WHAT IS CLAIMED IS:

1. A *Brassica* plant comprising a mutant allele at a fatty acyl-acyl-ACP thioesterase A2 (FATA2) locus, wherein said mutant allele results in the production of a FATA2 polypeptide having reduced thioesterase activity relative to a corresponding wild-type FATA2 polypeptide.

2. The plant of claim 1, wherein said mutant allele comprises a nucleic acid encoding a FATA2 polypeptide having a mutation in a region (SEQ ID NO:29) corresponding to amino acids 242 to 277 of the FATA2 polypeptide.

3. The plant of claim 2, wherein said FATA2 polypeptide comprises a substitution of a leucine residue for proline at position 255.

4. The plant of claim 1, said plant further comprising a mutant allele at a FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a lysine substituted for glutamic acid in a HECGH motif.

5. The plant of claim 1, said plant further comprising a mutant allele at a FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a glutamic acid substituted for glycine in the DRDYGILNKV motif or a histidine substituted for leucine in a KYLNNP motif.

6. The plant of claim 4, said plant further comprising a mutant allele at a different FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a glutamic acid substituted for glycine in the DRDYGILNKV motif or a histidine substituted for leucine in a KYLNNP motif.

7. The plant of claim 1 or claim 6, said plant further comprising mutant alleles at two different FAD3 loci, wherein one of said mutant alleles comprises a nucleic acid encoding a FAD3A polypeptide having a cysteine substituted for arginine at position 275, and wherein one of said mutant alleles comprises a fad3B nucleic acid sequence having a mutation in an exon-intron splice site recognition sequence.

8. The plant of claim 1, said plant further comprising mutant alleles at four different FATB loci.

9. The plant of claim 8, wherein at least one of said FATB mutant alleles comprises a nucleic acid encoding a truncated FATB polypeptide.

10. The plant of claim 9, wherein said nucleic acid encoding said truncated FATB polypeptide comprises a nucleotide sequence selected from the group consisting of: SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, and SEQ ID NO:4.

11. The plant of claim 10, said plant comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, and SEQ ID NO:4.

12. The plant of claim 1, wherein said plant is a *Brassica* napus, *Brassica* juncea, or *Brassica* rapa plant.

13. The plant of claim 1, wherein said plant is an F1 hybrid.

14. Progeny of the plant of claim 1, said progeny comprising said mutant allele.

15. Seeds of the plant of claim 1.

16. A *Brassica* plant comprising mutant alleles at two or more different fatty acytacyl carrier protein thioesterase B (FATB) loci, wherein said plant produces seeds yielding an oil having a total saturates content of about 2.5% to 5.5%.

17. The plant of claim 16, said oil having a palmitic acid content of about 1.5% to 3.5%.

18. The plant of claim 16, said oil having a stearic acid content of about 0.5% to 2.5%.

19. A *Brassica* plant comprising mutant alleles at two or more different fatty acyl-acyl carrier protein thioesterase B (FATB) loci, wherein each said mutant allele results in the production of a FATB polypeptide having reduced thioesterase activity relative to a corresponding wild-type FATB polypeptide.

20. The plant of claim 19, wherein at least one of said mutant alleles comprises a nucleic acid encoding a truncated FATB polypeptide.

21. The plant of claim 19, wherein at least one of said mutant alleles comprises a nucleic acid encoding a FATB polypeptide having a deletion of a helix/4-stranded sheet (4HBT) domain or a portion thereof.

22. The plant of claim 19, wherein at least one of said mutant alleles comprises a nucleic acid encoding a FATB polypeptide having a non-conservative substitution of a residue affecting substrate specificity.

23. The plant of claim 19, wherein at least one of said mutant alleles comprises a nucleic acid encoding a FATB polypeptide having a non-conservative substitution of a residue affecting catalytic activity.

24. The plant of claim 20, wherein said nucleic acid encoding said truncated FATB polypeptide comprises a nucleotide sequence selected from the group consisting of: SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, and SEQ ID NO:4.

25. The plant of claim 19 comprising mutant alleles at three different FATB loci.

26. The plant of claim 19 comprising mutant alleles at four different FATB loci.

27. The plant of claim 24 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1 and SEQ ID NO:2.

28. The plant of claim 24 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1 and SEQ ID NO:3.

29. The plant of claim 24 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1 and SEQ ID NO:4.

30. The plant of claim 24 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:3.

31. The plant of claim 24 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:4.

32. The plant of claim 24 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1, SEQ ID NO:3, and SEQ ID NO:4.

33. The plant of claim 19 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, and SEQ ID NO:4.

34. The plant of claim 19, said plant producing seeds yielding an oil having a total saturates content of about 2.5% to 5.5%.

35. The plant of claim 19, said plant producing seeds yielding an oil having a palmitic acid content of about 1.5% to 3.5%.

36. The plant of claim 19, said plant producing seeds yielding an oil having a stearic acid content of about 0.5% to 2.5%.

37. The plant of claim 34, said oil further having an oleic acid content of about 78% to 80%, a linoleic acid content of about 8% to 10%, and an α-linolenic acid content of about 2% to 4%.

38. The plant of claim 19, said plant further comprising a mutant allele at a delta-12 fatty acid desaturase (FAD2) locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a lysine substituted for glutamic acid in a His-Glu-Cys-Gly-His motif.

39. The plant of claim 19, said plant further comprising a mutant allele at a FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a glutamic acid substituted for glycine in the DRDYGILNKV motif or a histidine substituted for leucine in a KYLNNP motif.

40. The plant of claim 38, said plant further comprising a mutant allele at a different FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a glutamic acid substituted for glycine in the DRDYGILNKV motif or a histidine substituted for leucine in a KYLNNP motif.

41. The plant of claim 19, said plant further comprising mutant alleles at two different FAD3 loci, wherein one of said mutant alleles comprises a nucleic acid encoding a FAD3A polypeptide having a cysteine substituted for arginine at position 275, and wherein one of said mutant alleles comprises a fad3B nucleic acid sequence having a mutation in an exon-intron splice site recognition sequence.

42. The plant of claim 19, said plant further comprising a mutant allele at a fatty acyl-acyl-ACP thioesterase A2 (FATA2) locus, wherein said mutant allele results in the production of a FATA2 polypeptide having reduced thioesterase activity relative to a corresponding wild-type FATA2 polypeptide.

43. The plant of claim 19, wherein said plant is a *Brassica* napus, *Brassica* juncea, or *Brassica* rapa plant.

44. The plant of claim 19, wherein said plant is an F1 hybrid.

45. Progeny of the plant of claim 19, said progeny comprising said mutant alleles.

46. Seeds of the plant of claim 19.

47. A *Brassica* plant comprising mutant alleles at two or more different FATB loci, wherein each said mutant allele results in production of a FATB polypeptide having reduced thioesterase activity relative to a corresponding wild-type FATB polypeptide, and further comprising a mutant allele at a FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a lysine substituted for glutamic acid in a His-Glu-Cys-Gly-His motif.

48. The *Brassica* plant of claim 47, further comprising a mutant allele at a different FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a glutamic acid substituted for glycine in the DRDYGILNKV motif or a histidine substituted for leucine in a KYLNNP motif.

49. A method of producing an oil, said method comprising

a) crushing seeds produced from at least one *Brassica* plant of claim 1, claim 16 or claim 19; and

b) extracting said oil from said crushed seeds, said oil having, after refining, bleaching, and deodorizing, a total saturates content of about 2.5% to 5.5%.

50. The method of claim 49, wherein said oil further comprises an eicosenoic acid content of about 1.6% to 2.3%.

51. The method of claim 49 or claim 50, wherein said oil further comprises an oleic acid content of about 78% to 80%, a linoleic acid content of about 8% to 10%, and an α-linolenic acid content of about 2% to 4%.

52. The method of any one of claims 49-51, said plant further comprising a mutant allele at a FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a lysine substituted for glutamic acid in a His-Glu-Cys-Gly-His motif.

53. The method of claim 52, said plant further comprising a mutant allele at a different FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a glutamic acid substituted for glycine in the DRDYGILNKV motif or a histidine substituted for leucine in a KYLNNP motif.

54. The method of claim 53, said plant further comprising mutant alleles at two different FAD3 loci, wherein one of said FAD3 mutant alleles comprises a nucleic

acid encoding a FAD3A polypeptide having a cysteine substituted for arginine at position 275, and wherein one of said FAD3 mutant alleles comprises a fad3B nucleic acid sequence having a mutation in an exon-intron splice site recognition sequence.

55. A method for making a *Brassica* plant, said method comprising

a) crossing one or more first *Brassica* parent plants comprising a mutant allele at a FATB locus and one or more second *Brassica* parent plants comprising a mutant allele at a different FATB locus, wherein each said mutant allele results in the production of a FATB polypeptide having reduced thioesterase activity relative to a corresponding wild-type FATB polypeptide; and

b) selecting, for one to five generations, for progeny plants having mutant alleles at two or more different FATB loci thereby obtaining said *Brassica* plant.

56. A method for making a *Brassica* plant, said method comprising

a) obtaining one or more first *Brassica* parent plants comprising mutant alleles at two or more different FATB loci, wherein each said mutant allele results in the production of a FATB polypeptide having reduced thioesterase activity relative to a corresponding wild-type FATB polypeptide;

b) obtaining one or more second *Brassica* parent plants comprising a mutant allele at a FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a lysine substituted for glycine in a His-Glu-Cys-Gly-His motif;

c) crossing said one or more first *Brassica* parent plants and said one or more second *Brassica* parent plants; and

d) selecting, for one to five generations, for progeny plants having mutant alleles at two or more different FATB loci and a mutant allele at said FAD2 locus thereby obtaining said *Brassica* plant.

57. The method of claim 56, wherein said first *Brassica* parent plant comprises mutant alleles at three different FATB loci.

58. The method of claim 56, wherein said first *Brassica* parent plant comprises mutant alleles at four different FATB loci.

59. A method for making a *Brassica* plant, said method comprising a) obtaining one or more first *Brassica* parent plants comprising mutant alleles at two or

more different FATB loci, wherein each said mutant allele results in the production of a FATB polypeptide having reduced thioesterase activity relative to a corresponding wild-type FATB polypeptide;

b) obtaining one or more second *Brassica* parent plants comprising a mutant allele at a FADA2 locus, said mutant allele comprising a nucleic acid encoding a FATA2 polypeptide having a mutation in a region (SEQ ID NO:29) corresponding to amino acids 242 to 277 of the polypeptide;

c) crossing said one or more first *Brassica* parent plants and said one or more second *Brassica* parent plants; and

d) selecting, for one to five generations, for progeny plants having mutant alleles at two or more different FATB loci and a mutant allele at said FATA2 locus thereby obtaining said *Brassica* plant.

60. The method of claim 59, wherein said first *Brassica* parent plant comprises mutant alleles at four different FATB loci.

61. The method of claim 60, wherein said first *Brassica* parent plant further comprises a mutant allele at a FAD2 locus and mutant alleles at two different FAD3 loci, said FAD2 mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a lysine substituted for glutamic acid in a His-Glu-Cys-Gly-His motif, wherein one of said FAD3 mutant alleles comprises a nucleic acid encoding a FAD3A polypeptide having a cysteine substituted for arginine at position 275, and wherein one of said FAD3 mutant alleles comprises a fad3B nucleic acid sequence having a mutation in an exon-intron splice site recognition sequence.

62. A canola oil having an oleic acid content of about 78% to 80%, a linoleic acid content of about 8% to 10%, an α-linolenic acid content of no more than about 4%, and an eicosenoic acid content of about 1.6 to 2.3%.

63. The oil of claim 62, said oil further having a palmitic acid content of about 1.5% to 3.5%.

64. The oil of claim 62 or claim 63, said oil further having a stearic acid content of 0.5% to 2.5%.

65. The oil of any one of claims 62-64, wherein said eicosenoic acid content is about 1.9 to 2.2%.

66. The oil of any one of claims 62-65, wherein said α-linolenic acid content is about 2% to about 4%.

67. Seeds of a *Brassica* plant comprising a mutant allele at a FADA2 locus, said mutant allele comprising a nucleic acid encoding a FATA2 polypeptide having a mutation in a region (SEQ ID NO:29) corresponding to amino acids 242 to 277 of the polypeptide, said seeds yielding an oil having an oleic acid content of 78% to 80%, a linoleic acid content of about 8% to 10%, an α-linolenic acid content of no more than about 4%, and an eicosenoic acid content of 1.6 to 2.3%.

68. The seeds of claim 67, wherein said seeds are F2 seeds.

69. The seeds of claim 67, wherein said *Brassica* plant further comprises mutant alleles at four different FATB loci.

70. The seeds of any one of claims 67-69, wherein said *Brassica* plant further comprises a mutant allele at a FAD2 locus and mutant alleles at two different FAD3 loci, said FAD2 mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a lysine substituted for glutamic acid in a His-Glu-Cys-Gly-His motif, wherein one of said FAD3 mutant alleles comprises a nucleic acid encoding a FAD3A polypeptide having a cysteine substituted for arginine at position 275, and wherein one of said FAD3 mutant alleles comprises a fad3B nucleic acid sequence having a mutation in an exon-intron splice site recognition sequence.

71. A canola oil having a total saturated fatty acid content of no more than about 3.7% and an oleic acid content of about 72 to 75%.

72. The oil of claim 71, wherein said oil has a palmitic acid content of about 2.2 to 2.4%.

73. The oil of claim 71 or claim 72, wherein said oil has a stearic acid content of about 0.5 to 0.8%.

74. The oil of any one of claims 71-73, wherein said oil has a eicosenoic acid content of about 1.6 to 1.9%.

75. The oil of any one of claims 71-74, wherein said total saturated fatty acid content is about 3.4 to 3.7%.

76. A plant cell of the plant of any one of claims 1-13, 16-44 and 47-48, wherein said plant cell comprises one or more of said mutant alleles.

WHAT IS CLAIMED IS:

1. A *Brassica* plant comprising a mutant allele at a fatty acyl-acyl-ACP thioesterase A2 (FATA2) locus, wherein said mutant allele results in the production of a FATA2 polypeptide having reduced thioesterase activity relative to a corresponding wild-type FATA2 polypeptide.

2. The plant of claim 1, wherein said mutant allele comprises a nucleic acid encoding a FATA2 polypeptide having a mutation in a region (SEQ ID NO:29) corresponding to amino acids 242 to 277 of the FATA2 polypeptide.

3. The plant of claim 2, wherein said FATA2 polypeptide comprises a substitution of a leucine residue for proline at position 255.

4. The plant of claim 1, said plant further comprising a mutant allele at a FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a lysine substituted for glutamic acid in a HECGH motif.

5. The plant of claim 1, said plant further comprising a mutant allele at a FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a glutamic acid substituted for glycine in the DRDYGILNKV motif or a histidine substituted for leucine in a KYLNNP motif.

6. The plant of claim 4, said plant further comprising a mutant allele at a different FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a glutamic acid substituted for glycine in the DRDYGILNKV motif or a histidine substituted for leucine in a KYLNNP motif.

7. The plant of claim 1 or claim 6, said plant further comprising mutant alleles at two different FAD3 loci, wherein one of said mutant alleles comprises a nucleic acid encoding a FAD3A polypeptide having a cysteine substituted for arginine at position 275, and wherein one of said mutant alleles comprises a fad3B nucleic acid sequence having a mutation in an exon-intron splice site recognition sequence.

8. The plant of claim 1, said plant further comprising mutant alleles at four different FATB loci.

9. The plant of claim 8, wherein at least one of said FATB mutant alleles comprises a nucleic acid encoding a truncated FATB polypeptide.

10. The plant of claim 9, wherein said nucleic acid encoding said truncated FATB polypeptide comprises a nucleotide sequence selected from the group consisting of: SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, and SEQ ID NO:4.

11. The plant of claim 10, said plant comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, and SEQ ID NO:4.

12. The plant of claim 1, wherein said plant is a *Brassica* napus, *Brassica* juncea, or *Brassica* rapa plant.

13. The plant of claim 1, wherein said plant is an F1 hybrid.

14. Progeny of the plant of claim 1, said progeny comprising said mutant allele.

15. Seeds of the plant of claim 1.

16. The plant of claim 1, further comprising mutant alleles at two or more different fatty acyl-acyl carrier protein thioesterase B (FATB) loci, wherein each of said FATB mutant alleles results in the production of a FATB polypeptide having reduced thioesterase activity relative to a corresponding wild-type FATB polypeptide.

17. The plant of claim 16, wherein at least one of said FATB mutant alleles comprises a nucleic acid encoding a truncated FATB polypeptide.

18. The plant of claim 16, wherein at least one of said mutant alleles comprises a nucleic acid encoding a FATB polypeptide having a deletion of a helix/4-stranded sheet (4HBT) domain or a portion thereof.

19. The plant of claim 16, wherein at least one of said FATB mutant alleles comprises a nucleic acid encoding a FATB polypeptide having a non-conservative substitution of a residue affecting substrate specificity.

20. The plant of claim 16, wherein at least one of said FATB mutant alleles comprises a nucleic acid encoding a FATB polypeptide having a non-conservative substitution of a residue affecting catalytic activity.

21. The plant of claim 17, wherein said nucleic acid encoding said truncated FATB polypeptide comprises a nucleotide sequence selected from the group consisting of: SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, and SEQ ID NO:4.

22. The plant of claim 16 comprising mutant alleles at three different FATB loci.

23. The plant of claim 16 comprising mutant alleles at four different FATB loci.

24. The plant of claim 21 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1 and SEQ ID NO:2.

25. The plant of claim 21 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1 and SEQ ID NO:3.

26. The plant of claim 21 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1 and SEQ ID NO:4.

27. The plant of claim 21 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:3.

28. The plant of claim 21 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:4.

29. The plant of claim 21 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1, SEQ ID NO:3, and SEQ ID NO:4.

30. The plant of claim 16 comprising nucleic acids having the nucleotide sequences set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, and SEQ ID NO:4.

31. The plant of claim 16, said plant producing seeds yielding an oil having a total saturates content of about 2.5% to 5.5%.

32. The plant of claim 16, said plant producing seeds yielding an oil having a palmitic acid content of about 1.5% to 3.5%.

33. The plant of claim 16, said plant producing seeds yielding an oil having a stearic acid content of about 0.5% to 2.5%.

34. The plant of claim 31, said oil further having an oleic acid content of about 78% to 80%, a linoleic acid content of about 8% to 10%, and an α-linolenic acid content of about 2% to 4%.

35. The plant of claim 16, said plant further comprising a mutant allele at a delta-12 fatty acid desaturase (FAD2) locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a lysine substituted for glutamic acid in a His-Glu-Cys-Gly-His motif.

36. The plant of claim 16, said plant further comprising a mutant allele at a FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a glutamic acid substituted for glycine in the DRDYGILNKV motif or a histidine substituted for leucine in a KYLNNP motif.

37. The plant of claim 35, said plant further comprising a mutant allele at a different FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a glutamic acid substituted for glycine in the DRDYGILNKV motif or a histidine substituted for leucine in a KYLNNP motif.

38. The plant of claim 16, said plant further comprising mutant alleles at two different FAD3 loci, wherein one of said mutant alleles comprises a nucleic acid encoding a FAD3A polypeptide having a cysteine substituted for arginine at position 275, and wherein one of said mutant alleles comprises a fad3B nucleic acid sequence having a mutation in an exon-intron splice site recognition sequence.

39. The plant of claim 16, wherein said plant is a *Brassica* napus, *Brassica* juncea, or *Brassica* rapa plant.

40. The plant of claim 16, wherein said plant is an F1 hybrid.

41. Progeny of the plant of claim 16, said progeny comprising said mutant alleles.

42. Seeds of the plant of claim 16.

43. A method of producing an oil, said method comprising

a) crushing seeds produced from at least one *Brassica* plant of claim 1 or claim 16; and

b) extracting said oil from said crushed seeds, said oil having, after refining, bleaching, and deodorizing, a total saturates content of about 2.5% to 5.5%.

44. The method of claim 43, wherein said oil further comprises an eicosenoic acid content of about 1.6% to 2.3%.

45. The method of claim 43 or claim 44, wherein said oil further comprises an oleic acid content of about 78% to 80%, a linoleic acid content of about 8% to 10%, and an α-linolenic acid content of about 2% to 4%.

46. The method of any one of claims 43-45, said plant further comprising a mutant allele at a FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a lysine substituted for glutamic acid in a His-Glu-Cys-Gly-His motif.

47. The method of claim 46, said plant further comprising a mutant allele at a different FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a glutamic acid substituted for glycine in the DRDYGILNKV motif or a histidine substituted for leucine in a KYLNNP motif.

48. The method of claim 47, said plant further comprising mutant alleles at two different FAD3 loci, wherein one of said FAD3 mutant alleles comprises a nucleic acid encoding a FAD3A polypeptide having a cysteine substituted for arginine at position 275, and wherein one of said FAD3 mutant alleles comprises a fad3B nucleic acid sequence having a mutation in an exon-intron splice site recognition sequence.

49. The method of claim 50, wherein said first *Brassica* parent plant further comprises a mutant allele at a FAD2 locus, said mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a lysine substituted for glycine in a His-Glu-Cys-Gly-His motif.

50. A method for making a *Brassica* plant, said method comprising

a) obtaining one or more first *Brassica* parent plants comprising mutant alleles at two or more different FATB loci, wherein each said mutant allele results in the production of a FATB polypeptide having reduced thioesterase activity relative to a corresponding wildtype FATB polypeptide;

b) obtaining one or more second *Brassica* parent plants comprising a mutant allele at a FATA2 locus, said mutant allele comprising a nucleic acid encoding a FATA2 polypeptide having a mutation in a region (SEQ ID NO:29) corresponding to amino acids 242 to 277 of the polypeptide;

c) crossing said one or more first *Brassica* parent plants and said one or more second *Brassica* parent plants; and

d) selecting, for one to five generations, for progeny plants having mutant alleles at two or more different FATB loci and a mutant allele at said FATA2 locus thereby obtaining said *Brassica* plant.

51. The method of claim 50, wherein said first *Brassica* parent plant comprises mutant alleles at four different FATB loci.

52. The method of claim 51, wherein said first *Brassica* parent plant further comprises a mutant allele at a FAD2 locus and mutant alleles at two different FAD3 loci, said FAD2 mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a lysine substituted for glutamic acid in a His-Glu-Cys-Gly-His motif, wherein one of said FAD3 mutant alleles comprises a nucleic acid encoding a FAD3A polypeptide having a cysteine substituted for arginine at position 275, and wherein one of said FAD3 mutant alleles comprises a fad3B nucleic acid sequence having a mutation in an exon-intron splice site recognition sequence.

53. Seeds of a *Brassica* plant comprising a mutant allele at a FATA2 locus, said mutant allele comprising a nucleic acid encoding a FATA2 polypeptide having a mutation in a region (SEQ ID NO:29) corresponding to amino acids 242 to 277 of the polypeptide, said seeds yielding an oil having an oleic acid content of 78% to 80%, a linoleic acid content of

about 8% to 10%, an α-linolenic acid content of no more than about 4%, and an eicosenoic acid content of 1.6 to 2.3%.

54. The seeds of claim 53, wherein said seeds are F2 seeds.

55. The seeds of claim 54, wherein said *Brassica* plant further comprises mutant alleles at four different FATB loci.

56. The seeds of any one of claims 53-55, wherein said *Brassica* plant further comprises a mutant allele at a FAD2 locus and mutant alleles at two different FAD3 loci, said FAD2 mutant allele comprising a nucleic acid encoding a FAD2 polypeptide having a lysine substituted for glutamic acid in a His-Glu-Cys-Gly-His motif, wherein one of said FAD3 mutant alleles comprises a nucleic acid encoding a FAD3A polypeptide having a cysteine substituted for arginine at position 275, and wherein one of said FAD3 mutant alleles comprises a fad3B nucleic acid sequence having a mutation in an exon-intron splice site recognition sequence.