October 25, 2022

Bernadette Juarez
APHIS Deputy Administrator
Biotechnology Regulatory Services

Ms. Juarez,

With this letter we respectfully request a Regulatory Status Review from USDA-APHIS' Biotechnology Regulatory Services (BRS) for the following three Plant Trait Mechanisms 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. 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 the combination of those previously submitted PTMOAs in pennycress.   CBI-deleted

Additionally, these traits were evaluated in the AIR process. In response to each of three previously submitted AIR letters[1], BRS deregulated pennycress lines harboring disruptions in *FAE1*, *TT8*, [   ], and *AOP* genes, concluding that: "…your gene-edited pennycress lines are not themselves plant pests….Additionally, 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 your pennycress lines would increase the weediness of pennycress." *AOP2* is one of several genes that, when disrupted, reduce glucosinolate levels. This RSR requests evaluation of pennycress with mutations in one other gene that results in the same low glucosinolate phenotype, in addition to the same mutations in *FAE1, TT8,* and [   ] that lead to the same phenotypes as previously reviewed.   CBI-deleted

1. Information about Requestor

   First Name: Traci

   Last Name: Hagedorn

   Position: Consultant

   Organization Name (if applicable): Hjelle Advisors, LLC on behalf of CoverCress Inc.

   Contact information (choose one or both)

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[1] Cover Cress, Inc. Loss of *FAE1*, *TT8*, *AOP2* – USDA response January 29, 2020; CoverCress, Inc. Loss of *FAE1, TT8,* [   ] – USDA response May 7, 2020; CoverCress, Inc. Loss of *TT8, AOP2* – USDA response August 31, 2020   CBI-deleted

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. customarily and actually treats commercial and financial information as private and provides these information to the government under an assurance of privacy. We consider the information as 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:

CoverCress, Inc. has developed through selection and breeding several elite germplasm lines that have optimized agronomic characteristics. This improved germplasm is referred to as CoverCress™ and lines to date include B3, B28, B48, 2032, 183002-B-14, 183002-B-6, 183011-B-5, 183056-B-29, 182002-B-B-31, 183002-B-6, 183002-B-9, 183006-B-13, 183007-B-26, 183007-B-3, 183036-B-10, 183059-B-24, 183059-B-4 and 183059-B-20. It is envisioned that the above-mentioned lines and additional lines developed in the breeding program will undergo late stage editing to produce the lower glucosinolate, low erucic acid, and lower fiber phenotypes within germplasm that is already optimized for commercial production.

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

Nature of modification(s)

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

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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 was included in the plasmid to confer red fluorescence in plants that successfully take up the plasmid introduced by *A. tumefacians*. Presence of the construct in T_1 plants was 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 was screened for segregants that do not have the transgene as indicated by lack of red fluorescence. Resulting seedlings in the T_2 generation were screened again for negative presence of DsRED and Cas, as well as homozygous edits to [   ], *FAE1,* and *TT8* genes.   CBI-deleted

Examples of these edits are listed in the following section.

Sequence and Comparison of each Modification

[   ]   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 base pair insertion, marked in red. The full gene
sequences and sequence comparison are included in Appendix 1.
[

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[   ]   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 base pair insertion, highlighted in red. The full gene
sequences and sequence comparison are included in Appendix 1.
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FAE1

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

```
Ta_FAE1       GCCTTCACCGTTTTCGGTTTGGCTCTCTACATCGTAA-CCCGGCCCAAACCGGTTTACCT
Ta_fae1_mut1  GCCTTCACCGTTTTCGGTTTGGCTCTCTACATCGTAAACCCGGCCCAAACCGGTTTACCT
              ************************************* ********************
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TT8

The top line of the following sequence comparison is the unmodified sequence of *TT8*. Two representative modified gene sequences of *TT8* are included for comparison. One site in the gene is edited; one modified sequence includes a single G deletion and one modified sequence includes a single G insertion. The edits are highlighted in red. The full gene sequences and sequence comparison are included in Appendix 1.

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Ta_TT8_Wt    GGGAGAATGGATACTACAACGGTGCAATAAAG-ACGAGGAAGACAACTCAGCCGGCGGAA
Ta_TT8_Mut2  GGGAGAATGGATACTACAACGGTGCAATAAA--ACGAGGAAGACAACTCAGCCGGCGGAA
Ta_TT8_Mut1  GGGAGAATGGATACTACAACGGTGCAATAAAGGACGAGGAAGACAACTCAGCCGGCGGAA
             ****************************** ************************
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5. Description of new traits

Intended trait #1: low total glucosinolate seeds

Intended phenotype: 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 (Moser et al. 2009; Altendorf et al. 2019; McGinn et al. 2019). 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).

Reducing total glucosinolate levels will make pennycress or CoverCress more susceptible to diseases and environmental conditions than the wildtype. If low-glucosinolate seeds are

scattered during harvest, the likelihood of persistence and germination the following season is reduced compared to the wildtype.

Intended trait #2: low erucic acid seeds

Intended phenotype #2: 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 (McGinn et al. 2019; Chopra et al. 2020; Chopra 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 #3: lower fiber seeds

Intended phenotype #3: 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 thusly, 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 reduced seed dormancy, a major factor in the weediness of this plant (Ott et al. 2021; Chopra et al. 2018b).

6. Description of each MOA

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 1: 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 (Sedbrook et al. 2014; Chopra et al. 2018b; Chopra et al. 2020).
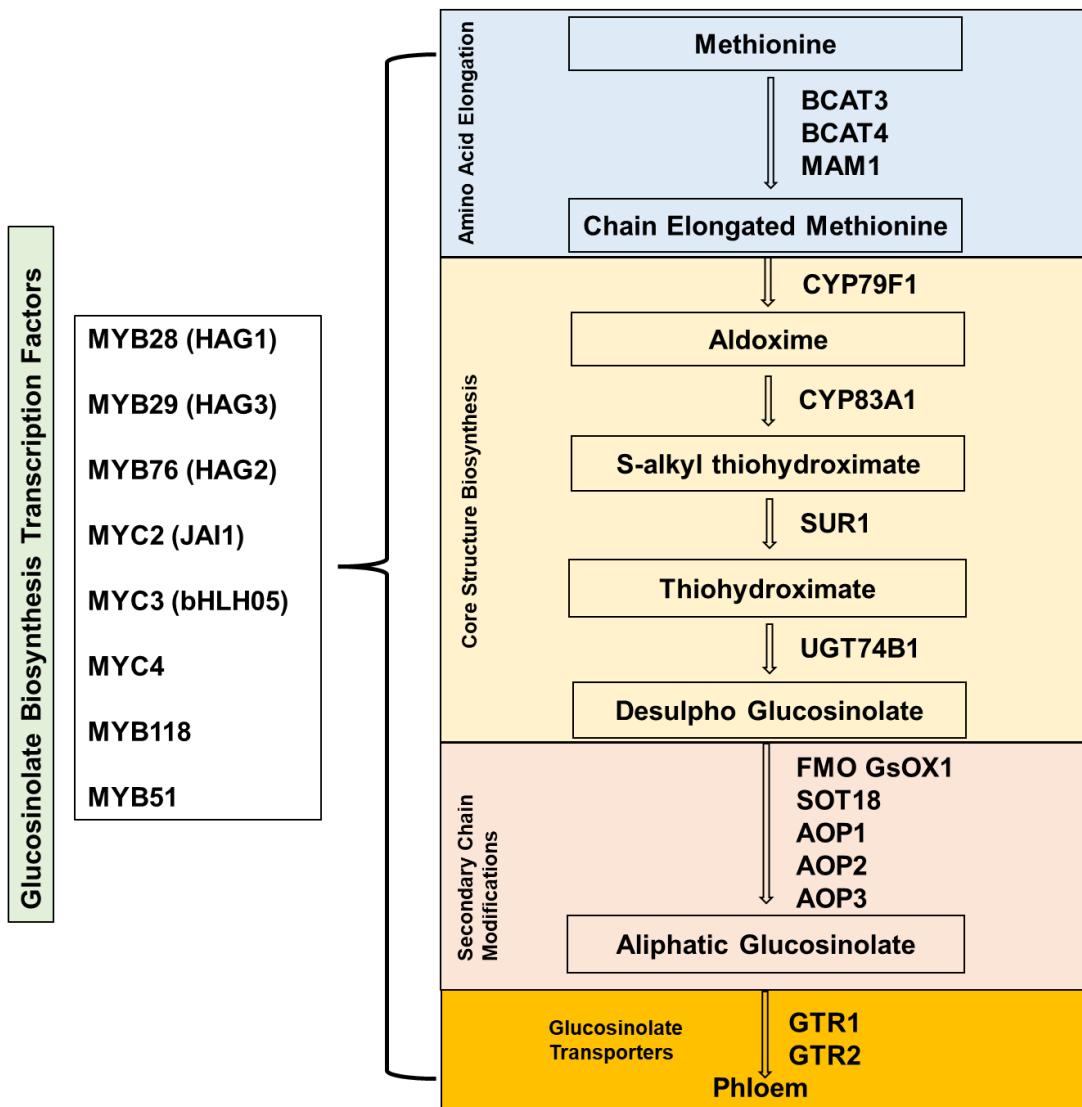
Figure 1: Major steps in glucosinolate biosynthesis

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. To reach the desired 70-80% reduction in glucosinolate levels will require loss of function mutations in a combination of the 2 gene targets in this RSR request.

These gene targets include the transcription factor [   ] and the transporter [   ]. Each gene and its respective contribution to achieve reduced glucosinolate levels is described below.

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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; Sedbrook et al. 2014; Moser et al. 2009).

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 that fact that the that 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 2), 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.
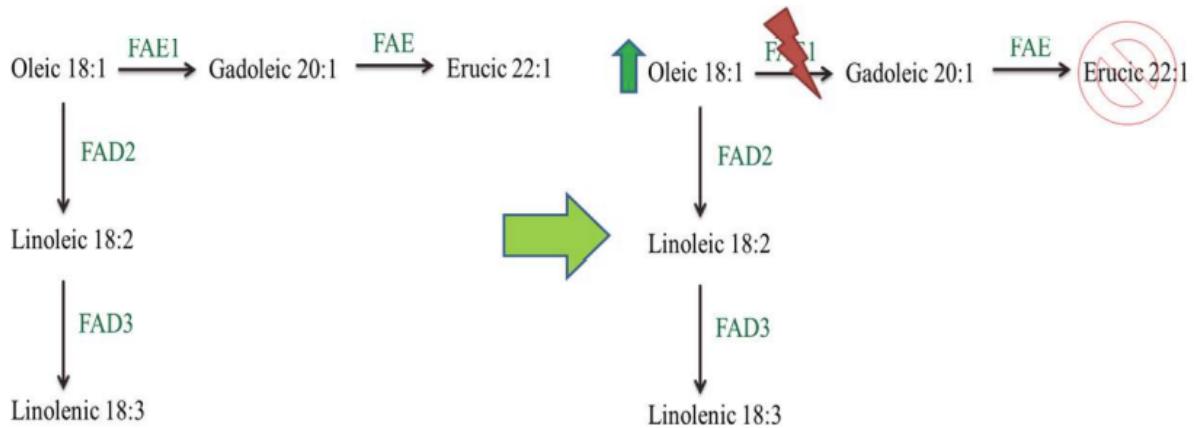
Figure 2: Fatty Acid Pathway to Reduce Erucic Acid Levels

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 and 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 3).

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 (Slominski et al. 1994 and 1999; Simbaya et al. 1995). 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.
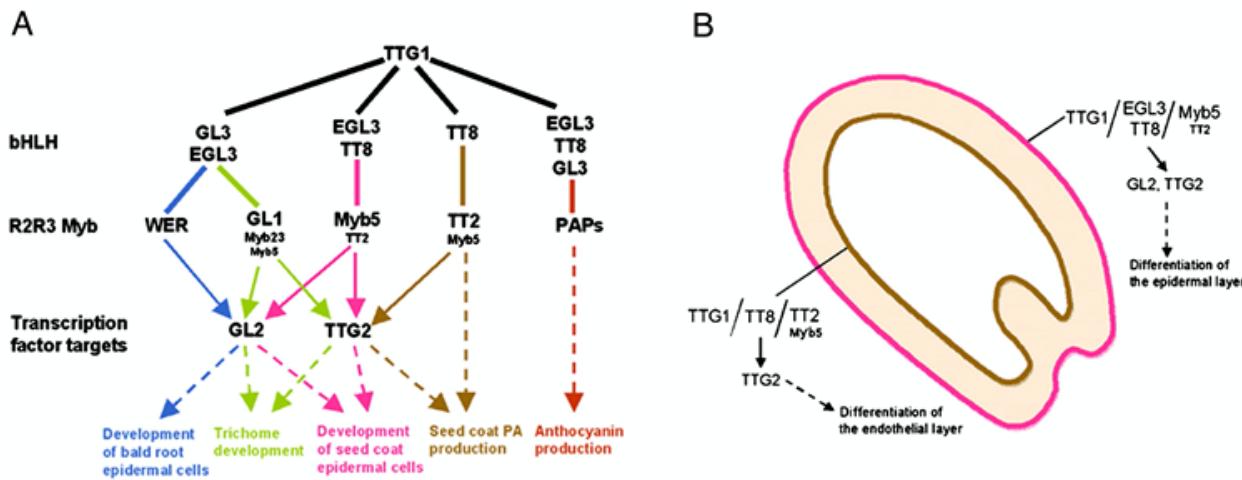
Figure 3: Models for the regulation of TTG-1 dependent pathways in seed coat development. (A) A regulatory network for the positive control of TTG1-dependent epidermal cell fates. Solid lines indicate interactions between members of a complex. Solid arrows indicate direct regulation of *GL2* or *TTG2* 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).

In conclusion, CoverCress™ is currently being developed as a new cash 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,* and *TT8* genes have resulted in the   CBI-deleted reduced total glucosinolates, low erucic acid, and lower fiber seed traits, respectively. The mechanism of action for the genetic changes leading to each phenotype is well-understood. Based on this information, we request USDA's review of the combination of these previously reviewed PTMOAs and confirmation that the traits, produced through simultaneous or sequential editing of any combination of [   ], *FAE1,* and *TT8* genes in pennycress, is not   CBI-deleted subject to regulation under Part 340.

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Appendix 1 – Full Sequences and Sequence Comparisons

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TaFAE1 Wild Type CDS;
ATGACGTCCGTTAACGTTAAGCTCCTTTACCATTACGTCATCACCAACTTTTTCAACCTTTGCTTCTTCCCG
TTAGCGGCGATCGTTGCCGGAAAAGCCTCTCGGCTTACCACAAACGATCTTCACCACTTCTACTATTCCTA
TCTCCAACACAACCTAATAACCATATCTCTACTCTTTGCCTTCACCGTTTTCGGTT<mark>TGGCTCTCTACATCGT</mark>
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TTCGTCCTGGCTTGATTTCTTGAGGAAGATTCAGGAGCGGTCTGGTCTAGGCGATGAAACCCACGGCCC

CGAGGGACTGCTTCAGGTCCCTCCACGGAAGACTTTTGCCGCGGCGCGTGAAGAAACAGAGCAAGTGA
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TaFAE1 Mutant1 CDS;
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CGTGATCGATGTGCTACAGAAGAACTTAGGTCTATTGCCGATCGATGTGGAGGCATCTAGGTCAACGTT
ACATAGATTTGGGAACACTTCGTCTAGCTCAATTTGGTATGAATTGGCGTACATAGAGGCAAAAGGAAG
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GGGTGGCTCTACGCAATGTCAAGGCTTCGACAAATAGTCCTTGGGAACATTGCATTGATAGATATCCAG
ATGCAATTGATTCTGATTCGGGTAAGTCAGAGACTCGTGTCCAAAACGGTCGGTCCTAA

TT8 Wild Type, unmodified sequence
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AGGTTCTTAAGGAACATGGTATAGAGACTACTGCAGTTCATACCGCGGTGAACGAGCGTGATTTCGAGG
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TT8 Modified Sequence, Representative Sequence #1
>Ta_TT8_Mut1
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AGAACAAGAAGAAGAAGAAGAAGAAGAAGTAGAAGAAGAAATGACAATGTCAGAGGAGATAAGGCTT
GGCTCTCCTGATGATGATGACGTCTCCAATCAAAACCTACTCTCTGATTTCCATGTAGAATCAACCCACAC
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TCCACATCTTCTTACATCCAATCATCATTTGCCACATGGAAGGCTGATAATTTTAAAGAGCATCAGCGAGT
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GACCACACTAAAGAAAAGAGGCTGCCTCGAGAAGAGCTTAATCACGTGGTGGCAGAGCGCCGCAGGA
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TCTCAATTCTTGGAGACACCATCAACTACGTAAACCATCTTCGAAATAGGGTCCAAGAGCTGGAGACTAA
TCATCACGAACAAAAACATAAGCGGATGCGTAGCTGTAAGGGAAAAACGTGGGAAGAGGTCGTTGAG
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ATCCTTCAGGTTCTTAAGGAACATGGTATAGAGACTACTGCAGTTCATACCGCGGTGAACGAGCGTGAT
TTCGAGGCCGAGATAAGGGCTATGGTGAGAGGGAAGAAACCAAGCATTGCTGAGGTCAAAAGAGCCA
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TT8 Modified Sequence, Representative Sequence #2
>Ta_TT8_Mut2
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GGAGAATGGATACT<mark>ACAACGGTGCAATAAA(-</mark>
<mark>)ACG</mark>AGGAAGACAACTCAGCCGGCGGAAGTGACGGCGGAAGAGGCTGCGTTAGAGAGGAGTCAGCAG
CTAAGGGAACTTTACGAGGCCCTTTTGGCCGGAGAGTCCTCATCGGAAGCTAGGGCATGCACGGCATTA
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CGGgtacccaactctctctctctctctctctctctctctctctctctctctctctttttgtctatactgaagtttcttaatttatcttttt
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taaaaaaaataacaaagggatgattaagggaaggagttggatacatgttgtttgtctgtgtgtgtgaagGTAAAAGAAGATATA
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TGTCACAACCCACGAGTCTTTTTTCAGATTCAGTTTCCACATCTTCTTACATCCAATCATCATTTGCCACAT
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ATCTTCGAAATAGGGTCCAAGAGCTGGAGACTAATCATCACGAACAAAAACATAAGCGGATGCGTAGCT
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Sequence Comparisons of the unmodified and modified genes

[

CBI-deleted

]

[

CBI-deleted

]

[

CBI-deleted

]

[

CBI-deleted

]

[

CBI-deleted

]

[

]

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. One site in the gene is edited and includes a single base pair insertion, highlighted in red.

```
Ta_FAE1      ATGACGTCCGTTAACGTTAAGCTCCTTTACCATTACGTCATCACCAACTTTTTCAACCTT
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
             ************************************************************
```

```
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*. Two representative modified gene sequences of *TT8* are included for comparison. One site in the gene is edited; one modified sequence includes a single G deletion and one modified sequence includes a single G insertion. The edits are highlighted in red.

```
Ta_TT8_Wt    ATGGATGAATCAAGTATTTTTACGGCAGAGAAAGTGATCGGAGCTGAGAAAAGAGAGCTT
Ta_TT8_Mut2  ATGGATGAATCAAGTATTTTTACGGCAGAGAAAGTGATCGGAGCTGAGAAAAGAGAGCTT
Ta_TT8_Mut1  ATGGATGAATCAAGTATTTTTACGGCAGAGAAAGTGATCGGAGCTGAGAAAAGAGAGCTT
             ************************************************************

Ta_TT8_Wt    CAAGGGCTGCTTAAGGCGGCGGTGCAATCTGTGGAGTGGACTTATAGTCTCTTCTGGCAA
Ta_TT8_Mut2  CAAGGGCTGCTTAAGGCGGCGGTGCAATCTGTGGAGTGGACTTATAGTCTCTTCTGGCAA
Ta_TT8_Mut1  CAAGGGCTGCTTAAGGCGGCGGTGCAATCTGTGGAGTGGACTTATAGTCTCTTCTGGCAA
             ************************************************************

Ta_TT8_Wt    CTTTGTCCTCAACAAAGGTTCTTTTTTTTTTTTAATAAATTTCATCGATCTCTCACAATA
Ta_TT8_Mut2  CTTTGTCCTCAACAAAGGTTCTTTTTTTTTTTTAATAAATTTCATCGATCTCTCACAATA
Ta_TT8_Mut1  CTTTGTCCTCAACAAAGGTTCTTTTTTTTTTTTAATAAATTTCATCGATCTCTCACAATA
             ************************************************************

Ta_TT8_Wt    AAAACCCTAAATTTTATATCATTTATTATTATATGTTTAACTACATAATTATCAGTATTT
Ta_TT8_Mut2  AAAACCCTAAATTTTATATCATTTATTATTATATGTTTAACTACATAATTATCAGTATTT
Ta_TT8_Mut1  AAAACCCTAAATTTTATATCATTTATTATTATATGTTTAACTACATAATTATCAGTATTT
             ************************************************************

Ta_TT8_Wt    TAACCGTCCATGTGCTTTATTTGGTTCCATTTCTGTCTCATATTTTACTTGAGGTTCAGA
Ta_TT8_Mut2  TAACCGTCCATGTGCTTTATTTGGTTCCATTTCTGTCTCATATTTTACTTGAGGTTCAGA
Ta_TT8_Mut1  TAACCGTCCATGTGCTTTATTTGGTTCCATTTCTGTCTCATATTTTACTTGAGGTTCAGA
             ************************************************************

Ta_TT8_Wt    CTGCCGAGCACATCTCTCGTTTGTCTCGAATCTGTGAGACTTTTTCGTTTATTGGCACTT
Ta_TT8_Mut2  CTGCCGAGCACATCTCTCGTTTGTCTCGAATCTGTGAGACTTTTTCGTTTATTGGCACTT
Ta_TT8_Mut1  CTGCCGAGCACATCTCTCGTTTGTCTCGAATCTGTGAGACTTTTTCGTTTATTGGCACTT
             ************************************************************

Ta_TT8_Wt    CTGTGTCAATTGAGTTATACTGAAGTAATTATATGTTTAAATGAATTAGGGTTTTGCTGT
Ta_TT8_Mut2  CTGTGTCAATTGAGTTATACTGAAGTAATTATATGTTTAAATGAATTAGGGTTTTGCTGT
Ta_TT8_Mut1  CTGTGTCAATTGAGTTATACTGAAGTAATTATATGTTTAAATGAATTAGGGTTTTGCTGT
             ************************************************************

Ta_TT8_Wt    GGGAGAATGGATACTACAACGGTGCAATAAAG-ACGAGGAAGACAACTCAGCCGGCGGAA
Ta_TT8_Mut2  GGGAGAATGGATACTACAACGGTGCAATAAA--ACGAGGAAGACAACTCAGCCGGCGGAA
Ta_TT8_Mut1  GGGAGAATGGATACTACAACGGTGCAATAAAGGACGAGGAAGACAACTCAGCCGGCGGAA
             *******************************  ***************************

Ta_TT8_Wt    GTGACGGCGGAAGAGGCTGCGTTAGAGAGGAGTCAGCAGCTAAGGGAACTTTACGAGGCC
Ta_TT8_Mut2  GTGACGGCGGAAGAGGCTGCGTTAGAGAGGAGTCAGCAGCTAAGGGAACTTTACGAGGCC
Ta_TT8_Mut1  GTGACGGCGGAAGAGGCTGCGTTAGAGAGGAGTCAGCAGCTAAGGGAACTTTACGAGGCC
             ************************************************************

Ta_TT8_Wt    CTTTTGGCCGGAGAGTCCTCATCGGAAGCTAGGGCATGCACGGCATTATCGCCGGAGGAT
Ta_TT8_Mut2  CTTTTGGCCGGAGAGTCCTCATCGGAAGCTAGGGCATGCACGGCATTATCGCCGGAGGAT
Ta_TT8_Mut1  CTTTTGGCCGGAGAGTCCTCATCGGAAGCTAGGGCATGCACGGCATTATCGCCGGAGGAT
             ************************************************************

Ta_TT8_Wt    CTGACGGAGACTGAATGGTTTTATCTAATGTGTGTCTCTTTCTCTTTCCCTCCTCCTTCC
Ta_TT8_Mut2  CTGACGGAGACTGAATGGTTTTATCTAATGTGTGTCTCTTTCTCTTTCCCTCCTCCTTCC
Ta_TT8_Mut1  CTGACGGAGACTGAATGGTTTTATCTAATGTGTGTCTCTTTCTCTTTCCCTCCTCCTTCC
             ************************************************************
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Ta_TT8_Wt      GGGTACCCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
Ta_TT8_Mut2    GGGTACCCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
Ta_TT8_Mut1    GGGTACCCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
               ************************************************************

Ta_TT8_Wt      CTCTTTTGTCTATACTGAAGTTTCTTAATTTATCTTTTTATCATCTCCTACTGAAGACAA
Ta_TT8_Mut2    CTCTTTTGTCTATACTGAAGTTTCTTAATTTATCTTTTTATCATCTCCTACTGAAGACAA
Ta_TT8_Mut1    CTCTTTTGTCTATACTGAAGTTTCTTAATTTATCTTTTTATCATCTCCTACTGAAGACAA
               ************************************************************

Ta_TT8_Wt      AAATAGTATTGTGTGTTAAATGCGAATCACGAATATTGTGGAAGCATTAAAAACAAACTG
Ta_TT8_Mut2    AAATAGTATTGTGTGTTAAATGCGAATCACGAATATTGTGGAAGCATTAAAAACAAACTG
Ta_TT8_Mut1    AAATAGTATTGTGTGTTAAATGCGAATCACGAATATTGTGGAAGCATTAAAAACAAACTG
               ************************************************************

Ta_TT8_Wt      AGGAGGTTGAGTTACTGAAAGAAGAAATGTATTGGAGTTGATGAAACGTACACTCCATTT
Ta_TT8_Mut2    AGGAGGTTGAGTTACTGAAAGAAGAAATGTATTGGAGTTGATGAAACGTACACTCCATTT
Ta_TT8_Mut1    AGGAGGTTGAGTTACTGAAAGAAGAAATGTATTGGAGTTGATGAAACGTACACTCCATTT
               ************************************************************

Ta_TT8_Wt      TAGTGAACATAATTGGACCGTTGAGATTCTTATTTTTTTGCTGATTGATTATCTAAAGTA
Ta_TT8_Mut2    TAGTGAACATAATTGGACCGTTGAGATTCTTATTTTTTTGCTGATTGATTATCTAAAGTA
Ta_TT8_Mut1    TAGTGAACATAATTGGACCGTTGAGATTCTTATTTTTTTGCTGATTGATTATCTAAAGTA
               ************************************************************

Ta_TT8_Wt      GAAGCATAAATAGATAATACATAAATGCATAACAAATTGTGTTAGTTATGGGTATAGTTA
Ta_TT8_Mut2    GAAGCATAAATAGATAATACATAAATGCATAACAAATTGTGTTAGTTATGGGTATAGTTA
Ta_TT8_Mut1    GAAGCATAAATAGATAATACATAAATGCATAACAAATTGTGTTAGTTATGGGTATAGTTA
               ************************************************************

Ta_TT8_Wt      ATGCTTTTTCTCTATGAGAGGAAAAAAAAAAAAAATATATAAATGTGGAAGTAATAATTTT
Ta_TT8_Mut2    ATGCTTTTTCTCTATGAGAGGAAAAAAAAAAAAAATATATAAATGTGGAAGTAATAATTTT
Ta_TT8_Mut1    ATGCTTTTTCTCTATGAGAGGAAAAAAAAAAAAAATATATAAATGTGGAAGTAATAATTTT
               ************************************************************

Ta_TT8_Wt      GTAGGATGCCAGGAAAGGCGTATGCGAGGAGGAAACACGTATGGCTATGTGGTGCAAATG
Ta_TT8_Mut2    GTAGGATGCCAGGAAAGGCGTATGCGAGGAGGAAACACGTATGGCTATGTGGTGCAAATG
Ta_TT8_Mut1    GTAGGATGCCAGGAAAGGCGTATGCGAGGAGGAAACACGTATGGCTATGTGGTGCAAATG
               ************************************************************

Ta_TT8_Wt      AGGTTGACAGTAAAATCTTTTCTAGGGCTATTCTCGCAAAGGTCTATTTCCTTTTTCATT
Ta_TT8_Mut2    AGGTTGACAGTAAAATCTTTTCTAGGGCTATTCTCGCAAAGGTCTATTTCCTTTTTCATT
Ta_TT8_Mut1    AGGTTGACAGTAAAATCTTTTCTAGGGCTATTCTCGCAAAGGTCTATTTCCTTTTTCATT
               ************************************************************

Ta_TT8_Wt      TACCACTACTCTATGCATCTACTTCTCTACCTATTTATATATCTCATCTTTCAAATTAAT
Ta_TT8_Mut2    TACCACTACTCTATGCATCTACTTCTCTACCTATTTATATATCTCATCTTTCAAATTAAT
Ta_TT8_Mut1    TACCACTACTCTATGCATCTACTTCTCTACCTATTTATATATCTCATCTTTCAAATTAAT
               ************************************************************

Ta_TT8_Wt      TAATTTTCTGTCTTTATTTTCTTGGATGCTCCTTCTACATCGGTCGGTTCCTTAATGGTT
Ta_TT8_Mut2    TAATTTTCTGTCTTTATTTTCTTGGATGCTCCTTCTACATCGGTCGGTTCCTTAATGGTT
Ta_TT8_Mut1    TAATTTTCTGTCTTTATTTTCTTGGATGCTCCTTCTACATCGGTCGGTTCCTTAATGGTT
               ************************************************************

Ta_TT8_Wt      AGAGTGCCAAAATCCAGGTAAACGTTGTCTTTATTGATTAATTCTAATTTTGAGTAATAT
Ta_TT8_Mut2    AGAGTGCCAAAATCCAGGTAAACGTTGTCTTTATTGATTAATTCTAATTTTGAGTAATAT
Ta_TT8_Mut1    AGAGTGCCAAAATCCAGGTAAACGTTGTCTTTATTGATTAATTCTAATTTTGAGTAATAT
               ************************************************************
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Ta_TT8_Wt      TTTACATTTATTTTACATGTTTGAAAATTGTTTTGTGATAAAAAAAAAGCAGACAGTGGT
Ta_TT8_Mut2    TTTACATTTATTTTACATGTTTGAAAATTGTTTTGTGATAAAAAAAAAGCAGACAGTGGT
Ta_TT8_Mut1    TTTACATTTATTTTACATGTTTGAAAATTGTTTTGTGATAAAAAAAAAGCAGACAGTGGT
               ************************************************************

Ta_TT8_Wt      TTGCATTCCCATGCTTGATGGCGTTGTGGAACTAGGCACAACGAACAAGGTACGGCGTAG
Ta_TT8_Mut2    TTGCATTCCCATGCTTGATGGCGTTGTGGAACTAGGCACAACGAACAAGGTACGGCGTAG
Ta_TT8_Mut1    TTGCATTCCCATGCTTGATGGCGTTGTGGAACTAGGCACAACGAACAAGGTACGGCGTAG
               ************************************************************

Ta_TT8_Wt      TTATCTTTTTATATATGCATAACCAAATGGTTAAGAAAAAGGTTAGAAGAGAAATAGATC
Ta_TT8_Mut2    TTATCTTTTTATATATGCATAACCAAATGGTTAAGAAAAAGGTTAGAAGAGAAATAGATC
Ta_TT8_Mut1    TTATCTTTTTATATATGCATAACCAAATGGTTAAGAAAAAGGTTAGAAGAGAAATAGATC
               ************************************************************

Ta_TT8_Wt      ATGCTTAAGTTTTATCAGTTAAATTAAAAATGTAAAAATAAGATATTATGTTCATTAATA
Ta_TT8_Mut2    ATGCTTAAGTTTTATCAGTTAAATTAAAAATGTAAAAATAAGATATTATGTTCATTAATA
Ta_TT8_Mut1    ATGCTTAAGTTTTATCAGTTAAATTAAAAATGTAAAAATAAGATATTATGTTCATTAATA
               ************************************************************

Ta_TT8_Wt      ATGTATAGTCCCTGTTAGTTAAAAAAAAAGAATAAAATATTTAACCATTTGAAGTCATAAT
Ta_TT8_Mut2    ATGTATAGTCCCTGTTAGTTAAAAAAAAAGAATAAAATATTTAACCATTTGAAGTCATAAT
Ta_TT8_Mut1    ATGTATAGTCCCTGTTAGTTAAAAAAAAAGAATAAAATATTTAACCATTTGAAGTCATAAT
               ************************************************************

Ta_TT8_Wt      ATAAAAATATTGTTTTTGGAGATAGTACATAATTCTCACAATAAAAAAAATAACAAAGGG
Ta_TT8_Mut2    ATAAAAATATTGTTTTTGGAGATAGTACATAATTCTCACAATAAAAAAAATAACAAAGGG
Ta_TT8_Mut1    ATAAAAATATTGTTTTTGGAGATAGTACATAATTCTCACAATAAAAAAAATAACAAAGGG
               ************************************************************

Ta_TT8_Wt      ATGATTAAGGGAAGGAGTTGGATACATGTTGTTTGTCTGTGTGTGTGAAGGTAAAAGAAG
Ta_TT8_Mut2    ATGATTAAGGGAAGGAGTTGGATACATGTTGTTTGTCTGTGTGTGTGAAGGTAAAAGAAG
Ta_TT8_Mut1    ATGATTAAGGGAAGGAGTTGGATACATGTTGTTTGTCTGTGTGTGTGAAGGTAAAAGAAG
               ************************************************************

Ta_TT8_Wt      ATATAGCGTTTGTTGAGCTCATAAAGAGTTTTTTTCCATAACCACCCCAAGTCAAACCCAA
Ta_TT8_Mut2    ATATAGCGTTTGTTGAGCTCATAAAGAGTTTTTTTCCATAACCACCCCAAGTCAAACCCAA
Ta_TT8_Mut1    ATATAGCGTTTGTTGAGCTCATAAAGAGTTTTTTTCCATAACCACCCCAAGTCAAACCCAA
               ************************************************************

Ta_TT8_Wt      AAGCTGCTCTTTCTGAACACTCCATCAACGAAGAGCACGAAGAAGACGAAGAACAAGAAG
Ta_TT8_Mut2    AAGCTGCTCTTTCTGAACACTCCATCAACGAAGAGCACGAAGAAGACGAAGAACAAGAAG
Ta_TT8_Mut1    AAGCTGCTCTTTCTGAACACTCCATCAACGAAGAGCACGAAGAAGACGAAGAACAAGAAG
               ************************************************************

Ta_TT8_Wt      AAGAAGAAGAAGAAGTAGAAGAAGAAATGACAATGTCAGAGGAGATAAGGCTTGGCT
Ta_TT8_Mut2    AAGAAGAAGAAGAAGTAGAAGAAGAAATGACAATGTCAGAGGAGATAAGGCTTGGCT
Ta_TT8_Mut1    AAGAAGAAGAAGAAGTAGAAGAAGAAATGACAATGTCAGAGGAGATAAGGCTTGGCT
               ************************************************************

Ta_TT8_Wt      CTCCTGATGATGATGACGTCTCCAATCAAAACCTACTCTCTGATTTCCATGTAGAATCAA
Ta_TT8_Mut2    CTCCTGATGATGATGACGTCTCCAATCAAAACCTACTCTCTGATTTCCATGTAGAATCAA
Ta_TT8_Mut1    CTCCTGATGATGATGACGTCTCCAATCAAAACCTACTCTCTGATTTCCATGTAGAATCAA
               ************************************************************

Ta_TT8_Wt      CCCACACTTTAGGTATACACTTATACATTAAATTAGTTAACGATATCATTACACGTATCT
Ta_TT8_Mut2    CCCACACTTTAGGTATACACTTATACATTAAATTAGTTAACGATATCATTACACGTATCT
Ta_TT8_Mut1    CCCACACTTTAGGTATACACTTATACATTAAATTAGTTAACGATATCATTACACGTATCT
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Ta_TT8_Wt    ATTTATTTTGTTAACAAGAAATTTAAAAATATTCGCCATTTCTTTGTTATGTCTAAAGAA
Ta_TT8_Mut2  ATTTATTTTGTTAACAAGAAATTTAAAAATATTCGCCATTTCTTTGTTATGTCTAAAGAA
Ta_TT8_Mut1  ATTTATTTTGTTAACAAGAAATTTAAAAATATTCGCCATTTCTTTGTTATGTCTAAAGAA
             ************************************************************

Ta_TT8_Wt    AATCTATAAAATTTTATGAATAGACACACACATGGACATGATGAATCTAATGGAGGAGGG
Ta_TT8_Mut2  AATCTATAAAATTTTATGAATAGACACACACATGGACATGATGAATCTAATGGAGGAGGG
Ta_TT8_Mut1  AATCTATAAAATTTTATGAATAGACACACACATGGACATGATGAATCTAATGGAGGAGGG
             ************************************************************

Ta_TT8_Wt    TGGAAACTATTCTCAGACAGTATCAACACTTCTTATGTCACAACCCACGAGTCTTTTTTC
Ta_TT8_Mut2  TGGAAACTATTCTCAGACAGTATCAACACTTCTTATGTCACAACCCACGAGTCTTTTTTC
Ta_TT8_Mut1  TGGAAACTATTCTCAGACAGTATCAACACTTCTTATGTCACAACCCACGAGTCTTTTTTC
             ************************************************************

Ta_TT8_Wt    AGATTCAGTTTCCACATCTTCTTACATCCAATCATCATTTGCCACATGGAAGGCTGATAA
Ta_TT8_Mut2  AGATTCAGTTTCCACATCTTCTTACATCCAATCATCATTTGCCACATGGAAGGCTGATAA
Ta_TT8_Mut1  AGATTCAGTTTCCACATCTTCTTACATCCAATCATCATTTGCCACATGGAAGGCTGATAA
             ************************************************************

Ta_TT8_Wt    TTTTAAAGAGCATCAGCGAGTGGAAACTAAATCGACGTCGTCGTCGCAATGGATGCTCAA
Ta_TT8_Mut2  TTTTAAAGAGCATCAGCGAGTGGAAACTAAATCGACGTCGTCGTCGCAATGGATGCTCAA
Ta_TT8_Mut1  TTTTAAAGAGCATCAGCGAGTGGAAACTAAATCGACGTCGTCGTCGCAATGGATGCTCAA
             ************************************************************

Ta_TT8_Wt    ACACATAATCTTGAGAGTTCCTTTACTCCACGACCACACTAAAGAAAAGAGGCTGCCTCG
Ta_TT8_Mut2  ACACATAATCTTGAGAGTTCCTTTACTCCACGACCACACTAAAGAAAAGAGGCTGCCTCG
Ta_TT8_Mut1  ACACATAATCTTGAGAGTTCCTTTACTCCACGACCACACTAAAGAAAAGAGGCTGCCTCG
             ************************************************************

Ta_TT8_Wt    AGAAGAGCTTAATCACGTGGTGGCAGAGCGCCGCAGGAGAGAGAAGCTGAATGAGAGATT
Ta_TT8_Mut2  AGAAGAGCTTAATCACGTGGTGGCAGAGCGCCGCAGGAGAGAGAAGCTGAATGAGAGATT
Ta_TT8_Mut1  AGAAGAGCTTAATCACGTGGTGGCAGAGCGCCGCAGGAGAGAGAAGCTGAATGAGAGATT
             ************************************************************

Ta_TT8_Wt    CATAACACTGAGATCATTGGTTCCCTTTGTGACCAAGATGGATAAAGTCTCAATTCTTGG
Ta_TT8_Mut2  CATAACACTGAGATCATTGGTTCCCTTTGTGACCAAGATGGATAAAGTCTCAATTCTTGG
Ta_TT8_Mut1  CATAACACTGAGATCATTGGTTCCCTTTGTGACCAAGATGGATAAAGTCTCAATTCTTGG
             ************************************************************

Ta_TT8_Wt    AGACACCATCAACTACGTAAACCATCTTCGAAATAGGGTCCAAGAGCTGGAGACTAATCA
Ta_TT8_Mut2  AGACACCATCAACTACGTAAACCATCTTCGAAATAGGGTCCAAGAGCTGGAGACTAATCA
Ta_TT8_Mut1  AGACACCATCAACTACGTAAACCATCTTCGAAATAGGGTCCAAGAGCTGGAGACTAATCA
             ************************************************************

Ta_TT8_Wt    TCACGAACAAAAACATAAGCGGATGCGTAGCTGTAAGGGAAAAACGTGGGAAGAGGTCGT
Ta_TT8_Mut2  TCACGAACAAAAACATAAGCGGATGCGTAGCTGTAAGGGAAAAACGTGGGAAGAGGTCGT
Ta_TT8_Mut1  TCACGAACAAAAACATAAGCGGATGCGTAGCTGTAAGGGAAAAACGTGGGAAGAGGTCGT
             ************************************************************

Ta_TT8_Wt    TGAGGTTTCCATCATAGAGAGTGATGTTTTGTTAGAGATGAGATGCGAGTACCGAGATGG
Ta_TT8_Mut2  TGAGGTTTCCATCATAGAGAGTGATGTTTTGTTAGAGATGAGATGCGAGTACCGAGATGG
Ta_TT8_Mut1  TGAGGTTTCCATCATAGAGAGTGATGTTTTGTTAGAGATGAGATGCGAGTACCGAGATGG
             ************************************************************

Ta_TT8_Wt    TCTATTGCTCGACATCCTTCAGGTTCTTAAGGAACATGGTATAGAGACTACTGCAGTTCA
Ta_TT8_Mut2  TCTATTGCTCGACATCCTTCAGGTTCTTAAGGAACATGGTATAGAGACTACTGCAGTTCA
Ta_TT8_Mut1  TCTATTGCTCGACATCCTTCAGGTTCTTAAGGAACATGGTATAGAGACTACTGCAGTTCA
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Ta_TT8_Wt      TACCGCGGTGAACGAGCGTGATTTCGAGGCCGAGATAAGGGCTATGGTGAGAGGGAAGAA
Ta_TT8_Mut2    TACCGCGGTGAACGAGCGTGATTTCGAGGCCGAGATAAGGGCTATGGTGAGAGGGAAGAA
Ta_TT8_Mut1    TACCGCGGTGAACGAGCGTGATTTCGAGGCCGAGATAAGGGCTATGGTGAGAGGGAAGAA
               ************************************************************

Ta_TT8_Wt      ACCAAGCATTGCTGAGGTCAAAAGAGCCATCCATCAAACTATATCCAATATTAAACTATA
Ta_TT8_Mut2    ACCAAGCATTGCTGAGGTCAAAAGAGCCATCCATCAAACTATATCCAATATTAAACTATA
Ta_TT8_Mut1    ACCAAGCATTGCTGAGGTCAAAAGAGCCATCCATCAAACTATATCCAATATTAAACTATA
               ************************************************************

Ta_TT8_Wt      G
Ta_TT8_Mut2    G
Ta_TT8_Mut1    G
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