CoverCress

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3/26/2024
Bernadette Juarez
U.S. Department of Agriculture
APHIS Deputy Administrator
Biotechnology Regulatory Services

RECEIVED
By ajdrummond for BRS Document Control Officer at 2:26 pm, Mar 26, 2024

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; [ ] to produce a lower glucosinolate phenotype; [ ] to produce a reduced-shatter phenotype; and [ ] to produce a lower PUFA/higher oleic acid phenotype. The first two PTMOAs are described in 22-069-01rsr. The third PTMOA is described in 22-241-01rsr. This RSR requests the evaluation of those previously submitted PTMOAs in combination with two additional PTMOAs. **CBI-Deleted (2)** **CBI-Deleted**

USDA has previously evaluated pennycress lines with the same phenotypes as three of the PTMO's in this RSR via the AIR process. Disruption of *TT8* and *FAE1* were reviewed in several AIR letters[1]. Additionally, lines containing disruption in genes (*AOP2*, [ ]) that are in the same biosynthesis pathway and that exhibit the same phenotype as our third trait [ ], were evaluated in some of these and other 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 an alternate gene that results in the same low glucosinolate phenotype, [ ]. In response to each of several previously submitted AIR letters, BRS deregulated pennycress lines harboring disruptions in *FAE1*, *TT8*, *AOP2* and other genes, concluding that: "…your gene-edited pennycress lines are not themselves plant pests". In other AIR response letters, USDA additionally stated 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 (2)** **CBI-Deleted** **CBI-Deleted**

Further, via the confirmation of exemption process, single edits in the [ ] (22-336-02cr), [ ] (22-107-02cr), and [ ] (23-208-01cr) 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

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)

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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, reduced-shatter, and higher oleic acid/lower PUFA 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, reduced-shatter, and higher oleic acid/lower PUFA 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_Mut1      GCCTTCACCGTTTTCGGTTTGGCTCTCTACATCGTAAACCCGGCCCAAACCGGTTTACCT
                  ************************************ ********************
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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_Mut1       GGGAGAATGGATACTACAACGGTGCAATAAAGGGACGAGGAAGACAACTCAGCCGGCGGAA
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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.

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One representative modified gene sequence of [ ] is included for comparison. One site CBI-Deleted
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.

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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 A insertion, highlighted in red. The full gene sequences and sequence comparison are included in Appendix 1.

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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., 2018b; 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., 2018b; 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 80 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., 2018b; 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 (e.g. 4% in broiler diets) (Chopra et al., 2020).

Intended trait #4: reduced shatter seedpods

Intended phenotype #4: reduced pod dehiscence, reduced seed dispersal

Pennycress seedpods often shatter due to high winds or mechanical harvest. This premature breakage can reduce yields by more than 50% in certain environmental conditions and limits economic viability in the domestication of pennycress for use in biofuels and bioproducts. Mutant pennycress lines, with reduced [ ] CBI-Deleted activity may have 60-90% reduction in pod dehiscence compared to its co-grown wild type resulting in improved agronomic properties (Chopra et. al., 2020). The reduction in pre-mature shatter and decreased loss during harvest also reduces the soil seed bank, easing management as a domesticated crop.

Intended trait #5: lower PUFA/higher oleic acid seeds

Intended phenotype #5: reduction of polyunsaturated fatty acids (PUFAs) in seeds, increase of oleic acid in seeds

A by-product of reducing erucic acid in pennycress oil via editing of the *FAE1* gene (trait #1), is an increase in polyunsaturated fatty acids (PUFAs), in particular linolenic acid with three double bonds (18:3) and linoleic acid with two double bonds (18:2). Higher levels of PUFAs in seed oil can reduce the stability of the oil, hence reducing its shelf life. The [ ] gene was identified as a gene target that, if loss of CBI-Deleted function occurs, results in [CBI-Deleted CBI-Deleted], but does not impact other biosynthetic pathways. CBI-Deleted

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.

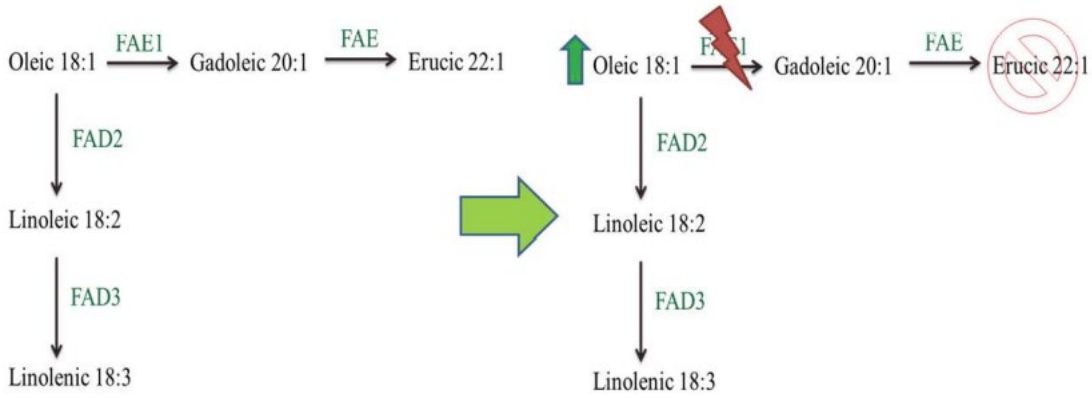

Figure 1: Fatty Acid Pathway to Reduce Erucic Acid Levels

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., 2018a). 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., 2018a). 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.

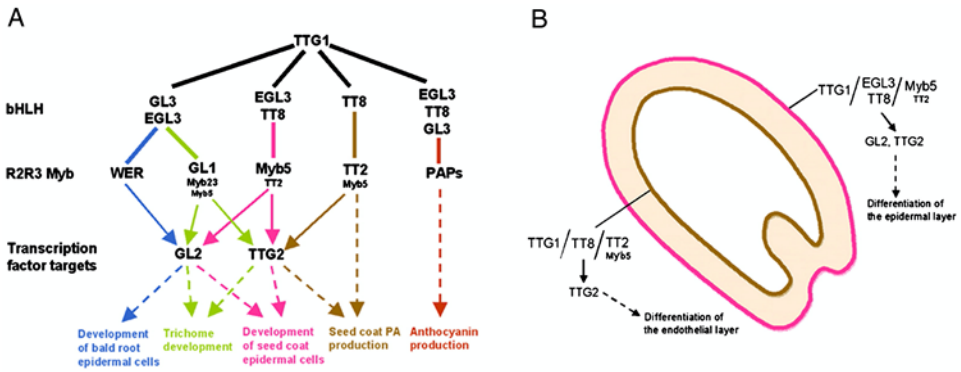

Figure 2: Models for the regulation of TTG-1 dependent pathways in seed coat development. (A) A regulatory network for the positive control of TTG1-dependent epidermal cell fates. Solid lines indicate interactions between members of a complex. Solid arrows indicate direct regulation of *GL2* or *TTG2* 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 resistance to insects and serve as defense compounds in different tissues of the plant and can help with suppressing 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 derived through the aliphatic glucosinolate pathway (Chopra et al., 2018b; Chopra et al., 2020; Sedbrook et al., 2014).

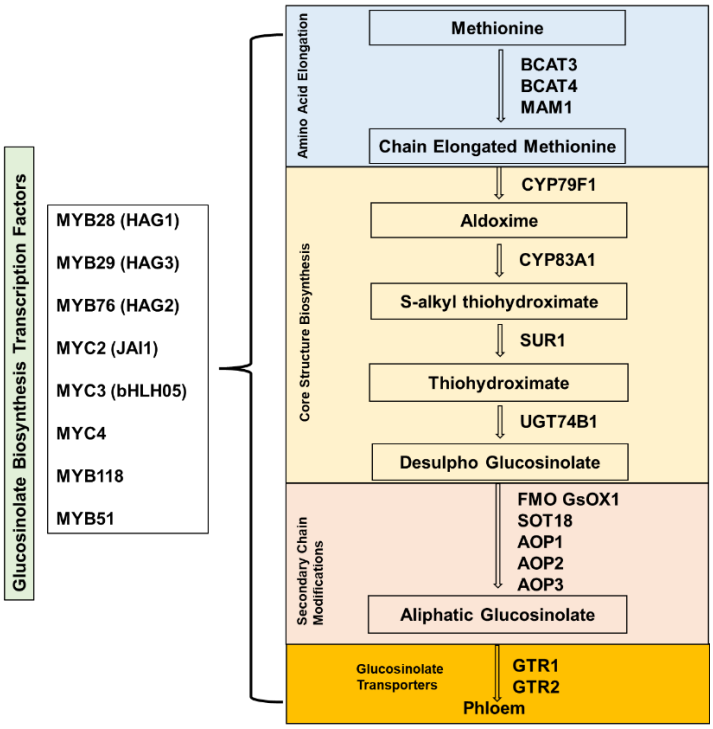

Figure 3: Major steps in glucosinolate biosynthesis

The rationale for gene target selection was to identify those genes that 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. The transcription factor [ ] was identified as the gene target in this RSR request. **CBI-Deleted**

[ ] is a bHLH protein that is known to interact directly with glucosinolate-related transcription factors, and it helps coordinate expression of several biosynthesis genes required to accumulate glucosinolate [ ]. We generated alleles in 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 results in a premature stop codon and a truncated, non-functional protein. Resulting sinigrin levels in [ ] pennycress mutants are reduced compared to its co-grown wild type. **CBI-Deleted** **CBI-Deleted** **CBI-Deleted** **CBI-Deleted**

Reduced Seedpod Shatter MOA

Wildtype pennycress seedpods often exhibit premature breakage by wind or during mechanical harvest. In the domestication of pennycress, improvements are necessary as this premature seedpod shatter can result in yield losses of over 50%. Mutants were identified with mutations in the pennycress candidate ortholog of the Arabidopsis [ ] gene. The seedpod contains a separation layer of cells flanking the septum (also called a replum) which divides the seedpod into two halves [ ]. [ ] encodes a [ ] regulating the formation of this separation layer, mediating pod breakage, and mutations in this gene generated mutants with a varying reduction in breakage of the dehiscence zones. The representative edited allele for [ ] has a 1-bp insertion that causes a frameshift resulting in a truncated, non-functional protein. [ ] pennycress mutants may have 60-90% reduction in pod dehiscence, compared to its co-grown wild type, reducing seed dispersal and yield loss (Chopra et al., 2020).

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Figure 4: An intact seedpod compared to a broken seedpod with released seeds (both are wild-type). The arrows show the septum of an intact pod (left) and the septum structure that remains after pod shatter. The arrows highlight the septum remaining after pod shatter. (Chopra et al., 2020)

Higher Oleic Acid/Lower PUFAs MOA

Pennycress *FAE1* mutants containing the desired decrease in erucic acid also contain a desirable elevation in oleic acid and an accumulation of higher levels of polyunsaturated fatty acids (PUFAs), in particular linolenic acid with three double bonds (18:3) and linoleic acid with two double bonds (18:2). Although linolenic acid, belonging to the omega3 class of fatty acids, is associated with reduced heart disease, reduced bone fracture risk and reduced childhood obesity (Perng et al., 2014; Rajaram, 2014), for many applications, PUFAs are not desirable. The extra bonds reduce the stability of the oil, shortening the shelf life of products containing the oil (Gordon, 1990).

A reduction in PUFA levels can be achieved by disrupting the activity of the [ ] gene, resulting in higher levels of oleic acid [

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]. [CBI-Deleted (2)
], modulates polyunsaturated fatty acid (PUFA) content CBI-Deleted
by interconverting PC and DAG, transferring 18:1 into PC for desaturation, and 18:2 and 18:3 into the triacylglycerol (TAG) biosynthetic pathway thereby increasing PUFA content in TAG (Figure 5). An edit to [ ] in pennycress may result in a frameshift leading to a CBI-Deleted
premature stop codon and a truncated, non-functional protein. The seeds of [ ] CBI-Deleted
pennycress edits may have a [CBI-Deleted
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], compared to its co-grown wild type, resulting in improved product quality and CBI-Deleted
stability.

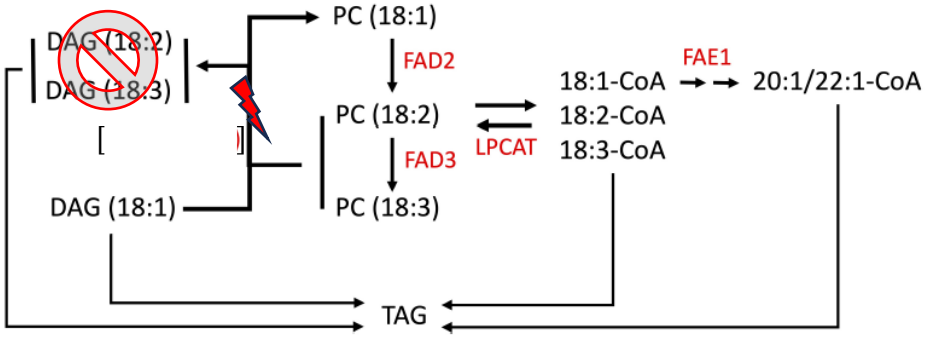

Figure 5: Simplified scheme for fatty acid modification in Brassicas illustrating reduction of polyunsaturated fatty acids via interruption of [ ] activity. CBI-Deleted

In conclusion, CoverCress™ is currently being developed as a new rotational oilseed crop that has the benefits of a cover crop that could be grown between the fall harvest and spring establishment of traditional crops in temperate regions. Edits and/or mutations to *FAE1, TT8,* [ ] genes have resulted in the low erucic acid, lower fiber, reduced total CBI-Deleted
glucosinolates, reduced shatter, and lower PUFAs/higher oleic acid seed traits, respectively. The mechanism of action for the genetic changes leading to each phenotype is well-understood and has a history of publication. Based on this information, we request USDA's review of the combination of these previously reviewed and new PTMOAs and confirmation that the traits, produced through simultaneous or sequential editing of any combination of *FAE1, TT8,* [CBI-Deleted
] genes in pennycress, are not subject to regulation under Part 340. CBI-Deleted

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Appendix 1 – Full Sequences and Sequence Comparisons

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

FAE1 Wild Type, Unmodified Sequence
Ta FAE1 WT CDS:
ATGACGTCCGTTAACGTTAAGCTCCTTTACCATTACGTCATCACCAACTTTTTCAACCTTTGCTTCTTCCCG
TTAGCGGCGATCGTTGCCGGAAAAGCCTCTCGGCTTACCACAAACGATCTTCACCACTTCTACTATTCCTA
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TTCGTCCTGGCTTGATTTCTTGAGGAAGATTCAGGAGCGGTCTGGTCTAGGCGATGAAACCCACGGCCC
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GTGGCTCTACGCAATGTCAAGGCTTCGACAAATAGTCCTTGGGAACATTGCATTGATAGATATCCAGAT
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FAE1 Modified Sequence, Representative Sequence
Ta fae1 Mutant1 CDS:
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TTAGCGGCGATCGTTGCCGGAAAAGCCTCTCGGCTTACCACAAACGATCTTCACCACTTCTACTATTCCTA
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TT8 Wild Type, Unmodified Sequence
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TT8 Modified Sequence, Representative Sequence
Ta tt8 Mutant1 CDS:
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[ ] Wild Type, Unmodified Sequence CBI-Deleted

Ta [ ] WT CDS: CBI-Deleted

[

CBI-Deleted

]

[ ] Modified Sequence, Representative Sequence CBI-Deleted

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[

CBI-Deleted

CBI-Deleted

]

[ ] Wild Type, Unmodified Sequence CBI-Deleted

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CBI-Deleted

]

[ ] Modified Sequence, Representative Sequence CBI-Deleted

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CBI-Deleted

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[ ] Wild Type, Unmodified Sequence CBI-Deleted
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[

CBI-Deleted

]

[ ] Modified Sequence, Representative Sequence CBI-Deleted
Ta [ ] Mutant1 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*. One representative modified gene sequence of *FAE1* is included for comparison (Ta_fae1_Mut1). One site in the gene is edited and includes a single A insertion, highlighted in red.

```
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Ta_fae1_Mut1      ATGACGTCCGTTAACGTTAAGCTCCTTTACCATTACGTCATCACCAACTTTTTCAACCTT
                  ************************************************************

Ta_FAE1           TGCTTCTTCCCGTTAGCGGCGATCGTTGCCGGAAAAGCCTCTCGGCTTACCACAAACGAT
Ta_fae1_Mut1      TGCTTCTTCCCGTTAGCGGCGATCGTTGCCGGAAAAGCCTCTCGGCTTACCACAAACGAT
                  ************************************************************

Ta_FAE1           CTTCACCACTTCTACTATTCCTATCTCCAACACAACCTAATAACCATATCTCTACTCTTT
Ta_fae1_Mut1      CTTCACCACTTCTACTATTCCTATCTCCAACACAACCTAATAACCATATCTCTACTCTTT
                  ************************************************************

Ta_FAE1           GCCTTCACCGTTTTCGGTTTGGCTCTCTACATCGTAA-CCCGGCCCAAACCGGTTTACCT
Ta_fae1_Mut1      GCCTTCACCGTTTTCGGTTTGGCTCTCTACATCGTAAACCCGGCCCAAACCGGTTTACCT
                  ************************************ ***********************

Ta_FAE1           CGTTGACCATTCCTGCTACCTTCCACCATCGCATCTTAGAAGCAGTATCTCTAAGGTCAT
Ta_fae1_Mut1      CGTTGACCATTCCTGCTACCTTCCACCATCGCATCTTAGAAGCAGTATCTCTAAGGTCAT
                  ************************************************************

Ta_FAE1           GGATATCTTCTATCAAGTAAGATTAGCCGATCCTTTACGGAACGCGGCAAGCGATGATTC
Ta_fae1_Mut1      GGATATCTTCTATCAAGTAAGATTAGCCGATCCTTTACGGAACGCGGCAAGCGATGATTC
                  ************************************************************

Ta_FAE1           GTCCTGGCTTGATTTCTTGAGGAAGATTCAGGAGCGGTCTGGTCTAGGCGATGAAACCCA
Ta_fae1_Mut1      GTCCTGGCTTGATTTCTTGAGGAAGATTCAGGAGCGGTCTGGTCTAGGCGATGAAACCCA
                  ************************************************************

Ta_FAE1           CGGCCCCGAGGGACTGCTTCAGGTCCCTCCACGGAAGACTTTTGCCGCGGCGCGTGAAGA
Ta_fae1_Mut1      CGGCCCCGAGGGACTGCTTCAGGTCCCTCCACGGAAGACTTTTGCCGCGGCGCGTGAAGA
                  ************************************************************

Ta_FAE1           AACAGAGCAAGTGATCATCGGTGCGCTCGAAAAACTATTCGAGAACACCAAAGTTAACCC
Ta_fae1_Mut1      AACAGAGCAAGTGATCATCGGTGCGCTCGAAAAACTATTCGAGAACACCAAAGTTAACCC
                  ************************************************************

Ta_FAE1           TAAAGAGATTGGTATACTTGTGGTGAACTCAAGCATGTTTAATCCGACTCCTTCGCTCTC
Ta_fae1_Mut1      TAAAGAGATTGGTATACTTGTGGTGAACTCAAGCATGTTTAATCCGACTCCTTCGCTCTC
                  ************************************************************

Ta_FAE1           GGCGATGGTTGTTAATACTTTCAAGCTCCGAAGCAACATCAGAAGCTTTAATCTTGGAGG
Ta_fae1_Mut1      GGCGATGGTTGTTAATACTTTCAAGCTCCGAAGCAACATCAGAAGCTTTAATCTTGGAGG
                  ************************************************************

Ta_FAE1           AATGGGTTGTAGTGCCGGCGTTATAGCCATTGATCTGGCTAAGGACTTGTTGCATGTCCA
Ta_fae1_Mut1      AATGGGTTGTAGTGCCGGCGTTATAGCCATTGATCTGGCTAAGGACTTGTTGCATGTCCA
                  ************************************************************
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Ta_FAE1          TAAAAACACTTATGCTCTTGTGGTGAGCACAGAGAACATCACTTACAACATTTATGCTGG
Ta_fae1_Mut1     TAAAAACACTTATGCTCTTGTGGTGAGCACAGAGAACATCACTTACAACATTTATGCTGG
                 ************************************************************

Ta_FAE1          TGATAACAGATCCATGATGGTTTCGAATTGCTTGTTCCGTGTTGGTGGGGCCGCGATTTT
Ta_fae1_Mut1     TGATAACAGATCCATGATGGTTTCGAATTGCTTGTTCCGTGTTGGTGGGGCCGCGATTTT
                 ************************************************************

Ta_FAE1          GCTCTCCAACAAGCCGAGGGACCGGAGACGGTCCAAGTACCAGCTACTTCACACGGTTCG
Ta_fae1_Mut1     GCTCTCCAACAAGCCGAGGGACCGGAGACGGTCCAAGTACCAGCTACTTCACACGGTTCG
                 ************************************************************

Ta_FAE1          GACGCATACCGGAGCTGACGACAAGTCTTTCCGATGTGTGCAACAAGAAGACGACGAGAG
Ta_fae1_Mut1     GACGCATACCGGAGCTGACGACAAGTCTTTCCGATGTGTGCAACAAGAAGACGACGAGAG
                 ************************************************************

Ta_FAE1          CGGTAAAACCGGGGTGTGTTTGTCCAAGGACATAACCGGTGTTGCCGGGAGAACTGTTCA
Ta_fae1_Mut1     CGGTAAAACCGGGGTGTGTTTGTCCAAGGACATAACCGGTGTTGCCGGGAGAACTGTTCA
                 ************************************************************

Ta_FAE1          GAAAAACATAACAACATTGGGTCCGTTGGTTCTTCCTTTTAGCGAGAAATTTCTTTTTTT
Ta_fae1_Mut1     GAAAAACATAACAACATTGGGTCCGTTGGTTCTTCCTTTTAGCGAGAAATTTCTTTTTTT
                 ************************************************************

Ta_FAE1          CGTTACCTTCATCGCCAAGAAACTCTTTAAAGACAAGATCAAACATTACTACGTCCCGGA
Ta_fae1_Mut1     CGTTACCTTCATCGCCAAGAAACTCTTTAAAGACAAGATCAAACATTACTACGTCCCGGA
                 ************************************************************

Ta_FAE1          TTTCAAGCTTGCTATCGACCATTTTTGTATTCATGCCGGAGGCAGAGCCGTGATCGATGT
Ta_fae1_Mut1     TTTCAAGCTTGCTATCGACCATTTTTGTATTCATGCCGGAGGCAGAGCCGTGATCGATGT
                 ************************************************************

Ta_FAE1          GCTACAGAAGAACTTAGGTCTATTGCCGATCGATGTGGAGGCATCTAGGTCAACGTTACA
Ta_fae1_Mut1     GCTACAGAAGAACTTAGGTCTATTGCCGATCGATGTGGAGGCATCTAGGTCAACGTTACA
                 ************************************************************

Ta_FAE1          TAGATTTGGGAACACTTCGTCTAGCTCAATTTGGTATGAATTGGCGTACATAGAGGCAAA
Ta_fae1_Mut1     TAGATTTGGGAACACTTCGTCTAGCTCAATTTGGTATGAATTGGCGTACATAGAGGCAAA
                 ************************************************************

Ta_FAE1          AGGAAGGATGAAGAGAGGGAACAAAGTTTGGCAGATTGCTTTAGGGTCAGGGTTTAAGTG
Ta_fae1_Mut1     AGGAAGGATGAAGAGAGGGAACAAAGTTTGGCAGATTGCTTTAGGGTCAGGGTTTAAGTG
                 ************************************************************

Ta_FAE1          TAATAGTGCGGTTTGGGTGGCTCTACGCAATGTCAAGGCTTCGACAAATAGTCCTTGGGA
Ta_fae1_Mut1     TAATAGTGCGGTTTGGGTGGCTCTACGCAATGTCAAGGCTTCGACAAATAGTCCTTGGGA
                 ************************************************************

Ta_FAE1          ACATTGCATTGATAGATATCCAGATGCAATTGATTCTGATTCGGGTAAGTCAGAGACTCG
Ta_fae1_Mut1     ACATTGCATTGATAGATATCCAGATGCAATTGATTCTGATTCGGGTAAGTCAGAGACTCG
                 ************************************************************

Ta_FAE1          TGTCCAAAACGGTCGGTCCTAA
Ta_fae1_Mut1     TGTCCAAAACGGTCGGTCCTAA
                 **********************
```

TT8

The top lines of the following sequence comparison are 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 (Ta_tt8_Mut1). The edits are highlighted in red.

```
Ta_TT8_Wt         ATGGATGAATCAAGTATTTTTACGGCAGAGAAAGTGATCGGAGCTGAGAAAAGAGAGCTT
Ta_tt8_Mut1       ATGGATGAATCAAGTATTTTTACGGCAGAGAAAGTGATCGGAGCTGAGAAAAGAGAGCTT
                  ************************************************************

Ta_TT8_Wt         CAAGGGCTGCTTAAGGCGGCGGTGCAATCTGTGGAGTGGACTTATAGTCTCTTCTGGCAA
Ta_tt8_Mut1       CAAGGGCTGCTTAAGGCGGCGGTGCAATCTGTGGAGTGGACTTATAGTCTCTTCTGGCAA
                  ************************************************************

Ta_TT8_Wt         CTTTGTCCTCAACAAAGGTTCTTTTTTTTTTTTAATAAATTTCATCGATCTCTCACAATA
Ta_tt8_Mut1       CTTTGTCCTCAACAAAGGTTCTTTTTTTTTTTTAATAAATTTCATCGATCTCTCACAATA
                  ************************************************************

Ta_TT8_Wt         AAAACCCTAAATTTTATATCATTTATTATTATATGTTTAACTACATAATTATCAGTATTT
Ta_tt8_Mut1       AAAACCCTAAATTTTATATCATTTATTATTATATGTTTAACTACATAATTATCAGTATTT
                  ************************************************************

Ta_TT8_Wt         TAACCGTCCATGTGCTTTATTTGGTTCCATTTCTGTCTCATATTTTACTTGAGGTTCAGA
Ta_tt8_Mut1       TAACCGTCCATGTGCTTTATTTGGTTCCATTTCTGTCTCATATTTTACTTGAGGTTCAGA
                  ************************************************************

Ta_TT8_Wt         CTGCCGAGCACATCTCTCGTTTGTCTCGAATCTGTGAGACTTTTTCGTTTATTGGCACTT
Ta_tt8_Mut1       CTGCCGAGCACATCTCTCGTTTGTCTCGAATCTGTGAGACTTTTTCGTTTATTGGCACTT
                  ************************************************************

Ta_TT8_Wt         CTGTGTCAATTGAGTTATACTGAAGTAATTATATGTTTAAATGAATTAGGGTTTTGCTGT
Ta_tt8_Mut1       CTGTGTCAATTGAGTTATACTGAAGTAATTATATGTTTAAATGAATTAGGGTTTTGCTGT
                  ************************************************************

Ta_TT8_Wt         GGGAGAATGGATACTACAACGGTGCAATAAAG-ACGAGGAAGACAACTCAGCCGGCGGAA
Ta_tt8_Mut1       GGGAGAATGGATACTACAACGGTGCAATAAAGGACGAGGAAGACAACTCAGCCGGCGGAA
                  ******************************* ************************

Ta_TT8_Wt         GTGACGGCGGAAGAGGCTGCGTTAGAGAGGAGTCAGCAGCTAAGGGAACTTTACGAGGCC
Ta_tt8_Mut1       GTGACGGCGGAAGAGGCTGCGTTAGAGAGGAGTCAGCAGCTAAGGGAACTTTACGAGGCC
                  ************************************************************

Ta_TT8_Wt         CTTTTGGCCGGAGAGTCCTCATCGGAAGCTAGGGCATGCACGGCATTATCGCCGGAGGAT
Ta_tt8_Mut1       CTTTTGGCCGGAGAGTCCTCATCGGAAGCTAGGGCATGCACGGCATTATCGCCGGAGGAT
                  ************************************************************

Ta_TT8_Wt         CTGACGGAGACTGAATGGTTTTATCTAATGTGTGTCTCTTTCTCTTTCCCTCCTCCTTCC
Ta_tt8_Mut1       CTGACGGAGACTGAATGGTTTTATCTAATGTGTGTCTCTTTCTCTTTCCCTCCTCCTTCC
                  ************************************************************

Ta_TT8_Wt         GGGTACCCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
Ta_tt8_Mut1       GGGTACCCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
                  ************************************************************

Ta_TT8_Wt         CTCTTTTGTCTATACTGAAGTTTCTTAATTTATCTTTTTATCATCTCCTACTGAAGACAA
Ta_tt8_Mut1       CTCTTTTGTCTATACTGAAGTTTCTTAATTTATCTTTTTATCATCTCCTACTGAAGACAA
                  ************************************************************
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Ta_TT8_Wt       AAATAGTATTGTGTGTTAAATGCGAATCACGAATATTGTGGAAGCATTAAAAACAAACTG
Ta_tt8_Mut1     AAATAGTATTGTGTGTTAAATGCGAATCACGAATATTGTGGAAGCATTAAAAACAAACTG
                ************************************************************

Ta_TT8_Wt       AGGAGGTTGAGTTACTGAAAGAAGAAATGTATTGGAGTTGATGAAACGTACACTCCATTT
Ta_tt8_Mut1     AGGAGGTTGAGTTACTGAAAGAAGAAATGTATTGGAGTTGATGAAACGTACACTCCATTT
                ************************************************************

Ta_TT8_Wt       TAGTGAACATAATTGGACCGTTGAGATTCTTATTTTTTTGCTGATTGATTATCTAAAGTA
Ta_tt8_Mut1     TAGTGAACATAATTGGACCGTTGAGATTCTTATTTTTTTGCTGATTGATTATCTAAAGTA
                ************************************************************

Ta_TT8_Wt       GAAGCATAAATAGATAATACATAAATGCATAACAAATTGTGTTAGTTATGGGTATAGTTA
Ta_tt8_Mut1     GAAGCATAAATAGATAATACATAAATGCATAACAAATTGTGTTAGTTATGGGTATAGTTA
                ************************************************************

Ta_TT8_Wt       ATGCTTTTTCTCTATGAGAGGAAAAAAAAAAAAATATATAAATGTGGAAGTAATAATTTT
Ta_tt8_Mut1     ATGCTTTTTCTCTATGAGAGGAAAAAAAAAAAAATATATAAATGTGGAAGTAATAATTTT
                ************************************************************

Ta_TT8_Wt       GTAGGATGCCAGGAAAGGCGTATGCGAGGAGGAAACACGTATGGCTATGTGGTGCAAATG
Ta_tt8_Mut1     GTAGGATGCCAGGAAAGGCGTATGCGAGGAGGAAACACGTATGGCTATGTGGTGCAAATG
                ************************************************************

Ta_TT8_Wt       AGGTTGACAGTAAAATCTTTTCTAGGGCTATTCTCGCAAAGGTCTATTTCCTTTTTCATT
Ta_tt8_Mut1     AGGTTGACAGTAAAATCTTTTCTAGGGCTATTCTCGCAAAGGTCTATTTCCTTTTTCATT
                ************************************************************

Ta_TT8_Wt       TACCACTACTCTATGCATCTACTTCTCTACCTATTTATATATCTCATCTTTCAAATTAAT
Ta_tt8_Mut1     TACCACTACTCTATGCATCTACTTCTCTACCTATTTATATATCTCATCTTTCAAATTAAT
                ************************************************************

Ta_TT8_Wt       TAATTTTCTGTCTTTATTTTCTTGGATGCTCCTTCTACATCGGTCGGTTCCTTAATGGTT
Ta_tt8_Mut1     TAATTTTCTGTCTTTATTTTCTTGGATGCTCCTTCTACATCGGTCGGTTCCTTAATGGTT
                ************************************************************

Ta_TT8_Wt       AGAGTGCCAAAATCCAGGTAAACGTTGTCTTTATTGATTAATTCTAATTTTGAGTAATAT
Ta_tt8_Mut1     AGAGTGCCAAAATCCAGGTAAACGTTGTCTTTATTGATTAATTCTAATTTTGAGTAATAT
                ************************************************************

Ta_TT8_Wt       TTTACATTTATTTTACATGTTTGAAAATTGTTTTGTGATAAAAAAAAAGCAGACAGTGGT
Ta_tt8_Mut1     TTTACATTTATTTTACATGTTTGAAAATTGTTTTGTGATAAAAAAAAAGCAGACAGTGGT
                ************************************************************

Ta_TT8_Wt       TTGCATTCCCATGCTTGATGGCGTTGTGGAACTAGGCACAACGAACAAGGTACGGCGTAG
Ta_tt8_Mut1     TTGCATTCCCATGCTTGATGGCGTTGTGGAACTAGGCACAACGAACAAGGTACGGCGTAG
                ************************************************************

Ta_TT8_Wt       TTATCTTTTTATATATGCATAACCAAATGGTTAAGAAAAAGGTTAGAAGAGAAATAGATC
Ta_tt8_Mut1     TTATCTTTTTATATATGCATAACCAAATGGTTAAGAAAAAGGTTAGAAGAGAAATAGATC
                ************************************************************

Ta_TT8_Wt       ATGCTTAAGTTTTATCAGTTAAATTAAAAATGTAAAAATAAGATATTATGTTCATTAATA
Ta_tt8_Mut1     ATGCTTAAGTTTTATCAGTTAAATTAAAAATGTAAAAATAAGATATTATGTTCATTAATA
                ************************************************************

Ta_TT8_Wt       ATGTATAGTCCCTGTTAGTTAAAAAAAAGAATAAAATATTTAACCATTTGAAGTCATAAT
Ta_tt8_Mut1     ATGTATAGTCCCTGTTAGTTAAAAAAAAGAATAAAATATTTAACCATTTGAAGTCATAAT
                ************************************************************
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Ta_TT8_Wt       ATAAAAATATTGTTTTTGGAGATAGTACATAATTCTCACAATAAAAAAAATAACAAAGGG
Ta_tt8_Mut1     ATAAAAATATTGTTTTTGGAGATAGTACATAATTCTCACAATAAAAAAAATAACAAAGGG
                ************************************************************

Ta_TT8_Wt       ATGATTAAGGGAAGGAGTTGGATACATGTTGTTTGTCTGTGTGTGTGAAGGTAAAAGAAG
Ta_tt8_Mut1     ATGATTAAGGGAAGGAGTTGGATACATGTTGTTTGTCTGTGTGTGTGAAGGTAAAAGAAG
                ************************************************************

Ta_TT8_Wt       ATATAGCGTTTGTTGAGCTCATAAAGAGTTTTTTCCATAACCACCCCAAGTCAAACCCAA
Ta_tt8_Mut1     ATATAGCGTTTGTTGAGCTCATAAAGAGTTTTTTCCATAACCACCCCAAGTCAAACCCAA
                ************************************************************

Ta_TT8_Wt       AAGCTGCTCTTTCTGAACACTCCATCAACGAAGAGCACGAAGAAGACGAAGAACAAGAAG
Ta_tt8_Mut1     AAGCTGCTCTTTCTGAACACTCCATCAACGAAGAGCACGAAGAAGACGAAGAACAAGAAG
                ************************************************************

Ta_TT8_Wt       AAGAAGAAGAAGAAGAAGTAGAAGAAGAAATGACAATGTCAGAGGAGATAAGGCTTGGCT
Ta_tt8_Mut1     AAGAAGAAGAAGAAGAAGTAGAAGAAGAAATGACAATGTCAGAGGAGATAAGGCTTGGCT
                ************************************************************

Ta_TT8_Wt       CTCCTGATGATGATGACGTCTCCAATCAAAACCTACTCTCTGATTTCCATGTAGAATCAA
Ta_tt8_Mut1     CTCCTGATGATGATGACGTCTCCAATCAAAACCTACTCTCTGATTTCCATGTAGAATCAA
                ************************************************************

Ta_TT8_Wt       CCCACACTTTAGGTATACACTTATACATTAAATTAGTTAACGATATCATTACACGTATCT
Ta_tt8_Mut1     CCCACACTTTAGGTATACACTTATACATTAAATTAGTTAACGATATCATTACACGTATCT
                ************************************************************

Ta_TT8_Wt       ATTTATTTTGTTAACAAGAAATTTAAAAATATTCGCCATTTCTTTGTTATGTCTAAAGAA
Ta_tt8_Mut1     ATTTATTTTGTTAACAAGAAATTTAAAAATATTCGCCATTTCTTTGTTATGTCTAAAGAA
                ************************************************************

Ta_TT8_Wt       AATCTATAAAATTTTATGAATAGACACACACATGGACATGATGAATCTAATGGAGGAGGG
Ta_tt8_Mut1     AATCTATAAAATTTTATGAATAGACACACACATGGACATGATGAATCTAATGGAGGAGGG
                ************************************************************

Ta_TT8_Wt       TGGAAACTATTCTCAGACAGTATCAACACTTCTTATGTCACAACCCACGAGTCTTTTTTC
Ta_tt8_Mut1     TGGAAACTATTCTCAGACAGTATCAACACTTCTTATGTCACAACCCACGAGTCTTTTTTC
                ************************************************************

Ta_TT8_Wt       AGATTCAGTTTCCACATCTTCTTACATCCAATCATCATTTGCCACATGGAAGGCTGATAA
Ta_tt8_Mut1     AGATTCAGTTTCCACATCTTCTTACATCCAATCATCATTTGCCACATGGAAGGCTGATAA
                ************************************************************

Ta_TT8_Wt       TTTTAAAGAGCATCAGCGAGTGGAAACTAAATCGACGTCGTCGTCGCAATGGATGCTCAA
Ta_tt8_Mut1     TTTTAAAGAGCATCAGCGAGTGGAAACTAAATCGACGTCGTCGTCGCAATGGATGCTCAA
                ************************************************************

Ta_TT8_Wt       ACACATAATCTTGAGAGTTCCTTTACTCCACGACCACACTAAAGAAAAGAGGCTGCCTCG
Ta_tt8_Mut1     ACACATAATCTTGAGAGTTCCTTTACTCCACGACCACACTAAAGAAAAGAGGCTGCCTCG
                ************************************************************

Ta_TT8_Wt       AGAAGAGCTTAATCACGTGGTGGCAGAGCGCCGCAGGAGAGAGAAGCTGAATGAGAGATT
Ta_tt8_Mut1     AGAAGAGCTTAATCACGTGGTGGCAGAGCGCCGCAGGAGAGAGAAGCTGAATGAGAGATT
                ************************************************************

Ta_TT8_Wt       CATAACACTGAGATCATTGGTTCCCTTTGTGACCAAGATGGATAAAGTCTCAATTCTTGG
Ta_tt8_Mut1     CATAACACTGAGATCATTGGTTCCCTTTGTGACCAAGATGGATAAAGTCTCAATTCTTGG
                ************************************************************
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Ta_TT8_Wt         AGACACCATCAACTACGTAAACCATCTTCGAAATAGGGTCCAAGAGCTGGAGACTAATCA
Ta_tt8_Mut1       AGACACCATCAACTACGTAAACCATCTTCGAAATAGGGTCCAAGAGCTGGAGACTAATCA
                  ************************************************************

Ta_TT8_Wt         TCACGAACAAAAACATAAGCGGATGCGTAGCTGTAAGGGAAAAACGTGGGAAGAGGTCGT
Ta_tt8_Mut1       TCACGAACAAAAACATAAGCGGATGCGTAGCTGTAAGGGAAAAACGTGGGAAGAGGTCGT
                  ************************************************************

Ta_TT8_Wt         TGAGGTTTCCATCATAGAGAGTGATGTTTTGTTAGAGATGAGATGCGAGTACCGAGATGG
Ta_tt8_Mut1       TGAGGTTTCCATCATAGAGAGTGATGTTTTGTTAGAGATGAGATGCGAGTACCGAGATGG
                  ************************************************************

Ta_TT8_Wt         TCTATTGCTCGACATCCTTCAGGTTCTTAAGGAACATGGTATAGAGACTACTGCAGTTCA
Ta_tt8_Mut1       TCTATTGCTCGACATCCTTCAGGTTCTTAAGGAACATGGTATAGAGACTACTGCAGTTCA
                  ************************************************************

Ta_TT8_Wt         TACCGCGGTGAACGAGCGTGATTTCGAGGCCGAGATAAGGGCTATGGTGAGAGGGAAGAA
Ta_tt8_Mut1       TACCGCGGTGAACGAGCGTGATTTCGAGGCCGAGATAAGGGCTATGGTGAGAGGGAAGAA
                  ************************************************************

Ta_TT8_Wt         ACCAAGCATTGCTGAGGTCAAAAGAGCCATCCATCAAACTATATCCAATATTAAACTATA
Ta_tt8_Mut1       ACCAAGCATTGCTGAGGTCAAAAGAGCCATCCATCAAACTATATCCAATATTAAACTATA
                  ************************************************************

Ta_TT8_Wt         G
Ta_tt8_Mut1       G
                  *
```

[ ] **CBI-Deleted**

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

[

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

One representative modified gene sequence of [ ] is included for CBI-Deleted comparison. One site in the gene is edited; the modified sequence includes a single A insertion. The edit is in red.

[

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

One representative modified gene sequence of [ ] is included for CBI-Deleted comparison. One site in the gene is edited; the modified sequence includes a single A insertion. The edit is in red.

[

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