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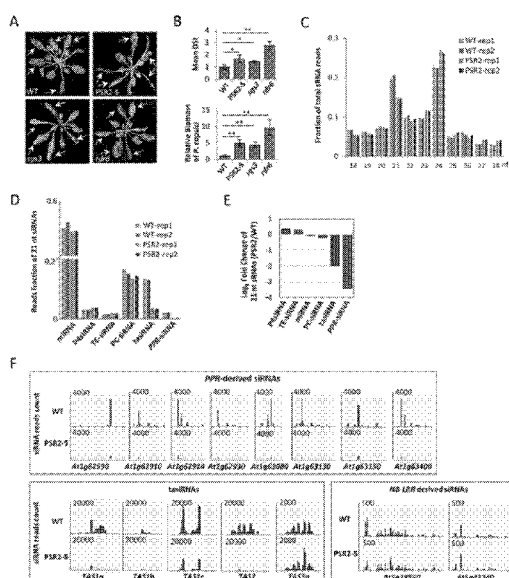


FIG. 1

(57) Abstract: Plants expressing miRNA and methods of making and their use are described. Specifically, the disclosure provides a transgenic plant engineered to heterologously express an miRNA, wherein the plant further heterologously expresses a pentatricopeptide repeat (PPR)- encoding transcript, and wherein the transgenic plant has enhanced resistance to a pathogen compared to a control plant that does not heterologously express the miRNA. Further disclosed are miRNA sequences that are used in the disclosure.

Declarations under Rule 4.17:

- *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*
- *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*

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- *with sequence listing part of description (Rule 5.2(a))*

sRNAS THAT ENHANCE PLANT RESISTANCE

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CROSS-REFERENCE TO RELATED PATENT APPLICATIONS

[0001] The present invention claims benefit of priority to U.S. Provisional Patent Application No. 62/714,342, filed August 3, 2018, which is incorporated by reference for all purposes.

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STATEMENT AS TO RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

[0002] This invention was made with Government support under U.S. Department of Agriculture National Institutes of Food and Agriculture (USDA-NIFA) Grant No. 2014-67013-21554. The government has certain rights in this invention.

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SEQUENCE LISTING

[0002.1] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on August 2, 2019, is named 081906-1146535_230610PC_SL.txt and is
20 332,041 bytes in size.

BACKGROUND OF THE INVENTION

[0003] *Phytophthora* are filamentous eukaryotic pathogens that exert major threats to food safety and human wellness (Kamoun et al., 2015). Hundreds of billions of dollars are lost each
25 year due to destructive crop diseases caused by *Phytophthora* species. For example, the notorious potato pathogen *Phytophthora infestans* was the culprit of the Irish Famine in the nineteenth century and remains a serious problem worldwide. Battling *Phytophthora* diseases is a major challenge in agriculture.

[0004] Plants have evolved a complex immune system during an arms race with potential
30 pathogens in the environment. However, successful pathogens are able to defeat host immunity,

mainly through the function of secreted proteins, called effectors (Jones and Dangl, 2006; Dou, and Zhou, 2012). Many effectors directly manipulate host cellular processes inside the host cells. The study of pathogen effectors and their targets has yielded important insights into basic plant cell biology in general, and immune signaling in particular (Win et al., 2012). Similar to many other filamentous fungi and oomycete pathogens, *Phytophthora* establishes intimate symbiotic associations with host plants through infection structures called haustoria, which are invaginations of host plasma membrane induced by extensions of *Phytophthora* hyphae (Bozkurt et al., 2014). Haustoria are believed to facilitate nutrient transportation from the host, and, more importantly, act as an essential interface for effector delivery from the pathogens (Petre and Kamoun, 2014). Each *Phytophthora* species is predicted to encode several hundreds to over one thousand effectors that have diverse cellular functions in plant hosts (Haas et al., 2009; Lamour et al., 2012; Pais et al., 2013; Tyler et al., 2006). This remarkably large effector repertoire reflects a high level of complexity in the defense/counter-defense crosstalk between *Phytophthora* and their plant hosts.

[0005] Recent studies have revealed that some *Phytophthora* effectors can inhibit the RNA silencing pathway in plants (Qiao et al., 2013). RNA silencing has a well-established role in anti-viral immunity and viral RNA silencing suppressors are indispensable for infection (Ding, 2010). These *Phytophthora* suppressors of RNA silencing (PSR) enhance plant susceptibility to *Phytophthora* (Qiao et al., 2013; Xiong et al., 2014). However, the role of RNA silencing in defense against eukaryotic pathogens is unclear; more importantly, how these pathogens can overcome RNAi-based defense mechanisms to establish successful infection remains unknown.

[0006] Gene silencing is mediated by small RNAs. Plants produce two major classes of sRNAs, microRNAs (miRNAs) and small interfering RNAs (siRNAs), which are distinctive in biosynthetic pathways and functions (Axtell, 2013). miRNAs are encoded from endogenous *MIR* loci, where the primary transcripts form foldback precursors that are subsequently processed. In contrast, the precursors of siRNAs are long double-stranded RNAs (dsRNAs) synthesized by RNA-dependent RNA polymerases (RDRPs) (Chen, 2009). A small number of miRNAs trigger the generation of secondary siRNAs, which are derived from a subset of miRNA-targeted transcripts. Land plants retain a complex pathway to generate numerous secondary siRNAs with

diverse sequences from both coding and non-coding transcripts, but the biological functions of these secondary siRNAs are largely unknown (Borges and Martienssen, 2015).

[0007] Among the RNA silencing suppressors identified from *Phytophthora sojae*, PSR2 was found to impair the accumulation of two secondary siRNAs, derived from the non-coding
5 *TAS1a/b/c* and *TAS2* transcripts respectively, in *Arabidopsis* (Qiao et al., 2013).

BRIEF SUMMARY OF THE INVENTION

[0008] miRNAs that can be expressed in plants and their use for increasing plant resistance to pathogens, including for example *Phytophthora* and *Verticillium*, are described. In some
10 embodiments, a transgenic plant engineered to heterologously express an miRNA comprising any one of SEQ ID NO: 1-19 is provided, wherein the transgenic plant has enhanced resistance to a pathogen compared to a control plant that does not heterologously express the miRNA. In some embodiments, the plant further heterologously expresses a pentatricopeptide repeat (PPR)-
15 encoding transcript. In some embodiments, the PPR-encoding transcript contains a mutation such that the transcript does not express a function protein. . In some embodiments, the PPR-encoding transcript and the miRNA are from the same species of plant and are different from the transgenic plant species. In some embodiments, the transgenic plant comprises an expression cassette, the expression cassette comprising a promoter operably linked to a polynucleotide encoding the miRNA, wherein the promoter is heterologous to the polynucleotide. In some
20 embodiments, the promoter is constitutive or tissue-specific or inducible.

[0009] In some embodiments, the plant is a dicot plant. In some embodiments, the plant is a cotton plant.

[0010] In some embodiments, the pathogen is one or more of a species of *Phytophthora* and/or *Verticillium* or other filamentous eukaryotic pathogen.

25 [0011] Also provided is a method of making the transgenic plant as described above or elsewhere herein. In some embodiments, the method comprises (i) modifying an endogenous promoter of the plant to heterologously express the miRNA or (ii) introducing the expression cassette into the plant. In some embodiments, the method further comprises selecting from a

plurality of modified plants, one or more plant with enhanced resistance to the pathogen (including but not limited to *Phytophthora*).

[0011] Also provided is a method of inducing resistance in a plant to a pathogen, the method comprising, contacting a plant with an miRNA comprising any one of SEQ ID NO: 1-19 in an amount to induce resistance to a pathogen. In some embodiments, the method further comprises contacting the plant with a pentatricopeptide repeat (PPR)-encoding transcript. In some embodiments, the PPR-encoding transcript contains a mutation such that the transcript does not express a function protein. In some embodiments, the PPR-encoding transcript and the miRNA are from the same (or different) species of plant and are different from the transgenic plant species. In some embodiments, the plant is a dicot plant. In some embodiments, the plant is a cotton plant. In some embodiments, the pathogen is one or more of a species of *Phytophthora* and/or *Verticillium*. In some embodiments, the contacting comprising spraying aerial parts of the plant or contacting roots of the plant with the miRNA (and optionally the PPR-encoding transcript).

DEFINITIONS

[0012] The term "pathogen-resistant" or "pathogen resistance" refers to an increase in the ability of a plant to prevent or resist pathogen infection or pathogen-induced symptoms. Pathogen resistance can be increased resistance relative to a particular pathogen species or genus (e.g., *Verticillium* or *Phytophthora*), increased resistance to multiple pathogens, or increased resistance to all pathogens (e.g., systemic acquired resistance). In some embodiments, resistance of a plant to a pathogen is "increased" when one or more symptoms of pathogen infection are reduced relative to a control (e.g., a plant in which a polynucleotide that inhibits expression of a pathogen target gene is not expressed).

[0013] "Pathogens" include, but are not limited to, viruses, bacteria, nematodes, fungi, oomycetes or insects (see, e.g., Agrios, *Plant Pathology* (Academic Press, San Diego, CA (1988))). In some embodiments, the pathogen is a fungal pathogen. In some embodiments, the pathogen is an oomycete pathogen. In some embodiments, the pathogen is *Phytophthora*. In some embodiments, the pathogen is *Verticillium*.

[0014] The term "nucleic acid" or "polynucleotide" refers to a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end. Nucleic

acids may also include modified nucleotides that permit correct read through by a polymerase and do not significantly alter expression of a polypeptide encoded by that nucleic acid.

[0015] The phrase "nucleic acid encoding" or "polynucleotide encoding" refers to a nucleic acid which directs the expression of a specific protein or peptide, or a non-coding RNA. The nucleic acid sequences include both the DNA strand sequence that is transcribed into RNA and, when encoding a protein, the RNA sequence that is translated into protein. The nucleic acid sequences include both the full length nucleic acid sequences as well as non-full length sequences derived from the full length sequences.

[0016] Two nucleic acid sequences or polypeptides are said to be "identical" if the sequence of nucleotides or amino acid residues, respectively, in the two sequences is the same when aligned for maximum correspondence as described below. "Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. When percentage of sequence identity is used in reference to proteins or peptides, it is recognized that residue positions that are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (*e.g.*, charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is

calculated according to, e.g., the algorithm of Meyers & Miller, *Computer Applic. Biol. Sci.* 4:11-17 (1988) e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California, USA).

[0017] The term "substantial identity" or "substantially identical," as used in the context of polynucleotide or polypeptide sequences, refers to a sequence that has at least 60% sequence identity to a reference sequence. Alternatively, percent identity can be any integer from 60% to 100%. Exemplary embodiments include at least: 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%, as compared to a reference sequence using the programs described herein; preferably BLAST using standard parameters, as described below.

One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

[0018] For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

[0019] A "comparison window," as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman *Add. APL. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman and Wunsch *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson and Lipman *Proc. Natl. Acad. Sci. (U.S.A.)* 85: 2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and

TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by manual alignment and visual inspection.

[0020] Algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.* (1990) *J. Mol. Biol.* 215: 403-410 and Altschul *et al.* (1977) *Nucleic Acids Res.* 25: 3389-3402, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (NCBI) web site. The algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al., supra*). These initial neighborhood word hits acts as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a word size (W) of 28, an expectation (E) of 10, M=1, N=-2, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word size (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)).

[0021] The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar

to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.01, more preferably less than about 10^{-5} , and most preferably less than about 10^{-20} .

[0022] A polynucleotide sequence is "heterologous" to an organism or a second polynucleotide sequence if it originates from a foreign species, or, if from the same species, is modified from its original form. For example, when a promoter is said to be operably linked to a heterologous coding sequence, it means that the coding sequence is derived from one species whereas the promoter sequence is derived another, different species; or, if both are derived from the same species, the coding sequence is not naturally associated with the promoter (*e.g.*, is a genetically engineered coding sequence, *e.g.*, from a different gene in the same species, or an allele from a different ecotype or variety).

[0023] An "expression cassette" refers to a nucleic acid construct, which when introduced into a host cell, results in transcription and/or translation of a RNA or polypeptide, respectively. Antisense constructs or sense constructs that are not or cannot be translated are expressly included by this definition. One of skill will recognize that the inserted polynucleotide sequence need not be identical, but may be only substantially similar to a sequence of the gene from which it was derived.

[0024] The term "promoter," as used herein, refers to a polynucleotide sequence capable of driving transcription of a coding sequence in a cell. Thus, promoters used in the polynucleotide constructs of the invention include cis-acting transcriptional control elements and regulatory sequences that are involved in regulating or modulating the timing and/or rate of transcription of a gene. For example, a promoter can be a cis-acting transcriptional control element, including an enhancer, a promoter, a transcription terminator, an origin of replication, a chromosomal integration sequence, 5' and 3' untranslated regions, or an intronic sequence, which are involved in transcriptional regulation. These cis-acting sequences typically interact with proteins or other biomolecules to carry out (turn on/off, regulate, modulate, *etc.*) gene transcription. A "constitutive promoter" is one that is capable of initiating transcription in nearly all tissue types, whereas a "tissue-specific promoter" initiates transcription only in one or a few particular tissue types. An "inducible promoter" is one that initiates transcription only under particular environmental conditions or developmental conditions.

[0025] The term "plant" includes whole plants, shoot vegetative organs and/or structures (*e.g.*, leaves, stems and tubers), roots, flowers and floral organs (*e.g.*, bracts, sepals, petals, stamens, carpels, anthers), ovules (including egg and central cells), seed (including zygote, embryo, endosperm, and seed coat), fruit (*e.g.*, the mature ovary), seedlings, plant tissue (*e.g.*, vascular tissue, ground tissue, and the like), cells (*e.g.*, guard cells, egg cells, trichomes and the like), and progeny of same. The class of plants that can be used in the method of the invention is generally as broad as the class of higher and lower plants amenable to transformation techniques, including angiosperms (monocotyledonous and dicotyledonous plants), gymnosperms, ferns, and multicellular algae. It includes plants of a variety of ploidy levels, including aneuploid, polyploid, diploid, haploid, and hemizygous.

BRIEF DESCRIPTION OF THE DRAWINGS

[0026] FIG. 1 PSR2 affects the accumulation of specific 21-nt siRNAs in *Arabidopsis*.

[0027] FIG. 1A Mutants defective in secondary siRNA production and a transgenic line expressing *PSR2* (*PSR2-5*) are hypersusceptible to *Phytophthora capsici*. *Arabidopsis* plants were inoculated with zoospore suspensions of *P. capsici* isolate LT263. Photos were taken at 3 days post inoculation (dpi). Arrows indicate inoculated leaves. WT: wild-type Col-0.

[0028] FIG. 1B Disease severity index (DSI) and pathogen biomass in inoculated *Arabidopsis* plants at 3 dpi. Values are mean $\pm$ SEM of three biological replicates. Student's t-test was used for comparisons (mutants versus WT). * and ** label results that are statistically different at $p \leq 0.05$ or $p \leq 0.01$. More than 20 leaves were inoculated in every biological replicate ($N \geq 20$).

[0029] FIG. 1C Size distribution of total small RNAs in WT and *PSR2-5* plants. Data from two biological replicates are presented.

[0030] FIG. 1D Reads fraction of 21-nt sRNAs in WT and *PSR2-5* plants. Percentage of reads count of miRNAs, and siRNAs produced from Pol IV transcripts (P4siRNA), transposable elements (TE), protein-coding transcripts (PC), *TAS* and *PPR* transcripts are presented. Data from two biological replicates are presented.

[0031] FIG. 1E Changes in the abundance (in a $\log_2$ scale) of 21-nt small RNAs derived from different classes of transcripts in *PSR2-5*. P4: RNA polymerase IV; TE: transposable elements;

PC: protein-coding genes; tasiRNA: *trans acting* siRNAs; *PPR*: pentatricopeptide repeat protein-coding genes.

[0032] FIG. 1F Secondary siRNAs generated from *PPR*, *TAS* and *NB-LRR* loci in WT and PSR2-5 plants. The number in each plot indicates the scale of sRNA reads count derived from each locus.

[0033] FIG. 2 Secondary siRNAs generated from a cluster of *PPR* genes contribute to *Arabidopsis* resistance to *P. capsici*.

[0034] FIG. 2A Northern blotting showing induced accumulation of miR161 and two representative *PPR*-derived secondary siRNAs in wild-type Col-0 (WT) plants during *P. capsici* infection (0-24 hours post inoculation with zoospore suspensions). Numbers represent relative signal intensities. U6 was used as a loading control. Water was used as the “mock” treatment. Similar results were obtained from two biological replicates. See also Figure 7A-D.

[0035] FIG. 2B Northern blotting showing that the abundance of miR161 and miR393 remained unchanged in *bak1/serk4* mutant after inoculated with *P. capsici*.

[0036] FIG. 2C miR161 is a positive regulator of plant immunity. The abundance of two *PPR*-derived siRNAs was determined in WT, *MIR161ox* and *MIR161cri* plants by northern blotting. Disease severity index (DSI) of WT, *MIR161ox* and *MIR161cri* plants was determined at 3 days after zoospore inoculation by *P. capsici*. Values are mean±SEM of three biological replicates. Student's t-test was used for comparisons (mutants versus WT). Statistically significant results are labeled with * ($p \leq 0.05$). $N \geq 20$. Northern blotting was used to examine the abundance of two *PPR*-derived siRNAs determined in WT, *MIR161ox* and *MIR161cri* plants. See also Figure 8A-J.

[0037] FIG. 2D *MIR173cri* mutants are hypersusceptible to *P. capsici*. The abundance of two *PPR*-derived siRNAs was evaluated in WT and the mutants. DSI was determined at 3 dpi. Values are mean±SEM of three biological replicates. Student's t-test was used for comparisons (mutants versus WT). Statistically significant results are labeled with * ($p \leq 0.05$). $N \geq 20$. The abundance of two *PPR*-derived siRNAs was evaluated in WT and *MIR173cri* mutants. See also Figure 8A-J.

[0038] FIG. 2E Secondary siRNA-producing *PPR* genes contribute to *Arabidopsis* resistance to *P. capsici*. DSI of eight *PPR* mutants was determined at 3 dpi. Values are mean±SEM of three biological replicates. Student's t-test was used for comparisons (mutants versus WT). * labels results that are statistically different at $p \leq 0.05$. $N \geq 20$. See also Figure 9.

5 **[0039]** FIG 3 A *PPR*-derived siRNA silences a gene in *Phytophthora* to confer resistance.

[0040] FIG 3A A flow chart describing the experimental procedure of the functional analysis of *PPR*-derived siRNAs.

[0041] FIG 3B Base pairing of the *PPR*-derived siR1310 and siR0513 with their predicted target site in *Phyca_554980* of *P. capsici* (SEQ ID NOS 1409-1412, respectively, in order of
10 appearance). See also Figure 10A-C.

[0042] FIG 3C Quantitative RT-PCR determining the transcript abundances of *Phyca_554980* and *Phyca_538731* (an off-target control) in *P. capsici* transformants harboring synthesized siR1310. *P. capsici* transformed with siRGFP was used as a negative control. Values are mean±SEM of three biological replicates. See also Figure 11A-G.

15 **[0043]** FIG 3D Numbers of sporangia produced by wild-type (WT) or transformants of *P. capsici* harboring siR1310 or siRGFP. Sporangia formation of *P. capsici* strains. Mycelium plugs were cultured in V8 medium for 2 days before sporangia were induced in sterilized water for 1 day in the dark. Number of sporangia were counted from four randomly selected fields of view under a microscope for each strain. Bars=200 μ m. Arrows indicate sporangia. Values are
20 mean±SEM of three biological replicates. One-way ANOVA and post-hoc Tukey testing were used for statistical comparison. Different letters indicate significant differences ($p \leq 0.05$). See also Figure 11A-G.

[0044] FIG 3E *P. capsici* transformants carrying siR1310 are no longer able to infect *N. benthamiana*. Mycelial plugs were used to inoculated detached leaves of *N. benthamiana*.
25 Photos of inoculated leaves were taken at 3 dpi under UV to better visualize the lesions. Lesion sizes are presented as mean±SEM of three replicates. One-way ANOVA and post-hoc Tukey testing were used for statistical comparison. Different letters indicate significant differences ($p \leq 0.05$).

[0045] FIG 3F Quantitative RT-PCR determining the abundances of siR1310 in leaves or extracellular vesicles (EV) of WT and PSR2-5 *Arabidopsis* plants with or without *P. capsici* infection. Values are mean±SEM of three biological replicates.

[0046] FIG 3G Transcript abundances of *Phyca_554980* in wild-type (WT), *MIR161ox*, PSR2-5 and *rd6* plants inoculated with *P. capsici*. The transcript levels at 1 dpi were determined by qRT-PCR. Values are mean±SEM of three biological replicates. Student's t-test was used for comparisons (mutants versus WT).

[0047] FIG. 4 PPR-derived siR1310 silences a reporter gene during *Phytophthora* infection.

[0048] FIG. 4A Schematic illustration of the construction of *mRFP* reporters containing either a target site of siR1310 (t-mRFP) or a mutated version of the target site (mt-mRFP).

[0049] FIG. 4 B- FIG. 4 C Red fluorescence intensity were monitored during *P. capsici* infection of WT, *MIR161ox*, or *MIR161cri* *Arabidopsis* plants. Because the t-mRFP and mt-mRFP constructs were independently transformed into *P. capsici*, their basal *mRFP* expression levels were different. Photos were taken at 2 dpi. Bars=20 µm. Values shown in panel C are mean±SEM. One-way ANOVA and post-hoc Tukey testing were used for statistical comparison. Different letters indicate values that are statistically different ($p \leq 0.05$). $N \geq 8$.

[0050] FIG. 4D *mRFP* transcript levels of the *P. capsici* strains infecting wild-type (WT), *MIR161ox* and *MIR161cri* plants were determined by qRT-PCR. Values are mean±SEM of at least four replicates. Student's t-test was used for comparisons (mutants versus WT). * represents statistical difference ($p \leq 0.05$); NS represents no statistical difference. Because t-mRFP and mt-mRFP constructs were independently transformed into *P. capsici*, their basal *mRFP* expression levels were different. See also Figure 1A-G.

[0051] FIG. 5 PSR2 associates with DRB4 in *Arabidopsis*.

[0052] FIG. 5A Schematic representation of the domain structure of PSR2 and DRB4. PSR2 has seven tandem repeat units consisting of W, Y and/or L motifs. S: secretion signal; R: RxLR domain. DRB4 has two double-stranded RNA-binding motifs (dsRBM) at the N-terminus.

[0053] FIG. 5B The two dsRNA-binding domains of DRB4 mediate interaction with PSR2 in planta. Flag-PSR2, DRB4-YFP, and DRB4 truncates were transiently expressed in *N.*

benthamiana. Total proteins were extracted and PSR2 was pulled down using anti-Flag agarose beads. Enrichment of DRB4 or its truncated mutants in the immune complexes was detected by western blotting. * labels corresponding protein band. The gel stained with Coomassie Brilliant Blue (CBB) was used as a loading control.

5 [0054] FIG. 5C WY1 and LWY2 are necessary and sufficient for PSR2 interaction with DRB4. PSR2, PSR2 Δ WY1, PSR2 Δ LWY2, and PSR2WY1+LWY2 were fused with a flag tag and individually expressed in *N. benthamiana* together with DRB4-YFP. Enrichment of DRB4 in the immune complexes pulled down by anti-Flag agarose beads was detected by western blotting. * labels corresponding protein band in each lane. The arrowhead labels signals
10 corresponding to DRB4.

[0055] FIG. 5D WY1 and LWY2 are necessary and sufficient for the transgene silencing suppression activity of PSR2. Leaves of *N. benthamiana* 16c plants were co-infiltrated with *Agrobacterium* carrying 35S:GFP and 35S:PSR2 constructs. Pictures were taken 5 days after *Agrobacterium* infiltration. EV: Empty vector. See also Figure 12A-D.

15 [0056] FIG. 5E Virulence activities of PSR2 and its derivatives were examined on *N. benthamiana* leaves inoculated with mycelial plugs of *P. capsici* strain LT263. Lesions were visualized under a UV lamp at 3 days post inoculation and lesion sizes were measured. YFP was used as a control. Values are mean $\pm$ SEM. Different letters indicate statistically different values ($p<0.01$). See also Figure 12A-D.

20 [0057] FIG. 5F Reduced dsRNA cleavage in PSR2-5 and a *drb4* mutant plants. In vitro synthesized 510-bp dsRNAs were labeled with 32 P, and then incubated with crude protein extracts. The cleavage products were analyzed by electrophoresis. A 22-nt DNA end-labeled with 32 P and a dsRNA ladder were used as size markers. The arrow labels the 510-bp dsRNAs and the arrowhead labels sRNA products. Numbers represent the relative abundances of the
25 sRNA products with the level in wild-type (WT) set to 1. Total proteins in the crude extracts were analyzed on SDS-PAGE and stained with Coomassie Brilliant Blue (CBB) as a loading control.

[0058] FIG. 6 A *drb4* mutant phenocopies PSR2-expressing plants.

[0059] FIG. 6A *drb4* and PSR2-5 plants were hypersusceptible to *P. capsici*. Roots of 14-day-old seedlings were inoculated by zoospore suspensions and the photos were taken at 3 dpi. This phenotype was complemented by introducing *DRB4-YFP* under its native promoter into the *drb4* mutant. See also Figure 12A-D.

5 **[0060]** FIG. 6B Five-week-old *drb4* and PSR2-5 plants exhibited a similar curly/narrow leaf phenotype.

[0061] FIG. 6C Venn diagram showing *PPR* loci with reduced secondary siRNA production in *rdr6*, *drb4* and PSR2-5 plants compared to wild-type *Arabidopsis* respectively.

10 **[0062]** FIG. 7A-D Accumulation of secondary siRNA-triggering miRNAs and tasiRNA in *Arabidopsis* during *P. capsici* infection, related to Figure 2.

[0063] FIG. 7A Quantitative RT-PCR showing transcript abundances of *pri-miRNAs* in wild-type *Arabidopsis* Col-0 during *P. capsici* infection at 0, 3, 6 and 12 hours post inoculation (hpi). Values are mean±SD. Water was used as a mock treatment.

15 **[0064]** FIG. 7B Northern blotting showing the abundances of miR173, miR390 and miR393 during *P. capsici* infection in wild-type (WT) *Arabidopsis* plants. Numbers represent relative signal intensities. U6 was used as a loading control.

[0065] FIG. 7C Sequence alignment of two *PPR*-siRNAs. *PPR*-siRNA-1 and *PPR*-siRNA-2 were used as representatives to show abundance changes in *Arabidopsis* (SEQ ID NOS 1413-1434, respectively, in order of appearance). Similar sequences could be produced from multiple
20 *PPR* loci.

[0066] FIG. 7D Northern blotting showing the abundances of two tasiRNAs (siR255 and siR1511) during *P. capsici* infection (0-24 hours post inoculation). The production of these tasiRNAs is triggered by miR173. Water was used as a mock treatment. U6 served as a loading control. Numbers represent relative signal intensities.

25 **[0067]** FIG. 8A-J. Disease susceptibility of miR161 and miR173 mutants, related to Figure 2.

[0068] FIG. 8A Sequences in the foldback region of *pri-miR161* in wild-type (WT) and *MIR161cri* lines (SEQ ID NOS 1435-1440, respectively, in order of appearance). The sequences in purple correspond to miR161. *MIR161cri-7* has one nucleotide insertion (in red), which

reduces, but not abolishes miR161 production. *MIR161cri-8* has a deletion of six nucleotides, abolishing miR161 production.

[0069] FIG. 8B Northern blotting showing the abundance of miR161 in wild-type *Arabidopsis* (WT), *MIR161* over-expression lines (*MIR161ox*), and crispr mutants (*MIR161cri*) lines.

5 Numbers represent relative signal intensities. U6 was used as a loading control.

[0070] FIG. 8C Disease symptoms of WT, *MIR161ox* and *MIR161cri* plants after inoculated with *P. capsici* zoospore suspension. Photos were taken at 3 dpi. Arrows indicate inoculated leaves.

10 **[0071]** FIG. 8D Northern blotting showing the increased accumulation of miR173 and tasiRNAs (represented by siR1511) in *MIR173* over-expression lines (*MIR173ox*). However, the abundance of *PPR*-derived siRNAs (represented by *PPR*-siRNA-2) was not increased. Numbers represent relative signal intensities. U6 was used as a loading control.

15 **[0072]** FIG. 8E *MIR173ox* plants exhibited similar susceptibility to wild-type (WT) when inoculated with *P. capsici* zoospore suspension. DSI was determined at 3 dpi. Values are mean±SEM of three biological replicates.

[0073] FIG. 8F Northern blotting showing the increased accumulation of miR390 in *MIR390* over-expression (*MIR390ox*) lines.

20 **[0074]** FIG. 8G *MIR390ox* plants exhibited similar susceptibility to wild-type (WT) when inoculated with *P. capsici* zoospore suspension. DSI was determined at 3 dpi. Values are mean±SEM of three biological replicates.

[0075] FIG. 8H Sequences in the foldback region of *MIR173* in wild-type and *MIR173cri* lines (SEQ ID NOS 1441-1446, respectively, in order of appearance). miR173 can be generated from both purple regions. Mutated nucleotides in *MIR173cri-3* are highlighted in red. In addition to mutations, *MIR173cri-7* also have a deletion of ten nucleotides, leading to abolishment of
25 miR173 production.

[0076] FIG. 8I Northern blotting showing the diminished accumulation of tasiRNAs (represented by siR255 and siR1511) in *MIR173cri* mutants. Numbers represent relative signal intensities. U6 was used as a loading control.

[0077] FIG. 8J Symptoms of *MIR173cri* mutants after *P. capsici* infection. Photos were taken at 3 dpi. Arrows indicate inoculated leaves.

[0078] FIG. 9A-C Characterization of the T-DNA insertion mutants of eight *PPR* genes that can generate secondary siRNAs, related to Figure 2.

5 [0079] FIG. 9A Schematic maps of the T-DNA insertion site in each mutant and the locations of the primers used for quantitative RT-PCR. Black arrows label the predicted target sites of miR161. White arrows label the predicted target sites of tasiRNAs.

[0080] FIG. 9B Quantitative RT-PCR measuring the transcript levels of the corresponding *PPR* gene in each mutant. Values are mean $\pm$ SD of at least three replicates.

10 [0081] FIG. 9C Disease symptoms of the mutants after *P. capsici* inoculation. Photos were taken at 3 dpi. Inoculated leaves were removed from the plants at 3 dpi to better show the symptoms.

[0082] FIG. 10A-C Potential targets of *PPR*-derived siRNAs in *Arabidopsis* and *Phytophthora*, related to Figure 3.

15 [0083] FIG. 10A Venn diagram showing a minimal overlap between genes up-regulated in PSR2-5 plants, compared to wild-type *Arabidopsis* Col-0, and the genes predicted to contain target site(s) of *PPR*-derived siRNAs.

20 [0084] FIG. 10B A list showing the 11 genes that are up-regulated in PSR2-5 and are also potential targets of *PPR*-derived siRNAs. Only two of the 11 genes contain *PPR* domains in their deduced amino acid sequences. At1g12775 can also produce siRNAs, but it is not in the gene cluster that produces the large majority of *PPR*-derived siRNAs.

[0085] FIG. 10C Amino acid sequence alignment of homologs of *Phyca_554980* encoded protein in *Phytophthora* species *P. capsici*, *P. parasitica*, *P. infestans*, *P. ramorum*, *P. cinnamomi*, and *P. sojae* (from the top to the bottom in the alignment) (SEQ ID NOS 1447-1452, respectively, in order of appearance). The protein sequences were identified using FungiDB (<http://fungidb.org/fungidb/>). Highlighted areas represent highly conserved sequences.

[0086] FIG. 11A-G Target gene silencing and developmental defects of *P. capsici* transformants carrying siR1310, related to Figure 3.

[0087] FIG. 11A Quantitative RT-PCR of the predicted target gene *Phyca_554980* in ten independent transformants of *P. capsici* that potentially carry siR1310. Transformants potentially carrying siRGFP were used as controls. Values are mean±SEM.

[0088] FIG. 11B Insufficient base pairing of the *PPR*-derived siR1310 and siR0513 with their predicted off-target *Phyca_538731* of *P. capsici* (SEQ ID NOS 1453-1456, respectively, in order of appearance).

[0089] FIG. 11C Mycelium growth of two siR1310 transformants with largely reduced transcript levels of the target gene *Phyca_554980*. *P. capsici* strains were grown on V8 plates. Pictures were taken after 5 days of growth. Transformants carrying siRGFP and wild-type (WT) strain were used as controls.

[0090] FIG. 11D Mycelium growth rate (shown as colony diameters) of *P. capsici* strains. Values are mean±SEM. Different letters indicate values that are statistically different ($p < 0.05$).

[0091] FIG. 11E Number of zoospores produced by *P. capsici* strains. Sporangia growing in sterilized water were stressed to release zoospores by illumination for 12 hours and then chilling at 4°C for 1 hour. Zoospores were counted from four randomly selected fields of view under a microscope for each strain using a hemocytometer. Values are mean±SEM. Different letters indicate values that are statistically different ($p < 0.05$).

[0092] FIG. 11F Quantitative RT-PCR showing the level of siR0513 in WT and PSR2-5 plants in EVs isolated from leaves tissues. Values are mean±SEM. * and ** label results that are statistically different with the WT value at $p \leq 0.05$ or $p \leq 0.01$.

[0093] FIG. 11G Stem loop qPCR showing the level of siR1310 in *MIR161ox* and *MIR161cri* mutant plants compared to wild-type (WT) *Arabidopsis*. Values are mean±SEM. * and ** label results that are statistically different with the WT value at $p \leq 0.05$ or $p \leq 0.01$.

[0094] FIG. 12A-D The RNAi suppression activity of PSR2 depends on its association with DRB4, related to Figure 5 and 6.

[0095] FIG. 12A Western blotting showing the abundance of GFP proteins in *N. benthamiana* 16c leaves expressing wild-type or truncated PSR2. Total proteins were extracted from leaves infiltrated with *Agrobacterium* carrying 35S-GFP and another strain carrying either the pEG100

empty vector (EV) or various truncates of PSR2-Flag at 5 dpi. Coomassie Brilliant blue staining (CBB) was used as loading control.

[0096] FIG. 12B Western blotting showing the protein levels of PSR2 or its derivatives in the infiltrated leaves. Total proteins were extracted from infiltrated leaves at 2 days after *Agro-*
5 infiltration and the proteins were detected by anti-Flag antibody. Coomassie Brilliant blue staining (CBB) was used as loading control.

[0097] FIG. 12C YFP-PSR2 and DRB4-YFP were expressed in *N. benthamiana* through *Agrobacterium*-mediated transient expression. Total proteins were extracted from the infiltrated leaves with treatment of RNase III and the immune complexes were pulled-down using anti-GFP
10 magnetic beads. The immuno-precipitated proteins were then incubated with in vitro synthesized dsRNA (510-bp in length). dsRNA enriched on the beads was extracted using Trizol/chloroform and then analyzed on 2% agarose gel along with Ethidium bromide staining. YFP was used as a negative control. The Arrowhead shows the position of the 510-bp dsRNA. Protein levels of immuno-precipitated YFP, PSR2 and DRB4 were confirmed by western blotting using anti-GFP
15 antibody.

[0098] FIG. 12D Detached leaves from four-week-old plants of wild-type (WT), PSR2-5, *drb4* and a complementation line of *drb4* (*DRB4* expressed under its native promoter) were inoculated with zoospore suspensions of *P. capsici* strain LT263. Inoculated leaves were stained with trypan blue to visualize the lesions at 3 dpi. Disease severity index (DSI) was also determined. Values
20 are mean±SD. * labels results that are statistically different at $p \leq 0.05$.

[0099] FIG. 13. A model illustrating an arms race centered on host-induced gene silencing in *Arabidopsis* during *Phytophthora* infection. *Phytophthora capsici* can be recognized by *Arabidopsis* in a BAK1-dependent manner, likely by receptor localized on the cell surface. miR161 is induced upon this recognition and the increased accumulation of miR161 leads to
25 increased production of secondary siRNAs from a small number of *PPR* transcripts. *PPR*-derived siRNA production is also affected by miR173-dependent tasiRNAs. These *PPR*-derived siRNAs confer resistance to *P. capsici*, likely through extracellular vesicle mediated transportation and conferring targeted gene(s) silencing in the pathogen. As a counter-defense strategy, some *Phytophthora* species evolved effectors possessing RNA silencing suppression

activity. In particular, PSR2 associates with the host protein DRB4 and interferes with secondary siRNA production from specific loci, especially the *PPR* loci, to promote the infection.

[0100] FIG. 14: Schematic illustration of inoculation method and construction of atlg62914m (SEQ ID NOS 1457-1459, respectively, in order of appearance). A codon encoding a tyrosine (Y144) was mutated into a stop codon.

[0101] FIG. 15: *Nicotiana benthamiana* leaves expressing both atMIR161 and atlg62914m produced a much higher amount of siRNAs derived from atlg62914m transcripts.

[0102] FIG. 16: Plants producing antimicrobial siRNAs exhibited enhanced resistance to *P. capsici*. Leaves of *Nicotiana benthamiana* that express atMIR161, atlg62914m, or atMIR161+atlg62914m were inoculated with *Phytophthora capsici* strain LT263. Disease severity was evaluated at 3 days post inoculation. The results show that plants expressing atMIR161+atlg62914m exhibited much enhanced resistance to *P. capsici*. This experiment was repeated three times with similar results. Images of representative inoculated leaves (two per treatment) are shown below (Panel A). Lesion size of each inoculated leaf was measured and analyzed (Panel B). Please note that not all leaves expressed the same amount of atMIR161 and/or atlg62914m transcripts, hence the variation within the same treatment.

DETAILED DESCRIPTION OF THE INVENTION

[0103] The inventors have discovered that certain miRNAs, when expressed in a plant, induce resistance to certain pathogens (including filamentous eukaryotic pathogens such as *Phytophthora* and *Verticilium*.) For example, expression of an miRNA161 family member in a plant is effective in increasing resistance to *Phytophthora* pathogens. Without intending to be bound by a certain mechanism of action, it is believed that expression of the miRNA results in causing production in the plant of numerous siRNAs, some of which are effective causing plant resistance to the pathogens. In some embodiments, the pathogen is *Phytophthora*. In some embodiments, the pathogen is an oomycete. In some embodiments, the pathogen is an ascomycete. In some embodiments, the pathogen is a hemi-ascomycete. In some embodiments, the pathogen is a basidiomycete.

[0104] Accordingly, in some embodiments, plants that heterologously express the miRNA are provided. In some embodiments, transgenic plants can be generated that comprise an expression cassette comprising a promoter operably linked to a polynucleotide encoding the miRNA. In some embodiments, the promoter is heterologous to the polynucleotide encoding the miRNA.

- 5 For example in some embodiments, the promoter is not endogenously linked to the polynucleotide, or is a modified form from the endogenous promoter (e.g., such that expression of the polynucleotide is increased). In some embodiments, the promoter is from the same species as the transgenic plant. In some embodiments, the promoter is from a different plant species. In some embodiments, the polynucleotide is from the same plant species or is
- 10 substantially identical to a polynucleotide from the same plant species. In some embodiments, the polynucleotide is from a different plant species from the transgenic plant or is substantially identical to the polynucleotide from a different plant species.

- [0105]** Exemplary miRNA161 sequences include but are not limited (i) to those listed below or (ii) to RNA sequences substantially identical to those listed below or (iii) to RNA sequences that
- 15 include 1, 2, 3, 4 or 5 nucleotide changes compared to any of the sequences below:

SEQ ID NO:1 >ath-MIR161.1 *Arabidopsis thaliana*
UGAAAGUGACUACAUCGGGGU

- 20 SEQ ID NO:2 >pav-miR161.1 *Prunus avium* L.
UUGAAAGUGAAAACAUCAGGC

SEQ ID NO:3 >Aca-miR161.1 *Azolla caroliniana*
UGAAAGUGACUACAUCGGGGU

- 25 SEQ ID NO:4 >Asp-miR161.1 *Alsophila spinulosa*
UGAAAGUGACUACAUCGGGGU

SEQ ID NO:5 >Cfo-miR161.1 *Cyrtomium fortunei*
UGAAAGUGACUACAUCGGGGU

- 30 SEQ ID NO:6 >Pnu-miR161.1 *Psilotum nudum*
UGAAAGUGACUACAUCGGGGU

- 35 SEQ ID NO:7>Scu-miR161.1 *Salvinia cucullata*
UGAAAGUGACUACAUCGGGGU

SEQ ID NO:8>Smo-miR161.1 *Salvinia molesta*
UGAAAGUGACUACAUCGGGGU

SEQ ID NO:9>Vst-miR161.1 *Vandenboschia striata*
UGAAAGUGACUACAUCGGGGU

5 SEQ ID NO:10>Isi-miR161.1 *Isoetes sinensis*
UGAAAGUGACUACAUCGGGGU

SEQ ID NO:11>Era-miR161.1 *Equisetum ramosissimum*
UGAAAGUGACUACAUCGGGGU

10

SEQ ID NO:12



{UGAAAGUGA(C/A)(U/A)ACAUC(G/A)GG(G/C)}

15 SEQ ID NO:13 >ath-MIR161.2 *Arabidopsis thaliana*
UCAAUGCAUUGAAAGUGACUA

SEQ ID NO:14>bna-miR161 *Brassica napus*
UCAAUGCACUGAAAGUGACUA

20

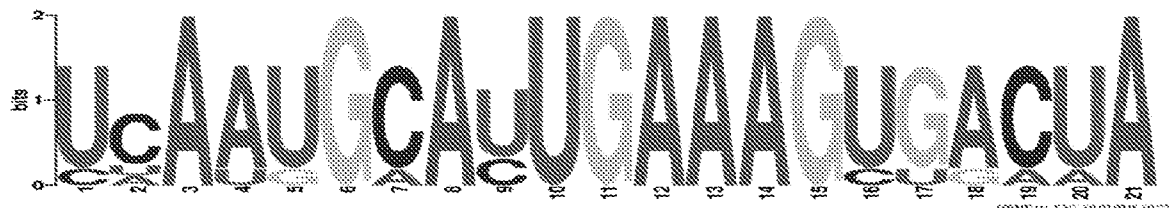
SEQ ID NO:15>bra-miR161-5p *Brassica rapa*
UCAAUGCACUGAAAGUGACUA

SEQ ID NO:16>cas-miR161 *Camelina sativa*
25 UCAAUGCAUUGAAAGUGACUA

SEQ ID NO:17>dlo-miR161.2 *Dimocarpus longan*
CAAUUGCAUUGAAAGCUGCUA

30 SEQ ID NO:18>pav-miR161.2 *Prunus avium* L.
UUAAGGAAUUGAAAGUGAAAA

SEQ ID NO:19



35 {(U/C)(C/U/A)A(A/U)(U/G)G(C/A)A(U/C)UGAAAG(U/C)(G/U)(A/G)(C/A)(U/A)A}

[0106] In some embodiments, one or more PPR transcript that serves as a target for miR161 is also expressed in the plant. In some embodiments, the PPR transcript is a P-type PPR transcript. *See, e.g.,* Barkan, *Annu. Rev. Plant Biol.* 2014.65:415-442. In some embodiments, the PPR transcript(s) is in the Rf-like (or RFL, “RF” stands for “restorer of fertility”) sub-clade of PPR-P genes. Related information of RF-like PPR genes, and RF-like transcripts, can be found in Dahan and Mireau, *RNA Biology* 10:9, 1469–1476, September 2013 as well as in Fujii *et al., Proc. Natl. Acad. Sci. USA* January 25, 2011, vol. 108, no. 4, pp. 1723–1728, including supplemental Table 1 therein listing a number of Rf-like PPR genes. Howell (*The Plant Cell*, Vol. 19: 926–942, March 2007) describes siRNAs that are specifically generated from PPR-P genes in *Arabidopsis* and other plant species. The PPR transcript will contain one or more (e.g., 2, 3, 4, 5, 6, 7, or more) sequences encoding anti-pathogen siRNAs. Exemplary anti-pathogen siRNAs are displayed for example in Table S3 as depicted in Hou, et al., A Phytophthora Effector Suppresses Trans-Kingdom RNAi to Promote Disease Susceptibility, 25(1) *Cell Host & Microbe* 153-165 (Jan. 9, 2019) or in U.S. Provisional Patent Application No. 62/714,342. Table S1 provides a listing of various *Arabidopsis* PPR transcripts. In some embodiments, the anti-pathogen siRNAs target one or more of the 249 *P. capsici* gene sequences as depicted in Table S4.

[0107] In some embodiments, the miR161 and the PPR transcript introduced into the plant are both from the same species. This will allow for optimal ability of the miR161 to generate siRNAs from the PPR transcript. However, this is optional and in other cases, the miR161 sequence and the PPR transcript are from different plant species. Exemplary sequences encoded by PPR genes are provided in Table S3 as depicted in Hou, et al., A Phytophthora Effector Suppresses Trans-Kingdom RNAi to Promote Disease Susceptibility, 25(1) *Cell Host & Microbe* 153-165 (Jan. 9, 2019). As shown in Example 2, the co-expression of at least one PPR gene with miR161 increases resistance in the plant to pathogens.

[0108] The isolation of polynucleotides (e.g., miRNA 161 members, PPR transcripts or promoters) may be accomplished by a number of techniques. For instance, oligonucleotide probes based on the sequences disclosed here can be used to identify the desired polynucleotide in a cDNA or genomic DNA library from a desired plant species. To construct genomic libraries, large segments of genomic DNA are generated by random fragmentation, e.g. using restriction endonucleases, and are ligated with vector DNA to form concatemers that can be

packaged into the appropriate vector. Alternatively, cDNA libraries from plants or plant parts may be constructed.

[0109] The cDNA or genomic library can then be screened using a probe based upon a sequence disclosed here. Probes may be used to hybridize with genomic DNA or cDNA sequences to isolate homologous genes in the same or different plant species. Alternatively, antibodies raised against a polypeptide can be used to screen an mRNA expression library.

[0110] Alternatively, the nucleic acids of interest can be amplified from nucleic acid samples using amplification techniques. For instance, polymerase chain reaction (PCR) technology to amplify the sequences of the genes directly from mRNA, from cDNA, from genomic libraries or cDNA libraries. PCR and other *in vitro* amplification methods may also be useful, for example, to clone nucleic acid sequences that code for proteins to be expressed, to make nucleic acids to use as probes for detecting the presence of the desired mRNA in samples, for nucleic acid sequencing, or for other purposes. For a general overview of PCR see PCR Protocols: A Guide to Methods and Applications. (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990).

[0111] Polynucleotides can also be synthesized by well-known techniques as described in the technical literature. See, e.g., Carruthers *et al.*, Cold Spring Harbor Symp. *Quant. Biol.* 47:411-418 (1982), and Adams *et al.*, *J. Am. Chem. Soc.* 105:661 (1983). Double stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

[0112] Once a desired polynucleotide sequence is obtained, it can be used to prepare an expression cassette for expression in a plant. In some embodiments, expression of the polynucleotide is directed by a heterologous promoter. Any of a number of means well known in the art can be used to drive expression of the polynucleotide sequence of interest in plants. Any organ can be targeted, such as shoot vegetative organs/structures (*e.g.* leaves, stems and tubers), roots, flowers and floral organs/structures (*e.g.* bracts, sepals, petals, stamens, carpels, anthers and ovules), seed (including embryo, endosperm, and seed coat) and fruit. Alternatively, expression can be conditioned to only occur under certain conditions (*e.g.*, using an inducible promoter).

[0113] For example, a plant promoter fragment may be employed to direct expression of the polynucleotide sequence of interest in all tissues of a regenerated plant. Such promoters are referred to herein as "constitutive" promoters and are active under most environmental conditions and states of development or cell differentiation. Examples of constitutive promoters include the cauliflower mosaic virus (CaMV) 35S transcription initiation region, the 1'- or 2'- promoter derived from T-DNA of *Agrobacterium tumefaciens*, and other transcription initiation regions from various plant genes.

[0114] Alternatively, the plant promoter may direct expression of the polynucleotide sequence of interest in a specific tissue (tissue-specific promoters) or may be otherwise under more precise environmental control (inducible promoters). Examples of tissue-specific promoters under developmental control include promoters that initiate transcription only in certain tissues, such as leaves or guard cells (including but not limited to those described in WO/2005/085449; U.S. Patent No. 6,653,535; Li *et al.*, *Sci China C Life Sci.* 2005 Apr;48(2):181-6; Husebye, *et al.*, *Plant Physiol*, April 2002, Vol. 128, pp. 1180-1188; and Plesch, *et al.*, *Gene*, Volume 249, Number 1, 16 May 2000, pp. 83-89(7)). Examples of environmental conditions that may affect transcription by inducible promoters include the presence of a pathogen, anaerobic conditions, elevated temperature, or the presence of light.

[0115] In some embodiments, the promoter is a constitutive promoter. In some embodiments, the promoter is an inducible promoter. In some embodiments, the promoter is stress inducible (e.g., inducible by abiotic stress). In some embodiments, the promoter is pathogen inducible. In some embodiments, the promoter is induced upon infection by *Phytophthora* or *Verticillium*. Non-limiting examples of pathogen inducible promoters include Botrytis-Induced Kinase 1 (BIK1) and the plant defending gene PDF1.2. See, e.g., Penninckx *et al.*, *Plant Cell* 10:2103-2113 (1998); see also Veronese *et al.*, *Plant Cell* 18:257-273 (2006).

[0116] In some embodiments, a polyadenylation region at the 3'-end of the coding region can be included. The polyadenylation region can be derived from a variety of plant genes, or from T-DNA.

[0117] The vector comprising the sequences will typically comprise a marker gene that confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance,

particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

[0118] As detailed herein, embodiments of the present invention provide for transgenic plants comprising recombinant expression cassettes for expressing a polynucleotide sequence as described herein. In some embodiments, a transgenic plant is generated that contains a complete or partial sequence of a polynucleotide (e.g., an miRNA161 sequence or a promoter) that is derived from a species other than the species of the transgenic plant. It should be recognized that transgenic plants encompass the plant or plant cell in which the expression cassette is introduced as well as progeny of such plants or plant cells that contain the expression cassette, including the progeny that have the expression cassette stably integrated in a chromosome.

[0119] In some embodiments, the transgenic plants comprising recombinant expression cassettes for expressing a polynucleotide sequence as described herein have increased or enhanced pathogen resistance compared to a plant lacking the recombinant expression cassette, wherein the transgenic plants comprising recombinant expression cassettes for expressing the polynucleotide sequence have about the same growth as a plant lacking the recombinant expression cassette. Methods for determining increased pathogen resistance are described below.

[0120] A recombinant expression vector as described herein may be introduced into the genome of the desired plant host by a variety of conventional techniques. For example, the DNA construct may be introduced directly into the genomic DNA of the plant cell using techniques such as electroporation and microinjection of plant cell protoplasts, or the DNA construct can be introduced directly to plant tissue using ballistic methods, such as DNA particle bombardment. Alternatively, the DNA construct may be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. While transient expression of the polynucleotide sequence of interest is also encompassed by the disclosure, generally expression will be from insertion of expression cassettes into the plant genome, e.g., such that at least some plant offspring also contain the integrated expression cassette.

[0121] Microinjection techniques are also useful for this purpose. These techniques are well known in the art and thoroughly described in the literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski *et al. EMBO J.* 3:2717-2722 (1984). Electroporation techniques are described in Fromm *et al. Proc. Natl. Acad. Sci. USA* 82:5824 (1985). Ballistic transformation techniques are described in Klein *et al. Nature* 327:70-73 (1987).

[0122] *Agrobacterium tumefaciens*-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example, Horsch *et al. Science* 233:496-498 (1984), and Fraley *et al. Proc. Natl. Acad. Sci. USA* 80:4803 (1983).

[0123] Transformed plant cells derived by any of the above transformation techniques can be cultured to regenerate a whole plant that possesses the transformed genotype and thus the desired phenotype such as enhanced pathogen resistance. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium, typically relying on a biocide and/or herbicide marker which has been introduced together with the desired nucleotide sequences. Plant regeneration from cultured protoplasts is described in Evans *et al.*, *Protoplasts Isolation and Culture*, Handbook of Plant Cell Culture, pp. 124-176, MacMillan Publishing Company, New York, 1983; and Binding, *Regeneration of Plants, Plant Protoplasts*, pp. 21-73, CRC Press, Boca Raton, 1985. Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee *et al. Ann. Rev. of Plant Phys.* 38:467-486 (1987).

[0124] After the expression cassette is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

Alternatively, an endogenous promoter sequence can be altered (e.g., by one or more nucleotide change) to generate a higher expressing promoter. This latter method can involve introduction of a new expression cassette into the plant or can involve *in vivo* mutation, for example using a targeted nuclease (e.g., CRISPR, talens, zinc fingers) in combination with a second polynucleotide that is introduced by homologous recombination (and optionally a third targeting polynucleotide).

[0125] Plant gene manipulations can be precisely tailored in non-transgenic organisms using the CRISPR/Cas9 genome editing method. In this bacterial antiviral and transcriptional regulatory system, a complex of two small RNAs - the CRISPR-RNA (crRNA) and the trans-activating crRNA (tracrRNA) - directs the nuclease (Cas9) to a specific DNA sequence

5 complementary to the crRNA. Binding of these RNAs to Cas9 involves specific sequences and secondary structures in the RNA. The two RNA components can be simplified into a single element, the single guide-RNA (sgRNA), which is transcribed from a cassette containing a target sequence defined by the user. This system has been used for genome editing in humans, zebrafish, *Drosophila*, mice, nematodes, bacteria, yeast, and plants. In this system the nuclease
10 creates double stranded breaks at the target region programmed by the sgRNA. These can be repaired by non-homologous recombination, which often yields inactivating mutations. The breaks can also be repaired by homologous recombination, which enables the system to be used for gene targeted gene replacement. Promoter mutations can be introduced into plants using the CAS9/CRISPR system. Accordingly, in some embodiments, instead of generating a transgenic
15 plant, a native promoter sequence in a plant or plant cell can be altered *in situ* to generate a plant or plant cell carrying a polynucleotide comprising a mutated miRNA promoter as described herein.

[0126] The CRISPR/Cas system has been modified for use in prokaryotic and eukaryotic systems for genome editing and transcriptional regulation. The "CRISPR/Cas" system refers to a
20 widespread class of bacterial systems for defense against foreign nucleic acid. CRISPR/Cas systems are found in a wide range of eubacteria and archaeal organisms. CRISPR/Cas systems include type I, II, and III sub-types. Wild-type type II CRISPR/Cas systems utilize the RNA-mediated nuclease, Cas9 in complex with guide and activating RNA to recognize and cleave foreign nucleic acid. Cas9 homologs are found in a wide variety of eubacteria, including, but not
25 limited to bacteria of the following taxonomic groups: *Actinobacteria*, *Aquificae*, *Bacteroidetes*, *Chlorobi*, *Chlamydiae*, *Verrucomicrobia*, *Chloroflexi*, *Cyanobacteria*, *Firmicutes*, *Proteobacteria*, *Spirochaetes*, and *Thermotogae*. An exemplary Cas9 protein is the *Streptococcus pyogenes* Cas9 protein. Additional non-limiting examples of Cas9 proteins and homologs thereof have been described in literature. In some embodiments, the RNA-guided nuclease is a Cpf1 nuclease or a
30 Cas9 nuclease.

[0127] Accordingly, in one aspect, a method can be provided using CRISPR/Cas9 or Cpf1 to introduce at least one of the promoter mutations described herein into a plant cell. In some embodiments, a method of altering a (e.g., native) nucleic acid encoding the miRNA in a plant is described. In some embodiments, the method can comprise introducing into the plant cell an engineered, non-naturally occurring Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-CRISPR associated (Cas) (CRISPR-Cas) system as well as a guide nucleic acid (e.g., RNA) to introduce one or more alteration in an endogenous miRNA promoter. In some embodiments, the CRISPR-Cas system comprises one or more vectors comprising: (a) a first regulatory element operable in a plant cell operably linked to at least one nucleotide sequence encoding a CRISPR-Cas system guide RNA that hybridizes with the target sequence, and (b) a second regulatory element operable in a plant cell operably linked to a nucleotide sequence encoding a Type-II Cas9 or Cpf1 protein, wherein components (a) and (b) are located on the same or different vectors of the system, whereby the guide RNA targets the target sequence and the Cas9 protein cleaves the DNA molecule, whereby at least one of the promoter mutations described herein is introduced into the target nucleic acid.

[0128] The expression cassettes and constructs (e.g., expressing an miRNA as described herein) can be used to confer increased or enhanced pathogen resistance on essentially any plant. Thus, the methods have use over a broad range of plants, including species from the genera *Asparagus*, *Atropa*, *Avena*, *Brassica*, *Citrus*, *Citrullus*, *Capsicum*, *Cucumis*, *Cucurbita*, *Daucus*, *Fragaria*, *Glycine*, *Gossypium*, *Helianthus*, *Heterocallis*, *Hordeum*, *Hyoscyamus*, *Lactuca*, *Linum*, *Lolium*, *Lycopersicon*, *Mahus*, *Manihot*, *Majorana*, *Medicago*, *Nicotiana*, *Oryza*, *Panicum*, *Pannisetum*, *Persea*, *Pisum*, *Pyrus*, *Prunus*, *Raphanus*, *Secale*, *Senecio*, *Sinapis*, *Solanum*, *Sorghum*, *Trigonella*, *Triticum*, *Vitis*, *Vigna*, and *Zea*. In some embodiments, the plant is a cotton plant. In some embodiments, the plant is an ornamental plant. In some embodiments, the plant is a vegetable- or fruit-producing plant. In some embodiments, the plant is a monocot. In some embodiments, the plant is a dicot.

[0129] Plants (or parts of plants) with increased pathogen resistance can be selected in many ways. The following methods are but a few of the possibilities. One method of selecting plants or parts of plants (e.g., fruits and vegetables) with increased pathogen resistance is to determine resistance of a plant to a specific plant pathogen. Possible pathogens include, but are not limited

to, viruses, bacteria, nematodes, oomycetes, fungi or insects (see, *e.g.*, Agrios, *Plant Pathology* (Academic Press, San Diego, CA) (1988)). Resistance responses of plants vary depending on many factors, including what pathogen, compound, or plant is used. Generally, increased resistance is measured by the reduction or elimination of disease symptoms (*e.g.*, reduction in the number or size of lesions or reduction in the amount of pathogen biomass on the plant or a part of the plant) when compared to a control plant. In some embodiments, resistance is increased when the number or sizes of lesions or amount of pathogen biomass on the plant or on a part of the plant is decreased by at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more relative to a control (*e.g.*, relative to a plant in which a heterologous polynucleotide has not been expressed).

[0130] Increased pathogen resistance can also be determined by measuring the increased expression of a gene operably linked a defense related promoter. Measurement of such expression can be measured by quantifying the accumulation of RNA or subsequent protein product (*e.g.*, using northern or western blot techniques, respectively (see, *e.g.*, Sambrook *et al.* and Ausubel *et al.*).

EXAMPLES

Example 1

[0131] Plants have evolved complex immunity that must be defeated by pathogens to establish infection. The destructive eukaryotic pathogen *Phytophthora* encodes suppressors of RNA interference (RNAi), but it remains unknown whether they target a specific host RNAi pathway that confers resistance. Here, we show that *Phytophthora* infection of *Arabidopsis* plants leads to increased production of a diverse pool of secondary siRNAs. Instead of regulating endogenous genes, these siRNAs are found in extracellular vesicles and silence target genes in *Phytophthora* during natural infection. Introduction of a plant siRNA in *Phytophthora* leads to developmental deficiency and abolished virulence while *Arabidopsis* mutants defective in secondary siRNA biogenesis are hypersusceptible. Notably, we show that the *Phytophthora* RNAi suppressor PSR2 specifically inhibits secondary siRNA biogenesis in *Arabidopsis* and promotes infection. These findings reveal siRNAs as antimicrobial agents targeting eukaryotic pathogens and highlight a defense/counter-defense arms race centered on trans-kingdom gene silencing between hosts and pathogens.

[0132] Here, we report that *Phytophthora* infection induces the production of a diverse pool of secondary siRNAs from specific transcripts in *Arabidopsis*. These siRNAs function as a collection of antimicrobial agents and silence target genes in *Phytophthora* during infection. As a counter-defense mechanism, PSR2 blocks this host-induced gene silencing by suppressing the biogenesis of specific secondary siRNAs. Thus, hosts and pathogens are engaged in an arms race centered on cross-kingdom RNAi-based immunity.

Results

Secondary siRNA pathway is required for *Arabidopsis* defense against *Phytophthora*

[0133] In *Arabidopsis*, RNA-dependent RNA polymerase 6 (RDR6) and Suppressor of Gene Silencing 3 (SGS3) are responsible for the synthesis of long dsRNA precursors from miRNA-targeted transcripts and thereby are key components of secondary siRNA production (Adenot et al., 2006; Peragine et al., 2004). Infection assays using *Phytophthora capsici* strain LT263, which does not have a PSR2 homolog, showed that *rdr6* and *sgs3* mutants are hypersusceptible, with the *rdr6* mutant exhibiting the most severe disease symptoms (Figure 1A and 1B). Similarly, a transgenic *Arabidopsis* line (PSR2-5) that constitutively expresses *PSR2* under the CaMV 35S promoter (Qiao et al., 2013; Xiong et al., 2014) also showed enhanced susceptibility (Figure 1A and 1B). These results support a role of the secondary siRNA pathway in plant defense during *Phytophthora* infection.

PSR2 diminishes the accumulation of specific secondary siRNAs in *Arabidopsis*

[0134] A genome-wide small RNA profiling of PSR2-5 revealed a significant reduction in the 21-nucleotide population (Figure 1C), which is mainly composed of miRNAs and secondary siRNAs (Li et al., 2016). Further analysis of changes in individual 21-nucleotide sRNA classes revealed a moderate, 5%, reduction in the miRNA level; however, drastic decreases were observed in the abundances of secondary siRNAs generated from transcripts of *TAS1a/b/c*, *TAS2*, and several pentatricopeptide-repeat protein (PPR)-encoding gene loci (Figure 1D-1F). In contrast, siRNAs produced from RNA polymerase IV-dependent transcripts, the non-coding *TAS3* transcripts, or transcripts of other loci, including transposable elements and protein-coding genes other than *PPR*, remained mostly unchanged (Figure 1D-1F). These results demonstrate a specific inhibitory effect of PSR2 on secondary siRNAs generated from *PPR* and *TAS1/2* transcripts in *Arabidopsis*.

[0135] The largest reduction (>90%) of sRNAs in PSR2-5 was observed from *PPR*-derived secondary siRNAs (Figure 1D and 1E). *PPR* represents a large gene family with approximately 450 members encoded in *Arabidopsis* (Schmitz-Linneweber and Small, 2008). The vast majority of *PPR*-siRNAs are produced from transcripts of fifteen *PPR* loci and PSR2 inhibits siRNA production from all of them (Table S1). Thirteen of siRNA-generating *PPR* transcripts contain target site(s) of microR161 (miR161), which is predicted to trigger sRNA production through the secondary siRNA pathway (Table S1). Another microRNA, miR173, can target *TASI/2* transcripts and trigger the production of *trans*-acting siRNAs (tasiRNAs) (Chen et al., 2007; Chen, 2009). Several of these *TASI/2*-derived siRNAs have predicted targets sites in the siRNA-producing *PPR* transcripts and may also trigger siRNA production (Howell et al., 2007). Since *TAS* loci derived tasiRNAs exhibit an approximately 75% reduction in PSR2-5 plants (Figure 1D and 7A-D), the largely diminished *PPR*-derived siRNAs in PSR2-5 is likely attributed to inhibition of both miR161- and miR173-triggered siRNA production.

miR161 and PPR-siRNAs are induced during Phytophthora infection

[0136] In order to investigate a potential contribution of miR161 and miR173 in plant defense, we conducted quantitative RT-PCR analysis to examine the primary transcript levels of their corresponding *MIR* genes during *P. capsici* infection. We detected an induction of *pri-miR161* whereas the *pri-miR173* level remained unchanged (Figure 7A). Consistently, northern blotting of mature miRNAs showed that miR161 accumulation was increased during *P. capsici* infection, especially at 6 and 24 hours post inoculation (hpi) (Figure 2A). A similar induction was also observed for miR393 (Figure 7B), which is known to be induced by microbial pathogens (e.g. bacterial flagella) and to contribute to plant basal defense (Navarro et al., 2006). In contrast to miR161 and miR393, the abundance of miR173 was unaltered, consistent with the unchanged *pri-miR173* transcript levels determined by qRT-PCR (Figure 7A and 7B). We also quantified the levels of *pri-miR390* transcripts and mature miR390, which is the trigger of secondary siRNAs produced from the non-coding *TAS3* transcripts (Adenot et al., 2006; Axtell et al., 2006). Similar to miR173, miR390 was not induced during *P. capsici* infection (Figure 7A and 7B).

[0137] The induction of miR161 at 6 hpi suggested that *P. capsici* induces an immune response during the initial stages of infection in *Arabidopsis*. Plant immunity can be activated by “non-self” molecules called microbe-associated molecular patterns (MAMP) (Jones and Dangl,

2006). Perception of MAMPs requires pattern recognition receptors and co-receptors located on the plant cell surface (Boutrot and Zipfel, 2017). In *Arabidopsis*, the leucine-rich repeat receptor-like kinases BRASSINOSTEROID INSENSITIVE 1-ASSOCIATED KINASE 1 (BAK1) and SOMATIC-EMBRYOGENESIS RECEPTOR-LIKE KINASE 4 (SERK4) are required for the
 5 activation of plant immunity by functioning as co-receptors for multiple unrelated MAMPs (Chinchilla et al., 2009; Roux et al., 2011). The induction of miR161 or miR393 was abolished in *bak1-5/serk4* plants inoculated with *P. capsici* (Figure 2B), indicating that the enhanced accumulation of miR161 is a plant defense response elicited upon perception of the *Phytophthora* pathogen.

10 **[0138]** As a major trigger of siRNA production from *PPR* transcripts, increased levels of miR161 would be expected to enhance accumulation of *PPR*-derived secondary siRNAs (Addo-Quaye et al., 2008; Howell et al., 2007). Indeed, northern blotting showed that, similar to miR161, the levels of two representative secondary siRNAs (named *PPR*-siRNA-1 and *PPR*-siRNA-2; Figure 7C) were also increased during *P. capsici* infection at and after 6 hpi (Figure
 15 2A). As a control, tasiRNAs dependent on miR173 did not exhibit differential accumulations in infected plants, consistent with the unchanged levels of their “trigger” miRNA during infection (Figure 7D).

miR161 contributes to Arabidopsis defense to P. capsici by triggering PPR-siRNA production

20 **[0139]** We next determined the contribution of miR161 to *Arabidopsis* defense against *P. capsici*. For this purpose, we generated transgenic lines that either over-express *MIR161* (*MIR161ox*) or have the *MIR161* knocked out (*MIR161cri*, Figure 8A and 8B) using CRISPR/Cas9-based mutagenesis. Northern blotting confirmed increased accumulation of miR161 in independent *MIR161ox* lines or reduced accumulation in *MIR161cri* lines (Figure 2C). The *MIR161ox* plants showed enhanced resistance to *P. capsici* whereas the *MIR161cri*
 25 mutants exhibited hypersusceptibility (Figure 2C and 8C), suggesting a role of miR161 as a positive regulator of *Arabidopsis* defense. On the contrary, overexpression of miR173 or miR390 had no effect on *Arabidopsis* resistance to *P. capsici* (Figure 8D-8G).

30 **[0140]** Although the accumulation of *PPR*-siRNA-1 and *PPR*-siRNA-2 was decreased in *MIR161cri* lines (Figure 2C), it was not abolished, probably because *PPR*-siRNAs could also be triggered by miR173-dependent tasiRNAs. Indeed, in *MIR173* knockout lines (*MIR173cri*,

Figure 8H), the abundance of *PPR*-derived siRNAs was diminished (Figure 2D), likely due to the largely reduced tasiRNA levels (Figure 8I). Similar to the *MIR161cri* mutants, *MIR173cri* plants also showed enhanced susceptibility to *P. capsici* (Figure 2D and 8J). Note that *PPR*-derived siRNA levels in *MIR173ox* lines were similar to those in wild-type plants, although the corresponding tasiRNA levels were significantly increased (Figure 8D). This is in agreement with the previous results that the susceptibility of *MIR173ox* lines to *P. capsici* remained unchanged.

[0141] These results prompted us to examine the function of the *PPR*-derived siRNAs in plant immunity by analyzing individual mutants of eight *PPR* genes in a cluster on *Arabidopsis* chromosome 1, from which secondary siRNAs are abundantly produced in a miR161- and tasiRNA-dependent manner (Addo-Quaye et al., 2008; Howell et al., 2007). We acquired T-DNA insertion mutants, one for each *PPR* gene (Figure 9A), and confirmed that the corresponding transcripts were largely reduced if not diminished (Figure 9B). Presumably, the low transcript levels would nearly abolish secondary siRNA production. Significantly, four of these eight mutants showed increased susceptibility to *P. capsici* (Figure 2E and 9C), providing further evidence supporting that *PPR*-derived siRNAs contribute to plant immunity.

PPR-siRNAs target Phytophthora transcripts to confer resistance

[0142] In plants, secondary siRNAs are believed to amplify miRNA-mediated gene silencing, specifically by miRNAs that potentially regulate large gene families (Adenot et al., 2006).

Arabidopsis encodes approximately 450 *PPR* genes (Barkan and Small, 2014) and it was proposed that siRNAs derived from a small number of *PPR* transcripts regulate a larger number of family members (Fei et al., 2013). We conducted RNA-seq analysis and compared transcriptome changes in PSR2-5 with wild-type Col-0. Two hundred and forty-nine genes were found to be up-regulated in PSR2-5 and 366 were down-regulated (Figure 10A and Table S2). However, only 11 of the up-regulated genes were predicted to have target site(s) of *PPR*-derived siRNAs (3922 siRNAs in total). This is surprising because 1326 *Arabidopsis* genes, including 134 *PPR* genes, were predicted as potential targets of this large pool of siRNAs (Table S3 as depicted in Hou, et al., A Phytophthora Effector Suppresses Trans-Kingdom RNAi to Promote Disease Susceptibility, 25(1) *Cell Host & Microbe* 153-165 (Jan. 9, 2019)). Furthermore, among the 11 up-regulated genes that could also be targeted by *PPR*-siRNAs, only two have PPR motifs

(Figure 10B). These results indicate that the primary targets of the *PPR*-derived siRNA population are not *Arabidopsis PPR* genes.

[0143] Gene silencing in eukaryotic pathogens by plant hosts have been observed. The first example of this host-induced gene silencing (HIGS) during natural infection was reported in cotton, where two miRNAs regulate virulence-related genes in the fungal pathogen *Verticillium dahlia* (Zhang et al., 2016). Furthermore, transgenic plants expressing artificial RNAi-inducing dsRNAs can trigger specific gene silencing in fungal and *Phytophthora* pathogens, as well as other parasites (Baulcombe, 2015; Hua et al., 2017; Jahan et al., 2015). These observations indicate that host-produced sRNAs can function, in part, to silence pathogen genes. We thus tested whether the *PPR*-derived siRNAs may be used by *Arabidopsis* to target genes in *P. capsici* for silencing. A prediction of potential targets in *P. capsici* transcripts using 3922 distinct *PPR*-derived siRNA sequences revealed 437 siRNA-*P. capsici* transcript pairs (Figure 3A). These matched pairs correspond to 249 *P. capsici* genes as potential targets of *PPR*-siRNAs (Table S4).

[0144] To test whether some of the predicted targets could be silenced by the corresponding plant siRNAs, we directly introduced synthesized 21-bp small RNA duplexes into *P. capsici*, mimicking what may occur during natural infection (Figure 3A). For this purpose, we focused on a *PPR*-derived siRNA-1310 (hereafter siR1310), which is predicted to target the *P. capsici* gene *Phyca_554980* (Figure 3B). *Phyca_554980* is constitutively expressed in *P. capsici* (Chen et al., 2013). Encoding a U2-associated splicing factor, homologs of *Phyca_554980* are also present in other *Phytophthora* species (Figure 10C), consistent with a conserved, housekeeping function. In addition to siR1310, *Phyca_554980* is predicted to be regulated by six other *PPR*-siRNAs (Table S4), including siR0513 (Figure 3B). Taken together, these results indicate that *Phyca_554980* might be an important target of *PPR*-siRNAs in *Phytophthora*.

[0145] Using a PEG-mediated transformation procedure, we incubated *P. capsici* protoplasts with the synthesized siR1310 duplex and a plasmid carrying a gene that confers resistance to the antibiotic G418. Transformants that gained G418 resistance potentially also took up the sRNAs. As a control, a 21-bp sRNA duplex designed to target a *GFP* gene was also synthesized and introduced into *P. capsici*. Seven of ten transformants potentially harboring siR1310 exhibited significantly reduced abundance of *Phyca_554980* transcripts (Figure 3C and 11A). This silencing effect is specific as *Phyca_554980* transcript levels were not affected in strains

transformed with siRGFP (Figure 3C and 11A). We further confirmed the silencing specificity of siR1310 by examining the transcript levels of another *P. capsici* gene *Phyca_538731*, which was used as an “off-target” control. *Phyca_538731* is predicted to be insufficient as a silencing target although it contains a sequence that partially matches siR1310 (Figure 11B). The transcript
5 abundance of *Phyca_538731* was not reduced in transformants harboring either siR1310 or siRGFP (Figure 3C).

[0146] Knowing that siR1310 can specifically silence target gene(s) in *Phytophthora*, we determined the consequence of the silencing event by analyzing the developmental phenotypes and virulence activities of the *P. capsici* transformants. Compared to a wild-type strain and the
10 transformants harboring siRGFP, transformants harboring siR1310 exhibited a moderate decrease in mycelial growth (Figure 11C and 11D) and significant defects in sporangia development (Figure 3D) and zoospore release (Figure 11E). Importantly, introduction of siR1310 nearly abolished the ability of *P. capsici* to cause disease on *Nicotiana benthamiana* (Figure 3E). Because the leaves were inoculated with mycelia plugs, the drastically reduced
15 virulence activity cannot be fully attributed to defects on sporulation of these transformants. These data indicate that *PPR*-derived siRNAs can specifically silence target gene(s) in *P. capsici* such as *Phyca_554980*, which is required for *Phytophthora* development and pathogenicity. As such, *PPR*-derived siRNAs may contribute to resistance to *P. capsici*.

PPR-siRNAs confer cross-kingdom gene silencing during Phytophthora infection

[0147] To explore whether *PPR*-derived siRNAs could be transported from host plants to
20 *Phytophthora*, we examined their presence in extracellular vesicles (EVs). A role of EVs in plant immunity has been proposed as they accumulate around fungal haustoria (An et al., 2006a; An et al., 2006b; Micali et al., 2011), and have recently been shown to carry stress-response proteins (Rutter et al., 2017) and small RNAs (Cai et al., 2018). Using qRT-PCR, we were able to detect
25 siR1310 in EVs isolated from wild-type *Arabidopsis* leaves (Figure 3F). The abundance of these siRNAs was significantly lower in EVs isolated from PSR2-5 leaves, consistent with an overall reduction of siR1310 in PSR2-5. Furthermore, *P. capsici* infection resulted in an increase of siR1310 abundance in EVs and this increase was abolished in PSR2-5 plants inoculated with *P. capsici* (Figure 3F). Similarly, siR0513, another *PPR*-siRNA that can target *Phyca_554980*,

could also be detected in EVs (Figure 11F). These results suggest that *PPR*-siRNAs are cargos of EVs and could be transported to silence target gene(s) in *Phytophthora*.

[0148] We next examined whether cross-kingdom gene silencing by *PPR*-siRNAs occurs during natural infection by monitoring the expression profiles of *Phyca_554980* when wild-type *P. capsici* was used to inoculate wild-type *Arabidopsis*, PSR2-5, *rdr6* or the *MIR161ox-3* plants. The transcript abundances of *Phyca_554980* were determined at one day post inoculation (dpi). We observed that *Phyca_554980* exhibited increased expression levels when *P. capsici* was used to infect PSR2-5 or *rdr6* plants (Figure 3G), which have decreased accumulation of *PPR*-siRNAs compared to wild-type plants. In contrast, *Phyca_554980* transcript level was decreased when *P. capsici* was used to infect *MIR161ox-3* plants (Figure 3G), which, at least in part, could be due to the enhanced silencing effect by an increased level of *PPR*-derived siRNAs. These results suggest that *Phyca_554980* expression in *P. capsici* is manipulated by host siRNAs during infection, potentially through the function of *PPR*-siRNAs in EVs such as siR1310 and siR0513.

[0149] Since *Phyca_554980* plays an important role in the development and virulence activity of *P. capsici*, its expression could be affected by multiple factors in addition to host siRNAs. To further demonstrate that cross-kingdom gene silencing occurs during natural infection, we generated *P. capsici* strains carrying a reporter to monitor the silencing effect of siR1310. A siR1310 target site (t) and a mutant version (mt) were incorporated into the 5' UTR sequence of an *mRFP* gene to generate *t-mRFP* and *mt-mRFP*, respectively (Figure 4A). These constructs were then introduced into *P. capsici*. Transformants with stable RFP expression were monitored for *mRFP* transcript levels during the infection of wild-type, *MIR161ox*, and *MIR161cri* plants, which accumulate different levels of siR1310 (Figure 11G). *P. capsici* carrying *t-mRFP* showed higher fluorescence intensities in hyphae when infecting *MIR161cri-8* plants compared to wild-type plants, whereas the lowest fluorescence signals were observed in hyphae infecting the *MIR161ox* plants (Figure 4B and 4C). In contrast, a strain carrying *mt-mRFP* did not show observable differences in fluorescence intensities from hyphae infecting these lines (Figure 4B and 4C). A similar conclusion was made by quantifying the transcript levels of *mRFP* by qRT-PCR (Figure 4D). Collectively, these results support direct gene silencing by siR1310, and possibly other *PPR*-derived siRNAs produced by *Arabidopsis*, in *P. capsici* during natural infection as an antimicrobial mechanism.

PSR2 interferes with secondary siRNA production by associating with DRB4

[0150] We next investigated the molecular basis underlying PSR2-mediated suppression of secondary siRNA accumulation in *Arabidopsis* by characterizing PSR2-interacting proteins. Using Yeast two-hybrid screening of an *Arabidopsis* cDNA library, we identified candidates that may associate with PSR2 in plant cells (Table S5). Among them, we were particularly interested in Double stranded RNA-binding protein 4 (DRB4), which has a known function in secondary siRNA biogenesis. DRB4 binds to dsRNA precursors through two double stranded RNA-binding domains (dsRBM1 and dsRBM2) and associates with Dicer-like 4 (DCL4), which processes the dsRNA substrates (Adenot et al., 2006; Fukudome et al., 2011). Co-immunoprecipitation of PSR2 with DRB4 after expressing both proteins in *N. benthamiana* confirmed their interaction in plant cells (Figure 5A and 5B). Furthermore, the two dsRBM domains of DRB4 are required for its interaction with PSR2.

[0151] PSR2 protein has a modular architecture, containing seven imperfect tandem repeats (Ye and Ma, 2016). Repeats 2-7 each includes three conserved motifs, which were named “L”, “W”, and “Y” after a conserved amino acid residue in their respective sequences (Jiang et al., 2008; Ye and Ma, 2016). Repeat 1 lacks an “L” motif, but contains the “W” and the “Y” motifs (Figure 5A). Analysis of truncated mutants of PSR2 revealed that the first (WY1) and the second (LWY2) repeat units are required for interaction with DRB4 (Figure 5C). Consistent with this observation, the mutants PSR2^{ΔWY1} and PSR2^{ΔLWY2} lost the ability to suppress transgene silencing (Figure 5D and 12A) or promote *Phytophthora* infection in *N. benthamiana* (Figure 5E and 12B). In addition, a fragment of PSR2 (55-215 aa), which spans WY1 and LWY2, is sufficient for association with DRB4 (Figure 5C). This fragment is also sufficient, although with an activity slightly weaker than full-length PSR2, to suppress transgene silencing (Figure 5D and 12A) and promote *Phytophthora* infection (Figure 5E and 12B). These results form a strong link between DRB4 interaction and the virulence function of PSR2.

[0152] Next, we explored how PSR2 may affect secondary siRNA biogenesis through the interaction with DRB4. We first examined whether PSR2 could interfere with the dicing of dsRNA substrates. Long dsRNAs (510 bp in length, corresponding to *GFP* sequence) were synthesized in vitro, labeled with ³²P, and then incubated with crude protein extracts of leaf tissues collected from wild-type, PSR2-5, or *drb4* plants. Cleavage products of sRNAs with 20-

25 nt in size were then detected by autoradiography. Extracts from both *drb4* and PSR2-5 plants showed reduced production of sRNAs, suggesting that PSR2 interferes with the dicing process (Figure 5F). We further examined whether PSR2 can bind dsRNAs in plant cells. YFP-PSR2 and DRB4-YFP were expressed independently in *N. benthamiana* and then pulled down using resins conjugated with an anti-GFP antibody. The protein-bound resins were incubated with the in vitro synthesized 510-bp dsRNAs and those bound to the immunoprecipitated proteins were detected. Our results show that both PSR2 and DRB4 associates with dsRNAs (Figure 12C). This might be due to a direct binding of PSR2 with dsRNAs, which may lead to competition with DRB4 for binding to dsRNA precursors. Or, it is also possible that PSR2 indirectly binds to dsRNAs by associating with the dicing complex and interferes with the processing of the dsRNA substrates.

drb4 phenocopies PSR2-5 plants

[0153] To further demonstrate that DRB4 is a virulence target of PSR2, we examined the development and disease susceptibility phenotypes of an *Arabidopsis drb4* mutant. Similar to PSR2-5, *drb4* is hypersusceptible to *P. capsici* (Figure 6A and 12D). In addition, both PSR2-5 and *drb4* exhibit a subtle developmental phenotype, i.e. narrow and curly leaves (Figure 6B). A similar, but more profound, leaf phenotype has been reported in *rdr6* (Peragine et al., 2004), indicating that it is likely associated with secondary siRNA production. Genome-wide sRNA profiling analysis further confirmed that as all siRNA-producing *PPR* loci were affected by *RDR6* and PSR2, most of them were also affected by *DRB4* (Figure 6C). On the contrary, siRNAs produced from transcripts encoding nucleotide-binding site leucine-rich repeat proteins (NB-LRR) were unaffected in either PSR2-5 or *drb4* plants although their production is fully dependent on RDR6 (Table S6). Encoding canonical disease resistance proteins, *NB-LRRs* constitute another large gene family that can produce secondary siRNAs (Zhai et al., 2011). The observation that PSR2 does not have a major impact on *NB-LRR*-derived siRNAs is intriguing because reduced abundance of these siRNAs may lead to increased expression of disease resistance genes that could be detrimental to the pathogen. Although it remains to be determined how PSR2 and DRB4 specifically affects *PPR*-derived but not *NB-LRR*-derived siRNAs, these results support DRB4 as a virulence target of PSR2 in *Arabidopsis*.

Discussion

[0154] Here, we show that siRNAs derived from endogenous plant transcripts target mRNAs of a eukaryotic pathogen *in trans*. Consistent with their importance as an antimicrobial strategy, the biogenesis of secondary siRNAs is specifically suppressed by the *Phytophthora* effector

5 PSR2. RNAi-based immunity thus represents an important battleground in the evolution of host-pathogen interactions.

[0155] Host-derived sRNAs have been found to facilitate plant defense to fungal pathogens.

Two miRNAs were shown to be exported from cotton and to reduce the virulence of *Verticillium dahlia* (Zhang et al., 2016). Furthermore, plant EVs were recently reported to mediate the

10 transportation of host sRNAs that can target virulence genes of another fungal pathogen *Botrytis cinerea* (Cai et al., 2018). In this study, we show secondary siRNAs are important executors of

host-induced gene silencing in an oomycete pathogen, which is evolutionarily very distant from fungi (Kamoun et al., 2015). Perception of *P. capsici* by *Arabidopsis* induces a transcriptional

induction of the trigger miRNA, miR161, which subsequently results in increased production and

15 accumulation of secondary siRNAs derived from specific *PPR* transcripts. The diverse *PPR*-siRNA pool includes numerous sequences, some of which can directly silence transcripts in *P. capsici*. Interestingly, miR161 can also be induced by bacterial flagellin (Li et al., 2010),

indicating that the production of secondary siRNAs is a general immune response triggered by a

broad spectrum of pathogens. Indeed, 216 siRNA-target pairs representing 150 potential targets

20 can be predicted from the fungal pathogen *Verticillium dahliae* (Table S4). It is therefore likely

that *PPR*-derived siRNAs also target mRNAs in *V. dahliae* for silencing. Consistent with this

notion, *rdr6* mutants of *Arabidopsis* exhibit hypersusceptibility to *V. dahlia* as well as *B. cinerea* (Ellendorff et al., 2009; Cai et al., 2018).

[0156] Secondary siRNAs have been implicated in playing a role in host-parasite interactions.

25 It was recently reported that miRNAs produced by the parasitic plant *Cuscuta campestris*

triggered siRNA production in host plants and manipulated host gene expression (Shahid et al.,

2018). In our study, secondary siRNAs produced by plant hosts function as antimicrobial agents.

The abundance and sequence complexity of secondary siRNAs is much higher than their miRNA triggers, which provides advantages during a co-evolutionary arms race with the pathogens.

30 During host-pathogen co-evolution, it would be expected that pathogen genes targeted by host

sRNAs are under strong selection to diversify, which could abolish sequence complementarity and thus evade silencing. Because *MIR* genes must maintain a foldback structure in their primary transcripts for processing, they are constrained in how rapidly they can evolve, which would be expected to compromise their utility as direct antimicrobial agents. The induction of a diverse pool of secondary siRNAs upon pathogen perception facilitates co-evolution with sequence changes in the targeted pathogen genes. This is particularly robust when the siRNAs are generated from non-coding genes (such as *TAS* in *Arabidopsis*) or genes within large families (such as *PPR*). Production of secondary siRNA from *PPR* transcripts is prevalent in eudicots, suggesting an ancient and potentially essential function (Xia et al., 2013). Most eudicot species encode over 400 *PPR* genes in their genome (Barkan and Small, 2014), but only a small number produce siRNAs. These siRNA-producing *PPRs* constitute a monophyletic clade that is evolving rapidly, possibly driven by the arms race with pathogens (Dahan and Mireau, 2013). None of the *PPR* mutants in the secondary siRNA-generating cluster that we examined exhibit morphological defects in *Arabidopsis*, indicating that these genes may tolerate sequence changes.

[0157] The presence of *PPR*-siRNAs in EVs suggests a potential mechanism for trafficking of pathogen-targeting sRNAs from plant hosts to pathogens. EVs mediate intercellular transport of sRNAs in mammals (Meldolesi, 2018), and have been shown to transport sRNAs from parasitic nematodes into mammalian host cells, where they suppress host immune responses (Buck et al., 2014). Notably, nematode EVs were recently shown to be specifically enriched in secondary siRNAs (Chow et al., 2018). In addition, purified plant EVs have been shown to be taken up by fungal hyphae in culture (Regente et al, 2017; Cai et al, 2018), indicating they could deliver sRNAs to pathogens. Global analysis of sRNA composition in plant EVs shows that siRNAs are the major sRNA cargo in terms of abundance (Baldrich, Rutter, Innes and Meyers, unpublished data). These results, together, support secondary siRNAs as prominent executors for cross-kingdom silencing.

[0158] Host defense mechanisms and pathogen virulence strategies are linked. Successful pathogens must defeat host immunity in order to establish infection. By investigating the function of PSR2, we demonstrate that *Phytophthora* pathogens have evolved effectors to suppress siRNA-based immunity. PSR2 is a conserved effector in *Phytophthora* (Xiong et al., 2014), thus, suppression of secondary siRNA production is likely a common virulence strategy

of *Phytophthora* and may also be employed by other fungal and oomycete pathogens that are potentially targeted by host-induced gene silencing.

[0159] Taken together, this work establishes a role for secondary siRNAs in plant immunity and sets the foundation for manipulating this particular pathway as a strategy to enhance broad-spectrum resistance to plant disease.

Materials and Methods

Plant Material and Growth Conditions

[0160] *Arabidopsis thaliana* ecotype Col-0 was used as wild-type and for generating transgenic lines. T-DNA insertion lines of AT1G62910 (SALK_152489), AT1G63130 (SAIL_119_G05), AT1G62930 (SAIL_18_E04), AT1G63080 (SALK_020638C), AT1G63400 (CS316928), AT1G63150 (SALK_152489), AT1G62590 (SALK_114012), and AT1G62914 (CS433098) were obtained from the Arabidopsis Biological Resource Center (ABRC). PSR2-5 are used from lab seeds stock. *Arabidopsis* and *Nicotiana benthamiana* plants were grown at 22±2°C with a 12 h light/12 h dark photoperiod.

Cloning and constructs

[0161] To construct miRNA overexpression lines in *Arabidopsis*, DNA sequences encoding the pri-miRNAs of miR161, miR173 and miR390 were amplified from cDNA of *Arabidopsis* Col-0 by PCR using gene-specific primers (listed in Table S7). The PCR products were inserted into pENTR/D-TOPO and subsequently pEG100 using Gateway cloning (Invitrogen) (Earley et al., 2006). To generate the knockout lines of miR161 and miR173, the *Yao* promoter-driven CRISPR/Cas9 system was utilized (Yan et al., 2015). The sgRNA cassettes were cloned into pCAMBIA1300-pYAO:Cas9 into the *SpeI* site. To construct an mRFP reporter containing the target site of siR1310, sequences corresponding to the sense and antisense strands of the siR1310 target site or mutated target site were synthesized and annealed respectively. The DNA fragments were then ligated with pTOR-mRFP into the *EcoRI* site.

Phytophthora capsici inoculation and phenotypic analysis

[0162] In most experiments, four-week-old *Arabidopsis* plants were inoculated with zoospore suspension (200-500 zoospores/μL) of *P. capsici* isolate LT263 as previously described (Hou and Ma, 2017). Disease symptoms were monitored three days after inoculation, and disease severity was evaluated as Mean DSI (Wang et al., 2013). Biomass of *P. capsici* was also

determined by qPCR using *P. capsici* specific primers (listed in Table S7) (Silvar et al., 2005). For root infection, roots of two-week old seedlings, grown on MS medium (Murashige and Skoog agar containing 1% (wt/vol) sucrose) were dipped in a zoospores suspension (100 zoospores/ μ L) for five seconds as described (Wang et al., 2013). The seedlings were immediately planted in soil and the disease symptoms were monitored at three days after inoculation. For inoculation of *N. benthamiana*, the abaxial sides of detached leaves were inoculated with fresh mycelial plugs (0.5 cm). Leaves were kept in sealed 0.8% water agar plates in the dark at 25°C. Lesions were observed under UV light three days after inoculation. Sizes of the lesion areas were analyzed using imageJ (imagej.net).

Isolation of extracellular vesicles (EVs)

[0163] For each biological replicate, EVs were isolated from the pooled apoplastic fluid of 36 five-week old *Arabidopsis* plants grown at 22 $\pm$ 2°C with a 9 h light/15 h dark photoperiod following the protocol of Rutter et al. (2017), including fractionation on an iodixanol density gradient (OptiPrep, Sigma Aldrich). Purified EVs were quantified using a ZetaView nanoparticle tracking analyzer from ParticleMetrix. Approximately 10 x 10⁹ EVs from each replicate were used for RNA extraction.

RNA extraction, northern blotting and quantitative real-time PCR

[0164] Total RNAs were extracted from *Arabidopsis* leaves and EVs with or without infection at different time points using TRIzol reagent (Invitrogen). Small RNA northern blotting was performed as described using 5 μ g of total RNA extract (Pall and Hamilton, 2008). U6 was used as a loading control. The results were visualized using a Typhoon phosphorimager and quantified with ImageQuant TL (GE). Sequences of the oligonucleotide probes are listed in Table S7. For quantitative RT-PCR, three biological repeats were performed, and relative expression levels were calculated using the $2^{-\Delta\Delta C_t}$ equation. *Actin2* was used as the internal control. Gene-specific primers used for qRT-PCR are listed in Table S7. For Figure 11G, siRNA levels were quantified using stem-loop qRT-PCR as described in (Varkonyi-Gasic et al., 2007) starting with 1.0 μ g total RNA from leaves. For Figures 3F and 11F, siRNA levels were quantified using the QuantiMir kit from System Biosciences (Mountain View, CA), starting with 2.0 μ g total RNA from leaves, diluting the resulting cDNA 100 fold, and then using 2-4 μ L of diluted cDNA for each 25 μ L

reaction. For both stem-loop and QuantiMir methods, the qRT-PCR step was performed using SYBR™ Green PCR Master Mix from Invitrogen and using U6 as an internal control.

Transformation of sRNAs into *Phytophthora* protoplasts

[0165] RNA oligonucleotides corresponding to siRGFP and siR1310 were synthesized and annealed to form siRNA duplex (listed in Table S7). A polyethylene glycol (PEG)-mediated protoplast transformation procedure was followed as described with modifications (Dou et al., 2008). Protoplasts of *P. capsici* isolate LT263 were prepared as described with a concentration of 2×10^4 protoplast per mL. 25 µg of *pTOR* plasmid DNA and 8 µg of siRNA duplex were added into 1 mL of protoplast suspension for transformation (Blanco and Judelson, 2005; Varkonyi-Gasic et al., 2007). Transformants were recovered in pea medium and then selected on V8 agar plates supplemented with 50 µg /mL of G418. Transformants with G418 resistance were sub-cultured and analyzed for development and virulence activity. Mycelia from each transformant were collected for RNA extraction and gene expression analysis.

Microscopy of *Phytophthora capsica* during infection

[0166] Four-week-old *Arabidopsis* plants were inoculated with a zoospore suspension (200-500 zoospores/µL) of *P. capsici* transformants expressing t-mRFP or mt-mRFP. Confocal images were captured at 2 dpi using a Leica SP5 confocal microscope under 40x lens. The average fluorescence strength of the entire hyphae in the images was estimated using Image J (<http://imagej.nih.gov/ij/>).

Co-immunoprecipitation assays of PSR2 and DRB4

[0167] 3xFlag-PSR2, DRB4-YFP and their derivatives were co-expressed in *N. benthamiana* using *Agrobacterium*-mediated infiltration. Total proteins were extracted using an IP buffer [10% (v/v) glycerol, 50 mM Tris-HCl pH 7.5, 150 mM NaCl, 5 mM DTT, 1x protease inhibitor mixture (Roche), 1 mM PMSF, and 0.1% CA-630], and then incubated with either anti-Flag agarose (Sigma-Aldrich) or anti-GFP magnetic beads (Chromotek) at 4°C for one hour. The beads were washed for five times using the IP buffer, and PSR2 and DRB4 in the immune complexes were detected by western blotting using anti-Flag (Sigma Aldrich) or anti-GFP antibody (Clontech) respectively.

Transgene silencing suppression assay using *N. benthamiana* 16c plants

[0168] PSR2 and its derivatives were cloned into the vector pEG100 and the recombinant plasmids were transformed into *Agrobacterium tumefaciens* strain GV3101. The bacteria were co-infiltrated into *N. benthamiana* 16c leaves together with *Agrobacterium* carrying 35S-GFP (Qiao et al., 2013). Green fluorescence was observed using a hand-held UV light at five days after *Agro*-infiltration. The protein levels of GFP were determined by western blotting using an anti-GFP antibody (Santa Cruz). The protein levels of PSR2 and its derivatives were examined by western blotting using an anti-PSR2 antisera generated in this study.

Double-stranded RNA binding and cleavage assays

[0169] Sense and antisense transcripts of green fluorescent protein (GFP) were synthesized from a plasmid template containing a partial GFP gene with 510-bp in length. In vitro transcription was conducted by incubating 0.1 μ M plasmid DNA in a 50 μ L reaction system with 0.5 μ M of T7 RNA polymerase and 5 mM of NTP mix for 3 hours at 37°C. 2 U Turbo DNase (Ambion) was added to the reaction mixture at 37°C for 15 minutes to remove the template DNA. Nucleotides and NTPs were also removed using Bio-Spin 6 columns (BioRad). Single-stranded RNAs were purified using acidic phenol/chloroform (Ambion), and precipitated using isopropanol (FisherChemical). RNA pellet was then dissolved in 30 μ L RNase-free water. Equal amounts of the ssRNAs were annealed as described and used for further analyses (Fukudome et al., 2011). For protein-dsRNA binding assay, YFP-PSR2 and DRB4-YFP fusion proteins were transiently expressed in *N. benthamiana* and total proteins were extracted using the IP buffer containing 10% (vol/vol) glycerol, 50 mM Tris-HCl (pH 7.5), 150 mM NaCl, 5 mM DTT, 1x protease inhibitor mixture (Roche), 1 mM PMSF, and 0.1% CA-630. Double-stranded RNA was removed by adding 7 μ L of RNaseIII (NEB), 10 μ L of 10x RNaseIII buffer and 10 μ L of 10x MnCl₂ to 1 mL of protein extract. Samples were then centrifuged at 12,000 rpm, 4°C for 15 min and the supernatant incubated with anti-GFP magnetic beads for two hours at 4°C (Chromotek). After washing beads, synthesized 510-bp dsRNAs were added to a final concentration of ~33 nM and incubated with the immune complexes at 4°C in a dsRNA-binding buffer containing 30 mM Tris-HCl (pH 7.0), 10 mM NaCl, 20 mM MgCl₂, 0.1 mM EDTA, and 5 mM DTT for 30 minutes. The beads were washed with binding buffer to remove the unbounded dsRNA before the protein-bounded RNAs were extracted using Trizol/Chloroform (Ambion) and then analyzed on 2% Agarose gel with ethidium bromide staining. For the dsRNA cleavage assay, 510-bp

dsRNAs synthesized as above were labeled with [α - 32 P] UTP as described (Fukudome et al., 2011). Crude protein extracts from 0.5 g leaves of four-week-old wild-type, *drb4* and PSR2-5 *Arabidopsis* plants were extracted using an extraction buffer containing 20 mM Tris-HCl (pH 7.5), 4 mM MgCl₂, 5 mM DTT, 1x protease inhibitor mixture (Roche) and 1 mM PMSF at 4°C. The 32 P-labeled dsRNAs (final concentration of ~1 nM) were incubated with 30 μ L of the cleavage buffer as described (Fukudome et al., 2011). One μ L of RNaseOUT (Invitrogen) was added to each 40 μ L reaction mixture. After incubation at 23°C for two hours, the cleavage products were purified by phenol/chloroform (Ambion), analyzed on 15% denaturing PAGE with 8 M urea, and detected by autoradiography.

10 RNA sequencing and data analysis

[0170] sRNA libraries were single-end sequenced on the Illumina HiSeq4000 platform with read lengths of 50 bases. Adapter sequences were trimmed from fastq reads using Cutadapt v1.4.1 (Martin, 2011), the remaining sequences in the size range of 18- to 28-nt were mapped to the *Arabidopsis thaliana* reference genome annotation (TAIR10) using Bowtie v1.0.1

(Langmead et al., 2009), allowing all alignments (-a) and zero mismatch (-v 0) per read. After removing the reads associated with t/r/sn/snoRNAs, the rest of the perfectly matched 18-28 nt sRNAs were used for further analysis. The sequences of mature miRNAs were from miRbase (version 21), and eight *TAS* loci: *TAS1a*, *TAS1b*, *TAS1c*, *TAS2*, *TAS3*, *TAS3b*, *TAS3c* and *TAS4* for trans-acting siRNAs identification. The list of Pol IV-dependent siRNA loci (P4siRNAs) has been previously described (Zhai et al., 2015). Protein-coding gene-derived siRNAs (PC-siRNAs) and transposon element derived siRNAs (TE-siRNAs) were calculated using Araport11 annotation (Cheng et al., 2017), with 27,655 protein-coding regions and 3,901 TEs. For normalization, the abundances of sRNAs in each library were normalized to transcripts per million (TPM), excluding t/r/sn/snoRNA-derived sequences. The abundance of sRNAs from each locus was summed by hits-normalized-abundance of all mapped reads from that region. Loci with normalized TPM >10 in WT were further analyzed for abundance changes in PSR2-5 (Table S1).

[0171] RNA-seq libraries were analyzed using paired-end sequencing on the Illumina HiSeq4000 platform with read lengths of 150 bases. Reads were mapped to the TAIR10 genome using HISAT2 v2-2.0.5 (Kim et al., 2015) allowing only one unique hit (-k 1) and length

less than 5000 (-X 5000). PCR duplicates were further removed using SAMTools v1.4 (Li et al., 2009). FPKM (Fragments Per Kilobase of transcript per Million mapped reads) of each gene was calculated using StringTie v1.3.3b (Pertea et al., 2015), and edgeR (Robinson et al., 2010) was used to identify genes that were differentially expressed between PSR and WT replicates.

5 siRNA target prediction in *Arabidopsis*, *Phytophthora capsici* and *Verticillium dahliae*

[0172] 3922 distinct *PPR*-derived siRNA sequences were used for target prediction using the psRNATarget web server (<http://plantgrn.noble.org/psRNATarget>) (Dai and Zhao, 2011).

Default setting of Schema V1 was used. For target prediction in *Arabidopsis*, “*Arabidopsis thaliana*, transcript, JGI genomic project, Phytozome 12, 167_TAIR10” was chosen as the target
10 file. For target prediction in *P. capsici*, “Phyca11_filtered_transcripts.fasta” was downloaded as the target file from JGI (<https://genome.jgi.doe.gov/Phyca11/Phyca11.home.html>). For target prediction in *V. dahliae*, “*Verticillium dahliae* v1.0” was downloaded as the target file from JGI (<https://genome.jgi.doe.gov/Verdal/Verdal.home.html>). Genes with expectation ≤ 2 were considered as potential targets of *PPR*-derived siRNAs.

15 Statistical data analysis

[0173] Data reported in this study were analyzed using JMP Pro v13.0 (SAS). To test for normal distribution of the collected data, normal quantile plots were inspected and Shapiro-Wilk goodness-of-fit tests were performed. To ensure that the variances are equal, the Levene's test was used. When comparing a test group to a control group, a two-tailed Student's t-test was used.

20 The significance values are reported as follows: $*$ = $p < 0.05$, $**$ = $p < 0.01$, and $***$ = $p < 0.001$. When comparing the means of multiple groups, a one-way ANOVA followed by Tukey's HSD post hoc test was performed. Significant differences between groups ($p < 0.05$) are denoted with different letters.

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[0174] The following references were referred to in this disclosure:

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Supplementary Tables

Table S1. Normalized reads of 21-nt siRNAs produced from individual loci in wild-type (WT) and PSR2-5 *Arabidopsis* plants. Note: The normalized reads of siRNAs are presented by transcripts per million (TPM).

5

TPM of 21nt siRNA

sRNA classes	Col-rep1	Col-rep2	PSR-rep1	PSR-rep2
miRNA	98440.62	107610.77	73074.24	72731.49
PolIV	6136.44	6197.19	5895.04	5758.75
PPR	4204.577	4442.467	332.482	257.305
TAS	26857.19	27664.42	5310.14	5015.75
TE	3083.74	3113.00	2809.61	2762.74
protein coding	33486.19	32038.30	20723.21	21878.18

TPM of 21nt sRNA from PPR loci

	Gene	annotation	Predicted target of miR161	Predicted target of tasiRNA	Col-rep1	Col-rep2	PSR-rep1	PSR-rep2
chr1:4183066-4186124	AT1G12300	Tetratricopeptide repeat (TPR)-like superfamily protein	N	Y	27.20	20.81	2.39	0.85
chr1:4353906-4355929	AT1G12775	Pentatricopeptide repeat (PPR) superfamily protein	N	Y	50.25	38.87	7.71	6.80
chr1:23176930-23179248	AT1G62590	pentatricopeptide (PPR) repeat-containing protein	Y	Y	1329.51	1411.09	114.64	70.81
chr1:23299057-23300958	AT1G62910	Pentatricopeptide repeat (PPR) superfamily protein	Y	Y	1835.84	1955.45	138.58	103.77
chr1:23301576-23303162	AT1G62914	pentatricopeptide (PPR) repeat-containing protein	Y	Y	2207.43	2240.55	165.44	126.53
chr1:23306534-23308683	AT1G62930	Tetratricopeptide repeat (TPR)-like superfamily protein	Y	Y	1659.49	1785.58	129.54	98.03
chr1:23385324-23387167	AT1G63070	Pentatricopeptide (PPR) repeat-containing protein	Y	Y	1429.051	1571.13	114.1079	76.97894
chr1:23387631-23390816	AT1G63080	Pentatricopeptide repeat (PPR) superfamily protein	Y	Y	2458.99	2592.41	172.62	141.20
chr1:23412730-23415149	AT1G63130	Tetratricopeptide repeat (TPR)-like superfamily protein	Y	Y	2551.81	2776.00	172.89	138.01

chr1:23419396-23421579	AT1G63150	Tetratricopeptide repeat (TPR)-like superfamily protein	Y	Y	1257.18	1291.52	119.69	88.25
chr1:23450654-23452311	AT1G63230	Tetratricopeptide repeat (TPR)-like superfamily protein	Y	Y	32.97	30.86	5.05	3.40
chr1:23489840-23491519	AT1G63330	Pentatricopeptide repeat (PPR) superfamily protein	Y	Y	1340.395	1422.751	116.5017	72.08801
chr1:23507320-23509053	AT1G63400	Pentatricopeptide repeat (PPR) superfamily protein	Y	Y	2269.20	2328.80	166.77	123.34
chr1:23587298-23588220	AT1G63630	Tetratricopeptide repeat (TPR)-like superfamily protein	Y	Y	142.75	109.74	43.89	34.45
chr5:5460976-5463017	AT5G16640	Pentatricopeptide repeat (PPR) superfamily protein	Y	Y	17.60	18.98	2.39	0.64

TPM of 21nt sRNA from TAS loci

annotation	Gene	Col-rep1	Col-rep2	PSR-rep1	PSR-rep2
TAS1a	AT2G27400	8209.76	7145.99	1020.06	997.75
TAS1b	AT1G50055	1623.00	1340.90	298.44	302.81
TAS1c	AT2G39675	14082.47	14370.17	4204.17	3546.56
TAS2	AT2G39681	10058.40	11524.90	508.03	460.39
TAS3a	AT3G17185	1172.05	1118.22	901.69	1178.93
TAS3b	AT5G49615	30.41	35.89	21.81	33.60
TAS3c	AT5G57735	0.64	2.06	0.53	0.64
TAS4	AT3G25795	8.00	6.40	5.85	12.76

Table S2. Differentially expressed genes in PSR2-5 compared to wild-type (WT) *Arabidopsis*

5

RMD-PSR2vsCol.up

Gene	logFC	logCPM	LR	PValue	p.ad
AT5G24240	7.502949	3.350601	220.1636	8.33E-50	3.26E-47
AT2G16660	3.707237	5.175004	435.0258	1.31E-96	2.30E-93
AT4G14130	3.699953	3.087442	117.7236	1.99E-27	2.44E-25
AT4G25100	3.671825	2.558724	85.83331	1.96E-20	1.33E-18
AT2G15880	3.135066	3.37708	113.7866	1.45E-26	1.70E-24
AT5G46330	3.085272	3.98353	165.4901	7.15E-38	1.65E-35
AT1G52040	2.740812	4.105898	151.9722	6.43E-35	1.29E-32
AT2G19800	2.645429	3.069461	76.49854	2.20E-18	1.19E-16
AT1G51940	2.562577	5.172258	267.4004	4.18E-60	2.68E-57

Gene	logFC	logCPM	LR	PValue	p.ad
AT3G47340	2.552249	7.041956	553.2558	2.46E-122	8.67E-119
AT4G31060	2.476966	3.34736	81.5164	1.74E-19	1.06E-17
AT1G16500	2.461926	3.721342	102.5801	4.14E-24	3.94E-22
AT1G19310	2.431091	3.662826	97.05833	6.73E-23	5.74E-21
AT3G47160	2.322041	4.188071	124.6911	5.95E-29	8.13E-27
AT5G02170	2.267654	3.13456	63.47816	1.62E-15	6.47E-14
AT1G22570	2.233476	2.794034	50.52581	1.18E-12	3.16E-11
AT5G02760	2.21795	5.462933	250.003	2.59E-56	1.40E-53
AT5G57780	2.195028	4.395229	131.3973	2.03E-30	3.17E-28
AT4G30410	2.152993	4.412997	128.6725	8.00E-30	1.19E-27
AT1G78170	2.135915	4.493168	133.9043	5.73E-31	9.38E-29
AT5G27920	2.132407	3.068713	55.44777	9.60E-14	2.98E-12
AT5G56870	2.096883	4.934546	169.7858	8.24E-39	2.03E-36
AT5G62730	2.019541	2.978234	48.34374	3.58E-12	9.07E-11
AT1G79700	1.982208	5.053666	165.8205	6.05E-38	1.42E-35
AT2G37025	1.97389	4.481799	116.9722	2.91E-27	3.47E-25
AT1G11740	1.971684	3.531549	64.0564	1.21E-15	4.92E-14
AT3G30775	1.928259	6.530167	306.1356	1.52E-68	1.33E-65
AT1G69040	1.925978	6.210203	268.755	2.12E-60	1.42E-57
AT2G42170	1.914366	3.691913	67.30218	2.33E-16	1.02E-14
AT5G04820	1.882771	4.413265	102.9711	3.40E-24	3.30E-22
AT2G33830	1.877903	5.003163	146.9497	8.05E-34	1.55E-31
AT3G50700	1.865444	3.928968	74.71815	5.43E-18	2.84E-16
AT1G76410	1.858853	3.155446	46.24928	1.04E-11	2.48E-10
AT2G15890	1.843736	5.408107	178.113	1.25E-40	3.45E-38
AT4G20140	1.831471	3.578929	58.14268	2.44E-14	8.11E-13
AT3G13065	1.826292	5.376703	172.8588	1.76E-39	4.67E-37
AT1G52750	1.817985	3.488648	54.5804	1.49E-13	4.52E-12
AT5G54190	1.795504	4.821994	123.254	1.23E-28	1.61E-26
AT3G62150	1.775038	4.474784	97.01024	6.90E-23	5.85E-21
AT2G31010	1.768041	3.458978	50.68668	1.08E-12	2.93E-11
AT1G56150	1.742507	2.883032	35.79065	2.20E-09	3.67E-08
AT3G51660	1.735102	3.335497	45.27936	1.71E-11	3.93E-10
AT1G22550	1.733088	3.748928	58.94168	1.62E-14	5.47E-13
AT5G06690	1.732088	4.76762	111.8045	3.94E-26	4.48E-24
AT1G70420	1.715052	3.000269	37.36539	9.79E-10	1.73E-08
AT5G65390	1.712067	3.870324	62.22344	3.07E-15	1.16E-13
AT2G30600	1.709636	6.417222	238.2293	9.57E-54	4.81E-51
AT3G62550	1.707982	4.711067	105.3255	1.04E-24	1.04E-22
AT2G25930	1.695291	3.890908	62.06362	3.33E-15	1.24E-13
AT1G28330	1.688552	4.432148	86.01107	1.79E-20	1.23E-18
AT5G42420	1.671915	3.616835	50.92041	9.62E-13	2.64E-11

Gene	logFC	logCPM	LR	PValue	p.ad
AT4G35770	1.664234	5.177903	131.4534	1.97E-30	3.12E-28
AT4G32280	1.663111	3.424676	44.6455	2.36E-11	5.26E-10
AT5G36700	1.660527	3.64819	51.427	7.43E-13	2.04E-11
AT1G77210	1.654193	4.540245	89.46247	3.13E-21	2.30E-19
AT4G13260	1.646034	3.118896	36.81996	1.30E-09	2.24E-08
AT2G22830	1.643134	3.110814	36.77277	1.33E-09	2.29E-08
AT5G22500	1.642957	4.355498	78.02563	1.02E-18	5.66E-17
AT1G05805	1.638331	5.909347	176.8005	2.42E-40	6.55E-38
AT4G04408	1.637953	2.95199	33.42628	7.40E-09	1.14E-07
AT2G15810	1.628932	2.533329	25.64465	4.10E-07	4.46E-06
AT3G53800	1.624301	5.164958	125.6449	3.68E-29	5.12E-27
AT2G42040	1.62139	4.713261	96.44627	9.17E-23	7.73E-21
AT5G54510	1.619989	3.972055	60.20761	8.54E-15	3.00E-13
AT5G43440	1.613493	4.220451	69.16704	9.05E-17	4.16E-15
AT4G37220	1.599104	3.624677	47.4668	5.59E-12	1.38E-10
AT1G78600	1.565105	3.580454	44.38785	2.69E-11	5.93E-10
AT5G57550	1.553518	3.401719	38.98747	4.27E-10	7.98E-09
AT4G30850	1.552898	2.789278	27.68408	1.43E-07	1.71E-06
AT1G02300	1.550311	4.294333	67.58068	2.02E-16	8.98E-15
AT4G16000	1.536328	4.247721	64.33109	1.05E-15	4.30E-14
AT5G56320	1.535272	2.916862	29.0814	6.94E-08	8.82E-07
AT1G69890	1.52348	4.251277	63.45855	1.64E-15	6.51E-14
AT1G11070	1.508233	4.260245	62.96175	2.11E-15	8.19E-14
AT5G22270	1.500339	4.306291	64.34216	1.05E-15	4.29E-14
AT2G33500	1.494807	3.563123	40.64124	1.83E-10	3.61E-09
AT5G01830	1.494559	3.61039	41.59369	1.12E-10	2.27E-09
AT5G62280	1.476166	4.367634	65.46928	5.90E-16	2.47E-14
AT1G53830	1.468811	3.018552	28.64664	8.69E-08	1.08E-06
AT1G12775	1.463787	3.603654	40.12151	2.39E-10	4.62E-09
AT1G79160	1.463528	5.172341	105.3763	1.01E-24	1.02E-22
AT2G44940	1.444197	5.05753	96.38269	9.47E-23	7.93E-21
AT1G53110	1.440929	3.166083	29.97078	4.39E-08	5.86E-07
AT4G34950	1.427547	6.273152	161.8909	4.37E-37	9.92E-35
AT4G03510	1.42487	4.151383	53.20408	3.01E-13	8.71E-12
AT2G40850	1.416095	3.173584	29.1694	6.63E-08	8.48E-07
AT4G31050	1.408999	3.467314	34.23522	4.88E-09	7.80E-08
AT4G04409	1.408807	3.141496	28.43812	9.67E-08	1.20E-06
AT1G47860	1.40573	3.845185	43.2801	4.74E-11	1.01E-09
AT2G20815	1.402987	3.415627	32.91677	9.62E-09	1.45E-07
AT5G62865	1.401723	3.376207	32.00727	1.54E-08	2.22E-07
AT2G04240	1.395125	4.455802	62.91721	2.16E-15	8.36E-14
AT2G44740	1.394997	4.482313	63.80357	1.37E-15	5.54E-14

Gene	logFC	logCPM	LR	PValue	p.ad
AT2G28660	1.3944	2.784534	22.70731	1.89E-06	1.76E-05
AT5G12050	1.388906	5.925339	132.2286	1.33E-30	2.13E-28
AT4G18170	1.38599	2.776581	22.3663	2.25E-06	2.06E-05
AT5G63930	1.385116	4.394435	59.32055	1.34E-14	4.59E-13
AT3G14460	1.380969	2.61972	20.50793	5.94E-06	4.88E-05
AT5G52882	1.380017	5.508703	112.7758	2.42E-26	2.79E-24
AT4G27870	1.373972	5.890034	127.8784	1.19E-29	1.71E-27
AT1G76090	1.365738	5.890561	126.425	2.48E-29	3.49E-27
AT2G21880	1.365507	3.969465	44.33058	2.77E-11	6.09E-10
AT4G36150	1.348473	4.330546	54.18734	1.82E-13	5.46E-12
AT4G16870	1.346717	6.004044	128.4764	8.83E-30	1.29E-27
AT5G34800	1.341371	3.225887	27.09114	1.94E-07	2.26E-06
AT1G75960	1.338206	3.594756	33.74274	6.29E-09	9.83E-08
AT4G03230	1.333963	4.868901	74.38119	6.44E-18	3.36E-16
AT5G24318	1.331962	3.088654	24.93948	5.92E-07	6.23E-06
AT2G42870	1.329761	3.556307	32.5052	1.19E-08	1.76E-07
AT5G28626	1.323192	3.427424	29.74793	4.92E-08	6.47E-07
AT3G48390	1.323167	4.040835	43.57655	4.08E-11	8.77E-10
AT3G27520	1.317977	2.970219	22.87564	1.73E-06	1.63E-05
AT5G08770	1.315073	2.960239	22.79976	1.80E-06	1.68E-05
AT2G37678	1.314295	3.537635	31.55789	1.94E-08	2.75E-07
AT4G21400	1.309815	3.382886	28.25331	1.06E-07	1.30E-06
AT2G05540	1.306842	5.993779	120.9522	3.91E-28	5.01E-26
AT3G53510	1.306507	3.625769	33.00064	9.21E-09	1.39E-07
AT4G38850	1.304339	4.222595	47.2283	6.32E-12	1.55E-10
AT5G67520	1.302267	3.969387	40.56984	1.90E-10	3.73E-09
AT4G23190	1.302056	3.687221	34.1505	5.10E-09	8.11E-08
AT2G23330	1.300194	3.139763	24.58736	7.10E-07	7.36E-06
AT1G61500	1.297954	4.190093	46.12907	1.11E-11	2.63E-10
AT3G52240	1.29519	5.204695	85.31418	2.55E-20	1.69E-18
AT3G20830	1.292758	3.712304	34.266	4.81E-09	7.69E-08
AT5G38040	1.292159	3.439988	28.81831	7.95E-08	9.97E-07
AT2G42320	1.289815	6.661237	155.0521	1.36E-35	2.87E-33
AT1G28130	1.288523	2.915619	21.40503	3.72E-06	3.21E-05
AT1G03457	1.286051	4.682461	62.27722	2.98E-15	1.13E-13
AT3G58620	1.277363	5.04442	76.44936	2.26E-18	1.22E-16
AT3G16740	1.276433	3.607914	31.20198	2.33E-08	3.24E-07
AT2G46310	1.271064	3.910925	37.66242	8.41E-10	1.50E-08
AT3G06455	1.255468	3.230179	24.17884	8.78E-07	8.91E-06
AT3G30180	1.254201	5.627047	98.71984	2.91E-23	2.57E-21
AT1G09570	1.249802	7.902887	150.1264	1.63E-34	3.22E-32
AT2G30250	1.24622	4.285456	45.31777	1.68E-11	3.87E-10

Gene	logFC	logCPM	LR	PValue	p.ad
AT5G07130	1.246126	2.95434	20.39933	6.29E-06	5.14E-05
AT1G44350	1.244687	4.998389	70.90721	3.74E-17	1.82E-15
AT3G60220	1.241346	4.03345	38.60691	5.18E-10	9.57E-09
AT3G46370	1.239916	5.308592	83.11784	7.73E-20	4.84E-18
AT5G66880	1.238712	4.023967	38.15322	6.54E-10	1.19E-08
AT2G32550	1.234465	2.854236	19.04059	1.28E-05	9.77E-05
AT1G20840	1.231684	5.193013	77.09102	1.63E-18	8.98E-17
AT5G18930	1.229743	2.943977	19.763	8.77E-06	6.92E-05
AT1G15020	1.227077	5.902622	104.1321	1.89E-24	1.86E-22
AT5G65925	1.224998	2.850617	18.69918	1.53E-05	0.000115
AT1G22740	1.224111	4.974158	67.60139	2.00E-16	8.93E-15
AT1G74930	1.222042	3.487951	26.8542	2.19E-07	2.52E-06
AT4G30940	1.220599	3.224071	22.97433	1.64E-06	1.56E-05
AT5G47240	1.219809	3.088553	21.14991	4.25E-06	3.61E-05
AT5G60860	1.214219	3.986978	36.09988	1.87E-09	3.16E-08
AT3G48290	1.211441	3.177373	21.96825	2.77E-06	2.48E-05
AT1G26580	1.204928	6.611458	134.2653	4.78E-31	7.92E-29
AT3G56720	1.204827	4.486138	48.50622	3.29E-12	8.36E-11
AT2G40620	1.203698	4.085546	37.56806	8.83E-10	1.57E-08
AT1G75240	1.199518	2.996388	19.55444	9.78E-06	7.65E-05
AT5G12950	1.198744	6.464421	126.5405	2.34E-29	3.33E-27
AT1G78210	1.195383	4.889649	61.64594	4.11E-15	1.51E-13
AT3G60965	1.190261	4.41167	45.30065	1.69E-11	3.89E-10
AT5G63620	1.189433	5.470368	83.73324	5.66E-20	3.61E-18
AT5G39020	1.188952	3.680828	28.65217	8.66E-08	1.08E-06
AT1G17147	1.187905	2.914222	18.22852	1.96E-05	0.000143
AT1G70430	1.187372	3.067435	19.88329	8.23E-06	6.54E-05
AT4G31890	1.185562	4.376172	43.76489	3.70E-11	8.01E-10
AT5G57785	1.184401	3.203079	21.37558	3.78E-06	3.25E-05
AT4G29050	1.184039	3.578594	26.66257	2.42E-07	2.76E-06
AT4G19540	1.178114	5.349475	77.50778	1.32E-18	7.30E-17
AT1G13210	1.174747	5.988185	98.7528	2.86E-23	2.55E-21
AT1G03090	1.168431	5.988779	97.69422	4.88E-23	4.24E-21
AT2G45920	1.167977	4.002143	33.72673	6.34E-09	9.90E-08
AT2G43200	1.167777	4.603099	49.61391	1.87E-12	4.94E-11
AT5G02260	1.165776	3.301992	21.81881	3.00E-06	2.66E-05
AT4G19700	1.16305	4.015137	33.91207	5.77E-09	9.07E-08
AT4G05631	1.151142	3.690203	27.35296	1.70E-07	1.99E-06
AT1G21730	1.1482	4.561669	46.86793	7.59E-12	1.84E-10
AT3G02860	1.147467	6.125715	101.0519	8.96E-24	8.19E-22
AT3G27880	1.145488	2.884207	16.78522	4.19E-05	0.000282
AT2G46490	1.142897	4.571171	46.58451	8.78E-12	2.11E-10

Gene	logFC	logCPM	LR	PValue	p.ad
AT5G03700	1.142268	3.472428	23.38633	1.33E-06	1.28E-05
AT1G33970	1.141822	5.018692	60.91676	5.95E-15	2.14E-13
AT1G56140	1.1418	4.361432	40.45073	2.02E-10	3.95E-09
AT1G75310	1.141434	6.159105	101.496	7.16E-24	6.63E-22
AT1G22400	1.14053	5.081909	63.06659	2.00E-15	7.81E-14
AT4G36790	1.139715	3.854706	29.56108	5.42E-08	7.09E-07
AT5G46500	1.137713	3.989695	32.02042	1.53E-08	2.21E-07
AT5G23955	1.134192	3.422528	22.18326	2.48E-06	2.24E-05
AT1G70820	1.133658	7.144148	131.0656	2.40E-30	3.71E-28
AT2G20250	1.130669	4.541425	44.92387	2.05E-11	4.62E-10
AT4G14270	1.130644	4.471263	42.8823	5.81E-11	1.22E-09
AT5G18640	1.125034	5.079609	61.20002	5.16E-15	1.88E-13
AT4G14230	1.124721	5.251004	67.27866	2.36E-16	1.03E-14
AT1G21830	1.115618	4.301225	37.18451	1.07E-09	1.88E-08
AT1G77170	1.115041	2.996488	16.98557	3.77E-05	0.000256
AT1G02640	1.108134	6.36924	104.9145	1.28E-24	1.26E-22
AT5G18130	1.101462	3.847341	27.54441	1.54E-07	1.82E-06
AT2G28360	1.098454	4.289898	35.82027	2.16E-09	3.62E-08
AT5G45960	1.091542	2.943772	15.95198	6.50E-05	0.000417
AT2G27770	1.09105	4.274844	35.22217	2.94E-09	4.83E-08
AT5G05890	1.087588	4.452316	39.38482	3.48E-10	6.58E-09
AT1G33770	1.084716	4.571974	42.30593	7.81E-11	1.60E-09
AT5G43730	1.084406	3.183998	17.8986	2.33E-05	0.000167
AT3G07010	1.08388	6.008312	85.68289	2.11E-20	1.42E-18
AT5G45830	1.083163	2.896996	15.2104	9.62E-05	0.000586
AT5G57130	1.081569	3.985951	29.07673	6.96E-08	8.84E-07
AT1G63260	1.079489	5.216801	61.15763	5.27E-15	1.91E-13
AT5G10570	1.078324	2.861972	14.88187	0.000114	0.000685
AT5G04770	1.078151	3.760344	25.0216	5.67E-07	6.00E-06
AT4G27450	1.076752	6.607938	108.1283	2.52E-25	2.63E-23
AT2G39480	1.075093	6.030845	85.45697	2.37E-20	1.58E-18
AT5G57565	1.074092	4.055906	29.87952	4.60E-08	6.07E-07
AT1G01240	1.068762	6.007118	83.41973	6.64E-20	4.19E-18
AT4G31240	1.066167	3.00839	15.816	6.98E-05	0.000444
AT2G22800	1.065279	4.531511	39.90376	2.67E-10	5.12E-09
AT5G65440	1.064355	6.199313	90.4243	1.92E-21	1.45E-19
AT3G63380	1.063735	3.22805	17.79658	2.46E-05	0.000176
AT4G00950	1.062264	5.047389	54.12631	1.88E-13	5.61E-12
AT5G28630	1.060269	3.269725	18.02946	2.18E-05	0.000157
AT3G15630	1.056793	4.141678	30.35883	3.59E-08	4.85E-07
AT5G11610	1.056551	3.928881	26.88448	2.16E-07	2.49E-06
AT1G05780	1.054908	2.999176	15.40693	8.67E-05	0.000534

Gene	logFC	logCPM	LR	PValue	p.ad
AT4G22540	1.054586	6.43741	98.14269	3.89E-23	3.40E-21
AT5G13860	1.049876	3.030823	15.4332	8.55E-05	0.000529
AT1G22540	1.049371	4.223632	31.49916	2.00E-08	2.83E-07
AT2G02220	1.048802	5.54941	68.5535	1.23E-16	5.59E-15
AT5G26340	1.047476	3.020707	15.38153	8.78E-05	0.00054
AT2G01340	1.042448	4.08756	28.64215	8.71E-08	1.09E-06
AT2G20780	1.039946	4.124063	29.24042	6.39E-08	8.23E-07
AT5G35370	1.038982	4.729981	43.21314	4.91E-11	1.04E-09
AT1G20390	1.031696	3.889763	25.09433	5.46E-07	5.81E-06
AT5G37930	1.028893	4.503288	36.61311	1.44E-09	2.46E-08
AT1G04360	1.028201	4.162962	29.35757	6.02E-08	7.80E-07
AT5G10790	1.027271	3.712719	22.18968	2.47E-06	2.23E-05
AT2G15960	1.025361	5.018198	49.67252	1.82E-12	4.82E-11
AT5G07610	1.025226	3.184896	16.17456	5.78E-05	0.000376
AT1G03990	1.023328	2.864461	13.36923	0.000256	0.00138
AT5G53550	1.017885	5.535395	64.40655	1.01E-15	4.17E-14
AT1G16030	1.01712	3.476721	18.88889	1.39E-05	0.000105
AT5G19530	1.016236	5.342903	58.15464	2.42E-14	8.08E-13
AT1G22530	1.016206	7.173876	106.3765	6.10E-25	6.22E-23
AT4G31000	1.016131	5.598149	65.69184	5.27E-16	2.22E-14
AT3G19553	1.010757	6.255349	84.1074	4.69E-20	3.04E-18
AT1G63240	1.010278	4.333709	31.66237	1.83E-08	2.63E-07
AT2G39580	1.00804	6.902308	102.6622	3.97E-24	3.81E-22
AT2G45400	1.005659	4.356409	31.94572	1.59E-08	2.29E-07
AT1G27460	1.004682	6.411598	88.68604	4.63E-21	3.32E-19
AT5G42250	1.002961	5.713079	66.69746	3.17E-16	1.36E-14
AT5G03050	1.00286	3.703478	21.20797	4.12E-06	3.52E-05
AT3G61350	1.00207	3.349519	16.90054	3.94E-05	0.000267
AT4G19890	1.001303	3.017574	14.04835	0.000178	0.00101
AT1G75140	1.000917	4.261786	29.53342	5.50E-08	7.18E-07

RMD-PSR2vsCol.down

Gene	logFC	logCPM	LR	PValue	p.ad
AT2G14610	-5.80435	1.654214	73.27472	1.13E-17	5.73E-16
AT3G24463	-4.12635	4.118576	260.9954	1.04E-58	6.11E-56
AT1G35140	-3.96708	5.989832	708.1141	5.14E-156	3.62E-152
AT1G26790	-3.86661	2.434913	88.17121	6.00E-21	4.25E-19
AT4G34550	-3.73457	3.17389	130.8612	2.66E-30	4.06E-28
AT3G24460	-3.45653	6.339527	711.7868	8.18E-157	1.15E-152
AT3G21890	-3.44419	2.602158	85.9575	1.84E-20	1.26E-18
AT2G27420	-3.03748	6.445434	625.603	4.52E-138	2.12E-134

Gene	logFC	logCPM	LR	PValue	p.ad
AT1G78440	-2.95519	2.99512	89.59435	2.92E-21	2.17E-19
AT3G17790	-2.90801	3.296977	103.4748	2.64E-24	2.58E-22
AT4G01080	-2.88749	5.866605	451.0064	4.36E-100	8.76E-97
AT1G07373	-2.88318	3.175543	95.36406	1.58E-22	1.29E-20
AT1G07367	-2.82844	2.943916	82.02055	1.35E-19	8.24E-18
AT5G61350	-2.79665	3.743117	128.8721	7.23E-30	1.08E-27
AT1G01520	-2.77384	4.440592	197.7545	6.45E-45	2.22E-42
AT4G08950	-2.7442	6.315754	510.2222	5.67E-113	1.60E-109
AT1G24580	-2.69028	3.748417	122.5102	1.78E-28	2.33E-26
AT5G08640	-2.6175	5.79005	379.3387	1.73E-84	2.22E-81
AT1G21910	-2.48894	5.676207	334.9356	8.09E-75	7.59E-72
AT3G21150	-2.42995	3.553299	93.44969	4.17E-22	3.24E-20
AT5G63160	-2.39068	6.796731	488.9003	2.47E-108	5.80E-105
AT1G24140	-2.38929	3.246441	75.71608	3.28E-18	1.75E-16
AT3G54810	-2.38091	6.157091	380.2167	1.12E-84	1.57E-81
AT5G37300	-2.33704	5.43189	273.9181	1.59E-61	1.18E-58
AT3G22840	-2.31835	4.091224	121.0036	3.81E-28	4.93E-26
AT5G37550	-2.31805	2.800877	56.29989	6.22E-14	1.97E-12
AT1G65870	-2.28486	4.836444	189.4131	4.27E-43	1.40E-40
AT1G02460	-2.26327	2.715897	51.43125	7.41E-13	2.04E-11
AT1G50040	-2.23761	5.225314	228.2609	1.43E-51	6.28E-49
AT5G14760	-2.20811	6.289865	356.8264	1.38E-79	1.50E-76
AT5G45340	-2.19232	4.917104	184.695	4.57E-42	1.37E-39
AT3G57540	-2.17676	2.869436	53.06819	3.22E-13	9.27E-12
AT4G23990	-2.16075	4.352601	128.0116	1.12E-29	1.62E-27
AT2G41240	-2.15383	3.87035	94.04329	3.09E-22	2.43E-20
AT1G62560	-2.14299	5.696509	266.508	6.55E-60	4.01E-57
AT2G41190	-2.1137	4.559338	140.7353	1.84E-32	3.32E-30
AT1G27020	-2.08841	2.726721	45.44474	1.57E-11	3.66E-10
AT5G52050	-2.08794	3.966204	94.74491	2.17E-22	1.73E-20
AT3G55580	-2.06607	3.17878	57.57163	3.26E-14	1.07E-12
AT4G03060	-2.04516	4.258103	108.891	1.71E-25	1.83E-23
AT1G60590	-2.04082	6.488475	340.1512	5.91E-76	5.95E-73
AT1G33760	-2.03632	3.355393	62.23129	3.05E-15	1.16E-13
AT3G19680	-2.02468	7.378412	384.4249	1.35E-85	2.12E-82
AT1G72520	-1.99	4.953312	161.3483	5.74E-37	1.28E-34
AT3G55840	-1.98322	2.656669	39.89162	2.68E-10	5.15E-09
AT5G57560	-1.97777	6.890558	361.9623	1.05E-80	1.23E-77
AT5G41750	-1.96965	5.598355	222.444	2.65E-50	1.10E-47
AT5G54130	-1.94977	6.319336	292.6639	1.31E-65	1.08E-62
AT1G23205	-1.94821	5.287017	189.1676	4.83E-43	1.55E-40
AT4G37320	-1.92202	4.326921	102.3442	4.67E-24	4.38E-22

Gene	logFC	logCPM	LR	PValue	p.ad
AT1G56600	-1.91584	4.254629	97.11945	6.53E-23	5.64E-21
AT1G72240	-1.91576	3.265095	53.51539	2.57E-13	7.52E-12
AT1G66090	-1.90332	4.869629	142.455	7.73E-33	1.43E-30
AT3G56260	-1.88733	2.963076	44.13863	3.06E-11	6.69E-10
AT5G42760	-1.88168	4.45417	108.1118	2.54E-25	2.63E-23
AT1G09350	-1.87186	3.540136	60.58647	7.04E-15	2.50E-13
AT5G64550	-1.84102	4.01971	79.32113	5.28E-19	3.02E-17
AT4G22620	-1.83793	2.766998	37.35782	9.83E-10	1.73E-08
AT4G32920	-1.83596	5.786431	211.3009	7.15E-48	2.58E-45
AT3G61490	-1.83485	4.066092	80.92013	2.35E-19	1.42E-17
AT1G65060	-1.83068	5.912277	219.7326	1.03E-49	3.94E-47
AT3G56980	-1.82522	3.689114	63.81541	1.37E-15	5.53E-14
AT5G25240	-1.79316	4.371859	94.07702	3.03E-22	2.40E-20
AT3G56970	-1.78751	3.194532	45.68529	1.39E-11	3.25E-10
AT1G19490	-1.77614	4.319899	89.3898	3.24E-21	2.38E-19
AT4G13990	-1.77555	3.266006	47.02625	7.00E-12	1.71E-10
AT3G22550	-1.76613	4.411053	94.62375	2.30E-22	1.83E-20
AT5G67300	-1.7661	6.108394	224.2983	1.04E-50	4.45E-48
AT3G23170	-1.75715	3.285852	46.58644	8.77E-12	2.11E-10
AT5G54930	-1.75479	2.80619	35.44908	2.62E-09	4.32E-08
AT5G49480	-1.75383	5.393102	166.0528	5.39E-38	1.31E-35
AT2G36590	-1.74795	5.551761	178.6533	9.54E-41	2.74E-38
AT1G60190	-1.74673	3.32658	47.58885	5.26E-12	1.30E-10
AT3G09600	-1.74627	6.10639	219.0048	1.49E-49	5.52E-47
AT5G01790	-1.74062	5.021022	134.2922	4.72E-31	7.90E-29
AT1G64780	-1.72327	7.124483	289.4401	6.58E-65	5.15E-62
AT2G21320	-1.7189	5.741178	184.781	4.38E-42	1.34E-39
AT2G32960	-1.71754	3.856554	63.27081	1.80E-15	7.12E-14
AT3G08770	-1.70762	2.891078	35.72495	2.27E-09	3.78E-08
AT2G36800	-1.70621	4.60266	100.6307	1.11E-23	1.01E-21
AT3G50800	-1.70072	3.463251	49.16165	2.36E-12	6.14E-11
AT3G26590	-1.68789	5.602366	170.6044	5.46E-39	1.37E-36
AT5G17300	-1.67501	6.288559	221.2249	4.89E-50	1.97E-47
AT3G50060	-1.67226	6.43578	234.3078	6.85E-53	3.33E-50
AT1G02820	-1.66741	5.953152	188.7073	6.09E-43	1.90E-40
AT3G14620	-1.65909	4.823626	109.512	1.25E-25	1.35E-23
AT4G11280	-1.65636	7.20258	270.204	1.02E-60	7.21E-58
AT3G27170	-1.65278	5.448615	154.1989	2.10E-35	4.27E-33
AT3G09450	-1.65181	4.810443	108.4522	2.14E-25	2.26E-23
AT3G19970	-1.64786	3.76595	55.98804	7.29E-14	2.28E-12
AT1G58520	-1.64455	7.705115	255.7671	1.44E-57	8.09E-55
AT2G17230	-1.64184	6.119244	198.1967	5.17E-45	1.82E-42

Gene	logFC	logCPM	LR	PValue	p.ad
AT2G41640	-1.63264	3.650698	50.81996	1.01E-12	2.76E-11
AT5G47910	-1.62443	6.551498	231.4129	2.93E-52	1.33E-49
AT5G53200	-1.61438	4.218603	70.42537	4.78E-17	2.28E-15
AT4G31800	-1.61383	4.201268	69.68136	6.97E-17	3.24E-15
AT5G19875	-1.6116	3.377445	41.9089	9.56E-11	1.95E-09
AT1G02380	-1.59419	4.078576	63.62651	1.50E-15	6.03E-14
AT5G50800	-1.59377	4.008607	61.33031	4.83E-15	1.76E-13
AT1G19640	-1.59111	4.20509	68.01019	1.63E-16	7.29E-15
AT5G15950	-1.57909	6.973379	243.5055	6.77E-55	3.53E-52
AT3G44860	-1.57428	4.35502	74.19116	7.09E-18	3.67E-16
AT4G25630	-1.57158	4.60285	87.15278	1.00E-20	7.03E-19
AT5G14700	-1.56877	3.61498	46.47473	9.28E-12	2.23E-10
AT1G56430	-1.56702	5.574638	148.0574	4.61E-34	9.01E-32
AT4G03450	-1.56041	2.908947	30.41858	3.48E-08	4.72E-07
AT3G17609	-1.56031	5.074862	113.7315	1.49E-26	1.74E-24
AT1G10640	-1.54415	4.577658	83.51799	6.31E-20	4.00E-18
AT1G69260	-1.54383	2.967162	31.08724	2.47E-08	3.43E-07
AT3G55980	-1.5312	7.317509	232.8876	1.40E-52	6.56E-50
AT4G35783	-1.52817	2.798981	27.8074	1.34E-07	1.60E-06
AT5G13200	-1.52214	4.434534	73.40378	1.06E-17	5.41E-16
AT1G27940	-1.51183	2.662405	25.14952	5.31E-07	5.67E-06
AT4G33040	-1.49287	2.599461	23.87251	1.03E-06	1.03E-05
AT3G18600	-1.49133	4.41131	70.11723	5.59E-17	2.64E-15
AT2G39710	-1.48559	4.466998	71.82174	2.36E-17	1.17E-15
AT2G40130	-1.47488	4.050132	54.41008	1.63E-13	4.90E-12
AT5G24155	-1.4729	4.304957	63.25795	1.81E-15	7.15E-14
AT3G58990	-1.47007	5.696849	137.3827	9.94E-32	1.75E-29
AT1G17100	-1.46917	6.357358	179.7094	5.61E-41	1.64E-38
AT3G06530	-1.46426	5.802592	141.7832	1.08E-32	1.98E-30
AT2G38210	-1.46094	4.157373	56.78354	4.87E-14	1.56E-12
AT1G72910	-1.45908	6.130389	160.4801	8.89E-37	1.95E-34
AT4G15248	-1.45763	3.674267	42.55656	6.87E-11	1.42E-09
AT2G27080	-1.45479	5.123598	102.8726	3.57E-24	3.45E-22
AT1G05170	-1.45274	5.200851	107.1221	4.19E-25	4.30E-23
AT1G35710	-1.44561	6.4188	178.5978	9.81E-41	2.76E-38
AT3G17130	-1.44147	2.997054	28.04608	1.18E-07	1.43E-06
AT2G39650	-1.43338	3.817169	44.81575	2.16E-11	4.85E-10
AT3G18950	-1.4331	4.943402	90.65062	1.71E-21	1.30E-19
AT5G59670	-1.42991	5.328591	111.1244	5.56E-26	6.16E-24
AT2G05632	-1.4295	2.644176	22.45927	2.15E-06	1.97E-05
AT3G14870	-1.42858	2.978689	27.38881	1.66E-07	1.96E-06
AT4G27940	-1.42776	4.823206	83.94828	5.08E-20	3.28E-18

Gene	logFC	logCPM	LR	PValue	p.ad
AT4G03960	-1.42684	3.241526	31.35829	2.15E-08	3.02E-07
AT3G44970	-1.41179	3.371074	33.07832	8.85E-09	1.34E-07
AT3G16910	-1.40703	7.039867	197.2526	8.31E-45	2.78E-42
AT5G04950	-1.40633	4.874226	83.94138	5.10E-20	3.28E-18
AT4G37260	-1.39621	6.009001	139.4959	3.43E-32	6.11E-30
AT5G62210	-1.39568	3.290724	30.8566	2.78E-08	3.84E-07
AT3G48240	-1.39349	2.673645	21.92857	2.83E-06	2.53E-05
AT1G65860	-1.39345	5.437021	112.0089	3.56E-26	4.07E-24
AT2G01300	-1.39299	3.233173	29.93406	4.47E-08	5.94E-07
AT1G66160	-1.38972	4.446331	62.88861	2.19E-15	8.46E-14
AT2G27840	-1.38773	4.322034	57.75308	2.97E-14	9.77E-13
AT4G12000	-1.38277	4.935673	84.81146	3.28E-20	2.16E-18
AT5G52320	-1.38185	5.584338	118.1046	1.64E-27	2.03E-25
AT2G28200	-1.38006	4.550048	66.49734	3.50E-16	1.50E-14
AT1G65560	-1.3787	4.231569	53.57277	2.49E-13	7.32E-12
AT1G76620	-1.37309	4.178523	51.74467	6.32E-13	1.77E-11
AT2G20560	-1.3703	2.932224	24.56193	7.20E-07	7.44E-06
AT5G61600	-1.35713	5.523291	111.1411	5.51E-26	6.16E-24
AT4G21760	-1.35646	3.4746	32.93203	9.54E-09	1.44E-07
AT1G10155	-1.35188	2.977575	24.50938	7.39E-07	7.62E-06
AT1G18850	-1.35138	3.774188	39.3597	3.52E-10	6.66E-09
AT1G48100	-1.3505	3.386444	30.57884	3.21E-08	4.39E-07
AT3G57260	-1.34702	3.250614	28.07578	1.17E-07	1.41E-06
AT3G48460	-1.34499	6.715632	172.1946	2.45E-39	6.28E-37
AT4G16140	-1.34367	3.937305	42.73597	6.26E-11	1.30E-09
AT2G40750	-1.33999	4.158856	48.72478	2.95E-12	7.54E-11
AT4G08040	-1.33867	3.557095	33.60248	6.76E-09	1.05E-07
AT4G26780	-1.32887	3.952952	42.46797	7.18E-11	1.48E-09
AT1G24020	-1.31933	4.505527	59.50299	1.22E-14	4.21E-13
AT5G60270	-1.31663	4.230707	49.15296	2.37E-12	6.16E-11
AT2G41905	-1.31515	3.029482	23.98474	9.71E-07	9.74E-06
AT3G47640	-1.30938	4.580461	61.65353	4.10E-15	1.51E-13
AT5G09590	-1.30741	6.195636	134.9695	3.35E-31	5.76E-29
AT3G56400	-1.30613	6.776017	165.9815	5.58E-38	1.33E-35
AT1G77450	-1.30543	3.717723	35.41119	2.67E-09	4.39E-08
AT3G03770	-1.30152	7.190513	172.4316	2.18E-39	5.68E-37
AT5G58120	-1.30046	6.050825	124.6332	6.12E-29	8.29E-27
AT4G04610	-1.29547	6.585584	154.3451	1.95E-35	4.03E-33
AT2G40150	-1.29421	4.414602	54.09712	1.91E-13	5.68E-12
AT4G23490	-1.29022	4.536686	58.13859	2.44E-14	8.11E-13
AT2G33380	-1.28527	5.922963	115.8128	5.22E-27	6.18E-25
AT3G04710	-1.28139	3.452289	29.11172	6.83E-08	8.69E-07

Gene	logFC	logCPM	LR	PValue	p.ad
AT1G55320	-1.2734	4.319682	48.93775	2.64E-12	6.83E-11
AT5G66740	-1.27018	5.168895	82.03711	1.34E-19	8.21E-18
AT1G47395	-1.26989	4.258049	46.66573	8.42E-12	2.04E-10
AT4G05410	-1.2655	4.341387	49.28152	2.22E-12	5.80E-11
AT5G18670	-1.26361	7.539231	158.4391	2.48E-36	5.29E-34
AT3G02020	-1.26035	6.384825	136.6245	1.46E-31	2.53E-29
AT5G15160	-1.25971	3.237315	24.83497	6.25E-07	6.54E-06
AT1G79150	-1.25865	4.815618	66.10651	4.27E-16	1.81E-14
AT4G01950	-1.2543	7.059153	159.3119	1.60E-36	3.46E-34
AT3G57660	-1.25227	5.551238	97.09296	6.61E-23	5.68E-21
AT1G69720	-1.25156	3.107933	22.98854	1.63E-06	1.55E-05
AT1G63810	-1.25033	4.539113	54.92126	1.25E-13	3.82E-12
AT1G31690	-1.24927	3.826019	35.03797	3.23E-09	5.27E-08
AT1G02390	-1.24758	4.359654	48.57546	3.18E-12	8.09E-11
AT2G38995	-1.24647	5.202052	80.64502	2.70E-19	1.61E-17
AT5G19600	-1.24518	3.02459	21.62112	3.32E-06	2.91E-05
AT1G66250	-1.24423	4.210499	43.67874	3.87E-11	8.34E-10
AT2G23340	-1.24412	5.530096	95.28118	1.65E-22	1.34E-20
AT2G23290	-1.2424	5.659682	99.20086	2.28E-23	2.05E-21
AT3G57150	-1.24166	6.409471	134.3222	4.65E-31	7.88E-29
AT5G42830	-1.23625	3.148195	22.90315	1.70E-06	1.61E-05
AT1G76600	-1.2304	4.661822	57.56894	3.26E-14	1.07E-12
AT1G32900	-1.22622	8.211745	143.047	5.74E-33	1.08E-30
AT5G13210	-1.22517	2.842808	18.89313	1.38E-05	0.000105
AT5G58760	-1.2247	4.159849	41.14448	1.41E-10	2.82E-09
AT5G24660	-1.22076	4.922569	66.30315	3.87E-16	1.64E-14
AT3G56990	-1.21771	4.585963	53.94942	2.06E-13	6.08E-12
AT1G77280	-1.21558	3.9767	36.66859	1.40E-09	2.40E-08
AT5G01260	-1.21172	5.777042	98.56934	3.14E-23	2.76E-21
AT1G18590	-1.21063	5.129795	73.19473	1.17E-17	5.95E-16
AT4G21940	-1.20719	3.98951	36.24107	1.74E-09	2.96E-08
AT3G01820	-1.20604	4.71069	57.08455	4.17E-14	1.35E-12
AT2G41050	-1.2038	3.633222	29.05447	7.04E-08	8.92E-07
AT4G12030	-1.20032	4.983405	66.45179	3.59E-16	1.53E-14
AT1G30530	-1.19941	6.595973	133.8066	6.02E-31	9.74E-29
AT5G40390	-1.199	6.906135	144.5706	2.67E-33	5.07E-31
AT3G44750	-1.19798	4.621065	53.43698	2.67E-13	7.80E-12
AT2G25140	-1.19708	5.190647	74.22466	6.97E-18	3.62E-16
AT5G19970	-1.19669	3.339623	23.79316	1.07E-06	1.07E-05
AT1G79520	-1.19568	6.141938	111.0563	5.75E-26	6.32E-24
AT1G47510	-1.19407	2.913525	18.85601	1.41E-05	0.000107
AT4G32480	-1.1921	6.146284	110.4787	7.70E-26	8.40E-24

Gene	logFC	logCPM	LR	PValue	p.ad
AT3G52370	-1.19208	5.538939	88.14576	6.08E-21	4.28E-19
AT5G58620	-1.18912	3.99836	35.42399	2.65E-09	4.37E-08
AT1G33265	-1.18642	3.205998	21.87032	2.92E-06	2.60E-05
AT4G27070	-1.18628	3.960167	34.56237	4.13E-09	6.66E-08
AT4G27280	-1.18424	6.183026	111.312	5.06E-26	5.69E-24
AT2G34655	-1.18152	3.370799	23.59262	1.19E-06	1.17E-05
AT3G62260	-1.17848	4.632252	52.20374	5.00E-13	1.40E-11
AT1G19970	-1.1778	4.117878	37.19099	1.07E-09	1.88E-08
AT5G65920	-1.17703	4.212501	39.53309	3.23E-10	6.13E-09
AT4G13410	-1.17541	3.544174	26.46807	2.68E-07	3.03E-06
AT5G41460	-1.17514	3.743431	29.76657	4.87E-08	6.42E-07
AT1G01210	-1.17178	3.98048	34.17975	5.02E-09	8.00E-08
AT5G06550	-1.16387	2.90713	17.97866	2.23E-05	0.000161
AT1G18900	-1.16327	5.37263	77.64741	1.23E-18	6.83E-17
AT3G23990	-1.15283	6.587086	123.6877	9.86E-29	1.32E-26
AT5G52310	-1.15197	6.49454	119.8885	6.69E-28	8.41E-26
AT5G13750	-1.15137	3.959917	32.73561	1.06E-08	1.58E-07
AT5G24150	-1.15046	7.70429	129.9251	4.26E-30	6.44E-28
AT3G59670	-1.1458	4.894129	58.04238	2.57E-14	8.50E-13
AT1G70985	-1.14579	4.095871	35.09166	3.15E-09	5.14E-08
AT2G30040	-1.14432	4.110491	35.30239	2.82E-09	4.64E-08
AT1G59660	-1.14392	2.687228	15.30623	9.14E-05	0.00056
AT5G12080	-1.14321	5.117173	65.40541	6.10E-16	2.54E-14
AT1G69310	-1.14028	3.004036	18.14378	2.05E-05	0.000149
AT3G30720	-1.1402	3.060921	18.65726	1.56E-05	0.000117
AT1G10490	-1.1398	5.000475	61.0713	5.50E-15	1.99E-13
AT3G23510	-1.13829	5.062615	63.11546	1.95E-15	7.66E-14
AT3G55120	-1.13581	5.23875	69.1466	9.14E-17	4.19E-15
AT1G69870	-1.13534	6.177086	102.4208	4.49E-24	4.24E-22
AT4G27010	-1.13368	3.473752	23.45601	1.28E-06	1.24E-05
AT4G35290	-1.13336	5.188329	66.98229	2.74E-16	1.18E-14
AT2G44500	-1.1332	5.230547	68.41032	1.33E-16	5.99E-15
AT1G04520	-1.13217	5.444876	76.54097	2.16E-18	1.17E-16
AT3G12270	-1.12725	4.22599	36.62684	1.43E-09	2.45E-08
AT3G47420	-1.12691	6.644904	120.7697	4.29E-28	5.44E-26
AT1G73390	-1.12589	6.55764	117.241	2.54E-27	3.06E-25
AT1G79270	-1.12546	6.72562	123.5167	1.07E-28	1.43E-26
AT1G22350	-1.12516	3.589184	24.93892	5.92E-07	6.23E-06
AT1G61890	-1.12471	5.864204	88.29422	5.64E-21	4.01E-19
AT1G29170	-1.12144	5.187821	65.61613	5.48E-16	2.30E-14
AT5G57685	-1.12129	3.607499	24.98268	5.78E-07	6.11E-06
AT5G28030	-1.12057	5.414577	73.72029	9.00E-18	4.62E-16

Gene	logFC	logCPM	LR	PValue	p.ad
AT5G58310	-1.11897	3.859308	29.07488	6.96E-08	8.84E-07
AT1G70000	-1.11724	5.764839	84.43379	3.97E-20	2.59E-18
AT5G47550	-1.11641	4.775057	51.54179	7.01E-13	1.95E-11
AT2G32295	-1.1164	4.826503	53.08981	3.19E-13	9.19E-12
AT4G13800	-1.11409	4.862015	53.98793	2.02E-13	5.99E-12
AT4G37310	-1.11144	6.639421	117.4017	2.34E-27	2.84E-25
AT1G47400	-1.10601	3.862664	28.59877	8.90E-08	1.11E-06
AT1G45249	-1.10553	5.879004	85.73078	2.06E-20	1.40E-18
AT2G36630	-1.09976	7.266761	125.5715	3.82E-29	5.27E-27
AT2G14247	-1.09909	4.541839	43.35203	4.57E-11	9.77E-10
AT4G20170	-1.09754	6.012828	88.88493	4.18E-21	3.04E-19
AT5G11650	-1.09652	6.045102	90.1432	2.22E-21	1.65E-19
AT1G78450	-1.09616	4.290683	36.22256	1.76E-09	2.98E-08
AT2G47440	-1.09509	7.646326	118.7375	1.20E-27	1.49E-25
AT2G37690	-1.09468	3.896444	28.37893	9.97E-08	1.23E-06
AT2G38860	-1.09459	5.134468	60.52468	7.27E-15	2.57E-13
AT1G32450	-1.09283	5.154111	61.09373	5.44E-15	1.97E-13
AT4G27560	-1.09267	4.44601	40.07247	2.45E-10	4.72E-09
AT3G25700	-1.09027	4.500328	41.373	1.26E-10	2.53E-09
AT3G16175	-1.08993	3.124726	17.81868	2.43E-05	0.000174
AT4G35320	-1.08967	5.50841	73.36547	1.08E-17	5.49E-16
AT5G02230	-1.08951	5.228673	63.59681	1.53E-15	6.10E-14
AT5G54250	-1.08943	6.346344	101.8687	5.93E-24	5.53E-22
AT1G80850	-1.08636	4.950761	54.2012	1.81E-13	5.43E-12
AT3G14850	-1.08629	2.70703	14.07577	0.000176	0.000997
AT3G27340	-1.08514	4.657427	45.34049	1.66E-11	3.83E-10
AT1G64620	-1.085	3.961354	29.27035	6.30E-08	8.14E-07
AT2G14050	-1.08353	3.357651	19.90817	8.13E-06	6.46E-05
AT1G29600	-1.08236	2.939056	15.87987	6.75E-05	0.00043
AT1G13609	-1.0804	5.673387	76.81404	1.88E-18	1.02E-16
AT1G02180	-1.07951	3.415213	20.53439	5.86E-06	4.82E-05
AT3G63110	-1.07828	5.459074	69.94347	6.10E-17	2.85E-15
AT1G73500	-1.07576	5.163311	59.87738	1.01E-14	3.52E-13
AT1G67470	-1.0746	4.265619	34.2684	4.80E-09	7.69E-08
AT5G08610	-1.07418	6.622774	109.5321	1.24E-25	1.34E-23
AT5G58770	-1.07336	6.59646	108.2296	2.39E-25	2.51E-23
AT5G11260	-1.07245	3.99622	29.19519	6.54E-08	8.38E-07
AT3G26960	-1.07041	4.173467	32.23571	1.37E-08	2.00E-07
AT5G02950	-1.0678	3.249406	18.43713	1.76E-05	0.00013
AT3G23580	-1.06757	5.801255	78.32411	8.74E-19	4.98E-17
AT1G15440	-1.0663	4.088087	30.46868	3.39E-08	4.61E-07
AT1G62180	-1.06599	6.282347	95.1162	1.80E-22	1.44E-20

Gene	logFC	logCPM	LR	PValue	p.ad
AT3G04140	-1.06435	6.302328	95.71142	1.33E-22	1.11E-20
AT1G80270	-1.06415	4.483652	39.12525	3.97E-10	7.48E-09
AT1G56670	-1.06362	4.180754	31.96407	1.57E-08	2.27E-07
AT2G46650	-1.06314	5.434334	67.56209	2.04E-16	9.04E-15
AT1G80830	-1.06122	5.31979	63.09348	1.97E-15	7.73E-14
AT1G72940	-1.06	5.326114	63.45035	1.64E-15	6.52E-14
AT3G55110	-1.05932	3.427313	20.01891	7.67E-06	6.13E-05
AT4G13750	-1.05879	4.705394	44.86158	2.11E-11	4.75E-10
AT4G10120	-1.05858	8.616721	105.0567	1.19E-24	1.18E-22
AT4G19450	-1.05819	6.082078	85.55851	2.25E-20	1.51E-18
AT5G27330	-1.05426	4.090582	29.94401	4.45E-08	5.92E-07
AT1G15710	-1.05378	5.156965	57.25877	3.82E-14	1.24E-12
AT2G25620	-1.05218	4.512864	39.16831	3.89E-10	7.33E-09
AT4G37240	-1.05208	4.821492	47.16694	6.52E-12	1.60E-10
AT1G65486	-1.04862	2.783319	13.74456	0.000209	0.001157
AT3G60360	-1.04851	3.814876	25.06135	5.55E-07	5.90E-06
AT1G60850	-1.0469	3.533009	20.80537	5.08E-06	4.24E-05
AT3G21750	-1.04606	5.974005	79.58944	4.61E-19	2.67E-17
AT5G11240	-1.04493	4.134785	30.0367	4.24E-08	5.68E-07
AT1G16130	-1.04486	3.04706	15.63957	7.66E-05	0.000481
AT4G30840	-1.04471	3.340804	18.4606	1.73E-05	0.000129
AT2G43500	-1.0441	5.022365	52.25815	4.87E-13	1.37E-11
AT1G01390	-1.04312	4.883507	48.20471	3.84E-12	9.70E-11
AT4G19820	-1.04268	2.947351	14.92568	0.000112	0.000671
AT2G23470	-1.04177	3.149118	16.60145	4.61E-05	0.000306
AT1G62540	-1.03855	3.629172	21.89639	2.88E-06	2.57E-05
AT2G34357	-1.03815	6.409675	95.4801	1.49E-22	1.22E-20
AT1G72810	-1.03688	4.342745	33.95321	5.65E-09	8.90E-08
AT1G04130	-1.03687	4.579169	39.45566	3.36E-10	6.37E-09
AT4G15430	-1.03571	5.647569	70.0841	5.68E-17	2.68E-15
AT3G04640	-1.03174	4.728644	42.98426	5.52E-11	1.16E-09
AT5G17050	-1.03097	6.063879	80.80829	2.49E-19	1.50E-17
AT1G24147	-1.02849	5.311602	59.3697	1.31E-14	4.49E-13
AT2G41410	-1.02805	6.38136	92.31927	7.38E-22	5.67E-20
AT3G57530	-1.02517	6.674774	101.4717	7.25E-24	6.67E-22
AT5G39785	-1.02508	3.747737	23.04207	1.58E-06	1.51E-05
AT2G46270	-1.02497	3.659533	21.68748	3.21E-06	2.83E-05
AT3G14900	-1.02479	4.686577	41.3875	1.25E-10	2.51E-09
AT3G09720	-1.02342	3.729868	22.83421	1.77E-06	1.66E-05
AT1G63780	-1.02147	4.353621	33.20781	8.28E-09	1.27E-07
AT1G27730	-1.02022	4.882756	46.45503	9.37E-12	2.25E-10
AT1G11130	-1.01843	4.75776	42.78654	6.11E-11	1.27E-09

Gene	logFC	logCPM	LR	PValue	p.ad
AT1G12380	-1.01749	3.772944	22.86091	1.74E-06	1.64E-05
AT5G23310	-1.01621	4.95169	47.71373	4.93E-12	1.23E-10
AT5G66540	-1.0149	4.756193	42.47467	7.16E-11	1.48E-09
AT4G12130	-1.0133	3.596519	20.4893	6.00E-06	4.92E-05
AT4G17770	-1.01027	6.21365	83.33601	6.92E-20	4.35E-18
AT2G40900	-1.00981	4.088366	27.34063	1.71E-07	2.01E-06
AT3G14200	-1.00936	4.395744	33.51403	7.08E-09	1.10E-07
AT5G20670	-1.00842	3.795318	22.77337	1.82E-06	1.71E-05
AT2G43110	-1.00824	3.81514	23.2488	1.42E-06	1.37E-05
AT1G32870	-1.00741	4.707506	40.69947	1.78E-10	3.51E-09
AT1G22190	-1.00734	6.138304	80.2558	3.29E-19	1.95E-17
AT5G58370	-1.00707	4.930022	46.45388	9.38E-12	2.25E-10
AT5G65870	-1.00663	3.534697	19.35195	1.09E-05	8.43E-05
AT2G31790	-1.00654	6.309963	86.23974	1.59E-20	1.10E-18
AT1G27760	-1.00648	6.498861	92.9523	5.36E-22	4.14E-20
AT4G30990	-1.00592	6.170636	81.15507	2.09E-19	1.27E-17
AT1G59740	-1.00446	2.891973	13.40192	0.000251	0.001362
AT5G26920	-1.00376	4.814384	42.74839	6.23E-11	1.30E-09
AT5G53486	-1.00266	3.814277	22.88829	1.72E-06	1.62E-05
AT1G33560	-1.00236	4.416829	33.35017	7.70E-09	1.18E-07
AT1G02220	-1.00168	3.303982	16.75978	4.24E-05	0.000285
AT3G03520	-1.00122	4.453436	34.20398	4.96E-09	7.92E-08

Predicted target Phytophthora

sRNA_Acc.	Target_Acc	Expectation	UP ES	sRNA_start	sRNA_end	Target_start	Target_end	sRNA_aligned_fragment	SE_QIDN	Target_aligned_fragment	SE_QIDN	Inhibition	Target_Desc.
ppR000	Phycal1_4	0.5	19.9	1	22	2066	2087	AUUUCAGUGAACAAAGUU	O: 20	UGCUCAACTUGUUCACUG	O: 45	Cleavage	1
ppR000	Phycal1_5	0.5	22.0	1	21	108	128	UCUCCAUCUUGUUGAGC	21	CUCUGCUCAACAAGGUGG	7	ge	1
ppR000	Phycal1_1	1	16.5	1	21	331	351	CACGUCUCGAGAUUUUGU	22	AAGAGCAAGGUCUCAGAC	8	ge	1
ppR000	Phycal1_1	1	15.5	1	21	1286	1307	GAUGUAUUU- GUGAAACAAGGC	23	UCCUUGUUUCACGAAUA	9	ge	1
ppR000	Phycal1_1	1	12.6	1	20	71	90	UAGGAUCUUAAGACCUU	24	CCAAAGGUCUAAAGAUCC	46	Transla	1
ppR000	Phycal1_4	1	19.7	1	22	2064	2085	UUCAGUGAACAAAGUUGA	25	GUUGCUCAACUUGUUCAC	1	tion	1
ppR000	Phycal1_5	1	21.2	1	21	1146	1166	AGUAGUCGAGAGCAUC	26	CAGUGAUGCUUCUGACU	2	ge	1
ppR000	Phycal1_5	1	21.2	1	22	1145	1166	AGUAGUCGAGAGCAUC	27	UCAGUGAUGCUUCUGAC	46	ge	1
ppR000	Phycal1_5	1	19.9	1	22	1028	1049	CAUGUGAAGUUGUCUGU	28	UUUCAAGGCGACUUC	4	ge	1
ppR000	Phycal1_5	1	19.9	1	21	1029	1049	CAUGUGAAGUUGUCUGU	29	UUCAACGGCGACUUC	5	ge	1
ppR000	Phycal1_5	1	21.4	1	21	122	142	AAUGAUGCACUCAUCU	30	UAGCAGAUUGGGUGAUC	6	ge	1
ppR000	Phycal1_5	1	21.4	1	22	121	142	AAUGAUGCACUCAUCU	31	GUAGCAGAUUGGGUGAUC	7	ge	1
ppR000	Phycal1_1	1.5	19.3	1	21	487	506	UUUGCAAAGACCAUCA	32	CUCGUUGA- GGUCUUUGCAA	8	ge	1
ppR000	Phycal1_1	1.5	15.9	1	22	65	86	UUACUUGAAGUCUGAAA	33	GCACAAUUCAGACUCAA	9	ge	1
ppR000	Phycal1_1	1.5	23.6	1	21	493	513	UCUAAACGAUCGUGCAU	34	CUGUAUGGACGAUCGUU	0	ge	1
ppR000	Phycal1_1	1.5	23.6	1	22	492	513	UCUAAACGAUCGUGCAU	35	GCUGUAUGGACGAUCGUU	1	ge	1
ppR000	Phycal1_1	1.5	23.6	1	20	494	513	UCUAAACGAUCGUGCAU	36	UGUAUGGACGAUCGUUUG	2	ge	1
ppR000	Phycal1_1	1.5	15.4	1	21	57	77	UAAAUAUCAGGUUCCAU	37	UCCAAGGAAACCUGAUU	3	ge	1
ppR000	Phycal1_1	1.5	18.9	1	21	91	111	UGCUUCUGAAGCUUUGU	38	GACAACGAAGCUUCAGGA	4	ge	1
			99					UGUG		GUA	5	ge	

sRNA_Acc.	Target_Ac_c	Expecta tion	UP ES	sRNA_s tart	sRNA_ end	Target_ start	Target_ end	sRNA_aligned_fragment	SE Q ID	Target_aligned_fragment	SE Q ID	Inhibit ion	Target_ Desc.
PPR000 2908	Phycal1_1 31320	1.5	18.1	1	24	52	76	GAUCUUAACA- CAAUCAUCGAUAG	39	GGCGCGGUGAUUGAUGUU	47	Transla tion	1
PPR000 2076	Phycal1_1 4558	1.5	19.6	1	22	157	179	UUGUAGACUCC- CUGUCGAAGGA	40	GGCUUCGACGGCGAGUC	47	Transla tion	1
PPR000 2076	Phycal1_1 4563	1.5	20.8	1	22	535	557	UUGUAGACUCC- CUGUCGAAGGA	41	GGCUUCGACGGCGAGUC	47	Transla tion	1
PPR000 0222	Phycal1_1 7852	1.5	18.0	1	21	620	640	UUGUAGAGGCGAGAAA UUUU	42	CCAUUUUCUCAGCCUCUA	47	Cleava ge	1
PPR000 2007	Phycal1_1 7852	1.5	15.9	1	21	621	641	UUUGUAGAGGCGAGAA AUUG	43	CAUUUUCUCAGCCUCUAC	48	Cleava ge	1
PPR000 2134	Phycal1_1 9397	1.5	19.9	1	21	500	521	UUGAAGAU- ACAACAUUAGCC	44	AGCUGAUUUUGUUGAUCU	48	Transla tion	1
PPR000 3112	Phycal1_2 1290	1.5	24.3	1	20	1534	1552	CAUUGAUCGAUGCGUUU GCG	45	CGCAAUUG- UCGAUCAAUG	48	Transla tion	1
PPR000 0180	Phycal1_3 8737	1.5	18.2	1	21	312	333	GAGGCUGA- GAAAUUGUACGAC	46	GUCGUACAUAUUAUCGG	48	Cleava ge	1
PPR000 0789	Phycal1_3 8737	1.5	18.2	1	22	311	333	GAGGCUGA- GAAAUUGUACGAC	47	CGUCGUACAUAUUAUCG	48	Cleava ge	1
PPR000 2927	Phycal1_3 8737	1.5	18.2	1	21	312	333	GAGGCUGA- GAAAUUGUACGAC	48	GUCGUACAUAUUAUCGG	48	Cleava ge	1
PPR000 2365	Phycal1_4 0140	1.5	21.0	1	21	193	213	UGCCAGACGUAGUAACU UAUA	49	CACGAGUUACUACGUCUG	48	Cleava ge	1
PPR000 2457	Phycal1_4 0140	1.5	20.8	1	21	195	215	UCUGCCAGCUGUAGUAA CUUA	50	CGAGUUACUACGUCUGG	48	Cleava ge	1
PPR000 3014	Phycal1_4 0140	1.5	21.3	1	21	194	214	CUGCCAGACGUAGUAAC UUUU	51	ACGAGUUACUACGUCUGG	48	Cleava ge	1
PPR000 2470	Phycal1_4 177	1.5	23.0	1	21	799	820	UCUCCAUUUUUGUAGC A-GAU	52	AUCGUGCUCAACAAGGUG	48	Cleava ge	1
PPR000 3110	Phycal1_4 501	1.5	19.9	1	21	2068	2088	CAUUUCAGUGAACAAAGU UGAG	53	CUCAACUUGUUCACUGAA	49	Cleava ge	1
PPR000 2908	Phycal1_5 0226	1.5	22.6	1	24	250	274	GAUCUUAACA- CAAUCAUCGAUAG	54	GGCGCGGUGAUUGAUGUU	49	Transla tion	1
PPR000 2995	Phycal1_5 02953	1.5	22.7	1	21	1700	1719	CUUCCUUCUUUACACACA AGCA	55	GGCUUUGUGAA- GAAGGAGG	49	Transla tion	1
PPR000 3599	Phycal1_5 06259	1.5	22.1	1	23	1491	1513	AGAGGCUGUCAACCAAAA UCUGGU	56	CGGAGAUUUUGGUGACAG	49	Cleava ge	1
PPR000 3600	Phycal1_5 06259	1.5	22.1	1	22	1492	1513	AGAGGCUGUCAACCAAAA UCUGG	57	GGAGAUUUUGGUGACAGU	49	Cleava ge	1
PPR000 3601	Phycal1_5 06259	1.5	22.1	1	21	1493	1513	AGAGGCUGUCAACCAAAA UCUG	58	GAGAUUUUGGUGACAGUC	49	Cleava ge	1
PPR000 3602	Phycal1_5 06259	1.5	22.1	1	20	1494	1513	AGAGGCUGUCAACCAAAA UCU	59	AGAUUUUGGUGACAGUCU	49	Cleava ge	1
PPR000 2547	Phycal1_5 09001	1.5	24.5	1	20	135	154	UCACUCCAUUUUCCAU ACU	60	AGUUUAUGGAAGUAGAC	49	Cleava ge	1
PPR000	Phycal1_5	1.5	21.0	1	21	994	1013	AGUGACUGUGUUGGCCAA	61	CUAGU- CUAGU-	49	Cleava ge	1

sRNA_Acc.	Target_Ac c	Expecta tion	UP ES	sRNA_s tart	sRNA_ end	Target_ start	Target_ end	sRNA_aligned_fragment	SE Q ID N O:	Target_aligned_fragment	SE Q ID N O:	Inhibit ion	Target_ Desc.
3502	24851		11					CUAA		GGCAGCACAGUCACU	8	ge	
PPR000	Phycal1_5	1.5	21.0	1	20	995	1013	AGUGACUGUGUUGGCCAA		UAGU-	49	Cleava	1
3503	24851		11					CUA	62	GGCAGCACAGUCACU	9	ge	
PPR000	Phycal1_5	1.5	20.2	1	21	1234	1254	CUGGUAGUUGGACUGAU		GGCAGCAGUCCGUCUAC	50	Cleava	1
3007	28722		95					GCGG	63	CAG	0	ge	
PPR000	Phycal1_5	1.5	17	1	21	933	954	UAAAUGGAUU-		CAGCCUACAACAUAUCCA	50	Transla	1
2771	30588		17					UUUAAGGCUA	64	UUUG	1	tion	
PPR000	Phycal1_5	1.5	17	1	20	934	954	UAAAUGGAUU-		AGCCUUACAACAUAUCCA	50	Transla	1
2772	30588		17					UUUAAGGCU	65	UUUG	1	tion	
PPR000	Phycal1_5	1.5	18.5	1	21	268	288	CAUCAUCCCAUUAUCCA		CUGCUGGUGGAGGGGAUG	50	Transla	1
3131	35284		11					GCAU	66	AUG	3	tion	
PPR000	Phycal1_5	1.5	18.5	1	21	378	398	CAUCAUCCCAUUAUCCA		CUGCUGGUGGAGGGGAUG	50	Transla	1
3131	35285		11					GCAU	67	AUG	4	tion	
PPR000	Phycal1_5	1.5	21.8	1	22	1636	1656	UUCUCCAUUUUUCUGA		AAUGCUCAGAAAAG-	50	Transla	1
2141	35726		19					GCAAC	68	UGGAGGAA	5	tion	
PPR000	Phycal1_5	1.5	21.8	1	21	1637	1656	UUCUCCAUUUUUCUGA		AUGCUCAGAAAAG-	50	Transla	1
2142	35726		19					GCAA	69	UGGAGGAA	6	tion	
1664	40026		81					UUUGAC	70	ACACCA	7	ge	
PPR000	Phycal1_5	1.5	17.5	1	24	2588	2611	UGGUGUGCUUCCCGAUA		CUACUGUCCAUUGGAUUU	50	Cleava	1
0803	48684		37					CUUGAAAA-	71	UUUCAAG	8	ge	
PPR000	Phycal1_5	1.5	10.6	1	21	509	528	AAUCCAUGGAUAAGAG		ACAGAG-	50	Cleava	1
3479	50985		11					AUAAAUUUUAUAGCCU	72	CUGAAGGAUUUUU	9	ge	
PPR000	Phycal1_5	1.5	14.3	1	22	47	67	UGAGGAUGAUGACUCA		UGAUUUG-	51	Cleava	1
2408	51551		88					ACUUG	73	GUGUAUUAUCCUCA	0	ge	
PPR000	Phycal1_5	1.5	14.3	1	21	48	67	UGAGGAUGAUGACUCA		GAGUUG-	51	Cleava	1
2409	51551		88					ACU	74	GUGUAUUAUCCUCA	1	ge	
PPR000	Phycal1_5	1.5	19.7	1	21	3610	3629	UUCUGUGGAUGGUUUC		ACGAGGAACCAUC-	51	Cleava	1
2144	53643		91					UCGU	75	AGCAGAA	2	ge	
PPR000	Phycal1_5	1.5	18.8	1	22	1794	1815	UUCAAAGAGGAUGUCAA		UCUGGUUGACAUCUUCU	51	Transla	1
0513	54980		18					CCAGA	76	UGAG	3	tion	
PPR000	Phycal1_5	1.5	19.1	1	21	1792	1812	AAAGAGGAUGUCAAACCA		UUU	51	Cleava	1
1310	54980		73					GAUC	77	UUU	4	ge	
PPR000	Phycal1_5	1.5	18.0	1	22	1452	1472	UCGCGUGACUCCUGAUA		GAUGA-	51	Cleava	1
2502	69294		35					UCAUA	78	AUCAGGAGUCGCGCGA	5	ge	
PPR000	Phycal1_5	1.5	18.0	1	21	1453	1472	UCGCGUGACUCCUGAUA		AUGA-	51	Cleava	1
2503	69294		35					UCAU	79	AUCAGGAGUCGCGCGA	6	ge	
PPR000	Phycal1_5	1.5	15.3	1	25	681	704	UUUGAGUUGAUGAUUAG		CCACGUUGCUG-	51	Cleava	1
1593	69323		79					CAAGGACU	80	UCAUCAAUCUCAA	7	ge	
PPR000	Phycal1_5	1.5	15.3	1	22	684	704	UUUGAGUUGAUGAUUAG		CGUUGCUG-	51	Cleava	1
1594	69323		79					CAAG	81	UCAUCAAUCUCAA	8	ge	
PPR000	Phycal1_5	1.5	19.7	1	21	808	828	AUGGAAGCUCGCGAAAAU		GUCUCUUUUCGCGGUUC	51	Cleava	1
3318	69939		65					AGAG	82	CAU	9	ge	
PPR000	Phycal1_5	1.5	13.8	1	21	658	677	UGGUUGAUUUCGAGUAU		GCA-	52	Cleava	1
1061	71554		16					CUGC	83	AUACUGAAUGCAACCA	0	ge	

sRNA_Acc.	Target_Acc	Expectation	UP ES	sRNA_start	sRNA_end	Target_start	Target_end	sRNA_aligned_fragment	SE Q ID N O:	Target_aligned_fragment	SE Q ID N O:	Inhibition	Target_Desc.
PPR000 1513	Phycal1_6 081	1.5	20.5	1	21	66	86	GCCACUGCUUCUGAAGC UCUG	84	GAGAGCUUCAGAAAGCUGU GGC	52	Cleavage	1
PPR000 1888	Phycal1_6 081	1.5	20.3	1	22	66	87	AGCCACUGCUUCUGAAG CUCUG	85	GAGAGCUUCAGAAAGCUGU GGCU	52	Cleavage	1
PPR000 1889	Phycal1_6 081	1.5	20.3	1	21	67	87	AGCCACUGCUUCUGAAG CUCU	86	AGAGCUUCAGAAAGCUGUG GCU	52	Cleavage	1
PPR000 0344	Phycal1_6 1568	1.5	19.3	1	21	405	425	UUGAUUUUCCUCUCAAU CAUA	87	UAUUUAGAGAGGGAAGA UCAA	52	Cleavage	1
PPR000 3081	Phycal1_6 2058	1.5	10.6	1	21	337	356	CCUUUAUUCUCGCGAGCU UCCA	88	AGGAGC- GCGAGAAUGAAGG	52	Cleavage	1
PPR000 0254	Phycal1_6 8972	1.5	22.7	1	21	57	76	CCUUUUGAUCUACUCUGU CGUA	89	UGCGAGC- GAUGAUCAAAAGG	52	Cleavage	1
PPR000 0798	Phycal1_6 8972	1.5	23.3	1	21	56	75	CUUUUGAUCUACUCGUC GUAC	90	CUGCGACG- GAUGAUCAAAAG	52	Cleavage	1
PPR000 3378	Phycal1_8 013	1.5	22.6	1	21	488	507	AUCGUUGAUCGCCUUUG CAAG	91	GUUGCAAAGG- GAUCGACGAU	52	Transla- tion	1
PPR000 1989	Phycal1_9 238	1.5	17.1	1	20	321	340	UUUUGAUCUACUCUCUG UAC	92	GUACGAGGAGAUCAUCAA CA	52	Cleavage	1
PPR000 3066	Phycal1_9 9132	1.5	23.3	1	21	535	555	CGGCUCUGUCACAAUCU CUAA	93	UUGGAGAUUGUGAUGGA GCCG	53	Cleavage	1
PPR000 1013	Phycal1_9 9498	1.5	19.3	1	21	487	506	UUUGCAAAGACCAUCAA UGAU	94	CUCGUUA- GGUCUUUGCAAA	53	Cleavage	1
PPR000 0158	Phycal1_1 00055	2	21.1	1	21	1328	1347	AACAUCAGCCUCUAUUU UCCC	95	UGGAAAGUGGAG- CUGAUGUU	53	Transla- tion	1
PPR000 0588	Phycal1_1 00055	2	21.1	1	22	1327	1347	AACAUCAGCCUCUAUUU UCCC	96	CUGGAAAAGUGGAG- CUGAUGUU	53	Transla- tion	1
PPR000 1374	Phycal1_1 00187	2	17.7	1	21	440	461	UGAUCUACAACACUAUC AUUG	97	UCAAUGGUGGCGUUUGUAG AUC	53	Cleavage	1
PPR000 1494	Phycal1_1 00187	2	17.7	1	21	441	461	UGAUCUACAACACUAUC AUUG	98	CAAUGGUGGCGUUUGUAGA UCA	53	Cleavage	1
PPR000 1766	Phycal1_1 00187	2	17.5	1	21	440	460	GAUCUACAACACUAUCA UUGA	99	UCAAUGGUGGCGUUUGUAG AUC	53	Transla- tion	1
PPR000 3326	Phycal1_1 02033	2	19.0	1	24	433	456	AUGCUGGUAGAGGGGAU GAUGGUG	100	CACUAUCAGUUAUCUAC CAGCAU	53	Cleavage	1
PPR000 0576	Phycal1_1 02925	2	22.0	1	21	327	347	AGAAGGUAGUGGAACUCU UCCG	101	CGUACGAGUUCUACUCCU UCU	53	Cleavage	1
PPR000 1259	Phycal1_1 02925	2	22.0	1	22	326	347	AGAAGGUAGUGGAACUCU UCCGC	102	CCGUACGAGUUCUACUACC UUUU	53	Cleavage	1
PPR000 0670	Phycal1_1 0317	2	18.7	1	22	605	626	UGAGACUUCUCGCGGAA GAGUU	103	AGCUCUACUGCGAGAUUGU UUUA	54	Cleavage	1
PPR000 0671	Phycal1_1 0317	2	18.7	1	21	606	626	UGAGACUUCUCGCGGAA GAGU	104	GCUCUACUGCGAGAUUGU UCA	54	Cleavage	1
PPR000 0637	Phycal1_1 04342	2	24.8	1	21	256	276	UGUAGUCACUUUCAGCG CAUU	105	AAUGCGUUUGAUGUGGCU ACA	54	Transla- tion	1
PPR000	Phycal1_1	2	12.4	1	21	83	102	AGUGUUGUAAGUGACUG	106	AGACA-	54	Cleavage	1

sRNA_Acc.	Target_Acc	Expectation	UP ES	sRNA_start	sRNA_end	Target_start	Target_end	sRNA_aligned_fragment	SE Q ID N O:	Target_aligned_fragment	SE Q ID N O:	Inhibition	Target_Desc.
3491	04418		38					UGUU	6				
PPR000 0104	Phycal1_1 04452	2	24.1	1	21	2991	3011	UUGAUCUUCUCUGUA CAAU	10 7	CGUGUACGACGAGGUGAU CGA	54 4	ge	1
PPR000 0329	Phycal1_1 04452	2	22.6	1	21	2992	3012	UUUGAUCUUCUCUGU ACAA	10 8	GUGUACGACGAGGUGAUC GAU	54 5	Cleava ge	1
PPR000 0349	Phycal1_1 04452	2	24.1	1	22	2990	3011	UUGAUCUUCUCUGUA CAAU	10 9	ACGUGUACGACGAGGUGA UCGA	54 6	Cleava ge	1
PPR000 0637	Phycal1_1 04721	2	16.7	1	21	256	276	UGUAGUCACUUCAGCG CAU	11 0	AAUGCGUUGAAUGUGGU ACA	54 7	Transla tion	1
PPR000 3046	Phycal1_1 05959	2	23.0	1	21	698	718	CUACUGAGUGUAUGAU UGAG	11 1	GUCACUCUAUUGUUCAG UAG	54 8	Cleava ge	1
PPR000 3922	Phycal1_1 06036	2	19.5	1	22	1375	1395	AAAAACCAUCCGUCUGA AAUU	11 2	AUUUUUGAGACGG- UGGUUUU	54 9	Transla tion	1
PPR000 3174	Phycal1_1 06199	2	13.5	1	21	80	99	CAAGGGCUUUUUGAUGA UGGC	11 3	GAAAGAGCUCUUG CCCAUCA-	55 0	ge	2
PPR000 3174	Phycal1_1 06199	2	18.2	1	21	134	153	CAAGGGCUUUUUGAUGA UGGC	11 4	GAAAGAGCUCUUG CCCAUCA-	55 5	Cleava ge	2
PPR000 0532	Phycal1_1 06247	2	20.2	1	21	283	303	UAAUUCAGGACUUUUU CUUC	11 5	CAGGAGAAUGUCGAUGAA UUA	55 2	Transla tion	1
PPR000 0063	Phycal1_1 06472	2	22.3	1	22	188	209	UUCUGACUACUCA- GUGAUUG	11 6	AGUAUCACGUGAGU- GUCGAGAA	55 3	Transla tion	1
PPR000 0225	Phycal1_1 06472	2	22.3	1	21	189	209	UUCUGACUACUCA- GUGAUU	11 7	GUUACACGUGAGU- GUCGAGAA	55 4	Transla tion	1
PPR000 0351	Phycal1_1 06472	2	22.3	1	24	186	209	UUCUGACUACUCA- GUGAUUGAU	11 8	CAAGUAUCACGUGAGU- GUCGAGAA	55 5	Transla tion	1
PPR000 0622	Phycal1_1 06472	2	22.3	1	20	190	209	UUCUGACUACUCA- GUGAU	11 9	UAUCACGUGAGU- GUCGAGAA	55 6	Transla tion	1
PPR000 0804	Phycal1_1 06472	2	23.3	1	21	190	210	CUUCUGACUACUCA- GUGAU	12 0	UAUCACGUGAGU- GUCGAGAG	55 7	Transla tion	1
PPR000 0805	Phycal1_1 06472	2	23.3	1	20	191	210	CUUCUGACUACUCA- GUGAU	12 1	AUCACGUGAGU- GUCGAGAG	55 8	Transla tion	1
PPR000 2148	Phycal1_1 06472	2	22.3	1	24	186	209	UUCUGACUACUCA- GUGAUUGCU	12 2	CAAGUAUCACGUGAGU- GUCGAGAA	55 9	Transla tion	1
PPR000 2149	Phycal1_1 06472	2	22.3	1	23	187	209	UUCUGACUACUCA- GUGAUUGC	12 3	AAGUAUCACGUGAGU- GUCGAGAA	56 0	Transla tion	1
PPR000 3768	Phycal1_1 06633	2	15.0	1	21	452	473	AAUACUAUGAU- CUCAGGAUUU	12 4	AAAUCCUGAGUAUCAUGG UGUU	56 1	Transla tion	1
PPR000 3030	Phycal1_1 06681	2	13.7	1	21	357	375	CUCGAAUACCAACAAUG CUU	12 5	GAAG-AUUG- UGGUUUUCGAG	56 2	Cleava ge	1
PPR000 3491	Phycal1_1 07719	2	13.2	1	21	290	309	AGUGUUUGAAGUGACUG UGUU	12 6	AGCAC- UCAUUUACACACU	56 3	Cleava ge	1
PPR000 3669	Phycal1_1 07852	2	15.3	1	21	30	51	ACGAGGAGA- UGAUCAAAAGGU	12 7	CUCUUUUUGACUCUCU UCGU	56 4	Transla tion	1
PPR000 1337	Phycal1_1 08533	2	21.6	1	21	81	100	UUGUAGAUCAACACACC AGGC	12 8	GCCUG- UGUUGGGAUCUACAA	56 5	Transla tion	1

sRNA_Acc.	Target_Ac	Expecta	UP	sRNA_s	sRNA_end	Target_start	Target_end	sRNA_aligned_fragment	SE	Target_aligned_fragment	SE	Inhibit	Target_Desc.
		tion	ES	tart					Q		Q	ion	
									ID		ID		
									N		N		
									O:		O:		
PPR000	Phycal1_1	2	21.4	1	21	80	99	UGUAGAUCAACAACCA	12	UGUAGAUCAACAACCA	12	Transla	1
1372	08533		42					GGCU	9	GGCU	9	tion	
PPR000	Phycal1_1	2	21.6	1	22	80	100	UUGUAGAUCAACAACCA	13	UUGUAGAUCAACAACCA	13	Transla	1
1613	08533		91					AGGCU	0	AGGCU	0	tion	
PPR000	Phycal1_1	2	21.4	1	20	81	99	UGUAGAUCAACAACCA	13	UGUAGAUCAACAACCA	13	Transla	1
1659	08533		42					GGC	1	GGC	1	tion	
PPR000	Phycal1_1	2	16.9	1	21	133	153	UUUUAUUCGCGAGCUUC	13	UUUUAUUCGCGAGCUUC	13	Transla	1
2049	08536		6					CAUC	2	CAUC	2	tion	
PPR000	Phycal1_1	2	15.3	1	21	1118	1139	CAGGUUGAUAAACGC-	13	CAGGUUGAUAAACGC-	13	Cleava	1
3137	08681		91					GUUGAU	3	GUUGAU	3	gc	
PPR000	Phycal1_1	2	16.2	1	21	1117	1138	AGGUUGAUAAACGC-	13	AGGUUGAUAAACGC-	13	Cleava	1
3520	08681		08					GUUGAU	4	GUUGAU	4	gc	
PPR000	Phycal1_1	2	19.3	1	21	85	104	AUUUUGACAUACAACAU	13	AUUUUGACAUACAACAU	13	Transla	1
1191	0889		37					UCUG	5	UCUG	5	tion	
PPR000	Phycal1_1	2	15.8	1	21	411	432	UGUCUGCAGACGUAG-	13	UGUCUGCAGACGUAG-	13	Cleava	1
2257	09101		25					UAACU	6	UAACU	6	gc	
PPR000	Phycal1_1	2	20.8	1	21	386	406	ACGUUUUUGUAGUUGCA	13	ACGUUUUUGUAGUUGCA	13	Cleava	1
1458	09114		56					AAGA	7	AAGA	7	gc	
PPR000	Phycal1_1	2	20.9	1	21	668	689	UUUACAUUCAC-	13	UUUACAUUCAC-	13	Transla	1
0003	09192		11					AACUCUAAU	8	AACUCUAAU	8	tion	
PPR000	Phycal1_1	2	20.9	1	22	667	689	UUUACAUUCAC-	13	UUUACAUUCAC-	13	Transla	1
0503	09192		11					AACUCUAAU	9	AACUCUAAU	9	tion	
PPR000	Phycal1_1	2	20.9	1	24	665	689	UUUACAUUCAC-	14	UUUACAUUCAC-	14	Transla	1
1017	09192		11					AACUCUAAU	0	AACUCUAAU	0	tion	
PPR000	Phycal1_1	2	20.9	1	20	669	689	UUUACAUUCAC-	14	UUUACAUUCAC-	14	Transla	1
1018	09192		11					AACUCUAAU	1	AACUCUAAU	1	tion	
PPR000	Phycal1_1	2	20.5	1	22	108	129	UGGUUUUCUGUUGGUGUG	14	UGGUUUUCUGUUGGUGUG	14	Cleava	1
0519	09473		04					CAUCC	2	CAUCC	2	gc	
PPR000	Phycal1_1	2	20.5	1	21	109	129	UGGUUUUCUGUUGGUGUG	14	UGGUUUUCUGUUGGUGUG	14	Cleava	1
1060	09473		04					CAUC	3	CAUC	3	gc	
PPR000	Phycal1_1	2	22.8	1	21	405	425	UUUGAUUUUCCUCUCAAU	14	UUUGAUUUUCCUCUCAAU	14	Cleava	1
0344	10173		22					CAUA	4	CAUA	4	gc	
PPR000	Phycal1_1	2	20.4	1	21	6928	6947	AGCAGUGGCUUUAGUUG	14	AGCAGUGGCUUUAGUUG	14	Cleava	1
1248	1199		89					AUCA	5	AUCA	5	gc	
PPR000	Phycal1_1	2	15.2	1	20	630	648	UUUGAAGUAAUUAUUGUC	14	UUUGAAGUAAUUAUUGUC	14	Cleava	1
2085	13560		38					GGC	6	GGC	6	gc	
PPR000	Phycal1_1	2	8.78	1	21	738	758	UUUGAGGUGACAAACAUU	14	UUUGAGGUGACAAACAUU	14	Cleava	1
2073	14431		3					AGGU	7	AGGU	7	gc	
PPR000	Phycal1_1	2	18.9	1	20	245	264	GAUGGUGUGGAACUCUU	14	GAUGGUGUGGAACUCUU	14	Cleava	1
2891	14778		27					CCG	8	CCG	8	gc	
PPR000	Phycal1_1	2	12.6	1	21	69	89	AGGAUCUUAUAGACCUUU	14	AGGAUCUUAUAGACCUUU	14	Cleava	1
3543	15329		09					GGAU	9	GGAU	9	gc	
PPR000	Phycal1_1	2	19.6	1	22	1414	1435	UUGAAGAGGAUUUGUG	15	UUGAAGAGGAUUUGUG	15	Cleava	1
2518	15436		58					CUAAU	0	CUAAU	0	gc	
PPR000	Phycal1_1	2	20.2	1	22	438	459	UUCAGUGAACAAAGUUGA	15	UUCAGUGAACAAAGUUGA	15	Transla	1

sRNA_Acc.	Target_Acc	Expectation	UP ES	sRNA_start	sRNA_end	Target_start	Target_end	sRNA_aligned_fragment	SE Q ID N O:	Target_aligned_fragment	SE Q ID N O:	Inhibition	Target_Desc.
2175	17293		77					GUGCA	1	UGGA	8	tion	
PPR000	Phycal1_1	2	17.5	1	24	502	525	AUGCUGGAGAU	15	CACUAUCAGUUAUCUAC	58	Cleavage	1
3326	18328		72					GAUGGUG	2	CAGCAU	9	ge	
PPR000	Phycal1_1	2	14.6	1	20	314	333	UUUGGCUUUGAGUUUGU	15	UUGAAAAACUCAAAGUCA	59	Cleavage	1
0599	19050		73					UUA	3	AA	0	ge	
PPR000	Phycal1_1	2	16.0	1	21	641	661	UGUAAUUACGGAAGAU	15	GCUCUAUCGCGCAAUU	59	Cleavage	1
0012	19085		02					GAGU	4	ACA	1	ge	
PPR000	Phycal1_1	2	16.0	1	22	640	661	UGUAAUUACGGAAGAU	15	CGCUCCAUCGUCGCAAU	59	Cleavage	1
0361	19085		02					GAGU	5	UACA	2	ge	
PPR000	Phycal1_1	2	16.0	1	24	638	661	UGUAAUUACGGAAGAU	15	GCCGCUCCAUCGUCGCA	59	Cleavage	1
0640	19085		02					GAGU	6	AUUACA	3	ge	
PPR000	Phycal1_1	2	16.0	1	20	642	661	UGUAAUUACGGAAGAU	15	CUCCAUCGUCGCAAUUA	59	Cleavage	1
0641	19085		02					GAG	7	CA	4	ge	
PPR000	Phycal1_1	2	19.0	1	22	462	481	ACUUUUCGCCACAACA	15	AGCUCU-UUGUGGC-	59	Cleavage	1
1904	19825		13					GAGCU	8	AAAAAGU	5	ge	
PPR000	Phycal1_1	2	16.7	1	21	589	609	CUCUUUGAACCAUUUGA	15	UUGGUCAAGUGGUUUGA	59	Cleavage	1
0550	19941		9					UCAA	9	AGAG	6	ge	
PPR000	Phycal1_1	2	24.5	1	20	873	892	UCUCAAUCUAUACACUG	16	ACGCAGUGAUGAUUGA	59	Cleavage	1
0676	19972		8					AGU	0	GG	7	ge	
PPR000	Phycal1_1	2	20.6	1	21	535	555	CUCUUUGAACCAUUUGA	16	UUGGUCAAGUGGUUUGA	59	Cleavage	1
0550	21035		18					UCAA	1	AGAG	8	ge	
PPR000	Phycal1_1	2	11.5	1	22	282	302	AUCUUUUUAACAAACU	16	UGCUGAGUUUGU-	59	Transla	1
0897	21390		9					CAAG	2	AAAGAAGAU	9	tion	
PPR000	Phycal1_1	2	23.5	1	21	407	429	GAUGGAGUGA-UGCCU-	16	AUCGAGGAGCAUACUC	60	Transla	1
2900	21453		58					CUCGAC	3	CCAUC	0	tion	
PPR000	Phycal1_1	2	23.9	1	22	407	430	AGAUUGGAGUGA-UGCCU-	16	AUCGAGGAGCAUACUC	60	Transla	1
3583	21453		91					CUCGAC	4	CCAUCU	1	tion	
PPR000	Phycal1_1	2	23.9	1	21	408	430	AGAUUGGAGUGA-UGCCU-	16	UCGAGGAGGCAUACUC	60	Transla	1
3584	21453		91					CUCGA	5	CAUCU	2	tion	
PPR000	Phycal1_1	2	21.8	1	21	386	406	ACGUUUUUGUAGUUUGCA	16	GCUGUGCAACUACGAAGA	60	Cleavage	1
1458	21499		87					AAGA	6	CGU	3	ge	
PPR000	Phycal1_1	2	18.6	1	22	820	840	UUCACUGAUCAUUGGGU	16	GGAAAAUCUAUUGA-	60	Cleavage	1
0226	22030		63					UUUGU	7	CGGUGAA	4	ge	
PPR000	Phycal1_1	2	18.6	1	21	821	840	UUCACUGAUCAUUGGGU	16	GAAAAUCUAUUGA-	60	Cleavage	1
0227	22030		63					UUUG	8	CGGUGAA	5	ge	
PPR000	Phycal1_1	2	19.4	1	21	839	859	UUUGUUUUUGUUGUUUGU	16	CUCAGCAGCAGCAAGAAC	60	Cleavage	1
2002	22338		96					UGAG	9	AAG	6	ge	
PPR000	Phycal1_1	2	17.5	1	22	593	614	ACAGCAACUCCACAU	17	AGAGACAUGUGGAAGCUG	60	Cleavage	1
3688	22637		25					UCUAU	0	UUUGU	7	ge	
PPR000	Phycal1_1	2	9.82	1	21	1242	1261	UGGUUUUCUGAUGGUGUG	17	GAAGCAAAACCA-	60	Transla	1
1487	22662		1					CUUC	1	CAGAAACCA	8	tion	
PPR000	Phycal1_1	2	9.82	1	22	1241	1261	UGGUUUUCUGAUGGUGUG	17	CGAAGCAAAACCA-	60	Transla	1
1662	22662		1					CUUCC	2	CAGAAACCA	9	tion	
PPR000	Phycal1_1	2	9.62	1	21	1243	1262	AUGGUUUUCUGAUGGUGU	17	AAGCAACCA-	61	Transla	1
1841	22662							GCUU	3	CAGAAACCAU	0	tion	

sRNA_Acc.	Target_Ac_c	Expecta tion	UP ES	sRNA_s tart	sRNA_ end	Target_ start	Target_ end	sRNA_aligned_fragment	SE Q ID	Target_aligned_fragment	SE Q ID	Inhibit ion	Target_ Desc.
PPR000 1973	Phycal1_1 23005	2	15.7	1	21	240	259	UUUUUGACUUGCGAAUA	17 O:	GGUAUAUUCG-	61 O:	Transla tion	1
PPR000 2310	Phycal1_1 24800	2	29	1	21	451	471	UUGGAAAGCUAGUACAG	4	AAGUCAAAG	1	Cleava	1
PPR000 1602	Phycal1_1 24969	2	92	1	23	77	100	UUUCAGAUCCCGU- AUCUCUUGU	5	CCA	2	ge	1
PPR000 2410	Phycal1_1 25360	2	22.3	1	21	1977	1997	UGAGCAUUGAUUGGUU	6	CUGAAC	3	ge	1
PPR000 3808	Phycal1_1 25444	2	11	1	21	597	617	CCC	17	UCA	4	Cleava	1
PPR000 3808	Phycal1_1 25481	2	89	1	22	591	611	AAGCUUCCGAAGCUGUG	7	AUGCCGCGAG-	61	ge	1
PPR000 3454	Phycal1_1 26185	2	19	1	22	591	611	GCUU	8	UUCCGAAGCUU	5	ge	1
PPR000 2835	Phycal1_1 26409	2	57	1	21	1269	1288	AAGCUUCCGAAGCUGUG	17	AUGCCGCGAG-	61	Cleava	1
PPR000	Phycal1_1	2	17.1	1	21	55	74	UUUCAGAUCCCGU- AUCUCUUGU	9	UUCGGAAGCUU	6	ge	1
PPR000	Phycal1_1	2	66	1	21	55	74	UUUCAGAUCCCGU- AUCUCUUGU	18	GCAGUUCUCUCC-	61	Transla tion	1
PPR000	Phycal1_1	2	18.9	1	21	57	76	UUUCAGAUCCCGU- AUCUCUUGU	0	GUCAGUAU	7	Cleava	1
PPR000	Phycal1_1	2	8	1	21	324	344	UUUCAGAUCCCGU- AUCUCUUGU	18	CUGCGGGAAGAGU-	61	ge	1
PPR000	Phycal1_1	2	18.2	1	21	324	344	UUUCAGAUCCCGU- AUCUCUUGU	1	CCACACC	8	Transla tion	1
PPR000	Phycal1_1	2	22.9	1	21	324	344	UUUCAGAUCCCGU- AUCUCUUGU	2	GGCGGAAGAGU-	61	ge	1
PPR000	Phycal1_1	2	04	1	22	323	344	UUUCAGAUCCCGU- AUCUCUUGU	18	CCACACCAG	9	Cleava	1
PPR000	Phycal1_1	2	22.9	1	22	323	344	UUUCAGAUCCCGU- AUCUCUUGU	3	UUCU	0	ge	1
PPR000	Phycal1_1	2	04	1	21	199	218	UUUCAGAUCCCGU- AUCUCUUGU	18	CCGUACGAGUCCAUACC	62	Cleava	1
PPR000	Phycal1_1	2	19.8	1	21	1128	1147	UUUCAGAUCCCGU- AUCUCUUGU	4	UUCU	1	ge	1
PPR000	Phycal1_1	2	32	1	21	1128	1147	UUUCAGAUCCCGU- AUCUCUUGU	5	GUGUAU-	62	Cleava	1
PPR000	Phycal1_1	2	18.9	1	21	1128	1147	UUUCAGAUCCCGU- AUCUCUUGU	18	UUCAAAGACAAUCA	2	ge	1
PPR000	Phycal1_1	2	36	1	21	54	74	UUUCAGAUCCCGU- AUCUCUUGU	6	UUCUUU-	62	Cleava	1
PPR000	Phycal1_1	2	11.5	1	21	54	74	UUUCAGAUCCCGU- AUCUCUUGU	18	UAAUCCAAUGGAACCCUGA	3	ge	1
PPR000	Phycal1_1	2	81	1	20	675	694	UUUCAGAUCCCGU- AUCUCUUGU	7	UAU	4	ge	1
PPR000	Phycal1_1	2	21.5	1	20	675	694	UUUCAGAUCCCGU- AUCUCUUGU	18	UACACACAUCAAUGGGUUU	62	Cleava	1
PPR000	Phycal1_1	2	96	1	22	55	77	UUUCAGAUCCCGU- AUCUCUUGU	8	UG	5	ge	1
PPR000	Phycal1_1	2	17.2	1	22	55	77	UUUCAGAUCCCGU- AUCUCUUGU	18	GCGGUAUUGAUUGUA	62	Cleava	1
PPR000	Phycal1_1	2	59	1	21	187	207	UUUCAGAUCCCGU- AUCUCUUGU	9	AGAUCG	6	ge	1
PPR000	Phycal1_1	2	14.8	1	21	2046	2066	UUUCAGAUCCCGU- AUCUCUUGU	19	AACAAACCGAAGCCAAA	62	Cleava	1
PPR000	Phycal1_1	2	86	1	21	2046	2066	UUUCAGAUCCCGU- AUCUCUUGU	0	UCA	7	ge	1
PPR000	Phycal1_1	2	19.6	1	21	2047	2067	UUUCAGAUCCCGU- AUCUCUUGU	19	GCGUACAUCCAGCGCAU	62	Cleava	1
PPR000	Phycal1_1	2	85	1	21	2047	2067	UUUCAGAUCCCGU- AUCUCUUGU	1	UGA	8	ge	1
PPR000	Phycal1_1	2	19.2	1	21	386	409	UUUCAGAUCCCGU- AUCUCUUGU	19	GCGUACAUCCAGCGCAU	62	Cleava	1
PPR000	Phycal1_1	2	84	1	24	386	409	UUUCAGAUCCCGU- AUCUCUUGU	2	GAC	9	ge	1
PPR000	Phycal1_1	2	13	1	22	388	409	UUUCAGAUCCCGU- AUCUCUUGU	19	CAAGCAUCCGACGGUCA	63	Cleava	1
PPR000	Phycal1_1	2	18.7	1	22	388	409	UUUCAGAUCCCGU- AUCUCUUGU	3	UGUAUA	0	ge	1
PPR000	Phycal1_1	2	13	1	21	389	409	UUUCAGAUCCCGU- AUCUCUUGU	19	AGCAUCCGACGGUCAUG	63	Cleava	1
PPR000	Phycal1_1	2	18.7	1	21	389	409	UUUCAGAUCCCGU- AUCUCUUGU	4	UAUA	1	ge	1
PPR000	Phycal1_1	2	13	1	21	382	402	UUUCAGAUCCCGU- AUCUCUUGU	19	GCAUCUCGACGUCAUG	63	Cleava	1
PPR000	Phycal1_1	2	22.7	1	21	382	402	UUUCAGAUCCCGU- AUCUCUUGU	5	AUA	2	ge	1
PPR000	Phycal1_1	2	22.7	1	21	382	402	UUUCAGAUCCCGU- AUCUCUUGU	19	UACGCGUGGUGUUGGUC	63	Cleava	1

sRNA_Acc.	Target_Ac	Expecta tion	UP ES	sRNA_s tart	sRNA_ end	Target_ start	Target_ end	sRNA_aligned_fragment	SE Q ID	Target_aligned_fragment	SE Q ID	Inhibit ion	Target_ Desc.
0535	4010		16										
PPR000	Phycal1_1	2	21.8	1	20	384	403	UGUAGAUCAACAACA	19	CGCUGGUGUUGGUCUA	63	ge	1
1058	4010		57					GCC	7	CA	4	ge	
PPR000	Phycal1_1	2	22.3	1	21	384	404	UUUGAUAACACACACC	19	CGCUGGUGUUGGUCUA	63	Cleava	1
1337	4010							AGGC	8	CAG	5	ge	
PPR000	Phycal1_1	2	22.3	1	22	383	404	UUUGAUAACACACACC	19	ACGCUGGUGUUGGUCU	63	Cleava	1
1613	4010							AGGCU	9	ACAG	6	ge	
PPR000	Phycal1_1	2	18.4	1	21	1523	1543	UCAACUUGUUCACUGAA	20	ACAUUUCGGUGACGAGU	63	Cleava	1
2564	4970		01					AUGG	0	UGG	7	ge	
PPR000	Phycal1_1	2	11.3	1	21	554	574	UUUGUUCUUGUUGUUGU	20	AUAAGCAACAACAAGAAC	63	Cleava	1
2002	6193		93					UGAG	1	AGA	8	ge	
PPR000	Phycal1_1	2	20.3	1	22	561	582	UUGCUGUUGACUUAUUC	20	GGAGCGAUGAGUCAACA	63	Cleava	1
2107	7835		88					ACUGA	2	GCGA	9	ge	
PPR000	Phycal1_1	2	20.3	1	21	562	582	UUGCUGUUGACUUAUUC	20	GAGCGAAUGAGUCAACAG	64	Cleava	1
2108	7835		88					ACUG	3	CGA	0	ge	
PPR000	Phycal1_1	2	19.4	1	22	562	583	GUUGCUGUUGACUUAUUC	20	GAGCGAAUGAGUCAACAG	64	Cleava	1
2782	7835		25					CACUG	4	CGAC	1	ge	
PPR000	Phycal1_1	2	19.4	1	21	563	583	GUUGCUGUUGACUUAUUC	20	AGCGAAUGAGUCAACAGC	64	Cleava	1
2783	7835		25					CACU	5	GAC	2	ge	
PPR000	Phycal1_1	2	17.7	1	22	539	560	UUUGGCUUUAAAUUCUC	20	AGUGGCAGAUUUUGAAG	64	Cleava	1
2017	8836		75					UCAAC	6	UCGAA	3	ge	
PPR000	Phycal1_1	2	20.0	1	24	539	562	GAUUUGGCUUUAAAUUCU	20	AGUGGCAGAUUUUGAAG	64	Cleava	1
2885	8836		14					GCUCAAC	7	UCGAAUC	4	ge	
PPR000	Phycal1_1	2	20.0	1	21	542	562	GAUUUGGCUUUAAAUUCU	20	GGGCAGAUUUUGAAGUCGA	64	Cleava	1
2886	8836		14					GCUC	8	AUC	5	ge	
PPR000	Phycal1_1	2	23.2	1	20	1763	1781	AACAAGAUUGGAAGCUCG	20	UUUCGGCGUUC-	64	Transla	1
3852	9221		01					GAA	9	GUCUUGU	6	tion	
PPR000	Phycal1_1	2	23.1	1	21	259	278	AAGACGGGCGUUCUCCA	21	UAUCUGGA-	64	Transla	1
3823	9518		97					GAUA	0	GACGCCCGUCU	7	tion	
PPR000	Phycal1_2	2	12.9	1	22	597	617	AAGCUUCCGAAGCUGUG	21	AUGGCCGCGAG-	64	Cleava	1
3808	0118		6					GCUUU	1	UUCGGAAGCUU	8	ge	
PPR000	Phycal1_2	2	20.9	1	22	95	115	UGUGGAACUCUUCGCGG	21	ACUCUUG-	64	Cleava	1
2253	0352		7					AGAUG	2	GGAGGAGUUCACCA	9	ge	
PPR000	Phycal1_2	2	16.1	1	21	537	557	AAUAUUGGGAUGGCACAC	21	CAUGGCGUGCAUCCGUAU	65	Cleava	1
3756	1138		2					CAUC	3	AUU	0	ge	
PPR000	Phycal1_2	2	24.3	1	21	1533	1552	CAUUGAUUGAUGCAUUU	21	CCGCAAAUGC-	65	Transla	1
0843	1290		45					GUGA	4	UCGAUCAUG	1	tion	
PPR000	Phycal1_2	2	23.8	1	21	1534	1553	UCAUUGAUCGAUGCGUU	21	CGCAAAUGC-	65	Cleava	1
2531	1290		21					UGCG	5	UUGCAUCAAUGG	2	ge	
PPR000	Phycal1_3	2	18.7	1	20	365	383	UAAAUGGAUUUUGUAAG	21	ACACU-	65	Cleava	1
2770	5826		06					UGU	6	AUGAAAUCCAUUUA	3	ge	
PPR000	Phycal1_3	2	18.9	1	21	365	384	AUAAAUGGAUUUUGUA	21	ACACU-	65	Cleava	1
3473	5826		88					GUGU	7	AUGAAAUCCAUUUAU	4	ge	
PPR000	Phycal1_3	2	14.5	1	20	311	331	GGCUGA-	21	CGUCGUACAUAUUCG	65	Cleava	1
0763	8737		23					GAAAUUGUACGACG	8	GCC	5	ge	

sRNA_Acc.	Target_Ac_c	Expecta tion	UP ES	sRNA_s tart	sRNA_ end	Target_ start	Target_ end	sRNA_aligned_fragment	SE Q ID	Target_aligned_fragment	SE Q ID	Inhibit ion	Target_ Desc.
PPR000 0938	Phycal1_3 8737	2	18.1	1	23	309	332	AGGCUGA- GAAAUUGUACGACGAG	21 O:	CCCGUCGUACAAUUUCAU	65 O:	Cleava ge	1
PPR000 0939	Phycal1_3 8737	2	18.1	1	21	311	332	AGGCUGA- GAAAUUGUACGACG	9	CGGCCU	6	Cleava ge	1
PPR000 2166	Phycal1_4 177	2	23.3	1	21	798	819	UCCAUUCUUGUGAGCA- GAUU	22	CAUCGUGUCUCAAAGGU	65	Cleava ge	1
PPR000 2978	Phycal1_4 177	2	21.0	1	25	798	823	CUUUCUCCAUUCUUGUG AGCA-GAUU	1	GGAG	8	Cleava ge	1
PPR000 2979	Phycal1_4 177	2	21.0	1	21	803	823	CUUUCUCCAUUCUUGUG AGCA-GAUU	22	GGAGAGC	65	Cleava ge	1
PPR000 0226	Phycal1_4 2707	2	19.6	1	22	208	228	UUCACUGAUCUAAUGGGU UUUGU	22	AGC	0	Cleava ge	1
PPR000 0227	Phycal1_4 2707	2	19.6	1	21	209	228	UUCACUGAUCUAAUGGGU UUUG	22	GAAACUCUUAUGA- CGGUGAA	66	Cleava ge	1
PPR000 1123	Phycal1_4 3385	2	13.6	1	21	27	46	UAAAUUCAGGUUCCAU UGUA	22	UAUGAUG- AACUCGAUUUA	66	Cleava ge	1
PPR000 3905	Phycal1_4 4195	2	12.6	1	20	2193	2212	AAAGAAUUGGAAACCAA AGG	22	CAUUUGGUUCCAUUUUCU	66	Cleava ge	1
PPR000 0867	Phycal1_4 501	2	19.9	1	22	2066	2087	AUUUCAGUAACAGAUU GAGUG	22	UGCUCACUUGUUCACUG	66	Cleava ge	1
PPR000 0868	Phycal1_4 501	2	19.9	1	21	2067	2087	AUUUCAGUAACAGAUU GAGU	8	GCUCACUUGUUCACUGA	66	Cleava ge	1
PPR000 2689	Phycal1_4 5605	2	9.92	1	22	760	781	UAGACUUAUUUUGUCAC UCUGG	9	UUAGUGUGCCAAAAAGAG	66	Cleava ge	1
PPR000 0373	Phycal1_4 583	2	24.8	1	21	1578	1598	UCGUCUAAACGACGUG CAUA	0	UCUA	7	Transla tion	1
PPR000 0682	Phycal1_4 583	2	24.8	1	22	1577	1598	UCGUCUAAACGACGUG CAUAC	23	GAUGCACGUAAGUUUGGA	66	Transla tion	1
PPR000 0809	Phycal1_4 583	2	21.2	1	22	1578	1599	CUCGUCUAAACGACGUG GCAUA	2	AUGA	9	Transla tion	1
PPR000 0810	Phycal1_4 583	2	21.2	1	21	1579	1599	CUCGUCUAAACGACGUG GCAU	23	GAUGCACGUAAGUUUGGA	67	Cleava ge	1
PPR000 0219	Phycal1_4 9400	2	21.0	1	21	314	334	UUUUCACUUAUAGUUCA CUGA	4	GAG	1	Transla tion	1
PPR000 2395	Phycal1_5 0226	2	21.7	1	22	253	275	UGAUUCUACAACA- CAUAUCGA	5	AGA	2	Cleava ge	1
PPR000 2832	Phycal1_5 02720	2	14.9	1	21	201	220	GGUUUUGAGCAUGGAUA UGAU	6	AGAUCG	67	Transla tion	1
PPR000 2595	Phycal1_5 02731	2	21.5	1	21	1061	1081	UAUGUCGGCAUUGAAUC CUUC	7	GCUUAAAACC	4	Transla tion	1
PPR000 3416	Phycal1_5 02731	2	46	1	21	1062	1082	AUAUGUCGGCAUUGAAU CCUU	8	AUG	5	Transla tion	1
PPR000 0617	Phycal1_5 02827	2	15.0	1	21	1220	1240	UUUGAGUUUUAUAAAGAA GAUG	9	UGU	6	Cleava ge	1
PPR000	Phycal1_5	2	14.9	1	21	1309	1329	UUUGAGUUUUAUAAAGAA	24	CAA	7	Cleava ge	1

sRNA_Acc.	Target_Ac c	Expecta tion	UP ES	sRNA_s tart	sRNA_ end	Target_ start	Target_ end	sRNA_aligned_fragment	SE Q ID	Target_aligned_fragment	SE Q ID	Inhibit ion	Target_ Desc.
0617	02829		96							CAA		ge	
PPR000	Phycal1_5	2	18.7	1	21	2042	2062	UAUAGGAUCUAUGGAC	24	AAAAGUUCUAAGAUCCUA	67	Cleava	1
2590	02941		48					CUU	2	GUA	9	ge	
PPR000	Phycal1_5	2	18.5	1	21	187	206	AGGAGUUGCAGGUUUGC	24	ACCAG-	68	Cleava	1
3544	03017		46					UGGC	3	AAACCUGCAGCUUCU	0	ge	
PPR000	Phycal1_5	2	14.4	1	22	1387	1407	UUCUUCACAAACAAAGCU	24	UAUGAAGCUGUGUU-	68	Cleava	1
1027	03168		79					UCAGA	4	UGAAGAA	1	ge	
PPR000	Phycal1_5	2	14.4	1	21	1388	1407	UUCUUCACAAACAAAGCU	24	AUGAAGCUGUGUU-	68	Cleava	1
1028	03168		79					UCAG	5	UGAAGAA	2	ge	
PPR000	Phycal1_5	2	21.7	1	21	583	602	AGUACUGUAAGUCACUA	24	GGCGUAGU-	68	Cleava	1
1235	03230		72					CGUU	6	ACUUGCAGUACU	3	ge	
PPR000	Phycal1_5	2	21.7	1	20	584	602	AGUACUGUAAGUCACUA	24	GCGUAGU-	68	Cleava	1
1236	03230		72					CGU	7	ACUUGCAGUACU	4	ge	
PPR000	Phycal1_5	2	20.2	1	21	1447	1466	AUGUAGUCACUUUUAGC	24	UGGUGUAAAAGG-	68	Transla	1
3275	03430		96					ACCC	8	GACUGCAU	5	tion	
PPR000	Phycal1_5	2	23.2	1	21	269	289	AGAUGAUGCGGUUAAUC	24	AGCAGAUUGACCGCAUCA	68	Cleava	1
1897	03678							UGUU	9	UCU	6	ge	
PPR000	Phycal1_5	2	21.1	1	23	701	723	GAAAGCAUUGGUGGUU	25	GGGCGAAUACCAUCAAUG	68	Cleava	1
2972	03915		73					UCGAGU	0	CUGUC	7	ge	
PPR000	Phycal1_5	2	21.1	1	20	704	723	GAAAGCAUUGGUGGUU	25	CGAAUACCAUCAAUGCUG	68	Cleava	1
2973	03915		73					UCG	1	UC	8	ge	
PPR000	Phycal1_5	2	19.2	1	21	520	540	AUCGUUGAUCGCCUUUG	25	CUGGCGAAGGUGAUCAAC	68	Cleava	1
3378	04528							CAAG	2	GAU	9	ge	
PPR000	Phycal1_5	2	19.3	1	21	308	329	UCUGGUCUA-	25	CAAUAAAGGUUAUCUGGAC	69	Transla	1
1081	04741		66					AUACCUUUGUA	3	CAGA	0	tion	
PPR000	Phycal1_5	2	16.7	1	25	14	38	CUUUUCCCAUUCUUUG	25	CAAGAGCUCGCCAAGAUG	69	Cleava	1
2978	05080		5					AGCAGAUU	4	GAGAAGG	1	ge	
PPR000	Phycal1_5	2	16.7	1	21	18	38	CUUUUCCCAUUCUUUG	25	AGCUCGCCAAGAUGGAGA	69	Cleava	1
2979	05080		5					AGCA	5	AGG	2	ge	
PPR000	Phycal1_5	2	15.6	1	21	1580	1600	AGAUGGAAGCUGCGAGA	25	AUAUUCGCCAGUUUUUCA	69	Cleava	1
3585	06007							AUAA	6	UCU	3	ge	
PPR000	Phycal1_5	2	20.8	1	21	151	172	AACGUGAAUGAUG-	25	CUUGAGUGGCAACAUAUCA	69	Transla	1
1330	06101		31					CACUCAU	7	CGUU	4	tion	
PPR000	Phycal1_5	2	20.8	1	24	148	172	AACGUGAAUGAUG-	25	UGCCUUGAGUGGCAACAUC	69	Transla	1
1570	06101		31					CACUCAUCUG	8	UCACGUU	5	tion	
PPR000	Phycal1_5	2	20.8	1	22	150	172	AACGUGAAUGAUG-	25	CCUUGAGUGGCAACAUAUC	69	Transla	1
1571	06101		31					CACUCAUC	9	ACGUU	6	tion	
PPR000	Phycal1_5	2	20.8	1	20	152	172	AACGUGAAUGAUG-	26	UUGAGUGGCAACAUAUCAC	69	Transla	1
1952	06101		31					CACUCA	0	GUU	7	tion	
PPR000	Phycal1_5	2	21.5	1	24	1142	1165	GUAGUCGAGAAGCAUCA	26	AAGUCAGUGAUGCUUCUC	69	Cleava	1
0750	06161		2					CUCCAUC	1	GACUGU	8	ge	
PPR000	Phycal1_5	2	21.0	1	21	1148	1168	UCAGUAGUUGAGAGGCA	26	GUGAUGCUUCUGACUGU	69	Cleava	1
2544	06161		28					UCAC	2	UGA	9	ge	
PPR000	Phycal1_5	2	22.1	1	24	1490	1513	AGAGCUGUCAACCAGA	26	ACGGAGAUUUGGUGACA	70	Cleava	1
3596	06259		32					UCUGGUU	3	GUCUCU	0	ge	

sRNA_Acc.	Target_Ac	Expecta tion	UP ES	sRNA_s tart	sRNA_ end	Target_ start	Target_ end	sRNA_aligned_fragment	SE Q ID	Target_aligned_fragment	SE Q ID	Inhibit ion	Target_ Desc.
PPR000 3597	Phycal1_5 06259	2	22.1 32	1	22	1492	1513	AGAGGCGUGUCAAACCAGA UCUGG	O: 26 4	GGAGAUUUGGUGACAGU CUCU	O: 70 1	Cleava ge	1
PPR000 3598	Phycal1_5 06259	2	22.1 32	1	21	1493	1513	AGAGGCGUGUCAAACCAGA UCUG	26 5	GAGAUUUGGUGACAGUC UCU	70 2	Cleava ge	1
PPR000 2166	Phycal1_5 06671	2	22.0 03	1	21	107	127	UUCCAUCUUGUUGAGCA GAUU	26 6	GCUCUGCUCAACAAGGUG GAG	70 3	Cleava ge	1
PPR000 2997	Phycal1_5 06671	2	22.0 1	1	22	107	128	CUUCCAUCUUGUUGAGC AGAUU	26 7	GCUCUGCUCAACAAGGUG GAGA	70 4	Cleava ge	1
PPR000 2998	Phycal1_5 06671	2	22.0 1	1	21	108	128	CUUCCAUCUUGUUGAGC AGAU	26 8	CUCUGCUCAACAAGGUG AGA	70 5	Cleava ge	1
PPR000 2999	Phycal1_5 06671	2	22.0 1	1	20	109	128	CUUCCAUCUUGUUGAGC AGA	26 9	UCUGCUCAACAAGGUGA GA	70 6	Cleava ge	1
PPR000 0792	Phycal1_5 06835	2	18.4 86	1	21	1415	1435	GAGAUUCUCUCAAAGAGG AUUG	27 0	AAAUCCUUUUUGAGGGC CUC	70 7	Cleava ge	1
PPR000 0830	Phycal1_5 06835	2	20.8 59	1	24	1413	1436	CGAGAUUCUCUCAAAGAG GAUUGU	27 1	GGAAAUCCUUUUUGAGGGC AUCUG	70 8	Cleava ge	1
PPR000 1027	Phycal1_5 06946	2	16.8 55	1	22	1571	1590	UUUUCACACAAACAGCU UCAGA	27 2	GAUGAAGCU-- GUUGUGAAGAA	70 9	Cleava ge	1
PPR000 1028	Phycal1_5 06946	2	16.8 55	1	21	1572	1590	UUUUCACACAAACAGCU UCAG	27 3	AUGAAGCU-- GUUGUGAAGAA	71 0	Cleava ge	1
PPR000 0943	Phycal1_5 07636	2	22.9 59	1	21	942	961	AGCCAAUCAAUAUCAC CUCU	27 4	AGAG- UGACAUUGAUUUUGGCU	71 1	Cleava ge	1
PPR000 1758	Phycal1_5 08164	2	19.0 69	1	22	893	914	GCAGUGGCUUUAAGUUGA CCGGA	27 5	AGUGGUCAGCUAAACCCA CUGC	71 2	Cleava ge	1
PPR000 1759	Phycal1_5 08164	2	19.0 69	1	21	894	914	GCAGUGGCUUUAAGUUGA CCG	27 6	GUGGUCAGCUAAACCCAC UGC	71 3	Cleava ge	1
PPR000 1760	Phycal1_5 08164	2	19.0 69	1	20	895	914	GCAGUGGCUUUAAGUUGA CCG	27 7	UGGUCAGCUAAACCCACU GC	71 4	Cleava ge	1
PPR000 0374	Phycal1_5 08585	2	17.4 24	1	21	138	158	UCGUCGUACAAUUUCUC AGCC	27 8	GGCUCAGAAUUCGUACGA CGA	71 5	Transla tion	1
PPR000 2002	Phycal1_5 08595	2	18.6 99	1	21	848	869	UUUUGUUCUUGUUGU- UGUUGAG	27 9	CUCAACGGACAACGAGAA CAAA	71 6	Cleava ge	1
PPR000 0014	Phycal1_5 08653	2	23.7 9	1	21	290	311	GAUUAUGAUUUUGGCU- UUGAGU	28 0	CCUCAUUGGCCAAAUCAA UGUC	71 7	Cleava ge	1
PPR000 0031	Phycal1_5 08653	2	23.7 9	1	22	289	311	GAUUAUGAUUUUGGCU- UUGAGU	28 1	UCCUCAUUGGCCAAAUUCA AUGUC	71 8	Cleava ge	1
PPR000 0135	Phycal1_5 08653	2	23.0 88	1	21	291	312	UGAUUAUGAUUUUGGCU- UUGAGU	28 2	CUCAUUGGCCAAAUCAAU GUCA	71 9	Cleava ge	1
PPR000 0364	Phycal1_5 08653	2	23.0 88	1	22	290	312	UGAUUAUGAUUUUGGCU- UUGAGU	28 3	CCUCAUUGGCCAAAUCAA UGUCA	72 0	Cleava ge	1
PPR000 0668	Phycal1_5 08653	2	23.0 88	1	20	292	312	UGAUUAUGAUUUUGGCU- UUGAGU	28 4	UCAAUUGGCCAAAUCAAUG UCA	72 1	Cleava ge	1
PPR000 0781	Phycal1_5 08653	2	23.7 9	1	23	288	311	GAUUAUGAUUUUGGCU- UUGAGUUU	28 5	UUUCCUCAUUGGCCAAAUUC AAUGUC	72 2	Cleava ge	1
PPR000	Phycal1_5	2	23.7	1	20	291	311	GAUUAUGAUUUUGGCU-	28	CUCAUUGGCCAAAUCAAU	72	Cleava	1

sRNA_Acc.	Target_Acc	Expectation	UP ES	sRNA_start	sRNA_end	Target_start	Target_end	sRNA_aligned_fragment	SE Q ID N O:	Target_aligned_fragment	SE Q ID N O:	Inhibition	Target_Desc.
0782	08653		9						6		3	ge	
PPR000	Phycal1_5	2	15.2	1	20	1692	1711	UUUUGAUCUCCUCG	28	GUACGAGGACAAGAUCAA	72	Transla	1
1989	09101		31					UAC	7	AA	4	tion	
PPR000	Phycal1_5	2	20.8	1	21	2682	2702	UGGAUCAUCCUCGUG	28	GUUGCACGAGUACAUGAU	72	Transla	1
2324	09101		03					CAAU	8	CCA	5	tion	
PPR000	Phycal1_5	2	18.8	1	21	157	176	AUUUUCUGUGAGUGCA	28	CCGAG-	72	Cleava	1
3207	09279		48					UGCA	9	CAUCUCGCAGAAAGAU	6	ge	
PPR000	Phycal1_5	2	20.3	1	21	1811	1831	UGCUUGGCCUUGUCUAG	29	CCGUCAGGACAAGGCCAA	72	Cleava	1
2346	09421		36					ACGA	0	GUA	7	ge	
PPR000	Phycal1_5	2	13.7	1	21	264	285	UUUCUGAUGGUGUGC-	29	AGGGAACGCACACUAUUA	72	Cleava	1
1597	10026		08					UUCGCG	1	GAAA	8	ge	
PPR000	Phycal1_5	2	14.5	1	21	627	646	UACAAUUUAUUGAUCAA	29	ACCAUUGA-	72	Cleava	1
2720	10032		1					UGGG	2	CAUUGAGUUGUA	9	ge	
0343	10073		88					CACU	3	GGUGAUUUUGUUGCCAAC	73	Cleava	1
PPR000	Phycal1_5	2	21.3	1	22	697	717	AGGGAAGCUUGUAGAGG	29	GCCAGCCCCUACA-	73	Transla	1
1242	10151		16					CUGAG	4	GCUCCCU	1	tion	
PPR000	Phycal1_5	2	19.2	1	21	1163	1182	UUUCACAGCCUCUACAA	29	GAGCUU-	73	Cleava	1
0602	10534		4					GCUU	5	UAGAGGUUGAGAAG	2	ge	
2038	10534		4					GCUU	6	GAGCUU-	73	Cleava	1
PPR000	Phycal1_5	2	16.0	1	21	2816	2836	UGUGAAGGAAGGGAAGC	29	UAGAGGUUGAGAAG	3	ge	
1054	11063		14					UUUG	7	UCAAUGUCCCCUCCUUC	73	Cleava	1
PPR000	Phycal1_5	2	19.6	1	21	655	675	UUCCUUCUUUACACAAA	29	ACA	4	ge	
1031	11064		46					UGCA	8	GGCAGCUGUGAAGGAAGG	73	Cleava	1
PPR000	Phycal1_5	2	20.0	1	20	37	56	AUCAGGACGAACACGCC	29	GAA	5	ge	
3396	113		8					GAG	9	GUCCGUGUGUUCGUCCUG	73	Cleava	1
PPR000	Phycal1_5	2	22.4	1	22	605	626	AGUCGAGAAGCAUCACU	30	GU	6	ge	
0931	11587		17					CCAUC	0	GUCU	7	ge	
PPR000	Phycal1_5	2	18.1	1	21	734	754	UCUUUACAUAUCCAU	30	CUAAGUGGAGUAUGUAG	73	Cleava	1
1497	11953		39					UUAC	1	GAGA	8	ge	
PPR000	Phycal1_5	2	15.0	1	21	880	900	ACUGUAAGUCACUACGU	30	ACAAACGUGGUGAAUUUAU	73	Cleava	1
0579	25051		31					UUGG	2	AGU	9	ge	
PPR000	Phycal1_5	2	14.3	1	21	881	901	UACUGUAAGUCACUACG	30	CAAACGUGGUGAAUUUAU	74	Transla	1
1113	25051		52					UUUG	3	GUA	0	tion	
PPR000	Phycal1_5	2	13.3	1	21	738	757	UUUGUAGUGUAAGUUU	30	CACGAAACUUUAU-	74	Cleava	1
2060	25051		87					CGUG	4	UCGACAA	1	ge	
PPR000	Phycal1_5	2	18.8	1	21	637	657	AGUAACUGUAUUAAGCAA	30	CUGAUUGUUGAUUCAGUU	74	Transla	1
3513	25248		4					UAC	5	ACU	2	tion	
PPR000	Phycal1_5	2	17.8	1	21	629	648	UCAUUGAUCGAGUGGUU	30	AGCAAACGCGUGCGAUCA-	74	Cleava	1
2531	26527		43					UGCG	6	UGA	3	ge	
PPR000	Phycal1_5	2	13.1	1	22	415	436	UUUCUCCAUCUUUUUA	30	GAUGUUGAGGAGGAUGG	74	Cleava	1
1014	26737		03					ACAA	7	AGAAG	4	ge	
PPR000	Phycal1_5	2	14.3	1	21	2782	2801	UUUGAUCUCUGUCUUCU	30	GUUGAGAAG-	74	Cleava	1
2100	27499		49					CAAC	8	CAGAGAUUUCGA	5	ge	

sRNA_Acc.	Target_Acc	Expectation	UP ES	sRNA_start	sRNA_end	Target_start	Target_end	sRNA_aligned_fragment	SE Q ID	Target_aligned_fragment	SE Q ID	Inhibition	Target_Desc.
PPR000 2463	Phycal1_5 27540	2	21.807	1	21	671	691	UCUCUUGGAAGAGUUUU UUGG	30 9	GCAAGAAACGCUUCCAGG AGA	74 6	Cleavage	1
PPR000 0599	Phycal1_5 28383	2	22.111	1	20	920	939	UUUGGCUUUGAGUUUGU UAA	31 0	UGAACAAAGUCAAAGCCA AA	74 7	Cleavage	1
PPR000 0611	Phycal1_5 28383	2	19.281	1	21	918	938	UUUGGCUUUGAGUUUGU AAAG	31 1	AUUGAACAAAGUCAAAGC CAA	74 8	Cleavage	1
PPR000 2980	Phycal1_5 28429	2	24.723	1	21	1596	1616	CUUUCGAUCAUACACG CAGC	31 2	GCUGAGUGAUGUGGUCGA AAG	74 9	Cleavage	1
PPR000 3749	Phycal1_5 28615	2	14.551	1	21	544	564	AAUGAGGGAUUUGUAGG UGAC	31 3	AUCGCCUACAUUUCCUC AUU	75 0	Transla	1
PPR000 0374	Phycal1_5 2871	2	19.106	1	21	48	67	UCGUCGUACAUAUUUCUC AGCC	31 4	GGCUG- GAAAUUCUACGACGA	75 1	Transla	1
PPR000 1452	Phycal1_5 28723	2	16.287	1	21	670	689	AUCUCACAGAUUGGCC UGAU	31 5	CUCAGAGCACAU- GAGAGAU	75 2	Cleavage	1
PPR000 0563	Phycal1_5 29319	2	16.223	1	21	43	63	AUCUGGUUGACAUCCUC UUUG	31 6	CAAGGAGGAGUCAAAGCA GAU	75 3	Cleavage	1
PPR000 1080	Phycal1_5 29319	2	17.049	1	21	42	62	UCUGGUUGACAUCCUCU UUGA	31 7	UCAAGGAGGAGUCAAAGC AGA	75 4	Cleavage	1
PPR000 1144	Phycal1_5 29319	2	16.216	1	21	44	64	GAUCUGGUUGACAUCCU CUU	31 8	AAGGAGGAGUCAAAGCAG AUC	75 5	Cleavage	1
PPR000 1161	Phycal1_5 29319	2	17.153	1	23	39	61	CUGGUUGACAUCCUCU UGAAC	31 9	AGAUCAAAGGAGGAGUACA AGCAG	75 6	Cleavage	1
PPR000 1350	Phycal1_5 29822	2	12.019	1	20	8089	8108	AUGAUGUGUUGUAGAU CAC	32 0	GUUCGUCUACAACACUGUC AU	75 7	Cleavage	1
PPR000 1358	Phycal1_5 29822	2	12.019	1	21	8088	8108	AUGAUGUGUUGUAGAU CACA	32 1	UGUCGUCUACAACACACUGU CAU	75 8	Cleavage	1
PPR000 1386	Phycal1_5 29822	2	12.037	1	21	8087	8107	UGAUGUGUUGUAGAU ACAA	32 2	UUUGUCGUCUACAACACUG UCA	75 9	Cleavage	1
PPR000 1396	Phycal1_5 29822	2	12.019	1	22	8087	8108	AUGAUGUGUUGUAGAU CACAA	32 3	UUUGUCGUCUACAACACUG UCAU	76 0	Cleavage	1
PPR000 1444	Phycal1_5 29822	2	11.731	1	21	8086	8106	GAUAGUGUUGUAGAU CAAC	32 4	AUUGUCGUCUACAACACU GUC	76 1	Cleavage	1
PPR000 1679	Phycal1_5 29822	2	12.037	1	22	8086	8107	UGAUGUGUUGUAGAU ACAAC	32 5	AUUGUCGUCUACAACACU GUCA	76 2	Cleavage	1
PPR000 1767	Phycal1_5 29822	2	11.731	1	20	8087	8106	GAUAGUGUUGUAGAU CAA	32 6	UUUGUCGUCUACAACACUG UC	76 3	Cleavage	1
PPR000 3058	Phycal1_5 29932	2	14.59	1	22	34	55	CGUUGCGAAGGAGGGG AAGCU	32 7	GCCUUCUUCUUCUUCGCG AACG	76 4	Cleavage	1
PPR000 3727	Phycal1_5 30588	2	19.844	1	22	930	952	AAUGGAUU- UUGUAAGGCUAAGA	32 8	GGUCAGCCUUACAACAAU CCAU	76 5	Cleavage	1
PPR000 3728	Phycal1_5 30588	2	19.844	1	21	931	952	AAUGGAUU- UUGUAAGGCUAAG	32 9	GUCAAGCCUUACAACAAUC CAU	76 6	Cleavage	1
PPR000 3854	Phycal1_5 30588	2	18.546	1	21	932	953	AAUGGAUU- UUGUAAGGCUAA	33 0	UCAGCCUUACAACAAUCC AUU	76 7	Transla	1
PPR000	Phycal1_5	2	23.4	1	21	1030	1049	CUUUUGAUCAUUCUGUC	33	CUACG-	76	Cleavage	1

sRNA_Acc.	Target_Ac_c	Expecta tion	UP ES	sRNA_s tart	sRNA_ end	Target_ start	Target_ end	sRNA_aligned_fragment	SE Q ID N O:	Target_aligned_fragment	SE Q ID N O:	Inhibit ion	Target_ Desc.
0798	30625		42						1	UGAGAUGAUCGAAAG	8	ge	
PPR000	Phycal1_5	2	23.4	1	21	1029	1049	CUUUCGAUCAUACAG	33	ACUACGUGAGAUGAUCGA	76	Cleava	1
2980	30625		42					CAGC	2	AAG	9	ge	
PPR000	Phycal1_5	2	14.7	1	21	220	239	AGAUUUUUACUUGAUG	33	GAAUCAUCGAAG-	77	Transla	1
3572	30998		37					GUUA	3	AAAAAUCU	0	tion	
PPR000	Phycal1_5	2	14.7	1	20	221	239	AGAUUUUUACUUGAUG	33	AAUCAUCGAAG-	77	Transla	1
3573	30998		37					GUU	4	AAAAAUCU	1	tion	
PPR000	Phycal1_5	2	19.1	1	22	7762	7784	UUGAUGAGAUGAUC-	33	GUCUUUUGCGAUCGUCUC	77	Cleava	1
2120	31377		91					CAAAAGGUC	5	AUCAA	2	ge	
PPR000	Phycal1_5	2	19.8	1	21	88	107	UCUGCUUGGCCUUGUCU	33	GUCUAU-	77	Cleava	1
2454	31549		43					AGAC	6	CAAGGCCAAGCAGA	3	ge	
PPR000	Phycal1_5	2	17.0	1	21	1017	1036	UUGCAGAUACUCGAAUA	33	AUUGUGUUCG-	77	Transla	1
0508	32200		8					CAAC	7	GUUUUUGCAA	4	tion	
PPR000	Phycal1_5	2	11.0	1	21	2455	2475	UGGUUUCUGAUGGCGUG	33	UAGACACGCCAUUAGAUG	77	Cleava	1
2304	33060		64					CCUC	8	CCA	5	ge	
PPR000	Phycal1_5	2	20.6	1	22	3688	3708	CUCAGCCUCUACAAGCU	33	GUGGAUGCUU-	77	Cleava	1
1164	33583		64					UCCCU	9	UAGAGGCUGAG	6	ge	
PPR000	Phycal1_5	2	20.6	1	21	3689	3708	CUCAGCCUCUUAAGCU	34	UGGAUGCUU-	77	Cleava	1
3032	33583		64					UCCC	0	UAGAGGCUGAG	7	ge	
PPR000	Phycal1_5	2	23.6	1	21	377	397	UCUUUCUGAGCAACUCC	34	UUUGGAGUUGCACAGAA	77	Transla	1
2446	33897		5					AUGG	1	AGA	8	tion	
PPR000	Phycal1_5	2	18.8	1	21	642	663	AUGCAUUUGU-	34	ACCCUUCUUUGCACAAAU	77	Transla	1
0155	34734		89					AAGGAAGGA	2	GCAG	9	tion	
PPR000	Phycal1_5	2	19.4	1	25	1528	1552	CUUUUCUCCAUUUUUG	34	GAUGAGUUCGAUAAGAU	78	Cleava	1
2978	36287		84					AGCAGAUU	3	GGAGGAAG	0	ge	
PPR000	Phycal1_5	2	19.4	1	21	1532	1552	CUUUUCUCCAUUUUUG	34	AGUUCGAUAAGAUGGAG	78	Cleava	1
2979	36287		84					AGCA	4	GAAAG	1	ge	
PPR000	Phycal1_5	2	11.6	1	21	4434	4455	AGGUGGAAGAUUG-	34	AAUCCAAACGCCAUCUUC	78	Cleava	1
1880	36369		18					GUGGAUC	5	ACCU	2	ge	
PPR000	Phycal1_5	2	17.0	1	21	2130	2150	UGAAGCGACAUGUUUG	34	CUUCCCAAGCAUUCGCU	78	Transla	1
2430	36610		61					GAAU	6	UCA	3	tion	
PPR000	Phycal1_5	2	21.6	1	21	2708	2727	CUUCGUCAUCUCUUA	34	UGGCUAAG-	78	Transla	1
1392	36711		36					GCCU	7	GAGGAGACGAAG	4	tion	
PPR000	Phycal1_5	2	18.8	1	21	464	485	AGGCUAAUGU-	34	AGAAGAUCACGCACAUUG	78	Transla	1
3535	37321		36					UGUGAUCUUA	8	GCCU	5	tion	
PPR000	Phycal1_5	2	18.8	1	20	465	485	AGGCUAAUGU-	34	GAAGAUCACGCACAUUGG	78	Transla	1
3536	37321		36					UGUGAUCUUC	9	CCU	6	tion	
PPR000	Phycal1_5	2	10.6	1	21	196	215	AGUUAGCCGGAUGGUUG	35	AUCACAACC-	78	Cleava	1
1875	38673		18					UGAA	0	UCCAGUCAACU	7	ge	
PPR000	Phycal1_5	2	16.4	1	21	632	651	AAUCUGCUUCCUCCUUU	35	GUUCAAGGGAGGAAG-	78	Cleava	1
1286	38759		13					GAAC	1	AGAUU	8	ge	
PPR000	Phycal1_5	2	13.0	1	21	1637	1657	UAAUGGACUACGUUUGG	35	CCUACCUAACGCAGUCAC	78	Transla	1
2743	39095		11					UAGA	2	UUA	9	tion	
PPR000	Phycal1_5	2	19.4	1	22	1478	1498	UGGUGUAAGUGACUGUG	35	GCCAGCAC-	79	Cleava	1
0048	43455		63					UUGCC	3	GUCAUUUACACCA	0	ge	

sRNA_Acc.	Target_Ac_c	Expecta tion	UP ES	sRNA_s tart	sRNA_ end	Target_ start	Target_ end	sRNA_aligned_fragment	SE Q ID	Target_aligned_fragment	SE Q ID	Inhibit ion	Target_ Desc.
PPR000 0064	Plycal1_5 43455	2	19.4	1	21	1479	1498	UGGUGUAAAGUGACUGUG UUGC	35 4	CCAGCAC- GUCAUUUACACCA	79 1	Cleava ge	1
PPR000 1123	Plycal1_5 44266	2	15.3	1	21	307	326	UAAAUACAGGUCCAU UGUA	35 5	UAUGAUG- AACUGAUUUUA GAUACAGUCACU-	79 2	Cleava ge	1
PPR000 0040	Plycal1_5 4441	2	18.4	1	21	967	986	AGUGGUGUAAAGUGACUG UGUU	35 6	GCACCA AUACAGUCACU-	79 3	Transla tion	1
PPR000 0179	Plycal1_5 4441	2	16.9	1	21	968	987	GAGUGGUGUAAAGUGACU GUGU	35 7	GCACCA GAUACAGUCACU-	79 4	Transla tion	1
PPR000 0786	Plycal1_5 4441	2	93	1	22	967	987	GAGUGGUGUAAAGUGACU GUGUU	35 8	GCACCA UCGUAUACAGUCACU-	79 5	Transla tion	1
PPR000 2293	Plycal1_5 4441	2	19.6	1	21	965	984	UGGUGUAAAGUGACUGUA UCCG	35 9	GCACCA AUCGUGUCCAUUCUCC	79 6	Cleava ge	1
PPR000 2557	Plycal1_5 44425	2	16.2	1	21	1652	1673	UCAAGGAGUAGUACGAC- ACGAG	36 0	UUGA GUUGAUAAGUGACU	79 7	Cleava ge	1
PPR000 1431	Plycal1_5 45468	2	16.8	1	21	772	792	UGAUAUGUACGACUCAAU CUGU	36 1	UUA GUCAAGAACAACAAGAGC	79 8	Cleava ge	1
PPR000 2002	Plycal1_5 45924	2	24.5	1	21	401	421	UUUUGUUUUUUUUUUUU UGAG	36 2	AAG AAUUGAUGUGGUUGAGAG	79 9	Cleava ge	1
PPR000 0217	Plycal1_5 469	2	21.0	1	22	946	967	UUUUCUCUCAUAUAUA UCACU	36 3	GAUU UUUGAUGUGGUUGAGAG	80 0	Cleava ge	1
PPR000 0218	Plycal1_5 469	2	21.0	1	21	947	967	UUUUCUCUCAUAUAUA UCAC	36 4	AAU AAUUGAUGUGGUUGAGAG	80 1	Cleava ge	1
PPR000 0332	Plycal1_5 469	2	20.3	1	21	946	966	UUUUCUCUCAUAUAUA CACU	36 5	GAAA AAUUGAUGUGGUUGAGAG	80 2	Cleava ge	1
PPR000 0623	Plycal1_5 469	2	21.0	1	21	945	965	UUUUCUCUCAUAUAUA ACUG	36 6	GGAA AAUUGAUGUGGUUGAGAG	80 3	Cleava ge	1
PPR000 0685	Plycal1_5 48193	2	17.2	1	21	576	596	UCCAUUUCAGUGAACAG AUUG	36 7	GGA AAUUGAUGUGGUUGAGAG	80 4	Cleava ge	1
PPR000 0686	Plycal1_5 48193	2	17.2	1	20	577	596	UCCAUUUCAGUGAACAG AUU	36 8	GA AAUUGAUGUGGUUGAGAG	80 5	Cleava ge	1
PPR000 3225	Plycal1_5 49021	2	12.7	1	22	582	603	AUUGGUCACCGGUUCU GUAUG	36 9	CAAU CCAUUUUUCUCAGCUUCUA	80 6	Cleava ge	1
PPR000 0222	Plycal1_5 49075	2	20.8	1	21	611	631	UUUGAGGGCUGAGAAA UUUG	37 0	CGA CGCAACAACAACAACGUG	80 7	Cleava ge	1
PPR000 1331	Plycal1_5 49870	2	14.4	1	21	4	24	AUUCACGUUUUUUGUAGU UGCA	37 1	AAU GCAACAACAACAACAACGUG	80 8	Transla tion	1
PPR000 1378	Plycal1_5 49870	2	14.4	1	20	5	24	AUUCACGUUUUUUGUAGU UGC	37 2	AU GCAACAACAACAACAACGUG	80 9	Transla tion	1
PPR000 1831	Plycal1_5 49870	2	14.4	1	24	1	24	AUUCACGUUUUUUGUAGU UGCAA	37 3	GUGAAU AUGGCAACAACAACAAC	81 0	Transla tion	1
PPR000 1832	Plycal1_5 49870	2	14.4	1	22	3	24	AUUCACGUUUUUUGUAGU UGCAA	37 4	GAUU GCGCAACAACAACAACAACGUG	81 1	Transla tion	1
PPR000 3270	Plycal1_5 50807	2	19.7	1	21	1028	1048	AUGGGAAGUUGUGUUGU GACU	37 5	CAU UUUCAAACGGGACUUCUA	81 2	Cleava ge	1
PPR000	Plycal1_5	2	19.8	1	21	1030	1050	ACAUUGGGAAGUUGCUG	37	UCAAACGGGACUUCUCCACA	81	Cleava ge	1

Target Desc.	Inhibit ion	SE Q ID N O:	Target_aligned_fragment	SE Q ID N O:	sRNA_aligned_fragment	Target_start	Target_end	sRNA_start	sRNA_end	UP E\$	Expecta tion	Target_Ac c	sRNA_Acc.
Cleava	ge	3	UGG	6	UUGA	701	723	1	24	76	2	50807	3678
	Cleava	81	ACGAUGAAAUUGGAUGA-AGAGGAA	37	UUCCUUUGUUAUCCAUUUCAGUGA	701	723	1	24	16.9	2	Physcall_5_51304	sPPR000_1622
	ge	4		7						65			
	Cleava	81	AUGAAAUUGGAUGA-AGAGGAA	37	UUCCUUUGUUAUCCAUUUCAG	704	723	1	21	16.9	2	Physcall_5_51304	sPPR000_1623
	ge	5		8						65			
	Cleava	81	CCGAAGAGUUCUACGCCAUC	37	GAUGGUGUGGAAACUCUUCCG	488	507	1	20	18.5	2	Physcall_5_54361	sPPR000_2891
	ge	6	UC	9						49			
	Cleava	81	CGCCGAAGAGUUCUACGC	38	AUGGUGUGGAAACUCUUC	486	506	1	21	18.5	2	Physcall_5_54361	sPPR000_3285
	ge	7	CAU	0	CCG					6			
	Cleava	81	UGGAUCUGGUUGACAUCA	38	AGAGGAUGUCAACCCAGAUCUG	1790	1810	1	21	19.7	2	Physcall_5_54980	sPPR000_0005
Cleava	ge	8	UCU	1						11			
	Cleava	81	GUGGAUCUGGUUGACAUC	38	AGAGGAUGUCAACCCAGAUCUGG	1789	1810	1	22	19.7	2	Physcall_5_54980	sPPR000_0062
	ge	9	AUCU	2						11			
	Cleava	82	CAGUGGAUCUGGUUGACA	38	AGAGGAUGUCAACCCAGAUCUGGUU	1787	1810	1	24	19.7	2	Physcall_5_54980	sPPR000_0311
	ge	0	UCAUCU	3						11			
	Cleava	82	AGUGGAUCUGGUUGACAUC	38	AGAGGAUGUCAACCCAGAUCUGGU	1788	1810	1	23	19.7	2	Physcall_5_54980	sPPR000_0312
	ge	1	CAUCU	4						11			
	Cleava	82	GGAUCUGGUUGACAUCAU	38	AGAGGAUGUCAACCCAGAUCU	1791	1810	1	20	19.7	2	Physcall_5_54980	sPPR000_0575
	ge	2	CU	5						11			
	Transla tion	82	AUCGAAGAGGCCUGGUUG	38	UGCCAACCAAUCCUCUU	514	534	1	21	19.8	2	Physcall_5_55924	sPPR000_2366
Cleava	ge	3	GCA	6	CGAG					02			
	Cleava	82	AGCCU-	38	CUCGAUCGCCUUGGUGA	482	501	1	21	22.9	2	Physcall_5_57010	sPPR000_3028
	ge	4	AUCAAGGUGAUCGAG	37	GGCU	2011	2032	1	21	8.37	2	Physcall_5_57900	sPPR000_0663
	Cleava	82	ACUUGCACAUUCCUAC	38	UGAU-					9			
	ge	5	AUCA	8	UGAAGGGAUGUGCAAGG	463	483	1	22	17.3	2	Physcall_5_57962	sPPR000_2444
	Cleava	82	CGUCAGCA-AGCUCAUUAAGA	38	UCUUUGAUGAGUUCUGC					07			
	ge	6	AGCUCAUUAAGA	9	UGAUG	121	141	1	21	21.4	2	Physcall_5_58930	sPPR000_0895
	Cleava	82	GUAGCAGAUUGGGUGCAU	39	AUGAUGCACUCAUUCUG	121	141	1	21	59	2	Physcall_5_58930	sPPR000_0895
	ge	7	CAU	0	UUCA					18.8	2	Physcall_5_59135	sPPR000_3668
	Transla tion	82	GGUUCUGCGGGA-	39	ACGGAACUCUCCGCGCA	2189	2208	1	21	29	2	Physcall_5_59135	sPPR000_3668
Cleava	ge	8	AGUUCUGU	1	GAUG	1382	1405	1	22	22.1	2	Physcall_5_59533	sPPR000_3642
	Cleava	82	AUUCGUAUUGCAGUCAUAA	39	ACUGUAUU-UGACUGC-					61			
	ge	9	UACAGU	2	AUCGAGC	1383	1405	1	21	22.1	2	Physcall_5_59533	sPPR000_3643
	Cleava	83	UUUGGAUUGCAGUCAUAAU	39	ACUGUAUU-UGACUGC-AUCGAG					61			
	ge	0	ACAGU	3	AUCGAG	674	694	1	21	16.3	2	Physcall_5_59533	sPPR000_2838
	Cleava	83	GUCUCUACGGAGCAUGUC	39	GGUGACAGUCUUCGUAG	674	694	1	21	11	2	Physcall_5_59533	sPPR000_2838
	ge	1	ACG	4	AGGU	124	145	1	22	16.7	2	Physcall_5_59533	sPPR000_2838
	Cleava	83	CUUCCGUUGGUUACCGCA	39	AUGGUGCGGUAAUUAUU	124	145	1	22	16.7	2	Physcall_5_59533	sPPR000_2838
	ge	2	CUAU	5	GGAU					96			
	Cleava	83	UUCCGUUGGUUACCGCAC	39	AUGGUGCGGUAAUUAUU	125	145	1	21	16.7	2	Physcall_5_59533	sPPR000_2838
Cleava	ge	3	UAU	6	GGAU					96			
	Cleava	83	UUGAAAGCAUUUGUGAA	39	CUUCCUUCACAAAUGC-	862	883	1	21	19.6	2	Physcall_5_62094	sPPR000_1158
	ge	4	GGAAG	7	AUCAA					54			
	Cleava	83	CAUGUGUUAUUAUACGUCUG	39	UGCCAGACGAGUUAUUAU	696	716	1	21	13.2	2	Physcall_5_66651	sPPR000_2365
	ge	5	GUA	8	UAUA					65			

sRNA_Acc.	Target_Ac_c	Expectation	UP ES	sRNA_start	sRNA_end	Target_start	Target_end	sRNA_aligned_fragment	SE Q ID	Target_aligned_fragment	SE Q ID	Inhibition	Target_Desc.
PPR000 2136	Phycal1_5 66673	2	10.3 08	1	21	893	912	UUGAAAUAAACCCUUGGA UAG	39 9	UUUAUCCA- GGGAUUUCAA	83 6	Transla tion	1
PPR000 2404	Phycal1_5 66746	2	14.7 76	1	22	1028	1049	UGAGGAAUUUGUAGGUG ACAAC	40 0	CGUAUCACCUACAAUUCU CUCG	83 7	Cleava ge	1
PPR000 2405	Phycal1_5 66746	2	14.7 76	1	21	1029	1049	UGAGGAAUUUGUAGGUG ACAA	40 1	GUUAUCCCUACAAUUCUC UCG	83 8	Cleava ge	1
PPR000 0541	Phycal1_5 67458	2	13.1 03	1	20	1053	1072	GAUGGUUUUCUGUUGGUG UGC	40 2	CCACACCAACAGAAAUUA UC	83 9	Cleava ge	1
PPR000 0572	Phycal1_5 67458	2	14.1 98	1	21	1053	1073	AGAUGGUUUUCUGUUGGU GUGC	40 3	CCACACCAACAGAAAUUA UCC	84 0	Cleava ge	1
PPR000 1140	Phycal1_5 67458	2	13.1 03	1	21	1052	1072	GAUGGUUUUCUGUUGGUG UGCA	40 4	ACCACACCAACAGAAAUU AUC	84 1	Cleava ge	1
PPR000 2832	Phycal1_5 67686	2	23.7 08	1	21	1618	1639	GGUUUUGAGCAUGGAU- AUGAU	40 5	UUCAUCAUCCAUUUUCAG AACC	84 2	Cleava ge	1
PPR000 3545	Phycal1_5 71683	2	16.5 17	1	22	110	131	AGGAGUUCUGGGUUUGU UGGAG	40 6	AACCAUAAAUCCAGAGC UUUU	84 3	Cleava ge	1
PPR000 3268	Phycal1_5 73054	2	24.2 42	1	21	68	89	AUGUGGAUGAUGCGCU- CAACC	40 7	CGUUGCAGCGCGUCAUCC ACGU	84 4	Cleava ge	1
PPR000 2771	Phycal1_5 75627	2	22.8 01	1	21	113	132	UAAUUGGAUUUUUGAAG GCUA	40 8	GAGCCU- AUAAGAUAUUAUUA	84 5	Cleava ge	1
PPR000 2772	Phycal1_5 75627	2	22.8 01	1	20	114	132	UAAUUGGAUUUUUGAAG GCU	40 9	AGCCU- AUAAGAUAUUAUUA	84 6	Cleava ge	1
PPR000 2978	Phycal1_5 77663	2	18.9 34	1	25	1177	1201	CUUUCUCCAUCUUGUUG AGCAGAUU	41 0	GAUGAUUCGAUAAGAU GGAGGAG	84 7	Cleava ge	1
PPR000 2979	Phycal1_5 77663	2	18.9 34	1	21	1181	1201	CUUUCUCCAUCUUGUUG AGCA	41 1	AGUUCGAUAAGAUUGGAG GAAG	84 8	Cleava ge	1
PPR000 0040	Phycal1_5 77733	2	18.4	1	21	911	930	AGUGGUGUAAGUGACUG UGUU	41 2	GAUACAGUCACU- GCACCACU	84 9	Transla tion	1
PPR000 0179	Phycal1_5 77733	2	16.9	1	21	912	931	GAGUGGUGUAAGUGACU GUGU	41 3	AUACAGUCACU- GCACCACUC	85 0	Transla tion	1
PPR000 0786	Phycal1_5 77733	2	16.9	1	22	911	931	GAGUGGUGUAAGUGACU GUGU	41 4	GAUACAGUCACU- GCACCACUC	85 1	Transla tion	1
PPR000 2293	Phycal1_5 77733	2	19.6 44	1	21	909	928	UGGUGUAAGUGACUGUA UCGC	41 5	UCGAUACAGUCACU- GCACCA	85 2	Cleava ge	1
PPR000 0040	Phycal1_5 8203	2	18.4	1	21	220	239	AGUGGUGUAAGUGACUG UGUU	41 6	GAUACAGUCACU- GCACCACU	85 3	Transla tion	1
PPR000 0179	Phycal1_5 8203	2	16.9	1	21	221	240	GAGUGGUGUAAGUGACU GUGU	41 7	AUACAGUCACU- GCACCACUC	85 4	Transla tion	1
PPR000 0786	Phycal1_5 8203	2	16.9	1	22	220	240	GAGUGGUGUAAGUGACU GUGU	41 8	GAUACAGUCACU- GCACCACUC	85 5	Transla tion	1
PPR000 2293	Phycal1_5 8203	2	19.6 44	1	21	218	237	UGGUGUAAGUGACUGUA UCGC	41 9	UCGAUACAGUCACU- GCACCA	85 6	Cleava ge	1
PPR000 0513	Phycal1_6 053	2	17.3 96	1	22	279	299	UUCAAAGAGGAUGUCAA CCAGA	42 0	AUUGGUUA- AUCUUCUUUGAG	85 7	Cleava ge	1
PPR000	Phycal1_6	2	20.3	1	21	67	87	AGCCACUGCUUCUCUGAAG	42	AGAGCUUCAGAAAGCUGUG	85	Cleava	1

sRNA_Acc.	Target_Acc	Expectation	UP ES	sRNA_start	sRNA_end	Target_start	Target_end	sRNA_aligned_fragment	SE Q ID N O:	Target_aligned_fragment	SE Q ID N O:	Inhibition	Target_Desc.
0571	081	9						UUU	1	GCU	8	ge	
PPR000	Phycal1_6	2	20.0	1	24	65	88	AAGCCACUGCUUCUGAA	42	GGAGAGCUUCAGAAAGCUG	85	Cleava	1
1294	081	01						GCUUUGU	2	UGGCUA	9	ge	
PPR000	Phycal1_6	2	20.0	1	24	65	88	AAGCCACUGCUUCUGAA	42	GGAGAGCUUCAGAAAGCUG	86	Cleava	1
1468	081	01						GCUCUGU	3	UGGCUA	0	ge	
PPR000	Phycal1_6	2	22.4	1	21	61	80	GCUUCUGAAGCUCUGUU	42	GCACGG-	86	Cleava	1
1754	081	37						GUGG	4	AGAGCUUCAGAAAGC	1	ge	
PPR000	Phycal1_6	2	24.1	1	21	331	350	CUACUGAGUGAUUGAU	42	GUCGAUC-	86	Cleava	1
3046	1617	84						UGAG	5	UAUCAUUCAGUAG	2	ge	
PPR000	Phycal1_6	2	14.1	1	21	317	336	AGAAAGAGGUAUGGAAC	42	CAGAGU-	86	Cleava	1
0577	6933	34						UCUU	6	CGAUACCUUCUUCU	3	ge	
PPR000	Phycal1_6	2	15.2	1	20	2236	2255	UGUUUGAACACCAUUUG	42	GCUCAAAUGGUGCUCAAA	86	Cleava	1
2240	695	22						GGC	7	UA	4	ge	
PPR000	Phycal1_6	2	24.8	1	21	469	489	AGUGCGUUUCGAUCUC	42	UGGGGAGAUCCGAAAGAGC	86	Cleava	1
3496	817	81						CCCA	8	GCU	5	ge	
PPR000	Phycal1_6	2	21.2	1	21	58	77	ACCUUUUGAUCAUCUCG	42	GCGACG-	86	Cleava	1
0477	8972	02						UCGU	9	GAUGAUCAAAAGGC	6	ge	
PPR000	Phycal1_7	2	20.9	1	22	4001	4022	CGCUGAAAGUGACUACA	43	CUGAAUUGUGUCACGUUC	86	Cleava	1
0826	3678	75						UUUG	0	AGCG	7	ge	
PPR000	Phycal1_7	2	21.1	1	25	229	253	CUUUCUCCAUUCUUGUG	43	GAUGAGUUCGAUAAAGAU	86	Cleava	1
2978	5053	72						AGCAGAUU	1	GGAGGAAG	8	ge	
PPR000	Phycal1_7	2	21.1	1	21	233	253	CUUUCUCCAUUCUUGUG	43	AGUUCGAUAAAGAUAGGAG	86	Cleava	1
2979	5053	72						AGCA	2	GAAG	9	ge	
PPR000	Phycal1_7	2	13.9	1	21	1798	1817	AGAGGCUGAGAAAUUGU	43	ACGUACAGUUUC-	87	Transla	1
0120	538	33						ACGA	3	CAGUCUCU	0	tion	
PPR000	Phycal1_8	2	22.9	1	21	121	140	UUGAUGGUUAGCAAAGA	43	CCAAUUCUUUG-	87	Transla	1
2117	0795	97						UUUG	4	UGAUCAUCA	1	tion	
PPR000	Phycal1_8	2	17.6	1	22	184	205	UCAGGAUUUGUGUAGUAA	43	AUCAUUUACUACAUGAUC	87	Cleava	1
2545	1678	83						ACGCC	5	CUGA	2	ge	
PPR000	Phycal1_8	2	15.1	1	21	262	281	UUUUUGACUUGCGAAUA	43	GGCAUUUCCGCAA-	87	Cleava	1
1973	2780	53						UGCG	6	UCAAGGA	3	ge	
PPR000	Phycal1_8	2	22.3	1	22	9214	9235	UUUUCGACGUUCCAUC	43	AACAACAUGGAGGCGCG	87	Cleava	1
1995	294	92						UUUGU	7	AAGA	4	ge	
PPR000	Phycal1_8	2	22.3	1	21	9215	9235	UUUUCGACGUUCCAUC	43	ACAACAUGGAGGCGCGGA	87	Cleava	1
1996	294	92						UUUG	8	AGA	5	ge	
PPR000	Phycal1_8	2	16.4	1	21	1462	1482	UGAUUUUGCUUUGAGUU	43	AACGAACUCAGAGCCGAG	87	Cleava	1
0169	3613	15						UUUG	9	UCA	6	ge	
PPR000	Phycal1_8	2	16.3	1	22	1462	1483	UUGAUUUGGCUUUGAGU	44	AACGAACUCAGAGCCGAG	87	Cleava	1
0613	3613	04						UUUGU	0	UCAA	7	ge	
PPR000	Phycal1_8	2	16.3	1	21	1463	1483	UUGAUUUGGCUUUGAGU	44	ACGAACUCAGAGCCGAGU	87	Cleava	1
0614	3613	04						UUUG	1	CAA	8	ge	
PPR000	Phycal1_9	2	18.1	1	21	318	338	UUGAUCAUCUCGUGUA	44	GUGGUACGAGGAGGAUGA	87	Cleava	1
0104	238	98						CAAU	2	UCAA	9	ge	
PPR000	Phycal1_9	2	18.1	1	22	317	338	UUGAUCAUCUCGUGUA	44	UGUGUACGAGGAGGAUG	88	Cleava	1
0349	238	98						CAAUU	3	AUCA	0	ge	

sRNA_Acc.	Target_Acc	Expectation	UP ES	sRNA_start	sRNA_end	Target_start	Target_end	sRNA_aligned_fragment	SE Q ID	Target_aligned_fragment	SE Q ID	Inhibition	Target_Desc.
PPR000 2373	Phycal1_9 238	2	17.0	1	22	5598	5619	UGCAAGAAAGACUGAAGA AGCGU	44 4	GUUCUUCUUCAGUCUUUU UGCG	88 1	Cleavage	1
PPR000 2322	Phycal1_9 576	2	18.1	1	22	110	130	UGGAUGGUUGGAACUU UUCGG	44 5	GCGAAGAGUCCCA- ACGUCCA	88 2	Translation	1
PPR000 2323	Phycal1_9 576	2	18.1	1	21	111	130	UGGAUGGUUGGAACUU UUCG	44 6	CGAAGAGUCCCA- ACGUCCA	88 3	Translation	1
PPR000 0550	Phycal1_9 6482	2	16.8	1	21	715	735	CUCUUUGAACCAUUUGA UCAA	44 7	CUUGUCAAGUGGUUCAA GAG	88 4	Cleavage	1
PPR000 0133	Phycal1_9 6874	2	19.1	1	21	1599	1619	UGUACGACGAGAUCAUC AAAA	44 8	AUUUGGUUAUCUCUUCGU ACA	88 5	Cleavage	1
PPR000 0338	Phycal1_9 6874	2	19.9	1	21	1600	1620	UUGUACGACGAGAUCAU CAAA	44 9	UUUGGUUAUCUCUUCGUA CAA	88 6	Translation	1
PPR000 0606	Phycal1_9 6874	2	19.9	1	24	1597	1620	UUGUACGACGAGAUCAU CAAAAGG	45 0	GAAUUGGUUAUCUCUUC GUACAA	88 7	Translation	1
PPR000 0607	Phycal1_9 6874	2	19.9	1	22	1599	1620	UUGUACGACGAGAUCAU CAAAA	45 1	AUUUGGUUAUCUCUUCGU ACAA	88 8	Translation	1
PPR000 0608	Phycal1_9 6874	2	19.9	1	20	1601	1620	UUGUACGACGAGAUCAU CAA	45 2	UUUGGUUAUCUCUUCGUAC AA	88 9	Translation	1
PPR000 3182	Phycal1_9 7685	2	20.0	1	21	20	39	CAACAGCAACUUCACACA UGUC	45 3	UUAUUG- GGAGGUUGUGUG	89 0	Cleavage	1
PPR000 0565	Phycal1_9 8429	2	22.2	1	21	580	599	AUCACAAUCUCUAGCUU GAAA	45 4	CUUCAGG- UAGAGGUUGUGAU	89 1	Cleavage	1
PPR000 2044	Phycal1_9 8462	2	17.7	1	21	145	165	UUUCCUUUCUCCAUUCU UGUU	45 5	GACGAGUAAGAAGGG GAAA	89 2	Cleavage	1
PPR000 1990	Phycal1_9 9039	2	17.8	1	21	75	94	UUUUGAAUUAUUUUUGA GCCA	45 6	AGGCUCAACAA- AUCAAAA	89 3	Translation	1

Predicted target_Verticillium

sRNA_Acc.	Target_Acc.	Expectation	UPE \$	sRNA_start	sRNA_end	Target_start	Target_end	sRNA_aligned_fragment	SEQ ID NO:	Target_aligned_fragment	SEQ ID NO:	Inhibition	Target_Desc.
PPR0001 513	VDAG_096 7570	1	24.7	1	21	1003	1023	GCCACUGCUUCUGAAGCU CUG	894	AAGAGCUUCACAAGCAGU GGC	1110	Translation	1
PPR0002 717	VDAG_058 6170	1	16.7	1	21	1473	1494	UACAGCACAGU- CAUAGAUAGU	895	UCUAUCUAUGUACUGUGC UGUA	1111	Translation	1
PPR0002 974	VDAG_097 2070	1	18.8	1	21	315	335	CUUUUGAUCAUCUCCUCG UAC	896	UUACGAGGAGAAGAUCAA AAG	1112	Translation	1
PPR0003 286	VDAG_080 7870	1	19.6	1	21	215	235	AUGGUGGAUCUGAUGAUU AGC	897	ACGAAUCAUCAGAUCCAC CAU	1113	Cleavage	1
PPR0000 102	VDAG_059 5970	1.5	11.4	1	22	1851	1872	GAGGAUGUCAACCAGAU UGGU	898	UACGAUCUGGUUGACCU CCUC	1114	Cleavage	1
PPR0000 199	VDAG_094 5570	1.5	51	1	21	818	838	UGUAGGUAAAAACAUCUG GUC	899	AGCCGAUGCUUUUACCU ACA	1115	Cleavage	1
PPR0000	VDAG_101	1.5	14.3	1	21	5171	5191	UUUUAAGGCUAAGAGAG GUA	900	AUUAUUCUUGGCCUUA AUCAAAA	1116	Cleavage	1

sRNA_A cc.	sRNA_A	Target_Acc.	Expectat ion	UPE \$	srNA_st art	srNA_end	Target_s tart	Target_end	srNA_aligned_fragment	SEQ ID NO:	Target_aligned_fragment	SEQ ID NO:	Inhibition	Targ et_sc.
327	PPR0000	VDAG_059	1.5	11.4	1	21	1852	1872	UAG GAGGAUGUCAACCCAGAU C	901	AGA AGAUCUGGUUGAGACCUC CUC	1117	Cleavage	1
543	PPR0000	VDAG_074	1.5	20.5	1	21	849	869	AUCUCGGGAAGAGAUUCC AUA	902	CAUGGACUUCUCCCGGA GAU	1118	Cleavage	1
898	PPR0001	VDAG_095	1.5	20.4	1	21	605	625	UAGGCUACUCCUUUAA GGC	903	CCUUGAGGGAGUGGAGC CUA	1119	Cleavage	1
500	PPR0001	VDAG_036	1.5	22.0	1	20	1734	1752	AGCAUCUCCAAACAACCU GC	904	GCAGUUUUUUGG- GAUGCU	1120	Cleavage	1
890	PPR0002	VDAG_086	1.5	24.2	1	21	1512	1532	UUUCUGAGCAACUCCAUG GCA	905	CGCCAUUGGAGGUGCUCAG AAG	1121	Translation	1
036	PPR0002	VDAG_021	1.5	16.1	1	21	732	752	UUGCAGAGACUAUCGAUG AUU	906	CAUCAUCGAUAGUCUGUG CAA	1122	Cleavage	1
111	PPR0002	VDAG_092	1.5	22.3	1	21	342	362	UUGAGGGAUUAUCAAG AGG	907	GCUCUUGGUCUAGUCCUU CAA	1123	Cleavage	1
125	PPR0002	VDAG_100	1.5	22.5	1	21	1636	1656	UGUCUGAAGAGGAUUGG UUG	908	AAACUAAUCCUCGUCGAG ACA	1124	Translation	1
258	PPR0002	VDAG_100	1.5	22.5	1	20	1637	1656	UGUCUGAAGAGGAUUGG UU	909	AACUAAUCCUCGUCGAGA CA	1125	Translation	1
259	PPR0002	VDAG_077	1.5	18.1	1	22	1117	1138	UGAGAUCAUUGUAUUGUA UGUU	910	AGCAUGCAGUACAAUGAU CUCG	1126	Cleavage	1
411	PPR0003	VDAG_066	1.5	12.7	1	21	2470	2490	CAUGGCUUUUUAACAC AAC	911	AUCGUGUUGAAAAAGCUC AUG	1127	Cleavage	1
121	PPR0003	VDAG_091	1.5	21.4	1	22	960	980	AUUCUGCGACGUUCCAUC UUGU	912	UGAAGAUUGAAGCUC- GAGAAU	1128	Cleavage	1
245	PPR0003	VDAG_007	1.5	48	1	21	516	536	AUGUGGAAGUUGCUGUUG ACU	913	CGUCAAACGGCAACGUC CAU	1129	Cleavage	1
270	PPR0003	VDAG_080	1.5	82	1	21	217	237	AGAUGGGAUCUCUGAUGA UUA	914	GAUCAUCAGAUCCACCA UUG	1130	Cleavage	1
580	PPR0003	VDAG_058	1.5	11	1	21	211	232	ACAUCUGCUUG- GCCUCGUCUA	915	AAGAUAGGCGCAAGCAG AUGU	1131	Translation	1
681	PPR0003	VDAG_058	1.5	16.6	1	20	212	232	ACAUCUGCUUG- GCCUCGUCU	916	AGAUGGCGCGCAAGCAGA UGU	1132	Translation	1
682	PPR0000	VDAG_042	2	24.1	1	22	751	772	UGGUGAAGUGACUGUGU UGCC	917	GACAAUGCAGUCACUUAC ACCU	1133	Cleavage	1
048	PPR0000	VDAG_042	2	31	1	21	752	772	UGGUGAAGUGACUGUGU UGC	918	ACAAUGCAGUCACUUACA CCU	1134	Cleavage	1
064	PPR0000	VDAG_081	2	31	1	20	161	180	AUCAUUGAUGGUCUUUUC AA	919	UUGCAAAGAACAUAUAG AG	1135	Translation	1
081	PPR0000	VDAG_095	2	64	1	21	544	564	AUGGAACUCUCCCGGAG AUG	920	GACCUCGCCGAAGAGUUC CAU	1136	Cleavage	1
087	PPR0000	VDAG_060	2	14.7	1	21	165	185	UUCUCCAUUCUUAUUAAC AAA	921	CUUGUUCAAGAAAGAUUGA GAU	1137	Cleavage	1
101	PPR0000	VDAG_081	2	26	1	21	160	180	AUCAUUGAUGGUCUUUUC AAA	922	AUUGCAAAGAACAUAU GAG	1138	Translation	1
126	PPR0000	VDAG_095	2	64	1	21	1343	1363	UUUUGAUCAUCUCGUCGU ACA	923	CGUACGACGACACGAUCA AAA	1139	Translation	1
131			2	7	1	21								

sRNA_A cc.	Target_Acc.	Expectat ion	UPE \$	sRNA_st art	sRNA_ end	Target_s tart	Target_ end	srna_aligned_fragment	SEQ ID NO:	Target_aligned_fragment	SEQ ID NO:	Inhibition	Targ et_ sc.
PPR0000	VDAG_064	2	18.2	1	21	683	703	AUGCAUUUGUGAAGGAAG	924	CCUUCUUUCACCA AUG	1140	Cleavage	1
155	VDAG_086	2	55	1	21	230	250	AGGAAAAUAGAGGCGUGA	925	CAU	1141	Cleavage	1
211	VDAG_092	2	79	1	21	972	992	UUU	926	CCU	1142	Cleavage	1
282	VDAG_056	2	7.72	1	21	1262	1281	AAUUGUACGACGAGAU	927	UUAUUCUUU	1143	Translation	1
322	VDAG_002	2	81	1	21	158	175	AAAGGUUAAGACCAGU	928	UUAUUCUUU	1144	Translation	1
379	VDAG_042	2	20.2	1	20	750	770	UUAUUCUUU	929	UUAUUCUUU	1145	Cleavage	1
406	VDAG_042	2	7	1	21	751	770	UUAUUCUUU	930	UUAUUCUUU	1146	Cleavage	1
407	VDAG_013	2	23.2	1	21	906	926	UUAUUCUUU	931	UUAUUCUUU	1147	Cleavage	1
445	VDAG_057	2	16.2	1	21	215	215	UUAUUCUUU	932	UUAUUCUUU	1148	Cleavage	1
448	VDAG_012	2	19.2	1	21	958	977	UUAUUCUUU	933	UUAUUCUUU	1149	Translation	1
PPR0000	VDAG_069	2	22.0	1	21	7161	7182	UUAUUCUUU	934	UUAUUCUUU	1150	Cleavage	1
512	VDAG_060	2	51	1	21	164	184	UUAUUCUUU	935	UUAUUCUUU	1151	Cleavage	1
524	VDAG_081	2	26	1	21	159	179	UUAUUCUUU	936	UUAUUCUUU	1152	Translation	1
525	VDAG_044	2	37	1	21	699	719	UUAUUCUUU	937	UUAUUCUUU	1153	Cleavage	1
PPR0000	VDAG_094	2	22.4	1	21	819	839	UUAUUCUUU	938	UUAUUCUUU	1154	Cleavage	1
547	VDAG_063	2	46	1	21	420	440	UUAUUCUUU	939	UUAUUCUUU	1155	Translation	1
563	VDAG_034	2	56	1	21	568	589	UUAUUCUUU	940	UUAUUCUUU	1156	Translation	1
646	VDAG_034	2	18.0	1	21	569	589	UUAUUCUUU	941	UUAUUCUUU	1157	Translation	1
647	VDAG_013	2	92	1	21	905	925	UUAUUCUUU	942	UUAUUCUUU	1158	Cleavage	1
651	VDAG_002	2	12.0	1	22	156	175	UUAUUCUUU	943	UUAUUCUUU	1159	Translation	1
698	VDAG_042	2	95	1	21	751	771	UUAUUCUUU	944	UUAUUCUUU	1160	Cleavage	1
757	VDAG_042	2	12.0	1	21	752	771	UUAUUCUUU	945	UUAUUCUUU	1161	Cleavage	1
758	VDAG_034	2	24.9	1	21	568	588	UUAUUCUUU	946	UUAUUCUUU	1162	Translation	1
760	VDAG_034	2	18	1	21	569	588	UUAUUCUUU	947	UUAUUCUUU	1163	Translation	1

sRNA_A cc.	Target_Acc.	Expectation	UPE \$	sRNA_start	sRNA_end	Target_start	Target_end	srna_aligned_fragment	SEQ ID NO:	Target_aligned_fragment	SEQ ID NO:	Inhibition	Target_s.
PPR0000 761	VDAG_037 82T0	2	63	1	21	89	108	AUGCAGAUUG	948	CAUGACAAAACCC	1164	Translation	1
PPR0000 788	VDAG_039 33T0	2	16.7	1	21	89	108	GAGGUAUUGAUUUUG	949	GUCACUUC	1165	Cleavage	1
PPR0000 791	VDAG_097 78T0	2	18.8	1	21	527	546	GAGGUAUUGGCGAC	950	AUCCUU	1166	Translation	1
PPR0000 798	VDAG_012 20T0	2	18.8	1	21	315	335	CUUUGAUCUUCGUC	951	UUACGAGGAGAAUCAA	1167	Translation	1
PPR0000 847	VDAG_013 68T0	2	23.0	1	21	959	978	CAUCUGUCGUACAAUUU	952	AAG	1168	Cleavage	1
PPR0000 887	VDAG_095 95T0	2	16.2	1	22	905	926	AUGGAUUUUUUAAGCUA	953	CGACUUCGCCGAG	1169	Cleavage	1
PPR0000 889	VDAG_031 50T0	2	17.3	1	22	543	564	AUGGAUCUUCGCCGAG	954	CCAU	1170	Cleavage	1
PPR0001 963	VDAG_017 57T0	2	24.1	1	21	1423	1442	ACAUGUCUUGGCCUCGU	955	GAGAUUGGCCAA-	1171	Translation	1
PPR0001 006	VDAG_003 87T0	2	21.3	1	21	173	194	UUUCCUUUC-	956	AAAA	1172	Cleavage	1
PPR0001 061	VDAG_000 42T0	2	21	1	21	347	367	UCCAUUCUUC	957	CGCAUG	1173	Cleavage	1
PPR0001 070	VDAG_029 47T0	2	14.1	1	21	173	194	UGGUUGUAUUCGAGUAUC	958	AGAAGAUUGGACGACAGGG	1174	Translation	1
PPR0001 080	VDAG_041 66T0	2	22.7	1	21	1715	1735	UGC	959	CUA	1175	Cleavage	1
PPR0001 158	VDAG_094 59T0	2	14.8	1	21	5083	5103	UGCUUCUGAAGCUUUUGU	960	AACAACAAGGCUUCAA	1176	Cleavage	1
PPR0001 159	VDAG_029 55T0	2	76	1	21	1715	1735	GUG	961	GCA	1177	Cleavage	1
PPR0001 161	VDAG_081 66T0	2	39	1	21	1715	1734	UCUGGUUGACAUCCUCUU	962	AGA	1178	Translation	1
PPR0001 217	VDAG_094 55T0	2	23.7	1	22	818	839	CUUCCUUCACAAAUGCAU	963	GUGUUGCAUUUG-	1179	Cleavage	1
PPR0001 224	VDAG_029 66T0	2	14.3	1	22	1712	1734	CUUAGGUAAAAACAUCU	964	AGCCAGAUUCUUUAACCU	1180	Cleavage	1
PPR0001 217	VDAG_081 14T0	2	56	1	23	1712	1734	GGUC	965	ACAU	1181	Cleavage	1
PPR0001 224	VDAG_004 69T0	2	23.7	1	22	159	180	CUUGUUGACAUCCUCUUU	966	ACGAG	1182	Translation	1
PPR0001 248	VDAG_027 49T0	2	42	1	21	343	362	AUCAUUUGAUGGUUUUUGC	967	UGAG	1183	Cleavage	1
PPR0001 278	VDAG_069 04T0	2	21.8	1	21	780	800	AAAU	968	GAGUACAC-	1184	Cleavage	1
PPR0001 308	VDAG_013 88T0	2	64	1	22	2975	2994	AUAUCAGGUUCCAUUGUA	969	GGAAUCCUGAUU	1185	Translation	1
PPR0001 345	VDAG_077 50T0	2	14.7	1	21	296	317	CUC	970	GGUCAAUUAGAGCCACU	1186	Cleavage	1
PPR0001 366	VDAG_096 75T0	2	19.1	1	21	1358	1378	UCCAGAGCAGUGGCU	971	GGU	1187	Cleavage	1
PPR0001 377	VDAG_022 79T0	2	31	1	21	152	171	ACCAGUUCUGGUUGACAA	972	AAAGACUGU	1188	Translation	1
PPR0001 392	VDAG_000 42T0	2	22.1	1	21	1002	1022	AAAGCU-	973	CGCCACUGCUUCUGACAG	1189	Cleavage	1
PPR0001 392	VDAG_000 42T0	2	17.5	1	21	296	317	UCCAGAGCAGUGGCU	974	UUUU	1190	Cleavage	1
PPR0001 392	VDAG_000 42T0	2	55	1	21	1358	1378	CUUUGUCAAAGCAGAUUCU	975	GGU	1191	Translation	1
PPR0001 392	VDAG_000 42T0	2	17.0	1	21	1358	1378	CUUUGUCAAAGCAGAUUCU	976	GGU	1192	Cleavage	1
PPR0001 392	VDAG_000 42T0	2	91	1	21	1358	1378	CUUUGUCAAAGCAGAUUCU	977	GGU	1193	Translation	1
PPR0001 392	VDAG_000 42T0	2	16.5	1	21	152	171	CUUUGUCAAAGCAGAUUCU	978	GCCACAACC-	1194	Cleavage	1
PPR0001 392	VDAG_000 42T0	2	43	1	21	1002	1022	GGC	979	AGCUUCAGAAAG	1195	Translation	1
PPR0001 392	VDAG_000 42T0	2	24.7	1	21	1002	1022	CCACUGCUUCUGAAGCUC	980	CAAGAGCUUCACAAAGCAG	1196	Cleavage	1
PPR0001 392	VDAG_000 42T0	2	6	1	21	1002	1022	UGU	981	UGG	1197	Translation	1
PPR0001 392	VDAG_000 42T0	2	22.1	1	21	164	183	CUUCCUUAACUCUUCUUA	982	GGGCGAGAGAG-	1198	Translation	1
PPR0001 392	VDAG_000 42T0	2	5	1	21	164	183	CCU	983	AGACGAGG	1199	Translation	1

sRNA_A cc.	Target_Acc.	Expectation	UPE \$	sRNA_start	sRNA_end	Target_start	Target_end	sRNA_aligned_fragment	SEQ ID NO:	Target_aligned_fragment	SEQ ID NO:	Inhibition	Target_s.
PPR0001	93T0	2	18.3	1	21	610	629	GUG	995	GGA	1211	Cleavage	1
PPR0001	VDAG_058	2	14	1	21	610	629	UUUUCAGCCUCUACAAG	995	GAGUUUG-	1211	Cleavage	1
PPR0001	VDAG_097	2	17.2	1	20	315	334	UUUUGAUAUCUCCUCGU	996	AGAGGCUGAAGAA	1212	Translation	1
PPR0002	VDAG_102	2	15.7	1	21	604	624	UUUUGUUUUUUUUUUUUUU	997	UUACGAGGAGAAAGAUCAA	1213	Cleavage	1
PPR0002	VDAG_094	2	20.9	1	21	940	960	GAG	998	AA	1214	Cleavage	1
PPR0002	VDAG_054	2	16.0	1	21	103	123	UUUUGUUUUUUUUUUUUUU	999	AACAACAACAACAAGAAC	1215	Translation	1
PPR0002	VDAG_089	2	17.6	1	21	940	960	UUUUGUUUUUUUUUUUUUU	1000	UACAACAACAACAAGAAC	1216	Cleavage	1
PPR0002	VDAG_088	2	18.1	1	21	598	618	UUUUGUUUUUUUUUUUUUU	1001	AG	1217	Cleavage	1
PPR0002	VDAG_029	2	20.5	1	21	290	310	GAG	1002	GUCAACUGCAACAAGAAC	1218	Translation	1
PPR0002	VDAG_000	2	22.5	1	21	114	134	UUUGGAAACUCUCCGCGA	1003	AAG	1219	Translation	1
PPR0002	VDAG_065	2	23.3	1	21	329	348	UUUGCAAAGGACGGGAACC	1004	GUUUUGUGGACGAGUUCC	1220	Cleavage	1
PPR0002	VDAG_037	2	17.1	1	22	1078	1100	UUUGAAUAGGUUGAGCGC	1005	AAA	1221	Translation	1
PPR0002	VDAG_037	2	87	1	21	1079	1100	AUC	1006	GAUGCG-	1222	Translation	1
PPR0002	VDAG_037	2	87	1	20	1080	1100	UUUGUAUC-	1007	UCAAACCUAUUAAC	1223	Translation	1
PPR0002	VDAG_097	2	14.5	1	21	239	260	GGAUGGUAAGA	1008	AAUUCUACCGUCCAGAUC	1224	Translation	1
PPR0002	VDAG_074	2	16.0	1	21	273	293	UUUGUAUC-	1009	GACAA	1225	Cleavage	1
PPR0002	VDAG_068	2	19.7	1	21	4783	4803	UUUGUAUC-	1010	AUCUACCGUCCAGAUCGA	1226	Cleavage	1
PPR0002	VDAG_101	2	21.9	1	21	5170	5190	UUUGUAUC-	1011	CAA	1227	Cleavage	1
PPR0002	VDAG_023	2	23.4	1	24	2547	2570	UUUGUAUC-	1012	GAG	1228	Cleavage	1
PPR0002	VDAG_023	2	23.4	1	21	2550	2570	UUUGUAUC-	1013	CAAGGCUUCCACGCCAU	1229	Cleavage	1
PPR0002	VDAG_000	2	16.9	1	22	2955	2976	UUUGUAUC-	1014	CUUCAA	1230	Translation	1
PPR0002	VDAG_000	2	16.9	1	21	2956	2976	UUUGUAUC-	1015	GGCUUCCACGCCAUUU	1231	Translation	1
PPR0002	VDAG_024	2	19.5	1	21	268	288	UUUGUAUC-	1016	CAA	1232	Cleavage	1
PPR0002	VDAG_033	2	24.2	1	21	1285	1304	UUUGUAUC-	1017	GGUGUGAGAAAAGUUGGA	1233	Cleavage	1
PPR0002	VDAG_033	2	75	1	21	1285	1304	UUUGUAUC-	1017	AGAA	1233	Cleavage	1
PPR0002	VDAG_033	2	75	1	21	1285	1304	UUUGUAUC-	1017	GUGUGAGAAAAGUUGGA	1233	Cleavage	1
PPR0002	VDAG_033	2	75	1	21	1285	1304	UUUGUAUC-	1017	GAA	1233	Cleavage	1
PPR0002	VDAG_033	2	75	1	21	1285	1304	UUUGUAUC-	1017	GAUCUGCUGACACGAUG	1233	Cleavage	1
PPR0002	VDAG_033	2	75	1	21	1285	1304	UUUGUAUC-	1017	GGA	1233	Cleavage	1
PPR0002	VDAG_033	2	75	1	21	1285	1304	UUUGUAUC-	1017	UAUUUG-	1233	Cleavage	1
PPR0002	VDAG_033	2	75	1	21	1285	1304	UUUGUAUC-	1017	UCAAACGAGAUUGGA	1233	Cleavage	1

sRNA_A cc.	Target Acc.	Expectat ion	UPE \$	sRNA_st art	sRNA_ end	Target_s tart	Target_ end	sRNA_aligned_fragment	SEQ ID NO:	Target_aligned_fragment	SEQ ID NO:	Inhibition	Targ et_sc.
PPR0002 173	VDAG_018 93T0	2	23.6	1	21	1017	1037	UUCAUGAUGGCGACUGUG	1018	GCUCAUGGUCGCCAUCAU	1234	Cleavage	1
PPR0002 173	VDAG_097 37T0	2	15.0	1	21	922	941	UUCAUGAUGGCGACUGUG	1019	GAA AAUCUCA-	1235	Cleavage	1
PPR0002 217	VDAG_054 73T0	2	9.77	1	21	1238	1258	UUAAGAGAAAUAGAAAGAAG	1020	UUGUUUUUUUUCAUUUCUC	1236	Cleavage	1
PPR0002 247	VDAG_066 54T0	2	20.9	1	21	3325	3344	UGUUCGUCCUGAUUAUUGU	1021	UGA GACA-	1237	Cleavage	1
PPR0002 258	VDAG_025 42T0	2	15.8	1	21	1512	1533	UGUCUCGAAGAGGAU-	1022	AGUAUCAGGCGGAACA	1238	Translation	1
PPR0002 289	VDAG_025 42T0	2	15.8	1	20	1513	1533	UGUCUGCAAGAGGAU-	1023	GACA CAACCAUCCUCCUCGAG	1239	Translation	1
PPR0002 284	VDAG_025 61T0	2	14.0	1	21	82	103	UGUAAAAGGG-	1024	UACAUCCUCAAGCCCUUU	1240	Translation	1
PPR0002 284	VDAG_077 70T0	2	15.4	1	21	295	314	UUGAGGAUGGU	1025	UACA UCCAUCUCA-	1241	Translation	1
PPR0002 289	VDAG_049 76T0	2	23.9	1	21	388	408	UGGUUGAGACUGGCCUUUC	1026	CCCUUUUCA	1242	Cleavage	1
PPR0002 297	VDAG_080 78T0	2	19.8	1	21	214	234	UGGUGGAUCUGAUGAUUA	1027	CCG CACGCU-	1243	Cleavage	1
PPR0002 313	VDAG_094 31T0	2	13.4	1	21	1317	1336	UGGCAAGGUGGGAGAAGC	1028	CCA CACGCU-	1244	Cleavage	1
PPR0002 313	VDAG_093 33T0	2	11.2	1	21	864	883	UGGCAAGGUGGGAGAAGC	1029	CUCUCAUUUGCCA	1245	Cleavage	1
PPR0002 327	VDAG_063 69T0	2	7.44	1	21	686	706	UGGAGUGGUAGUAAAUGG	1030	UUGCCU- CCA	1246	Translation	1
PPR0002 346	VDAG_094 95T0	2	22.8	1	21	964	983	UGCUUGGCCUUUGUCUAGA	1031	CCA CACGCU-	1247	Cleavage	1
PPR0002 353	VDAG_042 87T0	2	20.9	1	21	1068	1087	UGCUGAUGCGGCCUCUCUG	1032	AGACAAGGCCAAAGCA	1248	Translation	1
PPR0002 357	VDAG_017 62T0	2	18.7	1	22	872	893	UGCUCGAUCGCCUUUGGUG	1033	GGUGAC- GAGCCCAUCAGCA	1249	Translation	1
PPR0002 357	VDAG_026 87T0	2	18.6	1	22	221	242	UGCUCGAUCGCCUUUGGUG	1034	CCUUCGCCAAGGGGAUCG	1250	Cleavage	1
PPR0002 357	VDAG_002 18T0	2	20.5	1	22	530	551	UGCUCGAUCGCCUUUGGUG	1035	ACAUCACCAAGGCGCUCG	1251	Translation	1
PPR0002 367	VDAG_102 88T0	2	21.8	1	22	182	203	UGCAUGAUCGUCUAGAUG	1036	AGCA AGCA	1252	Cleavage	1
PPR0002 368	VDAG_102 88T0	2	21.8	1	21	183	203	UGCAUGAUCGUCUAGAUG	1037	CCUCAUCAAGAUGGUCAU	1253	Cleavage	1
PPR0002 422	VDAG_086 37T0	2	16.5	1	20	1028	1048	AGCAGAUUG-	1038	GCA AGGUUCCAAGUCCAUCG	1254	Translation	1
PPR0002 430	VDAG_063 81T0	2	17.7	1	21	1597	1615	UUUGGAACUCU	1039	UCA AUUCCCAA-CAU-	1255	Translation	1
PPR0002 444	VDAG_010 86T0	2	14.4	1	22	571	590	UCUUUGAUGAGUUCUGCU	1040	UUCGUUCA	1256	Cleavage	1
PPR0002 444	VDAG_008 86T0	2	15.3	1	20	932	950	UCUUUGGAAGAUUUUUUG	1041	GUUCAGCAG-- CUCAUCAAGA	1257	Translation	1

sRNA_A cc.	Target_Acc.	Expectation	UPE \$	sRNA_start	sRNA_end	Target_start	Target_end	sRNA_aligned_fragment	SEQ ID NO:	Target_aligned_fragment	SEQ ID NO:	Inhibition	Target_s.
448	39T0	2	64	1	21	32	51	GC	1042	CUUCCAAAGA	1258	Cleavage	1
PPR0002	VDAG_086	2	8.94	1	21	32	51	UGG	1043	CUUCCAAAGA	1259	Cleavage	1
463	VDAG_006	2	18.3	1	22	201	222	UCUCAUAGAGGAUUGGUU	1044	UGCCAAACCAUCCUCUAU	1260	Translation	1
PPR0002	VDAG_059	2	55	1	22	201	222	GGCG	1045	GUGG	1261	Cleavage	1
471	VDAG_084	2	21.4	1	24	855	878	UCGAUAUUGUGUUGAAG	1046	UGAUUCUUCGACACCAU	1262	Translation	1
506	VDAG_084	2	15.0	1	24	855	878	AUCACA	1047	CGCAUCUUUCACACAAU	1263	Cleavage	1
PPR0002	VDAG_059	2	32	1	24	1029	1052	UCGAUAUUGUGUUGAAG	1048	GAUUCUUCGACACCAU	1264	Translation	1
507	VDAG_084	2	21.4	1	23	856	878	AUCAC	1049	GUGG	1265	Cleavage	1
PPR0002	VDAG_084	2	15.0	1	23	1030	1052	UCGAUAUUGUGUUGAAG	1050	GCCAUUUUCACACAAU	1266	Translation	1
507	VDAG_059	2	32	1	23	1030	1052	AUCAC	1051	AUUG	1267	Cleavage	1
508	VDAG_084	2	21.4	1	21	858	878	UCGAUAUUGUGUUGAAG	1052	UACUUGCAGAGGCCUUCAA	1268	Cleavage	1
PPR0002	VDAG_084	2	15.0	1	21	1032	1052	AUC	1053	GGCAAGCGCAUCG-	1269	Cleavage	1
508	VDAG_081	2	18.7	1	21	1032	1052	UCGAUAUUGUGUUGAAG	1054	UUGGAGAAUUGUUGC	1270	Cleavage	1
530	VDAG_044	2	37	1	21	159	179	AAC	1055	UGA	1271	Translation	1
PPR0002	VDAG_044	2	22.4	1	21	699	719	UCAUUGAUGGUCUUUGCA	1056	CGC	1272	Translation	1
530	VDAG_016	2	46	1	21	699	719	AAC	1057	UUGGAGAAUUGUUGC	1273	Translation	1
PPR0002	VDAG_016	2	23.5	1	21	949	968	UACAUGAUCGUAUGCGUUU	1058	GGCAAGCGCAUCG-	1274	Cleavage	1
531	VDAG_101	2	39	1	21	949	968	GGC	1059	UUGGAGAAUUGUUGC	1275	Cleavage	1
PPR0002	VDAG_070	2	79	1	21	247	266	UCAUUGAUGGUCUUUGCA	1060	UUGGAGAAUUGUUGC	1276	Cleavage	1
533	VDAG_070	2	22.1	1	21	204	224	UACAACAAUUCUCA	1061	UUGGAGAAUUGUUGC	1277	Cleavage	1
539	VDAG_079	2	16	1	21	204	224	GCC	1062	UUGGAGAAUUGUUGC	1278	Translation	1
PPR0002	VDAG_079	2	22.6	1	21	792	811	UUAUUGCAGAGACUAUCG	1063	UUGGAGAAUUGUUGC	1279	Cleavage	1
577	VDAG_084	2	45	1	21	792	811	AUG	1064	UUGGAGAAUUGUUGC	1280	Cleavage	1
630	VDAG_084	2	19.3	1	22	1360	1381	UUAUUGCAGAGACUAUCG	1065	UUGGAGAAUUGUUGC	1281	Cleavage	1
PPR0002	VDAG_084	2	19.3	1	21	1361	1381	AGA	1066	UUGGAGAAUUGUUGC	1282	Cleavage	1
631	VDAG_077	2	23.5	1	21	1746	1765	UUAUUGCAGAGACUAUCG	1067	UUGGAGAAUUGUUGC	1283	Cleavage	1
634	VDAG_040	2	93	1	21	1746	1765	UUAUUGCAGAGACUAUCG	1068	UUGGAGAAUUGUUGC	1284	Cleavage	1
PPR0002	VDAG_040	2	11.9	1	21	350	371	UAGAUGGUUUUG-	1069	UUGGAGAAUUGUUGC	1285	Cleavage	1
681	VDAG_040	2	66	1	21	350	371	CAAGGAGA	1070	UUGGAGAAUUGUUGC	1286	Cleavage	1
PPR0002	VDAG_040	2	17.2	1	21	965	986	GGUGACAU-	1071	UUGGAGAAUUGUUGC	1287	Cleavage	1
838	VDAG_012	2	12	1	21	638	658	GGUGACAU-	1072	UUGGAGAAUUGUUGC	1288	Cleavage	1
PPR0002	VDAG_012	2	18.3	1	21	638	658	GGUGACAU-	1073	UUGGAGAAUUGUUGC	1289	Cleavage	1
842	VDAG_044	2	42	1	21	599	619	GGUGACAU-	1074	UUGGAGAAUUGUUGC	1290	Cleavage	1
PPR0002	VDAG_044	2	21.6	1	21	599	619	GGUGACAU-	1075	UUGGAGAAUUGUUGC	1291	Cleavage	1
857	VDAG_070	2	6	1	21	1001	1021	GGUGACAU-	1076	UUGGAGAAUUGUUGC	1292	Cleavage	1
PPR0002	VDAG_070	2	21.4	1	21	1001	1021	GGUGACAU-	1077	UUGGAGAAUUGUUGC	1293	Cleavage	1
857	VDAG_102	2	07	1	21	182	202	GGUGACAU-	1078	UUGGAGAAUUGUUGC	1294	Cleavage	1
PPR0002	VDAG_102	2	22.7	1	21	182	202	GGUGACAU-	1079	UUGGAGAAUUGUUGC	1295	Cleavage	1
871	88T0	2	41	1	21	182	202	GGUGACAU-	1080	UUGGAGAAUUGUUGC	1296	Cleavage	1

sRNA_A cc.	Target_Acc.	Expectat ion	UPE \$	sRNA_st art	sRNA_end	Target_s tart	Target_end	sRNA_aligned fragment	SEQ ID NO:	Target_aligned_fragment	SEQ ID NO:	Inhibition	Targ et_sc.
PPR0002	VDAG_038	2	14.8	1	21	2543	2562	GAGACUAUCGAUGAUUGU	1065	AACACAA-	1281	Translation	1
939	3670		83					GUU		CAUCAAUAGUCUC			
PPR0002	VDAG_041	2	11.7	1	21	124	143	GAAGCUGGAGAGAAAGCAUU	1066	CCCAAUGCAUU-	1282	Translation	1
964	3670		89					GGU		UCCAGCUUC			
PPR0002	VDAG_040	2	21.1	1	21	382	403	GAAGCUGC-	1067	CGCCUGAUUUCUCUGCAG	1283	Cleavage	1
965	7670		75					GAGAAUAAAGGCU		CUUC			
PPR0002	VDAG_074	2	16.0	1	21	274	294	CUUGUGAGCAGAUUUAA	1068	GCUUCAAAGCUGCUCAAC	1284	Cleavage	1
986	6670		05					AGC		AAG			
PPR0002	VDAG_021	2	24.5	1	21	1051	1070	CUUCUUUUUUCACACAA	1069	AGCUUGUG-	1285	Cleavage	1
995	6970		73					GCA		GAAAGAGGGGAG			
PPR0003	VDAG_071	2	21.3	1	21	703	722	CUGCUGAUGCGGCUCUGU	1070	AUGAC-	1286	Translation	1
011	1870		22					CAC		GAGCCUCAUCAGCAG			
PPR0003	VDAG_055	2	21.7	1	21	3535	3555	CUCGUAUCGCCUUGGUGAG	1071	AGCAUCAACAAGGCGAUC	1287	Cleavage	1
028	2470		16					GCU		GAG			
PPR0003	VDAG_065	2	23.9	1	21	1887	1907	CGUUGCAUCAUCUCCUUG	1072	GCUCAAGGAGAUUGGUGCA	1288	Cleavage	1
059	3770		86					AGC		UCG			
PPR0003	VDAG_091	2	19.4	1	21	347	367	CGAUGGCUAGCAAAGGGCU	1073	CUCAGCCAUUUGCUAGCCA	1289	Cleavage	1
070	6670		02					GCU		UGCAGCUCUUUGCUAGCC			
PPR0003	VDAG_012	2	20.4	1	21	484	505	CGAUGGCUAGC-	1074	UCUUGCGACACAUUCC	1290	Translation	1
071	9070		66					AAGAGCUGCU		CGG			
PPR0003	VDAG_041	2	21.3	1	21	1307	1327	CCGGACAUGUUCUUGAAG	1075	ACUCUUCGAGCUCUAGUC	1291	Cleavage	1
085	4070		16					AGG		CCGG			
PPR0003	VDAG_065	2	15.7	1	21	241	262	CCGGGACAUG-	1076	AGGGCUGCAGCUGGGAUC	1292	Translation	1
085	3470		14					UCUCGAAAGAGG		UGG			
PPR0003	VDAG_060	2	24.1	1	21	1618	1638	CCAGAUUCUGUUGACAGC	1077	CUGCGAAAAAAGCGGCCA	1293	Cleavage	1
095	6270		96					CUC		AUG			
PPR0003	VDAG_062	2	21.5	1	21	3476	3496	CAUUGGCCUCUAUUUUUG	1078	AGCUAAAAGAGAUUGGAGG	1294	Translation	1
111	7470		88					CAG		CUG			
PPR0003	VDAG_055	2	17.2	1	21	2018	2038	CAGCUUCCAUUUUGUUGA	1079	UGGAGGGGUUUCCCGAGG	1295	Cleavage	1
138	9470		17					GCA		AAAUGGUGUUGAUUGGC			
PPR0003	VDAG_024	2	17.6	1	21	1304	1324	CAGCCUCUGAAACCCUUC	1080	GUG	1296	Cleavage	1
141	3970		06					CUU		GGCGAAUUAAUGAUGGA			
PPR0003	VDAG_050	2	13.8	1	21	490	510	CACGCCAUCAGAUACCAU	1081	AUUG	1297	Cleavage	1
155	9170		09					CUU		GGCGAAUUAAUGAUGGA			
PPR0003	VDAG_021	2	16.8	1	22	37	58	CAAUUCCCUCAUUAAUUG	1082	AUUG	1298	Cleavage	1
166	1570		02					CCUU		GGCGCAACUUUGGAAGC			
PPR0003	VDAG_010	2	22.7	1	22	208	229	CAAAGCUUCCGAAAGCUGU	1083	UUUG	1299	Cleavage	1
194	0070		58					GGCU		AGAUGUGUUUGAGAAGAA			
PPR0003	VDAG_076	2	17.6	1	21	729	749	AUUUUUUUUUCUCAAAGCAUA	1084	GAU	1300	Cleavage	1
205	5470		23					UUA		GCUGGAAAAAAGCGGCC			
PPR0003	VDAG_062	2	21.3	1	21	3475	3495	AUUGGCCUCUAUUUUUGC	1085	AAU	1301	Translation	1
227	7470		23.9					AGC		UUGAAACCCAGUUUCAAAC			
PPR0003	VDAG_049	2	4					AUGGUUGAGACUGGCUUU	1086	CGU	1302	Cleavage	1
282	7670		18.2					CAA		CCUACUAACTUGGGCAC			
PPR0003	VDAG_100	2	59					AUGGUGCCAAAGUUUAUUGA	1087	CAU	1303	Translation	1
289	2770		7.39					GGG		CAUCCAUCUACAACCCACU	1304	Translation	1
PPR0003	VDAG_063	2	7.39					AUGGAGUGGUAGUAAAUG	1088				

sRNA_A cc.	Target_Acc.	Expectat ion	UPE \$	sRNA_st art	sRNA_end	Target_s tart	Target_end	SEQ ID NO:	Target_aligned_fragment	SEQ ID NO:	Inhibition	Targ et_sc.
313	69T0		4									
PPR0003	VDAG_102		22.4	1	22	183	204	1089	CCUACAAGAUGGUCU	1305	Cleavage	1
331	88T0	2	13						GAG			
PPR0003	VDAG_102		22.4	1	21	184	204	1090	AUGCAUGAUCGUCUAGAU	1306	Cleavage	1
332	88T0	2	13						GAG			
PPR0003	VDAG_007		9.13	1	21	1437	1457	1091	AUGAGGGAGCUGUAGGUG	1307	Cleavage	1
349	66T0	2	2						AUA			
PPR0003	VDAG_055		22.1	1	21			1092	AUGAGGAGUUCUGGGUUU	1308	Cleavage	1
354	80T0	2	5			47	67		GUU			
PPR0003	VDAG_051		16.2	1	21			1093	AUGAGGAGUUCUGGGUUU	1309	Cleavage	1
354	69T0	2	68			1258	1277		GUU			
PPR0003	VDAG_102		24.8	1	21			1094	AUCUGCUGGGCCUCAUCU	1310	Cleavage	1
366	96T0	2	55			179	200		AGAC			
PPR0003	VDAG_102		24.8	1	21			1095	AUCUGCUGGGCCUCAUCU	1311	Cleavage	1
367	96T0	2	55			180	200		AGA			
PPR0003	VDAG_102		24.8	1	20	181	200	1096	AUCUGCUGGGCCUCAUCU	1312	Cleavage	1
368	96T0	2	55			181	200		AG			
PPR0003	VDAG_009		11.3	1	21			1097	AUAUGGGAAGCUGGAGAA	1313	Cleavage	1
418	57T0	2	3			879	899		AGC			
PPR0003	VDAG_075		15.4	1	21			1098	AUAGAG-	1314	Cleavage	1
444	88T0	2	4			813	834		GCCAAUUGUUGAUC	1315	Cleavage	1
PPR0003	VDAG_015		19.8	1	21			1099	AGGGAUUGUAGGUGACA	1316	Cleavage	1
528	61T0	2	85			309	329		ACA			
PPR0003	VDAG_001		22.1	1	20	1695	1714	1100	AGCUCCGAAGCUGUGGC	1317	Cleavage	1
556	39T0	2	59						UU			
PPR0003	VDAG_049		15.2	1	21			1101	AGAGAUUGUUUCUCGGCG	1318	Translation	1
606	95T0	2	5			1084	1103		UGU			
PPR0003	VDAG_038		12.9	1	21			1102	AGACUACGAUGAUUGUG	1319	Cleavage	1
623	36T0	2	98			2541	2561		UUGA			
PPR0003	VDAG_041		21.6	1	22	1876	1896	1103	ACGUCUGGCAGACAAUCU	1320	Translation	1
662	49T0	2	11						UUGC			
PPR0003	VDAG_004		19.8	1	21	3917	3936	1104	AAUGAAUAACUUAUGGA	1321	Cleavage	1
752	19T0	2	61						CCG			
PPR0003	VDAG_021		19.9	1	21	1262	1281	1105	AAGCCAAGCAGAUGUUU	1322	Cleavage	1
797	10T0	2	89						GAG			
PPR0003	VDAG_065		19.9	1	21			1106	AAGAUGGAAGCUGCGAAA	1323	Cleavage	1
821	71T0	2	32			543	563		AUA			
PPR0003	VDAG_023		14.3	1	21			1107	AAGAGGGGAAGCUUUG	1324	Cleavage	1
822	95T0	2	85			54	74		AGG			
PPR0003	VDAG_010		23.1	1	21	208	228	1108	AAAGCUCCGAAGCUGUG	1325	Cleavage	1
891	00T0	2	28						GCU			
PPR0003	VDAG_010		23.1	1	20	209	228	1109	AAAGCUCCGAAGCUGUG			
892	00T0	2	28						GC			

Table S5. Candidate *Arabidopsis* proteins identified from a yeast two-hybrid screening that may associate with PSR2.

No.	Description	Sequence ID
1	Double-stranded-RNA-binding protein 4	NP_974480.1
2	Protein phosphatase 2A subunit A2	NP_189208.1
3	CTC-interacting domain 12 (CID12)/RNA-binding protein 37	NP_192799.1
4	Argonaut 1	NP_001185169.1
5	Cyclophilin ROC7	NP_200679.1
6	Multiple organellar RNA editing factor 8 (MORF8)	NP_566496.1

Table S6. Normalized reads of 21-nt siRNAs produced from individual *PPR* and *NB-LRR* loci in wild-type (WT), *rdrr6*, *drb4* and *PSR2-5 Arabidopsis* plants.

<u>PPR loci with reduced siRNA</u>									
	ID	Description	Col_1	Col_2	drb4_1	drb4_2	PSR_1	PSR_2	rdrr6_1 rdrr6_2
chr1:4183066-4186124	AT1G12300	Tetrahicopeptide repeat (TPR)-like superfamily protein	11.593	17.609	7.207	7.065	2.099	1.151	0.647 1.007
chr1:4353906-4355929	AT1G12775	Pentahicopeptide repeat (PPR) superfamily protein	18.888	31.716	18.555	16.799	6.619	6.141	1.780 1.612
chr1:23176930-23179248	AT1G62590	pentahicopeptide (PPR) repeat-containing protein	490.049	864.166	261.616	302.378	67.807	87.704	5.017 3.224
chr1:23299057-23300958	AT1G62910	Pentahicopeptide repeat (PPR) superfamily protein	719.051	1139.933	543.168	589.527	104.617	133.955	7.283 6.044
chr1:23301576-23303162	AT1G62914	pentahicopeptide (PPR) repeat-containing protein	930.468	1688.377	647.907	667.869	136.906	192.105	10.520 8.059
chr1:23306534-23308683	AT1G62930	Tetrahicopeptide repeat (TPR)-like superfamily protein	647.016	1063.937	509.278	547.138	99.612	125.895	7.768 5.843
chr1:23385324-23387167	AT1G63070	pentahicopeptide (PPR) repeat-containing protein	512.845	888.468	286.919	328.283	68.937	91.351	6.474 4.231
chr1:23387631-23390816	AT1G63080	Pentahicopeptide repeat (PPR) superfamily protein	960.428	1707.325	649.287	674.777	140.781	193.064	13.271 9.067
chr1:23412730-23415149	AT1G63130	Tetrahicopeptide repeat (TPR)-like superfamily protein	917.832	1540.402	648.367	694.559	122.860	160.631	10.034 8.261
chr1:23419396-23421579	AT1G63150	Tetrahicopeptide repeat (TPR)-like superfamily protein	415.669	597.255	246.281	285.736	58.443	79.452	2.751 2.015
chr1:23450654-23452311	AT1G63230	Tetrahicopeptide repeat (TPR)-like superfamily protein	7.686	15.343	5.367	2.512	0.646	1.919	0.486 0.000
chr1:23489840-23491519	AT1G63330	Pentahicopeptide repeat (PPR) superfamily protein	486.011	857.575	265.450	308.501	67.807	87.129	4.855 3.224
chr1:23507320-23509053	AT1G63400	Pentahicopeptide repeat (PPR) superfamily protein	966.290	1756.650	666.922	702.880	145.301	192.297	11.167 8.059

	ID	Description	Col_1	Col_2	drb4_1	drb4_2	PSR_1	PSR_2	rdr6_1	rdr6_2
chr1:23587298-23588220	AT1G63630	Tetrapeptide repeat (TPR)-like superfamily protein	27.355	35.732	10.428	6.908	7.588	7.868	0.647	0.403
chr5:5460976-5463017	AT5G16640	Pentapeptide repeat (PPR) superfamily protein	6.774	12.666	3.680	4.710	1.453	1.151	0.162	0.201
<u>NB-LRR loci with reduced siRNA</u>										
	ID	Description	Col_1	Col_2	drb4_1	drb4_2	PSR_1	PSR_2	rdr6_1	rdr6_2
chr5:17564738-17568802	AT5G43740	Disease resistance protein (CC-NBS-LRR class) family	119.842	229.840	195.369	203.155	137.552	159.672	4.532	3.828
chr5:25283063-25286002	AT5G63020	Disease resistance protein (CC-NBS-LRR class) family	12.375	17.506	22.543	26.219	16.467	19.575	2.104	3.828
chr5:15555156-15558732	AT5G38850	Disease resistance protein (TIR-NBS-LRR class)	435.729	763.456	825.487	852.185	671.453	888.365	5.665	7.656
chr5:17560179-17562929	AT5G43730	Disease resistance protein (CC-NBS-LRR class) family	18.758	37.380	43.858	52.751	25.186	31.858	1.133	0.806

Table S7. Oligonucleotides used in this study.

Usage	Oligo name	Oligo sequence	SEQ ID NO:
pri-miRNA cloning	pri-MIR161-F	CACCTTTGGGCCGATGTATCCAC	1326
	pri-MIR161-R	CACAAATTTCAA TGCTTTTCCT	1327
	pri-MIR173-F	CACCTGGAGACCGTCAGATTCGAA	1328
	pri-MIR173-R	ACGCATCAGATCTATCAAAACACA	1329
	pri-MIR390-F	CACCGATGACGTGTGTTCTTCGA	1330
	pri-MIR390-R	CTGCACCGGAGAAAGAGACT	1331
	AcGFP-qRT-F	GCAAGCTGACCCCTGAAGTTC	1332
	AcGFP-qRT-R	GTAGTTGCCGTCATCTCTCGAA	1333
	phyca-54980-qRT-F	AGGTGGTAGCAGACTTCA	1334
	phyca-54980-qRT-R	CTACACCATCAGCCTCCACA	1335
qPCR for Phytophthora genes	phyca_538731-qRT-F	GTGTGTTGCAAGTGGAGGAG	1336
	phyca_538731-qRT-R	CAGCCTTCACAAAGTGCCAAT	1337

Usage	Oligo name	Oligo sequence	SEQ ID NO:
qPCR for Arabidopsis genes	Pc76RTF	ATGGCCTATGTGACGCAGAT	1338
	Pc76RTR	TATTGGTCGATTGCTTGGC	1339
	mRFP-RT-F	GCCCCGTAATGCAGAAAGAAAG	1340
	mRFP-RT-R	GTCCAGCTTGATGTCGGTCTT	1341
	63400-RT-F	TTCCTTTGTAAATTACGA	1342
	63400-RT-R	AGCTTCCCTCCTTCACAAA	1343
	63150-RT-F	TTGAAGGGAATGTGCAAGGCT	1344
	63150-RT-R	ACCTCAGACTCTCTCTACCT	1345
	63130-RT-F	CTGATGGTGTGCTTCCCGAT	1346
	63130-RT-R	CCTCAGCATCTCTTCTCTCG	1347
	63080-RT-F	GTTTGCTGGCGATGCTTCAA	1348
	63080-RT-R	TACCGAACTAAAGCTGGTTACA	1349
	62930-RT-F	AGTTGGGGTTTGTGGAGA	1350
	62930-RT-R	TCACAAGGGAAGATGGTTGCT	1351
	62910-RT-F	AGGAGGAAGCAGATTCCTCG	1352
	62910-RT-R	AGCTTTTGTCCTCAATCTCCCA	1353
	62590-RT-F	CAC TTGCATCATCTCTTGAGGG	1354
	62590-RT-R	TCTGAAATGAGGGTATGIGGGT	1355
	62914-RT-F	GGTTCTGTGGTGTGCATCC	1356
	62914-RT-R	CCACCCATCTTCCACTTCCC	1357
	Actin2-RT-F	TAACTCTCCCGCTATGTATGTC	1358
	Actin2-RT-R	GAGAAACCCCTCGTAGATTGG	1359
stem loop qRT-PCR	siR1310-RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACgatactg	1360
	siR1310-forward primer	CGGCGAAAGAGGATGTCAAC	1361
	siR0513-RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACtctggt	1362
	siR0513-forward primer	CGGCGTTCAAAGAGGATGTCA	1363
	U6-RT-F	GATAAAATTGGAACGATACAG	1364
siRNA transformation	U6-RT-R	GGACCAATTTCGATTATTATGCG	1365
	Universal-RP	GTGCAGGGTCCGAGGT	1366
	siR2813-sense	CAAAGAGGAUGUCAAACAGAU	1367
	siR2813-antisense	CUGGUUGACAUCUUCUUUGTT	1368

Usage	Oligo name	Oligo sequence	SEQ ID NO:
northern blotting probes	AcGFP-siRNA-sense	GCAUCAAGGUGAACUUCAAAT	1369
	AcGFP-siRNA-antisense	UUGAAGUUCACCUUGAUGCCA	1370
	PPR-siRNA-1-probe	AGCCACTGCTTCTGAAAGCTCT	1371
	PPR-siRNA-2-probe	GTGATATTGAATTTGGCTTTGA	1372
	miR161-probe	ACCCCGATGTAGTCACTTTCA	1373
	miR173-probe	GTGATTTCTCTCTGTAAGCGA	1374
	miR390-probe	GGCGCTATCCCTCCTGAGCTT	1375
	miR393-probe	GATCAATGCGATCCCTTTGGA	1376
	siR255-probe	TACGCTATGTTGGACTTAGAA	1377
	siR1511-probe	AAGTATCATCATTCGCTTGGGA	1378
<i>P. capsici</i> biomass	AtRub-F4	GCAAGTGTTGGGTTCAAAAGCTGGTG	1379
	AtRub-R4	CCAGGTTGAGGAGTTACTCGGAATGCTG	1380
	CAP-Fw	TTTAGTTGGGGTCTTGTACC	1381
	CAP-Rv1	CCTCCACAACCAAGCAACA	1382
	sgR-161-S	ATTGGCAGTGAAAGTGACTAAACC	1383
	sgR-161-AS	AAACGGTTTAGTCACTTTCACTGC	1384
	siR2813t-S	AATTATCTGGTTGACATCATCTTTG	1385
	siR2813t-AS	AATTCAAAGATGATGTCAACCAGAT	1386
	siR2813mt-S	AATTACGTGCTTGACCTCATCTCCG	1387
	siR2813mt-AS	AATTCGGAGATGAGGTCAAGCACGT	1388
vector construction	pTSK108N3F-PSR2 ^{ΔWY1} -F	TCGGAAGCTTCCGCCGTTATG	1389
	pTSK108N3F-PSR2 ^{ΔWY1} -R	TTTCAAACCGGGCTTAGGCTTTA	1390
	pTSK108N3F-PSR2 ^{ΔLWY2} -F	CCCAAAGCCCCAAACGACTTTGA	1391
	pTSK108N3F-PSR2 ^{ΔLWY2} -R	GTCCGCTCTCCGCGACCGAG	1392
	pTSK108N3F-PSR2 ^{WY1+LWY2} -F	CGGAATTCGGAATCAACTTCAGTTCGGTG	1393
	pTSK108N3F-PSR2 ^{WY1+LWY2} -R	GCTCTAGA TTA CTGTTCGACAGCTTCATATAG	1394
	pENTRY1a-DRB4-F	tca GTC GAC TGG ATC CGG ATGGATCATGTATACAAAGGTCAACTGC	1395
	pENTRY1a-DRB4-R	tag ata tct cga gfg TGGGTTCAAGACGATAGGCTA	1396
	OV-pENTRY1a-DRB4MdsRBD1-F	ACGCCACAAAAGTCCAGAGGG	1397
	OV-pENTRY1a-D4RBMdsRBD1-R	TACATGATCCATGTCGACTGAA	1398
	OV-pENTRY1a-DRB4MdsRBD2-F	AAAAATGGGAACCTCGAACACAGAC	1399

Usage	Oligo name	Oligo sequence	SEQ ID NO:
	OV-pENTRY1a-DRB4MdsRBD2-R	GGCAACATCAATTCCCTCTGG	1400
	OV-pENTRY1a-DRB4ΔC-F	CACTCGAGATATCTAGACCCAGCT	1401
	OV-pENTRY1a-DRB4ΔC-R	GATACTCATGAATGCAACTTTAG	1402
	T7-gfp500-ss-F	GAAATTAAATACGACTCACTATA GGG GAAAACTACCTGTTCCATGGCCAAC	1403
	gfp500-scn-R	GAAAGGACCATGTTGGTCTCTCTTTTCG	1404
	gfp500-anti-F	GAAAACTACCTGTTCCATGGCCAAC	1405
	T7-gfp500-anti-R	GAAATTAAATACGACTCACTATA GGG GAAGGACCATGTTGGTCTCTCTTTTCG	1406
	22-nt DNA	GCCAGTTGGTATACTCAGGTGG	1407
	GFP 500 bp sequence	GAAAACTACCTGTTCCGTGGCCAACACTTGTCACTACTTTCTCTTATGGTGTTCATGCTTTT CAAGATACCCAGATCATATGAAGCGCACGACTTCTTCAAGAGCGCCATGCCCTGAGGGATA CGTGCAGGAGAGGACCATCTTCTTCAAGGACGACGGGAACCTACAAGACACGTGCTGAAGT CAAGTTTGAGGGGAGACACCTCTGTCACACAGGATCGAGCTTAAAGGGAATCGATTTCAAAGGA GGACGGAAACATCTCTCGGCCACAAGTTTGAATACAACTACAACCTCCCAACACGTATACATC ATGGCCGCAAGCAAAAGAACGGCATCAAAAGCCAACTTCAAGACCCGCCAACACATCGAA GACGGCGCGTGCAACTCGCTGATCATTTATCAACAAAATAC/TCCAAATTGGCGATGGCCCTG TCCTTTTACCAGAACCAATTA/CCTGTCCACACAAATCTGCCCTTTTCGAAAAGATCCCAACGAA AAGAGAGACCACATGGTCTCTTC	1408

Example 2

[0175] *Nicotiana benthamiana* plants producing antimicrobial siRNAs derived from an *Arabidopsis thaliana* mRNA show enhanced resistance to *Phytophthora capsici*

[0176] Leaves of *Nicotiana benthamiana* (a tobacco relative) were infiltrated with

5 *Agrobacterium tumefaciens* carrying one of the following constructs (see FIG. 14):

1. *atMIR161* (*at1g48267*, the gene encoding miR161 in *Arabidopsis thaliana*)
2. *at1g62914m* (a mutated *at1g62914* gene containing a premature stop codon – see Figure 1 below for details. Without the mutation, this gene in the ecotype Col-0 of *Arabidopsis thaliana* is predicted to encode a PPR protein; with the mutation, *at1g62914m* no longer
10 encodes a functional protein but can still be transcribed to mRNA, which carries the target site of miR161. Therefore, transcripts of *at1g62914m* are expected to serve as the precursor for secondary siRNA production if the same plant cell also produces miR161. This construct was used to eliminate the possible impact of At1g62914 protein on plant defense.)
- 15 3. *atMIR161* + *at1g62914m* (a mixture of the constructs above)

[0177] Levels of *at1g62914m*-derived siRNAs were determined by quantitative RT-PCR. Two siRNAs (i.e. siR1310 and siR0513) that can silence a virulence-related gene in *P. capsici* were examined as representatives. The results show that leaves expressing both *atMIR161* and *at1g62914m* produced a much higher amount of the siRNAs that can silence a virulence-related
20 gene in *Phytophthora capsici*. See FIG. 15.

[0178] Leaves of *Nicotiana benthamiana* that express *atMIR161*, *at1g62914m*, or *atMIR161+at1g62914m* were inoculated with *Phytophthora capsici* strain LT263. Disease severity was evaluated at 3 days post inoculation. The results show that plants expressing *atMIR161+at1g62914m* exhibited much enhanced resistance to *P. capsici*. This experiment was
25 repeated three times with similar results. Images of representative inoculated leaves (two per treatment) are shown below (Panel A, FIG. 16). Lesion size of each inoculated leaf was measured and analyzed (Panel B, FIG. 16). Please note that not all leaves expressed the same amount of *atMIR161* and/or *at1g62914m* transcripts, hence the variation within the same treatment.

[0179] All publications, patents and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing disclosure has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this disclosure that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

WHAT IS CLAIMED IS:

- 1 1. A transgenic plant engineered to heterologously express an miRNA
2 comprising any one of SEQ ID NO: 1-19, wherein the transgenic plant has enhanced resistance
3 to a pathogen compared to a control plant that does not heterologously express the miRNA.
- 1 2. The transgenic plant of claim 1, wherein the plant further heterologously
2 expresses a pentatricopeptide repeat (PPR)-encoding transcript.
- 1 3. The transgenic plant of claim 2, wherein the PPR-encoding transcript
2 contains a mutation such that the transcript does not express a function protein.
- 1 4. The transgenic plant of claim 2 or 3, wherein PPR-encoding transcript
2 and the miRNA are from the same species of plant and are different from the transgenic plant
3 species.
- 1 5. The transgenic plant of claim 1, wherein the transgenic plant comprises an
2 expression cassette, the expression cassette comprising a promoter operably linked to a
3 polynucleotide encoding the miRNA, wherein the promoter is heterologous to the
4 polynucleotide.
- 1 6. The transgenic plant of claim 5, wherein the promoter is a constitutive or
2 tissue-specific or inducible promoter.
- 1 7. The transgenic plant of any one of claim 1-6, wherein the plant is a dicot
2 plant.
- 1 8. The transgenic plant of claim 7, wherein the plant is a cotton plant.
- 1 9. The transgenic plant of any of claim 1-8, wherein the pathogen is one or
2 more of a species of *Phytophthora* and/or *Verticillium*.
- 1 10. A method of making the transgenic plant of any of claims 1-9, comprising
2 (i) modifying an endogenous promoter of the plant to heterologously express the miRNA or (ii)
3 introducing the expression cassette into the plant.

1 11. The method of claim 10, further comprising selecting from a plurality of
2 modified plants, one or more plant with enhanced resistance to the pathogen.

1 12. A method of inducing resistance in a plant to a pathogen, the method
2 comprising,
3 contacting a plant with an miRNA comprising any of SEQ ID NO: 1-19 in an
4 amount to induce resistance to a pathogen.

1 13. The method of claim 12, further comprising contacting the plant with a
2 pentatricopeptide repeat (PPR)-encoding transcript.

1 14. The method of claim 13, wherein the PPR-encoding transcript contains a
2 mutation such that the transcript does not express a function protein.

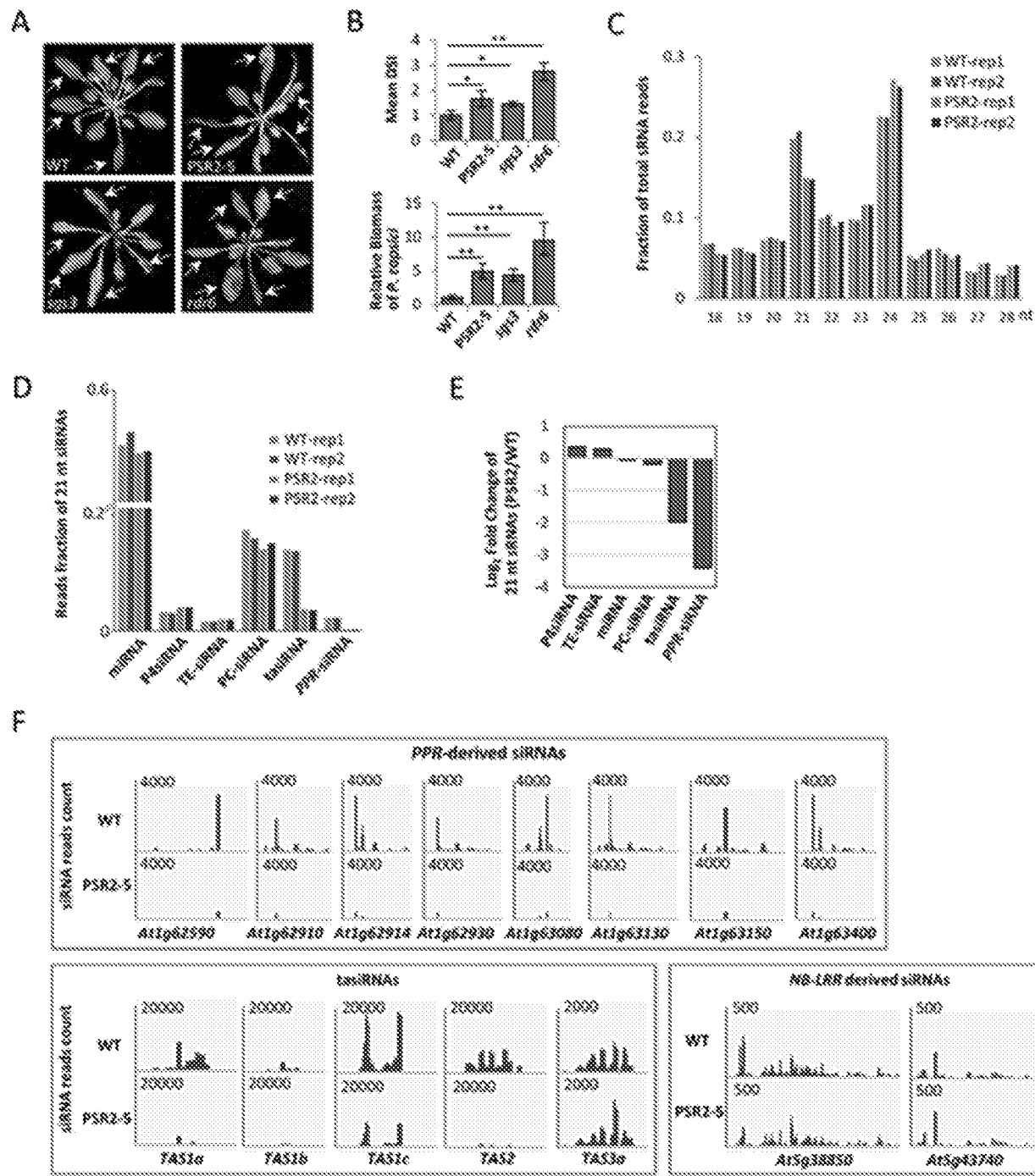
1 15 . The method of claim 2 or 3, wherein PPR-encoding transcript and the
2 miRNA are from the same species of plant and are different from the transgenic plant species.

1 16. The method of any one of claim 12-15, wherein the plant is a dicot plant.

1 17. The method of claim 16, wherein the plant is a cotton plant.

1 18. The method of any of claims 12-17, wherein the pathogen is one or more
2 of a species of *Phytophthora* and/or *Verticillium*.

1 19. The method of any of claims 12-18, wherein the contacting comprising
2 spraying aerial parts of the plant or contacting roots of the plant with the miRNA (and optionally
3 the PPR-encoding transcript).



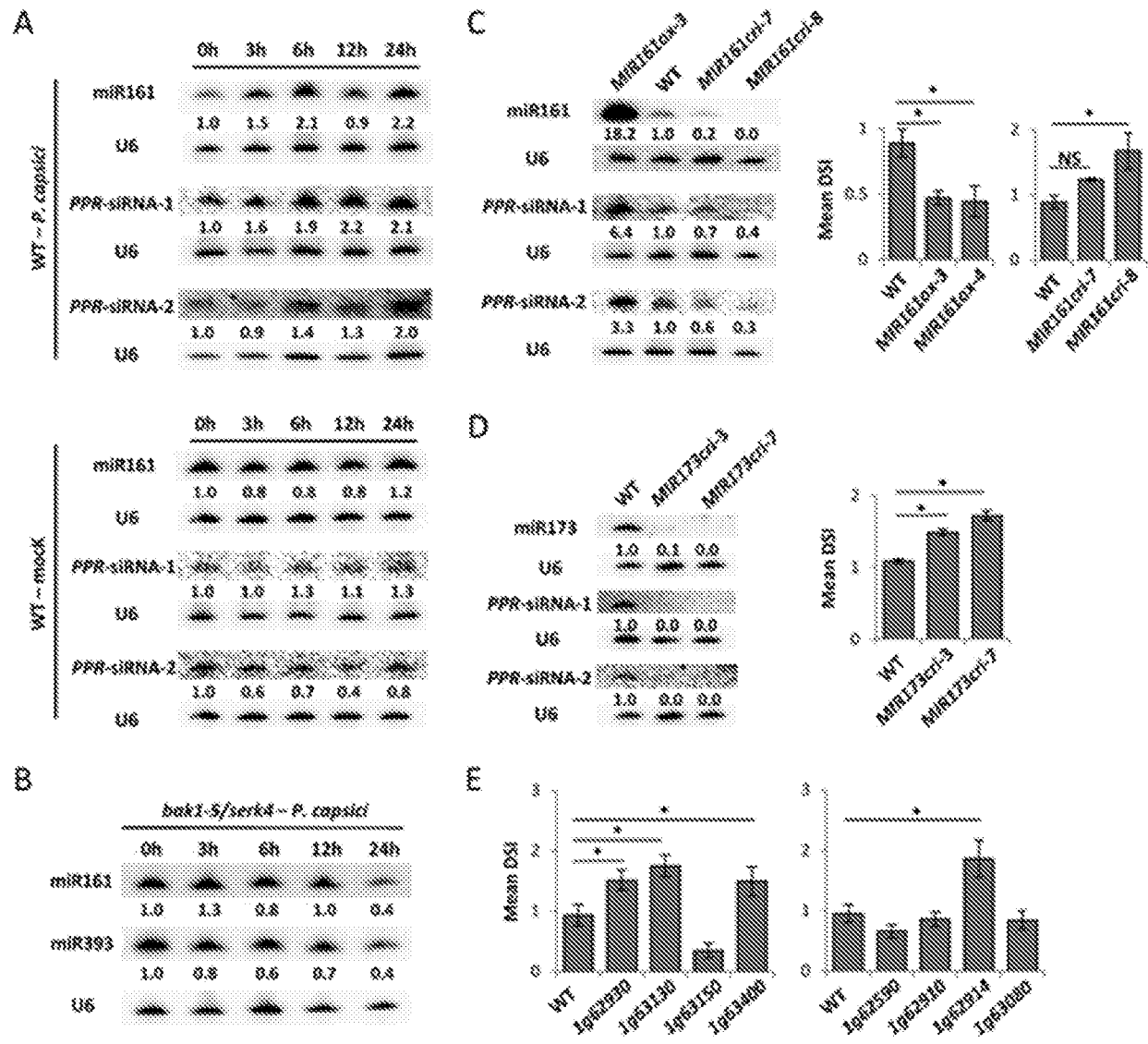


FIG. 2

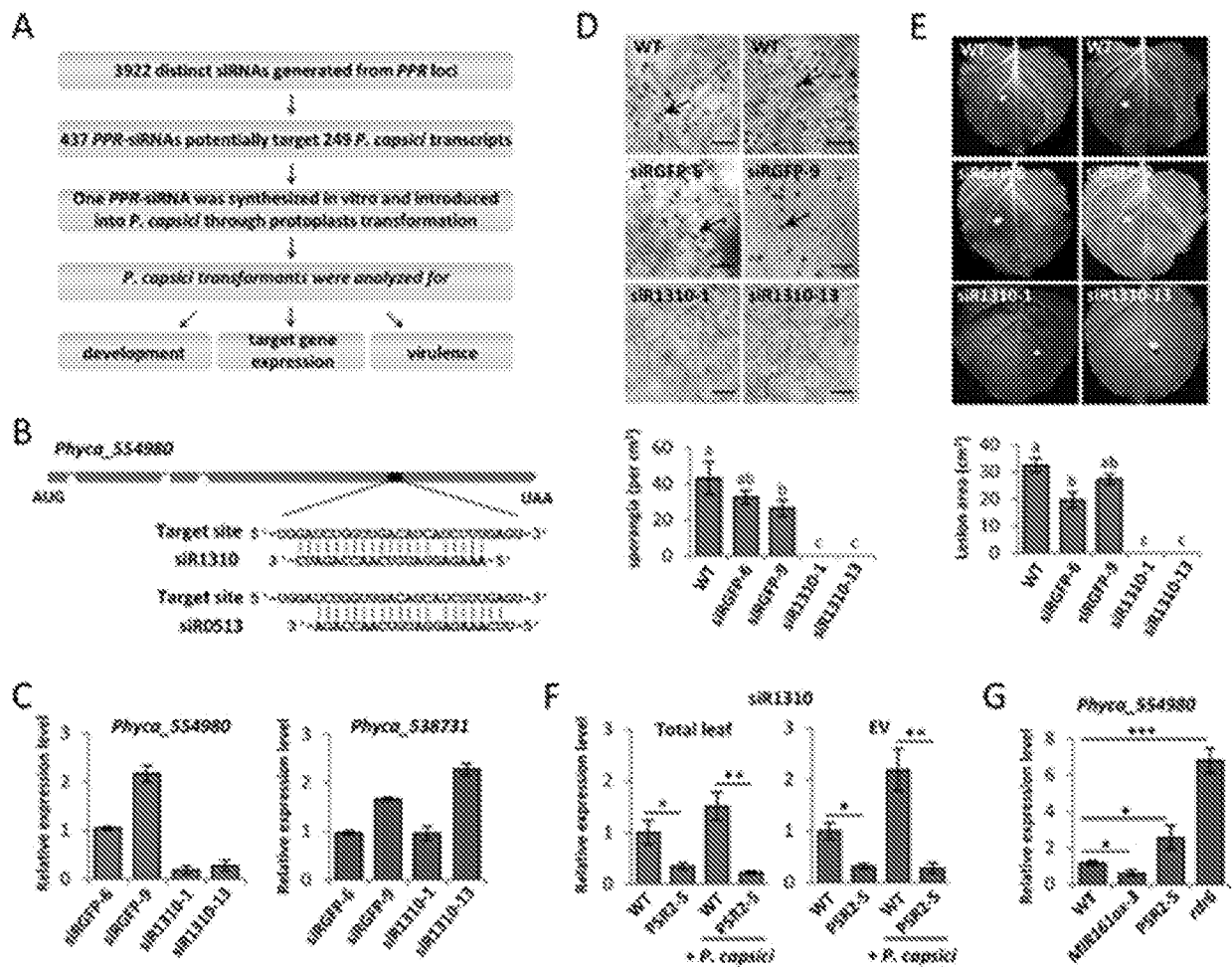


FIG. 3

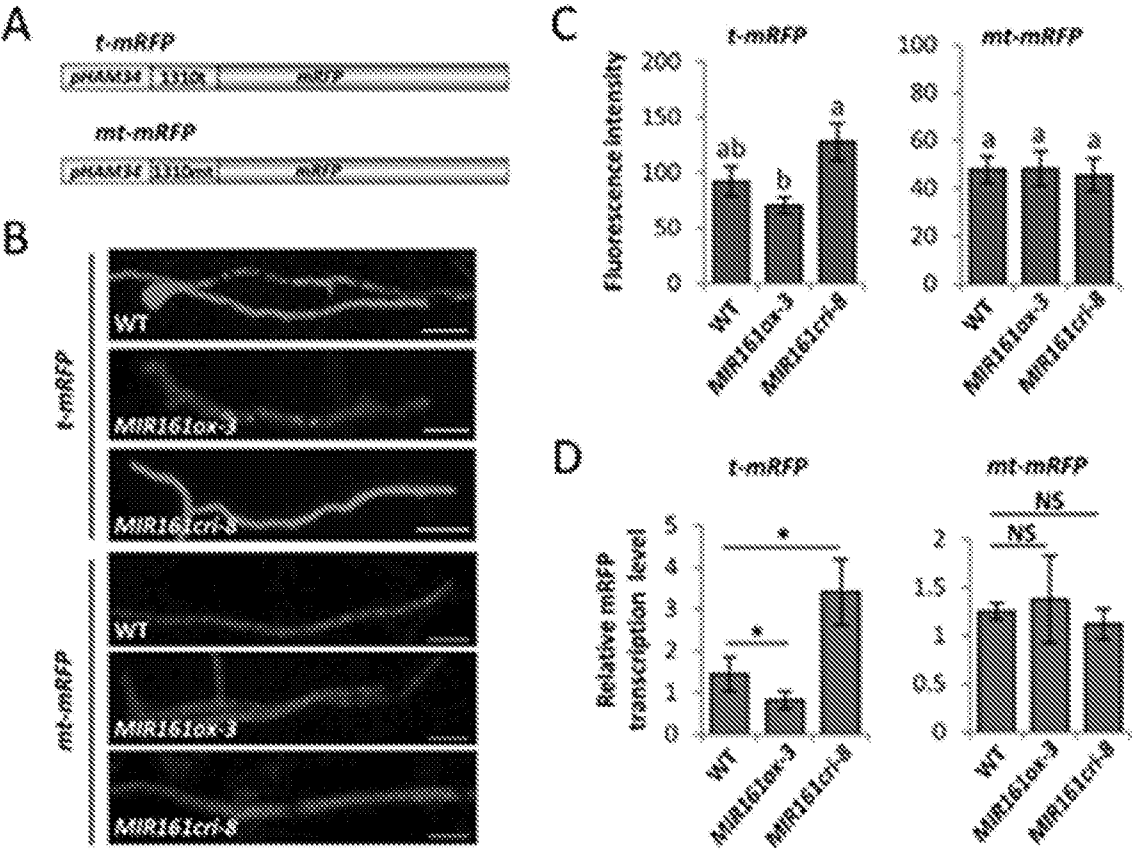


FIG. 4

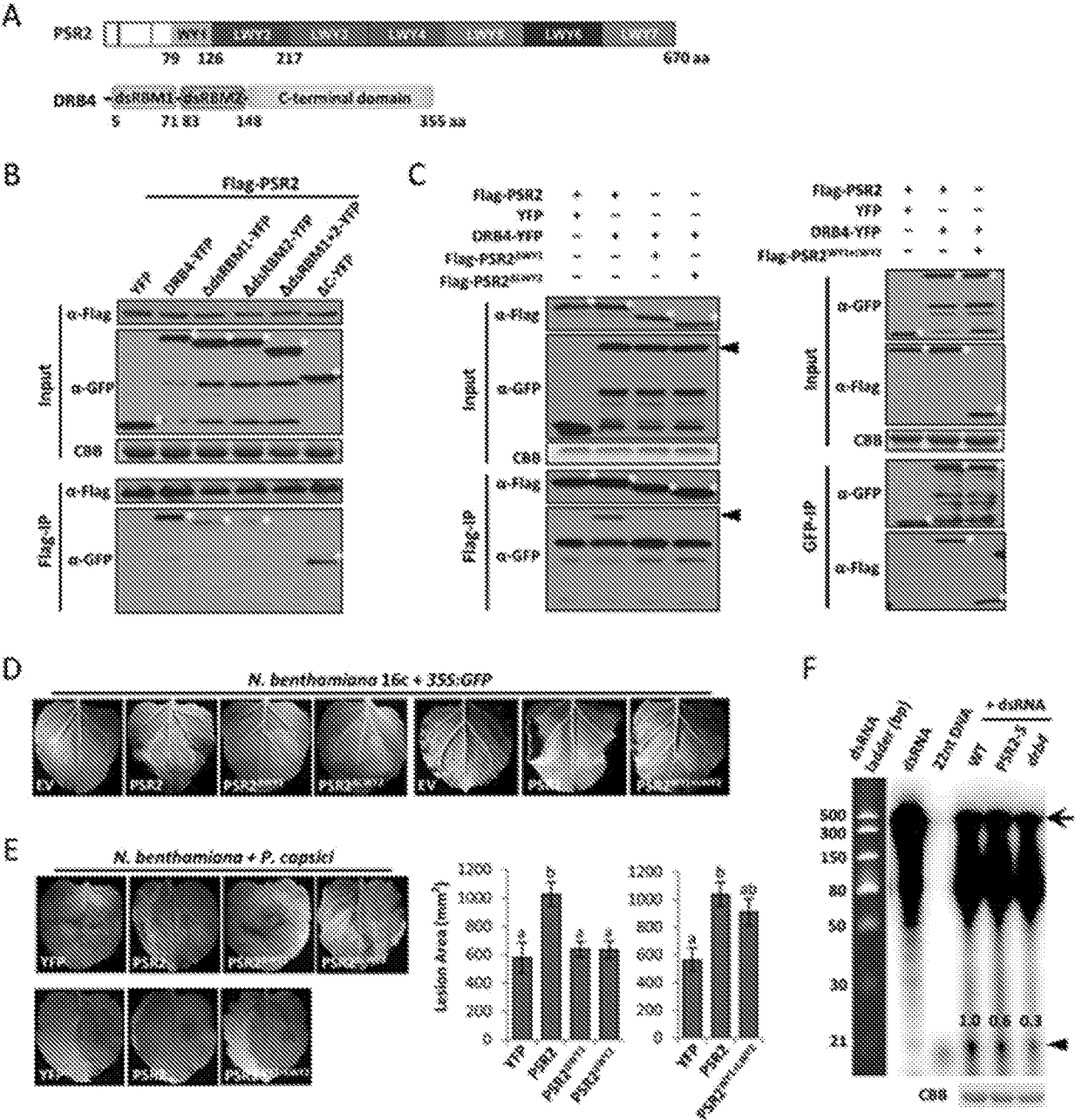


FIG. 5

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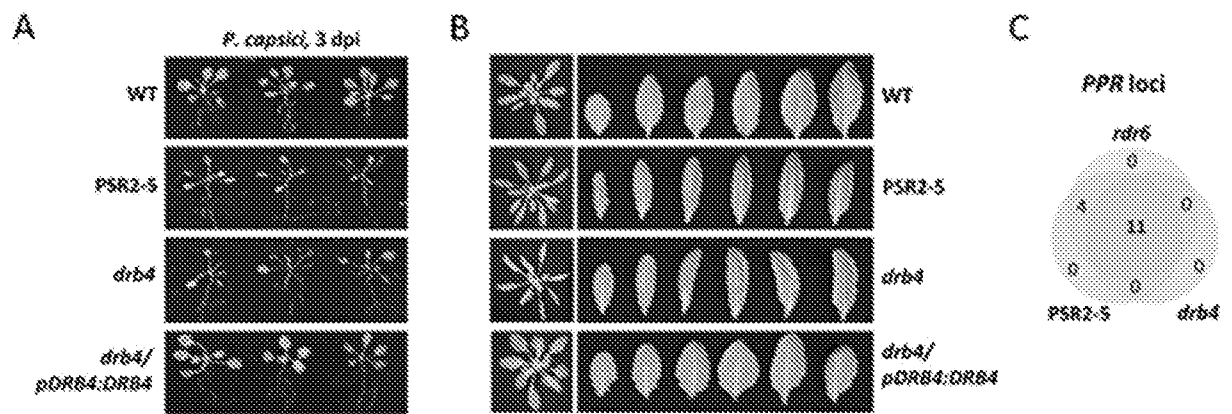


FIG. 6

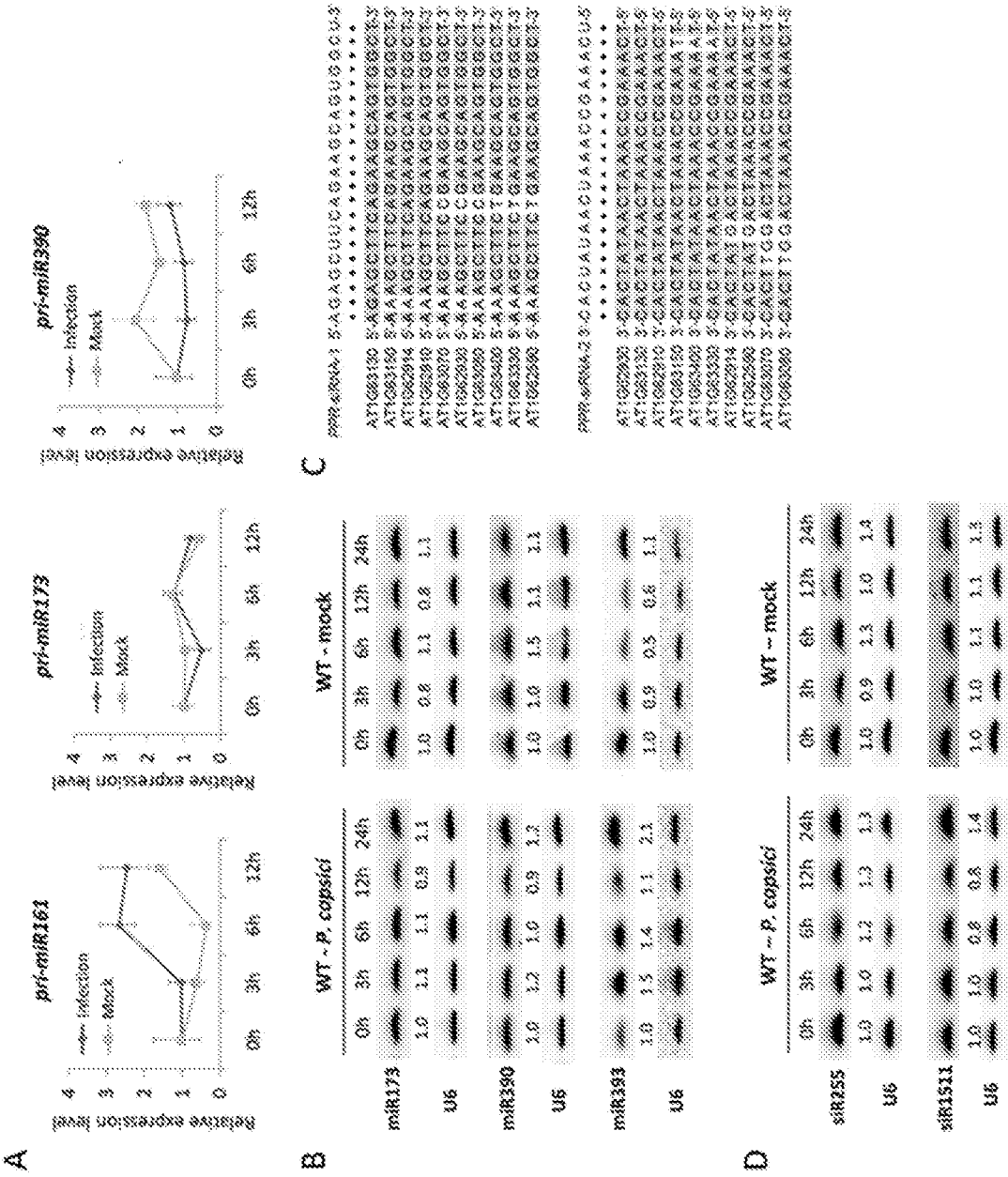


FIG. 7

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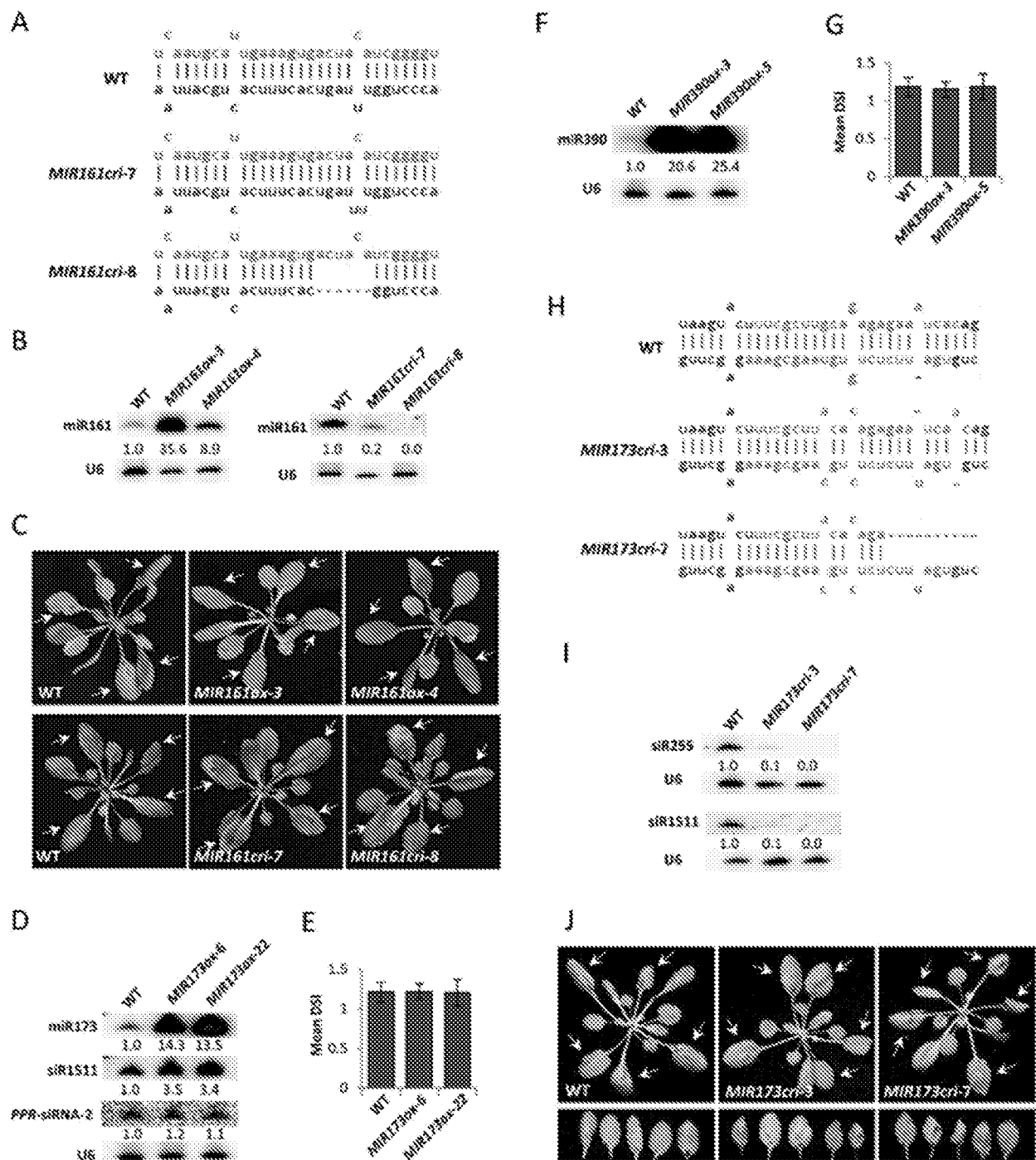


FIG. 8

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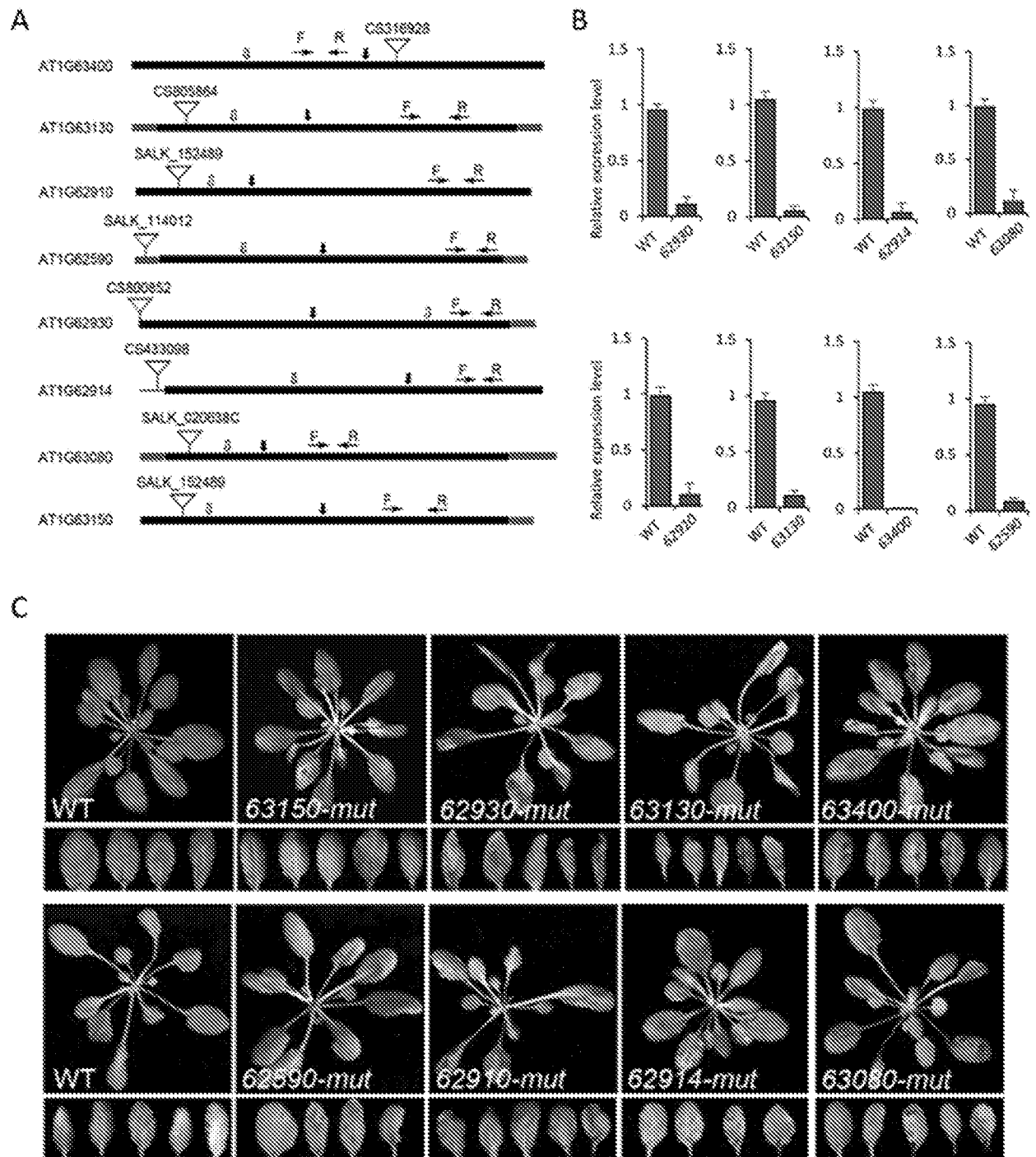


FIG. 9

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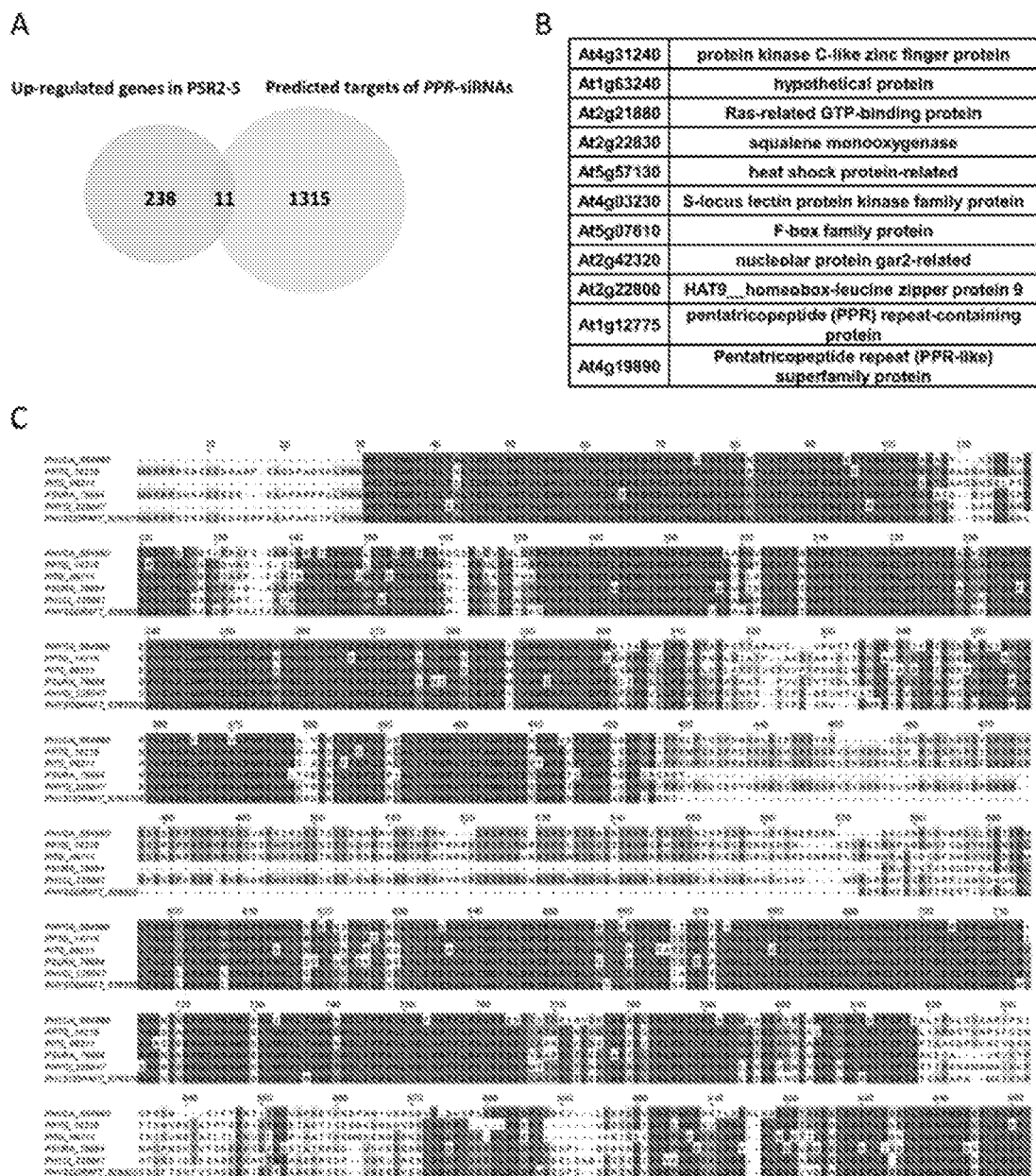
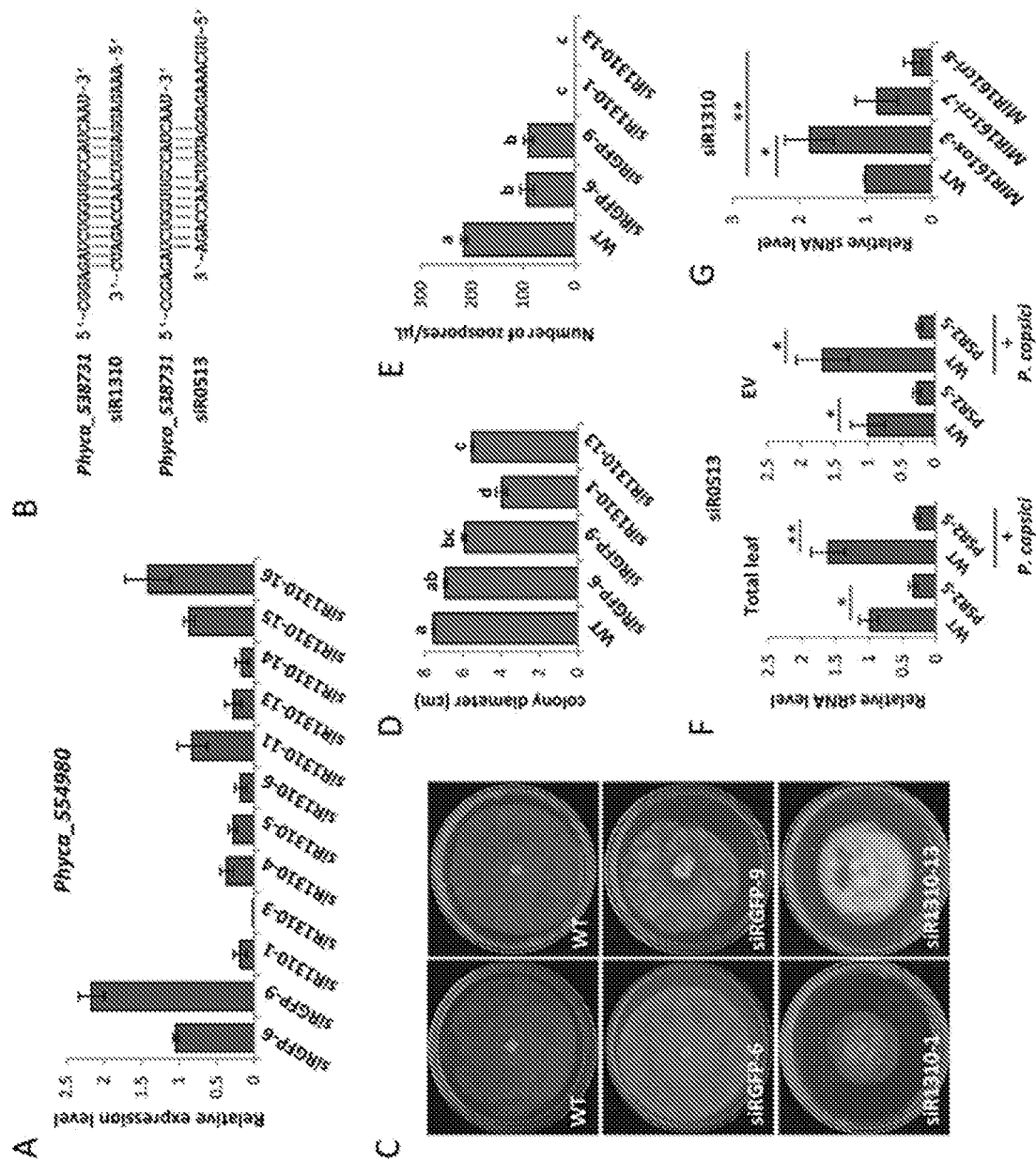


FIG. 10



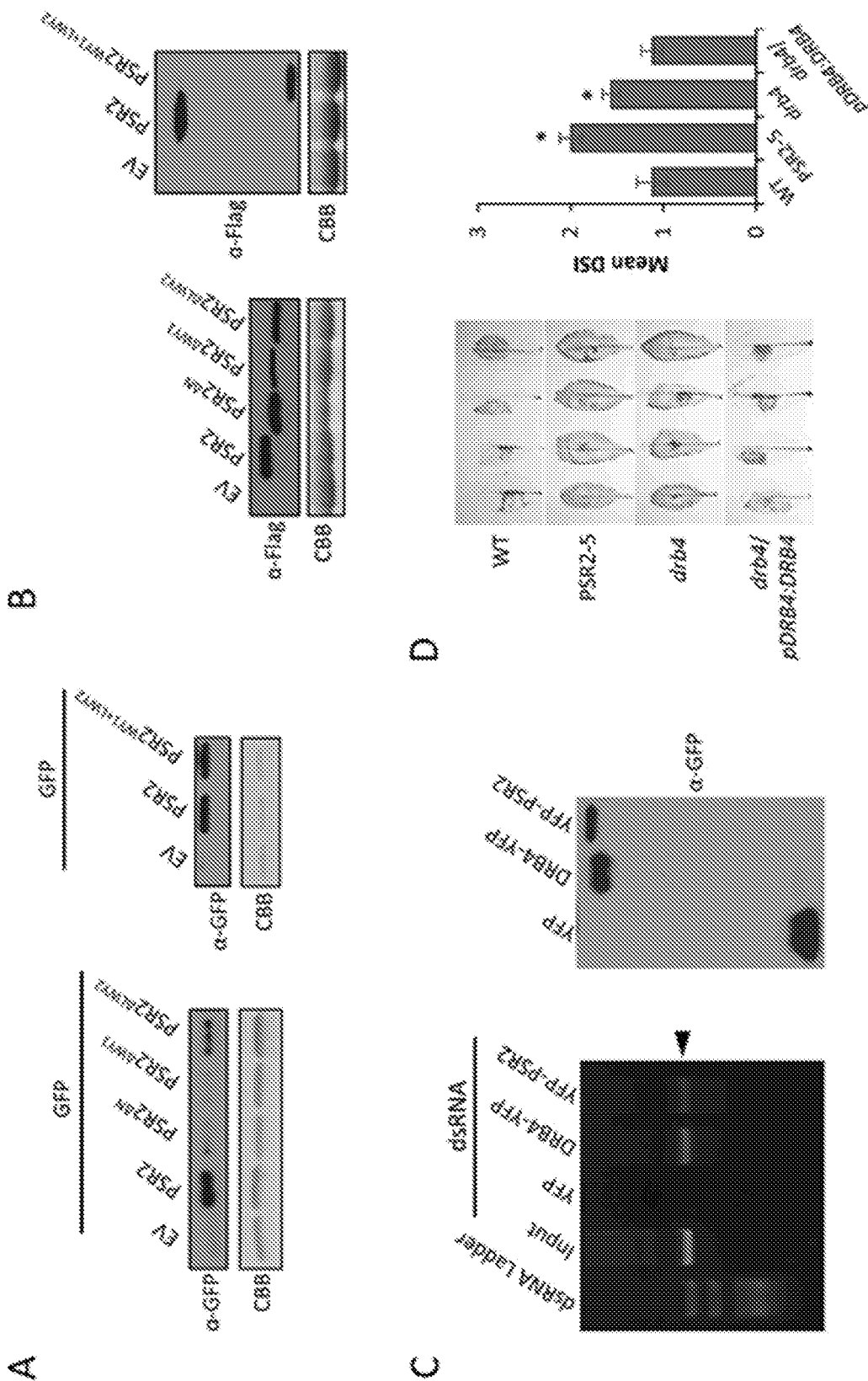


FIG. 12

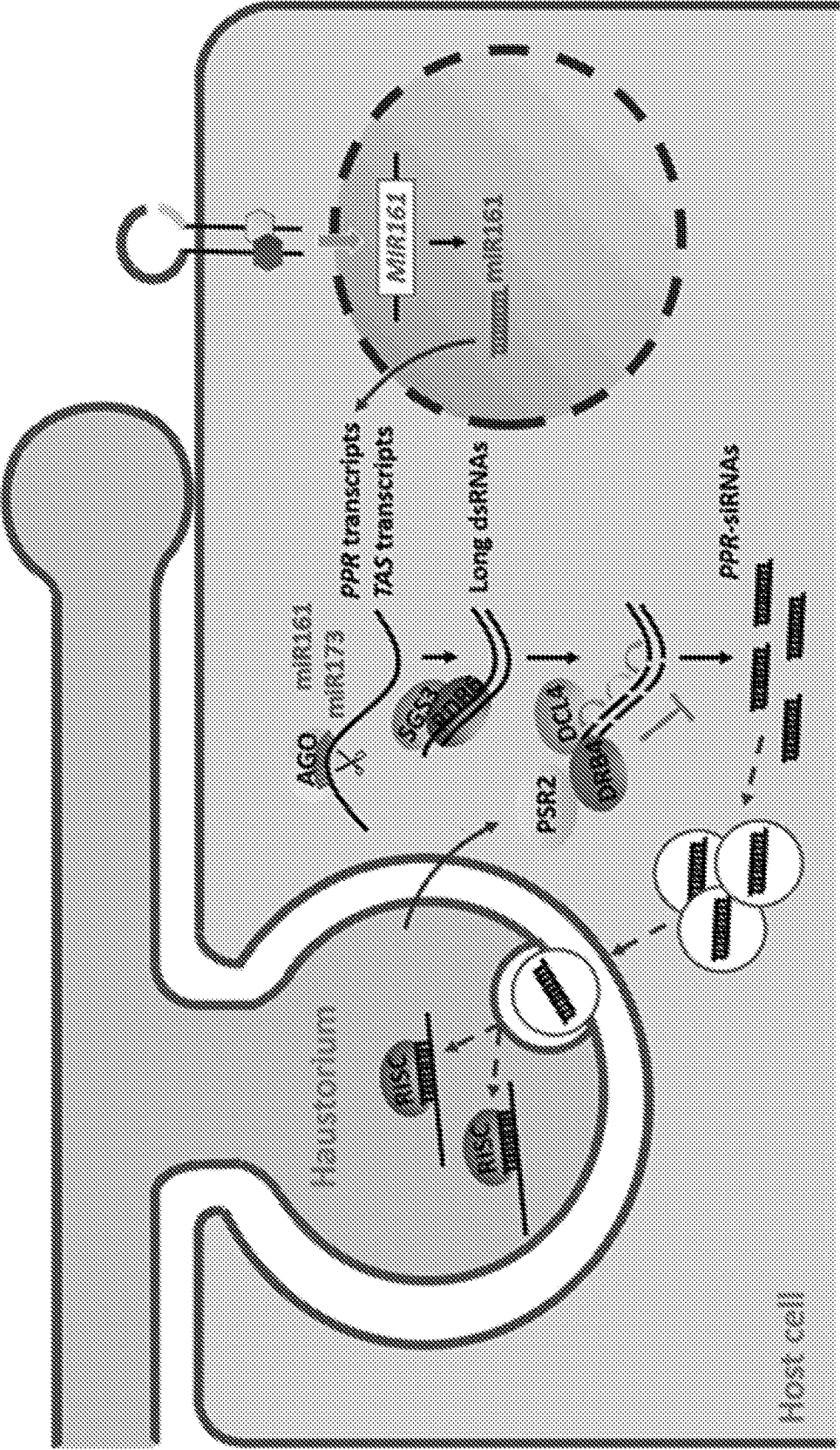


FIG. 13

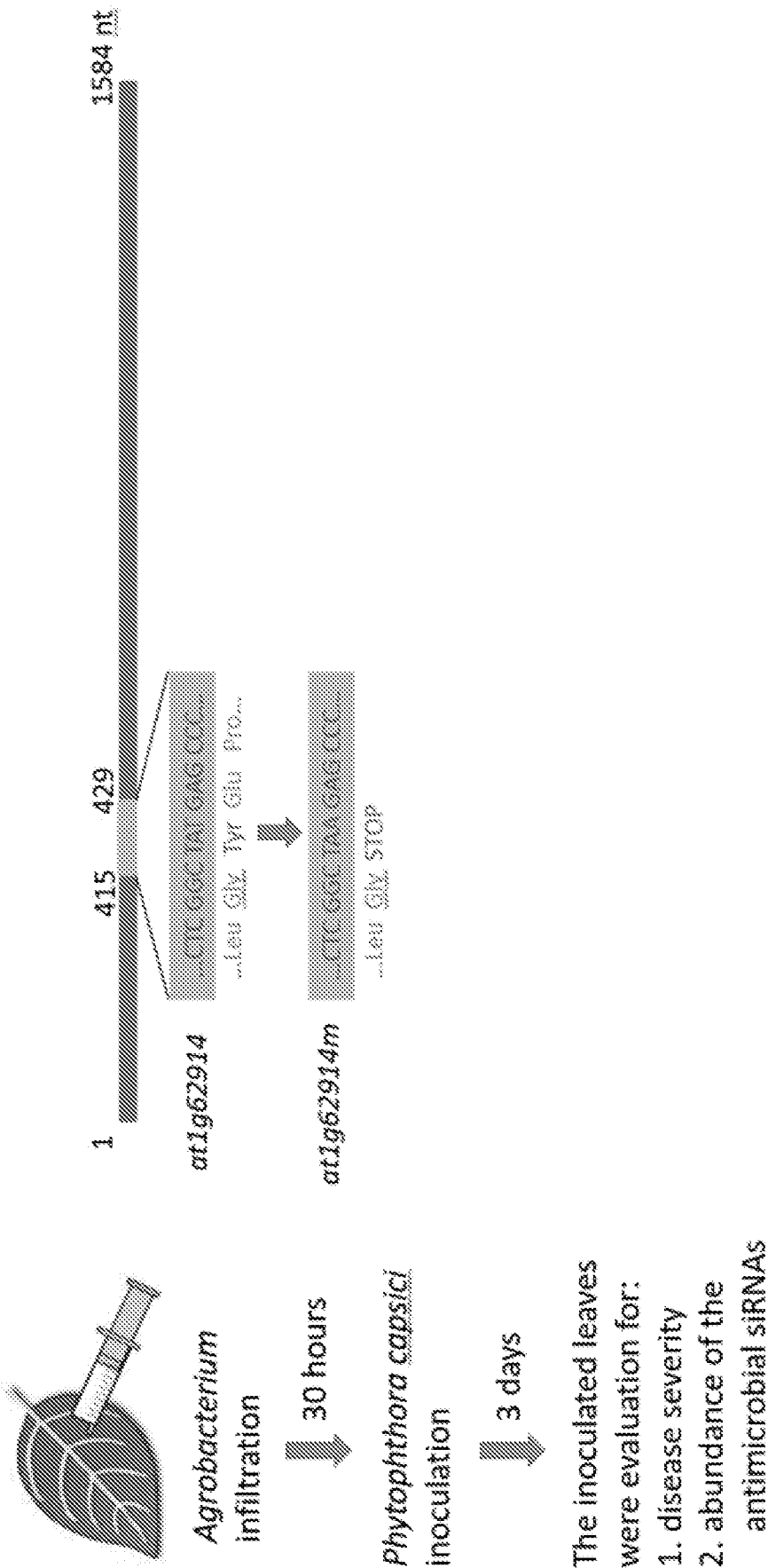


FIG. 14

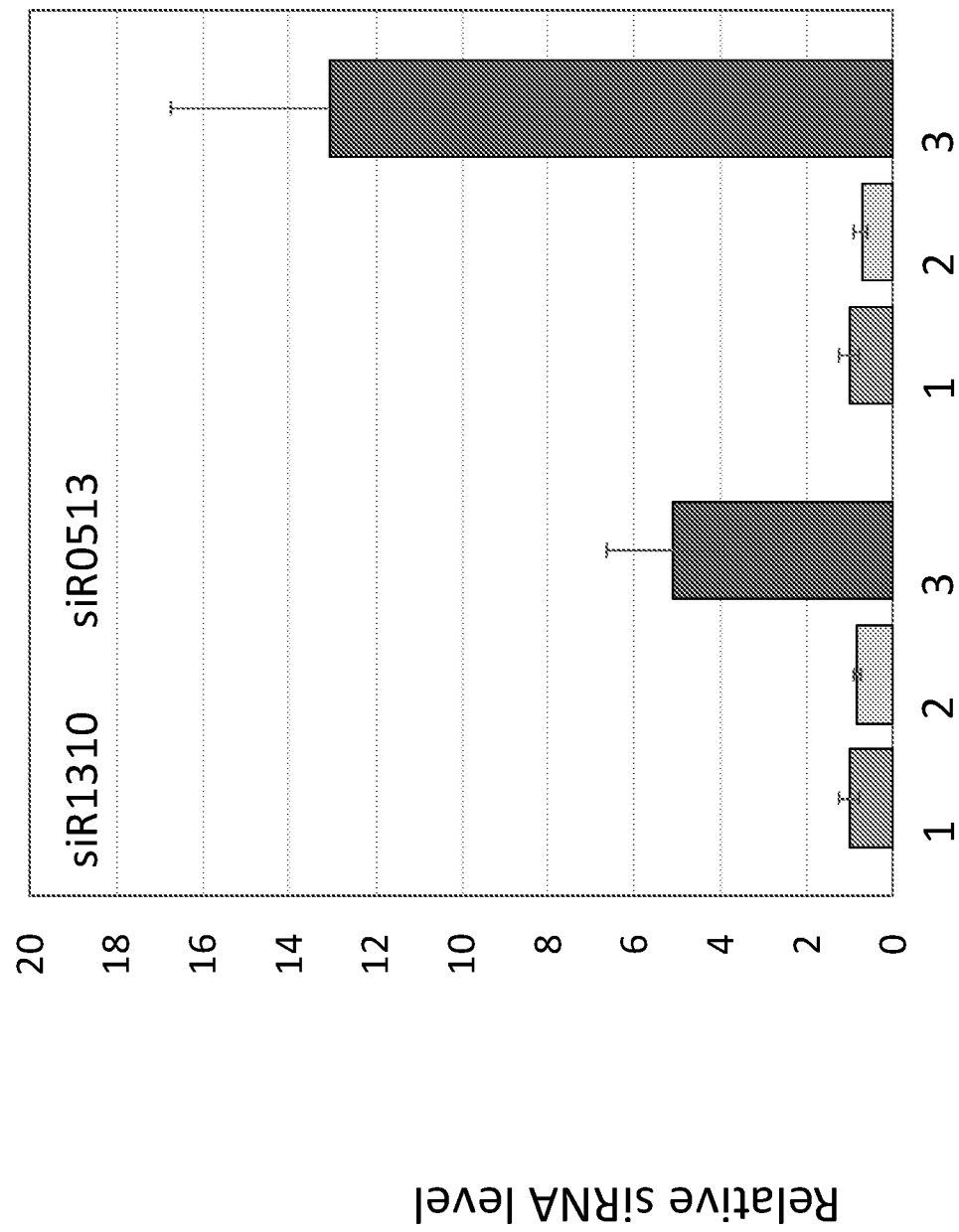


FIG. 15

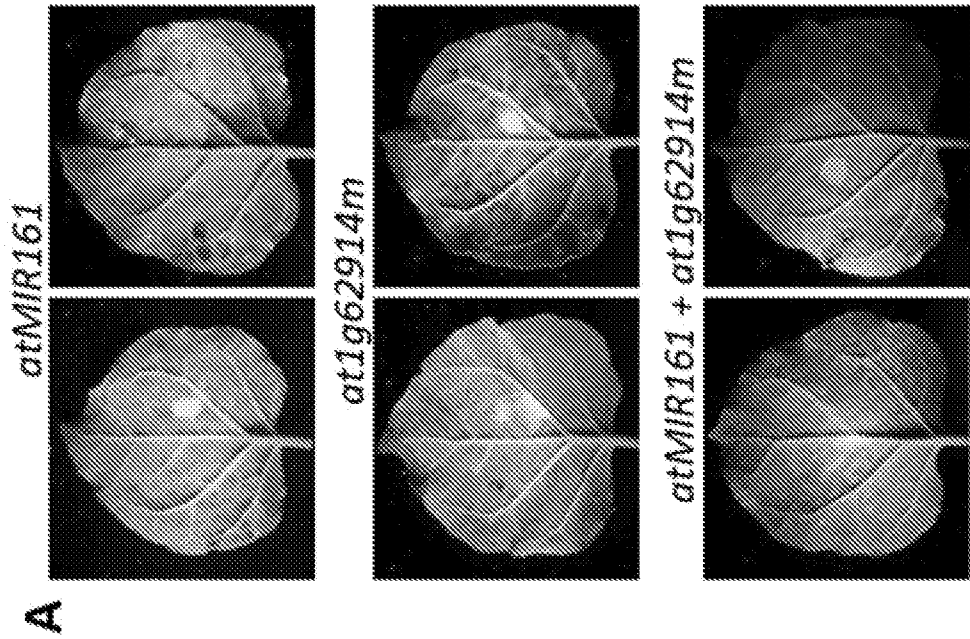
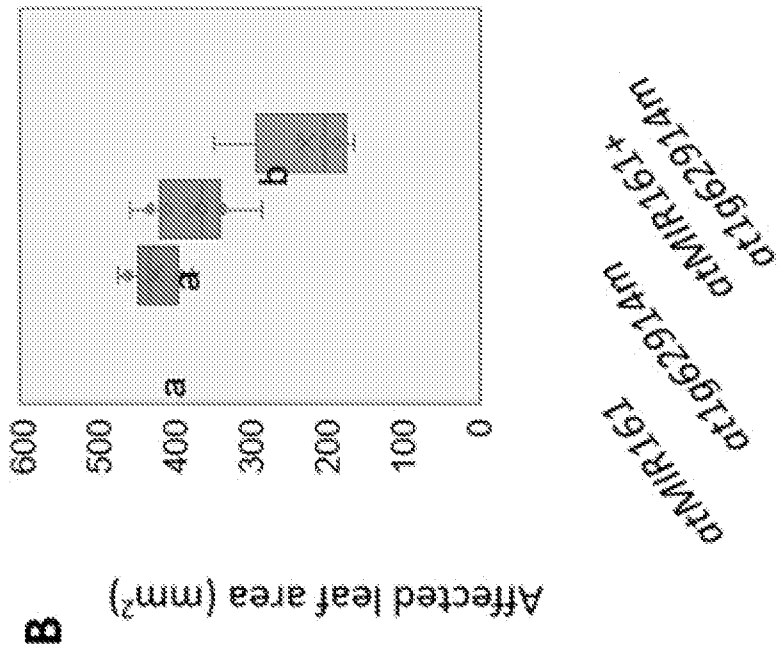


FIG. 16

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 19/44971

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - A01H 5/00; C12N 15/87; C12N 15/82; C12N 15/00; C07H 21/04 (2019.01)

CPC - C12N 15/8281; C12N 15/8282; C12N 15/8286; C07K 14/415; A01H 6/60; C12N 15/8216; C12N 15/00; C12N 15/82; C12N 2310/141; C12N 2310/14; C12N 15/113

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History Document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

See Search History Document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History Document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ---	US 2016/0257969 A1 (OREGON STATE UNIVERSITY) 08 September 2016 (08.09.2016), para [0012], [0064], [0138], [0163], [0169], [0173], [0182], [0190], [0197], [0272], [0306], [0370]; pg 30-32, Table 3; pg 46, Table 8A, SEQ ID NO: 222; and Fig 2B	1, 5-6 ----- 2-4
Y	YAGI et al., The potential for manipulating RNA with pentatricopeptide repeat proteins. Plant J. 2014, Vol. 78(5), p. 772-82. Abstract; pg 773, col 1, last para; pg 774, Table 1; pg 775, col 1, last para; and pg 776, col 2, middle para, and Fig 2	2-4
A	JEONG et al., Comprehensive Investigation of MicroRNAs Enhanced by Analysis of Sequence Variants, Expression Patterns, ARGONAUTE Loading, and Target Cleavage. Plant Physiol. 2013, Vol. 162(3), p. 1225-45. Entire documentation, especially Abstract; pg 1229, col 1, up para; and pg 1237, col 1, lower para, col 2, and Fig 8	1-6
A	XING et al., Genome-wide investigation of pentatricopeptide repeat gene family in poplar and their expression analysis in response to biotic and abiotic stresses. Sci Rep. 2018 Feb, Vol. 8(1):2817. PDF File: pg 1-9. Entire documentation, especially Abstract; pg 1, para 1; pg 2, para 3; pg 3, para 1 and Fig 1; pg 4, Fig 2; and pg 6, Fig 5	1-6

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

27 September 2019

Date of mailing of the international search report

27 NOV 2019

Name and mailing address of the ISA/US

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Lee W. Young

PCT Helpdesk: 571-272-4300
PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 19/44971

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 7-11, 16-19
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Groups I+, claims 1-6, directed to a transgenic plant engineered to heterologously express an miRNA. The miRNA will be searched to the extent that the miRNA encompasses SEQ ID NO: 1. It is believed that claims 1 (in part), 2-6 encompass this first named invention, and thus these claims will be searched without fee to the extent that they encompass wherein the miRNA encompasses SEQ ID NO: 1. Additional miRNA will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected miRNA(s). Applicants must further indicate, if applicable, the claims which encompass the first named invention, if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched. An exemplary election would be wherein the miRNA encompasses SEQ ID NO: 2 [claims: 1 (in part), (2-6)]. [Please note: in the situation that the selected SEQ ID NO is novel, Group II will be searched with the elected subgroup I]. *****Continued in the extra sheet*****

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1 (in part), 2-6, limited to SEQ ID NO: 1

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 19/44971

Continuation of:
Box No III (unity of invention is lacking)

Group II, claims 12-15, directed to a method of inducing resistance in a plant to a pathogen.

The inventions listed as Groups I+ and II do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special Technical Feature

Groups I+ and II are related as a product (Groups I+) and a method of making the product (Group II).

Group II includes the special technical feature of contacting a plant with an miRNA, not required by Groups I+.

Among Groups I+, each SEQ ID NO represents a structurally different nucleotide sequence.

Common Technical Features

The inventions of Groups I+ and II share the technical features of a transgenic plant comprising an miRNA comprising SEQ ID NO: 1, wherein the transgenic plant has enhanced resistance to a pathogen (part of claim 1 or part of claim 12); and --the inventions of Groups I+ further share the technical features of a transgenic plant engineered to heterologously express an miRNA comprising a specified sequence, wherein the transgenic plant has enhanced resistance to a pathogen compared to a control plant that does not heterologously express the miRNA (part of claim 1).

Therefore, in a summary, the common technical features shared by inventions of Groups I+ and II can be covered by:

A transgenic plant engineered to heterologously express an miRNA comprising SEQ ID NO: 1, wherein the transgenic plant has enhanced resistance to a pathogen compared to a control plant that does not heterologously express the miRNA (part of claim 1).

However, these shared technical features do not represent a contribution over prior art as being anticipated by US 2016/0257969 A1 to OREGON STATE UNIVERSITY (hereinafter 'Oregon') as follows:

Oregon discloses a transgenic plant engineered to heterologously express an miRNA (para [0190] - 'transgenic plants produced ... herbicide and/or pest resistance traits'; para [0138] - 'a plant that is modified to suppress a specific gene by an RNAi-inducing transgene. ... RNAi is triggered in transgenic plants'; para [0012] - 'employ constructs that yield single-stranded RNA transcripts, and take advantage of ... heterologous...in vivo-produced miRNAs or siRNAs to initiate production of siRNAs from an engineered RNAi-triggering cassette. ...to produce specific siRNAs in vivo for inactivation or suppression of one or more target genes or other entities, such as pathogens or pests (e.g., viruses, bacteria, nematodes'; para [0173] - 'heterologous miRNA or siRNA can be added to the cell ...by providing an expression cassette encoding such molecule... to mediate cleavage and release of siRNAs from a RNAi-triggering nucleic acid cassette')
-- comprising SEQ ID NO: 1 (para [0306] - 'Soybean is transformed by ... constructs 2A, 2B and 2C... transgenic soybean plants are regenerated which exhibit resistance to soybean cyst nematode infestation as compared to control plants'; Fig 2B, miR161.1; pg 46, Table 8A-continued, miR161.1...SEQ ID NO: 222, which is 100% identical to the claimed SEQ ID NO: 1),
--wherein the transgenic plant has enhanced resistance to a pathogen compared to a control plant that does not heterologously express the miRNA (para [0190] - 'transgenic plants produced using methods and cassettes described herein ... having an enhanced agronomic trait resulting from gene suppression from an siRNA-triggering nucleic acid cassette ... conferring another trait such as herbicide and/or pest resistance traits'; para [0064] - 'Agronomic trait: Characteristic of a plant, ... include,... disease or pest resistance'; para [0306] - 'Soybean is transformed by microprojectile bombardment using constructs 2A, 2B and 2C... transgenic soybean plants are regenerated which exhibit resistance to soybean cyst nematode infestation as compared to control plants'; Fig 2B, miR161.1; pg 46, Table 8A-continued, miR161.1... SEQ ID NO: 222; para [0370] - 'Soybean is transformed by Agrobacterium-mediated transformation of plasmid vectors ...and transgenic soybean plants are regenerated which exhibit resistance to soybean cyst nematode infestation as compared to control plants').

Without a shared special technical feature, the inventions lack unity with one another.

Groups I+ and II therefore lack unity under PCT Rule 13 because they do not share a same or corresponding special technical feature.

Continuation of item 4: Claims 7-11, 16-19 are not drafted in accordance with the second and third sentences of Rule 6.4 (a). These claims are improper multiple dependent claims.

Note:

1) Claim 15 lacks a proper antecedent basis for the "the method" limitation. For the purposes of this ISR, it is assumed that claim 15 depends from claim 12 or 13.