CLAIMS

What is claimed is:

1. A genetically modified *Saccharomyces cerevisiae* cell for producing a cannabinoid or a cannabinoid derivative, the genetically modified *Saccharomyces cerevisiae* cell comprising one or more heterologous nucleic acids integrated into a chromosome of the genetically modified *Saccharomyces cerevisiae* cell and encoding an active geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprising an amino acid sequence having at least 85% sequence identity to SEQ ID NO:110 or SEQ ID NO:100.

2. The genetically modified *Saccharomyces cerevisiae* cell of claim 1, wherein the geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO:110 or at least 85% sequence identity to SEQ ID NO:100.

3. The genetically modified *Saccharomyces cerevisiae* cell of claim 1 or claim 2, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more heterologous nucleic acids integrated into a chromosome of the genetically modified *Saccharomyces cerevisiae* cell and encoding a tetraketide synthase (TKS) polypeptide and one or more heterologous nucleic acids integrated into a chromosome of the genetically modified *Saccharomyces cerevisiae* cell and encoding an olivetolic acid (OAC) polypeptide, or one or more heterologous nucleic acids integrated into a chromosome of the genetically modified *Saccharomyces cerevisiae* cell and encoding a fusion TKS and OAC polypeptide.

4. The genetically modified *Saccharomyces cerevisiae* cell of claim 3, wherein the TKS polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:11 and the OAC polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:10.

5. The genetically modified *Saccharomyces cerevisiae* cell of any one of claims 1-4, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more of the following:
a) one or more heterologous nucleic acids encoding a polypeptide that generates an acyl-CoA compound or an acyl-CoA compound derivative; or

b) one or more heterologous nucleic acids encoding a polypeptide that generates geranyl pyrophosphate.

6. The genetically modified *Saccharomyces cerevisiae* cell of claim 5, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more heterologous nucleic acids encoding a polypeptide that generates an acyl-CoA compound or an acyl-CoA compound derivative and wherein the polypeptide that generates an acyl-CoA compound or an acyl-CoA compound derivative is an acyl-activating enzyme (AAE) polypeptide, a fatty acyl-CoA ligase polypeptide, or a fatty acyl-CoA synthetase (FAA) polypeptide.

7. The genetically modified *Saccharomyces cerevisiae* cell of claim 6, wherein the AAE polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:90, SEQ ID NO:92 or SEQ ID NO:149; the fatty acyl-CoA ligase polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:145 or SEQ ID NO:147; and
the FAA polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:169, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, or SEQ ID NO:200.

8. The genetically modified *Saccharomyces cerevisiae* cell of claim 5, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more heterologous nucleic acids encoding a polypeptide that generates geranyl pyrophosphate and wherein the polypeptide that generates geranyl pyrophosphate is a geranyl pyrophosphate synthetase (GPPS) polypeptide.

9. The genetically modified *Saccharomyces cerevisiae* cell of claim 8, wherein the GPPS polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:60.

10. The genetically modified *Saccharomyces cerevisiae* cell of any one of claims 1-9, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more of the following:

a) one or more heterologous nucleic acids encoding a HMG-CoA synthase (HMGS) polypeptide;
b) one or more heterologous nucleic acids encoding a 3-hydroxy-3-methyl-glutaryl-CoA reductase (HMGR) polypeptide;
c) one or more heterologous nucleic acids encoding a mevalonate kinase (MK) polypeptide;
d) one or more heterologous nucleic acids encoding a phosphomevalonate kinase (PMK) polypeptide;
e) one or more heterologous nucleic acids encoding a mevalonate pyrophosphate decarboxylase (MVD) polypeptide; or
f) one or more heterologous nucleic acids encoding a isopentenyl diphosphate isomerase (IDI) polypeptide.

11. The genetically modified *Saccharomyces cerevisiae* cell of claim 10, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more heterologous nucleic acids encoding an IDI polypeptide.

12. The genetically modified *Saccharomyces cerevisiae* cell of claim 11, wherein the IDI polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:58.

13. The genetically modified *Saccharomyces cerevisiae* cell of claim 10, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more heterologous nucleic acids encoding an HMGR polypeptide and wherein the HMGR polypeptide is a truncated HMGR polypeptide.

14. The genetically modified *Saccharomyces cerevisiae* cell of claim 13, wherein the HMGR polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:115 and the truncated HMGR polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:208.

15. The genetically modified *Saccharomyces cerevisiae* cell of claim 10, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more heterologous nucleic acids encoding an MK polypeptide and one or more heterologous nucleic acids encoding a PMK polypeptide.

16. The genetically modified *Saccharomyces cerevisiae* cell of claim 15, wherein the MK polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:64 the PMK polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:205.

17. The genetically modified *Saccharomyces cerevisiae* cell of claim 10, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more heterologous nucleic acids encoding a MVD polypeptide.

18. The genetically modified *Saccharomyces cerevisiae* cell of claim 17, wherein the MVD polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:66.

19. The genetically modified *Saccharomyces cerevisiae* cell of claim 10, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more heterologous nucleic acids encoding a polypeptide that condenses two molecules of acetyl-CoA to generate acetoacetyl-CoA and wherein the polypeptide that condenses two molecules of acetyl-CoA to generate acetoacetyl-CoA is an acetoacetyl-CoA thiolase polypeptide.

20. The genetically modified *Saccharomyces cerevisiae* cell of claim 19, wherein the acetoacetyl-CoA thiolase polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:25.

21. The genetically modified *Saccharomyces cerevisiae* cell of claim 1 or claim 2, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more heterologous nucleic acids encoding a cannabinoid synthase polypeptide, wherein the cannabinoid synthase polypeptide is a tetrahydrocannabinolic acid (THCA) synthase polypeptide or a cannabidiolic acid (CBDA) synthase polypeptide.

22. The genetically modified *Saccharomyces cerevisiae* cell of claim 21, wherein the THCA synthase polypeptide comprises an amino acid sequence having at least 85% sequence identity to NO:155 and the CBDA synthase polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:88 or SEQ ID NO:151.

23. The genetically modified *Saccharomyces cerevisiae* cell of claim 1 or claim 2, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more of the following:

a) one or more heterologous nucleic acids encoding a polypeptide that generates an acyl-CoA compound or an acyl-CoA compound derivative;

b) one or more heterologous nucleic acids encoding a polypeptide that generates geranyl pyrophosphate;

c) one or more heterologous nucleic acids encoding a HMG-CoA synthase (HMGS) polypeptide;

d) one or more heterologous nucleic acids encoding a 3-hydroxy-3-methyl-glutaryl-CoA reductase (HMGR) polypeptide;

e) one or more heterologous nucleic acids encoding a mevalonate kinase (MK) polypeptide;

f) one or more heterologous nucleic acids encoding a phosphomevalonate kinase (PMK) polypeptide;

g) one or more heterologous nucleic acids encoding a mevalonate pyrophosphate decarboxylase (MVD) polypeptide;

h) one or more heterologous nucleic acids encoding a isopentenyl diphosphate isomerase (IDI) polypeptide;

i) one or more heterologous nucleic acids encoding a polypeptide that condenses two molecules of acetyl-CoA to generate acetoacetyl-CoA, wherein the polypeptide that condenses two molecules of acetyl-CoA to generate acetoacetyl-CoA is an acetoacetyl-CoA thiolase polypeptide; or

j) one or more heterologous nucleic acids encoding a tetraketide synthase (TKS) polypeptide and one or more heterologous nucleic acids encoding an olivetolic acid cyclase (OAC) polypeptide, or one or more heterologous nucleic acids encoding a fusion TKS and OAC polypeptide.

24. A genetically modified *Saccharomyces cerevisiae* that produces a cannabinoid or cannabinoid derivative, wherein the *Saccharomyces cerevisiae* cell is genetically modified with:

a) one or more heterologous nucleic acids integrated into a chromosome of the genetically modified *Saccharomyces cerevisiae* cell and encoding a tetraketide synthase (TKS) polypeptide;

b) one or more heterologous nucleic acids integrated into a chromosome of the genetically modified *Saccharomyces cerevisiae* cell and encoding an olivetolic acid cyclase (OAC) polypeptide;

c) one or more heterologous nucleic acids integrated into a chromosome of the genetically modified *Saccharomyces cerevisiae* cell and encoding an active geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprising an amino acid sequence having at least 85% sequence identity to SEQ ID NO:110 or SEQ ID NO:100; and

d) at least one of

i) one or more heterologous nucleic acids encoding an ERG 8 polypeptide;

ii) one or more heterologous nucleic acids encoding an ERG 10 polypeptide;

iii) one or more heterologous nucleic acids encoding an ERG 12 polypeptide; and

iv) one or more heterologous nucleic acids encoding an ERG 13 polypeptide.

25. A genetically modified *Saccharomyces cerevisiae* cell that produces a cannabinoid or cannabinoid derivative, wherein the *Saccharomyces cerevisiae* cell is genetically modified with:

a) one or more heterologous nucleic acids integrated into a chromosome of the genetically modified *Saccharomyces cerevisiae* cell and encoding a fusion polypeptide comprising a tetraketide synthase (TKS) polypeptide and an olivetolic acid cyclase (OAC) polypeptide; and

b) one or more heterologous nucleic acids integrated into a chromosome of the genetically modified *Saccharomyces cerevisiae* cell and encoding an active geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprising an amino acid sequence having at least 85% sequence identity to SEQ ID NO:110 or SEQ ID NO:100.

26. The genetically modified *Saccharomyces cerevisiae* cell of claim 24 or 25, wherein the geranyl pyrophosphate olivetolic acid geranyltransferase polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO:110 or at least 85% sequence identity to SEQ ID NO:100.

27. The genetically modified *Saccharomyces cerevisiae* cell of claim 25, wherein the geranyl pyrophosphate olivetolic acid geranyltransferase polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO:110 or at least 85% sequence identity to SEQ ID NO: 100

28. The genetically modified *Saccharomyces cerevisiae* cell of any of claims 24 to 27, wherein the *Saccharomyces cerevisiae* cell is further genetically modified with:

a) one or more heterologous nucleic acids encoding a tetrahydrocannabinolic acid (THCA) synthase polypeptide or a cannabidiolic acid (CBDA) synthase polypeptide;

b) one or more heterologous nucleic acids encoding one or more polypeptides that generate geranyl pyrophosphate;

c) one or more heterologous nucleic acids encoding one or more polypeptides that generate hexanoyl-CoA or derivatives thereof; and

d) one or more heterologous nucleic acids encoding one or more polypeptides that generate malonyl-CoA.

29. The genetically modified *Saccharomyces cerevisiae* cell of claim 24 or 26, wherein the TKS polypeptide and OAC polypeptide exist in a fusion polypeptide.

30. The genetically modified *Saccharomyces cerevisiae* cell of claim 29, wherein the TKS-OAC fusion polypeptide has at least 85% sequence identity to SEQ ID NO: 80.

31. The genetically modified *Saccharomyces cerevisiae* cell of claim 28, wherein the one or more polypeptides that generate malonyl-CoA comprise an acetyl-CoA carboxylase-1 (ACC1) polypeptide.

32. The genetically modified *Saccharomyces cerevisiae* cell of claim 28, wherein the one or more polypeptides that generate hexanoyl-CoA or derivatives thereof comprise a hexanoyl-CoA synthetase (HCS) polypeptide.

33. The genetically modified *Saccharomyces cerevisiae* cell of claim 28, wherein the one or more polypeptides that generate geranyl pyrophosphate comprise a geranyl pyrophosphate synthetase (GPPS) polypeptide.

34. The genetically modified *Saccharomyces cerevisiae* cell of claim 33, wherein the GPPS polypeptide is a heterodimeric polypeptide comprising a GPPS large subunit polypeptide and a GPPS small subunit polypeptide.

35. The genetically modified *Saccharomyces cerevisiae* cell of claim 28, wherein the one or more polypeptides that generate hexanoyl-CoA or derivatives thereof comprise a MCT1 polypeptide, a PaaH1 polypeptide, a PhaB polypeptide, a PhaJ polypeptide, a Crt polypeptide, a Ter polypeptide, and/or a BktB polypeptide.

36. The genetically modified *Saccharomyces cerevisiae* cell of any one of the preceding claims, wherein at least one of the heterologous nucleic acids is operably linked to an inducible promoter.

37. The genetically modified *Saccharomyces cerevisiae* cell of claim 23, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more heterologous nucleic acids encoding a polypeptide that generates an acyl-CoA compound or an acyl-CoA compound derivative and wherein the polypeptide that generates an acyl-CoA compound or an acyl-CoA compound derivative is an acyl-activating enzyme (AAE) polypeptide, a fatty acyl-CoA ligase polypeptide, or a fatty acyl-CoA synthetase (FAA) polypeptide.

38. The genetically modified *Saccharomyces cerevisiae* cell of claim 37, wherein the AAE polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:90, SEQ ID NO:92 or SEQ ID NO:149; the fatty acyl-CoA ligase polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ

ID NO:145 or SEQ ID NO:147; and the FAA polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:169, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, or SEQ ID NO:200.

39. The genetically modified *Saccharomyces cerevisiae* cell of any of claims 23, 28, and 33, wherein the GPPS polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:60.

40. The genetically modified *Saccharomyces cerevisiae* cell of claim 23, wherein the IDI polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:58.

41. The genetically modified *Saccharomyces cerevisiae* cell of claim 23, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more heterologous nucleic acids encoding an HMGS polypeptide and one or more heterologous nucleic acids encoding a HMGR polypeptide and wherein the HMGR polypeptide is a truncated HMGR polypeptide.

42. The genetically modified *Saccharomyces cerevisiae* cell of claim 41, wherein the HMGS polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:115 and the truncated HMGR polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:208.

43. The genetically modified *Saccharomyces cerevisiae* cell of claim 23, wherein the genetically modified *Saccharomyces cerevisiae* cell further comprises one or more heterologous nucleic acids encoding an MK polypeptide and one or more heterologous nucleic acids encoding a PMK polypeptide.

44. The genetically modified *Saccharomyces cerevisiae* cell of claim 23, wherein the MK polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:64 and the PMK polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:205.

45. The genetically modified *Saccharomyces cerevisiae* cell of claim 23, wherein the MVD polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:66.

46. The genetically modified *Saccharomyces cerevisiae* cell of any one of claims 23 to 25, wherein the TKS polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:11 and the OAC polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:10.

47. The genetically modified *Saccharomyces cerevisiae* cell of claim 23 or 26, wherein the TKS-OAC fusion polypeptide has at least 85% sequence identity to SEQ ID NO: 80.

48. The genetically modified *Saccharomyces cerevisiae* cell of claim 24 or 25, wherein the ERG 8 polypeptide has at least 85% sequence identity to SEQ ID NO: 62, the ERG 10 polypeptide has at least 85% sequence identity to SEQ ID NO: 25, the ERG 12 polypeptide has at least 85% sequence identity to SEQ ID NO: 64, and/or the ERG 13 polypeptide has at least 85% sequence identity to SEQ ID NO: 24.

49. The genetically modified *Saccharomyces cerevisiae* cell of claim 28, wherein the THCA synthase polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:155 and the CBDA synthase polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:88 or SEQ ID NO:151.

50. The genetically modified *Saccharomyces cerevisiae* cell of claim 31, wherein the ACC1 polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:9.

51. The genetically modified *Saccharomyces cerevisiae* cell of claim 32, wherein the HCS polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4.

52. The genetically modified *Saccharomyces cerevisiae* cell of claim 35, wherein the MCT1 polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO: 42, the PaaH1 polypeptide comprises an amino acid sequence having at least

85% sequence identity to SEQ ID NO: 18 or SEQ ID NO: 46, the PhaB polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO: 94, the PhaJ polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO: 96, the Crt polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:19 or SEQ ID NO: 48, the Ter polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO: 20 or SEQ ID NO: 50, and/or the BktB polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO: 21 or SEQ ID NO: 44.

53. A method of producing a cannabinoid or a cannabinoid derivative in a genetically modified *Saccharomyces cerevisiae* cell, the method comprising:
a) culturing the genetically modified *Saccharomyces cerevisiae* cell of any one of claims 1-52 in a suitable medium; and
b) recovering the produced cannabinoid or cannabinoid derivative.

54. The method of claim 53, wherein the suitable medium comprises a carboxylic acid, hexanoic acid, olivetolic acid or an olivetolic acid derivative.

55. The method of claim 53 or 54, wherein the cannabinoid is cannabigerolic acid, cannabigerolic acid monomethylether (CBGAM), cannabigerol, cannabigerol monomethylether, Δ^9-trans-tetrahydrocannabinol, Δ^9-tetrahydrocannabinolic acid, Δ^9-tetrahydrocannabinol, Δ^8-tetrahydrocannabinolic acid, Δ^9-tetrahydrocannabinolic acid A, Δ^9-tetrahydrocannabinolic acid B, Δ^9-tetrahydrocannabinolic acid-C_4, Δ^9-tetrahydrocannabinol-C_4, Δ^9-tetrahydrocannabivarinic acid, Δ^9-tetrahydrocannabivarin, Δ^9-tetrahydrocannabiorcolic acid, Δ^9-tetrahydrocannabiorcol, Δ^7-cis-iso-tetrahydrocannabivarin, Δ^9-tetrahydrocannabinol, Δ^8-tetrahydrocannabinolic acid, Δ^8-trans-tetrahydrocannabinol, Δ^8-tetrahydrocannabinol, cannabidiolic acid, cannabidiol, cannabichromenic acid, cannabichromene, cannabinolic acid, cannabinol, cannabidiol monomethylether (CBDM), cannabidiol-C_4 (CBD-C_4), cannabidiorcol (CBD-C_1), cannabitriol, cannabichromenic acid, cannabichromene, cannabinolic acid, cannabinol, cannabinol methylether, cannabinol-C4, cannabinol-C2, cannabicyclovarin, cannabielsoic acid A, cannabielsoic acid B, cannabidivarinic acid, cannabidivarin, tetrahydrocannabivarinic acid, tetrahydrocannabivarin, cannabichromevarinic acid, cannabichromevarin,

cannabigerovarinic acid, cannabigerovarin, cannabicyclolic acid, cannabicyclol, cannabielsoinic acid, cannabielsoin, cannabicitranic acid, or cannabicitran.

56. A method of making a genetically modified *Saccharomyces cerevisiae* cell for producing a cannabinoid or a cannabinoid derivative, comprising introducing one or more heterologous nucleic acids encoding a geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprising an amino acid sequence having at least 85% sequence identity to SEQ ID NO:110 or SEQ ID NO:100 into the genetically modified *Saccharomyces cerevisiae* cell.

57. The method of claim 56, wherein the geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO:110 or at least 85% sequence identity to SEQ ID NO:100.

58. A method of producing a cannabinoid or a cannabinoid derivative, the method comprising mixing a geranyl pyrophosphate:olivetolic acid geranyltransferase (GOT) polypeptide with a prenyl group acceptor molecule and a prenyl group donor molecule, wherein the GOT polypeptide is an active GOT polypeptide comprising an amino acid sequence having at least 85% sequence identity to SEQ ID NO:110 or SEQ ID NO:100.

59. The method of claim 58, wherein the geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO:110 or at least 85% sequence identity to SEQ ID NO:100.

60. The method of claim 58 or 59, wherein the GOT polypeptide comprises the amino acid sequence of SEQ ID NO:110 or SEQ ID NO:100.

61. The method of any one of claims 56-60, wherein the cannabinoid is cannabigerolic acid, cannabigerolic acid monomethylether (CBGAM), cannabigerol, cannabigerol monomethylether, Δ^9-trans-tetrahydrocannabinol, Δ^9-tetrahydrocannabinolic acid, Δ^9-tetrahydrocannabinolic acid A, Δ^9-tetrahydrocannabinolic acid B, Δ^9-tetrahydrocannabinolic acid-C_4, Δ^9-tetrahydrocannabinol-C_4, Δ^9-tetrahydrocannabivarinic acid, Δ^9-tetrahydrocannabivarin, Δ^9-tetrahydrocannabiorcolic acid, Δ^9-tetrahydrocannabiorcol, Δ^7-cis-iso-tetrahydrocannabivarin, Δ^9-tetrahydrocannabinol, Δ^8-tetrahydrocannabinolic acid, Δ^8-

trans-tetrahydrocannabinol, Δ^8-tetrahydrocannabinol, cannabidiolic acid, cannabidiol, cannabidiol monomethylether (CBDM), cannabidiol-C_4 (CBD-C_4), cannabidiorcol (CBD-C_1), cannabitriol, cannabichromenic acid, cannabichromene, cannabinolic acid, cannabinol, cannabinol methylether, cannabinol-C4, cannabinol-C2, cannabidivarinic acid, cannabidivarin, tetrahydrocannabivarinic acid, tetrahydrocannabivarin, cannabichromevarinic acid, cannabichromevarin, cannabigerovarinic acid, cannabigerovarin, cannabicyclolic acid, cannabicyclol, cannabicyclovarin, cannabielsoic acid A, cannabielsoic acid B, cannabielsoinic acid, cannabielsoin, cannabicitranic acid, or cannabicitran.

62. The method of any one of claims 56-60, wherein the prenyl group acceptor molecule is olivetolic acid or an olivetolic acid derivative and the prenyl group donor molecule is geranyl pyrophosphate (GPP) or a GPP derivative.

63. The method of claim 62, wherein the prenyl group acceptor molecule is olivetolic acid and the prenyl group donor molecule is GPP.