CLAIMS

1. A *Vitis* sp. plant or part thereof having a reduced level of flower sex (FSL) polypeptide activity compared to a corresponding wildtype plant or part thereof having a *FSL* locus genotype which confers a male or hermaphrodite flower phenotype, wherein said plant or part thereof comprises an *FSL* locus comprising a polynucleotide sequence encoding the FSL polypeptide, and a region of the polynucleotide sequence encoding a plant AT-rich sequence- and zinc-binding (PLATZ) domain within the FSL polypeptide is modified relative to a corresponding polynucleotide sequence of a wildtype *FSL* locus allele which confers the male or hermaphrodite flower phenotype when expressed, wherein:

(a) an *FSL* locus genotype which confers a hermaphrodite flower phenotype comprises a hermaphrodite allele of the *FSL* locus encoding: (i) the FSL polypeptide comprising an amino acid sequence set forth in SEQ ID NO:1, (ii) a fragment of the FSL polypeptide set forth in SEQ ID NO:1 which retains the biological function thereof, or (iii) an amino acid sequence which is at least 80% identical to the sequence set forth in SEQ ID NO:1 across its full length and which retains the biological function thereof; and

an *FSL* locus genotype which confers a male flower phenotype comprises a male allele of the *FSL* locus encoding: (i) the FSL polypeptide comprising an amino acid sequence set forth in SEQ ID NO:3, (ii) a fragment of the FSL polypeptide set forth in SEQ ID NO:3 which retains the biological function thereof, or (iii) an amino acid sequence which is at least 80% identical to the sequence set forth in SEQ ID NO:3 across its full length and which retains the biological function thereof; 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, (i) a fragment of the FSL polypeptide set forth in SEQ ID NO:1 which retains the biological function 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 (ii) a fragment of the FSL polypeptide set forth in SEQ ID NO:3 which retains the biological function thereof.

2. The *Vitis* sp. plant or part thereof of claim 1, 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.

3. The *Vitis* sp. plant or part thereof of claim 1 or 2, wherein:

(a) the polynucleotide sequence encoding the PLATZ domain of 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;

(b) the reduced level of activity of the FSL polypeptide causes a male reproductive part of a flower of the *Vitis* sp. plant to be absent or non-functional; and/or

(c) the *Vitis* sp. plant or part thereof comprises a polynucleotide that confers dwarf stature to the plant, wherein the polynucleotide that confers dwarf stature is a variant of the gibberellic acid insensitive (*GAI1*) gene which comprises one or more mutations in the region encoding a DELLA domain relative to the corresponding wildtype polynucleotide sequence, or a fragment of the variant *GAI1* gene which retains its biological function.

4. A *Vitis* sp. plant or part thereof which produces seedless fruit, said plant comprising:

(i) a polynucleotide that confers dwarf stature to a *Vitis* sp. plant, wherein the polynucleotide that confers dwarf stature is a variant of the gibberellic acid insensitive (*GAI1*) gene which comprises one or more mutations in the region encoding a DELLA domain relative to the corresponding wildtype polynucleotide sequence, or a fragment of the variant *GAI1* gene which retains its biological function; and

(ii) a flower sex (*FSL*) locus which is homozygous for a female allele (f/f) conferring female flower phenotype, wherein the female allele of the *FSL* locus has an ORF which comprises 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 an A, and a region of the ORF of the *FSL* locus which encodes a plant AT-rich sequence- and zinc-binding (PLATZ) domain within the FSL polypeptide is modified relative to a corresponding region of a ORF for a wildtype *FSL* locus allele which confers the male or hermaphrodite flower phenotype when expressed.

5. The *Vitis* sp. plant or part thereof of claim 4, wherein:

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

(b) (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

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

6. The *Vitis* sp. plant or part thereof of claim 4 or 5, further comprising a polynucleotide that confers stenospermocarpy, wherein the polynucleotide that confers stenospermocarpy is a variant of the *Vitis vinifera* MADS-box protein 5 (VvMADS5) locus.

7. The *Vitis* sp. plant or part thereof of claim 6, wherein:

(a) 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

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

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

(d) said *Vitis* sp. plant produces parthenocarpic seedless fruit when flowers are unpollinated and stenospermocarpic fruit when flowers are pollinated with viable pollen.

8. A *Vitis* sp. plant or part thereof which produces seedless fruit, said *Vitis* sp. 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 *Vitis* sp. plant, wherein the polynucleotide that confers dwarf stature is a variant of the gibberellic acid insensitive (*GAI1*) gene comprising one or more mutations in the region encoding a DELLA domain relative to the corresponding wildtype polynucleotide sequence, or a fragment of said variant *GAI1* gene which retains its biological function; and

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

9. The *Vitis* sp. plant or part thereof of claim 8, wherein:

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

(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 comprising the 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 ID NO:8; and/or

(iii) 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.

10. The *Vitis* sp. plant or part thereof of claim 8 or 9, wherein:

(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 ID NO:10;

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

(iii) the variant *VvMADS5* locus which confers stenospermocarpy is present in a homozygous or heterozygous state.

11. A method of controlling flower sex in a *Vitis* sp. plant, said method comprising reducing a level of flower sex (FSL) polypeptide activity in the *Vitis* sp. 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, wherein the reduced level of FSL polypeptide activity in the *Vitis* sp. plant causes a male reproductive part of a flower to be absent or non-functional, wherein the level of FSL polypeptide activity is reduced in the *Vitis* sp. plant by modifying a region within the *FSL* locus encoding a plant AT-rich sequence- and zinc-binding (PLATZ) domain of the FSL polypeptide.

12. The method of claim 11, wherein:

(a) an *FSL* locus genotype which confers a hermaphrodite flower phenotype comprises a hermaphrodite allele of the *FSL* locus encoding: (i) the FSL

polypeptide comprising an amino acid sequence set forth in SEQ ID NO:1, (ii) a fragment of the FSL polypeptide set forth in SEQ ID NO:1 which retains the biological function thereof, or (iii) an amino acid sequence which is at least 80% identical to the sequence set forth in SEQ ID NO:1 across its full length and which retains the biological function thereof; and

an *FSL* locus genotype which confers a male flower phenotype comprises a male allele of the *FSL* locus encoding: (i) the FSL polypeptide comprising an amino acid sequence set forth in SEQ ID NO:3, (ii) a fragment of the FSL polypeptide set forth in SEQ ID NO:3 which retains the biological function thereof, or (iii) an amino acid sequence which is at least 80% identical to the sequence set forth in SEQ ID NO:3 across its full length and which retains the biological function thereof;

(b) a hermaphrodite allele of the *FSL* locus encodes the FSL polypeptide comprising the amino acid sequence set forth in SEQ ID NO:1, (ii) a fragment of the FSL polypeptide set forth in SEQ ID NO:1 which retains the biological function 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, (ii) a fragment of the FSL polypeptide set forth in SEQ ID NO:3 which retains the biological function thereof.

13. The method of claim 11 or 12, wherein the region within the *FSL* locus encoding the PLATZ domain is modified by:

(a) introducing one or more nucleotide additions, deletions or substitutions to the polynucleotide sequence encoding the PLATZ domain of 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

(b) introducing to the *Vitis* sp. 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 *Vitis* sp. plant or part thereof.

14. The method of any one of claims 11 to 13, wherein:

(i) the *Vitis* sp. plant or plant part in which the level of FSL polypeptide activity is reduced comprises a polynucleotide which confers dwarf stature, wherein the polynucleotide that confers dwarf stature is a variant of the gibberellic acid insensitive

(*GAI1*) gene comprising one or more mutations in the region encoding a DELLA domain relative to the corresponding wildtype polynucleotide sequence encoding the amino acid sequence set forth in SEQ ID No. 8, wherein the one or more mutations in the variant (*GAI1*) protein cause the DELLA domain to be deleted, truncated or altered and, wherein the variant (*GAI1*) protein has reduced gibberellic acid (GA) signalling relative to the corresponding wildtype protein;

(ii) the method comprises introducing to the plant or plant part the polynucleotide which confers dwarf stature is a variant of the GAI1 locus, relative to the wildtype GAI1 polynucleotide sequence set forth in SEQ ID NO: 8, wherein the one or more mutations result in a variant GAI1 protein in which the DELLA domain is deleted, truncated or altered, and wherein the variant protein has reduced GA signalling relative to the wildtype protein;

(iii) the plant or plant part in which FSL polypeptide activity is altered comprises a polynucleotide which confers stenospermocarpy is a variant of the *VvMADS5* locus comprising one or more mutations relative to the corresponding wildtype polynucleotide sequence encoding the VvMADS5 amino acid sequence set forth in SEQ ID NO: 10, wherein the one or more mutations result in a non-functional VvMADS5 protein; and/or

(iv) the method comprises introducing to the plant or plant part the polynucleotide which confers stenospermocarpy is a variant of the *VvMADS5* locus comprising one or more mutations relative to the corresponding wildtype polynucleotide sequence encoding the VvMADS5 amino acid sequence set forth in SEQ ID NO: 10, wherein the one or more mutations result in a non-functional VvMADS5 protein.

15. The method of claim 14, wherein:

the polynucleotide that confers dwarf stature is a variant of the *GAI1* gene encoding a variant GAI1 protein comprising a sequence set forth in SEQ ID NO: 9; and/or

the polynucleotide that confers stenospermocarpy is a variant of the *VvMADS5* locus that encodes a variant VvMADS5 protein comprising a sequence set forth in SEQ ID NO: 11.

16. The *Vitis* sp. plant or part thereof of any one of claims 1 to 10 or the method of any one of claims 11 to 15, wherein the plant part is selected from the group consisting of fruit, roots, stems, scion, cuttings, cells, seeds and seed parts.

17. A method of producing a *Vitis* sp. plant that produces flowers of known sex, said method comprising the steps of:

i) crossing two *Vitis* sp. parental plants,

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

iii) selecting a progeny *Vitis* sp. 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 *FSL* locus 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, and

(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 *Vitis* sp. plant having an *FSL* locus genotype which is homozygous for a female *FSL* locus allele (f/f) to thereby produce a *Vitis* sp. plant which produces female flowers,

wherein:

the female *FSL* locus allele (f) comprises an adenine (A) at position 621 of the open reading frame (ORF) sequence set forth in SEQ ID NO: 5;

the male *FSL* locus allele (M) comprises a cytosine (C) at position 627 of the ORF sequence set forth in SEQ ID NO: 7; and

the hermaphrodite *FSL* locus allele (H) comprises a cytosine (C) at position 627 of the ORF sequence set forth in SEQ ID NO: 6.

18. A method of producing a *Vitis* sp. plant which produces seedless fruit, said method comprising the steps of:

i) crossing two parental *Vitis* sp. plants, wherein the parental *Vitis* sp. plants each comprise a flower sex (*FSL*) locus genotype which is homozygous for a female *FSL* locus

allele (f/f), heterozygous for a female FSL locus allele and a hermaphrodite FSL locus allele (f/H), or heterozygous for a female FSL locus allele and a male FSL locus allele (f/M), and at least one of the parental *Vitis* sp. plants comprises a polynucleotide that confers dwarf stature;

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

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

thereby obtaining a *Vitis* sp. plant which produces seedless fruit,

wherein the female *FSL* locus allele (f) comprises an adenine (A) at position 621 of the open reading frame (ORF) sequence set forth in SEQ ID NO: 5, and

wherein the polynucleotide that confers dwarf stature is a variant of the gibberellic acid insensitive (*GAI1*) gene comprising one or more mutations in the region encoding a DELLA domain relative to the corresponding wildtype polynucleotide sequence, or a fragment of said variant *GAI1* gene which retains its biological function.

19. A method of producing a *Vitis* sp. plant which produces seedless fruit, said method comprising the steps of:

i) crossing two parental *Vitis* sp. plants, wherein (a) the parental *Vitis* sp. plants each comprise a flower sex (*FSL*) locus genotype which is homozygous for a female *FSL* locus allele (f/f) conferring a female flower phenotype, homozygous for a hermaphrodite allele (H/H), or heterozygous for the hermaphrodite *FLS* locus allele and female *FSL* locus allele (H/f), heterozygous for a female *FSL* locus allele and a male FSL locus allele (f/M) or heterozygous for a hermaphrodite *FSL* locus allele and a male FSL locus allele (H/M), (b) at least one of the parental *Vitis* sp. plants comprises a polynucleotide that confers dwarf stature, and (c) at least one of the parental *Vitis* sp. plants comprises a polynucleotide that confers stenospermocarpy;

ii) screening one or more progeny *Vitis* sp. plants from the cross for (a) the presence or absence of the *FSL* locus genotype which is homozygous for a female *FSL* allele (f/f) conferring a female flower phenotype, homozygous for a hermaphrodite *FSL* locus allele (H/H) conferring a hermaphrodite flower phenotype, or heterozygous for the hermaphrodite *FSL* locus allele and a female *FSL* locus allele (H/f) conferring a hermaphrodite flower phenotype, (b) the presence or absence of the polynucleotide that

confers dwarf stature, and (c) the presence or absence of the polynucleotide that confers stenospermocarpy; and

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

thereby producing a *Vitis* sp. plant which produces seedless fruit,

wherein the female *FSL* locus allele (f) comprises an adenine (A) at position 621 of the open reading frame (ORF) sequence set forth in SEQ ID NO: 5,

wherein the male *FSL* locus allele (M) comprises a cytosine (C) at position 627 of the ORF sequence set forth in SEQ ID NO: 7,

wherein the hermaphrodite *FSL* locus allele (H) comprises a cytosine (C) at position 627 of the ORF sequence set forth in SEQ ID NO: 6,

wherein the polynucleotide that confers dwarf stature is a variant of the gibberellic acid insensitive (*GAI1*) gene comprising one or more mutations in the region encoding a DELLA domain relative to the corresponding wildtype polynucleotide sequence, or a fragment of said variant *GAI1* gene which retains its biological function, and

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

20. The method of claim 19, wherein:

a *Vitis* sp. 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 *Vitis* sp. 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.

21. The method of claim 19 or 20, wherein:

(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 ID NO:10;

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

(iii) the variant *VvMADS5* locus which confers stenospermocarpy is present in a homozygous or heterozygous state.

22. The method of any one of claims 18 to 21, wherein:

(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; and/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.

23. Fruit of a *Vitis* sp. plant of any one of claims 1 to 10 or of a progeny thereof.

24. A method of producing seedless fruit, the method comprising:

(i) growing a *Vitis* sp. plant of any one of claim 1 to 10 to thereby produce fruit; and

(ii) optionally harvesting the fruit produced at (i); and

(iii) optionally processing the fruit harvested at (ii).

25. A product is a food, beverage product or ingredient which comprises part of a *Vitis* sp. plant of any one of claims 1 to 10 or a progeny 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.

26. A method of producing a food product, food ingredient, beverage product, beverage ingredient or combination thereof, comprising:

(a) obtaining fruit harvested from a Vitis sp. plant of any one of claims 1 to 10;

(b) processing the fruit to produce the food product, food ingredient, beverage product, beverage ingredient or combination thereof;

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.