CLAIMS

1. A recombinant genetic construct comprising one or more nucleic acid fragments adapted for insertion into the genetic material of a plant to alter or modify a trait of the plant selected from the group consisting of a disease resistance trait, an abiotic stress tolerance trait, or a morphological trait, wherein each of said one or more nucleic acid fragments consists of a plurality of nucleotide sequences of at least 15 nucleotides in length derived from one or more plants, and wherein upon insertion of said one or more nucleic acid fragments into the genetic material of a plant, nucleotide sequence that is introduced into the genetic material of the plant consists of said plant derived nucleotide sequence.

2. The recombinant genetic construct of claim 1, wherein the nucleotide sequences derived from one or more plants are derived from (i) one plant; or (ii) a plurality of plants of the same species.

3. The recombinant genetic construct of any preceding claim, wherein the total length of the one or more nucleic acid fragments of the genetic construct that are insertable into the genetic material of a plant is at least 100 base pairs; at least 500 base pairs; at least 1000; at least 2000 base pairs; or at least 3000 base pairs.

4. The recombinant genetic construct of any preceding claim, wherein the one or more nucleic acid fragments of the genetic construct that are insertable into the genetic material of a plant comprise one or more nucleotide sequences for expression in a plant.

5. The recombinant genetic construct of claim 4, wherein the one or more nucleotide sequences for expression in a plant are adapted for expression in the plant to alter or modify a trait of the plant.

6. The recombinant genetic construct of claim 4 or claim 5, wherein the one or more nucleotide sequences for expression in a plant are or comprise: (i) protein coding nucleotide sequences; or (ii) non- protein-coding nucleotide sequences.

7. The recombinant genetic construct of claim 6, wherein the protein coding nucleotide sequence comprises a nucleotide sequence set forth in SEQ ID NOS:38-46, 76, 78, or 98, or a fragment or variant thereof.

8. The recombinant genetic construct of claim 6, wherein the non- protein coding nucleotide sequences comprise one or more small RNA nucleotide sequences.

9. The recombinant genetic construct of claim 8, wherein the non- protein-coding nucleotide sequences for expression comprise a nucleotide sequence set forth in SEQ ID NOS:12-26, 64-66, 80-81, 83-92, 94, or 96-101, or a fragment or variant thereof.

10. The recombinant genetic construct of any one of claims 4-9, wherein the one or more nucleotide sequences for expression in a plant comprise one or more selectable marker nucleotide sequences.

11. The recombinant genetic construct of claim 10, wherein the selectable marker nucleotide sequence comprises a nucleotide sequence encoding an amino acid sequences set forth in SEQ ID NOS:38-46, or the nucleotide sequence set forth in SEQ ID NO:119, or a fragment or variant thereof.

12. The recombinant genetic construct of any preceding claim, wherein the one or more nucleic acid fragments of the genetic construct that are insertable into the genetic material of a plant comprise one or more regulatory nucleotide sequences.

13. The recombinant genetic construct of claim 12, wherein the regulatory nucleotide sequences comprise one or more promoter sequences.

14. The recombinant genetic construct of claim 13, wherein the promoter comprises a nucleotide sequence set forth in SEQ ID NOS:4-7, 67, 73, 74, 76, 78, or 98, or a fragment or variant thereof.

15. The recombinant genetic construct of any one of claims 12-14, wherein the regulatory sequences comprise one or more terminator sequences.

16. The recombinant genetic construct of claim 15, wherein the terminator comprises a nucleotide sequence set forth in SEQ ID NOS:8-11, 106, 108, 111, or 112, or a fragment or variant thereof.

17. The recombinant genetic construct of any preceding claim, further comprising flanking sequences of or surrounding the one or more nucleic acid fragments insertable into the genetic material of a plant.

18. The recombinant genetic construct of claim 17 wherein the flanking sequences comprise restriction digest sites.

19. The recombinant genetic construct of claim 18, wherein the flanking sequences comprise a nucleotide sequence set forth in SEQ ID NOS:102, 103, 109, 110, 115, 116, 117, 118, 120, or 121, or a fragment or variant thereof.

20. The recombinant genetic construct of any previous claim, comprising:

a first border nucleotide sequence;

a second border nucleotide sequence; and

one or more additional nucleotide sequences located between the first border nucleotide sequence and the second border nucleotide sequence,

wherein said additional nucleotide sequences, and at least a portion of said first border nucleotide sequence that is adjacent to said additional nucleotide sequences, are derived from one or more plants.

21. The recombinant genetic construct of claim 20, wherein at least a portion of the second border nucleotide sequence that is adjacent to said one or more additional nucleotide sequences is derived from one or more plants, wherein said one or more plants are the same one or more plants from which the additional nucleotide sequences and the at least a portion of the first border nucleotide sequence are derived.

22. The recombinant genetic construct of claim 20 or claim 21, wherein the one or more nucleic acid fragments insertable into the genetic material of a plant consisting

of a plurality of nucleotide sequences of at least 15 nucleotides in length derived from one or more plants consist of:

(i) the at least a portion of the first border nucleotide sequence derived from one or more plants;

(ii) the one or more additional nucleotide sequences derived from the one or more plants; and optionally

(iii) at least a portion of the second border nucleotide sequence derived from one or more plants.

23. The recombinant genetic construct of any one of claims 20-22, wherein the first border sequence is of a Right Border nucleotide sequence functional for *Agrobacterium*-mediated T-DNA plant transformation.

24. The genetic construct of any one of claims 20-23, wherein the second border nucleotide sequence is of a Left Border nucleotide sequence functional for *Agrobacterium*-mediated T-DNA plant transformation.

25. The recombinant genetic construct of any preceding claim, comprising a nucleotide sequence set forth in SEQ ID NOS:1-35, 49, 51-56, 66-68, 71-92, or 94-101, or a nucleic acid encoding an amino acid sequence set forth in SEQ ID NOS:38-46, or a fragment or variant thereof.

26. A method for producing a recombinant genetic construct, the method including the step of deriving from one or more plants one or more nucleic acid fragments adapted for insertion into the genetic material of a plant to alter or modify a trait of the plant selected from the group consisting of a disease resistance trait, an abiotic stress tolerance trait, or a morphological trait, wherein said one or more nucleic acid fragments consist of a plurality of nucleotide sequences of at least 15 nucleotides in length, to thereby produce the recombinant genetic construct, wherein upon insertion of said one or more nucleic acid fragments of the recombinant genetic construct into the genetic material of a plant, nucleotide sequence that is introduced into the genetic material of the plant consists of said plant derived nucleotide sequence.

27. The method of claim 26, including the step of adding a first border nucleotide sequence and a second border nucleotide sequence to respective ends of one or more additional nucleotide sequences, wherein the one or more additional nucleotide sequences and at least a portion of the first border nucleotide sequence are derived from one or more plants.

28. A recombinant genetic construct produced according to the method of claim 26 or claim 27.

29. The recombinant genetic construct of any one of claims 1-25, or the method of claim 26 or claim 27, wherein the one or more plants from which the nucleotide sequences are derived or derivable is or includes an organism of the classification Vegetabilia, Archaeplastida, Viridiplantae, or Embryophyta.

30. The recombinant genetic construct or method of claim 29, wherein the plant is monocotyledonous plant or a dicotyledonous plant.

31. The recombinant genetic construct or method of claim 30, wherein the plant is or includes a grass of the Poaceae family such as sugar cane; a *Gossypium* species such as cotton; a berry such as strawberry; a tree species inclusive of fruit trees such as apple and orange and nut trees such as almond; an ornamental plant such as an ornamental flowering plant, inclusive of rosaceous plants such as rose; a vine inclusive of fruit vines such as grapes; a cereal including sorghum, rice, wheat, barley, oats, and maize; a leguminous species including beans such as soybean and peanut; a solanaceous species including tomato and potato; a brassicaceous species including cabbage and oriental mustard; a cucurbitaceous plants including pumpkin and zucchini; a rosaceous plants including rose; an asteraceous plants including lettuce, chicory, and sunflower, or a relative of any of the preceding plants.

32. A vector comprising the recombinant genetic construct of any one of claims 1-25 or 28-31, and a backbone nucleotide sequence.

33. The vector of claim 32 wherein the backbone nucleotide sequence comprises a backbone insertion marker nucleotide sequence.

34. The vector of claim 33 wherein the backbone insertion marker nucleotide sequence comprises SEQ ID NO:36 or SEQ ID NO:37, or a fragment or variant thereof.

35. A host cell comprising the genetic construct of any one of claims 1-25 or 28-31, or the vector of any one of claims 32-34.

36. A method of genetically improving a plant, including the step of inserting at least a nucleic acid fragment of the genetic construct of any one of claims 1-25 or 28-31 into the genetic material of a plant cell or plant tissue, wherein said plant that is genetically improved is of the same species of the one or more plants from which the one or more nucleotide sequences of said nucleic acid fragment of the genetic construct is derived.

37. The method of claim 36, wherein said at least a nucleic acid fragment of the genetic construct is inserted into the genetic material of the plant cell or plant tissue via: (i) *Agrobacterium*-mediated transformation of the plant cell or plant tissue; or (ii) direct transformation.

38. The method of any one of claims 36-37, wherein the at least a nucleic acid fragment of the genetic construct that is introduced into the genetic material of the plant cell or plant tissue consists of the one or more nucleic acid fragments of the genetic construct insertable into the genetic material of a plant.

39. The method of any one of claims 36-38, including the further step of selecting a genetically improved plant wherein one or more traits of the plant are altered or modified as a result of insertion of the at least a nucleic acid fragment of the genetic construct, into the genetic material of the plant.

40. The method of claim 39, wherein the trait is modified according to the expression of one or more nucleotide sequences of the genetic construct suitable for expression in a plant to alter or modify a trait of the plant.

41. The method of claim 40, wherein the trait of the plant is: (i) relatively improved, increased, or otherwise positively altered by the expression of one or more nucleic acids in the plant comprising one or more small RNA sequences, wherein said nucleic acids are capable of altering the expression and/or replication of one or more nucleic acids of a plant pathogen and/or an endogenous plant nucleic acid; or (ii) relatively improved, increased, or otherwise positively altered by the expression of one or more protein-coding genes.

42. The method of any one of claims 39-41, wherein the trait is selected from the group consisting of disease resistance, abiotic stress tolerance, salt tolerance, a nutritional trait, a palatability trait and a morphological trait.

43. A plant or plant part produced according to the method of any one of claims 36-42.

44. A plant wherein at least a nucleic acid fragment of a recombinant genetic construct has been inserted into the genetic material of the plant, wherein said recombinant genetic construct comprises one or more nucleic acid fragments adapted for insertion into the genetic material of a plant to alter or modify a trait of the plant selected from the group consisting of a disease resistance trait, an abiotic stress tolerance trait, or a morphological trait, wherein said one or more nucleic acid fragments consist of a plurality of nucleotide sequences of at least 15 nucleotides in length, derived from one or more plants, and wherein nucleotide sequence of the recombinant genetic construct that has been inserted into the genetic material of the plant consists of said plant derived nucleotide sequence.

45. The method of any one of claims 36-42, or the plant of claim 43 or claim 44, wherein the plant is an organism of the classification Vegetabilia, Archaeplastida, Viridiplantae, or Embryophyta.

46. The method or plant of claim 45, wherein the plant is a monocotyledonous plant or a dicotyledonous plant.

47. The method or plant of claim 46, wherein the plant is or includes a grass of the Poaceae family such as sugar cane; a *Gossypium* species such as cotton; a berry such as strawberry; a tree species inclusive of fruit trees such as apple and orange and nut trees such as almond; an ornamental plant such as an ornamental flowering plant, inclusive of rosaceous plants such as rose; a vine inclusive of fruit vines such as grapes; a cereal including sorghum, rice, wheat, barley, oats, and maize; a leguminous species including beans such as soybean and peanut; a solanaceous species including tomato and potato; a brassicaceous species including cabbage and oriental mustard; a cucurbitaceous plants including pumpkin and zucchini; a rosaceous plants including rose; an asteraceous plants including lettuce, chicory, and sunflower, or a relative of any of the preceding plants.