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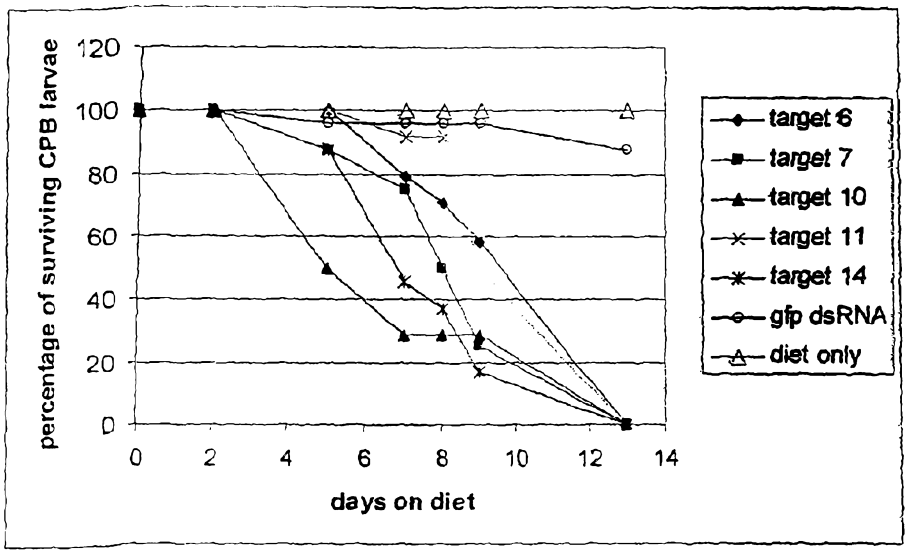
(54) Title: METHODS FOR CONTROLLING PESTS USING RNAI



(57) Abstract: The present invention relates to methods for controlling pest infestation using double stranded RNA molecules. The invention provides methods for producing transgenic cells expressing the double stranded RNA molecules, as well as compositions and commodity products containing or treated with such molecules.

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METHODS FOR CONTROLLING PESTS USING RNAi

FIELD OF THE INVENTION

The present invention relates generally to genetic control of pest infestations. More specifically, the present invention relates to recombinant technologies for repressing or inhibiting expression of target coding sequences in a pest.

INTRODUCTION

Insect and other pests can cause injury and even death by their bites or stings. Additionally, many pests transmit bacteria and other pathogens that cause diseases. For example, mosquitoes transmit pathogens that cause malaria, yellow fever, encephalitis, and other diseases. The bubonic plague, or black death, is caused by bacteria that infect rats and other rodents. Compositions for controlling microscopic pest infestations have been provided in the form of antibiotic, antiviral, and antifungal compositions. Methods for controlling infestations by pests, such as nematodes and insects, have typically been in the form of chemical compositions that are applied to surfaces on which pests reside, or administered to infested animals in the form of pellets, powders, tablets, pastes, or capsules.

Commercial crops are often the targets of insect attack. Substantial progress has been made in the last a few decades towards developing more efficient methods and compositions for controlling insect infestations in plants. Chemical pesticides have been very effective in eradicating pest infestations. However, there are several disadvantages to using chemical pesticides. Not only are they potentially detrimental to the environment, but chemical pesticides are not selective and can pose harm to non-target flora and fauna. Chemical pesticides persist in the environment and generally are slow to be metabolized, if at all. They accumulate in the food chain, and particularly in the higher predator species. Accumulation of chemical pesticides results in the development of resistance to the agents and in species higher up the evolutionary ladder, they can act as mutagens and/or carcinogens and cause irreversible and deleterious genetic modifications.

Because of the dangers associated with chemical pesticides, biological approaches have been developed for controlling pest infestations. For example, biological control using protein Cry3A from *Bacillus thuringiensis* have effectively controlled Colorado potato beetle larvae either as formulations sprayed onto the foliage or expressed in the leaves of potatoes. An alternative biological agent is double stranded RNA (dsRNA). Over the last few years,

downregulation of genes (also referred to as "gene silencing") in multicellular organisms by means of RNA interference has become a well-established technique.

RNA Interference (RNAi) provides a potentially powerful tool for controlling gene expression because of its specificity of target selection and remarkably high efficiency in target mRNA suppression. RNAi refers to the process of sequence-specific post-transcriptional gene silencing mediated by short interfering RNAs (siRNAs) (Zamore, P. et al., *Cell* 101:25-33 (2000); Fire, A. et al., *Nature* 391:806 (1998); Hamilton et al., *Science* 286, 950-951 (1999); Lin et al., *Nature* 402:128-129 (1999)). While the mechanics underlying RNAi are not fully characterized, it is thought that the presence of dsRNA in cells triggers RNAi by activating the ribonuclease III enzyme Dicer (Zamore, P. et al., (2000); Hammond et al., *Nature* 404, 293 (2000)). Dicer processes the dsRNA into short pieces called short interfering RNAs (siRNAs), which are about 21 to about 23 nucleotides long and comprise about 19 base pair duplexes (Zamore et al., (2000); Elbashir et al., *Genes Dev.*, 15, 188 (2001)). Following delivery into cells, the siRNA molecules associate with an endonuclease complex, commonly referred to as an RNA-induced silencing complex (RISC), which brings together the antisense strand of the siRNA and the cellular mRNA gene target. RISC cleaves the mRNA, which is then released and degraded. Importantly, RISC is then capable of degrading additional copies of the target mRNA.

Accordingly, the present invention provides methods and compositions for controlling pest infestation by repressing, delaying, or otherwise reducing gene expression within a particular pest.

SUMMARY OF THE INVENTION

In one aspect, the invention provides an isolated polynucleotide sequence comprising a nucleic acid sequence set forth in SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692,

1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481. In one embodiment, a double stranded ribonucleotide sequence is produced from the expression of a polynucleotide sequence, wherein contact of said ribonucleotide sequence by a pest inhibits the growth of said pest. In a further embodiment, contact of the sequence inhibits expression of a nucleotide sequence substantially complementary to said sequence. In another embodiment, a cell is transformed with the polynucleotide. In a further embodiment, the cell is a bacterial, yeast, or algal cell. In a still further embodiment, a food product, such as stored grains, pet food, or powdered chocolate, comprises the cell transformed with the polynucleotide. In yet another embodiment, a composition , such as a spray, powder, pellet, gel, capsule, food product, garment bag, and book, comprising the polynucleotide. In yet another embodiment, the invention provides a pesticide comprising the polynucleotide. In another embodiment, the invention provides a method for protecting an object, such as wood, tree, book binding, cloth, and a food storage container, from pest infestation, comprising treating said surface with a composition comprising the polynucleotide.

In another aspect, the invention provides a polynucleotide sequence having at least 70% sequence identity to a nucleic acid sequence set forth in SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481. In one embodiment, a double stranded ribonucleotide sequence is produced from the expression of a polynucleotide sequence, wherein contact of said ribonucleotide sequence by a pest inhibits the growth of said pest. In a further embodiment, contact of the sequence inhibits expression of a nucleotide sequence

substantially complementary to said sequence. In another embodiment, a cell is transformed with the polynucleotide. In a further embodiment, the cell is a bacterial, yeast, or algal cell. In a still further embodiment, a food product, such as stored grains, pet food, or powdered chocolate, comprises the cell transformed with the polynucleotide. In yet another embodiment, a composition , such as a spray, powder, pellet, gel, capsule, food product, garment bag, and book, comprising the polynucleotide. In yet another embodiment, the invention provides a pesticide comprising the polynucleotide. In another embodiment, the invention provides a method for protecting an object, such as wood, tree, book binding, cloth, and a food storage container, from pest infestation, comprising treating said surface with a composition comprising the polynucleotide.

In another aspect, the invention provides a method for controlling pest infestation, comprising exposing a pest to a composition comprising a polynucleotide sequence that inhibits a pest biological activity. In one embodiment, the polynucleotide sequence is set forth in any of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481.

In other embodiments, the invention provides for the use of the isolated nucleotide sequence, the double stranded ribonucleotide sequence, the cell, the composition, or the pesticide for preventing or treating an infestation, such as insect, nematode, or fungal infestation.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1-LD: Survival of *L. decemlineata* on artificial diet treated with dsRNA. Insects of the second larval stage were fed diet treated with 50 µl of topically-applied solution of dsRNA (targets or gfp control). Diet was replaced with fresh diet containing topically-applied dsRNA after 7 days. The number of surviving insects were assessed at days 2, 5, 7, 8, 9, & 13. The percentage of surviving larvae was calculated relative to day 0 (start of assay). Target LD006: (SEQ ID NO: 178); Target LD007 (SEQ ID NO: 183); Target LD010 (SEQ ID NO: 188); Target LD011 (SEQ ID NO: 193); Target LD014 (SEQ ID NO: 198); gfp dsRNA (SEQ ID NO: 235).

Figure 2-LD: Survival of *L. decemlineata* on artificial diet treated with dsRNA. Insects of the second larval stage were fed diet treated with 50 µl of topically-applied solution of dsRNA (targets or gfp control). Diet was replaced with fresh diet only after 7 days. The number of surviving insects was assessed at days 2, 5, 6, 7, 8, 9, 12, & 14. The percentage of surviving larvae was calculated relative to day 0 (start of assay). Target LD001 (SEQ ID NO: 163); Target LD002 (SEQ ID NO: 168); Target LD003 (SEQ ID NO: 173); Target LD015 (SEQ ID NO: 215); Target LD016 (SEQ ID NO: 220); gfp dsRNA (SEQ ID NO: 235).

Figure 3-LD: Average weight of *L. decemlineata* larvae on potato leaf discs treated with dsRNA. Insects of the second larval stage were fed leaf discs treated with 20 µl of a topically-applied solution (10 ng/µl) of dsRNA (target LD002 or gfp). After two days the insects were transferred on to untreated leaves every day.

Figure 4-LD: Survival of *L. decemlineata* on artificial diet treated with shorter versions of target LD014 dsRNA and concatemer dsRNA. Insects of the second larval stage were fed diet treated with 50 µl of topically-applied solution of dsRNA (gfp or targets). The number of surviving insects were assessed at days 3, 4, 5, 6, & 7. The percentage of surviving larvae were calculated relative to day 0 (start of assay).

Figure 5-LD: Survival of *L. decemlineata* larvae on artificial diet treated with different concentrations of dsRNA of target LD002 (a), target LD007 (b), target LD010 (c), target LD011 (d), target LD014 (e), target LD015 (f), LD016 (g) and target LD027 (h). Insects of the second larval stage were fed diet treated with 50 µl of topically-applied solution of dsRNA. Diet was replaced with fresh diet containing topically-applied dsRNA after 7 days. The number of surviving insects were assessed at regular intervals. The percentage of surviving larvae were calculated relative to day 0 (start of assay).

Figure 6-LD. Effects of *E. coli* strains expressing dsRNA target LD010 on survival of larvae of the Colorado potato beetle, *Leptinotarsa decemlineata*, over time. The two bacterial strains were tested in separate artificial diet-based bioassays: (a) AB309-105; data points for pGBNJ003 and pGN29 represent average mortality values from 5 different bacterial clones, (b) BL21(DE3); data points for pGBNJ003 and pGN29 represent average mortality values from 5 different and one single bacterial clones, respectively. Error bars represent standard deviations.

Figure 7-LD. Effects of different clones of *E. coli* strains (a) AB309-105 and (b) BL21(DE3) expressing dsRNA target LD010 on survival of larvae of the Colorado potato beetle, *Leptinotarsa decemlineata*, 12 days post infestation. Data points are average mortality values for each clone for pGN29 and pGBNJ003. Clone 1 of AB309-105 harbouring plasmid pGBNJ003 showed 100% mortality towards CPB at this timepoint. Error bars represent standard deviations.

Figure 8-LD. Effects of different clones of *E. coli* strains (a) AB309-105 and (b) BL21(DE3) expressing dsRNA target LD010 on growth and development of larval survivors of the Colorado potato beetle, *Leptinotarsa decemlineata*, 7 days post infestation. Data points are % average larval weight values for each clone (one clone for pGN29 and five clones for pGBNJ003) based on the data of Table 10. Diet only treatment represents 100% normal larval weight.

Figure 9-LD. Survival of larvae of the Colorado potato beetle, *Leptinotarsa decemlineata*, on potato plants sprayed by double-stranded RNA-producing bacteria 7 days post infestation. Number of larval survivors were counted and expressed in terms of % mortality. The bacterial host strain used was the RNaseIII-deficient strain AB309-105. Insect gene target was LD010.

Figure 10-LD. Growth/developmental delay of larval survivors of the Colorado potato beetle, *Leptinotarsa decemlineata*, fed on potato plants sprayed with dsRNA-producing bacteria 11 days post infestation. The bacterial host strain used was the RNaseIII-deficient strain AB309-105. Data figures represented as percentage of normal larval weight; 100 % of normal larval weight given for diet only treatment. Insect gene target was LD010. Error bars represent standard deviations.

Figure 11-LD. Resistance to potato damage caused by larvae of the Colorado potato beetle, *Leptinotarsa* decemlineata, by double-stranded RNA-producing bacteria 7 days post

infestation. Left, plant sprayed with 7 units of bacteria AB309-105 containing the pGN29 plasmid; right, plant sprayed with 7 units of bacteria Ab309-105 containing the pGBNJ003 plasmid. One unit is defined as the equivalent of 1 ml of a bacterial suspension at OD value of 1 at 600 nm. Insect gene target was LD010.

Figure 12-LD. Survival of *L. decemlineata* adults on potato leaf discs treated with dsRNA. Young adult insects were fed double-stranded-RNA-treated leaf discs for the first two days and were then placed on untreated potato foliage. The number of surviving insects were assessed regularly; mobile insects were recorded as insects which were alive and appeared to move normally; moribund insects were recorded as insects which were alive but appeared sick and slow moving – these insects were not able to right themselves once placed on their backs. Target LD002 (SEQ ID NO: 168); Target LD010 (SEQ ID NO: 188); Target LD014 (SEQ ID NO: 198); Target LD016 (SEQ ID NO: 220); gfp dsRNA (SEQ ID NO: 235).

Figure 13-LD. Effects of bacterial produced target double-stranded RNA against larvae of *L. decemlineata.* Fifty µl of an OD 1 suspension of heat-treated bacteria expressing dsRNA (SEQ ID NO: 188) was applied topically onto the solid artificial diet in each well of a 48-well plate. CPB larvae at L2 stage were placed in each well. At day 7, a picture was taken of the CPB larvae in a plate containing (a) diet with bacteria expressing target 10 double-stranded RNA, (b) diet with bacteria harbouring the empty vector pGN29, and, (c) diet only.

Figure 14-LD Effects on CPB larval survival and growth of different amounts of inactivated *E. coli* AB309-105 strain harbouring plasmid pGBNJ003 topically applied to potato foliage prior to insect infestation. Ten L1 larvae were fed treated potato for 7 days. Amount of bacterial suspension sprayed on plants: 0.25 U, 0.08 U, 0.025 U, 0.008 U of target 10 and 0.25 U of pGN29 (negative control; also included is Milli-Q water). One unit (U) is defined as the equivalent bacterial amount present in 1 ml of culture with an optical density value of 1 at 600nm. A total volume of 1.6 ml was sprayed on to each plant. Insect gene target was LD010.

Figure 15-LD Resistance to potato damage caused by CPB larvae by inactivated *E. coli* AB309-105 strain harbouring plasmid pGBNJ003 seven days post infestation. **(a)** water, **(b)** 0.25 U *E. coli* AB309-105 harbouring pGN29, **(c)** 0.025 U *E. coli* AB309-105 harbouring pGBNJ003, **(d)** 0.008 U *E. coli* AB309-105 harbouring pGBNJ003. One unit (U) is defined as the equivalent bacterial amount present in 1 ml of culture with an optical density value of 1

at 600nm. A total volume of 1.6 ml was sprayed on to each plant. Insect gene target was LD010.

Figure 1-PC: Effects of ingested target dsRNAs on survival and growth of *P. cochleariae* larvae. Neonate larvae were fed oilseed rape leaf discs treated with 25 µl of topically-applied solution of 0.1 µg/µl dsRNA (targets or gfp control). Afer 2 days, the insects were transferred onto fresh dsRNA-treated leaf discs. At day 4, larvae from one replicate for every treatment were collected and placed in a Petri dish containing fresh untreated oilseed rape foliage. The insects were assessed at days 2, 4, 7, 9 & 11. **(a)** Survival of *E. varivestis* larvae on oilseed rape leaf discs treated with dsRNA. The percentage of surviving larvae was calculated relative to day 0 (start of assay). **(b)** Average weights of *P. cochleariae* larvae on oilseed rape leaf discs treated with dsRNA. Insects from each replicate were weighed together and the average weight per larva determined. Error bars represent standard deviations. Target 1: SEQ ID NO: 473; target 3: SEQ ID NO: 478; target 5: SEQ ID NO: 483 --; target 10: SEQ ID NO: 488; target 14: SEQ ID NO: 493; target 16: SEQ ID NO: 498; target 27: SEQ ID NO: 503; gfp dsRNA: SEQ ID NO: 235.

Figure 2-PC: Survival of *P. cochleariae* on oilseed rape leaf discs treated with different concentrations of dsRNA of **(a)** target PC010 and **(b)** target PC027. Neonate larvae were placed on leaf discs treated with 25 µl of topically-applied solution of dsRNA. Insects were transferred to fresh treated leaf discs at day 2. At day 4 for target PC010 and day 5 for target PC027, the insects were transferred to untreated leaves. The number of surviving insects were assessed at days 2, 4, 7, 8, 9 & 11 for PC010 and 2, 5, 8, 9 & 12 for PC027. The percentage of surviving larvae was calculated relative to day 0 (start of assay).

Figure 3-PC: Effects of *E. coli* strain AB309-105 expressing dsRNA target PC010 on survival of larvae of the mustard leaf beetle, *P. cochleariae*, over time. Data points for each treatment represent average mortality values from 3 different replicates. Error bars represent standard deviations. Target 10: SEQ ID NO: 488

Figure 1-EV: Survival of *E. varivestis* larvae on bean leaf discs treated with dsRNA. Neonate larvae were fed bean leaf discs treated with 25 µl of topically-applied solution of 1 µg/µl dsRNA (targets or gfp control). Afer 2 days, the insects were transferred onto fresh dsRNA-treated leaf discs. At day 4, larvae from one treatment were collected and placed in a plastic box containing fresh untreated bean foliage. The insects were assessed for mortality at

days 2, 4, 6, 8 & 10. The percentage of surviving larvae was calculated relative to day 0 (start of assay). Target 5: SEQ ID NO: 576; target 10: SEQ ID NO: 586; target 15: SEQ ID NO: 591; target 16: SEQ ID NO: 596; gfp dsRNA: SEQ ID NO: 235.

Figure 2-EV: Effects of ingested target dsRNAs on surival of *E. varivestis* adults and resistance to snap bean foliar insect damage. **(a)** Surivival of *E. varivestis* adults on bean leaf treated with dsRNA. Adults were fed bean leaf discs treated with 75 µl of topically-applied solution of 0.1 µg/µl dsRNA (targets or gfp control). After 24 hours, the insects were transferred onto fresh dsRNA-treated leaf discs. After a further 24 hours, adults from one treatment were collected and placed in a plastic box containing potted fresh untreated whole bean plants. The insects were assessed for mortality at days 4, 5, 6, 7, 8, & 11. The percentage of surviving adults was calculated relative to day 0 (start of assay). Target 10: SEQ ID NO: 586; target 15: SEQ ID NO: 591; target 16: SEQ ID NO: 596; gfp dsRNA: SEQ ID NO: 235. **(b)** Resistance to bean foliar damage caused by adults of the *E. varivestis* by dsRNA. Whole plants containing insects from one treatment (see (a)) were checked visually for foliar damage on day 9. **(i)** target 10; **(ii)** target 15; **(iii)** target 16; **(iv)** gfp dsRNA; **(v)** untreated.

Figure 1-TC: Survival of *T. castaneum* larvae on artificial diet treated with dsRNA of target 14. Neonate larvae were fed diet based on a flour/milk mix with 1 mg dsRNA target 14. Control was water (without dsRNA) in diet. Four replicates of 10 first instar larvae per replicate were performed for each treatment. The insects were assessed for survival as average percentage means at days 6, 17, 31, 45 and 60. The percentage of surviving larvae was calculated relative to day 0 (start of assay). Error bars represent standard deviations. Target TC014: SEQ ID NO: 878.

Figure 1-MP: Effect of ingested target 27 dsRNA on the survival of *Myzus persicae* nymphs. First instars were placed in feeding chambers containing 50 µl of liquid diet with 2 µg/µl dsRNA (target 27 or gfp dsRNA control). Per treatment, 5 feeding chambers were set up with 10 instars in each feeding chamber. Number of survivors were assessed at 8 days post start of bioassay. Error bars represent standard deviations. Target MP027: SEQ ID NO: 1061; gfp dsRNA: SEQ ID NO: 235.

Figure 1-NL: Survival of *Nilaparvata lugens* on liquid artificial diet treated with dsRNA. Nymphs of the first to second larval stage were fed diet supplemented with 2 mg/ml

solution of dsRNA targets in separate bioassays: (a) NL002, NL003, NL005, NL010; (b) NL009, NL016; (c) NL014, NL018; (d) NL013, NL015, NL021. Insect survival on targets were compared to diet only and diet with gfp dsRNA control at same concentration. Diet was replaced with fresh diet containing dsRNA every two days. The number of surviving insects were assessed every day

Figure 2-NL: Survival of *Nilaparvata lugens* on liquid artificial diet treated with different concentrations of target dsRNA NL002. Nymphs of the first to second larval stage were fed diet supplemented with 1, 0.2, 0.08, and 0.04 mg/ml (final concentration) of NL002. Diet was replaced with fresh diet containing dsRNA every two days. The numbers of surviving insects were assessed every day.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides a means for controlling pest infestations by exposing a pest to a target coding sequence that post-transcriptionally represses or inhibits a requisite biological function in the pest. Following exposure to a target sequence, the target forms a the dsRNA corresponding to part or whole of an essential pest gene and causes down regulation of the pest target via RNA interference (RNAi). As a result of the down regulation of mRNA, the dsRNA prevents expression of the target pest protein and hence causes death, growth arrest, or sterility of the pest.

The present invention finds application in any area where it is desirable to inhibit viability, growth, development or reproduction of a pest, or to decrease pathogenicity or infectivity of a pest. Practical applications include, but are not limited to, (1) protecting plants against pest infestation; (2) pharmaceutical or veterinary use in humans and animals (for example to control, treat, or prevent insect infections in humans and animals); (3) protecting materials against damage caused by pests; and (4) protecting perishable materials (such as foodstuffs, seed, etc.) against damage caused by pests.

Administering or exposing a double stranded ribonucleic acid molecule to a pest results in one or more of the following attributes: reduction in feeding by the pest, reduction in viability of the pest, death of the pest, inhibition of differentiation and development of the pest, absence of or reduced capacity for sexual reproduction by the pest, muscle formation, juvenile hormone formation, juvenile hormone regulation, ion regulation and transport,

maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, sperm formation, pheromone synthesis, pheromone sensing, antennae formation, wing formation, leg formation, development and differentiation, egg formation, larval maturation, digestive enzyme formation, haemolymph synthesis, haemolymph maintenance, neurotransmission, cell division, energy metabolism, respiration, apoptosis, and any component of a eukaryotic cells' cytoskeletal structure, such as, for example, actins and tubulins. Any one or any combination of these attributes can result in an effective inhibition of pest infestation.

All technical terms employed in this specification are commonly used in biochemistry, molecular biology and agriculture; hence, they are understood by those skilled in the field to which this invention belongs. Those technical terms can be found, for example in: MOLECULAR CLONING: A LABORATORY MANUAL, 3rd ed., vol. 1-3, ed. Sambrook and Russel, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 2001; CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, ed. Ausubel *et al.*, Greene Publishing Associates and Wiley-Interscience, New York, 1988 (with periodic updates); SHORT PROTOCOLS IN MOLECULAR BIOLOGY: A COMPENDIUM OF METHODS FROM CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, 5th ed., vol. 1-2, ed. Ausubel *et al.*, John Wiley & Sons, Inc., 2002; GENOME ANALYSIS: A LABORATORY MANUAL, vol. 1-2, ed. Green *et al.*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1997.

Various techniques using PCR are described, for example, in Innis *et al.*, PCR PROTOCOLS: A GUIDE TO METHODS AND APPLICATIONS, Academic Press, San Diego, 1990 and in Dieffenbach and Dveksler, PCR PRIMER: A LABORATORY MANUAL, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 2003. PCR-primer pairs can be derived from known sequences by known techniques such as using computer programs intended for that purpose, *e.g.*, Primer, Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge, MA. Methods for chemical synthesis of nucleic acids are discussed, for example, in Beaucage & Caruthers, *Tetra. Letts.* 22: 1859-62 (1981), and Matteucci & Caruthers, *J. Am. Chem. Soc.* 103: 3185 (1981).

Restriction enzyme digestions, phosphorylations, ligations, and transformations were done as described in Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL, 2nd ed. (1989), Cold Spring Harbor Laboratory Press. All reagents and materials used for the growth and maintenance of bacterial cells were obtained from Aldrich Chemicals

(Milwaukee, Wis.), DIFCO Laboratories (Detroit, Mich.), Invitrogen (Gaithersburg, Md.), or Sigma Chemical Company (St. Louis, Mo.) unless otherwise specified.

Biological activity refers to the biological behavior and effects of a protein or peptide and its manifestations on a pest. For example, an inventive RNAi may prevent translation of a particular mRNA, thereby inhibiting the biological activity of the protein encoded by the mRNA or other biological activity of the pest.

In the present description, an RNAi molecule may inhibit a biological activity in a pest, resulting in one or more of the following attributes: reduction in feeding by the pest, reduction in viability of the pest, death of the pest, inhibition of differentiation and development of the pest, absence of or reduced capacity for sexual reproduction by the pest, muscle formation, juvenile hormone formation, juvenile hormone regulation, ion regulation and transport, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, sperm formation, pheromone synthesis, pheromone sensing, antennae formation, wing formation, leg formation, development and differentiation, egg formation, larval maturation, digestive enzyme formation, haemolymph synthesis, haemolymph maintenance, neurotransmission, cell division, energy metabolism, respiration, apoptosis, and any component of a eukaryotic cells' cytoskeletal structure, such as, for example, actins and tubulins.

Complementary DNA (cDNA) refers to single-stranded DNA synthesized from a mature mRNA template. Though there are several methods, cDNA is most often synthesized from mature (fully spliced) mRNA using the enzyme reverse transcriptase. This enzyme operates on a single strand of mRNA, generating its complementary DNA based on the pairing of RNA base pairs (A, U, G, C) to their DNA complements (T, A, C, G). Two nucleic acid strands are **substantially complementary** when at least 85% of their bases pair.

Desired Polynucleotide: a desired polynucleotide of the present invention is a genetic element, such as a promoter, enhancer, or terminator, or gene or polynucleotide that is to be transcribed and/or translated in a transformed cell that comprises the desired polynucleotide in its genome. If the desired polynucleotide comprises a sequence encoding a protein product, the coding region may be operably linked to regulatory elements, such as to a promoter and a terminator, that bring about expression of an associated messenger RNA transcript and/or a protein product encoded by the desired polynucleotide. Thus, a "desired

polynucleotide" may comprise a gene that is operably linked in the 5'- to 3'- orientation, a promoter, a gene that encodes a protein, and a terminator. Alternatively, the desired polynucleotide may comprise a gene or fragment thereof, in a "sense" or "antisense" orientation, the transcription of which produces nucleic acids that may affect expression of an endogenous gene in the host cell. A desired polynucleotide may also yield upon transcription a double-stranded RNA product upon that initiates RNA interference of a gene to which the desired polynucleotide is associated. A desired polynucleotide of the present invention may be positioned within a vector, such that the left and right border sequences flank or are on either side of the desired polynucleotide. The present invention envisions the stable integration of one or more desired polynucleotides into the genome of at least one host cell. A desired polynucleotide may be mutated or a variant of its wild-type sequence. It is understood that all or part of the desired polynucleotide can be integrated into the genome of a host. It also is understood that the term "desired polynucleotide" encompasses one or more of such polynucleotides. Thus, a vector of the present invention may comprise one, two, three, four, five, six, seven, eight, nine, ten, or more desired polynucleotides.

"**Exposing**" encompasses any method by which a pest may come into contact with a dsRNA, wherein the dsRNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of the nucleotide sequence of a pest target gene to be down-regulated. A pest may be exposed to the dsRNA by direct uptake (e.g. by feeding), which does not require expression of dsRNA within the pest. Alternatively, a pest may come into direct contact with a composition comprising the dsRNA. For example, a pest may come into contact with a surface or material treated with a composition comprising a dsRNA. A dsRNA may be expressed by a prokaryotic (for instance, but not limited to, a bacterial) or eukaryotic (for instance, but not limited to, a yeast) host cell or host organism.

Foreign: "foreign," with respect to a nucleic acid, means that that nucleic acid is derived from non-host organisms. According to the present invention, foreign DNA or RNA represents nucleic acids that are naturally occurring in the genetic makeup of viruses, mammals, fish or birds, but are not naturally occurring in the host that is to be transformed. Thus, a foreign nucleic acid is one that encodes, for instance, a polypeptide that is not naturally produced by the transformed host. A foreign nucleic acid does not have to encode a protein product.

Gene: refers to a polynucleotide sequence that comprises control and coding sequences necessary for the production of a polypeptide or precursor. The polypeptide can

be encoded by a full length coding sequence or by any portion of the coding sequence. A gene may constitute an uninterrupted coding sequence or it may include one or more introns, bound by the appropriate splice junctions. Moreover, a gene may contain one or more modifications in either the coding or the untranslated regions that could affect the biological activity or the chemical structure of the expression product, the rate of expression, or the manner of expression control. Such modifications include, but are not limited to, mutations, insertions, deletions, and substitutions of one or more nucleotides. In this regard, such modified genes may be referred to as "variants" of the "native" gene.

Genetic element: a "genetic element" is any discreet nucleotide sequence such as, but not limited to, a promoter, gene, terminator, intron, enhancer, spacer, 5'-untranslated region, 3'-untranslated region, or recombinase recognition site.

Genetic modification: stable introduction of a nucleic acid into the genome of certain organisms by applying methods in molecular and cell biology.

"**Gene suppression**" or "down-regulation of gene expression" or "inhibition of gene expression" are used interchangeably and refer to a measurable or observable reduction in gene expression or a complete abolition of detectable gene expression, at the level of protein product and/or mRNA product from the target gene. Down-regulation or inhibition of gene expression is "specific" when down-regulation or inhibition of the target gene occurs without manifest effects on other genes of the pest.

Depending on the nature of the target gene, down-regulation or inhibition of gene expression in cells of a pest can be confirmed by phenotypic analysis of the cell or the whole pest or by measurement of mRNA or protein expression using molecular techniques such as RNA solution hybridization, nuclease protection, Northern hybridization, reverse transcription, gene expression monitoring with a microarray, antibody binding, enzyme-linked immunosorbent assay (ELISA), Western blotting, radioimmunoassay (RIA), other immunoassays, or fluorescence-activated cell analysis (FACS).

Gymnosperm, as used herein, refers to a seed plant that bears seed without ovaries. Examples of gymnosperms include conifers, cycads, ginkgos, and ephedras.

Homology, as used herein relates to sequences; Protein, or nucleotide sequences are likely to be homologous if they show a "significant" level of sequence similarity or more preferably sequence identity. Truely homologous sequences are related by divergence from a common ancestor gene. Sequence homologs can be of two types:(i) where homologs exist in different species they are known as orthologs. e.g. the α-globin genes in mouse and human

are orthologs; (ii) paralogues are homologous genes in within a single species. e.g. the α- and β- globin genes in mouse are paralogs.

Host cell: refers to a microorganism, a prokaryotic cell, a eukaryotic cell, or cell line cultured as a unicellular entity that may be, or has been, used as a recipient for a recombinant vector or other transfer of polynucleotides, and includes the progeny of the original cell that has been transfected. The progeny of a single cell may not necessarily be completely identical in morphology or in genomic or total DNA complement as the original parent due to natural, accidental, or deliberate mutation.

Introduction: as used herein, refers to the insertion of a nucleic acid sequence into a cell, by methods including infection, transfection, transformation, or transduction.

Insect pests as used herein pests are include but are not limited to: from the order Lepidoptera, for example, *Acleris spp.*, *Adoxophyes spp.*, *Aegeria spp.*, *Agrotis spp.*, *Alabama argillaceae*, *Amylois spp.*, *Anticarsia gemmatalis*, *Archips spp*, *Argyrotaenia spp.*, *Autographa spp.*, *Busseola fusca*, *Cadra cautella*, *Carposina nipponensis*, *Chilo spp.*, *Choristoneura spp.*, *Clysia ambiguella*, *Cnaphalocrocis spp.*, *Cnephasia spp.*, *Cochylis spp.*, *Coleophora spp.*, *Crocidolomia binotalis*, *Cryptophlebia leucotreta*, *Cydia spp.*, *Diatraea spp.*, *Diparopsis castanea*, *Earias spp.*, *Ephestia spp.*, *Eucosma spp.*, *Eupoecilia ambiguella*, *Euproctis spp.*, *Euxoa spp.*, *Grapholita spp.*, *Hedya nubiferana*, *Heliothis spp.*, *Hellula undalis*, *Hyphantria cunea*, *Keiferia lycopersicella*, *Leucoptera scitella*, *Lithocollethis spp.*, *Lobesia botrana*, *Lymantria spp.*, *Lyonetia spp.*, *Malacosoma spp.*, *Mamestra brassicae*, *Manduca sexta*, *Operophtera spp.*, *Ostrinia Nubilalis*, *Pammene spp.*, *Pandemis spp.*, *Panolis flammea*, *Pectinophora gossypiella*, *Phthorimaea operculella*, *Pieris rapae*, *Pieris spp.*, *Plutella xylostella*, *Prays spp.*, *Scirpophaga spp.*, *Sesamia spp.*, *Sparganothis spp.*, *Spodoptera spp.*, *Synanthedon spp.*, *Thaumetopoea spp.*, *Tortrix spp.*, *Trichoplusia ni* and *Yponomeuta spp.*;

from the order *Coleoptera*, for example, *Agriotes spp.*, *Anthonomus spp.*, *Atomaria linearis*, *Chaetocnema tibialis*, *Cosmopolites spp.*, *Curculio spp.*, *Dermestes spp.*, *Epilachna spp.*, *Eremnus spp.*, *Leptinotarsa decemlineata*, *Lissorhoptrus spp.*, *Melolontha spp.*, *Orycaephilus spp.*, *Otiorhynchus spp.*, *Phlyctinus spp.*, *Popillia spp.*, *Psylliodes spp.*, *Rhizopertha spp.*, *Scarabeidae*, *Sitophilus spp.*, *Sitotroga spp.*, *Tenebrio spp.*, *Tribolium spp.* and *Trogoderma spp.*;

from the order *Orthoptera*, for example, *Blatta spp.*, *Blattella spp.*, *Gryllotalpa spp.*, *Leucophaea maderae*, *Locusta spp.*, *Periplaneta ssp.*, and *Schistocerca spp.*;

from the order *Isoptera*, for example,*Reticulitemes ssp*;

from the order *Psocoptera*, for example,*Liposcelis spp.*;

from the order *Anoplura*, for example,*Haematopinus spp.*, *Linognathus spp.*, *Pediculus spp.*, *Pemphigus spp.* and *Phylloxera spp.*;

from the order *Mallophaga*, for example,*Damalinea spp.* and *Trichodectes spp.*;

from the order *Thysanoptera*, for example,*Franklinella spp.*, *Hercinothrips spp.*, *Taeniothrips spp.*, *Thrips palmi*, *Thrips tabaci* and *Scirtothrips aurantii*;

from the order *Heteroptera*, for example, *Cimex spp.*, *Distantiella theobroma*, *Dysdercus spp.*, *Euchistus spp.*, *Eurygaster spp.*, *Leptocorisa spp.*, *Nezara spp.*, *Piesma spp.*, *Rhodnius spp.*, *Sahlbergella singularis*, *Scotinophara spp.*, *Triatoma spp.*, *Miridae family spp. such as Lygus hesperus* and *Lygus lineoloris*, *Lygaeida*e family *spp.* such as *Blissus leucopterus*, and *Pentatomidae* family *spp.*;

from the order *Homoptera*, for example, *Aleurothrixus floccosus*, *Aleyrodes brassicae*, *Aonidiella spp.*, *Aphididae*, *Aphis spp.*, *Aspidiotus spp.*, *Bemisia tabaci*, *Ceroplaster spp.*, *Chrysomphalus aonidium*, *Chrysomphalus dictyospermi*, *Coccus hesperidum*, *Empoasca spp.*, *Eriosoma larigerum*, *Erythroneura spp.*, *Gascardia spp.*, *Laodelphax spp.*, *Lacanium corni*, *Lepidosaphes spp.*, *Macrosiphus spp.*, *Myzus spp.*, *Nehotettix spp.*, *Nilaparvata spp.*, *Paratoria spp.*, *Pemphigus spp.*, *Planococcus spp.*, *Pseudaulacaspis spp.*, *Pseudococcus spp.*, *Psylla ssp.*, *Pulvinaria aethiopica*, *Quadraspidiotus spp.*, *Rhopalosiphum spp.*, *Saissetia spp.*, *Scaphoideus spp.*, *Schizaphis spp.*, *Sitobion spp.*, *Trialeurodes vaporariorum*, *Trioza erytreae* and *Unaspis citri*;

from the order *Hymenoptera*, for example, *Acromyrmex*, *Atta spp.*, *Cephus spp.*, *Diprion spp.*, *Diprionidae*, *Gilpinia polytoma*, *Hoplocampa spp.*, *Lasius sppp.*, *Monomorium pharaonis*, *Neodiprion spp*, *Solenopsis spp.* and *Vespa ssp.*;

from the order *Diptera*, for example, *Aedes spp.*, *Antherigona soccata*, *Bibio hortulanus*, *Calliphora erythrocephala*, *Ceratitis spp.*, *Chrysomyia spp.*, *Culex spp.*, *Cuterebra spp.*, *Dacus spp.*, *Drosophila melanogaster*, *Fannia spp.*, *Gastrophilus spp.*, *Glossina spp.*, *Hypoderma spp.*, *Hyppobosca spp.*, *Liriomysa spp.*, *Lucilia spp.*, *Melanagromyza spp.*, *Musca ssp.*, *Oestrus spp.*, *Orseolia spp.*, *Oscinella frit*, *Pegomyia hyoscyami*, *Phorbia spp.*, *Rhagoletis pomonella*, *Sciara spp.*, *Stomoxys spp.*, *Tabanus spp.*, *Tannia spp.* and *Tipula spp.*,

from the order *Siphonaptera*, for example,*Ceratophyllus spp. und Xenopsylla cheopis* and

from the order *Thysanura*, for example,*Lepisma saccharina*.

Monocotyledonous plant (monocot) is a flowering plant having embryos with one cotyledon or seed leaf, parallel leaf veins, and flower parts in multiples of three. Examples of monocots include, but are not limited to turfgrass, maize, rice, oat, wheat, barley, sorghum, orchid, iris, lily, onion, and palm.

Pest or **target pest** refers to insects, arachnids, crustaceans, fungi, bacteria, viruses, nematodes, flatworms, roundworms, pinworms, hookworms, tapeworms, trypanosomes, schistosomes, botflies, fleas, ticks, mites, and lice and the like that are pervasive in the human environment. A pest may ingest or contact one or more cells, tissues, or products produced by an organism transformed with a double stranded gene suppression agent, as well as a material or surface treated with a double stranded gene suppression agent.

Nematodes, or roundworms, are one of the most common phyla of animals, with over 20,000 different described species (over 15,000 are parasitic). They are ubiquitous in freshwater, marine, and terrestrial environments, where they often outnumber other animals in both individual and species counts, and are found in locations as diverse as Antarctica and oceanic trenches. Further, there are a great many parasitic forms, including pathogens in most plants and animals.

Nematode pests of a particular interest include, for example, *A. caninum, A. ceylancium, H. contortus, O. ostertagi, C. elegans, C. briggsae, P. pacificus, S. stercoralis, S. ratti, P. trichosuri, M. arenaria, M. chitwoodi, M. hapla, M. incognita, M. javanica, M. paraensis, G. rostochiensis, G. pallida, H. glycines, H. schattii, P. penetrans, P. vulnus, R. similis, Z. punctata, A. suum, T. canis, B. malayi, D. immitis, O. volvulus, T. vulpis, T. spiralis, X. index. A. duodenale, A. lumbricoides*, as well as species from the following genera: *Aphelenchoides*, *Nacobbus*, *Ditylenchus*, *Longidorus*, *Trichodorus*, and *Bursaphelenchus* .

Normal cell refers to a cell of an untransformed phenotype or exhibiting a morphology of a non-transformed cell of the tissue type being examined.

Operably linked: combining two or more molecules in such a fashion that in combination they function properly in a cell. For instance, a promoter is operably linked to a structural gene when the promoter controls transcription of the structural gene.

Orthologs are genes that are related by vertical descent from a common ancestor and encode proteins with the same function in different species. Due to their separation following a speciation event, orthologs may diverge, but usually have similarity at the seqence and structure levels. Two genes that are derived from a common ancestor and encode proteins

with similar function are refered to as orthologous. Identification of orthologs is critical for reliable predictions of gene function in newly sequenced genomes.

"**Pest control agent**", or "**gene suppression agent**" refers to a particular RNA molecule comprising a first RNA segment and a second RNA segment, wherein the complementarity between the first and the second RNA segments results in the ability of the two segments to hybridize *in vivo* and *in vitro* to form a double stranded molecule. It may generally be preferable to include a third RNA segment linking and stabilizing the first and second sequences such that a stem can be formed linked together at one end of each of the first and second segments by the third segment to forms a loop, so that the entire structure forms into a stem and loop structure, or even more tightly hybridizing structures may form into a stem-loop knotted structure. Alternatively, a symmetrical hairpin could be formed without a third segment in which there is no designed loop, but for steric reasons a hairpin would create its own loop when the stem is long enough to stabilize itself. The first and the second RNA segments will generally lie within the length of the RNA molecule and be substantially inverted repeats of each other and linked together by the third RNA segment. The first and the second segments correspond invariably and not respectively to a sense and an antisense sequence with respect to the target RNA transcribed from the target gene in the target insect pest that is suppressed by the ingestion of the dsRNA molecule.

The pest control agent can also be a substantially purified (or isolated) nucleic acid molecule and more specifically nucleic acid molecules or nucleic acid fragment molecules thereof from a genomic DNA (gDNA) or cDNA library. Alternatively, the fragments may comprise smaller oligonucleotides having from about 15 to about 250 nucleotide residues, and more preferably, about 15 to about 30 nucleotide residues.

Pesticide refers to any substance or mixture of substances intended for preventing, destroying, repelling, or mitigating any pest. A pesticide may be a chemical substance or biological agent used against pests including insects, pathogens, weeds, nematodes, and microbes that compete with humans for food, destroy property, spread disease, or are a nuisance.

Phenotype is a distinguishing feature or characteristic of an organism, which may be altered according to the present invention by integrating one or more "desired polynucleotides" and/or screenable/selectable markers into the genome of at least one cell of a transformed organism. The "desired polynucleotide(s)" and/or markers may confer a change in the phenotype of a transformed organism, by modifying any one of a number of genetic,

molecular, biochemical, physiological, or morphological characteristics or properties of the transformed cell or organism as a whole.

Plant and plant tissue: a "plant" is any of various photosynthetic, eukaryotic, multicellular organisms of the kingdom *Plantae* characteristically producing embryos, containing chloroplasts, and having cellulose cell walls. A part of a plant, *i.e.*, a "plant tissue" may be treated according to the methods of the present invention to prevent pest infestation on the plant or on the part of the plant. Many suitable plant tissues can be treated according to the present invention and include, but are not limited to, somatic embryos, pollen, leaves, stems, calli, stolons, microtubers, and shoots. Thus, the present invention envisions the treatment of angiosperm and gymnosperm plants such as acacia, alfalfa, apple, apricot, artichoke, ash tree, asparagus, avocado, banana, barley, beans, beet, birch, beech, blackberry, blueberry, broccoli, brussels sprouts, cabbage, canola, cantaloupe, carrot, cassava, cauliflower, cedar, a cereal, celery, chestnut, cherry, chinese cabbage, citrus, clemintine, clover, coffee, corn, cotton, cowpea, cucumber, cypress, eggplant, elm, endive, eucalyptus, fennel, figes, fir, geranium, grape, grapefruit, groundnuts, ground cherry, gum hemlock, hickory, kale, kiwifruit, kohlrabi, larch, lettuce, leek, lemon, lime, locust, pine, maidenhair, maize, mango, maple, melon, millet, mushroom, mustard, nuts, oak, oats, okra, onion, orange, an ornamental plant or flower or tree, papaya, palm, parsley, parsnip, pea, peach, peanut, pear, peat, pepper, persimmon, pigeon pea, pine, pineapple, plantain, plum, pomegranate, potato, pumpkin, radicchio, radish, rapeseed, raspberry, rice, rye, sorghum, , sallow, soybean, spinach, spruce, squash, strawberry, sugarbeet, sugarcane, sunflower, sweet potato, sweet corn, tangerine, tea, tobacco, tomato, trees, triticale, turf grasses, turnips, a vine, walnut, watercress, watermelon, wheat, yams, yew, and zucchini.

According to the present invention "plant tissue" also encompasses plant cells. Plant cells include suspension cultures, callus, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, seeds and microspores. Plant tissues may be at various stages of maturity and may be grown in liquid or solid culture, or in soil or suitable media in pots, greenhouses or fields. A plant tissue also refers to any clone of such a plant, seed, progeny, propagule whether generated sexually or asexually, and descendents of any of these, such as cuttings or seed.

Promoter is intended to mean a nucleic acid, preferably DNA that binds RNA polymerase and/or other transcription regulatory elements. As with any promoter, the promoters of the current invention will facilitate or control the transcription of DNA or RNA to generate an mRNA molecule from a nucleic acid molecule that is operably linked to the

promoter. As stated earlier, the RNA generated may code for a protein or polypeptide or may code for an RNA interfering, or antisense molecule.

Polynucleotide is a nucleotide sequence, comprising a gene coding sequence or a fragment thereof, a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker or the like. The polynucleotide may comprise single stranded or double stranded DNA or RNA. The polynucleotide may comprise modified bases or a modified backbone. The polynucleotide may be genomic, an RNA transcript (such as an mRNA) or a processed nucleotide sequence (such as a cDNA). The polynucleotide may comprise a sequence in either sense or antisense orientations.

An **isolated polynucleotide** is a polynucleotide sequence that is not in its native state, e.g., the polynucleotide is comprised of a nucleotide sequence not found in nature or the polynucleotide is separated from nucleotide sequences with which it typically is in proximity or is next to nucleotide sequences with which it typically is not in proximity.

Recombinant nucleotide sequence refers to a nucleic acid molecule that contains a genetically engineered modification through manipulation via mutagenesis, restriction enzymes, and the like.

RNA interference (RNAi) refers to sequence-specific or gene-specific suppression of gene expression (protein synthesis) that is mediated by short interfering RNA (**siRNA**).

Sequence identity: as used herein, "sequence identity" or "identity" in the context of two nucleic acid sequences includes reference to the residues in the two sequences which are the same when aligned for maximum correspondence over a specified region.

As used herein, percentage of sequence identity means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

"Sequence identity" has an art-recognized meaning and can be calculated using published techniques. See COMPUTATIONAL MOLECULAR BIOLOGY, Lesk, *ed.* (Oxford University Press, 1988), BIOCOMPUTING: INFORMATICS AND GENOME PROJECTS, Smith, *ed.* (Academic Press, 1993), COMPUTER ANALYSIS OF SEQUENCE DATA, PART I, Griffin & Griffin, *eds.*, (Humana Press, 1994), SEQUENCE ANALYSIS IN MOLECULAR BIOLOGY, Von Heinje *ed.*, Academic Press (1987), SEQUENCE ANALYSIS PRIMER, Gribskov & Devereux, *eds.* (Macmillan Stockton Press, 1991), and Carillo & Lipton, *SIAM J. Applied Math.* 48: 1073 (1988). Methods commonly employed to determine identity or similarity between two sequences include but are not limited to those disclosed in GUIDE TO HUGE COMPUTERS, Bishop, *ed.*, (Academic Press, 1994) and Carillo & Lipton, *supra*. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include but are not limited to the GCG program package (Devereux *et al., Nucleic Acids Research* 12: 387 (1984)), BLASTP, BLASTN, FASTA (Atschul *et al., J. Mol. Biol.* 215: 403 (1990)), and FASTDB (Brutlag *et al., Comp. App. Biosci.* 6: 237 (1990)).

Short hairpin RNA (shRNA) are short single-stranded RNAs having a high degree of secondary structure such that a portion of the RNA strand forms a hairpin loop.

Short interfering RNA (siRNA) refers to double-stranded RNA molecules from about 10 to about 30 nucleotides long that are named for their ability to specifically interfere with gene protein expression.

Target sequence refers to a nucleotide sequence in a pest that is selected for suppression or inhibition by double stranded RNA technology. A target sequence encodes an essential feature or biological activity within a pest.

Transcriptional terminators: The expression DNA constructs of the present invention typically have a transcriptional termination region at the opposite end from the transcription initiation regulatory region. The transcriptional termination region may be selected, for stability of the mRNA to enhance expression and/or for the addition of polyadenylation tails added to the gene transcription product. Translation of a nascent polypeptide undergoes termination when any of the three chain-termination codons enters the A site on the ribosome. Translation termination codons are UAA, UAG, and UGA.

Transformation: A process by which a nucleic acid is stably inserted into the genome of an organism. Transformation may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of nucleic acid sequences into a prokaryotic or eukaryotic host cell, including microorganism-mediated transformation, viral infection, whiskers, electroporation, microinjection, polyethylene glycol-treatment, heat shock, lipofection, and particle bombardment.

Transgenic organism comprises at least one cell in which an exogenous nucleic acid has been stably integrated. A transgenic organism according to the invention is for instance a bacterial, or eukaryotic, such as a yeast, host cell or host organism. The bacterium can be chosen from the group comprising Gram-negative and Gram-positive bacteria, such as, but not limited to, *Escherichia* spp. (e.g. *E. coli*), Bacillus spp. (e.g. *B. thuringiensis*), *Rhizobium* spp., *Lactobacilllus* spp., *Lactococcus* spp., etc.. The yeast can be chosen from the group comprising *Saccharomyces* spp., etc.

Variant: a "variant," as used herein, is understood to mean a nucleotide sequence that deviates from the standard, or given, nucleotide or amino acid sequence of a particular gene or protein. The terms, "isoform," "isotype," and "analog" also refer to "variant" forms of a nucleotide sequence. "Variant" may also refer to a "shuffled gene" such as those described in Maxygen-assigned patents.

It is understood that the present invention is not limited to the particular methodology, protocols, vectors, and reagents, etc., described herein, as these may vary. It is also to be understood that the terminology used herein is used for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention. It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a gene" is a reference to one or more genes and includes equivalents thereof known to those skilled in the art and so forth.

I. Target Pests

The present invention provides methodology and constructs for controlling pest infestations by administering, or otherwise exposing, to a pest a target coding sequence that post-transcriptionally represses or inhibits a requisite biological function in the pest. As used herein, the term "pest" refers to insects, arachnids, crustaceans, fungi, bacteria, viruses,

nematodes, flatworms, roundworms, pinworms, hookworms, tapeworms, trypanosomes, schistosomes, botflies, fleas, ticks, mites, and lice and the like that are pervasive in the human environment. A pest may ingest or contact one or more cells, tissues, or products produced by an organism transformed with a double stranded gene suppression agent, as well as a surface or material treated with a double stranded gene suppression agent.

A "pest resistance" trait is a characteristic of a transgenic host that causes the host to be resistant to attack from a pest that typically inflicts damage to the host. Such pest resistance can arise from a natural mutation or more typically from incorporation of recombinant DNA that confers pest resistance. To impart pest resistance to a transgenic host, a recombinant DNA can, for example, be transcribed into a RNA molecule that forms a dsRNA molecule within the tissues or fluids of the recombinant host. The dsRNA molecule is comprised in part of a segment of RNA that is identical to a corresponding RNA segment encoded from a DNA sequence within a pest that prefers to feed on the recombinant host. Expression of the gene within the target pest is suppressed by the dsRNA, and the suppression of expression of the gene in the target pest results in the host being pest resistant.

Suitable pests include any organism that causes damage to another organism. The invention contemplates insect, nematode, and fungal pests in particular.

Insect as used herein can be any insect, meaning any organism belonging to the Kingdom Animals, more specific to the Phylum Arthropoda, and to the Class Insecta or the Class Arachnida. The methods of the invention are applicable to all insects and that are susceptible to gene silencing by RNA interference and that are capable of internalising double-stranded RNA from their immediate environment.

In one embodiment of the invention, the insect may belong to the following orders: Acari, Araneae, Anoplura, Coleoptera, Collembola, Dermaptera, Dictyoptera, Diplura, Diptera, Embioptera, Ephemeroptera, Grylloblatodea, Hemiptera, Homoptera, Hymenoptera, Isoptera, Lepidoptera, Mallophaga, Mecoptera, Neuroptera, Odonata, Orthoptera, Phasmida, Plecoptera, Protura, Psocoptera, Siphonaptera, Siphunculata, Thysanura, Strepsiptera, Thysanoptera, Trichoptera, and Zoraptera.

In preferred, but non-limiting, embodiments and methods of the invention the insect is chosen from the group consisting of:

(1) an insect which is a plant pest, such as but not limited to *Nilaparvata* spp. (e.g. *N. lugens (brown planthopper)); Laodelphax* spp. (e.g. *L. striatellus (*small brown planthopper)); *Nephotettix* spp. (e.g. *N. virescens* or *N. cincticeps* (green leafhopper), or *N.nigropictus* (rice leafhopper)); *Sogatella* spp. (e.g. *S. furcifera* (white-backed planthopper)); *Blissus* spp. (e.g.

B. leucopterus leucopterus (chinch bug)); *Scotinophora* spp. (e.g. *S. vermidulate* (rice blackbug)); *Acrosternum* spp. (e.g. *A. hilare* (green stink bug)); *Parnara* spp. (e.g. *P. guttata* (rice skipper)); *Chilo* spp. (e.g. *C. suppressalis* (rice striped stem borer), *C. auricilius* (gold-fringed stem borer), or *C. polychrysus* (dark-headed stem borer)); *Chilotraea* spp. (e.g. *C. polychrysa* (rice stalk borer)); *Sesamia* spp. (e.g. *S. inferens* (pink rice borer)); *Tryporyza* spp. (e.g. *T. innotata* (white rice borer), or *T. incertulas* (yellow rice borer)); *Cnaphalocrocis* spp. (e.g. *C. medinalis* (rice leafroller)); *Agromyza* spp. (e.g. *A. oryzae* (leafminer), or *A. parvicornis* (corn blot leafminer)); *Diatraea* spp. (e.g. *D. saccharalis* (sugarcane borer), *or D. grandiosella* (southwestern corn borer)); *Narnaga* spp. (e.g. *N. aenescens* (green rice caterpillar)); *Xanthodes* spp. (e.g. *X. transversa* (green caterpillar)); *Spodoptera* spp. (e.g. *S. frugiperda* (fall armyworm), *S. exigua* (beet armyworm), *S. littoralis* (climbing cutworm) or *S. praefica* (western yellowstriped armyworm)); *Mythimna* spp. (e.g. *Mythmna (Pseudaletia) seperata* (armyworm)); *Helicoverpa* spp. (e.g. *H. zea* (corn earworm)); *Colaspis* spp. (e.g. *C. brunnea* (grape colaspis)); *Lissorhoptrus* spp. (e.g. *L. oryzophilus* (rice water weevil)); *Echinocnemus* spp. (e.g. *E. squamos* (rice plant weevil)); *Diclodispa* spp. (e.g. *D. armigera* (rice hispa)); *Oulema* spp. (e.g. *O. oryzae* (leaf beetle); *Sitophilus* spp. (e.g. *S. oryzae* (rice weevil)); *Pachydiplosis* spp. (e.g. *P. oryzae* (rice gall midge)); *Hydrellia* spp. (e.g. *H. griseola* (small rice leafminer), or *H. sasakii* (rice stem maggot)); *Chlorops* spp. (e.g. *C. oryzae* (stem maggot)); *Ostrinia* spp. (e.g. *O. nubilalis* (European corn borer)); *Agrotis* spp. (e.g. *A.ipsilon* (black cutworm)); *Elasmopalpus* spp. (e.g. *E. lignosellus* (lesser cornstalk borer)); *Melanotus* spp. (wireworms); *Cyclocephala* spp. (e.g. *C. borealis* (northern masked chafer), or *C. immaculata* (southern masked chafer)); *Popillia* spp. (e.g. *P. japonica* (Japanese beetle)); *Chaetocnema* spp. (e.g. *C. pulicaria* (corn flea beetle)); *Sphenophorus* spp. (e.g. *S. maidis* (maize billbug)); *Rhopalosiphum* spp. (e.g. *R. maidis* (corn leaf aphid)); *Anuraphis* spp. (e.g. *A. maidiradicis* (corn root aphid)); *Melanoplus* spp. (e.g. *M. femurrubrum* (redlegged grasshopper) *M. differentialis* (differential grasshopper) or *M. sanguinipes* (migratory grasshopper)); *Hylemya* spp. (e.g. *H. platura* (seedcorn maggot)); *Anaphothrips* spp. (e.g. *A. obscrurus* (grass thrips)); *Solenopsis* spp. (e.g. *S. milesta* (thief ant)); *or* spp. (e.g. *T. urticae* (twospotted spider mite), *T. cinnabarinus* (carmine spider mite); *Helicoverpa spp. (e.g. H. zea* (cotton bollworm), or *H. armigera* (American bollworm)); *Pectinophora* spp. (e.g. *P. gossypiella* (pink bollworm)); *Earias* spp. (e.g. *E. vittella* (spotted bollworm)); *Heliothis* spp. (e.g. *H. virescens* (tobacco budworm)); *Anthonomus* spp. (e.g. *A. grandis* (boll weevil)); *Pseudatomoscelis* spp. (e.g. *P. seriatus* (cotton fleahopper)); *Trialeurodes* spp. (e.g. *T. abutiloneus* (banded-winged whitefly) *T. vaporariorum*

(greenhouse whitefly)); *Bemisia* spp. (e.g. *B. argentifolii* (silverleaf whitefly)); *Aphis* spp. (e.g. *A. gossypii* (cotton aphid), *A. mellifera*); *Lygus* spp. (e.g. *L. lineolaris* (tarnished plant bug) or *L. hesperus* (western tarnished plant bug)); *Euschistus* spp. (e.g. *E. conspersus* (consperse stink bug)); *Chlorochroa* spp. (e.g. *C. sayi* (Say stinkbug)); *Nezara* spp. (e.g. *N. viridula* (southern green stinkbug)); *Thrips* spp. (e.g. *T. tabaci* (onion thrips)); *Frankliniella* spp. (e.g. *F. fusca* (tobacco thrips), or *F. occidentalis* (western flower thrips)); *Leptinotarsa* spp. (e.g. *L. decemlineata* (Colorado potato beetle), *L. juncta* (false potato beetle), or *L. texana* (Texan false potato beetle)); *Lema* spp. (e.g. *L. trilineata* (three-lined potato beetle)); *Epitrix* spp. (e.g. *E. cucumeris* (potato flea beetle), *E. hirtipennis* (flea beetle), or *E. tuberis* (tuber flea beetle)); *Epicauta* spp. (e.g. *E. vittata* (striped blister beetle)); *Empoasca* spp. (e.g. *E. fabae* (potato leafhopper)); *Myzus* spp. (e.g. *M. persicae* (green peach aphid)); *Paratrioza* spp. (e.g. *P. cockerelli* (psyllid)); *Conoderus* spp. (e.g. *C. falli* (southern potato wireworm), or *C. vespertinus* (tobacco wireworm)); *Phthorimaea* spp. (e.g. *P. operculella* (potato tuberworm)); *Macrosiphum spp. (e.g. M. euphorbiae* (potato aphid)); *Thyanta spp. (e.g. T. pallidovirens* (redshouldered stinkbug)); *Phthorimaea spp. (e.g. P. operculella* (potato tuberworm)); *Helicoverpa spp. (e.g. H. zea* (tomato fruitworm); *Keiferia spp. (e.g. K. lycopersicella* (tomato pinworm)); *Limonius* spp. (wireworms); *Manduca spp. (e.g. M. sexta* (tobacco hornworm), or *M. quinquemaculata* (tomato hornworm)); *Liriomyza spp. (e.g. L. sativae, L. trifolli* or *L. huidobrensis* (leafminer)); *Drosophilla* spp. (e.g. *D. melanogaster, D. yakuba, D. pseudoobscura* or *D. simulans); Carabus* spp. (e.g. *C. granulatus); Chironomus* spp. (e.g. *C. tentanus*); *Ctenocephalides* spp. (e.g. *C. felis* (cat flea)); *Diaprepes* spp. (e.g. *D. abbreviatus* (root weevil)); *Ips* spp. (e.g. *I. pini* (pine engraver)); *Tribolium* spp. (e.g. *T. castaneum* (red floor beetle)); *Glossina* spp. (e.g. *G. morsitans* (tsetse fly)); *Anopheles* spp. (e.g. *A. gambiae* (malaria mosquito)); *Helicoverpa* spp. (e.g. *H. armigera* (African Bollworm)); *Acyrthosiphon* spp. (e.g. *A. pisum* (pea aphid)); *Apis* spp. (e.g. *A. melifera* (honey bee)); *Homalodisca* spp. (e.g. H. *coagulate* (glassy-winged sharpshooter)); Aedes spp. (e.g. Ae. aegypti *(yellow fever mosquito)); Bombyx spp. (e.g. B. mori (silkworm), B. mandarina); Locusta spp. (e.g. L. migratoria (*migratory locust)); *Boophilus* spp. (e.g. *B. microplus* (cattle tick)); *Acanthoscurria* spp. (e.g. *A. gomesiana* (red-haired chololate bird eater)); *Diploptera* spp. (e.g. *D. punctata* (pacific beetle cockroach)); *Heliconius* spp. (e.g. *H. erato* (red passion flower butterfly) or *H. melpomene* (postman butterfly)); *Curculio* spp. (e.g. *C. glandium* (acorn weevil)); *Plutella* spp. (e.g. *P. xylostella* (diamontback moth)); *Amblyomma* spp. (e.g. *A. variegatum* (cattle tick)); *Anteraea* spp. (e.g. *A. yamamai* (silkmoth)); *Belgica* spp. (e.g. *B. antartica*), *Bemisa* spp. (e.g. *B. tabaci*), *Bicyclus* spp.,

Biphillus spp., *Callosobruchus* spp., *Choristoneura* spp., *Cicindela* spp., *Culex* spp.,*Culicoides* spp., *Diaphorina* spp., *Diaprepes* spp., *Euclidia* spp., *Glossina* spp., *Gryllus* spp., *Hydropsyche* spp., *Julodis* spp., *Lonomia* spp., *Lutzomyia* spp., *Lysiphebus* spp, *Meladema* spp, *Mycetophagus* spp., *Nasonia* spp., *Oncometopia* spp., *Papilio* spp., *Pediculus* spp., *Plodia* spp., *Rhynchosciara* spp., *Sphaerius* spp., *Toxoptera* spp., *Trichoplusa* spp., and *Armigeres* spp. (e.g. *A. subalbatus*);

(2) an insect capable of infesting or injuring humans and/or animals such as, but not limited to those with piercing-sucking mouthparts, as found in Hemiptera and some Hymenoptera and Diptera such as mosquitos, bees, wasps, lice, fleas and ants, as well as members of the Arachnidae such as ticks and mitesorder, class or familiy of Acarina (ticks and mites) e.g. representatives of the families *Argasidae*, *Dermanyssidae*, *Ixodidae*, *Psoroptidae* or *Sarcoptidae* and representatives of the species *Amblyomma* spp., *Anocentor* spp., *Argas* spp., *Boophilus* spp., *Cheyletiella* spp., *Chorioptes* spp., *Demodex* spp., *Dermacentor* spp., *Dermanyssus* spp., *Haemophysalis* spp., *Hyalomma* spp., *Ixodes* spp., *Lynxacarus* spp., *Mesostigmata* spp., *Notoedres* spp., *Ornithodoros* spp., *Ornithonyssus* spp., *Otobius* spp., *otodectes* spp., *Pneumonyssus* spp., *Psoroptes* spp., *Rhipicephalus* spp., *Sarcoptes* spp., or *Trombicula* spp. ; Anoplura (sucking and biting lice) e.g. representatives of the species *Bovicola* spp., *Haematopinus* spp., *Linognathus* spp., *Menopon* spp., *Pediculus* spp., *Pemphigus* spp., *Phylloxera* spp., or *Solenopotes* spp. ; Diptera (flies) e.g. representatives of the species *Aedes* spp., *Anopheles* spp., *Calliphora* spp., *Chrysomyia* spp., *Chrysops* spp., *Cochliomyia* spp., *Culex* spp., *Culicoides* spp., *Cuterebra* spp., *Dermatobia* spp., *Gastrophilus* spp., *Glossina* spp., *Haematobia* spp. , *Haematopota* spp., *Hippobosca* spp., *Hypoderma* spp., *Lucilia* spp., *Lyperosia* spp., *Melophagus* spp., *Oestrus* spp., *Phaenicia* spp., *Phlebotomus* spp., *Phormia* spp., *Sarcophaga* spp., *Simulium* spp., *Stomoxys* spp., *Tabanus* spp., *Tannia* spp. or *Tipula* spp.; Mallophaga (biting lice) e.g. representatives of the species *Damalina* spp., *Felicola* spp., *Heterodoxus* spp. or *Trichodectes* spp.; or Siphonaptera (wingless insects) e.g. representatives of the species *Ceratophyllus* spp., spp., *Pulex* spp., or *Xenopsylla* spp; Cimicidae (true bugs) e.g. representatives of the species *Cimex* spp., *Tritominae* spp., *Rhodinius* spp., or *Triatoma* spp.

and

(3) an insect that causes unwanted damage to substrates or materials, such as insects that attack foodstuffs, seeds, wood, paint, plastic, clothing etc.

The methods of the invention are applicable to all nematodes and that are susceptible to gene silencing by RNA interference and that are capable of internalising double-stranded RNA from their immediate environment.

In one embodiment of the invention, the nematode may belong to the family of the Heteroderidae, encompassing the genera Heterodera and Globodera.

In preferred, but non-limiting, embodiments and methods of the invention the insect is chosen from the group coprising but not limited to:

(1) a nematode which is a plant pathogenic nematode, such as but not limited to: *Meloidogyne spp. (e.g. M. incognita, M. javanica, M. graminicola,* M. arenaria, *M. chitwoodi, M. hapla or M. paranaensis); Heterodera spp. (e.g. H. oryzae, H. glycines, H. zeae or H. schachtii); Globodera spp. (e.g. G. pallida or G. rostochiensis); Rotylenchulus spp. (e.g. R. reniformis); Pratylenchus* spp. (e.g. *P. coffeae, P. Zeae* or *P. goodeyi*); *Radopholus* spp. (e.g. *R. similis*); *Hirschmaniella* spp. (e.g. *H. oryzae); Ancylostoma* spp. (e.g. *A. caninum, A. ceylanicum, A. duodenale* or *A. tubaeforme*); *Anisakid*; *Aphelenchoides* spp. (e.g. *A. Besseyi);* Ascarids*; Ascaris* spp., (e.g. *A. suum* or *A. lumbridoides*); *Belonolaimus* spp.; *Brugia* spp. (e.g. *B. malayi* or *B. pahangi*); *Bursaphelenchus* spp.; *Caenorhabditis* spp. (e.g. *C. elegans, C. briggsae* or *C. remanei*); *Clostridium* spp. (e.g. *C. acetobutylicum*); *Cooperia* spp. (e.g. *C. oncophora*); *Criconemoides* spp.; *Cyathostomum* spp. (e.g. *C. catinatum, C. coronatum* or *C. pateratum*); *Cylicocyclus* spp. (e.g. *C. insigne, C. nassatus* or *C. radiatus*); *Cylicostephanus* spp. (e.g. *C. goldi* or *C. longibursatus*); *Diphyllobothrium; Dirofilaria* spp. (e.g. *D. immitis*); *Ditylenchus* spp. (e.g. *D. dipsaci, D. destructor* or *D. Angustus); Enterobius* spp. (e.g. *E. vermicularis); Haemonchus* spp. (e.g. *H. contortus*); *Helicotylenchus* spp.; *Hoplolaimus* spp.; *Litomosoides* spp. (e.g. *L. sigmodontis*); *Longidorus* spp. (e.g. *L. macrosoma*); *Necator* spp. (e.g. *N. americanus*); *Nippostrongylus* spp. (e.g. *N. brasiliensis*) ; *Onchocerca* spp. (e.g. *O. volvulus*); *Ostertagia* spp. (e.g. *O. ostertagi); Parastrongyloides* spp. (e.g. *P. trichosuri*); *Paratrichodorus* spp. (e.g. *P. minor or P. teres); Parelaphostrongylus* spp. (e.g. *P. tenuis*); *Radophulus* spp.; *Scutellonerna.* spp.; *Strongyloides* spp. (e.g. *S. Ratti* or *S. stercoralis*); *Teladorsagia* spp. (e.g. *T. circumcincta*); *Toxascaris* spp. (e.g. *T. leonina); Toxocara* spp. (e.g. *T. canis* or *T. cati*); *Trichinella* spp. (e.g. *T. britovi, T. spiralis* or *T. spirae*); *Trichodorus spp. (e.g. T. similis);Trichuris* spp. (e.g. *T. muris, T. vulpis or T. trichiura*); *Tylenchulus* spp.; *Tylenchorhynchus* spp.; *Uncinaria* spp. (e.g. *U. stenocephala); Wuchereria* spp. (e.g. *W. bancrofti*); *Xiphinema* spp. (e.g. *X. Index* or *X. americanum*).

(2) a nematode capable of infesting humans such as, but not limited to: *Enterobius vermicularis*, the pinworm that causes enterobiasis; *Ascaris lumbridoides*, the large intestinal

roundworm that causes ascariasis; *Necator* and *Ancylostoma*, two types of hookworms that cause ancylostomiasis; *Trichuris trichiura*, the whipworm that causes trichuriasis; *Strongyloides stercoralis* that causes strongyloidiasis; and *Trichonella spirae* that causes trichinosis; *Brugia malayi* and *Wuchereria bancrofti*, the filarial nematodes associated with the worm infections known as lymphatic filariasis and its gross manifestation, elephantiasis, and *Onchocerca volvulus* that causes river blindness. Transfer of nematodes to humans may also occur through blood-feeding mosquitoes which have fed upon infected animals or humans;

(3) a nematode capable of infesting animals such as, but not limited to: dogs (Hookworms e.g. *Ancylostoma caninum* or *Uncinaria stenocephala,* Ascarids e.g. *Toxocara canis* or *Toxascaris leonina, or* Whipworms e.g. *Trichuris vulpis),* cats (Hookworms e.g. *Ancylostoma tubaeforme*, Ascarids e.g. *Toxocara cati),* fish (herring worms or cod worms e.g. *Anisakid*, or tapeworm e.g. *Diphyllobothrium*), sheep (Wire worms e. g. *Haemonchus contortus*) and cattle (Gastro-intestinal worms e.g. *Ostertagia ostertagi*, *Cooperia oncophora*);

(4) a nematode that causes unwanted damage to substrates or materials, such as nematodes that attack foodstuffs, seeds, wood, paint, plastic, clothing etc. Examples of such nematodes include but are not limited to *Meloidogyne* spp. (e.g. *M. incognita, M. javanica, M. arenaria, M. graminicola, M. chitwoodi* or *M. hapla); Heterodera* spp. (e.g. *H. oryzae, H. glycines, H. zeae* or *H. schachtii*); *Globodera* spp. (e.g. *G. pallida* or *G. rostochiensis); Ditylenchus* spp. (e.g. *D. dipsaci, D. destructor* or *D. angustus); Belonolaimus* spp.; *Rotylenchulus* spp. (e.g. *R. reniformis); Pratylenchus* spp. (e.g. *P. coffeae, P. goodeyi* or *P. zeae); Radopholus* spp. (e.g. *R. Similis); Hirschmaniella* spp. (e.g. *H. oryzae); Aphelenchoides* spp. (e.g. *A. besseyi); Criconemoides* spp.; *Longidorus* spp.; *Helicotylenchus* spp.; *Hoplolaimus* spp.; *Xiphinema* spp.; *Paratrichodorus* spp. (e.g. *P. minor); Tylenchorhynchus* spp;

(5) virus transmitting nematodes (e.g. *Longidorus macrosoma*: transmits prunus necrotic ring spot virus, *Xiphinema americanum*: transmits tobacco ring spot virus, *Paratrichadorus teres*: transmits pea early browning virus, or *Trichodorus similis*: transmits tobacco rattle virus).

Fungal pests of particular interest include but are not limited to the following. In one embodiment of the invention, the fungus may be a mold, or more particularly a filamentous fungus. In other embodiments of the invention, the fungus may be a yeast.

In one embodiment the fungus may be an ascomycetes fungus, i.e. a fungus belonging to the Phylum *Ascomycota.*

In preferred, but non-limiting, embodiments of the invention the fungal cell is chosen from the group consisting of:

(1) a fungal cell of, or a cell derived from a plant pathogenic fungus, such as but not limited to *Acremoniella* spp., *Alternaria* spp. (e.g. *Alternaria brassicola* or *Alternaria solani*), *Ascochyta* spp. (e.g. *Ascochyta pisi*), *Botrytis* spp. (e.g. *Botrytis cinerea* or *Botryotinia fuckeliana*), *Cladosporium* spp., *Cercospora* spp. (e.g. *Cercospora kikuchii or Cercospora zaea-maydis*), *Cladosporium* spp. (e.g. *Cladosporium fulvum*), *Colletotrichum* spp. (e.g. *Colletotrichum lindemuthianum*), *Curvularia* spp., *Diplodia* spp. (e.g. *Diplodia maydis*), *Erysiphe* spp. (e.g. *Erysiphe graminis f.sp. graminis, Erysiphe graminis f.sp. hordei* or *Erysiphe pisi*), *Erwinia armylovora, Fusarium* spp. (e.g. *Fusarium nivale, Fusarium sporotrichioides, Fusarium oxysporum, Fusarium graminearum, Fusarium germinearum, Fusarium culmorum, Fusarium solani, Fusarium moniliforme* or *Fusarium roseum*), *Gaeumanomyces* spp. (e.g. *Gaeumanomyces graminis f.sp. tritici*), *Gibberella* spp. (e.g. *Gibberella zeae*), *Helminthosporium* spp. (e.g. *Helminthosporium turcicum, Helminthosporium carbonum, Helminthosporium mavdis* or *Helminthosporium sigmoideum*), *Leptosphaeria salvinii, Macrophomina* spp. (e.g. *Macrophomina phaseolina*), *Magnaportha* spp. (e.g. *Magnaporthe oryzae*), *Mycosphaerella* spp., *Nectria* spp. (e.g. *Nectria heamatococca*), *Peronospora* spp. (e.g. *Peronospora manshurica* or *Peronospora tabacina*), *Phoma* spp. (e.g. *Phoma betae*), *Phakopsora* spp. (e.g. *Phakopsora pachyrhizi*), *Phymatotrichum* spp. (e.g. *Phymatotrichum omnivorum*), *Phytophthora* spp. (e.g. *Phytophthora cinnamomi, Phytophthora cactorum, Phytophthora phaseoli, Phytophthora parasitica, Phytophthora citrophthora, Phytophthora megasperma f.sp. soiae* or *Phytophthora infestans*), *Plasmopara* spp. (e.g. *Plasmopara viticola*), *Podosphaera* spp. (e.g. *Podosphaera leucotricha*), *Puccinia* spp. (e.g. *Puccinia sorghi, Puccinia striiformis, Puccinia graminis f.sp. tritici, Puccinia asparagi, Puccinia recondita* or *Puccinia arachidis*), *Pythium* spp. (e.g. *Pythium aphanidermatum*), *Pyrenophora* spp. (e.g. *Pyrenophora tritici-repentens* or *Pyrenophora teres*), *Pyricularia* spp. (e.g. *Pyricularia oryzae*), *Pythium* spp. (e.g. *Pythium ultimum*), *Rhincosporium secalis, Rhizoctonia* spp. (e.g. *Rhizoctonia solani, Rhizoctonia oryzae* or *Rhizoctonia cerealis*), *Rhizopus* spp. (e.g. *Rhizopus chinensid*), *Scerotium* spp. (e.g. *Scerotium rolfsii*), *Sclerotinia* spp. (e.g. *Sclerotinia sclerotiorum*), *Septoria* spp. (e.g. *Septoria lycopersici, Septoria glycines, Septoria nodorum* or *Septoria tritici*), *Thielaviopsis* spp. (e.g. *Thielaviopsis basicola*), *Tilletia* spp., *Trichoderma* spp. (e.g. *Trichoderma virde*), *Uncinula* spp. (e.g. *Uncinula necator*), *Ustilago maydis* (e.g. *corn*

smut), Venturia spp. (e.g. *Venturia inaequalis* or *Venturia pirina) or Verticillium* spp. (e.g. *Verticillium dahliae* or *Verticillium albo-atrum);*

(2) a fungal cell of, or a cell derived from a fungus capable of infesting humans such as, but not limited to, *Candida* spp., particularly *Candida albicans*; Dermatophytes including *Epidermophyton* spp., *Trichophyton* spp, and *Microsporum* spp.; *Aspergillus* spp. (particularly *Aspergillus flavus, Aspergillus fumigatus, Aspergillus nidulans, Aspergillus niger* or *Aspergillus terreus)*; *Blastomyces dermatitidis*; *Paracoccidioides brasiliensis; Coccidioides immitis*; *Cryptococcus neoformans*; *Histoplasma capsulatum* Var. *capsulatum* or Var. *duboisii*; *Sporothrix schenckii*; *Fusarium* spp.; *Scopulariopsis brevicaulis; Fonsecaea* spp.; *Penicillium* spp.; or *Zygomycetes* group of fungi (particularly *Absidia corymbifera, Rhizomucor pusillus* or *Rhizopus arrhizus)*;

(3) a fungal cell of, or a cell derived from a fungus capable of infesting animals such as, but not limited to *Candida* spp., *Microsporum* spp. (particularly *Microsporum canis* or *Microsporum gypseum), Trichophyton mentagrophytes, Aspergillus* spp., or *Cryptococcus neoforman;*

and

(4) a fungal cell of, or a cell derived from a fungus that causes unwanted damage to substrates or materials, such as fungi that attack foodstuffs, seeds, wood, paint, plastic, clothing etc. Examples of such fungi are the moulds, including but not limited to *Stachybotrys* spp., *Aspergillus* spp., *Alternaria* spp., *Cladosporium* spp., *Penicillium* spp. or *Phanerochaete chrysosporium.*

II. Identification of Target Sequences

The present invention provides a method for identifying and obtaining a nucleic acid comprising a nucleotide sequence for producing a dsRNA or siRNA. For example, such a method comprises: (a) probing a cDNA or genomic DNA library with a hybridization probe comprising all or a portion of a nucleotide sequence or a homolog thereof from a targeted pest; (b) identifying a DNA clone that hybridizes with the hybridization probe; (c) isolating the DNA clone identified in step (b); and (d) sequencing the cDNA or genomic DNA fragment that comprises the clone isolated in step (c) wherein the sequenced nucleic acid molecule transcribes all or a substantial portion of the RNA nucleotide acid sequence or a homolog thereof.

Additionally, the present invention contemplates a method for obtaining a nucleic acid fragment comprising a nucleotide sequence for producing a substantial portion of a dsRNA or siRNA comprising: (a) synthesizing first and a second oligonucleotide primers corresponding

to a portion of one of the nucleotide sequences from a targeted pest; and (b) amplifying a cDNA or genomic DNA template in a cloning vector using the first and second oligonucleotide primers of step (a) wherein the amplified nucleic acid molecule transcribes a substantial portion of a dsRNA or siRNA of the present invention.

In practicing the present invention, a target gene may be derived from any pest that causes damage to another organism. Several criteria may be employed in the selection of preferred target genes. The gene is one whose protein product has a rapid turnover rate, so that dsRNA inhibition will result in a rapid decrease in protein levels. In certain embodiments it is advantageous to select a gene for which a small drop in expression level results in deleterious effects for the recipient pest. If it is desired to target a broad range of insect species, for example, a gene is selected that is highly conserved across these species. Conversely, for the purpose of conferring specificity, in certain embodiments of the invention, a gene is selected that contains regions that are poorly conserved between individual insect species, or between insects and other organisms. In certain embodiments it may be desirable to select a gene that has no known homologs in other organisms.

As used herein, the term "derived from" refers to a specified nucleotide sequence that may be obtained from a particular specified source or species, albeit not necessarily directly from that specified source or species.

In one embodiment, a gene is selected that is expressed in the insect gut. Targeting genes expressed in the gut avoids the requirement for the dsRNA to spread within the insect. Target genes for use in the present invention may include, for example, those that share substantial homologies to the nucleotide sequences of known gut-expressed genes that encode protein components of the plasma membrane proton V-ATPase (Dow *et al.*, 1997,; Dow, 1999). This protein complex is the sole energizer of epithelial ion transport and is responsible for alkalinization of the midgut lumen. The V-ATPase is also expressed in the Malpighian tubule, an outgrowth of the insect hindgut that functions in fluid balance and detoxification of foreign compounds in a manner analogous to a kidney organ of a mammal.

In another embodiment, a gene is selected that is essentially involved in the growth, development, and reproduction of an insect. Exemplary genes include but are not limited to the structural subunits of ribosomal proteins and a beta-coatamer gene, CHD3 gene. Ribosomal proteins such as S4 (RpS4) and S9(RpS9) are structural constituents of the ribosome involved in protein biosynthesis and which are components of the cytosolic small ribosomal subunit, the ribosomal proteins such as L9 and L19 are structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome. The beta-

coatamer gene in *C. elegans* encodes a protein which is a subunit of a multimeric complex that forms a membrane vesicle coat Similar sequences have been found in diverse organisms such as *Arabidopsis thaliana*, *Drosophila melanogaster*, and *Saccharomyces cerevisiae*. Related sequences are found in diverse organisms such as *Leptinotarsa decemlineata*, *Phaedon cochleariae*, *Epilachna varivetis*, *Anthonomus grandis*, *Tribolium castaneum*, *Myzus persicae*, *Nilaparvata lugens*, *Chilo suppressalis*, *Plutella xylostella* and *Acheta domesticus*. Other target genes for use in the present invention may include, for example, those that play important roles in viability, growth, development, reproduction, and infectivity. These target genes include, for example, house keeping genes, transcription factors, and insect specific genes or lethal knockout mutations in *Caenorhabditis* or *Drosophila*. The target genes for use in the present invention may also be those that are from other organisms, *e.g.*, from a nematode (*e.g.*, *Meloidogyne* spp. or *Heterodera* spp.), other insects or arachnidae (e.g. *Leptinotarsa* spp., *Phaedon* spp., *Epilachna* spp., *Anthonomus* spp., *Tribolium* spp., *Myzus* spp., *Nilaparvata* spp., *Chilo* spp., *Plutella* spp., or *Acheta* spp.,. Additionally, the nucleotide sequences for use as a target sequence in the present invention may also be derived from viral, bacterial, fungal, insect or fungal genes whose functions have been established from literature and the nucleotide sequences of which share substantial similarity with the target genes in the genome of an insect.

For many of the insects that are potential targets for control by the present invention, there may be limited information regarding the sequences of most genes or the phenotype resulting from mutation of particular genes. Therefore, genes may be selected based on available information available concerning corresponding genes in a model organism, such as *Caenorhabditis* or *Drosophila*, or in some other insect species. Genes may also be selected based on available sequence information for other species, such as nematode or fungal species, in which the genes have been characterized. In some cases it will be possible to obtain the sequence of a corresponding gene from a target insect by searching databases, such as GenBank, using either the name of the gene or the gene sequence. Once the sequence is obtained, PCR may be used to amplify an appropriately selected segment of the gene in the insect for use in the present invention.

In order to obtain a DNA segment from the corresponding gene in an insect species, for example, PCR primers may be designed based on the sequence as found in *C. elegans* or *Drosophila*, or an insect from which the gene has already been cloned. The primers are designed to amplify a DNA segment of sufficient length for use in the present invention. Amplification conditions are selected so that amplification will occur even if the primers do

not exactly match the target sequence. Alternately, the gene, or a portion thereof, may be cloned from a genomic DNA or cDNA library prepared from the insect pest species, using a known insect gene as a probe. Techniques for performing PCR and cloning from libraries are known. Further details of the process by which DNA segments from target insect pest species may be isolated based on the sequence of genes previously cloned from an insect species are provided in the Examples. One of ordinary skill in the art will recognize that a variety of techniques may be used to isolate gene segments from insect pest species that correspond to genes previously isolated from other species.

III. Methods for inhibiting or suppressing a target gene

The present invention provides methods for inhibiting gene expression of one or multiple target genes in a target pest using stabilized dsRNA methods. The invention is particularly useful for modulating eukaryotic gene expression, in particular modulating the expression of genes present in pests that exhibit a digestive system pH level that is from about 4.5 to about 9.5, more preferably from about 5.0 to about 8.0, and even more preferably from about 6.5 to about 7.5. For pests with a digestive system that exhibits pH levels outside of these ranges, delivery methods may be desired for use that do not require ingestion of dsRNA molecules.

The methods of the invention encompass the simultaneous or sequential provision of two or more different double-stranded RNAs or RNA constructs to the same insect, so as to achieve down-regulation or inhibition of multiple target genes or to achieve a more potent inhibition of a single target gene.

Alternatively, multiple targets are hit by the provision of one double-stranded RNA that hits multiple target sequences, and a single target is more efficiently inhibited by the presence of more than one copy of the double stranded RNA fragment corresponding to the target gene. Thus, in one embodiment of the invention, the double-stranded RNA construct comprises multiple dsRNA regions, at least one strand of each dsRNA region comprising a nucleotide sequence that is complementary to at least part of a target nucleotide sequence of an insect target gene. According to the invention, the dsRNA regions in the RNA construct may be complementary to the same or to different target genes and/or the dsRNA regions may be complementary to targets from the same or from different insect species. Use of such dsRNA constructs in a plant host cell, thus establishes a more potent resistance to a single or to multiple insect species in the plant. In one embodiment, the double stranded RNA region comprises multiple copies of the nucleotide sequence that is complementary to the target

gene. Alternatively, the dsRNA hits more than one target sequence of the same target gene. The invention thus encompasses isolated double stranded RNA constructs comprising at least two copies of said nucleotide sequence complementary to at least part of a nucleotide sequence of an insect target. DsRNA that hits more than one of the above-mentioned targets, or a combination of different dsRNA against different of the above mentioned targets are developed and used in the methods of the present invention. Suitable dsRNA nucleotides and dsRNA constructs are described in WO2006/046148 by applicant, which is incorporated herein in its entirity.

The terms "hit", "hits", and "hitting" are alternative wordings to indicate that at least one of the strands of the dsRNA is complementary to, and as such may bind to, the target gene or nucleotide sequence.

The modulatory effect of dsRNA is applicable to a variety of genes expressed in the pests including, for example, endogenous genes responsible for cellular metabolism or cellular transformation, including house keeping genes, transcription factors, and other genes which encode polypeptides involved in cellular metabolism.

As used herein, the phrase "inhibition of gene expression" or "inhibiting expression of a target gene in the cell of an pest" refers to the absence (or observable decrease) in the level of protein and/or mRNA product from the target gene. Specificity refers to the ability to inhibit the target gene without manifest effects on other genes of the cell and without any effects on any gene within the cell that is producing the dsRNA molecule. The inhibition of gene expression of the target gene in the pest may result in novel phenotypic traits in the pest.

"Gene suppression" refers to any of the well-known methods for reducing the levels of gene transcription to mRNA and/or subsequent translation of the mRNA. Gene suppression is also intended to mean the reduction of protein expression from a gene or a coding sequence including posttranscriptional gene suppression and transcriptional suppression. Posttranscriptional gene suppression is mediated by the homology between of all or a part of a mRNA transcribed from a gene or coding sequence targeted for suppression and the corresponding double stranded RNA used for suppression, and refers to the substantial and measurable reduction of the amount of available mRNA available in the cell for binding by ribosomes. The transcribed RNA can be in the sense orientation to effect what is called co-suppression, in the anti-sense orientation to effect what is called anti-sense suppression, or in both orientations producing a dsRNA to effect what is called RNA interference (RNAi).

Transcriptional suppression is mediated by the presence in the cell of a dsRNA gene suppression agent exhibiting substantial sequence identity to a promoter DNA sequence or the complement thereof to effect what is referred to as promoter *trans* suppression. Gene suppression may be effective against a native host gene associated with a trait, *e.g.*, to provide hosts with reduced levels of a protein encoded by the native gene or with enhanced or reduced levels of an affected metabolite. Gene suppression can also be effective against target genes in pests that may ingest or contact material containing gene suppression agents, specifically designed to inhibit or suppress the expression of one or more homologous or complementary sequences in the cells of the pest.

A beneficial method of post transcriptional gene suppression in hosts employs both sense-oriented and anti-sense-oriented, transcribed RNA which is stabilized, *e.g.*, as a hairpin and stem and loop structure. A preferred DNA construct for effecting post transcriptional gene suppression is one in which a first segment encodes an RNA exhibiting an anti-sense orientation exhibiting substantial identity to a segment of a gene targeted for suppression, which is linked to a second segment in sense orientation encoding an RNA exhibiting substantial complementarity to the first segment. Such a construct forms a stem and loop structure by hybridization of the first segment with the second segment and a loop structure from the nucleotide sequences linking the two segments (see WO94/01550, WO98/05770, US 2002/0048814, and US 2003/0018993).

According to one embodiment of the present invention, there is provided a nucleotide sequence, for which *in vitro* expression results in transcription of a stabilized RNA sequence that is substantially homologous to an RNA molecule of a targeted gene in a pest that comprises an RNA sequence encoded by a nucleotide sequence within the genome of the pest. Thus, after the pest uptakes the stabilized RNA sequence, or is otherwise exposed to the dsRNA, a down-regulation of the nucleotide sequence corresponding to the target gene in the cells of a target pest is affected.

Inhibition of a target gene using the stabilized dsRNA technology of the present invention is sequence-specific in that nucleotide sequences corresponding to the duplex region of the RNA are targeted for genetic inhibition. RNA containing a nucleotide sequences identical to a portion of the target gene is preferred for inhibition. RNA sequences with insertions, deletions, and single point mutations relative to the target sequence have also been found to be effective for inhibition. In performance of the present invention, it is preferred that the inhibitory dsRNA and the portion of the target gene share at least from about 80% sequence identity, or from about 85% sequence identity, or from about 90%

sequence identity, or from about 95% sequence identity, or from about 99% sequence identity, or even about 100% sequence identity. Alternatively, the duplex region of the RNA may be defined functionally as a nucleotide sequence that is capable of hybridizing with a portion of the target gene transcript. A less than full length sequence exhibiting a greater homology compensates for a longer less homologous sequence. The length of the identical nucleotide sequences may be at least about 25, 50, 100, 200, 300, 400, 500 or at least about 1000 bases. Normally, a sequence of greater than 20-100 nucleotides should be used, though a sequence of greater than about 200-300 nucleotides would be preferred, and a sequence of greater than about 500-1000 nucleotides would be especially preferred depending on the size of the target gene. The invention has the advantage of being able to tolerate sequence variations that might be expected due to genetic mutation, strain polymorphism, or evolutionary divergence. The introduced nucleic acid molecule may not need to be absolute homology, may not need to be full length, relative to either the primary transcription product or fully processed mRNA of the target gene. Therefore, those skilled in the art need to realize that, as disclosed herein, 100% sequence identity between the RNA and the target gene is not required to practice the present invention.

IV. Methods for preparing dsRNA

dsRNA molecules may be synthesized either *in vivo* or *in vitro*. The dsRNA may be formed by a single self-complementary RNA strand or from two complementary RNA strands. Endogenous RNA polymerase of the cell may mediate transcription *in vivo*, or cloned RNA polymerase can be used for transcription *in vivo* or *in vitro*. Inhibition may be targeted by specific transcription in an organ, tissue, or cell type; stimulation of an environmental condition (*e.g.*, infection, stress, temperature, chemical inducers); and/or engineering transcription at a developmental stage or age. The RNA strands may or may not be polyadenylated; the RNA strands may or may not be capable of being translated into a polypeptide by a cell's translational apparatus.

A RNA, dsRNA, siRNA, or miRNA of the present invention may be produced chemically or enzymatically by one skilled in the art through manual or automated reactions or *in vivo* in another organism. RNA may also be produced by partial or total organic synthesis; any modified ribonucleotide can be introduced by *in vitro* enzymatic or organic synthesis. The RNA may be synthesized by a cellular RNA polymerase or a bacteriophage RNA polymerase (*e.g.*, T3, T7, SP6). The use and production of an expression construct are known in the art (see, for example, WO 97/32016; U.S. Pat. No's. 5,593, 874, 5,698,425, 5,712,135, 5,789,214, and 5,804,693). If synthesized chemically or by *in vitro* enzymatic

synthesis, the RNA may be purified prior to introduction into the cell. For example, RNA can be purified from a mixture by extraction with a solvent or resin, precipitation, electrophoresis, chromatography, or a combination thereof. Alternatively, the RNA may be used with no or a minimum of purification to avoid losses due to sample processing. The RNA may be dried for storage or dissolved in an aqueous solution. The solution may contain buffers or salts to promote annealing, and/or stabilization of the duplex strands.

V. Polynucleotide Sequences

Provided according to the invention are nucleotide sequences, the expression of which results in an RNA sequence which is substantially homologous to an RNA molecule of a targeted gene in a pest that comprises an RNA sequence encoded by a nucleotide sequence within the genome of the pest. Thus, after ingestion of the dsRNA sequence down-regulation of the nucleotide sequence of the target gene in the cells of the pest may be obtained resulting in a deleterious effect on the maintenance, viability, proliferation, reproduction, and infestation of the pest.

Each "nucleotide sequence" set forth herein is presented as a sequence of deoxyribonucleotides (abbreviated A, G, C and T). However, by "nucleotide sequence" of a nucleic acid molecule or polynucleotide is intended, for a DNA molecule or polynucleotide, a sequence of deoxyribonucleotides, and for an RNA molecule or polynucleotide, the corresponding sequence of ribonucleotides (A, G, C and U) where each thymidine deoxynucleotide (T) in the specified deoxynucleotide sequence in is replaced by the ribonucleotide uridine (U).

As used herein, "nucleic acid" refers to a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end. A nucleic acid may also optionally contain non-naturally occurring or altered nucleotide bases that permit correct read through by a polymerase and do not reduce expression of a polypeptide encoded by that nucleic acid. "Nucleotide sequence" or "nucleic acid sequence" refers to both the sense and antisense strands of a nucleic acid as either individual single strands or in the duplex.

The term "ribonucleic acid" (RNA) is inclusive of RNAi (inhibitory RNA), dsRNA (double stranded RNA), siRNA (small interfering RNA), mRNA (messenger RNA), miRNA (micro-RNA), tRNA (transfer RNA, whether charged or discharged with a corresponding acylated amino acid), and cRNA (complementary RNA) and the term "deoxyribonucleic acid" (DNA) is inclusive of cDNA and genomic DNA and DNA-RNA hybrids.

The words "nucleic acid segment", "nucleotide sequence segment", or more generally "segment" will be understood by those in the art as a functional term that includes both genomic sequences, ribosomal RNA sequences, transfer RNA sequences, messenger RNA sequences, operon sequences and smaller engineered nucleotide sequences that express or may be adapted to express, proteins, polypeptides or peptides.

Accordingly, the present invention relates to an isolated nucleic molecule comprising a polynucleotide having a sequence selected from the group consisting of any of the polynucleotide sequences of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481. The invention also provides functional fragments of the polynucleotide sequences of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481. The invention further provides complementary nucleic acids, or fragments thereof, to any of the polynucleotide sequences of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163,

168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481, as well as a nucleic acid, comprising at least 15 contiguous bases, which hybridizes to any of the polynucleotide sequences of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481.

The present invention also provides orthologous sequences, and complements and fragments thereof, of the polynucleotide sequences of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617,

1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481 of the invention. Accordingly, the invention encompasses target genes which are insect orthologs of a gene comprising a nucleotide sequence as represented in any of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481. By way of example, insect orthologues may comprise a nucleotide sequence as represented in any of SEQ ID NOs: 49-123, 275-434, 533-562, 621-738, 813-852, 908-1010, 1161-1437, 1730-1987, 2120-2290, 2384-2438, or a fragment thereof of at least 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26 or 27 nucleotides . A non-limiting list of insect or arachnida orthologs genes or sequences comprising at least a fragment of 15, preferably at least 17 bp of one of the sequences of the invention is given in **Tables 4.**

The invention also encompasses target genes which are nematode orthologs of a gene comprising a nucleotide sequence as represented in any of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686,

1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476, and 2481 of the invention. By way of example, nematode orthologs may comprise a nucleotide sequence as represented in any of SEQ ID NOs: 124-135, 435-446, 563, 564, 739-751, 853, 854, 1011-1025, 1438-1473, 1988-2001, 2291-2298, 2439-2440 of the invention, or a fragment of at least 15, 16, 17, 18, 19, 20 or 21 nucleotides thereof. According to another aspect, the invention thus encompasses any of the methods described herein for controlling nematode growth in an organism, or for preventing nematode infestation of an organism susceptible to nemataode infection, comprising contacting nematode cells with a double-stranded RNA, wherein the double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of the nucleotide sequence of a target gene comprising a fragment of at least 17, 18, 19, 20 or 21 nucleotides of any of the sequences as represented in SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481, whereby the double-stranded RNA is taken up by the fungus and thereby controls growth or prevents infestation. The invention also relates to nematode-resistant transgenic plants comprising a fragment of at least 17, 18, 19, 20 or 21 nucleotides of any of the sequences as represented in SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077,

1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481. A non-limiting list of nematode orthologs genes or sequences comprising at least a fragment of 15, preferably at least 17 bp of one of the sequences of the invention is given in Tables 5.

According to another embodiment, the invention encompasses target genes which are fungal orthologs of a gene comprising a nucleotide sequence as represented in any of SEQ ID NO:s 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481 of the invention. By way of example, fungal orthologs may comprise a nucleotide sequence as represented in any of SEQ ID NOs:136-158, 447-472, 565-575, 752-767, 855-862, 1026-1040, 1474-1571, 2002-2039, 2299-2338, 2441-2460, or a fragment of at least 17, 18, 19, 20, 21, 22, 23, 24, 25, 26 or 27 nucleotides thereof.. According to another aspect, the invention thus encompasses any of the methods described herein for controlling fungal growth on a cell or an organism, or for preventing fungal infestation of a cell or an organism susceptible to fungal infection, comprising contacting fungal cells with a double-stranded RNA, wherein the double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of the nucleotide sequence of a target gene comprising a fragment of at least 17, 18, 19, 20 or 21 nucleotides of any of the sequences as represented in SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163,

168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481, whereby the double-stranded RNA is taken up by the fungus and thereby controls growth or prevents infestation. The invention also relates to fungal-resistant transgenic plants comprising a fragment of at least 17, 18, 19, 20 or 21 of any of the sequences as represented in SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481. A non-limiting list of fungal orthologs genes or sequences comprising at least a fragment of 15, preferably at least 17 bp of one of the sequences of the invention is given in Tables 6.

In a further embodiment, a dsRNA molecule of the invention comprises any of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056,

1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481, though the sequences set forth in SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481 are not limiting. A dsRNA molecule of the invention can comprise any contiguous target gene from a pest species (e.g., about 15 to about 25 or more, or about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more contiguous nucleotides).

By "isolated" nucleic acid molecule(s) is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. For example, recombinant DNA molecules contained in a DNA construct are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include in vitro RNA transcripts of the DNA molecules of the present invention. Isolated nucleic acid molecules, according to the present invention, further include such molecules produced synthetically.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced synthetically. The DNA or RNA may be double-stranded or single-

stranded. Single-stranded DNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

VI. Sequence Analysis

Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer (such as the Model 373 from Applied Biosystems, Inc.). Therefore, as is known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 95% identical, more typically at least about 96% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence may be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion.

In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to a portion of the polynucleotide in a nucleic acid molecule of the invention described above. By a polynucleotide which hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides, and more preferably at least about 20 nucleotides, and still more preferably at least about 30 nucleotides, and even more preferably more than 30 nucleotides of the reference polynucleotide. These fragments that hybridize to the reference fragments are useful as diagnostic probes and primers. For the purpose of the invention, two sequences hybridize when they form a double-stranded complex in a hybridization solution of 6X SSC, 0.5% SDS, 5X Denhardt's solution and 100μg of non-specific carrier DNA. See Ausubel *et al.*, section 2.9, supplement 27 (1994). Sequences may hybridize at "moderate stringency," which is defined as a temperature of 60 °C in a hybridization solution of 6X SSC, 0.5% SDS, 5X Denhardt's solution and 100μg of non-specific carrier DNA. For "high stringency" hybridization, the temperature is increased to 68 °C. Following the moderate stringency hybridization reaction, the nucleotides are washed in a solution of 2X SSC plus 0.05% SDS for five times at room

temperature, with subsequent washes with 0.1X SSC plus 0.1% SDS at 60 °C for 1h. For high stringency, the wash temperature is increased to 68 °C. For the purpose of the invention, hybridized nucleotides are those that are detected using 1 ng of a radiolabeled probe having a specific radioactivity of 10,000 cpm/ng, where the hybridized nucleotides are clearly visible following exposure to X-ray film at -70 °C for no more than 72 hours.

The present application is directed to such nucleic acid molecules which are at least 60 %, 65 %, 70 %, 75 %, 80 %, 85 %, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to a nucleic acid sequence described in any of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481. Preferred, however, are nucleic acid molecules which are at least 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequence shown in of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481. Differences between two nucleic acid

sequences may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular nucleic acid molecule is at least 95%, 96%, 97%, 98% or 99% identical to a reference nucleotide sequence refers to a comparison made between two molecules using standard algorithms well known in the art and can be determined conventionally using publicly available computer programs such as the BLASTN algorithm. See Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997).

In one embodiment of the invention, a nucleic acid comprises an antisense strand having about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides, wherein the antisense strand is complementary to a RNA sequence or a portion thereof encoding a protein that controls cell cycle or homologous recombination, and wherein said siNA further comprises a sense strand having about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides, and wherein said sense strand and said antisense strand are distinct nucleotide sequences where at least about 15 nucleotides in each strand are complementary to the other strand.

In one embodiment, the present invention provides double-stranded nucleic acid molecules of that mediate RNA interference gene silencing. In another embodiment, the siNA molecules of the invention consist of duplex nucleic acid molecules containing about 15 to about 30 base pairs between oligonucleotides comprising about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides. In yet another embodiment, siNA molecules of the invention comprise duplex nucleic acid molecules with overhanging ends of about 1 to about 32 (e.g., about 1, 2, or 3) nucleotides, for example, about 21-nucleotide duplexes with about 19 base pairs and 3'-terminal mononucleotide, dinucleotide, or trinucleotide overhangs. In yet another embodiment, siNA molecules of the invention comprise duplex nucleic acid molecules with blunt ends, where both ends are blunt, or alternatively, where one of the ends is blunt.

An siNA molecule of the present invention may comprise modified nucleotides while maintaining the ability to mediate RNAi. The modified nucleotides can be used to improve in vitro or in vivo characteristics such as stability, activity, and/or bioavailability. For example, a siNA molecule of the invention can comprise modified nucleotides as a percentage of the

total number of nucleotides present in the siNA molecule. As such, a siNA molecule of the invention can generally comprise about 5% to about 100% modified nucleotides (e.g., about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% modified nucleotides). The actual percentage of modified nucleotides present in a given siNA molecule will depend on the total number of nucleotides present in the siNA. If the siNA molecule is single stranded, the percent modification can be based upon the total number of nucleotides present in the single stranded siNA molecules. Likewise, if the siNA molecule is double stranded, the percent modification can be based upon the total number of nucleotides present in the sense strand, antisense strand, or both the sense and antisense strands.

VII. Nucleic Acid Constructs

A recombinant nucleic acid vector may, for example, be a linear or a closed circular plasmid. The vector system may be a single vector or plasmid or two or more vectors or plasmids that together contain the total nucleic acid to be introduced into the genome of the bacterial host. In addition, a bacterial vector may be an expression vector. Nucleic acid molecules as set forth in SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 – 158, 159, 160, 161, 162, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 – 246, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 508-512, 513, 515, 517, 519, 521, 533 - 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 – 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 – 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908- 1040, 1041, 1046, 1051, 1056, 1061, 1066-1070, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 - 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 – 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 – 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 – 2460, 2461, 2466, 2471, 2476 and 2481, or fragments thereof can, for example, be suitably inserted into a vector under the control of a suitable promoter that functions in one or more microbial hosts to drive expression of a linked coding sequence or other DNA sequence. Many vectors are available for this purpose, and selection of the appropriate vector will depend mainly on the size of the nucleic acid to be inserted into the vector and the particular host cell to be transformed with the vector. Each vector contains various components

depending on its function (amplification of DNA or expression of DNA) and the particular host cell with which it is compatible. The vector components for bacterial transformation generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more selectable marker genes, and an inducible promoter allowing the expression of exogenous DNA.

Promoters

"Operably linked", as used in reference to a regulatory sequence and a structural nucleotide sequence, means that the regulatory sequence causes regulated expression of the linked structural nucleotide sequence. "Regulatory sequences" or "control elements" refer to nucleotide sequences located upstream (5' noncoding sequences), within, or downstream (3' non-translated sequences) of a structural nucleotide sequence, and which influence the timing and level or amount of transcription, RNA processing or stability, or translation of the associated structural nucleotide sequence. Regulatory sequences may include promoters, translation leader sequences, introns, enhancers, stem-loop structures, repressor binding sequences, and polyadenylation recognition sequences and the like.

An expression vector for producing a mRNA can also contain an inducible promoter that is recognized by the host bacterial organism and is operably linked to the nucleic acid encoding, for example, the nucleic acid molecule coding the *D. v. virgifera* mRNA or fragment thereof of interest. Inducible promoters suitable for use with bacterial hosts include β-lactamase promoter, *E. coli* λ phage PL and PR promoters, and *E. coli* galactose promoter, arabinose promoter, alkaline phosphatase promoter, tryptophan (trp) promoter, and the lactose operon promoter and variations thereof and hybrid promoters such as the tac promoter. However, other known bacterial inducible promoters are suitable.

In certain embodiments, the genes can be derived from different insects in order to broaden the range of insects against which the agent is effective. When multiple genes are targeted for suppression or a combination of expression and suppression, a polycistronic DNA element can be fabricated as illustrated and disclosed in Fillatti, Application Publication No. US 2004-0029283.

Selectable marker genes

A recombinant DNA vector or construct of the present invention will typically comprise a selectable marker that confers a selectable phenotype on transformed cells. Selectable markers may also be used to select for cells that contain the exogenous nucleic acids encoding polypeptides or proteins of the present invention. The marker may encode biocide resistance, such as antibiotic resistance (*e.g.*, kanamycin, G418 bleomycin,

hygromycin, *etc.*). Examples of selectable markers include, but are not limited to, a neo gene which codes for kanamycin resistance and can be selected for using kanamycin, G418, *etc.*, a bar gene which codes for bialaphos resistance; a nitrilase gene which confers resistance to bromoxynil, and a methotrexate resistant DHFR gene. Examples of such selectable markers are illustrated in U.S. Patents 5,550,318; 5,633,435; 5,780,708 and 6,118,047.

A recombinant vector or construct of the present invention may also include a screenable marker. Screenable markers may be used to monitor expression. Exemplary screenable markers include a β-glucuronidase or uidA gene (GUS) which encodes an enzyme for which various chromogenic substrates are known (Jefferson, 1987; Jefferson *et al.*, 1987); a β-lactamase gene (Sutcliffe *et al.*, 1978), a gene which encodes an enzyme for which various chromogenic substrates are known (*e.g.*, PADAC, a chromogenic cephalosporin); a luciferase gene (Ow *et al.*, 1986) a xylE gene (Zukowsky *et al.*, 1983) which encodes a catechol dioxygenase that can convert chromogenic catechols; an α-amylase gene (Ikatu *et al.*, 1990); a tyrosinase gene (Katz *et al.*, 1983) which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to melanin; an α-galactosidase, which catalyzes a chromogenic α-galactose substrate.

A transformation vector can be readily prepared using methods available in the art. The transformation vector comprises one or more nucleotide sequences that is/are capable of being transcribed to an RNA molecule and that is/are substantially homologous and/or complementary to one or more nucleotide sequences encoded by the genome of the insect, such that upon uptake of the RNA there is down-regulation of expression of at least one of the respective nucleotide sequences of the genome of the pest.

VIII. Methods for Genetic Engineering

The present invention contemplates introduction of a nucleotide sequence into a organism to achieve pest inhibitory levels of expression of one or more dsRNA molecules. The inventive polynucleotides and polypeptides may be introduced into a host cell, such as bacterial or yeast cell, by standard procedures known in the art for introducing recombinant sequences into a target host cell. Such procedures include, but are not limited to, transfection, infection, transformation, natural uptake, calcium phosphate, electroporation, microinjection biolistics and microorganism-mediated transformation protocols. The methods chosen vary with the host organism.

A transgenic organism of the present invention is one that comprises at least one cell it its genome in which an exogenous nucleic acid has been stably integrated. Thus, a

transgenic organism may contain only genetically modified cells in certain parts of its structure.

Accordingly, the present invention also encompasses a transgenic cell or organism comprising any of the nucleotide sequences or recombinant DNA constructs described herein. The invention further encompasses prokaryotic cells (such as, but not limited to, gram-positive and gram-negative bacterial cells) and eukaryotic cells (such as, but not limited to, yeast cells or plant cells).

For example, the present invention contemplates introducing a target gene into a bacterium, such as *Lactobacillus*. The nucleic acid constructs can be integrated into a bacterial genome with an integrating vector. Integrating vectors typically contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various Bacillus strains integrate into the Bacillus chromosome (EP 0 127,328). Integrating vectors may also be comprised of bacteriophage or transposon sequences. Suicide vectors are also known in the art.

Construction of suitable vectors containing one or more of the above-listed components employs standard recombinant DNA techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and re-ligated in the form desired to generate the plasmids required. Examples of available bacterial expression vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as Bluescript™ (Stratagene, La Jolla, CA), in which, for example, a *D. v. virgifera* protein or fragment thereof, may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of β-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke and Schuster, 1989); and the like.

The invention also contemplates introducing a target gene into a yeast cell. A yeast recombinant construct can typically include one or more of the following: a promoter sequence, fusion partner sequence, leader sequence, transcription termination sequence, a selectable marker. These elements can be combined into an expression cassette, which may be maintained in a replicon, such as an extrachromosomal element (*e.g.*, plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 (Botstein *et al.*, 1979), pCl/1 (Brake *et al.*, 1984), and YRp17

(Stinchcomb *et al.*, 1982). In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and typically about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20.

Useful yeast promoter sequences can be derived from genes encoding enzymes in the metabolic pathway. Examples of such genes include alcohol dehydrogenase (ADH) (EP 0 284044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EP 0 3215447). The yeast PHO5 gene, encoding acid phosphatase, also provides useful promoter sequences (Myanohara *et al.*, 1983). In addition, synthetic promoters that do not occur in nature also function as yeast promoters. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (U.S. Patent No. 4,876,197 and 4,880,734). Examples of transcription terminator sequences and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes, are known to those of skill in the art.

Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors typically contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome (Orr-Weaver *et al.*, 1983). An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, supra. One or more expression constructs may integrate, possibly affecting levels of recombinant protein produced (Rine *et al.*, 1983).

IX. Quantifying inhibition of target gene expression

Inhibition of target gene expression may be quantified by measuring either the endogenous target RNA or the protein produced by translation of the target RNA and the consequences of inhibition can be confirmed by examination of the outward properties of the cell or organism. Techniques for quantifying RNA and proteins are well known to one of ordinary skill in the art. Multiple selectable markers are available that confer resistance to ampicillin, bleomycin, chloramphenicol, gentamycin, hygromycin, kanamycin, lincomycin, methotrexate, phosphinothricin, puromycin, spectinomycin, rifampicin, and tetracyclin, and the like.

In certain embodiments gene expression is inhibited by at least 10%, preferably by at least 33%, more preferably by at least 50%, and yet more preferably by at least 80%. In particularly preferred embodiments of the invention gene expression is inhibited by at least 80%, more preferably by at least 90%, more preferably by at least 95%, or by at least 99% within cells in the pest so a significant inhibition takes place. Significant inhibition is intended to refer to sufficient inhibition that results in a detectable phenotype (*e.g.*, cessation of larval growth, paralysis or mortality, *etc.*) or a detectable decrease in RNA and/or protein corresponding to the target gene being inhibited. Although in certain embodiments of the invention inhibition occurs in substantially all cells of the pest, in other preferred embodiments inhibition occurs in only a subset of cells expressing the gene. For example, if the target gene plays an essential role in cells in an insect alimentary tract, inhibition of the gene within these cells is sufficient to exert a deleterious effect on the insect.

X. Exposing pest to dsRNA

A pest can be exposed to a dsRNA in any suitable manner that permits administering the dsRNA to the pest. For example, the pest can be contacted with the dsRNA in pure or substantially pure form, for example an aqueous solution containing the dsRNA. In one embodiment, the insect may be simply "soaked" or "sprayed" with an aqueous solution comprising the dsRNA. Alternatively, the pest may be "sprayed" with a solution comprising a dsRNA.

Alternatively, the dsRNA may be linked to a food component of the pest, such as a food component for a mammalian pathogenic pest, in order to increase uptake of the dsRNA by the insect. Ingestion by a pest permits delivery of the pest control agents to the pest and results in down-regulation of a target gene in the host. Methods for oral introduction may include, for example, directly mixing dsRNA with a, pest's food, as well as engineered approaches in which a species that is used as food is engineered to express the dsRNA or siRNA, then fed to the pest to be affected. For example, a bacteria, such as *Lactobacillus*, may be transformed with a target sequence and then fed to a pest. In one embodiment, for example, the dsRNA or siRNA molecules may be incorporated into, or overlaid on the top of, the insect's diet.

In other embodiments the pest may be contacted with a composition containing the inventive dsRNA. The composition may, in addition to the dsRNA, contain further excipients, diluents, or carriers.

The dsRNA may also be incorporated in the medium in which the pest grows or infests. For example, a dsRNA may be incorporated into a food container or protective

wrapping as a means for inhibiting pest infestation. Wood, for example, may be treated with a solution comprising a dsRNA to prevent pest infestation.

In other embodiments, the dsRNA is expressed in a bacterial or fungal cell and the bacterial or fungal cell is taken up or eaten by the insect species.

As illustrated in the examples, bacteria can be engineered to produce any of the dsRNA or dsRNA constructs of the invention. These bacteria can be eaten by the insect species. When taken up, the dsRNA can initiate an RNAi response, leading to the degradation of the target mRNA and weakening or killing of the feeding insect. Alternatively, dsRNA producing bacteria or yeast cells can be sprayed directly onto the crops.

Some bacteria have a very close interaction with the host plant, such as, but not limited to, symbiotic *Rhizobium* with the *Legminosea* (for example Soy). Such recombinant bacteria could be mixed with the seeds (for instance as a coating) and used as soil improvers.

A virus such as a baculovirus which specifically infects insects may be also be used. This ensures safety for mammals, especially humans, since the virus will not infect the mammal, so no unwanted RNAi effect will occur..

Possible applications include intensive greenhouse cultures, for instance crops that are less interesting from a GMO point of view, as well as broader field crops such as soy.

This approach has several advantages, eg: since the problem of possible dicing by a plant host is not present, it allows the delivery of large dsRNA fragments into the gut lumen of the feeding pest; the use of bacteria as insecticides does not involve the generation of transgenic crops, especially for certain crops where transgenic variants are difficult to obtain; there is a broad and flexible application in that different crops can be simultaneously treated on the same field and/or different pests can be simultaneously targeted, for instance by combining different bacteria producing distinct dsRNAs.

XI. Products

The present invention provides numerous products that can encompass a dsRNA for use in controlling pests. For example, the invention provides pharmaceutical or veterinary compositions for treating or preventing a pest disease or infection of humans or animals, respectively. Such compositions comprise at least one dsRNA or RNA construct, or nucleotide sequence or recombinant DNA construct encoding the dsRNA or RNA construct, wherein the RNA comprises annealed complementary strands, one of which has a nucleotide sequence which corresponds to a target nucleotide sequence of an pest target gene that causes the disease or infection, and at least one carrier, excipient, or diluent suitable for pharmaceutical use.

Alternatively, a pharmaceutical or veterinary composition may be used as a composition suitable for topical use, such as application on the skin of an animal or human. For example, a dsRNA may be used in a liquid composition to be applied to the skin as drops, gel, aerosol, cream, ointment, etc. Additionally, a dsRNA may be integrated into a transdermal patch or other medical device for treating or preventing a disease or condition. Other conventional pharmaceutical dosage forms may also be produced, including tablets, capsules, pessaries, transdermal patches, suppositories, etc. The chosen form will depend upon the nature of the target pest and hence the nature of the disease it is desired to treat.

Oral vaccines, for example, can be produced using the inventive constructs and methods. For example, a vaccine can be constructed by producing a dsRNA in bacteria (e.g. *lactobacillus*) which can be included in food and functions as an oral vaccine against insect infection. Accordingly, the invention provides constructs and methods for treating and/or preventing a pest disease or condition, comprising administering to a subject in need of such treatment and/or prevention, any of the compositions as herein described, said composition comprising at least one double-stranded RNA or double stranded RNA construct comprising annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of a nucleotide sequence of a pest target gene that causes the disease or condition.

While the inventive compositions may be used for treating a disease or condition in a subject patient, the compositions and methods may also be used as a means for protecting a substrate or material from pest infestation. The nature of the excipients included in the composition and the physical form of the composition may vary depending upon the nature of the substrate that it is desired to treat.

For example, such a composition may be a coating or a powder that can be applied to a substrate as a means for protecting the substrate from infestation by an insect and thereby preventing pest-induced damage to the substrate or material. Thus, in one embodiment, the composition is in the form of a coating on a suitable surface which adheres to, and is eventually ingested by an insect which comes into contact with the coating. Such a composition can be used to protect any substrate or material that is susceptible to infestation by or damage caused by a pest, for example foodstuffs and other perishable materials, and substrates such as wood.

For example, the composition may be a liquid that is brushed or sprayed onto or imprinted into the material or substrate to be treated. Thus, a human user can spray the insect or the substrate directly with the composition

For example, houses and other wood products can be destroyed by termites, powder post beetles, and carpenter ants. By treating wood or house siding with a composition comprising a dsRNA, it may be possible to reduce pest infestation. Likewise, a tree trunk may be treated with a composition comprising a dsRNA.

Flour beetles, grain weevils, meal moths, and other pests feed on stored grain, cereals, pet food, powdered chocolate, and almost everything else in the kitchen pantry that is not protected. Accordingly, the present invention provides a means for treating cereal boxes and other food storage containers and wrapping with a composition comprising a target dsRNA.

Larvae of clothes moths eat clothes made from animal products, such as fur, silk and wool. Thus, it may be desirable to treat hangers, closet organizers, and garment bags with the inventive dsRNA. Book lice and silverfish are pests of libraries because they eat the starchy glue in the bindings of books. Accordingly, the present invention provides compositions for treating books from pest infestation and destruction.

In one embodiment, the composition is in the form of a bait. The bait is designed to lure the insect to come into contact with the composition. Upon coming into contact therewith, the composition is then internalized by the insect, by ingestion for example and mediates RNAi to thus kill the insect. The bait may depend on the species being targeted. An attractant may also be used. The attractant may be a pheromone, such as a male or female pheromone for example. The attractant acts to lure the insect to the bait, and may be targeted for a particular insect or may attract a whole range of insects. The bait may be in any suitable form, such as a solid, paste, pellet or powdered form.

The bait may also be carried away by the insect back to the colony. The bait may then act as a food source for other members of the colony, thus providing an effective control of a large number of insects and potentially an entire insect pest colony. This is an advantage associated with use of the double stranded RNA or bacteria expressing the dsRNA of the invention, because the delayed action of the RNAi mediated effects on the pests allows the bait to be carried back to the colony, thus delivering maximal impact in terms of exposure to the insects.

The baits may be provided in a suitable "housing" or "trap". Such housings and traps are commercially available and existing traps may be adapted to include the compositions of the invention. The housing or trap may be box-shaped for example, and may be provided in pre-formed condition or may be formed of foldable cardboard for example. Suitable materials for a housing or trap include plastics and cardboard, particularly corrugated cardboard. The inside surfaces of the traps may be lined with a sticky substance in order to

restrict movement of the insect once inside the trap. The housing or trap may contain a suitable trough inside which can hold the bait in place. A trap is distinguished from a housing because the insect can not readily leave a trap following entry, whereas a housing acts as a "feeding station" which provides the insect arachnid with a preferred environment in which they can feed and feel safe from predators.

It is clear that numerous products and substrates can be treated with the inventive compositions for reducing pest infestation. Of course, the nature of the excipients and the physical form of the composition may vary depending upon the nature of the substrate that is desired to treat. For example, the composition may be a liquid that is brushed or sprayed onto or imprinted into the material or substrate to be treated, or a coating that is applied to the material or substrate to be treated.

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Specific examples are presented below of methods for identifying target sequences and introducing the sequences into various cells and compositions. They are meant to be exemplary and not as limitations on the present invention.

Example 1: Silencing *C.elegans* target genes in *C. elegans* in High Throughput Screening

A *C. elegans* genome wide library was prepared in the pGN9A vector (WO 01/88121) between two identical T7-promoters and terminators, driving its expression in the sense and antisense direction upon expression of the T7 polymerase, which was induced by IPTG.

This library was transformed into the bacterial strain AB301-105 (DE3) in 96 well plate format. For the genome wide screening, these bacterial cells were fed to the nuclease deficient *C. elegans nuc-1(e1392)* strain.

Feeding the dsRNA produced in the bacterial strain AB301-105 (DE3), to *C. elegans nuc-1 (e1392)* worms, was performed in a 96 well plate format as follows: *nuc-1* eggs were transferred to a separate plate and allowed to hatch simultaneously at 20 °C for synchronization of the L1 generation. 96 well plates were filled with 100 µL liquid growth medium comprising IPTG and with 10 µL bacterial cell culture of OD_{600}1 AB301-105 (DE3) of the C. elegans dsRNA library carrying each a vector with a C. elegans genomic fragment for expression of the dsRNA. To each well, 4 of the synchronized L1 worms were added and were incubated at 25 °C for at least 4 to 5 days. These experiments were performed in quadruplicate. In the screen 6 controls weree used:

- pGN29 = negative control, wild type
- pGZ1 = *unc-22* = twitcher phenotype
- pGZ18 = chitin synthase = embryonic lethal
- pGZ25 = *pos-1* = embryonic lethal
- pGZ59 = *bli-4D* = acute lethal
- ACC = acetyl co-enzym A carboxylase = acute lethal

After 5 days, the phenotype of the *C. elegans nuc-1 (e1392)* worms fed with the bacteria producing dsRNA were compared to the phenotype of worms fed with the empty vector (pGN29) and the other controls. The worms that were fed with the dsRNA were screened for lethality (acute or larval) lethality for the parent (Po) generation, (embryonic) lethality for the first filial (F1) generation, or for growth retardation of Po as follows: (i) Acute lethality of Po: L1's have not developed and are dead, this phenotype never gives progeny and the well looks quite empty; (ii) (Larval) lethality of Po: Po died in a later stage than L1, this phenotype also never gives progeny. Dead larvae or dead adult worms are found in the wells; (iii) Lethality for F1: L1's have developed until adult stage and are still alive. This phenotype has no progeny. This can be due to sterility, embryonic lethality (dead eggs on the bottom of well), embryonic arrest or larval arrest (eventually ends up being lethal): (iv) Arrested in growth and growth retardation/delay: Compared to a well with normal development and normal # of progeny.

For the target sequences presented in Table 1A, it was concluded that dsRNA mediated silencing of the *C. elegans* target gene in nematodes, such as *C. elegans*, had a fatal effect on the growth and viability of the worm.

Subsequent to the above dsRNA silencing experiment, a more detailed phenotyping experiment was conducted in *C. elegans* in a high throughput format on 24 well plates. The dsRNA library produced in bacterial strain AB301-105 (DE3), as described above, was fed to *C. elegans nuc-1 (e1392)* worms on 24 well plates as follows: *nuc-1* eggs were transferred to a separate plate and allowed to hatch simultaneously at 20 C for synchronization of the L1 generation. Subsequently 100 of the synchronized L1 worms were soaked in a mixture of 500 µL S-complete fed medium, comprising 5 µg/mL cholesterol, 4 µL/mL PEG and 1mM IPTG, and 500 µL of bacterial cell culture of OD_{600}1 AB301-105 (DE3) of the *C. elegans* dsRNA library carrying each a vector with a *C. elegans* genomic fragment for expression of the dsRNA. The soaked L1 worms were rolled for 2 hours at 25 C.

After centrifugation and removal of 950 µL of the supernatant, 5 µL of the remaining and resuspended pellet (comprising about 10 to 15 worms) was transferred in the middle of

each well of a 24 well plate, filled with a layer of agar LB broth. The inoculated plate was incubated at 25°C for 2 days. At the adult stage, 1 adult worm was singled and incubated at 25°C for 2 days for inspection of its progeny. The other adult worms are inspected *in situ* on the original 24 well plate. These experiments were performed in quadruplicate.

This detailed phenotypic screen was repeated with a second batch of worms, the only difference being that the worms of the second batch were incubated at 20 C for 3 days.

The phenotype of the worms fed with *C. elegans* dsRNA was compared to the phenotype of *C. elegans nuc-1 (e1392)* worms fed with the empty vector.

Based on this experiment, it was concluded that silencing the *C. elegans* target genes as represented in Table 1A had a fatal effect on the growth and viability of the worm and that the target gene is essential to the viability of nematodes. Therefore these genes are good target genes to control (kill or prevent from growing) nematodes via dsRNA mediated gene silencing. Accordingly, the present invention encompasses the use of nematode orthologs of the above *C. elegans* target gene to control nematode infestation in a variety of organisms and materials.

Example 2: Identification of *D. melanogaster* orthologs

As described above in Example 1, numerous *C. elegans* lethal sequenes were identified and can be used for identifying orthologs in other species and genera. For example, the *C. elegans* lethal sequences can be used to identify orthologous *D. melanogasters* sequences. That is, each *C. elegans* sequence can be querried against a public database, such as GenBank, for orthologous sequences in *D. melanogaster*. Potential *D. melanogaster* orthologs were selected that share a high degree of sequence homology (E value preferably less than or equal to 1E-30) and the sequences are blast reciprocal best hits, the latter means that the sequences from different organisms (e.g. *C. elegans* and *D. melanogaster*) are each other's top blast hits. For example, sequence C from *C. elegans* is compared against sequences in *D. melanogaster* using BLAST. If sequence C has the *D. melanogaster* sequence D as best hit and when D is compared to all the sequences of *C. elegans*, also turns out to be sequence C, then D and C are reciprocal best hits. This criterium is often used to define orthology, meaning similar sequences of different species, having similar function. The *D. melanogaster* sequence identifiers are represented in Table 1A.

Example 3: *Leptinotarsa decemlineata* (Colorado potato beetle)

A. Cloning partial gene sequences from *Leptinotarsa decemlineata*

High quality, intact RNA was isolated from 4 different larval stages of *Leptinotarsa decemlineata* (Colorado potato beetle; source: Jeroen van Schaik, Entocare CV Biologische Gewasbescherming, Postbus 162, 6700 AD Wageningen, the Netherlands) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manufacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the LD001, LD002, LD003, LD006, LD007, LD010, LD011, LD014, LD015, LD016 and LD018 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-LD**, which displays *Leptintarsa decemlineata* target genes including primer sequences and cDNA sequences obtained. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/topo vector (Cat. Nr. K2500 20, Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the respectiveSEQ ID NOs as given in **Table 2-LD** and are referred to as the partial sequences. The corresponding partial amino acid sequence are represented by the respective SEQ ID NOs as given in **Table 3-LD**, where the start of the reading frame is indicated in brackets.

B. dsRNA production of the *Leptinotarsa decemlineata* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-LD**. The conditions in the PCR reactions were as follows: 4 minutes at 95°C, followed by 35 cycles of 30 seconds at 95°C, 30 seconds at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-LD**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-LD**. Table 8-LD displays sequences for preparing ds RNA fragments of *Leptinotarsa decemlineata* target sequences and concatemer sequences, including primer sequences.

C. Screening dsRNA targets using artificial diet for activity against *Leptinotarsa decemlineata*

Artificial diet for the Colorado potato beetle was prepared as follows (adapted from Gelman *et al.*, 2001, J. Ins. Sc., vol. 1, no. 7, 1-10): water and agar were autoclaved, and the remaining ingredients (shown in Table 2 below) were added when the temperature dropped to 55 °C. At this temperature, the ingredients were mixed well before the diet was aliquoted into 24-well plates (Nunc) with a quantity of 1ml of diet per well. The artificial diet was allowed to solidify by cooling at room temperature. Diet was stored at 4 °C for up to three weeks.

Table 2: Ingredients for Artificial diet

Ingredients	Volume for 1 L
water	768ml
agar	14g
rolled oats	40g
Torula yeast	60g

lactalbumin hydrolysate	30g
casein	10g
fructose	20g
Wesson salt mixture	4g
tomato fruit powder	12.5g
potato leaf powder	25g
b-sitosterol	1g
sorbic acid	0.8g
methyl paraben	0.8g
Vanderzant vitamin mix	12g
neomycin sulfate	0.2g
aureomycin	0.130g
rifampicin	0.130g
chloramphenicol	0.130g
nystatin	0.050g
soybean oil	2ml
wheat germ oil	2ml

Fifty µl of a solution of dsRNA at a concentration of 1 mg/ml was applied topically onto the solid artificial diet in the wells of the multiwell plate. The diet was dried in a laminair flow cabin. Per treatment, twenty-four Colorado potato beetle larvae (2^{nd} stage), with two insects per well, were tested. The plates were stored in the insect rearing chamber at 25 ± 2 °C, 60 % relative humidity, with a 16:8 hours light:dark photoperiod. The beetles were assessed as live or dead every 1, 2 or 3 days. After seven days, for targets LD006, LD007, LD010, LD011, and LD014, the diet was replaced with fresh diet with topically applied dsRNA at the same concentration (1 mg/ml); for targets LD001, LD002, LD003, LD015, and LD016, the diet was replaced with fresh diet only. The dsRNA targets were compared to diet

only or diet with topically applied dsRNA corresponding to a fragment of the GFP (green fluorescent protein) coding sequence (SEQ ID NO: 235).

Feeding artificial diet containing intact naked dsRNAs to *L. decemlineata* larvae resulted in significant increases in larval mortalities as indicated in two separate bioassays (Figures 1LD-2LD).

All dsRNAs tested resulted ultimately in 100 % mortality after 7 to 14 days. Diet with or without GFP dsRNA sustained the insects throughout the bioassays with very little or no mortality.

Typically, in all assays observed, CPB second-stage larvae fed normally on diet with or without dsRNA for 2 days and molted to the third larval stage. At this new larval stage the CPB were observed to reduce significantly or stop altogether their feeding, with an increase in mortality as a result.

D. Bioassay of dsRNA targets using potato leaf discs for activity against the *Leptinotarsa decemlineata*

An alternative bioassay method was employed using potato leaf material rather than artificial diet as food source for CPB. Discs of approximately 1.1 cm in diameter (or 0.95 cm^2) were cut out off leaves of 2 to 3-week old potato plants using a suitably-sized cork borer. Treated leaf discs were prepared by applying 20 µl of a 10 ng/µl solution of target LD002 dsRNA or control gfp dsRNA on the adaxial leaf surface. The leaf discs were allowed to dry and placed individually in 24 wells of a 24-well multiplate (Nunc). A single second-larval stage CPB was placed into each well, which was then covered with tissue paper and a multiwell plastic lid. The plate containing the insects and leaf discs were kept in an insect chamber at 28°C with a photoperiod of 16h light/8h dark. The insects were allowed to feed on the leaf discs for 2 days after which the insects were transferred to a new plate containing fresh treated leaf discs. Thereafter, the insects were transferred to a plate containing untreated leaf discs every day until day 7. Insect mortality and weight scores were recorded.

Feeding potato leaf discs with surface-applied intact naked dsRNA of target LD002 to *L. decemlineata* larvae resulted in a significant increase in larval mortalities (i.e. at day 7 all insects were dead; 100 % mortality) whereas control gfp dsRNA had no effect on CPB survival. Target LD002 dsRNA severely affected the growth of the larvae after 2 to 3 days whereas the larvae fed with gfp dsRNA at the same concentration developed as normal (**Figure 3-LD**).

D. Screening shorter versions of dsRNAs using artificial diet for activity against *Leptinotarsa decemlineata*

This example exemplifies the finding that shorter (60 or 100bp) dsRNA fragments on their own or as concatemer constructs are sufficient in causing toxicity towards the Colorado potato beetle.

LD014, a target known to induce lethality in Colorado potato beetle, was selected for this example. This gene encodes a V-ATPase subunit E (SEQ ID NO:: 15).

A 100 base pair fragment, LD014_F1, at position 195-294 on SEQ ID NO:: 15 (SEQ ID NO: 159) and a 60 base pair fragment, LD014_F2, at position 235-294 on SEQ ID NO:: 15 (SEQ ID NO: 160) were further selected. See also **Table 7-LD.**

Two concatemers of 300 base pairs, LD014_C1 and LD014_C2, were designed (SEQ ID NO:: 161 and SEQ ID NO:: 162). LD014_C1 contained 3 repeats of the 100 base pair fragment described above (SEQ ID NO:: 159) and LD014_C2 contained 5 repeats of the 60 base pair fragment described above (SEQ ID NO:: 160). See also **Table 7-LD.**

The fragments LD014_F1 and LD014_F2 were synthesized as sense and antisense primers. These primers were annealed to create the double strands DNA molecules prior to cloning. *Xba*I and *Xma*I restrictions sites were included at the 5′ and 3′ ends of the primers, respectively, to facilitate the cloning.

The concatemers were made as 300 base pairs synthetic genes. *Xba*I and *Xma*I restrictions sites were included at the 5′ and 3′ ends of the synthetic DNA fragments, respectively, to facilite the cloning.

The 4 DNA molecules, i.e. the 2 single units (LD014_F1 & LD014_F2) and the 2 concatemers (LD014_C1 & LD014_C2), were digested with *Xba*I and *Xma*I and subcloned in pBluescriptII SK+ linearised by *Xba*I and *Xma*I digests, resulting in recombinant plasmids p1, p2, p3, & p4, respectively.

Double-stranded RNA production: dsRNA was synthesized using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter. For LD014_F1, the sense T7 template was generated using the specific T7 forward primer oGBM159 and the specific reverse primer oGBM164 (represented herein as SEQ ID NO:: 204 and SEQ ID NO: 205, respectively) in a PCR reaction with the following conditions: 4 minutes at 95°C, followed by 35 cycles of 30 seconds at 95°C, 30 seconds at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7

template was generated using the specific forward primer oGBM163 and the specific T7 reverse primer oGBM160 (represented herein as SEQ ID NO: 206 and SEQ ID NO:: 207, respectively) in a PCR reaction with the same conditions as described above. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, Dnase and Rnase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA is herein represented by SEQ ID NO: 203.

For LD014_F2, the sense T7 template was generated using the specific T7 forward primer oGBM161 and the specific reverse primer oGBM166 (represented herein as SEQ ID NO:: 209 and SEQ ID NO:: 210, respectively) in a PCR reaction with the following conditions: 4 minutes at 95°C, followed by 35 cycles of 30 seconds at 95°C, 30 seconds at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using the specific forward primer oGBM165 and the specific T7 reverse primer oGBM162 (represented herein as SEQ ID NO:: 211 and SEQ ID NO:: 212, respectively) in a PCR reaction with the same conditions as described above. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, Dnase and Rnase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA is herein represented by SEQ ID NO: 208.

Also for the concatemers, separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter. The recombinant plasmids p3 and p4 containing LD014_C1 & LD014_C2 were linearised with *Xba*I or *Xma*I, the two linear fragments for each construct purified and used as template for the *in vitro* transcription assay, using the T7 promoters flanking the cloning sites. Double-stranded RNA was prepared by *in vitro* transcription using the T7 RiboMAX™ Express RNAi System (Promega). The sense strands of the resulting dsRNA for LD014_C1 and LD014_C2 are herein represented by SEQ ID NO:: 213 and2114, respectively.

Shorter sequences of target LD014 and concatemers were able to induce lethality in *Leptinotarsa decemlineata*, as shown in **Figure 4-LD.**

G. Screening dsRNAs at different concentrations using artificial diet for activity against *Leptinotarsa decemlineata*

Fifty µl of a solution of dsRNA at serial ten-fold concentrations from 1 µg/µl (for target LD027 from 0.1 µg/µl)down to 0.01 ng/µl was applied topically onto the solid artificial diet in the wells of a 24-well plate (Nunc). The diet was dried in a laminair flow cabin. Per treatment, twenty-four Colorado potato beetle larvae (2nd stage), with two insects per well, were tested. The plates were stored in the insect rearing chamber at 25 ± 2 °C, 60 % relative humidity, with a 16:8 hours light:dark photoperiod. The beetles were assessed as live or dead at regular intervals up to day 14. After seven days, the diet was replaced with fresh diet with topically applied dsRNA at the same concentrations. The dsRNA targets were compared to diet only.

Feeding artificial diet containing intact naked dsRNAs of different targets to *L. decemlineata* larvae resulted in high larval mortalities at concentrations as low as between 0.1 and 10 ng dsRNA/µl as shown in **Figure 5-LD**.

H. Cloning of a CPB gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

While any efficient bacterial promoter may be used, a DNA fragment corresponding to an MLB gene target was cloned in a vector for the expression of double-stranded RNA in a bacterial host (See WO 00/01846).

The sequences of the specific primers used for the amplification of target genes are provided in Table 8. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in Table 8. The recombinant vector harboring this sequence is named pGBNJ003.

The sequences of the specific primers used for the amplification of target gene fragment LD010 are provided in Table 8 (forward primer SEQ ID NO:: 191 and reverse primer SEQ ID NO:: 190). The template used was the pCR8/GW/topo vector containing the LD010 sequence (SEQ ID NO:: 11). The primers were used in a PCR reaction with the

following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment was analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO 00/188121A1), and sequenced. The sequence of the resulting PCR product corresponds to SEQ ID NO:: 188 as given in Table 8. The recombinant vector harboring this sequence was named pGBNJ003.

I. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB309-105, and, (2) BL21(DE3)

The procedures described below were followed in order to express suitable levels of insect-active double-stranded RNA of target LD010 in bacteria. An RNaseIII-deficient strain, AB309-105, was used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB309-105 and BL21(DE3)

Three hundred ng of the plasmid was added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E.* coli strain AB309-105 or BL21(DE3). The cells were incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells were placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium was added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension was transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture was incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB309-105 and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGBNJ003, in the bacterial strain AB309-105 or BL21(DE3) was made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture was measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture was transferred to a 50 ml Falcon tube and the culture then

centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant was removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria were induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria were killed by heat treatment in order to minimize the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture was centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet was resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes were prepared and used in the bioassays for each refreshment. The tubes were stored at -20 °C until further use.

J. Laboratory trials to test Escherichia coli expressing dsRNA target LD010 against *Leptinotarsa decemlineata*

Two bioassay methods were employed to test double-stranded RNA produced in *Escherichia coli* against larvae of the Colorado potato beetle: (1) artificial diet-based bioassay, and, (2) plant-based bioassay.

Artificial diet-based bioassays

Artificial diet for the Colorado potato beetle was prepared as described previously in Example 4. A half milliliter of diet was dispensed into each of the wells of a 48-well multiwell test plate (Nunc). For every treatment, fifty µl of an OD 1 suspension of heat-treated bacteria (which is equivalent to approximately 5 x 10^7 bacterial cells) expressing dsRNA was applied topically onto the solid diet in the wells and the plates were allowed to dry in a laminair flow cabin. Per treatment, forty-eight 2nd stage Colorado potato beetle larvae, one in each well containing diet and bacteria, were tested. Each row of a plate (i.e. 8 wells) was considered as one replicate. The plates were kept in the insect rearing chamber at 25 ± 2 °C, 60 ± 5 % relative humidity, with a 16:8 hours light:dark photoperiod. After every 4 days, the beetles were transferred to fresh diet containing topically-applied bacteria. The beetles were assessed as alive or dead every one or three days post infestation. For the survivors, growth and development in terms of larval weight was recorded on day 7 post infestation.

For RNaseIII-deficient *E. coli* strain AB309-105, bacteria containing plasmid pGBNJ003 and those containing the empty vector pGN29 (reference to WO 00/188121A1) were tested in bioassays for CPB toxicity. Bacteria harboring the pGBNJ003 plasmid showed a clear increase in insect mortality with time, whereas little or no mortality was observed for pGN29 and diet only control **(Figures 6a-LD & 7a-LD)**. The growth and development of Colorado potato beetle larval survivors, 7 days after feeding on artificial diet containing bacteria expressing dsRNA target LD010, was severely impeded **(Table 10-LD, Figure 8a-LD)**.

For *E. coli* strain BL21(DE3), bacteria containing plasmid pGBNJ003 and those containing the empty vector pGN29 were tested against the Colorado potato beetle larvae. Similar detrimental effects were observed on larvae fed diet supplemented with BL21(DE3) bacteria as for the RNAseIII-deficient strain, AB309-105 **(Figures 6b-LD & 7b-LD)**. However, the number of survivors for the five clones were higher for BL21(DE3) than for AB309-105; at day 12, average mortality values were approximately 25 % lower for this strain compared to the RNase III deficient strain. Also, the average weights of survivors fed on diet containing BL21(DE3) expressing dsRNA corresponding to target LD010 was severely reduced **(Table 10-LD, Figure 8b-LD)**.

The delay in growth and development of the CPB larvae fed on diet containing either of the two bacterial strains harboring plasmid pGBNJ003 was directly correlated to feeding inhibition since no frass was visible in the wells of refreshed plates from day 4 onwards when compared to bacteria harboring the empty vector pGN29 or the diet only plate. This observation was similar to that where CPB was fed on *in vitro* transcribed double-stranded RNA topically applied to artificial diet (see Example 3D); here, cessation of feeding occurred from day 2 onwards on treated diet.

Plant-based bioassays

Whole potato plants were sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to CPB larvae. The potato plants of variety 'line 5' were grown from tubers to the 8-12 unfolded leaf stage in a plant growth room chamber with the following conditions: 25 ± 2°C, 60 % relative humidity, 16:8 hour light:dark photoperiod. The plants were caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent larval escape. Fifteen Colorado potato beetle larvae at the L1 stage were placed on each treated plant in the cage. Plants were treated with a suspension of *E. coli* AB309-105

harboring the pGBNJ003 plasmids (clone 1; **Figure 7a-LD**) or pGN29 plasmid (clone 1; see **Figure 7a-LD**). Different quantities of bacteria were applied to the plants: 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of 1.6 ml was sprayed on the plant with the aid of a vaporizer. One plant was used per treatment in this trial. The number of survivors were counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB309-105 expressing target dsRNA from pGBNJ003 led to a dramatic increase in insect mortality when compared to pGN29 control. The mortality count was maintained when the amount of bacteria cell suspension was diluted 9-fold (**Figure 9-LD**). The average weights of the larval survivors at day 11 on plants sprayed with bacteria harboring the pGBNJ003 vector were approximately 10-fold less than that of pGN29 (**Figure 10-LD**). Feeding damage by CPB larvae of the potato plant sprayed with bacteria containing the pGBNJ003 plasmid was much reduced when compared to the damage incurred on a potato plant sprayed with bacteria containing the empty vector pGN29 (**Figure 11-LD**).

These experiments showed that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification was provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

K. Testing various culture suspension densities of *Escherichia coli* expressing dsRNA target LD010 against *Leptinotarsa decemlineata*

Preparation and treatment of bacterial cultures are described in Example 3J. Three-fold serial dilutions of cultures (starting from 0.25 unit equivalents) of *Escherichia coli* RNAseIII-deficient strain AB309-105 expressing double-stranded RNA of target LD010 were applied to foliages of the potato plant of variety 'Bintje' at the 8-12 unfolded leaf stage. Ten L1 larvae of the *L. decemlineata* were placed on the treated plants with one plant per treatment. Scoring for insect mortality and growth impediment was done on day 7 (i.e., 7 days post infestation).

As shown in **Figure 14-LD**, high CPB larval mortality (90 to 100 %) was recorded after 1 week when insects were fed potato plants treated with a topical application by fine spray of heat-inactivated cultures of *E.coli* harboring plasmid pGBNJ003 (for target 10

dsRNA expression) at densities 0.25, 0.08 and 0.025 bacterial units. At 0.008 units, about a third of the insects were dead, however, the surviving insects were significantly smaller than those in the control groups (*E. coli* harbouring the empty vector pGN29 and water only). Feeding damage by CPB larvae of the potato plant sprayed with bacteria containing the pGBNJ003 plasmid at concentrations 0.025 or 0.008 units was much reduced when compared to the damage incurred on a potato plant sprayed with bacteria containing the empty vector pGN29 (**Figure 15-LD**).

L. Adults are extremely susceptible to orally ingested dsRNA corresponding to target genes.

The example provided below highlights the finding that adult insects (and not only insects of the larval stage) are extremely susceptible to orally ingested dsRNA corresponding to target genes.

Four targets were chosen for this experiment: targets 2, 10, 14 and 16 (SEQ ID NO: 168, 188, 198 and 220, respectively). GFP fragment dsRNA (SEQ ID NO: 235) was used as a control. Young adults (2 to 3 days old) were picked at random from our laboratory-reared culture with no bias towards insect gender. Ten adults were chosen per treatment. The adults were prestarved for at least 6 hours before the onset of the treatment. On the first day of treatment, each adult was fed four potato leaf discs (diameter 1.5 cm^2) which were pretreated with a topical application of 25 µl of 0.1µg/µl target dsRNA (synthesized as described in Example 3A; topical application as described in Example 3E) per disc. Each adult was confined to a small petridish (diameter 3 cm) in order to make sure that all insects have ingested equal amounts of food and thus received equal doses of dsRNA. The following day, each adult was again fed four treated leaf discs as described above. On the third day, all ten adults per treatment were collected and placed together in a cage consisting of a plastic box (dimensions 30 cm x 20 cm x 15 cm) with a fine nylon mesh built into the lid to provide good aeration. Inside the box, some moistened filter paper was placed in the base. Some (untreated) potato foliage was placed on top of the paper to maintain the adults during the experiment. From day 5, regular assessments were carried out to count the number of dead, alive (mobile) and moribund insects. For insect moribundity, adults were laid on their backs to check whether they could right themselves within several minutes; an insect was considered moribund only if it was not able to turn onto its front.

Clear specific toxic effects of double-stranded RNA correpsonding to different targets towards adults of the Colorado potato beetle, *Leptinotarsa decemlineata*, were demonstrated in this experiment (**Figure 12-LD**). Double-stranded RNA corresponding to a gfp fragment showed no toxicity towards CPB adults on the day of the final assessment (day 19). This experiment clearly showed that the survival of CPB adults was severely reduced only after a few days of exposure to dsRNA when delivered orally. For example, for target 10, on day 5, 5 out of 10 adults were moribund (sick and slow moving); on day 6, 4 out of 10 adults were dead with three of the survivors moribund; on day 9 all adults were observed dead.

As a consequence of this experiment, the application of target double-stranded RNAs against insect pests may be broadened to include the two life stages of an insect pest (i.e. larvae and adults) which could cause extensive crop damage, as is the case with the Colorado potato beetle.

Example 4: *Phaedon cochleariae* (mustard leaf beetle)

A. Cloning of a partial sequence of the *Phaedon cochleariae* (mustard leaf beetle) PC001, PC003, PC005, PC010, PC014, PC016 and PC027 genes via family PCR

High quality, intact RNA was isolated from the third larval stage of *Phaedon cochleariae* (mustard leaf beetle; source: Dr. Caroline Muller, Julius-von-Sachs-Institute for Biosciences, Chemical Ecology Group, University of Wuerzburg, Julius-von-Sachs-Platz 3, D-97082 Wuerzburg, Germany) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase (Cat. Nr. 1700, Promega) treatment following the manufacturer's instructions. cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the PC001, PC003, PC005, PC010, PC014, PC016 and PC027 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manafacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-PC**. Table 2-PC displays *Phaedon cochleariae* target genes including primer sequences and cDNA sequences obtained. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at

95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR4/TOPO vector (Cat. Nr. K4530-20, Invitrogen) and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NO:s as given in **Table 2-PC** and are referred to as the partial sequences.

The corresponding partial amino acid sequence are represented by the respective SEQ ID NO:s as given in **Table 3-PC**. Table 3-PC provides amino acid sequences of cDNA clones, and the start of the reading frame is indicated in brackets.

B. dsRNA production of the *Phaedon cochleariae* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-PC**. Table 8-PC provides details for preparing ds RNA fragments of *Phaedon cochleariae* target sequences, including primer sequences.

The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-PC**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-PC**.

C. Laboratory trials to test dsRNA targets, using oilseed rape leaf discs for activity against *Phaedon cochleariae* larvae

The example provided below is an exemplification of the finding that the mustard leaf beetle (MLB) larvae are susceptible to orally ingested dsRNA corresponding to own target genes.

To test the different double-stranded RNA samples against MLB larvae, a leaf disc assay was employed using oilseed rape (*Brassica napus* variety SW Oban; source: Nick Balaam, Sw Seed Ltd., 49 North Road, Abington, Cambridge, CB1 6AS, UK) leaf material as food source. The insect cultures were maintained on the same variety of oilseed rape in the insect chamber at 25 ± 2 °C and 60 ± 5 % relative humidity with a photoperiod of 16h light/8h dark. Discs of approximately 1.1 cm in diameter (or 0.95 cm^2) were cut out off leaves of 4- to 6-week old rape plants using a suitably-sized cork borer. Double-stranded RNA samples were diluted to 0.1 µg/µl in Milli-Q water containing 0.05% Triton X-100. Treated leaf discs were prepared by applying 25 µl of the diluted solution of target PC001, PC003, PC005, PC010, PC014, PC016, PC027 dsRNA and control gfp dsRNA or 0.05 % Triton X-100 on the adaxial leaf surface. The leaf discs were left to dry and placed individually in each of the 24 wells of a 24-well multiplate containing 1 ml of gellified 2% agar which helps to prevent the leaf disc from drying out. Two neonate MLB larvae were placed into each well of the plate, which was then covered with a multiwell plastic lid. The plate (one treatment containing 48 insects) was divided into 4 replicates of 12 insects per replicate (each row). The plate containing the insects and leaf discs were kept in an insect chamber at 25 ± 2 °C and 60 ± 5 % relative humidity with a photoperiod of 16h light/8h dark. The insects were fed leaf discs for 2 days after which they were transferred to a new plate containing freshly treated leaf discs. Thereafter, 4 days after the start of the bioassay, the insects from each replicate were collected and transferred to a Petri dish containing untreated fresh oilseed rape leaves. Larval mortality and average weight were recorded at days 2, 4 7, 9 and 11.

P. cochleariae larvae fed on intact naked target dsRNA-treated oilseed rape leaves resulted in significant increases in larval mortalities for all targets tested, as indicated in Figure 1(a). Tested double-stranded RNA for target PC010 led to 100 % larval mortality at day 9 and for target PC027 at day 11. For all other targets, signficantly high mortality values were reached at day 11 when compared to control gfp dsRNA, 0.05% Trition X-100 alone or

untreated leaf only: (average value in percentage ± confidence interval with alpha 0.05) PC001 (94.4 ± 8.2); PC003 (86.1 ± 4.1); PC005 (83.3 ± 7.8); PC014 (63.9 ± 20.6); PC016 (75.0 ± 16.8); gfp dsRNA (11.1 ± 8.2); 0.05% Triton X-100 (19.4 ± 10.5); leaf only (8.3 ± 10.5).

Larval survivors were assessed based on their average weight. For all targets tested, the mustard leaf beetle larvae had significantly reduced average weights after day 4 of the bioassay; insects fed control gfp dsRNA or 0.05% Triton X-100 alone developed normally, as for the larvae on leaf only **(Figure 1(b)-PC)**.

D. Laboratory trials to screen dsRNAs at different concentrations using oilseed rape leaf discs for activity against *Phaedon cochleariae* larvae

Twenty-five µl of a solution of dsRNA from target PC010 or PC027 at serial ten-fold concentrations from 0.1 µg/µl down to 0.1 ng/µl was applied topically onto the oilseed rape leaf disc, as described in Example 4D above. As a negative control, 0.05% Triton X-100 only was administered to the leaf disc. Per treatment, twenty-four mustard leaf beetle neonate larvae, with two insects per well, were tested. The plates were stored in the insect rearing chamber at 25 ± 2 °C, 60 ± 5 % relative humidity, with a 16:8 hours light:dark photoperiod. At day 2, the larvae were transferred on to a new plate containing fresh dsRNA-treated leaf discs. At day 4 for target PC010 and day 5 for target PC027, insects from each replicate were transferred to a Petri dish containing abundant untreated leaf material. The beetles were assessed as live or dead on days 2, 4, 7, 8, 9, and 11 for target PC010, and 2, 5, 8, 9 and 12 for target PC027.

Feeding oilseed rape leaf discs containing intact naked dsRNAs of the two different targets, PC010 and PC027, to *P. cochleariae* larvae resulted in high mortalities at concentrations down to as low as 1 ng dsRNA/µl solution, as shown in Figures 2 (a) and (b). Average mortality values in percentage ± confidence interval with alpha 0.05 for different concentrations of dsRNA for target PC010 at day 11, 0 µg/µl: 8.3 ± 9.4; 0.1 µg/µl: 100; 0.01 µg/µl: 79.2 ± 20.6; 0.001 µg/µl: 58.3 ± 9.4; 0.0001 µg/µl: 12.5 ± 15.6; and for target PC027 at day 12, 0 µg/µl: 8.3 ± 9.4; 0.1 µg/µl: 95.8 ± 8.2; 0.01 µg/µl: 95.8 ± 8.2; 0.001 µg/µl: 83.3 ± 13.3; 0.0001 µg/µl: 12.5 ± 8.2.

E. Cloning of a MLB gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to an MLB gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in Table 8. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in Table 8. The recombinant vector harbouring this sequence is named pGBNJ00(to be completed).

The sequences of the specific primers used for the amplification of target gene fragment PC010 are provided in **Table 8-PC**. The template used was the pCR8/GW/topo vector containing the PC010 sequence (SEQ ID NO: 253). The primers were used in a touch-down PCR reaction with the following conditions: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C with temperature decrease of -0.5 °C per cycle and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment was analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to SEQ ID NO: 488 as given in **Table 8-PC.** The recombinant vector harbouring this sequence was named pGCDJ001.

F. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli* AB309-105

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. In this experiment, an RNaseIII-deficient strain, AB309-105 is used.

Transformation of AB309-105

Three hundred ng of the plasmid were added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E.* coli strain AB309-105. The cells were incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after

which the cells were placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium was added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension was transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture was incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB309-105

Expression of double-stranded RNA from the recombinant vector, pGBNJ003, in the bacterial strain AB309-105 was made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture was measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture was transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant was removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria were induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria were killed by heat treatment in order to minimize the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture was centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet was resuspended in a total volume of 50 ml of 0.05% Triton X-100 solution. The tube was stored at 4 °C until further use

G. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Phaedon cochleariae*

Leaf disc bioassays

The leaf-disc bioassay method was employed to test double-stranded RNA from target PC010 produced in *Escherichia coli* (from plasmid pGCDJ001) against larvae of the mustard leaf beetle. Leaf discs were prepared from oilseed rape foliage, as described in Example 4. Twenty µl of a bacterial suspension, with an optical density measurement of 1 at 600 nm wavelength, was pipetted onto each disc. The leaf disc was placed in a well of a 24-multiwell plate containing 1 ml gellified agar. On each leaf disc were added two neonate larvae. For each treatment, 3 replicates of 16 neonate larvae per replicate were prepared. The plates were kept in the insect rearing chamber at 25 ± 2 °C and 60 ± 5 % relative humidity, with a 16:8 hours light:dark photoperiod. At day 3 (i.e. 3 days post start of bioassay), larvae were transferred to a new plate containing fresh treated (same dosage) leaf discs. The leaf material was refreshed every other day from day 5 onwards. The bioassay was scored on mortality and average weight. Negative controls were leaf discs treated with bacteria harbouring plasmid pGN29 (empty vector) and leaf only.

A clear increase in mortality of *P. cochleariae* larvae with time was shown after the insects were fed on oilseed rape leaves treated with a suspension of RNaseIII-deficient *E. coli* strain AB309-105 containing plasmid pGCDJ001, whereas very little or no insect mortality was observed in the case of bacteria with plasmid pGN29 or leaf only control (**Figure 3-PC**).

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to MLB. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. MLB are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB309-105 harbouring the pGBNJ001 plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB309-105 expressing target dsRNA from pGBNJ003 leed to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an

insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 5: *Epilachna varivetis* (Mexican bean beetle)

A. Cloning *Epilachna varivetis* partial gene sequences

High quality, intact RNA was isolated from 4 different larval stages of *Epilachna varivetis* (Mexican bean beetle; source: Thomas Dorsey, Supervising Entomologist, New Jersey Department of Agriculture, Division of Plant Industry, Bureau of Biological Pest Control, Phillip Alampi Beneficial Insect Laboratory, PO Box 330, Trenton, New Jersey 08625-0330, USA) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manafacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the EV005, EV009, EV010, EV015 and EV016 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-EV**, which displays *Epilachna varivetis* target genes including primer sequences and cDNA sequences obtained. These primers were used in respective PCR reactions with the following conditions: for EV005 and EV009, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute 30 seconds at 72°C, followed by 7 minutes at 72°C; for EV014, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 53°C and 1 minute at 72°C, followed by 7 minutes at 72°C; for EV010 and EV016, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 1 minute 40 seconds at 72°C, followed by 7 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr.

28706, Qiagen), cloned into the pCR4/TOPO vector (Cat. Nr. K4530-20, Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NO:s as given in **Table 2-EV** and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NO:s as given in **Table 3-EV**, where the start of the reading frame is indicated in brackets.

B. dsRNA production of the *Epilachna varivetis* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-EV**.

The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-EV**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-EV**.

C. Laboratory trials to test dsRNA targets using bean leaf discs for activity against *Epilachna varivetis* larvae

The example provided below is an exemplification of the finding that the Mexican bean beetle (MBB) larvae are susceptible to orally ingested dsRNA corresponding to own target genes.

To test the different double-stranded RNA samples against MBB larvae, a leaf disc assay was employed using snap bean (*Phaseolus vulgaris* variety Montano; source: Aveve NV, Belgium) leaf material as food source. The same variety of beans was used to maintain insect cultures in the insect chamber at 25 ± 2 °C and 60 ± 5 % relative humidity with a photoperiod of 16h light/8h dark. Discs of approximately 1.1 cm in diameter (or 0.95 cm^2) were cut out off leaves of 1- to 2-week old bean plants using a suitably-sized cork borer. Double-stranded RNA samples were diluted to 1 µg/µl in Milli-Q water containing 0.05% Triton X-100. Treated leaf discs were prepared by applying 25 µl of the diluted solution of target Ev005, Ev010, Ev015, Ev016 dsRNA and control gfp dsRNA or 0.05 % Triton X-100 on the adaxial leaf surface. The leaf discs were left to dry and placed individually in each of the 24 wells of a 24-well multiplate containing 1 ml of gellified 2 % agar which helps to prevent the leaf disc from drying out. A single neonate MBB larva was placed into each well of a plate, which was then covered with a multiwell plastic lid. The plate was divided into 3 replicates of 8 insects per replicate (row). The plate containing the insects and leaf discs were kept in an insect chamber at 25 ± 2 °C and 60 ± 5 % relative humidity with a photoperiod of 16h light/8h dark. The insects were fed on the leaf discs for 2 days after which the insects were transferred to a new plate containing freshly treated leaf discs. Thereafter, 4 days after the start of the bioassay, the insects were transferred to a petriplate containing untreated fresh bean leaves every day until day 10. Insect mortality was recorded at day 2 and every other day thereafter.

Feeding snap bean leaves containing surface-applied intact naked target dsRNAs to *E. varivestis* larvae resulted in significant increases in larval mortalities, as indicated in Figure 1. Tested double-stranded RNAs of targets Ev010, Ev015, & Ev016 led to 100 % mortality after 8 days, whereas dsRNA of target Ev005 took 10 days to kill all larvae. The majority of the insects fed on treated leaf discs containing control gfp dsRNA or only the surfactant Triton X-100 were sustained throughout the bioassay **(Figure 1-EV).**

D. Laboratory trials to test dsRNA targets using bean leaf discs for activity against *Epilachna varivestis* adults

The example provided below is an exemplification of the finding that the Mexican bean beetle adults are susceptible to orally ingested dsRNA corresponding to own target genes.

In a similar bioassay set-up as for Mexican bean beetle larvae, adult MBBs were tested against double-stranded RNAs topically-applied to bean leaf discs. Test dsRNA from each target Ev010, Ev015 and Ev016 was diluted in 0.05 % Triton X-100 to a final concentration of 0.1 μg/μl. Bean leaf discs were treated by topical application of 30 μl of the test solution onto each disc. The discs were allowed to dry completely before placing each on a slice of gellified 2 % agar in each well of a 24-well multiwell plate. Three-day-old adults were collected from the culture cages and fed nothing for 7-8 hours prior to placing one adult to each well of the bioassay plate (thus 24 adults per treatment). The plates were kept in the insect rearing chamber (under the same conditions as for MBB larvae for 24 hours) after which the adults were transferred to a new plate containing fresh dsRNA-treated leaf discs. After a further 24 hours, the adults from each treatment were collected and placed in a plastic box with dimensions 30 cm x 15 cm x 10 cm containing two potted and untreated 3-week-old bean plants. Insect mortality was assessed from day 4 until day 11.

All three target dsRNAs (Ev010, Ev015 and Ev016) ingested by adults of *Epilachna varivestis* resulted in significant increases in mortality from day 4 (4 days post bioassay start), as shown in **Figure 2(a)-EV**. From day 5, dramatic changes in feeding patterns were observed between insects fed initially with target-dsRNA-treated bean leaf discs and those that were fed discs containing control gfp dsRNA or surfactant Triton X-100. Reductions in foliar damage by MBB adults of untreated bean plants were clearly visible for all three targets when compared to gfp dsRNA and surfactant only controls, albeit at varying levels; insects fed target 15 caused the least damage to bean foliage (**Figure 2(b)-EV**).

E. Cloning of a MBB gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to an MLB gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in **Table 8-EV**. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed

on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-EV**. The recombinant vector harbouring this sequence is named pGBNJ00XX.

F. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB309-105, and, (2) BL21(DE3)

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB309-105, is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB309-105 and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E.* coli strain AB309-105 or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB309-105 and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGBNJ003, in the bacterial strain AB309-105 or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol)

supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimize the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

G. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Epilachna varivetis*

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to MBB. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. MMB are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB309-105 harbouring the pGBNJ001 plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB309-105 expressing target dsRNA from pGBNJ003 lead to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these

experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 6: *Anthonomus grandis* (cotton boll weevil)

A. Cloning *Anthonomus grandis* partial sequences

High quality, intact RNA was isolated from the 3 instars of *Anthonomus grandis* (cotton boll weevil; source: Dr. Gary Benzon, Benzon Research Inc., 7 Kuhn Drive, Carlisle, Pennsylvania 17013, USA) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manafacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the AG001, AG005, AG010, AG014 and AG016 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manafacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-AG**. These primers were used in respective PCR reactions with the following conditions: for AG001, AG005 and AG016, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C; for AG010, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 2 minutes and 30 seconds at 72°C, followed by 7 minutes at 72°C; for AG014, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 7 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/TOPO vector (Cat. Nr. K2500-20, Invitrogen) and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NO:s as given in **Table 2-AG** and are referred to as the partial sequences. The corresponding partial amino acid sequence are represented by the respective SEQ ID NO:s as given in **Table 3-AG**.

B. dsRNA production of the *Anthonomus grandis* (cotton boll weevil) genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-AG**. A touchdown PCR was performed as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C with a decrease in temperature of 0.5°C per cycle and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-AG**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-AG**.

C. Laboratory trials to test dsRNA targets, using artificial diet for activity against the larvae of the house cricket, *Acheta domesticus*

House crickets, *Acheta domesticus*, were maintained at Insect Investigations Ltd. (origin: Blades Biological Ltd., Kent, UK). The insects were reared on bran pellets and cabbage leaves. Mixed sex nymphs of equal size and no more than 5 days old were selected for use in the trial. Double-stranded RNA was mixed with a wheat-based pelleted rodent diet (rat and mouse standard diet, B & K Universal Ltd., Grimston, Aldbrough, Hull, UK). The diet, BK001P, contains the following ingredients in descending order by weight: wheat, soya, wheatfeed, barley, pellet binder, rodent 5 vit min, fat blend, dicalcium phosphate, mould carb. The pelleted rodent diet was finely ground and heat-treated in a microwave oven prior to mixing, in order to inactivate any enzyme components. All rodent diet was taken from the

same batch in order to ensure consistency. The ground diet and dsRNA were mixed thoroughly and formed into small pellets of equal weight, which were allowed to dry overnight at room temperature.

Double-stranded RNA samples from targets and gfp control at concentrations 10 µg/µl are applied in the ratio 1 g ground diet plus 1 ml dsRNA solution, thereby resulting in an application rate of 10 mg dsRNA per g pellet. Pellets are replaced weekly. The insects are provided with treated pellets for the first three weeks of the trial. Thereafter untreated pellets are provided. Insects are maintained within lidded plastic containers (9 cm diameter, 4.5 cm deep), ten per container. Each arena contains one treated bait pellet and one water source (damp cotton wool ball), each placed in a separate small weigh boat. The water is replenished *ad lib* throughout the experiment.

Assessments are made at twice weekly intervals, with no more than four days between assessments, until all the control insects had either died or moulted to the adult stage (84 days). At each assessment the insects are assessed as live or dead, and examined for abnormalities. From day 46 onwards, once moulting to adult commences, all insects (live and dead) are assessed as nyumph or adult. Surviving insects are weighed on day 55 of the trial. Four replicates are performed for each of the treatments. During the trial the test conditions are 25 to 33 °C and 20 to 25 % relative humidity, with a 12:12 hour light:dark photoperiod.

D. Cloning of a MLB gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to an MLB gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in Table 8. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence

of the resulting PCR product corresponds to the respective sequence as given in Table 8. The recombinant vector harbouring this sequence is named pGBNJ00XX.

E. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB309-105, and, (2) BL21(DE3)

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB309-105, is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB309-105 and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E. coli* strain AB309-105 or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB309-105 and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGBNJ003, in the bacterial strain AB309-105 or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

F. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Anthonomus grandis*

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to CBW. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. CBW are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB309-105 harbouring the pGBNJ001 plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB309-105 expressing target dsRNA from pGBNJ003 lead to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 7: *Tribolium castaneum* (red flour beetle)

A. Cloning *Tribolium castaneum* partial sequences

High quality, intact RNA was isolated from all the different insect stages of *Tribolium castaneum* (red flour beetle; source: Dr. Lara Senior, Insect Investigations Ltd., Capital Business Park, Wentloog, Cardiff, CF3 2PX, Wales, UK) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manafacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the TC001, TC002, TC010, TC014 and TC015 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manafacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-TC**. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C (TC001, TC014, TC015); 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 2 minutes and 30 seconds at 72°C, followed by 7 minutes at 72°C (TC010); 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 53°C and 1 minute at 72°C, followed by 7 minutes at 72°C (TC002) . The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/TOPO vector (Cat. Nr. K2500-20, Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NO:s as given in **Table 2-TC** and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NO:s as given in **Table 3-TC**.

B. dsRNA production of the *Tribolium castaneum* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-TC**. The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C (-0.5°C/cycle) and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-TC**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-TC**.

C. Laboratory trials to test dsRNA targets, using artificial diet for activity against *Tribolium castaneum* larvae

The example provided below is an exemplification of the finding that the red flour beetle (RFB) larvae are susceptible to orally ingested dsRNA corresponding to own target genes.

Red flour beetles, *Tribolium castaneum*, were maintained at Insect Investigations Ltd. (origin: Imperial College of Science, Technology and Medicine, Silwood Park, Berkshire, UK). Insects were cultured according to company SOP/251/01. Briefly, the beetles were housed in plastic jars or tanks. These have an open top to allow ventilation. A piece of netting was fitted over the top and secured with an elastic band to prevent escape. The larval rearing medium (flour) was placed in the container where the beetles can breed. The stored product

beetle colonies were maintained in a controlled temperature room at 25 ± 3 °C with a 16:8 hour light:dark cycle.

Double-stranded RNA from target TC014 (with sequence corresponding to SEQ ID NO: -799) was incorporated into a mixture of flour and milk powder (wholemeal flour: powdered milk in the ratio 4:1) and left to dry overnight. Each replicate was prepared separately: 100 µl of a 10 µg/µl dsRNA solution (1 mg dsRNA) was added to 0.1 g flour/milk mixture. The dried mixture was ground to a fine powder. Insects were maintained within Petri dishes (55 mm diameter), lined with a double layer of filter paper. The treated diet was placed between the two filter paper layers. Ten first instar, mixed sex larvae were placed in each dish (replicate). Four replicates were performed for each treatment. Control was Milli-Q water. Assessments (number of survivors) were made on a regular basis. During the trial, the test conditions were 25 – 33 °C and 20 – 25 % relative humidity, with a 12:12 hour light:dark photoperiod.

Survival of larvae of *T. castaneum* over time on artificial diet treated with target TC014 dsRNA was significantly reduced when compared to diet only control, as shown in Figure 1.

D. Cloning of a RFB gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to an RFB gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in **Table 8-TC**. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-TC**. The recombinant vector harbouring this sequence is named pGBNJ00 XX.

E. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB309-105, and, (2) BL21(DE3)

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB309-105, is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB309-105 and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E.* coli strain AB309-105 or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB309-105 and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGBNJ003, in the bacterial strain AB309-105 or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA

interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

F. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Tribolium castaneum*

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to RFB. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. RFB are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB309-105 harbouring the pGBNJ001 plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB309-105 expressing target dsRNA from pGBNJ003 leed to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 10: *Myzus persicae* (green peach aphid)

A. Cloning *Myzus persicae partial sequences*

High quality, intact RNA was isolated from nymphs of *Myzus persicae* (green peach aphid; source: Dr. Rachel Down, Insect & Pathogen Interactions, Central Science Laboratory, Sand Hutton, York, YO41 1LZ, UK) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manafacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the MP001, MP002, MP010, MP016 and MP027 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manafacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-MP**. These primers were used in respective PCR reactions with the following conditions: for MP001, MP002 and MP016, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute 30 seconds at 72°C, followed by 7 minutes at 72°C; for MP027, a touchdown program was used: 10 minutes at 95°C, followed by 10 cycles of 30 seconds at 95°C, 40 seconds at 60°C with a decrease in temperature of 1°C per cycle and 1 minute 10 seconds at 72°C, followed by 30 cycles of 30 seconds at 95°C, 40 seconds at 50°C and 1 minute 10 seconds at 72°C, followed by 7 minutes at 72°C; for MP010, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 3 minutes at 72°C, followed by 7 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/TOPO vector (Cat. Nr. K2500-20, Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NO:s as given in **Table 2-MP** and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NO:s as given in **Table 3-MP**.

B. dsRNA production of *Myzus persicae* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-MP**. A touchdown PCR was performed as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 55°C (for MP001, MP002, MP016, MP027 and gfp) or 30 seconds at 50°C (for MP010) with a decrease in temperature of 0.5°C per cycle and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 45°C and 1 minute at 72°C followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-MP**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-MP**.

C. Laboratory trials to test dsRNA targets using liquid artificial diet for activity against *Myzus persicae*

Liquid artificial diet for the green peach aphid, *Myzus persicae*, was prepared based on the diet suitable for pea aphids (*Acyrthosiphon pisum*), as described by Febvay et al. (1988) [Influence of the amino acid balance on the improvement of an artificial diet for a biotype of *Acyrthosiphon pisum* (Homoptera: Aphididae). *Can. J. Zool.* 66: 2449–2453], but with some modifications. The amino acids component of the diet was prepared as follows: in mg/100ml, alanine 178.71, beta-alanine 6.22, arginine 244.9, asparagine 298.55, aspartic acid 88.25, cysteine 29.59, glutamic acid 149.36, glutamine 445.61, glycine 166.56, histidine 136.02, isoleucine 164.75, leucine 231.56, lysine hydrochloride 351.09, methionine 72.35, ornithine (HCl) 9.41, phenylalanine 293, proline 129.33, serine 124.28, threonine 127.16, tryptophane 42.75, tyrosine 38.63, L-valine 190.85. The amino acids were dissolved in 30 ml Milli-Q H_2O except for tyrosine which was first dissolved in a few drops of 1 M HCl before adding to the amino acid mix. The vitamin mix component of the diet was prepared as a 5 x concentrate stock as follows: in mg/L, amino benzoic acid 100, ascorbic acid 1000, biotin 1, calcium panthothenate 50, choline chloride 500, folic acid 10, myoinositol 420, nicotinic acid 100, pyridoxine hydrochloride 25, riboflavin 5, thiamine hydrochloride 25. The riboflavin

was dissolved in 1 ml H2O at 50 °C and then added to the vitamin mix stock. The vitamin mix was aliquoted in 20 ml per aliquot and stored at -20 °C. One aliquot of vitamin mix was added to the amino acid solution. Sucrose and $MgSO_4.7H_2O$ was added with the following amounts to the mix: 20 g and 242 mg, respectively. Trace metal stock solution was prepared as follows: in mg/100ml, $CuSO_4.5H_2O$ 4.7, $FeCl_3.6H_2O$ 44.5, $MnCl_2.4H2O$ 6.5, NaCl 25.4, $ZnCl_2$ 8.3. Ten ml of the trace metal solution and 250 mg KH_2PO_4 was added to the diet and Milli-Q water was added to a final liquid diet volume of 100 ml. The pH of the diet was adjusted to 7 with 1 M KOH solution. The liquid diet was filter-sterilised through an 0.22 μm filter disc (Millipore).

Green peach aphids (*Myzus persicae*; source: Dr. Rachel Down, Insect & Pathogen Interactions, Central Science Laboratory, Sand Hutton, York, YO41 1LZ, UK) were reared on 4- to 6-week-old oilseed rape (*Brassica napus* variety SW Oban; source: Nick Balaam, Sw Seed Ltd., 49 North Road, Abington, Cambridge, CB1 6AS, UK) in aluminium-framed cages containing 70 μm mesh in a controlled environment chamber with the following conditions: 23 ±2 °C and 60 ±5 % relative humidity, with a 16:8 hours light:dark photoperiod.

One day prior to the start of the bioassay, adults were collected from the rearing cages and placed on fresh detached oilseed rape leaves in a Petri dish and left overnight in the insect chamber. The following day, first-instar nymphs were picked and transferred to feeding chambers. A feeding chamber comprised of 10 first instar nymphs placed in a small Petri dish (with diameter 3 cm) covered with a single layer of thinly stretched parafilm M onto which 50 μl of diet was added. The chamber was sealed with a second layer of parafilm and incubated under the same conditions as the adult cultures. Diet with dsRNA was refreshed every other day and the insects' survival assessed on day 8 i.e. 8th day post bioassay start. Per treatment, 5 bioassay feeding chambers (replicates) were set up simultaneously. Test and control (gfp) dsRNA solutions were incorporated into the diet to a final concentration of 2 μg/μl. The feeding chambers were kept at 23 ±2 °C and 60 ±5 % relative humidity, with a 16:8 hours light:dark photoperiod. A Mann-Whitney test was determined by GraphPad Prism version 4 to establish whether the medians do differ significantly between target 27 (MP027) and gfp dsRNA.

In the bioassay, feeding liquid artificial diet supplemented with intact naked dsRNA from target 27 (SEQ ID NO: 1061) to nymphs of *Myzus persicae* using a feeding chamber, resulted in a significant increase in mortality, as shown in Figure 1. Average percentage

survivors for target 27, gfp dsRNA and diet only treatment were 2, 34 and 82, respectively. Comparison of target 027 with gfp dsRNA groups using the Mann-Whitney test resulted in an one-tailed P-value of 0.004 which indicates that the median of target 027 is significantly different ($P < 0.05$) from the expected larger median of gfp dsRNA. The green peach aphids on the liquid diet with incorporated target 27 dsRNA were noticeably smaller than those that were fed on diet only or with gfp dsRNA control (data not presented).

D. Cloning of a GPA gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to a GPA gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in **Table 8-MP**. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-MP**. The recombinant vector harbouring this sequence is named pGBNJ00XX.

E. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB309-105, and, (2) BL21(DE3)

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB309-105, is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB309-105 and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E.* coli strain AB309-105 or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension

incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB309-105 and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGBNJ003, in the bacterial strain AB309-105 or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

F. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Myzus persicae*

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to GPA. The are grown from in a plant growth room

chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. GPA are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB309-105 harbouring the pGBNJ001 plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB309-105 expressing target dsRNA from pGBNJ003 lead to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 11: *Nilaparvata lugens* (Brown Plant Hopper)

A. Cloning *Nilaparvata lugens partial sequences*

From high quality total RNA of *Nilaparvata lugens* (source: Dr. J. A. Gatehouse, Dept. Biological Sciences, Durham University, UK) cDNA was generated using a commercially available kit (SuperScriptTM III Reverse Transcriptase, Cat N°. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's protocol.

To isolate cDNA sequences comprising a portion of the *Nilaparvata lugens* NL001, NL002, NL003, NL004, NL005, NL006, NL007, NL008, NL009, NL010, NL011, NL012, NL013, NL014, NL015, NL016, NL018, NL019, NL021, NL022, and NL027 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat N°. N8080240; Applied Biosystems) following the manufacturer's protocol.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-NL**. These primers were used in respective PCR reactions with the following conditions: for NL001: 5 minutes at 95°C, followed by 40 cycles of 30 seconds at

95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C: for NL002: 3 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C; for NL003: 3 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 61 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL004: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 51 °C and 1 minute at 72 °C; for NL005: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL006: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 55 °C and 3 minute 30 seconds at 72 °C, followed by 10 minutes at 72°C; for NL007: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 15 seconds at 72 °C, followed by 10 minutes at 72°C; for NL008: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 53 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL009: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 55 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL010: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 2 minute 30 seconds at 72 °C, followed by 10 minutes at 72°C; for NL011: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 55 °C and 1 minute at 72 °C; for NL012: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 55 °C and 1 minute at 72 °C; for NL013: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 10 seconds at 72 °C, followed by 10 minutes at 72°C; for NL014: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 53 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL015: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 40 seconds at 72 °C, followed by 10 minutes at 72°C; for NL016: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 40 seconds at 72 °C, followed by 10 minutes at 72°C; for NL018: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 35 seconds at 72 °C, followed by 10 minutes at 72°C; for NL019: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 55 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL021: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 45 seconds at 72 °C, followed by 10 minutes at 72°C: for NL022: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 45 seconds at 72 °C, followed by 10 minutes at 72°C; and for NL027: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1

minute 45 seconds at 72 °C, followed by 10 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/topo vector (Cat. Nr. K2500 20, Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NO:s as given in **Table 2-NL** and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NO:s as given in **Table 3-NL**.

B. Cloning of a partial sequence of the *Nilaparvata lugens* NL023 gene via EST sequence

From high quality total RNA of *Nilaparvata lugens* (source: Dr. J. A. Gatehouse, Dept. Biological Sciences, Durham University, UK) cDNA was generated using a commercially available kit (SuperScript™ III Reverse Transcriptase, Cat N°. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's protocol.

A partial cDNA sequence, NL023, was amplified from *Nilaparvata lugens* cDNA which corresponded to a *Nilaparvata lugens* EST sequence in the public database Genbank with accession number CAH65679.2. To isolate cDNA sequences comprising a portion of the NL023 gene, a series of PCR reactions with EST based specific primers were performed using PerfectShot™ ExTaq (Cat N°. RR005A, Takara Bio Inc.) following the manafacturer's protocol.

For NL023, the specific primers oGBKW002 and oGBKW003 (represented herein as SEQ ID NO: 1157 and SEQ ID NO: 1158, respectively) were used in two independent PCR reactions with the following conditions: 3 minutes at 95 °C, followed by 30 cycles of 30 seconds at 95 °C, 30 seconds at 56 °C and 2 minutes at 72 °C, followed by 10 minutes at 72°C. The resulting PCR products were analyzed on agarose gel, purified (QIAquick® Gel Extraction Kit; Cat. N°. 28706, Qiagen), cloned into the pCR4-TOPO vector (Cat N°. K4575-40, Invitrogen) and sequenced. The consensus sequence resulting from the sequencing of both PCR products is herein represented by SEQ ID NO: 1111 and is referred to as the partial sequence of the NL023 gene. The corresponding partial amino acid sequence is herein reperesented as SEQ ID NO: 1112.

C. dsRNA production of *Nilaparvata lugens* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5'

T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in Table 4. The conditions in the PCR reactions were as follows: for NL001: 4 minutes at 94 °C, followed by 35 cycles of 30 seconds at 94 °C, 30 seconds at 60 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL002: 4 minutes at 94 °C, followed by 35 cycles of 30 seconds at 94 °C, 30 seconds at 60 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL003: 4 minutes at 94 °C, followed by 35 cycles of 30 seconds at 94 °C, 30 seconds at 66 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL004: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 54 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL005: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 57 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL006: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 54 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL007: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 51 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL008: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 54 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL009: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 54 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL010: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 54 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL011: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 53 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL012: 4 minutes at 95 °C, followed by 35 cycles of 30secondes at 95 °C, 30 seconds at 53 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL013: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 55 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL014: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 51 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL015: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 55 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL016: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 57 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL018: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 55 °C and 1

minute at 72 °C, followed by 10 minutes at 72°C; for NL019: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 54 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL021: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 55 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL022: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 53 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL023: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 52 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; and for NL027: 4 minutes at 95 °C, followed by 35 cycles of 30secondes at 95 °C, 30 seconds at 52 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 4-NL**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen). The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions, but with the following modification: RNA peppet is washed twice in 70% ethanol. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-NL**.

The template DNA used for the PCR reactions with T7 primers on the green fluorescent protein (gfp) control was the plasmid pPD96.12 (the Fire Lab, http://genome-www.stanford.edu/group/fire/), which contains the wild-type gfp coding sequence interspersed by 3 synthetic introns. Double-stranded RNA was synthesized using the commercially available kit T7 RiboMAX™ Express RNAi System (Cat.N°. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter. For gfp, the sense T7 template was generated using the specific T7 FW primer oGAU183 and the specific RV primer oGAU182 (represented herein as SEQ ID NO: 236 and SEQ ID NO: 237 , respectively) in a PCR reaction with the following conditions: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 55 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using the specific FW primer oGAU181 and the specific T7 RV primer oGAU184 (represented herein as SEQ ID NO: 238 and SEQ ID NO: 239 , respectively) in a PCR reaction with the same conditions as described above. The

resulting PCR products were analyzed on agarose gel and purified (QIAquick® PCR Purification Kit; Cat. N°. 28106, Qiagen). The generated T7 FW and RV templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by precipitation with sodium acetate and isopropanol, following the manufacturer's protocol, but with the following modification: RNA peppet is washed twice in 70% ethanol. The sense strands of the resulting dsRNA is herein represented by SEQ ID NO: 235.

D. Laboratory trials to screen dsRNA targets using liquid artificial diet for activity against *Nilaparvata lugens*

Liquid artificial diet (MMD-1) for the rice brown planthopper, *Nilaparvata lugens*, was prepared as described by Koyama (1988) [Artificial rearing and nutritional physiology of the planthoppers and leafhoppers (Homoptera: Delphacidae and Deltocephalidae) on a holidic diet. *JARQ* 22: 20–27], but with a modification in final concentration of diet component sucrose: 14.4 % (weight over volume) was used. Diet components were prepared as separate concentrates: 10 x mineral stock (stored at 4 °C), 2 x amino acid stock (stored at -20 °C) and 10 x vitamin stock (stored at -20 °C). The stock components were mixed immediately prior to the start of a bioassay to 4/3 x concentration to allow dilution with the test dsRNA solution (4 x concentration), pH adjusted to 6.5, and filter-sterilised into approximately 500 µl aliquots.

Rice brown planthopper (*Nilaparvata lugens*) was reared on two-to-three month old rice (*Oryza sativa* cv Taichung Native 1) plants in a controlled environment chamber: 27 ± 2 °C, 80 % relative humidity, with a 16:8 hours light:dark photoperiod. A feeding chamber comprised 10 first or second instar nymphs placed in a small petri dish (with diameter 3 cm) covered with a single layer of thinly stretched parafilm M onto which 50 µl of diet was added. The chamber was sealed with a second layer of parafilm and incubated under the same conditions as the adult cultures but with no direct light exposure. Diet with dsRNA was refreshed every other day and the insects' survival assessed daily. Per treatment, 5 bioassay feeding chambers (replicates) were set up simultaneously. Test and control (gfp) dsRNA solutions were incorporated into the diet to a final concentration of 2 mg/ml. The feeding chambers were kept at 27 ± 2 °C, 80 % relative humidity, with a 16:8 hours light:dark photoperiod. Insect survival data were analysed using the Kaplan-Meier survival curve model and the survival between groups were compared using the logrank test (Prism version 4.0).

Feeding liquid artificial diet supplemented with intact naked dsRNAs to *Nilaparvata lugens in vitro* using a feeding chamber resulted in significant increases in nymphal

mortalities as shown in four separate bioassays (**Figures 1(a)-(d)-NL; Tables 1a-d-NL**). These results demonstrate that dsRNAs corresponding to different essential BPH genes showed significant toxicity towards the rice brown planthopper.

Effect of gfp dsRNA on BPH survival in these bioassays is not significantly different to survival on diet only

Tables 10a-d-NL show a summary of the survival of *Nilaparvata lugens* on artificial diet supplemented with 2 mg/ml (final concentration) of the following targets; in **Table 10(a)-NL**: NL002, NL003, NL005, NL010; in **Table 10(b)-NL** NL009, NL016; in **Table 10(c)-NL** NL014, NL018; and in **Table 10(d)-NL** NL013, NL015, NL021. In the survival analysis column, the effect of RNAi is indicated as follows: + = significantly decreased survival compared to gfp dsRNA control (alpha < 0.05); - = no significant difference in survival compared to gfp dsRNA control. Survival curves were compared (between diet only and diet supplemented with test dsRNA, gfp dsRNA and test dsRNA, and diet only and gfp dsRNA) using the logrank test.

E. Laboratory trials to screen dsRNAs at different concentrations using artificial diet for activity against *Nilaparvata lugens*

Fifty µl of liquid artificial diet supplemented with different concentrations of target NL002 dsRNA, namely 1, 0.2, 0.08, and 0.04 mg/ml (final concentration), was applied to the brown planthopper feeding chambers. Diet with dsRNA was refreshed every other day and the insects' survival assessed daily. Per treatment, 5 bioassay feeding chambers (replicates) were set up simultaneously. The feeding chambers were kept at 27 ± 2 °C, 80 % relative humidity, with a 16:8 hours light:dark photoperiod. Insect survival data were analysed using the Kaplan-Meier survival curve model and the survival between groups were compared using the logrank test (Prism version 4.0).

Feeding liquid artificial diet supplemented with intact naked dsRNAs of target NL002 at different concentrations resulted in significantly higher BPH mortalities at final concentrations of as low as 0.04 mg dsRNA per ml diet when compared with survival on diet only, as shown in **Figure 2-NL** and **Table 9-NL**. **Table 9-NL** summarizes the survival of *Nilaparvata lugens* artificial diet feeding trial supplemented with 1, 0.2, 0.08, & 0.04 mg/ml (final concentration) of target NL002. In the survival analysis column the effect of RNAi is indicated as follows: + = significantly decreases survival compared to diet only control (alpha < 0.05); - = no significant differences in survival compared to diet only control. Survival curves were compared using the logrank test.

F. Cloning of a BPH gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to a BPH gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in Table 8. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-NL**. The recombinant vector harbouring this sequence is named pGBNJ00.

G. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB309-105, and, (2) BL21(DE3)

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB309-105, is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB309-105 and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E.* coli strain AB309-105 or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB309-105 and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGBNJ003, in the bacterial strain AB309-105 or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

H. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Nilaparvata lugens*

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to BPH. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. BPH are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB309-105 harbouring the pGBNJ001 plasmids or pGN29 plasmid. Different

quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB309-105 expressing target dsRNA from pGBNJ003 leed to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 10: *Chilo suppressalis* (rice striped stem borer)

A. Cloning of partial sequence of the *Chilo suppressalis* genes via family PCR

High quality, intact RNA was isolated from the 4 different larval stages of *Chilo suppressalis* (rice striped stem borer) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manafacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the CS001, CS002, CS003, CS006, CS007, CS009, CS011, CS013, CS014, CS015, CS016 and CS018 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manafacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-CS**. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr.

28706, Qiagen), cloned into the pCR4/TOPO vector (Cat. Nr. K2500-20, Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NO:s as given in **Table 2-CS** and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NO:s as given in **Table 3-CS**.

B. dsRNA production of the *Chilo suppressalis* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-CS**. The conditions in the PCR reactions were as follows: 4 minutes at 95°C, followed by 35 cycles of 30 seconds at 95°C, 30 seconds at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-CS**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-CS**.

C. Laboratory trials to test dsRNA targets, using artificial diet for activity against *Chilo suppressalis* larvae

Rice striped stem borers, *Chilo suppressalis*, (origin: Syngenta, Stein, Switzerland) were maintained on a modified artificial diet based on that described by Kamano and Sato, 1985 (in: Handbook of Insect Rearing. Volumes I & II. P Singh and RF Moore, eds., Elsevier Science Publishers, Amsterdam and New York, 1985, pp 448). Briefly, a litre diet was made up as follows: 20 g of agar added to 980 ml of Milli-Q water and autoclaved; the agar solution was cooled down to approximately 55 °C and the remaining ingredients were added

and mixed thoroughly: 40 g corn flour (Polenta), 20 g cellulose, 30 g sucrose, 30 g casein, 20 g wheat germ (toasted), 8 g Wesson salt mixture, 12 g Vanderzant vitamin mix, 1.8 g sorbic acid, 1.6 g nipagin (methylparaben), 0.3 g aureomycin, 0.4 g cholesterol and 0.6 g L-cysteine. The diet was cooled down to approx. 45 °C and poured into rearing trays or cups. The diet was left to set in a horizontal laminair flow cabin. Rice leaf sections with oviposited eggs were removed from a cage housing adult moths and pinned to the solid diet in the rearing cup or tray. Eggs were left to hatch and neonate larvae were available for bioassays and the maintenance of the insect cultures. During the trials and rearings, the conditions were 28 ± 2 °C and 80 ± 5 % relative humidity, with a 16:8 hour light:dark photoperiod.

The same artificial diet is used for the bioassays but in this case the diet is poured equally in 24 multiwell plates, with each well containing 1 ml diet. Once the diet is set, the test formulations are applied to the diet's surface (2 cm^2), at the rate of 50 µl of 1 µg/µl dsRNA of target. The dsRNA solutions are left to dry and two first instar moth larvae are placed in each well. After 7 days, the larvae are transferred to fresh treated diet in multiwell plates. At day 14 (i.e. 14 days post bioassay start) the number of live and dead insects is recorded and examined for abnormalities. Twenty-four larvae in total are tested per treatment.

An alternative bioassay is performed in which treated rice leaves are fed to neonate larvae of the rice striped stem borer. Small leaf sections of *Indica* rice variety Taichung native 1 are dipped in 0.05 % Triton X-100 solution containing 1 µg/µl of target dsRNA, left to dry and each section placed in a well of a 24 multiwell plate containing gellified 2 % agar. Two neonates are transferred from the rearing tray to each dsRNA treated leaf section (24 larvae per treatment). After 4 and 8 days, the larvae are transferred to fresh treated rice leaf sections. The number of live and dead larvae are assessed on days 4, 8 and 12; any abnormalities are also recorded.

D. Cloning of a SSB gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to an SSB gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in Table 8. The template used is the pCR8/GW/topo vector containing any of target

sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-CS**. The recombinant vector harbouring this sequence is named pGBNJ00XX.

E. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB309-105, and, (2) BL21(DE3)

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB309-105, is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).
Transformation of AB309-105 and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E. coli* strain AB309-105 or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB309-105 and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGBNJ003, in the bacterial strain AB309-105 or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged

at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

F. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Chilo suppressalis*

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to SSB. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. SSB are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB309-105 harbouring the pGBNJ001 plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB309-105 expressing target dsRNA from pGBNJ003 leed to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial

expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 9: *Plutella xylostella* (Diamondback moth)

A. Cloning of a partial sequence of the *Plutella xylostella*

High quality, intact RNA was isolated from all the different larval stages of Plutella xylostella (Diamondback moth; source: Dr. Lara Senior, Insect Investigations Ltd., Capital Business Park, Wentloog, Cardiff, CF3 2PX, Wales, UK) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manufacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the PX001, PX009, PX010, PX015, PX016 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-PX**. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C (for PX001, PX009, PX015, PX016); 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 2 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C (for PX010). The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/TOPO vector (Cat. Nr. K2500-20, Invitrogen) and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NO:s as given in **Table 2-PX** and are referred to as the partial sequences. The corresponding partial amino acid sequence are represented by the respective SEQ ID NO:s as given in **Table 3-PX**.

B. dsRNA production of the *Plutella xylostella* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-PX**. The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C (-0.5°C/cycle) and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-PX**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-PX**.

C. Laboratory trials to test dsRNA targets, using artificial diet for activity against *Plutella xylostella* larvae

Diamond-back moths, *Plutella xylostella*, were maintained at Insect Investigations Ltd. (origin: Newcastle University, Newcastle-upon-Tyne, UK). The insects were reared on cabbage leaves. First instar, mixed sex larvae (approximately 1 day old) were selected for use in the trial. Insects were maintained in Eppendorf tubes (1.5 ml capacity). Commercially available Diamond-back moth diet (Bio-Serv, NJ, USA), prepared following the manafacturer's instructions, was placed in the lid of each tube (0.25 ml capacity, 8 mm diameter). While still liquid, the diet was smoother over to remove excess and produce an even surface.

Once the diet has set the test formulations are applied to the diet's surface, at the rate of 25 µl undiluted formulation (1 µg/µl dsRNA of targets) per replicate. The test formulations

are allowed to dry and one first instar moth larva is placed in each tube. The larva is placed on the surface of the diet in the lid and the tube carefully closed. The tubes are stored upside down, on their lids such that each larva remains on the surface of the diet. Twice weekly the larvae are transferred to new Eppendorf tubes with fresh diet. The insects are provided with treated diet for the first two weeks of the trial and thereafter with untreated diet.

Assessments are made twice weekly for a total of 38 days at which point all larvae are dead. At each assessment the insects are assessed as live or dead and examined for abnormalities. Forty single larva replicates are performed for each of the treatments. During the trial the test conditions are 23 to 26 °C and 50 to 65 % relative humidity, with a 16:8 hour light:dark photoperiod.

D. Cloning of a DBM gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to a DBM gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in **Table 8-PX**. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-PX**. The recombinant vector harbouring this sequence is named pGBNJ00XX.

E. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB309-105, and, (2) BL21(DE3)

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB309-105, is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB309-105 and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E. coli* strain AB309-105 or BL21(DE3). The cells are

incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB309-105 and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGBNJ003, in the bacterial strain AB309-105 or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

F. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Plutella xylostella*

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to DBM. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. DBM are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB309-105 harbouring the pGBNJ001 plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB309-105 expressing target dsRNA from pGBNJ003 leed to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 12: *Acheta domesticus* (house cricket)

A. Cloning *Acheta domesticus* partial sequences

High quality, intact RNA was isolated from all the different insect stages of *Acheta domesticus* (house cricket; source: Dr. Lara Senior, Insect Investigations Ltd., Capital Business Park, Wentloog, Cardiff, CF3 2PX, Wales, UK) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manafacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat.

Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the AD001, AD002, AD009, AD015 and AD016 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manafacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-AD**. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/topo vector (Cat. Nr. K2500 20, Invitrogen) and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NO:s as given in **Table 2-AD** and are referred to as the partial sequences. The corresponding partial amino acid sequence are represented by the respective SEQ ID NO:s as given in **Table 3-AD**.

B. dsRNA production of the *Acheta domesticus* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-AD**. The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C (-0.5°C/cycle) and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-AD**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed

and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-AD**.

C. Laboratory trials to test dsRNA targets, using artificial diet for activity against *Acheta domesticus* larvae

House crickets, *Acheta domesticus*, were maintained at Insect Investigations Ltd. (origin: Blades Biological Ltd., Kent, UK). The insects were reared on bran pellets and cabbage leaves. Mixed sex nymphs of equal size and no more than 5 days old were selected for use in the trial. Double-stranded RNA is mixed with a wheat-based pelleted rodent diet (rat and mouse standard diet, B & K Universal Ltd., Grimston, Aldbrough, Hull, UK). The diet, BK001P, contains the following ingredients in descending order by weight: wheat, soya, wheatfeed, barley, pellet binder, rodent 5 vit min, fat blend, dicalcium phosphate, mould carb. The pelleted rodent diet is finely ground and heat-treated in a microwave oven prior to mixing, in order to inactivate any enzyme components. All rodent diet is taken from the same batch in order to ensure consistency. The ground diet and dsRNA are mixed thoroughly and formed into small pellets of equal weight, which are allowed to dry overnight at room temperature.

Double-stranded RNA samples from targets and gfp control at concentrations 10 µg/µl were applied in the ratio 1 g ground diet plus 1 ml dsRNA solution, thereby resulting in an application rate of 10 mg dsRNA per g pellet. Pellets are replaced weekly. The insects are provided with treated pellets for the first three weeks of the trial. Thereafter untreated pellets are provided. Insects are maintained within lidded plastic containers (9 cm diameter, 4.5 cm deep), ten per container. Each arena contains one treated bait pellet and one water source (damp cotton wool ball), each placed in a separate small weigh boat. The water is replenished *ad lib* throughout the experiment.

Assessments are made at twice weekly intervals, with no more than four days between assessments, until all the control insects had either died or moulted to the adult stage (84 days). At each assessment the insects are assessed as live or dead, and examined for abnormalities. From day 46 onwards, once moulting to adult has commenced, all insects (live and dead) are assessed as nymph or adult. Surviving insects are weighed on day 55 of the trial. Four replicates are performed for each of the treatments. During the trial the test

conditions are 25 to 33 °C and 20 to 25 % relative humidity, with a 12:12 hour light:dark photoperiod.

D. Cloning of a HC gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to a HC gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in Table 8. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-AD**. The recombinant vector harbouring this sequence is named pGBNJ00XX.

E. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB309-105, and, (2) BL21(DE3)

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB309-105, is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB309-105 and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E.* coli strain AB309-105 or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB309-105 and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGBNJ003, in the bacterial strain AB309-105 or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

F. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Acheta domesticus*

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to HC. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. HC are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB309-105 harbouring the pGBNJ001 plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit

is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB309-105 expressing target dsRNA from pGBNJ003 leed to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 13: *Pyricularia grisea* (rice blast)

A. Cloning *P. grisea* partial sequences

High quality, intact RNA is isolated from different growth stages of *P. grisea* using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation is removed by DNase treatment following the manafacturer's instructions (Cat. Nr. 1700, Promega). cDNA is generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of a target gene, PCR is performed with degenerate primers using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manafacturer's instructions. The resultant PCR products are fractionated and sequenced.

B. dsRNA production of *P. grisea* genes

dsRNA is synthesized in milligram amounts using a commercially available kit, such as T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega), following the manufacturer's instructions. The resulting PCR products are analyzed on an agarose gel and purified by a PCR purification kit (e.g. Qiaquick PCR Purification Kit, Cat. Nr. 28106,

Qiagen) and $NaClO_4$ precipitation. The producr T7 forward and reverse templates are mixed and the resulting RNA strands are annealed, then DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions.

C. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB309-105, and, (2) BL21(DE3)

The procedures described below are followed in order to express suitable levels of fungal double-stranded RNA of fungal target in bacteria. An RNaseIII-deficient strain, AB309-105, is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB309-105 and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E. coli* strain AB309-105 or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB309-105 and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGBNJ003, in the bacterial strain AB309-105 or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

EDITORIAL NOTE

Number: 2006335978

The following claim pages are numbered 146 to 148

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THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. An isolated double stranded RNA sequence comprising annealed complementary strands, in which at least one of the strands comprises a polyribonucleotide selected from the group consisting of:

(i) polyribonucleotides complementary to at least 21 contiguous nucleotides of a target gene represented by any of SEQ ID NOs 2104, 11, 253, 517, 605, 797, 892, 1089, and 1115,

(ii) polyribonucleotides complementary to at least 21 contiguous nucleotides of a target gene encoding the amino acid sequence represented by any of SEQ ID NOs: 2105, 12, 254, 518, 606, 798, 893, 1090, and 1116,

(iii) polyribonucleotides having at least 80% sequence identity with the polyribonucleotides of (i) or (ii),

(iv) polyribonucleotides capable of hybridizing with at least 21 contiguous nucleotides of a target gene represented by any of SEQ ID NOs 2104, 11, 253, 517, 605, 797, 892, 1089, and 1115, and

(v) polyribonucleotides capable of hybridizing with at least 21 contiguous nucleotides of a target gene encoding the amino acid sequence represented by any of SEQ ID NOs: 2105, 12, 254, 518, 606, 798, 893, 1090, and 1116.

2. An isolated polynucleotide encoding a double stranded RNA sequence as claimed in claim 1.

3. A vector comprising at least one polynucleotide as claimed in claim 2.

4. A cell (other than a plant cell) transformed with at least one polynucleotide as claimed in claim 2.

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5. A method for controlling insect pest infestation in at least one object other than a plant, the method comprising the step of providing a pest with plant material comprising the double-stranded RNA of claim 1.

6. A method of controlling insect pest infestation in an object other than a plant, the method comprising the step of providing at least one double stranded RNA sequence as claimed in claim 1 in the diet of an insect pest or by spraying a surface of the object with at least one double stranded RNA sequence as claimed in claim 1.

7. A method of treating insect infestation in an object other than a plant, the method comprising the step of administering to the object, of one (or any two or more of):

(a) at least one double stranded RNA sequence as claimed in claim 1;

(b) at least one polynucleotide as claimed in claim 2;

(c) at least one vector as claimed in claim 3; and

(d) at least one cell as claimed in claim 4.

8. Use of one (or any two or more) of:

(a) at least one double stranded RNA sequence as claimed in claim 1;

(b) at least one polynucleotide as claimed in claim 2;

(c) at least one vector as claimed in claim 3; and

(d) at least one cell as claimed in claim 4;

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in order to treat insect infestation in an object other than a plant.

DATED: 30 January 2014

DEVGEN NV

5

By its Patent Attorneys

KNIGHTSBRIDGE PATENT ATTORNEYS

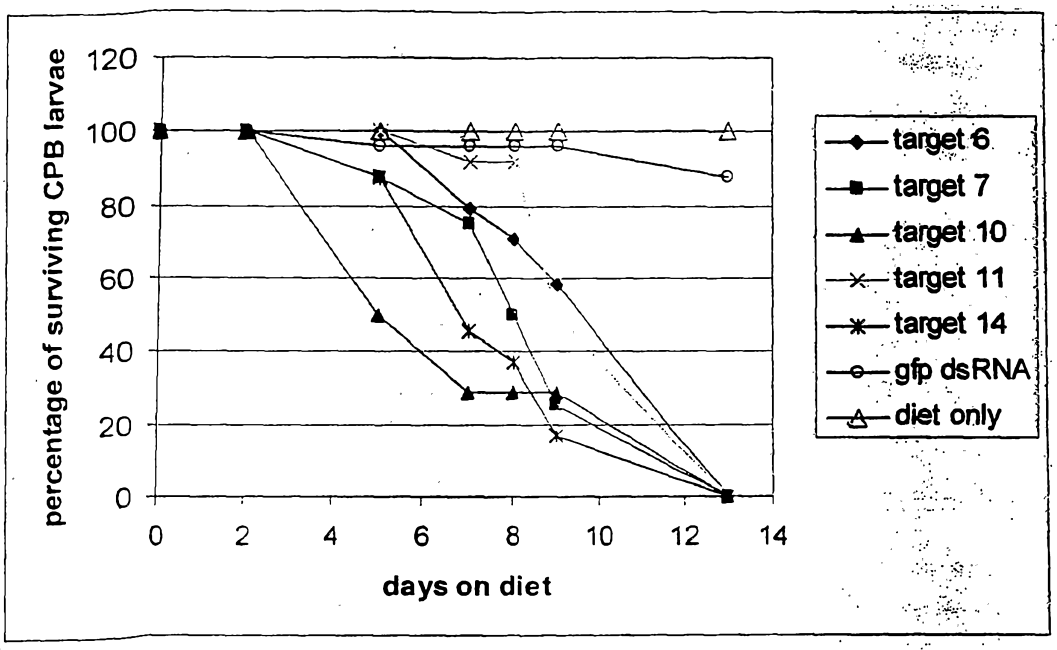

FIGURE 1-LD

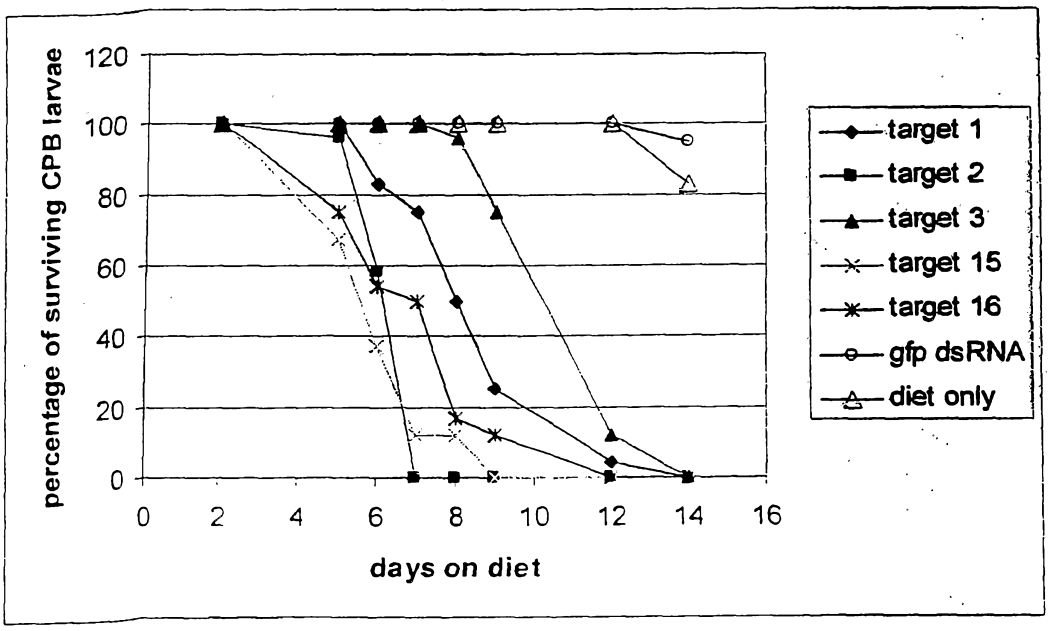

FIGURE 2-LD

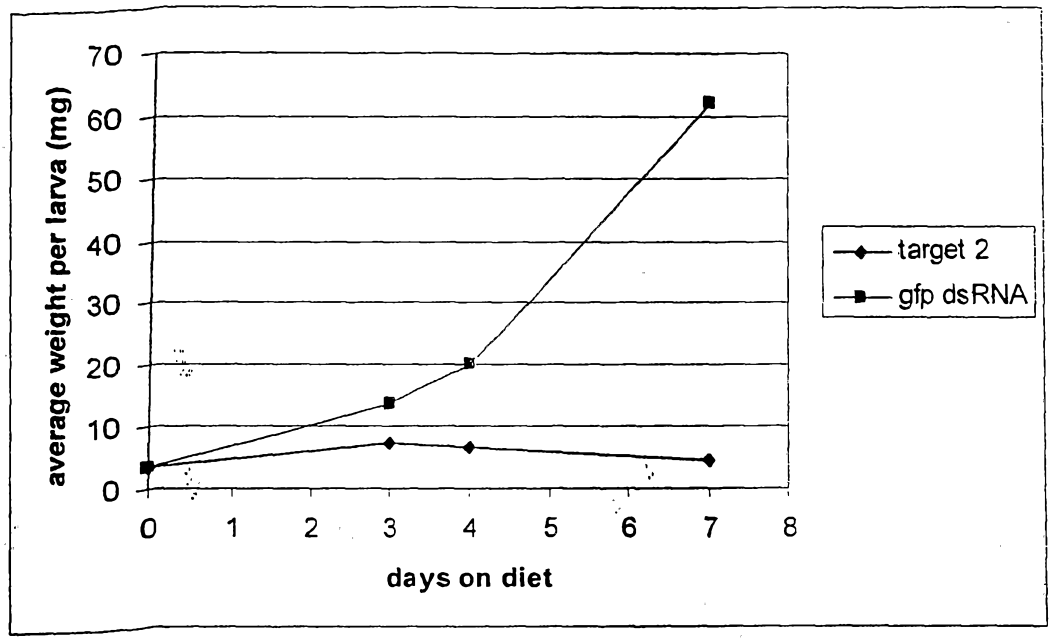

FIGURE 3-LD

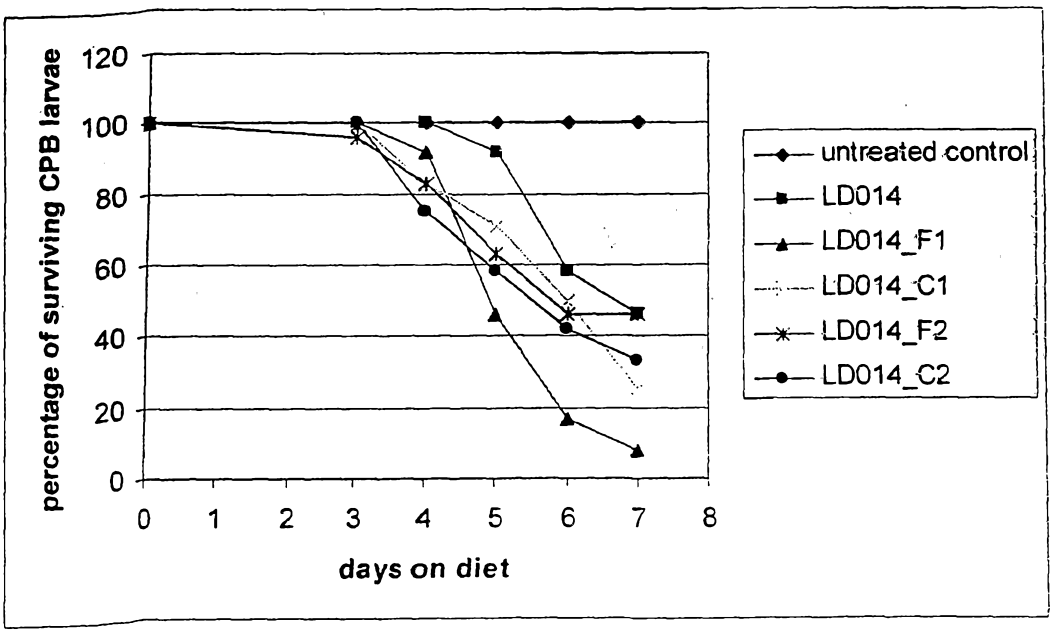

FIGURE 4-LD

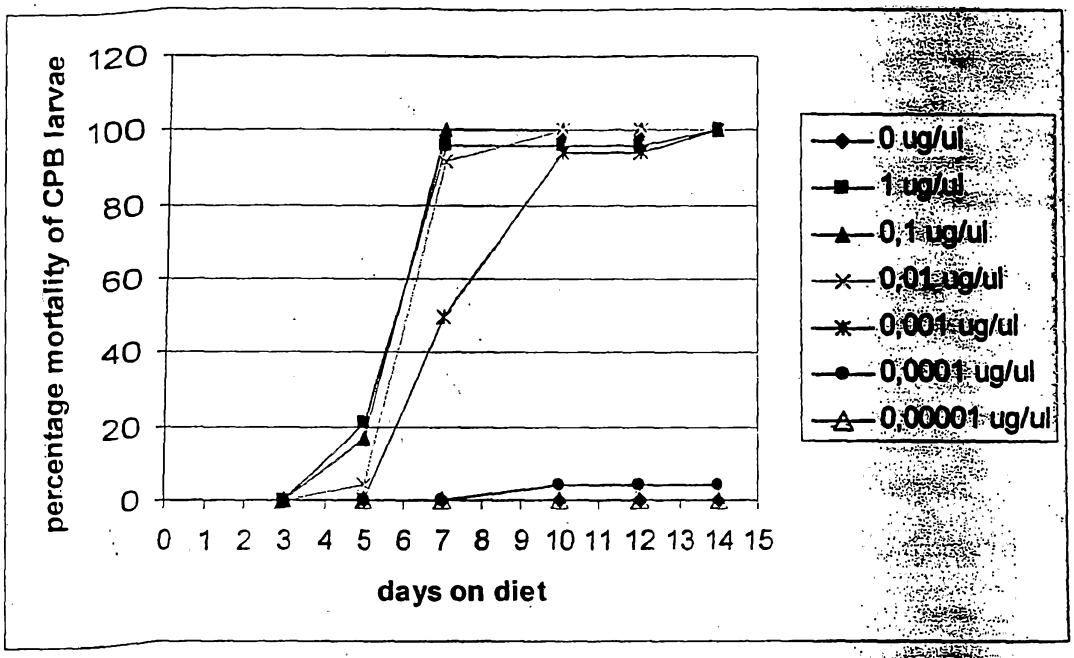

FIGURE 5(a)-LD

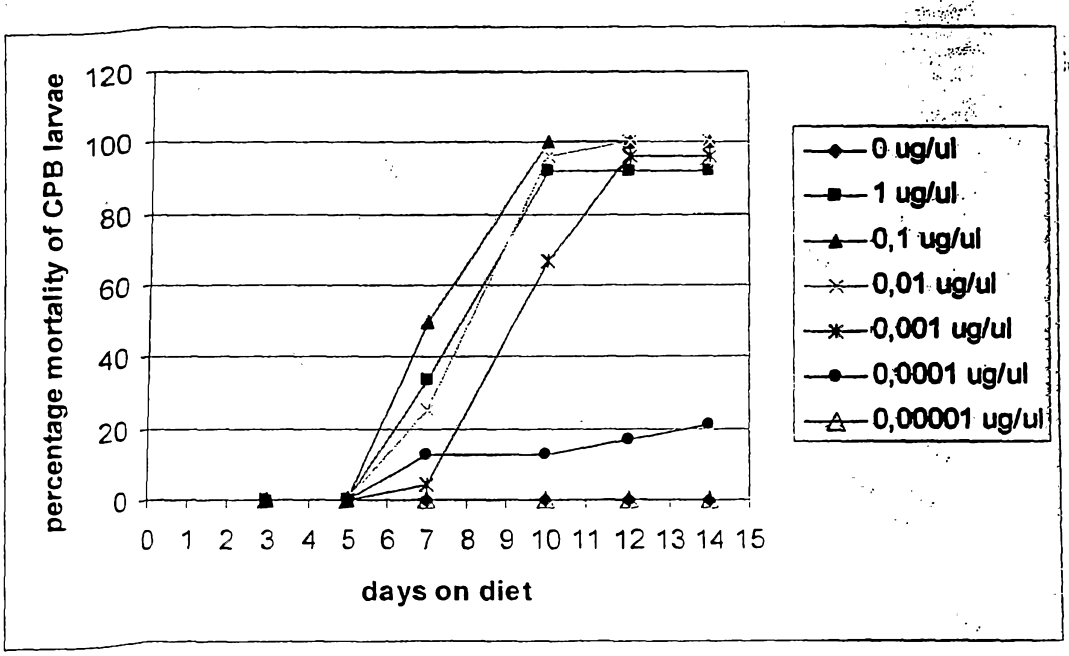

FIGURE 5(b)-LD

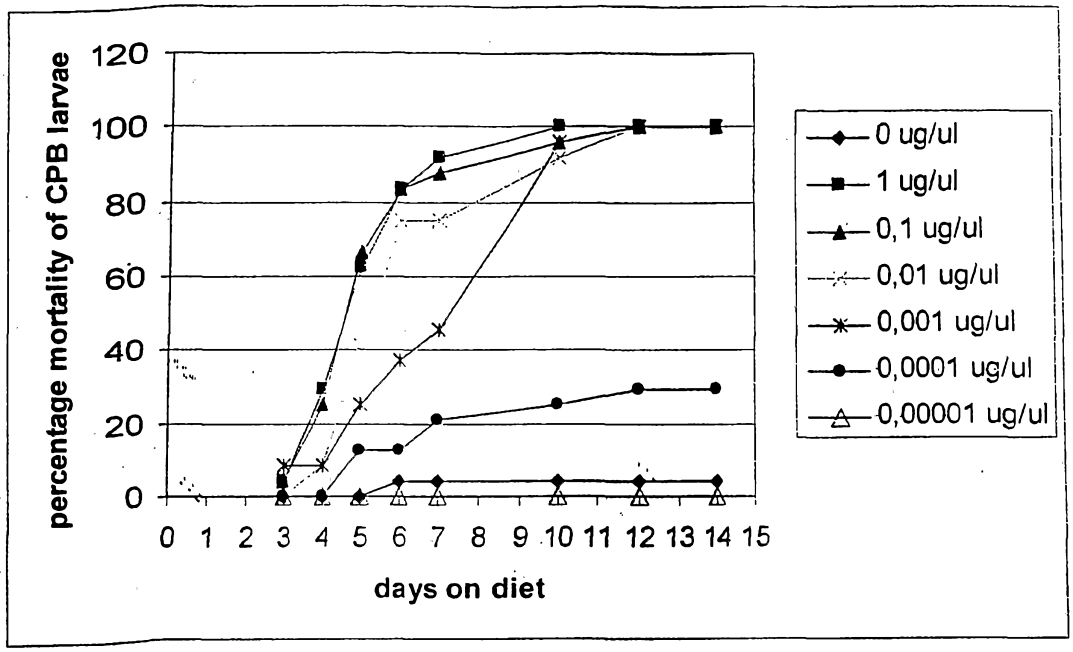

FIGURE 5(c)-LD

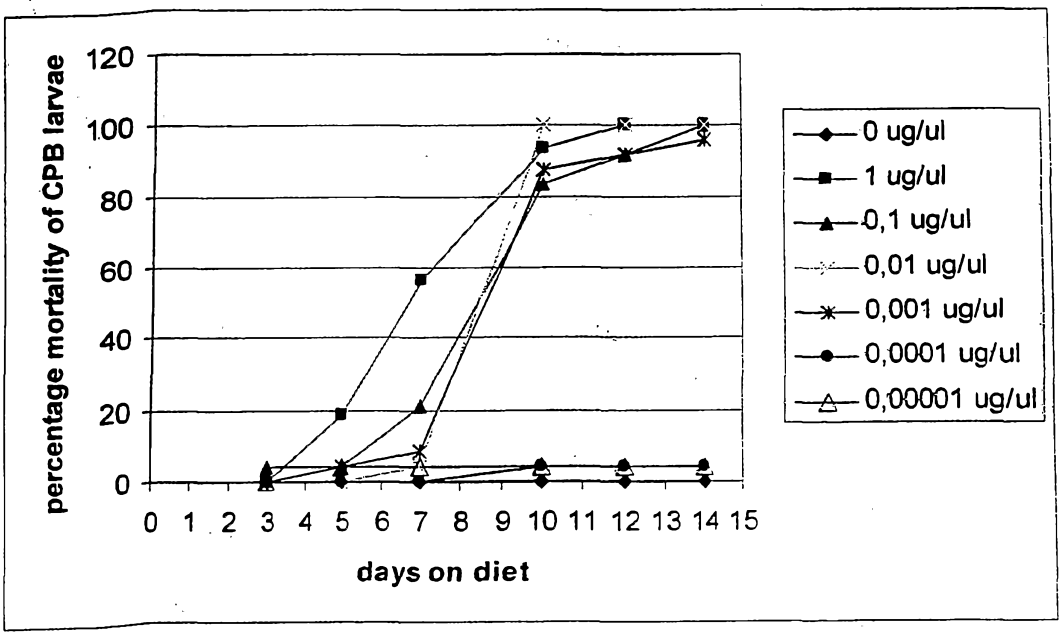

FIGURE 5(d)-LD

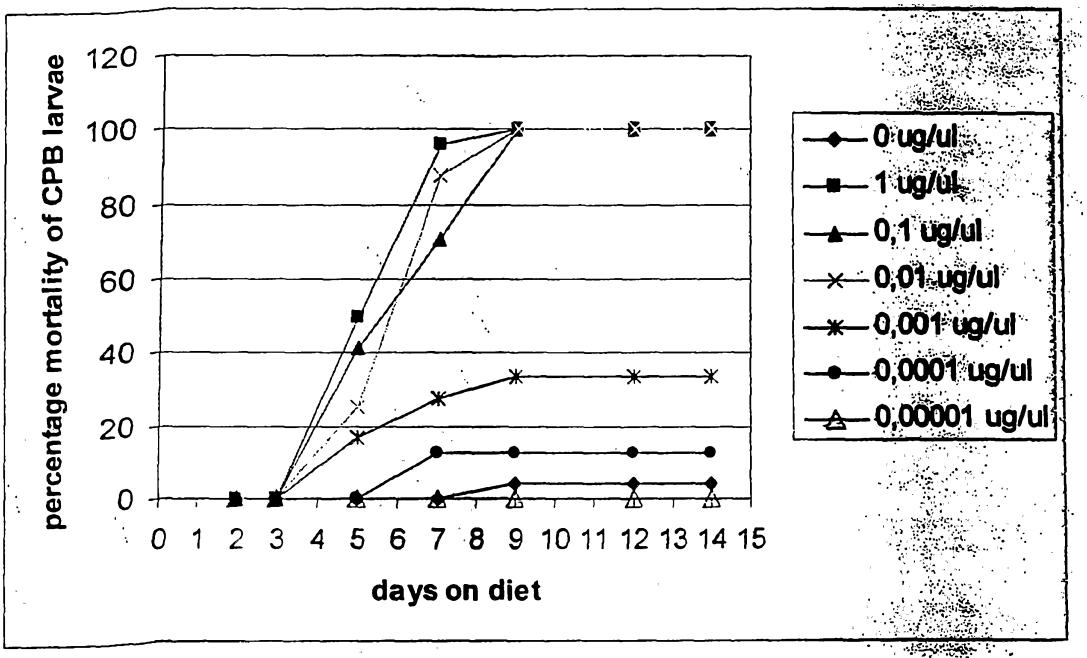

FIGURE 5(e)-LD

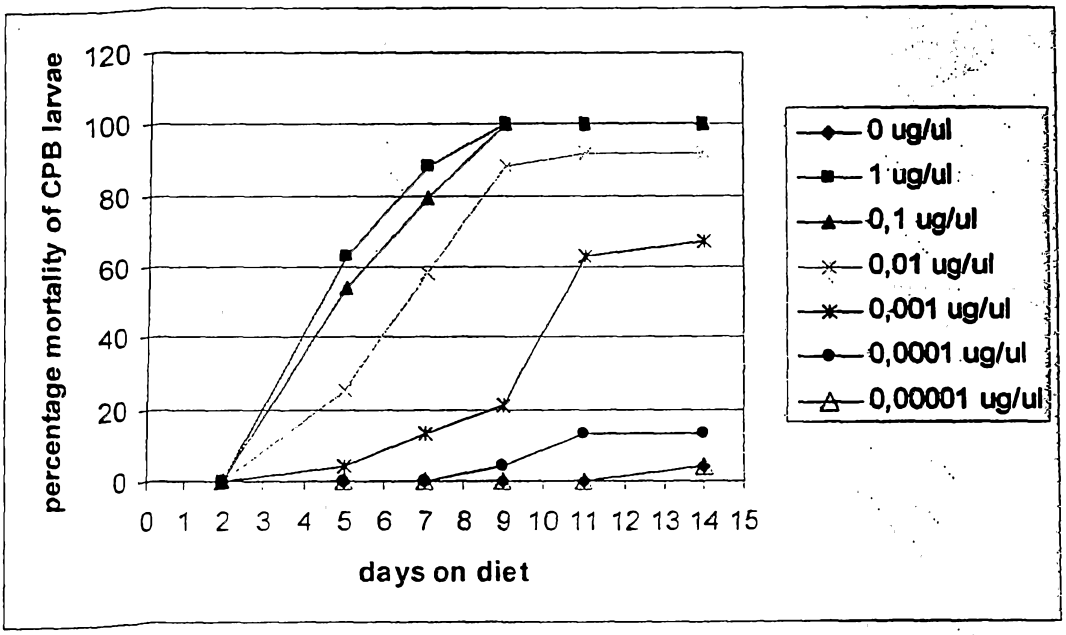

FIGURE 5(f)-LD

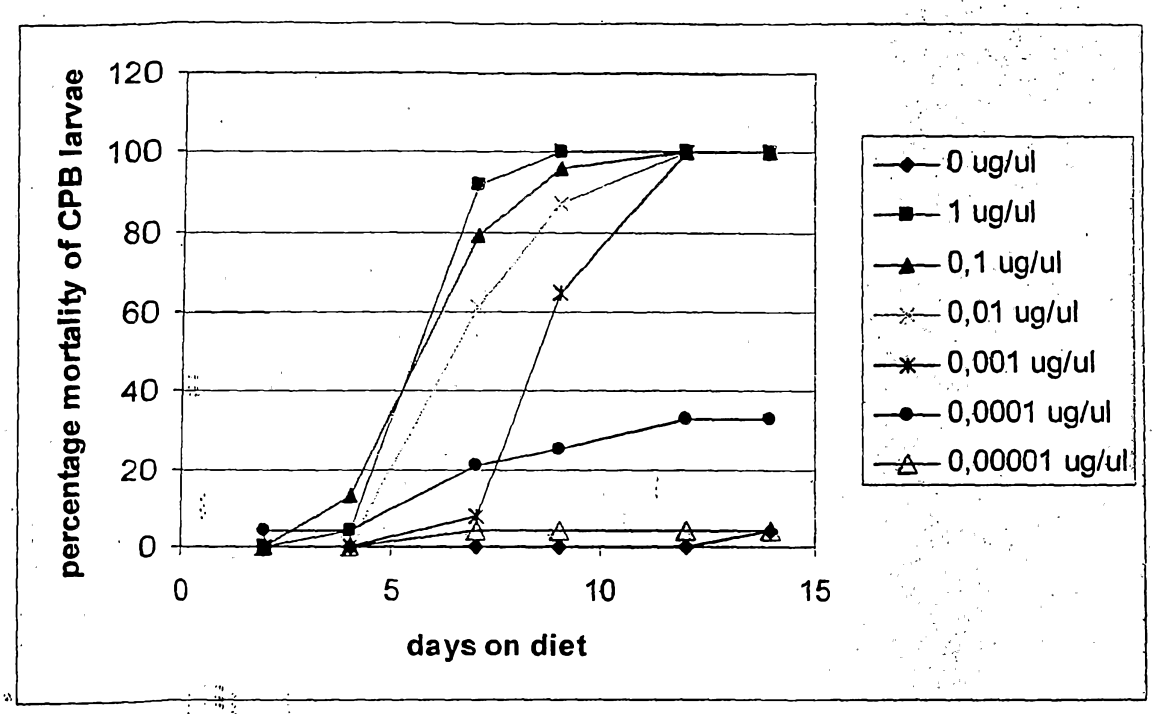

FIGURE 5(g)-LD

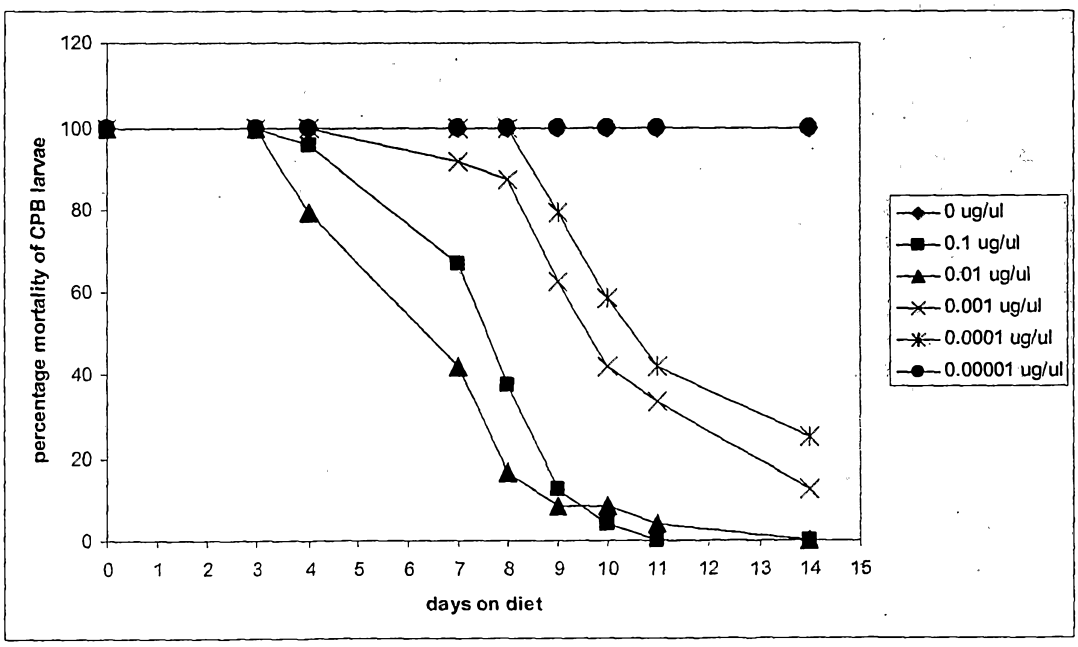

FIGURE 5(h)-LD

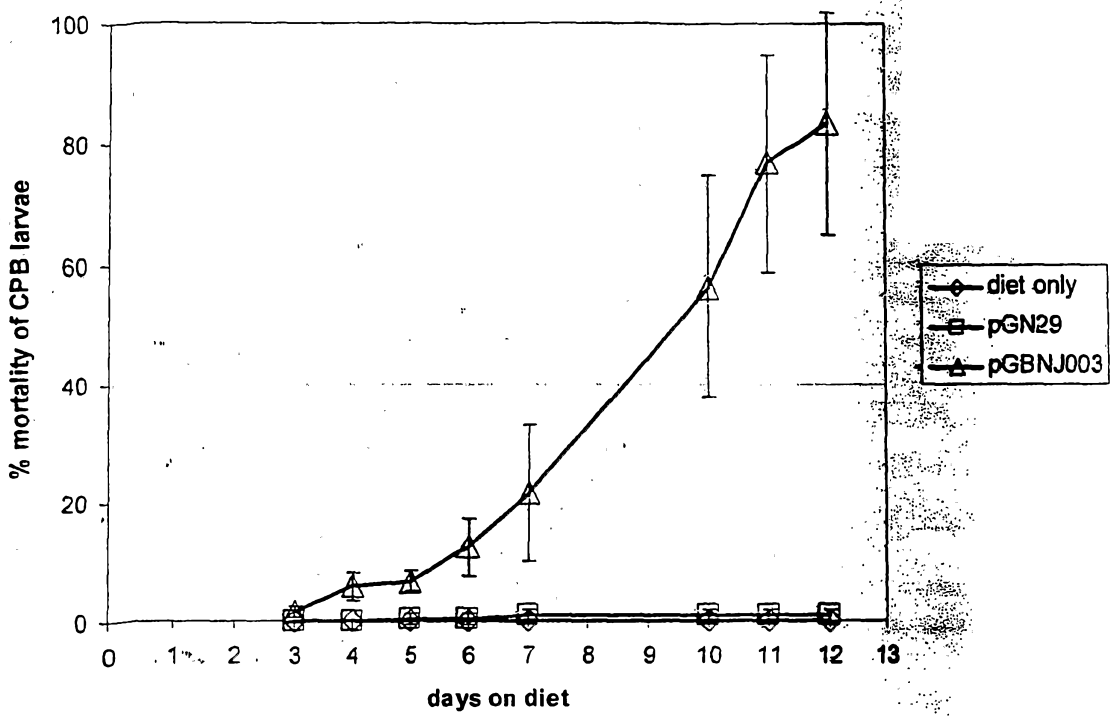

FIGURE 6(a)-LD

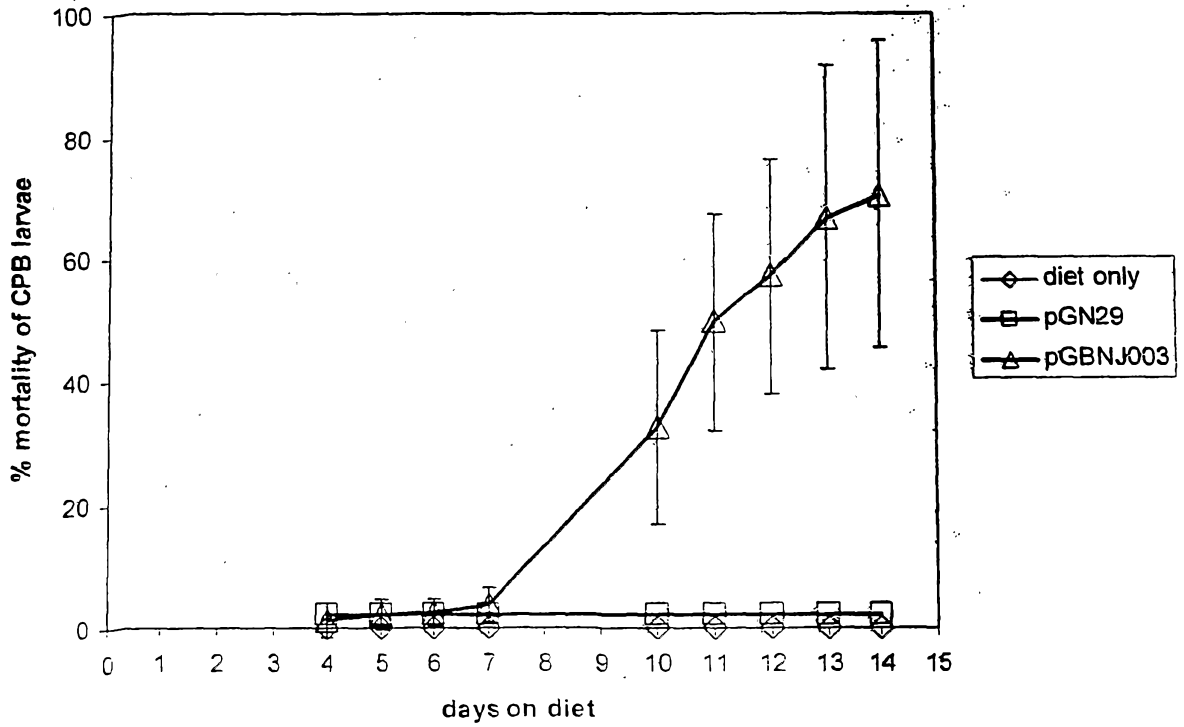

FIGURE 6(b)-LD

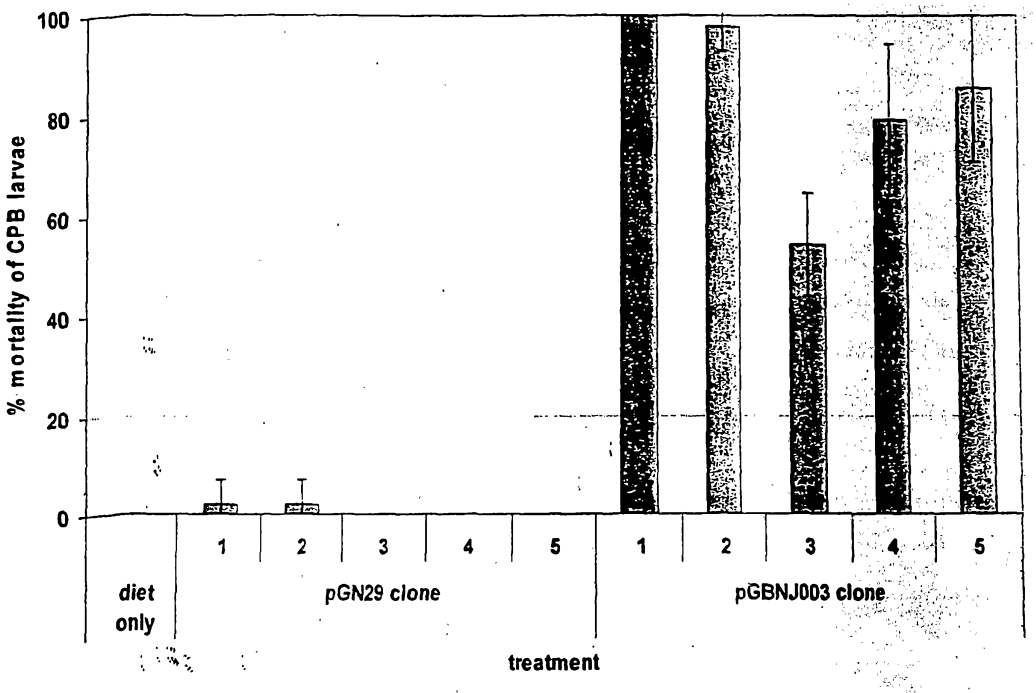

FIGURE 7(a)-LD

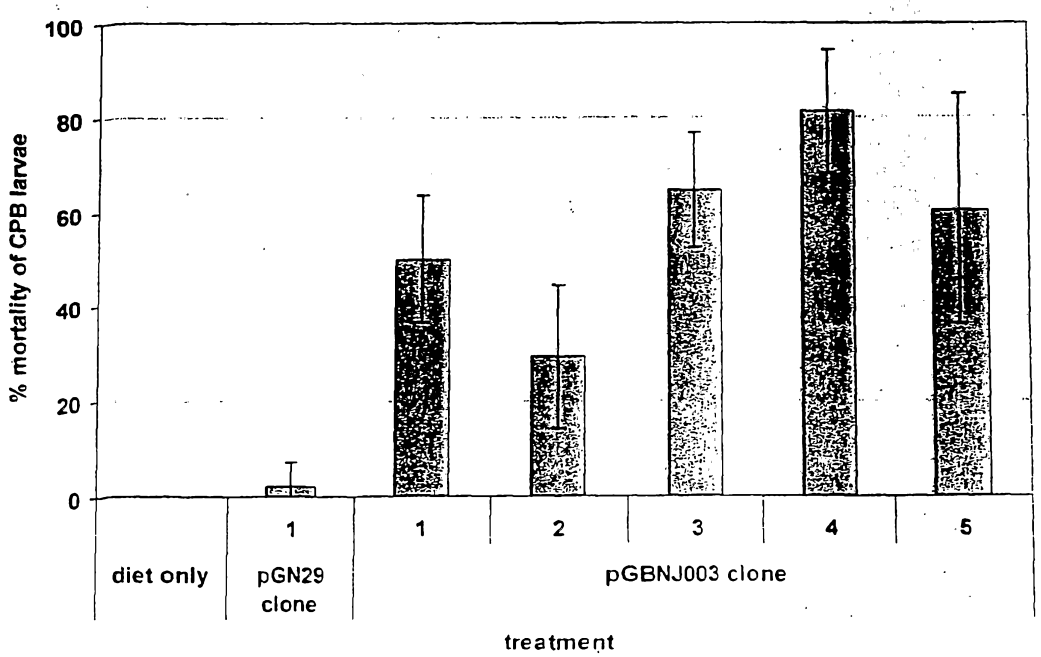

FIGURE 7(b)-LD

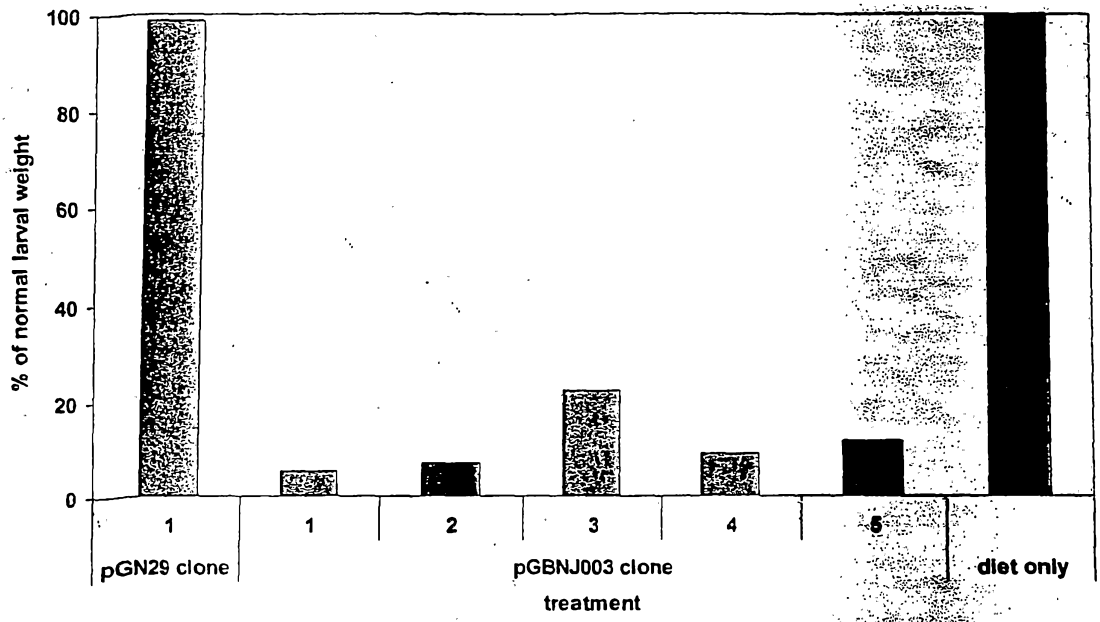

FIGURE 8(a)-LD

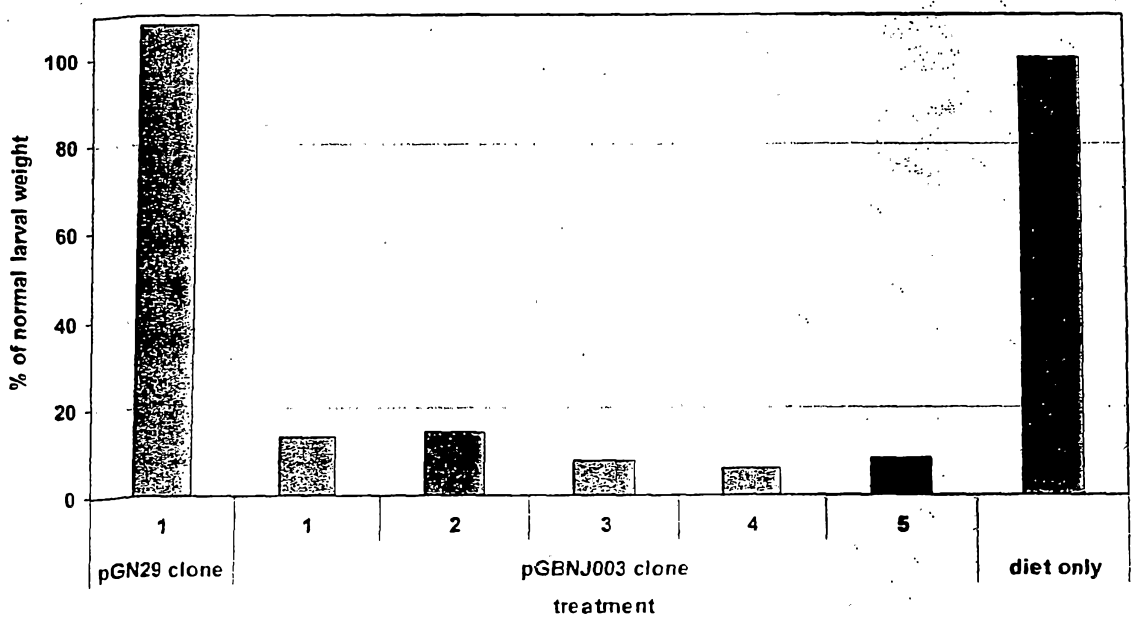

FIGURE 8(b)-LD

5

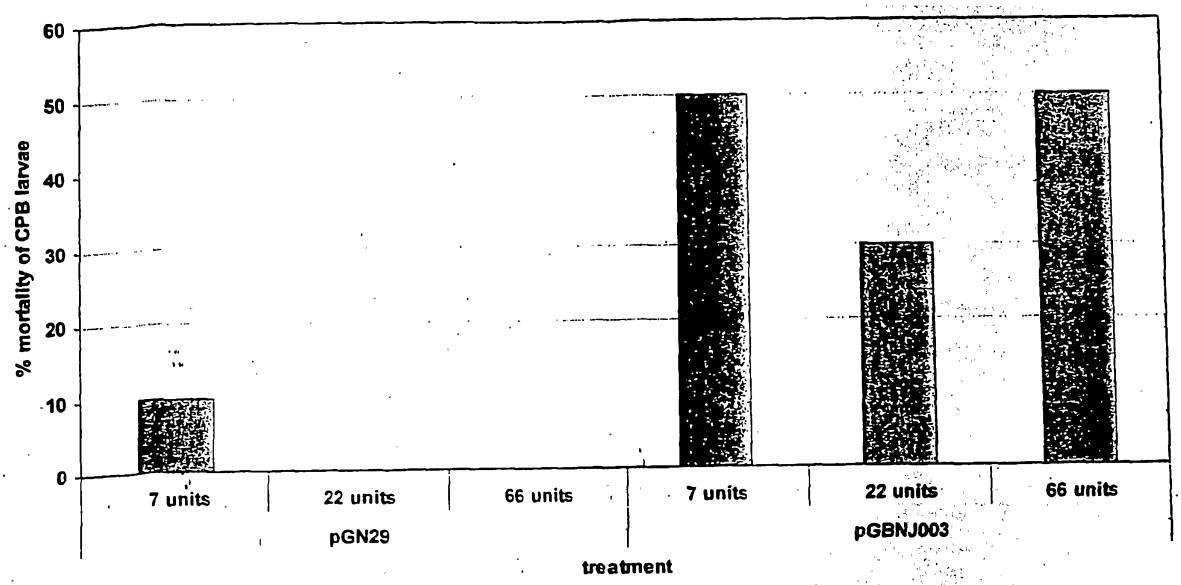

FIGURE 9-LD

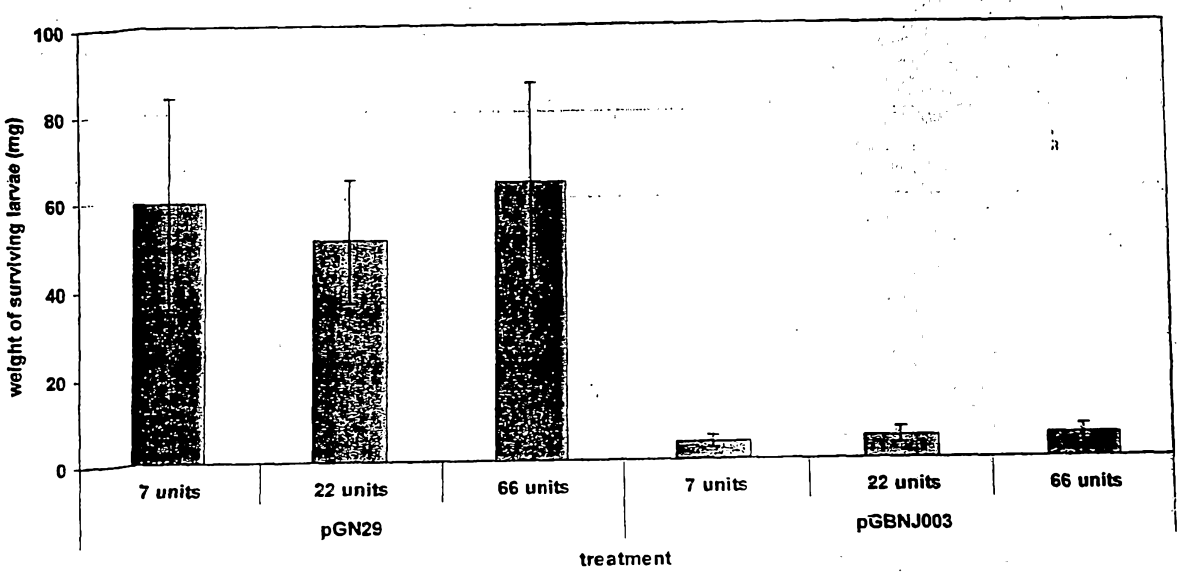

FIGURE 10-LD

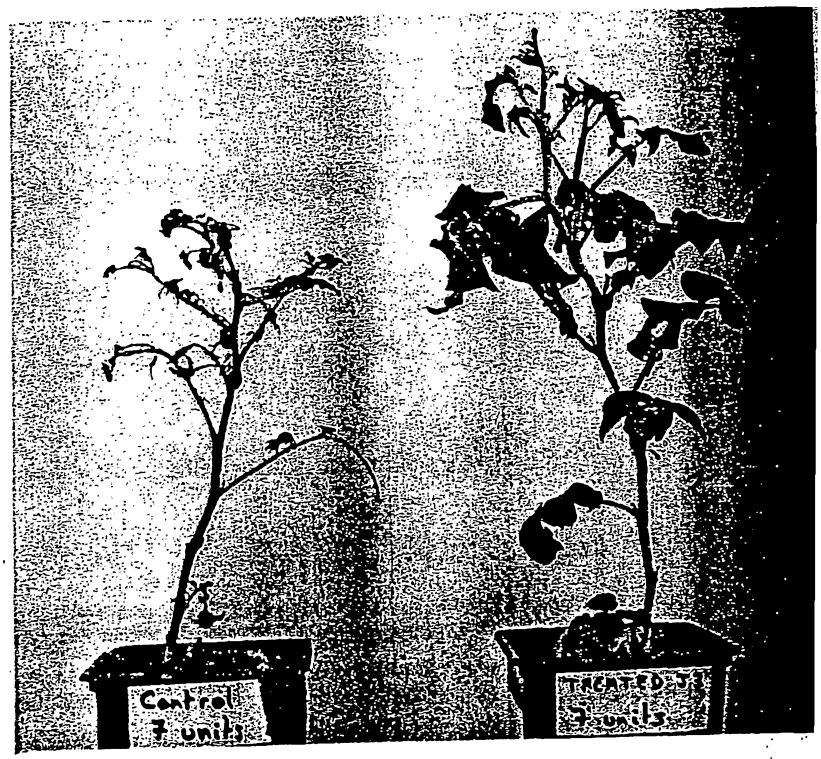

FIGURE 11-LD

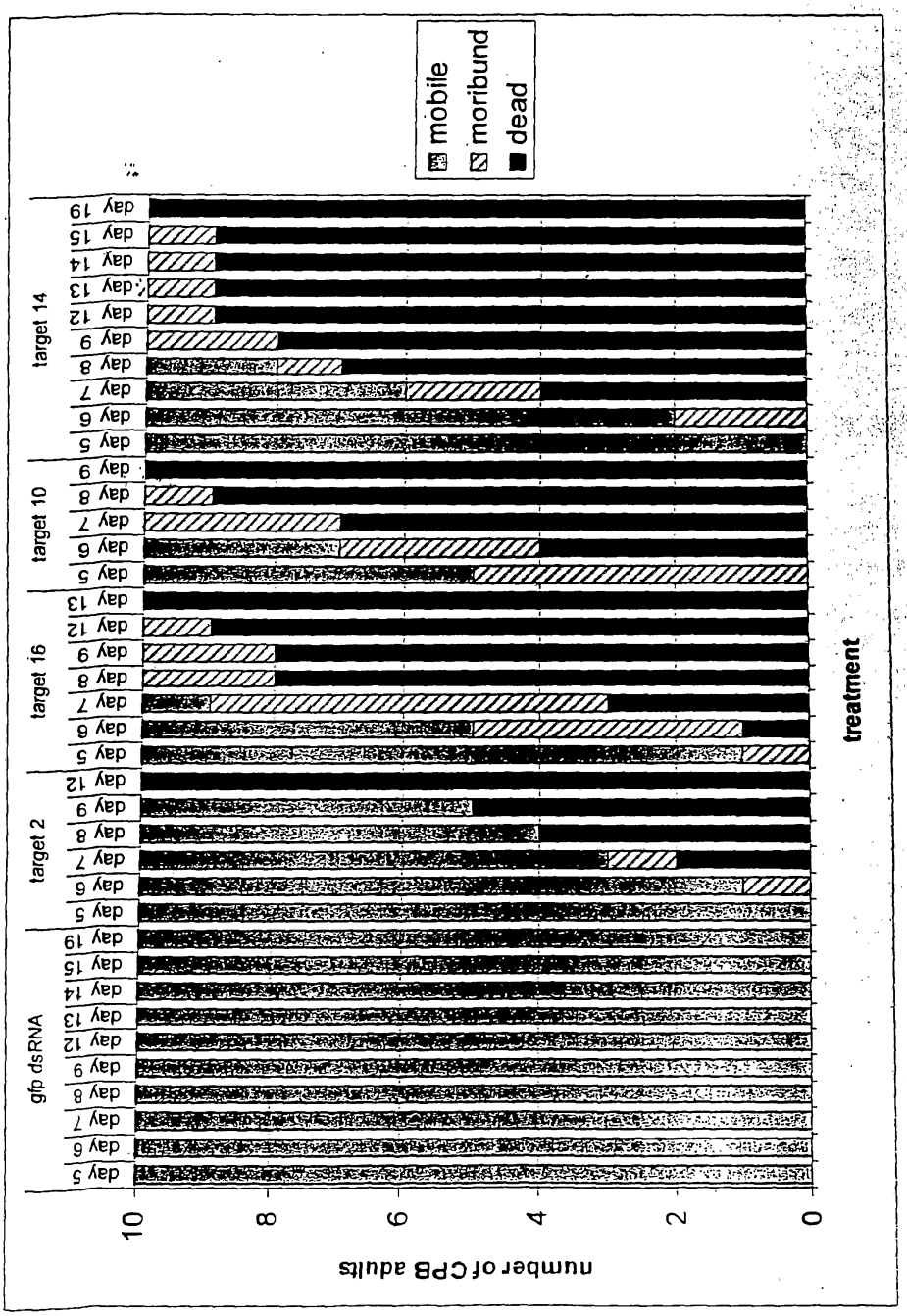
mobile
moribund
dead
number of CPB adults
0
2
4
6
8
10
treatment
gfp dsRNA
target 2
target 16
target 10
target 14
day 5
day 6
day 7
day 8
day 9
day 12
day 13
day 14
day 15
day 19

FIGURE 12-LD

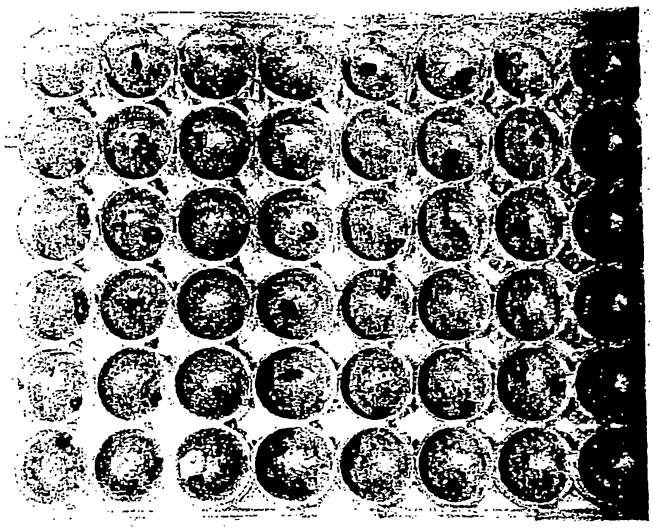

FIGURE 13(a)-LD

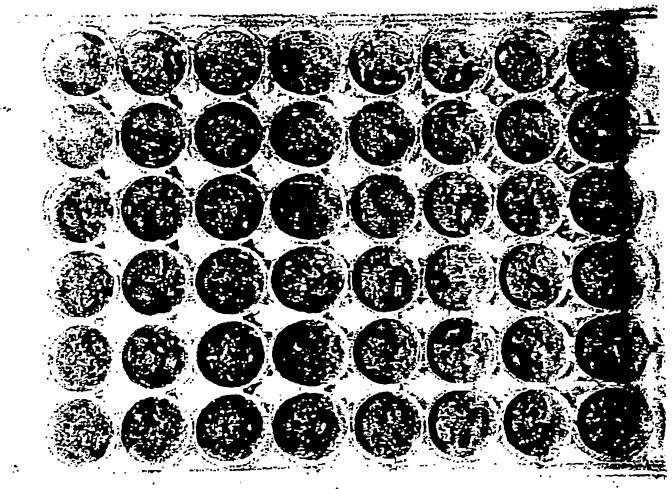

FIGURE 13(b)-LD

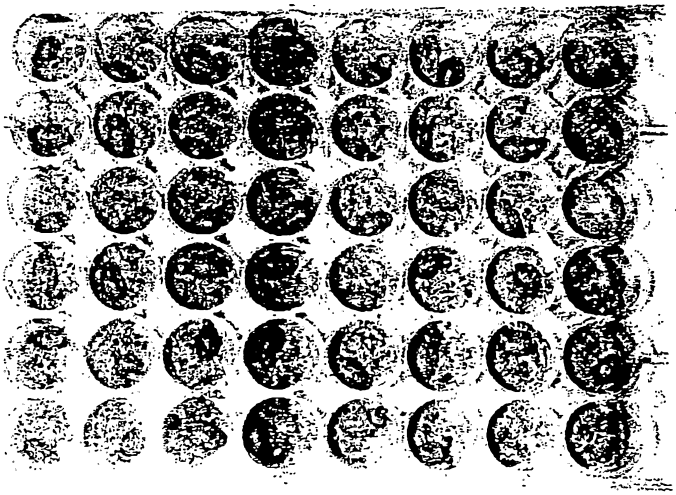

FIGURE 13(c)-LD

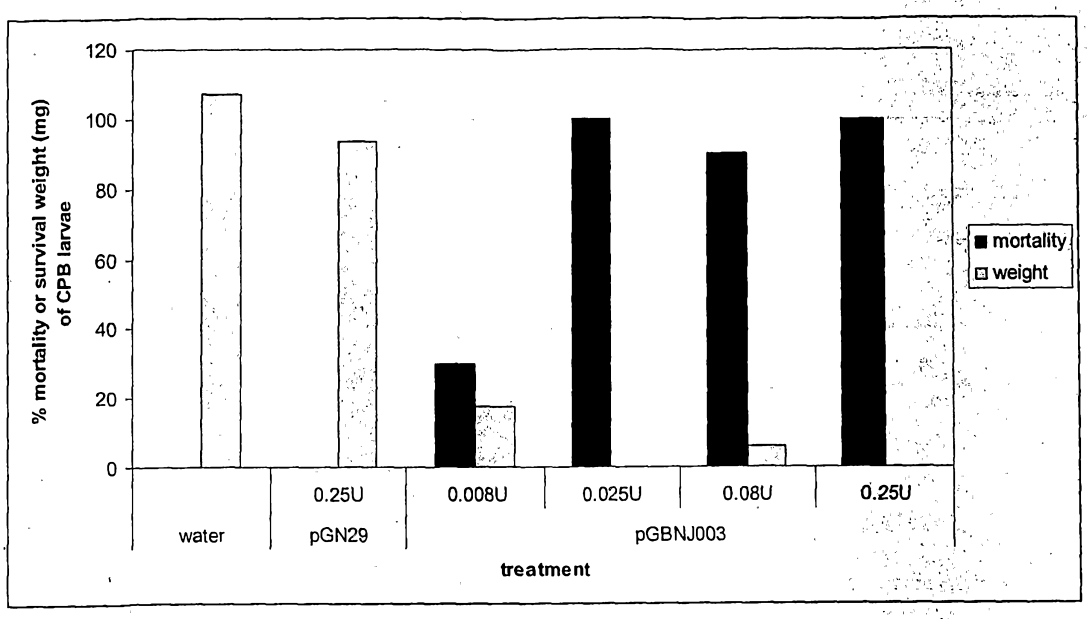
% mortality or survival weight (mg) of CPB larvae
120
100
80
60
40
20
0
water
0.25U
pGN29
0.008U
0.025U
0.08U
0.25U
pGBNJ003
treatment
mortality
weight

FIGURE 14-LD

FIGURE 15(a)-LD

FIGURE 15(b)-LD

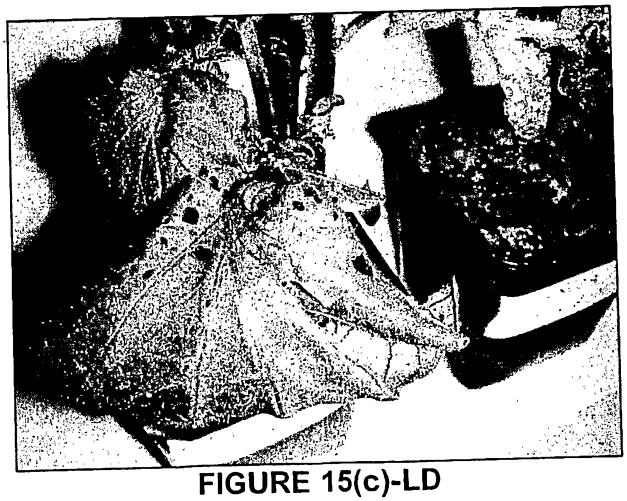

FIGURE 15(c)-LD

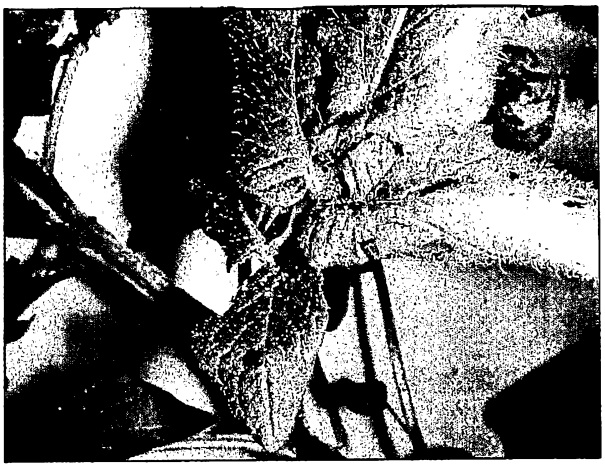

FIGURE 15(d)-LD

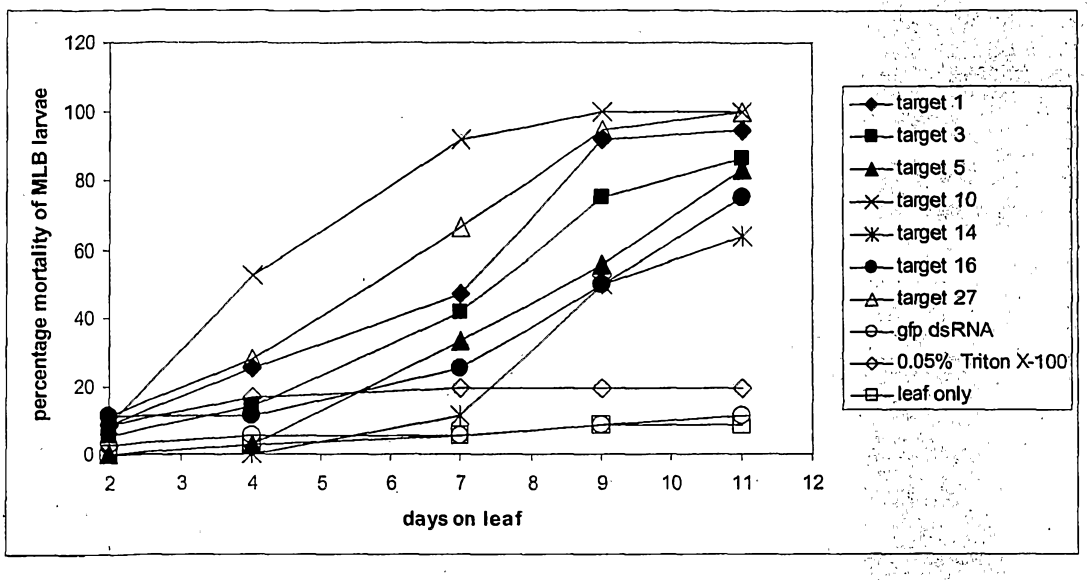

FIGURE 1(a)-PC

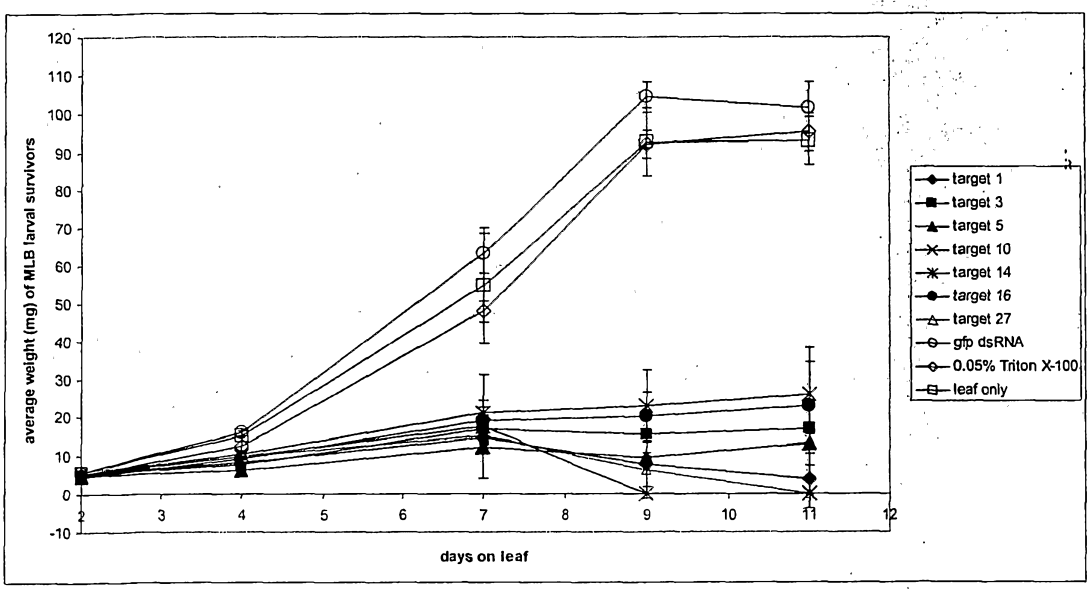

FIGURE 1(b)-PC

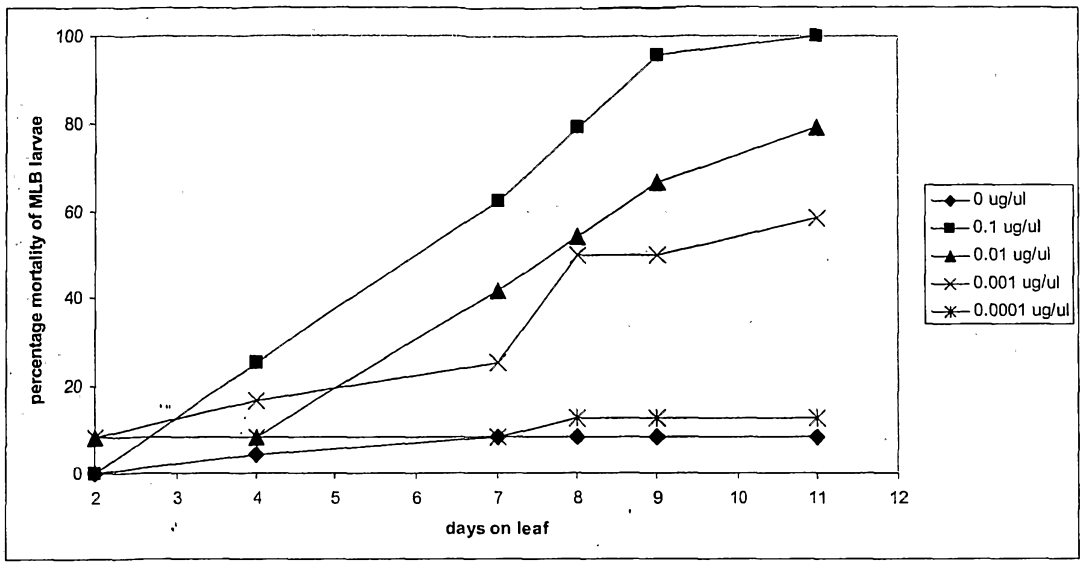

FIGURE 2(a)-PC

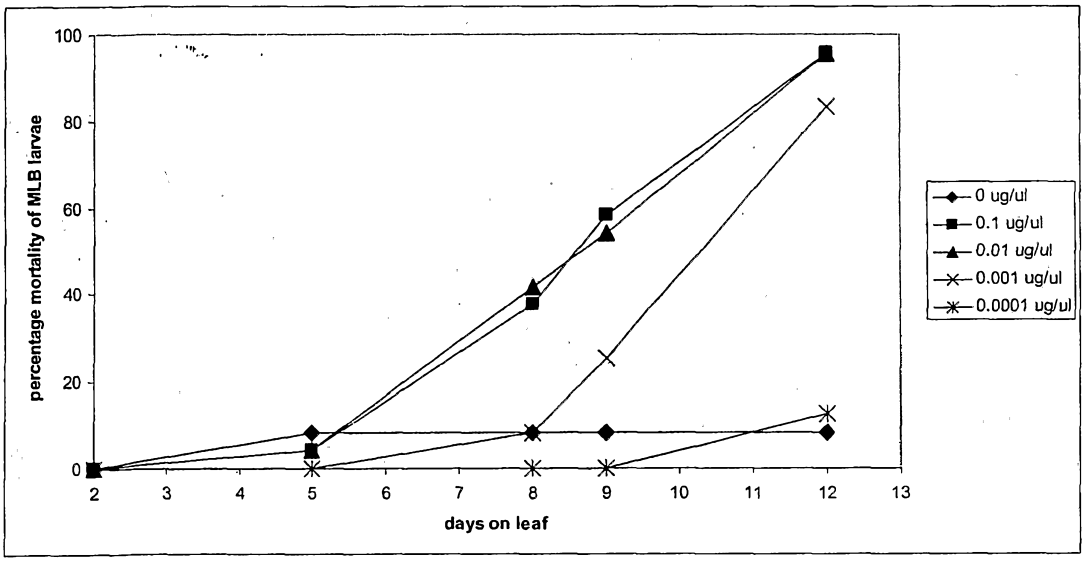

FIGURE 2(b)-PC

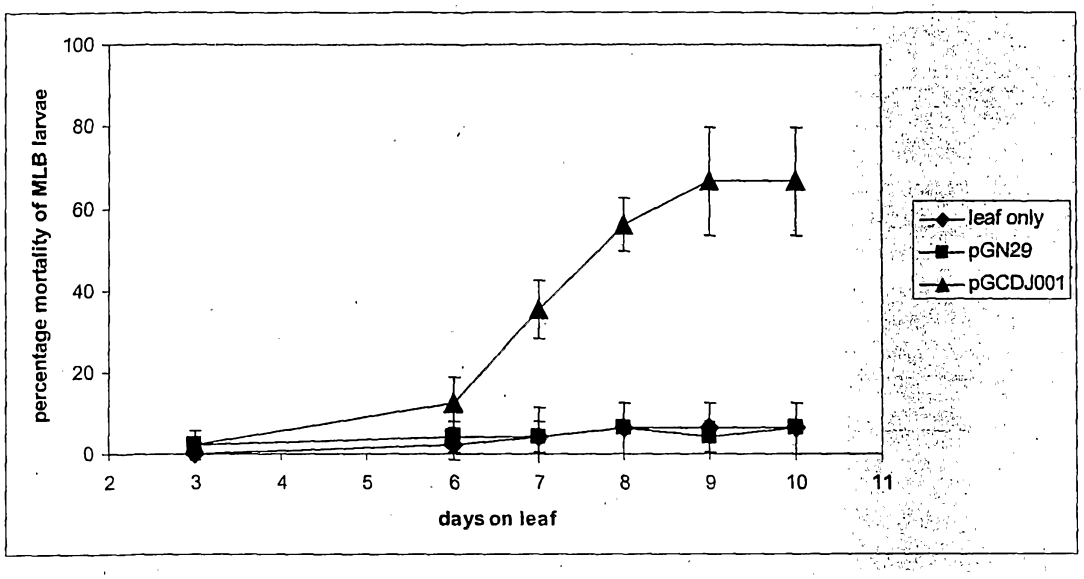
100
80
60
40
20
0
percentage mortality of MLB larvae
2
3
4
5
6
7
8
9
10
11
days on leaf
leaf only
pGN29
pGCDJ001

FIGURE 3-PC

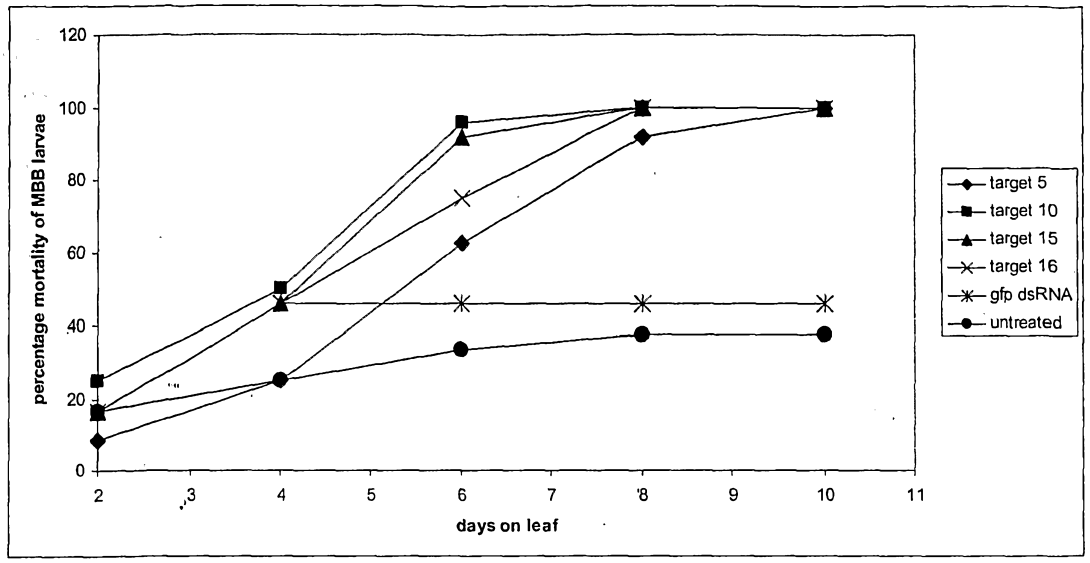

FIGURE 1-EV

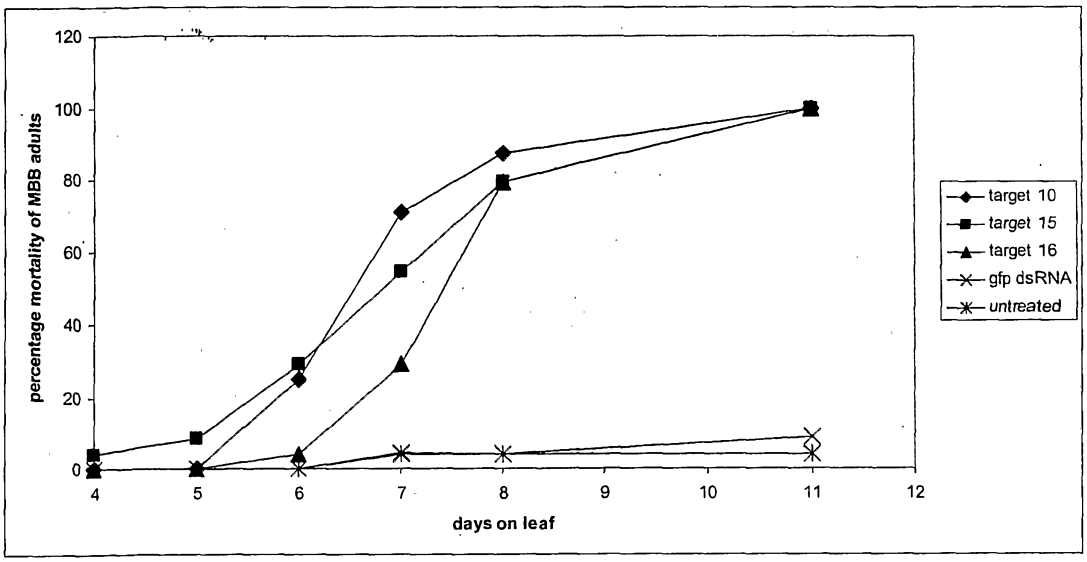

FIGURE 2(a)1-EV

FIGURE 2(b) (i)-EV

FIGURE 2(b) (ii)-EV

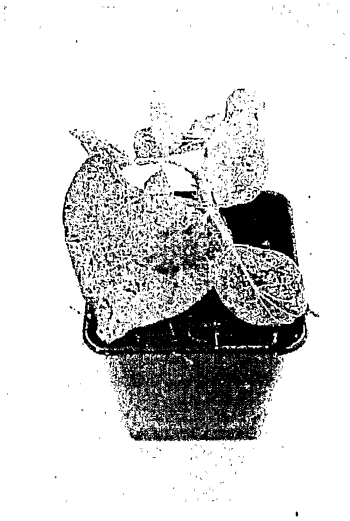

FIGURE 2(b) (iii)-EV

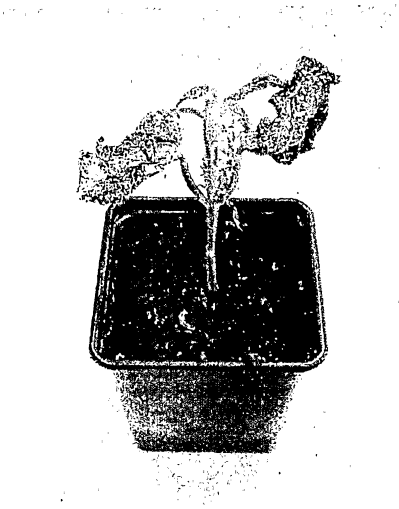

FIGURE 2(b) (iv)-EV

FIGURE 2(b) (v)-EV

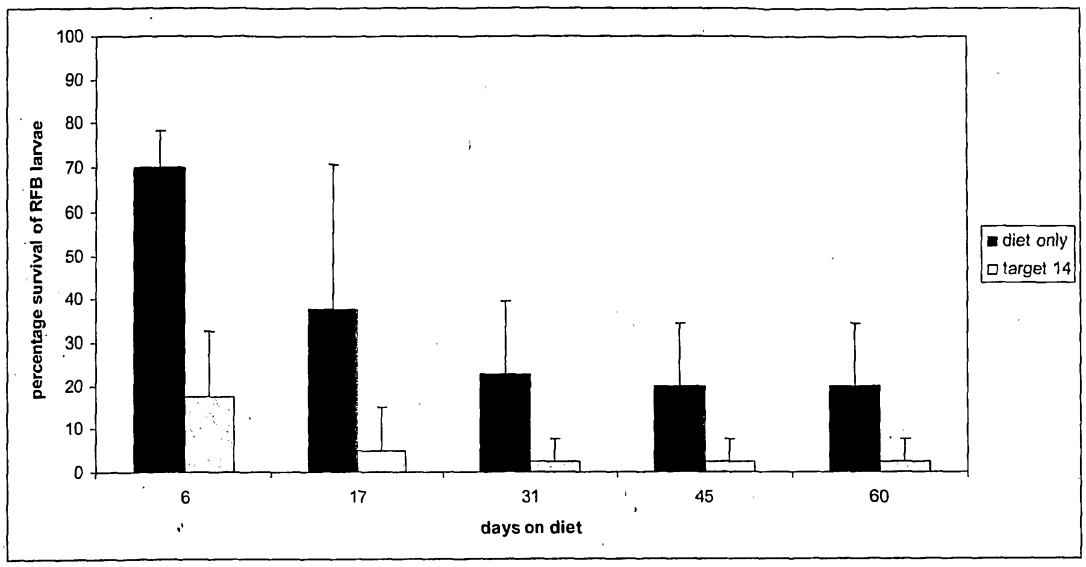
100
90
80
70
60
50
40
30
20
10
0
percentage survival of RFB larvae
6
17
31
45
60
days on diet
diet only
target 14

FIGURE 1-TC

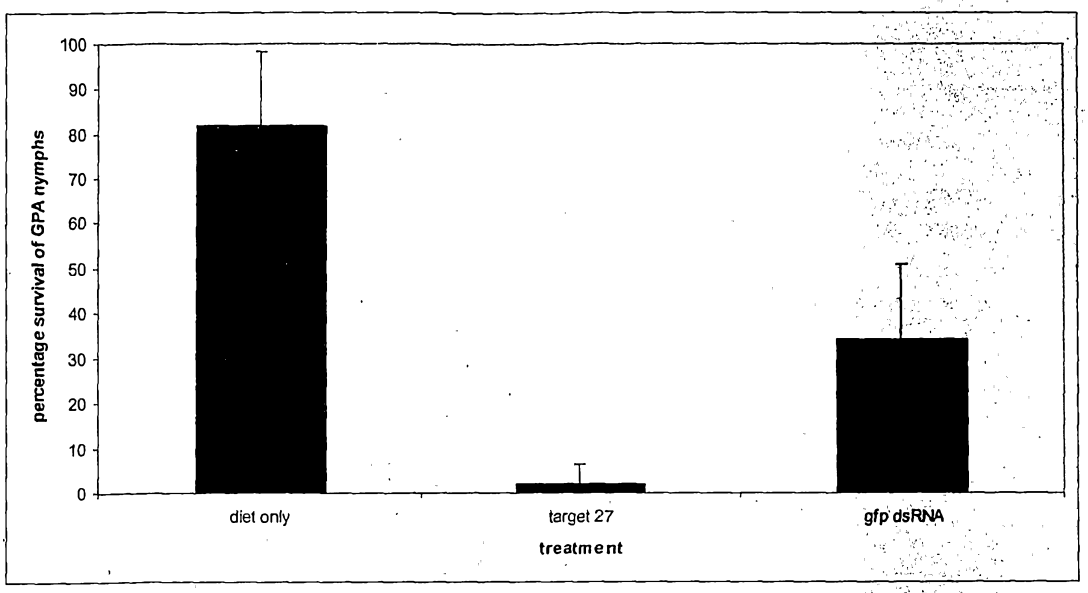
100
90
80
70
60
50
40
30
20
10
0
percentage survival of GPA nymphs
diet only
target 27
gfp dsRNA
treatment

FIGURE 1-MP

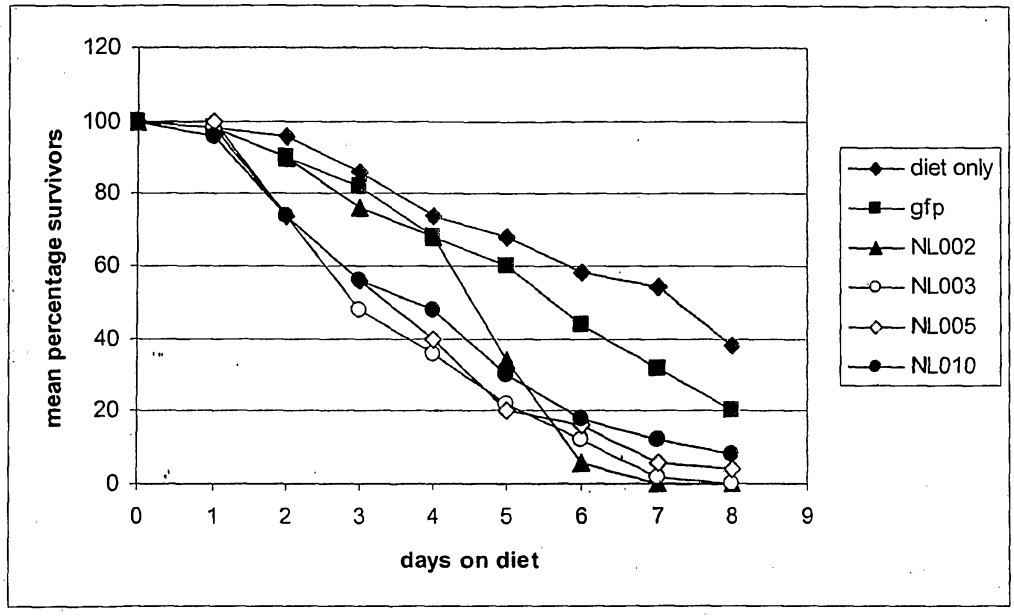

FIGURE 1 (a)-NL

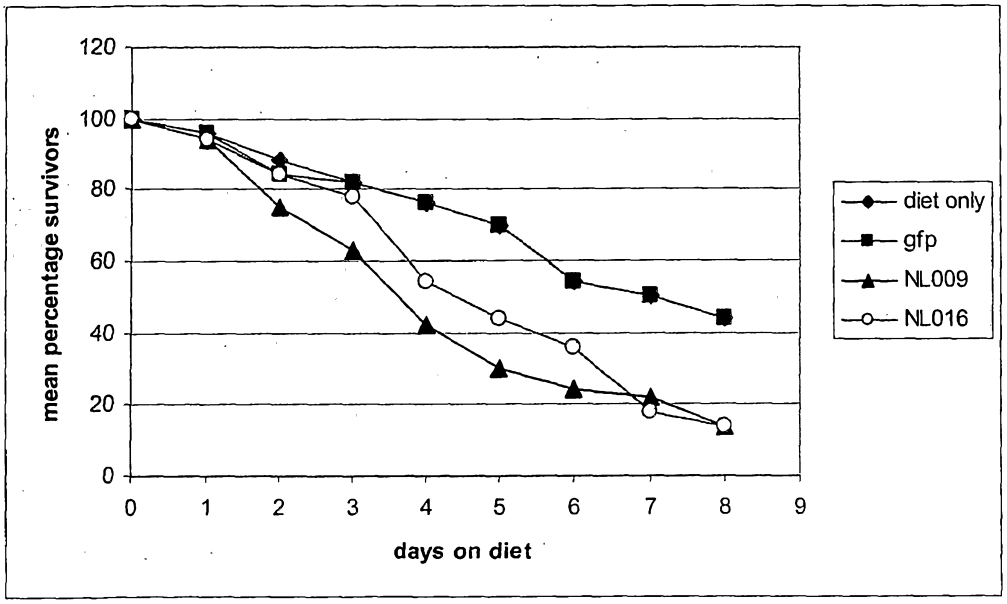

FIGURE 1 (b)-NL

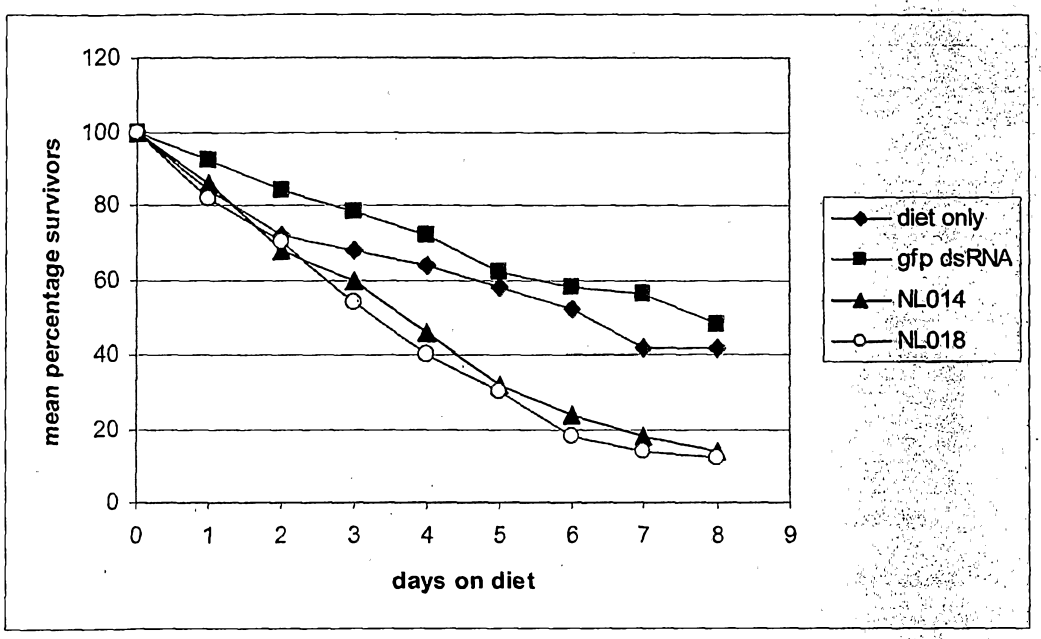

FIGURE 1 (c)-NL

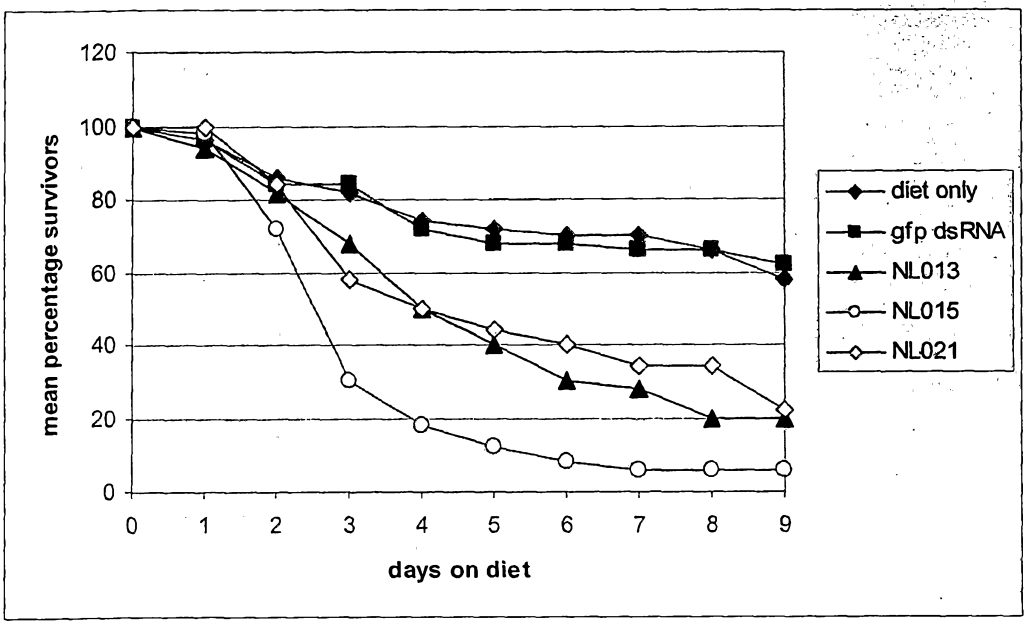

FIGURE 1 (d)-NL

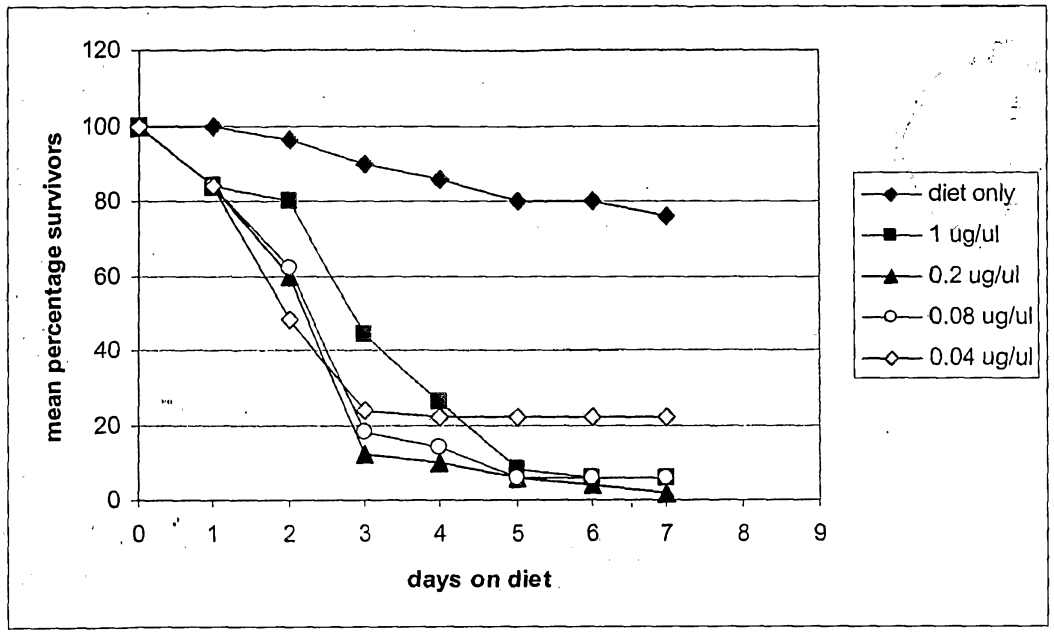
120
100
80
60
40
20
0
mean percentage survivors
0
1
2
3
4
5
6
7
8
9
days on diet
diet only
1 ug/ul
0.2 ug/ul
0.08 ug/ul
0.04 ug/ul

FIGURE 2-NL

Table 1A

C.elegans id	D. melanogaster id	description	devgen RNAi screen
B0250.1	CG1263	large ribosomal subunit L8 protein.	Acute lethal or lethal
B0336.10	CG3661	large ribosomal subunit L23 protein.	Acute lethal or lethal
B0336.2	CG8385	ADP-ribosylation factor	Acute lethal or lethal
B0464.1	CG3821	Putative aspartyl(D) tRNA synthetase.	Acute lethal or lethal
C01G8.5	CG10701	Ortholog of the ERM family of cytoskeletal linkers	Acute lethal or lethal
C01H6.5	CG33183	Nuclear hormone receptor that is required in all larval molts	Acute lethal or lethal
C02C6.1	CG18102	Member of the DYNamin related gene class	Acute lethal or lethal
C03D6.8	CG6764	Large ribosomal subunit L24 protein (Rlp24p)	Acute lethal or lethal
C04F12.4	CG6253	rpl-14 encodes a large ribosomal subunit L14 protein.	Acute lethal or lethal
C04H5.6	CG10689	Product with RNA helicase activity (EC:2.7.7.-) involved in nuclear mRNA splicing, via spliceosome which is a component of the spliceosome complex	Embryonic lethal or sterile
C13B9.3	CG14813	Delta subunit of the coatomer (COPI) complex	Acute lethal or lethal
C17H12.14	CG1088	Member of the Vacuolar H ATPase gene class	Acute lethal or lethal
C26E6.4	CG3180	DNA-directed RNA polymerase II	Acute lethal or lethal
F23F12.6	CG16916	Triple A ATPase subunit of the 26S proteasome's 19S regulatory particle (RP) base subcomplex	Acute lethal or lethal
F57B9.10	CG10149	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
K11D9.2	CG3725	sarco-endoplasmic reticulum Ca[2+] ATPase homolog	Embryonic lethal or sterile
T20G5.1	CG9012	Clathrin heavy chain	Acute lethal or lethal
T20H4.3	CG5394	Predicted cytoplasmic prolyl-tRNA synthetase (ProRS)	Acute lethal or lethal
T21E12.4	CG7507	Cytoplasmic dynein heavy chain homolog	Acute lethal or lethal
C05C10.3	CG1140	0rthologue to the human gene 3-OXOACID COA TRANSFERASE	Acute lethal or lethal
C09D4.5	CG2746	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome	Acute lethal or lethal

C09E10.2	CG31140	Orthologue of diacylglyerol kinase involved in movement, egg laying, and synaptic transmission, and is expressed in neurons.	Acute lethal or lethal
C13B9.3	CG14813	Delta subunit of the coatomer (COPI)	Acute lethal or lethal
C14B9.7	CG12775	Large ribosomal subunit L21 protein (RPL-21) involved in protein biosynthesis	Acute lethal or lethal
C15H11.7	CG30382	Type 6 alpha subunit of the 26S proteasome's 20S protease core particle (CP)	Acute lethal or lethal
C17E4.9	CG9261	Protein involved with Na+/K+- exchanging ATPase complex	Embryonic lethal or sterile
C17H12.14	CG1088	V-ATPase E subunit	Acute lethal or lethal
C23G10.4	CG11888	Non-ATPase subunit of the 26S proteasome's 19S regulatory paritcle base subcomplex (RPN-2)	Acute lethal or lethal
C26D10.2	CG7269	Product with helicase activity involved in nuclear mRNA splicing, via spliceosome which is localized to the nucleus	Acute lethal or lethal
C26E6.4	CG3180	RNA polymerase II 140kD subunit (RpII140), DNA-directed RNA polymerase activity (EC:2.7.7.6) involved in transcription from Pol II promoter which is a component of the DNA-directed RNA polymerase II, core complex	Acute lethal or lethal
C26F1.4	CG15697	Product with function in protein biosynthesis and ubiquitin in protein degradation.	Acute lethal or lethal
C30C11.1	CG12220	Unknown function	Acute lethal or lethal
C30C11.2	CG10484	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
C36A4.2	CG13977	cytochrome P450	Acute lethal or lethal
C37C3.6	CG33103	Orthologous to thrombospondin, papilin and lacunin	Acute lethal or lethal
C37H5.8	CG8542	Member of the Heat Shock Protein gene class	Acute lethal or lethal
C39F7.4	CG3320	Rab-protein 1 involved in cell adhesion	Acute lethal or lethal
C41C4.8	CG2331	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis	Growth delay or arrested in growth
C42D8.5	CG8827	ACE-like protein	Acute lethal or lethal

C47E12.5	CG1782	Ubiquitin-activating enzyme,function in an ATP-dependent reaction that activates ubiquitin prior to its conjugation to proteins that will subsequently be degraded by the 26S proteasome.	Acute lethal or lethal
C47E8.5	CG1242	Member of the abnormal DAuer Formation gene class	Acute lethal or lethal
C49H3.11	CG5920	Small ribosomal subunit S2 protein.	Acute lethal or lethal
C52E4.4	CG1341	Member of the proteasome Regulatory Particle, ATPase-like gene class	Acute lethal or lethal
C56C10.3	CG8055	Carrier protein with putatively involved in intracellular protein transport	Growth delay or arrested in growth
CD4.6	CG4904	Type 1 alpha subunit of the 26S proteasome's 20S protease core particle (CP).	Acute lethal or lethal
D1007.12	CG9282	Large ribosomal subunit L24 protein.	Acute lethal or lethal
D1054.2	CG5266	Member of the Proteasome Alpha Subunit gene class	Acute lethal or lethal
D1081.8	CG6905	MYB transforming protein	Acute lethal or lethal
F07D10.1	CG7726	Large ribosomal subunit L11 protein (RPL-11.2) involved in protein biosynthesis.	Acute lethal or lethal
F11C3.3	CG17927	Muscle myosin heavy chain (MHC B)	Acute lethal or lethal
F13B10.2	CG4863	Large ribosomal subunit L3 protein (rpl-3)	Acute lethal or lethal
F16A11.2	CG9987	Methanococcus hypothetical protein 0682 like	Acute lethal or lethal
F20B6.2	CG17369	V-ATPase B subunit	Growth delay or arrested in growth
F23F12.6	CG16916	Triple A ATPase subunit of the 26S proteasome's 19S regulatory particle (RP) base subcomplex (RPT-3)	Acute lethal or lethal
F25H5.4	CG2238	Translation elongation factor 2 (EF-2), a GTP-binding protein involved in protein synthesis	Growth delay or arrested in growth
F26D10.3	CG4264	Member of the Heat Shock Protein gene class	Acute lethal or lethal
F28C6.7	CG6846	Large ribosomal subunit L26 protein (RPL-26) involved in protein biosynthesis	Embryonic lethal or sterile
F28D1.7	CG8415	Small ribosomal subunit S23 protein (RPS-23) involved in protein biosynthesis	Acute lethal or lethal

F29G9.5	CG5289	Member of the proteasome Regulatory Particle, ATPase-like gene class	Acute lethal or lethal
F32H2.5	CG3523	Mitochondrial protein	Acute lethal or lethal
F37C12.11	CG2986	Small ribosomal subunit S21 protein (RPS-21) involved in protein biosynthesis	Acute lethal or lethal
F37C12.4	CG7622	Large ribosomal subunit L36 protein (RPL-36) involved in protein biosynthesis	Acute lethal or lethal
F37C12.9	CG1527	Small ribosomal subunit S14 protein (RPS-14) involved in protein biosynthesis	Acute lethal or lethal
F38E11.5	CG6699	beta' (beta-prime) subunit of the coatomer (COPI) complex	Acute lethal or lethal
F39B2.6	CG10305	Small ribosomal subunit S26 protein (RPS-26) involved in protein biosynthesis	Acute lethal or lethal
F39H11.5	CG12000	Member of the Proteasome Beta Subunit gene class	Acute lethal or lethal
F40F8.10	CG3395	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit	Acute lethal or lethal
F42C5.8	CG7808	Small ribosomal subunit S8 protein (RPS-8) involved in protein biosynthesis	Acute lethal or lethal
F49C12.8	CG5378	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
F53A3.3	CG2033	Small ribosomal subunit S15a protein.	Acute lethal or lethal
F53G12.10	CG4897	large ribosomal subunit L7 protein (rpl-7)	Acute lethal or lethal
F54A3.3	CG8977	Unknown function	Acute lethal or lethal
F54E2.3	CG1915	Product with sallimus (sls), myosin-light-chain kinase activity (EC:2.7.1.117) involved in mitotic chromosome condensation which is localized to the nucleus	
F54E7.2	CG11271	Small ribosomal subunit S12 protein (RPS-12) involved in protein biosynthesis	Acute lethal or lethal
F55A11.2	CG4214	Member of the SYNtaxin gene class	Acute lethal or lethal
F55A3.3	CG1828	transcritpion factor	Acute lethal or lethal

F55C10.1	CG11217	Ortholog of calcineurin B, the regulatory subunit of the protein phosphatase 2B	Acute lethal or lethal
F56F3.5	CG2168	rps-1 encodes a small ribosomal subunit S3A protein.	Acute lethal or lethal
F57B9.10	CG10149	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
F58F12.1	CG2968	ATP synthase	Acute lethal or lethal
F59E10.3	CG3948	Zeta subunit of the coatomer (COPI) complex	Acute lethal or lethal
JC8.3	CG3195	Large ribosomal subunit L12 protein (rpl-12)	Acute lethal or lethal
K01G5.4	CG1404	Putative RAN small monomeric GTPase (cell adhesion)	Acute lethal or lethal
K04F10.4	CG18734	Subtilase	Acute lethal or lethal
K05C4.1	CG12323	Member of the Proteasome Beta Subunit gene class	Acute lethal or lethal
K07D4.3	CG18174	Putative proteasome regulatory particle, lid subcomplex, rpn11	Acute lethal or lethal
K11D9.2	CG3725	Sarco-endoplasmic reticulum Ca[2+] ATPase	Embryonic lethal or sterile; Acute lethal or lethal
M03F4.2	CG4027	An actin that is expressed in body wall and vulval muscles and the spermatheca.	Acute lethal or lethal
R06A4.9	CG1109	six WD40 repeats	Acute lethal or lethal
R10E11.1	CG15319	Putative transcriptional cofactor	Acute lethal or lethal
R12E2.3	CG3416	Protein with endopeptidase activity involved in proteolysis and peptidolysis	Acute lethal or lethal
F10C1.2	CG10119	Member of the Intermediate Filament, B gene class	Embryonic lethal or sterile
F35G12.8	CG11397	Homolog of the SMC4 subunit of mitotic condensin	Embryonic lethal or sterile
F53G12.1	CG5771	GTPase homologue	Embryonic lethal or sterile
F54E7.3	CG5055	PDZ domain-containing protein	Embryonic lethal or sterile
H28O16.1	CG3612	ATP synthase	Growth delay or arrested in growth
K12C11.2	CG4494	Member of the SUMO (ubiquitin-related) homolog gene class	Embryonic lethal or sterile
R12E2.3	CG3416	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
R13A5.8	CG6141	Ribosomal protein L9, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome	Acute lethal or lethal

T01C3.6	CG4046	rps-16 encodes a small ribosomal subunit S16 protein.	Acute lethal or lethal
T01H3.1	CG7007	proteolipid protein PPA1 like protein	Acute lethal or lethal
T05C12.7	CG5374	Cytosolic chaperonin	Acute lethal or lethal
T05H4.6	CG5605	eukaryotic peptide chain release factor subunit 1	Acute lethal or lethal
T10H9.4	CG17248	N-synaptobrevin; v-SNARE, vesicle-mediated transport, synaptic vesicle	
T14F9.1	CG17332	ATPase subunit	Growth delay or arrested in growth
T20G5.1	CG9012	Clathrin heavy chain	Acute lethal or lethal
T21B10.7	CG7033	t-complex protein 1	Embryonic lethal or sterile
W09B12.1	CG17907	Acetylcholineesterase	
T27F2.1	CG8264	Member of the mammalian SKIP (Ski interacting protein) homolog gene class	Acute lethal or lethal
ZC434.5	CG5394	predicted mitochondrial glutamyl-tRNA synthetase (GluRS)	Acute lethal or lethal
B0511.6	CG6375	helicase	Embryonic lethal or sterile
DY3.2	CG10119	Nuclear lamin; LMN-1 protein	Growth delay or arrested in growth
R13G10.1	CG11397	homolog of the SMC4 subunit of mitotic condensin	Wild Type
T26E3.7	CG3612	Predicted mitochondrial protein.	Growth delay or arrested in growth
Y113G7A.3	CG1250	GTPase activator, ER to Golgi prot transport, component of the Golgi stack	Acute lethal or lethal
Y43B11AR.4	CG11276	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit	Acute lethal or lethal
Y46G5A.4	CG5931	Y46G5A.4 gene	Acute lethal or lethal
Y71F9AL.17	CG7961	Alpha subunit of the coatomer (COPI) complex	Acute lethal or lethal
Y76B12C.7	CG10110	Gene cleavage and polyadenylation specificity factor	Embryonic lethal or sterile
Y37D8A.10	CG1751	Unknown function	Embryonic lethal or sterile
CG7765	C06G3.2	Member of the Kinesin-Like Protein gene class	
CG10922	C44E4.4	RNA-binding protein	Embryonic lethal or sterile
CG4145	F01G12.5	alpha-2 type IV collagen	Embryonic lethal or sterile

CG13391	F28H1.3	apredicted cytoplasmic alanyl-tRNA synthetase (AlaRS)	Growth delay or arrested in growth
CG7765	R05D3.7	Member of the UNCoordinated gene class	Embryonic lethal or sterile
CG7398	R06A4.4	Member of the IMportin Beta family gene class	Embryonic lethal or sterile
CG7436	T17E9.2	Unknown function	Embryonic lethal or sterile
CG2666	T25G3.2	putative chitin synthase	Embryonic lethal or sterile
CG17603	W04A8.7	TATA-binding protein associated factor TAF1L (TAFII250)	Embryonic lethal or sterile

Table 1-LD

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
LD001	CG11276	1	2	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
LD002	CG8055	3	4	Carrier protein with putatively involved in intracellular protein transport
LD003	CG3395	5	6	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
LD006	CG3180	7	8	RNA polymerase II 140kD subunit (RpII140), DNA-directed RNA polymerase activity (EC:2.7.7.6) involved in transcription from Pol II promoter which is a component of the DNA-directed RNA polymerase II, core complex
LD007	CG7269	9	10	Helicase at 25E (Hel25E), also known in FlyBase as Dbp25F, Hel, l(2)25Eb and l(2)k11511, pre-mRNA splicing factor activity involved in nuclear mRNA splicing, via spliceosome which is localized to the nucleus
LD010	CG1250	11	12	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
LD011	CG1404	13	14	Tutative RAN small monomeric GTPase (cell adhesion)
LD014	CG1088	15	16	V-ATPase E subunit
LD015	CG2331	17	18	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
LD016	CG17369	19	20	V-ATPase B subunit
LD018	CG1915	21	22	Sallimus (sls), myosin-light-chain kinase activity (EC:2.7.1.117) involved in mitotic chromosome condensation which is localized to the nucleus
LD027	CG6699	23	24	Beta-coatamer protein, subunit of a multimeric complex that forms a membrane vesicle coat

Table 1-PC

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
PC001	CG11276	247	248	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit

PC003	CG3395	249	250	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
PC005	CG2746	251	252	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
PC010	CG1250	253	254	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
PC014	CG1088	255	256	V-ATPase E subunit
PC016	CG17369	257	258	V-ATPase B subunit
PC027	CG6699	259	260	Beta-coatamer protein, subunit of a multimeric complex that forms a membrane vesicle coat

Table 1-EV

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
EV005	CG2746	513	514	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
EV009	CG9261	515	516	Protein involved with Na+/K+- exchanging ATPase complex
EV010	CG1250	517	518	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
EV015	CG2331	519	520	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
EV016	CG17369	521	522	V-ATPase B subunit

Table 1-AG

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
AG001	CG11276	601	602	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
AG005	CG2746	603	604	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
AG010	CG1250	605	606	GTPase activator, ER to Golgi prot transport, component of the Golgi stack

AG014	CG1088	607	608	V-ATPase E subunit
AG016	CG17369	609	610	V-ATPase B subunit

Table 1-TC

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
TC001	CG11276	793	794	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
TC002	CG8055	795	796	Protein with putatively involved in intracellular protein transport
TC010	CG1250	797	798	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
TC014	CG1088	799	800	V-ATPase E subunit
TC015	CG2331	801	802	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis

Table 1-MP

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
MP001	CG11276	888	889	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
MP002	CG8055	890	891	Carrier protein with putatively involved in intracellular protein transport
MP010	CG1250	892	893	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
MP016	CG17369	894	895	V-ATPase B subunit
MP027	CG6699	896	897	Beta-coatamer protein, subunit of a multimeric complex that forms a membrane vesicle coat

Table 1-NL

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)

NL001	CG11276	1071	1072	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
NL002	CG8055	1073	1074	Protein with putatively involved in intracellular protein transport
NL003	CG3395	1075	1076	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
NL004	CG6141	1077	1078	Ribosomal protein L9, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
NL005	CG2746	1079	1080	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
NL006	CG3180	1081	1082	RNA polymerase II 140kD subunit (RpII140), DNA-directed RNA polymerase activity (EC:2.7.7.6) involved in transcription from Pol II promoter which is a component of the DNA-directed RNA polymerase II, core complex
NL007	CG7269	1083	1084	Helicase at 25E (Hel25E), also known in FlyBase as Dbp25F, Hel, l(2)25Eb and l(2)k11511, pre-mRNA splicing factor activity involved in nuclear mRNA splicing, via spliceosome which is localized to the nucleus
NL008	CG3416	1085	1086	Protein with endopeptidase activity involved in proteolysis and peptidolysis which is a component of the proteasome regulatory particle, lid subcomplex (sensu Eukarya)
NL009	CG9261	1087	1088	Protein involved with Na+/K+- exchanging ATPase complex
NL010	CG1250	1089	1090	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
NL011	CG1404	1091	1092	Putative RAN small monomeric GTPase (cell adhesion)
NL012	CG17248	1093	1094	N-synaptobrevin; v-SNARE, vesicle-mediated transport, synaptic vesicle
NL013	CG18174	1095	1096	Putative proteasome regulatory particle, lid subcomplex, rpn11
NL014	CG1088	1097	1098	V-ATPase E subunit
NL015	CG2331	1099	1100	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
NL016	CG17369	1101	1102	V-ATPase B subunit
NL018	CG1915	1103	1104	Sallimus (sls), myosin-light-chain kinase activity (EC:2.7.1.117) involved in mitotic chromosome condensation which is localized to the nucleus

NL019	CG3320	1105	1106	Rab-protein 1 involved in cell adhesion
NL021	CG10110	1107	1108	Gene cleavage and polyadenylation specificity factor
NL022	CG10689	1109	1110	Product with RNA helicase activity (EC:2.7.7.-) involved in nuclear mRNA splicing, via spliceosome which is a component of the spliceosome complex
NL023	CG17907	1111	1112	Acetylcholineesterase
NL027	CG6699	1113	1114	Beta-coatomer protein

Table 1-CS

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
CS001	CG11276	1682	1683	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
CS002	CG8055	1684	1685	Carrier protein with putatively involved in intracellular protein transport
CS003	CG3395	1686	1687	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
CS006	CG3180	1688	1689	RNA polymerase II 140kD subunit (RpII140), DNA-directed RNA polymerase activity (EC:2.7.7.6) involved in transcription from Pol II promoter which is a component of the DNA-directed RNA polymerase II, core complex
CS007	CG7269	1690	1691	Helicase at 25E (Hel25E), also known in FlyBase as Dbp25F, Hel, l(2)25Eb and l(2)k11511, pre-mRNA splicing factor activity involved in nuclear mRNA splicing, via spliceosome which is localized to the nucleus
CS009	CG9261	1692	1693	Protein involved with Na+/K+- exchanging ATPase complex
CS011	CG1404	1694	1695	Tutative RAN small monomeric GTPase (cell adhesion)
CS013	CG18174	1696	1697	Putative proteasome regulatory particle, lid subcomplex, rpn11
CS014	CG1088	1698	1699	V-ATPase E subunit
CS015	CG2331	1700	1701	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
CS016	CG17369	1702	1703	V-ATPase B subunit

CS018	CG1915	1704	1705	Sallimus (sls), myosin-light-chain kinase activity (EC:2.7.1.117) involved in mitotic chromosome condensation which is localized to the nucleus

Table 1-PX

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
PX001	CG11276	2100	2101	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
PX009	CG9261	2102	2103	Protein involved with Na+/K+- exchanging ATPase complex
PX010	CG1250	2104	2105	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
PX015	CG2331	2106	2107	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
PX016	CG17369	2108	2109	V-ATPase B subunit

Table 1-AD

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
AD001	CG11276	2364	2365	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
AD002	CG8055	2366	2367	Carrier protein with putatively involved in intracellular protein transport
AD009	CG9261	2368	2369	Protein involved with Na+/K+- exchanging ATPase complex
AD015	CG2331	2370	2371	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
AD016	CG17369	2372	2373	V-ATPase B subunit

Table 2-LD

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
LD001	SEQ ID NO: 25	SEQ ID NO: 26	SEQ ID NO: 1

	GGCCCCAAGA AGCATTTGAA GCG	TAGCGGATGG TGCGDCCRTC RTG	GGCCCCAAGAAGCATTTGAAGCGTTTGAATGCCCCAAAAGCATGGATGTTGGATA AATTGGGAGGTGTTTTCGCACCTCGCCCATCTACAGGACCTCACAAATTGCGAGA GTCTTTGCCCTTGGTGATCTTCCTACGTAACCGATTGAAGTATGCTTTGACTAACA GCGAAGTTACTAAGATTGTTATGCAAAGGTTAATCAAAGTAGATGGAAAAGTGAG GACCGACTCCAATTACCCTGCTGGGTTTATGGATGTTATTACCATTGAAAAAACTG GTGAATTTTTCCGACTCATCTATGATGTTAAAGGACGATTTGCAGTGCATCGTATT ACTGCTGAGGAAGCAAAGTACAAACTATGCAAAGTCAGGAGGATGCAAACTGGC CCCAAAGGAATTCCCTTCATAGTGACACACGACGGCCGCACCATCCGCTA
LD002	SEQ ID NO: 27 GAGCGGCCAT GCAAGCVCTB AARMRRAAG	SEQ ID NO: 28 GCAATGTCAT CCATCAKRTC RTGCAC	SEQ ID NO: 3 GCAATGTCATCCATCATGTCGTGTACATTGTCCACGTCCAAGTTTTTATGGGCTTT CTTAAGAGCTTCAGCTGCATTTTTCATAGATTCCAATACTGTGGTGTTCGTACTAG CTCCCTCCAGAGCTTCTCGTTGAAGTTCAATAGTAGTTAAAGTGCCATCTATTTGC AACTGATTTTTTTCTAATCGCTTCTTCCGCTTCAGCGCTTGCATGGCCGCTC
LD003	SEQ ID NO: 29 TCGGTCTTCTC GAAGACNTAY GTKAC	SEQ ID NO: 30 CAGGTTCTTC CTCTTKACRC GDCC	SEQ ID NO: 5 CAGGTTCTTCCTCTTGACGCGTCCAGGGCGACCACCACCGAATGGAGATTTGAGC GAGAAGTCAATATGCTTCTGGGAATCAAGTCTCACAATGAAGCTTGGAATATTCA CGACCTGCTTACGAACCCTGATATGTCTTTGACGGACCAGCACACGAGCATGATG GATTGATTTTGCAAGCCCCAACTTGAAAACTTGTGTTTGGAGACGTCGTTCCAAGA AATCTTCAATCTTCAAACCCAAGACGTAATCAAGCTTCATACGGGTTTCATCCAAC ACTCCAATACGCACCAACCGACGAAGAAGAGCATTGCCTTCAAACAACCTGCGCT GATCTTTCTCTTCCAAAGTCAGAAGTTCTCTGGCAGCTTTACGGATTTTTGCCAAG GTATACTTGACTCGCCACACTTCACGTTTGTTCCTAAGACCATATTCTCCTATGATT TTCAACTCCTGATCAAGACGTGCCTTTTCATAAGGTCGCCTGGGA
LD006	SEQ ID NO: 31 GGAGCGAGAC TACAACAAYK AYRGYTGGC	SEQ ID NO: 32 CTCGAACTGC TCYTCYTGAT CRCC	SEQ ID NO: 7 GGAGCGAGACTACACAACTATGGCTGGCAGGTGTTGGTTGCTTCTGGTGTGGTGG AATACATCGACACTCTTGAAGAAGAAACTGTCATGATTGCGATGAATCCTGAGGA TCTTCGGCAGGACAAAGAATATGCTTATTGTACGACCTACACCCACTGCGAAATC CACCCGGCCATGATCTTGGGCGTTTGCGCGTCTATTATACCTTTCCCCGATCATAA CCAGAGCCCAAGGAACACCTACCAGAGCGCTATGGGTAAGCAAGCTATGGGGGT CTACATTACGAATTTCCACGTGCGGATGGACACCCTGGCCCACGTGCTATACTACC CGCACAAACCTCTGGTCACTACCAGGTCTATGGAGTATCTGCGGTTCAGAGAATT ACCAGCCGGGATCAACAGTATAGTTGCTATTGCTTGTTATACTGGTTATAATCAAG AAGATTCTGTTATTCTGAACGCGTCTGCTGTGGAAAGAGGATTTTTCCGATCCGTG TTTTATCGTTCCTATAAAGATGCCGAATCGAAGCGAATTGGCGATCAAGAAGAGC

			AGTTCGAG
LD007	SEQ ID NO: 33 CCGAAGAAGG AYGTSAAGGG YAC	SEQ ID NO: 34 CGATGCAAGT AGGTGTCKGA RTCYTC	SEQ ID NO: 9 CCGAAGAAGGATGTGAAGGGTACTTACGTATCCATACACAGTTCAGGCTTCAGAG ATTTTTTATTGAAACCAGAAATTCTAAGAGCTATAGTTGACTGCGGTTTTGAACAC CCTTCAGAAGTTCAGCACGAATGTATTCCTCAAGCTGTCATTGGCATGGACATTTT ATGTCAAGCCAAATCTGGTATGGGCAAAACGGCAGTGTTTGTTCTGGCGACACTG CAACAATTGGAACCAGCGGACAATGTTGTTTACGTTTTGGTGATGTGTCACACTCG TGAACTGGCTTTCCAAATCAGCAAAGAGTACGAGAGGTTCAGTAAATATATGCCC AGTGTCAAGGTGGGCGTCTTTTTCGGAGGAATGCCTATTGCTAACGATGAAGAAG TATTGAAAAACAAATGTCCACACATTGTTGTGGGGACGCCTGGGCGTATTTTGGC GCTTGTCAAGTCTAGGAAGCTAGTCCTCAAGAACCTGAAACACTTCATTCTTGATG AGTGCGATAAAATGTTAGAACTGTTGGATATGAGGAGAGACGTCCAGGAAATCTA CAGAAACACCCCTCACACCAAGCAAGTGATGATGTTCAGTGCCACACTCAGCAAA GAAATCAGGCCGGTGTGCAAGAAATTCATGCAAGATCCAATGGAGGTGTATGTAG ACGATGAAGCCAAATTGACGTTGCACGGATTACAACAGCATTACGTTAAACTCAA AGAAAATGAAAAGAATAAAAAATTATTTGAGTTGCTCGATGTTCTCGAATTTAAT CAGGTGGTCATTTTTGTGAAGTCCGTTCAAAGGTGTGTGGCTTTGGCACAGTTGCT GACTGAACAGAATTTCCCAGCCATAGGAATTCACAGAGGAATGGACCAGAAAGA GAGGTTGTCTCGGTATGAGCAGTTCAAAGATTTCCAGAAGAGAATATTGGTAGCT ACGAATCTCTTTGGGCGTGGCATGGACATTGAAAGGGTCAACATTGTCTTCAACT ATGATATGCCAGAGGACTCCGACACCTACTTGCATCG
LD010	SEQ ID NO: 35 CTCTCAAGGA TTCKYTRCAR ATGTC	SEQ ID NO: 36 CGCCATTGGG CRATGGTYTC KCC	SEQ ID NO: 11 CTCTCAAGGATTCGTTGCAGATGTCTTTGAGCTTGTTGCCCCCGAATGCCTTGATA GGGTTGATTACCTTTGGGAAGATGGTCCAAGTGCACGAACTAGGTACCGAGGGCT GCAGCAAATCTTACGTTTTCCGAGGGACGAAAGACCTCACAGCTAAGCAAGTTCA AGAGATGTTGGAAGTGGGCAGAGCCGCAGTAAGTGCTCAACCTGCTCCTCAACAA CCAGGACAACCCATGAGGCCTGGAGCACTCCAGCAAGCTCCTACGCCACCAGGA AGCAGGTTCCTTCAACCCATCTCGAAATGCGACATGAACCTCACTGATCTTATTGG AGAGTTGCAAAGAGACCCATGGCCTGTCCACCAAGGCAAATGCGCCCTTAGATCG ACCGGGACAGCTTTATCGATAGCCATTGGGTTGTTGGAGTGCACATACGCCAATA CTGGTGCCAGGGTCATGCTATTCGTTGGAGGACCTTGCTCTCAAGGCCCTGGTCAA GTCTTGAATGATGATCTGAAGCAACCTATCAGATCTCACCACGACATCCAAAAAG ACAATGCCAAATACATGAAGAAAGCAATCAAGCACTATGATAATTTAGCGATGA GAGCAGCAACGAATGGCCACTGCGTTGACATATATTCATGCGCTTTGGATCAGAC

			AGGATTGATGGAGATGAAACAGTGTTGTAATTCAACAGGGGGACATATGGTCATG GGCGACTCGTTCAATTCTTCCCTGTTCAAGCAAACGTTCCAGCGCATATTTTCGAA AGATCAGAAAAAACGAGCTGAAGATGGCATTTAATGGTACTCTGGAGGGTCAAGT GTTCCAGGGAGTTGAAAATTCAAGGCGGTATTGGATCTTGTGTTTCGTTGAATGTG AAGAATCCTTTGGTTTCCGACACCGAAATAGGAATGGGTAACACGGTCCAGTGGA AAATGTGTACGGTAACTCCAAGTACTACCATGGCCTTGTTCTTCGAGGTCGTCAAC CAACATTCCGCTCCCATACCTCAAGGGGGAAGGGGCTGCATACAGTTCATCACGC AATATCAGCATGCTAGTGGCCAGAAGAGGATCCGAGTAACGACAGTTGCTAGAA ACTGGGCCGATGCTTCCGCTAATATACATCATGTCAGTGCTGGATTCGATCAGGA GGCAGCCGCAGTGATAATGGCGAGGATGGCAGTTTACAGAGCGGAATCAGACGA TAGCCCTGATGTTTTGAGATGGGTCGATAGGATGTTGATACGTCTGTGCCAGAAA TTCGGCGAATATAACAAGGACGACCCGAATTCGTTCCGCTTGGGCGAAAACTTCA GCCTCTACCCGCAGTTCATGTACCATTTGAGAAGGTCACAGTTCCTGCAGGTGTTT AACAATTCTCCCCGACGAAACGTCCTTCTACAGGCACATGCTTATGCGCGAAGACC TCACGCAGTCGCTGATCATGATCCAGCCGATACTCTACAGCTACAGTTTCAATGG ACCACCAGAACCTGTGCTTTTGGATACGAGTTCCATCCAACCCGATAGAATTCTGC TCATGGACACGTTCTTCCAGATTCTGATATTCCATGGCGAAACCATCGCCCAATGG CG
LD011	SEQ ID NO: 37 CCCACTTTCA AGTGYGTRYT RGTCGG	SEQ ID NO: 38 GTGGAAGCAG GGCWGGCAT KGCRAC	SEQ ID NO: 13 GTGGAAGCAGGGCTGGCATGGCGACAAATTCTAGATTGGGATCACCAATAAGCTT CCTAGCTAGCCATAGGAAAGGCTTCTCAAAGTTGTAGTTAGATTTGGCAGAGATA TCATAGTACTGCAAATTCTTCTTCCTATGAAAGACAATACTTTTCGCTTTTACTTTT CTGTCTTTGATGTCAACCTTGTTCCCGCAAAGTACTATCGGGATATTTTCACAGAC TCTGACAAGATCTCTGTGCCAATTTGGTACATTCTTGTATGTAACTCTGGAAGTTA CATCAAACATGATAATAGCACACACTGTCCCTGAATGTAATATCCATCACGGAGACC ACCAAACTTCTCCTGACCGGCAGTGTCCCATACATTGAACCGAATAGGGCCCCTG TTTGTATGGAAGACCAGAGGATGGACTTCAACTCCCAAAGTAGCTACATATCTTTT TTCAAATTCACCAGTCATATGACGTTTCACAAATGTCGTTTTTCCAGTACCTCCAT CTCCGACCAACACACACTTGAAAGTGGG
LD014	SEQ ID NO: 39 CGCAGATCAA RCAYATGATG GC	SEQ ID NO: 40 CGGATCTCGG GCASMARYTG C	SEQ ID NO: 15 CGCAGATCAAGCATATGATGGCTTTCATTGAACAAGAGGCAAACGAAAAGGCAG AAGAAATCGATGCCAAGGCCGAGGAAGAATTTAATATTGAAAAGGGGCGCCTTG TTCAGCAACAACGTCTCAAGATTATGGAATATTATGAGAAGAAAGAGAAACAGG TCGAACTCCAGAAAAAAATCCAATCGTCTAACATGTTGAATCAGGCTCGATTGAA AGTATTGAAGGTTAGGGAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAA

			CGACTTGGTCAGGTCACAAACGACCAGGGAAAATATTCCCAAATCCTGGAAAGCC TCATTTTGCAGGGATTATATCAGCTTTTTGAGAAAGATGTTACCATTCGAGTTCGG CCCCAGGACCGAGAACTGGTCAAATCCATCATTCCCACCGTCACGAACAAGTATA AAGATGCCACCGGTAAGGACATCCATCTGAAAATTGATGACGAAATCCATCTGTC CCAAGAAACCACCGGGGGAATCGACCTGCTGGCGCAGAAAAACAAAATCAAGAT CAGCAATACTATGGAGGCTCGTCTGGAGCTGATTTCGCAGCAACTTCTGCCCGAG ATCCG
LD014_F1			SEQ ID NO: 159 TCTAGAATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACG TTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGCCCG GG
LD014_F2			SEQ ID NO: 160 TCTAGAAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCA GGTCACAAACGCCCGGG
LD014_C1			SEQ ID NO: 161 TCTAGAATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACG TTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGATGT TGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTCGTACCGT ACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGATGTTGAATCAGG CTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTCGTACCGTACTAGAGGA GGCGCGTAAACGACTTGGTCAGGTCACAAACGCCCGGG
LD014_C2			SEQ ID NO: 162 TCTAGAAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCA GGTCACAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTT GGTCAGGTCACAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAA CGACTTGGTCAGGTCACAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGCGC GTAAACGACTTGGTCAGGTCACAAACGAAGATCACGTTCGTACCGTACTAGAGGA GGCGCGTAAACGACTTGGTCAGGTCACAAACGCCCGGG
LD015	SEQ ID NO: 41 CGCCATCCRT CGCTSTTCAA GGC	SEQ ID NO: 42 GCAATGGCAT CAAKYTCRTC RATG	SEQ ID NO: 17 GCAATGGCATCAAGTTCATCGATGAAGATGATCGCCGGAGAGTTTTTGTCAGCTT CTTCAAAAGCTTTGCGCAAGTTACTCTCAGACTCGCCAGCGAGTTTGCTCATGATC TCCGGCCCCGTTTATCAAGAAGAAGAACGCCCCCAGTCTCATTAGCCACCGGCGCGAG CAATCAGGGTCTTACCCGTACCAGGGGGACCATACAGCAGTATACCCCTAGGGGG CTTCACGCCGATAGCCTTGAAGAGCGATGGATGGCG

LD016	SEQ ID NO: 43 GACTGTGTCT GGTGTRAACG GWCC	SEQ ID NO: 44 GGAATAGGAT GGGTRATRTC GTCG	SEQ ID NO: 19 GGAATAGGATGGGTAATGTCGTCGTTGGGCATAGTCAATATAGGAATCTGGGTGA TGGATCCGTTACGTCCTTCAACACGGCCGGCACGTTCATAGATGGTAGCTAAATC GGTGTACATGTAACCTGGGAAACCACGACCAGGCACCTCTTCTCTGGCAGCA GATACCTCACGCAAAGCTTCTGCATACGAAGACATATCTGTCAAGATGACCAAGA CGTGCTTCTCACATTGGTAAGCCAAGAATTCGGCAGCTGTCAAAGCCAGACGAGG TGTAATAATTCTTTCAATGGTAGGATCGTTGGCCAAATTCAAGAACAGGCAGACA TTCTCCATAGAACCGTTCTCTTCGAAATCCTGTTTGAAGAACCTAGCTGTTTCCAT GTTAACACCCATAGCAGCGAAAACAATAGCAAAGTTATCTTCATGATCATCAAGT ACAGATTTACCAGGAATCTTGACTAAACCAGCCTGTCTACAGATCTGGGCAGCAA TTTCATTGTGAGGCAGACCAGCTGCAGAGAAAATGGGGATCTTCTGACCACGAGC AATGGAGTTCATCACGTCAATAGCTGTAATACCCGTCTGGATCATTTCCTCAGGAT AGATACGGGACCACGGATTGATTGGTTGACCCTGGATGTCCAAGAAGTCTTCAGC CAAAATTGGGGGACCTTTGTCGATGGGTTTTCCTGATCCATTGAAAACACGTCCCA ACATATCTTCAGAAACAGGAGTCCTCAAAATATCTCCTGTGAATTCACAAGCGGT GTTTTTGGCGTCGATTCCTGATGTGCCCTCGAACACTTGAACCACAGCTTTTGACC CACTGACTTCCAGAACTTGTCCCGAACGTATAGTGCCATCAGCCAGTTTGAGTTGT ACGATTTCATTGTACTTGGGGAACTTAACATCTTCGAGGATTACCAGAGGACCGTT CACACCAGACACAGTC
LD018	SEQ ID NO: 45 CACCTGGTTC AAGRATGGVC ARMG	SEQ ID NO: 46 GTGCATCGGT ACCAHSCHGC RTC	SEQ ID NO: 21 CACCTGGTTCAAGGATGGGCAGCGGATAACGGAGTCGCAGAAATACGAGAGCAC CTTCTCGAACAACCAAGCCTCCTTGAGGGTAAAACAAGCCCAGTCTGAGGACTCG GGACACTACACTTTGTTGGCGGAGAACCCTCAAGGCTGCATAGTGTCATCTGCTT ACTTAGCCATAGAACCGGTAACCACCCAGGAAGGGTTGATCCACGAGTCCACCTT CAAGCAGCAACAGACCGAAATGGAGCAAATCGACACCAGCAAGACCTTGGCGCC TAACTTCGTCAGGGTTTGCGGGGATAGAGACGTGACCGAGGGCAAGATGACCCGC TTCGACTGTCGCGTCACTGGTCGTCCTTATCCAGACGTGACATGGTACATAAACGG TCGACAAGTCACCGACGACCACAACCACAAGATTTTGGTTAACGAATCCGGAAAC CATGCCCTGATGATCACCACCGTGAGCAGGAACGACTCAGGAGTAGTGACCTGCG TCGCCAGGAACAAGACGGGAGAAACCTCCTTCCAGTGCAACCTTAACGTCATCGA AAAGGAACAGGTAGTCGCGCCCAAGTTCGTGGAGAGATTTACCACAGTCAACGTG GCAGAAGGAGAACCAGTGTCTCTGCGCGCTAGAGCTGTTGGCACCGCCGGTGCCGC GAATCACTTGGCAGAGGACGGGGCGCCCCTAGCCAGCGGGGCCCGACGTTCGCAT CGCGATTGACGGTGGAGCCTCTACTTTGAATATCTCGAGGGCCAAGGCCTCGGAT GCTGCATGGTACCGATGCAC

LD027	SEQ ID NO: 47 CCATGGTGGC GAYAARCCVT AC	SEQ ID NO: 48 GGTATAGATG AARCARTCDC CVACCCA	SEQ ID NO: 23 CCATGGTGGCGATAAACCATACTTGATATCGGGAGCAGACGATCGGTTGGTTAAA ATCTGGGACTATCAAAACAAAACGTGTGTCCAAACCTTGGAAGGACACGCCCAAA ACGTAACCGCGGTTTGTTTCCACCCTGAACTACCTGTGGCTCTCACAGGCAGCGA AGATGGTACCGTTAGAGTTTGGCATACGAATACACACAGATTAGAGAATTGTTTG AATTATGGGTTCGAGAGAGTGTGGACCATTTGTTGCTTGAAGGGTTCGAATAATG TTTCTCTGGGGTATGACGAGGGCAGTATATTAGTGAAAGTTGGAAGAGAAGAACC GGCAGTTAGTATGGATGCCAGTGGCGGTAAAATAATTTGGGCAAGGCACTCGGAA TTACAACAAGCTAATTTGAAGGCGCTGCCAGAAGGTGGAGAAATAAGAGATGGG GAGCGTTTACCTGTCTCTGTAAAAGATATGGGAGCATGTGAAATATACCCTCAAA CAATCCAACATAATCCGAATGGAAGATTCGTTGTAGTATGCGGAGACGGCGAATA TATCATTTACACAGCGATGGCTCTACGGAACAAGGCTTTTGGAAGCGCTCAAGAG TTTGTCTGGGCTCAGGACTCCAGCGAGTATGCCATTCGCGAGTCTGGTTCCACAAT TCGGATATTCAAAAACTTCAAAGAAAGGAAGAACTTCAAGTCGGATTTCAGCGCG GAAGGAATCTACGGGGGTTTTCTCTTGGGGATTAAATCGGTGTCCGGTTTAACGTT TTACGATTGGGAAACTTTGGACTTGGTGAGACGGATTGAAATACAACCGAGGGCG GTTTATTGGTCTGACAGTGGAAAATTAGTCTGTCTCGCAACGGAGGACAGCTACT TCATCCTTTCTTATGATTCGGAGCAAGTTCAGAAGGCCAGGGAGAACAATCAAGT CGCAGAGGATGGCGTAGAGGCCGCTTTCGATGTGTTGGGGGAAATGAACGAGTCT GTCCGAACAGGTCTTTGGGTCGGAGACTGTTTCATCTATACC

Table 2-PC

Target ID	**Primer Forward 5' → 3'**	**Primer Reverse 5' → 3'**	**cDNA Sequence (sense strand) 5' → 3'**
PC001	SEQ ID NO: 261 CATTTGAAGC GTTTWRMYG CYCC	SEQ ID NO: 262 CTTCGTGCCC TTGCCRATKA TRAABACG	SEQ ID NO: 247 CATTTGAAGCGTTTAGCTGCTCCCAAAGCATGGATGTTGGACAAATTGGGGGGTGTC TTCGCCCCTCGTCCATCCACCGGGCCTCACAAGTTGCGCGAATCCCTGCCTTTAGTGA TTTTCCTTCGTAACAGGCTGAAGTATGCCCTTACAAACAGTGAAGTCACTAAAATTGT CATGCAAAGGTTGATCAAAGTTGATGGTAAAGTGAGGACTGATTCTAATTACCCTGC TGGTTTCATGGATGTCATTACTATTGAGAAGACTGGTGAATTTTTCCGTCTGATCTAT GATGTTAAAGGAAGATTTGCTGTGCACCGTATTACAGCTGAAGAGGCAAAATACAAG TTGTGTAAAGTAAGGAGAGTCCAAACTGGTCCCAAAGGAATCCCATTTTTGGTAACA CATGATGGCAGAACCATTCGTTACCCTGACCCCAACATCAAAGTGAATGACACAATT CAAATGGAAATTGCTACATCTAAAATTCTTGACTACATCAAATTTGAATCTGGCAACC

			TCTGCATGATCACGGGGAGG
PC003	SEQ ID NO: 263 TCGGTCTTCT CGAAGACNTA YGTKAC	SEQ ID NO: 264 CCCTGGTTCT TCTTVRRRTT CTTCCTC	SEQ ID NO: 249 CCCTAGACGTCCCTATGAAAAGGCCCGTCTGGATCAGGAATTGAAAATTATCGGCGC CTTTGGTTTACGAAACAAACGTGAAGTGTGGAGAGTAAAGTACACTTTGGCTAAAAT CCGTAAAGCTGCTCGTGAACTGCTCACCCTAGAAGAAAAAGAGCCTAAAAGATTGTT TGAAGGTAATGCACTTCTACGTCGTTTGGTGCGAATTGGTGTTCTGGATGAGAACAG GATGAAGCTTGATTATGTTTTGGGTCTGAAAATTGAAGATTTCTTGGAAAGAAGGCTC CAAACTCAGGTGTTCAAATCTGGTCTGGCAAAGTCAATTCATCATGCTAGAGTACTG ATTAGGCAGAGACACATCCGGGTGCGCAAGCAGGTGGTGAACATCCCCCTCGTTCATC GTGCGGCTGGACTCGCAGAAGCACACATCGACTTCTCCCTGAAGTCGCCCTTCGGGGGT GGCCGACCTGGCCGTGTCAA
PC005	SEQ ID NO: 265 TGCGATGCGG CAARAARAAG GTBTGG	SEQ ID NO: 266 TCCTGCTTCT TSGYRGCRAT WCGYTC	SEQ ID NO: 251 TGCGATGCGGCAAAAAGAAGGTGTGGTTGGATCCAAATGAAATCAACGAAATCGCC AACACCAACTCAAGACAAAACATCCGTAAGCTCATCAAGGATGGTCTTATCATCAAG AAGCCAGTGGCAGTACACTCTAGGGCCCGTGTACGCAAGAACACTGAAGCCAGAAG GAAGGGAAGGCATTGTGGATTTGGAAAGAGGAAGGGTACGGCAAATGCCCGTATGC CTCAAAAGGAACTGTGGGTGCAGCGCATGCGCGTCCTCAGGCGCCTCCTCAAAAGT ACAGGGAGGCCAAGAAAATCGACCGCCATCTTTACCACGCCCTGTACATGAAAGCGA AGGGTAACGTGTTCAGGAACAAGAGGGTCCTTATGGAGTACATCCACAAGAAGAAG GCAGAGAAGGCCAGGGCCAAGATGCTGTCTGACCAGGCTAACGCCAGGAGATTGAA GGTGAAGCAGGCCAGGGAACGTAGGGAAGAGCGTATCGCCACCAAGAAGCAGG
PC010	SEQ ID NO: 267 CTCTCAAGGA TTCKYTRCAR ATGTC	SEQ ID NO: 268 CGCCATTGGG CRATGGTYTC KCC	SEQ ID NO: 253 CTCTCAAGGATTCTTTGCAGATGTCGCTCAGCCTATTACCGCCCAACGCGTTGATTGG ATTGATCACGTTCGGAAAAATGGTGCAAGTCCACGAACTGGGTACCGAAGGCTGCAG CAAGTCGTACGTGTTCTGTGGAACGAAAGATCTCACCGCCAAGCAAGTCCAGGAGAT GTTGGGCATTGGAAAAGGGTCACCAAATCCCCAACAACAGCCAGGGCAACCTGGGC GGCCAGGGCAGAATCCCCAAGCTGCCCCTGTACCACCGGGGAGCAGATTCTTGCAGC CCGTGTCAAAATGCGACATGAACTTGACAGATCTGATCGGGGAGTTGCAGAAAGACC CTTGGCCCGTACATCAGGGCAAAAGACCTCTTAGATCCACAGGCGCAGCATTGTCCA TCGCTGTCGGCCTCTTAGAATGCACCTATCCGAATACGGGTGGCAGAATCATGATATT CTTAGGAGGACCATGCTCTCAGGGTCCCGGCCAGGTGTTGAACGACGATTTGAAGCA GCCCATCAGGTCCCATCATGACATACACAAAGACAATGCCAAGTACATGAAGAAGGGC TATCAAACATTACGATCACTTGGCAATGCGAGCTGCCACCAACAGCCATTGCATCGA

			CATTTACTCCTGCGCCCTGGATCAGACGGGACTGATGGAGATGAAGCAGTGCTGCAA
			TTCCACCGGAGGGCACATGGTCATGGGCGATTCCTTCAATTCCTCTCTATTCAAACAA
			ACCTTCCAGCGAGTGTTCTCAAAAGACCCGAAGAACGACCTCAAGATGGCGTTCAAC
			GCCACCTTGGAGGTGAAGTGTTCCAGGGAGTTAAAAGTCCAAGGGGGCATCGGCTCG
			TGCGTGTCCTTGAACGTTAAAAGCCCTCTGGTTTCCGATACGGAACTAGGCATGGGG
			AATACTGTGCAGTGGAAACTTTGCACGTTGGCGCCGAGCTCTACTGTGGCGCTGTTCT
			TCGAGGTGGTTAACCAGCATTCGGCGCCCATACCACAGGGAGGCAGGGGCTGCATCC
			AGCTCATCACCCAGTATCAGCACGCGAGCGGGCAAAGGAGGATCAGAGTGACCACG
			ATTGCTAGAAATTGGGCGGACGCTACTGCCAACATCCACCACATTAGCGCTGGCTTC
			GACCAAGAAGCGGCGGCAGTTGTGATGGCCCGAATGGCCGGTTACAAGGCGGAATC
			GGACGAGACTCCCGACGTGCTCAGATGGGTGGACAGGATGTTGATCAGGCTGTGCCA
			GAAGTTCGGAGAGTACAATAAAGACGATCCGAATTCGTTCAGGTTGGGGGAGAACTT
			CAGTCTGTATCCGCAGTTCATGTACCATTTGAGACGGTCGCAGTTTCTGCAGGTGTTC
			AATAATTCTCCTGATGAAACGTCGTTTTATAGGCACATGCTGATGCGTGAGGATTTGA
			CTCAGTCTTTGATCATGATCCAGCCGATTTTGTACAGTTACAGCTTCAACGGGCCGCC
			CGAGCCTGTGTTGTTGGACACAAGCTCTATTCAGCCGGATAGAATCCTGCTCATGGAC
			ACTTTCTTCCAGATACTCATTTTCCATGGAGACCATTGCCCAATGGCG
PC014	SEQ ID NO: 269	SEQ ID NO: 270	SEQ ID NO: 255
	CGCAGATCAA	CGGATCTCGG	CTGATGTTCAAAAACAAATCAAACACATGATGGCTTTCATTGAACAAGAAGCCAATG
	RCAYATGATG	GCASMARYT	AGAAAGCAGAAGAAATTGATGCCAAGGCAGAGGAGGAATTCAACATTGAAAAAGGG
	GC	GC	CGTTTGGTCCAGCAACAGAGACTCAAGATCATGGAGTACTACGAGAAAAAGGAGAA
			GCAAGTCGAACTTCAAAAGAAAATTCAGTCCTCTAATATGTTGAATCAGGCTCGTTTG
			AAGGTGCTGAAAGTGAGAGAGGACCATGTCAGAGCAGTCCTGGAGGATGCTCGTAA
			AAGTCTTGGTGAAGTAACCAAAGACCAAGGAAAATACTCCCAAATTTTGGAGAGCCT
			AATCCTACAAGGACTGTTCCAGCTGTTCGAGAAGGAGGTGACGGTCCGCGTGAGACC
			GCAAGACAGGGACCTGGTCAGGTCCATCCTGCCCAACGTCGCTGCCAAATACAAGGA
			CGCCACCGGCAAAGACATCCTACTCAAGGTGGACGATGAGTCGCACCTGTCTCAGGA
			GATCACCGGAGGCGTCGATTTGCTCGCTCAGAAGAACAAGATCAAGATCAGCAACAC
			GATGGAGGCTAGGTTGGATCTGATCGCTCA
PC016	SEQ ID NO: 271	SEQ ID NO: 272	SEQ ID NO: 257
	GACTGTGTCT	GGAATAGGA	GGAATAGGATGGGTGATGTCGTCGTTGGGCATAGTCAAGATGGGGATCTGCGTGATG
	GGTGTRAACG	TGGGTRATRT	GAGCCGTTGCGGCCCTCCACACGACCGGCGCGCTCGTAAATGGTGGCCAGATCGGTG
	GWCC	CGTCG	TACATGTAACCGGGGGAAACCCCTACGGCCGGGCACTTCTTCTCGAGCGGCAGACACC
			TCACGCAACGCCTCCGCGTACGACGACATGTCGGTCAAGATGACCAGCACGTGCTTC
			TCGCACTGGTAGGCCAAGAATTCGGCGGCCGTCAGAGCCAAACGCGGCGTGATGATG

			CGCTCGATGGTCGGATCGTTGGCCAAGTTCAAGAACAGACACACGTTCTCCATCGAG CCGTTCTCTTCGAAGTCCTGCTTGAAGAACCTGGCAGTTTCCATGTTGACACCCATAG CAGCAAACACAATAGCAAAGTTGTCTTCATGGTCATCCAGCACAGACTTGCCAGGTA CTTTGACCAAGCCAGCCTGCCTACAAATCTGGGCTGCAATCTCATTGTGGGGCAGCCC AGCGGCGGAGAAGATCGGAATCTTCTGCCCTCTGGCGATAGAGTTCATCACGTCGAT GGCCGTGATCCCAGTCTGGATCATTTCCTCGGGATAAATACGCGACCACGGGTTGAT CGGCTGTCCTTGGATGTCGAGGTAGTCCTCAGCCAGGATCGGGGGACCTTTATCAAT GGGTTTTCCTGATCCATTGAAGACACGTCCCAGCATATCTTCTGATACTGGAGTTCTT AGAATATCTCCAGTGAACTCACACACCGTGTTCTTAGCATCAATACCTGATGTGCCTT CAAATACCTGAACAACTGCCTTTGATCCACTGACTTCCAAAACTTGTCCAGATCGTAG AGTTCCATCTGCCAATTTGAGCTGGACAATTTCATTGAATTTTGGAAACTTGACATCC TCAAGAATGACCAGTGGTCCGTTCACACCAGACACAGTC
PC027	SEQ ID NO: 273 GGGCCAAGCA CWSYGAAATR CAG	SEQ ID NO: 274 TGTGCCACCC TAGTRCGRTG YTC	SEQ ID NO: 259 GGGCCAAGCACAGTGAAATACAGCAAGCTAACTTGAAAGCACTACCAGAAGGAGCT GAAATCAGAGATGGAGAACGTTTGCCAGTCACAGTAAAGGACATGGGAGCATGCGA GATTTACCCACAAACAATCCAACACAACCCCAATGGGCGGTTTGTAGTGGTTTGTGG TGATGGAGAATACATAATATACACGGCTATGGCCCTTCGTAACAAAGCATTTGGTAG CGCTCAAGAATTTGTATGGGCACAGGACTCCAGTGAATATGCCATCCGCGAATCCGG ATCCACCATTCGAATCTTCAAGAATTTCAAAGAAAAAAAGAATTTCAAGTCCGACTT TGGTGCCGAAGGAATCTATGGTGGTTTTCTCTTGGGTGTGAAATCAGTGTCTGGCTTA GCTTTCTATGACTGGGAAACGCTTGAGTTAGTAAGGCGCATTGAAATACAGCCTAGA GCTATCTACTGGTCAGATAGTGGCAAGTTGGTATGCCTTGCTACCGAAGATAGCTATT TCATATTGTCCTATGACTCTGACCAAGTCCAGAAAGCTAGAGATAACAACCAAGTTG CCGAAGATGGAGTGGAGGCTGCCTTTGATGTCCTAGGTGAAATAAATGAATCCGTAA GAACAGGTCTTTGGGTAGGAGACTGCTTCATTTACACAAACGCAGTCAACCGTATCA ACTACTTTGTGGGTGGTGAATTGGTAACTATTGCACATCTGGACCGTCCTCTATATGT CCTGGGCTATGTACCTAGAGATGACAGGTTATACTTGGTTGATAAAGAGTTAGGAGT AGTCAGCTATCAATTGCTATTATCTGTACTCGAATATCAGACTGCAGTCATGCGACGA GACTTCCCAACGGCTGATCGAGTATTGCCTTCAATTCCAAAAGAACATCGCACTAGG GTGGCACA

Table 2-EV

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'

EV005	SEQ ID NO: 523 TGCGATGCGG CAARAARAAG GTBTGG	SEQ ID NO: 524 TCCTGCTTCT TSGYRGCRAT WCGYTC	SEQ ID NO: 513 TGCGATGCGGCAAGAAGAAGGTTTGGCTGGATCCTAATGAAATAACTGAAATTG CTAATACAAACTCTAGACAAAACATCCGCAAACTGATTAAAGATGGTCTTATTA TTAAAAAGCCTGTCGCGGTGCATTCTCGTGCACGTGTACGCAAAAATACTGAAG CCCGCAGGAAAGGTCGTCATTGTGGATTTGGTAAAAGGAAAGGAACTGCAAAT GCTAGGATGCCCAGAAAGGAATTATGGATTCAACGTATGAGAGTTCTCAGAAGG TTATTGAAGAAATATAGGGAAGCTAAGAAAATTGATAGGCATTTATACCATGCT TTATATATGAAAGCTAAGGGAAATGTATTCAAGAATAAGAGAGTAATGATGGAC TATATCCATAAAAAGAAGGCGGAGAAAGCACGTACAAAGATGCTCAATGATCA AGCTGATGCAAGGAGGCTGAAAGTCAAAGAGGCACGTAAGCGACGTGAAGAGC GTATCGCTACGAAGAAGCAGGA
EV009	SEQ ID NO: 525 GGGCCGTGGT CAGAAYATY WAYAAC	SEQ ID NO: 526 GCAGCCCACG CYYTGCACTC	SEQ ID NO: 515 CCAACTCTCGATCCAAGCATTCCAAAATACAGGACTGAAGAATCTATAATAGGA ACAAACCCAGGAATGGGTTTTAGGCCAATGCCCGACACAACGAAGAAAGTAC CCTGATTTGGTTACAGGGTTCTAATAAAACAAACTACGAAAAATGGAAAGGAAA TCTCCTCTCATATTTAGACAAGTATTACACTCCCGGAAAAATAGAAAAGGGAAA TATTCCAGTAAAGCGCTGTTCATACGGAGAAAAATTGATTAGGGGACAAGTATG TGATGTAGATGTGAGGAAATGGGAGCCGTGCACACCCCGGAAAATCATTTTGATTA CCTCAGAAATGCGCCTTGTATATTTCTGAAGCTGAACAGGATATATGGATGGGA ACCGGAGTACTACAACGATCCAAATGATCTTCCAGATGATATGCCGCAGCAGTT GAAGGACCATATACGTTATAATATCACCAATCCAGTGGAGAGAAATACCGTCTG GGTAACATGCGCAGGTGAAAATCCGGCAGACGTGGAGTACTTGGGCCCTGTGAA GTATTACCCATCTTTCCAGGGATTCCCCGGTTACTATTTTCCATATTTGAATTCTG AAGGGTACCTAAGTCCATTATTGGCGGTACAATTCAAGAGACCGGTGTCTGGTA TTGTTATAAATATCGAGTGCAAAGCGTGGGCTGC
EV010	SEQ ID NO: 527 CGGCTGACGT GGAAYGTKTG GCC	SEQ ID NO: 528 CGGCGTATTC TCCRAAYTTC TGGC	SEQ ID NO: 517 CTGGCGGCCACATGGTCATGGGTGATTCATTTAACTCTTCACTTTCAAACAAAC ATTTCAACGAGTATTTTCGAAAGATTCCAATGGAGACTTGAAGATGTCCTTCAAC GCCATATTAGAAGTGAAGTGTTCTAGAGAACTTAAAGTACAAGGAGGTATAGGT CCTTGTGTCTCTCTAAATGTCAAAAATCCTCTTGTTTCTGATTTAGAAATAGGCA TGGGTAACACAGTTCAGTGGAAACTGTGTAGCTTAAGTCCAAGCACTACGGTTG CCTTATTTTTCGAAGTTGTTAATCAGCATGCAGCACCCATTCCTCAAGGGGGACG TGGATGCATTCAGTTTATTACTCAATATCAGCATTCAAGTGGTCAGAAAAAAAT AAGGGTAACTACAATAGCAAGAAATTGGGCGGATGCCACTGCAAATATTCACCA TATTAGCGCTGGCTTTGACGAACAAACTGCGGCTGTTTTAATGGCGAGGATCGC

			TGTATATAGAGCAGAAACTGATGAGAGTTCAGATGTTCTCAGATGGGTTGACAG AATGTTGATACGATTGTGTCAGAAATTTGGAGAAATATAACAAAGATGACACCAA CAGCTTCAGGCTCAGTGAAAACTTCAGCTTATATCCACACAGTTTATGTATCATCTA CGTCGTTCCCAATTTCTACAAGTGTTCAATAATTCACCAGATGAAACTTCATTCT ATAGGCACATGTTGATGAGGGAAGATCGCAATCAG
EV015	SEQ ID NO: 529 CGCTGTCGCA RGCRAARATG G	SEQ ID NO: 530 CGATCAAAGC GWCCRAAVC GACG	SEQ ID NO: 519 CGCCATCCGTCGCTGTTCAAGGCGATCGGCGTTAAGCCTCCAAGGGGTATTCTCC TTTACGGGCCTCCCGGCACGGGGAAAACGCTGATCGCCAGGGCCGTTGCCAACG AAACTGGTGCGTTCTTCTTCCTCATCAATGGGCCCGAGATTATGAGCAAGCTGGC CGGAGAATCCGAGAGCAATCTTAGAAAGGCTTTGAAGAGGCTGATAAAAACTC TCCTGCAATCATCTTTATCGACGAATTAGACGCAATCGCTCCCAAGCGCGAGAA GACTCATGGTGAGGTAGAGAGACGCATCGTCTCCCAACTGTTGACTTTGATGGA CGGCATGAAGAAAAGTTCCCATGTGATCGTGATGGCGGCCACGAACAGGCCCA ATTCCATCGACCCTGCACTCAGACGTTTCGGCCGATTCGACAGAGAGATCGACA TCGGTATCCCCGACGCTACTGGAAGATTAGAAGTACTCAGAATACACACCAAAA ACATGAAATTGGCTGACGATGTAGATTTGGAACAGATTGCCGCAGAGACTCACG GTCATGTAGGTGCTGACTTGGCTTCTTTGTGCTCAGAGGCTGCCTTGCAACAAAT TAGAGAAAAAAATGGACCTCATCGACTTAGATGATGAGCAGATCGATGCCGAAGT CCTAAATTCTCTGGCAGTTACCATGGAGAACTTCCGTTACGCCATGTCTAAGAGC AGTCCGAGCGCTTTGCGCGAAACCGTCGT
EV016	SEQ ID NO: 531 GTTCACCGGC GAYATYCTGC G	SEQ ID NO: 532 CGGCATAGTC AGAATSGGRA TCTG	SEQ ID NO: 521 GACTGTGTCTGGTGTGAACGGACCGTTGGTGATCCTTGATAGTGTTAAGTTTCCA AAATTTAACGAAATTGTACAGCTCAAGTTATCAGATGGAACAGTTAGGTCTGGA CAAGTTTTGGAAGTCAGTGGACAGAAGGCGGTTGTCCAAGTTTTTGAAGGCACC TCCGGAATTGATGCTAAAAAACACTTTATGTGAATTTACAGGAGATATCTTAAGA ACTCCAGTGTCTGAAGATATGTTGGGTCGTGTGTTTAATGGATCTGGAAAGCCTA TCGATAAAGGGCCGCCAATCTTAGCTGAAGATTTTTCTTGACATTCAAGGTCAAC CTATAAATCCTTGGTCTCGTATCTATCCAGAAGAAATGATCCAGACTGGTATTTC TGCGATTGATGTGATGAATTCCATTGCCAGAGGACAAAAGATTCCAATTTTCTCT GCAGCTGGTTTACCCCACAATGAAATCGCTGCTCAAATCTGTAGACAAGCTGGT CTTGTCAAAATCCCAGGGAAATCTGTCTTAGATGATCATGAAGACAACTTTGCT ATCGTTTTCGCCGCTATGGGTGTCAATATGGAAACAGCCAGATTCTTCAAGCAA GATTTTGAAGAGAATGGCTCTATGGAAAATGTGTGCCTATTTTTGAACTTGGCCA ATGATCCTACCATTGAAAGAATTATAACACCCCGTTTGACTTTAACAGCGGCTG AATTTATGGCATATCAATGTGAGAAGCATGTGTTAGTCATATTGACTGACATGTC

			ATCTTATGCTGAGGCTTTGCGTGAGGTATCTGCTGCT

Table 2-AG

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
AG001	SEQ ID NO: 611 CATTTGAAGC GTTTWRMYGC YCC	SEQ ID NO: 612 CGCTTGTCCC GCTCCTCNGC RAT	SEQ ID NO: 601 CATTTGAAGCGTTTTGCTGCCCCCAAAGCATGGATGTTGGACAAATTGGGGGGTGTG TTCGCCCCCAGGCCCTCCACCGGGCCACACAAGCTCAGGGAGTCCCTTCCATTAGTG ATTTTCTTGCGTAACAGGTTGAAGTACGCCCTGACAAACTGTGAGGTGACCAAGATC GTTATGCAGAGACTTATTAAGGTCGACGGCAAAGTCAGGACTGATCCTAACTATCCT GCTGGATTCATGGATGTGATCACCATTGAAAAAACTGGTGAATTCTTCCGTTTGATCT ATGATGTTAAGGGAAGATTCACTATTCACAGGATCACTGCTGAAGAAGCAAAATACA AATTGTGCAAAGTCCGCAAGGTGCAAACCGGACCAAAAGGTATTCCATTCTTGGTCA CCCACGATGGTAGGACCATTAGGTACCCTGACCCAATGATCAAGGTAAACGACACCA TCCAACTGGAAATCGCCACCTCAAAGATCCTGGACTTTATCAAATTCGAATCCGGCA ACTTGTGCATGATCACCGGAGGCAGGAATTTGGGTAGAGTGGGAACGGTAGTGAAC AGGGAAAGGCATCCGGGATCATTCGATATTGTCCACATTAGGGACGCTAATGATCAC GTGTTCGCCACTAGATTAAACAACGTATTCGTCATCGGTAAAGGAAGCAAAGCTTTC GTGTCTCTGCCAAGGGGCAAGGGAGTGAAACTGTCCATCGCTG
AG005	SEQ ID NO: 613 GGTCTGGTTG GATCCHAATG AAATCAAYGA	SEQ ID NO: 614 TCCTGCTTCT TSGYRGCRAT WCGYTC	SEQ ID NO: 603 GGTCTGGTTGGATCCAAATGAAATCAATGAGATTGCCAACACCAACTCGAGGCAAAA CATCCGTAAATTGATCAAGGATGGTTTGATCATTAAGAAACCGGTGGCAGTGCACTC TAGGGCTCGTGTCCGTAAAAACACAGAAGCTCGCAGGAAGGGAAGGCACTGCGGTT TCGGTAAGAGGAAAGGTACAGCGAACGCTCGTATGCCTCAAAAGGAACTATGGATC CAAAGGATGCGTGTCTTGAGGCGTCTCCTGAAAAAATACAGGGAAGCCAAAAAGAT CGACAGGCATCTGTACCACGCCCTGTACATGAAGGCCAAGGGTAACGTGTTCAAGAA CAAGAGAGTGTTGATGGAATACATCCACAAGAAGAAGGCTGAGAAGGCCCGTGCCA AGATGTTGGCCGACCAAGCTAACGCCAGAAGGCAAAAGGTGAAACAAGTCCCGTGA GAGGAGGGAAGAGCGTATCGCCGCGAAGAAGCAGGA
AG010	SEQ ID NO: 615 CTGGCGGCCA CATGSTBATG G	SEQ ID NO: 616 CGCCATTGGG CRATGGTYTC KCC	SEQ ID NO: 605 CTGGCGGCCACATGCTTATGGGAGACTCTTTCAATTCGTCGTTGTTCAAACAAACTTT CCAAAGGGTGTTCGCGAAGGACCAGAATGGACATTTGAAGATGGCTTTCAACGGTAC TTTGGAGGTGAAGTGCTCTAGGGAATTAAAAGTTCAAGGCGGTATTGGCTCATGCGT GTCGCTAAATGTAAAAAGTCCTTTGGTAGCGGACACGGAAATAGGCATGGGAAACA

			CCGTGCAATGGAAGATGTGCACCTTCAACCCTAGCACGACGATGGCGCTGTTTTTCG AGGTGGTCAATCAGCATTCGGCCCCCATTCCTCAAGGTGGTAGAGGATGTATACAGT TTATTACACAATATCAGCACTCGAGTGGCCAAAGGAGGATAAGGGTGACGACGATA GCGAGAAATTGGGCGGACGCATCGGCGAATATATTCACCACATCAGCGCGGGTTTCGAT CAGGAACGTGCCGCGGTGATTATGGCCCGGATGGCTGTTTATAGAGCGGAGACCGAT GAGAGTCCCGATGTTTTAAGATGGGTCGATCGGATGCTGATTCGTTTGTGTCAAAAG TTTGGAGAATATAACAAAGATGACCAGGCATCCTTCAGATTAGGAGAAAATTTTAGC TTATACCCGCAATTCATGTACCACTTAAGGCGATCCCAGTTTTTGCAAGTGTTCAACA ATTCACCTGACGAAACGTCGTTTTACAGGCATATGCTTATGAGGGAAGATTTGACAC AGTCCCTGATAATGATTCAGCCGATCTTGTACAGTTACAGTTTTAATGGTCCTCCGGA GCCCGTTTTGTTGGACACCAGCTCAATACAACCGGACAGAATTCTCTGCTTATGGACAC GTTTTTCCAGATATTGATTTTTCCATGGAGAAACCATTGCCCAATGGCG
AG014	SEQ ID NO: 617 CGCAGATCAA RCAYATGATG GC	SEQ ID NO: 618 GAACTTGCGG TTGABGTTSC GDCC	SEQ ID NO: 607 CGCAGATCAAGCATATGATGGCCTTCATTGAGCAAGAGGCTAATGAAAAGGCCGAG GAAATTGATGCCAAGGCGGAAGAAGAATTTAACATTGAAAAGGGCCGCCTTGTGCA ACAACAAAGATTGAAGATCATGGAATACTATGAGAAGAAGGAGAAGCAAGTCGAAC TACAAAAGAAAATTCAATCCTCCAACATGCTGAACCAAGCCCGTCTTAAGGTTCTGA AAGTCCGCGAAGATCATGTTAGAGCTGTATTGGATGAGGCTCGCAAGAAGCTTGGTG AAGTCACCAGGGATCAAGGCAAATATGCCCAGATTCTGGAATCTTTGATCCTTCAGG GACTCTACCAGCTTTTCGAGGCAAACGTGACCGTACGCGTCCGCCCACAAGACAGAA CCTTAGTCCAATCAGTGCTGCCAACCATCGCAACCAAATACCGTGACGTCACCGGCC GAGATGTACACCTGTCCATCGATGACGAAACTCAACTGTCCGAATCCGTAACCGGCG GAATCGAACTTTTGTGCAAACAAAACAAAATTAAGGTCTGCAACACCCTGGAGGCAC GTTTGGACCTGATTTCGCAACAGTTGGTTCCGCAAATCCGTAACGCCTTGTTCGGACG CAACATCAACCGCAAGTTC
AG016	SEQ ID NO: 619 GTGTCGGAGG ATATGYTGGG YCG	SEQ ID NO: 620 GGAATAGGA TGGGTRATRT CGTCG	SEQ ID NO: 609 GTGTCGGAGGATATGTTGGGCCGAGTGTTCAACGGATCAGGAAAACCCATTGACAAA GGTCCTCCAATCTTAGCCGAAGATTTCTTGGACATCCAAGGTCAACCCATCAACCCAT GGTCGCGTATCTACCCGGAAGAAATGATCCAGACCGGTATCTCCGCCATCGACGTGA TGAACTCCATCGCGCGTGGGCAAAAAATCCCCATTTCTCCGCGGCCGGTTTACCGC ACAACGAAATCGCCGCCCAAATCTGTAGACAGGCCGGTTTAGTCAAACTGCCGGGCA AATCGGTAATCGACGATCACGAGGACAATTTCGCCATCGTGTTCGCCGCCATGGGTG TCAACATGGAAACCGCCCCGTTCTTCAAGCAGGACTTCGAAGAAAACGGTTCCATGG AGAACGTGTGTCTCTTCTTGAATTTGGCCAACGATCCCACCATCGAGAGAATCATCA CGCCCCGTTTGGCTCTGACCGCCGCCGAATTTTTGGCTTATCAATGCGAGAAACACGT

			GCTGGTTATCTTAACTGATATGTCTTCTTACGCCGAGGCTTTGCGTGAAGTATCCGCC GCCAGAGAAGAAGTACCCGGACGTCGTGGGTTCCCCGGTTACATGTACACCGATTTG GCCACCATTTACGAAAGAGCCGGTCGCGTTGAGGGTAGAAACGGTTCCATCACCCAG ATTCCCATCTTGACTATGCCGAACGACGACATCACCCATCCTATTCC

Table 2-TC

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
TC001	SEQ ID NO: 803 GGCCCCAAGA AGCATTTGAA GCG	SEQ ID NO: 804 CGCTTGTCCC GCTCCTCNGC RAT	SEQ ID NO: 793 GGCCCCAAGAAGCATTTGAAGCGTCTCAATGCGCCCAAAGCATGGATGTTGGATA AACTGGGGGGTGTGTTTGCCCCTCGGCCTTCCACCGGCCCCCACAAGCTACGGGAG TCGCTACCTTTGGTTATCTTCCTGCGAAACAGGCTGAAGTATGCCTTGACCAACTC AGAAGTGACGAAGATTGTTATGCAAAGATTGATTAAAGTTGACGGAAAAGTTAGG ACAGACCCCAACTACCCCGCGGGTTTCATGGATGTTGTGACTATTGAGAAAACTGG GGAATTCTTCCGCTTGATTTATGATGTTAAGGGAAGGTTCACAATCCATCGCATTA CTGGAGAAGAGGCCAAATATAAATTGTGCAAAGTGAAGAAAGTACAGACAGGCC CCAAGGGCATTCCCTTCTTGGTGACCCGCGACGGACGCACTATCAGATACCCAGAC CCCATGATCAAAGTGAATGACACCATTCAATTGGAGATTGCCACTTCGAAAATTCT TGATTTTATCAAATTTGAGTCCGGTAATTTGTGTATGATTACTGGAGGTCGTAACTT GGGGCGTGTCGGTACAGTGGTGAGCCGAGAACGTCACCCAGGTTCCTTCGACATC GTTCATATTAAGGATGCAAATGGGCACACC
TC002	SEQ ID NO: 805 CAGGAGTTCC TGGARRMBAA RATMGA	SEQ ID NO: 806 GCAATGTCAT CCATCAKRTC RTGTAC	SEQ ID NO: 795 CAGGAGTTCCTGGAGGCTAAAATCGACCAAGAGATCCTCACAGCGAAGAAAAACG CGTCGAAAAACAAACGAGCGGCCATCCAGGCCATCAAGAGGAAGAAACGCTACG AAAAGCAGCTCCAGCAGATCGATGGCACCCTCAGCACCATCGAGATGCAGCGGGA GGCCCTCGAGGGGGCCAACACCAACACAGCCGTACTCAAAACGATGAAAAACGCA GCGGACGCCCTCAAAAATGCCCACCTCAACATGGATGTTGATGAGGTACATGACA TGATGGATGACATTGC
TC010	SEQ ID NO: 807 GCATTCTGCG CTGGGTCGAT CG	SEQ ID NO: 808 TGCCGGAAGT TCTCRTAYTC KGGC	SEQ ID NO: 797 AAAATTCGGCGAATACAACAAAGACGACCCTAACAGTTTCCGTTTGAGTGAAAAC TTCAGTCTCTATCCCCAATTCATGTACCATTTGCGCCGCTCCCAATTCCTCCAAGTT TTCAACAACTCCCCAGACGAGACCTCGTTCTACCGCCACATGCTGATGCGGGAGGA CCTCACCCAAAGTCTCATTATGATCCAGCCGATTTTGTACAGTTATAGTTTCAACG GCCCCCCTGAACCCGTCCTCCTCGACACTAGTTCCATTCAACCCGATCGGATCCTTC

			TCATGGACACATTTTTCCAAATTTTGATTTTCCACGGTGAGACAATCGCCCAATGG AGGAACCTCAAGTACCAGGACATGCCCGAATACGAGAACTTCCGGCA
TC014	SEQ ID NO: 809 GAGAAAGCCG ARGARATYGA TGC	SEQ ID NO: 810 GAACTTGCGG TTGABGTTSC GDCC	SEQ ID NO: 799 GAGAAAGCCGAAGAAATCGATGCGAAAGCTGAGGAGGAGTTTAACATTGAAAAA GGGCGCCTGGTCCAACAACAGCGCTTGAAGATCATGGAATATTACGAGAAGAAGG AGAAACCGGTGGAATTGCAGAAGAAAATTCAGTCGTCAAACATGCTGAACCAAGC CCGTTTGAAAGTATTAAAAGTGCGTGAAGACCACGTCCACAATGTGCTGGATGAC GCCCGCAAACGTCTGGGCGAAATCACCAATGACCAGGCGAGATATTCACAACTTT TGGAGTCTCTTATCCTCCAGAGTCTCTACCAGTACTTGGGAATCAGTGATGAGTTG TTTGAGAACAATATAGTGGTGAGAGTCAGGCAACAGGACAGGAGTATAATCCAGG GCATTCTCCCAGTTGTTGCGACGAAATACAGGGACGCCACTGGTAAAGACGTTCAT CTTAAAATCGACGATGAGAGCCACTTGCCATCCGAAACCACCGGAGGAGTGGTTT TGTATGCGCAAAAGGGTAAAATCAAGATTGACAACACCTTGGAGGCTCGTTTGGA TTTAATTGCACAGCAACTTGTGCCAGAAATTCGTACGGCCTTGTTTGGACGCAACA TCAACCGCAAGTTC
TC015	SEQ ID NO: 811 GGATGAACTA CAGCTBTTCC GHGG	SEQ ID NO: 812 CGATCAAAG CGWCCRAAV CGACG	SEQ ID NO: 801 GGATGAACTACAGCTGTTCCGTGGCGATACAGTGTTGCTGAAAGGGAAGCGGCGG AAAGAGACCGTCTGCATTGTGCTGGCCGACGAAAACTGCCCCGATGAGAAGATCC GGATGAACAGGATCGTCAGGAATAATCTACGGGTTAGGCTCTCTGACGTCGTCTGG ATCCAGCCCTGTCCCGACGTCAAATACGGGAAGAGGATCCACGTTTTGCCCATCGA TGACACGGTCGAAGGGCTCGTCGGAAATCTCTTCGAGGTGTACTTAAAACCATACT TCCTCGAAGCTTATCGACCAATCCACAAAGGCGACGTTTTCATCGTCCGTGGTGGC ATGCGAGCCGTTGAATTCAAAGTGGTGGAAACGGAACCGTCACCATATTGTATCGT CGCCCCCGATACCGTCATCCATTGTGACGGCGATCCGATCAAACGAGAAGAAGAG GAGGAAGCCTTGAACGCCGTCGGCTACGACGATATCGGCGGTTGTCGCAAACAAC TCGCACAAATCAAAGAAATGGTCGAATTACCTCTACGCCACCCGTCGCTCTTCAAG GCCATTGGCGTGAAACCACCACGTGGTATCCTCTTGTACGGACCTCCAGGTACCGG TAAAACTTTAATCGCACGTGCAGTGGCCAACGAAACCGGTGCTTTCTTCTTCTTAA TCAACGGTCCCGAAATTATGAGTAAATTAGCCGGCGAATCCGAAAGTAATCTAAG GAAAGCGTTCGAAGAAGCCGATAAAAACTCACCGGCTATTATTTTCATCGATGAAT TGGACGCGATTGCACCGAAACGTGAAAAAACCCACGGCGAAGTCGAACGCCGAAT TGTCTCGCAATTGTTAACACTGATGGACGGCATGAAGAAAAGCTCGCATGTTATCG TGATGGCGGCCACAAATCGCCCGAACTCAATCGATCCGGCTTTGCGTCGGTTCGGT CGCTTTGATCG

Table 2-MP

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
MP001	SEQ ID NO: 898 GGCCCCAAGAAGCATTTGAAGCG	SEQ ID NO: 899 CGCTTGTCCCGCTCCTCNGCRAT	SEQ ID NO: 888 GGCCCCAAGAAGCATTTGAAGCGTTTAAACGCACCCAAAGCATGGATGTTGGACAAA TCGGGGGGTGTCTTCGCTCCACGTCCAAGCACCGGTCCACACAAACTTCGTGAATCAC TACCGTTATTGATCTTCTTGCGTAATCGTTTGAAGTATGCACTTACTGGTGCCGAAGTC ACCAAGATTGTCATGCAAAGATTAATCAAGGTTGATGGCAAAGTCCGTACCGACCCT AATTATCCAGCCGGTTTTATGGATGTTATATCTATCCAAAAGACCAGTGAGCACTTTA GATTGATCTATGATGTGAAAGGTCGTTTCACCATCCACAGAATTACTCCTGAAGAAGC AAAATACAAGTTGTGTAAAGTAAAGAGGGTACAAACTGGACCCAAAGGTGTGCCATT TTTAACTACTCATGATGGCCGTACTATTCGCTACCCTGACCCTAACATCAAGGTTAAT GACACTATTAGATACGATATTGCATCATCTAAAATTTTGGATCATATCCGTTTTGAAA CTGGAAACTTGTGCATGATAACTGGAGGTCGCAATTTAGGGCGTGTTGGTATTGTTAC CAACAGGGAAAGACATCCAGGATCTTTTGATATTGTTCACATTAAGGATGCAAATGA ACATATTTTTGCTACCCGGATGAACAATGTTTTTATTATTGGAAAAGGTCAAAAGAAC TACATTTCTCTACCAAGGAGTAAGGGAGTTAAATTGACTAT
MP002	SEQ ID NO: 900 GAGTTTCTTTAGTAAAGTATTCGGTGG	SEQ ID NO: 901 GCAATGTCATCCATCAKRTCRTGTAC	SEQ ID NO: 890 GAGTTTCTTTAGTAAAGTATTCGGTGGCAAAAAGGAAGAGAAGGGACCATCAACCGA AGATGCGATACAAAAGCTTCGATCCACTGAAGAGATGCTGATAAAGAAACAAGAATT TTTAGAAAAAAAAAATTGAACAAGAAGTAGCGATAGCCAAAAAAAATGGTACAACTA ATAAACGAGCTGCATTGCAAGCATTGAAGCGTAAGAAACGGTACGAACAACAATTAG CCCAAATTGATGGTACCATGTTAACTATTGAACAACAGCGGGAGGCATTAGAAGGTG CCAACACAAATACAGCAGTATTGACTACCATGAAAACTGCAGCAGATGCACTTAAAT CAGCTCATCAAAACATGAATGTAGATGATGTACATGATCTGATGGATGACATTGC
MP010	SEQ ID NO: 902 GTGGCTGCATACAGTTCATTACGCAG	SEQ ID NO: 903 CGCGGCTGCTCCATGAAYASYTG	SEQ ID NO: 892 GTGGCTGCATACAGTTCATTACGCAGTATCAACATTCCAGTGGCTATAAACGAATTAG AGTCACCACATTAGCTAGGAATTGGGCAGACCCTGTTCAGAATATGATGCATGTTAGT GCTGCATTTGATCAAGAAGCATCTGCCGTTTTAATGGCTCGTATGGTAGTGAACCGTG CTGAAACTGAGGATAGTCCAGATGTGATGCGTTGGGCTGATCGTACGCTTATACGCTT GTGTCAAAAATTTGGTGATTATCAAAAAGATGATCCAAATAGTTTCCGATTGCCAGAA AACTTCAGTTTATATCCACAGTTCATGTATCATTTAAGAAGGTCTCAATTTCTACAAGT TTTTAATAATAGTCCTGATGAAACATCATATTATAGGCACATGTTGATGCGTGAAGAT GTTACCCAAAGTTTAATCATGATACAGCCAATTCTGTATAGCTATAGTTTTAATGGTA

			GGCCAGAACCTGTACTTTGGATACCAGTAGTATTCAACCTGATAAAATATTATTGAT GGACACATTTTTCCATATTTTGATATTCCATGGAGAGACTATTGCTCAATGGAGAGCA ATGGATTATCAAAATAGACCAGAGTATAGTAACCTCAAGCAGTTGCTTCAAGCCCCCG TTGATGATGCTCAGGAAATTCTCAAAACTCGATTCCCAATGCCTCGGTATATTGACAC AGAACAAGGTGGTAGTCAGGCAAGATTTTTACTATGCAAAGTAAACCCATCTCAAAC ACATAATAATATGTATGCTTATGGAGGGTGATGGTGGAGCACCAGTTTTGACAGATGA TGTAAGCTTGCAGCTGTTCATGGAGCAGCCGCG
MP016	SEQ ID NO: 904 GTGTCGGAGG ATATGYTGGG YCG	SEQ ID NO: 905 GGAATAGGA TGGGTRATRT CGTCG	SEQ ID NO: 894 GTGTCGGAGGATATGTTGGGCCGCGTTTTCAATGGCAGTGGAAAGCCGATAGATAAA GGACCTCCTATTTTGGCTGAAGATTATTGGATATTGAAGGCCAACCTATTAATCCAT ACTCCAGAACATATCCTCAAGAAATGATTCAAACTGGTATTTCAGCTATTGATATCAT GAACTCTATTGCTCGTGGACAAAAAAATTCCAATATTTTCAGCTGCAGGTTTACCACAT AATGAGATTGCTGCTCAAATTTGTAGACAAGCTGGTCTCGTTAAAAAAACCTGGTAAAT CAGTTCTTGACGATCATGAAGACAATTTTGCTATAGTATTTGCTGCTATGGGTGTTAAT ATGGAAACAGCCAGATTCTTTAAACAAGATTTTGAGGAAAATGGTTCAATGGAGAAT GTTTGTTTGTTCTTGAATTTAGCTAATGATCCTACTATTGAGCGTATCATTACACCACG TCTTGCTTTAACTGCTGCTGAATTTTTAGCTTACCAATGTGAAAAGCATGTCTTAGTTA TTTTAACTGACATGAGTTCATATGCTGAAGCTTTAAGAGAAGTTTCTGCTGCTCGTGA AGAAGTACCTGGGCGTCGTGGTTTCCCTGGTTACATGTACACCGATTTAGCTACAATT TATGAACGTGCTGGGCGTGTAGAAGGAAGAAATGGTTCTATCACACAAATACCTATTT TAACTATGCCTAACGACGACATCACCCATCCTATTCC
MP027	SEQ ID NO: 906 CGCCGATTAC CAAAACAARA CBTG	SEQ ID NO: 907 GGGATACTGT CACAAYYTCD CCRCC	SEQ ID NO: 896 CGCCGATTACCAAAACAAGACGTGTGTTCAGACATTAGAAGGCCATGCTCAAAATAT TTCTGCTCGTTTGTTTCCATCCAGAACTTCCCATCGTGTTAACTGGCTCAGAAGATGGT ACCGTCAGAATTTGGCATTCTGGTACTTATCGATTAGAATCATCATTAAACTATGGGT TAGAACGTGTATGGACAATCTGTTGCTTACGGGGATCTAATAATGTAGCTCTAGGTTA TGATGAAGGAAGTATAATGGTTAAAGTTGGTCGTGAAGAGCCAGCAATGTCAATGGA TGTTCATGGGGGTAAAATTGTTTGGGCACGTCATAGTGAAATTCAACAAGCTAACCTT AAAGCGATGCTTCAAGCAGAAGGAGCCGAAATCAAAGATGGTGAACGTTTACCAATA CAAGTTAAAGACATGGGTAGCTGTGAAATTTATCCACAGTCAATATCTCATAATCCGA ATGGTAGATTTTTAGTAGTATGTGGTGATGGAGAGTATATTATATATACATCAATGGC TTTGCGTAATAAAGCATTTGGCTCCGCTCAGGATTTTGTATGGTCTTCTGATTCTGAGT ATGCCATTAGAGAAAATTCTTCTACAATCAAAGTTTTTAAAAATTTTAAAGAAAAAAAA GTCTTTTAAACCAGAAGGTGGAGCAGATGGTATTTTTGGAGGTTATTTGTTAGGTGTG AAATCTGTTACTGGGTTGGCTTTATATGATTGGGAAAATGGTAACTTAGTTCGAAGAA

			TTGAGACACAACCTAAACATGTATTTTGGTCAGAGTCTGGAGAATTAGTATGTCTTGC CACAGATGAAGCATACTTTATTTTACGTTTTGACGTCAATGTACTTAGTGCTGCAAGA GCATCCAATTATGAAGCTGCTAGTCCTGATGGTCTTGAAGATGCCTTTGAGATTTTAG GAGAAGTTCAAGAAGTTGTAAAAACTGGTCTATGGGTTGGTGATTGCTTTATTTACAC CAATGGAGTAAATCGTATCAACTATTATGTTGGTGGTGAAGTTGTGACAGTATCCC

Table 2-NL

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
NL001	SEQ ID NO: 1117 GAAATCATGG ATGTTGGACAA ATTGG	SEQ ID NO: 1118 ACTGAGCTTCACA CCCTTGCCC	SEQ ID NO: 1071 GAAATCATGGATGTTGGACAAATTGGGTGGTGTGTATGCACCCCGACCCAGCA CAGGTCCACACAAGCTGCGAGAATCTCTCCCACTTGTCATATTTTTGCGTAATC GGCTCAAGTACGCTTTAACTAACTGTGAAGTGAAGAAAATTGTGATGCAGCGT CTCATCAAGGTTGACGGCAAAGTGAGGACTGACCCCAACTATCCTGCAGGTTT TATGGACGTTGTTCAAATCGAAAAGACAAACGAGTTCTTCCGTTTGATCTATG ATGTTAAGGGACGTTTCACCATCCACAGGATCACAGCTGAAGAAGCTAAGTAC AAGCTGTGCAAAGTGAAGAGGGTTCAGACAGGACCCAAGGGCATTCCATTTTT GACCACTCACGATGGACGCACCATCAGGTATCCAGACCCCTTGGTAAAAGTCA ATGACACCATCCAATTGGACATTGCCACATCCAAAATCATGGACTTCATCAGA TTCGACTCTGGTAACCTGTGTATGATCACTGGAGGTCGTAACTTGGGTCGTGTG GGCACTGTCGTGAACAGGGAGCGACACCCGGGGTCTTTCGACATCGTGCACAT CAAGGACGTGTTGGGACACACTTTTGCCACTAGGTTGAACAACGTTTTCATCA TCGGCAAGGGTAGTAAAGCATACGTGTCTCTGCCCAAGGGCAAGGGTGTGAA GCTCAGT
NL002	SEQ ID NO: 1119 GATGAAAAGG GCCCTACAACT GGC	SEQ ID NO: 1120 CTGATCCACATCC ATGTGTTGATGAG	SEQ ID NO: 1073 GATGAAAAGGGCCCTACAACTGGCGAAGCCATTCAGAAACTACGCGAAACAG AGGAAATGCTGATAAAGAAACAAGACTTTTTAGAAAAGAAAATTGAAGTTGA AATTGGAGTTGCCAGGAAGAATGGAACAAAAAACAAAAGAGCCGCGATCCAG GCACTCAAAAGGAAGAAGAGGTATGAAAAGCAATTGCAGCAGATCGATGGAA CGTTATCAACAATTGAGATGCAGAGAGAGGCCCTCGAAGGAGCCAACACGAA TACGGCCGTACTGCAAACTATGAAGAACGCAGCAGATGCTCTCAAAGCGGCTC ATCAACACATGGATGTGGATCAG
NL003	SEQ ID NO: 1121 TCCGCGTCGTC	SEQ ID NO: 1122 TTGACGCGACCA	SEQ ID NO: 1075 TCCGCGTCGTCCTTACGAGAAGGCACGTCTCGAACAGGAGTTGAAGATCATCG

	CTTACGAGAA GGC	GGTCGGCCAC	GAGAGTATGGACTCCGTAACAAGCGTGAGGTGTGGAGAGTCAAATACGCCCT GGCCAAGATTCGTAAGGCCGCTCGTGAGCTGTTGACTCTGGAAGAGAAGGAC CAGAAACGTTTGTTGAAGGTAACGCCCTGCTGCGTCGCCTGGTGCGTATTGG AGTGTTGGACGAAGGAAGAATGAAGCTCGATTACGTCTTGGGTTTAAAAATTG AAGATTTCCTTGAACGTCGTCTACAGACTCAGGTGTACAAACTCGGTTTGGCC AAGTCCATCCATCACGCCCGTGTACTCATCAGACAAAGACATATCAGAGTGCG CAAACAAGTAGTGAACATTCCGAGCTTTGTGGTGCGCCTGGACTCGCAGAAGC ACATTGACTTCTCGCTGAAGTCGCCGTTCGGCGGTGGCCGACCTGGTCGCGTC AA
NL004	SEQ ID NO: 1123 TGAAGGTGGA GAARGGTTYG GMWCMAAG	SEQ ID NO: 1124 GTCGTCTTCTCDG AHACRTAVAGAC C	SEQ ID NO: 1077 AAGGAGTTGGCTGCTGTAAGAACTGTCTGCTCTCACATCGAAAACATGCTGAA GGGAGTCACAAAGGGATTCCTGTACAAGATGCGTGCCGTGTACGCCCATTTCC CCATCAACTGTGTGACGACCGAGAACAACTCTGTGATCGAGGTGCGTAACTTC CTGGGCGAGAAGTACATCCGACGGGTGAGGATGGCGCCCGGCGTCACTGTTA CCAACTCGACAAAGCAGAAGGACGAGCTCATCGTCGAAGGAAACAGCATAGA GGACGTGTCAAGATCAGCTGCCCTCATCCAACACAACACAGTCAACACAGTGAAGAAC AAGGATATTCGTAAATTCTTGGAC
NL005	SEQ ID NO: 1125 GGTCTGGTTGG ATCCHAATGA AATCAAYGA	SEQ ID NO: 1126 TCCTGCTTCTTSG YRGCRATWCGYT C	SEQ ID NO: 1079 TTGGATCCCAATGAAATAAATGAAATCGCAAACACAAATTCACGTCAAAGCAT CAGGAAGCTGATCAAAGACGGTCTTATCATCAAGAAACCGGTTGCAGTACATT CACGTGCTCGCGTTCGTAAAAACACTGAAGCCAGGAGAAAGGCAGACATTG TGGCTTTGGTAAGAGGAAAGGTACAGCCAACGCCCGTATGCCACACAAAGGTT CTATGGGTGAATCGTATGCGTGTCTTGAGAAGACTGTTGAAAAAATACAGACA AGATAAGAAAATCGACAGGCATCTGTACCATCACCTTTACATGAAGGCTAAGG GTAACGTATTCAAGAACAAGCGTGTATTGATGGAGTTCATTCATAAGAAGAAG GCCGAGAAAGCAAGAATGAAGATGTTGAACGACCAGGCTGAAGCTCGCAGAC AAAAGGTCAAGGAGGCCAAGAAGCGAAGGGAA
NL006	SEQ ID NO: 1127 GGAGCGAGAC TACAACAAYK AYRGYTGGC	SEQ ID NO: 1128 GAGATCTTCTGCA CRTTKACVGCATC	SEQ ID NO: 1081 AAGTGCTTGTGTCAAGTGGTGTGGTGGAGTACATTGACACCCTGGAGGAGGAG ACGACCATGATAGCGATGTCGCCGGATGACCTGCGTCAGGACAAGGAGTATG CCTACTGTACCACCTACACGCACTGCGAGATCCACCCGGCCATGATACTCGGT GTGTGCGCCTCTATTATTCCCTTCCCCGATCACACAACCAAAGTCCCAGGAACAC CTATCAGAGCGCTATGGGAAACAGGCGATGGGCGTGTACATCACCAACTTCC ACGTGCGAATGGACACGCTGGCTCACGTGCTGTTCTACCCGCACAAGCCACTG GTCACCACTCGCTCCATGGAGTACCTGCGCTTCAGGGAGCTTCCTGCCGGCAT

			CAACTCTGTGGTCGCCATCGCCTGCTACACTGGATACAACCAGGAGGACAGTG TCATTCTCAACGCCTCCGCTGTCGAGCGCGGATTCTTCAGATCGGTTTTCTTCC GATCTTACAAAGATGCAGAATCGAAGCGTATTGGCGACCAAGAGGAGCAATT CGAGAAGCCCACCAGACAGACGTGTCAGGGAATGAGGAATGCCATTTATGAC AAATTGGACGATGATGGCATCATTGCTCCCGGTCTGAGAGTGTCTGGTGACGA TGTGGTTATTGGCAAAACCATAACACTGCCCGATAATGATGACGAGCTGGAAG GTACAACAAAGAGGTTCACGAAGAGAGATGCCAGTACTTTCCTGCGTAACAGT GAGACGGGAATCGTCGACCAAGTCATGTTAACCTTGAACTCTGAGGGTTACAA GTTCTGCAAAATTCGAGTCAGGTCTGTGCGTATCCCGCAGATTGGCGATAAGT TCGCTTCCCGACATGGCCAAAAAGGAACGTGTGGAATACAGTATCGTCAAGA GGACATGCCTTTTACAAGCGAGGGAATCGCACCGGATATTATTATCAATCCTC ACGCTATCCCATCTCGTATGACAATTGGCCATTTAATTGAATGTCTCCAAGGA AAGGTGTCGTCGAACAAGGGCGAGATAGGTGACGCGACGCCGTTCAAC
NL007	SEQ ID NO: 1129 CGGTGTCCATT CACAGYTCCG G	SEQ ID NO: 1130 CGATGCAAGTAG GTGTCKGARTCYT C	SEQ ID NO: 1083 TTTCAGAGATTTCCTTCTGAAACCTGAAATTTTGAGAGCAATCCTTGACTGTGG TTTTGAACATCCATCTGAAGTACAACATGAATGCATTCCTCAAGCTGTACTTGG AATGGACATATTGTGTCAAGCGAAATCCGGTATGGGAAAAACTGCTGTATTTG TGTTGGCGACATTACAGCAAATTGAACCAACTGACAACCAAGTCAGTGTATTG GTCATGTGTCATACCAGAGAGCTTGCATTCCAAATCAGCAAAGAGTATGAACG ATTTTCGAAATGTATGCCAAATATCAAGGTTGGAGTTTTCTTCGGCGGACTGCC GATTCAGAGGGATGAGGAGACGTTGAAATTGAACTGTCCTCACATCGTGGTTG GAACACCCGGACGAATTTTGGCGTTGGTACGCAACAAGAAGCTGGACCTCAA GCATCTCAAGCACTTTGTCCTTGACGAATGTGACAAAATGTTGGAACTGTTAG ATATGCGAAGAGATGTGCAGGAAATATTCCGAAACACGCCGCACAGCAAACA AGTCATGATGTTCAGTGCAACTCTCAGCAAAGAAATTCGTCCAGTCTGCAAGA AATTCATGCAAGATCCGATGGAAGTGTACGTTGATGACGAGGCCAAGCTGAC GCTTCACGGCCTGCAGCAGCACTATGTCAAACTCAAAGAAAACGAAAAGAAC AAAAAGTTATTTGAATTACTTGACATACTTGAATTCAACCAGGTTGTTATATTT GTGAAGTCAGTGCAGCGCTGCATGGCCCTATCGCAACTCCTAACAGAGCAGAA CTTCCCTGCAGTGGCTATTCACCGTGGCATGACACAAGAAGAACGATTGAAGA AATATCAAGAGTTCAAAGAGTTCCTAAAGCGAATTTTGGTAGCAACGAATCTG TTTGGCAGAGGAATGGATATTGAGAGAGTCAACATTGTATTCAACTATGACAT GCCT
NL008	SEQ ID NO: 1131 GTGGTGGATCA	SEQ ID NO: 1132 GCGCATTTGATCG	SEQ ID NO: 1085 GGAAGGATAGAAAACCAGAAACGAGTTGTTGGTGTTCTTTTGGGATGCTGGAG

	CTTYAAYCGK ATG	TTBGTYTTCAC	ACCTGGAGGTGTATTAGATGTTTCAAACAGTTTTGCAGTTCCATTTGATGAGG ACGACAAAGAAAAGAATGTTTGGTTCTTAGACCATGATTACTTGGAAAACATG TTCGGGATGTTCAAGAAAGTTAATGCTAGAGAAAAGGTTGTGGGTTGGTACCA TACTGGACCCAAACTCCACCAAAACGATGTTGCAATCAATGAGTTGATTCGTC GTTACTGTCCAAACTGTGTCTTAGTCATAATCGATGCCAAGCCTAAAGATTTG GGTCTACCTACAGAGGCATACAGAGTCGTTGAAGAAATCCATGATGATGGATC GCCAACATCAAAAACATTTGAACATGTGATGAGTGAGATTGGGGCAGAAGAG GCTGAGGAGATTGGCGTTGAACATCTGTTGAGAGACATCAAAGATACAACAG TCGGGTCACTGTCACAGCGCGTCACAAATCAGCTGATGGGCTTGAAGGGCTTG CATCTGCAATTACAGGATATGCGAGACTATTTGAATCAGGTTGTCGAAGGAAA GTTGCCAATGAACCATCAAATCGTTTACCAACTGCAAGACATCTTCAACCTTCT ACCCGATATCGGCCACGGCAATTTTGTAGACTCGCTCTAC
NL009	SEQ ID NO: 1133 GGGCCGTGGTC AGAAYATYWA YAAC	SEQ ID NO: 1134 CCGCCAAAGGAC TSARRTADCCCTC	SEQ ID NO: 1087 TGCGACTATGATCGACCGCCGGGACGCGGTCAGGTGTGCGACGTCGACGTCAA GAACTGGTTTCCCTGCACCTCTGAGAACAATTTCAACTACCATCAATCGAGCC CTTGTGTTTTTCTCAAACTGAACAAGATAATTGGTTGGCAACCGGAGTACTAC AATGAGACTGAAGGCTTTCCAGATAATATGCCAGGTGACCTCAAGCGACACAT TGCCCAACAGAAGAGTATCAACAAGCTGTTTATGCAAACAATCTGGATAACTT GCGAAGGAGAGGGTCCTCTAGACAAGGAGAATGCAGGGAGATCCAGTACAT CCCTAGACAGGGATTTCCGGGCTACTTCTACCCTTACACTAATGCC
NL010	SEQ ID NO: 1135 CGGCTGACGTG GAAYGTKTGG CC	SEQ ID NO: 1136 TGCCGGAAGTTCT CRTAYTCKGGC	SEQ ID NO: 1089 (amino terminus) GTCCAGTCGACTGGAAGCCACCAGGCTTGTTGTTCCCGTTGGATGTCTGTATCA ACCTTTGAAGGAGAGACCTGATCTACCGCCTGTACAGTACGATCCAGTTCTTT GTACTAGGAATACTTGTCGTGCAATTCTGAATCCATTGTGCCAAGTCGACTATC GAGCCAAGCTATGGGTCTGCAACTTTTGTTTCCAGAGGAATCCTTTCCCCCCTC AATATGCAGCTATTTCGGAGCAGCATCAACCAGCAGAACTGATACCTTCATTT TCCACCATCGAATACATCATTACCAGAGCGCAAACGATGCCGCCGATGTTCGT GCTGGTGGTGGACACATGTCTGGACGACGAGGAGCTGGGAGCTTTGAAGGAC TCACTGCAGATGTCGCTGTCGCTGCCGCCCAATGCACTCATCGGTCTCATC ACGTTCGGCAAAATGGTGCAGGTGCACGAGCTTGGCTGCGACGGCTGCTCGAA GAGCTACGTGTTCCGTGGCGTGAAGGACCTGACTGCCAAGCAGATCCAGGAC ATGTTGGGCATTGGCAAGATGGCCGCCGCTCCACAGCCCATGCAACAGCGCAT TCCCGGCGCCGCTCCCTCCGCACCTGTCAACAGATTTCTTCAGCCTGTCGGAAA GTGCGATATGAGTTTAACTGATCTGCTTGGGGAATTGCAAAGAGATCCATGGA ATGTGGCTCAGGGCAAGAGACCTCTCCGATCTACTGGAGTTGCATTGTCCATT

			GCAGTTGGTCTGCTCGAGTGCACA SEQ ID NO: 1115 (carboxy terminus) CGTTGAACGTGAAAGGCTCGTGTGTGTCAGACACTGACATTGGCTTGGGCGGC ACCTCTCAATGGAAAATGTGCGCCTTCACTCCACACACAACTTGTGCATTCTTC TTCGAAGTTGTCAACCAGCACGCAGCCCCAATCCCACAGGGAGGAAGAGGAT GCATCCAATTCATTACGCAATACCAACATTCCAGTGGCCAGAGAAGGATACGT GTCACCACCATCGCTCGAAACTGGGCAGATGCGAGCACCAACCTGGCACACAT CAGTGCCGGCTTCGACCAGGAGGCAGGAGCCGTGCTGATGGCCCGCATGGTC GTGCATCGCGCCGAGACTGACGATGGACCTGACGTCATGCGCTGGGCTGACCG CATGCTCATCCGTCTCTGTCAGAGGTTCGGTGAATACAGTAAGGATGACCCTA ACAGTTTCCGTCTGCCAGAGAACTTCACACTTTATCCGCAGTTCATGTACCATC TGCGTCGATCCCAATTCTTGCAAGTGTTCAACAACAGTCCTGATGAAACATCTT ACTACAGGCACATTCTTATGCGAGAGGATCTGACTCAGAGTTTGATTATGATC CAGCCGATTTTGTACAGCTACAGCTTCAATGGTCCCCCCGAGCCAGTGCTGCT CGACACCAGCAGTATTCAACCCGACAGAATCCTATTGATGGACACATTTTTCC AAATTCTCATTTTCCATGGAGAGACGATTGCTCAATGGCGATCTCTCTGGGCTAC CAGGACAT
NL011	SEQ ID NO: 1137 CCCACTTTCAA GTGYGTRYTRG TCGG	SEQ ID NO: 1138 CGCTCTCTCTCTCGA TCTGYDSCTGCC	SEQ ID NO: 1091 AGATGGTGGTACCGGCAAAACTACATTTGTCAAACGACATCTTACCGGAGAAT TTGAAAAGAAGTATGTTGCCACCCTTGGAGTTGAAGTTCACCCCCTTGTATTTC ACACAAACAGAGGTGTGATTAGGTTCAATGTGTGGGACACAGCTGGCCAGGA AAAGTTCGGTGGACTTCGTGATGGATATTACATTCAGGGACAATGCGCCATCA TTATGTTTGACGTAACGTCAAGAGTCACCTACAAGAACGTTCCCAACTGGCAC AGAGATTTAGTGAGGGTTTGCGAAAACATTCCCATTGTACTATGCCGGCAACAA AGTAGACATCAAGGACAGGAAAGTCAAGGCCAAGAGCATAGTCTTCCATAGG AAGAAGAACCTTCAGTACTACGACATCAGTGCGAAAAGCAACTACAACTTCG AGAAGCCGTTCCTGTGGTTGGCAAAGAAGCTGATCGGTGACCCCAACCTGGAG TTCGTCGCCATGCCCGCCCTCCTCCCACCCGAGGTCACAATGGACCCCCCAAT
NL012	SEQ ID NO: 1139 GCAGGCGCAG GTBGABGARGT	SEQ ID NO: 1140 GAATTTCCTCTTS AGYTTBCCVGC	SEQ ID NO: 1093 GCAGCAGACGCAGGCACAGGTAGACGAGGTTGTCGATATAATGAAAACAAAC GTTGAGAAAGTATTGGAGAGGGATCAAAAACTATCAGAATTGGATGATCGAG CAGATGCTCTACAGCAAGGCGCTTCACAGTTTGAACAGCAAGCTGGCAAACTC AAGAGGAAATTC

NL013	SEQ ID NO: 1141 CAGATGCGCCC GTBGTDGAYA C	SEQ ID NO: 1142 GCCCTTGACAGA YTGDATVGGATC	SEQ ID NO: 1095 CGCAGAGCAAGTCTACATCTCTTCACTGGCCTTATTGAAAATGCTTAAGCACG GTCGCGCCGGTGTTCCCATGGAAGTTATGGGCCTAATGCTGGGCGAATTTGTA GACGACTACACTGTGCGTGTCATTGATGTATTCGCTATGCCACAGAGTGGAAC GGGAGTGAGTGTGGAGGCTGTAGACCCGGTGTTCCAAGCGAAGATGTTGGAC ATGCTAAAGCAGACAGGACGGCCCGAGATGGTGGTGGGCTGGTACCACTCGC ACCCGGGCTTCGGCTGCTGGCTGTCGACATCAACACGCAGGAGAGC TTCGAGCAACTATCCAAGAGAGCCGTTGCCGTCGTCGTC
NL014	SEQ ID NO: 1143 CGCAGATCAA RCAYATGATG GC	SEQ ID NO: 1144 GAACTTGCGGTTG ABGTTSCGDCC	SEQ ID NO: 1097 TTTCATTGAGCAAGAAGCCAATGAGAAAGCCGAAGAGATCGATGCCAAGGCC GAGGAAGAATTCAACATTGAAAAGGGAAGGCTCGTACAGCACCAGCGCCTTA AAATCATGGAGTACTATGACAGGAAAGAGAAGCAGGTTGAGCTCCAGAAAAA AATCCAATCGTCAAACATGCTGAACCAAGCGCGTCTGAAGGCACTGAAGGTG CGCGAAGATCACGTGAGAAGTGTGCTCGAAGAATCCAGAAAACGTCTTGGAG AAGTAACCAGAAACCCAGCCAAGTACAAGGAAGTCCTCCAGTATCTAATTGTC CAAGGACTCCTGCAGCTGCTAGAATCAAACGTAGTACTGCGCGTGCGCGAGGC TGACGTGAGTCTGATCGAGGGCATTGTTGGCTCATGCGCAGAGCAGTACGCGA AGATGACCGGCAAAGAGGTGGTGGTGAAGCTGGACGCTGACAACTTCCTGGC CGCCGAGACGTGTGGAGGCGTCGAGTTGTTCGCCCGCAACGGCCGCATCAAG ATCCCCAACACCCTCGAGTCCAGGCTCGACCTCATCTCCCAGCAACTTGTGCC CGAGATTAGAGTCGCGCTCTTT
NL015	SEQ ID NO: 1145 GCCGCAAGGA GACBGTVTGC	SEQ ID NO: 1146 GTCCGTGGGAYTC RGCHGCAATC	SEQ ID NO: 1099 ATTGTGCTGTCTGACGAGACATGTCCGTTCGAAAAGATCCGCATGAATCGAGT GGTCAGGAAGAATCTGCGAGTGCGCTTGTCCGACATTGTCTCGATCCAGCCTT GCCCAGACGTCAAGTATGGAAAGCGTATCCATGTGCTGCCCATTGATGATACC GTTGAGGGTCTTACAGGAAATCTGTTCGAAGTGTATTTGAAGCCATACTTCCT GGAAGCATACAGGCCAATTCACAAGGATGATGCATTCATTGTTCGCGGAGGTA TGAGAGCGGTCGAATTCAAGGTGGTTGAAACAGATCCATCGCCCTACTGCATT GTCGCGCCAGACACCGTCATCCATTGTGAGGGAGACCCCATCAAACGTGAGG ATGAAGAAGACGCAGCAAACGCAGTCGGCTACGACGACATTGGAGGCTGCAG AAAGCAGCTGGCGCAGATCAAAGAGATGGTGGAGTTGCCGCTGAGACATCCC AGTCTGTTCAAGGCGATCGGCGTGAAGCCGCCACGAGGCATCCTGCTGTACGG ACCACCGGGAACCGGAAAGACGTTGATAGCGCGCCGTCGCCAACGAAACG GGCGCCTTCTTCTTCCTCATCAACGGACCCGAGATTATGAGCAAATTGGCCGG CGAGTCGGAGAGTAACCTGCGCAAAGCTTTCGAGGAAGCGGACAAAAACGCA

			CCGGCCATCATCTTCATCGATGAGCTGGACGCAATCGCGCCAAAACGCGAGAA GACGCACGGCGAGGTGGAGCGACGCATCGTGTCGCAGCTGCTGACGCTGATG GACGGTCTCAAGCAGAGCTCGCACGTGATTGTCATGGCCGCCACCAATCGGCC CAACTCGATCGATGCCGCGCTTAGGCGCTTTGGCCGCTTTGATCGCGAAATCG ACATTGGCATTCCCGATGCCACCGGTCGTCTCGAGGTGCTGCGCATCCACACC AAGAACATGAAGTTGGCTGATGACGTCGATTTGGAACA
NL016	SEQ ID NO: 1147 GTTCACCGGCG AYATYCTGCG	SEQ ID NO: 1148 CGGCATAGTCAG AATSGGRATCTG	SEQ ID NO: 1101 GACGCCAGTATCAGAAGACATGCTTGGTCGTGTATTCAACGGAAGTGGTAAGC CCATCGACAAAGGACCTCCCATTCTTGCTGAGGATTATCTCCGACATTCAAGGT CAACCCATCAATCCTTGGTCGCGTATCTATCCCGAGGAAATGATCCAGACTGG AATTTCAGCCATCGACGTCATGAACTCGATTGCTCGTGGCCAGAAAATCCCCA TCTTTTCAGCTGCCGGTCTACCTCACAACGAAATTGCTGCTCAAATCTGTAGAC AGGCTGGTCTTGTCAAACTGCCAGGAAAGTCAGTTCTCGATGACTCTGAGGAC AACTTTGCTATTGTATTCGCAGCCATGGGAGTCAACATGGAAACTGCTCGATT CTTCAAACAGGATTTCGAGGAGAACGGCTCTATGGAGAACGTGTGCCTGTTCT TGAACCTGGCGAACGACCCGACGATCGAGCGTATCATCACACCACGCCTGGCG CTGACGGCCGCCGAGTTCCTGGCCTACCAGTGCGAGAAGCACGTGCTCGTCAT CCTCACCGACATGAGCTCCTACGCCGAGGCGCTGCGAGAGGTGTCCGCCGCCC GCGAGGAGGTGCCCGGCCGTCGTGGTTTCCCCGGTTACATGTACACCGATCTG GCCACCATCTACGAGCGCCGGACGAGTCGAGGGTCGCAACGGCTCCATCA CG
NL018	SEQ ID NO: 1149 GCTCCGTCTAC ATHCARCCNG ARGG	SEQ ID NO: 1150 GTGCATCGGTACC AHSCHGCRTC	SEQ ID NO: 1103 TATGCAAATGCCTGTGCCACGCCCACAAATAGAAAGCACACAACAGTTTATTC GATCCGAGAAAACAACATACTCGAATGGATTCACCACCATTGAGGAGGACTTC AAAGTAGACACTTTCGAATACCGTCTTCTGCGCGAGGTGTCGTTCCGCGAATC TCTGATCAGAAACTACTTGCACGAGGCGGACATGCAGATGTCGACGGTGGTGG ACCGAGCATTGGGTCCCCCCTCGGCGCCACACATCCAGCAGAAGCCGCGCAAC TCAAAAATCCAGGAGGGCGGCGATGCCGTCTTTTCCATCAAGCTCAGCGCCAA CCCCAAGCCTCGGCTGGTCTGGTTCAAGAACGGTCAGCGCATCGGTCAGACGC AGAAACACCAGGCCTCCTACTCCAATCAGACCGCCACGCTCAAGGTCAACAA AGTCAGCGCTCAAGACTCCGGCCACTACACGCTGCTTGCTGAAAATCCGCAAG GATGTACTGTGTCCTCAGCTTACCTAGCTGTCGAATCAGCTGGCACTCAAGAT ACAGGATACAGTGAGCAATACAGCAGACAAGAGGTGGAGACGACAGAGGCG GTGGACAGCAGCAAGATGCTGGCACCGAACTTTGTTCGCGTGCCGGCCGATCG CGACGCGAGCGAAGGCAAGATGACGCGGTTTGACTGCCGCGTGACGGGCCGA

			CCCTACCCGGACGTGGCCTGGTTCATCAACGGCCAACAGGTGGCTGACGACGC CACGCACAAGATCCTCGTCAACGAGTCTGGCAACCACTCGCTCATGATCACCG GCGTCACTCGCTTGGACCACGGAGTGGTCGGCTGTATTGCCCGCAACAAGGCT GGCGAAACCTCATTCCAGTGCAACTTGAATGTGATCGAGAAAGAACTGGTTGT GGCGCCGAAATTTGTGGAGAGATTCGCACAAGTGAATGTGAAGGAGGGTGAG CCGGTTGTGCTGAGCGCACGCGCTGTTGGCACACCTGTTCCAAGAATAACATG GCAGAAGGACGGCGCCCCGATCCAGTCGGGACCGAGCGTGAGTCTGTTTGTG GACGGAGGTGCGACCAGCCTGGACATCCCGTACGCGAAGGCGTCG
NL019	SEQ ID NO: 1151 GTCCTGTCTGC TGCTVMGWTT YGC	SEQ ID NO: 1152 CCTTGATCTCHGC MGCCATBGTC	SEQ ID NO: 1105 CGATGACACATACACAGAAAGTTACATCAGTACCATTGGTGTAGATTTTAAAA TTAGAACAATAGATCTCGATGGAAAAACCATAAAGCTTCAGATTTGGGACACG GCCGGCCAGGAGCGGTTCCGCACGATCACATCGAGCTACTACCGGGGCGCCC ACGGCATCATTGTGGTGTACGACTGCACCGACCAGGAGTCGTTCAACAACCTC AAACAGTGGCTCGAGGAGATTGACCGCTACGCCTGTGATAATGTCAACAAACT GCTCGTCGGCAACAAGTGTGATCAGACCAACAAAAAGGTCGTCGACTATACA CAGGCTAAGGAATACGCCGACCAGCTGGGCATTCCGTTCCTGGAGACGTCGGC GAAGAACGCGACCAATGTGGAGCAGGCGTTCAT
NL021	SEQ ID NO: 1153 CTCAATCAGAG CGTYCCHCCRT AYGG	SEQ ID NO: 1154 GGAATTGCCSAGV CGDGADCC	SEQ ID NO: 1107 CGTCAGTCTCAATTCTGTCACCGATATCAGCACCACGTTCATTCTCAAGCCACA AGAGAACGTGAAGATAACGCTTGAGGGCGCACAGGCCTGTTTCATTTCACACG AACGACTTGTGATCTCACTGAAGGGAGGAGAACTCTATGTTCTAACTCTCTAT TCCGATAGTATGCGCAGTGTGAGGAGTTTTCATCTGGAGAAAGCTGCTGCCAG TGTCTTGACTACTTGTATCTGTGTTTGTGAGGAGAACTATCTGTTCCTTGGTTC CCGTCTTGGAAACTCACTGTTGCTCAGGTTTACTGAGAAGGAATTGAACCTGA TTGAGCCGAGGGCCATCGAAAGCTCACAGTCCCAGAATCCGGCCAAGAAGAA AAAGCTGGATACTTTGGGAGATTGGATGGCATCTGACGTCACTGAAATACGCG ACCTGGATGAACTAGAAGTGTATGGCAGTGAAACACAAACCTCTATGCAAATT GCATCCTACATATTC
NL022	SEQ ID NO: 1155 GCGTGCTCAAG TAYATGACBG AYGG	SEQ ID NO: 1156 CCAGTTCATGCTT RTANGCCCANGC	SEQ ID NO: 1109 TACATTGCACAGAGAATTCCTTTCCGAGCCAGATCTGCAATCTTACAGTGTTAT GATAATTGATGAAGCTCACGAGAGGACGTTGCACACTGATATACTGTTCGGTT TGGTGAAAGATGTCGCCCGATTCAGACCTGACTTGAAGCTGCTCATATCAAGC GCCACACTGGATGCTCAGAAATTCTCCGAGTTTTTCGACGATGCACCCATCTTC AGGATTCCGGGCCGTAGATTTCCGGTGGACATCTACTACACAAAGGCGCCCGA GGCTGACTACGTGGACGCATGTGTCGTTTCGATCCTGCAGATCCACGCCACTC

			AGCCGCTGGGAGACATCCTGGTCTTCCTCACCGGTCAGGAGGATCGAAACC
			TGCCAGGAGCTGCTGCAGGACAGAGTGCGCAGGCTTGGGCCTCGTATCAAGG
			AGCTGCTCATATTGCCCGTCTATTCCAACCTACCCAGTGATATGCAGGCAAAG
			ATTTTCCTGCCCACTCCACCAAATGCTAGAAAGGTAGTATTGGCCACAAATAT
			TGCAGAAACCTCATTGACCATCGACAATATAATCTACGTGATTGATCCTGGTTT
			TTGTAAGCAGAATAACTTCAATTCAAGGACTGGAATGGAATCGCTTGTTGTAG
			TGCCTGTTTCAAAGGCATCGGCCAATCAGCGAGCAGGGCGGGCGGGACGGGT
			GGCGGCCGGCAAGTGCTTCCGTCTGTACACG
NL023	SEQ ID NO: 1157 CCGGAGCTTCT CTCAGGAACG C	SEQ ID NO: 1158 GAAAGCACACGC TGTTGCTCTGG	SEQ ID NO: 1111
			CCGGAGCTTCTCTCAGGAACGCCAGCACGAGGAAATGAAGGAATCCTCGGGT
			CGCATGCATCACAGCGATCCTCTAATCGTCGAGACTCATAGCGGTCACGTGAG
			AGGAATCTCGAAGACCGTCCTCGGACGGGAGGTCCACGTGTTTACCGGGATTC
			CGTTTGCGAAACCTCCCATCGGTCCGTTGCGATTCCGTAAACCGGTTCCCGTCG
			ACCCGTGGCACGGCGTTCTGGATGCGACCGCGCTTCCCAACAGCTGCTACCAG
			GAACGGTACGAGTATTTCCCGGGCTTCGAGGGAGAGGAAATGTGGAATCCGA
			ATACGAATTTGTCCGAAGATTGTCTGTATTTGAACATATGGGTGCCGCACCGG
			TTGAGAATCCGACACAGAGCCAACAGCGAGGAGAATAAACCAAGAGCGAAG
			GTGCCGGTGCTGATCTGGATCTACGGCGGGGGTTACATGAGCGGCACAGCTAC
			ACTGGACGTGTACGATGCTGACATGGTGGCCGCCACCGAGTGACGTCATCGTCG
			CCTCCATGCAGTACCGAGTGGGTGCGTTCGGCTTCCTCTACCTCGCACAGGAC
			TTGCCTCGAGGCAGCGAGGAGGCGCCGGGCAACATGGGGCTCTGGGACCAGG
			CCCTTGCCATCCGCTGGCTCAAGGACAACATTGCCCGCCTTCGGAGGCGATCCC
			GAACTCATGACGCTCTTTGGCGAGTCGGCTGGGGGTGGATCTGTAAGCATCCA
			CTTGGTATCACCGATAACTCGCGGCCTAGCGCGTCGTGGCATCATGCAGTCAG
			GAACGATGAACGCACCGTGGAGCTTCATGACGGCGGAACGCGCGACCGAAAT
			CGCCAAGACGCTCATTGACGACTGCGGCTGCAACTCGTCGCTCCTGACCGACG
			CTCCCAGTCGCGTCATGTCCTGTATGCGATCAGTCGAGGCAAAGATCATCTCC
			GTGCAGCAATGGAACAGCTACTCCGGCATTCTCGGACTTCCGTCTGCACCCAC
			CATCGACGGCATTTTCCTGCCCAAACATCCCCTCGATCTGCTCAAGGAAGGCG
			ACTTTCAGGACACTGAAATACTCATCGGCAGTAATCAGGATGAGGGTACCTAC
			TTCATATTGTACGATTTCATCGACTTCTTCCAAAAAGACGGGCCGAGTTTCTTG
			CAAAGAGATAAGTTCCTAGACATCATCAACACACAATTTTCAAGAATATGACGAA
			AATTGAGAGGGAAGCTATCATATTCCAGTACACAGATTGGGAGCATGTTATGG
			ATGGTTATCTGAACCAGAAAAATGATCGGAGATGTGGTTGGTGATTACTTCTTC
			ATCTGTCCGACAAATCATTTCGCACAGGCATTCGCAGAGCATGGAAAGAAGGT
			GTATTACTATTTCTTCACCCAGAGAACCAGTACAAGTTTATGGGCGAGTGGA

			TGGGAGTCATGCATGGAGATGAAATAGAATACGTTTTTGGTCATCCTCTCAAC ATGTCGCTGCAATTCAATGCTAGGGAAAGGGATCTCAGTCTGCGAATAATGCA AGCTTACTCTAGGTTTGCATTGACAGGTAAACCAGTGCCTGATGACGTGAATT GGCCTATCTACTCCAAGGACCAGCCGCAGTATTACATTTTCAATGCGGAGACT TCGGGCACAGGCAGAGGACCCAGAGCAACAGCGTGTGCTTTC
NL027	SEQ ID NO: 1159 GCCGATCGTKY TVACKGGCTC	SEQ ID NO: 1160 GGTATAGATGAA RCARTCDCCVACC CA	SEQ ID NO: 1113 AGAAGACGGCACGGTGCGTATTTGGCACTCGGGCACCTACAGGCTGGAGTCCT CGCTGAATTATGGCCTCGAAAGAGTGTGGACCATTTGCTGCATGCGAGGATCC AACAATGTGGCTCTTGGCTACGACGAAGGCAGCATAATGGTGAAGGTGGGTC GGGAGGAGCCGGCCATCTCGATGGATGTGAACGGTGAGAAGATTGTGTGGGC GCGCCACTCGGAGATACAACAGGTCAACCTCAAGGCCATGCCGGAGGGCGTC GAAATCAAAGATGGCGAACGACTGCCGGTCGCCGTTAAGGATATGGGCAGCT GTGAAATATATCCGCAGACCATCGCTCATAATCCCAACGGCAGATTCCTAGTC GTTTGTGGAGATGGAGAGTACATAATTCACACATCAATGGTGCTAAGAAATAA GGCGTTTGGCTCGGCCCAAGAGTTCATTTGGGGACAGGACTCGTCCGAGTATG CTATCAGAGAAGGAACATCCACTGTCAAAGTATTCAAAAACTTCAAAGAAAA GAAATCATTCAAGCCAGAATTTGGTGCTGAGAGCATATTCGGCGGCTACCTGC TGGGAGTTTGTTCGTTGTCTGGACTGGCGCTGTACGACTGGGAGACCCTGGAG CTGGTGCGTCGCATCGAGATCCAACCGAAACACGTGTACTGGTCGGAGAGTGG GGAGCTGGTGGCGCTGGCCACTGATGACTCCTACTTTGTGCTCCGCTACGACG CACAGGCCGTGCTCGCTGCACGCGACGCCGGTGACGACGCTGTCACGCCGGAC GGCGTCGAGGATGCATTCGAGGTCCTTGGTGAAGTGCACGAAACTGTAAAAA CTGGATTG

Table 2-CS

Target ID	**Primer Forward 5' → 3'**	**Primer Reverse 5' → 3'**	**cDNA Sequence (sense strand) 5' → 3'**
CS001	SEQ ID NO: 1706 CATTTGAAGCG TTTWRMYGCY CC	SEQ ID NO: 1707 CTTCGTGCCCTT GCCRATKATRA ABACG	SEQ ID NO: 1682 TAAAGCATGGATGTTGGACAAACTGGGTGGCGTGTACGCGCCGCGGCCGTCGA CCGGCCCCCACAAGTTGCGCGAGTGCCTGCCGCTGGTGATCTTCCTCAGGAACC GGCTCAAGTACGCGCTCACCGGAAATGAAGTGCTTAAGATTGTAAAGCAGCGA CTTATCAAAGTTGACGGCAAAGTCAGGACAGACCCCACATATCCCGCTGGATTT ATGGATGTTGTTTCCATTGAAAAGACAAATGAGCTGTTCCGTCTTATATATGATG TCAAAGGCAGATTTACTATTCACCGTATTACTCCTGAGGAGGCTAAATACAAGC

			TGTGCAAGGTGCGGCGCGTGGCGACGGGCCCCAAGAACGTGCCTTACCTGGTG ACCCACGACGGACGCACCGTGCGATACCCCGACCCACTCATCAAGGTCAACGA CTCCATCCAGCTCGACATCGCCACCTCCAAGATCATGGACTTCATCAAGTTTGA ATCTGGTAACCTATGTATGATCACGGGAGGCCGTAACTTGGGGCGCGTGGGCAC CATCGTGTCCCGCGAGCGACATCCCGGGTCCTTCGACATCGTGCATATACGGGA CTCCACCGGACATACCTTCGCTACCAGATTGAACAACGTGTTCATAATCGGCAA GGGCACGAAG
CS002	SEQ ID NO: 1708 GAGTTTCTTTA GTAAAGTATTC GGTGG	SEQ ID NO: 1709 GCAATGTCATC CATCAKRTCRT GTAC	SEQ ID NO: 1684 GAGTTTCTTTAGTAAAGTATTCGGTGGCAAGAAGGAGAGGAAGGGTCCATCAA CACACGAAGCTATACAGAAATTACGCGAAACGGAAGAGTTATTGCAGAAGAAA CAAGAGTTTCTAGAGCGAAAGATCGACACTGAATTACAAACGGCGAGAAAACA TGGCACAAAGAATAAGAGAGCTGCCATTGCGGCACTGAAGCGCAAGAAGCGTT ATGAAAAGCAGCTTACCCAGATTGATGGCACGCTTACCCAAATTGAGGCCCAAA GGGAAGCGCTAGAAGGAGCTAACACCAATACACAGGTGCTTAACACTATGCGA GATGCTGCTACCGCTATGAGACTCGCCCACAAGGATATCGATGTAGACAAGGTA CACGATCTGATGGATGACATTGC
CS003	SEQ ID NO: 1710 CAGGAGTTGAR RATHATYGGHS ARTA	SEQ ID NO: 1711 CAGGTTCTTCCT CTTKACRCGDC C	SEQ ID NO: 1686 TGGTCTCCGCAACAAGCGTGAGGTGTGGAGGGTGAAGTACACGCTGGCCAGGA TCCGTAAGGCTGCCCGTGAGCTGCTCACACTCGAGGAGAAAGACCCTAAGAGG TTATTCGAAGGTAATGCTCTCCTTCGTCGTCTGGTGAGGATCGGTGTGTTGGATG AGAAGCAGATGAAGCTCGATTATGTACTCGGTCTGAAGATTGAGGACTTCTTGG AACGTCGTCTCCAGACTCAGGTGTTCAAGGCTGGTCTAGCTAAGTCTATCCATC ATGCCCGTATTCTTATCAGACAGAGGCACATCCGTGTCCGCAAGCAAGTTGTGA ACATCCCTTCGTTCATCGTGCGGCTGGACTCTGGCAAGCACATTGACTTCTCGCT GAAGTCTCCGTTCGGCGGCGGCCGGCCG
CS006	SEQ ID NO: 1712 ACCTGCCAAGG AATGMGVAAY GC	SEQ ID NO: 1713 GAGATCTTCTG CACRTTKACVG CATC	SEQ ID NO: 1688 ACCTGCCAAGGAATGAGGAACGCTTTGTATGACAAATTGGATGATGGTATA ATTGCACCAGGGATTCGTGTATCTGGTGACGATGTAGTCATTGGAAAAACTATA ACTTTGCCAGAAAACGATGATGAGCTGGAAGGAACATCAAGACGATACAGTAA GAGAGATGCCTCTACATTCTTGCGAAACAGTGAAACTGGTATTGTTGACCAAGT TATGCTTACACTTAACAGCGAAGGATACAAATTTGTAAAATACGTGTGAGATC TGTGAGAATCCCACAAATTGGAGACAAATTTGCTTCTCGTCATGGTCAAAAAGG GACTTGTGGTATTCAATATAGGCAAGAAGATATGCCTTTCACTTGTGAAGGATT

			GACACCAGATATTATCATCAATCCACATGCTATCCCCTCTCGTATGACAATTGGT CACTTGATTGAATGTATTCAAGGTAAGGTCTCCTCAAATAAAGGTGAAATAGGT GATGCTACACCATTTAACGATGCTGTCAACGTGCAGAAGATCTC
CS007	SEQ ID NO: 1714 CGGTGTCCATT CACAGYTCCGG	SEQ ID NO: 1715 CGATGCAAGTA GGTGTCKGART CYTC	SEQ ID NO: 1690 TTTCAGAGATTTCTTGTTGGAACCAGAGATTTTGGGGGCTATCGTCGATTGCGGT TTCGAGCACCCTTCAGAAGTTCAACATGAATGTATTCCCCAAGCTGTTTTGGGA ATGGATATTCTTTGTCAAAGCTAAATCCGGAATGGGAAAAACCGCCGTATTTGT TTTAGCAACACTGCAACAGCTAGAACCTTCAGAAAACCATGTTTACGTATTAGT AATGTGCCATACAAGGGAACTCGCTTTCCAAATAAGCAAGGAATATGAGAGGT TCTCTAAATATATGGCTGGTGTTAGAGTATCTGTATTCTTTGGTGGGATGCCAAT TCAGAAAGATGAAGAAGTATTGAAGACAGCCTGCCCGCACATCGTTGTTGGTAC TCCTGGCAGAATATTAGCATTGGTTAACAACAAGAAACTGAATTTAAAACACCT GAAACACTTCATCCTGGATGAATGTGACAAAATGCTTGAATCTCTAGACATGAG ACGTGATGTGCAGGAAATATTCAGGAACACCCCTCACGGTAAGCAGGTCATGAT GTTTTCTGCAACATTGAGTAAGGAGATCAGACCAGTCTGTAAGAAATTTATGCA AGATCCTATGGAAGTTTATGTGGATGATGAAGCTAAACTTACATTGCACGGTTT GCAGCAACATTATGTTAAACTCAAGGAAAATGAAAAGAATAAGAAGTTATTTG AACTTTTGGATGTACTGGAGTTCAACCAAGTTGTCATATTTGTAAAGTCAGTGC AGCGCTGCATAGCTCTCGCACAGCTGCTGACAGACCAAAACTTCCCAGCTATTG GTATACACCGAAATATGACTCAAGATGAGCGTCTCTCCCGCTATCAGCAGTTCA AAGATTTCCAGAAGAGGATCCTTGTTGCGACAAATCTTTTTGGACGGGGTATGG ACATTGAAAGAGTCAACATAGTCTTCAATTATGACATGCCG
CS009	SEQ ID NO: 1716 CCTCGTTGCCA TYTGYWTKTG G	SEQ ID NO: 1717 CTGGATTCTCTC CCTCGCAMGAH ACC	SEQ ID NO: 1692 CCTCGTTGCCATTTGTATTTGGACGTTTCTGCAGCGGCTGGACTCACGGGAGCCC ATGTGGCAGCTGGACGAGAGCATCATCGGCACCAACCCCGGGCTCGGCTTCCGG CCCACGCCGCCAGAGGTCGCCAGCAGCGTCATCTGGTATAAAGGCAACGACCC CAACAGCCAACAATTCTGGGTGCAAGAAACCTCCAACTTTCTAACCGCGTACAA ACGAGACGGTAAGAAAGCAGGAGCAGGCCAGAACATCCACAACTGTGATTTCA AACTGCCTCCTCCGGCCGGTAAGGTGTGCGACGTGGACATCAGCGCCTGGAGTC CCTGTGTAGAGGACAAGCACTTTGGATACCACAAGTCCACGCCCTGCATCTTCC TCAAACTCAACAAGATCTTCGGCTGGAGGCCGCACTTCTACAACAGCTCCGACA GCCTGCCCACTGACATGCCCGACGACTTGAAGGAGCACATCAGGAATATGACA GCGTACGATAAGAATTATCTAAACATGGTATGGGTGTCTTGCGAGGGAGAGAAT CCAG
CS011	SEQ ID NO: 1718	SEQ ID NO: 1719	SEQ ID NO: 1694

	GGCTCCGGCAA GACVACMTTY GTC	GTGGAAGCAGG GCWGGCATKGC RAC	GGCTCCGGCAAGACGACCTTGTCAAACGACACTTGACTGGAGAGTTCGAGAA AAGATATGTCGCCACATTAGGTGTCGAGGTGCATCCCTTAGTATTCCACACAAA TAGAGGCCCTATAAGGTTTAATGTATGGATACTGCTGGCCAAGAAAAGTTTGG TGGTCTCCGAGATGGTTACTATATCCAAGGTCAATGTGCCATCATCATGTTCGAT GTAACGTCTCGTGTCACCTACAAAAATGTACCCAACTGGCACAGAGATTTAGTG CGAGTCTGTGAAGGCATTCCAATTGTTCTTTGTGGCAACAAAGTAGATATCAAG GACAGAAAAGTCAAAGCAAAAACTATTGTTTTCCACAGAAAAAAGAACCTTCA GTATTATGACATCTCTGCCAAGTCAAACTACAATTTCGAGAAACCCTTCCTCTGG TTAGCGAGAAAGTTGATCGGTGATGGTAACCTAGAGTTTGTCGCCATGCAGCCC TGCTTCCAC
CS013	SEQ ID NO: 1720 GGATCGTCTGC TAMGWYTWGG AGG	SEQ ID NO: 1721 CTATGGTGTCC AGCATSGCGC	SEQ ID NO: 1696 CAGATGCGCCCGTTGTTGATACTGCCGAACAGGTATACATCTCGTCTTTGGCCCT GTTGAAGATGTTAAAACACGGGCGCGCCGGTGTTCCAATGGAAGTTATGGGACT TATGTTAGGTGAATTTGTTGATGATTACACGGTGCGTGTCATAGACGTATTTGCC ATGCCTCAAACTGGCACAGGAGTGTCGGTTGAAGCTGTAGATCCTGTCTTCCAA GCAAAGATGTTGGATATGTTGAAGCAAACTGGACGACCTGAGATGGTAGTGGG ATGGTACCACTCGCATCCTGGCTTTGGATGTTGGTTATCTGGAGTCGACATTAAT ACTCAGCAGTCTTTCGAAGCTTTGTCTGAACGTGCTGTAGCTGTAGTGGTTGATC CCATTCAGTCTGTCAAGGGC
CS014	SEQ ID NO: 1722 ATGGCACTGAG CGAYGCHGAT G	SEQ ID NO: 1723 GAACTTGCGGT TGABGTTSCGDC C	SEQ ID NO: 1698 TTCAAAAGCAGATCAAGCATATGATGGCCTTCATCGAACAAGAGGCTAATGAA AAGGCCGAGGAAATCGATGCAAAGGCCGAAGAGGAGTTCAACATTGAAAAAG GCCGCCTGGTGCAGCAGCGCGCTCAAGATCATGGAATACTACGAAAAGAAA GAGAAACAAGTGGAACTCCAGAAAAAGATCCAATCTTCGAACATGCTGAATCA AGCCCGTCTGAAGGTGCTCAAAGTGCGTGAGGACCACGTACGCAACGTTCTCGA CGAGGCTCGCAAGCGCCTGGCTGAGGTGCCCAAAGACGTGAAACTTTACACAG ATCTGCTGGTCACGCTCGTCGTACAAGCCCTATTCCAGCTCATGGAACCCACAG TAACAGTTCGCGTTAGGCAGGCGGACGTCTCCTTAGTACAGTCCATATTGGGCA AGGCACAGCAGGATTACAAAGCAAAGATCAAGAAGGACGTTCAATTGAAGATC GACACCGAGAATTCCCTGCCCGCCGATACTTGTGGCGGAGTGGAACTTATTGCT GCTAGAGGGCGTATTAAGATCAGCAACACTCTGGAGTCTCGTCTGGAGCTGATA GCCCAACAACTGTTGCCCGAAATACGTACCGCATTGTTC
CS015	SEQ ID NO: 1724 GCCGCAAGGA	SEQ ID NO: 1725 CGATCAAAGCG	SEQ ID NO: 1700 ATCGTGCTTTCAGACGATAACTGCCCCGATGAGAAGATCCGCATGAACCGCGTC

	GACBGTVTGC	WCCRAAVCGAC G	GTGCGAAACAACTTGCGTGTACGCCTGTCAGACATAGTCTCCATAGCGCCTTGT CCATCGGTCAAATATGGGAAACGGGTACATATATTGCCCATTGATGATTCTGTC GAGGGTTTGACTGGAAATTTATTCGAAGTCTACTTGAAACCATACTTCATGGAA GCTTATCGGCCTATCCATCGCGATGACACATTCATGGTTCGCGGGGGCATGAGG GCTGTTGAATTCAAAGTGGTGGAGACTGATCCGTCGCCGTATTGCATCGTCGCT CCCGACACAGTGATACACTGCGAAGGAGACCCTATCAAACGAGAGGAAGAAGA AGAAGCCCTAAACGCCGTAGGGTACGACGACATCGGTGGCTGTCGTAAACAGC TCGCTCAGATCAAAGAGATGGTCGAGTTGCCTCTAAGGCATCCGTCGCTGTTCA AGGCAATTGGTGTGAAGCCGCCACGTGGAATCCTCATGTATGGGCCGCCTGGTA CCGGCAAAACTCTCATTGCTCGGGCAGTGGCTAATGAAACTGGTGCATTCTTCT TTCTGATCAACGGGCCGGAGATCATGTCCAAACTCGCGGGCGAGTCCGAATCGA ACCTTCGCAAGGCATTCGAGGAAGCGGACAAGAACTCCCCGGCTATAATCTTCA TCGATGAACTGGATGCCATCGCACCAAAGAGGGAGAAGACTCACGGTGAAGTG GAGCGTCGTATTGTGTCGCAACTACTTCTTATGGATGGAATGAAGAAGTCA TCGCACGTGATCGTAATGGCCGCCACCAACCGTCCGAATTCGATCGACCCGGCG CTA
CS016	SEQ ID NO: 1726 GTTCACCGGCG AYATYCTGCG	SEQ ID NO: 1727 GTCGCGCAGGT AGAAYTCKGC	SEQ ID NO: 1702 AGGATGGAAGCGGGGATACGTTTGAGCATCTCCTTGGGGAAGATACGGAGCAG CTGCCAGCCGATGTCCAGCGACTCGAATACTGTGCGGTTCTCGTAGTTGCCCTGT GTGATGAAGTTCTTCTCGAACTTGGTGAGGAACTCGAGGTAGAGCAGATCGTCG GGTGTCAGGGCTTCCTCACCGACGACAGCCTTCATGGCCTGCACCGTCCTTACCG ATGGCGTAGCAGGCGTACAGCTGGTTGGAAACATCAGAGTGGTCCTTGCGGGTC ATTCCCTCACCGATGGCAGACTTCATGAGACGAGACAGGGAAGGCAGCACGTTT ACAGGCGGGTAGATCTGTCTGTTGTGGAGCTGACGGTCTACGTAGATCTGTCCC TCAGTGATGTAGCCCGTTAAATCGGGAATAGGATGGGTGATGTCGTCGTTGGGC ATAGTCAAGATGGGGATCTGCGTGATGGATCCGTTTCTACCCTCTACACGCCCG GCTCTCTCGTAGATGGTGGCCAAATCGGTGTACATGTAACCTGGGAAACCACGT CGTCCGGGCACCTCCTCACGGGCGGCGGACACTTCACGCAGAGCCTCCGCGTAC GAAGACATGTCAGTCAAGATTACCAGCACGTGTTTCTCACACTGGTAGGCCAAG AACTCAGCAGCAGTCAAGGCCAAACGTGGTGTGATGATTCTCTCAATAGTGGGA TCGTTGGCCAGATTCAAGAACAGGCACACGTTCTCCATGGAGCCGTTCTCCTCG AAGTCCTGCTTGAAGAACCGGGCCGTCTCCATGTTCACACCCATGGCGGCGAAC ACGATGGCAAAGTTGTCCTCGTGGTCGTCCAGCACAGATTTGCCGGGGATCTTT ACAAGACCGGCTTGCCTACAGATCTGGGCGGCAATTTCGTTGTGTGGCAGACCG GCAGCCGAGAAAATGGGGATCTTTTGCCCGCGAGCAATGGAGTTCATCACGTCG ATAGCGGAGATACCAGTCTGGATCATTTCCTCAGGGTAGATACGGGACCAGGG

			GTTGATGGGCTGTCCCTGGATGTCCAAAAAGTCTTCAGCAAGGATTGGGGGACC TTTGTCAATGGGTTTTCCAGAGCCGTTGAATACGCGACCCAACATGTCTTCGGA GACAGGGGTGC
CS018	SEQ ID NO: 1728 GCTCCGTCTAC ATHCARCCNGA RGG	SEQ ID NO: 1729 GTGCATCGGTA CCAHSCHGCRT C	SEQ ID NO: 1704 GCTCCGTCTACATTCAGCCGGAAGGCGTCCCTGTACCTGCTCAGCAATCCCAAC AGCAGCAGAGTTACCGCCACGTCAGCGAGAGCGTCGAACACAAATCCTACGGC ACGCAAGGGTACACCACTTCGGAACAGACCAAGCAGACACAGAAGGTGGCGTA CACCAACGGTTCCGACTACTCTTCCACGGACGACTTTAAGGTGGATACGTTCGA ATACAGACTCCTCCGAGAAGTTTCGTTCAGGGAATCCATCACGAAGCGGTACAT TGGCGAGACAGACATTCAGATCAGCACGGAGGTCGACAAGTCTCTCGGTGTGGT GACCCCTCCTAAGATAGCACAAAAGCCTAGGAATTCCAAGCTGCAGGAGGGAG CCGACGCTCAGTTTCAAGTGCAGCTGTCGGGTAACCCGCGGCCACGGGTGTCAT GGTTCAAGAACGGGCAGAGGATAGTCAACTCGAACAAACACGAAATCGTCACG ACACATAATCAAACAATACTTAGGGTAAGAAACACACAAAAGTCTGATACTGG CAACTACACGTTGTTGGCTGAAAATCCTAACGGATGCGTCGTCACATCGGCATA CCTGGCCGTGGAGTCGCCTCAAGAAACTTACGGCCAAGATCATAAATCACAATA CATAATGGACAATCAGCAAACAGCTGTAGAAGAAAGAGTAGAAGTTAATGAAA AAGCTCTCGCTCCGCAATTCGTAAGAGTCTGCCAAGACCGCGATGTAACGGAGG GGAAAATGACGCGATTCGATTGCCGCGTCACGGGCAGACCTTACCCAGAAGTC ACGTGGTTCATTAACGATAGACAAATTCGAGACGATTATWATCATAAGATATTA GTAAACGAATCGTGTAATCATGCACTTATGATTACAAACGTCGATCTCAGTGAT AGTGGCGTAGTATCATGTATAGCACGCAACAAGACCGGCGAAACTTCGTTTCAG TGTAGGCTGAACGTGATAGAGAAGGAGCAAGTGGTCGCTCCCAAATTCGTGGA GCGGTTCAGCACGCTCAACGTGCGCGAGGGCGAGCCCGTGCAGCTGCACGCGC GCGCCGTCGGCACGCCTACGCCACGCATCACATGGCAGAAGGACGGCGTTCAA GTTATACCCAATCCAGAGCTACGAATAAATACCGAAGGTGGGGCCTCGACGCTG GACATCCCTCGAGCCAAGGCGTCGGACGCGGGATGGTACCGATGCAC

Table 2-PX

Target ID	**Primer Forward 5' → 3'**	**Primer Reverse 5' → 3'**	**cDNA Sequence (sense strand) 5' → 3'**
PX001	SEQ ID NO: 2110 GGCCCCAAGAAG CATTTGAAGCG	SEQ ID NO: 2111 CTTCGTGCCCTTG CCRATKATRAABA	SEQ ID NO: 2100 GGCCCCAAGAAGCATTTGAAGCGCCTGAACGCGCCGCGCGCATGGATGCT GGACAAGCTCGGCGGCGTGTACGCGCCGCGGCCCAGCACGGGCCCGCACA

	CG	AGCTGCGCGAGTGCCTGCCGCTCGTCATCTTCCTGCAACCGCCTCAAGTAC GCGCTCAGCGGCAACGAGGTGCTGAAGATCGTGAAGCAGCGCCTCATCAA GGTGGACGGCAAGGTCCGCACCGACCCACCTACCCGGCTGGATTCATGG ATGTTGTGTCGATTGAAAAGACCAATGAGCTGTTCCGTCTGATCTACGATG TGAAGGGACGCTTCACCATCCACCGCATCACTCCCGAGGAGGCCAAGTAC AAGCTGTGCAAGGTGAAGCGCGTGGCGACGGGCCCCAAGAACGTGCCGTA CATCGTGACGCACAACGGCCGCACCGCTGCGCTACCCCGACCCGCTCATCA AGGTCAACGACTCCATCCAGCTCGACATCGCCACCTGCAAGATCATGGAC ATCATCAAGTTCGACTCAGGTAACCTGTGCATGATCACGGGAGGGCGTAA CTTGGGGCGAGTGGGCACCATCGTGTCCCGCGAGAGGCACCCCGGGAGCT TCGACATCGTCCACATCAAGGACACCACCGGACACACCTTCGCCACCAGG TTGAACAACGTGTTCATCATCGGCAAGGGCACGAAG
PX009	SEQ ID NO: 2113 GCAGCCCACGCYY TGCACTC	SEQ ID NO: 2102 GCACGTTGATCTGGTACAAAGGAACCGGTTACGACAGCTACAAGTATTGG GAGAACCAGCTCATTGACTTTTTGTCAGTATACAAGAAGAAGGGTCAGAC AGCGGGTGCTGGTCAGAACATCTTCAACTGTGACTTCCGCAACCCGCCCCC ACACGGCAAGGTGTGCGACGTGGACATCCGCGGCTGGGAGCCCTGCATTG ATGAGAACCACTTCTCTTTCCACAAGTCTTCGCCTTGCATCTTCTTGAAGCT GAATAAGATCTACGGCTGGCGTCCAGAGTTCTACAACGACACGGCTAACC TGCCTGAAGCCATGCCCGTGGACTTGCAGACCCACATTCGTAACATTACTG CCTTCAACAGAGACTATGCGAACATGGTGTGGTGTCGTGCCACGGCGAG ACGCCGGCGGACAAGGAGAACATCGGGCCGGTGCGCTACCTGCCCTACCC GGGCTTCCCCGGGTACTTCTACCCGTACGAGAACGCCGAGGGGTATCTGA GCCCGCTGGTCGCCGTGCATTTGGAGAGGCCGAGGACCGGCATAGTGATC AACATCGAGTGCAAAGCGTGGGCTGC
PX010	SEQ ID NO: 2114 GTGGCTGCATAC AGTTCATTACGC AG	SEQ ID NO: 2104 CGCGGCTGCTCCA TGAAYASYTG GTGGCTGCATACAGTTCATTACGCAGTACCAGCACTCTAGTGGACAACGTC GCGTTCGGGTCACCACTGTCGCGCGCAATTGGGGCGACGCAGCCGCCAAC TTACACCACATATCGGCGGGCTTCGACCAGGAGGCGGCGGTGGTGAT GGCGCGGCTGGTGGTGTACCGCGCGGAGCAGGAGGACGGGCCCGACGTGC TGCGCTGGCTCGACCGCATGCTCATACGCCTGTGCCAGAAGTTCGGCGAGT ACGCGAAGGACGACCCGAACACAGCTTCCGTCTGTCGGAGAACTTCAGCCTG TACCCGCAGTTCATGTACCACCTGCGCCGCTCGCAGTTCCTGCAGGTCTTC AACAACTCGCCCGACGAGACCACCTTCTACAGACACATGCTGATGCGCGA AGACCTGACCCAATCCCTCATCATGATCCAGCCGATCCTCTACTCGTACAG

			CTTCGGAGGCGCGCCCGAACCCGTGCTGTTAGACACCAGCTCCATCCAGCC CGACCGCATCCTGCTCATGGACACCTTCTTCCAGATCCTCATCTACCATGG AGAGACAATGGCGCAATGGCGCGCTCTCCGCTACCAAGACATGGCTGAGT ACGAGAACTTCAAGCAGCTGCTGCGAGCGCCCGTGGACGACGCGCAGGAG ATCCTGCAGACCAGGTTCCCCGTGCCGCGGTACATTGATACAGAGCACGG CGGCTCACAGGCCCCGGTTCTTGCTTTCCAAAGTGAATCCCTCTCAGACTCA CAACAACATGTACGCGTATGGCGGGGCGATGCCGATACCATCAGCGGACG GTGGCGCCCCCGTGTTGACGGATGACGTGTCGCTGCAAGTGTTCATGGAGC AGCCGCG
PX015	SEQ ID NO: 2116 GCCGCAAGGAGA CBGTVTGC	SEQ ID NO: 2117 GCAATGGCATCAA KYTCRTCRATG	SEQ ID NO: 2106 GCCGCAAGGAGACCGTGTGCATTGTGCTGTCCGACGACAACTGCCCCGAC GAGAAGATCCGCATGAACCGCGTCGTCCGGAACACAACCTGCGAGTGCGCCT GTCAGACATTGTGTCCATCGCTCCTTGCCCGTCAGTGAAGTACGGCAAGAG AGTTCATATTCTGCCCATTGATGACTCTGTTGAGGGTTTGACTGGAAACCT GTTCGAAGTCTACCTGAAGCCGTACTTCATGGAGGCGTACCGGCCCATCCA CCGCGACGACACGTTCATGGTGCGCGGCGGCATGCGCGCCGTCGAGTTCA AGGTGGTGGAGACCGACCCCTCGCCCTACTGCATCGTGGCCCCCGACACG GTCATTCATTGTGAGGGAGAGCCGATTAAACGCGAGGAAGAAGAGGAGG CTCTCAACGCCGTCGGCTACGACGACATCGGCGGGTGCCGCAAGCAGCTG GCGCAGATCAAGGAGATGGTGGAGCTGCCGCTGCGCCACCCCTCGCTGTT CAAGGCCATCGGGGTCAAGCCGCCGCGGGGGATACTGATGTACGGGCCCC CGGGGACGGGGAAGACCTTGATCGCTAGGGCTGTCGCTAATGAGACGGGC GCATTCTTCTTCCTCATCAACGGCCCCGAGATCATGTCGAAACTCGCCGGT GAATCCGAGTCGAACCTGCGCAAGGCGTTCGAGGAGGCGGACAAGAACTC TCCGGCCATCATCCTCATTGATGAACTTGATGCCATTGC
PX016	SEQ ID NO: 2118 GTTCACCGGCGA YATYCTGCG	SEQ ID NO: 2119 CATCTCCTTGGGG AAGATACGCAGC	SEQ ID NO: 2108 GTTCACCGGCGATATTCTGCGCACGCCCGTCTCTGAGGACATGCTGGGTCG TATTTCAACGGCTCCGGCAAGCCCATCGACAAGGGGCCCCCGATCCTGGC CGAGGAGTACCTGGACATCCAGGGGCAGCCCATCAACCCGTGGTCCCGTA TCTACCCGGAGGAGATGATCCAGACTGGTATCTCCGCTATCGACGTGATGA ACTCCATCGCCCGTGGTCAGAAGATCCCCATCTTCTCCGCCGCCGGTCTGC CCCACAACGAGATTGCTGCTCAGATCTGTAGGCAGGCTGGTCTTGTCAAGG TCCCCGGAAAATCCGTGTTGGACGACCACGAAGACAACTTCGCCATCGTG TTCGCCGCCATGGGAGTCAACATGGAGACCGCCAGGTTCTTCAAGCAGGA CTTCGAGGAGAACGGTTCCATGGAGAACGTCTGTCTGTTCTTGAACTTGGC

			CAATGACCCGACCATTGAGAGGATTATCACGCCGAGGTTGGCGCTGACTG CTGCCGAGTTCTTGGCCTACCAGTGCGAGAAACACGTGTTGGTAATCTTGA CCGACATGTCTTCATACGCGGAGGCTCTTCGTGAAGTGTCAGCCGCCCGTG AGGAGGTGCCCGGACGACGTGGTTTCCCAGGTTACATGTACACGGATTTG GCCACAATCTACGAGCGCGCCGGGCGAGTCGAGGGCCGCAACGGCTCCAT CACGCAGATCCCCATCCTGACCATGCCCAACGACGACATCACCCACCCCAT CCCCGACTTGACCGGGTACATCACTGAGGGACAGATCTACGTGGACCGTC AGCTGCACAACAGGCAGATCTACCCGCCGGTGAATGTGCTCCCGTCGCTAT CTCGTCTCATGAAGTCCGCCATCGGAGAGGGCATGACCAGGAAGGACCAC TCCGACGTGTCCAACCAACTGTACGCGTGCTACGCCATCGGCAAGGACGT GCAGGCGATGAAGGCGGTGGTGGGCGAGGAGGCGCTCACGCCCGACGAC CTGCTCTACCTCGAGTTCCTCACCAAGTTCGAGAAGAACTTCATCACACAG GGAAGCTACGAGAACCGCACAGTGTTCGAGTCGCTGGACATCGGCTGGCA GCCCCTGCGTATCTTCCCCAAGGAGATG

Table 2-AD

Target ID	**Primer Forward 5' → 3'**	**Primer Reverse 5' → 3'**	**cDNA Sequence (sense strand) 5' → 3'**
AD001	SEQ ID NO: 2374 GGCCCCAAGAAGC ATTTGAAGCG	SEQ ID NO: 2375 CGCTTGTCCCG CTCCTCNGCRA T	SEQ ID NO: 2364 GGCCCCAAGAAGCATTTGAAGCGTTTAAATGCTCCTAAAGCATGGATGTTG GACAAACTCGGAGGAGTATTCGCTCCTCGCCCCAGTACTGGCCCCCACAAA TTGCGTGAATGTTTACCTTTGGTGATTTTTCTTCGCAATCGGCTCAAGTATGC TCTGACGAACTGTGAAGTAACGAAGATTGTTATGCAGCGACTTATCAAAGT TGACGGCAAGGTGCGAACCGATCCGAATTATCCCGCTGGTTTCATGGATGTT GTCACCATTGAGAAGACTGGAGAGTTCTTCAGGCTGGTGTATGATGTGAAA GGCCGTTTCACAATTCACAGAATTAGTGCAGAAGAAGCCAAGTACAAGCTC TGCAAGGTCAGGAGAGTTCAAACTGGGCCAAAAGGTATTCCATTCTTGGTG ACCCATGATGGCCGTACTATCCGTTATCCTGACCCAGTCATTAAAGTTAATG ACTCAATCCAATTGGATATTGCCACTTGTAAAATCATGGACCACATCAGATT TGAATCTGGCAACCTGTGTATGATTACTGGTGGACGTAACTTGGGTCGAGTG GGGACTGTTGTGAGTCGAGAACGTCACCCAGGCTCGTTTGATATTGTTCATA TCAAGGATACCCAAGGACATACTTTTGCCACAAGATTGAATAATGTATTCAT CATTGGAAAAGCTACAAAGCCTTACATTTCATTGCCAAAGGGTAAGGGTGT GAAATTGAGTATCGCCGAGGAGCGGGACAAGCG

AD002	SEQ ID NO: 2376 GAGTTTCTTTAGTA AAGTATTCGGTGG	SEQ ID NO: 2377 GCAATGTCATC CATCAKRTCRT GTAC	SEQ ID NO: 2366 GAGTTTCTTTAGTAAAGTATTCGGTGGGAAGAAAGATGGAAAGGCTCCGAC CACTGGTGAGGCCATTCAGAAACTCAGAGAAACAGAAGAAATGTTAATCAA AAAGCAGGAATTTTTAGAGAAGAAAATCGAACAAGAAATCAATGTTGCAA AGAAAAATGGAACGAAAAATAAGCGAGCTGCTATTCAGGCTCTGAAAAGG AAAAAGAGGTATGAAAAACAATTGCAGCAAATTGATGGCACCTTATCCACA ATTGAAATGCAAAGAGAAGCTTTGGAGGGTGCTAATACTAATACAGCTGTA TTACAAACAATGAAATCAGCAGCAGATGCCCTTAAAGCAGCTCATCAGCAC ATGGATGTGGACAAGGTACATGACCTGATGGATGACATTGC
AD009	SEQ ID NO: 2378 GAGTCCTAGCCGC VYTSGTKGC	SEQ ID NO: 2379 CTGGATTCTCT CCCTCGCAMG AHACC	SEQ ID NO: 2368 GAGTCCTAGCCGCCTTGGTTGCAGTATGTTTATGGGTCTTCTTCCAGACACT GGATCCTCGTATTCCCACCTGGCAGTTAGATTCTTCTATCATTGGCACATCA CCTGGCCTAGGTTTCCGGCCAATGCCAGAAGATAGCAATGTAGAGTCAACT CTCATCTGGTACCGTGGAACAGATCGTGATGACTTCCGTCAGTGGACAGAC ACCCTTGATGAATTTCTTGCTGTGTGTACAAGACTCCTGGTCTGACCCCTGGTC GAGGTCAGAACATCCACACAACTGTGACTATGATAAGCCGCCAAAGAAAGGCC AAGTTTGCAATGTGGACATCAAGAATTGGCATCCCTGCATTCAAGAGAATC ACTACAACTACCACACAAGAGCTCTCCATGCATATTCATCAAGCTCAACAAGA TCTACAATTGGATCCCTGAATACTACTACAATGAGAGTACGAATTTGCCTGAGCA GATGCCAGAAGACCTGAAGCAGTACATCCACACAACCTGGAGAGTAACAACTC GAGGGAGATGAACACGGTGTGGGTGTCGTGCGAGGGAGAGAATCCAG
AD015	SEQ ID NO: 2380 GGATGAACTACAG CTBTTCCGHGG	SEQ ID NO: 2381 GTCCGTGGGA YTCRGCHGCA ATC	SEQ ID NO: 2370 GGATGAACTACAGCTTTTCCGAGGAGATACAGTTCTTCTTAAAGGAAAAAG GAGGAAAGAAACTGTATGCATAGTGTTATCAGATGATACATGTCCTGATGG AAAAATAAGAATGAATAGAGTTGTACGCAACAATTTACGTGTTCGTTTGTCA GATGTTGTATCTGTACAACCTTGTCCTGATGTTAAGTATGGAAAAAGGATAC ATGTACTACCAATTGATGATACAGTTGAAGGACTAACCGGGAATTTGTTTGA GGTGTACTTAAAACCGTACTTTCTCGAAGCATACCGACCCATTCACAAAGAT GATGCGTTTATTGTTCGTGGTGGTATGCGAGCAGTAGAATTCAAAGTAGTGG AAACAGATCCTTCACCATATTGTATTGTTGCTCCTGATACTGTTATTCACTGT GAAGGTGATCCAATAAAACGTGAAGAGGAAGAAGCATTAAATGCTGT TGGTTATGATGACATTGGGGGTTGCCGAAAACAGCTAGCACAGATCAAGGA AATGGTGGAATTGCCATTACGGCACCCCAGTCTCTTTAAGGCTATTGGTGTT AAGCCACCGAGGGGAATACTGCTGTATGGACCCCCTGGAACTGGTAAAACC CTCATTGCCAGGGCTGTGGCTAATGAAACTGGTGCATTCTTCTTTTTAATAA

			ATGGTCCTGAAATTATGAGCAAGCTTGCTGGTGAATCTGAAAGCAACTTAC GTAAGGCATTTGAAGAAGCTGATAAGAATGCTCCGGCAATTATATTTATTGA TGAACTAGATGCAATTGCCCCTAAAAGAGAAAAAACTCATGGAGAGGTGGA ACGTCGCATAGTTTCACAACTACTAACTTTAATGGATGGTCTGAAGCAAAGT TCACATGTTATTGTTATGGCTGCCACAAATAGACCCAACTCTATTGATGGTG CCTTGCGCCGCTTTGGCAGATTTGATAGGGAAATTGATATTGGTATACCAGA TGCCACTGGTCGCCTTGAAATTCTTCGTATCCATACTAAGAATATGAAGTTA GCTGATGATGTTGATTTGGAACAGATTGCAGCCGAATCCCACGGAC
AD016	SEQ ID NO: 2382 GTTCACCGGCGAY ATYCTGCG	SEQ ID NO: 2383 GGAATAGGAT GGGTRATRTCG TCG	SEQ ID NO: 2372 GTTCACCGGCGATATTCTGCGCGTGCCCGTGTCCGAGGACATGCTGGGCCGC ACCTTCAACGGCAGCGGCATCCCCATCGACGGCGGCCCGCCCATCGTCGCA GAGACCTACCTCGACGTCCAGGGCATGCCGATTAATCCTCAAACGCGCATC TACCCGGAAGAAATGATCCAGACGGGGATCTCGACCATCGACGTGATGACG TCCATCGCGCGAGGGCAGAAGATCCCCATCTTCTCGGGCGCAGGGCTGCCA CACAACGAGATCGCTGCGCAGATCTGCCGACAGGCGGGGCTGGTGCAGCAC AAGGAGAACAAGGACGACTTCGCCATCGTGTTCGCGGCGATGGGCGTCAAC ATGGAGACGGCGCGCTTCTTCAAGCGCGAGTTCGCGCAGACGGGCGCGTGC AACGTGGTGCTGTTCCTCAACCTGGCCAACGACCCCACCATCGAGCGCATC ATCACCCCGCGCCTCGCGCTCACCGTGGCCGAGTTCCTGGCCTACCAGTGCA ACAAGCACGTGCTCGTCATCATGACCGACATGACCTCCTACGCGGAGGCGC TGCGCGAGGTGAGCGCGGCGCGCGAGGAGGTTCCTGGGCGAAGAGGCTTCC CAGGCTACATGTACACCGATCTCTCCACCATCTACGAGCGCGCTGGCCGTGT GCAAGGCCGCCCCGGCTCCATCACTCAGATCCCCATCCTGACGATGCCCAA CGACGACATCACCCATCCTATTC

Table 3-LD

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
LD001	1	SEQ ID NO: 2 (frame +1) GPKKHLKRLNAPKAWMLDKLGGVFAPRPSTGPHKLRESLPLVIFLRNRLKYALTNSEVTKIVMQRLIKV DGKVRTDSNYPAGFMDVITIEKTGEFFRLIYDVKGRFAVHRITAEEAKYKLCKVRRMQTGPKGIPFIVTH DGRTIR
LD002	3	SEQ ID NO: 4 (frame -3)

		AMQALKRKKRLEKNQLQIDGTLTTIELQREALEGASTNTTVLESMKNAAEALKKAHKNLDVDNVHDM MDDI
LD003	5	SEQ ID NO: 6 (frame -2) PRRPYEKARLDQELKIIGEYGLRNKREVWRVKYTLAKIRKAARELLTLEEKDQRRLFEGNALLRRLVRIG VLDETRMKLDYVLGLKIEDFLERRLQTQVFKLGLAKSIHHARVLVRQRHIRVRKQVVNIPSFIVRLDSQK HIDFSLKSPFGGGRPGRVKRKNL
LD006	7	SEQ ID NO: 8 (frame +1) HNYGWQVLVASGVVEYIDTLEEETVMIAMNPEDLRQDKEYAYCTTYTHCEIHPAMILGVCASIIPFPDHN QSPRNTYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPHKPLVTTRSMEYLRFRELPAGINSIVAIACYT GYNQEDSVILNASAVERGFFRSVFYRSYKDAESKRIGDQEEQFE
LD007	9	SEQ ID NO: 10 (frame +1) PKKDVKGTYVSIHSSGFRDFLLKPEILRAIVDCGFEHPSEVQHECIPQAVIGMDILCQAKSGMGKTAVFVL ATLQQLEPADNVVYVLVMCHTRELAFQISKEYERFSKYMPSVKVGVFFGGMPIANDEEVLKNKCPHIVV GTPGRILALVKSRKLVLKNLKHFILDECDKMLELLDMRRDVQEIYRNTPHTKQVMMFSATLSKEIRPVC KKFMQDPMEVYVDDEAKLTLHGLQQHYVKLKENEKNKKLFELLDVLEFNQVVIFVKSVQRCVALAQL LTEQNFPAIGIHRGMDQKERLSRYEQFKDFQKRILVATNLFGRGMDIERVNIVFNYDMPEDSDTYLH
LD010	11	SEQ ID NO: 12 (frame +1) VKCSRELKIQGGIGSCVSLNVKNPLVSDTEIGMGNTVQWKMCTVTPSTTMALFFEVVNQHSAPIPQGGR GCIQFITQYQHASGQKRIRVTTVARNWADASANIHHVSAGFDQEAAAVIMARMAVYRAESDDSPDVLR WVDRMLIRLCQKFGEYNKDDPNSFRLGENFSLYPQFMYHLRRSQFLQVFNNSPDETSFYRHMLMREDL TQSLIMIQPILYSYSFNGPPEPVLLDTSSIQPDRILLMDTFFQILIFHGETIAQW
LD011	13	SEQ ID NO: 14 (frame -1) PTFKCVLVGDGGTGKTTFVKRHMTGEFEKRYVATLGVEVHPLVFHTNRGPIRFNVWDTAGQEKFGGLR DGYYIQGQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFHRKKNLQ YYDISAKSNYNFEKPFLWLARKLIGDPNLEFVAMPALLP
LD014	15	SEQ ID NO: 16 (frame +3) QIKHMMAFIEQEANEKAEEIDAKAEEEFNIEKGRLVQQQRLKIMEYYEKKEKQVELQKKIQSSNMLNQA RLKVLKVREDHVRTVLEEARKRLGQVTNDQGKYSQILESLILQGLYQLFEKDVTIRVRPQDRELVKSIIPT VTNKYKDATGKDIHLKIDDEIHLSQETTGGIDLLAQKNKIKISNTMEARLELISQQLLPEI
LD015	17	SEQ ID NO: 18 (frame -1) RHPSLFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESESNLRKAFEEADKN SPAIIFIDELDAI

LD016	19	SEQ ID NO: 20 (frame -2) TVSGVNGPLVILEDVKFPKYNEIVQLKLADGTIRSGQVLEVSGSKAVVQVFEGTSGIDAKNTACEFTGDIL RTPVSEDMLGRVFNGSGKPIDKGPPILAEDFLDIQGQPINPWSRIYPEEMIQTGITAIDVMNSIARGQKIPIF SAAGLPHNEIAAQICRQAGLVKIPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLF LNLANDPTIERIITPRLALTAAEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTD LATIYERAGRVEGRNGSITQIPILTMPNDDITHPI
LD018	21	SEQ ID NO: 22 (frame +2) TWFKDGQRITESQKYESTFSNNQASLRVKQAQSEDSGHYTLLAENPQGCIVSSAYLAIEPVTTQEGLIHES TFKQQQTEMEQIDTSKTLAPNFVRVCGDRDVTEGKMTRFDCRVTGRPYPDVTWYINGRQVTDDHNHKI LVNESGNHALMITTVSRNDSGVVTCVARNKTGETSFQCNLNVIEKEQVVAPKFVERFTTVNVAEGEPVS LRARAVGTPVPRITWQRDGAPLASGPDVRIAIDGGASTLNISRAKASDAAWYRC
LD027	23	SEQ ID NO: 24 (frame +1) HGGDKPYLISGADDRLVKIWDYQNKTCVQTLEGHAQNVTAVCFHPELPVALTGSEDGTVRVWHTNTH RLENCLNYGFERVWTICCLKGSNNVSLGYDEGSILVKVGREEPAVSMDASGGKIIWARHSELQQANLKA LPEGGEIRDGERLPVSVKDMGACEIYPQTIQHNPNGRFVVVCGDGEYIIYTAMALRNKAFGSAQEFVWA QDSSEYAIRESGSTIRIFKNFKERKNFKSDFSAEGIYGGFLLGIKSVSGLTFYDWETLDLVRRIEIQPRAVY WSDSGKLVCLATEDSYFILSYDSEQVQKARENNQVAEDGVEAAFDVLGEMNESVRTGLWVGDCFIYT

Table 3-PC

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
PC001	247	SEQ ID NO: 248 (frame +1) AWMLDKLGGVFAPRPSTGPHKLRESLPLVIFLRNRLKYALTNSEVTKIVMQRLIKVDGKVRTDSNYPAG FMDVITIEKTGEFFRLIYDVKGRFAVHRITAEEAKYKLCKVRRVQTGPKGIPFLVTHDGRTIRYPDPNIKV NDTIQMEIATSKILDYIKFES
PC003	249	SEQ ID NO: 250 (frame: +2) PRRPYEKARLDQELKIIGAFGLRNKREVWRVKYTLAKIRKAARELLTLEEKEPKRLFEGNALLRRLVRIG VLDENRMKLDYVLGLKIEDFLERRLQTQVFKSGLAKSIHHARVLIRQRHIRVRKQVVNIPSFIVRLDSQK HIDFSLKSPFGGGRPGRV
PC005	251	SEQ ID NO: 252 (frame +3) PNEINEIANTNSRQNIRKLIKDGLIIKKPVAVHSRARVRKNTEARRKGRHCGFGKRKGTANARMPQKEL WVQRMRVLRRLLKKYREAKKIDRHLYHALYMKAKGNVFRNKRVLMEYIHKKKAEKARAKMLSDQA

		NARRLKVKQARERRE
PC010	253	SEQ ID NO: 254 (frame +3) LKDSLQMSLSLLPPNALIGLITFGKMVQVHELGTEGCSKSYVFCGTKDLTAKQVQEMLGIGKGSPNPQQ QPGQPGRPGQNPQAAPVPPGSRFLQPVSKCDMNLTDLIGELQKDPWPVHQGKRPLRSTGAALSIAVGLL ECTYPNTGGRIMIFLGGPCSQGPGQVLNDDLKQPIRSHHDIHKDNAKYMKKAIKHYDHLAMRAATNSH CIDIYSCALDQTGLMEMKQCCNSTGGHMVMGDSFNSSLFKQTFQRVFSKDPKNDLKMAFNATLEVKCS RELKVQGGIGSCVSLNVKSPLVSDTELGMGNTVQWKLCTLAPSSTVALFFEVVNQHSAPIPQGGRGCIQL ITQYQHASGQRRIRVTTIARNWADATANIHHISAGFDQEAAAVVMARMAGYKAESDETPDVLRWVDR MLIRLCQKFGEYNKDDPNSFRLGENFSLYPQFMYHLRRSQFLQVFNNSPDETSFYRHMLMREDLTQSLI MIQPILYSYSFNGPPEPVLLDTSSIQPDRILLMDTFFQILIFHGETIAQW
PC014	255	SEQ ID NO: 256 (frame +3) DVQKQIKHMMAFIEQEANEKAEEIDAKAEEEFNIEKGRLVQQQRLKIMEYYEKKEKQVELQKKIQSSNM LNQARLKVLKVREDHVRAVLEDARKSLGEVTKDQGKYSQILESLILQGLFQLFEKEVTVRVRPQDRDLV RSILPNVAAKYKDATGKDILLKVDDESHLSQEITGGVDLLAQKNKIKISNTMEARLDLIA
PC016	257	SEQ ID NO: 258 (frame +2) LVILEDVKFPKFNEIVQLKLADGTLRSGQVLEVSGSKAVVQVFEGTSGIDAKNTVCEFTGDILRTPVSED MLGRVFNGSGKPIDKGPPILAEDYLDIQGQPINPWSRIYPEEMIQTGITAIDVMNSIARGQKIPIFSAAGLPH NEIAAQICRQAGLVKVPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLAND PTIERIITPRLALTAAEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTDLATIYER AGRVEGRNGSITQIPILTMP
PC027	259	SEQ ID NO: 260 (frame +1) QANLKVLPEGAEIRDGERLPVTVKDMGACEIYPQTIQHNPNGRFVVVCGDGEYIIYTAMALRNKAFGSA QEFVWAQDSSEYAIRESGSTIRIFKNFKEKKNFKSDFGAEGIYGGFLLGVKSVSGLAFYDWETLELVRRIE IQPRAIYWSDSGKLVCLATEDSYFILSYDSDQVQKARDNNQVAEDGVEAAFDVLGEINESVRTGLWVGD CFIYTNAVNRINYFVGGELVTIAHLDRPLYVLGYVPRDDRLYLVDKELGVVSYXIAIICTRISDCSHATRL PNG*SSIAFNSK

Table 3-EV

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
EV005	513	SEQ ID NO: 514 (frame +3) RCGKKKVWLDPNEITEIANTNSRQNIRKLIKDGLIIKKPVAVHSRARVRKNTEARRKGRHCGFGKRKGTAN

		ARMPRKELWIQRMRVLRRLLKKYREAKKIDRHLYHALYMKAKGNVFKNKRVMMDYIHKKKAEKARTK MLNDQADARRLKVKEARKRREERIATKKQ
EV009	515	SEQ ID NO: 516 (frame +1) PTLDPSIPKYRTEESIIGTNPGMGFRPMPDNNEESTLIWLQGSNKTNYEKWKMNLLSYLDKYYTPGKIEKGN IPVKRCSYGEKLIRGQVCDVDVRKWEPCTPENHFDYLRNAPCIFLKLNRIYGWEPEYYNDPNDLPDDMPQQ LKDHIRYNITNPVERNTVWVTCAGENPADVEYLGPVKYYPSFQGFPGYYFPYLNSEGYLSPLLAVQFKRPV SGIVINIECKAWA
EV010	517	SEQ ID NO: 518 (frame +3) GGHMVMGDSFNSSLFKQTFQRVFSKDSNGDLKMSFNAILEVKCSRELKVQGGIGPCVSLNVKNPLVSDLEI GMGNTVQWKLCSLSPSTTVALFFEVVNQHAAPIPQGGRGCIQFITQYQHSSGQKKIRVTTIARNWADATAN IHHISAGFDEQTAAVLMARIAVYRAETDESSDVLRWVDRMLIRLCQKFGEYNKDDTNSFRLSENFSLYPQF MYHLRRSQFLQVFNNSPDETSFYRHMLMREDRNQ
EV015	519	SEQ ID NO: 520 (frame +1) RHPSLFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESESNLRKAFEEADKNSP AIIFIDELDAIAPKREKTHGEVERRIVSQLLTLMDGMKKSSHVIVMAATNRPNSIDPALRRFGRFDREIDIGIP DATGRLEVLRIHTKNMKLADDVDLEQIAAETHGHVGADLASLCSEAALQQIREKMDLIDLDDEQIDAEVLN SLAVTMENFRYAMSKSSPSALRETV
EV016	521	SEQ ID NO: 522 (frame +2) TVSGVNGPLVILDSVKFPKFNEIVQLKLSDGTVRSGQVLEVSGQKAVVQVFEGTSGIDAKNTLCEFTGDILR TPVSEDMLGRVFNGSGKPIDKGPPILAEDFLDIQGQPINPWSRIYPEEMIQTGISAIDVMNSIARGQKIPIFSAA GLPHNEIAAQICRQAGLVKIPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLAN DPTIERIITPRLTLTAAEFMAYQCEKHVLVILTDMSSYAEALREVSAA

Table 3-AG

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
AG001	601	SEQ ID NO: 602 (frame +1) HLKRFAAPKAWMLDKLGGVFAPRPSTGPHKLRESLPLVIFLRNRLKYALTNCEVTKIVMQRLIKVDGKVRT DPNYPAGFMDVITIEKTGEFFRLIYDVKGRFTIHRITAEEAKYKLCKVRKVQTGPKGIPFLVTHDGRTIRYPD PMIKVNDTIQLEIATSKILDFIKFESGNLCMITGGRNLGRVGTVVNRERHPGSFDIVHIRDANDHVFATRLNN VFVIGKGSKAFVSLPRGKGVKLSIA
AG005	603	SEQ ID NO: 604 (frame +2)

		VWLDPNEINEIANTNSRQNIRKLIKDGLIIKKPVAVHSRARVRKNTEARRKGRHCGFGKRKGTANARMPQK ELWIQRMRVLRRLLKKYREAKKIDRHLYHALYMKAKGNVFKNKRVLMEYIHKKKAEKARAKMLADQAN ARRQKVKQVP*EEGRAYRREEAG
AG010	605	SEQ ID NO: 606 (frame +3) GGHMLMGDSFNSSLFKQTFQRVFAKDQNGHLKMAFNGTLEVKCSRELKVQGGIGSCVSLNVKSPLVADTE IGMGNTVQWKMCTFNPSTTMALFFEVVNQHSAPIPQGGRGCIQFITQYQHSSGQRRIRVTTIARNWADASA NIHHISAGFDQERAAVIMARMAVYRAETDESPDVLRWVDRMLIRLCQKFGEYNKDDQASFRLGENFSLYP QFMYHLRRSQFLQVFNNSPDETSFYRHMLMREDLTQSLIMIQPILYSYSFNGPPEPVLLDTSSIQPDRILLMD TFFQILIFHGETIAQW
AG014	607	SEQ ID NO: 608 (frame +3) QIKHMMAFIEQEANEKAEEIDAKAEEEFNIEKGRLVQQQRLKIMEYYEKKEKQVELQKKIQSSNMLNQARL KVLKVREDHVRAVLDEARKKLGEVTRDQGKYAQILESLILQGLYQLFEANVTVRVRPQDRTLVQSVLPTIA TKYRDVTGRDVHLSIDDETQLSESVTGGIELLCKQNKIKVCNTLEARLDLISQQLVPQIRNALFGRNINRKF
AG016	609	SEQ ID NO: 610 (frame +1) VSEDMLGRVFNGSGKPIDKGPPILAEDFLDIQGQPINPWSRIYPEEMIQTGISAIDVMNSIARGQKIPIFSAAGL PHNEIAAQICRQAGLVKLPGKSVIDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLANDP TIERIITPRLALTAAEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTDLATIYERAG RVEGRNGSITQIPILTMPNDDITHPI

Table 3-TC

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
TC001	793	SEQ ID NO: 794 (frame +1) GPKKHLKRLNAPKAWMLDKLGGVFAPRPSTGPHKLRESLPLVIFLRNRLKYALTNSEVTKIVMQRLIKV DGKVRTDPNYPAGFMDVVTIEKTGEFFRLIYDVKGRFTIHRITGEEAKYKLCKVKKVQTGPKGIPFLVTR DGRTIRYPDPMIKVNDTIQLEIATSKILDFIKFESGNLCMITGGRNLGRVGTVVSRERHPGSFDIVHIKDAN GHTFATRLNNVFIIGKGSKPYVSLPRGKGVKLSI
TC002	795	SEQ ID NO: 796 (frame +1) QEFLEAKIDQEILTAKKNASKNKRAAIQAIKRKKRYEKQLQQIDGTLSTIEMQREALEGANTNTAVLKTM KNAADALKNAHLNMDVDEVHDMMDDI
TC010	797	SEQ ID NO: 798 (frame +3) PEVLVFGHVLVLEVPPLGDCLTVENQNLEKCVHEKDPIGLNGTSVEEDGFRGAVETITVQNRLDHNETL

		GEVLPHQHVAVERGLVWGVVENLEELGAAQMVHELGIETEVFTQTETVRVVFVVFAEF
TC014	799	SEQ ID NO: 800 (frame +1) EKAEEIDAKAEEEFNIEKGRLVQQQRLKIMEYYEKKEKPVELQKKIQSSNMLNQARLKVLKVREDHVHN VLDDARKRLGEITNDQARYSQLLESLILQSLYQYLGISDELFENNIVVRVRQQDRSIIQGILPVVATKYRD ATGKDVHLKIDDESHLPSETTGGVVLYAQKGKIKIDNTLEARLDLIAQQLVPEIRTALFGRNINRKF
TC015	801	SEQ ID NO: 802 (frame +2) DELQLFRGDTVLLKGKRRKETVCIVLADENCPDEKIRMNRIVRNNLRVRLSDVVWIQPCPDVKYGKRIH VLPIDDTVEGLVGNLFEVYLKPYFLEAYRPIHKGDVFIVRGGMRAVEFKVVETEPSPYCIVAPDTVIHCD GDPIKREEEEEALNAVGYDDIGGCRKQLAQIKEMVELPLRHPSLFKAIGVKPPRGILLYGPPGTGKTLIAR AVANETGAFFFLINGPEIMSKLAGESESNLRKAFEEADKNSPAIIFIDELDAIAPKREKTHGEVERRIVSQLL TLMDGMKKSSHVIVMAATNRPNSIDPALRRFGRFD

Table 3-MP

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
MP001	888	SEQ ID NO: 889 (frame +1) GPKKHLKRLNAPKAWMLDKSGGVFAPRPSTGPHKLRESLPLLIFLRNRLKYALTGAEVTKIVMQRLIKVDG KVRTDPNYPAGFMDVISIQKTSEHFRLIYDVKGRFTIHRITPEEAKYKLCKVKRVQTGPKGVPFLTTHDGRTI RYPDPNIKVNDTIRYDIASSKILDHIRFETGNLCMITGGRNLGRVGIVTNRERHPGSFDIVHIKDANEHIFATR MNNVFIIGKGQKNYISLPRSKGVKLT
MP002	890	SEQ ID NO: 891 (frame +2) SFFSKVFGGKKEEKGPSTEDAIQKLRSTEEMLIKKQEFLEKKIEQEVAIAKKNGTTNKRAALQALKRKKRYE QQLAQIDGTMLTIEQQREALEGANTNTAVLTTMKTAADALKSAHQNMNVDDVHDLMDDI
MP010	892	SEQ ID NO: 893 (frame +3) GCIQFITQYQHSSGYKRIRVTTLARNWADPVQNMMHVSAAFDQEASAVLMARMVVNRAETEDSPDVMR WADRTLIRLCQKFGDYQKDDPNSFRLPENFSLYPQFMYHLRRSQFLQVFNNSPDETSYYRHMLMREDVTQ SLIMIQPILYSYSFNGRPEPVLLDTSSIQPDKILLMDTFFHILIFHGETIAQWRAMDYQNRPEYSNLKQLLQAP VDDAQEILKTRFPMPRYIDTEQGGSQARFLLCKVNPSQTHNNMYAYGG*WWSTSFDR*CKLAAVHGAAA
MP016	894	SEQ ID NO: 895 (frame +1) VSEDMLGRVFNGSGKPIDKGPPILAEDYLDIEGQPINPYSRTYPQEMIQTGISAIDIMNSIARGQKIPIFSAAGL PHNEIAAQICRQAGLVKKPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLAND PTIERIITPRLALTAAEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTDLATIYERAG

		RVEGRNGSITQIPILTMPNDDITHPI
MP027	896	SEQ ID NO: 897 (frame +3) PITKTRRVFRH*KAMLKIFLLVCFHPELPIVLTGSEDGTVRIWHSGTYRLESSLNYGLERVWTICCLRGSNNV ALGYDEGSIMVKVGREEPAMSMDVHGGKIVWARHSEIQQANLKAMLQAEGAEIKDGERLPIQVKDMGSC EIYPQSISHNPNGRFLVVCGDGEYIIYTSMALRNKAFGSAQDFVWSSDSEYAIRENSSTIKVFKNFKEKKSFK PEGGADGIFGGYLLGVKSVTGLALYDWENGNLVRRIETQPKHVFWSESGELVCLATDEAYFILRFDVNVLS AARASNYEAASPDGLEDAFEILGEVQEVVKTGLWVGDCFIYTNGVNRINYYVGGEVVTVS

Table 3-NL

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
NL001	1071	SEQ ID NO: 1072 (frame +2) KSWMLDKLGGVYAPRPSTGPHKLRESLPLVIFLRNRLKYALTNCEVKKIVMQRLIKVDGKVRTDPNYPAGFM DVVQIEKTNEFFRLIYDVKGRFTIHRITAEEAKYKLCKVKRVQTGPKGIPFLTTHDGRTIRYPDPLVKVNDTIQL DIATSKIMDFIRFDSGNLCMITGGRNLGRVGTVVNRERHPGSFDIVHIKDVLGHTFATRLNNVFIIGKGSKAYV SLPKGKGVKLS
NL002	1073	SEQ ID NO: 1074 (frame +1) DEKGPTTGEAIQKLRETEEMLIKKQDFLEKKIEVEIGVARKNGTKNKRAAIQALKRKKRYEKQLQQIDGTLSTI EMQREALEGANTNTAVLQTMKNAADALKAAHQHMDVDQ
NL003	1075	SEQ ID NO: 1076 (frame +2) PRRPYEKARLEQELKIIGEYGLRNKREVWRVKYALAKIRKAARELLTLEEKDQKRLFEGNALLRRLVRIGVLD EGRMKLDYVLGLKIEDFLERRLQTQVYKLGLAKSIHHARVLIRQRHI RVRKQVVNIPSFVVRLDSQKHIDFSLKSPFGGGRPGRV
NL004	1077	SEQ ID NO: 1078 (frame +1) KELAAVRTVCSHIENMLKGVTKGFLYKMRAVYAHFPINCVTTENNSVIEVRNFLGEKYIRRVRMAPGVTVTN STKQKDELIVEGNSIEDVSRSAALIQQSTTVKNKDIRKFLD
NL005	1079	SEQ ID NO: 1080 (frame +1) LDPNEINEIANTNSRQSIRKLIKDGLIIKKPVAVHSRARVRKNTEARRKGRHCGFGKRKGTANARMPQKVLWV NRMRVLRRLLKKYRQDKKIDRHLYHHLYMKAKGNVFKNKRVLMEFIH KKKAEKARMKMLNDQAEARRQKVKEAKKRRE
NL006	1081	SEQ ID NO: 1082 (frame +3)

		VLVSSGVVEYIDTLEEETTMIAMSPDDLRQDKEYAYCTTYTHCEIHPAMILGVCASIIPFPDHNQSPRNTYQSA MGKQAMGVYITNFHVRMDTLAHVLFYPHKPLVTTRSMEYLRFRELPAGINSVVAIACYTGYNQEDSVILNAS AVERGFFRSVFFRSYKDAESKRIGDQEEQFEKPTRQTCQGMRNAIYDKLDDDGIIAPGLRVSGDDVVIGKTITL PDNDDELEGTTKRFTKRDASTFLRNSETGIVDQVMLTLNSEGYKFCKIRVRSVRIPQIGDKFASRHGQKGTCGI QYRQEDMPFTSEGIAPDIIINPHAIPSRMTIGHLIECLQGKVSSNKGEIGDATPFN
NL007	1083	SEQ ID NO: 1084 (frame +2) FRDFLLKPEILRAILDCGFEHPSEVQHECIPQAVLGMDILCQAKSGMGKTAVFVLATLQQIEPTDNQVSVLVMC HTRELAFQISKEYERFSKCMPNIKVGVFFGGLPIQRDEETLKLNCPHIVVGTPGRILALVRNKKLDLKHLKHFV LDECDKMLELLDMRRDVQEIFRNTPHSKQVMMFSATLSKEIRPVCKKFMQDPMEVYVDDEAKLTLHGLQQH YVKLKENEKNKKLFELLDILEFNQVVIFVKSVQRCMALSQLLTEQNFPAVAIHRGMTQEERLKKYQEFKEFLK RILVATNLFGRGMDIERVNIVFNYDMP
NL008	1085	SEQ ID NO: 1086 (frame +1) GRIENQKRVVGVLLGCWRPGGVLDVSNSFAVPFDEDDKEKNVWFLDHDYLENMFGMFKKVNAREKVVGW YHTGPKLHQNDVAINELIRRYCPNCVLVIIDAKPKDLGLPTEAYRVVEEIHDDGSPTSKTFEHVMSEIGAEEAE EIGVEHLLRDIKDTTVGSLSQRVTNQLMGLKGLHLQLQDMRDYLNQVVEGKLPMNHQIVYQLQDIFNLLPDI GHGNFVDSLY
NL009	1087	SEQ ID NO: 1088 (frame +1) CDYDRPPGRGQVCDVDVKNWFPCTSENNFNYHQSSPCVFLKLNKIIGWQPEYYNETEGFPDNMPGDLKRHIA QQKSINKLFMQTIWITCEGEGPLDKENAGEIQYIPRQGFPGYFYPYTN A
NL010	1089 1115	SEQ ID NO: 1090 (amino terminus end) (frame +2) SSRLEATRLVVPVGCLYQPLKERPDLPPVQYDPVLCTRNTCRAILNPLCQVDYRAKLWVCNFCFQRNPFPPQY AAISEQHQPAELIPSFSTIEYIITRAQTMPPMFVLVVDTCLDDEELGALKDSLQMSLSLLPPNALIGLITFGKMVQ VHELGCDGCSKSYVFRGVKDLTAKQIQDMLGIGKMAAAPQPMQQRIPGAAPSAPVNRFLQPVGKCDMSLTD LLGELQRDPWNVAQGKRPLR STGVALSIAVGLLECT SEQ ID NO: 1116 (carboxy terminus end) (frame +3) LNVKGSCVSDTDIGLGGTSQWKMCAFTPHTTCAFFFEVVNQHAAPIPQGGRGCIQFITQYQHSSGQRRIRVTTI ARNWADASTNLAHISAGFDQEAGAVLMARMVVHRAETDDGPDVMRWADRMLIRLCQRFGEYSKDDPNSFR LPENFTLYPQFMYHLRRSQFLQVFNNSPDETSYYRHILMREDLTQSLIMIQPILYSYSFNGPPEPVLLDTSSIQPD RILLMDTFFQILIFHGETIA
NL011	1091	SEQ ID NO: 1092 (frame +2) DGGTGKTTFVKRHLTGEFEKKYVATLGVEVHPLVFHTNRGVIRFNVWDTAGQEKFGGLRDGYYIQGQCAIIM FDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFHRKKNLQYYDISAKSNYNFEKPFL WLAKKLIGDPNLEFVAMPALLPPEVTMDPQX

NL012	1093	SEQ ID NO: 1094 (frame +2) QQTQAQVDEVVDIMKTNVEKVLERDQKLSELDDRADALQQGASQFEQQAGKLKRKF
NL013	1095	SEQ ID NO: 1096 (frame +2) AEQVYISSLALLKMLKHGRAGVPMEVMGLMLGEFVDDYTVRVIDVFAMPQSGTGVSVEAVDPVFQAKMLD MLKQTGRPEMVVGWYHSHPGFGCWLSGVDINTQESFEQLSKRAVAVVV
NL014	1097	SEQ ID NO: 1098 (frame +2) FIEQEANEKAEEIDAKAEEEFNIEKGRLVQHQRLKIMEYYDRKEKQVELQKKIQSSNMLNQARLKALKVRED HVRSVLEESRKRLGEVTRNPAKYKEVLQYLIVQGLLQLLESNVVLRVR EADVSLIEGIVGSCAEQYAKMTGKEVVVKLDADNFLAAETCGGVELFARNGRIKIPNTLESRLDLISQQLVPEI RVALF
NL015	1099	SEQ ID NO: 1100 (frame +1) IVLSDETCPFEKIRMNRVVRKNLRVRLSDIVSIQPCPDVKYGKRIHVLPIDDTVEGLTGNLFEVYLKPYFLEAYR PIHKDDAFIVRGGMRAVEFKVVETDPSPYCIVAPDTVIHCEGDPIKREDEEDAANAVGYDDIGGCRKQLAQIK EMVELPLRHPSLFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESESNLRKAFEE ADKNAPAIIFIDELDAIAPKREKTHGEVERRIVSQLLTLMDGLKQSSHVIVMAATNRPNSIDAALRRFGRFDREI DIGIPDATGRLEVLRIHTKNMKLADDVDLEX
NL016	1101	SEQ ID NO: 1102 (frame +2) TPVSEDMLGRVFNGSGKPIDKGPPILAEDYLDIQGQPINPWSRIYPEEMIQTGISAIDVMNSIARGQKIPIFSAAG LPHNEIAAQICRQAGLVKLPGKSVLDDSEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLANDP TIERIITPRLALTAAEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTDLATIYERAGRV EGRNGSIT
NL018	1103	SEQ ID NO: 1104 (frame +2) MQMPVPRPQIESTQQFIRSEKTTYSNGFTTIEEDFKVDTFEYRLLREVSFRESLIRNYLHEADMQMSTVVDRAL GPPSAPHIQQKPRNSKIQEGGDAVFSIKLSANPKPRLVWFKNGQRIGQTQKHQASYSNQTATLKVNKVSAQDS GHYTLLAENPQGCTVSSAYLAVESAGTQDTGYSEQYSRQEVETTEAVDSSKMLAPNFVRVPADRDASEGKM TRFDCRVTGRPYPDVAWFINGQQVADDATHKILVNESGNHSLMITGVTRLDHGVVGCIARNKAGETSFQCNL NVIEKELVVAPKFVERFAQVNVKEGEPVVLSARAVGTPVPRITWQKDGAPIQSGPSVSLFVDGGATSLDIPYA KAS
NL019	1105	SEQ ID NO: 1106 (frame +2) DDTYTESYISTIGVDFKIRTIDLDGKTIKLQIWDTAGQERFRTITSSYYRGAHGIIVVYDCTDQESFNNLKQWLE EIDRYACDNVNKLLVGNKCDQTNKKVVDYTQAKEYADQLGIPFLETSAKNATNVEQAF

NL021	1107	SEQ ID NO: 1108 (frame +2) VSLNSVTDISTTFILKPQENVKITLEGAQACFISHERLVISLKGGELYVLTLYSDSMRSVRSFHLEKAAASVLTT CICVCEENYLFLGSRLGNSLLLRFTEKELNLIEPRAIESSQSQNPAKKKKLDTLGDWMASDVTEIRDLDELEVY GSETQTSMQIASYIF
NL022	1109	SEQ ID NO: 1110 (frame +2) TLHREFLSEPDLQSYSVMIIDEAHERTLHTDILFGLVKDVARFRPDLKLLISSATLDAQKFSEFFDDAPIFRIPGR RFPVDIYYTKAPEADYVDACVVSILQIHATQPLGDILVFLTGQEEIETCQELLQDRVRRLGPRIKELLILPVYSNL PSDMQAKIFLPTPPNARKVVLATNIAETSLTIDNIIYVIDPGFCKQNNFNSRTGMESLVVVPVSKASANQRAGR AGRVAAGKCFRLYT
NL023	1111	SEQ ID NO: 1112 (frame +2) RSFSQERQHEEMKESSGRMHHSDPLIVETHSGHVRGISKTVLGREVHVFTGIPFAKPPIGPLRFRKPVPVDPWH GVLDATALPNSCYQERYEYFPGFEGEEMWNPNTNLSEDCLYLNIWVPHRLRIRHRANSEENKPRAKVPVLIWI YGGGYMSGTATLDVYDADMVAATSDVIVASMQYRVGAFGFLYLAQDLPRGSEEAPGNMGLWDQALAIRW LKDNIAAFGGDPELMTLFGESAGGGSVSIHLVSPITRGLARRGIMQSGTMNAPWSFMTAERATEIAKTLIDDCG CNSSLLTDAPSRVMSCMRSVEAKIISVQQWNSYSGILGLPSAPTIDGIFLPKHPLDLLKEGDFQDTEILIGSNQDE GTYFILYDFIDFFQKDGPSFLQRDKFLDIINTIFKNMTKIEREAIIFQYTDWEHVMDGYLNQKMIGDVVGDYFFI CPTNHFAQAFAEHGKKVYYYFFTQRTSTSLWGEWMGVMHGDEIEYVFGHPLNMSLQFNARERDLSLRIMQA YSRFALTGKPVPDDVNWPIYSKDQPQYYIFNAETSGTGRGPRATACAF
NL027	1113	SEQ ID NO: 1114 (frame +2) PIVLTGSEDGTVRIWHSGTYRLESSLNYGLERVWTICCMRGSNNVALGYDEGSIMVKVGREEPAISMDVNGE KIVWARHSEIQQVNLKAMPEGVEIKDGERLPVAVKDMGSCEIYPQTIAHNPNGRFLVVCGDGEYIIHTSMVLR NKAFGSAQEFIWGQDSSEYAIREGTSTVKVFKNFKEKKSFKPEFGAESIFGGYLLGVCSLSGLALYDWETLELV RRIEIQPKHVYWSESGELVALATDDSYFVLRYDAQAVLAARDAGDDAVTPDGVEDAFEVLGEVHETVKTGL WVGDCFIYT

Table 3-CS

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
CS001	1682	SEQ ID NO: 1683 (frame +1) KAWMLDKLGGVYAPRPSTGPHKLRECLPLVIFLRNRLKYALTGNEVLKIVKQRLIKVDGKVRTDPTYP AGFMDVVSIEKTNELFRLIYDVKGRFTIHRITPEEAKYKLCKVRRVATGPKNVPYLVTHDGRTVRYPDP LIKVNDSIQLDIATSKIMDFIKFESGNLCMITGGRNLGRVGTIVSRERHPGSFDIVHIRDSTGHTFATRLNN

		VFIIGKGTKAYISLPRGKGVRLT
CS002	1684	SEQ ID NO: 1685 (frame +1) SFFSKVFGGKKEEKGPSTHEAIQKLRETEELLQKKQEFLERKIDTELQTARKHGTKNKRAAIAALKRKK RYEKQLTQIDGTLTQIEAQREALEGANTNTQVLNTMRDAATAMRLAHKDIDVDKVHDLMDDI
CS003	1686	SEQ ID NO: 1687 (frame +1) GLRNKREVWRVKYTLARIRKAARELLTLEEKDPKRLFEGNALLRRLVRIGVLDEKQMKLDYVLGLKIE DFLERRLQTQVFKAGLAKSIHHARILIRQRHIRVRKQVVNIPSFIVRLDSGKHIDFSLKSPFGGGRP
CS006	1688	SEQ ID NO: 1689 (frame +1) TCQGMRNALYDKLDDDGIIAPGIRVSGDDVVIGKTITLPENDDELEGTSRRYSKRDASTFLRNSETGIVD QVMLTLNSEGYKFCKIRVRSVRIPQIGDKFASRHGQKGTCGIQYRQEDMPFTCEGLTPDIIINPHAIPSRM TIGHLIECIQGKVSSNKGEIGDATPFNDAVNVQKI
CS007	1690	SEQ ID NO: 1691 (frame +3) SEISCWNQRFWGLSSIAVSSTLQKFNMNVFPKLFWEWIFFVKAKSGMGKTAVFVLATLQQLEPSENHV YVLVMCHTRELAFQISKEYERFSKYMAGVRVSVFFGGMPIQKDEEVLKTACPHIVVGTPGRILALVNN KKLNLKHLKHFILDECDKMLESLDMRRDVQEIFRNTPHGKQVMMFSATLSKEIRPVCKKFMQDPMEV YVDDEAKLTLHGLQQHYVKLKENEKNKKLFELLDVLEFNQVVIFVKSVQRCIALAQLLTDQNFPAIGIH RNMTQDERLSRYQQFKDFQKRILVATNLFGRGMDIERVNIVFNYDMP
CS009	1692	SEQ ID NO: 1693 (frame +1) LVAICIWTFLQRLDSREPMWQLDESIIGTNPGLGFRPTPPEVASSVIWYKGNDPNSQQFWVQETSNFLTA YKRDGKKAGAGQNIHNCDFKLPPPAGKVCDVDISAWSPCVEDKHFGYHKSTPCIFLKLNKIFGWRPHF YNSSDSLPTDMPDDLKEHIRNMTAYDKNYLNMVWVSCEGENP
CS011	1694	SEQ ID NO: 1695 (frame +1) GSGKTTFVKRHLTGEFEKRYVATLGVEVHPLVFHTNRGPIRFNVWDTAGQEKFGGLRDGYYIQGQCAI IMFDVTSRVTYKNVPNWHRDLVRVCEGIPIVLCGNKVDIKDRKVKAKTIVFHRKKNLQYYDISAKSNY NFEKPFLWLARKLIGDGNLEFVAMQPCFH
CS013	1696	SEQ ID NO: 1697 (frame +2) DAPVVDTAEQVYISSLALLKMLKHGRAGVPMEVMGLMLGEFVDDYTVRVIDVFAMPQTGTGVSVEA VDPVFQAKMLDMLKQTGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVAVVVDPIQSVK G
CS014	1698	SEQ ID NO: 1699 (frame +2) QKQIKHMMAFIEQEANEKAEEIDAKAEEEFNIEKGRLVQQQRLKIMEYYEKKEKQVELQKKIQSSNML NQARLKVLKVREDHVRNVLDEARKRLAEVPKDVKLYTDLLVTLVVQALFQLMEPTVTVRVRQADVS

		LVQSILGKAQQDYKAKIKKDVQLKIDTENSLPADTCGGVELIAARGRIKISNTLESRLELIAQQLLPEIRT ALF
CS015	1700	SEQ ID NO: 1701 (frame +1) IVLSDDNCPDEKIRMNRVVRNNLRVRLSDIVSIAPCPSVKYGKRVHILPIDDSVEGLTGNLFEVYLKPYF MEAYRPIHRDDTFMVRGGMRAVEFKVVETDPSPYCIVAPDTVIHCEGDPIKREEEEEALNAVGYDDIGG CRKQLAQIKEMVELPLRHPSLFKAIGVKPPRGILMYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKL AGESESNLRKAFEEADKNSPAIIFIDELDAIAPKREKTHGEVERRIVSQLLTLMDGMKKSSHVIVMAATN RPNSIDPAL
CS016	1702	SEQ ID NO: 1703(frame -3) TPVSEDMLGRVFNGSGKPIDKGPPILAEDFLDIQGQPINPWSRIYPEEMIQTGISAIDVMNSIARGQKIPIFS AAGLPHNEIAAQICRQAGLVKIPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLF LNLANDPTIERIITPRLALTAAEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTD LATIYERAGRVEGRNGSITQIPILTMPNDDITHPIPDLTGYITEGQIYVDRQLHNRQIYPPVNVLPSLSRLM KSAIGEGMTRKDHSDVSNQLYACYAIGKDVQAMKAVVGEEALTPDDLLYLEFLTKFEKNFITQGNYEN RTVFESLDIGWQLLRIFPKEMLKRIPASI
CS018	1704	SEQ ID NO: 1705 (frame +2) SVYIQPEGVPVPAQQSQQQQSYRHVSESVEHKSYGTQGYTTSEQTKQTQKVAYTNGSDYSSTDDFKVD TFEYRLLREVSFRESITKRYIGETDIQISTEVDKSLGVVTPPKIAQKPRNSKLQEGADAQFQVQLSGNPRP RVSWFKNGQRIVNSNKHEIVTTHNQTILRVRNTQKSDTGNYTLLAENPNGCVVTSAYLAVESPQETYG QDHKSQYIMDNQQTAVEERVEVNEKALAPQFVRVCQDRDVTEGKMTRFDCRVTGRPYPEVTWFINDR QIRDDYXHKILVNESCNHALMITNVDLSDSGVVSCIARNKTGETSFQCRLNVIEKEQVVAPKFVERFSTL NVREGEPVQLHARAVGTPTPRITWQKDGVQVIPNPELRINTEGGASTLDIPRAKASDAGWYRC

Table 3-PX

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
PX001	2100	SEQ ID NO: 2101 (frame +1) GPKKHLKRLNAPRAWMLDKLGGVYAPRPSTGPHKLRECLPLVIFLQPPQVRAQRQRGAEDREAAPHQGGR QGPHRPHLPGWIHGCCVD*KDQ*AVPSDLRCEGTLHHPPHHSRGGQVQAVQGEARGDGPQERAVHRDAQ RPHAALPRPAHQGQRLHPARHRHLQDHGHHQVRLR*PVHDHGRA*LGASGHHRVPREAPRELRHRPHQG HHRTHLRHQVEQRVHHRQGHE
PX009	2102	SEQ ID NO: 2103 (frame +3)

		TLIWYKGTGYDSYKYWENQLIDFLSVYKKKGQTAGAGQNIFNCDFRNPPPHGKVCDVDIRGWEPCIDENH FSFHKSSPCIFLKLNKIYGWRPEFYNDTANLPEAMPVDLQTHIRNITAFNRDYANMVWVSCHGETPADKENI GPVRYLPYPGFPGYFYPYENAEGYLSPLVAVHLERPRTGIVINIECKAWA
PX010	2104	SEQ ID NO: 2105 (frame +3) GCIQFITQYQHSSGQRRVRVTTVARNWGDAAANLHHISAGFDQEAAAVVMARLVVYRAEQEDGPDVLRW LDRMLIRLCQKFGEYAKDDPNSFRLSENFSLYPQFMYHLRRSQFLQVFNNSPDETTFYRHMLMREDLTQSL IMIQPILYSYSFGGAPEPVLLDTSSIQPDRILLMDTFFQILIYHGETMAQWRALRYQDMAEYENFKQLLRAPV DDAQEILQTRFPVPRYIDTEHGGSQARFLLSKVNPSQTHNNMYAYGGAMPIPSADGGAPVLTDDVSLQVFM EQP
PX015	2106	SEQ ID NO: 2107 (frame +3) RKETVCIVLSDDNCPDEKIRMNRVVRNNLRVRLSDIVSIAPCPSVKYGKRVHILPIDDSVEGLTGNLFEVYLK PYFMEAYRPIHRDDTFMVRGGMRAVEFKVVETDPSPYCIVAPDTVIHCEGEPIKREEEEEALNAVGYDDIG GCRKQLAQIKEMVELPLRHPSLFKAIGVKPPRGILMYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAG ESESNLRKAFEEADKNSPAIILIDELDAI
PX016	2108	SEQ ID NO: 2109 (frame +2) FTGDILRTPVSEDMLGRIFNGSGKPIDKGPPILAEEYLDIQGQPINPWSRIYPEEMIQTGISAIDVMNSIARGQK IPIFSAAGLPHNEIAAQICRQAGLVKVPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVC LFLNLANDPTIERIITPRLALTAAEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTD LATIYERAGRVEGRNGSITQIPILTMPNDDITHPIPDLTGYITEGQIYVDRQLHNRQIYPPVNVLPSLSRLMKS AIGEGMTRKDHSDVSNQLYACYAIGKDVQAMKAVVGEEALTPDDLLYLEFLTKFEKNFITQGSYENRTVF ESLDIGWQPLRIFPKEM

Table 3-AD

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
AD001	2364	SEQ ID NO: 2365 (frame +1) GPKKHLKRLNAPKAWMLDKLGGVFAPRPSTGPHKLRECLPLVIFLRNRLKYALTNCEVTKIVMQRLIKVD GKVRTDPNYPAGFMDVVTIEKTGEFFRLVYDVKGRFTIHRISAEEAKYKLCKVRRVQTGPKGIPFLVTHDG RTIRYPDPVIKVNDSIQLDIATCKIMDHIRFESGNLCMITGGRNLGRVGTVVSRERHPGSFDIVHIKDTQGHTF ATRLNNVFIIGKATKPYISLPKGKGVKLSIAEERDK
AD002	2366	SEQ ID NO: 2367 (frame +2) SFFSKVFGGKKDGKAPTTGEAIQKLRETEEMLIKKQEFLEKKIEQEINVAKKNGTKNKRAAIQALKRKKRY

		EKQLQQIDGTLSTIEMQREALEGANTNTAVLQTMKSAADALKAAHQHMDVDKVHDLMDDI
AD009	2368	SEQ ID NO: 2369 (frame +3) VLAALVAVCLWVFFQTLDPRIPTWQLDSSIIGTSPGLGFRPMPEDSNVESTLIWYRGTDRDDFRQWTDTLDE FLAVYKTPGLTPGRGQNIHNCDYDKPPKKGQVCNVDIKNWHPCIQENHYNYHKSSPCIFIKLNKIYNWIPEY YNESTNLPEQMPEDLKQYIHNLESNNSREMNTVWVSCEGENP
AD015	2370	SEQ ID NO: 2371 (frame +2) DELQLFRGDTVLLKGKRRKETVCIVLSDDTCPDGKIRMNRVVRNNLRVRLSDVVSVQPCPDVKYGKRIHV LPIDDTVEGLTGNLFEVYLKPYFLEAYRPIHKDDAFIVRGGMRAVEFKVVETDPSPYCIVAPDTVIHCEGDPI KREEEEEALNAVGYDDIGGCRKQLAQIKEMVELPLRHPSLFKAIGVKPPRGILLYGPPGTGKTLIARAVANE TGAFFFLINGPEIMSKLAGESESNLRKAFEEADKNAPAIIFIDELDAIAPKREKTHGEVERRIVSQLLTLMDGL KQSSHVIVMAATNRPNSIDGALRRFGRFDREIDIGIPDATGRLEILRIHTKNMKLADDVDLEQIAAESHG
AD016	2372	SEQ ID NO: 2373 (frame +2) FTGDILRVPVSEDMLGRTFNGSGIPIDGGPPIVAETYLDVQGMPINPQTRIYPEEMIQTGISTIDVMTSIARGQ KIPIFSGAGLPHNEIAAQICRQAGLVQHKENKDDFAIVFAAMGVNMETARFFKREFAQTGACNVVLFLNLA NDPTIERIITPRLALTVAEFLAYQCNKHVLVIMTDMTSYAEALREVSAAREEVPGRRGFPGYMYTDLSTIYE RAGRVQGRPGSITQIPILTMPNDDITHPI

Table 4-LD

Target ID	SEQ ID NO	Sequences*	Example Gi-number and species
LD001	49	GGCCCCAAGAAGCATTTGAAGCGTTT	3101175 (Drosophila melanogaster), 92477283 (Drosophila erecta)
LD001	50	AATGCCCCAAAAGCATGGATGTTGGATA AATTGGGAGGTGT	70909480 (Carabus granulatus), 77325294 (Chironomus tentans), 900945 (Ctenocephalides felis), 60297219 (Diaprepes abbreviatus), 37951951 (Ips pini), 75735533 (Tribolium castaneum), 22039624 (Ctenocephalides felis)
LD001	51	GAAGTTACTAAGATTGTTATGCA	33368080 (Glossina morsitans)
LD001	52	ATTGAAAAAACTGGTGAATTTTTCCG	60297219 (Diaprepes abbreviatus)

LD001	53	ACACACGACGGCCGCACCATCCGCT	27555937 (Anopheles gambiae), 33355008 (Drosophila yakuba), 22474232 (Helicoverpa armigera), 3738704 (Manduca sexta)
LD001	54	ACACACGACGGCCGCACCATCCGCTA	92477283 (Drosophila erecta)
LD001	55	CCCAAGAAGCATTTGAAGCGTTTG	92954810 (Drosophila ananassae), 92231605 (Drosophila willistoni)
LD002	56	GCAATGTCATCCATCATGTCGTG	17861597 (Drosophila melanogaster), 92223378 (Drosophila willistoni), 92471309 (Drosophila erecta)
LD003	57	CAGGTTCTTCCTCTTGACGCGTCCAGG	24975810 (Anopheles gambiae), 3478578 (Antheraea yamamai), 42764756 (Armigeres subalbatus), 24661714 (Drosophila melanogaster), 68267151 (Drosophila simulans), 33355000 (Drosophila yakuba), 49532931 (Plutella xylostella), 76552910 (Spodoptera frugiperda), 92959651 (Drosophila ananassae), 92467993 (Drosophila erecta)
LD003	58	TTGAGCGAGAAGTCAATATGCTTCT	49558930 (Boophilus microplus)
LD003	59	TTCCAAGAAATCTTCAATCTTCAAACCCAA	62238687 (Diabrotica virgifera), 76169907 (Diploptera punctata), 67872253 (Drosophila pseudoobscura), 55877642 (Locusta migratoria), 66548956 (Apis mellifera)
LD003	60	TTCATCCAACACTCCAATACG	22040140 (Ctenocephalides felis)
LD003	61	AAGAGCATTGCCTTCAAACAACCT	2459311 (Antheraea yamamai)
LD003	62	AGTTCTCTGGCAGCTTTACGGATTTT	76169907 (Diploptera punctata)
LD003	63	CCACACTTCACGTTTGTTCCT	57963694 (Heliconius melpomene)
LD003	64	CCGTATGAAGCTTGATTACGT	108742527 (Gryllus rubens), 108742525 (Gryllus pennsylvanicus), 108742523 (Gryllus veletis), 108742521 (Gryllus bimaculatus), 108742519 (Gryllus firmus), 109194897 (Myzus persicae)
LD003	65	AGGAACAAACGTGAAGTGTGGCG	109194897 (Myzus persicae)
LD006	66	AGCGCTATGGGTAAGCAAGCTATGGG	27819970 (Drosophila melanogaster)
LD006	67	TGTTATACTGGTTATAATCAAGAAGAT	55801622 (Acyrthosiphon pisum), 66535130 (Apis mellifera)

LD007	68	GAAGTTCAGCACGAATGTATTCC	50563603 (Homalodisca coagulata)
LD007	69	CAAGCAAGTGATGATGTTCAGTGCCAC	50563603 (Homalodisca coagulata)
LD007	70	TGCAAGAAATTCATGCAAGATCC	21068658 (Chironomus tentans)
LD007	71	AAATGAAAAGAATAAAAAATT	49201437 (Drosophila melanogaster)
LD007	72	CAGAATTTCCCAGCCATAGGAAT	67895225 (Drosophila pseudoobscura)
LD007	73	AGCAGTTCAAAGATTTCCAGAAG	77848709 (Aedes aegypti)
LD007	74	TTCCAAATCAGCAAAGAGTACGAG	91083250 (Tribolium castaneum)
LD010	75	TACCCGCAGTTCATGTACCAT	29558345 (Bombyx mori)
LD010	76	CAGTCGCTGATCATGATCCAGCC	49559866 (Boophilus microplus)
LD010	77	CTCATGGACACGTTCTTCCAGAT	60293559 (Homalodisca coagulata)
LD010	78	GGGGCTGCATACAGTTCATCAC	92971011 (Drosophila mojavensis)
LD010	79	CCCGCAGTTCATGTACCATTTG	92952825 (Drosophila ananassae)
LD010	80	GACAATGCCAAATACATGAAGAA	92921253 (Drosophila virilis)
LD010	81	TTCGATCAGGAGGCAGCCGCAGTG	92921253 (Drosophila virilis)
LD011	82	AGCAGGGCTGGCATGGCGACAAA	28317118 (Drosophila melanogaster)
LD011	83	TTCTCAAAGTTGTAGTTAGATTTGGC	37951963 (Ips pini)
LD011	84	TACTGCAAATTCTTCTTCCTATG	55883846 (Locusta migratoria)
LD011	85	GGTACATTCTTGTATGTAACTC	67885713 (Drosophila pseudoobscura)
LD011	86	TCAAACATGATAATAGCACACTG	68771114 (Acanthoscurria gomesiana)
LD011	87	TCTCCTGACCGGCAGTGTCCCATA	17944197 (Drosophila melanogaster), 77843537 (Aedes aegypti), 94469127 (Aedes aegypti), 24664595 (Drosophila melanogaster)
LD011	88	GCTACTTTGGGAGTTGAAGTCCATCC	101410627 (Plodia interpuntella)
LD011	89	TAACTACAACTTTGAGAAGCCTTTCCT	90813103 (Nasonia vitripennis)

LD011	90	AAGTTTGGTGGTCTCCGTGATGG	84267747 (Aedes aegypti)
LD014	91	GCAGATCAAGCATATGATGGC	9732 (Manduca sexta), 90814338 (Nasonia vitripennis), 87266590 (Choristoneura fumiferana)
LD014	92	ATCAAGCATATGATGGCTTTCATTGA	75470953 (Tribolium castaneum), 76169390 (Diploptera punctata)
LD014	93	AATATTGAAAAGGGGCGCCTTGT	78055682 (Heliconius erato)
LD014	94	CAACGTCTCAAGATTATGGAATA	37659584 (Bombyx mori)
LD014	95	ATTATGGAATATTATGAGAAGAAAGA	66556286 (Apis mellifera)
LD014	96	AACAAAATCAAGATCAGCAATACT	25958976 (Curculio glandium)
LD016	97	ATGTCGTCGTTGGGCATAGTCA	27372076 (Spodoptera littoralis)
LD016	98	GTAGCTAAATCGGTGTACATGTAACCTG GGAAACCACGACG	27372076 (Spodoptera littoralis), 55797015 (Acyrthosiphon pisum), 73615307 (Aphis gossypii), 4680479 (Aedes aegypti), 9713 (Manduca sexta), 76555122 (Spodoptera frugiperda), 237458 (Heliothis virescens), 53883819 (Plutella xylostella), 22038926 (Ctenocephalides felis), 101403557 (Plodia interpuntella), 92969578 (Drosophila grimshawi), 91829127 (Bombyx mori)
LD016	99	GCAGATACCTCACGCAAAGCTTC	62239897 (Diabrotica virgifera)
LD016	100	GGATCGTTGGCCAAATTCAAGAACAGG CA	67882712 (Drosophila pseudoobscura), 92985459 (Drosophila grimshawi)
LD016	101	TTCTCCATAGAACCGTTCTCTTCGAAAT CCTG	4680479 (Aedes aegypti), 27372076 (Spodoptera littoralis)
LD016	102	GCTGTTTCCATGTTAACACCCAT	49558344 (Boophilus microplus)
LD016	103	TCCATGTTAACACCCATAGCAGCGA	62238871 (Diabrotica virgifera)
LD016	104	CTACAGATCTGGGCAGCAATTTCATTGT G	22038926 (Ctenocephalides felis), 16898595 (Ctenocephalides felis)
LD016	105	GGCAGACCAGCTGCAGAGAAAAT	22038926 (Ctenocephalides felis), 16898595 (Ctenocephalides

			felis)
LD016	106	GAGAAAATGGGGATCTTCTGACCACGA GCAATGGAGTTCATCACGTC	4680479 (Aedes aegypti), 9713 (Manduca sexta), 22038926 (Ctenocephalides felis), 16898595 (Ctenocephalides felis), 67877903 (Drosophila pseudoobscura), 10763875 (Manduca sexta), 76554661 (Spodoptera frugiperda), 77905105 (Aedes aegypti), 50562965 (Homalodisca coagulata), 27372076 (Spodoptera littoralis)
LD016	107	ATGGAGTTCATCACGTCAATAGC	9713 (Manduca sexta), 237458 (Heliothis virescens), 76554661 (Spodoptera frugiperda), 22474331 (Helicoverpa armigera)
LD016	108	GTCTGGATCATTTCCTCAGGATAGATAC GGGACCACGGATTGATTGGTTGACCCTG GATGTCCAAGAAGTCTTCAGCCAAAATT GGGGGACCTTTGTC	16898595 (Ctenocephalides felis), 22038926 (Ctenocephalides felis), 50562965 (Homalodisca coagulata), 49395165 (Drosophila melanogaster), 6901845 (Bombyx mori), 92931000 (Drosophila virilis)
LD016	109	ATTGGGGGACCTTTGTCGATGGG	10763875 (Manduca sexta)
LD016	110	ATGGGTTTTCCTGATCCATTGAAAACAC GTCCCAACATATCTTCAGAAACAGGAGT CCTCAAAATATCTCCTGTGAATTCACAA GCGGTGTTTTTGGCGTCGATTCCTGATG TGCCCTCGAACACTTGAACCACAGCTTT	49395165 (Drosophila melanogaster), 55905051 (Locusta migratoria)
LD016	111	ACAGCTTTTGACCCACTGACTTCCAG	21642266 (Amblyomma variegatum)
LD016	112	GACCCACTGACTTCCAGAACTTGTCCCG AACGTATAGTGCCATCAGCCAGTTTGAG T	49395165 (Drosophila melanogaster)
LD016	113	GGACCGTTCACACCAGACACAGT	24646342 (Drosophila melanogaster)
LD016	114	GACTGTGTCTGGTGTGAACGGTCCTCT	103769163 (Drosophila melanogaster), 92048971 (Drosophila willistoni)

LD016	115	TTCTCTTCGAAATCCTGTTTGAA	84116133 (Dermatophagoides farinae)
LD016	116	GACTGTGTVTGGTGTGAACGGTCC	24646342 (Drosophila melanogaster)
LD016	117	GGTCGTCGTGGTTTCCCAGGTTACATGT ACACCGATTT	92231646 (Drosophila willistoni), 91755555 (Bombyx mori), 84228226 (Aedes aegypti)
LD016	118	TGACAGCTGCCGAATTCTTGGC	92231646 (Drosophila willistoni)
LD018	119	CAAGTCACCGACGACCACAACCACAA	91080016 (Tribolium castaneum)
LD018	120	ATCGCGATTGACGGTGGAGCC	91080016 (Tribolium castaneum)
LD027	121	AGACGATCGGTTGGTTAAAATC	66501387 (Apis mellifera)
LD027	122	GATATGGGAGCATGTGAAATATA	77326476 (Chironomus tentans)
LD027	123	TTAGAGAATTGTTTGAATTAT	90129719 (Bicyclus anynana)

Table 4-PC

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PC001	275	AAAATTGTCATGCAAAGGTTGAT	37952206 (Ips pini)
PC001	276	AAAGCATGGATGTTGGACAAA	98994282 (Antheraea mylitta) 109978109 (Gryllus pennsylvanicus) 55904580 (Locusta migratoria)
PC001	277	AAAGCATGGATGTTGGACAAATT	31366663 (Toxoptera citricida)
PC001	278	AAAGCATGGATGTTGGACAAATTGGG	60311985 (Papilio dardanus)
PC001	279	AAAGCATGGATGTTGGACAAATTGGGGGGTGT	37951951 (Ips pini)
PC001	280	AAATACAAGTTGTGTAAAGTAA	84647793 (Myzus persicae)
PC001	281	AAGCATGGATGTTGGACAAATTGGGGGGTGT	70909486 (Mycetophagus quadripustulatus)
PC001	282	ATGGATGTCATTACTATTGAGAA	25957367 (Carabus granulatus)
PC001	283	CATCAAATTTGAATCTGGCAACCT	37952206 (Ips pini)
PC001	284	CATGATGGCAGAACCATTCGTTA	60303405 (Julodis onopordi)
PC001	285	CCAAAGCATGGATGTTGGACAA	90138164 (Spodoptera frugiperda)
PC001	286	CCATTTTTGGTAACACATGATGG	111011915 (Apis mellifera)
PC001	287	CCCAAAGCATGGATGTTGGACAA	50565112 (Homalodisca coagulata)

PC001	288	CCCAAAGCATGGATGTTGGACAAA	103790417 (Heliconius erato) 101419954 (Plodia interpunctella)
PC001	289	CCCAAAGCATGGATGTTGGACAAATT	73612809 (Aphis gossypii)
PC001	290	CCCAAAGCATGGATGTTGGACAAATTGGG	77329254 (Chironomus tentans)
PC001	291	CCCAAAGCATGGATGTTGGACAAATTGGGGGGTGT	60305420 (Mycetophagus quadripustulatus)
PC001	292	CCCAAAGCATGGATGTTGGACAAATTGGGGGGTGTCTTC GC	84647995 (Myzus persicae)
PC001	293	CGTTACCCTGACCCCAACATCAA	73613065 (Aphis gossypii)
PC001	294	GCAAAATACAAGTTGTGTAAAGTAA	83662334 (Myzus persicae)
PC001	295	GCATGGATGTTGGACAAATTGGG	92969396 (Drosophila grimshawi)
PC001	296	GCATGGATGTTGGACAAATTGGGGG	67885868 (Drosophila pseudoobscura)
PC001	297	GCATGGATGTTGGACAAATTGGGGGGTGT	25956479 (Biphyllus lunatus)
PC001	298	GCATGGATGTTGGACAAATTGGGGGGTGTCT	90814901 (Nasonia vitripennis)
PC001	299	GCTCCCAAAGCATGGATGTTGGA	110260785 (Spodoptera frugiperda)
PC001	300	GCTCCCAAAGCATGGATGTTGGACAA	76551269 (Spodoptera frugiperda)
PC001	301	GCTCCCAAAGCATGGATGTTGGACAAA	56085210 (Bombyx mori)
PC001	302	GCTCCCAAAGCATGGATGTTGGACAAATTGGG	22474232 (Helicoverpa armigera)
PC001	303	GGTCCCAAAGGAATCCCATTTTTGGT	50565112 (Homalodisca coagulata)
PC001	304	GGTGTCTTCGCCCCTCGTCCA	82575022 (Acyrthosiphon pisum)
PC001	305	GTGAAGTCACTAAAATTGTCATGCAAAG	25956820 (Biphyllus lunatus)
PC001	306	TCCACCGGGCCTCACAAGTTGCG	58371410 (Lonomia obliqua)
PC001	307	TCCCAAAGCATGGATGTTGGA	110263957 (Spodoptera frugiperda)
PC001	308	TGCTCCCAAAGCATGGATGTTGGACAA	48927129 (Hydropsyche sp.)
PC001	309	TGGATGTTGGACAAATTGGGGGGTGTCT	90814560 (Nasonia vitripennis)
PC003	310	AAAATTGAAGATTTCTTGGAA	108742519 (Gryllus firmus) 109978291 (Gryllus pennsylvanicus) 62083482 (Lysiphlebus testaceipes) 56150446 (Rhynchosciara americana)
PC003	311	AACAAACGTGAAGTGTGGAGAGT	57963755 (Heliconius melpomene)
PC003	312	AAGTCGCCCTTCGGGGGTGGCCG	77884026 (Aedes aegypti)
PC003	313	ACTTCTCCCTGAAGTCGCCCTTCGG	92992453 (Drosophila mojavensis)
PC003	314	AGATTGTTTGAAGGTAATGCACTTCT	60298816 (Diaphorina citri)
PC003	315	ATCCGTAAAGCTGCTCGTGAA	33373689 (Glossina morsitans)
PC003	316	ATCGACTTCTCCCTGAAGTCGCC	92987113 (Drosophila grimshawi)
PC003	317	ATCGACTTCTCCCTGAAGTCGCCCT	1899548 (Drosophila melanogaster)

PC003	318	ATGAAGCTTGATTATGTTTTGGGTCTGAAAATTGAAGAT TTCTTGGAAAGA	71539459 (Diaphorina citri)
PC003	319	ATTGAAGATTTCTTGGAAAGA	62240069 (Diabrotica virgifera)
PC003	320	CACATCGACTTCTCCCTGAAGTC	71550961 (Oncometopia nigricans)
PC003	321	CAGAAGCACATCGACTTCTCCCTGAAGTCGCCCTTCGG	68267151 (Drosophila simulans) 33355000 (Drosophila yakuba)
PC003	322	CAGAAGCACATCGACTTCTCCCTGAAGTCGCCCTTCGGG GG	2152719 (Drosophila melanogaster)
PC003	323	CGACTTCTCCCTGAAGTCGCC	107324644 (Drosophila melanogaster)
PC003	324	CTCCCTGAAGTCGCCCTTCGG	15461311 (Drosophila melanogaster)
PC003	325	CTGGACTCGCAGAAGCACATCGACTTCTCCCTGAA	38624772 (Drosophila melanogaster)
PC003	326	GACTTCTCCCTGAAGTCGCCCTTCGG	92959651 (Drosophila ananassae) 92981958 (Drosophila mojavensis) 76552467 (Spodoptera frugiperda)
PC003	327	GCTAAAATCCGTAAAGCTGCTCGTGA	60296953 (Diaprepes abbreviatus)
PC003	328	GCTAAAATCCGTAAAGCTGCTCGTGAACT	77329341 (Chironomus tentans)
PC003	329	GTGCGCAAGCAGGTGGTGAACATCCC	60312414 (Papilio dardanus)
PC003	330	TACACTTTGGCTAAAATCCGTAAAGCTGC	22040140 (Ctenocephalides felis)
PC003	331	TCGCAGAAGCACATCGACTTCTC	18883211 (Anopheles gambiae)
PC003	332	TCGCAGAAGCACATCGACTTCTCCCTGAAGTCGCCCTTC GG	92963738 (Drosophila grimshawi)
PC003	333	TCTCCCTGAAGTCGCCCTTCGG	38047836 (Drosophila yakuba) 27260897 (Spodoptera frugiperda)
PC003	334	TGAAAATTGAAGATTTCTTGGAA	61646980 (Acyrthosiphon pisum) 73615225 (Aphis gossypii) 83661890 (Myzus persicae) 37804775 (Rhopalosiphum padi) 30049209 (Toxoptera citricida)
PC003	335	TGAAAATTGAAGATTTCTTGGAAAGA	90813959 (Nasonia vitripennis)
PC003	336	TGGACTCGCAGAAGCACATCGACTTCTCCCT	25959408 (Meladema coriacea)
PC003	337	TGGCTAAAATCCGTAAAGCTGC	76169907 (Diploptera punctata)
PC003	338	TGGGTCTGAAAATTGAAGATTTCTTGGA	34788046 (Callosobruchus maculatus)
PC003	339	TTCTCCCTGAAGTCGCCCTTCGG	107331362 (Drosophila melanogaster) 110240861 (Spodoptera frugiperda)
PC003	340	TTGGGTCTGAAAATTGAAGATTTCTTGGAAAG	37952462 (Ips pini)

PC003	341	GGGTGCGCAAGCAGGTGGTGAAC	110887729 (Argas monolakensis)
PC005	342	CTCCTCAAAAAGTACAGGGAGGCCAAGAA	63512537 (Ixodes scapularis)
PC005	343	AAAAAGAAGGTGTGGTTGGATCC	33491424 (Trichoplusia ni)
PC005	344	AAAAAGAAGGTGTGGTTGGATCCAAATGAAATCAA	91759273 (Bombyx mori) 55908261 (Locusta migratoria)
PC005	345	AAAGAAGGTGTGGTTGGATCCAAATGAAATCA	101414616 (Plodia interpunctella)
PC005	346	AACACCAACTCAAGACAAAACAT	25957531 (Cicindela campestris)
PC005	347	AACACCAACTCAAGACAAAACATCCGTAA	25958948 (Curculio glandium)
PC005	348	AACTCAAGACAAAACATCCGTAA	60314333 (Panorpa cf. vulgaris APV-2005)
PC005	349	AAGAACACTGAAGCCAGAAGGAAGGGAAGGCATTGTGG	25958948 (Curculio glandium)
PC005	350	AATGAAATCAACGAAATCGCCAACAC	92979160 (Drosophila grimshawi) 92232072 (Drosophila willistoni)
PC005	351	ATGGAGTACATCCACAAGAAGAAGGC	15454802 (Drosophila melanogaster)
PC005	352	CAAGATGCTGTCTGACCAGGC	67872905 (Drosophila pseudoobscura)
PC005	353	CGCCTCCTCAAAAAGTACAGGGAGGC	75471260 (Tribolium castaneum)
PC005	354	CGTATCGCCACCAAGAAGCAG	68267374 (Drosophila simulans)
PC005	355	CTGTACATGAAAGCGAAGGGTAA	25957246 (Carabus granulatus)
PC005	356	GAACAAGAGGGTCCTTATGGAG	90977107 (Aedes aegypti)
PC005	357	GAACAAGAGGGTCCTTATGGAGTACATCCA	40544432 (Tribolium castaneum)
PC005	358	GAGCGTATCGCCACCAAGAAGCA	92480972 (Drosophila erecta) 33354497 (Drosophila yakuba)
PC005	359	GAGTACATCCACAAGAAGAAGGC	15516174 (Drosophila melanogaster)
PC005	360	GATCCAAATGAAATCAACGAAAT	56149737 (Rhynchosciara americana)
PC005	361	GCCAACACCAACTCAAGACAAAACATCCG	103019061 (Tribolium castaneum)
PC005	362	GCCAACACCAACTCAAGACAAAACATCCGTAAGCTCAT	56149737 (Rhynchosciara americana)
PC005	363	GGCAAAAAGAAGGTGTGGTTGGATCCAAATGAAATCA	101417042 (Plodia interpunctella)
PC005	364	GGGTCCTTATGGAGTACATCCACAAGAA	67885759 (Drosophila pseudoobscura)
PC005	365	TGCGATGCGGCAAAAAGAAGGT	56149531 (Rhynchosciara americana)
PC005	366	TGGTTGGATCCAAATGAAATCAACGAAAT	15355452 (Apis mellifera) 83662749 (Myzus persicae)
PC005	367	TTGGATCCAAATGAAATCAACGAAAT	110985444 (Apis mellifera) 111158439 (Myzus persicae)
PC010	368	CCGCAGTTCATGTACCATTTG	92952825 (Drosophila ananassae)
PC010	369	CTGATGGAGATGAAGCAGTGCTGCAATTC	58395529 (Anopheles gambiae str. PEST)
PC010	370	GACGTGCTCAGATGGGTGGACAG	56152422 (Rhynchosciara americana)

PC010	371	GCCCGAGCCTGTGTTGTTGGA	92939820 (Drosophila virilis)
PC010	372	GGCACATGCTGATGCGTGAGGAT	83937570 (Lutzomyia longipalpis)
PC010	373	GGGCACATGGTCATGGGCGATTC	3337934 (Drosophila melanogaster)
PC014	374	AAGATCATGGAGTACTACGAGAA	85577611 (Aedes aegypti)
PC014	375	ACGAGAAAAAGGAGAAGCAAG	67838315 (Drosophila pseudoobscura)
PC014	376	ATGGAGTACTACGAGAAAAAGGAGAAGCAAGT	92928915 (Drosophila virilis)
PC014	377	CAAAAACAAATCAAACACATGATGGC	82574001 (Acyrthosiphon pisum) 111160670 (Myzus persicae)
PC014	378	CTCAAGATCATGGAGTACTACGA	55692554 (Drosophila yakuba)
PC014	379	CTCAAGATCATGGAGTACTACGAGAA	92942301 (Drosophila ananassae) 92476196 (Drosophila erecta) 53884266 (Plutella xylostella)
PC014	380	GAACAAGAAGCCAATGAGAAAGC	111160670 (Myzus persicae)
PC014	381	GACTCAAGATCATGGAGTACT	112432414 (Myzus persicae)
PC014	382	GATGTTCAAAAACAAATCAAACACATGATGGC	73618688 (Aphis gossypii)
PC014	383	TACTACGAGAAAAAGGAGAAGC	62239529 (Diabrotica virgifera)
PC014	384	TTCATTGAACAAGAAGCCAATGA	15357365 (Apis mellifera)
PC016	385	ACACGACCGGCGCGCTCGTAAAT	75710699 (Tribolium castaneum)
PC016	386	ACCAGCACGTGCTTCTCGCACTGGTAGGCCAAGAATTCGGC	92048971 (Drosophila willistoni)
PC016	387	AGCACGTGCTTCTCGCACTGGTAGGC	92985459 (Drosophila grimshawi)
PC016	388	ATACGCGACCACGGGTTGATCGG	18868609 (Anopheles gambiae) 31206154 (Anopheles gambiae str. PEST)
PC016	389	ATCGGTGTACATGTAACCGGGGAAACC	2921501 (Culex pipiens) 62239897 (Diabrotica virgifera) 92957249 (Drosophila ananassae) 92477818 (Drosophila erecta) 92965644 (Drosophila grimshawi) 24646342 (Drosophila melanogaster) 67896654 (Drosophila pseudoobscura) 75710699 (Tribolium castaneum)
PC016	390	ATCGTTGGCCAAGTTCAAGAACAG	92950254 (Drosophila ananassae)
PC016	391	CACGTGCTTCTCGCACTGGTAGGCCAAGAA	4680479 (Aedes aegypti)
PC016	392	CCAGTCTGGATCATTTCCTCGGG	67884189 (Drosophila pseudoobscura)
PC016	393	CCAGTCTGGATCATTTCCTCGGGATA	92940287 (Drosophila virilis)

PC016	394	CGCTCGATGGTCGGATCGTTGGCCAAGTTCAAGAACA	2921501 (Culex pipiens)
PC016	395	CGCTCGATGGTCGGATCGTTGGCCAAGTTCAAGAACAG ACACACGTTCTCCAT	92477818 (Drosophila erecta) 15061308 (Drosophila melanogaster)
PC016	396	CGTGCTTCTCGCACTGGTAGGCCAAGAA	13752998 (Drosophila melanogaster)
PC016	397	CTGGCAGTTTCCATGTTGACACCCATAGC	16898595 (Ctenocephalides felis)
PC016	398	CTTAGCATCAATACCTGATGT	61646107 (Acyrthosiphon pisum)
PC016	399	GACATGTCGGTCAAGATGACCAGCACGTG	9713 (Manduca sexta)
PC016	400	GACATGTCGGTCAAGATGACCAGCACGTGCTTCTCGCAC TG	92933153 (Drosophila virilis)
PC016	401	GACATGTCGGTCAAGATGACCAGCACGTGCTTCTCGCAC TGGTA	2921501 (Culex pipiens)
PC016	402	GAGCCGTTCTCTTCGAAGTCCTG	237458 (Heliothis virescens)
PC016	403	GATGACCAGCACGTGCTTCTC	18883474 (Anopheles gambiae)
PC016	404	GATGACCAGCACGTGCTTCTCGCACTG	92477818 (Drosophila erecta)
PC016	405	GATGACCAGCACGTGCTTCTCGCACTGGTAGGCCAAGA A	15061308 (Drosophila melanogaster) 67883622 (Drosophila pseudoobscura)
PC016	406	GATGACCAGCACGTGCTTCTCGCACTGGTAGGCCAAGA ATTCGGC	31206154 (Anopheles gambiae str. PEST)
PC016	407	GATGGGGATCTGCGTGATGGA	101403557 (Plodia interpunctella)
PC016	408	GATGGGGATCTGCGTGATGGAGCCGTTGCGGCCCTCCAC	53883819 (Plutella xylostella)
PC016	409	GGAATAGGATGGGTGATGTCGTCGTTGGGCATAGT	110240379 (Spodoptera frugiperda)
PC016	410	GGAATAGGATGGGTGATGTCGTCGTTGGGCATAGTCA	27372076 (Spodoptera littoralis)
PC016	411	GGATCGTTGGCCAAGTTCAAGAA	91757299 (Bombyx mori)
PC016	412	GGATCGTTGGCCAAGTTCAAGAACA	103020368 (Tribolium castaneum)
PC016	413	GGATCGTTGGCCAAGTTCAAGAACAG	237458 (Heliothis virescens)
PC016	414	GGATGGGTGATGTCGTCGTTGGGCAT	101403557 (Plodia interpunctella)
PC016	415	GGCAGTTTCCATGTTGACACCCATAGC	4680479 (Aedes aegypti)
PC016	416	GGCATAGTCAAGATGGGGATCTG	92924977 (Drosophila virilis)
PC016	417	GTCTGGATCATTTCCTCGGGATA	92966144 (Drosophila grimshawi)
PC016	418	GTGATGATGCGCTCGATGGTCGGATCGTTGGCCAAGTTC AAGAACAGACACACGTTCTCCAT	15514750 (Drosophila melanogaster)
PC016	419	GTGTACATGTAACCGGGGAAACC	92924977 (Drosophila virilis)
PC016	420	GTTTCCATGTTGACACCCATAGC	91826756 (Bombyx mori)
PC016	421	TCAATGGGTTTTCCTGATCCATTGAA	49395165 (Drosophila melanogaster) 99009492 (Leptinotarsa decemlineata)

PC016	422	TCATCCAGCACAGACTTGCCAG	10763875 (Manduca sexta)
PC016	423	TCATCCAGCACAGACTTGCCAGG	9713 (Manduca sexta)
PC016	424	TCCATGTTGACACCCATAGCAGC	92962756 (Drosophila ananassae)
PC016	425	TCCATGTTGACACCCATAGCAGCAAACAC	60295607 (Homalodisca coagulata)
PC016	426	TCGAAGTCCTGCTTGAAGAACCTGGC	101403557 (Plodia interpunctella)
PC016	427	TCGATGGTCGGATCGTTGGCCAAGTTCAAGAACAGACA CACGTTCTCCAT	4680479 (Aedes aegypti)
PC016	428	TCGGATCGTTGGCCAAGTTCAAGAACAGACACACGTTCT CCAT	2793275 (Drosophila melanogaster)
PC016	429	TCGTTGGCCAAGTTCAAGAACAG	90137502 (Spodoptera frugiperda)
PC016	430	TGGGTGATGTCGTCGTTGGGCAT	53883819 (Plutella xylostella)
PC016	431	TTCTCGCACTGGTAGGCCAAGAA	110240379 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
PC016	432	TTCTCTTCGAAGTCCTGCTTGAAGAACCTGGC	9713 (Manduca sexta)
PC016	433	TTGGCCAAGTTCAAGAACAGACACACGTT	55905051 (Locusta migratoria)
PC016	434	GTTTCCATGTTGACACCCATAGCAGCAAA	84116133 (Dermatophagoides farinae)

Table 4-EV

Target ID	**SEQ ID NO**	**Sequence ***	**Example Gi-number and species**
EV005	533	AAGCGACGTGAAGAGCGTATCGC	76553206 (Spodoptera frugiperda)
EV005	534	ATTAAAGATGGTCTTATTATTAA	15355452 (Apis mellifera)
EV005	535	CGTAAGCGACGTGAAGAGCGTATCGC	33491424 (Trichoplusia ni)
EV005	536	GGTCGTCATTGTGGATTTGGTAAAAG	60314333 (Panorpa cf. vulgaris APV-2005)
EV005	537	TGCGATGCGGCAAGAAGAAGGT	15048930 (Drosophila melanogaster)
EV005	538	TGCGGCAAGAAGAAGGTTTGG	93002524 (Drosophila mojavensis) 92930455 (Drosophila virilis) 92044532 (Drosophila willistoni)
EV005	539	TTGTGGATTTGGTAAAAGGAA	60306723 (Sphaerius sp.)
EV010	540	CAAGTGTTCAATAATTCACCA	83937567 (Lutzomyia longipalpis)
EV010	541	CATTCTATAGGCACATGTTGATG	29558345 (Bombyx mori)
EV010	542	CTGGCGGCCACATGGTCATGGG	92476940 (Drosophila erecta) 92977931 (Drosophila grimshawi) 2871327 (Drosophila melanogaster)
EV015	543	AACAGGCCCAATTCCATCGACCC	92947821 (Drosophila ananassae)

EV015	544	AGAGAAAAAATGGACCTCATCGAC	62239128 (Diabrotica virgifera)
EV015	545	CGCCATCCGTCGCTGTTCAAGGCGATCGG	18866954 (Anopheles gambiae)
EV015	546	CTGGCAGTTACCATGGAGAACTTCCGTTACGCCATG	62239128 (Diabrotica virgifera)
EV015	547	GTGATCGTGATGGCGGCCACGAA	18887285 (Anopheles gambiae)
EV015	548	GTGATCGTGATGGCGGCCACGAAC	83423460 (Bombyx mori)
EV015	549	TGATGGACGGCATGAAGAAAAG	91086234 (Tribolium castaneum)
EV016	550	AATATGGAAACAGCCAGATTCTT	109193659 (Myzus persicae)
EV016	551	ATGATCCAGACTGGTATTTCTGC	92938857 (Drosophila virilis)
EV016	552	ATTGATGTGATGAATTCCATTGCC	55905051 (Locusta migratoria)
EV016	553	GAAATGATCCAGACTGGTATTTCTGC	50562965 (Homalodisca coagulata)
EV016	554	GAAGAAATGATCCAGACTGGTAT	92969748 (Drosophila mojavensis)
EV016	555	GACTGTGTCTGGTGTGAACGG	2286639 (Drosophila melanogaster) 92042621 (Drosophila willistoni)
EV016	556	GATATGTTGGGTCGTGTGTTTAA	92969748 (Drosophila mojavensis)
EV016	557	GATCCTACCATTGAAAGAATTAT	99011193 (Leptinotarsa decemlineata)
EV016	558	GTGTCTGAAGATATGTTGGGTCGTGT	76554661 (Spodoptera frugiperda)
EV016	559	GTGTCTGGTGTGAACGGACCG	22474331 (Helicoverpa armigera)
EV016	560	TCTGAAGATATGTTGGGTCGTGT	27372076 (Spodoptera littoralis)
EV016	561	TGGCATATCAATGTGAGAAGCA	60336595 (Homalodisca coagulata)
EV016	562	TTGAACTTGGCCAATGATCCTACCAT	91827863 (Bombyx mori)

Table 4-AG

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
AG001	621	AAAACTGGTGAATTCTTCCGTTTGAT	37953169 (Ips pini)
AG001	622	AAAGCATGGATGTTGGACAAA	98994282 (Antheraea mylitta) 109978109 (Gryllus pennsylvanicus) 55904580 (Locusta migratoria)
AG001	623	AAAGCATGGATGTTGGACAAATT	31366663 (Toxoptera citricida)
AG001	624	AAAGCATGGATGTTGGACAAATTGGG	60311985 (Papilio dardanus)
AG001	625	AAAGCATGGATGTTGGACAAATTGGGGGGTGT	37951951 (Ips pini) 109195107 (Myzus persicae)
AG001	626	AAATACAAATTGTGCAAAGTCCG	25958703 (Curculio glandium)
AG001	627	AACTTGTGCATGATCACCGGAG	22039624 (Ctenocephalides felis)
AG001	628	AAGCATGGATGTTGGACAAATTGGGGG	112433559 (Myzus persicae)

AG001	629	AAGCATGGATGTTGGACAAATTGGGGGGTGTGTT	70909486 (Mycetophagus quadripustulatus)
AG001	630	ACTGGTGAATTCTTCCGTTTGAT	77327303 (Chironomus tentans)
AG001	631	ATTGAAAAAACTGGTGAATTCTTCCGTTTGATCTATGATGTTAA	22039624 (Ctenocephalides felis)
AG001	632	CCAAAGCATGGATGTTGGACAA	90138164 (Spodoptera frugiperda)
AG001	633	CCCAAAGCATGGATGTTGGACAA	48927129 (Hydropsyche sp.) 76551269 (Spodoptera frugiperda)
AG001	634	CCCAAAGCATGGATGTTGGACAAA	91835558 (Bombyx mori) 103783745 (Heliconius erato) 101419954 (Plodia interpunctella)
AG001	635	CCCAAAGCATGGATGTTGGACAAATT	73619372 (Aphis gossypii)
AG001	636	CCCAAAGCATGGATGTTGGACAAATTGGG	77329254 (Chironomus tentans) 22474232 (Helicoverpa armigera)
AG001	637	CCCAAAGCATGGATGTTGGACAAATTGGGGG	84647382 (Myzus persicae)
AG001	638	CCCAAAGCATGGATGTTGGACAAATTGGGGGGTGT	84647995 (Myzus persicae)
AG001	639	CCCAAAGCATGGATGTTGGACAAATTGGGGGGTGTGTT	60305420 (Mycetophagus quadripustulatus)
AG001	640	CTGGATTCATGGATGTGATCA	27617172 (Anopheles gambiae)
AG001	641	GAATTCTTCCGTTTGATCTATGATGT	50565112 (Homalodisca coagulata) 71049326 (Oncometopia nigricans)
AG001	642	GCATGGATGTTGGACAAATTGGG	92969396 (Drosophila grimshawi) 93001617 (Drosophila mojavensis) 92929731 (Drosophila virilis)
AG001	643	GCATGGATGTTGGACAAATTGGGGG	67885868 (Drosophila pseudoobscura)
AG001	644	GCATGGATGTTGGACAAATTGGGGGGTGT	90814901 (Nasonia vitripennis)
AG001	645	GCATGGATGTTGGACAAATTGGGGGGTGTGTTCGCCCC	25956479 (Biphyllus lunatus)
AG001	646	GCCCCCAAAGCATGGATGTTGGACAA	50565112 (Homalodisca coagulata)
AG001	647	GCTGGATTCATGGATGTGATC	103775903 (Heliconius erato)
AG001	648	GGATCATTCGATATTGTCCACAT	113017118 (Bemisia tabaci)
AG001	649	GGCAACTTGTGCATGATCACCGGAGG	25958703 (Curculio glandium)
AG001	650	TACAAATTGTGCAAAGTCCGCAA	56161193 (Rhynchosciara americana)
AG001	651	TATCCTGCTGGATTCATGGATGT	40934103 (Bombyx mori)
AG001	652	TCACCATTGAAAAAACTGGTGAATTCTTC	62083410 (Lysiphlebus testaceipes)
AG001	653	TGCATGATCACCGGAGGCAGGAA	3478550 (Antheraea yamamai)
AG001	654	TGCATGATCACCGGAGGCAGGAATTTGGG	14627585 (Drosophila melanogaster) 33355008 (Drosophila yakuba)

AG001	655	TGGATGTTGGACAAATTGGGGGGTGT	90814560 (Nasonia vitripennis)
AG001	656	TGTGCATGATCACCGGAGGCAG	92949859 (Drosophila ananassae) 92999306 (Drosophila grimshawi)
AG001	657	TGTGCATGATCACCGGAGGCAGGAATTTGGG	67842487 (Drosophila pseudoobscura)
AG005	658	AAGATCGACAGGCATCTGTACCACG	83935651 (Lutzomyia longipalpis)
AG005	659	AAGATCGACAGGCATCTGTACCACGCCCTGTACATGAAGGC	76552995 (Spodoptera frugiperda)
AG005	660	AAGGGTAACGTGTTCAAGAACAA	18932248 (Anopheles gambiae) 60306606 (Sphaerius sp.)
AG005	661	AAGGGTAACGTGTTCAAGAACAAG	18953735 (Anopheles gambiae) 25957811 (Cicindela campestris) 60311920 (Euclidia glyphica)
AG005	662	AAGGGTAACGTGTTCAAGAACAAGAGAGT	25958948 (Curculio glandium) 90812513 (Nasonia giraulti)
AG005	663	ACAAGAAGAAGGCTGAGAAGGC	60311700 (Euclidia glyphica)
AG005	664	ATCAAGGATGGTTTGATCATTAA	25957811 (Cicindela campestris)
AG005	665	ATGGAATACATCCACAAGAAGAAG	56149737 (Rhynchosciara americana)
AG005	666	CAAAACATCCGTAAATTGATCAAGGATGGT	60314333 (Panorpa cf. vulgaris APV-2005)
AG005	667	CAAAACATCCGTAAATTGATCAAGGATGGTTTGATCAT	25958948 (Curculio glandium)
AG005	668	CAAGGGTAACGTGTTCAAGAA	476608 (Drosophila melanogaster) 38048300 (Drosophila yakuba)
AG005	669	CAAGGGTAACGTGTTCAAGAACAAG	92946023 (Drosophila ananassae) 2871633 (Drosophila melanogaster) 68267374 (Drosophila simulans) 33354497 (Drosophila yakuba) 83937096 (Lutzomyia longipalpis)
AG005	670	CATCTGTACCACGCCCTGTACATGAAGGC	101417042 (Plodia interpunctella)
AG005	671	GAAGAAGGCTGAGAAGGCCCG	40874303 (Bombyx mori)
AG005	672	GACAGGCATCTGTACCACGCCCTGTACATGAAGGC	90135865 (Bicyclus anynana)
AG005	673	GAGAAGGCCCGTGCCAAGATGTTG	82572137 (Acyrthosiphon pisum)
AG005	674	GATCCAAATGAAATCAATGAGATTGC	60312128 (Papilio dardanus)
AG005	675	GCTCGTATGCCTCAAAAGGAACTATGG	25957246 (Carabus granulatus)
AG005	676	GGGTAACGTGTTCAAGAACAAG	4447348 (Drosophila melanogaster)
AG005	677	GGTAACGTGTTCAAGAACAAG	18948649 (Anopheles gambiae)
AG005	678	TACATCCACAAGAAGAAGGCTGAGAAG	2871633 (Drosophila melanogaster)

AG005	679	TACCACGCCCTGTACATGAAGGC	10764114 (Manduca sexta)
AG005	680	TCAATGAGATTGCCAACACCAACTC	83935651 (Lutzomyia longipalpis)
AG005	681	TGATCAAGGATGGTTTGATCAT	77642775 (Aedes aegypti) 27615052 (Anopheles gambiae) 92982271 (Drosophila grimshawi) 67896961 (Drosophila pseudoobscura)
AG005	682	TGATCAAGGATGGTTTGATCATTAAGAA	92042883 (Drosophila willistoni)
AG005	683	TGGTTGGATCCAAATGAAATCA	40867709 (Bombyx mori) 101417042 (Plodia interpunctella)
AG005	684	TGGTTGGATCCAAATGAAATCAA	15355452 (Apis mellifera) 83662749 (Myzus persicae)
AG005	685	TGGTTGGATCCAAATGAAATCAATGAGAT	63013469 (Bombyx mori) 55908261 (Locusta migratoria)
AG005	686	TGTACCACGCCCTGTACATGAAGGC	23573622 (Spodoptera frugiperda)
AG005	687	TTGATCAAGGATGGTTTGATCA	113019292 (Bemisia tabaci)
AG005	688	TTGATCAAGGATGGTTTGATCAT	61674956 (Aedes aegypti) 41576849 (Culicoides sonorensis)
AG005	689	TTGATGGAATACATCCACAAGAAGAAGGC	92225847 (Drosophila willistoni)
AG005	690	AGGATGCGTGTCTTGAGGCGTCT	110887217 (Argas monolakensis)
AG005	691	AAGGCCAAGGGTAACGTGTTCAAGAACAAG	110887217 (Argas monolakensis)
AG010	692	CGTTTGTGTCAAAAGTTTGGAGAATA	78539702 (Glossina morsitans)
AG010	693	GATGTTTTAAGATGGGTCGATCG	110759793 (Apis mellifera)
AG010	694	TTTTACAGGCATATGCTTATGAGGGAAGATTT	55902158 (Locusta migratoria)
AG010	695	TTTTTCGAGGTGGTCAATCAGCATTCGGC	92925934 (Drosophila virilis)
AG014	696	AACATGCTGAACCAAGCCCGT	75466802 (Tribolium castaneum)
AG014	697	AACATGCTGAACCAAGCCCGTCT	87266590 (Choristoneura fumiferana) 103779114 (Heliconius erato)
AG014	698	AAGATCATGGAATACTATGAGAAGAA	101403826 (Plodia interpunctella)
AG014	699	AAGATCATGGAATACTATGAGAAGAAGGAGAA	81520950 (Lutzomyia longipalpis)
AG014	700	AATGAAAAGGCCGAGGAAATTGATGC	62239529 (Diabrotica virgifera)
AG014	701	ATGGAATACTATGAGAAGAAGGA	16901350 (Ctenocephalides felis)
AG014	702	CAATCCTCCAACATGCTGAACCA	53148472 (Plutella xylostella)
AG014	703	CAGATCAAGCATATGATGGCCTTCAT	53148472 (Plutella xylostella)

AG014	704	GCAGATCAAGCATATGATGGCCTTCAT	87266590 (Choristoneura fumiferana) 9732 (Manduca sexta) 90814338 (Nasonia vitripennis)
AG014	705	GCGGAAGAAGAATTTAACATTGAAAAGGG	50558386 (Homalodisca coagulata) 71552170 (Oncometopia nigricans)
AG016	706	AACGACGACATCACCCATCCTATTC	110248186 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
AG016	707	AACGGTTCCATGGAGAACGTGTG	2921501 (Culex pipiens) 92950254 (Drosophila ananassae) 110240379 (Spodoptera frugiperda)
AG016	708	AACGGTTCCATGGAGAACGTGTGTCT	24646342 (Drosophila melanogaster)
AG016	709	AACGGTTCCATGGAGAACGTGTGTCTCTTCTTGAA	91829127 (Bombyx mori)
AG016	710	ATGATCCAGACCGGTATCTCCGC	22474040 (Helicoverpa armigera)
AG016	711	ATGCCGAACGACGACATCACCCATCC	31206154 (Anopheles gambiae str. PEST)
AG016	712	CAATGCGAGAAACACGTGCTGGT	9713 (Manduca sexta)
AG016	713	CCGCACAACGAAATCGCCGCCCAAAT	75469507 (Tribolium castaneum)
AG016	714	CGTTTCTTCAAGCAGGACTTCGA	83937868 (Lutzomyia longipalpis)
AG016	715	CTTGGACATCCAAGGTCAACCCATCAACCCATGGTC	104530890 (Belgica antarctica)
AG016	716	GAAATGATCCAGACCGGTATCTC	2921501 (Culex pipiens) 92966144 (Drosophila grimshawi)
AG016	717	GAAATGATCCAGACCGGTATCTCCGCCATCGACGTGATG AACTC	31206154 (Anopheles gambiae str. PEST)
AG016	718	GAAGAAATGATCCAGACCGGTAT	75469507 (Tribolium castaneum)
AG016	719	GAAGAAGTACCCGGACGTCGTGG	22038926 (Ctenocephalides felis)
AG016	720	GACATCCAAGGTCAACCCATCAA	16898595 (Ctenocephalides felis)
AG016	721	GCCCGTTTCTTCAAGCAGGACTTCGA	31206154 (Anopheles gambiae str. PEST)
AG016	722	GCCGCCCAAATCTGTAGACAGGC	60295607 (Homalodisca coagulata)
AG016	723	GGATCAGGAAAACCCATTGACAAAGGTCC	49395165 (Drosophila melanogaster) 99009492 (Leptinotarsa decemlineata)
AG016	724	GGTTACATGTACACCGATTTGGC	91829127 (Bombyx mori)
AG016	725	GGTTACATGTACACCGATTTGGCCACCAT	77750765 (Aedes aegypti) 9713 (Manduca sexta) 110248186 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
AG016	726	GGTTACATGTACACCGATTTGGCCACCATTTACGAA	92231646 (Drosophila willistoni)

AG016	727	GTGTCGGAGGATATGTTGGGCCG	92460250 (Drosophila erecta) 24646342 (Drosophila melanogaster) 55694673 (Drosophila yakuba)
AG016	728	TACATGTACACCGATTTGGCCACCAT	31206154 (Anopheles gambiae str. PEST)
AG016	729	TTCAACGGATCAGGAAAACCCATTGACAAAGGTCC	99010653 (Leptinotarsa decemlineata)
AG016	730	TTCCCCGGTTACATGTACACCGATTTGGCCAC	2921501 (Culex pipiens) 75710699 (Tribolium castaneum)
AG016	731	TTCCCCGGTTACATGTACACCGATTTGGCCACCAT	62239897 (Diabrotica virgifera) 92957249 (Drosophila ananassae) 92477149 (Drosophila erecta) 67896654 (Drosophila pseudoobscura)
AG016	732	TTCCCCGGTTACATGTACACCGATTTGGCCACCATTTA	92969578 (Drosophila grimshawi)
AG016	733	TTCCCCGGTTACATGTACACCGATTTGGCCACCATTTAC GA	103744758 (Drosophila melanogaster)
AG016	734	TTCGCCATCGTGTTCGCCGCCATGGGTGT	31206154 (Anopheles gambiae str. PEST)
AG016	735	TTCTTCAAGCAGGACTTCGAAGA	9713 (Manduca sexta)
AG016	736	TTCTTGAATTTGGCCAACGATCC	92972277 (Drosophila grimshawi) 99011193 (Leptinotarsa decemlineata)
AG016	737	TTCTTGAATTTGGCCAACGATCCCACCATCGAG	67839381 (Drosophila pseudoobscura)
AG016	738	GCCGAATTTTTGGCTTATCAATG	84116133 (Dermatophagoides farinae)

Table 4-TC

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
TC001	813	AAAGCATGGATGTTGGATAAA	70909480 (Carabus granulatus) 16898765 (Ctenocephalides felis) 60298000 (Diaprepes abbreviatus)
TC001	814	AATTTGTGTATGATTACTGGAGG	55904576 (Locusta migratoria)
TC001	815	ACTGGAGGTCGTAACTTGGGGCGTGT	60298000 (Diaprepes abbreviatus)
TC001	816	ATGATTACTGGAGGTCGTAACTTGGGGCGTGT	73619372 (Aphis gossypii) 37804548 (Rhopalosiphum padi)
TC001	817	ATGCAAAGATTGATTAAAGTTGACGG	70909478 (Biphyllus lunatus)
TC001	818	ATTAAAGTTGACGGAAAAGTT	110763874 (Apis mellifera)
TC001	819	ATTGAGAAAACTGGGGAATTCTTCCG	37952206 (Ips pini)
TC001	820	ATTGTTATGCAAAGATTGATTAAAGTTGACGGAAAAGT	70909486 (Mycetophagus quadripustulatus)

TC001	821	CCAAGAAGCATTTGAAGCGTCT	55904580 (Locusta migratoria)
TC001	822	CCAAGAAGCATTTGAAGCGTCTC	83935971 (Lutzomyia longipalpis)
TC001	823	GCGCCCAAAGCATGGATGTTGGA	103790417 (Heliconius erato) 101419954 (Plodia interpunctella)
TC001	824	GGCCCCAAGAAGCATTTGAAGCGT	14700642 (Drosophila melanogaster)
TC001	825	TGATTACTGGAGGTCGTAACTTGGGGCGTGT	73612212 (Aphis gossypii)
TC001	826	TGTATGATTACTGGAGGTCGTAACTTGGGGCGTGT	70909478 (Biphyllus lunatus)
TC001	827	TTGATTTATGATGTTAAGGGA	77325485 (Chironomus tentans)
TC001	828	TTGTGTATGATTACTGGAGGTCGTAA	60305816 (Mycetophagus quadripustulatus)
TC002	829	AAAAACAAACGAGCGGCCATCCAGGC	18920284 (Anopheles gambiae)
TC002	830	ATCGACCAAGAGATCCTCACAGCGAAGAAAAACGCGTC GAAAAACAAACGAGCGGCCATCCAGGCC	75717966 (Tribolium castaneum)
TC002	831	CTCCAGCAGATCGATGGCACCCT	92475657 (Drosophila erecta) 13763220 (Drosophila melanogaster)
TC002	832	TCAAGAGGAAGAAACGCTACGAAAAGCAGCTCCAGCAG ATCGATGGCACCCTCAGCACCATCGAGATGCAGCGGGA GGCCCTCGAGGGGGCCAACACCAACACAGCCGTACTCA AAACGATGAAAAACGCAGCGGACGCCCTCAAAAATGCC CACCTCAACATGGATGTTGATGAGGT	75717966 (Tribolium castaneum)
TC010	833	AACCTCAAGTACCAGGACATGCCCGA	90973566 (Aedes aegypti)
TC010	834	AGCCGATTTTGTACAGTTATA	92944620 (Drosophila ananassae)
TC010	835	ATGGACACATTTTTCCAAATT	33427937 (Glossina morsitans)
TC010	836	ATGGACACATTTTTCCAAATTTTGATTTTCCACGG	56151768 (Rhynchosciara americana)
TC010	837	CAAGTACCAGGACATGCCCGA	18911059 (Anopheles gambiae)
TC010	838	CACATGCTGATGCGGGAGGACCTC	67893321 (Drosophila pseudoobscura)
TC010	839	CCTCAAGTACCAGGACATGCCCGA	67893324 (Drosophila pseudoobscura)
TC010	840	TCAAGTACCAGGACATGCCCGA	67893321 (Drosophila pseudoobscura)
TC010	841	TTCATGTACCATTTGCGCCGCTC	92952825 (Drosophila ananassae)
TC014	842	AAAATTCAGTCGTCAAACATGCTGAA	76169390 (Diploptera punctata)
TC014	843	AACATGCTGAACCAAGCCCGT	87266590 (Choristoneura fumiferana) 103779114 (Heliconius erato)
TC014	844	CACAGCAACTTGTGCCAGAAAT	92923718 (Drosophila virilis)
TC014	845	GAGAAAGCCGAAGAAATCGATGC	77325830 (Chironomus tentans)
TC014	846	GCCCGCAAACGTCTGGGCGAA	92232132 (Drosophila willistoni)
TC014	847	TAAAAGTGCGTGAAGACCACGT	58371699 (Lonomia obliqua)

TC015	848	ACACTGATGGACGGCATGAAGAA	78531609 (Glossina morsitans)
TC015	849	ATCGGCGGTTGTCGCAAACAACT	6904417 (Bombyx mori)
TC015	850	CCCGATGAGAAGATCCGGATGAA	83922984 (Lutzomyia longipalpis)
TC015	851	CTGCCCCGATGAGAAGATCCG	92948836 (Drosophila ananassae)
TC015	852	AACGAAACCGGTGCTTTCTTCTT	84116975 (Dermatophagoides farinae)

Table 4-MP

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
MP001	908	AAAGCATGGATGTTGGACAAA	98994282 (Antheraea mylitta) 108789768 (Bombyx mori) 109978109 (Gryllus pennsylvanicus) 55904580 (Locusta migratoria)
MP001	909	AAAGCATGGATGTTGGACAAAT	77325485 (Chironomus tentans) 37951951 (Ips pini) 60311985 (Papilio dardanus) 30031258 (Toxoptera citricida)
MP001	910	AAGAAGCATTTGAAGCGTTTAAACGCACC	3658572 (Manduca sexta)
MP001	911	AAGCATTTGAAGCGTTTAAACGC	103790417 (Heliconius erato) 22474232 (Helicoverpa armigera)
MP001	912	AAGCATTTGAAGCGTTTAAACGCACC	25957217 (Carabus granulatus)
MP001	913	AAGTCCGTACCGACCCTAATTATCCAGC	46994131 (Acyrthosiphon pisum)
MP001	914	ACGCACCCAAAGCATGGATGTT	46999037 (Acyrthosiphon pisum)
MP001	915	ACTATTAGATACGATATTGCA	46998791 (Acyrthosiphon pisum)
MP001	916	ACTGGACCCAAAGGTGTGCCATTTTTAACTACTCATGAT GGCCGTACTAT	46997137 (Acyrthosiphon pisum)
MP001	917	AGAAGCATTTGAAGCGTTTAAA	27620566 (Anopheles gambiae)
MP001	918	AGAAGCATTTGAAGCGTTTAAACGCACC	98994282 (Antheraea mylitta)
MP001	919	AGAAGCATTTGAAGCGTTTAAACGCACCCAAAGCATGG ATGTTGGACAAAT	73619191 (Aphis gossypii)
MP001	920	AGTAAGGGAGTTAAATTGACTA	46998791 (Acyrthosiphon pisum)
MP001	921	ATACAAGTTGTGTAAAGTAAAG	29553519 (Bombyx mori)
MP001	922	ATGGATGTTATATCTATCCAAAAGACCAGTGAGCACTTT AGATTGATCTATGATGTGAAAGGTCGTTTCAC	46998791 (Acyrthosiphon pisum)
MP001	923	ATTGATCTATGATGTGAAAGGTCGTTTCAC	46999037 (Acyrthosiphon pisum)

MP001	924	CAAAAGACCAGTGAGCACTTTAGATTGAT	30031258 (Toxoptera citricida)
MP001	925	CACAGAATTACTCCTGAAGAAGC	73619191 (Aphis gossypii)
MP001	926	CACAGAATTACTCCTGAAGAAGCAAAATACAAG	46998791 (Acyrthosiphon pisum) 30031258 (Toxoptera citricida)
MP001	927	CATCCAGGATCTTTTGATATTGTTCACATTAA	31364848 (Toxoptera citricida)
MP001	928	CATCCAGGATCTTTTGATATTGTTCACATTAAGGATGCA AATGAACATATTTTTGCTAC	37804548 (Rhopalosiphum padi)
MP001	929	CATCTAAAATTTTGGATCATATCCGTTTTGAAACTGGAA ACTTGTGCATGAT	46998791 (Acyrthosiphon pisum)
MP001	930	CATTTGAAGCGTTTAAACGCACC	30031258 (Toxoptera citricida)
MP001	931	CATTTGAAGCGTTTAAACGCACCCAAAGCATGGATGTT	46998791 (Acyrthosiphon pisum)
MP001	932	CCAAAGCATGGATGTTGGACAA	90138164 (Spodoptera frugiperda)
MP001	933	CCAAGGAGTAAGGGAGTTAAATTGACTA	73615238 (Aphis gossypii) 31364848 (Toxoptera citricida)
MP001	934	CCCAAAGCATGGATGTTGGAC	108789768 (Bombyx mori)
MP001	935	CCCAAAGCATGGATGTTGGACAA	50565112 (Homalodisca coagulata) 48927129 (Hydropsyche sp.) 76551269 (Spodoptera frugiperda)
MP001	936	CCCAAAGCATGGATGTTGGACAAA	56085210 (Bombyx mori) 103792451 (Heliconius erato) 101419954 (Plodia interpunctella)
MP001	937	CCCAAAGCATGGATGTTGGACAAAT	22474095 (Helicoverpa armigera)
MP001	938	CGTCCAAGCACCGGTCCACACAAACT	47537863 (Acyrthosiphon pisum)
MP001	939	CTGGAAACTTGTGCATGATAACTGGAGG	78524585 (Glossina morsitans)
MP001	940	GAAAGACATCCAGGATCTTTTGATATTGTTCACATTAAG GATGCAAATGAACATATTTTTGCTACCCGGATGAACAAT GTTTTTATTATTGGAAAAGGTCAAAAGAACTACATTTCT CTACCAAG	46997137 (Acyrthosiphon pisum)
MP001	941	GATCATATCCGTTTTGAAACTGGAAACTTGTGCATGAT	73614725 (Aphis gossypii)
MP001	942	GATGCAAATGAACATATTTTTGCTAC	31364848 (Toxoptera citricida)
MP001	943	GCACCCAAAGCATGGATGTTGGA	70909486 (Mycetophagus quadripustulatus)
MP001	944	GCACCCAAAGCATGGATGTTGGACAAAT	77329254 (Chironomus tentans) 60305420 (Mycetophagus quadripustulatus)
MP001	945	GGATCTTTTGATATTGTTCACAT	60303405 (Julodis onopordi)
MP001	946	GGATCTTTTGATATTGTTCACATTAAGGATGCAAATGAA	73619191 (Aphis gossypii)

		CATATTTTTGCTAC	
MP001	947	GGCCCCAAGAAGCATTTGAAGCGTTTAA	14693528 (Drosophila melanogaster)
MP001	948	GGGCGTGTTGGTATTGTTACCAACAG	31365398 (Toxoptera citricida)
MP001	949	GGGCGTGTTGGTATTGTTACCAACAGGGAAAG	73612212 (Aphis gossypii) 37804548 (Rhopalosiphum padi)
MP001	950	GGTACAAACTGGACCCAAAGG	60297572 (Diaprepes abbreviatus)
MP001	951	GTTTTTATTATTGGAAAAGGTCAAAAGAACTACATTTCT CT	73619191 (Aphis gossypii) 31364848 (Toxoptera citricida)
MP001	952	TGAAGTATGCACTTACTGGTGC	73619191 (Aphis gossypii)
MP001	953	TGTAAAGTAAAGAGGGTACAAACTGGACCCAAAGGTGT	73619191 (Aphis gossypii)
MP001	954	TGTGTAAAGTAAAGAGGGTACAAACTGGACCCAAAGGT GT	30031258 (Toxoptera citricida)
MP001	955	TTCTTGCGTAATCGTTTGAAGTATGCACTTACTGGTGCC GAAGTCACCAAGATTGTCATGCAAAGATTAATCAAGGTT GATGGCAAAGTCCGTACCGACCCTAATTATCCAGC	46998791 (Acyrthosiphon pisum)
MP001	956	TTGGAAAAGGTCAAAAGAACTACATTTCTCT	73615060 (Aphis gossypii)
MP001	957	TTGGATCATATCCGTTTTGAAACTGGAAACTTGTGCATG AT	37804548 (Rhopalosiphum padi)
MP002	958	AAAAAAAATGGTACAACTAATAAACGAGCTGCATTGCA AGC	47537017 (Acyrthosiphon pisum)
MP002	959	AAGAAACGGTACGAACAACAA	15363283 (Apis mellifera)
MP002	960	ACAAGAATTTTTAGAAAAAAAAATTGAACAAGAAGTAG CGATAGC	47537017 (Acyrthosiphon pisum)
MP002	961	CAAATTGATGGTACCATGTTAACTATTGAACAACAGCG	47537017 (Acyrthosiphon pisum)
MP002	962	GAAGATGCGATACAAAAGCTTCGATCCAC	47537017 (Acyrthosiphon pisum)
MP002	963	GAGTTTCTTTAGTAAAGTATTCGGTGG	110762684 (Apis mellifera)
MP010	964	AAAAGATGATCCAAATAGTTT	110759793 (Apis mellifera)
MP010	965	AAAATATTATTGATGGACACATTTTTCCATATTTTGATAT TCCA	47520567 (Acyrthosiphon pisum)
MP010	966	AATAGTCCTGATGAAACATCATATTATAG	47520567 (Acyrthosiphon pisum)
MP010	967	CAAAAAGATGATCCAAATAGTTTCCGATTGCCAGAAAA CTTCAGTTTATATCCACAGTTCATGTATCATTTAAGAAG GTCTCAATTTCTACAAGTTTTTAA	47520567 (Acyrthosiphon pisum)
MP010	968	CAACATTCCAGTGGCTATAAACGAAT	47520567 (Acyrthosiphon pisum)
MP010	969	CACATGTTGATGCGTGAAGATGTTAC	47520567 (Acyrthosiphon pisum)

MP010	970	CCAATTCTGTATAGCTATAGTTTTAATGGTAGGCCAGAA CCTGTACTTTTGGATACCAG	47520567 (Acyrthosiphon pisum)
MP010	971	CCATCTCAAACACATAATAATATGTATGCTTATGGAGG	55814942 (Acyrthosiphon pisum)
MP010	972	CTCAAAACTCGATTCCCAATGCCTCGGTATATTGACACA GAACAAGGTGGTAGTCAGGCAAGATTTTTACTATGCAA AGT	55814942 (Acyrthosiphon pisum)
MP010	973	GGTGATGGTGGAGCACCAGTTTTGACAGATGATGTAAG CTTGCA	55814942 (Acyrthosiphon pisum)
MP010	974	GTGGCTGCATACAGTTCATTACGCAGTA	28571527 (Drosophila melanogaster)
MP010	975	TAATGGCTCGTATGGTAGTGAACCGTGCTGAAACTGA	47520567 (Acyrthosiphon pisum)
MP010	976	TATAGGCACATGTTGATGCGTGAAGAT	40924332 (Bombyx mori)
MP010	977	TGGGCTGATCGTACGCTTATACGCTTGTGTCA	47520567 (Acyrthosiphon pisum)
MP010	978	TTAGCTAGGAATTGGGCAGACCCTGT	47520567 (Acyrthosiphon pisum)
MP016	979	AAACAAGATTTTGAGGAAAATGG	35508791 (Acyrthosiphon pisum)
MP016	980	AACCTGGTAAATCAGTTCTTGA	35508791 (Acyrthosiphon pisum)
MP016	981	AACGACGACATCACCCATCCTATTC	110240379 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
MP016	982	AATTTAGCTAATGATCCTACTATTGA	15366446 (Apis mellifera)
MP016	983	ACTATGCCTAACGACGACATCACCCATCC	237458 (Heliothis virescens)
MP016	984	ATAGTATTTGCTGCTATGGGTGTTAATATGGAAAC	30124460 (Toxoptera citricida)
MP016	985	CAAATTTGTAGACAAGCTGGTCT	103020368 (Tribolium castaneum)
MP016	986	CATGAAGACAATTTTGCTATAGTATTTGCTGCTATGGGT GTTAATATGGAAAC	35508791 (Acyrthosiphon pisum)
MP016	987	CCGATAGATAAAGGACCTCCTATTTTGGCTGAAGATTAT TTGGATATTGAAGGCCAACCTATTAATCCATA	35508791 (Acyrthosiphon pisum)
MP016	988	CCTATTTTGGCTGAAGATTAT	55905051 (Locusta migratoria)
MP016	989	CGTATCATTACACCACGTCTTGCTTTAACTGCTGCTGAAT TTTTAGCTTA	30124460 (Toxoptera citricida)
MP016	990	CGTCTTGCTTTAACTGCTGCTGAATTTTTAGCTTA	35508791 (Acyrthosiphon pisum)
MP016	991	GAAGAAGTACCTGGGCGTCGTGGTTTCCCTGGTTACATG TACAC	30124460 (Toxoptera citricida)
MP016	992	GAAGGAAGAAATGGTTCTATCACACAAATACCTATTTTA ACTATGCCTAA	30124460 (Toxoptera citricida)
MP016	993	GAAGGAAGAAATGGTTCTATCACACAAATACCTATTTTA ACTATGCCTAACGA	73615307 (Aphis gossypii)

MP016	994	GATTTAGCTACAATTTATGAACG	30124460 (Toxoptera citricida)
MP016	995	GCCAGATTCTTTAAACAAGATTTTGAGGAAAATGG	30124460 (Toxoptera citricida)
MP016	996	GCTATGGGTGTTAATATGGAAAC	75469507 (Tribolium castaneum)
MP016	997	GCTGCAGGTTTACCACATAATGAGATTGCTGCTCAAATT TG	35508791 (Acyrthosiphon pisum)
MP016	998	GCTGGGCGTGTAGAAGGAAGAAATGGTTCTATCACACA AATACCTATTTTAACTATGCCTAACGA	55813096 (Acyrthosiphon pisum)
MP016	999	GGTTACATGTACACCGATTTAGCTACAATTTATGAACG	55813096 (Acyrthosiphon pisum) 73615307 (Aphis gossypii)
MP016	1000	GTGGACAAAAAATTCCAATATTTTC	55813096 (Acyrthosiphon pisum)
MP016	1001	GTGTCGGAGGATATGTTGGGCCG	92460250 (Drosophila erecta) 2286639 (Drosophila melanogaster) 55694673 (Drosophila yakuba)
MP016	1002	GTTCTTGAATTTAGCTAATGATCCTACTATTGA	82563007 (Acyrthosiphon pisum)
MP016	1003	TCAATGGAGAATGTTTGTTTGTTCTTGAATTTAGCTAATG ATCCTACTATTGA	35508791 (Acyrthosiphon pisum) 30124460 (Toxoptera citricida)
MP016	1004	TCAGCTATTGATATCATGAACTCTATTGCTCGTGGACAA AAAATTCCAATATTTTC	35508791 (Acyrthosiphon pisum)
MP016	1005	TCATATGCTGAAGCTTTAAGAGAAGTTTCTGCTGCTCG	30124460 (Toxoptera citricida)
MP016	1006	TCCAGAACATATCCTCAAGAAATGATTCAAACTGGTAT	35508791 (Acyrthosiphon pisum)
MP016	1007	TCTATTGCTCGTGGACAAAAAATTCC	110764393 (Apis mellifera)
MP016	1008	TGTGAAAAGCATGTCTTAGTTATTTTAACTGACATGAGT TCATATGCTGAAGCTTTAAGAGAAGTTTCTGCTGCTCGT GAAGAAGTACCTGGGCGTCGTGGTTTCCC	55813096 (Acyrthosiphon pisum)
MP016	1009	TTAACTGACATGAGTTCATATGCTGAAGCTTTAAGAGAA GTTTCTGCTGCTCGTGAAGAAGTACCTGG	73615307 (Aphis gossypii)
MP027	1010	TTTTTAAAAATTTTAAAGAAAAAAA	47522167 (Acyrthosiphon pisum)

Table 4-NL

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
NL001	1161	CTGAAGAAGCTAAGTACAAGCT	16566724 (Spodoptera frugiperda)
NL001	1162	TTCTTCCGTTTGATCTATGATGTTAA	16900870 (Ctenocephalides felis)

NL001	1163	CAGCTGAAGAAGCTAAGTACAA	16900870 (Ctenocephalides felis), 56199521 (Culicoides sonorensis)
NL001	1164	GAGTTCTTCCGTTTGATCTATGATGTTAA	16900945 (Ctenocephalides felis)
NL001	1165	AAGTACAAGCTGTGCAAAGTGAAG	22474232 (Helicoverpa armigera)
NL001	1166	TTCGACATCGTGCACATCAAGGAC	22474232 (Helicoverpa armigera)
NL001	1167	ATCACAGCTGAAGAAGCTAAGTACAAG	25956820 (Biphyllus lunatus)
NL001	1168	TGTGTATGATCACTGGAGGTCGTAA	25957367 (Carabus granulatus)
NL001	1169	AACGTTTTCATCATCGGCAAG	27613698 (Anopheles gambiae)
NL001	1170	CCAAAATCATGGACTTCATCA	3738704 (Manduca sexta)
NL001	1171	TGATCTATGATGTTAAGGGACG	3738704 (Manduca sexta)
NL001	1172	CATGGATGTTGGACAAATTGGG	37951951 (Ips pini), 56772312 (Drosophila virilis), 60305420 (Mycetophagus quadripustulatus), 67885868 (Drosophila pseudoobscura), 77321575 (Chironomus tentans), 25956479 (Biphyllus lunatus), 22474232 (Helicoverpa armigera);
NL001	1173	TTTTGCCACTAGGTTGAACAACGT	37953169 (Ips pini)
NL001	1174	GCAGCGTCTCATCAAGGTTGACGGCAA	48927129 (Hydropsyche sp.)
NL001	1175	AAGGGACGTTTCACCATCCAC	50818668 (Heliconius melpomene)
NL001	1176	AACCTGTGTATGATCACTGGAGG	60293875 (Homalodisca coagulata)
NL001	1177	ACTAACTGTGAAGTGAAGAAAATTGT	60293875 (Homalodisca coagulata)
NL001	1178	TTCTTCCGTTTGATCTATGATGT	60293875 (Homalodisca coagulata), 71047771 (Oncometopia nigricans)
NL001	1179	TGTATGATCACTGGAGGTCGTAACTTGGG	60297219 (Diaprepes abbreviatus)
NL001	1180	CATGGATGTTGGACAAATTGGGTGG	60311985 (Papilio dardanus)
NL001	1181	GCTGAAGAAGCTAAGTACAAG	68758383 (Acanthoscurria gomesiana)
NL001	1182	GGAGGTCGTAACTTGGGTCGTGT	77327303 (Chironomus tentans)

NL001	1183	TATGATGTTAAGGGACGTTTCACCAT	77327303 (Chironomus tentans)
NL001	1184	CATGGATGTTGGACAAATTGGG	93002561 (Drosophila grimshawi) 93001617 (Drosophila mojavensis) 92939328 (Drosophila virilis) 112433559 (Myzus persicae) 90814922 (Nasonia vitripennis)
NL001	1185	CTGAAGAAGCTAAGTACAAGCT	110264122 (Spodoptera frugiperda)
NL001	1186	GAAGAAGCTAAGTACAAGCTGTG	90820001 (Graphocephala atropunctata)
NL001	1187	TTGCACAGCTTGTACTTAGCTTCTTC	90134075 (Bicyclus anynana)
NL001	1188	AAGTACAAGCTGTGCAAAGTGAAG	112350104 (Helicoverpa armigera)
NL001	1189	ATGATCACTGGAGGTCGTAACTTGGGTCG	113017118 (Bemisia tabaci)
NL001	1190	GGTCGTAACTTGGGTCGTGTGGG	109978109 (Gryllus pennsylvanicus)
NL001	1191	TTCGACATCGTGCACATCAAGGAC	112350104 (Helicoverpa armigera)
NL001	1192	ACATCGTGCACATCAAGGACG	90981811 (Aedes aegypti)
NL003	1193	CAGGAGTTGAAGATCATCGGAGAGTATGG	15457393 (Drosophila melanogaster), 76551770 (Spodoptera frugiperda)
NL003	1194	CGTAAGGCCGCTCGTGAGCTG	1797555 (Drosophila melanogaster)
NL003	1195	AAGGTAACGCCCTGCTGCGTCG	18863433 (Anopheles gambiae)
NL003	1196	CAGGAGTTGAAGATCATCGGAGAGTA	2459311 (Antheraea yamamai), 49532931 (Plutella xylostella)
NL003	1197	GCCAAGTCCATCCATCACGCCCG	33354488 (Drosophila yakuba), 60312414 (Papilio dardanus)
NL003	1198	AAGTCCATCCATCACGCCCGT	33528372 (Trichoplusia ni)
NL003	1199	TGTTTGAAGGTAACGCCCTGCT	34788046 (Callosobruchus maculatus)
NL003	1200	CAGGAGTTGAAGATCATCGGAGA	35505798 (Acyrthosiphon pisum), 56772256 (Drosophila virilis)
NL003	1201	GTGCGCCTGGACTCGCAGAAGCACAT	38624772 (Drosophila melanogaster)
NL003	1202	GAGTTGAAGATCATCGGAGAGTA	4158332 (Bombyx mori)
NL003	1203	TTGGGTTTAAAAATTGAAGATTTC	56150446 (Rhynchosciara americana)

NL003	1204	TCGCAGAAGCACATTGACTTCTC	56772256 (Drosophila virilis)
NL003	1205	AGAATGAAGCTCGATTACGTC	60306665 (Sphaerius sp.)
NL003	1206	TTTGTGGTGCGCCTGGACTCG	60312414 (Papilio dardanus)
NL003	1207	AGAAGCACATTGACTTCTCGCTGAAGTC	63514675 (Ixodes scapularis)
NL003	1208	TCGCAGAAGCACATTGACTTCTCGCT	70979521 (Anopheles albimanus)
NL003	1209	CTCATCAGACAAAGACATATCAGAGT	71536734 (Diaphorina citri)
NL003	1210	TTGAAGATCATCGGAGAGTATGG	73612958 (Aphis gossypii)
NL003	1211	AAAATTGAAGATTTCCTTGAA	75467497 (Tribolium castaneum)
NL003	1212	CAGAAGCACATTGACTTCTCGCT	77730066 (Aedes aegypti)
NL003	1213	CGTAAGGCCGCTCGTGAGCTG	24661714 (Drosophila melanogaster)
NL003	1214	GCGTGATGGATGGACTTGGCCAA	90813959 (Nasonia vitripennis)
NL003	1215	GCCAAGTCCATCCATCACGCCCG	92467993 (Drosophila erecta)
NL003	1216	GCCAAGTCCATCCATCACGCCCGT	112349903 (Helicoverpa armigera)
NL003	1217	CTCATCAGACAAAGACATATCAGAGT	110671455 (Diaphorina citri)
NL003	1218	CAGGAGTTGAAGATCATCGGAGA	86464397 (Acyrthosiphon pisum) 92938865 (Drosophila virilis)
NL003	1219	CAGGAGTTGAAGATCATCGGAGAGTATGG	101417830 (Plodia interpunctella) 110254389 (Spodoptera frugiperda)
NL003	1220	GAGTTGAAGATCATCGGAGAGTA	112984021 (Bombyx mori)
NL003	1221	TCGCAGAAGCACATTGACTTCTC	93002641 (Drosophila mojavensis) 92938865 (Drosophila virilis)
NL003	1222	TTGAAGATCATCGGAGAGTATGG	111158779 (Myzus persicae)
NL003	1223	CAGAAGCACATTGACTTCTCGCTGAA	92232387 (Drosophila willistoni)
NL003	1224	CTCCGTAACAAGCGTGAGGTGTGG	92232387 (Drosophila willistoni)
NL003	1225	CGTAACAAGCGTGAGGTGTGG	110558371 (Drosophila ananassae)
NL003	1226	GTCAAATACGCCCTGGCCAAGAT	93001117 (Drosophila grimshawi)
NL004	1227	TACGCCCATTTCCCCATCAACTGTGT	14994663 (Spodoptera frugiperda), 53883415 (Plutella xylostella)
NL004	1228	TGCTCTCACATCGAAAACATG	22039837 (Ctenocephalides felis)
NL004	1229	AACTTCCTGGGCGAGAAGTACATC	25959088 (Meladema coriacea)

NL004	1230	GCCGTGTACGCCCATTTCCCCATCAACTG	25959088 (Meladema coriacea)
NL004	1231	GTGTACGCCCATTTCCCCATCAACTGTGTGA C	2761563 (Drosophila melanogaster)
NL004	1232	GTGTACGCCCATTTCCCCATCAACTGTGT	33354902 (Drosophila yakuba)
NL004	1233	ATGCGTGCCGTGTACGCCCATTT	33433477 (Glossina morsitans)
NL004	1234	TCAGCTGCCCTCATCCAACAGTC	33491496 (Trichoplusia ni)
NL004	1235	AAGGATATTCGTAAATTCTTGGA	37952094 (Ips pini), 56199511 (Culicoides sonorensis)
NL004	1236	GCCCATTTCCCCATCAACTGTGT	42766318 (Armigeres subalbatus)
NL004	1237	AACTTCCTGGGCGAGAAGTACAT	49547659 (Rhipicephalus appendiculatus)
NL004	1238	AAGAACAAGGATATTCGTAAATTCTTGGA	56152793 (Rhynchosciara americana)
NL004	1239	AACTTCCTGGGCGAGAAGTACATCCG	58079798 (Amblyomma americanum), 49554219 (Boophilus microplus)
NL004	1240	CATTTCCCCATCAACTGTGTGAC	60312171 (Papilio dardanus)
NL004	1241	CGTAACTTCCTGGGCGAGAAGTACATCCG	63516417 (Ixodes scapularis)
NL004	1242	AGATCAGCTGCCCTCATCCAACA	71539722 (Diaphorina citri)
NL004	1243	GTGTACGCCCATTTCCCCATCAACTGTGT	24583601 (Drosophila melanogaster)
NL004	1244	TACGCCCATTTCCCCATCAACTGT	113017826 (Bemisia tabaci)
NL004	1245	TACGCCCATTTCCCCATCAACTGTGT	110263092 (Spodoptera frugiperda)
NL004	1246	GCCCATTTCCCCATCAACTGTGT	94468811 (Aedes aegypti)
NL004	1247	ACACAGTTGATGGGGAAATGGGC	90136736 (Bicyclus anynana)
NL004	1248	GCCCATTTCCCCATCAACTGTGT	110671493 (Diaphorina citri) 110249018 (Spodoptera frugiperda)
NL004	1249	GTCACACAGTTGATGGGGAAATGGGC	87266195 (Choristoneura fumiferana)
NL004	1250	CCATTTCCCCATCAACTGTGT	90981351 (Aedes aegypti)
NL005	1251	AAGGGTAACGTATTCAAGAACAAGCG	1900283 (Drosophila melanogaster)
NL005	1252	AAGGGTAACGTATTCAAGAACAAG	25956594 (Biphyllus lunatus)
NL005	1253	CGTGTATTGATGGAGTTCATTCA	30124405 (Toxoptera citricida), 60294294 (Homalodisca coagulata), 71046487 (Oncometopia nigricans), 73612243

			(Aphis gossypii)
NL005	1254	AAAGGTCAAGGAGGCCAAGAAG	67875089 (Drosophila pseudoobscura)
NL005	1255	AAGATGTTGAACGACCAGGCTGAAGC	77324118 (Chironomus tentans)
NL005	1256	ACGTTACCCTTAGCCTTCATGTA	90812513 (Nasonia girault)
NL005	1257	AAGGGTAACGTATTCAAGAACAAGCG	45552830 (Drosophila melanogaster)
NL005	1258	CGTGTATTGATGGAGTTCATTCA	112433619 (Myzus persicae)
NL005	1259	AGGTCAAGGAGGCCAAGAAGC	92941126 (Drosophila virilis)
NL005	1260	ACGTTACCCTTAGCCTTCATGTA	90812513 (Nasonia girault)
NL005	1261	AAGGGTAACGTATTCAAGAACAAGCG	45552830 (Drosophila melanogaster)
NL006	1262	AGTCCCAGGAACACCTATCAG	21464337 (Drosophila melanogaster)
NL006	1263	ATTATTCCCTTCCCCGATCACAA	24646762 (Drosophila melanogaster)
NL006	1264	CACGCTATCCCATCTCGTATGACAATTGG	24646762 (Drosophila melanogaster)
NL006	1265	TACAAGTTCTGCAAAATTCGAGT	49573116 (Boophilus microplus)
NL006	1266	ATGACAATTGGCCATTTAATTGAATG	50564037 (Homalodisca coagulata)
NL006	1267	ACCTACACGCACTGCGAGATCCA	58384759 (Anopheles gambiae str. PEST)
NL006	1268	GGTGTGGTGGAGTACATTGACAC	58384759 (Anopheles gambiae str. PEST)
NL006	1269	ATTATTCCCTTCCCCGATCACAA	24646762 (Drosophila melanogaster)
NL006	1270	AGTCCCAGGAACACCTATCAG	22026793 (Drosophila melanogaster)
NL006	1271	CACGCTATCCCATCTCGTATGACAATTGG	24646762 (Drosophila melanogaster)
NL006	1272	TCTCGTATGACAATTGGCCATTT	93000469 (Drosophila mojavensis)
NL007	1273	GCAAACAAGTCATGATGTTCAG	15354019 (Apis mellifera)
NL007	1274	GGTATGGGAAAAACTGCTGTATTTGTGTT	15354019 (Apis mellifera)
NL007	1275	GAATGCATTCCTCAAGCTGTA	21068658 (Chironomus tentans)
NL007	1276	TGCAAGAAATTCATGCAAGATCC	21068658 (Chironomus tentans)
NL007	1277	TTCCAAATCAGCAAAGAGTATGA	2890413 (Drosophila melanogaster)
NL007	1278	GATGACGAGGCCAAGCTGACGCT	49536419 (Rhipicephalus appendiculatus)
NL007	1279	TGTGGTTTTGAACATCCATCTGAAGTACAAC A	60308907 (Hister sp.)

NL007	1280	GAAAACGAAAAGAACAAAAAG	77642464 (Aedes aegypti)
NL007	1281	GGTATGGGAAAAACTGCTGTATTTGTGTT	110759359 (Apis mellifera)
NL007	1282	GCAAACAAGTCATGATGTTCAG	110759359 (Apis mellifera)
NL007	1283	CTGCAGCAGCACTATGTCAAACTCAA	90137538 (Spodoptera frugiperda)
NL007	1284	GAAAACGAAAAGAACAAAAAG	94468805 (Aedes aegypti)
NL008	1285	TGCCAAGCCTAAAGATTTGGG	60315277 (Dysdera erythrina)
NL008	1286	ATGTTCAAGAAAGTTAATGCTAGAGA	60336214 (Homalodisca coagulata)
NL008	1287	GAGTTGTTGGTGTTCTTTTGGGATG	66522334 (Apis mellifera)
NL008	1288	TTTCAAACAGTTTTGCAGTTCC	75735289 (Tribolium castaneum)
NL008	1289	GAGTTGTTGGTGTTCTTTTGGGATG	110762109 (Apis mellifera)
NL010_1	1290	AAGGACCTGACTGCCAAGCAG	2761430 (Drosophila melanogaster)
NL010_1	1291	GCCAAGCAGATCCAGGACATG	49559867 (Boophilus microplus)
NL010_1	1292	TGCTCGAAGAGCTACGTGTTCCG	49559867 (Boophilus microplus)
NL010_1	1293	AAGAGCTACGTGTTCCGTGGC	92043082 (Drosophila willistoni)
NL010_1	1294	AAGGACCTGACTGCCAAGCAG	92481328 (Drosophila erecta) 28571527 (Drosophila melanogaster)
NL010_2	1295	ATGGACACATTTTTCCAAATTCTCAT	33427937 (Glossina morsitans)
NL010_2	1296	ACCAGCAGTATTCAACCCGACA	47520567 (Acyrthosiphon pisum)
NL010_2	1297	TATTGATGGACACATTTTTCCA	47520567 (Acyrthosiphon pisum)
NL010_2	1298	TTCAACAACAGTCCTGATGAAAC	55891325 (Locusta migratoria)
NL010_2	1299	ATGGACACATTTTTCCAAATT	56151768 (Rhynchosciara americana), 75736992 (Tribolium castaneum)
NL010_2	1300	CCGCAGTTCATGTACCATCTGCG	6932015 (Anopheles gambiae), 29558345 (Bombyx mori)
NL010_2	1301	ATGGACACATTTTTCCAAATT	91086194 (Tribolium castaneum)
NL011	1302	AAGAAGTATGTTGCCACCCTTGG	21640529 (Amblyomma variegatum)
NL011	1303	GACATCAAGGACAGGAAAGTCAAGGCCAAG AGCATAGT	25959135 (Meladema coriacea)

NL011	1304	CAACTACAACTTCGAGAAGCCGTTCCTGTGG	25959135 (Meladema coriacea), 77646995 (Aedes aegypti)
NL011	1305	TACAAGAACGTTCCCAACTGGCA	3114090 (Drosophila melanogaster)
NL011	1306	TGCGAAAACATTCCCATTGTACT	37951963 (Ips pini)
NL011	1307	AGGAAGAAGAACCTTCAGTACTACGA	40544671 (Tribolium castaneum)
NL011	1308	AGCAACTACAACTTCGAGAAGCC	49565237 (Boophilus microplus), 49538692 (Rhipicephalus appendiculatus)
NL011	1309	AACAAAGTAGACATCAAGGACAGGAAAGTCAA	76552920 (Spodoptera frugiperda)
NL011	1310	CCCAACTGGCACAGAGATTTAGTG	78230577 (Heliconius erato/himera mixed EST library)
NL011	1311	GATGGTGGTACCGGCAAAACTAC	78538667 (Glossina morsitans)
NL011	1312	TACAAGAACGTTCCCAACTGGCAC	84267747 (Aedes aegypti)
NL011	1313	AACAAAGTAGACATCAAGGACAGGAAAGTCAA	110263840 (Spodoptera frugiperda)
NL011	1314	TTGACTTTCCTGTCCTTGATGTC	90136305 (Bicyclus anynana)
NL011	1315	GACATCAAGGACAGGAAAGTCAAGGC	90813103 (Nasonia vitripennis)
NL011	1316	AGGAAGAAGAACCTTCAGTACTACGA	91091115 (Tribolium castaneum)
NL011	1317	GATGTCGTAGTACTGAAGGTTCTT	90136305 (Bicyclus anynana)
NL011	1318	CAACTACAACTTCGAGAAGCCGTTCCTGTGG	90977910 (Aedes aegypti)
NL011	1319	CCAACCTGGAGTTCGTCGCCATGCC	92465523 (Drosophila erecta)
NL011	1320	GAATTTGAAAAGAAGTATGTTGC	113015058 (Bemisia tabaci)
NL011	1321	CTTCAGTACTACGACATCAGTGCGAA	110086408 (Amblyomma cajennense)
NL011	1322	AGCAACTACAACTTCGAGAAGCC	110086408 (Amblyomma cajennense)
NL011	1323	AAGCTGATCGGTGACCCCAACCTGGAGTT	110086408 (Amblyomma cajennense)
NL012	1324	CACAGTTTGAACAGCAAGCTGG	29552409 (Bombyx mori)
NL012	1325	GCAGCAGACGCAGGCACAGGTAGA	77823921 (Aedes aegypti)
NL012	1326	CACAGTTTGAACAGCAAGCTGG	94435913 (Bombyx mori)
NL013	1327	CAAGCGAAGATGTTGGACATGCT	15536506 (Drosophila melanogaster)
NL013	1328	ATGGTGGTGGGCTGGTACCACTCGCACCC	49547019 (Rhipicephalus appendiculatus)
NL013	1329	GTGGTGGGCTGGTACCACTCGCACCC	58079586 (Amblyomma americanum)

NL013	1330	GTGGGCTGGTACCACTCGCACCC	82848521 (Boophilus microplus)
NL013	1331	AAGATGTTGGACATGCTAAAGCAGACAGG	92229701 (Drosophila willistoni)
NL013	1332	TGTCGGGTGTCGACATCAACAC	92962655 (Drosophila ananassae)
NL013	1333	GTTCCCATGGAAGTTATGGGC	112433067 (Myzus persicae)
NL013	1334	GTGGGCTGGTACCACTCGCACCC	110085175 (Amblyomma cajennense)
NL014	1335	GAGATCGATGCCAAGGCCGAGGA	1033187 (Drosophila melanogaster)
NL014	1336	GAATTCAACATTGAAAAGGGA	16900951 (Ctenocephalides felis)
NL014	1337	GAAGAATTCAACATTGAAAAGGG	47518467 (Acyrthosiphon pisum)
NL014	1338	GAAGCCAATGAGAAAGCCGAAGA	47518467 (Acyrthosiphon pisum)
NL014	1339	TCGTCAAACATGCTGAACCAAGC	61954844 (Tribolium castaneum)
NL014	1340	TTTCATTGAGCAAGAAGCCAATGA	62239529 (Diabrotica virgifera), 76169390 (Diploptera punctata), 61954844 (Tribolium castaneum), 16900951 (Ctenocephalides felis)
NL014	1341	CAAGAAGCCAATGAGAAAGCCGA	111160670 (Myzus persicae)
NL014	1342	TTTCATTGAGCAAGAAGCCAATGA	91092061 (Tribolium castaneum)
NL014	1343	AGAAGCCAATGAGAAAGCCGA	112432414 (Myzus persicae)
NL014	1344	TCGTCAAACATGCTGAACCAAGC	91092061 (Tribolium castaneum)
NL014	1345	GCCAATGAGAAAGCCGAAGAGATCGATGCC AA	93001435 (Drosophila grimshawi)
NL014	1346	AAAGCCGAAGAGATCGATGCCAA	92936169 (Drosophila virilis)
NL014	1347	GAGATCGATGCCAAGGCCGAGGA	24644299 (Drosophila melanogaster)
NL014	1348	GAAGAATTCAACATTGAAAAGGG	86463006 (Acyrthosiphon pisum) 111160670 (Myzus persicae)
NL014	1349	GAAGAATTCAACATTGAAAAGGGAAGGCT	90819999 (Graphocephala atropunctata)
NL014	1350	AAGAATTCAACATTGAAAAGGG	111158385 (Myzus persicae)
NL015	1351	GAGGTGCTGCGCATCCACACCAA	18887285 (Anopheles gambiae)
NL015	1352	ATCCATGTGCTGCCCATTGATGA	21641659 (Amblyomma variegatum)
NL015	1353	CATGTGCTGCCCATTGATGAT	22039735 (Ctenocephalides felis)
NL015	1354	CTGCGCATCCACACCAAGAACATGAAGTTGG	22474136 (Helicoverpa armigera)
NL015	1355	TTCTTCTTCCTCATCAACGGACC	49552586 (Rhipicephalus appendiculatus)

NL015	1356	GAGATGGTGGAGTTGCCGCTG	58371722 (Lonomia obliqua)
NL015	1357	CAGATCAAAGAGATGGTGGAG	92947821 (Drosophila ananassae)
NL015	1358	ATCAACGGACCCGAGATTATG	92947821 (Drosophila ananassae)
NL015	1359	ATGAAGATGATGGCCGGTGCGTT	92470977 (Drosophila erecta)
NL015	1360	CCGGCCATCATCTTCATCGATGAG	92480997 (Drosophila erecta)
NL015	1361	ATCATCTTCATCGATGAGCTGGACGC	99007898 (Leptinotarsa decemlineata)
NL015	1362	CAGCTGCTGACGCTGATGGACGG	92941440 (Drosophila virilis)
NL015	1363	ATCGACATTGGCATTCCCGATGCCACCGG	92947821 (Drosophila ananassae)
NL016	1364	TCTATGGAGAACGTGTGCCTGTTCTTGAAC	27372076 (Spodoptera littoralis)
NL016	1365	TACCAGTGCGAGAAGCACGTGCT	2921501 (Culex pipiens)
NL016	1366	ATGGAGAACGTGTGCCTGTTCTTGAACCTGG C	31206154 (Anopheles gambiae str. PEST)
NL016	1367	CGTGGCCAGAAAATCCCCATCTT	3945243 (Drosophila melanogaster)
NL016	1368	TGGCCTACCAGTGCGAGAAGCACGTG	4680479 (Aedes aegypti)
NL016	1369	TGGCCACCATCTACGAGCGCGCCGG	53883819 (Plutella xylostella)
NL016	1370	ATGGAGAACGTGTGCCTGTTCTTGAA	67883622 (Drosophila pseudoobscura)
NL016	1371	CCCGAGGAAATGATCCAGACTGG	67883622 (Drosophila pseudoobscura)
NL016	1372	TGGCCTACCAGTGCGAGAAGCACGTGCT	67883622 (Drosophila pseudoobscura), 31206154 (Anopheles gambiae str. PEST)
NL016	1373	GAGGAGGTGCCCGGCCGTCGTGGTTTCCCCG GTTACATGTACACCGAT	67896654 (Drosophila pseudoobscura)
NL016	1374	GAGGGTCGCAACGGCTCCATCAC	67896654 (Drosophila pseudoobscura)
NL016	1375	GAGGTGCCCGGCCGTCGTGGTTTCCCCGGTT ACATGTACACCGAT	75710699 (Tribolium castaneum)
NL016	1376	ATGGAGAACGTGTGCCTGTTCTTGAAC	76554661 (Spodoptera frugiperda)
NL016	1377	TGGCCTACCAGTGCGAGAAGCACGTGCTCGT CATCCT	9992660 (Drosophila melanogaster)
NL016	1378	CGTCGTGGTTTCCCCGGTTACATGTACACCG	9992660 (Drosophila melanogaster), 2921501 (Culex

		AT	pipiens), 62239897 (Diabrotica virgifera)
NL016	1379	TGGTCGCGTATCTATCCCGAGGAAATGATCC AGAC	92999374 (Drosophila grimshawi)
NL016	1380	TGGTCGCGTATCTATCCCGAGGAAATGATCC AGACTGG	92940538 (Drosophila virilis)
NL016	1381	TCTATGGAGAACGTGTGCCTGTTCTTGAAC	92938622 (Drosophila virilis)
NL016	1382	ATGGAGAACGTGTGCCTGTTCTTGAAC	92950254 (Drosophila ananassae) 90137502 (Spodoptera frugiperda)
NL016	1383	AACGTGTGCCTGTTCTTGAAC	92946927 (Drosophila ananassae)
NL016	1384	TGGCCTACCAGTGCGAGAAGCACGTGCT	24646342 (Drosophila melanogaster) 92231646 (Drosophila willistoni)
NL016	1385	TGGCCTACCAGTGCGAGAAGCACGTGCTCGT CATCCT	107256717 (Drosophila melanogaster)
NL016	1386	GCCTACCAGTGCGAGAAGCACGTGCT	92985459 (Drosophila grimshawi)
NL016	1387	GAGGAGGTGCCCGGCCGTCGTGGTTTCCCCG GTTACATGTACAC	92938622 (Drosophila virilis)
NL016	1388	GAGGAGGTGCCCGGCCGTCGTGGTTTCCCCG GTTACATGTACACCGAT	92477818 (Drosophila erecta)
NL016	1389	GAGGTGCCCGGCCGTCGTGGTTTCCCCGGTT ACATGTACACCGAT	91090030 (Tribolium castaneum)
NL016	1390	CGTCGTGGTTTCCCCGGTTACAT	104530890 (Belgica antarctica)
NL016	1391	CGTCGTGGTTTCCCCGGTTACATGTACACCG AT	92981037 (Drosophila grimshawi) 24646342 (Drosophila melanogaster)
NL016	1392	CGTGGTTTCCCCGGTTACATGTACACCGAT	92957249 (Drosophila ananassae)
NL016	1393	ATCGGTGTACATGTAACCGGGGAAACCA	103744758 (Drosophila melanogaster)
NL016	1394	CGTCCGGCGCGCTCGTAGATGGT	91829127 (Bombyx mori)
NL016	1395	GAGGGTCGCAACGGCTCCATCAC	92957249 (Drosophila ananassae)
NL018	1396	CGGACGTGGCCTGGTTCATCA	92479742 (Drosophila erecta)
NL019	1397	GTGGTGTACGACTGCACCGACCAGGAGTCGT TCAACAAC	84343006 (Aedes aegypti)
NL019	1398	GAAAGTTACATCAGTACCATTGGTGT	113018639 (Bemisia tabaci)
NL019	1399	CACCGACCAGGAGTCGTTCAACAAC	85857059 (Aedes aegypti)
NL019	1400	AGTACCATTGGTGTAGATTTTAAAAT	91087112 (Tribolium castaneum)
NL019	1401	ATTGGTGTAGATTTTAAAATTAG	78542465 (Glossina morsitans)
NL019	1402	GGTGTAGATTTTAAAATTAGAAC	92232411 (Drosophila willistoni)

NL019	1403	GGTGTAGATTTTAAAATTAGAACAAT	90986845 (Aedes aegypti)
NL019	1404	GTTCTAATTTTAAAATCTACAC	92043152 (Drosophila willistoni)
NL019	1405	TGGGACACGGCCGGCCAGGAG	91091115 (Tribolium castaneum)
NL019	1406	TGGGACACGGCCGGCCAGGAGCG	90982219 (Aedes aegypti)
NL019	1407	TGGGACACGGCCGGCCAGGAGCGGT	94433465 (Bombyx mori)
NL019	1408	GACCAGCTGGGCATTCCGTTCCT	10708384 (Amblyomma americanum)
NL019	1409	ATTGGTGTAGATTTTAAAATT	18864897 (Anopheles gambiae)
NL019	1410	TGGGACACGGCCGGCCAGGAGCGGTT	18888926 (Anopheles gambiae)
NL019	1411	CAGGAGCGGTTCCGCACGATCAC	21640713 (Amblyomma variegatum)
NL019	1412	ATTGGTGTAGATTTTAAAATTAGAAC	22039832 (Ctenocephalides felis)
NL019	1413	ATTGGTGTAGATTTTAAAATTAG	33378174 (Glossina morsitans)
NL019	1414	TGGGACACGGCCGGCCAGGAG	3738872 (Manduca sexta), 25959135 (Meladema coriacea), 40542849 (Tribolium castaneum), 67840088 (Drosophila pseudoobscura)
NL019	1415	TGGGACACGGCCGGCCAGGAGCGGT	4161805 (Bombyx mori)
NL019	1416	GATGACACATACACAGAAAGTTACATCAGTAC	50562545 (Homalodisca coagulata), 71047909 (Oncometopia nigricans)
NL019	1417	ACGGCCGGCCAGGAGCGGTTCCG	58378591 (Anopheles gambiae str. PEST)
NL019	1418	AGTACCATTGGTGTAGATTTTAAAAT	61954135 (Tribolium castaneum)
NL019	1419	TAAAGCTTCAGATTTGGGACAC	68758530 (Acanthoscurria gomesiana)
NL019	1420	ATTTGGGACACGGCCGGCCAGGA	77667315 (Aedes aegypti)
NL019	1421	GTGGTGTACGACTGCACCGACCAGGAGTCGTTCAACAAC	77705629 (Aedes aegypti)
NL019	1422	GGTGTAGATTTTAAAATTAGAACAAT	77890715 (Aedes aegypti)
NL019	1423	TGGGACACGGCCGGCCAGGAGCG	82851662 (Boophilus microplus), 49536894 (Rhipicephalus appendiculatus)
NL022	1424	TCTTCCTCACCGGTCAGGAGGAGAT	6928515 (Anopheles gambiae)

NL022	1425	AAATTCTCCGAGTTTTTCGACGATGC	91082872 (Tribolium castaneum)
NL022	1426	TTCCTCACCGGTCAGGAGGAGAT	90976120 (Aedes aegypti)
NL022	1427	TAGTATTGGCCACAAATATTGCAGA	92042565 (Drosophila willistoni)
NL023	1428	TATTTGAACATATGGGTGCCGCA	20384699 (Plutella xylostella)
NL023	1429	GAGGGAGAGGAAATGTGGAATCC	22085301 (Helicoverpa armigera)
NL023	1430	CCGAAGATTGTCTGTATTTGAA	27531022 (Apis mellifera)
NL023	1431	GATTCCGTTTGCGAAACCTCC	57929927 (Anopheles gambiae str. PEST)
NL023	1432	GGTGCGTTCGGCTTCCTCTACCT	58380563 (Anopheles gambiae str. PEST)
NL023	1433	CAATTCAATGCTAGGGAAAGG	110759012 (Apis mellifera)
NL023	1434	GAGGGAGAGGAAATGTGGAATCC	55793188 (Helicoverpa assulta)
NL023	1435	CCGAAGATTGTCTGTATTTGAA	58585075 (Apis mellifera)
NL023	1436	GACGTCATCGTCGCCTCCATGCA	91077117 (Tribolium castaneum)
NL027	1437	GGAGACCCTGGAGCTGGTGCG	49543279 (Rhipicephalus appendiculatus)

Table 4-CS

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
CS001	1730	AAAGCATGGATGTTGGACAAA	73619372 (Aphis gossypii); 77325485 (Chironomus tentans); 22474232 (Helicoverpa armigera); 37951951 (Ips pini); 60305420 (Mycetophagus quadripustulatus); 84647995 (Myzus persicae)
CS001	1731	AAAGCATGGATGTTGGACAAACT	40877657 (Bombyx mori); 103783745 (Heliconius erato); 55904580 (Locusta migratoria); 101413238 (Plodia interpunctella)
CS001	1732	AACCGGCTCAAGTACGCGCTCAC	22474232 (Helicoverpa armigera)
CS001	1733	AACCGGCTCAAGTACGCGCTCACCGG	90134075 (Bicyclus anynana)
CS001	1734	AAGATCATGGACTTCATCAAGTT	90134075 (Bicyclus anynana)
CS001	1735	ACCAGATTGAACAACGTGTTCAT	71536878 (Diaphorina citri) 3658573 (Manduca sexta)

CS001	1736	ATCATGGACTTCATCAAGTTTGAATC	103783745 (Heliconius erato)
CS001	1737	CAAGATCATGGACTTCATCAAGTT	3478550 (Antheraea yamamai)
CS001	1738	CCCCACAAGTTGCGCGAGTGC	63011732 (Bombyx mori)
CS001	1739	CCCGCTGGATTTATGGATGTTGT	101403940 (Plodia interpunctella)
CS001	1740	CCTCCAAGATCATGGACTTCATCAAGTT	22474232 (Helicoverpa armigera)
CS001	1741	CCTGCCGCTGGTGATCTTCCT	27597800 (Anopheles gambiae)
CS001	1742	CGACGGGCCCCAAGAACGTGCC	22474232 (Helicoverpa armigera)
CS001	1743	CTCATCAAGGTCAACGACTCC	103783745 (Heliconius erato) 112350001 (Helicoverpa armigera) 101418268 (Plodia interpunctella)
CS001	1744	CTCATCAAGGTCAACGACTCCATCCAGCTC GACAT	3738704 (Manduca sexta)
CS001	1745	CTCATCAAGGTCAACGACTCCATCCAGCTC GACATCGCCACCT	53884106 (Plutella xylostella)
CS001	1746	CTGCCGCTGGTGATCTTCCTC	27603050 (Anopheles gambiae)
CS001	1747	GACCCCACATATCCCGCTGGATT	103783745 (Heliconius erato)
CS001	1748	GCAGCGACTTATCAAAGTTGA	109978109 (Gryllus pennsylvanicus)
CS001	1749	GCATGGATGTTGGACAAACTGGG	67899746 (Drosophila pseudoobscura)
CS001	1750	GCCACCTCCAAGATCATGGACTTCAT	110259010 (Spodoptera frugiperda)
CS001	1751	GCGCGTGGCGACGGGCCCCAAGAACGTGCC	53884106 (Plutella xylostella)
CS001	1752	GCTGGATTTATGGATGTTGTTT	29553519 (Bombyx mori)
CS001	1753	GGCTCAAGTACGCGCTCACCGG	5498893 (Antheraea yamamai)
CS001	1754	GTGGGCACCATCGTGTCCCGCGAG	3953837 (Bombyx mandarina) 53884106 (Plutella xylostella)
CS001	1755	GTGGGCACCATCGTGTCCCGCGAGCG	3478550 (Antheraea yamamai)
CS001	1756	GTGGGCACCATCGTGTCCCGCGAGCGACAT CCCGG	22474232 (Helicoverpa armigera)
CS001	1757	TAAAGCATGGATGTTGGACAA	58371410 (Lonomia obliqua)
CS001	1758	TAAAGCATGGATGTTGGACAAA	60311985 (Papilio dardanus) 31366663 (Toxoptera citricida)
CS001	1759	TAAAGCATGGATGTTGGACAAACT	109978109 (Gryllus pennsylvanicus)
CS001	1760	TAAAGCATGGATGTTGGACAAACTGGG	98994282 (Antheraea mylitta)
CS001	1761	TACAAGCTGTGCAAGGTGCGGCGCGTGGCG ACGGGCCC	98993531 (Antheraea mylitta)
CS001	1762	TACAAGCTGTGCAAGGTGCGGCGCGTGGCG	5498893 (Antheraea yamamai)

		ACGGGCCCCAA	
CS001	1763	TACCCCGACCCACTCATCAAGGT	90134075 (Bicyclus anynana)
CS001	1764	TGAACAACGTGTTCATAATCGG	98993531 (Antheraea mylitta)
CS001	1765	TGCGCGAGTGCCTGCCGCTGGT	22474232 (Helicoverpa armigera)
CS001	1766	TGTATGATCACGGGAGGCCGTAACTTGGG	60311445 (Euclidia glyphica)
CS001	1767	TGTATGATCACGGGAGGCCGTAACTTGGGG CG	3953837 (Bombyx mandarina)
CS001	1768	TGTATGATCACGGGAGGCCGTAACTTGGGG CGCGTGGGCACCATCGTGTCCCGCGAG	91826697 (Bombyx mori)
CS001	1769	TGTGCAAGGTGCGGCGCGTGGCGACGGGCC CCAAG	3478550 (Antheraea yamamai)
CS001	1770	TTGAACAACGTGTTCATAATCGGCAAGGGC ACGAA	3953837 (Bombyx mandarina) 40915191 (Bombyx mori)
CS002	1771	ATTGAGGCCCAAAGGGAAGCGCTAGAAGG	91849872 (Bombyx mori)
CS002	1772	CACGATCTGATGGATGACATTG	33498783 (Anopheles gambiae)
CS002	1773	GAGTTTCTTTAGTAAAGTATTCGGTGG	110762684 (Apis mellifera)
CS002	1774	TATGAAAAGCAGCTTACCCAGAT	49552807 (Rhipicephalus appendiculatus)
CS003	1775	AGGCACATCCGTGTCCGCAAGCA	10707186 (Amblyomma americanum)
CS003	1776	AAGATTGAGGACTTCTTGGAA	60295192 (Homalodisca coagulata)
CS003	1777	AAGCACATTGACTTCTCGCTGAA	92219983 (Drosophila willistoni)
CS003	1778	ATCAGACAGAGGCACATCCGTGT	27260897 (Spodoptera frugiperda)
CS003	1779	ATCCGTAAGGCTGCCCGTGAG	101413529 (Plodia interpunctella)
CS003	1780	ATCCGTAAGGCTGCCCGTGAGCTG	92042852 (Drosophila willistoni)
CS003	1781	ATCCGTAAGGCTGCCCGTGAGCTGCT	92959651 (Drosophila ananassae) 112349903 (Helicoverpa armigera)
CS003	1782	ATCCGTAAGGCTGCCCGTGAGCTGCTCAC	90138123 (Spodoptera frugiperda)
CS003	1783	CACATCCGTGTCCGCAAGCAAG	60306665 (Sphaerius sp.)
CS003	1784	CACATCCGTGTCCGCAAGCAAGT	77329341 (Chironomus tentans)
CS003	1785	CACATCCGTGTCCGCAAGCAAGTTG	60306676 (Sphaerius sp.)
CS003	1786	CGCAACAAGCGTGAGGTGTGG	92473214 (Drosophila erecta) 67888665 (Drosophila pseudoobscura)
CS003	1787	CGTGTCCGCAAGCAAGTTGTGAACATCCC	90134575 (Bicyclus anynana) 29553137 (Bombyx mori)
CS003	1788	CTCGCTGAAGTCTCCGTTCGGCGGCGGCCG	3986375 (Antheraea yamamai)

CS003	1789	CTCGGTCTGAAGATTGAGGACTT	112349903 (Helicoverpa armigera) 49532931 (Plutella xylostella)
CS003	1790	CTGGACTCTGGCAAGCACATTGACTTCTC	29553137 (Bombyx mori) 58371398 (Lonomia obliqua)
CS003	1791	GACTTCTCGCTGAAGTCTCCGTTCGGCGGCGG	60312414 (Papilio dardanus)
CS003	1792	GACTTCTCGCTGAAGTCTCCGTTCGGCGGCGGCCG	49532931 (Plutella xylostella)
CS003	1793	GAGGAGAAAGACCCTAAGAGGTTATTCGAAGGTAA	37952462 (Ips pini)
CS003	1794	GATCCGTAAGGCTGCCCGTGA	67568544 (Anoplophora glabripennis)
CS003	1795	GATCCGTAAGGCTGCCCGTGAGCTGCT	67843629 (Drosophila pseudoobscura) 56772258 (Drosophila virilis)
CS003	1796	GATTATGTACTCGGTCTGAAGATTGAGGACTT	101413529 (Plodia interpunctella)
CS003	1797	GGTCTGAAGATTGAGGACTTCTTGGA	2699490 (Drosophila melanogaster)
CS003	1798	GTGTGGAGGGTGAAGTACACGCT	60312414 (Papilio dardanus)
CS003	1799	GTGTTCAAGGCTGGTCTAGCTAAGTC	78230982 (Heliconius erato/himera mixed EST library)
CS003	1800	GTGTTGGATGAGAAGCAGATGAAGCTCGATTATGT	112349903 (Helicoverpa armigera)
CS003	1801	TGAAGATTGAGGACTTCTTGGA	3986375 (Antheraea yamamai)
CS003	1802	TGGACTCTGGCAAGCACATTGACTTCTC	78230982 (Heliconius erato/himera mixed EST library)
CS003	1803	TGGATGAGAAGCAGATGAAGCT	60312414 (Papilio dardanus)
CS003	1804	TGGTCTCCGCAACAAGCGTGAGGT	76552467 (Spodoptera frugiperda)
CS003	1805	TGGTCTCCGCAACAAGCGTGAGGTGTGG	33528372 (Trichoplusia ni)
CS006	1806	CGTATGACAATTGGTCACTTGATTGA	91831926 (Bombyx mori)
CS006	1807	GAAGATATGCCTTTCACTTGTGAAGG	55801622 (Acyrthosiphon pisum)
CS006	1808	GGAAAAACTATAACTTTGCCAGAAAA	40926289 (Bombyx mori)
CS006	1809	GGTGATGCTACACCATTTAACGATGCTGT	31366154 (Toxoptera citricida)
CS006	1810	TCTCGTATGACAATTGGTCACTTGAT	49201759 (Drosophila melanogaster)
CS006	1811	CTGTCAACGTGCAGAAGATCTC	49573116 (Boophilus microplus)
CS007	1812	TGGATGAATGTGACAAAATGCTTGAA	84114516 (Blomia tropicalis)
CS007	1813	TTTATGCAAGATCCTATGGAAGT	84114516 (Blomia tropicalis)
CS007	1814	AAATTTATGCAAGATCCTATGGAAGTTTATGT	78525380 (Glossina morsitans)

CS007	1815	AATATGACTCAAGATGAGCGTCT	90137538 (Spodoptera frugiperda)
CS007	1816	ATGACTCAAGATGAGCGTCTCTCCCG	103792212 (Heliconius erato)
CS007	1817	ATGCAAGATCCTATGGAAGTTTA	77336752 (Chironomus tentans)
CS007	1818	ATGCAAGATCCTATGGAAGTTTATGT	77873166 (Aedes aegypti)
CS007	1819	CGCTATCAGCAGTTCAAAGATTTCCAGAAG	77873166 (Aedes aegypti)
CS007	1820	GAAAATGAAAAGAATAAGAAG	110759359 (Apis mellifera) 78525380 (Glossina morsitans)
CS007	1821	GAAGTTCAACATGAATGTATTCC	110759359 (Apis mellifera)
CS007	1822	GATGAGCGTCTCTCCCGCTATCA	40932719 (Bombyx mori)
CS007	1823	TGCCAATTCAGAAAGATGAAGAAGT	110759359 (Apis mellifera)
CS007	1824	TGTAAGAAATTTATGCAAGATC	45244844 (Bombyx mori)
CS009	1825	AGGTGTGCGACGTGGACATCA	92460383 (Drosophila erecta)
CS009	1826	GACTTGAAGGAGCACATCAGGAA	29534871 (Bombyx mori)
CS009	1827	GGCCAGAACATCCACAACTGTGA	29534871 (Bombyx mori)
CS009	1828	TCTTGCGAGGGAGAGAATCCA	111005781 (Apis mellifera)
CS011	1829	AAAACTATTGTTTTCCACAGAAAAAAGAA	86465126 (Bombyx mori)
CS011	1830	ATCAAGGACAGAAAAGTCAAAGC	78230577 (Heliconius erato/himera mixed EST library)
CS011	1831	ATCTCTGCCAAGTCAAACTACAA	101406907 (Plodia interpunctella)
CS011	1832	CAATGTGCCATCATCATGTTCGA	110242457 (Spodoptera frugiperda)
CS011	1833	CCCAACTGGCACAGAGATTTAGTGCG	78230577 (Heliconius erato/himera mixed EST library)
CS011	1834	GACACTTGACTGGAGAGTTCGAGAAAAGAT A	101410627 (Plodia interpunctella)
CS011	1835	GATATCAAGGACAGAAAAGTCAA	60312108 (Papilio dardanus)
CS011	1836	GCCAAGTCAAACTACAATTTCGA	67873076 (Drosophila pseudoobscura)
CS011	1837	GCTGGCCAAGAAAAGTTTGGTGGT	111031693 (Apis mellifera)
CS011	1838	GGCCAAGAAAAGTTTGGTGGTCTCCG	84267747 (Aedes aegypti)
CS011	1839	TACAAAAATGTACCCAACTGGCA	92963426 (Drosophila grimshawi) 37951963 (Ips pini)
CS011	1840	TACAAAAATGTACCCAACTGGCACAGAGA	60312108 (Papilio dardanus)
CS011	1841	TATGGGATACTGCTGGCCAAGAA	40929360 (Bombyx mori)
CS011	1842	TATGGGATACTGCTGGCCAAGAAA	110749704 (Apis mellifera)
CS011	1843	TGGGATACTGCTGGCCAAGAA	73618835 (Aphis gossypii) 112432160 (Myzus persicae)
CS011	1844	TGTGCCATCATCATGTTCGATGT	84346664 (Aedes aegypti)

CS011	1845	TTGACTGGAGAGTTCGAGAAA	90136305 (Bicyclus anynana) 78230577 (Heliconius erato/himera mixed EST library) 60312108 (Papilio dardanus)
CS011	1846	TTGACTGGAGAGTTCGAGAAAA	86465126 (Bombyx mori) 110262261 (Spodoptera frugiperda)
CS011	1847	TGGGATACTGCTGGCCAAGAA	21639295 (Sarcoptes scabiei)
CS013	1848	GATCCCATTCAGTCTGTCAAGGG	3626535 (Drosophila melanogaster)
CS013	1849	TTCCAAGCAAAGATGTTGGATATGTTGAA	112433067 (Myzus persicae)
CS014	1850	AAAAAGATCCAATCTTCGAACATGCTGAA	103775905 (Heliconius erato)
CS014	1851	AAACAAGTGGAACTCCAGAAAAA	101403826 (Plodia interpunctella)
CS014	1852	AAAGTGCGTGAGGACCACGTACG	87266590 (Choristoneura fumiferana) 3738660 (Manduca sexta)
CS014	1853	AAGATCAGCAACACTCTGGAGTC	58371699 (Lonomia obliqua)
CS014	1854	AAGATCAGCAACACTCTGGAGTCTCG	91848497 (Bombyx mori)
CS014	1855	AAGATCCAATCTTCGAACATG	77790417 (Aedes aegypti)
CS014	1856	AAGATCCAATCTTCGAACATGCTGAA	91756466 (Bombyx mori)
CS014	1857	AAGCAGATCAAGCATATGATGGCCTTCATC GAACA	90814338 (Nasonia vitripennis)
CS014	1858	AAGCAGATCAAGCATATGATGGCCTTCATC GAACAAGAGGC	87266590 (Choristoneura fumiferana)
CS014	1859	ATGATGGCCTTCATCGAACAAGA	111158385 (Myzus persicae)
CS014	1860	ATGATGGCCTTCATCGAACAAGAGGC	98993392 (Antheraea mylitta) 91756466 (Bombyx mori) 103775905 (Heliconius erato)
CS014	1861	CAGATCAAGCATATGATGGCCTTCATCGA	53884266 (Plutella xylostella)
CS014	1862	CAGCAGCGGCTCAAGATCATGGAATACTA	101403826 (Plodia interpunctella)
CS014	1863	CATATGATGGCCTTCATCGAACAAGAGGC	101403826 (Plodia interpunctella)
CS014	1864	CTCAAAGTGCGTGAGGACCACGT	103775905 (Heliconius erato)
CS014	1865	CTCAAGATCATGGAATACTACGA	15068660 (Drosophila melanogaster)
CS014	1866	GAAATCGATGCAAAGGCCGAAGAGGAGTTC AA	103775905 (Heliconius erato)
CS014	1867	GAACTCCAGAAAAAGATCCAATC	76551032 (Spodoptera frugiperda)
CS014	1868	GAACTCCAGAAAAAGATCCAATCTTCGAAC ATGCTGAA	87266590 (Choristoneura fumiferana)
CS014	1869	GAGGAAATCGATGCAAAGGCCGA	76551032 (Spodoptera frugiperda)

CS014	1870	GCCGAAGAGGAGTTCAACATTGAAAAAGG	33374540 (Glossina morsitans)
CS014	1871	GCGCCTGGCTGAGGTGCCCAA	101403826 (Plodia interpunctella)
CS014	1872	GGCCGCCTGGTGCAGCAGCAGCG	24975647 (Anopheles gambiae)
CS014	1873	GGCTCAAGATCATGGAATACTA	37593557 (Pediculus humanus)
CS014	1874	GGCTCAAGATCATGGAATACTACGA	58371699 (Lonomia obliqua)
CS014	1875	TACGAAAAGAAAGAGAAACAAGT	33374540 (Glossina morsitans)
CS014	1876	TGAAGGTGCTCAAAGTGCGTGAGGA	92976185 (Drosophila grimshawi) 92994742 (Drosophila mojavensis)
CS014	1877	TTCAAAAGCAGATCAAGCATATGATGGCCT TCATCGAACAAGAGGC	3738660 (Manduca sexta)
CS015	1878	AACGGGCCGGAGATCATGTCCAA	92480997 (Drosophila erecta)
CS015	1879	AACTGCCCCGATGAGAAGATCCG	91086234 (Tribolium castaneum)
CS015	1880	ATCTTCATCGATGAACTGGATGC	56152379 (Rhynchosciara americana)
CS015	1881	CATATATTGCCCATTGATGATTC	58371642 (Lonomia obliqua)
CS015	1882	CTCATGTATGGGCCGCCTGGTACCGG	83423460 (Bombyx mori)
CS015	1883	CTGCCCCGATGAGAAGATCCGCATGAACCG	92948836 (Drosophila ananassae)
CS015	1884	GAGAAGATCCGCATGAACCGCGT	4691131 (Aedes aegypti) 92466521 (Drosophila erecta) 15070638 (Drosophila melanogaster)
CS015	1885	GTACATATATTGCCCATTGAT	90133859 (Bicyclus anynana)
CS015	1886	TCATCGCACGTGATCGTAATGGC	22474136 (Helicoverpa armigera)
CS015	1887	TTCATGGTTCGCGGGGGCATG	29551125 (Bombyx mori)
CS016	1888	AAATCGGTGTACATGTAACCTGGGAAACCA CG	55797015 (Acyrthosiphon pisum) 73615307 (Aphis gossypii)
CS016	1889	AAGTTGTCCTCGTGGTCGTCCA	91826756 (Bombyx mori)
CS016	1890	ACAGATCTGGGCGGCAATTTC	18950388 (Anopheles gambiae) 31206154 (Anopheles gambiae str. PEST)
CS016	1891	ACAGCCTTCATGGCCTGCACGTCCTT	76169888 (Diploptera punctata) 92953069 (Drosophila ananassae) 92477149 (Drosophila erecta) 8809 (Drosophila melanogaster) 55694467 (Drosophila yakuba)
CS016	1892	ACATCAGAGTGGTCCTTGCGGGTCAT	55694467 (Drosophila yakuba) 110248186 (Spodoptera frugiperda)
CS016	1893	ACCAGCACGTGTTTCTCACACTGGTA	91829127 (Bombyx mori)

CS016	1894	ACCTCCTCACGGGCGGCGGACAC	237458 (Heliothis virescens) 27372076 (Spodoptera littoralis)
CS016	1895	ACGACAGCCTTCATGGCCTGCACGTCCTT	67896654 (Drosophila pseudoobscura)
CS016	1896	ACGTAGATCTGTCCCTCAGTGATGTA	53883819 (Plutella xylostella)
CS016	1897	AGAGCCTCCGCGTACGAAGACATGTC	53883819 (Plutella xylostella)
CS016	1898	AGCAATGGAGTTCATCACGTC	60295607 (Homalodisca coagulata)
CS016	1899	AGCAGCTGCCAGCCGATGTCCAG	92953069 (Drosophila ananassae) 92477149 (Drosophila erecta) 55694467 (Drosophila yakuba) 112349870 (Helicoverpa armigera) 237458 (Heliothis virescens) 9713 (Manduca sexta) 110242332 (Spodoptera frugiperda)
CS016	1900	AGCATCTCCTTGGGGAAGATACG	63005818 (Bombyx mori) 92967975 (Drosophila mojavensis) 92938364 (Drosophila virilis) 92231646 (Drosophila willistoni) 237458 (Heliothis virescens)
CS016	1901	AGGGCTTCCTCACCGACGACAGCCTTCATG GCCTG	4680479 (Aedes aegypti)
CS016	1902	ATACCAGTCTGGATCATTTCCTCAGG	60295607 (Homalodisca coagulata)
CS016	1903	ATACGGGACCAGGGGTTGATGGGCTG	92953552 (Drosophila ananassae)
CS016	1904	ATAGCGGAGATACCAGTCTGGATCAT	237458 (Heliothis virescens) 76554661 (Spodoptera frugiperda)
CS016	1905	ATCTGGGCGGCAATTTCGTTGTG	83937869 (Lutzomyia longipalpis)
CS016	1906	ATGGCAGACTTCATGAGACGA	55894053 (Locusta migratoria)
CS016	1907	ATGGTGGCCAAATCGGTGTACATGTAACC	92965644 (Drosophila grimshawi)
CS016	1908	ATGGTGGCCAAATCGGTGTACATGTAACCT	92969578 (Drosophila grimshawi)
CS016	1909	ATGGTGGCCAAATCGGTGTACATGTAACCT GGGAAACCACG	92231646 (Drosophila willistoni)
CS016	1910	ATTCAAGAACAGGCACACGTTCTCCATGGA GCCGTTCTCCTCGAAGTCCTGCTTGAAGAA	67841091 (Drosophila pseudoobscura)
CS016	1911	ATTGGGGGACCTTTGTCAATGGGTTTTCC	49395165 (Drosophila melanogaster) 99009492 (Leptinotarsa decemlineata)
CS016	1912	CACACGTTCTCCATGGAGCCGTTCTCCTCGA	92477818 (Drosophila erecta)

		AGTCCTGCTTGAAGAA	
CS016	1913	CACTGGTAGGCCAAGAACTCAGC	4680479 (Aedes aegypti)
CS016	1914	CATCTCCTTGGGGAAGATACG	16899457 (Ctenocephalides felis) 9713 (Manduca sexta)
CS016	1915	CCCTCACCGATGGCAGACTTCAT	4680479 (Aedes aegypti) 92924977 (Drosophila virilis) 110248186 (Spodoptera frugiperda)
CS016	1916	CCGATGGCAGACTTCATGAGACG	71049259 (Oncometopia nigricans)
CS016	1917	CCGTCTCCATGTTCACACCCATGGCGGCGA ACACGATGGC	33547658 (Anopheles gambiae)
CS016	1918	CCGTTCTCCTCGAAGTCCTGCTTGAAGAA	31206154 (Anopheles gambiae str. PEST) 8809 (Drosophila melanogaster)
CS016	1919	CCGTTCTCCTCGAAGTCCTGCTTGAAGAACC	101403557 (Plodia interpunctella)
CS016	1920	CGAGCAATGGAGTTCATCACGTCGATAGCG GAGATACCAGTCTGGATCAT	27372076 (Spodoptera littoralis)
CS016	1921	CGGGCCGTCTCCATGTTCACACCCATGGCG GCGAACACGATGGC	31206154 (Anopheles gambiae str. PEST)
CS016	1922	CGTCCGGGCACCTCCTCACGGGCGGC	18883474 (Anopheles gambiae) 31206154 (Anopheles gambiae str. PEST)
CS016	1923	CGTCCGGGCACCTCCTCACGGGCGGCGGAC AC	9713 (Manduca sexta) 110248186 (Spodoptera frugiperda)
CS016	1924	CTACAGATCTGGGCGGCAATTTC	91826756 (Bombyx mori) 9713 (Manduca sexta) 27372076 (Spodoptera littoralis)
CS016	1925	CTACAGATCTGGGCGGCAATTTCGTTGTG	237458 (Heliothis virescens) 76554661 (Spodoptera frugiperda)
CS016	1926	CTCGTAGATGGTGGCCAAATC	53883819 (Plutella xylostella)
CS016	1927	CTCGTAGATGGTGGCCAAATCGGTGTACAT GTA	18883474 (Anopheles gambiae) 31206154 (Anopheles gambiae str. PEST)
CS016	1928	CTCGTAGATGGTGGCCAAATCGGTGTACAT GTAACC	92953069 (Drosophila ananassae) 92477818 (Drosophila erecta) 8809 (Drosophila melanogaster) 67896654 (Drosophila pseudoobscura)

CS016	1929	CTCGTAGATGGTGGCCAAATCGGTGTACAT GTAACCTGGGAAACCACG	9713 (Manduca sexta) 110248186 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
CS016	1930	GAACAGGCACACGTTCTCCATGGA	92962756 (Drosophila ananassae)
CS016	1931	GACTCGAATACTGTGCGGTTCTCGTAGTT	87266757 (Choristoneura fumiferana) 9713 (Manduca sexta)
CS016	1932	GACTTCATGAGACGAGACAGGGAAGGCAG CACGTT	9713 (Manduca sexta)
CS016	1933	GAGATACCAGTCTGGATCATTTC	92969748 (Drosophila mojavensis)
CS016	1934	GAGATACCAGTCTGGATCATTTCCTC	92935139 (Drosophila virilis)
CS016	1935	GATGAAGTTCTTCTCGAACTTGG	2921501 (Culex pipiens)
CS016	1936	GATGAAGTTCTTCTCGAACTTGGT	4680479 (Aedes aegypti) 31206154 (Anopheles gambiae str. PEST) 92953069 (Drosophila ananassae) 92477149 (Drosophila erecta) 8809 (Drosophila melanogaster) 67896654 (Drosophila pseudoobscura) 55694467 (Drosophila yakuba) 112349870 (Helicoverpa armigera) 237458 (Heliothis virescens)
CS016	1937	GATGAAGTTCTTCTCGAACTTGGTGAGGAA CTCGAGGTAGAGCA	76555122 (Spodoptera frugiperda)
CS016	1938	GATGGGGATCTGCGTGATGGA	101403557 (Plodia interpunctella) 53883819 (Plutella xylostella)
CS016	1939	GCACACGTTCTCCATGGAGCCGTTCTC	104530890 (Belgica antarctica)
CS016	1940	GCCAAATCGGTGTACATGTAACCTGGGAAA CCACGTCGTCCGGG	91829127 (Bombyx mori)
CS016	1941	GCCAAGAACTCAGCAGCAGTCA	237458 (Heliothis virescens)
CS016	1942	GCCGTCTCCATGTTCACACCCA	83937868 (Lutzomyia longipalpis)
CS016	1943	GCCGTCTCCATGTTCACACCCAT	92965644 (Drosophila grimshawi)
CS016	1944	GCCTGCACGTCCTTACCGATGGCGTAGCA	112349870 (Helicoverpa armigera) 237458 (Heliothis virescens) 110248186 (Spodoptera frugiperda)
CS016	1945	GCCTTCATGGCCTGCACGTCCTT	39675733 (Anopheles gambiae) 31206154 (Anopheles gambiae str. PEST)

CS016	1946	GCCTTCATGGCCTGCACGTCCTTACCGATGG CGTAGCA	2921501 (Culex pipiens)
CS016	1947	GCGGCGAACACGATGGCAAAGTT	2921501 (Culex pipiens) 92965644 (Drosophila grimshawi)
CS016	1948	GCGGCGAACACGATGGCAAAGTTGTCCTCG TG	77905105 (Aedes aegypti)
CS016	1949	GCGTACAGCTGGTTGGAAACATC	67896654 (Drosophila pseudoobscura)
CS016	1950	GGAATAGGATGGGTGATGTCGTCGTTGGGC ATAGT	110248186 (Spodoptera frugiperda)
CS016	1951	GGAATAGGATGGGTGATGTCGTCGTTGGGC ATAGTCA	27372076 (Spodoptera littoralis)
CS016	1952	GGATGGGTGATGTCGTCGTTGGGCAT	101403557 (Plodia interpunctella)
CS016	1953	GGCAGACCGGCAGCCGAGAAAATGGGGAT CTT	67841091 (Drosophila pseudoobscura)
CS016	1954	GGCATAGTCAAGATGGGGATCTG	92924977 (Drosophila virilis)
CS016	1955	GGCCGTCTCCATGTTCACACCCATGGC	101403557 (Plodia interpunctella)
CS016	1956	GGCGGGTAGATCTGTCTGTTGTG	2921501 (Culex pipiens) 92965644 (Drosophila grimshawi) 92924977 (Drosophila virilis)
CS016	1957	GGCGGGTAGATCTGTCTGTTGTGGAGCTGA CGGTCTACGTAGATCTGTCCCTCAGT	237458 (Heliothis virescens) 110248186 (Spodoptera frugiperda)
CS016	1958	GGGAAGATACGGAGCAGCTGCCA	60336551 (Homalodisca coagulata)
CS016	1959	GGGTTGATGGGCTGTCCCTGGATGTCCAA	76554661 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
CS016	1960	GGTTTTCCAGAGCCGTTGAATAC	62238871 (Diabrotica virgifera)
CS016	1961	GTGATGAAGTTCTTCTCGAACTTGGT	87266757 (Choristoneura fumiferana)
CS016	1962	GTGCGGTTCTCGTAGTTGCCCTG	31206154 (Anopheles gambiae str. PEST) 92477149 (Drosophila erecta) 8809 (Drosophila melanogaster) 67896654 (Drosophila pseudoobscura) 92938364 (Drosophila virilis) 92231646 (Drosophila willistoni) 55694467 (Drosophila yakuba)
CS016	1963	GTGGCCAAATCGGTGTACATGTAACC	2921501 (Culex pipiens) 75469507 (Tribolium castaneum)

CS016	1964	GTGTACATGTAACCTGGGAAACCACG	101403557 (Plodia interpunctella)
CS016	1965	GTGTACATGTAACCTGGGAAACCACGTCG	237458 (Heliothis virescens)
CS016	1966	GTGTACATGTAACCTGGGAAACCACGTCGT CCGGGCACCTCCTCACGGGCGGC	53883819 (Plutella xylostella)
CS016	1967	TCAGAGTGGTCCTTGCGGGTCAT	237458 (Heliothis virescens) 9713 (Manduca sexta)
CS016	1968	TCAGCAAGGATTGGGGGACCTTTGTC	10763875 (Manduca sexta)
CS016	1969	TCCTCACCGACGACAGCCTTCATGGCCTG	92969578 (Drosophila grimshawi)
CS016	1970	TCCTCAGGGTAGATACGGGACCA	76554661 (Spodoptera frugiperda)
CS016	1971	TCCTCAGGGTAGATACGGGACCAGGGGTTG ATGGGCTG	22474040 (Helicoverpa armigera) 237458 (Heliothis virescens) 9713 (Manduca sexta)
CS016	1972	TCGAAGTCCTGCTTGAAGAACC	9713 (Manduca sexta)
CS016	1973	TCGTAGATGGTGGCCAAATCGGTGTACATG TAACC	62239897 (Diabrotica virgifera)
CS016	1974	TCGTAGATGGTGGCCAAATCGGTGTACATG TAACCTGGGAAACCACG	4680479 (Aedes aegypti)
CS016	1975	TCTACGTAGATCTGTCCCTCAGTGATGTA	101403557 (Plodia interpunctella)
CS016	1976	TGCACGTCCTTACCGATGGCGTAGCA	9713 (Manduca sexta) 75710699 (Tribolium castaneum)
CS016	1977	TGGGTGATGTCGTCGTTGGGCAT	53883819 (Plutella xylostella)
CS016	1978	TGGTAGGCCAAGAACTCAGCAGC	9713 (Manduca sexta)
CS016	1979	TTCAAGAACAGGCACACGTTCTCCAT	18883474 (Anopheles gambiae) 31206154 (Anopheles gambiae str. PEST) 92933153 (Drosophila virilis) 27372076 (Spodoptera littoralis)
CS016	1980	TTCAAGAACAGGCACACGTTCTCCATGGA	92950254 (Drosophila ananassae) 76554661 (Spodoptera frugiperda)
CS016	1981	TTCTCACACTGGTAGGCCAAGAA	18883474 (Anopheles gambiae)
CS016	1982	TTCTCCTCGAAGTCCTGCTTGAAGAA	83937868 (Lutzomyia longipalpis)
CS016	1983	TTGAGCATCTCCTTGGGGAAGATACG	92477149 (Drosophila erecta) 8809 (Drosophila melanogaster) 67896654 (Drosophila pseudoobscura) 112349870 (Helicoverpa armigera)
CS016	1984	TTGAGCATCTCCTTGGGGAAGATACGGAGC	83928466 (Lutzomyia longipalpis)

		A	
CS016	1985	TTGAGCATCTCCTTGGGGAAGATACGGAGC AGCTGCCA	50559098 (Homalodisca coagulata) 71049259 (Oncometopia nigricans)
CS016	1986	TTGAGCATCTCCTTGGGGAAGATACGGAGC AGCTGCCAGCCGATGTC	87266757 (Choristoneura fumiferana)
CS018	1987	TCCGACTACTCTTCCACGGAC	31659029 (Anopheles gambiae)

Table 4-PX

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PX001	2120	AACAACGTGTTCATCATCGGCAAGGGCACGAA	112350001 (Helicoverpa armigera)
PX001	2121	AACGTGTTCATCATCGGCAAG	27562760 (Anopheles gambiae) 58378595 (Anopheles gambiae str. PEST)
PX001	2122	AACGTGTTCATCATCGGCAAGG	42764924 (Armigeres subalbatus)
PX001	2123	AACGTGTTCATCATCGGCAAGGG	71048604 (Oncometopia nigricans)
PX001	2124	AACGTGTTCATCATCGGCAAGGGCACGAA	112783858 (Anopheles funestus)
PX001	2125	AACTTGGGGCGAGTGGGCACCATCGTGTC	90132259 (Bicyclus anynana)
PX001	2126	AACTTGGGGCGAGTGGGCACCATCGTGTCCCGCGAG	112350001 (Helicoverpa armigera)
PX001	2127	AAGATCGTGAAGCAGCGCCTCATCAAGGTGGACGGCAA GGT	112350001 (Helicoverpa armigera)
PX001	2128	AAGGTCCGCACCGACCCCACCTA	14627585 (Drosophila melanogaster)
PX001	2129	AAGTACAAGCTGTGCAAGGTG	5498893 (Antheraea yamamai) 90132259 (Bicyclus anynana) 92969396 (Drosophila grimshawi) 50818668 (Heliconius melpomene) 58371410 (Lonomia obliqua)
PX001	2130	ACAACGTGTTCATCATCGGCAAGGGCACGAA	103783745 (Heliconius erato)
PX001	2131	ACGGCAAGGTCCGCACCGACCC	77890923 (Aedes aegypti)
PX001	2132	ACGGCCGCACGCTGCGCTACCCCGACCCGCTCATCAAGG TCAACGACTCC	101413238 (Plodia interpunctella)
PX001	2133	ACGTGTTCATCATCGGCAAGGGCAC	109509107 (Culex pipiens)
PX001	2134	AGGAGGCCAAGTACAAGCTGT	27566312 (Anopheles gambiae) 67889891 (Drosophila pseudoobscura)

PX001	2135	AGGAGGCCAAGTACAAGCTGTGCAAGGT	92944919 (Drosophila ananassae) 67886177 (Drosophila pseudoobscura) 92045792 (Drosophila willistoni)
PX001	2136	AGGAGGCCAAGTACAAGCTGTGCAAGGTG	92929731 (Drosophila virilis)
PX001	2137	CAACGTGTTCATCATCGGCAA	109509107 (Culex pipiens)
PX001	2138	CAACGTGTTCATCATCGGCAAGGGCA	55816641 (Drosophila yakuba)
PX001	2139	CACACCTTCGCCACCAGGTTGAACAACGTGTT	3986403 (Antheraea yamamai)
PX001	2140	CCCCAAGAAGCATTTGAAGCG	2886669 (Drosophila melanogaster)
PX001	2141	CCGAGGAGGCCAAGTACAAGCT	92944919 (Drosophila ananassae)
PX001	2142	CCGAGGAGGCCAAGTACAAGCTGTGCAAGGT	15480750 (Drosophila melanogaster)
PX001	2143	CCGCACAAGCTGCGCGAGTGCCTGCCGCT	22474232 (Helicoverpa armigera)
PX001	2144	CGACGGGCCCCAAGAACGTGCC	112350001 (Helicoverpa armigera)
PX001	2145	CGAGGAGGCCAAGTACAAGCT	58378595 (Anopheles gambiae str. PEST)
PX001	2146	CGAGGAGGCCAAGTACAAGCTG	18914191 (Anopheles gambiae)
PX001	2147	CGAGTGGGCACCATCGTGTCCCGCGAG	3986403 (Antheraea yamamai)
PX001	2148	CGCTACCCCGACCCGCTCATCAAGGTCAACGACTCC	112350001 (Helicoverpa armigera)
PX001	2149	CGCTTCACCATCCACCGCATCAC	103783745 (Heliconius erato)
PX001	2150	CGGCAACGAGGTGCTGAAGATCGT	90132259 (Bicyclus anynana)
PX001	2151	CGTAACTTGGGGCGAGTGGGCAC	60311985 (Papilio dardanus)
PX001	2152	CTACCCGGCTGGATTCATGGATGT	42764924 (Armigeres subalbatus)
PX001	2153	CTCATCAAGGTCAACGACTCC	103783745 (Heliconius erato)
PX001	2154	CTCATCAAGGTCAACGACTCCATCCAGCTCGACAT	3738704 (Manduca sexta)
PX001	2155	GACGGCAAGGTCCGCACCGAC	109509107 (Culex pipiens)
PX001	2156	GACGGCAAGGTCCGCACCGACCC	77759638 (Aedes aegypti)
PX001	2157	GAGGAGGCCAAGTACAAGCTGTGCAAGGT	67841491 (Drosophila pseudoobscura)
PX001	2158	GAGGAGGCCAAGTACAAGCTGTGCAAGGTG	56772971 (Drosophila virilis)
PX001	2159	GAGGCCAAGTACAAGCTGTGCAA	112350001 (Helicoverpa armigera)
PX001	2160	GAGGCCAAGTACAAGCTGTGCAAGGTG	98993531 (Antheraea mylitta)
PX001	2161	GCCAAGTACAAGCTGTGCAAGGT	67838306 (Drosophila pseudoobscura) 109978109 (Gryllus pennsylvanicus)
PX001	2162	GCCCCAAGAAGCATTTGAAGCG	2151718 (Drosophila melanogaster)
PX001	2163	GCGCGTGGCGACGGGCCCCAA	5498893 (Antheraea yamamai)
PX001	2164	GCGCGTGGCGACGGGCCCCAAG	3986403 (Antheraea yamamai)
PX001	2165	GGAGGCCAAGTACAAGCTGTGCAAGGT	92942537 (Drosophila ananassae)
PX001	2166	GGCCCCAAGAAGCATTTGAAGCG	4459798 (Drosophila melanogaster)

PX001	2167	GGCGGCGTGTACGCGCCGCGGCCC	98994282 (Antheraea mylitta)
PX001	2168	GTCCGCACCGACCCCACCTACCC	92472430 (Drosophila erecta) 55854272 (Drosophila yakuba)
PX001	2169	GTGGGCACCATCGTGTCCCGCGAGAG	3953837 (Bombyx mandarina) 29554802 (Bombyx mori)
PX001	2170	TCAAGGTGGACGGCAAGGTCCGCACCGACCC	92944919 (Drosophila ananassae)
PX001	2171	TGATCTACGATGTGAAGGGACG	83935965 (Lutzomyia longipalpis)
PX001	2172	TTCATGGATGTTGTGTCGATTGAAAA	90132259 (Bicyclus anynana)
PX001	2173	GCTGGATTCATGGATGTTGTG	10707240 (Amblyomma americanum)
PX001	2174	AAGCAGCGCCTCATCAAGGTGGACGGCAAGGTCCGCAC CGAC	49545866 (Rhipicephalus appendiculatus)
PX009	2175	AACATCTTCAACTGTGACTTC	93001544 (Drosophila mojavensis)
PX009	2176	TGATCAACATCGAGTGCAAAGC	110755556 (Apis mellifera)
PX009	2177	TTCTTGAAGCTGAATAAGATCT	103750396 (Drosophila melanogaster)
PX010	2178	CAGTTCCTGCAGGTCTTCAACAA	71553175 (Oncometopia nigricans)
PX010	2179	CCATCAGCGGACGGTGGCGCCCCCGTG	90139187 (Spodoptera frugiperda)
PX010	2180	CCCGCAGTTCATGTACCACCTGCGCCGCTCGCAGTTC	67893194 (Drosophila pseudoobscura)
PX010	2181	CCGAACAGCTTCCGTCTGTCGGAGAACTTCAG	29558345 (Bombyx mori)
PX010	2182	CGCCTGTGCCAGAAGTTCGGCGAGTACG	58395529 (Anopheles gambiae str. PEST)
PX010	2183	CTGCGCCGCTCGCAGTTCCTGCAGGT	18872210 (Anopheles gambiae)
PX010	2184	CTGTACCCGCAGTTCATGTACCA	29558345 (Bombyx mori)
PX010	2185	GACGTGCTGCGCTGGCTCGACCG	29558345 (Bombyx mori)
PX010	2186	GACGTGTCGCTGCAAGTGTTCATGGAGCA	18872210 (Anopheles gambiae)
PX010	2187	GAGTACGAGAACTTCAAGCAGCTGCTGC	77886140 (Aedes aegypti) 18872210 (Anopheles gambiae) 49376735 (Drosophila melanogaster) 67893324 (Drosophila pseudoobscura)
PX010	2188	GGCGGGGCGATGCCGATACCATC	91757875 (Bombyx mori)
PX010	2189	GTGGCTGCATACAGTTCATTACGCAGTACCAGCAC	28571527 (Drosophila melanogaster)
PX010	2190	TCGCAGTTCCTGCAGGTCTTCAACAA	92932090 (Drosophila virilis)
PX010	2191	TGCGCCGCTCGCAGTTCCTGCAGGTCTTCAACAA	67893324 (Drosophila pseudoobscura)
PX010	2192	TGCGCCGCTCGCAGTTCCTGCAGGTCTTCAACAACTCGC CCGACGAGACCAC	92952825 (Drosophila ananassae)
PX010	2193	TTCATGTACCACCTGCGCCGCTCGCAGTTCCTGCAGGTC TTCAACAACTCGCCCGACGAGACCAC	28571527 (Drosophila melanogaster)

PX010	2194	ATCCTGCTCATGGACACCTTCTTCCA	82842646 (Boophilus microplus)
PX015	2195	CACCGCGACGACACGTTCATGGTGCGCGGCGG	58371643 (Lonomia obliqua)
PX015	2196	CAGATCAAGGAGATGGTGGAG	92480997 (Drosophila erecta) 58371722 (Lonomia obliqua)
PX015	2197	CCCGACGAGAAGATCCGCATGAA	67873606 (Drosophila pseudoobscura)
PX015	2198	CCCGACGAGAAGATCCGCATGAACCGCGT	15070733 (Drosophila melanogaster)
PX015	2199	CCGACGAGAAGATCCGCATGAACCGCGT	92459970 (Drosophila erecta)
PX015	2200	CGCAAGGAGACCGTGTGCATTGTGCT	67873606 (Drosophila pseudoobscura)
PX015	2201	GACGAGAAGATCCGCATGAACCG	18914444 (Anopheles gambiae)
PX015	2202	GACGAGAAGATCCGCATGAACCGCGT	4691131 (Aedes aegypti)
PX015	2203	GCGCAGATCAAGGAGATGGTGGAGCT	99007898 (Leptinotarsa decemlineata)
PX015	2204	GGCATGCGCGCCGTCGAGTTC	6901917 (Bombyx mori)
PX015	2205	GTGCGCGGCGGCATGCGCGCC	67891252 (Drosophila pseudoobscura)
PX015	2206	TCAAGGAGATGGTGGAGCTGC	27819993 (Drosophila melanogaster)
PX015	2207	TGAAGCCGTACTTCATGGAGGC	29559940 (Bombyx mori)
PX015	2208	TGCCGCAAGCAGCTGGCGCAGATCAAGGAGATGGT	18914444 (Anopheles gambiae)
PX015	2209	TGGAGGCGTACCGGCCCATCCAC	18914444 (Anopheles gambiae)
PX016	2210	AAGGACCACTCCGACGTGTCCAA	101406307 (Plodia interpunctella)
PX016	2211	AAGGACGTGCAGGCGATGAAGGC	112349870 (Helicoverpa armigera) 110248186 (Spodoptera frugiperda)
PX016	2212	ACCAAGTTCGAGAAGAACTTCATC	4680479 (Aedes aegypti) 31206154 (Anopheles gambiae str. PEST) 92953069 (Drosophila ananassae) 92477149 (Drosophila erecta) 24646340 (Drosophila melanogaster) 67900295 (Drosophila pseudoobscura) 55694467 (Drosophila yakuba) 112349870 (Helicoverpa armigera) 237458 (Heliothis virescens)
PX016	2213	ACCAAGTTCGAGAAGAACTTCATCAC	87266757 (Choristoneura fumiferana)
PX016	2214	ACCGCCAGGTTCTTCAAGCAGGACTTCGA	9713 (Manduca sexta)
PX016	2215	ACCGGCGATATTCTGCGCACGCCCGTCTC	92940287 (Drosophila virilis)
PX016	2216	AGCAGGACTTCGAGGAGAACGG	67880606 (Drosophila pseudoobscura)
PX016	2217	ATCACGCAGATCCCCATCCTGACCATGCC	31206154 (Anopheles gambiae str. PEST)

PX016	2218	ATCTTGACCGACATGTCTTCATACGC	104530890 (Belgica antarctica) 92231646 (Drosophila willistoni)
PX016	2219	ATGACCAGGAAGGACCACTCCGACGT	75713096 (Tribolium castaneum)
PX016	2220	ATGCCCAACGACGACATCACCCA	101406307 (Plodia interpunctella) 76555122 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
PX016	2221	CAGAAGATCCCCATCTTCTCCGCCGCCGGTCTGCCCCAC AACGA	92460896 (Drosophila erecta) 24646340 (Drosophila melanogaster)
PX016	2222	CAGGACTTCGAGGAGAACGGTTCCATGGAGAACGT	2921501 (Culex pipiens) 76554661 (Spodoptera frugiperda)
PX016	2223	CCAAGTTCGAGAAGAACTTCATC	2921501 (Culex pipiens)
PX016	2224	CCCATCAACCCGTGGTCCCGTATCTACCCGGAGGA	2921501 (Culex pipiens)
PX016	2225	CCCGACTTGACCGGGTACATCACTGAGGGACAGATCTAC GT	101406307 (Plodia interpunctella)
PX016	2226	CCCGGACGACGTGGTTTCCCAGGTTACATGTACAC	91829127 (Bombyx mori)
PX016	2227	CCTGGACATCCAGGGGCAGCCCATCAACCC	91090030 (Tribolium castaneum)
PX016	2228	CGACGTGGTTTCCCAGGTTACATGTACACGGATTTGGC	237458 (Heliothis virescens)
PX016	2229	CGTCTCATGAAGTCCGCCATCGG	91829127 (Bombyx mori)
PX016	2230	CGTCTCATGAAGTCCGCCATCGGAGAGGGCATGACC	237458 (Heliothis virescens)
PX016	2231	CGTGGTCAGAAGATCCCCATCTTCTC	27372076 (Spodoptera littoralis)
PX016	2232	CGTGGTCAGAAGATCCCCATCTTCTCCGC	76554661 (Spodoptera frugiperda)
PX016	2233	CGTGGTTTCCCAGGTTACATGTACAC	55797015 (Acyrthosiphon pisum) 4680479 (Aedes aegypti) 73615307 (Aphis gossypii) 92231646 (Drosophila willistoni) 9713 (Manduca sexta) 76555122 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
PX016	2234	CGTGGTTTCCCAGGTTACATGTACACGGATTTGGCCACA ATCTACGAGCGCGCCGGGCG	101406307 (Plodia interpunctella)
PX016	2235	CTACGAGAACCGCACAGTGTTCGAGTC	112350031 (Helicoverpa armigera) 237458 (Heliothis virescens) 76555122 (Spodoptera frugiperda)

PX016	2236	CTGCGTATCTTCCCCAAGGAGAT	63005818 (Bombyx mori) 92477149 (Drosophila erecta) 24646340 (Drosophila melanogaster) 56773982 (Drosophila pseudoobscura) 92935600 (Drosophila virilis) 92220609 (Drosophila willistoni) 112350031 (Helicoverpa armigera) 237458 (Heliothis virescens) 9713 (Manduca sexta)
PX016	2237	CTGTACGCGTGCTACGCCATCGG	9713 (Manduca sexta)
PX016	2238	CTGTTCTTGAACTTGGCCAATGA	16898595 (Ctenocephalides felis)
PX016	2239	CTGTTCTTGAACTTGGCCAATGACCC	27372076 (Spodoptera littoralis)
PX016	2240	GACAACTTCGCCATCGTGTTCGC	92950254 (Drosophila ananassae)
PX016	2241	GACAACTTCGCCATCGTGTTCGCCGC	92477818 (Drosophila erecta) 24646340 (Drosophila melanogaster) 237458 (Heliothis virescens) 9713 (Manduca sexta) 76554661 (Spodoptera frugiperda)
PX016	2242	GACAACTTCGCCATCGTGTTCGCCGCCATGGG	31206154 (Anopheles gambiae str. PEST)
PX016	2243	GACCGTCAGCTGCACAACAGGCA	50564193 (Homalodisca coagulata)
PX016	2244	GACCTGCTCTACCTCGAGTTC	112349870 (Helicoverpa armigera)
PX016	2245	GACGTGATGAACTCCATCGCCCG	237458 (Heliothis virescens)
PX016	2246	GACGTGATGAACTCCATCGCCCGTGG	22474040 (Helicoverpa armigera)
PX016	2247	GAGAACGGTTCCATGGAGAACGT	91829127 (Bombyx mori)
PX016	2248	GAGGAGATGATCCAGACTGGTATCTCCGCTAT	237458 (Heliothis virescens) 76554661 (Spodoptera frugiperda)
PX016	2249	GAGGAGATGATCCAGACTGGTATCTCCGCTATCGACGTG ATGAACTCCAT	27372076 (Spodoptera littoralis)
PX016	2250	GAGGAGGCGCTCACGCCCGACGAC	9713 (Manduca sexta)
PX016	2251	GAGTTCTTGGCCTACCAGTGCGAGAA	4680479 (Aedes aegypti)
PX016	2252	GCCAGGTTCTTCAAGCAGGACTTCGAGGAGAACGG	101403557 (Plodia interpunctella)
PX016	2253	GCCCGTGGTCAGAAGATCCCCAT	67877903 (Drosophila pseudoobscura)
PX016	2254	GCCCGTGGTCAGAAGATCCCCATCTTCTC	6901845 (Bombyx mori)
PX016	2255	GCCCGTGGTCAGAAGATCCCCATCTTCTCCGCCGC	92950254 (Drosophila ananassae)
PX016	2256	GCCGAGTTCTTGGCCTACCAGTGCGAGAA	24646340 (Drosophila melanogaster)

PX016	2257	GCCGAGTTCTTGGCCTACCAGTGCGAGAAACACGTGTTGGT	110240379 (Spodoptera frugiperda)
PX016	2258	GCCGCCCGTGAGGAGGTGCCCGGACG	31206154 (Anopheles gambiae str. PEST) 9713 (Manduca sexta) 110240379 (Spodoptera frugiperda)
PX016	2259	GCCTACCAGTGCGAGAAACACGTGTTGGTAATCTTGACCGACATGTC	101406307 (Plodia interpunctella)
PX016	2260	GGCAGATCTACCCGCCGGTGAA	31206154 (Anopheles gambiae str. PEST)
PX016	2261	GGCGAGGAGGCGCTCACGCCCGACGA	31206154 (Anopheles gambiae str. PEST)
PX016	2262	GGTCAGAAGATCCCCATCTTCTC	60295607 (Homalodisca coagulata)
PX016	2263	GGTTACATGTACACGGATTTGGCCAC	92924977 (Drosophila virilis)
PX016	2264	GTGGTGGGCGAGGAGGCGCTCACGCC	112349870 (Helicoverpa armigera)
PX016	2265	GTTCACCGGCGATATTCTGCG	92997483 (Drosophila grimshawi)
PX016	2266	GTTCACCGGCGATATTCTGCGCAC	92950254 (Drosophila ananassae) 92048971 (Drosophila willistoni)
PX016	2267	TACCAGTGCGAGAAACACGTGTTGGT	237458 (Heliothis virescens)
PX016	2268	TACGCCATCGGCAAGGACGTGCAGGCGATGAAGGC	87266757 (Choristoneura fumiferana)
PX016	2269	TCCATCACGCAGATCCCCATCCT	101406307 (Plodia interpunctella)
PX016	2270	TCCGGCAAGCCCATCGACAAGGG	92460896 (Drosophila erecta) 24646340 (Drosophila melanogaster) 22474040 (Helicoverpa armigera) 237458 (Heliothis virescens)
PX016	2271	TCTACGAGCGCGCCGGGCGAGTC	33528180 (Trichoplusia ni)
PX016	2272	TCTCGTCTCATGAAGTCCGCCATCGG	9713 (Manduca sexta)
PX016	2273	TGACTGCTGCCGAGTTCTTGGCCTACCAGTGCGAGAAACACGTGTTGGT	27372076 (Spodoptera littoralis)
PX016	2274	TGCACAACAGGCAGATCTACCC	62239897 (Diabrotica virgifera)
PX016	2275	TGCGTATCTTCCCCAAGGAGAT	16900620 (Ctenocephalides felis) 92967975 (Drosophila mojavensis)
PX016	2276	TGCTACGCCATCGGCAAGGACGTGCAGGC	31206154 (Anopheles gambiae str. PEST) 92953069 (Drosophila ananassae) 92477149 (Drosophila erecta) 24646340 (Drosophila melanogaster) 67898824 (Drosophila pseudoobscura) 55694467 (Drosophila yakuba)

PX016	2277	TGCTCTACCTCGAGTTCCTCACCAAGTTCGAGAAGAACT TCATC	76555122 (Spodoptera frugiperda)
PX016	2278	TGTCTGTTCTTGAACTTGGCCAA	4680479 (Aedes aegypti) 92477818 (Drosophila erecta) 24646340 (Drosophila melanogaster)
PX016	2279	TGTCTGTTCTTGAACTTGGCCAATGA	55905051 (Locusta migratoria)
PX016	2280	TGTTCTTGAACTTGGCCAATGA	91090030 (Tribolium castaneum)
PX016	2281	TTCAACGGCTCCGGCAAGCCCAT	76554661 (Spodoptera frugiperda)
PX016	2282	TTCAACGGCTCCGGCAAGCCCATCGACAAGGG	4680479 (Aedes aegypti) 31206154 (Anopheles gambiae str. PEST) 67877903 (Drosophila pseudoobscura)
PX016	2283	TTCGAGGAGAACGGTTCCATGGAGAA	92972277 (Drosophila grimshawi)
PX016	2284	TTCGAGGAGAACGGTTCCATGGAGAACGT	92950254 (Drosophila ananassae)
PX016	2285	TTCTTCAAGCAGGACTTCGAGGAGAA	83937868 (Lutzomyia longipalpis)
PX016	2286	TTCTTCAAGCAGGACTTCGAGGAGAACGG	92477818 (Drosophila erecta)
PX016	2287	TTCTTCAAGCAGGACTTCGAGGAGAACGGTTC	31206154 (Anopheles gambiae str. PEST)
PX016	2288	TTCTTCAAGCAGGACTTCGAGGAGAACGGTTCCATGGAG AACGT	24646340 (Drosophila melanogaster)
PX016	2289	TTCTTGAACTTGGCCAATGACCC	9713 (Manduca sexta)
PX016	2290	TTCTTGGCCTACCAGTGCGAGAA	31206154 (Anopheles gambiae str. PEST) 67883622 (Drosophila pseudoobscura) 92231646 (Drosophila willistoni)

Table 4-AD

Target ID	**SEQ ID NO**	**Sequence ***	**Example Gi-number and species**
AD001	2384	AAAGCATGGATGTTGGACAAA	73619372 (Aphis gossypii); 77325485 (Chironomus tentans); 22474232 (Helicoverpa armigera); 37951951 (Ips pini); 60305420 (Mycetophagus quadripustulatus); 84647995 (Myzus persicae)

AD001	2385	AAAGCATGGATGTTGGACAAACT	94432102 (Bombyx mori); 103790417 (Heliconius erato); 55904580 (Locusta migratoria); 101419954 (Plodia interpunctella)
AD001	2386	AAAGGTATTCCATTCTTGGTGACCCATGATGG CCGTACTATCCGTTATCCTGACCCAGTCATTA AAGT	109978109 (Gryllus pennsylvanicus)
AD001	2387	AACTGTGAAGTAACGAAGATTGTTATGCAGC GACTTATCAAAGTTGA	109978109 (Gryllus pennsylvanicus)
AD001	2388	AAGAAGCATTTGAAGCGTTTAAA	3658572 (Manduca sexta)
AD001	2389	AAGGGTAAGGGTGTGAAATTGAGTAT	109978109 (Gryllus pennsylvanicus)
AD001	2390	AATGTATTCATCATTGGAAAAGC	55904577 (Locusta migratoria)
AD001	2391	AGAAGCATTTGAAGCGTTTAAA	98994282 (Antheraea mylitta) 73619372 (Aphis gossypii)
AD001	2392	AGAAGCATTTGAAGCGTTTAAATGC	27620566 (Anopheles gambiae)
AD001	2393	AGTACTGGCCCCCACAAATTGCG	109978109 (Gryllus pennsylvanicus)
AD001	2394	AGTGCAGAAGAAGCCAAGTACAAGCT	109978109 (Gryllus pennsylvanicus)
AD001	2395	ATCGCCGAGGAGCGGGACAAGC	3953837 (Bombyx mandarina) 94432102 (Bombyx mori)
AD001	2396	CAAGGACATACTTTTGCCACAAGATTGAATAA TGTATTCATCATTGGAAA	109978109 (Gryllus pennsylvanicus)
AD001	2397	CAGAAGAAGCCAAGTACAAGCT	42764924 (Armigeres subalbatus)
AD001	2398	CATGATGGCCGTACTATCCGTTA	73613065 (Aphis gossypii)
AD001	2399	CATGATGGCCGTACTATCCGTTATCCTGACCC	31365398 (Toxoptera citricida)
AD001	2400	CATTTGAAGCGTTTAAATGCTCC	27557322 (Anopheles gambiae)
AD001	2401	CCTAAAGCATGGATGTTGGAC	77324536 (Chironomus tentans)
AD001	2402	CCTAAAGCATGGATGTTGGACAA	58371410 (Lonomia obliqua)
AD001	2403	CCTAAAGCATGGATGTTGGACAAA	60311985 (Papilio dardanus) 30031258 (Toxoptera citricida)
AD001	2404	CCTAAAGCATGGATGTTGGACAAACT	98994282 (Antheraea mylitta)
AD001	2405	CGTACTATCCGTTATCCTGACCC	37804548 (Rhopalosiphum padi)
AD001	2406	GAATGTTTACCTTTGGTGATTTTTCTTCGCAAT CGGCT	109978109 (Gryllus pennsylvanicus)
AD001	2407	GCAGAAGAAGCCAAGTACAAGCT	37953169 (Ips pini)
AD001	2408	GCATGGATGTTGGACAAACTCGG	83935968 (Lutzomyia longipalpis)

AD001	2409	GCTGGTTTCATGGATGTTGTCAC	109978109 (Gryllus pennsylvanicus)
AD001	2410	GGCCCCAAGAAGCATTTGAAGCGTTTAA	14693528 (Drosophila melanogaster)
AD001	2411	GGTTTCATGGATGTTGTCACCAT	25958683 (Curculio glandium)
AD001	2412	TATGATGTGAAAGGCCGTTTCACAATTCACAG AAT	109978109 (Gryllus pennsylvanicus)
AD001	2413	TCATTGCCAAAGGGTAAGGGT	77324972 (Chironomus tentans)
AD001	2414	TGGATATTGCCACTTGTAAAATCATGGACCAC ATCAGATTTGAATCTGG	109978109 (Gryllus pennsylvanicus)
AD001	2415	TTAAATGCTCCTAAAGCATGGATGTTGGACAA ACT	109978109 (Gryllus pennsylvanicus)
AD001	2416	TTTGAATCTGGCAACCTGTGTATGAT	60311985 (Papilio dardanus)
AD001	2417	TTTGATATTGTTCATATCAAGGATAC	109978109 (Gryllus pennsylvanicus)
AD002	2418	AAGAAAATCGAACAAGAAATC	55902553 (Locusta migratoria)
AD002	2419	CAGCACATGGATGTGGACAAGGT	67899569 (Drosophila pseudoobscura)
AD002	2420	GAGTTTCTTTAGTAAAGTATTCGGTGG	110762684 (Apis mellifera)
AD009	2421	CACTACAACTACCACAAGAGC	84226228 (Aedes aegypti) 18941376 (Anopheles gambiae)
AD009	2422	CAGAACATCCACAACTGTGACT	29534871 (Bombyx mori)
AD009	2423	GGTGTGGGTGTCGTGCGAGGG	83926368 (Lutzomyia longipalpis)
AD009	2424	TGGATCCCTGAATACTACAATGA	83926506 (Lutzomyia longipalpis)
AD015	2425	GAGCAGTAGAATTCAAAGTAGT	99012451 (Leptinotarsa decemlineata)
AD015	2426	GCAATTATATTTATTGATGAA	83936542 (Lutzomyia longipalpis)
AD015	2427	TCACCATATTGTATTGTTGCT	31366806 (Toxoptera citricida)
AD015	2428	TTGTCCTGATGTTAAGTATGG	84114691 (Blomia tropicalis)
AD016	2429	ACGATGCCCAACGACGACATCACCCATCC	101406307 (Plodia interpunctella)
AD016	2430	ATGCCCAACGACGACATCACCCA	53883819 (Plutella xylostella)
AD016	2431	ATGCCCAACGACGACATCACCCATCCTATT	110240379 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
AD016	2432	CAGAAGATCCCCATCTTCTCGG	91827264 (Bombyx mori) 22474331 (Helicoverpa armigera) 60295607 (Homalodisca coagulata)
AD016	2433	CGGCTCCATCACTCAGATCCCCAT	67896654 (Drosophila pseudoobscura)
AD016	2434	GCCAACGACCCCACCATCGAG	101406307 (Plodia interpunctella)
AD016	2435	GCCCGTGTCCGAGGACATGCTGGG	83937868 (Lutzomyia longipalpis) 75473525 (Tribolium castaneum)

AD016	2436	GGCAGAAGATCCCCATCTTCTC	2286803 (Drosophila melanogaster)
AD016	2437	GTTCACCGGCGATATTCTGCG	92997483 (Drosophila grimshawi)
AD016	2438	GTTCACCGGCGATATTCTGCGC	92953552 (Drosophila ananassae) 92042621 (Drosophila willistoni)

Table 5-LD

Target ID	SEQ ID No	Sequences*	Example Gi-number and species
LD001	124	AAGAAGCATTTGAAGCGTTTG	8005678 (Meloidogyne incognita), 9829015 (Meloidogyne javanica)
LD003	125	GTTCTTCCTCTTGACGCGTCC	7710484 (Zeldia punctata)
LD003	126	GCAGCTTTACGGATTTTTGCCAA	32183696 (Meloidogyne chitwoodi)
LD003	127	TTTCAACTCCTGATCAAGACGT	1662318 (Brugia malayi), 31229562 (Wuchereria bancrofti)
LD006	128	GCTATGGGTAAGCAAGCTATGGG	520506 (Caenorhabditis elegans)
LD007	129	AAAGAATAAAAAATTATTTGA	17539725 (Caenorhabditis elegans)
LD007	130	AAGCAAGTGATGATGTTCAGTGC	7143515 (Globodera pallida)
LD014	131	ATGATGGCTTTCATTGAACAAGA	10122191 (Haemonchus contortus)
LD015	132	AACGCCCCAGTCTCATTAGCCAC	20064339 (Meloidogyne hapla)
LD016	133	TTTTGGCGTCGATTCCTGATG	71999357 (Caenorhabditis elegans)
LD016	134	GTGTACATGTAACCTGGGAAACC	13418283 (Necator americanus)
LD016	135	GTGTACATGTAACCTGGGAAACCACGAC G	10819046 (Haemonchus contortus)

Table 5-PC

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PC001	435	ATGGATGTTGGACAAATTGGG	7143612 (Globodera rostochiensis)
PC003	436	GCTAAAATCCGTAAAGCTGCTCGTGAACT	9831177 (Strongyloides stercoralis)
PC003	437	GAGTAAAGTACACTTTGGCTAAA	28914459 (Haemonchus contortus)
PC003	438	AAAATCCGTAAAGCTGCTCGTGAACT	32185135 (Meloidogyne chitwoodi)
PC003	439	CTGGACTCGCAGAAGCACATCGACTT	51334250 (Radopholus similis)

PC003	440	CGTCTGGATCAGGAATTGAAA	61115845 (Litomosoides sigmodontis)
PC005	441	TGGTTGGATCCAAATGAAATCAA	5430825 (Onchocerca volvulus)
PC005	442	GTGTGGTTGGATCCAAATGAAATCAA	6845701 (Brugia malayi); 45215079 (Wuchereria bancrofti)
PC014	443	CACATGATGGCTTTCATTGAACAAGAAGC	10122191 (Haemonchus contortus)
PC014	444	TACGAGAAAAAGGAGAAGCAAGT	21265518 (Ostertagia ostertagi)
PC016	445	GTCTGGATCATTTCCTCGGGATAAAT	18081287 (Globodera rostochiensis)
PC016	446	CCAGTCTGGATCATTTCCTCGGGATA	108957716 (Bursaphelenchus mucronatus); 108962248 (Bursaphelenchus xylophilus)

Table 5-EV

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
EV005	563	TTAAAGATGGTCTTATTATTAA	21819186 (Trichinella spiralis)
EV016	564	GCTATGGGTGTCAATATGGAAAC	54554020 (Xiphinema index)

Table 5-AG

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
AG001	739	GCTGGATTCATGGATGTGATCA	15666884 (Ancylostoma ceylanicum)
AG001	740	ATGGATGTTGGACAAATTGGG	18081843 (Globodera rostochiensis)
AG001	741	TTCATGGATGTGATCACCATTGA	27002091 (Ascaris suum)
AG005	742	GTCTGGTTGGATCCAAATGAAATCAATGA	2099126 (Onchocerca volvulus)
AG005	743	GGATCCAAATGAAATCAATGA	2099309 (Onchocerca volvulus)
AG005	744	TGATCAAGGATGGTTTGATCAT	2130916 (Brugia malayi)
AG005	745	TGGTTGGATCCAAATGAAATCAATGA	6845701 (Brugia malayi)
AG005	746	CCAAGGGTAACGTGTTCAAGAACAAG	29964728 (Heterodera glycines)
AG005	747	TGGTTGGATCCAAATGAAATCAATGA	45215079 (Wuchereria bancrofti)
AG005	748	TGGATCCAAATGAAATCAATGA	61116961 (Litomosoides sigmodontis)
AG014	749	GAAGAATTTAACATTGAAAAGGG	10122191 (Haemonchus contortus)
AG014	750	GAATTTAACATTGAAAAGGGCCG	28252967 (Trichuris vulpis)
AG016	751	GGTTACATGTACACCGATTTGGC	54552787 (Xiphinema index)

Table 5-TC

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
TC014	853	ATCATGGAATATTACGAGAAGAA	6562543 (Heterodera schachtii); 15769883 (Heterodera glycines)
TC015	854	AACGGTCCCGAAATTATGAGTAAATT	108966476 (Bursaphelenchus xylophilus)

Table 5-MP

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
MP001	1011	GATCTTTTGATATTGTTCACATTAA	13099294 (Strongyloides ratti)
MP001	1012	ACATCCAGGATCTTTTGATATTGTTCAC	15275671 (Strongyloides ratti)
MP001	1013	TCTTTTGATATTGTTCACATTAA	32183548 (Meloidogyne chitwoodi)
MP016	1014	TATTGCTCGTGGACAAAAAAT	9832367 (Strongyloides stercoralis)
MP016	1015	TCTGCTGCTCGTGAAGAAGTACCTGG	13418283 (Necator americanus)
MP016	1016	GCTGAAGATTATTTGGATATT	20064440 (Meloidogyne hapla)
MP016	1017	GGTTTACCACATAATGAGATTGCTGC	20064440 (Meloidogyne hapla)
MP016	1018	AAGAAATGATTCAAACTGGTATTTCAGCTATTGAT	31545172 (Strongyloides ratti)
MP016	1019	TATTGCTCGTGGACAAAAAATTCCAAT	31545172 (Strongyloides ratti)
MP016	1020	GTTTCTGCTGCTCGTGAAGAAGT	31545172 (Strongyloides ratti)
MP016	1021	CGTGGTTTCCCTGGTTACATGTACAC	31545172 (Strongyloides ratti)
MP016	1022	CCTGGTTACATGTACACCGATTT	54552787 (Xiphinema index)
MP027	1023	TTTAAAAATTTTAAAGAAAAA	27540724 (Meloidogyne hapla)
MP027	1024	CTATTATGTTGGTGGTGAAGTTGT	34026304 (Meloidogyne arenaria)
MP027	1025	AAAGTTTTTAAAAATTTTAAA	34028558 (Meloidogyne javanica)

Table 5-NL

Target ID	SEQ ID No	Sequence *	Example Gi-number and species
NL001	1438	AGTACAAGCTGTGCAAAGTGAAGA	18087933 (Globodera rostochiensis), 54547517 (Globodera pallida)
NL001	1439	ATGGATGTTGGACAAATTGGGTGG	7143612 (Globodera rostochiensis)
NL001	1440	TGGATGTTGGACAAATTGGGTGG	7235910 (Meloidogyne incognita)
NL001	1441	AGTACAAGCTGTGCAAAGTGAAGA	111164813 (Globodera rostochiensis)
NL003	1442	AGTCCATCCATCACGCCCGTGT	6081031 (Pristionchus pacificus)
NL003	1443	CTCCGTAACAAGCGTGAGGTGTGG	5815927 (Pristionchus pacificus)

NL003	1444	GACTCGCAGAAGCACATTGACTTCTC	5815618 (Pristionchus pacificus)
NL003	1445	GCAGAAGCACATTGACTTCTC	6081031 (Pristionchus pacificus)
NL003	1446	GCCAAGTCCATCCATCACGCCC	6081133 (Pristionchus pacificus)
NL003	1447	GCCAAGTCCATCCATCACGCCCGTGT	1783663 (Pristionchus pacificus)
NL003	1448	TCGCAGAAGCACATTGACTTCTC	10804008 (Ascaris suum)
NL003	1449	TCGCAGAAGCACATTGACTTCTCGCTGAA	18688500 (Ascaris suum)
NL003	1450	GCCAAGTCCATCCATCACGCCCGTGT	91102596 (Pristionchus pacificus)
NL003	1451	GACTCGCAGAAGCACATTGACTTCTC	91102596 (Pristionchus pacificus)
NL003	1452	CTCCGTAACAAGCGTGAGGTGTGG	91102596 (Pristionchus pacificus)
NL004	1453	AAGAACAAGGATATTCGTAAATT	3758529 (Onchocerca volvulus), 6200728 (Litomosoides sigmodontis)
NL004	1454	AAGAACAAGGATATTCGTAAATTCTTGGA	21056283 (Ascaris suum), 2978237 (Toxocara canis)
NL004	1455	CCGTGTACGCCCATTTCCCCATCAAC	1783477 (Pristionchus pacificus)
NL004	1456	TACGCCCATTTCCCCATCAAC	2181209 (Haemonchus contortus)
NL007	1457	CAACATGAATGCATTCCTCAAGC	39747064 (Meloidogyne paranaensis)
NL007	1458	GAAGTACAACATGAATGCATTCC	6721002 (Onchocerca volvulus)
NL007	1459	GCTGTATTTGTGTTGGCGACA	27541378 (Meloidogyne hapla)
NL008	1460	AGAAAAGGTTGTGGGTTGGTA	108958003 (Bursaphelenchus mucronatus)
NL011	1461	GGACTTCGTGATGGATATTACATTCAGGGACAATG	33138488 (Meloidogyne incognita)
NL011	1462	CAACTACAACTTCGAGAAGCC	108984057 (Bursaphelenchus xylophilus)
NL014	1463	GAAGAATTCAACATTGAAAAGGG	11927908 (Haemonchus contortus)
NL014	1464	GAGCAAGAAGCCAATGAGAAAGC	108985855 (Bursaphelenchus mucronatus)
NL014	1465	TTTCATTGAGCAAGAAGCCAATGAGAAAGCCGAAGA	108979738 (Bursaphelenchus xylophilus)
NL015	1466	ATGAGCAAATTGGCCGGCGAGTCGGAG	18090737 (Globodera rostochiensis)
NL015	1467	CACACCAAGAACATGAAGTTGGCTGA	68276872 (Caenorhabditis remanei)
NL015	1468	CAGGAAATCTGTTCGAAGTGT	45564676 (Meloidogyne incognita)
NL015	1469	CTGGCGCAGATCAAAGAGATGGT	18090737 (Globodera rostochiensis)
NL015	1470	TGGCGCAGATCAAAGAGATGGT	27428872 (Heterodera glycines)
NL016	1471	TATCCCGAGGAAATGATCCAGAC	18081287 (Globodera rostochiensis)
NL016	1472	CGTATCTATCCCGAGGAAATGATCCAGACTGGAATT TC	108957716 (Bursaphelenchus mucronatus) 108962248 (Bursaphelenchus xylophilus)

NL023	1473	TGGATGGGAGTCATGCATGGA	13959786 (Nippostrongylus brasiliensis)

Table 5-CS

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
CS001	1988	ATACAAGCTGTGCAAGGTGCG	10803803 (Trichuris muris)
CS003	1989	AAGCACATTGACTTCTCGCTGAA	18850138 (Ascaris suum)
CS003	1990	CGCAACAAGCGTGAGGTGTGG	40305701 (Heterodera glycines)
CS003	1991	CGTCTCCAGACTCAGGTGTTCAAG	91102965 (Nippostrongylus brasiliensis)
CS011	1992	TTTAATGTATGGGATACTGCTGG	9832495 (Strongyloides stercoralis)
CS011	1993	CACTTGACTGGAGAGTTCGAGAAAA	18082874 (Globodera rostochiensis)
CS011	1994	CTCGTGTCACCTACAAAAATGTACC	71182695 (Caenorhabditis remanei)
CS011	1995	CACTTGACTGGAGAGTTCGAGAA	108987391 (Bursaphelenchus xylophilus)
CS013	1996	TAGGTGAATTTGTTGATGATTA	40305096 (Heterodera glycines)
CS014	1997	AAGAAAGAGAAACAAGTGGAACT	51871231 (Xiphinema index)
CS016	1998	GTGTACATGTAACCTGGGAAACCACG	10819046 (Haemonchus contortus)
CS016	1999	GTGTACATGTAACCTGGGAAACC	13418283 (Necator americanus)
CS016	2000	GCCAAATCGGTGTACATGTAACC	54552787 (Xiphinema index)
CS016	2001	AAGTTCTTCTCGAACTTGGTGAGGAACTC	111163626 (Globodera rostochiensis)

Table 5-PX

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PX001	2291	CTCGACATCGCCACCTGCAAG	11069004 (Haemonchus contortus); 27770634 (Teladorsagia circumcincta)
PX001	2292	GACGGCAAGGTCCGCACCGAC	32320500 (Heterodera glycines)
PX001	2293	CCCGGCTGGATTCATGGATGT	51334233 (Radopholus similis)
PX001	2294	ATCAAGGTGGACGGCAAGGTCCGCAC	108959807 (Bursaphelenchus xylophilus)
PX001	2295	ACAACGTGTTCATCATCGGCAA	111166840 (Globodera rostochiensis)
PX016	2296	CGTGGTTTCCCAGGTTACATGTACACGGATTTGGC	10819046 (Haemonchus contortus)
PX016	2297	GGTTTCCCAGGTTACATGTACAC	13418283 (Necator americanus)
PX016	2298	GAGTTCCTCACCAAGTTCGAGAAGAACTT	111163626 (Globodera rostochiensis)

Table 5-AD

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
AD015	2439	ATAAATGGTCCTGAAATTATGA	9832193 (Strongyloides stercoralis)
AD016	2440	GTCAACATGGAGACGGCGCGCTT	30220804 (Heterodera glycines)

Table 6-LD

Target ID	SEQ ID No	Sequences*	Example Gi-number and species
LD001	136	TAGCGGATGGTGCGGCCGTCGTG	54625255 (Phlebiopsis gigantea)
LD003	137	TTCCAAGAAATCTTCAATCTTCAAA	50294437 (Candida glabrata CBS 138)
LD007	138	GACTGCGGTTTTGAACACCCTTCAGAAGT TCA	110463173 (Rhizopus oryzae)
LD007	139	TGTCAAGCCAAATCTGGTATGGG	110463173 (Rhizopus oryzae)
LD011	140	GGCTTCTCAAAGTTGTAGTTA	48898288 (Aspergillus flavus)
LD011	141	CCATCACGGAGACCACCAAACTT	60673229 (Alternaria brassicicola)
LD011	142	AAAGGCTTCTCAAAGTTGTAGTTA	58157923 (Phytophthora infestans)
LD011	143	TGTGCTATTATCATGTTTGATGT	110458937 (Rhizopus oryzae)
LD011	144	ACTGCCGGTCAGGAGAAGTTTGG	90638500 (Thermomyces lanuginosus)
LD011	145	AATACAACTTTGAGAAGCCTTTCCT	90549582 (Lentinula edodes), 90381505 (Amorphotheca resinae)
LD011	146	CAGGAGAAGTTTGGTGGTCTCCG	90544763 (Gloeophyllum trabeum)
LD011	147	ACCACCAAACTTCTCCTGACC	90368069 (Aureobasidium pullulans)
LD011	148	GGTCAGGAGAAGTTGGTGGTCTCCG	90355148 (Coprinopsis cenerea)
LD016	149	GCAGCAATTTCATTGTGAGGCAGACCAG	50285562 (Candida glabrata CBS 138)
LD016	150	ATGGAGTTCATCACGTCAATAGC	68419480 (Phytophthora parasitica)
LD016	151	GGTCTGCCTCACAATGAAATTGCTGCCCA GAT	85109950 (Neurospora crassa)
LD016	152	CTATTGTTTTCGCTGCTATGGGTGTTAACA TGGA	50423336 (Debaryomyces hansenii), 90540142 (Gloeophyllum trabeum)
LD016	153	ATGAACTCCATTGCTCGTGGTCAGAAGAT	84573655 (Aspergillus oryzae)
LD016	154	ATAGGAATCTGGGTGATGGATCCGTT	90562068 (Leucosporidium scottii), 90359845 (Aureobasidium pullulans)

LD016	155	TCCTGTTTCTGAAGATATGTTGGG	90388021 (Cunninghamella elegans)
LD016	156	TTTGAAGATTGAAGATTTCTTGGAACG	50294437 (Candida glabrata CBS 138), 110468393 (Rhizopus oryzae), 90388664 (Cunninghamella elegans), 90376235 (Amorphotheca resinae)
LD027	157	TCACAGGCAGCGAAGATGGTACC	90546087 (Gloeophyllum trabeum)
LD027	158	TTCTTTGAAGTTTTTGAATAT	50292600 (Candida glabrata CBS 138)

Table 6-PC

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PC001	447	CCCTGCTGGTTTCATGGATGTCAT	110469463 (Rhizopus oryzae)
PC003	448	ATTGAAGATTTCTTGGAAAGAAG	50294437 (Candida glabrata CBS 138)
PC003	449	TTGAAGATTTCTTGGAAAGAAG	50310014 (Kluyveromyces lactis NRRL Y-1140)
PC003	450	CTTCTTTCCAAGAAATCTTCAA	622611 (Saccharomyces cerevisiae)
PC003	451	GACTCGCAGAAGCACATCGACTT	109744873 (Allomyces macrogynus); 59284959 (Blastocladiella emersonii); 90623359 (Corynascus heterothallicus); 29427071 (Verticillium dahliae)
PC003	452	GACTCGCAGAAGCACATCGACTTC	59298648 (Blastocladiella emersonii); 90565029 (Leucosporidium scottii)
PC003	453	TCGCAGAAGCACATCGACTTC	47032157 (Mycosphaerella graminicola)
PC003	454	CAGAAGCACATCGACTTCTCCCT	34332427 (Ustilago maydis)
PC005	455	CTTATGGAGTACATCCACAAG	98997063 (Spizellomyces punctatus)
PC005	456	AAGAAGAAGGCAGAGAAGGCCA	84572408 (Aspergillus oryzae)
PC010	457	GTGTTCAATAATTCTCCTGATGA	50288722 (Candida glabrata CBS 138)
PC010	458	ATTTTCCATGGAGAGACCATTGC	70990481 (Aspergillus fumigatus)
PC010	459	GGGCAGAATCCCCAAGCTGCC	90631635 (Thermomyces lanuginosus)
PC014	460	AATACAAGGACGCCACCGGCA	30394561 (Magnaporthe grisea)
PC016	461	ATGCCCAACGACGACATCACCCA	59281308 (Blastocladiella emersonii)
PC016	462	TGGGTGATGTCGTCGTTGGGCAT	38353161 (Hypocrea jecorina)
PC016	463	GGTTTCCCCGGTTACATGTACAC	34447668 (Cryphonectria parasitica)
PC016	464	ACTATGCCCAACGACGACATCAC	34447668 (Cryphonectria parasitica)
PC016	465	CCGGGCACTTCTTCTCGAGCGGC	38353161 (Hypocrea jecorina)
PC016	466	CCGACCATCGAGCGCATCATCAC	59281308 (Blastocladiella emersonii)
PC016	467	TTCTTGAACTTGGCCAACGATCC	50285562 (Candida glabrata CBS 138)

PC016	468	TGTTCTTGAACTTGGCCAACGA	66909391 (Phaeosphaeria nodorum)
PC016	469	GCTATGGGTGTCAACATGGAAACTGC	110463410 (Rhizopus oryzae)
PC016	470	TGCTATGGGTGTCAACATGGA	71006197 (Ustilago maydis)
PC016	471	CTATTGTGTTTGCTGCTATGGGTGT	68488910 (Candida albicans)
PC016	472	TACGAGCGCGCCGGTCGTGTGGA	90347883 (Coprinopsis cinerea)

Table 6-EV

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
EV010	565	TTCAATAATTCACCAGATGAAAC	50405834 (Debaryomyces hansenii)
EV015	566	CGATCGCCTTGAACAGCGACG	22502898 (Gibberella zeae)
EV015	567	GTTACCATGGAGAACTTCCGTTA	67900533 (Aspergillus nidulans FGSC A4)
EV015	568	GTTACCATGGAGAACTTCCGTTACGCC	70820241 (Aspergillus niger)
EV015	569	ACCATGGAGAACTTCCGTTACGCC	84573628 (Aspergillus oryzae)
EV015	570	ATGGAGAACTTCCGTTACGCC	71002727 (Aspergillus fumigatus)
EV016	571	TCTGAAGATATGTTGGGTCGTGT	90396765 (Cunninghamella elegans)
EV016	572	CAAAAGATTCCAATTTTCTCTGCA	50306984 (Kluyveromyces lactis NRRL Y-1140)
EV016	573	CCCCACAATGAAATCGCTGCTCAAAT	68001221 (Schizosaccharomyces pombe 972h-)
EV016	574	ATCGTTTTCGCCGCTATGGGTGT	58271359 (Cryptococcus neoformans var.)
EV016	575	TTCAAGCAAGATTTTGAAGAGAATGG	50285562 (Candida glabrata CBS 138)

Table 6-AG

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
AG001	752	CGTAACAGGTTGAAGTACGCCCT	16931515 (Coccidioides posadasii)
AG001	753	AAGGTCGACGGCAAAGTCAGGACTGAT	33515688 (Cryptococcus neoformans var.)
AG001	754	CCATTCTTGGTCACCCACGATG	38132640 (Hypocrea jecorina)
AG001	755	ATCAAGGTAAACGACACCATC	56939474 (Puccinia graminis f. sp.)
AG005	756	TGTACATGAAGGCCAAGGGTAACGTGTTCAAGAACAAG	98997063 (Spizellomyces punctatus)
AG005	757	CCAAGGGTAACGTGTTCAAGAACAAG	109744763 (Allomyces macrogynus); 59297176 (Blastocladiella emersonii)
AG005	758	AAGGGTAACGTGTTCAAGAACAAG	109741162 (Allomyces macrogynus)
AG005	759	CAAGAAGAAGGCTGAGAAGGC	67903433 (Aspergillus nidulans FGSC A4)

AG005	760	CAAGAAGAAGGCTGAGAAGGC	4191107 (Emericella nidulans)
AG005	761	AAGAAGAAGGCTGAGAAGGCC	66909252 (Phaeosphaeria nodorum)
AG005	762	CAAAACATCCGTAAATTGATCAAGGATGGTTT	21649803 (Conidiobolus coronatus)
AG016	763	TTCGCCGCCATGGGTGTCAAC	50554108 (Yarrowia lipolytica)
AG016	764	ATGGGTGTCAACATGGAAACCGC	90639144 (Trametes versicolor)
AG016	765	TGGAAACCGCCCGTTTCTTCA	85109950 (Neurospora crassa)
AG016	766	GGTTACATGTACACCGATTTG	32169825 (Mucor circinelloides)
AG016	767	GTCAAGATGGGAATCTGGGTGATGGA	38353161 (Hypocrea jecorina)

Table 6-TC

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
TC001	855	AACAGGCTGAAGTATGCCTTGACC	90545567 (Gloeophyllum trabeum)
TC015	856	TTCATCGTCCGTGGTGGCATG	46122304 (Gibberella zeae PH-1)
TC015	857	AGTTTTACCGGTACCTGGAGG	50310636 (Kluyveromyces lactis NRRL Y-1140)
TC015	858	CCTCCAGGTACCGGTAAAACT	85114224 (Neurospora crassa)
TC015	859	CCTCCAGGTACCGGTAAAACTTT	50290674 (Candida glabrata CBS 138)
TC015	860	ATTAAAGTTTTACCGGTACCTGGAGG	3356460 (Schizosaccharomyces pombe)
TC015	861	GGTGCTTTCTTCTTCTTAATCAA	21649889 (Conidiobolus coronatus)
TC015	862	ATCAACGGTCCCGAAATTATG	82610024 (Phanerochaete chrysosporium)

Table 6-MP

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
MP002	1026	AATTTTTAGAAAAAAAAATTG	68026454 (Schizosaccharomyces pombe 972h-)
MP010	1027	GTCACCACATTAGCTAGGAAT	48564349 (Coccidioides posadasii)
MP016	1028	AAGAAATGATTCAAACTGGTAT	90396765 (Cunninghamella elegans)
MP016	1029	AAGAAATGATTCAAACTGGTATTTC	110463410 (Rhizopus oryzae)
MP016	1030	CATGAACTCTATTGCTCGTGG	50285562 (Candida glabrata CBS 138)
MP016	1031	GCTGCTATGGGTGTTAATATGGA	90348219 (Coprinopsis cinerea)
MP016	1032	TGCTATGGGTGTTAATATGGAAAC	90396964 (Cunninghamella elegans)
MP016	1033	CCTACTATTGAGCGTATCATTAC	90524974 (Geomyces pannorum)
MP016	1034	GAAGTTTCTGCTGCTCGTGAAGAAGTACCTGG	90396313 (Cunninghamella elegans)
MP016	1035	GTTTCTGCTGCTCGTGAAGAAGT	32169825 (Mucor circinelloides)
MP016	1036	GTGTACATGTAACCAGGGAAACCACG	45392344 (Magnaporthe grisea)

MP016	1037	CCTGGTTACATGTACACCGATTT	32169825 (Mucor circinelloides)
MP016	1038	GGTTACATGTACACCGATTTA	47067814 (Eremothecium gossypii)
MP016	1039	CCTATTTTAACTATGCCTAACGA	90396313 (Cunninghamella elegans)
MP027	1040	ACTCTCCATCACCACATACTA	60673889 (Alternaria brassicicola)

Table 6-NL

Target ID	SEQ ID No	Sequence *	Example Gi-number and species
NL001	1474	CCAAGGGCAAGGGTGTGAAGCTCA	30418788 (Magnaporthe grisea)
NL001	1475	TCTCTGCCCAAGGGCAAGGGTGT	22500578 (Gibberella zeae), 46128672 (Gibberella zeae PH-1), 70662858 (Gibberella moniliformis), 71000466 (Aspergillus fumigatus)
NL001	1476	TCTGCCCAAGGGCAAGGGTGT	14664568 (Fusarium sporotrichioides)
NL001	1477	TCTCTGCCCAAGGGCAAGGGT	50550586 (Yarrowia lipolytica)
NL001	1478	TCTCTGCCCAAGGGCAAGGGTGT	71000466 (Aspergillus fumigatus) 92459259 (Gibberella zeae)
NL001	1479	CTGCCCAAGGGCAAGGGTGTGAAG	90545567 (Gloeophyllum trabeum)
NL003	1480	ATGAAGCTCGATTACGTCTTGG	24446027 (Paracoccidioides brasiliensis)
NL003	1481	CGTAAGGCCGCTCGTGAGCTG	10229753 (Phytophthora infestans)
NL003	1482	CGTAAGGCCGCTCGTGAGCTGTTGAC	58082846 (Phytophthora infestans)
NL003	1483	GACTCGCAGAAGCACATTGACTT	21393181 (Pratylenchus penetrans), 34330401 (Ustilago maydis)
NL003	1484	TGAAGCTCGATTACGTCTTGG	46346864 (Paracoccidioides brasiliensis)
NL003	1485	TGGCCAAGTCCATCCATCACGCCCGTGT	58113938 (Phytophthora infestans)
NL004	1486	CGTAACTTCCTGGGCGAGAAG	58127885 (Phytophthora infestans)
NL003	1487	ATGAAGCTCGATTACGTCTTGG	90366381 (Aureobasidium pullulans)
NL003	1488	TCGGTTTGGCCAAGTCCATCCA	90353540 (Coprinopsis cinerea)
NL003	1489	GACTCGCAGAAGCACATTGACTT	71012467 (Ustilago maydis)
NL003	1490	GACTCGCAGAAGCACATTGACTTCTC	90616286 (Ophiostoma piliferum)
NL004	1491	TACGCCCATTTCCCCATCAAC	15771856 (Gibberella zeae), 29426217 (Verticillium dahliae), 30399988 (Magnaporthe grisea), 34330394 (Ustilago maydis), 39945691 (Magnaporthe grisea 70-15), 46108543 (Gibberella zeae PH-1), 70660620 (Gibberella

			moniliformis)
NL004	1492	CGTGTACGCCCATTTCCCCATCAAC	90615722 (Ophiostoma piliferum)
NL004	1493	TACGCCCATTTCCCCATCAAC	90367524 (Aureobasidium pullulans) 90372622 (Cryptococcus laurentii) 109654277 (Fusarium oxysporum f. sp.) 90535059 (Geomyces pannorum) 46108543 (Gibberella zeae PH-1) 90566138 (Leucosporidium scottii) 39945691 (Magnaporthe grisea 70-15) 110115733 (Saitoella complicata) 110081735 (Tuber borchii) 71021510 (Ustilago maydis) 50554252 (Yarrowia lipolytica)
NL004	1494	TACGCCCATTTCCCCATCAACTG	90640952 (Trametes versicolor)
NL004	1495	CGTGTACGCCCATTTCCCCATCAAC	90615722 (Ophiostoma piliferum)
NL005	1496	AAAAGGTCAAGGAGGCCAAGA	14662414 (Fusarium sporotrichioides)
NL005	1497	TTCAAGAACAAGCGTGTATTGATGGA	90395504 (Cunninghamella elegans)
NL005	1498	TTCAAGAACAAGCGTGTATTGATGGAGT	90542553 (Gloeophyllum trabeum)
NL006	1499	CCTGGAGGAGGAGACGACCAT	70998503 (Aspergillus fumigatus)
NL006	1500	TCCCATCTCGTATGACAATTGG	68471154 (Candida albicans)
NL006	1501	ATGGTCGTCTCCTCCTCCAGG	70998503 (Aspergillus fumigatus)
NL006	1502	TCCCATCTCGTATGACAATTGG	68471154 (Candida albicans) 50425488 (Debaryomyces hansenii)
NL007	1503	CAAGTCATGATGTTCAGTGCAAC	70984614 (Aspergillus fumigatus)
NL007	1504	TGACGCTTCACGGCCTGCAGCAG	10229203 (Phytophthora infestans)
NL007	1505	CAAGTCATGATGTTCAGTGCAAC	70984614 (Aspergillus fumigatus)
NL010_2	1506	CAATTCTTGCAAGTGTTCAACAA	68478799 (Candida albicans)
NL010_2	1507	TTCAACAACAGTCCTGATGAAAC	21649260 (Conidiobolus coronatus)
NL010_2	1508	TTCTTGCAAGTGTTCAACAAC	47031965 (Mycosphaerella graminicola)
NL011	1509	AAGAACGTTCCCAACTGGCAC	68132303 (Trichophyton rubrum)
NL011	1510	ACAAGAACGTTCCCAACTGGCA	68132303 (Trichophyton rubrum)
NL011	1511	ACCTACAAGAACGTTCCCAACT	68132303 (Trichophyton rubrum)
NL011	1512	ACCTACAAGAACGTTCCCAACTGGCAC	70674996 (Gibberella moniliformis)

NL011	1513	CAACTACAACTTCGAGAAGCC	22500425 (Gibberella zeae), 34331122 (Ustilago maydis), 46108433 (Gibberella zeae PH-1), 47029512 (Mycosphaerella graminicola), 56236507 (Setosphaeria turcica), 62926335 (Fusarium oxysporum f. sp.), 70674996 (Gibberella moniliformis), 70992714 (Aspergillus fumigatus)
NL011	1514	CAAGAACGTTCCCAACTGGCAC	68132303 (Trichophyton rubrum)
NL011	1515	CACCTACAAGAACGTTCCCAAC	68132303 (Trichophyton rubrum)
NL011	1516	CCTACAAGAACGTTCCCAACTG	68132303 (Trichophyton rubrum)
NL011	1517	CTACAAGAACGTTCCCAACTGG	68132303 (Trichophyton rubrum)
NL011	1518	GCAACTACAACTTCGAGAAGCC	22505588 (Gibberella zeae)
NL011	1519	TACAAGAACGTTCCCAACTGGC	68132303 (Trichophyton rubrum)
NL011	1520	TCACCTACAAGAACGTTCCCA	68132303 (Trichophyton rubrum)
NL011	1521	TCACCTACAAGAACGTTCCCAA	68132303 (Trichophyton rubrum)
NL011	1522	TCACCTACAAGAACGTTCCCAACT	30405871 (Magnaporthe grisea)
NL011	1523	TCACCTACAAGAACGTTCCCAACTGGCAC	13903501 (Blumeria graminis f. sp.), 3140444 (Emericella nidulans), 34331122 (Ustilago maydis), 49096317 (Aspergillus nidulans FGSC A4)
NL011	1524	TGGGACACAGCTGGCCAGGAAA	14180743 (Magnaporthe grisea), 39950145 (Magnaporthe grisea 70-15)
NL011	1525	TTCGAGAAGCCGTTCCTGTGG	38056576 (Phytophthora sojae), 45244260 (Phytophthora nicotianae), 58091236 (Phytophthora infestans)
NL011	1526	TTCGAGAAGCCGTTCCTGTGGTTGGC	58090083 (Phytophthora infestans)
NL011	1527	TGGGACACAGCTGGCCAGGAAA	39950145 (Magnaporthe grisea 70-15)
NL011	1528	TATTACATTCAGGGACAATGCG	110134999 (Taphrina deformans)
NL011	1529	TCACCTACAAGAACGTTCCCAACTGGCAC	84573903 (Aspergillus oryzae) 90355199 (Coprinopsis cinerea) 90624693 (Corynascus heterothallicus) 90638500 (Thermomyces lanuginosus)
NL011	1530	ACCTACAAGAACGTTCCCAACTGGCAC	113544700 (Cordyceps bassiana) 85114463 (Neurospora crassa)
NL011	1531	TACAAGAACGTTCCCAACTGGCA	110269748 (Hypocrea lixii)
NL011	1532	TACAAGAACGTTCCCAACTGGCAC	110458937 (Rhizopus oryzae)
NL011	1533	AGGAAGAAGAACCTTCAGTACT	90557551 (Leucosporidium scottii)

NL011	1534	AAGAAGAACCTTCAGTACTACGA	113551594 (Cordyceps bassiana)
NL011	1535	AAGAAGAACCTTCAGTACTACGACATC	90036917 (Trichophyton rubrum)
NL011	1536	AAGAACCTTCAGTACTACGACATC	90624693 (Corynascus heterothallicus)
NL011	1537	GGCTTCTCGAAGTTGTAGTTGC	89975123 (Hypocrea lixii)
NL011	1538	CAACTACAACTTCGAGAAGCC	70992714 (Aspergillus fumigatus) 90368808 (Aureobasidium pullulans) 90629512 (Corynascus heterothallicus) 109656121 (Fusarium oxysporum f. sp.) 90532849 (Geomyces pannorum) 110272576 (Hypocrea lixii) 47029512 (Mycosphaerella graminicola) 85114463 (Neurospora crassa) 90617165 (Ophiostoma piliferum) 90036917 (Trichophyton rubrum)
NL011	1539	GGCTTCTCGAAGTTGTAGTTG	92233975 (Gibberella zeae)
NL013	1540	CCCGAGATGGTGGTGGCTGGTACCA	49069733 (Ustilago maydis)
NL013	1541	GGTACCACTCGCACCCGGGCTT	58134950 (Phytophthora infestans)
NL013	1542	GTGGGCTGGTACCACTCGCACCCGGGCTTCG GCTGCTGGCTGTCGGG	38062327 (Phytophthora sojae)
NL013	1543	TGGTACCACTCGCACCCGGGCTT	58084933 (Phytophthora infestans)
NL013	1544	CCCGAGATGGTGGTGGGCTGGTACCA	71006043 (Ustilago maydis)
NL015	1545	ATCCACACCAAGAACATGAAG	10181857 (Aspergillus niger), 22505190 (Gibberella zeae), 30394634 (Magnaporthe grisea), 33507832 (Cryptococcus neoformans var.), 3773467 (Emericella nidulans), 39940093 (Magnaporthe grisea 70-15), 46122304 (Gibberella zeae PH-1), 47032030 (Mycosphaerella graminicola), 49106059 (Aspergillus nidulans FGSC A4)
NL015	1546	CACACCAAGAACATGAAGTTGG	21649889 (Conidiobolus coronatus)
NL015	1547	GCCTTCTTCTTCCTCATCAACGG	46122304 (Gibberella zeae PH-1)
NL015	1548	TTGGAGGCTGCAGAAAGCAGCT	90369178 (Cryptococcus laurentii)
NL015	1549	GCCTTCTTCTTCCTCATCAACGG	46122304 (Gibberella zeae PH-1)
NL015	1550	ATCCACACCAAGAACATGAAG	70820941 (Aspergillus niger) 58260307 (Cryptococcus neoformans var.) 85691122 (Encephalitozoon cuniculi GB-M1)

			46122304 (Gibberella zeae PH-1) 39940093 (Magnaporthe grisea 70-15) 85082882 (Neurospora crassa) 50555821 (Yarrowia lipolytica)
NL015	1551	CACACCAAGAACATGAAGTTGGC	110272618 (Hypocrea lixii)
NL016	1552	CATGAACTCGATTGCTCGTGG	30418452 (Magnaporthe grisea), 39942327 (Magnaporthe grisea 70-15)
NL016	1553	CCACCATCTACGAGCGCGCCGGACG	39942327 (Magnaporthe grisea 70-15), 45392344 (Magnaporthe grisea)
NL016	1554	CATGAACTCGATTGCTCGTGG	90367610 (Aureobasidium pullulans) 39942327 (Magnaporthe grisea 70-15)
NL016	1555	CATGTCGGTGAGGATGACGAG	90562068 (Leucosporidium scottii)
NL016	1556	CCACCATCTACGAGCGCGCCGGACG	39942327 (Magnaporthe grisea 70-15)
NL019	1557	CAGATTTGGGACACGGCCGGCCAGGAGCG	9834078 (Phytophthora sojae)
NL019	1558	GACCAGGAGTCGTTCAACAAC	9834078 (Phytophthora sojae)
NL019	1559	TGGGACACGGCCGGCCAGGAG	38056576 (Phytophthora sojae), 40545332 (Phytophthora nicotianae), 58083674 (Phytophthora infestans)
NL019	1560	TGGGACACGGCCGGCCAGGAGCG	29426828 (Verticillium dahliae), 38057141 (Phytophthora sojae)
NL019	1561	TGGGACACGGCCGGCCAGGAGCGGTT	70981934 (Aspergillus fumigatus)
NL019	1562	TTCCTGGAGACGTCGGCGAAGAACGC	90643518 (Trametes versicolor)
NL019	1563	CAGATTTGGGACACGGCCGGCCAGGAGCG	90616605 (Ophiostoma piliferum)
NL019	1564	TGGGACACGGCCGGCCAGGAG	110272626 (Hypocrea lixii)
NL019	1565	TGGGACACGGCCGGCCAGGAGCG	50550714 (Yarrowia lipolytica)
NL019	1566	TGGGACACGGCCGGCCAGGAGCGGTT	70981934 (Aspergillus fumigatus)
NL019	1567	TGGGACACGGCCGGCCAGGAGCGGTTCCG	50553761 (Yarrowia lipolytica)
NL022	1568	CAGGCAAAGATTTTCCTGCCCA	58124185 (Phytophthora infestans)
NL022	1569	GGCAAGTGCTTCCGTCTGTACAC	58124872 (Phytophthora infestans)
NL023	1570	GGATGACCAAAAACGTATTCT	46137132 (Gibberella zeae PH-1)
NL023	1571	AGAATACGTTTTTGGTCATCC	46137132 (Gibberella zeae PH-1)

Table 6-CS

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
CS003	2002	TGGTCTCCGCAACAAGCGTGA	46356829 (Paracoccidioides brasiliensis)
CS003	2003	GGTCTCCGCAACAAGCGTGAG	71012467 (Ustilago maydis)
CS003	2004	TGGTCTCCGCAACAAGCGTGAGGT	5832048 (Botryotinia fuckeliana)
CS003	2005	TGGTCTCCGCAACAAGCGTGAGGT	40545704 (Sclerotinia sclerotiorum)
CS003	2006	GGTCTCCGCAACAAGCGTGAGGT	21907821 (Colletotrichum trifolii); 90623359 (Corynascus heterothallicus); 94331331 (Pyronema omphalodes); 29427071 (Verticillium dahliae)
CS003	2007	TGGTCTCCGCAACAAGCGTGAGGTGTGG	27439041 (Chaetomium globosum); 47032270 (Mycosphaerella graminicola)
CS003	2008	CGCAACAAGCGTGAGGTGTGG	71000428 (Aspergillus fumigatus); 67537265 (Aspergillus nidulans FGSC A4); 70825441 (Aspergillus niger); 84573806 (Aspergillus oryzae); 3773212 (Emericella nidulans); 90632673 (Thermomyces lanuginosus); 34332427 (Ustilago maydis)
CS006	2009	TCCCCTCTCGTATGACAATTGGT	68011927 (Schizosaccharomyces pombe 972h-)
CS007	2010	ATTTAGCTTTGACAAAGAATA	50305206 (Kluyveromyces lactis NRRL Y-1140)
CS007	2011	GAGCACCCTTCAGAAGTTCAACA	90553133 (Lentinula edodes)
CS011	2012	TGGGATACTGCTGGCCAAGAA	90385536 (Amorphotheca resinae); 68475609 (Candida albicans); 50304104 (Kluyveromyces lactis NRRL Y-1140); 85105150 (Neurospora crassa)
CS011	2013	AAGTTTGGTGGTCTCCGAGATGGTTACTA	90355199 (Coprinopsis cinerea)
CS011	2014	CAATGTGCCATCATCATGTTCGA	15276938 (Glomus intraradices)
CS011	2015	CATCATCATGTTCGATGTAAC	28268268 (Chaetomium globosum)
CS011	2016	CACTTGACTGGAGAGTTCGAGAA	90368808 (Aureobasidium pullulans); 34331122 (Ustilago maydis)
CS011	2017	TGAAGGTTCTTTTTTCTGTGGAA	6831345 (Pneumocystis carinii)
CS013	2018	GGATGGTACCACTCGCATCCTGG	109651225 (Fusarium oxysporum f. sp.)
CS015	2019	AACGAGAGGAAGAAGAAGAAG	39944615 (Magnaporthe grisea 70-15)
CS015	2020	AGGGCTTCTTCTTCTTCCTCTC	14662870 (Fusarium sporotrichioides)

CS015	2021	TAGGGCTTCTTCTTCTTCCTC	85112692 (Neurospora crassa)
CS015	2022	GAGATGGTCGAGTTGCCTCTA	71005073 (Ustilago maydis)
CS016	2023	GCTGAAGACTTTTTGGACATC	30418452 (Magnaporthe grisea)
CS016	2024	CCTCACCAAGTTCGAGAAGAACTTC	90566317 (Leucosporidium scottii)
CS016	2025	GTCGTCGGTGAGGAAGCCCTG	84573655 (Aspergillus oryzae)
CS016	2026	TCCTCACCGACGACAGCCTTCATGGCC	29427786 (Verticillium dahliae)
CS016	2027	GATGTTTCCAACCAGCTGTACGCC	90368806 (Aureobasidium pullulans)
CS016	2028	GGCGTACAGCTGGTTGGAAACATC	29427786 (Verticillium dahliae)
CS016	2029	TGATGTTTCCAACCAGCTGTACGCC	46107507 (Gibberella zeae PH-1)
CS016	2030	ATGGCAGACTTCATGAGACGAGA	29427786 (Verticillium dahliae)
CS016	2031	ATGCCCAACGACGACATCACCCA	59281308 (Blastocladiella emersonii)
CS016	2032	TGGGTGATGTCGTCGTTGGGCAT	38353161 (Hypocrea jecorina)
CS016	2033	ACTATGCCCAACGACGACATCAC	34447668 (Cryphonectria parasitica)
CS016	2034	GGTTACATGTACACCGATTTG	32169825 (Mucor circinelloides)
CS016	2035	CCCAGGTTACATGTACACCGATTT	47067814 (Eremothecium gossypii)
CS016	2036	ACACCACGTTTGGCCTTGACT	68488910 (Candida albicans)
CS016	2037	GCCATGGGTGTGAACATGGAGAC	82608508 (Phanerochaete chrysosporium)
CS016	2038	GACGACCACGAGGACAACTTTGCCATCGTGTTCG	59277641 (Blastocladiella emersonii)
CS016	2039	AAGATCCCCATTTTCTCGGCTGC	90348219 (Coprinopsis cinerea)

Table 6-PX

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PX001	2299	CTCATCAAGGTGGACGGCAAGGT	85080580 (Neurospora crassa)
PX001	2300	TCGGTGCGGACCTTGCCGTCCACCTTGA	70768092 (Gibberella moniliformis)
PX001	2301	GACGGCAAGGTCCGCACCGAC	109745014 (Allomyces macrogynus); 60673542 (Alternaria brassicicola); 90368699 (Aureobasidium pullulans); 59299145 (Blastocladiella emersonii); 27438899 (Chaetomium globosum); 90623992 (Corynascus heterothallicus); 89975695 (Hypocrea lixii); 99039195 (Leptosphaeria maculans); 39970560 (Magnaporthe grisea); 47731115 (Metarhizium anisopliae); 90036859 (Trichophyton rubrum); 29427127

			(Verticillium dahliae)
PX001	2302	GACGGCAAGGTCCGCACCGACCC	70823112 (Aspergillus niger); 90633197 (Thermomyces lanuginosus)
PX001	2303	AAGGTCCGCACCGACCCCACCTACCC	71015993 (Ustilago maydis)
PX001	2304	CGCTTCACCATCCACCGCATCAC	90639458 (Trametes versicolor)
PX001	2305	CGAGGAGGCCAAGTACAAGCTG	78177454 (Chaetomium cupreum); 27438899 (Chaetomium globosum)
PX001	2306	GAGGCCAAGTACAAGCTGTGCAAGGT	109745014 (Allomyces macrogynus)
PX001	2307	GCCAAGTACAAGCTGTGCAAG	45923813 (Coccidioides posadasii)
PX001	2308	CCCGACCCGCTCATCAAGGTCAACGAC	78177454 (Chaetomium cupreum)
PX001	2309	CGACATCGTCCACATCAAGGAC	82603501 (Phanerochaete chrysosporium)
PX001	2310	CCGCACAAGCTGCGCGAGTGCCTGCCGCTC	109745014 (Allomyces macrogynus)
PX010	2311	TTCGACCAGGAGGCGGCGGCGGT	90542152 (Gloeophyllum trabeum)
PX010	2312	CACCACCGCCGCCGCCTCCTG	84578035 (Aspergillus oryzae)
PX010	2313	TGCAGGTCTTCAACAACTCGCCCGACGA	39978050 (Magnaporthe grisea)
PX010	2314	TTCAACAACTCGCCCGACGAGAC	90618424 (Corynascus heterothallicus)
PX015	2315	CATGCGCGCCGTCGAGTTCAAGGTGGT	59282860 (Blastocladiella emersonii)
PX015	2316	GCATTCTTCTTCCTCATCAACGG	68323226 (Coprinopsis cinerea)
PX015	2317	ATCAACGGCCCCGAGATCATGTC	85082882 (Neurospora crassa)
PX015	2318	TGCGCAAGGCGTTCGAGGAGGC	71002727 (Aspergillus fumigatus)
PX016	2319	CCTCACCAAGTTCGAGAAGAACTTC	90566317 (Leucosporidium scottii)
PX016	2320	GAGGAGATGATCCAGACTGGTAT	90639144 (Trametes versicolor)
PX016	2321	GAGGAGATGATCCAGACTGGTATCTC	58271359 (Cryptococcus neoformans)
PX016	2322	ATGAACTCCATCGCCCGTGGTCAGAAGATCCC	90545177 (Gloeophyllum trabeum)
PX016	2323	GTCAGAAGATCCCCATCTTCTCCGCC	9651842 (Emericella nidulans)
PX016	2324	CAGAAGATCCCCATCTTCTCCGC	70825597 (Aspergillus niger); 90611576 (Ophiostoma piliferum); 90639144 (Trametes versicolor)
PX016	2325	CAGAAGATCCCCATCTTCTCCGCC	67540123 (Aspergillus nidulans)
PX016	2326	CAGAAGATCCCCATCTTCTCCGCCGCCGG	59283275 (Blastocladiella emersonii)
PX016	2327	AAGATCCCCATCTTCTCCGCCGCCGGTCT	34447668 (Cryphonectria parasitica)
PX016	2328	CCCATCTTCTCCGCCGCCGGTCTGCC	90621827 (Corynascus heterothallicus)
PX016	2329	GGTCTGCCCCACAACGAGATTGCTGC	90367610 (Aureobasidium pullulans); 66909391 (Phaeosphaeria nodorum)
PX016	2330	TTCGCCGCCATGGGAGTCAACATGGAGAC	90562163 (Leucosporidium scottii)

PX016	2331	ACCGCCAGGTTCTTCAAGCAGGA	47067814 (Eremothecium gossypii)
PX016	2332	CTGTTCTTGAACTTGGCCAATGA	90545177 (Gloeophyllum trabeum)
PX016	2333	GGTTACATGTACACGGATTTG	34447668 (Cryphonectria parasitica); 90545177 (Gloeophyllum trabeum); 39942327 (Magnaporthe grisea); 82608506 (Phanerochaete chrysosporium); 71006197 (Ustilago maydis)
PX016	2334	GGCAAGCCCATCGACAAGGGGCCC	59283275 (Blastocladiella emersonii)
PX016	2335	ATGGGGTGGGTGATGTCGTCGTTGGGCATGGTCA	38353161 (Hypocrea jecorina)
PX016	2336	ACCATGCCCAACGACGACATCACCCACCC	59281308 (Blastocladiella emersonii)
PX016	2337	TGCACAACAGGCAGATCTACCC	107889579 (Encephalitozoon cuniculi)
PX016	2338	CCGTCGCTATCTCGTCTCATGAA	48521040 (Coccidioides posadasii)

Table 6-AD

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
AD001	2441	CCCGCTGGTTTCATGGATGTT	58259586 (Cryptococcus neoformans)
AD001	2442	GACAACATCCATGAAACCAGCGGG	21649877 (Conidiobolus coronatus)
AD001	2443	TTCATGGATGTTGTCACCATTG	90616000 (Ophiostoma piliferum)
AD001	2444	GAAGAAGCCAAGTACAAGCTCTG	110469512 (Rhizopus oryzae)
AD001	2445	AAGAAGCCAAGTACAAGCTCTG	110469518 (Rhizopus oryzae)
AD001	2446	GCCAAGTACAAGCTCTGCAAGGT	98996590 (Spizellomyces punctatus)
AD001	2447	GCCAAGTACAAGCTCTGCAAGGTCA	109743129 (Allomyces macrogynus)
AD001	2448	AGTACAAGCTCTGCAAGGTCA	71000466 (Aspergillus fumigatus); 67537247 (Aspergillus nidulans); 70823112 (Aspergillus niger); 40886470 (Emericella nidulans)
AD015	2449	TATGGACCCCCTGGAACTGGTAAAACC	46349704 (Paracoccidioides brasiliensis)
AD016	2450	TGCCCGTGTCCGAGGACATGCTGGGCCG	109743322 (Allomyces macrogynus)
AD016	2451	TGCCCGTGTCCGAGGACATGCTGGGCCGC	59283275 (Blastocladiella emersonii)
AD016	2452	CGTGTCCGAGGACATGCTGGGCCGCA	90612905 (Ophiostoma piliferum)
AD016	2453	ATGGGCGTCAACATGGAGACGGC	59277641 (Blastocladiella emersonii)
AD016	2454	TGGAGACGGCGCGCTTCTTCA	90611376 (Ophiostoma piliferum)
AD016	2455	TTCCTCAACCTGGCCAACGACCCCAC	90611376 (Ophiostoma piliferum)
AD016	2456	ACCATCGAGCGCATCATCACCCCGCGCCTCGC	59281308 (Blastocladiella emersonii)
AD016	2457	TCCACCATCTACGAGCGCGCTGG	90368806 (Aureobasidium pullulans)

AD016	2458	CTGACGATGCCCAACGACGACATCAC	90611301 (Ophiostoma piliferum)
AD016	2459	ATGCCCAACGACGACATCACCCA	59281308 (Blastocladiella emersonii)
AD016	2460	TGGGTGATGTCGTCGTTGGGCAT	38353161 (Hypocrea jecorina)

Table 7-LD

Target ID	SEQ ID NO and DNA Sequence (sense strand) 5' → 3' of fragments and concatemer constructs
LD014_F1	SEQ ID NO: 159 TCTAGAATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTCGTACCGTACTAGAGGAG GCGCGTAAACGACTTGGTCAGGTCACAAACGCCCGGG
LD014_F2	SEQ ID NO: 160 TCTAGAAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGCCCGGG
LD014_C1	SEQ ID NO: 161 TCTAGAATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTCGTACCGTACTAGAGGAG GCGCGTAAACGACTTGGTCAGGTCACAAACGATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGA TCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGATGTTGAATCAGGCTCGAT TGAAAGTATTGAAGGTTAGGGAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCA CAAACGCCCGGG
LD014_C2	SEQ ID NO: 162 TCTAGAAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGAAGATCACGT TCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGAAGATCACGTTCGTACCGTACTAGAG GAGGCGCGTAAACGACTTGGTCAGGTCACAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGAC TTGGTCAGGTCACAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAA CGCCCGGG

Table 8-LD

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
LD001	SEQ ID NO: 164 GCGTAATACGACT CACTATAGGGGCC CCAAGAAGCATTT	SEQ ID NO: 165 CCTTTGGGGCCAG TTTGCATC	SEQ ID NO: 163 GGCCCCAAGAAGCATTTGAAGCGTTTGAATGCCCCAAAAGCATGGA TGTTGGATAAATTGGGAGGTGTTTTCGCACCTCGCCCATCTACAGG ACCTCACAAATTGCGAGAGTCTTTGCCCTTGGTGATCTTCCTACGTA

	GAAGCG SEQ ID NO: 166 GGCCCCAAGAAGC ATTTGAAGCG	ACCGATTGAAGTATGCTTTGACTAACAGCGAAGTTACTAAGATTGT TATGCAAAGGTTAATCAAAGTAGATGGAAAAGTGAGGACCGACTC CAATTACCCTGCTGGGTTTATGGATGTTATTACCATTGAAAAAACTG GTGAATTTTTCCGACTCATCTATGATGTTAAAGGACGATTTGCAGTG CATCGTATTACTGCTGAGGAAGCAAAGTACAAACTATGCAAAGTCA GGAGGATGCAAACTGGCCCCAAAGG
	SEQ ID NO: 167 GCGTAATACGACT CACTATAGGCCTT TGGGGCCAGTTTG CATC	
LD002	SEQ ID NO: 169 GCGTAATACGACT CACTATAGGGTCC ACGTCCAAGTTTTT ATGGGC SEQ ID NO: 171 GTCCACGTCCAAG TTTTTATGGGC	SEQ ID NO: 168 GTCCACGTCCAAGTTTTTATGGGCTTTCTTAAGAGCTTCAGCTGCAT TTTTCATAGATTCCAATACTGTGGTGTTCGTACTAGCTCCCTCCAGA GCTTCTCGTTGAAGTTCAATAGTAGTTAAAGTGCCATCTATTTGCAA CTGATTTTTTTCTAATCGCTT
	SEQ ID NO: 170 AAGCGATTAGAAA AAAATCAGTTGC SEQ ID NO: 172 GCGTAATACGACT CACTATAGGAAGC GATTAGAAAAAAA TCAGTTGC	
LD003	SEQ ID NO: 174 GCGTAATACGACT CACTATAGGCCCA GGCGACCTTATGA AAAGGC SEQ ID NO: 176 CCCAGGCGACCTT ATGAAAAGGC	SEQ ID NO: 173 GGTGACCACCACCGAATGGAGATTTGAGCGAGAAGTCAATATGCTT CTGGGAATCAAGTCTCACAATGAAGCTTGGAATATTCACGACCTGC TTACGAACCCTGATATGTCTTTGACGGACCAGCACACGAGCATGAT GGATTGATTTTGCAAGCCCCAACTTGAAAACTTGTGTTTGGAGACG TCGTTCCAAGAAATCTTCAATCTTCAAACCCAAGACGTAATCAAGC TTCATACGGGTTTCATCCAACACTCCAATACGCACCAACCGACGAA GAAGAGCATTGCCTTCAAACAACCTGCGCTGATCTTTCTCTTCCAAA GTCAGAAGTTCTCTGGCAGCTTTACGGATTTTTGCCAAGGTATACTT GACTCGCCACACTTCACGTTTGTTCCTAAGACCATATTCTCCTATGA TTTTCAACTCCTGATCAAGACGTGCCTTTTCATAAGGTCGCCTGGG
	SEQ ID NO: 177 GCGTAATACGACT CACTATAGGGGTG ACCACCACCGAAT GGAG	
LD006	SEQ ID NO: 179 GCGTAATACGACT CACTATAGGGGTG TTGGTTGCTTCTGG TGTG	SEQ ID NO: 178 GGTGTTGGTTGCTTCTGGTGTGGTGGAATACATCGACACTCTTGAA GAAGAAACTGTCATGATTGCGATGAATCCTGAGGATCTTCGGCAGG ACAAAGAATATGCTTATTGTACGACCTACACCCACTGCGAAATCCA CCCGGCCATGATCTTGGGCGTTTGCGCGTCTATTATACCTTTCCCCG ATCATAACCAGAGCCCAAGGAACACCTACCAGAGCGCTATGGGTA AGCAAGCTATGGGGGTCTACATTACGAATTTCCACGTGCGGATGGA
	SEQ ID NO: 180 GCTTCGATTCGGC ATCTTTATAGG SEQ ID NO: 182 GCGTAATACGACT	

	SEQ ID NO: 181 GGTGTTGGTTGCTTCTGGTGTG	CACTATAGGGCTTCGATTCGGCATCTTTATAGG	CACCCTGGCCCACGTGCTATACTACCCGCACAAACCTCTGGTCACTACCAGGTCTATGGAGTATCTGCGGTTCAGAGAATTACCAGCCGGGATCAACAGTATAGTTGCTATTGCTTGTTATACTGGTTATAATCAAGAAGATTCTGTTATTCTGAACGCGTCTGCTGTGGAAAGAGGATTTTTCCGATCCGTGTTTTATCGTTCCTATAAAGATGCCGAATCGAAGC
LD007	SEQ ID NO: 184 GCGTAATACGACTCACTATAGGGACTGGCGGTTTTGAACACCC SEQ ID NO: 186 GACTGGCGGTTTTGAACACCC	SEQ ID NO: 185 CCTTTCAATGTCCATGCCACG SEQ ID NO: 187 GCGTAATACGACTCACTATAGGCCTTTCAATGTCCATGCCACG	SEQ ID NO: 183 GACTGGCGGTTTTGAACACCCTTCAGAAGTTCAGCACGAATGTATTCCTCAAGCTGTCATTGGCATGGACATTTTATGTCAAGCCAAATCTGGTATGGGCAAAACGGCAGTGTTTGTTCTGGCGACACTGCAACAATTGGAACCAGCGGACAATGTTGTTTACGTTTTGGTGATGTGTCACACTCGTGAACTGGCTTTCCAAATCAGCAAAGAGTACGAGAGGTTCAGTAAATATATGCCCAGTGTCAAGGTGGGCGTCTTTTTCGGAGGAATGCCTATTGCTAACGATGAAGAAGTATTGAAAAACAAATGTCCACACATTGTTGTGGGGACGCCTGGGCGTATTTTGGCGCTTGTCAAGTCTAGGAAGCTAGTCCTCAAGAACCTGAAACACTTCATTCTTGATGAGTGCGATAAAATGTTAGAACTGTTGGATATGAGGAGAGACGTCCAGGAAATCTACAGAAACACCCCTCACACCAAGCAAGTGATGATGTTCAGTGCCACACTCAGCAAAGAAATCAGGCCGGTGTGCAAGAAATTCATGCAAGATCCAATGGAGGTGTATGTAGACGATGAAGCCAAATTGACGTTGCACGGATTACAACAGCATTACGTTAAACTCAAAGAAAATGAAAAGAATAAAAAATTATTTGAGTTGCTCGATGTTCTCGAATTTAATCAGGTGGTCATTTTTGTGAAGTCCGTTCAAAGGTGTGTGGCTTTGGCACAGTTGCTGACTGAACAGAATTTCCCAGCCATAGGAATTCACAGAGGAATGGACCAGAAAGAGAGGTTGTCTCGGTATGAGCAGTTCAAAGATTTCCAGAAGAGAATATTGGTAGCTACGAATCTCTTTGGGCGTGGCATGGACATTGAAAGG
LD010	SEQ ID NO: 189 GCGTAATACGACTCACTATAGGGCTTGTTGCCCCCGAATGC SEQ ID NO: 191 GCTTGTTGCCCCC	SEQ ID NO: 190 CTATCGGGTTGGATGGAACTCG SEQ ID NO: 192 GCGTAATACGACTCACTATAGGCTATCGGGTTGGATGGA	SEQ ID NO: 188 GCTTGTTGCCCCCGAATGCCTTGATAGGGTTGATTACCTTTGGGAAGATGGTCCAAGTGCACGAACTAGGTACCGAGGGCTGCAGCAAATCTTACGTTTTCCGAGGGACGAAAGACCTCACAGCTAAGCAAGTTCAAGAGATGTTGGAAGTGGGCAGAGCCGCAGTAAGTGCTCAACCTGCTCCTCAACAACCAGGACAACCCATGAGGCCTGGAGCACTCCAGCAAGCTCCTACGCCACCAGGAAGCAGGTTCCTTCAACCCATCTCGAAATGCGACATGAACCTCACTGATCTTATTGGAGAGTTGCAAAGAGACCCATGGCCTGTCCACCAAGGCAAATGCGCCCTTAGATCGACCGGGACAGCT

	GAATGC	ACTCG
LD011	SEQ ID NO:194 GCGTAATACGACT CACTATAGGGCCA TAGGAAAGGCTTC TCAAAG SEQ ID NO: 196 GCCATAGGAAAGG CTTCTCAAAG	SEQ ID NO: 195 GGAAAAACGACAT TTGTGAAACGTC SEQ ID NO: 197 GCGTAATACGACT CACTATAGGGGAA AAACGACATTTGT GAAACGTC

TTATCGATAGCCATTGGGTTGTTGGAGTGCACATACGCCAATACTG
GTGCCAGGGTCATGCTATTCGTTGGAGGACCTTGCTCTCAAGGCCC
TGGTCAAGTCTTGAATGATGATCTGAAGCAACCTATCAGATCTCAC
CACGACATCCAAAAAGACAATGCCAAATACATGAAGAAAGCAATC
AAGCACTATGATAATTTAGCGATGAGAGCAGCAACGAATGGCCACT
GCGTTGACATATATTCATGCGCTTTGGATCAGACAGGATTGATGGA
GATGAAACAGTGTTGTAATTCAACAGGGGGACATATGGTCATGGGC
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CATTCCGCTCCCATACCTCAAGGGGGAAGGGGCTGCATACAGTTCA
TCACGCAATATCAGCATGCTAGTGGCCAGAAGAGGATCCGAGTAAC
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GCCATAGGAAAGGCTTCTCAAAGTTGTAGTTAGATTTGGCAGAGAT
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TCGGGATATTTTCACAGACTCTGACAAGATCTCTGTGCCAATTTGGT
ACATTCTTGTATGTAACTCTGGAAGTTACATCAAACATGATAATAG
CACACTGTCCCTGAATGTAATATCCATCACGGAGACCACCAAACTT
CTCCTGACCGGCAGTGTCCCATACATTGAACCGAATAGGGCCCCTG
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CATATCTTTTTTCAAATTCACCAGTCATATGACGTTTCACAAATGTC
GTTTTTCC

LD014	SEQ ID NO: 199 GCGTAATACGACT CACTATAGGTTTC ATTGAACAAGAGG CAAACG SEQ ID NO: 201 TTTCATTGAACAA GAGGCAAACG	SEQ ID NO: 200 GCGAAATCAGCTC CAGACGAGC SEQ ID NO: 202 GCGTAATACGACT CACTATAGGGCGA AATCAGCTCCAGA CGAGC	SEQ ID NO: 198 TTTCATTGAACAAGAGGCAAACGAAAAGGCAGAAGAAATCGATGC CAAGGCCGAGGAAGAATTTAATATTGAAAAGGGGCGCCTTGTTCAG CAACAACGTCTCAAGATTATGGAATATTATGAGAAGAAAGAGAAA CAGGTCGAACTCCAGAAAAAAATCCAATCGTCTAACATGTTGAATC AGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTCGTAC CGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGA CCAGGGAAAATATTCCCAAATCCTGGAAAGCCTCATTTTGCAGGGA TTATATCAGCTTTTTGAGAAAGATGTTACCATTCGAGTTCGGCCCCA GGACCGAGAACTGGTCAAATCCATCATTCCCACCGTCACGAACAAG TATAAAGATGCCACCGGTAAGGACATCCATCTGAAAATTGATGACG AAATCCATCTGTCCCAAGAAACCACCGGGGGAATCGACCTGCTGGC GCAGAAAAACAAAATCAAGATCAGCAATACTATGGAGGCTCGTCT GGAGCTGATTTCGC
LD014_F1	SEQ ID NO: 204 GCGTAATACGACT CACTATAGGATGT TGAATCAGGCTCG ATTG SEQ ID NO: 206 ATGTTGAATCAGG CTCGATTG	SEQ ID NO: 205 CGTTTGTGACCTG ACCAAGTC SEQ ID NO: 207 GCGTAATACGACT CACTATAGGCGTT TGTGACCTGACCA AGTC	SEQ ID NO: 203 ATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATC ACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGT CACAAACG
LD014_F2	SEQ ID NO: 209 GCGTAATACGACT CACTATAGGAAGA TCACGTTCGTACC GTAC SEQ ID NO: 211 AAGATCACGTTCG TACCGTAC	SEQ ID NO: 210 CGTTTGTGACCTG ACCAAG SEQ ID NO: 212 GCGTAATACGACT CACTATAGGCGTT TGTGACCTGACCA AG	SEQ ID NO: 208 AAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGG TCAGGTCACAAACG
LD014_C1			SEQ ID NO: 213

			AATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGAT CACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGG TCACAAACGATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTA GGGAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGAC TTGGTCAGGTCACAAACGATGTTGAATCAGGCTCGATTGAAAGTAT TGAAGGTTAGGGAAGATCACGTTCGTACCGTACTAGAGGAGGCGC GTAAACGACTTGGTCAGGTCACAAACGC
LD014_C2			SEQ ID NO: 214 AAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTG GTCAGGTCACAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGC GCGTAAACGACTTGGTCAGGTCACAAACGAAGATCACGTTCGTACC GTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGAA GATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTC AGGTCACAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGCGC GTAAACGACTTGGTCAGGTCACAAACGC
LD015	SEQ ID NO: 216 GCGTAATACGACT CACTATAGGCGCC GGAGAGTTTTTGT CAGC SEQ ID NO: 218 CGCCGGAGAGTTT TTGTCAGC	SEQ ID NO: 217 CTATCGGCGTGAA GCCCCC SEQ ID NO: 219 GCGTAATACGACT CACTATAGGCTAT CGGCGTGAAGCCC CC	SEQ ID NO: 215 CGCCGGAGAGTTTTTGTCAGCTTCTTCAAAAGCTTTGCGCAAGTTAC TCTCAGACTCGCCAGCGAGTTTGCTCATGATCTCCGGCCCGTTTATC AAGAAGAAGAACGCCCCAGTCTCATTAGCCACGGCGCGAGCAATC AGGGTCTTACCCGTACCAGGGGGACCATACAGCAGTATACCCCTAG GGGGCTTCACGCCGATAG
LD016	SEQ ID NO: 221 GCGTAATACGACT CACTATAGGGGCA TAGTCAATATAGG AATCTGGGTG SEQ ID NO: 223 GGCATAGTCAATA TAGGAATCTGGGT	SEQ ID NO: 222 GGTAATCCTCGAA GATGTTAAGTTCC SEQ ID NO: 224 GCGTAATACGACT CACTATAGGGGTA ATCCTCGAAGATG TTAAGTTCC	SEQ ID NO: 220 GGCATAGTCAATATAGGAATCTGGGTGATGGATCCGTTACGTCCTT CAACACGGCCGGCACCGTTCATAGATGGTAGCTAAATCGGTGTACAT GTAACCTGGGAAACCACGACGACCAGGCACCTCTTCTCTGGCAGCA GATACCTCACGCAAAGCTTCTGCATACGAAGACATATCTGTCAAGA TGACCAAGACGTGCTTCTCACATTGGTAAGCCAAGAATTCGGCAGC TGTCAAAGCCAGACGAGGTGTAATAATTCTTTCAATGGTAGGATCG TTGGCCAAATTCAAGAACAGGCAGACATTCTCCATAGAACCGTTCT CTTCGAAATCCTGTTTGAAGAACCTAGCTGTTTCCATGTTAACACCC ATAGCAGCGAAAACAATAGCAAAGTTATCTTCATGATCATCAAGTA

	G		CAGATTTACCAGGAATCTTGACTAAACCAGCCTGTCTACAGATCTG GGCAGCAATTTCATTGTGAGGCAGACCAGCTGCAGAGAAAATGGG GATCTTCTGACCACGAGCAATGGAGTTCATCACGTCAATAGCTGTA ATACCCGTCTGGATCATTTCCTCAGGATAGATACGGGACCACGGAT TGATTGGTTGACCCTGGATGTCCAAGAAGTCTTCAGCCAAAATTGG GGGACCTTTGTCGATGGGTTTTCCTGATCCATTGAAAACACGTCCCA ACATATCTTCAGAAACAGGAGTCCTCAAAATATCTCCTGTGAATTC ACAAGCGGTGTTTTTGGCGTCGATTCCTGATGTGCCCTCGAACACTT GAACCACAGCTTTTGACCCACTGACTTCCAGAACTTGTCCCGAACG TATAGTGCCATCAGCCAGTTTGAGTTGTACGATTTCATTGTACTTGG GGAACTTAACATCTTCGAGGATTACC
LD018	SEQ ID NO: 226 GCGTAATACGACT CACTATAGGGAG TCGCAGAAATACG AGAGCAC SEQ ID NO: 228 GGAGTCGCAGAAA TACGAGAGCAC	SEQ ID NO: 227 GTAGAGGCTCCAC CGTCAATCGC SEQ ID NO: 229 GCGTAATACGACT CACTATAGGGTAG AGGCTCCACCGTC AATCGC	SEQ ID NO: 225 GGAGTCGCAGAAATACGAGAGCACCTTCTCGAACAACCAAGCCTC CTTGAGGGTAAAACAAGCCCAGTCTGAGGACTCGGGACACTACACT TTGTTGGCGGAGAACCCTCAAGGCTGCATAGTGTCATCTGCTTACTT AGCCATAGAACCGGTAACCACCCAGGAAGGGTTGATCCACGAGTC CACCTTCAAGCAGCAACAGACCGAAATGGAGCAAATCGACACCAG CAAGACCTTGGCGCCTAACTTCGTCAGGGTTTGCGGGGATAGAGAC GTGACCGAGGGCAAGATGACCCGCTTCGACTGTCGCGTCACTGGTC GTCCTTATCCAGACGTGACATGGTACATAAACGGTCGACAAGTCAC CGACGACCACAACCACAGATTTTGGTTAACGAATCCGGAAACCAT GCCCTGATGATCACCACCGTGAGCAGGAACGACTCAGGAGTAGTG ACCTGCGTCGCCAGGAACAAGACGGGAGAAACCTCCTTCCAGTGC AACCTTAACGTCATCGAAAAGGAACAGGTAGTCGCGCCCAAGTTCG TGGAGAGATTTACCACAGTCAACGTGGCAGAAGGAGAACCAGTGT CTCTGCGCGCTAGAGCTGTTGGCACGCCGGTGCCGCGAATCACTTG GCAGAGGGACGGGGCGCCCCTAGCCAGCGGGCCCGACGTTCGCAT CGCGATTGACGGTGGAGCCTCTAC
LD027	SEQ ID NO: 231 GCGTAATACGACT CACTATAGGGGGA GCAGACGATCGGT TGG	SEQ ID NO: 232 TCGGACAGACTCG TTCATTTCCC SEQ ID NO: 234	SEQ ID NO: 230 GGGAGCAGACGATCGGTTGGTTAAAATCTGGGACTATCAAAACAA AACGTGTGTCCAAACCTTGGAAGGACACGCCCAAAACGTAACCGC GGTTTGTTTCCACCCTGAACTACCTGTGGCTCTCACAGGCAGCGAA GATGGTACCGTTAGAGTTTGGCATACGAATACACACAGATTAGAGA ATTGTTTGAATTATGGGTTCGAGAGAGTGTGGACCATTTGTTGCTTG

	SEQ ID NO: 233 GGGAGCAGACGAT CGGTTGG	GCGTAATACGACT CACTATAGGTCGG ACAGACTCGTTCA TTTCCC	AAGGGTTCGAATAATGTTTCTCTGGGGTATGACGAGGGCAGTATAT TAGTGAAAGTTGGAAGAGAAGAACCGGCAGTTAGTATGGATGCCA GTGGCGGTAAAATAATTTGGGCAAGGCACTCGGAATTACAACAAG CTAATTTGAAGGCGCTGCCAGAAGGTGGAGAAATAAGAGATGGGG AGCGTTTACCTGTCTCTGTAAAAGATATGGGAGCATGTGAAATATA CCCTCAAACAATCCAACATAATCCGAATGGAAGATTCGTTGTAGTA TGCGGAGACGGCGAATATATCATTTACACAGCGATGGCTCTACGGA ACAAGGCTTTTGGAAGCGCTCAAGAGTTTGTCTGGGCTCAGGACTC CAGCGAGTATGCCATTCGCGAGTCTGGTTCCACAATTCGGATATTC AAAAACTTCAAAGAAAGGAAGAACTTCAAGTCGGATTTCAGCGCG GAAGGAATCTACGGGGGTTTTCTCTTGGGGATTAAATCGGTGTCCG GTTTAACGTTTTACGATTGGGAAACTTTGGACTTGGTGAGACGGAT TGAAATACAACCGAGGGCGGTTTATTGGTCTGACAGTGGAAAATTA GTCTGTCTCGCAACGGAGGACAGCTACTTCATCCTTTCTTATGATTC GGAGCAAGTTCAGAAGGCCAGGGAGAACAATCAAGTCGCAGAGGA TGGCGTAGAGGCCGCTTTCGATGTGTTGGGGGAAATGAACGAGTCT GTCCGA
gfp	SEQ ID NO: 236 GCGTAATACGACT CACTATAGGAGAT ACCCAGATCATAT GAAACGG SEQ ID NO: 238 AGATACCCAGATC ATATGAAACGG	SEQ ID NO: 237 CAATTTGTGTCCA AGAATGTTTCC SEQ ID NO: 239 GCGTAATACGACT CACTATAGGCAAT TTGTGTCCAAGAA TGTTTCC	SEQ ID NO: 235 AGATACCCAGATCATATGAAACGGCATGACTTTTTCAAGAGTGCCA TGCCCGAAGGTTATGTACAGGAAAGAACTATATTTTTCAAAGATGA CGGGAACTACAAGACACGTAAGTTTAAACAGTTCGGTACTAACTAA CCATACATATTTAAATTTTCAGGTGCTGAAGTCAAGTTTGAAGGTG ATACCCTTGTTAATAGAATCGAGTTAAAAGGTATTGATTTTAAAGA AGATGGAAACATTCTTGGACACAAATTG

Table 8-PC

Target ID	**Primers Forward 5' → 3'**	**Primers Reverse 5' → 3'**	**dsRNA DNA Sequence (sense strand) 5' → 3'**
PC001	SEQ ID NO: 474 GCATGGATGTTGG ACAAATTGGG	SEQ ID NO: 475 GCGTAATACGACT CACTATAGGAGAT	SEQ ID NO: 473 GCATGGATGTTGGACAAATTGGGGGGTGTCTTCGCCCCTCGTCCATCCA CCGGGCCTCACAAGTTGCGCGAATCCCTGCCTTTAGTGATTTTCCTTCG

	SEQ ID NO: 476 GCGTAATACGACT CACTATAGGGCAT GGATGTTGGACAA ATTGGG	TCAAATTTGATGT AGTCAAGAATTTT AG SEQ ID NO: 477 AGATTCAAATTTG ATGTAGTCAAGAA TTTTAG	TAACAGGCTGAAGTATGCCCTTACAAACAGTGAAGTCACTAAAATTGT CATGCAAAGGTTGATCAAAGTTGATGGTAAAGTGAGGACTGATTCTAA TTACCCTGCTGGTTTCATGGATGTCATTACTATTGAGAAGACTGGTGAA TTTTTCCGTCTGATCTATGATGTTAAAGGAAGATTTGCTGTGCACCGTA TTACAGCTGAAGAGGCAAAATACAAGTTGTGTAAAGTAAGGAGAGTCC AAACTGGTCCCAAAGGAATCCCATTTTGGTAACACATGATGGCAGAA CCATTCGTTACCCTGACCCCAACATCAAAGTGAATGACACAATTCAAAT GGAAATTGCTACATCTAAAATTCTTGACTACATCAAATTTGAATCT
PC003	SEQ ID NO: 479 CCCTAGACGTCCC TATGAAAAGGCCC SEQ ID NO: 481 GCGTAATACGACT CACTATAGGCCCT AGACGTCCCTATG AAAAGGCCC	SEQ ID NO: 480 GCGTAATACGACT CACTATAGGTTGA CACGGCCAGGTCG GCCACC SEQ ID NO: 482 TTGACACGGCCAG GTCGGCCACC	SEQ ID NO: 478 CCCTAGACGTCCCTATGAAAAGGCCCGTCTGGATCAGGAATTGAAAAT TATCGGCGCCTTTGGTTTACGAAACAAACGTGAAGTGTGGAGAGTAAA GTACACTTTGGCTAAAATCCGTAAAGCTGCTCGTGAACTGCTCACCCTA GAAGAAAAAGAGCCTAAAAGATTGTTTGAAGGTAATGCACTTCTACGT CGTTTGGTGCGAATTGGTGTTCTGGATGAGAACAGGATGAAGCTTGATT ATGTTTTGGGTCTGAAAATTGAAGATTTCTTGGAAAGAAGGCTCCAAA CTCAGGTGTTCAAATCTGGTCTGGCAAAGTCAATTCATCATGCTAGAGT ACTGATTAGGCAGAGACACATCCGGGTGCGCAAGCAGGTGGTGAACAT CCCCTCGTTCATCGTGCGGCTGGACTCGCAGAAGCACACATCGACTTCTCC CTGAAGTCGCCCTTCGGGGGTGGCCGACCTGGCCGTGTCAA
PC005	SEQ ID NO: 484 ATCCTAATGAAAT CAACGAAATCGCC SEQ ID NO: 486 GCGTAATACGACT CACTATAGGATCC TAATGAAATCAAC GAAATCGCC	SEQ ID NO: 485 GCGTAATACGACT CACTATAGGTTCC CTACGTTCCCTGG CCTGCTTC SEQ ID NO: 487 TTCCCTACGTTCCC TGGCCTGCTTC	SEQ ID NO: 483 ATCCTAATGAAATCAACGAAATCGCCAACACCAACTCAAGACAAAACA TCCGTAAGCTCATCAAGGATGGTCTTATCATCAAGAAGCCAGTGGCAG TACACTCTAGGGCCCGTGTACGCAAGAACACTGAAGCTAGAAGGAAGG GAAGGCATTGTGGATTTGGAAAGAGGAAGGGTACGGCAAATGCCCGTA TGCCTCAAAAGGAACTGTGGGTGCAGCGCATGCGCGTCCTCAGGCGCC TCCTCAAAAAGTACAGGGAGGCCAAGAAAATCGACCGCCATCTTTACC ACGCCCTGTACATGAAAGCGAAGGGTAACGTGTTCAGGAACAAGAGG GTCCTTATGGAGTACATCCACAAGAAGAAGGCAGAGAAGGCCAGGGC CAAGATGCTGTCTGACCAGGCTAACGCCAGGAGATTGAAGGTGAAGCA GGCCAGGGAACGTAGGGAA
PC010	SEQ ID NO: 489 GCTCAGCCTATTA CCGCCCAACGC	SEQ ID NO: 490 GCGTAATACGACT CACTATAGGATGG AAAATGAGTATCT	SEQ ID NO: 488 GCTCAGCCTATTACCGCCCAACGCGTTGATTGGATTCACGTTCGGA AAAATGGTGCAAGTCCACGAACTGGGTACCGAAGGCTGCAGCAAGTCG TACGTGTTCTGTGGAACGAAAGATCTCACCGCCAAGCAAGTCCAGGAG

	SEQ ID NO: 491 GCGTAATACGACT CACTATAGGGCTC AGCCTATTACCGC CCAACGC	GGAAGAAAG SEQ ID NO: 492 ATGGAAAATGAGT ATCTGGAAGAAAG	ATGTTGGGCATTGGAAAAGGGTCACCAAATCCCCAACAACAGCCAGGG CAACCTGGGCGGCCAGGGCAGAATCCCCAAGCTGCCCCTGTACCACCG GGGAGCAGATTCTTGCAGCCCGTGTCAAAATGCGACATGAACTTGACA GATCTGATCGGGGAGTTGCAGAAAGACCCTTGGCCCGTACATCAGGGC AAAAGACCTCTTAGATCCACAGGCGCAGCATTGTCCATCGCTGTCGGC CTCTTAGAATGCACCTATCCGAATACGGGTGGCAGAATCATGATATTCT TAGGAGGACCATGCTCTCAGGGTCCCGGCCAGGTGTTGAACGACGATT TGAAGCAGCCCATCAGGTCCCATCATGACATACACAAAGACAATGCCA AGTACATGAAGAAGGCTATCAAACATTACGATCACTTGGCAATGCGAG CTGCCACCAACAGCCATTGCATCGACATTTACTCCTGCGCCCTGGATCA GACGGGACTGATGGAGATGAAGCAGTGCTGCAATTCCACCGGAGGGCA CATGGTCATGGGCGATTCCTTCAATTCCTCTCTATTCAAACAAACCTTC CAGCGAGTGTTCTCAAAAGACCCGAAGAACGACCTCAAGATGGCGTTC AACGCCACCTTGGAGGTGAAGTGTTCCAGGGAGTTAAAAGTCCAAGGG GGCATCGGCTCGTGCGTGTCCTTGAACGTTAAAAGCCCTCTGGTTTCCG ATACGGAACTAGGCATGGGGAATACTGTGCAGTGGAAACTTTGCACGT TGGCGCCGAGCTCTACTGTGGCGCTGTTCTTCGAGGTGGTTAACCAGCA TTCGGCGCCCATACCACAGGGAGGCAGGGGCTGCATCCAGCTCATCAC CCAGTATCAGCACGCGAGCGGGCAAAGGAGGATCAGAGTGACCACGA TTGCTAGAAATTGGGCGGACCGCTACTGCCAACATCCACCACATTAGCG CTGGCTTCGACCAAGAAGCGGCGGCAGTTGTGATGGCCCGAATGGCCG GTTACAAGGCGGAATCGGACGAGACTCCCGACGTGCTCAGATGGGTGG ACAGGATGTTGATCAGGCTGTGCCAGAAGTTCGGAGAGTACAATAAAG ACGATCCGAATTCGTTCAGGTTGGGGGAGAACTTCAGTCTGTATCCGCA GTTCATGTACCATTTGAGACGGTCGCAGTTTCTGCAGGTGTTCAATAAT TCTCCTGATGAAACGTCGTTTTATAGGCACATGCTGATGCGTGAGGATT TGACTCAGTCTTTGATCATGATCCAGCCGATTTTGTACAGTTACAGCTT CAACGGGCCGCCCGAGCCTGTGTTGTTGGACACAAGCTCTATTCAGCC GGATAGAATCCTGCTCATGGACACTTTCTTCCAGATACTCATTTTCCAT
PC014	SEQ ID NO: 494 CTGATGTTCAAAA ACAAATCAAACAC ATG SEQ ID NO: 496	SEQ ID NO: 495 GCGTAATACGACT CACTATAGGTGAG CGATCAGATCCAA CCTAGCCTCC	SEQ ID NO: 493 CTGATGTTCAAAAACAAATCAAACACATGATGGCTTTCATTGAACAAG AAGCCAATGAGAAAGCAGAAGAAATTGATGCCAAGGCAGAGGAGGAA TTCAACATTGAAAAAGGGCGTTTGGTCCAGCAACAGAGACTCAAGATC ATGGAGTACTACGAGAAAAAGGAGAAGCAAGTCGAACTTCAAAAGAA AATTCAGTCCTCTAATATGTTGAATCAGGCTCGTTTGAAGGTGCTGAAA GTGAGAGAGGACCATGTCAGAGCAGTCCTGGAGGATGCTCGTAAAAGT

	GCGTAATACGACT CACTATAGGCTGA TGTTCAAAAACAA ATCAAACACATG	SEQ ID NO: 497 TGAGCGATCAGAT CCAACCTAGCCTC C	CTTGGTGAAGTAACCAAAGACCAAGGAAAATACTCCCAAATTTGGAG AGCCTAATCCTACAAGGACTGTTCCAGCTGTTCGAGAAGGAGGTGACG GTCCGCGTGAGACCGCAAGACAGGGACCTGGTCAGGTCCATCCTGCCC AACGTCGCTGCCAAATACAAGGACGCCACCGGCAAAGACATCCTACTC AAGGTGGACGATGAGTCGCACCTGTCTCAGGAGATCACCGGAGGCGTC GATTTGCTCGCTCAGAAGAACAAGATCAAGATCAGCAACACGATGGAG GCTAGGTTGGATCTGATCGCTCA
PC016	SEQ ID NO: 499 ACTGGTCATTCTTG AGGATGTCAAGT SEQ ID NO: 501 GCGTAATACGACT CACTATAGGACTG GTCATTCTTGAGG ATGTCAAGT	SEQ ID NO: 500 GCGTAATACGACT CACTATAGGTTGG GCATAGTCAAGAT GGGGATCTGC SEQ ID NO: 502 TTGGGCATAGTCA AGATGGGGATCTG C	SEQ ID NO: 498 ACTGGTCATTCTTGAGGATGTCAAGTTTCCAAAATTCAATGAAATTGTC CAGCTCAAATTGGCAGATGGAACTCTACGATCTGGACAAGTTTTGGAA GTCAGTGGATCAAAGGCAGTTGTTCAGGTATTTGAAGGCACATCAGGT ATTGATGCTAAGAACACGGTGTGTGAGTTCACTGGAGATATTCTAAGA ACTCCAGTATCAGAAGATATGCTGGGACGTGTCTTCAATGGATCAGGA AAACCCATTGATAAAGGTCCCCCGATCCTGGCTGAGGACTACCTCGAC ATCCAAGGACAGCCGATCAACCCGTGGTCGCGTATTTATCCCGAGGAA ATGATCCAGACTGGGATCACGGCCATCGACGTGATGAACTCTATCGCC AGAGGGCAGAAGATTCCGATCTTCTCCGCCGCTGGGCTGCCCCACAAT GAGATTGCAGCCCAGATTTGTAGGCAGGCTGGCTTGGTCAAAGTACCT GGCAAGTCTGTGCTGGATGACCATGAAGACAACTTTGCTATTGTGTTTG CTGCTATGGGTGTCAACATGGAAACTGCCAGGTTCTTCAAGCAGGACTT CGAAGAGAACGGCTCGATGGAGAACGTGTGTCTGTTCTTGAACTTGGC CAACGATCCGACCATCGAGCGCATCATCACGCCGCGTTTGGCTCTGAC GGCCGCCGAATTCTTGGCCTACCAGTGCGAGAAGCACGTGCTGGTCAT CTTGACCGACATGTCGTCGTACGCGGAGGCGTTGCGTGAGGTGTCTGCC GCTCGAGAAGAAGTGCCCGGCCGTAGGGTTTCCCCGGTTACATGTAC ACCGATCTGGCCACCATTTACGAGCGCGCCGGTCGTGTGGAGGGCCGC AACGGCTCCATCACGCAGATCCCCATCTTGACTATGCCCAA
PC027	SEQ ID NO: 504 CAAGCTAACTTGA AAGTACTACCAGA AGG SEQ ID NO: 506 GCGTAATACGACT CACTATAGGCAAG	SEQ ID NO: 505 GCGTAATACGACT CACTATAGGTTTT GGAATTGAAGGCA ATACTCGATCAG SEQ ID NO: 507 TTTTGGAATTGAA	SEQ ID NO: 503 CAAGCTAACTTGAAAGTACTACCAGAAGGAGCTGAAATCAGAGATGGA GAACGTTTGCCAGTCACAGTAAAGGACATGGGAGCATGCGAGATTTAC CCACAAACAATCCAACACAACCCCAATGGGCGGTTTGTAGTGGTTTGT GGTGATGGAGAATACATAATATACACGGCTATGGCCCTTCGTAACAAA GCATTTGGTAGCGCTCAAGAATTTGTATGGGCACAGGACTCCAGTGAA TATGCCATCCGCGAATCCGGATCCACCATTCGAATCTTCAAGAATTTCA AAGAAAAAAAGAATTTCAAGTCCGACTTTGGTGCCGAAGGAATCTATG

	CTAACTTGAAAGT ACTACCAGAAGG	GGCAATACTCGAT CAG	GTGGTTTTCTCTTGGGTGTGAAATCAGTTTCTGGCTTAGCTTTCTATGAC TGGGAAACGCTTGAGTTAGTAAGGCGCATTGAAATACAGCCTAGAGCT ATCTACTGGTCAGATAGTGGCAAGTTGGTATGCCTTGCTACCGAAGATA GCTATTTCATATTGTCCTATGACTCTGACCAAGTCCAGAAAGCTAGAGA TAACAACCAAGTTGCTGAAGATGGAGTGGAGGCTGCCTTTGATGTCCT AGGTGAAATAAATGAATCCGTAAGAACAGGTCTTTGGGTAGGAGACTG CTTCATTTACACAAACGCAGTCAACCGTATCAACTACTTTGTGGGTGGT GAATTGGTAACTATTGCACATCTGGACCGTCCTCTATATGTCCTGGGCT ATGTACCTAGAGATGACAGGTTATACTTGGTTGATAAAGAGTTAGGAG TAGTCAGCTATCNAATTGCTATTATCTGTACTCGAATATCAGACTGCAG TCATGCGACGAGACTTCCCAACGGCTGATCGAGTATTGCCTTCAATTCC AAAA

Table 8-EV

Target ID	**Primers Forward 5' → 3'**	**Primers Reverse 5' → 3'**	**dsRNA DNA Sequence (sense strand) 5' → 3'**
EV005	SEQ ID NO: 577 GACAAAACATCCG CAAACTG SEQ ID NO: 579 GCGTAATACGACT CACTATAGGGACA AAACATCCGCAAA CTG	SEQ ID NO: 578 GCGTAATACGACT CACTATAGGCTCC TTGCATCAGCTTG ATC SEQ ID NO: 580 CTCCTTGCATCAG CTTGATC	SEQ ID NO: 576 GACAAAACATCCGCAAACTGATTAAAGATGGTCTTATTATTAAAAAGC CTGTCGCGGTGCATTCTCGTGCACGTGTACGCAAAAATACTGAAGCCC GCAGGAAAGGTCGTCATTGTGGATTTGGTAAAAGGAAAGGAACTGCAA ATGCTAGGATGCCCAGAAAGGAATTATGGATTCAACGTATGAGAGTTC TCAGAAGGTTATTGAAGAAATATAGGGAAGCTAAGAAAATTGATAGGC ATTTATACCATGCTTTATATATGAAAGCTAAGGGAAATGTATTCAAGAA TAAGAGAGTAATGATGGACTATATCCATAAAAAGAAGGCGGAGAAAG CACGTACAAAGATGCTCAATGATCAAGCTGATGCAAGGAG
EV009	SEQ ID NO: 582 CAGGACTGAAGAA TCTATAATAGG SEQ ID NO: 584 GCGTAATACGACT CACTATAGGCAGG	SEQ ID NO: 583 GCGTAATACGACT CACTATAGGCTGG AAAGATGGGTAAT ACTTC SEQ ID NO: 585	SEQ ID NO: 581 CAGGACTGAAGAATCTATAATAGGAACAAACCCAGGAATGGGTTTTAG GCCAATGCCCGACAACAACGAAGAAAGTACCCTGATTTGGTTACAGGG TTCTAATAAAACAAACTACGAAAAATGGAAAATGAATCTCCTCTCATA TTTAGACAAGTATTACACTCCCGGAAAAATAGAAAAGGGAAATATTCC AGTAAAGCGCTGTTCATACGGAGAAAAATTGATTAGGGGACAAGTATG TGATGTAGATGTGAGGAAATGGGAGCCGTGCACCCCGGAAAATCATTT

	ACTGAAGAATCTA TAATAGG	CTGGAAAGATGGG TAATACTTC	TGATTACCTCAGAAATGCGCCTTGTATATTTCTGAAGCTGAACAGGATA TATGGATGGGAACCGGAGTACTACAACGATCCAAATGATCTTCCAGAT GATATGCCGCAGCAGTTGAAGGACCATATACGTTATAATATCACCAAT CCAGTGGAGAGAAATACCGTCTGGGTAACATGCGCAGGTGAAAATCCG GCAGACGTGGAGTACTTGGGCCCTGTGAAGTATTACCCATCTTTCCAG
EV010	SEQ ID NO: 587 CCAATGGAGACTT GAAGATGTC SEQ ID NO: 589 GCGTAATACGACT CACTATAGGCCAA TGGAGACTTGAAG ATGTC	SEQ ID NO: 588 GCGTAATACGACT CACTATAGGCTTC CCTCATCAACATG TGC SEQ ID NO: 590 CTTCCCTCATCAAC ATGTGC	SEQ ID NO: 586 CCAATGGAGACTTGAAGATGTCCTTCAACGCCATATTAGAAGTGAAGT GTTCTAGAGAACTTAAAGTACAAGGAGGTATAGGTCCTTGTGTCTCTCT AAATGTCAAAAATCCTCTTGTTTCTGATTTAGAAATAGGCATGGGTAAC ACAGTTCAGTGGAAACTGTGTAGCTTAAGTCCAAGCACTACGGTTGCCT TATTTTTCGAAGTTGTTAATCAGCATGCAGCACCCATTCCTCAAGGGGG ACGTGGATGCATTCAGTTTATTACTCAATATCAGCATTCAAGTGGTCAG AAAAAAATAAGGGTAACTACAATAGCAAGAAATTGGGCGGATGCCAC TGCAAATATTCACCATATTAGCGCTGGCTTTGACGAACAAACTGCGGCT GTTTTAATGGCGAGGATCGCTGTATATAGAGCAGAAACTGATGAGAGT TCAGATGTTCTCAGATGGGTTGACAGAATGTTGATACGATTGTGTCAGA AATTTGGAGAATATAACAAAGATGACACCAACAGCTTCAGGCTCAGTG AAAACTTCAGCTTATATCCACAGTTTATGTATCATCTACGTCGTTCCCA ATTTCTACAAGTGTTCAATAATTCACCAGATGAAACTTCATTCTATAGG CACATGTTGATGAGGGAAG
EV015	SEQ ID NO: 592 GTTAAGCCTCCAA GGGGTATTC SEQ ID NO: 594 GCGTAATACGACT CACTATAGGGTTA AGCCTCCAAGGGG TATTC	SEQ ID NO: 593 GCGTAATACGACT CACTATAGGGAGC ACAAAGAAGCCAA GTCAG SEQ ID NO: 595 GAGCACAAAGAAG CCAAGTCAG	SEQ ID NO: 591 GTTAAGCCTCCAAGGGGTATTCTCCTTTACGGGCCTCCCGGCACGGGGA AAACGCTGATCGCCAGGGCCGTTGCCAACGAAACTGGTGCGTTCTTCTT CCTCATCAATGGGCCCGAGATTATGAGCAAGCTGGCCGGAGAATCCGA GAGCAATCTTAGAAAGGCTTTTGAAGAGGCTGATAAAAACTCTCCTGC AATCATCTTTATCGACGAATTAGACGCAATCGCTCCCAAGCGCGAGAA GACTCATGGTGAGGTAGAGAGACGCATCGTCTCCCAACTGTTGACTTTG ATGGACGGCATGAAGAAAAGTTCCCATGTGATCGTGATGGCGGCCACG AACAGGCCCAATTCCATCGACCCTGCACTCAGACGTTTCGGCCGATTCG ACAGAGAGATCGACATCGGTATCCCCGACGCTACTGGAAGATTAGAAG TACTCAGAATACACACCAAAAACATGAAATTGGCTGACGATGTAGATT TGGAACAGATTGCCGCAGAGACTCACGGTCATGTAGGTGCTGACTTGG CTTCTTTGTGCTC
EV016	SEQ ID NO: 597 GGTGATCCTTGAT	SEQ ID NO: 598 GCGTAATACGACT	SEQ ID NO: 596 GGTGATCCTTGATAGTGTTAAGTTTCCAAAATTTAACGAAATTGTACAG

	AGTGTTAAG SEQ ID NO: 599 GCGTAATACGACT CACTATAGGGGTG ATCCTTGATAGTG TTAAG	CACTATAGGCCTC AGCATAAGATGAC ATG SEQ ID NO: 600 CCTCAGCATAAGA TGACATG	CTCAAGTTATCAGATGGAACAGTTAGGTCTGGACAAGTTTTGGAAGTC AGTGGACAGAAGGCGGTTGTCCAAGTTTTTGAAGGCACCTCCGGAATT GATGCTAAAAACACTTTATGTGAATTTACAGGAGATATCTTAAGAACTC CAGTGTCTGAAGATATGTTGGGTCGTGTGTTTAATGGATCTGGAAAGCC TATCGATAAAGGGCCGCCAATCTTAGCTGAAGATTTTCTTGACATTCAA GGTCAACCTATAAATCCTTGGTCTCGTATCTATCCAGAAGAAATGATCC AGACTGGTATTTCTGCGATTGATGTGATGAATTCCATTGCCAGAGGACA AAAGATTCCAATTTTCTCTGCAGCTGGTTTACCCCACAATGAAATCGCT GCTCAAATCTGTAGACAAGCTGGTCTTGTCAAAATCCCAGGGAAATCT GTCTTAGATGATCATGAAGACAACTTTGCTATCGTTTTCGCCGCTATGG GTGTCAATATGGAAACAGCCAGATTCTTCAAGCAAGATTTTGAAGAGA ATGGCTCTATGGAAAATGTGTGCCTATTTTTGAACTTGGCCAATGATCC TACCATTGAAAGAATTATAACACCCCGTTTGACTTTAACAGCGGCTGAA TTTATGGCATATCAATGTGAGAAGCATGTGTTAGTCATATTGACTGACA TGTCATCTTATGCTGAGG

Table 8-AG

Target ID	**Primers Forward 5' → 3'**	**Primers Reverse 5' → 3'**	**dsRNA DNA Sequence (sense strand) 5' → 3'**
AG001	SEQ ID NO: 769 GCGTAATACGACT CACTATAGGGCAT GGATGTTGGACAA ATTGG SEQ ID NO: 771 GCATGGATGTTGG ACAAATTGG	SEQ ID NO: 770 GATTTCCAGTTGG ATGGTGTCG SEQ ID NO: 772 GCGTAATACGACT CACTATAGGGATT TCCAGTTGGATGG TGTCG	SEQ ID NO: 768 GCATGGATGTTGGACAAATTGGGGGGTGTGTTCGCCCCCAGGCCCTCC ACCGGGCCACACAAGCTCAGGGAGTCCCTTCCATTAGTGATTTTCTTGC GTAACAGGTTGAAGTACGCCCTGACAAACTGTGAGGTGACCAAGATCG TTATGCAGAGACTTATTAAGGTCGACGGCAAAGTCAGGACTGATCCTA ACTATCCTGCTGGATTCATGGATGTGATCACCATTGAAAAAACTGGTGA ATTCTTCCGTTTGATCTATGATGTTAAGGGAAGATTCACTATTCACAGG ATCACTGCTGAAGAAGCAAAATACAAATTGTGCAAAGTCCGCAAGGTG CAAACCGGACCAAAAGGTATTCCATTCTTGGTCACCCACGATGGTAGG ACCATTAGGTACCCTGACCCAATGATCAAGGTAAACGACACCATCCAA CTGGAAATC
AG005	SEQ ID NO: 774 GCGTAATACGACT CACTATAGGCAAC ACCAACTCGAGGC	SEQ ID NO: 775 CCTTTTGCCTTCTG GCGTTAG	SEQ ID NO: 773 CAACACCAACTCGAGGCAAAACATCCGTAAATTGATCAAGGATGGTTT GATCATTAAGAAACCGGTGGCAGTGCACTCTAGGGCTCGTGTCCGTAA AAACACAGAAGCTCGCAGGAAGGGAAGGCACTGCGGTTTCGGTAAGA

	AAAAC SEQ ID NO: 776 CAACACCAACTCG AGGCAAAAC	SEQ ID NO: 777 GCGTAATACGACT CACTATAGGCCTT TTGCCTTCTGGCGT TAG	GGAAAGGTACAGCGAACGCTCGTATGCCTCAAAGGAACTATGGATCC AAAGGATGCGTGTCTTGAGGCGTCTCCTGAAAAAATACAGGGAAGCCA AAAAGATCGACAGGCATCTGTACCACGCCCTGTACATGAAGGCCAAGG GTAACGTGTTCAAGAACAAGAGAGTGTTGATGGAATACATCCACAAGA AGAAGGCTGAGAAGGCCCGTGCCAAGATGTTGGCCGACCAAGCTAACG CCAGAAGGCAAAAGG
AG010	SEQ ID NO: 779 GCGTAATACGACT CACTATAGGCAAA CTTTCCAAAGGGT GTTCG SEQ ID NO: 781 CAAACTTTCCAAA GGGTGTTCG	SEQ ID NO: 780 GAAGGATGCCTGG TCATCTTTG SEQ ID NO: 782 GCGTAATACGACT CACTATAGGGAAG GATGCCTGGTCAT CTTTG	SEQ ID NO: 778 CAAACTTTCCAAAGGGTGTTCGCGAAGGACCAGAATGGACATTTGAAG ATGGCTTTCAACGGTACTTTGGAGGTGAAGTGCTCTAGGGAATTAAAA GTTCAAGGCGGTATTGGCTCATGCGTGTCGCTAAATGTAAAAAGTCCTT TGGTAGCGGACACGGAAATAGGCATGGGAAACACCGTGCAATGGAAG ATGTGCACCTTCAACCCTAGCACGACGATGGCGCTGTTTTTCGAGGTGG TCAATCAGCATTCGGCCCCCATTCCTCAAGGTGGTAGAGGATGTATACA GTTTATTACACAATATCAGCACTCGAGTGGCCAAAGGAGGATAAGGGT GACGACGATAGCGAGAAATTGGGCGGACGCATCGGCGAATATTCACCA CATCAGCGCGGGTTTCGATCAGGAACGTGCCGCGGTGATTATGGCCCG GATGGCTGTTTATAGAGGCGGAGACCGATGAGAGTCCCGATGTTTTAAG ATGGGTCGATCGGATGCTGATTCGTTTGTGTCAAAAGTTTGGAGAATAT AACAAAGATGACCAGGCATCCTTC
AG014	SEQ ID NO: 784 GCGTAATACGACT CACTATAGGGAAA AGGCCGAGGAAAT TGATG SEQ ID NO: 786 GAAAAGGCCGAGG AAATTGATG	SEQ ID NO: 785 CAACTGTTGCGAA ATCAGGTCC SEQ ID NO: 787 GCGTAATACGACT CACTATAGGCAAC TGTTGCGAAATCA GGTCC	SEQ ID NO: 783 GAAAAGGCCGAGGAAATTGATGCCAAGGCGGAAGAAGAATTTAACAT TGAAAAGGGCCGCCTTGTGCAACAACAAAGATTGAAGATCATGGAATA CTATGAGAAGAAGGAGAAGCAAGTCGAACTACAAAAGAAAAATTCAAT CCTCCAACATGCTGAACCAAGCCCGTCTTAAGGTTCTGAAAGTCCGCG AAGATCATGTTAGAGCTGTATTGGATGAGGCTCGCAAGAAGCTTGGTG AAGTCACCAGGGATCAAGGCAAATATGCCCAGATTCTGGAATCTTTGA TCCTTCAGGGACTCTACCAGCTTTTCGAGGCAAACGTGACCGTACGCGT CCGCCCACAAGACAGAACCTTAGTCCAATCAGTGCTGCCAACCATCGC AACCAAATACCGTGACGTCACCGGCCGAGATGTACACCTGTCCATCGA TGACGAAACTCAACTGTCCGAATCCGTAACCGGCGGAATCGAACTTTT GTGCAAACAAAACAAAATTAAGGTCTGCAACACCCTGGAGGCACGTTT GGACCTGATTTCGCAACAGTTG
AG016	SEQ ID NO: 789 GCGTAATACGACT CACTATAGGGTGT	SEQ ID NO: 790 CGACCGGCTCTTT CGTAAATG	SEQ ID NO: 788 GTGTTCAACGGATCAGGAAAACCCATTGACAAAGGTCCTCCAATCTTA GCCGAAGATTTCTTGGACATCCAAGGTCAACCCATCAACCCATGGTCG

	TCAACGGATCAGGAAAACC SEQ ID NO: 791 GTGTTCAACGGATCAGGAAAACC	 SEQ ID NO: 792 GCGTAATACGACTCACTATAGGCGACCGGCTCTTTCGTAAATG	CGTATCTACCCGGAAGAAATGATCCAGACCGGTATCTCCGCCATCGAC GTGATGAACTCCATCGCGCGTGGGCAAAAAATCCCCATTTTCTCCGCGG CCGGTTTACCGCACAACGAAATCGCCGCCCAAATCTGTAGACAGGCCG GTTTAGTCAAACTGCCGGGCAAATCGGTAATCGACGATCACGAGGACA ATTTCGCCATCGTGTTCGCCGCCATGGGTGTCAACATGGAAACCGCCCG TTTCTTCAAGCAGGACTTCGAAGAAAACGGTTCCATGGAGAACGTGTG TCTCTTCTTGAATTTGGCCAACGATCCCACCATCGAGAGAATCATCACG CCCCGTTTGGCTCTGACCGCCGCCGAATTTTTGGCTTATCAATGCGAGA AACACGTGCTGGTTATCTTAACTGATATGTCTTCTTACGCCGAGGCTTT GCGTGAAGTATCCGCCGCCAGAGAAGAAGTACCCGGACGTCGTGGGTT CCCCGGTTACATGTACACCGATTTGGCCACCATTTACGAAAGAGCCGGT CG

Table 8-TC

Target ID	**Primers Forward 5' → 3'**	**Primers Reverse 5' → 3'**	**dsRNA DNA Sequence (sense strand) 5' → 3'**
TC001	SEQ ID NO: 864 GCGTAATACGACTCACTATAGGCTGCGAAACAGGCTGAAGTATGC SEQ ID NO: 866 CTGCGAAACAGGCTGAAGTATGC	SEQ ID NO: 865 GGTGTGCCCATTTGCATCCT SEQ ID NO: 867 GCGTAATACGACTCACTATAGGGGTGTGCCCATTTGCATCCT	SEQ ID NO: 863 CTGCGAAACAGGCTGAAGTATGCCTTGACCAACTCAGAAGTGACGAAG ATTGTTATGCAAAGATTGATTAAAGTTGACGGAAAAGTTAGGACAGAC CCCAACTACCCCGCGGGTTTCATGGATGTTGTGACTATTGAGAAAACTG GGGAATTCTTCCGCTTGATTTATGATGTTAAGGGAAGGTTCACAATCCA TCGCATTACTGGAGAAGAGGCCAAATATAAATTGTGCAAAGTGAAGAA AGTACAGACAGGCCCCAAGGGCATTCCCTTCTTGGTGACCCGCGACGG ACGCACTATCAGATACCCAGACCCCATGATCAAAGTGAATGACACCAT TCAATTGGAGATTGCCACTTCGAAAATTCTTGATTTTATCAAATTTGAG TCCGGTAATTTGTGTATGATTACTGGAGGTCGTAACTTGGGGCGTGTCG GTACAGTGGTGAGCCGAGAACGTCACCCAGGTTCCTTCGACATCGTTC ATATTAAGGATGCAAATGGGCACACC
TC002	SEQ ID NO: 869 GCGTAATACGACTCACTATAGGCATCCATGTTGAGGTGGGCA	SEQ ID NO: 870 CTTTGTGAACAGCGGCCATC SEQ ID NO: 872	SEQ ID NO: 868 CATCCATGTTGAGGTGGGCATTTTTGAGGGCGTCCGCTGCGTTTTTCAT CGTTTTGAGTACGGCTGTGTTGGTGTTGGCCCCCTCGAGGGCCTCCCGC TGCATCTCGATGGTGCTGAGGGTGCCATCGATCTGCTGGAGCTGCTTTT CGTAGCGTTTCTTCCTCTTGATGGCCTGGATGGCCGCTGTTCACAAAG

	SEQ ID NO: 871 CATCCATGTTGAG GTGGGCA	GCGTAATACGACT CACTATAGGCTTT GTGAACAGCGGCC ATC	
TC010	SEQ ID NO: 874 GCGTAATACGACT CACTATAGGATGT ACCATTTGCGCCG CTC SEQ ID NO: 876 ATGTACCATTTGC GCCGCTC	SEQ ID NO: 875 ATGTCCTGGTACTT GAGGTTCCTCC SEQ ID NO: 877 GCGTAATACGACT CACTATAGGATGT CCTGGTACTTGAG GTTCCTCC	SEQ ID NO: 873 ATGTCCTGGTACTTGAGGTTCCTCCATTGGGCGATTGTCTCACCGTGGA AAATCAAAATTTGGAAAAATGTGTCCATGAGAAGGATCCGATCGGGTT GAATGGAACTAGTGTCGAGGAGGACGGGTTCAGGGGGGCCGTTGAAA CTATAACTGTACAAAATCGGCTGGATCATAATGAGACTTTGGGTGAGG TCCTCCCGCATCAGCATGTGGCGGTAGAACGAGGTCTCGTCTGGGGAG TTGTTGAAAACTTGGAGGAATTGGGAGCGGCGCAAATGGTACAT
TC014	SEQ ID NO: 879 GCGTAATACGACT CACTATAGGCAAC AGCGCTTGAAGAT CATGG SEQ ID NO: 881 CAACAGCGCTTGA AGATCATGG	SEQ ID NO: 880 ACAAGGCCGTACG AATTTCTGG SEQ ID NO: 882 GCGTAATACGACT CACTATAGGACAA GGCCGTACGAATT TCTGG	SEQ ID NO: 878 CAACAGCGCTTGAAGATCATGGAATATTACGAGAAGGAGAAACC GGTGGAATTGCAGAAGAAAATTCAGTCGTCAAACATGCTGAACCAAGC CCGTTTGAAAGTATTAAAAGTGCGTGAAGACCACGTCCACAATGTGCT GGATGACGCCCGCAAACGTCTGGGCGAAATCACCAATGACCAGGCGAG ATATTCACAACTTTTGGAGTCTCTTATCCTCCAGAGTCTCTACCAGTACT TGGGAATCAGTGATGAGTTGTTTGAGAACAATATAGTGGTGAGAGTCA GGCAACAGGACAGGAGTATAATCCAGGGCATTCTCCCAGTTGTTGCGA CGAAATACAGGGACGCCACTGGTAAAGACGTTCATCTTAAAATCGACG ATGAGAGCCACTTGCCATCCGAAACCACCGGAGGAGTGGTTTTGTATG CGCAAAAGGGTAAAATCAAGATTGACAACACCTTGGAGGCTCGTTTGG ATTTAATTGCACAGCAACTTGTGCCAGAAATTCGTACGGCCTTGT
TC015	SEQ ID NO: 884 GCGTAATACGACT CACTATAGGCGAT ACAGTGTTGCTGA AAGGGAAG SEQ ID NO: 886 CGATACAGTGTTG	SEQ ID NO: 885 TCGGATTCGCCGG CTAATTTAC SEQ ID NO: 887 GCGTAATACGACT CACTATAGGTCGG ATTCGCCGGCTAA	SEQ ID NO: 883 CGATACAGTGTTGCTGAAAGGGAAGCGGCGGAAAGAGACCGTCTGCAT TGTGCTGGCCGACGAAAACTGCCCCGATGAGAAGATCCGGATGAACAG GATCGTCAGGAATAATCTACGGGTTAGGCTCTCTGACGTCGTCTGGATC CAGCCCTGTCCCGACGTCAAATACGGGAAGAGGATCCACGTTTTGCCC ATCGATGACACGGTCGAAGGGCTCGTCGGAAATCTCTTCGAGGGTGTAC TTAAAACCATACTTCCTCGAAGCTTATCGACCAATCCACACAAAGGCGAC GTTTTCATCGTCCGTGGTGGCATGCGAGCCGTTGAATTCAAAGTGGTGG

	CTGAAAGGGAAG	TTTAC	AAACGGAACCGTCACCATATTGTATCGTCGCCCCCGATACCGTCATCCA TTGTGACGGCGATCCGATCAAACGAGAAGAAGAGGAGGAAGCCTTGA ACGCCGTCGGCTACGACGATATCGGCGGTTGTCGCAAACAACTCGCAC AAATCAAAGAAATGGTCGAATTACCTCTACGCCACCCGTCGCTCTTCAA GGCCATTGGCGTGAAACCACCACGTGGTATCCTCTTGTACGGACCTCCA GGTACCGGTAAAACTTTAATCGCACGTGCAGTGGCCAACGAAACCGGT GCTTTCTTCTTCTTAATCAACGGTCCCGAAATTATGAGTAAATTAGCCG GCGAATCCGA

Table 8-MP

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
MP001	SEQ ID NO: 1042 GCGTAATACGACT CACTATAGGGTTT AAACGCACCCAAA GCATGG SEQ ID NO: 1044 GTTTAAACGCACC CAAAGCATGG	SEQ ID NO: 1043 CAATACCAACACG CCCTAAATTGC SEQ ID NO: 1045 GCGTAATACGACT CACTATAGGCAAT ACCAACACGCCCT AAATTGC	SEQ ID NO: 1041 GTTTAAACGCACCCAAAGCATGGATGTTGGACAAATCGGGGGGTGTCT TCGCTCCACGTCCAAGCACCGGTCCACACAAACTTCGTGAATCACTACC GTTATTGATCTTCTTGCGTAATCGTTTGAAGTATGCACTTACTGGTGCC GAAGTCACCAAGATTGTCATGCAAAGATTAATCAAGGTTGATGGCAAA GTCCGTACCGACCCTAATTATCCAGCCGGTTTTATGGATGTTATATCTA TCCAAAAGACCAGTGAGCACTTTAGATTGATCTATGATGTGAAAGGTC GTTTCACCATCCACAGAATTACTCCTGAAGAAGCAAAATACAAGTTGT GTAAAGTAAAGAGGGTACAAACTGGACCCAAAGGTGTGCCATTTTTAA CTACTCATGATGGCCGTACTATTCGCTACCCTGACCCTAACATCAAGGT TAATGACACTATTAGATACGATATTGCATCATCTAAAATTTTGGATCAT ATCCGTTTTGAAACTGGAAACTTGTGCATGATAACTGGAGGTCGCAATT TAGGGCGTGTTGGTATTG
MP002	SEQ ID NO: 1047 GCGTAATACGACT CACTATAGGGGTG GCAAAAAGGAAG AGAAGG SEQ ID NO: 1049 GGTGGCAAAAAGG	SEQ ID NO: 1048 GCTGATTTAAGTG CATCTGCTGC SEQ ID NO: 1050 GCGTAATACGACT CACTATAGGGCTG ATTTAAGTGCATC	SEQ ID NO: 1046 GGTGGCAAAAAGGAAGAGAAGGGACCATCAACCGAAGATGCGATACA AAAGCTTCGATCCACTGAAGAGATGCTGATAAAGAAACAAGAATTTTT AGAAAAAAAAAATTGAACAAGAAGTAGCGATAGCCAAAAAAAATGGTA CAACTAATAAACGAGCTGCATTGCAAGCATTGAAGCGTAAGAAACGGT ACGAACAACAATTAGCCCAAATTGATGGTACCATGTTAACTATTGAAC AACAGCGGGAGGCATTAGAAGGTGCCAACACAAATACAGCAGTATTG ACTACCATGAAAACTGCAGCAGATGCACTTAAATCAGC

	AAGAGAAGG	TGCTGC	
MP010	SEQ ID NO: 1052 GCGTAATACGACT CACTATAGGCAGA CCCTGTTCAGAAT ATG SEQ ID NO: 1054 CAGACCCTGTTCA GAATATG	SEQ ID NO: 1053 GCATTGGGAATCG AGTTTTGAG SEQ ID NO: 1055 GCGTAATACGACT CACTATAGGGCAT TGGGAATCGAGTT TTGAG	SEQ ID NO: 1051 CAGACCCTGTTCAGAATATGATGCATGTTAGTGCTGCATTTGATCAAGA AGCATCTGCCGTTTTAATGGCTCGTATGGTAGTGAACCGTGCTGAAACT GAGGATAGTCCAGATGTGATGCGTTGGGCTGATCGTACGCTTATACGCT TGTGTCAAAAATTTGGTGATTATCAAAAAGATGATCCAAATAGTTTCCG ATTGCCAGAAAACTTCAGTTTATATCCACAGTTCATGTATCATTTAAGA AGGTCTCAATTTCTACAAGTTTTTAATAATAGTCCTGATGAAACATCAT ATTATAGGCACATGTTGATGCGTGAAGATGTTACCCAAAGTTTAATCAT GATACAGCCAATTCTGTATAGCTATAGTTTTAATGGTAGGCCAGAACCT GTACTTTTGGATACCAGTAGTATTCAACCTGATAAAATATTATTGATGG ACACATTTTTCCATATTTTGATATTCCATGGAGAGACTATTGCTCAATG GAGAGCAATGGATTATCAAAATAGACCAGAGTATAGTAACCTCAAGCA GTTGCTTCAAGCCCCCGTTGATGATGCTCAGGAAATTCTCAAAACTCGA TTCCCAATGC
MP016	SEQ ID NO: 1057 GCGTAATACGACT CACTATAGGGTTT TCAATGGCAGTGG AAAGC SEQ ID NO: 1059 GTTTTCAATGGCA GTGGAAAGC	SEQ ID NO: 1058 CGTGGTGTAATGA TACGCTC SEQ ID NO: 1060 GCGTAATACGACT CACTATAGGCGTG GTGTAATGATACG CTC	SEQ ID NO: 1056 GTTTTCAATGGCAGTGGAAAGCCGATAGATAAAGGACCTCCTATTTTG GCTGAAGATTATTTGGATATTGAAGGCCAACCTATTAATCCATACTCCA GAACATATCCTCAAGAAATGATTCAAACTGGTATTTCAGCTATTGATAT CATGAACTCTATTGCTCGTGGACAAAAAATTCCAATATTTTCAGCTGCA GGTTTACCACATAATGAGATTGCTGCTCAAATTTGTAGACAAGCTGGTC TCGTTAAAAAACCTGGTAAATCAGTTCTTGACGATCATGAAGACAATTT TGCTATAGTATTTGCTGCTATGGGTGTTAATATGGAAACAGCCAGATTC TTTAAACAAGATTTTGAGGAAAATGGTTCAATGGAGAATGTTTGTTTGT TCTTGAATTTAGCTAATGATCCTACTATTGAGCGTATCATTACACCACG
MP027	SEQ ID NO: 1062 GCGTAATACGACT CACTATAGGGCTC GTTTGTTTCCATCC AGAAC SEQ ID NO: 1064 GCTCGTTTGTTTCC ATCCAGAAC	SEQ ID NO: 1063 CCAAAAATACCAT CTGCTCCACC SEQ ID NO: 1065 GCGTAATACGACT CACTATAGGCCAA AAATACCATCTGC TCCACC	SEQ ID NO: 1061 GCTCGTTTGTTTCCATCCAGAACTTCCCATCGTGTTAACTGGCTCAGAA GATGGTACCGTCAGAATTTGGCATTCTGGTACTTATCGATTAGAATCAT CATTAAACTATGGGTTAGAACGTGTATGGACAATCTGTTGCTTACGGGG ATCTAATAATGTAGCTCTAGGTTATGATGAAGGAAGTATAATGGTTAA AGTTGGTCGTGAAGAGCCAGCAATGTCAATGGATGTTCATGGGGGTAA AATTGTTTGGGCACGTCATAGTGAAATTCAACAAGCTAACCTTAAAGC GATGCTTCAAGCAGAAGGAGCCGAAATCAAAGATGGTGAACGTTTACC AATACAAGTTAAAGACATGGGTAGCTGTGAAATTTATCCACAGTCAAT

			ATCTCATAATCCGAATGGTAGATTTTTAGTAGTATGTGGTGATGGAGAG TATATTATATATACATCAATGGCTTTGCGTAATAAAGCATTTGGCTCCG CTCAGGATTTTGTATGGTCTTCTGATTCTGAGTATGCCATTAGAGAAAA TTCTTCTACAATCAAAGTTTTTAAAAATTTTAAAGAAAAAAAGTCTTTT AAACCAGAAGGTGGAGCAGATGGTATTTTTGG

Table 8-NL

Target ID	**Primers Forward 5' → 3'**	**Primers Reverse 5' → 3'**	**dsRNA DNA Sequence 5' → 3'**
NL001	SEQ ID NO: 1573 GCGTAATACGACTC ACTATAGGGAAATC ATGGATGTTGGACA AATTGG SEQ ID NO: 1575 GAAATCATGGATGT TGGACAAATTGG	SEQ ID NO: 1574 ACTGAGCTTCAC ACCCTTGCCC SEQ ID NO: 1576 GCGTAATACGAC TCACTATAGGAC TGAGCTTCACAC CCTTGCCC	SEQ ID NO: 1572 GAAATCATGGATGTTGGACAAATTGGGTGGTGTGTATGCACCCCGACC CAGCACAGGTCCACACAAGCTGCGAGAATCTCTCCCACTTGTCATATTT TTGCGTAATCGGCTCAAGTACGCTTTAACTAACTGTGAAGTGAAGAAA ATTGTGATGCAGCGTCTCATCAAGGTTGACGGCAAAGTGAGGACTGAC CCCAACTATCCTGCAGGTTTTATGGACGTTGTTCAAATCGAAAAGACAA ACGAGTTCTTCCGTTTGATCTATGATGTTAAGGGACGTTTCACCATCCA CAGGATCACAGCTGAAGAAGCTAAGTACAAGCTGTGCAAAGTGAAGA GGGTTCAGACAGGACCCAAGGGCATTCCATTTTTGACCACTCACGATG GACGCACCATCAGGTATCCAGACCCCTTAGTAAAAGTCAATGACACCA TCCAATTGGACATTGCCACATCCAAAATCATGGACTTCATCAGATTCGA CTCTGGTAACCTGTGTATGATCACTGGAGGTCGTAACTTGGGTCGTGTG GGCACTGTCGTGAACAGGGAGCGACACCCGGGGTCTTTCGACATCGTG CACATCAAGGACGTGTTGGGACACACTTTTGCCACTAGGTTGAACAAC GTTTTCATCATCGGCAAGGGTAGTAAAGCATACGTGTCTCTGCCCAAGG GCAAGGGTGTGAAGCTCAGT
NL002	SEQ ID NO: 1578 GCGTAATACGACTC ACTATAGGGATGAA AAGGGCCCTACAAC TGGC SEQ ID NO: 1580 GATGAAAAGGGCCC	SEQ ID NO: 1579 CTGATCCACATC CATGTGTTGATG AG SEQ ID NO: 1581 GCGTAATACGAC TCACTATAGGCT	SEQ ID NO: 1577 GATGAAAAGGGCCCTACAACTGGCGAAGCCATTCAGAAACTACGCGAA ACAGAGGAAATGCTGATAAAGAAACAAGACTTTTTAGAAAAGAAAATT GAAGTTGAAATTGGAGTTGCCAGGAAGAATGGAACAAAAAACAAAAG AGCCGCGATCCAGGCACTCAAAAGGAAGAAGAGGTATGAAAAGCAAT TGCAGCAGATCGATGGAACGTTATCAACAATTGAGATGCAGAGAGAGG CCCTCGAAGGAGCCAACACGAATACGGCCGTACTGCAAACTATGAAGA ACGCAGCAGATGCTCTCAAAGCGGCTCATCAACACATGGATGTGGATC AG

	TACAACTGGC	GATCCACATCCA TGTGTTGATGAG	
NL003	SEQ ID NO: 1583 GCGTAATACGACTC ACTATAGGTCCGCG TCGTCCTTACGAGA AGGC SEQ ID NO: 1585 TCCGCGTCGTCCTTA CGAGAAGGC	SEQ ID NO: 1584 TTGACGCGACCA GGTCGGCCAC SEQ ID NO: 1586 GCGTAATACGAC TCACTATAGGTT GACGCGACCAGG TCGGCCAC	SEQ ID NO: 1582 TCCGCGTCGTCCTTACGAGAAGGCACGTCTCGAACAGGAGTTGAAGAT CATCGGAGAGTATGGACTCCGTAACAAGCGTGAGGTGTGGAGAGTCAA ATACGCCCTGGCCAAGATTCGTAAGGCCGCTCGTGAGCTGTTGACTCTG GAAGAGAAGGACCAGAAACGTTTGTTTGAAGGTAACGCCCTGCTGCGT CGCCTGGTGCGTATTGGAGTGTTGGACGAAGGAAGAATGAAGCTCGAT TACGTCTTGGGTTTAAAAATTGAAGATTTCCTTGAACGTCGTCTACAGA CTCAGGTGTACAAACTCGGTTTGGCCAAGTCCATCCATCACGCCCGTGT ACTCATCAGACAAAGACATATCAGAGTGCGCAAACAAGTAGTGAACAT TCCGAGCTTTGTGGTGCGCCTGGACTCGCAGAAGCACATTGACTTCTCG CTGAAGTCGCCGTTCGGCGGTGGCCGACCTGGTCGCGTCAA
NL004	SEQ ID NO: 1588 GCGTAATACGACTC ACTATAGGGGAGTT GGCTGCTGTAAGAA CTG SEQ ID NO: 1590 GGAGTTGGCTGCTG TAAGAACTG	SEQ ID NO: 1589 CTGTTGTTGACTG TTGGATGAGG SEQ ID NO: 1591 GCGTAATACGAC TCACTATAGGCT GTTGTTGACTGTT GGATGAGG	SEQ ID NO: 1587 GGAGTTGGCTGCTGTAAGAACTGTCTGCTCTCACATCGAAAACATGCTG AAGGGAGTCACAAAGGGATTCCTGTACAAGATGCGTGCCGTGTACGCC CATTTCCCCATCAACTGTGTGACGACCGAGAACAACTCTGTGATCGAG GTGCGTAACTTCCTGGGCGAGAAGTACATCCGACGGGTGAGGATGGCG CCCGGCGTCACTGTTACCAACTCGACAAAGCAGAAGGACGAGCTCATC GTCGAAGGAAACAGCATAGAGGACGTGTCAAGATCAGCTGCCCTCATC CAACAGTCAACAACAG
NL005	SEQ ID NO: 1593 GCGTAATACGACTC ACTATAGGCGCAAA CACAAATTCACGTC AAAGC SEQ ID NO: 1595 CGCAAACACAAATT CACGTCAAAGC	SEQ ID NO: 1594 CCTTCGCTTCTTG GCCTCCTTGAC SEQ ID NO: 1596 GCGTAATACGAC TCACTATAGGCC TTCGCTTCTTGGC CTCCTTGAC	SEQ ID NO: 1592 CGCAAACACAAATTCACGTCAAAGCATCAGGAAGCTGATCAAAGACGG TCTTATCATCAAGAAACCGGTTGCAGTACATTCACGTGCTCGCGTTCGT AAAAACACTGAAGCCAGGAGGAAAGGCAGACATTGTGGCTTTGGTAA GAGGAAAGGTACAGCCAACGCCCGTATGCCACAAAAGGTTCTATGGGT GAATCGTATGCGTGTCTTGAGAAGACTGTTGAAAAAATACAGACAAGA TAAGAAAATCGACAGGCATCTGTACCATCACCTTTACATGAAGGCTAA GGGTAACGTATTCAAGAACAAGCGTGTATTGATGGAGTTCATTCATAA GAAGAAGGCCGAGAAAGCAAGAATGAAGATGTTGAACGACCAGGCTG AAGCTCGCAGACAAAAGGTCAAGGAGGCCAAGAAGCGAAGG
NL006	SEQ ID NO: 1598	SEQ ID NO: 1599	SEQ ID NO: 1597

	GCGTAATACGACTCACTATAGGGTGCTTGTGTCAAGTGGTGTGG SEQ ID NO: 1600 GTGCTTGTGTCAAGTGGTGTGG	CGAGATGGGATAGCGTGAGG SEQ ID NO: 1601 GCGTAATACGACTCACTATAGGCGAGATGGGATAGCGTGAGG	GTGCTTGTGTCAAGTGGTGTGGTGGAGTACATTGACACCCTGGAGGAG GAGACGACCATGATAGCGATGTCGCCGGATGACCTGCGTCAGGACAAG GAGTATGCCTACTGTACCACCTACACGCACTGCGAGATCCACCCGGCC ATGATACTCGGTGTGTGCGCCTCTATTATTCCCTTCCCCGATCACAACC AAAGTCCCAGGAACACCTATCAGAGCGCTATGGGGAAACAGGCGATG GGCGTGTACATCACCAACTTCCACGTGCGAATGGACACGCTGGCTCAC GTGCTGTTCTACCCGCACAAGCCACTGGTCACCACTCGCTCCATGGAGT ACCTGCGCTTCAGGGAGCTTCCTGCCGGCATCAACTCTGTGGTCGCCAT CGCCTGCTACACTGGATACAACCAGGAGGACAGTGTCATTCTCAACGC CTCCGCTGTCGAGCGCGGATTCTTCAGATCGGTTTTCTTCCGATCTTAC AAAGATGCAGAATCGAAGCGTATTGGCGACCAAGAGGAGCAATTCGA GAAGCCCACCAGACAGACGTGTCAGGGAATGAGGAATGCCATTTATGA CAAATTGGACGATGATGGCATCATTGCTCCCGGTCTGAGAGTGTCTGGT GACGATGTGGTTATTGGCAAAACCATAACACTGCCCGATAATGATGAC GAGCTGGAAGGTACAACAAAGAGGTTCACGAAGAGAGATGCCAGTAC TTTCCTGCGTAACAGTGAGACGGGAATCGTCGACCAAGTCATGTTAAC CTTGAACTCTGAGGGTTACAAGTTCTGCAAAATTCGAGTCAGGTCTGTG CGTATCCCGCAGATTGGCGATAAGTTCGCTTCCCGACATGGCCAAAAA GGAACGTGTGGAATACAGTATCGTCAAGAGGACATGCCTTTTACAAGC GAGGGAATCGCACCGGATATTATTATCAATCCTCACGCTATCCCATCTC G
NL007	SEQ ID NO: 1603 GCGTAATACGACTCACTATAGGTGAGAGCAATCCTTGACTGTGG SEQ ID NO: 1605 TGAGAGCAATCCTTGACTGTGG	SEQ ID NO: 1604 CCACGGTGAATAGCCACTGC SEQ ID NO: 1606 GCGTAATACGACTCACTATAGGCCACGGTGAATAGCCACTGC	SEQ ID NO: 1602 TGAGAGCAATCCTTGACTGTGGTTTTGAACATCCATCTGAAGTACAACA TGAATGCATTCCTCAAGCTGTACTTGGAATGGACATATTGTGTCAAGCG AAATCCGGTATGGGAAAAACTGCTGTATTTGTGTTGGCGACATTACAG CAAATTGAACCAACTGACAACCAAGTCAGTGTATTGGTCATGTGTCAT ACCAGAGAGCTTGCATTCCAAATCAGCAAAGAGTATGAACGATTTTCG AAATGTATGCCAAATATCAAGGTTGGAGTTTTCTTCGGCGGACTGCCGA TTCAGAGGGATGAGGAGACGTTGAAATTGAACTGTCCTCACATCGTGG TTGGAACACCCGGACGAATTTTGGCGTTGGTACGCAACAAGAAGCTGG ACCTCAAGCATCTCAAGCACTTTGTCCTTGACGAATGTGACAAAATGTT GGAACTGTTAGATATGCGAAGAGATGTGCAGGAAATATTCCGAAACAC GCCGCACAGCAAACAAGTCATGATGTTCAGTGCAACTCTCAGCAAAGA AATTCGTCCAGTCTGCAAGAAATTCATGCAAGATCCGATGGAAGTGTA CGTTGATGACGAGGCCAAGCTGACGCTTCACGGCCTGCAGCAGCACTA

			TGTCAAACTCAAAGAAAACGAAAAGAACACAAAAAGTTATTTGAATTACT TGACATACTTGAATTCAACCAGGTTGTTATATTTGTGAAGTCAGTGCAG CGCTGCATGGCCCTATCGCAACTCCTAACAGAGCAGAACTTCCCTGCA GTGGCTATTCACCGTGG
NL008	SEQ ID NO: 1608 GCGTAATACGACTC ACTATAGGGATGCT GGAGACCTGGAGGT G SEQ ID NO: 1610 GATGCTGGAGACCT GGAGGTG	SEQ ID NO: 1609 GAGCGAGTCTAC AAAATTGCCG SEQ ID NO: 1611 GCGTAATACGAC TCACTATAGGGA GCGAGTCTACAA AATTGCCG	SEQ ID NO: 1607 GATGCTGGAGACCTGGAGGTGTATTAGATGTTTCAAACAGTTTTGCAGT TCCATTTGATGAGGACGACAAAGAAAAGAATGTTTGGTTCTTAGACCA TGATTACTTGGAAAACATGTTCGGGATGTTCAAGAAAGTTAATGCTAG AGAAAAGGTTGTGGGTTGGTACCATACTGGACCCAAACTCCACCAAAA CGATGTTGCAATCAATGAGTTGATTCGTCGTTACTGTCCAAACTGTGTC TTAGTCATAATCGATGCCAAGCCTAAAGATTTGGGTCTACCTACAGAG GCATACAGAGTCGTTGAAGAAATCCATGATGATGGATCGCCAACATCA AAAACATTTGAACATGTGATGAGTGAGATTGGGGCAGAAGAGGCTGAG GAGATTGGCGTTGAACATCTGTTGAGAGACATCAAGATACAACAGTC GGGTCACTGTCACAGCGCGTCACAAATCAGCTGATGGGCTTGAAGGGC TTGCATCTGCAATTACAGGATATGCGAGACTATTTGAATCAGGTTGTCG AAGGAAAGTTGCCAATGAACCATCAAATCGTTTACCAACTGCAAGACA TCTTCAACCTTCTACCCGATATCGGCCACGGCAATTTTGTAGACTCGCT C
NL009	SEQ ID NO: 1613 GCGTAATACGACTC ACTATAGGGCGACT ATGATCGACCGCC SEQ ID NO: 1615 GCGACTATGATCGA CCGCC	SEQ ID NO: 1614 GTGTAAGGGTAG AAGTAGCCCGG SEQ ID NO: 1616 GCGTAATACGAC TCACTATAGGGT GTAAGGGTAGAA GTAGCCCGG	SEQ ID NO: 1612 GCGACTATGATCGACCGCCGGGACGCGGTCAGGTGTGCGACGTCGACG TCAAGAACTGGTTTCCCTGCACCTCTGAGAACAATTTCAACTACCATCA ATCGAGCCCTTGTGTTTTTCTCAAACTGAACAAGATAATTGGTTGGCAA CCGGAGTACTACAATGAGACTGAAGGCTTTCCAGATAATATGCCAGGT GACCTCAAGCGACACATTGCCCAACAGAAGAGTATCAACAAGCTGTTT ATGCAAACAATCTGGATAACTTGCGAAGGAGAGGGTCCTCTAGACAAG GAGAATGCAGGGGAGATCCAGTACATCCCTAGACAGGGATTTCCGGGC TACTTCTACCCTTACAC
NL010	SEQ ID NO: 1618 GCGTAATACGACTC ACTATAGGGCTTGT TGTTCCCGTTGGAT GTC	SEQ ID NO: 1619 GCAACTCCAGTA GATCGGAGAGGT C SEQ ID NO: 1621	SEQ ID NO: 1617 GCTTGTTGTTCCCGTTGGATGTCTGTATCAACCTTTGAAGGAGAGACCT GATCTACCGCCTGTACAGTACGATCCAGTTCTTTGTACTAGGAATACTT GTCGTGCAATTCTGAATCCATTGTGCCAAGTCGACTATCGAGCCAAGCT ATGGGTCTGCAACTTTTGTTTCCAGAGGAATCCTTTCCCCCCTCAATAT GCAGCTATTTCGGAGCAGCATCAACCAGCAGAACTGATACCTTCATTTT

	SEQ ID NO: 1620 GCTTGTTGTTCCCGT TGGATGTC	GCGTAATACGAC TCACTATAGGGC AACTCCAGTAGA TCGGAGAGGTC	CCACCATCGAATACATCATTACCAGAGCGCAAACGATGCCGCCGATGT TCGTGCTGGTGGTGGACACATGTCTGGACGACGAGGAGCTGGGAGCTT TGAAGGACTCACTGCAGATGTCGCTGTCGCTGCCGCCCAATGCACT CATCGGTCTCATCACGTTCGGCAAAATGGTGCAGGTGCACGAGCTTGG CTGCGACGGCTGCTCGAAGAGCTACGTGTTCCGTGGCGTGAAGGACCT GACTGCCAAGCAGATCCAGGACATGTTGGGCATTGGCAAGATGGCCGC CGCTCCACAGCCCATGCAACAGCGCATTCCCGGCGCCGCTCCCTCCGCA CCTGTCAACAGATTTCTTCAGCCTGTCGGAAAGTGCGATATGAGTTTAA CTGATCTGCTTGGGGAATTGCAAAGAGATCCATGGAATGTGGCTCAGG GCAAGAGACCTCTCCGATCTACTGGAGTTGC
NL011	SEQ ID NO: 1623 CCCACTTTCAAGTG YGTRYTRGTCGG SEQ ID NO: 1625 GTTGCCACCCTTGG AGTTGAAG	SEQ ID NO: 1624 GTCCATTGTGAC CTCGGGAGG SEQ ID NO: 1626 GCGTAATACGAC TCACTATAGGGT CCATTGTGACCTC GGGAGG	SEQ ID NO: 1622 GTTGCCACCCTTGGAGTTGAAGTTCACCCCCTTGTATTTCACACAAACA GAGGTGTGATTAGGTTCAATGTGTGGGACACAGCTGGCCAGGAAAAGT TCGGTGGACTTCGTGATGGATATTACATTCAGGGACAATGCGCCATCAT TATGTTTGACGTAACGTCAAGAGTCACCTACAAGAACGTTCCCAACTG GCACAGAGATTTAGTGAGGGTTTGCGAAAACATTCCCATTGTACTATGC GGCAACAAAGTAGACATCAAGGACAGGAAAGTCAAGGCCAAGAGCAT AGTCTTCCATAGGAAGAAGAACCTTCAGTACTACGACATCAGTGCGAA AAGCAACTACAACTTCGAGAAGCCGTTCCTGTGGTTGGCAAAGAAGCT GATCGGTGACCCCAACCTGGAGTTCGTCGCCATGCCCGCCCTCCCTCCCA CCCGAGGTCACAATGGAC
NL012	SEQ ID NO: 1628 GCGTAATACGACTC ACTATAGGGCAGCA GACGCAGGCACAGG TAG SEQ ID NO: 1630 GCAGCAGACGCAGG CACAGGTAG	SEQ ID NO: 1629 GAATTTCCTCTTG AGTTTGCCAGCTT G SEQ ID NO: 1631 GCGTAATACGAC TCACTATAGGGA ATTTCCTCTTGAG TTTGCCAGCTTG	SEQ ID NO: 1627 GCAGCAGACGCAGGCACAGGTAGACGAGGTTGTCGATATAATGAAAA CAAACGTTGAGAAAAGTATTGGAGAGGGATCAAAAACTATCAGAATTGG ATGATCGAGCAGATGCTCTACAGCAAGGCGCTTCACAGTTTGAACAGC AAGCTGGCAAACTCAAGAGGAAATTC
NL013	SEQ ID NO: 1633 GCGTAATACGACTC ACTATAGGCGCAGA	SEQ ID NO: 1634 GGCAACGGCTCT CTTGGATAG	SEQ ID NO: 1632 CGCAGAGCAAGTCTACATCTCTTCACTGGCCTTATTGAAAATGCTTAAG CACGGTCGCGCCGGTGTTCCCATGGAAGTTATGGGCCTAATGCTGGGC

	GCAAGTCTACATCT CTTC SEQ ID NO: 1635 CGCAGAGCAAGTCT ACATCTCTTC	SEQ ID NO: 1636 GCGTAATACGAC TCACTATAGGGG CAACGGCTCTCTT GGATAG	GAATTTGTAGACGACTACACTGTGCGTGTCATTGATGTATTCGCTATGC CACAGAGTGGAACGGGAGTGAGTGTGGAGGCTGTAGACCCGGTGTTCC AAGCGAAGATGTTGGACATGCTAAAGCAGACAGGACGGCCCGAGATG GTGGTGGGCTGGTACCACTCGCACCCGGGCTTCGGCTGCTGGCTGTCGG GTGTCGACATCAACACGCAGGAGAGCTTCGAGCAACTATCCAAGAGAG CCGTTGCC
NL014	SEQ ID NO: 1638 GCGTAATACGACTC ACTATAGGCATTGA GCAAGAAGCCAATG AG SEQ ID NO: 1640 CATTGAGCAAGAAG CCAATGAG	SEQ ID NO: 1639 GAGCGCGACTCT AATCTCGG SEQ ID NO: 1641 GCGTAATACGAC TCACTATAGGGA GCGCGACTCTAA TCTCGG	SEQ ID NO: 1637 CATTGAGCAAGAAGCCAATGAGAAAGCCGAAGAGATCGATGCCAAGG CCGAGGAAGAATTCAACATTGAAAAGGGAAGGCTCGTACAGCACCAG CGCCTTAAAATCATGGAGTACTATGACAGGAAAGAGAAGCAGGTTGAG CTCCAGAAAAAAATCCAATCGTCAAACATGCTGAACCAAGCGCGTCTG AAGGCACTGAAGGTGCGCGAAGATCACGTGAGAAGTGTGCTCGAAGA ATCCAGAAAACGTCTTGGAGAAGTAACCAGAAACCCAGCCAAGTACAA GGAAGTCCTCCAGTATCTAATTGTCCAAGGACTCCTGCAGCTGCTAGAA TCAAACGTAGTACTGCGCGTGCGCGAGGCTGACGTGAGTCTGATCGAG GGCATTGTTGGCTCATGCGCAGAGCAGTACGCGAAGATGACCGGCAAA GAGGTGGTGGTGAAGCTGGACGCTGACAACTTCCTGGCCGCCGAGACG TGTGGAGGCGTCGAGTTGTTCGCCCGCAACGGCCGCATCAAGATCCCC AACACCCTCGAGTCCAGGCTCGACCTCATCTCCCAGCAACTTGTGCCCG AGATTAGAGTCGCGCTC
NL015	SEQ ID NO: 1643 GCGTAATACGACTC ACTATAGGCTGCGA GTGCGCTTGTCCG SEQ ID NO: 1645 CTGCGAGTGCGCTT GTCCG	SEQ ID NO: 1644 GGCCAAAGCGCC TAAGCGC SEQ ID NO: 1646 GCGTAATACGAC TCACTATAGGGG CCAAAGCGCCTA AGCGC	SEQ ID NO: 1642 CTGCGAGTGCGCTTGTCCGACATTGTCTCGATCCAGCCTTGCCCAGACG TCAAGTATGGAAAGCGTATCCATGTGCTGCCCATTGATGATACCGTTGA GGGTCTTACAGGAAATCTGTTCGAAGTGTATTTGAAGCCATACTTCCTG GAAGCATACAGGCCAATTCACAAGGATGATGCATTCATTGTTCGCGGA GGTATGAGAGCGGTCGAATTCAAGGTGGTTGAAACAGATCCATCGCCC TACTGCATTGTCGCGCCAGACACCGTCATCCATTGTGAGGGAGACCCC ATCAAACGTGAGGATGAAGAAGACGCAGCAAACGCAGTCGGCTACGA CGACATTGGAGGCTGCAGAAAGCAGCTGGCGCAGATCAAAGAGATGG TGGAGTTGCCGCTGAGACATCCCAGTCTGTTCAAGGCGATCGGCGTGA AGCCGCCACGAGGCATCCTGCTGTACGGACCACCGGGAACCGGAAAGA CGTTGATAGCGCGCCGTCGCCAACGAAACGGGCGCCTTCTTCTTCCT CATCAACGGACCCGAGATTATGAGCAAATTGGCCGGCGAGTCGGAGAG TAACCTGCGCAAAGCTTTCGAGGAAGCGGACAAAAACGCACCGGCCAT

			CATCTTCATCGATGAGCTGGACGCAATCGCGCCAAAACGCGAGAAGAC GCACGGCGAGGTGGAGCGACGCATCGTGTCGCAGCTGCTGACGCTGAT GGACGGTCTCAAGCAGAGCTCGCACGTGATTGTCATGGCCGCCACCAA TCGGCCCAACTCGATCGATGCCGCGCTTAGGCGCTTTGGCC
NL016	SEQ ID NO: 1648 GCGTAATACGACTC ACTATAGGGACGCC AGTATCAGAAGACA TGC SEQ ID NO: 1650 GACGCCAGTATCAG AAGACATGC	SEQ ID NO: 1649 GATGGAGCCGTT GCGACC SEQ ID NO: 1651 GCGTAATACGAC TCACTATAGGGA TGGAGCCGTTGC GACC	SEQ ID NO: 1647 GACGCCAGTATCAGAAGACATGCTTGGTCGTGTATTCAACGGAAGTGG TAAGCCCATCGACAAAGGACCTCCCATTCTTGCTGAGGATTATCTCGAC ATTCAAGGTCAACCCATCAATCCTTGGTCGCGTATCTATCCCGAGGAAA TGATCCAGACTGGAATTTCAGCCATCGACGTCATGAACTCGATTGCTCG TGGCCAGAAAATCCCCATCTTTTCAGCTGCCGGTCTACCTCACAACGAA ATTGCTGCTCAAATCTGTAGACAGGCTGGTCTTGTCAAACTGCCAGGAA AGTCAGTTCTCGATGACTCTGAGGACAACTTTGCTATTGTATTCGCAGC CATGGGAGTCAACATGGAAACTGCTCGATTCTTCAAACAGGATTTCGA GGAGAACGGCTCTATGGAGAACGTGTGCCTGTTCTTGAACCTGGCGAA CGACCCGACGATCGAGCGTATCATCACACCACGCCTGGCGCTGACGGC CGCCGAGTTCCTGGCCTACCAGTGCGAGAAGCACGTGCTCGTCATCCTC ACCGACATGAGCTCCTACGCCGAGGCGCTGCGAGAGGTGTCCGCCGCC CGCGAGGAGGTGCCCGGCCGTCGTGGTTTCCCCGGTTACATGTACACC GATCTGGCCACCATCTACGAGCGCGCCGGACGAGTCGAGGGTCGCAAC GGCTCCATC
NL018	SEQ ID NO: 1653 GCGTAATACGACTC ACTATAGGGCAAAT GCCTGTGCCACGC SEQ ID NO: 1655 GCAAATGCCTGTGC CACGC	SEQ ID NO: 1654 GCAATACAGCCG ACCACTCCG SEQ ID NO: 1656 GCGTAATACGAC TCACTATAGGGC AATACAGCCGAC CACTCCG	SEQ ID NO: 1652 GCAAATGCCTGTGCCACGCCCACAAATAGAAAGCACACAACAGTTTAT TCGATCCGAGAAAACAACATACTCGAATGGATTCACCACCATTGAGGA GGACTTCAAAGTAGACACTTTCGAATACCGTCTTCTGCGCGAGGTGTCG TTCCGCGAATCTCTGATCAGAAACTACTTGCACGAGGCGGACATGCAG ATGTCGACGGTGGTGGACCGAGCATTGGGTCCCCCCTCGGCGCCACAC ATCCAGCAGAAGCCGCGCAACTCAAAAATCCAGGAGGGCGGCGATGC CGTCTTTTCCATCAAGCTCAGCGCCAACCCCAAGCCTCGGCTGGTCTGG TTCAAGAACGGTCAGCGCATCGGTCAGACGCAGAAACACCAGGCCTCC TACTCCAATCAGACCGCCACGCTCAAGGTCAACAAAGTCAGCGCTCAA GACTCCGGCCACTACACGCTGCTTGCTGAAAATCCGCAAGGATGTACT GTGTCCTCAGCTTACCTAGCTGTCGAATCAGCTGGCACTCAAGATACAG GATACAGTGAGCAATACAGCAGACAAGAGGTGGAGACGACAGAGGCG GTGGACAGCAGCAAGATGCTGGCACCGAACTTTGTTCGCGTGCCGGCC GATCGCGACGCGAGCGAAGGCAAGATGACGCGGTTTGACTGCCGCGTG

			ACGGGCCGACCCTACCCGGACGTGGCCTGGTTCATCAACGGCCAACAG GTGGCTGACGACGCCACGCACAAGATCCTCGTCAACGAGTCTGGCAAC CACTCGCTCATGATCACCGGCGTCACTCGCTTGGACCACGGAGTGGTCG GCTGTATTGC
NL019	SEQ ID NO: 1658 GCGTAATACGACTC ACTATAGGGCTTCA GATTTGGGACACGG C SEQ ID NO: 1660 GCTTCAGATTTGGG ACACGGC	SEQ ID NO: 1659 GAACGCCTGCTC CACATTGG SEQ ID NO: 1661 GCGTAATACGAC TCACTATAGGGA ACGCCTGCTCCA CATTGG	SEQ ID NO: 1657 GCTTCAGATTTGGGACACGGCCGGCCAGGAGCGGTTCCGCACGATCAC ATCGAGCTACTACCGGGGCGCCCACGGCATCATTGTGGTGTACGACTG CACCGACCAGGAGTCGTTCAACAACCTCAAACAGTGGCTCGAGGAGAT TGACCGCTACGCCTGTGATAATGTCAACAAACTGCTCGTCGGCAACAA GTGTGATCAGACCAACAAAAAGGTCGTCGACTATACACAGGCTAAGGA ATACGCCGACCAGCTGGGCATTCCGTTCCTGGAGACGTCGGCGAAGAA CGCGACCAATGTGGAGCAGGCGTTC
NL021	SEQ ID NO: 1663 GCGTAATACGACTC ACTATAGGCGTCAG TCTCAATTCTGTCAC CG SEQ ID NO: 1665 CGTCAGTCTCAATT CTGTCACCG	SEQ ID NO: 1664 CTTCTAGTTCATC CAGGTCGCG SEQ ID NO: 1666 GCGTAATACGAC TCACTATAGGCTT CTAGTTCATCCA GGTCGCG	SEQ ID NO: 1662 CGTCAGTCTCAATTCTGTCACCGATATCAGCACCACGTTCATTCTCAAG CCACAAGAGAACGTGAAGATAACGCTTGAGGGCGCACAGGCCTGTTTC ATTTCACACGAACGACTTGTGATCTCACTGAAGGGAGGAGAACTCTAT GTTCTAACTCTCTATTCCGATAGTATGCGCAGTGTGAGGAGTTTTCATC TGGAGAAAGCTGCTGCCAGTGTCTTGACTACTTGTATCTGTTTGTGA GGAGAACTATCTGTTCCTTGGTTCCCGTCTTGGAAACTCACTGTTGCTC AGGTTTACTGAGAAGGAATTGAACCTGATTGAGCCGAGGGCCATCGAA AGCTCACAGTCCCAGAATCCGGCCAAGAAGAAAAAGCTGGATACTTTG GGAGATTGGATGGCATCTGACGTCACTGAAATACGCGACCTGGATGAA CTAGAAG
NL022	SEQ ID NO: 1668 GCGTAATACGACTC ACTATAGGCTCACG AGAGGACGTTGCAC AC SEQ ID NO: 1670 CTCACGAGAGGACG	SEQ ID NO: 1669 CAGACGGAAGCA CTTGCCG SEQ ID NO: 1671 GCGTAATACGAC TCACTATAGGCA GACGGAAGCACT	SEQ ID NO: 1667 CTCACGAGAGGACGTTGCACACTGATATACTGTTCGGTTTGGTGAAAG ATGTCGCCCGATTCAGACCTGACTTGAAGCTGCTCATATCAAGCGCCAC ACTGGATGCTCAGAAATTCTCCGAGTTTTTCGACGATGCACCCATCTTC AGGATTCCGGGCCGTAGATTTCCGGTGGACATCTACTACACAAAGGCG CCCGAGGCTGACTACGTGGACGCATGTGTCGTTTCGATCCTGCAGATCC ACGCCACTCAGCCGCTGGGAGACATCCTGGTCTTCCTCACCGGTCAGG AGGAGATCGAAACCTGCCAGGAGCTGCTGCAGGACAGAGTGCGCAGG CTTGGGTCTCGTATCAAGGAGCTGCTCATATTGCCCGTCTATTCCAACC

	TTGCACAC	TGCCG	TACCCAGTGATATGCAGGCAAAGATTTTCCTGCCCACTCCACCAAATGC TAGAAAGGTAGTATTGGCCACAAATATTGCAGAAACCTCATTGACCAT CGACAATATAATCTACGTGATTGATCCTGGTTTTTGTAAGCAGAATAAC TTCAATTCAAGGACTGGAATGGAATCGCTTGTTGTAGTGCCTGTTTCAA AGGCATCGGCCAATCAGCGAGCAGGGCGGGCGGGACGGGTGGCGGCC GGCAAGTGCTTCCGTCTG
NL023	SEQ ID NO: 1673 GCGTAATACGACTC ACTATAGGGTCCTC GGACGGGAGGTCC SEQ ID NO: 1675 GTCCTCGGACGGGA GGTCC	SEQ ID NO: 1674 GCAATGTTGTCCT TGAGCCAGC SEQ ID NO: 1676 GCGTAATACGAC TCACTATAGGGC AATGTTGTCCTTG AGCCAGC	SEQ ID NO: 1672 GTCCTCGGACGGGAGGTCCACGTGTTTACCGGGATTCCGTTTGCGAAAC CTCCCATCGGTCCGTTGCGATTCCGTAAACCGGTTCCCGTCGACCCGTG GCACGGCGTTCTGGATGCGACCGCGCTTCCCAACACAGCTGCTACCAGGA ACGGTACGAGTATTTCCCGGGCTTCGAGGGAGAGGAAATGTGGAATCC GAATACGAATTTGTCCGAAGATTGTCTGTATTTGAACATATGGGTGCCG CACCGGTTGAGAATCCGACACAGAGCCAACAGCGAGGAGAATAAACC AAGAGCGAAGGTGCCGGTGCTGATCTGGATCTACGGCGGGGGTTACAT GAGCGGCACAGCTACACTGGACGTGTACGATGCTGACATGGTGGCCGC CACGAGTGACGTCATCGTCGCCTCCATGCAGTACCGAGTGGGTGCGTTC GGCTTCCTCTACCTCGCACAGGACTTGCCTCGAGGCAGCGAGGAGGCG CCGGGCAACATGGGGCTCTGGGACCAGGCCCTTGCCATCCGCTGGCTC AAGGACAACATTGC
NL027	SEQ ID NO: 1678 GCGTAATACGACTC ACTATAGGAGAAGA CGGCACGGTGCG SEQ ID NO: 1680 AGAAGACGGCACGG TGCG	SEQ ID NO: 1679 CAATCCAGTTTTT ACAGTTTCGTGC SEQ ID NO: 1681 GCGTAATACGAC TCACTATAGGCA ATCCAGTTTTTAC AGTTTCGTGC	SEQ ID NO: 1677 AGAAGACGGCACGGTGCGTATTTGGCACTCGGGCACCTACAGGCTGGA GTCCTCGCTGAATTATGGCCTCGAAAGAGTGTGGACCATTTGCTGCATG CGAGGATCCAACAATGTGGCTCTTGGCTACGACGAAGGCAGCATAATG GTGAAGGTGGGTCGGGAGGAGCCGGCCATCTCGATGGATGTGAACGGT GAGAAGATTGTGTGGGCGCGCCACTCGGAGATACAACAGGTCAACCTC AAGGCCATGCCGGAGGGCGTCGAAATCAAAGATGGCGAACGACTGCC GGTCGCCGTTAAGGATATGGGCAGCTGTGAAATATATCCGCAGACCAT CGCTCATAATCCCAACGGCAGATTCCTAGTCGTTTGTGGAGATGGAGA GTACATAATTCACACATCAATGGTGCTAAGAAATAAGGCGTTTGGCTC GGCCCAAGAGTTCATTTGGGGACAGGACTCGTCCGAGTATGCTATCAG AGAAGGAACATCCACTGTCAAAGTATTCAAAAACTTCAAAGAAAAGAA ATCATTCAAGCCAGAATTTGGTGCTGAGAGCATATTCGGCGGCTACCTG CTGGGAGTTTGTTCGTTGTCTGGACTGGCGCTGTACGACTGGGAGACCC TGGAGCTGGTGCGTCGCATCGAGATCCAACCGAAACACGTGTACTGGT CGGAGAGTGGGGAGCTGGTGGCGCTGGCCACTGATGACTCCTACTTTG

			TGCTCCGCTACGACGCACAGGCCGTGCTCGCTGCACGCGACGCCGGTG ACGACGCTGTCACGCCGGACGGCGTCGAGGATGCATTCGAGGTCCTTG GTGAAGTGCACGAAACTGTAAAAACTGGATTG

Table 8-CS

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
CS001	SEQ ID NO: 2041 TAAAGCATGGATG TTGGACAAACTGG G SEQ ID NO: 2043 GCGTAATACGACT CACTATAGGTAAA GCATGGATGTTGG ACAAACTGGG	SEQ ID NO: 2042 GCGTAATACGACT CACTATAGGGGTG AGTCGCACGCCCT TGCC SEQ ID NO: 2044 GGTGAGTCGCACG CCCTTGCC	SEQ ID NO: 2040 TAAAGCATGGATGTTGGACAAACTGGGTGGCGTGTACGCGCCGCGGCC GTCGACCGGCCCCCACAAGTTGCGCGAGTGCCTGCCGCTGGTGATCTTC CTCAGGAACCGGCTCAAGTACGCGCTCACCGGAAATGAAGTGCTTAAG ATTGTAAAGCAGCGACTTATCAAAGTTGACGGCAAAGTCAGGACAGAC CCCACATATCCCGCTGGATTTATGGATGTTGTTTCCATTGAAAAGACAA ATGAGCTGTTCCGTCTTATATATGATGTCAAAGGCAGATTTACTATTCA CCGTATTACTCCTGAGGAGGCTAAATACAAGCTGTGCAAGGTGCGGCG CGTGGCGACGGGCCCCAAGAACGTGCCTTACCTGGTGACCCACGACGG ACGCACCGTGCGATACCCCGACCCACTCATCAAGGTCAACGACTCCAT CCAGCTCGACATCGCCACCTCCAAGATCATGGACTTCATCAAGTTTGAA TCTGGTAACCTATGTATGATCACGGGAGGCCGTAACTTGGGGCGCGTG GGCACCATCGTGTCCCGCGAGCGACATCCCGGGTCCTTCGACATCGTGC ATATACGGGACTCCACCGGACATACCTTCGCTACCAGATTGAACAACG TGTTCATAATCGGCAAGGGCACGAAGGCGTACATCTCGCTGCCGCGCG GCAAGGGCGTGCGACTCACC
CS002	SEQ ID NO: 2046 CAAGAAGGAGGA GAAGGGTCCATCA AC SEQ ID NO: 2048 GCGTAATACGACT CACTATAGGCAAG AAGGAGGAGAAG GGTCCATCAAC	SEQ ID NO: 2047 GCGTAATACGACT CACTATAGGCTTG TCTACATCGATAT CCTTGTGGGC SEQ ID NO: 2049 CTTGTCTACATCG ATATCCTTGTGGG C	SEQ ID NO: 2045 CAAGAAGGAGGAGAAGGGTCCATCAACACACGAAGCTATACAGAAAT TACGCGAAACGGAAGAGTTATTGCAGAAGAAACAAGAGTTTCTAGAGC GAAAGATCGACACTGAATTACAAACGGCGAGAAAACATGGCACAAAG AATAAGAGAGCTGCCATTGCGGCACTGAAGCGCAAGAAGCGTTATGAA AAGCAGCTTACCCAGATTGATGGCACGCTTACCCAAATTGAGGCCCAA AGGGAAGCGCTAGAAGGAGCTAACACCAATACACAGGTGCTTAACACT ATGCGAGATGCTGCTACCGCTATGAGACTCGCCCACAAGGATATCGAT GTAGACAAG

CS003	SEQ ID NO: 2051 TGGTCTCCGCAAC AAGCGTGAGG SEQ ID NO: 2053 GCGTAATACGACT CACTATAGGTGGT CTCCGCAACAAGC GTGAGG	SEQ ID NO: 2052 GCGTAATACGACT CACTATAGGCGAA CGGAGACTTCAGC GAGAAGTCA SEQ ID NO: 2054 CGAACGGAGACTT CAGCGAGAAGTCA	SEQ ID NO: 2050 TGGTCTCCGCAACAAGCGTGAGGTGTGGAGGGTGAAGTACACGCTGGC CAGGATCCGTAAGGCTGCCCGTGAGCTGCTCACACTCGAGGAGAAAGA CCCTAAGAGGTTATTCGAAGGTAATGCTCTCCTTCGTCGTCTGGTGAGG ATCGGTGTGTTGGATGAGAAGCAGATGAAGCTCGATTATGTACTCGGT CTGAAGATTGAGGACTTCTTGGAACGTCGTCTCCAGACTCAGGTGTTCA AGGCTGGTCTAGCTAAGTCTATCCATCATGCCCGTATTCTTATCAGACA GAGGCACATCCGTGTCCGCAAGCAAGTTGTGAACATCCCTTCGTTCATC GTGCGGCTGGACTCTGGCAAGCACATTGACTTCTCGCTGAAGTCTCCGT TCG
CS006	SEQ ID NO: 2056 GGATGATGATGGT ATAATTGCACCAG GG SEQ ID NO: 2058 GCGTAATACGACT CACTATAGGGGAT GATGATGGTATAA TTGCACCAGGG	SEQ ID NO: 2057 GCGTAATACGACT CACTATAGGCGTT AAATGGTGTAGCA TCACCTATTTCACC SEQ ID NO: 2059 CGTTAAATGGTGT AGCATCACCTATT TCACC	SEQ ID NO: 2055 GGATGATGATGGTATAATTGCACCAGGGATTCGTGTATCTGGTGACGA TGTAGTCATTGGAAAAACTATAACTTTGCCAGAAAACGATGATGAGCT GGAAGGAACATCAAGACGATACAGTAAGAGAGATGCCTCTACATTCTT GCGAAACAGTGAAACTGGTATTGTTGACCAAGTTATGCTTACACTTAAC AGCGAAGGATACAAATTTTGTAAAATACGTGTGAGATCTGTGAGAATC CCACAAATTGGAGACAAATTTGCTTCTCGTCATGGTCAAAAAGGGACT TGTGGTATTCAATATAGGCAAGAAGATATGCCTTTCACTTGTGAAGGAT TGACACCAGATATTATCATCAATCCACATGCTATCCCCTCTCGTATGAC AATTGGTCACTTGATTGAATGTATTCAAGGTAAGGTCTCCTCAAATAAA GGTGAAATAGGTGATGCTACACCATTTAACG
CS007	SEQ ID NO: 2061 CTTGTTGAAACCA GAGATTTTGAGGG C SEQ ID NO: 2063 GCGTAATACGACT CACTATAGGCTTG TTGAAACCAGAGA TTTTGAGGGC	SEQ ID NO: 2062 GCGTAATACGACT CACTATAGGCGGC ATGTCATAATTGA AGACTATGTTGAC TC SEQ ID NO: 2064 CGGCATGTCATAA TTGAAGACTATGT TGACTC	SEQ ID NO: 2060 CTTGTTGAAACCAGAGATTTTGAGGGCTATCGTCGATTGCGGTTTCGAG CACCCTTCAGAAGTTCAACATGAATGTATTCCCCAAGCTGTTTTGGGAA TGGATATTCTTTGTCAAAGCTAAATCCGGAATGGGAAAAACCGCCGTA TTTGTTTTAGCAACACTGCAACAGCTAGAACCTTCAGAAAACCATGTTT ACGTATTAGTAATGTGCCATACAAGGGAACTCGCTTTCCAAATAAGCA AGGAATATGAGAGGTTCTCTAAATATATGGCTGGTGTTAGAGTATCTGT ATTCTTTGGTGGGATGCCAATTCAGAAAGATGAAGAAGTATTGAAGAC AGCCTGCCCGCACATCGTTGTTGGTACTCCTGGCAGAATATTAGCATTG GTTAACAACAAGAAACTGAATTTAAAACACCTGAAACACTTCATCCTG GATGAATGTGACAAAATGCTTGAATCTCTAGACATGAGACGTGATGTG

			CAGGAAATATTCAGGAACACCCCTCACGGTAAGCAGGTCATGATGTTT TCTGCAACATTGAGTAAGGAGATCAGACCAGTCTGTAAGAAATTTATG CAAGATCCTATGGAAGTTTATGTGGATGATGAAGCTAAACTTACATTGC ACGGTTTGCAGCAACATTATGTTAAACTCAAGGAAAATGAAAAGAATA AGAAGTTATTTGAACTTTTGGATGTACTGGAGTTCAACCAAGTTGTCAT ATTTGTAAAGTCAGTGCAGCGCTGCATAGCTCTCGCACAGCTGCTGACA GACCAAAACTTCCCAGCTATTGGTATACACCGAAATATGACTCAAGAT GAGCGTCTCTCCCGCTATCAGCAGTTCAAAGATTTCCAGAAGAGGATC CTTGTTGCGACAAATCTTTTTGGACGGGGTATGGACATTGAAAGAGTCA ACATAGT CTTCAATTAT GACATGCCG
CS009	SEQ ID NO: 2066 ACGTTTCTGCAGC GGCTGGACTC SEQ ID NO: 2068 GCGTAATACGACT CACTATAGGACGT TTCTGCAGCGGCT GGACTC	SEQ ID NO: 2067 GCGTAATACGACT CACTATAGGGATA ATTCTTATCGTACG CTGTCATATTCCTG SEQ ID NO: 2069 GATAATTCTTATC GTACGCTGTCATA TTCCTG	SEQ ID NO: 2065 ACGTTTCTGCAGCGGCTGGACTCACGGGAGCCCATGTGGCAGCTGGAC GAGAGCATCATCGGCACACCAACCCCGGGCTCGGCTTCCGGCCCACGCCG CCAGAGGTCGCCAGCAGCGTCATCTGGTATAAAGGCAACGACCCCAAC AGCCAACAATTCTGGGTGCAAGAAACCTCCAACTTTCTAACCGCGTAC AAACGAGACGGTAAGAAAGCAGGAGCAGGCCAGAACATCCACAACTG TGATTTCAAACTGCCTCCTCCGGCCGGTAAGGTGTGCGACGTGGACATC AGCGCCTGGAGTCCCTGTGTAGAGGACAAGCACTTTGGATACCACAAG TCCACGCCCTGCATCTTCCTCAAACTCAACACAAGATCTTCGGCTGGAGGC CGCACTTCTACAACAGCTCCGACAGCCTGCCCACTGACATGCCCGACG ACTTGAAGGAGCACATCAGGAATATGACAGCGTACGATAAGAATTATC
CS011	SEQ ID NO 2071 CGACACTTGACTG GAGAGTTCGAGA SEQ ID NO: 2073 GCGTAATACGACT CACTATAGGCGAC ACTTGACTGGAGA GTTCGAGA	SEQ ID NO: 2072 GCGTAATACGACT CACTATAGGCTCT AGGTTACCATCAC CGATCAACT SEQ ID NO: 2074 CTCTAGGTTACCA TCACCGATCAACT	SEQ ID NO: 2070 CGACACTTGACTGGAGAGTTCGAGAAAAGATATGTCGCCACATTAGGT GTCGAGGTGCATCCCTTAGTATTCCACACAAATAGAGGCCCTATAAGG TTTAATGTATGGGATACTGCTGGCCAAGAAAAGTTTGGTGGTCTCCGAG ATGGTTACTATATCCAAGGTCAATGTGCCATCATCATGTTCGATGTAAC GTCTCGTGTCACCTACAAAAATGTACCCAACTGGCACAGAGATTTAGT GCGAGTCTGTGAAGGCATTCCAATTGTTCTTTGTGGCAACAAAGTAGAT ATCAAGGACAGAAAAGTCAAAGCAAAAACTATTGTTTTCCACAGAAAA AAGAACCTTCAGTATTATGACATCTCTGCCAAGTCAAACTACAATTTCG AGAAACCCTTCCTCTGGTTAGCGAGAAAGTTGATCGGTGATGGTAACC TAGAG
CS013	SEQ ID NO: 2076 TGCCGAACAGGTA TACATCTCGTCTTT	SEQ ID NO: 2077 GCGTAATACGACT	SEQ ID NO: 2075 TGCCGAACAGGTATACATCTCGTCTTTGGCCCTGTTGAAGATGTTAAAA CACGGGCGCGCCGGTGTTCCAATGGAAGTTATGGGACTTATGTTAGGT

	GG SEQ ID NO: 2078 GCGTAATACGACT CACTATAGGTGCC GAACAGGTATACA TCTCGTCTTTGG	CACTATAGGCCAC TACAGCTACAGCA CGTTCAGAC SEQ ID NO: 2079 CCACTACAGCTAC AGCACGTTCAGAC
CS014	SEQ ID NO: 2081 CAGATCAAGCATA TGATGGCCTTCAT CGA SEQ ID NO: 2083 GCGTAATACGACT CACTATAGGCAGA TCAAGCATATGAT GGCCTTCATCGA	SEQ ID NO: 2080 AGATCAAGCATATGATGGCCTTCATCGAACAAGAGGCTAATGAAAAGG CCGAGGAAATCGATGCAAAGGCCGAAGAGGAGTTCAACATTGAAAAA GGCCGCCTGGTGCAGCAGCGGCTCAAGATCATGGAATACTACGAA AAGAAAGAGAAACAAGTGGAACTCCAGAAAAAGATCCAATCTTCGAA CATGCTGAATCAAGCCCGTCTGAAGGTGCTCAAAGTGCGTGAGGACCA CGTACGCAACGTTCTCGACGAGGCTCGCAAGCGCCTGGCTGAGGTGCC CAAAGACGTGAAACTTTACACAGATCTGCTGGTCACGCTCGTCGTACA AGCCCTATTCCAGCTCATGGAACCCACAGTAACAGTTCGCGTTAGGCA GGCGGACGTCTCCTTAGTACAGTCCATATTGGGCAAGGCACAGCAGGA TTACAAAGCAAAGATCAAGAAGGACGTTCAATTGAAGATCGACACCGA GAATTCCCTGCCCGCCGATACTTGTGGCGGAGTGGAACTTATTGCTGCT AGAGGGCGTATTAAGATCAGCAACACTCTGGAGTCTCGTCTGGAGCTG ATAGCCCAACAACTGTTGCCCGAAATACGTACCGCATTGTTC
CS015	SEQ ID NO: 2086 ATCGTGCTTTCAG ACGATAACTGCCC C SEQ ID NO: 2088 GCGTAATACGACT CACTATAGGATCG TGCTTTCAGACGA TAACTGCCCC	SEQ ID NO: 2087 GCGTAATACGACT CACTATAGGCCAT TACGATCACGTGC GATGACTTC SEQ ID NO: 2089 CCATTACGATCAC GTGCGATGACTTC	SEQ ID NO: 2085 ATCGTGCTTTCAGACGATAACTGCCCCGATGAGAAGATCCGCATGAAC CGCGTCGTGCGAAACAACTTGCGTGTACGCCTGTCAGACATAGTCTCCA TAGCGCCTTGTCCATCGGTCAAATATGGGAAACGGGTACATATATTGCC CATTGATGATTCTGTCGAGGGTTTGACTGGAAATTTATTCGAAGTCTAC TTGAAACCATACTTCATGGAAGCTTATCGGCCTATCCATCGCGATGACA CATTCATGGTTCGCGGGGGCATGAGGGCTGTTGAATTCAAAGTGGTGG AGACTGATCCGTCGCCGTATTGCATCGTCGCTCCCGACACAGTGATACA CTGCGAAGGAGACCCTATCAAACGAGAGGAAGAAGAAGCCCTAA ACGCCGTAGGGTACGACGACATCGGTGGCTGTCGTAAACAGCTCGCTC AGATCAAAGAGATGGTCGAGTTGCCTCTAAGGCATCCGTCGCTGTTCA AGGCAATTGGTGTGAAGCCGCCACGTGGAATCCTCATGTATGGGCCGC

			CTGGTACCGGCAAAACTCTCATTGCTCGGGCAGTGGCTAATGAAACTG GTGCATTCTTCTTTCTGATCAACGGGCCGGAGATCATGTCCAAACTCGC GGGCGAGTCCGAATCGAACCTTCGCAAGGCATTCGAGGAAGCGGACAA GAACTCCCCGGCTATAATCTTCATCGATGAACTGGATGCCATCGCACCA AAGAGGGAGAAGACTCACGGTGAAGTGGAGCGTCGTATTGTGTCGCAA CTACTTACTCTTATGGATGGAATGAAGAAGTCATCGCACGTGATCGTAA TGG
CS016	SEQ ID NO: 2091 AGGATGGAAGCGG GGATACGTTTGAG SEQ ID NO: 2093 GCGTAATACGACT CACTATAGGAGGA TGGAAGCGGGGAT ACGTTTGAG	SEQ ID NO: 2092 GCGTAATACGACT CACTATAGGGCAC CCCTGTCTCCGAA GACATGTT SEQ ID NO: 2094 GCACCCCTGTCTC CGAAGACATGTT	SEQ ID NO: 2090 AGGATGGAAGCGGGGATACGTTTGAGCATCTCCTTGGGGAAGATACGG AGCAGCTGCCAGCCGATGTCCAGCGACTCGAATACTGTGCGGTTCTCGT AGTTGCCCTGTGTGATGAAGTTCTTCTCGAACTTGGTGAGGAACTCGAG GTAGAGCAGATCGTCGGGTGTCAGGGCTTCCTCACCGACGACAGCCTT CATGGCCTGCACGTCCTTACCGATGGCGTAGCAGGCGTACAGCTGGTT GGAAACATCAGAGTGGTCCTTGCGGGTCATTCCCTCACCGATGGCAGA CTTCATGAGACGAGACAGGGAAGGCAGCACGTTTACAGGCGGGTAGAT CTGTCTGTTGTGGAGCTGACGGTCTACGTAGATCTGTCCCTCAGTGATG TAGCCCGTTAAATCGGGAATAGGATGGGTGATGTCGTCGTTGGGCATA GTCAAGATGGGGATCTGCGTGATGGATCCGTTTCTACCCTCTACACGCC CGGCTCTCTCGTAGATGGTGGCCAAATCGGTGTGTACATGTAACCTGGGA AACCACGTCGTCCGGGCACCTCCTCACGGGCGGCGGACACTTCACGCA GAGCCTCCGCGTACGAAGACATGTCAGTCAAGATTACCAGCACGTGTT TCTCACACTGGTAGGCCAAGAACTCAGCAGCAGTCAAGGCCAAACGTG GTGTGATGATTCTCTCAATAGTGGGATCGTTGGCCAGATTCAAGAACA GGCACACGTTCTCCATGGAGCCGTTCTCCTCGAAGTCCTGCTTGAAGAA CCGGGCCGTCTCCATGTTCACACCCATGGCGGCGAACACGATGGCAAA GTTGTCCTCGTGGTCGTCCAGCACAGATTTGCCGGGGATCTTTACAAGA CCGGCTTGCCTACAGATCTGGGCGGCAATTTCGTTGTGTGGCAGACCGG CAGCCGAGAAAATGGGGATCTTTTGCCCGCGAGCAATGGAGTTCATCA CGTCGATAGCGGAGATACCAGTCTGGATCATTTCCTCAGGGTAGATAC GGGACCAGGGGTTGATGGGCTGTCCCTGGATGTCCAAAAAGTCTTCAG CAAGGATTGGGGGACCTTTGTCAATGGGTTTTCCAGAGCCGTTGAATAC GCGACCCAACATGTCTTCGGAGACAGGGGTGC
CS018	SEQ ID NO: 2096 CGTCCCTGTACCT GCTCAGCAATCCC	SEQ ID NO: 2097 GCGTAATACGACT CACTATAGGCAGC	SEQ ID NO: 2095 CGTCCCTGTACCTGCTCAGCAATCCCAACAGCAGCAGAGTTACCGCCA CGTCAGCGAGAGCGTCGAACACAAATCCTACGGCACGCAAGGGTACAC

	A SEQ ID NO: 2098 GCGTAATACGACT CACTATAGGCGTC CCTGTACCTGCTC AGCAATCCCA	GTCGAGGCCCCAC CTT SEQ ID NO: 2099 CAGCGTCGAGGCC CCACCTT	CACTTCGGAACAGACCAAGCAGACACAGAAGGTGGCGTACACCAACG GTTCCGACTACTCTTCCACGGACGACTTTAAGGTGGATACGTTCGAATA CAGACTCCTCCGAGAAGTTTCGTTCAGGGAATCCATCACGAAGCGGTA CATTGGCGAGACAGACATTCAGATCAGCACGGAGGTCGACAAGTCTCT CGGTGTGGTGACCCCTCCTAAGATAGCACAAAAGCCTAGGAATTCCAA GCTGCAGGAGGGAGCCGACGCTCAGTTTCAAGTGCAGCTGTCGGGTAA CCCGCGGCCACGGGTGTCATGGTTCAAGAACGGGCAGAGGATAGTCAA CTCGAACAAACACGAAATCGTCACGACACATAATCAAACAATACTTAG GGTAAGAAACACACAAAAGTCTGATACTGGCAACTACACGTTGTTGGC TGAAAATCCTAACGGATGCGTCGTCACATCGGCATACCTGGCCGTGGA GTCGCCTCAAGAAACTTACGGCCAAGATCATAAATCACAATACATAAT GGACAATCAGCAAACAGCTGTAGAAGAAAGAGTAGAAGTTAATGAAA AAGCTCTCGCTCCGCAATTCGTAAGAGTCTGCCAAGACCGCGATGTAA CGGAGGGGAAAATGACGCGATTCGATTGCCGCGTCACGGGCAGACCTT ACCCAGAAGTCACGTGGTTCATTAACGATAGACAAATTCGAGACGATT ATWATCATAAGATATTAGTAAACGAATCGTGTAATCATGCACTTATGA TTACAAACGTCGATCTCAGTGATAGTGGCGTAGTATCATGTATAGCACG CAACAAGACCGGCGAAACTTCGTTTCAGTGTAGGCTGAACGTGATAGA GAAGGAGCAAGTGGTCGCTCCCAAATTCGTGGAGCGGTTCAGCACGCT CAACGTGCGCGAGGGCGAGCCCGTGCAGCTGCACGCGCGCGCCGTCGG CACGCCTACGCCACGCATCACATGGCAGAAGGACGGCGTTCAAGTTAT ACCCAATCCAGAGCTACGAATAAATACCGAAGGTGGGGCCTCGACGCT G

Table 8-PX

Target ID	**Primers Forward 5' → 3'**	**Primers Reverse 5' → 3'**	**dsRNA DNA Sequence (sense strand) 5' → 3'**
PX001	SEQ ID NO: 2340 GCGTAATACGACT CACTATAGGCGAG GTGCTGAAGATCG TGAAG SEQ ID NO: 2342 CGAGGTGCTGAAG	SEQ ID NO: 2341 CTTGCCGATGATG AACACGTTG SEQ ID NO: 2343 GCGTAATACGACT CACTATAGGCTTG	SEQ ID NO: 2339 CGAGGTGCTGAAGATCGTGAAGCAGCGCCTCATCAAGGTGGACGGCAA GGTCCGCACCGACCCCACCTACCCGGCTGGATTCATGGATGTTGTGTCG ATTGAAAAGACCAATGAGCTGTTCCGTCTGATCTACGATGTGAAGGGA CGCTTCACCATCCACCGCATCACTCCCGAGGAGGCCAAGTACAAGCTG TGCAAGGTGAAGCGCGTGGCGACGGGCCCCAAGAACGTGCCGTACATC GTGACGCACAACGGCCGCACGCTGCGCTACCCCGACCCGCTCATCAAG

	ATCGTGAAG	CCGATGATGAACA CGTTG	GTCAACGACTCCATCCAGCTCGACATCGCCACCTGCAAGATCATGGAC ATCATCAAGTTCGACTCAGGTAACCTGTGCATGATCACGGGAGGGCGT AACTTGGGGCGAGTGGGCACCATCGTGTCCCGCGAGAGGCACCCCGGG AGCTTCGACATCGTCCACATCAAGGACACCACCGGACACACCTTCGCC ACCAGGTTGAACAACGTGTTCATCATCGGCAAG
PX009	SEQ ID NO: 2345 GCGTAATACGACT CACTATAGGCAGC TACAAGTATTGGG AGAACCAG SEQ ID NO: 2347 CAGCTACAAGTAT TGGGAGAACCAG	SEQ ID NO: 2346 TGTTGATCACTAT GCCGGTCCT SEQ ID NO: 2348 GCGTAATACGACT CACTATAGGTGTT GATCACTATGCCG GTCCT	SEQ ID NO: 2344 CAGCTACAAGTATTGGGAGAACCAGCTCATTGACTTTTTGTCAGTATAC AAGAAGAAGGGTCAGACAGCGGGTGCTGGTCAGAACATCTTCAACTGT GACTTCCGCAACCCGCCCCCACACGGCAAGGTGTGCGACGTGGACATC CGCGGCTGGGAGCCCTGCATTGATGAGAACCACTTCTCTTTCCACAAGT CTTCGCCTTGCATCTTCTTGAAGCTGAATAAGATCTACGGCTGGCGTCC AGAGTTCTACAACGACACGGCTAACCTGCCTGAAGCCATGCCCGTGGA CTTGCAGACCCACATTCGTAACATTACTGCCTTCAACAGAGACTATGCG AACATGGTGTGGGTGTCGTGCCACGGCGAGACGCCGGCGGACAAGGA GAACATCGGGCCGGTGCGCTACCTGCCCTACCCGGGCTTCCCCGGGTA CTTCTACCCGTACGAGAACGCCGAGGGGTATCTGAGCCCGCTGGTCGC CGTGCATTTGGAGAGGCCGAGGACCGGCATAGTGATCAACA
PX010	SEQ ID NO: 2350 GCGTAATACGACT CACTATAGGACCA GCACTCTAGTGGA CAACGTC SEQ ID NO: 2352 ACCAGCACTCTAG TGGACAACGTC	SEQ ID NO: 2351 CTGTATCAATGTA CCGCGGCAC SEQ ID NO: 2353 GCGTAATACGACT CACTATAGGCTGT ATCAATGTACCGC GGCAC	SEQ ID NO: 2349 ACCAGCACTCTAGTGGACAACGTCGCGTTCGGGTCACCACTGTCGCGC GCAATTGGGGCGACGCAGCCGCCAACTTACACCACATATCGGCGGGCT TCGACCAGGAGGCGGCGGCGGTGGTGATGGCGCGGCTGGTGGTGTACC GCGCGGAGCAGGAGGACGGGCCCGACGTGCTGCGCTGGCTCGACCGCA TGCTCATACGCCTGTGCCAGAAGTTCGGCGAGTACGCGAAGGACGACC CGAACAGCTTCCGTCTGTCGGAGAACTTCAGCCTGTACCCGCAGTTCAT GTACCACCTGCGCCGCTCGCAGTTCCTGCAGGTCTTCAACAACTCGCCC GACGAGACCACCTTCTACAGACACATGCTGATGCGCGAAGACCTGACC CAATCCCTCATCATGATCCAGCCGATCCTCTACTCGTACAGCTTCGGAG GCGCGCCCGAACCCGTGCTGTTAGACACCAGCTCCATCCAGCCCGACC GCATCCTGCTCATGGACACCTTCTTCCAGATCCTCATCTACCATGGAGA GACAATGGCGCAATGGCGCGCTCTCCGCTACCAAGACATGGCTGAGTA CGAGAACTTCAAGCAGCTGCTGCGAGCGCCCGTGGACGACGCGCAGGA GATCCTGCAGACCAGGTTCCCCGTGCCGCGGTACATTGATACAG
PX015	SEQ ID NO: 2355 GCGTAATACGACT CACTATAGGGACG	SEQ ID NO: 2356 GATGATGGCCGGA GAGTTCTTG	SEQ ID NO: 2354 GACGAGAAGATCCGCATGAACCGCGTCGTCCGGAACAACCTGCGAGTG CGCCTGTCAGACATTGTGTCCATCGCTCCTTGCCCGTCAGTGAAGTACG

	AGAAGATCCGCAT GAACC SEQ ID NO: 2357 GACGAGAAGATCC GCATGAACC	SEQ ID NO: 2358 GCGTAATACGACT CACTATAGGGATG ATGGCCGGAGAGT TCTTG	GCAAGAGAGTTCATATTCTGCCCATTGATGACTCTGTTGAGGGTTTGAC TGGAAACCTGTTCGAAGTCTACCTGAAGCCGTACTTCATGGAGGCGTA CCGGCCCATCCACCGCGACGACACGTTCATGGTGCGCGGCGGCATGCG CGCCGTCGAGTTCAAGGTGGTGGAGACCGACCCCTCGCCCTACTGCAT CGTGGCCCCCGACACGGTCATTCATTGTGAGGGAGAGCCGATTAAACG CGAGGAAGAAGAGGAGGCTCTCAACGCCGTCGGCTACGACGACATCG GCGGGTGCCGCAAGCAGCTGGCGCAGATCAAGGAGATGGTGGAGCTG CCGCTGCGCCACCCCTCGCTGTTCAAGGCCATCGGGGTCAAGCCGCCG CGGGGGATACTGATGTACGGGCCCCCGGGGACGGGGAAGACCTTGATC GCTAGGGCTGTCGCTAATGAGACGGGCGCATTCTTCTTCCTCATCAACG GCCCCGAGATCATGTCGAAACTCGCCGGTGAATCCGAGTCGAACCTGC GCAAGGCGTTCGAGGAGGCGGACAAGAACTCTCCGGCCATCATC
PX016	SEQ ID NO: 2360 GCGTAATACGACT CACTATAGGCTGG GTCGTATTTTCAAC GGCTC SEQ ID NO: 2362 CTGGGTCGTATTTT CAACGGCTC	SEQ ID NO: 2361 AGTGATGTACCCG GTCAAGTCG SEQ ID NO: 2363 GCGTAATACGACT CACTATAGGAGTG ATGTACCCGGTCA AGTCG	SEQ ID NO: 2359 CTGGGTCGTATTTTCAACGGCTCCGGCAAGCCCATCGACAAGGGGCCC CCGATCCTGGCCGAGGAGTACCTGGACATCCAGGGGCAGCCCATCAAC CCGTGGTCCCGTATCTACCCGGAGGAGATGATCCAGACTGGTATCTCCG CTATCGACGTGATGAACTCCATCGCCCGTGGTCAGAAGATCCCCATCTT CTCCGCCGCCGGTCTGCCCCACAACGAGATTGCTGCTCAGATCTGTAGG CAGGCTGGTCTTGTCAAGGTCCCCGGAAAATCCGTGTTGGACGACCAC GAAGACAACTTCGCCATCGTGTTCGCCGCCATGGGAGTCAACATGGAG ACCGCCAGGTTCTTCAAGCAGGACTTCGAGGAGAACGGTTCCATGGAG AACGTCTGTCTGTTCTTGAACTTGGCCAATGACCCGACCATTGAGAGGA TTATCACGCCGAGGTTGGCGCTGACTGCTGCCGAGTTCTTGGCCTACCA GTGCGAGAAACACGTGTTGGTAATCTTGACCGACATGTCTTCATACGCG GAGGCTCTTCGTGAAGTGTCAGCCGCCCGTGAGGAGGTGCCCGGACGA CGTGGTTTCCCAGGTTACATGTACACGGATTTGGCCACAATCTACGAGC GCGCCGGGCGAGTCGAGGGCCGCAACGGCTCCATCACGCAGATCCCCA TCCTGACCATGCCCAACGACGACATCACCCACCCCATCCCCGACTTGAC CGGGTACATCACT

Table 8-AD

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
AD001	SEQ ID NO: 2462	SEQ ID NO: 2463	SEQ ID NO: 2461

	GCGTAATACGACT CACTATAGGGCTC CTAAAGCATGGAT GTTGG SEQ ID NO: 2464 GCTCCTAAAGCAT GGATGTTGG	CAATATCAAACGA GCCTGGGTG SEQ ID NO: 2465 GCGTAATACGACT CACTATAGGCAAT ATCAAACGAGCCT GGGTG	GCTCCTAAAGCATGGATGTTGGACAAACTCGGAGGAGTATTCGCTCCT CGCCCCAGTACTGGCCCCCACAAATTGCGTGAATGTTTACCTTTGGTGA TTTTTCTTCGCAATCGGCTCAAGTATGCTCTGACGAACTGTGAAGTAAC GAAGATTGTTATGCAGCGACTTATCAAAGTTGACGGCAAGGTGCGAAC CGATCCGAATTATCCCGCTGGTTTCATGGATGTTGTCACCATTGAGAAG ACTGGAGAGTTCTTCAGGCTGGTGTATGATGTGAAAGGCCGTTTCACA ATTCACAGAATTAGTGCAGAAGAAGCCAAGTACAAGCTCTGCAAGGTC AGGAGAGTTCAAACTGGGCCAAAAGGTATTCCATTCTTGGTGACCCAT GATGGCCGTACTATCCGTTATCCTGACCCAGTCATTAAAGTTAATGACT CAATCCAATTGGATATTGCCACTTGTAAAATCATGGACCACATCAGATT TGAATCTGGCAACCTGTGTATGATTACTGGTGGACGTAACTTGGGTCGA GTGGGGACTGTTGTGAGTCGAGAACGTCACCCAGGCTCGTTTGATATTG
AD002	SEQ ID NO: 2467 GCGTAATACGACT CACTATAGGGAAG AAAGATGGAAAGG CTCCGAC SEQ ID NO: 2469 GAAGAAAGATGGA AAGGCTCCGAC	SEQ ID NO: 2468 CATCCATGTGCTG ATGAGCTGC SEQ ID NO: 2470 GCGTAATACGACT CACTATAGGCATC CATGTGCTGATGA GCTGC	SEQ ID NO: 2466 GAAGAAAGATGGAAAGGCTCCGACCACTGGTGAGGCCATTCAGAAACT CAGAGAAACAGAAGAAATGTTAATCAAAAAGCAGGAATTTTTAGAGA AGAAAATCGAACAAGAAATCAATGTTGCAAAGAAAAATGGAACGAAA AATAAGCGAGCTGCTATTCAGGCTCTGAAAAGGAAAAAGAGGTATGAA AAACAATTGCAGCAAATTGATGGCACCTTATCCACAATTGAAATGCAA AGAGAAGCTTTGGAGGGTGCTAATACTAATACAGCTGTATTACAAACA ATGAAATCAGCAGATGCCCTTAAAGCAGCTCATCAGCACATGGAT G
AD009	SEQ ID NO: 2472 GCGTAATACGACT CACTATAGGGTCT TCTTCCAGACACT GGATCCTC SEQ ID NO: 2474 GTCTTCTTCCAGAC ACTGGATCCTC	SEQ ID NO: 2473 CGTGTTCATCTCCC TCGAGTTG SEQ ID NO: 2475 GCGTAATACGACT CACTATAGGCGTG TTCATCTCCCTCGA GTTG	SEQ ID NO: 2471 GTCTTCTTCCAGACACTGGATCCTCGTATTCCCACCTGGCAGTTAGATT CTTCTATCATTGGCACATCACCTGGCCTAGGTTTCCGGCCAATGCCAGA AGATAGCAATGTAGAGTCAACTCTCATCTGGTACCGTGGAACAGATCG TGATGACTTCCGTCAGTGGACAGACACCCTTGATGAATTTCTTGCTGTG TACAAGACTCCTGGTCTGACCCCTGGTCGAGGTCAGAACATCCACAAC TGTGACTATGATAAGCCGCCAAAGAAAGGCCAAGTTTGCAATGTGGAC ATCAAGAATTGGCATCCCTGCATTCAAGAGAATCACTACAACTACCAC AAGAGCTCTCCATGCATATTCATCAAGCTCAACAAGATCTACAATTGG ATCCCTGAATACTACAATGAGAGTACGAATTTGCCTGAGCAGATGCCA GAAGACCTGAAGCAGTACATCCACAACCTGGAGAGTAACAACTCGAGG GAGATGAACACG
AD015	SEQ ID NO: 2477 GCGTAATACGACT	SEQ ID NO: 2478 AGAATTTCAAGGC	SEQ ID NO: 2476

	CACTATAGGGTTG AAGGACTAACCGG GAATTTG SEQ ID NO: 2479 GTTGAAGGACTAA CCGGGAATTTG	GACCAGTGG SEQ ID NO: 2480 GCGTAATACGACT CACTATAGGAGAA TTTCAAGGCGACC AGTGG	GTTGAAGGACTAACCGGGAATTTGTTTGAGGTGTACTTAAAACCGTACT TTCTCGAAGCATACCGACCCATTCACAAAGATGATGCGTTTATTGTTCG TGGTGGTATGCGAGCAGTAGAATTCAAAGTAGTGGAAACAGATCCTTC ACCATATTGTATTGTTGCTCCTGATACTGTTATTCACTGTGAAGGTGAT CCAATAAAACGTGAAGAGGAAGAAGAAGCATTAAATGCTGTTGGTTAT GATGACATTGGGGGTTGCCGAAAACAGCTAGCACAGATCAAGGAAATG GTGGAATTGCCATTACGGCACCCCAGTCTCTTTAAGGCTATTGGTGTTA AGCCACCGAGGGGAATACTGCTGTATGGACCCCCTGGAACTGGTAAAA CCCTCATTGCCAGGGCTGTGGCTAATGAAACTGGTGCATTCTTCTTTTT AATAAATGGTCCTGAAATTATGAGCAAGCTTGCTGGTGAATCTGAAAG CAACTTACGTAAGGCATTTGAAGAAGCTGATAAGAATGCTCCGGCAAT TATATTTATTGATGAACTAGATGCAATTGCCCCTAAAAGAGAAAAAAC TCATGGAGAGGTGGAACGTCGCATAGTTTCACAACTACTAACTTTAATG GATGGTCTGAAGCAAAGTTCACATGTTATTGTTATGGCTGCCACAAATA GACCCAACTCTATTGATGGTGCCTTGCGCCGCTTTGGCAGATTTGATAG GGAAATTGATATTGGTATACCAGATGCCACTGGTCGCCTTGAAATTCT
AD016	SEQ ID NO: 2482 GCGTAATACGACT CACTATAGGACCC GGAAGAAATGATC CAGAC SEQ ID NO: 2484 ACCCGGAAGAAAT GATCCAGAC	SEQ ID NO: 2483 ATGTAGCCTGGGA AGCCTCTTC SEQ ID NO: 2485 GCGTAATACGACT CACTATAGGATGT AGCCTGGGAAGCC TCTTC	SEQ ID NO: 2481 ACCCGGAAGAAATGATCCAGACGGGGATCTCGACCATCGACGTGATGA CGTCCATCGCGCGAGGGCAGAAGATCCCCATCTTCTCGGGCGCAGGGC TGCCACACAACGAGATCGCTGCGCAGATCTGCCGACAGGCGGGGCTGG TGCAGCACAAGGAGAACAAGGACGACTTCGCCATCGTGTTCGCGGCGA TGGGCGTCAACATGGAGACGGCGCGCTTCTTCAAGCGCGAGTTCGCGC AGACGGGCGCGTGCAACGTGGTGCTGTTCCTCAACCTGGCCAACGACC CCACCATCGAGCGCATCATCACCCCGCGCCTCGCGCTCACCGTGGCCG AGTTCCTGGCCTACCAGTGCAACAAGCACGTGCTCGTCATCATGACCG ACATGACCTCCTACGCGGAGGCGCTGCGCGAGGTGAGCGCGGCGCGCG AGGAGGTTCCTGGGCGAAGAGGCTTCCCAGGCTACAT

Table 9-LD

Target ID	Hairpin Sequence 5' → 3'
LD002	SEQIDNO: 240 GCCCTTGCAATGTCATCCATCATGTCGTGTACATTGTCCACGTCCAAGTTTTTATGGGCTTTCTTAAGAGCTTCAGCTG

	CATTTTTCATAGATTCCAATACTGTGGTGTTCGTACTAGCTCCCTCCAGAGCTTCTCGTTGAAGTTCAATAGTAGTTAA
	AGTGCCATCTATTTGCAACTGATTTTTTTCTAATCGCTTCTTCCGCTTCAGCGCTTGCATGGCCGCTCAAGGGCGAATT
	CACCAGCTTTCTTGTACAAAGTGGTATATCACTAGTGCGGCCGCCTGCAGGTCGACCATATGGTCGACCTGCAGGCG
	GCCGCACTAGTGATGCTGTTATGTTCAGTGTCAAGCTGACCTGCAAACACGTTAAATGCTAAGAAGTTAGAATATAT
	GAGACACGTTAACTGGTATATGAATAAGCTGTAAATAACCGAGTATAAACTCATTAACTAATATCACCTCTAGAGTA
	TAATATAATCAAATTCGACAATTTGACTTTCAAGAGTAGGCTAATGTAAAATCTTTATATATTTCTACAATGTTCAAA
	GAAACAGTTGCATCTAAACCCCTATGGCCATCAAATTCAATGAACGCTAAGCTGATCCGGCGAGATTTTCAGGAGCT
	AAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATT
	TTGAGGCATTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAAGACCG
	TAAAGAAAAATAAGCACACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGGAATTCC
	GTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTACACCGTTTTCCATGAGCAAACT
	GAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCG
	TGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTG
	AGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTTTCACCATGGGCAAATATTAT
	ACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAG
	AATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAAACGCGTGGATCAGCTTAATATGACT
	CTCAATAAAGTCTCATACCAACACAAGTGCCACCTATTCAACCATCAAGAAAAAAGCCAAAATTTATGCTACTCTAAG
	GAAAACTTCACTAAAGAAGACGATTTAGAGTGTTTACCAAGAAATTTCTGTCATCTTACTAAACAACTAAAGATCGG
	TGTGATACAAAAACCTAATTCTCATTAAAGTTTATGCTAAAATAAGCATAATTTTACCCACTAAGCGTGACCAGATAAA
	CATAACTCAGCACACCAGAGCATATATATTGGTGGCTCAAATCATAGAAACTTACAGTGAAGACACAGAAAGCCGT
	AAGAAGAGGCAAGAGTATGAAACCTTACCTCATCATTTCCATGAGGTTGCTTCTGATCCCGCGGGATATCACCACTT
	TGTACAAGAAAGCTGGGTCGAATTCGCCCTTGAGCGGCCATGCAAGCGCTGAAGCGGAAGAAGCGATTAGAAAAAA
	ATCAGTTGCAAATAGATGGCACTTTAACTATTGAACTTCAACGAGAAGGCTCTGGAGGGAGCTAGTACGAACACC
	ACAGTATTGGAATCTATGAAAAATGCAGCTGAAGCTCTTAAGAAAGCCCATAAAAACTTGGACCGTGGACAATGTAC
	ACGACATGATGGATGACATTGCAAGGGC
LD006	SEQIDNO: 241
	GCCCTTGGAGCGAGACTACAACAACTATGGCTGGCAGGTGTTGGTTGCTTCTGGTGTGGTGGAATACATCGACACTC
	TTGAAGAAGAAACTGTCATGATTGCGATGAATCCTGAGGATCTTCGGCAGGACAAAGAATATGCTTATTGTACGACC
	TACACCCACTGCGAAATCCACCCGGCCATGATCTTGGGCGTTTGCGCGTCTATTATACCTTTCCCCGATCATAACCAG
	AGCCCAAGGAACACCTACCAGAGCGCTATGGGTAAGCAAGCTATGGGGGTCTACATTACGAAATTTCCACGTGCGGAT
	GGACACCCTGGCCCACGTGCTATACTACCCGCACAAACCTCTGGTCACTACCAGGTCTATGGAGTATCTGCGGTTCA
	GAGAATTACCAGCCGGGATCAACAGTATAGTTGCTATTGCTTGTTATACTGGTTATAATCAAGAAGATTCTGTTATTC
	TGAACGCGTCTGCTGTGGAAAGAGGATTTTTCCGATCCGTGTTTTATCGTTCCTATAAAGATGCCGAAATCGAAGCGA
	ATTGGCGATCAAGAAGAGCAGTTCGAGAAGGGCGAATTCACCAGCTTTCTTGTACAAAGTGGTATATCACTAGTGCG
	GCCGCCTGCAGGTCGACCATATGGTCGACCTGCAGGCGGCCGCACTAGTGATGCTGTTATGTTCAGTGTCAAGCTGA
	CCTGCAAACACGTTAAATGCTAAGAAGTTAGAATATATGAGACACGTTAACTGGTATATGAATAAGCTGTAAATAAC

	CGAGTATAAACTCATTAACTAATATCACCTCTAGAGTATAATATAATCAAATTCGACAATTTGACTTTCAAGAGTAG
	GCTAATGTAAAATCTTTATATATTTCTACAATGTTCAAAGAAACAGTTGCATCTAAACCCCTATGGCCATCAAATTCA
	ATGAACGCTAAGCTGATCCGGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATAC
	CACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTCAGTCAGTTGCTCAATGTACCTATAACCA
	GACCGTTCAGCTGGATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTTATTCA
	CATTCTTGCCCGCCTGATGAATGCTCATCCGGAATTCCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATA
	GTGTTCACCCTTGTTACACCGTTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATT
	TCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTA
	TTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACA
	ACTTCTTCGCCCCCCGTTTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAG
	GTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCA
	GGGCGGGGCGTAAACGCGTGGATCAGCTTAATATGACTCTCAAATAAAGTCTCATACCAACAAGTGCCACCTTATTCA
	ACCATCAAGAAAAAAGCCAAAATTTATGCTACTCTAAGGAAAACTTCACTAAAGAAGACGATTTAGAGTGTTTTACC
	AAGAATTTCTGTCATCTTACTAAACAACTAAAGATCGGTGTGATACAAAACCTAATCTCATTAAAGTTTATGCTAAA
	ATAAGCATAATTTTACCCACTAAGCGTGACCAGATAAACATAACTCAGCACACCAGAGCATATATATTGGTGGCTCA
	AATCATAGAAACTTACAGTGAAGACACAGAAAGCCGTAAGAAGAGGCAAGAGTATGAAACCTTACCTCATCATTTC
	CATGAGGTTGCTTCTGATCCCGCGGGATATCACCACTTTGTACAAGAAAGCTGGGTCGGCCCTTCTCGAACTGCTCTT
	CTTGATCGCCAATTCGCTTCGATTCGCATCTTTATAGGAACGATAAAACACGGATCGGAAAAATCCTCTTTCCACAG
	CAGACGCGTTCAGAATAACAGAATCTTCTTGATTATAACCAGTATAACAAGCAATAGCAACTATACTGTTGATCCCG
	GCTGGTAATTCTCTGAACCGCAGATACTCCATAGACCTGGTAGTGACCAGAGGTTTGTGCGGGTAGTATAGCACCGTG
	GGCCAGGGTGTCCATCCGCACCGTGGAAATTCGTAATGTAGACCCCCATAGCTTGCTTACCCATAGCGCTCTGGTAGG
	TGTTCCTTGGGCTCTGGTTATGATCGGGGAAAGGTATAATAGACGCGCAAACGCCCAAGATCATGGCCGGGTGGATT
	TCGCAGTGGGTGTAGGTCGTACAATAAGCATATTCTTTGTCCTGCCGAAGATCCTCAGGATTCATCGCAATCATGACA
	GTTTCTTCTTCAAGAGTGTCGATGTATTCCACCACACCAGAAGCAACCAACACCTGCCAGCCATAGTTGTTGTAGTCT
	CGCTCCAAGGGC
LD007	SEQIDNO: 242
	GCCCTTCCGAAGAAGGATGTGAAGGGTACTTACGTATCCATACACAGTTCAGGCTTCAGAGATTTTTTATTGAAACC
	AGAAATTCTAAGAGCTATAGTTGACTGCGGTTTTGAACACCCTTCAGAAGTTCAGCACGAATGTATTCCTCAAGCTGT
	CATTGGCATGGACATTTTATGTCAAGCCAAATCTGGTATGGGCAAAACGGCAGTGTTTGTTCTGGCGACACTGCAAC
	AATTGGAACCAGCGGACAATGTTGTTTACGTTTGGTGATGTGTCACACTCGTGAACTGGCTTTCCAAATCAGCAAA
	GAGTACGAGAGGTTCAGTAAATATATGCCCAGTGTCAAGGTGGGCGTCTTTTTCGGAGGAATGCCTATTGCTAACGA
	TGAAGAAGTATTGAAAAACAAATGTCCACACATTGTTGTGGGACGCCTGGGCGTATTTTGGCGCTTGTCAAGTCTA
	GGAAGCTAGTCCTCAAGAACCTGAAACACTTCATTCTTGATGAGTGCGATAAATGTTAGAACTGTTGGATATGAGG
	AGAGACGTCCAGGAAATCTACAGAAACACCCCTCACACCAAGCAAGTGATGATGTTCAGTGCCACACTCAGCAAAG
	AAATCAGGCCGGTGTGCAAGAAATTCATGCAAGATCCAATGGAGGTGTATGTAGACGATGAAGCCAAATTGACGTT
	GCACGGATTACAACAGCATTACGTTAAACTCAAAGAAAATGAAAAGAATAAAAAATTATTTGAGTTGCTCGATGTTC

TCGAATTTAATCAGGTGGTCATTTTTGTGAAGTCCGTTCAAAGGTGTGTGGCTTTGGCACAGTTGCTGACTGAACAGA
ATTTCCCAGCCATAGGAATTCACAGAGGAAATGGACCAGAAAGAGAGGTTGTCTCGGTATGAGCAGTTCAAAGATTTC
CAGAAGAGAATATTGGTAGCTACGAATCTCTTTGGGCGTGGCATGGACATTGAAAGGGTCAACATTGTCTTCAACTA
TGATATGCCAGAGGACTCCGACACCTACTTGCATCGAAGGGCGAATTCACCAGCTTTCTTGTACAAAGTGGTATATC
ACTAGTGCGGCCGCCTGCAGGTCGACCATATGGTCGACCTGCAGGCGGCCGCACTAGTGATGCTGTTATGTTCAGTG
TCAAGCTGACCTGCAAACACGTTAAATGCTAAGAAGTTAGAATATATGAGACACGTTAACTGGTATATGAATAAGCT
GTAAATAACCGAGTATAAACTCATTAACTAATATCACCTCTAGAGTATAATATAATCAAATTCGACAATTTGACTTTC
AAGAGTAGGCTAATGTAAAATCTTTATATATTTCTACAATGTTTCAAAGAAACAGTTGCATCTAAACCCCTATGGCCAT
CAAATTCAATGAACGCTAAGCTGATCCGGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACT
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Table 9-PC

Target ID	Hairpin Sequence 5' → 3'
PC001	SEQ ID NO: 508 AGATTCAAATTTGATGTAGTCAAGAATTTTAGATGTAGCAATTTCCATTTGAATTGTGTCATTCACTTTGATGTTGGGGT CAGGGTAACGAATGGTTCTGCCATCATGTGTTACCAAAAATGGGATTCCTTTGGGACCAGTTTGGACTCTCCTTACTTT ACACAACTTGTATTTTGCCTCTTCAGCTGTAATACGGTGCACAGCAAATCTTCCTTTAACATCATAGATCAGACGGAAA AATTCACCAGTCTTCTCAATAGTAATGACATCCATGAAACCAGCAGGGTAATTAGAATCAGTCCTCACTTTACCATCAA CTTTGATCAACCTTTGCATGACAATTTTAGTGACTTCACTGTTTGTAAGGGCATACTTCAGCCTGTTACGAAGGAAAAT CACTAAAGGCAGGGATTCGCGCAACTTGTGAGGCCCGGTGGATGGACGAGGGGCGAAGACACCCCCCAATTTGTCCA ACATCCATGCAAGGGCGAATTCGACCCAGCTTTCTTGTACAAAGTGGTGATATCACTAGTGCGGCCGCCTGCAGGTCG ACCATATGGTCGACCTGCAGGCGGCCGCACTAGTGATGCTGTTATGTTCAGTGTCAAGCTGACCTGCAAACACGTTAA ATGCTAAGAAGTTAGAATATATGAGACACGTTAACTGGTATATGAATAAGCTGTAAATAACCGAGTATAAACTCATTA ACTAATATCACCTCTAGAGTATAATATAATCAAATTCGACAATTTGACTTTCAAGAGTAGGCTAATGTAAAATCTTTAT ATATTTCTACAATGTTCAAAGAAACAGTTGCATCTAAACCCCTATGGCCATCAAATTCAATGAACGCTAAGCTGATCCG GCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGG CATCGTAAAGAACATTTTGAGGCATTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGG CCTTTTTAAAGACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGC TCATCCGGAATTCCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTACACCGTTTTC CATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGC AAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAA TCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTTTCACCATGGGC AAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCATGCCGTCTGTGATGGCTTCCATG TCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAAACGCGTGGATCAGCTTAAT ATGACTCTCAATAAAGTCTCATACCAACAAGTGCCACCTTATTCAACCATCAAGAAAAAAGCCAAAATTTATGCTACT CTAAGGAAAACTTCACTAAAGAAGACGATTTAGAGTGTTTTACCAAGAATTTCTGTCATCTTACTAAACAACTAAAGA TCGGTGTGATACAAAACCTAATCTCATTAAAGTTTATGCTAAAATAAGCATAATTTTACCCACTAAGCGTGACCAGATA AACATAACTCAGCACACCAGAGCATATATATTGGTGGCTCAAATCATAGAAACTTACAGTGAAGACACAGAAAGCCGT AAGAAGAGGCAAGAGTATGAAACCTTACCTCATCATTTCCATGAGGTTGCTTCTGATCCCGCGGGATATCACCACTTTG TACAAGAAAGCTGGGTCGAATTCGCCCTTGCATGGATGTTGGACAAATTGGGGGGTGTCTTCGCCCCTCGTCCATCCAC CGGGCCTCACAAGTTGCGCGAATCCCTGCCTTTAGTGATTTTCCTTCGTAACAGGCTGAAGTATGCCCTTACAAACAGT

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	ACCGTATTACAGCTGAAGAGGCAAAATACAAGTTGTGTAAAGTAAGGAGAGTCCAAACTGGTCCCAAAGGAATCCCA
	TTTTTGGTAACACATGATGGCAGAACCATTCGTTACCCTGACCCCAACATCAAAGTGAATGACACAATTCAAATGGAA
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PC010	SEQ ID NO: 509
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	CATTGTCCATCGCTGTCGGCCTCTTAGAATGCACCTATCCGAATACGGGTGGCAGAATCATGATATTCTTAGGAGGACC
	ATGCTCTCAGGGTCCCGGCCAGGTGTTGAACGACGATTTGAAGCAGCCCATCAGGTCCCATCATGACATACACAAAGA
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	CTCAAGATGGCGTTCAACGCCACCTTGGAGGTGAAGTGTTCCAGGGAGTTAAAAGTCCAAGGGGGCATCGGCTCGTGC
	GTGTCCTTGAACGTTAAAAGCCCTCTGGTTTCCGATACGGAACTAGGCATGGGAATACTGTGCAGTGGAAACTTTGC
	ACGTTGGGCGCCGAGCTCTACTGTGGCGCTGTTCTTCGAGGTGGTTAACCAGCATTCGGCGCCCATACCACACGGGAGGC
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	AAATTGGGCGGACGCTACTGCCAACATCCACCACATTAGCGCTGGCTTCGACCAAGAAGCGGCGGCAGTTGTGATGGC
	CCGAATGGCCGGTTACAAGGCGGAATCGGACGAGACTCCCGACGTGCTCAGATGGGTGGACAGGATGTTGATCAGGC
	TGTGCCAGAAGTTCGGAGAGTACAATAAAGACGATCCGAATTCGTTCAGGTTGGGGGAGAACTTCAGTCTGTATCCGC
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	CATGCTGATGCGTGAGGATTTGACTCAGTCTTTGATCATGATCCAGCCGATTTTGTACAGTTACAGCTTCAACGGGCCG
	CCCGAGCCTGTGTTGTTGGACACAAGCTCTATTCAGCCGGATAGAATCCTGCTCATGGACACTTTCTTCCAGATACTCA
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	ATGAACGCTAAGCTGATCCGGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACC
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	GCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCG
	TAAACGCGTGGATCAGCTTAATATGACTCTCAATAAAGTCTCATACCAACAAGTGCCACCTTATTCAACCATCAAGAA
	AAAAGCCAAAATTTATGCTACTCTAAGGAAAACTTCACTAAAGAAGACGATTTAGAGTGTTTTACCAAGAATTTCTGT
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	CAGTGAAGACACAGAAAGCCGTAAGAAGAGGCAAGATGAAACCTTACCTCATCATTTCCATGAGGTTGCTTCTGA
	TCCCGCGGGATATCACCACTTTGTACAAGAAAGCTGGGTCGAATTCGCCCTTCGCCATTGGGCAATGGTCTCTCCATGG
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	GGCACAGCCTGATCAACATCCTGTCCACCCATCTGAGCACGTCGGAGTCTCGTCCGATTCCGCCTTGTAACCGGCCAT
	TCGGGCCATCACAACTGCCGCCGCTTCTTGGTCGAAGCCAGCGCTAATGTGGTGGATGTTGGCAGTAGCGTCCGCCCA
	ATTTCTAGCAATCGTGGTCACTCTGATCCTCCTTTGCCCGCTCGCGTGCTGATACTGGGTGATGAGCTGGATGCAGCCC
	CTGCCTCCCCTGTGGTATGGGCGCCGAATGCTGGTTAACCACCTCGAAGAACAGCGCCACAGTAGAGGCTCGGCGCCAAC
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	GAGATCTTTCGTTCCACAGAACACGTACGACTTGCTGCAGCCTTCGGTACCCAGTTCGTGGACTTGCACCATTTTTCCG
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PC014	SEQ ID NO: 510
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	CCCAGCTTTCTTGTACAAAGTGGTGATATCACTAGTGCGGCCGCCTGCAGGTCGACCATATGGTCGACCTGCAGGCGG
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	GCCCTTCGGATCTCGGGCACCAATTGCTGAGCGATCAGATCCAACCTAGCCTCCATCGTGTTGCTGATCTTGATCTTGT
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PC016	SEQ ID NO: 511
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	TAGGGGTTTCCCCGGTTACATGTACACCGATCTGGCCACCATTTACGAGCGCGCCGGTCGTGTGGAGGGCCGCAACGG CTCCATCACGCAGATCCCCATCTTGACTATGCCCAA
PC027	SEQ ID NO: 512 GGGCCAAGCACAGCGAAATGCAGCAAGCTAACTTGAAAGCACTACCAGAAGGAGCTGAAATCAGAGATGGAGAACGT TTGCCAGTCACAGTAAAGGACATGGGAGCATGCGAGATTTACCCACAAACAATCCAACACAACCCCAATGGGCGGTTT GTAGTGGTTTGTGGTGATGGAGAATACATAATATACACGGCTATGGCCCTTCGTAACAAAGCATTTGGTAGCGCTCAA GAATTTGTATGGGCACAGGACTCCAGTGAATATGCCATCCGCGAATCCGGATCCACCATTCGAATCTTCAAGAATTTCA AAGAAAAAAAGAATTTCAAGTCCGACTTTGGTGCCGAAGGAATCTATGGTGGTTTTCTCTTGGGTGTGAAATCAGTGT CTGGCTTAGCTTTCTATGACTGGGAAACGCTTGAGTTAGTAAGGCGCATTGAAATACAGCCTAGAGCTATCTACTGGTC AGATAGTGGCAAGTTGGTATGCCTTGCTACCGAAGATAGCTATTTCATATTGTCCTATGACTCTGACCAAGTCCAGAAA GCTAGAGATAACAACCAAGTTGCCGAAGATGGAGTGGAGGCTGCCTTTGATGTCCTAGGTGAAATAAATGAATCCGTA AGAACAGGTCTTTGGGTAGGAGACTGCTTCATTTACACAAACGCAGTCAACCGTATCAACTACTTTGTGGGTGGTGAA TTGGTAACTATTGCACATCTGGACCGTCCTCTATATGTCCTGGGCTATGTACCTAGAGATGACAGGTTATACTTGGTTG ATAAAGAGTTAGGAGTAGTCAGCTATCAATTGCTATTATCTGTACTCGAATATCAGACTGCAGTCATGCGACGAGACTT CCCAACGGCTGATCGAGTATTGCCTTCAATTCCAAAAGAACACCGCACTAGGGTGGCACAAAGGGCGAATTCGACCCA GCTTTCTTGTACAAAGTGGTGATATCACTAGTGCGGCCGCCTGCAGGTCGACCATATGGTCGACCTGCAGGCGGCCGC ACTAGTGATGCTGTTATGTTCAGTGTCAAGCTGACCTGCAAACACGTTAAATGCTAAGAAGTTAGAATATATGAGACA CGTTAACTGGTATATGAATAAGCTGTAAATAACCGAGTATAAACTCATTAACTAATATCACCTCTAGAGTATAATATAA TCAAATTCGACAATTTGACTTTCAAGAGTAGGCTAATGTAAAATCTTTATATATTTCTACAATGTTCAAAGAAACAGTT GCATCTAAACCCCTATGGCCATCAAATTCAATGAACGCTAAGCTGATCCGGCGAGATTTTCAGGAGCTAAGGAAGCTA AAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTC AGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATA AGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGGAATTCCGTATGGCAATGAA AGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTACACCGTTTTCCATGAGCAAACTGAAACGTTTTCATCG CTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACC TGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGAT TTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTG CTGATGCCGCTGGCGATTCAGGTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAAC AGTACTGCGATGAGTGGCAGGGCGGGGCGTAAACGCGTGGATCAGCTTAATATGACTCTCAATAAAGTCTCATACCAA CAAGTGCCACCTTATTCAACCATCAAGAAAAAAGCCAAAATTTATGCTACTCTAAGGAAAACTTCACTAAAGAAGACG ATTTAGAGTGTTTTACCAAGAATTTCTGTCATCTTACTAAACAACTAAAGATCGGTGTGATACAAAACCTAATCTCATT AAAGTTTATGCTAAAATAAGCATAATTTTACCCACTAAGCGTGACCAGATAAACATAACTCAGCACACCAGAGCATAT ATATTGGTGGCTCAAATCATAGAAACTTACAGTGAAGACACAGAAAGCCGTAAGAAGAGGCAAGAGTATGAAACCTT ACCTCATCATTTCCATGAGGTTGCTTCTGATCCCGCGGGATATCACCACTTTGTACAAGAAAGCTGGGTCGAATTCGCC CTTTGTGCCACCCTAGTGCGGTGTTCTTTTGGAATTGAAGGCAATACTCGATCAGCCGTTGGGAAGTCTCGTCGCATGA CTGCAGTCTGATATTCGAGTACAGATAATAGCAATTGATAGCTGACTACTCCTAACTCTTTATCAACCAAGTATAACCT

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Table 9-MP

Target ID	Hairpin Sequence 5' → 3'
MP001	SEQ ID NO: 1066 GTTTAAACGCACCCAAAGCATGGATGTTGGACAAATCGGGGGGGTGTCTTCGCTCCACGTCCAAGCACCGGTCCACAC AAACTTCGTGAATCACTACCGTTATTGATCTTCTTGCGTAATCGTTTGAAGTATGCACTTACTGGTGCCGAAGTCACC AAGATTGTCATGCAAAGATTAATCAAGGTTGATGGCAAAGTCCGTACCGACCCTAATTATCCAGCCGGTTTTATGGA TGTTATATCTATCCAAAAGACCAGTGAGCACTTTAGATTGATCTATGATGTGAAAGGTCGTTTCACCATCCACAGAAT TACTCCTGAAGAAGCAAAATACAAGTTGTGTAAAGTAAAGAGGGTACAAACTGGACCCAAAGGTGTGCCATTTTTA ACTACTCATGATGGCCGTACTATTCGCTACCCTGACCCTAACATCAAGGTTAATGACACTATTAGATACGATATTGCA TCATCTAAAATTTTGGATCATATCCGTTTTGAAACTGGAAACTTGTGCATGATAACTGGAGGTCGCAATTTAGGGCGT GTTGGTATTGAAGGGCGAATTCGACCCAGCTTTCTTGTACAAAGTGGTGATATCACTAGTGCGGCCGCCTGCAGGTC GACCATATGGTCGACCTGCAGGCGGCCGCACTAGTGATGCTGTTATGTTCAGTGTCAAGCTGACCTGCAAACACGTT AAATGCTAAGAAGTTAGAATATATGAGACACGTTAACTGGTATATGAATAAGCTGTAAATAACCGAGTATAAACTCA TTAACTAATATCACCTCTAGAGTATAATATAATCAAATTCGACAATTTGACTTTCAAGAGTAGGCTAATGTAAAATCT TTATATATTTCTACAATGTTCAAAGAAACAGTTGCATCTAAACCCCTATGGCCATCAAATTCAATGAACGCTAAGCTG ATCCGGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATC CCAATGGCATCGTAAAGAACATTTTGAGGCATTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGG ATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCC TGATGAATGCTCATCCGGAATTCCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGT TACACCGTTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTA CACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTT TTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCC

	GTTTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCATGCCGT
	CTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAAA
	CGCGTGGATCAGCTTAATATGACTCTCAATAAAGTCTCATACCAACAAGTGCCACCTTATTCAACCATCAAGAAAAA
	AGCCAAAATTTATGCTACTCTAAGGAAAACTTCACTAAAGAAGACGATTTAGAGTGTTTTACCAAGAATTTCTGTCA
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	CCCACTAAGCGTGACCAGATAAACATAACTCAGCACACCAGAGCATATATATTGGTGGCTCAAATCATAGAAACTTA
	CAGTGAAGACACAGAAAGCCGTAAGAAGAGGCAAGAGTATGAAACCTTACCTCATCATTTCCATGAGGTTGCTTCTG
	ATCCCGCGGGATATCACCACTTTGTACAAGAAAGCTGGGTCGAATTCGCCCTTCAATACCAACACGCCCTAAATTGC
	GACCTCCAGTTATCATGCACACAAGTTTCCAGTTTCAAAACGGATATGATCCAAAATTTTAGATGATGCAATATCGTATC
	TAATAGTGTCATTAACCTTGATGTTAGGGTCAGGGTAGCGAATAGTACGGCCATCATGAGTAGTTAAAAATGGCACA
	CCTTTGGGTCCAGTTTGTACCCTCTTTACTTTACACAACTTGTATTTTGCTTCTTCAGGAGTAATTCTGTGGATGGTGA
	AACGACCTTTCACATCATAGATCAATCTAAAGTGCTCACTGGTCTTTTGGATAGATATAACATCCATAAAACCGGCTG
	GATAATTAGGGTCGGTACGGACTTTGCCATCAACCTTGATTAATCTTTGCATGACAATCTTGGTGACTTCGGCACCAG
	TAAGTGCATACTTCAAACGATTACGCAAGAAGATCAATAACGGTAGTGATTCACGAAGTTTGTGTGGACCGGTGCTT
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MP002	SEQ ID NO: 1067
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	GCTGTTGTTCAATAGTTAACATGGTACCATCAATTTGGGCTAATTGTTGTTCGTACCGTTTCTTACGCTTCAATGCTTG
	CAATGCAGCTCGTTTATTAGTTGTACCATTTTTTTTGGCTATCGCTACTTCTTGTTCAAATTTTTTTTCTAAAAATTCTT
	GTTTCTTTATCAGCATCTCTTCAGTGGATCGAAGCTTTTGTATCGCATCTTCGGTTGATGGTCCCTTCTCTTCCTTTTTG
	CCACCAAGGGCGAATTCGACCCAGCTTTCTTGTACAAAGTGGTGATATCACTAGTGCGGCCGCCTGCAGGTCGACCA
	TATGGTCGACCTGCAGGCGGCCGCACTAGTGATGCTGTTATGTTCAGTGTCAAGCTGACCTGCAAACACGTTAAATG
	CTAAGAAGTTAGAATATATGAGACACGTTAACTGGTATATAGCTGTAAATAACCGAGTATAAACTCATTAAC
	TAATATCACCTCTAGAGTATAATATAATCAAATTCGACAATTTGACTTTCAAGAGTAGGCTAATGTAAAATCTTTATA
	TATTTCTACAATGTTCAAAGAAACAGTTGCATCTAAACCCCCTATGGCCATCAAATTCAATGAACGCTAAGCTGATCC
	GGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATATACCACCGTTGATATATCCCAA
	TGGCATCGTAAAGAACATTTTGAGGCATTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATT
	ACGGCCTTTTTAAAGACCGTAAAGAAAAATAAGCACACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATG
	AATGCTCATCCGGAATTCCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTACAC
	CGTTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACAT
	ATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGT
	CTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTTT
	CACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCATGCCGTCTGTG
	ATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAAACGCGT
	GGATCAGCTTAATATGACTCTCAATAAAGTCTCATACCAACAAGTGCCACCTTATTCAACCATCAAGAAAAAAGCCA
	AAATTTATGCTACTCTAAGGAAAACTTCACTAAAGAAGACGATTTAGAGTGTTTTACCAAGAATTTCTGTCATCTTAC

	TAAACAACTAAAGATCGGTGTGATACAAAACCTAATCTCATTAAAGTTTATGCTAAAATAAGCATAATTTTACCCAC
	TAAGCGTGACCAGATAAACATAACTCAGCACACCAGAGCATATATATTGGTGGCTCAAATCATAGAAACTTACAGTG
	AAGACACAGAAAGCCGTAAGAAGAGGCAAGAGTATGAAACCTTACCTCATCATTTCCATGAGGTTGCTTCTGATCCC
	GCGGGATATCACCACTTTGTACAAGAAAGCTGGGTCGAATTCGCCCTTGGTGGCAAAAAGGAAGAGAAGGGACCAT
	CAACCGAAGATGCGATACAAAAGCTTCGATCCACTGAAGAGATGCTGATAAAGAAACAAGAATTTTTAGAAAAAAAA
	AATTGAACAAGAAGTAGCGATAGCCAAAAAAAATGGTACAACTAATAAACCGAGCTGCATTGCAAGCATTGAAGCGT
	AAGAAACGGTACGAACAACAATTAGCCCAAATTGATGGTACCATGTTAACTATTGAACAACAGCGGGAGGCATTAG
	AAGGTGCCAACACAAATACAGCAGTATTGACTACCATGAAAACTGCAGCAGATGCACTTAAATCAGC
MP010	SEQ ID NO: 1068
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	TAGTGAACCGTGCTGAAACTGAGGATAGTCCAGATGTGATGCGTTGGGCTGATCGTACGCTTATACGCTTGTGTCAA
	AAATTTGGTGATTATCAAAAAGATGATCCAAATAGTTTCCGATTGCCAGAAAACTTCAGTTTATATCCACACAGTTCATG
	TATCATTTAAGAAGGTCTCAATTTCTACAAGTTTTTAATAATAGTCCTGATGAAACATCATATTATAGGCACACATGTTG
	ATGCGTGAAGATGTTACCCAAAGTTTAATCATGATACAGCCAATTCTGTATAGCTATAGTTTTAATGGTAGGCCAGA
	ACCTGTACTTTTGGATACCAGTAGTATTCAACCTGATAAAATATTATTGATGGACACATTTTTCCATATTTTGATATTC
	CATGGAGAGACTATTGCTCAATGGAGAGCAATGGATTATCAAAATAGACCAGAGTATAGTAACCTCAAGCAGTTGCT
	TCAAGCCCCCGTTGATGATGCTCAGGAAATTCTCAAAACTCGATTCCCAATGCAAGGGCGAATTCGACCCAGCTTTC
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	TGATGCTGTTATGTTCAGTGTCAAGCTGACCTGCAAACACGTTAAATGCTAAGAAGTTAGAATATATGAGACACGTT
	AACTGGTATATGAATAAGCTGTAAATAACCGAGTATATAAACTCATTAATCACCTCTAGAGTATATAATATAATC
	AAATTCGACAATTTGACTTTCAAGAGTAGGCTAATGTAAAATCTTTATATATTTCTACAATGTTCAAAGAAACAGTTG
	CATCTAAACCCCCTATGGCCATCAAATTCAATGAACGCTAAGCTGATCCGGCGAGATTTTTCAGGAGCTAAGGAAGCTA
	AAATGGAGAAAAAAATCACTGGATATATACCCAATGGCATCGTAAAGAACATTTTGAGGCATTT
	CAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAAGACCGTAAAGAAAAA
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	GAAAGACGGGTGAGCTGGTGATATGGGATAGTGTTCACACCGTTTTCCATGAGCAAACTGAAACGTTTT
	CATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTG
	AAAACCTGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCA
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	ACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATG
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	TCTCATACCAACAAGTGCCACCTTATTCAACCATCAAGAAAAAAGCCAAAATTTATGCTACTCTAAGGAAAACTTCA
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	CACACCAGAGCATATATATTGGTGGCTCAAATCATAGAAACTTACAGTGAAGACACAGAAAGCCGTAAGAAGAGGC
	AAGAGTATGAAACCTTACCTCATCATTTCCATGAGGTTGCTTCTGATCCCGCGGGATATCACCACTTTGTACAAGAAA

	GCTGGGTCGAATTCGCCCTTGCATTGGGAATCGAGTTTTGAGAATTTCCTGAGCATCATCAACGGGGGCTTGAAGCA
	ACTGCTTGAGGTTACTATACTCTGGTCTATTTTGATAATCCATTGCTCTCCATTGAGCAATAGTCTCTCCATGGAATAT
	CAAAATATGGAAAAATGTGTCCATCAATAATATTTTATCAGGTTGAATACTACTGGTATCCAAAAGTACAGGTTCTG
	GCCTACCATTAAAACTATAGCTATACAGAATTGGCTGTATCATGATTAAACTTTGGGTAACATCTTCACGCATCAACA
	TGTGCCTATAATATGATGTTTCATCAGGACTATTATTAAAAACTTGTAGAAATTGAGACCTTCTTAAATGATACATGA
	ACTGTGGATATAAACTGAAGTTTTCTGGCAATCGGAAACTATTTGGATCATCTTTTTGATAATCACCAAATTTTTGAC
	ACAAGCGTATAAGCGTACGATCAGCCCAACGCATCACATCTGGACTATCCTCAGTTTCAGCACGGTTCACTACCATA
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MP016	SEQ ID NO: 1069
	GTTTTCAATGGCAGTGGAAAGCCGATAGATAAAGGACCTCCTATTTTGGCTGAAGATTATTTGGATATTGAAGGCCA
	ACCTATTAATCCATACTCCAGAACATATCCTCAAGAAATGATTCAAACTGGTATTTCAGCTATTGATATCATGAACTC
	TATTGCTCGTGGACAAAAAATTCCAATATTTTCAGCTGCAGGTTTACCACATAATGAGATTGCTGCTCAAATTTGTAG
	ACAAGCTGGTCTCGTTAAAAAAACCTGGTAAATCAGTTCTTGACGATCATGAAGACAATTTTGCTATAGTATTTGCTGC
	TATGGGTGTTAATATGGAAACAGCCAGATTCTTTAAACACAAGATTTTGAGGAAAATGGTTCAATGGAGAATGTTTGTT
	TGTTCTTGAATTTAGCTAATGATCCTACTATTGAGCGTATCATTACACCACGAAGGGCGAATTCGACCCAGCTTTCTT
	GTACAAAGTGGTGATATCACTAGTGCGGCCGCCTGCAGGTCGACCATATGGTCGACCTGCAGGCGGCCGCACTAGTG
	ATGCTGTTATGTTCAGTGTCAAGCTGACCTGCAAACACGTTAAATGCTAAGAAGTTAGAATATATGAGACACGTTAA
	CTGGTATATGAATAAGCTGTAAATAACCGAGTATAAACTCATTAACTATCACCTCTAGAGTATAATAATCAA
	ATTCGACAATTTGACTTTCAAGAGTAGGCTAAATGTAAAATCTTTATATATTTCTACAATGTTCAAAGAAACAGTTGCA
	TCTAAACCCCTATGGCCATCAAATTCAATGAACGCTAAGCTGATCCGGCGAGATTTTCAGGAGCTAAGGAAGCTAAA
	ATGGAGAAAAAAATCACTGGATATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTCA
	GTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATA
	AGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGGAATTCCGTATGGCAATGA
	AAGACGGTGAGCTGGTGATATGGGATAGTGTTCACACCGTTTTCCATGAGCAAACTGAAACGTTTTCAT
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	AAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGA
	ATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAAACGCGTGGATCAGCTTAATATGACTCTCTTCAATAAAGTC
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	AAAGAAGACGATTTAGAGTGTTTTACCAAGAAATTTCTGTCATCTTACTAAACAACTAAAGATCGGTGTGATACAAAA
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	GAGTATGAAACCTTACCTCATCATTTCCATGAGGTTGCTTCTGATCCCGCGGGATATCACCACTTTGTACAAGAAAGC
	TGGGTCGAATTCGCCCTTCGTGGTGTAATGATACGCTCAATAGTAGGATCATTAGCTAAATTCAAGAACACAAACAAC
	ATTCTCCATTGAACCATTTTCCTCAAAATCTTGTTTAAAGAATCTGGCTGTTTCCATATTAACACCCATAGCAGCAAA

	TACTATAGCAAAATTGTCTTCATGATCGTCAAGAACTGATTTACCAGGTTTTTTAACGAGACCAGCTTGTCTACAAAT TTGAGCAGCAATCTCATTATGTGGTAAACCTGCAGCTGAAAATATTGGAATTTTTTGTCCACGAGCAATAGAGTTCAT GATATCAATAGCTGAAATACCAGTTTGAATCATTTCTTGAGGATATGTTCTGGAGTATGGATTAATAGGTTGGCCTTC AATATCCAAATAATCTTCAGCCAAAATAGGAGGTCCTTTATCTATCGGCTTTCCACTGCCATTGAAAAC
MP027	SEQ ID NO: 1070 CCAAAAATACCATCTGCTCCACCTTCTGGTTTAAAAGACTTTTTTTCTTTAAAATTTTTAAAAACTTTGATTGTAGAAG AATTTTCTCTAATGGCATACTCAGAATCAGAAGACCATACAAAATCCTGAGCGGAGCCAAATGCTTTATTACGCAAA GCCATTGATGTATATATAATATACTCTCCATCACCACATACTACTAAAAATCTACCATTCGGATTATGAGATATTGAC TGTGGATAAATTTCACAGCTACCCATGTCTTTAACTTGTATTGGTAAACGTTCACCATCTTTGATTTCGGCTCCTTCTG CTTGAAGCATCGCTTTAAGGTTAGCTTGTTGAATTTCACTATGACGTGCCCAAACAATTTTACCCCCATGAACATCCA TTGACATTGCTGGCTCTTCACGACCAACTTTAACCATTATACTTCCTTCATCATAACCTAGAGCTACATTATTAGATCC CCGTAAGCAACAGATTGTCCATACACGTTCTAACCCATAGTTTAATGATGATTCTAATCGATAAGTACCAGAATGCC AAATTCTGACGGTACCATCTTCTGAGCCAGTTAACACGATGGGAAGTTCTGGATGGAAACAAACGAGCAAGGGCGA ATTCGACCCAGCTTTCTTGTACAAAGTGGTGATATCACTAGTGCGGCCGCCTGCAGGTCGACCATATGGTCGACCTGC AGGCGGCCGCACTAGTGATGCTGTTATGTTCAGTGTCAAGCTGACCTGCAAACACGTTAAATGCTAAGAAGTTAGAA TATATGAGACACGTTAACTGGTATATGAATAAGCTGTAAATAACCGAGTATAAACTCATTAACTAATATCACCTCTA GAGTATAATATAATCAAATTCGACAATTTGACTTTCAAGAGTAGGCTAATGTAAAATCTTTATATATTTCTACAATGT TCAAAGAAACAGTTGCATCTAAACCCCTATGGCCATCAAATTCAATGAACGCTAAGCTGATCCGGCGAGATTTTCAG GAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGA ACATTTTGAGGCATTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAA GACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGGA ATTCCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTACACCGTTTTCCATGAGC AAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATG TGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCT GGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTTTCACCATGGGCAAAT ATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCATGCCGTCTGTGATGGCTTCCATGTC GGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAAACGCGTGGATCAGCTTAAT ATGACTCTCAATAAAGTCTCATACCAACAAGTGCCACCTTATTCAACCATCAAGAAAAAAGCCAAAATTTATGCTAC TCTAAGGAAAACTTCACTAAAGAAGACGATTTAGAGTGTTTTACCAAGAATTTCTGTCATCTTACTAAACAACTAAA GATCGGTGTGATACAAAACCTAATCTCATTAAAGTTTATGCTAAAATAAGCATAATTTTACCCACTAAGCGTGACCA GATAAACATAACTCAGCACACCAGAGCATATATATTGGTGGCTCAAATCATAGAAACTTACAGTGAAGACACAGAA AGCCGTAAGAAGAGGCAAGAGTATGAAACCTTACCTCATCATTTCCATGAGGTTGCTTCTGATCCCGCGGGATATCA CCACTTTGTACAAGAAAGCTGGGTCGAATTCGCCCTTGCTCGTTTGTTTCCATCCAGAACTTCCCATCGTGTTAACTG GCTCAGAAGATGGTACCGTCAGAATTTGGCATTCTGGTACTTATCGATTAGAATCATCATTAAACTATGGGTTAGAA CGTGTATGGACAATCTGTTGCTTACGGGGATCTAATAATGTAGCTCTAGGTTATGATGAAGGAAGTATAATGGTTAA AGTTGGTCGTGAAGAGCCAGCAATGTCAATGGATGTTCATGGGGGTAAAATTGTTTGGGCACGTCATAGTGAAATTC

AACAAGCTAACCTTAAAGCGATGCTTCAAGCAGAAGGAGCCGAAATCAAAGATGGTGAACGTTTACCAATACAAGT TAAAGACATGGGTAGCTGTGTGAAATTTATCCACAGTCAATATCTCATAATCCGAATGGTAGATTTTTAGTAGTATGTGG TGATGGAGAGTATATTATATACATCAATGGCTTTGCGTAATAAAGCATTTGGCTCCGCTCAGGATTTTGTATGGTC TTCTGATTCTGAGTATGCCATTAGAGAAAATTCTTCTACAATCAAAGTTTTTAAAAATTTTAAAGAAAAAAAGTCTTT TAAACCAGAAGGTGGAGCAGATGGTATTTTTTGG

Table10-LD

bioassay	bacterial host strain	treatment	no. of survivors	total weight	average weight / larvae
I		diet only	8*	1.0245	0.1281
	AB309-105	pGN29	8*	1.0124	0.1266
		pGBNJ003 clone 1	4	0.0273	0.0068
		pGBNJ003 clone 2	1	0.0091	0.0091
		pGBNJ003 clone 3	25	0.7113	0.0285
		pGBNJ003 clone 4	12	0.1379	0.0115
		pGBNJ003 clone 5	12	0.1808	0.0151
II		diet only	8*	1.0435	0.1304
	BL21(DE3)	pGN29	8*	1.1258	0.1407
		pGBNJ003 clone 1	33	0.5879	0.0178
		pGBNJ003 clone 2	42	0.8034	0.0191
		pGBNJ003 clone 3	33	0.3441	0.0104
		pGBNJ003 clone 4	21	0.1738	0.0083
		pGBNJ003 clone 5	33	0.3628	0.0120

Tables 10-NL (a)

RNAi	Mean % survival (days post start)									Survival analysis[1]
	0	1	2	3	4	5	6	7	8	
gfp	100	98	90	82	68	60	44	32	20	-
diet only	100	98	96	86	74	68	58	54	38	-
NL002	100	98	90	76	68	34	6	0	0	+
NL003	100	98	74	48	36	22	12	2	0	+
NL005	100	100	74	56	40	20	16	6	4	+
NL010	100	96	74	56	48	30	18	12	8	+

[1] = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif.[2]
diet versus:			
NL002	29.06	<0.0001	Yes
NL003	39.59	<0.0001	Yes
NL005	29.55	<0.0001	Yes
NL010	21.04	<0.0001	Yes
gfp dsRNA versus:			
NL002	15.09	0.0001	Yes
NL003	22.87	<0.0001	Yes
NL005	15.12	<0.0001	Yes
NL010	8.838	0.0029	Yes
diet versus gfp dsRNA	4.030	0.0447 (~0.05)	No

[2] alpha < 0.05

Tables 10-NL (b)

RNAi	Mean % survival (days post start)									Survival analysis[1]
	0	1	2	3	4	5	6	7	8	
gfp	100	96	84	82	76	70	54	50	44	-
diet only	100	96	88	82	76	70	54	50	44	-
NL009	100	94	75	63	42	30	24	22	14	+
NL016	100	94	84	78	54	44	36	18	14	+

[1] = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif. [2]
diet versus:			
NL009	11.98	0.0005	Yes
NL016	8.98	0.0027	Yes
gfp dsRNA versus:			
NL009	13.69	0.0002	Yes
NL016	11.37	0.0007	Yes
diet versus gfp dsRNA	0.03317	0.8555	No

[2] alpha < 0.05

Tables 10-NL (c)

RNAi	Mean % survival (days post start)									Survival analysis[1]
	0	1	2	3	4	5	6	7	8	
gfp	100	92	84	78	72	62	58	56	48	-
diet only	100	84	72	68	64	58	52	42	42	-
NL014	100	86	68	60	46	32	24	18	14	+
NL018	100	82	70	54	40	30	18	14	12	+

[1] = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif. [2]
diet versus:			
NL014	8.088	0.0045	Yes
NL018	10.47	0.0012	Yes
gfp dsRNA versus:			
NL014	14.55	0.0001	Yes
NL018	17.64	<0.0001	Yes
diet versus gfp dsRNA	0.6548	0.4184	No

[2] alpha < 0.05

Tables 10-NL (d)

RNAi	Mean % survival (days post start)										Survival analysis[1]
	0	1	2	3	4	5	6	7	8	9	
gfp	100	96	84	84	72	68	68	66	66	62	-
diet only	100	96	86	82	74	72	70	70	66	58	-
NL013	100	94	82	68	50	40	30	28	20	20	+
NL015	100	100	72	30	18	12	8	6	6	6	+
NL021	100	100	84	58	50	44	40	34	34	22	+

[1] = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif. [2]
diet versus:			
NL013	15.73	<0.0001	Yes
NL015	39.44	<0.0001	Yes
NL021	12.75	0,0004	Yes
gfp dsRNA versus:			
NL013	16.42	<0.0001	Yes
NL015	39.15	<0.0001	Yes
NL021	14.1	0,0002	Yes
diet versus gfp dsRNA	0.1031	0,7481	No

[2] alpha < 0.05

Table 11-NL

NL002 RNAi	Mean % survival (days post start)								Survival analysis[1]
	0	1	2	3	4	5	6	7	
diet only	100	100	96	90	86	78	78	78	-
1 µg/µl	100	84	80	44	26	8	6	6	+
0.2 µg/µl	100	84	60	12	8	4	2	2	+
0.08 µg/µl	100	84	62	18	14	6	6	6	+
0.04 µg/µl	100	84	48	24	22	22	22	22	+

[1] = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif. [2]
diet versus:			
NL002 1 µg/µl	57.53	<0.0001	Yes
NL002 0.2 µg/µl	74.54	<0.0001	Yes
NL002 0.08 µg/µl	64	<0.0001	Yes
NL002 0.04 µg/µl	39.49	<0.0001	Yes

[2] alpha < 0.05