected from the group consisting of: C. tropicalis and C. viswanathii.

5. The genetically modified yeast of claim , wherein the Candida spp. yeast is a genetically modified ATCC20336 yeast.

6. The genetically modified yeast of any one of claim 2-5, wherein the endogenous acyl-CoA oxidase polypeptide is a POX4 polypeptide.

7. The genetically modified yeast of claim 6, wherein the POX4 polypeptide comprises a modified amino acid sequence of SEQ ID NO: 30.

8. The genetically modified yeast of any one of claims 6-7, wherein the POX4 polypeptide comprises an amino acid modification at one or more amino acid positions selected from the group consisting of: 88, 90, 96, 98, 99, 100, 102, 103, 302, 309, 310, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504 and 505.

9. The genetically modified yeast of any one of claims 3-5, wherein the endogenous acyl-CoA oxidase polypeptide is a POX5 polypeptide.

10. The genetically modified yeast of claim 9, wherein the POX5 polypeptide comprises a modified amino acid sequence of SEQ ID NO: 32.

11. The genetically modified yeast of any one of claims 9-10, wherein the POX5 polypeptide comprises an amino acid modification at one or more amino acid positions selected from the group consisting of: 81, 82, 83, 84, 85, 86, 88, 93, 94, 95, 96, 98, 102, 284, 287, 290, 291, 292, 294, 295, 428, 429, 436, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462 and 463.

12. The genetically modified yeast of any one of claims 3-5, wherein the acyl-CoA dehydrogenase polypeptide is selected from the group consisting of: ACAD, VLCAD, LCAD, MCAD and SCAD polypeptides.

13. The genetically modified yeast of claim 12, wherein the acyl-CoA dehydrogenase polypeptide comprises a modified amino acid sequence of SEQ ID NO: 3685.

14. The genetically modified yeast of any one of claims 12-13, wherein the acyl-CoA dehydrogenase polypeptide comprises an amino acid modification at VLCAD position 461.

15. The genetically modified yeast of any one of claims 8, 11 and 14, wherein at least one of the amino acid modifications is an amino acid substitution.

16. The genetically modified yeast of claim 15, wherein at least one of the one or more amino acid substitutions is conservative.

17. The genetically modified yeast of claim 15, wherein at least one of the one or more amino acid substitutions is not conservative.

18. The genetically modified yeast of claim 2, wherein the yeast is a genetically modified Yarrowia spp. yeast.

19. The genetically modified yeast of claim 18, wherein the Yarrowia spp. yeast is Y. lipolytica.

20. The genetically modified yeast of any one of claims 18-19, wherein the endogenous acyl-CoA oxidase polypeptide is selected from the group consisting of: a POX1 polypeptide, POX2 polypeptide, POX3 polypeptide, POX4 polypeptide, POX5 polypeptide or POX6 polypeptide.

21. The genetically modified yeast of claim 20, wherein the endogenous acyl-CoA oxidase polypeptide is selected from the group consisting of: SEQ ID NOs: 3778 to 3783.

22. The genetically modified yeast of claim 2, wherein the yeast is a genetically modified Pichia spp. yeast.

23. The genetically modified yeast of claim 22, wherein the Pichia spp. yeast is selected from the group consisting of: P. pastoris, P. membranifaciens, P. kluyveri, P. guilliermondii, P. heedii and P. subpelliculosa.

24. The genetically modified yeast of claim 2, wherein the yeast is a genetically modified Saccharomyces spp. yeast.

25. The genetically modified yeast of claim 24, wherein the Saccharomyces spp. yeast is selected from the group consisting of: S. cerevisiae, S. bayanus, S. pastorianus and S. carlsbergensis.

26. The genetically modified yeast of claim 2, wherein the yeast is a genetically modified Kluyveromyces spp. yeast.

27. The genetically modified yeast of claim 26, wherein the Kluyveromyces spp. yeast is selected from the group consisting of: K. lactis and K. marxianus.

28. The genetically modified yeast of any one of claims 2-27, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the N-terminal loop.

29. The genetically modified yeast of any one of claims 2-28, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the D alpha helix.

30. The genetically modified yeast of any one of claims 2-29, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop between the D alpha helix and the E' alpha helix.

31. The genetically modified yeast of any one of claims 2-30, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification to an amino acid in effective contact with carbons 6 to 9 in a feedstock component.

32. The genetically modified yeast of any one of claims 2-31, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification to an amino acid in effective contact with carbons 10 to 12 in a feedstock component.

33. The genetically modified yeast of any one of claims 2-32, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the L alpha helix.

34. The genetically modified yeast of any one of claims 2-33, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop C-terminal to the L alpha helix.

35. The genetically modified yeast of any one of claims 2-34, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop between the L alpha helix and the M alpha helix.

36. The genetically modified yeast of any one of claims 28-35, wherein the amino acid modification comprises an amino acid substitution.

37. The genetically modified yeast of claim 36, wherein the amino acid substitution is conservative.

38. The genetically modified yeast of claim 36, wherein the amino acid substitution is not conservative.

39. A genetically modified yeast comprising (i) an active, modified endogenous acyl-CoA oxidase polypeptide or an active, modified endogenous acyl-CoA dehydrogenase polypeptide and (ii) a genetic modification that alters an enoyl CoA isomerase activity, wherein the yeast is capable of producing a diacid from a feedstock comprising one or more components from a vegetable oil.

40. The genetically modified yeast of any one of claims 2-39, which comprises a genetic modification that reduces an enoyl CoA isomerase activity.

41. The genetically modified yeast of claim 40, which comprises a disruption, deletion or knockout of (i) a polynucleotide that encodes an enoyl CoA isomerase polypeptide or (ii) a promoter operably linked to a polynucleotide that encodes an enoyl CoA isomerase polypeptide, whereby the enoyl CoA isomerase activity is reduced or removed.

42. The genetically modified yeast of claim 41, wherein the genetic modification disrupts a polynucleotide that encodes an enoyl CoA isomerase polypeptide.

43. The genetically modified yeast of any one of claims 2-42, which comprises a genetic modification that increases an enoyl CoA isomerase activity.

44. The genetically modified yeast of claim 43, which comprises (i) an increased copy number of a polynucleotide that encodes an enoyl CoA isomerase polypeptide or (ii) a promoter inserted and operably linked to a polynucleotide that encodes an enoyl CoA isomerase polypeptide.

45. The genetically modified yeast of any one of claims 40-44, wherein the enoyl CoA isomerase polypeptide is a polypeptide native to the yeast.

46. The genetically modified yeast of any one of claims 39-45, wherein the activity of one or more or all enoyl CoA isomerase polypeptide types in the yeast is altered.

47. The genetically modified yeast of claim 46, wherein the yeast comprises two enoyl CoA isomerase polypeptide types, and one or both of the polypeptide types are altered.

48. The genetically modified yeast of any one of claims 39-45, wherein the enoyl CoA isomerase activity is provided by a polypeptide present in a Candida spp. yeast.

49. The genetically modified yeast of any one of claims 39-48, wherein the enoyl CoA isomerase activity is provided by a polypeptide comprising the amino acid sequence of SEQ ID NO: 3675, 3677, 3800, 3802, 3803 or 3805.

50. The genetically modified yeast of any one of claims 39-48, wherein the yeast is a Yarrowia yeast.

51. The genetically modified yeast of claim 50, wherein the yeast is a Y. lipolytica yeast.

52. The genetically modified yeast of claim 51, wherein the enoyl CoA isomerase activity is provided by a polypeptide present in a Yarrowia yeast or a Y. lipolytica yeast.

53. The genetically modified yeast of claim 51, wherein the enoyl CoA isomerase activity is provided by a polypeptide comprising the amino acid sequence of SEQ ID NO: 3804 or 3806.

54. The genetically modified yeast of any one of claims 2-53, which comprises a genetic modification that reduces the cytoplasmic activity of an acyl-CoA synthetase (ACS) polypeptide.

55. The genetically modified yeast of any one of claims 2-54, which comprises a genetic modification that reduces the peroxisomal activity of an acyl-CoA synthetase (ACS) polypeptide.

56. The genetically modified yeast of claim 54 or 55, wherein the genetic modification disrupts a polynucleotide that encodes the acyl-CoA synthetase (ACS) polypeptide.

57. The genetically modified yeast of claim 56, wherein the genetic modification disrupts an ACS1 polypeptide or ACS2 polypeptide.

58. The genetically modified yeast of any one of claims 54-57, wherein the genetic modification disrupts a polynucleotide that encodes a long-chain acyl-CoA synthetase polypeptide.

59. The genetically modified yeast of claim 58, wherein the genetic modification disrupts a FAT1 polypeptide.

60. The genetically modified yeast of any one of claims 54-59, wherein the acyl-CoA synthetase (ACS) polypeptide is a polypeptide native to the yeast.

61. The genetically modified yeast of claim 60, wherein the yeast is a Candida spp. yeast.

62. The genetically modified yeast of claim 61, wherein the acyl-CoA synthetase (ACS) polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs: 80, 82, 84, 158 and 159.

63. The genetically modified yeast of claim 61, wherein the FAT1 polypeptide comprises the amino acid sequence of SEQ ID NO: 90.

64. The genetically modified yeast of any one of claims 2-63, which comprises a genetic modification that reduces the activity of a PXA polypeptide.

65. The genetically modified yeast of claim 64, wherein the genetic modification disrupts a polynucleotide that encodes the PXA polypeptide.

66. The genetically modified yeast of claim 64 or 65, wherein the PXA polypeptide is a PXA1 polypeptide or a PXA2 polypeptide, or a PXA1 polypeptide and a PXA2 polypeptide.

67. The genetically modified yeast of any one of claims 64-66, wherein the PXA polypeptide is native to the yeast.

68. The genetically modified yeast of claim 67, wherein the yeast is a Candida spp. yeast.

69. The genetically modified yeast of claim 68, wherein the PXA1 polypeptide comprises the amino acid sequence of SEQ ID NO: 92.

70. The genetically modified yeast of claim 68, wherein the PXA2 polypeptide comprises the amino acid sequence of SEQ ID NO: 94.

71. The genetically modified yeast of any one of claims 2-70, comprising an active, modified endogenous acyl-CoA oxidase polypeptide and no active, modified endogenous acyl-CoA dehydrogenase polypeptide.

72. The genetically modified yeast of any one of claims 2-70, comprising no active, modified endogenous acyl-CoA oxidase polypeptide and an active, modified endogenous acyl-CoA dehydrogenase polypeptide.

73. A method for producing a diacid, comprising:

(1) contacting a genetically modified yeast of any of claims 1-72 with a feedstock comprising one or more components from a feedstock containing at least one unsaturated vegetable fatty acid capable of being converted by the yeast to a diacid;

(2) culturing the yeast under conditions in which the diacid is produced from the feedstock; and

(3) hydrogenating the diacid to remove any unsaturation in the carbon chain.

74. The method of claim 73, wherein the unsaturated vegeteable fatty acid is linoleic acid or linolenic acid.

75. The method of claim 74, wherein the diacid is dodecanedioic acid or sebacic acid.

76. A genetically modified yeast, comprising a heterologous acyl-CoA oxidase polypeptide or a heterologous acyl-CoA dehydrogenase polypeptide, which yeast is capable of producing a diacid from a feedstock comprising one or more components from a vegetable oil.

77. The genetically modified yeast of claim 76, wherein the heterologous acyl-CoA oxidase polypeptide is a native polypeptide.

78. The genetically modified yeast of claim 76, wherein the heterologous acyl-CoA oxidase polypeptide is an active, modified polypeptide.

79. The genetically modified yeast of claim 76, wherein the heterologous acyl-CoA dehydrogenase polypeptide is a native polypeptide.

80. The genetically modified yeast of claim 76, wherein the heterologous acyl-CoA dehydrogenase polypeptide is an active, modified polypeptide.

81. The genetically modified yeast of claim 76 or 77, wherein the heterologous acyl-CoA oxidase polypeptide is selected from the group consisting of: a polypeptide having an amino acid sequence set forth in SEQ ID NO: 51 to SEQ ID NO: 3673.

82. The genetically modified yeast of claim 76 or 79, wherein the heterologous acyl-CoA dehydrogenase polypeptide is selected from the group consisting of: SEQ ID NOs: 3679 to 3683, 3686, 3689, 3691, 3693, 3695, 3697, 3699, 3701 and 3703.

83. The genetically modified yeast of any one of claims 76-82, which is selected from the group consisting of: a Candida spp. yeast, Yarrowia spp. yeast, Pichia spp. yeast, Saccharomyces spp. yeast and Kluyveromyces spp. yeast.

84. The genetically modified yeast of claim 83, which is selected from the group consisting of: C. tropicalis, C. viswanathii, Y. lipolytica, P. pastoris, P. membranifaciens, P. kluyveri, P. guilliermondii, P. heedii, P. subpelliculosa, S. cerevisiae, S. bayanus, S. pastorianus, S. carlsbergensis, K. lactis and K. marxianus.

85. The genetically modified yeast of any one of claims 76-84, which comprises a genetic modification that reduces the activity of an enoyl CoA isomerase polypeptide.

86. The genetically modified yeast of claim 85, wherein the genetic modification disrupts a polynucleotide that encodes the enoyl CoA isomerase polypeptide.

87. The genetically modified yeast of claim 85 or 86, wherein the enoyl CoA isomerase polypeptide is a polypeptide native to the yeast.

88. The genetically modified yeast of claim 87, wherein the yeast is a Candida spp. yeast.

89. The genetically modified yeast of claim 88, wherein the enoyl CoA isomerase polypeptide comprises the amino acid sequence of SEQ ID NO: 3675 or 3677.

90. The genetically modified yeast of any one of claims 76-89, which comprises a genetic modification that reduces the cytoplasmic activity of an acyl-CoA synthetase (ACS) polypeptide.

91. The genetically modified yeast of any one of claims 76-90, which comprises a genetic modification that reduces the peroxisomal activity of an acyl-CoA synthetase (ACS) polypeptide.

92. The genetically modified yeast of claim 90 or 91, wherein the genetic modification disrupts a polynucleotide that encodes the acyl-CoA synthetase (ACS) polypeptide.

93. The genetically modified yeast of claim 92, wherein the genetic modification disrupts an ACS1 polypeptide or ACS2 polypeptide.

94. The genetically modified yeast of any one of claims 90-93, wherein the genetic modification disrupts a polynucleotide that encodes a long-chain acyl-CoA synthetase polypeptide.

95. The genetically modified yeast of claim 94, wherein the genetic modification disrupts a FAT1 polypeptide.

96. The genetically modified yeast of any one of claims 90-95, wherein the acyl-CoA synthetase (ACS) polypeptide is a polypeptide native to the yeast.

97. The genetically modified yeast of claim 96, wherein the yeast is a Candida spp. yeast.

98. The genetically modified yeast of claim 97, wherein the acyl-CoA synthetase (ACS) polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs: 80, 82, 84, 158 and 159.

99. The genetically modified yeast of claim 96, wherein the FAT1 polypeptide comprises the amino acid sequence of SEQ ID NO: 90.

100. The genetically modified yeast of any one of claims 76-99, which comprises a genetic modification that reduces the activity of a PXA polypeptide.

101. The genetically modified yeast of claim 100, wherein the genetic modification disrupts a polynucleotide that encodes the PXA polypeptide.

102. The genetically modified yeast of claim 100 or 101, wherein the PXA polypeptide is a PXA1 polypeptide or a PXA2 polypeptide, or a PXA1 polypeptide and a PXA2 polypeptide.

103. The genetically modified yeast of any one of claims 100-102, wherein the PXA polypeptide is native to the yeast.

104. The genetically modified yeast of claim 103, wherein the yeast is a Candida spp. yeast.

105. The genetically modified yeast of claim 104, wherein the PXA1 polypeptide comprises the amino acid sequence of SEQ ID NO: 92.

106. The genetically modified yeast of claim 104, wherein the PXA2 polypeptide comprises the amino acid sequence of SEQ ID NO: 94.

107. The genetically modified yeast of any one of claims 76-106, comprising an active, modified endogenous acyl-CoA oxidase polypeptide and no active, modified endogenous acyl-CoA dehydrogenase polypeptide.

108. The genetically modified yeast of any one of claims 76-106, comprising no active, modified endogenous acyl-CoA oxidase polypeptide and an active, modified endogenous acyl-CoA dehydrogenase polypeptide.

109. The genetically modified yeast of any one of claims 1-108, comprising one or more genetic modifications that reduce the activity of one or more native endogenous acyl-CoA oxidase polypeptides.

110. The genetically modified yeast of claim 109, comprising genetic modifications that reduce the activity of all native endogenous acyl-CoA oxidase polypeptides.

111. The genetically modified yeast of claim 109 or 110, wherein the genetic modifications partially block beta oxidation activity.

112. The genetically modified yeast of any one of claims 1-111, wherein the diacid is a C4 to C24 diacid.

113. The genetically modified yeast of claim 112, wherein the diacid is a C10, C12, C14, C16, C18 or C20 diacid.

114. The genetically modified yeast of claim 113, wherein the diacid is a C10 diacid.

115. The genetically modified yeast of claim 113, wherein the diacid is a C12 diacid.

116. The genetically modified yeast of claim 113, wherein the diacid is a C18 diacid.

117. The genetically modified yeast of any one of claims 112-116, wherein the diacid contains no unsaturation.

118. The genetically modified yeast of any one of claims 112-116, wherein the diacid contains one or more unsaturations.

119. The genetically modified yeast of any one of claims 112-118, wherein the diacid is the predominant diacid in a mixture of diacids.

120. The genetically modified yeast of any one of claims 1-119, wherein the feedstock comprises a substantially pure oil.

121. The genetically modified yeast of any one of claims 1-120, wherein the feedstock comprises a plurality of fatty acids.

122. The genetically modified yeast of claim 121, wherein the feedstock comprises a soapstock.

123. The genetically modified yeast of claim 121, wherein the feedstock comprises a fatty acid distillate.

124. The genetically modified yeast of any one of claims 1-123, wherein the vegetable oil is from a plant selected from the group consisting of: palm, palm kernel, coconut, soy, safflower, canola, palm, palm kernel or combination thereof.

125. A method for producing a desired diacid, comprising:

contacting a genetically modified yeast of any one of claims 1-124 with a feedstock comprising one or more components from a vegetable oil capable of being converted by the yeast to a diacid; and

culturing the yeast under conditions in which the desired diacid is produced from the feedstock.

126. The method of claim 125, wherein the desired diacid is a C4 to C24 diacid.

127. The method of any one of claims 125-126, wherein the desired diacid contains no unsaturation.

128. The method of any one of claims 125-126, wherein the desired diacid contains one or more unsaturations.

129. The method of any one of claims 125-128, wherein the desired diacid is the predominant diacid in a mixture of diacids.

130. The method of any one of claims 125-129, wherein the feedstock comprises a substantially pure oil.

131. The method of any one of claims 125-129, wherein the feedstock comprises a plurality of fatty acids.

132. The method of claim 131, wherein the feedstock comprises a soapstock.

133. The method of claim 131, wherein the feedstock comprises a fatty acid distillate.

134. The method of any one of claims 125-133, wherein the vegetable oil is from a plant selected from the group consisting of: palm, palm kernel, coconut, soy, safflower, canola, palm, palm kernel or combination thereof.

135. An isolated nucleic acid, comprising a polynucleotide that encodes a modified acyl-CoA oxidase polypeptide from a yeast.

136. The isolated nucleic acid of claim 135, wherein the modified acyl-CoA oxidase polypeptide comprises an amino acid modification in the N-terminal loop.

137. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the D alpha helix.

138. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop between the D alpha helix and the E' alpha helix.

139. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification to an amino acid in effective contact with carbons 6 to 9 in a feedstock component.

140. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification to an amino acid in effective contact with carbons 10 to 12 in a feedstock component.

141. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the L alpha helix.

142. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop C-terminal to the L alpha helix.

143. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop between the L alpha helix and the M alpha helix.

144. The isolated nucleic acid of any one of claims 135-143, wherein the yeast is selected from the group consisting of: a Candida spp. yeast, Yarrowia spp. yeast, Pichia spp. yeast, Saccharomyces spp. yeast and Kluyveromyces spp. yeast.

145. The isolated nucleic acid of claim 144, wherein the yeast is selected from the group consisting of: C. tropicalis, C. viswanathii, Y. lipolytica, P. pastoris, P. membranifaciens, P. kluyveri, P. guilliermondii, P. heedii, P. subpelliculosa, S. cerevisiae, S. bayanus, S. pastorianus, S. carlsbergensis, K. lactis and K. marxianus.

146. The isolated nucleic acid of claim 144, wherein the yeast is a Candida spp. Yeast selected from the group consisting of: C. tropicalis and C. viswanathii.

147. The isolated nucleic acid of claim 146, wherein the yeast is a genetically modified ATCC20336 yeast.

148. The isolated nucleic acid of any one of claims 144-147, wherein the endogenous acyl-CoA oxidase polypeptide is a POX4 polypeptide.

149. The isolated nucleic acid of claim 148, wherein the POX4 polypeptide comprises a modified amino acid sequence of SEQ ID NO: 30.

150. The isolated nucleic acid of claim 148 or 149, wherein the POX4 polypeptide comprises amino acid modifications at one or more amino acid positions selected from the group consisting of: 88, 90, 96, 98, 99, 100, 102, 103, 302, 309, 310, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504 and 505.

151. The isolated nucleic acid of any one of claims 144-147, wherein the endogenous acyl-CoA oxidase polypeptide is a POX5 polypeptide.

152. The isolated nucleic acid of claim 141, wherein the POX5 polypeptide comprises a modified amino acid sequence of SEQ ID NO: 32.

153. The isolated nucleic acid of claim 151 or 152, wherein the POX5 polypeptide comprises amino acid modifications at one or more amino acid positions selected from the group consisting of: 81, 82, 83, 84, 85, 86, 88, 93, 94, 95, 96, 98, 102, 284, 287, 290, 291, 292, 294, 295, 436, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462 and 463.

154. An expression vector comprising the isolated nucleic acid of any one of claims 135-153.

155. A host cell comprising a nucleic acid of any one of claims 135-153.

156. A host cell of claim 155, which is a Candida spp. yeast cell selected from the group consisting of: C. tropicalis and C. viswanathii.

157. The host cell of claim 156, wherein the Candida spp. yeast is a genetically modified ATCC20336 yeast.

158. The host cell of claim 155, which is selected from the group consisting of: a Yarrowia spp. yeast, Pichia spp. yeast, Saccharomyces spp. yeast and Kluyveromyces spp. yeast.

159. The host cell of claim 158, which is selected from the group consisting of: Y. lipolytica, P. pastoris, P. membranifaciens, P. kluyveri, P. guilliermondii, P. heedii, P. subpelliculosa, S. cerevisiae, S. bayanus, S. pastorianus, S. carlsbergensis, K. lactis and K. marxianus.

160. A genetically modified yeast comprising (i) an active, modified endogenous acyl-coA oxidase polypeptide or an active, modified endogenous acyl-coA dehydrogenase polypeptide; (ii) a genetic modification that alters an enoyl co-A isomerase activity; and (iii) a genetic modification that alters a dieneoyl CoA reductase (DCR) activity, wherein the yeast is capable of producing a diacid from a feedstock comprising one or more components from a vegetable oil.

161. The genetically modified yeast of claim 160, wherein the feedstock comprises at least one long chain unsaturated fatty acid.

162. The genetically modified yeast of claim 161, wherein the long chain unsaturated fatty acid is linoleic acid or linolenic acid.

163. The genetically modified yeast of any one of claims 160-162, which comprises a genetic modification that reduces an enoyl CoA isomerase activity.

164. The genetically modified yeast of claim 163, which comprises a disruption, deletion or knockout of (i) a polynucleotide that encodes an enoyl CoA isomerase polypeptide or (ii) a promoter operably linked to a polynucleotide that encodes an enoyl CoA isomerase polypeptide, whereby the enoyl CoA isomerase activity is reduced or removed.

165. The genetically modified yeast of claim 164, wherein the genetic modification disrupts a polynucleotide that encodes an enoyl CoA isomerase polypeptide.

166. The genetically modified yeast of any one of claims 160-165, which comprises a genetic modification that increases an enoyl CoA isomerase activity.

167. The genetically modified yeast of claim 166, which comprises (i) an increased copy number of a polynucleotide that encodes an enoyl CoA isomerase polypeptide or (ii) a promoter

inserted and operably linked to a polynucleotide that encodes an enoyl CoA isomerase polypeptide.

168. The genetically modified yeast of any one of claims 160-167, wherein the enoyl CoA isomerase activity is provided by a polypeptide comprising the amino acid sequence of SEQ ID NO: 3675, 3677, 3800, 3802, 3803 or 3805.

169. The genetically modified yeast of any one of claims 160-167, wherein enoyl CoA isomerase activity is provided by a polypeptide present in a Yarrowia yeast.

170. The genetically modified yeast of claim 169, wherein the Yarrowia yeast is a Y. lipolytica yeast.

171. The genetically modified yeast of any one of claims 160-167, wherein enoyl CoA isomerase activity is provided by a polypeptide comprising the amino acid sequence of SEQ ID NO: 3804 or 3806.

172. The genetically modified yeast of any one of claims 160-171, which comprises a genetic modification that reduces a dieneoyl CoA reductase activity.

173. The genetically modified yeast of claim 172, which comprises a disruption, deletion or knockout of (i) a polynucleotide that encodes a dieneoyl CoA reductase polypeptide or (ii) a promoter operably linked to a polynucleotide that encodes a dieneoyl CoA reductase polypeptide, whereby the dieneoyl CoA reductase activity is reduced or removed.

174. The genetically modified yeast of claim 173, wherein the genetic modification disrupts a polynucleotide that encodes a dieneoyl CoA reductase polypeptide.

175. The genetically modified yeast of any one of claims 160-171, which comprises a genetic modification that increases a dieneoyl CoA reductase activity.

176. The genetically modified yeast of claim 175, which comprises (i) an increased copy number of a polynucleotide that encodes a dieneoyl CoA reductase polypeptide or (ii) a

promoter inserted and operably linked to a polynucleotide that encodes a dieneoyl CoA reductase polypeptide.

177. The genetically modified yeast of any one of claims 160-176, wherein the dieneoyl CoA reductase activity is provided by a polypeptide comprising the amino acid sequence of SEQ ID NO: 3789, 3791, 3792 or 3793.

178. The genetically modified yeast of any one of claims 160-177, wherein the dieneoyl CoA reductase activity is provided by a polypeptide present in a Yarrowia yeast.

179. The genetically modified yeast of claim 178, wherein the Yarrowia yeast is a Y. lipolytica yeast.

180. The genetically modified yeast of any one of claims 160-177, wherein the dieneoyl CoA reductase activity is provided by a polypeptide comprising the amino acid sequence of SEQ ID NO: 3794 or 3795.

181. The genetically modified yeast of any one of claims 160-180, wherein the endogenous acyl-CoA oxidase polypeptide is a POX4 polypeptide.

182. The genetically modified yeast of claim 181, wherein the POX4 polypeptide comprises a modified amino acid sequence of SEQ ID NO: 30.

183. The genetically modified yeast of claim 181 or 182, wherein the POX4 polypeptide comprises an amino acid modification at one or more amino acid positions selected from the group consisting of: 88, 90, 96, 98, 99, 100, 102, 103, 302, 309, 310, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504 and 505.

184. The genetically modified yeast of any one of claims 160-180, wherein the endogenous acyl-CoA oxidase polypeptide is a POX5 polypeptide.

185. The genetically modified yeast of claim 184, wherein the POX5 polypeptide comprises a modified amino acid sequence of SEQ ID NO: 32.

186. The genetically modified yeast of claim 184, wherein the POX5 polypeptide comprises an amino acid modification at one or more amino acid positions selected from the group consisting of: 81, 82, 83, 84, 85, 86, 88, 93, 94, 95, 96, 98, 102, 284, 287, 290, 291, 292, 294, 295, 428, 429, 436, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462 and 463.

187. The genetically modified yeast of any one of claims 160-186, wherein the acyl-CoA dehydrogenase polypeptide is selected from the group consisting of: ACAD, VLCAD, LCAD, MCAD and SCAD polypeptides.

188. The genetically modified yeast of claim 187, wherein the acyl-CoA dehydrogenase polypeptide comprises a modified amino acid sequence of SEQ ID NO: 3685.

189. The genetically modified yeast of any one of claims 160-188, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the N-terminal loop.

190. The genetically modified yeast of any one of claims 160-189, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the D alpha helix.

191. The genetically modified yeast of any one of claims 160-190, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop between the D alpha helix and the E' alpha helix.

192. The genetically modified yeast of any one of claims 160-191, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification to an amino acid in effective contact with carbons 6 to 9 in a feedstock component.

193. The genetically modified yeast of any one of claims 160-192, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification to an amino acid in effective contact with carbons 10 to 12 in a feedstock component.

194. The genetically modified yeast of any one of claims 160-193, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the L alpha helix.

195. The genetically modified yeast of any one of claims 160-194, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop C-terminal to the L alpha helix.

196. The genetically modified yeast of any one of claims 160-195, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop between the L alpha helix and the M alpha helix.

197. A method for producing a diacid, comprising:

(a) contacting a genetically modified yeast of any one of claims 160-196 with a feedstock comprising a vegetable oil; and

(b) culturing the yeast under conditions in which diacid is produced from the feedstock.

198. The method of claim 197, comprising purifying the diacid from the yeast.

199. A method for producing a diacid, comprising:

(a) contacting a genetically modified yeast of any of embodiments 1-124 and 160-198 with a feedstock comprising an unsaturated vegetable fatty acid capable of being converted by the yeast to a diacid;

(b) culturing the yeast under conditions in which diacid containing one or more unsaturations is produced from the feedstock; and

(c) hydrogenating and removing one or more of the unsaturations.

200. The method of claim 199, wherein the unsaturated vegeteable fatty acid is linoleic acid or linolenic acid.

201. A diacid obtained by the method of any one of claims 199-200.

202. The diacid of claim 201, wherein said diacid is is dodecanedioic acid or sebacic acid.

What is claimed is:

1. A genetically modified Yarrowia lipoytica yeast comprising (i) an active, modified endogenous acyl-coA oxidase polypeptide or an active, modified endogenous acyl-coA dehydrogenase polypeptide; (ii) a genetic modification that alters a native enoyl co-A isomerase activity; and (iii) a genetic modification that alters a native dieneoyl CoA reductase (DCR) activity, wherein the yeast is capable of producing a diacid from a feedstock comprising one or more components from a vegetable oil.

2. A genetically modified yeast comprising an active, modified endogenous acyl-CoA oxidase polypeptide or an active, modified endogenous acyl-CoA dehydrogenase polypeptide, which yeast is capable of producing a diacid from a feedstock comprising one or more components from a vegetable oil.

3. The genetically modified yeast of claim 2, wherein the yeast is a genetically modified Candida spp. yeast.

4. The genetically modified yeast of claim 3, wherein the Candida spp. yeast is selected from the group consisting of: C. tropicalis and C. viswanathii.

5. The genetically modified yeast of claim 3, wherein the Candida spp. yeast is a genetically modified ATCC20336 yeast.

6. The genetically modified yeast of any one of claim 2-5, wherein the endogenous acyl-CoA oxidase polypeptide is a POX4 polypeptide.

7. The genetically modified yeast of claim 6, wherein the POX4 polypeptide comprises a modified amino acid sequence of SEQ ID NO: 30.

8. The genetically modified yeast of any one of claims 6-7, wherein the POX4 polypeptide comprises an amino acid modification at one or more amino acid positions

selected from the group consisting of: 88, 90, 96, 98, 99, 100, 102, 103, 302, 309, 310, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504 and 505.

9. The genetically modified yeast of any one of claims 3-5, wherein the endogenous acyl-CoA oxidase polypeptide is a POX5 polypeptide.

10. The genetically modified yeast of claim 9, wherein the POX5 polypeptide comprises a modified amino acid sequence of SEQ ID NO: 32.

11. The genetically modified yeast of any one of claims 9-10, wherein the POX5 polypeptide comprises an amino acid modification at one or more amino acid positions selected from the group consisting of: 81, 82, 83, 84, 85, 86, 88, 93, 94, 95, 96, 98, 102, 284, 287, 290, 291, 292, 294, 295, 428, 429, 436, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462 and 463.

12. The genetically modified yeast of any one of claims 3-5, wherein the acyl-CoA dehydrogenase polypeptide is selected from the group consisting of: ACAD, VLCAD, LCAD, MCAD and SCAD polypeptides.

13. The genetically modified yeast of claim 12, wherein the acyl-CoA dehydrogenase polypeptide comprises a modified amino acid sequence of SEQ ID NO: 3685.

14. The genetically modified yeast of any one of claims 12-13, wherein the acyl-CoA dehydrogenase polypeptide comprises an amino acid modification at VLCAD position 461.

15. The genetically modified yeast of any one of claims 8, 11 and 14, wherein at least one of the amino acid modifications is an amino acid substitution.

16. The genetically modified yeast of claim 15, wherein at least one of the one or more amino acid substitutions is conservative.

17. The genetically modified yeast of claim 15, wherein at least one of the one or more amino acid substitutions is not conservative.

18. The genetically modified yeast of claim 2, wherein the yeast is a genetically modified Yarrowia spp. yeast.

19. The genetically modified yeast of claim 18, wherein the Yarrowia spp. yeast is Y. lipolytica.

20. The genetically modified yeast of any one of claims 18-19, wherein the endogenous acyl-CoA oxidase polypeptide is selected from the group consisting of: a POX1 polypeptide, POX2 polypeptide, POX3 polypeptide, POX4 polypeptide, POX5 polypeptide or POX6 polypeptide.

21. The genetically modified yeast of claim 20, wherein the endogenous acyl-CoA oxidase polypeptide is selected from the group consisting of: SEQ ID NOs: 3778 to 3783.

22. The genetically modified yeast of claim 2, wherein the yeast is a genetically modified Pichia spp. yeast.

23. The genetically modified yeast of claim 22, wherein the Pichia spp. yeast is selected from the group consisting of: P. pastoris, P. membranifaciens, P. kluyveri, P. guilliermondii, P. heedii and P. subpelliculosa.

24. The genetically modified yeast of claim 2, wherein the yeast is a genetically modified Saccharomyces spp. yeast.

25. The genetically modified yeast of claim 24, wherein the Saccharomyces spp. yeast is selected from the group consisting of: S. cerevisiae, S. bayanus, S. pastorianus and S. carlsbergensis.

26. The genetically modified yeast of claim 2, wherein the yeast is a genetically modified Kluyveromyces spp. yeast.

27. The genetically modified yeast of claim 26, wherein the Kluyveromyces spp. yeast is selected from the group consisting of: K. lactis and K. marxianus.

28. The genetically modified yeast of any one of claims 2-27, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the N-terminal loop.

29. The genetically modified yeast of any one of claims 2-28, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the D alpha helix.

30. The genetically modified yeast of any one of claims 2-29, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop between the D alpha helix and the E' alpha helix.

31. The genetically modified yeast of any one of claims 2-30, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification to an amino acid in effective contact with carbons 6 to 9 in a feedstock component.

32. The genetically modified yeast of any one of claims 2-31, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification to an amino acid in effective contact with carbons 10 to 12 in a feedstock component.

33. The genetically modified yeast of any one of claims 2-32, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the L alpha helix.

34. The genetically modified yeast of any one of claims 2-33, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop C-terminal to the L alpha helix.

35. The genetically modified yeast of any one of claims 2-34, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop between the L alpha helix and the M alpha helix.

36. The genetically modified yeast of any one of claims 28-35, wherein the amino acid modification comprises an amino acid substitution.

37. The genetically modified yeast of claim 36, wherein the amino acid substitution is conservative.

38. The genetically modified yeast of claim 36, wherein the amino acid substitution is not conservative.

39. A genetically modified yeast comprising (i) an active, modified endogenous acyl-CoA oxidase polypeptide or an active, modified endogenous acyl-CoA dehydrogenase polypeptide and (ii) a genetic modification that alters an enoyl CoA isomerase activity, wherein the yeast is capable of producing a diacid from a feedstock comprising one or more components from a vegetable oil.

40. The genetically modified yeast of any one of claims 2-39, which comprises a genetic modification that reduces an enoyl CoA isomerase activity.

41. The genetically modified yeast of claim 40, which comprises a disruption, deletion or knockout of (i) a polynucleotide that encodes an enoyl CoA isomerase polypeptide or (ii) a promoter operably linked to a polynucleotide that encodes an enoyl CoA isomerase polypeptide, whereby the enoyl CoA isomerase activity is reduced or removed.

42. The genetically modified yeast of claim 41, wherein the genetic modification disrupts a polynucleotide that encodes an enoyl CoA isomerase polypeptide.

43. The genetically modified yeast of any one of claims 2-42, which comprises a genetic modification that increases an enoyl CoA isomerase activity.

44. The genetically modified yeast of claim 43, which comprises (i) an increased copy number of a polynucleotide that encodes an enoyl CoA isomerase polypeptide or (ii) a promoter inserted and operably linked to a polynucleotide that encodes an enoyl CoA isomerase polypeptide.

45. The genetically modified yeast of any one of claims 40-44, wherein the enoyl CoA isomerase polypeptide is a polypeptide native to the yeast.

46. (he genetically modified yeast of any one of claims 39-45, wherein the activity of one or more or all enoyl CoA isomerase polypeptide types in the yeast is altered.

47. The genetically modified yeast of claim 46, wherein the yeast comprises two enoyl CoA isomerase polypeptide types, and one or both of the polypeptide types are altered.

48. The genetically modified yeast of any one of claims 39-45, wherein the enoyl CoA isomerase activity is provided by a polypeptide present in a Candida spp. yeast.

49. The genetically modified yeast of any one of claims 39-48, wherein the enoyl CoA isomerase activity is provided by a polypeptide comprising the amino acid sequence of SEQ ID NO: 3675, 3677, 3800, 3802, 3803 or 3805.

50. The genetically modified yeast of any one of claims 39-48, wherein the yeast is a Yarrowia yeast.

51. The genetically modified yeast of claim 50, wherein the yeast is a Y. lipolytica yeast.

52. The genetically modified yeast of claim 51, wherein the enoyl CoA isomerase activity is provided by a polypeptide present in a Yarrowia yeast or a Y. lipolytica yeast.

53. The genetically modified yeast of claim 51, wherein the enoyl CoA isomerase activity is provided by a polypeptide comprising the amino acid sequence of SEQ ID NO: 3804 or 3806.

54. The genetically modified yeast of any one of claims 2-53, which comprises a genetic modification that reduces the cytoplasmic activity of an acyl-CoA synthetase (ACS) polypeptide.

55. The genetically modified yeast of any one of claims 2-54, which comprises a genetic modification that reduces the peroxisomal activity of an acyl-CoA synthetase (ACS) polypeptide.

56. The genetically modified yeast of claim 54 or 55, wherein the genetic modification disrupts a polynucleotide that encodes the acyl-CoA synthetase (ACS) polypeptide.

57. The genetically modified yeast of claim 56, wherein the genetic modification disrupts an ACS1 polypeptide or ACS2 polypeptide.

58. The genetically modified yeast of any one of claims 54-57, wherein the genetic modification disrupts a polynucleotide that encodes a long-chain acyl-CoA synthetase polypeptide.

59. The genetically modified yeast of claim 58, wherein the genetic modification disrupts a FAT1 polypeptide.

60. The genetically modified yeast of any one of claims 54-59, wherein the acyl-CoA synthetase (ACS) polypeptide is a polypeptide native to the yeast.

61. The genetically modified yeast of claim 60, wherein the yeast is a Candida spp. yeast.

62. The genetically modified yeast of claim 61, wherein the acyl-CoA synthetase (ACS) polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs: 80, 82, 84, 158 and 159.

63. The genetically modified yeast of claim 61, wherein the FAT1 polypeptide comprises the amino acid sequence of SEQ ID NO: 90.

64. The genetically modified yeast of any one of claims 2-63, which comprises a genetic modification that reduces the activity of a PXA polypeptide.

65. The genetically modified yeast of claim 64, wherein the genetic modification disrupts a polynucleotide that encodes the PXA polypeptide.

66. The genetically modified yeast of claim 64 or 65, wherein the PXA polypeptide is a PXA1 polypeptide or a PXA2 polypeptide, or a PXA1 polypeptide and a PXA2 polypeptide.

67. The genetically modified yeast of any one of claims 64-66, wherein the PXA polypeptide is native to the yeast.

68. The genetically modified yeast of claim 67, wherein the yeast is a Candida spp. yeast.

69. The genetically modified yeast of claim 68, wherein the PXA1 polypeptide comprises the amino acid sequence of SEQ ID NO: 92.

70. The genetically modified yeast of claim 68, wherein the PXA2 polypeptide comprises the amino acid sequence of SEQ ID NO: 94.

71. The genetically modified yeast of any one of claims 2-70, comprising an active, modified endogenous acyl-CoA oxidase polypeptide and no active, modified endogenous acyl-CoA dehydrogenase polypeptide.

72. The genetically modified yeast of any one of claims 2-70, comprising no active, modified endogenous acyl-CoA oxidase polypeptide and an active, modified endogenous acyl-CoA dehydrogenase polypeptide.

73. A method for producing a diacid, comprising:

(1) contacting a genetically modified yeast of any of claims 1-72 with a feedstock comprising one or more components from a feedstock containing at least one unsaturated vegetable fatty acid capable of being converted by the yeast to a diacid;

(2) culturing the yeast under conditions in which the diacid is produced from the feedstock; and

(3) hydrogenating the diacid to remove any unsaturation in the carbon chain.

74. The method of claim 73, wherein the unsaturated vegetable fatty acid is linoleic acid or linolenic acid.

75. The method of claim 74, wherein the diacid is dodecanedioic acid or sebacic acid.

76. A genetically modified yeast, comprising a heterologous acyl-CoA oxidase polypeptide or a heterologous acyl-CoA dehydrogenase polypeptide, which yeast is capable of producing a diacid from a feedstock comprising one or more components from a vegetable oil.

77. The genetically modified yeast of claim 76, wherein the heterologous acyl-CoA oxidase polypeptide is a native polypeptide.

78. The genetically modified yeast of claim 76, wherein the heterologous acyl-CoA oxidase polypeptide is an active, modified polypeptide.

79. The genetically modified yeast of claim 76, wherein the heterologous acyl-CoA dehydrogenase polypeptide is a native polypeptide.

80. The genetically modified yeast of claim 76, wherein the heterologous acyl-CoA dehydrogenase polypeptide is an active, modified polypeptide.

81. The genetically modified yeast of claim 76 or 77, wherein the heterologous acyl-CoA oxidase polypeptide is selected from the group consisting of: a polypeptide having an amino acid sequence set forth in SEQ ID NO: 51 to SEQ ID NO: 3673.

82. The genetically modified yeast of claim 76 or 79, wherein the heterologous acyl-CoA dehydrogenase polypeptide is selected from the group consisting of: SEQ ID NOs: 3679 to 3683, 3686, 3689, 3691, 3693, 3695, 3697, 3699, 3701 and 3703.

83. The genetically modified yeast of any one of claims 76-82, which is selected from the group consisting of: a Candida spp. yeast, Yarrowia spp. yeast, Pichia spp. yeast, Saccharomyces spp. yeast and Kluyveromyces spp. yeast.

84. The genetically modified yeast of claim 83, which is selected from the group consisting of: C. tropicalis, C. viswanathii, Y. lipolytica, P. pastoris, P. membranifaciens, P. kluyveri, P. guilliermondii, P. heedii, P. subpelliculosa, S. cerevisiae, S. bayanus, S. pastorianus, S. carlsbergensis, K. lactis and K. marxianus.

85. The genetically modified yeast of any one of claims 76-84, which comprises a genetic modification that reduces the activity of an enoyl CoA isomerase polypeptide.

86. The genetically modified yeast of claim 85, wherein the genetic modification disrupts a polynucleotide that encodes the enoyl CoA isomerase polypeptide.

87. The genetically modified yeast of claim 85 or 86, wherein the enoyl CoA isomerase polypeptide is a polypeptide native to the yeast.

88. The genetically modified yeast of claim 87, wherein the yeast is a Candida spp. yeast.

89. The genetically modified yeast of claim 88, wherein the enoyl CoA isomerase polypeptide comprises the amino acid sequence of SEQ ID NO: 3675 or 3677.

90. The genetically modified yeast of any one of claims 76-89, which comprises a genetic modification that reduces the cytoplasmic activity of an acyl-CoA synthetase (ACS) polypeptide.

91. The genetically modified yeast of any one of claims 76-90, which comprises a genetic modification that reduces the peroxisomal activity of an acyl-CoA synthetase (ACS) polypeptide.

92. The genetically modified yeast of claim 90 or 91, wherein the genetic modification disrupts a polynucleotide that encodes the acyl-CoA synthetase (ACS) polypeptide.

93. The genetically modified yeast of claim 92, wherein the genetic modification disrupts an ACS1 polypeptide or ACS2 polypeptide.

94. The genetically modified yeast of any one of claims 90-93, wherein the genetic modification disrupts a polynucleotide that encodes a long-chain acyl-CoA synthetase polypeptide.

95. The genetically modified yeast of claim 94, wherein the genetic modification disrupts a FAT1 polypeptide.

96. The genetically modified yeast of any one of claims 90-95, wherein the acyl-CoA synthetase (ACS) polypeptide is a polypeptide native to the yeast.

97. The genetically modified yeast of claim 96, wherein the yeast is a Candida spp. yeast.

98. The genetically modified yeast of claim 97, wherein the acyl-CoA synthetase (ACS) polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs: 80, 82, 84, 158 and 159.

99. The genetically modified yeast of claim 96, wherein the FAT1 polypeptide comprises the amino acid sequence of SEQ ID NO: 90.

100. The genetically modified yeast of any one of claims 76-99, which comprises a genetic modification that reduces the activity of a PXA polypeptide.

101. The genetically modified yeast of claim 100, wherein the genetic modification disrupts a polynucleotide that encodes the PXA polypeptide.

102. The genetically modified yeast of claim 100 or 101, wherein the PXA polypeptide is a PXA1 polypeptide or a PXA2 polypeptide, or a PXA1 polypeptide and a PXA2 polypeptide.

103. The genetically modified yeast of any one of claims 100-102, wherein the PXA polypeptide is native to the yeast.

104. The genetically modified yeast of claim 103, wherein the yeast is a Candida spp. yeast.

105. The genetically modified yeast of claim 104, wherein the PXA1 polypeptide comprises the amino acid sequence of SEQ ID NO: 92.

106. The genetically modified yeast of claim 104, wherein the PXA2 polypeptide comprises the amino acid sequence of SEQ ID NO: 94.

107. The genetically modified yeast of any one of claims 76-106, comprising an active, modified endogenous acyl-CoA oxidase polypeptide and no active, modified endogenous acyl-CoA dehydrogenase polypeptide.

108. The genetically modified yeast of any one of claims 76-106, comprising no active, modified endogenous acyl-CoA oxidase polypeptide and an active, modified endogenous acyl-CoA dehydrogenase polypeptide.

109. The genetically modified yeast of any one of claims 1-108, comprising one or more genetic modifications that reduce the activity of one or more native endogenous acyl-CoA oxidase polypeptides.

110. The genetically modified yeast of claim 109, comprising genetic modifications that reduce the activity of all native endogenous acyl-CoA oxidase polypeptides.

111. The genetically modified yeast of claim 109 or 110, wherein the genetic modifications partially block beta oxidation activity.

112. The genetically modified yeast of any one of claims 1-111, wherein the diacid is a C4 to C24 diacid.

113. The genetically modified yeast of claim 112, wherein the diacid is a C10, C12, C14, C16, C18 or C20 diacid.

114. The genetically modified yeast of claim 113, wherein the diacid is a C10 diacid.

115. The genetically modified yeast of claim 113, wherein the diacid is a C12 diacid.

116. The genetically modified yeast of claim 113, wherein the diacid is a C18 diacid.

117. The genetically modified yeast of any one of claims 112-116, wherein the diacid contains no unsaturation.

118. The genetically modified yeast of any one of claims 112-116, wherein the diacid contains one or more unsaturations.

119. The genetically modified yeast of any one of claims 112-118, wherein the diacid is the predominant diacid in a mixture of diacids.

120. The genetically modified yeast of any one of claims 1-119, wherein the feedstock comprises a substantially pure oil.

121. The genetically modified yeast of any one of claims 1-120, wherein the feedstock comprises a plurality of fatty acids.

122. The genetically modified yeast of claim 121, wherein the feedstock comprises a soapstock.

123. The genetically modified yeast of claim 121, wherein the feedstock comprises a fatty acid distillate.

124. The genetically modified yeast of any one of claims 1-123, wherein the vegetable oil is from a plant selected from the group consisting of: palm, palm kernel, coconut, soy, safflower, canola, palm, palm kernel or combination thereof.

125. A method for producing a desired diacid, comprising:

contacting a genetically modified yeast of any one of claims 1-124 with a feedstock comprising one or more components from a vegetable oil capable of being converted by the yeast to a diacid; and

culturing the yeast under conditions in which the desired diacid is produced from the feedstock.

126. The method of claim 125, wherein the desired diacid is a C4 to C24 diacid.

127. The method of any one of claims 125-126, wherein the desired diacid contains no unsaturation.

128. The method of any one of claims 125-126, wherein the desired diacid contains one or more unsaturations.

129. The method of any one of claims 125-128, wherein the desired diacid is the predominant diacid in a mixture of diacids.

130. The method of any one of claims 125-129, wherein the feedstock comprises a substantially pure oil.

131. The method of any one of claims 125-129, wherein the feedstock comprises a plurality of fatty acids.

132. The method of claim 131, wherein the feedstock comprises a soapstock.

133. The method of claim 131, wherein the feedstock comprises a fatty acid distillate.

134. The method of any one of claims 125-133, wherein the vegetable oil is from a plant selected from the group consisting of: palm, palm kernel, coconut, soy, safflower, canola, palm, palm kernel or combination thereof.

135. An isolated nucleic acid, comprising a polynucleotide that encodes a modified acyl-CoA oxidase polypeptide from a yeast.

136. The isolated nucleic acid of claim 135, wherein the modified acyl-CoA oxidase polypeptide comprises an amino acid modification in the N-terminal loop.

137. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the D alpha helix.

138. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop between the D alpha helix and the E' alpha helix.

139. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification to an amino acid in effective contact with carbons 6 to 9 in a feedstock component.

140. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification to an amino acid in effective contact with carbons 10 to 12 in a feedstock component.

141. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the L alpha helix.

142. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop C-terminal to the L alpha helix.

143. The isolated nucleic acid of claim 135, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop between the L alpha helix and the M alpha helix.

144. The isolated nucleic acid of any one of claims 135-143, wherein the yeast is selected from the group consisting of: a Candida spp. yeast, Yarrowia spp. yeast, Pichia spp. yeast, Saccharomyces spp. yeast and Kluyveromyces spp. yeast.

145. The isolated nucleic acid of claim 144, wherein the yeast is selected from the group consisting of: C. tropicalis, C. viswanathii, Y. lipolytica, P. pastoris, P. membranifaciens, P. kluyveri, P. guilliermondii, P. heedii, P. subpelliculosa, S. cerevisiae, S. bayanus, S. pastorianus, S. carlsbergensis, K. lactis and K. marxianus.

146. The isolated nucleic acid of claim 144, wherein the yeast is a Candida spp. Yeast selected from the group consisting of: C. tropicalis and C. viswanathii.

147. The isolated nucleic acid of claim 146, wherein the yeast is a genetically modified ATCC20336 yeast.

148. The isolated nucleic acid of any one of claims 144-147, wherein the endogenous acyl-CoA oxidase polypeptide is a POX4 polypeptide.

149. The isolated nucleic acid of claim 148, wherein the POX4 polypeptide comprises a modified amino acid sequence of SEQ ID NO: 30.

150. The isolated nucleic acid of claim 148 or 149, wherein the POX4 polypeptide comprises amino acid modifications at one or more amino acid positions selected from the group consisting of: 88, 90, 96, 98, 99, 100, 102, 103, 302, 309, 310, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504 and 505.

151. The isolated nucleic acid of any one of claims 144-147, wherein the endogenous acyl-CoA oxidase polypeptide is a POX5 polypeptide.

152. The isolated nucleic acid of claim 141, wherein the POX5 polypeptide comprises a modified amino acid sequence of SEQ ID NO: 32.

153. The isolated nucleic acid of claim 151 or 152, wherein the POX5 polypeptide comprises amino acid modifications at one or more amino acid positions selected from the group consisting of: 81, 82, 83, 84, 85, 86, 88, 93, 94, 95, 96, 98, 102, 284, 287, 290, 291, 292, 294, 295, 436, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462 and 463.

154. An expression vector comprising the isolated nucleic acid of any one of claims 135-153.

155. A host cell comprising a nucleic acid of any one of claims 135-153.

156. A host cell of claim 155, which is a Candida spp. yeast cell selected from the group consisting of: C. tropicalis and C. viswanathii.

157. The host cell of claim 156, wherein the Candida spp. yeast is a genetically modified ATCC20336 yeast.

158. The host cell of claim 155, which is selected from the group consisting of: a Yarrowia spp. yeast, Pichia spp. yeast, Saccharomyces spp. yeast and Kluyveromyces spp. yeast.

159. The host cell of claim 158, which is selected from the group consisting of: Y. lipolytica, P. pastoris, P. membranifaciens, P. kluyveri, P. guilliermondii, P. heedii, P. subpelliculosa, S. cerevisiae, S. bayanus, S. pastorianus, S. carlsbergensis, K. lactis and K. marxianus.

160. A genetically modified yeast comprising (i) an active, modified endogenous acyl-coA oxidase polypeptide or an active, modified endogenous acyl-coA dehydrogenase polypeptide; (ii) a genetic modification that alters an enoyl co-A isomerase activity; and (iii) a genetic modification that alters a dieneoyl CoA reductase (DCR) activity, wherein the yeast is capable of producing a diacid from a feedstock comprising one or more components from a vegetable oil.

161. The genetically modified yeast of claim 160, wherein the feedstock comprises at least one long chain unsaturated fatty acid.

162. The genetically modified yeast of claim 161, wherein the long chain unsaturated fatty acid is linoleic acid or linolenic acid.

163. The genetically modified yeast of any one of claims 160-162, which comprises a genetic modification that reduces an enoyl CoA isomerase activity.

164. The genetically modified yeast of claim 163, which comprises a disruption, deletion or knockout of (i) a polynucleotide that encodes an enoyl CoA isomerase polypeptide or (ii) a promoter operably linked to a polynucleotide that encodes an enoyl CoA isomerase polypeptide, whereby the enoyl CoA isomerase activity is reduced or removed.

165. The genetically modified yeast of claim 164, wherein the genetic modification disrupts a polynucleotide that encodes an enoyl CoA isomerase polypeptide.

166. The genetically modified yeast of any one of claims 160-165, which comprises a genetic modification that increases an enoyl CoA isomerase activity.

167. The genetically modified yeast of claim 166, which comprises (i) an increased copy number of a polynucleotide that encodes an enoyl CoA isomerase polypeptide or (ii) a promoter inserted and operably linked to a polynucleotide that encodes an enoyl CoA isomerase polypeptide.

168. The genetically modified yeast of any one of claims 160-167, wherein the enoyl CoA isomerase activity is provided by a polypeptide comprising the amino acid sequence of SEQ ID NO: 3675, 3677, 3800, 3802, 3803 or 3805.

169. The genetically modified yeast of any one of claims 160-167, wherein enoyl CoA isomerase activity is provided by a polypeptide present in a Yarrowia yeast.

170. The genetically modified yeast of claim 169, wherein the Yarrowia yeast is a Y. lipolytica yeast.

171. The genetically modified yeast of any one of claims 160-167, wherein enoyl CoA isomerase activity is provided by a polypeptide comprising the amino acid sequence of SEQ ID NO: 3804 or 3806.

172. The genetically modified yeast of any one of claims 160-171, which comprises a genetic modification that reduces a dieneoyl CoA reductase activity.

173. The genetically modified yeast of claim 172, which comprises a disruption, deletion or knockout of (i) a polynucleotide that encodes a dieneoyl CoA reductase polypeptide or (ii) a

promoter operably linked to a polynucleotide that encodes a dieneoyl CoA reductase polypeptide, whereby the dieneoyl CoA reductase activity is reduced or removed.

174. The genetically modified yeast of claim 173, wherein the genetic modification disrupts a polynucleotide that encodes a dieneoyl CoA reductase polypeptide.

175. The genetically modified yeast of any one of claims 160-171, which comprises a genetic modification that increases a dieneoyl CoA reductase activity.

176. The genetically modified yeast of claim 175, which comprises (i) an increased copy number of a polynucleotide that encodes a dieneoyl CoA reductase polypeptide or (ii) a promoter inserted and operably linked to a polynucleotide that encodes a dieneoyl CoA reductase polypeptide.

177. The genetically modified yeast of any one of claims 160-176, wherein the dieneoyl CoA reductase activity is provided by a polypeptide comprising the amino acid sequence of SEQ ID NO: 3789, 3791, 3792 or 3793.

178. The genetically modified yeast of any one of claims 160-177, wherein the dieneoyl CoA reductase activity is provided by a polypeptide present in a Yarrowia yeast.

179. The genetically modified yeast of claim 178, wherein the Yarrowia yeast is a Y. lipolytica yeast.

180. The genetically modified yeast of any one of claims 160-177, wherein the dieneoyl CoA reductase activity is provided by a polypeptide comprising the amino acid sequence of SEQ ID NO: 3794 or 3795.

181. The genetically modified yeast of any one of claims 160-180, wherein the endogenous acyl-CoA oxidase polypeptide is a POX4 polypeptide.

182. The genetically modified yeast of claim 181, wherein the POX4 polypeptide comprises a modified amino acid sequence of SEQ ID NO: 30.

183. The genetically modified yeast of claim 181 or 182, wherein the POX4 polypeptide comprises an amino acid modification at one or more amino acid positions selected from the group consisting of: 88, 90, 96, 98, 99, 100, 102, 103, 302, 309, 310, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504 and 505.

184. The genetically modified yeast of any one of claims 160-180, wherein the endogenous acyl-CoA oxidase polypeptide is a POX5 polypeptide.

185. The genetically modified yeast of claim 184, wherein the POX5 polypeptide comprises a modified amino acid sequence of SEQ ID NO: 32.

186. The genetically modified yeast of claim 184, wherein the POX5 polypeptide comprises an amino acid modification at one or more amino acid positions selected from the group consisting of: 81, 82, 83, 84, 85, 86, 88, 93, 94, 95, 96, 98, 102, 284, 287, 290, 291, 292, 294, 295, 428, 429, 436, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462 and 463.

187. The genetically modified yeast of any one of claims 160-186, wherein the acyl-CoA dehydrogenase polypeptide is selected from the group consisting of: ACAD, VLCAD, LCAD, MCAD and SCAD polypeptides.

188. The genetically modified yeast of claim 187, wherein the acyl-CoA dehydrogenase polypeptide comprises a modified amino acid sequence of SEQ ID NO: 3685.

189. The genetically modified yeast of any one of claims 160-188, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the N-terminal loop.

190. The genetically modified yeast of any one of claims 160-189, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the D alpha helix.

191. The genetically modified yeast of any one of claims 160-190, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop between the D alpha helix and the E' alpha helix.

192. The genetically modified yeast of any one of claims 160-191, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification to an amino acid in effective contact with carbons 6 to 9 in a feedstock component.

193. The genetically modified yeast of any one of claims 160-192, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification to an amino acid in effective contact with carbons 10 to 12 in a feedstock component.

194. The genetically modified yeast of any one of claims 160-193, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the L alpha helix.

195. The genetically modified yeast of any one of claims 160-194, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop C-terminal to the L alpha helix.

196. The genetically modified yeast of any one of claims 160-195, wherein the modified endogenous acyl-CoA oxidase polypeptide comprises an amino acid modification in the loop between the L alpha helix and the M alpha helix.

197. A method for producing a diacid, comprising:

(a) contacting a genetically modified yeast of any one of claims 160-196 with a feedstock comprising a vegetable oil; and

(b) culturing the yeast under conditions in which diacid is produced from the feedstock.

198. The method of claim 197, comprising purifying the diacid from the yeast.

199. A method for producing a diacid, comprising:

(a) contacting a genetically modified yeast of any of embodiments 1-124 and 160-198 with a feedstock comprising an unsaturated vegetable fatty acid capable of being converted by the yeast to a diacid;

(b) culturing the yeast under conditions in which diacid containing one or more unsaturations is produced from the feedstock; and

(c) hydrogenating and removing one or more of the unsaturations.

200. The method of claim 199, wherein the unsaturated vegetable fatty acid is linoleic acid or linolenic acid.