FIG. 1

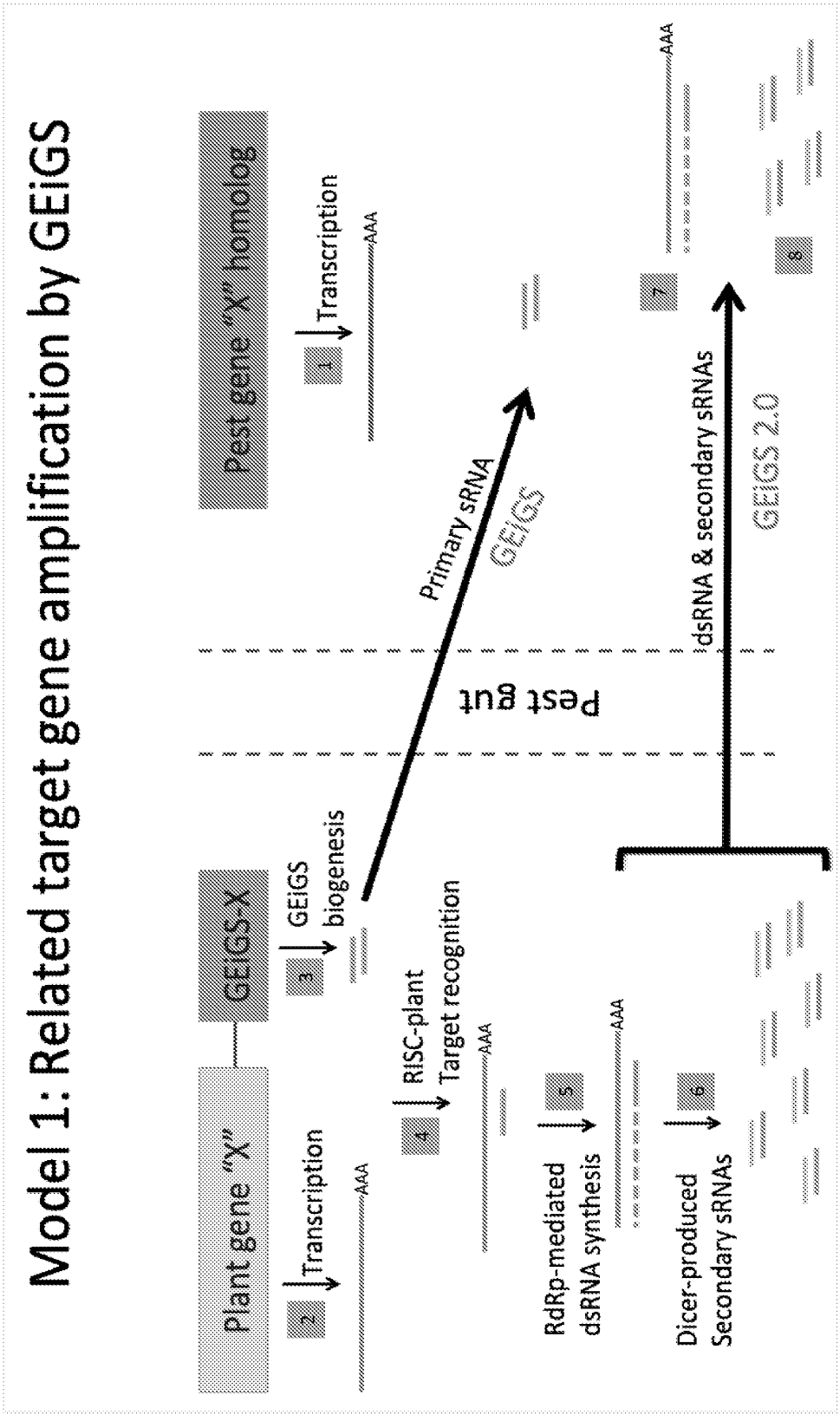

Model 1: Related target gene amplification by GEiGS
Plant gene "X"
GEiGS-X
Pest gene "X" homolog
1 Transcription
2 Transcription
3 GEiGS biogenesis
4 RISC-plant Target recognition
5 RdRp-mediated dsRNA synthesis
6 Dicer-produced Secondary sRNAs
7
8
AAA
Primary sRNA
GEiGS
Pest gut
dsRNA & secondary sRNAs
GEiGS 2.0

FIG. 2

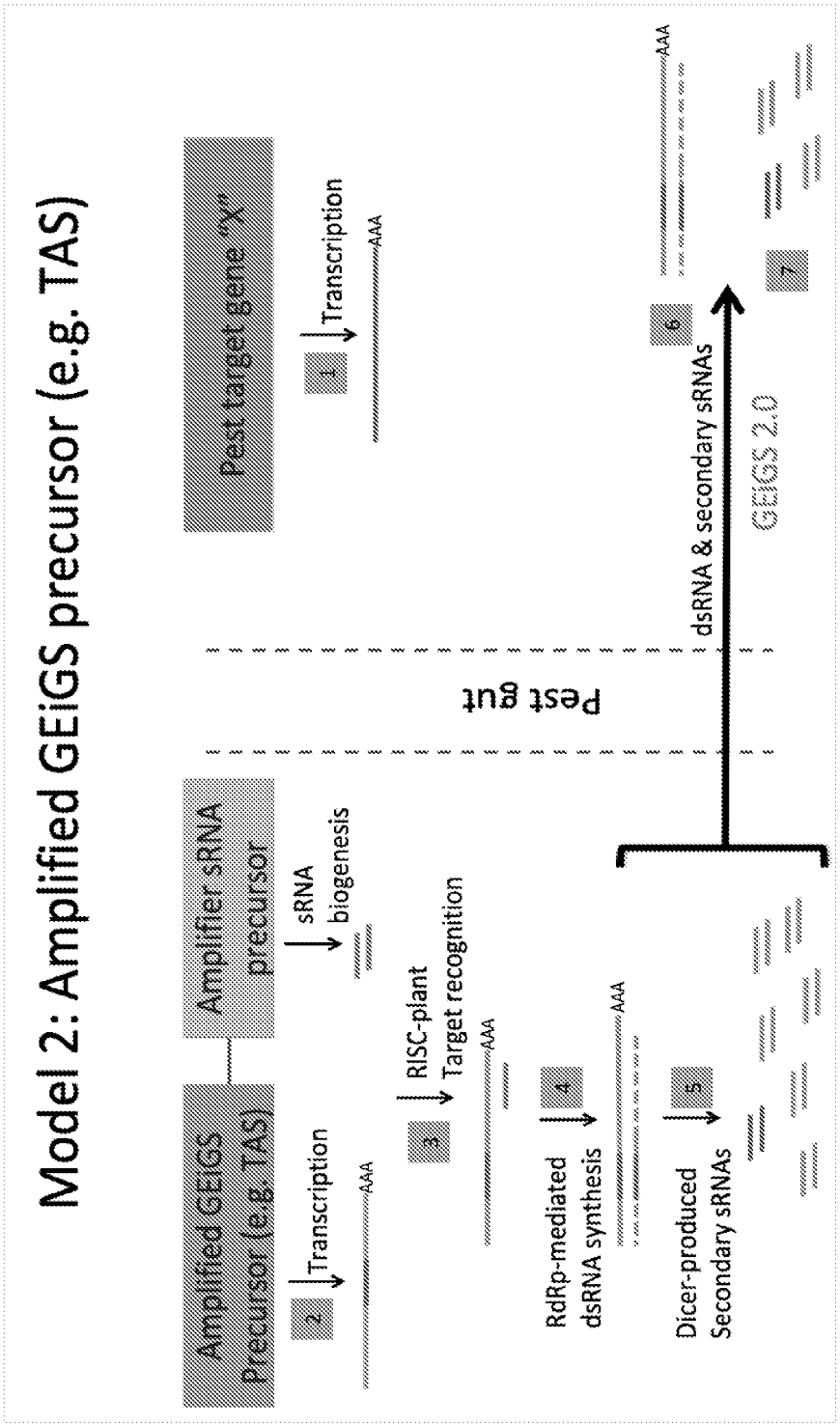

Model 2: Amplified GEiGS precursor (e.g. TAS)
Amplified GEiGS Precursor (e.g. TAS)
Amplifier sRNA precursor
Pest target gene "X"
2
Transcription
AAA
sRNA biogenesis
1
Transcription
AAA
3
RISC-plant Target recognition
AAA
Pest gut
RdRp-mediated dsRNA synthesis
4
AAA
Dicer-produced Secondary sRNAs
5
dsRNA & secondary sRNAs
GEiGS 2.0
6
AAA
7

FIG. 3A

```
Query: AF502391.1
       Heterodera glycines putative gland protein G10A06 mRNA, complete cds

  Hit: gi|79332368|ref|NM_001037071.1| (1591)
       Arabidopsis thaliana bZIP transcription factor family protein (TGA1),...

 HSPs: ----  --------  ---------  ------  ---------------  ----------------------
          #   E-value  Bit score    Span      Query range               Hit range
       ----  --------  ---------  ------  ---------------  ----------------------
          0      0.36      40.96      27        [365:392]            [1259:1286]
      Query: AF502391.1 Heterodera glycines putative gland protein G10A06 mRN...
        Hit: gi|79332368|ref|NM_001037071.1| Arabidopsis thaliana bZIP transc...
Query range: [365:392] (1)
  Hit range: [1259:1286] (1)
Quick stats: evalue 0.36; bitscore 40.96
  Fragments: 1 (27 columns)

Pest seq  Query - AAATGAAGAAAATGCACAGACCTCAAA      SEQ ID NO: 1
                  |||||||||||||| | ||||||||||
Plant seq   Hit - AAATGAAGAAAATGGAAAGACCTCAAA      SEQ ID NO: 2
```

FIG. 3B

Ath-MIR173 based GEiGS molecule **SEQ ID NO: 3**

GAAGGACUuuguaaaacaauuucagaauuaCUGAGGACAAAAAUGUUGUAGUACACUUAAAGUCGCAAACCGC
GGUGAUUUGAAUUUGUUUGUAAAGACCUUC

>NM_001037071.1 Arabidopsis thaliana bZIP transcription factor family protein (TGA1), mRNA **SEQ ID NO: 4**

ACACCTTCCAAACACTATTGGGGAAATGGCTTCTTCTCTTTTTTCCGGTGTAGGTTTAAGGTTTTAGATTTG
AAGGCGGATGGTGAGGAGTTTGTGTTGATGAAATGGGTGATTTGAATTGAGGAAAACATGAATTCGACATCG
ACACATTTTGTGCCACCGAGAAGAGTTGGTATATACGAACCTGTCCATCAATTCGGTATGTGGGGGGAGAGT
TTCAAAAGCAATATTAGCAATGGGACTATGAACACACCAAACCACATAATAATACCGAATAATCAGAAACTA
GACAACAACGTGTCAGAGGATACTTCCCATGGAACAGCAGGAACTCCTCACATGTTCGATCAAGAAGCTTCA
ACGTCTAGACATCCCGATAAGATACAAAGACGGCTTGCTCAAAACCGCGAGGCTGCTAGGAAAAGTCGCTTG
CGCAAGAAGGCTTATGTTCAGCAACTGGAAACAAGCAGGTTGAAGCTAATTCAATTAGAGCAAGAACTCGAT
CGTGCTAGACAACAGGGATTCTATGTAGGAAACGGAATAGATACTAATTCTCTCGGTTTTTCGGAAACCATG
AATCCAGGGATTGCTGCATTTGAAATGGAATATGGACATTGGGTTGAAGAACAGAACAGACAGATATGTGAA
CTAAGAACAGTTTTACACGGACACATTAACGATATCGAGCTTCGTTCGCTAGTCGAAAACGCCATGAAACAT
TACTTTGAGCTTTTCCGGATGAAATCGTCTGCTGCCAAAGCCGATGTCTTCTTCGTCATGTCAGGGATGTGG
AGAACTTCAGCAGAACGATTCTTCTTATGGATTGGCGGATTTCGACCCTCCGATCTTCTCAAGGTTCTTTTG
CCACATTTTGATGTCTTGACGGATCAACAACTTCTAGATGTATGCAATCTAAAACAATCGTGTCAGCAAGCA
GAAGACGCGTTGACTCAAGGTATGGAGAAGCTGCAACACACCCTTGCGGACTGCGTTGCAGCGGGACAACTC
GGTGAAGGAAGTTACATTCCTCAGGTGAATTCTGCTATGGATAGATTAGAAGCTTTGGTCAGTTTCGTAAAT
CAGGCTGATCACTTGAGACATGAAACATTGCAACAAATGTATCGGATATTGACAACGCGACAAGCGGCTCGA
GGATTATTAGCTCTTGGTGAGTATTTTCAACGGCTTAGAGCCTTGAGCTCAAGTTGGGCAACTCGACATCGT

GAACCAACGTAGGTTTGAGTTATTTTGTAACAACCaaatgaagaaaatggaaagacctcaaaAAATGAAGAA
||||||||||||| | ||||||||||
AAATGAAGAAAATGCACAGACCTCAAA **SEQ ID NO: 1**

TGAGTGCATCTGAAAACAGAGGACTACTCTGAATAAATAGAGGGGTTGCTGCTGATATTTATTTTTACTCTG
CGGCGGAATTAGAAAATTTGAAAAACATCATGTATTGATAAGTTGTAAATATCAGAAAAAGGTGGGGGTGCA
AAAATTTGTACTTTTTAGCTTTTGAAAGAGGCAAGTTTTTCGAATGTTTGTTTGATttgtaaacaatttcag
aattaTATAAACTTGGTTCCAAATCCCCTGTAATAATGTCGAGCTATCTGCAATTTGAAAACTATAGGGGCT
TTACTTA

FIG. 4A

```
Query: AF500024.1
       Heterodera glycines putative gland protein G8H07 mRNA, complete cds

  Hit: gi|1063720382|ref|NM_116351.7| (3676)
       Arabidopsis thaliana glycosyl transferase family 1 protein (AT4G01210...

 HSPs: ----  --------  ---------  ------  ---------------  ---------------------
          #   E-value  Bit score    Span      Query range               Hit range
       ----  --------  ---------  ------  ---------------  ---------------------
          0         4      38.26      28      [1161:1189]               [553:581]
      Query: AF500024.1 Heterodera glycines putative gland protein G8H07 mRNA...
        Hit: gi|1063720382|ref|NM_116351.7| Arabidopsis thaliana glycosyl tra...
Query range: [1161:1189] (1)
  Hit range: [553:581] (1)
Quick stats: evalue 4; bitscore 38.26
  Fragments: 1 (28 columns)

Pest seq   Query - CAGCAACAACAGAATCAGGAACAGCAAC    SEQ ID NO: 5
                   |||||||||||| | ||| ||||||||
Plant seq    Hit - CAGCAACAACAGCAACAGCAACAGCAAC    SEQ ID NO: 6
```

FIG. 4B

Ath-MIR156a based GEiGS molecule

CAAGAGAAACGCAAAGAUAAAGAUUGAACUGGGGUAUCACACAAAGGCAAGAUGCAGACCAGUGCAGUUGCUUCGCUUGCGUGaugcucauggcuuuuaaauuuaA
UCCGGUGCCGAUCUCUUC **SEQ ID NO: 7**

>NM_116351.7 Arabidopsis thaliana glycosyl transferase family 1 protein (AT4G01210), mRNA **SEQ ID NO: 8**

AAATTAAATTATGCGTCTAAGTTGTAACATATAATAAAAGGATAATATATTTTTCAGTCACACCAAAAAAAAAATTGATAAGAAAGAAAAAAAAAAGAGTGAAAATTAGAAAGACAGAGAA
GCAAAGATTCTTGCTCCCTGCGAATCCGCAGCTGCTTCGAAACGCAAATCCGATTTGTAGTCTCCTTTGATTCTTCCATTGACGATACAGCTTCTCTTTCTCTCTTCTCTCTGCTTACTT
TGCTTTTTACTAAGCTCACAAGAATCTACGCATCTGTACTGTTATTATGCTGATGCTCTCTACTTAATCATCACCACCGCACGCAGTTCGAGATTTCTGGAATTTTCTGTGTCGGATGCG
TTTGAGATTCATCGAATCTACTTGGTTATAGATTGGAAATTTAGGTGGGGATTTGAGTTGCTTAGCTTGTGGTAGGTTACATTTTCTTGTTTGAGATTCAGTGAATCTCTCCAGAGTTGC

ATGTATAGAAATGGGTTCTTTGGAATCTGGGATTCCGACGAAGCGAGATAACGGCGGCGTAAGAGGTGGAAGAcagcaacaacagcaacagcaacagcaacAGTTCTTCTTGCAGAGAAA
||||||||||| | ||| |||||||||
CAGCAACAACAGAATCAGGAACAGCAAC **SEQ ID NO: 5**

CAGATCGAGACTCTCCAGATTCTTTCTATTGAAGAGTTTTAATTACCTCCTATGGATTTCTATAATTTGTGTCTTCTTCTTCTTCGCTGTGCTGTTCCAGATGTTTTTGCCGGGTTTGGT
GATTGATAAATCGGATAAACCATGGATTAGTAAGGAGATTTTGCCACCTGATTTGGTTGGTTTTAGGGAGAAAGGGTTTTTGGATTTTGGTGATGATGTTAGAATTGAGCCCACCAAGCT
TCTGATGAAATTCCAAAGAGatgccatggttcaatttaCATCTTCTTCTCTCAATACCACTCTGCAGCGTTTTGGATTCAGAAAGCCTAAGCTAGCTCTGGTTTTTGGCGATTTGTT
AGCTGATCCAGAACAGGTGTTAATGGTGTCTCTCTCCAAGGCACTGCAAGAGGTTGGCTATGCAATTGAGGTTTACTCGCTTGAAGATGGTCCAGTGAATAGTATTTGGCAGAAAATGGG
AGTTCCAGTCACAATACTCAAGCCTAATCAGGAATCGAGTTGTGTTATCGACTGGCTCTCCTATGATGGCATAATTGTGAACTCTCTCCGAGCTAGGAGTATGTTTACTTGCTTCATGCA
AGAACCTTTCAAATCTTTGCCTCTTATTTGGGTCATCAATGAAGAAACTCTTGCTGTTCGGTCTAGACAGTACAACTCAACAGGGCAGACTGAACTCCTCACTGACTGGAAAAAGATTTT
CAGCCGGGCATCGGTTGTAGTCTTCCATAATTATCTCCTTCCGATACTCTACACCGAGTTTGATGCTGGCAACTTCTATGTGATTCCCGGATCTCCTGAAGAAGTATGTAAAGCAAAGAA
TCTAGAGTTTCCTCCACAGAAAGATGATGTGGTCATTTCCATTGTGGGAAGTCAGTTCTTGTACAAGGGTCAATGGCTGGAACATGCCCTGCTTCTGCAAGCTCTACGGCCTTTATTTTC
GGGCAATTACCTTGAAAGTGATAATTCCCATCTCAAGATCATAGTTTTAGGTGGAGAGACAGCGTCCAACTACAGCGTAGCTATTGAGACAATTTCCCAGAACTTGACATATCCAAAAGA
GGCTGTGAAGCACGTAAGAGTTGCGGGGAATGTTGATAAGATTCTTGAAAGTTCTGATCTTGTTATATATGGATCATTTCTTGAGGAGCAGTCTTTTCCAGAAATTTTGATGAAGGCCAT
GTCCTTGGGGAAACCTATAGTTGCACCAGACCTCTTCAACATTAGAAAATATGTTGACGACAGGGTTACTGGGTATCTCTTCCCCAAGCAGAATCTTAAAGTTCTATCGCAAGTTGTGCT
TGAAGTGATAACAGAAGGGAAGATATCTCCATTGGCTCAGAAGATTGCCATGATGGGGAAAACAACTGTTAAAAATATGATGGCTCGGGAAACCATAGAAGGTTATGCAGCTCTACTAGA
GAATATGCTCAAGTTTTCTTCGGAAGTTGCTTCTCCTAAGGATGTACAAAAAGTTCCTCCAGAACTGAGAGAAGAGTGGAGTTGGCATCCGTTTGAAGCTTTTATGGATACATCGCCTAA
TAATAGAATAGCAAGAAGTTATGAGTTCTTAGCGAAGGTTGAGGGGCATTGGAATTATACCCCAGGAGAAGCTATGAAATTTGGAGCTGTTAATGATGATTCGTTCGTGTATGAAATTTG
GGAAGAAGAGAGATATCTTCAAATGATGAATAGTAAAAAAAGACGAGAAGACGAGGAGCTGAAAAGCAGAGTCTTGCAGTATCGTGGGACATGGGAAGATGTATATAAAAGCGCCAAAAG
GGCAGACCGAAGTAAGAATGATCTACATGAGAGGGATGAAGGGGAGCTGCTAAGAACCGGTCAACCTTTATGCATATATGAACCCTATTTTGGTGAAGGAACCTGGTCGTTTCTACATCA
AGATCCCCTCTATCGTGGGGTTGGCCTGTCAGTTAAAGGACGTAGACCTAGGATGGATGATGTCGATGCATCATCACGTCTTCCGCTTTTCAACAATCCGTACTATCGCGATGCTCTTGG
TGACTTTGGAGCTTTTTTTGCAATCTCAAACAAGATTGATCGGTTACACAAGAATTCATGGATTGGGTTTCAGTCCTGGAGAGCGACTGCCAGGAAGGAATCTTTATCCAAGATTGCTGA
AGACGCATTACTTAATGCTATACAAACACGAAAACACGGAGATGCCTTATATTTTTGGGTTCGCATGGACAAAGATCCCAGAAATCCTCTGCAGAAACCCTTTTGGTCGTTCTGTGATGC
CATAAATGCTGGGAATTGCAGGTTTGCTTACAACGAAACTTTGAAGAAAATGTACAGTATCAAGAACTTGGACTCATTGCCACCAATGCCCGAGGATGGGGATACATGGTCTGTGATGCA
GAGCTGGGCATTGCCAACAAGATCCTTCTTAGAGTTTGTCATGTTCTCAAGGATGTTTGTGGATTCACTAGATGCACAGATATATGAAGAGCATCATCGAACAAACCGTTGCTATCTGAG
TTTAACCAAAGACAAGCATTGCTATTCGCGGGTACTAGAGCTTCTGGTGAACGTATGGGCTTACCACAGTGCAAGACGCATTGTCTACATAGATCCTGAGACTGGTTTGATGCAAGAGCA
ACACAAACAGAAGAACCGGCGAGGGAAAATGTGGGTGAAGTGGTTCGATTACACAACTCTGAAAACAATGGACGAAGATCTAGCTGAAGAAGCCGACTCAGACCGTCGTGTGGGTCACTG
GCTATGGCCATGGACTGGCGAGATCGTGTGGCGCGGTACATTAGAGAAAGAGAAGCAAAAGAAGAATTTAGAGAAAGAGGAGAAGAAGAAGAAGAGTCGAGATAAGCTGAGTAGAATGAG
AAGTAGAAGTGGTCGTCAGAAAGTGATCGGAAAATATGTAAAACCACCGCCTGAGAACGAAACTGTTACCGGAAATTCCACTTTGTTAAATGTAGTAGACGCATAAAAGAAAACAAATTA
AAATTGCTTCTTTTTTTTGTTAGGTCACTAATTTGTTTCATTCATTGTTTTTGGAAAGATTACTGTATAAAAGGTCT

FIG. 5A

```
Query: AF469060.1
       Heterodera glycines ubiquitin extension protein mRNA, complete cds
 Hit: gi|1063721094|ref|NM_001203752.2| (901)
       Arabidopsis thaliana ubiquitin 11 (UBQ11), mRNA
HSPs: ----  --------  ---------  ------  ---------------  ---------------------
         #   E-value  Bit score    Span      Query range               Hit range
       ----  --------  ---------  ------  ---------------  ---------------------
          0   7.3e-62     242.04     231         [68:299]               [396:627]
          1   9.5e-48     194.25     227         [72:299]               [172:399]
      Query: AF469060.1 Heterodera glycines ubiquitin extension protein mRNA,...
        Hit: gi|1063721094|ref|NM_001203752.2| Arabidopsis thaliana ubiquitin...
Query range: [68:299] (1)
  Hit range: [396:627] (1)
Quick stats: evalue 7.3e-62; bitscore 242.04
  Fragments: 1 (231 columns)

Pest seq  Query - TGGCATGCAAATTTTCGTGAAGACATTGACGGGCAAAACGATCACTTTGGAGGTGGAGAGCTCGGAC
                  ||| ||||| |||||||| || ||  | ||||| || ||||| ||| | |||||||||||||| |||
Plant seq   Hit - TGGTATGCAGATTTTCGTTAAAACCCTAACGGGAAAGACGATTACTCTTGAGGTGGAGAGCTCTGAC

Pest seq  Query - ACTGTGGACAATGTGAAGGAGAAGATCCAAGAGAAGGAGGGCATTCCGCCGGATCAGCAACGGCTGA
                  ||  | ||||| || ||||  |||||||||| |||||||||||||| ||||| ||||| || || |
Plant seq   Hit - ACCATTGACAACGTCAAGGCCAAGATCCAAGATAAGGAGGGCATTCCTCCGGACCAGCAGCGTCTCA

Pest seq  Query - TCTTCGCCGGCAAACAGCTCGAGGACGGACGAACGTTGGCCGACTACAACATACAGAAGGAGTCCAC
                  ||||||| || || ||||| ||||| ||||| || |||||||||||||||| |||||||||| ||
Plant seq   Hit - TCTTCGCTGGAAAGCAGCTTGAGGATGGACGTACTTTGGCCGACTACAACATCCAGAAGGAGTCTAC

Pest seq  Query - GCTCCACTTGGTCCTCCGTCTCCGGGGCGG
                   || ||||||||||||||||||| || ||
Plant seq   Hit - TCTTCACTTGGTCCTCCGTCTCCGTGGTGG
```

SEQ ID NO: 9

SEQ ID NO: 10

FIG. 5B

Ath-MIR156c based GEiGS molecule **SEQ ID NO: 11**

CGCACAGAAAGGGUGAUAAUGGCUUGGUUGCACUAAGGCACGUUGCAUGGCCGAUGCAUAUGCUUCUCUAGCGC*aaccaaguucauguauogu*uuA
UUCCCGCA

>NM_001203752.2 Arabidopsis thaliana ubiquitin 11 (UBQ11), mRNA **SEQ ID NO: 12**

```
CAAATCTCTCAACCGTGATCAAGGTAGATTTCTGAGTTCTTATTGTATTTCTTCGATTTGTTTCGTTCGATC
GCAATTTAGGCTCTGTTCTTTGATTTTGATCTCGTTAATCTCTGATCGGAGGCAAATTACATAGTTTCATCG
TTAGATCTCTTCTTATTTCTCGATTAGGATGCAGATCTTCGTTAAGACTCTCACCGGAAAGACTATCACCCT
CGAGGTGGAAAGCTCTGACACCATCGACAACGTTAAGGCCAAGATCCAGGATAAGGAAGGTATTCCTCCGGA
TCAGCAGAGGCTTATCTTCGCCGGAAAGCAGTTGGAGGATGGCCGCACGTTGGCGGATTACAATATCCAGAA

GGAATCCACCCTCCACTTGGTTCTCAGGCTCCGTGGtggtatgcagattttcgttaaaaccctaacgggaaa
                                  ||| ||||| |||||||| || ||  | ||||| ||
                                  TGGCATGCAAATTTTCGTGAAGACATTGACGGGCAA   SEQ ID NO: 9

gacgattactcttgaggtggagagctctgacaccattgacaacgtcaaggccaagatccaagataaggaggg
 ||||| ||| | ||||||||||||||| |||||  | ||||| || ||||  |||||||||| ||||||||
AACGATCACTTTGGAGGTGGAGAGCTCGGACACTGTGGACAATGTGAAGGAGAAGATCCAAGAGAAGGAGGG

cattcctccggaccagcagcgtctcatcttcgctggaaagcagcttgaggatggacgtactttggccgacta
|||||| ||||| ||||| || || |||||||| || || ||||| ||||| ||||| || ||||||||||
CATTCCGCCGGATCAGCAACGGCTGATCTTCGCCGGCAAACAGCTCGAGGACGGACGAACGTTGGCCGACTA

caacatccagaaggagtctactcttcacttggtcctccgtctccgtggtggTTTCTAAACCTTGTCTCTCTC
|||||| |||||||||| || || |||||||||||||||||||| || ||
CAACATACAGAAGGAGTCCACGCTCCACTTGGTCCTCCGTCTCCGGGGCGG

TCTTATGGTTACTGaaccaagttcatgtatcgtttCATCTAGTACTTTGGTGGTTTATGTTTTGGGGCCATG
TACAGCCTCTGATAAATAATTGATCGACTATGTTTCCGTTTCTTTCATCTCTCTTTTCTTTCAAACAACAAA
TCGAACTTATTCTCTATTGCAATTATCTCTTTCGATTCACTTTTGTCATCGTTGTCTCTTTATATGATGTGC
TTAGTTTGATGAGTGTGAGAAGTACAGAGTCTCTATC
```

FIG. 6

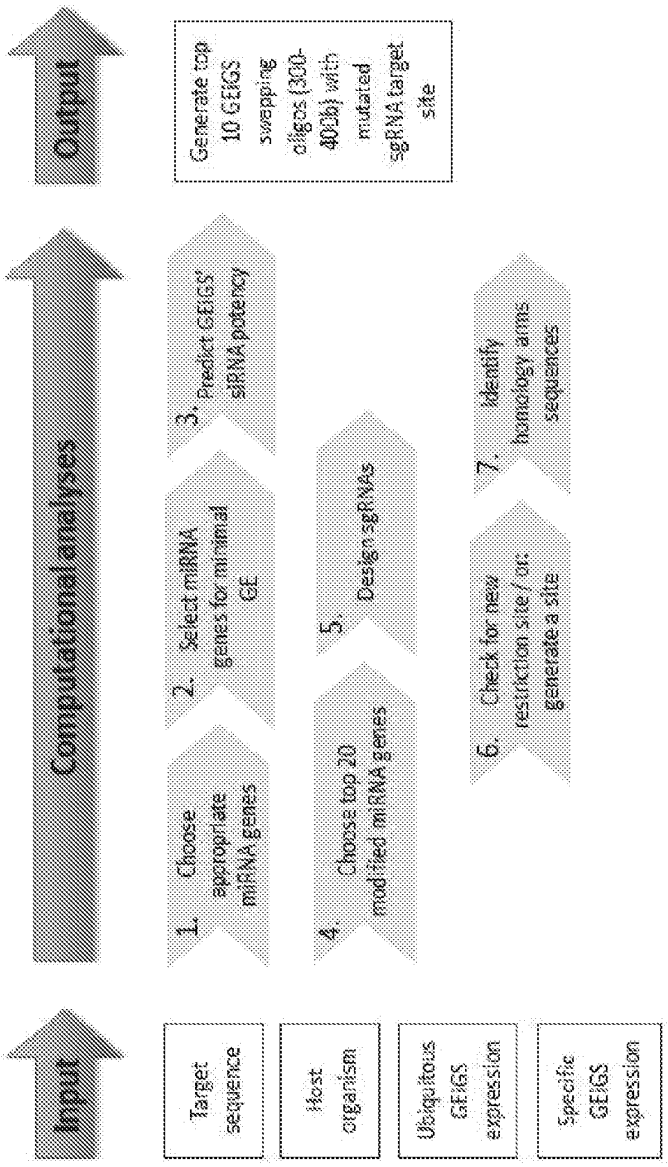
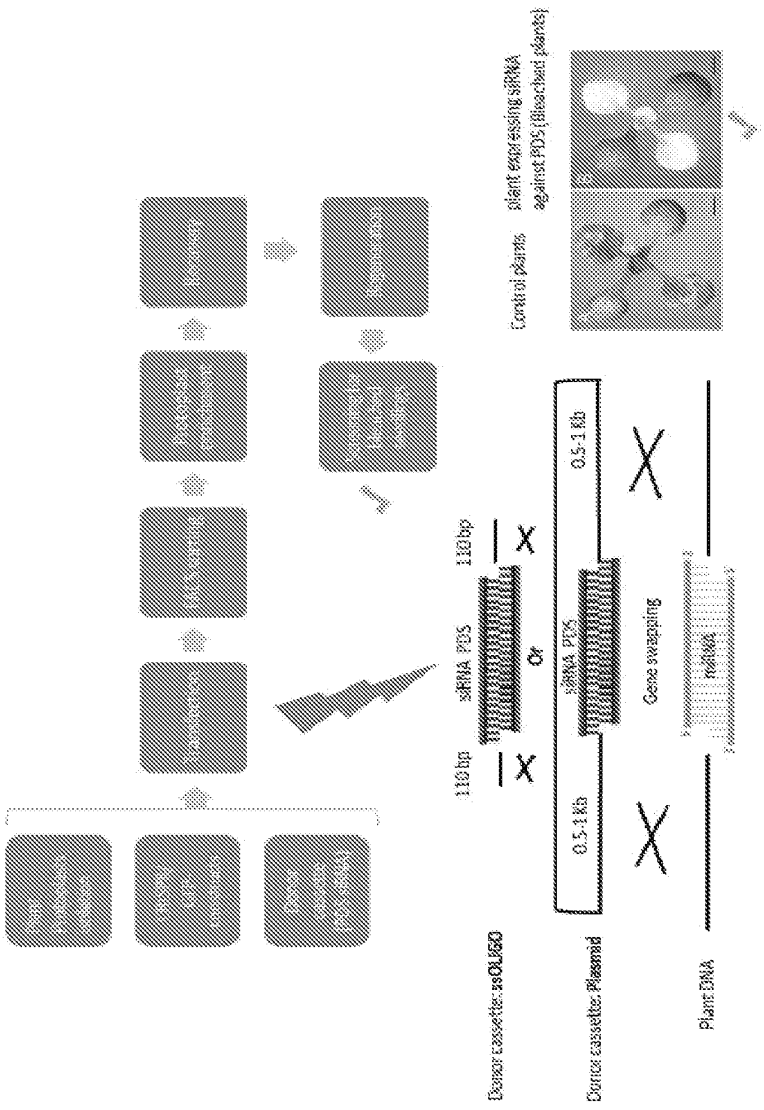

Input
Target sequence
Host organism
Ubiquitous GEiGS expression
Specific GEiGS expression
Computational analyses
1. Choose appropriate miRNA genes
2. Select miRNA genes for minimal GE
3. Predict GEiGS' siRNA potency
4. Choose top 20 modified miRNA genes
5. Design sgRNAs
6. Check for new restriction site / or generate a site
7. Identify homology arms sequences
Output
Generate top 10 GEiGS swapping oligos (300-400bp) with mutated sgRNA target site

FIG. 7


Control plants
Plant expressing siRNA against PDS (Bleached plants)
Donor cassette: pSOL650
Donor cassette: Plasmid
Plant DNA
110 bp
siRNA PDS
110 bp
OR
0.5-1 Kb
siRNA PDS
0.5-1 Kb
Gene swapping
Native

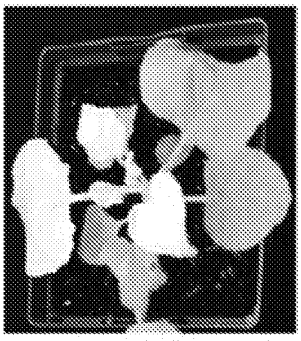


FIG. 8B

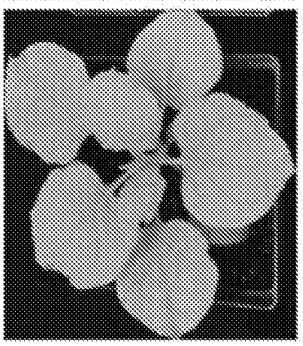


FIG. 8A

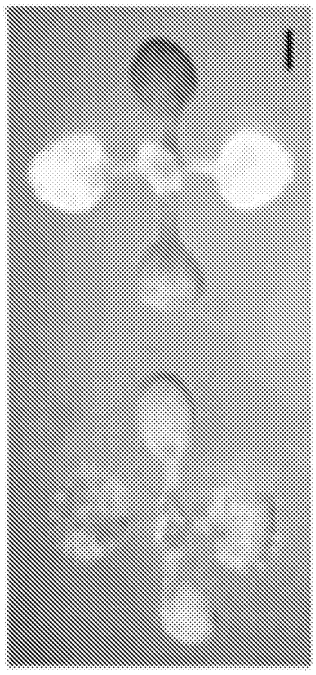


FIG. 8C

FIG. 9A

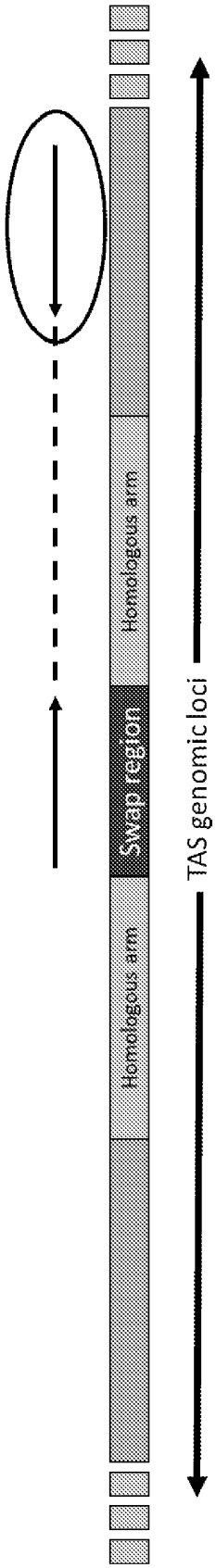

Homologous arm
Swap region
Homologous arm
TAS genomic loci

FIG. 9B

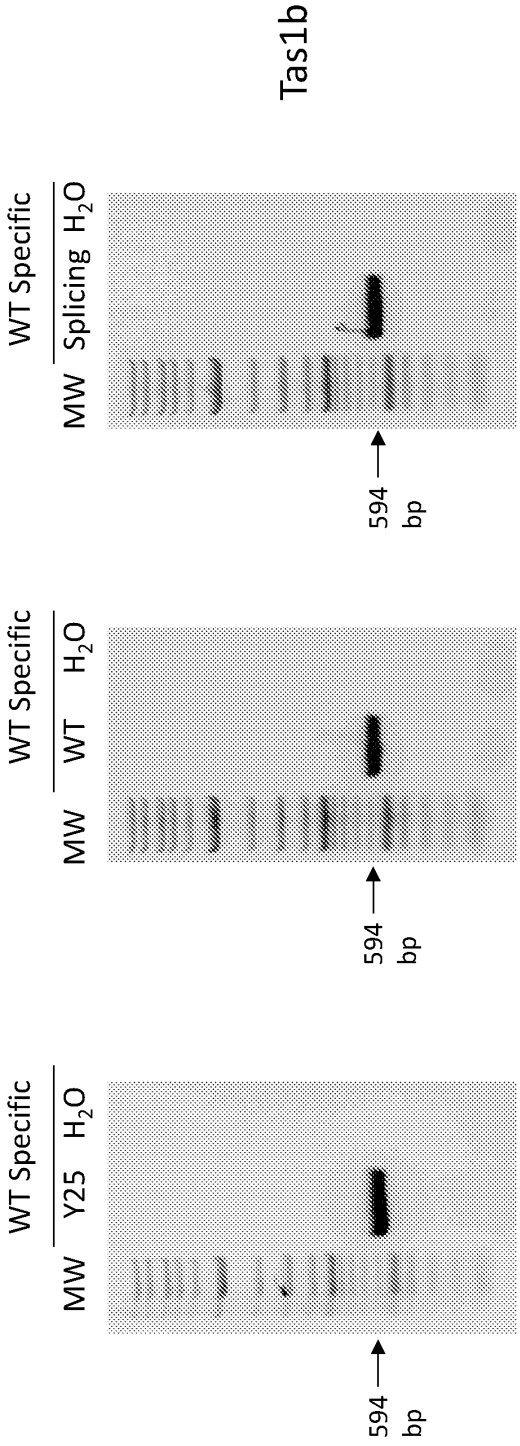

WT Specific
MW Y25 H2O
594 bp
WT Specific
MW WT H2O
594 bp
WT Specific
MW Splicing H2O
594 bp
Tas1b

FIG. 9C

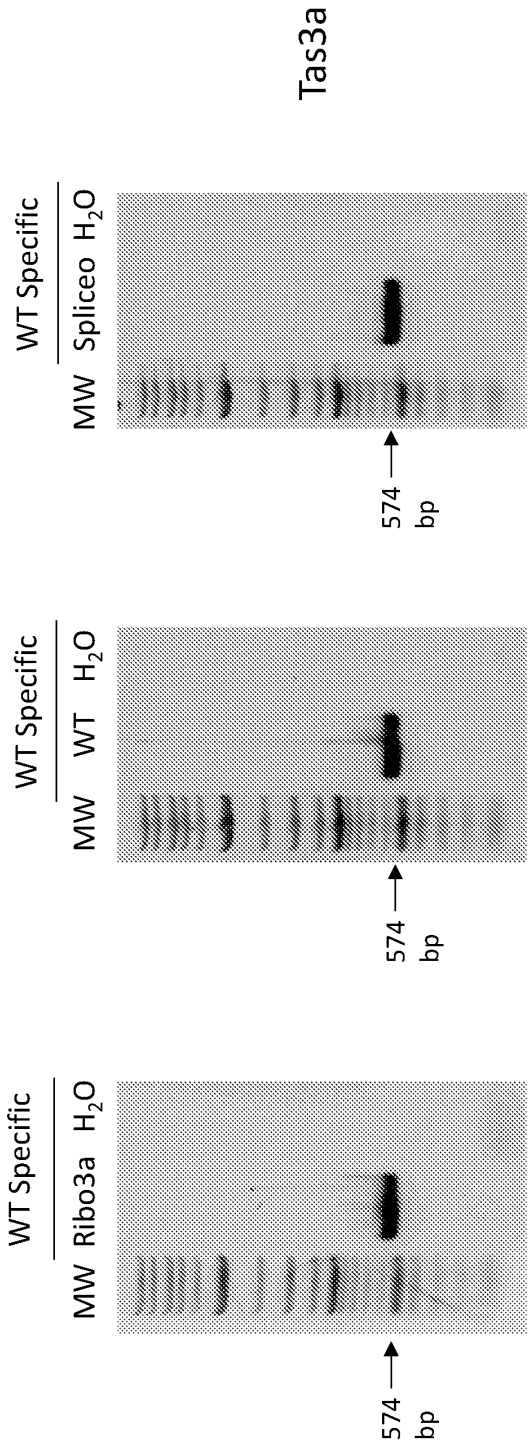
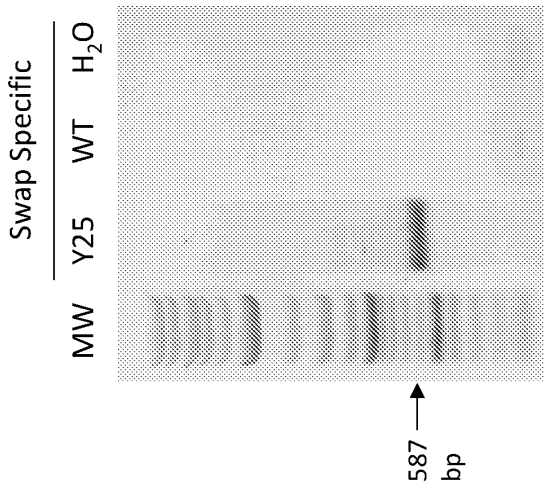

WT Specific
MW Ribo3a H2O
574 bp
WT Specific
MW WT H2O
574 bp
WT Specific
MW Spliceo H2O
574 bp
Tas3a

FIG. 9D


Swap Specific
MW
Y25
WT
H2O
587
bp

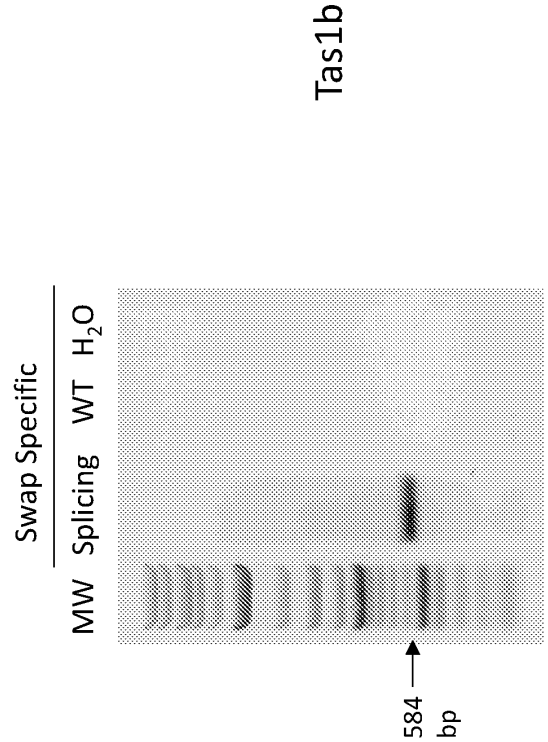
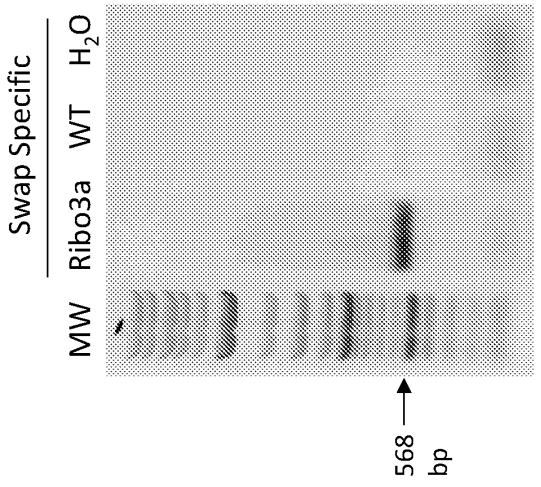

Tas1b
Swap Specific
MW
Splicing
WT
H2O
584
bp

FIG. 9E


Swap Specific
MW
Ribo3a
WT
H2O
568
bp

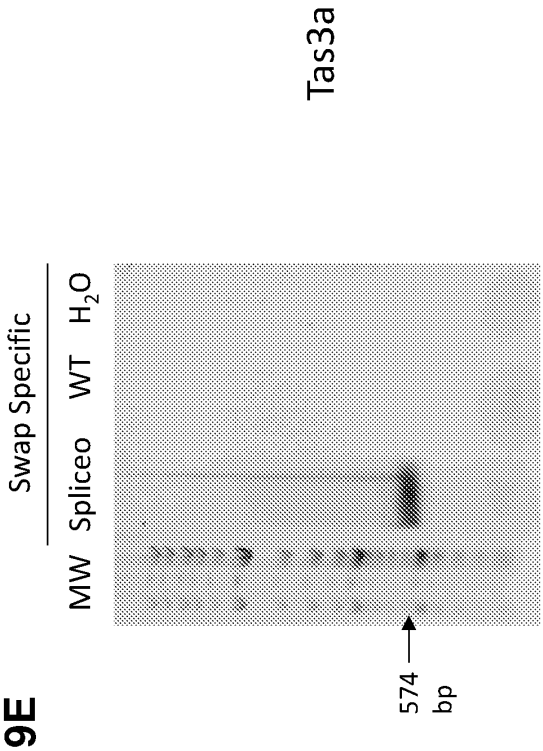
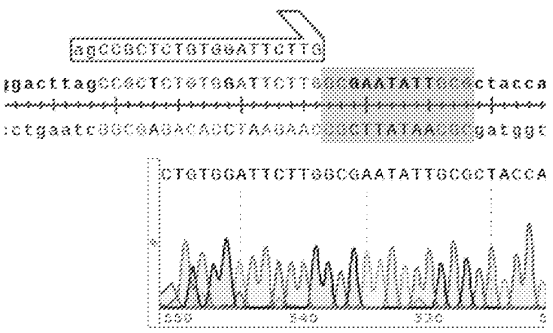

Tas3a
Swap Specific
MW
Spliceo
WT
H2O
574
bp

FIG. 9F

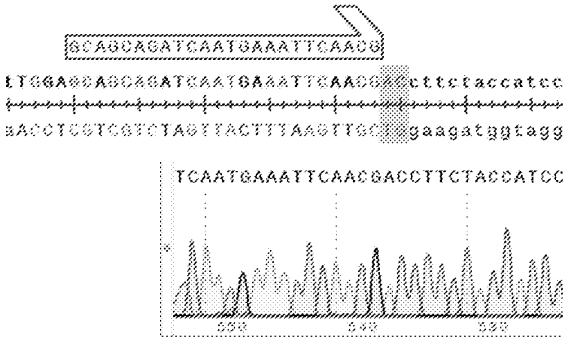
Tas1b

Y25



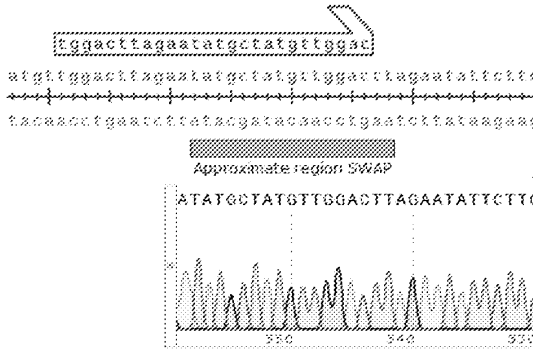
SEQ ID Nos: 79, 80

Splicing



SEQ ID Nos: 77, 78

WT



SEQ ID No: 73

FIG. 9G

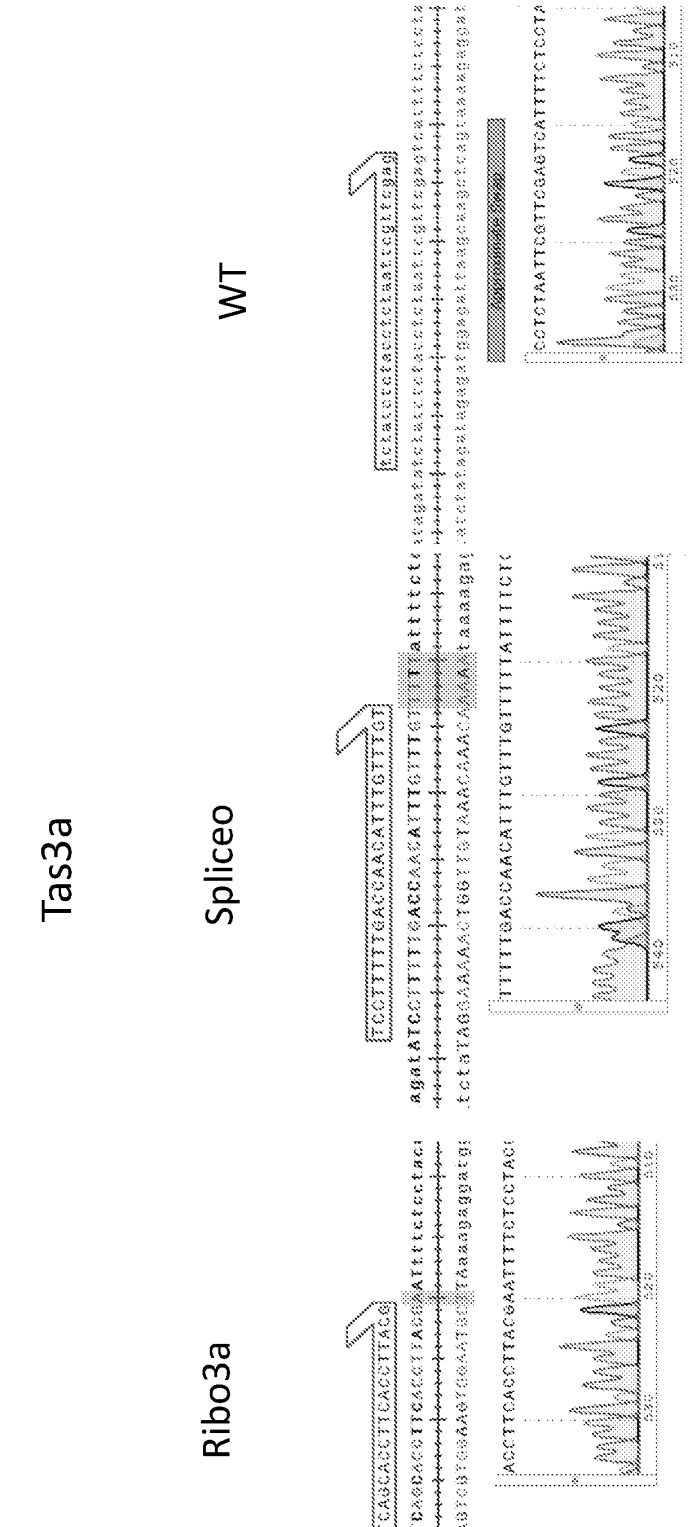

Tas3a
Spliceo
WT
Ribo3a
SEQ ID Nos: 85, 86
SEQ ID Nos: 89, 90
SEQ ID No: 83

FIG. 10A

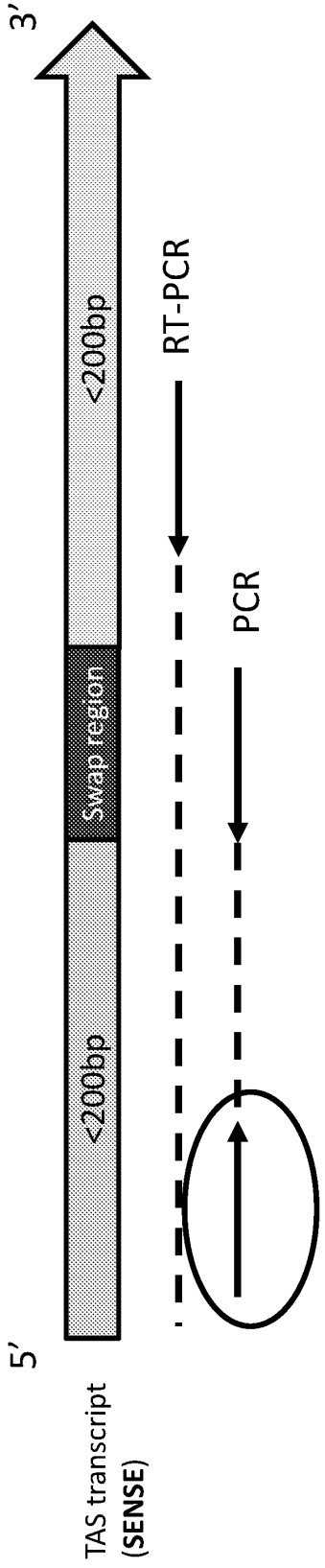


FIG. 10B

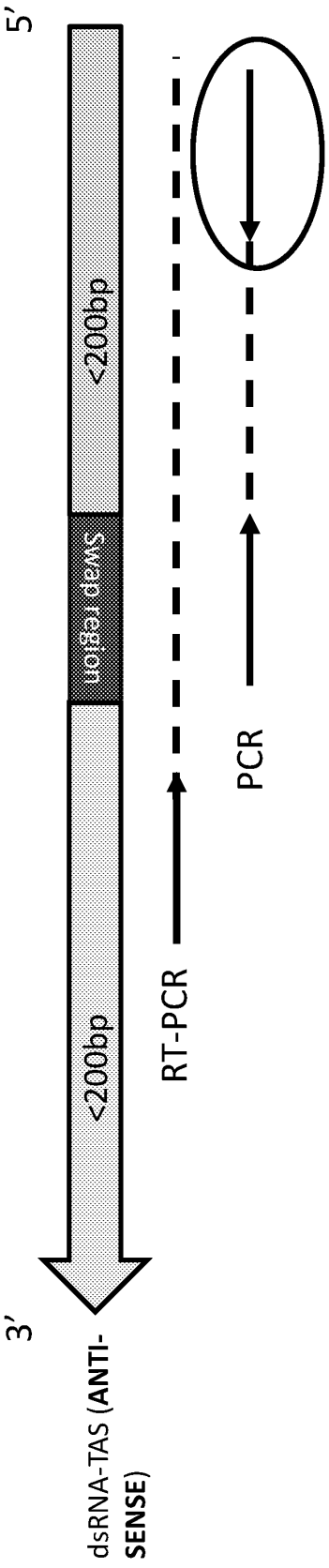


FIG. 10C Tas1b - SENSE

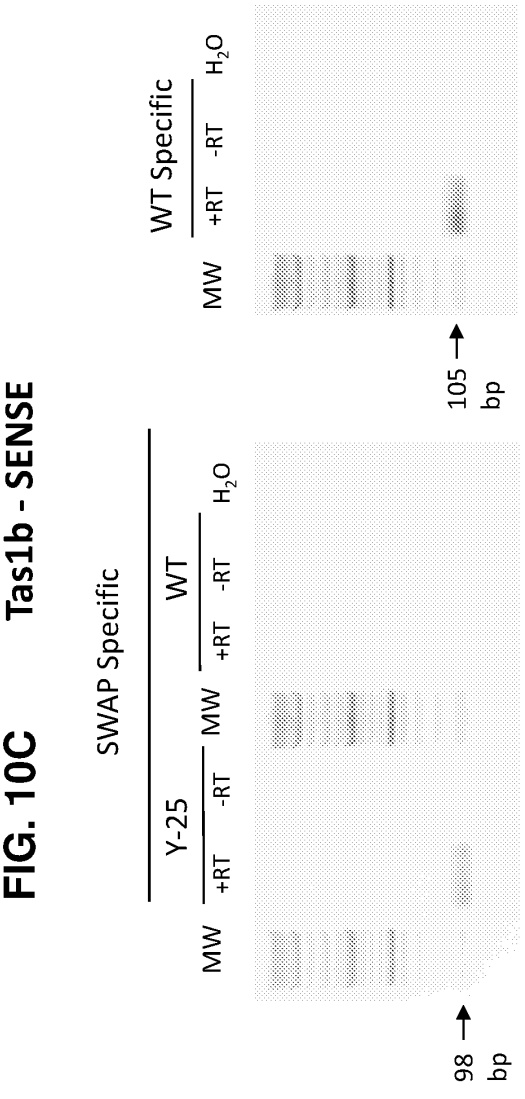


FIG. 10D Tas1b ANTI-SENSE

FIG. 10E Tas3a - SENSE

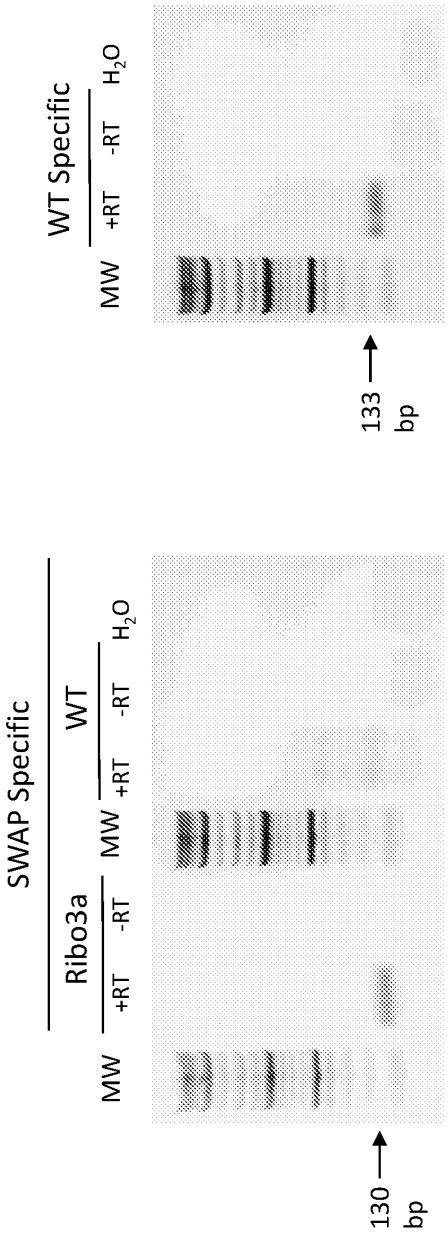


FIG. 10F Tas3a - ANTI-SENSE

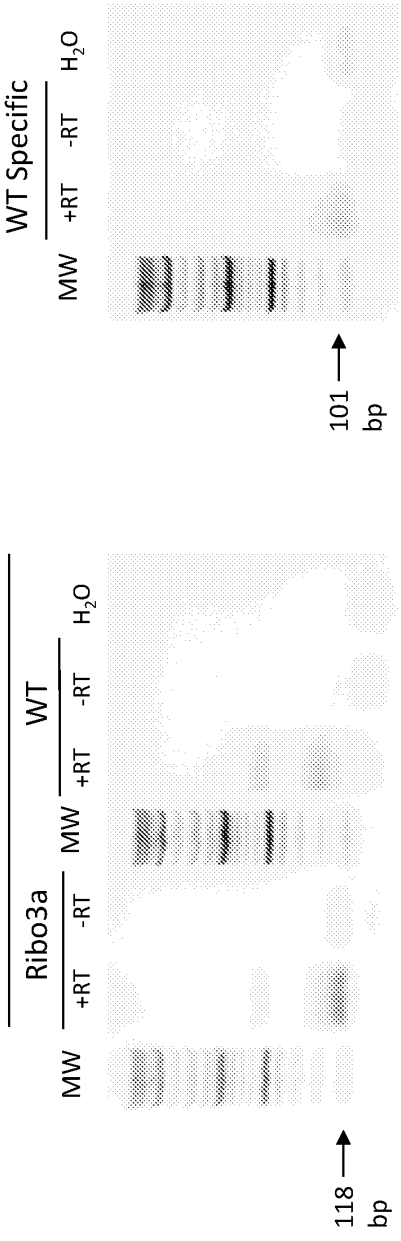
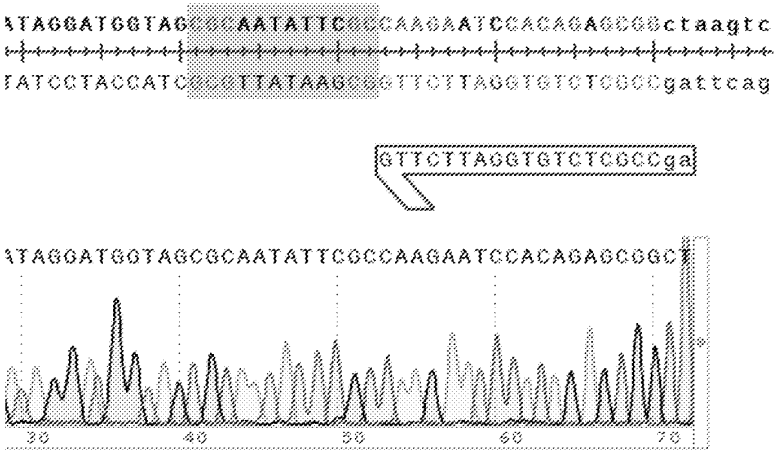


FIG. 10G

Y-25

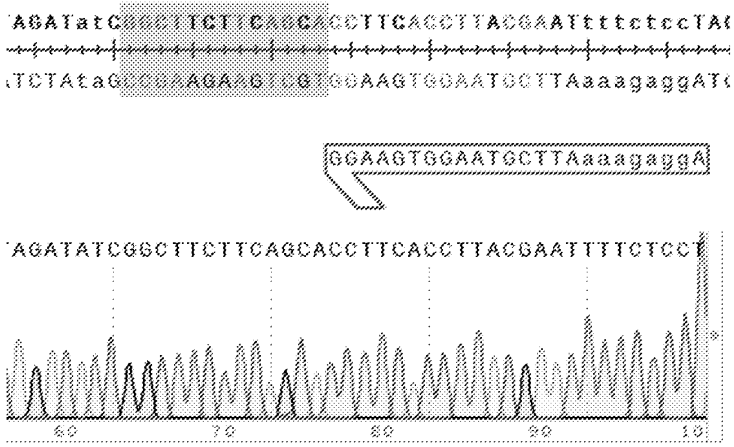
SEQ ID Nos:
79, 80



Tas1b - SENSE

Ribo3a

SEQ ID Nos:
85, 86

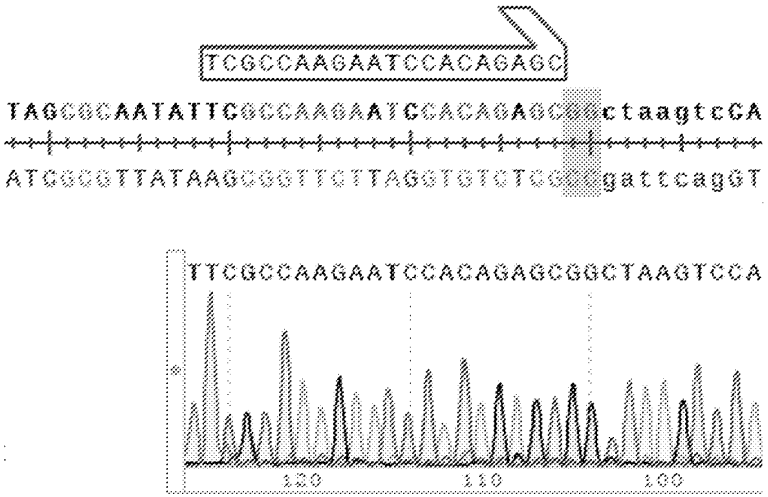


Tas3a - SENSE

FIG. 10H

Y-25

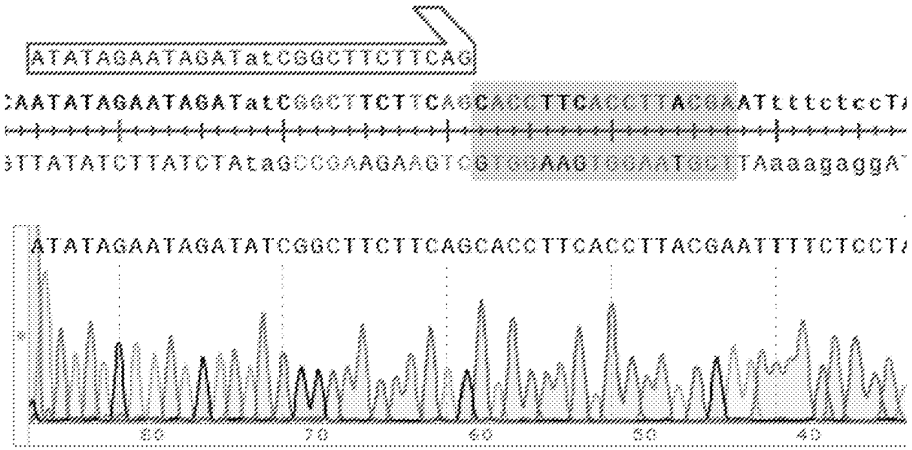
SEQ ID Nos: 79, 80



Tas1b – ANTI-SENSE

Ribo3a

SEQ ID Nos: 85, 86

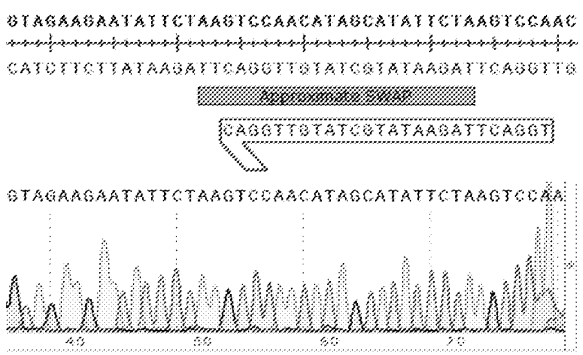


Tas3a – ANTI-SENSE

FIG. 10I

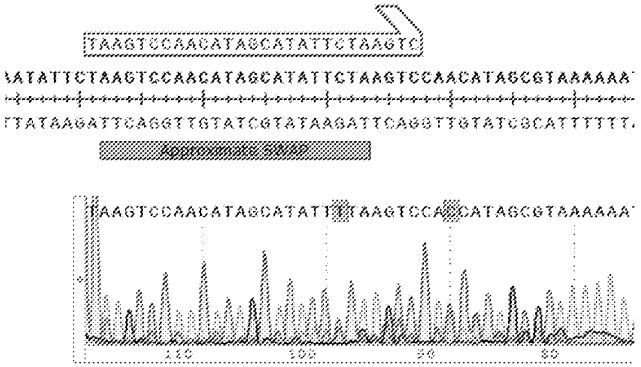
Tas1b WT Sense

SEQ ID No: 73



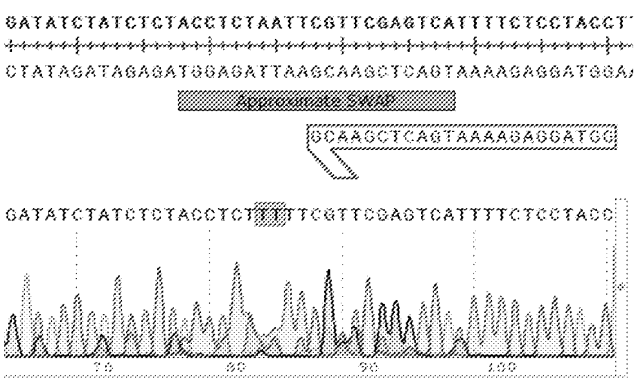
Tas1b WT Anti-Sense

SEQ ID No: 73



Tas3a WT Sense

SEQ ID No: 83



Tas3a WT Anti-Sense

SEQ ID No: 83

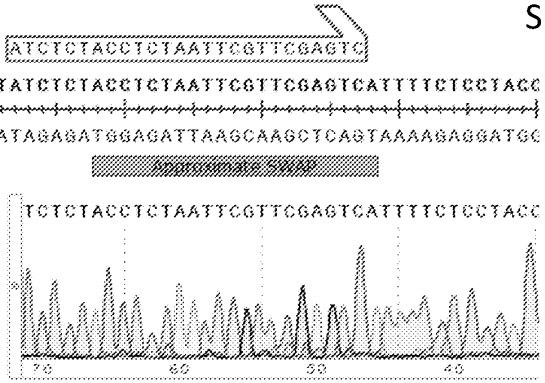


FIG. 11A

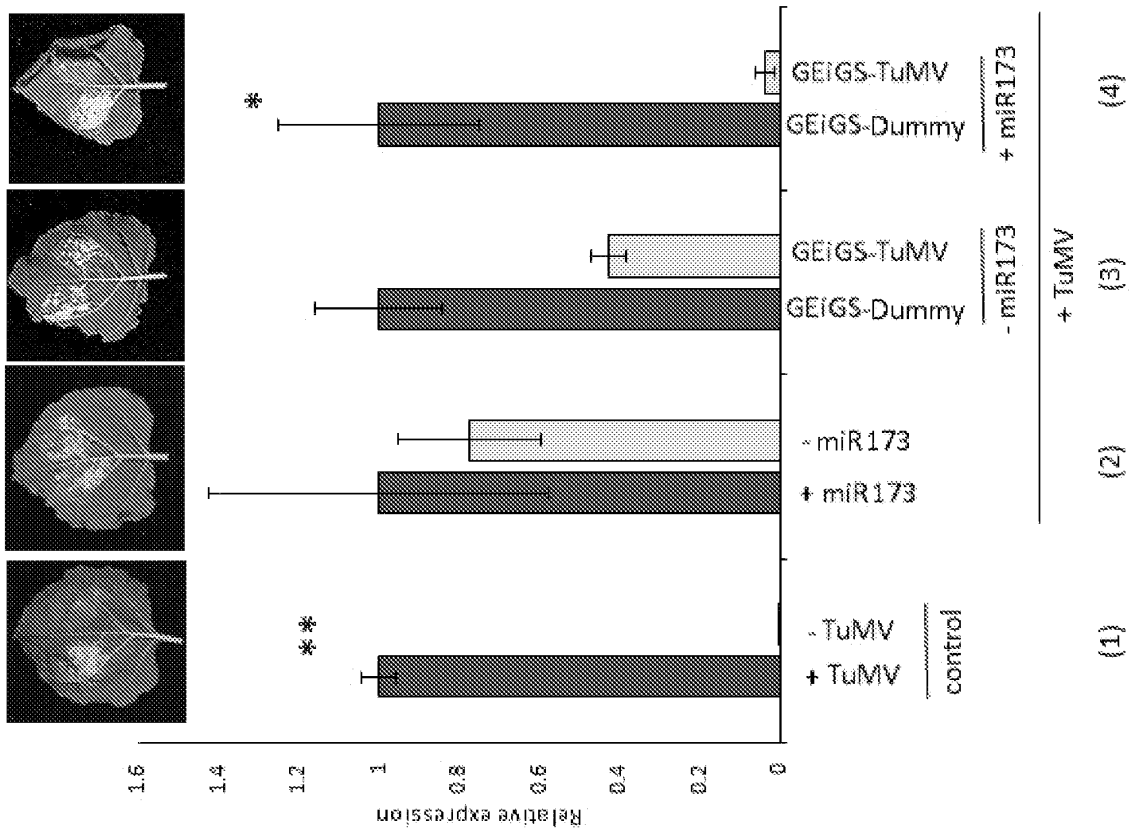

Relative expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
**
*
- TuMV
+ TuMV
control
- miR173
+ miR173
GEiGS-Dummy
GEiGS-TuMV
- miR173
+ miR173
GEiGS-Dummy
GEiGS-TuMV
+ TuMV
(1)
(2)
(3)
(4)

FIG. 11B

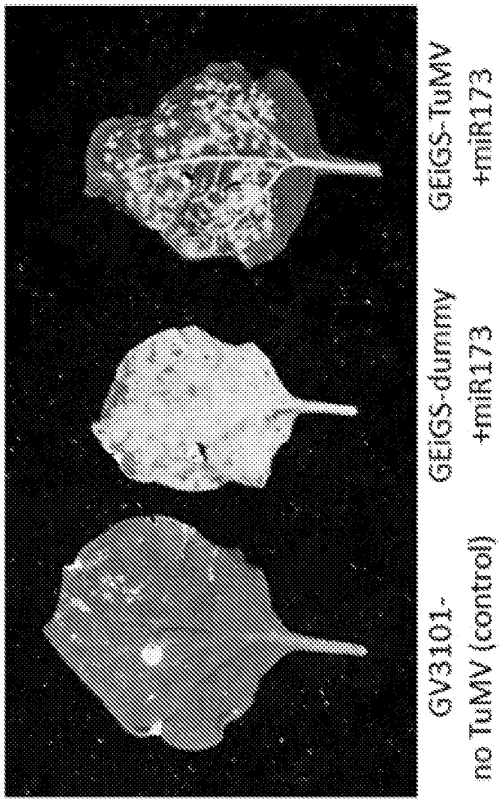

GV3101-
no TuMV (control)
GEiGS-dummy
+miR173
GEiGS-TuMV
+miR173

FIG. 12A

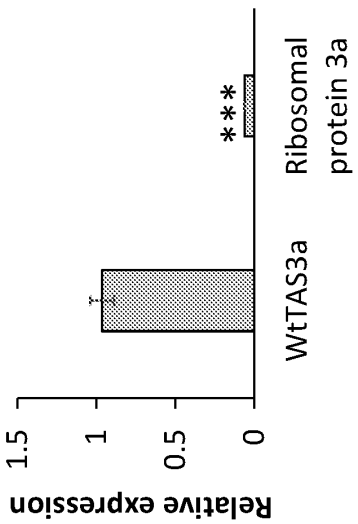


FIG. 12B

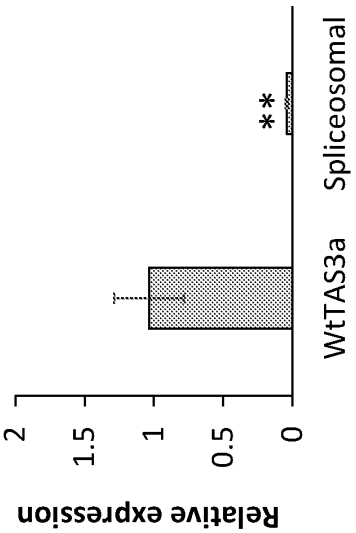


FIG. 13A

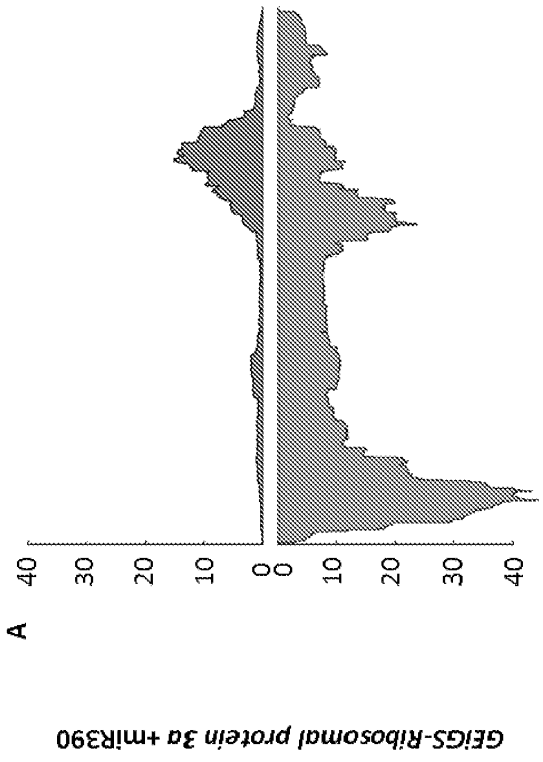


FIG. 13B

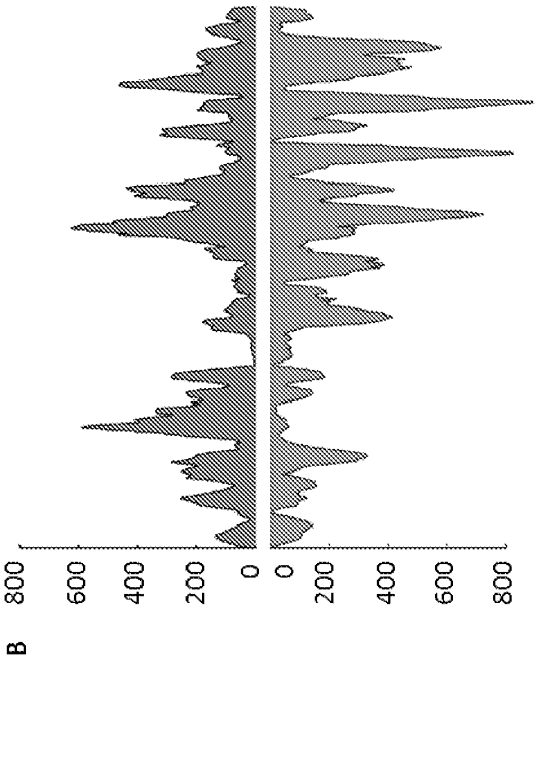


FIG. 13C

FIG. 13D