FIG. 1

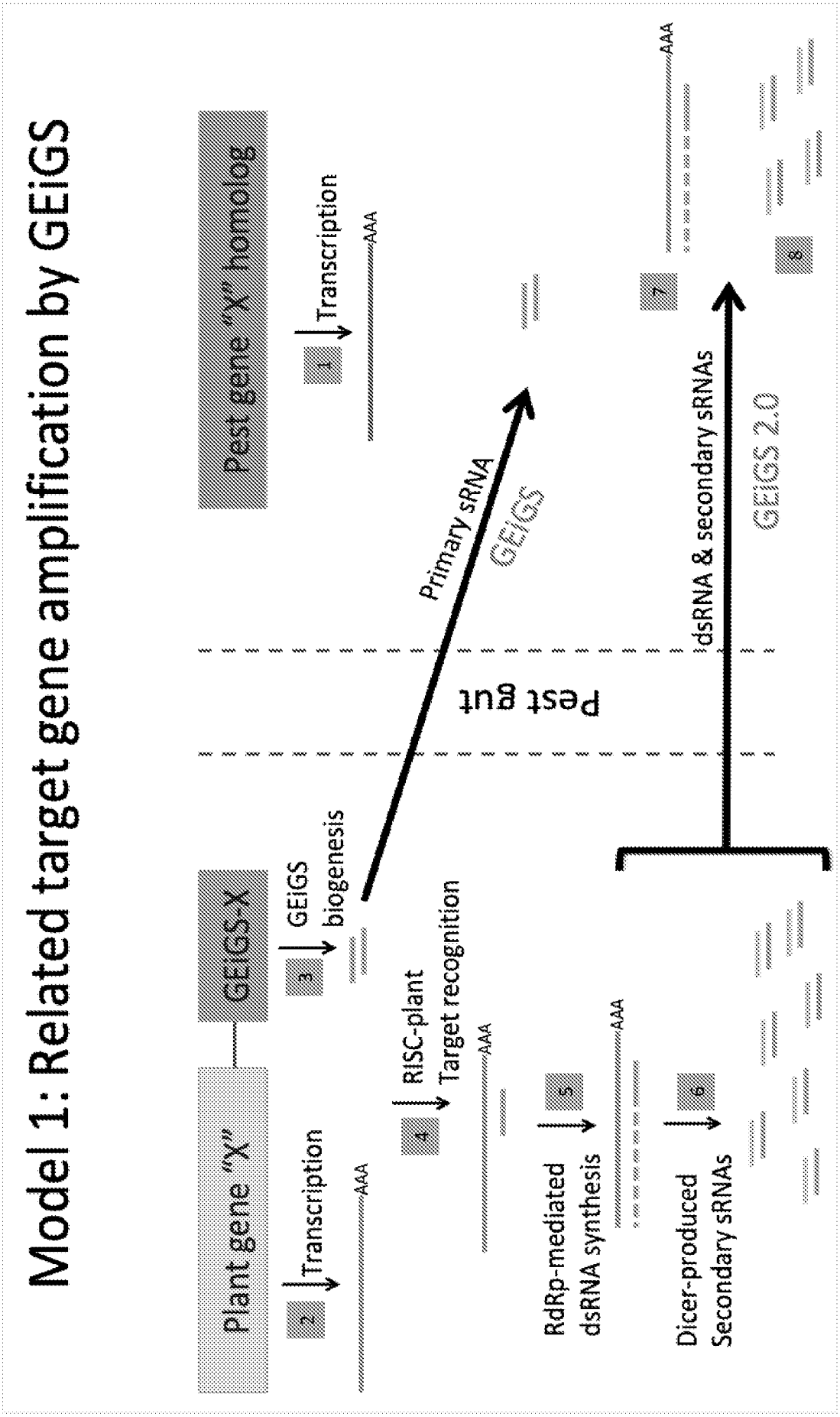

Model 1: Related target gene amplification by GEiGS
Plant gene "X"
GEIGS-X
Pest gene "X" homolog
1 Transcription
2 Transcription
3 GEiGS biogenesis
4 RISC-plant Target recognition
5 RdRp-mediated dsRNA synthesis
6 Dicer-produced Secondary sRNAs
7
8
AAA
Primary sRNA
GEIGS
Pest gut
dsRNA & secondary sRNAs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

FIG. 2

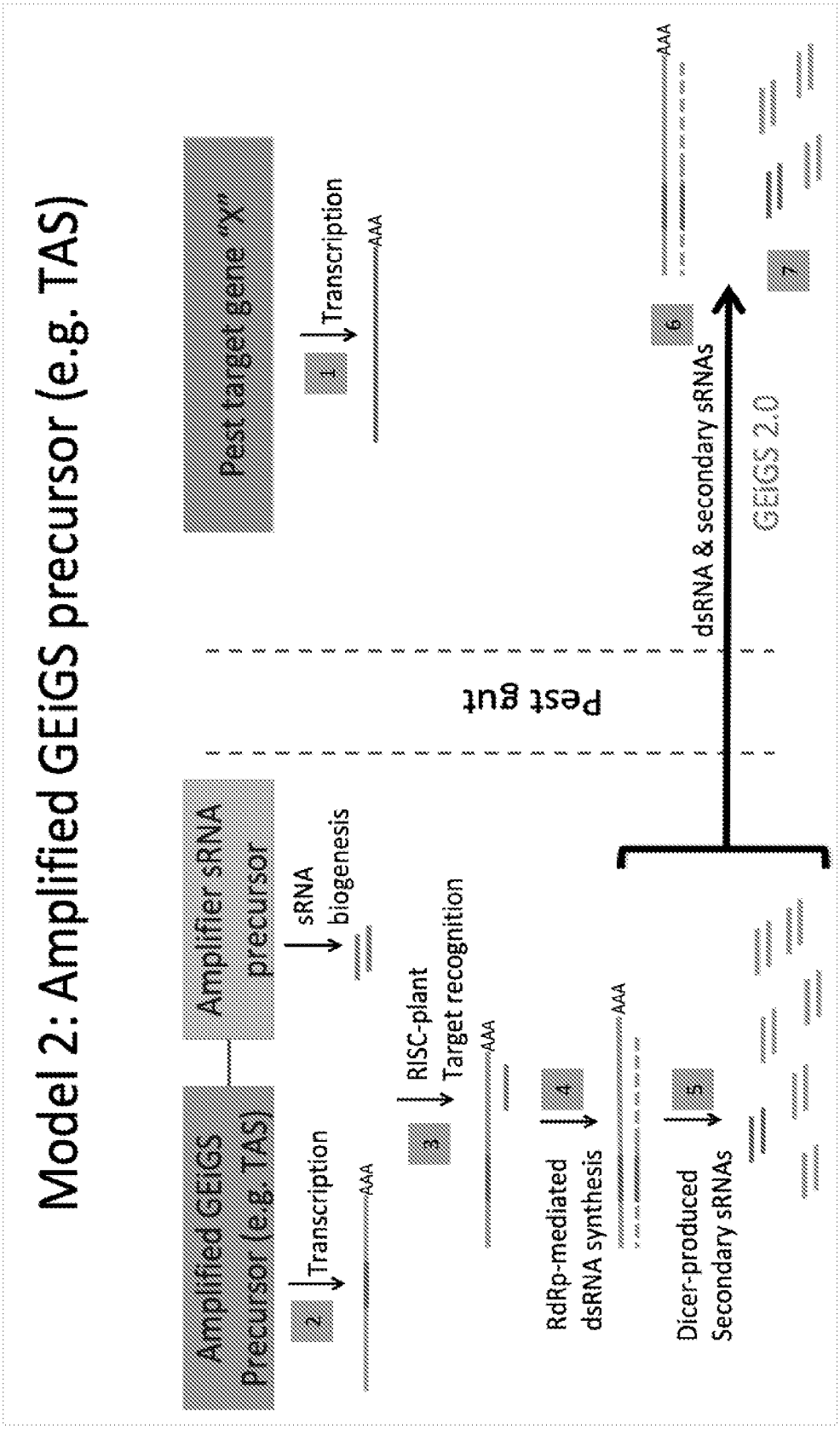

Model 2: Amplified GEiGS precursor (e.g. TAS)
Amplified GEiGS Precursor (e.g. TAS)
Amplifier sRNA precursor
Pest target gene "X"
1
Transcription
AAA
2
Transcription
AAA
sRNA biogenesis
3
RISC-plant Target recognition
AAA
Pest gut
RdRp-mediated dsRNA synthesis
4
AAA
Dicer-produced Secondary sRNAs
5
dsRNA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

GAAGGACUnnqnaaaacaaunncagaaunaCUGAGGACAAAAAUGUUGUAGUACACUUAAAGUCGCAAACCGC
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

CAAGAGAAACGCAAAGAUAAAGAUUGAACUGGGGUAUCACACAAAGGCAAGAUGCAGACCAGUGCAGUUGCUUCGCUUGCGUGaugcucauggunnuaaauuuaA
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
TCTGATGAAATTCCAAAGAGatgccatggtttcaatttcatcCATCTTCTTCTCTCAATACCACTCTGCAGCGTTTTGGATTCAGAAAGCCTAAGCTAGCTCTGGTTTTTGGCGATTTGTT
AGCTGATCCAGAACAGGTGTTAATGGTGTCTCTCTCCAAGGCACTGCAAGAGGTTGGCTATGCAATTGAGGTTTACTCGCTTGAAGATGGTCCAGTGAATAGTATTTGGCAGAAAATGGG
AGTTCCAGTCACAATACTCAAGCCTAATCAGGAATCGAGTTGTGTTATCGACTGGCTCTCCTATGATGGCATAATTGTGAACTCTCTCCGAGCTAGGAGTATGTTTACTTGCTTCATGCA
AGAACCTTTCAAATCTTTGCCTCTTATTTGGGTCATCAATGAAGAAACTCTTGCTGTTCGGTCTAGACAGTACAACTCAACAGGGCAGACTGAACTCCTCACTGACTGGAAAAAGATTTT
CAGCCGGGCATCGGTTGTAGTCTTCCATAATTATCTCCTTCCGATACTCTACACCGAGTTTGATGCTGGCAACTTCTATGTGATTCCCGGATCTCCTGAAGAAGTATGTAAAGCAAAGAA
TCTAGAGTTTCCTCCACAGAAAGATGATGTGGTCATTTCCATTGTGGGAAGTCAGTTCTTGTACAAGGGTCAATGGCTGGAACATGCCCTGCTTCTGCAAGCTCTACGGCCTTTATTTTC
GGGCAATTACCTTGAAAGTGATAATTCCCATCTCAAGATCATAGTTTTAGGTGGAGAGACAGCGTCCAACTACAGCGTAGCTATTGAGACAATTTCCCAGAACTTGACATATCCAAAAGA
GGCTGTGAAGCACGTAAGAGTTGCGGGGAATGTTGATAAGATTCTTGAAAGTTCTGATCTTGTTATATATGGATCATTTCTTGAGGAGCAGTCTTTTCCAGAAATTTTGATGAAGGCCAT
GTCCTTGGGGAAACCTATAGTTGCACCAGACCTCTTCAACATTAGAAAATATGTTGACGACAGGGTTACTGGGTATCTCTTCCCCAAGCAGAATCTTAAAGTTCTATCGCAAGTTGTGCT
TGAAGTGATAACAGAAGGGAAGATATCTCCATTGGCTCAGAAGATTGCCATGATGGGGAAAACAACTGTTAAAAATATGATGGCTCGGGAAACCATAGAAGGTTATGCAGCTCTACTAGA
GAATATGCTCAAGTTTTCTTCGGAAGTTGCTTCTCCTAAGGATGTACAAAAAGTTCCTCCAGAACTGAGAGAAGAGTGGAGTTGGCATCCGTTTGAAGCTTTTATGGATACATCGCCTAA
TAATAGAATAGCAAGAAGTTATGAGTTCTTAGCGAAGGTTGAGGGGCATTGGAATTATACCCCAGGAGAAGCTATGAAATTTGGAGCTGTTAATGATGATTCGTTCGTGTATGAAATTTG
GGAAGAAGAGAGATATCTTCAAATGATGAATAGTAAAAAAAGACGAGAAGACGAGGAGCTGAAAAGCAGAGTCTTGCAGTATCGTGGGACATGGGAAGATGTATATAAAAGCGCCAAAAG
GGCAGACCGAAGTAAGAATGATCTACATGAGAGGGATGAAGGGGAGCTGCTAAGAACCGGTCAACCTTTATGCATATATGAACCCTATTTTGGTGAAGGAACCTGGTCGTTTCTACATCA
AGATCCCCTCTATCGTGGGGTTGGCCTGTCAGTTAAAGGACGTAGACCTAGGATGGATGATGTCGATGCATCATCACGTCTTCCGCTTTTCAACAATCCGTACTATCGCGATGCTCTTGG
TGACTTTGGAGCTTTTTTTGCAATCTCAAACAAGATTGATCGGTTACACAAGAATTCATGGATTGGGTTTCAGTCCTGGAGAGCGACTGCCAGGAAGGAATCTTTATCCAAGATTGCTGA
AGACGCATTACTTAATGCTATACAAACACGAAAACACGGAGATGCCTTATATTTTTGGGTTCGCATGGACAAAGATCCCAGAAATCCTCTGCAGAAACCCTTTTGGTCGTTCTGTGATGC
CATAAATGCTGGGAATTGCAGGTTTGCTTACAACGAAACTTTGAAGAAAATGTACAGTATCAAGAACTTGGACTCATTGCCACCAATGCCCGAGGATGGGGATACATGGTCTGTGATGCA
GAGCTGGGCATTGCCAACAAGATCCTTCTTAGAGTTTGTCATGTTCTCAAGGATGTTTGTGGATTCACTAGATGCACAGATATATGAAGAGCATCATCGAACAAACCGTTGCTATCTGAG
TTTAACCAAAGACAAGCATTGCTATTCGCGGGTACTAGAGCTTCTGGTGAACGTATGGGCTTACCACAGTGCAAGACGCATTGTCTACATAGATCCTGAGACTGGTTTGATGCAAGAGCA
ACACAAACAGAAGAACCGGCGAGGGAAAATGTGGGTGAAGTGGTTCGATTACACAACTCTGAAAACAATGGACGAAGATCTAGCTGAAGAAGCCGACTCAGACCGTCGTGTGGGTCACTG
GCTATGGCCATGGACTGGCGAGATCGTGTGGCGCGGTACATTAGAGAAAGAGAAGCAAAAGAAGAATTTAGAGAAAGAGGAGAAGAAGAAGAAGAGTCGAGATAAGCTGAGTAGAATGAG
AAGTAGAAGTGGTCGTCAGAAAGTGATCGGAAAATATGTAAAACCACCGCCTGAGAACGAAACTGTTACCGGAAATTCCACTTTGTTAAATGTAGTAGACGCATAAAAGAAAACAAATTA
AAATTGCTTCTTTTTTTGTTAGGTCACTAATTTGTTTCATTCATTGTTTTTGGAAAGATTACTGTATAAAAGGTCT

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*aaccaaguucauguaucguuu*A
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

TCTTATGGTTACTG*aaccaagttcatgtatcgttt*CATCTAGTACTTTGGTGGTTTATGTTTTGGGGCCATG
TACAGCCTCTGATAAATAATTGATCGACTATGTTTCCGTTTCTTTCATCTCTCTTTTCTTTCAAACAACAAA
TCGAACTTATTCTCTATTGCAATTATCTCTTTCGATTCACTTTTGTCATCGTTGTCTCTTTATATGATGTGC
TTAGTTTGATGAGTGTGAGAAGTACAGAGTCTCTATC
```

FIG. 6

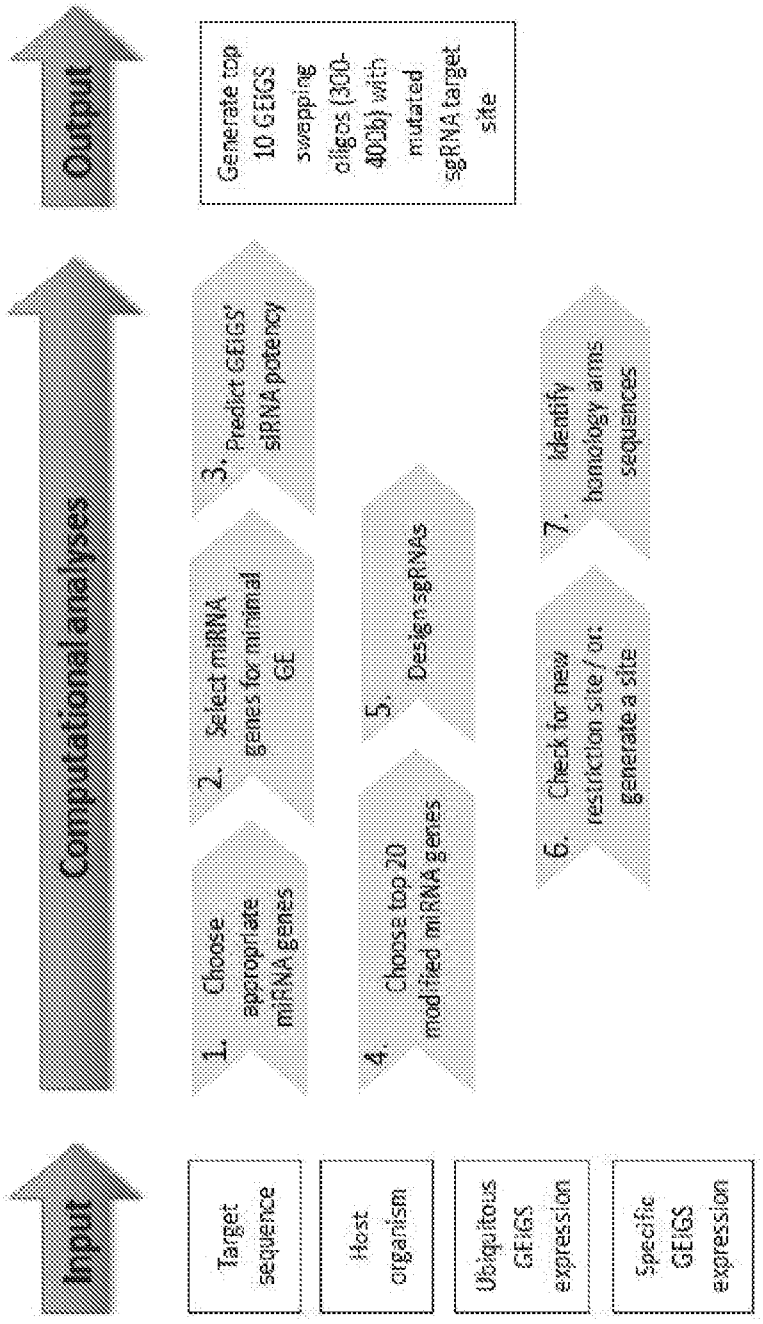
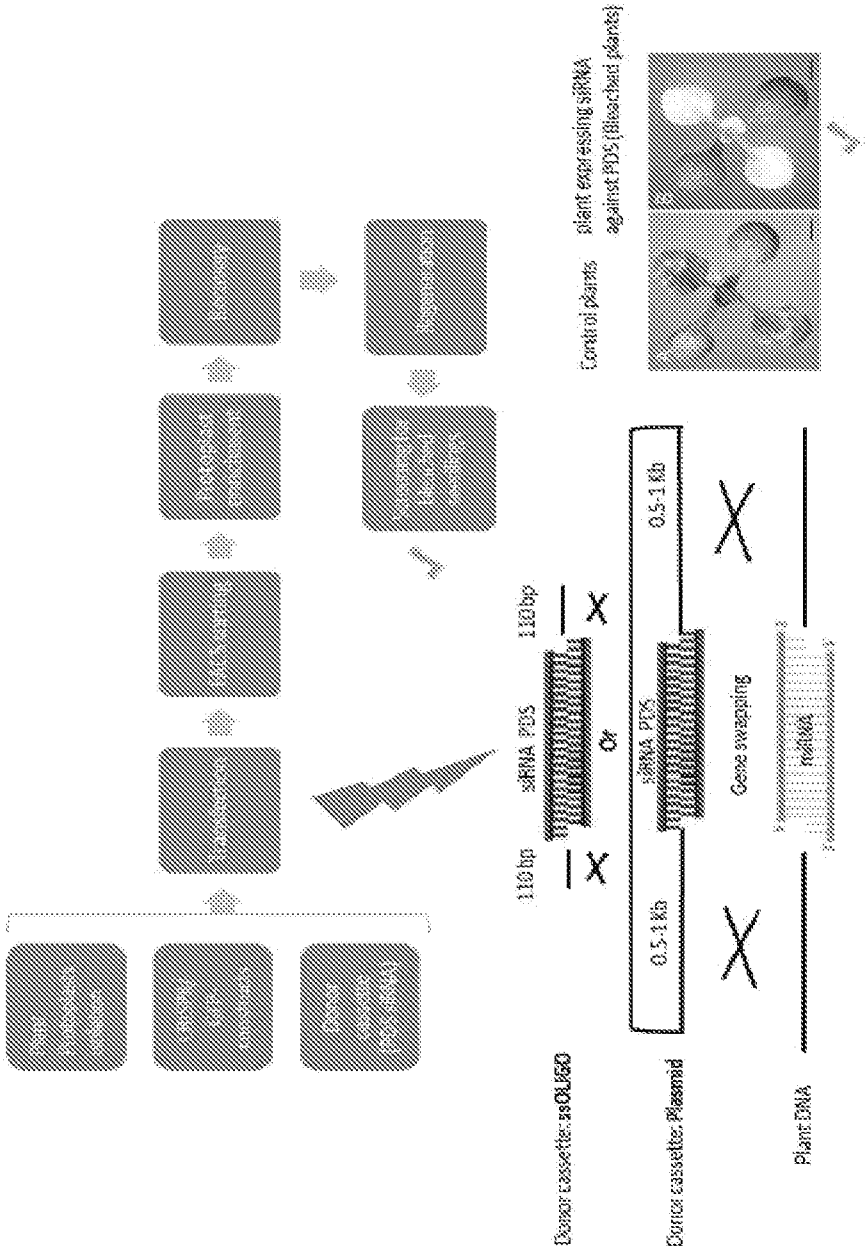

Input
Target sequence
Host organism
Ubiquitous GEiGS expression
Specific GEiGS expression
Computational analyses
1. Choose appropriate miRNA genes
2. Select miRNA genes for miramod GE
3. Predict GEiGS' siRNA potency
4. Choose top 20 modified miRNA genes
5. Design sgRNAs
6. Check for new restriction site / 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)
116 bp
siRNA PDS
116 bp
Or
0.5-1 Kb
siRNA PDS
0.5-1 Kb
Gene swapping
Donor cassette: ssODN
Donor cassette: Plasmid
Plant DNA

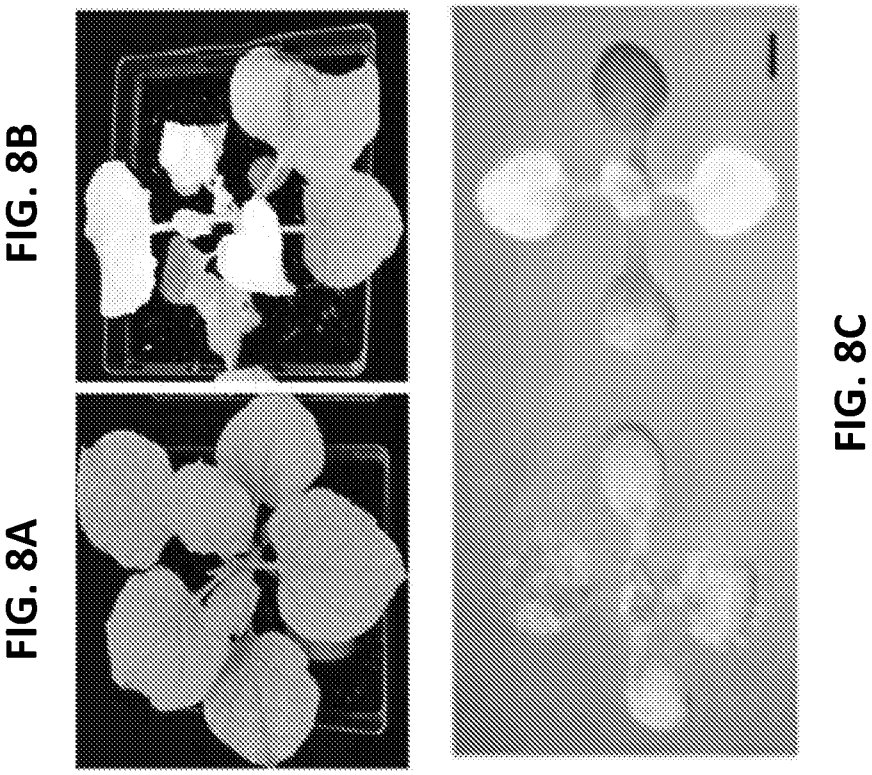


FIG. 8A

FIG. 8B

FIG. 8C

FIG. 9A

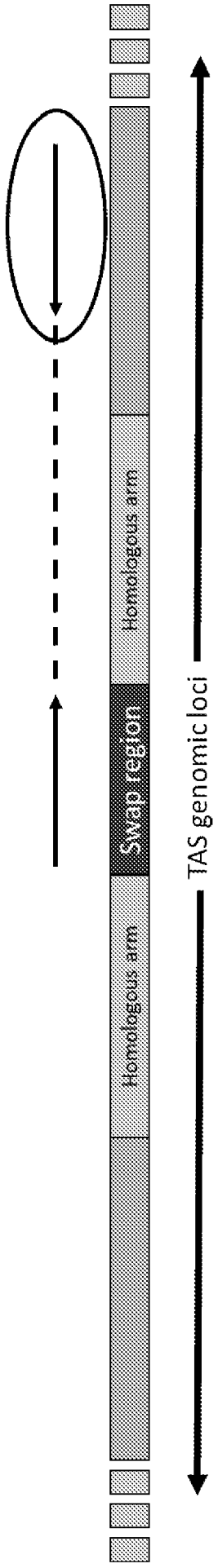

Homologous arm
Swap region
Homologous arm
TAS genomic loci

FIG. 9B

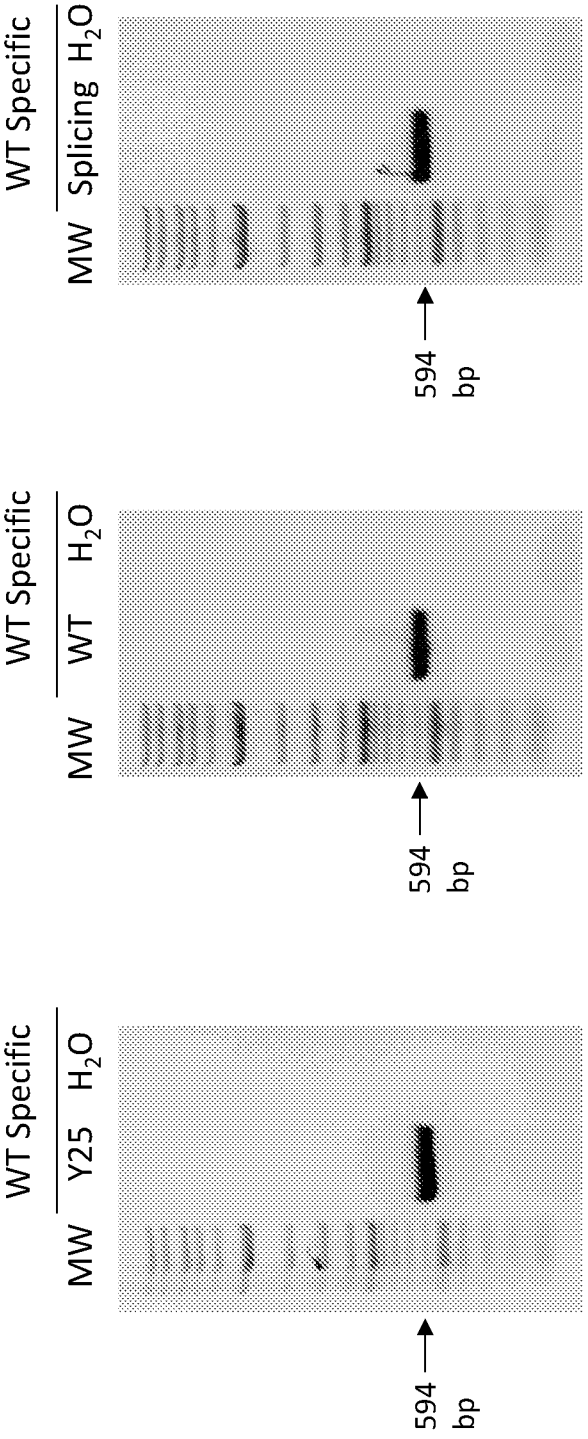

WT Specific
MW Y25 H2O
594 bp
WT Specific
MW WT H2O
594 bp
WT Specific
MW Splicing H2O
594 bp
Tas1b

FIG. 9C

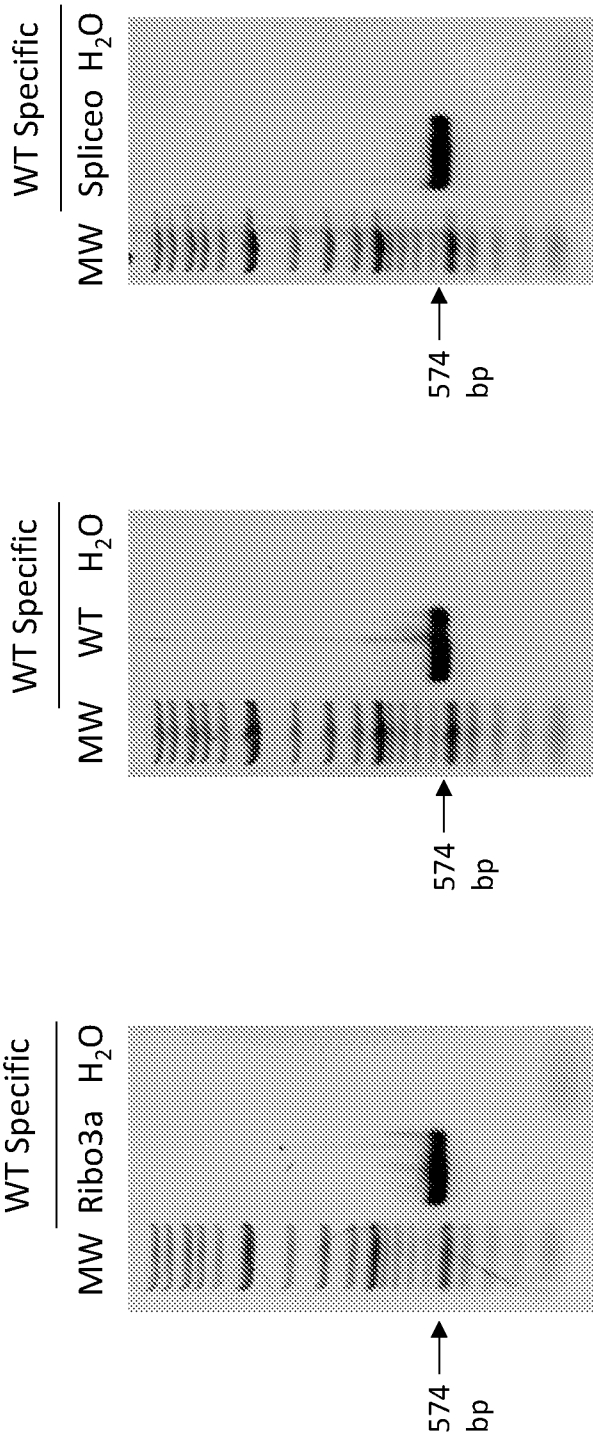
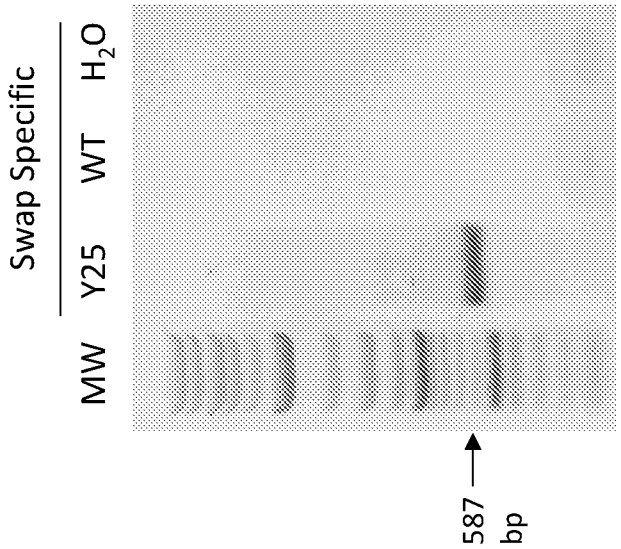

WT Specific
MW Ribo3a H2O
574 bp
WT Specific
MW WT H2O
574 bp
WT Specific
MW Spliceo H2O
574 bp
Tas3a

FIG. 9D


Swap Specific
MW Y25 WT H_2O
587 bp

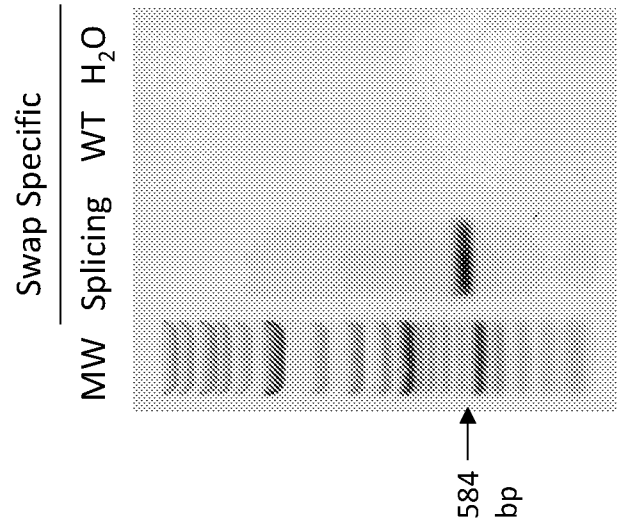
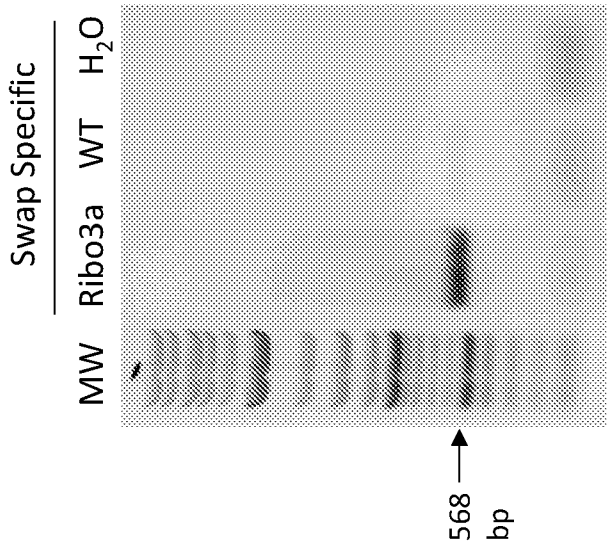

Tas1b
Swap Specific
MW Splicing WT H_2O
584 bp

FIG. 9E


Swap Specific
MW Ribo3a WT H_2O
568 bp

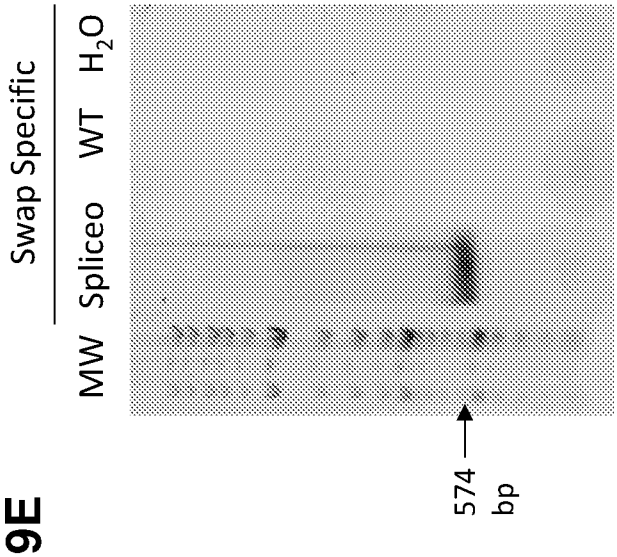

Tas3a
Swap Specific
MW Spliceo WT H_2O
574 bp

FIG. 9F

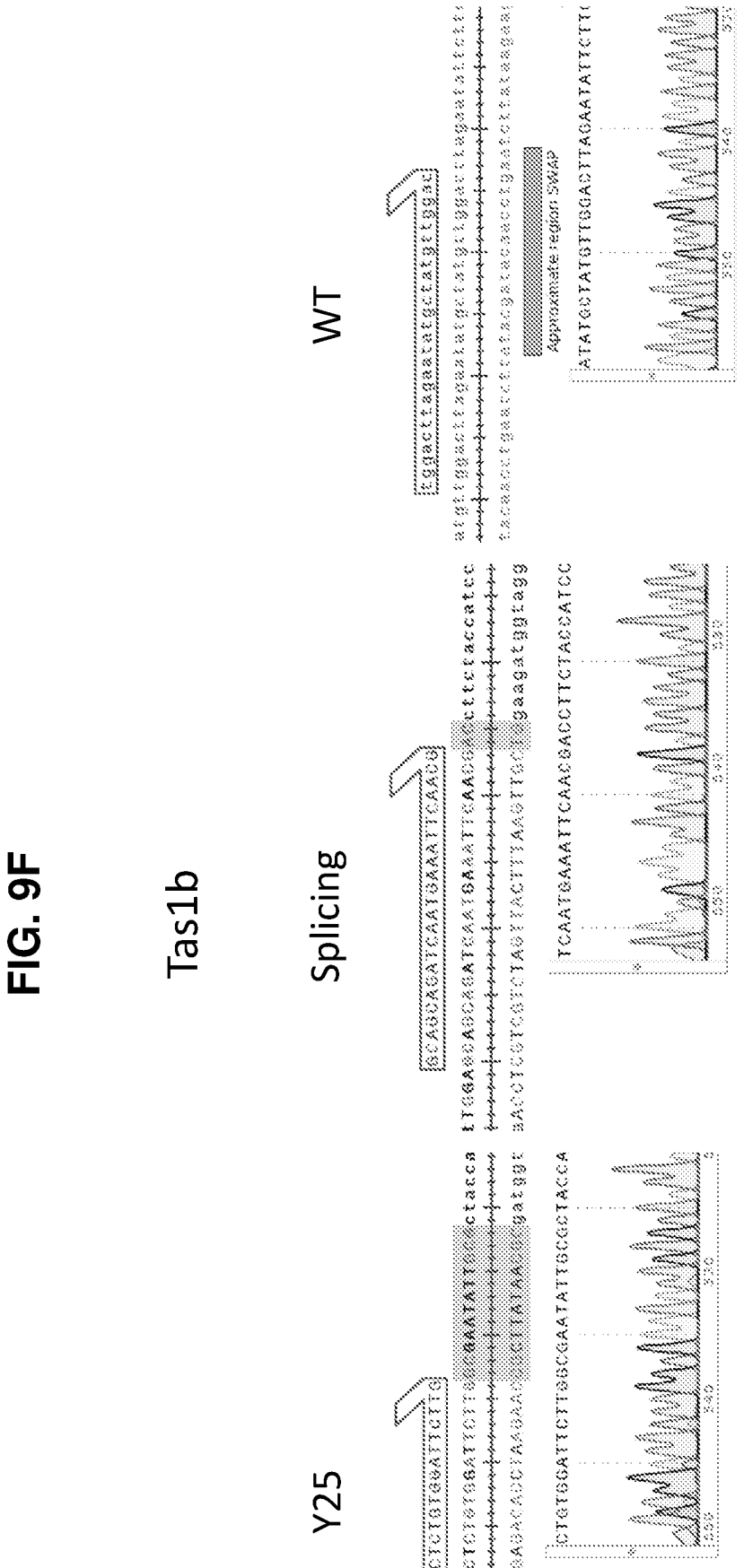
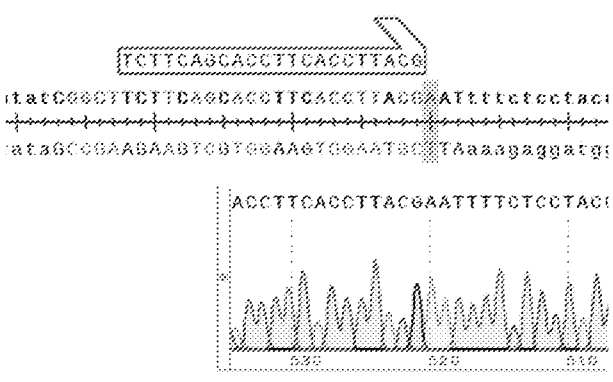

Tas1b
Splicing
WT
Y25
Approximate region SWAP
SEQ ID Nos: 79, 80
SEQ ID Nos: 77, 78
SEQ ID No: 73

FIG. 9G

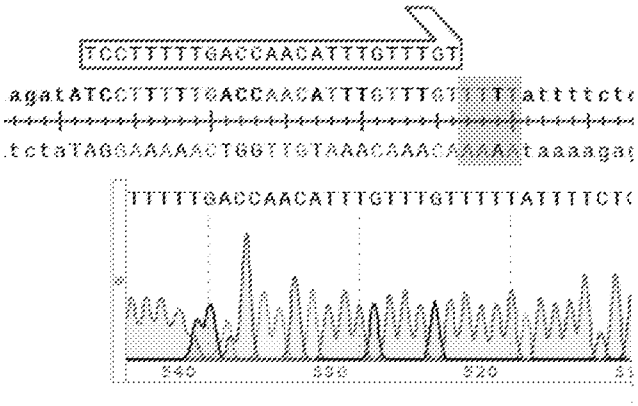
Tas3a

Ribo3a



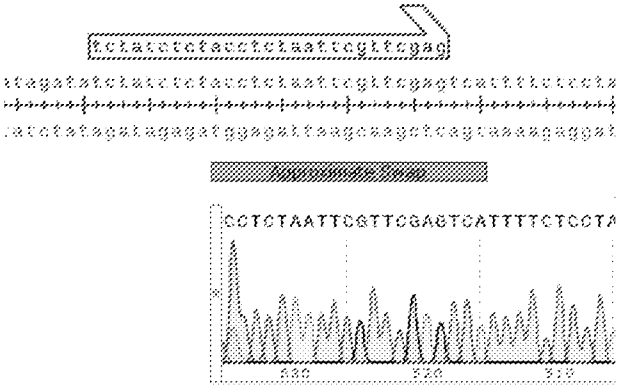
SEQ ID Nos: 85, 86

Spliceo



SEQ ID Nos: 89, 90

WT



SEQ ID No: 83

FIG. 10A

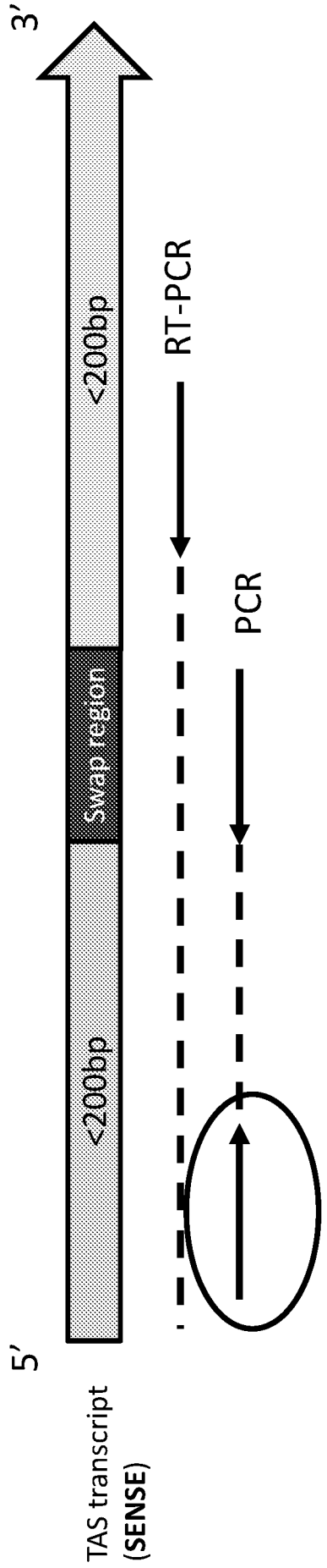


FIG. 10B

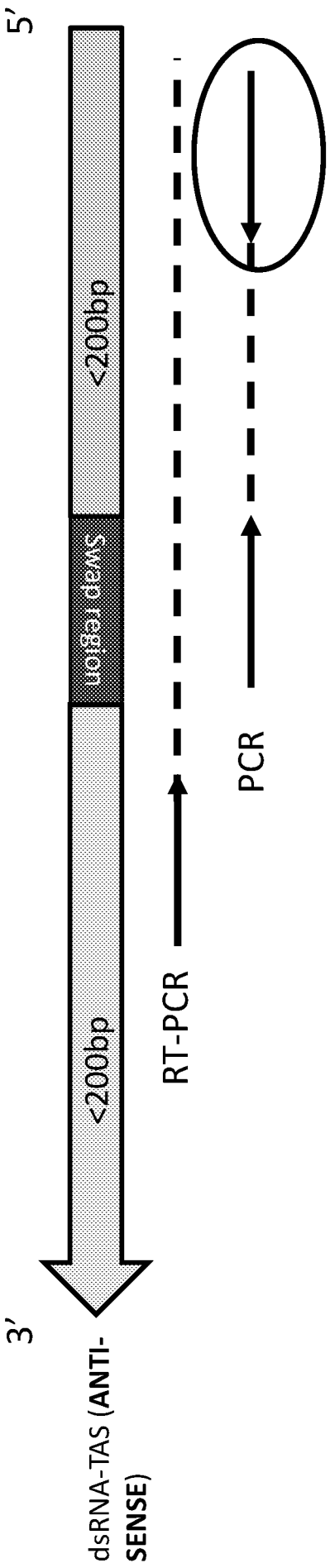


FIG. 10C Tas1b - SENSE

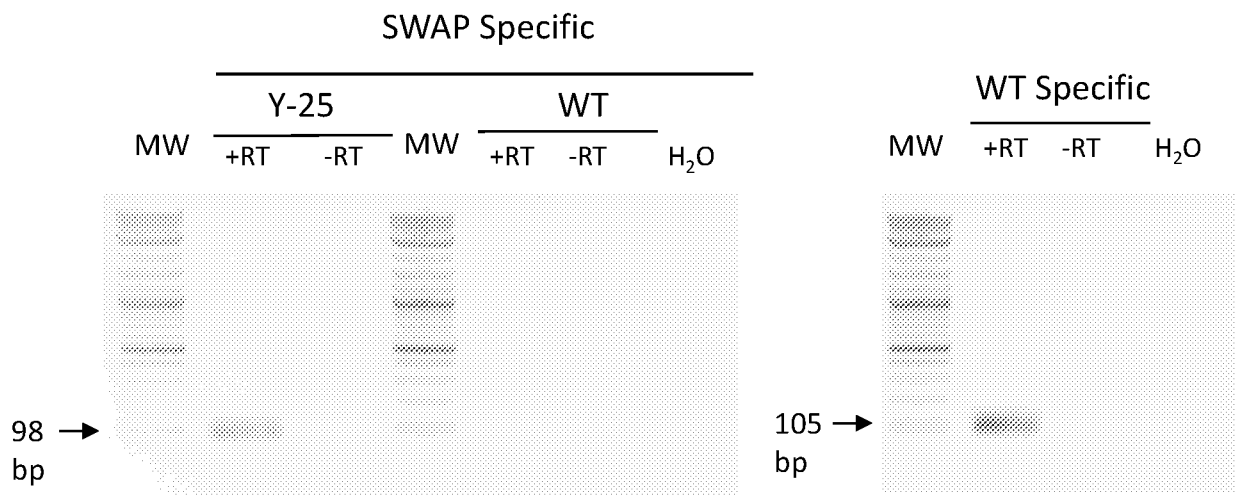


FIG. 10D Tas1b ANTI-SENSE

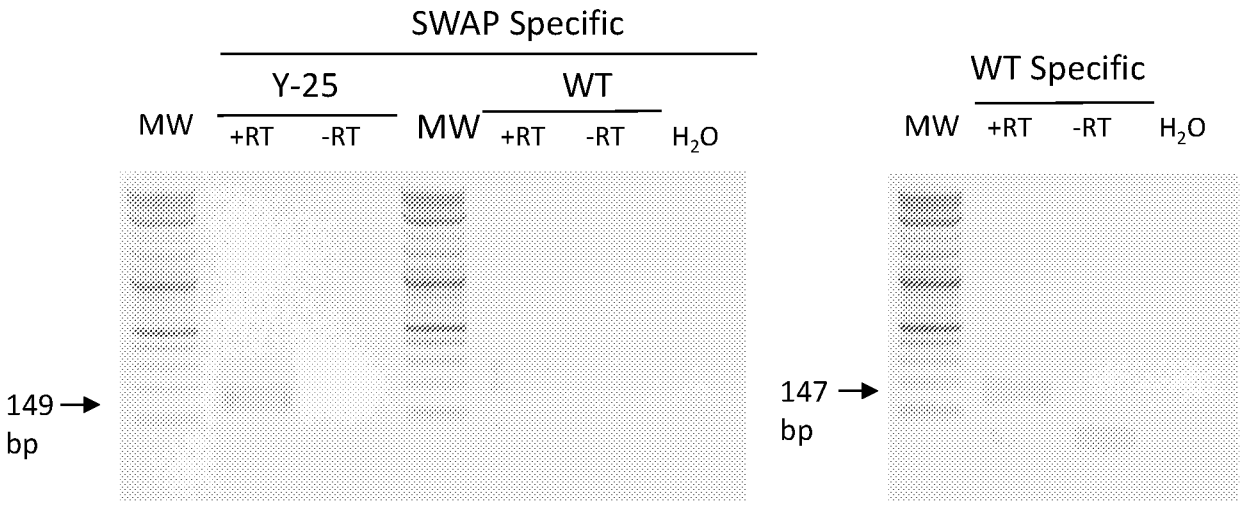


FIG. 10E Tas3a - SENSE

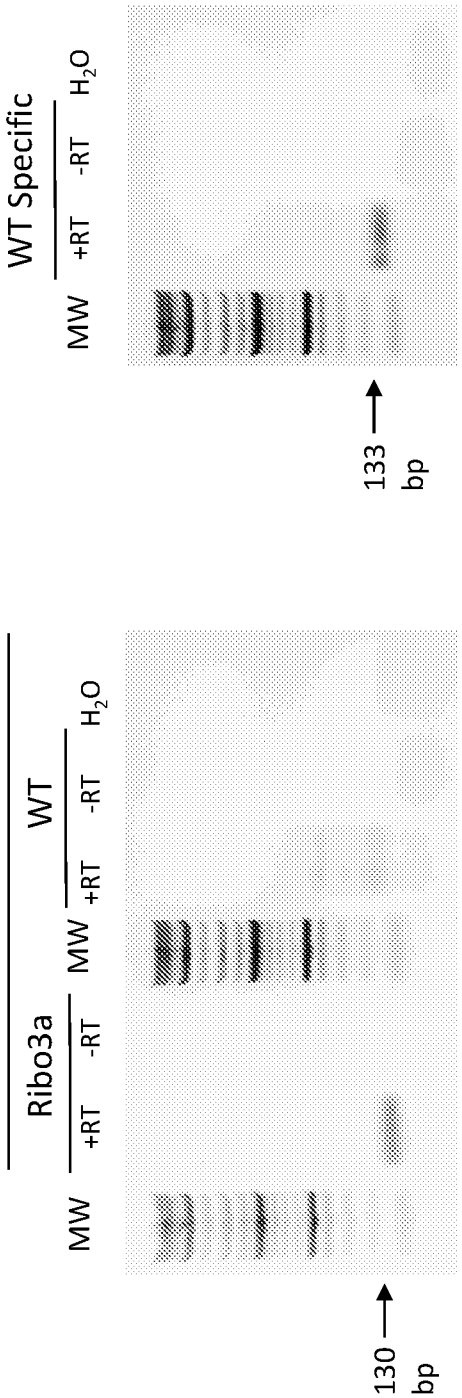


FIG. 10F Tas3a - ANTI-SENSE

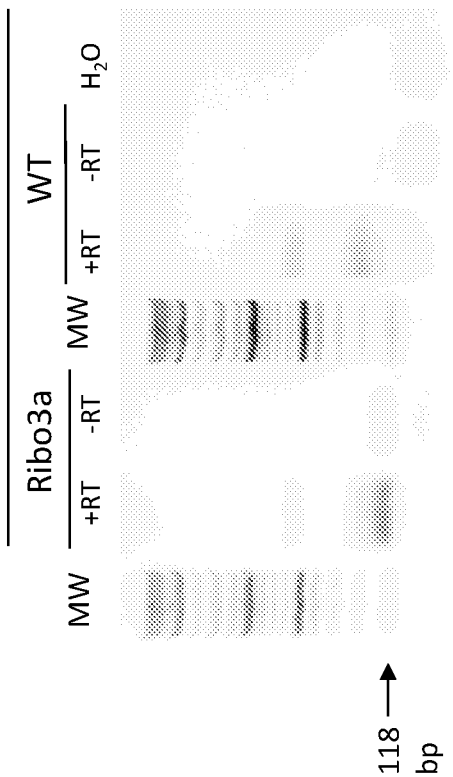
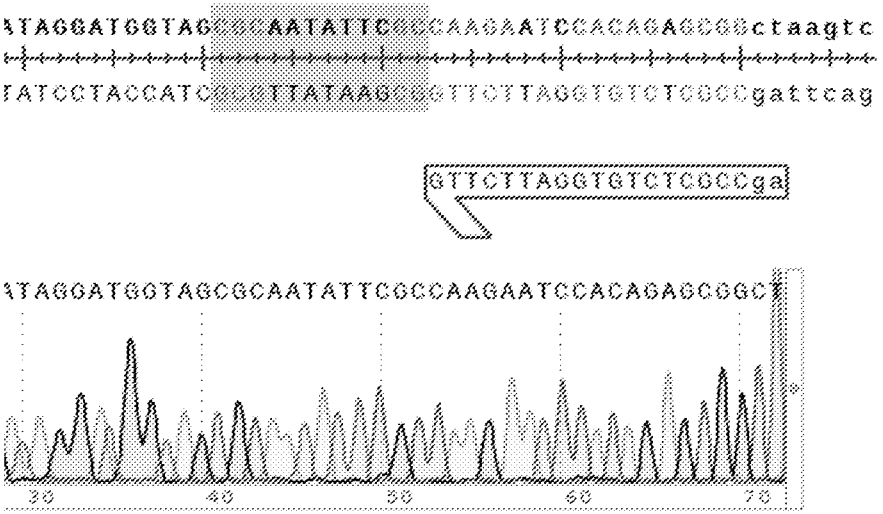


FIG. 10G

Y-25

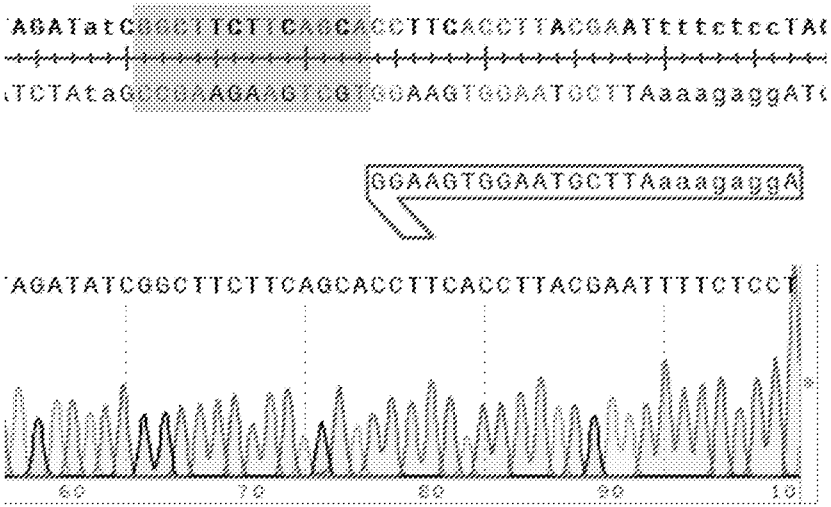
SEQ ID Nos:
79, 80



Tas1b - SENSE

Ribo3a

SEQ ID Nos:
85, 86

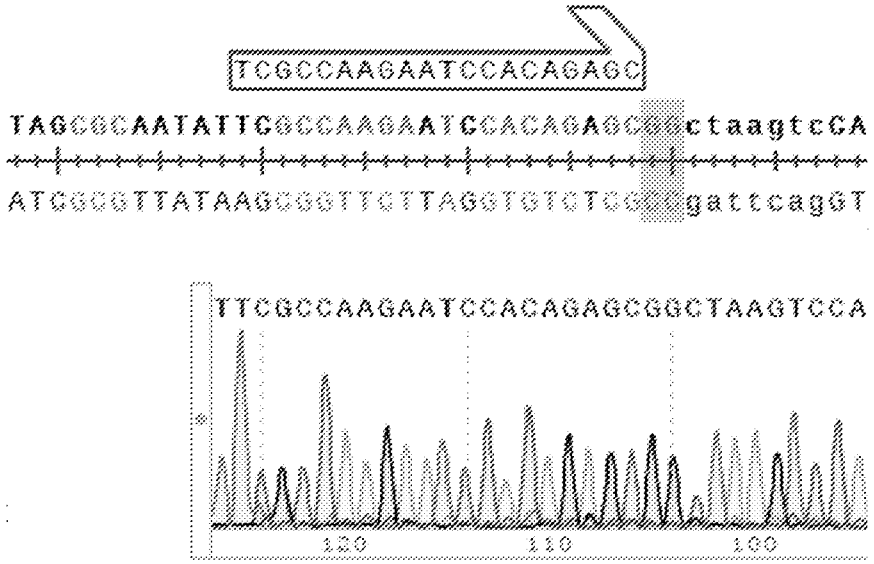


Tas3a - SENSE

FIG. 10H

Y-25

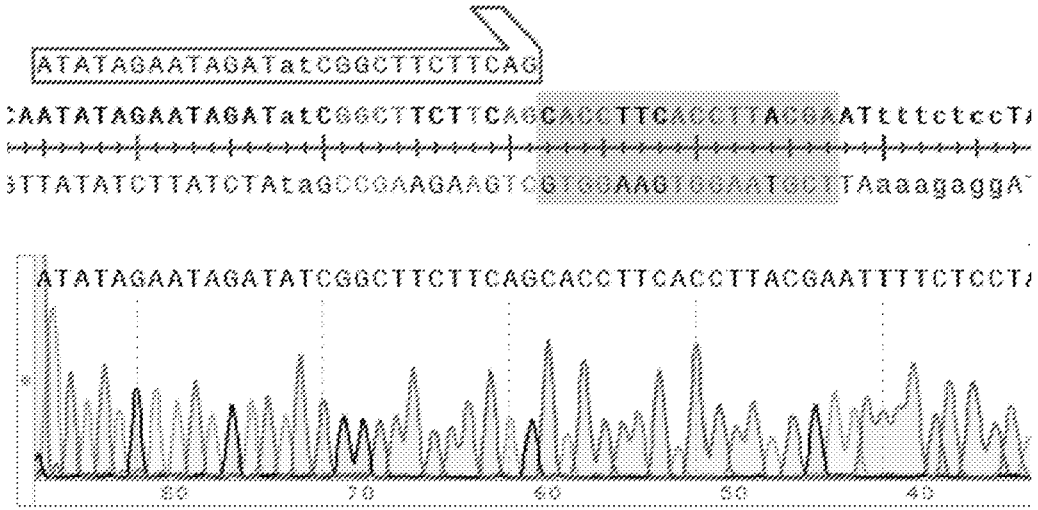
SEQ ID Nos: 79, 80



Tas1b – ANTI-SENSE

Ribo3a

SEQ ID Nos: 85, 86



Tas3a – ANTI-SENSE

FIG. 10I

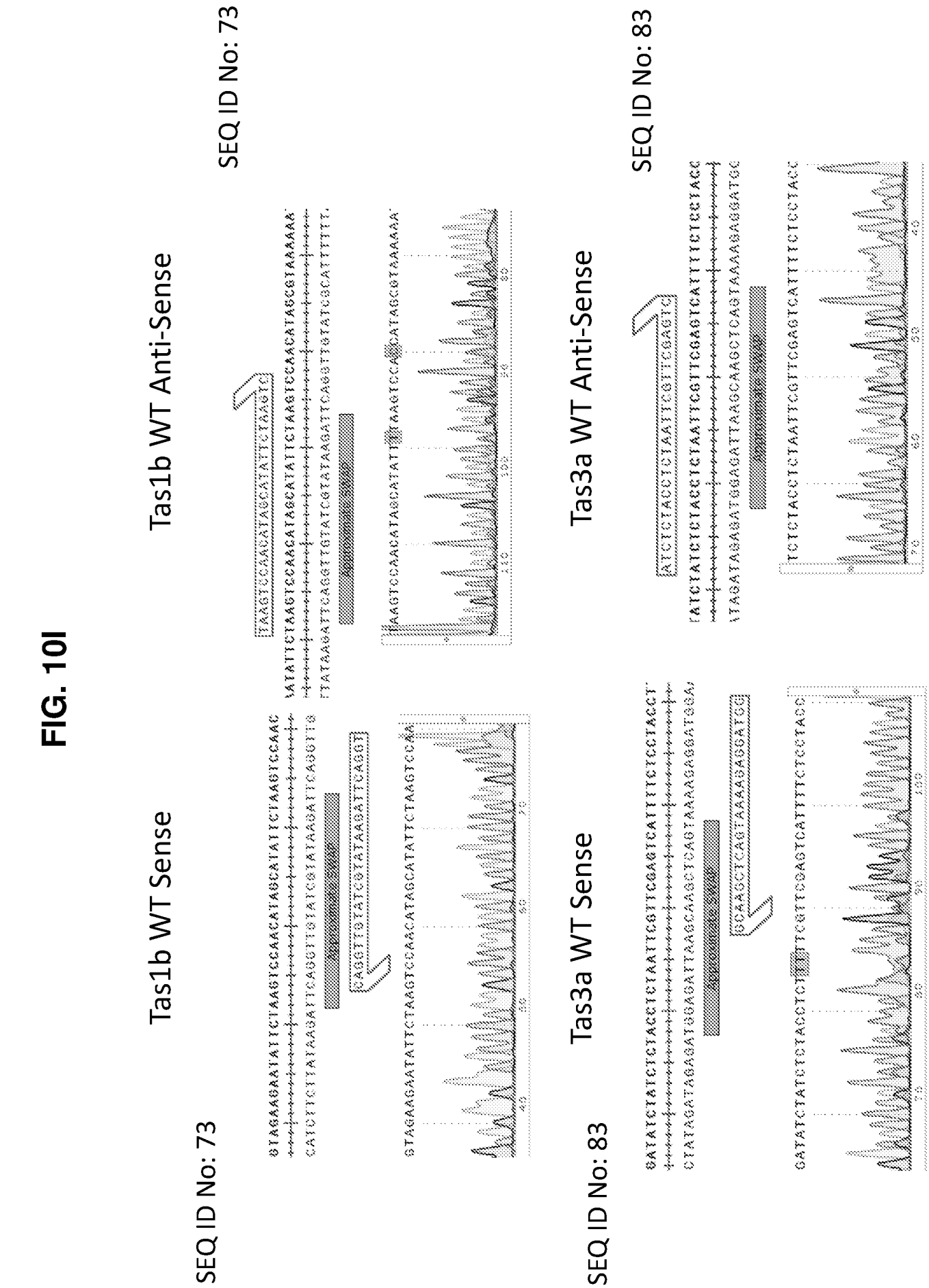

SEQ ID No: 73
Tas1b WT Sense
SEQ ID No: 73
Tas1b WT Anti-Sense
SEQ ID No: 83
Tas3a WT Sense
SEQ ID No: 83
Tas3a WT Anti-Sense

FIG. 11A

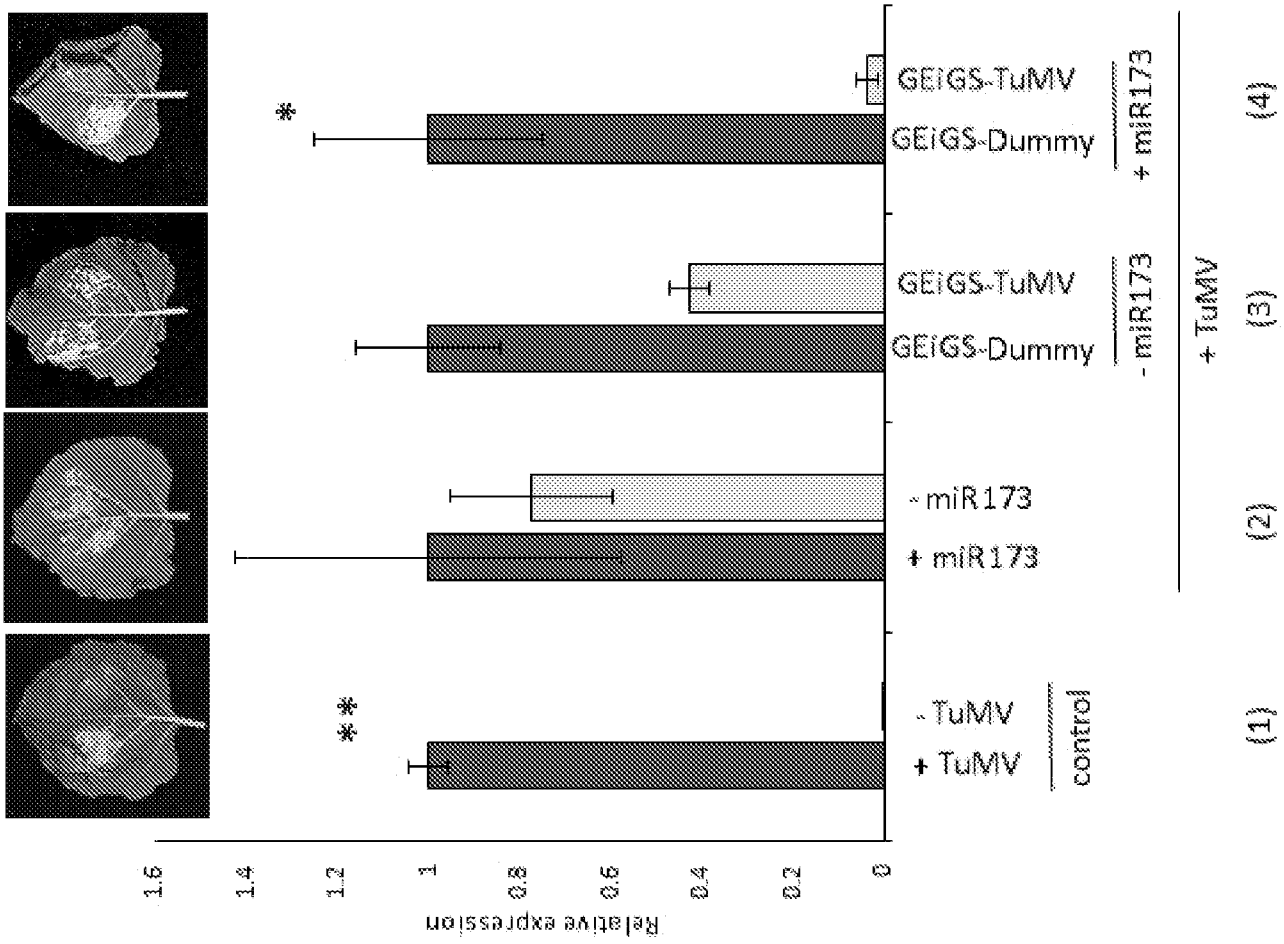

Relative expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
- TuMV
+ TuMV
control
- miR173
+ miR173
GEiGS-Dummy
GEiGS-TuMV
- miR173
GEiGS-Dummy
GEiGS-TuMV
+ miR173
+ TuMV
(1)
(2)
(3)
(4)
**
*
*

FIG. 11B

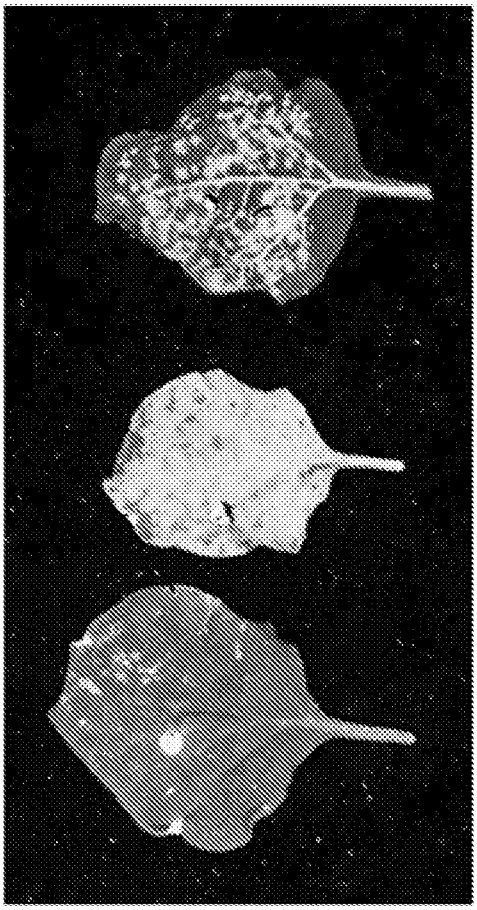

GV3101-
no TuMV (control)
GEiGS-dummy
+miR173
GEiGS-TuMV
+miR173

FIG. 12A

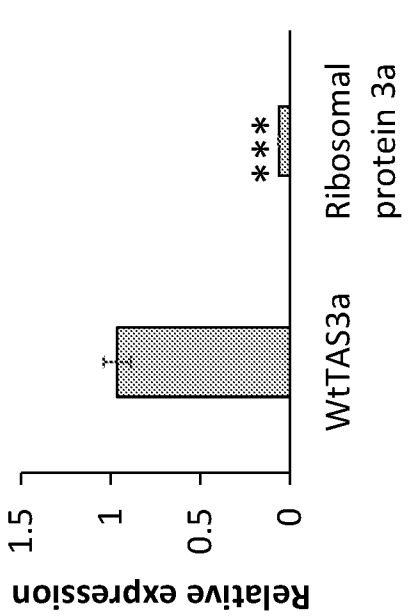


FIG. 12B

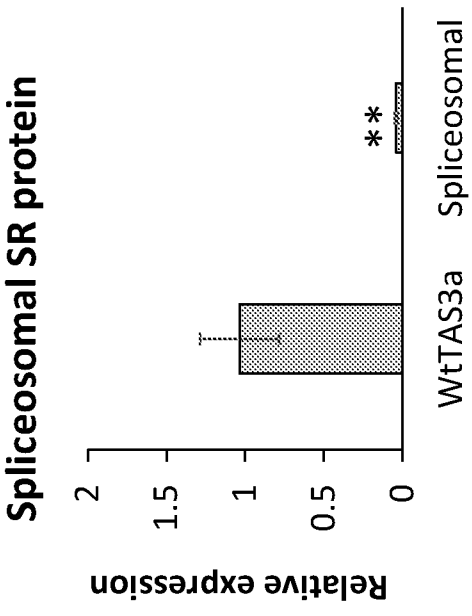
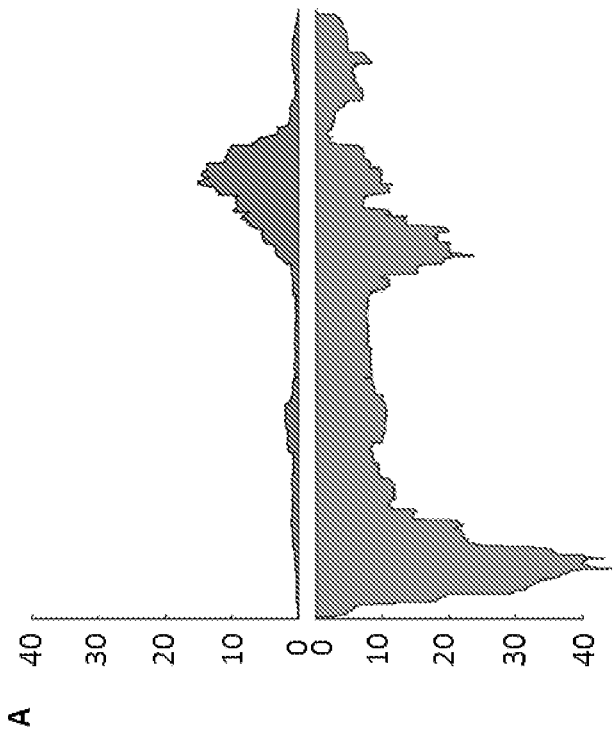


FIG. 13A



GEIGS-Ribosomal protein 3a +miR390

FIG. 13B

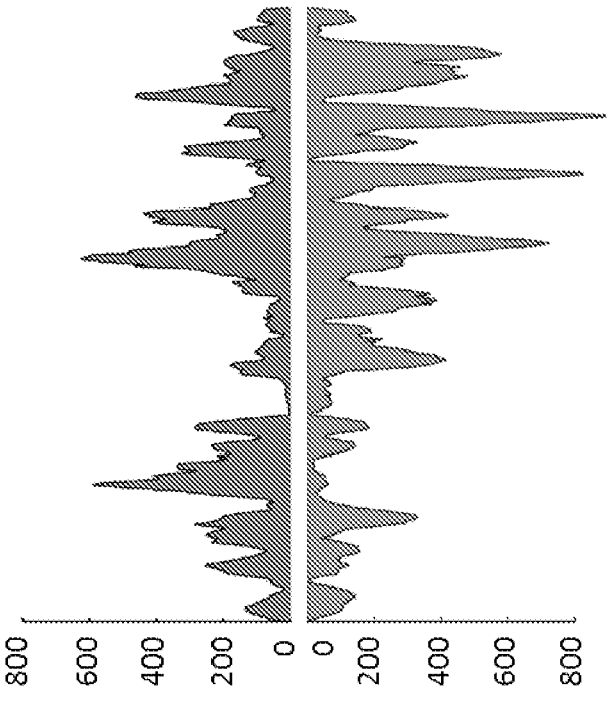


FIG. 13C

GEIGS-Spliceosomal SR protein +miR390

FIG. 13D