CLAIMS

We claim:

1. 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 seed 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; and

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

2. A canola plant, or a part thereof, comprising the genome of the seed of claim 1, produced by growing the seed 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, protoplast, cotyledon, half-cotyledon, hypocotyl, radicle, cell culture, tissue culture, protein, oil, lipid, fatty acid, gamete, or nucleic acid.

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

(a) planting a collection of seed comprising seed of a hybrid, one of whose parent is the plant of claim 2, or a canola plant having all the physiological and morphological characteristics of the canola plant of claim 2, said collection also comprising seed of said inbred line;

(b) growing canola plants from said collection of seeds;

(c) identifying an inbred plant from said inbred line;

(d) selecting said inbred plant; and

(e) controlling pollination in a manner which preserves the homozygosity of said inbred plant.

5. The method according to claim 4, wherein said one parent 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. A method of detecting the presence of event NS-B50027-4 of claim 1 in a sample comprising plant DNA, comprising the steps of:

contacting said sample with:

(a) a first primer that binds to a flanking junction region of *Brassica* genome of NS-B50027-4, and

(b) a second primer that binds to a transgene of NS-B50027-4;

subjecting said sample to polymerase chain reaction; and

characterizing the amplicons generated between said primers.

10. The method of claim 9, wherein said primers are the primers shown in SEQ. ID. NO:1 to SEQ ID NO:90.

11. A segregant obtained from the seed of claim 1, wherein said segregant comprises either said first transgenic locus or said second transgenic locus.

12. 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 segregating the genome of the seed of claim 1 to obtain a segregant 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.

13. The method of claim 12, wherein the *Brassica* is *B. juncea* or *B. napus*.

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

15. 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.

16. A method of detecting the presence of at least one transgenic locus of claim 1 in a sample comprising plant DNA, wherein said method comprises

contacting said sample with:

at least one first primer that binds to a first transgene-flanking junction region of said first transgenic locus, said at least one first primer selected from the group of primers consisting of SEQ ID NO:17 – SEQ ID NO:31 and SEQ ID NO:83 – SEQ ID NO:86; or

at least one second primer that binds to a second transgene-flanking junction region of said first transgenic locus, said at least one second primer selected from the group of primers consisting of SEQ ID NO:32 – SEQ ID NO:41; or

at least one third primer that binds to a first transgene-flanking junction region of said second transgenic locus, said at least one third primer selected from the group of primers consisting of SEQ ID NO:42 – SEQ ID NO:62; or

at least one fourth primer that binds to a second transgene-flanking junction region of said second transgenic locus, said at least one fourth primer selected from the group of primers consisting of SEQ ID NO:63 – SEQ ID NO:90; or

at least ten contiguous nucleotides or complements thereof;

subjecting said sample to polymerase chain reaction; and

assaying for amplicons generated between said primers,

wherein said assay is, optionally, a KASP™ genotyping assay.

17. The method of claim 16, further comprising the step of contacting said sample with a third primer that binds to a transgene sequence, said second primer selected from the group of primers consisting of those depicted in SEQ ID NO:1 – SEQ ID NO:8, at least ten contiguous nucleotides thereof, or complements thereof.

18. The method of claim 16, further comprising the step of contacting said sample with a primer that binds to a transgene sequence, said primer selected from the group consisting of those depicted in SEQ ID NO:1 - SEQ ID NO:16, at least ten contiguous nucleotides thereof, or complements thereof.

19. A plant, plant material, or plant-derived material identified by the method of claim 16.

20. A kit comprising components to carry out the method of claim 16.