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(54) Title: ENDORNAVIRAL SATELLITE RNA AMPLIFICATION SYSTEMS FOR PLANTS

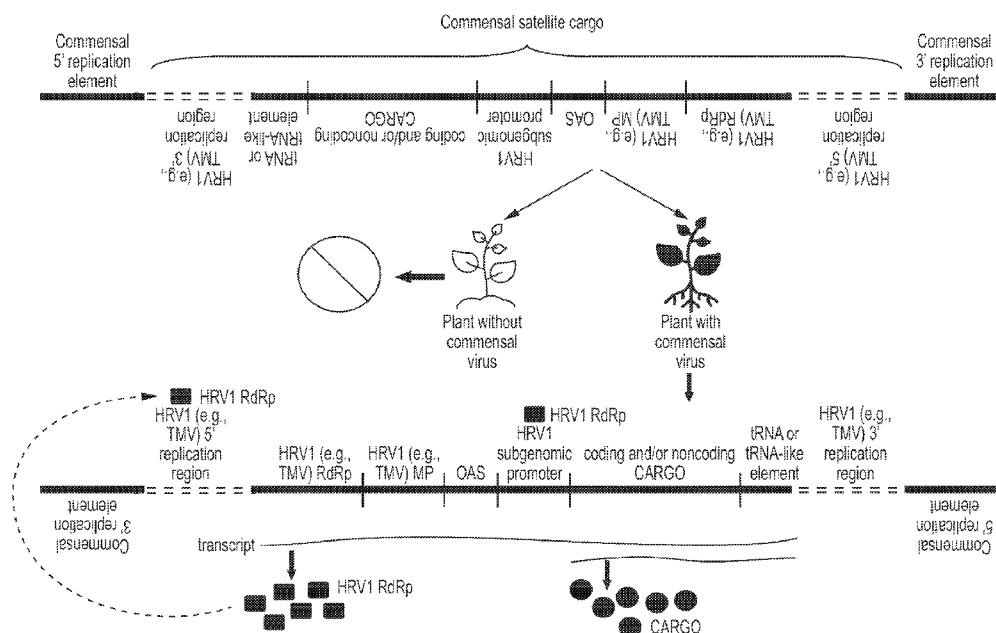


Figure 6

(57) Abstract: Synthetic endornavirus satellite RNA molecules and satellite particles containing the same are disclosed. Synthetic endornavirus satellite RNA molecules which contain internal heterologous TNA virus (HRV) amplicons are also disclosed. Also disclosed are methods of using the endornavirus satellite RNA molecules and satellite particles containing the same to change plant phenotypes, improve plant stress resistance, and improve plant pest and pathogen resistance.

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ENDORNAVIRAL SATELLITE RNA AMPLIFICATION SYSTEMS FOR PLANTS**CROSS-REFERENCE TO RELATED APPLICATIONS**

[0001] This application claims priority to provisional application U.S. Serial No. 63/499,746 filed May 3, 2023, which is hereby incorporated herein by reference in its entirety.

INCORPORATION OF SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in XML file format and is hereby incorporated by reference in its entirety. The XML file, created on April 27, 2024, is named P14020WO00.xml, and is 6,095,495 bytes in size. The XML file, created on April 30, 2023, is named P14020US00.xml, which is 1,380,742 bytes in size and was filed in provisional application U.S. Serial No. 63/499,746 on May 3, 2023, is also incorporated herein by reference in its entirety.

BACKGROUND

[0003] There is need in the art for modifying polynucleotides for improving phenotypes and genotypes of organisms; in particular, for agricultural applications to improve plants such as crop plants.

[0004] Endornaviruses (EV) are RNA viruses having an a linear single-stranded (+) genome of about 14 to about 17.6 kilobases (kb) in length. The endornavirus genome encodes an RNA-dependent RNA polymerase (RdRP) but does not encode a capsid protein.

SUMMARY

[0005] This disclosure provides recombinant RNA molecules comprising from 5' terminus to 3' terminus: (a) a 5' RNA replication element recognized by an endornavirus RNA-dependent RNA polymerase (RdRP); (b) a cargo RNA molecule (cargo RNA sequence); and (c) a 3' RNA replication element recognized by the RdRP; wherein the 5' RNA replication element, the cargo RNA molecule, and the 3' RNA replication element are operably linked, and wherein the cargo RNA molecule is heterologous to the 5' RNA replication element and the 3' RNA replication element. In certain embodiments, (i) the 5' RNA replication element and the 3' RNA replication element are obtained from the same endornavirus genome or from endornavirus genomes having at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another and which are optionally related; (ii) the 5' RNA replication element, the 3' RNA replication element, and the RdRP are obtained from the same endornavirus genome or from endornavirus genomes having at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another and which are optionally related; or (iii) the 5' RNA replication element, the 3' RNA replication element, and/or the RdRP coding region are obtained from different endornavirus genomes, and the members of each respective set of the 5' RNA replication elements, 3' RNA replication elements, and/or RdRP coding regions have at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another. In certain embodiments, the RNA molecule comprises: at least one heterologous RNA virus (HRV) amplicon in sense or antisense orientation to the first 5' RNA replication element comprising: I. (i) a heterologous RNA virus (HRV) 5' replication region (HRV 5'RR); (ii) the cargo RNA molecule; and

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(iii) the heterologous RNA virus (HRV) 3' RNA replication region (HRV 3'RR); wherein the HRV 5' RR and HRV 3' RR HRV are recognized by a heterologous RNA virus RNA-dependent RNA polymerase (hrvRdRP); and wherein the HRV 5'RR, cargo RNA molecule, and HRV 3'RR are operably linked; or II. a heterologous RNA virus (HRV) subgenomic promoter operably linked to the cargo RNA molecule; wherein the subgenomic promoter is recognized by a heterologous RNA virus RNA-dependent RNA polymerase (hrvRdRP). Agricultural formulations as well as bacterial, fungal, plant, insect, and invertebrate animal cells comprising the herein disclosed recombinant RNAs are also provided.

[0006] Also provided are expression systems comprising: (a) an RNA molecule comprising the herein disclosed recombinant RNA molecules; and (b) a cell containing the recombinant RNA molecule and an RdRP protein that recognizes the 5' and 3' RNA replication elements of the recombinant RNA molecule. In certain embodiments, the cell further comprises one or more of: (i) a viral capsid protein (CP); (ii) an RNA-binding protein (RBP) that binds to the RNA molecule, optionally wherein the RBP binds to an RNA effector; (iii) an RNA cleavage agent that cleaves the RNA molecule; (iv) a second RNA-dependent RNA polymerase (2nd RdRP) protein that recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter in the RNA molecule; (v) a viral movement protein (MP); (vi) a heterologous RNA virus (HRV); or (vii) an hrvRdRP, optionally wherein the hrvRdRP recognizes the HRV 5' or 3' replication region and/or the subgenomic promoter.

[0007] Also provided are methods of providing a synthetic endornavirus satellite RNA to a plant, comprising contacting the plant with any of the herein disclosed recombinant RNA molecules.

[0008] Also provided are methods of establishing a synthetic endornavirus satellite RNA in a plant cell, comprising: providing to a plant cell any of the herein disclosed recombinant RNA molecules, wherein the plant cell comprises an RdRP protein that recognizes the 5' RNA replication element and 3' RNA replication element, wherein the RNA molecule optionally comprises an encapsidation recognition element (ERE) and is or can be encapsidated by a capsid protein, whereby the RdRP protein catalyzes synthesis of the synthetic endornavirus satellite RNA from the recombinant RNA molecule.

[0009] Also provided are methods of obtaining a phenotypic change in a plant or plant cell, comprising: providing to a plant or plant cell any of the herein disclosed recombinant RNA molecules, wherein the cargo RNA molecule comprises RNA that effects a phenotypic change in the plant or plant cell in comparison to a plant or plant cell lacking the recombinant RNA, wherein the plant or plant cell comprises an RdRP protein that recognizes the 5' RNA replication element and 3' RNA replication element and catalyzes synthesis of a synthetic endornavirus satellite RNA from the recombinant RNA molecule and the cargo RNA molecule effects the phenotypic change. In certain embodiments, the methods further comprise providing an hrvRdRP to the plant which recognizes the HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA, optionally wherein the hrvRdRP is provided by introducing a recombinant DNA or RNA encoding the hrvRdRP into the plant or a part thereof.

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[0010] Also provided are methods of manufacturing a synthetic endornavirus satellite particle, comprising combining any of the herein disclosed recombinant RNA molecules with a viral capsid protein, wherein the recombinant RNA molecule comprises an encapsidation recognition element (ERE), and wherein the ERE provides for encapsidation of the RNA by the viral capsid protein.

[0011] Also provided are plant propagules comprising any of the herein disclosed recombinant RNA molecules and an endornavirus RdRP, optionally wherein the plant propagule further comprises a heterologous RNA virus RdRP which recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter in the synthetic endornavirus satellite RNA. In certain embodiments, the plant propagule further comprises a heterologous RNA virus RdRP which recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter in the synthetic endornavirus satellite RNA, and the heterologous RNA virus RdRP is an Alphaflexivirus, Betaflexivirus, Bromovirus, Celavirus, Closterovirus, Comovirus, Potexvirus, Potyvirus, Tobamovirus, Tombusvirus, Tospoviridae, Trivirinae, Tymovirus, Varicosavirus, or Secoviridae RdRP.

[0012] Also provided are plants comprising any of the herein disclosed recombinant RNA molecules and an endornavirus RdRP, optionally wherein the plant propagule further comprises a heterologous RNA virus RdRP which recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter in the synthetic endornavirus satellite RNA.

[0013] Endornavirus satellite systems that are self-replicating when introduced into a plant or plant cell, comprising: (1) any of the herein disclosed recombinant endornavirus satellite RNAs (*e.g.*, recombinant RNA molecules); and (2) an exogenous endornavirus that is capable of replication in the plant or plant cells and that encodes the endornavirus RdRP that recognizes the 5' and 3' RNA replication elements in the recombinant endornavirus satellite RNA, optionally wherein the endornavirus satellite system further comprises a heterologous RNA virus RdRP which recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter in the synthetic endornavirus satellite RNA.

BRIEF DESCRIPTION OF THE DRAWINGS

[0014] Figure 1 shows a non-limiting embodiment of a structure of an endornavirus satellite construct. In this embodiment, the 5' RNA replication element is labelled "5' RRE" and the 3' RNA replication element is labeled "3' RRE."

[0015] Figure 2 shows non-limiting embodiments of an endornavirus satellite construct containing a heterologous RNA virus (HRV) amplicon comprising: (i) a heterologous RNA virus (HRV) 5' replication region (HRV 5'RR); (ii) the cargo RNA molecule; and (iii) the heterologous RNA virus (HRV) 3' RNA replication region (HRV 3'RR). Both sense and antisense orientations of the HRV amplicon relative to the endornavirus 5' RNA replication element are shown. In certain embodiments, at least one cleavable sequence is located: (i) 5' to the 5' RNA replication element or 3' to the 3' RNA replication element; and/or (ii) between the 3' end of the 5' RNA replication element and the HRV amplicon and/or between the HRV amplicon and the 5' end of the 3' RNA replication element, wherein the cleavable sequence is optionally a self-cleaving ribozyme, a self-cleaving inducible ribozyme, or an

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siRNA or miRNA recognition site. In certain embodiments, a subgenomic promoter and/or an IRES is/are operably linked to the cargo RNA.

[0016] Figure 3 shows non-limiting embodiments of an endornavirus satellite construct containing a heterologous RNA virus (HRV) amplicon comprising a heterologous RNA virus (HRV) subgenomic promoter (HRV sgp) which is recognized by a heterologous RNA virus RNA-dependent RNA polymerase (hrvRdRP) and which is operably linked to the cargo RNA molecule. Embodiments where the HRV sgp and cargo RNA are in sense and antisense orientation relative to the endornavirus 5' RRE are shown.

[0017] Figure 4 depicts an endornavirus satellite construct comprising heterologous RNA virus (HRV) subgenomic promoters (HRV sgp) with: (i) one HRV sgp operably linked to a cargo RNA; and (ii) one HRV sgp operably linked to RNA encoding an hrvRdRP which recognizes both of the HRV sgp (*i.e.*, can drive expression of the operably linked hrvRdRP and cargo RNA). In certain embodiments, an IRES is operably linked to the cargo RNA and/or an IRES is operably linked to the RNA encoding the hrvRdRP.

[0018] Figure 5 depicts non-limiting embodiments of an endornavirus satellite construct containing a heterologous RNA virus (HRV) amplicon comprising a heterologous RNA virus (HRV) subgenomic promoter (HRV sgp) which is recognized by a heterologous RNA virus RNA-dependent RNA polymerase (hrvRdRP) and which is operably linked to the cargo RNA molecule flanked by HRV 5' RR and HRV 3' RR. Embodiments where the HRV sgp and cargo RNA are in sense or antisense orientation relative to the endornavirus 5' RRE are shown. The HRV 5' RR and 3' RR which flank the cargo RNA provide for hrvRdRP-mediated replication of an RNA comprising from 5' to 3' the HRV 5' RR, cargo RNA, and HRV 3' RR. In certain embodiments, the HRV 5' RR and 3' RR are flanked by ribozymes.

[0019] Figure 6 depicts a commensal satellite with a cargo RNA molecule including an HRV ("HRV1", e.g., tobacco mosaic virus, TMV) amplicon designed to be amplified by the HRV ("HRV1", e.g., TMV) RdRP binding to either the replication regions or to the subgenomic promoter, where the commensal satellite is an endornavirus satellite. The resulting transcripts include RNA encoding the HRV RdRP ("HRV1 RdRP", solid squares), which can further amplify the HRV amplicon, as well as RNA encoding another cargo (solid circles). In the absence of the commensal virus, no amplification of the commensal satellite occurs.

[0020] Figure 7 depicts a commensal satellite with a cargo RNA molecule including an HRV (HRV1, e.g., tobacco mosaic virus, TMV) amplicon designed to be amplified by the HRV RdRP ("HRV1 RdRP", solid squares) binding to the HRV1 replication regions, where the commensal satellite is an endornavirus satellite. The resulting transcripts include RNA encoding the HRV (HRV1) RdRP which can further amplify the HRV amplicon. The HRV1 amplicon includes sequence for a HRV2 amplicon (indicated in italicized text), encoding a coding and/or noncoding cargo (solid circles) and designed to be amplified in the presence of a second acute viral RdRP ("HRV2 RdRP", hexagonal symbol), which can be provided, e.g., by introduction of a second acute virus ("HRV2", e.g., cowpea mosaic virus, CPMV) into the plant. In the absence of the commensal virus, no amplification of the commensal satellite occurs

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[0021] Figure 8 depicts a commensal satellite with a cargo RNA molecule including an HRV ("HRV1", e.g., tobacco mosaic virus, TMV) amplicon designed to be amplified by the HRV ("HRV1", e.g., TMV) RdRP binding to either of two subgenomic promoters, where the commensal satellite is an endornavirus satellite. The resulting transcripts include RNA encoding the HRV RdRP ("HRV1 RdRP", solid squares), which can further amplify the HRV amplicon, as well as RNA encoding a noncoding RNAi cargo, the sense and antisense strands of which are formed during the amplification process to yield a double-stranded RNA molecule (dsRNA) for silencing of a target gene. In the absence of the commensal virus, no amplification of the commensal satellite occurs.

DETAILED DESCRIPTION

Definitions

[0022] The term "and/or" where used herein is to be taken as specific disclosure of each of the two specified features or components with or without the other. Thus, the term "and/or" as used in a phrase such as "A and/or B" herein is intended to include "A and B," "A or B," "A" (alone), and "B" (alone). Likewise, the term and/or as used in a phrase such as "A, B, and/or C" is intended to encompass each of the following embodiments: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

[0023] As used herein, the terms "F₁," "F₂," and the like refer to filial generations of plants or seed obtained from a parent plant which has been selfed or that has been crossed to another plant.

[0024] As used herein, the term "heterologous", when used to describe a first element in reference to a second element means that the first element and second element do not exist in nature disposed as described. For example, a heterologous nucleic acid molecule or sequence is a nucleic acid molecule or sequence that (a) is not native to a cell in which it is expressed, (b) is linked or fused to a nucleic acid molecule or sequence with which it is not linked to or fused to in nature, or with which it is not linked to or fused to in nature in the same way, (c) has been altered or mutated by the hand of man relative to its native state, or (d) has altered expression as compared to its native expression levels under similar conditions. For example, a "heterologous promoter" is used to drive transcription of a sequence that is not one that is natively transcribed by that promoter (*e.g.*, a eukaryote promoter used to drive transcription of a DNA molecule encoding an endornavirus RNA sequence); thus, a "heterologous promoter" sequence can be included in an expression construct by a recombinant nucleic acid technique. In embodiments, a recombinant polynucleotide such as those provided by this disclosure includes genetic sequences of two or more different endornaviruses, which genetic sequences are "heterologous" in that they would not naturally occur together. In some embodiments "heterologous" refers to a molecule or to a discrete part of a molecule; for example, referring to a cargo RNA molecule (*e.g.*, a nucleic acid such as a protein-encoding RNA, an ssRNA, a regulatory RNA, an interfering RNA, or a guide RNA), which can be part of a larger molecule, or referring to a structure (*e.g.*, structures including a promoter (*e.g.*, for a DNA dependent RNA polymerase) or subgenomic promoter (*e.g.*, for an RNA-dependent RNA polymerase), an RNA effector, RNA cleavage agent recognition site, or a polynucleotide comprising or

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encoding an expression-enhancing element, encapsidation recognition element (ERE), selectable or scoreable marker, DNA aptamer, RNA aptamer; a transcription factor binding site, internal ribosome entry site (IRES), DNA spacer, an RNA cleavage agent recognition site, tRNA-like element, or a transcript-stabilizing or transcript-destabilizing RNA sequence) that is not found naturally in a plant endornavirus.

[0025] As used herein, the terms “include,” “includes,” and “including” are to be construed as at least having the features to which they refer while not excluding any additional unspecified features. The terms “comprise,” “comprises,” and “comprising” mean “include,” “includes,” and “including”, respectively.

[0026] As used herein, the term “internal ribosome entry site” or “IRES” refers to a sequence (*e.g.*, an RNA sequence) capable of recruiting a ribosome and translation machinery to initiate translation from an RNA sequence. An IRES element is generally between 100-800 nucleotides. An appropriate IRES can be obtained from plant and plant viral IRES sequences such as encephalomyocarditis virus IRES (ECMV), maize hsp101 IRES 5'UTR, crucifer infecting tobamovirus crTMV CR-CP 148 IRES, tobacco etch virus (TEV) IRES 5'UTR and hibiscus chlorotic ringspot virus (HCRSV) IRES. In addition, in embodiments, an IRES sequence is derived from non-plant eukaryotic virus sequences that include but are not limited to: acute bee paralysis virus (ABPV), classical swine fever virus (CSFV), coxsackievirus B3 virus (CVB3), encephalomyocarditis virus (ECMV), enterovirus 71 (E71), hepatitis A virus (HAV), human rhinovirus (HRV2), human rhinovirus (HRV2), human lymphotropic virus (HTLV), polyoma virus (PV), and *Zea mays* (ZmHSP101). Examples of IRES sequences useful in the compositions and methods described herein are shown in Table 5.

[0027] As used herein, the phrase “operably linked” refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. For instance, a promoter is operably linked to a coding sequence if the promoter provides for transcription or expression of the coding sequence.

[0028] As used herein the term “percent identity” refers to percent (%) sequence identity with respect to a reference polynucleotide or polypeptide sequence following alignment by standard techniques. Alignment for purposes of determining percent nucleic acid or amino acid sequence identity can be achieved in various ways that are within the capabilities of one of skill in the art, for example, using publicly available computer software such as BLAST, BLAST-2, PSI-BLAST, or Megalign software. In some embodiments, the software is MUSCLE (Edgar, *Nucleic Acids Res.*, 32(5): 1792-1797, 2004). Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For example, in embodiments, percent sequence identity values are generated using the sequence comparison computer program BLAST (Altschul *et al.* (1990) *J. Mol. Biol.*, 215:403-410). As an illustration, the percent sequence identity of a given nucleic acid or amino acid sequence, A, to, with, or against a given nucleic acid or amino acid sequence, B, (which can alternatively be phrased as a given

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nucleic acid or amino acid sequence, A that has a certain percent sequence identity to, with, or against a given nucleic acid or amino acid sequence, B) is calculated as follows: 100 multiplied by (the fraction X/Y), where X is the number of nucleotides or amino acids scored as identical matches by a sequence alignment program (*e.g.*, BLAST) in that program's alignment of A and B, and where Y is the total number of nucleotides or amino acids in B.

[0029] As used herein, the term “plant” includes a whole plant and any descendant, cell, tissue, or part of a plant. The term “plant parts” include any part(s) of a plant, including, for example and without limitation: seed (including mature seed and immature seed); a plant cutting; a plant cell; a plant cell culture; or a plant organ (*e.g.*, pollen, mature or immature embryos, flowers, fruits, shoots, leaves, roots, stems, and explants). In embodiments, a plant tissue or plant organ is or includes a seed, protoplast, callus, or any other group of plant cells that is organized into a structural or functional unit. In embodiments, a plant cell or tissue culture is capable of regenerating a plant having the physiological and morphological characteristics of the plant from which the cell or tissue was obtained, and of regenerating a plant having substantially the same genotype as the plant. Regenerable cells in a plant cell or tissue culture can include embryos, protoplasts, meristematic cells, callus, pollen, leaves, anthers, roots, root tips, flowers, and/or stalks. In contrast, some plant cells are not capable of being regenerated to produce plants and are referred to herein as “non-regenerable” plant cells.

[0030] As used herein, the term “transcriptome” refers to the sum total of all RNA molecules expressed in a cell. Such RNA molecules include mRNAs, tRNAs, ribosomal RNAs, miRNAs, viral RNAs (both genomic and sub-genomic), and long non-coding RNAs.

[0031] To the extent to which any of the preceding definitions is inconsistent with definitions provided in any patent or non-patent reference incorporated herein by reference, any patent or non-patent reference cited herein, or in any patent or non-patent reference found elsewhere, it is understood that the preceding definition will be used herein.

[0032] Unless otherwise stated, nucleic acid sequences described herein are given, when read from left to right, in the 5' to 3' direction. Nucleic acid sequences may be provided as DNA or as RNA, as specified. Furthermore, because of known codon degeneracy, different nucleic acid sequences can encode the same polypeptide sequence, and such modified nucleic acid sequences (*e.g.*, for the purposes of codon optimization for a given species) are within the scope of the present disclosure. Where a term is provided in the singular, it also contemplates aspects of the invention described by the plural of that term.

[0033] This disclosure provides, *inter alia*, recombinant polynucleotides (*e.g.*, recombinant DNA, recombinant RNA, recombinant ssRNAs, recombinant dsRNAs, recombinant vectors, etc.) including one or more sequences of or derived from an endornavirus (EV); in particular, a 5' or 3' RNA replication element that is recognized by an endornavirus RNA-dependent RNA polymerase (RdRP). This disclosure is further related to methods of making and using such recombinant polynucleotides, for example, by employing such recombinant polynucleotides to express a heterologous cargo sequence in a plant and optionally thereby modifying expression of an endogenous target sequence and/or genotype or phenotype

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of the plant. In embodiments, the endornavirus is a commensal endornavirus, that is, an endornavirus that is endemic or native to a given eukaryote host (such as a host plant) without causing apparent negative effects on the host (*i.e.*, is considered non-pathogenic), is often present at a persistent but low population (*i.e.*, low viral titer), and is often vertically transmitted to succeeding generations of the host.

[0034] In one aspect, this disclosure is related to a recombinant DNA molecule that includes a promoter that is functional in a cell and is operably linked to a DNA sequence encoding an RNA molecule. The RNA molecule includes, in 5' to 3' order: (a) a 5' RNA replication element that is capable of being recognized by an endornavirus RNA-dependent RNA polymerase (RdRP); (b) a cargo RNA sequence; and (c) a 3' RNA replication element that is capable of being recognized by the endornavirus RdRP. Figure 1 shows an embodiment of a generalized structure of a DNA polynucleotide encoding an endornavirus satellite, where in certain embodiments the 5' RNA replication element corresponds to the 5' untranslated region (UTR) of an endornavirus and where the 3' RNA replication element corresponds to the 3' untranslated region (UTR) of an endornavirus. In some embodiments, the 5' RNA replication element and/or the 3' RNA replication element include nucleotides that extend into the predicted coding sequence or open reading frame of the endornavirus.

[0035] Recombinant DNA molecules provided herein can include a promoter that is functional in a cell (*e.g.*, a bacterial cell, a plant cell, a fungal cell, or an animal cell) and is operably linked to a DNA sequence encoding an RNA molecule (*e.g.* a 5' RNA replication element, a cargo RNA sequence; and a 3' RNA replication element; a ribozyme, an intron, or a RNA encoding a protein (*e.g.*, a capsid, movement, RdRP, or an RdRP protein that recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter).

[0036] In embodiments, a promoter functional in a plant cell provides for systemic gene expression, or alternatively for cell-, tissue-, or organ-specific gene expression, or expression that is inducible by external signals or agents (for example, light-, pathogen-, wound-, stress-, or hormone-inducible elements, or chemical inducers) or elements that are capable of cell-cycle regulated gene transcription; such elements may be located in the 5' or 3' regions of the native gene or engineered into a polynucleotide.

[0037] Promoters include those from viruses, bacteria, fungi, animals, and plants. Suitable promoters can be used to drive expression by any RNA polymerase (*e.g.*, RNA pol I, pol II, or pol III). Embodiments of promoters include those from cauliflower mosaic virus (*e.g.*, p35S), bacteriophage (*e.g.*, pT7), and plants (*e.g.*, pATUBQ10). In certain embodiments, the promoter is operably linked to nucleotide sequences encoding multiple guide RNAs, wherein the sequences encoding guide RNAs are separated by a cleavage site such as a nucleotide sequence encoding a microRNA recognition/cleavage site or a self-cleaving ribozyme (see, *e.g.*, Ferré-D'Amaré and Scott (2010) Cold Spring Harbor Perspectives Biol., 2:a003574). In certain embodiments, the promoter is a pol II promoter operably linked to a nucleotide sequence encoding the RNA. In certain embodiments, the promoter operably linked to one or more polynucleotides encoding elements of a genome-editing system is a constitutive promoter that

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drives DNA expression in plant cells. In certain embodiments, the promoter drives DNA expression in the nucleus or in an organelle such as a chloroplast or mitochondrion. Examples of constitutive promoters active in plant cells include a CaMV 35S promoter as disclosed in U.S. Pat. Nos. 5,858,742 and 5,322,938, a rice actin promoter as disclosed in U.S. Pat. No. 5,641,876, a maize chloroplast aldolase promoter as disclosed in U.S. Pat. No. 7,151,204, and a nopaline synthase (NOS) and octopine synthase (OCS) promoter from *Agrobacterium tumefaciens*. In certain embodiments, the promoter operably linked to one or more polynucleotides encoding elements of a genome-editing system is a promoter from figwort mosaic virus (FMV), a RUBISCO promoter, or a pyruvate phosphate dikinase (PDK) promoter, which is active in the chloroplasts of mesophyll cells. In some embodiments, the promoter is heterologous to the cell it is functional in and/or to the other elements to which the promoter is operably linked. All of the patent publications referenced in this paragraph are incorporated herein by reference in their entirety.

[0038] Embodiments of recombinant polynucleotides provided herein comprise or encode RNA molecules containing 5' and 3' RNA replication elements recognized by an endornavirus RNA-dependent RNA polymerase (RdRP). In certain embodiments, recognition by an endornavirus RdRP is identified in an in vitro RdRP assay (*e.g.*, an assay adapted from Horiuchi et al. *Plant Cell Physiol.* 42(2):197-203, 2001). In certain embodiments, recognition by an endornavirus RdRP is identified by an in vivo RdRP assay wherein an RNA comprising 5' and 3' RNA replication elements is introduced into a cell comprising the RdRP, and replication of the RNA is assayed (*e.g.*, by an RT-PCR assay or an assay for a reporter gene encoded by a cargo RNA located in the RNA comprising 5' and 3' RNA replication elements). In certain embodiments, cells comprising the RdRP are engineered by introducing a gene or RNA molecule encoding the RdRP into the cell. In other embodiments, the cell comprising the RdRP is a cell which contains an endornavirus which expresses the RdRP; in such embodiments the endornavirus can be one that is native to or is known to naturally occur in the cell, or it can be a non-native endornavirus. Alternatively, a recombinant virus of any suitable viral family can be engineered to express the endornavirus RdRP. In certain embodiments, the recombinant polynucleotides (*e.g.*, recombinant DNAs or recombinant RNAs) comprise a 5' RNA replication element and a 3' RNA replication element obtained from the same endornavirus genome or from endornavirus genomes having at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another and which are optionally related. In embodiments, the endornavirus genomes having at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another are taxonomically related, *e.g.*, genomes classified as belonging to the same genus, family, and/or order. In certain embodiments, the recombinant polynucleotides (*e.g.*, recombinant DNAs or recombinant RNAs) comprise a 5' RNA replication element, a 3' RNA replication element, and an RdRP are obtained from the same endornavirus genome or from endornavirus genomes having at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another and which are optionally taxonomically related, *e.g.*, genomes classified as belonging to the same genus, family, and/or order. Non-limiting examples of a 5' RNA replication element and a 3' RNA replication element from the same endornavirus

genome include those set forth in each row of Table 18. Non-limiting examples of a 5' RNA replication element and a 3' RNA replication element from the same endornavirus RdRP genome and the corresponding RdRP protein that recognizes that 5' RNA replication element and 3' RNA replication element include those set forth in each row of Table 18. The RdRPs set forth in Table 17 also recognize the corresponding 5' RNA replication element and a 3' RNA replication element from the endornavirus genome corresponding to the same endornavirus (*i.e.*, an endornavirus having the genome of Table 1 or Table 18). In certain embodiments, the recombinant polynucleotides (*e.g.*, recombinant DNAs or recombinant RNAs) comprise a 5' RNA replication element, a 3' RNA replication element, and/or an RdRP coding region are obtained from two endornavirus genomes wherein the members of each pair of the 5' RNA replication elements, 3' RNA replication elements, and RdRP coding regions of the two endornavirus genomes have at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another. In certain embodiments, the recombinant polynucleotides (*e.g.*, recombinant DNAs or recombinant RNAs) comprise a 5' RNA replication element and a 3' RNA replication element obtained from distinct endornavirus genomes. In certain embodiments, the recombinant polynucleotides (*e.g.*, recombinant DNAs or recombinant RNAs) comprise a 5' RNA replication element, a 3' RNA replication element, and an RdRP are obtained from distinct endornavirus genomes. In certain embodiments, the distinct endornavirus genomes will have less than 85%, 80%, 75%, or 70% sequence identity to one another. In certain embodiments, the distinct endornavirus genomes will have 50%, 60%, or 65% to any one of 70%, 75%, 80%, or 84% sequence identity to one another.

[0039] In certain embodiments, the combination of 5' RNA replication elements, 3' RNA replication elements, and RdRP set forth in a single row of Table 18, or variants thereof having at least 85%, 90%, 95%, 98%, or 99% sequence identity to the 5' RNA replication element, 3' RNA replication elements, and RdRP, or variants thereof wherein the secondary structures of the RNA replication elements are conserved, are used together in an expression system, plant cell, plant propagule, plant, or method provided herein. In certain embodiments, the 5' RNA replication elements and 3' RNA replication elements in a given row of Table 18 or variants thereof are operably linked to a cargo RNA and replicated by the corresponding RdRP or variant thereof in the row. In certain embodiments, the combination of 5' RNA replication elements, 3' RNA replication elements, and RdRP set forth in any one of the rows of Table 18 or aforementioned or otherwise disclosed variants thereof are used in a dicot plant cell-based expression system, dicot plant cell, dicot plant propagule, dicot plant, or related dicot plant-based method provided herein. In certain embodiments, the aforementioned dicot is a member of the genus *Brassica*, *Capsicum*, *Citrus*, *Cucumis*, *Cucurbita*, *Gossypium*, *Helianthus*, *Nicotiana*, *Phaseolus*, *Solanum*, *Vicia*, *Vitis*, or *Glycine*. In certain embodiments, the combination of 5' RNA replication elements, 3' RNA replication elements, and RdRP set forth in a row of Table 18 or aforementioned or otherwise disclosed variants thereof are used in a monocot plant cell-based expression system, monocot plant cell, monocot plant propagule, monocot plant, or related monocot plant-based

method provided herein. In certain embodiments, the aforementioned monocot is a member of the genus *Avena*, *Hordeum*, *Oryza*, *Secale*, *Triticum*, *Sorghum*, or *Zea*.

[0040] Examples of DNA molecules which encode RNA molecules comprising or containing 5' and 3' RNA replication elements recognized by an endornavirus RdRP are set forth in Table 1. DNA molecules which encode RNAs comprising or containing 5' RNA replication elements recognized by an endornavirus RdRP include SEQ ID NOs: 466 to 522, 727, or 924 to 1017 (**EV** genome 5' UTRs). DNA molecules which encode RNAs comprising or containing 3' RNA replication elements recognized by an endornavirus RdRP include SEQ ID NOs: 523 to 595, 728, or 1019 to 1129 (EV genome 3' UTRs).

[0041] Structural features (e.g., dsRNA hairpins and ssRNA loops) identified in endornavirus 5' and 3' RNA replication elements are shown in **Tables 19 to 25** by way of dot bracket notation. The dot bracket notation provided in **Tables 19 to 25** was generated using RNA Fold software for predicting RNA secondary structure based on minimum free energy predictions of base pair probabilities. A dot '.' signifies an unpaired base and a bracket '(' or ')' represents a paired base. Dot bracket notation is further described in Mattei et al., *Nucleic Acids Research*, 42(10): 6146-6157, 2014; Ramlan and Zauner In International Workshop on Computing With Biomolecules, E. Csuhaj-Varju, R. Freund, M. Oswald and K. Salomaa (Eds.), 27 August 2008, Wien, Austria, pp. 75-86, From: Austrian Computer Society, 2008; and Hofacker et al., *Monatshefte für Chemie Chem. Monthly*, 125: 167-188, 1994. Such structural features can range in size from 20, 30, or 40 to about 500 nucleotides (nt). These structural features are useful for designing engineered polynucleotide sequences that function as endornavirus RNA replication elements and/or for constructing variants of the sequences set forth in **SEQ ID NO: 466 to 595, 727, 728, and 924 to 1129** that function as 5' and 3' RNA replication elements. In certain embodiments, one or more residues in the RNA secondary structure set forth in **Tables 19 to 25** or in equivalent RNAs are substituted with distinct nucleotides which maintain the RNA secondary structure (e.g., presence or absence of base pairing). In certain embodiments the RNA secondary structure set forth in **Tables 19 to 25** or in equivalent RNAs, the RNA secondary structure is maintained by making substitutions in the nucleotide sequence that result in no changes in the position of base-paired nucleotides or non-base-paired nucleotides. In certain embodiments the RNA secondary structure set forth in **Table 19 to 25** or in equivalent RNAs is maintained by substituting nucleotides in the secondary structure which are not base paired with nucleotides which will not base pair, and/or by substituting nucleotides in the secondary structure which are base paired with nucleotides which will base pair. In this context, it is understood that, in some embodiments, maintaining the RNA secondary structure need not be absolute (e.g., the structure is partially maintained). In certain embodiments, a dsRNA structure is partially maintained when one, two, three or more nucleotides, particularly at the 5' end and/or 3' end of a hairpin-forming structure are substituted with nucleotides which do not base pair and thus reduce the total length of dsRNA in the structure. In certain embodiments, an unpaired RNA structure is partially maintained when one, two, three or more nucleotides, particularly at the 5' end and/or 3' end of a loop structure are substituted with nucleotides which base pair and thus reduce the total length of ssRNA in the loop

structure. The ability of such partially maintained secondary structures to be recognized by the corresponding endornavirus RdRP is monitored by in vitro or in vivo assays. Embodiments of endornavirus satellite RNAs include those where the 5' RNA replication element includes one or more of these 5' structural features and/or wherein the 3' RNA replication element includes one or more of these 3' structural features. In certain embodiments, the 5' RNA replication elements comprise an RNA encoded by a DNA having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or 100% sequence identity to **SEQ ID NO: 466 to 522, 727, or 924 to 1017** optionally wherein the encoded RNA maintains or partially maintains a corresponding structural feature set forth in Table 19 to 25. In certain embodiments, the 3' RNA replication elements comprise an RNA encoded by a DNA having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or 100% sequence identity to **SEQ ID NO: 523 to 595, 728, or 1019 to 1129**, wherein the encoded RNA optionally maintains or partially maintains a corresponding structural feature set forth in **Table 19 to 25**.

[0042] Recombinant polynucleotides (*e.g.*, recombinant DNA, recombinant RNA, recombinant ssRNAs, recombinant dsRNAs, recombinant vectors, etc.) provided herein can also comprise or encode additional RNA elements.

[0043] Embodiments of additional RNA elements include RNAs encoding an endornavirus RdRP. Examples of DNA sequences encoding endornavirus RdRP include the corresponding sequences of **EV** genomes set forth in Table 1 under descriptors "NC_XXXXXX" which refer to the National Center for Biotechnology Information database accession number for entries in the world wide web internet database "ncbi[dot]nlm[dot]nih.gov/nuccore". Examples of DNA sequences encoding endornavirus RdRP also include the sequences set forth in Table 17 as well as DNA sequences having at least 85%, 90%, 95%, 98%, or 99% identity thereto. Examples of DNA sequences encoding endornavirus RdRP also include the sequence of the DNA encoding the EV RdRP disclosed in **SEQ ID NO: 632 to 681 and 1130 to 1260** as well as DNA sequences having at least 85%, 90%, 95%, 98%, or 99% identity thereto. Examples of DNA sequences encoding endornavirus RdRP and endornavirus RdRP protein sequences also include the DNA and amino acid sequences set forth in Table 17 as well as the DNA and protein sequences having at least 85%, 90%, 95%, 98%, or 99% identity thereto. RNA molecules which encode the RdRP amino sequences of Table 17 and protein sequences having at least 85%, 90%, 95%, 98%, or 99% identity thereto are also provided by this disclosure.

[0044] Embodiments of additional RNA elements include RNAs encoding a viral movement protein (MP). In certain embodiments, the cargo RNA comprises an RNA encoding a viral MP. Without being bound to hypothesis or theory, the viral movement protein is believed to bind to the RNA and to assist its movement (and thus the movement of the cargo RNA) throughout the plant, *e.g.*, via the plasmodesmata. Viral MPs include movement proteins identified from tobacco mosaic virus (TMV), cowpea mosaic virus, potato leafroll virus, tomato spotted wilt virus, and tomato mosaic virus. MPs from a variety of viruses are described in **Table 3**.

[0045] Embodiments of additional RNA elements include tRNA-like sequences (TLS). TLS can trigger mobility of otherwise nonmobile RNAs, assisting to increase systemic delivery of the RNA molecule. TLS include tRNAs and tRNA-like sequences identified from other genetic elements, *e.g.*, mRNAs. An isoleucine tRNA encoded by residues 2431-2512 of SEQ ID NO: 630 is an example of a useful tRNA-like sequence. Other mobile RNAs including TLS identified in *Arabidopsis* which are useful for building polynucleotides are described in **Table 4**. In assembling Table 4, mobile mRNA sequences were downloaded from the PLAMOM database for *Arabidopsis*. The tRNA “seed alignment” from the RFAM database was downloaded in stockholm format (multiple sequence alignment + secondary structure). A covariance model was created with INFERNAL for the tRNA stockholm alignment. PLAMOM mRNA sequences were scanned for significant similarity to tRNAs based on primary and secondary structure features. mRNA sequences with significant hits ($E\text{-val} < 1$) were then saved to a fasta file. In one embodiment, such a tRNA-like sequence includes a tRNA-like sequence from an *Arabidopsis* Flowering Time T (FT) mRNA. In some embodiments, the RNA molecule includes at least one RNA encoding a viral MP, a tRNA-like sequence from an *Arabidopsis* FT mRNA, and an encapsidation recognition element (ERE) comprising TMV-OAS. In some embodiments, the RNA molecule includes a tRNA-like sequence encoded by a DNA sequence selected from the group consisting of SEQ ID NOs: 76-123 and 790 (*e.g.*, isoleucine tRNA encoded by residues 2431-2512 of SEQ ID NO: 630). In some embodiments, the RNA molecule includes a modified tRNA-like sequence that has at least 90%, 95%, 98%, or 99% sequence identity to a scaffold tRNA-like sequence encoded by a DNA sequence selected from the group consisting of SEQ ID NOs: 76-123 and 790, and that maintains the secondary structure of the scaffold tRNA-like sequence.

[0046] Embodiments of additional RNA elements include RNAs encoding a viral capsid protein (CP). Such capsid proteins are also sometimes referred to as coat proteins, with both capsid and coat proteins being referred to as “CP.” In embodiments where a CP is provided, the capsid protein is heterologous to the endornavirus. In certain embodiments, the cargo RNA comprises an RNA encoding a viral CP. CP can be provided, *e.g.*, by co-expression of a recombinant construct encoding the CP or by native expression by a virus endogenous to or introduced into a plant cell. Encapsidation of an RNA molecule by the CP is achieved provided it contains an encapsidation recognition element (ERE), *e.g.*, an origin of assembly sequence (OAS). **Table 2** describes several OAS and CP sequences from a variety of viruses useful in engineering constructs which provide for RNA encapsidation. In embodiments, the OAS is positioned near the 3' end of a construct, *e.g.*, within the 3' region of a cargo RNA or 3' to a cargo RNA. For example, in some embodiments, the OAS is found 5' to the 3' RNA replication elements (*e.g.*, the 3' RNA replication elements set forth in Table 1). In embodiments, a TMV-OAS positioned at the 3' end of the RNA molecule is recognized by the TMV capsid protein, leading to assembly of a TMV virion around the RNA.

[0047] Embodiments wherein the recombinant RNAs are complexed with RNA binding proteins (RBPs) are also provided herein. Embodiments of RBPs include RNA recognition motifs (RRMs) such

as: (i) Lys/Arg-Gly-Phe/Tyr-Gly/Ala-Phe/Tyr-Val/Ile/Leu-X-Phe/Tyr, where X can be any amino acid (SEQ ID NO: 464); (ii) Ile/Val/Leu-Phe/Tyr-Ile/Val/Leu-X-Asn-Leu, where X can be any amino acid (SEQ ID NO: 465). Such RBP and RRM include those disclosed in Maris et al. 2005, doi.org/10.1111/j.1742-4658.2005.04653.x.

[0048] Embodiments of additional RNA elements include at least one ribozyme. Ribozymes include self-cleaving ribozyme, a ligand-responsive ribozyme (aptazyme), a trans-cleaving ribozyme designed to cleave a target sequence (e.g., a trans-cleaving hammerhead ribozyme designed to cleave the pepper phytoene desaturase (PDS) sequence (e.g., the RNA encoded by SEQ ID NO: 421), a hepatitis delta virus (HDV) ribozyme (e.g., the RNA encoded by SEQ ID NO: 423), or a hammerhead ribozyme (e.g., the RNA encoded by SEQ ID NO: 420). In various embodiments, multiple ribozymes are included in a polynucleotide. Useful ribozymes include Twister, Hammerhead, Hairpin, and other ribozymes. Non-limiting examples of useful ribozymes include those provided in Table 14. In certain embodiments, such a ribozyme (e.g., a self-cleaving ribozyme) is located 5' to the 5' RNA replication element and/or 3' to the 3' RNA replication element in the recombinant RNA. In certain embodiments, such a ribozyme (e.g., a self-cleaving ribozyme) is located 5' to the HRV 5' RNA replication region and/or 3' to the HRV 3' RNA replication region in a recombinant RNA comprising an imbedded heterologous RNA virus (HRV) amplicon.

[0049] Embodiments of additional RNA elements include intronic sequences. Examples of intronic sequences that can be included in the recombinant polynucleotides provided herein are described in **Table 6**. In certain embodiments, intronic sequences are placed in a 5'UTR downstream of a promoter (e.g., a promoter active in plant cells) used to drive expression of a recombinant RNA. In certain embodiments, intronic sequences are placed 5' to a 5' RNA replication element, in a cargo RNA, or 3' to a 3' RNA replication element.

[0050] Embodiments of recombinant polynucleotides and additional RNA elements include subgenomic promoters recognized by an RNA-dependent RNA polymerase (RdRP) and/or RNA molecules encoding an RNA-dependent RNA polymerase (RdRP). Examples of such subgenomic promoters and RdRP include a Brome Mosaic Virus subgenomic promoter and RdRP (Siegal et al. 1998, doi: 10.1073/pnas.95.20.11613), barley yellow dwarf virus (BYDV) sgRNA1, sgRNA2, and sgRNA3 subgenomic promoters and RdRP (Koev and Miller; J Virol. 2000 Jul;74(13):5988-96. doi: 10.1128/jvi.74.13.5988-5996.2000), *Alternanthera* mosaic virus (AltMV-MU) sgp1, sgp2, and sgp3 subgenomic promoters and RdRP (Putlyaev et al., Biochemistry (Mosc.);80(8):1039-46DOI: 10.1134/S000629791508009X). Additional examples of subgenomic promoters are provided in Table 16. In certain embodiments, such subgenomic promoters are placed either 5' and/or 3' to an RNA molecule comprising a 5' RNA replication element, a cargo RNA, and a 3' RNA replication element to permit production of either or both + and – strands of the RNA molecule when the RdRP is provided. In certain embodiments, such subgenomic promoters are operably linked to a cargo RNA molecule and/or to any additional RNA element to permit production of the corresponding cargo and/or additional RNA

when the RdRP is provided. In certain embodiments, the subgenomic promoters are operably linked to a cargo RNA comprising an HRV-inhibitory RNA or to a cargo RNA that encodes a protein which inhibits infection, movement, transmission, and/or replication of the HRV. In certain embodiments, the subgenomic promoters are operably linked to a cargo RNA comprising an RNA having at least 20 (e.g., 20, 21, 22, 23, 24, or 25) contiguous nucleotides having an identical or complementary sequence to a segment of equivalent length of the genomic RNA of the HRV. In certain embodiments, the subgenomic promoters are operably linked to a cargo RNA comprising an RNA having at least 20 (e.g., 20, 21, 22, 23, 24, or 25) contiguous nucleotides having an identical or complementary sequence to a segment of equivalent length of the genomic RNA of the HRV which does not encode the hrvRdRP.

[0051] Embodiments of other optional elements in the recombinant polynucleotides provided herein include: a) a discrete expression cassette including a second promoter operably linked to a DNA sequence to be transcribed, and optionally a terminator element (see, e.g., a NOS or CaMV35S terminator); (b) an expression-enhancing element (e.g., a DNA encoding an expression-enhancing intronic sequence); (c) a DNA or RNA sequence encoding a marker (e.g., a selectable marker such as DNA or RNA encoding an antibiotic resistance or herbicide resistance sequence; DNA encoding a scorable marker or detectable label (e.g., a beta-glucuronidase, fluorescent protein, luciferase, etc.); (d) a DNA aptamer; (e) a DNA or RNA sequence encoding an RNA aptamer; (f) T-DNA left and right border DNA sequences; (g) a spacer DNA sequence; (h) a DNA sequence encoding a transcription factor binding site; (i) a DNA sequence encoding a localization sequence (e.g., DNA encoding a targeting peptide, such as a nuclear localization signal (NLS), a mitochondrial localization signal, or a plastid localization signal); or (j) a DNA sequence encoding at least one sequence-specific recombinase recognition site (SSRRS: e.g., a pair of sequence-specific recombinase recognition sites that are recognized by a given recombinase, such as LOX sites recognized by a CRE recombinase); and (k) a DNA sequence encoding a transcript-stabilizing or transcript-destabilizing sequence (see, e.g., US Published Patent Application 2007/0011761, incorporated herein by reference in its entirety; Geisberg et al. (2014) *Cell*, 156: 812-824).

[0052] Provided herein are recombinant polynucleotides comprising a cargo RNA molecule or comprising DNA encoding a cargo RNA molecule. In some embodiments, the recombinant polynucleotide includes a single cargo RNA molecule. In other embodiments, the recombinant polynucleotide includes at least two cargo RNA molecules, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, or more than 10 cargo RNA molecules; in embodiments, the at least two cargo RNA molecules are the same (e.g., multiple copies of a non-coding RNA sequence or multiple copies of a RNA sequence encoding a polypeptide) or are different (e.g., two or more different non-coding RNA sequences, or two or more different coding RNA sequences, or combinations of non-coding and coding cargo RNA sequences).

[0053] In certain embodiments, a cargo RNA molecule is up to about 14, 15, 16, or 17 kilobases (kb) in length. Cargo RNA molecules can range in length from any one of about 20 nucleotides (nt), 100nt, 200nt, 300nt, 400nt, 500nt, 600nt, 700nt, 800nt, or 900nt to any one of about 1kb, 2kb, 3kb, 4kb, 5kb,

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6kb, 7kb, 8kb, 9kb, 10kb, 11kb, 12kb, 13 kb, 14kb, 15kb, 16kb, or 17kb in length. Other lengths of the cargo RNA molecule are less than or equal to 100 nucleotides (nt) can range in length from any one of about 20nt, 30nt, or 40nt to any one of about 50nt, 60nt, 70nt, 80nt, 90nt, or 100nt in length.

Recombinant RNAs comprising a cargo RNA of up to about 14, 15, 16, or 17kb in length can in certain embodiments be encapsidated by a viral capsid protein. In such embodiments, cargo RNAs can range in length from any one of about 20nt, 100nt, 200nt, 300nt, 400nt, 500nt, 600nt, 700nt, 800nt, or 900nt to any one of about 1kb, 2kb, 3kb, 3.2kb, 4kb, 5kb, 6kb, 7kb, 8kb, 9kb, 10kb, 11kb, 12kb, 13kb, or 14 kb in length. Recombinant RNAs comprising a cargo RNA of up to about 3kb, 4kb, 5kb, 6kb, 7kb, 8kb, 9kb, 10kb, 11kb, 12kb, 13 kb, 14kb, 15kb, 16kb, or 17kb in length can in certain embodiments be encapsidated by a heterologous viral capsid protein set forth in Table 2. In certain embodiments, recombinant RNAs comprising a cargo RNA of up to about 14kb, 15kb, 16kb, or 17kb and encapsidated by a heterologous viral capsid protein can comprise an OAS element set forth in Table 2 and be encapsidated by a corresponding capsid protein set forth in Table 2. In some embodiments, the cargo RNA molecule is greater than 14kb, for example, 15kb, 16kb, 17kb, 18kb, 19kb, or even 20kb. In embodiments, the cargo RNA molecule includes: (a) at least one coding sequence, (b) at least one non-coding sequence, or (c) both at least one coding sequence and at least one non-coding sequence. Such cargo RNA molecules include combinations of coding/non-coding sequence; multiple non-coding/coding sequences; as well as aptamers, ribozymes, and other elements as is described herein. In embodiments, the cargo RNA molecule includes (a) a coding sequence to be expressed in a plant, and (b) at least one non-coding sequence that modifies expression or translation of the coding sequence, such as a recognition and cleavage sequence for an siRNA or miRNA that is endogenously expressed in the plant (see, e.g., US Patent Nos. 8,334,430, 9,139,838, 9,976,152, 10,793,869, 10,876,126) and can bind to and cleave an RNA transcript containing the recognition and cleavage sequence; in such embodiments, it is possible to achieve spatially or temporally or developmentally specific expression of the coding sequence in the plant. In embodiments, a coding or non-coding cargo RNA can be optimized for expression in plants by methods which include using codons which occur more frequently in plant genes and/or by eliminating polyadenylation sites in the cargo RNA (e.g., as described in at least US Pat. Nos. 5380831, 5689052, and 7741118, which are each incorporated herein by reference in their entireties).

[0054] In embodiments, the cargo RNA molecule includes at least one coding sequence (e.g., a translatable sequence). In some embodiments, the coding sequence is accordingly a protein or a polypeptide such as those described in this disclosure's working examples. In some embodiments, a cargo RNA comprises a selectable marker RNA encoding an antibiotic resistance or herbicide resistance polypeptide sequence or a scorable marker RNA encoding a scorable marker protein (e.g., a beta-glucuronidase, fluorescent protein, luciferase, etc.). Examples of selectable marker/selection agent combinations include glyphosate-resistant EPSPS enzymes and/or glyphosate oxidases/glyphosate, a bialaphos resistance (bar) or phosphinothricin acyl transferase (pat) enzyme/glufosinate, or a neomycin phosphotransferase (npt)/neomycin or kanamycin. Examples of scorable markers include β -glucuronidase

(GUS), luciferase, and fluorescent proteins such as green fluorescent protein (GFP), yellow fluorescent protein (YFP), and cyan fluorescent protein (CFP). In embodiments, the cargo RNA sequence encodes at least one protein or polypeptide that provides a desirable trait in a plant in which the protein or polypeptide is expressed. Non-limiting examples of polypeptides useful in agricultural applications include, for example, bacteriocins, lysins, antimicrobial peptides, nodule C-rich peptides, and bacteriocyte regulatory peptides. Such polypeptides can be used to alter the level, activity, or metabolism of target microorganisms for increasing the fitness of beneficial insects (such as honeybees and silkworms) or for decreasing the fitness of pest invertebrates (such as aphids, caterpillars, beetle larvae, and mites). Embodiments of agriculturally useful polypeptides include peptide toxins, such as those naturally produced by entomopathogenic bacteria (e.g., *Bacillus thuringiensis*, *Photorhabdus luminescens*, *Serratia entomophila*, or *Xenorhabdus nematophila*), as is known in the art. Embodiments of agriculturally useful polypeptides include polypeptides (including small peptides such as cyclodipeptides or diketopiperazines) for controlling agriculturally important pests or pathogens, e.g., antimicrobial polypeptides or antifungal polypeptides for controlling diseases in plants, or pesticidal polypeptides (e.g., insecticidal polypeptides and/or nematocidal polypeptides) for controlling invertebrate pests such as insects or nematodes. Embodiments of antimicrobial polypeptides include cathelicidins, cecropins, beta-defensins, amphibian antimicrobial peptides (e.g., aurein-like peptides, esculentin, gaegurin, brevinin, rugosin, ranatuerin, ranacyclin, uperin, ocellatin, grahamin, nigrocin, dermoseptin, temporin, bombinin, maximin), enterocins, ponicerins, megourins, apidaecins, abaecins, attacin, bacteriocins and lantibiotics, dermcidin, formaecin, halocidins, lactocin, tachystatins, and some insecticidal toxins produced by spiders and scorpions. Embodiments of agriculturally useful polypeptides include antibodies, nanobodies, and fragments thereof, e.g., antibody or nanobody fragments that retain at least some (e.g., at least 10%) of the specific binding activity of the intact antibody or nanobody. Embodiments of agriculturally useful polypeptides include transcription factors, e.g., plant transcription factors; see, e.g., the “AtTFDB” database listing the transcription factor families identified in the model plant *Arabidopsis thaliana*), publicly available at [agris-knowledgebase\[dot\]org/AtTFDB/](http://agris-knowledgebase[dot]org/AtTFDB/). Embodiments of agriculturally useful polypeptides include nucleases, for example, exonucleases or endonucleases (e.g., Cas nucleases such as Cas9 or Cas12a). Embodiments of agriculturally useful polypeptides further include cell-penetrating peptides, enzymes (e.g., amylases, cellulases, peptidases, lipases, chitinases), peptide pheromones (for example, yeast or fungal mating pheromones, invertebrate reproductive and larval signaling pheromones, see, e.g., Altstein (2004) *Peptides*, 25:1373–1376). Embodiments of agriculturally useful polypeptides confer a beneficial agronomic trait, e.g., herbicide tolerance, insect control, modified yield, increased fungal or oomycete disease resistance, increased virus resistance, increased nematode resistance, increased bacterial disease resistance, plant growth and development, modified starch production, modified oils production, high oil production, modified fatty acid content, high protein production, fruit ripening, enhanced animal and human nutrition, production of biopolymers, environmental stress resistance, pharmaceutical peptides

(e.g., hormones, enzymes, transcription factors, antigens, antibodies, or antibody fragments) and secretable peptides, improved processing traits, improved digestibility (e.g., reduced levels of toxins or reduced levels of compounds with “anti-nutritive” qualities such as lignins, lectins, and phytates), enzyme production, flavor, nitrogen fixation, hybrid seed production, fiber production, and biofuel production. Non-limiting examples of agriculturally useful polypeptides include polypeptides that confer herbicide resistance (US Patent Nos. 6,803,501; 6,448,476; 6,248,876; 6,225,114; 6,107,549; 5,866,775; 5,804,425; 5,633,435; and 5,463,175), increased yield (US Patent Nos. RE38,446; 6,716,474; 6,663,906; 6,476,295; 6,441,277; 6,423,828; 6,399,330; 6,372,211; 6,235,971; 6,222,098; and 5,716,837), insect control (US Patent Nos. 6,809,078; 6,713,063; 6,686,452; 6,657,046; 6,645,497; 6,642,030; 6,639,054; 6,620,988; 6,593,293; 6,555,655; 6,538,109; 6,537,756; 6,521,442; 6,501,009; 6,468,523; 6,326,351; 6,313,378; 6,284,949; 6,281,016; 6,248,536; 6,242,241; 6,221,649; 6,177,615; 6,156,573; 6,153,814; 6,110,464; 6,093,695; 6,063,756; 6,063,597; 6,023,013; 5,959,091; 5,942,664; 5,942,658; 5,880,275; 5,763,245; 5,763,241; 10,017,549; 10,233,217; 10,487,123; 10,494,408; 10,494,409; 10,611,806; 10,612,037; 10,669,317; 10,827,755; 11,254,950; 11,267,849; 11,130,965; 11,136,593; and 11,180,774), fungal disease resistance (US Patent Nos. 6,653,280; 6,573,361; 6,506,962; 6,316,407; 6,215,048; 5,516,671; 5,773,696; 6,121,436; 6,316,407; and 6,506,962), virus resistance (US Patent Nos. 6,617,496; 6,608,241; 6,015,940; 6,013,864; 5,850,023; and 5,304,730), nematode resistance (US Patent No. 6,228,992), bacterial disease resistance (US Patent No. 5,516,671), plant growth and development (US Patent Nos. 6,723,897 and 6,518,488), starch production (US Patent Nos. 6,538,181; 6,538,179; 6,538,178; 5,750,876; 6,476,295), modified oils production (US Patent Nos. 6,444,876; 6,426,447; and 6,380,462), high oil production (US Patent Nos. 6,495,739; 5,608,149; 6,483,008; and 6,476,295), modified fatty acid content (US Patent Nos. 6,828,475; 6,822,141; 6,770,465; 6,706,950; 6,660,849; 6,596,538; 6,589,767; 6,537,750; 6,489,461; and 6,459,018), high protein production (US Patent No. 6,380,466), fruit ripening (US Patent No. 5,512,466), enhanced animal and human nutrition (US Patent Nos. 6,723,837; 6,653,530; 6,5412,59; 5,985,605; and 6,171,640), biopolymers (US Patent Nos. RE37,543; 6,228,623; 5,958,745; and 6,946,588), environmental stress resistance (US Patent No. 6,072,103), pharmaceutical peptides (e.g., hormones, enzymes, transcription factors, antigens, antibodies, or antibody fragments) and secretable peptides (US Patent Nos. 6,812,379; 6,774,283; 6,140,075; and 6,080,560), improved processing traits (US Patent No. 6,476,295), improved digestibility (US Patent No. 6,531,648) low raffinose (US Patent No. 6,166,292), industrial enzyme production (US Patent No. 5,543,576), improved flavor (US Patent No. 6,011,199), nitrogen fixation (US Patent No. 5,229,114), hybrid seed production (US Patent No. 5,689,041), fiber production (US Patent Nos. 6,576,818; 6,271,443; 5,981,834; and 5,869,720) and biofuel production (US Patent No. 5,998,700). In certain embodiments, the cargo RNA encodes one or more small signaling peptides (SSPs), also called peptide hormones, which are an attractive option for use as cargoes in RNA commensal satellites due to their small size (5-75 amino acids) and potency. In certain embodiments, SSPs result from processing longer precursor polypeptides (derived from ORF regions). In other embodiments, SSPs originate from a wider

range of sources including intergenic/intronic regions, long non-coding RNAs, pri-miRNAs, and 5' and 3' UTRs of mRNAs. Non-limiting examples of SSPs include miPEP172c, miPEP171d, BomiPEP397a, AtmiPEP397a, BvmiPEP164b, and AtmiPEP164b peptides set forth in Table 13.

[0055] In some embodiments, the RNA molecule further includes an internal ribosome entry site (IRES) located 5' and immediately adjacent to the at least one coding sequence. In yet other embodiments, the cargo RNA molecule includes multiple coding sequences, and the RNA molecule further includes an IRES located 5' and immediately adjacent to each of the coding sequences (*e.g.*, open translational reading frames encoding a protein of interest. Useful IRES sequences include those depicted in Table 5.

[0056] In certain embodiments, the cargo RNA molecule includes a non-coding sequence such as those described in this disclosure's working examples. Such non-coding sequences include a hairpin RNA (hpRNA); an RNA that forms multiple stem-loops; an RNA pseudoknot; an RNA sequence that forms at least partially double-stranded RNA; a small interfering RNA (siRNA) or siRNA precursor; a microRNA (miRNA) or miRNA precursor; a ribozyme; a ligand-responsive ribozyme (aptazyme); an RNA aptamer; or a long noncoding RNA (lncRNA). In certain embodiments, the cargo RNA includes a selectable or scorable RNA marker, such as an RNA aptamer or a regulatory RNA, such as an siRNA or siRNA precursor (see, *e.g.*, US Patent No. 8,404,927, 8,455,716, 9,777,288, 10,378,012), a miRNA or a miRNA precursor (see, *e.g.*, US Patent Nos. 8,410,334, 8,395,023, 9,708,620), a trans-acting siRNA or trans-acting siRNA precursor (see, *e.g.*, US Patent Nos. 8,030,473, 8,476,422, 8,816,061, 9,018,002), a phased sRNA or phased sRNA precursor (see, *e.g.*, US Patent No. 8,404,928), an siRNA or miRNA decoy (see, *e.g.*, US Patent Nos. 8,946,511, 9,873,888), an siRNA or miRNA cleavage blocker (see, *e.g.*, US Patent 9,040,774), an siRNA or miRNA recognition and cleavage sequence (see, *e.g.*, US Patent Nos. 8,334,430, 9,139,838, 9,976,152, 10,793,869, 10,876,126), a riboswitch (see, *e.g.* U.S. Patent Application Public. No. 20130102651; U.S. Patent No. 6,630,306; U.S. Patent No. 6,949,379), or a ribozyme. Suitable RNA aptamers include those that exhibit fluorescence upon binding a molecule. For example, the fluorescent RNA aptamer can be the Broccoli RNA aptamer. Other fluorescent RNA aptamers that can be used include, but are not limited to, Spinach, Spinach2, Carrot, Radish, Corn, Red Broccoli, Orange Broccoli, and Broccoli Fluorets. Other useful RNA aptamers that can be used include those provided in Table 15. Suitable regulatory RNAs can be used to down-regulate (*i.e.*, silence) the expression of a marker gene. For example, phytoene desaturase (PDS) is widely used as a marker gene because silencing of the gene yields a photobleached phenotype. Regulatory RNAs such as decoys or cleavage blockers can also be used to interfere with endogenous small RNA-regulated pathways, resulting in a visible phenotype; see, *e.g.*, US Patent Nos. 8,946,511, 9,873,888, 9,040,774).

[0057] Antiviral cargo RNAs, and in particular antiviral cargo RNAs directed against viral pathogens are provided herein. In certain embodiments, the antiviral cargo RNAs comprise a heterologous RNA Virus (HRV)-inhibitory RNA or encode an HRV-inhibitory protein, wherein the HRV-inhibitory RNA or protein inhibits infection, movement, transmission, and/or replication of the HRV. Target viral pathogens

include an Alphaflexivirus, Betaflexivirus, Bromovirus, Celavirus, a Closterovirus, a Comovirus, a Potexvirus, Potyvirus, Tobamovirus, Tombusvirus, Tospoviridae, Trivirinae, Tymovirus, Varicosavirus, or Secoviridae. In certain embodiments the target viral pathogen is Cucumber Mosaic Virus, Brome mosaic virus, Citrus tristeza virus, Beet yellows virus, Cowpea mosaic virus, Potato virus X; Pepper mottle virus, Bean yellow mosaic virus, Barley stripe mosaic virus, Wheat stripe mosaic virus, Rice yellow mottle virus, Maize dwarf mosaic virus, zucchini yellow mosaic virus, watermelon mosaic virus, sugarcane mosaic virus, Tobacco mosaic virus, Tomato mosaic virus, Tomato brown rugose fruit virus, Turnip vein-clearing virus, Pepper mild mottle virus, Turnip crinkle virus, Tomato bushy stunt virus, Tomato spotted wilt virus, watermelon bud necrosis virus, Turnip yellow mosaic virus, Spinach latent virus, Olive latent virus 2, Citrus yellow vein clearing virus, Potato latent virus, Apple stem grooving virus, Citrus leaf blotch virus, Apple latent spherical virus, Soybean latent spherical virus, Celery latent virus, Black grass varicosavirus-like virus, Maize suscal virus, Horseradish latent virus, Bean latent virus, Rice latent virus 1, or Rice latent virus 2. In certain embodiments, the targeted viral pathogen is a heterologous RNA virus disclosed in Table 7. In certain embodiments, antiviral inhibitory RNAs (RNAi sequences) used as cargo RNAs are obtained for a chosen target gene of a viral pathogen using siRNA/miRNA prediction tools (see, e.g., on the world wide web internet site “zhaolab[dot]org/pssRNAit/). Other examples of non-coding RNA sequences having antiviral activity (e.g., dsRNA molecules which produce miRNA or siRNA) that can be used as antiviral cargo RNAs include those disclosed in US Patent No. 8,455,716, which is incorporated herein by reference in its entirety. Non-limiting examples of viral targets for antiviral cargo RNA molecules include the viral genes and genomes provided in Table 7 as well as other variants of those viral sequences. In certain embodiments, cargo RNAs encoding antiviral proteins are provided. Non-limiting examples of antiviral proteins include the N protein (e.g., the protein encoded by nt 491-3925 in SEQ ID NO: 630; Whitham, S. *et al. Cell* **78**, 1101–1115 (1994)) and endogenous plant viral resistance proteins provided in Table 8, [0058] Antifungal cargo RNAs, and in particular antifungal cargo RNAs directed against plant fungal pathogens, are provided herein. Target fungal pathogens include *Botrytis*, *Fusarium*, *Magnaporthe*, *Phytophthora*, *Rhizoctonia*, *Sclerotinia*, and *Verticillium* sp. In certain embodiments, the antifungal cargo RNA comprises a non-coding RNA sequence having antifungal activity (e.g., dsRNA molecules which produce miRNA or siRNA) and in particular a dsRNA directed against a fungal pathogen target gene. In certain embodiments, such antifungal cargo RNAs comprising dsRNA-mediated control of fungal pathogens are modeled after those described in Qiao et al., 2021, doi: 10.1111/pbi.13589; Duanis-Assaf, et al., 2022, DOI: 10.1111/pbi.13708; Yang et al., 2022, doi: 10.3389/fmicb.2021.660976; Sundaresha et al., 2021, doi: 10.20944/preprints202102.0280.v1; and Gaffar et al., 2019, doi: 10.3389/fmicb.2019.01662. Non-limiting examples of antifungal cargo RNAi targets are provided in Table 10. In certain embodiments, antifungal inhibitory RNAs (RNAi sequences) used as cargo RNAs are obtained for a chosen target gene of a fungal pathogen (e.g., a fungal pathogen gene set forth in Table 10) using siRNA/miRNA prediction tools (see, e.g., on the world wide web internet site

“zhaolab[dot]org/pssRNAit/). In other embodiments, antifungal cargo RNAs encode antifungal proteins. Useful antifungal proteins include nodule-specific cysteine-rich antimicrobial peptides (Vellivelli et al., 2020, doi: 10.1073/pnas.2003526117), defensins (Asano et al., 2013, doi: 10.1371/journal.ppat.1003581), the conidial germination-inhibiting antifungal peptides disclosed in International Patent Application publication WO2023/004435, which is herein incorporated by reference in its entirety, including their homodimers, heterodimers, and fusions with signal or cell-penetrating peptides (e.g., the sequences provided in Tables 4 and 5 of WO2023/004435); the various antifungal antimicrobial peptides disclosed in De Cesare *et al.* (2020) mBio 11:e02123-20; doi.org/10.1128/mBio.02123-20, including Table 1 (supplemental material, journals[dot]asm[dot]org/doi/suppl/10.1128/mbio.02123-20/suppl_file/mbio.02123-20-st001[dot]pdf), and other antifungal proteins provided in Table 11.

[0059] Insecticidal cargo RNAs, and in particular insecticidal or insect inhibitory cargo RNAs directed against insects are provided herein. Target insects include sucking insects (*e.g.*, heteropteran and homopteran insects including aphids, whiteflies, and plant bugs), caterpillars (*e.g.*, lepidopteran insects including fall army, black cutworm, corn earworm, soybean looper, and velvetbean caterpillar), beetles (*e.g.*, coleopteran insects including Colorado Potato Beetle and corn rootworms), and flies (*e.g.*, dipteran insects including *Ceratitis capitata*). Insecticidal or insect inhibitory cargo RNAs provided herein can be directed against insects at various stages of their development (*e.g.*, embryonic, larval, pupal, or adult stages). In certain embodiments, the insecticidal or insect inhibitory cargo RNA comprises a non-coding RNA sequence having insecticidal or insect inhibitory activity (*e.g.*, dsRNA molecules which produce miRNA or siRNA) and in particular a dsRNA directed against an insect target gene. In certain embodiments, such insecticidal cargo RNAs comprising dsRNA-mediated control of insects comprise or are modeled after those described in US Patent Nos. 11,091,770 and 11,186,837, which are each incorporated herein by reference in their entireties. Non-limiting examples of insecticidal or insect-inhibitory cargo RNAi targets are provided in Table 9. Non-limiting examples of insecticidal cargo RNAi targets include insect Actin, SNF7, Tyrosine hydroxylase, C002, Hunchback, V-ATPase subunit A, COPI coatomer beta prime subunit, ribosomal protein L19, and ubiquitin C genes. In certain embodiments, insecticidal or insect inhibitory RNAs (RNAi sequences) used as cargo are obtained for a chosen target gene of an insect (*e.g.*, an insect gene set forth in Table 9 or US Patent Nos. 11,091,770 and 11,186,837) using siRNA/miRNA prediction tools (see, *e.g.*, on the world wide web internet site “zhaolab[dot]org/pssRNAit/). In other embodiments, insecticidal cargo RNAs encode insecticidal proteins. Useful insecticidal proteins encoded by insecticidal cargo RNAs include native and modified *Bacillus thuringiensis* Cry, vegetative insecticidal proteins (VIP), and Cyt proteins (Palma et al. 2014, doi: 10.3390/toxins6123296; US Patent No. 11,267,849, incorporated herein by reference in its entirety) as well as insecticidal or insect-inhibitory proteins provided in Table 9.

[0060] Cargo RNAs can also encode “resistance” or “R” genes which confer resistance to certain arthropods, bacteria such as *Pseudomonas* sp., *Xanthomonas* sp., and *Erwinia* sp., and fungal pathogens

including *Cochliobolus*, *Blumeria*, *Fusarium*, *Melampsora*, and *Magnaporthe* sp. Non-limiting examples of R genes encoded by cargo RNAs include those provided in Table 12.

[0061] In some embodiments, the cargo RNA molecule comprises a CRISPR guide RNA, e.g., a crRNA, gRNA, or sgRNA. CRISPR-associated endonucleases such as Cas9, Cas12, and Cas13 endonucleases are used as genome editing tools in different plants; see, e.g., Wolter et al. (2019) BMC Plant Biol., 19:176-183; Aman et al. (2018) Genome Biol., 19:1-10. CRISPR/Cas9 requires a two-component crRNA:tracrRNA “guide RNA” (“gRNA”) that contains a targeting sequence (the “CRISPR RNA” or “crRNA” sequence) and a Cas9 nuclease-recruiting sequence (tracrRNA). Efficient Cas9 gene editing is also achieved with the use of a chimeric “single guide RNA” (“sgRNA”), an engineered (synthetic) single RNA molecule that mimics a naturally occurring crRNA-tracrRNA complex and contains both a tracrRNA (for binding the nuclease) and at least one crRNA (to guide the nuclease to the sequence targeted for editing); see, for example, Cong et al. (2013) Science, 339:819-823; Xing et al. (2014) BMC Plant Biol., 14:327-340. Chemically modified sgRNAs have been demonstrated to be effective in genome editing; see, for example, Hendel et al. (2015) Nature Biotechnol., 985-991. Commercial manufacturers of CRISPR nucleases and guide RNAs provide algorithms for designing guide RNA sequences; see, e.g., guide design tools provided by Integrated DNA Technologies at [www\[idtdna\]com/pages/products/crispr-genome-editing/alt-r-crispr-cas9-system](http://www.idtdna.com/pages/products/crispr-genome-editing/alt-r-crispr-cas9-system). Some Cas nucleases, including Cas12a and Cas13, do not require a tracrRNA.

[0062] Also provided herein are recombinant polynucleotides wherein the 5' and 3' RNA replication elements of the endornavirus flank an internal sequence wherein the cargo RNA is operably linked to one or more elements of a heterologous RNA virus (HRV).

[0063] In certain embodiments, cargo RNAs are imbedded within a heterologous RNA virus (HRV) amplicon comprising: (i) an HRV 5' replication region (HRV 5' RR); (ii) the cargo RNA molecule; and (iii) the heterologous RNA virus (HRV) 3' RNA replication region (HRV 3' RR), wherein (i), (ii), and (iii) are operably linked. An illustrative example of an endornavirus satellite construct with such an HRV amplicon is shown in Figure 2. Amplification of such an HRV amplicon in plants comprising a COMMENSAL satellite construct, the COMMENSAL, and an HRV RdRP is illustrated in Figure 6. Examples of HRV 5' replication regions (5'RR), 3' replication regions (3'RR), and corresponding HRV RNA-dependent RNA Polymerases (RdRP) that recognize such replication regions are set forth in Table 7. In certain embodiments where the cargo RNA encodes a protein, an internal ribosome entry site (IRES; e.g. an IRES in Table 5) is typically operably linked to the coding cargo RNA. In certain embodiments one or more self-cleaving or inducible ribozymes are operably linked to the 5' end of the HRV 5' RR and to the 3' end of the HRV 3' RR. In certain embodiments, the HRV amplicon further comprises a subgenomic promoter which is operably linked to the cargo RNA molecule. Examples of subgenomic promoters include a subgenomic promoter of the HRV and/or a Brome Mosaic Virus subgenomic promoter (Siegal et al. 1998, doi: 10.1073/pnas.95.20.11613), barley yellow dwarf virus (BYDV) sgRNA1, sgRNA2, and sgRNA3 subgenomic promoters (Koev and Miller; J Virol. 2000

Jul;74(13):5988-96, doi: 10.1128/jvi.74.13.5988-5996.2000), and an *Alternanthera* mosaic virus (AltMV-MU) sgp1, sgp2, or sgp3 subgenomic promoter (Putlyaev et al., Biochemistry (Mosc.);80(8):1039-46, DOI: 10.1134/S000629791508009X). Further examples of subgenomic promoters include those in Table 16. Such HRV amplicons can be in the sense or antisense orientation with respect to the endornavirus 5' RNA replication element. When the HRV amplicon is oriented in the sense orientation relative to the endornavirus 5' RNA replication element, the HRV 5' RR and 3' RR are present in the recombinant RNA molecule in the sense orientation, as in the corresponding sequences found in the plus (+) strand of the HRV genomic RNA. When the HRV amplicon is oriented in the antisense orientation relative to the endornavirus 5' RNA replication element, the HRV 5' RR and 3' RR are present in the recombinant RNA molecule in antisense orientation, as in the corresponding sequences found in the negative (-) strand of the HRV genomic RNA. Under certain conditions where a plant cell or plant containing the recombinant RNA containing the HRV amplicon are provided with an RNA-dependent RNA polymerase that recognizes the HRV 5' RR and 3'RR (hrvRdRP), the HRV amplicon undergoes amplification (e.g., hrvRdRP-mediated replication). Such hrvRdRP can be provided by sources that include: (i) infection by the HRV; (ii) introduction by vector-mediated delivery of a polynucleotide encoding the hrvRdRP (e.g., *Agrobacterium*-mediated delivery or viral vector mediated delivery); or (iii) introduction of a nucleic acid encoding the hrvRdRP. A non-limiting example of a recombinant satellite RNA that contains HRV 5'RR and 3'RR sequence pairs that are respectively recognized by two distinct HRV RdRP ("HRV1 RdRP" and "HRV2 RdRP") is illustrated in Figure 7. Amplification (e.g., an increase in copy number of the HRV amplicon) provides for additional copies of the cargo RNA and an enhancement of desirable phenotypes conferred by the cargo RNA (e.g., increased antiviral, antifungal, or insecticidal activity in comparison to control plants lacking the amplified cargo RNA or lacking the cargo RNA).

[0064] In other embodiments, the recombinant nucleotides provided herein comprise endornavirus 5' and 3' RNA replication elements flanking a heterologous RNA virus (HRV) subgenomic promoter operably linked to the cargo RNA molecule; wherein the subgenomic promoter is recognized by a heterologous RNA virus RNA-dependent RNA polymerase (hrvRdRP). An illustrative example of an endornavirus satellite construct with subgenomic promoters in sense or antisense orientation relative to the 5' RRE is shown in Figure 3. Another illustrative example where subgenomic promoters drive expression of an HRV RdRP and a dsRNA cargo in plants comprising an endornavirus satellite construct is shown in Figure 8. In certain embodiments where the cargo RNA linked to the subgenomic promoter encodes a protein, an internal ribosome entry site (IRES; e.g. an IRES in Table 5) is typically operably linked to the cargo RNA. Embodiments of subgenomic promoters include a subgenomic promoter of the HRV and/or a Brome Mosaic Virus subgenomic promoter (Siegal et al. 1998, doi: 10.1073/pnas.95.20.11613), barley yellow dwarf virus (BYDV) sgRNA1, sgRNA2, and sgRNA3 subgenomic promoters (Koev and Miller; J Virol. 2000 Jul;74(13):5988-96. Doi: 10.1128/jvi.74.13.5988-5996.2000), and an *Alternanthera* mosaic virus (AltMV-MU) sgp1, sgp2, or sgp3 subgenomic promoter

(Putlyaev et al., Biochemistry (Mosc.);80(8):1039-46DOI: 10.1134/S000629791508009X). Further subgenomic promoters include those in Table 16. Such subgenomic promoters and operably linked cargo RNAs can be in the sense or antisense orientation with respect to the endornavirus 5' RNA replication element. Expression of cargo RNAs from subgenomic promoters provides for additional copies of the cargo RNA and an enhancement of desirable phenotypes conferred by the cargo RNA (*e.g.*, increased antiviral, antifungal, or insecticidal activity in comparison to control plants lacking the additional expressed cargo RNA or lacking the cargo RNA). When the subgenomic promoters and operably linked cargo RNAs are oriented in the sense orientation relative to the endornavirus 5' RNA replication element, the subgenomic promoters and operably linked cargo RNAs are present in the recombinant RNA molecule as a sense strand where the subgenomic promoter is recognized by the hrvRdRP to produce the desired cargo RNA. When the subgenomic promoters and operably linked cargo RNAs are oriented in the sense orientation relative to the endornavirus 5' RNA replication element in the recombinant RNA molecule (positive strand), the subgenomic promoter can be recognized by the hrvRdRP to produce the desired cargo RNA. When the HRV amplicon is oriented in the antisense orientation relative to the endornavirus 5' RNA replication element in the recombinant RNA molecule, the subgenomic promoter cannot be recognized by the hrvRdRP to produce the desired cargo RNA. However, the negative strand of the recombinant RNA molecule produced by the endornavirus RdRP would contain the subgenomic promoters and operably linked cargo RNA in a sense orientation where the subgenomic promoter can be recognized by the hrvRdRP to produce the desired cargo RNA. In certain embodiments, the HRV amplicons further comprise a HRV 5' RR and 3' RR which flank the cargo RNA and provide for hrvRdRP-mediated replication of an RNA comprising from 5' to 3' the HRV 5' RR, cargo RNA, and HRV 3' RR (*e.g.*, as illustrated in the non-limiting example of Figure 5). Under certain conditions where a plant cell or plant containing the recombinant RNA containing the subgenomic promoters and operably linked cargo RNA are provided with an RNA-dependent RNA polymerase that recognizes the subgenomic promoter (hrvRdRP), an RNA encoding the cargo molecule can be produced (*e.g.*, via hrvRdRP-mediated synthesis of the cargo RNA from the subgenomic promoter). Such hrvRdRP can be provided by sources that include: (i) infection by the HRV; (ii) introduction by vector-mediated delivery (*e.g.*, *Agrobacterium*-mediated delivery or viral vector mediated delivery); (iii) introduction of a nucleic acid encoding the hrvRdRP; or (iv) inclusion of a cargo RNA in the recombinant nucleotides comprising endornavirus 5' and 3' RNA replication elements. In one particular embodiment, the subgenomic promoter and operably linked cargo RNA are present in the recombinant RNA molecule as the antisense strand, and the cargo RNA encodes both an hrvRdRP and a second coding or non-coding RNA where both the hrvRdRP and a second coding or non-coding RNA are operably linked to a subgenomic promoter recognized by the hrvRdRP. In certain embodiments, an IRES is operably linked to the RNA encoding the hrvRdRP. Production of the negative strand of the recombinant nucleotides comprising endornavirus 5' and 3' RNA replication elements results in an RNA where the subgenomic promoters recognized by the hrvRdRP can drive expression of the HRV RdRp and a second coding or non-coding

RNA. An illustrative example of an endornavirus satellite construct with subgenomic promoters in antisense orientation relative to the 5' RRE and driving expression of both an hrvRdRP that recognizes the subgenomic promoters and a second cargo RNA is shown in Figure 4.

[0065] In a related aspect, an RNA molecule including at least one HRV amplicon is amplified directly by the hrvRdRP (*e.g.*, without initial or further amplification by the commensal viral RdRP). In one embodiment, the HRV amplicon includes, in 5' to 3' order, (i) a heterologous RNA virus (HRV) 5' replication region (HRV 5'RR); (ii) a cargo RNA molecule; and (iii) a heterologous RNA virus (HRV) 3' RNA replication region (HRV 3'RR); wherein the HRV 5' RR and HRV 3' RR HRV are recognized by a heterologous RNA virus RNA-dependent RNA polymerase (hrvRdRP); and wherein the HRV 5'RR, cargo RNA molecule, and HRV 3'RR are operably linked. In another embodiment, the HRV amplicon includes, in 5' to 3' order, a subgenomic promoter that is operably linked to (v) a cargo RNA molecule, wherein the subgenomic promoter is recognized by the hrvRdRP. Such HRV amplicons can be provided in either an isolated form or in a composition. In embodiments, the RNA molecule including the HRV amplicon can be provided to a plant, for example, by transcription in the plant from a recombinant DNA molecule encoding the RNA molecule that is transiently expressed in the plant or that is stably integrated into the plant's genome, or by delivery to the plant of an exogenous RNA molecule including the HRV amplicon, for example, by contacting a surface of the plant with the exogenous RNA molecule including the HRV amplicon, or by introducing the exogenous RNA molecule including the HRV amplicon into the plant's vascular system (*e.g.*, by injection, infusion, petiole uptake, root uptake). In embodiments, RNA molecules (or DNA encoding such RNA molecules) are delivered by injection into the vascular system of plants, such as perennial or woody plants. Examples of devices and methods for delivery via injection into plant vascular systems include those described in US Patent No. 11844318; examples of delivery via injection into olive trees are described in PCT published application WO 2023/161802 and Grandi *et al.* (2023) *Front. Plant Sci.*, 14:2023; doi.org/10.3389/fpls.2023.1180632; and examples of delivery via injection into citrus trees are described in PCT published application WO 2023/240208 and Al-Rimawi *et al.* (2019) *Antibiotics*, 8, 196; doi:10.3390/antibiotics8040196.

[0066] In embodiments, the cargo RNA molecule includes at least one antiviral RNA (*e.g.*, an antiviral inhibitory RNA or an RNA encoding an antiviral polypeptide) that provides the plant with resistance to at least one viral pathogen (which in some instances can be the heterologous RNA virus itself). Such embodiments are useful as antiviral treatments for plants, to prevent or decrease the severity of infection of a plant by a viral pathogen.

[0067] In certain embodiments, plants including solanaceous plants (Solanaceae), legumes (Fabaceae), cucurbits (Cucurbitaceae), *Vitis* spp., Asteraceae, and cereals (Graminaceae) that comprise endornavirus satellite RNAs containing HRV amplicons disclosed herein can exhibit control of a wide variety HRV. In one embodiment, solanaceous plants including *Capsicum* spp. that comprise endornavirus satellite RNAs with Bell pepper alphaendornavirus 5' RRE and 3'RRE (*e.g.*, Table 1) that contain an HRV amplicon with suitable antiviral cargo can exhibit control of HRV that include Fabaceae Bean common mosaic

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necrosis virus, Bean common mosaic virus, Bean leafroll virus, Bean mild mosaic virus, Bean necrotic mosaic orthospovirus, Bean pod mottle virus, Bean rugose mosaic virus, Bean yellow disorder virus, Bean yellow mosaic virus, Broad bean mottle virus, Broad bean necrosis virus, Broad bean stain virus, Broad bean true mosaic virus, Broad bean wilt virus 1, Broad bean wilt virus 2, Faba bean polerovirus 1, Southern bean mosaic virus, Southern cowpea mosaic virus, Soybean dwarf virus, Soybean latent spherical virus, Soybean mosaic virus, Soybean scleroulivirus 1, Soybean scleroulivirus 2, Soybean vein necrosis orthospovirus, Soybean yellow common mosaic virus, Soybean yellow mottle mosaic virus, Soybean-associated deltaflexivirus 1, Lupinus mosaic virus, Peanut clump virus, Peanut mottle virus, Peanut stunt virus, Peanut yellow mosaic virus, Pea early-browning virus, Pea enation mosaic virus 1, Pea enation mosaic virus 2, Pea green mottle virus, Pea mild mosaic virus, Pea seed-borne mosaic virus, Pea stem necrosis virus, and Pea streak virus. In one embodiment, leguminous plants such as common bean, faba bean, winged bean, and cluster bean that comprise endornavirus satellite RNA's with Cluster bean alphaendornavirus, Phaseolus vulgaris alphaendornavirus, Vicia faba alphaendornavirus, or Winged bean alphaendornavirus 5' RRE and 3' RRE (e.g., Table 1) containing an HRV amplicon with suitable antiviral cargo can exhibit control of HRV that include Bean common mosaic necrosis virus, Bean common mosaic virus, Bean leafroll virus, Bean mild mosaic virus, Bean necrotic mosaic orthospovirus, Bean pod mottle virus, Bean rugose mosaic virus, Bean yellow disorder virus, Bean yellow mosaic virus, Broad bean mottle virus, Broad bean necrosis virus, Broad bean stain virus, Broad bean true mosaic virus, Broad bean wilt virus 1, Broad bean wilt virus 2, Faba bean polerovirus 1, Southern bean mosaic virus, Southern cowpea mosaic virus, Soybean dwarf virus, Soybean latent spherical virus, Soybean mosaic virus, Soybean scleroulivirus 1, Soybean scleroulivirus 2, Soybean vein necrosis orthospovirus, Soybean yellow common mosaic virus, Soybean yellow mottle mosaic virus, Soybean-associated deltaflexivirus 1, Lupinus mosaic virus, Peanut clump virus, Peanut mottle virus, Peanut stunt virus, Peanut yellow mosaic virus, Pea early-browning virus, Pea enation mosaic virus 1, Pea enation mosaic virus 2, Pea green mottle virus, Pea mild mosaic virus, Pea seed-borne mosaic virus, Pea stem necrosis virus, and Pea streak virus. In one embodiment, plants such as *Vitis* spp. that comprise endornavirus satellite RNAs with Grapevine endophyte alphaendornavirus 5' RRE and 3' RRE (e.g., Table 1) and containing an HRV amplicon with suitable antiviral cargo can exhibit control of HRV that include Australian grapevine viroid, Grapevine Algerian latent virus, Grapevine asteroid mosaic associated virus, Grapevine berry inner necrosis virus, Grapevine Bulgarian latent virus, Grapevine chrome mosaic virus, Grapevine coguvirus, Grapevine deformation virus, Grapevine enamovirus 1, Grapevine fabavirus, Grapevine fanleaf virus, Grapevine fleck virus, Grapevine laulaviruses, Grapevine leafroll-associated viruses, Grapevine rubodviruses, Grapevine viruses A, B, D, E, F, G, H, I, J, and T, and Grapevine yellow speckle viroids. In one embodiment, cucurbit plants such as cucumbers and the like that comprise endornavirus satellite RNAs with Cucumis melo alphaendornavirus or Lagenaria siceraria alphaendornavirus 5' RRE and 3' RRE (e.g., Table 1) and containing an HRV amplicon with suitable antiviral cargo can exhibit control of HRV that include Cucumber Bulgarian latent virus,

Cucumber fruit mottle mosaic virus, Cucumber green mottle mosaic virus, Cucumber leaf spot virus, Cucumber mosaic virus, Cucumber mottle virus, Cucumber necrosis virus, Cucumber soil-borne virus, Cucumber vein yellowing virus, Cucumber vein-clearing virus, Cucumis melo alphaendornavirus, Cucurbit aphid-borne yellows virus, Cucurbit mild mosaic virus, Cucurbit vein banding virus, Cucurbit yellow stunting disorder virus, Melon aphid-borne yellows virus, Melon mild mottle virus, Melon necrotic spot virus, Melon rugose mosaic virus, Melon severe mosaic orthotospovirus, Melon tenuivirus, Melon yellow spot orthotospovirus, Melon yellowing-associated virus, Wild cucumber mosaic virus, and Wild melon banding virus. In one embodiment, *Helianthus* spp. plants that comprise endornavirus satellite RNAs with *Helianthus annuus* alphaendornavirus 5' RRE and 3' RRE (*e.g.*, Table 1) that contain an HRV amplicon with suitable antiviral cargo can exhibit control of HRV that include Sunflower chlorotic mottle virus, Sunflower mild mosaic virus, and Sunflower ring blotch virus. In one embodiment, Gramineae plants such as *Hordeum vulgare* that comprise endornavirus satellite RNAs with *Hordeum vulgare* alphaendornavirus 5' RRE and 3' RRE (*e.g.*, Table 1) that contain an HRV amplicon with suitable antiviral cargo can exhibit control of HRV that include Barley yellow dwarf viruses, Barley stripe mosaic virus, Barley mild mosaic virus, Barley yellow mosaic virus, Brome mosaic virus, Maize aumavirus, Maize chlorotic dwarf virus, Maize chlorotic mottle virus, Maize dwarf mosaic virus, Maize necrotic streak virus, Maize rayado fino virus, Maize rough dwarf virus, Maize stripe tenuivirus, Maize white line mosaic virus, Maize yellow dwarf virus, Maize yellow mosaic virus, Oat blue dwarf virus, Oat chlorotic stunt virus, Oat golden stripe virus, Oat mosaic virus, Oat necrotic mottle virus, Rice black streaked dwarf virus, Rice dwarf virus, Rice gall dwarf virus, Rice grassy stunt tenuivirus, Rice hoja blanca tenuivirus, Rice necrosis mosaic virus, Rice ragged stunt virus, Rice stripe necrosis virus, Rice stripe tenuivirus, Rice tungro spherical virus, Rice yellow mottle virus, Southern rice black-streaked dwarf virus, Wheat eglid mosaic virus, Wheat spindle streak mosaic virus, Wheat streak mosaic virus, Wheat yellow leaf virus, Wheat yellow mosaic virus, Chinese wheat mosaic virus, European wheat striate mosaic tenuivirus, Iranian wheat stripe tenuivirus, Japanese soil-born wheat mosaic virus, Ryegrass cryptic virus, Ryegrass mosaic virus, Ryegrass mottle virus, Sorghum chlorotic spot virus, Sorghum mosaic virus, Sugarcane mosaic virus, Sugarcane streak mosaic virus, Sugarcane yellow leaf virus, Soil-borne cereal mosaic virus, Soil-borne wheat mosaic virus, and Bamboo mosaic virus. In one embodiment, *Oryza* spp. plants that comprise endornavirus satellite RNAs with *Oryza rufipogon* alphaendornavirus or *Oryza sativa* alphaendornavirus 5' RRE and 3' RRE (*e.g.*, Table 1) that contain an HRV amplicon with suitable antiviral cargo can exhibit control of HRV that include Barley yellow dwarf viruses, Barley stripe mosaic virus, Barley mild mosaic virus, Barley yellow mosaic virus, Brome mosaic virus, Maize aumavirus, Maize chlorotic dwarf virus, Maize chlorotic mottle virus, Maize dwarf mosaic virus, Maize necrotic streak virus, Maize rayado fino virus, Maize rough dwarf virus, Maize stripe tenuivirus, Maize white line mosaic virus, Maize yellow dwarf virus, Maize yellow mosaic virus, Oat blue dwarf virus, Oat chlorotic stunt virus, Oat golden stripe virus, Oat mosaic virus, Oat necrotic mottle virus, Rice black streaked dwarf virus, Rice dwarf virus, Rice gall dwarf virus, Rice

grassy stunt tenuivirus, Rice hoja blanca tenuivirus, Rice necrosis mosaic virus, Rice ragged stunt virus, Rice stripe necrosis virus, Rice stripe tenuivirus, Rice tungro spherical virus, Rice yellow mottle virus, Southern rice black-streaked dwarf virus, Wheat eglid mosaic virus, Wheat spindle streak mosaic virus, Wheat streak mosaic virus, Wheat yellow leaf virus, Wheat yellow mosaic virus, Chinese wheat mosaic virus, European wheat striate mosaic tenuivirus, Iranian wheat stripe tenuivirus, Japanese soil-born wheat mosaic virus, Ryegrass cryptic virus, Ryegrass mosaic virus, Ryegrass mottle virus, Sorghum chlorotic spot virus, Sorghum mosaic virus, Sugarcane mosaic virus, Sugarcane streak mosaic virus, Sugarcane yellow leaf virus, Soil-borne cereal mosaic virus, Soil-borne wheat mosaic virus, and Bamboo mosaic virus. In one embodiment, avocado plants comprise endornavirus satellite RNAs with *Persea americana* alphaendornavirus 1 5' RRE and 3' RRE (*e.g.*, Table 1) that contain an HRV amplicon with suitable antiviral cargo can exhibit control of HRV that include Avocado sunblotch viroid.

[0068] Without seeking to be limited by theory, RNA molecules that contain HRV amplification sequences (such as the HRV amplicons described herein which contain either (1) a pair of HRV 5' and 3' RNA replication regions, or (2) a subgenomic promoter that is recognized by the hrvRdRP) potentially also serve as a "sponge" or "decoy" that reduces the corresponding hrvRdRP's efficiency in recognizing and amplifying the HRV viral genome itself, thus potentially decreasing a pathogenic HRV's deleterious effects on an infected plant.

[0069] RNA polynucleotides comprising at least one cleavable sequence are provided. In certain embodiments, the at least one cleavable sequence is located: (i) 5' to the 5' RNA replication element or 3' to the 3' RNA replication element; and/or (ii) between the 3' end of the 5' RNA replication element and the HRV amplicon and/or between the HRV amplicon and the 5' end of the 3' RNA replication element. In certain embodiments, the cleavable sequence is a self-cleaving ribozyme (*e.g.*, a hammerhead ribozyme; Tang and Breaker. *Proc Natl Acad Sci USA*. 2000 May 23;97(11):5784-9. doi:

10.1073/pnas.97.11.5784), a self-cleaving inducible ribozyme, or an siRNA or miRNA recognition site.

[0070] In an embodiment, a cargo RNA molecule that is integrated into a polynucleotide includes at least one CRISPR guide RNA; release of the guide RNA is mediated, *e.g.*, by flanking DR sequences, ribozyme sequences, or other self-cleaving or trans-cleaving RNAs, or by cleavage by an endogenous ribonuclease. The corresponding Cas nuclease can be provided by separate or concurrent delivery, *e.g.*, by co-delivery with a vector or polynucleotide, or by transient or stable expression of the corresponding Cas nuclease in the cell to which the polynucleotide is delivered. For many Cas nucleases, guide sequence designs are constrained by the requirement that the DNA target sequence (to which the crRNA is designed to be complementary) must be adjacent to a proto-spacer adjacent motif ("PAM") sequence that is recognized by the specific Cas nuclease to be employed. Cas nucleases recognize specific PAM sequences and there is a diversity of nucleases and corresponding PAM sequences; see, *e.g.*, Smakov et al. (2017) *Nature Reviews Microbiol.*, doi:10.1038/nrmicro.2016.184. For example, Cas9 nucleases cleave dsDNA, require a GC-rich PAM sequence located 3' to the DNA target sequence to be targeted by the crRNA component of the guide RNA, and cleave leaving blunt ends. Cas12a nucleases cleave

dsDNA, require a T-rich PAM sequence located 5' to the DNA target sequence to be targeted by the crRNA component of the guide RNA, and cleave leaving staggered ends with a 5' overhang. Cas13 nucleases cleave single-stranded RNAs and do not require a PAM sequence; instead, Cas13 nucleases are guided to their targets by a single crRNA with a direct repeat ("DR"). In practice, the crRNA component of a guide RNA is generally designed to have a length of between 17 – 24 nucleotides (frequently 19, 20, or 21 nucleotides) and exact complementarity (i. e., perfect base-pairing) to the targeted gene or nucleic acid sequence that is itself adjacent to a PAM motif (when required by the Cas nuclease). A crRNA component having less than 100% complementarity to the target sequence can be used (e. g., a crRNA with a length of 20 nucleotides and between 1 – 4 mismatches to the target sequence) but this increases the potential for off-target effects.

[0071] Non-limiting examples of effective guide RNA design are found, e.g., in US Patent Application Publications US 2019/0032131, 2015/0082478, and 2019/0352655, which are each incorporated by reference in their entirety herein. For the purposes of gene editing, CRISPR "arrays" can be designed to include one or multiple guide RNA sequences corresponding to one or more desired target DNA sequence(s); see, for example, Cong et al. (2013) *Science*, 339:819-823; Ran et al. (2013) *Nature Protocols*, 8:2281-2308.

[0072] In certain embodiments, the 5' RNA replication element includes a 5' UTR element of an endornavirus genome (e.g., an EV 5' UTR set forth in Table 1). In embodiments, the 5' RNA replication element further includes a genomic sequence of the endornavirus that is natively located 3' to and optionally adjacent or immediately adjacent to the 5' UTR sequence. In embodiments, the 3' RNA replication element includes a 3' UTR sequence of an endornavirus genome (e.g., an EV 3' UTR set forth in Table 1). In embodiments, the 3' RNA replication element further includes a genomic sequence of the endornavirus that is natively located 5' to and optionally adjacent or immediately adjacent to the 3' UTR sequence.

[0073] In other embodiments, the RNA molecule further includes at least one RNA molecule encoding a viral MP. In certain embodiments, the at least one RNA molecule encoding an MP is located (a) before the cargo RNA molecule, (b) after the cargo RNA molecule, or (c) both before and after the cargo RNA molecule. In embodiments, the at least one RNA sequence encoding an MP includes at least two RNA sequences encoding different MPs or a single RNA sequence encoding multiple copies of MPs.

[0074] In some embodiments, the recombinant DNA molecule further includes a discrete expression cassette including a second promoter that is functional in the cell and is operably linked to a DNA sequence encoding at least one viral movement protein, and optionally a terminator element.

[0075] In some embodiments, the RNA molecule further includes an encapsidation recognition element (ERE), where the ERE is located close to or adjacent to the 3' RNA replication element, and optionally wherein the 3' RNA replication element includes a 3' UTR sequence of the endornavirus. In embodiments, the ERE includes a viral OAS such as a tobacco mosaic virus OAS (TMV-OAS) or an OAS set forth in Table 2.

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[0076] In embodiments, the RNA molecule further includes at least one tRNA-like sequence (TLS), and wherein the at least one tRNA-like sequence includes a tRNA-like sequence from an *Arabidopsis* FT mRNA (e.g. a TLS in an *Arabidopsis* FT mRNA of **Table 4**). In some embodiments, the RNA molecule includes a tRNA-like sequence encoded by a DNA sequence selected from the group consisting of SEQ ID NOs: 76-123, and 790. In some embodiments, the RNA molecule includes a modified tRNA-like sequence that has at least 90% sequence identity to a scaffold tRNA-like sequence encoded by a DNA sequence selected from the group consisting of SEQ ID NOs: 76-123, and 790 and that maintains the secondary structure of the scaffold tRNA-like sequence. In still other embodiments, the RNA molecule further includes at least one RNA encoding a viral MP, a tRNA-like sequence from an *Arabidopsis* FT mRNA, and an encapsidation recognition sequence including TMV-OAS.

[0077] In some embodiments, the cargo RNA molecule is up to about 3kb, 4kb, 5kb, 6kb, 7kb, 8kb, 9kb, 10kb, 11kb, 12kb, 13 kb, 14kb, 15kb, 16kb, or 17kb in length. In certain embodiments, the cargo RNA molecule is up to about 14kb, 15kb, 16kb, or 17kb in length. In certain embodiments, the cargo molecule is up to about 17kb, 18kb, or 19kb in length. In embodiments, the cargo RNA molecule includes: (a) at least one coding sequence, (b) at least one non-coding sequence, or (c) both at least one coding sequence and at least one non-coding sequence. In other embodiments, the cargo RNA molecule includes at least one coding sequence, and wherein the RNA molecule further includes an internal ribosome entry site (IRES) located 5' and immediately adjacent to the at least one coding sequence. In other embodiments, the cargo RNA molecule includes multiple coding sequences, and wherein the RNA molecule further includes an IRES located 5' and immediately adjacent to each of the coding sequences.

[0078] In other embodiments, the cargo RNA molecule includes at least one non-coding sequence, and wherein the at least one non-coding sequence is selected from the group consisting of a hairpin RNA (hpRNA); an RNA that forms multiple stem-loops; an RNA pseudoknot; an RNA sequence that forms at least partially double-stranded RNA; a small interfering RNA (siRNA) or siRNA precursor; a microRNA (miRNA) or miRNA precursor; a ribozyme; a ligand-responsive ribozyme (aptazyme); an RNA aptamer; and a long noncoding RNA (lncRNA).

[0079] In embodiments, a DNA sequence encoding at least one ribozyme is provided. In embodiments, the at least one ribozyme is located 5' to the 5' RNA replication element or 3' to the 3' RNA replication element. In embodiments, a DNA sequence encoding at least one ligand-responsive ribozyme (aptazyme) is provided. In embodiments, the at least one ligand-responsive ribozyme is located 5' to the 5' RNA replication element or 3' to the 3' RNA replication element.

[0080] Recombinant RNA molecules comprising the aforementioned or otherwise disclosed 5' RNA replication elements, a cargo RNA molecule(s), and 3' RNA replication elements, as well as additional aforementioned or otherwise disclosed elements are also provided herein. In certain embodiments, the recombinant RNA molecules are produced by a recombinant DNA molecule provided herein. In certain embodiments, the recombinant RNA molecules are produced by an in vivo or in vitro (e.g., cell free)

RNA replication process through the action of a RdRP acting on: (i) 5' and 3' RNA replication elements; and/or (ii) a subgenomic promoter.

[0081] Expression systems comprising the recombinant polynucleotides are also provided. Such expression systems include both cell-based and cell free expression systems. In certain embodiments, cell-free expression system can include (a) an RNA molecule comprising, in 5' to 3' order: (i) a 5' RNA replication element; (ii) a cargo RNA molecule; and (iii) a 3' RNA replication element; and, optionally, further comprising at least one additional RNA or other element. Embodiments of additional elements include at least one RNA encoding a viral MP, at least one tRNA-like sequence, an OAS, an RdRP protein that recognizes the 5' and 3' RNA replication elements, a subgenomic promoter, and/or an RdRP that recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter. In some embodiments, the RdRP protein is provided by an endornavirus, *e.g.* an endornavirus that is endogenous to a cell in which expression is desired. In certain embodiments, cell-based expression system can include (a) a recombinant DNA molecule including a heterologous promoter that is functional in a cell and is operably linked to a DNA sequence encoding an RNA molecule comprising, in 5' to 3' order: (i) a 5' RNA replication element; (ii) a cargo RNA molecule; and (iii) a 3' RNA replication element; and, optionally, further comprising at least one additional RNA or other element. Embodiments of additional elements include at least one RNA encoding a viral MP, at least one tRNA-like sequence, an OAS, an RdRP protein that recognizes the 5' and 3' RNA replication elements, a subgenomic promoter, and/or an RdRP that recognizes the subgenomic promoter. In certain embodiments, cell-based expression system can include (a) a recombinant RNA molecule comprising, in 5' to 3' order: (i) a 5' RNA replication element; (ii) a cargo RNA molecule; and (iii) a 3' RNA replication element; and, optionally, further comprising at least one additional RNA or other element. Embodiments of additional RNA elements include at least one RNA encoding a viral MP, at least one tRNA-like sequence, an OAS, an RdRP protein that recognizes the 5' and 3' RNA replication elements, a subgenomic promoter, and/or an RdRP that recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter. In some embodiments, the RdRP protein is provided by an endornavirus. In some embodiments, an RdRP that recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter is provided by a heterologous RNA virus (HRV) or by another nucleic acid introduced into the cell (*e.g.*, by a vector or other recombinant nucleic acid). In still other embodiments, the 5' RNA replication element and the 3' RNA replication element are obtained from the same endornavirus and/or from the same endornavirus genome (*e.g.*, both obtained from the same EV genome) or from endornavirus genomes having at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another and which are optionally related. In some embodiments, a cell used in the expression system is a bacterial cell, a plant cell, a fungal cell, or an animal cell (*e.g.*, an insect cell). In embodiments, a cell used in the expression system endogenously contains an endornavirus having a genome that encodes an RdRP that recognizes the 5' and 3' RNA replication elements. In some embodiments, the expression system further includes a viral capsid protein that is recognized by the encapsidation recognition element and encapsidates the RNA molecule. In some

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embodiments, the viral capsid protein is: (a) expressed by the recombinant DNA molecule in the cell (*e.g.*, where the recombinant DNA molecule further includes a discrete expression cassette comprising a second promoter operably linked to a DNA sequence encoding the viral capsid protein, and optionally a terminator element), (b) co-expressed by a second recombinant DNA molecule in the cell; (c) provided exogenously to the cell; or (d) expressed by a virus in the cell. In embodiments, the RdRP protein is heterologous to the cell. In embodiments, the RdRP protein is provided exogenously to the cell. In certain embodiments, the RdRP protein that recognizes the 5' and 3' RNA replication elements is endogenously expressed in the plant cell by the endornavirus (*e.g.*, where the endornavirus virus occurs naturally in the plant cell). In embodiments, the endornavirus is native to or endemic to the plant cell. In embodiments, the endornavirus that is endemic to the plant cell is non-pathogenic. In embodiments, the endornavirus that is endemic to the plant cell is non-pathogenic and commensal. In embodiments, the endornavirus is an exogenously introduced endornavirus (*i.e.*, not endemic or native to the host, but artificially introduced). For example, an endornavirus natively found in one plant species, variety, or germplasm can be introduced, with or without a corresponding recombinant endornavirus satellite RNA, into a different plant species, variety, or germplasm. In embodiments, a complete self-replicating endornavirus satellite system is introduced into a plant or plant cells, wherein the self-replicating endornavirus satellite system includes: (1) a recombinant endornavirus satellite RNA comprising, from 5' terminus to 3' terminus: (a) a 5' RNA replication element recognized by an endornavirus RNA-dependent RNA polymerase (RdRP); (b) a cargo RNA molecule; and (c) a 3' RNA replication element recognized by the RdRP; wherein the 5' RNA replication element, the cargo RNA molecule, and the 3' RNA replication element are operably linked, and wherein the promoter and the cargo RNA molecule are heterologous to the 5' RNA replication element and the 3' RNA replication element; and (2) an exogenous endornavirus (*e.g.*, an endornavirus that is not endemic or native to the plant or plant cells) that is capable of replication in the plant or plant cells and that encodes the endornavirus RdRP that recognizes the 5' and 3' RNA replication element sequences in the recombinant endornavirus satellite RNA. In embodiments, the EV RdRP comprises a protein having at least 85%, 90%, 95%, 97%, or 99% sequence identity to SEQ ID NO: 613 to 725, or 726. In embodiments, the recombinant DNA molecule or recombinant RNA molecule further comprises at least one RNA encoding a viral MP, a tRNA-like sequence from an *Arabidopsis* FT mRNA, and an encapsidation recognition sequence including a TMV-OAS.

[0082] Cells comprising any of the aforementioned or otherwise disclosed recombinant polynucleotides (*e.g.*, recombinant DNAs, recombinant RNAs, or vectors comprising or encoding the same) are provided herein. Cells comprising the recombinant polynucleotides include prokaryotic (*e.g.*, a bacterium, such as a bacterium capable of transforming a eukaryotic cell) or eukaryotic (*e.g.*, a plant cell, fungal cell, or animal cell such as an insect cell) cells. In certain embodiments, the cells are bacterial cells capable of transforming a plant cell (*e.g.*, an *Agrobacterium* sp., a *Sinorhizobium* sp., a *Mesorhizobium* sp., *Bradyrhizobium* sp., *Rhizobium* sp., or an *Ensifer* sp. cell. Bacterial cells capable of transforming a

plant cell suitable for use with the recombinant polynucleotides provided herein include *Agrobacterium* sp., a *Sinorhizobium* sp., a *Mesorhizobium* sp., *Bradyrhizobium* sp., *Rhizobium* sp., or an *Ensifer* sp. cell are disclosed in US patent application publications US20170369898 and US20180312854, each incorporated herein by reference in their entireties.

[0083] Vectors suitable for maintenance, propagation, and/or expression of the recombinant polynucleotides in the aforementioned prokaryotic or eukaryotic cells are also provided herein. Such vectors can comprise any of the aforementioned or otherwise disclosed recombinant polynucleotides, recombinant DNA molecules, and recombinant RNA molecules as well as those polynucleotides molecules described in the Examples. In some embodiments, the bacterium that mediates the plant transformation is an *Agrobacterium* sp., a *Sinorhizobium* sp., a *Mesorhizobium* sp., *Bradyrhizobium* sp., *Rhizobium* sp., or an *Ensifer* sp. In embodiments where an *Agrobacterium* sp. is used, the vector includes T-DNAs flanking the recombinant DNA molecule encoding the recombinant RNA molecule (*e.g.*, as described in US patent application publications US20170369898 and US20180312854, each incorporated herein by reference in their entireties). In some embodiments, the vector is contained within a plant cell or within a bacterial cell (*Agrobacterium* sp., a *Sinorhizobium* sp., a *Mesorhizobium* sp., *Bradyrhizobium* sp., *Rhizobium* sp., or an *Ensifer* sp. cell).

[0084] Viral particles comprising any of the aforementioned or otherwise disclosed recombinant RNA molecules are also provided. In one embodiment, the recombinant RNA is introduced into a host or production plant using *Agrobacterium*-mediated transformation with a polynucleotide comprising (5' to 3'): (i) a promoter which is operably linked to a viral MP coding sequence and a TLS element, flanked by endornavirus 5' and 3' RNA replication elements; (ii) a promoter which is operably linked to a cargo RNA molecule and a TLS element, flanked by endornavirus 5' and 3' RNA replication elements; (iii) a promoter operably linked to an RdRP coding sequence; and (iv) a promoter operably linked to a CP encoding sequence. Heterologous promoters independently drive expression of the capsid protein and the cargo as depicted. The RNA expressed from the polynucleotide includes an OAS. A host plant is transformed for production of the synthetic endornavirus satellite RNA and satellite particles comprising the encapsidated RNA. The expressed and encapsidated endornavirus satellite RNA is subsequently isolated from leaf material or other tissue of the host plant, purified (and, if desired, formulated) for high pressure spraying onto plants that endogenously contain the corresponding endornavirus or a recombinant source of the EV RdRP for subsequent expression and replication of the endornavirus satellite RNA and satellite particles comprising the same in encapsidated form. In certain embodiments, spraying with the encapsidated satellite particles with certain cargo RNA molecules can be used to modify the plant as desired. The presence of a movement protein and/or tRNA-like sequences facilitates systemic movement throughout the plant receiving the high-pressure spray satellite particles comprising the desired recombinant RNA molecules comprising the encoded MP and cargo RNA. In certain embodiments, plants without a systemic endornavirus which provides the EV RdRP can further comprise a recombinant DNA or RNA molecule which encodes and provides the RdRP.

[0085] Target plants and plant cells used as hosts for synthetic endornavirus satellite RNAs (*e.g.*, recombinant RNAs) provided herein include both monocot and dicot plants and plant cells which can support endornavirus replication. In embodiments, the endornavirus is endogenous to (endemic to or natively found in) the plant or plant cell. In other embodiments, the endornavirus is introduced to and becomes established in the plant or plant cell. Embodiments include row crop plants, fruit-producing plants and trees, vegetables, trees, and ornamental plants including ornamental flowers, shrubs, trees, groundcovers, and turf grasses. In certain embodiments, the host plants and plant cells for synthetic **endornavirus** satellite RNAs include row crop plants, fruit-producing plants and trees, vegetables, trees, and ornamental plants including ornamental flowers, shrubs, trees, groundcovers, and turf grasses. In embodiments, the host plants and plant cells for synthetic endornavirus satellite RNAs include commercially important cultivated crops, trees, and plants, including: alfalfa (*Medicago sativa*), almonds (*Prunus dulcis*), apples (*Malus x domestica*), apricots (*Prunus armeniaca*, *P. brigantine*, *P. mandshurica*, *P. mume*, *P. sibirica*), asparagus (*Asparagus officinalis*), bananas (*Musa* spp.), barley (*Hordeum vulgare*), beans (*Phaseolus* spp.), blueberries and cranberries (*Vaccinium* spp.), cacao (*Theobroma cacao*), canola and rapeseed or oilseed rape, (*Brassica napus*), Polish canola (*Brassica rapa*), and related cruciferous vegetables including broccoli, kale, cabbage, and turnips (*Brassica carinata*, *B. juncea*, *B. oleracea*, *B. napus*, *B. nigra*, and *B. rapa*, and hybrids of these), carnation (*Dianthus caryophyllus*), carrots (*Daucus carota sativus*), cassava (*Manihot esculentum*), cherry (*Prunus avium*), chickpea (*Cicer arietinum*), chicory (*Cichorium intybus*), chili peppers and other capsicum peppers (*Capsicum annuum*, *C. frutescens*, *C. chinense*, *C. pubescens*, *C. baccatum*), chrysanthemums (*Chrysanthemum* spp.), coconut (*Cocos nucifera*), coffee (wild and domesticated *Coffea* spp. including *Coffea arabica*, *Coffea canephora*, and *Coffea liberica*), cotton (*Gossypium hirsutum* L.), cowpea (*Vigna unguiculata* and other *Vigna* spp.), fava beans (*Vicia faba*), cucumber (*Cucumis sativus*), currants and gooseberries (*Ribes* spp.), date (*Phoenix dactylifera*), duckweeds (family Lemnoideae), eggplant or aubergine (*Solanum melongena*), eucalyptus (*Eucalyptus* spp.), flax (*Linum usitatissimum* L.), geraniums (*Pelargonium* spp.), grapefruit (*Citrus x paradisi*), grapes (*Vitis* spp.) including wine grapes (*Vitis vinifera* and hybrids thereof), guava (*Psidium guajava*), hops (*Humulus lupulus*), hemp and cannabis (*Cannabis sativa* and *Cannabis* spp.), irises (*Iris* spp.), lemon (*Citrus limon*), lettuce (*Lactuca sativa*), limes (*Citrus* spp.), maize (*Zea mays* L.), mango (*Mangifera indica*), mangosteen (*Garcinia mangostana*), melon (*Cucumis melo*), millets (*Setaria* spp., *Echinochloa* spp., *Eleusine* spp., *Panicum* spp., *Pennisetum* spp.), oats (*Avena sativa*), oil palm (*Ellis quineensis*), olive (*Olea europaea*), onion (*Allium cepa*) and other alliums (*Allium* spp.), orange (*Citrus sinensis*), papaya (*Carica papaya*), peaches and nectarines (*Prunus persica*), pear (*Pyrus* spp.), pea (*Pisa sativum*), peanut (*Arachis hypogaea*), peonies (*Paeonia* spp.), petunias (*Petunia* spp.), pineapple (*Ananas comosus*), plantains (*Musa* spp.), plum (*Prunus domestica*), poinsettia (*Euphorbia pulcherrima*), poplar (*Populus* spp.), potato (*Solanum tuberosum*), pumpkins and squashes (*Cucurbita pepo*, *C. maxima*, *C. moschata*), rice (*Oryza sativa* L.), roses (*Rosa* spp.), rubber (*Hevea brasiliensis*), rye (*Secale cereale*), safflower (*Carthamus tinctorius* L), sesame seed (*Sesame*

indium), sorghum (*Sorghum bicolor*), soybean (*Glycine max* L.), strawberries (*Fragaria* spp., *Fragaria x ananassa*), sugar beet (*Beta vulgaris*), sugarcane (*Saccharum* spp.), sunflower (*Helianthus annuus*), sweet potato (*Ipomoea batatas*), tangerine (*Citrus tangerina*), tea (*Camellia sinensis*), tobacco (*Nicotiana tabacum* L.), tomato (*Solanum lycopersicum* or *Lycopersicon esculentum*), tulips (*Tulipa* spp.), walnuts (*Juglans* spp. L.), watermelon (*Citrullus lanatus*), wheat (*Triticum aestivum*), and yams (*Discorea* spp.). Wild relatives of domesticated plants are also of interest. In certain embodiments, the host plant or plant cells for synthetic endornavirus satellite RNAs is a dicot plant or plant cell selected from the genera *Brassica*, *Capsicum*, *Cucumis*, *Cucurbita*, *Gossypium*, *Nicotiana*, *Solanum*, or *Glycine*. In certain embodiments, the host plant or plant cells for synthetic endornavirus satellite RNAs is a monocot plant or plant cell selected from the genera *Avena*, *Hordeum*, *Oryza*, *Secale*, *Triticum*, *Sorghum*, or *Zea*. In certain embodiments, monocot target plants and plant cells used as hosts for synthetic endornavirus satellite RNAs (e.g., recombinant RNAs) provided herein include oats (*Avena sativa*), barley (*Hordeum vulgare*), rice (*Oryza sativa*, *Oryza glaberrima*, *Oryza rufipogon*), rye (*Secale cereale*), wheat (*Triticum aestivum*), sorghum (*Sorghum bicolor*), and maize (*Zea mays*) plants and plant cells.

[0086] Methods of using or use of any of the aforementioned or otherwise disclosed recombinant polynucleotides, expression systems, cells, and /or vectors to: (i) provide a synthetic endornavirus satellite RNA to a plant cell, (ii) obtain a phenotypic change in a plant or plant cell; (iii) increase a plant's resistance of a pest or pathogen, (iv) increase a plant's resistance to stress, (v) express a polypeptide in a plant or plant cell, and/or (vi) manufacture a synthetic endornavirus virus particle are also provided. In certain embodiments of the methods, the recombinant RNA molecule or a formulation thereof is provided by contacting the plant or plant cell with the recombinant RNA molecule or formulation thereof. In other embodiments, the recombinant RNA molecule is provided by expressing in the plant or plant cell a DNA molecule that encodes the recombinant RNA molecule or a formulation. In other embodiments, the recombinant RNA molecule is provided by contacting the plant or plant cell with cells (such as bacterial cells) which comprise a DNA molecule that encodes the recombinant RNA molecule and are capable of transforming the plant or plant cell. In other embodiments, the recombinant RNA molecule is provided by contacting the plant or plant cell with a satellite particle comprising an encapsidated recombinant RNA molecule or a formulation thereof. In embodiments, the 5' RNA replication element has a nucleotide sequence obtained or derived from an endornavirus genomic sequence; and/or the 3' RNA replication element has a nucleotide sequence obtained or derived from an endornavirus genomic sequence. In certain embodiments, the 5' and/or 3' RNA replication element can be obtained from the corresponding endornavirus genomic sequence by synthesizing or cloning a copy of the corresponding endornavirus genomic sequence. In certain embodiments, the 5' and/or 3' RNA replication element can be derived from the corresponding endornavirus genomic sequence by synthesizing a copy of a modified endornavirus genomic sequence or sequences. Such modifications of endornavirus genomic sequences present in a derived sequence include: (i) substitutions of nucleotides which maintain the RNA secondary structure; (ii) substitution of nucleotides based on a consensus obtained by alignment of 5' or 3' RNA

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replication elements; (iii) insertions, deletions, and/or substitution of nucleotides to facilitate assembly and/or operable linkage to other elements in the satellite RNA which include cargo RNA molecules, tRNA-like elements, encapsidation recognition element (ERE), RNA encoding a viral movement protein (MP), IRES elements, an HRV 5'RR, HRV 3'RR, and/or HRV subgenomic promoter; or (iv) any combination of (i), (ii), or (iii). In certain embodiments, the plant cell includes the endornavirus virus, and the RdRP protein is provided to the plant cell by the endornavirus virus. In embodiments, the endornavirus is endemic to the plant cell. In embodiments, the endornavirus that is endemic to the plant cell is non-pathogenic and/or commensal to the plant cell. In other embodiments, the endornavirus is exogenously provided to the plant cell. In some embodiments, the RdRP protein is exogenously provided to the plant cell. In embodiments, the recombinant RNA molecule is produced in a fermentation system. In embodiments, the recombinant RNA molecule is provided to the plant cell by transcribing in the plant cell a recombinant DNA construct including a promoter functional in the plant cell and operably linked to a DNA sequence encoding the recombinant RNA molecule. In embodiments, the recombinant RNA molecule further includes an encapsidation recognition element (ERE), and the plant cell further includes a viral capsid protein (CP) capable of encapsidating the synthetic endornavirus satellite RNA. In embodiments, wherein the viral capsid protein is exogenously provided to the plant cell. In other embodiments, the recombinant DNA construct further includes a DNA sequence encoding a viral capsid protein. Still in other embodiments, the recombinant DNA construct further includes a second promoter functional in the plant cell and operably linked to the DNA sequence encoding the viral capsid protein. In embodiments, the viral capsid protein is expressed in the plant cell and encapsidates the synthetic endornavirus satellite RNA. In yet other embodiments, the plant cell includes the endornavirus, and the endornavirus provides the RdRP protein to the plant cell. In certain embodiments, the methods can further comprise a first step of providing a population of plants comprising the plant cells comprising: (i) the endornavirus which provides the RdRP; or (ii) recombinant polynucleotide molecule that encodes the RdRP; and then providing the recombinant RNA molecule to the plants comprising the plant cells. In certain embodiments, the methods can further comprise the step of determining if the plant cell comprises an endornavirus which can provide the RdRP. In embodiments wherein it is determined that the plant cell comprises the endornavirus which can provide the RdRP, the endornavirus, the RdRP protein, and/or the recombinant polynucleotide encoding the RdRP is optionally not exogenously provided to the plant cell. In other embodiments wherein it is determined that the plant cell does not comprise the endornavirus which can provide the RdRP and the endornavirus is exogenously provided to the cell, the RdRP protein or the recombinant polynucleotide encoding the RdRP is exogenously provided to the plant cell, or a combination of the endornavirus, RdRP protein, or polynucleotide encoding the RdRP is exogenously provided to the plant cell. In embodiments, a complete self-replicating endornavirus satellite system is introduced into a plant or plant cells, wherein the self-replicating endornavirus satellite system includes: (1) a recombinant endornavirus satellite RNA comprising, from 5' terminus to 3' terminus: (a) a 5' RNA replication element recognized by an endornavirus RNA-dependent RNA polymerase (RdRP); (b) a

cargo RNA molecule; and (c) a 3' RNA replication element recognized by the RdRP; wherein the 5' RNA replication element, the cargo RNA molecule, and the 3' RNA replication element are operably linked, and wherein the promoter and the cargo RNA molecule are heterologous to the 5' RNA replication element and the 3' RNA replication element; and (2) an exogenous endornavirus (e.g., an endornavirus that is not endemic or native to the plant or plant cells) that is capable of replication in the plant or plant cells and that encodes the endornavirus RdRP that recognizes the 5' and 3' RNA replication element sequences in the recombinant endornavirus satellite RNA. In embodiments, the endornavirus RdRP comprises a protein having at least 85%, 90%, 95%, 97%, or 99% sequence identity to SEQ ID NO: 613 to 725, or 726. The presence or absence of an endornavirus in a target plant can be determined by an RNA detection assay (e.g., an RT-PCR assay) using nucleic acid probes and/or primers which can detect any part of an endornavirus genome including a 5' RNA replication element, a CP and/or RdRP coding region, and/or a 3' RNA replication element. Such probes and primers include those which detect any of the 5' or 3' RNA replication elements set forth in Table 1 or having significant sequence identity thereto (e.g., at least about 80%, 85%, 90%, 95%, 98%, or 99% of a length of at least about 18, 20, 30, 40 or 50 nt). The presence or absence of an endornavirus in a target plant can be determined by a protein detection assay (e.g., an immunoassay) directed to an EV RdRP (e.g., an RdRP encoded by a EV genome disclosed in Table 1 or an RdRP disclosed in Table 17).

[0087] In certain embodiments of any of the aforementioned or otherwise disclosed methods, the recombinant RNA that effects: (i) a phenotypic change in the plant or plant cell; (ii) increases a plant's resistance to a pest or pathogen; or (iii) increases a plant's resistance to stress can include an RNA for modulating a target gene's expression relative to the target gene's expression in a control plant or plant cell not provided with the recombinant RNA molecule, and the phenotypic change, increased resistance to the pest or pathogen, or increased resistance to stress is a result of the modulation. In embodiments, the modulation is (a) an increase of the target gene's expression; or (b) a decrease of the target gene's expression. In some embodiments, expression of the target gene is increased by up to about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 100%, or more than 100% relative to a reference level (e.g., a level found in a control plant or plant cell lacking the recombinant RNA). In certain embodiments, expression of the target gene is increased by up to about 2-, 3-, 4-, 5-, 6-, 8-, 9-, 10-fold, or more relative to a reference level (e.g., a level found in a control plant or plant cell lacking the recombinant RNA molecule). In some embodiments, expression of the target gene is decreased by at least about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%,

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44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 100%, or more than 100% relative to a reference level (*e.g.*, a level found in a level found in a control plant or plant cell lacking the recombinant RNA). In certain embodiments, expression of the target gene is decreased by up to about 2-, 3-, 4-, 5-, 6-, 8-, 9-, 10-fold, or more relative to a reference level (*e.g.*, a level found in a control plant or plant cell lacking the recombinant RNA molecule).

Modulation of target gene expression can be effected by one or more RNAs for modifying the genome, epigenome, and/or transcriptome of the plant or plant cell. RNAs for modifying the genome include gRNAs recognized by CAS nucleases, RNAs encoding TALENs or artificial zinc finger proteins (aZFN). RNAs for modifying the epigenome include RNAs which provide RNA directed DNA methylation such as in promoter regions of target genes (Matzke and Mosher (2014); doi: 10.1038/nrg3683). Embodiments of an RNA for modifying the transcriptome include one or more RNAs that comprise any of: a hairpin RNA (hpRNA); an RNA that forms multiple stem-loops; an RNA pseudoknot; an RNA molecule that forms at least partially double-stranded RNA; a small interfering RNA (siRNA) or siRNA precursor; a microRNA (miRNA) or miRNA precursor; a phased siRNA or phased siRNA precursor (see, *e.g.*, US Patent No. 8,404,928); a ribozyme; a ligand-responsive ribozyme (aptazyme); an RNA aptamer; or a long noncoding RNA (lncRNA).

[0088] In any of the aforementioned or otherwise disclosed methods wherein a phenotypic change is obtained or effected in a plant or plant cell, the cargo RNA molecule can comprise an RNA that effects a phenotypic change in the plant or plant cell in comparison to a plant or plant cell lacking the recombinant RNA. In certain embodiments, phenotypes that are changed include developmental rate, growth rate, size, yield (*e.g.*, intrinsic yield), vigor, photosynthetic capability, flavor, starch production, protein content, carbohydrate content, oil content, fatty acid content, lipid content, digestibility, biomass, shoot length, root length, root architecture, seed set, seed weight, seed quality (*e.g.*, nutritional content), germination, fruit set, rate of fruit ripening, production of biopolymers, production of fibers, production of biofuels, production of pharmaceutical peptides (*e.g.*, hormones, enzymes, transcription factors, antigens, antibodies, or antibody fragments), production of secretable peptides, enzyme production, improved processing traits, or amount of harvestable produce. In some embodiments, phenotypes that are changed include taste, appearance, or shelf-life of a product harvested from the plant. In other embodiments, phenotypes that are changed include flower size, flower color, flower patterning, flower morphology including presence or absence of stamens, flower number, flower longevity, flower fragrance, leaf size, leaf color, leaf patterning, leaf morphology, plant height, or plant architecture.

[0089] In any of the aforementioned or otherwise disclosed methods wherein a plant's resistance to a pest or pathogen is increased, the recombinant RNA can comprise an RNA that inhibits expression of a gene of the pest or pathogen and/or inhibits replication of the genome of the pest or pathogen. In certain embodiments, the pest or pathogen is selected from the group comprising: a bacterium, a virus other than

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an endornavirus, a fungus, an oomycete, and an invertebrate (*e.g.*, an arthropod or a nematode). Target viruses other than an endornavirus include; (i) positive-strand RNA viruses in the *Bromoviridae*, *Closteroviridae*, *Luteoviridae*, or *Potyviridae* family; (ii) negative strand RNA viruses in the *Bunyaviridae* and *Rhabdoviridae* family; (iii) dsDNA viruses in the family *Caulimoviridae*; and (iv) ssDNA viruses in the family *Geminiviridae*. Target arthropods pests include coleopteran and lepidopteran insects. Target fungal pathogens include *Magnaporthe* spp., *Botrytis* spp., *Puccinia* spp., *Fusarium* spp., *Blumeria* spp., *Mycosphaerella* spp., *Colletotrichum* spp., *Ustilago* spp., *Melampsora* spp., *Phakopsora* spp., *Phytophthora* spp., and *Rhizoctonia* spp. In embodiments, the cargo RNA molecule effects an increase in the plant's resistance to a pest or pathogen, relative to that in a plant not provided with the recombinant RNA molecule.

[0090] In any of the aforementioned or otherwise disclosed methods wherein a plant's resistance to stress is increased, the recombinant RNA can comprise an RNA that targets a plant gene which provides such resistance. In embodiments, the RNA that effects an increase in the plant's resistance to stress in the plant or plant cell includes an RNA for modulating the target gene's expression relative to the target gene's expression in a control plant or plant cell not provided with the recombinant RNA molecule, and wherein the increase stress resistance is a result of the modulation. In embodiments, the modulation is (a) an increase of the target gene's expression; or (b) a decrease of the target gene's expression. In still other embodiments, the RNA that effects an increase in the plant's resistance to stress in the plant or plant cell comprises a messenger RNA encoding a protein which confers the stress resistance. In still other embodiments, the messenger RNA includes an RNA sequence absent in the transcriptome of the plant or plant cell lacking the recombinant RNA. In embodiments, the stress includes at least one abiotic stress selected from the group including: nutrient stress, light stress, drought stress, heat stress, and cold stress. In other embodiments, the stress includes at least one biotic stress selected from the group including: crowding, shading, and allelopathy (*e.g.*, resulting from allelopathic chemicals including a juglone produced by walnut trees).

[0091] In any of the aforementioned or otherwise disclosed methods wherein an exogenous polypeptide (*e.g.*, an exogenous polypeptide) is expressed in a plant or plant cell, the cargo RNA can encode the exogenous polypeptide. In embodiments, the polypeptide is isolated (*e.g.*, separated from at least one other cellular components such as a carbohydrate, a lipid, or another protein) or polypeptide is purified.

[0092] In any of the aforementioned or otherwise disclosed methods wherein a synthetic endornavirus satellite particle is manufactured, such manufacture can occur in either a cell-based system or a cell-free system. Cell-based methods of manufacturing a synthetic endornavirus satellite particle can comprise: (a) providing to a plant cell the recombinant RNA molecule, wherein the recombinant RNA molecule comprises an encapsidation recognition element (ERE), and wherein the plant cell comprises an RdRP protein that recognizes the 5' RNA replication element and 3' RNA replication element catalyzes synthesis of a synthetic endornavirus satellite RNA from the recombinant RNA molecule and a viral

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capsid protein, wherein the ERE provides for encapsidation of the RNA by the viral capsid protein; and optionally isolating the synthetic endornavirus satellite particle from the plant cell, a plant comprising the plant cell, or from media in which the plant cell or the plant had been grown. Cell-free methods of manufacturing a synthetic endornavirus satellite particle include methods where the recombinant RNA molecule is combined with a viral capsid protein in a vessel, wherein the recombinant RNA molecule comprises an ERE, and wherein the ERE provides for encapsidation of the RNA by the viral capsid protein in the vessel; optionally wherein the method further comprises isolating the synthetic endornavirus satellite particle from uncombined RNA and/or viral capsid protein in the vessel. In certain embodiments of either cell-based or cell-free methods, the synthetic satellite particle is isolated (*e.g.*, separated from at least one other cellular components such as an organelle, a membrane, a carbohydrate, a lipid, or another protein) or is purified. In certain embodiments, the methods can further comprise formulating the synthetic endornavirus satellite particle.

[0093] Synthetic endornavirus satellite particles comprising the recombinant RNA, including those made by the aforementioned methods are also provided. Methods of providing any of the aforementioned synthetic endornavirus satellite particles to a plant, including contacting (*e.g.*, spraying, dusting, injecting, soaking, etc.) the plant with the synthetic endornavirus satellite particle or a formulation thereof are also provided.

[0094] The recombinant polynucleotides, cells comprising the same, and synthetic endornavirus satellite particles described herein can be formulated either in pure form (*e.g.*, the composition contains only the recombinant polynucleotide) or together with one or more additional formulation components to facilitate application or delivery of the compositions. In embodiments, the additional formulation component includes, *e.g.*, a carrier (*i.e.*, a component that has an active role in delivering the active agent (*e.g.*, recombinant polynucleotide); for example, a carrier can encapsulate, covalently or non-covalently modify, or otherwise associate with the active agent in a manner that improves delivery of the active agent) or an excipient (*e.g.*, a delivery vehicle, adjuvant, diluent, surfactant, stabilizer, or tonicity agent). In some embodiments, the composition is formulated for delivery to a plant.

[0095] In some aspects, the disclosure provides a formulation comprising any of the compositions described herein. In some embodiments, the formulation is a liquid, a gel, or a powder. In some embodiments, the formulation is configured to be sprayed on plants, to be injected into plants (see, *e.g.*, US Patent No. 11,844,318) or otherwise introduced into the vascular system of a plant, to be rubbed on leaves, to be soaked into plants, to be coated onto plants, or be coated on seeds, or to be delivered through root uptake (*e.g.*, in a hydroponic system or via soil).

[0096] Depending on the intended objectives and prevailing circumstances, the composition can be formulated into emulsifiable concentrates, suspension concentrates, directly sprayable or dilutable solutions, coatable pastes, diluted emulsions, spray powders, soluble powders, dispersible powders, wettable powders, dusts, granules, encapsulations in polymeric substances, microcapsules, foams, aerosols, carbon dioxide gas preparations, or tablets. In some instances, the composition is a liquid. In

some instances, the composition is a solid. In some instances, the composition is an aerosol, such as in a pressurized aerosol can.

[0097] In some instances, the recombinant polynucleotide makes up about 0.1% to about 100% of the composition, such as any one of about 0.01% to about 100%, about 1% to about 99.9%, about 0.1% to about 10%, about 1% to about 25%, about 10% to about 50%, about 50% to about 99%, or about 0.1% to about 90% of active ingredients (*e.g.*, recombinant polynucleotides). In some instances, the composition includes at least any of 0.1%, 0.5%, 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or more active ingredients (*e.g.*, recombinant polynucleotides). In some instances, the concentrated agents are preferred as commercial products, the final user normally uses diluted agents, which have a substantially lower concentration of active ingredient.

[0098] In some embodiments, the composition is formulated for topical delivery to a plant. In some embodiments, the topical delivery is spraying, leaf rubbing (*e.g.*, with or without an abrasive), soaking, coating (*e.g.*, coating using micro-particulates or nano-particulates), or delivery through root uptake (*e.g.*, delivery in a hydroponic system or by a root drench).

[0099] In some embodiments, the composition further comprises a carrier and/or an excipient. In other embodiments, the composition does not comprise a carrier or excipient, *e.g.*, comprises a naked polynucleotide (*e.g.*, a naked RNA).

[0100] In some embodiments, the recombinant polynucleotide is delivered at a concentration of at least 0.1 grams per acre, *e.g.*, at least 0.1, 1, 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 grams per acre. In some embodiments, less than 120 liters per acre is delivered, *e.g.*, less than 110, 100, 90, 80, 70, 60, 50, 40, 30, 20, 15, 10, 5, or 2 liters per acre or less than 1 liter per acre.

[0101] In some aspects, the formulation comprises a carrier. In some embodiments the formulation is an emulsion or a reverse emulsion, a liquid, or a gel. In embodiments, the formulation includes a carrier that serves as a physical support (*e.g.*, solid or semi-solid surfaces or matrices, powders, or particles or nanoparticles). In embodiments, the active agent is encapsulated or enclosed in or attached to or complexed with a carrier including a liposome, vesicle, micelle, or other fluid compartment. In embodiments, the active agent is encapsulated or enclosed in or attached to or complexed with a carrier including a naturally occurring or synthetic, branched or linear polymer (*e.g.*, pectin, agarose, chitin, chitosan, DEAE-dextran, polyvinylpyrrolidone ("PVP"), or polyethylenimine ("PEI")). In embodiments the carrier includes cations or a cationic charge, such as cationic liposomes or cationic polymers such as polyamines (*e.g.*, spermine, spermidine, putrescine). In embodiments, the carrier includes a polypeptide such as an enzyme, (*e.g.*, cellulase, pectolyase, maceroenzyme, pectinase), a cell penetrating or pore-forming peptide (*e.g.*, poly-lysine, poly-arginine, or polyhomarginine peptides).

[0102] Non-limiting examples of carriers include cationic liposomes and polymer nanoparticles such as those reviewed by Zhang et al. (2007) J. Controlled Release, 123:1 - 10, and the cross-linked multilamellar liposomes described in US Patent Application Publication 2014/0356414 A1, incorporated by reference in its entirety herein. In embodiments, the carrier includes a nanomaterial, such as carbon or

silica nanoparticles, carbon nanotubes, carbon nanofibers, or carbon quantum dots. Non-limiting examples of carriers include particles or nanoparticles (*e.g.*, particles or nanoparticles made of materials such as carbon, silicon, silicon carbide, gold, tungsten, polymers, or ceramics) in various size ranges and shapes, magnetic particles or nanoparticles (*e.g.*, silenceMag Magnetotransfection™ agent, OZ Biosciences, San Diego, CA), abrasive or scarifying agents, needles or microneedles, matrices, and grids.

[0103] In certain embodiments, particulates and nanoparticulates are useful in delivery of the polynucleotide composition or the nuclease or both. Useful particulates and nanoparticles include those made of metals (*e.g.*, gold, silver, tungsten, iron, cerium), ceramics (*e.g.*, aluminum oxide, silicon carbide, silicon nitride, tungsten carbide), polymers (*e.g.*, polystyrene, polydiacetylene, and poly(3,4-ethylenedioxythiophene) hydrate), semiconductors (*e.g.*, quantum dots), silicon (*e.g.*, silicon carbide), carbon (*e.g.*, graphite, graphene, graphene oxide, or carbon nanosheets, nanocomplexes, or nanotubes), and composites (*e.g.*, polyvinylcarbazole/graphene, polystyrene/graphene, platinum/graphene, palladium/graphene nanocomposites). In certain embodiments, such particulates and nanoparticulates are further covalently or non-covalently functionalized, or further include modifiers or cross-linked materials such as polymers (*e.g.*, linear or branched polyethylenimine, poly-lysine), polynucleotides (*e.g.*, DNA or RNA), polysaccharides, lipids, polyglycols (*e.g.*, polyethylene glycol, thiolated polyethylene glycol), polypeptides or proteins, and detectable labels (*e.g.*, a fluorophore, an antigen, an antibody, or a quantum dot). In various embodiments, such particulates and nanoparticles are neutral, or carry a positive charge, or carry a negative charge.

[0104] Embodiments of compositions including particulates include those formulated, *e.g.*, as liquids, colloids, dispersions, suspensions, aerosols, gels, and solids. Embodiments include nanoparticles affixed to a surface or support, *e.g.*, an array of carbon nanotubes vertically aligned on a silicon or copper wafer substrate. Embodiments include polynucleotide compositions including particulates (*e.g.*, gold or tungsten or magnetic particles) delivered by a Biolistic-type technique or with magnetic force. The size of the particles used in Biolistics is generally in the "microparticle" range, for example, gold microcarriers in the 0.6, 1.0, and 1.6 micrometer size ranges (see, *e.g.*, instruction manual for the Helios® Gene Gun System, Bio-Rad, Hercules, CA; Randolph-Anderson et al. (2015) "Submicron gold particles are superior to larger particles for efficient Biolistic® transformation of organelles and some cell types", Bio-Rad US/EG Bulletin 2015), but successful Biolistics delivery using larger (40 - 48 - WO 2019/144124 PCT/US2019/014559 nanometer) nanoparticles has been reported in cultured animal cells; see O'Brian and Lummis (2011) BMC Biotechnol., 11 :66 - 71.

[0105] Other embodiments of useful particulates are nanoparticles, which are generally in the nanometer (nm) size range or less than 1 micrometer, *e.g.*, with a diameter of less than about 1 nm, less than about 3 nm, less than about 5 nm, less than about 10 nm, less than about 20 nm, less than about 40 nm, less than about 60 nm, less than about 80 nm, and less than about 100 nm. Specific, non-limiting embodiments of nanoparticles commercially available (all from Sigma-Aldrich Corp., St. Louis, MO) include gold nanoparticles with diameters of 5, 10, or 15 nm; silver nanoparticles with particle sizes of

10, 20, 40, 60, or 100 nm; palladium "nanopowder" of less than 25 nm particle size; single-, double-, and multi-walled carbon nanotubes, *e.g.*, with diameters of 0.7 - 1.1, 1.3 - 2.3, 0.7 - 0.9, or 0.7 - 1.3 nm, or with nano tube bundle dimensions of 2 - 10 nm by 1 - 5 micrometers, 6 - 9 nm by 5 micrometers, 7 - 15 nm by 0.5 - 10 micrometers, 7 - 12 nm by 0.5 - 10 micrometers, 110 - 170 nm by 5 - 9 micrometers, 6 - 13 nm by 2.5 - 20 micrometers. Embodiments include polynucleotide compositions including materials such as gold, silicon, cerium, or carbon, *e.g.*, gold or gold-coated nanoparticles, silicon carbide whiskers, carborundum, porous silica nanoparticles, gelatin/silica nanoparticles, nanoceria or cerium oxide nanoparticles (CNPs), carbon nanotubes (CNTs) such as single-, double-, or multi-walled carbon nanotubes and their chemically functionalized versions (*e.g.*, carbon nanotubes functionalized with amide, amino, carboxylic acid, sulfonic acid, or polyethylene glycol moieties), and graphene or graphene oxide or graphene complexes; see, for example, Wong et al. (2016) *Nano Lett.*, 16: 1161 - 1172; Giraldo et al. (2014) *Nature Materials*, 13:400-409; Shen et al. (2012) *Theranostics*, 2:283 - 294; Kim et al. (2011) *Bioconjugate Chem.*, 22:2558 - 2567; Wang et al. (2010) *J. Am. Chem. Soc. Comm.*, 132:9274 - 9276; Zhao et al. (2016) *Nanoscale Res. Lett.*, 11: 195 - 203; and Choi et al. (2016) *J. Controlled Release*, 235:222 - 235. See also, for example, the various types of particles and nanoparticles, their preparation, and methods for their use, *e.g.*, in delivering polynucleotides and polypeptides to cells, disclosed in US Patent Application Publications 2010/0311168, 2012/0023619, 2012/0244569, 2013/0145488, 2013/0185823, 2014/0096284, 2015/0040268, 2015/0047074, and 2015/0208663, all of which are incorporated herein by reference in their entirety.

[0106] In some aspects, the composition includes an excipient, *e.g.*, a delivery vehicle, adjuvant, diluent, surfactant, stabilizer, or tonicity agent or a combination thereof. In some embodiments, the excipient is a crop oil concentrate, a vegetable oil concentrate, a modified vegetable oil, a nitrogen source, a deposition (drift control) and/or retention agent (with or without ammonium sulfate and/or defoamer), a compatibility agent, a buffering agent and/or acidifier, a water conditioning agent, a basic blend, a spreader-sticker and/or extender, an adjuvant plus foliar fertilizer, an antifoam agent, a foam marker, a scent, or a tank cleaner and/or neutralizer. In some embodiments, the excipient is an adjuvant described in the *Compendium of Herbicide Adjuvants* (Young et al. (2016). *Compendium of Herbicide Adjuvants* (13th ed.), Purdue University).

[0107] Examples of delivery vehicles and diluents include, but are not limited to, lactose, dextrose, sucrose, sorbitol, mannitol, starches, gum acacia, calcium phosphate, alginates, tragacanth, gelatin, calcium silicate, microcrystalline cellulose, polyvinylpyrrolidone, cellulose, water, saline solution, syrup, methylcellulose, methyl- and propylhydroxybenzoates, talc, magnesium stearate, and mineral oil. Further examples of delivery vehicles include, but are not limited to, solid or liquid excipient materials, solvents, stabilizers, slow-release excipients, colorings, and surface-active substances (surfactants). In some instances, the excipient (*e.g.*, delivery vehicle) is a stabilizing vehicle. In embodiments, the stabilizing vehicle includes, *e.g.*, an epoxidized vegetable oil, an antifoaming agent, *e.g.* silicone oil, a preservative, a viscosity regulator, a binding agent, or a tackifier. In some instances, the stabilizing

vehicle is a buffer suitable for the recombinant polynucleotide. In some instances, the composition is microencapsulated in a polymer bead delivery vehicle. In some instances, the stabilizing vehicle protects the recombinant polynucleotide against UV and/or acidic conditions. In some instances, the delivery vehicle contains a pH buffer. In some instances, the composition is formulated to have a pH in the range of about 4.5 to about 9.0, including for example pH ranges of about any one of 5.0 to about 8.0, about 6.5 to about 7.5, or about 6.5 to about 7.0.

[0108] In some instances, the composition provided herein includes an adjuvant. Adjuvants are agents that do not possess the polynucleotide activity, but impart beneficial properties to a formulation. For example, adjuvants are either pre-mixed in the formulation or added to a spray tank to improve mixing or application or to enhance performance. They are used extensively in products designed for foliar applications. Adjuvants can be used to customize the formulation to specific needs and compensate for local conditions. Adjuvants can be designed to perform specific functions, including wetting, spreading, sticking, reducing evaporation, reducing volatilization, buffering, emulsifying, dispersing, reducing spray drift, and reducing foaming. No single adjuvant can perform all these functions, but compatible adjuvants often can be combined to perform multiple functions simultaneously.

[0109] Among nonlimiting examples of adjuvants included in the formulation are binders, dispersants and stabilizers, specifically, for example, casein, gelatin, polysaccharides (*e.g.*, starch, gum arabic, cellulose derivatives, alginic acid, etc.), lignin derivatives, bentonite, sugars, synthetic water-soluble polymers (*e.g.*, polyvinyl alcohol, polyvinylpyrrolidone, polyacrylic acid, etc.), PAP (acidic isopropyl phosphate), BHT (2,6-di-*t*-butyl-4-methylphenol), BHA (a mixture of 2-*t*-butyl-4-methoxyphenol and 3-*t*-butyl-4-methoxyphenol), vegetable oils, mineral oils, fatty acids and fatty acid esters.

[0110] In embodiments, the compositions provided herein are in a liquid formulation. Liquid formulations are generally mixed with water, but in some instances are used with crop oil, diesel fuel, kerosene, or other light oil as an excipient. The amount of active ingredient (*e.g.*, recombinant polynucleotides) often ranges from about 0.5 to about 80 percent by weight.

[0111] In embodiments, an emulsifiable concentrate formulation contains a liquid active ingredient, one or more petroleum-based solvents, and an agent that allows the formulation to be mixed with water to form an emulsion. Such concentrates can be used in agricultural, ornamental and turf, forestry, structural, food processing, livestock, and public health pest formulations. In embodiments, these are adaptable to application equipment from small portable sprayers to hydraulic sprayers, low-volume ground sprayers, mist blowers, and low-volume aircraft sprayers. Some active ingredients readily dissolve in a liquid excipient. When mixed with an excipient, they form a solution that does not settle out or separate, *e.g.*, a homogenous solution. In embodiments, formulations of these types include an active ingredient, a carrier and/or an excipient, and one or more other ingredients. Solutions can be used in any type of sprayer, indoors and outdoors.

[0112] In some instances, the composition is formulated as an invert emulsion. An invert emulsion is a water-soluble active ingredient dispersed in an oil excipient. Invert emulsions require an emulsifier that

allows the active ingredient to be mixed with a large volume of petroleum-based excipient, usually fuel oil. Invert emulsions aid in reducing drift. With other formulations, some spray drift results when water droplets begin to evaporate before reaching target surfaces; as a result the droplets become very small and lightweight. Because oil evaporates more slowly than water, invert emulsion droplets shrink less and more active ingredient reaches the target. Oil further helps to reduce runoff and improve rain resistance. It further serves as a sticker-spreader by improving surface coverage and absorption. Because droplets are relatively large and heavy, it is difficult to get thorough coverage on the undersides of foliage. Invert emulsions are most commonly used along rights-of-way where drift to susceptible non-target areas can be a problem.

[0113] A flowable or liquid formulation combines many of the characteristics of emulsifiable concentrates and wettable powders. Manufacturers use these formulations when the active ingredient is a solid that does not dissolve in either water or oil. The active ingredient, impregnated on a substance such as clay, is ground to a very fine powder. The powder is then suspended in a small amount of liquid. The resulting liquid product is quite thick. Flowables and liquids share many of the features of emulsifiable concentrates, and they have similar disadvantages. They require moderate agitation to keep them in suspension and leave visible residues, similar to those of wettable powders.

[0114] Flowables/liquids are easy to handle and apply. Because they are liquids, they are subject to spilling and splashing. They contain solid particles, so they contribute to abrasive wear of nozzles and pumps. Flowable and liquid suspensions settle out in their containers. Because flowable and liquid formulations tend to settle, packaging in containers of five gallons or less makes remixing easier.

[0115] Aerosol formulations contain one or more active ingredients and a solvent. Most aerosols contain a low percentage of active ingredients. There are two types of aerosol formulations—the ready-to-use type commonly available in pressurized sealed containers and those products used in electrical or gasoline-powered aerosol generators that release the formulation as a smoke or fog.

[0116] Ready to use (RTU) aerosol formulations are usually small, self-contained units that release the formulation when the nozzle valve is triggered. The formulation is driven through a fine opening by an inert gas under pressure, creating fine droplets. These products are used in greenhouses, in small areas inside buildings, or in localized outdoor areas. Commercial models, which hold five to 5 pounds of active ingredient, are usually refillable.

[0117] Smoke or fog aerosol formulations are not under pressure. They are used in machines that break the liquid formulation into a fine mist or fog (aerosol) using a rapidly whirling disk or heated surface.

[0118] In some embodiments, the composition comprises a liquid excipient. In embodiments, a liquid excipient includes, for example, aromatic or aliphatic hydrocarbons (*e.g.*, xylene, toluene, alkylnaphthalene, phenylxylethane, kerosene, gas oil, hexane, cyclohexane, etc.), halogenated hydrocarbons (*e.g.*, chlorobenzene, dichloromethane, dichloroethane, trichloroethane, etc.), alcohols (*e.g.*, methanol, ethanol, isopropyl alcohol, butanol, hexanol, benzyl alcohol, ethylene glycol, etc.), ethers

(*e.g.*, diethyl ether, ethylene glycol dimethyl ether, diethylene glycol monomethyl ether, diethylene glycol monoethyl ether, propylene glycol monomethyl ether, tetrahydrofuran, dioxane, etc.), esters (*e.g.*, ethyl acetate, butyl acetate, etc.), ketones (*e.g.*, acetone, methyl ethyl ketone, methyl isobutyl ketone, cyclohexanone, etc.), nitriles (*e.g.*, acetonitrile, isobutyronitrile, etc.), sulfoxides (*e.g.*, dimethyl sulfoxide, etc.), amides (*e.g.*, N,N-dimethylformamide, N,N-dimethylacetamide, cyclic imides (*e.g.* N-methylpyrrolidone) alkylidene carbonates (*e.g.*, propylene carbonate, etc.), vegetable oil (*e.g.*, soybean oil, cottonseed oil, etc.), vegetable essential oils (*e.g.*, orange oil, hyssop oil, lemon oil, etc.), or water.

[0119] In some embodiments, the composition comprises a gaseous excipient. Gaseous excipients include, for example, butane gas, flaron gas, liquefied petroleum gas (LPG), dimethyl ether, and carbon dioxide gas.

[0120] In some embodiments, the compositions are provided as a dry formulation. Dry formulations can be divided into two types: ready-to-use and concentrates that must be mixed with water to be applied as a spray. Most dust formulations are ready to use and contain a low percentage of active ingredients (less than about 10 percent by weight), plus a very fine, dry inert excipient (*e.g.*, talc, chalk, clay, nut hulls, or volcanic ash). The size of individual dust particles varies. A few dust formulations are concentrates and contain a high percentage of active ingredients. In some embodiments, these are mixed with dry inert excipients before applying. In some embodiments, dusts are used dry and can easily drift to non-target sites.

[0121] In some instances, the composition is formulated as a powder. In some instances, the composition is formulated as a wettable powder. Wettable powders are dry, finely ground formulations that look like dusts. They usually must be mixed with water for application as a spray. A few products, however, can be applied either as a dust or as a wettable powder—the choice is left to the applicator. Wettable powders have about 1 to about 95 percent active ingredient by weight; in some cases more than about 50 percent. The particles do not dissolve in water. They settle out quickly unless constantly agitated to keep them suspended. They can be used for most pest problems and in most types of spray equipment where agitation is possible. Wettable powders have excellent residual activity. Because of their physical properties, most of the formulation remains on the surface of treated porous materials such as concrete, plaster, and untreated wood. In such cases, only the water penetrates the material.

[0122] In some instances, the composition is formulated as a soluble powder. Soluble powder formulations look like wettable powders. However, when mixed with water, soluble powders dissolve readily and form a true solution. After they are mixed thoroughly, no additional agitation is necessary. The amount of active ingredient in soluble powders ranges from about 15 to about 95 percent by weight; in some cases more than about 50 percent. Soluble powders have all the advantages of wettable powders and none of the disadvantages, except the inhalation hazard during mixing.

[0123] In some instances, the composition is formulated as a water-dispersible granule. Water-dispersible granules, also known as dry flowables, are like wettable powders, except instead of being dust-like, they are formulated as small, easily measured granules. Water-dispersible granules must be

mixed with water to be applied. Once in water, the granules break apart into fine particles similar to wettable powders. The formulation requires constant agitation to keep it suspended in water. The percentage of active ingredient is high, often as much as 90 percent by weight. Water-dispersible granules share many of the same advantages and disadvantages of wettable powders, except they are more easily measured and mixed. Because of low dust, they cause less inhalation hazard to the applicator during handling.

[0124] In some embodiments, the composition comprises a solid excipient. Solid excipients include finely-divided powder or granules of clay (*e.g.* kaolin clay, diatomaceous earth, bentonite, Fubasami clay, acid clay, etc.), synthetic hydrated silicon oxide, talc, ceramics, other inorganic minerals (*e.g.*, sericite, quartz, sulfur, activated carbon, calcium carbonate, hydrated silica, etc.), a substance which can be sublimated and is in the solid form at room temperature (*e.g.*, 2,4,6-triisopropyl-1,3,5-trioxane, naphthalene, p-dichlorobenzene, camphor, adamantane, etc.); wool; silk; cotton; hemp; pulp; synthetic resins (*e.g.*, polyethylene resins such as low-density polyethylene, straight low-density polyethylene and high-density polyethylene; ethylene-vinyl ester copolymers such as ethylene-vinyl acetate copolymers; ethylene-methacrylic acid ester copolymers such as ethylene-methyl methacrylate copolymers and ethylene-ethyl methacrylate copolymers; ethylene-acrylic acid ester copolymers such as ethylene-methyl acrylate copolymers and ethylene-ethyl acrylate copolymers; ethylene-vinylcarboxylic acid copolymers such as ethylene-acrylic acid copolymers; ethylene-tetracyclododecene copolymers; polypropylene resins such as propylene homopolymers and propylene-ethylene copolymers; poly-4-methylpentene-1, polybutene-1, polybutadiene, polystyrene; acrylonitrile-styrene resins; styrene elastomers such as acrylonitrile-butadiene-styrene resins, styrene-conjugated diene block copolymers, and styrene-conjugated diene block copolymer hydrides; fluororesins; acrylic resins such as poly(methyl methacrylate); polyamide resins such as nylon 6 and nylon 66; polyester resins such as polyethylene terephthalate, polyethylene naphthalate, polybutylene terephthalate, and polycyclohexylenedimethylene terephthalate; polycarbonates, polyacetals, polyacrylsulfones, polyarylates, polyacrylates, hydroxybenzoic acid polyesters, polyetherimides, polyester carbonates, polyphenylene ether resins, polyvinyl chloride, polyvinylidene chloride, polyurethane, and porous resins such as foamed polyurethane, foamed polypropylene, or foamed ethylene, etc.), glasses, metals, ceramics, fibers, cloths, knitted fabrics, sheets, papers, yarn, foam, porous substances, and multifilaments.

[0125] In some instances, the composition is provided in a microencapsulated formulation (*e.g.*, a nanocapsule). Microencapsulated formulations are mixed with water and sprayed in the same manner as other sprayable formulations. After spraying, the encapsulation shell or coating breaks down and slowly releases the active ingredient.

[0126] In some instances, the composition is provided in a liposome. In some instances, the composition is provided in a vesicle.

[0127] In some instances, a composition provided herein includes a surfactant. Surfactants, also called wetting agents and spreaders, physically alter the surface tension of a spray droplet. For a

formulation to perform its function properly, a spray droplet must be able to wet the foliage and spread out evenly over a leaf. Surfactants enlarge the area of formulation coverage, thereby increasing exposure to the active agent. Surfactants are particularly important when applying a formulation to waxy or hairy leaves. Without proper wetting and spreading, spray droplets often run off or fail to cover leaf surfaces adequately. Too much surfactant, however, can cause excessive runoff and reduce efficacy.

[0128] Surfactants can be classified as anionic, cationic, or nonionic. Formulation activity in the presence of a nonionic surfactant can be quite different from activity in the presence of a cationic or anionic surfactant. Selecting the wrong surfactant can reduce the efficacy of a product and injure the target plant. For example, anionic surfactants are most effective when used with contact pesticides (pesticides that control a pest by direct contact rather than being absorbed systemically). Cationic surfactants are not typically used as stand-alone surfactants because they usually are phytotoxic.

[0129] Nonionic surfactants, often used with systemic pesticides, help sprays to penetrate plant cuticles. Nonionic surfactants are compatible with most pesticides, and most EPA-registered pesticides that require a surfactant recommend a nonionic type. Adjuvants include, but are not limited to, stickers, extenders, plant penetrants, compatibility agents, buffers or pH modifiers, drift control additives, defoaming agents, and thickeners.

[0130] Among nonlimiting examples of surfactants included in the compositions described herein are alkyl sulfate ester salts, alkyl sulfonates, alkyl aryl sulfonates, alkyl aryl ethers and polyoxyethylenated products thereof, polyethylene glycol ethers, polyvalent alcohol esters and sugar alcohol derivatives. In some embodiments, the surfactant is a nonionic surfactant, a surfactant plus nitrogen source, an organo-silicone surfactant, or a high surfactant oil concentrate.

[0131] In formulations and in the use forms prepared from these formulations, the recombinant polynucleotide can, in embodiments, be in a mixture with other active compounds, such as pesticidal agents (*e.g.*, insecticides, sterilants, acaricides, nematocides, molluscicides, or fungicides, attractants, growth-regulating substances, or herbicides). As used herein, the term “pesticidal agent” refers to any substance or mixture of substances intended for preventing, destroying, repelling, or mitigating any pest. A pesticide can be a chemical substance or biological agent used against pests including insects, mollusks, pathogens, weeds, nematodes, and microbes that compete with humans for food, destroy property, spread disease, or are a nuisance. The term “pesticidal agent” further encompasses other bioactive molecules such as antibiotics, antivirals pesticides, antifungals, antihelminthics, nutrients, pollen, sucrose, and/or agents that stun or slow insect movement.

[0132] In instances where the recombinant polynucleotide is applied to plants, a mixture with other known compounds, such as herbicides, fertilizers, growth regulators, safeners, semiochemicals, or else with agents for improving plant properties is also possible.

[0133] In another aspect, this disclosure is related to a method of producing a modified plant propagule that comprises at least one plant cell comprising a recombinant RNA molecule. The method, in general, includes the steps of: isolating a plant propagule comprising at least one plant cell comprising a

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recombinant RNA molecule and an endornavirus RNA-dependent RNA polymerase (RdRP) from a mixed population of plant cells comprising both plant cells comprising the recombinant RNA molecule and plant cells lacking the recombinant RNA molecule, wherein the recombinant RNA molecule comprises, in 5' to 3' order, a 5' RNA replication element that is capable of being recognized by the endornavirus RdRP; a cargo RNA sequence; and a 3' RNA replication element that is capable of being recognized by the endornavirus RdRP. In certain embodiments, the isolated plant propagule comprising at least one plant cell comprising a recombinant RNA molecule will be free or substantially free of plant cells lacking the recombinant RNA. Such isolated plant propagules which are substantially free of plant cells lacking the recombinant RNA can in certain embodiments comprise plant propagules where at least 75%, 80%, 85%, 90%, 95%, 98%, or 99% of the plant cells in the plant propagule contain the recombinant DNA molecule. In embodiments, the mixed population of plant cells comprise a population of protoplasts or a population of cells in callus, an explant, a plant part, or whole plant. In embodiments, the mixed population of plant cells can comprise a population of plant cells where less than 70%, 60%, 50%, 40%, 30%, 20%, 10%, 5%, or 1% of the plant cells in the population contain the recombinant RNA molecule. In some embodiments, the mixed population of plant cells comprise plant cells comprising the endornavirus RdRP and plant cells lacking the endornavirus RdRP. In certain embodiments, the plant cells lacking the endornavirus RdRP will also lack the recombinant RNA. In other embodiments, the mixed population of plant cells comprise plant cells comprising the endornavirus RdRP. In certain embodiments, the plant cells comprising the endornavirus RdRP can further comprise the recombinant RNA. In some embodiments, the cargo RNA sequence comprises RNA that encodes a selectable or scorable marker. In embodiments, the mixed population of plant cells is screened or selected for the presence of the plant cell comprising the recombinant RNA molecule prior to isolating the plant propagule. In such screens, the mixed population of cells or a portion thereof are subjected to an assay for a screenable marker for the presence of the recombinant RNA molecule (*e.g.*, an RNA sequence diagnostic for presence of the recombinant RNA molecule or a polypeptide encoded by the recombinant RNA molecule) and separated from plant cells lacking the recombinant RNA molecule. In some embodiments, the isolation comprises selecting for the plant cell comprising the recombinant RNA molecule prior to isolating the plant propagule. Examples of such selections in instances where the recombinant RNA encodes a selectable marker (*e.g.*, a protein which confers resistance to a selection agent such as an herbicide or antibiotic) can comprise exposing the mixed population of plant cells to a selection agent (*e.g.*, an herbicide or antibiotic) and isolating plant cells which survive exposure to the selection agent. Examples of selectable marker/selection agent combinations include glyphosate-resistant EPSPS enzymes and/or glyphosate oxidases/glyphosate, a bialaphos resistance (*bar*) or phosphinothricin acyl transferase (*pat*) enzyme/glufosinate, or a neomycin phosphotransferase (*npt*)/neomycin or kanamycin. In certain embodiments, the selectable or scorable marker is an RNA aptamer (*e.g.*, a Broccoli aptamer) or a regulatory RNA (*e.g.*, an siRNA, siRNA precursor, miRNA, or miRNA precursor, or a phased siRNA or phased siRNA precursor that downregulates expression of an endogenous gene in

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the plant, resulting in a detectable phenotype, e.g., bleaching caused by downregulation of a pigment-producing gene). In embodiments, the mixed population is located within a plant or a plant part. In some embodiments, the plant or plant part is screened or selected for presence of the recombinant RNA molecule prior to isolating the plant propagule. In other embodiments, the plant or plant part is screened or selected for systemic presence of the recombinant RNA molecule prior to isolating the plant propagule. In some embodiments, the plant cells, plant, or plant part in the mixed population or that are isolated lack DNA that encodes the recombinant RNA molecule. In embodiments, the plant propagule comprising the recombinant RNA molecule is isolated by detecting the RNA molecule in one or more plant cells comprising the recombinant RNA molecule and separating the one or more plant cells comprising the recombinant RNA molecule from the plant cells lacking the recombinant DNA molecule. In some embodiments, the plant propagule is a mosaic comprising both plant cells comprising the recombinant RNA molecule and plant cells lacking the recombinant RNA molecule. In other embodiments, the modified plant propagule is a mosaic comprising both plant cells comprising the endornavirus RdRP and plant cells lacking the endornavirus RdRP. In certain embodiments, at least 99%, 98%, 95%, 90%, 85%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, 10%, 5%, or 1% of the plant cells in the mosaic can comprise the recombinant RNA molecule. In certain embodiments that are particularly advantageous for at least regulatory reasons, the plant propagule lacks DNA that encodes the recombinant RNA molecule. In embodiments, the modified plant propagule comprises the cell comprising the recombinant RNA molecule, or a seed, seedling, ovule, embryo, pollen, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, explant, or callus comprising the cell comprising the recombinant RNA molecule. Plant propagules made by any of the aforementioned methods and/or incorporating any of the aforementioned features are also provided herein.

[0134] In some embodiments, any of the aforementioned methods can further comprise multiplying the cell, seed, seedling, ovule, embryo, pollen, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, explant, or callus to obtain progeny, wherein the progeny comprise the recombinant RNA molecule. In other embodiments, the multiplying of the cells consists of culturing a plurality of explants obtained from the cell, seed, seedling, ovule, embryo, pollen, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, explant, or callus. In yet other embodiments, the isolated propagule comprises the cell and the aforementioned methods can further comprise regenerating a plant, seedling, ovule, embryo, pollen, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, explant, or callus comprising the recombinant RNA from the cell. In still other embodiments, the isolated propagule comprises callus and the aforementioned methods can further comprise regenerating a plant, seedling, ovule, embryo, pollen, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, or explant comprising the recombinant RNA from said callus. In embodiments, a plant is regenerated and the aforementioned methods can further comprise recovering F1 seed or F1 progeny or clonal progeny comprising the recombinant RNA from the plant.

[0135] In another aspect, this disclosure is related to a method of providing a synthetic endornavirus satellite RNA to a plant or plant part by grafting one plant part to another plant part. In certain

embodiments, the methods can comprise grafting a scion onto a rootstock comprising any of the aforementioned or otherwise disclosed recombinant DNA molecules and/or recombinant RNA molecules (*e.g.*, a recombinant RNA comprising, in 5' to 3' order, a 5' RNA replication element that is capable of being recognized by an endornavirus RNA-dependent RNA polymerase (RdRP); a cargo RNA sequence; and a 3' RNA replication element that is capable of being recognized by the endornavirus RdRP), wherein at least one cell of the rootstock and/or the scion comprises the endornavirus RdRP. In certain embodiments, the scion can comprise a plant shoot, an apical or other meristem, a leaf attached to a petiole, or other plant part and the rootstock can comprise roots and aerial portions of the plant including the main stem, secondary stems, leaves, and/or reproductive structures of the plant. In embodiments, DNA that encodes the recombinant RNA molecule is absent in the scion and/or the rootstock. In embodiments, the scion lacks the recombinant RNA molecule prior to grafting. In embodiments, the rootstock comprises the endornavirus RdRP. In some embodiments, the endornavirus RdRP is provided by an endornavirus endemic to the rootstock (*e.g.*, an endornavirus which is non-pathogenic and/or commensal). In other embodiments, the endornavirus RdRP is exogenously provided to the rootstock (*e.g.*, via DNA expression cassette which is integrated into the chromosomal or plastidic DNA of the rootstock or via a recombinant viral vector comprising DNA or RNA encoding the RdRP). In embodiments, the scion comprises the endornavirus RdRP. In some embodiments, the RdRP is provided by an endornavirus endemic to the scion (*e.g.*, an endornavirus which is non-pathogenic and/or commensal). In other embodiments, the RdRP is exogenously provided to the scion (*e.g.*, via DNA expression cassette which is integrated into the chromosomal or plastidic DNA of the scion or via a recombinant viral vector comprising DNA or RNA encoding the RdRP). In embodiments, the endornavirus RdRP comprises a protein having at least 85%, 90%, 95%, 97%, or 99% sequence identity to SEQ ID NO: 613 to 725, or 726. In embodiments, the rootstock and/or the scion comprises a heterologous viral coat protein which can encapsidate the recombinant RNA molecule. In some embodiments, the rootstock and/or the scion comprises the recombinant RNA molecule encapsidated by a heterologous viral coat protein.

[0136] In another aspect, this disclosure is related to a method of producing a grafted plant comprising a recombinant RNA molecule comprising, in 5' to 3' order, a 5' RNA replication element that is capable of being recognized by an endornavirus RNA-dependent RNA polymerase (RdRP); a cargo RNA sequence; and a 3' RNA replication element that is capable of being recognized by an the endornavirus RdRP. In certain embodiments, the recombinant RNA molecule is provided by contacting the scion, the rootstock, or both the scion and the rootstock with a composition comprising the recombinant RNA molecule prior to grafting the scion onto the rootstock to produce the grafted plant. In certain embodiments, at least one cell of the rootstock and/or the scion comprises an endornavirus RdRP prior to contacting the scion, the rootstock, or both the scion and the rootstock with the composition. In embodiments, the rootstock comprises the endornavirus RdRP. In some embodiments, the endornavirus RdRP is provided by an endornavirus endemic to the rootstock (*e.g.*, an endornavirus which is non-

pathogenic and/or commensal). In other embodiments, the endornavirus RdRP is exogenously provided to the rootstock (*e.g.*, via DNA expression cassette which is integrated into the chromosomal or plastidic DNA of the rootstock or via a recombinant viral vector comprising DNA or RNA encoding the RdRP). In embodiments, the scion comprises the endornavirus RdRP. In some embodiments, the RdRP is provided by an endornavirus endemic to the scion (*e.g.*, an endornavirus which is non-pathogenic and/or commensal). In other embodiments, the RdRP is exogenously provided to the scion (*e.g.*, via DNA expression cassette which is integrated into the chromosomal or plastidic DNA of the scion or via a recombinant viral vector comprising DNA or RNA encoding the RdRP). In embodiments, the endornavirus RdRP comprises a protein having at least 85%, 90%, 95%, 97%, or 99% sequence identity to SEQ ID NO: 613 to 725, or 726. In embodiments, DNA that encodes the recombinant RNA molecule is absent in the scion, the rootstock, and/or the grafted plant. The composition can be provided to the scion, the rootstock, or both the scion and the rootstock according to any of the formulations disclosed herein. In some embodiments, the formulation is a liquid, a gel, or a powder. In some embodiments, the formulation is configured to be sprayed on to the scion, the rootstock, or both the scion and the rootstock; to be injected into the scion, the rootstock, or both the scion and the rootstock; to be soaked into the scion, the rootstock, or both the scion and the rootstock; or to be coated onto the scion, the rootstock, or both the scion and the rootstock. In certain embodiments, the contacting comprises dipping the scion, the rootstock, or both the scion and the rootstock into the composition prior to grafting.

[0137] In another aspect, this disclosure is related to a method for producing a plant that transmits any of the aforementioned or otherwise disclosed recombinant RNA molecules provided herein to progeny plants or seed. In certain embodiments, the methods include the steps of: isolating an F₁ progeny plant or seed comprising at least one cell comprising an endornavirus RNA-dependent RNA polymerase (RdRP) and the recombinant RNA molecule comprising, in 5' to 3' order, a 5' RNA replication element that is capable of being recognized by the endornavirus RdRP; a cargo RNA sequence; and a 3' RNA replication element that is capable of being recognized by the endornavirus RdRP from a population of F₁ plants or seed obtained from at least one parent plant comprising the recombinant RNA molecule. In embodiments, the parent plant or a part thereof comprising the plant cell is screened or selected for presence of the recombinant RNA molecule prior to isolating the F₁ progeny plant or seed. In some embodiments, the parent plant or one or more parts thereof are screened for systemic presence of the recombinant RNA molecule prior to isolating the F₁ progeny plants. In other embodiments, floral tissue (*e.g.*, whole flowers or buds, sepal, calyx, or petal), male reproductive tissue (*e.g.*, stamen, anther, or pollen), or female reproductive tissue (*e.g.*, whole fruit, ovary, pericarp, ovule, seed coat, endosperm, or embryo) of the parent plant is screened or selected for presence of the recombinant RNA molecule. In embodiments, F₁ seeds are obtained from a parent plant selected for presence of the recombinant RNA molecule in pericarp tissue. In embodiments, the F₁ progeny plant or seed comprising the cell is isolated by screening the population of F₁ plants or seed obtained from a parent plant for the presence of the recombinant RNA molecule and propagating the F₁ progeny plant or seed comprising the recombinant

RNA molecule. In such screens, the progeny plants or seed thereof are subjected to an assay for a screenable marker for the presence of the recombinant RNA (*e.g.*, an RNA sequence diagnostic for presence of the recombinant RNA molecule or a polypeptide encoded by the recombinant RNA molecule) and separated from progeny plants and seed lacking the recombinant RNA progeny plants and seed lacking the recombinant RNA. Such screening assays can be non-destructive assays wherein a portion of the progeny seed or plant is removed and assayed without loss of the viability or ability to propagate the seed or plant tissue comprising the recombinant RNA. In some embodiments, an F₁ seed of the parent plant is non-destructively screened for presence of the recombinant RNA molecule. In other embodiments, the F₁ seed of the parent plant is non-destructively screened by assaying maternally derived or endosperm tissue of the seed for the presence of the recombinant RNA molecule. Methods for non-destructive assays of seed or other plant tissue which can be adapted for such screens include but are not limited to those disclosed in US patent applications US20220221377 and US20210259176, both incorporated herein by reference in their entireties. In some embodiments, the cargo RNA sequence comprises RNA that encodes a selectable or scorable marker. In some embodiments, the recombinant RNA molecule encodes a selectable marker and the F₁ progeny plant or seed comprising the recombinant RNA molecule is isolated by selecting the F₁ progeny plant or seed comprising the recombinant RNA molecule for presence of the selectable marker. Examples of such selections in instances where the recombinant RNA encodes a selectable marker (*e.g.*, a protein which confers resistance to a selection agent such as an herbicide or antibiotic) can comprise exposing the progeny seeds or plants to a selection agent (*e.g.*, an herbicide or antibiotic) and isolating progeny seeds or plants which survive exposure to the selection agent. Examples of selectable marker/selection agent combinations include glyphosate-resistant EPSPS enzymes and/or glyphosate oxidases/glyphosate, a bialaphos resistance (*bar*) or phosphinothricin acyl transferase (*pat*) enzymes/glufosinate, and neomycin phosphotransferase (*npt*)/neomycin or kanamycin. In certain embodiments, the selectable or scorable marker is an RNA aptamer or a regulatory RNA. In some embodiments, the F₁ progeny plant or seed lacks DNA that encodes the recombinant RNA molecule. In other embodiments, the parent plant lacks DNA that encodes the recombinant RNA molecule. In embodiments, the selected F₁ progeny plant transmits the recombinant RNA molecule to at least F₂ progeny. In some embodiments, the F₁ progeny plant or seed population is obtained from a parent plant used as a pollen recipient. In other embodiments, the F₁ progeny plant or seed population is obtained from a parent plant used as a pollen donor. In embodiments, the F₁ progeny plant or seed population is obtained by selfing the parent plant. In other embodiments, the F₁ progeny plant or seed population is obtained from the sexual crossing of two parent plants. In some embodiments, the parent plant that comprises the recombinant RNA molecule is the female parent plant. In other embodiments, the parent plant that comprises the recombinant RNA molecule is the male parent plant, and the recombinant RNA molecule is transmitted in pollen of the male parent plant.

[0138] In certain embodiments, the methods can further comprise introducing the recombinant RNA molecule or a polynucleotide encoding the recombinant RNA molecule into a plant cell and obtaining the

parent plant comprising the recombinant RNA molecule from the plant cell. In embodiments, the recombinant RNA molecule further comprises at least one additional element selected from the group consisting of: (a) at least one RNA encoding a viral movement protein (MP); (b) at least one tRNA-like sequence; and c) an origin-of-assembly sequence (OAS). In embodiments, a parent and/or plant comprises a heterologous viral coat protein which can encapsidate the recombinant RNA molecule. In some embodiments, the parent and/or progeny plant comprises the recombinant RNA molecule encapsidated by a heterologous viral coat protein.

[0139] In another aspect, this disclosure is related to a method of barcoding a plant, plant cell, progeny thereof, or part thereof. The methods comprise providing to the plant or plant cell any of the aforementioned or otherwise disclosed recombinant RNA molecules provided herein, wherein the cargo RNA of the recombinant RNA molecule comprises a barcode RNA molecule, and wherein the plant or plant cell comprises an endornavirus RdRP. In embodiments, the barcode RNA molecule comprises a sequence that uniquely identifies the plant, plant cell, progeny thereof, or part thereof. In some embodiments, the barcode RNA can be a randomly generated sequence. In some embodiments, the barcode RNA molecule comprises a sequence that is not present in the genome and/or transcriptome of a wild-type plant of the same species, a pathogen thereof, or a symbiont thereof. In some embodiments, the barcode RNA molecule comprises a forward primer binding site and a reverse primer binding site for detection of the barcode RNA molecule. In embodiments, the barcode RNA molecule comprises a non-protein coding sequence. In some embodiments, the barcode RNA sequence is up to about 3.2 kb in length. In some embodiments, the barcode RNA has a length of 10 to 5000 nucleotides, 20 to 1000 nucleotides, or 50 to 500 nucleotides. In certain embodiments, the barcode RNA molecule has a length of 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, or 5000 nucleotides. In embodiments, the plant transmits the recombinant RNA molecule comprising the barcode RNA to progeny. In some embodiments, the plant, plant cell, progeny thereof, or part thereof lacks DNA that encodes the recombinant RNA molecule. In some embodiments, the methods can further comprise isolating an F₁ progeny plant or seed comprising at least one cell comprising the endornavirus RdRP and the recombinant RNA molecule. In some embodiments, the F₁ progeny plant or seed is obtained from the plant used as a pollen recipient. In other embodiments, the F₁ progeny plant or seed is obtained from the plant used as a pollen donor. In embodiments, the F₁ progeny plant or seed is obtained by selfing the parent plant. In embodiments, the methods can further comprise propagating the plant or plant cell to obtain a plant part or a plant propagule comprising the barcode RNA molecule.

[0140] In another aspect, this disclosure is related to a method of identifying a barcoded plant, plant part, or plant cell. The methods comprise screening for the presence of a barcode RNA molecule in the plant, plant part, or plant cell, wherein the plant, plant part, or plant cell comprises any of the aforementioned or otherwise disclosed recombinant RNA molecules provided herein, and wherein the cargo RNA of the recombinant RNA molecule comprises the barcode RNA molecule. In certain

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embodiments, the methods comprise obtaining a nucleic acid sample from the plant, plant part, or plant cell; and detecting the presence of the barcode RNA molecule in the sample. Assays for detection of a barcode RNA include RNA detection assays (*e.g.*, an RT-PCR assay) using nucleic acid probes and/or primers which can detect the barcode RNA and/or sequencing of the barcode RNA. Such screening assays can be non-destructive assays wherein a portion of the seed or plant is removed and assayed without loss of the viability or ability to propagate the seed or plant tissue comprising the barcode RNA. Methods for non-destructive assays of seed or other plant tissue which can be adapted for such screens include but are not limited to those disclosed in US patent applications US20220221377 and US20210259176, both incorporated herein by reference in their entireties. In some embodiments, a seed of the plant is non-destructively screened for presence of the barcode RNA molecule. In other embodiments, a seedling, ovule, embryo, pollen, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, explant, or callus is screened for the presence of the barcode RNA molecule.

[0141] In certain optional embodiments, the methods disclosed herein are not processes for modifying the germ line or genetic identity of human beings. In certain optional embodiments, the methods disclosed herein are not processes for modifying the genetic identity of animals which are likely to cause them suffering without any substantial medical benefit to man or animal, and are also not drawn to animals resulting from such processes. In certain optional embodiments, the methods disclosed herein are not methods for treatment of the human or animal body by surgery or therapy. In certain optional embodiments, the cells disclosed herein are not human embryos. In certain optional embodiments, the cells disclosed herein are not the human body or its parts, at the various stages of its formation and development. In certain optional embodiments provided herein, the plant cells, plant propagules (*e.g.*, a seed, seedling, ovule, embryo, pollen, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, explant, or callus), and plants provided herein are not produced by an exclusively biological process. In certain optional embodiments provided herein, the methods for producing plant cells, plant propagules (*e.g.*, a seed, seedling, ovule, embryo, pollen, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, explant, or callus), and plants provided herein are not exclusively biological processes.

Embodiments

[0142] Various embodiments of the compositions, systems, and methods described herein are set forth in the following set of numbered embodiments.

[0143] 1. A recombinant RNA molecule comprising from 5' terminus to 3' terminus:

- (a) a 5' RNA replication element recognized by an endornavirus RNA-dependent RNA polymerase (RdRP);
- (b) a cargo RNA molecule; and
- (c) a 3' RNA replication element recognized by the RdRP;

wherein the 5' RNA replication element, the cargo RNA molecule, and the 3' RNA replication element are operably linked and wherein the cargo RNA molecule is heterologous to the 5' RNA replication element and the 3' RNA replication element, optionally wherein: (i) the 5' RNA replication element and

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the 3' RNA replication element are obtained from the same endornavirus genome or from endornavirus genomes having at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another and which are optionally related; (ii) the 5' RNA replication element, the 3' RNA replication element, and the RdRP are obtained from the same endornavirus genome or from endornavirus genomes having at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another and which are optionally related; or (iii) the 5' RNA replication element, the 3' RNA replication element, and/or the RdRP coding region are obtained from different endornavirus genomes, and wherein the members of each respective set of the 5' RNA replication elements, 3' RNA replication elements, and/or RdRP coding regions have at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another..

[0144] 2. The recombinant RNA molecule of embodiment 1, wherein:

(a) the 5' RNA replication element comprises at least one RNA secondary structure provided in Table 19, 20, 21, and/or 25 or adopted by an RNA molecule encoded by SEQ ID NO: 466 to 522, 727, or 924 to 1017; and/or

(b) the 3' RNA replication element comprises at least one RNA secondary structure provided in Table 22, 23, 24, and/or 25 or adopted by an RNA molecule encoded by SEQ ID NO: 523 to 595, 728, or 1019 to 1129.

[0145] 3. The recombinant RNA molecule of embodiment 1, wherein:

(a) the 5' RNA replication element comprises an RNA molecule encoded by SEQ ID NO: 466 to 522, 727, or 924 to 1017; a variant thereof encoded by a DNA molecule having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% sequence identity to SEQ ID NO: 466 to 522, 727, or 924 to 1017; or a variant thereof wherein one or more nucleotides in the RNA secondary structure are substituted with distinct nucleotides which maintain the RNA secondary structure; and/or

(b) the 3' RNA replication element comprises an RNA molecule encoded by SEQ ID NO: 523 to 595, 728, or 1019 to 1129; a variant thereof encoded by a DNA molecule having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% sequence identity to SEQ ID NO: 523 to 595, 728, or 1019 to 1129; or a variant thereof wherein one or more base-paired residues in the RNA secondary structure are substituted with distinct nucleotides which maintain the RNA secondary structure.

[0146] 4. The recombinant RNA molecule of embodiment 3, wherein the RNA secondary structure is maintained by substituting nucleotides in the secondary structure which are not base paired with nucleotides which will not base pair, and/or by substituting nucleotides in the secondary structure which are base paired with nucleotides which will base pair.

[0147] 5. The recombinant RNA molecule of any one of embodiments 1 to 4, wherein:

(a) the 5' RNA replication element comprises at least a segment of the 5' untranslated region (UTR) of the endornavirus genome or a variant thereof having one or more nucleotide substitutions, insertions, and/or deletions, wherein the variant is recognized by the RdRP, optionally wherein the 5' RNA replication element further comprises a genomic sequence of the endornavirus that is natively located 3' to and adjacent to the 5' UTR sequence; and/or

(b) the 3' RNA replication element comprises at least a segment of the 3' UTR of the endornavirus genome or a variant thereof having one or more nucleotide substitutions, insertions, and/or deletions, wherein the variant is recognized by the RdRP, optionally wherein the 3' RNA replication element further comprises a genomic sequence of the endornavirus that is natively located 5' to and adjacent to the 3' UTR sequence, and optionally wherein the endornavirus genome of (a) and (b) are the same.

[0148] 6. The recombinant RNA molecule of any one of embodiments 1 to 5, wherein the RNA molecule further comprises at least one of: (i) a tRNA-like element, optionally wherein the tRNA-like element provides for intercellular movement of the RNA and optionally wherein the intercellular movement is mediated by a viral movement protein (MP); (ii) an encapsidation recognition element (ERE), optionally wherein the ERE provides for encapsidation of the RNA by a viral capsid protein; (iii) an RNA effector; and/or (iv) RNA encoding a viral movement protein (MP), optionally wherein an internal ribosome entry site (IRES) is operably linked to the RNA encoding the MP.

[0149] 7. The recombinant RNA molecule of embodiment 6, wherein the tRNA-like element comprises a tRNA-like molecule from an *Arabidopsis* FT mRNA or is a tRNA-like sequence encoded by a DNA sequence selected from the group consisting of SEQ ID NOs: 76-123, and 790 or is a modified tRNA-like sequence that has at least 90% sequence identity to a scaffold tRNA-like sequence encoded by a DNA sequence selected from the group consisting of SEQ ID NOs: 76-123, and 790, and that maintains the secondary structure of the scaffold tRNA-like sequence, and/or wherein the ERE is a tobacco mosaic virus (TMV) OAS.

[0150] 8. The recombinant RNA molecule of embodiment 1, wherein the cargo RNA molecule is up to about 3.2kb in length.

[0151] 9. The recombinant RNA molecule of embodiment 1, wherein the cargo RNA molecule comprises: (a) at least one coding sequence, optionally wherein the coding sequence encodes a selectable or scoreable marker; (b) at least one non-coding sequence; or (c) both at least one coding sequence and at least one non-coding sequence.

[0152] 10. The recombinant RNA molecule of embodiment 1, wherein the cargo RNA molecule comprises at least one coding sequence, and wherein the RNA molecule further comprises an internal ribosome entry site (IRES) which is operably linked to at least one coding sequence, optionally wherein the operably linked IRES is located 5' and immediately adjacent to the coding sequence.

[0153] 11. The recombinant RNA molecule of embodiment 1, wherein the cargo RNA molecule comprises at least one non-coding sequence, and wherein the at least one non-coding sequence is a hairpin RNA (hprRNA); an RNA that forms multiple stem-loops; an RNA pseudoknot; an RNA molecule that forms at least partially double-stranded RNA; a small interfering RNA (siRNA) or siRNA precursor; a microRNA (miRNA) or miRNA precursor; a phased RNA or phased RNA precursor; a ribozyme; a ligand-responsive ribozyme (aptazyme); an RNA aptamer; or a long noncoding RNA (lncRNA).

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[0154] 12. The recombinant RNA molecule of embodiment 1, further comprising an RNA comprising encoding at least one ribozyme, optionally wherein the at least one ribozyme is located 5' to the 5' RNA replication element or 3' to the 3' RNA replication element.

[0155] 13. The recombinant RNA molecule of embodiment 1, further comprising an RNA molecule comprising at least one ligand-responsive ribozyme (aptazyme), optionally wherein the at least one ligand-responsive ribozyme is located 5' to the 5' RNA replication element or 3' to the 3' RNA replication element.

[0156] 14. The recombinant RNA molecule of embodiment 1, wherein: (i) the RNA further comprises at least a segment of its reverse complementary RNA molecule; and/or (ii) the recombinant RNA molecule is complexed with one or more RNA binding proteins or encapsidated by a viral capsid protein, optionally wherein the viral capsid protein comprises a viral capsid protein of SEQ ID NO: 26 to 50, and/or optionally wherein the RNA binding proteins comprise an RNA recognition motif.

[0157] 15. The recombinant RNA molecule of embodiment 1, wherein the RNA molecule comprises: at least one heterologous RNA virus (HRV) amplicon in sense or antisense orientation to the first 5' RNA replication element comprising:

I. (i) a heterologous RNA virus (HRV) 5' replication region (HRV 5'RR); (ii) the cargo RNA molecule; and (iii) the heterologous RNA virus (HRV) 3' RNA replication region (HRV 3'RR); wherein the HRV 5' RR and HRV 3' RR HRV are recognized by a heterologous RNA virus RNA-dependent RNA polymerase (hrvRdRP); and wherein the HRV 5'RR, cargo RNA molecule, and HRV 3'RR are operably linked; or

II. a heterologous RNA virus (HRV) subgenomic promoter operably linked to the cargo RNA molecule; wherein the subgenomic promoter is recognized by a heterologous RNA virus RNA-dependent RNA polymerase (hrvRdRP).

[0158] 16. The recombinant RNA of embodiment 15, wherein the RNA molecule comprises from 5' terminus to 3' terminus:

(a) the 5' RNA replication element;

(b) the HRV amplicon in antisense orientation to the first 5' RNA replication element; optionally wherein the HRV amplicon further comprises:

(i) an RNA molecule encoding an HRV RNA-dependent RNA polymerase (hrvRdRP) which is operably linked to the HRV 5'RR and HRV 3'RR, wherein the RNA molecule encoding the HRV RNA-dependent RNA polymerase (hrvRdRP) is optionally operably linked to a subgenomic promoter recognized by the hrvRdRP; or

(ii) an RNA molecule encoding an HRV RNA-dependent RNA polymerase (hrvRdRP) which is operably linked to linked to a subgenomic promoter recognized by the hrvRdRP; and

(c) the 3' RNA replication element.

[0159] 17. The recombinant RNA of embodiment 15 or 16, wherein the HRV 5'RR, HRV 3'RR, and hrvRdRP comprise an HRV 5'RR, HRV 3'RR, and hrvRdRP from a virus selected from the group

consisting of a Alphaflexivirus, Betaflexivirus, Bromovirus, Celavirus, a Closterovirus, a Comovirus, a Potexvirus, Potyvirus, Tobamovirus, Tombusvirus, Tospoviridae, Trivirinae, and Tymovirus, Varicosavirus, and Secoviridae.

[0160] 18. The recombinant RNA of embodiment 17, wherein: (i) the Bromovirus is a Cucumber Mosaic Virus, Spinach latent virus, Olive latent virus, or Brome mosaic virus; (ii) the Closterovirus is a Citrus tristeza virus or Beet yellows virus; (iii) the Comovirus is Cowpea mosaic virus, Apple latent spherical virus, or Soybean latent spherical virus; (iv) the Potexvirus is Potato virus X or Citrus yellow vein clearing virus; (v) the Potyvirus is a Pepper mottle virus, Bean yellow mosaic virus, Barley stripe mosaic virus, Wheat stripe mosaic virus, Rice yellow mottle virus, Maize dwarf mosaic virus, zucchini yellow mosaic virus, watermelon mosaic virus, or sugarcane mosaic virus; (vi) the Tobamovirus is a Tobacco mosaic virus, Tomato mosaic virus, Tomato brown rugose fruit virus, Turnip vein-clearing virus, or Pepper mild mottle virus; (vii) the Tombusvirus is a Turnip crinkle virus or Tomato bushy stunt virus; (iv) the Tospoviridae is a Tomato spotted wilt virus or watermelon bud necrosis virus; or (viii) the Tymovirus is a Turnip yellow mosaic virus, Citrus yellow vein clearing virus, Potato latent virus, Apple stem grooving virus, or Citrus leaf blotch virus.

[0161] 19. The recombinant RNA of any one of embodiments 1 to 18, wherein the HRV 5' RR and the HRV 3' RR are obtained from the same HRV genome.

[0162] 20. The recombinant RNA of any one of embodiments 1 to 18, wherein the HRV 5' RR and the HRV 3' RR are obtained from distinct HRV genomes.

[0163] 21. The recombinant RNA molecule of any one of embodiments 1 to 20, wherein:

(a) the HRV 5' RR comprises at least one RNA secondary structure adopted by an RNA encoded by SEQ ID NO: 161 to 185, or 186, or comprises the RNA sequence encoded by SEQ ID NO: 161 to 185, or 186, or comprises a contiguous fragment of at least 80%, 85%, 90%, or 95% of the full sequence of the RNA encoded by SEQ ID NO: 161 to 185, or 186; and/or

(b) the HRV 3' RR comprises at least one RNA secondary structure adopted by an RNA encoded by SEQ ID NO: 187 to 211, or 212, or comprises the RNA sequence of the RNA encoded by SEQ ID NO: 187 to 211, or 212, or comprises a contiguous fragment of at least 80%, 85%, 90%, or 95% of the full sequence of the RNA encoded by SEQ ID NO: 187 to 211, or 212.

[0164] 22. The recombinant RNA molecule of any one of embodiments 1 to 20, wherein:

(a) the HRV 5' RR is encoded by a DNA molecule comprising SEQ ID NO: 161 to 185, or 186; or a variant thereof comprising DNA having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% sequence identity to SEQ ID NO: 161 to 185, or 186; or a variant thereof wherein one of more residues in the RNA secondary structure are substituted with distinct nucleotides which maintain the RNA secondary structure; and/or

(b) the HRV 3' RR is encoded by a DNA molecule comprising SEQ ID NO: 187 to 211, or 212; or a variant thereof comprising DNA having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% sequence identity to SEQ ID NO: 187 to 211, or 212; or a variant thereof wherein one of more residues in

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the RNA secondary structure are substituted with distinct nucleotides which maintain the RNA secondary structure.

[0165] 23. The recombinant RNA molecule of embodiment 15, wherein:

(a) the HRV 3' RR comprises an RNA molecule containing at least a segment of the 3' untranslated region (UTR) of the HRV genome, or a variant thereof having one or more nucleotide substitutions, insertions, and/or deletions, wherein the HRV 3' RR or the variant is recognized by the hrvRdRP, optionally wherein the RNA comprising the HRV 3' RR further comprises a genomic sequence of the HRV that is natively located 5' to and adjacent to the 3' UTR sequence;

and/or

(b) the HRV 5' RR comprises an RNA molecule containing at least a segment of the 3' untranslated region (UTR) of the HRV genome, or a variant thereof having one or more nucleotide substitutions, insertions, and/or deletions, wherein the HRV 5' RR or the variant is recognized by the hrvRdRP, optionally wherein the RNA comprising the HRV 5' RR further comprises a genomic sequence of the HRV that is natively located 3' to and adjacent to the 5' UTR sequence.

[0166] 24. The recombinant RNA molecule of any one of embodiments 1 to 23, wherein the cargo RNA comprises an HRV-inhibitory RNA or encodes an HRV-inhibitory protein, wherein the HRV-inhibitory RNA or HRV-inhibitory protein inhibits infection, movement, transmission, and/or replication of the HRV.

[0167] 25. The recombinant RNA molecule of any one of embodiments 1 to 24, wherein the cargo RNA comprises an RNA having at least 20 to 25 contiguous nucleotides having an identical or complementary sequence to a segment of equivalent length of the genomic RNA of the HRV.

[0168] 26. The recombinant RNA molecule of any one of embodiments 1 to 24, wherein the cargo RNA comprises an RNA having at least 20 to 25 contiguous nucleotides having an identical or complementary sequence to a segment of equivalent length of the genomic RNA of the HRV which does not encode the hrvRdRP.

[0169] 27. The recombinant RNA molecule of any one of embodiments 1 to 26, wherein:

(i) the HRV is a Cucumber Mosaic Virus and the HRV 5'RR comprises an RNA encoded by the Cucumber Mosaic Virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Cucumber Mosaic Virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Cucumber Mosaic Virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Cucumber Mosaic Virus 3' RR DNA sequence in Table 7; or _____;

(ii) the HRV is a Brome mosaic virus and the HRV 5'RR comprises an RNA encoded by the Brome mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Brome mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Brome mosaic virus 3' RR DNA sequence in Table 7, or

an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Brome mosaic virus 3' RR DNA sequence in Table 7;

(iii) the HRV is a Citrus tristeza virus and the HRV 5'RR comprises an RNA encoded by the Citrus tristeza virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus tristeza virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Citrus tristeza virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus tristeza virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus tristeza virus RdRP sequence in Table 7;

(iv) the HRV is Beet yellows virus and the HRV 5'RR comprises an RNA encoded by the Beet yellows virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Beet yellows virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Beet yellows virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Beet yellows virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Beet yellows virus RdRP sequence in Table 7

(v) the HRV is Cowpea mosaic virus and the HRV 5'RR comprises an RNA encoded by the Cowpea mosaic virus 5' RR DNA sequence in Table 7 or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Cowpea mosaic virus 5' RR DNA sequence in Table 7;

(vi) the HRV is Potato virus X and the HRV 5'RR comprises an RNA encoded by the Potato virus X 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Potato virus X 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Potato virus X 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Potato virus X 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Potato virus X RdRP sequence in Table 7;

(vii) the HRV is Pepper mottle virus and the HRV 5'RR comprises an RNA encoded by the Pepper mottle virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Pepper mottle virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Pepper mottle virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Pepper mottle virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Pepper mottle virus RdRP sequence in Table 7;

(viii) the HRV is Bean yellow mosaic virus and the HRV 5'RR comprises an RNA encoded by the Bean yellow mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Bean yellow mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Bean yellow mosaic virus 3' RR DNA

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sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Bean yellow mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Bean yellow mosaic virus RdRP sequence in Table 7;

(ix) the HRV is Barley stripe mosaic virus and the HRV 5'RR comprises an RNA encoded by the Barley stripe mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Barley stripe mosaic virus 5' RR DNA sequence in Table 7, and the HRV 3' RR comprises an RNA encoded by the Barley stripe mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Barley stripe mosaic virus 3' RR DNA sequence in Table 7;

(x) the HRV is Wheat stripe mosaic virus and the HRV 5'RR comprises an RNA encoded by the Wheat stripe mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Wheat stripe mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Wheat stripe mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Wheat stripe mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Wheat stripe mosaic virus RdRP sequence in Table 7;

(xi) the HRV Rice yellow mottle virus and the HRV 5'RR comprises an RNA encoded by the Rice yellow mottle virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Rice yellow mottle virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Rice yellow mottle virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Rice yellow mottle virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Rice yellow mottle virus RdRP sequence in Table 7;

(xii) the HRV is Maize dwarf mosaic virus and the HRV 5'RR comprises an RNA encoded by the Maize dwarf mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Maize dwarf mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Maize dwarf mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Maize dwarf mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Maize dwarf mosaic virus RdRP sequence in Table 7;

(xiii) the HRV is zucchini yellow mosaic virus and the HRV 5'RR comprises an RNA encoded by the Zucchini yellow mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Zucchini yellow mosaic virus 5' RR

DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Zucchini yellow mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Zucchini yellow mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Zucchini yellow mosaic virus RdRP sequence in Table 7;

(xiv) the HRV is watermelon mosaic virus and the HRV 5'RR comprises an RNA encoded by the Watermelon mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Watermelon mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Watermelon mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Watermelon mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Watermelon mosaic virus RdRP sequence in Table 7;

(xv) the HRV is sugarcane mosaic virus and the HRV 5'RR comprises an RNA encoded by the Sugarcane mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Sugarcane mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Sugarcane mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Sugarcane mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Sugarcane mosaic virus RdRP sequence in Table 7;

(xvi) the HRV is Tobacco mosaic virus and the HRV 5'RR comprises an RNA encoded by the Tobacco mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tobacco mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Tobacco mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tobacco mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Tobacco mosaic virus RdRP sequence in Table 7;

(xvii) the HRV is Tomato mosaic virus and the HRV 5'RR comprises an RNA encoded by the Tomato mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Tomato mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato mosaic virus RdRP sequence in Table 7;

(xviii) the HRV is Tomato brown rugose fruit virus and the HRV 5'RR comprises an RNA encoded by the Tomato brown rugose fruit virus 5' RR DNA sequence in Table 7, an RNA encoded by a

DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato brown rugose fruit virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Tomato brown rugose fruit virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato brown rugose fruit virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato brown rugose fruit virus RdRP sequence in Table 7;

(xix) the HRV is Turnip vein-clearing virus and the HRV 5'RR comprises an RNA encoded by the Turnip vein-clearing virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip vein-clearing virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Turnip vein-clearing virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip vein-clearing virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip vein-clearing virus RdRP sequence in Table 7;

(xx) the HRV is Pepper mild mottle virus and the HRV 5'RR comprises an RNA encoded by the Pepper mild mottle virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Pepper mild mottle virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Pepper mild mottle virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Pepper mild mottle virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Pepper mild mottle virus RdRP sequence in Table 7;

(xxi) the HRV is Turnip crinkle virus and the HRV 5'RR comprises an RNA encoded by the Turnip crinkle virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip crinkle virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Turnip crinkle virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip crinkle virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip crinkle virus RdRP sequence in Table 7;

(xxii) the HRV is Tomato bushy stunt virus and the HRV 5'RR comprises an RNA encoded by the Tomato bushy stunt virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato bushy stunt virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Tomato bushy stunt virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato bushy stunt virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato bushy stunt virus RdRP sequence in Table 7;

(xxiii) the HRV is Tomato spotted wilt virus and the HRV 5'RR comprises an RNA encoded by the Tomato spotted wilt virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato spotted wilt virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Tomato spotted wilt virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato spotted wilt virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato spotted wilt virus RdRP sequence in Table 7;

(xxiv) the HRV is watermelon bud necrosis virus and the HRV 5'RR comprises an RNA encoded by the Watermelon bud necrosis virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Watermelon bud necrosis virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Watermelon bud necrosis virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Watermelon bud necrosis virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Watermelon bud necrosis virus RdRP sequence in Table 7; or

(xxv) the HRV is Turnip yellow mosaic virus and the HRV 5'RR comprises an RNA encoded by the Turnip yellow mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip yellow mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Turnip yellow mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip yellow mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip yellow mosaic virus RdRP sequence in Table 7;

(xxvi) the HRV is Spinach latent virus and the HRV 5'RR comprises an RNA encoded by the Spinach latent virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Spinach latent virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Spinach latent virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Spinach latent virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Spinach latent virus RdRP sequence of SEQ ID NO: 516;

(xxvii) the HRV is Spinach latent virus and the HRV 5'RR comprises an RNA encoded by the Spinach latent virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Spinach latent virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Spinach latent virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Spinach

latent virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Spinach latent virus RdRP sequence of SEQ ID NO: 517;

(xxviii) the HRV is Olive latent virus 2 and the HRV 5'RR comprises an RNA encoded by the Olive latent virus 2 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Olive latent virus 2 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Olive latent virus 2 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Olive latent virus 2 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Olive latent virus 2 RdRP sequence in Table 7;

(xxix) the HRV is Citrus yellow vein clearing virus and the HRV 5'RR comprises an RNA encoded by the Citrus yellow vein clearing virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus yellow vein clearing virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Citrus yellow vein clearing virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus yellow vein clearing virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus yellow vein clearing virus RdRP sequence in Table 7;

(xxx) the HRV is Potato latent virus and the HRV 5'RR comprises an RNA encoded by the Potato latent virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Potato latent virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Potato latent virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Potato latent virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Potato latent virus RdRP sequence in Table 7;

(xxxi) the HRV is Apple stem grooving virus and the HRV 5'RR comprises an RNA encoded by the Apple stem grooving virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Apple stem grooving virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Apple stem grooving virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Apple stem grooving virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Apple stem grooving virus RdRP sequence in Table 7;

(xxxii) the HRV is Citrus leaf blotch virus and the HRV 5'RR comprises an RNA encoded by the Citrus leaf blotch virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus leaf blotch virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Citrus leaf blotch virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the

Citrus leaf blotch virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus leaf blotch virus RdRP sequence in Table 7;

(xxxiii) the HRV is Apple latent spherical virus and the HRV 5'RR comprises an RNA encoded by the Apple latent spherical virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Apple latent spherical virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Apple latent spherical virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Apple latent spherical virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Apple latent spherical virus RdRP sequence in Table 7;

(xxxiv) the HRV is Soybean latent spherical virus and the HRV 5'RR comprises an RNA encoded by the Soybean latent spherical virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Soybean latent spherical virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Soybean latent spherical virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Soybean latent spherical virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Soybean latent spherical virus RdRP sequence in Table 7; .

(xxxv) the HRV is Celery latent virus and the HRV 5'RR comprises an RNA encoded by the Celery latent virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Celery latent virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Celery latent virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Celery latent virus 3' RR DNA sequence in Table 7, and the RdRP comprise a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Celery latent virus RdRP sequence in Table 7;

(xxxvi) the HRV is Black grass varicosavirus-like virus and the HRV 5'RR comprises an RNA encoded by the Black grass varicosavirus-like virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Black grass varicosavirus-like virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Black grass varicosavirus-like virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Black grass varicosavirus-like virus 3' RR DNA sequence in Table 7, and the RdRP comprise a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Black grass varicosavirus-like virus sequence in Table 7; or

(xxxvii) the HRV is Maize suscal virus and the HRV 5'RR comprises an RNA encoded by the Maize suscal virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Maize suscal virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Maize suscal virus 3' RR DNA sequence in Table 7, or

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an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Maize suscal virus 3' RR DNA sequence in Table 7, and the RdRP comprise a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Maize suscal virus sequence in Table 7.

[0170] 28. The recombinant RNA molecule of any one of embodiments 1 to 27, further comprising an RNA comprising encoding at least one cleavable sequence, optionally wherein the at least one cleavable sequence is located: (i) 5' to the 5' RNA replication element or 3' to the 3' RNA replication element; and/or (ii) between the 3' end of the 5' RNA replication element and the HRV amplicon and/or between the HRV amplicon and the 5' end of the 3' RNA replication element. wherein the cleavable sequence is optionally a self-cleaving ribozyme, a self-cleaving inducible ribozyme, or an siRNA or miRNA recognition site.

[0171] 29. An agricultural formulation comprising the recombinant RNA molecule of any one of embodiments 1 to 28.

[0172] 30. The agricultural formulation of embodiment 29, wherein the recombinant RNA molecule is complexed with one or more RNA binding proteins or encapsidated by a viral capsid protein, optionally wherein the RNA comprises an ERE which provides for encapsidation of the RNA by the viral capsid protein.

[0173] 31. The agricultural formulation of embodiment 30, wherein the RNA binding proteins comprise an RNA recognition motif.

[0174] 32. The agricultural formulation of embodiment 30 or 31, wherein the viral capsid protein comprises the viral capsid protein of SEQ ID NO: 26 to 50.

[0175] 33. The agricultural formulation of anyone of embodiments 29 to 32, wherein the formulation comprises the recombinant RNA molecule and a carrier, an excipient, and/or an adjuvant.

[0176] 34. A cell comprising the recombinant RNA molecule of any one of embodiments 1 to 28, wherein the cell is a bacterial cell, a fungal cell, a plant cell, an insect cell, or an invertebrate animal cell.

[0177] 35. The cell of embodiment 34, wherein the cell is a plant cell and DNA which encodes the recombinant RNA molecule is absent from the cell.

[0178] 36. The cell of embodiment 34, wherein the cell comprises a recombinant DNA molecule which encodes the recombinant RNA molecule.

[0179] 37. An expression system comprising:

(a) an RNA molecule comprising the recombinant RNA molecule of any one of embodiments 1 to 28; and

(b) a cell containing the recombinant RNA molecule and an RdRP protein that recognizes the 5' and 3' RNA replication elements of the recombinant RNA molecule.

[0180] 38. The expression system of embodiment 37, wherein the recombinant RNA molecule comprises an operably linked encapsidation recognition element (ERE) recognized by a viral capsid protein, and wherein the cell contains the viral capsid protein.

[0181] 39. The expression system of embodiment 38, wherein the RNA molecule is encapsidated by the viral capsid protein and/or wherein the viral capsid protein comprises the viral capsid protein of any one of SEQ ID NOs: 26 to 50.

[0182] 40. The expression system of embodiment 37, 38, or 39, further comprising the reverse complement of the recombinant RNA molecule.

[0183] 41. The expression system of any one of embodiments 37 to 40, wherein the cell is a bacterial cell, a plant cell, a fungal cell, an insect cell, or an invertebrate animal cell.

[0184] 42. The expression system of any one of embodiments 37 to 41, wherein the cell further comprises: (i) a viral capsid protein (CP), (ii) an RNA-binding protein (RBP) that can bind to the RNA molecule, optionally wherein the RBP binds to an RNA effector; (iii) an RNA cleavage agent that cleaves the RNA molecule; (iv) a second RNA-dependent RNA polymerase (RdRP) protein that recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter in the RNA molecule (2nd RdRP); (v) a viral movement protein (MP); (vi) a heterologous RNA virus (HRV); or (vii) an hrvRdRP, optionally wherein the hrvRdRP recognizes the HRV 5' or 3' replication region and/or the subgenomic promoter.

[0185] 43. The expression system of embodiment 42, wherein the CP, RBP, RdRP, 2nd RdRP, hrvRdRP, and/or the MP is: (a) expressed by a recombinant DNA molecule in the cell; (b) provided exogenously to the cell; (c) expressed by a recombinant RNA molecule in the cell; or (d) expressed by a virus in the cell.

[0186] 44. The expression system of embodiment 42, wherein the RdRP, CP, RBP, 2nd RdRP, hrvRdRP, and/or the MP protein is heterologous to the cell.

[0187] 45. The expression system of embodiment 42 or 44, wherein the RdRP, 2nd RdRP, or hrvRdRP protein or a polynucleotide encoding the RdRP, 2nd RdRP, or hrvRdRP protein is (a) expressed by a recombinant DNA molecule in the cell; (b) provided exogenously to the cell; (c) expressed by a recombinant RNA molecule in the cell; or (d) expressed by a virus in the cell.

[0188] 46. The expression system of any one of embodiments 37 to 45, wherein the cell is a plant cell.

[0189] 47. The expression system of embodiment 46, wherein the plant cell contains an endornavirus which expresses the RdRP protein that recognizes the 5' RNA replication element and the 3' RNA replication element and/or wherein the plant cell contains an HRV that expresses the 2nd RdRP or hrvRdRP protein.

[0190] 48. The expression system of embodiment 47, wherein the endornavirus occurs naturally in the plant cell.

[0191] 49. A method of providing a synthetic endornavirus satellite RNA to a plant, comprising contacting the plant with the recombinant RNA molecule of any one of embodiments 1 to 28.

[0192] 50. The method of embodiment 49, wherein contacting comprises spraying, dusting, injecting, or soaking the plant or a part thereof with the recombinant RNA molecule or the formulation.

[0193] 51. The method of embodiment 49 or 50, further comprising providing an hrvRdRP to the plant which recognizes the HRV 5' or 3' replication region and/or the subgenomic promoter, optionally

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wherein the hrvRdRP is provided by introducing a recombinant DNA or RNA encoding the hrvRdRP into the plant or a part thereof.

[0194] 52. A method of establishing a synthetic endornavirus satellite RNA in a plant cell, comprising: providing to a plant cell the recombinant RNA molecule of any one of embodiments 1 to 28; wherein the plant cell comprises an RdRP protein that recognizes the 5' RNA replication element and 3' RNA replication element, wherein the RNA molecule is optionally comprises an ERE and is encapsidated by a capsid protein, whereby the RdRP protein catalyzes synthesis of the synthetic endornavirus satellite RNA from the recombinant RNA molecule.

[0195] 53. The method of embodiment 52, wherein the plant cell comprises an endornavirus and wherein the RdRP protein is provided to the plant cell by the endornavirus.

[0196] 54. The method of embodiment 52 or 53, wherein the endornavirus is endemic to the plant cell, optionally wherein the endornavirus which is endemic to the plant cell is non-pathogenic and/or commensal.

[0197] 55. The method of embodiment 52, 53, or 54, wherein the recombinant RNA molecule comprises an operably linked encapsidation recognition element (ERE) recognized by a viral capsid protein.

[0198] 56. The method of any one of embodiments 52 to 55, further comprising providing an hrvRdRP to the plant which recognizes the HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA, optionally wherein the hrvRdRP is provided by introducing a recombinant DNA or RNA encoding the hrvRdRP into the plant or a part thereof.

[0199] 57. A method of obtaining a phenotypic change in a plant or plant cell, comprising: providing to a plant or plant cell a recombinant RNA molecule of any one of embodiments 1 to 28, wherein the cargo RNA molecule comprises RNA that effects a phenotypic change in the plant or plant cell in comparison to a plant or plant cell lacking the recombinant RNA, wherein the plant or plant cell comprises an RdRP protein that recognizes the 5' RNA replication element and 3' RNA replication element and catalyzes synthesis of a synthetic endornavirus RNA from the recombinant RNA molecule, and wherein the cargo RNA molecule effects the phenotypic change.

[0200] 58. The method of embodiment 57, wherein the RNA that effects a phenotypic change in the plant or plant cell comprises at least one RNA selected from an siRNA or siRNA precursor, a miRNA or miRNA precursor, and a phased siRNA or phased siRNA precursor.

[0201] 59. The method of embodiment 57, wherein the RNA that effects a phenotypic change in the plant or plant cell comprises a messenger RNA.

[0202] 60. The method of embodiment 59, wherein the messenger RNA comprises an RNA molecule absent in the genome of the plant or plant cell.

[0203] 61. The method of embodiment 57, wherein the RNA that effects a phenotypic change in the plant or plant cell comprises an RNA for modifying the genome of the plant or plant cell.

[0204] 62. The method of embodiment 57, wherein the RNA that effects a phenotypic change in the plant or plant cell comprises an RNA for modifying the transcriptome and/or epigenome of the plant or plant cell, optionally wherein the RNA for modifying the epigenome targets an endogenous plant gene for RNA-induced transcriptional silencing.

[0205] 63. The method of any one of embodiments 57 to 62, wherein the phenotypic change comprises an increase in the plant's resistance to a pest or pathogen, optionally wherein the pest or pathogen is selected from the group comprising a bacterium, a virus other than an endornavirus, a fungus, an oomycete, and an invertebrate.

[0206] 64. The method of embodiment 63, wherein the pathogen is a heterologous RNA virus (HRV), optionally wherein the HRV is a virus selected from the group consisting of an Alphaflexivirus, Betaflexivirus, Bromovirus, Celavirus, a Closterovirus, a Comovirus, a Potexvirus, Potyvirus, Tobamovirus, Tombusvirus, Tospoviridae, Trivirinae, and Tymovirus, Varicosavirus, and Secoviridae.

[0207] 65. The method of embodiment 64, wherein: (i) the Bromovirus is a Cucumber Mosaic Virus, Spinach latent virus, Olive latent virus, or Brome mosaic virus; (ii) the Closterovirus is a Citrus tristeza virus or Beet yellows virus; (iii) the Comovirus is Cowpea mosaic virus, Apple latent spherical virus, or Soybean latent spherical virus; (iv) the Potexvirus is Potato virus X or Citrus yellow vein clearing virus; (v) the Potyvirus is a Pepper mottle virus, Bean yellow mosaic virus, Barley stripe mosaic virus, Wheat stripe mosaic virus, Rice yellow mottle virus, Maize dwarf mosaic virus, zucchini yellow mosaic virus, watermelon mosaic virus, or sugarcane mosaic virus; (vi) the Tobamovirus is a Tobacco mosaic virus, Tomato mosaic virus, Tomato brown rugose fruit virus, Turnip vein-clearing virus, or Pepper mild mottle virus; (vii) the Tombusvirus is a Turnip crinkle virus or Tomato bushy stunt virus; (iv) the Tospoviridae is a Tomato spotted wilt virus or watermelon bud necrosis virus; or (viii) the Tymovirus is a Turnip yellow mosaic virus, Citrus yellow vein clearing virus, Potato latent virus, Apple stem grooving virus, or Citrus leaf blotch virus.

[0208] 66. The method of any one of embodiments 57 to 62, wherein the phenotypic change comprises an increase in the plant's resistance to stress, optionally wherein the stress comprises at least one abiotic stress comprising nutrient stress, light stress, water stress, heat stress, and/or cold stress, or optionally wherein the stress comprises at least one biotic stress comprising crowding, shading, or allelopathy.

[0209] 67. The method of any one of embodiments 57 to 66, wherein the recombinant RNA molecule is provided to the plant or plant cell in the form of an RNA, an encapsidated RNA, or a formulation thereof.

[0210] 68. The method of embodiment 67, wherein the encapsidated RNA comprises a synthetic endornavirus satellite particle.

[0211] 69. The method of any one of embodiments 57 to 68, wherein the providing comprises contacting the plant or plant cell with the RNA, encapsidated RNA, or formulation thereof, optionally

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wherein contacting comprises spraying, dusting, injecting, or soaking the plant or plant cell with the RNA, encapsidated RNA, or formulation thereof.

[0212] 70. The method of any one of embodiments 57 to 69, wherein the recombinant RNA further comprises its reverse complementary RNA molecule.

[0213] 71. The method of any one of embodiments 57 to 70, further comprising providing an hrvRdRP to the plant which recognizes the HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA, optionally wherein the hrvRdRP is provided by introducing a recombinant DNA or RNA encoding the hrvRdRP into the plant or a part thereof.

[0214] 72. A method of manufacturing a synthetic endornavirus satellite particle, comprising combining the recombinant RNA molecule of any one of embodiments 1 to 28 with a viral capsid protein, wherein the recombinant RNA molecule comprises an encapsidation recognition element (ERE), and wherein the ERE provides for encapsidation of the RNA by the viral capsid protein.

[0215] 73. The method of embodiment 72, wherein the recombinant RNA molecule is combined with a viral capsid protein in a vessel.

[0216] 74. The method of embodiment 73, wherein the combining comprises

(a) providing to a plant cell the recombinant RNA molecule, wherein the recombinant RNA molecule comprises an encapsidation recognition element (ERE), and wherein the plant cell comprises an RdRP protein that recognizes the 5' RNA replication element and 3' RNA replication element catalyzes synthesis of a synthetic endornavirus satellite RNA from the recombinant RNA molecule and a viral capsid protein, wherein the ERE provides for encapsidation of the RNA by the viral capsid protein; and optionally

(b) isolating the synthetic endornavirus satellite particle from the plant cell, a plant comprising the plant cell, or from media in which the plant cell or the plant had been grown.

[0217] 75. The method of embodiment 72, 73, or 74, further comprising the step of formulating the synthetic endornavirus satellite particle wherein the formulating comprises combining the synthetic endornavirus satellite particle with a carrier, an excipient, and/or an adjuvant.

[0218] 76. A plant propagule comprising the recombinant RNA molecule of any one of embodiments 1 to 28 and an endornavirus RdRP, optionally wherein the plant propagule further comprises a heterologous RNA virus RdRP which recognizes an HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA.

[0219] 77. The plant propagule of embodiment 76, wherein the plant propagule is a seed, a seedling, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, explant, embryo, or callus.

[0220] 78. The plant propagule of embodiment 76 or 77, wherein the plant propagule is a mosaic comprising both plant cells comprising the recombinant RNA molecule and plant cells lacking the recombinant RNA molecule.

[0221] 79. The plant propagule of embodiment 76, 77, or 78, wherein the plant propagule lacks DNA encoding the recombinant RNA molecule.

[0222] 80. The plant propagule of any one of embodiments 76 to 79, wherein the plant propagule further comprises a heterologous RNA virus RdRP which recognizes an HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA, and the heterologous RNA virus RdRP is an Alphaflexivirus, Betaflexivirus, Bromovirus, Cclavirus, a Closterovirus, a Comovirus, a Potexvirus, Potyvirus, Tobamovirus, Tombusvirus, Tospoviridae, Trivirinae, Tymovirus, Varicosavirus, or Secoviridae RdRP or an RdRP set forth in Table 7.

[0223] 81. A plant comprising the recombinant RNA molecule of any one of embodiments 1 to 28 and an endornavirus RdRP, optionally wherein the plant propagule further comprises a heterologous RNA virus RdRP which recognizes an HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA.

[0224] 82. The plant of embodiment 81, wherein the plant is a monocot or a dicot plant.

[0225] 83. The plant of embodiment 81, wherein the plant is of the family Asteraceae, Cucurbitaceae, Fabaceae, Lauraceae, Poaceae, or Solanaceae, optionally wherein the plant is a member of the genus *Capsicum*, *Cucumis*, *Cucurbita*, *Helianthus*, *Hordeum*, *Nicotiana*, *Oryza*, *Secale*, *Solanum*, or *Triticum*.

[0226] 84. The plant of embodiment 81, 82, or 83, wherein the plant lacks DNA that encodes the recombinant RNA molecule.

[0227] 85. The plant of any one of embodiments 81 to 84, wherein the plant comprises an endornavirus, and wherein the endornavirus RdRP is provided to the plant cell by the endornavirus, optionally wherein the endornavirus RdRP comprises a protein having at least 85%, 90%, 95%, 97%, or 99% sequence identity to SEQ ID NO: 613 to 725, or 726.

[0228] 86. The plant of any one of embodiments 81 to 85, wherein the endornavirus is endemic to the plant, optionally wherein the endemic endornavirus is non-pathogenic and/or commensal.

[0229] 87. The plant of any one of embodiments 81 to 86, wherein the endornavirus RdRP, the 5' RNA replication element, and/or the 3' RNA replication element are derived from an endornavirus comprising one or both of the endornavirus RdRP, 5' RNA replication element, and/or 3' RNA replication elements.

[0230] 88. The plant of any one of embodiments 81 to 87, wherein the RdRP has at least 85%, 90%, 95%, 97%, 98%, or 99% identity to SEQ ID NO: 613 to 725, or 726, wherein the 5' RNA replication element has at least 85%, 90%, 95%, 97%, 98%, or 99% identity to the RNA encoded by SEQ ID NO: 466 to 522, 727, or 924 to 1017 and/or wherein the 3' RNA replication element has at least 85%, 90%, 95%, 97%, 98%, or 99% identity to the RNA encoded by SEQ ID NO: 523 to 595, 728, or 1019 to 1129.

[0231] 89. The plant of any one of embodiments 81 to 88, wherein the plant is a grafted plant and wherein the rootstock and/or scion of the grafted plant comprise at least one cell comprising the recombinant RNA and the endornavirus RdRP.

[0232] 90. The plant of any one of embodiments 81 to 89, wherein the plant is not produced by an essentially biological process.

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[0233] 91. The plant of any one of embodiments 81 to 90, wherein the plant further comprises a heterologous RNA virus (HRV) RdRP which recognizes an HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA, and the heterologous RNA virus RdRP is an Alphaflexivirus, Betaflexivirus, Bromovirus, Celavirus, a Closterovirus, a Comovirus, a Potexvirus, Potyvirus, Tobamovirus, Tombusvirus, Tospoviridae, Trivirinae, Tymovirus, Varicosavirus, or Secoviridae RdRP or an RdRP set forth in Table 7.

[0234] 92. A endornavirus satellite system that is self-replicating when introduced into a plant or plant cell, comprising: (1) a recombinant endornavirus satellite RNA of any one of embodiments 1 to 28; and (2) an exogenous endornavirus that is capable of replication in the plant or plant cells and that encodes the endornavirus RdRP that recognizes the 5' and 3' RNA replication element sequences in the recombinant endornavirus satellite RNA, optionally wherein the endornavirus satellite system further comprises a heterologous RNA virus RdRP which recognizes an HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA.

[0235] 93. The self-replicating endornavirus satellite system of embodiment 92, wherein the exogenous endornavirus is endemic or native to a different species, variety, or germplasm of plant.

[0236] 94. The self-replicating endornavirus satellite system of embodiment 92, wherein the endornavirus satellite system further comprises a heterologous RNA virus (HRV) RdRP which recognizes an HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA, and the heterologous RNA virus RdRP is optionally an Alphaflexivirus, Betaflexivirus, Bromovirus, Celavirus, a Closterovirus, a Comovirus, a Potexvirus, Potyvirus, Tobamovirus, Tombusvirus, Tospoviridae, Trivirinae, Tymovirus, Varicosavirus, or Secoviridae RdRP or an RdRP set forth in Table 7.

[0237] 95. A recombinant DNA molecule comprising a first promoter which is operably linked to DNA encoding the RNA molecule of any one of embodiments 1-28.

[0238] 96. A cell comprising the recombinant DNA molecule of embodiment 95, wherein the cell is a bacterial cell, a fungal cell, a plant cell, an insect cell, or an invertebrate animal cell.

[0239] 97. A vector for bacterially mediated plant transformation, comprising the recombinant DNA molecule of embodiment 95.

[0240] 98. The vector of embodiment 97, wherein the bacterium that mediates the plant transformation is an *Agrobacterium* sp., a *Sinorhizobium* sp., a *Mesorhizobium* sp., a *Bradyrhizobium* sp., *Rhizobium* sp., or an *Ensifer* sp. and the vector is adapted for transformation with the bacterium.

[0241] 99. The vector of embodiment 97 or 98, wherein the bacterium that mediates the plant transformation is an *Agrobacterium* sp., and wherein the vector further comprises T-DNAs flanking the DNA molecule encoding the recombinant RNA molecule.

[0242] 100. The vector of embodiment 97, 98, or 99, contained within a bacterial or plant cell.

[0243] 101. An expression system comprising: (a) the recombinant DNA molecule of embodiment 95; and (b) a cell containing the recombinant DNA molecule and an RdRP protein that recognizes the 5' and 3' RNA replication elements encoded by the DNA molecule.

[0244] 102. The expression system of embodiment 101, wherein the recombinant DNA molecule further comprises at least one additional element comprising: (i) DNA encoding at least one RNA encoding a viral movement protein (MP); (ii) DNA encoding at least one tRNA-like molecule; (iii) DNA encoding an encapsidation recognition element (ERE); (iv) DNA encoding an RNA comprising, from 5' to 3' and operably linked, a 5' RNA replication element recognized by an endornavirus RNA-dependent RNA polymerase (RdRP), the RNA of (i) and optionally an operably linked RNA of (ii) and/or (iii), and a 3' RNA replication element; (v) DNA encoding an RNA promoter; (vi) DNA encoding an RNA-dependent RNA polymerase (RdRP) that recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter; and/or (vii) a DNA molecule comprising a promoter which is operably linked to the DNA encoding the RNA of at least one of (i), (ii), (iii), (iv), (v), or (vi).

[0245] 103. The expression system of embodiments 101 or 102, wherein the cell is a bacterial cell, a plant cell, a fungal cell, an insect cell, or a non-human animal cell, optionally wherein the bacterial cell is an *Agrobacterium* sp., a *Sinorhizobium* sp., a *Mesorhizobium* sp., *Bradyrhizobium* sp., *Rhizobium* sp., or an Ensifer sp. cell.

[0246] 104. The expression system of any one of embodiment 101, 102, or 103, further comprising: (i) a viral capsid protein that can encapsidate an RNA molecule comprising the encapsidation recognition element (ERE); (ii) an RNA-binding protein (RBP) that can bind to the RNA molecule encoded by the DNA molecule, optionally wherein the RBP binds to an RNA effector; (iii) an RNA cleavage agent that cleaves the RNA molecule; and/or (iv) an RNA promoter dependent RNA polymerase (RdRP) protein that recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter recognizes an RNA promoter in the RNA molecule.

[0247] 105. The expression system of embodiment 104, wherein the viral capsid protein is: (a) expressed by the recombinant DNA molecule in the cell, (b) co-expressed by a second recombinant DNA molecule in the cell; (c) provided exogenously to the cell; or (d) expressed by a virus in the cell.

[0248] 106. The expression system of embodiment 104 or 105, wherein: (i) the capsid protein, viral movement protein (MP), RdRP protein, and/or the RdRP protein that recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter is heterologous to the cell and/or (ii) wherein the RdRP protein or a polynucleotide encoding the RdRP protein is provided exogenously to the cell.

[0249] 107. The expression system of any one of embodiments 101 to 106, wherein the cell is a plant cell.

[0250] 108. The expression system of 107, wherein the plant cell contains an endornavirus which expresses the RdRP protein that recognizes the 5' RNA replication element and the 3' RNA replication element.

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[0251] 109. The expression system of embodiment 108, wherein the endornavirus occurs naturally in the plant cell.

[0252] 110. The expression system of any one of embodiments 101 to 109, wherein the recombinant DNA molecule further comprises at least one RNA encoding a viral MP, a tRNA-like molecule from an Arabidopsis FT mRNA, and an encapsidation recognition element comprising a TMV-OAS.

[0253] 111. An agricultural formulation comprising the expression system of any one of embodiments 101 to 110.

[0254] 112. The agricultural formulation of embodiment 111, wherein the formulation comprises the expression system and a carrier, an excipient and/or an adjuvant.

[0255] 113. An agricultural formulation comprising the recombinant DNA molecule of embodiment 95.

[0256] 114. The agricultural formulation of embodiment 112, wherein the formulation comprises the recombinant DNA molecule and a carrier, an excipient and/or an adjuvant.

[0257] 115. A method of producing an exogenous polypeptide in a plant or plant cell, comprising: providing a plant or plant cell comprising the recombinant RNA molecule of any one of embodiments 1 to 28 or the recombinant DNA molecule of embodiment 95, wherein the cargo RNA molecule encoded by the RNA or DNA molecule comprises a translatable messenger RNA encoding the exogenous polypeptide, wherein the plant or plant cell comprises an RdRP protein that recognizes the 5' RNA replication element and the 3' RNA replication element of the recombinant RNA and that catalyzes synthesis of a synthetic endornavirus satellite RNA from the recombinant RNA molecule, and wherein the exogenous polypeptide is translated from the translatable messenger; optionally wherein the plant or plant cell further comprises a heterologous RNA virus (HRV) RNA promoter dependent RNA polymerase (hrvRdRP) protein that recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter recognizes an RNA promoter in the RNA molecule.

[0258] 116. The method of embodiment 115, further comprising a first step of providing a population of plants comprising the plant cells comprising the endornavirus which provides the RdRP protein; and then providing the recombinant RNA or DNA molecule, the cell, the vector, the recombinant RNA or DNA molecule, or formulation thereof to the plants comprising the plant cells and optionally further comprising providing the hrvRdRP to the plants comprising the plant cells.

[0259] 117. The method of embodiment 115 or 116, wherein the endornavirus is exogenously provided to the plant cell and/or wherein an HRV encoding the hrvRdRP is provided to the plant cell.

[0260] 118. The method of embodiment 115, 116, or 117, wherein the RdRP and/or hrvRdRP protein or a recombinant polynucleotide encoding the RdRP and/or hrvRdRP protein is exogenously provided to the plant cell.

[0261] 119. The method of any one of embodiments 115 to 118, further comprising a first step of providing a population of plants comprising the plant cells comprising the RdRP protein or the

recombinant polynucleotide encoding the RdRP; and then providing the recombinant RNA molecule to the plants comprising the plant cells.

[0262] 120. The method of any one of embodiments 115 to 119, wherein the recombinant RNA molecule has been produced in a fermentation system.

[0263] 121. The method of any one of embodiments 115 to 120, further comprising the step of determining if the plant cell comprises an endornavirus which can provide the RdRP.

[0264] 122. A method of producing a modified plant propagule that comprises at least one plant cell comprising a recombinant RNA molecule of embodiment 1 to 28, comprising isolating a plant propagule comprising at least one plant cell comprising the recombinant RNA molecule and an endornavirus RNA-dependent RNA polymerase (RdRP) from a mixed population of plant cells comprising both plant cells comprising the recombinant RNA molecule and plant cells lacking the recombinant RNA molecule.

[0265] 123. The method of embodiment 122, wherein the mixed population of plant cells comprise a population of protoplasts or a population of cells in callus or an explant.

[0266] 124. The method of embodiment 122 or 123, wherein the mixed population of plant cells comprise plant cells comprising the endornavirus RdRP and plant cells lacking the endornavirus RdRP.

[0267] 125. The method of embodiment 122, 123, or 124, wherein the mixed population of plant cells comprise plant cells comprising the endornavirus RdRP.

[0268] 126. The method of any one of embodiments 121 to 125, wherein the mixed population of plant cells is screened or selected for the presence of the plant cell comprising the recombinant RNA molecule prior to isolating the plant propagule.

[0269] 127. The method of any one of embodiments 122 to 126, wherein the isolation comprises selecting for the plant cell comprising the recombinant RNA molecule prior to isolating the plant propagule.

[0270] 128. The method of any one of embodiments 122 to 127, wherein the mixed population is located within a plant or a plant part.

[0271] 129. The method of any one of embodiments 122 to 128, wherein the plant or plant part is screened or selected for presence of the recombinant RNA molecule prior to isolating the plant propagule.

[0272] 130. The method of any one of embodiments 122 to 128, wherein the plant or plant part is screened or selected for systemic presence of the recombinant RNA molecule prior to isolating the plant propagule.

[0273] 131. The method of any one of embodiments 122 to 130, wherein the recombinant RNA molecule encodes a selectable marker and the plant propagule comprising the recombinant RNA molecule is isolated by selecting for presence of the selectable marker.

[0274] 132. The method of embodiment 131, further comprising selecting a plant propagule comprising a recombinant RNA molecule wherein the selectable marker has been removed.

- [0275] 133. The method of any one of embodiments 122 to 132, wherein the plant propagule comprising the recombinant RNA molecule is isolated by detecting the RNA molecule in one or more plant cells comprising the recombinant RNA molecule and separating the one or more plant cells comprising the recombinant RNA molecule from the plant cells lacking the recombinant DNA molecule.
- [0276] 134. The method of any one of embodiments 122 to 133, wherein the plant propagule is a mosaic comprising both plant cells comprising the recombinant RNA molecule and plant cells lacking the recombinant RNA molecule.
- [0277] 135. The method of any one of embodiments 121 to 134, wherein the plant propagule is a mosaic comprising both plant cells comprising the endornavirus RdRP and plant cells lacking the endornavirus RdRP.
- [0278] 136. The method of any one of embodiments 122 to 134, wherein the plant propagule lacks DNA that encodes the recombinant RNA molecule.
- [0279] 137. The method of any one of embodiments 122 to 136, wherein the plant or plant part lacks DNA that encodes the recombinant RNA molecule.
- [0280] 138. The method of any one of embodiments 122 to 137, wherein the plant propagule comprises the cell, or a seed, seedling, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, explant, or callus comprising the cell.
- [0281] 139. The method of embodiment 138, further comprising multiplying the cell, seed, seedling, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, explant, or callus to obtain progeny, wherein the progeny comprise the recombinant RNA molecule.
- [0282] 140. The method of embodiment 139, wherein the multiplying comprises culturing a plurality of explants obtained from the cell, seed, seedling, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, explant, or callus.
- [0283] 141. The method of any one of embodiments 122 to 140, wherein the isolated propagule comprises the cell and the method further comprises regenerating a plant, seedling, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, explant, or callus comprising the recombinant RNA from said cell.
- [0284] 142. The method of any one of embodiments 122 to 140, wherein the isolated propagule comprises callus and the method further comprises regenerating a plant, seedling, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, or explant comprising the recombinant RNA from said callus.
- [0285] 143. The method of embodiment 141 or 142, wherein a plant is regenerated and wherein the method further comprises recovering F₁ seed or F₁ progeny comprising the recombinant RNA from the plant.
- [0286] 144. A method of providing a synthetic endornavirus satellite RNA to a plant comprising: grafting a scion onto a rootstock comprising recombinant RNA molecule of any one of embodiments 1 to 28, wherein at least one cell of the rootstock and/or the scion comprises the endornavirus RdRP.
- [0287] 145. The method of embodiment 144, wherein the scion lacks the recombinant RNA molecule prior to grafting.

[0288] 146. The method of embodiment 144 or 145, wherein the rootstock comprises the endornavirus RdRP.

[0289] 147. The method of any one of embodiments 144 to 146, wherein the RdRP is provided by an endornavirus endemic to the rootstock, optionally wherein the endornavirus endemic to the rootstock is non-pathogenic and/or commensal.

[0290] 148. The method of any one of embodiments 144 to 146, wherein the RdRP is exogenously provided to the rootstock.

[0291] 149. The method of any one of embodiments 144 to 148, wherein the scion comprises the endornavirus RdRP.

[0292] 150. The method of any one of embodiments 144 to 149, wherein the RdRP is provided by an endornavirus endemic to the scion and/or wherein the RdRP is exogenously provided to the scion, optionally wherein the endornavirus endemic to the scion is non-pathogenic and/or commensal.

[0293] 151. A method for producing a plant that transmits a recombinant RNA molecule to progeny plants or seed comprising isolating an F₁ progeny plant or seed comprising at least one cell comprising an endornavirus RNA-dependent RNA polymerase (RdRP) and the recombinant RNA molecule of any one of embodiments 1 to 28 from a population of F₁ plants or seed obtained from a parent plant comprising the recombinant RNA molecule.

[0294] 152. The method of embodiment 151, wherein the F₁ progeny plant or seed comprising the cell is isolated by screening the population of F₁ plants or seed obtained from a parent plant for the presence of the recombinant RNA molecule and propagating the F₁ progeny plant or seed comprising the recombinant RNA molecule.

[0295] 153. The method of embodiment 151, wherein the recombinant RNA molecule encodes a selectable marker and the F₁ progeny plant or seed comprising the recombinant RNA molecule is isolated by selecting the F₁ progeny plant or seed comprising the recombinant RNA molecule for presence of the selectable marker.

[0296] 154. The method of any one of embodiments 151 to 153, wherein the F₁ progeny plant or seed lack DNA that encodes the recombinant RNA molecule.

[0297] 155. The method of any one of embodiments 151 to 154, wherein the parent plant lacks DNA that encodes the recombinant RNA molecule.

[0298] 156. The method of embodiment 153, wherein the selected F₁ progeny plant transmits the recombinant RNA molecule to at least F₂ progeny.

[0299] 157. The method of any one of embodiments 151 to 156, wherein the F₁ progeny plant or seed population is obtained from a parent plant used as a pollen recipient.

[0300] 158. The method of any one of embodiments 151 to 156, wherein the F₁ progeny plant or seed population is obtained from a parent plant used as a pollen donor.

[0301] 159. The method of any one of embodiments 151 to 156, wherein the F₁ progeny plant or seed population is obtained by selfing the parent plant.

[0302] 160. The method of any one of embodiments 151 to 159, wherein the parent plant or a part thereof comprising the plant cell is screened or selected for presence of the recombinant RNA molecule prior to isolating the F₁ progeny plant or seed.

[0303] 161. The method of any one of embodiments 151 to 160, wherein the parent plant or one or more parts thereof are screened for systemic presence of the recombinant RNA molecule prior to isolating the F₁ progeny plants, optionally wherein the part comprises floral tissue or male or female reproductive tissue.

[0304] 162. The method of any one of embodiments 151 to 161, wherein the pericarp of the parent plant is screened or selected for presence of the recombinant RNA molecule.

[0305] 163. The method of any one of embodiments 151 to 162, wherein F₁ seeds are obtained from a parent plant selected for presence of the recombinant RNA molecule in pericarp tissue.

[0306] 164. The method of any one of embodiments 151 to 163, wherein an F₁ seed of the parent plant is non-destructively screened for presence of the recombinant RNA molecule.

[0307] 165. The method of embodiment 164, wherein the F₁ seed of the parent plant is non-destructively screened by assaying maternally derived or endosperm tissue of the seed for the presence of the recombinant RNA molecule.

[0308] 166. The method of any one of embodiments 151 to 165, further comprising introducing the recombinant RNA molecule or a polynucleotide encoding the recombinant RNA molecule into a plant cell and obtaining the parent plant comprising the recombinant RNA molecule from the plant cell.

[0309] 167. The method of any one of embodiments 151 to 166, wherein the propagule, plant, plant part, scion, and/or rootstock comprises a heterologous viral coat protein which can encapsidate the recombinant RNA molecule and/or comprises the recombinant RNA molecule encapsidated by a heterologous viral coat protein.

[0310] 168. A method of barcoding a plant, plant cell, progeny thereof, or part thereof comprising providing to the plant or plant cell the recombinant RNA molecule of any one of embodiments 1 to 28, wherein the cargo RNA of the recombinant RNA molecule comprises a barcode RNA molecule, and wherein the plant or plant cell comprises an endornavirus RNA-dependent RNA polymerase (RdRP).

[0311] 169. The method of embodiment 168, wherein the barcode RNA molecule comprises a sequence that uniquely identifies the plant, plant cell, progeny thereof, or part thereof.

[0312] 170. The method of embodiment 168 or 169, wherein the barcode RNA molecule comprises a sequence that is not present in the genome and/or transcriptome of a wild-type plant of the same species, a pathogen thereof, or a symbiont thereof.

[0313] 171. The method of any one of embodiments 168 to 170, wherein the barcode RNA molecule comprises a random sequence.

[0314] 172. The method of any one of embodiments 168 to 171, wherein the barcode RNA molecule comprises a forward primer binding site and a reverse primer binding site that is not present in the

genome and/or transcriptome of a wild-type plant of the same species, a pathogen thereof, or a symbiont thereof.

[0315] 173. The method of any one of embodiments 168 to 172, wherein the barcode RNA molecule is up to about 3.2 kb in length.

[0316] 174. The method of any one of embodiments 168 to 172, wherein the barcode RNA molecule has a length of 10 to 3200 nucleotides, 20 to 1000 nucleotides, or 50 to 500 nucleotides, optionally wherein the barcode RNA molecule has a length of 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1500, 2000, 2500, 3000, or 3200 nucleotides.

[0317] 175. The method of any one of embodiments 168 to 174, wherein the barcode RNA molecule comprises a non-protein coding sequence.

[0318] 176. The method of any one of embodiments 168 to 175, wherein the plant transmits the recombinant RNA molecule to progeny.

[0319] 177. The method of any one of embodiments 168 to 176, wherein the plant, plant cell, progeny thereof, or part thereof lacks DNA that encodes the recombinant RNA molecule.

[0320] 178. The method of any one of embodiments 168 to 176, further comprising isolating an F₁ progeny plant or seed comprising at least one cell comprising the endornavirus RdRP and the recombinant RNA molecule.

[0321] 179. The method of embodiment 178, wherein the F₁ progeny plant or seed is obtained from the plant used as a pollen recipient.

[0322] 180. The method of embodiment 178, wherein the F₁ progeny plant or seed is obtained from the plant used as a pollen donor.

[0323] 181. The method of embodiment 178, wherein the F₁ progeny plant or seed is obtained by selfing the plant.

[0324] 182. The method of any one of embodiments 168 to 181, further comprising propagating the plant or plant cell to obtain a plant part or a plant propagule comprising the barcode RNA molecule, optionally wherein said propagule comprises callus, tubers, and/or rootstock.

[0325] 183. A method of identifying a barcoded plant, plant part, or plant cell, the method comprising screening for the presence of a barcode RNA molecule in the plant, plant part, or plant cell, wherein the plant, plant part, or plant cell comprises the recombinant RNA molecule of any one of embodiments 1 to 28, wherein the cargo RNA of the recombinant RNA molecule comprises the barcode RNA molecule.

Summary of Tables

Table 1. Endornavirus 5' and 3' RNA Replication Element (RRE) DNA Coding Sequences

Name ¹	Sequences	
endo5UTR consensus		
>endFiveUTRMSA-consensus	SEQ ID NO: 466	
endornavirus	5' RNA replication element (5'-most 500 bases)	5' RNA replication element
Oryza sativa endornavirus >NC_007647	SEQ ID NO: 467	
Vicia faba endornavirus >NC_007648	SEQ ID NO: 468	
Oryza rufipogon endornavirus >NC_007649	SEQ ID NO: 469	
Persea americana endornavirus >NC_016648	SEQ ID NO: 470	
Lagenaria siceraria endornavirus >NC_023641	SEQ ID NO: 471	
Yerba mate endornavirus strain INTA >NC_024455	SEQ ID NO: 472	
Hot pepper alphaendornavirus >NC_027920	SEQ ID NO: 473	
Hordeum vulgare endornavirus >NC_028949	SEQ ID NO: 474	
Cucumis melo endornavirus isolate CL-01 >NC_029064	SEQ ID NO: 475	
Winged bean alphaendornavirus 1 >NC_031336	SEQ ID NO: 476	SEQ ID NO: 491
Lagenaria siceraria endornavirus Hubei isolate >NC_034216	SEQ ID NO: 477	GTA
Phaseolus vulgaris endornavirus 2 isolate PvEV-2 >NC_038422	SEQ ID NO: 478	
Bell pepper endornavirus isolate Penol >NC_039216	SEQ ID NO: 479	SEQ ID NO: 489
Phaseolus vulgaris alphaendornavirus 1 isolate PvEV-1 >NC_039217	SEQ ID NO: 480	
Phaseolus endornavirus 3 isolate LA >NC_040558	SEQ ID NO: 481	GGGGAAAT
Helianthus annuus alphaendornavirus isolate BJ >NC_040799	SEQ ID NO: 482	SEQ ID NO: 517
Cluster bean endornavirus isolate: 593049 >NC_040825	SEQ ID NO: 483	SEQ ID NO: 492
Basella alba endornavirus 1, BaEV1 >NC_043109	SEQ ID NO: 484	
Bell pepper endornavirus >AB597230		SEQ ID NO: 485
Cucumis melo endornavirus isolate CL-01		GGTA

>NC_029064		
Bell pepper endornavirus isolate Maor		SEQ ID NO: 486
>KP455654		
Bell pepper endornavirus		SEQ ID NO: 487
>KT149366		
Bell pepper endornavirus isolate BPEV-YW		SEQ ID NO: 488
>JN019858		
Persea americana endornavirus isolate Fuerte		GTA
>JN880414		
Bell pepper endornavirus isolate lj		SEQ ID NO: 490
>KF709944		
Oryza sativa endornavirus		TGAA
>D32136		
Oryza rufipogon endornavirus		TGAA
>AB014344		
Cucumber endornavirus 1 isolate CuEV1		SEQ ID NO: 493
>MT586998		
Bell pepper endornavirus strain IS		SEQ ID NO: 494
>JQ951943		
Fagopyrum esculentum endornavirus 2 isolate SK		SEQ ID NO: 495
>MZ517186		
Capsicum frutescens endornavirus 1 isolate LA-C		SEQ ID NO: 496
>MT013202		
Cucumis melo alphaendornavirus strain CmEV/BRA/TO-23/2014		SEQ ID NO: 497
>MH365458		
Bell pepper alphaendornavirus isolate Antioquia May 5		SEQ ID NO: 498
>MN073197		
Capsicum frutescens endornavirus 1 isolate LA-A		SEQ ID NO: 499
>MT013200		
Capsicum frutescens endornavirus 1 isolate LA-B		TAAAAAGGT
>MT013201		

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Plant associated alphaendornavirus 1 isolate BER19SW1		SEQ ID NO: 500
>OL472077		
Tomato associated alphaendornavirus 1 isolate BOL20S		GTCAAG
>OL472079		
Bell pepper alphaendornavirus isolate MS1		SEQ ID NO: 501
>MN175323		
Brown algae endornavirus 1 Chiba1		GTCTCAAG
>LC521321		
Brown algae endornavirus 2 Chiba2		ACA
>LC521322		
Bell pepper alphaendornavirus isolate BPEV_Panama		SEQ ID NO: 502
>MZ127290		
Lily alphaendornavirus isolate BJ		SEQ ID NO: 503
>MZ614632		
Phaseolus vulgaris alphaendornavirus 2		SEQ ID NO: 504
>OM112199		
Basella alba alphaendornavirus strain Oahu4		AAT
>OM108480		
Pumpkin alphaendornavirus isolate Anhui		SEQ ID NO: 505
>MW018478		
Oryza sativa alphaendornavirus isolate BXCFS134		SEQ ID NO: 506
>MZ209990		
Oryza sativa alphaendornavirus isolate DHCFY127945		SEQ ID NO: 507
>MZ209614		
Pterostylis alphaendornavirus strain HR		SEQ ID NO: 508
>OL471320		
Bell pepper alphaendornavirus isolate LA-E		SEQ ID NO: 509
>MT013204		
Triticeae associated alphaendornavirus isolate Wheeler		SEQ ID NO: 510
>MW091544		
Hordeum vulgare alphaendornavirus isolate HYT-37		

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>MN107382		SEQ ID NO: 511
Hordeum vulgare alphaendornavirus isolate HYT-38		SEQ ID NO: 512
>MN107383		
Cucumis melo alphaendornavirus isolate IL		TTCCGTA
>MN398900		
Phaseolus vulgaris alphaendornavirus 1 isolate PVAV1/CG6		SEQ ID NO: 513
>MN832719		
Phaseolus vulgaris alphaendornavirus 2 isolate PVAV2/CG6		SEQ ID NO: 514
>MN832720		
Bell pepper alphaendornavirus isolate XJ		SEQ ID NO: 515
>MH182675		
Bell pepper alphaendornavirus isolate Marinilla		SEQ ID NO: 516
>MK284997		
Bell pepper alphaendornavirus isolate San Vicente		GGTTTT
>MK284998		
Bell pepper alphaendornavirus isolate May8A		SEQ ID NO: 518
>MK116548		
Endornavirus identified from rice cultivar M-102		SEQ ID NO: 520
Johnsongrass virus isolate JVG-1		SEQ ID NO: 521
>MW756210		
Johnsongrass virus isolate JVG-2		SEQ ID NO: 522
>MW756211		
Endornavirus identified from Rutgers tomato		SEQ ID NO: 519
Bell Pepper Endornavirus 5' RRE		SEQ ID NO: 727
endo3UTR consensus		
>endThreeUTRMSA-consensus	SEQ ID NO: 523	
endornavirus	3' RNA replication element (3'-most 500 bases)	3' RNA replication element

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Oryza sativa endornavirus	SEQ ID NO: 524	
>NC_007647		
Vicia faba endornavirus	SEQ ID NO: 525	
>NC_007648		
Oryza rufipogon endornavirus >NC_007649	SEQ ID NO: 526	
Persea americana endornavirus	SEQ ID NO: 527	
>NC_016648		
Lagenaria siceraria endornavirus, LsEV	SEQ ID NO: 528	
>NC_023641		
Yerba mate endornavirus strain INTA	SEQ ID NO: 529	
>NC_024455		
Hot pepper alphaendornavirus	SEQ ID NO: 530	
>NC_027920		
Hordeum vulgare endornavirus	SEQ ID NO: 531	
>NC_028949		
Cucumis melo endornavirus isolate CL-01	SEQ ID NO: 532	
>NC_029064		
Winged bean alphaendornavirus 1	SEQ ID NO: 533	SEQ ID NO: 551
>NC_031336		
Lagenaria siceraria endornavirus-Hubei	SEQ ID NO: 534	SEQ ID NO: 588
>NC_034216		
Phaseolus vulgaris endornavirus 2 isolate PvEV-2	SEQ ID NO: 535	
>NC_038422		
Bell pepper endornavirus isolate Penol	SEQ ID NO: 536	SEQ ID NO: 547
>NC_039216		
Phaseolus vulgaris alphaendornavirus 1	SEQ ID NO: 537	
>NC_039217		
Phaseolus endornavirus 3 isolate LA	SEQ ID NO: 538	SEQ ID NO: 548
>NC_040558		
Helianthus annuus alphaendornavirus isolate BJ	SEQ ID NO: 539	SEQ ID NO: 586
>NC_040799		

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Cluster bean endornavirus 1	SEQ ID NO: 540	SEQ ID NO: 552
>NC_040825		
Basella alba endornavirus 1, baEV1	SEQ ID NO: 541	
>NC_043109		
Bell pepper endornavirus		SEQ ID NO: 542
>AB597230		
Cucumis melo endornavirus isolate CL-01		SEQ ID NO: 543
>NC_029064		
Bell pepper endornavirus isolate Maor		SEQ ID NO: 544
>KP455654		
Bell pepper endornavirus		SEQ ID NO: 545
>KT149366		
Bell pepper endornavirus isolate BPEV-YW		SEQ ID NO: 546
>JN019858		
Persea americana endornavirus isolate Fuerte		SEQ ID NO: 549
>JN880414		
Bell pepper endornavirus isolate lj		SEQ ID NO: 550
>KF709944		
Oryza sativa endornavirus		SEQ ID NO: 553
>D32136		
Oryza rufipogon endornavirus		SEQ ID NO: 554
>AB014344		
Cucumber endornavirus 1 isolate CuEV1		SEQ ID NO: 555
>MT586998		
Bell pepper endornavirus strain IS		SEQ ID NO: 556
>JQ951943		
Fagopyrum esculentum endornavirus 2 isolate SK		SEQ ID NO: 557
>MZ517186		
Capsicum frutescens endornavirus 1 isolate LA-C		SEQ ID NO: 558
>MT013202		
Cucumis melo alphaendornavirus strain CmEV/BRA/TO-23/2014		SEQ ID NO: 559

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>MH365458		
Bell pepper alphaendornavirus isolate Antioquia May 5		SEQ ID NO: 560
>MN073197		
Capsicum frutescens endornavirus 1 isolate LA-A		SEQ ID NO: 561
>MT013200		
Capsicum frutescens endornavirus 1 isolate LA-B		SEQ ID NO: 562
>MT013201		
Plant associated alphaendornavirus 1 isolate BER19SW1		SEQ ID NO: 563
>OL472077		
Tomato associated alphaendornavirus 1 isolate BOL20S		SEQ ID NO: 564
>OL472079		
Bell pepper alphaendornavirus isolate MS1		SEQ ID NO: 565
>MN175323		
Brown algae endornavirus 1 Chiba1		SEQ ID NO: 566
>LC521321		
Brown algae endornavirus 2 Chiba2		SEQ ID NO: 567
>LC521322		
Bell pepper alphaendornavirus isolate BPEV_Panama		SEQ ID NO: 568
>MZ127290		
Lily alphaendornavirus isolate BJ		SEQ ID NO: 569
>MZ614632		
Phaseolus vulgaris alphaendornavirus 2		SEQ ID NO: 570
>OM112199		
Basella alba alphaendornavirus strain Oahu4		SEQ ID NO: 571
>OM108480		
Pumpkin alphaendornavirus isolate Anhui		SEQ ID NO: 572
>MW018478		
Oryza sativa alphaendornavirus isolate BXCFS134		SEQ ID NO: 573
>MZ209990		
Oryza sativa alphaendornavirus isolate DHCFY127945		SEQ ID NO: 574
>MZ209614		

Pterostylis alphaendornavirus strain HR		SEQ ID NO:
>OL471320		575
Bell pepper alphaendornavirus isolate LA-E		SEQ ID NO:
>MT013204		576
Triticeae associated alphaendornavirus isolate Wheeler		SEQ ID NO:
>MW091544		577
Hordeum vulgare alphaendornavirus isolate HYT-37		SEQ ID NO:
>MN107382		578
Hordeum vulgare alphaendornavirus isolate HYT-38		SEQ ID NO:
>MN107383		579
Cucumis melo alphaendornavirus isolate IL		SEQ ID NO:
>MN398900		580
Phaseolus vulgaris alphaendornavirus 1 isolate PVAV1/CG6		SEQ ID NO:
>MN832719		581
Phaseolus vulgaris alphaendornavirus 2 isolate PVAV2/CG6		SEQ ID NO:
>MN832720		582
Bell pepper alphaendornavirus isolate XJ		SEQ ID NO:
>MH182675		583
Bell pepper alphaendornavirus isolate Marinilla		SEQ ID NO:
>MK284997		584
Bell pepper alphaendornavirus isolate San Vicente		SEQ ID NO:
>MK284998		585
Bell pepper alphaendornavirus isolate May8A		SEQ ID NO:
>MK116548		587
Capsicum frutescens endornavirus 1 isolate MC7		SEQ ID NO:
>MN175322		589
Geranium carolinianum endornavirus		SEQ ID NO:
>MH577297		590
Endornavirus identified from rice cultivar M-102		SEQ ID NO:
		592
Johnsongrass virus isolate JVG-1		SEQ ID NO:
>MW756210		593

Johnsongrass virus isolate JVG-2		SEQ ID NO: 594
>MW756211		
Endornavirus identified from Rutgers tomato		SEQ ID NO: 591
Bell pepper endornavirus 3'RRE		SEQ ID NO: 728
Endornavirus	5' RRE (SEQ ID NO)	3'RRE (SEQ ID NO)
Agaricus bisporus alphaendornavirus 1	924	1018
Alphaendornavirus sp.	925	1019
Basella alba alphaendornavirus 1	926	1020
Bell pepper alphaendornavirus	927	1023
Cucumis melo alphaendornavirus	928	1024
Dicrocoelium alphaendornavirus	929	
Erysiphe cichoracearum alphaendornavirus	930	1025
Grapevine endophyte alphaendornavirus	931	1026
Helianthus annuus alphaendornavirus	932	1027
Helicobasidium mompa alphaendornavirus 1	933	1028
Hordeum vulgare alphaendornavirus	934	1029
Hot pepper alphaendornavirus	935	1030
Lagenaria siceraria alphaendornavirus	936	1032
Lily alphaendornavirus	937	1033
Oryza sativa alphaendornavirus	938	1035
Persea americana alphaendornavirus 1	939	1036
Phaseolus vulgaris alphaendornavirus 1	940	1038
Phaseolus vulgaris alphaendornavirus 2	941	1039
Phaseolus vulgaris alphaendornavirus 3	942	1040
Phytophthora cactorum alphaendornavirus 1	943	
Phytophthora cactorum alphaendornavirus 2	944	
Phytophthora cactorum alphaendornavirus 3	945	
Plant associated alphaendornavirus 1	946	1043
Pterostylis alphaendornavirus	947	1044
Pumpkin alphaendornavirus	948	1045
Rhizoctonia cerealis alphaendornavirus 1	949	1046

Rhizoctonia solani alphaendornavirus 1	950	1047
Rhizoctonia solani alphaendornavirus 2	951	1048
Triticeae associated alphaendornavirus	952	1051
Tvarminne alphaendornavirus	953	1052
Vicia faba alphaendornavirus	954	1053
Winged bean alphaendornavirus 1	955	1054
Yerba mate alphaendornavirus	956	1055
Alternaria brassicicola betaendornavirus 1	957	1056
Betaendornavirus sp.	958	1057
Botrytis cinerea betaendornavirus 1	959	1058
Gremmeniella abietina betaendornavirus 1	960	1059
Rosellinia necatrix betaendornavirus 1	961	1060
Sclerotinia minor betaendornavirus 1	962	1061
Sclerotinia sclerotiorum betaendornavirus 1	963	1062
Sclerotinia sclerotiorum betaendornavirus 1	964	1063
Sclerotinia sclerotiorum betaendornavirus 1	965	1064
Tuber aestivum betaendornavirus	966	1065
Arthrocladiella mougeotii alphaendornavirus	967	1068
Botrytis cinerea endornavirus 2	968	1070
Botrytis cinerea endornavirus 3	969	1071
Botrytis cinerea endornavirus 4	970	1072
Botrytis endornavirus 1	971	
Bremia lactucae associated endornavirus 1	972	1074
Capsicum frutescens endornavirus 1	973	1077
Carteria obtusa associated endorna-like virus	974	1078
Ceratobasidium endornavirus 1	975	1079
Ceratobasidium endornavirus 2	976	1080
Ceratobasidium endornavirus A	977	1081
Ceratobasidium endornavirus B	978	1082
Ceratobasidium endornavirus C	979	1083
Ceratobasidium endornavirus D	980	1084

Ceratobasidium endornavirus G	981	1086
Chalara endornavirus CeEV1	982	
chieh-qua endornavirus	983	1088
Cluster bean endornavirus 1	984	1089
Cucumber endornavirus 1	985	1090
Diplodia seriata endornavirus 1	986	1091
Fagopyrum esculentum endornavirus 1	987	1092
Fagopyrum esculentum endornavirus 2	988	1093
Geranium carolinianum endornavirus	989	1094
Grapevine-associated endornavirus 1	990	
Hydrocotyle umbellata endornavirus	991	1095
Hygrophorus penarioides endornavirus 1	992	1096
Hymenoscyphus fraxineus endornavirus 1	993	1097
Lagenaria siceraria endornavirus-Hubei	994	1099
Lonicera maackii endornavirus	995	1100
Macrophomina phaseolina endornavirus 1	996	1101
Macrophomina phaseolina endornavirus 2	997	1102
Morchella importuna endornavirus 1	998	1103
Morchella importuna endornavirus 2	999	1104
Morchella importuna endornavirus 3	1000	1105
Phomopsis vexans endornavirus 2	1001	1108
Phytophthora endornavirus 2	1002	1109
Phytophthora endornavirus 3	1003	1110
Rhizoctonia solani endornavirus	1004	1111
Rhizoctonia solani endornavirus - RS002	1005	1112
Rhizoctonia solani endornavirus 4	1006	1113
Rhizoctonia solani endornavirus 5	1007	1114
Rhizoctonia solani endornavirus 6	1008	1115
Rhizoctonia solani endornavirus 7	1009	1116
Rhizopus microsporus endornavirus 1	1010	1117
Rhizopus microsporus endornavirus 2	1011	1118

Sanya endornavirus 1	1012	
Sclerotinia sclerotiorum endornavirus 11	1013	1119
Sclerotinia sclerotiorum endornavirus 1-WX	1014	1120
Setosphaeria turcica endornavirus 1	1015	1125
Setosphaeria turcica endornavirus 2	1016	1126
Soybean leaf-associated endornavirus 1	1017	1127
Sclerotinia sclerotiorum endornavirus 2-A		1121
Sclerotinia sclerotiorum endornavirus 3		1122
Sclerotinia sclerotiorum endornavirus 8		1123
Sclerotinia sclerotiorum endornavirus 9		1124
Staurostrum sebaldi endornavirus		1128
Volvox aureus endorna-like virus		1129
Beijing alphaendornavirus 3		1021
Beijing sediment alphaendornavirus 2		1022
Jiangsu alphaendornavirus 1		1031
Oryza rufipogon alphaendornavirus		1034
Phaseolus leptostachyus alphaendornavirus		1037
Phytophthora alphaendornavirus 1		1041
Phytophthora heveae alphaendornavirus 1		1042
Sichuan alphaendornavirus 22		1049
Tomato associated alphaendornavirus 1		1050
Almopos endorna-like virus 1		1066
Althepos endorna-like virus 1		1067
Bolbocoleon piliferum endorna-like virus		1069
Brachiomonas submarina endorna-like virus		1073
Brown algae endornavirus 1		1075
Brown algae endornavirus 2		1076
Ceratobasidium endornavirus F		1085
Ceratobasidium endornavirus H		1087
Krauss' spikemoss associated endorna-like virus		1098
Ophiostoma bicolor endornavirus 1		1106

Phomopsis vexans endornavirus 1		1107
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¹ The descriptors “NC_XXXXXX” refer to the National Center for Biotechnology Information database accession number for entries in the world wide web internet database

“ncbi[dot]nlm[dot]nih.gov/nuccore.”

² DNA sequences which encode the corresponding RNA molecules of the replication elements are provided are provided.

Table 2. Viral capsid protein and origin of assembly sequences

Virus¹	Origin of assembly sequence²	Capsid Protein
NC_001367.1 Tobacco mosaic virus, complete genome Tobacco mosaic virus	SEQ ID NO: 1	SEQ ID NO: 26
NC_001556.1 Tobacco mild green mosaic virus, complete genome Tobacco mild green mosaic virus	SEQ ID NO: 2	SEQ ID NO: 27
NC_002692.1 Tomato mosaic virus, complete genome Tomato mosaic virus	SEQ ID NO: 3	SEQ ID NO: 28
NC_003630.1 Pepper mild mottle virus, complete genome Pepper mild mottle virus	SEQ ID NO: 4	SEQ ID NO: 29
NC_004106.1 Paprika mild mottle virus, complete genome Paprika mild mottle virus	SEQ ID NO: 5	SEQ ID NO: 30
NC_009642.1 Bell pepper mottle tobamovirus, complete genome Bell pepper mottle virus	SEQ ID NO: 6	SEQ ID NO: 31
NC_022230.1 Tomato mottle mosaic virus isolate MX5, complete genome Tomato mottle mosaic virus	SEQ ID NO: 7	SEQ ID NO: 32
NC_001728.1 Odontoglossum ringspot virus, complete genome Odontoglossum ringspot virus	SEQ ID NO: 8	SEQ ID NO: 33
NC_003852.1 Obuda pepper virus, complete genome Obuda pepper virus	SEQ ID NO: 9	SEQ ID NO: 34
NC_009041.1 Rehmannia mosaic virus, complete genome Rehmannia mosaic virus	SEQ ID NO: 10	SEQ ID NO: 35
NC_010944.1 Brugmansia mild mottle virus, complete genome Brugmansia mild mottle virus	SEQ ID NO: 11	SEQ ID NO: 36
NC_022801.1 Yellow tailflower mild mottle virus isolate Cervantes, complete genome Yellow tailflower mild mottle virus	SEQ ID NO: 12	SEQ ID NO: 37
NC_030229.1 Tropical soda apple mosaic virus isolate Okcechobce, complete genome Tropical soda apple mosaic virus	SEQ ID NO: 13	SEQ ID NO: 38
NC_001801.1 Cucumber green mottle mosaic virus, complete genome Cucumber green mottle mosaic virus	SEQ ID NO: 14	SEQ ID NO: 39
NC_002633.1 Cucumber fruit mottle mosaic virus, complete genome Cucumber fruit mottle mosaic virus	SEQ ID NO: 15	SEQ ID NO: 40

Virus¹	Origin of assembly sequence²	Capsid Protein
NC_003610.1 Kyuri green mottle mosaic virus, complete genome Kyuri green mottle mosaic virus	SEQ ID NO: 16	SEQ ID NO: 41
NC_003878.1 Zucchini green mottle mosaic virus, complete genome Zucchini green mottle mosaic virus	SEQ ID NO: 17	SEQ ID NO: 42
NC_008614.1 Cucumber mottle virus, complete genome Cucumber mottle virus	SEQ ID NO: 18	SEQ ID NO: 43
watermelon green mottle mosaic virus	SEQ ID NO: 19	SEQ ID NO: 44
NC_001873.1 Turnip vein-clearing virus, complete genome Turnip vein-clearing virus	SEQ ID NO: 20	SEQ ID NO: 45
NC_002792.2 Ribgrass mosaic virus, complete genome Ribgrass mosaic virus	SEQ ID NO: 21	SEQ ID NO: 46
NC_003355.1 Wasabi mottle virus, complete genome Wasabi mottle virus	SEQ ID NO: 22	SEQ ID NO: 47
NC_004422.1 Youcai mosaic virus, complete genome Youcai mosaic virus	SEQ ID NO: 23	SEQ ID NO: 48
NC_008365.1 Streptocarpus flower break virus, complete genome Streptocarpus flower break virus	SEQ ID NO: 24	SEQ ID NO: 49
NC_016442.1 Rattail cactus necrosis associated virus, complete genome Rattail cactus necrosis-associated virus	SEQ ID NO: 25	SEQ ID NO: 50

¹ The descriptors “NC_XXXXXX.1” refer to the National Center for Biotechnology Information

database accession number for entries in the world wide web internet database

“ncbi[dot]nlm[dot]nih.gov/nuccore.”

² RNA equivalents of the DNA sequences are also contemplated and can be obtained from the DNA sequences provided.

Table 3. Movement proteins.

Virus	Movement protein (MP)
NC_001367.1 Tobacco mosaic virus, complete genome Tobacco mosaic virus	SEQ ID NO: 51
NC_001556.1 Tobacco mild green mosaic virus, complete genome Tobacco mild green mosaic virus	SEQ ID NO: 52
NC_002692.1 Tomato mosaic virus, complete genome Tomato mosaic virus	SEQ ID NO: 53
NC_003630.1 Pepper mild mottle virus, complete genome Pepper mild mottle virus	SEQ ID NO: 54
NC_004106.1 Paprika mild mottle virus, complete genome Paprika mild mottle virus	SEQ ID NO: 55
NC_009642.1 Bell pepper mottle tobamovirus, complete genome Bell pepper mottle virus	SEQ ID NO: 56
NC_022230.1 Tomato mottle mosaic virus isolate MX5, complete genome Tomato mottle mosaic virus	SEQ ID NO: 57

Virus	Movement protein (MP)
NC_001728.1 Odontoglossum ringspot virus, complete genome Odontoglossum ringspot virus	SEQ ID NO: 58
NC_003852.1 Obuda pepper virus, complete genome Obuda pepper virus	SEQ ID NO: 59
NC_009041.1 Rehmannia mosaic virus, complete genome Rehmannia mosaic virus	SEQ ID NO: 60
NC_010944.1 Brugmansia mild mottle virus, complete genome Brugmansia mild mottle virus	SEQ ID NO: 61
NC_022801.1 Yellow tailflower mild mottle virus isolate Cervantes, complete genome Yellow tailflower mild mottle virus	SEQ ID NO: 62
NC_030229.1 Tropical soda apple mosaic virus isolate Okeechobee, complete genome Tropical soda apple mosaic virus	SEQ ID NO: 63
NC_001801.1 Cucumber green mottle mosaic virus, complete genome Cucumber green mottle mosaic virus	SEQ ID NO: 64
NC_002633.1 Cucumber fruit mottle mosaic virus, complete genome Cucumber fruit mottle mosaic virus	SEQ ID NO: 65
NC_003610.1 Kyuri green mottle mosaic virus, complete genome Kyuri green mottle mosaic virus	SEQ ID NO: 66
NC_003878.1 Zucchini green mottle mosaic virus, complete genome Zucchini green mottle mosaic virus	SEQ ID NO: 67
NC_008614.1 Cucumber mottle virus, complete genome Cucumber mottle virus	SEQ ID NO: 68
watermelon green mottle mosaic virus	SEQ ID NO: 69
NC_001873.1 Turnip vein-clearing virus, complete genome Turnip vein-clearing virus	SEQ ID NO: 70
NC_002792.2 Ribgrass mosaic virus, complete genome Ribgrass mosaic virus	SEQ ID NO: 71
NC_003355.1 Wasabi mottle virus, complete genome Wasabi mottle virus	SEQ ID NO: 72
NC_004422.1 Youcai mosaic virus, complete genome Youcai mosaic virus	SEQ ID NO: 73
NC_008365.1 Streptocarpus flower break virus, complete genome Streptocarpus flower break virus	SEQ ID NO: 74
NC_016442.1 Rattail cactus necrosis associated virus, complete genome Rattail cactus necrosis-associated virus	SEQ ID NO: 75

¹ The descriptors “NC_XXXXXX.1” refer to the National Center for Biotechnology Information database accession number for entries in the world wide web internet database “ncbi[dot]nlm[dot]nih.gov/nuccore.”

Table 4. tRNA-like sequences

Name ¹ of Arabidopsis gene containing tRNA-like sequence that can confer cell-to-cell mobility	Sequence ²
>AT1G59870.1	SEQ ID NO: 76
>AT1G71697.1	SEQ ID NO: 77
>AT1G77885.1	SEQ ID NO: 78
>AT2G04400.1	SEQ ID NO: 79
>AT2G20230.1	SEQ ID NO: 80
>AT2G24790.1	SEQ ID NO: 81
>AT2G32540.1	SEQ ID NO: 82
>AT3G15850.1	SEQ ID NO: 83
>AT3G25770.1	SEQ ID NO: 84
>AT4G15570.1	SEQ ID NO: 85
>AT4G26050.1	SEQ ID NO: 86
>AT4G26050.1	SEQ ID NO: 87
>AT4G27430.2	SEQ ID NO: 88
>AT4G27430.2	SEQ ID NO: 89
>AT5G46330.1	SEQ ID NO: 90
>AT5G54110.1	SEQ ID NO: 91
>AT5G65730.1	SEQ ID NO: 92
>AT3G02020.1	SEQ ID NO: 93
>AT5G63840.1	SEQ ID NO: 94
>AT2G36930.1	SEQ ID NO: 95
>AT5G59950.5	SEQ ID NO: 96
>AT5G20180.1	SEQ ID NO: 97
>AT5G20180.2	SEQ ID NO: 98
>AT1G07940.2	SEQ ID NO: 99
>AT2G14260.2	SEQ ID NO: 100
>AT3G05520.2	SEQ ID NO: 101
>AT4G10840.1	SEQ ID NO: 102
>AT4G10840.2	SEQ ID NO: 103
>AT1G73650.3	SEQ ID NO: 104
>AT2G45990.1	SEQ ID NO: 105
>AT2G45990.3	SEQ ID NO: 106
>AT2G45990.4	SEQ ID NO: 107
>AT3G03160.1	SEQ ID NO: 108
>AT5G64870.1	SEQ ID NO: 109
>AT1G13600.1	SEQ ID NO: 110
>AT1G73177.1	SEQ ID NO: 111
>AT1G07670.1	SEQ ID NO: 112
>AT1G55490.1	SEQ ID NO: 113
>AT1G55490.2	SEQ ID NO: 114

Name ¹ of Arabidopsis gene containing tRNA-like sequence that can confer cell-to-cell mobility	Sequence ²
>AT1G55680.1	SEQ ID NO: 115
>AT2G14120.1	SEQ ID NO: 116
>AT2G14120.2	SEQ ID NO: 117
>AT2G14120.3	SEQ ID NO: 118
>AT2G32730.1	SEQ ID NO: 119
>AT3G10760.1	SEQ ID NO: 120
>AT4G10320.1	SEQ ID NO: 121
>AT4G16990.4	SEQ ID NO: 122
>AT5G59380.1	SEQ ID NO: 123

¹ The descriptors “ATXXXXXXX.X” refer to the Arabidopsis Information Resource (TAIR) database accession number for entries in the world wide web internet database “arabidopsis.org.”

Table 5. IRES sequences

IRES source	NCBI Accession ID ¹	Sequence ²
Cardiovirus A		SEQ ID NO: 124
Tobacco mosaic virus		SEQ ID NO: 125
Hibiscus chlorotic ringspot virus		SEQ ID NO: 126
Zea mays HSP101		SEQ ID NO: 127
Plautia stali intestine virus	AB006531.1	SEQ ID NO: 128
Kashmir bee virus	NC_004807	SEQ ID NO: 129
Solenopsis invicta virus	NC_006559	SEQ ID NO: 130
Triatoma virus	NC_003783	SEQ ID NO: 131
Cricket paralysis virus		SEQ ID NO: 132, SEQ ID NO: 133
Hepacivirus C		SEQ ID NO: 134
Turnip crinkle virus		SEQ ID NO: 135
Turnip vein-clearing virus		SEQ ID NO: 136
Rhopalosiphum padi virus		SEQ ID NO: 137
<i>Homo sapiens</i> C-myc		SEQ ID NO: 138
Israeli acute paralysis virus	NC_009025	SEQ ID NO: 139
Drosophila C virus		SEQ ID NO: 140
Black queen cell virus		SEQ ID NO: 141
Homalodisca coagulata virus 1		SEQ ID NO: 142
Aphid lethal paralysis virus		SEQ ID NO: 143
Himetobi P virus		SEQ ID NO: 144
Mud crab virus		SEQ ID NO: 145
Canine picodistrovirus		SEQ ID NO: 146

¹ The descriptors “NC_XXXXXX.1” refer to the National Center for Biotechnology Information database accession number for entries in the world wide web internet database “ncbi[dot]nlm[dot]nih.gov/nuccore.”

² RNA equivalents of the DNA sequences are also contemplated and can be obtained from the DNA sequences provided.

Table 6. Intron sequences

Intron number	Sequence
1	SEQ ID NO: 147
2	SEQ ID NO: 148
3	SEQ ID NO: 149
4	SEQ ID NO: 150
5	SEQ ID NO: 151
6	SEQ ID NO: 152
7	SEQ ID NO: 153
8	SEQ ID NO: 154
9	SEQ ID NO: 155
10	SEQ ID NO: 156
11	SEQ ID NO: 157
12	SEQ ID NO: 158
13	SEQ ID NO: 159
Potato ST-LS1 intron2	SEQ ID NO: 160

Table 7: Heterologous RNA viruses (HRVs) and Target Viral Pathogens

HRV or Target Viral Pathogen name	NCBI Accession ID ¹	5' RR Sequence ² (SEQ ID NO:)	3' RR Sequence ² (SEQ ID NO:)	RdRP or REPLICASE NT Sequence (SEQ ID NO:)	RdRP or REPLICASE AA Sequence (SEQ ID NO:)
Cucumber mosaic virus	NC_002034.1, NC_002035, NC_001440.1	161	187	-	-
Brome mosaic virus	NC_002026.1, NC_002027.1, NC_002028.2	162	188	-	-
Citrus tristeza virus	NC_001661.1 (SEQ ID NO: 1439)	163	189	-1440	223, 1441
Beet yellows virus	NC_001598	164	190	-	224
Cowpea mosaic virus	NC_003549.1, NC_003550.1	165	-	-	-
Potato virus X	NC_011620	166	191	-	225
Potato virus A	NC_004039	167	192	-	226
Potato virus Y	NC_001616	168	193	-	227

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HRV or Target Viral Pathogen name	NCBI Accession ID¹	5' RR Sequence² (SEQ ID NO:)	3' RR Sequence² (SEQ ID NO:)	RdRP or REPLICASE NT Sequence (SEQ ID NO:)	RdRP or REPLICASE AA Sequence (SEQ ID NO:)
Pepper mottle virus	NC_001517	169	194	-	228
Bean yellow mosaic virus	NC_003492	170	195	-	229
Barley stripe mosaic virus	NC_003469, NC_003481, NC_003478	171	196	-	-
Wheat stripe mosaic virus	NC_040760, NC_040761	172	197	-	230
Rice yellow mottle virus	L20893	173	198	-	231
Maize dwarf mosaic virus	NC_003377	174	199	-	232
Zucchini yellow mosaic virus	NC_003224	175	200	-	233
Watermelon mosaic virus	NC_006262	176	201	-	234
Sugarcane mosaic virus	KY548506	177	202	-	235
Tobacco mosaic virus	NC_001367.1	178	203	212	236
Tomato mosaic virus	NC_002692.1	179	204	213	237
Turnip vein-clearing virus	NC_001873.1	180	205	214	238
Pepper mild mottle virus	NC_003630.1	181	206	215	239
Turnip crinkle virus	NC_003821.3	182	207	216, 217	240, 241
Tomato bushy stunt virus	NC_001554.1	183	208	218, 219	242, 243
Tomato spotted wilt virus	KT160280.1, KT160281.1, KT160282.1	184	209	220	244
Watermelon bud necrosis virus	NC_038288.1, NC_038289.1, NC_038290.1	185	210	221	245
Turnip yellow mosaic virus	NC_004063.1	186	211	222	246
Spinach latent virus	NC_003808 (SEQ ID NO: 1394)	1403	1412	1430	1421
Spinach latent virus	NC_003809 (SEQ ID NO: 1395)	1404	1413	1431	1422
Olive latent virus 2 RNA 2	NC_003674 (SEQ ID NO: 1396)	1405	1414	1432	1423
Citrus yellow vein clearing virus isolate CQ	NC_026592.1 (SEQ ID NO: 1397)	1406	1415	1433	1424

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HRV or Target Viral Pathogen name	NCBI Accession ID¹	5' RR Sequence² (SEQ ID NO:)	3' RR Sequence² (SEQ ID NO:)	RdRP or REPLICASE NT Sequence (SEQ ID NO:)	RdRP or REPLICASE AA Sequence (SEQ ID NO:)
Potato latent virus, complete genome	NC_011525 (SEQ ID NO: 1398)	1407	1416	1434	1425
Apple stem grooving virus	NC_001749.2 (SEQ ID NO: 1399)	1408	1417	1435	1426
Citrus leaf blotch virus, complete genome	NC_003877.1 (SEQ ID NO: 1400)	1409	1418	1436	1427
Apple latent spherical virus segment 1	NC_003787.1 (SEQ ID NO: 1401)	1410	1419	1437	1428
Soybean latent spherical virus isolate ND1	NC_032270 (SEQ ID NO: 1402)	1411	1420	1438	1429
Tomato brown rugose fruit virus (ToBRFV)	SEQ ID NO: 1499	1507	1511	1515	1523
Celery latent virus	NC_055507.1 SEQ ID NO: 1500	1508	1512	1516	1524
Black grass varicosavirus-like virus	NC_026801.1 SEQ ID NO: 1501	1509	1513	1517	1525
Maize suscal virus	MZ270532.1 SEQ ID NO: 1502	1510	1514	1518	1526
Horseradish latent virus (DNA Virus)	NC_018858.1 SEQ ID NO: 1503			1519	1527
Bean latent virus (DNA Virus)	NC_055589.1 SEQ ID NO: 1504			1520	1528
Rice latent virus 1 (DNA Virus)	NC_075432.1 SEQ ID NO: 1505			1521	1529
Rice latent virus 2 (DNA Virus)	NC_040537.1 SEQ ID NO: 1506			1522	1530

¹ The descriptors "NC_XXXXXX.1" refer to the National Center for Biotechnology Information database accession number for entries in the world wide web internet database

"ncbi[dot]nlm[dot]nih.gov/nuccore."

² RNA equivalents of the DNA sequences are also contemplated and can be obtained from the DNA sequences provided.

Table 8.

Antiviral Cargo Molecules

Gene	NCBI or TAIR ¹ Accession ID	NT Sequence (SEQ ID NO)	AA Sequence (SEQ ID NO)	Target	Examples of Target Crops
Ty-1	XM_010323869.3	247		Tomato yellow leaf curl virus	
HRT	AT5G43470	248		Turnip crinkle virus	
RCY1	AT2G26430 AK317155	249, 1442	1451	Cucumber mosaic virus	Various (broad spectrum)
BcTuR3	AB498796	250		Turnip mosaic virus	
Pvr4	KT359375.1	251		Potato virus Y, Pepper mottle virus	
RTM1	NM_001331575.1	252		Tobacco etch virus	
Sw5b	KY006959.1	253	1452	Tomato spotted wilt virus	Various (broad spectrum)
N	U15605.1	254		Tobacco mosaic virus, Tomato brown rugose fruit virus	
Tm-2-2	AF536201.1	255, 1443	1453	Tomato mosaic virus	Tomato
L4	AB523377	256		Tobacco mosaic virus, Tomato mosaic virus, Tomato brown rugose fruit virus, Tobacco mild green mosaic virus, Bell pepper mottle virus, Pepper mild mottle virus	
Rx	AJ011801.1	257	1454	Potato virus X	Potato
JAX1	AT1G58160	258		Broad spectrum Potexvirus	
Nucleotides 3411 to 4388 of PMMoV genomic sequence	M81413	259		Pepper mild mottle virus	
TMV coat protein (CP)	NP_597750.1	1445	1455	Plant pathogenic viruses	Tomato
SMV coat protein (CP)	AB100443	1446	1456	Plant pathogenic viruses	Soybean

Gene	NCBI or TAIR ¹ Accession ID	NT Sequence (SEQ ID NO)	AA Sequence (SEQ ID NO)	Target	Examples of Target Crops
CMV coat protein (CP)	AF350450	1447	1457	Plant pathogenic viruses	Black pepper
PVX coat protein (CP)	X12804	1448	1458	Plant pathogenic viruses	Potato
TSWV nucleocapsid protein (NP)	NC_002051.1	1449	1459	Plant pathogenic viruses	Tobacco
Rsv4	LC325439.1	1450	1460	Soybean mosaic virus	Soybean

¹ The descriptors “ATXGXXXXX” refer to the Arabidopsis Information Resource (TAIR) database accession number for entries in the world wide web internet database “arabidopsis.org.” The other descriptors refer to the National Center for Biotechnology Information database accession number for entries in the world wide web internet database “ncbi[dot]nlm[dot]nih.gov/nuccore.”

Table 9

Insecticidal or Insect Inhibitory Cargo and Nematocidal or Nematode Inhibitory Molecules

Gene name	NCBI Accession ID	NT Sequence (SEQ ID NO)	AA Sequence (SEQ ID NO)	Cargo type	Target	Examples of Target Crop
Vip3Aa	HM132043.2	260		Protein	Insect (lepidopteran)	
Vip3	KF499114.1	261		Protein	Insect (lepidopteran)	
Vip1	KF499112.1	262		Protein	Insect (coleoptera, Hemiptera)	
Vip2	KF499113.1	263		Protein	Insect (coleoptera, Hemiptera)	
Sip1A	DQ350881.1	264		Protein	Insect (colcoptera)	
<i>Spodoptera exigua</i> integrin beta 1 subunit	HQ829425.1	265		dsRNA	Insect (Beet armyworm)	
Pheromone biosynthesis activating neuropeptide	U08109.1	266		dsRNA	Insect (Corn earworm)	
Cry 1A	HM132043.2	267		Protein	Insect (lepidopteran, diptera)	
Cry 1Ab	KR612322.1	268		Protein	Gastropoda	

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Gene name	NCBI Accession ID	NT Sequence (SEQ ID NO)	AA Sequence (SEQ ID NO)	Cargo type	Target	Examples of Target Crop
Cry1B	EF102874.1	269		Protein	Insect (lepidopteran, diptera, coleoptera)	
Cry1C	EU679502.1	270		Protein	Insect (lepidopteran, diptera)	
Cry1D	JN205068.1	271		Protein	Insect (lepidopteran)	
Cry1Ea	ON508055.1	272		Protein	Insect (lepidopteran)	
Cry1F	EU679501.1	273		Protein	Insect (lepidopteran)	
Cry1I	AF211190.1	274		Protein	Insect (lepidopteran, coleoptera)	
Cry1K	U28801.1	275		Protein	Insect (lepidopteran)	
Cry2A	KJ710647.1	276		Protein	Insect (lepidopteran, diptera, Hemiptera)	
Cry3A	EU332160.1	277		Protein	Insect (coleoptera, Hemiptera, Hymenoptera)	
Cry4A	EF208904.1	278		Protein	Insect (diptera)	
Cry4B	MN539646.1	279		Protein	Insect (diptera)	
Cry5A	EF219060.1	280		Protein	Insect, Rhabditida (Hymenoptera)	
Cry5B	EU822809.1	281	1468	Protein	Rhabditida, Root Knot Nematode	Tomato, potato, peppers, eggplants, cotton
Cry8B	FJ770571.1	282		Protein	Insect (coleoptera)	
Cry8D	AB303980.1	283		Protein	Insect (lepidopteran, coleoptera)	
Cry8F	KC778983.1	284		Protein	Insect (coleoptera)	
Cry8G	FJ198072.1	285		Protein	Insect (coleoptera)	
Cry9A	KX094977.1	286		Protein	Insect (lepidopteran)	

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Gene name	NCBI Accession ID	NT Sequence (SEQ ID NO)	AA Sequence (SEQ ID NO)	Cargo type	Target	Examples of Target Crop
Cry 10	MN539645.1	287		Protein	Insect (diptera)	
Cry 11Aa	MK184471.1	288		Protein	Insect (diptera, Hemiptera)	
Cry 11B	HQ845255.1	289		Protein	Insect (diptera)	
Cry 19A	Y07603.1	290		Protein	Insect (diptera)	
Cry 19B	D88381.1	291		Protein	Insect (diptera)	
Cry21A	KC898940.2	292		Protein	Rhabditida	
Cry22A	EU715020.1	293		Protein	Insect (lepidopteran, coleoptera, Hymenoptere)	
Cry32A	GU063850.1	294		Protein	Insect (lepidopteran)	
Cry35A	AY536895.1	295		Protein	Insect (coleoptera)	
Cry35B	AY536894.1	296		Protein	Insect (coleoptera)	
Cry39A	AB074413.2	297		Protein	Insect (diptera)	
Cry51A	MT882335.1	298		Protein	Insect (lepidopteran)	
Cyt1A	EF656359.1	299		Protein	Insect (diptera, coleoptera)	
Cyt2Ba	MK690503.1	300		Protein	Insect (diptera)	
snf7	XM_028287710.2	301		dsRNA	Insect (Western corn rootworm)	
snf7	XM_023156793.1	302		dsRNA	Insect (Colorado potato beetle)	
Actin	XM_023168674.1	303		dsRNA	Insect (Colorado potato beetle)	
vATPaseI	XM_023156515.1	304		dsRNA	Insect (Colorado potato beetle)	
Tyrosine hydroxylase	NM_001305520.1	305		dsRNA	Insect (Diamondback moth)	
C002	XM_015524104.1	306		dsRNA	Insect (Russian wheat aphid)	
hunchback	NM_001162510.1	307		dsRNA	Insect (Pea Aphid)	

Gene name	NCBI Accession ID	NT Sequence (SEQ ID NO)	AA Sequence (SEQ ID NO)	Cargo type	Target	Examples of Target Crop
Mi-1.2	AF039682.1	1461	1469	Protein	Root knot nematode	Tomato, potato, peppers, eggplants, cotton
Gpa-2	AF195939.1	1462	1470	Protein	Cyst nematode	Tomato, potato, peppers, eggplants, cotton
Rhg1	NM_001248836.2	1463	1471	Protein	Cyst nematode	Soybean, potato, corn
Rhg4	NM_001249781.3	1464	1472	Protein	Cyst nematode	Soybean, potato, corn
Zea mays cystatin 2	NM_001112543.1	1465	1473	Protein	Root knot/burrowing/spiral nematodes	Banana, soybean, tomato, potato, cotton, eggplants
<i>Colocasia esculenta</i> cysteine proteinase inhibitor (CeCPI)	AF525880.1	1466	1474	Protein	Root knot nematode, plant fungal pathogens	Tomato, potato, peppers, eggplants, cotton
Cry6A (plant-codon optimized)		1467	1475	Protein	Root knot nematode	Tomato, potato, peppers, eggplants, cotton

¹ The descriptors refer to the National Center for Biotechnology Information database accession number for entries in the world wide web internet database “ncbi[dot]nlm[dot]nih.gov/nuccore.”

Table 10

Antifungal Cargo RNAi Targets

Cargo	NCBI Accession ID ¹	Sequence	Target pathogen	Examples of target crop
Bc_Chitin synthase 1	AY515145	SEQ ID NO: 308	<i>Botrytis cinerea</i>	bell pepper, tomato
Bc_Chitin synthase 3a	AF494188	SEQ ID NO: 309	<i>Botrytis cinerea</i>	bell pepper, tomato
Bc_Chitin synthase 3b	AF529208.1	SEQ ID NO: 310	<i>Botrytis cinerea</i>	bell pepper, tomato
Bc_Chitin synthase 6	AY515144	SEQ ID NO: 311	<i>Botrytis cinerea</i>	bell pepper, tomato

Cargo	NCBI Accession ID ¹	Sequence	Target pathogen	Examples of target crop
Bc_DCL1	XM_024696562.1	SEQ ID NO: 312	<i>Botrytis cinerea</i>	bell pepper, tomato
Bc_DCL2	XM_037334035.1	SEQ ID NO: 313	<i>Botrytis cinerea</i>	bell pepper, tomato
Bc_ERG1	XM_001547426.2	SEQ ID NO: 314	<i>Botrytis cinerea</i>	bell pepper, tomato
Bc_ERG11	MT430876.1	SEQ ID NO: 315	<i>Botrytis cinerea</i>	bell pepper, tomato
Bc_ERG13	XM_001552372.2	SEQ ID NO: 316	<i>Botrytis cinerea</i>	bell pepper, tomato
Bc_EF2	XM_024693463	SEQ ID NO: 317	<i>Botrytis cinerea</i>	bell pepper, tomato
Fgr_chs3b	AF484941.1	SEQ ID NO: 318	<i>Fusarium</i>	wheat, soybean, corn
Fgr_chs6	XM_011319518.1	SEQ ID NO: 319	<i>Fusarium</i>	wheat, soybean, corn
Fgr_gls	XM_011329487.1	SEQ ID NO: 320	<i>Fusarium</i>	wheat, soybean, corn
Fgr_Pkc	XM_011329746.1	SEQ ID NO: 321	<i>Fusarium</i>	wheat, soybean, corn
FO_chs5	AF484941.1	SEQ ID NO: 322	<i>Fusarium oxysporum</i>	tomato, tobacco, cucurbits, banana
FO_W2	AB266616.1	SEQ ID NO: 323	<i>Fusarium oxysporum</i>	tomato, tobacco, cucurbits, banana
FO_FRP1	AY673970.1	SEQ ID NO: 324	<i>Fusarium oxysporum</i>	tomato, tobacco, cucurbits, banana
FO_OPR	AFQF01002613	SEQ ID NO: 325	<i>Fusarium oxysporum</i>	tomato, tobacco, cucurbits, banana
Mo_chs1	MGG_01802.6	SEQ ID NO: 326	<i>Magnaporthe</i> +C19	rice, wheat, maize
Mo_chs6	MGG_13013.6	SEQ ID NO: 327	<i>Magnaporthe</i>	rice, wheat, maize
Mo_chs7	MGG_06064.6	SEQ ID NO: 328	<i>Magnaporthe</i>	rice, wheat, maize
Sorbitol dehydrogenase (SDH)	NW_003303753.1	SEQ ID NO: 329	<i>Phytophthora infestans</i>	potato
AGO1	XM_011321673.1	SEQ ID NO: 330	<i>Fusarium graminearum</i>	wheat, soybean, corn
AGO2	XM_011317703.1	SEQ ID NO: 331	<i>Fusarium graminearum</i>	wheat, soybean, corn
FgQIP	XM_011328057.1	SEQ ID NO: 332	<i>Fusarium graminearum</i>	wheat, soybean, corn
FG_DCL1	XM_011330473.1	SEQ ID NO: 333	<i>Fusarium graminearum</i>	wheat, soybean, corn
FG_DCL2	XM_011322896.1	SEQ ID NO: 334	<i>Fusarium graminearum</i>	wheat, soybean, corn
VD_DCL1	MK015620.1	SEQ ID NO: 335	<i>Verticillium dahliae</i>	potato, peppermint, eggplant, tomato
VD_DCL2	MK015621.1	SEQ ID NO: 336	<i>Verticillium dahliae</i>	potato, peppermint, eggplant, tomato
Suppressor of actin (SAC1)	XM_028639311.1	SEQ ID NO: 337	<i>Verticillium dahliae</i>	potato, peppermint, eggplant, tomato

Cargo	NCBI Accession ID¹	Sequence	Target pathogen	Examples of target crop
Dynactin (DCTN1)	KAH6702269.1	SEQ ID NO: 338	<i>Verticillium dahliae</i> , <i>Rhizoctonia solani</i>	potato, peppermint, eggplant, tomato
Polygalacturonase (PG)	XM_043324583.1	SEQ ID NO: 339	<i>Rhizoctonia solani</i>	tomato, wheat, soybean, potato
Bc_vacuolar protein sorting 51 (VPS51)	XM_024698195.1	SEQ ID NO: 340	<i>Botrytis cinerea</i>	bell pepper, tomato
Bc_dynactin (DCTN1)	XM_001550899.2	SEQ ID NO: 341	<i>Botrytis cinerea</i>	bell pepper, tomato
Bc_suppressor of actin (SAC1)	XM_024697060.1	SEQ ID NO: 342	<i>Botrytis cinerea</i>	bell pepper, tomato
Ss_DCL1	XM_001585129.1	SEQ ID NO: 343	<i>S. sclerotiorum</i>	soybean, pea, canola
Ss_DCL2	XM_001588771.1	SEQ ID NO: 344	<i>S. sclerotiorum</i>	soybean, pea, canola
Ss_vacuolar protein sorting 51 (VPS51)	XM_001590214.1	SEQ ID NO: 345	<i>S. sclerotiorum</i>	soybean, pea, canola
Ss_dynactin (DCTN1)	XM_001594287.1	SEQ ID NO: 346	<i>S. sclerotiorum</i>	soybean, pea, canola
Ss_suppressor of actin (SAC1)	CP017829.1	SEQ ID NO: 347	<i>S. sclerotiorum</i>	soybean, pea, canola
Fmk1 (FOXG_08140)	XM_018386908.1	SEQ ID NO: 348	<i>Fusarium oxysporum</i>	tomato, tobacco, cucurbits, banana
Hog1 (FOXG_06318)	XM_018384930.1	SEQ ID NO: 349	<i>Fusarium oxysporum</i>	tomato, tobacco, cucurbits, banana
PBS2 (FOXG_03107)	XM_018380643.1	SEQ ID NO: 350	<i>Fusarium oxysporum</i>	tomato, tobacco, cucurbits, banana
Cfa6-HrpL		SEQ ID NO: 1476	<i>Pseudomonas syringae</i>	tomato, bean

¹ The descriptors refer to the National Center for Biotechnology Information database accession number for entries in the world wide web internet database “ncbi[dot]nlm[dot]nih.gov/nuccore.”

Table 11.

Antifungal and Antibacterial cargo protein

Cargo (RNAi target gene)	NCBI Accession ID¹	NT Sequence (SEQ ID NO)	AA Sequence (SEQ ID NO)	Target pathogen	Examples of target crop
Antifungal symbiotic peptide NCR044	6U6G_A	SEQ ID NO: 351	SEQ ID NO: 361	<i>Botrytis cinerea</i> , <i>Fusarium spp.</i>	tomato, tobacco, bell pepper
Buckwheat Antifungal Protein, Fa-AMP1	P0DKH7	SEQ ID NO: 352	SEQ ID NO: 362	<i>Fusarium oxysporum</i>	tomato, tobacco, cucurbits, banana
Buckwheat Antifungal Protein, Fa-AMP2	P0DKH8	SEQ ID NO: 353	SEQ ID NO: 363	<i>Fusarium oxysporum</i>	tomato, tobacco, cucurbits, banana

Cargo (RNAi target gene)	NCBI Accession ID ¹	NT Sequence (SEQ ID NO)	AA Sequence (SEQ ID NO)	Target pathogen	Examples of target crop
Pepper Antimicrobial Protein CaAMP1	AAT35532.1	SEQ ID NO: 354	SEQ ID NO: 364	<i>Fusarium oxysporum</i> , <i>Alternaria brassicicola</i> , <i>Phytophthora</i> spp.	tomato, rice, bell pepper, soybean
Bean CH5B chitinase protein	P36361.1	SEQ ID NO: 355	SEQ ID NO: 365	<i>Alternaria</i> spp., <i>Rhizoctonia solani</i>	soybean, rice, tomato, bell pepper
Rice RC7 chitinase	Q7DNA1.1	SEQ ID NO: 356	SEQ ID NO: 366	<i>Rhizoctonia solani</i>	rice, bell pepper, tomato, soybean
Tomato chitinase pcht28	Q40114.1	SEQ ID NO: 357	SEQ ID NO: 367	<i>Verticillium dahliae</i>	strawberry
Barley chitinase II	M62904.1	SEQ ID NO: 358	-	<i>Fusarium graminearum</i>	wheat, soybean, corn
Rice chitinase RCH10	P25765.2	SEQ ID NO: 359	SEQ ID NO: 368	<i>Rhizoctonia solani</i> , <i>Magnaporthe oryzae</i>	rice
Arabidopsis Thionin 2.4	NP_179105.1	-	SEQ ID NO: 369	<i>Fusarium graminearum</i> , <i>F. sporotrichoides</i>	wheat, corn
<i>Brassica juncea</i> BjCHI1 chitinase	AY714982.1	SEQ ID NO: 360	-	<i>Rhizoctonia solani</i>	potato
Mungin protein from mung bean	-	-	SEQ ID NO: 370	<i>R. solani</i> , <i>Coprinus comatus</i> , <i>Mycosphaerella arachidicola</i> , <i>B. cinerea</i> , <i>F. oxysporum</i>	tomato, bell pepper, potato, tomato, soybean
Camptothecin from Camptotheca	UUY85546.1	-	SEQ ID NO: 371	<i>Magnaporthe oryzae</i>	rice
NaD1 defensin from <i>Nicotiana glauca</i>	Q8GTM0.1	-	SEQ ID NO: 372	<i>Fusarium oxysporum</i> f.sp. <i>vasinfectum</i> , <i>Botrytis cinerea</i>	cotton, tomato, bell pepper
Tk-AMP-X1 from wheat	CCP19154.1	-	SEQ ID NO: 373	<i>Fusarium graminearum</i>	wheat, corn
CBP from spindle tree	AAP35269.1	-	SEQ ID NO: 374	<i>Alternaria brassicicola</i> MUCL 20297	brassica crops
Chitinase from spindle tree	AAP35270.1	-	SEQ ID NO: 375	<i>Alternaria brassicicola</i> MUCL 20297	brassica crops
Antimicrobial peptide 1, ToAMP1 from wigg flower	B3EWQ1.1	-	SEQ ID NO: 376	<i>Fusarium oxysporum</i> TSKHA-4	banana, tomato, cucurbits

Cargo (RNAi target gene)	NCBI Accession ID ¹	NT Sequence (SEQ ID NO)	AA Sequence (SEQ ID NO)	Target pathogen	Examples of target crop
Antimicrobial peptide 2, ToAMP2	B3EWQ2.1	-	SEQ ID NO: 377	<i>Fusarium oxysporum</i> TSKHA-4	banana, tomato, cucurbits
Antimicrobial peptide 3, ToAMP3	B3EWQ3.1	-	SEQ ID NO: 378	<i>Fusarium oxysporum</i> TSKHA-4	banana, tomato, cucurbits
Defensin Tk-AMP-D1	P84963.1	-	SEQ ID NO: 379	<i>Alternaria consortialis</i>	brassica crops
Defensin Ec-AMP-D2	P86519.1	-	SEQ ID NO: 380	<i>Fusarium oxysporum</i>	banana, tomato, cucurbits
Defensin Ec-AMP-D1	P86518.1	-	SEQ ID NO: 381	<i>Fusarium graminearum</i>	wheat, corn
Antimicrobial peptide Ar-AMP	AAB22102.1	-	SEQ ID NO: 382	<i>Bipolaris sorokiniana</i>	wheat
AtCDR1	NM_122858.3	1477	1489	<i>P. syringae</i> , <i>Liberibacter</i> sp.	Citrus, tomato
PtCDR2	Consensus sequence	1478		<i>P. syringae</i> , <i>Liberibacter</i> sp.	Citrus, tomato
PtCDR8	Consensus sequence	1479		<i>P. syringae</i> , <i>Liberibacter</i> sp.	Citrus, tomato
cecropin B	NM_001102561.1	1480	1490	<i>P. syringae</i> , <i>Liberibacter</i> sp., plant fungal pathogens	Citrus, tomato, grapevines
BP100		1481	1491	<i>P. syringae</i> , <i>Liberibacter</i> sp.	Citrus, tomato, grapevines
CA-3.1		1482	1492	<i>P. syringae</i> , <i>Liberibacter</i> sp.	Citrus, tomato, grapevines
<i>Medicago truncatula</i> defensin (Def1)	AY313166.1	1483	1493	<i>P. syringae</i> , <i>Liberibacter</i> sp., plant fungal pathogens	Citrus, tomato, grapevines
RsAFP2	KF498667.1	1484	1494	plant fungal pathogens	Citrus, tomato, grapevines
<i>Arabidopsis thaliana</i> defensin 1.1 (PDF1.1)	NM_106233.4	1485	1495	plant fungal and/or bacterial pathogens	Grapevines, tomato
JLA-9		1486	1496	<i>P. syringae</i> , <i>Liberibacter</i> sp.	Grapevines, tomato, potato, citrus
Darobactin		1487	1497	<i>P. syringae</i> , <i>Liberibacter</i> sp.	Grapevines, tomato, potato, citrus
Urechistachykinin II	NM_122858.3	1488	1498	<i>P. syringae</i> , <i>Liberibacter</i> sp.	Grapevines, tomato, potato, citrus

¹ The descriptors refer to the National Center for Biotechnology Information database accession number for entries in the world wide web internet database “ncbi[dot]nlm[dot]nih.gov/nuccore.”

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Table 12.

Resistance Gene

Gene name	Source species	Effector Target	NCBI or TAIR Accession ID ¹	NT Sequence	AA Sequence	Target
Bph1/9	<i>Oryza sativa</i>	-	KX681919.1	SEQ ID NO: 383	-	<i>Nilaparvata lugens</i>
Bph14	<i>Oryza sativa</i>	-	FJ941067.1	SEQ ID NO: 384	-	<i>Nilaparvata lugens</i>
TAO1	<i>Arabidopsis thaliana</i>	AvrB	NM_001344554	SEQ ID NO: 385	-	<i>Pseudomonas syringae</i>
CAR1	<i>Arabidopsis thaliana</i>	AvrE, HopAA	AT1G50180	SEQ ID NO: 386	-	<i>Pseudomonas syringae</i>
RPS5	<i>Arabidopsis thaliana</i>	AvrPphB	AT1G12220	SEQ ID NO: 387	-	<i>Pseudomonas syringae</i>
RPS2	<i>Arabidopsis thaliana</i>	AvrRpm1, AvrRpt2	AT3G03600	SEQ ID NO: 388	-	<i>Pseudomonas syringae</i>
ZAR1	<i>Arabidopsis thaliana</i>	HopO, HopX, HopBA1, HopZ1a, HopF2a, AvrAc	AT3G50950	SEQ ID NO: 389	-	<i>Pseudomonas syringae</i> , <i>Xanthomonas campestris</i>
RPS6	<i>Arabidopsis thaliana</i>	HopA1	AT4G31700	SEQ ID NO: 390	-	<i>Pseudomonas syringae</i>
SUMM2	<i>Arabidopsis thaliana</i>	HopA1	AT1G12280	SEQ ID NO: 391	-	<i>Pseudomonas syringae</i>
BAR1	<i>Arabidopsis thaliana</i>	HopB	AT5G18360	SEQ ID NO: 392	-	<i>Pseudomonas syringae</i>
CaPtr1	<i>Capsicum annuum</i>	AvrRpt2, RipBN	-	-	-	<i>Pseudomonas syringae</i> , <i>Ralstonia pseudosolanacearum</i>
Bs2	<i>Capsicum chacoense</i>	AvrBs2	AF202179.1	SEQ ID NO: 393	-	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i>
Rpg1b	<i>Glycine max</i>	AvrB	NM_001353616.2	SEQ ID NO: 394	-	<i>Pseudomonas savastanoi</i>
Rpg1r	<i>Glycine max</i>	AvrRpm1	KF958751	SEQ ID NO: 395	-	<i>Pseudomonas syringae</i>
Pbr1.b	<i>Hordeum vulgare</i>	AvrPphB	MH595618	SEQ ID NO: 396	-	<i>Pseudomonas savastanoi</i>
Pbr1.c	<i>Hordeum vulgare</i>	AvrPphB	MH595619	SEQ ID NO: 397	-	<i>Pseudomonas savastanoi</i>
FB_MR5	<i>Malus x robusta</i>	AvrRpt2_E A	CCH50986.1	-	SEQ ID NO: 407	<i>Erwinia amylovora</i>
NbPtr1	<i>Nicotiana benthamiana</i>	AvrRpt2, RipBN	-	-	-	<i>Pseudomonas syringae</i> , <i>Ralstonia pseudosolanacearum</i>

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Gene name	Source species	Effector Target	NCBI or TAIR Accession ID ¹	NT Sequence	AA Sequence	Target
Roq1	<i>Nicotiana benthamiana</i>	HopQ1-1, XopQ, RipB	MF773579.1	SEQ ID NO: 398	-	<i>Pseudomonas syringae</i> , <i>Xanthomonas</i> , <i>Ralstonia solanacearum</i>
NbZAR1	<i>Nicotiana benthamiana</i>	XopJ4	MH532570.1	SEQ ID NO: 399	-	<i>Xanthomonas perforans</i>
Rpa1	<i>Nicotiana tabacum</i>	AvrRpm1_Psy, AvrRpm1_Psa	-	-	-	<i>Pseudomonas syringae</i>
NitabPtr1	<i>Nicotiana tabacum</i>	AvrRpt2, RipBN	-	-	-	<i>Pseudomonas syringae</i> , <i>Ralstonia pseudosolanacearum</i>
NtomPtr1	<i>Nicotiana tomentosiformis</i>	AvrRpt2, RipBN	-	-	-	<i>Pseudomonas syringae</i> , <i>Ralstonia pseudosolanacearum</i>
Xo1	<i>Oryza sativa</i>	pthXo1, tal2g, tal8, tal2, tal1c, tal5, talC, AvrXa10, AvrXa7	MT395901.1	SEQ ID NO: 400	-	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> , <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i>
Xa1	<i>Oryza sativa</i>	pthXo1, Tal9d, Tal4	-	-	-	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i>
Ptr1	<i>Solanum lycopersicum</i>	AvrRpt2, RipBN	-	-	-	<i>Pseudomonas syringae</i> , <i>Ralstonia pseudosolanacearum</i>
Bs4	<i>Solanum lycopersicum</i>	AvrBs4, Hax3, Hax4, AvrBs3	NM_001329525.1	SEQ ID NO: 401	-	<i>Xanthomonas</i>
Prf	<i>Solanum lycopersicum</i>	AvrPto, AvrPtoB	-	-	-	<i>Pseudomonas syringae</i>
StrPtr1	<i>Solanum tuberosum</i>	AvrRpt2, RipBN	-	-	-	<i>Pseudomonas syringae</i> , <i>Ralstonia pseudosolanacearum</i>
Rxo1	<i>Zea mays</i>	AvrRxo1-ORF1	AY935244.1	SEQ ID NO: 402	-	<i>Xanthomonas oryzae</i> , <i>Burkholderia andropogonis</i>

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Gene name	Source species	Effector Target	NCBI or TAIR Accession ID ¹	NT Sequence	AA Sequence	Target
RRS1-S	<i>Arabidopsis thaliana</i>	AvrRps4	-	-	-	<i>Pseudomonas syringae</i> , <i>Ralstonia solanacearum</i> , <i>Colletotrichum higginsianum</i>
RPS4	<i>Arabidopsis thaliana</i>	AvrRps4, PopP2	-	-	-	<i>Pseudomonas syringae</i> , <i>Ralstonia solanacearum</i> , <i>Colletotrichum higginsianum</i>
RRS1-R	<i>Arabidopsis thaliana</i>	AvrRps4, PopP2	-	-	-	<i>Pseudomonas syringae</i> , <i>Ralstonia solanacearum</i> , <i>Colletotrichum higginsianum</i>
RRS1B	<i>Arabidopsis thaliana</i>	PopP2	-	-	-	<i>Pseudomonas syringae</i> , <i>Ralstonia solanacearum</i> , <i>Colletotrichum higginsianum</i>
RPS4B	<i>Arabidopsis thaliana</i>	PopP2	-	-	-	<i>Pseudomonas syringae</i> , <i>Ralstonia solanacearum</i> , <i>Colletotrichum higginsianum</i>
LOV1	<i>Arabidopsis thaliana</i>	Victorin	-	-	-	<i>Cochliobolus victoriae</i>
WRR4A	<i>Arabidopsis thaliana</i>	CCG28, CCG30, CCG33, CCG40, CCG67, CCG71, CCG79, CCG104	-	-	-	<i>Albugo candida</i> (Ac2V)
WRR4B	<i>Arabidopsis thaliana</i>	CCG45, CCG57, CCG61, CCG70	-	-	-	<i>Albugo candida</i> (Ac2V)
Fom-2	<i>Cucumis melo</i>	AvrFom2	-	-	-	<i>Fusarium oxysporum</i> f. sp. <i>melonis</i>
MLA1	<i>Hordeum vulgare</i>	AVRal	-	-	-	<i>Blumeria graminis</i> f. sp. <i>hordei</i>

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Gene name	Source species	Effector Target	NCBI or TAIR Accession ID ¹	NT Sequence	AA Sequence	Target
MLA10	<i>Hordeum vulgare</i>	AVRa10	-	-	-	<i>Blumeria graminis</i> f. sp. <i>hordei</i>
MLA13	<i>Hordeum vulgare</i>	AVRa13	-	-	-	<i>Blumeria graminis</i> f. sp. <i>hordei</i>
MLA22	<i>Hordeum vulgare</i>	AVRa22	-	-	-	<i>Blumeria graminis</i> f. sp. <i>hordei</i>
MLA7	<i>Hordeum vulgare</i>	AVRa7	-	-	-	<i>Blumeria graminis</i> f. sp. <i>hordei</i>
MLA9	<i>Hordeum vulgare</i>	AVRa9	-	-	-	<i>Blumeria graminis</i> f. sp. <i>hordei</i>
L2	<i>Linum usitatissimum</i>	AvrL2-A	-	-	-	<i>Melampsora lini</i>
L6	<i>Linum usitatissimum</i>	AvrL567-A, AvrL567-B, AvrL567-D, AvrL567-E, AvrL567-F, AvrL567-J, AvrL567-L	-	-	-	<i>Melampsora lini</i>
L7	<i>Linum usitatissimum</i>	AvrL567-A, AvrL567-B, AvrL567-D, AvrL567-E, AvrL567-F, AvrL567-J, AvrL567-L	-	-	-	<i>Melampsora lini</i>
L5	<i>Linum usitatissimum</i>	AvrL567-A, AvrL567-B, AvrL567-E, AvrL567-F, AvrL567-J, AvrL567-L	-	-	-	<i>Melampsora lini</i>
M	<i>Linum usitatissimum</i>	AvrM:ABB 96264;1632 6930	-	-	-	<i>Melampsora lini</i>
P	<i>Linum usitatissimum</i>	AvrP:ACD4 9721;19633 228	-	-	-	<i>Melampsora lini</i>
P2	<i>Linum usitatissimum</i>	AvrP123:A BB96267;16 326930	-	-	-	<i>Melampsora lini</i>
Pi54	<i>Oryza sativa</i>	Avr-Pi54	KM043887.1	SEQ ID NO: 403	-	<i>Magnaporthe oryzae</i>
Pi9	<i>Oryza sativa</i>	AvrPi9	MZ327710.1	SEQ ID NO: 404	-	<i>Magnaporthe oryzae</i>

Gene name	Source species	Effector Target	NCBI or TAIR Accession ID ¹	NT Sequence	AA Sequence	Target
Pia-2	<i>Oryza sativa</i>	Avr-Pia. Avr1-CO39	-	-	-	<i>Magnaporthe oryzae</i>
Pib	<i>Oryza sativa</i>	AvrPiB	AB013449.2	SEQ ID NO: 405	-	<i>Magnaporthe oryzae</i>
Pi5-1	<i>Oryza sativa</i>	AvrPii	EU869185.1	SEQ ID NO: 406	-	<i>Magnaporthe oryzae</i>

¹ The descriptors “ATXGXXXXX” refer to the Arabidopsis Information Resource (TAIR) database accession number for entries in the world wide web internet database “arabidopsis.org.” The other descriptors refer to the National Center for Biotechnology Information database accession number for entries in the world wide web internet database “ncbi[dot]nlm[dot]nih.gov/nuccore.”

Table 13

Bioactive Plant peptides

Peptide name	Sequence	Function
miPEP172c	SEQ ID NO: 408	Increase nodulation in soybean (improved nitrogen fixation, improved yield)
miPEP171d	SEQ ID NO: 409	Increase adventitious root formation in grapevine
BomiPEP397a	SEQ ID NO: 410	Increase foliar surface (36%) and root development in cabbage
AtmiPEP397a	SEQ ID NO: 411	Increase root development in <i>Arabidopsis</i>
BvmiPEP164b	SEQ ID NO: 412	Growth inhibition of <i>Barbarea vulgaris</i> (a weed)
AtmiPEP164b	SEQ ID NO: 413	Root growth inhibition in <i>Arabidopsis</i>

Table 14

Ribozymes

Ribozyme	NCBI Accession ID	Rfam ID	Sequence ¹
Twister	KV767472.1 (20283-20218)	RF03160	SEQ ID NO: 414
Twister	CM001069.2 (36212529-36212469)	RF03160	SEQ ID NO: 415
Twister	-	RF03160; URS0000D6C74A_4558 (1-52)	SEQ ID NO: 416
Twister	-	RF03160; URS0000D69167_4558 (1-52)	SEQ ID NO: 417
Twister	-	RF03160; URS0000D66A77_4558 (1-52)	SEQ ID NO: 418
Twister	AP014967.1 (27291338-27291417)	RF03160	SEQ ID NO: 419
Hammerhead	-	-	SEQ ID NO: 420

Ribozyme	NCBI Accession ID	Rfam ID	Sequence ¹
Hammerhead targeting pepper phytoene desaturase	-	-	SEQ ID NO: 421
GlmS	FJ935779.1 (2022-2192)	RF00234	SEQ ID NO: 422
HDV	-	-	SEQ ID NO: 423
VS_ribozyme	4R4V	-	SEQ ID NO: 424
Hairpin	D00721.1 (306-255)	RF00173	SEQ ID NO: 425
Hairpin	M21212.1 (157-106)	RF00173	SEQ ID NO: 426
Hairpin	M14879.1 (224-175)	RF00173	SEQ ID NO: 427
Hairpin	D00685.1 (306-255)	RF00173	SEQ ID NO: 428
Hairpin	D00721.1 (306-255)	RF00173	SEQ ID NO: 429
Hairpin	M17439.1 (226-177)	RF00173	SEQ ID NO: 430
Hairpin	-	RF04190; URS000080E2EB_32630 (1-68)	SEQ ID NO: 431
Group I self-splicing intron	AP014966.1 (20467201-20466676)	RF00028	SEQ ID NO: 432
Group I self-splicing intron	ADWL01007159.1 (31477-32002)	RF00028	SEQ ID NO: 433
Group II self-splicing intron	ASAF01074251.1 (11469-11396)	RF00029	SEQ ID NO: 434
Group II self-splicing intron	CM001068.2 (57579158-57579287)	RF00029	SEQ ID NO: 435
Group II self-splicing intron	CAJW011389724.1 (98-22)	RF00029	SEQ ID NO: 436
Group II self-splicing intron	CAJW011360013.1 (116-194)	RF00029	SEQ ID NO: 437
Group II self-splicing intron	KL543661.1 (216201-216123)	RF00029	SEQ ID NO: 438

¹ RNA equivalents of the DNA sequences are also contemplated and can be obtained from the DNA sequences provided.

Table 15. RNA Aptamers

RNA aptamer	Sequence ¹
Pepper	SEQ ID NO: 439
Broccoli	SEQ ID NO: 440
Corn-SAM	SEQ ID NO: 441
Mango	SEQ ID NO: 442
Mango II	SEQ ID NO: 443
Mango III	SEQ ID NO: 444
Mango III (A10U)	SEQ ID NO: 445
Mango IV	SEQ ID NO: 446
Squash	SEQ ID NO: 447
Chili	SEQ ID NO: 448
Spinach	SEQ ID NO: 449
Spinach2	SEQ ID NO: 450
Orange broccoli	SEQ ID NO: 451
DIR2s	SEQ ID NO: 452

¹ DNA equivalents of the RNA sequences are also contemplated and can be obtained from the RNA sequences provided.

Table 16. Subgenomic promoters

Subgenomic promoter	Sequence¹
Pea early-browning virus CP	SEQ ID NO: 453
Tobacco rattle virus strain TCM CP*	SEQ ID NO: 454
Tobacco rattle virus strain PSG CP*	SEQ ID NO: 455
Tobacco rattle virus strain PLB CP*	SEQ ID NO: 456
Tobacco rattle virus strain PRV CP*	SEQ ID NO: 457
Pea early-browning virus 12K	SEQ ID NO: 458
Pea early-browning virus 29.6K	SEQ ID NO: 459
Pea early-browning virus 29K	SEQ ID NO: 460
Tobacco mosaic virus CP	SEQ ID NO: 461
Tobacco mosaic virus MP	SEQ ID NO: 462
Cucumber mosaic virus CP	SEQ ID NO: 463

¹ RNA equivalents of the DNA sequences are also contemplated and can be obtained from the DNA sequences provided.

*See Goulden *et al.* (1990) *Nucleic Acids Res.*, 18:4507 – 4512, DOI:10.1093/NAR/18.15.4507.

Table 17. Endornavirus RdRP sequences

Name	NT Sequence SEQ ID NO¹	Amino Acid Sequence SEQ ID NO
Oryza sativa endornavirus (NC_007647) RdRP	596	613
Vicia faba endornavirus (NC_007648) RdRP	597	614
Oryza rufipogon endornavirus (NC_007649) RdRP	598	615
Persea americana endornavirus (NC_016648) RdRP	599	616
Lagenaria siceraria endornavirus (NC_023641) RdRP	600	617
Yerba mate endornavirus strain INTA (NC_024455) RdRP	601	618
Hot pepper alphaendornavirus (NC_027920) RdRP	602	619
Hordeum vulgare endornavirus (NC_028949) RdRP	603	620
Cucumis melo endornavirus isolate CL-01 (NC_029064) RdRP	604	621
Winged bean alphaendornavirus 1 (NC_031336) RdRP	605	622
Lagenaria siceraria endornavirus Hubei isolate (NC_034216) RdRP	606	623
Phaseolus vulgaris endornavirus 2 isolate PvEV-2 (NC_038422) RdRP	607	624
Bell pepper endornavirus isolate Penol (NC_039216) RdRP	608	625
Phaseolus vulgaris alphaendornavirus 1 isolate PvEV-1 (NC_039217) RdRP	609	626
Phaseolus endornavirus 3 isolate LA (NC_040558) RdRP	610	627
Helianthus annuus alphaendornavirus isolate BJ (NC_040799) RdRP	611	628
Cluster bean endornavirus isolate: 593049 (NC_040825) RdRP	612	629
Bell pepper endornavirus (AB597230) RdRP	632	682
Cucumis melo endornavirus isolate CL-01 (NC_029064) RdRP	633	683

Name	NT Sequence SEQ ID NO ¹	Amino Acid Sequence SEQ ID NO
Bell pepper endornavirus isolate Maor (KP455654) RDRP	634	684
Bell pepper endornavirus (KT149366) RDRP	635	685
Bell pepper endornavirus isolate BPEV-YW (JN019858) RDRP	636	686
Bell pepper endornavirus isolate Penol (NC_039216) RDRP	637	687
Persea americana endornavirus isolate Fuerte (JN880414) RDRP	638	688
Bell pepper endornavirus isolate lj (KF709944) RDRP	639	689
Oryza sativa endornavirus (D32136) RDRP	640	690
Oryza rufipogon endornavirus (AB014344) RDRP	641	691
Cucumber endornavirus 1 isolate CuEV1 (MT586998) RDRP	642	692
Bell pepper endornavirus strain IS (JQ951943) RDRP	643	693
Fagopyrum esculentum endornavirus 2 isolate SK (MZ517186) RDRP	644	694
Capsicum frutescens endornavirus 1 isolate LA-C (MT013202) RDRP	645	695
Cucumis melo alphaendornavirus strain CmEV/BRA/TO- 23/2014 (MH365458) RDRP	646	696
Bell pepper alphaendornavirus isolate Antioquia May 5 (MN073197) RDRP	647	697
Capsicum frutescens endornavirus 1 isolate LA-A (MT013200) RDRP	648	698
Capsicum frutescens endornavirus 1 isolate LA-B (MT013201) RDRP	649	699
Plant associated alphaendornavirus 1 isolate BER19SW1 (OL472077) RDRP	650	700
Tomato associated alphaendornavirus 1 isolate BOL20S (OL472079) RDRP	651	701
Bell pepper alphaendornavirus isolate MS1 (MN175323) RDRP	652	702
Brown algae endornavirus 1 Chiba1 (LC521321) RDRP	653	703
Brown algae endornavirus 2 Chiba2 (LC521322) RDRP	654	704
Bell pepper alphaendornavirus isolate BPEV_Panama	655	705

Name	NT Sequence SEQ ID NO ¹	Amino Acid Sequence SEQ ID NO
(MZ127290) RDRP		
Lily alphaendornavirus isolate BJ (MZ614632) RDRP	656	706
Phaseolus vulgaris alphaendornavirus 2 (OM112199) RDRP	657	707
Basella alba alphaendornavirus strain Oahu4 (OM108480) RDRP	658	708
Pumpkin alphaendornavirus isolate Anhui (MW018478) RDRP	659	709
Oryza sativa alphaendornavirus isolate BXCFS134 (MZ209990) RDRP	660	710
Oryza sativa alphaendornavirus isolate DHCFY127945 (MZ209614) RDRP	661	711
Pterostylis alphaendornavirus strain HR (OL471320) RDRP	662	712
Bell pepper alphaendornavirus isolate LA-E (MT013204) RDRP	663	713
Triticeae associated alphaendornavirus isolate Wheeler (MW091544) RDRP	664	714
Hordeum vulgare alphaendornavirus isolate HYT-37 (MN107382) RDRP	665	715
Hordeum vulgare alphaendornavirus isolate HYT-38 (MN107383) RDRP	666	716
Cucumis melo alphaendornavirus isolate IL (MN398900) RDRP	667	717
Phaseolus vulgaris alphaendornavirus 1 isolate PVAV1/CG6 (MN832719) RDRP	668	718
Phaseolus vulgaris alphaendornavirus 2 isolate PVAV2/CG6 (MN832720) RDRP	669	719
Bell pepper alphaendornavirus isolate XJ (MH182675) RDRP	670	720
Bell pepper alphaendornavirus isolate Marinilla (MK284997) RDRP	671	721
Bell pepper alphaendornavirus isolate San Vicente (MK284998) RDRP	672	722
Bell pepper alphaendornavirus isolate May8A (MK116548) RDRP	673	723
Endornavirus RDRP from <i>Oryza sativa</i> M-102	674	-
Johnsongrass virus isolate JVG-1 (MW756210) RDRP	675	724
Johnsongrass virus isolate JVG-2 (MW756211) RDRP	676	725
Consensus endornavirus RdRP partial sequence identified from <i>Oryza sativa</i> cultivars M-102 and Colusa	677	726
Endornavirus RdRP fragment identified from <i>Oryza sativa</i> Colusa	678	-

Name	NT Sequence SEQ ID NO ¹	Amino Acid Sequence SEQ ID NO
Endornavirus RdRP fragment identified from <i>Oryza sativa</i> M102	679	-
Endornavirus RdRP identified from Rutgers tomato	680	-
Endornavirus RdRP identified from Early Girl (F ₁) tomato	681	-
Agaricus bisporus alphaendornavirus 1	1130	1261
Alphaendornavirus fimbriatae-1	1131	1262
Alphaendornavirus fimbriatae-2	1132	1263
Alphaendornavirus fimbriatae-3	1133	1264
Alphaendornavirus sp.	1134	1265
Basella alba alphaendornavirus 1	1135	1266
Beijing alphaendornavirus 3	1136	1267
Beijing sediment alphaendornavirus 1	1137	1268
Beijing sediment alphaendornavirus 2	1138	1269
Bell pepper alphaendornavirus	1139	1270
Cucumis melo alphaendornavirus	1140	1271
Erysiphe cichoracearum alphaendornavirus	1141	1273
Grapevine endophyte alphaendornavirus	1142	1274
Helianthus annuus alphaendornavirus	1143	1275
Helicobasidium mompa alphaendornavirus 1	1144	1276
Hordeum vulgare alphaendornavirus	1145	1277
Hot pepper alphaendornavirus	1146	1278
Jiangsu alphaendornavirus 1	1147	1279
Lagenaria siceraria alphaendornavirus	1148	1280
Lily alphaendornavirus	1149	1281
Nansha Islands sediment alphaendornavirus 2	1150	1282
Oryza rufipogon alphaendornavirus	1151	1283
Oryza sativa alphaendornavirus	1152	1284
Persea americana alphaendornavirus 1	1153	1285
Phaseolus leptostachyus alphaendornavirus	1154	1286
Phaseolus lunatus alphaendornavirus	1155	1287
Phaseolus vulgaris alphaendornavirus 1	1156	1288
Phaseolus vulgaris alphaendornavirus 2	1157	1289
Phaseolus vulgaris alphaendornavirus 3	1158	1290
Phytophthora alphaendornavirus 1	1159	1291
Phytophthora cactorum alphaendornavirus 1	1160	1292
Phytophthora cactorum alphaendornavirus 1	1161	1293
Phytophthora cactorum alphaendornavirus 2	1162	1294
Phytophthora cactorum alphaendornavirus 2	1163	1295
Phytophthora cactorum alphaendornavirus 3	1164	1296
Phytophthora cactorum alphaendornavirus 3	1165	1297
Phytophthora heveae alphaendornavirus 1	1166	1298
Plant associated alphaendornavirus 1	1167	1299
Pterostylis alphaendornavirus	1168	1300
Pumpkin alphaendornavirus	1169	1301
Rhizoctonia cerealis alphaendornavirus 1	1170	1302

Name	NT Sequence SEQ ID NO ¹	Amino Acid Sequence SEQ ID NO
Rhizoctonia solani alphaendornavirus 1	1171	1303
Rhizoctonia solani alphaendornavirus 2	1172	1304
Sichuan alphaendornavirus 22	1173	1305
Tomato associated alphaendornavirus 1	1174	1306
Triticeae associated alphaendornavirus	1175	1307
Vicia faba alphaendornavirus	1176	1309
Winged bean alphaendornavirus 1	1177	1310
Yerba mate alphaendornavirus	1178	1311
Yunnan alphaendornavirus 4	1179	1312
Alternaria brassicicola betaendornavirus 1	1180	1313
Betaendornavirus sp.	1181	1314
Botrytis cinerea betaendornavirus 1	1182	1315
Gremmeniella abietina betaendornavirus 1	1183	1316
Rosellinia necatrix betaendornavirus 1	1184	1317
Sclerotinia minor betaendornavirus 1	1185	1318
Sclerotinia sclerotiorum betaendornavirus 1	1186	1319
Sclerotinia sclerotiorum betaendornavirus 1	1187	1320
Sclerotinia sclerotiorum betaendornavirus 1	1188	1321
Tuber aestivum betaendornavirus	1189	1322
Almopos endorna-like virus 1	1190	1323
Althepos endorna-like virus 1	1191	1324
Arthrocladiella mougeotii alphaendornavirus	1192	1325
Bolbocoleon piliferum endorna-like virus	1193	1326
Botrytis cinerea endornavirus 2	1194	1327
Botrytis cinerea endornavirus 3	1195	1328
Botrytis cinerea endornavirus 4	1196	1329
Botrytis endornavirus 1	1197	1330
Brachiomonas submarina endorna-like virus	1198	1331
Bremia lactucae associated endornavirus 1	1199	1332
Brown algae endornavirus 1	1200	1333
Brown algae endornavirus 2	1201	1334
Capsicum frutescens endornavirus 1	1202	1335
Carteria obtusa associated endorna-like virus	1203	1336
Ceratobasidium endornavirus 1	1204	1337
Ceratobasidium endornavirus 2	1205	1338
Ceratobasidium endornavirus A	1206	1339
Ceratobasidium endornavirus B	1207	1340
Ceratobasidium endornavirus C	1208	1341
Ceratobasidium endornavirus D	1209	1342
Ceratobasidium endornavirus F	1210	1343
Ceratobasidium endornavirus G	1211	1344
Ceratobasidium endornavirus H	1212	1345
Chalara endornavirus CeEV1	1213	1346
chieh-qua endornavirus	1214	1347
Cluster bean endornavirus 1	1215	1348

Name	NT Sequence SEQ ID NO ¹	Amino Acid Sequence SEQ ID NO
Cucumber endornavirus 1	1216	1349
Diplodia seriata endornavirus 1	1217	1350
Fagopyrum esculentum endornavirus 1	1218	1351
Fagopyrum esculentum endornavirus 2	1219	1352
Geranium carolinianum endornavirus	1220	1353
Grapevine-associated endornavirus 1	1221	1354
Hydrocotyle umbellata endornavirus	1222	1355
Hygrophorus penarioides endornavirus 1	1223	1356
Hymenoscyphus fraxineus endornavirus 1	1224	1357
Krauss' spikemoss associated endorna-like virus	1225	1358
Lagenaria siceraria endornavirus-Hubei	1226	1359
Lonicera maackii endornavirus	1227	1360
Macrophomina phaseolina endornavirus 1	1228	1361
Macrophomina phaseolina endornavirus 2	1229	1362
Morchella importuna endornavirus 1	1230	1363
Morchella importuna endornavirus 2	1231	1364
Morchella importuna endornavirus 3	1232	1365
Neofusicoccum parvum endornavirus 1	1233	1366
Ophiostoma bicolor endornavirus 1	1234	1367
Phomopsis vexans endornavirus 1	1235	1368
Phomopsis vexans endornavirus 2	1236	1369
Phytophthora endornavirus 2	1237	1370
Phytophthora endornavirus 3	1238	1371
Rhizoctonia solani endornavirus	1239	1372
Rhizoctonia solani endornavirus - RS002	1240	1373
Rhizoctonia solani endornavirus 1	1241	1374
Rhizoctonia solani endornavirus 3	1242	1375
Rhizoctonia solani endornavirus 4	1243	1376
Rhizoctonia solani endornavirus 5	1244	1377
Rhizoctonia solani endornavirus 6	1245	1378
Rhizoctonia solani endornavirus 7	1246	1379
Rhizopus microsporus endornavirus 1	1247	1380
Rhizopus microsporus endornavirus 2	1248	1381
Sanya endornavirus 1	1249	1382
Sclerotinia sclerotiorum endornavirus 11	1250	1383
Sclerotinia sclerotiorum endornavirus 1-WX	1251	1384
Sclerotinia sclerotiorum endornavirus 2-A	1252	1385
Sclerotinia sclerotiorum endornavirus 3	1253	1386
Sclerotinia sclerotiorum endornavirus 8	1254	1387
Sclerotinia sclerotiorum endornavirus 9	1255	1388
Setosphaeria turcica endornavirus 1	1256	1389
Setosphaeria turcica endornavirus 2	1257	1390
Soybean leaf-associated endornavirus 1	1258	1391
Staurastrum sebaldi endornavirus	1259	1392
Volvox aureus endorna-like virus	1260	1393

Name	NT Sequence SEQ ID NO ¹	Amino Acid Sequence SEQ ID NO
Dicrocoelium alphaendornavirus		1272
Tvarminne alphaendornavirus		1308

¹ DNA equivalents of the RNA sequences are also contemplated and can be obtained from the RNA sequences provided.

Table 18. Endornavirus Genome 5' and 3' RNA Replication Element Pairs and RdRP

Row	endornavirus	EV Genome-5' RNA Replication Element	EV Genome-3' RNA Replication Element	EV RdRP
		SEQ ID NO	SEQ ID NO	Protein
				SEQ ID NO
1	Oryza sativa endornavirus	467	524	613
	>NC_007647			
2	Vicia faba endornavirus	468	525	614
	>NC_007648			
3	Oryza rufipogon endornavirus	469	526	615
	>NC_007649			
4	Persea americana endornavirus	470	527	616
	>NC_016648			
5	Lagenaria siceraria endornavirus	471	528	617
	>NC_023641			
6	Yerba mate endornavirus strain INTA	472	529	618
	>NC_024455			
7	Hot pepper alphaendornavirus	473	530	619
	>NC_027920			
8	Hordeum vulgare endornavirus	474	531	620
	>NC_028949			
9	Cucumis melo endornavirus isolate CL-01	475	532	621
	>NC_029064			
10	Winged bean alphaendornavirus 1	476	533	622
	>NC_031336			
11	Lagenaria siceraria endornavirus Hubei isolate	477	534	623
	>NC_034216			
12	Phaseolus vulgaris endornavirus 2 isolate PvEV-2	478	535	624
	>NC_038422			
13	Bell pepper endornavirus isolate Penol	479	536	625
	>NC_039216			
14	Phaseolus vulgaris alphaendornavirus 1 isolate PvEV-1	480	537	626

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Row	endornavirus	EV Genome-5' RNA Replication Element	EV Genome-3' RNA Replication Element	EV RdRP
	>NC_039217			
15	Phaseolus endornavirus 3 isolate LA	481	538	627
	>NC_040558			
16	Helianthus annuus alphaendornavirus isolate BJ	482	539	628
	>NC_040799			
17	Cluster bean endornavirus isolate: 593049	483	540	629
	>NC_040825			
18	Agaricus bisporus alphaendornavirus 1	924	1018	1261
19	Alphaendornavirus sp.	925	1019	
20	Basella alba alphaendornavirus 1	926	1020	1266
21	Bell pepper alphaendornavirus	927	1023	1270
22	Cucumis melo alphaendornavirus	928	1024	1271
23	Erysiphe cichoracearum alphaendornavirus	930	1025	1273
24	Grapevine endophyte alphaendornavirus	931	1026	1274
25	Helianthus annuus alphaendornavirus	932	1027	1275
26	Helicobasidium mompa alphaendornavirus 1	933	1028	1276
27	Hordeum vulgare alphaendornavirus	934	1029	1277
28	Hot pepper alphaendornavirus	935	1030	1278
29	Lagenaria siceraria alphaendornavirus	936	1032	1280
30	Lily alphaendornavirus	937	1033	1281
31	Oryza sativa alphaendornavirus	938	1035	
32	Persea americana alphaendornavirus 1	939	1036	1285
33	Phaseolus vulgaris alphaendornavirus 1	940	1038	1288
34	Phaseolus vulgaris alphaendornavirus 2	941	1039	1289
35	Phaseolus vulgaris alphaendornavirus 3	942	1040	1290
36	Plant associated alphaendornavirus 1	946	1043	1299
37	Pterostylis alphaendornavirus	947	1044	1300
38	Pumpkin alphaendornavirus	948	1045	1301
39	Rhizoctonia cerealis alphaendornavirus 1	949	1046	1302
40	Rhizoctonia solani alphaendornavirus 1	950	1047	1303

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Row	endornavirus	EV Genome-5' RNA Replication Element	EV Genome-3' RNA Replication Element	EV RdRP
41	Rhizoctonia solani alphaendornavirus 2	951	1048	1304
42	Triticeae associated alphaendornavirus	952	1051	1307
43	Tvarminne alphaendornavirus	953	1052	
44	Vicia faba alphaendornavirus	954	1053	1309
45	Winged bean alphaendornavirus 1	955	1054	1310
46	Yerba mate alphaendornavirus	956	1055	1311
47	Alternaria brassicicola betaendornavirus 1	957	1056	1313
48	Betaendornavirus sp.	958	1057	1314
49	Botrytis cinerea betaendornavirus 1	959	1058	1315
50	Gremmeniella abietina betaendornavirus 1	960	1059	1316
51	Rosellinia necatrix betaendornavirus 1	961	1060	1317
52	Sclerotinia minor betaendornavirus 1	962	1061	1318
53	Sclerotinia sclerotiorum betaendornavirus 1	963	1062	1319
54	Sclerotinia sclerotiorum betaendornavirus 1	964	1063	1320
55	Sclerotinia sclerotiorum betaendornavirus 1	965	1064	1321
56	Tuber aestivum betaendornavirus	966	1065	1322
57	Arthrocladiella mougeotii alphaendornavirus	967	1068	1325
58	Botrytis cinerea endornavirus 2	968	1070	1327
59	Botrytis cinerea endornavirus 3	969	1071	1328
60	Botrytis cinerea endornavirus 4	970	1072	1329
61	Bremia lactucae associated endornavirus 1	972	1074	1332
62	Capsicum frutescens endornavirus 1	973	1077	1335
63	Carteria obtusa associated endorna- like virus	974	1078	1336
64	Ceratobasidium endornavirus 1	975	1079	1337
65	Ceratobasidium endornavirus 2	976	1080	1338
66	Ceratobasidium endornavirus A	977	1081	1339
67	Ceratobasidium endornavirus B	978	1082	1340
68	Ceratobasidium endornavirus C	979	1083	1341
69	Ceratobasidium endornavirus D	980	1084	1342
70	Ceratobasidium endornavirus G	981	1086	1344
71	chieh-qua endornavirus	983	1088	1345
72	Cluster bean endornavirus 1	984	1089	1348
73	Cucumber endornavirus 1	985	1090	1349
74	Diplodia seriata endornavirus 1	986	1091	1350

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Row	endornavirus	EV Genome-5' RNA Replication Element	EV Genome-3' RNA Replication Element	EV RdRP
75	Fagopyrum esculentum endornavirus 1	987	1092	1351
76	Fagopyrum esculentum endornavirus 2	988	1093	1352
77	Geranium carolinianum endornavirus	989	1094	1353
78	Hydrocotyle umbellata endornavirus	991	1095	1355
79	Hygrophorus penarioides endornavirus 1	992	1096	1356
80	Hymenoscyphus fraxineus endornavirus 1	993	1097	1357
81	Lagenaria siceraria endornavirus- Hubei	994	1099	1359
82	Lonicera maackii endornavirus	995	1100	1360
83	Macrophomina phaseolina endornavirus 1	996	1101	1361
84	Macrophomina phaseolina endornavirus 2	997	1102	1362
85	Morchella importuna endornavirus 1	998	1103	1363
86	Morchella importuna endornavirus 2	999	1104	1364
87	Morchella importuna endornavirus 3	1000	1105	1365
88	Phomopsis vexans endornavirus 2	1001	1108	1368
89	Phytophthora endornavirus 2	1002	1109	1369
90	Phytophthora endornavirus 3	1003	1110	1371
91	Rhizoctonia solani endornavirus	1004	1111	1372
92	Rhizoctonia solani endornavirus - RS002	1005	1112	1373
93	Rhizoctonia solani endornavirus 4	1006	1113	1376
94	Rhizoctonia solani endornavirus 5	1007	1114	1377
95	Rhizoctonia solani endornavirus 6	1008	1115	1378
96	Rhizoctonia solani endornavirus 7	1009	1116	1379
97	Rhizopus microsporus endornavirus 1	1010	1117	1380
98	Rhizopus microsporus endornavirus 2	1011	1118	1381
99	Sclerotinia sclerotiorum endornavirus 11	1013	1119	1383
100	Sclerotinia sclerotiorum endornavirus 1-WX	1014	1120	1384
101	Setosphaeria turcica endornavirus 1	1015	1125	1389
102	Setosphaeria turcica endornavirus 2	1016	1126	1390
103	Soybean leaf-associated endornavirus 1	1017	1127	1391

Table 19: 5' RRE conserved motif 1

ID	start	end	score	Sequence SEQ ID NO	Dot-bracket
NC_028949	61	94	28.6539	729	((((((((((((((((...))))))))))))))
NC_023641	54	87	28.6539	730	((((((((((((((((...))))))))))))))
NC_034216	54	87	28.6539	731	((((((((((((((((...))))))))))))))
NC_027920	92	125	28.3124	732	(((((((((((((((((...))))))))))))))
NC_039216	92	125	28.3124	733	(((((((((((((((((...))))))))))))))
NC_040825	70	103	28.3124	734	(((((((((((((((((...))))))))))))))
NC_038422	92	125	28.3124	735	(((((((((((((((((...))))))))))))))
NC_043109	58	91	27.6697	736	(((((((((((((((((.....))))))))))))))
NC_029064	58	91	26.9303	737	(((((((((((((((((.....))))))))))))))
NC_007647	95	128	26.1285	738	..(((((((((((((((.....))))))))))))..

Table 20: 5' RRE conserved motif 2

ID	start	end	score	Sequence SEQ ID NO	Dot-bracket
NC_040799	451	484	26.5814	739	...(((.(.....))).))...))
NC_023641	107	140	26.2301	740	(.(((.(.....))).).))....
NC_038422	147	180	26.0438	741	..(((((((.....).)))))).
NC_040825	177	210	24.6702	742	..(((((((.....)))))).).))
NC_039216	464	497	24.3448	743	)(((.(.....))).))...))
NC_007647	130	163	24.2612	744	(((((((((.....))))))))).((
NC_007648	370	403	23.5937	745	(((((((((.....))))....)).)
NC_039217	366	399	22.8964	746	...(((.....))))))....))
NC_027920	302	335	22.58	747	..(((((((.....)))))).).

Table 21: 5' RRE conserved motif 3

ID	start	end	score	Sequence SEQ ID NO	Dot-bracket
NC_007647	54	81	18.065	748	((((((((((((((((...))))))))))))))
NC_039216	420	447	18.065	749	..((((((((((((((...)).))))))))
NC_038422	55	82	18.065	750	))((((((((((((((((...))))))))))
NC_024455	36	63	18.065	751	((((((((((((((((((...))))))))))
NC_007649	54	81	18.065	752	((((((((((((((((((...))))))))))
NC_040825	324	351	18.065	753	((...((((((((((((((((...))))))))
NC_016648	55	82	18.065	754	((((((((((((((((((...))))))))))
NC_029064	381	408	17.3838	755	((((((((((((((((((...)).))))....

ID	start	end	score	Sequence SEQ ID NO	Dot-bracket
NC_043109	102	129	17.3672	756	(..(((((((.....))).))).)...
NC_023641	260	287	15.4922	757	(.(((((((((((.....)))))).))))))
NC_034216	108	135	15.4922	758	..(((((((.....))).))).))
NC_028949	273	300	15.4922	759	(((((((((.....)))))).))))
NC_040799	385	412	15.0744	760	..(((((((.....))).))))
NC_007648	76	103	14.0185	761	...(((((((((((.....)))))).))))

Table 22: 3' RRE conserved motif 1

ID	start	end	score	Sequence SEQ ID NO	Dot-bracket
NC_016648	33	58	24.5196	762	((((((.....))))).)
NC_031336	56	81	24.0017	763	..((((.....)))).
NC_043109	206	231	23.8605	764	((((((.....))))))
NC_039216	11	36	23.8447	765	(..((((.....))).)
NC_040799	433	458	22.9536	766	((((((.....))))).
NC_024455	435	460	22.7717	767	((((((.....))))))
NC_029064	56	81	21.6556	768	((((((.....))))))
NC_038422	131	156	20.4816	769	((((((.....))))))
NC_040558	375	400	19.8443	770	..((((.....))))
NC_007647	377	402	19.6202	771	((((((.....))))))

Table 23: 3' RRE conserved motif 2

ID	start	end	score	Sequence SEQ ID NO	Dot-bracket
NC_016648	78	118	21.3334	772	)((((.....(((((((.....))).)))).....))))
NC_038422	177	217	20.5634	773	(((((.....(((((((.....)))))).)))).....)).)
NC_027920	360	400	19.0346	774	..(((((((.....(((((((.....))).)))).....))).
NC_043109	158	198	17.9168	775	..(((((((.....))).)))).....)))).
NC_029064	342	382	16.9873	776	(..(((((((.....))).)))).....)).)
NC_007647	411	451	16.8916	777	..((((.....(((((((.....)))))).)))).....))))(
NC_023641	327	367	16.499	778	(((((((((((((.....)))))).)))).....))))
NC_039216	149	189	14.378	779	((((((((.....(((((((.....)))))).)))).....))))

Table 24: 3' RRE conserved motif 3

ID	start	end	score	Sequence SEQ ID NO	Dot-bracket
NC_024455	20	50	19.7807	780	((...(((.....(((((((.....))).)))).....)))

ID	start	end	score	Sequence SEQ ID NO	Dot-bracket
NC_039217	30	60	19.5078	781	(((((.(....(((...)))...)).)))
NC_031336	259	289	18.2695	782	((..(((....(((....)))....)).)
NC_040825	243	273	18.2345	783	..(((((((....(((....)))....))))))
NC_007648	137	167	17.5665	784	((..(((....(((....)))....))))..
NC_034216	117	147	17.4943	785	(((((....(((....)))....)).))
NC_028949	309	339	16.5839	786	(...(((....(((....)))....)).)
NC_040558	37	67	15.2611	787	(((((....(((....)))....))))

Table 25. Endornavirus 5'RRE and 3' RRE Secondary Structures

Endornavirus	5' RRE SEQ ID NO	5' RRE Dot-Bracket
Agaricus bisporus alphaendornavir s 1	924	
Alphaendornavir s sp.	925	(((((((.....))))).((....(((.....((((.....))..))))))....).. .))....((((.....)))).....
Basella alba alphaendornavir s 1	926	(((((....(((.....)))))).((((.....((((.....((((.....))))))))))))....(((((((....(((....)))....)).))))....(((....(((....((((.....))..((.....))....)).))))....))....((((.....((((.....))))....((((..... ..((((.....))))....((((.....((((.....))))....))))....))....))....)))....((((.....))....((.....))....))))....))....))))....
Bell pepper alphaendornavir s	927	
Cucumis melo alphaendornavir s	928	..(((((((.....))))).((((.....((((.....((((.....((((.....)))))))))) ..))))....((((.....((((.....))))....))....((((.....))....((((.....))....)))))....))....))....))....
Erysiphe cichoracearum alphaendornavir s	930	
Grapevine endophyte alphaendornavir s	931	
Helianthus annuus alphaendornavir s	932	..(((((((.....))))....
Helicobasidium momp alphaendornavir s 1	933	
Hordeum vulgare alphaendornavir s	934	((.....(((((((.....))))....))....((((.....((((.....((((.....))))))))))....((((.....((((.....((((.....))))....))))....))))....))))....)))))....))....

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

Endornavirus	5' RRE SEQ ID NO	5' RRE Dot-Bracket
alphaendornavir s 1		
Plant associated alphaendornavir s 1	1043	
Pterostylis alphaendornavir s	1044	...(((.(.({(.....)).}).)))...
Pumpkin alphaendornavir s	1045	(((((((.....))))))....
Rhizoctonia cerealis alphaendornavir s 1	1046	((((((((((((.((((((((((.....)).).))))))(((((.({(.....)).....}).)(((((.((((..... ..)))))..)))).....).))))..))))..)))..)).....(((((((.....)).)).((((.(.({(.....)).)((({.....}))..(((((((.....)).))))..))))..
Rhizoctonia solani alphaendornavir s 1	1047	(((((((.....))).).(.....(((((((.....)))))).-.))
Rhizoctonia solani alphaendornavir s 2	1048	
Sichuan alphaendornavir s 22	1049	(((((((.({(.....)).}.)...))))....
Tomato associated alphaendornavir s 1	1050	.(((((((.....))))))....(((((((.....)).....))).(((((((.....)))))).....
Triticeae associated alphaendornavir s	1051	{..({(.....))..}.
Tvarminne alphaendornavir s	1052	.(((.....)))(((((((((.....))))))))
Vicia faba alphaendornavir s	1053	(((((((((.({(......(((((((.((((((((.....)))))).).))....).)))))).....)))).....))))..)))))))..{{(.....)}})
Winged bean alphaendornavir s 1	1054	(((({{{.....}})})....
Yerba mate alphaendornavir s	1055	(((({{{.....}})}).(((.....(((({{{.....}})....}))))..
Alternaria brassicicola betaendornavirus 1	1056	{{(.({(.....)))))}

[illegible]

Endornavirus	5' RRE SEQ ID NO	5' RRE Dot-Bracket
Bremia lactucae associated endornavirus 1	1074	.(((((((.....)))))).(((.....)))......
Brown algae endornavirus 1	1075	(((((((((((.....))).))))))))......
Brown algae endornavirus 2	1076	...(((.....(((.....))))))....(((.....))).))
Capsicum frutescens endornavirus 1	1077	(((((((.....))))))
Carteria obtusa associated endorna-like virus	1078	(((.....))).))
Ceratobasidium endornavirus 1	1079	(((((.....(((.....))))))....)))).....
Ceratobasidium endornavirus 2	1080	..(((.....)))..
Ceratobasidium endornavirus A	1081	(((((((((((.....))))))....)))).....
Ceratobasidium endornavirus B	1082	
Ceratobasidium endornavirus C	1083	(((((((((((.....))))))....)))).....
Ceratobasidium endornavirus D	1084	(((((((((((.....))))))....)))).....
Ceratobasidium endornavirus F	1085	..(((.....)))......((((.....)))
Ceratobasidium endornavirus G	1086	(((.....))).(((.....)))..
Ceratobasidium endornavirus H	1087	(((.....))).((((.....))).....
chieh-qua endornavirus	1088	(((((((((((.....))))))....)))).....
Cluster bean endornavirus 1	1089	(((.....))).
Cucumber endornavirus 1	1090	(((.....)))......
Diplodia seriata endornavirus 1	1091	(((((((((((.....))))))....)))).....
Fagopyrum esculentum endornavirus 1	1092	(((.....))).
Fagopyrum esculentum endornavirus 2	1093	((((.....)))...
Geranium carolinianum endornavirus	1094	((((.....))).....

Endornavirus	5' RRE SEQ ID NO	5' RRE Dot-Bracket
Hydrocotyle umbellata endornavirus	1095	
Hygrophorus penarioides endornavirus 1	1096	(((((((...)).)))))......
Hymenoscyphus fraxineus endornavirus 1	1097	{(.((((.((((.....))))))))}
Krauss' spikemoss associated endorna-like virus	1098	
Lagenaria siceraria endornavirus- Hubei	1099	...(((((((.....))))))..{(.((((((((.....))))))..)).}.....
Lonicera maackii endornavirus	1100	..{(..{(..(((.....)))..})..)}(((((((.(.....)).)))))......
Macrophomina phaseolina endornavirus 1	1101	..{(.....)}...{(.....((((((((((((.....(((((((.....)))))).....)).))))))))..)}....
Macrophomina phaseolina endornavirus 2	1102	{(.....((((.....))).....)}.....(((((((.(.....)).)))))..
Morchella importuna endornavirus 1	1103	..((((.....((((.....))))))..){(.(.....((((.....))))..)}..(((((((.(.....))))..))..)
Morchella importuna endornavirus 2	1104	(((((((.....(((((((.....)))))).....))))))..
Morchella importuna endornavirus 3	1105	((.....(((.(.....)).))).....).(((((((.(.....)).))).....))..
Ophiostoma bicolor endornavirus 1	1106	(((((((.....)).)))..).(((((((.....)).)))..).
Phomopsis vexans endornavirus 1	1107	(((((((.....)).))).....
Phomopsis vexans endornavirus 2	1108	{(.((((.(.....(((((((.....)).)))..))))))(((((((.....)).)))((.....))..((((((((.....(((((((.....))))))..)))))).....))))..)}..
Phytophthora endornavirus 2	1109	..(((((((.....))))))(((((((.....)))))......
Phytophthora endornavirus 3	1110	
Rhizoctonia solani endornavirus	1111	(((((((.....))))).(((((((.....)))))......
Rhizoctonia solani endornavirus 1	1112	{(.....((((.....))))..}
Rhizoctonia solani endornavirus 4	1113	(((((((.....((((.....))))..))))

Endornavirus	5' RRE SEQ ID NO	5' RRE Dot-Bracket
Rhizoctonia solani endornavirus 5	1114	..(((((((((((.....)))))).))))..(((((((((((.(((.(.....)))))).))))))))....
Rhizoctonia solani endornavirus 6	1115	
Rhizoctonia solani endornavirus 7	1116	
Rhizopus microsporus endornavirus 1	1117	{((((((((.....)))))))).
Rhizopus microsporus endornavirus 2	1118	
Sclerotinia sclerotiorum endornavirus 11	1119	(((((.....))))).(((.(.(((.....)))))).((((((((.....)))))))).
Sclerotinia sclerotiorum endornavirus 1- WX	1120	((((((((((.....)))))))).((((.....((((((((.....))))))))......((((((((.....)))))).)))).....
Sclerotinia sclerotiorum endornavirus 2-A	1121	(((((.(((.....)))))).((((.....)))).....((((.(.(((.....((((((((.....)))))))))))).)).
Sclerotinia sclerotiorum endornavirus 3	1122	((((((((.....)))))).
Sclerotinia sclerotiorum endornavirus 8	1123	((((((((.....))))))......((((((((.....))))))......((((((((..... ((((((((.....)))))).)))))).
Sclerotinia sclerotiorum endornavirus 9	1124	((((.....)))).....((((((((.....)))))).
Setosphaeria turcica endornavirus 1	1125	..(((((((((((.(((.(.....)))))).)))))))).((((.....)))).....((((.....))))).
Setosphaeria turcica endornavirus 2	1126	((((((((((.....(((.(((.(((.....))))).(((.(((.(((.....))))).(((.(((.....))))).))))).))))).)
Soybean leaf- associated endornavirus 1	1127	..((((((((.....)))))))((((.....)))).....
Staurostrum sebaldi endornavirus	1128	((((((((.....))))).(((.....((((((((.....))))).))))).))))..... ((((((((.....))))).)))).....((((.....)))).....((((((((.....))))).))))..... ((((.....)))).....((((.....)))).....((((.....)))).....
Volvox aureus endorna-like virus	1129	{((.....))}.....

EXAMPLES**Example 1. An antiviral endornavirus satellite with an imbedded HRV amplicon and RNAi cargo**

[0326] An endornavirus satellite (COMSAT) that carries an antiviral inhibitory RNA (RNAi) cargo is generally provided in 5' to 3' orientation as follows: (i) 5' RNA replication element from the endornavirus virus; (ii) a heterologous RNA virus (HRV) 5' replication region (HRV 5'RR); (iii) an antiviral RNA molecule which induces an RNAi response; (iv) the heterologous RNA virus (HRV) 3' RNA replication region (HRV 3'RR); and (v) and the 3' RNA replication element from the endornavirus virus.

[0327] A COMSAT comprising endornavirus 5' and 3' RNA replication elements flanking a TMV amplicon containing a cargo RNA containing a Pepper mild mottle virus (PMMoV) RNAi inducing sequence (*e.g.*, a PMMoV sequence which can form a dsRNA) is provided as SEQ ID NO: 630. The elements of the satellite are set forth in Table 26.

Table 26.

Genetic element	Nucleotide position in SEQ ID NO: 630
endornavirus 5' RNA replication element	1-226
TMV 5' replication region	227-294
Antiviral RNAi cargo (PMMoV RNAi inducing sequence)	295-1272
TMV 3' replication region	1273-1476
ZmHSP101 IRES (optional)	1477-1623
TMV MP (optional)	1624-2430
Ileu tRNA	2431-2512
endornavirus 3' RNA replication element	2513-2566

Example 2. An antiviral endornavirus satellite with an imbedded HRV amplicon and antiviral protein cargo

[0328] A endornavirus satellite (COMSAT) with an imbedded HRV amplicon that carries an antiviral protein cargo is generally provided in 5' to 3' orientation as follows: (i) 5' RNA replication element from the endornavirus virus; (ii) a heterologous RNA virus (HRV) 5' replication region (HRV 5'RR); (iii) an antiviral protein cargo; (iv) the heterologous RNA virus (HRV) 3' RNA replication region (HRV 3'RR); and (v) the 3' RNA replication element from the endornavirus virus.

[0329] A COMSAT comprising endornavirus 5' and 3' RNA replication elements flanking a tobacco mosaic virus (TMV) amplicon containing an antiviral cargo protein containing the coding sequence of the N gene of tobacco is provided as SEQ ID NO: 631. This satellite includes TMV 5' and 3' replication region sequences (HRV 5' and 3' RR sequences) to promote secondary amplification by TMV, which is a pathogenic tobamovirus. The elements of this satellite are set forth in Table 26. Similar antiviral endornavirus satellites are designed for secondary amplification by tomato mosaic virus or tomato brown

rugose fruit virus (which are also pathogenic tobamoviruses), and include an N protein (SEQ ID NO:254), L4 protein (SEQ ID NO:256), or a combination of N and L4 protein as the antiviral cargo sequence(s), and replacing the HRV 5' and 3' RR sequences of TMV with the HRV 5' and 3' RR sequences of either tomato mosaic virus or tomato brown rugose fruit virus as provided in Table 7, to promote secondary amplification by tomato mosaic virus or tomato brown rugose fruit virus, respectively. Solanaceous plants containing the endornavirus (or that otherwise are provided with the appropriate endornavirus RdRP, e.g., through transient or transgenic expression) and that are provided with these antiviral endornavirus satellites are expected to exhibit resistance to tobacco mosaic virus, tomato mosaic virus, or tomato brown rugose fruit virus, respectively.

Table 27

Genetic element	Nucleotide position in SEQ ID NO: 631
endornavirus 5' RNA replication element	1-226
TMV 5' replication region	227-294
PSVI IRES	295-490
Antiviral protein cargo (coding sequence of N gene)	491-3925
TMV 3' replication region	3926-4129
ZmHSP101 IRES (optional)	4130-4276
TMV MP (optional)	4277-5083
Ileu tRNA	5084-5165
endornavirus 3' RNA replication element	5166-5219

Example 3. Assaying plants comprising antiviral endornavirus commensal satellite with antiviral cargo for antiviral activity

[0330] Antiviral COMSATs (e.g., of Examples 1 or 2) or control RNAs (e.g., RNAs lacking the antiviral cargo) are delivered into target host plants, such as pepper or tomato plants via micro-bombardment ("biolistic" delivery) using a "gene gun" or by bacterially mediated (e.g., by *Agrobacterium*) transient expression. Plants, e.g., pepper and tomato plants, are grown in growth chambers using a long-day photoperiod (16 h light/8 h dark) with light intensity 100-150 micromole, until seedlings are about 2 weeks old. Antiviral COMSATs are prepared either as *in vitro* transcribed (IVT) products (capped or uncapped), or as *Agrobacterium* binary vectors. For micro-bombardment, the IVT product is coated onto the surface of gold nanoparticles which are precipitated on inner surface of bullet tubes; these are accelerated at the abaxial surface of the seedlings' leaves with helium pressure from 100 to 180 psi. For agroinfiltration, COMSAT-carrying clones in binary vector are transformed into *Agrobacterium* GV 2260, and the transformed *Agrobacterium* is selected by growing at 28°C under appropriate antibiotic selection. The positive transformants are verified by PCR and then grown at 28°C overnight in liquid LB medium with appropriate antibiotics plus rifamycin to maintain the

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Agrobacterium and prevent contamination. *Agrobacterium* cells are collected by centrifugation and resuspended in MMA buffer at an OD600 of 0.2, incubated at 28°C on a shaker for 2 hours, and then infiltrated into the abaxial sides of the leaves. Control plants are treated in the same way but with non-COMSAT control IVT transcripts, or empty buffers. At different timepoints after COMSAT delivery, tissues from systemic leaves (leaves distal to the treated leaves) are collected and subjected to RNA extraction, followed by cDNA syntheses. COMSAT titers are monitored in systemic tissue by qRT-PCR with COMSAT-specific primers.

[0331] The efficacy of an antiviral COMSAT can be tested by challenging the COMSAT-treated plants with the viral pathogen of interest (e.g., cucumber mosaic virus, CMV, or tobacco mosaic virus, TMV), for example, by mechanical infection. Infectious preparations of such acute viral pathogens are prepared *in planta* (e.g., in *Nicotiana benthamiana*) or in the form of GFP-fused infectious clones in a binary vector or T7-based vector. Suitable viral inoculums can be prepared as infectious sap extracted from an infected plant, as an *Agrobacterium*-based inoculum, or as IVT products. The inoculum is introduced into leaves of the COMSAT-treated plants by rub-inoculation (for infectious sap or IVT product), by agroinfiltration (for GFP-fused infectious clone in binary vector), or by micro-bombardment (for IVT product or plasmid of infectious clone in binary vector). For rub-inoculation, the infectious sap or IVT products are respectively diluted 3 times or to 50ng/microliter in phosphate buffer 0.05M, pH 7.4 and dropped onto leaf adaxial surfaces which is pre-dusted with an abrasive such as carborundum or bentonite. The inoculum is gently spread on the abrasive-dusted leaf surface by gloved fingers or cotton buds; after 30 seconds the inoculated leaf is washed with water. Micro-bombardment of infectious clones is conducted following previously described methods (see, e.g., delivery techniques described in PCT/US22/78963; see also Bio-Rad Tech Note 2531 “Inoculation of Viral RNA and cDNA to Potato and Tobacco Plants Using the Helios™ Gene Gun”). Infiltration with an *Agrobacterium*-based viral pathogen inoculum is performed using methods similar to that used for COMSAT infiltration, but the *Agrobacterium* suspension is diluted at OD600 of 0.1.

[0332] Symptoms and titre of the acute viral pathogens are monitored in the plants, typically over time to confirm progress or decline of viral infection. Effectiveness of antiviral COMSATs is evaluated by comparing relative titres of systemic infected viruses in antiviral COMSAT-treated plants and the control plants. Tissues from inoculated leaves and systemic leaves (distal to the inoculated leaves) are collected, total RNA is extracted, optionally followed by cDNA synthesis. The viral titre can be quantitatively measured by qRT-PCR with virus-specific primers. Viral titre or presence can be measured by immunoassay methods; for example, Tobacco mosaic virus (TMV) is routinely detected in plants using a commercially available strip assay (Agdia ImmunoStrip® for TMV Agdia, Inc., Elkhart, IN, USA). Alternatively, viral titre is qualitatively evaluated by viral disease symptoms, or by proxy measurement (e.g., measuring GFP expressed by GFP-fused viral constructs). Generally, qRT-PCR measurements are normalized to endogenous reference gene controls (e.g., actin, tubulin, ubiquitin-3, GADPH, or translation elongation factor EF1a, used individually or preferably in multiples, e.g., at least 3 reference

genes or at least three deltaCt values). The viral titre (as fold changed, relative to an endogenous reference gene) is compared to that of controls.

Example 4. Vertical transmission of an anti-botrytis cargo RNA in pepper plants

[0333] This example demonstrates how an endonaviral satellite can be used to generate fungal resistant germplasm without necessitating transgenesis.

[0334] In vitro transcribed RNA molecules encoding the following constructs (listed from 5' to 3') were ballistically delivered into leaves of twelve "Ace F₁" hybrid pepper plants: (Construct 1, carrying a cargo RNA encoding dsRNAs targeting the *Botrytis cinerea* genes DCL1 and DCL2) 5'UTR_226bp-BcDCL1_dsRNA-BcDCL2_dsRNA-ZmHSP101_IRES-TMVMP-Ile-3'UTR_113bp_w_PolyC_tail (SEQ ID NO: 788); (Construct 2, carrying a cargo RNA encoding a heterologous pathogenesis-related (PR) protein that enhances resistance to bacterial and fungal pathogen infection, *Panax ginseng* pathogenesis-related protein family 10 gene, "PgPR10") 5'UTR_226bp-HCRSV_IRES-PgPR10_1-ZmHSP101_IRES-TMVMP-Ile-3'UTR_113bp_w_PolyC_tail (SEQ ID NO: 789).

[0335] Systemic mobility and persistence of these molecules was further demonstrated across these plants using RT-PCR in systemic tissues (tissue samples taken from parts of the plant distal to the site of treatment). The plants were then grown to maturity and their fruits were harvested. The pericarp of the pepper fruits was screened using RT-PCR for the presence of delivered RNA and 32% of all the assayed fruit were positive.

[0336] Seeds were collected from RT-PCR positive mature fruit of these plants, vernalized, and then planted in soil. Cotyledons from these second-generation seedlings were then collected and RNA was extracted from individual seedlings. A pooled screening strategy was used where RNA from 8 seedlings were combined, and RT-PCR was used to look for presence of the delivered RNA molecules in these tissues. A positive signal was observed in four of the 12 pooled groups. Each of the 8 individuals in two of these four positive pooled groups was analyzed by RT-PCR and one positive individual per pool was identified. Thus, these results indicate a vertical transmission rate of at least 1/24 (i.e., about 4%).

[0337] The two second-generation plants with successful vertical transmission were then grown to maturity. Here the antifungal cargo in the RNA satellite should lead to a reduction in viral virulence. Leaves from these plants were harvested and used to perform a botrytis challenge assay, using leaves from a wild-type plant as a control. A significant reduction of botrytis infection (size and severity of fungal lesions on the detached leaves) was observed in detached leaves of the second-generation plants with positive vertical transmission as compared to leaves of the wild-type control plant. Furthermore, RT-PCR confirmed the presence of the satellite PgPR10 polypeptide-encoding cargo RNA in the second-generation plants with positive vertical transmission. Resistance to *Botrytis* infection was observed in the detached leaves of second-generation plants with systemic distribution of Construct 1 (COM1) or Construct 2 (COM2).

Example 5. Detection of Satellite RNA Negative-Sense Strand

[0338] Where only the positive-sense strand of a satellite RNA is provided to a plant or plant cell (e.g., by delivery of the RNA itself or by delivery of DNA encoding the satellite RNA's positive-sense strand), replication of the satellite RNA in a plant or plant cell can be verified by detection of the satellite RNA's negative-sense strand, for example, by using a negative-sense-strand-specific Taqman® assay.

[0339] In one non-limiting example, a bell pepper endornavirus (BPEV) satellite of 2357 nucleotides was constructed with the following elements in 5' to 3' orientation: (1) BPEV 5' RNA replication element; (2) a first IRES sequence (PSVI IRES, with the addition of spacer nucleotides on the 5' end); (3) RNA encoding a reporter protein (GFP); (4) a second IRES sequence (ZmHSP IRES); (5) a viral movement protein; (6) a zebrafish sequence (as a non-plant heterologous sequence for detection purposes); (7) an isoleucine tRNA sequence; (8) BPEV 3' RNA replication element. This construct included several genetic elements that were also incorporated in the constructs described in Examples 1 and 2, but without the TMV 5' and 3' replication region sequences. Similar satellites can be designed and constructed using alternative genetic elements such as those provided elsewhere in this specification, such as other pairs of 5' and 3' RNA replication elements, other pairs of HRV 5' and 3' replication region sequences, and/or other cargo sequences.

[0340] The positive-sense strand of this BPEV satellite RNA was produced through in vitro transcription (IVT), and biolistically delivered with a gene gun into bell pepper plant leaves. Samples were collected 4 weeks post gene gun firing from a local leaf. Samples underwent RNA extraction, library prep, and Illumina® sequencing using a stranded kit (NEBNext® Ultra™ II Directional RNA Library Prep Kit for Illumina®, catalogue numbers E7760S or E7760L, New England Biolabs, Ipswich, MA) with added DMSO treatment and plant rRNA depletion. Reads were mapped against the BPEV satellite RNA's sequence and negative-sense reads were identified using the Integrative Genomics Viewer (IGV) browser (Robinson et al., Bioinformatics, 39(1) (2023), btac830). Negative-sense reads mapping to the BPEV satellite were present, confirming that replication of the BPEV satellite had occurred. BPEV negative-sense reads were also identified in BPEV infected plants that served as a positive control for the analysis.

Example 6. Detection of Satellite RNA Negative-Sense Strand in a Tomato Plant

[0341] Where only the positive-sense strand of a satellite RNA is provided to a plant or plant cell (e.g., by delivery of the RNA itself or by delivery of DNA encoding the satellite RNA's positive-sense strand), replication of the satellite RNA in a plant or plant cell can be verified by detection of the satellite RNA's negative-sense strand, for example, by using a negative-sense-strand-specific Taqman® assay.

[0342] Negative sense GFP produced by a satellite RNA containing a GFP protein encoding cargo sequences is detected using Taqman® qPCR. The reference sequence that can be used is an endogenous tomato gene, "Tom06" (NCBI Gene ID 101249087, ubiquitin-conjugating enzyme E2-17 kDa, from *Solanum lycopersicum*). Taqman® qPCR primers and probes were ordered from Integrated DNA Technology, Coralville, IA. The negative sense GFP probe is labeled with FAM520 dye with ZEN/Iowa

Black FQ quencher. The Tom06 probe is labeled with SUN5544 with ZEN/Iowa Black FQ quencher. Primers and probes are used at a 2:1 ratio. cDNA is synthesized via reverse transcription (30 minutes at 60 degrees C, then 10 minutes at 85 degrees C) using Maxima H Minus First Strand cDNA synthesis Kit (K1652, Thermo Fisher Scientific, Waltham MA) using the RT primers in Table 28. This was followed by treatment (30 minutes at 37 degrees C, then 1 minute at 80 degrees C) with thermolabile exonuclease I (E1050 New England Biolabs, Ipswich MA) to remove excess RT primers. The synthesized cDNA was cleaned with RNAClean XP beads (A63987 Beckman Coulter, Brea CA). Taqman® qPCR is carried out using Taqman® Advanced Fast MasterMix (444965, Thermo Fisher Scientific, Waltham MA) and the primer and probes in Table 29.

Table 28. Description of Reverse Transcriptase Primers

RT Primer Name	RT Primer Sequence
negative GFP reverse transcription primer	ccactggattcagcgaagtATGCGTAAAGGCGAAGAG (SEQ ID NO: 1531)
Tom06 (solanaceous house keeping reverse transcription primer)	CTGAGTCCAGCTACGAGCAG (SEQ ID NO: 1532)

Table 29. Description of qPCR primers and probes

qPCR Primer/Probe Name	qPCR Primer/Probe Sequence
negative GFP forward primer	CCACTGGATTCAGCGAAGT (SEQ ID NO: 1533)
negative GFP reverse primer	AACTTCAGCGTCAGTTTACCA (SEQ ID NO: 1534)
negative GFP probe	/6-FAM/CGAGGGTGA/ZEN/AGGTGACGCAACTA/3IABkFQ/ (SEQ ID NO: 1535)
Tom06 forward primer	CCTGCTGTCCATCTGCTCTC (SEQ ID NO: 1536)
Tom06 reverse primer	CTGAGTCCAGCTACGAGCAG (SEQ ID NO: 1537)
Tom06 probe	/5SUN/ACAAGACTG/ZEN/ACAGGGCCAAA /3IABkFQ/ (SEQ ID NO: 1538)

Example 7. Injection of citrus trees with an antiviral Endornaviral satellite for resistance to Citrus tristeza virus

[0343] An antiviral endornaviral satellite with an imbedded HRV amplicon designed to promote secondary amplification by Citrus tristeza virus is provided in 5' to 3' orientation as follows: (i) 5' replication element from an endornavirus; (ii) an HRV amplicon in either sense or anti-sense orientation comprising a Citrus tristeza virus 5' replication region (HRV 5'RR) which is operably linked to RNA encoding an antiviral protein cargo or antiviral RNA cargo (*e.g.*, an RNA molecule which induces an RNAi response) which is operably linked to the Citrus tristeza virus 3' RNA replication region (HRV 3'RR); and (iii) the 3' RNA replication element from an endornavirus is provided. The antiviral protein or RNA cargo can be specifically anti-CTV or have broader antiviral activity.

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[0344] The endornaviral satellite is delivered via application and/or injection into citrus trees (see, e.g., US Patent No. 11,844,318, International Patent Application publication WO2023/240208, Al-Rimawi *et al.* (2019) *Antibiotics*, 8, 196; doi:10.3390/antibiotics8040196, each incorporated herein by reference in their entirety). In embodiments, the endornaviral satellite is delivered into the vascular system (e.g., xylem) of a citrus tree, for example, by injection directly into the tree's vascular system. Citrus trees containing the endornavirus or that otherwise are provided with the appropriate endornaviral RdRP that recognizes the 5' and 3' RNA replication element of the endornaviral satellites (and, in the case of constructs containing an HRV amplicon, also containing or otherwise provided with a CTV RdRP) and that are provided with these antiviral endornaviral satellites are expected to exhibit resistance to Citrus tristeza virus.

Other Embodiments

[0345] Although the foregoing disclosure has been described in some detail by way of illustration and example for purposes of clarity of understanding, the descriptions and examples should not be construed as limiting the scope of the disclosure.

[0346] Other embodiments are within the claims.

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WHAT IS CLAIMED IS:

1. A recombinant RNA molecule comprising from 5' terminus to 3' terminus:

- (a) a 5' RNA replication element recognized by an endornavirus RNA-dependent RNA polymerase (RdRP);
- (b) a cargo RNA molecule; and
- (c) a 3' RNA replication element recognized by the RdRP;

wherein the 5' RNA replication element, the cargo RNA molecule, and the 3' RNA replication element are operably linked; wherein the cargo RNA molecule is heterologous to the 5' RNA replication element and the 3' RNA replication element; and, optionally, wherein: (i) the 5' RNA replication element and the 3' RNA replication element are obtained from the same endornavirus genome or from endornavirus genomes having at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another; (ii) the 5' RNA replication element, the 3' RNA replication element, and the RdRP are obtained from the same endornavirus genome or from endornavirus genomes having at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another; or (iii) the 5' RNA replication element, the 3' RNA replication element, and/or the RdRP coding region are obtained from different endornavirus genomes, and wherein the members of each respective set of the 5' RNA replication elements, 3' RNA replication elements, and/or the RdRP coding regions have at least 85%, 90%, 95%, 98%, or 99% sequence identity to one another.

2. The recombinant RNA molecule of claim 1, wherein:

(a) the 5' RNA replication element comprises at least one RNA secondary structure provided in Table 19, 20, 21, and/or 25 or adopted by an RNA molecule encoded by SEQ ID NO: 466 to 522, 727, or 924 to 1017; and/or

(b) the 3' RNA replication element comprises at least one RNA secondary structure provided in Table 22, 23, 24, and/or 25 or adopted by an RNA molecule encoded by SEQ ID NO: 523 to 595, 728, or 1019 to 1129.

3. The recombinant RNA molecule of claim 1, wherein:

(a) the 5' RNA replication element comprises an RNA molecule encoded by SEQ ID NO: 466 to 522, 727, or 924 to 1017; a variant thereof encoded by a DNA molecule having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% sequence identity to SEQ ID NO: 466 to 522, 727, or 924 to 1017; or a variant thereof wherein one or more nucleotides in the RNA secondary structure are substituted with distinct nucleotides which maintain the RNA secondary structure; and/or

(b) the 3' RNA replication element comprises an RNA molecule encoded by SEQ ID NO: 523 to 595, 728, or 1019 to 1129, or; a variant thereof encoded by a DNA molecule having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% sequence identity to SEQ ID NO: 523 to 595, 728, or 1019 to 1129; or a variant thereof wherein one or more base-paired residues in the RNA secondary structure are substituted with distinct nucleotides which maintain the RNA secondary structure.

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4. The recombinant RNA molecule of claim 3, wherein the RNA secondary structure is maintained by substituting nucleotides in the secondary structure which are not base paired with nucleotides which will not base pair, and/or by substituting nucleotides in the secondary structure which are base paired with nucleotides which will base pair.

5. The recombinant RNA molecule of claim 1, wherein:

(a) the 5' RNA replication element comprises at least a segment of the 5' untranslated region (UTR) of the endornavirus genome or a variant thereof having one or more nucleotide substitutions, insertions, and/or deletions, wherein the variant is recognized by the RdRP, optionally wherein the 5' RNA replication element further comprises a genomic sequence of the endornavirus that is natively located 3' to and adjacent to the 5' UTR sequence; and/or

(b) the 3' RNA replication element comprises at least a segment of the 3' UTR of the endornavirus genome or a variant thereof having one or more nucleotide substitutions, insertions, and/or deletions, wherein the variant is recognized by the RdRP, optionally wherein the 3' RNA replication element further comprises a genomic sequence of the endornavirus that is natively located 5' to and adjacent to the 3' UTR sequence, and optionally wherein the endornavirus genome of (a) and (b) are the same.

6. The recombinant RNA molecule of claim 1, wherein the RNA molecule further comprises at least one of: (i) a tRNA-like element, optionally wherein the tRNA-like element provides for intercellular movement of the RNA and optionally wherein the intercellular movement is mediated by a viral movement protein (MP); (ii) an encapsidation recognition element (ERE), optionally wherein the ERE provides for encapsidation of the RNA by a endornavirus capsid protein or optionally wherein the ERE provides for encapsidation of the RNA by a non-endornavirus capsid protein; (iii) an RNA effector; and/or (iv) RNA encoding a viral movement protein (MP), optionally wherein an internal ribosome entry site (IRES) is operably linked to the RNA encoding the MP.

7. The recombinant RNA molecule of claim 6, wherein the tRNA-like element comprises a tRNA-like molecule from an *Arabidopsis* FT mRNA or is a tRNA-like sequence encoded by a DNA sequence selected from the group consisting of SEQ ID NOs: 76-123, and 790, or is a modified tRNA-like sequence that has at least 90% sequence identity to a scaffold tRNA-like sequence encoded by a DNA sequence selected from the group consisting of SEQ ID NOs: 76-123, or 790 and that maintains the secondary structure of the scaffold tRNA-like sequence, and/or wherein the ERE is a tobacco mosaic virus (TMV) OAS.

8. The recombinant RNA molecule of claim 1, wherein the cargo RNA molecule is up to about 14kb, 15kb, 16kb, or 17kb in length.

9. The recombinant RNA molecule of claim 1, wherein the cargo RNA molecule comprises: (a) at least one coding sequence, optionally wherein the coding sequence encodes a selectable or scoreable marker;

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(b) at least one non-coding sequence; or (c) both at least one coding sequence and at least one non-coding sequence.

10. The recombinant RNA molecule of claim 1, wherein the cargo RNA molecule comprises at least one coding sequence, and wherein the RNA molecule further comprises an internal ribosome entry site (IRES) which is operably linked to at least one coding sequence, optionally wherein the operably linked IRES is located 5' and immediately adjacent to the coding sequence.

11. The recombinant RNA molecule of claim 1, wherein the cargo RNA molecule comprises at least one non-coding sequence, and wherein the at least one non-coding sequence is a hairpin RNA (hpRNA); an RNA that forms multiple stem-loops; an RNA pseudoknot; an RNA molecule that forms at least partially double-stranded RNA; a small interfering RNA (siRNA) or siRNA precursor; a microRNA (miRNA) or miRNA precursor; a phased RNA or phased RNA precursor; a ribozyme; a ligand-responsive ribozyme (aptazyme); an RNA aptamer; or a long noncoding RNA (lncRNA).

12. The recombinant RNA molecule of claim 1, further comprising an RNA comprising encoding at least one ribozyme, optionally wherein the at least one ribozyme is located 5' to the 5' RNA replication element or 3' to the 3' RNA replication element.

13. The recombinant RNA molecule of claim 1, further comprising an RNA molecule comprising at least one ligand-responsive ribozyme (aptazyme), optionally wherein the at least one ligand-responsive ribozyme is located 5' to the 5' RNA replication element or 3' to the 3' RNA replication element.

14. The recombinant RNA molecule of claim 1, wherein: (i) the RNA further comprises at least a segment of its reverse complementary RNA molecule; and/or (ii) the recombinant RNA molecule is complexed with one or more RNA binding proteins or encapsidated by a viral capsid protein, optionally wherein the viral capsid protein is a endornavirus capsid protein, optionally wherein the RNA comprises an ERE which provides for encapsidation of the RNA by the endornavirus capsid protein, and/or optionally wherein the RNA binding proteins comprise an RNA recognition motif.

15. The recombinant RNA molecule of claim 1, wherein the RNA molecule comprises:
at least one heterologous RNA virus (HRV) amplicon in sense or antisense orientation to the first 5' RNA replication element comprising:

I. (i) a heterologous RNA virus (HRV) 5' replication region (HRV 5'RR); (ii) the cargo RNA molecule; and (iii) the heterologous RNA virus (HRV) 3' RNA replication region (HRV 3'RR); wherein the HRV 5' RR and HRV 3' RR HRV are recognized by a heterologous RNA virus RNA-dependent RNA polymerase (hrvRdRP); and wherein the HRV 5'RR, cargo RNA molecule, and HRV 3'RR are operably linked; or

II. a heterologous RNA virus (HRV) subgenomic promoter operably linked to the cargo RNA molecule; wherein the subgenomic promoter is recognized by a heterologous RNA virus RNA-dependent RNA polymerase (hrvRdRP).

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16. The recombinant RNA of claim 15, wherein the RNA molecule comprises from 5' terminus to 3' terminus:

(a) the 5' RNA replication element;

(b) the HRV amplicon in antisense orientation to the first 5' RNA replication element; optionally wherein the HRV amplicon further comprises:

(i) an RNA molecule encoding an HRV RNA-dependent RNA polymerase (hrvRdRP) which is operably linked to the HRV 5'RR and HRV 3'RR, wherein the RNA molecule encoding the HRV RNA-dependent RNA polymerase (hrvRdRP) is optionally operably linked to a subgenomic promoter recognized by the hrvRdRP; or

(ii) an RNA molecule encoding an HRV RNA-dependent RNA polymerase (hrvRdRP) which is operably linked to linked to a subgenomic promoter recognized by the hrvRdRP; and

(c) the 3' RNA replication element.

17. The recombinant RNA of claim 15, wherein the HRV 5'RR, HRV 3'RR, and hrvRdRP comprise an HRV 5'RR, HRV 3'RR, and hrvRdRP from a virus selected from the group consisting of a Alphaflexivirus, Betaflexivirus, Bromovirus, Celavirus, a Closterovirus, a Comovirus, a Potexvirus, Potyvirus, Tobamovirus, Tombusvirus, Tospoviridae, Trivirinae, and Tymovirus, Varicosavirus, and Secoviridae.

18. The recombinant RNA of claim 17, wherein: (i) the Bromovirus is a Cucumber Mosaic Virus, Spinach latent virus, Olive latent virus, or Brome mosaic virus; (ii) the Closterovirus is a Citrus tristeza virus or Beet yellows virus; (iii) the Comovirus is Cowpea mosaic virus, Apple latent spherical virus, or Soybean latent spherical virus; (iv) the Potexvirus is Potato virus X or Citrus yellow vein clearing virus; (v) the Potyvirus is a Pepper mottle virus, Bean yellow mosaic virus, Barley stripe mosaic virus, Wheat stripe mosaic virus, Rice yellow mottle virus, Maize dwarf mosaic virus, zucchini yellow mosaic virus, watermelon mosaic virus, or sugarcane mosaic virus; (vi) the Tobamovirus is a Tobacco mosaic virus, Tomato mosaic virus, Tomato brown rugose fruit virus, Turnip vein-clearing virus, or Pepper mild mottle virus; (vii) the Tombusvirus is a Turnip crinkle virus or Tomato bushy stunt virus; (iv) the Tospoviridae is a Tomato spotted wilt virus or watermelon bud necrosis virus; or (viii) the Tymovirus is a Turnip yellow mosaic virus, Citrus yellow vein clearing virus, Potato latent virus, Apple stem grooving virus, or Citrus leaf blotch virus.

19. The recombinant RNA of claim 15, wherein the HRV 5' RR and the HRV 3' RR are obtained from the same HRV genome.

20. The recombinant RNA of claim 15, wherein the HRV 5' RR and the HRV 3' RR are obtained from distinct HRV genomes.

21. The recombinant RNA molecule of claim 15, wherein:

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(a) the HRV 5' RR comprises at least one RNA secondary structure adopted by an RNA encoded by SEQ ID NO: 161 to 185, or 186, or comprises the RNA sequence encoded by SEQ ID NO: 161 to 185, or 186, or comprises a contiguous fragment of at least 80%, 85%, 90%, or 95% of the full sequence of the RNA encoded by SEQ ID NO: 161 to 185, or 186; and/or

(b) the HRV 3' RR comprises at least one RNA secondary structure adopted by an RNA encoded by SEQ ID NO: 187 to 211, or 212, or comprises the RNA sequence encoded by SEQ ID NO: 187 to 211, or 212, or comprises a contiguous fragment of at least 80%, 85%, 90%, or 95% of the full sequence of the RNA encoded by SEQ ID NO: 187 to 211, or 212.

22. The recombinant RNA molecule of claim 15, wherein:

(a) the HRV 5' RR is encoded by a DNA molecule comprising SEQ ID NO: 161 to 185, or 186 ; or a variant thereof comprising DNA having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% sequence identity to SEQ ID NO: 161 to 185, or 186 ; or a variant thereof wherein one of more residues in the RNA secondary structure are substituted with distinct nucleotides which maintain the RNA secondary structure; and/or

(b) the HRV 3' RR is encoded by a DNA molecule comprising SEQ ID NO: 187 to 211, or 212; or a variant thereof comprising DNA having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% sequence identity to SEQ ID NO: 187 to 211, or 212; or a variant thereof wherein one of more residues in the RNA secondary structure are substituted with distinct nucleotides which maintain the RNA secondary structure.

23. The recombinant RNA molecule of claim 15, wherein:

(a) the HRV 3' RR comprises an RNA molecule containing at least a segment of the 3' untranslated region (UTR) of the HRV genome, or a variant thereof having one or more nucleotide substitutions, insertions, and/or deletions, wherein the HRV 3' RR or the variant is recognized by the hrvRdRP, optionally wherein the RNA comprising the HRV 3' RR further comprises a genomic sequence of the HRV that is natively located 5' to and adjacent to the 3' UTR sequence; and/or

(d) the HRV 5' RR comprises an RNA molecule containing at least a segment of the 3' untranslated region (UTR) of the HRV genome, or a variant thereof having one or more nucleotide substitutions, insertions, and/or deletions, wherein the HRV 5' RR or the variant is recognized by the hrvRdRP, optionally wherein the RNA comprising the HRV 5' RR further comprises a genomic sequence of the HRV that is natively located 3' to and adjacent to the 5' UTR sequence.

24 The recombinant RNA molecule of claim 15, wherein the cargo RNA comprises an HRV-inhibitory RNA or encodes an HRV-inhibitory protein, wherein the HRV-inhibitory RNA or HRV-inhibitory protein inhibits infection, movement, transmission, and/or replication of the HRV.

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25. The recombinant RNA molecule of claim 15, wherein the cargo RNA comprises an RNA having at least 20 to 25 contiguous nucleotides having an identical or complementary sequence to a segment of equivalent length of the genomic RNA of the HRV.

26. The recombinant RNA molecule of claim 15, wherein the cargo RNA comprises an RNA having at least 20 to 25 contiguous nucleotides having an identical or complementary sequence to a segment of equivalent length of the genomic RNA of the HRV which does not encode the hrvRdRP.

27. The recombinant RNA molecule of claim 15, wherein:

(i) the HRV is a Cucumber Mosaic Virus and the HRV 5'RR comprises an RNA encoded by the Cucumber Mosaic Virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Cucumber Mosaic Virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Cucumber Mosaic Virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Cucumber Mosaic Virus 3' RR DNA sequence in Table 7; or _____;

(ii) the HRV is a Brome mosaic virus and the HRV 5'RR comprises an RNA encoded by the Brome mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Brome mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Brome mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Brome mosaic virus 3' RR DNA sequence in Table 7;

(iii) the HRV is a Citrus tristeza virus and the HRV 5'RR comprises an RNA encoded by the Citrus tristeza virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus tristeza virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Citrus tristeza virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus tristeza virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus tristeza virus RdRP sequence in Table 7;

(iv) the HRV is Beet yellows virus and the HRV 5'RR comprises an RNA encoded by the Beet yellows virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Beet yellows virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Beet yellows virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Beet yellows virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Beet yellows virus RdRP sequence in Table 7

(v) the HRV is Cowpea mosaic virus and the HRV 5'RR comprises an RNA encoded by the Cowpea mosaic virus 5' RR DNA sequence in Table 7 or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Cowpea mosaic virus 5' RR DNA sequence in Table 7;

(vi) the HRV is Potato virus X and the HRV 5'RR comprises an RNA encoded by the Potato virus X 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Potato virus X 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Potato virus X 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Potato virus X 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Potato virus X RdRP sequence in Table 7;

(vii) the HRV is Pepper mottle virus and the HRV 5'RR comprises an RNA encoded by the Pepper mottle virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Pepper mottle virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Pepper mottle virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Pepper mottle virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Pepper mottle virus RdRP sequence in Table 7;

(viii) the HRV is Bean yellow mosaic virus and the HRV 5'RR comprises an RNA encoded by the Bean yellow mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Bean yellow mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Bean yellow mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Bean yellow mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Bean yellow mosaic virus RdRP sequence in Table 7;

(ix) the HRV is Barley stripe mosaic virus and the HRV 5'RR comprises an RNA encoded by the Barley stripe mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Barley stripe mosaic virus 5' RR DNA sequence in Table 7, and the HRV 3' RR comprises an RNA encoded by the Barley stripe mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Barley stripe mosaic virus 3' RR DNA sequence in Table 7;

(x) the HRV is Wheat stripe mosaic virus and the HRV 5'RR comprises an RNA encoded by the Wheat stripe mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Wheat stripe mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Wheat stripe mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Wheat stripe mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Wheat stripe mosaic virus RdRP sequence in Table 7;

(xi) the HRV Rice yellow mottle virus and the HRV 5'RR comprises an RNA encoded by the Rice yellow mottle virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Rice yellow mottle virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Rice yellow mottle virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Rice yellow mottle virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Rice yellow mottle virus RdRP sequence in Table 7;

(xii) the HRV is Maize dwarf mosaic virus and the HRV 5'RR comprises an RNA encoded by the Maize dwarf mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Maize dwarf mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Maize dwarf mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Maize dwarf mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Maize dwarf mosaic virus RdRP sequence in Table 7;

(xiii) the HRV is zucchini yellow mosaic virus and the HRV 5'RR comprises an RNA encoded by the Zucchini yellow mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Zucchini yellow mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Zucchini yellow mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Zucchini yellow mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Zucchini yellow mosaic virus RdRP sequence in Table 7;

(xiv) the HRV is watermelon mosaic virus and the HRV 5'RR comprises an RNA encoded by the Watermelon mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Watermelon mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Watermelon mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Watermelon mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Watermelon mosaic virus RdRP sequence in Table 7;

(xv) the HRV is sugarcane mosaic virus and the HRV 5'RR comprises an RNA encoded by the Sugarcane mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Sugarcane mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Sugarcane mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the

Sugarcane mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Sugarcane mosaic virus RdRP sequence in Table 7;

(xvi) the HRV is Tobacco mosaic virus and the HRV 5'RR comprises an RNA encoded by the Tobacco mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tobacco mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Tobacco mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tobacco mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Tobacco mosaic virus RdRP sequence in Table 7;

(xvii) the HRV is Tomato mosaic virus and the HRV 5'RR comprises an RNA encoded by the Tomato mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Tomato mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato mosaic virus RdRP sequence in Table 7;

(xviii) the HRV is Tomato brown rugose fruit virus and the HRV 5'RR comprises an RNA encoded by the Tomato brown rugose fruit virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato brown rugose fruit virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Tomato brown rugose fruit virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato brown rugose fruit virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato brown rugose fruit virus RdRP sequence in Table 7;

(xix) the HRV is Turnip vein-clearing virus and the HRV 5'RR comprises an RNA encoded by the Turnip vein-clearing virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip vein-clearing virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Turnip vein-clearing virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip vein-clearing virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip vein-clearing virus RdRP sequence in Table 7;

(xx) the HRV is Pepper mild mottle virus and the HRV 5'RR comprises an RNA encoded by the Pepper mild mottle virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Pepper mild mottle virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Pepper mild mottle virus 3' RR DNA

sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Pepper mild mottle virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Pepper mild mottle virus RdRP sequence in Table 7;

(xxi) the HRV is Turnip crinkle virus and the HRV 5'RR comprises an RNA encoded by the Turnip crinkle virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip crinkle virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Turnip crinkle virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip crinkle virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip crinkle virus RdRP sequence in Table 7;

(xxii) the HRV is Tomato bushy stunt virus and the HRV 5'RR comprises an RNA encoded by the Tomato bushy stunt virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato bushy stunt virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Tomato bushy stunt virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato bushy stunt virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato bushy stunt virus RdRP sequence in Table 7;

(xxiii) the HRV is Tomato spotted wilt virus and the HRV 5'RR comprises an RNA encoded by the Tomato spotted wilt virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato spotted wilt virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Tomato spotted wilt virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato spotted wilt virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Tomato spotted wilt virus RdRP sequence in Table 7;

(xxiv) the HRV is watermelon bud necrosis virus and the HRV 5'RR comprises an RNA encoded by the Watermelon bud necrosis virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Watermelon bud necrosis virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Watermelon bud necrosis virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Watermelon bud necrosis virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Watermelon bud necrosis virus RdRP sequence in Table 7; or

(xxv) the HRV is Turnip yellow mosaic virus and the HRV 5'RR comprises an RNA encoded by the Turnip yellow mosaic virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at

least 85%, 90%, 95%, or 99% sequence identity to the Turnip yellow mosaic virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Turnip yellow mosaic virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip yellow mosaic virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Turnip yellow mosaic virus RdRP sequence in Table 7;

(xxvi) the HRV is Spinach latent virus and the HRV 5'RR comprises an RNA encoded by the Spinach latent virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Spinach latent virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Spinach latent virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Spinach latent virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Spinach latent virus RdRP sequence of SEQ ID NO: 516;

(xxvii) the HRV is Spinach latent virus and the HRV 5'RR comprises an RNA encoded by the Spinach latent virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Spinach latent virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Spinach latent virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Spinach latent virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Spinach latent virus RdRP sequence of SEQ ID NO: 517;

(xxviii) the HRV is Olive latent virus 2 and the HRV 5'RR comprises an RNA encoded by the Olive latent virus 2 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Olive latent virus 2 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Olive latent virus 2 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Olive latent virus 2 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Olive latent virus 2 RdRP sequence in Table 7;

(xxix) the HRV is Citrus yellow vein clearing virus and the HRV 5'RR comprises an RNA encoded by the Citrus yellow vein clearing virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus yellow vein clearing virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Citrus yellow vein clearing virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus yellow vein clearing virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus yellow vein clearing virus RdRP sequence in Table 7;

(xxx) the HRV is Potato latent virus and the HRV 5'RR comprises an RNA encoded by the Potato latent virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%,

90%, 95%, or 99% sequence identity to the Potato latent virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Potato latent virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Potato latent virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Potato latent virus RdRP sequence in Table 7;

(xxxix) the HRV is Apple stem grooving virus and the HRV 5'RR comprises an RNA encoded by the Apple stem grooving virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Apple stem grooving virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Apple stem grooving virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Apple stem grooving virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Apple stem grooving virus RdRP sequence in Table 7;

(xxxix) the HRV is Citrus leaf blotch virus and the HRV 5'RR comprises an RNA encoded by the Citrus leaf blotch virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus leaf blotch virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Citrus leaf blotch virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus leaf blotch virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Citrus leaf blotch virus RdRP sequence in Table 7;

(xxxix) the HRV is Apple latent spherical virus and the HRV 5'RR comprises an RNA encoded by the Apple latent spherical virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Apple latent spherical virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Apple latent spherical virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Apple latent spherical virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Apple latent spherical virus RdRP sequence in Table 7; or

(xxv) the HRV is Soybean latent spherical virus and the HRV 5'RR comprises an RNA encoded by the Soybean latent spherical virus 5' RR DNA sequence in Table 7, an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Soybean latent spherical virus 5' RR DNA sequence in Table 7, the HRV 3' RR comprises an RNA encoded by the Soybean latent spherical virus 3' RR DNA sequence in Table 7, or an RNA encoded by a DNA having at least 85%, 90%, 95%, or 99% sequence identity to the Soybean latent spherical virus 3' RR DNA sequence in Table 7, and the RdRP comprises a protein having at least 85%, 90%, 95%, or 99% sequence identity to the Soybean latent spherical virus RdRP sequence in Table 7.

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28. The recombinant RNA molecule of claim 15, further comprising an RNA comprising encoding at least one cleavable sequence, optionally wherein the at least one cleavable sequence is located: (i) 5' to the 5' RNA replication element or 3' to the 3' RNA replication element; and/or (ii) between the 3' end of the 5' RNA replication element and the HRV amplicon and/or between the HRV amplicon and the 5' end of the 3' RNA replication element, wherein the cleavable sequence is optionally a self-cleaving ribozyme, a self-cleaving inducible ribozyme, or an siRNA or miRNA recognition site.

29. An agricultural formulation comprising the recombinant RNA molecule of any one of claims 1 to 28.

30. The agricultural formulation of claim 29, wherein the recombinant RNA molecule is complexed with one or more RNA binding proteins or encapsidated by a viral capsid protein, optionally wherein the viral capsid protein is a endornavirus capsid protein and optionally wherein the RNA comprises an ERE which provides for encapsidation of the RNA by the endornavirus capsid protein.

31. The agricultural formulation of claim 30, wherein the RNA binding proteins comprise an RNA recognition motif.

32. The agricultural formulation of claim 30, wherein the viral capsid protein is heterologous to the endornavirus.

33. The agricultural formulation of claim 29, wherein the formulation comprises the recombinant RNA molecule and a carrier, an excipient, and/or an adjuvant.

34. A cell comprising the recombinant RNA molecule of any one of claims 1 to 28, wherein the cell is a bacterial cell, a fungal cell, a plant cell, an insect cell, or an invertebrate animal cell.

35. The cell of claim 34, wherein the cell is a plant cell and DNA which encodes the recombinant RNA molecule is absent from the cell.

36. The cell of claim 34, wherein the cell comprises a recombinant DNA molecule which encodes the recombinant RNA molecule.

37. An expression system comprising:

(a) an RNA molecule comprising the recombinant RNA molecule of any one of claims 1 to 28; and

(b) a cell containing the recombinant RNA molecule and an RdRP protein that recognizes the 5' and 3' RNA replication elements of the recombinant RNA molecule.

38. The expression system of claim 37, wherein the recombinant RNA molecule comprises an operably linked encapsidation recognition element (ERE) recognized by a viral capsid protein, and wherein the cell contains the viral capsid protein.

39. The expression system of claim 37, wherein the viral capsid protein comprises the viral capsid protein of any one of SEQ ID NOs: 26 to 50.

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40. The expression system of claim 37, further comprising the reverse complement of the recombinant RNA molecule.

41. The expression system of claim 37, wherein the cell is a bacterial cell, a plant cell, a fungal cell, an insect cell, or an invertebrate animal cell.

42. The expression system of claim 37, wherein the cell further comprises: (i) a viral capsid protein (CP), (ii) an RNA-binding protein (RBP) that can bind to the RNA molecule, optionally wherein the RBP binds to an RNA effector; (iii) an RNA cleavage agent that cleaves the RNA molecule; (iv) a second RNA-dependent RNA polymerase (RdRP) protein that recognizes an HRV 5' or 3' replication region and/or a subgenomic promoter in the RNA molecule (2nd RdRP); (v) a viral movement protein (MP); (v) a heterologous RNA virus (HRV); or (vi) an hrvRdRP, optionally wherein the hrvRdRP recognizes the HRV 5' or 3' replication region and/or the subgenomic promoter.

43. The expression system of claim 42, wherein the CP, RBP, RdRP, 2nd RdRP, hrvRdRP, and/or the MP is: (a) expressed by a recombinant DNA molecule in the cell; (b) provided exogenously to the cell; (c) expressed by a recombinant RNA molecule in the cell; or (d) expressed by a virus in the cell.

44. The expression system of claim 42, wherein the RdRP, CP, RBP, 2nd RdRP, hrvRdRP, and/or the MP protein is heterologous to the cell.

45. The expression system of claim 42, wherein the RdRP, 2nd RdRP, or hrvRdRP protein or a polynucleotide encoding the RdRP, 2nd RdRP, or hrvRdRP protein is (a) expressed by a recombinant DNA molecule in the cell; (b) provided exogenously to the cell; (c) expressed by a recombinant RNA molecule in the cell; or (d) expressed by a virus in the cell.

46. The expression system of claim 37, wherein the cell is a plant cell.

47. The expression system of claim 46, wherein the plant cell contains an endornavirus which expresses the RdRP protein that recognizes the 5' RNA replication element and the 3' RNA replication element and/or wherein the plant cell contains an HRV that expresses the 2nd RdRP or hrvRdRP protein.

48. The expression system of claim 47, wherein the endornavirus occurs naturally in the plant cell.

49. A method of providing a synthetic endornavirus satellite RNA to a plant, comprising contacting the plant with the recombinant RNA molecule of any one of claims 1 to 28.

50. The method of claim 49, wherein contacting comprises spraying, dusting, injecting, or soaking the plant or a part thereof with the recombinant RNA molecule or the formulation.

51. The method of claim 49, further comprising providing an hrvRdRP to the plant which recognizes the HRV 5' or 3' replication region and/or the subgenomic promoter, optionally wherein the hrvRdRP is provided by introducing a recombinant DNA or RNA encoding the hrvRdRP into the plant or a part thereof.

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52. A method of establishing a synthetic endornavirus satellite RNA in a plant cell, comprising:
providing to a plant cell the recombinant RNA molecule of any one of claims 1 to 28;
wherein the plant cell comprises an RdRP protein that recognizes the 5' RNA replication element and 3' RNA replication element, wherein the RNA molecule is optionally comprises an ERE and is encapsidated by a capsid protein,
whereby the RdRP protein catalyzes synthesis of the synthetic endornavirus satellite RNA from the recombinant RNA molecule.
53. The method of claim 52, wherein the plant cell comprises an endornavirus and wherein the RdRP protein is provided to the plant cell by the endornavirus.
54. The method of claim 52, wherein the endornavirus is endemic to the plant cell, optionally wherein the endornavirus which is endemic to the plant cell is non-pathogenic and/or commensal.
55. The method of claim 52, wherein the capsid protein comprises a viral capsid protein of SEQ ID NO: 26 to 50.
56. The method of claim 52, further comprising providing an hrvRdRP to the plant which recognizes the HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA, optionally wherein the hrvRdRP is provided by introducing a recombinant DNA or RNA encoding the hrvRdRP into the plant or a part thereof.
57. A method of obtaining a phenotypic change in a plant or plant cell, comprising: providing to a plant or plant cell a recombinant RNA molecule of any one of claims 1 to 28, wherein the cargo RNA molecule comprises RNA that effects a phenotypic change in the plant or plant cell in comparison to a plant or plant cell lacking the recombinant RNA, wherein the plant or plant cell comprises an RdRP protein that recognizes the 5' RNA replication element and 3' RNA replication element and catalyzes synthesis of a synthetic endornavirus RNA from the recombinant RNA molecule, and wherein the cargo RNA molecule effects the phenotypic change.
58. The method of claim 57, wherein the RNA that effects a phenotypic change in the plant or plant cell comprises at least one RNA selected from an siRNA or siRNA precursor, a miRNA or miRNA precursor, and a phased siRNA or phased siRNA precursor.
59. The method of claim 57, wherein the RNA that effects a phenotypic change in the plant or plant cell comprises a messenger RNA.
60. The method of claim 59, wherein the messenger RNA comprises an RNA molecule absent in the genome of the plant or plant cell.
61. The method of claim 57, wherein the RNA that effects a phenotypic change in the plant or plant cell comprises an RNA for modifying the genome of the plant or plant cell.

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62. The method of claim 57, wherein the RNA that effects a phenotypic change in the plant or plant cell comprises an RNA for modifying the transcriptome and/or epigenome of the plant or plant cell, optionally wherein the RNA for modifying the epigenome targets an endogenous plant gene for RNA-induced transcriptional silencing.

63. The method of claim 57, wherein the phenotypic change comprises an increase in the plant's resistance to a pest or pathogen, optionally wherein the pest or pathogen is selected from the group comprising a bacterium, a virus other than an endornavirus, a fungus, an oomycete, and an invertebrate.

64. The method of claim 63, wherein the pathogen is a heterologous RNA virus (HRV), optionally wherein the HRV is a virus selected from the group consisting of an Alphaflexivirus, Betaflexivirus, Bromovirus, Celavirus, a Closterovirus, a Comovirus, a Potexvirus, Potyvirus, Tobamovirus, Tombusvirus, Tospoviridae, Trivirinae, and Tymovirus, Varicosavirus, and Secoviridae.

65. The method of claim 64, wherein: (i) the Bromovirus is a Cucumber Mosaic Virus, Spinach latent virus, Olive latent virus, or Brome mosaic virus; (ii) the Closterovirus is a Citrus tristeza virus or Beet yellows virus; (iii) the Comovirus is Cowpea mosaic virus, Apple latent spherical virus, or Soybean latent spherical virus; (iv) the Potexvirus is Potato virus X or Citrus yellow vein clearing virus; (v) the Potyvirus is a Pepper mottle virus, Bean yellow mosaic virus, Barley stripe mosaic virus, Wheat stripe mosaic virus, Rice yellow mottle virus, Maize dwarf mosaic virus, zucchini yellow mosaic virus, watermelon mosaic virus, or sugarcane mosaic virus; (vi) the Tobamovirus is a Tobacco mosaic virus, Tomato mosaic virus, Tomato brown rugose fruit virus, Turnip vein-clearing virus, or Pepper mild mottle virus; (vii) the Tombusvirus is a Turnip crinkle virus or Tomato bushy stunt virus; (iv) the Tospoviridae is a Tomato spotted wilt virus or watermelon bud necrosis virus; or (viii) the Tymovirus is a Turnip yellow mosaic virus, Citrus yellow vein clearing virus, Potato latent virus, Apple stem grooving virus, or Citrus leaf blotch virus.

66. The method of claim 57, wherein the phenotypic change comprises an increase in the plant's resistance to stress, optionally wherein the stress comprises at least one abiotic stress comprising nutrient stress, light stress, water stress, heat stress, and/or cold stress, or optionally wherein the stress comprises at least one biotic stress comprising crowding, shading, or allelopathy.

67. The method of claim 57, wherein the recombinant RNA molecule is provided to the plant or plant cell in the form of an RNA, an encapsidated RNA, or a formulation thereof.

68. The method of claim 67, wherein the encapsidated RNA comprises a synthetic endornavirus satellite particle.

69. The method of claim 57, wherein the providing comprises contacting the plant or plant cell with the RNA, encapsidated RNA, or formulation thereof, optionally wherein contacting comprises spraying, dusting, injecting, or soaking the plant or plant cell with the RNA, encapsidated RNA, or formulation thereof.

70. The method of claim 57, wherein the recombinant RNA further comprises its reverse complementary RNA molecule.

71. The method of claim 57, further comprising providing an hrvRdRP to the plant which recognizes the HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA, optionally wherein the hrvRdRP is provided by introducing a recombinant DNA or RNA encoding the hrvRdRP into the plant or a part thereof.

72. A method of manufacturing a synthetic endornavirus satellite particle, comprising combining the recombinant RNA molecule of any one of claims 1 to 28 with a viral capsid protein, wherein the recombinant RNA molecule comprises an encapsidation recognition element (ERE), and wherein the ERE provides for encapsidation of the RNA by the viral capsid protein.

73. The method of claim 72, wherein the recombinant RNA molecule is combined with a viral capsid protein in a vessel.

74. The method of claim 73, wherein the combining comprises

(a) providing to a plant cell the recombinant RNA molecule, wherein the recombinant RNA molecule comprises an encapsidation recognition element (ERE), and wherein the plant cell comprises an RdRP protein that recognizes the 5' RNA replication element and 3' RNA replication element catalyzes synthesis of a synthetic endornavirus satellite RNA from the recombinant RNA molecule and a viral capsid protein, wherein the ERE provides for encapsidation of the RNA by the viral capsid protein; and optionally

(b) isolating the synthetic endornavirus satellite particle from the plant cell, a plant comprising the plant cell, or from media in which the plant cell or the plant had been grown.

75. The method of claim 72, further comprising the step of formulating the synthetic endornavirus satellite particle wherein the formulating comprises combining the synthetic endornavirus satellite particle with a carrier, an excipient, and/or an adjuvant.

76. A plant propagule comprising the recombinant RNA molecule of any one of claims 1 to 28 and an endornavirus RdRP, optionally wherein the plant propagule further comprises a heterologous RNA virus RdRP which recognizes an HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA.

77. The plant propagule of claim 76, wherein the plant propagule is a seed, a seedling, root, stem, leaf, shoot, tuber, rhizome, stolon, bulb, explant, embryo, or callus.

78. The plant propagule of claim 76, wherein the plant propagule is a mosaic comprising both plant cells comprising the recombinant RNA molecule and plant cells lacking the recombinant RNA molecule.

79. The plant propagule of claim 76, wherein the plant propagule lacks DNA encoding the recombinant RNA molecule.

80. The plant propagule of claim 76, wherein the plant propagule further comprises a heterologous RNA virus RdRP which recognizes an HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA, and the heterologous RNA virus RdRP is an Alphaflexivirus, Betaflexivirus, Bromovirus, Celavirus, a Closterovirus, a Comovirus, a Potexvirus, Potyvirus, Tobamovirus, Tombusvirus, Tospoviridae, Trivirinae, Tymovirus, Varicosavirus, or Secoviridae RdRP or an RdRP set forth in Table 7.
81. A plant comprising the recombinant RNA molecule of any one of claims 1 to 28 and an endornavirus RdRP, optionally wherein the plant propagule further comprises a heterologous RNA virus RdRP which recognizes an HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA.
82. The plant of claim 81, wherein the plant is a monocot or a dicot plant.
83. The plant of claim 81, wherein the plant is of the family Asteraceae, Cucurbitaceae, Fabaceae, Lauraceae, Poaceae, or Solanaceae, optionally wherein the plant is a member of the genus *Capsicum*, *Cucumis*, *Cucurbita*, *Helianthus*, *Hordeum*, *Nicotiana*, *Oryza*, *Secale*, *Solanum*, or *Triticum*.
84. The plant of claim 81, wherein the plant lacks DNA that encodes the recombinant RNA molecule.
85. The plant of claim 81, wherein the plant comprises an endornavirus, and wherein the endornavirus RdRP is provided to the plant cell by the endornavirus, optionally wherein the endornavirus RdRP comprises a protein having at least 85%, 90%, 95%, 97%, or 99% sequence identity to SEQ ID NO: 613 to 725, or 726.
86. The plant of claim 81, wherein the endornavirus is endemic to the plant, optionally wherein the endemic endornavirus is non-pathogenic and/or commensal.
87. The plant of claim 81, wherein the endornavirus RdRP, the 5' RNA replication element, and/or the 3' RNA replication element are derived from an endornavirus comprising one or both of the endornavirus RdRP, 5' RNA replication element, and/or 3' RNA replication elements.
88. The plant of claim 81, wherein the RdRP has at least 85%, 90%, 95%, 97%, 98%, or 99% identity to SEQ ID NO: 613 to 725, or 726, wherein the 5' RNA replication element has at least 85%, 90%, 95%, 97%, 98%, or 99% identity to the RNA encoded by SEQ ID NO: 466 to 522, 727, or 924 to 1017 and/or wherein the 3' RNA replication element has at least 85%, 90%, 95%, 97%, 98%, or 99% identity to the RNA encoded by SEQ ID NO: 523 to 595, 728, or 1019 to 1129.
89. The plant of claim 81, wherein the plant is a grafted plant and wherein the rootstock and/or scion of the grafted plant comprise at least one cell comprising the recombinant RNA and the endornavirus RdRP.
90. The plant of claim 81, wherein the plant is not produced by an essentially biological process.

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91. The plant of claim 81, wherein the plant further comprises a heterologous RNA virus (HRV) RdRP which recognizes an HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA, and the heterologous RNA virus RdRP is an Alphaflexivirus, Betaflexivirus, Bromovirus, Celavirus, a Closterovirus, a Comovirus, a Potexvirus, Potyvirus, Tobamovirus, Tombusvirus, Tospoviridae, Trivirinae, Tymovirus, Varicosavirus, or Secoviridae RdRP or an RdRP set forth in Table 7.

92. A endornavirus satellite system that is self-replicating when introduced into a plant or plant cell, comprising: (1) a recombinant endornavirus satellite RNA of any one of claims 1 to 28; and (2) an exogenous endornavirus that is capable of replication in the plant or plant cells and that encodes the endornavirus RdRP that recognizes the 5' and 3' RNA replication element in the recombinant endornavirus satellite RNA, optionally wherein the endornavirus satellite system further comprises a heterologous RNA virus RdRP which recognizes an HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA.

93. The self-replicating endornavirus satellite system of claim 92, wherein the exogenous endornavirus is endemic or native to a different species, variety, or germplasm of plant.

94. The self-replicating endornavirus satellite system of claim 92, wherein the endornavirus satellite system further comprises a heterologous RNA virus (HRV) RdRP which recognizes an HRV 5' or 3' replication region and/or the subgenomic promoter in the synthetic endornavirus satellite RNA, and the heterologous RNA virus RdRP is optionally an Alphaflexivirus, Betaflexivirus, Bromovirus, Celavirus, a Closterovirus, a Comovirus, a Potexvirus, Potyvirus, Tobamovirus, Tombusvirus, Tospoviridae, Trivirinae, Tymovirus, Varicosavirus, or Secoviridae.



Figure 1

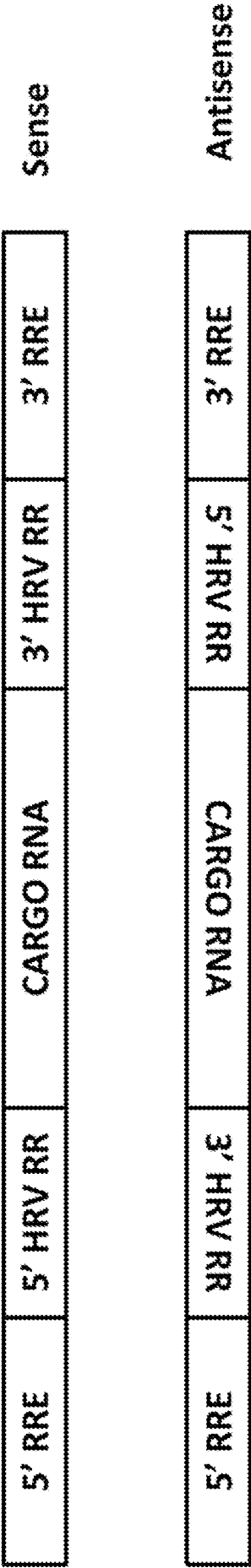


Figure 2

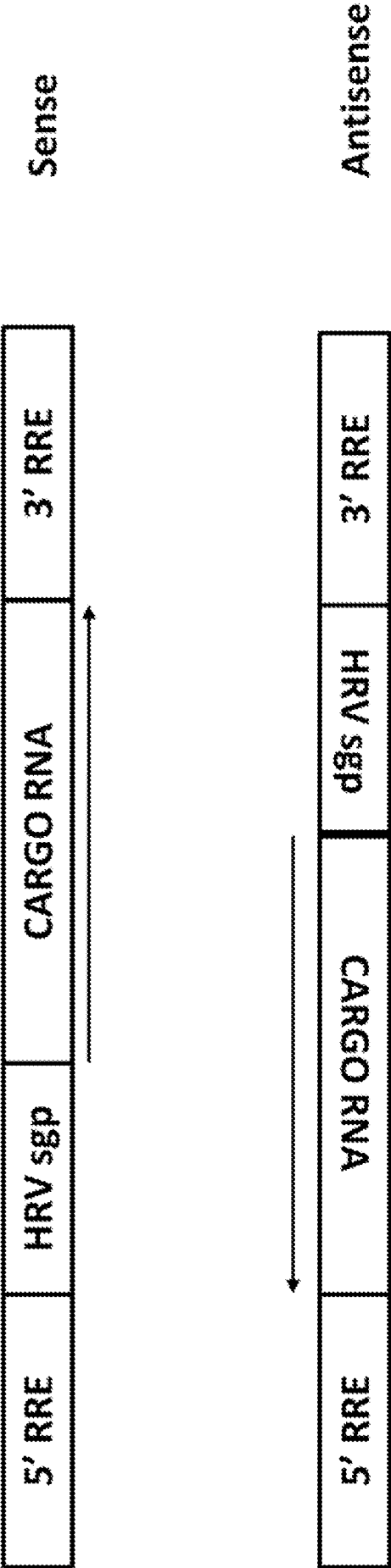


Figure 3

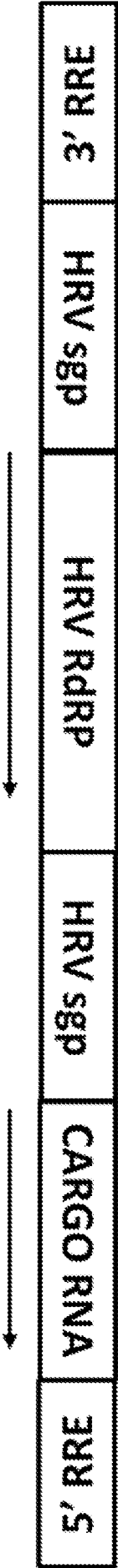


Figure 4

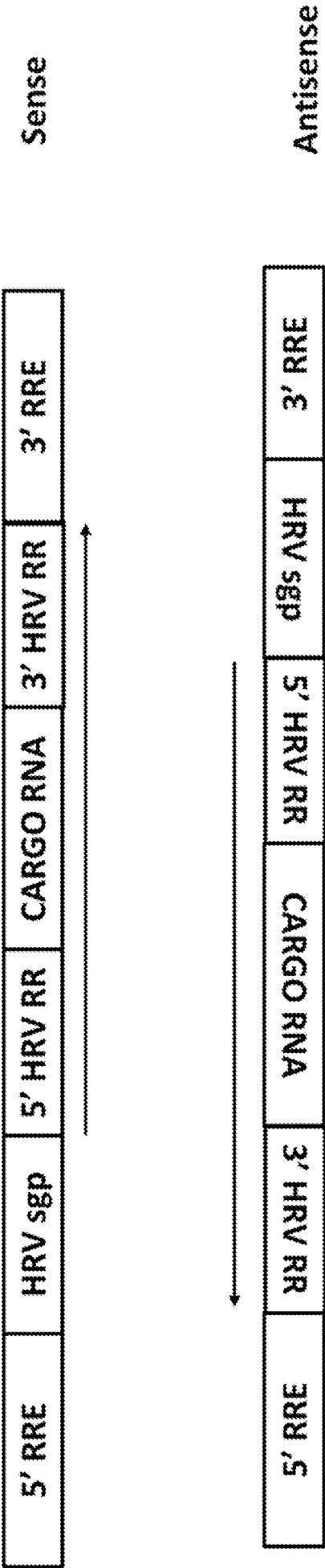


Figure 5

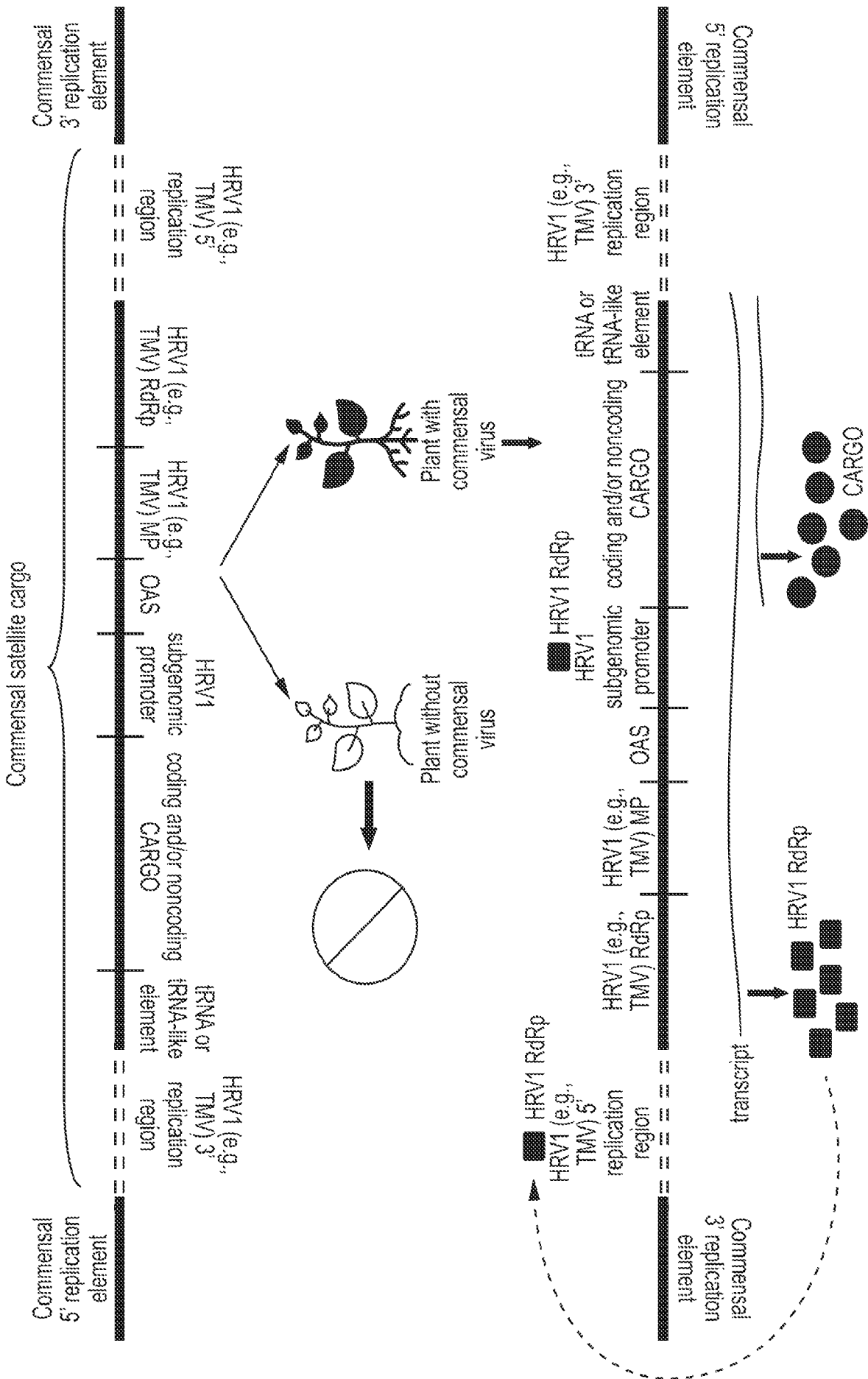


Figure 6

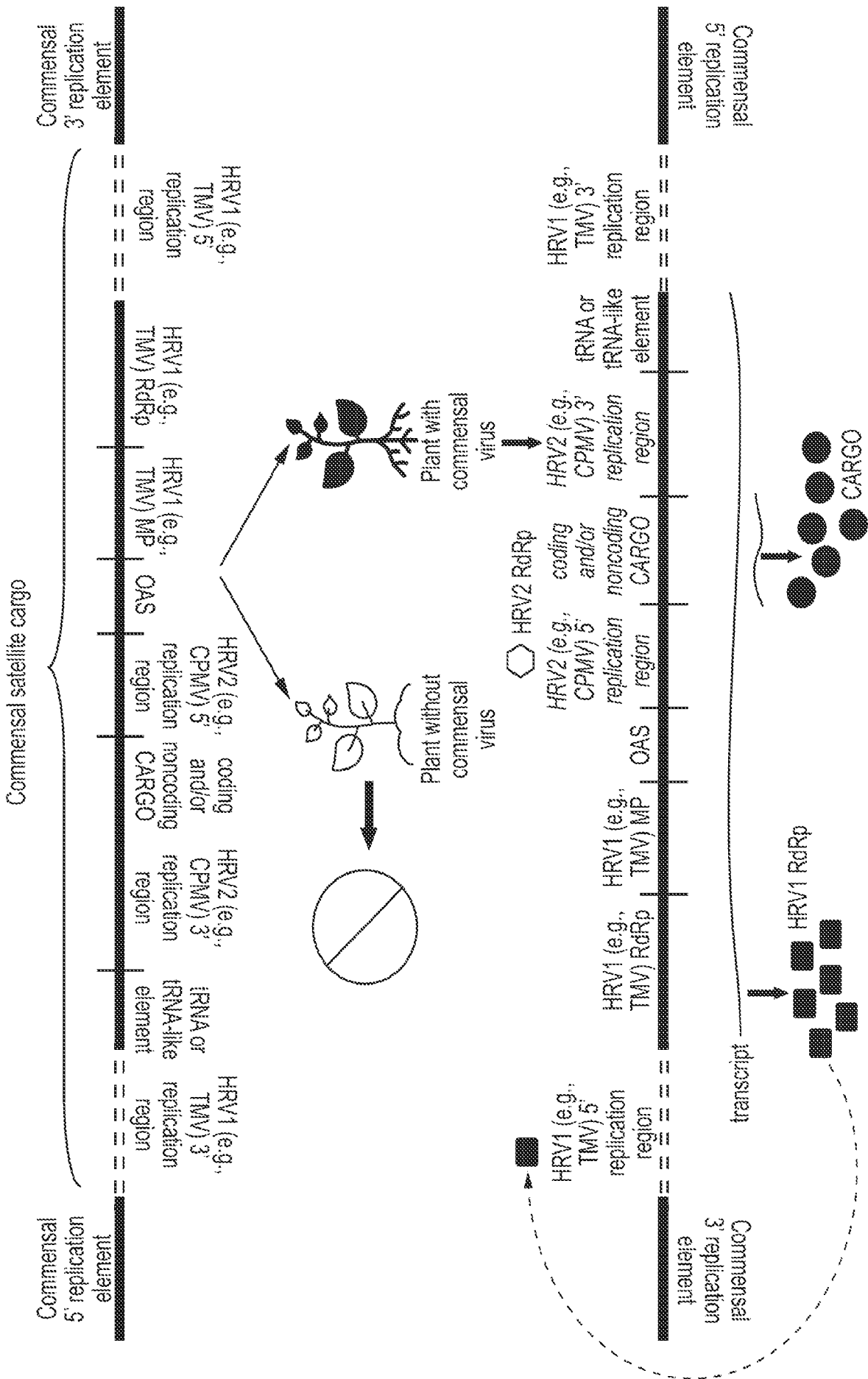


Figure 7

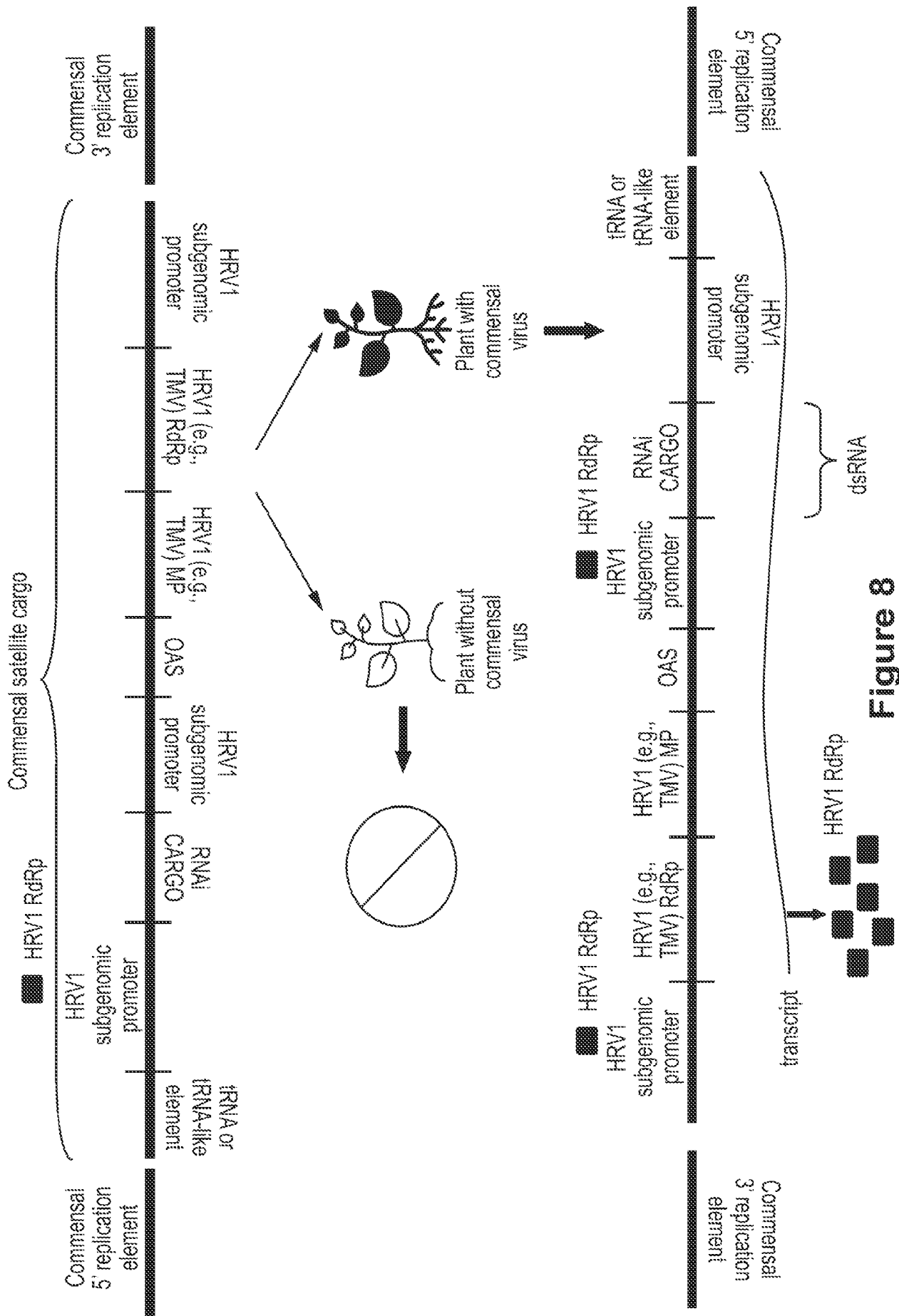


Figure 8

INTERNATIONAL SEARCH REPORT

International application No

PCT/US2024/027778

A. CLASSIFICATION OF SUBJECT MATTER

INV. C12N15/82

ADD.

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)

C12N

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

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

EPO-Internal, WPI Data, BIOSIS, CHEM ABS Data, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DE 102 25 066 A1 (BASF PLANT SCIENCE GMBH [DE]) 18 December 2003 (2003-12-18)	1,3-5,9, 11-14, 30,31, 33-37, 41-50, 52-54, 57, 59-63, 66,67, 69, 81-87, 90-94
Y	[0012], [0018], [0020], [0022] - [0026]; claims 1-19 ----- -/-	1-94



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

12 August 2024

Date of mailing of the international search report

22/10/2024

Name and mailing address of the ISA/

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Marchesini, Patrizia

INTERNATIONAL SEARCH REPORT

International application No

PCT/US2024/027778

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KHAKHAR ARJUN ET AL: "RNA Viral Vectors for Accelerating Plant Synthetic Biology", FRONTIERS IN PLANT SCIENCE , vol. 12 23 June 2021 (2021-06-23), XP093047125, DOI: 10.3389/fpls.2021.668580 Retrieved from the Internet: URL:https://www.frontiersin.org/articles/10.3389/fpls.2021.668580/full the whole document -----	1-94
Y	WO 2005/049839 A2 (ICON GENETICS AG [DE]; MARILLONNET SYLVESTRE [DE] ET AL.) 2 June 2005 (2005-06-02) pages 19-21, last and first paragraph respectively; claims 1-57 -----	1-94
Y	WO 2021/257987 A2 (HALO BIO RNAI THERAPEUTICS INC [US]) 23 December 2021 (2021-12-23) claims 1-20 -----	1-94
Y	ABRAHAMIAN PETER ET AL: "Annual Review of Virology Plant Virus-Derived Vectors: Applications in Agricultural and Medical Biotechnology", ANNU. REV. VIROL , vol. 7 10 June 2020 (2020-06-10), pages 513-535, XP093047962, DOI: 10.1146/annurev-virology-010720- Retrieved from the Internet: URL:https://www.annualreviews.org/doi/suppl/10.1146/annurev-virology-010720-054958 pages 515-518 "Vector engineering" the whole document -----	1-94
Y	CANDRESSE THIERRY ET AL: "Complete genomic sequence of barley (Hordeum vulgare) endornavirus (HvEV) determined by next-generation sequencing", ARCHIVES OF VIROLOGY, vol. 161, no. 3, 1 March 2016 (2016-03-01), pages 741-743, XP093194267, AT ISSN: 0304-8608, DOI: 10.1007/s00705-015-2709-3 sequence KT721705 (Genbank) ----- -/-	1-94

INTERNATIONAL SEARCH REPORT

International application No

PCT/US2024/027778

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P	WO 2023/077118 A1 (FLAGSHIP PIONEERING INNOVATIONS VII LLC [US]) 4 May 2023 (2023-05-04) claims 1-29; sequence 279 the whole document -----	1 - 94

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2024/027778

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:
 - a. ☒ forming part of the international application as filed.
 - b. ☐ furnished subsequent to the international filing date for the purposes of international search (Rule 13*ter*.1(a)).

☐ accompanied by a statement to the effect that the sequence listing does not go beyond the disclosure in the international application as filed.
2. ☐ With regard to any nucleotide and/or amino acid sequence disclosed in the international application, this report has been established to the extent that a meaningful search could be carried out without a WIPO Standard ST.26 compliant sequence listing.
3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2024/027778

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.:
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:

see additional 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 an 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.:
1-94 (partially)

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.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-94 (partially)

Relates to a recombinant RNA molecule comprising a 5' RNA replication element depicted by SEQ ID No. 729, a cargo RNA molecule , and a 3 ' replication element operably linked. Also relates to an agricultural formulation, cell, expression system, plant, plant propagule and methods comprising said recombinant RNA molecule.

2. claims: 1-94 (partially)

Relates to a recombinant RNA molecule comprising a 5' RNA replication element , a cargo RNA molecule , and a 3 ' replication element operably linked, wherein each combination of possible replication element recognized by a endornovirus RNA-dependent RNA polymerase with any possible cargo RNA is a separate invention. Also relates to an agricultural formulation, cell, expression system, plant, plant propagule and methods comprising said recombinant RNA molecule.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2024/027778

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