CLAIMS

1. A plant or part thereof having an altered level of flower sex (FSL) polypeptide activity compared to a corresponding plant or part thereof having a *FSL* locus genotype which confers a male or hermaphrodite flower phenotype, wherein:

(a) an *FSL* locus genotype which confers a hermaphrodite flower phenotype comprises a hermaphrodite allele of the *FSL* locus encoding the FSL polypeptide comprising an amino acid sequence set forth in SEQ ID NO:1, a biologically active fragment thereof, or an amino acid sequence which is at least 40% identical to the sequence set forth in SEQ ID NO:1; and

an *FSL* locus genotype which confers a male flower phenotype comprises a male allele of the *FSL* locus encoding the FSL polypeptide comprising an amino acid sequence set forth in SEQ ID NO:3, a biologically active fragment thereof, or an amino acid sequence which is at least 40% identical to the sequence set forth in SEQ ID NO:3; or

(b) a hermaphrodite allele of the *FSL* locus encodes the FSL polypeptide comprising the amino acid sequence set forth in SEQ ID NO:1, or a biologically active fragment thereof; and

a male allele of the *FSL* locus encodes the FSL polypeptide comprising the amino acid sequence set forth in SEQ ID NO:3, or a biologically active fragment thereof.

~~2. The plant or part thereof of claim 1, wherein:~~

~~an *FSL* locus genotype which confers a hermaphrodite flower phenotype comprises a hermaphrodite allele of the *FSL* locus encoding the FSL polypeptide comprising an amino acid sequence set forth in SEQ ID NO:1, a biologically active fragment thereof, or an amino acid sequence which is at least 40% identical to the sequence set forth in SEQ ID NO:1; and~~

~~an *FSL* locus genotype which confers a male flower phenotype comprises a male allele of the *FSL* locus encoding the FSL polypeptide comprising an amino acid sequence set forth in SEQ ID NO:3, a biologically active fragment thereof, or an amino acid sequence which is at least 40% identical to the sequence set forth in SEQ ID NO:3.~~

~~3. The plant or part thereof of claim 1, wherein:~~

~~a hermaphrodite allele of the *FSL* locus encodes the FSL polypeptide comprising the amino acid sequence set forth in SEQ ID NO:1, or a biologically active fragment thereof; and~~

~~a male allele of the *FSL* locus encodes the FSL polypeptide comprising the amino acid sequence set forth in SEQ ID NO:3, or a biologically active fragment thereof.~~

2~~4~~. The plant or part thereof of ~~any one of claims 1 to 3~~claim 1 or 2, comprising:

(a) an *FSL* locus comprising a polynucleotide sequence encoding the FSL polypeptide, where the polynucleotide sequence is modified relative to a corresponding polynucleotide sequence of a wildtype *FSL* locus allele which confers a male or hermaphrodite flower phenotype when expressed, optionally wherein the polynucleotide sequence encoding the FSL polypeptide comprises one or more nucleotide additions, deletions or substitutions relative to the corresponding polynucleotide sequence of an *FSL* locus allele which confers a male or hermaphrodite flower phenotype when expressed; or

(b) an *FSL* locus comprising a polynucleotide sequence encoding the FSL polypeptide, wherein a region of the polynucleotide sequence encoding a plant AT-rich sequence- and zinc-binding (PLATZ) domain of the *FSL* locus is modified relative to a corresponding polynucleotide sequence of a wildtype *FSL* locus allele which confers a male or hermaphrodite flower phenotype when expressed, optionally wherein the polynucleotide sequence encoding the FSL polypeptide comprises one or more nucleotide additions, deletions or substitutions relative to the corresponding polynucleotide sequence of an *FSL* locus allele which confers a male or hermaphrodite flower phenotype when expressed.

~~5. The plant or part thereof of claim 4, wherein a region of the polynucleotide sequence encoding a plant AT-rich sequence- and zinc-binding (PLATZ) domain of the *FSL* locus is modified.~~

~~6. The plant or part thereof of claim 4 or 5, wherein the polynucleotide sequence encoding the FSL polypeptide comprises one or more nucleotide additions, deletions or substitutions relative to the corresponding polynucleotide sequence of an *FSL* locus allele which confers a male or hermaphrodite flower phenotype when expressed.~~

~~7~~3. The plant or part thereof of claim 1 or 2~~ any one of claims 1 to 6~~, wherein:

(a) FSL polypeptide activity is reduced in the plant or plant part relative to a level of FSL polypeptide activity in a corresponding wildtype plant or part thereof;

(b) the altered activity of the FSL polypeptide causes a male reproductive part of a flower of the plant to be absent or non-functional; and/or

(c) the plant or part thereof comprises a polynucleotide that confers dwarf stature to the plant.

~~8. The plant or part thereof of any one of claims 1 to 7, wherein the altered activity of the FSL polypeptide causes a male reproductive part of a flower of the plant to be absent or non-functional.~~

~~9~~4. A plant or part thereof which produces seedless fruit, said plant comprising:

(i) a polynucleotide that confers dwarf stature to a plant; and

(ii) a flower sex (*FSL*) locus which is homozygous for a female allele (f/f) conferring female flower phenotype.

~~10~~5. The plant or part thereof of claim ~~9~~4, wherein the *FSL* locus has an ORF which comprise a sequence set forth in SEQ ID NO: 5 or a sequence which is at least 70% thereto provided that the nucleotide corresponding to position 621 of the sequence set forth in SEQ ID NO: 5 is a A.

~~11. The plant or part thereof of any one of claims 1 to 8, comprising a polynucleotide that confers dwarf stature to the plant.~~

~~12~~6. The plant or part thereof of any one of claims ~~9~~ 4 to ~~11~~6, wherein:

(a) the polynucleotide that confers dwarf stature is altered relative to the corresponding wildtype polynucleotide sequence; and/or

(b) the polynucleotide that confers dwarf stature is a variant of the gibberellic acid insensitive (*GAI1*) gene or a fragment thereof.

~~13. The plant or part thereof of any one of claims 9 to 12, wherein the polynucleotide that confers dwarf stature is a variant of the gibberellic acid insensitive (*GAI1*) gene or a fragment thereof.~~

~~14~~7. The plant or part thereof of claim 6~~13~~, wherein:

(a) the variant of the *GAI1* gene or fragment thereof that confers dwarf stature to the plant comprises one or more mutations in the region encoding a DELLA domain;

(b) the variant of the *GAI1* gene or fragment thereof is present in a homozygous (GAI1/GAI1) or heterozygous (GAI1/Gai1) state;

(c) (i) the *GAI1* gene encodes a GAI1 protein comprising the amino acid sequence set forth in SEQ ID NO: 8 or an amino acid sequence which is at least 90% identical to the sequence set forth in SEQ ID NO:8 which retains the GA signalling function thereof, and wherein the variant of the *GAI1* gene encodes a variant GAI1 protein comprising an amino acid sequence set forth in SEQ ID NO: 9 or an amino acid sequence which is at least 90% identical to the sequence set forth in SEQ ID NO:9 provided that the amino acid sequence of the variant GAI1 protein comprises a Leu to His substitution at position 38 relative to the sequence set forth in SEQ IDNO: 8; or

(ii) the *GAI1* gene encodes a GAI1 protein comprising the amino acid sequence set forth in SEQ ID NO: 8 or an amino acid sequence which is at least 90% identical to the sequence set forth in SEQ ID NO:8 which retains the GA signalling function thereof, and wherein the variant of the *GAI1* gene encodes a variant GAI1 protein in which the DELLA domain is deleted, truncated or altered; and/or

(d) said plant produces parthenocarpic seedless fruit when flowers are unpollinated and fruit containing seeds when flowers are pollinated with viable pollen.

~~15. The plant or part thereof of claim 13 or 14, wherein the variant of the *GAI1* gene or fragment thereof is present in a homozygous (GAI1/GAI1) or heterozygous (GAI1/Gai1) state.~~

~~16. The plant or part thereof of any one of claims 13 to 15, wherein the *GAI1* gene encodes a GAI1 protein comprising the amino acid sequence set forth in SEQ ID NO: 8 or an amino acid sequence which is at least 90% identical to the sequence set forth in SEQ ID NO:8 which retains the GA signalling function thereof, and wherein the variant of the *GAI1* gene encodes a variant GAI1 protein comprising an amino acid sequence set forth in SEQ ID NO: 9 or an amino acid sequence which is at least 90% identical to the sequence set forth in SEQ ID NO:9 provided that the amino acid sequence of the variant GAI1 protein comprises a Leu to His substitution at position 38 relative to the sequence set forth in SEQ IDNO: 8.~~

~~17. The plant or part thereof of any one of claims 13 to 15, wherein the *GAI1* gene encodes a GAI1 protein comprising the amino acid sequence set forth in SEQ ID NO: 8 or an amino acid sequence which is at least 90% identical to the sequence set forth in~~

~~SEQ ID NO:8 which retains the GA signalling function thereof, and wherein the variant of the *GAI1* gene encodes a variant GAI1 protein in which the DELLA domain is deleted, truncated or altered.~~

~~18. The plant or part thereof of any one of claims 9 to 17, wherein said plant produces parthenocarpic seedless fruit when flowers are unpollinated and fruit containing seeds when flowers are pollinated with viable pollen.~~

~~19~~8. The plant or part thereof of any one of claims ~~9 to 18~~4 to 7, comprising a polynucleotide that confers stenospermocarpy.

~~20~~9. The plant or part thereof of claim ~~19~~8, wherein:

(a) the polynucleotide that confers stenospermocarpy is a variant of the *Vitis vinifera* MADS-box protein 5 (VvMADS5) locus;

(b) (i) the *VvMADS5* locus encodes a VvMADS5 protein comprising the amino acid sequence set forth in SEQ ID NO: 10 or an amino acid sequence which is at least 90% identical to the sequence set forth in SEQ ID NO:10 which retains the biological function thereof, and wherein the variant VvMADS5 protein comprises the amino acid sequence set forth in SEQ ID NO: 11 or an amino acid sequence which is at least 90% identical to the sequence set forth in SEQ ID NO:11 provided that the amino acid sequence of the variant VvMADS5 protein comprises an R197L substitution relative to the sequence set forth in SEQ IDNO: 10; or

(ii) the variant *VvMADS5* locus comprises one or more mutations which results in deletion or truncation of the VvMADS5 protein;

(b) the variant *VvMADS5* locus which confers stenospermocarpy is present in a homozygous or heterozygous state; and/or

(c) said plant produces parthenocarpic seedless fruit when flowers are unpollinated and stenospermocarpic fruit when flowers are pollinated with viable pollen.

~~21. The plant or part thereof of claim 20, wherein the *VvMADS5* locus encodes a VvMADS5 protein comprising the amino acid sequence set forth in SEQ ID NO: 10 or an amino acid sequence which is at least 90% identical to the sequence set forth in SEQ ID NO:10 which retains the biological function thereof, and wherein the variant VvMADS5 protein comprises the amino acid sequence set forth in SEQ ID NO: 11 or an amino acid sequence which is at least 90% identical to the sequence set forth in SEQ ID~~

~~NO:11 provided that the amino acid sequence of the variant VvMADS5 protein comprises an R197L substitution relative to the sequence set forth in SEQ IDNO: 10.~~

~~22. The plant or part thereof of claim 20, wherein the variant *VvMADS5* locus comprises one or more mutations which results in deletion or truncation of the VvMADS5 protein.~~

~~23. The plant or part thereof of any one of claims 20 to 22, wherein the variant *VvMADS5* locus which confers stenospermocarpy is present in a homozygous or heterozygous state.~~

~~24. The plant or part thereof of any one of claims 19 to 23, wherein said plant produces parthenocarpic seedless fruit when flowers are unpollinated and stenospermocarpic fruit when flowers are pollinated with viable pollen.~~

~~25~~10. A plant or part thereof which produces seedless fruit, said plant comprising:

(i) a flower sex (*FSL*) locus genotype which is heterozygous for a female *FSL* locus allele and a hermaphrodite *FSL* locus allele (*FSL/fsl*), or homozygous for the hermaphrodite *FSL* locus allele (*FSL/FSL*);

(ii) a polynucleotide that confers dwarf stature to a plant; and

(iii) polynucleotide that confers stenospermocarpy.

~~26. The plant or part thereof of any one of claims 1 to 25, wherein the plant is a dioecious plant species.~~

~~27~~11. The plant or part thereof of any one of claims 1 to ~~25~~10, wherein:

(a) the plant is a hermaphroditic plant species;

(b) the plant is a fruit producing plant;

(c) the plant is a *Vitis* sp.; and/or

(b) the plant part is a fruit, roots, stems, scion, cuttings, cells, seeds and seed parts.

~~28. The plant or part thereof of any one of claims 1 to 27, wherein the plant is a fruit producing plant.~~

~~29. The plant or part thereof of any one of claims 1 to 28, wherein the plant is a *Vitis* sp.~~

~~30. The plant or part thereof of any one of claims 1 to 29, wherein the plant part is a fruit, roots, stems, scion, cuttings, cells, seeds and seed parts.~~

~~31~~12. A method of controlling flower sex in a plant, said method comprising altering a level of flower sex (FSL) polypeptide activity in the plant or part thereof compared to a level of FSL polypeptide activity in a corresponding plant or part thereof having an *FSL* locus genotype which confers a male or hermaphrodite flower phenotype.

~~32~~13. The method of claim ~~31~~12, wherein:

(a) an *FSL* locus genotype which confers a hermaphrodite flower phenotype comprises a hermaphrodite allele of the *FSL* locus encoding the FSL polypeptide comprising an amino acid sequence set forth in SEQ ID NO:1, a biologically active fragment thereof, or an amino acid sequence which is at least 40% identical to the sequence set forth in SEQ ID NO:1; and

an *FSL* locus genotype which confers a male flower phenotype comprises a male allele of the *FSL* locus encoding the FSL polypeptide comprising an amino acid sequence set forth in SEQ ID NO:3, a biologically active fragment thereof, or an amino acid sequence which is at least 40% identical to the sequence set forth in SEQ ID NO:3;

(b) a hermaphrodite allele of the *FSL* locus encodes the FSL polypeptide comprising the amino acid sequence set forth in SEQ ID NO:1, or a biologically active fragment thereof; and

a male allele of the *FSL* locus encodes the FSL polypeptide comprising the amino acid sequence set forth in SEQ ID NO:3, or a biologically active fragment thereof; and/or

(c) a plant or plant part having an altered level of FSL polypeptide activity comprises an FSL polypeptide comprising an amino acid sequence set forth in SEQ ID NO:2, a biologically active fragment thereof, or an amino acid sequence which is at least 40% identical to the sequence set forth in SEQ ID NO:2.

~~33. The method of claim 32, wherein:~~

~~a hermaphrodite allele of the *FSL* locus encodes the FSL polypeptide comprising the amino acid sequence set forth in SEQ ID NO:1, or a biologically active fragment thereof; and~~

~~a male allele of the *FSL* locus encodes the FSL polypeptide comprising the amino acid sequence set forth in SEQ ID NO:3, or a biologically active fragment thereof.~~

~~34. The method of any one of claims 31 to 33, wherein a plant or plant part having an altered level of FSL polypeptide activity comprises an FSL polypeptide comprising an amino acid sequence set forth in SEQ ID NO:2, a biologically active fragment thereof, or an amino acid sequence which is at least 40% identical to the sequence set forth in SEQ ID NO:2.~~

~~35~~14. The method of ~~any one of claims 31 to 34~~claim 12 or 13, comprising:

(a) modifying a *FSL* locus comprising a polynucleotide sequence encoding the FSL polypeptide or a biologically active fragment thereof, optionally comprising introducing one or more nucleotide additions, deletions or substitutions to the polynucleotide sequence encoding the FSL polypeptide relative to a corresponding polynucleotide sequence of a wildtype *FSL* locus allele which confers a male or hermaphrodite flower phenotype when expressed;

(b) modifying a region within the *FSL* locus encoding a plant AT-rich sequence- and zinc-binding (PLATZ) domain, optionally comprising introducing one or more nucleotide additions, deletions or substitutions to the polynucleotide sequence encoding the FSL polypeptide relative to a corresponding polynucleotide sequence of a wildtype *FSL* locus allele which confers a male or hermaphrodite flower phenotype when expressed; and/or

(c) introducing to the plant or plant part a RNA interference (RNAi) agent which targets a messenger RNA (mRNA) of the *FSL* locus or an allele thereof, thereby reducing FSL polypeptide activity in the plant or part thereof.

~~36. The method of claim 35, comprising modifying a region within the *FSL* locus encoding a plant AT-rich sequence- and zinc-binding (PLATZ) domain.~~

~~37. The method of claim 335 or 36, comprising introducing one or more nucleotide additions, deletions or substitutions to the polynucleotide sequence encoding the FSL polypeptide relative to a corresponding polynucleotide sequence of a wildtype *FSL* locus allele which confers a male or hermaphrodite flower phenotype when expressed.~~

~~38. The method of any one of claims 31 to 34, comprising introducing to the plant or plant part a RNA interference (RNAi) agent which targets a messenger RNA (mRNA) of the *FSL* locus or an allele thereof, thereby reducing FSL polypeptide activity in the plant or part thereof.~~

~~39~~15. The method of any one of claims ~~31 to 38~~12 to 14, wherein:

(a) FSL polypeptide activity is reduced in the plant or plant part relative a level of FSL polypeptide activity in a corresponding wildtype plant or part thereof; and/or

(b) reducing the activity of the FSL polypeptide in the plant or plant part causes a male reproductive part of a flower of the plant or plant part to be absent or non-functional.

~~40. The method of any one of claims 31 to 39, wherein reducing the activity of the FSL polypeptide in the plant or plant part causes a male reproductive part of a flower of the plant or plant part to be absent or non-functional.~~

~~41. The method of any one of claims 31 to 40, wherein the plant is a dioecious plant species.~~

~~42~~16. The method of any one of claims ~~31 to 40~~12 to 15, wherein:

(a) the plant is a hermaphroditic plant species;

(b) the plant is a fruit producing plant;

(c) the plant is a *Vitis* sp.; and/or

(d) the plant part is selected from the group consisting of fruit, roots, stems, scion, cuttings, cells, seeds and seed parts.

~~43. The method of any one of claims 31 to 42, wherein the plant is a fruit producing plant.~~

~~44. The method of any one of claims 31 to 43, wherein the plant is a *Vitis* sp.~~

~~45. The method of any one of claims 31 to 44, wherein the plant part is selected from the group consisting of fruit, roots, stems, scion, cuttings, cells, seeds and seed parts.~~

~~46~~17. A method of producing a plant that produces flowers of known sex, said method comprising the steps of:

i) crossing two parental plants,

ii) screening one or more progeny plants from the cross to determine the genotype at a flower sex (*FSL*) locus, and

iii) selecting a progeny plant capable of exhibiting a desired flower sex phenotype on the basis of the FSL locus genotype, wherein

(a) an *FSL* locus genotype which is homozygous for a female *FSL* locus allele (f/f) confers a female flower phenotype,

(b) an *FSL* locus genotype which is heterozygous for a female allele and a hermaphrodite *FSL* locus allele (f/H) confers a hermaphrodite flower phenotype, and an *FSL* locus genotype which is homozygous for a hermaphrodite *FSL* locus allele (H/H) confers a hermaphrodite flower phenotype,

(c) an *FSL* locus genotype which is heterozygous for a male *FSL* locus allele and either a female *FSL* locus allele (M/f) or a hermaphrodite *FSL* locus allele (M/H) confers a male flower phenotype, and an *FSL* locus genotype which is homozygous for a male *FSL* locus allele (M/M) confers a male flower phenotype,

thereby producing a plant which produces flower of known sex,

and optionally comprising selecting a progeny plant having an *FSL* locus genotype which is homozygous for a female allele (f/f) to thereby produce a plant which produces female flowers.

~~47. The method of claim 46, comprising selecting a progeny plant having an *FSL* locus genotype which is homozygous for a female allele (f/f) to thereby produce a plant which produces female flowers.~~

~~48~~18. A method of producing a plant which produces seedless fruit, said method comprising the steps of:

i) crossing two parental plants, wherein one of the parental plants comprises a flower sex (*FSL*) locus which is homozygous for a female allele (f/f) conferring female flower phenotype, and the other parental plant comprises a polynucleotide that confers dwarf stature,

ii) screening one or more progeny plants from the cross for the presence or absence of the *FSL* locus which is homozygous for a female allele (f/f), and the presence or absence of the polynucleotide that confers dwarf stature, and

iii) selecting a progeny plant which comprises the *FSL* locus which is homozygous for a female allele (f/f) and which comprises the polynucleotide that confers dwarf stature,

thereby producing a plant which produces seedless fruit.

~~49~~19. A method of producing a plant which produces seedless fruit, said method comprising the steps of:

i) crossing two parental plants, wherein at least one of the parental plants comprises (a) a flower sex (*FSL*) locus which is homozygous for a female allele (f/f) conferring a female flower phenotype, homozygous for *FSL* allele (*FSL/FSL*), or heterozygous for *FSL* (*FSL/fsl*) conferring a hermaphrodite flower phenotype, (b) at least one of the parental plants comprises a polynucleotide that confers dwarf stature, and (c) at least one of the parental plants comprises a polynucleotide that confers stenospermocarpy,

ii) screening one or more progeny plants from the cross for the presence or absence of the *FSL* locus which is homozygous for FSL (*fsl/fsl*), homozygous for a hermaphrodite allele (*FSL/FSL*), or heterozygous for a hermaphrodite allele and a female allele (*FSL/fsl*), (b) the presence or absence of the polynucleotide that confers dwarf stature, and (b) the presence or absence of the polynucleotide that confers stenospermocarpy, and

iii) selecting a progeny plant which comprises (a) an *FSL* locus genotype that confers a female or hermaphrodite flower phenotype, (b) a polynucleotide that confers dwarf stature, and (c) the polynucleotide that confers stenospermocarpy,

thereby producing a plant which produces seedless fruit.

~~50~~20. The method of claim ~~49~~19, wherein:

a progeny plant which comprises (a) an *FSL* locus genotype that confers a hermaphrodite flower phenotype, (b) the polynucleotide that confers dwarf stature, and (c) the polynucleotide that confers stenospermocarpy, produces stenospermocarpic seedless fruit; and

a progeny plant which comprises (a) an *FSL* locus genotype that confers a female flower phenotype, (b) the polynucleotide that confers dwarf stature, and (c) the polynucleotide that confers stenospermocarpy, produces parthenocarpic seedless fruit.

~~51. A method of producing a plant which produces parthenocarpic seedless fruit, said method comprising the steps of:~~

~~i) crossing two parental plants, wherein at least one of the parental plants comprises a flower sex (*FSL*) locus which is homozygous for a female allele (f/f) conferring female flower phenotype, at least one of the parental plants comprises a polynucleotide that confers dwarf stature, and at least one of the parental plants comprises a polynucleotide that confers stenospermocarpy,~~

~~ii) screening one or more progeny plants from the cross for the presence or absence of the *FSL* locus which is homozygous *fsl/fsl* which gives rise to female flower~~

~~morphology. the presence or absence of the polynucleotide that confers dwarf stature, and the presence or absence of the polynucleotide that confers stenospermocarpy, and~~

~~iii) selecting a progeny plant which comprises the *FSL* locus which is homozygous for a female allele (f/f), the polynucleotide that confers dwarf stature, and the polynucleotide that confers stenospermocarpy,~~

~~thereby producing a plant which produces parthenocarpic seedless fruit.~~

~~52~~21. The method of any one of claims ~~46 to 51~~17 to 20, wherein the *FSL* locus or an allele thereof is as structurally defined in any one or more of the preceding claims.

~~53~~22. The method of any one of claims ~~48~~ 18 to ~~52~~21, wherein:

(a) the polynucleotide that confers dwarf stature is a variant of the gibberellic acid insensitive (*GAI1*) gene or a fragment thereof as structurally defined in any one of the preceding claims;

(b) the polynucleotide that confers stenospermacarpy is a variant of the *Vitis vinifera* MADS-box protein 5 (VvMADS5) locus as structurally defined in any one of the preceding claims;

(c) the plant is a hermaphroditic plant species;

(d) the plant is a fruit producing plant; and/or

(e) the plant is a *Vitis* sp..

~~54. The method of any one of claims 49 to 53, wherein the polynucleotide that confers stenospermacarpy is a variant of the *Vitis vinifera* MADS-box protein 5 (VvMADS5) locus as structurally defined in any one of the preceding claims.~~

~~55. The method of any one of claims 46 to 54, wherein the plant is a dioecious plant species.~~

~~56. The method of any one of claims 46 to 54, wherein the plant is a hermaphroditic plant species.~~

~~57. The method of any one of claims 46 to 56, wherein the plant is a fruit producing plant.~~

~~58. The method of any one of claims 46 to 57, wherein the plant is a *Vitis* sp.~~

~~59~~23. Fruit of a plant of any one of claims 1 to ~~30~~ 11 or of a progeny thereof, preferably wherein the plant is a *Vitis* sp..

~~60~~24. A method of producing seedless fruit, the method comprising:
(i) growing a plant of any one of claim 1 to ~~30~~ 11 to thereby produce fruit; and
(ii) optionally harvesting the fruit produced at (i); and
(iii) optionally processing the fruit harvested at (ii).

~~61~~25. A product produced from a plant of any one of claims 1 to ~~30~~ 11 or produced from a fruit thereof, preferably wherein the product is a food product, food ingredient, beverage product or beverage ingredient, optionally wherein:
(i) the food product is selected from the group consisting of table grapes, jam, marmalade, jelly, sultana, and raisins;
(ii) the food ingredient is vincotto, vinegar or grape must syrup (mosto cotto);
(iii) the beverage product is wine, grappa, brandy or grape juice;
(iv) the beverage ingredient is wine grapes or table grapes .

~~62. The product of claim 61, wherein the product is a food product, food ingredient, beverage product or beverage ingredient.~~

~~63. The product of claim 62, wherein:~~
~~(i) the food product is selected from the group consisting of table grapes, jam, marmalade, jelly, sultana, and raisins;~~
~~(ii) the food ingredient is vincotto, vinegar or grape must syrup (mosto cotto);~~
~~(iii) the beverage product is wine, grappa, brandy or grape juice;~~
~~(iv) the beverage ingredient is wine grapes or table grapes.~~

~~64~~26. A flower sex (FSL) polypeptide comprising an amino acid sequence selected from the sequences set forth in SEQ ID NOs: 1, 2 or 3 or a biologically active fragment thereof, or an amino acid sequence which is at least 40% identical to a sequence set forth in SEQ ID NOs: 1, 2 or 3.

~~65~~27. An isolated nucleic acid molecule encoding a flower sex (FSL) polypeptide, comprising (a) a polynucleotide sequence selected from the sequences set forth in SEQ ID NOs: 5-7 or a polynucleotide having an open reading frame (ORF) selected from the sequences set forth in SEQ ID NOs: 5-7 or (b) a polynucleotide sequence having at least

40% identity to one of the sequences set forth in SEQ ID NOs: 5-7 or a polynucleotide having an open reading frame (ORF) having at least 40% identity to one of the sequences set forth in SEQ ID NOs: 5-7; or (c) a polynucleotide sequence which is complementary to any of the polynucleotide sequences of (a) or (b), optionally wherein the nucleic acid molecule is operably-linked to a promoter and comprised within an expression vector.

~~66. An expression vector comprising the isolated nucleic acid molecule of claim 65 operably linked to a promoter.~~

~~67. A host cell comprising the nucleic acid molecule of claim 65 or an expression vector of claim 66.~~

~~68. The host cell of claim 67 which is a yeast, bacteria or plant cell.~~