THAT WHICH IS CLAIMED IS:

1. A mustard (e.g., *Brassicaceae*) plant or part thereof comprising at least one non-natural mutation in an endogenous gene encoding a cytochrome P450 mono-oxygenase (i.e., CYP79F1, homomethionine N-monooxygenase; EC 1.14.14.42), an endogenous gene encoding a 2-oxo acid-dependent dioxygenase (i.e., AOP2, 2-oxoglutarate-dependent dioxygenase; EC 1.14.11.M8) and/or an endogenous gene encoding a myrosinase (i.e., glucosinolase, thioglucosidase (e.g., β-thioglucosidase), thioglucoside glucohydrolase; EC 3.2.1.147 (EC 3.2.3.1 transferred to 3.2.1.147)).)), an endogenous gene encoding a cytochrome P450 mono-oxygenase (i.e., CYP79F1, homomethionine N-monooxygenase; EC 1.14.14.42), and/or an endogenous gene encoding a 2-oxo acid-dependent dioxygenase (i.e., AOP2, 2-oxoglutarate-dependent dioxygenase; EC 1.14.11.M8), optionally, wherein the plant or part thereof comprising at least one non-natural mutation in an endogenous gene exhibits a reduction in the activity of the myrosinase, the AOP2, and/or the CYP79F.

2. The mustard plant or part thereof of claim 1, wherein the plant or part thereof comprising at least one non-natural mutation in an endogenous gene exhibits a reduction in the activity of the CYP79F1, the AOP2, and/or the myrosinase.

3. The mustard plant or part thereof of claim 1 or claim 2, wherein the plant or part thereof comprising at least one non-natural mutation in an endogenous gene exhibits reduced hydrolysis of glucosinolates (e.g., reduced production/amounts of thiocyanates (e.g., allyl isothiocyanate), reduced production of glucose (e.g., reduced hydrolysis of sinigrin (i.e., allylglucosinolate or 2-propenylglucosinolate)).propenylglucosinolateand/or reduced amounts/production of alkenyl glucosinolates and/or aliphatic glucosinolates.

43. The mustard plant or part thereof of any one of claimsclaim 1-3, wherein the plant or part thereof comprising at least one non-natural mutation in an endogenous gene exhibits reduced amounts/production of alkenyl glucosinolates.

5. The mustard plant or part thereof of any one of the preceding claims, wherein the plant or part thereof comprising at least one non-natural mutation in an endogenous gene exhibits reduced amounts/production of aliphatic glucosinolates.

6. The mustard plant or part thereof of any one of the preceding claimsclaim 2, wherein when eaten the plant or part thereof comprising at least one non-natural mutation in an endogenous gene exhibits reduced pungency and/or reduced bitterness.

7. The mustard plant or part thereof of any one of the preceding claims, wherein the at least one non-natural mutation is a dominant-negative allele, semi-dominant allele, weak loss of function allele, null allele, a hypermorphic mutation or a hypomorphic mutation.

84. The mustard plant or part thereof of any one of the preceding claims, wherein the null allele is a full knockout mutant CYP79F1 allele, a full knockout mutant AOP2 allele and/or a full knockout mutant myrosinase allele., optionally, wherein the full knockout mutant CYP79F1 allele results in the production of a nonfunctional CYP79F1 protein or no production of a CYP79F1 protein, the full knockout mutant AOP2 allele results in the production of a nonfunctional AOP2 protein or no production of a AOP2 protein, the full knockout mutant myrosinase allele results in the production of a nonfunctional myrosinase protein or no production of a myrosinase protein.

9. The mustard plant or part thereof of any one of the preceding claims, wherein the full knockout mutant CYP79F1 allele results in the production of a nonfunctional CYP79F1 protein or no production of a CYP79F1 protein, the full knockout mutant AOP2 allele results in the production of a nonfunctional AOP2 protein or no production of a AOP2 protein, the full knockout mutant myrosinase allele results in the production of a nonfunctional myrosinase protein or no production of a myrosinase protein.

105. The mustard plant or part thereof of any one of the preceding claims, wherein the mustard plant or part thereof is a kale plant or part thereof, a collard plant or part thereof, a spinach plant or part thereof, a cabbage plant or part thereof, a beet plant or part thereof, a watercress plant or

part thereof, a lettuce plant or part thereof (e.g. romaine), a swiss chard plant or part thereof, an arugula plant or part thereof, an endive plant or part thereof, a bok choy plant or part thereof, a rutabaga plant or part thereof, a turnip plant or part thereof, a mustard plant or part thereof, a cabbage plant or part thereof, a broccoli plant or part thereof, a cauliflower plant or part thereof, a Brussels sprout plant or part thereof, a radish plant or part thereof, or a kohlrabi plant or part thereof~~.~~

~~11. The mustard plant or part thereof of any one of the preceding claims~~, optionally, wherein the mustard plant or part thereof is *Brassica oleracea* (e.g., *B. oleracea* var. *oleracea*, *B. oleracea* var. *capitata*, *B. oleracea* var. *botrytis*, *B. oleracea* var. *gemmifera*, *B. oleracea* var. *sabauda*, *B. oleracea* var. *gongyiodes*, *B. oleracea* var. *italic*, *B. oleracea* var. *sabellica*, *B. oleracea* var. *acephala*), *Brassica juncea*, *Brassica rapa (B. rapa* subsp. *pekinensis*, *B. rapa* subsp. *Chinensis*, *B. rapa* subsp. *rapa)*, *Brassica napas*, *Brassica carinata*, *Brassica campestris*, *Brassica nigra* or *Raphanus raphanistrum* (e.g., *Raphanus raphanistrum* subsp. *Sativus*).

~~12~~6. The mustard plant or part thereof of any one of the preceding claims, wherein the at least one non-natural mutation is a base substitution, a base deletion and/or a base insertion.

~~13~~7. The mustard plant or part thereof of any one of the preceding claims, wherein the endogenous gene encoding a myrosinase comprising at least one non-natural mutation ~~is a base substitution to an A, a T, a G, or a C.~~

~~14. The mustard plant or part thereof~~ comprises a nucleotide sequence of any one of **SEQ ID NOs:141-599**, ~~the preceding claims, wherein the~~endogenous gene encoding a cytochrome P450 mono-oxygenase comprising at least one non-natural mutation ~~is a substitution of at least one base pair (e.g., 1, 2, 3, 4, or 5 base pairs).~~

~~15. The mustard plant or plant part thereof~~ comprises a nucleotide sequence of any one of ~~the preceding claims, wherein the~~**SEQ ID NOs:788-799**, and/or the endogenous gene encoding a 2-oxo acid-dependent dioxygenase comprising at least one non-natural mutation ~~is~~comprises a ~~deletion.~~

~~16. The mustard plant or part thereof of claim 18, wherein the deletion is a deletion of at least one base pair (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100 or more base pairs).~~

~~17. The mustard plant or part thereof of claim 16, wherein the deletion results in-frame or out of frame mutation.~~

~~18. The mustard plant or part thereof~~nucleotide sequence of any one of ~~the preceding claims, wherein the at least one non-natural mutation results in a premature stop codon~~**SEQ ID NOs:600-616 or 800-816**.

~~19. The mustard plant or plant part thereof of any one of the preceding claims, wherein the at least one non-natural mutation of the endogenous gene results in a truncation of the CYP79F1, the AOP2 and/or the myrosinase.~~

~~20. The mustard plant or plant part thereof of any one of the preceding claims, wherein the at least one non-natural mutation results in a deletion of at least one amino acid (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 450, 500, or 550 or more amino acids).~~

~~21. The mustard plant or part thereof of claim 20, wherein the deletion of at least one amino acid is a deletion of two or more consecutive amino acids (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 450, 500, or 550 or more consecutive amino acids).~~

~~22. A mustard plant cell, comprising a base editing system comprising:~~

~~(a) a CRISPR-associated effector protein;~~

~~(b) a cytidine deaminase or adenosine deaminase; and~~

~~(c) a guide nucleic acid (gRNA) having a spacer sequence with complementarity to an endogenous target gene encoding a CYP79F1, an endogenous target gene encoding an AOP2, and/or an endogenous target gene encoding an myrosinase.~~

~~23. The mustard plant cell of claims 22 , wherein the gRNA comprises a spacer sequence having at least 80% identity to any one of **SEQ ID NO:115** or **SEQ ID NO:116**, **SEQ ID NOs:132-139** and/or **SEQ ID NOs:105-111**.~~

~~24. A mustard plant regenerated from the plant part of any one of claims 1 to 21 or the plant cell of claim 22 or claim 23.~~

~~25~~8. A mustard plant or part thereof (e.g., a plant cell) having reduced pungency or bitterness [when eaten] (e.g., reduced hydrolysis of glucosinolates and/or reduced amounts/production of alkenyl glucosinolates and/or aliphatic glucosinolates) comprising at least one non-natural mutation an endogenous myrosinase gene, an endogenous *AOP2* gene and/or an endogenous *CYP79F1* gene, wherein the at least one mutation is a substitution, insertion or a deletion that is introduced using an editing system that comprises a nucleic acid binding domain that binds to a target site in the endogenous myrosinase gene, in the endogenous *AOP2* gene or in the endogenous *CYP79F1* gene.

~~26. The mustard plant or part thereof of any one of claim 33, wherein the at least one non-natural mutation is a dominant-negative allele, semi-dominant allele, weak loss of function allele, null mutation, a hypermorphic mutation or a hypomorphic mutation, optionally wherein the at least one non-natural mutation is a null mutation.~~

~~27. The mustard plant or part thereof of claim 26~~9. The mustard plant or part thereof of claim 8, wherein the null mutation is a full knockout mutant CYP79F1 allele, a full knockout mutant AOP2 allele and/or a full knockout mutant myrosinase allele~~.~~, optionally, wherein the full knockout mutant CYP79F1 allele results in the production of a nonfunctional CYP79F1 protein or no production of a CYP79F1 protein, the full knockout mutant AOP2 allele results in the production of a nonfunctional AOP2 protein or no production of a AOP2 protein, the full knockout mutant myrosinase allele results in the production of a nonfunctional myrosinase protein or no production of a myrosinase protein.

~~28. The mustard plant or part thereof of claim 27, wherein the full knockout mutant CYP79F1 allele results in the production of a nonfunctional CYP79F1 protein or no production of a CYP79F1 protein, the full knockout mutant AOP2 allele results in the production of a nonfunctional AOP2 protein or no production of a AOP2 protein, the full knockout mutant myrosinase allele results in the production of a nonfunctional myrosinase protein or no production of a myrosinase protein.~~

~~29. The mustard plant or part thereof of any one of claims 25-28, wherein the at least one non-natural mutation is a point mutation.~~

~~30. The mustard plant or part thereof of anyone of claims 25-29, wherein the at least one non-natural mutation of the endogenous myrosinase gene, the endogenous *AOP2* gene and/or the endogenous *CYP79F1* gene results in a truncated protein.~~

~~31. The mustard plant or part thereof of any one of claims 25-30~~10. The mustard plant or part thereof of claim 8 or claim 9, wherein the at least one non-natural mutation is a base substitution, a base deletion and/or a base insertion.

~~32~~11. The mustard plant or part thereof of ~~any one of~~ claims ~~25-31~~8-10, wherein the ~~at least one non-natural mutation comprises a base substitution to an A, a T, a G, or a C.~~

~~33. The mustard plant or plant part thereof of any one of claims 25-31, wherein the~~ endogenous gene encoding a myrosinase comprising at least one non-natural mutation is ~~a deletion of at least one base pair (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100 or more base pairs).~~

~~34. The mustard plant or part thereof of claim 31 or 33, wherein~~ comprises a nucleotide sequence of any one of **SEQ ID NOs:141-599**, the endogenous gene encoding a cytochrome P450 mono-oxygenase comprising at least one non-natural mutation comprises a nucleotide sequence of any one of **SEQ ID NOs:788-799**, and/or the ~~deletion results in-frame or out of frame mutation.~~

~~35. The mustard plant or part thereof of anyone of claims 25-34, wherein the~~endogenous gene encoding a 2-oxo acid-dependent dioxygenase comprising at least one non-natural mutation ~~results~~comprises a ~~premature stop codon.~~

~~36. The mustard plant or plant part thereof~~nucleotide sequence of any one of ~~the preceding claims, wherein the at least one non-natural mutation results in a deletion of at least one amino acid (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 450, 500, or 550 or more amino acids), optionally wherein the deletion of at least one amino acid is a deletion of two or more consecutive amino acids~~**SEQ ID NOs:600-616** or **800-816**.

~~37~~12. The mustard plant or part thereof of any one of claims ~~25 to 36, wherein the nucleic acid binding domain of the editing system is from a polynucleotide-guided endonuclease, a CRISPR-Cas endonuclease (e.g., CRISPR-Cas effector protein), a zinc finger nuclease, a transcription activator-like effector nuclease (TALEN) and/or an Argonaute protein.~~

~~38. The mustard plant or part thereof of any one of claims 25 to 37~~8 to 11, wherein the mustard plant or part thereof is a kale plant or part thereof, a collard plant or part thereof, a spinach plant or part thereof, a cabbage plant or part thereof, a beet plant or part thereof, a watercress plant or part thereof, a lettuce plant or part thereof (e.g. romaine), a swiss chard plant or part thereof, an arugula plant or part thereof, an endive plant or part thereof, a bok choy plant or part thereof, a rutabaga plant or part thereof, a turnip plant or part thereof, a mustard plant or part thereof, a cabbage plant or part thereof, a broccoli plant or part thereof, a cauliflower plant or part thereof, a Brussels sprout plant or part thereof, a radish plant or part thereof, or a kohlrabi plant or part thereof~~.~~

~~39. The mustard plant or part thereof of any one of claims 25 to 38~~, optionally, wherein the plant or part thereof *is Brassica oleracea* (e.g., *B. oleracea* var. *oleracea*, *B. oleracea* var. *capitata*, *B. oleracea* var. *botrytis*, *B. oleracea* var. *gemmifera*, *B. oleracea* var. *sabauda*, *B. oleracea* var. *gongyiodes*, *B. oleracea* var. *italic*, *B. oleracea* var. *sabellica*, *B. oleracea* var. *acephala*), *Brassica juncea*, *Brassica rapa* (*B. rapa* subsp. *pekinensis*, *B. rapa* subsp. *Chinensis*,

B. rapa subsp. *rapa), Brassica napas, Brassica carinata, Brassica campestris Brassica nigra* or *Raphanus raphanistrum* (e.g., *Raphanus raphanistrum* subsp. *Sativus*).

~~40. The mustard plant or part thereof of any one of claims 25 to 39, wherein the plant part is a cell.~~

~~41~~13. A mustard plant regenerated from the plant part of any one of claims ~~25 to 40.~~

~~42. The mustard plant of claim 41~~1-12 optionally, wherein the plant exhibits reduced pungency and/or bitterness.

~~43. A method of producing/breeding a transgene-free base-edited mustard plant, comprising: (a) crossing the plant of any one of claims 1 to 21 or 24-42 with a transgene free mustard plant, thereby introducing the at least one mutation, the mutation, or the modification into the mustard plant that is transgene-free; and~~
~~(b) selecting a progeny plant that comprises the at least one single nucleotide substitution but is transgene-free, thereby producing a transgene-free base-edited mustard plant.~~

~~44. A method of providing a plurality of mustard plants exhibiting reduced pungency or bitterness, the method comprising planting two or more plants of any one of claims 1 to 21 or 24-42 in a growing area (e.g., a field (e.g., a cultivated field, an agricultural field), a growth chamber, a greenhouse, a recreational area, a lawn, and/or a roadside and the like), thereby providing a plurality of mustard plants exhibiting reduced pungency or bitterness as compared to a plurality of control mustard plants not comprising the mutation.~~

~~45~~14. A method for editing a specific site in the genome of a mustard plant cell, the method comprising: cleaving, in a site specific manner, a target site within an endogenous myrosinase gene, an endogenous *AOP2* gene and/or an endogenous *CYP79F1* gene, thereby generating an edit in the endogenous myrosinase gene, the endogenous AOP2 gene and/or the endogenous CYP79F1 gene of the plant cell.

~~46~~15. The method of claim ~~45~~14, further comprising regenerating a mustard plant from the mustard plant cell comprising an edit in the endogenous myrosinase gene, the endogenous AOP2 gene and/or the endogenous CYP79F1 gene to produce a plant comprising the edit in its endogenous myrosinase gene, endogenous AOP2 gene and/or endogenous CYP79F1 gene~~.~~, optionally, wherein the edit results in a non-natural mutation.

~~47~~16. The method of claim ~~46, wherein the edit results in a non-natural mutation.~~

~~48. The method of claim 47~~15, wherein the mustard plant comprising the edit in its endogenous myrosinase gene, endogenous AOP2 gene and/or endogenous CYP79F1 gene exhibits reduced pungency and/or bitterness.

~~49. The method of claim 47 or claim 48, wherein the mutation is a dominant-negative allele, semi-dominant allele, weak loss of function allele, null allele, a hypermorphic mutation or a hypomorphic mutation.~~

~~50~~17. The method of claim any one of claims ~~47-49~~14-16, wherein the edit in the ~~mutation is a deletion.~~

~~51. The method of claim 50, wherein the deletion~~endogenous myrosinase gene results in a ~~full knockout mutant CYP79F1 allele, a full knockout mutant AOP2 allele~~myrosinase gene having a nucleotide sequence of any one of **SEQ ID NOs:141-599**, the edit in the endogenous cytochrome P450 mono-oxygenase gene results in a cytochrome P450 mono-oxygenase gene having a nucleotide sequence of any one of **SEQ ID NOs:788-799** and/or ~~a full knockout mutant myrosinase allele.~~

~~52. The method of claim 51, wherein the full knockout mutant CYP79F1 allele results in~~ the ~~production of a nonfunctional CYP79F1 protein or no production of a CYP79F1 protein, the full knockout mutant AOP2 allele results in the production of a nonfunctional AOP2 protein or no production of a AOP2 protein, the full knockout mutant myrosinase allele results in the production of a nonfunctional myrosinase protein or no production of a myrosinase protein.~~

53. A method for making a mustard plant, comprising:
(a) contacting a population of mustard plant cells comprising a DNA sequence that encodes a wild type endogenous myrosinase, a wild type endogenous *AOP2* and/or a wild type edit in the endogenous *CYP79F1* with a nuclease linked to a DNA binding domain (e.g., editing system) that binds to a target sequence in the wild type endogenous myrosinase, the wild type endogenous *AOP2* or the wild type endogenous *CYP79F1*, (b) selecting a mustard plant cell from said population in which at least one DNA sequence encoding the wild type endogenous myrosinase, the wild type endogenous *AOP2* and/or the wild type endogenous *CYP79F1* has been mutated, wherein the mutation comprises a deletion of at least one nucleotide in the at least one DNA sequence; and (c) growing the selected plant cell into a mustard plant.

54. A method for producing a mustard plant or part thereof comprising at least one cell in which an endogenous myrosinase gene, an endogenous *AOP2* gene and/or an endogenous *CYP79F1* gene is mutated, the method comprising contacting a target site in the endogenous myrosinase gene, the endogenous *AOP2*2-oxo acid-dependent dioxygenase gene and/or the endogenous *CYP79F1*results in a 2-oxo acid-dependent dioxygenase gene in the mustard plant or plant part with a nuclease linked to a DNA binding domain (e.g., editing system) that binds to the target site, thereby producing a mustard plant or part thereof comprising at least one cell having a mutation in the endogenous myrosinase gene, the endogenous *AOP2* gene and/or the endogenous *CYP79F1* gene.

55. A method for producing a mustard plant having a phenotype of reduced pungency and/or reduced bitterness, comprising (a) contacting a mustard plant cell comprising a wild type endogenous myrosinase gene, a wild type endogenous *AOP2* gene and/or a wild type endogenous *CYP79F1* gene with a nuclease targeting the wild type endogenous myrosinase gene, the wild type endogenous *AOP2* gene or the wild type endogenous *CYP79F1* gene, wherein the nuclease is linked to a DNA binding domain that binds to a target site in the wild type endogenous wild type endogenous myrosinase gene, the wild type endogenous *AOP2* gene or the wild type endogenous *CYP79F1* gene, (b) growing the plant cell into a mustard plant, thereby producing a mustard plant having a phenotype of reduced pungency and/or reduced bitternessnucleotide sequence of any one of **SEQ ID NOs:600-616** or **800-816**.

~~56. A method for producing a mustard plant or part thereof comprising at least one cell having a mutated endogenous myrosinase gene, a mutated endogenous *AOP2* gene and/or a mutated endogenous *CYP79F1* gene, the method comprising contacting a target site in an endogenous myrosinase gene, an endogenous *AOP2* gene and/or an endogenous *CYP79F1* gene in the mustard plant or plant part with a nuclease comprising a cleavage domain and a DNA-binding domain, wherein the DNA binding domain binds to a target site in the endogenous myrosinase gene, the endogenous *AOP2* gene and/or the endogenous *CYP79F1* gene, thereby producing the plant or part thereof comprising at least one cell having a mutated endogenous myrosinase gene, a mutated endogenous *AOP2* gene and/or a mutated endogenous *CYP79F1* gene.~~

~~57~~18. A method of producing a mustard plant or part thereof comprising a mutated endogenous myrosinase gene, a mutated endogenous *AOP2* gene and/or a mutated endogenous *CYP79F1* gene and having a phenotype of reduced pungency and/or bitterness, the method comprising contacting a target site in an endogenous myrosinase gene, an endogenous *AOP2* gene and/or an endogenous *CYP79F1* gene with a nuclease comprising a cleavage domain and a DNA binding domain (e.g., editing system) comprising a nucleic acid binding domain that binds to the target site in the endogenous myrosinase gene, the endogenous *AOP2* gene and/or the endogenous *CYP79F1* gene, thereby producing a mustard plant or part thereof comprising a mutated endogenous myrosinase gene, a mutated endogenous *AOP2* gene and/or a mutated endogenous *CYP79F1* gene and having reduced pungency and/or bitterness.

~~58. The method of any one of claims 53-57, wherein the nuclease cleaves the endogenous myrosinase gene, the endogenous *AOP2* gene and/or the endogenous *CYP79F1* gene and a mutation is introduced into the endogenous myrosinase gene, the endogenous *AOP2* gene and/or the endogenous *CYP79F1* gene.~~

~~59. The method of any one of claims 53, 54 or 58, wherein the mutation is a non-natural mutation.~~

~~60. The method of any one of claims 53, 54, 58 or 59, wherein the mutation is a dominant-negative allele, semi-dominant allele, weak loss of function allele, null allele, a hypermorphic mutation or a hypomorphic mutation.~~

~~61. The method of any one of claims 53, 54, 58, 59 or 60, wherein the mutation is a full knockout mutant CYP79F1 allele, a full knockout mutant AOP2 allele and/or a full knockout mutant myrosinase allele.~~

~~62. The method of claim 61, wherein the full knockout mutant CYP79F1 allele results in the production of a nonfunctional CYP79F1 protein or no production of a CYP79F1 protein, the full knockout mutant AOP2 allele results in the production of a nonfunctional AOP2 protein or no production of a AOP2 protein, the full knockout mutant myrosinase allele results in the production of a nonfunctional myrosinase protein or no production of a myrosinase protein.~~

~~63. The method of any one of claims 53, 54, 58, or 59-62~~19. The method of claim 18, wherein the mutation is a base substitution, a base insertion and/or a base deletion.

~~64~~20. The method of claim ~~63~~18 or claim 19, wherein the ~~base deletion is an in-frame deletion or an out-of-frame deletion.~~

~~65. The method of any one of claims 53, 54, 58, or 59-64, wherein the mutation results in a premature stop codon.~~

~~66. The method of any one of claims 53, 54, 58, or 59-65, wherein the mutation of the~~mutated endogenous myrosinase gene~~, the endogenous *AOP2* gene and/or the endogenous *CYP79F1* gene results in a truncated CYP79F1 protein, a truncated AOP2 protein, and/or a truncated myrosinase protein.~~

~~67. The method of any one of claims 53, 54, 58, or 59-66, wherein the mutation results in a phenotype of reduced pungency and/or reduced bitterness.~~

68. The method of any one of claims 53, 54, 58, or 59-67, wherein the nuclease is a zinc finger nuclease, a transcription activator-like effector nucleases (TALEN), an endonuclease (e.g. Fok1) or a CRISPR-Cas effector protein.

69. The method of any one of claims 53, 54, 58, or 59-68, wherein the DNA binding domain is a zinc finger, a transcription activator-like DNA binding domain (TAL), an argonaute or a CRISPR-Cas effector DNA binding domain.

70. A guide nucleic acid (e.g., gRNA, gDNA, crRNA, crDNA) that binds to a target site in an endogenous myrosinase gene, in an endogenous *AOP2* gene or in an endogenous *CYP79F1* gene.

71. The guide nucleic acid of claim 70, wherein the guide nucleic acid comprises a spacer sequence having the nucleotide sequence of **SEQ ID NO:115** or **SEQ ID NO:116**, any one of **SEQ ID NOs:105-111**, or any one of **SEQ ID NOs:132-139**.

72. A system comprising the guide nucleic acid of claim 70 or claim 71 and a CRISPR-Cas effector protein that associates with the guide nucleic acid.

73. The system of claim 72, further comprising a tracr nucleic acid that associates with the guide nucleic acid and a CRISPR-Cas effector protein, optionally wherein the tracr nucleic acid and the guide nucleic acid are covalently linked.

74. A gene editing system comprising a CRISPR-Cas effector protein in association with a guide nucleic acid, wherein the guide nucleic acid comprises a spacer sequence that binds to an endogenous myrosinase gene, in an endogenous *AOP2* gene or in an endogenous *CYP79F1* gene.

75. The gene editing system of claim 74 , wherein the guide nucleic acid comprises a spacer sequence having at least 80% identity to the nucleotide sequence of **SEQ ID NO:115** or **SEQ ID NO:116**, to the nucleotide sequence of any one of **SEQ ID NOs:105-111**, or to the **141-599**, the mutated endogenous cytochrome P450 mono-oxygenase gene comprises a nucleotide sequence of any one of **SEQ ID NOs:132-139**.

~~76. The gene editing system of claim 74 or claim 75, further comprising a tracr nucleic acid that associates with the guide nucleic acid and a CRISPR-Cas effector protein, optionally wherein the tracr nucleic acid and the guide nucleic acid are covalently linked.~~

~~77. A complex comprising a CRISPR-Cas effector protein comprising a cleavage domain and a guide nucleic acid, wherein the guide nucleic acid binds to a target site in an endogenous myrosinase gene, in an endogenous *AOP2* gene or in an endogenous *CYP79F1* gene, wherein the cleavage domain cleaves a target strand in the endogenous myrosinase gene, in the endogenous *AOP2* gene or in the endogenous *CYP79F1* gene.~~

~~78. An expression cassette comprising a (a) polynucleotide encoding CRISPR-Cas effector protein comprising a cleavage domain and (b) a guide nucleic acid that binds to a target site in an endogenous myrosinase gene, in an endogenous *AOP2* gene or in an endogenous *CYP79F1* gene.~~ **~~SPEC~~** ~~wherein the guide nucleic acid comprises a spacer sequence that is complementary to and binds to a sequence having at least 80% sequence identity to at least a portion of a sequence having at least 80% sequence identity to the~~ **788-799**, and/or the mutated endogenous 2-oxo acid-dependent dioxygenase gene comprises a nucleotide sequence of any one of **SEQ ID NOs:~~66-91~~, ~~SEQ ID NO:112~~, ~~SEQ ID NO:113~~,** or **~~SEQ ID NOs:117-126~~**, ~~optionally wherein a portion is about 2 to about 22 consecutive nucleotides in length~~**600-616** or **800-816**.

~~79. A nucleic acid encoding a dominant-negative allele, semi-dominant allele, weak loss of function allele, null allele, a hypermorphic mutation or a hypomorphic mutation of a myrosinase, a CYP79F1 or an AOP2.~~

~~80. The nucleic acid of claim 79, wherein the nucleic acid encodes a null allele that is a full knockout mutant CYP79F1 allele, a full knockout mutant AOP2 allele and/or a full knockout mutant myrosinase allele.~~

~~81. The nucleic acid of claim 80, wherein the full knockout mutant CYP79F1 allele results in the production of a nonfunctional CYP79F1 protein or no production of a CYP79F1 protein, the full knockout mutant AOP2 allele results in the production of a nonfunctional AOP2 protein or~~

no production of a AOP2 protein, the full knockout mutant myrosinase allele results in the production of a nonfunctional myrosinase protein or no production of a myrosinase protein.

8221. A mustard plant or part thereof comprisingproduced by the nucleic acidmethod of any one of claims 79-81.

83. The mustard plant or part thereof of claim 8214-20, wherein the plant or part thereof exhibits reduced pungency and/or reduced bitterness.,

84. The mustard plant or part thereof of claim 82 or claim 83optionally, wherein the mustard plant or part thereof is a kale plant or part thereof, a collard plant or part thereof, a spinach plant or part thereof, a cabbage plant or part thereof, a beet plant or part thereof, a watercress plant or part thereof, a lettuce plant or part thereof (e.g. romaine), a swiss chard plant or part thereof, an arugula plant or part thereof, an endive plant or part thereof, a bok choy plant or part thereof, a rutabaga plant or part thereof, a turnip plant or part thereof, a mustard plant or part thereof, a cabbage plant or part thereof, a broccoli plant or part thereof, a cauliflower plant or part thereof, a Brussels sprout plant or part thereof, a radish plant or part thereof, or a kohlrabi plant or part thereof.

85. The mustard plant or part thereof of any one of claims 82 to 84, wherein the plant or part thereof *is Brassica oleracea* (e.g., *B. oleracea* var. *oleracea*, *B. oleracea* var. *capitata*, *B. oleracea* var. *botrytis*, *B. oleracea* var. *gemmifera*, *B. oleracea* var. *sabauda*, *B. oleracea* var. *gongyiodes*, *B. oleracea* var. *italic*, *B. oleracea* var. *sabellica*, *B. oleracea* var. *acephala*), *Brassica juncea*, *Brassica rapa* (*B. rapa* subsp. *pekinensis*, *B. rapa* subsp. *Chinensis*, *B. rapa* subsp. *rapa*), *Brassica napas*, *Brassica carinata*, *Brassica campestris*, *Brassica nigra* or *Raphanus raphanistrum* (e.g., *Raphanus raphanistrum* subsp. *Sativus*).

86. A method of producing a mustard plant having at least one myrosinase gene and/or by at least one *AOP2* gene and/or by a *CYP79F1* gene with reduced expression (e.g., 5%-100% reduced), and/or reduced production (e.g., 5%-100% reduced) of at least one myrosinase, at least one AOP2 or a CYP79F1, the method comprising (a) contacting a population of mustard plant

~~cells comprising a DNA sequence that encodes a wild type endogenous myrosinase, a wild type endogenous *AOP2* and/or a wild type endogenous *CYP79F1* with (i) a nuclease linked to a nucleic acid binding domain (e.g., editing system) that binds to a target sequence in the wild type endogenous myrosinase, the wild type endogenous *AOP2* or the wild type endogenous *CYP79F1*, (ii) an RNAi that targets the wild type endogenous myrosinase, the wild type endogenous *AOP2* or the wild type endogenous *CYP79F1*, or (iii) or an siRNA that targets the wild type endogenous myrosinase, the wild type endogenous *AOP2* or the wild type endogenous *CYP79F1*, (b) selecting a mustard plant cell from said population having reduced expression of at least one myrosinase gene, of at least one *AOP2* gene or of the *CYP79F1* gene, and/or reduced production of the at least one myrosinase, the at least one AOP2 or the CYP79F1; and (c) growing the selected plant cell into a mustard plant.~~

~~87. A mustard plant produced by the method of claim 86.~~

~~88. The mustard plant of claim 87, wherein the plant or a part thereof exhibits reduced pungency and/or reduced bitterness.~~

~~89. A mustard plant comprising an RNAi or a siRNA that is complementary to at least one myrosinase gene, at least one *AOP2* gene and/or a *CYP79F1* gene and reduced expression of the at least one myrosinase gene, the at least one *AOP2* gene and/or the *CYP79F1* gene.~~