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(71) Applicant: **ARBOR BIOTECHNOLOGIES, INC.** [US/US]; 20 Acorn Park Drive, Tower 500, Cambridge, Massachusetts 02140 (US).

(72) Inventors: **SCOTT, David A.**; c/o Arbor Biotechnologies, Inc., 20 Acorn Park Drive, Tower 500, Cambridge, Massachusetts 02140 (US). **CHENG, David R.**; c/o Arbor Technologies, Inc., 20 Acorn Park Drive, Tower 500, Cambridge, Massachusetts 02140 (US). **YAN, Winston X.**; c/o Arbor Biotechnologies, Inc., 20 Acorn Park Drive, Tower 500, Cambridge, Massachusetts 02140 (US).

(74) Agent: **BEHROOZ, Alireza** et al.; Saul Ewing LLP, Centre Square West, 38th Floor, 1500 Market Street, Philadelphia, Pennsylvania 19102 (US).

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(54) Title: TYPE V NUCLEASES

(57) Abstract: The present invention relates to nucleases or nucleic acids encoding the nucleases, RNA guides or nucleic acids encoding the RNA guides, processes for characterizing the nucleases and/or RNA guides, compositions comprising the nucleases and/or RNA guides, and kits and/or methods for preparing and/or using the nucleases and/or RNA guides.

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TYPE V NUCLEASES

CROSS-REFERENCE TO RELATED APPLICATION

The present application is entitled to priority under 35 U.S.C. § 119(e) to U.S. Provisional Patent Application No. 63/278,685, filed November 12, 2021, which is hereby incorporated by reference in its entirety herein.

REFERENCE TO AN ELECTRONIC SEQUENCE LISTING

The contents of the electronic sequence listing (File Name: 381834-7008WO1 Sequence Listing.xml; Size: 5.21 megabytes; and Date of Creation: November 7, 2022) is herein incorporated by reference in its entirety.

BACKGROUND

Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and CRISPR-associated (Cas) genes, collectively known as CRISPR-Cas or CRISPR/Cas systems, are adaptive immune systems in archaea and bacteria that defend particular species against foreign genetic elements, *e.g.*, phage infection. The CRISPR-Cas systems of prokaryotic adaptive immunity are an extremely diverse group of proteins effectors, non-coding elements, as well as loci architectures, some examples of which have been engineered and adapted to produce important biotechnologies.

The components of the system involved in host defense include one or more effector proteins capable of modifying DNA or RNA and an RNA guide element that targets these protein activities to a specific sequence on the target (*e.g.*, phage) DNA or RNA. The RNA guide is composed of a CRISPR RNA (crRNA) and may require an additional trans-activating RNA (tracrRNA) to enable targeted nucleic acid manipulation by the effector protein(s). The crRNA consists of a direct repeat responsible for protein binding to the crRNA and a spacer sequence that is complementary to the desired nucleic acid target sequence. CRISPR systems can be reprogrammed to target alternative DNA or RNA targets by modifying the spacer sequence of the crRNA.

There remains a need for additional programmable effectors and systems for modifying nucleic acids and polynucleotides (*i.e.*, DNA, RNA, or any hybrid, derivative, or modification) beyond the current CRISPR-Cas systems that enable novel applications through their unique properties.

SUMMARY OF THE INVENTION

It is against the above background that the present invention provides certain advantages and advancements over the prior art.

Although this invention disclosed herein is not limited to specific advantages or functionalities, the present invention provides, in one aspect, a composition comprising:

(a) a nuclease or a nucleic acid encoding the nuclease, wherein the nuclease comprises an amino acid sequence with at least 80% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1**; and

(b) an RNA guide or a nucleic acid encoding the RNA guide, wherein the RNA guide comprises a direct repeat sequence and a spacer sequence,

wherein the nuclease binds to the RNA guide, and wherein the spacer sequence binds to a target nucleic acid.

In another aspect, the present invention provides a cell comprising a composition comprising:

(a) a nuclease or a nucleic acid encoding the nuclease, wherein the nuclease comprises an amino acid sequence with at least 80% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1**; and

(b) an RNA guide or a nucleic acid encoding the RNA guide,

wherein the RNA guide comprises a direct repeat sequence and a spacer sequence, wherein the nuclease binds to the RNA guide, and wherein the spacer sequence binds to a target nucleic acid.

In some aspects, the present invention provides a method of binding a composition to a target nucleic acid in a cell, the method comprising:

(a) providing the composition, wherein the composition comprises a nuclease or a nucleic acid encoding the nuclease, wherein the nuclease comprises an amino acid sequence with at least 80% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1**; and an RNA guide or a nucleic acid encoding the RNA guide, wherein the RNA guide comprises a direct repeat sequence and a spacer sequence, wherein the nuclease binds to the RNA guide, and wherein the spacer sequence binds to a target nucleic acid; and

(b) delivering the composition to the cell,

wherein the cell comprises the target nucleic acid, wherein the nuclease binds to the RNA guide, and wherein the spacer sequence binds to the target nucleic acid.

In other aspects, the present invention provides a method of introducing an indel into a target nucleic acid in a cell, the method comprising:

(a) providing a composition comprising a nuclease or a nucleic acid encoding the nuclease, wherein the nuclease comprises an amino acid sequence with at least 80% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1**; and an RNA guide or a nucleic acid

encoding the RNA guide, wherein the RNA guide comprises a direct repeat sequence and a spacer sequence, wherein the nuclease binds to the RNA guide, and wherein the spacer sequence binds to a target nucleic acid; and

(b) delivering the composition to the cell,

wherein recognition of the target nucleic acid by the composition results in a modification of the target nucleic acid.

DETAILED DESCRIPTION

Definitions

The present invention will be described with respect to particular embodiments, but the invention is not limited thereto but only by the claims. Terms as set forth hereinafter are generally to be understood in their common sense unless indicated otherwise.

Unless otherwise defined, scientific and technical terms used herein have the meanings that are commonly understood by those of ordinary skill in the art. In the event of any latent ambiguity, definitions provided herein take precedent over any dictionary or extrinsic definition. Unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. The use of "or" means "and/or" unless stated otherwise. The use of the term "including," as well as other forms, such as "includes" and "included," is not limiting.

Generally, nomenclature used in connection with cell and tissue culture, molecular biology, immunology, microbiology, genetics, and protein and nucleic acid chemistry and hybridization described herein is well-known and commonly used in the art. The methods and techniques provided herein are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated. Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art or as described herein. The nomenclatures used in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well-known and commonly used in the art. Standard techniques are used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

That the disclosure may be more readily understood, select terms are defined below.

The articles "a" and "an" are used herein to refer to one or to more than one (i.e., to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

"About" as used herein when referring to a measurable value such as an amount, a temporal duration, and the like, is meant to encompass variations of ±20% or ±10%, more preferably ±5%, even more preferably ±1%, and still more preferably ±0.1% from the specified value, as such variations are appropriate to perform the disclosed methods.

As used herein, the term "catalytic residue" refers to an amino acid that activates catalysis. A catalytic residue is an amino acid that is involved (e.g., directly involved) in catalysis.

As used herein, the terms "domain" and "protein domain" refer to a distinct functional and/or structural unit of a polypeptide. In some embodiments, a domain may comprise a conserved amino acid sequence. As used herein, the term "RuvC domain" refers to a conserved domain or motif of amino acids having nuclease (e.g., endonuclease) activity. As used herein, a protein having a split RuvC domain refers to a protein having two or more RuvC motifs, at sequentially disparate sites within a sequence, that interact in a tertiary structure to form a RuvC domain.

As used herein, the term "effector" refers to a polypeptide or protein, such as an enzyme, having at least one "effector activity." For example, effectors can include nucleases, e.g., CRISPR-associated nucleases.

As used herein, the term "effector activity" refers to a biological activity. In some embodiments, effector activity includes enzymatic activity, e.g., catalytic ability of an effector. For example, effector activity can include nuclease activity.

As used herein, the term "nuclease" refers to an enzyme capable of cleaving a phosphodiester bond. A nuclease hydrolyzes phosphodiester bonds in a nucleic acid backbone. As used herein, the term "endonuclease" refers to an enzyme capable of cleaving a phosphodiester bond between nucleotides.

As used herein, the terms "parent," "parent polypeptide," and "parent sequence" refer to an original polypeptide (e.g., reference or starting polypeptide) to which an alteration is made to produce a variant polypeptide of the present invention.

As used herein, the term "protospacer adjacent motif" or "PAM" refers to a DNA sequence adjacent to a target sequence to which a complex comprising an effector and an RNA guide binds. In some embodiments, a PAM is required for enzyme activity. As used herein, the term "adjacent" includes instances in which an RNA guide of the complex specifically binds, interacts, or associates with a target sequence that is immediately adjacent to a PAM. In such instances, there are no nucleotides between the target sequence and the PAM. The term "adjacent" also includes instances in which there are a small number (e.g., 1, 2, 3, 4, or 5) of nucleotides between the target sequence, to which the targeting moiety binds, and the PAM.

As used herein, the terms "reference composition," "reference sequence," and "reference" refer to a control, such as a negative control or a parent (e.g., a parent sequence, a parent protein, a wild-type protein, or a complex comprising a parent sequence).

As used herein, the terms "RNA guide" or "RNA guide sequence" refer to any RNA molecule that facilitates the targeting of a polypeptide described herein to a target nucleic acid. For example, an RNA guide can be a molecule that recognizes (e.g., binds to) a target nucleic acid. An RNA guide may be designed to be complementary to a specific nucleic acid sequence. An RNA guide comprises a DNA targeting sequence and a direct repeat (DR) sequence. The terms CRISPR RNA (crRNA), pre-crRNA, mature crRNA, and gRNA are also used herein to refer to an RNA guide. As used herein, the term "pre-crRNA" refers to an unprocessed RNA molecule comprising a DR-spacer-DR sequence. As used herein, the term "mature crRNA" refers to a processed form of a pre-crRNA; a mature crRNA may comprise a DR-spacer sequence, wherein the DR is a truncated form of the DR of a pre-crRNA and/or the spacer is a truncated form of the spacer of a pre-crRNA. The RNA guide can further comprise a tracrRNA sequence. In some embodiments, the tracrRNA sequence is fused to the direct repeat sequence of the RNA guide. In some embodiments, the RNA guide is a single molecule RNA guide (e.g., an sgRNA).

As used herein, the terms "single molecule guide RNA," "single molecule RNA guide," "single guide RNA," "sgRNA," and the like are used to refer to an RNA guide (comprising a direct repeat sequence and a spacer sequence) fused to a tracrRNA. The RNA guide and tracrRNA can be transcribed together as a single transcript (e.g., with intervening linker nucleotides). The RNA guide and tracrRNA can be covalently linked (e.g., linked by intervening nucleotides). In some embodiments, the 3' end of the RNA guide is linked to the 5' end of the tracrRNA. In some cases, the 5' end of the RNA guide is linked to the 3' end of the tracrRNA. In some cases, the 5' end of the RNA guide is linked to the 5' end of the tracrRNA. In some cases, the 3' end of the RNA guide is linked to the 3' end of the tracrRNA.

It will be understood that when a nucleotide sequence is represented by a DNA sequence (i.e., A, T, C, G), this also includes an RNA sequence (i.e., A, U, C, G), such as an RNA transcript of the DNA sequence, in which "U" replaces "T" in the sequence.

As used herein, the term "substantially identical" refers to a sequence, polynucleotide, or polypeptide, that has a certain degree of identity to a reference sequence.

As used herein, the terms "target nucleic acid" and "target sequence" refer to a nucleic acid sequence to which a targeting moiety (e.g., RNA guide) specifically binds. In some embodiments, the DNA targeting sequence of an RNA guide binds to a target nucleic acid.

As used herein, the term "targeting moiety" refers to a molecule or component (e.g., nucleic acid and/or RNA guide) that facilitates the targeting of another molecule or component to a target nucleic acid. In some embodiments, the targeting moiety specifically interacts or associates with the target nucleic acid.

As used herein, the terms "trans-activating crRNA" and "tracrRNA" refer to an RNA molecule involved in or required for the binding of a targeting moiety (e.g., an RNA guide) to a target nucleic acid.

In one aspect, the present invention provides novel nucleases and methods of use thereof. In some aspects, a composition, kit, or cell comprising a nuclease of the present invention having one or more characteristics is described herein. In some aspects, a method of preparing a nuclease of the present invention is described. In some aspects, a method of delivering a composition comprising a nuclease of the present invention is described.

COMPOSITION

In some aspects, the invention described herein comprises compositions comprising a nuclease. In some embodiments, a composition of the invention includes a nuclease, and the composition has nuclease activity. In some aspects, the invention described herein comprises compositions comprising a nuclease and a targeting moiety. In some embodiments, a composition of the invention includes a nuclease and an RNA guide sequence, and the RNA guide sequence directs the nuclease activity to a site-specific target. In some embodiments, a nuclease of the composition of the present invention is a recombinant nuclease.

In some embodiments, the composition described herein comprises an RNA-guided nuclease (e.g., a nuclease comprising multiple components). In some embodiments, a nuclease of the present invention comprises enzyme activity (e.g., a protein comprising a RuvC domain or a split RuvC domain). In some embodiments, the composition comprises a targeting moiety (e.g., an RNA guide). In some embodiments, the composition comprises a ribonucleoprotein (RNP) comprising a nuclease and a targeting moiety (e.g., RNA guide).

In some embodiments, the composition of the present invention includes an effector (e.g., nuclease) described herein.

Nuclease

In various embodiments, the nuclease of the present invention is a Type V CRISPR-associated nucleases.

In some embodiments, the nuclease is an isolated or purified nuclease.

A nucleic acid sequence encoding a nuclease described herein may be substantially identical to a reference nucleic acid sequence if the nucleic acid encoding the nuclease comprises a sequence having least about 60%, least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or at least about

99.5% sequence identity to the reference nucleic acid sequence. The percent identity between two such nucleic acids can be determined manually by inspection of the two optimally aligned nucleic acid sequences or by using software programs or algorithms (e.g., BLAST, ALIGN, CLUSTAL) using standard parameters. One indication that two nucleic acid sequences are substantially identical is that the two nucleic acid molecules hybridize to each other under stringent conditions (e.g., within a range of medium to high stringency).

In some embodiments, a nuclease described herein is encoded by a nucleic acid sequence having at least about 60%, least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or at least about 99.5% sequence identity to a reference nucleic acid sequence.

A nuclease described herein may be substantially identical to a reference polypeptide if the nuclease comprises an amino acid sequence having at least about 60%, least about 65%, least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or at least about 99.5% sequence identity to the amino acid sequence of the reference polypeptide. The percent identity between two such polypeptides can be determined manually by inspection of the two optimally aligned polypeptide sequences or by using software programs or algorithms (e.g., BLAST, ALIGN, CLUSTAL) using standard parameters. One indication that two polypeptides are substantially identical is that the first polypeptide is immunologically cross-reactive with the second polypeptide. Typically, polypeptides that differ by conservative amino acid substitutions are immunologically cross-reactive. Thus, a polypeptide is substantially identical to a second polypeptide, for example, where the two peptides differ only by a conservative amino acid substitution or one or more conservative amino acid substitutions.

In some embodiments, a nuclease of the present invention comprises a polypeptide sequence having 50, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1** (*e.g.*, SEQ ID NOs: 1, 6, 11, and the like). In some embodiments, a nuclease of the present invention comprises a polypeptide sequence having greater than 50, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identity to, or having 100% identity to, any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1**.

One skilled in the art can identify a suitable nucleic acid sequence to encode a polypeptide sequence having 50, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1**.

In some embodiments, a nuclease of the present invention is a nuclease having a specified degree of amino acid sequence identity to one or more reference polypeptides, e.g., at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or even at least 99% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1**. Homology or identity can be determined by amino acid sequence alignment, e.g., using a program such as BLAST, ALIGN, or CLUSTAL, as described herein. In some embodiments, a nuclease having a specified degree of amino acid sequence identity to one or more reference polypeptides retains one or more characteristics, e.g., nuclease activity, as the one or more reference polypeptides.

In some embodiments, a nuclease of the present invention comprises a protein with an amino acid sequence with at least about 60%, least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or at least about 99.5% sequence identity to the reference amino acid sequence of any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1**. In some embodiments, a nuclease having a specified degree of amino acid sequence identity to one or more reference polypeptides retains one or more characteristics, e.g., nuclease activity, as the reference amino acid sequence.

Also provided is a nuclease of the present invention having enzymatic activity, e.g., nuclease activity, and comprising an amino acid sequence which differs from the amino acid sequences of any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1** by no more than 50, no more than 40, no more than 35, no more than 30, no more than 25, no more than 20, no more than 19, no more than 18, no more than 17, no more than 16, no more than 15, no more than 14, no more than 13, no more than 12, no more than 11, no more than 10, no more than 9, no more than 8, no more than 7, no more than 6, no more than 5, no more than 4, no more than 3, no more than 2, or no more than 1 amino acid residue(s), when aligned using any of the previously described alignment methods.

In some embodiments, a nuclease of the present invention comprises a RuvC domain. In some embodiments, a nuclease of the present invention comprises a split RuvC domain or two or more partial RuvC domains. For example, a nuclease comprises RuvC motifs that are not contiguous with respect to the primary amino acid sequence of the nuclease but form a RuvC domain once the protein folds. In some embodiments, the catalytic residue of a RuvC motif is a glutamic acid residue and/or an aspartic acid residue.

In some embodiments, the invention includes an isolated, recombinant, substantially pure, or non-naturally occurring nuclease comprising a RuvC domain, wherein the nuclease has enzymatic activity, e.g., nuclease activity, wherein the nuclease comprises an amino acid sequence having at least about 60%, 65%,

70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1**.

In some embodiments, an effector (e.g., a nuclease) of the present invention forms a dimer. In some embodiments, the dimer is a homodimer (e.g., a homodimer comprising two identical RuvC domains). In some embodiments, the dimer is a heterodimer (e.g., a heterodimer comprising two non-identical RuvC domains). For example, in some embodiments, a first effector polypeptide of SEQ ID NO: 1 forms a homodimer with a second effector polypeptide of SEQ ID NO: 1. In other embodiments, a first effector polypeptide of SEQ ID NO: 1 forms a heterodimer with a second effector polypeptide of any one of SEQ ID NOs: 6-3875 which is referred to as an effector in Column 2 of **Table 1**. In some embodiments, a dimer of the present invention (e.g., a dimer comprising two RuvC domains) is capable of cleaving two target nucleic acid molecules. In some embodiments, a dimer of the present invention (e.g., a dimer comprising two RuvC domains) is capable of cleaving two sites within a single nucleic acid target. In some embodiments, a dimer of the present invention (e.g., a dimer comprising two RuvC domains) is capable of cleaving each strand of a double-stranded DNA target sequence. In some embodiments, a dimer of the present invention (e.g., a dimer comprising one active RuvC domain and one inactive RuvC domain) is capable of cleaving only a single strand of a double-stranded DNA target sequence (i.e., the dimer nicks the double-stranded DNA target).

Table 1: Amino acid and nucleotide sequences

SEQ ID NO:		
1	CLUST.048080_OJQP01000557-M effector>	MSQKVVLERVTLDGARPFTGYADRHDPESERLYARSGGQAMDWLCDAWRYRFNQLRSNRCKYGKGKTLVPIGGEPDTRSVSQSRSECSWLAAVPSLILESPTRIERVEWFTAVQRRKTLLGKRLKPGRMPRFKSYKRDGQRFVCWHNGGRNAVYRRVNRNHGIITITGQNPKGMSLPGEPLRYRILLHVRVSQPIREYTAIQVDWTNRTVVFNNTPTPVKHEPTGRAVGIDRGCVHAAADSDGRFMDLPKDRLKAIDREIRKRQKAQARRAGNAGYSSEREYAKSGKTSRAYRRTRLEIGRLHAKSKRILDDVYQKYTTRLVRDNDLIVLENLRLANMSRRNKPVPDPLHEGRCLPNGQAAKRGLNHSLRQASMGRLASMLAYKTRLAEGVGMILVNPAYTSQTCSRCGYVDERNRESQAVFVCKKCSYTANADVNAARNILERGLDTLAVTSENLWGADGTPVEQGRKTNGNAARESVAVS
2	CLUST.048080_OJQP01000557-M direct repeat 1>	cuaccccgcacacgcggggauaaacc
3	CLUST.048080_OJQP01000557-M	gguuuaucccccgcgugugcgggguag

	direct repeat 2>	
4	CLUST.048080_OJQP01000557-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
5	CLUST.048080_OJQP01000557-M non-coding>	ttcaaccgtcagggccgcaaacttacgttccacactgtcgaatacacgggagagatca ctatcaccgaccgtgacaagctaacccaaacgatgctctcgggtatcggccacggcaa ggcctatggattgggtctgatgctgcttttctaaccaccgttttgccgtgagggtgcc cccgcctttaggcgtggggaggaatcacggcttaccctcaccatattatatataatgt ggtattatgggagtcatgagtcagaaagtcgtgttggaacgtgtgacgttggacggag ccaggccgttcaccggctacgccgacaggcacgaccccgaatccgaaagactgtacgc gcgttcgggcggtcaggcgatggactggctgtgcgacgcttggcgatacgacgtgaac gccgcccggaacatcctcgaacggggattggacacgctcgccgtcacgtcggaaaacc tgtggggcgcggacggcaccccggtcgaacaggggcgtaagaccaacggaaacgctgc acgcgaatccgtggcagtctcttagggaccagaacctctcccatcgtcaggacgggag gaatcccccggcttcagccgaggggaggacgtcaatgacatgcgatagtcgaaagaag tcttatggcaaaccattcattcaacctcgtcaccgaaccatgggtccccgtactcgca aacggcaagcacgagtcctactctctggaaaccctgttcgatcagccgacctctatcc gacaactggatatagccgacccgttggaacgagtcagcgccgcaccattctgtctgag aataatccgactgttgaacgagtatgacattccactggaccacgccctgctggcattg gacttggccagactcaacaaaccggactccgcagacatggtgcgacgcgactggagcc gactgctcgactgattgtccaccagattgccagcactggacaatcggctcagaaaata ggaacaaatttgcataatagacccatgcatagtctcgaaaacgttgaaaactaaacta caaagtcaagcgaaatgcgaaacacggcgtgtcacttaccccgcgcatgcgggggtgg tttcttaaaatgttttcccatttgcctgttatactgaatacgttcacatagaaatgaa agaggaaaaacaatgagcccttcggaagccagtgccacgaaaatccctgccacctcca tagaccggcactaattggagtgggggcaaaaatgaatcatccagaccaactcagccgt gaatatgcggcgatccttcccgccttgaaagaccacggctatcgagccgacgtgaaag caagcatcgccgacgaacgtttcatcttggtcgtcagcggcaaacccaccacacaagaat ctaccgg
6	CLUST.048080_S.3P3UU1-M effector>	MSQVVKITKVSIKGATPYLGDRDNDSSQPIFSRSPNQVIEWLCSAWRKRFNDHRSQRK KYGKDKVLVPLGDTVVETTDKQAREEHSFLKAVPSLVLQSPEQIEAKEWFASIKRRKT LKESGRNPGKMPKFKSYKKHDHTFVCWFNSGRNARFEKVGRRTGIVSITGMNPKGKKN PGDKGQRFVIRIHVRLSQDIRPYTSVQVNWTKKQLVFVNEPLAVTPREQRGQGSAVGI DRGVVHMSADSQGGFENLPWDTITSLDNKVRRLQRSQERSAEDLGFDSYHAAKKAGKN SKSSQRRDKEIAKTKAKISRVVQDVQHKVSRRLVEENDIIAIEKLNLAGMSKRAKAKV DPHNPGEFLPNGQSAKRALNHKLRLSALAQFGEFLQYKARLSGGQIIEVDPRNTSRRC SSCGHVSQENRESQAVFLCKKCGYSDNADHNAAINILERALRDHKEEITNFWGGKHPS VRTYQSDPRGLTTSQRSSTIRKPHVLATR
7	CLUST.048080_S.3P3UU1-M direct repeat 1>	gggaacaaccccgcgugugcggggaa
8	CLUST.048080_S.3P3UU1-M direct repeat 2>	uuccccgcacacgcgggguuguuccc
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89	CLUST.097864_S.19YDUM-M non-coding>	gagcggcggcagacggtggcgtggtggatggggctcattgacggcttcaaggctgcgt tccgggacggtctgcgcaaggggccgcatcggcggtcgccgccctggtcatctcggg cgcgttgctcgccgcggggtacttcctccgcgactgcgcgcacgcggtcgtcaagacg gggacctcgaacgaggtgccgaagtttcgcggtgcgccgtgaggcgtcgtgagcgtgc cttgttcgtcgcgatgactcgaaacgccaagcaagccagcgatctgcgagcagatttc cgcacactgctcaacgtgacggcaagttgtgtcgttcggcgaaaccccgcgccgcgcg ctgctccgcgagcgtgaccggaatccggatcgagcgggttcgctgcttcatttcttcc ctgttgtacgccaaaagggcgtgttgaacaagaactaaccatttgttgaacaagtttg accacctgttggacacgcgctacacccgatctcaccccgcatggctcgcgtcgaactg caccgcgcctacaagttccggctctacccgacgccggcgcaggtcgccgagctgtcgg aatgcgaacggcagttgagacgcctctggaatctctcgcatgagcagcggctcatggc gctcgggcggcacttgcagctatgtttgacgacgcgactgggcgacgtcaacgccgcc gtgaatgtcctccggcgcgcgcgtagggctcctggggatgctccggcgtccgcgaaga aaaagcgcgtgaccatcgggatcaagggtcggaaaaagagggcggcgtgagttccccg accattgcacaaacttttgcggttcatcgaggaccgcggagccttcggaaactctccg gaggaatgctgcggaggggaagcgcccgtaagggctcccgacgaggcagcaacgtgac ggggaaacccgccacaccctgatcgcacggttctgccgtttgacaatcgacgccacgg gacatccgccctcgggtaggccaatttctcttgtagtttccaagagggcgaggggtac tggtcgcgcagggacgagcgggagcctgatggctcatgcactcgttcattcccggtgt ggtattcttttcgccgatgtacgagatgaagcaggcgacgatagcgcgcgccatcgac atcctgcgcgccgggccgatgacgggtgccgcgttcgcggccaggatgtggccggagc gagtcgtcggc
90	CLUST.097864_S.19YDUM-M direct repeat homology 1>	ugcgcgcac
91	CLUST.097864_S.19YDUM-M direct repeat homology 2>	gugcgcgca
92	CLUST.097864_S.19YDUM-M direct repeat homology -containing sequence>	gagcggcggcagacggtggcgtggtggatggggctcattgacggcttcaaggctgcgt tccgggacggtctgcgcaaggggccgcatcggcggtcgccgccctggtcatctcggg cgcgttgctcgccgcggggtacttcctccgcgactgcgcgcacgcggtcgtcaagacg gggacctcgaacgaggtgccgaagcttcgcggtgcgccgtgaggcgtcgtgagcgtgc cttgttcgtcgcgatgactcgaaacgccaagcaagccagcgatctgcgagcagatttc cgcacactgctcaacgtga
93	CLUST.097864_S.0I3GCV-M effector>	MSRVELHRAYKFRLYPTPAQVAELAEWERQLRRLYNLAHSQRLAAMQRHVRPKSPGVL KSECLSCGAVAVAEIGTDGKAKKTVKHAVGCSVLECRSCGGSPDAEGRTAHTAACSFV DYYRQGREMTQLLEEDDQLARVVCSARQETLRDLEKAWQRWHKMPGFGKPHFKKRIDS CRIYFSTPKSWAVDLGYLSFTGVASSVGRIKIRQDRVWPGDAKFSSCHVVRDVDEWYA VFPLTFTKEIEKPKGGAVGINRGAVHAIADSTGRVVDSPKFYARSLGVIRHRARLLDR KVPFGRAVKPSPTKYHGLPKADIDAAAARVNASPGRLVYEARARGSIAAAEAHLAALV LPAPRQTSQLPSEGRNRERARRFLALAHQRVRRQREWFLHNESAHYAQSYTKIAIEDW

		STKEMTSSEPRDAEEMKRVTRARNRSILDVGWYELGRQIAYKSEATGAEFAKVDPGLR ETETHVPEAIVRERDVDVSGMLRGEAGISGTCSRCGGLLRASASGHADAECEVCLHVE VGDVNAAVNVLKRAMFPGAAPPSKEKAKVTIGIKGRKKKRAA
94	CLUST.097864_S.0 I3GCV-M direct repeat 1>	ggcuagcccgugcgcgcagggacgagugg
95	CLUST.097864_S.0 I3GCV-M direct repeat 2>	ccacucgucccugcgcgcacgggcuagcc
96	CLUST.097864_S.0 I3GCV-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
97	CLUST.097864_S.0 I3GCV-M non-coding>	ctgctggttcggccggctcttggggctctcgtcccgcagcatcttgcgcaccagctgt gtgagcggcacatcgagccgttcggcgagtttctgcgcctcacgctgctcggcgagcg tgaccgggattcggatcgagtgggttcgtttcatttgctcgaaaagaagtgtacgacg actttgtttgcagttcaacacttgaccaacggatgaacagtagctaatgaaacggtca tgagccgcgtcgaactccaccgcgcctacaagttccggctctacccgacgccggcaca ggtcgcggagcttgccgagtgggagcggcagctgcggcggctctacaacctcgcccac agccagcggctcgctgcgatgcagcggcacgtggaatcccgccgggcggtggccgatt tttgacggcctgacgctcatcaaaactttcgcgccgcttcggcgacgcggggctgccgg aaactctccggtggaaggctgcggaggggacctgcttgtagaggagcctgtcgaggca gcaacgtgagagagcgacttctcacaccctgatcgcacggtttagccgtttgacaatt cgcacgggacttgcacgggctccggtttcttctgtagtttcgaagagacaacgaacat cacggccccgcgtccggggcacatagacgaattgttcaagctgcgctcgcgcccatct ccccccccatggcgttgtttccgtaaggggtagggtgttacgctccaggacatgcccgt ctccgccgtcgtcgaggctttcaagcaagcgatccgtggcaaacacaccacccgcaag gaccccgacctcgcgctcgtgtcgcactgcatcgcgcaagcgctcgcgctgacgcccg cggcgctcgcggaggtgacggccaag
98	CLUST.097864_S.1 FGTX8-M effector >	MSRVELHRAYKFRLYPTPVQVAELSEWERQLRRLYNLGHEQRLLTLTRHLRPKSPGVL KGECLSCDSTQVQEVGADGRPKTTVRHAEQCPTLACRSCGALRDAEGRTAHTVACAFV DYYRQGREMTELLAADDQLARVVCSARQEVLRDLDKAWQRWRKMPGFGKPRFKRRTDS CRIYFSTPKAWKLEGGHLSFTGAATTVGAIKMRQDRNWPASVQFSSCHVVRDVDEWYA VFPLTFVAEVARPKGGAVGINRGAVHAIADSTGRVVDSPRYYARALGVIRHRARLFDR KVPSGHAVKPSPTKYRGLSAIEVDRVARATGFTPGRVVTEALNRGGVAYAECALAAIA VLGHGPERPLTSDGRNREKARKFLALAHQRVRRQREWFLHNESAHYARTYSKIAIEDW STKEMTASEPQGEETRRVTRSRNRSILDVGWYELGRQLAYKTEATGAEFAQVDPGLKE TETNVPKAIADARDVDVSGMLRGEAGISGTCSKCGGLLRAPASGHADAECEICLNVEV GDVNAAVNVLKRAMFPGDAPPASGEKPKVSIGIKGRQKKKKAA
99	CLUST.097864_S.1 FGTX8-M direct repeat 1>	ggcaggcccgugcgcgcagggacgagugg
100	CLUST.097864_S.1 FGTX8-M direct	ccacucgucccugcgcgcacgggccugcc

	repeat 2>	
101	CLUST.097864_S.1 FGTX8-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
102	CLUST.097864_S.1 FGTX8-M non-coding>	cggcggccgcgtgggcacgcacgccgtcatctgctggcgcccgcacgtgccgctggcc gttgacccgaagcctggccggtgggagtttcaggggacgagtctcgacgacctgacgc tcgttgccggctcgtcgagcgtcctgctcagcgggccctgcggcgcgcactttcacgt ccgaggcggcgcgatcgagggcgaataggttttcttgccgcatcctgcaacatctccc gcatcagtttcgtgagcggcaggtcgaggcgctcagcgagccgcctggccgcgcgcat ctccgcgagcgtgaccgggactcggatcgagtgtgttcgcttcattttgaacaccact tgaccaacgggtgaacagcggctagacagatcggcgtgagccgcgttgaactccaccg cgcgtacaagttccggctctacccgacgccggtgcaggtcgccgagctgtccgagtgg gagcgacaactccggcgcctctacaacctcgggcatgagcagcgcctgctgaccttga cgcggcacctggacgatcgacgagctgtggccgacttcgacggcctgacgctcgtcaa gactttcgcgttgcttcggcgacgcgtggccgccggaaactctccggtggaaggctgc ggaggggacctgtctgcaagagggcccgacgaggcagcaacgtgaagaggcgactctt cacaccctgatcgcacggttctgccgggcatttgacaatccgcacgggcgccttcggg ctctgttttcttctgtagtttcgaagaggaaaactcaccgctatggctcgacaaaggc aggcccgttgcgcgtaagggactagtggaagccggcttctgttgccaggtgccggccc aaggcaggccgtgcgcgcagggacgagtgggcatcgaacccgtcgcagcgcggacggt ctgtgtccggtcacgggtatttgttctcgcgcgggtacggcgcatccgggatcggttt gcgcaaaaagccgcagagttcgtaccagcccgcgcccgcgctcatgttcagcaccaag agatcgcgtggtcggtccttgaagtgcttgaggacctcggcgttgtggcggcgaaacc gcgcgcgcatcaccggctcgttgaacttgatgcccccgtagagcttgcggtggatctt gtgggtgaac
103	CLUST.097864_S.1 FGTX8-M direct repeat homology 1>	ggacgag
104	CLUST.097864_S.1 FGTX8-M direct repeat homology 2>	ctcgtcc
105	CLUST.097864_S.1 FGTX8-M direct repeat homology-containing sequence>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn cggcggccgcgtgggcacgcacgccgtcatctgctggcgcccgcacgtgccgctggcc gttgacccgaagcctggccggtgggagtttcaggggacgagtctcgacgacctgacgc tcgttgccggctcgtcgagcgtcctgctcagcgggccctgcggcgcgcactttcacgt ccgaggcggcgcgatcgagggcgaataggttttcttgccgcatcctgcaacatctccc gcatcagtttcgtgagc
106	CLUST.097864_S.0 BE3W0-M	MARVELHRAYKFRLYPTPAQVAELSECERQLRRLWNLSHEQRLMALGRHLRPAQPVEC RSCGAVRAKGDDDDKTEHLATCAAHEEIARDKTWKRWTTQSECRSCGALKGADGKIEH TESCAFVDYYRQAPEMTELLQGGDDQLARVVCSARQEILRDLDRAWQRWRKAPQQWGK PRFKRRGDRCRIYFSNPKAWRVEAGFLSFAGAAASVGQIRIRQDRPWPGDAKFSSCHI

	effector>	TRDGDEWYAVFPLVFSKEVVRPTGGAVGINRGAIHAIADSNGRVVDSPQFYARALGII RHRARLFSRKVPFGHCVKPSPTKYRGFSPAVVDALARDLATSPGRVVYEAQKRGGLEA ARTYLAANPPAPPRASLSIPSDGRNRERARQYLARAHQRVRRQREWFLHNESTHYASR FSTIAIEDWSTKGMTSSEPEGDEPRSVVRGRNRSILDVGWYEFGRQLKYKVEPTGGEF VPVDPGLMETETVVPAATTRERGADASLLKGEAGISRTCSSCGGLLPEAASGHREAEC QLCLTTRLGDVNAAVNVLRRARRAPGDAPASAKKKRVTIGIKGRKKRAA
107	CLUST.097864_S.0 BE3W0-M direct repeat 1>	ggcaggcccgugcgcgcaggggcgagugg
108	CLUST.097864_S.0 BE3W0-M direct repeat 2>	ccacucgccccugcgcgcacgggccugcc
109	CLUST.097864_S.0 BE3W0-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
110	CLUST.097864_S.0 BE3W0-M non-coding>	cgcttccttccccatcttctcggcggcttcccgcagcatcttgcgtacgagctgcgtg agcggcaagttgtgtcgttcggcgaaaccccgcgccgcgcgctgctccgcgagcgtga ccgagatccggatcgagcgggttcgctgcttcatttcttccctgttgtacgccaaaag ggcgtgttgaacaagaactaaccgtttgttgaacgagcttgaccacctgttggacacg cgctacatcccgatctgccccgcatggctcgcgtcgaactgcaccgcgcctacaagtt ccggctctacccgacgccggcgcaggtcgccgagctgtcggaatgcgaacggcagttg agacgcctctggaatctctcgcatgagcagcggctcatggcgctcgggcggcacttgc agctatgtttgacgacgcgactgggcgacgtcaacgccgccgtgaatgtcctccggcg cgcgcgtagggctcctggggatgctccggcgtccgcgaagaaaaagcgcgtgaccatc gggatcaagggtcggaaaaagagggcggcgtgagttccccgaccattgcacaaacttt tgcggttcatcgaggaccgcggagccttcggaaactctccggaggaatgctgcggagg ggaagcgcccgtaagggctcccgacgaggcagcaacgtgacgggggacccgccacac cctgatcgcacggttctgccgtttgacaatcgacgccacgggacatccgccctcgggt aggccaatttctcttgtagtttccaagagggcgaggggtatcggtcgcgcagggacga gcgggagcctgatggctcatgcactcgttcattcccggtgtggtattcttttcgccga tgtacgagatgaagcaggcgacgatagcgcgcgccatcgacatcctgcgcgccgggcc gatgacgggtgccgcgttcgcggccaggatgtggccggagcgagtcgtcggcaaatcc
111	CLUST.097864_S.0 BE3W0-M direct repeat homology 1>	cugcgcg
112	CLUST.097864_S.0 BE3W0-M direct repeat homology 2>	cgcgcag
113	CLUST.097864_S.0 BE3W0-M	gggcgaggggtaccggtcgcgcagggacgagcgggagcctgatggctcatgcactcgt tcattcccggtgtggtattcttttcgccgatgtacgagatgaagcaggcgacgatagc gcgcgccatcgacatcctgcgcgccgggccgatgacgggtgccgcgttcgcggccagg

	direct repeat homology - containing sequence >	atgtggccggagcgagtcgtcggcaaatccnnnnnnnnnnnnnnnnnnnnnnnnnnnn nnnnnnnnnnnnnnnnnnnn

	homology 1>	
120	CLUST.097864_S.2 RMY1P-M direct repeat homology 2>	gggacag
121	CLUST.097864_S.2 RMY1P-M direct repeat homology - containing sequence >	acgtaccaggtccagcccgcacgttgcagggttggggcgggattcgaaagcgatctag agctgtcccaaacgcgcgtaagcgcggtgggacagcgaaacactaaaaaaggggactc cgtgcgaatcaacgaccttcatttgctcccgcgtgtggaggatggcctcacgtttctc tacgcggacaggtgccgcgtggagcaatcggattcggccatcg
122	CLUST.097864_S.0 NVIQC-M effector >	MKTVIHRAYKFRLYPTEAQDAELCEWERQLRWLYNLAHEQRLAALSRPRGEQPRVDYY RQGREMTEIVRADPQLARVVCSARQEVLRDLDKAWQRWRKRLGGKPHFKRRTDAVRIY LSTPKHWKVDGLGHLLLSGIASTVGPIKIKQDRTWPGDAKFTACHLVRDVDQWFAVFP LEFSVQAEKPKGGAIGINRGAVHAIADSYGRVVDSPRHYTRALERIQKLSRDLARKES GSRNRHKAAMKLARAHRTVRRQREYFLHGESAYYTQRYGLIGIEDWSTKEMTSSEPDP KIEAPKNLLNRKILDVGWYELARQIDYKAEARGSRVVRVLPGITDQDLDGISTIDSFT NLPMQHSASGEQYAENGYLGDVNAARNVLVRALRAGGKPPVEKKPRTPIKIKGRTKRP ETSGKPPDEACGGDAPVRAPVEAGTLDREVGHHERTVEP
123	CLUST.097864_S.0 NVIQC-M direct repeat 1>	ggcucacccgugcgcgcguggauggcugg
124	CLUST.097864_S.0 NVIQC-M direct repeat 2>	ccagccauccacgcgcgcacgggugagcc
125	CLUST.097864_S.0 NVIQC-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
126	CLUST.097864_S.0 NVIQC-M non-coding>	atcaagatcaaaggccgcaccaagcggccagagacgtccggcaagccgccggatgaag cctgcggaggggacgcgccagtaagggcacccgttgaggcaggaacgctcgaccgcga ggttgggcaccacgaacgcacggttgagccgtaggagacatccagccatcaaaggtga acattgatcaatggtttcgaagagggaatccgcccgtaaggggacccgtcgaggcaga aaaggggacggcgacgtcccccaccctgaacgcacggttttgccgaacgaagagacg cctgacacatccagcccatgaggagacggtttgttgaatggttccgaagaggcaagcc cgtgcgcgcaggggcggatgg
127	CLUST.097864_S.0 NVIQC-M direct repeat	ccgugcgcg

	homology 1>	
128	CLUST.097864_S.0 NVIQC-M direct repeat homology 2>	cgcgcacgg
129	CLUST.097864_S.0 NVIQC-M direct repeat homology - containing sequence >	ggggatccgcccgtaaggggacccgtcgaggcagaaaaggggacggcgacgtccccc accctgaacgcacggttttgccgaacgaagagacgcctgacacatccagcccatgagg agacggtttgttgaatggttccgaagaggcaagcccgtgcgcgcaggggcggatggnn nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn nnnnnnnnnnnnnnnnnn
130	CLUST.097864_OVJK010000038-M effector >	MDKTDTHQRGYKYRLYPTPVQEEILRGWQETHRRVWNELIGPYAEAIQQGVQRKKTNA ECMAEAVAKGITGDDALKAAVKELKLADGARFKQDVLNLFKSKGWTAGTRLVSERNIL RKKRAGSPFCAQIPFSVMDEIVQAHVKAWDSYLAGITKMPCFKAKHESMSSVRTRLAA SFKIHDHHVELSMFELNGERTKIRFHKHRPLPTEPTRVCITSQGRRWFVVFGVKVLSI PLDPDRPAVGIDCGVVNLLTDSTSRSVPGIRTSERLDARERWLQRRLAKKKKGSGHWH KINDQINRLRRHKADVRADVLHKESLHYARTYSTVVLEDLKVKNMTKTAKGTKEAPGK NVAQKSGLNRAILSQGWGMFGDMLRYKIAQRHGNLVHVQPNGTSQTCFKCGHVSALNR TTQAEFKCVNCGYEVNADVNAAQNILARAVPGSTHVVEKKAPRKLHTVTGRKKPRTTL SVGETSQNAAVGRTVKLPVEDGETAPPDETGTTCPSTTVSRTLRSSMNGTLPTPAIVI LDMLENVTESPSESTDLQNGSAE
131	CLUST.097864_OVJK010000038-M direct repeat 1>	ccgcggaauagcgguugguggguagguuggcuucac
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133	CLUST.097864_OVJK010000038-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
134	CLUST.097864_OVJK010000038-M non-coding>	agatttgcgaccccatgaatgactttgtgggggtctgccaggggcccggcaccgggg gtcaatcggtatgaagatgaaagtccgccccaacttggattcagagggattctgcgaa cctatttgggtttggcagaaggaatgaccctatgttggtggggcttcgggcgtaatac ctggcagaggtacaacccggatgacgcaggacgaaaagaagtcgattctggccaggat tatcagtgggattcacgtcaccaaggtggtggcgacccgtagcgtgaagggtaagtac ggggacaccttcgtcgggtggcctactacaagaagctggtggaactcaacgagaaggg tctatctggttgggctatgaatgggcagccggttcccttgaccgaccaggacaaggaa

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135	CLUST.097864_OVJK010000038-M direct repeat homology 1>	uuggugg
136	CLUST.097864_OVJK010000038-M direct repeat homology 2>	ccaccaa
137	CLUST.097864_OVJK010000038-M direct repeat homology -containing sequence>	agatttgcgaccccatgaatgactttgtgggggtctgccaggggcccggtaccgggg gtcaatcggtatgaagatgaaagtccgccccaacttggattcagaggaattctgcgaa cctatttgggtttggcagaaggaatgaccctatgttggtggggcttcgggcgtaatac ctggcagaggtacaacccggatgacgcaggacgaaaagaagtcgattctggccaggat tatcagtgggattcacgtcaccaaggtggtggcgacccgtagcgtgaagggtaagtac ggggacaccttcgtcgg
138	CLUST.118237_S.05PZVL-M effector>	MNHKSTVKASVRHLTRHALQKPGEESDPGETTKTLKFRVDAKGHTRTRLDQIFTAQRQ FVRDLLNKLEGMWDKDPQRFIRMVESSASDPFESKTSCYGWMMTKFLTGSDLPEHLSR SAATASVATLSGNMKSFVTRRENVLKDMAVVIERNMENCEAGLKDLCAELKIDRFKSP PSVDLESINAKTVEKYNEWVAAARVWCNLILAQKHKIPRGDAFFPTRLKAYPGFPGSV IHKEATYFATAIKELRKCLADLKQSHQKLFGALSNEEWSLVLERFPAPEGTGGKGMRH QLGKTLAVLGKKHPEWKPRQYIEELVAGLERGADSMAKHLENRQFSDRPAAIKLINLL NNACVVLMEPLRVKSLYKEYFEQDTPRRNAFGQARGSLAEPTDQADSLQILGFSLMDE

		VRGICRYDGFLAFAGDKEKDQWAFFFDPDGPGGMGIADPVKHPKGSTDSGYIGFGTMG GSRKRAQAAEKRLVRERLWIRRDRKPLQLPLHFGTRQGREYLWNFDHGLKKSSDPWML TNGRLLRIYPHNRPQFSDYFLTITLQKDTPPLAISSGEKLVGVDRGEQNPASFAVVDA KGRLLERGNVGEKYTAKIRQFAEMKSDLQRTAGGYTRKLRAKERNTASALGGLVMREL LDLLVRHPGALVFERLSSGITTRGGRGTLMGNMHYERILSGLRASWPRQVATRHPVPP STAKESRRSCDL
139	CLUST.118237_S.05PZVL-M direct repeat 1>	gguuugcugaccucgauuguuggaggagugcaaaag
140	CLUST.118237_S.05PZVL-M direct repeat 2>	cuuuugcacuccuccaacaaucgaggucagcaaacc
141	CLUST.118237_S.05PZVL-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
142	CLUST.118237_S.05PZVL-M non-coding>	ctctctggattgggttggtcttcgccacgatggtctactttcacggcaacgtgaaaga cttggaacccaaacccggttcggtcacaccgatccagaaaacggccgcggggctgatg tttcttgtcgatgcgatcatgctgggactcgctctttatttgatccttcgctaacgcg aaccgatcgataaggattaagtcgcactacccctgcatcgattcccgtttttttcgatt cccttccaggtatttaatttttacttctcaacgaggtatttggcttggcatggtttcc tctgcgccccctgcccccctgtcccctgcccccctttcacttccagcctaccaattccca gtgttcaaaacgtcggtgttttggcgtttatccctttcctgagataacgcccaggactg tttttgtcccacctcctaatttacacttatccttattatgaactggaatagctccgtt aaaagtccgattatgactgcttgcttaatacgatgaatcacaaaagcactgtcaaagc ctctgttcgccatcttactcggcatgcattgcagaaacccggggaggagagtgatccg ggagaaacgacaaagactttaaagttccgggtagatgccaaaggacatacccgaaccc gactcgacacccggggtggtcggggaacattgatgggcaacatgcactatgagcgaat tttgtctgggttgagggcaagttggccgaggcaggttgctacaaggcacccagtgccg ccaagtaccgcaaaggaatcacgccgttcttgcgatttgtaaatccagcatataccag tgccacctgttcagcttgtggtgaggtgttcagttctagttggtataagaaaaccgca gccacaatcagtaaggaatcacccggttcatggtcagtgacgcttcccaacggaaaaa aacttcagttgccatgctcctacacctcatacatgcgtgggcgcggtgaaaagacatg gaacaccgctgaacggctggaggaacttttcaaggatcgaacatggtcagatcttccc cccagcacccgaaaaacagtagagggattggttgctcgcctgactcatcatcgcccca aacggggtcaggcagcactgaacattgcccgcaaaagcatctgggtcagctcccttcc accccgtcaggcaaagcaatcggaaggtgaagaccggcgttccaccgaggaaccatgg cgcgtttggtacaaaaagcagatcatggaaaagtggtcttaaaaaatcccttgccacc cggctatcataggatcattttagtctcttagtattttctttgcacaacgtcgactgcc ctgccaaggagcggctgacaaccaacaagttcttttacatttgaggtgcaaaccgttc ttgtgatttttttacaaaaggatgcacccgaaagggttggccataccc
143	CLUST.118237_S.1OLNUI-M effector>	MPQTIELKLFMNSIHKSVRSLLSLGLSRSASASPQTITRTVKFKINTDIRPELIPVLN RHFDAFEKFRRKVLDELEAWWNKKPDDFTSMVRATAKERFQDKSSCYGWLYRHFLSGK DLPAGLTREAANSVLWSLKGGLKSFLTRRENVAKELEENYTTNANLWNESIIRIIRDH KLDKPTPPTAPPTVNFKKLTDDQIEKYNGWVGIVRMWGNLILHQQLVQKGLVDREDAK LPRRLKGYPGFPGSQRYLQGASLADSLKRLDDITGKFAKDSEKRFAKITSEHWGAVLE RFFPPEAKEDETRRRPRTVKQMAAERLHYLCKHNPDWKPEQTAKEVLAGLFRLADKLH AHLKNNSPHDRRAVIKLANVLNVAAVFSLEPLRASGDYIACFEADEPRRQAFADLRGA LAQPGDDTVAIEVTGFSLSSNSPQYCGLLACREIKPDCDEWAFFYTLDNQDLKIFAKP GPRPPRDFQPTNWHGFATKGSDDEKEIVRGTVWLPTEISKTKPALALPLAFGARQGRE

		YLWHFDRDLRTRNEWTPLNARLLRVMPAAQESESEKERALRANRADFYVTITFLRLAP PIASVKSKELIGVDRGEVVPAAFAVVGATGRFLAKPSRLREFMEYLRQLDNWEKLNLA HPENARENERKPRWEARPDDGFGFIAPEYRDQQREFNKLKRELQQTKGGYTRWLRAKE RNRARALGGQVMRELLMLCATHKAPLVFESLGSGLATRGGKGTMMSQMQYSRVFTSVE QKLAEAGLCAIARQPKFRKWDNGFIKLVGPACTSATCSVCGQVHSTSFYATIAATLKE SSKGNWQVTLPNGKVRRLPKEYGYWLRGKGEQTANTDERIHQLLNKPFAELSTTNHNA LISLLKSRWLPFRPDQATFQCLACGYSVNADVQAALNIARKHLFRIGREKKSDEENEA ARRKVMGEWETWYRQKLASVWNK
144	CLUST.118237_S.1 OLNUI-M direct repeat 1>	gugagaaccgcugcgguucgcggggaugguuucaaag
145	CLUST.118237_S.1 OLNUI-M direct repeat 2>	cuuugaaaccaucccgcgaaccgcagcgguucucac
146	CLUST.118237_S.1 OLNUI-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
147	CLUST.118237_S.1 OLNUI-M non-coding>	caccacgccgtcttcgatggcattgaacaacgtctccagaaacttccgttcccgggcc aatcgttggacaaccgtttgcaacccttcggcatccaggcgtccgatcctgcccagga ctttatcgagaaaagtcgatattaccgcagccataatgatgatacccgccaatgcgca accaccgcgccaatttgacgcacccaaagtattcaagcaattctgattaggcaagcat tgctttcaatttgaaaggccggaaaaaaccgtgaaaaattcggggtttttcaattaaa caagaaagttgtcaaggggaaaattgcgcaaaaaaaacagtcaaaatttcggcatttt tgacctaagcaattgcaaaccaaacacttacgaatttccacctgcttgctgcccatga ctgcaaaatggtagcttgggactgatggacgaatgcgactgatggtctggcaaccagc cagtggtcaaggcgggtttctgccagatggacagataggattgtaatcataagacgat tcgggcaaaaccagggcggacagggaaagcaggaattggacggtggggcgagattcca tcgagccgtaaaatcgagtcggagcacagcccgtcacgttgcaggattaatggtgaaa atgggtcttggcaggacgttctgtttgggccataatcttgcccgctccacaaaacgaa gggaaaaagaagatgagtgcggaaacttcagaggctggcaaaaccatgtgggctttcg acttgggcacagactgcgaattgcgcgtcgaatgccgcaaaccatcgaattgaaacta tttataaattcaatccacaaatccgttcgttcgctgctatcgcttggcctgtcgcgta gcgcttcggcaagtccgcaaacaattacgcgcacagtaaaattcaagatcaataccga cattcggcaagccgcgctcaatatcgccagaaagcatctgtttcgcattggccgcgaa aaaaaatcagatgaggagaatgaagccgcacgacgcaaagttatgggtgagtgggaaa cttggtatcggcagaaactcgccagcgtttggaataaataattcacccttagccattt tgactgtgagcgagatatgaagaccgacgatttccttccaatctattcgctcgcggag tggcattattgcccacgctcgtcttttctgtcgtggttcggcgcggaacgtgaggatc gcgtcaccccggcttaccagaagatgcgtgaagtccatgccgtgagcaatcatgtggc gtttcggggcgcattggaacgcggcggctggctggatggcaaacacgcgctgctggtt tatcccttgcatgatgacgaccttgaaaatgtggaacgttacggcgcggtacgggtgt ggcaggcaacgtttgaatttctttgaatttaggcttgcagttggatgggagcaggcat aatacttctcccgttagctgtctcctcggaggcagatttactttgattctgtgcgcct ttacgccccacgtatttgacgcacttcgcgaacttcagcggttaacggaaaccgccag cggtggatggacgattcacccggcgttccttgacaacacagtccgtagcagttggtta tatacgaaacggactaaaagcggtttgccatgcgtaacttgttgccagacaatggagt catcatctcggcagaaattttgcatttaggtcttgatgcaaatatttggacggcaggg cgtgaagagcgggccggcctggttcgtcagcggctggtgagaaccgctgcggttcgcg gggatggtttcaaagactgtctttatctcacgccggaaagattcaacgcgtgagaacc

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148	CLUST.118237_S.1 OLNUI-M direct repeat homology 1>	caucccc
149	CLUST.118237_S.1 OLNUI-M direct repeat homology 2>	ggggaug
150	CLUST.118237_S.1 OLNUI-M direct repeat homology - containing sequence >	gcgggccggcctggttcgtcagcggctggtgagaaccgctgcggttcgcggggatggt ttcaaagactgtctttatctcacgccggaaagattcaacgcgtgagaaccgctgcggt tcgcggggatggtttcaaaggctaaggaaatgtccatccccgtcgtgtccgccgtgag aaccgctgcggttcgcggggatggtttcaaaggtttgcacgcaaattccataagcatt tgtcacatgtgagaaccgctgcggttcgcggggatggtttcaaaggttacggccgtaa cggttgctgcaacggtc
151	CLUST.118237_OCZT010053476-M effector >	MSKEPRKNSTHASLRQLLELGLSKSSSAEPQKITRTVKFKIHTLARPELVAPLNKHFN AFDQFREKVLAELESWWDKDPDSFTHMVKCSTKLKFEEKSSCYAWLYKKFLTGAELPP ELSRDAANAMLDNLGGGLKSFLTRRATVSLEIKKRYEQNKEEWEKELSLIAKERNLKL PEVPREIDFNNLTAKKIDFYNEWVGLVRMWCNLILIQKEKLTRENACLPRYLKSYPGF PGSQRFRKPVTIEQTLAELETIAREQAGKASQRFADLKPEVWQAIQERFSPPKKEEAE TTPRPRTASQTVSRRFTALIQANPNWKPQQIAEEILAGIFRAADKLKKHLVTTKYTDR RATIKFANLFNVAVVFAREPFRARGDYVASYEADIARQKAFGDLRGALHQPSDESSAI QISGFSIKDGGTPNYNGLLVCKSEANGKDSWAFLYCHQEGQIFQLADEKAKLRGKKLS EWTGFASRGGSRKKAEASPKQLVKSSVWVSEKNPPTVLPLAFGTRLGREYLWHFDRNL RTKSEWVLGNGRLLRVMPPGRTDLAEFYLAITMERETPPVASVVANKLIGIDRGEAVP ASYAVVDGEERLLDSGRIAENYREEQRAFNKSKRELQSERGGYTRTLRSKERNRARAL GGEVTRKLLSLAAEHCAPLVLENLNSSLATRGGKNTMMSQMQYERVFTALEQKLAEAG LYSLPSAPKFRKGDNAFIKLVGPAYTSQTCSACGHVHWAEFYEKILDTLAPCGEKQWQ VTVEGKARTLPESYTYWLRGKGEQTKNTHERIIELLKDRPVSKLNKTDRKSLVSLFKN RWMPYRPKQADFQCVVCGHKMNADEQGALNIARKFLFASGRGKKSGEMTEAERRKVRG EWEKWYKEKLATVWKKQ
152	CLUST.118237_OCZT010053476-M direct repeat 1>	guuugcaugaugacguuugcgggguugguuuca
153	CLUST.118237_OCZT010053476-M	ugaaaccaaccccgcaaacgucaucaugcaaac

	direct repeat 2>	
154	CLUST.118237_OCZT010053476-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
155	CLUST.118237_OCZT010053476-M non-coding>	ctggaatccccggccatcaatcccgccaacgccgccgagcgcgatgagttccgtctga ataccttcccaccggacaaccacaccgcgcccgcgccgccgactccgcccgcgacacc gaagccgtaaaatcaaatttggaaaacgcaaagcggcctttgggaatggaggccgctt tttgttttggattgttcctgttcacgaaatccgctattcaggctacaaatctaaaagg gtaaatatgagcaaagagcctcggaaggattcgactcacgcctcgcttcgccagttgc ttgaacttggtttgagcaaaagcagttcggcagagccacagaagatcacgcgcacggt gaagttcaagattcacacgcttgcacgaccggaactcgttggcgcgttgaacatcgcc cgcaaattcctgttcgcctcgggacgcggaaaaaagtccggtgaaatgaccgaagccg agcggcgcaaagtgcggggcgagtgggaaaagtggtataaggaaaaacttgcgaccgt ctggaaaaaacaatgaaaggcttgcgtcagttctgcgaaaggcgtaaacaggcggcgt tagtatttactttgatacgatctagcgtgcctttccgtccaacggattcgacacgacc cgtgaacttcagcgtgcaaaaggaaatcacaagtggtggttgaccgctgcctgtagcg atccttgaaaacttaaaccgagcgaatcagttaggttcggaaagaagcccgaactggt ttcaaagtcaatcgcgtcaatgatttcctgcaaaccataaacgggtctaaacgggtca gtcctaacttt
156	CLUST.118237_S.1IZOEO-M effector>	MKAKYRSNSIHASLRQLLELGLSKSSSAEPQKITRTAKFKINTDIRPDLVPVLNRHFD AFEKFRRKVLDELEARWNKDQKSFQAMVQCSAKEPYQKKSSCYAWLDTHFITEAKAVL DLPRKPATSLLYNLSGGLKGFLTRRETVTEDIQKRFNDNLREWNGDLSQLASDLKAPL PPAPPNLDFENLTERAIERYNDWVGRTRAWCNLILVQQKKVERRDACLPRYLKGYPGF FGSQRYATTASLAENLKKLEQEAREQSKKAPTRFAKLSPEIWTAIQERFSPPEGHEAG EKRRPRTAHQTVCLRFAALRAAHPEWTPAQLAGEILAGIFHGTEKLKKHLAANGFEDR RAVIKLANLYNVVVAFSLDPIRAAGNYISFYKEETPKRNAFGDVRGGLHQPSDESAAI EIMGFGLQKESGKPLYNGLLVCKKSEKEHDDSWAFLYCHTEGQMFELANEKAKLRGKL LTDWTGFASRGGSRKKAEASAKQLVRGRVWISEKTPPTVMPLAFGSRQGREYLWHFDR DLREKNEWVLGNGRLLRIMPPGRPNAADFYLTITLERQAPPVAEFIASKLIGIDRGEA VPAAYALIDREGRWLVNQKRFQEFLKALGTWHDELDEWWKKNKNTPINDRVKRPRLQW TSELEDGFGFVASEYREQQADFNDQKRELQRTQGGYTRWLRSKERNRARALGGEVTRA VLSLASEHRSPLVLEKLGSALATRGGKGTMMSQMQYERMLTTLEQKLAEVGLYAMPSA PKYRKLTNGFINFAAPHYTSSTCSSCGQVHDSIFYNELAKKIVRPNDSKWQVTLPSGQ TRTLPQTYSYWLKGKGEQTKQTNERLNELLGERTVTQLSKSSYMTLVSLLKNSWLPYR PQQADFCCLNCGYTTNADVQGALNIARKFLFRSERGKKTDDAGEEGEAKRGKYKDDWQ TWYRQKLEKVWCK
157	CLUST.118237_S.1IZOEO-M direct repeat 1>	uucggaaucgcugacgcucgcggggcugguuucaaag
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160	CLUST.118237_S.1 IZOEO-M non-coding>	cggggaatataacaaaccaaatccgtcttgcaacaactatttcgcccgatttgcggtc ttaactcatcgtagcggcggtcggcagaccgccgcatttcttctggaaattgcgctgt ccggcactttgccgggagccgctgcgcccgttttgcagaggtttcgttttaatccttt tggaaagcaccgcgaagccagcttcaactaccgcttgccgccgccgggacacgggcgt agcatcactccacaatcagccatcaggaaaatgggtatgaaaatctctttggggattt catcatgaaagcaaagtatcggtctaactcaattcatgcctcgctccggcagcttttg gagcttggcttaagcaagagcagttcggcagaaccacagaaaatcacgcgcactgcca agttcaagattaataccgacatccggccggatttggttttaaacattgcccgaaagtt tttgttccgttccgaacgaggcaaaaagactgacgacgcaggcgaagaaggtgaggca aagcgtggtaaatacaaagacgactggcagacttggtatcgccaaaagttggaaaagg tctggtgcaagtaatctgacatcgcccattcgagactcgcgagcatgacatggaggcc gacgatttccttcctatctactcgctcgcggagtggcattattgcccgcgctcgtctt ttctgtcgtggtttggtgcagagcgtgaggatcgcgtcaccccggcttaccagaaaat gcgcgaagtccacgcggtgagcaatgta
161	CLUST.118237_S.1 IZOEO-M direct repeat homology 1>	ccgcgag
162	CLUST.118237_S.1 IZOEO-M direct repeat homology 2>	ctcgcgg
163	CLUST.118237_S.1 IZOEO-M direct repeat homology -containing sequence>	tgttccgttccgaacgaggcaaaaagactgacgacgcaggcgaagaaggtgaggcaaa gcgtggtaaatacaaagacgactggcagacttggtatcgccaaaagttggaaaaggtc tggtgcaagtaatctgacatcgcccattcgagacccgcgagcatgacatggagaccga cgatttccttcctatctactcgctcgcggagtggcattattgcccgcgctcgtctttt ctgtcgtggtttggtgcagagcgtgaggatcgcgtcaccccggcttaccagaaaatgc gcgaagtccacgcggtg
164	CLUST.118237_S.10WVPV-M effector>	MIHKSTVKASVRHLTRHALDKPGEGDPGKPTTKTLKFRIDAKGHTRTRLDQIFTAQNH FRRDLYIKLEGMWDKDPESFISMVNSSPSKPFQKKTSCSGWIETKFVTGVALPEHLSR ETAAATAVAVGNSLTATFERRKNVISQLAKNIEENRSVWRGNLKELCSELKITPFKAP PSIHPAKINAKTVEKYNEWVAAARIWCNLILVQKHRVPRNSACLPVRLKHYPGFPGSV IFKKGASLATAIKEFRKCLAGLKRSQLKLFDGLTAEEWGLVIDRFPAPEGEGGKGMRH QLGKTLAVLGKKHPDWKPRQLVEELVAGLERGADSLVNHLKDRDFSDRPAAIKLINLL NNACVVLMEPLRVKNLYRELFEVGTPRRDAFGQARGALAEPTDQSEGLEIRGFSIRTN RPPIGHSSFNGFLAVRQTEGKDEWSFFFDPDGPGGMGLSGLPPAGSIPTDYIGFGSTG GSRKKAQASEKKLVRERLWIRRDRNPLQLPLQFGKRQGREYLWNFDHGLKKSSDPWML ANGRLLRVYPPNQPQFSDYFLTITLQKDTPPLALSAGEMLIGVDQGEVNPASYAVTDA KGKLLTRGNVGESYSAKIRQFAEMKSAEQRTAGGYTRKLRSKERNTASACGGLVIREL LDLLVRYPGALVFERLSSGIATRGGRGTLMSNMHYQRITGGIEKKLSEAGCHRITDFK SNFSPFLRMVQPHYTSATCSNCGEVFDSDWYEKLTATIRKSVSGSWVVTLPDGKELWL QGREEIPWNPTDRLEEIFKGRTFPDLTSRSQKIVQGIVGRLVAFRPKRGEFVCPCCGH TDDADLQAALNIARKSIWLSTLPKRSKKETLAEARGSTKPAWKKWYQNRISENWC
165	CLUST.118237_S.1	gguuagcucccauccuuguugggugguuugcaaaag

	0WVPV-M direct repeat 1>	
166	CLUST.118237_S.10WVPV-M direct repeat 2>	cuuuugcaaaccacccaacaaggaugggagcuaacc
167	CLUST.118237_S.10WVPV-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
168	CLUST.118237_S.10WVPV-M non-coding>	aaatacggttccgtcaaataagttgcctgaagagtcactggcgttccctgaaaattcg tattttccaaccaagccataattgaggttaaccacggcagacttcgctgttgaaccca tcaacaagatggctaatgcgaccacccgattcatatattaattaaaccatgttctttt gttttttcaatgtcccacaggctctttttttgactaaataaaatatatccctttggt atatccttggttggtttcgtattatcgcataaaacaaatggtttgtgaccggtcatgt tttgagcgttccatctctgtaggtttcattggggttttgtgattacccctcctaata ccgtatttgtaccacccccctaccttagggttagccctgttttgaactggaatacgtac cttaatcgtctgattataacccttcggttaaaacgatgattcataagagtactgttaa agcatccgttcgccacctgacccgccatgctctggacaaacccggcgagggcgatccg ggtaaaccaacaacaaaaaccctgaagttccggattgatgccaaggggcacacccgca cccggctcgaccaagccgctttaaatatagctcgcaagagtatctggctgagtacttt gcccaaaagatccaaaaaggaaacactggctgaagcacgtgggtccacaaaaccagcg tggaaaaagtggtatcaaaatcgtatcagcgagaattggtgttaaaaatacttgtctt acactcgaaaatattataaaaagcagtcttagtattttcttagcaacacgttgtctgt cctcgccaaggaacggtcaacaatccaacaagttctttcgcaacgggggggcaaacca gaaaattttcccttaaatttgaatcttaggactttagatactgccatgcgcggatact acaaaaccaaatgcatatttttcgta
169	CLUST.118237_S.19HPUJ-M effector>	MSKEYRPDSIHASLRHLLELGLSKTGSSEPQKITRTVKFKVHTLARPELVAPLNQHFN AFDEFRHKVLADLESWWDKAPDSFTRMVKSSTKAKYEEKSSCYAWLYRKYLTGAELPT ELSRDAANAMLDNLAGSLKSFLTRRATVSLEIKKRYEQNREEWEKELSLVAKEKNLTL PKPPPEIDFDHLNVMAIGLYNEWVGLVRMWCNLILIQKEKLTRENACLPRYLKSYPGF PGSQRFRKPVTIEQTFGELEAAARDQAGNATNRFANVKPEVWQAIEERFKPPAKDEVE IEARPRSRTASQTVARRLAALVKANPNWTPDQLAVEILAGIFRAADKLQKHLAATEYT DHRATIKLANLFNAAVVFAREPFRASGDYVASYGADMARQKAFGDLRGALHQPSDESS AIQITGFSVNEDGSPNYNGLLVCKPEADGKDSWAFLYCHQEGQTFQLADEKAKLRGKK LSEWTGFASRGGSRKKAEASAKQLVKGRVWVSEKKPPTVLPLAFGTRMGREYLWHFDR NLRTKSAWVLGNGRLLRVMPPARPDLAEFYLTITMEREAPPVASVVANKLIGIDRGEA VPAAYAVVDSEGRLLDSGRIAEKYREEQRAFNKSKRELQSERGGYTRTLRSKERNRAR ALGGEVTRRLLSLAAEHRAPLVLENLNSSLATRGGKNTMMSQMQYERVFTALEQKLAE AGLYSLPSAPKYRKGDNAFIKLVGPAYTSQTCSACGHVHSSEFYDQLTDTLAPCGDKQ WRVTVEGKPRILPESYTYWLRGKGDQTRNTNERIVELLKDRPISKLTKTDRKSLVSLV KNRWMQYRPTQADFQCVVCGHKMNADEQGALNIARKFLFALGRGKKSGEMTEAERRKV RGEWEKWYKEKLGTVWRK
170	CLUST.118237_S.19HPUJ-M direct repeat 1>	cucugacgcgcugacguucgcgggguugguuucaaag
171	CLUST.118237_S.19HPUJ-M	cuuugaaaccaaccccgcgaacgucagcgcgucagag

	direct repeat 2>	
172	CLUST.118237_S.19HPUJ-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
173	CLUST.118237_S.19HPUJ-M non-coding>	tgccgggcggcggggaaagcgtatgatttgcgccgtcaccagaaaacaaacgaaggca caaaatggggcggaaaagaaaaggcatcgggcagaaagagcaagcccagccggatttg ggtccggccgggcttgtccaagaaacgcttttgaacaggtgtatccgcatggaggata agtccatattcagcttcccttgcttgaccactttactttacaacacttcgaatttatg agcaaagaataccgaccggattcgattcacgcctcgcttcgccatctgcttgaacttg gcttgagcaaaaccggttcgagtgaaccgcaaaagatcacgcgcacagttaagttcaa ggtacacacgcttgcccgaccggaactggtgcaaggcgcattgaacatcgcccgcaag ttccttttcgccttgggacgcgggaagaaatccggcgagatgaccgaagcggagcggc gcaaagtcaggggcgagtgggaaaaatggtataaggaaaaactcggaaccgtttggag aaagtgataagtctggattttcgcccattgcgggcctgatatggaaaacgatgatttt ctgcccatctactcgctggcggaatggcattattgcccgcgctcggcgtttctctcct ggttcggcgctgaacgcgaagaccgcgtgacgccggcttaccagaagatgcgtgaagt ccatgccgtgagcaaccatgtggccttccgcggcgaactcgaacggggcggttggctg ggcggaaaaaacgcgctgctcatttacccgcttcacgatgacgaccttgaaaatgtgg agcggttcggggcggtgcgcgtctggcaggccacatttgaacttctttaagaaaacgc ttgcgtctgtcctgctaatggcgtaaaaaggccccgttagtatttactttgatacgat ctggcgtgcctttccgcccaacggattcgacacgacccacgaacttcagcgtgtctga ggaaacctcaagcggtggatgagccgctgcttgtcgcgatccttgataagtcaaacgg agcgagtcggttaggtttggaaaaagccttgaaccgttctcagcggtttcctatgcgt aacttgcctaaaatcaacacgagtttgcgcgttagccgctgcgacagcagcggctcac gcgcaaactcgtgtgatccaagggccgaagaagattcgcgatggccagcgggacttcg accgctctgacgcgctgacgttcgcggggttggtttcaaagcaagctgacctggacca aggccgcgacggggaggctctgacgcgctgacgttcgcggggttggtttcaaagcgaa ccggtcgcgcgtcagggccaggatttcctccctctgacgcgctgacgttcgcggggtt ggtttcaaaggagaaggcgatgggatggccgtggaaaaggactatctctgacgcgctg acgttcgcggggttggtttcaaagggtggcaaggatcgcgccggccgc
174	CLUST.118237_S.19HPUJ-M direct repeat homology 1>	cgcguca
175	CLUST.118237_S.19HPUJ-M direct repeat homology 2>	ugacgcg
176	CLUST.118237_S.19HPUJ-M direct repeat homology - containing	agattcgcgatggccagcgggacttcgaccgctctgacgcgctgacgttcgcggggtt ggtttcaaagcaagctgacctggaccaaggccgcgacggggaggctctgacgcgctga cgttcgcggggttggtttcaaagcgaaccggtcgcgcgtcagggccaggatttcctcc ctctgacgcgctgacgttcgcggggttggtttcaaaggagaaggcgatgggatggccg tggaaaaggactatctctgacgcgctgacgttcgcggggttggtttcaaagggtggca aggatcgcgccggccgc

	sequence>	
177	CLUST.118237_S.0DXSGL-M effector>	MIHKSTVKASVRHLTRHALDKPGEGDPGETTKTLKFRIDAKGHTRTRLDQIFSAQRQF VRDLLNKLEGMWDKDPERFIRMARSSPSEPFEKKTSCAGWMLTKFLTGSDLPKHLSRQ SARATLSPLSRNMKSFITRRKNVLKDMAVVIGRNRDNWDSGLKELCAELKVDQFKGPP SVDPDKLNAKTVEKYNEWVAAARVWCNLILAQKHKIPRGDAFFPTRLKAYPGFPGSVI HKEAVPFSTAIEELRKCLADLKRSQLKLFDGLTAEEWVLVLERFPATEGEGGKGMRHQ LGKTLAVLGKKHSDWKPRQLVEELVAGLERGADSLVNHLKDRDFSDRPAAIKLINLLN NACVVLMEPLRVKNLYREYFEQDTPRRNAFGQARGSLAEPTDQADSLEIEGFSLKKGD AGSCNFDGLLAVTPKDGKDQWSFFFDPEGPGGMGIAEITKHPRGSTTTEHLSFGSSGG SRKKAQASEKKLVRERLWIRRDRKPLQLPLQFGTRQGREYLWNFDHGLKKSSDPWLLA NGRLLRVYPINRPQFSQYNLTITLQKDTPPLALSAGEMLIGVDRGEVNPASFAVVDAK GKLLKCGNVGEKYTAKIRQLAEMKSDLQRTAGGYTRKLRAKERNTASALGGLVIRELL DLLVRHPGDLVFERLTSGITTRGGRGTLMGNMHYERIMSGVEGKLAEAGCYKVPRATK FRSKDTRFVRFVHPAYTSATCSACGDVFSSGWYKKTAATIAKESPGSWSVTLPSGKKI QLPSSYTYYMRGRGEKTWNTAERLEELFKGRKWSDLPPSTRKTVEGLVARLIHHRPKR GEFVCPSCGHKDDADLQAALNIARKSIWVRSLPPRQAKQSEGEDRRSTEEPWREWYKK QIREKWA
178	CLUST.118237_S.0DXSGL-M direct repeat 1>	gguuucgcacucccucauuguuggugugugcaaaag
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	effector>	HKEGIAFDTAIKELRKCLADLKRSHLKLFDGLTVEEWGLVLERFPAPEGEGGKGMRHQ LGKTLAVLGKKHSDWKPRQLAEELVTGLERGADSLANHLKDRDFSDRPAAIKLINLLN NACVVLMEPLRVKNLYREYFEQDTPRRNAFGQARGSLAEPTDQADSLQIMGFAIRKTP EGHSGFDGFLAVSQKEGKDIWSFFFDPDGPGGMGLCDASKHPRGSTTTDQIGFGTSGG SRKRAQAAEKRLVRERLWIRRDRKPLQLPLQFGTRQGREYLWNFDHGLKKSSDPWMLT NGRLLRIYPPNRPQFSQYYLTIALQKDTPPPALTAGEMLIGVDRGEQNPASYAVTDGK GKLLAKGNVGESYSAKIRQFAEMKSEMQRTAGGYTRKLRAKERNTASALGGLVIRELL DLLVRHPGALVFERLTSGITTRGGRGTLMGNMHYERILSGVEGKLAEAGCYKAPSAAK YRKGITPFLRFVNPAYTSATCSACGDVFSSGWYRKAAATISRESSGSWSVTLPSGKKV QLPSSYTSYMRGRGEKTWNTAERLEELFKGRKWSDLPPSTRKTVDGLVARLIHHRPKR GEFVCPSCAHKDDADLQAALNIARKSIWVSSLPHRQAKQSEGEDRRSTEEPWREWYKK RIREKWA
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218	CLUST.17 8956_S.0 RPEAW-M direct repeat 1>	ugggugagagaccuugugcaucaggggaaggaugcaccg
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220	CLUST.17 8956_S.0 RPEAW-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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225	CLUST.192185_OGCH01002141-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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227	CLUST.192185_OGCH01002141-M direct repeat homology 1>	uuucaauuccuuaacggauucuca
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231	CLUST.192185_S.0QHQRG-M direct repeat 1>	ggugaaggaacaaaaaugggugcgac
232	CLUST.192185_S.0QHQRG-M direct	gucgcacccauuuuuguuccuucacc

	repeat 2>	
233	CLUST.192185_S.0 QHQRG-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
234	CLUST.192185_S.0 QHQRG-M non-coding>	gctgtagtctatagtccacttgctatgcttacagcatctctcataccatgtatctgga tctgttttgtataggtttactagctccttactcatcaatatataaataaagatacatt ttccagagggtcattatttaaagggaatcctttcccatttttagaaattcagacaaag aaatcctatcccaaatttctaaaaaataggataggatttcctatcccaaacttctaaa aagtgggaaaggattttacggtgtttattgtaatttaccttctaacagacattctact agtgttcgtaagtcgtctgcagatactgtgagagggatgactgcttgcatgttggatt ctgctttgctataagggaagtaaataaaatgctgatagagcgagggttcaagcaaccg aaggtaaggatgtctaaggttaaagaagatgagataaaaaaggaagaataggagtaag gatgaagtatgagaggttcatggttattatttagggtacgtattgcagtgtaaaatat acagtgttatcaacccttttcttttgtgttaaatgttaatatgtaaagtaactacatg ttagaatccgttaggaattgaaagtataatgtttatatatttaacaaatgatatttaa tattgaggttgaaactcacaaagactatacttaagctagagttaaaaggagatcctac cagtttaaatagtctaaacgatctctttaataaatatgatcaattggtaaagatagca gacagttttatctataatgtttatcccatttatgttgtcgcacataccatgtctaacg taacaagcaccctacaaggtaatggtgagggacgtcctcttagagggcaaaccgagtt accttgtagtgtaagaagacttgttacgttagacgaatttatatacgaaaagatagga aatggcggataagtaacgattgtaatatataaaggtagtatataagttttaatggtat tggtgagtct
235	CLUST.192185_S.0 QHQRG-M direct repeat homology 1>	ccauuuu
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		LKDLKKIKKVLGKLYNDVNSNGIKSIDEYIKNEAKGKTKDILEILNKIKEYANNHNHN HNHNIRKVTKYILKQRDRIEKRIFLLSVFAYYQFKNELETEALWHDKLLYEVKPSYTS QQCLACRNIDKLNRLTQRQFRCIKCNFKMNADFNASANIALRYVEKLLKIELIPMRNN NDNNDNSSSSSSKQGKGSGTMTITSATTPLHASINASSKAGVVCNNTDGIVAHTMSNV TSTLQGNGEGRPLRVRGQTELPCSVRRLVTLDEFIYEKRGNGG
239	CLUST.192185_S.3 D61XP-M direct repeat 1>	ggugaaggaacaaaaaugggugcgac
240	CLUST.192185_S.3 D61XP-M direct repeat 2>	gucgcacccauuuuuguuccuucacc
241	CLUST.192185_S.3 D61XP-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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243	CLUST.192185_S.3 D61XP-M direct repeat homology 1>	ccauuuu
244	CLUST.192185_S.3 D61XP-M direct repeat homology 2>	aaaaugg
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247	CLUST.192185_S.0AKDY4-M direct repeat 1>	guuagagcaguacaauaguuagacugcgac
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251	CLUST.19 2185_S.2 BZ4LU-M effector >	MIGRVKLSTILILKLKYQNKQLYTRLRLSLISTQATARATTKVKAKKLTKTMLKLELK CEPNSLKFLDNLFNEYEQLVRIADSFIQHLYPYYANINEQEKLERLKELIKSLDEKAI RKNKRRKRELYEEEEQATTAKTKTETKHQYTHSNLLKTLLHRFIKYAKQYYGIDAKYA YLEMQGGLTDLMHSNAESAYKHRTIPNLRGLSNVMPIRVSKRPLLENRRSKDNNIDEY YQRTAEFIFNNGKIMFRIGSKRNGLTFKIAERFNDVERLGMLIDAIQGKNGLTIGDPS YLIRKDTDNGYRYYIMVSISKNVDVKVLREAVNNKNKIRIIGIDSNISKYIATMFCIE VDKENKEFKLVNAKGIDSKNYINAVKKYEEERRKLQQGRMKGKINKKKGSRYKEEEDY TVKNRCGDSKRIDIRRQLIGYICNQILEFANKNNADIILIEDLKGLNKELKTLRIIRN ELGKLYNNVNDKGNNAIDDKINEVNKDKKYKNKIGKPLLEILNKIKECSNNNKNNTKV AKYILKQKQMIERRIFLLSIMAYYQFKQELEVEALWNGKLLYIINPKYTSQQCLRCNH TNKLNRITQRQFKCIRCKFEMNADFNASANIALRFATKLKLELELKQGESSSMMTITS ATTPLHASINAGSKASEQGYRYNNANLVRNGSVAATMSSVASIALQGEGERRFPCLRG QTDEPCSAKRSIATLDEFLEKKGNGG
252	CLUST.19 2185_S.2 BZ4LU-M direct repeat 1>	ggugaaguagcgaugaugcaugcgac
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257	CLUST.192185_S.2BZ4LU-M direct repeat homology 2>	gcgauga
258	CLUST.192185_S.2BZ4LU-M direct repeat homology -containing sequence>	aatgtgtttatttattgatgttgttgttattctcatcatctccgtcattatcatcgc caacataaagtctgttcagattctcaatgacttctttatgtttgtttattaattcctt atagttactaacatcattatcatcgttacctttatcatcgctgttaacattaccaaca ttaccaagacttctaacagcttctattatctcatcataaatttcattcacaacattaa ctttgtttctgaagaacgtatcaaccttcaacttcaataccttacatcggcttcctt ccagcagtaaccattcc
259	CLUST.219656_QJWJ01000458-M effector>	MKQAGTIKVEIVPDGDGARVYARLRAMRGSLPLALNFAFRDVFPEAMAQLESALNGER GDAKWQGSVRKRLRHHWNAQLQSRLAFASRTKGQGKKSSAKPPDPTVFEPTLDTLCSE TSDHIVSRFSGEHFRDLMAGRAGVPTFKGGGKSFFAEGRAVSLSGTLSTLRMRFPLWG SGKKATPFKVFTEGNAARATMRQLLLSSGDRENVIELERRVRRKESREQAEFELEQLG AIKMGRVGISYDENRQKWFALISWTRHAPEGYKEGQAAALHLGCQVFLQAATEKGELW QRPGFDILAARARFHGARWRLSKCKRSFGKGSRGHGKKRRELPFTKLSERESQWVKNW IRTMASDLIKWCLLHGVSDLYLEDLSGIRDTFEKETEGDAPEPLKRMIHQWPYYETQQ AIERQAAEFGVRCHKTAQAISTHRCPSCGHTDPENVTFTNMLSHDEVRVLNGMLFKRV DKRAWFSCTACKHRGSADVVSCMNHLALVGRDHSFGAMQEASKKRKGIQRKKVASAAN GIGVGSDAAE
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261	CLUST.219656_QJWJ01000458-M direct repeat 2>	cuccaaacaccugaccguccacggaucgacuuugcc
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263	CLUST.219656_QJWJ01000458-M non-coding>	agcacagccctcgtgctctcgctcgtcgtccccggtgacgagtgccggttgtgtgggc tcaaaccggacccgaaggcgttgagccggaaggatgtccgggcgttggtcagagaagc caagctgaaagggaagtctactgagcagagatgagggttcaggccggaatcaccctcg gtccaccagaggcgaaagcgaggcctcagtcctcgctaggcacacagtgccagttccg cccgctccaaggcggaaaacacctgacccaaccgctctgaaccctcttttctgctcag aaggagaaccatgaaacaagcaggcaccatcaaagtcgagatagtcccggacggcgac ggggcacgcgtgtatgccaggcttcgcgcgatgcgtgggtcactcccgctcgcgctga actttgcgttccgtgacgtgttccccgaggccatggctcagctggtcagctgcatgaa ccacctcgccctggttgggcgtgaccattcattcggcgccatgcaagaggcgtccaag aaacgaaagggtattcaacggaagaaggttgcgagtgctgccaatggcattggagttg gaagcgatgctgcggagtaggcgctcgcaaagcagtttgcaagacgtcgggatcgttg ctgtgcgtgaactactgaagtccagtaggcgatccgctatcggttaaggtgtttggag ttggtcaggtgtttggaatagttgagttggagcctcagaaaaaccaaagcaggagaac cacatgtcactagtgaagtacaacgaagcagtaacccacgccaggcagctactcacga attggctagacgcaggcgtccagctcttcctggcgctgcgtgagatcgaaaccagcgg cgactggcagaacggcgagcacgccaatttccaggactcgcgttcgtccctagcgatt cgccgcaccagtgagcaacaggaaaccatcgcgcgcctgcgggacgaggtggcaaccc tgcgcaaagagaacaaggcactgaagcgaaaactgcagcgcctggagaagccggcgga agcggcggagtaatagatcggatgatgaatctgacagagcgcgctgcacgcgaacaac tgcaacgcgatggggttgaactgctcaagctgatcggtgccgagttgcgcaagcagac ggacgccaatgtcagcgtcagaccgaaacggctgaaggtatgcttgctgccaaaaaaa ggaagacggcccgaagcgctgagcttgggccgtctttgagttttgcgctagatcacgc tatttttgagctggatgcgcattgttacggatacctccaggcgctgcattggttgcc ttgccctgaagcgtctggagcgctagcttgtgaccgtccctcccaacatttatggacc gcccgctcgatcaacgaacagg
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266	CLUST.219656_QJWJ01000458-M direct repeat homology-containing sequence>	aaaggaagacggcccgaagcgctgagcttgggccgtctttgagttttgcgctagatca cgctatttttgagctggatgcgcattgttacggatacctccaggcgctgcattggtt gccttgccctgaagcgtctggagcgctagcttgtgaccgtccctcccaacatttatgg accgcccgctcgatcaacgaacaggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn nnnnnnnnnnnnnnnnn
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	effector>	TAMTEARTAMAKTSDERRTFVRREYNKWALVAEDAAKLALPLWGTGKKVVEFVVRPAG GSHRAFWRRLVHHFVRRDEVCKAEAELKKIGWNEAEKQALRNLRATRKSEADKEKRKE IFTKIAALINAANKRVQSDKDPIEKKLYGLVKMGRVGVVYNERRRKWFATISFIEYKP DVAAKGQKAALNFGVNVFVQALAENGAEWHEDGDQILVKRIAAHMQRKSIQRSQRTFG PGSQNRGHKRRDLPLSKRKGDESNFVQTYIRQLASRIIKWCARHGVADLYIENLKGIR EQFERDTKEQAHEEVKRRIHSWPFHDTATAIIYEGAQHNIRVHRKGARYVSQRCPDCE HTAPENVQAISVPGIPLLLKPVGPHRWVSGHKAGRDGVMYRRVKKTCRFECVDCGKRG GADFIACLNHLIDVGAQFKGGSPLAKAQEKTRKRVSNDRRKKVKRSA
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269	CLUST.219656_S.359KQ6-M direct repeat 2>	cuuccaacaccauuccuu
270	CLUST.219656_S.359KQ6-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
271	CLUST.219656_S.359KQ6-M non-coding>	gcggcgctataaacaatgttatgaagggttgtaacgaacgttcgcacattgaagccga tccccgatccaagaaagtcgattcggcgacttgaaagcgaggctggtcctcgctgccc ctttccgggggacctccggtgcttgcaccgcgacaacaccattccggatcggagatcg ggcttcaacgtgcgagcggtgcctacatcagcttgaaaggaggtccaagctgctgaga ttactaaccgctcagcgagtgccgtgggggcgcagacttcatcgcgtgcctgaaccat ctcatcgatgtcggcgcgcaattcaagggcgggtcgccgctcgctaaagctcaggaga agacgcgcaagcgcgtgagcaacgatcggaggaagaaggtcaagcgatcggcgtgaag gaatggtgttggaagccgtcagatctttcgttgcccaagtcgaatggaaggaatggtg ttggaagcgaggacagcacagtgtttcgagcgcttgaaaaggaatggtgttggaagcg cacgcgccatcggggcacacgtgccagagcgaaacggacgcgaagaaggaatggtgtt ggaagggtcccctgcaccggtaggttgagcctgtcggtgtacccagcgaaacggacgc gaagaaggaatggtgttggaagtgctcgcctacgtggttcagcgaaaaagggctgaac tggaaggagtggtgttggaaaggtagcgtcgtatcgaaaggaatggtgttggaaggga gttcgcgattgaaaggagtggtgttggaaggagaacttgccgtcggtggttcgcaaat cctcgttgagcattgcagtgctacgaaaaaggaatcgaaggtaaatgaccaaaaaact aagcaagagttcatacgacagcgcggtgaagcggattcgcgcgctgatgcaaaactgg ttcgagaggggtgtcgacctcttcatcgaactgcgcagtatcgatcagtccggtgtat ggcgccaccccggtcacgccatcacgaagcctgagcaagatgtgcgtgcgcttcgaaa agacaacgccatgttgaagatgaagcggaaagcgaagccgctggagcgcgtgcgtctc gccaagaagaagaaagcaggtgcgaagagaagcagcgcgcgggcgccgaactgaagtg aggcacccttgttcgagggatagaactactacggagtttagaggtagagcgaaacgga cgcgaagaaggaatggtgttggaagggtcccctgcaccggtagattgagcctgtcggt gtacccagcgaaacggacgcgaagaaggaatggtgttggaagaacaggccgcgtcgat ggcgaaagcgaaacggacgcgaagaaggaagggtgttggaagcctccagtgacccgcg cgtcggcggcttgtaagcaggagcgaaacggacgcgaagaaggaatggtgttggaagg gagaggtgcgcgtccgctgtggagttctggaatggtgttggaagattgagcacccctc ggcacgggcgtgcgcacgacctcaaagtaggtgccgaaaaggaatggtgttggaagcg aagatactggttccgtaatggcgcatagcaattcgcttggagcgtgccgtgaagtgga atggtgttggaagtgaatctcccgtgggccaaagtgttgcgcgacgttataaagaatg ttatgaggtgactcatgagtacgaagtggcccccgcagcgattcgtcggcttcgtaa gaagctcgggctcgctcaagaagggctcgctcggcgcctcgacgtgtccgtagtgtct gtgaaccgatgggagcgcggacacagcacgccgacagggctcagtgcgaaggcgctcg

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272	CLUST.21 9656_S.3 59KQ6-M direct repeat homology 1>	aacaccauuc
273	CLUST.21 9656_S.3 59KQ6-M direct repeat homology 2>	gaaugguguu
274	CLUST.21 9656_S.3 59KQ6-M direct repeat homology - containi ng sequence >	gcggcgctataaacaatgttatgaagggttgtaacgaacgttcgcacattgaagccga tccccgatccaagaaagtcgattcggcgacttgaaagcgaggctggtcctcgctgccc ctttccgggggacctccggtgcttgcaccgcgacaacaccattccggatcggagatcg ggcttcaacgtgcgagcggtgcctacatcagcttgaaaggaggtccaagctgctgaga ttactaaccgctcagcgagtgc
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276	CLUST.21 9656_S.0 2973R-M direct repeat 1>	gagaaagaauggaaucggaaga
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278	CLUST.21 9656_S.0 2973R-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
279	CLUST.21 9656_S.0	acgtagaaaggtactggtccagaccatttgcgagggattgaaacgccctcggagaatg aatggaattggaagctgctctgctgaaggcgttgcgtcgagcatcttgtgttgaaaca

	2973R-M non-coding>	ccttcgctgaaaacgcccttcgaagaaggaatggaatcggaagcacgctggcgatctt cggcgccctagtcgaggagcagggctgaaacagtcttcagagtgcggtgctgaggcca agaaggaatggggttggaagcgtcgcggcagtcgatcttcgacgaaggaacgggttcg gaagatgtcgatgcggcgtttcaattgaatggaactggaagatgcggcgtctcgcttt caagtcgagcgctagaaagctaaaatagatgaaagacgttggaaccctactcatcgag atcaaaaaaccagtcggcgacgtgccgctcgtttacaggcgcctgcgcgcgctgaccc gttcggtagcgcaagctctcaacatgacgatgcaggactcgcacccgagcgccgtcgc gcaa
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284	CLUST.219656_S.2B0JKQ-M direct repeat 1>	gcagaucagaaauggaaacgucagguguucagag
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288	CLUST.219656_S.2B0JKQ-M direct repeat homology 1>	aacaccugac
289	CLUST.219656_S.2B0JKQ-M direct repeat homology 2>	gucagguguu
290	CLUST.219656_S.2B0JKQ-M direct repeat homology -containing sequence>	acgagatatcgtgtcagggtacgcaccgtaaacagccattagtacgccaacgaccggg aactgctggccgatctaccggcccgaaagcgaggcttgtcctcgctaagtggcgcaag tcgccacgggtcccgcgctctacggagtcgggagaacacctgacggcccggtcgctgg cgtgctcatgcttgtttgctgggggattcagtgtccaggtgtttagagggtcaggggt ccggctgtgcgagccgtcaggtgtgcagagtgctttttttccgacgaagcgtcaggtgt ccagaaaggccagcggattc
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	effector>	VGISYCERKRNWYALISWTGEVEVEMQKGQQAACNFGVNVFLQAVAEDGSSFRVDGSD ILVTRKRFAHRRWSIQKSLDTMGRGSRGHGKRRRLAPITKIEDAENRWMETKCRTVAA ELVKWCVRHRVGVINLEDLEGIRDGKAASMHHTNVKRLIHQWSFYELRLAVERQASEF GVQVKVDTAEFNSQRCPRCGYTSEENTKQVSGREEYIIHHGKAYSRRDKMRMFECVSC GFKADGDVVAAANHLNDAAGVIAKLKSLHRNSVREKTNVALEA
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294	CLUST.219656_S.3J5O8F-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
295	CLUST.219656_S.3J5O8F-M non-coding>	ctaggtcgcaaagaagtgttcacggtgtcgaagtatcgagcggtgttatacgggcaag atgtcggttatcccgatgaggtggagcgtgtctggagattctgcgcacggttcgaaac cgaagaaggagttgaagtcgaggactccgcttgattacgtctgccccgagaatcgtgt ctggttctcgcgtaaggagcgcgaatggccccatcctggcccctcagcgccccgctga cggcctttccccggccgcccctcccctttggagccccctgccccctcccccgtttacg gggcgctgaggggctttctcatggaaagtcgtgtttccatcggaggggttccagtccg gcggtatctatgtctccgtggccaggattcccctcaagtccctcgcggtcccgaagaa gcggctcaaggtcgctggcaccctgaagtgcgagattgttcgccccgaaggcgaaaca tgggacttcgagtgtgtgtcgtgtggtttcaaagcagatggcgatgtcgtcgctgctg cgaaccacctgaatgatgcggctggcgttatcgccaagctgaagagtctccatcgcaa ttcagttcgagagaaaacgaacgttgcgttggaagcctaagaggtcggtcagacggcc tgaatgcgagcggtcctgccaaaggtgggggtttaccgactcgcaaagaggcccaact cggggaccgctcgctaagcggttcgtagatagccgaaaccaaagcggaacacaggtca gcccttctcct
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297	CLUST.300348_S.078WZM-M direct repeat 1>	gaugcagaaaggguaauugaguuaaguguugugcaagcug
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	repeat 2>	
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302	CLUST.300348_S.21TS8J-P direct repeat 1>	guugcagaacccgaauagacgaaugaaggaaugcaac
303	CLUST.300348_S.21TS8J-P direct repeat 2>	guugcauuccuucauucgucuauucggguucugcaac
304	CLUST.300348_S.21TS8J-P spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
305	CLUST.300348_S.21TS8J-P non-coding>	acagtaaaggttgatttgtcaaataagcagaaagttttatatgccgtggggcagataa gaggaattattgggggagaaaagttcccgccgccgacggaatggaaaaagcggtgcgt ggactgttactataacaagctgtgttgggggtaagatggaagtacaaaaaactgtgat gaagacactttctttgagaatattaagacctctgtactcacaagaaatagaaaaagag attaaagaagaaaaagaaagaagaaaacaagccggaggaactggagagcttgacgggg gattttataaacgaaaagtaaataaattcccaaaatttaaatgtgaaaagtgtaactt agaaataagtgctgactataacgctgctcgcaatctatcaactcccgatatagagaaa

		tttgtggcaaaagctacaaaaggcattaatttgccagaaaaatgagaatgttattcca taataacatttgatgcacacgattcctccctacagtagttaggtatagccgaaaggta gagactaaatctgtagttggagtgggccgcttgcatcggcctaaagttgagaagtgtc agactctgataaccctcaacgacgatattctttatttcggttcaaagttctgcacaaa acaggtgagtccttataaaccggtgtgcagaacgccggctcacctttttccttcatcc gattttacgcttaaaagccgtaaaaacgcgggattcggcgcctgctttagtttatgaa acttgccgacaatgtcctgcctgccttttacataacgtgcaagcaatttttccgcctt gctgtttgccgtatagatttcatacataggtggattgaatgatgaaactcatatataa acaatgccctccaacgagaatagacgaatgaaggaatgcaatcttgacagagcccgat tgcgttatctccgggagaaacatataaaagcatcaaccactgatcggaatgatatcca aaaacatggccaccatcacccgatggattgaggagcgggcacgatattccacccccat catccgcatctccctt
306	CLUST.300348_S.21TS8J-P direct repeat homology 1>	uccuuca
307	CLUST.300348_S.21TS8J-P direct repeat homology 2>	ugaagga
308	CLUST.300348_S.21TS8J-P direct repeat homology - containing sequence >	agttggagtgggccgcttgcatcggcctaaagttgagaagtgtcagactctgataacc ctcaacgacgatattctttatttcggttcaaagttctgcacaaaacaggtgagtcctt ataaaccggtgtgcagaacgccggctcacctttttccttcatccgattttacgcttaa aagccgtaaaaacgcggaattcggcgcc
309	CLUST.300348_S.0QW2KE-M effector >	MRISKTLSLRIVRPFYTPEVEAGIKAEKDKREAQGQTRSLDAKFFNELKKKHSEIILS SEFYSLLSEVQRQLTSIYNHAMSNLYHKIIVEGEKTSTSKALSNIGYDECKAIFPSYM ALGLRQKIQSNFRRRDLKNFRMAVPTAKSDKFPIPIYRQVDGSKGGFKISENDGKDFI VELPLVDYVAEEVKTAKGRFTKINISKPPKIKNIPVILSTLRRRQSGQWFSDDGTNAE IRRVISGEYKVSWIEIVRRTRFGKHDDWFVNMVIKYDKPEEGLDSKVVGGIDVGVSSP LVCALNNSLDRYFVKSSDIIAFNKRAMARRRTLLRQNKYKRSGHGSKNKLEPITVLTE KNERFKKSIMQRWAKEVAEFFRGKGASVVRMEELSGLKEKDNFFSSYLRMYWNYGQLQ QIIENKLKEYGIKVNYVSPKDTSKKCHSCTHINEFFTFEYRQKNNFPLFKCEKCGVEC SADYNAAKNMAIA
310	CLUST.300348_S.0QW2KE-M direct repeat 1>	gucucagagauacuuccaauaaaacaaggauugaaac
311	CLUST.300348_S.0QW2KE-M direct	guuucaauccuuguuuuauuggaaguaucucugagac

	repeat 2>	
312	CLUST.300348_S.0QW2KE-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
313	CLUST.300348_S.0QW2KE-M non-coding>	aatgtaaatatctaaattcagattttcttgacactctcacatacacttccacttacac agatgtctttatatccgcctcagttcttcttgagtacctttctgcccacgttttatt tatttcatgaactgtctgtgtatagatcagaatgaagataagaggtacaaggtattga aaggcagagagattcatgaaggaaaagagagagtgaatattgattatcttaggagaag gattggctgcgtgaataaagagataggcgtctatatggcttcagacaaatatcatatt aaaggtgaagtggatgaagtattaactctgtctgatggtacaatggcgcctcttgact ataagtacgcagaatacaaggagacagtttttagaactcaacgatatcagtctgtatt ctatggcttacttataaagcagaactacagcaaagaggttaaaaagggctttatctgc tatacaagaagcaagaattatttaaaagaggttcagataactgaaaaggactttatcg aattacagaatatgatttctgaaataattgatatcacccagaagggctattatcctaa gggtacaaagtataaagcacaatgcatagattgttgttatagaaatatctgcaagggg taaaagatgagaatttcaaaaacactatctcttagaattgttcggcctttctatacgc ctgaagttgaagctggtataaaggcagagaaggataagcgtgaagcacaggggcaaac aagaagtctcgatgccaaatttttcaacgaactcaagaaatccaagaaatgtcatagc tgcactcatataaatgaatttttacatttgagtatagacagaagaataacttccctc tctttaagtgcgaaaaatgtggagtcgagtgtagtgctgattacaatgcagctaaaaa catggctattgcttaaatgacttgatttcttactgtgaatttggaaaaatagcattaa gcattgttctttgacaacataaatttgaaattagtaatcgtcccaaagggttggctat agcaggctgttgcttgcagaggataagttgacatgaatttgtcatccagcctgatgga ataaggtgcggctgatttcaacagccgaatatcgaggtgccagaatcatttttgatc tttggataacaccctcgaaacaactaactattggaagttaatgatgtaaatttatgag gtaaaatgtgatctggcggtaaaagtcatcgaatatcaatgattttaccgccaagatt ctatgtaaaagacagtgaaaattgagactttggatacaaaaatgagagggtttttaac caaaataggcatttctaaagttgcgagagaatggcaatcttcaaggatttctgaacaa aatgagctaatctgagcgattcataggtaataaaaacatagaaaaaatcacttagagg gcgatagatccttgttataataggtttgcaaaacaacaaaaaaatatcacccaataag tgaggaaattatgaaacaaagagaaaacaaaagcaagtgcaaaatcagcaaagtagag gtaacggcagatacattgacaggcagagggggggatggcgttatttgtta
314	CLUST.300348_S.0QW2KE-M direct repeat homology 1>	uccuugu
315	CLUST.300348_S.0QW2KE-M direct repeat homology 2>	acaagga
316	CLUST.300348_S.0QW2KE-M direct repeat homology - containi	ctaatctgagcgattcataggtaataaaaacatagaaaaaatcacttagagggcgata gatccttgttataataggtttgcaaaacaacaaaaaaatatcacccaataagtgagga aattatgaaacaaagagaaaacaaaagcaagtgcaaaatcagcaaagtagaggtaacg gcagatacattgacaggcagagggggggatggcgttatttgtta

	ng sequence >	
317	CLUST.304860_S.0OLHZC-M effector >	MHKKPKAAADDILDYGEVDAELTRLTTLMKEKLDHLKPEPDAAPEVMKAEADAVYARL EALIPELKKTVRDSLLRLANRELPLRGRDWVWNDAKGQLEEGNFSDDTLGRWIRGQRG LSMDRIEQIEMLRKRFMALKRQMALAPGVEVSQGVEDKGRRIDEPCQKILDKLDRLKQ QRVNQTAHLILVQALGLRLRPHQESAQDRHEKDIHGEYEPMPGRKPVDFIVMEDLSRY LSSQGRAPSENRRLMKWCHRAVLGKLKQMCEPFGIAVLEVPAAYSSRFCALTGVPGFR AMEVHDGNADDFRWKRLIKKAEKDKSSKDAVAAATHFDQLRRLNAELREKKILDKGTP LRTLLVPVAGGPIFVPIQGGGPRQADMNAAINLGLRALASPTCLQARPKVRAELKDGT HHAIHGNKLEKAAGLELQPPPQPSKELATQKRTNFFFDEDGVGGFDTGWVIAGGKRIR VSGSMALWKAVKDRAWQRVAELNQKRIAKWLGLAPDSDDEIPM
318	CLUST.304860_S.0OLHZC-M direct repeat 1>	gcuucagucccacgauucagaggagcuugaggcgg
319	CLUST.304860_S.0OLHZC-M direct repeat 2>	ccgccucaagcuccucugaaucgugggacugaagc
320	CLUST.304860_S.0OLHZC-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
321	CLUST.304860_S.0OLHZC-M non-coding>	gaatccacaaaaagcccaaggctgcggcggatgacatcctagactacggggaggtcga tgcggaactgacgcggctgacgacgctcatgaaggaaaagttggaccacctgaagcca gagcctgatgccgccccagaggtaatgaaggcagagggggggaagcggattcgcgtct ccggctcaatggccctgtggaaggccgtcaaggacagggcgtggcagcgcgttgctga actcaatcaaaagcggatcgccaaatggcttgggctcgcgcctgattcagacgacgaa atcccaatgtagatataaccgccgcgccgccgccccagcggaccagatctcccgtcat gaacattcgcctcagcgtccgcgtgagttgacacggctcggtaagttatgaagctatc aaaacttttcgagaagaccctgaatgcaccgcagtccgtgcgctttgctgacctgtgc cggttggtggtggcgtttggctacgttttggatcgggtgaagggcagtcatcacattt ttattcatccggatgccccccgcaagatgaaggcggaactgcccccccctgctgaacca tgaggaggaccagatcctctttgtgagcctagggccggaagacagcgcgcacgggctg cggatcgaggcgatggggcagccgtatctggtgcggagtcgggtcgtgatcgtctgag gggggcggaaaatccggaaatctcatttgatctctggggcgacccggtcagaatgcgg gcggccatgtgccaccgaccacccttcctccgccattggaatgggcaagctctaagaa tcgagtttgatttgatctctgacatcgtgacgactgaagcgcggcgctcctcgcgagc gcggaaatgccgggcaagtgcccggcccgcgctcgcgaggcgcgtcacaacttaattc aagaggcaaggtcgccgatgacggaccacgcaaaagcgggttgatggaggagcgctcg caaagtgagcacgaaacgtccacgggacaagcctcgggaagtgccaggaaagtgtgga cagcctggccaggctgacg
322	CLUST.304860_S.0OLHZC-M direct repeat homology 1>	acugaag
323	CLUST.304860_S.0	cuucagu

	OLHZC-M direct repeat homology 2>	
324	CLUST.304860_S.0 OLHZC-M direct repeat homology - containing sequence >	aggggggcggaaaatccggaaatctcatttgatctctggggcgacccggtcagaatgc gggcggccatgtgccaccgaccacccttcctccgccattggaatgggcaagctctaag aatcgagtttgatttgatctctgacatcgtgacgactgaagcgcggcgctcctcgcga gcgcggaaatgccgggcaagtgcccggcccgcgctcgcgaggcgcgtcacaacttaat tcaagaggcaaggtcgccgatgacggaccacgcaaaagcgggttgatggaggagcgct cgcaaagtgagcacgaa
325	CLUST.304860_S.0 DWX15-M effector >	MPGWQELANGDETRLLQLREALKQHIIEQRQRIQRELLRLTGRILPLRGRDWVWAPHP DKPDCHLLRQAREDARRQKVKLRGQRGLSMARIEQLSELRRRWQSLNQALRRKIGDRP LTASEMRNDPIPDPCPDILIKLENIREQRVNQTAHLILAQALGLRLRQPQLSPESRQA ADIHGEYDVVRPPVDMIVVEDLSRYLSNQGRAKAENTRLMKWCHRAIILKLNMLAKPF GIPVLETPAAYSSRFCCLSGAAGFRAAEVSWKDRHEFRWRVLLGEEAKARAEGAEPSP SAMHAARLFSSLEKIAASERPNRTLLAPQPGGPIFVTAKAIPHPAPAGNRKLSGNKDI LPMQADLNAAVNLALRAVAHPSVADIHHRLRTERKKGEKGQPDTFIVREPRRFGKDKV PIQIRDGDSLPKERNPNLFYDRHEIAPFGRARLETDSAGRFDYASGPGVWKTVNDREY QWRRCEAINNERLRRWLNHEQVKDDVPM
326	CLUST.304860_S.0 DWX15-M direct repeat 1>	gccgcagucgccgcgauuucaggaagcaugaggcgg
327	CLUST.304860_S.0 DWX15-M direct repeat 2>	ccgccucaugcuuccugaaaucgcggcgacugcggc
328	CLUST.304860_S.0 DWX15-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
329	CLUST.304860_S.0 DWX15-M non-coding>	caatccgacctgctgaacgacatccctgacgccgccgccttaaaacaaagactcagct tccccgagcagaacgacaaattactcgtcgcgttgcggcgcgcgcaaaactggatcgc gacctgcgtctcatggcactggaaactcacctagccggatgccgagccgcagcgccaa ggcgcgctggaacaaattcgcgaacagcagcgaatgcctggctggcaggaactggcga atggcgatgggacccgcctgctccaactgcgggaggcgttgaaacaacatatcatcga gcaacgccagcggatacagcgggaattgttgcggctgaccgggcggatactcccgctg cgcgggcgcgctgggcgattcgactacgcctccggtcccggtgtttggaagaccgtga atgatcgggaataccagtggaggcggtgcgaggccatcaacaacgaacggcttcggcg gtggctgaatcatgagcaagtgaaggacgatgtcccaatgtaggcgtaatgagcgacg cgccggtccaaacccaaaccgcactcgaagcccagccgcctctgccagtgcggcgctt gcacaacttcatctattgtccgcgcctgttctactatcaatgggtcgagaatattttt caggaaaatgccgataccgtcgcccaggtcaagtccgccctgcaccccatcctcaaac acgacgaggaccaggtgttgtttgtcgctcttgggccttcaggcaacgacgccagcct ggtcatcgaggccatgggtctgccctatctcacaagaacgcgggttaccattatctga ttcatcgccgccggacgcgcccttatttttcgaatttttggcattgaccgaaccatt

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330	CLUST.304860_S.14XMT9-M effector>	MATIAEWEEAREIAEKLGMNADKVLGDSLTRYSFPEMNDRLLYALRRAQARLARLQSW SSVAWEERDDARRAAFEKRRTRIKEQITEAIAARAEAETRPEKDREQELPARGQWLDE VKPFVERQAWDCVRDRILREIQNEREIIQAQLVRIANRIQPLRERQWEWASRDDGSKC HVLRQTPRGTDVRSKLLAGQRGLSLARIEQLESLRQRCQSLNRALMQRPGEPAKLGFG KRGVELPDPCPELLERLEALKKQRVNQTSHLILAQALGVRLRAHASDAATREALDIHG EYERIPGRKPVDFLVLENLDRYLASQGRSRSENSRLMKWCHRAILGKLKQLCMPYGLR VLETPAAYSSKFCSLTGIAGFRAVELTPDDAQEFLWRKHLERLVDPERAEKLSMEERS ESQAVKRVFDSLREWNRALLIERDTARAEGRPFRPKWRTLLAPMHLGPIFVPMHGKPM QADINAAINIGLRAIASPEADAIHTRIRAMRDGETFKVRAENSREKARWGAKPPEIAL PPEADEKAQGNRLKLLAEARLNFFVDLGRVATFDHADIVDLPHPVSSGRGLWRAVNQF AWRRCEEINQARIAKSKLEADEIPR
331	CLUST.304860_S.14XMT9-M direct repeat 1>	gccgcagcgcccgcgaugccagagacguugaggcgg
332	CLUST.304860_S.14XMT9-M direct repeat 2>	ccgccucaacgucucuggcaucgcgggcgcugcggc
333	CLUST.304860_S.14XMT9-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
334	CLUST.304860_S.14XMT9-M non-coding>	gaaagctgggggaggcagaaggccgtccttggtgggccacggtccgagccatgggaat gttgcggcttcctggcgaggatactctcgtcctgcgagagggactgcctcaggaagag ctgtccggcagtcggggacgaatggcgaccattgccgaatgggaagaagcccgagaaa ttgccgagaagctcgggatgaacgcggacaaggtgcttggcgattccctgacgcggta ttccttccccgaaatgaacgaccgcctcctctatgcattgcgtcgagcgcaggcgcac gcggatattgtcgatctcccgcacccagtttcgagcggtcgcggactatggcgcgcgg tcaaccagttcgcgtggcgacgttgcgaagaaatcaatcaagcccgaatcgcaaagtc aaaactcgaagctgacgagattcccagatagagatcagagttcctcaagctacctatc tggccaccagagatttcgggatttaccagatttcatgatctggtaggatttcccccaa tctgccatgagcgcacgccgctccatctcaaaccgctcgcgtcggatcggaagagacg cagcggattcgtcgcaggccgagctaccgctcgccgcgctgcagccgcaaatccatga tgcgctcgaaaaagctctgggccagacgcctgagatcgcaattt
335	CLUST.304860_S.14CKDXI-M effector>	MVKPEKPEQTAAALKELREQKRCPEVAKMAADPARTNELISFIHARIAELRRTIQEHL LALTERILPLRERSWEFVAHPQVEHFPGCHLLQPTDKGSGAKTKKLPGQRGLSMARIE QLSELRRRWQSLNQSLRRSIGEPPLTAAQMRANPIPDPCPHILRKLDDIREQRVNQTA HLILAEALGVRLIAPEKDRKEREVADVHGEYVSFRPPVDFIVLENLDRYKATQGRAKS ENSRLMQWCHRAVVDKIKELAEPFGIPVLETPAAYSSRFCSLTGIAGFRAVEVGLRDR DDYRWRKLLREADEKGEAASDEAKATRQLFMNLEQANAGRVGKQLRTLLAPQVGGPIF VTATGVPHPAPRHERKPSPALVPPMQSDLNAAINLALRGIAHPTRADIHHRVRTERID PKEAKQKQTTTSHVFRTREKRRFGEQQPQIVTAPDNSLPKERNSNLFYDPWSLALFGR ARWDSEPEGAFPYASGPGLWKRVNDSAFQWQRCEEIYRQRMEKLGFKAASDVPVNTLR AEEDDVPYRLT

336	CLUST.304860_S.1 CKDXI-M direct repeat 1>	gccgcagucgccgcgaacucagagaccgugaggcgg
337	CLUST.304860_S.1 CKDXI-M direct repeat 2>	ccgccucacggucucugaguucgcggcgacugcggc
338	CLUST.304860_S.1 CKDXI-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
339	CLUST.304860_S.1 CKDXI-M non-coding>	ctggtaaaaccagagaagccggagcaaacggcagcggccttgaaagaactgcgggagc aaaagcgctgccccgaagttgctaagatggcggctgatcctgccaggacgaacgaatt gatcagtttcatccatgctcgtatagcggaactgcaggtgaaggcggcgctgggaacg gaagtgaatcacgatgaggaccaggtgctttttgtgtcgctggggccgcaggcgtgcg acgcgagtttggtgattgaagcgatgggattgccgtatcaaacgcgctcgcgggtgac gatcatttgagggaagattttggtttgcaaaggggcggaattgggatttatatcgaag cggccattggccaccgaccagtaaacctccgccattggtttaccacgtttttgaaat agcgggtgactgcgtgtttgcgcgctgggcgagcgagcgcgacggtgctgcggctcgc ccgcaggggcgctcgtgatatataagagtctctatcggatggggttgcgtgtgagaga tggtgagatgaatgcgaagctgcggaaaaagatagccgtcgctcgccaaacggtcagc gggcgacggagtggaggggagtttggaagacagcatcc
340	CLUST.304860_S.1 VILGX-M effector >	MASEGEWNESLELAKALLAEEPENWIGAHRFEKSYPEQNDALLKLANRRLSRLQTFHR WSCFDPEKEDDPERRSSLVSKLVAELEHWEDDDVSAWATKLEGGDVAAFQIAAGEAFA TYRAELLPLLVALANRVAPLREDRWSWKLRGNESPYGDLVRIPREPRSKLPVRGQRGL SLARIEQMENLRRLFLRYNRTLDREPGKPAKFGRADEGRDSGEPCRDLLEKIDRIKEQ RVNQTAHLMLAQALGVKLAPHTLDPQTRREGDHHGEYTRIPGREPVDLVVIEDLGRYL SSQGRAPSENSRLMKWAHRAVRDKVKMLIEEPFGIPVLEVPAAYSSRFSAVTGEPGSR CEERPFLDDYLEESLLRRSHTPPGTGQSDMRPWNSKLIAQFERLAEINAQRKASGRTP LTLLLPKTGGPLFVGAKASPVVQSDMNAAINLGFRAVAAPDALHLLHRIRSERDGKEI RTVTRNAREKAAFGKKGIVIGLRSEASPKLSKSSNFFYDEKAVAMFDRGELSLEGKTM PVSSGIGLWHAVNSAILPRIVALNEERLLRMGSGFGNDPRDEIPM
341	CLUST.304860_S.1 VILGX-M direct repeat 1>	gcugcagucgccgcuguuucgaagauccugaggcgg
342	CLUST.304860_S.1 VILGX-M direct repeat 2>	ccgccucaggaucuucgaaacagcggcgacugcagc
343	CLUST.304860_S.1 VILGX-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
344	CLUST.304860_S.1 VILGX-M	cgcatggcctccgaaggggagtggaatgagtccttggaactcgccaaggctctcctcg ccgaggagcctgagaactggatcggggcgcatcgcttcgagaaatcgtatcccgagca gaatgatgctctgctcaaactggctaaccgccgtctcggaaagaccatgccagtctcc

	non-coding>	tcaggtatcggcctctggcatgcggtggattccgccattcttcccagaatcgttgctc tcaatgaggagcgcctcctgcggatgggctcaggatttggaaacgacccacgcgacga aatcccgatgtaagcccatgaggaaggaaccggatctcctgatgccggttcggcgttt gcaaaactacgcctactgcccgcgtctcttctactatcagtgggtggagggaatcttt gtcgagaatgcggatgtcaccgagggcaaggccgtacattcacgaacggacaaggcaa agaccgctctggctgacatcatcgacttaaccgaggatcagattctcttcatttgcct tggtcccgaagtcaccgatacggggttgatgctggaatccttggggcgaccctaccgg aaaagaacgatggtcaccatcgtctgatttggagttgcaaccacggatgaagcagcta tgaagagagtgcccatgttggcaatgacctcttttcttccgccctcggaaaagcaagt tctttgaaattgcgacgactgcggtctgcgagcacccagagttgtgctcatttcctgt gataacgctcgcgtacgatgctgaaagagaaaatcggggcgctccttggtcgtcataa acagattgacccgttaatcggcaccacttgaggagacgcactcgcaaccttctcggcg cctctctgaaaagttaaggaaattcgtggggtgagtcgatgaaagcaatggcctcgtc t
345	CLUST.455941_S.15YLU3-M effector>	MNEVLPIPAVGEDAADTIMRGSKMRIYPSVRQAATMDLWRRRCIQLWNLLLELEQAAY SGENRRTQIGWRSIWATVVEDSHAEAVRVAREGKKRKDGTFRKAPSGKEIPPLDPAML AKIQRQMNGAVDVDPKTGEVTPAQPRLFMWEHELQKIMARLKQAPRTHWIDDLPSHAA QSVVKDLIKALQAMLRERKKRASGIGGRDTGFPKFKKNRYAAGSVYFANTQLRFEAKR GKAGDPDAVRGEFARVKLPNGVGWMECRMPRHINAAHAYAQATLMGGRIWRQGENWYL SCQWKMPKPAPLPRAGRTAAIKIAAAIPITTVDNRGQTREYAMPPIDRERIAAHAAAG RAQSRALEARKRRAKKREAYAKKRHAKKLERGIAAKPPGRARIKLSPGFYAAAAKLAK LEAEDANAREAWLHEITTQIVRNFDVIAVPRMEVAKLMKKPEPPEEKEEQVKAPWQGK RRSLKAARVMMRRTAMALIQTTLKYKAVDLRGPQAYEEIAPLDVTAAACSGCGVLKPE WKMARAKGREIMRCQEPLPGGKTCNTVLTYTRNSARVIGRELAVRLAERQKA
346	CLUST.455941_S.15YLU3-M direct repeat 1>	ggcugcuccgggugcgcguggagcgagg
347	CLUST.455941_S.15YLU3-M direct repeat 2>	ccucgcuccacgcgcacccggagcagcc
348	CLUST.455941_S.15YLU3-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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351	CLUST.455941_S.15YLU3-M direct repeat homology 2>	gctgctcc
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388	CLUST.103834_S.7 UARU8-M non-coding>	tgggagcgcgcctttggcggcggcggtgtgcaaaagcaaaagccggcaaagaagcgcg agcggtccggtggggcgaagccagcccggggcgctcgcaaacgggtatcccgcggtag tcgtggggaaagtctggatagcgcagcggagtagtctgctgatatggtcgaaccctgg ccgagccgggggggagggcgctcgcaaagcgctttgcaggtctttgacaacttagcaat ttgtagcgcgctgcaagagggagacatgccgcggtggcgagacggagacaagtacaat caacgcgggcagttccccgccctggagaggggacccccacgcagatctgctcgaatac gtaaggcagttccccgccttgagagggagatggatggagctaggtctacgctgcgagc gcagcaagatggcagcaagcagcaagatggcagcaagacaagggaagcgtcgaaggat ctccaacggcgtctctgtctcgcgaaagcagcttcccgccaagagggagacacgggcg cagtgagcctgaaagccgcttcgagacggaggccggcgcaaaggggcgcctactgtg cgcacgcttggggaaggcgacggttgtcaaccggtggtggacggtacggtcgtgcgaa gcggctccccgctttgagagggagacacgagcagtgccagtacctcagtcagtatcag tcgaggtcgcgcgaagcagctccccgctttcgagagggagacatccaagccatgaacc gcgagcagctccccgctttttgagagggagactggggatcagccaaggcagacccaac gcaccggtcgtccgctggtcagacacctgatgtcgcaaggcagctccccgccttgagt gggagacagcgccttgttgctgaggtacgccgagccatcggagggcgtcgcaaggcag ctccccgccttgagtgggagacagcgccttgttgctgaggtacgccgaggcgtcggag ggcttcgcaaggccgttccccg
389	CLUST.103834_S.7 UARU8-M direct repeat homology 1>	gcuucgc
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471	CLUST.173825_S.1OTRSZ-M direct repeat 1>	guuaggaauaacagaggaugucaugugauuggcaag
472	CLUST.173825_S.1OTRSZ-M direct repeat 2>	cuugccaaucacaugacauccucuguuauuccuaac
473	CLUST.173825_S.1OTRSZ-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
474	CLUST.173825_S.1OTRSZ-M non-coding>	atacaaccaagcaaatacggataatttggattcaagttgtagacgaaataacatttca tcaagttttttttgagcttcggttctttggtcactcatgataagcactgaaaaacata actttagcgtcaccggagcaagtataagcctcatcacgattttatagcaaccaacata gggattatttcactaattggggctttttctagcttattgctcattatgatatgatctt aatattaaacctagtcgcgtgatggtgttgatagcaccgattcaccactaggagtagg tatagcacacccacatttcaagtctacatgaaaactatcgaatttaaaatttatccca cactcgcacagtcacagactattgataaatggctgcaagatattaaatgggtgtggaa taaaggtctatctctcaaacttgctgatagacagaagtattacagaactcaaataggc gattatcatccttcattatttctgggaacttcggttgcttgccatgactcaatttcag ccaatccaacagccaaaaataaaaagaaaatgccaaaaaaacagcgaccttcggaaag tgcctctcaaaaccatacacagcttactctctggtgacagggtcaaatctcccgcatc cactcataagacaattcattttctatctccccaaaa
475	CLUST.173825_APIZ01000218-M effector>	MKTLEFKIYPTLAQSQTIDKWLDKLKWVWNTGLSLKLAGRQKYYREKEIGDQVIPDGV VLQWKWRKVVTEDKKGKSTEKWEKVRLVGTGVIRPKNGYPYCEIRQHLNIEDPDKYGQ CEFYRSDKIPDFMADVPTKFKAGVIDSLKKSWKAYVTPKHPGRKPKFKGRNDKIKSLV NLNAGGKSKELKPEKIPGSNNGYVQFPKLGKIRVKGLFDRYDWQEWGAARIVIEPSGY YLHVCVDVPDEPLPKSDKSVGIDPGLLSVITTDQGREVEPPRLFRKQQAKLRRLQRKA SRQVKGGCNQKKTYRKIALHHEKIRRSRNAFNHKLSTKIVREYSGIVMEDIKIQNLNR KPKAKKREDGNGYEQNGAKRKAGLNKSFADSALGDLISKIETKCQDTDREFVKVAAHY TTVDCSNCGAKIKKALSQRTHRCTECGHTEGRDSNAAKNILLKGKKQLQTVYRAWAWE

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476	CLUST.173825_API Z0100021 8-M direct repeat 1>	ggugaaauuagcuuugaguaaucagguuaauugcaag
477	CLUST.173825_API Z0100021 8-M direct repeat 2>	cuugcaauuaaccugauuacucaaagcuaauuucacc
478	CLUST.173825_API Z0100021 8-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
479	CLUST.173825_API Z0100021 8-M non-coding>	ccttatatcaattttgatgttcagcgttgtattgaatatgctaaacaggtaaatccca aaatccaagtgttccaagtttctgctactactggggaagggttagatgagtggtatgg gtttttgtttagtaaggttgtggtttctgtttaattgcaatttttcttttgataaacta atcaaaacttgggctagtttacgctagtaagctgttttgcatttaatttacacaggat taagcaagggagcaatatgctcccatgacattaatttttataaaaatttgacgttttt acattattcaatttagtagcaggttagctgatcatatataatatgggtataattaaga ctacccaatctagttctgtcataattaccataaattcacaactgtaagtacgatgtgg gcgatcgcacaagcatattttatatgaaaaccctggaatttaaaatctatccgactct tgcacagtcacagacaattgataaatggctggataaactcaagtgggtatggaacacg ggcttatcactgaaattagcaggaagacagaaatattatagggagaaagaaataggt
480	CLUST.173825_S.2H87QC-M effector>	MKTLEFKLDPTLAQVQTINQWLDKLKWVWNTGLSLKLAGRQKYYREKEIGDRIIPDGV VLRWKWRKVVTEDKKGKSTEKWEKVRLVGTGVIRPKSGHPYCEIRQHLNIENPDKYGQ CEFYRSDNIPDFMADVPSKFKAGVIDSLKKSWKAYVTPKHPGKKPKFKGRNDKIKSLV NLNAGGKAKELKPEKIPGSNNGYVQFPKLGKIKVKGLFDRYDWQEWGAARIVKEPSGY YLHVCVDVPNDPLPKSDKAVGIDPGLLSVITTDQGREIEPPKLFRKQQTKLRRLQRKA SRQQKGGCNQKKTYEKIALHHEKIRRRRNAFNHKLSTKVVREYSGIVMEDIKIQNLNR KPKAKKREDGNGYEQNGAKRKAGLNKSFADSALGDLISKIETKCKDTDREFVKVAPHH TTVDCSKCGAKIKKALSQRTHRCTECGHTEGRDSNAAKNILLKGKKQLQTVYRAWAWE HGETRKPGSDSNTECHQEVKTDLSELTPSPEHGDPTTYPSSVTLQDKQAVNTVNLDSV SAKSQSHIQLTLW
481	CLUST.173825_S.2H87QC-M direct repeat 1>	gcugacgcaggaugaucgcauuauuguaguuggcaag
482	CLUST.173825_S.2H87QC-M direct repeat 2>	cuugccaacuacaauaaugcgaucauccugcgucagc
483	CLUST.173825_S.2	nnnnnnnnnnnnnnnn

	H87QC-M spacer>	
484	CLUST.173825_S.2 H87QC-M non-coding>	ctaatccttgggcttgtcttggatatagattctgaactcgggtttaaacattttaaca ttcccatacaggttttaattccgacaatctgaaatatttgcgatcgcccgtcgcatcg gtcaaaatagcctatttatatggtaaaatattagctagtcgcgtgatggtgttcgtag caccgattcaccactagcagtaggtctacaccacccacaaattaattctacatgaaaa ctcttgaatttgagcttgaccccacacttgcacaggtacaaaccattaatcaatggct agacaaactcaagtgggtctggaacacagggctatcactcaaactagcaggaagacag aaatattatagagagaaagaaataggcttatcggaattgacaccatcacctgaacatg gtgatccaactacatatccttcttctgtcactctccaagataaacaagcagtaaatac agtaaatttagactcggtttcagccaaatctcaaagtcatattcagcttaccctctgg tagcagggttagggctgacgcaggatgatcgcattattgtagttggcaagaatctggg tttttgcgcctcttgcagaccttgcgccaagctgacgcaggatgatcgcattattgta gttggcaaggtaggaaggagcgccgccatttgccccgaggga
485	CLUST.173825_LJOV01000322-M effector>	MKTLEFKIYPTLAQSQTIDKWLDKLKWVWNTGLSLKLAGRQKYYREKEIGDQVIPDGV VLQWKWRKVVTEDKKGKSTEKWEKVRLVGTGVIRPKNGYPYCEIRQHLNIEDPDKYGQ SEFFKKNNIPNFMADVPTRFKAGVVDSLKKSWKAYVTPKHPGRKPKFKRRNDKIKSLV NRNAGGKSKELKPKKIPGSNNGYVQFPELGKIRVKGLFDRYDWQEWGAARIVKEPSGY YLHVCVDVPNNPLPKSDKSVGIDPGLLSVITTDQGREVAPPKLFRKQQTKLRRLQRKA SKQKKGGCNQKKTYRKIALHHEKIRRSRNAFNHKLSTKVVREYSGIVMEDIKIQNLNR KPKAKKREDGNGYEQNGAKRKAGLNKSFADSALGDLISKIETKCKDTDREFVKVAAHY TTVDCSNCGAKIKKALSQRTHRCTECGHTEGRDSNAAKNILLKGKKQLSTVYRAWAWE HGETRKPGSDSTAECHQEGVQTPPEDEHSSQLTPARGTKRGRGDVKTSDPAKMDSKLD TVSDPNLDNKPDTRAPCTSSISPNSVENKIPKTKKKKRSAQSSSESFTQLTIWDTAGE ISFE
486	CLUST.173825_LJOV01000322-M direct repeat 1>	ggugaaauuagcuuugaguaauuagguuaauugcaag
487	CLUST.173825_LJOV01000322-M direct repeat 2>	cuugcaauuaaccuaauuacucaaagcuaauuucacc
488	CLUST.173825_LJOV01000322-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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490	CLUST.173825_S.1 QCULD-M effector>	MKTLEFKIYPTLAQSQTIDKWLDKLKWVWNTGLSLKLAGRQKYYREKEVGDSEVLLQA VRPIPDGVVLQWKWRKVVTTDKKGKSTEKWEKVRLVGTGVIRPKNGYPYCEIRQHLNI EDPDKYGQCEFYRSDKIPEFIADVPTKFKAGVVDSLKKSWKAYVTPKHPGRKPRFKGR NDKIKSLVNLNAGGKSKELKPEKIPGSNNGYVQFPKLGRIRVKGLFDRYDWHEWGSAR IVKEPSGYYLHVCVNIPNEPLPKSDKSVGIDPGLLSVITTDQGREVAPPKLFRKQQVK LRRLQRKASRQKKGGCNQKKTYQKIALHHEKIRRSRNAFNHKLSTKVVREYSGIVMED IKIQNLNRKPKAKKREDGNGYEQNGAKRKAGLNKSFADSALGDLISKIETKCKDTDRE FVKVAAHYTTVDCSNCGAKIKKALSQRTHRCTECGHTEGRDSNAAKNILLKGKKQLST VYRAWAWEHGETRKPGSDSTAECHQEGVQTPPEDEHSSQLTPARGTKRGRGDVKTSDP AKMDSKLDTVSDPNLDNKPDTRAPCTSSISPNSVENKIPKTKKKKRSAQSSSESFTQL TIWDTAGEISFE
491	CLUST.173825_S.1 QCULD-M direct repeat 1>	ggugaaauuagcuuugaguaauuagguuaauugcaag
492	CLUST.173825_S.1 QCULD-M direct repeat 2>	cuugcaauuaaccuaauuacucaaagcuaauuucacc
493	CLUST.173825_S.1 QCULD-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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495	CLUST.173825_S.1 QCULD-M direct	accuaau

	repeat homology 1>	
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497	CLUST.173825_S.1 QCULD-M direct repeat homology -containing sequence>	cacgtctcatgtacgcagcaccctacaaagattatttttgaaaaaccgttaataatac aaatcctaataagtcataatgacctacacaagttaatccagcattattacccatttct tctctttgtttctgactataaaacctaattcctgtgggagaatggggcgtaatttgac atggtgatgagttattaaaagtaatgtccactaaatagaatttaccaccaggagaaag taccccttgctacctcatttaaaacctgttctggttgaggataatgcaaaaagctgatg gtatt
498	CLUST.248729_S.2 PEV7N-M effector>	MEIVKSIGIKLDTLVDQDNELRQLFEAFRLGINWSLKEIEKRYQTFLKSYTEIPRDRQ VEGICLACSKEARLSYTDSAGKKVCMACARRCYSEYTVRKEIYGVGDRQVETDLKSIT EVPNKTHYTMMFSQAYAMWSSYNAWRSKRNKEKEMILNTLDEYERSSDRTYLEAARLV EKNAQEIISSNKNMSWKQAKAQAFKGVYSAYPQEKRKKIEQMHDKLMDIRRLSRPIHF PELDECRTVMMSSGFVNWDQGKLYLTLFHKGRKEIGYFGKEYLAQFIPKMEEDNNVYC NLTKKNGVYYLMYPLAIKVKQPIDINECDPFVFMTSPTKTAIIGYDSDGTMQSVKWFP AGLLAFSKRHFKEKRKEIGSRQDIRDARRRGLTGTARENHHEPMRNIRRRKKKIKRMG STEARMVSSFNHQLTREMIDYVMSQSENPKILIWDIGNGITQNFGRSLNYLKSLWPAV QQQEYLKHKAMQVSIPVIEIKYNKCNDLVCSSCEAKQVNENGSEKKKKSMKVITQMIK GIKNFKCQKCGYEVNMLINQGNNVCNALL
499	CLUST.248729_S.2 PEV7N-M direct repeat 1>	aguaacauucaucaaaaguaggguuguaac
500	CLUST.248729_S.2 PEV7N-M direct repeat 2>	guuacaacccuacuuuugaugaauguuacu
501	CLUST.248729_S.2 PEV7N-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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503	CLUST.248729_S.2 PEV7N-M direct repeat homology 1>	aacccua
504	CLUST.248729_S.2 PEV7N-M direct repeat homology 2>	uaggguu
505	CLUST.248729_S.2 PEV7N-M direct repeat homology -containing sequence>	cttatatataccctaaaatcaatactgtatatcgcgtaagcgaggtcgcctggtgct acatgcgcccgcgattctatgaattgcaaaaggtgacgcgtgcccgttacagcgcgct ggtgatccccgtatgtgaaaacatgcggaggatcaaccctacgataatggggtcaagg ggaggtagttcacatataatctggagagaaaatggaaatcgttaaatcaattggtatt aaattagatactttagtcgatcaggataatgaactcagacagctatttgaggcattcc ggcttggtataaactgg
506	CLUST.248729_DAJM01000001-M effector>	MAPVILAESQPYFNTGDILENVMKTVGIKLNLIIPQEQELKTLFEAFRTGINWSLNEI EKRYQVFVSRFEEIPKENRIDGVCPECNTEKNLTFLNRYTNRKYCSSCAMKTYSEYTV RKEIYGVGDRVVANDLKSVIEIPVKTHYAMLFSQAYAMWKSYNAWRIKRNRELGVVEA ELSSYPDQRYLHAAMLIEQKAADTKRSNPKMIWKTAKAHATKEVFRDFSDKEQKEIRR LHDKLMDVRRLKRPISFPHLEECRTIMMASGFVQWDNGELYLTLWGKGRKRIDFWGKE YLKQYILKMEADNNVYCNITKKNGDYYLMYPLEIKVKQPPAIEECDPFVVLSSPTRIG VFGYDEDGALNSVKWMSTGQLAFSKRHFKEKRAEITVRKSPDEKMRKIRRRRKKIRRR GNVEQRYVSTYNHQISRKVVDYIMEQSENPKILLWDVGNGITQNFGKQLNYLKNLWPV VQQQDYLRHKAMQVSIPIVEIKYNKCNDLVCSSCGAKQKNGKKPAKAITQLIKGIKNF KCESCGYEVNQLINQANNIVSMQ
507	CLUST.248729_DAJM01000001-M direct repeat 1>	aacugucuaaaaaugagguaucucaagguaucuca
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511	CLUST.24 8729_S.1 HFIGL-M effector >	MEQETKRTVQIKLRQTPDQAEEIEKLFLAFKIGLNFCLEEIEKAYQKTAGEYLRVKDG EEIKGTCPGCHKEKTLAYRSSNKMYCSSCVMRNFSEYTVRTAIISTKERKVEHDLKDA VQLENQTHFHMMFSQAYANWKSFDAWRKKREYERDNLKKELSDLEKGKETGKVIAAAK LIWKNAALICLNNEKITRRNAMALASKDVYNLFPDIVPRDISRAVSKIRRLNSLSRPV RFPRYDAVQAIQIHNNFVKFKEVKLHMSLFYKKKNQQVMDFYSNKYLDQFLSAMEEDN EVYTNLIKRIDGKKISYYLMYPLTVKMDIPTIFDLVDVFTICFSPDRVLVHCHYNEVN GNGSGNTLKWYKLGWLIDKKTHGYEKRRELQEHNTRNSLRRIKKMGNAEQRTTRTFNH QLSHNIVEYVTEKSDNALIVMWDISTGITADYGRKLNLAKKVWPVVQQQEFIKHKAFL RCVPVKLFSYKEENNLRCSFCGKTILKKDELGKTTKDPIKTITAILRGAKNLKCEKCG HELNLLLNQARNLSKLPLSEENKK
512	CLUST.24 8729_S.1 HFIGL-M direct repeat 1>	guuuaucagggacuuucgaaggaacagggacuucaac
513	CLUST.24 8729_S.1 HFIGL-M direct repeat 2>	guugaagucccuguuccuucgaaagucccugauaaac
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556	CLUST.308062_S.4 LJ3RY-M direct repeat homology 2>	agugguu
557	CLUST.308062_S.4 LJ3RY-M direct repeat homology - containing sequence >	ctgaaaatctcgcatctgattcccatgtagtcataagtaaccaggtggtttgtatcac ctatatggttcactgatctaccgggagtcaggtaggactcatgctgagatggttatgc agaccctctcgcatgtagtgttgcaaaggtatagaaccactggggatctcatactgag

558	CLUST.308062_S.1 UHPF4-P effector>	MKSIANGHHGATSVSERALQSRKGGKKDRFAEEARRPRTQPTEDISRVRVAASSTLHP RKSPLGDHKPSQQSKLDPEQLASREWLKEQLTARQVAKPVAFLYNGSWVCRNGNTKIG IIPAALVTARDASAVDGIFVIRASVGVEIVQPISSSTKQAAQYRVKSKTAKSDDERKK FLADAERAEKSAWDELGAMLRTASRVYPFMMRAVTEWCLKGCLPQNPREGEPTSDNYL VAFRADKEWHELHPDAPPQLLHSGIKSVAKKRAYDDWHGWDRSPKTRMSKGPPWNTRE GFSLPESCFTLRSEGGQMVCELRLHAKTDDGKNSPPVRVVVAARSGGSWAQLRALTDP TSGCSIDQARILWSEDERKWLMRISFSKPLPPVPTGDGPAIVVRRGVKRFMVVVRSDG ERIPREDFQGHPLPNLEDAWGAVTTLRRLEARRGKNRRKAIGPSILELKEAIDNRRRQ IKGHLPAQGRGARGHGKKRYLRALESIRRAEANFSQTWWRQWASWLARVAETIRASEV LIEDWCSVPAPWHEDEVIRTMLRRFPTAMARDAIVWALKKRGIKCRLIAAWYDLKRCP SCGADTEVDGKRVYCTKCPAAAPRDQWAAWHVFTKAGYTEIQLSHYISWASAILRAKK GKSNEQDPRNKAAE
559	CLUST.308062_S.1 UHPF4-P direct repeat 1>	gucgcaacaggcaacaggaugaagagguauuggagc
560	CLUST.308062_S.1 UHPF4-P direct repeat 2>	gcuccaauaccucuucauccuguugccuguugcgac
561	CLUST.308062_S.1 UHPF4-P spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
562	CLUST.308062_S.1 UHPF4-P non-coding>	ctcttcatcgatggcgatgaccagccagctgttcagctgagctacgaagtcgactctt cggaactcgaaatcgaggaagggcctccacagctggtagggatgcttgaatggctgcg gcaagatcaccactatgacggggatgagccgtgagagttatggcgtctccatcgacga actgtcacggtgggggactctcacaattgatttgacaatcaaccaccgaaggactaga tgaaatctatagctaatggtcaccacggggcgactagcgttagtgagcgggctctcca atctcgcaaaggcggcaagaaggatcgttttgccgaagaggcgcgtcgcccgcgtact cagccaacagaggacatatcccgtgttcgggtt
563	CLUST.377319_S.83NSIP-M effector>	MTSTHSKTAKGSDIPAEIARSHSNGKPYIFGKASVLNPKKKKNEEDSKEHINPVDPDA KESGILCHKIMMAPDAEGYDFLFSLCRASGQAFAAYARQYNVRYKRMRESEEWKQAHA LDTPQNIAAKREIRIISRKISRTRRQAKAISPEALKAAEPTIEALKKQREKIASSMES QPQKDKKKKNGRKRLTKEEKEAHKILKAQEKALAKDEKSARRLAFEHAYEHHGVGLAI VPWLRGNRNGAYSEDLDILGPRSWIRSHLSTFNAAAVFKEAEAACKNARKEDASKVFI QRTLLRPCPSGRLGIAEGTIGINPDGSMFYIKRRGENTGKRGLNSDTISIPLIKRHEG NVYEENALSYILSGGLRNISVVPVRSHGKIHFELAISYKGKSIPDADPTTQGVIGVDF GTQHTAVFGKAVGGQILKHSPNGGSHEKEILRRKRQLSRKQVSNNPHSFDSNGAYIKG TKITRSKRMILLKRKIKALEEQQARCRKQESNIAGKQISRMGKVIIMEDCLMEGWSKV AGKGVRAGTPSAVKSSLIKHAKRAGSEVVEVNTRKIRATQYDPISGNYNKIPLDQRTV VVGGVKVDRDLKSAYILSHVNNNEIDVVTARKEWQASCGQLQGRLDS
564	CLUST.377319_S.83NSIP-M direct repeat 1>	ccuguacaagagcccgcuuuugcgggaguccacagg
565	CLUST.377319_S.83NSIP-M direct	ccuguggacucccgcaaaagcgggcucuuguacagg

	repeat 2>	
566	CLUST.377319_S.83NSIP-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
567	CLUST.377319_S.83NSIP-M non-coding>	gtttttccatgaaatgttctcacgcgtaaagaaggggcagtcattctcacacggagac attatccacgatcttatcgcaaacgactacgtcgtccgtctcatcgacgcaacagagt gcgaccgcccagttcttcgcattattttcgcggacaaggataacaacgtcatgcccta cgacatgtctcccaatgaggcaatcgctcagtacgggtactcaaaggcagaaccctga ttttttcgggggagaataatcacccccactagaatgaggtcatgacaagcactcattc taagactgccaaaggttccgacattccagcagagatcgcccggtcccattccaatggt aagccatacatatttggaaaagcctctgtcctcaatcccaagaagaaaaagaacgagg aagactccaaagagcatacagttgttgtaggggtgtaaaagttgaccgagatttaaa gtcagcctacattctttctcatgtaaataataatgaaatcgatgtcgtaaccgctcgt aaagagtggcaagcaagctgtggtcagctgcaggggcggctcgattcgtaaataaatg cgcctcctgcatggagaggacaccacccatagggaacggatctactaccaaggcagaa gcgtatcccctgcaacgagttgcgtgataaaaggacagcgcttccattgtcaacgtgt cagttttcggaaagaaatttctgaactcttcgagcgctctgtcggatggatgggattg cgagatccaccagaattatcctcgctcaataaaatgagcatcgcgcagcaagaatccg cgaaagcggggctcaaatacaggagctttgtattgtttttttcggggcaaaacagact caagtacaggtaatataagtacttacatagatcacaagtccacagcacaggcatcaca tcagagacaattttatatgcgaaaaattaaagaaataaccataaaaaaggttcgcgac ccctcagcgtcacccgaacttctcctcaaagcaatggacagtaagtttgaaggcgttc gatattttgcagctagaaatgcgaatttcactccagagattctcttaagagctattga cgattctttttctcaaaagagattcag
568	CLUST.377319_S.3N2XJO-M effector>	MSDPTPSAITISQKIAAAHAKGKPFIFGKAPVLKPKKKSDAPQEEDDSTSEPTDATGI LCHKIMMAPDKEGYDFLLKLCRASGHAFAAYARQYNVRYKRMRESDEWRQAHALDTPK NIAAKREMRIIGRKISRTRRQAAAISPEALKAAKPAIEALKKQMEKIASSMENRKPKK EKKNKKGRKRLTKEEKDAHKILKAQEKALAKEENSARKLAFEHAYEHHGVGLAIVPWL RGNRNGAYSEDLDILGPRSWIRSHLSTFNAGAIFKEAEAACKTARKEHSSKVFITRPP LRPCPSGRMGIAEGTIGINPDGSLFYIKRRGENKGKKGLSSRTISIPLRTRHEGDPYE EKVLSYIMSGCMRNVSVVPVRSHGKIHFELAVSYKGEALPDSLPHAQGKVGVDFGTQS TAVFGSHMGGRTIAHSPKGRRLDSLIKALQRRFSRAQVANNPHAFDSKGAYIKGSKIN RSQRMIALKRQIKALQEQQARCRKQEANLAGKHISRMGDHFVFEDCLMDGWSKAAGKG VRAGTPSAVRDALVKHAERAGGKISQVSTKEIKATQYDPLSGDYNKIPLTQRTVVVGG VEVDRDLKSAYVLSHVNNDQIDAVAARNEWQASCGQLQGRVDP
569	CLUST.377319_S.3N2XJO-M direct repeat 1>	ccuguauaucagcccgcuuucucgggaggcuacagg
570	CLUST.377319_S.3N2XJO-M direct repeat 2>	ccuguagccucccgagaaagcgggcugauauacagg
571	CLUST.377319_S.3N2XJO-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
572	CLUST.377319_S.3N2XJO-M	ggctacctagcccgcctcatcgatgccacggagaacgggcgcccagtgctccgcatcg tctttgcggacaagcacaaccgcatcatgcccgaagagatgtctcccaacgaggcaat cgcccagtacgggtactcaaggacatccccctgatttttcgggggaaattatccct

	non-coding>	gccactagaatggcaggatatgagcgaccctacccccagcgccatcaccatcagccag aagatcgcagcagcccacgccaagggcaagccgttcatcttcggcaaggcgcctgtcc tcaagcccaagaagaagtccgatgctccccaagaggaggacgattccacttcgaccgt tgtcgtagggggcgtagaagttgaccgcgacttgaagtcagcctacgttctttctcat gtgaacaacgatcagatcgacgccgtagccgctcgcaacgagtggcaagcaagctgtg gtcagctgcaggggcgggtcgatccgtgaatgaatgcgcctgctgcatggagaggaca ccgcccatagggaacggatctactaccaaggcacaggcgcatcccctgcaacgagctg cgtgataaagggacagcgcttccattggcaacgtgtcggaatttatcgaaaactggat tcctcgaacgccctgccggatggatgaggatcgcaagatccacgagaattatcctcgc tcaataaaacgagcatcgcgcagccagaatccgcgaaagcgggcttacatacaggttt tacaggcttgctttttttcggggcaaaacaggcttaaatacaggtaaggaaagcactt acgagcgtaaccctgcaagggttgcgaagtacaagtgccttcggtccagccctttatc tgagccctcttttgcgggaggctacaggaaaataacgtccgataaaactatcgcctaa accgatagttgaaacccaaacccaatacttcgttcccgtactagagcccgctttcgtg aaatactacagtgagctttcgttcctccttctcctcgtcacgatgctgctttggcttc atccgcctcatgtcccgcccaagtggaggacgccgttcctcctcttcaaggcagcagt aggcgcggcagccatagcggcatccgtctac
573	CLUST.377319_S.3N2XJO-M direct repeat homology 1>	aaagcgggc
574	CLUST.377319_S.3N2XJO-M direct repeat homology 2>	gcccgcttt
575	CLUST.377319_S.3N2XJO-M direct repeat homology -containing sequence>	gtgataaagggacagcgcttccattggcaacgtgtcggaattcatcgaaaactggatt cctcgagcgccctgccggatggatgaggatcgcaagatccacgagaattatcctcgct caataaaacgagcatcgcgcagccagaatccgcgaaagcgggcttacatacaggtttt acaggcttgctttttttcggggcaaaacaggcttaaatacaggtaaggaaagcactta cgagcgtaa
576	CLUST.377319_S.1A4227-M effector>	MVAMTTKKTAKGSDVGSEISAAHAKGKPYICGKAPVRNPKNKPAEEGEATASAVSAPE GGMLCHKIPLAPDERDYKFLVAACKASRQVYNAFVRQYNTRYKRMRESPQWKAALLME PEEMREARRGIRIARKARGRLSRSAKSASPEDAEKIKQEIEAMDSRIASAHKILDDLR KTMPKDIGKAMGEAFLDLYKKHLNRGDIEKWMRGRRNGVYDENRDMIGPRSWIRRYIS SFNFSQICTEAEASCQTARKQHRSRVKAGLSLRPLPSGRIGMAEGTISVELDGSMSFI KRSGENKGKKGLNAEHVRIPLRLRPDGDPYEANVLSHILSGGPQRIRNMSIVPVHSHG RMHFELAISYIGKPLPDDSPSLHGTVGIDFGTQHTAVYNRTVNHGEHVRHSPHGRRLE DRIARLQRRYAHAQILNNPHAFDEKGAPIRGARIRRSRRMLKLKKKIRALHEQAARCR KQEANLAGKRISRMGDAFIMEDCSMEGWSAQAGRGIHAGTPSAVRDSLCKHAQRANKE IVEISTAKIKATQYDPVSGCYNRIPLHQRTVVVGGVEVDRDLKSAYVLSHVKNNTIDS VAARNEWQASCGQLQGRSDS
577	CLUST.377319_S.1A4227-M	ccuguguucuaucccuguuuugugggagcccacag

	direct repeat 1>	
578	CLUST.377319_S.1 A4227-M direct repeat 2>	cugugggcucccacaaaacagggauagaacacagg
579	CLUST.377319_S.1 A4227-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
580	CLUST.377319_S.1 A4227-M non-coding>	ccttgggatctcaccacggaggcgtggctggagttcgtgggcgagtacggatacgatt gcttcataacgaggatcgtgccaccgtacgtcctgaaccttccccaatacaagaccac gcgcaggctgtcgaggctggcaagggagaattagagatcgtctccaacttatcttttc ctcttgcccttgacaaccagtaaagtaggctgttatccttttgaaagaggagaaaacc gcctgctcggatgcgtcatgaagaccactatattctataatggttgccatgaccacca agaagacagccaaaggatctgatgtaggctctgaaatatccgccgcccacgccaaggg caagccttacatttgcggcaaggcccccgtgcgtaatcctaaaaataaaccagcggaa gaaggcgaagcgactacagtcgtggtgggaggcgtagaggttgacagggatcttaagt cagcctacgttctttctcatgtaaaaaacaatacaatcgactccgtagccgctcgcaa cgagtggcaggcaagctgtggtcagcttcaggggcggagcgattcgtaaacgaatgcg gtacgggcgttcgtgggttttcgcgcccgagccgtgccgcatcccctgaaacgagccg tgcgataaaaggacagcgcttccattgttaacgtatcagagcatgccaagcgtgctcc ccgagcgctctatcggatggatgggatcgcaagatccgcaagaattatccccgcgtta tcaaaacgcatcgtacggcgagaatccgcgaaacaggaataaagcacagggcatgcag ggcttctttttcggccaagaaaagtatttaagttcatgtctgtaaagaatttatgaaa gatacctccgcgaagtactccccagcggaatcccacccatgattttcgggggaaggaa aaaccccacggagtcaacgatgtcactgtccctccacccgcccacgccgcggtcccct tccctttcctacgtccgctcccagatcattgcattcctccacagcaggaacggagacg ccccagcgaaggaagatgattgccactttttcgggggtaagataaccacaagtactt gtaaataaagaacttgtgtcttcatccctccgccacggctccacgccacgcccacaca gtaatatcgggcaaaccgatattcataaggcaaacccaatagtcacactcccacaatg ccccatatgcagtacatcatctcagccatagcattcatcgcctgtgcagcagtcctct acgtgtccctggctccactcatgaacatggagaatccaggtgacagcgcggacgagca gtgaacagcctcttccatgccagtgcattgc
581	CLUST.377319_S.1 A4227-M direct repeat homology 1>	ucccaca
582	CLUST.377319_S.1 A4227-M direct repeat homology 2>	uguggga
583	CLUST.377319_S.1 A4227-M direct repeat	gatgattgccactttttttcgggggtaagataaccacaagtacttgtaaataaagaact tgtgtcttcatccctccgccacggctccacgccacgcccacacagtaatatcgggcaa accgatattcataaggcaaacccaatagtcacactcccacaatgccccatatgcagta catcatctcagccatagcattcatcgcctgtgcagcagtcctctacgtgtccctggct

	homology-containing sequence>	ccactcatgaacatggaggatccaggtgacagcgcggacgagcagtgaacagcctcttccatgccagtgcattgc
584	CLUST.377319_S.6 MJ2B1-M effector>	MYKLEYANPEHPIVSKIAAAHKKGKAFIFGSAEVRNPRKKKGANAELPEPKDSEADVESAMPERMESGVGVLCHKMLLCPDRHGFNFFRSLCHASGHVFATFVREYNIRYKRMRESPEWKTAHAMSSDEDKERSRKIRMKEREKSRISRRARADSKEAVDAADLVIKQIDNDIKALRKEMGMVDVPERDENGKRLTKKQRQEWKANHKKMDKPQGDAFKAAYRKHGVGIDIVSWIQGGAGAGYDEAHDILGSNSWIRNHLSSKNLYAICKTAYTACTNARKEDGSRVFCRRPGLRPCPTGVMGVASGTIGLSPDGSMFFVKRRGEGDGKKGMSSRKMIVPIRRRHADNAYESRALSHILSGGMRNISVVPVFSGGMLHFELAISYIGKPIPDSIKPSAGVIGVDFGASSTAVFGPSAGGHILEHSPNGLIHSSEIKRLQRSYSRKSIANSPESFDENGAWIRGTKTKRSRRMKLLKRRIKMLEECGARCREQEANLLGKRISRMGDIVKVEDCSMEEWSKAAGKGVKKGTPATVKKSLIKHARRAGSQVFEVNTIKIKATQYDPVSGAYNKLSLKQRRVVVGGVEVDRDLKSAYVLSHVNNDQIDTVAARNEWQASCGQLQGRVDP
585	CLUST.377319_S.6 MJ2B1-M direct repeat 1>	acuguaacucaucccgcauuuucggguggcuacagg
586	CLUST.377319_S.6 MJ2B1-M direct repeat 2>	ccuguagccacccgaaaaugcgggaugaguuacagu
587	CLUST.377319_S.6 MJ2B1-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
588	CLUST.377319_S.6 MJ2B1-M non-coding>	aagattgtcagtcatgaggtcattggcgccgctgtgacataccagtacaccgaaaagagcgatatcgacaccacggtgttcatcaacatcggcatggatgaccaccgcttcaaggtcatcaacgcctggatcggtgataatgttgatgggaagatgctccatgaacagcaccctttcagttcaagataaagccggcttcatccatgggtcatcacgaccacgccgattccatctacgatccgaccactgttgagttcaggaagatgcctgacctagcgcgcgcgcgcaaggacttcgagagtctcatcgggtctggaagttcgaaggagcgaattgcctaccaacgcatggaggggaagatcagggacatgacaaggtcttgggcggatgcgggcaggcaggccatccagtcgggcagaccagacgaatattccaaatggctcacacctccagcccaggaaatcctgaatgagttggagaggatcaaggaaatgaggagtgagtcttacggccagccaaccaaaccgacaaggatcagtcaaaactggggaacgggcaatattatcttcaagttccttgagcgcgatgactacatcggcctgttcaagatgatcaaggaatcgcttgccgatggcattgtccatccggacgaactgaaggcgtctgtggagatggcggaagggatcatgaatcaggacattggctacaatccgcacggcgggcggtagtcgccgaactctgaaatcctgcaactgcagcagcgtatgattgcaccgacccaccgtctccctgttgtgatggcggacttatccatttggaaacttccttgcggttggagcagacacttgtacaggcttgaatatgccaatccagaacatcctattgtttctaagatcgcagctgcccacaagaaggggaaggcatttatcttcggatcggctgaagtccgcaatccgaggaagaagaagggtgcaaatgcggaactcccgagccccgagtcgttgtgggaggggtcgaggttgacagggacttgaagtcagcctacgttctttcgcatgtgaataatgatcagatcgacaccgtagccgctcgcaatgagtggcaagcaagctgtggtcagctgcaggggcgggtcgatccgtgattgaatgcaccccctcaggggcgcatcccctgcaatgagctgcgtgtaaccaggacagcgtttccattgtcaacgtgtcggataagtggagaaatccatcgagtccccgagcgccctgacggatggaag

		agagccttcgggttctcaagaattatccaaggtgggtcatcatcaatgatggctccgc gcagcgagaacccgcgaatgcgggataagttacagaacaccggcttgc
589	CLUST.377319_S.6MJ2B1-M direct repeat homology 1>	augcggga
590	CLUST.377319_S.6MJ2B1-M direct repeat homology 2>	ucccgcau
591	CLUST.377319_S.6MJ2B1-M direct repeat homology -containing sequence>	acagcgtttccattgtcaacgtgtcggataagtggagaaatccatcgagtcctcgagc gccctgacggatggaagagagccttcgggttctcaagaattatccaaggtgggtcatc atcaatgatggctccgcgcagcgagaacccgcgaatgcgggataagttacagaacacc ggcttgc
592	CLUST.420457_S.7SM14I-M effector>	MAAIYRSYEVLVEETAGNHKSRQNGKTRKELRANCDNTRRALKVTHELFQDAVCYYIF CLAGLVKDARDQNGEPINRMWEYLHSESMLSTTNRIAAHLGKKYFKQPDLGANPTEKL LESIYASTPTKRLAHDTAALNGLYRKLAGEAVQIKKQGKGKNAKTKAALTDMAQFASN WYQRLSNPASTQGGEEVISQNNAYWLKVAAELTPVAEQELRSDFDDAAYAKRLELKYC FNSPVTELSSEDALKDYGLAFGVTEPGKPNSFWNKPLKTAVAALTRYASPRDPSVPKV TFEDAVAKLRECAQDRQLSSTFAYPAVASGSKPSGTYWLCLRYKFSPSPQTRRHLYEN IQKRKPTDPTNPLAAIRAEFGLVFPFFTNLLGLSPKSGEGAVWTGFDKSAFKRAAEEV FKYRLRSDERAEQVRKRRAKIAALNERGEWIDEKGKTKQLGGIEGDEERPRLMRQLLD RLGGAIGYGMRRATIGGWADLRQDFLKIAKKGEPIDEDELLAAIEKAREESSGGFGSG AFFKALCDEDYHLLWLTKWDNPQAHHPKNFVRWWVLYSEANEELTKVWDDQKNAPKPI AFTWPSSENRRGDTSFRPLDFEIPVAPAPSIDLFDREDDGKPIKLVRTNAEPPKKKAK EDSAEPPPFMDGDGNALYPLTLSYRRFKRDRIAKADGSSVEAVYAPPLVALNPPSFQE TGNKKPLLASASLLPGDKHGCWHFMFSFALEREMQQALVDESARIPGEKDGSVRKIKK NGKWIGLYLRWPVDAKTEKKKDAAAPVETEEVEATDAKFSPTKLWCSSKFEPFDILSV DLGVRYAGAWCRAHIKVGHDPDRPNQRTISPAGSAPEIVFDAYDFGTFRLQGEDAKIW RKDKHKGFGNEPEQEKCGSLGRIASDPERTEFAKLAAQVFPVTTRLPVPNDPAELKFF PDLGDHLVFRLRRRLGRIRFLFKLRWQISGKVKKLVHDYNVLDGAELKEFRGEQRFNV LKSLAYVPKEDMPEDEEGEDDFMRGLRLTLAPDDVWLTLSYEHAGKPYPLFSKVKAGH TPSEKENAKTQKAAQKAAWAALKRELESDCNAKWNWSALAKQTETELQDAMRLFSGEQ SVIAEVARFVWPLQDKKWKWISCTINKDGKIEQSYVERDELSNEPKRPIHGMRGLSMK RIRSMQDFRQCCQSLAKLERRFYTEEQHGLEPSPVRSGDRIHEPARPFRDKINELRDQ RVNQTAHMILAEALGLELMKPTEVTIDGKSKWELKSERDLHGRYEKKKSRAAAIVLED LSRYRTSQDRSRYENSQLMEWSHRAVIGKLQDMAQVFGVQIITVDARFSSRFCSRTGV PGIRCAQISKEFENEYPWKKWKEETIGKPDKDGKRKPTERADMILLAAKALNLADNPK ATLVLPMDGGPAFLPVITRNSNKDGIQENADIGAAVNIGLRAVAHPDRLDVFPVLRTE AKADGRLEIKNRRGSLSEAVAKAEERTVQLVEPPEKKSKAEDQGATGAEDDSGGDEEL ESGKFPYLYAAVSVGKTLSVPIADGKRYQLPLTADGRKIATGDGDWAGAAQGKDFWTL VKQDCWTRIKQINARRLEALGIAPPDEEDNIPY

593	CLUST.420457_S.7 SM14I-M direct repeat 1>	guuucagucgccgcgauuucagagagcuugaggcgg
594	CLUST.420457_S.7 SM14I-M direct repeat 2>	ccgccucaagcucucugaaaucgcggcgacugaaac
595	CLUST.420457_S.7 SM14I-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
596	CLUST.420457_S.7 SM14I-M non-coding>	tggtcggtcagttcggagcgtaaaatttccgctggcgtcctcgcaatggcggcgagtc ttttattgtttgcgctggggacactcctggcattggcgaaacagaaatggaatcatca ttcaaacgttccgccaacggcattggaacaatgaggttccgcccattctgaaactgca agagatcaacgagtaatccacttgtctccgccctccatttttgctatcacgctgcggg actagacggaactgagggctgccgccatctgagcaatctctgtgcggcgggtggaatc gtttgccgaacgcgggcgggaattttgaaacggaggaacaaccatgaatcgcatttac cagggtcgcgtcacgaaagtcgaaatcctgaacgggaaggacgaatcaggtaaaccgc aatgggtgttgcttgggttcacgcgcgagaagctcgatgaactcaagaagcaacgtga acaactgcgcgagtgtgcacgcaaagaactcgccgagatcaatcgccaactgaatgaa ccgtggcagacggcgctctggaaacaccacgagcttttcaggacgcggtgaattatt acacgcttgcgccaacggcagttcacgggtacggcaaaaaggagggaaattgacatgg cagctatctatcgcagctacgaagtgctcgttgaggaaacggctggcaatcacaaatc gcgtcagaacggcaagacgcgcaaagaactcagagccaactgcgacaacacgcggcgt gcgctcaaggtaacacatgagctttttcaagacggagattgggcgggagcagcacaag gcaaagacttctggacactggttaagcaagattgctggacgcggatcaaacaaatcaa tgcgagacgccttgaagcgttaggaatcgcgcctccagacgaagaagacaacattccc tactgagatcctatgagcgacgcgccggtacagacacaggccgggcttgaagcgcagc cgccgctgccggtgcgacggctgcataactacatctactgtccgcgtctgttttattt tcagtgggtcgagaacatttttcaggagaatgcggatacggtggcgcaactcaaagcc gcgctcgcggtcgaaatcaacgcggatgaagaccaagtgcttttcgtttcgcttggac ctgaatcgaatgacgccagcctcatcattgacgccatggggcgcgcttatacggttcg cacacgagtcacgataatttagggtagcgcaagcatcctgcttgcgagattccgccaa aaacctcattgacagagcagcagccgagtggtttcatgctcgcggccaaggccaccga ccatcaaccttccgccattgggttgacaggtttttttgaaatcgcgagcgacttcaatt ggattgaaacgcggctgacgagcgcctcagcgccggagcgtcgccgcaccggtgctcg ctttatgtaagtggctctgaaccaagctcctgagcgcggcgactgccgcctctctgaa aacggtggctgaaatttctcgtcccgctcgattttcaccaactcactcgccttgaaaa caggcgttttgcaggggggtcg
597	CLUST.420457_S.7 SM14I-M direct repeat homology 1>	ucucugaa
598	CLUST.420457_S.7 SM14I-M direct repeat	uucagaga

	homology 2>	
599	CLUST.420457_S.7SM14I-M direct repeat homology-containing sequence>	attgggttgacaggtttttgaaatcgcgagcgacttcaattggattgaaacgcggctgacgagcgcctcagcgccggagcgtcgccgcaccggtgctcgctttatgtaagtggctctgaaccaagctcctgagcgcggcgactgccgcctctctgaaaacggtggctgaaatttctcgtcccgctcgattttcaccaactcactcgccttgaaaacaggcgttttgcagggggtcg
600	CLUST.420457_PLTX01000084-M effector>	MASIYRSYEVLVEETAGNHKTRGAGKTRKDFKAHHENTCRALRVTHELFQDAVCYYILCLVGLVKNERDKDGEPINRMWQYLQIDPKTNVVIARLASRYPDAPFHEAGNIQGLLSQTYEWLADESEKTTPASLLTTYRILFQQAAKADSDEDASAALENLKTFAGNWIAILCNENGDTTIPGQGVFDKLHRELSGVAGKEPGRMWKTIEALAQESLCDKSKADAGWQLRETAKANAKNAKAKKPKTGEELARLSRENLDEKLQSDRAALKALFVKAFSASKIKKYCSLKPEEIQAAITEIESATFDDKRFLRLRFGARDNNMEQPLFRYLWLREDAKCGGAVTNDLLEYVAKETPETELRDDDGKGISKMPYQKTGKEPLFPYFTNCLGIKHTDRAAWFEFDKSAFKRAAEEVFKYKLRTDERAELNTERKHKLDTLQAEIKDDPRAPLMEHLLAGLGGAIGYGMRRATIGGWADLRKDFLRIAKKGEPIDEDELLAAIEKAREESSGGFGSGALFKALCDEKYQPLWLPEWENKQPHHPKNFVRWWVLYSEAKEELKKVWDEDTTQPKPIAFTWPGTENRHSETSFRPLDFDIDITPTPPIYLFDQGSEGKPIILIQTNAKPPKKRQSAEVQPADVPAFTDGDGNALYPLTLSYRRFKRDRIANADGSSVEAEFATPLIVGEFPKFPRKEKDKGKPLDSSASLLPADKRGCWHFMFSFKLERGMQKKLVDETVQIPGEKSVRKNRKWVGLYLRWPIDATTEKPPKKKHVQAVPDASDVTKEPDANFSVKKIWCSVDFKPFDILSVDLGVRYAGAWCRGRVKVGRDADRPGQRTISPAGHAHEIVFDAYDFGTFRLQGEDAKIWRKDKHKGFGSEPELEKCGSRGRITSETERQEFAKLAGQLFAPTAWLPIPSEPDELKFFPDLGGHLAYRLRRRLGRVRFLFKLHWQINGKIKKVGHDYIALDGDDLKTFRCEQRSNVLASLAYIPKEDMPEDSDEGEDDFMRELRLTLAPDDVWAALTYEHDGKTYPLFSKIKGGRTKEEKEKSKGQKAVQKAAGAALKKELASDGVGKWNWQALAKAADTELVHTMRAFAGENSLIAEVARFVWPLQNKKWKWNNCTIAKDGKLVQSLLERDDESSEPKRFIHGMRGLNMKRIRLMQDFRQCCQSLAKLERRFTEENHGLEPSPVRPGDRVHEPAPAFLDKINELRDQRVNQTAHMILAEALGLELMNPTEVMIDGKSKWVLKSERDLHGRYKQKKARVAAIVLEDLSRYRTSQDRSRYENSQLMEWSHRAIIGKLQDMAQVFGIQIITVDARFSSRFCSRTGVPGIRCAQVAKGFDNDYPWKKWKEETFGKADKDGKRQLTERANMIVLAAKALNLSDNLKATLILPMDGGPAFLPVISHSPTKEGLQENADIGAAVNIGLRPVAHPDRLDVFPVLRTEAKADGKLEIKNRRGSLSEAASKAEDRTVQTIEPPAEKKAASAEDDIGGDEELESGKFPYLYAAVRVGNNLSVPIADQHRYQLPLAADGRKLVAGDTVGVGAAQSKDFWPRVKRDCWERIKRINATRLRNLGIEPPKEWNI
601	CLUST.420457_PLTX01000084-M direct repeat 1>	gccgcagucgccgcgauuccagcgagcuugaggcgg
602	CLUST.420457_PLTX01000084-M direct repeat 2>	ccgccucaagcucgcuggaaucgcggcgacugcggc

603	CLUST.420457_PLTX01000084-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
604	CLUST.420457_PLTX01000084-M non-coding>	atttttgaagactcaacatttcgccacttatgtggagccccacataagtggcggagcg agcactgtccaggtggaggctgtcgtttgcactaccttgacagcgcacagcgagccgt acaatggaggcgggattcacgcaagtctactggaacccagcgcgaatgcgctccacat tgggattgggaaaagcgatgtgccccgacatccgctgtcgggggacatcgggtcggta tcgcatcgtcaacggcaagccaatgtcttcgggttttgcagcggagcatcgccattgt gtcaaagcgaaaaacacgaagtcttggctgcccgcgcgggtggttgcggtcgtgacgg tcaaccgatgcgggacgcgaatgccaggtggaaacgggcggtcaggttttcggcagcg atgtgaccgcgcgtgatgtccaagcggtgacatcgccagcaaatcgaacagctacagc caagcagagtctcggagctttgcgggcggcggcgttgggcggcgggggcaagccgcag cagcaaagtccgagtcttggattggcccttcctgatgggaaaccgatccggcgttatc accgtccgtgtgttttgtgtaaactttggctgtgtacaagttttgaaacgcgggaatt tgtggattacgctcgttgcgttacgctgacagcgtaacgcctgcttcggagagttagc ttgtacttggccacgctgtggcaagtggtcagtccgctttgaattacctcgcgaactc tgtgctggtagcactgagtgaatcaagttaatacttacagactcaaccacagagcgag gttatgaatcgcatctaccaaggccgcgtcatcaaggtcgaaccgctcaatgacggcc aaccggagccgctgccgaaacgggagtggcagaaagcctcctggcaacgccacaaatt cttccggaacgccgtcaactatcacccccttgcctccgccgcatattgagatttcgaa agggaagtaacccatatggcttcgatctaccgcagctacgaagttctcgttgaaaaga ccgcaggcaaccacaagacgcgcggtgccggtaagacgagaaaagatttcaaagcgca tcacgagaatacttgccgggcattgagggtgacgcacgagttgtttcaagttgccggt gacacagtcggcgtaggagcagcacaaagcaaagacttctggccacgggttaagcgtg attgctgggaacgcatcaagcgaatcaacgcgacgcgcctccgcaatttaggcattga gccaccgaaggagtggaacatctagggaaccgttatgagcgacgcgccagtacaaacc caagctggacttgaagcacaaccgccgatgccggtgcggcggttgcacaacttcacct actgtccgcgactgttttatttccagtgggtcgagaatatctttcaggaaaatgctga cacggttgcccaacttaaagccgcgctcgcgcccgagatgaactacgaccaggatcaa gtgctgttcgtgtcccttggcttggagagtgccgacgcgacgttgatcattgaagcga tgggtcagccatacacggttcgctcgcgcgtcacgatcatctgattgactgcgggttc gaaatgtgtttccatgctggtggctaaggccaccgaccacttgttctccgccattgag caagcatgttctctgaaatcgcgagtgactgaggtttaacgacacgaggcgcgcgagc gcggcaatgctcgaccagagcttcggcggcgctcgctgtatgcaaacggctgaaccgc tggaagatgcgcgagacagctctcatggttataataagtgaaggacaatataaggctg gcactcgattccaatgcaggaatccactggccggcctatcgaacggtggggcca
605	CLUST.420457_S.0YQP83-M effector>	MNTVYRTYEILIEETLSTSDPKRQKSSKPSRENLKTRRAFETTHRVFQDAVCYYMLCL IGLVRNATETGSDGTVTDINPLWRTLTTGEQGKKTNELVCQLRVRYPNAAWSSSSNLT EFRTRVYDWKKNNLELENASLEQTYRILFSQAVGSKSGDDFAEALENLKSFAGTWIAI LCNENGNTTIPGGGVYDVVHRRLKSCLNNDSHILKNVVTDAVVKALEERTASVEQWHT SRLERSNRENETAKGKKSPEKIRALIDKAVAGKIQKEAITLRDAYLKSLSPEKTTKYC SLSPEQIQRAIALLGTKQVSVDSFPRLRFEARDNSFEQPLLRYLLLRSEESCSEAVTR DVWDYVRKEDPEHAILDEVKHPLTCMPYQSVGNEPLFPYFTNCLGVSCKDRSVWWDFD KSAFKRAAEEVFKYRIRSDKRLADYRSKANRVLAMQGKGEWADLRGATKQLGGLLEDP RGPLMEQLLAEIGGSIGYGLRRGTIGGWGDLREDFLKAAKIGDPDGESLEVLVTTAQS DSGGGFGSAALFKKLCEPEYFSLWQENWSPWQPWHPKNFLSWYVRYAEAVEELKALAE DDIGSASSVKTSLRLKPISVTLPGTKNKHGEVSFRPFDFYCPIEQHPNIDLFDRDETK QYRLVRTNTTSVKEKIKDSGPEGADYPLTLSYRRLKRDRITLADGSSMEAFYQPPLVV EGAPDFHQEAKAKAMKGNKPYLAVSVEVSSTLLPPTRESGPFHLTMAMLVDIDGLSAA TPKIDDKKHPDPAKRTENSVRFGPPLNGKYTHQYLRWPIDAVTEKKTTDASEAHTTDE AEGEKPTKFSAGKLWCVKNFDSFHILSVDLGVRFAGAWCRAKVFKGEPQAGQRIISAE TDQAKTGKVVFGVEDVGTFRLQGEDVKLWRKRKGQAHHTFEQEPCGSRGRKATEAEIA TFVHLAKQLVPATSRSPLLDAAETKYYPQLASHLQFRLARRLGQLRMLFNLRWRAVGR WKKDGHVYRELSGTELEAFQLEQRLRTIDMLDFSQREDIPDDQEEEHMEKLRLSVVDR SEWEKLTFALKGKTARTFGKQRTKAGKEAQAIARNAFRRKLTDTSSPWDWNALEREAT

		RQIEEAMTSFSGTGGLISRVAHFVWPLIKKRWNWQPCGKEKGGKQSVLECVADETAED QNITGMRGLNMRRVELLQEFRRCCQSLAKLERRRYQDSNGGLEPSPVRERDEVHEPAP AWIDKVNELREQRVNQTAHLILAEALGVDLMNPDEVEIDGLKKAVLKTERDVHGRYKK NPNRPRVAAIVLEDLSRYRTSQDRSRFENRQLMEWSHRQVLTKLQDMSQVFGIPIFTV DARFSSRFSSRTGVPGIRCVEVSKGFEAEHPWKKWAKETVIKPNGGGERMPSERAKLI ETAATQLTTADSRASLILPLDGGPSFLPVQSHHEGHEGLEANADINAAVSIGLRAVAH PDRLDVFPLLKAIPKTNGGMEIVAKRGSFAAKSRVLTPAALPVVAAMQEGATEMPSTD DDEAESGKIKYVFACPKIHVEPAFNIPNEKRYELLGTASGAVSKIYWSRVKETCLSRI TNINAARLAKWRDCKDEIPM
606	CLUST.420457_S.0 YQP83-M direct repeat 1>	guuccccccgugcgauuucaggaagcgugaggcgg
607	CLUST.420457_S.0 YQP83-M direct repeat 2>	ccgccucacgcuuccugaaaucgcacgggggggaac
608	CLUST.420457_S.0 YQP83-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
609	CLUST.420457_S.0 YQP83-M non-coding>	ctcgtcgtcttcaccaatctcgaaagcctcaattccgtttttatccgtcaggagctac cccagtcggagcgactgcgtcagttgaacaaaattgccatctcccagatgcacacgct cctcgccgccaacaacgtcaagcgcctcaagtaagggcagccccaagggacctttccc cagcgtcggcgagcacagtgagcccgcccaaaaaaacccaccaccccaccacgcgcag aaaaaccactgacacgacccgaatttcccccattattctgcccaccccagcctgtcct ccgaagccttggcgaaggaggaaccccaaaaccccagcccttatttcccccctctca tgaaccgcatctaccaaggccgtatctcgtctgtcgaaattcccaagctcggagccaa gaatgaatgggagcagcttcctaacggacaggacgctttttgggagcaccacaggttg tttcaggatgctgcaaattactaacttaatggacggaatttatgaatactgtatatcg aacttatgaaatactgatcgaggaaacgctatcgaccagtgaccctaagcggcagaag tcctccaagccatcgagggaaaacctgaagactcggcgcgcgttcgagacaacacacc gcgtgtttcaggatgcgaagcgctatgaattgcttggcactgcatctggtgccgtttc caagatttactggagtcgagttaaggagacgtgcttgagccgaattaccaatatcaac gcagcccgtttggccaaatggcgcgactgcaaggacgagattccaatgtaaccgatcc cctttatgtccgactccggtcttcacacttcgggcgaactcgcggctcagccgccgat gccggtgcggcggctccataactatctctattgtccgcggctcttctatctccagtgg gtggaaaatatattcgaggaaaatgccgatacggccacccaagccagggccgcgctcg cggagatcatcaacaccgaccacgatcaggtgcttttcgtttcgctcggcccggcagc gggcgatgcgacgctcatcatcgaggctctcgggttaccctatgcggtgagatcgcgc gtgacgattatttgaaggattgacctgggacctttgcggtttggctgttttcggcca ccggccaccgaccagtttacctccgccattggtaaaccacgctatttgaaatcgcgac ggatgcggcgagcaccgcaagtgcgggagtgctccccgaggagcgctcgcaaatctaa tttgagagggagaattaattacgacgtcagctagctgggctggtcgccgtctatttgt tgcgggcactcgatattcacaaagtccttcgaggaggaataggtggttattcacagga gcgctat
610	CLUST.420457_S.0 YQP83-M direct repeat	gaaaucg

	homology 1>	
611	CLUST.420457_S.0 YQP83-M direct repeat homology 2>	cgauuuc
612	CLUST.420457_S.0 YQP83-M direct repeat homology - containing sequence >	ctcatcatcgaggctctcgggttaccctatgcggtgagatcgcgcgtgacgattatttgaaggattgacctgggacctttgcggtttggctgttttcggccaccggccaccgaccagtttacctccgccattggtaaaccacgctatttgaaatcgcgacggatgcggcgagcaccgcaagtgcgggagtgctccccgaggagcgctcgcaaatctaatttgagagggagaattaattacgacgtcagctagctgggctggtcgccgtctatttgttgcgggcactcgatattcacaaagtccttc
613	CLUST.420457_S.5 8ZRNE-M effector >	MSTVYRTYEVLIEETLSASDPKRQKSAKPPRENAATRRALEMTHRIFQDAVCYYILCLIGLVRDAKESAPDGSEIEVNPLWHTLTTGAQGGRTDELVRALAKRYPDAPWHDSQGFSSFHSAVYDWKRLGLNTGPAQLALTYKLLFSQAVGENIDDNAAAALENLKSFAGTWIAILCNEDGDTTVPGGGVYDTVHRHLKSCPNADAQRLEQVIGKSIEQSLRQRLIDLREWKTARVHRLTQDNLQSKRKKNSEQIQASAEALVEGKSKKECLTLREAYLKALSPDKTRKYCSLSADQIQAALRLAHAMPLTIESFPRLRFGTRDNSFEQPLFRYLLLKNVDDCSEAVVRDLWNYIRNEKPEAALQDEEGRPLQILPYQATGKEPLFPYFTNCLGISVVDRSVWFDFDKSAFKRAAEEVFKYRIRSDKRRTDYAAKAARVRALEGTGDWQDSKGLPKQLGGMRDDPRWKKMEQLLAEIGGGIGYGLRRSTIGGWGDLREEFLKSAEAGEPDGVELEILVVAAQASSSGGFGSAAFFKKLGEPEYFVLWQEDWAPKQPWHAKNFVAWYVRYAEAKDELKILSEEGADTPENSEATTGTAAAPRLKPISITLPGTTNRYGDESFRPLDFECKIEPHPHLDLFDRDEAGQYRLVRTNTFLAKDKFKDGGPEGAEYPLTLSYRRFKRDRIVSGDGLSMEAFYQPPLVIEGAPDFHQETREKALKSKKAYAPAALTVSASLLPPTRESGPYHLTMAMPVDVDGLTAATRKIDDKKHLDPAKRSENSIRFGPPLNGEFTRMYFRWPVDAEAEKRRPPGASAEGLEESSKPAKISPAKIWCAKDFDPFHILSVDLGVRYAGAWCRAKVFKGEAAPRQRVISAEADEARTGKIVFGVEQVGTFRLQGEDAKHWRKRKGQERHSFEQEPFGSQGRKATEDEVKAFVELAKDIVPESPCNPLPPADETQYFHQLAGHLQFRLARRLGQLRLLFNLRWRATGRVKKDGHIYRELNGEELDAFRLDQRLRVIEMLDFKPRTDVADDREESHMEKLRLILADAAAWDGLVFVFKEQPVRLFAKQRTKSGNAAQEAARNTLKSQFVQSASTWHWEALTEEVTRQIDATMATLTGDSGLVARAAHFVWPLIEKRWVWRPCERSDSGSQSLLVCVADSAAVAQNITGMRGLNMRRIELFQEFRRCCQSLAKLERRYYREAHKGLEPSPVRADDVIHEPAPAWIEKVNELRTQRVNQTANLILAEALGLDLMNPDEVSIDGLKKAALKNERDVHGRYVKNPDKPRVAAIVLEDLSRYRTSQDRSRFENRQLMEWSHRQVLTKLIDMAWKVFGIPVFTVDARFSSRFSSRTGAPGIRCAEVAQGFEHEHPWKKWAEETVLDPKSKDGTRAPSERANLIRETAARLAVAPRKISLLLPLDGGSSFLPVVPHLPDHEGLEPNADINAAANIGLRAVAHPDRFDIFPLLRGKAKPDDALEILAKRGQYAIEVQTLMPVQPAGDRRAASHDPNGSDVEEEDVESGRIKYLFACPNVGNAPALRIDAQNRYELTPGTSAAVSKIYWSRVKQVCLARIEAINAARLAKWRDGQGEKDVRY
614	CLUST.420457_S.5 8ZRNE-M direct repeat 1>	guuccccccgucgcgauuucaggaagcgugaggcgg
615	CLUST.420457_S.5	ccgccucacgcuuccugaaaucgcgacgggggaac

	8ZRNE-M direct repeat 2>	
616	CLUST.420457_S.58ZRNE-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
617	CLUST.420457_S.58ZRNE-M non-coding>	atcgaccggactctgctcctgcacgattccgccctgcgcgatctgtatcaaaaactgc ggccgttgcttgcgccccgccggaaccgccgcgccgggaactcggtttccacaccgg cctgaagaaaccccaggggccactccgcccatgaaccgcatctaccaaggccgcgtga cggccgacacggacagcatcgaaactaaagcataacctgccatgagcaccgtctatcg aacctatgaagtcctaattgaggaaacgctttctgccagcgatcccaagcgccagaag tcggccaagcctccacgagaaaatgcggcgacacgccgggcactggaaatgactcatc ggatttttcaggatgcgtatgagctgacacccggcacaagtgccgctgtttcgaaaat ctattggtcttgcgtaaaacaggtatgtcttgcccggattgaggccatcaacgccgcc cgcctcgccaagtggcgtgatggccaggggggaaaaggacgtccggtattagccgtcgt gtccaccaccggtccccagtgttcgcatgttcccgccggccggccgcggcgtccgggg ccgcatttaccgtttgcgcccggccgcccggccgggttggctgtggcccatgagttat cgcgaggccctctcccgctggcgggcgctcccgccggagcggcgccgggctttgcgct gggcggccatcccccgccaggtcgcggccagcatggccttcgagggcgagccggttga cccccaatggctggagaaactacacgcccgcgcgacgccacccgctggatcgaaacca gccgcgggaccctcagctacacgcagctagccccgctgctcgccgagcgggtgctgcg cgtgcagcagcggcttgaggccgagacttacgcggacctgcaagccaaggccgcgctc gcggaaatcatcaaccgcgaccacgatcagatcctgttcgtgtcgctcggccccgagg ccgccgatgcgaccttgattatcgaggcgctggggctgccctacacggtgcgctcgcg ggtgaccatcgtttgaaggattgacccggtccggcggatggcttggctttgctccggc caaggccaccgaccagtttacctccgccattggtaaaccacgctatttgaaatcgcga gggattcggaccgggcgagcaccccgagtgcgagagggctgccctgtggagcgctcgc aaactatatttcagacgggaaacctggagacgtgcgcgcaactcgggcgcagcacaag ctgcagatctcgggtgctcgttcctcacaatcgcgcccgtgcggagaatgccggttat ccacagggtct
618	CLUST.420457_S.58ZRNE-M direct repeat homology 1>	gaaaucgcg
619	CLUST.420457_S.58ZRNE-M direct repeat homology 2>	cgcgauuuc
620	CLUST.420457_S.58ZRNE-M direct repeat homology - containing	ttgattatcgaggcgctggggctgccctacacggtgcgctcgcgggtgaccatcgttt gaaggattgacccggtccggcggatggcttggctttgctccggccaaggccaccgacc agtttacctccgccattggtaaaccacgctatttgaaatcgcgagggattcggaccgg gcgagcaccccgagtgcgagagggctgccctgtggagcgctcgcaaactatatttcag acgggaaacctggagacgtgcgcgcaactcgggcgcagcacaagctgcagatctcggg tgctcgttcctcacaatcg

621	CLUST.420457_S.513CCY-M effector>	MPNELYRTYEVLVEESVHPDHPKRAKDKTNKPSRFNAEIDGALRDTHMIFQDAVCYNT LCFAGLAGMERHKSGERAGGLLNPLWQHLTTPASKGGIKEETEKVIRRLATHYKPLAD ITIADEFLNRVYSEPLRINSGMTEAERKAVLDLRARCYRILEMFGAPQKDNGGQECAD MSAFANTWAGLTSKPESDTEIPGNLAYDCVSRELQAKLTDEMNEKEVVEVLEKTLLRY SQVAEERNKKDSEQKYLEELEELKNAICVAEKLPDTNETKARKIRSAKGVAEEFEKEK DQFIKKFFENRRTGLGRAVVSALGKPFATEKASDLGLSEAEFSAAKQHIARIAVATET IDKQHIRLHYKGGNPNNFEKAIFRYWLLRNDETSLDGNGKKTVKAAALADFRNFIKND KPEKEPKLDEKHIAAMPFTAKGAKFAFQLFGKLCLGIETIHSSPDWAFDKTAYATAAE DVFKYKIRTDTRKVKVAKLLNVVQAYENKGTSLTAEESPTGKRLTVRGMDGDPRWKED KEDCKGVVRLLAKMSQDKEISGYGLRAGTIGGWAEVRKALLGVYRKATKNGRDVNETQ LTTDLEKAVDDEMEANRQGFGSADFFHELCEPAFFHLWLEDKEKDNEKDKDGNVIQKF EHNGIKDFIPHYVSYCEWREKLISLLMQDGGELEWKSEVELPATELRKLANRPIRYTW PGLLNRHKKPSYRYFDFAENLNTSLQLKSLFRRVRTESDPHGVPIYKKLDGDDAKLTL AARRLKRDKIVNKDTGNSVDALWCPPLILAGESEPTKEKYPRAGKYEDGKAKTWTKGD AEVSFSLIASPLPGDYWNEVAGVPSASEKYPVHMTVSFKLEANALALLQNEGVHFIRK SLKGVGEEDDKREFFRWPVDIETDRVAAQEAAAKDKKEAEKTGKPPKKQTRKPDVKPD ELWCNYANGFLVKESRYIKAERTKRVPEFHLLSIDLGNRFAAAFTRLRIHADPKSDGR VVSAEGFLPVIKAQSVRQGKLCLQGEGADVWRLVSEKNKEHIATKLRAQGIKRDPVVG QYDLVEEAYGNGGRGRFPTDLEYKQQFVPVAEHLVPVSSLSLAGTNKQTYPELGDHLI FRLKRRIGRLRTLLNLIWRLRGTHERNNNIGKHDKQREDKDWLFHRRMTVETLARSKF PKRPRQEGEVEEPNDASLRASLASDDQWQKLKEHGLLDSVKGAAEKKRRQDLENALKQ LGVWNWDKLADAVKNQIEENFSGNDSLDKLLVDVIEFCLPLRGRHWGWDRSRKARLHW DKKDETHNPNIQGMRGLSLKRLEQILNLRQRCQSFAKLEDRYHRQFKLKNYNPPDSIA RELIEDVCPLLLERSNRIRDQRVEQTAHLILAEALGMELKNPSEVVNKKARKMAVDLH GEYKRRKDKNRRDYPRCSVIVLENLERYKTSQERTKTENSRLMQWAHRAIIEKLEDMC RPFGITLMLVDPAFSSHFDARTGLPGVRMNQVSPGFHEQYPYNKWVNDKTKTGKQTQL AKDIEAVKKLFADNPDFKGDLILAVEGGKEFLPVLSPDGGEGLINADICAAGNVGLRG VADPLRWDIFPRLRTKQISETEVSVTNWRGWFGKYLNDAEERRMRALATETAPAKAAA TEKKKRRNSATNANESESPDSSDSQSGESSEFPAFFVAHPNHDWGIGLRDRAYRFVQN GKEILTYPQSAYLKRVEKVCSEHIIRINQDRIHKPPKA
622	CLUST.420457_S.513CCY-M direct repeat 1>	guuucagucgccgcgauuucagagagcuugaggcgg
623	CLUST.420457_S.513CCY-M direct repeat 2>	ccgccucaagcucucugaaaucgcggcgacugaaac
624	CLUST.420457_S.513CCY-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
625	CLUST.420457_S.513CCY-M non-coding>	tggtcggtcagttcggagcgtaaaatttccgctggcgtcctcgcaatggcggcgagtc tcttgttgtttgcgttggggacactcctggcattggcgaaacagaaatggaatcatca ttcaaacgttccgtcaacagcattggaacaatgaggttccgcccactctgaaacgacg agagacaacgagtaatccacttgtctccgccctccatttttgctatcacgctgcggga ctagacggaactgagggctgccgctttctgaagcattttctgagcggcgggtggaatc gtttgccgaacgcgggcgggaatttttgaaacggaggaacaaccatgaatcgcattta ccagggtcgcgtcacgaaagtcgaaatcctgaacgggaaggacgaatcaggtaaaccg caatgggtgttgcttgggttcacgcgcgagaagctcgatgaactcaagaagcaacgtg

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626	CLUST.420457_S.513CCY-M direct repeat homology 1>	ucucugaa
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667	CLUST.019581_S.5 FSZZE-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
668	CLUST.019581_S.5 FSZZE-M non-coding>	aagattaagattgggaggaaccgaaagctgtgcagtgatccccttttttgatttcttgc tcgtaagccttttgatatcagatgggcttttgctacagccaattagccctacaaaaa ataacacaacacaaaggcttaatgttttacgcatgatgtacctggggatagagttaac atcgctggctcatagcttaataggaccccagtttatattcaagcattatccaacatct aagtaaacaatcgcctaaaacttccagttcttctattgcattacagatcccgcatatg

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	direct repeat 2>	
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1627	CLUST.210119_S.6	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

	1WV0Z-M spacer>	
1628	CLUST.210119_S.61WV0Z-M non-coding>	aaataaacaaactaattgaaaggaaaacgaagacacttataaaaatagaaaaggggcg aatcaaattcaaggcaacgcgaataaccctgcaccaaggctcttttaaaattagattc ggcgataaacccgcttttctgataaaggcgttgtcttgcttaaatcctaactgccaaa accacaagaaacaaattgacgctgacctaaacgcggcaagagtaatagctagttgtta cgccttaaaaattaatgattcccaaccatttggaacaaggaaaagatttaaaaaaaga acaacgaattaatttaacggtaacctgtggaatccagtttactttggcagtcctaaaa gaaccgtgtataccaacggatatggaatcggtgtaaatcgaaccatcctttgggacgg gtgctcttctatatggcgagcaccttaagaagactcgttgcaagtcttttgggctcat aaaccattgtcgcgatggataacggcctgacttagtttcggttcaaaattggttggtc tttttaaataaggctacaaaaaggcccttatccgattacgctttttatccgggcattt tcctgccttttaggcgaatttcaacgatttttcggcttaagcgaggtgcgtt
1629	CLUST.229769_UPSR01022669-M effector>	MVKTLQLKIHKPTKYKKMLLDKTIKRYNLVYNEMLKDAKTNIDIIISHYCNDNGKYTA QTISKFFSGKDYHKKYGIEPLYDSLKFYVSTNIASYLELKKYLQSKNLEDNTQFPFIK RNKKNIIKKIKKYEYKIINDIMFTNEQQHELEQKIKKLKAEIDRINDFVPISFSRFDE NRDACLLYSPKKNRYYVKLYIMGREESIKVFKNHKPKNIEAVKDFDELIYLPSGHRFE TDKTKPQPYIILPLEFGLWHEKYLKMIRKGEATPSAMKLIKRNEDYYIDLPVNIGTDR QEKWKKFDKEKIIKTETRLGIDMGVACIASIAVVKDIKTEPIFTKKFIEETKEYNEAF ERYVEKLIIAQKNCSNYPQDKKYIQGILHRVANEIIKIAVEYKSDIYVEDLNIDKSTK RIESTPKFQKYNKKTIKRIVKQLNRWAYGELYKILKYKAEINNLTKVRKVNPKFTSEE CSMCGHNEIITSNAKNENRETQSLFVCKKCGFTYDADINAAINIANRYYNTVKLKSKE LNNMIIVEHNLFDIQGMGCDSYYAIQDFLNKLKKYYDEYKNMSAELKKDKKLKQQYAI LAKLDYSDYEKYFSLV
1630	CLUST.229769_UPSR01022669-M direct repeat 1>	guuuuaaaacuacuauaguguaaauguaac
1631	CLUST.229769_UPSR01022669-M direct repeat 2>	guuacauuuacacuauaguaguuuuaaaac
1632	CLUST.229769_UPSR01022669-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1633	CLUST.229769_UPSR01022669-M non-coding>	ataaaatattaatataaaagtattgacaaattcaaaatgaaatactataataaatgtg gaaatgaggctcgaaaatggttaaaacattacaattaaaaatacacaaaccaaccaaa tacaaaaagatgttattagataaaactataaaaaggtataatttagtatataatgaaa tgctaaaagatgctaaaactaatattgatataataatatctcactattgtcaagactt tttaaataaattgaaaaagtattatgatgaatataaaaacatgagtgcagaacttaaa aaagataaaaaattaaaacaacagtatgctattttggcaaaattagattattctgatt atgaaaaatatttcagtttagtttgacaaaatattaaaataatattatactaaatatg aacattgaaaatttaatataaaaaaagtggttacattttcactgacttatctatgcag aaattggtagataggtcgaatgttgcagagcaacaaaaatttgtctaccttcgataat gtaaaaattataggaggtcgacaattaaaacagctaaattaattaacaaaaaagtcaa aatatgtaaaacaaaactatatattgtgtttttaaattaatattatacaatatatagg gtgtgtaaatggtaaattaataatctttaaatcaaatcaaaatttgatggaaaagagg attaattatgatattaaaaaagcaattgacaaataaaaacaaaattgctattataata

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1634	CLUST.229769_S.C670MG-M effector>	MALPKLSASQFHTAKFKVHNPSGYKRRRLIAAIDLISKEYTLLLDILSKDPDAVEQGA THEYVNKNNGVVKQFYSKINLSSYIRSVLNEHSDRFNCRGSLKDIIVEEATGSILSYL QLKTGDKQDDTSFPSGKEDIREEKIDELLDEVLEVDDLEKEKELKASLKRRERHYQRP ISFVRFRDAALVRTKDGTKIYAIVNIGADAKKTVFRNDLLQVTDNKPYKDKPSTTKIT LPLEMGRWSMYKFFRKGTPKTSKLYYEEETDTFYLNYTFSFETPTVEPQSFMGIDRGK VIVGAYGVVDFDNNVLIQGTATGQKLKDKLNDLDEEIRTLQAKSVERIPFNKWRRVVN AEMHNIANEIVRVAKQYNSVIAFENLQNITRTHKRVKGAPRNPFNKALRKSQYRNLKQ LVEYKANFEGLPVVEVNPAYTSQTCHVCGKVDSSFRLDQASFKCDCGNEMNADINASL VIASKANWIYNYDGLKGKYKNTGHFISELRNTRISA
1635	CLUST.229769_S.C670MG-M direct repeat 1>	guugcaacuggaccagagugggauugagauu
1636	CLUST.229769_S.C670MG-M direct repeat 2>	aaucucaaucccacucugguccaguugcaac
1637	CLUST.229769_S.C670MG-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1638	CLUST.229769_S.C670MG-M non-coding>	attcagaagaccaaactggctaccatcgtggcaaccatctcgctggtcgtatcccagc tggccaactggctggggcccaagatacctgcgatgttcaagtagtgaacatttatacc ctgaccgacctagtcagtctgaccgaccccggcagtctgaccgaccccggcagtccga ccgacctcggcagtctgactgaccccggcagtcagagtgtccgttagggacagactgt ccctcccaaacagactgtccctcccaaacagactgtccctcccaaacagactgtccct cccagacagactgtccctcccagacagactgtccctcccagacagactgtccctccca gacagactgtccctcccagacagactgtccctcctggatcgaagattgaagccaccct atagatggggtggctttgttatagattaactattattattgcttgacattttagatct caaatcgtattatatattattcacatagttggtttaatttatggcactgccgaagttg tctgcttcgcagtttcatacagcgaagtttaaggttcacaatccaagtgggtataaga ggcgtcgcctgatagcggccattgacctcatcagcaaggaatacacccttttgttgga tatcctgtctaaagactgcggcaacgagatgaacgccgatatcaacgccagtctggtg attgcttccaaggccaactggatatataattatgacggactgaaaggcaagtataaga acacaggacactttatcagtgaactccggaacacccgaatatcagcttaaacagatta acaggaagatctataatctggttgagcatctgaagaaacatagaggcgaccggatagc tatgcgtcagttagagcgtaagctacgccagcgccgtggtcttttaacatatatgaat gggcgtcgtctaactgcttcgtgagaagtgttatcttttacgccctggccgagtctgg tccgtatcaccggcgattcccgcttgcgggatgaaccgggttaggccagtcaagaccg aatccacgatgtcgtagagattaaaaacccttcgggtatctacggcgatgtccagtat attggtcgtcgttcccctgggtaaatcgtacaaccggagatcgacgacgaatactccc gaaccgttctatctaaggcattgtttttattgagcccgacgtagggggagatattgcc ttccctgatagttggccggaggctgcacttgttgtaactgaactatagtcatatctca taaaccatcaggacgcttatgagaggaagaactacactcttcaccctcatcctgctaa ccaccctcaccctgctccaggcaggctccaataccagagtcacccgcgtcatcgacgg cgacaccttcgtcatctcttccggtgagaaagtacgcctcattggagtagataccccc gagacaaaacacccccgtaaaggagttgagtatttcggcccccaagcctctgccttct cccgggagatgctcgaaggtaaaaccgtccgtcttgaatccgatgtccaggagcacga ccgctatggccgcctcctcgcatacgt

1639	CLUST.229769_S.2 YNMEV-M effector>	MVKTLQLKIHKPTKYKKMLLDKTIKRYNLVYNEMLKDAKTNIDIIISHYCNDNGKYTA QTISKFFSGKDYHKKYGIEPLYDSLKFYVSTNIASYLELKKYLQSKNLEDNTQFPFIK RNKKNIIKKIKKYEYKIINDIMLTNEQQHELEQKIKKLKAEIDRINDFVPISFSRFDE KRDACLLYSPKKNRYYVKLYIMGRKESIKVFKNHKPKNIEAVKDFDELIYLPSGHRFE TDKTKPQPYIILPLEFGLWHEKYLKMIRKGEATPSAMKLIKRNEDYYIDLPVNIGTDR QEKWKKFDKEKIIKTETRLGIDMGVACIASIAVVKDIKTEPIFTKKFIEETKEYNEAF ERYVEKLIIAQKNCSNYPQDKKYIQGILHRVANEIIKIAVEYKSDIYVEDLNIDKSTK RIKSTPKFQKYNKKTIKRIVKQLNRWAYGELYKILKYKAEINNLTKVRKVNPKFTSEE CSMCGHNEIITSNAKNENRETQSLFVCKKCGFTYDADINAAINIANRYYNTVKLKSKE LNNMIIVEHNLFDIQGMGCDSYYAIQDFLNKLKKYYDEYKNMSAELKKDKKLKQQYAI LAKLDYSDYEKYFSLV
1640	CLUST.229769_S.2 YNMEV-M direct repeat 1>	guuuuaaaacuacuauagugua
1641	CLUST.229769_S.2 YNMEV-M direct repeat 2>	uacacuauaguaguuuuaaaac
1642	CLUST.229769_S.2 YNMEV-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1643	CLUST.229769_S.2 YNMEV-M non-coding>	atggttgtagtggaggataaaattgttaatggatttagagtagtacattgtataccaa atataacagatgaagaaagagaaaagaaaaagaaggagatttatgataggtggaaatg aggctcgaaaatggttaaaacattacaattaaaaatacacaaaccaaccaaatacaaa aagatgttattagataaaactataaaaaggtataatttagtatataatgaaatgctaa aagatgctaaaactaatattgatataataatatctcactattgtcaagacttttaaa taaattgaaaaagtattatgatgaatataaaaacatgagtgcagaacttaaaaaagat aaaaaattaaaacaacagtatgctattttggcaaaattagattattctgattatgaaa aatatttcagtttagtttgacaaaatataaaaataataatataataagaatagaagtg aagtatctacgtattgcttaggcaagaagtagtagaaggtgtgaacccaccctatcga aaggtagttgcttagttagtgtatgactatacttccgttgcttacaacgaagatatgt aacaacatatctgtgaaggtagtaatacatgatgctaagaaactccaacctctaagcg aagcgtaggttggagaggttcattataaaaaaagtggttacattttcactgacttatc tatgcagaaattggtagataggtcgaatgttgcagagcaacaaaaatttgtctacctt cgataatgtaaaaattataggaggtcgacaattaaaacagctaaattaattaacaaaa aagtcaaaatatgtaaaacaaaactatatattgtgtttttaaattaatagtatacaat atatagggtgtgtaaatggtaaattaataatctttaaatcaaatcaaaatttgattta aaaaaggaggaaatttttcatgcat
1644	CLUST.229769_S.B TGQD0-M effector>	MIKTLQVKLHNLSNYKTLILNKTMKNYSLAYKEMLQVAKENIDIITEKYCNDKGEYKA QAISSFFNGMNIHAKYGLEKLNDVLKLDVGGNIASYLELKKEDDNTNYPTIKTNKLNI IRKIKKANDKILNDINITHEECHDLEQNIKKYEKKLNKSKKYKPISFGRYEEKRDCCL LYNPITNKYFAKLYLLNDSDSKTMFKNRPKLKRTTYNENHQLYYIPSMNKFKEDIKKP QSFILVPLEFGRWHEKWFKKIRRYEVKTCPFKLIKRNNEFYLDIPIEDEIVKCTECNG YLNKRGICVKCGKKFESKEVGKIKKETFVKTYKPETKLGIDLGISNIATITVLDNKNN LLFTKRYDGKEYCKKIEHYVLKMSQAQRNAAALPQDKKYLEGFLHTVANDIIKIAREY KSQIYMEDLKMDKSKKKLEEHKKFKMFSKKAKKKVIERINRWSYGQMIDIMEYKCGIN KIPKPKLINPKFTSEKCHVCGHNEVISSKGKDKNRESQDSFICKKCGLTMNADENASI NIACYYDSKITLKLEEKDGLYTVKNKLFKFNIQEKTPEDTLKKWLECLKEYKQEYDNI PWDKKKKGSKLAKQYAVLKHLEKDNYKEYFIIEP

1645	CLUST.229769_S.BTGQD0-M direct repeat 1>	gcuuuaaagauacuauauagaauguuaacuugaua
1646	CLUST.229769_S.BTGQD0-M direct repeat 2>	uaucaaguuaacauucuauauaguaucuuuaaagc
1647	CLUST.229769_S.BTGQD0-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1648	CLUST.229769_S.BTGQD0-M non-coding>	aaattcaaaacaggaaatacaacttttgtgtcaggaagtctatgttataaaatagtta aaggaatagctgtgccattagataagcctagtacaaaattacaaagatttagtttgtg ggtattaagaaaacttggattgactgaaatttagaatatgcaaagaacaatatgaaaa aaatattaaaagagttagaaggtttgtaggtaataattaaaatataaaatttaagagg tgatatagtgataaaaacattacaagttaaattacataatttaagtaattataaaact ttaatattaaataaaacaatgaaaaattactccttagcatacaaagaaatgctacaag ttgcaaaagaaaatatagatataattacagagaagtattgttggttggagtgtttaaa ggaatataaacaagaatatgacaatattccttgggataaaaagaaaaaaggaagtaaa ttagcaaaacaatacgcagttttaaaacatttagaaaaagacaattataaagaatatt ttattattgaaccttgaaattaaaatataaaagttgttaacatttctattatctttttt ataactatgtagtttgtagttatatgaggatagaacgatacttagtatcggctgaagt ttatatagatttgcagtaaacctaaaattaggtttgtaaatttattgtaaaaacactt gaaatgcagtagtaatacatactggatgaatttataaataaatgaggttcactgcaaa ataggcttcaaaatagtagtatttttaaaaattaaacaaattgatacaatatgtagtt attggattattgttagcatactatatgttgcgtatagtatttcaagtcgtaacagata caaagttttaaagatactattttgtaatataatttttaacatgaaaaacgaagtgtcaa ctaaccagctaccctaaagggatagtggttttctgctaagtttttataaacgagcata agtgagtatataagagataaattttacagattttgctataaaataagagttttatagc aaaatgaaaaggagggatatagtggataaaataaaatttaaaaatggaagtgaaataa agattattgatgtagatgtagctagcacaagaagtaaaagaggacataggcaattgca aaagataaagtattattacaaacatagacaattgcaa
1649	CLUST.229769_S.9F71YP-M effector >	MIKTLQVKLHNLSNYKTLILNKTMKNYSLAYKEMLQVAKENIDIITEKYCNDKGEYKA QAISSFFNGMNIHAKYGLEKLNDVLKLDVGGNIASYLELKKEDDNTNYPTIKTNKLNI IRKIKKVNDKILNDINITHEECHDLEQNIKKYEKKLNKSKKYKPISFGRYEEKRDCCL LYNPVTNKYFAKLYLLNDSDSKTMFKNRPKLKRTTYNENHQLYYIPSMNKFKEDIKKP QSFILVPLEFGRWHEKWFKKIRRYEVKTCPFKLIKRNNEFYLDIPIEDEIVKCTECNG YLNKRGICVKCGKKFESKEVGKIKKETFVKTYKPETKLGIDLGISNIATITVLDNKNN LLFTKRYDGEEYCKKIEHYVLKMSQAQRNAAALPQDKKYLEGFLHTVANDIIKIAREY KSQIYMEDLKMDKSKKKLEEHKKFKMFSKKAKKKVIERINRWSYGQMIDIMEYKCGIN KIPKPKLINPKFTSEKCHVCGHNEVISSKGKDKNRESQDSFICKKCGLTMNADENASI NIACYYDSKITLKLEEKDGLYTVKNKLFKFNIQEKTPEDTLKKWLECLKEYKQEYDNI PWDKKKKGSKLAKQYAVLKHLEKDNYKEYFIIEP
1650	CLUST.229769_S.9F71YP-M direct repeat 1>	gcuuuaaagauacuauauagaauguuaac
1651	CLUST.229769_S.9	guuaacauucuauauaguaucuuuaaagc

	F71YP-M direct repeat 2>	
1652	CLUST.229769_S.9 F71YP-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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1654	CLUST.229769_FZPS01000186-P effector>	MIKTLQVKLHNLSNYKTLILNKTMKNYSLAYKEMLQVAKENIDIITEKYCNDKGEYKA QAISSFFNGMNIHAKYGLEKLNDVLKLDVGGNIASYLELKKEDDNTNYPTIKTNKLNI IRKIKKVNDKILNDINITHEECHDLEQNIKKYEKKLNKSKKYKPISFGRYEEKRDCCL LYNPITNKYFAKLYLLNDSDSKTMFKNRPKLKRTTYNENHQLYYIPSMNKFKEDIKKP QSFILVPLEFGRWHEKWFKKIRRYEVKTCPFKLIKRNNEFYLDIPIEDEIVKCTECNG YLNKRGICVKCGKKFESKEVGKIKKETFVKTYKPETKLGIDLGISNIATIAVLDDKNN LLFTKRYDGKEYCKKIEHYVLKMSQAQRNAAALPQDKKYLEGFLHTVANDIIKIAREY KSQIYMEDLKMDKSKKKLEEHKKFKMFSKKAKKKVIERINRWSYGQMIDIMEYKCGIN KIPKPKLINPKFTSEKCHVCGHNEVISSKGKDKNRESQDSFICKKCGLTMNADENASI NIACYYDSKITLKLEEKDGLYTVKNKLFKFNIQEKTPEDTLKRWLECLKEYKQEYDNI PWDKKKKGSKLAKQYAVLKYLEKDNYKEYFIIEP
1655	CLUST.229769_FZPS01000186-P direct repeat 1>	agcuuuaaagauacuauauagaauguuaacu
1656	CLUST.229769_FZPS01000186-P direct repeat 2>	aguuaacauucuauauaguaucuuuaaagcu
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1659	CLUST.229769_S.0W10HD-M effector>	MYLTGVFKIHNPSRRKRQVLDHALESYTRAMDKILVDASRRADKIREDTCSRKRDGTA IEKWVDRRVGGKLLAPQSTGEMLSGALSDGLRTDAGRQVASHFALTAMGEDASFPEAR DPRPDAIDNAMHDFCFASIDEYDKYRDRMLRQARGSVTPILFPRERDCPLVVSADGQS FFAMLNILAMKSPLGVRTTIDDGNLIHAQTGEVISYRGKSKVLFPLQVGKRNGAFAWQ YERFLDPIINGDGAIKECHLVRRDGKKGDHEYFVHYAIDVPEPEPYTPETYLGVDVGI LYTMAYAIVAPDGGVIKMVERDDGYAEQARRFGKRVQERQRRGKRVTMRSYGRKAQEQ LLHEMVNEIIEEAIEHRSQIVLEGLSVMVRGKFVKSAWAKIKRYFEYKCALAGVPLRT DMWAAYTSKVCLHCGEINAERQLGHAFVCPCCGATYPSDAGAAVNIARRMFYRKKEWS KAGGWKAFHKSFANVTHLNAENGLRDVELIWSGISRERQLGVTVNN
1660	CLUST.229769_S.0W10HD-M direct repeat 1>	guuacagugaacaacuaguguagauggacaaugcgac
1661	CLUST.229769_S.0W10HD-M direct repeat 2>	gucgcauuguccaucuacacuaguuguucacuguaac
1662	CLUST.229769_S.0	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

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	effector>	RQAALDLNWRVLDDKILRIGMLWDGTQHTALHFPAPLMARWRSLQDLQRQVAEALTAC KTTLEMVWKDTPLPEDLQPDAWAQMGQRGLLRLLRAVLALPLVVPSRTATLAILEPWE RRTGKLWREVRGLQGHLERAKQAWYRVLAKELCSQYDVLAVEDLDVRQMSQRRSEMSP RLQASMVYRQLVAPGAFLQRLVHTAAREGVTVIKVNPAYSTLTCPVCQAILPSQEGEL WLTCPHGHRYDQDRAAATTLFRRAFASGDTRSTEGPCA
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1732	CLUST.380028_S.9 CRN9E-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1733	CLUST.380028_S.9 CRN9E-M non-coding>	gcgtgagatctttgatataatccttaaaggatattatcctaaaaagagtagatggcag aataggtgcattgattgttgttacaggaatatttgcaaagggtagaaggtgaaaattt caaagacactatctcttagaattattcggccctactatacgcctgaggttgagtctgc cataaaagcagagaaagataagcgtgaagctcaagggcagacaagaaatctcgatgcc aaatttttcaatgaacttaagaaatccaagaaatgtcatagctgcggatatataaatg aatttttttacatttgagtttagacagaagaataacttcccacttttttaagtgcaaaaa atgtggtgttgagtgtaacgctgattacaatgcagctaaaaacatagctattgcttaa atgggttgacttttttagtgagaattttagaaaatattattgagttttgttctttgaca atatagattcggagtaatcgccccaaaaaggttggctatagcaggctattgcttgcag aggataagttgacaataaatttgtcatccagcctgatggaataaggcgcggctgattt caacagcctaatatcgaggtgccagaatcatgcatgatctctggaggacaccctcgaa acaattattggaagctaatgatgcaaatttatgggacaaaatgtggtctggcggtgaa agtcattgaatatcaacggtttcaccgccaggattccatgtaaaacatagcgaatttt gagacttttggatacgaaaatgaaagggtttttaaccaaaataggcatttgtaaaatc ctaatggaatggctattatcaaggctttaagggcaaaatgctacca
1734	CLUST.416732_S.5 JS1C1-M effector >	MSDYKFSNNGVTNTGSAHIGLSPENSSTVMDMFKVITKDADFLLKNLLIMEGGEYMLN REIHNGDKEFDKIISKLGLSKKEKENLKMKCKDFFFDFVKLQNGRSLANILFETKGTT LIGCGKDKKGEKVDGEYPTIYHDHETLRSTGLLPLKFSKNIDDVDYKYLICYLVHNVL SSFIEKRDAYNDNKKEWESKLSNSNLPQLERMSEFLNGINHLGNIIGWNGKKYIGFIK KWTDEESSMYDFFVQKLQDNPKYKFGKKDQFLYGYEPEFLNYLFHDFRDLWHPDNLIG KDEYVDLISGKNNTDAETANKGAYHWLKDFINISSFDAYGKMATIGMGNNLINYSMNI DKDGKIIVNMDNIFDRSKPIVFNVYRNSYFRNFKIIESDDKKGIYKVEFSTSNNGVIY EGYIKSPSLRFATKGGTIKIDFPISDKRIKGGREMNTDLMWFLNRASPCSTKNKEVNS FIGKNFVGLAIDRGINPLMAWYVAEWTYDKDGKAKIVRSIANGRVDSGHNESEVKFVR ETTNRIVGIKSLVWNTVKYRTGGSEGIDRCRKSQNGQVDLFEMFDIDYNNYLKEVNNL PYDPNSERSIIQTWVSSPWKVKDLVKDAKNRMVQIKTQYHNAKDKEKYITTQNRAGFY DFLKIEMEKQFTSLQRMFSGGQKDICKNNEEYRRGLRRRINLYTSSVIMSLARKFNVD CIFLEDLDSSKSSWDDAKKNSLKDLWSTGGADDILGKMANKYKYPIVKVNSHLTSLVD NKTGKIGYRDPKKKSNLYVERGKKIEIIDSDENAAINILKRGISKHIDIREFFAEKIE VSGKTLYRISNKLGKQRMGSLYYLEGNKEILFGLGKNGEPIVCKRGLCKKERLAPRIA EKKSTYLIMNGSKWMFRHEAKKIVETYKDRYCANHKVASKDG
1735	CLUST.416732_S.5 JS1C1-M direct repeat 1>	ggugcaaucaucuggaaauaccagagauaauugcaac
1736	CLUST.416732_S.5 JS1C1-M	guugcaauuaucucugguauuuccagaugauugcacc

	direct repeat 2>	
1737	CLUST.416732_S.5 JS1C1-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1738	CLUST.416732_S.5 JS1C1-M non-coding>	gtggagtttataataattgtcttaattcccttaaaagaatagagccatctgtagaccc taaatggtttccggttctaaggaaatcgcttcaaattgcctctatatatcatgatctg ggtaaacttgacgatcaggcccaatctttttgcatggcgagattaaatccaaaatga tcaaccacgtagatgctggcgtggcatttactctatctcaatattcaaaaaccaagga catgtcttatcttatagccgcttatttaattttggcacatcatattggtttacctaat tatgactatatgtttaagacagaaagacaaatgcttagtcttattgtttctccaacaa aatcattcagagataggaagtcgctaaagaaatatgacatgggtaagaatatggttaa gacccacgtaaataagaatctaaataattatttaaaaatacatagaggcctttgtgaa ttagcaccagatgacgttaaaatatccaagagttcagcgttatcttttattagtaatc ctcttgctattaaagttgccataagtattttggttgatgctgatcatgaagatacatc ggaaaattatggcgacacttatccggtcagagtaaagcatattaactccaaatattat ctaggaaatctacaaaaagctgtaaaaaaaatggaagacgattacaagaacggactta tttcttgttccaaagaaaggtttaatcttcggcaggaattttataagttatgtggcaa tgttgaatttgatagttcgttttatcttgtagacggaactgttggcataggaaaaaca ttagccataatgaacttagcattaaccatggctataaaacttaatgtagacactctaa tatttattcttccgtatatagccttaattgaccaatcggcccatgaatatattagatg tctttttgatgatcccaaagacgcaatgtacaaccttaataccattcattctatttttt aaaacaaaaaatgtttttcatcgcaagtataataagggatttaatgctccaattaaca tgacaactagtgttaacttttccaaattatatcaagtaatcatacgtgtgtttttaa gaatattcacaagtttattgggagcgtcattgttatagacgaatattctagtattgcc tcatatgaattttggccctcaatgctgaaaattatgaacgatttggctaaacacttct cttgcaagtttatattttcttcgggtacgcctgtcagattctggaatgttgatgatat atctaaaatggtgggagaaaacatatctgttaaacaagtaatttcttccaagatgtat aagaaaatgattgctcttgaaaagaacagagtaatcattagaaattcaatcaaggaag aatggagttttaaaaaactcgcaagagaaattttaaaacaaaagaaatccacttttgt tattctaaataccagaaaaaaaacggttgcctttgcacaagaactaatgaagaaaaca agcagaaaaatttaccttagattttctggtttgtcgccaaaagataggatagcacaat ttgagaaaataaaagccgacatcatagagcaaaagccaataatagttattgctacaca gggatcagatataggacttgatatttctttttattgcggttttaaagaatcaagtaat tacgattctatatctcaaatgaaaggtagaatcaataggggtaacgaatttgaaaaat ccttccttcatatatttaggttaagtaaatgtcctaatggcggaaccgaaatttttta taacaatcccgcctttaaacacaagactgaaatttttgagtcggaagtaaaattgcaa aagagtatgtcgcctgagtatagcacatatattgcagaaaaagaaatagatagaatgt ctattccgtcaaaggataaaatgaactctcttattagaatgtgggatcataaggagtt tgagaattttggtgataatttctctctaattgacatgcctatgatgcacttattaata aatccagacttgtttgccaaaatgaagaaagacgaatatgttccgtataacgaactcc agaataatatcgttaacgttatatggagtgaaaaaaatatggatcttttaagggatca tattgttttagtggacgacgaacttggcataaacaatgaaggcgaagatacagataat aaagaaaagaaaggtttttatggattgtatttttggaaaggtgcctatgatcctgaaa attttggtatttttgcagatcccatttggggccttgttgatttgaaaacattaattgt ttgaaaatagttcttgacttttttaagaaaagagtatatactgtttaataataaatata aaacaaaaggagaaaaacaatgagtgattataaattcagtaataatggtgttacaaat actggttctgcgcatataggactttctccagaaaattcatctactgttatggacatgt ttaaagtaataacaaaagatgcggattttcttttgaaaaacctccttattatgaggct tgctcctagaattgctgagaaaaagagtacctatcttattatgaatggatcaaaatgg atgtttagacatgaggctaaaaaaattgtagaaacatataaagatcgttattgcgcga accacaaggtagcatcaaaagacgggtaggttcgcgctagccgtaagtagttcattga caattgaatataaaaatatccttgcatcaaggatattttgggcagcaaaaatcaggg gattcgcggaaaagactctggaacccccctgattttattacaaatttatagtataca

1739	CLUST.416732_S.17EH7F-M effector>	MYKKGEAMKKQTIVKKDSKAETKENKMYPDKDTDFPVNSQFSRSISIRANVDPKDLLV LKRTFEETTKISDELLSTLLMLRGKDYCLDNVVCKGEEVLENLYKKLSKNATVNRDKF ISTAKAFYEYFHGCSYHKGFKSFFFSSKEIDSIQSEKFGYLREIGLFPIKIDAQISND LQYSIVASNHAKIKGFEKIDKEYQANKEKWNKTIGESTLKHLNRYGEMLKGLSDLGTM GNFNGKKYDRFMGHWRNEQKIPDHISMLDFFRKIYQEKGKSHRFTAIDNFTYGYESEF MNHIYLNFSDLWLKEDVIGDEEYVSLIRGAYHWQKDVVGIASFSGYNKYEKLFMGDNK INYALDFSNKDQWLMKFNNVISKEPETITLRLCKNGYFNNLSVLEKNDENGRYKIRFS TEKQGKYFYEAFIREPFLRYNKDNDKIYVHFCLSEEIKENCPNHLDTRSDKYLFKSAL LTNSRQKLGKLHYRDFHIVGVDLGINPVAKITVCKVHVDKNENLKITKIITEETRKNI DTNYLDQLNLLYKKIVSLKRLIRATVAFKKDGEEIPKMFKMGKKSPYFLNWTEVLNVN YDDYIKEISTFSVDRLSGLTLPMQWARSQNKWVVKDLTKMVRKGISDLIYARYFNCSD KTQYVTENNAVDITTFKKHDIISEIIGLQKMFSGGGKDVAKKDYLYLRGLRKHIGNYT ASAIVSIAQKYNAVFIFIEDLDLKISGMNGKKENKVKILWGVGQLKKRLSEKAEKFGI GIVPVNPELTSQMDRETFLLGYRNPTNKKELYVKRDDKIEILDADETASYNVALRGLG HHANLIQFRADKMPNGCFRVMPDRKYKQGALYGYLNSTAVLFKDKGDGVLTIHKSKLT KKERDSRPIKGKKTFVVKNGKRWILRHVLDEEVKKYPEMYNSQN
1740	CLUST.416732_S.17EH7F-M direct repeat 1>	gugcaauuaaguagaaauacugcuagugauugcaac
1741	CLUST.416732_S.17EH7F-M direct repeat 2>	guugcaaucacuagcaguauuucuacuuaauugcac
1742	CLUST.416732_S.17EH7F-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1743	CLUST.416732_S.17EH7F-M non-coding>	ggatataaacttgaattggcaattggtgtaagtatgggcgtagaacttttgtctatg cggatcaatatggtaaagacgtaaattctatgggacttggcttcaggggcagtacttt tacatttattcccggagtaaacgtaaaaagataataaagaatagggcaacattgggaa taaaaataatgaaagaaatttatatagcacattctgaagataaagaaaaaggagctaa gatacaaacctatgaaaatcatgtttcgggcgttcttaaaagttgtaaaagagagctt aaaaaaataagacctttttgtaataaaggttggtatagggttcaaaaggataaaaaag aaaatgaagaaaaagaagaaaacgttcagtctcaagattttggggacatctattattg gactggagaatatgatcctaataactttggtattatggttggttgggataaattgcca aagcctatgatggtttagaaaataatatttttaaaaaaaataaaatagttgttgacaa atttactagaaaatctataatatagacaaatcaaggtataatatatatagaatgtata aaaaaggagaagcaatgaaaaaacaaacgatagtaaaaaaggacagtaaggcggaaac aaaggaaaacaaaatgtatccagataaggatacggattttcctgtaaattctcaattc tcaagatcaatttcgataagggcaaataaaagcaaacttaccaaaaaggaaagggatt ctaggccaattaaaggtaaaaaaactttgtggtaaaaaatggaaaaagatggatact aagacatgtacttgatgaagaagttaagaagtatcccgaaatgtataatagtcaaaac tgaagtttgcgaacccctagtgaacgtaaattcattaaggggttcgcatttttataa aatgttcattgacaactgaatatgacgatagcacttcattgattgtatgattagtgct attattttgataggttcgcagaaatcgctcattagacccttttatttataagggtctaa tgagcgtactttaaccgcagact
1744	CLUST.416732_S.C6EQWX-M effector>	MRKNDDFPISDTFSRGASVKATCNKSIKDLFEKMTDMEEIVAPLILSMLGKDFSFNGE LVDGTKYFKEYCEKNKIKFDDELVLVAKAFAQEFLSTSKSTGFVSFLFSSKDINNEYT KVHEERVQDALEKYNKKLESGKLKAGELFKEPKKRICFSIIRDRIFPIKNSFTSQQSF SVCKSIHSALTSYFQISTAREEEVEKWRSAIFESDRLDEYQRVGQFFSDFEAIEDKSF KFSTKTFLTFLKNWQQKGKNEKSLKDFFEEKTKEDPNKKFVDLDKFMYGYDASFLNLL

		FFEYKDLWTLFSEDISSSFLNTIVTNFHFKKEHVLFSTRKFNEKNLTMCLGNNQIHYS MSFDGSFHFKVKELSLDIDTPKGIFTYFEMLNVDDKKGIYTFRYATDSKAKHKFIGSL KEPRLRLVGDQYYLDFLMSGAYLESNKDFEFKELSKQQSLFKTSFTKRKGFIEGNHNF VAFDVGLNPLFTGVCGSFEGKEDSISYSFGSVVRPYKNSINKSDYYKEANRFTRSISH LLRVSANHKNEKIVVWKFKHDGIYVDCASVLDIDKDKFLKELDSLPKLSDQFGFQPLF QKGWSVASLIKKANGYVSKIRSEYRMSADKASYTTSNNFSDYSLVRKIEVCKSYISLQ KSLSKNKKDCCKSLKIYTQNLVEKMTKDMAAAFISIAVEKKARFIFLEDLDAKTSSFE DRDKNSMKRIMRVAELRKWIANRAEKFGIAVVSVDPYLTSLTDNETRHIGHRDAKNKK NLYVVRNNKIETIDSDINAAKNIAIRAFEHHSDLNHFRVEEIEKGYRLNGSELGVRRQ GALKKQFGSSSLLIRDIGNGLKSEKLLGQSKKHPKLNKKSIFAYFVGDDWYLRHEADE KVYSMAKKAGLIDYDLK
1745	CLUST.416732_S.C6EQWX-M direct repeat 1>	gugcagacauuaggaaaaaccuaaguccauugcaac
1746	CLUST.416732_S.C6EQWX-M direct repeat 2>	guugcaauggacuuagguuuuuccuaaugucugcac
1747	CLUST.416732_S.C6EQWX-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1748	CLUST.416732_S.C6EQWX-M non-coding>	gccatctaagttaacaaacttaatacctcgattaagtgatctgtcttcatttaaggct tcaattaaacgtttggcaatggttgtttttccagagcaaggaagaccagttagccaaa tagtgaaaaatggattttcagattctttttttcataatttaatcttcaatgatcctctt gcgagtacagacattaggaagaacctaagtccgttgtaacataatggtatttattact taatgaatcgtgaataatcctcttgacaatatgaacttttgcagtatattaatggcaa tagattaaaaaatattttaggggaataatgtatttagctcattcaaaagatgacgatt taggagtatcatgtcaaacatattctgatcacattcatggggtcttatcagaggctca caaaaggataaattatattagaggtattgataataaaatcttcgatgtagtggagaag gtaaaactgcttgacaaatcgttagttaaggttaagttatatgatgacgatgagttgt attgctggttaggcgaatatgatcctgataattatggattgatgtacgctattgatcc aggctatccatatccaataaatgatataattatttaaattaataaaaataaggaataa caatgcgtaagaatgacgattttccaattagtgatacctttagtagaggtgcttctgt aaaagccacatgcaataaaagcattaaagatctttttgaaaaaatgacagatatggag gagatagttgctcctctaattctttcgatgttaggacttggtcaaagtaagaaacatc ccaaattaaacaagaaaagcatttttgcatattttgttggggatgattggtatcttcg tcatgaagctgatgaaaaagtttattcaatggctaagaaagctggattaattgattat gatttaaaataactgatttaaaataatcgcgaacctatagttagcatgtcgttaggtt agaggttcgcgatttgcaaaattaccctagaaataggcataaaatattatgtttatgg gtgtattctttaaaaatattaaatagagttcttaggttcgcgaaagtggccttataag ttattggtgttgagggatttatacccccttgct
1749	CLUST.002248_AP008972 effector>	MENQTVQDKKYNIYKCYIKDDNPLYNTLDEWSHLANNLYNESIFIMRQLFTGLTKSSD KRQKLETTTIENVLKIAKLYNKNIILNEEYRLVNYPFLDFYFKKTNNENYYSSLPRQT AQSVIKEANTKFSDWLKALKDYKKNPSRYTGKPKMPKYKTSGGCATFSLTNQDVVFKK NKHNYIIKLPKTKATLSFNKKLKNERLKSVNVKKEYGTLKVTFLFENLCDKKANLKSG VFCGIDLGVNNLAAIVTSNGNSLLVKGEFIKSKNQWFNKKIAKNLKGQTIGTDKKAIS SKALNNLYKKRQFFIEDAMHKVAKKIVFWCIGENVSNIVIGKNKGWKQKSNIGKVNNQ NFIQIPHALLINYIKTIAEKIGMQVVETDESYTSKASFVDIDQIPTYKKDANMTYFFS GSRVKRGLYKDSLGRIINADLNGAGNIMRKILADENIKVNVNNLISPIKLTASEIYA

1750	CLUST.002248_AP008972 direct repeat 1>	gaaaaacacucgcuuauugcgagaaa
1751	CLUST.002248_AP008972 direct repeat 2>	uuucucgcaauaagcgaguguuuuuc
1752	CLUST.002248_AP008972 spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1753	CLUST.002248_AP008972 non-coding>	atttaaataccttgcggtatagtcttttataaactcatcaaccttgttttgtaaaact ggttttctgtattttgttacaagcactaaatgatactgtagtaaaaaagatgcgtgcc tgtttttgtaataaccttgtttggttttttcatgataaactcctttatttacaaaac tgtcttttacaactatagctgtttatggtataattatatcataaataaggtttaaaag aaaggagtaattttaatggaaaatcaaacagttcaagacaaaaaatacaacatttata agtgctatataaaagatgataacccttttatataacacattagatgagtggtcacatct tgcaaataatttatataatgaaagcatctttatcatgagacaacttttttataaagat agccttggcaggataattaatgctgacctaaatggtgctggcaacattatgagaaaaa tattagccgatgaaaacattaaggtaaatgttaataatttaatatcaccaattaaatt aacagcttctgaaatatatgcttaaatgtgatccagttaaatggatagagggtgcagt gaaccatccttataggaaagacaacttgtattattaagttgttggagcttattaaaaa actgtagttttgttttctacaaacaaagaaactccactctatagcttgctataggtgg agaggttcattaatcgtctcttgacataaaaaacataaaaaacataaaaggaataata cttgataaatataaattaatattatcatcagctttttctttctctttctttcgcttt tttctataatttatatatttcagtaaaaccgttagctattccttcatttgacaacac atttaagttgtcttcataataccattctgaatctgttctgctcgcaaaaacctgatta ttattgttaagcattgttagaaaaaagccaacaataacaacactgattaacattttct taattttgtttaatttcatttataataccccctcattatttatcactcgctatttgcg agaaattattaacctatgcaacattagtaaattccttctgaaacacactcgctatttg cgagaaaaaggttaattgtccttaatcttgttatcccactatctggtcgtgtgtagcc gccagaaacacccccgcttgtgcgggtaaaatttttatttagaactaactgagtcaggc aacaggaacaccctcgcttgtgcgggtaaaagggaactaatatgaattaaggaatggc aatataagaaacacccccgcctgtgcgggtaatattaattaaggaatagttttcatca gaaacgccatcgccatcaggaacacactcgcttgtgcgagtaaaataaaaaaaattta ggaaatggtgttatgagacagaaacacactcgccattgcgagaaatatataaacgaaa cctgcaaaatagttgaatttcaggaagggaaaccatatatacacgattatgttatttt ttatataaatctttttgcatagtttcgctatattcttttagagtctttgtagcctcaa ttgttctgttaattttaattaactgttcttccttatctttagaatttataatatttct tagataatctatagaatattgtttgta
1754	CLUST.002248_CP017982 effector>	MRKKVVPRNKAKYEHLASEYLVAGNSKLDQCSHASHDLYNRALYDLRQGFFKRNYVKG YCDLDQRFKKRYSARESMLYHSLFYVQSAQQTLKEVNTIWSAWLKALKAYQANPGKFT GRPRMPKYLAKGQRHVFFVTNQNAKVKDDYLIIPKLGFKLKLTPHLKAIQRVAFKPVY GGYKAIVQYKTNRDIDYLPDNGRYMGIDPGVDNAFACVANIQKAPLLVNGRAIKSVNQ YYNKERSRLKALQARYHQLESIVDTQQGKKPVYRETKAMRRITAWRNRKIRQFAHKAS KRIVDYALSCGANTIVIGNNKSWKRSSDMGRKNNQNFIGIPHKVMIDMIQYKANLAGI SVIRTNESYTSQTSALDHEKPCWENGSQSRKRQGKTPINRRIHRGLFQSNNGRLVNAD INGALQIIRKVFPKFSSDEGIEDAVLHPVKWSPLI
1755	CLUST.002248_CP017982	cguggguucaaaucccacau

	direct repeat 1>	
1756	CLUST.002248_CP017982 direct repeat 2>	auguggauuugaacccacg
1757	CLUST.002248_CP017982 spacer>	nnnn

1761	CLUST.002248_CP003642 direct repeat 2>	guuucaaucccuaauagggauuuugaugaauugcaac
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1763	CLUST.002248_CP003642 non-coding>	atgattgaagtacatcccaatcctgccaaagccttatctgacgggccacaatctttga caccagaaggttttgataagttgatgccagaattagcagtcattgctaaagcgatggg acgctgggaacaaccagcagttgccttagtgtaaacctttcttttgtgaggggaactg ctttgaatttttaccctttatagctggatttcatgatgctagttgcgcggatgggtgg gtgtagaatttcgatgctggaaaaaaatgcttggatctcaatcactgcaagggtttca gcctctaatcgcccaatatcgatccgcgcgatctctgaaagccttaaccttaaagggt ttcagccttttttttctgacccctattttcaaaccaacggctgtaatggtatattgat gatcgatccgcgcaactgtaccttgaaaactaaatatggtaaggtttccagaccccag cgttcctacatgacacagataccaccaaatacattgttgcaactcaagccattggctt ttgcattcttgaaaagaaatctgtaagcgagtctacgattcctgttaccaggagcaat taagaaatcaggcttcaacagattacgctaaaagaactaattttctgggtaaatctag caagggtgttaccaggggcaagtagtatttaagtaggttgggttgaggcacaaaaccc aatattatcaataaatttgttgggttctcacacggtaagcccaacttacaatttctc aagtgaaccgcattgatcataaaaatactcggtatgcgggaaagtcagggtctttaga cctgagagggaagcgacacgagcggttttaaccgccgtggtatgagtctatattatcc gtggtgtgggtcttcaatataacgcctaactgcttcgctgctaacattccctgctgta ctcacaaaataactttgtagtcgattatgatatggatatcaacgaaactctggaaagt agagccagtggctaaagtcaagaaaataatcggagtgcaacaagtcttgctgtctcct aacaatgagataaaagcgttattagagtacctttgtcaacaagcaggaaagctgtata acgcagcaaatattctcagaaaagtagccagcaatctcagcttagacttaggcttact gggtagacggtctttgacaaccgtagcgagagttagactttggaaactacctaagttt actctgtccgcagaatctcagcggcttcagccctgagactgtcaattatttgaattac atctttcgtaggggcacagccaatacggttcggttaacgtttgaatctgtggaagatc cccccaaccccccttaaaaaggggggctttagactgtttttagccctttttaagggg ggctttagactgtttttagccctttttaaggggactttgactctcttttaccccct tttcaaggggtcgccgcagacgggggatcttaacggaaccctattgggggcacagc aatgctcattggtgtcaacttaagctgaaagctcttccaaataacactttgagccatt atctcgttcccaatctccgacgcttaatgcaatcagtgcggctctgccgcttatacgg aaggcggcagccctaaagtaggcattcccagcccagaggctaggaacgagattttaaa agggttttcgcttaagttgacatctatgtagattgtcgtgcctctacatgttcaaatt gtctaacgtcgtctgctgccaaaaccagatgagcgacggctagaagaacggcccccgc taccaaaaccactaccagaattacgtcgggttgggctggagttcccagaaggtctgag tgtgctgctaccataaccggaacctgtggcgcggct
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1765	CLUST.002248_AZYY01000030-M direct	agcgcugcugcaagcaguucgcuguu

	repeat 1>	
1766	CLUST.002248_AZYY01000030-M direct repeat 2>	aacagcgaacugcuugcagcagcgcu
1767	CLUST.002248_AZYY01000030-M spacer>	nnnn

	repeat 1>	
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1951	CLUST.026133_S.9549BP-M direct repeat 2>	ugcaacgaccugccgaaucccacagacuguugcac
1952	CLUST.026133_S.9549BP-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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2111	CLUST.035812_S.0 LOFCB-M direct repeat 2>	cucccaaccacccacgcgccugugggggugcau
2112	CLUST.035812_S.0 LOFCB-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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2119	CLUST.035812_S.0 DN0N3-M direct repeat homology 1>	gauugcauggg
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2698	CLUST.046082_S.02FTO2-M effector>	MMAKKKPKHEEKEYVGAIRVQPVGIQAVDGESPKAFREAMEPIAVAVQQLKNVAMFAW YSWHRKVGNVQLVMDWVDEILAWDREVKPVAQKFVADTRQYEKDAAAWKKSPKGTRGK RPTKPKKLHADRPKCPVLPYPKACSNAIYHEVSGAIPLLNKRVVVLALNRMFSNLKTH QVAFRPGQWNQWTGFREWHVMLAGYGLFSQCHKPQPIPIDRDNCTLIPPDAEESRWRA LIRVDRVPTTTKAGKEVFRSTPWVVTLKTGGRHDAKIRNMLEKCHSGEWKFCGSNLVW RNGMFDVEVSYKQEKLEPIKADPNKVAVLVPGRKRGWRLRINGRSWWLGGKGSDRLVG VFRRQTAERKATFHASYRHGGTARQGHGRQTAMRGFYSKKNILARYQQQYNGRIVREV IQQMERHGVGTLVFRSPSGSVEKTRLLCTAGAGRKGGSWPWHQVDTRLKAVCHRHELV YESPRRKRRKREGSGGAKNPGTARKVATADGNKDWGDRSKANGRKKRANGAARRDLSK TATQKAVG
2699	CLUST.046082_S.02FTO2-M direct repeat 1>	gugaaaacgugugggagagggagagggauugcagg
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2701	CLUST.046082_S.02FTO2-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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	5XCV4-M direct repeat 1>	
2705	CLUST.046082_S.95XCV4-M direct repeat 2>	ccugaacaacacaccguuuaguucacccacugacac
2706	CLUST.046082_S.95XCV4-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2707	CLUST.046082_S.95XCV4-M non-coding>	gtgtcagcctgcggtgaactgtaccactgcaagaggtgcggaggcctgttcgacgacg acccggaagagggtggcgattacgacgaccgtgacccagggaagcgtttggagagaag agagcggacgaagacaaggaggcggtgagtattaccactgcacacagaacgtcttcgg atgaggaagacgaacgattcattggggcgtcctgacgtccctagggtccaagggagaa cccttggcagaaatggagaatagctacggacttcgcgtgccgggcagcactcaccaaa acacaccgtttaattttgtggggtattcgatggtaggactgattcgcatctctcgtgt tcgtaccgcaaagtttcgcgtggctttgcgcggtggaacaaaggagtttctggctagg tctggtgtccgtgaagccgaccgttacggaggatggtcttggttcgagtttggccaga agctcaagaacgcgtgtgagcgagccggcattgagtgcaaggacgcgagcaagatcga agaagacgcgagcggtggttgatatgggtgtggttttgtgtcgtgtttttggcaccgc tcgcaaagtgcattgcaacccattggcacgggtgatgttgagacggtgccaacaaaac atttaaagccgtgtgatgtatgcggaaagatgtttctggcaaaaccgatcacgaagaa gtattgctcgaatgcctgtgtcgggtattcgaagtttgtgtcacggttgagaagggag tttgatcatgatcgttccgaacgacttcaacccgagactggcgctgaggaagtggcag gccgaggcgaagacggcgagcgttaaccaacattacgacaacgcggtcgacctcgtcg cgatctacgaaagcgagtggttcaacgaccactacaagaca
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2709	CLUST.046082_S.B34L2J-M direct repeat 1>	auaggugauuggugcgag
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	34L2J-M non-coding>	cgaagagtttacgccagagcttgaagaagaatgaaagccactcggcttaggccgagca caaggggtcactcgcgaccctgaaggcgggaatagctgcggacttcgagagccgcgta gcgctcgccaaaccaatcacctttctattaaggagatcaacagatggctgtgcgtacc atgcgatatgagatcatcggctggcaaggcgatccgaaagaggccaaagcccggtggc gtgaaatcgccgatgactgccgcgaggtagtcaactgcatttggcagcaatgggaagt ctggcacgtttctcgtggccacgagcgggttgcctttgccgtcatgtgttcctataag tgcaaggacgcaggcattcattttgtaatcaagaagtctgcgagcggtccgaaaaaac aaggaccgaaagtgacgaaaaagtcgaaccgctcgcaaaaggcttctggggctgttgc ggcgaaatgagttacggcgacggggtggcagtggctagttccacttggtagtacagca tgccaaacaagctatacgacaaatgccgcatatgctttggacttatagcggtagaacc ggaggtgatcgtcaaaaagaaaaaacgtttatgtagcgagtgccgttttctatatgga tttatttcacgacaggagaaacgtgatggcaaaaatgaagtgggaagtaacgctgaag aagatcgacgctctgatcgcggagagcaacggaacgctctatgaccgcgtgatcatgc tcaaggaagtatgggacgatcccggcttt
2713	CLUST.046082_S.B34L2J-M direct repeat homology 1>	accaaucaccu
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2715	CLUST.046082_S.B34L2J-M direct repeat homology -containing sequence>	tattacggggttcgggttaaacgcgaagagtttacgccagagcttgaagaagaatgaa agccactcggcttaggccgagcacaaggggtcactcgcgaccctgaaggcgggaatag ctgcggacttcgagagccgcgtagcgctcgccaaaccaatcacctttctattaaggag atcaacagatggctgtgcgtaccatgcgatatgagatcatcggctggcaaggcgatcc gaaagaggccaaagcccggtggcgtgaaatcgccgatgactgccgcgaggtagtcaac tgcatttggcagcaatgggaa
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2717	CLUST.046082_S.0WGLO2-M direct repeat 1>	aguggagaacaccgcuagaugaugggguaacuacagg
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	direct repeat 2>	
2719	CLUST.046082_S.0WGLO2-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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2721	CLUST.046082_S.590OHR-P effector>	MREFKESVRVDRIEIKGVRWIAESKRTISPEAQAWHAMHERWLALSEEIQCISNAVWRHWTSWHTAAGNDVAIRAYMHDLRLWNQTEKKDRVGDKPKCTVTLWPKEFASHLMQKLQADFPSVNARPLGLAVNKLMGTIKNGRGVLSAFPRSMQVLGDEVGPPSFCYAQPIPLCNARCKMVPPEDDKGDWQAEFRIDRIERDGAQAVSTCDTVSLKAKARPRATLEKLEKSKYHRNGGMLQYDRRKNAWFLMVGYRLPIIRSGALDETRTATVRAGIKCPLIVEIDGREIPVGGYGDNVAAIRAMIDRERQSRNENYRWSPGGSKGHGRETAQGQRMADFVNRWLRFCTNMNYTLTAKVIGLAQEHNCGGILFHQPTAETQGEYLLFSAGKSEQTRIASGWPWHRLAQIIQQKANQNGMETLVFQEKKVAQQPNSEGVATDEVESS
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2724	CLUST.046082_S.590OHR-P spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2725	CLUST.046082_S.8GJBZA-M effector>	MENSYGLRVPGSTHQNTPFNFVGYSMVGLIRISRVRTAKFRVALRGGTKEERSARYKDLVSIVDKFKRASNRLLREWLLWHEANGSANAIREWLDTPRQDRPKFTLQCVSKDNAARQREAIRRLYGDINGRCVDLMSQKIKRNLESKSRTVPSLKAWWSILLDNENVSSYVTDIPVPIDKANWKLCVEYDGNGRPTYLSKCNLGRYRVIGKNGKEKTVGEVYDFEINTQGKENKSLAWIIKTHIDEESRDVPDDKRTVVVGGSSVKFYSGKNQWYLLLSYTCYENVRPMDSSMSASLEAGDDVPFVLSLPDNRNKSGVYAKWIHSRGADGIGEVRSMISAQRIARMANYRHASGAAKGHGRKRAMKSWEGKLAQRWKQYQNNVNLKCAREITDELIRRGIGTLHYSLPTKTAAKTKFLARSGVREADRYGGWSWFEFGQKLKNACERAGIECKDASKIEEDASGG

2726	CLUST.046082_S.8GJBZA-M direct repeat 1>	cgugucaguggugaacuaaacgguguguuguucagg
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2739	CLUST.046082_S.07180U-M non-coding>	gaccccgagccgccgccgcagaacgtgccggagctgctgaaggctcaggagcggcagtggcgtcaggtcggccgtgcgaccgggcagagcctgccgctggtcctcagccaggtcgcctcggcgctgcggcgactgggctggaaggggtgagttgagggttgagagttgagggttgagcgaccgcgcaagcggaggatcagacggaccccaaggagttttgcgttcggccgattggacggccggaggcgagaatagctgcggacttcgagcgccgcggagccctcgccgatttctgacctgggttgccccggggcttcggcccccgggcgcccttttccgacgggaggcgaatatggcgaacaacgccaacaagaatgatcggctgagcctgacgcagatgaccagcttcgaggtcaagacggtcggcggcgactggcaggaggtgaccggccggtggcacgagctttcgcgcgactgccgcgacctggccaacttcttctgg
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2741	CLUST.046082_OVQ	gugugaagacagauagagacaaggugugguauucag

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2743	CLUST.04 6082_OVQ U0100679 1-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2744	CLUST.04 6082_OVQ U0100679 1-M non-coding>	actcctcgggagcccaataaatactgggccgactgaacggccttatggtcgagaatag ctgcggacttagagagccgtgtagcactcgccaaacacacctttcaagaggattggta atgccaaatcgtaatgacagaaagatgcgggaatccattcgagcggcacggtttgagg tcgattcagtcgacggggccgagtggaaggtaacggtgacgcgatggtttgcaacgat ggatctttgccgacgtgcgtcaaatctttactacattgtggagtgtggcaagtcgagc ggtccagagcagagcgaaacatcagcaccgctcgcaacgccagaagtgactgacggca atgaagttacaacgcagtcaagaaaggggcagcgaaaagtaatcgcaaaacaaaccg gaaaaagtgaaccgctcgaaagtgcgtgcgtaagtggcttgtgctgaatggattgcga gtccatccgcgccttctgcaaactggtccactttgcaccatcgttttcgttgcaatag ctgaaacttaaaggtgtgtattcaggttctataaacgttttccagacttttgtcgcg gacgggtgtaagaacaaaagaatacaaggtgtgtattcaggttgacgtgccacagatc ggtggcgttgttagggccgagtgtgaacacagaaattcaaaggtgtgtattcagggcg catcctgggtctgtgtgcaaacaacaggtgtattcagcatgcttatcccaattcgctt aagtgtgtgtgaactctgcgaaacgccactcgcagccaaaagaaagcggagacgattt tgcgggcactgtgctcgactctctgccgtggtggaagagatccaacagttggagatgc gtcaagatgatgaactacaaaaagatcgaactcgaaattcaggacttcgtgaagcagg gacaacacacagcgtgggagatcgcgaccaggtgtgtgaagctcttgaacgaatccga cagctacgctcaaagcgtggggctgaaaccagacgacgtt
2745	CLUST.04 6082_OVQ U0100679 1-M direct repeat homology 1>	acacaccuu
2746	CLUST.04 6082_OVQ U0100679 1-M direct repeat homology 2>	aaggugugu
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	repeat homology - containing sequence>	tcgattcagtcgacggggccgagtggaaggtaacggtgacgcgatggtttgcaacgatggatctttgccgacgtgcg
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2749	CLUST.046082_S.0RT0AW-M direct repeat 1>	gucgcaguggaugcaggaauggguaugcacugcgg
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2796	CLUST.046082_S.0TFDO5-M direct repeat 2>	cucgcaucgauuguuguuguguucggucacu
2797	CLUST.046082_S.0TFDO5-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2798	CLUST.046082_S.0TFDO5-M non-coding>	acgttatcgcagttgatttcgatgggcaggatacgtggggtaaagctgtttactggtg gtcatccaaagtacaagcggttggacctggatgaacttattgagtctctggagtacgg cgcgggtttttgtgccgcaacacagagctattaaaaatacatcgatttagaagcgtca ccagtcgtacagactggtaagcgggatcgcacccgttaaggcgagaaaagctgcggac ttatagagccgtgtagcactcaccacgattgttgtgcgggtggctcggtgaaagccga gtcacccctttttaaaaaggaataataatgacggttcgtaatattcgggtcgaggtga tagtgcccaaggaacgtcgcgaggcgttgcgtgatacgtcggtggcttgccaacgtat gcacaatcgactgtggcagatttggctttgccaccatagcaaccatggttccgcagcc aatgaggaaggtttggagtatggaaaaaagccaaaaacaaaaacgaaaaagtcaacga ccaaaactgccgccggtagcgtgcgtggcgtgcggaaggctaatgaaccaaagcgtaa agagcgttctggaggatcagttagcggtttgcggtaagtgtttgtttcttaggaatgt atacgggaggttgcgagatggccaagaagtgggaattgaaaatgaacgaacagcgaga actgcggaagcaggggattgccgttctgtatcagcgggtcgtgttgttgtctgagtgc tacgcggataaaaatttttctagcgtggtgcgaggctcacaaccgtagtgagatgtcat cggaaaagcgaggtccatctgatcgcattggatggaaggatcgttgcctggctgccga gaaggagatcgatcggctgcgtgctgaactcgacattctgaatcgcgctatggaaatt gcagggttgaaaaagttagcagcttagttttttgaggtgctcgcaaaacgtgccgta catccagtgatttattgcgcgttttgcgtgtgctgcagccacctaacgtaagccagca gtcaatgaatacaacagcaattaatgcgaaaaaggagcttcgtatgggcaaagtgaat

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2801	CLUST.046082_S.0TFDO5-M direct repeat homology -containing sequence>	ggagtacggcgcgggtttttgtgccgcaacacagagctattaaaaatacatcgattta gaagcgtcaccagtcgtacagactggtaagcgggatcgcacccgttaaggcgagaaaa gctgcggacttatagagccgtgtagcactcaccacgattgttgtgcgggtggctcggt gaaagccgagtcacccctttttaaaaaggaataataatgacggttcgtaatattcggg tcgaggtgatagtgcccaaggaacgtcgcgaggcgttgcgtgatacgtcggtggcttg ccaacgtatgcacaatcgac
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2809	CLUST.046082_S.3 X5BXO-M direct repeat 2>	caucuccauucuuucaugcacu
2810	CLUST.046082_S.3 X5BXO-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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2812	CLUST.046082_S.5 G75YW-P effector>	MSKLKKPAEKKPRKKKPEGLTKIIRVQLCGIDDGFAEEKERLAKISLQMQQIANDFHS QWFSLHLEAGSPTALRKWIQEDKEWAQKYGELDKAQKAQKRKGKKELLPSFDVKIPPR AKCPVQPYSNKMANEIYKRLTTQHCNLGTKPIGIVSRRLSSTLLSTPATKSKYKRWFM ILCGYGEYSQFSRPQPVPFYTANSNFVVPKSNNDPWKLIVRYEKVDGQRTLRPMVFKL RTGGRHLAPIRKVLWKITSGEYIFGTSQIIKCENTGKWYADICYLMPGVVAPSDSKKT AVVSGGRYHGVMLRIDGKTHMKLRSCRHIKHARRSLTLQRFGKSESYKYASSARKNHG RKVHNWRRKSERNWRNQTKTFNNTWAAEVIGRCVRAGVGQLVTYQPTGKWRDTRYLSN VGKIGRNESTAWDWYHMQQQLEAVGAAAGMKVIARQGGKPRKKEVNR
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	repeat 2>	
2815	CLUST.046082_S.5G75YW-P spacer>	nnnnnnnnnnnnnnnnnnnn
2816	CLUST.046082_S.5G75YW-P non-coding>	gacagtgtttgcatcgattgcgatttcggtgcgtttatcgttgaatttcgtttgggct ttccacccgtattgattatacatcccaatctgactaaaagggattgcgtcttttggac gtggtgggtagatgtaccgtttgcttagcttcatttttaaacctctacccttttatag cacgacaaatatggctatttaattaattaataccagcgtcgtgctataaaaaactacc agcgtgctaaaggattatatcagagcacatatgaataaaaatcaaagaaatccgagat gacacttcttcgtgaataactacaggaggatctgcaatatcttttcataacagccgaa tggagaatagcgttcgttcccaggtaactacaggtgctccgataacgtggcccttagc gtcaatggagaatagcgttcgttcaaaatgtaaatggagacgaaatggagaatagcgt tcgttcccaggtaactacaggactacaggcttcacaagagattaatcgaagttaacta cctattaatgtgatgctaaaacagtccagataaactatgatcaccaaatagaggcgtc ctgtacgtctcgaaggcgagaatagctgcgggcattccgtaccgtgttagctctcgcc agagttacttttttaaccacccgttagcgtactacaggcccctgaataaagccgctta ttttgtgtaggagactatagtgagtaaattgaagaaaccggcagaaaagaaaccacgt aaaaagaagccagaaggacttacgaagattattcgcgtccagctatgtggtattgacg acggctttgcagaggaaaaagaacgtctcgccaagatatcgcttcaaatgcagtctaa tgtcggaaaaattggccgtaatgaatcgacggcctgggattggtgccacatgcagcag cagttggaagcggttggagcagcagccgggatgaaagtaatcgctaggcaaggaggta agccccgtaaaaaagaagttaatcgataattgtttttgtgctataagtttgcagaatc actaattgaggcgtcctgtacgtctcgaaggcgagaatagctgcgggcattccgtacc gtgttagctctcgccagagttacctttttaacctacagaggacgatatggccgactt tcgagttgttaagaacaagcgaatcagtttacttggcggtgacgatgactataagtca cacaaaaagtacatcggcactcttgcttctgatattcagagaatcgtcaacgatttta tgtcagcatggttgcaaattcattttgaagctggcaatcatcttctcgttcgtgaatg ggcagaacaagatcgccgctggctttacgagcctgagactcgcgttggcccccgtacg cggtgccctgtcgatccatgcagtaccgaaatggctcagcagcttgacgaaatcatgt ctgctacatatccctcgatgaacaagcactgtaagctagcaaccgagaaagcgttgag aatactgcagaaacatgggtataagtcggcttatcctcgctggataacagtccttttg ggccgaggaggcctcctacagtcgtctcaacgaagtagcattccgtttcataaacgtg actgccgaatcatcgttccgcaga
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2820	CLUST.046082_S.0OJK53-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnn
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2822	CLUST.046082_S.0OJK53-M direct repeat homology 1>	acaccugucgu
2823	CLUST.046082_S.0OJK53-M direct repeat homology 2>	acgacaggugu
2824	CLUST.046082_S.0OJK53-M direct repeat homology -containing sequence>	acccccaagcggattcgggagcagacgaaagactcgttcaaaccaacgaactagagga gttttgaggcagcccccgaaaggggacgggccgattggacggcccaaggcgagaatag ctgcggaccccgagagccgtgtagccctcgcttaacacctgtcgtgcggcgatcgggt tcaccacctggcccggtcgccgcgacttttacgaggaaatgatcatggccgaattga ctgccatgcggatcacatcattcgaggtggccaatgttgatggtgattgggggagac caccaagcggtggcatcaact
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2834	CLUST.046082_UINC01018500-M direct repeat 1>	aggcaucggaauguguaaaugcag
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2837	CLUST.046082_UINC01018500-M non-coding>	gaggtggacaacaagaagccccgagaggctggctggaaacagcgtttcgaggaacttc aggagcaatatgacgctctggagcggaaattcgaattgaccgaggctcaacttagcga gcttcgggcagtcgtcacgcaccagaccgtgtaataaatgcggcagttagagccgcgc gccctcgactgcacgggggaaggtgagaatagctgcgaacttcgcgagtcgagtagca ctcaccattacacgttggccagtccaccttaacgggtgggctggctttttaacacaa gcgaggagagcctacgatgcatacagtcaagttcgaggttgccaagtttcaaggcgac aatcgtaagcggcgagcgttcttcttggaactggcgcgtaactgccagcgagtaaaga accgtgtcatgcagcattggctccaggcccatgcggaggcgggcaacgtcgtgcagga cgcgtggtgccgatcaataacatgtaagtgcaggtggactgtgcaggcgggccggtaa agaagaaaaagaagaaggcagtgtaagtgcaggtcggcttgccgtcagcgaatgtaaa tgcaggagcgatgcaagtcattgagtgtaaatgcaggagatgtaatcaagcagcccga caagtgtaagtgcagggaagggatatggccacttacccgccttcgtggtatctcgccg ctggcggtcatccccaagtgtaagtgcaggacaacccgtggaggacaacccgacatca cgtgtaagtgcaggcaccgcatcgcagattgaatctaccgtgcaagcgatggcgacgt gtaagtgcaggatgcggcaacgcgaaatctacagtgtaagtgcaggggtttgtgatcc atcacgacgtgtaaatgcagacacaagacggagcattatagatgtgtaaatgcaggca agcggtctggtcggggccttactaatcgtgcgtgtaaatgcagtaggacaaaagtatc gtgcgtgtaaatgcagtgagagtcagatagatcgtgcgtgtaaatgcagtgggggaa ctcagacgctggtgcgtgtaagtgcagggtctaccaggcactggtgcgtgtaagtgca ggacgggtgtaaatgcagatgtggtcctttggcgcgtgtaaatgcaggtagagctttg gcgcgtgtaaatgcaggataggaatcctatcagaggatgtgtaagtgcagggaataat gtcacgaactaagacgtgtaaatgcaggaaccgtttccgtctctaggtcgccgcttaa tcaggcatcggaatgtgtaaatgcaggaaaggagcaggaaaggaattgtcgccgctta atcagacatcggaatgtgtaaatgcagttagccctgtttgcgtccaaatggattacgg tagattaggcatcggaaagtgtaaatgcaggtttcttttcgtcgatccagatgcgagt atgtcttatgagtattcttagtcgttcacaacttgaaaagattgaccccggtggccac ggccattatcaggggctgctgagtgatctcaaggaaaccgctctccactttcaaggga tgaccgacccggaagtagccgagatcgacaagatgcgtgtc

2838	CLUST.046082_UORX01017215-M effector>	MAAGKKRKTNSNGDNLRAAVRVAKCEVDWGSSVKDMNAKTREHYEATTKRWHAATRLV QEISNCFYDYWLAWHVLNQSDIKTKAWLDERQRVRDAMSGQPEKIINAALKEQVGPCP VETFPPDLMDSKRPTSFYRVLTIRFGELPAHIVSVILNGLQGKLTGKAAHGSLPKPTA MFLHHERVPNFTRPLPIPFVKQDCTLRKEGDEFYIDLKVWRVETTSKKGQPKMVCLTD SIKLRTKGAKCANERAMLSKIFTGEWEFKGSTLQWDDRCRKWLVNVCHQRPSHVMPVD PSKIAYLMAGCRNAFSVFYRDGKRWRRKWFQGRGLHIIEMRRKLWEYRAERNANYRHA TARKGRGFDNANRWRATSAQTWKYFVRRVNHNLTAEVVKWWYGALVYKQPEGRYATSR FVAGEFKNSTWEFYQIGSQLAYKCQDAGIAFSVQKVGASADVATGVLGDARDSSDVTG SDATQINKIGRNAGRQQDRSRKAAGSMSRQ
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2840	CLUST.046082_UORX01017215-M direct repeat 2>	ccugcauaacccuuuugauu
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2845	CLUST.046082_S.2 OME3E-M direct repeat 2>	cucgcaucgauuguuguuguguucagucacugcugc
2846	CLUST.046082_S.2 OME3E-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2847	CLUST.046082_S.2 OME3E-M non-coding>	taaggatacgtggggtgaagctgtttactggtggtcatccaaagtacaagcggttgga cctggatgaactgattgagtctctggagtacggcgcgggtttttgtgccgcaacacag agctattaaaaatacatcgatttagaagcgtcaccagtcgtacagactggtaagcggg atcgcacccgttaaggcgagaaaagctgcggacttatagagccgtgtagcactcacca cgattgttgtgcgggtggctcggtgaaagccgagtcacccctttttaaaaaggaataa taatgacggttcgtaatattcgggtcgaggtgatagtgcccaaggaacgtcgcgaggc gttgcgtgatacgtcggtggcttgccaacgtatgcacaatcgactgtggcagatttgg ctttgccaccatagcaaccatggttccgcagccaaggaggaaggtttggagtatggaa aaaagccaaaaacaaaaacgaaaaagtcaacgaccaaaactgccgccggtagcgtgcg tggcgtgcggaaggctaatgaaccaaagcgtaaagagcgttctggaggatcagttagc ggtttgcggtaagtgtttgtttcttaggaatgtatacgggaggttgcgagatggccaa gaagtgggaattgaaaatgaacgaacagcgagaactgcggaagcaggggattgccgtt ctgtatcagcgggtcgtgttgttgtctgagtgctacgcggataaaagttttctagcgt ggtgcgaggctcacaaccgtagtgagatgtcatcggaaaagcgaggtccatctgatcg cattggatggaaggatcgttgcctggctgccgagaaggagatcgatcggctgcgtgct gaactcgacattctgaatcgcgctatggaaattgcagggttgaaaaagttagcagctt agtgtttttgaggtgctcgcaaaacgtgccgtacatccagtgatttattgcgcgtttt gcgtgtgctcacctaacgtaagccagcagtcaatgaatacaacagcaattaatgcgaa aaggagcttcgtatgggcaaattaaacatggcagtactcgatcccattacggtccagt gctttagccagacgtacttggttggcctgcataacgcgtgcgaggtcaagcggacaat cggctgcttggcacggcaacttgcgacgagcgaaggctgga
2848	CLUST.046082_S.2 OME3E-M direct repeat homology 1>	cgauuguugu
2849	CLUST.046082_S.2 OME3E-M direct repeat homology 2>	acaacaaucg
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2851	CLUST.046082_S.1 NLO7U-M effector>	MRCLKLEIAELDTDSRRRWWSLCDQAKQVVNRIWRKWLVYHSQNDSELKLRTFLNSLA AWNAADKKTRGEKPKNPVNCITNDLWNAVYADLRATFPDWHTRPLTLLMNSERGKITA LKASKGSLPGWVAILLDQQGLPSSTRPIPVPFDAANTKVTTSDDESVQVTVNLERPEI DGKKQTISVTFGVITTGKARRYAEPIQAVATGTHKLKGSSVMYDQGRKKWYMLVAYEP CGQEKPNVDPTKAMILRAAYRTPWRVRIAGRSWRVGSDGKFIAERRREVLMSRWNRQN NYRWAATSTKGHGRERALQSPMKLSRSWNLFVKTYNQQVVAEVIRQAVSRGCGRIVLL KDSPGRFLEKAGKVEGRHDSTAWAWFQFEAILKDHCHPLGIKVETRKASGKVKAGGEA A
2852	CLUST.046082_S.1 NLO7U-M direct repeat 1>	gaaaugggacguaaaugcagg
2853	CLUST.046082_S.1 NLO7U-M direct repeat 2>	ccugcauuuacgucccauuuc
2854	CLUST.046082_S.1 NLO7U-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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2856	CLUST.046082_S.0 PBUC3-M effector>	MSNDKFLRVLTVEVSRLSDDKDEHWRQFRELESLMQQVQEIQNAFFDHWRAWHFENGS AAKIKAFHAAWKEHLEAKRPKSERPKLDVHPLSSELGKRIYHFIVKTWPNVHTRVVAL SMNRLKQLVMSSKSAHGNWPAWHSWLLFRQQIPMFTSPCPLPFSKENLAMFSPSERDG QHSLKCSLSRHPVAGKSMQKSVVYNLTIWDKGRRMASRRITLAKIVRGEFEFCGSQLF IKNGKLFAAIAYRQDKPSRSSGNGVAVVVASPNTPLRMRAGGRSWRIGGDGRVVATVR RQLMGQRWSRQQTYRVSASSARKGHGLHRALDKVTLLSNRWRDFVRTYNRNMAVEICK RAVATGCGVVFLSKRSDDSRWLSRAGKFDCRDKSGWDWYGLEKTLRDKAVEFGLEVET RESKRQPDSAEKVVTTNQVNSTVI
2857	CLUST.046082_S.0 PBUC3-M direct repeat 1>	ggugaauucgacugugauuuaagugguugaugcagg
2858	CLUST.046082_S.0	ccugcaucaaccacuuaaaucacagucgaauucacc

	PBUC3-M direct repeat 2>	
2859	CLUST.046082_S.0 PBUC3-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2860	CLUST.046082_S.0 PBUC3-M non-coding>	gtcgagatggggttgctgaatctggaagaggagtcaccgcacccggaactgttcttca aacgagacgttactttggtcgcggaagagatgtttgcggcgaggttcgcgccaaagac cggcgacgacggcgacccgttttcgtgggattgaaagaaaatgtatacatttttggtg tttcttcattgattccgtggttggcctcgataagctgcctgcggcactggccgagatg gggaacctgcaagcccctatggcgagaatagctgcggactccgagagccgcgtagcgc tcgccaacaaccacaaccaataaccagcgaagcaaccgcttcgctgagactctcggcc agtgccattttccaatttcacaggaatgcacaatgtcgaatgacaaatttctgcgtgt gctcacggtcgagatctcccgcttgagcgatgataaagacgagcactggaggcaattc cgtgaactcgaatctttgatgcagcaggttcaggaaattcaaaacgctttcttcgatc actggcgattgccgaacgtctctcgcgttctctggtgggtaaattcgacagtgatcta agtggttgatgcagtatccagcgttgcaactcggctggcgaaaacggtgaatttggcc gtgatttaagtggttgatgcaggaaggacctccgtgtcagtctgaatttctgtggtga atttgacagtaatttgagtggttgatgcaggttgagccattggtgcaatcgagccacc aaaggttaactcgacagtgatttaggcggatcacgtagatgccgacgtgcaaattatg ttttcggttgattgatcgcggcaacttctgtcgcggttgtgtttcccttcgctccttt gcggagcgtcttcaggaggacttgcgaaatgtctcgtcagaccagtgtgggctacaaa aagaaattgatcgtcgcttcagaactgcggacacatggaagggccgcgctctttcagc gggcgactctgttggtcgaggtgtttgaggaccgagaatttcgagcagacaacgatca gttc
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2863	CLUST.046082_S.0 7OOX0-M direct repeat 2>	gcgcgcuaacguccgcccg
2864	CLUST.046082_S.0 7OOX0-M spacer>	nnnnnnnnnnnnnnnnnnnnn
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2866	CLUST.046082_S.3 WWULE-M effector>	MREEERMGIKCTRVEIRRLNNDAENDARRKIWRSIATECLRATNCFWETWWQWHLAGQ SQTALATWIKTLIAWHDADPKTRGKKPPCPVKAMAKEASNIIYHRLTETCQNLHTRTI VLLTNRLTKRLTSQRSAHGSLAWWCNLLLYRERTPASIDPQPIPFDKANSKLLPPTES GGNWGIELRLARVAKGISVSQLCELWTSGKKRHSIATILSRIASGEYIAKGSQLLLVR GKWYAALSYQMPDADKVSLSAAKRAILLPGRNDPWLLQIEGGVYWRGGTGRHIAAVRK RVIQERRERQENYRWAATAQKGRGRPRATAAWTRLRSVWTHCCTNYNRHVAKAIVDEC VRRGVGQLEYWQPEGKRSDSRFLGRAGKFDGYRDQTTYPWYQMALLLSDKCVEKGITF AVRKFGHETKENPADDVLQTV
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2868	CLUST.046082_S.3 WWULE-M direct repeat 2>	auuggcccggcggagaucggc
2869	CLUST.046082_S.3 WWULE-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2870	CLUST.046082_S.3 WWULE-M non-coding>	ggctatcgggatcagaccacgtatccctggtatcagatggccttgttgctgtcggata aatgcgtcgaaaaaggaatcacgttcgcggtgcggaagttcggccatgagacaaaaga aaatcccgctgacgacgtactgcagactgtgtaggaggatcgttgtgatcacgccggc gcaggtgctggctgatcatttaaagctctgtagtgagtgttgcggctttcgacaagtc gcgaaccatctgaggagggtagagcggtatgggaagcaaaaacgaaaagacatggacg atgaaaatggccgaggtcgatgaactgatcagccatgacgcgggctcgttatacgatc gcgtgaaactgttgatcgagatctacgaggacagtgagttccgtgcacactgcaaggc acgtatctccgcggggccgatctccgccgggccaatatcttaggggccacattttgcg gcgcaacaatcgacggtgctgtcctgcagcctgaagacattggtggtccaggttggat actgtgcgctctgaccgacctcaagtggtcaactattgcggcagagagacagaagctc ttgacacccagctctccagtgtgagatgcgccatggctccagcaccagaaatcacgat

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2871	CLUST.073508_S.7WI0O6-P effector>	MFVYTLKLDANNKLKQQLGRRFKMAQDIYQRTIHEILKRDDKQKKDPRNKTIKAIYRQ IHALKDQITELENDLSNKSKKEQTAIKKVTKDLTKQIKELEAEAKPIFRQMAEDYDIV GKYTFGKYANDYRNARNYSFYIPSDAAGVLGMRAWSSYEKMKFNKGAKKINRYPQLNS FETMKKTGIMIKDGLLKMGTKNKKIEVPVIYKNDEFEQEVFKNELKYNRLLRKFENGE VQYYVQMIFDGIPPQRMDNYIKGTVGLDVGLTKVAISTPNEVKILPLAPNLQNFDKEI RRLSRKLTRQRIANNPDNYNADGTIKKGKKVWINSKGYLETKHKLADLKRKQAEYRKI SHKELANAIIQMGDKFIIKQSNFEKLKEKSRVDRKSTTGKNLSKKRAGKTINSHAPGF FIQQLLYKAEFQGKETQVITNKDFNPYEYNHASKEVIENKAHLKSINIDGFEVQKNLY AAFLVSQYENMENDNVIKSNFEKFLQNQEFYIENIA
2872	CLUST.073508_S.7WI0O6-P direct repeat 1>	guuuguuuagcauggugccaaaag
2873	CLUST.073508_S.7WI0O6-P direct repeat 2>	cuuuuggcaccaugcuaaacaaac
2874	CLUST.073508_S.7WI0O6-P spacer>	nnnn

	effector>	VATSSRLGTNLEELAPDIDKNEKLIAKLQRKLDRQRRANNPNNYNPDGTIKKGRKTWH DSKNYLKTKKKLAELSRIQAETRKLAHNNLANKLVEIGNEFVVEKMNFADLAKRLEDG EISKITGKNLSKKQFGKLIGRRAPAALIEKLRYKAEFRGSKFILVDNEKIAATQLNHL DGEHHPIKLSERVKMVGEHPVQRDLYSAFILEHVTEGGENVDLKSCGKDFNRFLHNQE HTMDNLTNVTPSMGVKRFKAIKNKK
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2886	CLUST.073508_S.2XBYJV-M direct repeat 2>	aacagaaugguuccaaaa
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		gtacagagcattgaatgaaaaggcagtgtacagtaccaaccttgtgatttgacccctt gtaaggttatggttttacaaggttccaaaggagtggcaataatatttcagattttcag ctcccttgtaaggttatggttttacaaggttccaaaggatatttgtttaatgcgtttc agacgatgatttttccaaattggggaaaatttggatttttttatataaaaaaatggtac tttagaaatgaaatatcggggtgagttggcacccttttttgaaaaagaaataaatcgg tactggaaactgtacagagcattgaatgaaaaggcagtgtacagtaccaaccttgtga tttgacaaaatctatgttttcgattttatcaacgcttcattgttcgacttccttattt taaatatctcacaatttttttctccgggattttcccggagtttttttttaggtcaaaaaa tcaatatcgtaattccatcatctcagttccaacatcatcgtagatcagaaaaattccc tttaacctctgcttgtctccatttttcttttgtgaaaacagggtgtaccctatttttac tcat
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2897	CLUST.073508_UPQM01006119-M effector>	MDKKEDEKHLFIYTLKLKTSQQDRERLNKRFRMAQDIYRKALIEVHKRYLKFKKDPLY KKAIKLDKGDKEKTALFKELREKHQLQGKFTFGQFANDYRNARNYSPYIPSDVATKLG FRAYEAYEKIMFAKGAKTVDFRKVVNSMEGKSDAGITIRNGIFKMGTKTDRAKFSCPV IYEEDNFEEEILRNKVKFVRLVRRLEYGQYNFYAQVILEGTPVLKNPQNDLKTNVGID IGLTSVAVATDYETQLIELAPSVKNNDKKLAKLNQKMDRQRRANNPQNYNPDGTIKTG RKTWNDSKRYLKTKAQYQELERLGREQRRHAHERLSNQIVEMGDSFIVEQMSFAELAK RHETPTKNESGKFLSSAGFGKHVKRRAPASLISLIKYKAFFRGRKFLEVNVDDITATQ LDHSTGERKPLELSQRIKIVDNQVVQRDLYSAFLLKNVYPSAIGVNLDSCKKDFPHFL SLQEETMENLEFEKTTPSMGLKKWKSLKKKHK
2898	CLUST.073508_UPQM01006119-M direct repeat 1>	guuuuggcaucagucuguuugacacggugcuaaagg

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2901	CLUST.073508_UPQM01006119-M non-coding>	tcttgaccaaaatgatttacttttagattggtcagttaatgctccaatataaacaata caagtccgtagcatcttattgatatgattagttaaaatgcctcttacttcattgtctt caatataagaaggcatccctttttatttcaagcatagtttacctacttcttctttttta gttataatattagtatgccataaatccaactaatttcgtctatttttctaaaaaagcc ctcgtattttccgagagcttcttatttttattatttgtgtgaggctaacatgcgaga tgttttatccatttcgcgcgtgaccttgcgattttcttttctgatttcttttaatgtt tctggaaaactcatacctatatctcactttctttgtttcttactaagattgtattata ttttttccgaaatgtcaacatttattattgacatttttaaaaaatgttgtatgattt cattataggggttcatttagcaacctctttaggcagtcgttaaggagtacaggggtat tcttggctgctaagagtaaacggtcttagtacatgaaactgaaacgcaatgtagaaag tttactttctagtaacgtcagggcatctactattgccgaactcaaccagttaaataga aaaagccaaaaatagacttacgagaacatggtgttaaaggtattgattagttagaata tctaccgcttgagctttaacattagccttttaacatggtgctaaaagaataactatg gagaaatcatcaaagacgaagttttagcattagcaacataatgctaaaagtttctaat cggtagtgttttataattatgtgaggtgttatatggacaaaaaagaagatgaaaaaca tctttttatttatactttgaaattaaaaactagccaacaagatagagagcgattgaat aaacgttttagaatggctcaagatatttatagaaaagcacttatcgaagtacataaac ggtatttagcaatcggtgttaatcttgactcttgtaagaaagattttcctcatttctt atctttgcaagaagaaacaatggaaaatcttgaatttgaaaaaaccactccttcgatg ggcttgaaaaaatggaagagtctaaaaaagaaacataaataaaagtttagagaatttc taagttttttgtctgctcttgcgtttcaaatcttgtgacgtttttttgaagacttcca tgtattgttggtaatggtaataaatgctattactttcttcttctaatgaattatgcaa ccaatctaaaggcgaataaaatttagttttata
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	5-M direct repeat 2>	
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2910	CLUST.073508_S.9DHXZU-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2911	CLUST.073508_S.9DHXZU-M	tatgggcaatactctccgcagtatgatgaaatacatcagttgttatttctcacgccat tggcaacgccttctggtaatatgagttccttaataacatacgaggagagactttgcaa gatagaatcgataatcaaagaaactatttcttaacactttctctctaaatctgcaaag

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2921	CLUST.073508_S.33E4Q3-M direct repeat 1>	gguuuuggcaucagucuguuuga
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2923	CLUST.073508_S.33E4Q3-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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2926	CLUST.073508_UPJM01000070-M direct repeat 1>	guuuugaaacaaucauguuuaacaugguaccaaaag
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2928	CLUST.073508_UPJM01000070-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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		tgtccccctgttatgttatattactttctttaaatttttggtgggggtttatcccc ctattatggagcgatacccaagttggctgaaggggcggtcttgaaaaccgctagacg gcagagatgtcgtgcgtgggttcgaatcccactcgctcctttctaccgttactttgga aacggtaaatgccataattatgattatcataatggcattaaacatttaattaaaatta ttctttactcatatagcaatgtttttaatatcttatgaaagacaataattttaataaa taacatgttacgagttaaacaaaagcgaagaaacactttaatattattacacgcaaca tgattacaaaagttacgtccagttcgttcaaaaaaaacttaacattttaatccaaaag gctgcgatattgtctcaataaaaattaacatgtttcaaaagcgctatgtagatactta aaaaataaacttaatataaaaatccaaaaggtcgtataccaaatataacataaacgga atttagcgcagtttggttagcgcactcgctttgggagcgaggggtcgcaggttcgaat cctgcaattccgatagagacagagtttattcaagattaaatctaaaataagcatctct agttgattagtgttgaatctctagtgtcagtaggacaaggttttagacattgactgaa gttatgtcctagacttcactaatcaaaatcagactcgataactcagctggtagagtag cggacttttaatccgtaggtcgcaggttcgaatcctgctcgggtcataaaaccgttcc tttggaaacggtagacatcctaaatgtaaatattacattgatgtcagaattttatgta aaaattattctttaatcattaagcaatgttttattctaaaatatcttatgaaaaacaa taattttaatatgaacatgttgtgaggttttagaaccgtcatatttgacatggtgccg aaaggcgcttgctcaagaagttaactctgaactagttttagaaccgttatgattagca taataccaaaaggctagtgcaactcttatgagtttatcatatctaaagcgataccaaa agagtcaatttttttgcttatctaatcacatagttttaaaaccatcatgttaaacata ataccaaaagtggcatgataaggatattaatactggaatagctttaaaatcatgttta ccacaacaacaaacggtgaataaccatcataacatctaaatgtcgcaaaaaggtgtca aaaacacctaaagcataataattaacaaacggcttatataaaaattcatacattatat tagaaacaaattaacaattgaaacaaaaattgtcccaagcatgacactaaactgccaa tgaataatattagaaagacatgacttctaactgaaaattattcatgatttttcatta tatatctccaaagcaaaggggtttggggttcaactccccactccctcatatatctaat tagcaattagatagaaccatattaatagggaaaaaataatatggtgctcctatatgga ttcccaatgggtaactatggaataggcgtaccaatgaatgtacgttgtgaaggaacaa ttgttctaattgttctgtatcacagaaactctatccgtggtaatacggttgaagtatt tcatttccatttatttatattctcctaacaaaagacctttgttattacaaaggtcact attggggtatagccaagcggtaaggcaaaggactttgactcctttacgcgttggttcg aatccagctaccccagtcgaaatatttaccataaatatttccaaccaagtaaacctac atataaaccaaaagcggttctacctcacacagcaggtggtaatgacacaacaacatca aatattggtttagcggtacttgcaacgtcatcagttttagcaacactaggtcttgcaa aacgtaaaaagaatgactaatctataacatataaaaaacagttaattaaattaactgt ttttttgttttacttaaggtgcaattcattgcacctatttaatttatgtaaaaatgt aacataaataataaacgtcaaaggagatatatacatgtttgtttatacactaaaatta aacactaataactatcaccacaatcgactagctcgtcgattcaaaatggctcaagaca tttatcgcaaatcgattttagaaatcttgaaacgtgaagctaaacaaaagaaagaccc tcgtaacaaaaaaatcaaagattcatacgagaaaatcaattcacttaaagaccaaatt ttgaatctaaataaagatttaacacgtctaatcaacggtgttgacgttcagcgtaatc tttacgcagcattcttaacttcacaatatgaaaatctcgataacagtaagattgttca aagcaatttcgaaacattcctacgtaatcaagaacattacttagaaactgcataaaca tgagcatttacatatcatcaactaatgttatatacactgaccaagattttcctgacac tcttgaaaaaaacaaattttggagagatagagaatctaatggtctaatcgtaaaaagt ctcgaagatttaacttcagaattgaaattagat
2930	CLUST.073508_OBLG01000980-M effector>	MRKKYDGMTSIIELPLKTEKWQGDVINKKMDHAVQIYNDMLHYKLGQYKELTERKDWK ENEREIIHFYDLTNPIETVTKKYDSFYNKKLDIIMNQEHGEDFNQEEVKKQILAEKEE VISKLLQERDTFEEEILSEINQNKIERKARQNIKKSGVPITDDGMNAEIKKVLEEEKK KITEEKVKICKKEAFQKKNDMLREARFTEFGFNGDVAKFSAHYATTISSNMACLTIAA PLWVAFSKFLFGNGKMVHYKKWGSINTIKTNGKSGIRLITENNRYYLILSNSPYKKEK NGEIYRFKARYSSSHPVKIEVLVGEKEYNKEMLQADISSICIKRVKIRDQYKYFVQFS VRRSPYKKKDENGDLIHPISDGTVGLCIWRNRLCAVSKDQVKSYDLSPGYSEYSDQLS EIGQKMDQLLRLNNPDNYNENGTVKSGIMVDGEKQKLTWVKSRQYKELSKKYREASRK YVETRSIWQNKIVYELLSMGNKFFICDTSYLTKKVDLESKTKKEQQTKADRRRSIMQA APSEFINKLNRKLQSDLLTPVNKVVIPEQLYWYNHAKGLCNKDDFWDDYMMLNMFESI PHTLYRAFMMLYYDSDRKEYRNIPEDEWNSFLEKAKMENVVKTNKNKI

2931	CLUST.073508_OBLG01000980-M direct repeat 1>	uuguaagguuacgguuuuacaagguuccaaagg
2932	CLUST.073508_OBLG01000980-M direct repeat 2>	ccuuuggaaccuuguaaaaccguaaccuuacaa
2933	CLUST.073508_OBLG01000980-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2934	CLUST.073508_OBLG01000980-M non-coding>	taaaacgtgattgtggtatcttataaataagactatgccgaaaaaataaaggacatat cggggtgagttggcatccttctttgaaatagaagtaaatcggtactggaaactgtaca gagcgtattttatgaaaaggcagtgtacagtaccaaccttgtaatttgaccagtgtaa gtgtaaaaaaggagagaaaaacggatgaggaagaaatatgatggaatgacatcaatca tcgagttgccattaaagacagaaaaatggcaaggggatgtaatcaataagaagatgga tcatgcagtccagatttataatgacatgttgcattataaattggggcaatataaagag attcctcatacattatacagggcttttatgatgctatattatgattctgaccggaaag aatataggaatatcccggaagatgaatggaactcatttttggaaaaagccaaaatgga aaatgtcgtaaagacgaataagaataagatataggaaataatattggggtgagttggc acccttctttgagatagaagtaaatcggtactggaaactgtacagagcattgaatgaa aaggcagtgtacagtaccgaccttgtaatttgactatttgtttaatgcttttcagacg atgatctttccaaattgggaaaaatttggatttttatatataaaaaaaatggtacttta gaaatgaaatatcggggtgagttggcacccttttttgaaaaagaaataaatcggtact ggaaactgtacagagcatattttatgataaggcagtgtacagtgccaaccttgtaatt tgaccccaaatctatgtttctcgattttatcaacgcttcattgttcgacttccttatt tcaaatatttcacaatttttttttctccgggatttttcccggagtttttttttaggtcaa aaaatcaatatcgtaattccatcatctcagttccaacatcatcgtagatcagaaaaat tctctttgacctctgcttatctccatttttcttttgtgaaaacagggtgtaccctgtct ttactcat
2935	CLUST.073508_OBLG01000980-M direct repeat homology 1>	accuuguaa
2936	CLUST.073508_OBLG01000980-M direct repeat homology 2>	uuacaaggu

2937	CLUST.073508_OBLG01000980-M direct repeat homology-containing sequence>	aaaagccaaaatggaaaatgtcgtaaagacgaataagaataagatataggaaataata ttggggtgagttggcacccttctttgagatagaagtaaatcggtactggaaactgtac agagcattgaatgaaaaggcagtgtacagtaccgaccttgtaatttgac
2938	CLUST.073508_S.A19AKJ-M effector>	MKNDKEKSMTVFEIPLICNEIVKGNLNKRMRVACDIYNDLNNFYQRRYKELTLSKEYV KDQKELIQCYQLEDLYEEYKKDKKSHKKKEWDFEAWINLTSEIIKAKIKSNKEKLQLL SKEEDKEELADEELVDETDDISSNKQFKLKSEIKKLRRQLLFLKGLDSSSEEELIYRF KEIAQTKKDIFDRRNKKCLELGLTEFGFVGEVSKYAKKYNHLVPSVMAARTVAKRLWA GYQKLLYGNGTKVNYCKREFFNTLETDDKHGIKLLKDNRGLYLSLSNNRAEAKREPLK IYLRRSDSDYDDYYLRELEKNVEDKLYRTLKVIRIVRRFEKNHLLKNTNFYVQFTLEN VKPYIKKNRDGSDKHIIKDGPVALSIWRNVLVAINNDEYKTWDLAAGEEEYAERRALL QRKLDENRRANNPDNFNDDGTVKKGRHTWNIDTDYIRLKNSISELSRKHTATSKLEKR HIVYELLKMGNSFTIYDTKYDVKRKKPSKESLEDLSQTEMRKKARDRRAIQNGAPSTF KTYLQQKISMYKLEEIKSVRVPDDVFWYKHDVDSSSEDFFKNGSVKVNNIDIDSVLYH AFVLKHYDIENKCLDKQGMETEFYKIFA
2939	CLUST.073508_S.A19AKJ-M direct repeat 1>	ccuugagaagguuauccauuuacaaggguaucgagg
2940	CLUST.073508_S.A19AKJ-M direct repeat 2>	ccucgauacccuuguaaauggauaaccuucucaagg
2941	CLUST.073508_S.A19AKJ-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2942	CLUST.073508_S.A19AKJ-M non-coding>	cataaggctataataactaagaaaaaagtgttaagttgcaagaatgaggtagaaatat tagatatgcttacagagtcatttttgaacagcataccattacaaaatgaacacaaagg gctgaaagatgttgataaaatcattatgacataaattacgacatgcttgggtagttat tgcattagtgaaaggataaacgatgaagaatgataaagaaaaaagcatgacagtattt gaaataccttaatatgcaacgagattgtcaagggaaaccttaataaaagaatgaggg tagcttgcgatatatataatgacttaaataacttctaccaaagaagatataaagagga cttctttaagaatggtagcgttaaagtcaacaatatagatatagatagtgttttatat cacgcctttgttcttaagcactatgacattgaaaataaatgcctggataaacaaggaa tggaaacagagttttataagatatttgcctaatatcaaacagtctgattggccagact ttaaacactagagacggtatgctgacaattaaaacaacgatagataattgcatcaaca atagttttattaataggtatatcatagctagatatgtgaatttggggctttagagcag tataaatttacacaggtgtcaaggtggtgttacatgcataaatgaagacgaggggctt tagggcagtacgaatagatgatataaaaagaaataagataaaatagtctgctcgatca gactataaacaataaacattagagacgatatactaacaattaaaacaacgatagataa ttgcatcaacaatagttttattaataggtatatcataactaaacttgtaatttggccc ttgagaaggttattcagttacaagggtatcgagggaagacactgttgttagatgcctt agttgaccttgagaaggttattcagttacaagggtatcgaggttgaaaaaccagtttg

		ggacaagataatataaaaaaatgaaataagataaaatagtctgctcgatcagactata aacattagagacgatatgctgacaattaaaacaacgatagataattgcatcaacaata gttttattaaaataggtatatcataactaaacttgtaatttggctaatatggcatagc ttataacctgtgtgggtgagaaaacccacggtttcaactgtgaggatgataaaccacc tcgctactttctgtagatagattttgactacaaggccgtaggtgtaaatatgcaaaaa ggcgttaagggagcaagttttattgcatgggaacagctcgaactgatagataaagtca agaaaatagggttttaaattactttgctaaagcagtaaaatcgtaggggacataatg atttctgcattttagctttgttggaggagattatggcgggaaagatagattattcggc tctcaatatagaaccgtatccacatgagctggctattgcagaattgttttcgcaacaa gggaaggacgtgatttttcttaagcccagtaacataccgggagtatatgtaccggata ttgtggtc
2943	CLUST.073508_S.1 S66CQ-M effector>	MFVYTLKLDANNKLKQQLGRRFKMAQDIYQRTIHEILKRDEKQKKDPRNKTIKAIYRQ IHALKDQITELETNLNDKPKKEQTAIKKITKDLTKQIKELEAEAKPIFRQMAEDYDIV GKYTFGKYANDYRNARNYSFYIPSDAAGVLGMRAWSSYEKMKFNKGAKKINRYPQLNS FETMKKTGIMIKDGLLKMGTKNKKIEVPVIYKNDEFEQEVFKNELKYNRLLRKFENGE VQYYVQMIFDGIPPQRMDNYIKGTVGIDVGLTKVAISTPNEVKILSLAPNLQNFDKEI RRLSRKLTRQRIANNPDNYNSDGTIKKGKKTWVNSKGYLKTKHKLADLKRKQAEYRKI SHKELANAIIQMGDKFIIKQSNFEKLKEKSKVDRKSATGKNLSKKHAGKTINSHAPGF FIQQLLYKAEFQGKETQVITNKDFNPYEYNHASKEAIENKAHLKSINIDGFEVQKNLY AAFLVSQYENMENDNVIKSNFEKFLRNQEFYIENIA
2944	CLUST.073508_S.1 S66CQ-M direct repeat 1>	ucagcuuuuucuuuaucagcuuuuucuuuugca
2945	CLUST.073508_S.1 S66CQ-M direct repeat 2>	ugcaaaagaaaaagcugauaaagaaaaagcuga
2946	CLUST.073508_S.1 S66CQ-M spacer>	nnnnnnnnnnnn
2947	CLUST.073508_S.1 S66CQ-M non-coding>	acttaggaatacatctttcggttcgaatccgattatttcaatattgaaatttatttttc aataaggtcatttagggaatgacaaaattaagttaaagaaccctcgttacgtccaaat gtgcactaaacgacgtagaagttgaatccactttagataaagattcgttggagcatat ccaagcggtaaggataggtgctcgtcaccgaaatcgtgggttcgaatcccactacttc aattcagaacagtttctgttctgaaaaatacaagctaattgtattttctggttggtat agattacggtacatgccaaataaaaatggaagatgatactaaaaaattaaacacctac aaaaaagatggcatcacatatgtgactttagacgaatccattcttgacacagattctt ggttaccaaaagaagccatccaacaaattgtagacgcaatcaaaagacaataagaaaa agaaaataaaggagaataaaacatgttcgtatacacactaaaactagacgctaacaac aaattaaaacaacaattaggtcgtcgctttaagatggctcaagatatttaccaacgta cgattcacgagattttaaaacgagatgaaaaacaaaaaaaagaccctcgaaataaaat caatatagatggttttgaagttcaaaagaatttgtacgcagctttccttgtatcgcaa tatgagaacatggaaaatgacaacgtcattaagtcaaacttcgaaaaattccttcgaa accaagaactctacattgaaaatattgcataatatggctatttacaatccaaaaaaca atactgtttatacagacctagacttttagataccttatctaaaaacaaattttggaa agaaaaagatactaatggtttaaccatcaaaacattagacgattttgcaaaagaattg ggttatgatgggatctcctttacggttggttaatatttctataacacaattataccaa aaattgaagtaatgttcaagtgataggtgagattttatttacagttgaaaaaagcta ctcacatgagtagctttttttttagttttctctcttacgttttgttgcggctagacc caatacggacgcaagcgttagtgcaccaagtgcatttaaagctgtattgttaccacct

		gctgtatttggtaattgacttactggtttttcgcttcttggtttttcggaagatttaa catcagttgatggtttttcatccttaacaggaatgaattgcaaatcatccttcttaac ttccttcttcagaccaaaatcgttcaaaccagttccgaggtcaggtttcttttcaggt tctttttcaagtgttgacaaattaaattctggtttttcgttaactaacggcttcactt cgttaccatcttcattaataccattacttgtcaaaggacctttatattcaggtttctc attaaccaatggtttaatttcattaccgttttcgtctacaccattacttgattcaaca cctttataatcagacatatcattaactaaaacttcaccagattttgcaatcacaattc cacgaattgctttcaaaccttcttctttcgctttcattctagcttcagaggaagtcgc attattgatagcttcaattgctttattcttttcagcttcaacttttgtttcaatttc acagcctgatcaggcgaaagtccagcagactcaatatccatcaatttcttgtcgaact cgttaatgattaaattgatagagtcagctttttctttatcagctttttctttagcaag tctttctgcttcagctttttctttatcagctttttctttgcaagtctttctgcttca gctttttctttatctgctttttctttgca
2948	CLUST.073508_S.1 S66CQ-M direct repeat homology 1>	aaaagaaaa
2949	CLUST.073508_S.1 S66CQ-M direct repeat homology 2>	ttttctttt
2950	CLUST.073508_S.1 S66CQ-M direct repeat homology -containing sequence >	aaaaatggaagatgatactaaaaaattaaacacctacaaaaaagatggcatcacatat gtgactctagacgaatccattcttgacacagattcttggttaccaaaagaagccatcc aacaaattgtagacgcaatcaaaagacaataagaaaaagaaaataaaggagaataaaa catgttcgtatacacactaaaactagacgctaacaacaaattaaaacaacaattaggt cgtcgctttaagatggctcaagatatttaccaacgtacgattcacgagattttaaaac gagatgaaaaacaaaaaaa
2951	CLUST.073508_OOZQ01000117-M effector >	MRKKYDGMTSIIELPLKTEKWQGDVINKKMDHAVQIYNDMLHYKLGQYKELTEREDWK ENEREIIHFYDLTNPIETVTKKYDSFYNKKLDIIMNQEHGEDFNQEEVEKQILAEKEE VISKLLQERDTFEEEILSEINQNKIERKARQNIKKSGVPITDDGMNAEIKKVLKEEKK KITEEKVKICKKEAFQKKNDMLREARFTEFGFNGDVAKFSAHYATTISSNMACLTIAA PLWVAFSKFLFGNGKMVHYKKWGSINTIKTNGKSGIRLITENNRYYLILSNSPYKKEK NGEIYRFKARYSSSHPVKIEVLVGEKEYNKEMLQADISSICIKRVKIRDQYKYFVQFS VRRSPYKKKDENGDLIHPISDGTVGLCIWRNRLCAVSKDQVKSYDLSPGYSEYSDQLS EIGQKMDQLLRLNNPDNYNENGTVKSGIMVDGEKQKLTWVKSRQYKELSKKYREASRK YVETRSIWQNKIVYELLSMGNKFFICDTSYLTKKVDLESKTKKEQQTKADRRRSIMQA APSEFINKLNRKLQSDLLTPVNKVVIPEQLYWYNHAKGLCNKDDFWDDYMMLNMFESI PHTLYRAFMMLYYDSDRKEYRNIPEDEWNSFLEKAKMENVVKTNKNKI
2952	CLUST.073508_OOZQ01000117-M direct repeat 1>	cccuuguaagguuacgauuuuacaagguuccaaagg

2953	CLUST.073508_OOZQ01000117-M direct repeat 2>	ccuuuggaaccuuguaaaaucguaaccuuacaaggg
2954	CLUST.073508_OOZQ01000117-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2955	CLUST.073508_OOZQ01000117-M non-coding>	aaaaataacgtactgcttggaattaaagttgataaggataaagaatatttatttgtat caacaatgtttgatatatcagaatctaaaatacaaagacgtttgcatagtggaagatt aaaagaatttttcgttgacacaacgaaaaaataatggtattttattagaaaaaagaga atatgataataaaaagcatagttattttgaggtcggaaatggttcccgacacactctg aaaagagtacctgagatgatggatacaccgcccatccataataattatgctttattat atttatggattagataaaaaaggaatagagagagatccagttctttcgtagaacaaca aaaacctcagtgctgcaccactgggggtttttttccccatatttattcccaagtccgg ttgccgatattccatccttccatatcggttaaagatgcaaacgagcagaaattgttcc aaccccagtattctacaaaaatccaaccagaataggggggagcagcacaggggaagaa taagaaaaagagaaaaaagataatttctctgacctcaatcctattctacatatttcca ctattggaatcatatattaacctgagtagatcgaggggtgactttggaacaggattgt ggtatattacaaacaaggcaatgccgaaaaaataaaggacatatcggggtgagttggc atccttctttgaaatagaagtaaatcggtactggaaactgtacagagcgtattttatg aaaaggcagtgtacagtaccaaccttgtaatttgacagtgtaagtgtaaaaaaggaga gaaaaacggatgaggaagaaatatgatggaatgacatcaatcatcgagttgccattaa agacagaaaaatggcaaggggatgtaatcaataagaagatggatcatgcagtccagat ttataatgacatgttgcattataaattggggcaatataaagagattcctcatacatta tacagggcttttatgatgctatattatgattctgaccggaaagaatataggaatatcc cggaagatgaatggaactcatttttggaaaaagccaaaatggaaaatgtcgtaaagac gaataagaataagatataggaaataatattggggtgagttggcacccttctttgagat agaagtaaaccggtactggaaactgtacagagcattgaatgaaaaggcagtgtacagt accgaccttgtaatttgacccttgtaaggttacggttttacaaggttccaaaggtgg tttgcatatttgagcttaaaacctcctcccttgtaaggttacggttttacaaggttcc aaaggatatttgtttaatgcttttcagacgatgatctttccaaattgggtaaaatttg gatttttttatataaaaaaatggtactttagaaatgaaatatcggggtgagttggcatc cctctttgagatagaagtaaattggtactggaaactgtacagagcatagaatgaaaag gcagtgtacagtaccaaccttgtgatttgacg
2956	CLUST.073508_OOZQ01000117-M direct repeat homology 1>	accuuguaa
2957	CLUST.073508_OOZQ01000117-M direct repeat homology 2>	uuacaaggu

2958	CLUST.073508_OOZQ01000117-M direct repeat homology-containing sequence>	aaaagccaaaatggaaaatgtcgtaaagacgaataagaataagatataggaaataata ttggggtgagttggcacccttctttgagatagaagtaaaccggtactggaaactgtac agagcattgaatgaaaaggcagtgtacagtaccgaccttgtaatttgacccccttgtaa ggttacggttttacaaggttccaaaggtggtttgcatatttgagcttaaaacctcctc ccttgtaaggttacggttttacaaggttccaaaggatatttgtttaatgcttttcaga cgatgatctttccaaattg
2959	CLUST.073508_UMLR01012367-M effector>	MANEKEPVSVLELPLKMEKWQADRINSVMDAVTKIYNIVLRKTNNRYKELIKTKAWRA DTTRLVDLYNIQKSTEDAVKEQRSYLNKILKKETENLPDDDPNKEKIIADKSQKLEEE IEAFEQKILELKKSFIENYYDEFEAISGDKKAEKKFIDKLNKKLEGKTKARKFSDEEF EDAFIYTKAEAEKKVIYDARHEQTKFTTPYGISDTIKPVRYYFSNLVPSAVANITISE PMGKAFEKLIYGNGKRVYYRKFNETNTICSNNKSGLRVVEENGEHYLLYSCQYAEGEK NAEKQAKREAYQKENKIKPYKIRAKYNKSHEMRIKIGNPKTKYETEMLKGKIARVTLV RKFEKTKYHYYIQLTLKREPYIKVDENGEPLHKVKDGVVGINIWRNRLCAVSKTEAKV FDLSPGYIEKSKLQADYNRKLDELSRAENPDNYNEDGTVKKGTKGHKLTWSRSDEWKF YKRKLSELYRVDNVNKDYNRRKIVYALLEMGNEFIMMDSSNITKKIGVTEMTNKEQEK AKDRRSSIQEASPSAFVNALNARLNSYGLPSVKKVKINEELYWYNAFLNKIDKTLFTD DAVRISDIPASDGYYLEVPHTLYRAFMLLHYDNKKHCYLDVSDEELDNFVEITKEHDI LLTNKKKRQLENA
2960	CLUST.073508_UMLR01012367-M direct repeat 1>	guuuuggagccuuauaggauuacaagauuccaaagg
2961	CLUST.073508_UMLR01012367-M direct repeat 2>	ccuuuggaaucuuguaauccuauaaggcuccaaaac
2962	CLUST.073508_UMLR01012367-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2963	CLUST.073508_UMLR01012367-M non-coding>	aatggaattgttgacaaaggtggtgcatggtacacatatcaaggcaacagatttcagg gaagaagcaatgccattgcatatcttgttgaaaatgcagatgtatgcaaagaaataga aatgaagattagagagtcagaaaaaaataaatagtacatatttacaataagatgattt ggcatcttaaaactgcaaaagcagatacttcctagataggcagatataggcatggaac atttgtgttctgtgagaaaatgcagcataggagtaaacttgtaattgaatatttgagt agcatagaattgttattccatacagaatgttttggaatcttatgaaactacaagattc caaaggggtaaagaatgtaaacaatcgttatatacaaaaagaattgcgagattcatgg ttgctttgtgtcttgtagaattgtaagatttagaagaaatagagatttatacagatgt tagaaggtttatttcatatatataacaaatcatattcaaaatatatgattatataat ggaggacaatatatggaatgtaaatatacatgctttgatagagttatgaacttggtaa agccactaccaaaagaaaagttttgggatgcttgtgacttaatcacaaattacagttt cattgattttcttgacttttgtgtagaaaatgaatgttttacagaagattgtgagtca atggttgcagagtacattgttgatcaaggaatagcaaaagatgaaaatgaagcagaag

		aaaaagttcaatatatgtgtgatgaaaacatattaaaagactttgttataagaaatga acttgtaattcatttctgctaaaattaaaaactcctatttcaaaataggagtttttat ttgcaaaaaataaatcaaatatttttatgttataataacaaaaaataaaaaaggagag aaaataaaatggcaaatgaaaaggaacctgtatcagtattggaattaccactcaagat ggaaaagtggcaggcagacagaattaactctgtaatggatgctgttacgaaaatctat aatatagttttaagaaaaaccaacaacagatacaaggagttatatcgggcatttatgc ttttgcattatgataacaagaagcattgttatttggatgtttcagatgaagaacttga taactttgttgagattacaaaagagcatgatattcttctgacgaataagaagaagaga cagcttgaaaatgcttaaatcacaatgtcctacctaatagaaatattaggtaggatgt tctttttttggaggaaatatatgaaactaggagataagttatattatgtattatcagat tttagtggggttagtataagtgagattacggttacatcaataaaggataagtattttg tatgcaaatacaaaagaacatccaatgaagaattaatattcaccaataaagat
2964	CLUST.073508_UMLR01012367-M direct repeat homology 1>	uuuggaaucuu
2965	CLUST.073508_UMLR01012367-M direct repeat homology 2>	aagauuccaaa
2966	CLUST.073508_UMLR01012367-M direct repeat homology - containing sequence >	tagcatagaattgttattccatacagaatgttttggaatcttatgaaactacaagatt ccaaaggggtaaagaatgtaaacaatcgttatatacaaaaagaattgcgagattcatg gttgctttgtgtcttgtagaattgtaagatttagaagaaatagagatttatacagatg ttagaaggtttatttca
2967	CLUST.073508_OQSP01001034-M effector >	MRKKYDGMTSIIELPLKTEKWQGDVINKKMDHAVQIYNDMLHYKLGQYKELTEREDWK ENECEIIHFYDLTNPIETVTKKYDSFYNKKLDIILNQEHGEDFNQEEVEKQLLAEKEE VISKLLQERAAFEEEILSEIDQNKIERKARQNIKKSGVPITDDGMNTEIKKVLEEEKK KITEEKVKICKKEAFQKKNDMLKEARFTEFGFNGDVAKFSAHYTTTVSSNMACLTIAA PLWVAFSKFLFGNGKKVHYKKRGSINTIKTNGKSGIRLITENNRYYLILSNSPYKKEK NGEIYRFKARYNSSHPVKIEVLVGEKEYNKEMLQADISSICIKRVKIRDQYKYFVQFS VRRFPYKKKDENGDLIHPISDGTVGLCIWRNRLCAVSKDQVKTYDLSPGYSEYSDQLS EIGQKMDQLLRLNNPDNYNENGTVKSGIMVDGEKQRLIWVKSRQYKELSKKYREVSRK YVETRSIWQNKIVYKLLSMGNEFFIYDTSYLTKKVDLESKTKKEQQTKADRRRSIMQA APSEFINKLNRKLQSDLLAPVNKVIIPEQLYWYNHAKGFCNKDDFGDDYMMLNMFESI PHTLYRAFMMLYYDSDRKEYRNIPEDEWNSFLERAKMENVVKTNKNKI
2968	CLUST.073508_OQSP01001034-M direct	uuuguaggguuacgauuuuacaaggucccaaagg

	repeat 1>	
2969	CLUST.073508_OQSP01001034-M direct repeat 2>	ccuuugggaccuuguaaaaucguaacccuacaaa
2970	CLUST.073508_OQSP01001034-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2971	CLUST.073508_OQSP01001034-M non-coding>	gcagcatcaaagcagtttgagtttggtttcgggcaaaataagaccaatcatcaaaccg gagctatcggattctatctcgacacaaacatgatcaaggaaccattgcgggcggtatt aaggtcttgcggatatcgaaagtcaatttttctaattagaaaaaatttgtatttcataa aaaaaacaaaccatggcagtgacaaatttagaacaactgtggtataataacagtgtta aaaatattggggtgagttggcacccttctttgagatagaagtaaaccggtactggaaa ctgtacagagcatattttatgaaaaggcagtgtacaataccaaccttgtaatttgaca ccttgtagggttacgattttacaaggttccaaaggcttgcggtcgggattccactgac ccggtataccttgtatggttacgattttacaaggttccaaaggatcgagaaaaattat ctctttacgattttacaaggctccaaaggttagacctaggattgtagagaatgtgaca acccttgtaaggttacggttttgaaaggtcccaaagcagcgtaagtgtaaaaaaaagg agagaaaaacggatgaggaagaaatatgatggaatgacatcaatcatcgagttgccat taaagacagaaaaatggcaaggggatgtaataaataagaagatggatcatgcagttca gatttataatgacatgttacattacaaattggggcaatataaggagattcctcataca ttatacagggcttttatgatgctatattatgattctgaccggaaagaatataggaata tcccggaagatgaatggaactcatttttggaaagagccaaaatggaaaatgtcgtaaa gacaaataagaataagatataagaaataatatcggggtgagttggcacccttctttga gatagaagtaaaccggtactggaaactgtacagagcattgaatgaaaaggcagtgtac agtaccgaccttgtaatttgacatatttgtttaatgcttttcagacgatgatctttcc aaattgggaaaaatttgaatttttttatataaaaaattggtactttagaaatgaaatat cggggtgagttggcatccctctttgagatagaagtaaattggtactggaaactgtaca gagcatataaatgaaaaggcagtgtacagtaccgaccttgtgatttgacacaaatcta tgtttctcgatttcaccaacgcttcaatgttcgacttccctattccaaatatctcata atttttctccgggatttcccggagttttttttaggtcaaaaaaatcaatatcgtaa ttcagaaaaattctctttgacctctgcttatctccaatttttttgtgaaaatagggtg taccctgtttttactcatgcgttccacctctattgttgtaaaaacagggttatttttt tatttatttacaaaatgtaaacgaagtctttgattttgattttacatttgctataat aaagaaaaacggaaaggcagataaaacatgagaattgcatatgtgagggttagtacca tcgaacaaaacgaagcaaggcagattgagggcttagcaaaatataatatagaaaaatg gtttactgagaaaaaatctggaaaggacaccaatcgggaaaagctgcaggaaatgtta gat
2972	CLUST.073508_OQSP01001034-M direct repeat homology 1>	accuuguaa
2973	CLUST.073508_OQSP01001034-M	uuacaaggu

	direct repeat homology 2>	
2974	CLUST.073508_OQSP0100103 4-M direct repeat homology - containing sequence >	aagagccaaaatggaaaatgtcgtaaagacaaataagaataagatataagaaataata tcggggtgagttggcacccttctttgagatagaagtaaaccggtactggaaactgtac agagcattgaatgaaaaggcagtgtacagtaccgaccttgtaatttgac
2975	CLUST.073508_ODLH0100206 8-M effector >	MEEDKKHFVYTLKLKTTNKHVEQLNRRFKMTQDIFKKSLIECLRRDKASKKDPLYKQA MKHEASSKERKKILKELDKKYDLSDFSIRKFANDYRNARNYSHYIPSDVAISLGKRAW GAFSKVKFAKGANHISLNNPFTSMEGIHDAALTIRNGVFKMGTVTDKAKFSCPVIYED DEMERNILRNKVKYCRLIRKQEHNKTNFYVQVVLEGYPHIKTTEPLDAKVGVDIGLTT VATSSRLGTNLEELAPDIDKNEKLIAKLQRKLDRQRRANNPNNYNPDGTIKKGRKTWH DSKNYLKTKKKLAELSRIQAETRKLAHNNLANKLVEIGNEFVVEKMNFADLAKRLEDG EISKITGKNLSKKQFGKLIGRRAPAALIEKLRYKAEFRGSKFTLVDNEKIAATQLNHL DGEHHPIKLSERVKMVGEHPVQRDLYSAFILEHVTEGGEKVDLKSCGKDFNRFLHNQE HTMDNLTNVTPSMGVKRFKAIKNKK
2976	CLUST.073508_ODLH0100206 8-M direct repeat 1>	guuuuggaaccauucuguuugacaugguaccaaagg
2977	CLUST.073508_ODLH0100206 8-M direct repeat 2>	ccuuugguaccaugucaaacagaaugguuccaaaac
2978	CLUST.073508_ODLH0100206 8-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2979	CLUST.073508_ODLH0100206 8-M non-coding>	ttgattaaggtacgttcgttagaaacgcaatggcaaattcaatttgtttaacgcctga aaatctatcttagtcaactccaatcatgttaaatagaagaatgcgaggtaatcgaaga tttggcaatgttgtgagccaaaaacttatatactatgaaaggaaaagttgtgactaaa acatttcaagattttaaagaggaatatttggaagaattaggttctgaagctaaagaag aatacaatagagctttagaagaatccaaagaagaaaaacaaaaataaattacgaaggc ttagaaaatggaagaagataaaaaacattttgtatatactttaaaattaaaaacaaca aacaaacacgtcgagcaattgaatcgacgttttaaaatgactcaggacatcttcaaaa agagtttgattgaatgcctaagaagagataaagctcccaaaactgagggtggtgaaaa agtagatttgaagagttgtggtaaagactttaatcgtttcttacataaccaagaacac accatggacaatttaacaaatgtaaccccatctatgggtgttaaacgttttaaagcta ttaaaaataaaaaataaaaggactaatatagtccttttttttattacaacaaaataaaa gattagcatgggaataaattcctcttgaaataagaataacaaatcatagagcaaattg

		caagtaaaaaatgaagaaaaggcttcttataacctaatgagcttagacataaaagtcg caatatgttataattatattgtagaaaaaaagaaaaagaggacttgattcaatggtaa aagaattagataattttgaagatgaagaaatgaatatttttgatgagaaagtaaaaga aaaagaagattcatcgtctaataaaaccttagcatacgggatggatgaacgtgagact attttcctttatagtgaaattgacaat
2980	CLUST.073508_S.2 CDW54-M effector>	MAQDIYRKSILEILKRESKQKKDPRNKKIKDSYEKINSLKDQILNLNNDLETKPKSEQ KTIKDNIKSFNKEIKELDKQIKALYKELDTDYDLRGSFSFGKFANNYRNARNYSNYIP SDVAIKLGMRAWDAYEKVKFKKGAKQINKYPELMSFEAKSDSGIIIRNGVLKMGTKGK GIEIPVIYKNDDFEREVFTNEFKFNRILRRFENNKWNYYVQMIFDGIPPQKIDNYLTG TVGIDVGITKVTISTPNEVKILPLAPELQNFDAEIRRLSRKLDRQRRANNPDNYNEDG TIKRGKKTWVQSKGYIKTKNKLANLKRKQAEYRKISHKTLANAIIAMGDKFIIKQSNF EELMKRSSETKVSKTGKFLSKKRAGKKIENHAPAYFIQQLTYKAMFQGKEVITLTNKE FNPYEYNHVTQEFQEVNKNSQTRLINGIDVQRNLYAAFLTSQYENLDDNNAVQSNFET FLRNQELYLETA
2981	CLUST.073508_S.2 CDW54-M direct repeat 1>	guuuuagaacaaucauuuuua
2982	CLUST.073508_S.2 CDW54-M direct repeat 2>	uaaaaaugauuguucuaaaac
2983	CLUST.073508_S.2 CDW54-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2984	CLUST.073508_S.2 CDW54-M non-coding>	ttctttatttccatttatatattctcctaataaacgaccgttgtaatcacaaaggtca ctaatggggtatagccaagcggtaaggcaaaggactttgactccttcactcgttggtt cgaatccagctaccccagtcgaaatatttatcataaatatttccaaagtctttattac ggtggttaattaaaagtgtagtaaaaactttgttagactagccagtctccttttctaat aaatcaggtgtaacaatttgaataaggttgttgcatcattatctcttattggggaaat aattatttcaataattattataagagtaaatttaaatttcatataactctatcgcctc gtaatatagtcatttggggaatgacaaaataattcttaaagaacccccgttacgtcta agatagacataaagacgtaggagttaagctgatactctggatgacagcttgttgaagt atatctaagcagtaaagataggtcttattgaccaaaaccgtgggttcgaatcccacta cttcagttgaatgaaagaagggtgattaccttgttaaattttcgttcaagaattaaac aacccaagcaaaataatttgtaaaagacacatatattgatgtctttttttcataccgt tcatttggaaacggttaatgtcataattatgataatcataatgacattattcatttca ttaaagttattctttactcatatagcaatgttattaacatcttgtagaaaacaataac tttaataaatgacatgttgaatttaaacacaaaacataataccaaaaggcacctttag aattactctcaaaacatccagttttaaagtaatcataattgacatagtaccaaaagta gacttccttgacatgcttaaaaactaatattttaaaacattaatatttaacaaaatct caaaagatatgaatatcgttttattaaaaacacttttagaaatattatatttaacat gagatcaaacgtttctttaataaaaatgtaaaaatcacttaataattaaaaataaaat agtttaaatttatatatcattttgatacataaatttaagctatttttttacatattag aaaataaataattagtgcaatatattgcacctatttaatttctgtaaaaatataccat aaataataaacattaaaggagaatatacatgtttgtttacacattaaaattaaatact aataattatcaccataatcgactcgctcgacgattcaaaatggctcaagatatttatc gcaaatcaattttagaaattttgaaacgtgaatctaaacaaaagaaagaccctcgtaa caaaaaaatcaaagactcatacgagaaaatcaattcacttaaagaccaaattttgaat ctgaataacgatttaacacgtctaatcaacggtatcgatgttcaacgtaatctctacg ctgcattcttgacttcacagtatgaaaacctagatgacaataacgctgttcaaagcaa

		ctttgaaacattcttgcgtaatcaagaactttacttagaaaccgcataatcatgagca tttatatcgcatcaactaatgttatatatacagaccaagattttcctgataccctgga aaaaaacaaattttggagagatagagaatctaatggtctaatcataaaaagtctcgaa gatttaacttcagaattgaaacttgat
2985	CLUST.073508_S.6W88CN-P effector>	MNEESKKILTVTYPLIVNTAAVDELNKRLRIGCDIYNAMLCAKLKRLRQMEQTRAWRE NQKIIQEEYALESADEDIEKNKEKRRHSERLKAAFKAKQDMLKENGFTKFSFVSDVLL YAKPYARQIPSKMASLSIGAPMWHAFEKYFFSNGQKIHFKKYRDFNSLETDNKSGLRL LTDEKGKDYLFLSNRNSGAKPLRINLYPYQTDYDKAMRSGDIKIIRVVRRHQNNKDRF YAQAVVNVVPFVKTDGDGSALHPFGTGAVGLAIWQGTMYAVSDSQVKKFDLMPNNEAY QMQKNEMNRQLTILRQELNPDNFEEDGQIKKGIIDSNGKRVKLTWKYNKHYYRLRNRK REMERKHTENMSILKNKIVYELLMMGDEFFIYDTSYRTDKPEWDEEEPLTQKEYRKKK KRRKSIQDSAPAELIVKLNNKLAMYDKPAVTKVHIKDKDYWYDHTKDMENPAAFTGDM VRIADDVIPHTAYRAFLVRFYNGTYNNDNIQAAWNLFLNALK
2986	CLUST.073508_S.6W88CN-P direct repeat 1>	guuaaguacuuauauacuuuugcauagguacaaagga
2987	CLUST.073508_S.6W88CN-P direct repeat 2>	uccuuuguaccuaugcaaaaguauauaaguacuuaac
2988	CLUST.073508_S.6W88CN-P spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2989	CLUST.073508_S.6W88CN-P non-coding>	tacaataaaataaagaaatactgtatggggcaggaaagctgtgaggactgtctgtttg ccatggaggatggcgctgatgcggaatgtcttatggaatatcaggatacaccgaatga atggcagctccttgatatagattaagtgtgcaaaatgcaaaagcattttcataaataa aaagccggtaaggcagaaagaggtacttataatgacaaaagcagaattagcaacagcg atctcagagaaagcacaaatcagcaagaaagatgcggaaaatgttgtaagagcattta cggatgttatcggggatgagcggcttttacaggcgatatggtccgtattgcggacgat gtaatacctcacacggcttatagggcatttctggtacgtttttacaacggaacgtata ataatgataatatacaggcggcttggaatctgtttctgaacgcattaaaatgatttaa atggatgaattgtcatccttagctaaatagctaaaataccggctggatcataatgtat ggctgtacttactgcggtagacgggtagatagcaggagttatgggatggcggctatgt aaaaactttgaggttaagtacttataagtacttatatacttttgcataggtacaaagg attggattaacaacaattgcaattacgatggttaagtacttatatacttttgcatagg tacaaaggaggttaggaataggtttatccttataaagtgtacattcgatgtaaaggaa agatgagttttacaatttattgaatgggattatttttacatagatacataagaatcgt aatataaaactgttatagaatgctgctaagtacttatatcataagtacaaagatacat tttacaggcataatttatagcttaataaaggagccgattattgtgatgttacatgatt ttttgatggcttatggtggcaatgtttgtatttcaatagttggtttttgcgaagaagc tgaacagagtgaagttatgacctctgattga
2990	CLUST.073508_S.6W88CN-P direct repeat homology 1>	uaaguacuua
2991	CLUST.073508_S.6	uaaguacuua

	W88CN-P direct repeat homology 2>	
2992	CLUST.073508_S.6 W88CN-P direct repeat homology - containing sequence >	ggttaggaataggtttatccttataaagtgtacattcgatgtaaaggaaagatgagtt ttacaatttattgaatgggattatttttacatagatacataagaatcgtaatataaaa ctgttatagaatgctgctaagtacttatatcataagtacaaagatacattttacaggc ataatttatagcttaataaaggagccgattattgtgatgttacatgatttttgatgg cttatggtggcaatgtttgtatttcaatagttggtttttgcgaagaagctgaacagag tga
2993	CLUST.073508_ULNQ01033742-M effector >	MISIKSSGGSNMGKINKYDGVTSVIELPLKTEKWQEDRINKKMKNIAAIYNAMLRYEL DKLTCLKSSSEWQENERTISHIYDLTKPFETVKKKYDRIYEFKIKSAIKEQDESSDDV DKDKIKETFLAEKKELLETLEADRKAFEDEILQQIDMDAISKKAKAQTKKKSQSSDIY EDAVNNLLSKKKSELIEKTGKVMLKEAYGIKGELLKNAKFTQFGFASDVAMFTKHYIT SIGANMASLTVANPMWVAFSEYFYGNGRRIKYKKPDSIDAIRTDGKSGIRLIFENEKY YLLISNSSYKKEKNGNVYTFKSCYGQANPIKIEVKMDDKEYNREMMNAKISGICIKRK LIRNRYRYYVQFSVRRHPYQKKDADGNLKHSVARGKVGVCIWRDVIGAYSSNGVKFFN LASGSEKYDKERGELSRKMDEILRMNNPDNFDEKGRIKKGKIVDGKRVRLTWVKSNLY KDLSMQYRELSRRFVENRTIEQNKIIYDLLTLGDEFYIYDGNYSTIKGNLEDKSIEEQ KKKADRRRSIQTVAPYMFISKLNNKLAALGCDPVVKVNVSNDTYWYNHAKGRQDKDSF GANYMMLNSFESVNHTIYRAFLILYYESKTKQYVIPEEDWKLFLERTKNTSFLRARNE
2994	CLUST.073508_ULNQ01033742-M direct repeat 1>	cauuuguaugcuuauggaaucgcaagg
2995	CLUST.073508_ULNQ01033742-M direct repeat 2>	ccuugcgauuccauaagcauacaaaug
2996	CLUST.073508_ULNQ01033742-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
2997	CLUST.073508_ULNQ01033742-M non-coding>	atcatacttgaaaattaccgtaagtacggtaatgagacaaaatgggatttgacgaatg ctataactgattatgcacatgttgttgatattagttcacgcataaagttagagtctgc tgcatttaaaattgcataaaaaaataaaaaaaaactaacgtaaaagaaaaagagatac atatttaattatatgtatctttttttgcaaaaagtgaaatgatttgtaaaatgctat gatttctataaaaagtagtggaggaagcaacatgggtaaaataaataaatacgatgga gtaacatctgttatagagttgccattaaaaactgagaagtggcaggaagatagaataa ataagaaaatgaaaaatatagcagcaatatactttgaaagtgtaaatcatacaatata tagagcatttttgattttatattatgaatcaaaaacaaaacaatatgttattccagaa gaagattggaaactgtttttagagcgaacaaaaaatacaagttttctccgcgcaagga atgaataatatattattgttttcttttgttcataatgaacaaaagaaaagtttaattt

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2998	CLUST.079467_OLGI01004405-M effector>	MAHKENQKAFVVTFPLRTEKWQEDRIDKMMRMLTTFYNDRQRKLVRRYIYLSHSKAYK EAKGKGVVAFKNYMKENGFSQYGLDAFFKADTKGALYQCRLNSMFLQYLSQCAWSAWD KKLFGKGDFVKTDKVVNIFCSRNKKGRFCGFDYDLSTFTIRIKSTCTKEIICSIPFVV NKKSDYELFALSQRICRIGIVRKLIRGKYKYYVQFTFDGVPYHKGRNIGTGIVGIDPG PSKIAIVGDNKVEIAKLAPNIEEDERKTARLKRKLDRSRRATNPHMYKEDGTIIKGQR QTCFSKVYNETRKQLADAQRKLAAKRKIAHNELANTLLEYGDTFKVEANSYKSMQART KATSMTKSGRIRSKKRYGKSIKN
2999	CLUST.079467_OLGI01004405-M direct repeat 1>	cuuguaugugacauggaaaugaaggguaguuacaag
3000	CLUST.079467_OLGI01004405-M direct repeat 2>	cuuguaacuacccuucauuuccaugucacauacaag
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3093	CLUST.096738_S.10ASJA-M effector>	MMRKAFKFRCYPNKQTQQRLWDVMQRGVTPVWNACVAERQAVRTEYAHLCDEAICDRV YDLKRDLSPKEEKAIRKKMANQVSWPSAYSQYKHIRKRDHPEYADFYAKMLECTVAEV DGAEKSYRALWILGDTKARPPSEQRVHRVITYRLSGFKLNGSYLWLSRIGTMKIRLHR PVEGIIKTVTIREKNWKWYVSFSSEAEHFSGPCRSVSEDNPVIGRYLRQKHPITGGAT REKTGAYNVLPRSQPSGGATREKTGAYNYNDHSLELSFRPHCFVEDSAGRIFDHPDFY FEGIETLRRLSRELSRKMKWHCADCDGVCEKYRTVRDTPTCWHCGSEVIRPQRSQNWY KARKRLGAHQEHIARQRRYWLWHVANFYAGHYRQIIVYEKMWKYKIKYARTGDEAIRL CDGAAALFVAMLKTKCQDFGTELILRKDVKWQHQEKDLIERAELEGLHKLMRRLQRIL NDPRPVHLPFLKRASKQRPTLKRYA
3094	CLUST.096738_S.10ASJA-M direct repeat 1>	gguguaagagacccgaaaaugagguguagauacaac
3095	CLUST.096738_S.10ASJA-M direct repeat 2>	guuguaucuacaccucauuuucgggucucuuacacc
3096	CLUST.096738_S.10ASJA-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3097	CLUST.096738_S.10ASJA-M non-coding>	tttacagccggcgatttgcgacgaatgtaccctgaaggcgttccggactggatcacag gcggcaaggatcatagatggtcctattggcttaaagatcaaatcaatgggagatttga agagatgaaagatgaaactcgactgcttttataaataatagtctgttggcggcggggt tttccaccgccccaaggggaaagatatagcggtctttcctggccccgccgctctgaat gaaaacagtcagcagaaaggaaatagattagaaatgatgagaaaagcgttcaaatttc

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3098	CLUST.096738_S.10ASJA-M direct repeat homology 1>	gguguaagagacccgaaaaugagguguagauacaac
3099	CLUST.096738_S.10ASJA-M direct repeat homology 2>	guuguaucuacaccucauuuucgggucucuuacacc
3100	CLUST.096738_S.10ASJA-M direct repeat homology - containing sequence >	ctttttttgagaaaaccatctttatcaggtgtaagagacccgaaaatgaggtgtagat acaacgagttcgtcccagtcgtcgagctccagctggtgtaagagacccgaaaatgagg tgtagatacaacgatcaatggctggcgggcgtctggtgtaagagacccgaaaatgagg tgtagatacaaccgccactgtctgtctaccggggaatagaacggtgtaagagacccga aaatgaggtgtagatacaactgttga
3101	CLUST.096738_S.10T1L2-M effector >	MDENKQLKTGEKGRMEMKKRRSKCKQEKCRKAFKFRAYPNRELQNRMFDMMRVNTIAY NGCVGEYDVAYGSFRRKIAEFKKSGAGWDSLDEKRREKLVKEAIKSVDWPTRSKLYGN YVSKRNNPQNDGFYIAAIQNTMLQVFNAVHGYQSKRDKGDPDVRRPKKQDFHRGIIYR QSGFFPKKAVKNKVRLSGIGTIKFKRHREIEGRIKAVIVKFEHGKWYVIFSCESPVKK RKRTGKKVTIKFSDLYFIEDSSGRIIEQPGYYFGSLPKIRELSRAYSKKSLQYKDGDY KKLVVDAEKDFKKKNLKKAKRKLGKFHGKIKGRRRDFINKIVRNYVMEYDIITVYEQP FYLRQQCQLSSRDAIRLADAAPGIFLRMLKHKCNEYGVKLILIKNELLWDAGRQITAD KKSIKQQKQFLRNVKRRMK
3102	CLUST.096738_S.10T1L2-M direct repeat 1>	ggugcaaaggaccucgauuugugauguagauacaac
3103	CLUST.096738_S.10T1L2-M direct	guuguaucuacaucacaaaucgagguccuuugcacc

	repeat 2>	
3104	CLUST.096738_S.1 OT1L2-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3105	CLUST.096738_S.1 OT1L2-M non-coding>	gaatgggacgaaaaaaaggcggtcgcccgggcggcgaaccagttcaggctgttcgaag gctgccacctggcggagctgcgggcggcatttgacccggagtacgcgaaagaattaga gcgtatgacaaagcaggctataaaaggagaatgagaaatgagcaagacatgtagttgt tgtcctaacaaagcaaagtatgatgtagatggtgaattatgttgtggtaaacatttga cttatactgttgattatgcactaaaaatgagtccacatcaagtcaaagtagagaaagt caaagagcaatacgatgaatgataaacttaaaataatattagaatcaatcagtcgtga attattgaagtggatgagaataaacagctaaagacaggagaaaaaggcaggatggaaa tgaaaaaacgccgctcaaaatgcaagcaagaaaaatgcagaaaggcatttaagttcag ggcttatcctaacagggagctgcagaaccggatgttcgatatgacgaacaggcagaca gagaacagcaatgcagcgctgctgtttaacatagtttgctcgattacggacgattcgg aagttaagagaaaattcctcgaagagtatcagccgtcgctgaaaaaattgagtccggg caggagaaagacggcctgaccgtgagttttgctctttgtaaaataaataaacgtggcg atggtattcgccttcccgggcccgcaaatgtgggctggcgggagaactgcaccgaatc gagcgaactgacatcggccaacctttcggctgccctcgatgtgctcggcgtaaaaaaa ttaatttgaaggatttccatgtataatttcctcaattgttccatattgaaatattcga tataactaaggcacaggtttaatattgtaatcgcgaatcgaggtgacttatggaaaag cctttgagatgtagactcggcctgcataaataaaacaaaatattttggacccaggagc taaattacgcaggcgatagaaggcattattgtgcacattgcggcaattattttgatgt cgatgtcgatgccggggatg
3106	CLUST.096738_S.1 OT1L2-M direct repeat homology 1>	aaucgaggu
3107	CLUST.096738_S.1 OT1L2-M direct repeat homology 2>	accucgauu
3108	CLUST.096738_S.1 OT1L2-M direct repeat homology-containing sequence>	agcgaactgacatcggccaacctttcggctgccctcgatgtgctcggcgtaaaaaaat taatttgaaggatttccatgtataatttcctcaattgttccatattgaaatattcgat ataactaaggcacaggtttaatattgtaatcgcgaatcgaggtgacttatggaaaagc ctttgagatgtagactcggcctgcataaataaaacaaaatattttggacccaggagct aaattacgcaggcgatagaaggcattattgtgcacattgcggcaattattttgatgtc gatgtcgatgccggggatg
3109	CLUST.096738_S.3 UZALR-M effector>	MRVFGGIWCDAVNERFRTYRQWERAVYTETKKTENEICGPLSQEKIKQIEKSVADNIV KPVNSFYSQYRLIRKRDHTEYEPYNAKSMQCVLGKVDSSFKSYWQVRKSNPKAKPPGQ KRLHKTIEYHQSGWKIEGNILFLSKLGKFRIRLHRPIDGTIKSVSISERNRKWYAYFS CEIDKKPGVCSPVTEVKSNMDNNLRQEYAPSGGDDPEKAGTYNSLKDLNKLGRGGDDP EKAGTYNSCALEVDSYGGGDDPEKAGTYNRYVSNNLNNTGGDDPEKAGEIQIAYGWKA NIFLIDSDGFLVEHPEFYFNELERLERLNQSLSRKTRWMCRNCGKLGEKYRSDKKGKY

		CIDCGSDRISKYSSKNWYKARHTIRKWHERIANKRAYYLWNLARFYAGNYKRVIINKW PIAKEIEYATDNKTARKLCDGAYGLFVNMLKHKCNELGTEFIIRKDLSWQNEIDRITE QAKMEQLEKLLRETKKTVKRNNRARFRYLETAFERLTMLRI
3110	CLUST.096738_S.3 UZALR-M direct repeat 1>	uacuguaagagaccucgauuugaggguaguuacaac
3111	CLUST.096738_S.3 UZALR-M direct repeat 2>	guuguaacuaccccucaaaucgaggucucuuacagua
3112	CLUST.096738_S.3 UZALR-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3113	CLUST.096738_S.3 UZALR-M non-coding>	aaagttaaaaaaaatctgcgttcatctgcgtaaatctgcggttaaaaaattaatcaat aataaataatcaatagtcaatgaaaagtcccggccggaaccggggattgacaggaaca ataaatcgaaaggagaaacgacgaaaaaagaaaagagcgacaatcttatcaggaaaac attcaaatatcggtgctacccgaacatcgggacaaaaaagcgtgcgtatcaaaccatg agagtctttggaggtatctggtgtgacgcagtaaacgaaagattcaggacttacaggc aatgggagcgtgcggtttacaccgagatcaaaaaaaccgagaatgaaatatgcggacc attatcacaagaaaaaataaagcagatagaaaaatccaaatcgcttatggctggaagg ccaatatattcctgatagacagtgacggttttcttgtcgagcatcccgagttttattt taacgaactcgaaaggttggagcgactcaatcagagtctgagcagaaagacgagatgg atgtgcaggaactgcgggaagttgggcgagaagtaccgaagcgacaaaaaaggtaaat actgtatagactgcgggagtgatagaatatcgaagtatagctcaaagaactggtacaa ggccaggcacacaataagaaaatggcacgagagaattgccaacaaaagagcttattat ctctggaatctggcaagattttatgcgggcaattacaagcgggtgataataaataaat ggccgattgccaaagaaatcgaatacgcaacggacaataaaaccgcaagaaaattatg cgatggcgcgtatggattgtttgtcaacatgctcaagcataagtgtaacgaattagga accgaatttatcatacgaaaggatttatcatggcaaaacgaaatcgacagaataacag aacaggcaaagatggaacaactggaaaaactgctgcgagaaacgaaaaagacggtgaa aagaaacaatcgtgcgcgcttcaggtacttagagacggccttcgaacgcttgacgatg ctgcggatttgattcgcggggcattgatagatttggagatgggcgtgagtccgacgag tcggacaagccagcatttgaacggtgtgggtaaggtgcttcagatcaaaaaaatgaag gataacgcaggagataccattaaaaaaacatgcaaacaagccggttttctgccgggaa gcgctcgaaaatttgcataatattttatgctctttgaaaaaaaaataccagtgtgtgt agcactgtgggtgtatagtcccaagatacaacttttacat
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3115	CLUST.096738_S.8 I0G0N-M direct	agguggagccgaccucgauuggggugguaggugcaac

	repeat 1>	
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3120	CLUST.096738_S.30K4G8-M direct repeat 1>	ccgucgcgacucgcgcacgcgcgcgagaggcaac
3121	CLUST.096738_S.30K4G8-M direct repeat 2>	guugccucucgcgcgcgugcgcgagucgcgacgg
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3124	CLUST.096738_S.11CB3O-M effector>	MKHGVTPVWNACVAEREEAKKQYKELVDRAITDWVMDNKRDIPAKVEKEIRKSLVKKV AWPSAYSQYKHCSHTVNPHLSRFSSKMLQCTTGQVDGSEKSYREQRKKGDSKARPPKQ KFMHRSIMYRQSGWYPKTAEEINAMDVPAVTLTKLGRTGQSGRIRIKLHRPIEGRIKA VSLTQKNGRYYICFSCELDDFSGACGPIAAPKSGDIPDLRQKHTSTGGSDPKKGGAHN GKVSGIIFRRGGSDPKKGGAHNLIRLDSSATKGGSDPKKGGAHNVSYCSANVAIGGSD PKKGVVIEFLFWSGKFLRDSDGLEIPFPEFYWRDIEKLRELSRQFSAKKNARHEKRDG LGEKEFRGRNRLKAKRRLARWHEHKANKRLYWIWHVVGYYVANYRRIVIPKWPIKKEI EYALTNKDARTLCDGSYGKFVKCLKQKAGQFGVEVIEVKDERYEQEIARLLRVKENED HRQLLRETRKAVKHDQTWRFAYIRHRIKNVMLKQERKKDHGKKRKRK
3125	CLUST.096738_S.11CB3O-M direct repeat 1>	gguggaagcgaccccaaaaaggguggugcacacaac
3126	CLUST.096738_S.11CB3O-M direct repeat 2>	guugugugcaccacccuuuuuggggucgcuuccacc
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3134	CLUST.096738_S.6XHCYG-M direct repeat homology 1>	cggccucga
3135	CLUST.096738_S.6	ucgaggccg

	XHCYG-M direct repeat homology 2>	
3136	CLUST.096738_S.6 XHCYG-M direct repeat homology -containing sequence>	nnnn

		catgccgagccagagaaaatcactggataaatgcggtgtcgctctttgacagctacag attttcggggccgtgcagtcccttgccgcttccaagctatgcgttccgcgtggcttg cggcagaactacaggctctctaaagatcggtgcgtgccgcaccttgctggatcaactg taacgtttcgtcacagtccagcagaacacgaaccagcaggcaatgcccgctgg
3142	CLUST.096738_S.22SYVE-M effector>	MNQAIDEATTPIWNACVRERRAAFEHYLRKVEAIMVLEGMYAAADETAVRKRVARSHH WPTKYDQYALIRKRDLPPEHPYQRYNTAMLQCVVGQVDGAYQAFWGHWRSGDKEARPP QESRHFDCLMFRHSRVIQRDGYITSSGWRFEYAAGRRFARLTLHGIGVLKVRWHRSIE GRVKAVSVTRRRGKWYVSFSCEIDDFSGACSPLPASKSCVQQDLRQEHPVPGGADPNL AGADNHTVNMLSAMEGGADPNLAGADNRKCLRSCARRGGADPNLAGADNVRAGTPIRV RGGADPNLGGADNCESGGKTKRGGGADPNLGGADNGRAAAGGARVGGACTIWFPDGAF LCDSRGRTVNHPAFYQRQIATLRRLSRSLSRKLEARKHRTAAERERIAALPRWQRDRN IFKARRRLARWHEHVAAKRTDFLWRLAREYAERFDAVTLYTRPAKTPIQYAITSNTAL RLCDAAYGRFETMLRQKCQQFGTELTIKENPTWPQQKETLRQARQWQDLGKALRTAKS ALKKGSHKRLQSSLRDCARAVTREI
3143	CLUST.096738_S.22SYVE-M direct repeat 1>	gguggagccgacccgaauuuggcgggugcagacaac
3144	CLUST.096738_S.22SYVE-M direct repeat 2>	guugucugcacccgccaaauucgggucggcuccacc
3145	CLUST.096738_S.22SYVE-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3146	CLUST.096738_S.22SYVE-M non-coding>	ccgaaaaaggaccggcagctggcggtcgcgtcgatctacccgcagtacggagcgcagc tcggcgacgatcccggcggtgacatggccgacggcctgggcctggcggcgtggtggct gcggcagcgggcgggaaaggagttgtggacgtgagacgggcattcaaatatcgctgtt atccattgcgggcgacactgcggcggttgaatcaggcgattgacgaggcaaccacgcc gatctggaacgcctgtgttcgcgagcgtcgcgcggcgtttgaacactacctgcggaag gtggaggcgatcatggttctggagggcatgtatgccgctgcagacgaaacggcggtgc gcgggcgcgcagcggccgggggcgcacgcgtcggcggcgcgtgcacgatctggtttcc tgacggcgcctttctgtgcgactcgcgcgggcgcacggtgaaccacccggcattttac cagcggcagatcgccacgttgcggcggctgtcacggtcgttgagccgcaagcccgagg cgcggaagcaccgcacggcggccgaacgcgaacggatcgcggcactgccccgctggca acgcgaccgcaacattttcaaggcgaggcgccggctggcgcgctggcatgagcacgtg gcggccaagcggactgacttttgtggcgtttggcccgggaatacgccgaacggtttg acgcggtgacgctctacacgcggccagccaagacgccgatccaatatgcgattaccag caacacggcgttgcgcttgtgtgacgcggcctacggccgcttcgaaacgatgctgcgg caaaagtgccagcagtttggaacggaacttacgattaaggagaaccccacatggcctc agcaaaaggaaacgcttcggcaagcaagacagtggcaggatctgggcaaggccctgcg gacggcgaaaagcgccctgaagaaagggagtcacaagcgcttgcagtcgtcgctaagg gattgcgcacgagcggtgacgcgggaaatatgatccgtgcgacgatcttcgatacgct caacggcgcgatctcggtaggccagagcaacgtggtgctcaacgggctgggtaagttg atccagatcaagaagctggagcaccaattcggcgtggcccgcaaagcgatgcaggcgc agagtttcccgctcccgggcggggatgaataagggtcaagaaccgacttttccacggg ggtttggggtcccctgtcgcaccaaagtcctgcatgtagcggaacttgcggcaaaact acaccggcaccacccatgactgacgtaatggctattcccggcggtgtcggcgaccgga a
3147	CLUST.096738_S.3	MLRKTFKYRCFTNIGTAKKAFKEFDRNALVWNEALAVRNLYFELSKTYDQIRPIYDYK QQYWMIGQKYNPRFKGIDAQGLQDVQVKLHGSFRSFFELRKNGDKNARPPRYKNRYKC

	NWIJ5-M effector >	IVRRQSGWKLEEKNLYISGVGRFKIKLHRPIEGKIKTVTITRKGPKWFVSFSVEMPEP ELKNGKRKISLIFDDYFFLIDSEGGFVEFPEFYFSEIAELRRLNRSLSRKEKASNSRK KAKRALARWHEKIANRRDNFIKNKAFYYAENYDIIEISVLPYKNMIQYAGSSEKAMKL CDASRSKFTQALKFKCLEKGTILIERKDEQWQQQKEKSLETAKMQELQRLLRQAKRAV KRKCRARFKFLEMACERLTTLQI
3148	CLUST.096738_S.3 NWIJ5-M direct repeat 1>	auugcaagagacccugauuugggauguaguuac
3149	CLUST.096738_S.3 NWIJ5-M direct repeat 2>	guaacuacaucccaaaucagggucucuugcaau
3150	CLUST.096738_S.3 NWIJ5-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3151	CLUST.096738_S.3 NWIJ5-M non-coding>	tcggaaggtgttggagtggcgaaggaaatatctgacctggcaaagcgcgttcaggctg gcgaggaaataacggacatcgaaatagaggctgcccgtcagcaggtggcggattcggt tgccgaatgggacaaagcggccgggaatagttgataatgtaaacggccccgccctctt ttcgaaggtactttccgggcgggactgattttgaaaaattatggaaaatggaaatgtt aaaaatatacgagcatagcgaggcaggcagggatttttttgaggattatcaatacgga aatcaaaaaacttattgagtagtaaaagataatcagtggaatcagtgtctaagaaaaa cggataaagatgctaaggaaaacctttaaataccgatgctttacgaatataggaactg caaagaaagcgtttaaggaatccgatagaaatgcgttggtttggaacgaggcccttgc cgtaagaaatttgtatttcgaattatcgaagacctacgatcaacagcaaaaagaaaaa tcactggaaacggcaaagatgcaagagctgcaaaggttgctccggcaggcgaagagag cggtgaaaagaaaatgtcgtgcgcgcttcaagttcttagagatggcctgcgaacgctt gaccacgctgcagatctgattcaggcggcgcttatcgatctggagacgggcacgagca acagcggccgggcaagccagcatctgaacggaataggcaagattctgcagataaaaaa gatgcaggatagcgctctggattcggtaaaaaaaatcaacaaagatataggcaaattg ccgggaaccggtagaaaattcgcataattaatatcgaaaaaagttctttgaaaaataa acaaatggtcagtgtaatggccatggccacttaaaaaatcatataggatattaatccg tagatgatttttgtgaccgaatacaacctcttgttttggcaaagaatttgacaaaggc tgatatacttgatagatttgccgcgatgatacgggagcgtggccggcagctcggctac ggctctttcgtactcgattgtacattcga
3152	CLUST.096738_S.1 TWMT0-M effector >	MMRRSFKYRAYPNKGTRRRLFNVMRRAATPVWNVCIAEREQSRLLYRQKLDEACSGAV YDLRRDLTEKEEKAIRREVGKDIHWPTAYDQYKHIRKSDHAEYAPYSASMLECTVALA DSSEKSFRALWLKGHRDARPPKQTNFLRVLTFRKSGWSLDADKLTLMGIGTIPVRMHR PIEGKVKTVTIRQTRTGKWHVCFSCEITNFQGSCGPLSQPKTCVPQGLRQKHAPSDGS DPNLGGAHNNDAAGSVVGTDGSDPNLGGAHNGGGVCSSSRTDGSDPNLGGAHNGRGSS PQLAQDGSDPNLGGAHNNQRMLGQVQIYFPDDGFIVDSAGFEIPHPEFYTSEIAKLRR LSRSLSRKQKRSPNAEPDGSTNRGGAQPCLGRNRRRARRALAKWHERIAAKRDYFLWH VANYYARNYREVTVWTRPAKPPIQYAVTSQTARRLCDGAYAKFVNMLKQKCEQYESVI EIKENQEWQEQKETLTEVARIEAIQPILRKAKRAVRKNRVGHLKSLQRDCARAATVQI
3153	CLUST.096738_S.1 TWMT0-M direct repeat 1>	gcaaggcaaggcaagggaauuuugugaggtggga

3154	CLUST.096738_S.1 TWMT0-M direct repeat 2>	ucccaccucacaaaauucccuugccuugccuugc
3155	CLUST.096738_S.1 TWMT0-M spacer>	nnnn

		cggataaagatgctaaggaaaacctttaaataccgatgctttacgaatataggaactg caaagaaagcgtttaaggaatccgatagaaatgcgttggtttggaacgaggcccttgc cgtaagaaatttgtatttcgaattatcgaagacctacgatcaacagcaaaaagaaaaa tcactggaaacggcaaagatgcaagagctgcaaaggttgctccggcaggcgaagagag cggtgaaaagaaaatgtcgtgcgcgcttcaagttcttagagatggcctgcgaacgctt gaccacgctgcagatctgattcaggcggcgcttatcgatctggagacgggcacgagca acagcggccgggcaagccagcatctgaacggagtaggcaagattctgcagataaaaag gatgcaggatagcgctctggattcggtaaaaaaaatcaacaaagatataggcaaattg ccgggaaccggtagaaaattcgcataattaatatcgaaaaaagttctttgaaaaataa acaaatggtcagtgtaatggccatggccacttaaaaaatcatataggatattaatccg tagatgatttttgtgaccgaatacaacctcttgtttt
3162	CLUST.096738_S.5 BVMF9-M effector>	MLRKTFKYRCFTNIGTAKKAFKEFDRNALVWNEALAVRNLYFELSKTYDQIRPIYDYK QQYWMIGQKYNPRFKGIDAQGLQDVQVKLHGSFRSFFELRKNGDKNARPPRYKNRYKC IVRRQSGWKLEDKNLYISGVGRFKIKLHRPIEGTIKTVTINRKGPKWFVSFSVEMPEP ELKNGKRKISLIFDDYFFLIDSEGGFVEFPEFYFSEIAELRRLNRSLSRKEKASNSRK KAKRALARWHEKIANRRDNFIKNKAFYYAENYDIIEISVLPYKNMIQYAGSSEKAMKL CDASRSKFTQALKFKCLEKGTILIERKDEQWQQQKEKSLETAKMQELQRLLRQAKRAV KRKCRARFKFLEMACERLTTLQI
3163	CLUST.096738_S.5 BVMF9-M direct repeat 1>	auuguaagagacccugauuugggauguaguuacaac
3164	CLUST.096738_S.5 BVMF9-M direct repeat 2>	guuguaacuacaucccaaaucagggucucuuacaau
3165	CLUST.096738_S.5 BVMF9-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3166	CLUST.096738_S.5 BVMF9-M non-coding>	tgaaaaattatggaaaatggaaatgttaaaaatatacgagcatagcgaggcaggcagg gatttttttgaggattatcaatacggaaatcaaaaagcctattgagtagtaaaagata atcagtggaatcagtgtctaagaaaaacggataaagatgctaaggaaaacctttaaat accgatgctttacgaatataggaactgcaaagaaagcgtttaaggagttcgatagaaa tgcgttggtttggaacgaggcccttgccgtaagaaatttgtatttcgaattatcgaag acctacgatcaacagcaaaaagaaaaatcactggaaacggcaaagatgcaagagctgc aaaggttgctccggcaggcgaagagagcggtgaaaagaaaatgtcgtgcgcgcttcaa gttcttagagatggcctgcgaacgcttgaccacgctgcagatctgattcaggcggcgc ttatcgatctggagacgggcacgagcaatagcggccgggcaagccagcatctgaacgg aataggcaagattctgcagataaaaaggatgcaggatagcgctctggattcggtaaaa aaaatcaacaaagatataggcaaattgccgggaaccggtagaaaattcgcataattaa tatcgaaaaaagttctttgaaaaataaacaaatggtcagtgtaatggccatggccact taaaaaatcatataggatattaatccgtagatgatttttgtgaccgaatacaacctct tgttcggatcgccgccgcctatcggaggcgcggatt
3167	CLUST.104413_S.8 C75ZW-M effector>	MAKSDRKQPVDSGVGLLEVRLGAALSCPTRRLVADLEHVGLQVARAKTAMVRAFERWH EDHPGYDPGAVTRKDGAPCLLRGRPRPVNQPLPARMPVERELKCRKCKGTGALSAAPC PSCDGRGSKSWIDPATWLYHVGRRASPDVDATVMASCSKAVWAALQAELPWNHHGASA YRWQAIVNHEAGPGEVERTVYRSLAVPAPNSQTVLGYVGAVSRELPAKDARRVADCSA SSAVARFCLFSEESGRGTRDAIVRVEARQLTPGNRNVLRRVASGEWKMRDSALVYKEG KGRGKSRRKAKRNGAWFLQLCYHQPRVNLGLDPNREAVVEALPPDAGKPFRVECGPAC WGLGAAAMLEREALRLDARRRALRERFAVTGHGRRGHGRQRVERDIRPITRAVRDLVE

		RFIDGLVAEVVRFCVRFNAGSVLYREPGVRGRERSWFAGKGLFFDWTNFWMKLSQKCA HHGIELRKERPAKAGRAAAGV
3168	CLUST.104413_S.8 C75ZW-M direct repeat 1>	ugacaagagagugagugaaucggugg
3169	CLUST.104413_S.8 C75ZW-M direct repeat 2>	ccaccgauucacucacucucuuguca
3170	CLUST.104413_S.8 C75ZW-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3171	CLUST.104413_S.8 C75ZW-M non-coding>	acaagcagggcggagccggtgggtcgtaaagacgagggacgtacacggggttattgat caactcaccgccccgcgaaaccgcaaccgacacgaacaaacacaaggggtaatcgccg atggccaaatccgaccggaagcagcccgtggacagcggcgtcggactgttagaagtcc gcctcggcgccgccctctcctgcccgacccgccgcctggtggcggacctggagcacgt cgggctgcaagtcgcccgcgcgaaaaccgcgatggggagggagcggtcctggttcgcg gggaaggggctgtttttcgactggacgaatttctggatgaagctgtcgcagaagtgcg cgcaccacgggattgagctgcgcaaagagcggccggcgaaggcggggcgggcggcggc gggggtgtgaaggtgtgggcgggtcggctcacggcgggccggagtgccgaaggattc
3172	CLUST.104413_S.3 OMB2Y-M effector>	MKAITILKLPLAPTTEQLESLDAVARACRKSRNSAVENWLLRERGLPLSARQATPPQP RHVRNRITGQTEMRARETSSESTKLYHAMTAAVPKLDTSLVSSLASEINSHLRAQVDW RKRNGQKRTRADDILDYEQRPPFSQAMRVPVVSRKACFTYGPQTTLSVRFLRSGHGDV ETFAIPTERLGTRIKRKLLDIANGDRKLRDSYFHYRPERNRWYWYLPVEEDVAQPLDA TIILELRPSVDVADRPFQIGRRYVGDGRYLQSQLSRILTAEKEIGMSYRDRRTGAGHG RKKRDKAIAIKRLQRRHRMDEFRRKLIVDIVRTCERNNAGRILYREPSLPVRKRCWFA LVGIDFDWTRFLSDLKNAATRAGIEIDKRQWKWKEAFPSEEEPTEQLLQEPCVANS
3173	CLUST.104413_S.3 OMB2Y-M direct repeat 1>	gggcgcgguggauauaugaccggauugggaaugcgag
3174	CLUST.104413_S.3 OMB2Y-M direct repeat 2>	cucgcauucccaauccggucauauauccaccgcgccc
3175	CLUST.104413_S.3 OMB2Y-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3176	CLUST.104413_S.3 OMB2Y-M non-coding>	tggactagatttctgagcgatctgaaaaatgcggcgacgagggctggcattgaaattg acaagaggcaatggaagtggaaggaagcgtttccatcggaggaagaacccaccgagca gttgctccaggagccgtgcgtggcgagttcgtagggggcctcgccgccccaatggcga gcagccaacgaccccaacgtggtcgctggaactctcgctggaccgtggaaaatcacga gcccatcccaatcgggcaagtcgattttccaattcccaatccgcgtcacgcgcggccc ctggtgcaactatttaccaggaacgctagagcaaggagttgaacgatgcaaaaaaagt cgaccagccagaaacacgctgaattgaagtcgctcggaaaggactgccgagacaagat

		ttggaggaggcttcagcttaccgaggaaatcttgagggaccacgaatatgtcgacgcg aacttcggaagcgaggcgcgatctcggtccacgaaggacgaaccggacccaaaaggac gcactgactggaaggctgaatgccagaggctacaacttcgcgtcaaggaactagaggc agagattcgtgttctgcgtgaagtgctggagaaatccacaagtgtcaagagttagaac acttccgtgcgcgagttgcgacgtgctcgtccgtgtcgcgaatcgcgaggctttcctg gcgatggtgcgaacggggcgccagccgctgtgctcgcagtgtgggcgatacgtgtcac gcgagcggtcgagtgctggcgaaataccggcagccgctcgcgtgacgcaacgccacga cggagatggagttgcgtccactagactcatcggcgataggatggttcgcgacaagcgt gctatggctctcgcgagcaggcgcgtaaagcgagtgctggatgcaccttgcgacagcg ggtcgcgatccctcttggcttgccggtcccaacgagggcgcggtgg
3177	CLUST.104413_S.3 OMB2Y-M direct repeat homology 1>	auucccaauccg
3178	CLUST.104413_S.3 OMB2Y-M direct repeat homology 2>	cggauugggaau
3179	CLUST.104413_S.3 OMB2Y-M direct repeat homology - containing sequence >	gcagttgctccaggagccgtgcgtggcgaattcgtaggggcctcgccgccccaatgg cgagcagccaacgaccccaacgtggtcgctggaactctcgctggaccgtggaaaatca cgagcccatcccaatcgggcaagtcgattttccaattcccaatccgcgtcacgcgcgg cccctggtgcaactatttaccaggaacgctagagcaaggagttgaacgatgcaaaaaa agtcgaccagccagaaacacgctgaattgaagtcgctcggaaaggactgccgagacaa gatttggaggaggcttcagctt
3180	CLUST.104413_S.1 688F7-M effector >	MKSITVLKLKLTDPPAELTEVARLCREARNVASEDWLLRARGRKESAKQAKLNRQGKP LSESTKLYHAITTSVPRLGTDVASNIAQQVNSFLAAKVDWRKGVADNGKRPKRKDAIL RREERPAFYTDLSVPIANKHTTIVFEDDVQVHVRNIMRNSLQISLDFTISLKGVPTGI KRIIHDLARGERKLADSKLLERRGKWYWYIPVAFETEQLDTDRIATLSPVIGKGEIER PFSLEIPGRSRAWGIGAGRYLISQTLRLVGVRKQIGWRYRQRMGAGHGRKKIDIAVSK RNLQLADIVTEVRRRAIVDVVKQCERHRCGVLEYLEPTNPTKEKCWFEANGLTWNWTR WLDDLKNAAARRGIEVKVRKLRLGDIDNGEDSS
3181	CLUST.104413_S.1 688F7-M direct repeat 1>	guugcagcgaacgaaugauugguuugggauugugag
3182	CLUST.104413_S.1 688F7-M direct repeat 2>	cucacaaucccaaaccaaucauucguucgcugcaac
3183	CLUST.104413_S.1	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

	688F7-M spacer>	
3184	CLUST.104413_S.1 688F7-M non-coding>	agaggcgaagtgggagcaatcaatcaggcacagccgtagtcaaacgggtgctcacagc ccgaatggcgagcagccggaggtcttaatgtgacagccggacctctcgccaaattccg taaatccgcgatgtggattacgtcaggacgcggaaatcccaaaccgagcggctgtgtc tgattgatggttcctgttttaagtcttcgtttttgaaaggaaaatgaaatgagtacga gtggacagaagcgagcagaattaaagaagctcgccaaacaatcgcgagagaatatctt tcgcatgctgcaactggttgagaaaaatgctggttcgaggcaaacggcttgacttgga actggacgcgatggctggacgatttgaaaaatgcggcagcgcgtcgtggaatcgaagt caaggttcgcaaattgcgactgggagatattgacaatggcgaagattcgtcgtgagtt gccatgcgaagtgtgtggcaagtcggtgcgactgtcgcgcaaaagatttttgcaaatg gtgaaatctgatcagttaccgatttgcgagcagtgccgtagatttgtgaggccgggaa ccgctcgcgtgtcagaacttccttctgagcaagagtttccgaagctgggacttgcaag gaaggttggaagaggtgccaatcggcaggggctctcgcaagtatgtctttggcccgt tgtggcgaaaggacttatggcgacggaccggagaggttccggctacgtttagggaggt tgcagcgaacgaatgattggtttgggattgtgaggggactggcggacgccgccgccg cgcggacgtggcttgttgcagcgaacgaatgattggtttgggattgtgaggcgggcat gtatcgctgcaagccgctttccttcgcgttgcagcgaacgaatgattggtttgggatt gtgagttccgcagtacgctgatgtagtaacctttgtgatggttgcagcgaacgaatga ttggtttgggattgtgaggtgccggctaaaggatggagcccttatcttggggacatat ttggatgcaactaaccgcccaccaactcgacgccctcaactccgcaaccatcggcacg gtggggctactcaccggcggacccggcagcggcaagactacttgccttgggcacctga tccgccagctacgccaacgcaacggcagcagcggaatg
3185	CLUST.104413_S.1 688F7-M direct repeat homology 1>	ucgcugcaa
3186	CLUST.104413_S.1 688F7-M direct repeat homology 2>	uugcagcga
3187	CLUST.104413_S.1 688F7-M direct repeat homology -containing sequence>	ccggagaggttccggctacgtttagggaggttgcagcgaacgaatgattggtttggga ttgtgaggggactggcggacgccgccgccgcgcggacgtggcttgttgcagcgaacg aatgattggtttgggattgtgaggcgggcatgtatcgctgcaagccgctttccttcgc gttgcagcgaacgaatgattggtttgggattgtgagttccgcagtacgctgatgtagt aacctttgtgatggttgcagcgaacgaatgattggtttgggattgtgaggtgccggct aaaggatggagcccttatc
3188	CLUST.104413_S.1 58IE3-M effector>	MGQPETTKCVLKLRLGASLTGPTKRMARDLHQASLLYNQCRNAIVRAWERSAEDNPSE TFAMFVCRCGAAERRASRKAAGESKVREHCTCEDNPCEVARQACPLLAAKITTSCATQ EVSAKLRSKLPWNRPNKAHRYIWQGILANQVARPCYRGSELPVPCQDAKLSLTDSGYT LSFPVWSLASGRQHRNFLCRIPTKRLTRGYKRILFNIVKGEWNLCDSRLQFHEPRSRQ KKGFWAIHLVYDRKQDPIAGLDSKQVARLTLQPKDAKKPFDVSTDGVFKPWLLGDVDV YLGFLSRLETRRLEMRLRHKEKGSGRRGHGRGRTEKAIRPATRKARNIARLFQWRIVA QLVRFCERYGCGVVEFSEPKQGQKNASWFAVPGRPWTWADFMSRLKHKLWVNGIDLRE SEGGEQKQARRSRGPKVNGGTGNGKMPHNGGEVANGKNGVARKTGRKAGRGRDEK

3189	CLUST.104413_S.158IE3-M direct repeat 1>	cagcaggugauggugagac
3190	CLUST.104413_S.158IE3-M direct repeat 2>	gucucaccaucaccugcug
3191	CLUST.104413_S.158IE3-M spacer>	nnnn

	homology 2>	
3195	CLUST.104413_S.158IE3-M direct repeat homology-containing sequence>	actgcggtaacgacgtaaataagcacaccggaccggcaggttcgggtgtccctcgtcg tccagtcgccacgcacgaaggcgatgcactctcgcttaaggccacgccctcaggggca aaacacgcgggagatgtgtcgatggcctcccgcaaccatcaccgaccgcgccggccat cctattgctctcgacggaagcgtggtgcgaggaagttttctcttccatgcctttactg tgacaagccagtgtccatgaatgctggccgtttcatcgagttgttcgacgccgacaag cgtccggtatgcagaaggt
3196	CLUST.104413_S.3X18JK-M effector>	MKSFTVLRLKLEDDEATSATLASIGQLCRRARNAGLEDWLLRQRGKPESPRQSQRLVK RKDVDPDSEKSESTKIYHALRAAVPELGTTQCTMLAAALWSNLTAKQDWRRGATEEGR RLRRLHAILDYQDRPPFFTTLEIPLHNAHTTVRFTDTLTVTVNRPTSAIPALTVQVCL GGMPSGYKLLLHRLARGELKLADSKLVERDGIWFWHVPFTFETDPRSEIVAELWPRIP AAEKAKAEADSPRRADPNGNGQHNGKLPPAPAQARAAKHAQRPFRLDLPGGDEWFVGD GDYLKAQTARLIGLRKQIGWRYRNRMGAGHGRRKIDAAVRRRRQQERNMRQEVLRHMI ADIVRQCLKANVGTLIYHEPSGPLREHSWFAAAGLTWDWTRFCQDLKNAAARQSIAVT VKMWKRGEAIPEDQADPGTQSASAAGAVASKRFGKARNERCGGAVDD
3197	CLUST.104413_S.3X18JK-M direct repeat 1>	ggcgcaguagaugacuaagaggcuuggugaugcgag
3198	CLUST.104413_S.3X18JK-M direct repeat 2>	cucgcaucaccaagccucuuagucaucuacugcgcc
3199	CLUST.104413_S.3X18JK-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3200	CLUST.104413_S.3X18JK-M non-coding>	gaactcgaacaggccaaagccgccctggaagagtaccgccgcaccaacgccgaactgc gcaataaccacgaagcgcatctcggcgagatcggcgaactgcgcggccggctggcggt gctggaatcgctcaccaagaaccgggcggcctgagcccagtggccggcgggcaccgaa cgccggccggcgcggcgagtgaaggagcggcaagatgcaacggcgcaaccgcccctgt gaagtctgcgggcgcgacgtggcgatccgcagccggcgcaggttcctgcagttagtcc gggacgatcagccggtacgctgcgagcagtgccgtcgctacgtttccccagggaccgc tcgcgtgtcacaactacccagcgagcacgtacttccggcgatgggattacgggccaaa ctgcgccgtaatgcgaaacggcgcggggtgctcgaaagctgccccctgggccgttgcg gcgcaagcagttcgggagccgcacgaggtaatgcgtgcccagaagggcgcgaagaaaa aggaggcgcaggcccatgaaatccttcacagttttgagactgaaactcgaagacgacg aggccaccagcgccacgctggcgagcatcggccaactctgccgccgagcccgcaacgc tggcctggaggattggctgctgcgccagcgcggcaagccggaatcgccggtgaccgtc aaaatgtggaaacgcggcgaggcgatccctgaggatcaggcggaccccggcacacaaa gcgcgagcgccgcgggcgcagtcgcaagtaagaggtttggcaaggcgaggaatgagcg ctgtggcggcgcggtggatgactgaaaggtttggcaatgcgagggaaccagccgccgc ctggagtacttcactgagcgcggcgcagtggatcagtgaaaactttggcaatgcgagg cgatgcgagcgagacgaacgccatttagtcattcgtccttcgttattccttagacatt cgtcattgggttttcgtcattccccccagcctacaccttcgccctctgccccttttcc tccgccttcttccgctcccgctgccgccggctccagatccgctgggcggcgttgagtt

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3207	CLUST.104413_S.6 PRVDY-M direct repeat 1>	aaugaaggguaagugcaag
3208	CLUST.104413_S.6 PRVDY-M direct repeat 2>	cuugcacuuacccuucauu
3209	CLUST.104413_S.6 PRVDY-M spacer>	nnnn

	repeat 1>	
3213	CLUST.104413_S.68OT58-M direct repeat 2>	cucgcaacacacauucguucguucacucguucucac
3214	CLUST.104413_S.68OT58-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnn
3215	CLUST.104413_S.68OT58-M non-coding>	gttgccaaattgaccgaggagggcgcacggcttcgcgaggagaatgcggacatgcgtg accgagtggctcggctggaaggagccattgacgaacgccgttctctcgcacgagtagg gtaatgcaagcgattctcgaagtgaaactcggccgtccctaccagatgcctgccaagc ggctccagaggctgcttgagcaggcaaggcgggactgttgcaagaccaggaatgcggc gatcacgcactggctgttgtggcgacgatcgaatccccctttgcgagaggaagaactc tttgctcgtgagagcatgccgttcgactggacggcgttgtgtgggcgacttcgtttca aagccgagtctaaggggctcgcatttgagacaacacggatcggaatggccgaatggag ggaagggaagtgaaagatcgcggaccaagtcgactgacgatcgattgcgagatttgcg gtgaaccaatgcaggtgaatcggaagcgatacgtcgagttggtgaaagcgggtgagcg cccccgatgccggaagaacggttgcgagaggttgtgtggcgcgaaaaacccccgtacc tctcgcacgtcagaagtggttctcggtgaacgagttggggcgttgttggtcagcagga ctggtcgcaagaagagccggaaaccgggggccctcgaaaagctgcgtgtaacacgttt gactgtcgagggttgcgcggactgct
3216	CLUST.104413_S.3ZK1L6-M effector>	MPPAILEIKLGRPYEMPERRLHELLARRRLECCIARNAAVTHWLVWRRTHPDWEPGGP YDSPPRKIKRAAKPQAKPASGPPKDPPFAPREFLSRELYSVAAAAAPALNTSVISSCV QEVNARLRAKTPYDHDGMARWVWQAILASEVSLPTWRGGRIPAPRSVTVLHYDADSCS LRFALSSKRSGYRVLSPEVRLHAGDLTAGNRRLLQRIAAGEVRMADSQIVERKGKWYF QLCYEMPKASECDSERVLTLMPGKPEAEYPFRLLWTDRDGKLRDWTAGKAKPLIAEYR RVQARRRAMRFRYRDGAGSGHGRQRWAKGIKPLERAVRDMCGRWQKQFISDMLKVALK EGCGMVLYREPTKPLREKEFFARSDMPFDWTAFIGRLKFKCESKGLRFESERIGLAEW RGESEKQETAT
3217	CLUST.104413_S.3ZK1L6-M direct repeat 1>	agggaaugugugaugcgag
3218	CLUST.104413_S.3ZK1L6-M direct repeat 2>	cucgcaucacaccauucccu
3219	CLUST.104413_S.3ZK1L6-M spacer>	nnnnnnnnnnnnnnnnnnnn

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3221	CLUST.10 4413_S.3 4FVZI-M effector >	MPPAILEIKLGRPYEMPERRLHELLARRRLECCIARNAAVTHWLVWRRTHPDWEPGGP YDSPPRKIKRAAKPQAKPTSGPPKDPPFAPREFLSRELYSVAAAAAPALNTSVISSCV QEVNARLRAKTPYDHDGMARWVWQAILASEVSLPTWRGGRIPAPRSVTVLHYDADSCS LRFALSSKRSGYRVLSPEVRLHAGDLTAGNRRLLQRIAAGEVRMADSQIVERKGKWYF QLCYEMPKASECDSERVLTLMPGKPEAEYPFRLLWTDRDGKLRDWTAGKAKPLIAEYR RVQARRRAMRFRYRDGAGSGHGRQRWAKGIKPLERAVRDMCGRWQKQFISDLLKVALK EGCGMVLYREPTKPLREKEFFARSDMPFDWTAFIGRLKFKCESKGLRFESERIGLAEW RGESEKQETAT
3222	CLUST.10 4413_S.3 4FVZI-M direct repeat 1>	agagggaaugugugaugcgag
3223	CLUST.10 4413_S.3 4FVZI-M direct repeat 2>	cucgcaucacaccauucccucu
3224	CLUST.10 4413_S.3 4FVZI-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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3226	CLUST.10 4413_S.0	MAKQNPARKRLKPTKVLIDLELGKCLTINTKKAHEVLHFIAHSCNLARNKVVRDWEAW RRENPDWQPQQRTGRGKMPKFINKKVPVKGTSKFAVQKIPKMEHPAISQEIENMLYHS

	BYHJ1-M effector >	VVSVSPHLHTNLTSKCKQEALVPIMAKAAWTDGGYKYERILSYEDRLPSFHGSVIPVQ NADAILCYDGVTWAGGKVSDNSKAVTQKHSASCVFGIRLLRYPKANSDFAWPEQLPKK KQLEFLLFRLKIDDLHDGIKKKLKEIASFVAPPKTKDGKESKKLMKFGDSKLVFSGGK WRLQLLTTAHPSDPLDTSKVAILVPMPSGSFYPFVLHLPDGTTRKIGNQRGCTSCYRD RSIQFEHHKRLRCDRFRKGIGKGHGRARIFDERSRLTGKSRAYQKHFLQNVVIDAVRE ATRAGCGSVIYREPNLWLRQMMWNEVLAERIDKDTKRYTLVGLVLNSKGRQIHAPYSL PRNFSLYFDWTKFDGYLKYKMEQAGICVTSSRIGYKEYNLFLTTGKITVGEKKGEKAK KNGEVSAKKQSANGSNCKTPARNGSANGAKKTSKKGPLAKSKIRRKGAKKGSRKPDNA PSASK
3227	CLUST.104413_S.0 BYHJ1-M direct repeat 1>	aucgcaagaugguagaaaaaccgagaguguuguga
3228	CLUST.104413_S.0 BYHJ1-M direct repeat 2>	ucacaacacucucgguuuuucuaccaucuugcgau
3229	CLUST.104413_S.0 BYHJ1-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3230	CLUST.104413_S.0 BYHJ1-M non-coding>	aatggtaagagttctatggccaatgacgtagcatgcgttgcatgccacgtgtttcagt tgaacgcggccacgagctttatcacattatgtgacgggccatctggtgctaaaaaagt tttggaggaggcgatcaagcgttttccgaggtaagtacctcgggggtctatcacagg cccaagaaaggcgagaagtactgtggtcaagtttgcttggtgtatagacaactcggac ccgaactcacaacgtttgggataatccgatgtcacctgttgcctaccgcacagccact ctcgcataactgccccgaatgccgtctggatagcttactcagtaagcgctaaggcccg gacggaacactctcactgctggggccccatgaggggccccagctttattttgaaagga cgccacgaaatggccaaacaaaaccccgcaagaaaacgcctcaaaccaaccaaggtgc tgattgacttagaactcggcaaatgccttacaatcaacacaaaaaaggcacatgaagt tttgcatttcatcgcgcactcttgtaacctcgcacgtaacaagtcgaactgcaaaact cctgcgagaaatggctctgcaaatggtgcgaagaagacctcgaagaaaggacctctcg caaaaagcaaaatacggcgaaaaggtgctaagaaaggctctcggaagccagacaacgc accttcagcttctaagtagctagcaatgatatttactctttattgtaagttgccgctt gcaaaacggtgttgtgaccgttgatgcttattattggatcgtcgtagtgttgtgaggc gggcttgcccttgttctcatcgcggagacaaagtagtactatgggctgtattaaaagc ccaagcgatttggtgttgatttggtgttataaaaacaccaaatcaccaatcacatatt ttaactagttatagagcagttttcgtggattttaaaatagtcagtcaattcgggaaga gcaaaacgggccttcagatatcggagggcatgtatcacggcaagatgcaatatggcat caaggcgctctaccctctacagcgtgccgcgtttgaggcactggttggcaagcaatat ttcctgcttgagagcccaaccgcgtctggtaaatctgtgactctgcaggctctaattc ttgctaaaatggcacgtagccgaaaaactaagtgtattatagcagtgccgcaaacaaa tatcgcaagatctttctgcaacaaacaccgcatacaacttcctgtcgggggcatttac tcgtggagcactagaacgtccagacctgttgagcttagaacattcttagacttcctca gacagtctccggagtcgcggccttcgagaacgatagtggttacacacgctatgttgct caatgtcgcgcgacaatccgataaatttggggatatactagagtatctatcggacact gtcatcgtcattgatgaggctcaccatcttaatatgggaggcatagaaaacaatcaac ttgcgaagttcataaaacgaataattgttaataagctgaacacatgtgtgtggctagc aacagctactacatgtcgcggcgacaacagtccaataatagacgccgcgcatatagat aattttgaagtgttctcggtgtctttcgaagagttctgggacagcacaaacctcagat ggtt

3231	CLUST.104413_S.0 BYHJ1-M direct repeat homology 1>	aacacucuc
3232	CLUST.104413_S.0 BYHJ1-M direct repeat homology 2>	gagaguguu
3233	CLUST.104413_S.0 BYHJ1-M direct repeat homology -containing sequence>	agtttgcttggtgtatagacaactcggacccgaattcacaacgtttgggataatccga tgtcacctgttgcctaccgcacagccactctcgcataactgccccgaatgccgtctgg atagcttactcagtaagcgctaaggcccggacggaacactctcactgctggggcccca tgaggggccccagctttattttgaaaggacgccacgaaatggccaaacaaaaccccgc aagaaaacgcctcaaaccaaccaaggtgctgattgacttagaactcggcaaatgcctt acaatcaacacaaaaaagg
3234	CLUST.104413_S.13J5ZE-M effector>	MLQGRKDNDGMITDAKGVTSILKLKIGRPLNMPAKRLAELLEQGRRDCCRARNATVTH WLLWRKQRPDWKPGDPYDAPEAKIKRKPADPAKPPPKDSPIGPRLFLSRELYEVATRT AVNLSATVASSCVQEVVDRLKSNTPYNHDGDARWNWQAILNAEVSLPTWRGGTIPSPK QTATFTYNDHECTLRFPLLSKSSGYATISPTVRLEVGDMSAGHRRLLQRIASGEIRMA DSNICERDGKWYFNLCYTVPTVVSGLDTERVLTVYPTLPDEKWPFVVTWPTEGTETAR WYIGKAKPIVADYRRVVARRRAIRYRYSDGTGSGHGKQRWYQTIKPMARYVVDMQARF EKLTCSDIVKLALREKCGTILYREPTMPVRDNSWWAKQDVPFNWTSFDARLRHAVTKA GLQYEVERIRMGEWRPKEQKSAS
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3237	CLUST.104413_S.13J5ZE-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3238	CLUST.104413_S.13J5ZE-M non-coding>	ctcttggacatgctgaaagactgccacacactggaacggcacgccgaactctgccaac gctgggaacaggacgtggaacagatggacgccggggtgcatcaggaggggacgaagat cctcgcagaacacaaggccaagctaggcggttgagtgctggggtttgggccgcacggg cgagttgcggctaacgtggagcgtgttgtaggcacgttcctcaaggccagtcggtgaa gctggccagttttgaatcactaggggcacttgcagccccaacgagaggcgagaagtac catgacacccaaaggacaccaatgccgcatccatgccgttcgcttcggcgagcggttc ggtcggcagtccaatggctcaggcaactctcgcagaattgccggcggaaaaggctcga

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3239	CLUST.104413_S.13J5ZE-M direct repeat homology 1>	acaugcucuc
3240	CLUST.104413_S.13J5ZE-M direct repeat homology 2>	gagagcaugu
3241	CLUST.104413_S.13J5ZE-M direct repeat homology - containing sequence >	gacacccaaaggacaccaatgccgcatccatgccgttcgcttcggcgagcggttcggt cggcagtccaatggctcaggcaactctcgcagaattgccggcggaaaaggctcgatat acggactctcgcaagagactccacggccgggccgacatgctctcgcctctacgcggtg gttcgctgccgcgtagaggtttttcaaatcacaccgtttctgtatcccaatcacacga ggagtacgtatgaacgcaacgaagaaggcattgttggaactgaagcaactcgccaaca aggcggcagacacgctctac
3242	CLUST.104413_S.75W8SR-M effector >	MASKSLKSITVLKLKLDLSDEQKELLTDVAKLCRKARNAALENWLLRKRGLPETEKQA KPSRKNVGEGLKESTKIYHAVRLAAPTLNTAMVSMIANGIDSNLRSKLDWRKQPGAVD GGEKPKKAVRADAILAYDDRPPFFTKFEIPIRSAISSFTFVEWPELSTPFYVGAKVDL KLRTSQLKGGHKRLLHELAAGTRKLSDSRIVEKDGEWFWHVPIMFETVVRSEIEATLW PVFDAKSSRPFDMDLPGDRTWGIGDGRYYIGQATRFIALRKAIGWRYKQRSGAGHGRK KIDDAMRKRWCQWQCIATEFRRRAINDVVKQCVRGNIGTLIYREPSLVVREKSWFDLN GLDWDWTRFLGDLTNAAARQGIDVVKRPLKLKEYKGNEPSPATV

3243	CLUST.104413_S.75W8SR-M direct repeat 1>	cccgugagguggaucaauagauggaugaggguugcgag
3244	CLUST.104413_S.75W8SR-M direct repeat 2>	cucgcaacccucauccaucuauugauccaccucacggg
3245	CLUST.104413_S.75W8SR-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3246	CLUST.104413_S.75W8SR-M non-coding>	aattgtgggatatagctacgagaggagtgaaaaatggctagtaagagtctgaaatcaa tcactgtcttgaaactcaaactcgatttgagcgacgagcaaaaggaactgcttaccga cgtggcgaagctctgccggaaggcacgcaacgccgcgctcaagaactggttgctgcgg aaacgcgggtggtttgacttaaacggtctggattgggactggactcggtttctgggcg acctcacgaatgcagctgcacggcagggaatcgacgtggtgaagcgaccactgaagct aaaggagtacaagggaaatgagccatcgccggctaccgtgtgattgttgcggcaagga agtttcgatccaaagccagaagcgttttctggcgatggtgcatggcaatcacaaaccg ctttgcgagcagtgcggtaggtacataagaccggccaccgctcgcgttccagaagtca gcaaggggttagtcttacggcattgggcttggtcggtgctattggggcatcgggcaa gagtcgtaagccgctcgcaagttatcgtctgggtcgttgcggcgtaacgggttacgag agtgg
3247	CLUST.104413_S.1EXWHV-M effector>	MPTQVLEIKLGACLTMPTRRCHALLAEVARDCNLARNGALRHWIRWREDNPDWQPAQR RRRDGSPKVSAAGKPVLEDPAMSQAEENEMYYAARRLAPRVSSNVITHVRGEVLAKLK AKMPWNHPGSARYFWQGILAYEISAPSWRGEAIPVPNNSAAICYCGEFNRETNAEAMR HCGASSCVVRFPLLSKNAGMRERSPICRLEVRQLSKGNRAVVRRIAHGELKMSDSKLV HKRGAWFFQLTYKQPARDHALTIDRVAVLTPTGPDCRRGPFELLFPPEGDASGRAFQR RWYVGDAAPLEAEYRRLAIRRRVIRNRYKDGAKRGHGKQGFYRALRPFSRAFCDMEDR FTKHLVTDIVAACIKQDCGALAYREPTMPLRDKLWFGVRGIPFPWTQFAGRLKFKMAA NAIEWQTTKRLGVAQHRQEYGWGQDDEKAS
3248	CLUST.104413_S.1EXWHV-M direct repeat 1>	ggugcagcggaugaauaacgacaggaaugaugcgag
3249	CLUST.104413_S.1EXWHV-M direct repeat 2>	cucgcaucauuccugucguuauucauccgcugcacc
3250	CLUST.104413_S.1EXWHV-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3251	CLUST.104413_S.1EXWHV-M non-coding>	aaagcgctcctggaatggacggaagcgaaagacgaagcatctgcctgcaagaagaatt tcgaccgtctgaacgacgagctgctcgacatgattcacggcgggccggactggcaaaa caagctgccgttcgatgaaggggaagaggagtagcacaaaacactgggggactcgcac ccccatgagaggcgagtagtaccgtggtcaagaaaaccggaaaccgcctgcgttacgc acggagcaattcgttcgtccaggtatccggtacacgagcgcacggcaactctcgcaga

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3252	CLUST.104413_S.1 EXWHV-M direct repeat homology 1>	ucauuccugu
3253	CLUST.104413_S.1 EXWHV-M direct repeat homology 2>	acaggaauga
3254	CLUST.104413_S.1 EXWHV-M direct repeat homology -containing sequence>	taccgtggtcaagaaaaccggaaaccgcctgcgttacgcacggagcaattcgttcgtc caggtatccggtacacgagcgcacggcaactctcgcagaaggccggcgaaacgaaagc ccggatattcgcgcataggcgcacggcctgggcgtcattcctgttttggcggtgggcg tcttcgggcgcctgccgctgttttcaacagaaggagactgacggatggaccgagcgga aactaaacagcgtcttatcgagctgcggcaacttgcaaagctggcagaccagaacatt taccgccgcgtcagccttgc
3255	CLUST.104413_S.0 H259E-M effector>	MPTLVIELKLGSAISMPTHRLNALLTQTALDCDHARNAAVRFWERWREDNPEWKPEQR RTRDGSPKANADGKPVLESEMISQAAENEMYHAARRAAPNVNASIVTHCRGQVLDALK ARTPYNHEGTDQFVWQAILANERARPCYRGGTIPVPNNTAGFVYSGSASKKASKAAIE AGQDQAVLQFALLSKDSGYHCMSPIVRLHVRELSAGTRRILKAIAEGRDGYSFCDSSI VNKGNFWSFQLVAKVPTKDAGLTPSREAVLFPQPGDQRRPFVLEMPDNGRRYIGNGDV LKRIRQQQVIRRKTLQARYREGVAPGHGKGRFFERLRPHSRQWPLVESMFTKMAVADI VKSCLRNDCGTVVYREPTMPVREHRRMWFAEHGIPFDWTRFEAQLLNACEKVGISVKV FGRKQKEMRADRINMAEWRERIGDVSTAEENDAGSGNASLPDVRSGSAAGNGKAAGTG ASRGKAVLR
3256	CLUST.104413_S.0 H259E-M direct repeat 1>	gugagaacaagucgaagugagag

3257	CLUST.104413_S.0 H259E-M direct repeat 2>	cucucacuucgacuuguucucac
3258	CLUST.104413_S.0 H259E-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3259	CLUST.104413_S.0 H259E-M non-coding>	tggatcggtttgagccagtcgtgcgcgactgctggcgatgcagcggagagggagccgt tgttgagccggctgtcgagttcgtccagcgcgtcacggagggcgcgtcggcggatgtt ctgcgtgaggctctggcgtgctgtctggcgcggacagagttcgaggctggcgaagtct gcgtgcaggagcggcagacgatcgaaggcgtgatcgctgcgggcgtgagcaggcagtg actgtctgttctgaatatagaaggcgtgctgcaaagggagtctctcactcccatgagt ggcgagaagtgctgatgtcacgaactcggaatcactgtgcgactggtttgcattactt cgacgcgaaccagccacggctccgaatcagcggtcagtaactctcgcagaaggccggt gaaacgaagtccggatagacggcgtgtaaacgccacggcctggacgcttcgacgccga caggggggctgagtgcagcctcagccccctgtctctttcacgattcttttcttcaacgc gggaggagcgaacgacatggcgaaagcgaaaagtacgaagcagttgctggttgagttg atgaacctgtctgagacggtgtcgcccagcatttaccgcatgattcagattgcggcgg cagtgtttggtgatgcggcgtggatcgctgaggagcacggcggcagcagcagagaggg gaccgaccatgccaacacttgtgattgagttgaaactcggctcggcgatttccatgcc gacacatcgcttgaacgcgctactgacgcaaacggcactcgattgcgatcacgcccgt aacgctgccgtgcggttctgggaacggtggcgtgaggacaatagagaaaggattggcg atgtctcgacggcagaagaaaacgatgccgggtcagggaacgcttccctgccggatgt gcgatcgggaagtgccgctggcaacggcaaagcggctggcactggtgcgagccggggt aaggccgttctgcggtgattgtcgaagattcgagcggttctgtgccggcgaaagtgcc ggaagcgttcgcagtgaggaagtgcgtgaggatacgggagttgcgtgtttgcgatttg tgccggctggtggtgtgagaggccatcaatacggaccgctcgcaagggggcgtgtaac gtgtgttgggacttcgccttgcgatgcgcgcg
3260	CLUST.104413_S.1 RDYWU-M effector>	MKSITVLKLKLDISDDVRQQLESVASHCRHARNAAVEDWLLRMRGKPETAKQSTRLCK HAKHEGKPKSESTKLYHAITAAVPELGTTNASMLASAISSHLSAKVDWRRGKSPDGTT PKRKDAILAYEDRVPFFTGDCIPVRSKDSTLAVSDGQWSLTVRRPLRDLDYLAGDIAS RGLSPGIKKILAAVATGERKFADSQILLTSKGWMWHLPVQFEADQLDATTEAHLWPVI GAEKNGRQADRPFAIHLPNQQRPWYAGDGRYLLAQTQRLIGLKKQIGWRYRQRMGAGH GRQKIDAAVRRRSKQLDNIRAEVRRRAIADIVSQCVRAKCGKLVYHEPTNPAKDRLWF AAMQLDWDWTRFGVDLKNAAARKGVEVVIQKLKIKEVINAA
3261	CLUST.104413_S.1 RDYWU-M direct repeat 1>	ggcggaggagaugagugaaggguuugggaaugcgag
3262	CLUST.104413_S.1 RDYWU-M direct repeat 2>	cucgcauucccaaacccuucacucaucuccuccgcc
3263	CLUST.104413_S.1 RDYWU-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3264	CLUST.104413_S.1	tcgccacgacataaggaatagccacacaagcaatcgcagtcagttgacagtcgggttc tcgcaccccgaatggcgagcagccggaagccgcaaccctcggcagccggacctctcgc

	RDYWU-M non-coding>	caaaccccacaagtgccggattaacgggccggcaattcccaaacccgctgactgcgat tgcttgtttggctaaccgtttttcactggaggcaatgaagatgacaaagaaaatgacg acgtcacaaaaacgcgcggagttgaagcgcgtgagcaaggccgcaaaagatggcgtgt ggcagatgcttaatctggctgaccagcaaaggacaggctgtggtttgccgcgatgcag ctcgattgggactggacacgattcggtgtcgacctgaaaaacgcggcagcgagaaagg gcgtggaggtcgtgattcagaagctgaaaatcaaggaggtgatcaatgcggcgtgaac taccctgcgaatgctgtggcgtgatggtgcggttaggcaaggcgagattgcgcgactt agcacgccgcgacgcgctgccattttgcgagcagtgccgtaggtacgttaggccgggg accgctcgcgtgtcacaactcacgacagagcaagtagatccgtcgctggggttatcgc gaaagcgcggcaggggcgcgaaaccggcgagggtgctcgcaaacctgcctttggcgcg ttgcgggcaaagggtttgcgacgacggcc
3265	CLUST.104413_S.1 RDYWU-M direct repeat homology 1>	auucccaaaccc
3266	CLUST.104413_S.1 RDYWU-M direct repeat homology 2>	ggguuugggaau
3267	CLUST.104413_S.1 RDYWU-M direct repeat homology -containing sequence>	tcgccacgacataaggaatagccacacaagcaatcgcagtcagttgacagtcgggttc tcgcaccccgaatggcgagcagccggaagccgcaaccctcggcagccggacctctcgc caaaccccacaagtgccggattaacgggccggcaattcccaaacccgctgactgcgat tgcttgtttggctaaccgtttttcactggaggcaatgaagatgacaaagaaaatgacg acgtcacaaaaacgcgcggagttgaagcgcgtgagcaaggccgcaaaagatggcgtgt ggcagatgcttaatctggctga
3268	CLUST.104413_S.2 VXDYA-M effector>	MPTKRFLALMDNAVSDCNRVRNAVVRKWQRWREDNPDWKPAQRRLRNGEPKVSKAGKP VMEHDMISQDIQNGLYHCYKEVSPNLSSNVASGCWAEVLSDLADSTPYNHVGAKYRWQ AILNYEVQAPTYRGPVIPCAKKNAKIIFTEDRLEFSFPLLSMASGYRERSPIVRLKGH RSAGLSKGNQELLKRIVAGEVKWCDSKLVRKDHGWEFQLCYHVPIKDHGLDVDRVAIL TPLRKDSRRPFELRMSDGARWTVGDGVPYFKECERVEIRRKAIRYRYRDGAGSGHGKA NFYTAIRPSSRKVIDQQDRFIKHMVSDIIKFCIRNNCGTVRYREPTMPLRKLLWFDQQ GCPFDWTRFAGHLAFKLEGNTIAQEFRHERKKSPVRIGVEGHKEEYPRSWPTK
3269	CLUST.104413_S.2 VXDYA-M direct repeat 1>	guagaaguggucauuugaaagcugaaacguugcgag
3270	CLUST.104413_S.2 VXDYA-M direct repeat 2>	cucgcaacguuucagcuuucaaaugaccacuucuac

3271	CLUST.104413_S.2VXDYA-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3272	CLUST.104413_S.2VXDYA-M non-coding>	gaacagtcggacgaattgctcaagtcccgcaatgaagatctcgacggactgcgcggtc gggttgccgaacttgagagcgagaatgccacgcttcgcgggcggatttccgagcttaa acgggtggtggaccgtcagttgcaaccggcataggaagctgaaacgttgtgagtaaga cgcctcgctgcaccaatactagaggggtaatccagtgcccacgggagtcctaccaatc aagctcggcagttctgttaacatgccgacaaagcggtttctggctctgatggacaacg ccgtcagtgattgcaaccgcgtccgtaatgccgttgtccggaagtggcagcggtggcg tgaggacaatcccgactggaagcccgcacagcggcgactccgcaacggagaaccagac tggacgcggtttgctggtcacttggccttcaagctggagggcaacacgatcgcccagg agtttcggcacgagcgaaagaagtcaccggtgcggatcggtgttgagggccacaaaga agagtacccgcgatcatggccaaccaagtagcgtacgaactcgactgtgctctctgcc gcgagcccgtgaggctgagtggtccgtcgttgctgaagcatgtcagggcgggaactca accgctgtgccgcgtgaatgggtgctttcgatacgaacgaccaggtggcggcgaaaac acggggaccgctcgcaagtcgcaaggtgtgttggtgacacacgttgcggggaaggtgt ttgtgtctggacgtggcgagcgaggctaccaacaggcaccgctcgcaaacggtcgcgt gaggcgttgtggggtaagggtttagggatggggcctgatctccttcttctt
3273	CLUST.104413_S.29WNPF-M effector>	MTASVIKLKLGRPYQMPKKRFDALLRQQGREADKARNAAMMHWYRWRKDHPEWTPGAP YDAPQAKIKRQPKEGAKPAKDSPIGPRLFLSRELYQAARQAAPTLAGSLASACVQDVI QRLRAKTPYNHDGEARFVWQAILGHETSVPTWRSGVIPVMRNTSSFGYCGQVTRASND AERAAEHEAVLQFQLLSNVSGYRVRSPSVRLEVGDMSRGHRRLLRRIAAGQVRMADSS IGENKGKWFLALCYAVDPIDHGLDAERTITLLPALPEDRWPFVLRFGEDGTWKVGKAK PMVAEYQRIVARRRAIRYRYADGCGKGHGKKRWYKSLRPMGRAVKDLQDRFEKQLVAD IVQYAIRQGFGKLSYREPTMPVRQNSWFEGQGKVPFGWVEFEARLKFKCEQHGIEYSK QRIGMGEWGPRKEKNAG
3274	CLUST.104413_S.29WNPF-M direct repeat 1>	gugagaacggcuaaaggaagggaaguguguugcgag
3275	CLUST.104413_S.29WNPF-M direct repeat 2>	cucgcaacacacuucccuuccuuuagccguucucac
3276	CLUST.104413_S.29WNPF-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3277	CLUST.104413_S.29WNPF-M non-coding>	agccggaacaagccggcagcagcaagcgcaccgcgtggaaagagatcgccgaggagcg gcaggagacgatcgacgcccaggccgccgagctgggcaagatgcgggacgaagtcgga cacctgcgtgacgaaaacgctcgcctgcatgggcgaatcgagcagctggagaagttgc tggattacgagacgatgcccgtgtgaaccgaaagggatagttatgactgcgtcggtaa tcaagctgaagctcggcaggccgtaccagatgccgaaaaagcggttcgacgccttgct gcggcagcaggggcgcgaagccgacaaggcccgcaatgcggcgatgatgcactggtat cgctggcgcaaagaccactggttcgaggggcaggggaaagtgccgttcggctgggttg agttcgaggcccggttgaagttcaagtgcgagcagcacggaattgaatactccaaaca acgcatcgggatgggcgaatggggaccacgaaaagaaaaaaacgccggctgatgctgg actgcgacatatgcggggagccgatggagctgtcgccggcgcggtacgtggcgtgggt ccgggcgggtgagcggccgcggtgccgccgcaacggctgcgagcggttgtgtggcgtg aaaaccccccgggaccgctcgcggcgcggaagacgaatccggccaacgggttggggttt

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3278	CLUST.104413_S.7QFM5L-P effector>	MKSITVLKLKVSSNPHEALERIAIASRKARNAWLDDWLLRARGTPESKKQPRQSPKLD KHGNSKPLSESTKLYHAITASVPDLGTTQASMLAAAVNSNLSAKIDWRRGATDNGKRP KRRDAILNYEDRPPFFTGLEIPLHNAHTTLTCGDRMVIEIRRPMRDIQSLRVELSLRD IPPGVQKVLREIASGTRKLSDSKLLFKDRNKAWYWHLPVTFETEQRSDIEAELFATIG TPKGRQSDRPFAMKLPGRTWYAGDGRYLLSQVSRLVGLRKQIGWRYRLRQGAGHGRKK VDDAVKRRREQEHNVRNEFRRRLIVDILRQCERSEVGKLVYREPSLPLREKCWFGCVG LEFDWTRFASDLKNAAARKGIVVESKQYKWKDAQNDGYLPKKAKASEDAS
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3285	CLUST.104413_S.83BD33-M direct repeat 2>	cucgcaacacacguucguucauu
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3287	CLUST.104413_S.83BD33-M non-coding>	ggagtgggctcaaggctcacgacgcactgcagtccgagttctttccggacctcgggga ctacctgtccctgggaaagctggtccagatgtttcgctgcgcgcctaaggcgcagtgg gttgagcaccgctacgacatcgcagctgttgaggccatctacgacgagcagcggcggg ccactacgctggaggagaaagggacgcgtacgtcatggaaaacgttggccatggagcg ggccgagcggattgtgcaactggaggccattgtcgcgaagctgacggccgacaacgac cagctgaaggccgagaacgccgagttccgcatccgtattgccacgttggagggcgcga tcagcgagcggcgagcatccgcagcaagggcagggagggctcgctgatgcaagcaatc ctcgaaatcaagctcggcaggccataccagatgccgaccaggcggatgatccagctct tggagcagggtaggcgggactgctgcaaggcccgtaacgcagcgatcatgcattggtt gatctggcatcgcatgcacccgacccctacctgcgtggtggtagtgaccaaccagcag gtgagaacggataactgaccgagcgtgtgttgcgagaggaagtcaagctcgcccgtgt gaaaacgggtgtgttgacgagctggtttgtgccggtggggaacaggcagaaaggagtg tagcatgggacgactgacgatcgacataccagacgcactggagcggcagctggacgca tatcgtcgaaatcacaagctggaggccggcaagatgctcatgcggagtacggcatgct gccggctgctggcacaagccctggctggcgtgcaggag
3288	CLUST.104413_S.0Y20H3-M effector>	MSAKGEVAVAKTKDTLTYTTVLRLKIVEADTSNGYCSKEDLDKLACICRHGWNAAIED WLLRQRGMPESEKQARPGRVKESLGEATKLYHAVGSRVPSLFGTQTAVTVARNVWSYL QADADWRLQKKGAKKIKRRDLILAYDSRPPFSAAKNIPTYGASTKVNFADSLTVSFRR LTRESGVTTIKVTSKKLPKSHKALLREMAEGTRKVPDSKLVFRNDHWYMHIPVRYTKP KPKQDVVAHLYPVIGNPDNQDRMYNLYLPGREDKVWKVGDGRYLRSQVSRLVALRKHI GWRYRQRQGAGHGRKKVDAAVVKRWNQQRNQFYAVRQRAILDIVKQCQKYDVGTLIYH EPTGPLKNHCWFSTVKLDWDWTSFLMNLRNSLAHRYIDLSVKKWKLGEAKKALPDSFD SSSSSGEGSSQ
3289	CLUST.104413_S.0Y20H3-M direct repeat 1>	ugcugugaugaauuguugccaaccauguuguaaggugcuguga
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3291	CLUST.104413_S.0Y20H3-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnn
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3332	CLUST.111915_S.1FAO0R-M direct repeat 2>	ccugcacccauuacccagaauucuucccguugccag
3333	CLUST.111915_S.1FAO0R-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3334	CLUST.111915_S.1FAO0R-M non-coding>	ggggcgaaggtcagagcgttgatcggtaatgtgccatcgacgcacatcagcagaccgc tcatgcaggaactgaaggaagccgggtgtgtgcagttcgaggttccgatcgagcatgg gctgtacaggacggacgtggagccggaggaatagattcgtcttgacatgttcgccgtc gggcgtacactgcacccaatggaaacgggatgcgcgagcaggacgccaaggcttagaa agcgggtagagcagttggagaaacaagcattttgcagaagctgcggggctcctgttct atggggcatcacggaatcgttcaacaagatgcctttggacgaagtgccggatctgaat ggcatgtggcagctggaagacggctacatttcgaaggctaccgagcagtcgagtcgca aatatacgtctcattttgctacatgcccgaacgccgataaacacaggaagcgcaggtg atcgtggaaagaagtgagtccgcagagagagggctgactgcacagcctcaaggcgagg aaattgcgcgatacaccgacattgtcggggaagccaaccgcgcaatgctcgccaattc gcccctgaccggggcgtccgttacccacccggggtaatgggtgcaggtggccgaagtc gaagaagccgctggccggtgcctggcaacgggaagaaacacgggtgacgggtgcaggg aggcgcgcccctgggatgcgctagcgtcggccttgtggcaatggcaaggagtctgggt agcgagtgcaggagccccgccgagtgccaccttaacgggtagcgggtgcaggtgatct ggacgtcgccctggcaatggcaaggaatctgggtagcggatgcgcaggtcggggcaaa acgccgacagcacaaaacaagggtgacggatgcaggatatgggtgatggaagcaggga

		gcccgacgtgttctgggcgtgggtgacgaatgcaggccgaggacgcaagaaggatggc aacagcaagaactctgggtaacggggtgacggttgcaggacacgagttctgtccgcga tggcgtgacaatgggaagaagtctgggtgacggttgcaggccgctgagctgctgagca atataggtaacgggtgcagggatgggtggcacgccgattgtgttggcaatgggaagaa tgctgggtagcgggtgcaggaccgggcacgcgaagactcgctggagtctggcaaggaa tccgggtagcggatgcaggtgggtggcacgccgattgtgttgtcatgaccctcagcga acggcgggtgactggcaagggatctgtggtgacggatgcagggtgggcgatgacgtcg aggatgatcgcgggcagggtaaaacgggtgcaggatgggtggcacgctggcaatagca ggaatctgggtaacgggtgcaggccgctgagttgctgatcaatatgggtaacgggtgc aggctagaccgcccggggctgggtgacgggtgcaggcagctccaggtgcttgcttttt tgcttagtcttgacttaccactttaattatgcagatcaagccgggtttggaacgacgg ctcgtctcccgagccagctccatcgtcgaagattgcgggcaggacgaaacgttcgggc tgctcgcccagtcagccgcaaaggccgcactggtctttgcttcctccgcctcccaact cgtc
3335	CLUST.11 1915_S.0 IO4ZO-M effector >	MYGDSRIEEGNMDALGKSSRDGTNQHPPCDAASTAVCETAVIVRATARMTIDFMAMEE PERIRARQLLYEARRNSAAAANAVLRAFWRADGDALDGYMVEHGHGPKKAVDWPMPKI QSYGLARLVAPMLPSGIGSAVARMAETKWRQTRFEALVRNTEKPAHYREANPIPIRQQ DYSLTKEDGRWCLSMMLRSGEPRVKLPLDIRDSFQRSILENVSEWKGSRALARKKGES REAYKQRVASLEAAQRGWEAGELRIEQDSKRKARWYVRMAYKRIVDKQADGKRASLHR GIKNFLVCVTDDGQEWKYEGADIEAFLAQMQARRRQYQRNSLASSRSGHGRRVILRPI DKLQGKADRWRRTKNQTLARRLAEWLRDRGVSVLFIEDLSGIRSGEPEKLEGGERIYK RVQEWPFYDAGQRIHSCCEELGINVKTVSPAYDSQRCPVCGAIDPEHKDLRYWKLSCK SCGARRDLDVAAAYNVLARGLAVHGGKGEDYKDIGRAKRAAKGKKNAG
3336	CLUST.11 1915_S.0 IO4ZO-M direct repeat 1>	gucgcaacggaugaauggaugcugauugauggaagg
3337	CLUST.11 1915_S.0 IO4ZO-M direct repeat 2>	ccuuccaucaaucagcauccauucauccguugcgac
3338	CLUST.11 1915_S.0 IO4ZO-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3339	CLUST.11 1915_S.0 IO4ZO-M non- coding>	tcggattggatctggtttgacgatctgctctggccggagcggtatcgaaggtgcgaat tgaaatacgggcacatcgggacctcgtgcatcgcgcaccgcaaatccgtccgctcccg atggaccgacggctacggccatgattggcggttcgtccaagacctcatggccgaggcc tcgaactatcggtacgccggagatggtggctacatcgtctgccacgttcctggctgtc tcgacaggtgaaggttgacacgtgagtccctcgcaccaatgatgagttcttcaggttg acatttaggcaacgagtgagtacaagcaatgcagcaaacgacggtagaggcagcgtcg cggggttttaatgggccgacttcccggcctgaagccgaggtagcagccatgtacggcg attctcgaatcgaggaaggaaacatggacgcgctcggtaaatcgtcccgagatgggac caatcagcatccgccttgcgacgctgcctcaaccgccgtttgcgaaacggccgtcatc gttcgtgcgactgctcgcatgacgaagtcttgcggcgctcgtcgcgacctcgacgtcg ccgccgcctacaacgtcctcgcgcgcgggcttgcggtccacgggggcaagggagagga ttacaaggacattggccgcgccaagcgcgctgccaagggcaagaagaatgctggttga tggtaaggaggcgtggctcgctgcgcgct
3340	CLUST.11 1915_S.1 JWWCF-M	MLESQSKKQEIPDSIRNVSTDAAEGDDMDLVRASTRFEIRLSPKHEDGTPHTLNLETL HALDEASQLVARCRNRVARWLYGQDSDWLYAQPLPWPKKIAWSPAPVGPRRDGTTGPI ALTTLAYRQAISSQDVARLSSDVVAWASKDVVSKWTEKRWDILVRQTEALLHYKPHQP IAIPHKAVKFALREDGSADVAFRVLSLKAEDAKPIHVHIVPRDAWQREELRALAAGDW

	effector>	KLGQLVVSRHHEKRGRWFLRFSYTKRVPRAEGNGVIAIRRGMRSFIVTASTTGDVRAL VDGGDILAFKRQMLGRRRSIGRRARAWQAGQGATGHGTRRRVGALISLSGKEQAWVKE RCKQIAAAVVHWAKEQKASEVVIEDFTIPWKEDAWREVKSWPWYLTKESVKTAVENAG LKFRELSVASNRKRCPVCKHEHQVEPVDSYGRWECESCGVKRSVESIVVLNMLADAGR PEAVERAEDKRQAVAKIVARATVSQKPLEPLAGKNEKSRAKMCNGIRGKRNGSGKK
3341	CLUST.111915_S.1 JWWCF-M direct repeat 1>	guggagacggcuaucgauuuggagagcaagcgcgag
3342	CLUST.111915_S.1 JWWCF-M direct repeat 2>	cucgcgcuugcucuccaaaucgauagccgucuccac
3343	CLUST.111915_S.1 JWWCF-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3344	CLUST.111915_S.1 JWWCF-M non-coding>	gttttcccgaacgccgcggcgaggcgcgccgcggacgacgccatcgacaagctcgacc cgaagctgccgatgacggcgtacttggacgcgtgggagagcgcttatttcgagatcgc gaaaaagtccctattccgcgagccaaatagctgatttacgcctggaaatggcccgctt gactttcgccaagtggtacggcaatctgacggcagttgtgttggagagcagagagcaa gtgcgagcatgagcacgatcgatcacaaagcgagggaatcgaagagtcagaatcagaa atcgtagtggacggacgcgtggctttgatgccgatcgggaagaacccgcgtagcgctc gctacacagcatccctcacaggatgcagctctccaatccgcgcgagcggaaacgtcct ttctccaagggaccgctggtatcgcagccggctaaagcgagggagctacgaaggacgt cgcgtccgtcctctacggtttctgatttttggagagcaagtgcgaggccggactgtaa cgaggtgacgtgatgctggagagtcagtcgaagaaacaagagatccctgacagcatcc ggaacgtgtccacagatgccgcagagggcgatgacatggacctcgttcgcgcctcgac ccgcttcgagatccgcctaagccccaagcatgaggacgggacgccggaagacaagcgc caggccgtcgcgaagatcgtcgcgagagcgaccgtgagtcaaaaacccctggaacctc tcgcgggcaaaaacgagaagagtcgcgcgaagatgtgcaacgggatacgtgggaagag gaacggatcgggcaagaagtagttaccgctcgcatatcgttcgctaggtctttgaaat cattgtgacgtaatcgatgctttcgtctcggggtcgaacgtgacgatgtttggggtcg tggagacggctatcgatttggagagcaagcgcgagcagacgccccgtaagaggtgccg tacgtgcaggtgcagtggagacggctatcgatttggagagcaagcgcgagttcgtccc gaggtcgaacgtgacgatgtttggggtcgtggagacggctattgatttggagagcaag cgcgaggggaaactggtacgcatgattagacggttctcttggtaagtggagacggcta tcgatttggagagcaagcgcaagttcgtttcgaggtcgaacgtgacgatgtttggggt cgtggagacggctatcga
3345	CLUST.111915_S.1 JWWCF-M direct repeat homology 1>	gcucuccaa
3346	CLUST.111915_S.1 JWWCF-M direct repeat	uuggagagc

	homology 2>	
3347	CLUST.111915_S.1JWWCF-M direct repeat homology-containing sequence>	agagcaagtgcgagcatgagcacgatcgatcacaaagcgagggaatcgaagagtcagaatcagaaatcgtagtggacggacgcgtggctttgatgccgatcgggaagaacccgcgtagcgctcgctacacagcatccctcacaggatgcagctctccaatccgcgcgagcggaaacgtccttttctccaagggaccgctggtatcgcagccggctaaagcgagggagctacgaaggacgtcgcgtccgtcctctacggtttctgatttttggagagcaagtgcgaggccggactgtaacgaggtgacgtg
3348	CLUST.111915_S.15UNY3-M effector>	MGPDEGSDAVSSTETSKEIVRATCRLQLDISEMCATTELRDAHRRRTCGGVEGGCAACVASKALRSARRECARIANVSLRLRWAADAELIDRYQLAHGRAPKGREWEETDLRQAIQRVTAGMDPAQRSVVLEKCVRTTGAGKKAIYPYPLLCLLAPSLAAGIVSAVDQAVMQKWNETRWASLVQMDKSPPHYNWDNPIPLRKADTNLQHVEGKRFKVSFSVSSRDPNRRGKEFSIPIYGRDDYQQNILTMLASDDSRMGAAQITEDRKRPGRWYLRIAYRKRIEKTTDVKTAGINKGIICFLAAATEDGRRWTHDGADIEAYLKQVQSRRQRYQRQVKSSGRIGHGRTRTLRPIEHLRGQGEAWRDTRCQTIARRFVDWLVTEKVGRLYIDDFSGIRDSLPENLEKGDWIWNRIQEWPFYKLQMKVISCCEERGIETVIRNPKHISGTCPKCRSREVTLIGRKRLRCSSCKHVVHWDVAAAEVNMQDGESERRGDKEIEPKKNAKKPRPVKPATGPSRKP
3349	CLUST.111915_S.15UNY3-M direct repeat 1>	gcgccggaagauaccagaagugauggugauugcagg
3350	CLUST.111915_S.15UNY3-M direct repeat 2>	ccugcaaucaccaucacuucugguaucuuccggcgc
3351	CLUST.111915_S.15UNY3-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3352	CLUST.111915_S.15UNY3-M non-coding>	tttgcctacctcgccagtcgaatcaacgaagggcgcgcctgttgcggcatgaaccaatgcttcgagcgcgccgccaccggcagcgcctggtgcgccgagcacaccgatcatatgaataaactctacaacgtctcgtccaaccccaagtgacacgagccgcaaaggtttccatgcccgaggctgcgtctgactctataacaccagggtccttggcgctccctgcagagcgcaaaggcgagaagcgatcggacatgccgcacgcgcaagcgttcggggaagaaagtctgactggcgcgctcgctaattcacgggaggtttcctcctgcaccatcactcgaccgtcgtcaccagacgggttgggtcctgatgaggggtcagacgcagtcccgagcacggaaaccagcaaggagatcgtgcgggccacgtgccgcctgcagctcgacatctccgagatgtgcgccacgacggagctacgcgacgcgcaccggcgccgcacctgtgggggccacgtggtgcactgggacgtggccgctgctgaggtcaatatgcaggacggcgagagcgagcgccgtggtgataaggagatcgaacccaagaaaaacgcgaagaaaccgaggccagtaaaaccggcaactggaccctctcgcaaaccgtaatgcaggtgctcggaattacatggcgccccagcgacggaagcctgacctcgtcgctggcgtttgggcctttctatgtacgaacgtctatcgaaagtggtgatggttgcaggaagtgcaagccctagactgcgacgcgcgctgtgtgaacgtccaaaagaagtgcaaggaaagtggtgatggttgcagggcatactgctgggccgatggtgattgcaggttgcgagcaaggcggcttgcgcctgcctggcgccgtatgtttcgcacgaacaagtaagcccgcgcgctcgtcgggacgagaggtgccgatgcgcagagggggggtgcagggcaacgccacgatcgacggagatctaggcgccgcgcaccccgcacccccctggacttttg

		gcagaaatgactgggtgcccttaacctaacggggccccatggagttcgaggagatcgg ctacgcccccccccctgtcaccagagcccccgcgtcccgtggtgccggtggcagtagcg agccccatgccggcgcccgccatggggcacctgggcgctccgcggtcgcttgcgcctg cccgagtgcgcgcc
3353	CLUST.11 1915_S.1 5UNY3-M direct repeat homology 1>	caccaucac
3354	CLUST.11 1915_S.1 5UNY3-M direct repeat homology 2>	gugauggug
3355	CLUST.11 1915_S.1 5UNY3-M direct repeat homology - containi ng sequence >	cgaggctgcgtctgactctataacaccaggatccttggcgctccctgcagagcgcaaa ggcgagaagcgatcggacatgccgcacgcgcaagcgttcggggaagaaagtctgactg gcgcgctcgctaattcacgggaggtttcctcctgcaccatcactcgaccgtcgtcacc agacgggttgggtcctgatgaggggtcagacgcagtctcgagcacggaaaccagcaag gagatcgtgcgggccacgtgccgcctgcagctcgacatctccgagatgtgcgccacga cggagctacgcgacgcgca
3356	CLUST.11 1915_S.0 TNEOO-M effector >	MLESQSKKQEIPDSIRNVSTDAAEGDDMDLVRASTRFEIRLSPKHEDGTPHTLNLETL HALDEASQLVARCRNRVARWLYGQDSDWLYAQPLPWPKKIAWSPAPVGPRRDGTTGPI ALTTLAYRQAISSQDVARLSSDVVAWASKDVVSKWTEKRWDILVRQTEALLHYKPHQP IAIPHKAVKFALREDGSADVAFRVLSLKAEDAKPIHVHIVPRDAWQREELRALAAGDW KLGQLVVSRHHEKRGRWFLRFSYTKRVPRAEGNGVIAIRRGMRSFIVTASTTGDVRAL VDGGDILAFKRQMLGRRRSIGRRARAWQAGQGATGHGTRRRVGALISLSGKEQAWVKE RCKQIAAAVVHWAKEQKASEVVIEDFTIPWKEDAWREVKSWPWYLTKESVKTAVENAG LKFRELSVASNRKRCPVCKREHQVEPVDSYGRWECESCGVKRSVESIVVLNMLADAGR PEAVERAEDKRQAVAKIVARATVSQKPLEPLAGKNEKSRAKMRNGIRGKRNGSGKK
3357	CLUST.11 1915_S.0 TNEOO-M direct repeat 1>	guguggagacggcuaucgauuuggagagcaagcgcgaga
3358	CLUST.11 1915_S.0 TNEOO-M direct repeat 2>	ucucgcgcuugcucuccaaaucgauagccgucuccacac
3359	CLUST.11 1915_S.0 TNEOO-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3360	CLUST.11 1915_S.0	gttttcccgaacgccgcggcgaggcgcgccgcggacgacgccatcgacaagctcgacc cgaagctgccgatgacggcgtacttggacgcgtgggagagcgcttatttcgagatcgc

	TNEOO-M non-coding>	gaaaaagtccccattccgcgagccaaatagctgatttacgcctggaaatggcccgctt gactttcgccaagtggtacggcaatctgacggcagttgtgttggagagcagagagcaa gtgcgagcatgagcacgatcgatcacaaagcgagggaatcgaagagtcagaatcagaa atcgtagtggacggacgcgtggctttgatgccgatcgggaagaacccgcgtagcgctc gctacacagcatccctcacaggatgcagctctccaatccgcgcgagcggaaacgtcct ttctccaagggaccgctggtatcgcagccggctaaagcgagggagctacgaaggacgt cgcgtccgtcctctacggtttctgatttttggagagcaagtgcgaggccggactgtaa cgaggtgacgtgatgctggagagtcagtcgaagaaacaagagatccctgacagcatcc ggaacgtgtccacagatgccgcagagggcgatgacatggacctcgttcgcgcctcgac ccgcttcgagatccgcctaagccccaagcatgaggacgggacgccggaagacaagcgc caggccgtcgcgaagatcgtcgcgagagcgaccgtgagtcaaaaacccctggaacctc tcgcgggcaaaaacgagaagagtcgcgcgaagatgcgcaacgggatacgtgggaagag gaacggatcgggcaagaagtagttaccgctcgcatatcgttcgctaggtctttgaaat cattgtgacgtaatcgatgtgattccatctcctcctcgtccggtggggtctgcgatgt ggagac
3361	CLUST.111915_S.0 TNEOO-M direct repeat homology 1>	gcucuccaa
3362	CLUST.111915_S.0 TNEOO-M direct repeat homology 2>	uuggagagc
3363	CLUST.111915_S.0 TNEOO-M direct repeat homology -containing sequence>	agagcaagtgcgagcatgagcacgatcgatcacaaagcgagggaatcgaagagtcaga atcagaaatcgtagtggacggacgcgtggctttgatgccgatcgggaagaacccgcgt agcgctcgctacacagcatccctcacaggatgcagctctccaatccgcgcgagcggaa acgtcctttctccaagggaccgctggtatcgcagccggctaaagcgagggagctacga aggacgtcgcgtccgtcctctacggtttctgatttttggagagcaagtgcgaggccgg actgtaacgaggtgacgtg
3364	CLUST.111915_S.0 BCWM1-M effector>	MAEAKGGGSTESPVQMQEVTRASMVIPLEPWRIAEDPEKHKKGKCREEKKKKKTKKQQ SEEKKCSACELINALYETQRATASVYNFITRSLWRQDADFLDAFMVRHGRKPLSKEWD KPNVYYYAEARAAHPDMASGIVATIQKKASGKWILSRWKALVTQEESPPHYRDTQPIP LRKQDYALVESEERDTFELAFTLHSGRRAQKGKEYIIPLRTKDQKQYNCLRKIARGEW KGGEVALLRERKDRGKGGGPVNKWFVRISYKKQVEVTTEPNYAALNRGIAFFLVGYTS TGQKYILDGNDIRSHLRALQNRRRDRQRGYKHAGRNRKGHGRKRALQPIAHLYKKGEM WRQTYNQTKARNFAKWCKKNEVDRVYLADFSNIRNDYVDKLEGGKRLWDLIQEWPYYN LQMRLVSCLEEEGIEVYQMPAQNITRTCPRCGNVKEEAVISRQYKCETCGYERHRDIV ACQNELARGERLRREGELEQISFGESKGKKKKDLGKKPKK
3365	CLUST.111915_S.0 BCWM1-M direct repeat 1>	gaaggaaacguuacgaauuggagg

3366	CLUST.111915_S.0BCWM1-M direct repeat 2>	ccuccaauucguaacguuuccuuc
3367	CLUST.111915_S.0BCWM1-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3368	CLUST.111915_S.0BCWM1-M non-coding>	cagtacgtcaggtttttgtggtggatgtggcgcgtactgcaaaaggtgattggctgg ttattgagcttaatgacgggcagcagtcgggattgtcagcgattgagccaaatgactt gtatcggtctttggataagaagttgagggaataaagggcagtcgactgccgggaggag aaggctgaaaggcctgtgactgcagcagtgggaataatagaaagaggtgttacgaatt ggagggttccagccgatgctcaccaccatagaatgaaacgttacgaattggaggtcgc cccacaggaggaatccattgcccatgtccaagtgggaacaatagaatgaggcgttacg aattggaggtcgggagatctggagtaagcagcaacaatagaaggaagcgttacgaatt ggaggcccgacgctcccatctcaccgcagtatcagatgtctcatgggagtacttaaaa aagttgttacgaattggaggcggacgggcggttacaccatgcaggtaaaaacaacaga agaaaagcgttacgaattggaggatcggatttagtaaggagagcggcgaggtagatta tgagagtacttaaagagaacgttacgaattggaagcagcctagaatcggatgacaaaa aagtgttatgtagaaaaaacgcttgacaatcgcttttgtacctatagaatgggacaag tatgaatcagaaggttacagagggctcttgccttatatcaaccgaggcgcattcagac gtgggtgcgcacggttcaggttgcctccacaacctaaaggtgagaagtaaaactttcc gtcatgccgaccagtatcggggaagtcagtcgggaaacgctcacaaaaagcgatgatg acatcgtgggatatgagcggcatcgggatattgtggcctgccagaacgagttggcgag gggcgagcgattgcggcgggaaggcgagttggagcagatttcgtttggcgagtcaaag ggaaagaaaaagaaagacctaggtaagaagcccaagaagtgattttgaaagcgttacg agttggaggcaaagtcgggactaacaccacgcgttacgaattggaggatcatgaggct cgtcacttattgatttttgtacaaagaaagcgttacgaaccggaggacaaggtacag gatgtcatccaataagctggtttttaccataatgacgtagatggtttcactggcgcc tgggtttttggcgtcaatggggcgatgatgcggcgtattgtctggtggattatggag agggtgatgaggatattcctttgccgcctgtggaa
3369	CLUST.111915_S.152GW2-M effector>	MGPDAASSTDTEIVRATCRLQLDLSDLCATAELREAHRRRACGGAEGGCPACLAAKTL RTVRRECARVANVSMRLRWAADAELVDRYQIAHGRAPKGKEWEDTDLSQAIERVTAGM PHAVRAALLEKCTRITQPKNDKPSKKVLYPYPLLCAMAPGISAGIVSAIDQAVMQKWN ETRWAALVQMDKSPPHYAWTNPIPLRKADVKLQHVEGERFKLSFSVSSKDAGRRGKEF SIPIHARDDYQMGLLTMLSSDAARMGALQLTEDRKRPGRWYVRIAYRKLAAKTTATKA AGINKGLVCFLAAATEDGQKWMYDGADVEAYLKQIQARRQRYQRQVKASGRIGHGRMR TLRPIEHLQGQGEAWRDTRCQTIARRFVGWLITEGVGRLYIDDFSGIRDQPPEGLRRG EWIWNRIQEWPFYKLQMKVISCCEEHGIETVIRNPKHISGTCPKCRSREVKYINRKLH CSACRHVVHWDIGAAQVNMLDGERERRGEKEIEPKKSSKKSTAKKPPGGTARKA
3370	CLUST.111915_S.152GW2-M direct repeat 1>	guggcgaaagucgaagcgagugaugguuguugcagg
3371	CLUST.111915_S.152GW2-M direct repeat 2>	ccugcaacaaccaucacucgcuucgacuuucgccac
3372	CLUST.111915_S.1	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

	52GW2-M spacer>	
3373	CLUST.111915_S.152GW2-M non-coding>	cgtaccgtttttttttgaagactgctaccaatggggccgcggacgctacgagtgcgaggcgctgtgggcgcagaagcaaagccatgtgttcgatggttcgcccacgcatgaatgggtcgatgagatcaactgctcgaatgaggtgaagtgatgtcacgcgcgacaacgacgcgcgaatgcaaagaacatcaggggagatgaataacaccagacgttcctcgtctgaccaggagatgaaacgatgacgatgcccgaggctgcaccagggtccttggcgttccctgcagaacgcaaaggcgagaagcgaccggacatggcccgcgcgaaagcgctggcggaagcaagcccggctggcgcgctcgctaatactgatcctccgggatctaccatcactccgccctctcacgagggattgggccctgatgcagcttcgagcaccgacaccgagattgtgcgtgccacctgcagactgcagctcgatctgagcgatctctgcgccaccgccgagctgcgcgaagcgcaccgacgccgggcctgcggcggcgccgagggtggctgcccgcatgtggtgcactgggacatcggcgcggctcaagtcaacatgctcgacggtgagcgcgagcggcgaggtgagaaggagatcgaaccgaagaaatcctcgaagaaatcgactgccaagaaaccaccaggtggaaccgctcgcaaagcgtgatgcaagtctatgaaattagacaactgacacgggacgcgcgcaagagatcttcgtgagtgatggtgattgcaggcagctggccgatggtgattgcagggagcctgagcacggccgtagagagttggcgaccgatcggcagaagcgttgccctagatccaaaaacttgtatggttggtccgagctgcggcagactaggaccatgaagctccaagacttgccgcggctactgcccggcgccgacgtgcgcattaagctacgcaggaggctctgcttcgtgaccctgcgccacgaagggcgcgtcgggcacgggatctataagaagctcacgttcgcgacgagaaatgccgct
3374	CLUST.111915_S.152GW2-M direct repeat homology 1>	accaucacuc
3375	CLUST.111915_S.152GW2-M direct repeat homology 2>	gagugauggu
3376	CLUST.111915_S.152GW2-M direct repeat homology - containing sequence>	gaaacgatgacgatgctcgaggctgcaccagggtccttggcgttccctgcagaacgcaaaggcgagaagcgaccggacatggcccgcgcgaaagcgctggcggaagcaagcccggctggcgcgctcgctaatactgatcctccgggatctaccatcactccgccctctcacgaggattgggccctgatgcagcctcgagcaccgacaccgagattgtgcgtgccacctgcagactgcagctcgatctgagcgatctctgcgccaccgccgagctgcgcgaagcgcaccgacgccgggcctgcggcggcg
3377	CLUST.111915_S.1U6VGI-M effector>	MDTDPTSIPAVDRLKLVRASTRFEVRIRPRDDDGNELSENIALLRSLDEVARMVATARNVTMRSLERADAAVLDAFVEEHHRLPARADEIKWPSSDALASASPIYTYRTIRAACPQLDTACAAWLSKDVHSKWREKRWLTLIAQTEARPHCKPTHPIPIPAAAVRLGRREDGSMQITFRLFSTEVEGARRIMITLVPRDARQRMEIDSIASGEWKLGQVVLSRHHEKRGRWFVRLTHTRLVAPVAHAGVVAVRRGMRAFLVGAASDGDVRTLDDGADLLEHKRRFDARRREIGRRLAGDAANGHGTRRRTAALIDLTTTEKDYSTTRCARSAAAVVEYAKKCAASRVVLEDLTIPKSSDAWWLVKRWPWFMLKTAITNACEAAGLAVEERRVSNRRTRCPECTHEHLAPPVDTRGTWQCVNCAMTRSADQVDALNMLRDAGAADGVAQAAGNRRVAVRALAAAARGDVARKPAKEVERKCESESSEGRGRRRGPTVPSARKPTRKCAE

3378	CLUST.111915_S.1 U6VGI-M direct repeat 1>	gucgaagcgacaaaggaaguggagaggaagugcgag
3379	CLUST.111915_S.1 U6VGI-M direct repeat 2>	cucgcacuuccucuccacuuccuuugucgcuucgac
3380	CLUST.111915_S.1 U6VGI-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3381	CLUST.111915_S.1 U6VGI-M non-coding>	ggcatcggcgagcgcgatgcgcgcatcacgaagttgctcgcggacatccgagagcgcg atgcgcgcatcaaggaattggaggagaagaaaacgaaggctcgggtagccacccgaag cgctgccgatggtggcgaagatgcccatgcctaaggagcactcgtagctggtcgaccg ctggaatggacgtcggaggaagaataccatggacactctcaccaaaccgcagcgtgat gctgcacctctccatcctcacctcggtgaggctcggtctttgaccgatagggcgatcg cacgccctcaaggtgaatcagtggacacagatccgacgtccattccagcggtcgaccg gctcaagctcgtccgggcgagcacgcgcttcgaggtgcgcatccgcccccgagacgac gacggcaacgagctgtcggagaacatcgccctgctgcgttcgctcgacgaggttctgg cggcggcggcgagaggcgatgtggcgcgcaaacctgcgaaggaagtggagaggaagtg cgagtccgaaagcagtgagggccgcgggcgcagacgggggccgactgtgcccagcgct cgaaaaccaacacgcaagtgcgcggaatgatgggtgtgtagacggggtct
3382	CLUST.111915_S.0 MPO29-P effector >	MNTMHTTIDSALGATRSGEATGLTLDNHDAPVASHVAPAKAVGRTPPPEVEQVKTDAT QVAPGALSIVRATCRILLDVAVLAADRREHIAKRCGGTEGGCKACQLQQELRGAQREA VRAANAAMRVHWRADADILDQALLATGAPPAKAADWKRFAQIDPERLVRAVSPGLSRG ETKLAAGELVKTSKADKTYLSTYRLVRVIAPDLPGGIASAISDSVQSKWQRERFASLV RCTKSPPHYTGTMPLPLRAADCALTHCVDDDYEFTFAIRGGLGHRWTLPISARDGATK KRYLAKLLSELAGSNVKFGACQISEDRMRPGRWFVRIAYTRRVDAAVVGKNDCAIHLG IVNFMAALGSDGERFIIEGNDIRTHLAQIQARRRSYQRQIKYSNRTGRGREAALAASR KLAGAHERWVDTTIQRIARSIANWVKEHGYSRVYMPDFTRVRDSVPELLERSDSVYQW LQEWPYYRMQQAIRSCLEEVGIGCNHECSGSRARPPTCSCIAERGSGVDDGVLSRHAC PACGETEALIEDLGIRTFRCESCGHHGPLDVVLAELILARGRERRGDSDSLIGENGSK LGPPKGKNGGARKASRKYPKSKGPRRAGSEESSVCNVIGAMARRPAAQQLLRQKRVQC AT
3383	CLUST.111915_S.0 MPO29-P direct repeat 1>	gucagaagagaguucagugugcaacgugauuggagg
3384	CLUST.111915_S.0 MPO29-P direct repeat 2>	ccuccaaucacguugcacacugaacucucuucugac
3385	CLUST.111915_S.0 MPO29-P spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

3386	CLUST.111915_S.0MPO29-Pnon-coding>	tacgccgcgatgactgagttgatcgcgggcgcggaagatagcgtctggaccattctagtaatcgccggccagctcgtgccttcggggcagatacgctgctcctgttccgacggaactagtgtctggttggattgggctaggacgtcataacgatgaataccatgcacacgacaatcgatagcgccctcggcgccacccggagtggggaagctactggcttgacgctcgacaatcatgacgccccagtggcgtcacacgttgcacccgcgaaagcggtagggcggactccaccgcccgaagtc
3387	CLUST.111915_S.1FK0JU-Meffector>	MYGDSRIEEGNMDALGKSSRDGTNQHPPCDAASTAVCETAVIVRATARMTIDFMAMEEPERIRVRQLLYEARRNSAAAANAVLRAFWRADGDALDGYMVEHGHGPKKAVDWPMPKIQSYGLARLVAPMLPSGIGSAVARMAETKWRQTRFEALVRNTEKPAHYREANPIPIRQQDYSLTKEDGRWCLSMMLRSGEPRVKLPLDIRDSFQRSILENVSEWKGSRALARKKGESREAYKQRVASLEAAQRGWEAGELRIEQDSKRKARWYVRMAYKRIVDKQADGKRASLHRGIKNFLVCVTDDGQEWKYEGADIEAFLAQMQARRRQYQRNSLASSRSGHGRRVILRPIDKLQGKADRWRRTKNQTLARRLAEWLRDRGVSVLFIEDLSGIRSGEPEKLEGGERIYKRVQEWPFYDAGQRIHSCCEELGINVKTVSPAYDSQRCPVCGAIDPEHKDLRYWKLSCKSCGARRDLDVAAAYNVLARGLAVHGGKGEDYKDIGRAKRAAKGKKNAG
3388	CLUST.111915_S.1FK0JU-Mdirectrepeat1>	gucgcaacggaugaauggaugcugauugauggaagg
3389	CLUST.111915_S.1FK0JU-Mdirectrepeat2>	ccuuccaucaaucagcauccauucauccguugcgac
3390	CLUST.111915_S.1FK0JU-Mspacer>	nnnnnnnnnnnnnnnnnnnn
3391	CLUST.111915_S.1FK0JU-Mnon-coding>	caccgcaaatccgtccgctcccgatggaccgacggctacggccatgattggcggttcgtccaagacctcatggccgagatctcgaactatcggtacgccggagatggtggctacatcgtctgccacgttcctggctgtctcgacaggtgaaggttgacacgtgagtccctcgccaccaatgatgagttcttcaggttgacatttaggcaacgagtgagtacaagcaatgcagcaaacgacggtagaggcagcgtcgcggggttttaatgggccgacttcccggcctgaagccgaggtagcagccatgtacggcgattctcgaatcgaggaaggaaacatggacgcgctcggtaaatcgtcccgagatgggaccaatcagcatccgccttgcgacgctgcctcaaccgccgtttgcgaaacggccgtcatcgttcgtgcgactgctcgcatgacgaagtcttgcggcgctcgtcgcgacctcgacgtcgccgccgcctacaacgtcctcgcgcgcgggcttgcggtccacgggggcaagggagaggattacaaggacattggccgcgccaagcgcgctgccaagggcaagaagaatgctggttgatggtaaggaggcgtggctcgctgcgcgctaaggaacgccctgcacgagtgcctggatgctgattcgaaggcgatacggtcagcggacgcgcgaaaggagagcccatgacggagtggtttcaacgcaaagcgggagatgagttctcgattcaccacgaggacgagagcgtcgttctgattggcgaccaaacacccgattgggtaaagctcccgcctgagcttggtggggcaacgcttcggattgcttcatcgtttcgcatggaatgtccgatgtgtgaagacggtgctccggtcaggcattttgcttgctcggacggttacggcgttgccgagtgcagtcgccatggtttcgtttggtatcgaaggaagacctcatgacgttgtcgttcgctgtcggaatcccgaccatcaatcgtgcagacctgctcgaaatgagcgttgcggacttggcctcaacgtgcccgaacgcgacgctcatcgtcgtcgacaacggccatcaggt
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		IVRKIHKVNYRLRITKLNFVKLNGHVKIFPKKSPLVRDIYKDLPILHKLEYEKKKLFE KRDRTLRHIRRTAINALLRFLRERGVTHVVVGYPYNINKNRNELTVNLFQYRKTINDL KIIGERYGIKVDEIVEYNTSITCSVCGEVHKNGRIERGLYKCEKTGKMINADVNGALN IFYKAFSKMPKQLKKIETIKLTSSPSTRLFAPLTT
3393	CLUST.13 1247_S.5 J7C87-P direct repeat 1>	cccgcacuucgauaguguugcagc
3394	CLUST.13 1247_S.5 J7C87-P direct repeat 2>	gcugcaacacuaucgaagugcggg
3395	CLUST.13 1247_S.5 J7C87-P spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3396	CLUST.13 1247_S.5 J7C87-P non- coding>	gaagaactgaagaagaagcacaacgttgagaaatttgcagtattctatgttgtcaagg acacaactccagatcctttaccagaaaaatactatctagttccagtagatgaagccga ggcttacaaattcattagtaatatagaacagtgagcacccgcactttaaaatttttata tacctcttcacagccgtccgcatcgacacttcttcacgtgggggtgcgtgccccacag gacgcgggtctacccttacgggaaccccgcttaaacatactttatctatgcaaaaatt taagccttttgccacctttaaccgtaagaagtaaggtttaaatatggcaaaagtaaa cccatatgtatgaaaaaggtaacaataaacgtcgatgaaaaactgaaggaagttttct ccaggttatgcgatgaggaagggatagaccttgctcagggtattagagagttgatgat tgaggcaataaacaggggctatgtaaacaaagagagaaaggaaggtgcagaaaaggtg agaagaaataccaagtaaaacatcatctgataaaaagaacggtaaacattcagggcag aaagaaagtggtaataaacgtgcacttactgttagattgaacctaagtgtgggacagc aaatatatctcacttctttaattaaggcatacacaacaatagctgggaaattaaatag ggacgcttacgctaaatttatggaacttacagctaacggagtagtagagaatataaag cagttgaaagatattaagaaaaaaactggtaagatgataaacgccgacgtgaacggtg cacttaacatattttacaaagcgttctctaagatgccaaaacaattgaagaaaattga aactataaaactgacctcctccccgtctacgaggcttttcgccccttaactacctag ggcttttgggttagatttttatttttaagttttaagtccggattcttcatatgcagta tttagtcttacttttgctcatattcgtcgcagtcgccatcatcataacgttactacct tacgtgagtctcatcataacgaatattaacaacgtcaacgcacgtgtgtatacactat ataattcaagcacgtatatgagcggcacgtggctagtcaacggtagtaaaattcaaca ggtccctcaaacgccgacaaacaaactcgtcattgaggtagaagagggttcttacatt tacgtgtccaaccagacgtggagtgaaatgctgtcggataacggcgataacggaccga
3397	CLUST.13 1247_S.5 NODOF-P effector >	MSSKTSSDKKNGKHSRQKESDNKRSLTVRLNLSMEQQIYLTSLIKAYTSIAKKLHEEA RAKFMELTNGEIKNIKELKDVKKKFNSWFNEYFKTQRKWITDSLGSNISDQLFQFLMA QYKNFFANYENFFEHKVDGRPSFPSLPELFQIRDRGVEVDFDKKILIIKLKGKQLRLK FQSDRILYHGDPGAVTIKKVDGKFYAYIPFDFNPKFNEEKKGAIDIGLSNFFAAVTED GDVILVKAKQYTYIYNMYKQRIKELDRMIGNIRKHTLKMYVTPPKSFRYHPLLGFTNN REVSKILISLYTSRYDEKRGKKKKLTREDMTNIVKKIRKVNYSLRIKRLNFMKVDGHI KLFPKKSRFMNDVYRDLPMLHKLEYERRKLFEKRDRTLTHIRRTAINALLRILKERGV TRIVVGYPRYINKNRNELTVNLFQYRKTINDLKIIGERYGIKVEELEEYGTSIRCSIC GEEHKNGRIERGLYRCEKTGKTINADVNGALNIFYKAFSKMPKQLKKIETIKLTSSPP QRDEVSHLLSYRKL
3398	CLUST.13 1247_S.5 NODOF-P direct	gcugcaacucuauagaagugcggg

	repeat 1>	
3399	CLUST.131247_S.5 NODOF-P direct repeat 2>	cccgcacuucuauagaguugcagc
3400	CLUST.131247_S.5 NODOF-P spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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3403	CLUST.131247_S.858TOV-P direct repeat 1>	cccgcacuucgauagaguugcauc
3404	CLUST.131247_S.858TOV-P direct repeat 2>	gaugcaacucuaucgaagugcggg
3405	CLUST.131247_S.858TOV-P spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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3407	CLUST.13 1247_S.6 GYS2S-M effector >	MASKTSSDKKNGKHSGQKESDNKRSLTVRLNLSTGQQIYLTSLIKAYTTISGKLNKDA YAKFMELTADGVVENIKQLKDVKKKFYAWFYEYVKTQRKWITDSLGSYVSDQLLHFLD AQYKNFFSNYENFFKRKIDGRPSFPSLPELFQIRDHGVEVDFNKKELMIKLKGKRLSL RFQADKLLYHGEPGSVTIKRVDGKFYAYIPFDFTPKLEEGKKGAIDIGLANFFAAVTE DGDVILVKAKEYTYIYNMYKEKIKELDRIIGKIRKHTLRMYVTPPKSFKRYPFLGFTN NRQVSKIITSLYTSRYDVGRAKKKRLRREDMTSIVKKIRKVNYRLRITKLNFVKLNGH VKLFPKKSQFIRDIYKDLPILHKLEYERKKLFEKRDRTLMNIRRTAINTLLRILKQRG TTHVVVGYPYNISKNRNELTVNLFQYRKTINDLKIIGERYGIKVDEIVEYNTSITCSV CGEVHKNGRIERGLYKCEKNGNVINADVNGALNIFYKAFSKMPKQLKKIETIKLTSSS P
3408	CLUST.13 1247_S.6 GYS2S-M direct repeat 1>	gcugcaacccuauacaagugcggg
3409	CLUST.13 1247_S.6 GYS2S-M direct repeat 2>	cccgcacuuguauaggguugcagc
3410	CLUST.13 1247_S.6 GYS2S-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3411	CLUST.13 1247_S.6 GYS2S-M non-coding>	tgatgaaaaactaaaggaagtttttactagattatgtgacgaagaagggatagatatg gctcagggtataagagagttaatgatcgaggcgataaacaggggctatataaacaagc agaggaaagaaggagctgaaaaggtgagaagaaatgagtgaacccgcacttctatagg gttgcagctggccgaggcggaagaaggagaagaagaagatgatctcccgcacttctat agagttgcagcatagtgaaaacgttgaggaaaagctaacccaaaaactttaaattcta ctacacgtctatgtactcaagcggggttcccgcaagggtagacccgtgtcctgtgggg cacgcacccccacgtgaataagagacgttgcggacagatgcggacggctataaagagg tatacaaactttcattcaaagattttgctgcaaccctatacaagtgcgggcatggtct tttgtccccatacttttgttacgtacccgagctgcaaccctatacaagtgcgggtcca ttgtcgccgaattgaggctaattgcggcatcgaaatgctacaaccctatacaagtgcg ggcttttcagttcgtacagcttaaaactgtaaaaagtaaggtttaaatattgcaaagg taaggatacaatatagatatgaacatgaaaaaggaaggttcggaaaaggtgagaagaa atggcaagcaaaacatcatctgataaaaagaacggtaaacattcagggcagaaagaaa gtgataacaaacgttcacttactgttagattaaacctaagtacgggacagcaaatata tctcacttctttaattaaggcatacacaacaatagaaagaggcttgtataagtgtgag aaaaatggaaacgtgataaacgccgacgtgaacggtgcacttaacatattttacaaag cgttctctaaaatgccaaaacaactgaagaaaattgaaactataaaactgacctcctc ctcgccctgagaggcgaggtttttcgccccttaactaccgaaaactataaattcttc tgcacgtctatgtactcaagcggggttcccgtaagggtagacccgtgtcctgtggggc acgcacccccacgtgaataagcaacgatgcggacagatgctgacggctgtgaagaggt atataaactttcagctacaactctatagaagtgcgggtaatccatttgagcttttat gcgtctaaaaaggtatgcagctacaactctatagaagtgcgggattcggcgtgtcctg ctctcttttactctcgccacgaactgctgcacctctatagaagtgctggtgaatggct ttgagggcttgaaacaggcacagaaaacatttttagggataggtgcccattttatgac atgcaaaggttacccaagacgcttaagttcgtggcgagagttactgagagcagggcac

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3412	CLUST.13 1247_S.6 52TIS-M effector >	MPSNTDSKRALTVRLNLSTGQQIYLTSLIKAYTTIAGKLNKDAYAKFMELTPNGVVEN IKQLKDVKKKFYAWFYEYVKTQRKWITDSLGSYVSDQLLHFLDAQYKNFFSNYENFFK RKIDGRPSFPSLPELFQIRDHGVEVDFNKKELMIKLKGKRLSLRFQADKLLYHGEPGS VTIKRVDGKFYAYIPFDFTPKFEEGKKGAIDIGLANFFAAVTEDGDVILVKAKEYTYI YNMYKEKIKELDRIIGKIRKHTLRMYVTPPKSFKRYPFLGFTNNRQVSKIITSLYTSR YDVGRAKKKRLRREDMTSIVKKIRKVNYKLRITKLNFVKLNGHVKLFPKKSQFIRDIY KDLPILHKLEYERKKLFEKRDRTLRHIRRTAINTLLRILKERGTTHVVVGYPYNISKN RNELTVNLFQYRKTINDLKIIGERYGIKVDEIVEYNTSITCSVCGEVHKNGRIERGLY RCDKNGHVINADVNGALNIFYKAFFKMPKQLKKIETIKLTSSSP
3413	CLUST.13 1247_S.6 52TIS-M direct repeat 1>	cccgcacuuguauaggguugcagc
3414	CLUST.13 1247_S.6 52TIS-M direct repeat 2>	gcugcaacccuauacaagugcggg
3415	CLUST.13 1247_S.6 52TIS-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3416	CLUST.13 1247_S.6 52TIS-M non- coding>	aatcattatagtatcagcaaaaataacgtgatgtatatcttacacaaatgtacaattc ttgatgaagagtattgtactcaagggatttttaacgtgaccttgagtacccttgagta acgttgcgggcgttataatataatataatatgtctttcaatataatatattatata tatagccgcctaacgttactcaacgttattcaaggttactcaaggtattttggttgaa ataagggggtcaaaatttttgtcgtaaatagtcggatgatatcagtataaatttatt atgatatatattgtataataaataattatgtatagtgcttattaatgtttataatgat tttattattaatacataataaacacatatattattatcttgtatttatataaataatg catatattataatttatggttttaaagataaatattaatatggataaatatatcatat ataataaaataatgaatatatattagtttattcattactggataaagtgaaaatgatt ctaacacatatataggtatgaaacacattttgccttgagtacccttgaataacgttga gtaagggcagccccgttgtggattacacatgtagtgtgcggtgtaatatatatggtgt cataatgtagccttacataactaacgcaaattcagtgccttactcaaggttactcaaa ctgaggatttctgcccttgagtaacgtagaggtttgaagcaatcaattagtttattga ttactggataaagtgaaaatgattataacacatatacaggtatgaaacacattttgcc ttgagtacccttgaataacgttgagtaagggcagccccgttgtggatatggtatacag tgtgcgatatcaggtaaagaatatcgtaatgaagcgttacgtcagtatctcaacccaa atgccttactcaaggttactcaaactgaggatttctgcccttgagtaacgtagaggtt tgaagcccttgaaagtttatatacctctttacagccgtccgcatctgtccgcatcatc acttcttcacgtgggggtgcgtgccccacaggacacgggtctacccttgcgggaaccc cgcttaaacatactttacctatgcaaaaatttgagctttttgccaacttttaaccgta agaagtaaggcttaaatatggcaaaagtaaacccatatgtatgaaaaaggtaacaata aacgtcgatgaaaaactgaaggaagttttctccaggttatgcgatgaggaagggatag accttgctcagggtataagagagttgatgattgaggcaataaacaggggctatgtaaa caaagagagaaaagaagaaagaggcttgtataggtgtgacaaaaatggacacgtgata aacgccgacgtgaacggtgcacttaacatattttacaaagcgttctttaaaatgccaa aacaactgaagaaaattgaaactataaaactgacctcctcctcgccctgagaggcgag

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3417	CLUST.13 1247_S.6 OS0AV-M effector >	MSESKRALIVKLNPTRDECVYLISLIKAYTAIARKLHADAYAKFMELTANGLIENIKQ LKDIKKKFNSWFNEYFKTQRKWITDTLGSNITDQLFQFLRGQYENFFANYENFFKHKI EGRPSFPTLPELFQIRDRGVEIDFDKKILTIKLKGKRLSLRFQADRILYRGEPGAVTI KQLDGKFYAYIPFDFTPKFEEGKKGAIDIGLTNFFATVTEDGDAILIKAKEYTYGYNM YKEKIKELDRIIGKIRKHTLRMYITPPKSFRRNPFLGFTNNREVSKIITSLYTSWYDI GRAKKKRLRREDMTSIVKKIRKVNYRLRITKLDFVKLNGHVKLFPKKSQFVKDVYKDL PILHKLEYEKKKLFEKRDKTLMHIRRTAINALLRFLREKGVTHVIVGYPYNINKNRNE LTVNLFQYRKTINDLKIIGERYGIKVDEIVEYNTSITCSICGEVHKNGRIERGLYKCE KTGKMINADVNGALNIFYKAFSKMPKQLKKIETIKLTSSSP
3418	CLUST.13 1247_S.6 OS0AV-M direct repeat 1>	uguaacucuauagaagugcggg
3419	CLUST.13 1247_S.6 OS0AV-M direct repeat 2>	cccgcacuucuauagaguuaca
3420	CLUST.13 1247_S.6 OS0AV-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3421	CLUST.13 1247_S.6 OS0AV-M non- coding>	acagacattttgaaaaaaatactatacacagtagacacattttacgggctaaaactag atatgcaaaaaactatgaacgaactgtacagggagatggatttcagaaaagctattga cgtgcttgagaaaatgattgttatggcgatctaagcaacgagcctcgctattagtcta aaagcaagtacgtcatataacaccccaacagcttcatttagaaagatcctcatcgcac tgaaagcctccccgcacttttttctgatctctgaccatcagcatatagtcgctatcgtt tctttttcacgtgggggtgcgtgccccacagatcgcgggtctacccttacgggaaccc cgcttaactagcagttagtacagtgtaatttaaagttttcggtgcatatacagctcag agctgtaagaaataaagtttaaaaactgcaaaaataaagtcaaatacatgaagaagat aacaataaacattgatgaaaaactaaaggaggttttttctggattatgcgaagaggaa gggatagatatgactcaggggataagagagctaatgatcgaggcgataaacaggggtt atataaataaacagaggaaagaagaaagaggattgtataagtgtgagaaaactggtaa gatgataaacgccgacgtgaacggtgcacttaacatattttataaagcgttctctaag atgccaaaacaactaaagaaaattgaaactataaaactgacctcctcctcaccctgaa ggcgaggctttctaccccttaactacctgctttgtggtgttcttcagtttttctcaa aagaaacgtatagctagcttttaactaagcataagatttagaatttatttttatctct ctagtttaagatctaagaaatttcaactaatccacaaagcgttaactaccgaaaactt taaattacactgtactaactgctagttaagcggggttcccgtaagggtagacccgcga tctgtggggcacgcacccccacgtgaaaaagaaacgatagcgactgcgtgcagaagct ataatgaaaatactggt
3422	CLUST.13 1247_S.2 SHT3Q-M effector >	MASKTSSDKKNGKHSGQKESDNKRSLTVRLNLSTGQQIYLTSLIKAYTTISGKLNKDA YAKFMELTADGVVENIKQLKDVKKKFYAWFYEYVKTQRKWITDSLGSYVSDQLLHFLD AQYKNFFSNYENFFKRKIDGRPSFPSLPELFQVRDHGVEVDFNKKELMIKLKGKRLSL RFQADKLLYHGEPGSVTIKRVDGKFYAYIPFDFTPKLEEGKKGAIDIGLANFFAAVTE DGDVILVKAKEYTYIYNMYKEKIKELDRIIGKIRKHTLRMYVTPPKSFKRYPFLGFTN NRQVSKIITSLYTSRYDVGRAKKKRLRREDMTSIVKKIRKVNYRLRITKLNFVKLNGH VKLFPKKSQFIRDIYKDLPILHKLEYERKKLFEKRDRTLRHIRRTAINTLLRILKERG TTHVVVGYPYNISKNRNELTVNLFQYRKTINDLKIIGQRYGIKVDEIVEYNTSITCSV

		CGEVHKNGRIERGLYKCEKTGKMINADVNGALNIFYKAFSKIPKQLKKIETVKLTSSP STRLSAPLTT
3423	CLUST.131247_S.2 SHT3Q-M direct repeat 1>	uugcugcaacccuauacaagugcggg
3424	CLUST.131247_S.2 SHT3Q-M direct repeat 2>	cccgcacuuguauaggguugcagcaa
3425	CLUST.131247_S.2 SHT3Q-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3426	CLUST.131247_S.2 SHT3Q-M non-coding>	cttttcagttcgtacagcttaaaactgtaaaaagtaaggtttaaatattgcaaaggta aggatacaatatagatatgaacatgaaaaaggaaggttcggaaaaggtgagaagaaat ggcaagcaaaacatcatctgataaaaagaacggtaaacattcagggcagaaagaaagt gataacaaacgttcacttactgttagattaaacctaagtacgggacagcaaatatatc tcacttctttaattaaggcatacacaacaataactggtaagatgataaacgccgacgt gaacggtgcacttaacatattttacaaagcgttctctaaaataccaaaacaactgaag aaaattgaaactgtaaaactgacctcctccccgtctacgaggctttccgcccccttaa ctacctagggcttttaggttagatttttatttttaactcttaagtccgagttcttcat atgcagtatttagtcttacttttgctcatattcgtcgcagtcgccatcatcataacct tactaccttacataagcctcattataacgaatattaacaacgtcaacgcgcgtgtgta cacactatacaattcaagcacgtatatgagcggcacgtggctagtcaacggtagtaaa cttcaacaggcctctcaaacgccgacaaacaaactcgtcattgaggtagaagagggtt cttacatttacgtgtccaaccagacgtggagtgaaatgctgtcggataacggcgataa cgggccgatattctccccctatgcgtcgttcaacctctcagccggctactacaagttt aacatacctacgcaggccttcgacttcgaacaaccggtctacagtgtcttatcaagtc tggcgttcttcttcgcagctgcagtagtgtttattctcttcatggttttgtcgtatag tcgtagaaggtaacgtagtatatttttaatatgatcttatacgtataacttaatgac gtacaaagaacacatctacgccaaatctgaaaggcaacta
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3428	CLUST.131247_S.4 UV6F4-M direct repeat 1>	cccgcacuuccauagaguugcaac
3429	CLUST.131247_S.4 UV6F4-M direct	guugcaacucuauggaagugcggg

	repeat 2>	
3430	CLUST.131247_S.4UV6F4-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3431	CLUST.131247_S.4UV6F4-M non-coding>	aactgacaccgacattttgaaaaaaatattgtacacagtagacacattttacggactg aagttggacatgcaaaaaactatgaacgaactgtacagagagatggatttcagaaaag ctattgacgtgctagagaaaatgatcgccatgacaatctaagcgacgagcctcgccat taggctagaagcaagtacgtcatataacactaaaagtttatataccccgcacttttg cagaactctgaccgtcattatcgtcagcatcatcgcttcttcacgtgggggtgcgtgc cccacagatcgcgggtctacccctttcggggaaccccgcttaactagtagttaacgta gtgcaatttaaaggtttcggtgtatatacagctcagagctgtaagaaataaagtttaa aaactgcaaaaataaggtcatagcacatgaagaagataacaataaacattgatgaaaa actaaaggaggtttttctaaattatgtgaagaggaagggatagatatggctcagggg ataagagagttaatgatcgaggcgataaacaggggttatataaacaagcagaggaaac aagaaagaggcttgtataagtgtgagaaaactggtaagatgataaacgctgacgtgaa cggtgcactcaatatattttacaaagcgttctctaagatgccaaaacaactaaagaaa attgaaactataaaactaaccttctcccagccttgaaggcgaggctttccgttccctt aactacttgctttgtggtgttcttcagtttttcccaaaagaaacgtatagctagcttt taactaagcataagatttagaatttatttttatctctctagtttaagatctaagaaat ttcaactaatctacaaagcgttaaccaccgaaaactttaaattgtactatattaactg ctagtcaagcggggttccccgaaaggggtagacccgcgatctgtggggcacgcacccc cacgtgaagaagcgatgatgctgacgataatgacggtcagagttctgcaaaagtgcgg gggtatataaacttttagt
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3433	CLUST.131247_S.52UZ7R-P direct repeat 1>	cccgcacuccaaucggguuucagc
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3435	CLUST.131247_S.52UZ7R-P spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3436	CLUST.131247_S.52UZ7R-P non-coding>	atcgtctcttcttcacgtgggggtgcgtgccccacaggtttgcgggtctacccccttgc ggggaaccccgcatgtttattatatactacacaagaatttaaagttttcggttcacat acagcttaaagctgtaagacataaagtttattaactccaaaaatacagtcataataca tgaaaaagataacaataaacgtagatgaaaaactaaaggaggctttttctaaattatg tgaagaagaaggaatagatatggctcagggtttaagagagttaatgatcgaagcaata

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3437	CLUST.13 1247_S.2 4AWJ6-M effector >	MSSKTTSDKKNGKRLGQKESDNKRSLTVRLNLSTEQQIYLTSLIKAYTTIARKLNNDA YAKFVELTTNGVVENIKQLKDVKKKFNLWFNEYFKTQRKWITDTLGSNVTDQLFQFLR GQYENFFANYENFFKHKIEGRPSFPTLPELFQIRDRGVEIDFDKKILTIKLKGKRLSL RFQADRLLYHGEPGAVTIKQLDGKFYAYIPFDFTPNLEKGKKAAIDIGLINFFAAVTE DGDVILVKAKEYTYVYNMYKEKIKELDRIIGKIRKHTLQMYITPPKSFKRYPFLGFTN NRQVSKIITSLYTSRYDVGRAKKKRLRREDMTSIVKKIHKVNYKLRIAKLNFMKLNGT VKLFPKKSPLVRDIYKDLPILHKLEYERKKLYEKRDRTLRHIRRTYINTLLCILKERG VTYVVVGYPYNINKNRNELTVNLFQYRKTINDLKIIGERYGIKVDEIMEYNTSITCSI CGEVHKNGRIERGLYKCEKTGKMINADVNGALNIFYKAFSKMPKQLKKTETIKAKLHL LNVN
3438	CLUST.13 1247_S.2 4AWJ6-M direct repeat 1>	uguugaaguacugcaaaaguguggg
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3440	CLUST.13 1247_S.2 4AWJ6-M spacer>	nnnnnnnnnnnnnnnnnnnnnnn
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3443	CLUST.13 1247_S.5 HF75D-M direct repeat 1>	cuucuucgucaccaucuaauacuccaacaucuacaccgu
3444	CLUST.13 1247_S.5 HF75D-M direct repeat 2>	acgguguagauguuggaguauuagauggugacgaagaag
3445	CLUST.13 1247_S.5 HF75D-M spacer>	nnnn

	effector>	VILVKAKEYTHVYNMYKEKIKELDRIIGKIKKHTLRMYITPPKSFRRYPFLGFTNNRQ VSKIITSLYTSWYDAGRAKKKRLRREDMTSIVKKIRTVNYRLRITKLDFVKLNGHVKL FPKKSQFVKDVYKDLPILHKLEYEKKKLFEKRDRTLMHIRRTAINALFRILRERGVTH VVVGYPYNINKNRNELTVNLFQYRKTINDLKIIGERYGIKVDEIVEYNTSITCSICGE VHKNGRIERGLYKCEKTGKMINADVNGALNIFYKAFSKMPKQLKKIETIKLTSSSP
3448	CLUST.131247_S.6J9JOH-M direct repeat 1>	guugcaacucuauggaagugcgggua
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	non-coding>	tgggcgtagaccccgatcaagatagtttcagcggagaagtcgtcgaaatggcgttgcg tcttttcatttcggcgctcggcaagactcgcggaacagtttggcccatcggacacggg agcgccggtatgcgcggaaacagactcgtgacgagcatgacaaccgatttgtccgtgg ggaaaccgatgaccgccgggaagtcagaagcctgttttggaaaaaatcaattcttgat ttggtgttcatttgaacatttgttaagatctaaagttaatggttcgctgctaccgcta ctgcctgaatccttcagcgacgcaaatcgccgcgattcatcgtgcggcgaaagcggcg cgagcgtactggaacggcctcgtggcggtccaacgttgggcggaacgtgagatcaagg ccggtcgccaaggtgtgccgggccagttccagggaggcgctcgcgcgtctcttggggc tgtagcgccaggggatagcaatatcatcttggcgtggtcacgccctgcaaccggacca aaggcccgaggaccgctcgcagagtgcgcggtggacgactccaattgaggtaatggcg gaggcaacgagcagagcgactgagacagaaaaagcgtcgcagttatatcgcttttgt gggagagatctgggttgtcatctgagacagaaacccgccaaaaatatctcccaaattg ctttttgcggagccagcgcatggatttcctccgagaggagttaaaagcgcgtgagcgg gaacggggtgttttagtaacgccgatgcctccagcctgcctaaaaatctgtctcagat gacagtaagtgcgccattcacagcggggtaggcgcgtctctggtaatcccatattgtc atctgaggcagaaattctctgtatcctgggattgaaactgccgttcgttatctgaagc agaaatttcccgagctggcgcagatccccctattgtcatccgagacagaaaacggttc ggattctggattggacctgcgcgtgtcgtcatttgaagcagaaattcccgtgctgcgc agatccccctattatcatccgagacagaaaacggttcggattctgggattgaaactgc ggtgacgtcatctgaagcagaaatttacccgggctggcgcagggtcccatactgtcat ctgaggcagaaaatctctgaatcctgggattgaaaccccgtattgtcatctgagacag acgatattgtcttttgagacagacgacattgtcacatgaagcagatttttgctttac tattgtcattggaaacagaaaatactgtcatttgagacagaaaagcatccggtaagga gttgaatattaacgggttacgaaaagataactttctaaatctgttgtttaaaaactta aaaaacaacaactggctgttgttttttgaagtgaacactctgtcagctaaagcagac agcttctttgagcacccggcccaacggctgggttacgctcaaccggcccgttccaggc caggcgcgattaaggatattaatcgccgcgttgtggtcccgatcgagcaccagaccgc aaccgcaccggtgaacgcg
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	effector>	RKGESVALQRQVQSNSPFKLKRFSDLSALGGQALKKCEVIIHRPLPDSAEIKQIAVSG RRGQRHLIVMFKAASSDVAKNFPATNRTAGVDPGIKVALTITPLDSPDFGTSDKIEKQ PDLARDACFLKRLRRLQRKHDRQRRQNNPECFDEKGRWIKGKRLHNESKNMQRTQSRI TAMNTHLAESRRDFYHNAACEILRSFDNVAVGKWRPAQTRQRKPTTPSPKGLGAARRA TNRISYDHAISLFISYLKDKAERSVTTKHVQEVSEFGSTRSCPKCGKLTGPVGTEGLA VRDWTCVNCNTTFQRDAASAWQIAKRFKAEVASTSQPAESQDSANSASVLTQV
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	IIXZY-M direct repeat homology - containing sequence>	aacgccgatgcctccagcctgcctaaaaatctgtctcagatgacagtaagtgcgccat tcacagcggggtaggcgcgtctctggtaatcccatatt
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3560	CLUST.187051_S.0 SV2QT-M direct repeat 2>	guugcggucagcccgcauuugaggggucucccgcac
3561	CLUST.187051_S.0 SV2QT-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3562	CLUST.187051_S.0 SV2QT-M non-coding>	agagacagccggcaaaacacgctagaaccgcaccggccccgacgggccgtcgccgggt tagctcagcggtagagcagcggttttgtaaaccgaaggtcgggggttcaatcccctca cccggcaccaaaatttccaacccaaacaacaagatataagatggccgggcccttgacg attttgatcgtcatttcggggaagcgctggggaagcacagggttcggtttcggtcccc agaatgcacagcctgcacagggccgggccggcttcccccctcacccacatgcccgctag cttagtgaggtgtcggaacccgccacctacattcccaagccgccggtccaatacctga ccgccgtattcgagctgcggccgacgcggcggaaggcggctgcgctggagcgggtgcg tgcgaccgccgaggccatattctggaaccagctggagcgtcaccgggttgaggtttga cgccagtgcgtgggacatcacttgcggcccacgatggctgcgatgagccgtagatagc gcaccgcctccctcgctctccgcctcgccaacgcggctgcgcggctcctctcgccgtg cttccaagcgttccggttgcccttgggcgcaccggagccgtcagcgccgccgtgcatg cgacagcgccggcgcccccttcaccgctggcgactggcaaggcgtcccccgccgtgtcc gggctcggcagcgcagcgccaagtgcatggggttgtccgtcgtcatttctgttatcgc cctccccctccgggtg
3563	CLUST.187051_S.18YWL7-M effector>	MPPRAAKPPEEQFLTAVFELRPTRRKAGALERVRDAAETVFWESLGRAEASARGAESL PKPERRRILQEIGAAARRAAISAGLNEPIAQGLGRDAEAAAGATIEARAKGRVAGWPT RPEPRRVAPLPERLGALAASCTLLAEQEARDSLNQKDWTPRARPLTLARERDCRIHRD AEGRLAVALNLLRASDTRSREARISAGSDACTGEVLPAQRRKTVLMIPLACSKWHEDR FLSGKATLKSALVFPRDGRWWLQAQFALPVRARPVSGQILGIDRGVVNPAALALVDAA GAVLAIPGRQGAAISAAVSARVAQQRRRQQDGDDGFRRKLGRAIGATRSAGETRARTR

		IGRHIDMGLHLLANEVVALARGAGARVALEKLDGLKRSMRMARPKGARRGGWGTVLRK AQLAKLETLLTYKLTLAGLPPPREVIAAGTSVTCAACGTRDPKSRPAQDRFLCTACGF AAHADDNAAVLVARRGAMEIKKGDTLDALHKNMVARLRTRGDGGLGPLASGQRIVAAR AAGPGPYAPPAREGTGLDPELGQNVSQSGAENGREAVVAERGAPLSRPPDSPNSPTGS EPCATSGCGDRRDGG
3564	CLUST.187051_S.18YWL7-M direct repeat 1>	cggguguggagaccggcgcgaugggggcugaccgcaac
3565	CLUST.187051_S.18YWL7-M direct repeat 2>	guugcggucagcccccaucgcgccggucuccacacccg
3566	CLUST.187051_S.18YWL7-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnn
3567	CLUST.187051_S.18YWL7-M non-coding>	ggcgggagcagggcggccagatggcgacgatgaagcatgccggggataatgcaggatc ggggccggggctggccagcgcccccgggcggcaggggcggaaagctggaaaaacctag gaaactctagtttcggacaaatacccaaggggcgatcgcgccgcccggtgttacgatt ttttggacgtttttcgggggtcccgaggcggggtcggggccctgaagcccacaaggc gggcatgcggtggcgcccgcgcggggcggcggtggaggggccgatgcacagcttcaa agagcgcgcggcgcagctgatgaatcgtggccacgctttcggtggcaacgcgcatgaa aaagcgattattgccattggcgaatgggatcgctggctgttagcctgacggcaatgcc accccgcgcggcgaaaccacccgaggaacaattccttactgccgttttcgaactgcgc cccacccggcgcaaggcgggggcgctggagcgggtgcgcgatgccgccgagacggtgt tctgggagagcctgggccgcgccgaggccc
3568	CLUST.187051_S.18YWL7-M direct repeat homology 1>	aucgcgccg
3569	CLUST.187051_S.18YWL7-M direct repeat homology 2>	cggcgcgau
3570	CLUST.187051_S.18YWL7-M direct repeat homology-containing sequence>	ggcgggagcagggcggccagatggcgacgatgaagcatgccggggataatgcaggatc ggggccggggctggccagcgcccccgggcggcaggggcggaaagctggaaaaacctag gaaactctagtttcggacaaatacccaaggggcgatcgcgccgcccggtgttacgatt ttttggacgtttttcgggggtcccgaggcggggtcggggccctgaagcccacaaggc gggcatgcggtggcgcccgcgcggggcggcggtggaggggccgatgcacagcttcaa agagcgcgcggcgcagctg

3571	CLUST.187051_S.6 DMUUP-M effector>	MPEFLTAVFELRPSRRKAAAVERVRAPAESLFWDAVGKLRDPADAIVAIEAPRKRQTA AAAMKVDIAKNTMASASKAGLNEAVAQGLTRDITASVMSYVGLRANGHAAEWPSPVAP DAADHGAALNQFLTATTKGAEDAARDALARISRLPGRRPLLIARARDCALVRKKDGGQ IVAVLNILRADDKRAREAKIDDGFDAASGLPILRQSDAEKERKARQARGAPRKSRSEP RNLVMPETSDSRLIIPVTCSKWHEQKFLNGRTKLRSSLIVRRGTRWFLCAQFEMAEPK KPQMTGARLGIDRGIANPIAVSVVAHDAAVIAAPKPAGAEIGQAIHKAEQRRRAEQRR RGVSSRKHARQVDHHLHHLANDIVRDAKTFGAQVVVEKLDGFKATIRTKRVKGARKNP WQKSLKNVQLGKLEAILDYKLKLAGLPPAREVFAARTSISCPACGQTDPKSRVAQDKF VCTGCGFEVHADTCGAVNIARRDIAFTKHTKGGDFAALERDMVAGLRSRDDGGLGPLA AGLMAAGGFVAVRATADRLYETQLVLNLSAEQNAYPDAVQNRRSAVFAERSGAFSGHS KQRRSVESQRLTQERLL
3572	CLUST.187051_S.6 DMUUP-M direct repeat 1>	guuguugugagccggcauuugcaggggggcagcaac
3573	CLUST.187051_S.6 DMUUP-M direct repeat 2>	guugcugccccccugcaaaugccggcucacaacaac
3574	CLUST.187051_S.6 DMUUP-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3575	CLUST.187051_S.6 DMUUP-M non-coding>	ccagggtcagccagtcgctggcaacgtgtagcgcccgaacataatcgtcccatgcgtt gcgcaccggcgcccggccgctggttaccaatgccggttcctatcaagccgcacctgca taatattatttttccttatatcggtgcggccggtgaatgccggcgccaaggtcgtcaac agagtttgtggaaaaacacgttcaggtcaagccgttggcgcccgcgcatgtttcagag gaaacttccatggcggcaaatacgtcagtcccggaaaagatctgtccgcactgtagga agacattcacccccgcgattgaccgctctctagcaagtctcgctcgtggcgcgagac gatctggctgagcagcgagaacagcatgtcaagggtgtgctcgacacccttgtccgtc atgttccgccgcaggtcatgaagctcggcgtggaatttgtaccattcggtcacggctg tgttccccctacgttcaacgaaatatgaggcaacatgccgttgacggcaaactaaacc aacagaatagtatgccgctatgcaattaacattccgtgtgcgcgtgtatctgactaag aggcaacacgctatactggcggattacttgaaccatacgcgtcgactgggttgtatcc tgtcgccgagattaccatgcccgaatttctgacggccgttttcgagccccgtccatct cgtcgcaaggcagcggcggtggagcgagttcgtgcgccggctgaaagcctgttctggg acgcggtgggcaaactgcgtgacccagctgacgccatcgttgcaatcgag
3576	CLUST.187051_S.6 DMUUP-M direct repeat homology 1>	aaugccggc
3577	CLUST.187051_S.6 DMUUP-M direct repeat homology 2>	gccggcauu

3578	CLUST.187051_S.6 DMUUP-M direct repeat homology-containing sequence>	ccagggtcagccagtcgctggcaacgtgtagcgcccgaacataatcgtcccatgcgtt gcgcaccggcgcccggccgctggttaccaatgccggttcctatcaagccgcacctgca taatattattttccttatatcggtgcggccggtgaatgccggcgccaaggtcgtcaac agagtttgtggaaaaacacgttcaggtcaagccgttggcgcccgcgcatgtttcagag gaaacttccatggcggcaaatacgtcagtcccggaaaagatctgtccgcactgtagga agacattcacccccgcga
3579	CLUST.187051_S.097P5Q-M effector>	MGQFLTAVFELRPTRRKAAALERVRAPAEAVFWEVMATLRPSFESLPLPGEDQESKKL AKTARIEACRNAQKLALQKATKAGLVEPVAAGLARDVEMAVSSFAELRAKGQEASWPV KHEPTESDYVAALQALAASTDQESESKARDELARVRKPPKARGLTLARSRDGNIIRDQ MGRLAAVLNCLRANDKRSRQATINPGVDPSTGEGFKKNRSSKTKLVIPLACSKWHENK FLAPRRDGRRPTLRSSIIFPRDDRWWMAAQFEMPQEKAHLSGAVLGVDRGCVYPVAAA LVDANGALIELPEPVGKEVGEIIVEMEQRRREESRRRGITSQSYFNAVNDNLHRIANS IVDLAREHGAVVAVEKLGEFKRTIVTKRIRGSRKGGWRRVLKKAQLGKLEMILKYKLE LAGLPQMVEVVAAGSSQSCAACGHRAKKNRADRDAFKCVECGHEMHADSNAAIIVARR GVFVLQRKLRKGDKLDQLHKNMIAGLRAGGMTGLGRHGLAVPVVSGRGSAE
3580	CLUST.187051_S.097P5Q-M direct repeat 1>	gggucucgcacccccagauucguggagugacugagac
3581	CLUST.187051_S.097P5Q-M direct repeat 2>	gucucagucacuccacgaaucuggggugcgagaccc
3582	CLUST.187051_S.097P5Q-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3583	CLUST.187051_S.097P5Q-M non-coding>	ccgaaaaagcccaagggcatgtggtggcgaacttacgagcgcctgcgcgacgaatgtt tcgacgctgagatgcgtgccgacgaggcctttgcgatccatgccgaacgaatgctcgc ccacatcgacaaccgaaaacccacaaggagatagtgatgctgaccgaacccaaaacca tcctgccgctggcgattgtttccactatcgacatcccatccccttcaatcggcaggg gggaggggtcggttacagggaatcccttaccgcctcgctagcgttgcggtttttag gcttcggcggcggctgcggtgagcaaagcctcagcgcaggaccggagtggcgaattta aggccagacacgcctccacagtcgagcaggattatcatgtgacctgtccatgggccag ttcctgacagccgtctttgagcttcggccgacccggcgcaaagctgctgctttggagc gcgtccgcgcacccgccgaggcggtattttgggaagtcatggcaacgctgcgcccgag cttcgaatccctgccgctccccggtttcgtgttgcagcggaaactaagaaaaggggat aaactggatcagctacacaagaacatgatcgctggccttcgggctggcggcatgaccg gcctcgggcggcacggattggccgtgccggtcgtctcgggtcggggttctgccgaata ggcgtatgcgtgccttcgggtgccttacctattcgcgggccgaacacttacgaccaaa acccctgtgggtattcgcagagcgggtcggcacgattcaatggggtgagatggaaag tggcatttcacgtttcagggcaaccagttacgaattatcaca
3584	CLUST.187051_S.2CRVWO-M effector>	MGQFLTAVSALNPTRRKAAALERVRAANEEAFWESMASAKERADDIIAMPKKERRSAL RQACKHVLKIAGKHKLVEPVACGLMRDVEMAVSSYIELRVGEHEATWPERDLGQRPDI GMALDQLAAAISIEDENAARDAFAKARKIPATRGLTFARARDARIVKDSAGRVAVVLN CLWASDPRSRKTVIHEGVDPTTGEVLGQAKSKAKLVIPMSCSRWHQNKFLNGEAVLRS SLVFKRAERWFIASQFEMPEKQAPPSGAVLGIDRGIVYPVSVGVVDADGALLDLEAPA

		GNEIGNRIRLSDERRKRQAQRRGVTTLRHEKVVHHSLHRLANEIVRTATRYGAEVAVE KLGEMKKVITTARPTGARKGGWRRSLKKAQLGELEQFLSYKLKLAGLPKVREVIAAGT SMTCPACGHKAKENRPGRDVFKCVACGHAAHADQNASIIIARRAVLMRKLKKGDKLDA LHMDMVASLRTRGDGGLGRRELFTMVVPAHVSGVEANEGKASLLTSASGQEVTLVDQN VPTGVLAERIGAYSGRGTPHIREPDQ
3585	CLUST.187051_S.2 CRVWO-M direct repeat 1>	gguggagccgccuccggaaugcagggugacuggaac
3586	CLUST.187051_S.2 CRVWO-M direct repeat 2>	guuccagucacccugcauuccggaggcggcuccacc
3587	CLUST.187051_S.2 CRVWO-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3588	CLUST.187051_S.2 CRVWO-M non-coding>	ctctcggcaacattcataaaatggcagctgccggaccgcttcgagtatctggatgcga tcccgcgtacctcgacgggaaaattctggaaggtgaagctgcggaagcgcttctcggg agcgccctcgggggctgattcgggcgcaccctagcccggatcacctgcgccggggtgg acgccaacgccgagcaggtccgaaggggttgggcgtgggtattcgagcgctacgcacc gaagggatcgcccctgtatggcattcaggccgaggcccgtcttgctaggcgcggcctg tgggcggatgatggggcggtagcaccttgggagtggaggcgccggtagctagatgggc cagttcctaaccgccgtgtccgcgctgaatccgacacgccgtaaggcagcggcgctca agcgcgtgcgcgctgcgaatgaggaggcgttctgggagtcgatggcgagcgcgaaaga gcgcgccgacgacatcatcgccatgcccgcgaatgagggcaaagcatcgctccttacc tcagcatcgggacaagaagtcacacttgtcgatcaaaacgtcccaacgggcgtactcg cagagcggattggcgcttattctggaaggggcacccccacattcgggagccagatca atgagttccgcagcatcaacgcccctcaacatgctcgtacggcagatcggacgacaag ccgccttgggggtgggtccgttgaaaccacttcgtcgcagtgcgacgtctaccccggc gttcaagtgggggaatgcgggcagcccaatttctgacatccggcgagtcgagtctac aaaacagtctacacgccgacggataaacggaacccgttcgagaaattgttctaagcct ttgattattggctccccgaccagggctcgaacctgggacctgcggattaacagtccgt cgctctaccgactgagctatcggggaccggaaaaaggccgcaattctaccggattacc ttcgaaatggcgtcggcgacgtagtcgaggttcttcgtcgtgagcgcggcgacgcaga tgcggccggtcttgatggtgtagatcgagtactccgcgcgcagtcgcagcacctgctc cttcgtgaggcccgagtagga
3589	CLUST.187051_S.2 RX87F-M effector >	MARPVVQFLTAVFELRPSRRKAAALERVRAAAETVFWQQLDSYRARADEVAADPDRKA RRTALSGIRAATAKLATRAGLSESVAEGVARDVEQNISSYVGKKAKGGEAGWPARTDA VTPEDRANVLASLCTATTSKHEAAGRDELARVAKGERVHPFVLVRARDCQIVRDGAGR IAVVLNVLRAKDARAREAVVRDGFDATTGEVINRSKRKTVLVVPLACSRWHENKFLSG KAQLKSALVVRREDRWFLCAQFALPVTVLAPSGAALGVDRGCVFPAATALVSGDGAVI EVPGGQGEKIGQTIVRADDRRRRQQRRRGWTELRHVRAVDHALHGLANGIVALARTHH AEVVIEKLGEFKRTIVAQRQKGTRKGGWRRVLKKAQLGKLEQILTYKLALAGLPPLRE VYAAGTSQTCPACGHRDPKSRPEQALFRCTSCGHELHADANAAVVIARRGVLMRTIKK GDKLDALHRDMVAGLRSRDDGGLGPLASSRRVVAAHVPAAVANDLKEASASGGLTAAA GQEATIAAENARKGVLAERSGRISSKAPVPGSKGSSKSSRRIGCGEPEDAG
3590	CLUST.187051_S.2 RX87F-M direct	ggugcggugagccugaagaugcgggguagcugcaac

	repeat 1>	
3591	CLUST.187051_S.2 RX87F-M direct repeat 2>	guugcagcuaccccgcaucuucaggcucaccgcacc
3592	CLUST.187051_S.2 RX87F-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3593	CLUST.187051_S.2 RX87F-M non-coding>	gaggatcatcgccatggctccccaggagatctccaaggccgagctgctcgccaagctg agggtcggcaacgacaacgccaggttgccccgctctacgcgggaacttaccgaggcgc tgcgcagattggggccggacctagaagcagcgggcgtccgcatcgaggaaaaaaggag ggctacgggccgcttctacatcatcacccggacgtgacggtgggggggcttcggcccc cttcccgatgacacatgacacagatgacacaggattttcgaaagtctcccgtcccctg cggactcgaaagtagcctgacgctggcttgaccctgatgcgcccgatatcgttgcggg atggcgcgtccggtcgtccagttcctgacagcggtcttcgagctgcgccccagcaggc gcaaggctgcggctctggagcgcgtgcgcgcggcggcggagacggtcttctggcagca gctcgacagctaccgtgcgcgggccgacgaggtccgtaactagttgctgaataacccc gggtctgca
3594	CLUST.187051_S.AC7B0Y-M effector>	MGQFLTAVFEMRPTRRKAAIMERVRREAEDVFWSVMAPANRAAAEQAVATEDKTERRK LLSTYEVRMRAEAARAGLIEAVAQGLARDAGMAVSSYVELRRKGQSAEWPERKLAKAS GHEDGLAALAAAMTREEENAARDLFTSATREPSPRPLTFARERDARIVRKTVNGPISV VLNIITAKDRRAKQMMMAEGLDAATGEALREHRSKTKLIVPLSCSLWHEQKFLGGKAI LRSSMILRRGERWFLQSQFEFPDATPVKTEGSLGVDRGLVNTLVGAAVDMEGAVTGLP IISGPAIGDTIRALDKKDRAYKRRTGRVGLQHRRRVDHMLHEMTNRIVAEAKNRRLQV TMEDLKGFKQTIVQKRAKGGRRNPWARSLKKAQLGKIEQILDYKLTLAGLPKMRIVPP GGTSITCSRCGHAAKENRTEQASFKCVSCGFEAHADANAAVQIARRGLMKVRKGDKLA VLHTNMAVALSKRGGDGGLGLLAASAAGGFVAAHASAPEPYEAEAPQGVEVLSFDAGQ ELTDAAKNLRKDVFAERGGSDFEGQNTGNRNKRHGLDEA
3595	CLUST.187051_S.AC7B0Y-M direct repeat 1>	gaugcgguccccccucgauuuguccggugagcgcaac
3596	CLUST.187051_S.AC7B0Y-M direct repeat 2>	guugcgcucaccggacaaaucgaggggaccgcauc
3597	CLUST.187051_S.AC7B0Y-M spacer>	nnnnnnnnnnnnnnnnnnnnn
3598	CLUST.187051_S.AC7B0Y-M non-coding>	cgcctcctgaagcccgccgaggtggcccgcgcggtggcctatctgtcaagcgaggagt ccggcatgatgaccggctcgatcatcgacttcgaccagcaggtgctgggcgcggccaa cgccacccccggagccgccgcccgccacgtggtgatgactttggtgcgccggcggttgc cagaatggagccgccggtagccggatcgtagccgcccgtcgccacgcaatggctatgg cgggcctgttgcaaaaaacccgtctcacgcggttgacagcgcgcgctgtcagcccgtg ttttttgtcaattttgatggatgaaatttcgcaatccattacagccattgcgggctga aatcataaattgcagattggggatgccgtcgagtcgccaaccccagggcttccatggg ccagttcctgaccgccgtcttcgagatgcgcccgacccgccgcaaggcggcgatcatg

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3599	CLUST.187051_S.5P2O0I-M effector>	MAGQYLTAVFKLRPSRRKAAIMEKLRAKAEDVFWDILAQKRPRADAVAAEADKKARRE QSRALEQEITRDVIRDATKAGLNEPIAQGLGRDIAMAIGSYIELRAGGHEAEYPARLV TSEADHATALDALALATTREEENAARDSLARVARKPGPRPLTIARARDGLIIRKGPNG ALALVLNIMRATDEKARPAQLAPGMEAATGEVFKGGVSKTRIILPLECSLWHQNKFLS GKTILRSGLLLRRGDEWFYCAQFEMPERKAALSEARLGVDRGIVNPIALSVVAGDGRI IRVSEPLGQEVGASIAAADRRRRAEQKRRGATSHRHVDRVDQALHLLANRIVAEAKAF RAQVVLEKLDGLKRTITEARPKGARRGGWRRHLKKAQLGKLEVLLGYKLKLAGLPAPR DVVAGGTSQTCPACAARDKKNRPSQERFCCIACGFSAHADSVGAVNIARRGVAMIGIT KGDKLAPREQDMVARLRLRDDGGLGPLAANAAGGFVADRASTAKGVSSPQGELPGLEQ KTTHGDQNARKGVFAARGATFFRGQNGKKPLRGKGVTHDPPE
3600	CLUST.187051_S.5P2O0I-M direct repeat 1>	cccggagugacccugaauuuguggggguggccgcaac
3601	CLUST.187051_S.5P2O0I-M direct repeat 2>	guugcggccaccccacaaauucagggucacuccggg
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3604	CLUST.187051_S.5P2O0I-M	uugcggcca

	direct repeat homology 1>	
3605	CLUST.187051_S.5 P2O0I-M direct repeat homology 2>	uggccgcaa
3606	CLUST.187051_S.5 P2O0I-M direct repeat homology - containing sequence >	nnnn

		agacgggcaaggatatttttatattctccccctataaagcggttaatagccgtagtgc ggtggcagacccgattctcttcaccctactttggaatcatcaggtgcaactcctgaac cgcacatttatgtctttgtaatggctttgtacataaattgtacagcagaggcatatcg ctcactaatactcacagacaagcctgtgggggggtgtctaacagccctgagtgagtag tctaagctctgaacaggggctacgttaagagagaaaacagttcttgaggtatagggggg tggtttctcccacggataaacctgtgggtttcccgccaaaattttatgattcatttttt catcgagttctccttaagaaatcgggcttatctgaagcacggagcttaccgcatcttc cgatgcggggaataggctaaaatctatgtagggcggggaccgcccgaactaaagcctg tggagctggctctgacggggtatacctttagcggggtatgctagttaccaccagtctt gaagcaggaagctcggctacttgtagccgagtagttcacgcgataacaaggaatacag acatgaatgatacaataacagccagaaaatatgatatcagtctggtaaagatagcttc atatacaatgaaagcccgcctttatccgaacatacatcaggaaaaatatatgcaggcc atcttggatggtataagaaaagccagcaacgggacagaggcatataaaaatccttttg ttcttgtagataaggatggaaatgtgatcgatgatgcccagggatacggctttacaaa ggctgctgatgcgagaaagtattggaatgaccatataagaaagaaaaagaaggcagca gaagctgtctgataataaaaaacggtgaggcttagccaccgtgtagtgcgaaccctta atacacatcatgcctgcgtgatgttcgcactacgaaatgtctggtctacggtctttta ataggcataaaaacctgtaactgaccggcaggaaacagaccgataccatatattgaca tgcggattatgctataacagaatattgcgtaagagatggcaatagatttattttcggg agctggtggtttgtatataggctttaaaagcaggattcgatatgaacctcacatgact aaagtcgcaggtgttggcctgctgaattataaaaaagccacccggcgtgaccaggtgg ttaagaggggg
3612	CLUST.192220_S.5 LDOXB-P direct repeat homology 1>	caugcggauu
3613	CLUST.192220_S.5 LDOXB-P direct repeat homology 2>	aauccgcaug
3614	CLUST.192220_S.5 LDOXB-P direct repeat homology -containing sequence>	cggtgaggcttagccaccgtgtagtgcgaacccttaatacacatcatgcctgcgtgat gttcgcactacgaaatgtctggtctacggtcttttaataggcataaaaacctgtaact gaccggcaggaaacagaccgataccatatattgacatgcggattatgctataacagaa tattgcg
3615	CLUST.192220_S.AQA19H-M effector>	MNDTITARKYDISLVKIASYTMKARLYPNIHQEKYMQAILDGIRKASNGTKYCLKNHL YPELEKPGKDGVTMFPDWKYIGSSAWLEKLRDLYPGIRGIVPGASLSSSVGGAIACDL KKGWEKLGKLPTDKWMNLKDKKGRPRVKNYCKRFPRTSFWIQIPTDRIEYVDEKHVWI NLFPTKKFEDDTPFGRIRIRGWNSKITFDENGSPVPVQKNVGVRISINACGEWYIAFS FQNAYRPVKVRTDIERTPIGIDPGIKYSLTDSDGEHYENRRYKERLQDQINFYKDQMS RRQGSCNAEFRKNRKEAWKWNDEHKEEIEAGKAERKSVAESKRYLKAKYRAARLEKKA VDRRNNDQGVMTSEIIAKASHLYLESPDIKAIMQDQEMGILAADAAMGENLLKLKYKA EWSGIGYHAIDREALSTQKCSACGYVLKDDEKLKLGDREFVCPVCGHKEDRDENAAKV

		ILATGKQEEADGIPSYVPPKEKPVREYKDTPVSKKHPDVFVHFSNEMKEAYKNPFVLV DKDGNVIDDAQGYGFTKAADARKYWNDHIRKKKKAAEAV
3616	CLUST.192220_S.AQA19H-M direct repeat 1>	guugcaauccgcauggauuauacggauuaagag
3617	CLUST.192220_S.AQA19H-M direct repeat 2>	cucuuaauccguauaauccaugcggauugcaac
3618	CLUST.192220_S.AQA19H-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3619	CLUST.192220_S.AQA19H-M non-coding>	gaatgggcaggaatgatgctccttgcaatagctttttcaagatttctgatgatagtga ccaattctgatccggattccgtatgggacgctacaactaaagctgaagataaagtcat ggatttttgggaaacatacaggaccctgcctgaagagcaaaaaataaaacaaataca aaaaatatagcaaaaaactatttacatattagcgtaatatgatatagttatatctgtc aagaggaaattattgcggatggccgaaaataatttttctatggaccattagcccaact ggtcagagcaggcggctcataaccgctcggtttggggttcgaatccccggtggtccat ttgcaggatataccaacctttcccgacagtttggttaacagcggactgctgacaccga tatatcctgcgcaggggcctgtaaaggtttcgacggtggattgaaaacttaatatgcg tgccagtccggaagatctgtaaaacttccacccaaatgtaaacgacgaaaatcgtgag tacgcttttgctgcctgagtaatcagacatgctcctcccgttaagaggataagctcca tggatatcaccgctgtaatccacggggtcaaatgaagcggttatacagagacagtcat gccgtaataaacctctgaagaatttttttattccggcacagacgaatacacattgcctg ttctgtgtaccgtccaagcatgggaacagtgatacgcacgtagtatattatgtgatta gattgcatcggacacgggttcgactcccgtcaggtccacttagcgtgataaatgacag gtcaaaggggcccctgaatatccataccagggttttaacctgtaatgctcgtgtagct cagccggtagagcacgtgacttttaatcacggtgtcgagggttcgatcccctccacgg gcacttggggactgcgatcatcagtatcgtatccccgctttgacatgaaactcctttc cgtagcggtcaacaaccgctatacctgcatggtgtatacgaagagtatatcagtggtt cgactccctgacaggtatttgcccgtattatcagacgggcaaggatattttcatattc tccccctataaagcggttaacagccgtagtgcggtggcagacccgattctcttcaccc tactttggaatcatcaggtgcaactcctgaaccgcacatttatgtctttgtaatggct ttgtacataaattgtacagcagaggcatatcgctcactaatactcacagacaagcctg tgggggtgtctaacagccctgagtgagtagtctaagctctgaacaggggctacgtta agagagaaaacagttcttgaggtatagggggtggtttctcccacggataaacctgtgg gtttcccgccaaaatttttatgattcatttttcatcgagttctacttaagaaatcgggc ttatctgaagcacggagcttaccgcatcttccgatgcggggaataggctaaaatctat gtagggcggggaccgcccgaactaaagcctgtggagctggctctgacggggtatacct ttagcggggtatgctagttaccaccagtcttgaagcaggaagctcggctacttgtagc cgagtagttcactatatagcagagtctgcatgggtcgcaggctccgtctgctcgtgta gctcagtcggtagagcacgtgacttttaatcacggtgtcgagggttcaatcccctcca cgggcatttctgctctggttagagtgcgggaatgactatgttgccataggcactcctt tagtgagcagctgagcctttgtacgccggttgcttacatttaagcgataacaaggaat acagacatgaatgatacaataacagccagaaaatatgatatcagtctggtaaagatag cttcatatacaatgaaagcccgcctttatccgaacatacatcaggaaaaatatatgca ggccatcttggatggtataagaaaagccagtaacgggacagaggcatataaaaatcct tttgttcttgtagataaggatggaaatgtgatcgatgatgcccagggatacggcttta caaaggctgctgatgcgagaaagtattggaatgaccatataagaaagaaaaagaaggc agcagaagctgtctgataataaaaaacggtgaggcttagccaccgtgtagtgcgaacc

		cttaatacacatcatgcctgcgtgatgttcgcactacgaaatgtctggtctacggtct tttaataggcataaaaacctgtaactgaccggcaggaaacagaccgataccatatatt gacatgcggattatgctataacagaatattgcgatggcaatagatttattttcgggag ctggtggtttgcatataggctttaaaagcaggatt
3620	CLUST.19 2220_S.A QA19H-M direct repeat homology 1>	caugcggauu
3621	CLUST.19 2220_S.A QA19H-M direct repeat homology 2>	aauccgcaug
3622	CLUST.19 2220_S.A QA19H-M direct repeat homology - containi ng sequence >	cggtgaggcttagccaccgtgtagtgcgaacccttaatacacatcatgcctgcgtgat gttcgcactacgaaatgtctggtctacggtcttttaataggcataaaaacctgtaact gaccggcaggaaacagaccgataccatatattgacatgcggattatgctataacagaa tattgcg
3623	CLUST.19 2220_OUP M0100032 0-M effector >	MEVQYNKIDVYPMKIRLYPTKEQAKTIDGWLMGLQKAYNMTLYALKEGVPELRQKSKS GDAEFPNWKYIGKREWLDELRKNSPCVANVPGGCLSSTVGGALGADMRKAWESQGKLP VDAWFRATDANGRHIVRWYSDAKPRKSCFFQIEAGKISREKQSVYITLRKDFRVKARG WNDKIRFSEESDEGFFEKYRDSKKVLSLRVSRDNCGDYFATITLKDVYRPTKVEAERK GVGIDVGVRAMATDSDGRVYENPRIKQKFEDKKTELGRQLSRRYGAKNKQFRQDCKEA RSFNRLHESEINEKLVVPKTVLPSRRYNQAQLKLSKLERKMRRKRDMAQHVYSAEVVR KASLVAIENLNVKGMMADSNLADRLSDAAMSELLRKLKYKAEWSGASYHAIGTFTAST QRCAKCGYILRGENKLARDDSVFVCPVCRNVDGRDANAAKSILQVAQKEISEGVPSAD LIKKLEVKKTKTYPDKPIGKAFPNVFTHFSEEYKKQKRNPFVIVDENKNVLNDAQGYG YRNRQSAQKFWAHKMNQ
3624	CLUST.19 2220_OUP M0100032 0-M direct repeat 1>	gucacaaccuaugugugguuaugaacugcaag
3625	CLUST.19 2220_OUP M0100032 0-M direct repeat 2>	cuugcaguucauaaccacacauagguugugac
3626	CLUST.19 2220_OUP M0100032	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

	0-M spacer>	
3627	CLUST.192220_OUPM01000320-M non-coding>	ctgaaaatgcgccgccgcaccaccctggagccgatgaacgcctatgagcgtcatgtca tccatgccgcccttcaggacatggacaacatcaccacccattccaccggcgtcgaacc aaaccgctgcgtcgtcatcgagtacgtccgttaaacaggcacccccccatgggctgcgg cccatgggggtttatcgcttccataaggtacacaaactgaaagtggggaatgaaggc aacaccgcgcaattgtgtctgcgagccgcagccgtttttttgccccacttcttcagtt tgaaaaacgagaaatacatacagtataccttcgttttccaaactttgaattgagccaa aaatccaggctggggcttcttgccaaattgtgcggtgttgcctgaacattgcaatgtg tgtcatatattggacataatgtgtggtagtatttatctgcgaaagaaaaagcacacaa atacgaagttaaggttgacattctgcaaattgtagaataaagtaaagaaaaggggcga ctgcagtggaagttcagtacaataaaattgatgtttacccgatgaaaataaggcttta ccctacaaaagaacaggcaaaaacaatcgatgggtggctaatgggattgcaaaaggcg tataacatgacgctgtatgccctgaaagaggggtgccgacccatttagcgaggagt ataagaagcaaaagagaaatccatttgtaattgttgatgagaataaaaatgtcctgaa tgatgcccaaggatatgggtatcgtaacagacagagtgcgcagaaattctgggcacat aaaatgaaccaataaattttatttcgtgaggtgcagccacgaggtgcgaataggaagt acgcagcaatgtgctgaatcgttcgcacgaaaattggcatttttgaaaaccaaagcca ataatcatatccataaaaacagaggtagacgcaacatgctgtaaccctattagccact agacacaggatcttgcaagcctaggctatccgtacccttgtttctgcttttgctacaa cttatgaacggtaagccgtggcaaatatttaggtggggcttggcaaaatgggctgaca taaaaaatacacttactgcctatctgttctgccgagatagaaaagaaacgtggcgtga gtaagctacagatcatatggcaaagtttttcccccttgctcgttgacagaggtgagca aggggaaacttttgtgccctgacaggggccggtccttcacaccaggcggaaggctgc tgccccgtgggcggggaggggacctccagggaaccgcggaggggggaaaacttccccg gtccacagggattcggcctgggcggcgttctcggcctccaggtcgatgagcggaacgg aaacagtgccgga
3628	CLUST.192220_UPOH01022078-M effector>	METQYYKVAAYPMKIRLYPTKEQAKTIDSWLLGLQKAYNMTLYALKEGVPEEPEEPEE PGEKKPELRRKSEDGSTEFPNWKYIGSGDWIERLERKNQSLKGIPHDAYYNAVGGMLS VDMKKAWESQGKLPVDKWFQARDEKGHLIVRWYNKGKTRSSAYLQVEARKIVQQGKSV FITLQKGFSVKARGWNEKIRFSEDLTQSFFDKYQGDKRKVGVRISRDNCGDYYAVISL KDVYRPVKVEAERRSVGVDAGTRVMATDSDGMTYENPRIKKRNEAEKAELDRQLARRF GARNEQFRAECKAARKYNKSHQEEIAEKVVELKRVLPSKRYLKAQLKLSKLERKAARQ RDMVQHIHTAQIVAKANLVAIEHLNVEGMKKDSNSASSVEDAAMSGLLQKIKYKAQWS GGNYHSIGTFDPSTQRCAQCGYVLKDEEKLKRGDDTFVCPRCGNVDGRDENAAKSILI VAKERIERGLPSADTIKKPKEKKKKTYPDKPIGKNYPGVFTHFSEEFRQQYKNPFVIV NDKQEVLDDAQGYGYSDRQSAQKFWTHKMKTQQKQ
3629	CLUST.192220_UPOH01022078-M direct repeat 1>	gguaacaaucugcggauggaugugaacugcaag
3630	CLUST.192220_UPOH01022078-M direct repeat 2>	cuugcaguucacauccauccgcagauuguuacc
3631	CLUST.192220_UPOH01022078-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn

3632	CLUST.192220_UPOH01022078-M non-coding>	aggcttttcccaaaaaatgatttttaggaaagtgggaaacctattggacacaatgcg tgctattatgcagaaaaagagattgacatcccatataaatgtgagataataaaggaaa aagcaggggaggtgcagcaatggaaacacaatattataaggttgcagcatacccgat gaaaatccggctgtaccccacaaaggaacaggcgaagaccatagacagctggcttctg ggcttgcagaaggcatataatatgacgctgtacgcactgaaagagggtgtgccggagg aatttagacaacaatataaaaatccgtttgtaattgtaaatgataagcaggaagtatt ggatgatgcccaggggtatgggtacagtgatagacagagtgcccagaaattctggaca cataaaatgaaaacacaacaaaaacagtaaagaaaatcttatcgtgaggtgcagccac gatgtgcgaatctaaagtgaacagaaatgggaacagacgttcgcacgaatgttggcgg atttcttcggaaatcgagccaataatcatatccatattaccgggttgctctatagata gtgttgggtacacttgctgaacacaagatattgcaccgtcctcgttcatcagctgaaa attca
3633	CLUST.192220_S.AS97E5-M effector>	MRKAWESQGKLPVDKWFQARDEKGHLIVRWYNKGKTRSSAYLQVEARKIVQQGKSVFI TLQKGFSVKARGWNKKIRFSEDLTQSFFDKYQGDERKVGVRISRDNCGDYYAVISLKD VYRPVKVEAERRSVGVDAGTRVMATDSDGMTYENPRIKKRNEAEKAELDRQLARRFGA RNEQFRAECKAARKYNKSHQGEIAEKVVELKRVLPSKRYLKAQLKLSKLERKAARQRD MVQHIHTAQIVAKANLVAIEHLNVEGMKKDSNSASSVEDAAMSGLLQKIKYKAQWSGG NYHSIGTFDPSTQRCAQCGYVLKDEEKLKRGDDTFVCPRCGNVDGRDENAAKSILIVA KERIERGLPSADTIKKPKEKKKKTYPDKPIGKNYPGVFTHFSEEFRQQYKNPFVIVND KQEVLDDAQGYGYSDRQSAQKFWTHKMKTQQKQ
3634	CLUST.192220_S.AS97E5-M direct repeat 1>	guaacaaucugcggauggaugugaacugcaag
3635	CLUST.192220_S.AS97E5-M direct repeat 2>	cuugcaguucacauccauccgcagauuguuac
3636	CLUST.192220_S.AS97E5-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3637	CLUST.192220_S.AS97E5-M non-coding>	atgaggaaggcgtgggaaagtcaggggaaattacctgttgataaatggtttcaggcta gggatgagaagggccacttgattgtacgatggtataacaaggggaagacgagaagttc cgcctaccttcaggttgaagccagaaaaattgttgaggaatttagacaacaatataaa aatccgtttgtaattgtaaatgataagcaggaagtattggatgatgcccaggggtatg ggtacagtgatagacagagtgcccagaaattctggacacacaaaatgaaaacacaaca aaaacaataaagaaaatcttatcgtgaggtgcagccacgatgtgcgaatctaaagtaa acagaaatgggaacagacgttcgcacgaatgttggcggatttcttcggaaatcgagcc aataatcatatccatattaccgggttgctctatagatagtgttgggtacacttgctga acacaagatattgcgaaaccgtaggcaaaataaagatctataataatatgctccctttt ccggttttatgtgg
3638	CLUST.192220_UPEJ01009172-M effector>	METQYYKVAAYPMKIRLYPTKEQAKTIDSWLLGLQKAYNMTLYALKEGVPELRQKSKD GSTEFPNWKYIGSKAWLDSLRERSSYVASVPGGCLSSSVGGALGADIKKAWESQGKLP VDAWFKATDAKGHSIIRWYSDSRPRKSCFFQIEANRFTRTNQSVYITLRKDFTIKARG WNDKIRFAADSTESFFERYRDGNDVFSFRISRDNCGDYYAVITLKDVYRPFNVEPERR GIGIDAGVNAMATDSDGVSYENPRIKKKNETLKAEFGRQMARRYGIKNEQFRKERKET RKYNTLHNEEIANQTVEPRCISPSKRYLKAQVKLSELERKVRRQRDLIQHTYTARIIA KANLVAIENLNVKGMMGNSNLADSLSDAAMSEFLRKLKYKAQWSGGEYHAIGTFTAST ERCAQCGYVLQGTEKLTLADRIFTCPICGNTDDRDANAAKSILEIAEEEIKEGIPSAD TVKKPKEKKKKTYPDKPIGKNYPDVFTHFSEELVQQHKNPFVIVNDRQEVLDDAQGYG YSDRQSAQKFWTHKMKTQQKQ

3639	CLUST.192220_UPEJ0100917 2-M direct repeat 1>	uaacaaucugcggauggaugugaacugcaag
3640	CLUST.192220_UPEJ0100917 2-M direct repeat 2>	cuugcaguucacauccauccgcagauuguua
3641	CLUST.192220_UPEJ0100917 2-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3642	CLUST.192220_UPEJ0100917 2-M non-coding>	caccacccattccaccggtgtggagcctaaccgctgcgtcgtgattgaatacgtccga taaacgtacataagaagtccccacaggaagaaattcctgtggggacttctttgacgat gcgaaagtttttccaaaaaaatgattgtttttaggaaagtgggaaaactattggacac aatgcgtgctattatgcagaaaaagagattgacatcccatataaatgtgagataataa aagaataagcagagggaggtgcagcaatggaaacacaatattataaggttgcagcata cccgatgaaaatccggctgtaccccacaaaggaacaggcgaagaccatagacagctgg cttctgggcttgcagaaggcatataatatgacgctgtacgcgctgaaagagggcgtgc cggaagaacttgttcaacagcataaaaatccgtttgtaattgtaaatgataggcaaga agtattggatgatgcccagggatatgggtacagtgacagacagagtgcccagaaattc tggacacataaaatgaaaacacaacaaaaacagtaaagaaaatcttatcgtgaggtgc agccacgatgtgcgaatctaaagtggacagaaatgggaacagacgttcgcacgaatgt tggcggatttcttcggaaatcgagccaatcatcatatccatattaccgggttgctcta tagatagtgttgggtacatttgctgaacacaagatattgcaggttgtgagccgatgaa tgcctatgagcgccatgtgattcatgccgccttgcaggatatggataacatcaccacc cattccaccggtgtggagcctaaccgctgcgtcgtgattgaatacgtcagataa
3643	CLUST.192220_S.0OKRAA-M effector>	MTPAQRITKAKTGRSKREIQMADYVYRKIPTYSLKVRIYPNRAQKEIFSTYFLALEKA ANMTLYALHEHDEAICTEKEGVFWPDFYAMAKKDWLDRLREENDLVRELPGSALSSQL GGLFLSDLKKTWEKQGRLPIDAWFERVNKKGKRVLHYYKGAKKKNSYFTQIRANKFVL QDGRIYVTPSKKIGRIRIRGWNDTLGFGDDGNFSFFDYYAGFPEKALSCRISKNNVDE WYLSVTLSDVWRRFTDDPAKADIGIDLNLSGDHGVVSTANGSYENPYFKKHALAELAE LQRRTSRRYGPSNGEYRKDLSKARRENRRRMENGEKELTELPMPSNRYLKADLKAKRL ALRTARQREDHQHRIASAEVAKAKMIGIEDLDVKGMQKDSNYSESLSDAAFGAQKQKI LYKAAWKGVPVITIEPVPASTLVCPVCGCVTEDAKKEPSKTWTCPECQTTKDFYAVKA ETVLALALQEPNDKGSPGEGPDKKKQAKKKDEIHPKEIPKDRPFDKKHPDLLIHYDEN FVKDFKNPFVVTDRAGNILDDAQGYGYSTAQAARKAYRYKYG
3644	CLUST.192220_S.0OKRAA-M direct repeat 1>	aaaaaugaccccaaaauccucgcacaaaaauaaaaauaaccccaaaauccucgcacaa cagcaaaaaugaccccgaaauccucgcacaaaca
3645	CLUST.192220_S.0OKRAA-M direct repeat 2>	uguuugugcgaggauuucggggucauuuuugcuguugugcgaggauuuuggggguuauu uuuauuuuugugcgaggauuuuggggucauuuuu

3646	CLUST.192220_S.0OKRAA-Mspacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3647	CLUST.192220_S.0OKRAA-Mnon-coding>	gcctttaaccatatcggtccatattccaaccgcaatatcatatagcggttccgtaaaa taacgctccccttttatgtagatcataaaaatcgactaatttctggtcgatgtcatcaa tcagactctttaaaagcctttcagaatatttcataggataacctctttctcgattaat atttctgattccctattccattatagcaaaccaaatttgttgcgcgaaaccatgaggc atgaaaaaatggctccataatactcgcacaaacagcctatttttaaagattgacgcca aaatcgcttctctttaatttttttttaaacgtaatctacaatgatgccgtaagcaacca aacgtgttccggaggatgattgggatgatcactgtgacgtgctccataggacaaagcg tcctgagatcggccataaggctgcgcgataactacatcacgcgtaaaacgatccctaa catgccagcaggcgagggcgtcactattgtctataacaatgagactaaccgttacaag gtgggcaatccgattaaccgcaatgccatacttctgttactgctgctgcatctatcgc atcccgattcaaacggtattatccgctcttttgatctgatccactacgacgagaactt cgtcaaagacttcaaaaacccctttgttgtcacagaccgcgccggaaacatcctcgac gacgctcagggctacggctattcaacggcacaggccgcccgcaaggcctatcgataca aatacggttaagattaatttttggggatgaggctcaaccatccccggtgcgaaccgca agctcccagaagatccctgaggggttcgcaccgaaacgacaggaaacgaccattggat cggggctcacacgagccaggcgtaagctgtctgtcccaacacatagcgcggcaaagct catccagcacaagatgtcgcggtcgcaacccgcgtgtgggcgggatttgagagctgca tgtatgctggcgtcgtcgaatgccgcaagtcgcaacccgcgtgtgggcgggatttgag aaagttcgccggagtacgcacacagtacgcattggtgtcgcaacccgcgcgcaggcgg gaaacaggggtgatgctcaccagtactcatgaataaaaattatggggatgaggcttaa ccatccccggtgcgaaccgcaagctcccagagggtccccgggtggttcgcaccgaaat gacagggaacgcccattggatcggggctcgcacgagccgggcgtaagctgtctgtccc aacacatggcgaggcggagcacatcccgcacaagatgtcgcggtcgcaacccgcgcgc gtgtgggaattaagatgtaattgcttcgcgtgtgaccgaatctttgactgtcgcaacc cgcgcgtgtgggaattaagatgagatatctcgcatgctttaaattctgcgcgacgtcg caacccgcgtgcaggcgggaaacaggggtgatgctcaccagtactcattgaataacaa aaattatgggaatgagactcaaccattcccgctgccagccaaatccggagggtccccg gtggatgtcagctaaatgacagggaacgcccatcggatcggggccataaacggccggg cataagctgtctgtcccaacacagagcgcggcaaagctcctcccgcacaagatgtcgc ggtcgaaatccgcgtgtgggcgggatttgagatttgaatcatttctggccttgttgcg ataatatatacgtcgcaatccgcgtgtgggcgggaattgagatacagcctaaaaaata ctttttttacagtggctgacaagtcgcaatccgcgcgcaggcgggaattgagaaagtga cgccattaaaacttggtcgcccttgcccaggcgcaacctgcacacacttggataaagc cgaatgggtgcgcaaggtttaaagacatccaaagccgaagtaccgacagttcgcagcg cttatcgtgccctttttatcgcactataccgataagacagttacgaaataagacgaaa taaatttttttttaaaatttttggcccgaaaacgggctttttttttcttaaaaaaaccca atcttccctataataaaattagaagatatccgaagcacaccactccggttaaaaggca ttaagagaagggagcatcattatgaagcaattcgcaaaaagagccggcgcgatcctgt tggcagggattatggcaatcggcagcgcggccctgtcattggcggcaggcccgtcggc gcctgtcgagacagaagcggcaggcaaggttaggtatgatgagtatttcaaccttcct aatatttatgattggctgaaagaccatcaggagcgcggctactacacagggacatttt atttccccggaggagtcgaccatccctacaatacaaacgtcatggcggcacacgaccc ggcgtatgatggggcgaacaacggcttcaactgtaccggctttctgagccgcgtcttc tgggattccgagacgaatggggcggcctatccgggagacgcgaacttcaacgccttct ttgtctcccacggatggccggatcacggcactgcgaacagtacagccaatgccacgca gctcatgtccggcttctacggcaaggacgccgccggcaatattgtggtcccgcacgcc aacgagatcgaatattattatttcgactcgacgagccccatgatcgccgg
3648	CLUST.263724_S.3Q1QOB-Meffector>	MRKIKEHPGREMRGLRVKVYPSPEQELALLGMQRRLRRIWNWLVSQSQQTFNARDAFA AKNGAGPKPIRPENDAGEQPWKQYHDDMREWRSRVRAVLAEHKDDPGLKFRSIRDYCT QFLVEHDYQLYPHVIEDETPPPAHLQQALYKDYQSALAGTKRGQMPPRRRKRDEDMPL RVGSATCFRLLPTTKGRKLISTHPKGPQLSGILNAQVKLPEIGWIDAHISGAQPLEDD QFWVEGVSIRKEADGWYAAIRQHVLPKPVTKGTGSCGIDVGLVHVFAVVGDDGEKLLA DNTRRGSRRGHLRTPGGYVELIAERQAAGLPVSKLHCRSARHIREYIRRELFPFTDRY

		EFVAVEDLPSDVGFQHTPHLSFMRTVRSMLVQRYGSERVIDVDATGTSRICSMCGEIQ PRSWSELPNRIGKCGACGHEEHSDINAARNVLRRLLESQAAE
3649	CLUST.263724_S.3Q1QOB-M direct repeat 1>	cuaccaacgacuaccaggcccggcugucuccgggac
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3738	CLUST.347685_MKRX01000006 direct repeat homology 2>	agcacucuuag
3739	CLUST.347685_MKRX01000006 direct repeat homology - containing sequence>	cgtgccgcgctgagaaggattgtgatatagtttctaagttccatctcgatgcggaacg gatactacgctgtagtctatacgacacgagtgatagccctgcggggttcgcccctaag tccgtatgacaagcctctttcaggcggtggacttctaagagtgctggtgggtggaatc cctaagccacccacctccttcacaatctggcagaatcacgagttccattaagaaaagg tgacgttaacctaatttgtgcgttacgaaattgttgatggttatggtagccaggtcct caagcatagcgagcgtctcgt
3740	CLUST.347685_QEUN01000014 effector>	MSPLERSLRKVGENRLERLRVREEKIRKHIEQHPRGKNDHQALHFLLHQIEVERNDLY RNLKDPEYVPKPAKQRRERRQINVAKPPTRPKKEKGPQPESTKYVIRPPVPGKNLPAF ASKYEARDTRDDSYQDGRSWTSAPYVEVELPILGADKVIQKLMKFVQKDERSIVRDWA TKTYSSIEAAREALLVGAQVSEDVSVWRGLLAETKNAQNFAALSDDQIEAAMSKEAKG ADLRPRRAALLVAQRHWVDQTVKAIKESAPSGVDKDTLDRRLRAGLRGFHTAANSGKH TNPQFPYLTAEKPVVPMESVVQSVLAFLDDPDDQRYTKDKEDDKKRHRVTVLQKELGK ARPRKRLELQTPKWAGRPTVKGTISKRRDAALVWDTSKEANGLCLALPIGGMPKIDVE QFIYQDGTSLLSDCQIASKTTKKGAACAVLPLKPKHDFLRWFTKHVENHNPDAPLERR CLHNTTQFVIVDPEGPRPRLFVRPVFKFYDPGKTVPNTHETWKKPDCRYLVGIDRGIN YVLRAVVVDTEEKKVIADIGLPGRKHEWRMIRDEIAYHQQMRDLARNTGKHASVVAKH VRALALARKKDRALGKFATVEAVAELVKKCEQDYGSGNYCFVLEDLDMGAMNLKRNNR VKHMAVMEEALVNQMRKQGYAYDGRRGRVDGVRHEGAWYTSQVSPFGWWAKRDEVEEA WKRDKTRPIGRKVGNWYEMPEPGQDGDRPDTYRKGYWSKPKNAEGKPYGRNRFSVEPG DEKPDAERRFCWGSELFWDPNVKSFKGKEFPEGVVLDADFVGALNIALRPLVNDGQGK GFKAEDMAREHTILNPQFKIACQIPVYEFVEEDGDKWAALRRIML
3741	CLUST.347685_QEUN01000014 direct repeat 1>	gucgcaggggaucaagaacgcucuuagggaaugaaag

3742	CLUST.347685_QEUN01000014 direct repeat 2>	cuuucauucccuaagagcguucuugaucccccugcgac
3743	CLUST.347685_QEUN01000014 spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3744	CLUST.347685_QEUN01000014 non-coding>	gacgaaatcgtggtttattgcctgatgggctcgcgcagcgccgacgcatgcaggttcc tccgcgcggcgggttttcagaaggtgcgcaacctccgcggcggcatccgctcgtggat cgatgaggtcgagccggggatggtgaagtattgagtcccgcgttcagtgcgggttgca actcccaattggttgggggtaacaagcaaggatgggtaagaatcgatcctcgtcctcg gatttgagcccgctcgaacggtccttgcggaaggtcggtgagaatcgccttgagcggc tgcgggtgcgagaggagaagattaggaagcacatagaacagcacccccgcggtaagaa cgatcatcaggctctccacttcttattgcaccaaatcggccagggtaaaggcttcaag gccgaggacatggcgagggagcacacgatactaaacccgcagttcaagatcgcctgcc agataccagtttacgagttcgtcgaagaggacggcgacaagtgggcagctctgcgccg gatcatgctatagttaggcgttccgtctcgactatgccgtaccactagaccgagccta cacggcacgcggtcatagcgttaaccaaggcgtggtgacaagcctctttcaggcgtcg gacacttaagagcgttaggcgggcggtccctaagccgcccgcccccttatttgcacgt tttccccgaaccccgtaactctgccagccacaaacacccagaagcgcgtctacactcc ctacgggggtagacagacatgcgctatgagatcgtagacggttacgggtgccaagtgc tcaagcacagcgagcgcctcgttcttcgatacccccctcgcccctccgggggagagggg gccaggggtgaggggaagcaacccaagcgcgaggtgcccgtcttgcaccttattcag gcgatcggcgagaggtggggagcgcgcgtcctgcatcaagcccggaaactgcaattgc gatctgtcctccagcttcaggcacgcgacgccgcaaggcacttccagggcaaggcgga gtacatcgcgttccgcctgaggtggtaggccatgaagtggctcgtgtgctacgacatc gagaaggatagtgtccgaaacaaggtggcagacttctgcctggacaaggggcttgagc gggttcaatacagcgtcttccttgggtcgatgacaagaacgctcgccaaagaacttgg cgcacaggaactcgtccctagagttaggcgcgcagtcaaatgcaccctagacgaggct cgcgaaggcctctccgccccggaactcccctggccaacgctccaccgcggaaagtgcc aagactgcgagttccgacggttttgcaatgacgtctggtagatggggttcgaaaccct cgcaaccgctcggatttcggggcgatgtgcgaatcctaacgcccccgacactcaagat gatggaggccttcgacccacaatcaagcccgactcagacagcgaagagccaatggtgt gcgcaaattcgctctcaccgggtacattcattcgcacaacggcggactttgtaagcta aatagcgggtttcgaaacgacgcggccgaacctgttagggcagggttgcagcaaatgg acggcgtgcttgagtccggccatgcatgattgaggtaaacagagttgtggcggacttc atttgcgtcaggaggcgacgatgaggcgagagagaacggttctgtacttgttggcggg cggatttcttctgaccgcgatcgaggtgcgatatctgcaccgggaggtcttaggggag cactggcaaacttgggttcctgtggcttatggggcgctaggcacggccgtagcc
3745	CLUST.347685_QEUN01000014 direct repeat homology 1>	uaagagcguu
3746	CLUST.347685_QEUN01000014 direct repeat	aacgcucuua

	homology 2>	
3747	CLUST.347685_QEUN01000014 direct repeat homology-containing sequence>	acggcgacaagtgggcagctctgcgccggatcatgctatagttaggcgttccgtctcg actatgccgtaccactagaccgagcctacacggcacgcggtcatagcgttaaccaagg cgtggtgacaagcctctttcaggcgtcggacacttaagagcgttaggcgggcggtccc taagccgcccgccccttatttgcacgttttccccgaaccccgtaactctgccagcca caaacacccagaagcgcgtctacactccctacgggggtagacagacatgcgctatgag atcgtagacggttacgggtg
3748	CLUST.360654_S.3F1DBS-M effector>	MTVKAFKIHCKSLTVKKREILFNMCNNYAEIYNYLSQFLRSVDYKKYMSNAERNYLYN KYITNQDKIGGIIDKKLPSNYIVICKDQLLSNFKSNGGKFAPIIEKPNIIIFDDASII KNKDTFYCIIPKAKKYNIPQIVLPLNTGNWEECNEFLDNLISKKCPQVIYNYRDNTIS ISSKKENEKRKKKAEVETIIGVDRGINNIIVLSALNRKKEVIAVKTFSGKEYNDILRR VRIQQNILKSKNIEINNKVANITETTLRQIAYTASEWIKQFPNPIIVFENLKMQKSKV RRKHGGKSGKNLRKLINRWTYNKIKMMILQKVGQRGIYDISINPRYTSQFCNRCGTKG IRDGIHFGCSKCGLGFGSNPKSVIGQYNADVNGSINIAKKGYFSLYEKDKGKVVVPKR HPNERDGQPTAYWILEGMTNSQSNENQVNTCEKVDIHLHDNSTMPEPNVMVNVVSCTP ENNHFSSPYKEENKKSIRIESEQKIDIGEVLLQSKF
3749	CLUST.360654_S.3F1DBS-M direct repeat 1>	guugcagagcaaguucugauagauguuggacuacaac
3750	CLUST.360654_S.3F1DBS-M direct repeat 2>	guuguaguccaacaucuaucagaacuugcucugcaac
3751	CLUST.360654_S.3F1DBS-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3752	CLUST.360654_S.3F1DBS-M non-coding>	atatgcccgctcaccaccagtcatggtacatcacccattataatttctttttttaaca tattacctacttacttataaattataaactatcaatagtataaatttcatttataatg taaataatatttaataggtaaaagtatatatatgagtaaaacaatgtagtattaatga cagtaaaggcgtttaaaattcattgtaaatcattaaccgttaaaaaaagagaaattct ttttaatatgtgtaataattatgctgaaatttataattatttatcccaatttttacgt tcagtcgattataaaaaatatatgagtaatctaaaattatacttatctatatagtagt tctatattttaatagactaacttccaggatgtactgaaaatagtttatataactcgca actttgcgctcactcgtcattttaaaaatatcataaccagccaatgactttctaaaac ttttttataattcgttttatttcatcacgatcttctaacattcgagttc
3753	CLUST.360654_S.7ANXNT-M effector>	MTINSFKVFCLPLSKSKQETLQNMINEYSQIYNYASRLIPSMKGSKHLKFSNPSTLYT KWIKSKKIERKYIGSLEAFNAIKDAVANFKTHGNLSEMKEPNIIKFEKSRYEIIKLNN HYGIKIGGKNGIYLPLVTGDYEKLNEFLDVIIKTDSNPGNVLYNLKENSISISHDINE NNTIPKYKKDIEIDTIIGVDLGSNNLAALSVLKFKKEDVEQKIIDFKMNGKKFISRND IPIEIAKVELISGLGNRHRLKYLKKVNKWKQKHRKDVGNRIRNIQQSNEHLISAKIAE IAKEYPNSLVVLEANLTNVRTRYSLFNPGGTKQKIEYKLNNIGIRTKEIHPAYTSQRC NKCGAIGIRQKGTVYFQCPSCGLGGSTPSSTIGQYNADVNASINIGLKGLFSLYGKKE RNVDRVLNIDPNEHTQEDEPKPISEVCNGKKLCKDAILDCQNRKEVDNKENDKQTFFE FRRNCVPEKIQNLPDINEKIISQEDRKSEEKPLSDYWCR

3754	CLUST.360654_S.7 ANXNT-M direct repeat 1>	gucgaugagcaaguucugauagauguugc
3755	CLUST.360654_S.7 ANXNT-M direct repeat 2>	gcaacaucuaucagaacuugcucaucgac
3756	CLUST.360654_S.7 ANXNT-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3757	CLUST.360654_S.7 ANXNT-M non-coding>	agataattgtcaaatacaatgatacatattccaatgtatcggtggtccccccgaccac ccaagattgtatttgataccctaaataagtcaactttccaaagaaaaatcggacatgg gtcgcgaacctaattcggaggaaagtgttattgtagattgtcaagtccggtttgtctg cagcaattgacaatcattatattaatttttttatgatttttagaatatccgataagt atatataggttaaagactaataaggatatattatgacaataaattcgtttaaagtttt ttgtttgcctcttagtaaatctaaacaagaaacactacaaaatatgataaacgaatat agtcaaatctataattatgcttcaagattaattccttcaatgaaaggaagtaaacatc ttaaattt
3758	CLUST.360654_S.416239-M effector>	MIINSFKVFCLPLSKSKQETLQNMINEYSQIYNYASRLIPSMKGSKHLKFSNPSTLYT KWIKSKKIERKYIGSLEAFNAIKDAVANFKTHGNLSEMKEPNIIKFEKSRYEIIKLNN HYGIKIGGKNGIYLPLVTGDYEKLNEFLDVIIKTDSNPGNVLYNLKENSISISHDINE NNTIPKYKKDIEIDTIIGVDLGSNNLAALSVLKFKKEDVEQKIIDFKMNGKKFISRND IPIEIAKVELISGLGNRHRLKYLKKVNKWKQKHRKYVGNRIRNIQQSNEHLISAKIAE IAKEYPNSLVVLEANLTNVRTRYSLFNPGGTKQKIEYKLNNIGIRTKEIHPAYTSQRC NKCGAIGIRQKGTVYFQCPSCGLGGSTPSSTIGQYNADVNASINIGLKGLFSLYGKKE RNVDRVLNIDPNEHTQEGEPKPISEVCNGKKLCKDAILDCQNRKEVDNKENDKQTFFE FRRNCVPEKIQNLPDINEKIISQEDRKSEEKPLSDYWCR
3759	CLUST.360654_S.416239-M direct repeat 1>	gucgaugagcaaguucugauagauguugcacaucaac
3760	CLUST.360654_S.416239-M direct repeat 2>	guugaugugcaacaucuaucagaacuugcucaucgac
3761	CLUST.360654_S.416239-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3762	CLUST.360654_S.416239-M non-coding>	ctgatatttttctactaacaattcagttattataccatctatttctttaaacaatttt tgtgttcttagaaattcataaacattcaatgggatactgatatgcaatttccttgtgg aatatgtagcatttatttcaaaatcgacagtcatattaatctattaaatataaatttc atttataaagtcaactaaattaaatatccgataagtatatatagatgtaatgatatat agataattgttaagtgtaatgatgaacattccatatacttaacaaataaataccttc caaagaaaaatcggacatgggtcgcgaacctaattcggaggaaagtgttattgtagat tgtcaagtccggtttgtctgcagcaattgacaatcattatattaatttttttatgatt

		ttttagaatatccgataagtatatataggttaaagactaataaggatatattatgata ataaattcgtttaaagttttttgtttgcctcttagtaaatctaaacaagaaacactac aaaatatgataaacgaatatagtcaaatctataattatgcttcaagattaattccttc aatgaaaggaagtaaacatcttaaattta
3763	CLUST.360654_S.2R4B9S-M effector>	MATTSFKVQCAELTQKKEMWLVQRINEYAKIYNIASQYIPSLPEKYLKSENPSELYTK WIKGNDSSQMLQSPILTGLQMLNALKDACSNYKTRRALKQKKSSISFIKIPNIIKFEN SEYQILKINDRTYAIHVGGKEGITIPLITNAPEKEAIRKVKGIEWGLIDHLNLGIKMQ VAKKERNKELALKKRKTPTANKEKGVKAGLGAIVYNLRDNTVSIPHTFETPRFKKKNT RCTFIGVDRGVRNSVVLSAIFVDTAKLNGIQEYQELFNEPSISKHMFRSLRGLNVNVV GVKIIKSSTTNDKKRQIRNIGDKRREKRKYVGNRYRNVSETVSHQISAEAVKFISQFR NPVVFFEDLNMDKKKRRHKFGKKNAKGSRRMLSRWDYGAIRRKIEYKLEAYGIWTMGI NPMFTSQTCNNCGAIGIRDGIGFKCERCGLGIGSNPVGTIGQYNADVNASTNIALKGL FALYGQKVGVVADPYEQPDRSVMKPIPTAMSDMDGKDTQEIEKLPDETNVSRSNLRQE GVSLVLPFAEKHCQNAQPMVEIHQVGCAPENGFSSSYKGKDNYAGRTELEEKTNIGEV VSQTEF
3764	CLUST.360654_S.2R4B9S-M direct repeat 1>	ugucgcagacugaguucugaugaauguaggacugcaac
3765	CLUST.360654_S.2R4B9S-M direct repeat 2>	guugcaguccuacauucaucagaacucagucugcgaca
3766	CLUST.360654_S.2R4B9S-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3767	CLUST.360654_S.2R4B9S-M non-coding>	cttctctatgtatagtcttccattatcttcataaaatgcaattaagtcgccttttttt gtgtttaataattccacagctcgctctatgagcgtcattttattatctgtacttaatt ttgaaatgcctaacaatttatgcttttctgacatcgatatactatatgtacgatatac ttatatagtttgccgtctttaaagtatgtatagtacataaggtatgtaaatggcaaca acttcatttaaagtgcaatgcgctgaattaacacaaaaaaaggaaatgtggttagttc agcgcatcaatgaatatgctaaaatttataatatagcatcccaatatattccatcact tcctgaaaaatacctgaaatcagaggggagagccagcaagtagcaataatactaaaga gatgaacttaagaaatgaaacgtgatggtgatatcacacgcagggtttttctcctttc ttcctctacccttacattaaattcgggctcatcgattatcctggataactcgcccaaa acgtggtttttgttgtaaaataaagaatgaacgagcagtcgatgctgcatcagc
3768	CLUST.360654_S.3MEYEW-M effector>	MTTKAFKVQMLPLTKIKVDKLNNMAEAYGRVYNFAANFMPSLPEKYLDKNASLLYTKW IKSKVIDYTGIQAGDAHLAVIDAAANWKATHYRTQMKEPHIIKLASTRYKIVKETSGH FGLIIKSEKIYLPLITGNHDRDLKRPEKRRWGLVEHLETAIAIQNGDAKILDKRGRVK KGVGAITLNLRDNSISIPITIESQKFKKKTELTTFIGIDRNVRPQNFVSVAAIQIIKP LTRQNVIDLDKALDSGARISRNLLTAIGVEYKISVELFGGLKTASQMKHLKKIRKERQ KSGKIVGHRLENIQESTADQVSRKIVNFSKQFQNPIIFFEDLQNFTGAKKKTGKSGGK SLRKMLNSWNYGELKSKTEYKLKESGMYVMEVNPQYTSQRCSKCGAIGIRSQKDNTFM CSACGYGVGSSPTGVIGQMHADINASINIALKGFWVLYGSKKGKVYNPNVEPSENITN PIPTEMTGVDGIKTRKSEPIEQKTKSKESRSIVRGSRQSIVAMTNAVDSVPEKLQVGS HRFSSLYKGSNKKPVRTKSKQKIDSGEVP
3769	CLUST.360654_S.3MEYEW-M direct	guaacagagcaaguucugauagaugucgaauguaaac

	repeat 1>	
3770	CLUST.360654_S.3 MEYEW-M direct repeat 2>	guuuacauucgacaucuaucagaacuugcucuguuac
3771	CLUST.360654_S.3 MEYEW-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3772	CLUST.360654_S.3 MEYEW-M non-coding>	gagtgttggaactggaaagatgtctgaatgtcctatttttatctgtaaaaataatata aacgatttaacttttaacgtggttccattaggaaccatggaagcgcgcaaagtcatgt tgaatgcggataatatcggcaaattacttactgtaaaattcatcggtcgcactgaaga tggtatccctaaattcgcagtcggaaaggttatcagattggcaaaagatttggataga aaagtataaatagtaataagacatataggatattatgacaactaaagcgttcaaagtg caaatgcttccacttacaaaaataaaagtggataaacttaataatatggcagaagcct atggacgcgtttataattttgcagctaattttatgccatcacttccagaaaaatattt agataaaaactggtaatagaaaactataaatactaataaaataatatgagtgatatag tcccgtagtgtagtcaggtcaatcattctggactttgaagtatttgtggaaaaacgct agctaatgccgcaaatcgaagtaatccggagacgttttgggttcgaatcccaccggga ctattaactcgatatggtgtaatagaag
3773	CLUST.360654_S.3 8YTA7-M effector >	MTINSFKVFCLPLSKSKQETLQNMINEYSQIYNYASRLIPSMKGSKHLKFSNPSTLYT KWIKSKKIERKYIGSLEAFNAIKDAVANFKTHGNLSEMKEPNIIKFEKSRYEIIKLNN HYGIKIGGKNGIYLPLVTGDYEKLNEFLDVIIKTDSNPGNVLYNLKENSISISHDINE NNTIPKYKKDIEIDTIIGVDLGSNNLAALSVLKFKKEDVEQKIIDFKMNGKKFISRND IPTEIAKVELISGLGNRHRLKYFKKMNKWKQKHRKYVGNRIRNIQQSNEHLISAKIAE IAKEYPNSLVVLEANLTNVRTRYSLFNPGGTKQKIEYKLNNIGIRTKEIYPAYTSQRC NKCGAIGIRQKGTVYFQCPSCGLGGSTPSSTIGQYNADVNASINIGLKGLFSLYGKKE RNVDRVLNIDPNEHTQEGEPKPISEVCNGKKLCKDAILDCQNRKEVDNKENDKQTFFE FRRNCVPKNSKSS
3774	CLUST.360654_S.3 8YTA7-M direct repeat 1>	gucgaugagcaaguucugauagauguugcgcaucaac
3775	CLUST.360654_S.3 8YTA7-M direct repeat 2>	guugaugcgcaacaucuaucagaacuugcucaucgac
3776	CLUST.360654_S.3 8YTA7-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3777	CLUST.360654_S.3 8YTA7-M non-coding>	atgaaccaaaaacttactgcagcaaaacgcggtgagaaaaccgggatgaattttccgt atattgaaaaagtaatagatatgcgaaaaattatgaagaaagtttatctaaattaatt ttttttgtttttcttaaccgataagtatttatagtttaaagattaataaggatatatt atgacaataaattcgtttaaagttttttgtttgcctcttagtaaatctaaacaagaaa cactacaaaatatgataaacgaatatagtcaaatctataattatgcttcaagattaat tccttcaatgaaaggaagtaaacatcttaaatttattagtgaggtatgtaatggaaaa aaattgtgtaaagacgcaatacttgattgtcaaaaccggaaggaagtagacaacaagg aaaacgataagcaaacgttttttgaatcccgtaggaactgcgttccaaaaaattcaaa

		atcttcctgatataaatgaaaaaataatttcgcaggaagatagaaaatcagaagaaaa accgctatcggattactggttgatacttccgccg
3778	CLUST.432266_S.0 DQOKW-M effector>	MKDNVLKNDRNDEEIDFIKKTKWNRKTYPLKLNLTDIQLVRLENLIYQYKKGINRIIE ILLKEYFPNYLLRLSEDNIEEGVCPSCQTKKKLRFELSDFEFVRYSELKGKPLYKPIL KKGNKVKICEMCSCSHYSLRKFLLPSSKREVPIKEWDFTKDINLGSGSSIYDSCLQKA VETIKSQQEIKKKIDYKINFYRKRILENTIKLNNTHKKDFLNFIESKNLNEKDGLSLL KKFIKRDEISIEKEKKKKAENIVYKNDSIRLYENSYEFIEEEEDFFIKFKDYSRDKCM TLSFYGKDYQKKLAEKFIKSKKAETEIVRKGDDFYLQYIYRKELNVPTPNKSFNAVGI DVNIINLSSYVAINSRGDILKIKFYSGRNMRFKRRRFKEVRKIWQSKTKYVSKGGKGR AWKWYLKKQKSQNERNYVKYIIHNLTTDIVQNIKENFDKPVIVLEELKNIRDRIGKEL KITKSSIDKLKKNQQKAIRGDKLLNSELNNWNFDEFQKFLEYKANWLGIPIVKVPAKN TSICCNKCGECDKSNYEDYHKVKFKCKKCGYECNADFNASLNIARSFYKNLETN
3779	CLUST.432266_S.0 DQOKW-M direct repeat 1>	guuacauuguaaauuauuaugaaacu
3780	CLUST.432266_S.0 DQOKW-M direct repeat 2>	aguuucauaauaauuuacaauguaac
3781	CLUST.432266_S.0 DQOKW-M spacer>	nnnnnnnnnnnnnnnnnnnnnnn
3782	CLUST.432266_S.0 DQOKW-M non-coding>	ttctagtgggttttctgtatctttaaactcaaagaaatctgcataaacacttttaaca taaccatttctccaagtattattattaagggtaatatgtaatttaatttttttagaat aagattcttttattaattcttgattaataaccatgttcgtttgttcgttgttcatagt gtatattaaaagactactctttatatatctttatttttcattttgtagttacaatttcc aattaaaagtatttttgattttaaataacctataaattgttttatttttttatctat gttatcgtcggatattcttttatttattaatttgataatatttatttttgctttttca tttaataaaccatctttatttaacgtctgctttacattgaagctaccttcatatactt aatcaaaattaagctgattatctccgacgggagaaaagataatcgggctttgtaacac agccctatattttaacatatagctaaaatataatattcataataaacactactatata aatgtttcgtttttaaaggatataatgtattaaaacaaaaccaaaaggtttatatata tcaatacattataattcttatgaaagataatgtattaaaaaatgatagaaatgatgaa gaaatagattttataaaaaaaacaaaatggaatagaaaaacctatcctttaaaattaa atcttacagatattcaattagtaagattagaaaatctaatctatcaatataaaaataa atgtggagagtgtgataaatctaattatgaagattatcataaggtaaaatttaagtgt aaaaagtgtggttatgagtgtaatgctgattttaatgcaagtttaaacatagcaagga gtttttataagaatttagaaacaaattaataatttttatcgtcgataaaaaaccttaa actccatataaagccctacaatcaaagatttttatttgttaagggtttactattcaa atcttttgttttatttcaggcaattctaataatatctcataccacaccttacatctgg aacaataacccctatcaccataaacattttcaaataaaactatatcttcatgtaaggg acaattcat
3783	CLUST.432266_S.0 DQOKW-M direct repeat homology 1>	uucauaauaa

3784	CLUST.432266_S.0 DQOKW-M direct repeat homology 2>	uuauuaugaa
3785	CLUST.432266_S.0 DQOKW-M direct repeat homology - containing sequence >	cgtctgctttacattgaagctaccttcatatacttaatcaaaattaagctgattatct ccgacgggagaaaagataatcgggctttgtaacacagccctatattttaacatatagc taaaatataatattcataataaacactactatataaatgtttcgtttttaaaggatat aatgtattaaaacaaaaccaaaaggtttatatatatcaatacattataattcttatga aagataatgtattaaaaaatgatagaaatgatgaagaaatagattttataaaaaaa
3786	CLUST.432266_S.003CRT-M effector >	MEHNVVKTEDFLIKTNWQRKTYPLKLNLTDTQTARVENLIYQYKKATNKIIQIITKEY FQNHLRRLAEENIKEGQCPLCQKKKKLKFELIGFDFVKYATTKGKPNYKPVIKNCNKL NICEMCHCSHYSLRKFLLPSSKRDIPIKQWDFTKDINLGKSSVIYDSCLQKAVECIKS QVEIKKKIDWKIKFYRERIIDNTVKLNQEDDKENKFKDKELIKKLKNYIRYDTKNIDK EKKKVSDGIIYKNDAIRLYDNSYKLIQEDGDFFIKFKDYSKDKWLTFSFYGKKYQKVL AEKFIKSKNAETEIIRKGDDFFLQYIYRKESDVPIPNKNFTAIGIDVNIINLASYTCI KENSINFNTKFYSGRRMRKKRKRFNDMRAIWNKKRKYSESGGKGRSKKWFLRKVESQN EKNYVKYIIHNITTEIVQDIKENVLKPVIILENLKDIRDRIGNELKISKCSIEKLNKD QQKKIRADKLLNSELNNWNFDDFQKFIEYKANWLGIPVVYVKAKDTSIKCNKCGNIDP HNYTDYHKVKFKCSKCNYKCNSDFNASVNIARRFYEDLNNTK
3787	CLUST.432266_S.003CRT-M direct repeat 1>	guuacacaaacauaaauuaugauac
3788	CLUST.432266_S.003CRT-M direct repeat 2>	guaucauaauuuauguuuguguaac
3789	CLUST.432266_S.003CRT-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnn
3790	CLUST.432266_S.003CRT-M non-coding>	ttcttcaccctcaattgttggcttaataatgccaaaacatttctttaataattctccg caatcttgacatttatagattggtgttgacctataagactttccacgttcatacaatc tcctcttgtttttgtgttcacatttttctaccatgtaacataatgtatacattcttat ttataaatgtttgtttaaactaaaaaatagttatatagttatgaacaccaactaaaat tattctttgatttaagaaagcccttaaattctttaattttaatatctatatttttatt ttctattctgctgcttattaattctataatctttaatcttgcagtttcttttaatttt ccatctttttttataattgatgattgacttgttaacactatgtcattcaaatctttg gaatcaaatattcactcattttcttttgattgatataatcaaatcctgatacatggat tcttaaattactcttctctattttgcacggatattctattattttcattttattaaat attatttttgaatgttaccgtcttttgtttttgaagctacctccattgggttaaatat aaaatctaactgataatcctcgacgggcgataaagattatcgggcattgtaacattac ccaacataataacatatagctaatatgtaaaataatgaacacgacttactatttaaat

		gtttgtaattttatgaccataatgtatatttatgttgcccataagtatataaatagta atactttataattctcatggaacataatgtagtaaaaactgaggatttttgataaag actaattggcaaagaaaaacttatcctcttaaactaaaccttacagatactcaaactg caagagttgaaaatcttatatatcaatataaaaaagctacgaataaaataaagtgtgg gaatatagatcctcataactatactgattatcacaaggttaaatttaaatgttccaaa tgtaactataaatgtaattcagattttaatgctagtgtaaatatagcaagaagattct atgaagatcttaataatactaaatagttatgtaattatatataactaatgaaccaaga aggatttgaacctccgatctatgccatgtaaggacattgctttaccagactaagctat tggttctttttaaaaagcaaatcccctaaaaaaaataagtggggacgaatttaaatta ttaaataaattttgcagtttcttccattaaagttatgccaacaatattttctacacct tgtccaacaaagtccattgtgtttttatctttcttcttagctaactttatgttttctc ctgctagtgcaacagattgtgccaatggaactaa
3791	CLUST.432266_S.003CRT-M direct repeat homology 1>	auuuauguu
3792	CLUST.432266_S.003CRT-M direct repeat homology 2>	aacauaaau
3793	CLUST.432266_S.003CRT-M direct repeat homology - containing sequence >	taaatataaaatctaactgataatcctcgacgggcgataaagattatcgggcattgta acattacccaacataataacatatagctaatatgtaaaataatgaacacgacttacta tttaaatgtttgtaattttatgaccataatgtatatttatgttgcccataagtatata aatagtaatactttataattctcatggaacataatgtagtaaaaactgaggatttttt gataaagactaattggcaaagaaaaacttatcctcttaaactaaaccttacagatact caaactgcaagagttgaaa
3794	CLUST.432266_S.1SQ6OZ-M effector >	MEDKVLKNEDLLKKTEWQRKTYPLKLNLTDVQQVRLDQLFYEYKKATNFIIDIIRNKF HINHIAQLTKDEEEKGICPMCNQERKLVYNLFDFDFVKYGESKGKPHFKPVYKKGNVL KICQGCPTSHYSLRKFLYSTSKRDVPVKDWDFTKGIRLERGVWDSCVQKAIETIKSAY EIKKKIEYKIKWHREKIMENNIELNKELKKPNQDKELIKKLRNFIKGSERIIEKEKKK LAEEVYFNGTAVRLYDSAYSLIKEQDDFYIKLKDFTTNKFLTVEFYGADYQKKLADKF IKSKKAETEIIKRGDNYYLQYIYRQEAEVPIPNESFTAIGIDVNIINLASYLSITKDT LDKPKDINFFSGREMRHKRKRMSKVRQKWAEKTKYKEKGGKGRSRRWFREKCKSQREM LYVKYNIHNITTKIVQDIKDKYDKPVIVLENLKDIRDRIGKEIKITKCSMEKLTLKQS KSIRGEKLLNKDLNNWNFDDFQKMIEYKAKWLGIPVVFVSAKNTSITCNKCGHISQDN YEDYHKVHFKCKKCGYQCNADFNASVNIARQFYKDIEEEKK
3795	CLUST.432266_S.1SQ6OZ-M direct repeat 1>	guuacauaaguaaauaauaugaauc
3796	CLUST.432266_S.1SQ6OZ-M	gauucauauuauuuacuuauguaac

	direct repeat 2>	
3797	CLUST.432266_S.1SQ6OZ-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnn
3798	CLUST.432266_S.1SQ6OZ-M non-coding>	taagttacataagtaaataatatgaatccaatttatcaagtagggtagcaatagttacataagtaaataatatgaatctttgtgaatgtctatgaagagaatggttacataagtaaataatatgaatcccgtcttttacttttgtggctatccacatccagagattataaatccccttattattccacgacgggggtgaaacaattgggcgttgtaacacagccctgtaaataaacatatagctaatttacaatttttattaaaactttaatctttataaacctttctttttgtatttccttttatgtatctttattaacctaaaagtatataaatactaatacattccatattttatggaagataaagtattaaaaaatgaggatttgcttaaaaaaacagaatggcaaagaaaaacctatcctcttaaattaaacctcacagatgttcaacaggtaagattagaccagttatttttatgagtataaaaaggcaactaattttatttgtgggcatatctctcaggacaattatgaggattatcataaggttcattttaagtgtaaaaaatgtggttatcaatgtaatgctgattttaatgcttcagttaacattgctagacaattctataaagatatagaggaagagaaaaaataatctaaatcttcacctttttattctttcattcttttaatttcttctgccaataaataaactgtttgagttaatccattaacctccccctgcattgctcttaatacaatagcttgttgttgaataaccattcttaggctcattgtattttctgataagtccttatcttg
3799	CLUST.432266_S.0XJP3Q-M effector>	MKEEVIKNQEKEEKDLLKKTDWQRKTYPLKLKLTDIQQSRIEGIIFEYKKAINQIIQTITKDYFKNYLIQISEEDIKKGLCASCHKERKLEYELSDFEFIKYAGTKDKPNYKPIFKKNNKVLICNNCHNSHYSLRKFLYATSKRDVPIPQWDFTKKVNLNRGLWDACVQKAVETIKSQVEINKKINRNLKFYRERIMDNTVKLNKEKSKIKKDIEEIKKLSNYIKHDERTIQKEKNKISGEIEYKANSIRLYETSYKLIKDDNDYFIKLKDYSKNNWMTIQFFGEDYQKKLADKFIKSKNAETEIVRKGDDFYLQYIYRQKTEIPIPDDSFTTIGIDVNILNLASLVSMNKDFKPIDIKFYSGRNLRSKRKRFRKVRAIWKSKTKQKEKGGKGRAYKWYINKQKAQNERDYVKYQIHNLTTNIIQFIKDKYDKPVIILENLKDIRNRITKEIKIANRNLIKFLPKDLRKQADELYKKKKYKEFNDILSQVSSKQKKYYQKAVRELKSLNADLNNWNFDDFQNYLEYKANWFGIPIVKVPSKDTSIKCNKCDNVDEENYLDFHTVNFKCKSCGYQCNADFNASVNIARSFYEGLKNEK
3800	CLUST.432266_S.0XJP3Q-M direct repeat 1>	guuacauuagccuuauaauauaauc
3801	CLUST.432266_S.0XJP3Q-M direct repeat 2>	gauuauauuauaaggcuaauguaac
3802	CLUST.432266_S.0XJP3Q-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnn
3803	CLUST.432266_S.0XJP3Q-M non-coding>	ataatataatctttttcgtcaccttcatcatctcctacccgtcattcgactattggagctacctccattaaaacaaataaattgtcctgatatttatcgacggggaataaatatcgtggattgtaacatcccacaataatctaacatatagctaaattacattattattagaatttatactttaaatacttttctattttattggctctaaagtaatataaataatcgaaaagtatttaaatagtattactttatataatctatgaaagaagaagtaataaaaaatcaagaaaaagaagaaaaagatttattaaaaaaaacagattggcaaagaaaaacttatccttt

		taaagttgaaacttactgatattcaacaatcaagaatagaagggataattttcgaata taaaaaa
3804	CLUST.432266_S.0 MTL4O-M effector>	MEKEEKTKGEWSRKTYPLKTIIQDSDRQKISDFLDEYVKVTNFVLNKCMYDILPFYKE LTEEEHVEGKCPLCYNPKNQKEKKLKFKWKRPDGKIERNCGCLIGHYSLRKIFLPSSK RTLMQNGSLPGFDMRMAGELYDWEVELTPGGDNELKKHNLQLYDSCLQKAVETIKSHK AINEDIDKDIRYLRGRNEVIDAVISEDTSHIKNKKLLTMTQKYTARRLKTFKRKNSEK IEKLENRKAEKIEYKQKVARIYNTYYRWVERCENDHILSLKIFKDPIDVDFYGKEYQK KKTDIFSRVEKQPEIEIIEREGGQIWFQYVYKEQKKVKIPTESFASIGVNFGILNTLT YAVCDPETKESKGCMFFSGRPVRRRRRQMWKVRKIWQKKMRMKKNGGKGRTLRWFKSK VWQQKEKKYLKDYIHNTTTSCIYSLMKRDDRDIVIILPNFKKLRDSVNADKKKIYREL KGKGRTWYKKEKFLIHELNTSPFLQTYNFLAYKLNWIGVPVVEMPCAYKTRQCNKCGH VREEIEGKDLHELHFKCQNTECGYECNADFNNSINLSRDFYDYMSNSEYELVMCKDGI YRFRKVKKS
3805	CLUST.432266_S.0 MTL4O-M direct repeat 1>	gauucuuuaaguaauuaucaugaaac
3806	CLUST.432266_S.0 MTL4O-M direct repeat 2>	guuucaugauaauuacuuaaagaauc
3807	CLUST.432266_S.0 MTL4O-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnn
3808	CLUST.432266_S.0 MTL4O-M non-coding>	aaatctaaaatcaaggataaaaaatcaaaaaaaatttcaggctcacaaaagtgaggcg ggtttttcttcttacccgtagtaagccatttgggacttacctcccgtttaattacttt tggagcatgctcctcagaccaccaaacccaattatttagcagcgatttatgggaaaac gggttaagaaaccccacaatcgggggaagaatcatctcccctgtcaatccaacatata gtcagatttcctgttgatagattattgtatttcaagtatataaatcagaaaggtttta taaatacacccaatattctgatattcacataaaaaaactaaaccccccaaattcattta tatacttctgataccttataaaatatacaatggaaaaagaagaaaaaactaagggtga atggagtagaaaaacgtaccctctaaaaacgataatacaagactcagatagacagaaa atatctgatttttagatgaatatgttaaggttacaaattttgtacttaataagtgca tgtac
3809	CLUST.432266_S.0 MTL4O-M direct repeat homology 1>	uaauuacuu
3810	CLUST.432266_S.0 MTL4O-M direct repeat homology 2>	aaguaauua
3811	CLUST.432266_S.0 MTL4O-M	ccgtttaattacttttggagcatgctcctcagaccaccaaacccaattatttagcagc gatttatgggaaaacgggttaagaaaccccacaatcgggggaagaatcatctcccctg tcaatccaacatatagtcagatttcctgttgatagattattgtatttc

	direct repeat homology-containing sequence>	
3812	CLUST.484501_S.99UFQX-M effector>	MAKDKTTKLSRTVVTPVRLTRKKRAQVAALMAAQRWCYNELVNAMRLHSQPIFPIANG DAVRHCFIKGKGAERARRIFADTGEVIAGVPVAEYRKDAMLEPWPYLKALTDRQPAPF DAGCKYGISSKQVSALCRGMRGQIKGFWTHRKKGNYRAQLPMRFRSVRKPSGRKWDVL KAECRWVGTHLQLGSKTQIGGFVTVSVPPKMVGMEVLQASISFDDGGDAWIHLSYSLP KPDADEVKALTNVAAVDPGQLRAMVVADSKGRIRSVSGHDILAVKRQRERSQKAINRK RARVFRGQVRYYLSSEERETMTSMEAKSSGAGTKYAHQRIAAHRRREQLERHVAAGNS PETFRYRRRYSNRDWKLKHALGRHNAIARRKLRYANHCVTKRIANWCIAQDVGTLYFG DVFNIPKGRKKGETRKLQSKRNALWEVGRQRDLLQQKLEEHGATLSLQSERYTSQTCP KCGARRKPRGRLYVCRSCGWTGDRDGVGAANILSDALDSKSRILPGRLKPLSLSPVMS KKGALVSVSDAPSRFDGLCSSPESGDSQVRTLVRESGDILSSNLVNHPEIPATRDRRR KVQPKGSARVAESPTHLRSPQAERSHDPTSDTFGISANNQSAQKEAQSPI
3813	CLUST.484501_S.99UFQX-M direct repeat 1>	gcugaaauccaucggaauccuuccuagggauugaaag
3814	CLUST.484501_S.99UFQX-M direct repeat 2>	cuuucaaucccuaggaaggauuccgauggauuucagc
3815	CLUST.484501_S.99UFQX-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3816	CLUST.484501_S.99UFQX-M non-coding>	cctactgattccgagctagaaattcacttgaatgcagagcttctgttgcgcggcttgg cagccattgacgaaagcgatattgaccgatgccccaaccagcaatctctgcgcattgc ggctgaagggctagacaccgaagccaacaaataaagctagttaaggcagacccgacca ctctctcctggaacattgctattctgaaatcagtatcaattttcattagatatgaccg gctgagccacttatccagatggcgaaagataaaaccactaaactgtcgcgaactgtcg tcacgccagtgcgcttgacgagaaagaagcgggcacaggttgcggcgctaatggctgc tcaacgatggtgttacaacgagctggttaatgcaatgaggttgcattcacaggtgcag cctaaagggtccgcgcgagtcgcggaaagcccaacacatctgcgatcgccacaggctg agcgatcgcacgatcccacttccgacacctttggaatatcagctaataatcaatccgc gcaaaaggaggctcaatcaccgatatagcttgggctataggacaccacatgaa
3817	CLUST.484501_S.9RDN22-M effector>	MPTDTKYRTVKIPLRLTAVKQSQVKSLMACERWLYNEAIAAMNALSQPVYPIGDGGAV MACWLHGAQKIQDTYLKSKQQDKDKIKLSLQWATVAAKERDSYAKSGEVSPGHPVREY RKWESFDAWQYFKSLCEVLPNPKRGNAKSNYGVSAKTASAMCRMLRGQVSSFFTKRKK GDFRAKLPNRFRSADTPQGWLWTVPDKECRWLPNGQLQLGCKNQVGGFFVVNINREWQ NLAIQKAQVSLDQSRQFWLHLSYEVQPIEDNRLNRSAGIDLGQKRAIAITLNNGRSAQ ISGQDITKLKARRDRITRKIQRKRSRAFRGQIRHFLSADEQQTMRSLEAKSPGSGTKY AHRMVAQRRREDGLRRRSRRDYRLLLAQRKLATKTRRSLVYANHCITRKATDWLIHHS VGSVFVGDVGTVPKRRRKGATRIKQVRNNVLWESGTQIKYLTEKLEMHGATLQTVPEH YTSQTCPNCGTRHKPRNRRYHCRNCGWTGDRDAVGSANILAKSLSSDWPATGQIKPLS MIALAVSPAIAKQPGRKLRRFGHRCQLNGRPSREVACLDGCDSLPRTSVREPVDVSAG

		RQVIQPRNPCLARNPAGKGAKEVRAIAETLTLFELPGAQVTHNDLRSSPKPKTKRRSA QAMPQSFAQLDLWSAAPETG
3818	CLUST.484501_S.9 RDN22-M direct repeat 1>	ccugaaacggguugaccgguugggcgaucguugcaag
3819	CLUST.484501_S.9 RDN22-M direct repeat 2>	cuugcaacgaucgcccaaccggucaacccguuucagg
3820	CLUST.484501_S.9 RDN22-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3821	CLUST.484501_S.9 RDN22-M non-coding>	aaacaccgcatcaacaatccgcccgatcgcgcctactgcactatctgcggcgaggtgt tgcgccgtggtgggctatccgaaaagtttgggttccatcagaagtgcgatcgtgcctg gttccaggcgttgtaccgggaattgaagaagtaggcgatcgctaagaagtttgtcggt atgcttgcattattgatttgtagtgtgtagtatctggttagatacatacacagtcatg cctacagacaccaagtatcgtactgtcaaaattccgttgcggttgaccgcagtcaaac aatctcaggttaagtcgttaatggcttgtgagcgttggctgtacaatgaggcgatcgc cgcaatgaatgcactgagtcagccggtctatccaagctaaacaacctaaaatacaaca tgccattacgagccttgtccgttgaaactaaaaaatcagttatttctttttggtttaa aagctcaaatgaagctcgatttaagcatcccaaaggctttatttgtcccggatgcaag caaaagatgtatgttcgaggcgggggagtaacaaaatttcaaacacattttgctcata caaaaagtcttgagcaatgttttattgctcaaaaaactcaatctacaccaaaagatct aactcatcacacgctagccgttcaacaagtatacaactggctgcttcctcaattgcct gaagggttttctatggagccagagtattttgacccaaaagttcctgatagaattgcag acattggagtattagactctaatgggtcttttgttcaagcggttgaaattcaactaac caaaatttcaattgaaagattggaggcaagaacagattcttacgaaaatgctggaata gaagttctttggtttttgggaaaggctgtgatcaagaagatatcagaatgtggcctc accgaagatttggatgttatttgctgcctgagtttgacttccgaagcacagagttcgc agaattatcagcctcttgacgatcacaaatttgattttcagcacaaaggacagtctag gctg
3822	CLUST.484501_S.A8IP67-M effector>	MKTGNRIKPDLDHALTIKIIFSQRVKFVNIFERRRNTCATIKVIQRQLPKSMVEVRTV KIQFNPTQQQKQILDSALWNSRRLYNLLVEQLTVIRNRAKRISSDVDIIFELVLCGLD INIAVKFLQLKQSWRNPYLNILRPGWATEFLRSVEAQKGCTYPKALELKKVKSGKNKG KQSFTPVIRTPDGKKNASPSASGVPGQSLGLIAQSFEASIKSCFTHWRNGNYDAKLPR RYKSSFPLPISNQQIKVLGHHVYQFGAGKTTIALKLPELARFNKIADAKFSRSRSGNY HIFVSGYVDVEVNPQLNNVAAIDFGQKRAIVISTVVDGKTKTAMVSGKNIIGLKRERD RRYRELNRKRARTFRGHLRQYLSAEERNTCRRLQQEDNQRQIKGKKRTGADQKYAHRL INQRRREGVDGKGRRLVDLNQAPHDGICKVNRPDLKLGVLRKYSKQNYKLKRTLAKVS EYYRLRLTYANHCITRTTVDWAIAHDVGKIYVGDLDSLPKGRKKGKRRVKQVSRNNLW EMPTQKKYLEEKLILAGSPFKEPVEKHHERLTSQTCPVCQSRTKSRNRVYRCRVCHWI GDRDGLGSTNLLSLIKTGSCGNIMPDSIPRTLPIAPAIGQRIPMHRVAHIEQSNMRGG SAEASVPILTKSTISVLQASAIVDCCEKDGLTETLVDKGRRRKETGSGCMNNSASPIS REFLMPVGDSQTAKSGAKSKSKSRSLSNSLPSYIQLTLWDVEV
3823	CLUST.484501_S.A8IP67-M direct repeat 1>	gguguaacuagcuucuuaucuuuagcuguuuggcag

3824	CLUST.484501_S.A8IP67-M direct repeat 2>	cugccaaacagcuaaagauaagaagcuaguuacacc
3825	CLUST.484501_S.A8IP67-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3826	CLUST.484501_S.BKO4ZC-M effector >	MPKKNQNKTPYRTAKISIALTQKQRRQVRSLMDCERWLYNEAIAALRLLNQPVYLIGD GGPVRACSVGDRKARKRFEQTGALCDGFPVREWREWKSFSAERYLVASESTRGLCYYI PNRYRFDDTKSRYGVSSSSLTALSEAIKGTIKGFFTSRSHGDFRAKLPAQFRSHDRPK GRIWTIKKEEIRWKHGRLRLGCKNQNGGYVTLKVPKEWYGRAVDAAKVTQDDRGDFWL HLSYEAQIKPLGLTGSAGIDMGQKRAVTIATDAGKSVTISGADIVRLKERRDRYTRRI QRLEARRFRGEVRHTLTAAEQQTMRDLEAKSSGAGTQYAHRMIAQRRRENAQRRRSRR QFKLLRSRRNLSVKIKRSLKYANHCITRKTADWLIDQGVGQVYVGEISSVPKGRKKGS RRIKQVRNNALWEAPAQIKQLEEKLKMVGGTLHHTAEHYTSQTCPNCGARHKPRNRRY NCRTCGWVGDRDSVGAANILAKSLSDGWPAQGRIVPHAPRSLAVSPAIAKQPRRKLER LGQRSPLLGRPESQGVDRLDGCDSLPRTPVRESVDVPADLAGESTRKPCSARNPAVKD AKEVRAIAETLTLFELPVAEAAHNDLSSKPKSSRRRRSAPTPPQRQAQLGLWDSAAKN G
3827	CLUST.484501_S.BKO4ZC-M direct repeat 1>	gcgaaaaacgguugaccgguuggggcgaucguugcaag
3828	CLUST.484501_S.BKO4ZC-M direct repeat 2>	cuugcaacgaucgcccaaccggucaaccguuuuucgc
3829	CLUST.484501_S.BKO4ZC-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3830	CLUST.484501_S.BKO4ZC-M non-coding>	cagcatactgaacctcattgaggagcgagagtgggacaatgacgtaattgaatcgcca cagtttcaattactggagtctacgtttcagcagtttgtggactcgattcagggcttga ctcgttttgaggtggattacagtattgctgttttgctaggagaaagcgacaaaaatca aggaacaggagcttggtaagcctaggcgcgatcgccctcccctcagtcagtcactatg cccaagaaaaatcaaaacaaaaccccgtatcgtacagcaaaaatctcgatcgccctca cccaaaagcagcggcggcaggtgcgatcgcttatggattgtgagcggtggctctacaa cgaggcgatcgcggcattgcggttgctaaatcgccatctcctgctagtgttgactctg agtcgggggaaatgctaggcttaatgcattcatgggtttctccccgtg
3831	CLUST.484501_LIRO01000096-M effector >	MGKPKPIYRTAKISLKVSRRQQKQLRRLMSAQRWCYNVVIAALRAANSPIYPIVPGVG PVRACSLKSAPKRRKQYLADGKPAEGYIVREWRDWQQFKPWDALKGHCDLYPYHDRDE GGSKYGVSAKTASGVTQTIRGFIQGYWTKRKRGDFAAQMPNQFRSAQFESGWIWEVDK QELDWDGDRLVLGTRNQIGGVVSLPIPKRYVGCSINKASITRDGAGDFWLHLSYAAAG EHGFAPDPDLTRSAGIDMGQIRAMVLTLDSGKSVSLSGRQICGLKRERDRRFRGIQRA RARVFRAQVRQYLTDEQKATMAAMEAKSPGQGTKYARRMVSAARKELGLKKRSRRDHH LWQTQKRVATQVNRNLKYANHSITRRAVDWLRGNKVGKVYLGDIGSIPKGRKKGSKRL KQVKRNAQWEYGNQEKMMTEKLEEYGATLHKAHEHFTSQTCPNCGARHKPRGRLYRCR VCGWQGDRDAVGSANILARSIDPAWPDSGRIVPHTLKPLAISPAMKKAGRLHVGAARP

		QPLGGPPTSREVGCRPPECVDRSPRITREPEATAEGLVAESTRKPRPAGKTAVRADKK VRASRESLAPSAIPASEGLHDDLANTQKQDTRSRFAQQPPETPVQLNLWDLADATEV
3832	CLUST.484501_LIRO01000096-M direct repeat 1>	gaugcaacggaagucugacuugggcgaucguugcaag
3833	CLUST.484501_LIRO01000096-M direct repeat 2>	cuugcaacgaucgcccaagucagacuuccguugcauc
3834	CLUST.484501_LIRO01000096-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3835	CLUST.484501_LIRO01000096-M non-coding>	gccgcgatcgccctgttgttagccccagtgatggatgcttactccctttgggcgatcg gtctttttgggcctctgtggccctaaccacaatctccggcgcaatttatctcattcc ggttggtaaacagagcgttgaatccggtgcttagatcacgtctttcttgatttttctc acacagaaaaacattagaattaacaaagaatcaagcggggttaaaacacaaagccgaa cccacccctcggcaggggttgcactttaacctaacttatagcactgggtaagaaccca tgggcaagcccaaaccgatctatcgcacggccaagatctcgctgaaggtttcgcgccg ccagcaaaagcagttgcggcggctgatgagcgcccagcggtggtgctacaacgtcgtg attgcggcattgcgggccgccaattcaccgattggtttttcctgccccggtcggtgct ggatgcaacggaagtctgacttgggcgatcgttgcaagcgaagggagacagctagctg ttttgcatcccctcaatcatcttaatcacccgctgcatctcggtttgtaaaccggtaa tctggctttgcagcggctcgactgtttgggcgatcgcctgctgaatgccatggtcgat cgccgctaggattgaatcagtgcggtc
3836	CLUST.485489_S.3F0LXT-M effector>	MKRIASSLILSFLFALVVLVFLAPSTSASPSSVSHQPLVTSHLITQSITMTTISTIEV SLGDIFAVVGDRAIVGSRREWERMPSVVAIIHPNESPWYHTITVTAVPTDVSLSDNMI DVGGGRLYVPYSGDLLLVESDTITTLYRSPEPNNWYRCESDGKYVYCKASNSNTWSVV SFDTNVPTVVYTTSVVSWGGVKWTARELLFVSVSTRRDEEGIIETVCVTDFTTGSNVC RDRGPMSSGVFRLALFPHLSTLYLQEANTLYVYSVPTLTLEAATTLPSDFRIVAYNRD WILVHDGIVYTSPDTLYIYQPRQLQPPVLYKEILVRGASVKAINNHMAIVGWAETGII DFTSEAQTFHYRSFSERPAVVSLKDRLILAYPHFLSVYSTTTWTENGRYLLSLTEIFT PVTDHDHRLLMMGSQHYYLFDFSSYPPEVVSGTVSPNVASCLWKAIRGDYVYGTCAPQ KAAVTEDRYKDAVYGYPATLKLSSMQIASVLNAPLFGPIVSSGGIYAFVTQTVGTDRM SITFSVLSDDPENLFVAQTFSNSITMPSFMYWNTVDRYDHKMFIVAFDPYSYWFRATR WDLNTQQVITRVLTPNIYWEKVDDLYVYVKYVTGNGAFLRVFSHDFTRYYTISPAVSF AYIETAPPYVVGMDYYYFQVFMRPEISLPFKVYLPFVTRQ
3837	CLUST.485489_S.3F0LXT-M direct repeat 1>	guccgaacgccuccaaugcccgacagggcauuaagac
3838	CLUST.485489_S.3F0LXT-M direct	gucuuaaugcccugucgggcauuggaggcguucggac

	repeat 2>	
3839	CLUST.485489_S.3F0LXT-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3840	CLUST.485489_S.3F0LXT-M non-coding>	acaaaagtgtccagcatccgcgatagggaggcctaaattgggtgtacatgcccagaaatagaaaacgcggtggctggtgcaaaacaggagagtaatcaaaaacaacctgggcgggaatatcaaattaaccactggaggtgaaaaatgaaaagaattgcatcatccctaatccttttcgttcctgtttgctctcgtggttctcgtctttcttgccccaagcaccagcgcatctccatcttcagtttcccaccagcctcttgtaacctctcatcttattacacagtccatcactatgtacaccatttctcccgcagtttcatttgcatatatagaaaccgccccaccatatgttgtggggatggattactattacttccaagtattcatgcgtccagaaatttctttgcctttaaggtgtacctcccgtttgttaccagacaatagttgctgatgtttcttggcaaccttgctagggtgtgtcccaatttcgtcgggctgggccgtcggcctttccgcttggccgtcaacggccaggctcaggcaaagacgaggcgctaaagcgccccttccgccctgcaacccacgttcccgaacatctaccgggggggaagagggcgcttccagcgccctgcgcaacctcagccaagccgattacggccttgccccccaggcctccgccactacccggcgggacccgccgacact
3841	CLUST.485489_S.12IVJQ-M effector>	MKRIASSLILSFLFALVVLVFLAPSTSASPSSVSYQPLVASHLITQSITMTTISAIEVSPNDIFAVVGDRAIVGKRGEWEKPSVIAIIQPNENPWYHTITVTAVPTDISLSSNMIDVGEGRLYVPYRGNLLLVESDTITTLYRSPEPNNWYRCESDGKYVYCEASNSDTWSVVSFDTNVPTVVYTTSVVSWGGVKWTARELLFVSVSTRRDEGGIIETVCVTDFTTGSNVCRDRGPASSGVFRLALFPHLSTLYLQEANTLYVYSVPTLTLEATTTLPSDFRIVAYNHDWLLVHDGIVYTSPDTLYIYQPRQLQPPVLYKEILVREASVKAINNHMAIVGGAETSIIDFTSEEQTFYRSFSRQCTVVSLKDRLIFAYPRFLSVYSTTTWTENGQYLLSLTEIFTPVTDYDHRLLMMGSQHYYLFDFSSYPPGAISGTVSPDVASCLWKAIRGDYVYGTCAPQRSILGDRYKDAVYGYPATLKLSSMQIASVLNTPLFGPIVSSGGIYAFVTQTVGTNMMSLTLSMLSNDPENLSVVQTFSNSITVPSFWYWNTVDRYDRKMFIVAYDPSSYRLRATRWDLDTQQVITMTFPSNIYWEKVDDLYVYVRQAASTGTFLRGFSHDFTRYYTISPAISSAYIETAPPYVVGMDYYYFQVFMRPEISLPFKVYLPFVTRQ
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3843	CLUST.485489_S.12IVJQ-M direct repeat 2>	gucuuaaugcccugucgggcauuggaggcguucggac
3844	CLUST.485489_S.12IVJQ-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3845	CLUST.485489_S.12IVJQ-M non-coding>	cgcgcagtgacaaaagtgtccagcatccgcgatagggaggcctaaattgggtgtacatgcccagaaatagaaaacgcggtggctggtgcaaaacaggagagtaatcaaaaacaacctgggcgggaatatcaaattaaccactggaggtgaaaaatgaaaagaattgcatcatccctaatcctttcgttcctgtttgctctcgtggttctcgtctttcttgccccaagcaccagcgcatctccatcttcagtttcctaccagcctcttgtagcctctcatcttattacacagtccatcactatgtacaccatttctcctgctatctcatctgcatatatagaaaccgccccaccatatgttgtggggatggattactattacttccaagtattcatgcgtccagaaattttctttgccttttaaggtgtacctcccgtttgttaccagacaatagttgggtgtttcttggcaaccttgctagggtgtgtcccaatttcgtcgggctgggccgtcggcctttccg

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3846	CLUST.485489_OQUW0101071 4-M effector>	MKKILMPIFLPLAATLLVLLAFSKGGNADSSNSPIEHPLSASTSYITSFLPLTRVSVV EIRPYWIGVAAGDKAVLGGRSFAAVVSVGNSPWYHTITVTSVLSDPGYLGGNTAIDIG EGRVYKVGNGKVVKLSNDAISVVYTPPENPNWYRCEGDGEYVYCAHRTSGRWSVLSFE TITPTVVYSISWPSRHYVWTARNRWFAFAIGTWPQDSGPKEYLVLLDSVSNTEITRFL WRDWMTDQLLLFPHLDTLYLIDKNQVLYVYSVPTLTLEMTDTLPSGLWVSGYSEDWIL GYNQPDWNSPGTLYVYKPQQLQPPVLYKEVYGVESPSNFNGRLAILGEGEAIMDFTSP ELPIYPYWDSLREIKAVEQLGDRLVFALPRMLSVYNTRNWSENGRYLLSLTEVFTPTT DRNHRLLMVGSEHYYLFDFSSYPPEIVSGTVSPDVSSCYWSIIRGDDVYGVCEIQREY SSRVYYGRPARMSLSSMQIEVIGPSPMIGPVVTSRGFFGFTQTAEMNGDIVVYELDPE SLGIVRTSLVDIDMYYIMWRDLVHYDYRAFVSGREASYSLWLTLIGIDLSVPKAVTVS IPGLYSLVGADDTYVYLEANRPCALSHDFTRLYFLDFPLGSRPRLASPFLLGDYWSYH EIFLRPGPSEMPYKVYLPLVIRQKP
3847	CLUST.485489_OQUW0101071 4-M direct repeat 1>	guugcaacgccuccgauccgacugaggauacugaaag
3848	CLUST.485489_OQUW0101071 4-M direct repeat 2>	cuuucaguauccucagucggaucggaggcguugcaac
3849	CLUST.485489_OQUW0101071 4-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3850	CLUST.485489_OQUW0101071 4-M non-coding>	gtggtaattctttgttggcaacgaggctataatagacatggctttttctcccagcggg agagagatagttgtggtggaggagagcggaaaagccgtccgaatgaaagcgtatttaa gcagggcaacccccccccaattcaaccaagcaggaggtgtaaaatgaaaaagattctga tgcccatctttcttccattagccgccacccttctggttctcctcgcgttcagcaaggg tggtaatgcagactcatccaattcccccatagaacatcctctatcggcatccacatcc tatatcacctctttccttcttgacttcccgttaggatctcggccgcgcctcgcgtcgc cgtttctgttgggagattactggagttaccacgagatatttttgcgaccaggtccctc agagatgccctacaaggtatatctgccgctggtcattcgccaaaagccctgacacctg ttgttctgggagggagtaagcaaagccagcgcggcgcctttgccaattcccgctacca gaagcggagaggggcaacacgacgaagttgccccctctctgcaatatcaggaaaga agaagagatgtcatcagaacaggcgttggtatgcccttgtggtctgtcgtctgtggtc tgtcgtccgtggtctgtcgtcggtggtctgtcgtctgtggtctg
3851	CLUST.485489_S.4M6LU5-P effector>	MKRVALSIVIPVLAVCFVLCALNSANALSHTSPVTANVSTSPSVTYTLPATLLGHVEI GPWNFYAVVGEKVLLGSLPYIAIVSNCNNPWQCQITTTAVSTDVPRVYEGVDIGGGRL YEQDQGAVISVTESGTITVLYRPPEQARWERCEGDGTYVYCMLSWPNTLSVLSFDTNT PTVIYSITTSYVWTARDLLVASLNSRQVSGSWEYTVCVSDLRSSLQTCNYIGQYPTGE KEGLALFPHLNTLYVQISSHLYVYSVPTLTLQPEEEITLPLGSYIQGYGRDWLLVGAG SYNPNMSRLYVYRPRRLQGAVFQKEFLVPLYLYVQGYNDSLAIIGLDREVGFVDFTRP EPQFYLYSYRKYGGLGTRTFRFGDRLIFAYPYYLSAYSLTNMAESGRYLLTPTEVYTP

		ATNHDHRLLMMGSRYYYLFDFSSYPPEVVSGTVSPEVASCWWKAIRGNYAYGTCSPRR GWPRDLSTGPDENIAYGYPATLDLSSMQIASTMNSQMFGPFVTNDKIYAFVTQTVGTG IIITVSVLSNDPNNLSVSQVLPNSVSLPNWGWQQSGRYEHSLFMQMIDIDNCRWLPYL VKLDLSVPQVITTTPFYNDRLAGADDLYVYLYDMTRLYHGFSHDFTRHYIFDSLPAFG TLLVAPRLLIVQFDWSSGCWVYARPEISLSYKAYLPVVIRSGGN
3852	CLUST.485489_S.4 M6LU5-P direct repeat 1>	gucugaacgccuccaaugcccgacagggcauuaagac
3853	CLUST.485489_S.4 M6LU5-P direct repeat 2>	gucuuaaugcccugucgggcauuggaggcguucagac
3854	CLUST.485489_S.4 M6LU5-P spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3855	CLUST.485489_S.4 M6LU5-P non-coding>	ctccgcaatgtgattcaacaagcagaaatgggaggcctggattttctcgcgtatggtg aaccggtcgcgacggttgcggctaatattgagggagtcgatgataatataatagagtt cttcggaaattaggggagcaggcattatgttttgagtctgggctttaaacaaaccggg aatagacaggacggatacctaaaatatatagccctacggtttctgcaaaaaaccggcc cggcaaattagccccaagttacaagcatgtaagttagaaaggaggtacaaaatgaaaa gggttgctctatcaatagttattcccgttcttgctgtttgcttcgtgctgtgtgccct taatagcgccaacgccctatcacatacctctcccgttaccgcaaacgtatcaacctcc ccttctgtcacatacactcttcccgccctcccagcatttgggaccttgctggttgcgc cgcggctactgattgtgcaatttgattggtcatccggttgctgggtatatgccagacc tgaaatctctctctcatataaggcatacctgccagtagttatcaggtcgggagggaac tagccggtcaggtgattaaaggagcacggtggggtcagcaaagaccacctggcaagcc ggcccatggttgcaaataagtaagttagaggaaagacgcagaatagaaaggcttgttc tatcaatagcgaacgagccacagaacggttcggggcgggaccgccttctggcggaggc tacc
3856	CLUST.485489_S.3 W1NWX-P effector>	MKRVILSTAIPVLAVCFVLCALNSANALSPTSPVTANVSPAPSVTYTLTATLLGHVEI EPWDFYAVVGKKVLLGRWPYITIVSNCNNPWQCQITTTAVSTDVPRVYGGIDVGGGKL YERTWGTVISVTESGTITVLYQPPEQWRSGWSRCEGDGTYAYCWKSVQGTLGVLSFDT NTPTVVYSITTSYVWTARDLLVASLNSEWVSGSWEYTVCVSDLRSGLQTCNYIGQYPT GEKEGLAIFPHLNTLYVQIGSHLYTYSVPTLTLQLEEEITLPLGSYIQAYGRDWLLVG AGSYDPNVSRLYVYRPQRLQKAVFQKEFLVPLYLYVQGYNDSLAIIGLAQEVGFVDFT RPEPQFYLYSYRKYGGLGTRTFRFGDRLIFAYPYYLSAYSLTNMAESGRYLLTPTEIY TPVTDYDHRLLMMGSRYYYLFDFSSYPPEVVSGTVSPEVASCWWKAIRGNYAYGTCSP RRGWPRDLSTSPDENVVYGYPATLDLSSMQIASTMNSRMFGPFVTNDKIYAFVTQTVG TGIVITVSVLSNDPNNLFVSRVLPNSVSLPNWGWMQSGRYEHSLFVQMIDTDNYGWRP YLVKLDLGVPQVITTPIGSNDQLAGADDLYVYLHNLTGQHHGFSHDFTRHYIFDLPPA FGTLLVAPRLLIVQFSGCWIYARPEISFPYKAYLPLVIRSGGN
3857	CLUST.485489_S.3 W1NWX-P direct repeat 1>	guugcaucgccuccgauccgaccgaggauacugaaag
3858	CLUST.485489_S.3 W1NWX-P	cuuucaguauccucggucggaucggaggcgaugcaac

	direct repeat 2>	
3859	CLUST.485489_S.3 W1NWX-P spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3860	CLUST.485489_S.3 W1NWX-P non-coding>	tttactggccaaatggtttcgcaagattctggcccacacagtatgtgtgtggctgaac ctccaatacgggaggccacctttggatttcgctggcttggtcgcagtaaaataatgtt gcacatggcgtcccatattatatatagatctgtctcgaatttagacaaatgagcccca tgcaggccaaaattgatttcggctcacgacagatggcccatatatggtgcataagcgc cgtgttaatcccatatatgggcagtcacactaccggtttccggtttgtctaaactcgg gtctataatttctgcaaaaatccggcccggcaaattagctcaaagttacaagtatgta agttagaaaggaggtacaaaatgaaaagggttattctatcaacggccattcctgttct tgctgtctgcttcgtactgtgtgctcttaatagcgccaacgccctatcacccacctct cctgttaccgcaaacgtatcacctgccccttctgtcacatatacccttactgcttttg atctccccccagcatttgggaccttgctggttgcgccgcggctgctgattgtgcaatt ctctggttgctggatatatgccaggcccgaaatctctttcccatataaggcatacctg ccattggttatcaggtcgggagggaattagccggtcatggtgattaaagaggcacggt gatgtattgcaaagtggttatcatcggggcatttggcgctgggaagagtttatccgat tagcaccctccggcaacgctgttgtcagcacagaaagatgcggggactatatataaag cctcttccttcgcagacaatctctggctaagaaggtgtgtaatgacgaccacagttgc ccagatggccggaacgggctcagagagatgatagagacttttagtttccgctaacttt gcctgctacaggcaggggaaatccccctgggccagcacccgccgcagccgtcccgggc tccgttggggctgccgatcccagaagccggtcggcaccagcggtaacaccgccgccag gtagagcaagatgttcgccaacagcagggctaactccggcagccgccaatgctcttcg gcgcgtaactgttcagccccacccctcccccagcggcttcgccgctacccccctcctct ctcctgaacgaagttcaggagaggggaagaggtgccgccacaggcggcgggggtgggg tgaggaagtctgaatagttactccggcgcaaacacccactgccgttcccgccccagga gaggcttggtcacgggtgtgtcccaaaatcgtcggagcccggtgggccaggccgtaaa cggcctggctgaggctgcatagggcgctggaagcgccctctcccggttgtaggacaac tgcttgcagttgtcctacaaacggaacatgggttgcccaggtggagagggcgctttag cgcctcatccttgcctgagcctggccgtttacggccaggcgaaaaggccagcagccca gcccgacaaaactgggacacacccgaaaggcacagccttttccggccaacgccagaat tttccgcctgatgcgacaccgtcgggcggattgctcttgccaatccgggcgttcttgg gtatccttactcgtgcccaggagccaaaatgaaaccgcgcatccgactggaccggttg ctggtggagcgggggctggcggagagccgcactgaggcccagcagtgggtccgcgcgg gccaggtgcgcgtcgccgaacaggtggtggaccagcccggggcgctggtatcccccga cgcc
3861	CLUST.724765_S.1 H18U1-M effector >	MAFQSKRRIVGNFVKEQCLKAVDGKVILTDQEKRELIKRYELHLEPHKWLLRLFLSGY EGRDDGFYEELGNTNLDKEKFFEVTAGLRDALLRQSGSSRALKSSMLGKCPPSAAVGK AAKHIQTLRDAGILPFKTGLTSGEDYNVLQQAVQQLRSWVACDHRTREAYAEQQEKTS QAEEAAKKAANEVKPEDAKSLERHERVLTKLRKQERRLERMKSHAQFSLDEMDCTGYS LCMGANYLKDYCLEKEGRGLRLTLKNSTMAGSYYVSVGDGQHAGMKNPGTPAGGSPEK GRRRNILFDFTVEKCGDNYLFRYDENGKRPRAGVVKEPRFCWRRKGNSVELYLAMPIN IENSMRNIFVGKQKSGKHSAFTRQWPKEVEGLDELRDAVVLGVDIGINRAAFCAALKT SRFENGLPADVQVMDTTCDALTEKGQEYRQLRKDATCLAWLIRTTRRFKADPGNKHNQ IKEKDVERFDSADGAYRRYMDAIAEMPSDPLQVWEAARITGYGEWAKEIFARFNHYKH EHACCAVSLSLSDRLVWCRLIDRILSLKKCLHFGGYESKHRKGFCKSLYRLRHNARND VRKKLARFIVDAAVDAGASVIAMEKLPSSGGKQSKDDNRIWDLMAPNTLATTVCLMAK VEGIGFVQVDPEFTSQWVFEQRVIGDREGRIVSCLDAEGVRRDYDADENAAKNIAWLA LTREAEPFCMAFEKRNGVVEPKGLRFDIPEEPTREQDESDQDFKKRLEERDKLIERLQ AKADRMQAIVQRLFGDRRPWDAFADRIPEGKSKRLFRHRDGLVLNKPFKGLCGSENSE QKASARNSR
3862	CLUST.724765_S.1	guguaggccuccucugaaugggguggcuaaugacac

	H18U1-M direct repeat 1>	
3863	CLUST.724765_S.1 H18U1-M direct repeat 2>	gugucauuagccaccccauucagaggaggccuacac
3864	CLUST.724765_S.1 H18U1-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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3866	CLUST.724765_S.1 8PUDW-M effector>	MAFQSKRRIVGNFVKEQCLKAVDGKVILTDQEKRELIKRYELHLEPHKWLLRLFLSGY EGRDDGFYEELGNTNLDKEKFFEVTAGLRDALLRQSGSSRALKSSMLGKCPPSAAVGK AAKHIQTLRDAGILPFKTGLTSGEDYNVLQQAVQQLRSWVACDHRTREAYAEQQEKTS QAEEAAKKAANEVKPEDAKSLERHERVLTKLRKQERRLERMKSHAQFSLDEMDCTGYS LCMGANYLKDYCLEKEGRGLRLTLKNSTMAGSYYVSVGDGQHAGMKNPGTPAGGSPEK GRRRNILFDFTVEKCGDNYLFRYDENGKRPRAGVVKEPRFCWRRKGNSVELYLAMPIN IENSMRNIFVGKQKSGKHSAFTRQWPKEVEGLDELRDAVVLGVDIGINRAAFCAALKT SRFENGLPADVQVMDTTCDALTEKGQEYRQLRKDATCLAWLIRTTRRFKADPGNKHNQ IKEKDVERFDSADGAYRRYMDAIAEMPSDPLQVWEAARITGYGEWAKEIFARFNHYKH EHACCAVSLSLSDRLVWCRLIDRILSLKKCLHFGGYESKHRKGFCKSLYRLRHNARND VRKKLARFIVDAAVDAGASVIAMEKLPSSGGKQSKDDNRIWDLMAPNTLATTVCLMAK VEGIGFVQVDPEFTSQWVFEQRVIGDREGRIVSCLDAEGVRRDYDADENAAKNIAWLA LTREAEPFCMAFEKRNGVVEPKGLRFDIPEEPTREQDESDQDFKKRLEERDKLIERLQ AKADRMQAIVQRLFGDRRPWDAFADRIPEGKSKRLFRHRDGLVLNKPFKGLCGSENSG QKASARNSR
3867	CLUST.724765_S.1 8PUDW-M direct repeat 1>	guguaggccuccucugaaugggguggcuaaugacac
3868	CLUST.724765_S.1 8PUDW-M direct	gugucauuagccaccccauucagaggaggccuacac

	repeat 2>	
3869	CLUST.724765_S.18PUDW-M spacer>	nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
3870	CLUST.724765_S.18PUDW-M non-coding>	cggcggctttgcgaccagcttctccgccgggacatgcgtatgcgcgtcaattctttcg gtgatgttcatggggactatctccttgtctctccatttttttccatgcattcgccaaaa tcccctttttttcgggaaatcggcttgaatttcataggacaggagctaagtttctgaat gcgattccaactgaacaacagatcacgcgcattgtcgactcaatgagagtgaactacc ccgccctatcgggcgcgcgccttcggcacgcaccctatagaggacggggtcttctcgc ccgatgaggataaaaaacgccctttgacttgacttccaatatgcgcgcgctatagtgc cgcaaccacaacaaaggaactcatatggcatttcagtcgaaaagaaggatcgtcggca acttcgtcaaggaacagtgcctcaaggctgtcgacggcaaggtcattctgacggacca ggaaaaacgggaactcattaagcggtacgagccccatctggagccgcacaaatggctc ccgtgggacgccttcgccgacagaatccccgaaggcaagtcgaagaggctcttccgcc atcgtgacgggcttgtcttgaacaagccgttcaaaggtctttgtggcagtgaaaacag tgggcaaaaggcatccgctcgcaattcgcgatgatgccgatgcgatctttgacaactg aatatcgagcggctgaatgggagtgcggcgagccatagccgctcgaaggtgcggatat tgaacgccttatgccccttgagatcaccaaatacgcgcgtttctgagacatgacttca ggaaccgctcggaatctggctcacaacgcatcagatacaagatagatacaacgcagac acgcggaaatgggagccagctctctcgacgaggacctggaggtctggatagaggcgac aagaaggcttctcagcattccgcagagaaccgtcaagcagcccgacggcgccgtcgtg tgtgccgtggagccccgcctgctccagtccatcctgcggttc
3871	CLUST.724765_S.0V4LO3-M effector>	MGRFGKKKIAVNGYVEQDCIKTISAKCLLTRAQIDELRAKYDAVLDTMRPLIRLILAG YEGRDDGIYEEIAPEMSKKKFFEAATEWRESIVKNASPRAMKASVFGDKEPCKSTGGA RAVIGKLRKSGVFPIETGLSGGDEYNLIEQAIEYAKSWLKSDEATREAYADQQKDIKR LIGEAKKLALKIEKAEKKLEATNPQTKSWKKTTEIIKKSKREFGSVTTKTEKAEKRFE RMKPFSKLELQNMDCTKYSTYLGTNYSPFKLKKEGDLLQITVTSSVMKGTYLASYGDG QYGSRRNNGQSRRDDFVPNMNQKRRRNLMFDCTVEPFGDGSLLRYEENGLRPRVAELK EPRLCWRRRNGNYELYLMMPVKMHVKSPEMFAGDHLAFSRYWPKEVEGLDSDTKITAL GVDVGIIRSAYCVAVTAERFVDGLPTEMTVGKASFDAQTEKGREYFELGRRATMLGWL IKTTRRYKKDPKNEHNQIKESDVAAFDGSPGAFEHYILAVDEMSDDPLDVWGHANITG YGKWTKQIFKEFNQLKRERAEGQVEPNMTDDLTWCSLIDYIISLKKTLHFGGYETKER ESFCPALYNERANCRDVVRKRLARYVVERAIAAEAQVISVENLSKCRRDDKRKNRVWD LMSQQSWIGVLTNMARMENIAVVSVNPDLTSQWVEQCGAIGDRKARTIACRDVNGKFV SLDADLNAAYNIASRALTRHAEPFSITFKKKDGILEQKDVCFDPGVIPVLEKNENEEK FRERVEKYEKSLVIKQERAVRWRAILQHLFGNERPWDEFTDEVKEGRHVSLYRHHGKL VRTKQYAGLVKEANNELVPVCAVAR
3872	CLUST.724765_S.0V4LO3-M direct repeat 1>	guguugauccguucugaaug
3873	CLUST.724765_S.0V4LO3-M direct repeat 2>	cauucagaacggaucaacac
3874	CLUST.724765_S.0V4LO3-M spacer>	nnnnnnnnnnnnnnnnnnnn

3875	CLUST.724765_S.0 V4LO3-M non-coding>	ctcggggaggacggcgacgattcgttcaccgaaggacagcagaagagcctggacaagg tgggggaaatggtgaggagcaacggtggcaccgtgctgacgttgcttcagaaggtggc ggactatttcaataaaatatcaaaatccacctgacataaatgcgatgagtgctatact aacattttcagacaatcaaagtcacaaataaaggaacacatcatgggacgcttcggta aaaaaaagatagccgttaatggttatgtcgagcaagactgtatcaagaccatttccgc gaaatgcctgcttaccagggcacagatcgacgagctacgcgccaagtacgacgccgtt ctcgataccatgcgtccaccttgggacgaatttacagacgaagtcaaggaaggaaggc acgtctccctctatcgccaccatggtaaacttgtcagaacaaagcagtatgcagggtt ggtaaaagaagcgaataacgagttagttccggtatgtgctgtggctcgctgaagaatt ttatggcgttcctgcaccaagtgatctttgaaaatttagaaatcgagcgcctccgttg ttcagcgttcagtataggtgctcgaacatattgtaggcaaaggggatatgccgcatta taaagtgtatgaccgccccaaatacactgccgatagggtgcctctcgaaaagcgattt gtaatatactataaacgactacctatgattaaaaccatcaaaaaaaaatcaaaatccc cttgacataaagggattctggtttacgttagagtatactgaaaactcacaagacggat tcaacaggaaactaaaatgttcacagcaaccttcaattggaatgattggaataacgat cggaacctccggtcgacggttgcttacgtcctgatttcctgacggaaacagatttcaa agcccctcgatcgaaaggtcgaggggctttttgtgtttataggatctcagcaggtggg tactgcggtcagtctccaaaactgatgctcagggagttcgatcctcccggattctgcc agaaaattgaatatagtactgatgccgaagagtcgaggcgccgccctgtcacggcggt atttttgaagcgggttcgagtcccgtcagtgctgccaaataattgaatagtagttcat cggtagccgagctggtagcaggcagcagactgttaatctgtcgggattttattcccca tcgttggttcgaatccaactcgatgagccagagaaggaaaagaaaacccttctgttgt attaacagataatgttaataaatcaggagggtttctatgtccaagcgatcagaggcaa cacaaagatggcgtgaaaaaacgaaaaagcgtgttatcgaagccatgggggcgcatg tgtaatctgtggttacaacaaatgtgacaaagtaatgtgcctacaccatcttgatcca tcccagaaagag

Biochemical Characteristics

In some embodiments, the biochemistry of a nuclease described herein is analyzed using one or more assays. In some embodiments, the biochemical characteristics of a nuclease of the present invention are analyzed in bacterial cells, as described in Example 1. In some embodiments, the biochemical characteristics of a nuclease of the present invention are analyzed in mammalian cells, as described in Example 2.

Described herein are compositions and methods relating to a nuclease of the present invention. The compositions and methods are based, in part, on the observation that cloned and expressed effectors of the present invention have nuclease activity.

In some embodiments, a nuclease and an RNA guide as described herein form a complex (e.g., an RNP). In some embodiments, the complex includes other components. In some embodiments, the complex is activated upon binding to a nucleic acid substrate that has complementarity to a spacer sequence in the RNA guide (e.g., a target nucleic acid). In some embodiments, the target nucleic acid is a double-stranded DNA (dsDNA). In some embodiments, the target nucleic acid is a single-stranded DNA (ssDNA). In some embodiments, the target nucleic acid is a single-stranded RNA (ssRNA). In some embodiments, the target nucleic acid is a double-stranded RNA (dsRNA). In some embodiments, the sequence-specificity requires a complete match of the spacer sequence in the RNA guide to the target substrate. In other embodiments,

the sequence specificity requires a partial (contiguous or non-contiguous) match of the spacer sequence in the RNA guide to the target substrate.

In some embodiments, the target nucleic acid is present in a cell. In some embodiments, the target nucleic acid is present in the nucleus of the cell. In some embodiments, the target nucleic acid is endogenous to the cell. In some embodiments, the target nucleic acid is a genomic DNA. In some embodiments, the target nucleic acid is a chromosomal DNA. In one embodiment, the target nucleic acid is an extrachromosomal nucleic acid. In some embodiments, the target nucleic acid is a protein-coding gene or a functional region thereof, such as a coding region, or a regulatory element, such as a promoter, enhancer, a 5' or 3' untranslated region, etc. In some embodiments, the target nucleic acid is a non-coding gene, such as transposon, miRNA, tRNA, ribosomal RNA, ribozyme, or lincRNA. In some embodiments, the target nucleic acid is a plasmid.

In some embodiments, the target nucleic acid is exogenous to a cell. In some embodiments, the target nucleic acid is a viral nucleic acid, such as viral DNA or viral RNA. In some embodiments, the target nucleic acid is a horizontally transferred plasmid. In some embodiments, the target nucleic acid is integrated in the genome of the cell. In some embodiments, the target nucleic acid is not integrated in the genome of the cell. In some embodiments, the target nucleic acid is a plasmid in the cell. In some embodiments, the target nucleic acid is present in an extrachromosomal array.

In some embodiments, the target nucleic acid is an isolated nucleic acid, such as an isolated DNA or an isolated RNA. In some embodiments, the target nucleic acid is present in a cell-free environment. In some embodiments, the target nucleic acid is an isolated vector, such as a plasmid. In some embodiments, the target nucleic acid is an ultrapure plasmid.

In some embodiments, the complex becomes activated upon binding to the target substrate. In some embodiments, the activated complex exhibits "multiple turnover" activity, whereby upon acting on (e.g., cleaving) the target nucleic acid, the activated complex remains in an activated state. In some embodiments, the activated complex exhibits "single turnover" activity, whereby upon acting on the target nucleic acid, the complex reverts to an inactive state.

In some embodiments, a nuclease described herein binds to a target nucleic acid at a sequence defined by the region of complementarity between the RNA guide and the target nucleic acid.

In some embodiments, a nuclease described herein targets a sequence adjacent to a PAM sequence. In some embodiments, the PAM sequence of a nuclease described herein is located directly upstream of the target sequence of the target nucleic acid (e.g., directly 5' of the target sequence). In some embodiments, the PAM sequence of a nuclease described herein is located directly 5' of the non-complementary strand (e.g., non-target strand) of the target nucleic acid. As used herein, the "complementary strand" of the target

hybridizes to the RNA guide. As used herein, the "non-complementary strand" of the target does not directly hybridize to the RNA.

In some embodiments, a nuclease described herein cleaves ssDNA. In some embodiments, a nuclease described herein cleaves dsDNA. In some embodiments, a nuclease described herein is a nickase (e.g., the nuclease cleaves one strand of a double-stranded target nucleic acid).

In some embodiments, a nuclease of the present invention has enzymatic activity, e.g., nuclease activity, over a broad range of pH conditions. In some embodiments, the nuclease has enzymatic activity, e.g., nuclease activity, at a pH of from about 3.0 to about 12.0. In some embodiments, the nuclease has enzymatic activity at a pH of from about 4.0 to about 10.5. In some embodiments, the nuclease has enzymatic activity at a pH of from about 5.5 to about 8.5. In some embodiments, the nuclease has enzymatic activity at a pH of from about 6.0 to about 8.0. In some embodiments, the nuclease has enzymatic activity at a pH of about 7.0.

In some embodiments, a nuclease of the present invention has enzymatic activity, e.g., nuclease activity, at a temperature range of from about 10° C to about 100° C. In some embodiments, a nuclease of the present invention has enzymatic activity at a temperature range from about 20° C to about 90° C. In some embodiments, a nuclease of the present invention has enzymatic activity at a temperature of about 20° C to about 25° C or at a temperature of about 37° C.

In some embodiments wherein a nuclease of the present invention induces double-stranded breaks or single-stranded breaks in a target nucleic acid, (e.g. genomic DNA), the double-stranded break can stimulate cellular endogenous DNA-repair pathways, including Homology Directed Recombination (HDR), Non-Homologous End Joining (NHEJ), or Alternative Non-Homologues End-Joining (A-NHEJ). NHEJ can repair cleaved target nucleic acid without the need for a homologous template. This can result in deletion or insertion of one or more nucleotides at the target locus. HDR can occur with a homologous template, such as the donor DNA. The homologous template can comprise sequences that are homologous to sequences flanking the target nucleic acid cleavage site. In some cases, HDR can insert an exogenous polynucleotide sequence into the cleave target locus. The modifications of the target DNA due to NHEJ and/or HDR can lead to, for example, mutations, deletions, alterations, integrations, gene correction, gene replacement, gene tagging, transgene knock-in, gene disruption, and/or gene knock-outs.

In some embodiments, binding of a nuclease/RNA guide complex to a target locus in a cell recruits one or more endogenous cellular molecules or pathways other than DNA repair pathways to modify the target nucleic acid. In some embodiments, binding of a nuclease/RNA guide complex blocks access of one or more endogenous cellular molecules or pathways to the target nucleic acid, thereby modifying the target nucleic acid. For example, binding of a nuclease/RNA guide complex may block endogenous transcription or translation machinery to decrease the expression of the target nucleic acid.

Variants

In some embodiments, the present invention includes variants of a nuclease described herein. In some embodiments, a nuclease described herein can be mutated at one or more amino acid residues to modify one or more functional activities. For example, in some embodiments, a nuclease of the present invention is mutated at one or more amino acid residues to modify its nuclease activity (e.g., cleavage activity). For example, in some embodiments, a nuclease may comprise one or more mutations that increase the ability of the nuclease to cleave a target nucleic acid. In some embodiments, a nuclease is mutated at one or more amino acid residues to modify its ability to functionally associate with an RNA guide. In some embodiments, a nuclease is mutated at one or more amino acid residues to modify its ability to functionally associate with a target nucleic acid.

In some embodiments, a variant nuclease has a conservative or non-conservative amino acid substitution, deletion or addition. In some embodiments, the variant nuclease has a silent substitution, deletion or addition, or a conservative substitution, none of which alter the polypeptide activity of the present invention. Typical examples of the conservative substitution include substitution whereby one amino acid is exchanged for another, such as exchange among aliphatic amino acids Ala, Val, Leu and Ile, exchange between hydroxyl residues Ser and Thr, exchange between acidic residues Asp and Glu, substitution between amide residues Asn and Gln, exchange between basic residues Lys and Arg, and substitution between aromatic residues Phe and Tyr. In some embodiments, one or more residues of a nuclease disclosed herein are mutated to an Arg residue. In some embodiments, one or more residues of a nuclease disclosed herein are mutated to a Gly residue.

A variety of methods are known in the art that are suitable for generating modified polynucleotides that encode variant nucleases of the invention, including, but not limited to, for example, site-saturation mutagenesis, scanning mutagenesis, insertional mutagenesis, deletion mutagenesis, random mutagenesis, site-directed mutagenesis, and directed-evolution, as well as various other recombinatorial approaches. Methods for making modified polynucleotides and proteins (e.g., nucleases) include DNA shuffling methodologies, methods based on non-homologous recombination of genes, such as ITCHY (See, Ostermeier et al., 7:2139-44 [1999]), SCRACHY (See, Lutz et al. 98:11248-53 [2001]), SHIPREC (See, Sieber et al., 19:456-60 [2001]), and NRR (See, Bittker et al., 20:1024-9 [2001]; Bittker et al., 101:7011-6 [2004]), and methods that rely on the use of oligonucleotides to insert random and targeted mutations, deletions and/or insertions (See, Ness et al., 20:1251-5 [2002]; Coco et al., 20:1246-50 [2002]; Zha et al., 4:34-9 [2003]; Glaser et al., 149:3903-13 [1992]).

In some embodiments, a nuclease of the present invention comprises an alteration at one or more (e.g., several) amino acids in the nuclease, wherein at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16,

17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 162, 164, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 193, 194, 195, 196, 197, 198, 199, 200, or more amino acids are altered. In one embodiment, the alteration is relative to a parent polypeptide, wherein the alteration comprises one or more substitutions, insertions, deletions, and/or additions in the nuclease relative to the parent polypeptide.

As used herein, a "biologically active portion" is a portion that maintains the function (e.g. completely, partially, minimally) of a nuclease (e.g., a "minimal" or "core" domain). In some embodiments, a nuclease fusion protein is useful in the methods described herein. Accordingly, in some embodiments, a nucleic acid encoding the fusion nuclease is described herein. In some embodiments, all or a portion of one or more components of the nuclease fusion protein are encoded in a single nucleic acid sequence.

Although the changes described herein may be one or more amino acid changes, changes to a nuclease may also be of a substantive nature, such as fusion of polypeptides as amino- and/or carboxyl-terminal extensions. For example, nuclease may contain additional peptides, e.g., one or more peptides. Examples of additional peptides may include epitope peptides for labelling, such as a polyhistidine tag (His-tag), Myc, and FLAG. In some embodiments, a nuclease described herein can be fused to a detectable moiety such as a fluorescent protein (e.g., green fluorescent protein (GFP) or yellow fluorescent protein (YFP)).

A nuclease described herein can be modified to have diminished nuclease activity, e.g., nuclease inactivation of at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 97%, or 100%, as compared to a reference nuclease. Nuclease activity can be diminished by several methods known in the art, e.g., introducing mutations into the RuvC domain (e.g, one or more catalytic residues of the RuvC domain).

In some embodiments, the nuclease described herein can be self-inactivating. See, Epstein et al., "Engineering a Self-Inactivating CRISPR System for AAV Vectors," Mol. Ther., 24 (2016): S50, which is incorporated by reference in its entirety.

Nucleic acid molecules encoding the nucleases described herein can further be codon-optimized. The nucleic acid can be codon-optimized for use in a particular host cell, such as a bacterial cell or a mammalian cell.

Targeting Moiety

In some embodiments, the composition described herein comprises a targeting moiety.

The targeting moiety may be substantially identical to a reference nucleic acid sequence if the targeting moiety comprises a sequence having least about 60%, least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or at least about 99.5% sequence identity to the reference nucleic acid sequence. The percent identity between two such nucleic acids can be determined manually by inspection of the two optimally aligned nucleic acid sequences or by using software programs or algorithms (e.g., BLAST, ALIGN, CLUSTAL) using standard parameters. One indication that two nucleic acid sequences are substantially identical is that the two nucleic acid molecules hybridize to each other under stringent conditions (e.g., within a range of medium to high stringency).

In some embodiments, the targeting moiety has at least about 60%, least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or at least about 99.5% sequence identity to the reference nucleic acid sequence.

RNA Guide Sequence

In some embodiments, the targeting moiety comprises, or is, an RNA guide sequence. In some embodiments, the RNA guide sequence directs a nuclease described herein to a particular nucleic acid sequence. Those skilled in the art reading the below examples of particular kinds of RNA guide sequences will understand that, in some embodiments, an RNA guide sequence is site-specific. That is, in some embodiments, an RNA guide sequence associates specifically with one or more target nucleic acid sequences (e.g., specific DNA or genomic DNA sequences) and not to non-targeted nucleic acid sequences (e.g., non-specific DNA or random sequences).

In some embodiments, the composition as described herein comprises an RNA guide sequence that associates with a nuclease described herein and directs a nuclease to a target nucleic acid sequence (e.g., DNA). The RNA guide sequence may associate with a nucleic acid sequence and alter functionality of a nuclease (e.g., alters affinity of the nuclease to a molecule, e.g., at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more).

The RNA guide sequence may target (e.g., associate with, be directed to, contact, or bind) one or more nucleotides of a sequence, e.g., a site-specific sequence or a site-specific target. In some embodiments, a nuclease (e.g., a nuclease plus an RNA guide) is activated upon binding to a nucleic acid substrate that is

complementary to a spacer sequence in the RNA guide (e.g., a sequence-specific substrate or target nucleic acid).

In some embodiments, an RNA guide sequence comprises a spacer sequence. In some embodiments, the spacer sequence of the RNA guide sequence may be generally designed to have a length of between 15 and 50 nucleotides and be complementary to a specific nucleic acid sequence. In some embodiments, the spacer is about 15-20 nucleotides in length, about 20-25 nucleotides in length, about 25-30 nucleotides in length, about 30-35 nucleotides in length, about 35-40 nucleotides in length, about 40-45 nucleotides in length, or about 45-50 nucleotides in length. In some particular embodiments, the RNA guide sequence may be designed to be complementary to a specific DNA strand, e.g., of a genomic locus. In some embodiments, the spacer sequence is designed to be complementary to a specific DNA strand, e.g., of a genomic locus.

In certain embodiments, the RNA guide sequence comprises a direct repeat sequence linked to a spacer sequence. In some embodiments, the RNA guide sequence includes a direct repeat sequence and a spacer sequence or a direct repeat-spacer-direct repeat sequence. In some embodiments, the RNA guide sequence includes a truncated (i.e., processed) direct repeat sequence and a spacer sequence, which is typical of processed or mature crRNA. Exemplary direct repeat sequences (e.g., exemplary unprocessed direct repeat sequences) are provided in **Table 1**. In some embodiments, the spacer sequence comprises from about 10 nucleotides to about 60 nucleotides. Exemplary spacer sequences are provided in **Table 1**. In some embodiments, a nuclease forms a complex with the RNA guide sequence, and the RNA guide sequence directs the complex to associate with site-specific target nucleic acid that is complementary to at least a portion of the RNA guide sequence.

In some embodiments, the RNA guide sequence comprises a sequence, e.g., RNA sequence, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% complementary to a target nucleic acid sequence. In some embodiments, the RNA guide sequence comprises a sequence at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% complementary to a DNA sequence. In some embodiments, the RNA guide sequence comprises a sequence at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% complementary to a target nucleic acid sequence. In some embodiments, the RNA guide sequence comprises a sequence at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% complementary to a genomic sequence. In some embodiments, the RNA guide sequence comprises a sequence complementary to or a sequence comprising at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% complementarity to a genomic sequence.

In some embodiments, an RNA guide (e.g., the spacer of the RNA guide) of the present invention binds a target adjacent to a PAM.

In some embodiments, a nuclease described herein includes one or more (e.g., two, three, four, five, six, seven, eight, or more) RNA guide sequences, e.g., RNA guides.

In some embodiments, the RNA guide has an architecture similar to, for example, RNA guides described in International Publication Nos. WO 2014/093622 and WO 2015/070083, the entire contents of each of which are incorporated herein by reference.

In some embodiments, an RNA guide sequence of the present invention comprises a direct repeat sequence having 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% identity to any one of SEQ ID NOs: 1-3875 which is referred to as a direct repeat sequence in Column 2 of **Table 1**, or to a portion thereof. In some embodiments, an RNA guide of the present invention comprises a direct repeat sequence having greater than 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identity to, or having 100% identity to, any one of SEQ ID NOs: 1-3875 which is referred to as a direct repeat sequence in Column 2 of **Table 1**, or to a portion thereof.

In some embodiments, a CRISPR-associated protein and an RNA guide (e.g., an RNA guide comprising a direct repeat and a spacer) form a complex. In some embodiments, a CRISPR-associated protein and an RNA guide (e.g., an RNA guide comprising direct repeat-spacer-direct repeat sequence or pre-crRNA) form a complex. In some embodiments, the complex binds a target nucleic acid.

In some embodiments, the CRISPR-associated protein comprises an amino acid sequence that is at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identical to the amino acid sequence of any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1**, and the direct repeat sequence comprises a nucleotide sequence that is at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identical to the nucleotide sequence of any one of SEQ ID NOs: 1-3875 which is referred to as a direct repeat in Column 2 of **Table 1**, or to a portion of said sequence. For example, in some embodiments, the CRISPR-associated protein comprises an amino acid sequence that is at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identical to the amino acid sequence of SEQ ID NO: 1, and the direct repeat sequence comprises a nucleotide sequence that is at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identical to the nucleotide sequence of SEQ ID NO: 2 or SEQ ID NO: 3 or to a portion of the nucleotide sequence of SEQ ID NO: 2 or SEQ ID NO: 3.

Transactivating RNA (tracrRNA)

In addition to an effector protein and an RNA guide (e.g., a crRNA), some CRISPR systems also include an additional small RNA (which activates robust enzymatic activity of the effector protein) referred

to as a transactivating RNA (tracrRNA). Such tracrRNAs typically include a complementary region that hybridizes to the crRNA. The crRNA-tracrRNA hybrid forms a complex with an effector resulting in the activation of programmable enzymatic activity.

In some embodiments, the RNA guide further comprises a trans-activating RNA (tracrRNA). In some embodiments, the RNA guide forms a complex (e.g., a duplex) with the tracrRNA. In some embodiments, an RNA guide is fused to a tracrRNA. The term single-guide RNA (sgRNA) is used herein to refer to an RNA guide-tracrRNA fusion. In some embodiments, the RNA guide-tracrRNA duplex or sgRNA binds to a CRISPR-associated protein.

TracrRNA sequences can be identified by searching genomic sequences flanking CRISPR arrays for short sequence motifs that are homologous to the direct repeat portion of the crRNA. Search methods include exact or degenerate sequence matching for the complete direct repeat (DR) or DR subsequences. For example, a DR of length *n* nucleotides can be decomposed into a set of overlapping 6-10 nt kmers. These kmers can be aligned to sequences flanking a CRISPR locus, and regions of homology with 1 or more kmer alignments can be identified as DR homology regions for experimental validation as tracrRNAs. Exemplary kmers are provided in **Table 1** and referred to as "direct repeat homology" sequences and exemplary DR homology regions are provided in **Table 1** and referred to as "direct repeat homology-containing" sequences.

Alternatively, RNA cofold free energy can be calculated for the complete DR or DR subsequences and short kmer sequences from the genomic sequence flanking the elements of a CRISPR system. Flanking sequence elements with low minimum free energy structures can be identified as DR homology regions for experimental validation as tracrRNAs.

TracrRNA elements frequently occur within close proximity to CRISPR associated genes or a CRISPR array. As an alternative to searching for DR homology regions to identify tracrRNA elements, non-coding sequences flanking CRISPR associated proteins or the CRISPR array can be isolated by cloning or gene synthesis for direct experimental validation of tracrRNAs.

Experimental validation of tracrRNA elements can be performed using small RNA sequencing of the host organism for a CRISPR system or synthetic sequences expressed heterologously in non-native species. Alignment of small RNA sequences from the originating genomic locus can be used to identify expressed RNA products containing DR homology regions and sterotyped processing typical of complete tracrRNA elements.

Complete tracrRNA candidates identified by RNA sequencing can be validated *in vitro* or *in vivo* by expressing the crRNA and effector in combination with or without the tracrRNA candidate, and monitoring the activation of effector enzymatic activity.

In engineered constructs, the expression of tracrRNAs can be driven by promoters including, but not limited to U6, U1, and H1 promoters for expression in mammalian cells or J23119 promoter for expression in bacteria.

In some embodiments, a tracrRNA can be fused with a crRNA and expressed as a single RNA guide.

In some embodiments, the CRISPR-associated protein comprises an amino acid sequence that is at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identical to the amino acid sequence of any one of SEQ ID NOs: 1-3875 referred to as an effector in Column 2 of **Table 1**, and the tracrRNA sequence comprises a nucleotide sequence, or an RNA transcript thereof, having at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identity to a portion of, or to a portion of the reverse complement of, any one of SEQ ID NOs: 1-3875 referred to as a non-coding sequence in Column 2 of **Table 1**. For example, in some embodiments, the CRISPR-associated protein comprises an amino acid sequence that is at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identical to the amino acid sequence of SEQ ID NO: 1, and the tracrRNA sequence comprises a nucleotide sequence, or an RNA transcript thereof, having at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identity to a portion of SEQ ID NO: 5, or to a portion of the reverse complement of SEQ ID NO: 5. In some embodiments, the tracrRNA sequence is encoded by a nucleotide sequence having at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identity to a portion of, or to a portion of the reverse complement of, any one of SEQ ID NOs: 1-3875 referred to as a non-coding sequence in Column 2 of **Table 1**. In some embodiments, the tracrRNA sequence comprises an RNA transcript of a nucleotide sequence having at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identity to a portion of, or to a portion of the reverse complement of, any one of SEQ ID NOs: 1-3875 referred to as a non-coding sequence in Column 2 of **Table 1**.

In some embodiments, the CRISPR-associated protein comprises an amino acid sequence that is at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identical to the amino acid sequence of any one of SEQ ID NOs: 1-3875 referred to as an effector in Column 2 of **Table 1**, and the tracrRNA sequence comprises a nucleotide sequence, or an RNA transcript thereof, having at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identity to any one of SEQ ID NOs: 1-3875 referred to as a direct repeat homology-containing sequence in Column 2 of **Table 1**, to a

portion thereof, to the reverse complement thereof, or to a portion of the reverse complement thereof. For example, in some embodiments, the CRISPR-associated protein comprises an amino acid sequence that is at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identical to the amino acid sequence of SEQ ID NO: 11, and the tracrRNA sequence comprises a nucleotide sequence, or an RNA transcript thereof, having at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identity to SEQ ID NO: 18, to a portion of SEQ ID NO: 18, to the reverse complement of SEQ ID NO: 18, or to a portion of the reverse complement of SEQ ID NO: 18. In some embodiments, the tracrRNA sequence is encoded by a nucleotide sequence having at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identity to any one of SEQ ID NOs: 1-3875 referred to as a direct repeat homology-containing sequence in Column 2 of **Table 1**, to a portion thereof, to the reverse complement thereof, or to a portion of the reverse complement thereof. In some embodiments, the tracrRNA sequence comprises an RNA transcript of a nucleotide sequence having at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identity to any one of SEQ ID NOs: 1-3875 referred to as a direct repeat homology-containing sequence in Column 2 of **Table 1**, to a portion thereof, to the reverse complement thereof, or to a portion of the reverse complement thereof.

In some embodiments, the CRISPR-associated protein comprises an amino acid sequence that is at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identical to the amino acid sequence of any one of SEQ ID NOs: 1-3875 referred to as an effector in Column 2 of **Table 1**, and the tracrRNA sequence comprises a nucleotide sequence having at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identity to any one or more of SEQ ID NOs: 1-3875 referred to as a direct repeat homology sequence in Column 2 of **Table 1**. For example, in some embodiments, the CRISPR-associated protein comprises an amino acid sequence that is at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identical to the amino acid sequence of SEQ ID NO: 11, and the tracrRNA sequence comprises a nucleotide sequence having at least 80% (e.g., 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%) identity to SEQ ID NO: 16 and/or SEQ ID NO: 17.

Novel RNA Modulators of Enzymatic Activity

In addition to the effector protein and an RNA guide (e.g., a crRNA), some CRISPR systems may also include an additional small RNA to activate or modulate the effector activity, referred to herein as an RNA modulator.

RNA modulators are expected to occur within close proximity to CRISPR-associated genes or a CRISPR array. To identify and validate RNA modulators, non-coding sequences flanking CRISPR-associated proteins or the CRISPR array can be isolated by cloning or gene synthesis for direct experimental validation.

Experimental validation of RNA modulators can be performed using small RNA sequencing of the host organism for a CRISPR system or synthetic sequences expressed heterologously in non-native species. Alignment of small RNA sequences to the originating genomic locus can be used to identify expressed RNA products containing DR homology regions and sterotyped processing.

Candidate RNA modulators identified by RNA sequencing can be validated *in vitro* or *in vivo* by expressing a crRNA and an effector in combination with or without the candidate RNA modulator and monitoring alterations in effector enzymatic activity.

In engineered constructs, RNA modulators can be driven by promoters including U6, U1, and H1 promoters for expression in mammalian cells, or J23119 promoter for expression in bacteria.

In some embodiments, the RNA modulators can be artificially fused with either a crRNA, a tracrRNA, or both and expressed as a single RNA element.

In some embodiments wherein an effector of the present invention forms a dimer, the dimer forms a complex with one or more RNA guide sequences. In some embodiments wherein an effector of the present invention forms a dimer, the dimer forms a complex with one or more tracrRNA sequences. In some embodiments, the dimer forms a complex with one tracrRNA sequence and one RNA guide sequence. In some embodiments, the dimer forms a complex with one tracrRNA sequence and two RNA guide sequences. In some embodiments, the dimer forms a complex with two tracrRNA sequences and one RNA guide sequence. In some embodiments, the dimer forms a complex with two tracrRNA sequences and two RNA guide sequences. In some embodiments, the dimer forms a complex with one sgRNA sequence. In some embodiments, the dimer forms a complex with two sgRNA sequences.

In some embodiments, a homodimer comprising two identical RuvC domains forms a complex with one tracrRNA sequence and one RNA guide sequence. In some embodiments, a heterodimer comprising two non-identical RuvC domains forms a complex with one tracrRNA sequence and one RNA guide sequence. In some embodiments, a homodimer comprising two identical RuvC domains forms a complex with one tracrRNA sequence and two RNA guide sequences. In some embodiments, a heterodimer comprising two non-identical RuvC domains forms a complex with one tracrRNA sequence and two RNA guide sequences. In some embodiments, a homodimer comprising two identical RuvC domains forms a

complex with two tracrRNA sequences and one RNA guide sequence. In some embodiments, a heterodimer comprising two non-identical RuvC domains forms a complex with two tracrRNA sequences and one RNA guide sequence. In some embodiments, a homodimer comprising two identical RuvC domains forms a complex with two tracrRNA sequences and two RNA guide sequences. In some embodiments, a heterodimer comprising two non-identical RuvC domains forms a complex with two tracrRNA sequences and two RNA guide sequences. In some embodiments, a homodimer comprising two identical RuvC domains forms a complex with one sgRNA sequence. In some embodiments, a heterodimer comprising two non-identical RuvC domains forms a complex with one sgRNA sequence. In some embodiments, a homodimer comprising two identical RuvC domains forms a complex with two sgRNA sequences. In some embodiments, a heterodimer comprising two non-identical RuvC domains forms a complex with two sgRNA sequences.

Unless otherwise noted, all compositions and nucleases provided herein are made in reference to the active level of that composition or nuclease, and are exclusive of impurities, for example, residual solvents or by-products, which may be present in commercially available sources. Nuclease component weights are based on total active protein. All percentages and ratios are calculated by weight unless otherwise indicated. All percentages and ratios are calculated based on the total composition unless otherwise indicated. In the exemplified composition, the nuclease levels are expressed by pure enzyme by weight of the total composition and unless otherwise specified, the ingredients are expressed by weight of the total compositions.

Modifications

The RNA guide sequence, tracrRNA sequence, sgRNA sequence, or any of the nucleic acid sequences encoding a nuclease may include one or more covalent modifications with respect to a reference sequence, in particular the parent polyribonucleotide, which are included within the scope of this invention.

Exemplary modifications can include any modification to the sugar, the nucleobase, the internucleoside linkage (e.g. to a linking phosphate/to a phosphodiester linkage/to the phosphodiester backbone), and any combination thereof. Some of the exemplary modifications provided herein are described in detail below.

The RNA guide sequence, tracrRNA sequence, sgRNA sequence, or any of the nucleic acid sequences encoding components of a nuclease may include any useful modification, such as to the sugar, the nucleobase, or the internucleoside linkage (e.g. to a linking phosphate/to a phosphodiester linkage/to the phosphodiester backbone). One or more atoms of a pyrimidine nucleobase may be replaced or substituted with optionally substituted amino, optionally substituted thiol, optionally substituted alkyl (e.g., methyl or ethyl), or halo (e.g., chloro or fluoro). In certain embodiments, modifications (e.g., one or more

modifications) are present in each of the sugar and the internucleoside linkage. Modifications may be modifications of ribonucleic acids (RNAs) to deoxyribonucleic acids (DNAs), threose nucleic acids (TNAs), glycol nucleic acids (GNAs), peptide nucleic acids (PNAs), locked nucleic acids (LNAs) or hybrids thereof). Additional modifications are described herein.

In some embodiments, the modification may include a chemical or cellular induced modification. For example, some nonlimiting examples of intracellular RNA modifications are described by Lewis and Pan in "RNA modifications and structures cooperate to guide RNA-protein interactions" from Nat Reviews Mol Cell Biol, 2017, 18:202-210.

Different sugar modifications, nucleotide modifications, and/or internucleoside linkages (e.g., backbone structures) may exist at various positions in the sequence. One of ordinary skill in the art will appreciate that the nucleotide analogs or other modification(s) may be located at any position(s) of the sequence, such that the function of the sequence is not substantially decreased. The sequence may include from about 1% to about 100% modified nucleotides (either in relation to overall nucleotide content, or in relation to one or more types of nucleotide, i.e. any one or more of A, G, U or C) or any intervening percentage (e.g., from 1% to 20%>, from 1% to 25%, from 1% to 50%, from 1% to 60%, from 1% to 70%, from 1% to 80%, from 1% to 90%, from 1% to 95%, from 10% to 20%, from 10% to 25%, from 10% to 50%, from 10% to 60%, from 10% to 70%, from 10% to 80%, from 10% to 90%, from 10% to 95%, from 10% to 100%, from 20% to 25%, from 20% to 50%, from 20% to 60%, from 20% to 70%, from 20% to 80%, from 20% to 90%, from 20% to 95%, from 20% to 100%, from 50% to 60%, from 50% to 70%, from 50% to 80%, from 50% to 90%, from 50% to 95%, from 50% to 100%, from 70% to 80%, from 70% to 90%, from 70% to 95%, from 70% to 100%, from 80% to 90%, from 80% to 95%, from 80% to 100%, from 90% to 95%, from 90% to 100%, and from 95% to 100%).

In some embodiments, sugar modifications (e.g., at the 2' position or 4' position) or replacement of the sugar at one or more ribonucleotides of the sequence may, as well as backbone modifications, include modification or replacement of the phosphodiester linkages. Specific examples of a sequence include, but are not limited to, sequences including modified backbones or no natural internucleoside linkages such as internucleoside modifications, including modification or replacement of the phosphodiester linkages. Sequences having modified backbones include, among others, those that do not have a phosphorus atom in the backbone. For the purposes of this application, and as sometimes referenced in the art, modified RNAs that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides. In particular embodiments, a sequence will include ribonucleotides with a phosphorus atom in its internucleoside backbone.

Modified sequence backbones may include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other

alkyl phosphonates such as 3'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates such as 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included. In some embodiments, the sequence may be negatively or positively charged.

The modified nucleotides, which may be incorporated into the sequence, can be modified on the internucleoside linkage (e.g., phosphate backbone). Herein, in the context of the polynucleotide backbone, the phrases "phosphate" and "phosphodiester" are used interchangeably. Backbone phosphate groups can be modified by replacing one or more of the oxygen atoms with a different substituent. Further, the modified nucleosides and nucleotides can include the wholesale replacement of an unmodified phosphate moiety with another internucleoside linkage as described herein. Examples of modified phosphate groups include, but are not limited to, phosphorothioate, phosphoroselenates, boranophosphates, boranophosphate esters, hydrogen phosphonates, phosphoramidates, phosphorodiamidates, alkyl or aryl phosphonates, and phosphotriesters. Phosphorodithioates have both non-linking oxygens replaced by sulfur. The phosphate linker can also be modified by the replacement of a linking oxygen with nitrogen (bridged phosphoramidates), sulfur (bridged phosphorothioates), and carbon (bridged methylene-phosphonates).

The α-thio substituted phosphate moiety is provided to confer stability to RNA and DNA polymers through the unnatural phosphorothioate backbone linkages. Phosphorothioate DNA and RNA have increased nuclease resistance and subsequently a longer half-life in a cellular environment.

In specific embodiments, a modified nucleoside includes an alpha-thio-nucleoside (e.g., 5'-*O*-(1-thiophosphate)-adenosine, 5'-*O*-(1-thiophosphate)-cytidine (a-thio-cytidine), 5'-*O*-(1-thiophosphate)-guanosine, 5'-*O*-(1-thiophosphate)-uridine, or 5'-*O*-(1-thiophosphate)-pseudouridine).

Other internucleoside linkages that may be employed according to the present invention, including internucleoside linkages which do not contain a phosphorous atom, are described herein.

In some embodiments, the sequence may include one or more cytotoxic nucleosides. For example, cytotoxic nucleosides may be incorporated into sequence, such as bifunctional modification. Cytotoxic nucleoside may include, but are not limited to, adenosine arabinoside, 5-azacytidine, 4'-thio-aracytidine, cyclopentenylcytosine, cladribine, clofarabine, cytarabine, cytosine arabinoside, 1-(2-C-cyano-2-deoxy-beta-D-arabino-pentofuranosyl)-cytosine, decitabine, 5-fluorouracil, fludarabine, floxuridine, gemcitabine, a combination of tegafur and uracil, tegafur ((RS)-5-fluoro-1-(tetrahydrofuran-2-yl)pyrimidine-2,4(1H,3H)-dione), troxacitabine, tezacitabine, 2'-deoxy-2'-methylidenecytidine (DMDC), and 6-mercaptopurine. Additional examples include fludarabine phosphate, N4-behenoyl-1-beta-D-

arabinofuranosylcytosine, N4-octadecyl-1-beta-D-arabinofuranosylcytosine, N4-palmitoyl-1-(2-C-cyano-2-deoxy-beta-D-arabino-pentofuranosyl) cytosine, and P-4055 (cytarabine 5'-elaidic acid ester).

In some embodiments, the sequence includes one or more post-transcriptional modifications (e.g., capping, cleavage, polyadenylation, splicing, poly-A sequence, methylation, acylation, phosphorylation, methylation of lysine and arginine residues, acetylation, and nitrosylation of thiol groups and tyrosine residues, etc.). The one or more post-transcriptional modifications can be any post-transcriptional modification, such as any of the more than one hundred different nucleoside modifications that have been identified in RNA (Rozenski, J, Crain, P, and McCloskey, J. (1999). The RNA Modification Database: 1999 update. Nucl Acids Res 27: 196-197) In some embodiments, the first isolated nucleic acid comprises messenger RNA (mRNA). In some embodiments, the mRNA comprises at least one nucleoside selected from the group consisting of pyridin-4-one ribonucleoside, 5-aza-uridine, 2-thio-5-aza-uridine, 2-thiouridine, 4-thio-pseudouridine, 2-thio-pseudouridine, 5-hydroxyuridine, 3-methyluridine, 5-carboxymethyl-uridine, 1-carboxymethyl-pseudouridine, 5-propynyl-uridine, 1-propynyl-pseudouridine, 5-taurinomethyluridine, 1-taurinomethyl-pseudouridine, 5-taurinomethyl-2-thio-uridine, 1-taurinomethyl-4-thio-uridine, 5-methyl-uridine, 1-methyl-pseudouridine, 4-thio-1-methyl-pseudouridine, 2-thio-1-methyl-pseudouridine, 1-methyl-1-deaza-pseudouridine, 2-thio-1-methyl-1-deaza-pseudouridine, dihydrouridine, dihydropseudouridine, 2-thio-dihydrouridine, 2-thio-dihydropseudouridine, 2-methoxyuridine, 2-methoxy-4-thio-uridine, 4-methoxy-pseudouridine, and 4-methoxy-2-thio-pseudouridine. In some embodiments, the mRNA comprises at least one nucleoside selected from the group consisting of 5-aza-cytidine, pseudoisocytidine, 3-methyl-cytidine, N4-acetylcytidine, 5-formylcytidine, N4-methylcytidine, 5-hydroxymethylcytidine, 1-methyl-pseudoisocytidine, pyrrolo-cytidine, pyrrolo-pseudoisocytidine, 2-thio-cytidine, 2-thio-5-methyl-cytidine, 4-thio-pseudoisocytidine, 4-thio-1-methyl-pseudoisocytidine, 4-thio-1-methyl-1-deaza-pseudoisocytidine, 1-methyl-1-deaza-pseudoisocytidine, zebularine, 5-aza-zebularine, 5-methyl-zebularine, 5-aza-2-thio-zebularine, 2-thio-zebularine, 2-methoxy-cytidine, 2-methoxy-5-methyl-cytidine, 4-methoxy-pseudoisocytidine, and 4-methoxy-1-methyl-pseudoisocytidine. In some embodiments, the mRNA comprises at least one nucleoside selected from the group consisting of 2-aminopurine, 2, 6-diaminopurine, 7-deaza-adenine, 7-deaza-8-aza-adenine, 7-deaza-2-aminopurine, 7-deaza-8-aza-2-aminopurine, 7-deaza-2,6-diaminopurine, 7-deaza-8-aza-2,6-diaminopurine, 1-methyladenosine, N6-methyladenosine, N6-isopentenyladenosine, N6-(cis-hydroxyisopentenyl)adenosine, 2-methylthio-N6-(cis-hydroxyisopentenyl) adenosine, N6-glycinylcarbamoyladenosine, N6-threonylcarbamoyladenosine, 2-methylthio-N6-threonyl carbamoyladenosine, N6,N6-dimethyladenosine, 7-methyladenine, 2-methylthio-adenine, and 2-methoxy-adenine. In some embodiments, mRNA comprises at least one nucleoside selected from the group consisting of inosine, 1-methyl-inosine, wyosine, wybutosine, 7-deaza-guanosine, 7-deaza-8-aza-

guanosine, 6-thio-guanosine, 6-thio-7-deaza-guanosine, 6-thio-7-deaza-8-aza-guanosine, 7-methyl-guanosine, 6-thio-7-methyl-guanosine, 7-methylinosine, 6-methoxy-guanosine, 1-methylguanosine, N2-methylguanosine, N2,N2-dimethylguanosine, 8-oxo-guanosine, 7-methyl-8-oxo-guanosine, 1-methyl-6-thio-guanosine, N2-methyl-6-thio-guanosine, and N2,N2-dimethyl-6-thio-guanosine.

The sequence may or may not be uniformly modified along the entire length of the molecule. For example, one or more or all types of nucleotide (e.g., naturally-occurring nucleotides, purine or pyrimidine, or any one or more or all of A, G, U, C, I, pU) may or may not be uniformly modified in the sequence, or in a given predetermined sequence region thereof. In some embodiments, the sequence includes a pseudouridine. In some embodiments, the sequence includes an inosine, which may aid in the immune system characterizing the sequence as endogenous versus viral RNAs. The incorporation of inosine may also mediate improved RNA stability/reduced degradation. See for example, Yu, Z. et al. (2015) RNA editing by ADAR1 marks dsRNA as "self". Cell Res. 25, 1283-1284, which is incorporated by reference in its entirety.

VECTORS

The present invention provides a vector for expressing a nuclease described herein or nucleic acids encoding a nuclease described herein may be incorporated into a vector. In some embodiments, a vector of the invention includes a nucleotide sequence encoding a nuclease described herein. In some embodiments, a vector of the invention includes a nucleotide sequence encoding a nuclease described herein.

The present invention also provides a vector that may be used for preparation of a nuclease described herein or compositions comprising a nuclease described herein. In some embodiments, the invention includes the composition or vector described herein in a cell. In some embodiments, the invention includes a method of expressing the composition comprising a nuclease of the present invention, or vector or nucleic acid encoding the nuclease, in a cell. The method may comprise the steps of providing the composition, e.g., vector or nucleic acid, and delivering the composition to the cell.

Expression of natural or synthetic polynucleotides is typically achieved by operably linking a polynucleotide encoding the gene of interest, e.g., nucleotide sequence encoding a nuclease of the present invention, to a promoter and incorporating the construct into an expression vector. The expression vector is not particularly limited as long as it includes a polynucleotide encoding a nuclease of the present invention and can be suitable for replication and integration in eukaryotic cells.

Typical expression vectors include transcription and translation terminators, initiation sequences, and promoters useful for expression of the desired polynucleotide. For example, plasmid vectors carrying a recognition sequence for RNA polymerase (pSP64, pBluescript, etc.). may be used. Vectors including

those derived from retroviruses such as lentivirus are suitable tools to achieve long-term gene transfer since they allow long-term, stable integration of a transgene and its propagation in daughter cells. Examples of vectors include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. The expression vector may be provided to a cell in the form of a viral vector.

Viral vector technology is well known in the art and described in a variety of virology and molecular biology manuals. Viruses which are useful as vectors include, but are not limited to phage viruses, retroviruses, adenoviruses, adeno-associated viruses, herpes viruses, and lentiviruses. In general, a suitable vector contains an origin of replication functional in at least one organism, a promoter sequence, convenient restriction endonuclease sites, and one or more selectable markers.

The kind of the vector is not particularly limited, and a vector that can be expressed in host cells can be appropriately selected. To be more specific, depending on the kind of the host cell, a promoter sequence to ensure the expression of a nuclease of the present invention from a polynucleotide is appropriately selected, and this promoter sequence and the polynucleotide are inserted into any of various plasmids etc. for preparation of the expression vector.

Additional promoter elements, e.g., enhancing sequences, regulate the frequency of transcriptional initiation. Typically, these are located in the region 30-110 bp upstream of the start site, although a number of promoters have recently been shown to contain functional elements downstream of the start site as well. Depending on the promoter, it appears that individual elements can function either cooperatively or independently to activate transcription.

Further, the disclosure should not be limited to the use of constitutive promoters. Inducible promoters are also contemplated as part of the disclosure. The use of an inducible promoter provides a molecular switch capable of turning on expression of the polynucleotide sequence which it is operatively linked when such expression is desired or turning off the expression when expression is not desired. Examples of inducible promoters include, but are not limited to a metallothionine promoter, a glucocorticoid promoter, a progesterone promoter, and a tetracycline promoter.

The expression vector to be introduced can also contain either a selectable marker gene or a reporter gene or both to facilitate identification and selection of expressing cells from the population of cells sought to be transfected or infected through viral vectors. In other aspects, the selectable marker may be carried on a separate piece of DNA and used in a co-transfection procedure. Both selectable markers and reporter genes may be flanked with appropriate transcriptional control sequences to enable expression in the host cells. Examples of such a marker include a dihydrofolate reductase gene and a neomycin resistance gene for eukaryotic cell culture; and a tetracycline resistance gene and an ampicillin resistance gene for culture of *E. coli* and other bacteria. By use of such a selection marker, it can be confirmed whether the

polynucleotide encoding a nuclease of the present invention has been transferred into the host cells and then expressed without fail.

The preparation method for recombinant expression vectors is not particularly limited, and examples thereof include methods using a plasmid, a phage or a cosmid.

CELLS

The nucleases described herein can be introduced into a variety of cells. In some embodiments, the cell is an isolated cell. In some embodiments the cell is in cell culture. In some embodiments, the cell is ex vivo. In some embodiments, the cell is obtained from a living organism, and maintained in a cell culture. In some embodiments, the cell is a single-cellular organism.

In some embodiments, the cell is a prokaryotic cell. In some embodiments, the cell is a bacterial cell or derived from a bacterial cell. In some embodiments, the cell is an archaeal cell or derived from an archaeal cell.

In some embodiments, the cell is a eukaryotic cell. In some embodiments, the cell is a plant cell or derived from a plant cell. In some embodiments, the cell is a fungal cell or derived from a fungal cell. In some embodiments, the cell is an animal cell or derived from an animal cell. In some embodiments, the cell is an invertebrate cell or derived from an invertebrate cell. In some embodiments, the cell is a vertebrate cell or derived from a vertebrate cell. In some embodiments, the cell is a mammalian cell or derived from a mammalian cell. In some embodiments, the cell is a human cell. In some embodiments, the cell is a zebra fish cell. In some embodiments, the cell is a rodent cell. In some embodiments, the cell is synthetically made, sometimes termed an artificial cell.

In some embodiments, the cell is derived from a cell line. A wide variety of cell lines for tissue culture are known in the art. Examples of cell lines include, but are not limited to, 293T, MF7, K562, HeLa, and transgenic varieties thereof. Cell lines are available from a variety of sources known to those with skill in the art (see, e.g., the American Type Culture Collection (ATCC) (Manassas, Va.)). In some embodiments, a cell transfected with one or more nucleic acids (such as nuclease polypeptide encoding vector and RNA guide) is used to establish a new cell line comprising one or more vector-derived sequences to establish a new cell line comprising modification to the target nucleic acid or target locus. In some embodiments, the cell is an immortal or immortalized cell.

In some embodiments, the method comprises introducing into a host cell one or more nucleic acids comprising nucleotide sequences encoding a DNA-targeting RNA (e.g., RNA guide) and/or the nuclease. In one embodiment, a cell comprising a target DNA is in vitro, in vivo, or ex vivo. In other embodiments, nucleic acids comprising nucleotide sequences encoding a DNA-targeting RNA (e.g., RNA guide) and/or

the nuclease include recombinant expression vectors e.g., including but not limited to adeno-associated virus constructs, recombinant adenoviral constructs, recombinant lentiviral constructs, recombinant retroviral constructs, and the like.

In some embodiments, the cell is a primary cell. In some embodiments, the cell is a stem cell such as a totipotent stem cell (e.g., omnipotent), a pluripotent stem cell, a multipotent stem cell, an oligopotent stem cell, or an unipotent stem cell. In some embodiments, the cell is an induced pluripotent stem cell (iPSC) or derived from an iPSC. In some embodiments, the cell is a differentiated cell. For example, in some embodiments, the differentiated cell is a muscle cell (e.g., a myocyte), a fat cell (e.g., an adipocyte), a bone cell (e.g., an osteoblast, osteocyte, osteoclast), a blood cell (e.g., a monocyte, a lymphocyte, a neutrophil, an eosinophil, a basophil, a macrophage, a erythrocyte, or a platelet), a nerve cell (e.g., a neuron), an epithelial cell, an immune cell (e.g., a lymphocyte, a neutrophil, a monocyte, or a macrophage), a liver cell (e.g., a hepatocyte), a fibroblast, or a sex cell. In some embodiments, the cell is a terminally differentiated cell. For example, in some embodiments, the terminally differentiated cell is a neuronal cell, an adipocyte, a cardiomyocyte, a skeletal muscle cell, an epidermal cell, or a gut cell. In some embodiments, the cell is a mammalian cell, e.g., a human cell or a murine cell. In some embodiments, the murine cell is derived from a wild-type mouse, an immunosuppressed mouse, or a disease-specific mouse model.

In some embodiments, a method for modifying a target DNA molecule in a cell is provided. The method comprises contacting the target DNA molecule inside of a cell with a nuclease described herein; and a single molecule DNA-targeting RNA comprising, in 5' to 3' order, a first nucleotide segment that hybridizes with a target sequence of the target DNA molecule; a nucleotide linker; and a second nucleotide segment that hybridizes with the first nucleotide segment to form a double-stranded RNA duplex. The variant polypeptide forms a complex with the single molecule DNA-targeting RNA inside the cell and the target DNA molecule is modified.

PREPARATION

In some embodiments, a nuclease of the present invention can be prepared by (I) culturing bacteria which produce a nuclease of the present invention, isolating the nuclease, and optionally, purifying the nuclease. The nuclease can be also prepared by (II) a known genetic engineering technique, specifically, by isolating a gene encoding a nuclease of the present invention from bacteria, constructing a recombinant expression vector, and then transferring the vector into an appropriate host cell for expression of a recombinant protein. Alternatively, a nuclease can be prepared by (III) an *in vitro* coupled transcription-translation system. Bacteria that can be used for preparation of a nuclease of the present invention are not

particularly limited as long as they can produce a nuclease of the present invention. Some non-limiting examples of the bacteria include *E. coli* cells described herein.

Methods of Expression

The present invention includes a method for protein expression, comprising translating a nuclease described herein.

In some embodiments, a host cell described herein is used to express a nuclease. The host cell is not particularly limited, and various known cells can be preferably used. Specific examples of the host cell include bacteria such as *E. coli*, yeasts (budding yeast, *Saccharomyces cerevisiae*, and fission yeast, *Schizosaccharomyces pombe*), nematodes (*Caenorhabditis elegans*), *Xenopus laevis* oocytes, and animal cells (for example, CHO cells, COS cells and HEK293 cells). The method for transferring the expression vector described above into host cells, i.e., the transformation method, is not particularly limited, and known methods such as electroporation, the calcium phosphate method, the liposome method and the DEAE dextran method can be used.

After a host is transformed with the expression vector, the host cells may be cultured, cultivated or bred, for production of a nuclease. After expression of the nuclease, the host cells can be collected and nuclease purified from the cultures etc. according to conventional methods (for example, filtration, centrifugation, cell disruption, gel filtration chromatography, ion exchange chromatography, etc.).

In some embodiments, the methods for nuclease expression comprises translation of at least 5 amino acids, at least 10 amino acids, at least 15 amino acids, at least 20 amino acids, at least 50 amino acids, at least 100 amino acids, at least 150 amino acids, at least 200 amino acids, at least 250 amino acids, at least 300 amino acids, at least 400 amino acids, at least 500 amino acids, at least 600 amino acids, at least 700 amino acids, at least 800 amino acids, at least 900 amino acids, or at least 1000 amino acids of a nuclease. In some embodiments, the methods for protein expression comprises translation of about 5 amino acids, about 10 amino acids, about 15 amino acids, about 20 amino acids, about 50 amino acids, about 100 amino acids, about 150 amino acids, about 200 amino acids, about 250 amino acids, about 300 amino acids, about 400 amino acids, about 500 amino acids, about 600 amino acids, about 700 amino acids, about 800 amino acids, about 900 amino acids, about 1000 amino acids or more of a nuclease.

A variety of methods can be used to determine the level of production of a mature nuclease in a host cell. Such methods include, but are not limited to, for example, methods that utilize either polyclonal or monoclonal antibodies specific for a nuclease. Exemplary methods include, but are not limited to, enzyme-linked immunosorbent assays (ELISA), radioimmunoassays (MA), fluorescent immunoassays (FIA), and fluorescent activated cell sorting (FACS). These and other assays are well known in the art (See, e.g., Maddox et al., J. Exp. Med. 158:1211 [1983]).

The present disclosure provides methods of *in vivo* expression of a nuclease in a cell, comprising providing a polyribonucleotide encoding the nuclease to a host cell wherein the polyribonucleotide encodes the nuclease, expressing the nuclease in the cell, and obtaining the nuclease from the cell.

DELIVERY

Nucleases, RNA guides, tracrRNA sequences, sgRNA sequences, and/or compositions described herein may be formulated, for example, including a carrier, such as a carrier and/or a polymeric carrier, e.g., a liposome, and delivered by known methods to a cell (e.g., a prokaryotic, eukaryotic, plant, mammalian, etc.). Such methods include, but not limited to, transfection (e.g., lipid-mediated, cationic polymers, calcium phosphate, dendrimers); electroporation or other methods of membrane disruption (e.g., nucleofection), viral delivery (e.g., lentivirus, retrovirus, adenovirus, AAV), microinjection, microprojectile bombardment ("gene gun"), fugene, direct sonic loading, cell squeezing, optical transfection, protoplast fusion, impalefection, magnetofection, exosome-mediated transfer, lipid nanoparticle-mediated transfer, and any combination thereof.

In some embodiments, the method comprises delivering one or more nucleic acids (e.g., nucleic acids encoding a nuclease, RNA guide, donor DNA, etc.), one or more transcripts thereof, and/or a pre-formed nuclease/RNA guide complex to a cell. Exemplary intracellular delivery methods, include, but are not limited to: viruses or virus-like agents; chemical-based transfection methods, such as those using calcium phosphate, dendrimers, liposomes, or cationic polymers (e.g., DEAE-dextran or polyethylenimine); non-chemical methods, such as microinjection, electroporation, cell squeezing, sonoporation, optical transfection, impalefection, protoplast fusion, bacterial conjugation, delivery of plasmids or transposons; particle-based methods, such as using a gene gun, magnectofection or magnet assisted transfection, particle bombardment; and hybrid methods, such as nucleofection. In some embodiments, the present application further provides cells produced by such methods, and organisms (such as animals, plants, or fungi) comprising or produced from such cells.

KITS

The invention also provides kits that can be used, for example, to carry out a method described herein. In some embodiments, the kits include a nuclease of the present invention. In some embodiments, the kits include a polynucleotide that encodes such a nuclease, and optionally the polynucleotide is comprised within a vector, *e.g.,* as described herein. The kits also can optionally include an RNA guide, *e.g.,* as described herein. The RNA guide of the kits of the invention can be designed to target a sequence of interest, as is known in the art. The nuclease and the RNA guide can be packaged within the same vial

or other vessel within a kit or can be packaged in separate vials or other vessels, the contents of which can be mixed prior to use. The kits can additionally include, optionally, a buffer and/or instructions for use of the nuclease and/or RNA guide.

All references and publications cited herein are hereby incorporated by reference.

EXAMPLES

The following examples are provided to further illustrate some embodiments of the present invention but are not intended to limit the scope of the invention; it will be understood by their exemplary nature that other procedures, methodologies, or techniques known to those skilled in the art may alternatively be used.

Example 1 – Expression of Effectors in *E. coli*

In this Example, a system individually comprising an effector of any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1** is engineered and introduced into *E. coli*.

For each effector, a polynucleotide encoding the effector is *E. coli* codon-optimized, synthesized (Genscript), and individually cloned into a custom expression system derived from pET-28a(+) (EMD-Millipore). The vector includes a polynucleotide encoding each effector under the control of a *lac* promoter and an *E. coli* ribosome binding sequence. The vector also includes sites for a tracrRNA and an RNA guide or a sgRNA as described herein following the open reading frame for the effector. Plasmid configurations are shown in **Table 2**. The spacers are designed to target sequences of a pACYC184 plasmid and *E. coli* essential genes.

Table 2. Bacterial Plasmids.

Configuration
Effector-non-coding RNA-full length DR-spacer-full length DR
Effector-non-coding RNA-mature DR-spacer
Effector-TracrRNA-full length DR-spacer-full length DR
Effector-TracrRNA-mature DR-spacer
Effector-TracrRNA-sgRNA
Effector-sgRNA

The plasmids described in **Table 2** are electroporated into E. Cloni electrocompetent *E. coli* (Lucigen). The plasmids are either co-transformed with purified pACYC184 plasmid or directly transformed into pACYC184-containing E. Cloni electrocompetent *E. coli* (Lucigen), plated onto agar containing the proper antibiotics, and incubated for 10-12 hours at 37 °C.

A proxy for activity of the engineered effector systems in *E. coli* is investigated, wherein bacterial cell death is used as the proxy for system activity. An active effector associated with an RNA guide and tracrRNA or with an sgRNA can disrupt expression of a spacer sequence target, e.g., a pACYC184 plasmid sequence or an *E. coli* essential gene, resulting in cell death. Using this proxy, the ability of the effectors disclosed herein can be determined in *E. coli*.

Example 2 – Expression of Effectors in Mammalian Cells

This Example describes an indel assessment on mammalian targets by the effector of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1** introduced into mammalian cells by transient transfection.

The effectors of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1** are individually cloned into a pcda3.1 backbone (Invitrogen). The plasmids are then maxi-prepped and diluted to 1 μg/μL. The sgRNA sequences are further individually cloned into a plasmid, purified, and diluted. Targets are selected to be adjacent to PAM sequences for effectors for which a PAM sequence is required.

Approximately 16 hours prior to transfection, 100 μl of 25,000 HEK293T cells in DMEM/10%FBS+Pen/Strep are plated into each well of a 96-well plate. On the day of transfection, the cells are 70-90% confluent. For each well to be transfected, a mixture of 0.5 μl of Lipofectamine 2000 and 9.5 μl of Opti-MEM is prepared and then incubated at room temperature for 5-20 minutes (Solution 1). After incubation, the lipofectamine:OptiMEM mixture is added to a separate mixture containing 182 ng of effector plasmid and 14 ng of sgRNA and water up to 10 μL (Solution 2). In the case of negative controls, the sgRNA is not included in Solution 2. The solution 1 and solution 2 mixtures are mixed by pipetting up and down and then incubated at room temperature for 25 minutes. Following incubation, 20 μL of the Solution 1 and Solution 2 mixture are added dropwise to each well of a 96 well plate containing the cells. 72 hours post transfection, cells are trypsinized by adding 10 μL of TrypLE to the center of each well and incubated for approximately 5 minutes. 100 μL of D10 media is then added to each well and mixed to

resuspend cells. The cells are then spun down at 500g for 10 minutes, and the supernatant is discarded. QuickExtract buffer is added to 1/5 the amount of the original cell suspension volume. Cells are incubated at 65°C for 15 minutes, 68°C for 15 minutes, and 98°C for 10 minutes.

Samples for Next Generation Sequencing are prepared by two rounds of PCR. The first round (PCR1) is used to amplify specific genomic regions depending on the target. PCR1 products are purified by column purification. Round 2 PCR (PCR2) is done to add Illumina adapters and indexes. Reactions are then pooled and purified by column purification. Sequencing runs are done with a 150 cycle NextSeq v2.5 mid or high output kit.

Presence of indels at the analyzed targets, as determined by NGS, are indicative of mammalian activity of the effectors of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of **Table 1**.

Enumerated Embodiments

The following enumerated embodiments are provided, the numbering of which is not to be construed as designating levels of importance.

Enumerated embodiment 1 provides a composition comprising:

(a) a nuclease or a nucleic acid encoding the nuclease, wherein the nuclease comprises an amino acid sequence with at least 80% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1; and

(b) an RNA guide or a nucleic acid encoding the RNA guide, wherein the RNA guide comprises a direct repeat sequence and a spacer sequence,

wherein the nuclease binds to the RNA guide, and wherein the spacer sequence binds to a target nucleic acid.

Enumerated embodiment 2 provides the composition of enumerated embodiment 1, wherein the nuclease comprises a RuvC domain or a split RuvC domain.

Enumerated embodiment 3 provides the composition of any previous enumerated embodiment, wherein the nuclease comprises a catalytic residue.

Enumerated embodiment 4 provides the composition of enumerated embodiment 3, wherein the catalytic residue is aspartic acid or glutamic acid.

Enumerated embodiment 5 provides the composition of any previous enumerated embodiment, wherein the nuclease comprises an amino acid sequence with at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1.

Enumerated embodiment 6 provides the composition of any previous enumerated embodiment, wherein the nuclease comprises an amino acid sequence with at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1 and the direct repeat sequence comprises a nucleotide sequence with at least 90% or at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as a direct repeat in Column 2 of Table 1, or to a portion of any one of SEQ ID NOs: 1-3875 which is referred to as a direct repeat in Column 2 of Table 1.

Enumerated embodiment 7 provides the composition of any previous enumerated embodiment, wherein the RNA guide further comprises a trans-activating crRNA (tracrRNA) sequence.

Enumerated embodiment 8 provides the composition of any previous enumerated embodiment, wherein the nuclease comprises an amino acid sequence with at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1 and the tracrRNA sequence comprises a nucleotide sequence, or an RNA transcript thereof, with at least 90% or at least 95% identity to a portion of any one of SEQ ID NOs: 1-3875 which is referred to as a non-coding sequence in Column 2 of Table 1, to the reverse complement thereof, or to a portion of the reverse complement thereof.

Enumerated embodiment 9 provides the composition of any previous enumerated embodiment, wherein the nuclease comprises an amino acid sequence with at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1 and the tracrRNA sequence comprises a nucleotide sequence, or an RNA transcript thereof, with at least 90% or at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as a direct repeat homology-containing sequence in Column 2 of Table 1, to a portion thereof, to the reverse complement thereof, or to a portion of the reverse complement thereof.

Enumerated embodiment 10 provides the composition of any previous enumerated embodiment, wherein the nuclease comprises an amino acid sequence with at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1 and the tracrRNA sequence comprises a nucleotide sequence set forth in any one or more of SEQ ID NOs: 1-3875 which is referred to as a direct repeat homology sequence in Column 2 of Table 1.

Enumerated embodiment 11 provides the composition of any one of enumerated embodiments 8-10, wherein the direct repeat sequence is fused to the tracrRNA sequence.

Enumerated embodiment 12 provides the composition of any previous enumerated embodiment, wherein the RNA guide is a single molecule RNA guide (sgRNA).

Enumerated embodiment 13 provides the composition of any previous enumerated embodiment, wherein the spacer sequence comprises between about 10 nucleotides and about 60 nucleotides in length.

Enumerated embodiment 14 provides the composition of any previous enumerated embodiment, wherein the spacer sequence comprises between about 10 nucleotides and about 35 nucleotides in length.

Enumerated embodiment 15 provides the composition of any previous enumerated embodiment, wherein the spacer sequence comprises between about 20 nucleotides and about 25 nucleotides in length.

Enumerated embodiment 16 provides the composition of any previous enumerated embodiment, wherein the target nucleic acid comprises a sequence complementary to a nucleotide sequence in the spacer sequence.

Enumerated embodiment 17 provides the composition of any previous enumerated embodiment, wherein the target nucleic acid is adjacent to a protospacer adjacent motif (PAM) sequence.

Enumerated embodiment 18 provides the composition of any previous enumerated embodiment, wherein the composition further comprises a modulator RNA.

Enumerated embodiment 19 provides the composition of any previous enumerated embodiment, wherein the nuclease comprises the amino acid sequence set forth in any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1.

Enumerated embodiment 20 provides the composition of any previous enumerated embodiment, wherein the nuclease cleaves the target nucleic acid.

Enumerated embodiment 21 provides the composition of any previous enumerated embodiment, wherein the target nucleic acid is single-stranded DNA or double-stranded DNA.

Enumerated embodiment 22 provides the composition of any previous enumerated embodiment, wherein the target nucleic acid is double-stranded DNA and wherein the nuclease cleaves one strand of the target sequence or both strands of the target sequence.

Enumerated embodiment 23 provides the composition of any previous enumerated embodiment, wherein the composition comprises at least 10% greater enzymatic activity than that of a reference composition.

Enumerated embodiment 24 provides the composition of enumerated embodiment 23, wherein the enzymatic activity is nuclease activity or nickase activity.

Enumerated embodiment 25 provides the composition of any previous enumerated embodiment, wherein the nuclease further comprises a peptide tag, a fluorescent protein, a base-editing domain, a DNA methylation domain, a histone residue modification domain, a localization factor, a transcription modification factor, a light-gated control factor, a chemically inducible factor, or a chromatin visualization factor.

Enumerated embodiment 26 provides the composition of any previous enumerated embodiment, wherein the nucleic acid encoding the nuclease is codon-optimized for expression in a cell.

Enumerated embodiment 27 provides the composition of any previous enumerated embodiment, wherein the nucleic acid encoding the nuclease is operably linked to a promoter.

Enumerated embodiment 28 provides the composition of any previous enumerated embodiment, wherein the nucleic acid encoding the nuclease is in a vector.

Enumerated embodiment 29 provides the composition of any previous enumerated embodiment, wherein the vector comprises a retroviral vector, a lentiviral vector, a phage vector, an adenoviral vector, an adeno-associated vector, or a herpes simplex vector.

Enumerated embodiment 30 provides the composition of any previous enumerated embodiment, wherein the composition is present in a delivery composition comprising a nanoparticle, a liposome, an exosome, a microvesicle, or a gene-gun.

Enumerated embodiment 31 provides a cell comprising the composition of any previous enumerated embodiment.

Enumerated embodiment 32 provides the cell of enumerated embodiment 31, wherein the cell is a eukaryotic cell or a prokaryotic cell.

Enumerated embodiment 33 provides the cell of any previous enumerated embodiment, wherein the cell is a mammalian cell or a plant cell.

Enumerated embodiment 34 provides the cell of any previous enumerated embodiment, wherein the cell is a human cell.

Enumerated embodiment 35 provides a method of binding the composition of any previous enumerated embodiment to the target nucleic acid in a cell, the method comprising:

(a) providing the composition; and

(b) delivering the composition to the cell,

wherein the cell comprises the target nucleic acid, wherein the nuclease binds to the RNA guide, and wherein the spacer sequence binds to the target nucleic acid.

Enumerated embodiment 36 provides a method of introducing an indel into a target nucleic acid in a cell, the method comprising:

(a) providing the composition of any previous enumerated embodiment; and

(b) delivering the composition to the cell,

wherein recognition of the target nucleic acid by the composition results in a modification of the target nucleic acid.

Enumerated embodiment 37 provides the method of enumerated embodiment 35 or enumerated embodiment 36, wherein delivering the composition to the cell is by transfection.

Enumerated embodiment 38 provides the method of any previous enumerated embodiment, wherein the cell is a eukaryotic cell.

Enumerated embodiment 39 provides the method of any previous enumerated embodiment, wherein the cell is a prokaryotic cell.

Enumerated embodiment 40 provides the method of any previous enumerated embodiment, wherein the cell is a human cell.

Other Embodiments

The disclosures of each and every patent, patent application, and publication cited herein are hereby incorporated herein by reference in their entirety. While this invention has been disclosed with reference to specific embodiments, it is apparent that other embodiments and variations of this invention may be devised by others skilled in the art without departing from the true spirit and scope of the invention. The appended claims are intended to be construed to include all such embodiments and equivalent variations.

CLAIMS

What is claimed is:

1. A composition comprising:
   (a) a nuclease or a nucleic acid encoding the nuclease, wherein the nuclease comprises an amino acid sequence with at least 80% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1; and
   (b) an RNA guide or a nucleic acid encoding the RNA guide, wherein the RNA guide comprises a direct repeat sequence and a spacer sequence,
   wherein the nuclease binds to the RNA guide, and wherein the spacer sequence binds to a target nucleic acid.

2. The composition of claim 1, wherein the nuclease comprises a RuvC domain or a split RuvC domain.

3. The composition of any previous claim, wherein the nuclease comprises a catalytic residue.

4. The composition of claim 3, wherein the catalytic residue is aspartic acid or glutamic acid.

5. The composition of any previous claim, wherein the nuclease comprises an amino acid sequence with at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1.

6. The composition of any previous claim, wherein the nuclease comprises an amino acid sequence with at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1 and the direct repeat sequence comprises a nucleotide sequence with at least 90% or at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as a direct repeat in Column 2 of Table 1, or to a portion of any one of SEQ ID NOs: 1-3875 which is referred to as a direct repeat in Column 2 of Table 1.

7. The composition of any previous claim, wherein the RNA guide further comprises a trans-activating crRNA (tracrRNA) sequence.

8. The composition of any previous claim, wherein the nuclease comprises an amino acid sequence with at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1 and the tracrRNA sequence comprises a nucleotide sequence, or an RNA transcript thereof, with at least 90% or at least 95% identity to a portion of any one of SEQ ID NOs: 1-3875 which is referred to as a non-coding sequence in Column 2 of Table 1, to the reverse complement thereof, or to a portion of the reverse complement thereof.

9. The composition of any previous claim, wherein the nuclease comprises an amino acid sequence with at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1 and the tracrRNA sequence comprises a nucleotide sequence, or an RNA transcript thereof, with at least 90% or at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as a direct repeat homology-containing sequence in Column 2 of Table 1, to a portion thereof, to the reverse complement thereof, or to a portion of the reverse complement thereof.

10. The composition of any previous claim, wherein the nuclease comprises an amino acid sequence with at least 95% identity to any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1 and the tracrRNA sequence comprises a nucleotide sequence set forth in any one or more of SEQ ID NOs: 1-3875 which is referred to as a direct repeat homology sequence in Column 2 of Table 1.

11 The composition of any one of claims 8-10, wherein the direct repeat sequence is fused to the tracrRNA sequence.

12. The composition of any previous claim, wherein the RNA guide is a single molecule RNA guide (sgRNA).

13. The composition of any previous claim, wherein the spacer sequence comprises between about 10 nucleotides and about 60 nucleotides in length.

14. The composition of any previous claim, wherein the spacer sequence comprises between about 10 nucleotides and about 35 nucleotides in length.

15. The composition of any previous claim, wherein the spacer sequence comprises between about 20 nucleotides and about 25 nucleotides in length.

16. The composition of any previous claim, wherein the target nucleic acid comprises a sequence complementary to a nucleotide sequence in the spacer sequence.

17. The composition of any previous claim, wherein the target nucleic acid is adjacent to a protospacer adjacent motif (PAM) sequence.

18. The composition of any previous claim, wherein the composition further comprises a modulator RNA.

19. The composition of any previous claim, wherein the nuclease comprises the amino acid sequence set forth in any one of SEQ ID NOs: 1-3875 which is referred to as an effector in Column 2 of Table 1.

20. The composition of any previous claim, wherein the nuclease cleaves the target nucleic acid.

21. The composition of any previous claim, wherein the target nucleic acid is single-stranded DNA or double-stranded DNA.

22. The composition of any previous claim, wherein the target nucleic acid is double-stranded DNA and wherein the nuclease cleaves one strand of the target sequence or both strands of the target sequence.

23. The composition of any previous claim, wherein the composition comprises at least 10% greater enzymatic activity than that of a reference composition.

24. The composition of claim 23, wherein the enzymatic activity is nuclease activity or nickase activity.

25. The composition of any previous claim, wherein the nuclease further comprises a peptide tag, a fluorescent protein, a base-editing domain, a DNA methylation domain, a histone residue

modification domain, a localization factor, a transcription modification factor, a light-gated control factor, a chemically inducible factor, or a chromatin visualization factor.

26. The composition of any previous claim, wherein the nucleic acid encoding the nuclease is codon-optimized for expression in a cell.

27. The composition of any previous claim, wherein the nucleic acid encoding the nuclease is operably linked to a promoter.

28. The composition of any previous claim, wherein the nucleic acid encoding the nuclease is in a vector.

29. The composition of any previous claim, wherein the vector comprises a retroviral vector, a lentiviral vector, a phage vector, an adenoviral vector, an adeno-associated vector, or a herpes simplex vector.

30. The composition of any previous claim, wherein the composition is present in a delivery composition comprising a nanoparticle, a liposome, an exosome, a microvesicle, or a gene-gun.

31. A cell comprising the composition of any previous claim.

32. The cell of claim 31, wherein the cell is a eukaryotic cell or a prokaryotic cell.

33. The cell of any previous claim, wherein the cell is a mammalian cell or a plant cell.

34. The cell of any previous claim, wherein the cell is a human cell.

35. A method of binding the composition of any previous claim to the target nucleic acid in a cell, the method comprising:

(a) providing the composition; and

(b) delivering the composition to the cell,

wherein the cell comprises the target nucleic acid, wherein the nuclease binds to the RNA guide, and wherein the spacer sequence binds to the target nucleic acid.

36. A method of introducing an indel into a target nucleic acid in a cell, the method comprising:

(a) providing the composition of any previous claim; and

(b) delivering the composition to the cell,

wherein recognition of the target nucleic acid by the composition results in a modification of the target nucleic acid.

37. The method of claim 35 or claim 36, wherein delivering the composition to the cell is by transfection.

38. The method of any previous claim, wherein the cell is a eukaryotic cell.

39. The method of any previous claim, wherein the cell is a prokaryotic cell.

40. The method of any previous claim, wherein the cell is a human cell.