CLAIMS

1. A segregant of inbred canola line NS-B50027-4, representative seed of said inbred canola line having been deposited under ATCC Accession Number PTA-123186, wherein said NS-B50027-4 contains within its genome:

a first transgenic locus comprising one copy of each of a *M. pusilla* Δ6-desaturase, a *P. cordata* Δ5-elongase, a *P. salina* Δ5-desaturase, and a *P. pastoris* Δ15/ω3-desaturase gene,

a second transgenic locus comprising two copies of each of a *Micromonas pusilla* Δ6-desaturase, a *Pyramimonas cordata* Δ5-elongase, a *Pavlova salina* Δ5-desaturase, a *Pichia pastoris* Δ15/ω3-desaturase, a *Pavlova salina* Δ4-desaturase, a *Lachancea kluyveri* Δ12-desaturase, and a *P. cordata* Δ6-elongase gene;

wherein said first transgenic locus is located on a first chromosome, and said second transgenic locus is located on a second chromosome;

wherein said segregant comprises either said first transgenic locus or said second transgenic locus.

2. A canola plant, or a part thereof, comprising the genome of the segregant of claim 1.

3. The canola plant, or part thereof, of claim 2, wherein said part is at least one of seed, leaf, pollen, embryo, root, root tip, pod, flower, ovule, stalk, cell, cotyledon, half-cotyledon, hypocotyl, radicle, or gamete.

4. A method for obtaining a canola inbred line comprising:

(a) producing a hybrid plant by crossing (i) a first plant grown from seed of inbred canola line NS-B50027-4, representative seed of said inbred canola line having been deposited under ATCC Accession Number PTA-123186, wherein said NS-B50027-4 contains within its genome (1) a first transgenic locus comprising one copy of each of a *M. pusilla* Δ6-desaturase, a *P. cordata* Δ5-elongase, a *P. salina* Δ5-desaturase, and a *P. pastoris* Δ15/ω3-desaturase gene, and (2) a second transgenic locus comprising two copies of each of a *Micromonas pusilla* Δ6-desaturase, a *Pyramimonas cordata* Δ5-elongase, a *Pavlova salina* Δ5-desaturase, a *Pichia pastoris* Δ15/ω3-desaturase, a *Pavlova salina* Δ4-desaturase, a *Lachancea kluyveri* Δ12-desaturase, and a *P. cordata* Δ6-elongase gene, wherein said first transgenic locus is located on a first chromosome and said

second transgenic locus is located on a second chromosome, with (ii) a plant of a second canola line, wherein said hybrid plant comprises at least one transgenic locus of NS-B50027-4;

(b) crossing said hybrid with a plant of said second canola line; and;

(c) repeating step (b) at least once to obtain said canola inbred line, wherein said canola inbred line comprises at least one of said transgenic loci.

5. The method according to claim 4, wherein said inbred canola line has all the physiological and morphological characteristics of inbred canola line NS-B50027-4, seed of said line having been deposited under ATCC Accession No. PTA-123186.

6. A method of producing eicosapentaenoic acid (EPA); docosapentaenoic acid (DPA), or docosahexaenoic acid (DHA) in the seed of a plant comprising cultivating a plant comprising the first transgenic locus and/or the second transgenic locus of claim 1, wherein transgenes of said locus or loci are expressed in the seed of said plant.

7. The seed of the plant cultivated as in claim 6.

8. A method of making docosahexaenoic acid (DHA)-containing canola oil comprising the steps of:

(a) introgressing the DHA trait of NS-B50027-4, deposited under ATCC Accession Number PTA-123186, into an elite *Brassica* line that is male sterile;

(b) introgressing the DHA trait of NS-B50027-4 into a second elite *Brassica* line that is fertile;

(c) crossing the two lines (a) and (b) to obtain a hybrid progeny;

(d) cultivating the seed of the hybrid progeny;

(e) harvesting the grain produced by the cultivated hybrid progeny; and

(f) extracting the oil from the progeny of the hybrid seed.

9. The segregant of claim 1, wherein said segregant comprises said second transgenic locus.

10. A method of increasing production of long chain polyunsaturated fatty acids (LC-PUFA) in *Brassica* that produces long chain-polyunsaturated fatty acid (LC-PUFA) comprising the steps of

obtaining a segregant of claim 1 comprising said first transgenic locus, and introgressing the segregant with a recipient *Brassica* that comprises LC-PUFA biosynthesis genes to obtain introgressed progeny *Brassica* that contain both recipient LC-PUFA biosynthesis genes and said first transgenic locus, wherein said introgressed *Brassica* progeny produces increased LC-PUFA.

11. The method of claim 10, wherein the *Brassica* is *B. juncea* or *B. napus*.

12. The method of claim 10, wherein the LC-PUFA comprises more docosapentaenoic acid (DPA) than docosahexaenoic acid (DHA).

13. The method of claim 8, wherein the hybrid progeny further comprises at least one trait selected from herbicide resistance, insect resistance, bacterial disease resistance, fungal disease resistance, viral disease resistance, or sterility.

14. A canola inbred line produced by the method of claim 4, wherein said canola inbred line comprises at least one trait selected from herbicide resistance, insect resistance, bacterial disease resistance, fungal disease resistance, viral disease resistance, or sterility.

15. A method for obtaining a segregant of NS-B50027-4-derived canola plant or a part thereof, representative seed of an inbred NS-B50027-4 canola line having been deposited under ATCC Accession Number PTA-123186, characterized by comprising:

(a) crossing a first plant grown from a segregant of said NS-B50027-4 canola line with a second plant of another canola line to yield a hybrid plant, and

(b) growing the hybrid plant under plant growing conditions to yield the segregant of NS-B50027-4-derived canola plant,

wherein said segregant of NS-B50027-4 contains within its genome:

a first transgenic locus comprising one copy of each of a *M. pusilla* Δ6-desaturase, a *P. cordata* Δ5-elongase, a *P. salina* Δ5-desaturase, and a *P. pastoris* Δ15/ω3-desaturase gene,

a second transgenic locus comprising two copies of each of a *Micromonas pusilla* Δ6-desaturase, a *Pyramimonas cordata* Δ5-elongase, a *Pavlova salina* Δ5-desaturase, a *Pichia pastoris* Δ15/ω3-desaturase, a *Pavlova salina* Δ4-desaturase, a *Lachancea kluyveri* Δ12-desaturase, and a *P. cordata* Δ6-elongase gene;

wherein said first transgenic locus is located on a first chromosome, and said second transgenic locus is located on a second chromosome;

wherein said segregant comprises either said first transgenic locus or said second transgenic locus.

16. The method of claim 15, characterized by said NS-B50027-4-derived canola plant or a part thereof is transformed such that its genetic material contains one or more transgenes, operably linked to one or more regulatory elements, in addition to the transgenes present in said NS-B50027-4 canola line.

17. The method of claim 15, characterized by said canola part thereof being at least one of seed, leaf, pollen, embryo, root, root tip, pod, flower, ovule, stalk, cell, cotyledon, half-cotyledon, hypocotyl, radicle, or gamete.

18. The method of claim 15, characterized by said NS-B50027-4-derived canola plant or a part thereof being the product of traditional breeding techniques and not having been modified by recombinant, mutagenic, or other genetic modification other than the elite event associated with said NS-B50027-4 line.

19. The method of claim 15, characterized by said method further comprising:

(a) crossing said segregant of NS-B50027-4-derived canola plant with itself or another canola plant to yield the additional segregant of NS-B50027-4-derived canola plants;

(b) growing said segregant of NS-B50027-4-derived canola plant of step (a) under plant growing conditions, to yield additional NS-B50027-4-derived canola plants; and

(c) repeating the crossing and growing steps of (a) and (b) from 0 to 7 times to generate further NS-B50027-4-derived canola plants, said NS-B50027-4-derived canola plants expressing a combination of at least two NS B50027-4-traits selected from DHA production and at least one additional agronomically desirable trait.