CoverCress

CBI-Deleted Copy

RECEIVED
By ajdrummond for BRS Document Control Officer at 2:50 pm, Apr 03, 2024

4/3/2024
Bernadette Juarez
U.S. Department of Agriculture
APHIS Deputy Administrator
Biotechnology Regulatory Services

Dear Deputy Administrator Juarez,

With this letter we respectfully request a Regulatory Status Review from USDA-APHIS's Biotechnology Regulatory Services (BRS) for the following Plant Trait Mechanism of Action: *Thlaspi arvense* L. (pennycress; field pennycress) CRISPR/Cas9 generated mutant lines, featuring disruption of any combination of: *FAE1* to produce a low erucic acid phenotype; *TT8* to produce a lower fiber phenotype; and [ ] to produce a lower glucosinolate phenotype. These PTMOA's are described in previously submitted RSR's 22-069-01rsr, 22-292-01rsr, 23-264-01rsr, 23-342-01rsr, 23-355-01rsr, 24-064-01rsr, and 24-065-01rsr. CBI-Deleted

USDA has previously evaluated pennycress lines with the same phenotypes as the PTMOA's in this RSR via the AIR and RSR processes. Disruption of *TT8* and *FAE1* were reviewed in several AIR letters[1], and in the recently reviewed 22-069-01rsr and 22-292-01rsr, the USDA did not identify any plausible pathway by which the modified plants would pose an increased plant pest risk. Lines containing disruptions in genes (*AOP2*, [ ]) that are in the same biosynthesis pathway and that exhibit the same phenotype as our third trait [ ], were evaluated in AIR requests[2]. *AOP2*, [ ] are examples of several genes that, when disrupted, reduce glucosinolate levels in pennycress. This RSR requests evaluation of pennycress with mutations in one of the aforementioned genes [ ] in addition to two other genes [ ] resulting in the same low glucosinolate phenotype, in combination with the previously evaluated disruptions in *TT8* and *FAE1*. In response to each of several previously submitted AIR letters, BRS deregulated pennycress lines harboring disruptions in *AOP2,* [ ], and other genes, concluding that: "…your genome edited pennycress lines are not themselves plant pests". USDA additionally stated in several AIR response letters that pennycress is not listed as a Federal noxious weed pursuant to 7 CFR part 360 and USDA has no reason to believe that the intended phenotypes of the pennycress lines would increase the weediness of pennycress.

CBI-Deleted
CBI-Deleted
CBI-Deleted
CBI-Deleted (2)
CBI-Deleted
CBI-Deleted

Further, via the confirmation of exemption process, single edits in the [ ] (22-336-01cr), [ ] (23-107-01cr), and [ ] (22-336-02cr) genes have been deemed "achievable by conventional breeding and unlikely to pose an increased plant pest risk relative to their conventionally bred counterparts".

CBI-Deleted
CBI-Deleted (2)

[1] Illinois State University, USDA response August 8, 2018; Illinois State University, USDA response April 9, 2019; Cover Cress, Inc., USDA response January 29, 2020; CoverCress, Inc., USDA response May 7, 2020; CoverCress, Inc., USDA response August 31, 2020

[2] Cover Cress, Inc., USDA response January 29, 2020; CoverCress, Inc., USDA response May 7, 2020; CoverCress, Inc., USDA response August 31, 2020; Illinois State University, USDA response August 24, 2020

CoverCress

CBI-Deleted Copy

**1. Information about Requestor**

**First Name:** Marcia

**Last Name:** Weldon

**Position:** Regulatory & Stewardship Manager

**Organization Name (if applicable):** CoverCress, Inc.

**Contact information (choose one or both)**

**Telephone:** [ ] CBI-Deleted

**Email address:** mweldon@covercress.com

**2. Does the request contain Confidential Business Information (CBI)?**

Yes, this RSR request contains CBI.

This RSR for gene-edited pennycress contains confidential business information that could harm CoverCress, Inc. if publicly disclosed prior to publication of patent applications or other disclosures with that information. The specific information that could cause competitive harm are the names and sequences of the low glucosinolate target genes, as well as the specific modifications and the mechanism of action. Premature disclosure of that information could allow competitors to develop competitive products much more quickly than if the information was kept as CBI and/or trade secret. CoverCress, Inc. treats this information as private both customarily and actually and provides this information to the government under an assurance of privacy. The information is confidential within the meaning of 5 U. S. C. §552(b)(4), the Freedom of Information Act's Exemption 4.

**3. Description of the comparator plant:**

**Scientific name (genus, species):** *Thlaspi arvense*

**Common Name:** pennycress; field pennycress; CoverCress®

**Subspecies / Cultivar / Breeding Line:**

Field pennycress is an oilseed crop undergoing domestication for use as an alternative source of biofuel and feedstock. Besides the economic benefit(s), the crop will provide ecosystem services as a cover crop in a two-year corn-soybean rotation. Although a prolific seed producer, interspecific hybridization is uncommon in the genus *Thlaspi* and there are no reports of interspecific hybrids with *Thlaspi arvense* (Al-Shehbaz, 1986; Best & McIntyre, 1975; Warwick et al., 2002).

CoverCress, Inc. has developed, through selection and breeding, several elite germplasm pennycress lines that have optimized agronomic characteristics. The improved germplasm are referred to as CoverCress® lines. It is envisioned that current and future lines from the breeding program, optimized for commercial production, will undergo late stage editing to produce the low erucic acid, lower fiber, lower glucosinolate phenotypes.

## 4. Genotype of the modified plant (if genetic material is not inserted into the genome):

### Nature of modification(s):

Mutations will be introduced into pennycress cultivars using a CRISPR/SpCas9 DNA construct designed to target genomic edits to the *FAE1*, *TT8*, [ ] genes. This transgene construct will be delivered to the plant using a disarmed *Agrobacterium tumefaciens* strain (GV3101) and a standard floral dip transformation method. When integrated into the plant genome, the expressed *Streptococcus pyogenes* CRISPR-associated protein 9 (SpCas9) endonuclease will be guided to five unique, targeted loci (the *FAE1*, *TT8*, [ ] genes). At these locations, the SpCas9 endonuclease will catalyze double-stranded DNA breaks, which would then be repaired by the plant's error-prone endogenous non-homologous end joining (NHEJ DNA) repair mechanisms, resulting in heritable mutations at the targeted loci. CBI-Deleted CBI-Deleted

The design pipeline has two steps to ensure the gRNA is specific to the gene and to reduce off-targeting. First, an online gRNA design tool that has an inbuilt pennycress genome is used to identify gRNA target sites and provide a list of putative off-target sites. Furthermore, a blast search is performed with a candidate protospacer sequence against the pennycress genome to avoid the use of a protospacer with potential off targets.

DsRED fluorescent protein from Discosoma will be included in the plasmid to confer red fluorescence in plants that successfully take up the plasmid introduced by *A. tumefacians*. The presence of the edits in $T_1$ plants will be confirmed through visualization of red fluorescent protein under a light system and confirmatory PCR screening of a fragment of the T-DNA. Seed from the progeny $T_2$ generation will then be screened for segregants that do not have the transgene as indicated by lack of red fluorescence. Resulting seedlings in the $T_2$ generation will be screened again for negative presence of DsRED and Cas, as well as homozygous edits to *FAE1*, *TT8*, [ ]. CBI-Deleted

Examples of these edits are listed in the following section.

### Sequence and Comparison of each Modification

*FAE1, Fatty Acid Elongation 1*

The top line of the following sequence comparison is the unmodified sequence of *FAE1*. One representative modified gene sequence of *FAE1* is included for comparison. One site in the gene is edited and includes a single A insertion, highlighted in red. The full gene sequences and sequence comparison are included in Appendix 1.

```
Ta_FAE1_WT    GCCTTCACCGTTTTCGGTTTGGCTCTCTACATCGTAA-CCCGGCCCAAACCGGTTTACCT
Ta_fae1_Mut   GCCTTCACCGTTTTCGGTTTGGCTCTCTACATCGTAAACCCGGCCCAAACCGGTTTACCT
              ************************************ ********************
```

*TT8*, *Transparent Testa 8*

The top line of the following sequence comparison is the unmodified sequence of *TT8*. A representative modified gene sequence of *TT8* is included for comparison. One site in the

gene is edited and includes a single G insertion, highlighted in red. The full gene sequences and sequence comparison are included in Appendix 1.

```
Ta_TT8_WT     GGGAGAATGGATACTACAACGGTGCAATAAAG-ACGAGGAAGACAACTCAGCCGGCGGAA
Ta_tt8_Mut    GGGAGAATGGATACTACAACGGTGCAATAAAGGACGAGGAAGACAACTCAGCCGGCGGAA
              ****************************** **************************
```

[ ] CBI-Deleted

The top line of the following sequence comparison is the unmodified sequence of the [ ] CBI-Deleted gene. One representative modified gene sequence of [ ] is included for comparison. One CBI-Deleted site in the gene is edited and includes a single T insertion, highlighted in red. The full gene sequences and sequence comparison are included in Appendix 1.

[

CBI-Deleted

]

[ ] CBI-Deleted

The top line of the following sequence comparison is the unmodified sequence of the [ ] CBI-Deleted gene. One representative modified gene sequence of [ ] is included for comparison. CBI-Deleted One site in the gene is edited and includes a 2 bp deletion, highlighted in red. The full gene sequences and sequence comparison are included in Appendix 1.

[

CBI-Deleted

]

[ ] CBI-Deleted

The top line of the following sequence comparison is the unmodified sequence of [ ]. CBI-Deleted One representative modified gene sequence of [ ] is included for comparison. One site CBI-Deleted in the gene is edited and includes a single T insertion, highlighted in red. The full gene sequences and sequence comparison are included in Appendix 1.

[

CBI-Deleted

]

## 5. Description of new trait

**Intended trait #1:** low erucic acid seeds

**Intended phenotype #1:** low accumulation of erucic acid in seeds

Erucic acid in seed oil in homozygous *fae1* mutants is consistently <2% of total fatty acids, compared with >35% of total fatty acids in wild-type pennycress seeds (Chopra et al., 2018a;

Chopra et al., 2020; McGinn et al., 2019). The fatty acid profile of homozygous *fae1* mutants is comprised predominantly of oleic acid (C18:1), linoleic acid (C18:2) and linolenic acid (C18:3), which have known nutritional and energy value.

**Intended trait #2:** lower fiber seeds

**Intended phenotype #2:** yellow seed (as a marker for lower fiber)

In homozygous *tt8* mutants, the seed coats of pennycress are light yellow colored in contrast to the naturally dark seeds produced by wild-type pennycress, signifying the absence or reduction of condensed tannins in the seed coat. These seeds contain lower levels of undigestible fiber, and thus, higher metabolizable energy for animal feed.

In a composition study of several light-colored pennycress mutants versus 95 wild type pennycress accessions harvested at various locations across the USA, NIR spectroscopy analysis revealed that the light-colored pennycress contained 10-19.7% Acid Detergent Fiber (ADF) and 13.1-24.1% Neutral Detergent Fiber (NDF), while the dark-colored pennycress contained 20.8-37.9% ADF and 26.3-35.1% NDF (Ulmasov et al., 2020). Additional composition studies consistently show a 25-37% reduction in various fiber components relative to the dark wild type seed (Ulmasov et al., 2020). The lower fiber (yellow seed) phenotype is also associated with more consistent germination and reduced seed dormancy, a major factor in the weediness of this plant (Chopra et al., 2018a; Koirala et al., 2023; Ott et al., 2021).

**Intended trait #3:** reduced glucosinolate seeds

**Intended phenotype #3:** low accumulation of total glucosinolates in seeds; reduction of total glucosinolate levels to below 30 µmol/g of total seed weight

Pennycress contains high levels of oil (~25-35%) that makes it a desirable ultra-low carbon fuel feedstock (Altendorf et al. 2019; McGinn et al. 2019; Moser et al. 2009). In addition to this primary value for fuel, the seed could provide an energy source for animal feeds such as chicken feed. Field pennycress or CoverCress® also contains 80-110µmol/g glucosinolates derived through the aliphatic glucosinolate pathway (Chopra et al., 2018a; Chopra et al., 2020; Sedbrook et al., 2014). Glucosinolates are biologically active compounds found in the Brassicaceae family of plants, including broccoli, cabbage, cauliflower, rapeseed, mustard, and horseradish, and provide defense mechanisms for plants. Over 200 types of glucosinolates are found in brassicas (Prieto et al., 2019); pennycress contains the glucosinolate sinigrin (Chopra et al., 2020). Sinigrin and its metabolite allyl isothiocyanate can reduce palatability of food and feed at lower levels and result in toxic effects at higher levels. Therefore, presence of glucosinolates (which is almost all sinigrin) in field pennycress or CoverCress® impacts the ability to include the seed or meal in feed applications above limited inclusion rates (Chopra et al., 2020).

**Description of each MOA:**

**Low erucic acid MOA**

Field pennycress contains high levels of oil (~25-35%) that makes it a desirable ultra-low carbon fuel feedstock (McGinn et al., 2019; Moser et al., 2009; Sedbrook et al., 2014). In addition to this primary value for fuel, the seed, meal and/or oil could provide an energy source for animal feeds. The utility of pennycress for this use, however, is limited by the fact that the oil contains >35% erucic acid (Altendorf et al., 2019; McGinn et al., 2019). Erucic acid is a 22-carbon monounsaturated acid that is absorbed, distributed, and metabolized like other fatty acids involving primarily metabolism via mitochondrial beta-oxidation and, to a lesser extent, peroxisomal beta-oxidation. Like other longer-chain fatty acids, the rate of mitochondrial beta oxidation is comparatively lower for erucic acid; however, elevated erucic acid levels induce liver peroxisomal oxidation pathways as a mechanism of compensation. Interest in the safety of erucic acid occurred when results of studies in rats associated the dietary intake of high doses of erucic acid with myocardial lipidosis and heart lesions. Oilseed rape conventionally contains similarly high levels of erucic acid. Low erucic acid varieties were identified and marketed as canola, which have been shown to be safe for inclusion in animal feed.

Reduction in erucic acid is achieved through disruption of *fatty acid elongation 1* (*FAE1*) (Figure 1), resulting in higher levels of oleic (18:1) (Qiu et al., 2006). It is through this same mechanism that erucic acid levels are lowered in pennycress (McGinn et al., 2019). The edit to *FAE1* causes a frameshift which results in a premature stop codon and a truncated, non-functional protein.

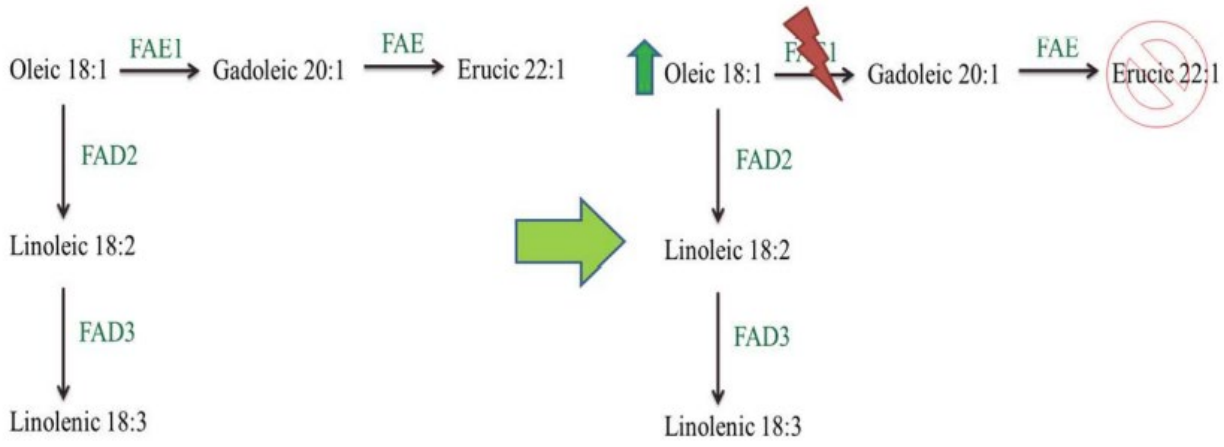


**Figure 1:** Fatty Acid Pathway to Reduce Erucic Acid Levels

**Lower fiber MOA**

Field Pennycress is high in fiber (level is variable, but Acid Detergent Fraction values of up to 40% mass on a dry weight basis have been observed (Ulmasov et al., 2020), which can impact digestibility as a feed ingredient.

The production of seed coat fiber was first characterized in the model plant Arabidopsis. Arabidopsis seed coats derive their brown color from the accumulation of proanthocyanidins (PAs), a class of flavonoid chemicals (polymerized flavan-3-ols, or condensed tannins) that protect against a variety of biotic and abiotic stresses and help maintain seed dormancy and viability (Debeaujon et al., 2003). PAs start out as colorless epicatechin compounds until they are transported to the vacuole where they are polymerized and oxidized as the seed desiccates. In Arabidopsis, PAs are only produced in a narrowly defined cell layer in the endothelium of the seed, and TTG1, TT8/bHLH042, and TT2/MYB123 have been demonstrated as being the three main regulators of PA biosynthesis in seed coat (Baudry et al., 2004; Lepiniec et al., 2006). Gonzalez et al. (2009) described how TTG1 works in a complex with a particular combination of MYB class and bHLH class transcription factors to regulate epidermal development of the seed coat (Figure 2).

Loss-of-function mutants in these genes exhibit the transparent "testa" phenotype as a result of low levels of oxidized PAs in the seed coat (Chopra et al., 2018b). The transparent testa phenotype has been observed in brassicas, including canola, and is characterized by yellow seeds that have more oil because of the resulting thinner seed coat and larger embryo (Abraham and Bhatia, 1986). Meal from these brassicas have also been shown to be useful in animal feed because of the relatively lower fiber and higher metabolizable energy (Simbaya et al., 1995; Slominski et al., 1994 and 1999). Similarly, the transparent testa phenotype was observed with loss-of-function mutations in orthologs of these genes in pennycress, resulting in reduced fiber content (Chopra et al., 2018b). In CoverCress® the *TT8* gene was edited for loss of function. The edit to *TT8* causes a frameshift which results in a premature stop codon and a truncated, non-functional protein.

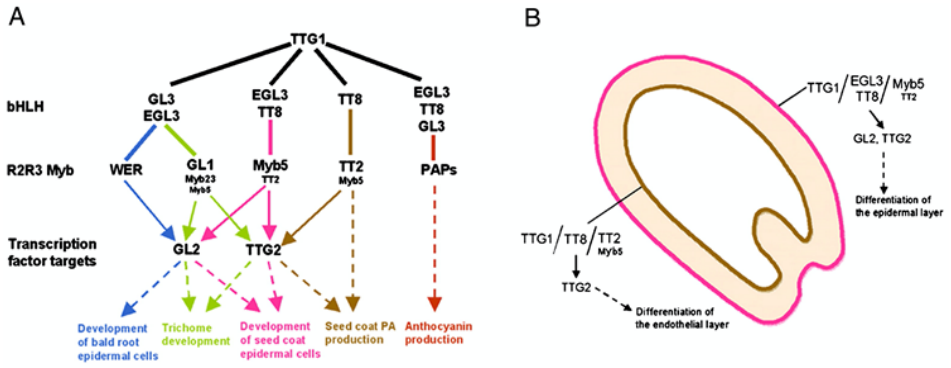


**Figure 2:** Models for the regulation of TTG-1 dependent pathways in seed coat development. (A) A regulatory network for the positive control of TTG1-dependent epidermal cell fates.

Solid lines indicate interactions between members of a complex. Solid arrows indicate direct regulation of *GL2* or *TTG2* targets. Dashed arrows indicate a multi-step differentiation pathway. Colored lines and arrows indicate specific regulator combinations and the pathway controlled. Text size in the case of the MYBs indicates their relative contributions to cell fate regulation. (B) A regulatory model for the differentiation of the seed coat outer and inner layers specified by specific TTG1-dependent transcriptional complexes. Text size in the case of MYB5 and TT2 MYBs indicates their relative contributions to the development of the outer and inner testa layers (Figure from Gonzalez et al., 2009).

**Low total glucosinolate MOA**

Glucosinolates are secondary metabolites important for plant defense during development and exposure to biotic and abiotic environmental conditions, as well as helpful in the suppression of weeds. Sønderby et al. (2010) gives an overview of the glucosinolate biosynthesis pathway. Glucosinolate biosynthesis in brassicas requires three steps, outlined in Figure 3: 1) amino acid chain elongation, 2) oxidation and sulfation to generate the core glucosinolate structure and 3) secondary side chain modifications to generate unique forms of glucosinolates. Levels of glucosinolate in the seed are regulated by transporters. There are more than 200 glucosinolates identified and classified in brassicas. Field pennycress or CoverCress® contains 80-100µmol/g glucosinolates in the form of sinigrin (>99% of the glucosinolate found in pennycress) derived through the aliphatic glucosinolate pathway (Chopra et al., 2018a; Chopra et al., 2020; Sedbrook et al., 2014).

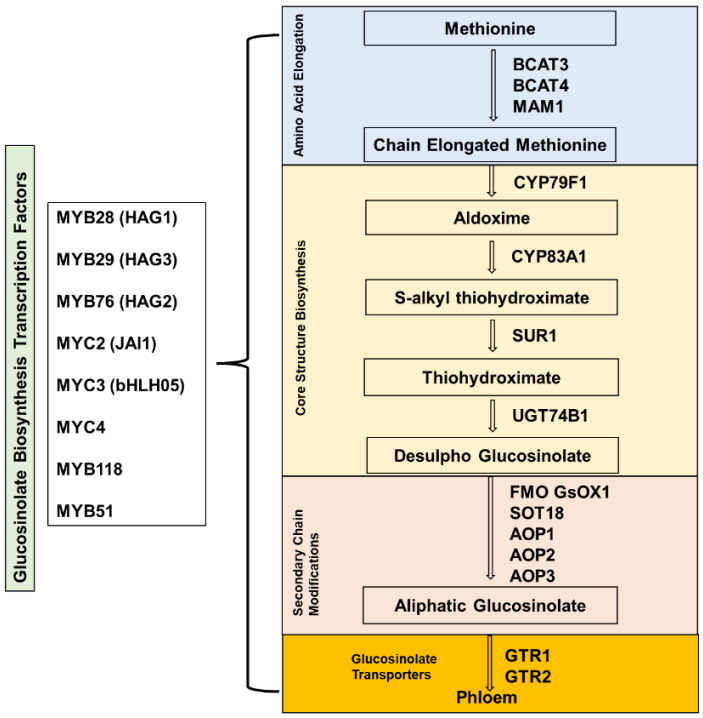


**Figure 3:** Major steps in glucosinolate biosynthesis

The rationale for gene target selection was to identify those genes that could result in reduced glucosinolate levels in the seed through a combination of reduced production and mobilization, but do not impact other biosynthetic pathways or cause accumulation of glucosinolates in other parts of the plant. To reach the desired 70-80% reduction in glucosinolate levels will require loss of function mutations in a combination of gene targets in this RSR request.

These three targets include transcription factors ([ ]), and transporter ([ ]). CBI-Deleted (2)
The genes and their respective contribution to achieve reduced glucosinolate levels are described below.

[ ] encodes a high-affinity, proton-dependent glucosinolate-specific transporter that is CBI-Deleted
crucial for the transport of both methionine- and tryptophan-derived glucosinolates to seeds
[ ]. Gene edited alleles for loss of function of [ ] in pennycress CBI-Deleted (2)
resulted in a reduction in sinigrin levels compared to wild type, with no impact on other biosynthetic pathways or observed accumulation of glucosinolates in other parts of the plant. The representative edited allele for [ ] provided has a 1-bp insertion that causes CBI-Deleted
a frameshift which results in a premature stop codon and a truncated, non-functional protein. Evidence from both greenhouse and field studies demonstrates that plants with this loss of function grow normally throughout their lifecycle unlike observations in *Brassica juncea* (Tan et al. 2022).

[ ] is a MYB protein that directly regulates the expression of aliphatic CBI-Deleted
glucosinolates biosynthesis in brassicas [ ]. The representative edited CBI-Deleted
allele for [ ] has a 2-bp deletion that causes a frameshift which results in a premature CBI-Deleted
stop codon and a truncated, non-functional protein. This results in a reduction in sinigrin levels compared to wild type. Evidence from greenhouse and field studies demonstrates that plants grow normally throughout their lifecycle and no apparent reduction in plant height or changes in leaf morphology have been observed.

[ ] is a bHLH protein that is known to interact directly with glucosinolate-related CBI-Deleted
transcription factors, and it helps coordinate expression of several biosynthesis genes
required to accumulate glucosinolate [ ]. We generated alleles in CBI-Deleted
pennycress to test this hypothesis and found via RT-PCR that genes involved in glucosinolate biosynthesis were reduced significantly in various stages of plant development. The representative edited allele for [ ] has a 1-bp insertion that causes a frameshift which CBI-Deleted
results in a premature stop codon and a truncated, non-functional protein. [ ] CBI-Deleted
pennycress edits will have a reduction in sinigrin levels compared to its co-grown wild type. Evidence from both greenhouse and field studies demonstrates that plants grow normally throughout their lifecycle and no apparent reduction in plant height or changes in leaf morphology have been observed.

To achieve meaningful reduction in glucosinolate levels, knockouts in multiple gene targets across the various stages of production and transport are needed to reach the phenotype goal of below 30 µmol/g of total seed weight.

## References

Abraham, V., Bhatia, C. R., (1986). Development of Strains with Yellow Seedcoat in Indian Mustard (*Brassica juncea* Czern. & Coss.). *Plant Breeding*, 97, 86–88.

Al-Shehbaz, I. A. (1986). The genera of Lepidieae (Cruciferae; Brassicaceae) in the southeastern United States. *J. Arnold Arbor.,* Harv. Univ., 67, 265–311.

Altendorf, K., Isbell, T., Wyse, D. L., Anderson, J. A. (2019). Significant variation for seed oil content, fatty acid profile, and seed weight in natural populations of field pennycress (*Thlaspi arvense* L.). *Industrial crops and products,* 129, 261-268. DOI:10.1016/j.indcrop.2018.11.054

Baudry, A., Heim, M. A., Dubreucq, B., Caboche, M., Weisshaar, B., Lepiniec, L. (2004). *TT2*, *TT8*, and *TTG1* synergistically specify the expression of *BANYULS* and proanthocyanidin biosynthesis in *Arabidopsis thaliana*. *Plant J*, 39, 366-380.

Best, K. F., & McIntyre, G. I. (1975). The Biology of Canadian Weeds. Can. J. Plant Sci., 55, 279–292.

Chopra, R., Folstad, N., Lyons, J., Ulmasov, T., Gallaher, C., Sullivan, L., McGovern, A., Mitacek, R., Frels, K., Altendorf, K., Killam, A., Ismail, B., Anderson, J. A., Wyse, D. L., Marks, M. D. (2018a). The adaptable use of Brassica NIRS calibration equations to identify pennycress variants to facilitate the rapid domestication of a new winter oilseed crop. *Industrial crops and products, 128*, 55-61. DOI:10.1016/j.indcrop.2018.10.079

Chopra, R., Johnson, E. B., Daniels, E., McGinn, M., Dorn, K. M., Esfahanian, M., Folstan, N., Amundson, K., Altendorf, K., Betts, K., Frels, K., Anderson, J. A., Wyse, D. L., Sedbrook, J. C., Marks, M. D. (2018b). Translational genomics using Arabidopsis as a model enables the characterization of pennycress genes through forward and reverse genetics. *Plant J.,* Dec, 96(6), 1093-1105. DOI:10.1111/tpj.14147. PMID: 30394623

Chopra, R., Johnson, E. B., Emenecker, R., Cahoon, E. B., Lyons, J., Kliebenstein, D. J., Daniels, E., Dorn, K. M., Esfahanian, M., Folstad, N., Frels, K., McGinn, M., Ott, M., Gallaher, C., Altendorf, K., Berroyer, A., Ismail, B., Anderson, J. A., Wyse, D. L., Marks, M. D. (2020). Identification and stacking of crucial traits required for the domestication of pennycress. *Nature Food*, *1*(1), 84-91. DOI:10.1038/s43016-019-0007-z

Debeaujon, B. P., Stupar, R. M., Gingerich, D. J., Vierstra, R. D. (2003). Proanthocyanidin-accumulating cells in *Arabidopsis* testa: regulation of differentiation and role in seed development. Plant Cell, 15, 2514-2531.

Gonzalez, A., Mendenhall, J., Huo, Y., Lloyd, M. (2009). TTG1 complex MYBs, MYB5 and TT2,

control outer seed coat differentiation. *Dev. Biol.*, 325, 412-421.

[

CBI-Deleted

]

Koirala, N., Barker, D. J., Gesch, R. W., Heller, N. J., Hard, A. W., Wells, S. S., Phippen, W. B., Lindsey, A. J. (2023). Seed pelleting and storage effects on germination of Pennycress (*Thlaspi arvense* L.). *Crop Science*, 1–12. DOI:10.1002/csc2.21077

Lepiniec, L., Debeaujon, I., Routaboul, J., Baudry, A., Pourcel, L., Nesi, N., Caboche, M. (2006). Genetics and biochemistry of seed flavonoids. *Annu. Rev. Plant Biol*., 57, 405-430.

McGinn, M., Phippen, W. B., Chopra, R., Bansal, S., Jarvis, B. A., Phippen, M. E., Dorn, K. M., Esfahanian, M., Nazarenus, T. J., Cahoon, E. B., Durrett, T. P., Marks, M. D., Sedbrook, J. C. (2019). Molecular tools enabling pennycress (*Thlaspi arvense*) as a model plant and oilseed cash cover crop. *Plant Biotechnol J*., Apr 17(4), 776-788. DOI:10.1111/pbi.13014. Epub 2018 Oct 25. PMID: 30230695; PMCID: PMC6419581

Moser, B. R., Shah, S. N., Winkler-Moser, J. K., Vaughn, S. F., Evangelista, R. L. (2009). Composition and physical properties of cress (*Lepidium sativum* L.) and field pennycress (*Thlaspi arvense* L.) oils. *Industrial Crops and products,* Sep 30 (2), 199-205. DOI:10.1016/j.indcrop.2009.03.007

[

CBI-Deleted

]

Ott, M. A., G. Gardner, K. M. Rai, D. L. Wyse, M. D. Marks, R. Chopra (2021) TRANSPARENT TESTA 2 allele confers major reduction in pennycress (*Thlaspi arvense* L.) seed dormancy, Industrial Crops and Products, Volume 174

Prieto, M. A., López, C. J., Simal-Gandara, J. (2019). Glucosinolates: Molecular structure, breakdown, genetic, bioavailability, properties and healthy and adverse effects. *Adv Food Nutr Res.,* 90, 305-350. DOI:10.1016/bs.afnr.2019.02.008. Epub Mar 25. PMID: 31445598

Qiu, D., Morgan, C., Shi, J., Long, Y., Liu, J., Li, R., Zhuang, X., Wang, Y., Tan, X., Dietrich, E., Weihmann, T., Everett, C., Vanstraelen, S., Beckett, P., Fraser, F., Trick, M., Barnes, S., Wilmer, J., Schmidt, R., Li, J., Bancroft, I. (2006). A comparative linkage map of oilseed rape and its use for QTL analysis of seed oil and erucic acid content. *Theoretical and applied genetics*, *114*(1), 67–80. DOI:10.1007/s00122-006-0411-2

[

CBI-Deleted

]

Sedbrook, J. C., Phippen, W. B., Marks, M. D. (2014). New approaches to facilitate rapid domestication of a wild plant to an oilseed crop: example pennycress (*Thlaspi arvense* L.). *Plant Sci.* 227, 122–132.

Simbaya, J, Slominski, B. A., Rakow, G., Campbell, L. D., Downey, R. K., Bell, J. M. (1995). Quality Characteristics of Yellow-Seeded Brassica Seed Meals: Protein, Carbohydrate, and Dietary Fiber Components. *Journal of Agricultural and Food Chemistry, 43* (8), 2062-2066.

Slominski, B. A., Simbaya, J., Campbell, L. D., Guenter, W. (1994). Carbohydrates and dietary fiber components of yellow and brown-seeded canola. *J. Agric. Food Chem.,* 42, 704–707.

Slominski, B. A., Simbaya, J., Campbell, L. D., Rakow, G., Guenter, W. (1999). Nutritive value for broilers of meals derived from newly developed varieties of yellow-seeded canola. *Animal Feed Science and Technology,* 78, 249-262.

Sønderby I. E., Geu-Flores, F., Halkier, B. A. (2010). Biosynthesis of glucosinolates – gene discovery and beyond, *Trends in Plant Science*, 15(5), 283-290, DOI:10.1016/j.tplants.2010.02.005

Tan, Z, Xie Z, Dai, L, Zhang, Y, Zhao, H, Tang, S, Wan, L, Yao, X, Guo, L, Hong, D (2022) Genome- and transcriptome-wide association studies reveal the genetic basis and the breeding history of seed glucosinolate content in *Brassica napus*. Plant Biotechnol J. Jan;20(1):211-225. DOI:10.1111/pbi.13707. Epub 2021 Oct 28. PMID: 34525252; PMCID: PMC8710833

Ulmasov, T., Hartnell, G., Sedbrook, J. C., Marks, M. D., Chopra, R., Esfahanian, M. (2020). Low fiber pennycress meal and methods of making (U.S. Patent No. 10,709,151). U.S. Patent and Trademark Office.

Warwick, S. I., Francis, A., & Susko, D. J. (2002). The biology of Canadian weeds. 9. *Thlaspi arvense* L. (updated). *Canadian journal of plant science*, *82*(4), 803-823.

## Appendix 1 – Full Sequences and Sequence Comparisons

**Unmodified and Modified Sequences of FAE1, TT8, [ ]** CBI-Deleted

Protospacer Sequence Highlighted Yellow, Edit Highlighted Red

*FAE1* Wild Type, Unmodified Sequence

*Ta FAE1* WT CDS:

ATGACGTCCGTTAACGTTAAGCTCCTTTACCATTACGTCATCACCAACTTTTTCAACCTTTGCTTCTTCCCG
TTAGCGGCGATCGTTGCCGGAAAAGCCTCTCGGCTTACCACAAACGATCTTCACCACTTCTACTATTCCTA
TCTCCAACACAACCTAATAACCATATCTCTACTCTTTGCCTTCACCGTTTTCGGTTTGGCTCTCTACATCGT
AACCCGGCCCAAACCGGTTTACCTCGTTGACCATTCCTGCTACCTTCCACCATCGCATCTTAGAAGCAGTA
TCTCTAAGGTCATGGATATCTTCTATCAAGTAAGATTAGCCGATCCTTTACGGAACGCGGCAAGCGATGA
TTCGTCCTGGCTTGATTTCTTGAGGAAGATTCAGGAGCGGTCTGGTCTAGGCGATGAAACCCACGGCCC
CGAGGGACTGCTTCAGGTCCCTCCACGGAAGACTTTTGCCGCGGCGCGTGAAGAAACAGAGCAAGTGA
TCATCGGTGCGCTCGAAAAACTATTCGAGAACACCAAAGTTAACCCTAAAGAGATTGGTATACTTGTGG
TGAACTCAAGCATGTTTAATCCGACTCCTTCGCTCTCGGCGATGGTTGTTAATACTTTCAAGCTCCGAAGC
AACATCAGAAGCTTTAATCTTGGAGGAATGGGTTGTAGTGCCGGCGTTATAGCCATTGATCTGGCTAAG
GACTTGTTGCATGTCCATAAAAACACTTATGCTCTTGTGGTGAGCACAGAGAACATCACTTACAACATTT
ATGCTGGTGATAACAGATCCATGATGGTTTCGAATTGCTTGTTCCGTGTTGGTGGGGCCGCGATTTTGCT
CTCCAACAAGCCGAGGGACCGGAGACGGTCCAAGTACCAGCTACTTCACACGGTTCGGACGCATACCG
GAGCTGACGACAAGTCTTTCCGATGTGTGCAACAAGAAGACGACGAGAGCGGTAAAACCGGGGTGTGT
TTGTCCAAGGACATAACCGGTGTTGCCGGGAGAACTGTTCAGAAAAACATAACAACATTGGGTCCGTTG
GTTCTTCCTTTTAGCGAGAAATTTCTTTTTTTCGTTACCTTCATCGCCAAGAAACTCTTTAAAGACAAGATC
AAACATTACTACGTCCCGGATTTCAAGCTTGCTATCGACCATTTTTGTATTCATGCCGGAGGCAGAGCCG
TGATCGATGTGCTACAGAAGAACTTAGGTCTATTGCCGATCGATGTGGAGGCATCTAGGTCAACGTTAC
ATAGATTTGGGAACACTTCGTCTAGCTCAATTTGGTATGAATTGGCGTACATAGAGGCAAAAGGAAGGA
TGAAGAGAGGGAACAAAGTTTGGCAGATTGCTTTAGGGTCAGGGTTTAAGTGTAATAGTGCGGTTTGG
GTGGCTCTACGCAATGTCAAGGCTTCGACAAATAGTCCTTGGGAACATTGCATTGATAGATATCCAGAT
GCAATTGATTCTGATTCGGGTAAGTCAGAGACTCGTGTCCAAAACGGTCGGTCCTAA

*FAE1* Modified Sequence, Representative Sequence

*Ta fae1* Mutant CDS:

ATGACGTCCGTTAACGTTAAGCTCCTTTACCATTACGTCATCACCAACTTTTTCAACCTTTGCTTCTTCCCG
TTAGCGGCGATCGTTGCCGGAAAAGCCTCTCGGCTTACCACAAACGATCTTCACCACTTCTACTATTCCTA
TCTCCAACACAACCTAATAACCATATCTCTACTCTTTGCCTTCACCGTTTTCGGTTTGGCTCTCTACATCGT
AA(A)CCCGGCCCAAACCGGTTTACCTCGTTGACCATTCCTGCTACCTTCCACCATCGCATCTTAGAAGCAGTA
TCTCTAAGGTCATGGATATCTTCTATCAAGTAAGATTAGCCGATCCTTTACGGAACGCGGCAAGCGATGA
TTCGTCCTGGCTTGATTTCTTGAGGAAGATTCAGGAGCGGTCTGGTCTAGGCGATGAAACCCACGGCCC
CGAGGGACTGCTTCAGGTCCCTCCACGGAAGACTTTTGCCGCGGCGCGTGAAGAAACAGAGCAAGTGA
TCATCGGTGCGCTCGAAAAACTATTCGAGAACACCAAAGTTAACCCTAAAGAGATTGGTATACTTGTGG
TGAACTCAAGCATGTTTAATCCGACTCCTTCGCTCTCGGCGATGGTTGTTAATACTTTCAAGCTCCGAAGC
AACATCAGAAGCTTTAATCTTGGAGGAATGGGTTGTAGTGCCGGCGTTATAGCCATTGATCTGGCTAAG
GACTTGTTGCATGTCCATAAAAACACTTATGCTCTTGTGGTGAGCACAGAGAACATCACTTACAACATTT

ATGCTGGTGATAACAGATCCATGATGGTTTCGAATTGCTTGTTCCGTGTTGGTGGGGCCGCGATTTTGCT
CTCCAACAAGCCGAGGGACCGGAGACGGTCCAAGTACCAGCTACTTCACACGGTTCGGACGCATACCG
GAGCTGACGACAAGTCTTTCCGATGTGTGCAACAAGAAGACGACGAGAGCGGTAAAACCGGGGTGTGT
TTGTCCAAGGACATAACCGGTGTTGCCGGGAGAACTGTTCAGAAAAACATAACAACATTGGGTCCGTTG
GTTCTTCCTTTTAGCGAGAAATTTCTTTTTTTCGTTACCTTCATCGCCAAGAAACTCTTTAAAGACAAGATC
AAACATTACTACGTCCCGGATTTCAAGCTTGCTATCGACCATTTTTGTATTCATGCCGGAGGCAGAGCCG
TGATCGATGTGCTACAGAAGAACTTAGGTCTATTGCCGATCGATGTGGAGGCATCTAGGTCAACGTTAC
ATAGATTTGGGAACACTTCGTCTAGCTCAATTTGGTATGAATTGGCGTACATAGAGGCAAAAGGAAGGA
TGAAGAGAGGGAACAAAGTTTGGCAGATTGCTTTAGGGTCAGGGTTTAAGTGTAATAGTGCGGTTTGG
GTGGCTCTACGCAATGTCAAGGCTTCGACAAATAGTCCTTGGGAACATTGCATTGATAGATATCCAGAT
GCAATTGATTCTGATTCGGGTAAGTCAGAGACTCGTGTCCAAAACGGTCGGTCCTAA

*TT8* Wild Type, Unmodified Sequence
*Ta TT8* WT CDS:
ATGGATGAATCAAGTATTTTTACGGCAGAGAAAGTGATCGGAGCTGAGAAAAGAGAGCTTCAAGGGCT
GCTTAAGGCGGCGGTGCAATCTGTGGAGTGGACTTATAGTCTCTTCTGGCAACTTTGTCCTCAACAAAGg
ttctttttttttttaataaatttcatcgatctctcacaataaaaaccctaaattttatatcatttattattatatgtttaactacataattatcag
tattttaaccgtccatgtgctttatttggttccatttctgtctcatattttacttgaggttcagactgccgagcacatctctcgtttgtctcgaat
ctgtgagacttttcgtttattggcacttctgtgtcaattgagttatactgaagtaattatatgtttaaatgaattagGGTTTTGCTGTG
GGAGAATGGATACTACAACGGTGCAATAAAGACGAGGAAGACAACTCAGCCGGCGGAAGTGACGGCG
GAAGAGGCTGCGTTAGAGAGGAGTCAGCAGCTAAGGGAACTTTACGAGGCCCTTTTGGCCGGAGAGTC
CTCATCGGAAGCTAGGGCATGCACGGCATTATCGCCGGAGGATCTGACGGAGACTGAATGGTTTTATCT
AATGTGTGTCTCTTTCTCTTTCCCTCCTCCTTCCGGgtacccaactctctctctctctctctctctctctctctctctctctctc
tctctctctctttgtctatactgaagtttcttaatttatctttttatcatctcctactgaagacaaaaatagtattgtgtgttaaatgcgaatca
cgaatattgtggaagcattaaaaacaaactgaggaggttgagttactgaaagaagaaatgtattggagttgatgaaacgtacactccat
tttagtgaacataattggaccgttgagattcttatttttttgctgattgattatctaaagtagaagcataaatagataatacataaatgcata
acaaattgtgttagttatgggtatagttaatgctttttctctatgagaggaaaaaaaaaaaaatatataaatgtggaagtaataatttttgta
gGATGCCAGGAAAGGCGTATGCGAGGAGGAAACACGTATGGCTATGTGGTGCAAATGAGGTTGACAGT
AAAATCTTTTCTAGGGCTATTCTCGCAAAGgtctatttccttttttcatttaccactactctatgcatctacttctctacctatttat
atatctcatctttcaaattaattaattttctgtctttatttttcttggatgctccttctacatcggtcggttccttaatggttagAGTGCCAAA
ATCCAGgtaaacgttgtctttattgattaattctaattttgagtaatattttacatttattttacatgtttgaaaattgttttgtgataaaaaa
aaagCAGACAGTGGTTTGCATTCCCATGCTTGATGGCGTTGTGGAACTAGGCACAACGAACAAGgtacggc
gtagttatctttttatatatgcataaccaaatggttaagaaaaaggttagaagagaaatagatcatgcttaagttttatcagttaaattaaa
aatgtaaaaataagatattatgttcattaataatgtatagtccctgttagttaaaaaaaagaataaaatatttaaccatttgaagtcataat
ataaaaatattgtttttggagatagtacataattctcacaataaaaaaaataacaaagggatgattaagggaaggagttggatacatgtt
gtttgtctgtgtgtgtgaagGTAAAAGAAGATATAGCGTTTGTTGAGCTCATAAAGAGTTTTTTCCATAACCACC
CCAAGTCAAACCCAAAAGCTGCTCTTTCTGAACACTCCATCAACGAAGAGCACGAAGAAGACGAAGAAC
AAGAAGAAGAAGAAGAAGAAGAAGTAGAAGAAGAAATGACAATGTCAGAGGAGATAAGGCTTGGCTC
TCCTGATGATGATGACGTCTCCAATCAAAACCTACTCTCTGATTTCCATGTAGAATCAACCCACACTTTAG
gtatacacttatacattaaattagttaacgatatcattacacgtatctatttattttgttaacaagaaatttaaaaatattcgccatttctttgt
tatgtctaaagaaaatctataaaattttatgaatagACACACACATGGACATGATGAATCTAATGGAGGAGGGTGGA
AACTATTCTCAGACAGTATCAACACTTCTTATGTCACAACCCACGAGTCTTTTTTCAGATTCAGTTTCCACA
TCTTCTTACATCCAATCATCATTTGCCACATGGAAGGCTGATAATTTTAAAGAGCATCAGCGAGTGGAAA

CTAAATCGACGTCGTCGTCGCAATGGATGCTCAAACACATAATCTTGAGAGTTCCTTTACTCCACGACCA
CACTAAAGAAAAGAGGCTGCCTCGAGAAGAGCTTAATCACGTGGTGGCAGAGCGCCGCAGGAGAGAG
AAGCTGAATGAGAGATTCATAACACTGAGATCATTGGTTCCCTTTGTGACCAAGATGGATAAAGTCTCA
ATTCTTGGAGACACCATCAACTACGTAAACCATCTTCGAAATAGGGTCCAAGAGCTGGAGACTAATCATC
ACGAACAAAAACATAAGCGGATGCGTAGCTGTAAGGGAAAAACGTGGGAAGAGGTCGTTGAGGTTTCC
ATCATAGAGAGTGATGTTTTGTTAGAGATGAGATGCGAGTACCGAGATGGTCTATTGCTCGACATCCTTC
AGGTTCTTAAGGAACATGGTATAGAGACTACTGCAGTTCATACCGCGGTGAACGAGCGTGATTTCGAGG
CCGAGATAAGGGCTATGGTGAGAGGGAAGAAACCAAGCATTGCTGAGGTCAAAAGAGCCATCCATCAA
ACTATATCCAATATTAAACTATAG

*TT8* Modified Sequence, Representative Sequence
*Ta tt8* Mutant CDS:
ATGGATGAATCAAGTATTTTTACGGCAGAGAAAGTGATCGGAGCTGAGAAAAGAGAGCTTCAAGGGCT
GCTTAAGGCGGCGGTGCAATCTGTGGAGTGGACTTATAGTCTCTTCTGGCAACTTTGTCCTCAACAAAGg
Ttctttttttttttaataaatttcatcgatctctcacaataaaaaccctaaattttatatcatttattattatatgtttaactacataattatcag
Tattttaaccgtccatgtgctttatttggttccatttctgtctcatattttacttgaggttcagactgccgagcacatctctcgtttgtctcgaat
ctgtgagacttttcgtttattggcacttctgtgtcaattgagttatactgaagtaattatatgtttaaatgaattagGGTTTTGCTGTG
GGAGAATGGATACTACAACGGTGCAATAAAG(G)ACGAGGAAGACAACTCAGCCGGCGGAAGTGACGGCG
GAAGAGGCTGCGTTAGAGAGGAGTCAGCAGCTAAGGGAACTTTACGAGGCCCTTTTGGCCGGAGAGTC
CTCATCGGAAGCTAGGGCATGCACGGCATTATCGCCGGAGGATCTGACGGAGACTGAATGGTTTTATCT
AATGTGTGTCTCTTTCTCTTTCCCTCCTCCTTCCGGgtacccaactctctctctctctctctctctctctctctctctctctctc
Tctctctctcttttgtctatactgaagtttcttaatttatctttttatcatctcctactgaagacaaaaatagtattgtgtgttaaatgcgaatca
Cgaatattgtggaagcattaaaaacaaactgaggaggttgagttactgaaagaagaaatgtattggagttgatgaaacgtacactccat
Tttagtgaacataattggaccgttgagattcttatttttttgctgattgattatctaaagtagaagcataaatagataatacataaatgcata
acaaattgtgttagttatgggtatagttaatgctttttctctatgagaggaaaaaaaaaaaaatatataaatgtggaagtaataattttgt
agGATGCCAGGAAAGGCGTATGCGAGGAGGAAACACGTATGGCTATGTGGTGCAAATGAGGTTGACAGT
AAAATCTTTTCTAGGGCTATTCTCGCAAAGgtctatttccttttttcatttaccactactctatgcatctacttctctacctatttat
atatctcatctttcaaattaattaattttctgtctttatttttcttggatgctccttctacatcggtcggttccttaatggttagAGTGCCAAA
ATCCAGgtaaacgttgtctttattgattaattctaattttgagtaatattttacatttattttacatgtttgaaaattgttttgtgataaaaaa
aaagCAGACAGTGGTTTGCATTCCCATGCTTGATGGCGTTGTGGAACTAGGCACAACGAACAAGgtacggc
gtagttatctttttatatatgcataaccaaatggttaagaaaaaggttagaagagaaatagatcatgcttaagttttatcagttaaattaaa
aatgtaaaaataagatattatgttcattaataatgtatagtccctgttagttaaaaaaaagaataaaatatttaaccatttgaagtcataat
ataaaaatattgtttttggagatagtacataattctcacaataaaaaaaataacaaagggatgattaagggaaggagttggatacatgtt
gtttgtctgtgtgtgtgaagGTAAAAGAAGATATAGCGTTTGTTGAGCTCATAAAGAGTTTTTTCCATAACCACC
CCAAGTCAAACCCAAAAGCTGCTCTTTCTGAACACTCCATCAACGAAGAGCACGAAGAAGACGAAGAAC
AAGAAGAAGAAGAAGAAGAAGAAGTAGAAGAAGAAATGACAATGTCAGAGGAGATAAGGCTTGGCTC
TCCTGATGATGATGACGTCTCCAATCAAAACCTACTCTCTGATTTCCATGTAGAATCAACCCACACTTTAG
Gtatacacttatacattaaattagttaacgatatcattacacgtatctatttatttttgttaacaagaaatttaaaaatattcgccatttctttgt
tatgtctaaagaaaatctataaaatttttatgaatagACACACACATGGACATGATGAATCTAATGGAGGAGGGTGGA
AACTATTCTCAGACAGTATCAACACTTCTTATGTCACAACCCACGAGTCTTTTTTCAGATTCAGTTTCCACA
TCTTCTTACATCCAATCATCATTTGCCACATGGAAGGCTGATAATTTTAAAGAGCATCAGCGAGTGGAAA
CTAAATCGACGTCGTCGTCGCAATGGATGCTCAAACACATAATCTTGAGAGTTCCTTTACTCCACGACCA
CACTAAAGAAAAGAGGCTGCCTCGAGAAGAGCTTAATCACGTGGTGGCAGAGCGCCGCAGGAGAGAG

AAGCTGAATGAGAGATTCATAACACTGAGATCATTGGTTCCCTTTGTGACCAAGATGGATAAAGTCTCA
ATTCTTGGAGACACCATCAACTACGTAAACCATCTTCGAAATAGGGTCCAAGAGCTGGAGACTAATCATC
ACGAACAAAAACATAAGCGGATGCGTAGCTGTAAGGGAAAAACGTGGGAAGAGGTCGTTGAGGTTTCC
ATCATAGAGAGTGATGTTTTGTTAGAGATGAGATGCGAGTACCGAGATGGTCTATTGCTCGACATCCTTC
AGGTTCTTAAGGAACATGGTATAGAGACTACTGCAGTTCATACCGCGGTGAACGAGCGTGATTTCGAGG
CCGAGATAAGGGCTATGGTGAGAGGGAAGAAACCAAGCATTGCTGAGGTCAAAAGAGCCATCCATCAA
ACTATATCCAATATTAAACTATAG

[ ] Wild Type, Unmodified Sequence CBI-Deleted

*Ta* [ ] WT CDS: CBI-Deleted

[

CBI-Deleted

]

[ ] Modified Sequence, Representative Sequence CBI-Deleted

*Ta* [ ] Mutant CDS: CBI-Deleted

[

CBI-Deleted

**CBI-Deleted**

]

[ ] Wild Type, Unmodified Sequence **CBI-Deleted**

*Ta* [ ] WT CDS: **CBI-Deleted**

[

**CBI-Deleted**

]

[ ] Modified Sequence, Representative Sequence CBI-Deleted

*Ta* [ ] Mutant CDS: CBI-Deleted

[

CBI-Deleted

]

[ ] Wild Type, Unmodified Sequence CBI-Deleted

*Ta* [ ] WT CDS: CBI-Deleted

[

CBI-Deleted

CBI-Deleted

]

[ ] Modified Sequence, Representative Sequence CBI-Deleted
*Ta* [ ] Mutant CDS: CBI-Deleted
[

CBI-Deleted

]

**Sequence Comparisons of the unmodified and modified genes**

*FAE1*

The top lines of the following sequence comparison are the unmodified sequence of *FAE1* (Ta_FAE1_WT). One representative modified gene sequence of *FAE1* (Ta_fae1_Mut) is included for comparison. One site in the gene is edited and includes a single A insertion, highlighted in red.

```
Ta_FAE1_WT        ATGACGTCCGTTAACGTTAAGCTCCTTTACCATTACGTCATCACCAACTTTTTCAACCTT
Ta_fae1_Mut       ATGACGTCCGTTAACGTTAAGCTCCTTTACCATTACGTCATCACCAACTTTTTCAACCTT
                  ************************************************************

Ta_FAE1_WT        TGCTTCTTCCCGTTAGCGGCGATCGTTGCCGGAAAAGCCTCTCGGCTTACCACAAACGAT
Ta_fae1_Mut       TGCTTCTTCCCGTTAGCGGCGATCGTTGCCGGAAAAGCCTCTCGGCTTACCACAAACGAT
                  ************************************************************

Ta_FAE1_WT        CTTCACCACTTCTACTATTCCTATCTCCAACACAACCTAATAACCATATCTCTACTCTTT
Ta_fae1_Mut       CTTCACCACTTCTACTATTCCTATCTCCAACACAACCTAATAACCATATCTCTACTCTTT
                  ************************************************************

Ta_FAE1_WT        GCCTTCACCGTTTTCGGTTTGGCTCTCTACATCGTAA-CCCGGCCCAAACCGGTTTACCT
Ta_fae1_Mut       GCCTTCACCGTTTTCGGTTTGGCTCTCTACATCGTAAACCCGGCCCAAACCGGTTTACCT
                  ************************************ **********************

Ta_FAE1_WT        CGTTGACCATTCCTGCTACCTTCCACCATCGCATCTTAGAAGCAGTATCTCTAAGGTCAT
Ta_fae1_Mut       CGTTGACCATTCCTGCTACCTTCCACCATCGCATCTTAGAAGCAGTATCTCTAAGGTCAT
                  ************************************************************

Ta_FAE1_WT        GGATATCTTCTATCAAGTAAGATTAGCCGATCCTTTACGGAACGCGGCAAGCGATGATTC
Ta_fae1_Mut       GGATATCTTCTATCAAGTAAGATTAGCCGATCCTTTACGGAACGCGGCAAGCGATGATTC
                  ************************************************************

Ta_FAE1_WT        GTCCTGGCTTGATTTCTTGAGGAAGATTCAGGAGCGGTCTGGTCTAGGCGATGAAACCCA
Ta_fae1_Mut       GTCCTGGCTTGATTTCTTGAGGAAGATTCAGGAGCGGTCTGGTCTAGGCGATGAAACCCA
                  ************************************************************

Ta_FAE1_WT        CGGCCCCGAGGGACTGCTTCAGGTCCCTCCACGGAAGACTTTTGCCGCGGCGCGTGAAGA
Ta_fae1_Mut       CGGCCCCGAGGGACTGCTTCAGGTCCCTCCACGGAAGACTTTTGCCGCGGCGCGTGAAGA
                  ************************************************************

Ta_FAE1_WT        AACAGAGCAAGTGATCATCGGTGCGCTCGAAAAACTATTCGAGAACACCAAAGTTAACCC
Ta_fae1_Mut       AACAGAGCAAGTGATCATCGGTGCGCTCGAAAAACTATTCGAGAACACCAAAGTTAACCC
                  ************************************************************

Ta_FAE1_WT        TAAAGAGATTGGTATACTTGTGGTGAACTCAAGCATGTTTAATCCGACTCCTTCGCTCTC
Ta_fae1_Mut       TAAAGAGATTGGTATACTTGTGGTGAACTCAAGCATGTTTAATCCGACTCCTTCGCTCTC
                  ************************************************************

Ta_FAE1_WT        GGCGATGGTTGTTAATACTTTCAAGCTCCGAAGCAACATCAGAAGCTTTAATCTTGGAGG
Ta_fae1_Mut       GGCGATGGTTGTTAATACTTTCAAGCTCCGAAGCAACATCAGAAGCTTTAATCTTGGAGG
                  ************************************************************

Ta_FAE1_WT        AATGGGTTGTAGTGCCGGCGTTATAGCCATTGATCTGGCTAAGGACTTGTTGCATGTCCA
Ta_fae1_Mut       AATGGGTTGTAGTGCCGGCGTTATAGCCATTGATCTGGCTAAGGACTTGTTGCATGTCCA
                  ************************************************************
```

```
Ta_FAE1_WT        TAAAAACACTTATGCTCTTGTGGTGAGCACAGAGAACATCACTTACAACATTTATGCTGG
Ta_fae1_Mut       TAAAAACACTTATGCTCTTGTGGTGAGCACAGAGAACATCACTTACAACATTTATGCTGG
                  ************************************************************

Ta_FAE1_WT        TGATAACAGATCCATGATGGTTTCGAATTGCTTGTTCCGTGTTGGTGGGGCCGCGATTTT
Ta_fae1_Mut       TGATAACAGATCCATGATGGTTTCGAATTGCTTGTTCCGTGTTGGTGGGGCCGCGATTTT
                  ************************************************************

Ta_FAE1_WT        GCTCTCCAACAAGCCGAGGGACCGGAGACGGTCCAAGTACCAGCTACTTCACACGGTTCG
Ta_fae1_Mut       GCTCTCCAACAAGCCGAGGGACCGGAGACGGTCCAAGTACCAGCTACTTCACACGGTTCG
                  ************************************************************

Ta_FAE1_WT        GACGCATACCGGAGCTGACGACAAGTCTTTCCGATGTGTGCAACAAGAAGACGACGAGAG
Ta_fae1_Mut       GACGCATACCGGAGCTGACGACAAGTCTTTCCGATGTGTGCAACAAGAAGACGACGAGAG
                  ************************************************************

Ta_FAE1_WT        CGGTAAAACCGGGGTGTGTTTGTCCAAGGACATAACCGGTGTTGCCGGGAGAACTGTTCA
Ta_fae1_Mut       CGGTAAAACCGGGGTGTGTTTGTCCAAGGACATAACCGGTGTTGCCGGGAGAACTGTTCA
                  ************************************************************

Ta_FAE1_WT        GAAAAACATAACAACATTGGGTCCGTTGGTTCTTCCTTTTAGCGAGAAATTTCTTTTTTT
Ta_fae1_Mut       GAAAAACATAACAACATTGGGTCCGTTGGTTCTTCCTTTTAGCGAGAAATTTCTTTTTTT
                  ************************************************************

Ta_FAE1_WT        CGTTACCTTCATCGCCAAGAAACTCTTTAAAGACAAGATCAAACATTACTACGTCCCGGA
Ta_fae1_Mut       CGTTACCTTCATCGCCAAGAAACTCTTTAAAGACAAGATCAAACATTACTACGTCCCGGA
                  ************************************************************

Ta_FAE1_WT        TTTCAAGCTTGCTATCGACCATTTTTGTATTCATGCCGGAGGCAGAGCCGTGATCGATGT
Ta_fae1_Mut       TTTCAAGCTTGCTATCGACCATTTTTGTATTCATGCCGGAGGCAGAGCCGTGATCGATGT
                  ************************************************************

Ta_FAE1_WT        GCTACAGAAGAACTTAGGTCTATTGCCGATCGATGTGGAGGCATCTAGGTCAACGTTACA
Ta_fae1_Mut       GCTACAGAAGAACTTAGGTCTATTGCCGATCGATGTGGAGGCATCTAGGTCAACGTTACA
                  ************************************************************

Ta_FAE1_WT        TAGATTTGGGAACACTTCGTCTAGCTCAATTTGGTATGAATTGGCGTACATAGAGGCAAA
Ta_fae1_Mut       TAGATTTGGGAACACTTCGTCTAGCTCAATTTGGTATGAATTGGCGTACATAGAGGCAAA
                  ************************************************************

Ta_FAE1_WT        AGGAAGGATGAAGAGAGGGAACAAAGTTTGGCAGATTGCTTTAGGGTCAGGGTTTAAGTG
Ta_fae1_Mut       AGGAAGGATGAAGAGAGGGAACAAAGTTTGGCAGATTGCTTTAGGGTCAGGGTTTAAGTG
                  ************************************************************

Ta_FAE1_WT        TAATAGTGCGGTTTGGGTGGCTCTACGCAATGTCAAGGCTTCGACAAATAGTCCTTGGGA
Ta_fae1_Mut       TAATAGTGCGGTTTGGGTGGCTCTACGCAATGTCAAGGCTTCGACAAATAGTCCTTGGGA
                  ************************************************************

Ta_FAE1_WT        ACATTGCATTGATAGATATCCAGATGCAATTGATTCTGATTCGGGTAAGTCAGAGACTCG
Ta_fae1_Mut       ACATTGCATTGATAGATATCCAGATGCAATTGATTCTGATTCGGGTAAGTCAGAGACTCG
                  ************************************************************

Ta_FAE1_WT        TGTCCAAAACGGTCGGTCCTAA
Ta_fae1_Mut       TGTCCAAAACGGTCGGTCCTAA
                  **********************
```

*TT8*

The top lines of the following sequence comparison are the unmodified sequence of *TT8* (Ta_TT8_WT). A representative modified gene sequence of *TT8* (Ta_tt8_Mut) is included

for comparison. One site in the gene is edited and includes a single G insertion, highlighted in red.

```
Ta_TT8_WT         ATGGATGAATCAAGTATTTTTACGGCAGAGAAAGTGATCGGAGCTGAGAAAAGAGAGCTT
Ta_tt8_Mut        ATGGATGAATCAAGTATTTTTACGGCAGAGAAAGTGATCGGAGCTGAGAAAAGAGAGCTT
                  ************************************************************

Ta_TT8_WT         CAAGGGCTGCTTAAGGCGGCGGTGCAATCTGTGGAGTGGACTTATAGTCTCTTCTGGCAA
Ta_tt8_Mut        CAAGGGCTGCTTAAGGCGGCGGTGCAATCTGTGGAGTGGACTTATAGTCTCTTCTGGCAA
                  ************************************************************

Ta_TT8_WT         CTTTGTCCTCAACAAAGGTTCTTTTTTTTTTTTTAATAAATTTCATCGATCTCTCACAATA
Ta_tt8_Mut        CTTTGTCCTCAACAAAGGTTCTTTTTTTTTTTTTAATAAATTTCATCGATCTCTCACAATA
                  ************************************************************

Ta_TT8_WT         AAAACCCTAAATTTTATATCATTTATTATTATATGTTTAACTACATAATTATCAGTATTT
Ta_tt8_Mut        AAAACCCTAAATTTTATATCATTTATTATTATATGTTTAACTACATAATTATCAGTATTT
                  ************************************************************

Ta_TT8_WT         TAACCGTCCATGTGCTTTATTTGGTTCCATTTCTGTCTCATATTTTACTTGAGGTTCAGA
Ta_tt8_Mut        TAACCGTCCATGTGCTTTATTTGGTTCCATTTCTGTCTCATATTTTACTTGAGGTTCAGA
                  ************************************************************

Ta_TT8_WT         CTGCCGAGCACATCTCTCGTTTGTCTCGAATCTGTGAGACTTTTTCGTTTATTGGCACTT
Ta_tt8_Mut        CTGCCGAGCACATCTCTCGTTTGTCTCGAATCTGTGAGACTTTTTCGTTTATTGGCACTT
                  ************************************************************

Ta_TT8_WT         CTGTGTCAATTGAGTTATACTGAAGTAATTATATGTTTAAATGAATTAGGGTTTTGCTGT
Ta_tt8_Mut        CTGTGTCAATTGAGTTATACTGAAGTAATTATATGTTTAAATGAATTAGGGTTTTGCTGT
                  ************************************************************

Ta_TT8_WT         GGGAGAATGGATACTACAACGGTGCAATAAAG-ACGAGGAAGACAACTCAGCCGGCGGAA
Ta_tt8_Mut        GGGAGAATGGATACTACAACGGTGCAATAAAGGACGAGGAAGACAACTCAGCCGGCGGAA
                  ******************************* ****************************

Ta_TT8_WT         GTGACGGCGGAAGAGGCTGCGTTAGAGAGGAGTCAGCAGCTAAGGGAACTTTACGAGGCC
Ta_tt8_Mut        GTGACGGCGGAAGAGGCTGCGTTAGAGAGGAGTCAGCAGCTAAGGGAACTTTACGAGGCC
                  ************************************************************

Ta_TT8_WT         CTTTTGGCCGGAGAGTCCTCATCGGAAGCTAGGGCATGCACGGCATTATCGCCGGAGGAT
Ta_tt8_Mut        CTTTTGGCCGGAGAGTCCTCATCGGAAGCTAGGGCATGCACGGCATTATCGCCGGAGGAT
                  ************************************************************

Ta_TT8_WT         CTGACGGAGACTGAATGGTTTTATCTAATGTGTGTCTCTTTCTCTTTCCCTCCTCCTTCC
Ta_tt8_Mut        CTGACGGAGACTGAATGGTTTTATCTAATGTGTGTCTCTTTCTCTTTCCCTCCTCCTTCC
                  ************************************************************

Ta_TT8_WT         GGGTACCCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
Ta_tt8_Mut        GGGTACCCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
                  ************************************************************

Ta_TT8_WT         CTCTTTTGTCTATACTGAAGTTTCTTAATTTATCTTTTTATCATCTCCTACTGAAGACAA
Ta_tt8_Mut        CTCTTTTGTCTATACTGAAGTTTCTTAATTTATCTTTTTATCATCTCCTACTGAAGACAA
                  ************************************************************

Ta_TT8_WT         AAATAGTATTGTGTGTTAAATGCGAATCACGAATATTGTGGAAGCATTAAAAACAAACTG
Ta_tt8_Mut        AAATAGTATTGTGTGTTAAATGCGAATCACGAATATTGTGGAAGCATTAAAAACAAACTG
                  ************************************************************
```

```
Ta_TT8_WT       AGGAGGTTGAGTTACTGAAAGAAGAAATGTATTGGAGTTGATGAAACGTACACTCCATTT
Ta_tt8_Mut      AGGAGGTTGAGTTACTGAAAGAAGAAATGTATTGGAGTTGATGAAACGTACACTCCATTT
                ************************************************************

Ta_TT8_WT       TAGTGAACATAATTGGACCGTTGAGATTCTTATTTTTTTGCTGATTGATTATCTAAAGTA
Ta_tt8_Mut      TAGTGAACATAATTGGACCGTTGAGATTCTTATTTTTTTGCTGATTGATTATCTAAAGTA
                ************************************************************

Ta_TT8_WT       GAAGCATAAATAGATAATACATAAATGCATAACAAATTGTGTTAGTTATGGGTATAGTTA
Ta_tt8_Mut      GAAGCATAAATAGATAATACATAAATGCATAACAAATTGTGTTAGTTATGGGTATAGTTA
                ************************************************************

Ta_TT8_WT       ATGCTTTTTCTCTATGAGAGGAAAAAAAAAAAAATATATAAATGTGGAAGTAATAATTTT
Ta_tt8_Mut      ATGCTTTTTCTCTATGAGAGGAAAAAAAAAAAAATATATAAATGTGGAAGTAATAATTTT
                ************************************************************

Ta_TT8_WT       GTAGGATGCCAGGAAAGGCGTATGCGAGGAGGAAACACGTATGGCTATGTGGTGCAAATG
Ta_tt8_Mut      GTAGGATGCCAGGAAAGGCGTATGCGAGGAGGAAACACGTATGGCTATGTGGTGCAAATG
                ************************************************************

Ta_TT8_WT       AGGTTGACAGTAAAATCTTTTCTAGGGCTATTCTCGCAAAGGTCTATTTCCTTTTTCATT
Ta_tt8_Mut      AGGTTGACAGTAAAATCTTTTCTAGGGCTATTCTCGCAAAGGTCTATTTCCTTTTTCATT
                ************************************************************

Ta_TT8_WT       TACCACTACTCTATGCATCTACTTCTCTACCTATTTATATATCTCATCTTTCAAATTAAT
Ta_tt8_Mut      TACCACTACTCTATGCATCTACTTCTCTACCTATTTATATATCTCATCTTTCAAATTAAT
                ************************************************************

Ta_TT8_WT       TAATTTTCTGTCTTTATTTTCTTGGATGCTCCTTCTACATCGGTCGGTTCCTTAATGGTT
Ta_tt8_Mut      TAATTTTCTGTCTTTATTTTCTTGGATGCTCCTTCTACATCGGTCGGTTCCTTAATGGTT
                ************************************************************

Ta_TT8_WT       AGAGTGCCAAAATCCAGGTAAACGTTGTCTTTATTGATTAATTCTAATTTTGAGTAATAT
Ta_tt8_Mut      AGAGTGCCAAAATCCAGGTAAACGTTGTCTTTATTGATTAATTCTAATTTTGAGTAATAT
                ************************************************************

Ta_TT8_WT       TTTACATTTATTTTACATGTTTGAAAATTGTTTTGTGATAAAAAAAAAGCAGACAGTGGT
Ta_tt8_Mut      TTTACATTTATTTTACATGTTTGAAAATTGTTTTGTGATAAAAAAAAAGCAGACAGTGGT
                ************************************************************

Ta_TT8_WT       TTGCATTCCCATGCTTGATGGCGTTGTGGAACTAGGCACAACGAACAAGGTACGGCGTAG
Ta_tt8_Mut      TTGCATTCCCATGCTTGATGGCGTTGTGGAACTAGGCACAACGAACAAGGTACGGCGTAG
                ************************************************************

Ta_TT8_WT       TTATCTTTTTATATATGCATAACCAAATGGTTAAGAAAAAGGTTAGAAGAGAAATAGATC
Ta_tt8_Mut      TTATCTTTTTATATATGCATAACCAAATGGTTAAGAAAAAGGTTAGAAGAGAAATAGATC
                ************************************************************

Ta_TT8_WT       ATGCTTAAGTTTTATCAGTTAAATTAAAAATGTAAAAATAAGATATTATGTTCATTAATA
Ta_tt8_Mut      ATGCTTAAGTTTTATCAGTTAAATTAAAAATGTAAAAATAAGATATTATGTTCATTAATA
                ************************************************************

Ta_TT8_WT       ATGTATAGTCCCTGTTAGTTAAAAAAAAGAATAAAATATTTAACCATTTGAAGTCATAAT
Ta_tt8_Mut      ATGTATAGTCCCTGTTAGTTAAAAAAAAGAATAAAATATTTAACCATTTGAAGTCATAAT
                ************************************************************

Ta_TT8_WT       ATAAAAATATTGTTTTTGGAGATAGTACATAATTCTCACAATAAAAAAAATAACAAAGGG
Ta_tt8_Mut      ATAAAAATATTGTTTTTGGAGATAGTACATAATTCTCACAATAAAAAAAATAACAAAGGG
                ************************************************************
```

```
Ta_TT8_WT       ATGATTAAGGGAAGGAGTTGGATACATGTTGTTTGTCTGTGTGTGTGAAGGTAAAAGAAG
Ta_tt8_Mut      ATGATTAAGGGAAGGAGTTGGATACATGTTGTTTGTCTGTGTGTGTGAAGGTAAAAGAAG
                ************************************************************

Ta_TT8_WT       ATATAGCGTTTGTTGAGCTCATAAAGAGTTTTTTCCATAACCACCCCAAGTCAAACCCAA
Ta_tt8_Mut      ATATAGCGTTTGTTGAGCTCATAAAGAGTTTTTTCCATAACCACCCCAAGTCAAACCCAA
                ************************************************************

Ta_TT8_WT       AAGCTGCTCTTTCTGAACACTCCATCAACGAAGAGCACGAAGAAGACGAAGAACAAGAAG
Ta_tt8_Mut      AAGCTGCTCTTTCTGAACACTCCATCAACGAAGAGCACGAAGAAGACGAAGAACAAGAAG
                ************************************************************

Ta_TT8_WT       AAGAAGAAGAAGAAGAAGTAGAAGAAGAAATGACAATGTCAGAGGAGATAAGGCTTGGCT
Ta_tt8_Mut      AAGAAGAAGAAGAAGAAGTAGAAGAAGAAATGACAATGTCAGAGGAGATAAGGCTTGGCT
                ************************************************************

Ta_TT8_WT       CTCCTGATGATGATGACGTCTCCAATCAAAACCTACTCTCTGATTTCCATGTAGAATCAA
Ta_tt8_Mut      CTCCTGATGATGATGACGTCTCCAATCAAAACCTACTCTCTGATTTCCATGTAGAATCAA
                ************************************************************

Ta_TT8_WT       CCCACACTTTAGGTATACACTTATACATTAAATTAGTTAACGATATCATTACACGTATCT
Ta_tt8_Mut      CCCACACTTTAGGTATACACTTATACATTAAATTAGTTAACGATATCATTACACGTATCT
                ************************************************************

Ta_TT8_WT       ATTTATTTTGTTAACAAGAAATTTAAAAATATTCGCCATTTCTTTGTTATGTCTAAAGAA
Ta_tt8_Mut      ATTTATTTTGTTAACAAGAAATTTAAAAATATTCGCCATTTCTTTGTTATGTCTAAAGAA
                ************************************************************

Ta_TT8_WT       AATCTATAAAATTTTATGAATAGACACACACATGGACATGATGAATCTAATGGAGGAGGG
Ta_tt8_Mut      AATCTATAAAATTTTATGAATAGACACACACATGGACATGATGAATCTAATGGAGGAGGG
                ************************************************************

Ta_TT8_WT       TGGAAACTATTCTCAGACAGTATCAACACTTCTTATGTCACAACCCACGAGTCTTTTTTC
Ta_tt8_Mut      TGGAAACTATTCTCAGACAGTATCAACACTTCTTATGTCACAACCCACGAGTCTTTTTTC
                ************************************************************

Ta_TT8_WT       AGATTCAGTTTCCACATCTTCTTACATCCAATCATCATTTGCCACATGGAAGGCTGATAA
Ta_tt8_Mut      AGATTCAGTTTCCACATCTTCTTACATCCAATCATCATTTGCCACATGGAAGGCTGATAA
                ************************************************************

Ta_TT8_WT       TTTTAAAGAGCATCAGCGAGTGGAAACTAAATCGACGTCGTCGTCGCAATGGATGCTCAA
Ta_tt8_Mut      TTTTAAAGAGCATCAGCGAGTGGAAACTAAATCGACGTCGTCGTCGCAATGGATGCTCAA
                ************************************************************

Ta_TT8_WT       ACACATAATCTTGAGAGTTCCTTTACTCCACGACCACACTAAAGAAAAGAGGCTGCCTCG
Ta_tt8_Mut      ACACATAATCTTGAGAGTTCCTTTACTCCACGACCACACTAAAGAAAAGAGGCTGCCTCG
                ************************************************************

Ta_TT8_WT       AGAAGAGCTTAATCACGTGGTGGCAGAGCGCCGCAGGAGAGAGAAGCTGAATGAGAGATT
Ta_tt8_Mut      AGAAGAGCTTAATCACGTGGTGGCAGAGCGCCGCAGGAGAGAGAAGCTGAATGAGAGATT
                ************************************************************

Ta_TT8_WT       CATAACACTGAGATCATTGGTTCCCTTTGTGACCAAGATGGATAAAGTCTCAATTCTTGG
Ta_tt8_Mut      CATAACACTGAGATCATTGGTTCCCTTTGTGACCAAGATGGATAAAGTCTCAATTCTTGG
                ************************************************************

Ta_TT8_WT       AGACACCATCAACTACGTAAACCATCTTCGAAATAGGGTCCAAGAGCTGGAGACTAATCA
Ta_tt8_Mut      AGACACCATCAACTACGTAAACCATCTTCGAAATAGGGTCCAAGAGCTGGAGACTAATCA
                ************************************************************
```

```
Ta_TT8_WT         TCACGAACAAAAACATAAGCGGATGCGTAGCTGTAAGGGAAAAACGTGGGAAGAGGTCGT
Ta_tt8_Mut        TCACGAACAAAAACATAAGCGGATGCGTAGCTGTAAGGGAAAAACGTGGGAAGAGGTCGT
                  ************************************************************

Ta_TT8_WT         TGAGGTTTCCATCATAGAGAGTGATGTTTTGTTAGAGATGAGATGCGAGTACCGAGATGG
Ta_tt8_Mut        TGAGGTTTCCATCATAGAGAGTGATGTTTTGTTAGAGATGAGATGCGAGTACCGAGATGG
                  ************************************************************

Ta_TT8_WT         TCTATTGCTCGACATCCTTCAGGTTCTTAAGGAACATGGTATAGAGACTACTGCAGTTCA
Ta_tt8_Mut        TCTATTGCTCGACATCCTTCAGGTTCTTAAGGAACATGGTATAGAGACTACTGCAGTTCA
                  ************************************************************

Ta_TT8_WT         TACCGCGGTGAACGAGCGTGATTTCGAGGCCGAGATAAGGGCTATGGTGAGAGGGAAGAA
Ta_tt8_Mut        TACCGCGGTGAACGAGCGTGATTTCGAGGCCGAGATAAGGGCTATGGTGAGAGGGAAGAA
                  ************************************************************

Ta_TT8_WT         ACCAAGCATTGCTGAGGTCAAAAGAGCCATCCATCAAACTATATCCAATATTAAACTATA
Ta_tt8_Mut        ACCAAGCATTGCTGAGGTCAAAAGAGCCATCCATCAAACTATATCCAATATTAAACTATA
                  ************************************************************

Ta_TT8_WT         G
Ta_tt8_Mut        G
                  *
```

[ ] CBI-Deleted

The top lines of the following sequence comparison are the unmodified sequence of the [ ] gene. One representative modified gene sequence of [ ] is included for comparison. One site in the gene is edited; the modified sequence includes a single T insertion. The edit is in red. CBI-Deleted CBI-Deleted (2)

[

CBI-Deleted

CBI-Deleted

CoverCress

CBI-Deleted Copy

CBI-Deleted

CoverCress

CBI-Deleted Copy

CBI-Deleted

]

[ ] CBI-Deleted

The top lines of the following sequence comparison are the unmodified sequence of the [ CBI-Deleted
] gene. One representative modified gene sequence of [ ] is CBI-Deleted (2)
included for comparison. One site in the gene is edited; the modified sequence includes a 2 bp deletion. The edit is in red.

[

CBI-Deleted

CBI-Deleted

]

[ ] CBI-Deleted

The top lines of the following sequence comparison are the unmodified sequence of the [ CBI-Deleted

] gene. One representative modified gene sequence of [ ] is CBI-Deleted (2)

included for comparison. One site in the gene is edited; the modified sequence includes a single T insertion. The edit is in red.

[

CBI-Deleted

CBI-Deleted

CBI-Deleted

]