CLAIMS

1. A method of reducing the content of at least one steroidal alkaloid, a derivative thereof, a metabolite thereof, or a biosynthetic intermediate thereof; of at least on steroidal glycoalkaloid; of at least one steroidal saponin, a derivative thereof, a metabolite thereof, or a biosynthetic intermediate thereof; or of at least one triterpenoid saponin, a derivative thereof, a metabolite thereof, or a biosynthetic intermediate thereof, in at least one cell of a plant or a plant part, the method comprising genetically modifying said at least one plant cell, said genetic modification comprising:

    (a) transforming said at least one plant cell with at least one silencing molecule targeted to a nucleic acid gene sequence encoding a Cellulose Synthase Like G (CSLG) enzyme wherein the nucleic acid sequence encoding said CSLG gene is set forth in any one of SEQ ID NOS: 30, 32, 34, 36, 38, 40, 65, 80, 93, 95, 97, 99, 101, 103, or 105; or a homolog thereof having at least 55% identity to and at least 55% coverage of, the nucleic acid sequence set forth in any one of SEQ ID NOS: 30, 32, 34, 36, 38, 40, 65, 80, 93, 95, 97, 99, 101, 103, or 105; or

    (b) mutagenizing at least one nucleic acid sequence encoding a Cellulose Synthase Like G (CSLG) enzyme, wherein the nucleic acid sequence encoding said CSLG gene is set forth in any one of SEQ ID NOS: 30, 32, 34, 36, 38, 40, 65, 80, 93, 95, 97, 99, 101, 103, or 105; or a homolog thereof having at least 55% identity to and at least 55% coverage of, the nucleic acid sequence set forth in any one of SEQ ID NOS: 30, 32, 34, 36, 38, 40, 65, 80, 93, 95, 97, 99, 101, 103, or 105, and wherein the mutagenesis comprises introducing (1) one or more point mutations into the nucleic acid sequence, (2) deletions within the nucleic acid sequence, or (3) insertions within the nucleic acid, or (4) any combination thereof, wherein said introducing comprising mutagenizing coding or non-coding sequence;

wherein expression of the gene encoding the CSLG enzyme is reduced in the genetically

modified plant cell compared to its expression in a corresponding unmodified plant cell, wherein the plant comprising said genetically modified cell comprises reduced content of at least one steroidal alkaloid; of at least one steroidal glycoalkaloid; of at least one steroidal saponin; or of at least one triterpenoid saponin, compared to the corresponding unmodified plant.

2. The method of claim 1, wherein:

(a) when the nucleic acid of the CSLG is set forth in SEQ ID NO: 30, the silencing molecule is set forth in SEQ ID NO: 42 or a complementary sequence thereof, or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in SEQ ID NO: 42 or a complementary sequence thereof;

(b) when the nucleic acid of the CSLG is set forth in SEQ ID NO: 34, the silencing molecule is set forth in SEQ ID NO: 43 or a complementary sequence thereof, or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in SEQ ID NO: 43 or a complementary sequence thereof;

(c) when the nucleic acid of the CSLG is set forth in SEQ ID NO: 38, the silencing molecule is set forth in SEQ ID NO: 44 or a complementary sequence thereof, or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in SEQ ID NO: 44 or a complementary sequence thereof;

(d) when the nucleic acid of the CSLG is set forth in SEQ ID NO: 65 or SEQ ID NO: 93, the silencing molecule is set forth in SEQ ID NO: 106 or a complementary sequence thereof, or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in SEQ ID NO: 65 or the nucleic acid sequence set forth in SEQ ID NO: 93; or

(e) when the nucleic acid of the CSLG is set forth in SEQ ID NO: 95, the silencing molecule is set forth in SEQ ID NO: 107 or a complementary sequence thereof, or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in SEQ

ID NO: 95.

3. The method of any one of claims 1-2, wherein

(a) said steroidal alkaloid, said steroidal saponin, or said triterpenoid saponin comprises a toxin or a bitter tasting compound or having hormone mimicking properties, or a combination thereof; or

(b) said steroidal glycoalkaloid comprises an esculeoside, a dehydroesculeoside, alpha-tomatine, tomatine, alpha-chaconine, alpha-solanine, alpha-solasonine, alpha-solmargine, or any combination thereof; or

(c) said steroidal saponin comprises uttroside B, a tomatoside, or any combination thereof; or

(d) said triterpenoid saponin comprises medicagenic acid 3-O-glucuronide (MA-3-GlcA) (Compound 6), 3-O-β-D-glucuronopyranosyl-28-O-β-D-fucopyranosyl-medicagenic acid (compound 7), 3-O-[β-D-glucuronopyranosyl]-28-O-[α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 8), 3-O-[β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 9), 3-O-[β-D-xylopyranosyl-(1–>3)-β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 10), 3-O-[β-D-xylopyranosyl-(1–>3)-β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-4-acetyl-β-D-fucopyranosyl]-medicagenic acid (compound 11), glycyrrhizin (Compound 14), Glycyrrhetinic acid 3-O-monoglucuronide (compound 15), bayogenin (Compound 25), bayogenin-hexA-hex-hex (Compound 31), serjanic acid (Compound 26), serjanic acid-hexA-hex (Compound 32), soyasapogenol A (Compound 29), soyasapogenol B (Compound 30), soyasapogenol A–hexA-hex-pent (Compound 34), soyasaponin VI (Compound 35), betavulgaroside IV (Compound 33), hederagenin-3GlcA, gypsogenin-3GlcA, gypsogenic

acid-3GlcA, or a QS-21 adjuvant, or any combination thereof; or

(e) a combination thereof.

4. The method according to any one of claims 1-3, said method further comprising reducing the content of at least one triterpenoid saponin biosynthetic intermediate, wherein said triterpenoid saponin biosynthetic intermediate comprises (S)-2,3-Oxidosqualene, β-Amyrin, Medicagenic acid (MA), Oleanolic acid (OA), oleanolic acid-3GlcA, Augustic acid (AA), augustic acid-3GlcA, or glycyrrhetinic acid, or any combination thereof.

5. The method according to any one of claims 1-4, further comprising altering the content of a phytosterol; a cholesterol; a phytocholesterol; a cholestenol; or a phytocholestenol.

6. A genetically modified cell having increased expression of at least one heterologous gene compared to a corresponding unmodified cell, said at least one heterologous gene encoding a cellulose synthase like G (CSLG) enzyme wherein the amino acid sequence of said encoded CSLG enzyme is set forth in any one of SEQ ID NOS: 31, 33, 35, 37, 39, 41, 66, 81, 94, 96, 98, 100, 102, or 104; or a homolog thereof having at least 55% identity to and at least 55% coverage of, the amino acid sequence set forth in any one of SEQ ID NOS: 31, 33, 35, 37, 39, 41, 66, 81, 94, 96, 98, 100, 102, or 104, wherein said genetically modified cell comprises an increased content of at least one steroidal alkaloid; of at least one steroidal glycoalkaloid; of at least one steroidal saponin; or of at least one triterpenoid saponin, compared to a corresponding unmodified cell.

7. The genetically modified cell according to claim 6, wherein said genetically modified cell comprising an increased content of at least one steroidal alkaloid; of at least one steroidal glycoalkaloid; of at least one steroidal saponin; or of at least one triterpenoid saponin, further expresses at least one additional heterologous gene encoding an enzyme, said enzyme selected from the group consisting of a saponin beta-amyrin synthase, a cytochrome P450, a glycosyltransferase, an acyltransferase, and an UDP-glucose 6-dehydrogenase 1, or any combination thereof.

8. The genetically modified cell according to any one of claims 6-7, wherein the nucleic acid sequence encoding said at least one heterologous CSLG gene is set forth in any one of SEQ ID NOS: 30, 32, 34, 36, 38, 40, 65, 80, 93, 95, 97, 99, 101, 103, or 105; or a homolog thereof having at least 55% identity to and at least 55% coverage of, the nucleic acid sequence set forth in any one of SEQ ID NOS: 30, 32, 34, 36, 38, 40, 65, 80, 93, 95, 97, 99, 101, 103, or 105.

9. The genetically modified cell according to any one of claims 7-8, wherein the nucleic acid sequence encoding said at least one additional heterologous gene encodes

   (a) a β-amyrin synthase, said nucleic acid sequence set forth in SEQ ID NO: 45; or a homolog thereof having at least 80% identity to and at least 80% coverage of the nucleic acid sequence set forth in SEQ ID NO: 45; or

   (b) a cytochrome P450, said nucleic acid sequence set forth in any one of SEQ ID NO: 46, 51, or 53; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in any one of SEQ ID NO: 46, 51, or 53; or

   (c) a glycosyl transferase, said nucleic acid sequence set forth in any one of SEQ ID NO: 55, 57, 59, or 61; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in any one of SEQ ID NO: 55, 57, 59, or 61; or

   (d) an acetyltransferase, said nucleic acid sequence set forth in SEQ ID NO: 63; or a homolog thereof having at least 80% identity to and at least 80% coverage of the nucleic acid sequence set forth in SEQ ID NO: 63; or

   (e) a UDP-glucose 6-dehydrogenase 1, said nucleic acid sequence set forth in SEQ ID NO: 74; or a homolog thereof having at least 80% identity to and at least 80% coverage of the nucleic acid sequence set forth in SEQ ID NO: 74; or

   (f) any combination thereof of (a), (b), (c), (d), and (e).

10. The genetically modified cell according to any one of claims 7-9, wherein the amino acid sequence of said encoded at least one additional heterologous gene encodes

(a) a β-amyrin synthase, said amino acid sequence set forth in SEQ ID NO: 48; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the amino acid sequence set forth in SEQ ID NO: 48; or

(b) a cytochrome P450, said amino acid sequence set forth in any one of SEQ ID NO: 49, 52, or 54; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the amino acid sequence set forth in any one of SEQ ID NO: 49, 52, or 54; or

(c) a glycosyl transferase, said amino acid sequence set forth in any one of SEQ ID NO: 56, 58, 60, or 62; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the amino acid sequence set forth in any one of SEQ ID NO: 56, 58, 60, or 62; or

(d) an acetyltransferase, said amino acid sequence set forth in SEQ ID NO: 64; or a homolog thereof having at least 80% identity to and at least 80% coverage of the amino acid sequence set forth in SEQ ID NO: 64; or

(e) a UDP-glucose 6-dehydrogenase 1, said amino acid sequence set forth in SEQ ID NO: 75; or a homolog thereof having at least 80% identity to and at least 80% coverage of the amino acid sequence set forth in SEQ ID NO: 75; or

(f) any combination thereof of (a), (b), (c), (d), and (e).

11. The genetically modified cell according to any one of claims 6-10, wherein said triterpenoid saponin comprises a sweetener, foaming agent, emulsifier, preservative, anti-carcinogen, hypocholesterolemic agent, anti-inflammatory agent, anti-oxidant, biological adjuvant, anti-microbial agent, insecticidal agent, antifeedant, anti-fungal agent, or any combination thereof.

12. The genetically modified cell according to any one of claims 6-11,

(a) wherein said steroidal glycoalkaloid comprises an esculeoside, a dehydroesculeoside, alpha-tomatine, tomatine, dehydrotomatine, alpha-chaconine, alpha-solanine, alpha-solasonine, alpha-solmargine, or any combination thereof; or

(b) wherein said steroidal saponin comprises uttroside B, a tomatoside, or any combination thereof; or

(c) wherein said triterpenoid saponin comprises medicagenic acid 3-O-glucuronide (MA-3-GlcA) (Compound 6), 3-O-β-D-glucuronopyranosyl-28-O-β-D-fucopyranosyl-medicagenic acid (compound 7), 3-O-[β-D-glucuronopyranosyl]-28-O-[α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 8), 3-O-[β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 9), 3-O-[β-D-xylopyranosyl-(1–>3)-β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 10), 3-O-[β-D-xylopyranosyl-(1–>3)-β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-4-acetyl-β-D-fucopyranosyl]-medicagenic acid (compound 11), glycyrrhizin (Compound 14), glycyrrhetinic acid 3-O-monoglucuronide (Compound 15), bayogenin (Compound 25), bayogenin-hexA-hex-hex (Compound 31), serjanic acid (Compound 26), serjanic acid-hexA-hex (Compound 32), soyasapogenol A (Compound 29), soyasapogenol B (Compound 30), soyasapogenol A–hexA-hex-pent (Compound 34), soyasaponin VI (Compound 35), betavulgaroside IV (Compound 33), hederagenin-3GlcA, gypsogenin-3GlcA, gypsogenic acid-3GlcA, or a QS-21 adjuvant, or any combination thereof; or

(d) a combination thereof.

13. The genetically modified cell according to any one of claims 6-12, further comprising an increased content of at least one triterpenoid saponin biosynthetic intermediate, wherein said triterpenoid saponin biosynthetic intermediate comprises (S)-2,3-Oxidosqualene, β-Amyrin, Medicagenic acid (MA), Oleanolic acid (OA), oleanolic acid-3GlcA, Augustic acid (AA), augustic acid-3GlcA, or glycyrrhetinic acid, or any combination thereof.

14. The genetically modified cell according to any one of claims 6-13, having an altered content of a phytosterol; a cholesterol; a phytocholesterol; a cholestenol;

or a phytocholestenol.

15. The genetically modified cell according to any one of claims 6-14, wherein said cell comprises a plant cell, a yeast cell, or an alga cell.

16. The genetically modified cell according to claim 15, wherein said plant cell comprises a cell from a plant in the *Poales* order, the *Caryophyllales* order, the *Solanales* order, the *Fabales* order, the *Malvales* order, the *Apiales* order, the *Brassicales* order, the *Asparagales* order, the *Dioscoreales* order, or the *Liliales* order.

17. The genetically modified cell according to claim 16, wherein:
    (a) when said plant cell comprises a cell from a plant in the *Poales* order, said plant is selected from the group of genera consisting of the *Oryza* genus, the *Hordeum* genus, the *Avena* genus, and the *Triticum* genus;
    (b) when said plant cell comprises a cell from a plant in the *Caryophyllales* order, said plant is selected from the group of genera consisting of the *Spinacia* genus, the *Chenopodium* genus, the *Beta* genus, the *Rheum* genus, the *Vaccaria* genus, the *Saponaria* genus, and the *Gypsophila* genus;
    (c) when said plant cell comprises a cell from a plant in the *Solanales* order, said plant is selected from the group of genera consisting of the *Solanum* genus, the *Capsicum* genus, the *Nicotiana* genus, the *Hyoscyamus* genus, the *Datura* genus, and the *Atropa* genus;
    (d) when said plant cell comprises a cell from a plant in the *Fabales* order, said plant is selected from the group of genera consisting of the *Glycyrrhiza* genus, the *Medicago* genus, the *Glycine* genus, the *Lotus* genus, the *Cicer* genus, the *Phaseolus* genus, the *Pisum* genus, the *Arachis* genus, the *Lupinus* genus, and the *Acacia* genus;
    (e) when said plant cell comprises a cell from a plant in the *Malvales* order, said plant is selected from the *Theobroma* genus;
    (f) when said plant cell comprises a cell from a plant in the *Apiales* order, said plant is selected from the group of genera consisting of the *Daucus*

genus, the *Apium* genus, the *Petroselinum* genus, the *Panax* genus, the *Bupleurum* genus, the *Hedera* genus, and the *Centella* genus; or

(g) when said plant cell comprises a cell from a plant in the *Brassicales* order, said plant is selected from the group of genera consisting of the *Arabidopsis* genus, the *Brassica* genus, the *Capparis* genus, and the *Carica* genus.

18. The genetically modified cell according to claim 17, wherein:

(a) when said plant cell comprises a cell from a plant in the *Caryophyllales* order, said plant is selected from the group consisting of spinach, beetroot, and quinoa;

(b) when said plant cell comprises a cell from a plant in the *Solanales* order, said plant is selected from the group consisting of tomato, wild tomato, potato, wild potato, eggplant, pepper, bell pepper, cayenne pepper, chili pepper, pimiento, tabasco pepper, ground cherry, tobacco, and bittersweet; or

(c) when said plant cell comprises a cell from a plant in the *Fabales* order, said plant is selected from the group consisting of alfalfa, soy, *Lotus japonicus*, and licorice.

19. The genetically modified cell according to claim 18, wherein:

(a) the plant cell is from a tomato plant having:

(i) an increased content of alpha-tomatine; or tomatidine; or dehydrotomatine; or a steroidal saponin; or

(ii) an altered content of a phytosterol; a cholesterol ; a phytocholesterol; a cholestenol; or a phytocholestenol; or

(b) the plant cell is from a potato plant having:

(i) an increased content of alpha-chaconine; or alpha-solanine ; or a steroidal saponin; or

(ii) an altered content of a phytosterol; a cholesterol ; a phytocholesterol; a cholestenol; or a phytocholestenol; or

(c) the plant cell is from an eggplant plant having:

(i) an increased content of alpha-solasonine; or alpha-

solamargine; or a steroidal saponin;

(ii) an altered content of a phytosterol; a cholesterol ; a phytocholesterol; a cholestenol; or a phytocholestenol.

20. The genetically modified cell according to any one of claims 15-19, wherein said plant cell comprises a leaf cell, a petiole cell, a plant stem or stalk cell, a root cell, a bud cell, a tuber cell, a bean cell, a grain or kernel cell, a fruit cell, a nut cell, a legume cell, a seed or seed cell, a callus cell, a bract cell, or a flower cell.

21. The genetically modified cell according to any one of claims 15-19, wherein said plant cell is comprised in a plant or a portion thereof, said portion thereof comprising a plant leaf, a plant petiole, a plant stem or stalk, a plant root, a plant bud, a plant tuber, a plant bean, a plant grain or kernel, a plant fruit, a plant nut, a plant legume, a plant seed, a plant bract, or a plant flower.

22. The genetically modified cell according to claim 15, wherein said yeast is selected from a *Saccharomyces* genus, a *Schizosaccharomyces* genus, a *Pichia* genus, a *Yarrowia* genus, a *Kluyveromyces* genus, or a *Candida* genus.

23. The genetically modified cell according to claim 15, wherein said alga is selected from a microalga, a multi-cellular alga, a cyanobacterium, a diatom, chlorophytes (green algae), rhodophytes (red algae), or phaeo-phytes (brown algae), a *Dunaliella*, a *Chlamydamonas*, or a *hematococus*.

24. A genetically modified plant comprising at least one cell having altered expression of at least a cellulose synthase like G (CSLG) gene compared to the expression of CSLG in a corresponding unmodified plant wherein the amino acid sequence of said CSLG enzyme is set forth in any one of SEQ ID NOS: 31, 33, 35, 37, 39, 41, 66, 81, 94, 96, 98, 100, 102, or 104; or a homolog thereof having at least 55% identity to and at least 55% coverage of, the amino acid sequence set forth in any one of SEQ ID NOS: 31, 33, 35, 37, 39, 41, 66, 81, 94, 96, 98, 100, 102, or 104, and wherein the genetically modified plant has an altered content of at least one steroidal alkaloid; of at least one steroidal glycoalkaloid; of at least one steroidal saponin; or of at least one triterpenoid saponin compared to the corresponding unmodified plant.

25. The genetically modified plant of claim 24, wherein said CSLG gene comprises the endogenous CSLG gene.

26. The genetically modified plant of claim 25, wherein said endogenous CSLG gene comprises a mutation, said mutation comprising at least one or more point mutations, or an insertion, or a deletion, or any combination thereof, and

    (a) wherein said expressed CSLG enzyme has increased stability or increased activity or both and the altered content comprises an increased amount of the at least one steroidal alkaloid; of at least one steroidal glycoalkaloid; of the at least one steroidal saponin; or of the at least one triterpenoid saponin compared to the corresponding unmodified plant; or

    (b) wherein said expressed CSLG enzyme has decreased stability or decreased activity or both and the altered content comprises a decreased amount of the at least one steroidal alkaloid; of at least one steroidal glycoalkaloid; of the at least one steroidal saponin; or of the at least one triterpenoid saponin compared to the corresponding unmodified plant.

27. The genetically modified plant of any one of claims 25-26, wherein:

    (a) said endogenous CSLG gene is selectively silenced, repressed, or has reduced expression and said altered content comprises a reduced amount of the at least one steroidal alkaloid; of at least one steroidal glycoalkaloid; of the at least one steroidal saponin; or of the at least one triterpenoid saponin compared to the corresponding unmodified plant; or

    (b) said endogenous CSLG gene is overexpressed and said altered content comprises an increased amount of the at least one steroidal alkaloid; of at least one steroidal glycoalkaloid; of the at least one steroidal saponin; or of the at least one triterpenoid saponin compared to the corresponding unmodified plant.

28. The genetically modified plant of any one of claims 24-27, further comprising an altered content of at least one biosynthetic intermediate of a triterpenoid saponin, said altered content comprising an increased amount or a decrease amount of (S)-2,3-Oxidosqualene, β-Amyrin, Medicagenic acid (MA), Oleanolic acid (OA),

oleanolic acid-3GlcA, Augustic acid (AA), augustic acid-3GlcA, or glycyrrhetinic acid, or any combination thereof.

29. The genetically modified plant of claim 25, wherein when said endogenous CSLG gene is selectively silenced, repressed, or has reduced expression, said cell further comprises at least one silencing molecule targeted to the polynucleotide encoding said CSLG gene, wherein the silencing molecule is selected from an RNA interference molecule or an antisense molecule, or wherein the silencing molecule is a component of a viral induced gene silencing system.

30. The genetically modified plant of claim 24, wherein said CSLG gene comprises a heterologous CSLG gene, and said altered expression comprises a *de novo* expression of said gene.

31. The genetically modified plant according to claim 30, wherein said expression comprises increased expression compared to a corresponding unmodified cell, and said altered content comprising increased content of at least one steroidal alkaloid; of at least one steroidal glycoalkaloid; of at least one steroidal saponin; or of at least one triterpenoid saponin, compared to the corresponding unmodified plant.

32. The genetically modified plant of claim 31, further comprising an altered content of at least one biosynthetic intermediate of a triterpenoid saponin, said altered content comprising an increased amount or a decrease amount of (S)-2,3-Oxidosqualene, β-Amyrin, Medicagenic acid (MA), Oleanolic acid (OA), oleanolic acid-3GlcA, Augustic acid (AA), augustic acid-3GlcA, or glycyrrhetinic acid, or any combination thereof.

33. The genetically modified plant according to any one of claims 24-32, wherein the nucleic acid sequence encoding said CSLG gene is set forth in any one of SEQ ID NOS: 30, 32, 34, 36, 38, 40 , 65, 80, 93, 95, 97, 99, 101, 103, or 105; or a homolog thereof having at least 55% identity to and at least 55% coverage of, the nucleic acid sequence set forth in any one of SEQ ID NOS: 30, 32, 34, 36, 38, 40, 65, 80, 93, 95, 97, 99, 101, 103, or 105.

34. The genetically modified plant according to any one of claims 24-33, wherein the altered expression of the at least one cellulose synthase like G (CSLG) gene is

altered by introducing (1) one or more point mutations into the nucleic acid sequence, (2) deletions within the nucleic acid sequence, or (3) insertions within the nucleic acid, any combination thereof, or (4) any combination thereof, wherein said introducing comprising mutagenizing coding or non-coding sequence.

35. The genetically modified plant according to claim 34, wherein the altered expression of the at least one CSLG gene is altered by introducing a silencing molecule targeted to the at least one CSLG gene and wherein:

(a) when the nucleic acid of the CSLG is set forth in SEQ ID NO: 30, the silencing molecule is set forth in SEQ ID NO: 42 or a complementary sequence thereof, or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in SEQ ID NO: 42 or a complementary sequence thereof;

(b) when the nucleic acid of the CSLG is set forth in SEQ ID NO: 34, the silencing molecule is set forth in SEQ ID NO: 43 or a complementary sequence thereof, or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in SEQ ID NO: 43 or a complementary sequence thereof;

(c) when the nucleic acid of the CSLG is set forth in SEQ ID NO: 38, the silencing molecule is set forth in SEQ ID NO: 44 or a complementary sequence thereof, or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in SEQ ID NO: 44 or a complementary sequence thereof;

(d) when the nucleic acid of the CSLG is set forth in SEQ ID NO: 65 or SEQ ID NO: 93, the silencing molecule is set forth in SEQ ID NO: 106 or a complementary sequence thereof, or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in SEQ ID NO: 65 or the nucleic acid sequence set forth in SEQ ID NO: 93; or

(e) when the nucleic acid of the CSLG is set forth in SEQ ID NO: 95, the silencing molecule is set forth in SEQ ID NO: 107 or a complementary sequence thereof, or a homolog thereof having at least 80% identity to

and at least 80% coverage of, the nucleic acid sequence set forth in SEQ ID NO: 95.

36. The genetically modified plant according to any one of claims 24-35, wherein said triterpenoid saponin comprises a sweetener, foaming agent, emulsifier, preservative, anti-carcinogen, hypocholesterolemic agent, anti-inflammatory agent, anti-oxidant, biological adjuvant, anti-microbial agent, insecticidal agent, antifeedant, anti-fungal agent, or any combination thereof.

37. The genetically modified plant according to any one of claims 24-35,

(a) wherein said steroidal glycoalkaloid comprises an esculeoside, a dehydroesculeoside, alpha-tomatine, tomatine, alpha-chaconine, alpha-solanine, alpha-solasonine, alpha-solmargine, or any combination thereof; or

(b) wherein said steroidal saponin comprises uttroside B, a tomatoside, or any combination thereof; or

(c) wherein said triterpenoid sapoinin comprises medicagenic acid 3-O-glucuronide (MA-3-GlcA) (Compound 6), 3-O-β-D-glucuronopyranosyl-28-O-β-D-fucopyranosyl-medicagenic acid (compound 7), 3-O-[β-D-glucuronopyranosyl]-28-O-[α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 8), 3-O-[β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 9), 3-O-[β-D-xylopyranosyl-(1–>3)-β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 10), 3-O-[β-D-xylopyranosyl-(1–>3)-β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-4-acetyl-β-D-fucopyranosyl]-medicagenic acid (compound 11), glycyrrhizin (Compound 14), Glycyrrhetinic acid 3-O-monoglucuronide (compound 15), bayogenin (Compound 25), bayogenin-hexA-hex-hex (Compound 31), serjanic acid (Compound 26), serjanic acid-hexA-hex (Compound

32), soyasapogenol A (Compound 29), soyasapogenol B (Compound 30), soyasapogenol A–hexA-hex-pent (Compound 34), soyasaponin VI (Compound 35), betavulgaroside IV (Compound 33), hederagenin-3GlcA, gypsogenin-3GlcA, gypsogenic acid-3GlcA, or a QS-21 adjuvant, or any combination thereof; or

(d) a combination thereof.

38. The genetically modified plant according to claim 24, having an altered content of a phytosterol; a cholesterol; a phytocholesterol; a cholestenol; or a phytocholestenol.

39. The genetically modified plant according to any one of claims 24-38, wherein said plant is selected from the *Poales* order, the *Caryophyllales* order, the *Solanales* order, the *Fabales* order, the *Malvales* order, the *Apiales* order, the *Brassicales* order, the *Asparagales* order, the *Dioscoreales* order, or the *Liliales* order.

40. The genetically modified plant according to claim 39, wherein:

(a) when said plant comprises a plant in the *Poales* order, said plant is selected from the group of genera consisting of the *Oryza* genus, the *Hordeum* genus, the *Avena* genus, and the *Triticum* genus;

(b) when said plant comprises a plant in the *Caryophyllales* order, said plant is selected from the group of genera consisting of the *Spinacia* genus, the *Chenopodium* genus, the *Beta* genus, the *Rheum* genus, the *Vaccaria* genus, the *Saponaria* genus, and the *Gypsophila* genus;

(c) when said plant comprises a plant in the *Solanales* order, said plant is selected from the group of genera consisting of the *Solanum* genus, the *Capsicum* genus, the *Nicotiana* genus, the *Hyoscyamus* genus, the *Datura* genus, and the *Atropa* genus;

(d) when said plant comprises a plant in the *Fabales* order, said plant is selected from the group of genera consisting of the *Glycyrrhiza* genus, the *Medicago* genus, the *Glycine* genus, the *Lotus* genus, the *Cicer* genus, the *Phaseolus* genus, the *Pisum* genus, the *Arachis* genus, the *Lupinus* genus, and the *Acacia* genus;

(e) when said plant comprises a plant in the *Malvales* order, said plant is selected from the *Theobroma* genus;

(f) when said plant comprises a plant in the *Apiales* order, said plant is selected from the group of genera consisting of the *Daucus* genus, the *Apium* genus, the *Petroselinum* genus, the *Panax* genus, the *Bupleurum* genus, the *Hedera* genus, and the *Centella* genus; or

(g) when said plant comprises a plant in the *Brassicales* order, said plant is selected from the group of genera consisting of the *Arabidopsis* genus, the *Brassica* genus, the *Capparis* genus, and the *Carica* genus.

41. The genetically modified plant according to claim 40, wherein:

(a) when said plant comprises a plant in the *Caryophyllales* order, said plant is selected from the group consisting of spinach, beetroot, and quinoa;

(b) when said plant comprises a plant in the *Solanales* order, said plant is selected from the group consisting of tomato, wild tomato, potato, wild potato, eggplant, pepper, bell pepper, cayenne pepper, chili pepper, pimiento, tabasco pepper, ground cherry, tobacco, and bittersweet; or

(c) when said plant comprises a plant in the *Fabales* order, said plant is selected from the group consisting of alfalfa, soy, *Lotus japonicus*, and licorice.

42. The genetically modified plant according to claim 41, wherein:

(a) the plant is a tomato plant having:

(i) an increased content of alpha-tomatine; or tomatidine; or dehydrotomatine; or a steroidal saponin; or

(ii) an altered content of a phytosterol; a cholesterol; a phytocholesterol; a cholestenol; or a phytocholestenol; or

(b) the plant is a potato plant having:

(i) an increased content of alpha-chaconine; or alpha-solanine; or a steroidal saponin; or

(ii) an altered content of a phytosterol; a cholesterol; a phytocholesterol; a cholestenol; or a phytocholestenol; or

(c) the plant is an eggplant plant having:

(i) an increased content of alpha-solasonine; or alpha-solamargine; or a steroidal saponin

(ii) an altered content of a phytosterol; a cholesterol; a phytocholesterol a cholestenol; or a phytocholestenol .

43. The genetically modified plant according to any one of claims 24-42, wherein said plant cell comprises a leaf cell, a petiole cell, a plant stem or stalk cell, a root cell, a bud cell, a tuber cell, a bean cell, a grain or kernel cell, a fruit cell, a nut cell, a legume cell, a seed or seed cell, a callus cells, a bract cell, a callus cell, and a flower cell.

44. A method of producing a steroidal alkaloid, a steroidal glycoalkaloid, a steroidal saponin, or a triterpenoid saponin in a genetically modified cell, the method comprising:

(a) introducing an at least one heterologous gene into said cell, said at least one heterologous gene encoding a cellulose synthase like G (CSLG) enzyme wherein the amino acid sequence of said encoded CSLG enzyme is set forth in any one of SEQ ID NOS: 31, 33, 35, 37, 39, 41, 66, 81, 94, 96, 98, 100, 102, or 104; or a homolog thereof having at least 55% identity to and at least 55% coverage of, the amino acid sequence set forth in any one of SEQ ID NOS: 31, 33, 35, 37, 39, 41, 66, 81, 94, 96, 98, 100, 102, or 104, wherein said heterologous gene is optionally comprised in a vector; and

(b) expressing said at least one heterologous gene in said cell;

wherein said cell comprises an increased content of at least one steroidal alkaloid, at least one steroidal glycoalkaloid; at least one steroidal saponin, or at least one triterpenoid saponin compared to a corresponding unmodified cell.

45. The method of producing a steroidal alkaloid, a steroidal glycoalkaloid, a steroidal saponin, or a triterpenoid saponin of claim 44, said introducing further comprising introducing an at least one additional heterologous gene into said cell, said heterologous gene selected from the group consisting of the group encoding a saponin beta-amyrin synthase, a cytochrome P450, a glycosyltransferase, an

acyltransferase, and a UDP-glucose 6-dehydrogenase I, or any combination thereof, wherein said at least one additional heterologous gene is optionally comprised in a vector; and further comprising expressing said at least one additional heterologous gene in said cell.

46. The method of producing a steroidal alkaloid, a steroidal glycoalkaloid, a steroidal saponin, or a triterpenoid saponin of claim 45, wherein

    (a) said at least one heterologous gene is operably linked to a promoter, a transcription termination sequence, or a combination thereof; or

    (b) said at least one additional heterologous gene is operably linked to a promoter, a transcription termination sequence, or a combination thereof; or

    (c) a combination thereof of (a) and (b).

47. The method of producing a steroidal alkaloid, a steroidal glycoalkaloid, a steroidal saponin, or a triterpenoid saponin according to any one of claims 44-46, wherein said introducing comprises transforming said at least one cell with

    (a) said at least one heterologous gene or a polynucleotide sequence encoding said at least one heterologous gene, or the vector comprising said at least one heterologous gene; or

    (b) said at least one additional heterologous gene or a polynucleotide sequences encoding said at least one additional heterologous gene, or the vector comprising said at least one additional heterologous gene; or

    (c) a combination thereof of (a) and (b);

wherein said expressing comprises transient expression or constitutive expression.

48. The method of producing a steroidal alkaloid, a steroidal glycoalkaloid, a steroidal saponin, or a triterpenoid saponin according to any one of claims 45-47, wherein the nucleic acid sequence encoding said at least one heterologous CSLG gene is set forth in any one of SEQ ID NOS: 30, 32, 34, 36, 38, 40 , 65, 80, 93, 95, 97, 99, 101, 103, or 105; or a homolog thereof having at least 55% identity to and at least 55% coverage of, the nucleic acid sequence set forth in any one of SEQ ID NOS: 30, 32, 34, 36, 38, 40, 65, 80, 93, 95, 97, 99, 101, 103, or 105.

49. The method of producing a steroidal alkaloid, a steroidal glycoalkaloid, a steroidal saponin, or a triterpenoid saponin according to any one of claims 45-48, wherein the nucleic acid sequence encoding said at least one additional heterologous gene encodes

(a) a β-amyrin synthase, said nucleic acid sequence set forth in SEQ ID NO: 45; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in SEQ ID NO: 45; or

(b) a cytochrome P450, said nucleic acid sequence set forth in any one of SEQ ID NO: 46, 51, or 53; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in any one of SEQ ID NO: 46, 51, or 53; or

(c) a glycosyl transferase, said nucleic acid sequence set forth in any one of SEQ ID NO: 55, 57, 59, or 61; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in any one of SEQ ID NO: 55, 57, 59, or 61; or

(d) an acyltransferase, said nucleic acid sequence set forth in SEQ ID NO: 63; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in SEQ ID NO: 63; or

(e) a UDP-glucose 6-dehydrogenase 1, said nucleic acid sequence set forth in SEQ ID NO: 74; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the nucleic acid sequence set forth in SEQ ID NO: 74; or

(f) any combination thereof of (a), (b), (c), (d), and (e).

50. The method of producing a steroidal alkaloid, a steroidal glycoalkaloid, a steroidal saponin, or a triterpenoid saponin according to any one of claims 45-49, wherein the amino acid sequence of said encoded at least one additional heterologous gene encodes

(a) a β-amyrin synthase, said amino acid sequence set forth in SEQ ID NO: 48; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the amino acid sequence set forth in SEQ ID NO: 48; or

(b) a cytochrome P450, said amino acid sequence set forth in any one of SEQ

ID NO: 49, 52, or 54; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the amino acid sequence set forth in any one of SEQ ID NO: 49, 52, or 54; or

(c) a glycosyl transferase, said amino acid sequence set forth in any one of SEQ ID NO: 56, 58, 60, or 62; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the amino acid sequence set forth in any one of SEQ ID NO: 56, 58, 60, or 62; or

(d) an acyltransferase, said amino acid sequence set forth in SEQ ID NO: 64; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the amino acid sequence set forth in SEQ ID NO: 64; or

(e) a UDP-glucose 6-dehydrogenase 1, said amino acid sequence set forth in SEQ ID NO: 75; or a homolog thereof having at least 80% identity to and at least 80% coverage of, the amino acid sequence set forth in SEQ ID NO: 75; or

(f) any combination thereof of (a), (b), (c), (d), and (e).

51. The method of producing a steroidal alkaloid, a steroidal glycoalkaloid, a steroidal saponin, or a triterpenoid saponin according to any one of claims 44-50, wherein

(a) said triterpenoid saponin comprises a sweetener, foaming agent, emulsifier, preservative, anti-carcinogen, hypocholesterolemic agent, anti-inflammatory agent, anti-oxidant, biological adjuvant, anti-microbial agent, insecticidal agent, antifeedant, anti-fungal agent, or any combination thereof; or

(b) said steroidal glycoalkaloid comprises an esculeoside, a dehydroesculeoside, alpha-tomatine, tomatine, alpha-chaconine, alpha-solanine, alpha-solasonine, alpha-solmargine, or any combination thereof; or

(c) said steroidal saponin comprises uttroside B, a tomatoside, or any combination thereof; or

(d) said triterpenoid saponin comprises medicagenic acid 3-O-glucuronide (MA-3-GlcA) (Compound 6), 3-O-β-D-glucuronopyranosyl-28-O-β-D-fucopyranosyl-medicagenic acid (compound 7), 3-O-[β-D-

glucuronopyranosyl]-28-O-[α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 8), 3-O-[β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 9), 3-O-[β-D-xylopyranosyl-(1–>3)-β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 10), 3-O-[β-D-xylopyranosyl-(1–>3)-β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-4-acetyl-β-D-fucopyranosyl]-medicagenic acid (compound 11), glycyrrhizin (Compound 14), Glycyrrhetinic acid 3-O-monoglucuronide (compound 15), bayogenin (Compound 25), bayogenin-hexA-hex-hex (Compound 31), serjanic acid (Compound 26), serjanic acid-hexA-hex (Compound 32), soyasapogenol A (Compound 29), soyasapogenol B (Compound 30), soyasapogenol A–hexA-hex-pent (Compound 34), soyasaponin VI (Compound 35), betavulgaroside IV (Compound 33), hederagenin-3GlcA, gypsogenin-3GlcA, gypsogenic acid-3GlcA, or a QS-21 adjuvant, or any combination thereof; or

(e) a combination thereof.

52. The method according to any one of claims 44-51, further comprising altering the content of a phytosterol; a cholesterol; a phytocholesterol; a cholestenol; or a phytocholestenol.

53. The method of producing a steroidal alkaloid, a steroidal glycoalkaloid, a steroidal saponin, or a triterpenoid saponin according to any one of claims 44-52, wherein said cell comprises a plant cell, a yeast cell, or an alga cell.

54. The method of producing a steroidal alkaloid, a steroidal glycoalkaloid, a steroidal saponin, or a triterpenoid saponin according to claim 53, wherein

(a) said plant cell comprises a cell from a plant in the *Poales* order, the *Caryophyllales* order, the *Solanales* order, the *Fabales* order, the *Malvales* order, the *Apiales* order, the *Brassicales* order, the *Asparagales*

order, the *Dioscoreales* order, or the *Liliales* order; or

(b) said yeast is selected from a *Saccharomyces* genus, a *Schizosaccharomyces* genus, a *Pichia* genus, a *Yarrowia* genus, a *Kluyveromyces* genus, or a *Candida* genus; or

(c) said alga is selected from a microalga, a multi-cellular alga, a cyanobacterium, a diatom, chlorophytes (green algae), rhodophytes (red algae), or phaeo-phytes (brown algae), a *Dunaliella*, a *Chlamydamonas*, or a *hematococus.*

55. The method of producing a steroidal alkaloid, a steroidal glycoalkaloid, a steroidal saponin, or a triterpenoid saponin according to claim 54, wherein:

(a) when said plant cell comprises a cell from a plant in the *Poales* order, said plant is selected from the group of genera consisting of the *Oryza* genus, the *Hordeum* genus, the *Avena* genus, and the *Triticum* genus;

(b) when said plant cell comprises a cell from a plant in the *Caryophyllales* order, said plant is selected from the group of genera consisting of the *Spinacia* genus, the *Chenopodium* genus, the *Beta* genus, the *Rheum* genus, the *Vaccaria* genus, the *Saponaria* genus, and the *Gypsophila* genus;

(c) when said plant cell comprises a cell from a plant in the *Solanales* order, said plant is selected from the group of genera consisting of the *Solanum* genus, the *Capsicum* genus, the *Nicotiana* genus, the *Hyoscyamus* genus, the *Datura* genus, and the *Atropa* genus;

(d) when said plant cell comprises a cell from a plant in the *Fabales* order, said plant is selected from the group of genera consisting of the *Glycyrrhiza* genus, the *Medicago* genus, the *Glycine* genus, the *Lotus* genus, the *Cicer* genus, the *Phaseolus* genus, the *Pisum* genus, the *Arachis* genus, the *Lupinus* genus, and the *Acacia* genus;

(e) when said plant cell comprises a cell from a plant in the *Malvales* order, said plant is selected from the *Theobroma* genus;

(f) when said plant cell comprises a cell from a plant in the *Apiales* order, said plant is selected from the group of genera consisting of the *Daucus*

genus, the *Apium* genus, the *Petroselinum* genus, the *Panax* genus, the *Bupleurum* genus, the *Hedera* genus, and the *Centella* genus; or

(g) when said plant cell comprises a cell from a plant in the *Brassicales* order, said plant is selected from the group of genera consisting of the *Arabidopsis* genus, the *Brassica* genus, the *Capparis* genus, and the *Carica* genus.

56. The method according to claim 55, wherein:

(a) when said plant cell comprises a cell from a plant in the *Caryophyllales* order, said plant is selected from the group consisting of spinach, beetroot, and quinoa; or

(b) when said plant cell comprises a cell from a plant in the *Solanales* order, said plant is selected from the group consisting of tomato, wild tomato, potato, wild potato, eggplant, pepper, bell pepper, cayenne pepper, chili pepper, pimiento, tabasco pepper, ground cherry, tobacco, and bittersweet; or

(c) when said plant cell comprises a cell from a plant in the *Fabales* order, said plant is selected from the group consisting of alfalfa, soy, *Lotus japonicus*, and licorice.

57. A method of increasing the content of at least one steroidal alkaloid; of at least one steroidal glycoalkaloid; of at least one steroidal saponin; or of at least one triterpenoid saponin, in at least one cell of a plant or plant part, the method comprising genetically modifying said at least one plant cell, said genetic modification comprising:

(a) mutagenizing at least one nucleic acid sequence encoding a Cellulose Synthase Like G (CSLG) enzyme wherein the amino acid sequence of said CSLG enzyme is set forth in any one of SEQ ID NOS: 31, 33, 35, 37, 39, 41, 66, 81, 94, 96, 98, 100, 102, or 104; or a homolog thereof having at least 55% identity to and at least 55% coverage of, the amino acid sequence set forth in any one of SEQ ID NOS: 31, 33, 35, 37, 39, 41, 66, 81, 94, 96, 98, 100, 102, or 104, wherein the mutagenesis comprises introducing (1) one or more point mutations into the nucleic

acid sequence, (2) deletions within the nucleic acid sequence, or (3) insertions within the nucleic acid, or (4) any combination thereof, wherein said introducing comprising mutagenizing coding or non-coding sequence; and

(b) expressing said nucleic acid encoding said CSLG;

wherein the plant comprising said genetically modified cell comprises increased content of at least one steroidal alkaloid; of at least one steroidal glycoalkaloid; of at least one steroidal saponin; or of at least one triterpenoid saponin, compared to the corresponding unmodified plant.

58. The method of claim 57, wherein the nucleic acid sequence encoding said CSLG gene is set forth in any one of SEQ ID NOS: 30, 32, 34, 36, 38, 40, 65, 80, 93, 95, 97, 99, 101, 103, or 105; or a homolog thereof having at least 55% identity to and at least 55% coverage of, the nucleic acid sequence set forth in any one of SEQ ID NOS: 30, 32, 34, 36, 38, 40, 65, 80, 93, 95, 97, 99, 101, 103, or 105.

59. The method of any one of claims 57-58, wherein

(a) said steroidal alkyloid, said steroidal saponin, or said triterpenoid saponin comprises a sweetener, foaming agent, emulsifier, preservative, anti-carcinogen, hypocholesterolemic agent, anti-inflammatory agent, anti-oxidant, biological adjuvant, anti-microbial agent, insecticidal agent, antifeedant, anti-fungal agent, or any combination thereof; or

(b) said steroidal glycoalkaloid comprises an esculeoside, a dehydroesculeoside, alpha-tomatine, tomatine, alpha-chaconine, alpha-solanine, alpha-solasonine, alpha-solmargine, or any combination thereof; or

(c) wherein said steroidal saponin comprises uttroside B, a tomatoside, or any combination thereof; or

(d) said triterpenoid saponin comprises medicagenic acid 3-O-glucuronide (MA-3-GlcA) (Compound 6), 3-O-β-D-glucuronopyranosyl-28-O-β-D-fucopyranosyl-medicagenic acid (compound 7), 3-O-[β-D-glucuronopyranosyl]-28-O-[α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 8), 3-O-[β-D-

glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 9), 3-O-[β-D-xylopyranosyl-(1–>3)-β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-β-D-fucopyranosyl]-medicagenic acid (compound 10), 3-O-[β-D-xylopyranosyl-(1–>3)-β-D-glucuronopyranosyl]-28-O-[β-D-glucopyranosyl-(1–>4)-α-L-rhamnopyranosyl-(1–>2)-4-acetyl-β-D-fucopyranosyl]-medicagenic acid (compound 11), glycyrrhizin (Compound 14), Glycyrrhetinic acid 3-O-monoglucuronide (compound 15), bayogenin (Compound 25), bayogenin-hexA-hex-hex (Compound 31), serjanic acid (Compound 26), serjanic acid-hexA-hex (Compound 32), soyasapogenol A (Compound 29), soyasapogenol B (Compound 30), soyasapogenol A–hexA-hex-pent (Compound 34), soyasaponin VI (Compound 35), betavulgaroside IV (Compound 33), hederagenin-3GlcA, gypsogenin-3GlcA, gypsogenic acid-3GlcA, or a QS-21 adjuvant, or any combination thereof; or

(e) a combination thereof.

60. The methods of any one of claims 57-59, wherein said plant comprising said genetically modified cell further comprises increased content of at least one biosynthetic intermediate of a triterpenoid saponin, said intermediate comprising (S)-2,3-Oxidosqualene, β-Amyrin, Medicagenic acid (MA), Oleanolic acid (OA), oleanolic acid-3GlcA, Augustic acid (AA), augustic acid-3GlcA, or glycyrrhetinic acid, or any combination thereof.

61. The method of any one of claims 57-60, wherein

(a) expression of the gene encoding the CSLG enzyme is increased in the genetically modified plant cell compared to its expression in a corresponding unmodified plant cell; or

(b) said encoded CSLG enzyme has increased activity in the genetically modified plant cell compared to its activity in a corresponding unmodified plant cell; or

(c) said encoded CSLG enzyme has increased stability in the genetically

modified plant cell compared to its stability in a corresponding unmodified plant cell; or

(d) any combination thereof of (a), (b), and (c).

62. The method according to any one of claims 57-61, further comprising altering the content of a phytosterol; a cholesterol; a phytocholesterol; a cholestenol; or a phytocholestenol.