

Supplementary Materials

Update on the inactivation procedures for the vaccine development prospects of a new highly virulent RGNNV isolate

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| Table S1. Representative genotype sequences for designing broad-spectrum NNV RNA1 amplification primers. | | | | | | |
|--|--------------------------------|----------|------------------------|--|-----------|-------|
| Acc. no. | Isolate ref. | Genotype | Species host | | Country | Ref. |
| | | | Common name | Scientific name | | |
| NC_013458.1 | JFIwa98 | BFNNV | Barfin flounder | <i>Verasper moseri</i> | Japan | [1] |
| NC_008040.1 | SGWak97 | RGNNV | Red-spotted grouper | <i>Epinephelus akaara</i> | | [2] |
| NC_003448.1 | | SJNNV | Striped Jack | <i>Pseudocaranx dentex</i> | | [3] |
| NC_013460.1 | TPKag93 | TPNNV | Tiger puffer | <i>Takifugu rubripes</i> | Japan | [1] |
| KF386163.1 | 389/I96 | SJNNV | European seabass | <i>Dicentrarchus labrax</i> | Italy | [4] |
| JN189814.2 | 484.2.2009 | SJNNV | Senegalese sole | <i>Solea senegalensis</i> | Spain | [5] |
| FJ789783.1 | 1 | RGNNV | European seabass | <i>Dicentrarchus labrax</i> | Tunisia | [6] |
| JN189909.2 | 367.2.2005 | RGNNV | European seabass | <i>Dicentrarchus labrax</i> | Italy | [5] |
| AF319555.1 | Singapore | RGNNV | Greasy grouper | <i>Epinephelus tauvina</i> | Singapore | [7] |
| AY369136.1 | | RGNNV | Orange-spotted grouper | <i>Epinephelus coioides</i> | China | [1,8] |
| AY721616.1 | | RGNNV | Dragon grouper | <i>Epinephelus lanceolatus</i> | China | [1] |
| EF558368.1 | China 1 | RGNNV | Red-spotted grouper | <i>Epinephelus akaara</i> | China | [9] |
| JN189865.2 | 283.2009 | RGNNV | European seabass | <i>Dicentrarchus labrax</i> | Italy | [5] |
| KP455643.1 | SBN147 | RGNNV | Sea Perch | <i>Lateolabrax japonicus</i> | China | [10] |
| MN309751.1 | RGNNV201 | RGNNV | Hybrid tiger grouper | <i>Epinephelus fuscoguttatus</i> x <i>Epinephelus lanceolatus</i> | China | [11] |
| MT157513.1 | CNPgg2018 | RGNNV | Pearl gentian grouper | <i>Epinephelus lanceolatus</i> x <i>Epinephelus fuscoguttatus</i> | China | [12] |
| AJ401165.2 | AH99NorA | BFNNV | Atlantic halibut | <i>Hippoglossus hippoglossus</i> | Norway | [13] |
| MF144242.1 | KS1 | RGNNV | Orange-spotted grouper | <i>Epinephelus coioides</i> | Taiwan | [14] |
| KY315688.1 | MENNV1310 | RGNNV | Marbled eel | <i>Anguilla marmorata</i> | Taiwan | |
| KY354681.1 | VNNV/S.aurata/I/425-10/Sep2008 | RGNNV | Gilthead seabream | <i>Sparus aurata</i> | Italy | [15] |
| MN245301.1 | SK-07 1324 | BFNNV | Atlantic cod | <i>Gadus morhua</i> | Norway | [16] |
| Reference sequences are shaded. | | | | | | |

| Table S2. Representative genotype sequences for designing broad-spectrum NNV RNA2 amplification primers. | | | | | | |
|--|-----------------------------------|----------|-----------------------|--|-------------------|------|
| Acc. no. | Isolate ref. | Genotype | Species host | | Country | Ref. |
| | | | Common name | Scientific name | | |
| NC_013459.1 | JFIwa98 | BFNNV | Barfin flounder | <i>Verasper moseri</i> | Japan | [1] |
| NC_008041.1 | SGWak97 | RGNNV | Red-spotted grouper | <i>Epinephelus akaara</i> | | [2] |
| NC_003449.1 | | SJNNV | Striped Jack | <i>Pseudocaranx dentex</i> | | [3] |
| NC_013461.1 | TPKag93 | TPNNV | Tiger puffer | <i>Takifugu rubripes</i> | Japan | [1] |
| KY315689.1 | MENNV1310 | RGNNV | Marbled eel | <i>Anguilla marmorata</i> | Taiwan | |
| AY744705.1 | RGNNV-CN | RGNNV | Red-spotted grouper | <i>Epinephelus akaara</i> | China | [17] |
| JF412263.1 | BVN-CIBA10 | RGNNV | Barramundi | <i>Lates calcarifer</i> | India | |
| KF386164.1 | 389/I96 | RGNNV | European seabass | <i>Dicentrarchus labrax</i> | Italy | [4] |
| MN309752.1 | RGNNV201 | RGNNV | Hybrid tiger grouper | <i>Epinephelus fuscoguttatus</i> x <i>Epinephelus lanceolatus</i> | China | [11] |
| EF617327.1 | Ac06NorPp | BFNNV | Atlantic cod | <i>Gadus morhua</i> | Norway | |
| FJ789784.1 | 1 | RGNNV | European seabass | <i>Dicentrarchus labrax</i> | Tunisia | [6] |
| JN189992.2 | 283.2009 | RGNNV | European seabass | <i>Dicentrarchus labrax</i> | Italy | [5] |
| MG637439.1 | ZN521 | RGNNV | Pearl gentian grouper | <i>Epinephelus lanceolatus</i> x <i>Epinephelus fuscoguttatus</i> | China | |
| KM588181.1 | GGNNV20131122 | RGNNV | Giant grouper | <i>Epinephelus lanceolatus</i> | Taiwan | [18] |
| JN189919.2 | 484.2.2009 | SJNNV | Senegalese sole | <i>Solea senegalensis</i> | Spain | [5] |
| JN189936.2 | 367.2.2005 | SJNNV | European seabass | <i>Dicentrarchus labrax</i> | Italy | [5] |
| KY354694.1 | VNNV/S.aurata/I/425-10/Sep2008 | RGNNV | Gilthead seabream | <i>Sparus aurata</i> | Italy | |
| GU592791.1 | LcNNV | RGNNV | Barramundi | <i>Lates calcarifer</i> | India | |
| KY354702.2 | VNNV/S.aurata/Farm1/461-1/Nov2014 | SJNNV | Gilthead seabream | <i>Sparus aurata</i> | Mediterranean Sea | [19] |
| AF245003.1 | | RGNNV | Malabar grouper | <i>Epinephelus malabaricus</i> | Taiwan | [20] |
| AF245004.1 | | RGNNV | Giant grouper | <i>Epinephelus lanceolatus</i> | Taiwan | [20] |
| KM576685.1 | PCNNV | BFNNV | Pacific cod | <i>Gadus macrocephalus</i> | China | [21] |
| AF499774.1 | | RGNNV | Guppy | <i>Poecilia reticulata</i> | Singapore | [22] |
| KU705815.1 | VI37 | RGNNV | Mouse grouper | <i>Cromileptes altivelis</i> | Vietnam | [23] |
| JX402858.1 | Tilapia-CU-2011 | RGNNV | Nile tilapia | <i>Oreochromis niloticus</i> | Thailand | [24] |
| Reference sequences are shaded. | | | | | | |

| Table S3. BLASTn top resulting records similar to the RNA1 sequence from the NNV isolated in this work. | | | | | | | | |
|---|-------------------|---|-----------|-------------|-------------|---------|------------|----------|
| Accession | Coverage | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. ident | Acc. Len |
| JN189865.2 | complete cds | Dicentrarchus labrax betanodavirus | 1415 | 1415 | 100% | 0.0 | 99.49 | 3103 |
| MF144242.1 | complete sequence | Epinephelus coioides nervous necrosis virus | 1349 | 1349 | 100% | 0.0 | 97.95 | 3100 |
| KY930893.1 | complete cds | Betanodavirus sp. | 1349 | 1349 | 100% | 0.0 | 97.95 | 2946 |
| MH758753.1 | complete cds | Redspotted grouper nervous necrosis virus | 1343 | 1343 | 100% | 0.0 | 97.82 | 3024 |
| KC696563.1 | complete cds | Redspotted grouper nervous necrosis virus | 1343 | 1343 | 100% | 0.0 | 97.82 | 2991 |
| AY324869.1 | complete cds | Sevenband grouper nervous necrosis virus | 1343 | 1343 | 100% | 0.0 | 97.82 | 3105 |
| GQ402010.1 | complete cds | Redspotted grouper nervous necrosis virus | 1338 | 1338 | 100% | 0.0 | 97.69 | 2998 |
| KY354681.1 | complete cds | Sparus aurata betanodavirus | 1332 | 1332 | 100% | 0.0 | 97.56 | 3051 |
| FJ809938.1 | complete cds | Redspotted grouper nervous necrosis virus | 1332 | 1332 | 100% | 0.0 | 97.56 | 2949 |
| FJ803915.1 | complete cds | Sea bass Iberian betanodavirus | 1327 | 1327 | 100% | 0.0 | 97.43 | 3089 |
| AY690597.1 | partial cds | Redspotted grouper nervous necrosis virus | 1327 | 1327 | 100% | 0.0 | 97.43 | 2968 |
| KT390713.1 | partial cds | Grouper betanodavirus | 1321 | 1321 | 100% | 0.0 | 97.30 | 2871 |
| FJ748760.1 | complete sequence | Japanese flounder nervous necrosis virus | 1321 | 1321 | 100% | 0.0 | 97.30 | 3104 |
| AB373028.1 | complete sequence | Sevenband grouper nervous necrosis virus | 1321 | 1321 | 100% | 0.0 | 97.30 | 3105 |
| AF319555.1 | complete cds | Epinephelus tauvina nervous necrosis virus | 1321 | 1321 | 100% | 0.0 | 97.30 | 3103 |
| AF326776.1 | complete sequence | Epinephelus tauvina nervous necrosis virus | 1321 | 1321 | 100% | 0.0 | 97.30 | 3007 |
| MH181161.1 | complete cds | Redspotted grouper nervous necrosis virus | 1315 | 1315 | 100% | 0.0 | 97.18 | 3090 |
| HQ859913.1 | complete cds | Tiger grouper Nervous Necrosis Virus | 1315 | 1315 | 100% | 0.0 | 97.18 | 3024 |
| HQ859908.1 | complete cds | Tiger grouper Nervous Necrosis Virus | 1315 | 1315 | 100% | 0.0 | 97.18 | 3024 |
| HQ859892.1 | complete cds | Mouse grouper Nervous Necrosis Virus | 1315 | 1315 | 100% | 0.0 | 97.18 | 3024 |
| AY721616.1 | complete cds | Dragon grouper nervous necrosis virus | 1315 | 1315 | 100% | 0.0 | 97.18 | 3103 |
| HQ859895.1 | complete cds | Tiger grouper Nervous Necrosis Virus | 1310 | 1310 | 100% | 0.0 | 97.05 | 3024 |
| HQ859890.1 | complete cds | Asian seabass Nervous Necrosis Virus | 1310 | 1310 | 100% | 0.0 | 97.05 | 3024 |
| HQ859887.1 | complete cds | Asian seabass Nervous Necrosis Virus | 1310 | 1310 | 100% | 0.0 | 97.05 | 3024 |
| EF558368.1 | complete cds | Redspotted grouper nervous necrosis virus | 1310 | 1310 | 100% | 0.0 | 97.05 | 3103 |
| KM095958.1 | complete sequence | Sevenband grouper nervous necrosis virus | 1304 | 1304 | 100% | 0.0 | 96.92 | 3103 |

| | | | | | | | | |
|------------|-------------------|--|------|------|------|-----|-------|------|
| MN097800.1 | partial cds | Betanodavirus sp. | 1299 | 1299 | 100% | 0.0 | 96.79 | 2727 |
| MN097798.1 | complete cds | Betanodavirus sp. | 1299 | 1299 | 100% | 0.0 | 96.79 | 2961 |
| HQ859916.1 | complete cds | Asian seabass Nervous Necrosis Virus | 1299 | 1299 | 100% | 0.0 | 96.79 | 3024 |
| HQ859911.1 | complete cds | Asian seabass Nervous Necrosis Virus | 1299 | 1299 | 100% | 0.0 | 96.79 | 3024 |
| FJ803913.1 | complete cds | Gilthead sea bream Iberian betanodavirus | 1299 | 1299 | 100% | 0.0 | 96.79 | 3101 |
| GQ904198.1 | complete cds | Golden pompano nervous necrosis virus | 1299 | 1299 | 100% | 0.0 | 96.79 | 3024 |
| FJ789783.1 | complete sequence | Redspotted grouper nervous necrosis virus | 1299 | 1299 | 100% | 0.0 | 96.79 | 3104 |
| KU705814.1 | complete sequence | Mouse grouper Nervous Necrosis Virus | 1293 | 1293 | 100% | 0.0 | 96.66 | 3017 |
| FJ803914.1 | complete cds | Senegalese sole Iberian betanodavirus | 1293 | 1293 | 100% | 0.0 | 96.66 | 3042 |
| FJ803912.1 | complete cds | Gilthead sea bream Iberian betanodavirus | 1293 | 1293 | 100% | 0.0 | 96.66 | 3065 |
| MG387122.1 | complete cds | Betanodavirus sp. | 1288 | 1288 | 100% | 0.0 | 96.53 | 3105 |
| KP455643.1 | complete sequence | Sevenband grouper nervous necrosis virus | 1288 | 1288 | 100% | 0.0 | 96.53 | 3103 |
| FJ803911.2 | complete cds | Senegalese sole Iberian betanodavirus | 1288 | 1288 | 100% | 0.0 | 96.53 | 3105 |
| KJ541747.1 | complete cds | Redspotted grouper nervous necrosis virus | 1288 | 1288 | 100% | 0.0 | 96.53 | 3103 |
| JN189909.2 | complete cds | Dicentrarchus labrax betanodavirus | 1288 | 1288 | 100% | 0.0 | 96.53 | 3104 |
| KY354688.2 | complete sequence | Sparus aurata betanodavirus | 1288 | 1288 | 100% | 0.0 | 96.53 | 2984 |
| FJ803916.1 | complete cds | Gilthead sea bream Iberian betanodavirus | 1288 | 1288 | 100% | 0.0 | 96.53 | 3051 |
| MG874757.1 | complete sequence | Epinephelus coioides nervous necrosis virus | 1282 | 1282 | 100% | 0.0 | 96.41 | 3103 |
| KF668184.1 | complete cds | Redspotted grouper nervous necrosis virus | 1277 | 1277 | 100% | 0.0 | 96.28 | 3024 |
| GQ402012.1 | complete cds | Redspotted grouper nervous necrosis virus | 1277 | 1277 | 100% | 0.0 | 96.28 | 2998 |
| MN309751.1 | complete sequence | Hulong grouper nervous necrosis virus | 1271 | 1271 | 100% | 0.0 | 96.15 | 3103 |
| KY785170.1 | partial cds | Sparus aurata betanodavirus | 1269 | 1269 | 100% | 0.0 | 96.02 | 2826 |
| MT157513.1 | complete cds | Pearl gentian grouper nervous necrosis virus | 1249 | 1249 | 100% | 0.0 | 95.64 | 3103 |
| AY369136.1 | complete sequence | Redspotted grouper nervous necrosis virus | 1249 | 1249 | 100% | 0.0 | 95.64 | 3103 |
| MG600032.1 | complete cds | Betanodavirus sp. | 1238 | 1238 | 100% | 0.0 | 95.38 | 3109 |
| MN709776.1 | complete cds | Redspotted grouper nervous necrosis virus | 1232 | 1232 | 100% | 0.0 | 95.25 | 3024 |
| KY315688.1 | complete sequence | Redspotted grouper nervous necrosis virus | 1232 | 1232 | 100% | 0.0 | 95.25 | 3095 |
| HQ859906.1 | complete cds | Tiger grouper Nervous Necrosis Virus | 1232 | 1232 | 100% | 0.0 | 95.25 | 3024 |
| HQ859903.1 | complete cds | Asian seabass Nervous Necrosis Virus | 1232 | 1232 | 100% | 0.0 | 95.25 | 3024 |

| | | | | | | | | |
|------------|--------------|---------------------------------------|------|------|------|-----|-------|------|
| HQ859900.1 | complete cds | Golden pompano nervous necrosis virus | 1232 | 1232 | 100% | 0.0 | 95.25 | 3024 |
| HQ859898.1 | complete cds | Asian seabass Nervous Necrosis Virus | 1227 | 1227 | 100% | 0.0 | 95.12 | 3024 |

| Table S4. BLASTn top resulting records similar to the RNA2 sequence from the NNV isolated in this work. | | | | | | | | |
|---|-------------------|--|-----------|-------------|-------------|---------|------------|----------|
| Accession | Coverage | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. ident | Acc. Len |
| JN189992.2 | complete cds | Dicentrarchus labrax betanodavirus | 1799 | 1799 | 100% | 0.0 | 99.59 | 1433 |
| MN709777.1 | complete cds | Redspotted grouper nervous necrosis virus | 1600 | 1600 | 100% | 0.0 | 95.95 | 1362 |
| HQ859938.1 | complete cds | Tiger grouper Nervous Necrosis Virus | 1594 | 1594 | 100% | 0.0 | 95.85 | 1363 |
| HQ859935.1 | complete cds | Asian seabass Nervous Necrosis Virus | 1589 | 1589 | 100% | 0.0 | 95.74 | 1363 |
| HQ859945.1 | complete cds | Tiger grouper Nervous Necrosis Virus | 1583 | 1583 | 100% | 0.0 | 95.64 | 1363 |
| HQ859924.1 | complete cds | Mouse grouper Nervous Necrosis Virus | 1583 | 1583 | 100% | 0.0 | 95.64 | 1363 |
| HQ859930.1 | complete cds | Asian seabass Nervous Necrosis Virus | 1583 | 1583 | 100% | 0.0 | 95.65 | 1363 |
| AY721615.1 | complete cds | Dragon grouper nervous necrosis virus | 1578 | 1578 | 100% | 0.0 | 95.54 | 1433 |
| MH758754.1 | complete cds | Redspotted grouper nervous necrosis virus | 1572 | 1572 | 100% | 0.0 | 95.44 | 1358 |
| GU826692.1 | complete sequence | Lates calcarifer nervous necrosis virus | 1572 | 1572 | 100% | 0.0 | 95.44 | 1434 |
| KC696562.1 | complete cds | Redspotted grouper nervous necrosis virus | 1567 | 1567 | 100% | 0.0 | 95.34 | 1366 |
| HQ859948.1 | complete cds | Asian seabass Nervous Necrosis Virus | 1567 | 1567 | 100% | 0.0 | 95.34 | 1363 |
| HM485328.1 | complete sequence | Lates calcarifer nervous necrosis virus | 1567 | 1567 | 100% | 0.0 | 95.34 | 1434 |
| AY324870.1 | complete cds | Sevenband grouper nervous necrosis virus | 1567 | 1567 | 100% | 0.0 | 95.34 | 1434 |
| AF281657.1 | complete cds | Epinephelus tauvina nervous necrosis virus | 1567 | 1567 | 100% | 0.0 | 95.34 | 1368 |
| MG637439.1 | complete cds | Pearl gentian grouper nervous necrosis virus | 1561 | 1561 | 100% | 0.0 | 95.24 | 1432 |
| HQ859927.1 | complete cds | Tiger grouper Nervous Necrosis Virus | 1561 | 1561 | 100% | 0.0 | 95.24 | 1363 |
| AB373029.1 | complete sequence | Sevenband grouper nervous necrosis virus | 1561 | 1561 | 100% | 0.0 | 95.24 | 1433 |
| AY690596.1 | complete cds | Redspotted grouper nervous necrosis virus | 1561 | 1561 | 100% | 0.0 | 95.24 | 1430 |
| MF510920.1 | complete cds | Epinephelus coioides nervous necrosis virus | 1555 | 1555 | 100% | 0.0 | 95.14 | 1433 |
| KY354694.1 | complete cds | Sparus aurata betanodavirus | 1555 | 1555 | 100% | 0.0 | 95.14 | 1416 |
| MW590702.1 | complete sequence | Redspotted grouper nervous necrosis virus | 1555 | 1555 | 100% | 0.0 | 95.14 | 1316 |
| GU826693.1 | complete cds | Lates calcarifer nervous necrosis virus | 1555 | 1555 | 100% | 0.0 | 95.14 | 1089 |
| MT157514.1 | complete cds | Pearl gentian grouper nervous necrosis virus | 1550 | 1550 | 100% | 0.0 | 95.04 | 1434 |

Figure S1. Multiple sequence alignment of RNA1 sequences from the selected genotype representatives.

| GB acc. no | | bp |
|-------------|---|-----|
| AY369136.1 | TAACATCACCTTCTTGCTCTGTTGAGTCATCACTTACGCAAGGTTACCGTTCAGCTTAGA | 60 |
| KY315688.1 | -----CTTCTTGCTCTGTTGAGTAATCACTTACGCAAGGTTACCGTTCAGCTTAGA | 51 |
| JN189909.2 | TAACATCACCTTCTTGCTCTGTTGAGTAATCACTTACGCAAGGTTACCGTTCAGCTTAGA | 60 |
| MT157513.1 | TTACATCACCTTCTTGCTCTGTTGAGTAATCACTTACGCAAGGTTACCGTTCAGCTTAGA | 60 |
| JN189865.2 | TAACATCACCTTCTTGCTCTGTTGAGTAATCACTTACGCAAGGTTACCGTTCAGCTTAGA | 60 |
| MF144242.1 | TAACATCACCTTCTTGCTCTGTTGAGTAATCACTTACGCAAGGTTACCGTTCAGCTTAGA | 60 |
| AF319555.1 | TAACATCACCTTCTTGCTCTGTTGAGTAATCACTTACGCAAGGTTACCGTTCAGCTTAGA | 60 |
| FJ789783.1 | TAACATCACCTTCTTGCTCTGTTGAGTAATCACTTACGCAAGGTTACCGTTCAGCTTAGA | 60 |
| NC_008040.1 | TAACATCACCTTCTTGCTCTGTTGAGTAATCACTTACGCAAGGTTACCGTTTAGCTTAGA | 60 |
| EF558368.1 | TAACATCACCTTCTTGCTCTGTTGAGTCATCACTTACGCAAGGTTACCGTTCAGCTTAGA | 60 |
| AY721616.1 | TAACATCACCTTCTTGCTCTGTTGAGTAATCACTTACGCAAGGTTACCGTTCAGCTTAGA | 60 |
| KY354681.1 | ---CATCACCTTCTTGCTCTGTTGAGTAATCACTTACGCAAGGTTACCGTTCAGCTTAGA | 57 |
| KP455643.1 | TAACATCACCTTCTTGCTCTGTTGAGTAATCACTTACGCAAGGTTACCGTTCAGCTTAGA | 60 |
| MN309751.1 | TAACATCACCTTCTTGCTCTGTTGAGTAATCACTTACGCAAGGTTACCGTTCAGCTTAGA | 60 |
| | ***** | |
| AY369136.1 | CAACGACAAGTCTACGCCATGCGTCGCTTTGAGTTCGCACTCGCACGCATGTCTGGAGCA | 120 |
| KY315688.1 | CAACGACAAGTCTAGGCCATGCGTCGCTTTGAGTTCGCACTCGCACGCATGACTGGAGCA | 111 |
| JN189909.2 | CAACGACAAGTCTACGCCATGCGTCGCTTTGAGTTCGCACTCGCACGCATGTCTGGAGCA | 120 |
| MT157513.1 | CA-AGACAAGTCTACGCCATGCGTCGCTTTGAGTTTGCACTCGCACGCATGTCTGGAGCA | 119 |
| JN189865.2 | CAACGACAAGTCTACGCCATGCGTCGCTTTGAGTTTGCACTCGCACGCATGTCTGGAGCA | 120 |
| MF144242.1 | CAACGACAAGTCTACGCCATGCGTCGCTTTGAGTTCGCACTCGCACGCATGTCTGGAGCA | 120 |
| AF319555.1 | CAACGACAAGTCTACGCCATGCGTCGCTTTGAGTTTGCACTCGCACGCATGTCTGGAGCA | 120 |
| FJ789783.1 | CAACGACAAGTCTACGCCATGCGTCGCTTTGAGTTTGCACTCGCACGCATGTCTGGAGCA | 120 |
| NC_008040.1 | CAACGACAAGTCTACGCCATGCGTCGCTTTGAGTTTGCACTCGCACGCATGTCTGGAGCA | 120 |
| EF558368.1 | CAACGACAAGTCTACGCCATGCGTCGCTTTGAGTTTGCACTCGCACGCATGTCTGGAGCA | 120 |
| AY721616.1 | CAACGACAAGTCTACGCCATGCGTCGCTTTGAGTTTGCACTCGCACGCATGTCTGGAGCA | 120 |
| KY354681.1 | CAACGACAAGTCTACGCCATGCGTCGCTTTGAGTTTGCACTCGCACGCATGTCTGGAGCA | 117 |
| KP455643.1 | CAACGACAAGTCTACGCCATGCGTCGCTTTGAGTTTGCACTCGCACGCATGTCTGGAGCA | 120 |
| MN309751.1 | CAACGACAAGTCTACGCCATGCGTCGCTTTGAGTTTGCACTCGCACGCATGTCTGGAGCA | 120 |
| | ** ***** | |
| AY369136.1 | GCATTTTGTGTGTACACAGGCTACCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTT | 180 |
| KY315688.1 | GCATTTTGTGTGTACACAGGCTACCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTT | 171 |
| JN189909.2 | GCATTTTGTGTGTACACAGGCTACCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTT | 180 |
| MT157513.1 | GCATTTTGTGTGTACACAGGCTACCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTT | 179 |
| JN189865.2 | GCATTTTGTGTGTACACAGGCTATCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTC | 180 |
| MF144242.1 | GCATTTTGTGTGTACACAGGCTACCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTT | 180 |
| AF319555.1 | GCATTTTGTGTGTACACAGGCTACCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTT | 180 |
| FJ789783.1 | GCATTTTGTGTGTACACAGGCTATCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTC | 180 |
| NC_008040.1 | GCATTTTGTGTGTACACAGGCTACCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTT | 180 |
| EF558368.1 | GCATTTTGTGTGTACACAGGCTACCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTT | 180 |
| AY721616.1 | GCATTTTGTGTGTACACAGGCTACCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTT | 180 |
| KY354681.1 | GCATTTTGTGTGTACACAGGCTACCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTT | 177 |
| KP455643.1 | GCATTTTGTGTGTACACAGGCTACCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTT | 180 |
| MN309751.1 | GCATTTTGTGTGTACACAGGCTACCGCTGTTGACCTCAAAATGGCTCGCGGACCGTGTT | 180 |
| | ***** | |
| AY369136.1 | GAGGATTATCGCCAACGCATCATCGCTGAGAAGAAACAAGTTCTCCGTGATGCGGCCATG | 240 |
| KY315688.1 | GAGGATTATCGCCATCGCATCATCGCTGAGAAGAAACAAGTTCTCCGTGATGCGGCCATG | 231 |
| JN189909.2 | GAGGATTATCGCCAACGCATCATCGCTGAGAAGAAACAAGTTCTCCGTGATGCGGCCATG | 240 |
| MT157513.1 | GAGGATTATCGCCAACGCATCATCGCTGAGAAGAAACAAGTTCTCCGTGATGCGGCCATG | 239 |
| JN189865.2 | GAGGATTATCGCCAACGCGTCATTGCTGAGAAGAAACAAGTTCTCCGTGATGCGGCCATG | 240 |
| MF144242.1 | GAGGATTATCGCCAACGCGTCATCGCTGAGAAGAAACAAGTTCTCCGTGACGCGGCCATG | 240 |
| AF319555.1 | GAGGATTATCGCCAACGCATCATCGCTGAGAAGAAACAAGTTCTCCGTGATGCGGCCATG | 240 |
| FJ789783.1 | GAGGATTATCGCCAACGCGTCATTGCTGAGAAGAAACAAGTTCTCCGTGATGCGGCCATG | 240 |
| NC_008040.1 | GAGGATTATCGCCAACGCGTCATCGCTGAGAAGAAACAAGTTCTCCGTGATGCGGCCATG | 240 |
| EF558368.1 | GAGGATTATCGCCAACGCGTCACCGCTGAGAAGAAACAAGTTCTCCGTGATGCGGCCATG | 240 |
| AY721616.1 | GAGGATTATCGCCAACGCGTCATCGCTGAGAAGAAACAAGTTCTCCGTGACGCGGCCATG | 240 |
| KY354681.1 | GAGGATTATCGCCAACGCGTCATCGCTGAGAAGAAACAAGTTCTCCGTGACGCGGCCATG | 237 |
| KP455643.1 | GAGGATTATCGCCAACGCGTCATCGCTGAGAAGAAACAAGTTCTCCGTGACGCGGCCATG | 240 |
| MN309751.1 | GAGGATTATCGCCAACGCGTCATCGCTGAGAAGAAACAAGTTCTCCGTGACGCGGCCATG | 240 |
| | ***** | |
| AY369136.1 | ATCCGGACTCAGATCCAGCGGAAATGGAATTGGTGCGCATCTCGGTGCGCAAAGGCCAT | 300 |
| KY315688.1 | ATCCGGACTCAGATCCAGCGGAAATGGAATTGGTGCGCATTTCCGGTGCGBAAAGGCCAT | 291 |
| JN189909.2 | ATCCGGACTCAGATCCAGCGGAAATGGAATTGGTGCGCATCTCGGTGCGCAAAGGCCAT | 300 |
| MT157513.1 | ATCCGGACTCAGATCCAGCGGAAATGGAGCTGGTGCGCATCTCGGTGCGCAAAGGCCAT | 299 |
| JN189865.2 | ATCCGGACTCAGATCCAGCGGAAATGGAACCTGGTACGCATTTCCGGTGCGBAAAGGCCAT | 300 |
| MF144242.1 | ATCCGGACTCAGATCCAGCGGAAATGGAGCTAGTGCGCATTTCCGGTGCGBAAAGGCCAT | 300 |
| AF319555.1 | ATCCGTACTCAGATCCAGCGGAAATGGAGCTGGTGCGCATCTCGGTGCGCAAAGGCCAT | 300 |
| FJ789783.1 | ATCCGGACTCAGATCCAGCGGAAATGGAACCTGGTGCGCATTTCCGGTGCGBAAAGGCCAT | 300 |

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| NC_008040.1 | ATCCGGACTCAGATCCAGCGGGAAATGGAAGTGGTGCGTATCTCGGTGCGCAAAGGCCAT | 300 |
| EF558368.1 | ATCCGGACTCAGATCCAGCGGGAAATGGAAGTGGTGCGTATCTCGGTGCGCAAAGGCCAT | 300 |
| AY721616.1 | ATCCGGACTCAGATCCAGCGGGAAATGGAGCTAGTGCGTATCTCGGTGCGCAAAGGCCAT | 300 |
| KY354681.1 | ATCCGGACTCAGATCCAGCGGGAAATGGAGCTAGTGCGCATTTTCGGTGCGCAAAGGCCAT | 297 |
| KP455643.1 | ATCCGGACTCAGATCCAGCGGGAAATGGAGCTAGTGCGCATTTTCGGTGCGCAAAGGCCAT | 300 |
| MN309751.1 | ATCCGGACCCAGATCCAGCGGGAAATGGAGCTAGTGCGCATCTCGGTGCGCAAAGGCCAT | 300 |
| | ***** ** ***** * ** * * ***** * | |
| AY369136.1 | TCCCATCAGGAAGCTGCTACTGAGCGTAACAGCGCCACTGAGACCATGCTCGGTGTGGTG | 360 |
| KY315688.1 | TCCCATCAGGAAGCTGCTACTGAGCGTAACAGCGCCACTGAGACCATGCTCGGTGTGGTG | 351 |
| JN189909.2 | TCCCATCAGGAAGCTGCTACTGAGCGTAACAGCGCCACTGAGACCATGCTCGGTGTGGTG | 360 |
| MT157513.1 | TCCCACCAGGAAGCTGCTACTGAGCGTAACAGCGCCACTGAAACCATGCTCGGTGTGGTG | 359 |
| JN189865.2 | TCCCACCAGGAAGCTGCTACTGAGCGTAACAGCGCCACTGAGACCATGCTCGGTGTGGTG | 360 |
| MF144242.1 | TCCCATCAGGAAGCCGCTACTGAGCGTAACAGCGCTACTGAGACCATGCTCGGTGTGGTG | 360 |
| AF319555.1 | TCCCACCAGGAAGCTGCTACTGAGCGTAACAGCGCCACTGAGACCATGCTCGGTGTGGTG | 360 |
| FJ789783.1 | TCCCATCAGGAAGCCGCTACTGAGCGTAACAGCGCTACTGAGACCATGCTCGGTGTGGTG | 360 |
| NC_008040.1 | TCCCATCAGGAAGCCGCTACTGAGCGTAACAGCGCTACTGAGACCATGCTCGGTGTGGTG | 360 |
| EF558368.1 | TCCCATCAGGAAGCCGCTACTGAGCGTAACAGCGCTACTGAGACCATGCTCGGTGTGGTG | 360 |
| AY721616.1 | TCCCATCAGGAAGCCGCTACTGAGCGTAACAGCGCCACTGAGACCATGCTCGGTGTGGTG | 360 |
| KY354681.1 | TCCCATCAGGAAGCCGCTACTGAGCGTAACAGCGCTACTGAGACCATGCTCGGTGTGGTG | 357 |
| KP455643.1 | TCCCATCAGGAAGCCGCTACTGAGCGTAACAGCGCTACTGAGACCATGCTCGGTGTGGTG | 360 |
| MN309751.1 | TCCCATCAGGAAGCCGCTACTGAGCGTAACAGCGCTACTGAGACCATGCTCGGTGTGGTG | 360 |
| | ***** ***** ***** ***** ***** ***** ***** | |
| AY369136.1 | GAGAAATGTGGCTATGAGCCATATGTCAATTTACCATCACCCCGTGAGGTTGGATACCAC | 420 |
| KY315688.1 | GAGAAATGTGGCTATGAGCCATATGTCAATTTACCATCACCCCGTGAGGTTGGATACCAC | 411 |
| JN189909.2 | GAGAAATGTGGCTATGAGCCATATGTCAATTTACCATCACCCCGTGAGGTTGGATACCAC | 420 |
| MT157513.1 | GAGAAATGTGGCTACGAGCCATATGTATCTCTCCATCACCCCGTGAGGTTGGATACCAC | 419 |
| JN189865.2 | GAGAAATGCGGCTACGAGCCATATGTCAATTTACCATCACCCCGTGAGGTTGGATACCAC | 420 |
| MF144242.1 | GAGAAATGTGGCTACGAGCCATATGTCAATTTACCATCACCCCGTGAGGTTGGATACCAC | 420 |
| AF319555.1 | GAGAAATGTGGCTACGAGCCATATGTCAATTTCTCCATCACCCCGTGAGGTTGGATACCAC | 420 |
| FJ789783.1 | GAGAAATGTGGCTACGAGCCATATGTCAATTTACCATCACCCCGTGAGGTTGGATACCAC | 420 |
| NC_008040.1 | GAGAAATGTGGCTACGAGCCATATGTCAATTTACCATCACCCCGTGAGGTTGGATACCAC | 420 |
| EF558368.1 | GAGAAATGTGGCTACGAGCCATATGTCAATTTACCATCACCCCGTGAGGTTGGATACCAC | 420 |
| AY721616.1 | GAGAAATGTGGCTACGAGCCATATGTCAATTTACCATCACCCCGTGAGGTTGGATACCAC | 420 |
| KY354681.1 | GAGAAATGTGGCTACGAGCCATATGTCAATTTACCATCACCCCGTGAGGTTGGATACCAC | 417 |
| KP455643.1 | GAGAAATGTGGCTACGAGCCATATGTCAATTTACCATCACCCCGTGAGGTTGGATACCAC | 420 |
| MN309751.1 | GAGAAATGTGGCTACGAGCCATATGTCAATTTACCATCACCCCGTGAGGTTGGATACCAC | 420 |
| | ***** ***** ***** ** ** * ***** ***** ***** * | |
| AY369136.1 | GGGTCACGTCAGTTCTACAGTCTGGCGGATTTCCGCCAAGACTACCGTCGCGATGACATC | 480 |
| KY315688.1 | GGGTCACGTCAGTTCTACAGTCTGGCGGATTTCCGCCAAGACTACCGTCGCGATGACATC | 471 |
| JN189909.2 | GGGTCACGTCAGTTCTATAGTCTGGCAGATTTTCGCCAAGACTACCGTCGCGATGACATC | 480 |
| MT157513.1 | GGGTCACGTCAGTTCTATAGTCTGGCAGATTTTCGCCAAGACTACCGTCGCGATGACATC | 479 |
| JN189865.2 | GGGTCACGTCAGTTCTATAGTCTGGCAGATTTTCGCCAAGACTACCGTCGCGATGACATC | 480 |
| MF144242.1 | GGGTCACGTCAGTTCTATAGTCTGGCAGATTTTCGCCAAGACTACCGTCGCGATGACATC | 480 |
| AF319555.1 | GGGTCACGTCAGTTCTATAGTCTGGCAGATTTTCGCCAAGACTACCGTCGCGATGACATC | 480 |
| FJ789783.1 | GGGTCACGTCAGTTCTATAGTCTGGCAGATTTTCGCCAAGACTACCGTCGCGATGACATC | 480 |
| NC_008040.1 | GGGTCACGTCAGTTCTATAGTCTGGCAGATTTTCGCCAAGACTACCGTCGCGATGACATC | 480 |
| EF558368.1 | GGGTCACGTCAGTTCTATAGTCTGGCAGATTTTCGCCAAGACTACCGTCGCGATGACATC | 480 |
| AY721616.1 | GGGTCACGTCAGTTCTATAGTCTGGCAGATTTTCGCCAAGACTACCGTCGCGATGACATC | 480 |
| KY354681.1 | GGGTCACGTCAGTTCTATAGTCTGGCAGATTTTCGCCAAGACTACCGTCGCGATGACATC | 477 |
| KP455643.1 | GGGTCACGTCAGTTCTATAGTCTGGCAGATTTTCGCCAAGACTACCGTCGCGATGACATC | 480 |
| MN309751.1 | GGGTCACGTCAGTTCTATAGTCTGGCAGATTTTCGCCAAGACTACCGTCGCGATGACATC | 480 |
| | ***** ** ** ***** ** ** ***** ***** ***** * | |
| AY369136.1 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTACTACGTGGACATGCATGAGTTG | 540 |
| KY315688.1 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTATTACGTGGACATGCATGAGTTG | 531 |
| JN189909.2 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTACTACGTGGACATGCATGAGTTG | 540 |
| MT157513.1 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTACTACGTGGACATGCATGAGTTG | 539 |
| JN189865.2 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTACTACGTGGACATGCATGAGTTG | 540 |
| MF144242.1 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTACTACGTGGACATGCATGAGTTG | 540 |
| AF319555.1 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTACTACGTGGACATGCATGAGTTG | 540 |
| FJ789783.1 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTACTACGTGGACATGCATGAGTTA | 540 |
| NC_008040.1 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTACTACGTGGACATGCATGAGTTG | 540 |
| EF558368.1 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTACTACGTGGACATGCATGAGTTG | 540 |
| AY721616.1 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTACTACGTGGACATGCATGAGTTG | 540 |
| KY354681.1 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTACTACGTGGACATGCATGAGTTG | 537 |
| KP455643.1 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTACTACGTGGACATGCATGAGTTG | 540 |
| MN309751.1 | ACCGACCGTCACATCATTGTGATGACTGATGTTGACTACTACGTGGACATGCATGAGTTG | 540 |
| | ***** ** ***** ***** ***** ***** ***** | |
| AY369136.1 | ATTGGTTTGGGTGTTCCGATATTGTTGTACACCTTCCAGCCAAGTACTGTGTCGGGAGAA | 600 |
| KY315688.1 | ATTGGATTGGGTGTTCCGATATTGTTGTACACCTTCCAGCCAGTACTGTGTCGGGAGAA | 591 |
| JN189909.2 | ATTGGTCTGGGTGTTCCGATATTACTGTACACCTTCCAGCCAAGTACTGTGTCGGGAGAG | 600 |
| MT157513.1 | ATTGGTTTGGGTGTTCCGATATTGCTGTACACCTTCCAGCCAAGTACTGTGTCGGGAGAG | 599 |
| JN189865.2 | ATTGGTTTGGGTGTTCCGATATTGCTGTACACCTTCCAGCCAAGTACTGTGTCGGGGAG | 600 |

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| MF144242.1 | ATTGGTTTGGGTGTTCCGATACTGCTATACACCTTCCAGCCAAGTACTGTGTCCGGAGAG | 600 |
| AF319555.1 | ATTGGTTTGGGTGTTCCGATAATTGTTGTACACCTTCCAGCCAAGTACTGTGTCCGGAGAG | 600 |
| FJ789783.1 | ATTGGTTTGGGTGTTCCAATATTGCTGTACACCTTCCAGCCAAGTACTGTGTCCGGAGAG | 600 |
| NC_008040.1 | ATTGGTTTGGGTGTTCCGATAATTGCTGTACACCTTCCAGCCAAGTACTGTGTCCGGAGAG | 600 |
| EF558368.1 | ATTGGTTTGGGTGTTCCGATAATTGCTGTACACCTTCCAGCCAAGTACTGTGTCCGGAGAG | 600 |
| AY721616.1 | ATTGGTTTGGGTGTTCCGATACTGCTGTACACCTTCCAGCCAAGTACTGTGTCCGGAGAG | 600 |
| KY354681.1 | ATTGGTTTGGGTGTTCCGATACTGCTATACACCTTCCAGCCAAGTACTGTGTCCGGAGAG | 597 |
| KP455643.1 | ATTGGTTTGGGTGTTCCGATACTGCTATACACCTTCCAGCCAAGTACTGTGTCCGGAGAG | 600 |
| MN309751.1 | ATTGGTTTGGGTGTTCCGATACTGCTATACACCTTCCAGCCAAGTACTGTGTCCGGAGAG | 600 |
| | ***** | |
| AY369136.1 | GTTAAGGATGGTTACTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGTGGG | 660 |
| KY315688.1 | GTTAAGGATGGTTATTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGTGGG | 651 |
| JN189909.2 | GTTAAGGATGGTTACTTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGCGGG | 660 |
| MT157513.1 | GTTAAGGATGGTTACTTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGCGGG | 659 |
| JN189865.2 | GTCAAGGATGGTTATTTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGCGGG | 660 |
| MF144242.1 | GTTAAGGATGGTTACTTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGCGGG | 660 |
| AF319555.1 | GTTAAGGATGGTTACTTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGCGGG | 660 |
| FJ789783.1 | GTTAAGGATGGTTACTTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGCGGG | 660 |
| NC_008040.1 | GTTAAGGATGGTTACTTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGCGGG | 660 |
| EF558368.1 | GTTAAGGATGGTTACTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGCGGG | 660 |
| AY721616.1 | GTTAAGGATGGTTACTTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGCGGG | 660 |
| KY354681.1 | GTTAAGGATGGTTACTTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGCGGG | 657 |
| KP455643.1 | GTTAAGGATGGTTACTTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGCGGG | 660 |
| MN309751.1 | GTTAAGGATGGTTACTTTACCATCACTGACGACTCCGTTCACTACCGTGTTGCTGGCGGG | 660 |
| | ** ***** | |
| AY369136.1 | AAGGATGTGCGCCACCGCATTTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 720 |
| KY315688.1 | AAGGATGTGCGCCACCGCATTTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 711 |
| JN189909.2 | AAGGATGTGCGCCATCGCATCTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 720 |
| MT157513.1 | AAGGATGTGCGTCATCGCATCTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 719 |
| JN189865.2 | AAGGATGTGCGCCATCGCATTTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 720 |
| MF144242.1 | AAGGATGTGCGCCATCGCATCTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 720 |
| AF319555.1 | AAGGATGTGCGCCACCGCATCTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 720 |
| FJ789783.1 | AAGGATGTGCGCCATCGCATCTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 720 |
| NC_008040.1 | AAGGATGTGCGCCATCGCATCTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 720 |
| EF558368.1 | AAGGATGTGCGCCATCGCATCTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 720 |
| AY721616.1 | AAGGATGTGCGCCATCGCATCTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 720 |
| KY354681.1 | AAGGATGTGCGCCATCGCATCTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 717 |
| KP455643.1 | AAGGATGTGCGCCATCGCATCTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 720 |
| MN309751.1 | AAGGATGTGCGCCATCGCATCTGGAACACAAAGATACCATGTATGTGTGCTCCCGA | 720 |
| | ***** | |
| AY369136.1 | CCTCGTGGTTTCTGGGCGAATCTGGTGCAGATTCTACGTGACATCACTGGTGTACCGCG | 780 |
| KY315688.1 | CCTCGTGGTTTCTGGGCGAATCTGGGCGGATCCTGCGTGACATCACTGGTGTACCGCG | 771 |
| JN189909.2 | CCTCGCGGTCTCTGGGCGAATCTGTTGCAGATCCTGCGTGACATCACTGGTGTACCGCG | 780 |
| MT157513.1 | CCTCGTGGTTTCTGGGCGAATCTGATGCAGATCCTGCGCGACATCACTGGTGTACCGCG | 779 |
| JN189865.2 | CCTCGTGGTTTCTGGGCGAATCTGATGCAGATCCTGCGTGACATCACTGGTGTACCGCG | 780 |
| MF144242.1 | CCTCGTGGTTTCTGGGCGAATCTGATGCAGATCCTGCGTGACATCACTGGTGTACCGCG | 780 |
| AF319555.1 | CCTCGTGGTTTCTGGGCGAATCTGATGCAGATCCTGCGTGACATCACTGGTGTACCGCG | 780 |
| FJ789783.1 | CCTCGTGGTTTCTGGGCGAATCTGATGCAGATCCTGCGTGATATCACTGGTGTACCGCG | 780 |
| NC_008040.1 | CCTCGTGGTTTCTGGGCGAATTTGATGCAGATCCTGCGTGACATCACTGGTGTACCGCG | 780 |
| EF558368.1 | CCTCGTGGTTTCTGGGCGAATCTGATGCAGATCCTGCGTGATATCACTGGTGTACCGCG | 780 |
| AY721616.1 | CCTCGTGGTTTCTGGGCGAATCTGATGCAGATCCTGCGTGATATCACTGGTGTACCGCG | 780 |
| KY354681.1 | CCTCGTGGTTTCTGGGCGAATCTGATGCAGATCCTGCGTGACATCACTGGTGTACCGCG | 777 |
| KP455643.1 | CCTCGTGGTTTCTGGGCGAATCTGATGCAGATCCTGCGTGACATCACTGGTGTACCGCG | 780 |
| MN309751.1 | CCTCGTGGTTTCTGGGCGAATCTGATGCAGATCCTGCGTGACATCACTGGTGTACCGCG | 780 |
| | ***** | |
| AY369136.1 | ATCTGTGGTTTCTTTACGCCAAGCTCGGTATTGCGCCCTTCGGCGACCCGTGTACCATG | 840 |
| KY315688.1 | ATCTGTGGTTTCTTTACGCCAAGCTCGGTATTGCGCCCTTCGGCGACCCGTGTACCATG | 831 |
| JN189909.2 | ATTTGTAGTTATCTTTACACCAAGCTCGGTATTGCGCCCTTCGGCGACCCGTGTACCATG | 840 |
| MT157513.1 | ATCTGCAGCTTTCTTTACACCAAGCTCGGTATTGCGCCCTTCGGCGACCCGTGTACCATG | 839 |
| JN189865.2 | ATCTGTAGCTTTCTTTACACCAAGCTCGGTATTGCGCCCTTCGGCGACCCGTGTACCATG | 840 |
| MF144242.1 | ATCTGTAGCTTTCTTTACGCCAAGCTCGGTATTGCGCCCTTCGGCGACCCGTGTACCATG | 840 |
| AF319555.1 | ATCTGTAGCTTTCTTTACACCAAGCTCGGTATTGCGCCCTTCGGCGACCCGTGTACCATG | 840 |
| FJ789783.1 | ATCTGTAGCTTTCTCTACGCCAAGCTCGGTATTGCGCCCTTCGGCAACCCGTGTACCATG | 840 |
| NC_008040.1 | ATCTGTAGCTTTCTTTACACCAAGCTCGGTATTGCGCCCTTCGGCGACCCGTGTACCATG | 840 |
| EF558368.1 | ATCTGTAGTTTCTTTATACCAAGCTCGGTATTGCGCCCTTCGGCGACCCGTGTACCATG | 840 |
| AY721616.1 | ATCTGTAGCTTTCTTTACACCAAGCTCGGTATTGCGCCCTTCGGCGACCCGTGTACCATG | 840 |
| KY354681.1 | ATCTGTAGCTTTCTATACGCCAAGCTCGGTATTGCGCCCTTCGGCGACCCGTGTACCATG | 837 |
| KP455643.1 | ATCTGTAGCTTTCTTTACGCCAAGCTCGGTATTGCGCCCTTCGGCGACCCGTGTACCATG | 840 |
| MN309751.1 | ATCTGTAGCTTTCTTTACGCCAAGCTCGGTATTGCGCCCTTCGGCGACCCGTGTACCATG | 840 |
| | ** * * | |
| AY369136.1 | TTCACCGTCGATCAATTCAAGATGGGTGAGCACCCTAACATCGTGTGATTGTGCCCTTT | 900 |
| KY315688.1 | TTCACCGTCGATCAATTTAGGATGGGTGAGCACCCTAACATCGTGTGATTGTGCCCTTT | 891 |

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| JN189909.2 | TTCACCGTTGATCAATTCAAGATGGGTGAGCACCGTAATATCGTGTGCGATTGTGCCCTTT | 900 |
| MT157513.1 | TTCACCGTTGATCAATTCAAGATGGGTGAGCATCGTAACATCGTGTCAATTGTGCCCTTT | 899 |
| JN189865.2 | TTCACCGTTGATCAATTCAAGATGGGTGAGCATCGTAACATCGTGTCAATTGTGCCCTTT | 900 |
| MF144242.1 | TTCACCGTTGATCAATTCAAGATCGGTGAGCATCGTAACATCGTCTCGATTGTGCCCTTT | 900 |
| AF319555.1 | TTCACCGTTGATCAATTCAAGATGGGTGAGCATCGTAACATCGTGTCAATTGTGCCCTTT | 900 |
| FJ789783.1 | TTCACCGTTGATCAATTCAAGATGGGTGAGCATCGTAACATCGTGTGCGATTGTGCCCTTT | 900 |
| NC_008040.1 | TTCACCGTTGATCAATTCAAGATGGGTGAGCATCGTAACATCGTGTGCGATTGTGCCCTTT | 900 |
| EF558368.1 | TTCACCGTTGATCAATTCAAGATGGGTGAGCATCGTAACATCGTGTGCGATTGTGCCCTTT | 900 |
| AY721616.1 | TTCACCGTTGATCAATTCAAGATGGGTGAGCATCGTAACATCGTGTGCGATTGTGCCCTTT | 900 |
| KY354681.1 | TTCACCGTTCGATCAATTCAAGATGGGTGAGCATCGTAACATCGTGTGCGATTGTGCCCTTT | 897 |
| KP455643.1 | TTCACCGTTGATCAATTCAAGATGGGTGAGCATCGTAACATCGTCTCGATTGTGCCCTTT | 900 |
| MN309751.1 | TTCACCGTTGATCAATTCAAGATGGGTGAGCATCGTAACATCGTCTCGATTGTGCCCTTT | 900 |
| | ***** ** ***** ** * ** | |
| AY369136.1 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTATGGTGCTGAGTTGGAGTACATG | 960 |
| KY315688.1 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTATGGTGCTGAGTTGGAGTACATG | 951 |
| JN189909.2 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTATGGTACTGAGTTGGAGTATATG | 960 |
| MT157513.1 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTATGGTGCTGAGTTGGAGTATATG | 959 |
| JN189865.2 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTACGGTGCTGAGTTGGAGTATATG | 960 |
| MF144242.1 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTACGGTGCTGAGTTGGAGTATATG | 960 |
| AF319555.1 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTATGGTGCTGAGTTGGAGTATATG | 960 |
| FJ789783.1 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTACGGTGCTGAGTTGGAGTATATG | 960 |
| NC_008040.1 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTACGGTGCTGAGTTGGAGTATATG | 960 |
| EF558368.1 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTACGGTGCTGAGTTGGAGTATATG | 960 |
| AY721616.1 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTACGGTGCTGAGTTGGAGTATATG | 960 |
| KY354681.1 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTACGGTGCTGAGTTGGAGTATATG | 957 |
| KP455643.1 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTACGGTGCTGAGTTGGAGTATATG | 960 |
| MN309751.1 | GCAACTTGCCGTTCAAACCTGCTCAAGATCAGTGAGTACGGTGCTGAGTTGGAGTATATG | 960 |
| | ***** ** ***** ** ***** ** | |
| AY369136.1 | CGCTACCAGCAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTACATCTCTGAGAAT | 1020 |
| KY315688.1 | CGCTATCAACAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTACATCTCTGAGAAT | 1011 |
| JN189909.2 | CGCTACCAACAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTACATCTCTGAGAAT | 1020 |
| MT157513.1 | CGCTATCAACAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTATATCTCTGAGAAT | 1019 |
| JN189865.2 | CGCTACCAGCAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTACATCTCTGAGAAT | 1020 |
| MF144242.1 | CGCTACCAACAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTATATCTCTGAGAAT | 1020 |
| AF319555.1 | CGCTACCAACAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTACATCTCTGAGAAT | 1020 |
| FJ789783.1 | CGCTACCAACAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTACATCTCTGAGAAT | 1020 |
| NC_008040.1 | CGCTACCAACAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTACATCTCTGAGAAT | 1020 |
| EF558368.1 | CGCTACCAACAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTACATCTCTGAGAAT | 1020 |
| AY721616.1 | CGCTATCAACAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTACATCTCTGAGAAT | 1020 |
| KY354681.1 | CGCTACCAACAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTATATCTCTGAGAAT | 1017 |
| KP455643.1 | CGCTACCAACAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTATATCTCTGAGAAT | 1020 |
| MN309751.1 | CGCTACCAACAGCGCAACAACATTGCCAACTTCAACGCAGTCACCTTATATCTCTGAGAAT | 1020 |
| | ***** ** ***** ** ***** ** | |
| AY369136.1 | GGGCCACTCATCAGTCTGGGTTTGAAGGCAATTTTGCAAGCGTCCAGCTTCCCCTGCAA | 1080 |
| KY315688.1 | GGGCCACTCATCAGTCTGGGTTTGAAGGCAATTTTGCAAGCGTCCAGCTTCCCCTGCG | 1071 |
| JN189909.2 | GGGCCGCTCATCAGTCTGGGTTTGAAGGCAATTTTGCAAGTGTCCAGCTTCCCCTGCG | 1080 |
| MT157513.1 | GGGCCACTCATCAGTCTGGGTTTGAAGGCAATTTTGCAAGCGTCCAGCTTCCCTGCG | 1079 |
| JN189865.2 | GGGCCACTCATCAGTCTGGGTTTGAAGGCAATTTTGCAAGCGTCCAGCTTCCCCTGCG | 1080 |
| MF144242.1 | GGGCCCTCATCAGCTTGGGTTTGAAGGCAACTTTTGCAAGCGTCCAGCTTCCCCTGCG | 1080 |
| AF319555.1 | GGGCCACTCATCAGTCTGGGTTTGAAGGCAATTTTGCAAGCGTCCAACTTCCCTGCG | 1080 |
| FJ789783.1 | GGGCCACTTATCAGCTTGGGTTTGAAGGCAACTTTTGCAAGCGTCCAGCTTCCCCTGCG | 1080 |
| NC_008040.1 | GGGCCACTCATCAGCTTGGGTTTGAAGGCAACTTTTGCAAGCGTCCAACTTCCCTTGCAG | 1080 |
| EF558368.1 | GGGCCACTCATCAGCTTGGGTTTGAAGGCAACTTTTGCAAGCGTCCAGCTTCCCCTGCG | 1080 |
| AY721616.1 | GGGCCCTCATCAGCTTGGGTTTGAAGGCAACTTTTGCAAGCGTCCAGCTTCCCCTGCG | 1080 |
| KY354681.1 | GGGCCCTCATCAGCTTGGGTTTGAAGGCAACTTTTGCAAGTGTCCAGCTTCCCCTGCG | 1077 |
| KP455643.1 | GGGCCCTCATCAGCTTGGGTTTGAAGGCAACTTTGCAAGCGTCCAGCTTCCCCTGCG | 1080 |
| MN309751.1 | GGGCCCTCATCAGCTTGGGTTTGAAGGCAACTTTTGCAAGCGTCCAGCTTCCCCTGCG | 1080 |
| | ***** * ***** ***** ** ***** ***** ***** | |
| AY369136.1 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1140 |
| KY315688.1 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1131 |
| JN189909.2 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1140 |
| MT157513.1 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1139 |
| JN189865.2 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1140 |
| MF144242.1 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1140 |
| AF319555.1 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1140 |
| FJ789783.1 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1140 |
| NC_008040.1 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1140 |
| EF558368.1 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1140 |
| AY721616.1 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1140 |
| KY354681.1 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1137 |
| KP455643.1 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1140 |
| MN309751.1 | GATTTTCGAGAACATCCGCACTGCATACGAACTGTCCAAGACTAACAACCTTGTGAGACT | 1140 |
| | ***** ***** ***** ***** ***** ***** ***** | |

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| AY369136.1 | GTTTCGCCGGTCAGGGCGCCCCGTGCAAGGAGGCAGCTATCATACATAAGTGTCTCCAAGCC | 1200 |
| KY315688.1 | GTTTCGCCGGTCAGGGCGCCCCGTGCAAGGAGGCAGCTATCATACATAAGTGTCTCCAAGCC | 1191 |
| JN189909.2 | GTTTCGCCGGTCAGGACGCCCGTGCAAGGAGGCAGCTATCATCCACAAATGTCTCCAAGCT | 1200 |
| MT157513.1 | GTTTCGCCGGTCAGGGCGCCCCGTGCAAGGAGGCAGCTATCATCCATAAATGTCTCCAAGCC | 1199 |
| JN189865.2 | GTTTCGCCGGTCAGGGCGCCCCGTGCAAGGAGGCAGCTATCATCCATAAATGTCTCCAAGCC | 1200 |
| MF144242.1 | GTTTCGCCGGTCAGGGCGCCCCGTGCAAGGAGGCAGCTATCATCCATAAATGTCTCCAAGCC | 1200 |
| AF319555.1 | GTTTCGCCGGTCAGGGCGCCCCGTGCAAGGAGGCAGCTATCATCCATAAATGTCTCCAAGCC | 1200 |
| FJ789783.1 | GTTTCGCCGGTCAGGGCGCCCCGTGCAAGGAGGCAGCTATCATCCATAAATGTCTCCAAGCC | 1200 |
| NC_008040.1 | GTTTCGCCGGTCAGGGCGCCCCGTGCAAGGAGGCAGCTATCATCCATAAATGTCTCCAAGCC | 1200 |
| EF558368.1 | GTTTCGCCGGTCAGGGCGCCCCGTGCAAGGAGGCAGCTATCATCCATAAATGTCTCCAAGCC | 1200 |
| AY721616.1 | GTTTCGCCGGTCAGGGCGCCCCGTGCAAGGAGGCAGCTATCATCCACAAATGTCTCCAAGCC | 1200 |
| KY354681.1 | GTTTCGCCGGTCAGGGCGCCCCGTGCAAGGAGGCAGCTATCATCCATAAATGTCTCCAAGCC | 1197 |
| KP455643.1 | GTTTCGCCGGTCAGGGCGCCCCGTGCAAGGAGGCAGCTATCATCCATAAATGTCTCCAAGCC | 1200 |
| MN309751.1 | GTTTCGCCGGTCAGGGCGCCCCGTGCAAGGAGGCAGCTATCATCCATAAATGTCTCCAAGCC | 1200 |
| ***** | | |
| AY369136.1 | GAGTGTGCCGTCGTCAGCGAGGTCGTGCATAAACTGGCGATCTCGCTCGCCATTACCAA | 1260 |
| KY315688.1 | GAGTGTGCCGTCGTCAGCGAGGTCGTGCATAAACTGGCGATCTCGCTCGCCATTACCAA | 1251 |
| JN189909.2 | GAGTGTGTGTCGTCAGCGAGGTCGTACATAAACTGGCGATCTTGCTCGTCATTACCAA | 1260 |
| MT157513.1 | GAGTGTGCCGTCGTCAGCGAGGTCGTGCATAAACCCGGCGATCTCGCTCGTCATTACCAA | 1259 |
| JN189865.2 | GAGTGTGCCGTCGTCAGCGAGGTCGTGCATAAACTGGCGATCTTGCTCGTCATTACCAA | 1260 |
| MF144242.1 | GAGTGTGCCGTCGTCAGCGAGGTCGTGCATAAACTGGCGATCTTGCTCGTCATTACCAA | 1260 |
| AF319555.1 | GAGTGTGCCGTCGTCAGCGAGGTCGTGCATAAACTGGCGATCTTGCTCGTCATTACCAA | 1260 |
| FJ789783.1 | GAGTGTGCCGTCGTCAGCGAGGTCGTGCATAAACTGGCGATCTTGCTCGTCATTACCAA | 1260 |
| NC_008040.1 | GAGTGTGCCGTCGTCAGCGAGGTCGTGCATAAACTGGCGATCTTGCTCGTCATTACCAA | 1260 |
| EF558368.1 | GAGTGTGCCGTCGTCAGCGAGGTCGTGCATAAACTGGCGATCTTGCTCGTCATTACCAA | 1260 |
| AY721616.1 | GAGTGTGCCGTCGTCAGCGAGGTCGTGCATAAACTGGCGATCTTGCTCGTCATTACCAA | 1260 |
| KY354681.1 | GAGTGTGCCGTCGTCAGCGAGGTCGTGCATAAACTGGCGATCTTGCTCGTCATTACCAA | 1257 |
| KP455643.1 | GAGTGTGCCGTCGTCAGCGAGGTCGTGCATAAACTGGCGATCTTGCTCGTCATTACCAA | 1260 |
| MN309751.1 | GAGTGTGCCGTCGTCAGCGAGGTCGTGCATAAACTGGCGATCTTGCTCGTCATTACCAA | 1260 |
| ***** | | |
| AY369136.1 | GCAGTTGGTAGTGCTACGACACTGATCCGGCCGAGCAGGGCAAGTGTATGCTCGTGAG | 1320 |
| KY315688.1 | GCAGTTGGTAGTGCTACGACACTGATCCGGCCGAGCAGGGCAAGTGTATGCTCGTGAG | 1311 |
| JN189909.2 | GCAGTTGGTAGTGCTACGACACTGATCCGGCCGAGCAGGGCAAGTGTATGCTCGTGAG | 1320 |
| MT157513.1 | GCAGTTGGTAGTGCTACGACACTGATCCGGCCGAGCAGGGCAAGTGTATGCTCGTGAG | 1319 |
| JN189865.2 | GCTGTTGGTAGTGCTACGACACTGATCCAGCCGAGCAGGGCAAGTGTATGCTCGTGAG | 1320 |
| MF144242.1 | GCAGTTGGTAGTGCTACGACACTGATCCAGCTGAGCAGGGCAAGTGTATGCTCGTGAG | 1320 |
| AF319555.1 | GCAGTTGGTAGTGCTACGACACTGATCCAGCCGAGCAGGGCAAGTGTATGCTCGTGAG | 1320 |
| FJ789783.1 | GCAGTTGGTAGTGCTACGACACTGATCCAGCTGAGCAGGGCAAGTGTATGCTCGTGAG | 1320 |
| NC_008040.1 | GCAGTTGGTAGTGCTACGACACTGATCCAGCTGAGCAGGGCAAGTGTATGCTCGTGAG | 1320 |
| EF558368.1 | GCAGTTGGTAGTGCTACGACACTGATCCAGCTGAGCAGGGCAAGTGTATGCTCGTGAG | 1320 |
| AY721616.1 | GCAGTTGGTAGTGCTACGACACTGATCCAGCTGAGCAGGGCAAGTGTATGCTCGTGAG | 1320 |
| KY354681.1 | GCAGTTGGTAGTGCTACGACACTGATCCAGCTGAGCAGGGCAAGTGTATGCTCGTGAG | 1317 |
| KP455643.1 | GCAGTTGGTAGTGCTACGACACTGATCCAGCTGAGCAGGGCAAGTGTATGCTCGTGAG | 1320 |
| MN309751.1 | GCAGTTGGTAGTGCTACGACACTGATCCAGCTGAGCAGGGCAAGTGTATGCTCGTGAG | 1320 |
| ***** | | |
| AY369136.1 | TATGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1380 |
| KY315688.1 | TATGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1371 |
| JN189909.2 | TATGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1380 |
| MT157513.1 | TATGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1379 |
| JN189865.2 | TATGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1380 |
| MF144242.1 | TACGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1380 |
| AF319555.1 | TATGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1380 |
| FJ789783.1 | TATGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1380 |
| NC_008040.1 | TATGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1380 |
| EF558368.1 | TATGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1380 |
| AY721616.1 | TACGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1380 |
| KY354681.1 | TACGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1377 |
| KP455643.1 | TACGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1380 |
| MN309751.1 | TACGCTCCTGGACCGTTGACTCAAACCTGCTGTATTTCCAAGTGAGTCACGTTCCAACGAG | 1380 |
| ***** | | |
| AY369136.1 | CTTGCCACAATCGACGGTCGTATTGCTGGTCCGCAAGCCAAGGCAAAGAGCCGCGAGCAC | 1440 |
| KY315688.1 | CTTGCCACAATCGACGGTCGTATTGCTGGTCCGCAAGCCAAGGCAAAGAGCCGCGAGCAC | 1431 |
| JN189909.2 | CTTGCCACAATCGACGGTCGTATTGCTGGTCCGCAAGCTAAGGCAAAGAGCCGCGAGCAC | 1440 |
| MT157513.1 | CTTGCCACGATTGACGGTCGTATTGCTGGTCCGCAAGCTAAGGCAAAGAGCCGCGAGCAC | 1439 |
| JN189865.2 | CTTGCCACAATCGACGGTCGTATTGCTGGTCCGCAAGCCAAGGCAAAGAGCCGCGAGCAC | 1440 |
| MF144242.1 | CTTGCCACAATCGACGGTCGTATTGCTGGTCCGCAAGCCAAGGCAAAGAGCCGCGAGCAC | 1440 |
| AF319555.1 | CTTGCCACAATCGACGGTCGTATTGCTGGTCCGCAAGCCAAGGCAAAGAGCCGCGAGCAC | 1440 |
| FJ789783.1 | CTTGCCACGATTGACGGTCGTATTGCTGGTCCGCAAGCCAAGGCAAAGAGCCGCGAGCAC | 1440 |
| NC_008040.1 | CTTGCCACAATCGACGGTCGTATTGCTGGTCCGCAAGCCAAGGCAAAGAGCCGCGAGCAC | 1440 |
| EF558368.1 | CTTGCCACAATCGACGGTCGTATTGCTGGTCCGCAAGCCAAGGCAAAGAGCCGCGAGCAC | 1440 |
| AY721616.1 | CTTGCCACAATCGACGGTCGTATTGCTGGTCCGCAAGCCAAGGCAAAGAGCCGCGAGCAT | 1440 |
| KY354681.1 | CTTGCCACAATCGACGGTCGTATTGCTGGTCCGCAAGCCAAGGCAAAGAGCCGCGAGCAC | 1437 |

KP455643.1 CTTGCCACAATCGACGGTCGTATTGCTGGTCCGCAAGCCAAGGCAAAGAGCCGCGAGCAC 1440
MN309751.1 CTTGCCACAATCGACGGTCGTATTGCTGGTCCGCAAGCCAAGGCAAAGAGCCGCGAGCAC 1440
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AY369136.1 ATAACACCTAAGATGCGCAAAGTGGCTAGGGACTTCGTGCACCATTGGTGCCGGTTGCC 1500
KY315688.1 ATAACACCTAAGATGCGCAAAGTGGCTAGGGACTTCGTGCACCATTGGTGCCGGTTGCC 1491
JN189909.2 ATAACACCTAAGATGCGCAAAGTGGCTAGGGACTTCGTGCACCATTGGTGCCGGTTGCC 1500
MT157513.1 ATAACACCTAAGATGCGCAAAGTGGCTAGGGATTTCGTGCACCATCTGGTGCCGATTGCC 1499
JN189865.2 ATAACACCTAAAATGCGCAAAGTGGCTAGGGATTTCGTGCACCATTGGTGCCGGTTGCC 1500
MF144242.1 ATAACACCTAAGATGCGCAAAGTGGCTAGGGACTTCGTGCACCATCTGGTGCCGATTGCC 1500
AF319555.1 ATAACACCTAAGATGCGCAAAGTGGCTAGGGACTTCGTGCACCATCTGGTGCCGATTGCC 1500
FJ789783.1 ATAACACCTAAGATGCGCAAAGTGGCTAGGGACTTCGTGCACCATCTGGTGCCGATTGCC 1500
NC_008040.1 ATAACACCTAAGATGCGCAAAGTGGCTAGGGACTTCGTGCACCATCTGGTGCCGATTGCC 1500
EF558368.1 ATAACACCTAAGATGCGCAAAGTGGCTAGGGACTTCGTGCACCATCTGGTGCCGATTGCC 1500
AY721616.1 ATAACACCTAAGATGCGCAAAGTGGCTAGGGACTTCGTGCACCATCTGGTGCCGATTGCC 1500
KY354681.1 ATAACACCTAAGATGCGCAAAGTGGCTAGGGACTTCGTGCACCATCTGGTGCCGATTGCC 1497
KP455643.1 ATAACACCTAAGATGCGCAAAGTGGCTAGGGACTTCGTGCACCATCTGGTGCCGATTGCC 1500
MN309751.1 ATAACACCTAAGATGCGCAAAGTGGCTAGGGACTTCGTGCACCATCTGGTGCCGATTGCC 1500
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AY369136.1 GGTACTGGCCGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1560
KY315688.1 GGTACTGGCCGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1551
JN189909.2 GGTACTGGCCGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1560
MT157513.1 GGTACTGGCCGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1559
JN189865.2 GGCACCTGGCCGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1560
MF144242.1 GGTACGGGCGGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1560
AF319555.1 GGCACCTGGCCGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1560
FJ789783.1 GGCACCTGGCCGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1560
NC_008040.1 GGTACTGGCCGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1560
EF558368.1 GGCACCTGGCCGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1560
AY721616.1 GGCACCTGGCCGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1560
KY354681.1 GGTACTGGCCGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1557
KP455643.1 GGTACGGGCGGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1560
MN309751.1 GGTACGGGCGGTCCCTACCCCTCACGTATGTCGAGGAGCAGCAGACCAAGCCGTTACAG 1560
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Conventional PCR/qPCR forward primer:CCGATATCACGATGAGTTCAC

AY369136.1 CGGGCTCGGAATGATGCTAAACCGATATCACGATGAGTTCACATATGATGGTCAAAGCGTTC 1620
KY315688.1 CGGGCTCGGAATGATGCTAAACCGATATCACGATGAGTTCACATATGATGGTCAAAGCGTTC 1611
JN189909.2 CGGGCTCGGAATGATGCTAAACCGATATCACGATGAGTTCACATATGATGGTCAAAGCGTTC 1620
MT157513.1 CGGGCTCGGAATGATGCTAAACCGATATCACGATGAGTTCACATATGATGGTCAAAGCGTTC 1619
JN189865.2 CGGGCTCGGAATGATGCTAAACCGATAACACGATGAGTTCACATATGATGGTCAAAGCGTTC 1620
MF144242.1 CGGGCTCGGAATGATGCTAAACCGATATCACGATGAGTTCACATATGAAGGGCAAAGCGTTC 1620
AF319555.1 CGGGCTCGGAATGATGCTAAACCGATATCACGATGAGTTCACATATGATGGTCAAAGCGTTC 1620
FJ789783.1 CGGGCTCGGAATGATGCTAAACCGATATCACGATGAGTTCACATATGATGGTCAAAGCGTTC 1620
NC_008040.1 CGGGCTCGGAATGATGCTAAACCGATATCACGATGAGTTCACATATGATGGTCAAAGCGTTC 1620
EF558368.1 CGGGCTCGGAATGATGCTAAACCGATATCACGATGAGTTCACATATGATGGTCAAAGCGTTC 1620
AY721616.1 CGGGCTCGGAATGATGCTAAACCGATATCACGATGAGTTCACATATGATGGTCAAAGCGTTC 1620
KY354681.1 CGGGCTCGGAATGATGCTAAACCGATATCACGATGAGTTCACATATGATGGTCAAAGCGTTC 1617
KP455643.1 CGGGCTCGGAATGATGCTAAACCGATATCACGATGAGTTCACATATGATGGTCAAAGCGTTC 1620
MN309751.1 CGGGCTCGGAATGATGCTAAACCGATATCACGATGAGTTCACATATGATGGTCAAAGCGTTC 1620
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AY369136.1 CAAAAGAAAGAAGCATACAACGCCCCAAATTACCCAGGAACATCTCAACCGTTCCGCAC 1680
KY315688.1 CAAAAGAAAGAAGCATACAACGCCCCAAATTACCCAGGAACATCTCAACCGTTCCACAC 1671
JN189909.2 CAAAAGAAAGAAGCATACAACGCCCCAAATTATCCCAGGAACATTTCAACCGTTCCGCAC 1680
MT157513.1 CAAAAGAAAGAAGCATACAACGCCCCAAATTATCCCAGGAACATTTCAACCGTTCCGCAT 1679
JN189865.2 CAAAAGAAAGAAGCATACAACGCCCCAAATTACCCAGGAACATTTCAACCGTTCCGCAC 1680
MF144242.1 CAAAAGAAAGAAGCATACAACGCCCCAAACTACCCAGGAACATTTCAACCGTTCCGCAC 1680
AF319555.1 CAAAAGAAAGAAGCATACAACGCCCCAAATTATCCCAGGAACATTTCAACCGTTCCGCAT 1680
FJ789783.1 CAAAAGAAAGAAGCATACAACGCCCCAAATTATCCCAGGAACATTTCAACCGTTCCGCAT 1680
NC_008040.1 CAAAAGAAAGAAGCATACAACGCCCCAAATTACCCAGGAACATTTCAACCGTTCCGCAT 1680
EF558368.1 CAAAAGAAAGAAGCATACAACGCCCCAAATTATCCCAGGAACATTTCAACCGTTCCGCAT 1680
AY721616.1 CAAAAGAAAGAAGCATACAACGCCCCAAATTACCCAGGAACATTTCAACTGTTCCGCAT 1680
KY354681.1 CAAAAGAAAGAAGCATACAACGCCCCAAATTATCCCAGGAACATTTCAACCGTTCCGCAC 1677
KP455643.1 CAAAAGAAAGAAGCATACAACGCCCCAAATTACCCAGGAACATTTCAACCGTTCCGCAT 1680
MN309751.1 CAAAAGAAAGAAGCATACAACGCCCCAAATTATCCCAGGAACATCTCAACCGTTCCGCAT 1680
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qPCR reverse primer:CCAGCTACACCTACGCTTTC

AY369136.1 ACCCAAACGTCAGTTGTCCAGCTACACCTACGCTTTCAAAGCCAGTGTTCTCCAGCAT 1740
KY315688.1 ACCCAAACGTCAGTTGTCCAGCTACACCTACGCTTTCAAAGCCAGTGTTCTCCAGCAT 1731
JN189909.2 ACCCAGAACGTCAGTTGTCCAGCTACACCTACGCTTTCAAAGCCAGTGTTCTCCAGCAT 1740
MT157513.1 ACCCAGAACGTCAGTTGTCCAGCTACACCTACGCTTTCAAAGCCAGTGTTCTCCAGCAT 1739
JN189865.2 ACCCAAACGTCAGTTGTCCAGCTACACCTACGCTTTCAAAGCCAGTGTTCTCCAGCAT 1740
MF144242.1 ACCCAAACGTCAGTTGTCCAGCTACACCTACGCTTTCAAAGCCAGTGTTCTCCAGCAT 1740
AF319555.1 ACCCAAACGTCAGTTGTCCAGCTACACCTACGCTTTCAAAGCCAGTGTTCTCCAGCAT 1740
FJ789783.1 ACCCAAACGTCAGTTGTCCAGCTACACCTACGCTTTCAAAGCTAGTGTTCTCCAGCAT 1740
NC_008040.1 ACCCAAACGTCAGTTGTCCAGCTACACCTACGCTTTCAAAGCCAGTGTTCTCCAGCAT 1740

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| EF558368.1 | ACCCAAAACGTTAAGTTGTCCAGCTACACCTATGCTTTC | AAAGCCAGTGTTCTCCAGCAT | 1740 |
| AY721616.1 | ACCCAAAACGTTCAAGTTGTCCAGCTACACCTACGCTTTC | AAAGCCAGTGTTCTCCAGCAT | 1740 |
| KY354681.1 | ACCCAAAACGTTCAAGTTGTCCAGCTACACCTACGCTTTC | AAAGCCAGTGTTCTCCAGCAT | 1737 |
| KP455643.1 | ACCCAGAACGTTCAAGTTGTCCAGCTACACCTACGCTTTC | AAAGCCAGTGTTCTCCAGCAT | 1740 |
| MN309751.1 | ACCCAAAACGTTCAAGTTGTCCAGCTACACCTACGCTTTC | AAAGCCAGTGTTCTCCAGCAT | 1740 |
| | ***** | | |
| AY369136.1 | GTTCCGTGGTACATGCCAACGCACACACCAGCTGAAATTGCTGACGCAGTGCAAAAACCTTG | | 1800 |
| KY315688.1 | GTTCCGTGGTACATGCCAACGCACACACCAGCTGAAATTGCTGACGCAGTGCAAAAACCTTG | | 1791 |
| JN189909.2 | GTTCCGTGGTACATGCCAACGCACACACCAGCTGAAATCGCTGACGCAGTGCAAAAACCTTG | | 1800 |
| MT157513.1 | GTTCCGTGGTACATGCCAACGCACACACCAGCTGAAATTGCTGACGCAGTGCAAAAACCTTG | | 1799 |
| JN189865.2 | GTTCCGTGGTACATGCCAACGCACACACCAGCGGAAATCGCTGACGCAGTGCAAAAACCTTG | | 1800 |
| MF144242.1 | GTTCCGTGGTACATGCCAACGCACACACCAGCGGAAATCGCTGACGCAGTGCAAAAACCTTG | | 1800 |
| AF319555.1 | GTTCCGTGGTACATGCCAACGCACACACCAGCTGAAATCGCTGACGCAGTGCAAAAACCTTG | | 1800 |
| FJ789783.1 | GTTCCGTGGTACATGCCAACGCACACACCAGCTCAAATCGCTGACGCAGTGCAAAAACCTTG | | 1800 |
| NC_008040.1 | GTTCCGTGGTACATGCCAACGCACACACCAGCTGAAATCGCTGACGCAGTGCAAAAACCTTG | | 1800 |
| EF558368.1 | GTTCCGTGGTACATGCCAACGCACACACCAGCTGAAATCGCTGACGCAGTGCAAAAACCTTG | | 1800 |
| AY721616.1 | GTTCCGTGGTACATGCCAACGCACACACCAGCTGAAATCGCTGACGCAGTGCAAAAACCTTG | | 1800 |
| KY354681.1 | GTTCCGTGGTACATGCCAACGCACACACCAGCTGAAATCGCTGACGCAGTGCAAAAACCTTG | | 1797 |
| KP455643.1 | GTTCCGTGGTACATGCCAACGCACACACCAGCTGAAATTGCTGACGCAGTGCAAAAATTTG | | 1800 |
| MN309751.1 | GTTCCGTGGTACATGCCAACGCACACACCAGCTGAAATTGCTGACGCAGTGCAAAAACCTTG | | 1800 |
| | ***** | | |
| AY369136.1 | GCCGCAAGTTCCTACTGAGCTGGTTGAAACTGACTACAGCAAGTTCGATGGCACATTCTTG | | 1860 |
| KY315688.1 | GCCGCAAGTTCCTACTGAGCTGGTTGAAACTGACTACAGCAAGTTCGATGGCACATTCTTG | | 1851 |
| JN189909.2 | GCCGCAAGTTCCTACTGAGCTGGTCGAAACTGACTACAGCAAGTTCGATGGCACATTTTCTG | | 1860 |
| MT157513.1 | GCTGCAAGTTCCTACTGAGCTGGTTGAAACTGACTACAGCAAGTTCGATGGCACATTCTTG | | 1859 |
| JN189865.2 | GCCGCAAGTTCCTACTGAGCTGGTTGAAACTGACTACAGCAAGTTCGATGGCACATTCTTG | | 1860 |
| MF144242.1 | GCCGCAAGTTCCTACTGAGCTGGTCGAAACTGACTACAGCAAGTTCGATGGCACATTCTTG | | 1860 |
| AF319555.1 | GCTGCAAGTTCCTACTGAGCTGGTTGAAACCGACTACAGCAAGTTCGATGGCACATTCTTG | | 1860 |
| FJ789783.1 | GCCGCAAGTTCCTACTGAGCTGGTTGAAACTGACTACAGCAAGTTCGATGGCACATTCTTG | | 1860 |
| NC_008040.1 | GCCGCAAGTTCCTACTGAGCTGGTTGAAACTGACTACAGCAAGTTCGATGGCACATTCTTG | | 1860 |
| EF558368.1 | GCCGCAAGTTCCTACTGAGCTGGTTGAGACTGACTACAGCAAGTTCGATGGCACATTCTTG | | 1860 |
| AY721616.1 | GCCGCAAGTTCCTACTGAGCTGGTTGAAACTGACTACAGCAAGTTCGATGGCACATTCTTG | | 1860 |
| KY354681.1 | GCCGCAAGTTCCTACTGAGCTGGTTGAAACTGACTACAGCAAGTTCGATGGCACATTCTTG | | 1857 |
| KP455643.1 | GCCGCAAGTTCCTACTGAGCTGGTTGAAACTGACTACAGCAAGTTCGATGGCACATTCTTG | | 1860 |
| MN309751.1 | GCCGCAAGTTCCTACTGAGCTGGTTGAAACTGACTACAGCAAGTTCGATGGCACATTCTTG | | 1860 |
| | ** ***** | | |
| AY369136.1 | CGCTTTATGCGTGAGTGCGTCGAGTTTGCTATTTATAAGCGCTGGGTTACCTGGACCAC | | 1920 |
| KY315688.1 | CGCTTCATGCGTGAGTGCGTCGAATTTGCTATTTATAAGCGCTGGGTTACCTGGACCAC | | 1911 |
| JN189909.2 | CGCTTTATGCGTGAGTGCGTCGAATTTGCCATCTATAAGCGCTGGGTTACCTGGACCAC | | 1920 |
| MT157513.1 | CGCTTCATGCGTGAGTGCGTCGAGTTTGCGATCTATAAGCGCTGGGTTACCTGGACCAC | | 1919 |
| JN189865.2 | CGCTTTATGCGTGAGTGCGTCGAATTTGCCATCTATAAGCGCTGGGTTACCTGGACCAC | | 1920 |
| MF144242.1 | CGCTTCATGCGTGAGTGCGTCGAATTTGCCATTTATAAGCGCTGGGTTCCACCTGGACCAC | | 1920 |
| AF319555.1 | CGCTTTATGCGTGAGTGCGTCGAATTTGCTATCTATAAGCGCTGGGTTACCTGGACCAC | | 1920 |
| FJ789783.1 | CGCTTTATGCGTGAGTGCGTTGAATTTGCTATCTATAAGCGCTGGGTTACCTGGACCAC | | 1920 |
| NC_008040.1 | CGCTTCATGCGTGAGTGCGTCGAATTTGCTATCTATAAGCGCTGGGTTACCTGGACCAC | | 1920 |
| EF558368.1 | CGCTTCATGCGTGAGTGCGTCGAATTTGCTATCTATAAGCGCTGGGTTACCTGGACCAC | | 1920 |
| AY721616.1 | CGCTTCATGCGTGAGTGCGTCGAATTTGCTATCTATAAGCGCTGGGTTACCTGGACCAC | | 1920 |
| KY354681.1 | CGCTTTATGCGTGAGTGCGTTGAATTTGCTATCTATAAGCGCTGGGTTACCTGGACCAC | | 1917 |
| KP455643.1 | CGCTTTATGCGTGAGTGCGTCGAATTTGCCATCTATAAGCGCTGGGTTACCTGGACCAC | | 1920 |
| MN309751.1 | CGCTTTATGCGTGAGTGCGTCGAATTTGCTATTTATAAGCGCTGGGTTACCTGGACCAC | | 1920 |
| | ***** | | |
| AY369136.1 | TTGCCAGAATTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACCCGATTG | | 1980 |
| KY315688.1 | TTGCCGGAGTTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACCCGACTG | | 1971 |
| JN189909.2 | TTGCCAGAGTTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACACGATTG | | 1980 |
| MT157513.1 | TTGCCAGAATTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACACGATTG | | 1979 |
| JN189865.2 | TTGCCAGAGTTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACACGACTG | | 1980 |
| MF144242.1 | TTGCCGGAGTTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACACGACTG | | 1980 |
| AF319555.1 | TTGCCAGAGTTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACACGACTG | | 1980 |
| FJ789783.1 | TTGCCAGAGTTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACACGATTG | | 1980 |
| NC_008040.1 | TTGCCAGAGTTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACACGATTG | | 1980 |
| EF558368.1 | TTGCCAGAATTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACACGATTG | | 1980 |
| AY721616.1 | TTGCCAGAGTTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACACGATTG | | 1980 |
| KY354681.1 | TTGCCAGAGTTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACACGATTG | | 1977 |
| KP455643.1 | TTGCCAGAGTTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACACGATTG | | 1980 |
| MN309751.1 | TTGCCAGAGTTAACAACCTTTATTGGCTAATGAGATCCAAGCACCTGCTGTTACACGATTG | | 1980 |
| | ***** | | |
| AY369136.1 | GGCATTAATATGACCTGATTGCAGTCGCCTCAGCGGTTCTGCTCTCACGACAGACGGA | | 2040 |
| KY315688.1 | GGCATCAAATACGACCTGATTGCAGCCGCCTCAGCGGTTCTGCTCTCACACAGACGGA | | 2031 |
| JN189909.2 | GGCATCAAGTATGACCTGACTGCAGTCGCCTTAGTGGTTCTGCTCTCACTACAGACGGA | | 2040 |
| MT157513.1 | GGCATCAAGTATGATCCTGATTGCAGCCGCCTCAGTGGTCTGCTCTCACGACCGACGGA | | 2039 |
| JN189865.2 | GGCATCAAGTATGATCCTGATTGCAGTCGCCTCAGTGGTCTGCTCTCACGACAGACGGA | | 2040 |
| MF144242.1 | GGCATCAAGTATGATCCTGATTGCAGTCGCCTCAGTGGTCTGCTCTCACGACAGACGGA | | 2040 |

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| AF319555.1 | GGCATCAAGTATGACCCTGATTGCAGTCGCCTCAGTGGTTCTGCTCTCACAAACGACGGA | 2040 |
| FJ789783.1 | GGCATCAAGTATGACCCTGATTGCAGCCGCTCAGCGGTTCTGCTCTCACGACGACGGA | 2040 |
| NC_008040.1 | GGCATCAAGTATGACCCTGATTGCAGTCGCCTCAGTGGTTCTGCTCTCACGACAGACGGA | 2040 |
| EF558368.1 | GGCATCAAGTATGAACCTGATTGCAGTCGCCTCAGTGGTTCTGCTCTCACGACAGACGGA | 2040 |
| AY721616.1 | GGCATTAAGTATGACCCTGATTGCAGTCGCCTCAGTGGTTCTGCTCTCACAAACAGACGGA | 2040 |
| KY354681.1 | GGCATCAAGTATGACCCTGATTGCAGTCGCCTCAGTGGTTCTGCACTCACGACAGACGGA | 2037 |
| KP455643.1 | GGCATCAAGTATGACCCTGATTGCAGTCGCCTCAGCGGCTCTGCTCTCACAAACAGACGGA | 2040 |
| MN309751.1 | GGCATCAAGTATGACCCTGATTGCAGTCGCCTCAGTGGCTCTGCTCTCACAAACAGACGGA | 2040 |
| | ***** ** ** ** ***** ***** ***** ** ** ***** ***** ** ***** | |
| AY369136.1 | AACAGCATTGCCAATGCTTTCGTCTCATACCTTGCTGGTCGTATGGCTGGCATGGATGAT | 2100 |
| KY315688.1 | AACAGCATTGCCAATGCATTCGTCTCGTACCTTGCTGGTCGCATGGCTGGCATGGATGAT | 2091 |
| JN189909.2 | AACAGCATTGCCAATGCTTTCGTCTCATACCTTGCTGGTCGTATGGCTGGCATGGATGAT | 2100 |
| MT157513.1 | AACAGCATTGCCAATGCATTCGTCTCGTACCTTGCTGGTCGCATGGCTGGTATGGATGAC | 2099 |
| JN189865.2 | AACAGCATTGCCAATGCTTTCGTCTCATACCTTGCTGGTCGCATGGCTGGCATGGATGAT | 2100 |
| MF144242.1 | AACAGCATTGCCAATGCTTTCGTCTCATACCTTGCCGGTCGCATGGCTGGCATGGATGAT | 2100 |
| AF319555.1 | AACAGCATTGCTAATGCTTTCGTCTCATACCTTGCTGGTCGCATGGCTGGCATGGATGAT | 2100 |
| FJ789783.1 | AACAGCATTGCCAATGCTTTCGTCTCATACCTTGCTGGTCGCATGGCTGGCATGGATGAT | 2100 |
| NC_008040.1 | AACAGCATTGCCAACGCTTTCGTCTCATACCTTGCTGGTCGCATGGCTGGCATGGATGAT | 2100 |
| EF558368.1 | AACAGCATTGCCAATGCTTTCGTCTCATACCTTGCTGGTCGCATGGCTGGCATGGATGAT | 2100 |
| AY721616.1 | AACAGCATTGCCAATGCTTTCGTCTCATACCTTGCTGGTCGCATGGCTGGCATGGATGAC | 2100 |
| KY354681.1 | AACAGCATTGCCAATGCTTTCGTCTCATACCTTGCTGGTCGCATGGCTGGCATGGATGAC | 2097 |
| KP455643.1 | AACAGCATTGCCAATGCTTTCGTCTCATACCTTGCTGGTCGTATGGCTGGCATGGATGAC | 2100 |
| MN309751.1 | AACAGCATTGCCAATGCTTTCGTCTCATACCTTGCTGGTCGTATGGCTGGCATGGATGAC | 2100 |
| | ***** ** ** ***** ***** ***** ***** ***** ***** ***** | |
| AY369136.1 | GACGAAGCTTGGTCTTGGATCGGCATTGTATACGGTGATGACGGGCTCAGATCTGGTAAT | 2160 |
| KY315688.1 | GACGAAGCTTGGTCTTGGATCGGCATTGTATACGGTGATGATGGGCTCAGATCTGGTAAC | 2151 |
| JN189909.2 | GATGAAGCTTGGTCTTGGATCGGCATTGTGTACGGTGATGATGGGCTCCGATCTGGTAAT | 2160 |
| MT157513.1 | GATGAAGCTTGGTCTTGGATCGGCATTGTGTACGGTGATGACGGGCTCCGATCTGGTAAT | 2159 |
| JN189865.2 | GATGAAGCTTGGTCTTGGATCGGCATTGTGTACGGTGATGATGGGCTCCGATCTGGTAAT | 2160 |
| MF144242.1 | GATGAAGCTTGGTCTTGGATCGGCATTGTGTACGGTGATGATGGGCTCCGATCTGGTAAT | 2160 |
| AF319555.1 | GATGAAGCTTGGTCTTGGATCGGCATTGTGTACGGTGATGATGGGCTCCGATCTGGTAAT | 2160 |
| FJ789783.1 | GATGAAGCTTGGTCTTGGATCGGCATTGTGTACGGTGATGATGGGCTCCGATCTGGTAAT | 2160 |
| NC_008040.1 | GATGAAGCTTGGTCTTGGATCGGCATTGTGTACGGTGATGATGGGCTCCGATCTGGTAAT | 2160 |
| EF558368.1 | GATGAAGCTTGGTCTTGGATCGGCATTGTGTACGGTGATGATGGGCTCCGATCTGGTAAT | 2160 |
| AY721616.1 | GATGAAGCTTGGTCTTGGATCGGCATTGTGTACGGTGATGACGGGCTCCGATCTGGTAAT | 2160 |
| KY354681.1 | GATGAAGCTTGGTCTTGGATCGGCATTGTGTACGGTGATGATGGGCTCCGATCTGGTAAT | 2157 |
| KP455643.1 | GATGAGGCTTGGTCTTGGATCGGCATTGTGTACGGTGATGATGGGCTCCGATCTGGTAAT | 2160 |
| MN309751.1 | GATGAGGCTTGGTCTTGGATCGGCATTGTGTACGGTGATGACGGGCTCCGATCTGGTAAT | 2160 |
| | ** ** ***** ***** ***** ***** ***** ***** ***** | |
| AY369136.1 | GTTTCAAATGAGCTCCTCACCAACACTGCTTCTCCCTTGGCTTTGACTTGAAGATAGTG | 2220 |
| KY315688.1 | GTTTCAAATGAGCTCCTCACCAACACTGCTTCTCCCTTGGCTTTGACTTGAAGATAGTG | 2211 |
| JN189909.2 | GTTTCAAATGAGCTCCTCACCAACACTGCTTCTCCCTCGGCTTTGACTTGAAGATCGTG | 2220 |
| MT157513.1 | GTTTCAAATGAGCTCCTCACCAACACTGCTTCTCCCTTGGCTTTGACTTGAAGATTGTG | 2219 |
| JN189865.2 | GTTTCAAATGAGCTCCTCACCAACACTGCTTCTCCCTCGGCTTTGACTTGAAGATAGTG | 2220 |
| MF144242.1 | GTTTCAAATGAGCTCCTCACCAACACTGCTTCTCCCTCGGCTTTGACTTGAAGATAGTG | 2220 |
| AF319555.1 | GTTTCAAACGAGCTCCTCACCAACACTGCTTCTCCCTCGGCTTTGACTTGAAGATAGTG | 2220 |
| FJ789783.1 | GTTTCAAACGAGCTCCTCACCAACACTGCTTCTCCCTCGGCTTTGACTTGAAGATAGTG | 2220 |
| NC_008040.1 | GTTTCAAATGAGCTCCTCACCAACACTGCTTCTCCCTCGGCTTTGACTTGAAGATAGTG | 2220 |
| EF558368.1 | GTTTCAAATGAGCTCCTCACCAACACTGCTTCTCCCTCGGCTTTGACTTGAAGATAGTG | 2220 |
| AY721616.1 | GTTTCAAATGAGCTCCTCACCAACACTGCTTCTCCCTCGGCTTTGACTTGAAGATAGTG | 2220 |
| KY354681.1 | GTTTCAAATGAGCTCCTCACCAACACTGCTTCTCCCTCGGCTTTGACTTGAAGATAGTG | 2217 |
| KP455643.1 | GTTTCAAATGAGCTCCTCACCAACACTGCTTCTCCCTCGGCTTTGACTTGAAGATAGTG | 2220 |
| MN309751.1 | ATTTCAAATGAGCTCCTCACCAACACTGCTTCTCCCTCGGCTTTGACTTGAAGATAGTG | 2220 |
| | ***** ***** ***** ***** ***** ***** ***** | |
| AY369136.1 | AACCGCGCGCCACGTGGCTCCCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2280 |
| KY315688.1 | AACCGCGCGCCACGTGGCTCCCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2271 |
| JN189909.2 | AACCGCGCGCCACGTGGCTCTCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2280 |
| MT157513.1 | AATCGCGCACCCACGTGGCTCTCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2279 |
| JN189865.2 | AATCGCGCGCCACGTGGCTCTCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2280 |
| MF144242.1 | AATCGCGCGCCACGTGGCTCTCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2280 |
| AF319555.1 | AATCGCGCGCCACGTGGCTCTCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2280 |
| FJ789783.1 | AATCGCGCGCCACGTGGCTCTCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2280 |
| NC_008040.1 | AATCGCGCGCCACGTGGCTCTCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2280 |
| EF558368.1 | AATCGCGCGCCACGTGGCTCTCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2280 |
| AY721616.1 | AATCGCGCGCCACGTGGCTCTCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2280 |
| KY354681.1 | AATCGCGCGCCACGTGGCTCTCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2277 |
| KP455643.1 | AATCGCGCGCCACGTGGCTCTCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2280 |
| MN309751.1 | AATCGCGCGCCACGTGGCTCTCCAGTGACATTCTGTCTCGAGTATACCTCGATCCTTGG | 2280 |
| | ** ***** ** ** ***** ** ***** ***** ***** ***** ***** | |
| AY369136.1 | TCCTCACCGGCTTCCGTGCAGTCGCCATTAAAGAACATTGTTGAAATTGCATACCACCTGT | 2340 |
| KY315688.1 | TCCTCACCGGCTCCGTGCAGTCGCCATTAAAGAACATTGTTGAAATTGCATACCACCTGT | 2331 |
| JN189909.2 | TCCTCACCGGCTTCCGTGCAGTCGCCATTAAAGAACATTGTTGAAATTGCACACCACCTGT | 2340 |

MT157513.1 TCCTCACC GGCTTCCGTGCAGTCGCCATTAAGAACATTGTTGAAATTGCACACCACCTGT 2339
JN189865.2 TCCTCACC GGCTTCCGTGCAGTCGCCATTAAGAACATTATTGAAATTGCACACCACCTGT 2340
MF144242.1 TCCTCACC GGCTTCCGTGCAGTCGCCATTAAGAACATTATTGAAATTGCACACCACCTGT 2340
AF319555.1 TCCTCACC GGCTTCCGTGCAGTCGCCATTAAGAACATTGTTGAAATTGCACACCACCTGT 2340
FJ789783.1 TCCTCACC GGCTTCCGTGCAGTCGCCATTAAGAACATTGTTGAAATTGCACACCACCTGT 2340
NC_008040.1 TCCTCACC GGCTTCCGTGCAGTCGCCATTAAGAACATTGTTGAAATTGCACACCACCTGT 2340
EF558368.1 TCCTCACC GGCTTCCGTGCAGTCGCCATTAAGAACATTGTTGAAATTGCACACCACCTGT 2340
AY721616.1 TCCTCACC GGCTTCCGTGCAGTCGCCATTAAGAACATTGTTGAAATTGCACACCACCTGT 2340
KY354681.1 TCCTCACC GGCTTCCGTGCAGTCGCCATTAAGAACATTGTTGAAATTGCACACCACCTGT 2337
KP455643.1 TCCTCACC GGCTTCCGTGCAGTCGCCATTAAGAACATTGTTGAAATTGCACACCACCTGT 2340
MN309751.1 TCCTCACC GGCTTCCGTGCAGTCGCCATTAAGAACATTGTTGAAATTGCACACCACCTGT 2340

Conventional PCR reverse primer: GACATTGGCTGGGCTAAG

AY369136.1 GACACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2400
KY315688.1 GACACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2391
JN189909.2 GACACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2400
MT157513.1 GATACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2399
JN189865.2 GATACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2400
MF144242.1 GATACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2400
AF319555.1 GATACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2400
FJ789783.1 GATACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2400
NC_008040.1 GATACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2400
EF558368.1 GATACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2400
AY721616.1 GATACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2400
KY354681.1 GATACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2397
KP455643.1 GATACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2400
MN309751.1 GATACCCAGTCAGAGATTGACGACATTGGCTGGGCTAAGACACAGGCGTATTTGGTCACT 2400

AY369136.1 GATAGCAAGACACCTTTTATTGGTCATTGGTGCCGGGCTTATCAGAGAAATTGCACTGCA 2460
KY315688.1 GATAGCAAGACACCTTTTATTGGTCATTGGTGCCGGGCTTATCAGAGAAATTGCACTGCA 2451
JN189909.2 GATGGCAAGACACCTTTTATTGGTCATTGGTGCCGGGCTTATCAGAGAAATTGCACTGCA 2460
MT157513.1 GATAGCAAGACACCTTTTATTGGTCATTGGTGCCGGGCTTATCAGAGAAATTGCACTGCA 2459
JN189865.2 GATAGCAAGACACCTTTTATTGGTCATTGGTGCCGGGCTTATCAGAGAAATTGCACTGCA 2460
MF144242.1 GATAGCAAGACACCTTTT-TGGTCATTGGTGCCGGGCTTATCAGAGAAATTCC-CTGCA 2458
AF319555.1 GATAGCAAGACACCTTTTATTGGTCATTGGTGCCGGGCTTATCAGAGAAATTGCACTGCA 2460
FJ789783.1 GATAGCAAGACACCTTTTATTGGTCATTGGTGCCGAGCTTATCAGAGAAATTGCACTGCA 2460
NC_008040.1 GATAGCAAGACACCTTTTATTGGTCATTGGTGCCGGGCTTATCAGAGAAATTGCACTGCA 2460
EF558368.1 GATAGCAAGACACCTTTTATTGGTCATTGGTGCCGGGCTTATCAGAGAAATTGCACTGCA 2460
AY721616.1 GATAGCAAGACACCTTTTATTGGTCATTGGTGCCGGGCTTATCAGAGAAATTGCACTGCA 2460
KY354681.1 GATAGCAAGACACCTTTTATTGGTCATTGGTGCCGGGCTTATCAGAGAAATTGCACTGCA 2457
KP455643.1 GATAGCAAGACACCTTTTATTGGTCATTGGTGCCGGGCTTATCAGAGAAATTGCACTGCA 2460
MN309751.1 GATAGCAAGACACCTTTTATTGGTCATTGGTGCCGGGCTTATCAGAGAAATTGCACTGCA 2460

AY369136.1 CGTGTGGTCCAGTATGCAGACTACACTGACATTCCATTCTGGGTGAAGAATGACGACCAC 2520
KY315688.1 CGTGTGGTCCAGTATGCAGACTACACTGATATCCATTCTGGGTGAAGAATGACGACCAC 2511
JN189909.2 CGTGTGGTCCAGTATGCAGACTACACTGACATTCCATTCTGGGTGAAGAATGACGACCAC 2520
MT157513.1 CGTGTGGTCCAGTATGCAGACTACCTGACATTCCATTCTGGGTGAAGAATGACGACCAC 2519
JN189865.2 CGTGTGGTCCAGTATGCAGACTACACTGACATTCCATTCTGGGTGAAGAATGACGACCAC 2520
MF144242.1 CGTGTGGTCCAGT-ATGCGACTACACTGACATTCCATTCTGGGTGAAGAATGACGACCAC 2517
AF319555.1 CGTGTGGTCCAGTATGCAGACTACCTGACATTCCATTCTGGGTGAAGAATGACGACCAC 2520
FJ789783.1 CGTGTGGTCCAGTATGCAGACTACACTGACATTCCATTCTGGGTGAAGAATGACGACCAC 2520
NC_008040.1 CGTGTAGTTCAGTATGCAGACTACACTGACATTCCATTCTGGGTGAAGAATGACGACCAC 2520
EF558368.1 CGTGTGGTCCAGTATGCAGACTACACTGACATTCCATTCTGGGTGAAGAATGACGACCAC 2520
AY721616.1 CGTGTGGTCCAGTATGCAGACTACACTGACATTCCATTCTGGGTGAAGAATGACGACCAC 2520
KY354681.1 CGTGTGGTCCAGTATGCAGACTACACTGACATTCCATTCTGGGTGAAGAATGACGACCAC 2517
KP455643.1 CGTGTGGTCCAGTATGCAGACTACACTGACATTCCATTCTGGGTGAAGAATGACGACCAC 2520
MN309751.1 CGTGTGGTCCAGTATGCAGACTACACTGACATTCCATTCTGGGTGAAGAATGACGACCAC 2520

AY369136.1 GTTGGCAACTCGTGGCCGAGTCTGAATCCGATGACTGGAATGACATTGTAGCCAATGAG 2580
KY315688.1 GTTGGCAACTCGTGGCCGAGTCTGAATCCGATGACTGGAACGACATTGTAGCCAATGAG 2571
JN189909.2 GCTGGCAAGTCTGGCCGAGTCTGATCCGATGACTGGAATGACGTTGTAGCCAACGAG 2580
MT157513.1 GTTGGCAACTCGTGGCCGAGTCTGAATCTGATGACTGGAATGACATTGTAGCCAACGAG 2579
JN189865.2 GTTGGCAACTCGTGGCCGAGTCTGAATCCGATGACTGGAATGACGTTGTAGCCAACGAG 2580
MF144242.1 GTTGGCAACTCGTGGCCGAGTCTGAATCCGATGACTGGAATGACGTTGTAGCCAACGAG 2577
AF319555.1 GTTGGCAACTCGTGGCCGAGTCTGAATCCGATGACTGGAATGACATTGTAGCCAACGAG 2580
FJ789783.1 GTTGGCAACTCGTGGCCGAGTCTGAATCCGATGACTGGAATGACGTTGTAGCCAACGAG 2580
NC_008040.1 GTCGGCAACTCGTGGCCGAGTCTGAATCCGATGACTGGAATGACGTTGTAGCCAACGAG 2580
EF558368.1 GTTGGCAACTCGTGGCCGAGTCTGAATCTGATGACTGGAATGACGTTGTAGCCAACGAG 2580
AY721616.1 GTTGGCAACTCGTGGCCGAGTCTGAATCCGATGACTGGAATGACGTTGTAGCCAACGAG 2580
KY354681.1 GTTGGCAACTCGTGGCCGAGTCTGAATCCGATGACTGGAATGACGTTGTAGCCAACGAG 2577
KP455643.1 GTTGGCAACTCGTGGCCGAGTCTGAATCCGATGACTGGAATGACGTTGTAGCCAACGAG 2580
MN309751.1 GTTGGCAACTCGTGGCCGAGTCTGAATCCGATGACTGGAATGACGTTGTAGCCAACGAG 2580

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| AY369136.1 | CTTGGCGTCACCACCGCCGAGCTGTTGAAGCATCTTGCACTTCTAGATGCTTATACTGGT | 2640 |
| KY315688.1 | CTTGGCGTCACCACCGCCGAGCTGTTGAAGCATCTTGCACTTCTAGATGCTTATACTGGT | 2631 |
| JN189909.2 | CTTGGCGTCACCACCGCCGAGCTGTTGAAGCATCTTGCACTTCTGGATGCTTATGCTGGT | 2640 |
| MT157513.1 | CTTGGCGTCACCACCGCTGAGCTGTTGAAGCATCTTGCACTTCTGGATGCTTATGCTGGT | 2639 |
| JN189865.2 | CTTGGCGTCACCACCGCTGAGCTGTTGAAGCATCTTGCACTCCTGGATGCTTATACTGGT | 2640 |
| MF144242.1 | CTTGGCGTCACCACCGCTGAGCTGTTGAAGCATCTTGCACTCCTGGATGCTTATACTGGT | 2637 |
| AF319555.1 | CTTGGCGTCACCACCGCTGAGCTGTTGAAGCATCTTGCACTTCTGGATGCTTATGCTGGT | 2640 |
| FJ789783.1 | CTTGGCGTCACCACCGCTGAGCTGTTGAAGCATCTTGCACTCCTGGATGCTTATACTGGT | 2640 |
| NC_008040.1 | CTCGGCGTCACCACCGCTGAGCTGTTGAAGCATCTTGCACTTCTGGATGCTTATACTGGT | 2640 |
| EF558368.1 | CTTGGCGTCACCACCGCTGAGCTGTTGAAGCATCTCGCACTTCTGGATGCTTATACTGGT | 2640 |
| AY721616.1 | CTTGGCGTCACCACCGCTGAGCTGTTGAAGCATCTTGCACTTCTGGATGCTTATACTGGT | 2640 |
| KY354681.1 | CTTGGCGTCACCACCGCTGAGCTGTTGAAGCATCTTGCACTTCTGGATGCTTATACTGGT | 2637 |
| KP455643.1 | CTTGGCGTCACCACCGCTGAGCTGTTGAAGCATCTTGCACTTCTGGATGCTTATACTGGT | 2640 |
| MN309751.1 | CTTGGCGTCACCACCGCTGAGCTGTTGAAGCATCTTGCACTTCTGGATGCTTATACTGGT | 2640 |
| | ** ***** | |
| AY369136.1 | CCCATTAATGGCCTCCACGCTCTGACGACATCAATCGATTTGGAACCAAAGATGCTCTGTC | 2700 |
| KY315688.1 | CCCATTAATGGCCTCCACGCTCTGACAACATCAATCGATTTGGAACCAAAGATGCTCTGTC | 2691 |
| JN189909.2 | CCCATCAGTGGCCTCCACGTTTGACAACATCAATCGATTTGGAACCAAAGATGCTCTGTC | 2700 |
| MT157513.1 | CCCATCAGTGGCCTCCCGCTCTGACAACATCAATTGATTTGGAACCAAAGATGCTCTGTC | 2699 |
| JN189865.2 | CCCATTAGTGGCCTCCACGCTCTGACAACATCAATCGATTTGGAACCAAAGATGCTCTGTC | 2700 |
| MF144242.1 | CCCATTAGTGGCCTCCACGCTCTGACAACATCAATCGATTTGGAACCAAAGATGCTCTGTC | 2697 |
| AF319555.1 | CCCATCAGTGGCCTCCACGCTCTGACAACATCAATCGATTTGGAACCAAAGATGCTCTGTC | 2700 |
| FJ789783.1 | CCCATCAGTGGCCTCCACGCTCTGACAACATCAATCGATTTGGAACCAAAGATGCTCTGTC | 2700 |
| NC_008040.1 | CCCATCAGTGGCCTCCACGCTCTGACAACATCAATCGATTTGGAACCAAAGATGCTCTGTC | 2700 |
| EF558368.1 | CCCATCAGTGGCCTCCACGCTCTGACAACATCAATCGATTTGGAACCAAAGATGCTCTGTC | 2700 |
| AY721616.1 | CCCATTAGTGGCCTCCACGCTCTGACAACATCAATCGATTTGGAACCAAAGATGCTCTGTC | 2700 |
| KY354681.1 | CCCATTAGTGGCCTCCACGCTCTGACAACATCAATCGATTTGGAACCAAAGATGCTCTGTC | 2697 |
| KP455643.1 | CCCATTAGCGGCTCCACGCTCTGACAACATCAATCGATTTGGAACCAAAGATGCTCTGTC | 2700 |
| MN309751.1 | CCCATTAGCGGCTCCCGCTCTGACAACATCAATTGATTTGGAACCAAAGATGCTCTGTC | 2700 |
| | ***** | |
| AY369136.1 | GCATTAGACGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAAAGTAGCAAGGATGGAACA | 2760 |
| KY315688.1 | GCATTAGACGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAACACTAGCAAGGATGGAACA | 2751 |
| JN189909.2 | GCATTAGACGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAAAGTAGCAAGGATGGAACA | 2760 |
| MT157513.1 | GCATTAGACGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAAAGTAGCAAGGATGGAACA | 2759 |
| JN189865.2 | GCATTAGACGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAAAGTAGCAAGGATGGAACA | 2760 |
| MF144242.1 | GCATTAGACGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAAAGTAGCAAGGATGGAACA | 2757 |
| AF319555.1 | GCATTAGATGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAAAGTAGCAAGGATGGAACA | 2760 |
| FJ789783.1 | GCATTAGACGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAAAGTAGCAAGGATGGAACA | 2760 |
| NC_008040.1 | GCATTGGACGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAAAGTAGCAAGGATGGAACA | 2760 |
| EF558368.1 | GCATTAGACGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAAAGTAGTAAGGATGGAACA | 2760 |
| AY721616.1 | GCATTAGACGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAAAGTAGTAAGGATGGAACA | 2760 |
| KY354681.1 | GCATTGGACGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAAAGTAGTAAGGATGGAACA | 2757 |
| KP455643.1 | GCATTAGACGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAAAGTAGTAAGGATGGAACG | 2760 |
| MN309751.1 | GCATTAGACGGGGAGATCCAAGCCGGTCCTAGTCAAAACAAAAGTAGTAAGGATGGAACA | 2760 |
| | ***** | |
| AY369136.1 | AATCCAACAAGCGATCGATCAGCACCTCGTCGAGCTCGAGCAGCTCTTCCAGGTGATGAT | 2820 |
| KY315688.1 | AATCCAACAAGCGATCGATCAGCACCTCGTCGAGCTCGAGCAGCTCTTCCAGGTGATGAT | 2811 |
| JN189909.2 | AATCCAACAAGCGATCGATCAGCACCTCGTCGAGCTCGAACAGCTCTTCCAGGTGATGAT | 2820 |
| MT157513.1 | AATCCAACAAGCGATCGATCAGCACCTCGTCGAGCTCGAGCAGCTCTTCCAGGTGATGAT | 2819 |
| JN189865.2 | AATCCAACAAGCGATCGATCAGCACCTCGTCGAGCTCGAGCAGCTCTTCCAGGTGATGAT | 2820 |
| MF144242.1 | AATCCAACAAGCGATCGATCAGCACCTCGTCGAGCTCGAGCAGCTCTTCCAGGTGATGAT | 2817 |
| AF319555.1 | AATCCAACAAGCGATCGATCAGCACCTCGTCGAGCTCGAGCAGCTCTTCCAGGTGATGAT | 2820 |
| FJ789783.1 | AATCCAACAAGCGATCGATCAGCACCTCGTCGAGCTCGAGCAGCTCTTCCAGGTGATGAT | 2820 |
| NC_008040.1 | AATCCAACAAGCGATCGATCAGCACCTCGTCGAGCTCGAGCAGCTCTTCCAGGTGATGAT | 2820 |
| EF558368.1 | AATCCAACAAGCGATCGATCAGCACCTCGTCGAGCTCGAGCAGCTCTTCCAGGTGATGAT | 2820 |
| AY721616.1 | AATCCAACAAGCGATCGATCAGCACCTCGTCGAGCTCGAGCAGCTCTTCCAGGTGATGAT | 2820 |
| KY354681.1 | AATCCAACAAGCGATCGATCAGCACCTCGTCGAGCTCGAGCAGCTCTTCCAGGTGATGAT | 2817 |
| KP455643.1 | AATCCAACAAGCGATCGATCAGCTCCTCGTCGAGCTCGAGCAGCTCTTCCAGGTGATGAT | 2820 |
| MN309751.1 | AATCCAACAAGCGATCGATCAGCACCTCGTCGAGCTCGAGCAGCTCTTCCAGGTGATGAT | 2820 |
| | ***** | |
| AY369136.1 | GGACACGCGCTCGCTCTCGGCGGAGTGACCGCGATCCAGGTAAACGAGATGCGCACGTT | 2880 |
| KY315688.1 | GGACACGCGCTCGCTCTCGGCGGAGTGACCGCGATCCAGGTAAACGAGATGCGCACGTT | 2871 |
| JN189909.2 | GGACACGCGCTCGCTCTCGGCGGAGTGACCGCGATCCAGGTAAACGAGATGCGCACGTT | 2880 |
| MT157513.1 | GGACACGCGCTCGCTCTCGGCGGAGTGACCGCGATCCAGGTAAACGAGATGCGCACGTT | 2879 |
| JN189865.2 | GGACACGCGCTCGCTCTCGGCGGAGTGACCGCGATCCAGGTAAACGAGATGCGCACGTT | 2880 |
| MF144242.1 | GGACACGCGCTCGCTCTCGGCGGAGTGACCGCGATCCAGGTAAACGAGATGCGCACGTT | 2877 |
| AF319555.1 | GGACACGCGCTCGCTCTCGGCGGAGTGACCGCGATCCAGGTAAACGAGATGCGCACGTT | 2880 |
| FJ789783.1 | GGACACGCGCTCGCTCTCGGCGGAGTGACCGCGATCCAGGTAAACGAGATGCGCACGTT | 2880 |
| NC_008040.1 | GGACACGCGCTGCTCTCGGCGGAGTGACCGCGATCCAGGTAAACGAGATGCGCACGTT | 2880 |
| EF558368.1 | GGACACGCGCTCGCTCTCGGCGGAGTGACCGCGATCCAGGTAAACGAGATGCGCACGTT | 2880 |
| AY721616.1 | GGACACGCGCTCGCTCTCGGCGGAGTGACCGCGATCCAGGTAAACGAGATGCGCACGTT | 2880 |
| KY354681.1 | GGACACGCGCTCGCTCTCGGCGGAGTGACCGCGATCCAGGTAAACGAGATGCGCACGTT | 2877 |
| KP455643.1 | GGACACGCGCTCGCTCTCGGCGGAGTGACCGCGATCCAGGTAAACGAGATGCGCACGTT | 2880 |

| | | |
|-------------|--|------|
| MN309751.1 | GGACACGCGCGTCGCTCTCGGCGGAGTGACCGCGATCCAGGTAACAGAGATGCGTACGTT ***** | 2880 |
| AY369136.1 | CGTGATAAGCGCTCAGCCCGCAGCTCGCCGCCTACACGTCTGTACGCCGGTTTCCGCC | 2940 |
| KY315688.1 | CGTGACAAGTGCTCAGCCCGCAGCTCGCCGCCTACACGTCTGTCTCGCCGGTTTCCGCC | 2931 |
| JN189909.2 | CGTGATAAGCGCCACGCCCGCAGCCCGTCGCTACACGTCTGTACGCCGGTTTCCGCC | 2940 |
| MT157513.1 | CGTGATAAGCGCCACGCCCGCAGCTCGCCGCCTGCACGTCTGTACGCCGGTTTCCGCC | 2939 |
| JN189865.2 | CGTGATAAGCGCCACGCCCGCAGCTCGCCGCCTGCACGTCTGTACGCCGGTTTCCACC | 2940 |
| MF144242.1 | CGTGATAAGCGCCACGCCCGCAGCTCGCCGCCTGCACGTCTGTACGCCGGTTTCCACC | 2937 |
| AF319555.1 | CGTGATAAGCGCCACGCCCGCAGCTCGCCGCCTACACGTCTGTACGCCGGTTTCCACC | 2940 |
| FJ789783.1 | CGTGATAAGCGCCACGCCCGCAGCTCGCCGCCTACACGTCTGTACGCCGGTTTCCACC | 2940 |
| NC_008040.1 | CGTGGTAAGCGCTCAGCCCGCAGCTCGCCGCCTGTACGTCTGTACGCCGGTTTCCACC | 2940 |
| EF558368.1 | CGTGATAAGCGCCACGCCCGGGCTCGCCGCCTACACGTCTGTACGCCGGTTTCCACC | 2940 |
| AY721616.1 | CGTGATAAGCGCCACGCCCGCAGCTCGCCGCCTGCACGTCTGTACGCCGGTTTCCACC | 2940 |
| KY354681.1 | CGTGATAAGCGCCACGCCCGCAGCTCGCCGCCTGCACGTCTGTACGCCGGTTTCCACC | 2937 |
| KP455643.1 | CGTGATAAGCGCCACGCCCGCAGCTCGCCGCCTGCACGTCTGTACGCCGGTTTCCACC | 2940 |
| MN309751.1 | CGTGATAAGCGCCACGCCCGCAGCTCGCCGCCTGCACGTCTGTACGCCGGTTTCCACC **** * * * * * | 2940 |
| AY369136.1 | CGCTCTAGCGGTGATCGAGGAACCGATGGAGACAGACTAGGCCGAGCTGTTGTGCGTCAG | 3000 |
| KY315688.1 | CGCTTTAGCGGTGATCGAGGAACCGGTGGAGACAGACTAGGCCGAGCTGTTGTGCGTCAG | 2991 |
| JN189909.2 | CGCTCTAGCGGTGATCGTGGAACCGATGGAGACGGAAGTGGAGCCGAGCTGCTGTGCGTCAG | 3000 |
| MT157513.1 | TCTTCCAGCAGTGGTCGAGGAACCGATGGAGACGGAAGTGGAGCCGAGCTGCTGTGCGTCAG | 2999 |
| JN189865.2 | CCTTCCAGCGGTGATCGAGGAACCGATGGAGACGGAAGTGGAGCCGAGCTGCTGTGCGCCAG | 3000 |
| MF144242.1 | CCTTCCAGTGGTGATCGAGGAACCGATGGAGACGGAAGTGGAGCCGAGCTGCTGTGCGTCAG | 2997 |
| AF319555.1 | CCTTCCAGCGGTGATCGAGGAACCGATGGAGACGGAAGTGGAGCCGAGCTGCTGTGCGTCAG | 3000 |
| FJ789783.1 | CCTTCCAGCGGTGATCGAGGAACCGATGGAGACGGAAGTGGAGCCGAGCTGCTGTGCGTCAG | 3000 |
| NC_008040.1 | CCTTCCAGCGGTGATCGAGGAACCGATGGAGACGGAAGTGGAGCCGAGCTGCTGTGCGTCAG | 3000 |
| EF558368.1 | CCTTCCAGCGGTGATCGAGGAGCCGATGGAGACGGAAGTGGAGCCGAGCTGCTGTGCGTCAG | 3000 |
| AY721616.1 | CCTTCCAGCGGTGATCGAGGAACCGATGGAGACGGAAGTGGAGCCGAGCTGCTGTGCGTCAG | 3000 |
| KY354681.1 | CCTTCCAACGCTGATCGAGGAGCCGATGGAGACGGAAGTGGAGCCGAGCTGCTGTGCGTCAG | 2997 |
| KP455643.1 | CCTTCCAGCGGTGATCGAGGAACCGATGGAGACGGAAGTGGAGCCGAGCTGCTGTGCGTCGG | 3000 |
| MN309751.1 | CCTTCCAGCGGTGATCGAGGAACCGATGGAGACGGAAGTGGAGCCGAGCTGCTGTGCGTCAG * * * * * | 3000 |
| AY369136.1 | CGTCAACGACGTCGCACTCAAGTGATAGACAGGTCACCTGCCTGCTCCACCCCC-CTGGAC | 3059 |
| KY315688.1 | CGTCAACGACGTCGCACTCAAGTGATAGACAGGTCACCTGCCTGCTCCACCCCC-CTGGAC | 3050 |
| JN189909.2 | CGTCAGCGACGTCGCACTCAGGTGTAGACAGGTCACCTGCCTGCTCCACCCCCCGGAC | 3060 |
| MT157513.1 | CGTCAGCGACGTCGCACTCAAGTGATAGACAGGTCACCTGCCTGCTCCACCCCCCT-GGAC | 3058 |
| JN189865.2 | CGTCAGCGACGTCGCACTCAAGTGATAGACAGGTCACCTGCCTGCTCCACCCCCCT-GGAC | 3059 |
| MF144242.1 | CGTCAGCGACGTCGCACTCAAGTGATAGACAGGTCACCTGCCTGCTCCACCCCCCT-GGAC | 3056 |
| AF319555.1 | CGTCAGCGACGTCGCACTCAAGTGATAGACAGGTCACCTGCCTGCTCCACCCCCCT-GGAC | 3059 |
| FJ789783.1 | CGCCATCGACGTCGCACTCAAGTGATAGACGGGTACCTGCCTGCTCCACCCCCCG-GAC | 3059 |
| NC_008040.1 | CCCCGCGACGTCGCACTCAAGTGATAGACAGGTCACCTGCCTGCTCCACCCCCCTGGAC | 3060 |
| EF558368.1 | CGCCAGGGACGTCGCACTCAAGTGATAGACAGGTCACCTGCCTGCTCCACCCCC-CTGGAC | 3059 |
| AY721616.1 | CGCCAGCGACGTCGCACTCAAGTGATAGACAGGTCACCTGCCTGCTCCACCCCC-CTGGAC | 3059 |
| KY354681.1 | CGCCAGCGACGTCGCACTCAAGTGATAGACAGGTCACCTGCCTGCTCCACCCCC-C---- | 3051 |
| KP455643.1 | CGTCAGCGACGTCGCACTCAAGTGATAGACAGGTCACCTGCCTGCTCCACCCCC-CTGGAC | 3059 |
| MN309751.1 | CGTCAGCGACGTCGCACTCAAGTGATAGACAGGTCACCTGCCTGCTCCACCCCC-CTGGAC * * * * * | 3059 |
| AY369136.1 | CGTTTTGGTCCCTTAATCAGCTTTATGCTGTCTACGCTTCGGC- | 3103 |
| KY315688.1 | CGTTTTGGTCCCTTAATCAGCTTTATGCTATCTTACGCTTCGGCA | 3095 |
| JN189909.2 | CGTCTTGGTCCCTTAATCAGCTTTATGCTGTCTTACGCTTCGGC- | 3104 |
| MT157513.1 | CGTTTTGGTCCCTTAATCAGCTTTATGCTGTCTTACGCTTCGGCG | 3103 |
| JN189865.2 | CGTTTTGGTCCCTTAATCAGCTTTATGCTGTCTTACGCTTCGGC- | 3103 |
| MF144242.1 | CGTTTTGGTCCCTTAATCAGCTTTATGCTGTCTTACGCTTCGGC- | 3100 |
| AF319555.1 | CGTTTTGGTCCCTTAATCAGCTTTATGCTGTCTTACGCTTCGGC- | 3103 |
| FJ789783.1 | CGGTTTTGGTCCCTTAATCAGCTTTATGCTGTCTTACGCTTCGGCG | 3104 |
| NC_008040.1 | CGTTTTGGTCCCTTAATCAGCTTTATGCTGTCTTACGCTTCGGCG | 3105 |
| EF558368.1 | CGTTTTGGTCCCTTAATCAGCTTTATGCTGTCTTACGCTTCGGC- | 3103 |
| AY721616.1 | CGTTTTGGTCCCTTAATCAGCTTTATGCTGTCTTACGCTTCGGC- | 3103 |
| KY354681.1 | ----- | 3051 |
| KP455643.1 | CATTTTTGGTCCCTTAATCAGCTTTATGCTGTCTTACGCTTCGGC- | 3103 |
| MN309751.1 | CGTTTTGGTCCCTTGATCAGCTTTATGCTGTCTTACGCTTCGGC- | 3103 |

Figure S2. Multiple sequence alignment of RNA2 sequences from the selected genotype representatives.

| GB acc. no | Conventional PCR forward primer:AATGGTACGCAAAGGTGA | bp |
|-------------|---|-----|
| KY354702.2 | -----CCGCTTTGCAATCAAAATGGTACGCAAAGGTGATAAGAAATTGGCAAAA | 50 |
| KF386164.1 | TAATTCGACATCGCTTTGCATCTCAAAATGGTACGCAAAGGTGAGAAGAAATTGGCTAAA | 60 |
| JX402858.1 | ----- | 0 |
| KY315689.1 | -TAATTCAGCACCGCTTTGCAATCAAAATGGTACGCAAAGGTGAGAAGAAATTGGCAAAA | 59 |
| JN189992.2 | -TAATCCATCACCGCTTTGCAATCAAAATGGTACGCAAAGGTGAGAAGAAATTGGCAAAA | 59 |
| GU592791.1 | -----TNNTNCNACNAATGGTACGCAAAGGTGAGAAGAAATTGGCAAAA | 44 |
| AF499774.1 | -----ATGGTACGCAAAGGTGATAAGAAATTGGCAAAA | 33 |
| MG637439.1 | -TAATCCATCACCGCTTTGCAATCAAAATGGTACGCAAAGGTGAGAAGAAATTGGCAAAAG | 59 |
| KU705815.1 | -----CCCCCTACAAATGGTACGCAAAGGTGAGAAGAAATTGGCAAAA | 43 |
| AF245004.1 | -----CTTTGCAAGTCAAAATGGTACGCAAAGGTGAGAAGAAATTGGCAAAA | 47 |
| JF412263.1 | -TAATCCATCACCGCTTTGCAATCAAAATGGTACGCAAAGGTGAGAAGAAATTGGCAAAA | 59 |
| MN309752.1 | -TAATCCATCACCGCTTTGCAATCAAAATGGTACGCAAAGGTGAGAAGAAATTGGCAAAA | 59 |
| KM588181.1 | ---TCCTTCATCGCTTTGCAATCAAAATGGTACGCAAAGGTGAGAAGAAATTGGCAAAA | 56 |
| FJ789784.1 | -TAATCCACCACCGCTTTGCAATCAAAATGGTACGCAAAGGTGAGAAGAAATTGGCAAAA | 59 |
| AF245003.1 | -----CTTTGCAAGTCAAAATGGTACGCAAAGGTGAGAAGAAATTGGCAAAA | 47 |
| NC_008041.1 | -TAATCCATCACCGCTTTGCAATCAAAATGGTACGCAAAGGTGAGAAGAAATTGGCAAAA | 59 |
| AY744705.1 | -TAATCCATCACCGCTTTGCAATCAAAATGGTACGCAAAGGTGAGAAGAAATTGGCAAAA | 59 |
| KY354702.2 | CCTGCGACCACAAAGGCCGCGCAATCCTCAACCACGTCGACGTGCAACACAGCGCCGTCGC | 110 |
| KF386164.1 | ACAGCGACCACCAAGGCCGCTAATCCTCAACCCCGTCGACGTGCCGCCAACCGGCGGCGT | 120 |
| JX402858.1 | -CCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGTCGACGTGCTAACAATCGTCGGCGT | 59 |
| KY315689.1 | CCCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGCGACGTGCTAACAATCGTCGGCGT | 119 |
| JN189992.2 | CCCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGCGACGTGCTAACAATCGTCGGCGT | 119 |
| GU592791.1 | CCCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGCGACGTGCTAACAATCGTCGGCGT | 104 |
| AF499774.1 | CCCGCGACCACCAAGGCCGCGCAATCCGCAATCCCGCGACGTGCTAACAATCGTCGGCGT | 93 |
| MG637439.1 | CCCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGCGACGTGCTAACAATCGTCGGCGT | 119 |
| KU705815.1 | CCCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGCGACGTGCTAACAATCGTCGGCGT | 103 |
| AF245004.1 | CCCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGCGACGTGCTAACAATCGTCGGCGT | 107 |
| JF412263.1 | CCCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGCGACGTGCTAACAATCGTCGGCGT | 119 |
| MN309752.1 | CCCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGCGACGTGCTAACAATCGTCGGCGT | 119 |
| KM588181.1 | CCCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGCGACGTGCTAACAATCGTCGGCGT | 116 |
| FJ789784.1 | CCCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGCGACGTGCTAACAATCGTCGGCGT | 119 |
| AF245003.1 | CCCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGCGACGTGCTAACAATCGTCGGCGT | 107 |
| NC_008041.1 | CCCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGCGACGTGCTAACAATCGTCGGCGT | 119 |
| AY744705.1 | CCCGCGACCACCAAGGCCGCGCAATCCGCAACCCCGCGACGTGCTAACAATCGTCGGCGT | 119 |
| | * | |
| KY354702.2 | AGTGGTAGGGCTGATGCACCTTAGCTAAGGCATCGACTATCACGGGATTGGACGTGCG | 170 |
| KF386164.1 | AGTAATCGACCTGACGCGCTTTAGCAAAGGCTTCGACTGTCACGGGATTCGGACGTGGG | 180 |
| JX402858.1 | AGTAACCGCATTGACGCACCCGTGTCTAAGGCTCGACCGTAACCTGGGTTTGGACGTGGG | 119 |
| KY315689.1 | AGTAATCGCACTGACGCACCTGTGTCTAAGGCTCGACTGTAACCTGGGTTTGGACGTGGG | 179 |
| JN189992.2 | AGTAATCGCACTGACGCACCTGTGTCTAAGGCTCGACCGTAACCTGGATTGGACGTGGG | 179 |
| GU592791.1 | AGTAATCGCACTGACGCACCTGTGTCTAAGGCTCGACTGTAACCTGGATTGGACGTGGG | 164 |
| AF499774.1 | AGTAATCGCACTGACGCACCTGTGTCTAAGGCTCGACTGTAACCTGGATTGGACGTGGG | 153 |
| MG637439.1 | AGTAACCGCACTGACGCACCTGTGTCTAAGGCTCGACTGTGACTGGATTGGACGTGGG | 179 |
| KU705815.1 | AGTAATCGCACTGACGCACCTGTGTCTAAGGCTCGACTGTGACTGGATTGGACGTGGG | 163 |
| AF245004.1 | AGTAATCGCACTGACGCACCTGTGTCTAAGGCTCGACTGTGACTGGATTGGACGTGGG | 167 |
| JF412263.1 | AGTAATCGCACTGACGCACCTGTGTCTAAGGCTCGACTGTGACTGGATTGGACGTGGG | 179 |
| MN309752.1 | AGTAACCGCACTGACGCACCTGTGTCTAAGGCTCGACTGTGACCGGATTGGACGTGGG | 179 |
| KM588181.1 | AGTAATCGCACTGACGCACCTGTGTCTAAGGCTCGACTGTGACTGGATTGGACGTGGG | 176 |
| FJ789784.1 | AGTAATCGCACTGACGCACCTGTGTCTAAGGCTCGACTGTAACCTGGATTGGACGTGGG | 179 |
| AF245003.1 | AGCAATCGCACTGACGCACCTGTGTCTAAGGCTCGACTGTAACCTGGATTGGACGTGGG | 167 |
| NC_008041.1 | AGTAATCGCACTGACGCACCTGTGTCTAAGGCTCGACTGTAACCTGGATTGGACGTGGG | 179 |
| AY744705.1 | AGTAATCGCACTGACGCACCTGTGTCTAAGGCTCGACTGTAACCTGGATTGGACGTGGG | 179 |
| | ** | |
| KY354702.2 | ACCAATGATGTCCACATCTCGGGAATGTCACGGATCGCTCAGGCAGTTGTTCCAGCCGGG | 230 |
| KF386164.1 | ACCAATGACGTCCATCTCTCGGGTATGTCGAGAATCTCCCAAGCAGTCCTCGCGCCGGG | 240 |
| JX402858.1 | ACCAATGACGTCCATCTCTCAGGTATGTCGAGAATCGCCCAAGCCGTCCTCCAGCCGGG | 179 |
| KY315689.1 | ACCAATGACGTCCATCTCTCAGGTATGTCGAGAATCTCCAGGCCGTCCTCCAGCCGGG | 239 |
| JN189992.2 | ACCAATGACGTCCATCTCTCAGGTATGTCGAGAATCTCCAGGCCGTCCTCCAGCCGGG | 239 |
| GU592791.1 | ACCAATGACGTCCATCTCTCAGGTATGTCGAGAATCTCCAGGCCGTCCTCCAGCCGGG | 224 |
| AF499774.1 | ACCAATGAAGTCTATCTCTCAGGTATGTCGAGAATCTCCAGGCCGTCCTCCAGCCGGG | 213 |
| MG637439.1 | ACCAATGACGTCCATCTCTCAGGTATGTCGAGAATCTCCAGGCCGTCCTCCAGCCGGG | 239 |
| KU705815.1 | ACCAATGACGTCCATCTCTCAGGTATGTCGAGAATCTCCAGGCCGTCCTCCAGCCGGG | 223 |
| AF245004.1 | ACCAATGACGTCCATCTCTCAGGTATGTCGAGAATCTCCAGGCCGTCCTCCAGCCGGG | 227 |
| JF412263.1 | ACCAATGACGTCCATCTCTCAGGTATGTCGAGAATCTCCAGGCCGTCCTCCAGCCGGG | 239 |
| MN309752.1 | ACCAATGACGTCCATCTCTCAGGTATGTCGAGAATCTCCAGGCCGTCCTCCAGCCGGG | 239 |
| KM588181.1 | ACCAATGACGTCCATCTCTCAGGTATGTCGAGAATCTCCAGGCCGTCCTCCAGCCGGG | 236 |
| FJ789784.1 | ACCAATGACGTCCATCTCTCAGGTATGTCGAGAATCTCCAGGCCGTCCTCCAGCCGGG | 239 |
| AF245003.1 | ACCAATGACGTCCATCTCTCAGGTATGTCGAGAATCTCCAGGCCGTCCTCCAGCCGGG | 227 |

| | | |
|-------------|--|-----|
| AY744705.1 | ACTGACAACGATCACACCTTCGACGCGCTTCAAGCAACTCGTGGTGCAGTCGTTGCCAAA | 479 |
| | ***** | |
| | TGGTGGGAAAG | |
| KY354702.2 | TGGTGGGAAAGCCGAACGGTCCGGCCCCAGTATACTCGAACGCTTCTCTGGACCTCAACC | 530 |
| KF386164.1 | TGGTGGGAGCAGGACAGTACGTCACAGTACACTCGAACCATGCTCTGGACCTCAACA | 540 |
| JX402858.1 | TGGTGGGAAAGCAGAAGTGTCCGACCACAGTACACCCGCACGCTCCTTTGGACCTCATCG | 479 |
| KY315689.1 | TGGTGGGAAAGCAGAACAGTCCGACCTCAGTACACCCGTACGCTCCTCTGGACCTCGTCG | 539 |
| JN189992.2 | TGGTGGGAAAGCAGAACAGTCCGACCGCAGTTCACCTCGCACGCTCCTCTGGACCTCGTCG | 539 |
| GU592791.1 | TGGTGGGAAAGCAGAACAGTCCGACCTCAGTACACCCGCACGCTCCTCTGGACCTCGTCG | 524 |
| AF499774.1 | TGGTGGGAAAGCAGAACAGTCCGACCTCAGTACACCCGCACGCTCCTCTGGACCTCGTCG | 513 |
| MG637439.1 | TGGTGGGAAAGCAGAACAGTCCGACCTCAGTACACCCGCACGCTCCTCTGGACCTCGTCG | 539 |
| KU705815.1 | TGGTGGGAAAGCAGAACAGTCCGACCTCAGTACACCCGTACGCTCCTCTGGACCTCGTCG | 523 |
| AF245004.1 | TGGTGGGAAAGCAGAACAGTCCGACCTCAGTACACCCGCACGCTCCTCTGGACCTCGTCG | 527 |
| JF412263.1 | TGGTGGGAAAGCAGAACAGTCCGACCTCAGTACACCCGCACGCTCCTCTGGACCTCGTCG | 539 |
| MN309752.1 | TGGTGGGAAAGCAGAACAGTCCGACCCAGTACACCCGCACGCTCCTCTGGACCTCGTCG | 539 |
| KM588181.1 | TGGTGGGAAAGCAGAACAGTCCGACCTCAGTACACCCGTACGCTCCTCTGGACCTCGTCG | 536 |
| FJ789784.1 | TGGTGGGAAAGCAGTACAGTCCGACCTCAGTACACCCGCACGCTCCTCTGGACCTCGTCG | 539 |
| AF245003.1 | TGGTGGGAAAGCAGAACAGTCCGACCTCAGTACACCCGCACGCTCCTCTGGACCTCGTCG | 527 |
| NC_008041.1 | TGGTGGGAAAGCAGAACAGTCCGACCTCAGTACACCCGCACGCTCCTCTGGACCTCGTCG | 539 |
| AY744705.1 | TGGTGGGAAAGCAGAACAGTCCGACCTCAGTACACCCGCACGCTCCTCTGGACCTCGTCG | 539 |
| | ***** | |
| KY354702.2 | GGGAAGGAGCAGCGATTGACGTCACCTGGCCGGCTGGTACTCCTGTGTGTTGGCAGCAAC | 590 |
| KF386164.1 | GGAAAGGAGCAGCGTTTGACTTCACCTGGACGCTTCATTCTCCTCTGTGTGCGCAGCAAC | 600 |
| JX402858.1 | GGAAAGGAGCAGCGCTCTCACGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 539 |
| KY315689.1 | GGAAAGGAGCAGCGCTCTCACGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAGCAAC | 599 |
| JN189992.2 | GGAAAGGAGCAGCGCTCTTACATCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 599 |
| GU592791.1 | GGAAAGGAGCAGCGCTCTCACGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 584 |
| AF499774.1 | GGAAAGGAGCAGCGCTCTCATGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 573 |
| MG637439.1 | GGAAAGGAGCAGCGCTCTCACGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 599 |
| KU705815.1 | GGAAAGGAGCAGCGCTCTCACGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 583 |
| AF245004.1 | GGAAAGGAGCAGCGCTCTCACGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 587 |
| JF412263.1 | GGAAAGGAGCAGCGCTCTCACGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 599 |
| MN309752.1 | GGAAAGGAGCAGCGCTCTCACGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 599 |
| KM588181.1 | GGAAAGGAGCAGCGCTCTCACGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 596 |
| FJ789784.1 | GGAAAGGAGCAGCGCTCTCACGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 599 |
| AF245003.1 | GGAAAGGAGCAGCGCTCTCACGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 587 |
| NC_008041.1 | GGAAAGGAGCAGCGCTCTCACGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 599 |
| AY744705.1 | GGAAAGGAGCAGCGCTCTCACGTCACCTGGTCGGCTGATACTCCTGTGTGTGCGCAACAAC | 599 |
| | ** ***** | |
| KY354702.2 | ACTGACGTTGTCAACGTGTGTCAGTCATGTGTCGCTGGAGCGTTGCGCTTAGTGTCCCGTCC | 650 |
| KF386164.1 | ACTGACGTGGTTAACGTGTGTCGGTGTTATGTGCTGAGGTGTGCGCCTCAGTGTCCCATCT | 660 |
| JX402858.1 | ACTGACGTGGTTAACGTTTTCAGTGCTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCGTCC | 599 |
| KY315689.1 | ACTGATGTGGTCAACGTGTGTCAGTGCTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCATCT | 659 |
| JN189992.2 | ACTGACGTGGTTAACGTGTGTCGGTGCTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCGTCT | 659 |
| GU592791.1 | ACTGATGTGGTCAACGTGTGTCAGTGCTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCATCT | 644 |
| AF499774.1 | ACTGATGTGGTCAACGTGTGTCAGTGCTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCATCT | 633 |
| MG637439.1 | ACTGACGTGGTCAACGTGTGTCGGTGCTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCATCT | 659 |
| KU705815.1 | ACTGATGTGGTCAACGTGTGTCAGTGCTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCATCT | 643 |
| AF245004.1 | ACTGATGTGGTCAACGTGTGTCAGTGCTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCATCT | 647 |
| JF412263.1 | ACTGATGTGGTCAACGTGTGTCAGTACTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCATCT | 659 |
| MN309752.1 | ACTGATGTGGTCAACGTGTGTCAGTACTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCATCT | 659 |
| KM588181.1 | ACTGATGTGGTCAACGTGTGTCAGTGCTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCATCT | 656 |
| FJ789784.1 | ACCGATGTGGTCAACGTGTGTCGGTGCTATGTGTCGCTGGAGTGTTCGATTGAGCGTTCCATCT | 659 |
| AF245003.1 | ACTGATGTGGTCAACGTGTGTCAGTGCTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCATCT | 647 |
| NC_008041.1 | ACTGATGTGGTCAACGTGTGTCAGTGCTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCATCT | 659 |
| AY744705.1 | ACTGATGTGGTCAACGTGTGTCAGTGCTGTGTCGCTGGAGTGTTCGACTGAGCGTTCCATCT | 659 |
| | ** ** * | |
| KY354702.2 | CTTGAGACACCTGAGGACACCACCGCTCCAATTACTACCCAGGCGCCACTCCACAACGAT | 710 |
| KF386164.1 | CTCGAGACGCTGAGGACACAGCTGCACCGATTTCGTCACAGGGTCCCCTCTACAACGAT | 720 |
| JX402858.1 | CTTGAAACACCTGAAGAGACCAACCGTCCCATCATGACACAGGGTCCCCTGTACAACGAT | 659 |
| KY315689.1 | CTTGAGACACCTGAAGAGACCACCGTCCCATCATGACACAAGGTTCCCTGTACAACGAT | 719 |
| JN189992.2 | CTTGAAACACCTGAAGAGACCACCGTCCCATCATGACACAAGGTTCCCTGTACAATGAT | 719 |
| GU592791.1 | CTTGAGACACCTGAAGAGACCACCGTCCCATCATGACACAAGGTTCCCTGTACAACGAT | 704 |
| AF499774.1 | CTTGAGACACCTGAAGAGACCACCGTCCCATCATGACACAAGGTTCCCTGTACAACGAT | 693 |
| MG637439.1 | CTTGAGACACCTGAAGAGACCACCGTCCCATCATGACACAAGGTTCCCTGTACAACGAT | 719 |
| KU705815.1 | CTTGAGACACCTGAAGAGACCACCGTCCCATCATGACACAAGGTTCCCTGTACAACGAT | 703 |
| AF245004.1 | CTTGAGACACCTGAAGAGACCACCGTCCCATCATGACACAAGGTTCCCTGTACAACGAT | 707 |
| JF412263.1 | CTTGAGACACCTGAGGAGACACCAGTCCCATCATGACACAAGGTTCCCTGTACAACGAT | 719 |
| MN309752.1 | CTTGAGACACCTGAGGAGACACCAGTCCCATCATGACACAAGGTTCCCTGTACAACGAT | 719 |
| KM588181.1 | ATTGAGACACCTGAAGAGACCACCGACCCATCATGACACAAGGTTCCCTGTACAACGAT | 716 |
| FJ789784.1 | CTTGAGACACCTGAAGAGACCACCGTCCCATCATGACACAAGGTTCCCTGTACAACGAT | 719 |
| AF245003.1 | CTTGAGACACCTGAAGAGACCACCGTCCCATCATGACACAAGGTTCCCTGTACAACGAT | 707 |
| NC_008041.1 | CTTGAGACACCTGAAGAGACCACCGTCCCATCATGACACAAGGTTCCCTGTACAACGAT | 719 |

| | | |
|-------------|---|-----|
| AY744705.1 | CTTGAGACACCTGAAGAGACCACCGTCCCATGATGACACAAGGTTCCTGTGTAACACGAT * | 719 |
| KY354702.2 | TCCATTAAACAACGGTTACTGATTTTCGGTCCATTCTTTTGGGCTCGACCCAACCTCGAC | 770 |
| KF386164.1 | TCCCTTGCACAAA-----CTGACTTCAAATCCATCCTCCTGGGTTCCACACAGCTGGAC | 774 |
| JX402858.1 | TCCCTCGCTGCAC-----ATGACTTCAAGTCCATCCTCCTAGGATCCACACCACTGGAC | 713 |
| KY315689.1 | TCCCTTTCCACAAA-----ATGACTTCAAGTCCATCCTCCTAGGATCCATACCACTGGAC | 773 |
| JN189992.2 | TCCCTCGCTGCCAA-----CTGACTTCAAGTCCATCCTCCTAGGATCCACAGCACTGGAC | 773 |
| GU592791.1 | TCCCTTTCCACAAA-----ATGACTTCAAGTCCATCCTCCTAGGATCCACACCACTGGAC | 758 |
| AF499774.1 | TCCCTTTCCACAAA-----CTGACTTCAAGTCCATCCTCCTAGGATCCACACCACTGGAC | 747 |
| MG637439.1 | TCCCTTTCCACAAA-----ATGACTTCAAGTCCATCCTCCTAGGATCCACGCCACTGGAC | 773 |
| KU705815.1 | TCCCTTTCCACAAA-----ATGACTTCAAGTCCATCCTCCTAGGATCCACGCCACTGGAT | 757 |
| AF245004.1 | TCCCTTTCCACAAA-----ATGACTTTAAGTCCATCCTCCTAGGATCCACACCACTGGAC | 761 |
| JF412263.1 | TCCCTTTCCACAAA-----ATGACTTCAAGTCCATCCTCCTAGGATCCACACCACTGGAC | 777 |
| MN309752.1 | TCCCTTTCCACAAA-----ATGACTTCAAGTCCATCCTCCTAGGATCCACACCACTGGAC | 773 |
| KM588181.1 | TCCCTTTCCACAAA-----CTGACTTCAAGTCCATCCTCCTAGGATCCACACCACTGGAT | 770 |
| FJ789784.1 | TCCCTTTCCACAAA-----ATGACTTCAAGTCCATCCTCCTAGGATCCACACCACTGGAC | 773 |
| AF245003.1 | TCCCTTTCCACAAA-----ATGACTTCAAATCCATCCTCCTAGGATCCACACCACTGGAC | 761 |
| NC_008041.1 | TCCCTTTCCACAAA-----ATGACTTCAAGTCCATCCTCCTAGGATCCACACCACTGGAC | 773 |
| AY744705.1 | TCCCTTTCCACAAA-----ATGACTTCAAGTCCATCCTCCTAGGATCCACACCACTGGAC *** * ** * * **** * * * * * * * * | 773 |
| KY354702.2 | CTCGCTCCTGCAAACGCTGTCTTTGTCACTGACAAAACCGTTGCCCATTTGATTACAGTCTT | 830 |
| KF386164.1 | ATATCCCCGGAGCGGCCCATCTTCCAGATGGACCGCCCGCTGTCCATTGATTACAAGCTG | 834 |
| JX402858.1 | ATAGCCCCTGACGGTGCAGTCTACACAGCTGGACCGTCCGCTGTCCATCGATTACAGCCTT | 773 |
| KY315689.1 | ATTGCCCCGTGATGGAGCAGTCTTCCAGCTGGACCGCCCGCTGTCCATTGACTACAGCCTT | 833 |
| JN189992.2 | ATTGCTCCTGACGGAGCAATCTTCCAGCTGGACCGTCCGCTGTCTCATTGACTACAACCTT | 833 |
| GU592791.1 | ATTGCCCTGATGGAGAGCTTCTCCAGCTGGACCGTCCGCTGTCCATTGACTACAGCCTT | 818 |
| AF499774.1 | ATTGCCCCCTGATGGAGCAGTCTTCCAGCTGGACCGTCCGCTGTCCATTGACTACACCTT | 807 |
| MG637439.1 | ATTGCCCCCTGATGGAGCAGTCTTCCAGCTGGACCGTCCGCTGTCCATCGACTACAGCCTT | 833 |
| KU705815.1 | ATTGCCCCCTGATGGAGCAGTCTTCCAGCTGGACCGTCCGCTGTCCATCGACTACAGCCTT | 817 |
| AF245004.1 | ATTGCCCTGATGGAGCAGTCTTCCAGCTGGATCGACCGTGTCCATTGACTACAGCCTT | 821 |
| JF412263.1 | ATTGCCCCCTGATGGAGCAGTCTTCCAGCTGGACCGTCCGCTGTCCATTGACTACAGCCTT | 833 |
| MN309752.1 | ATTGCCCCCTGATGGAGCAGTCTTCCAGCTGGACCGTCCGCTGTCCATTGACTACAGCCTT | 833 |
| KM588181.1 | ATTGCCCCCTGATGGAGCAGTCTTCCAGCTGGACCGTCCGCTGTCCATTGACTACAGCCTT | 830 |
| FJ789784.1 | ATTGCCCTGATGGAGCAGTCTTCCAGCTGGACCGTCCGCTATCCATTGACTACAGCCTT | 821 |
| AF245003.1 | ATTGCCCCCTGATGGAGCAGTCTTCCAGCTGGACCGTCCGCTGTCCATTGACTACAGCCTT | 833 |
| NC_008041.1 | ATTGCCCCCTGATGGAGCAGTCTTCCAGCTGGACCGTCCGCTGTCCATTGACTACAGCCTT | 833 |
| AY744705.1 | ATTGCCCCCTGATGGAGCAGTCTTCCAGCTGGACCGTCCGCTGTCCATTGACTACAGCCTT * * * * * ** * * * * * * * * * * | 833 |
| KY354702.2 | GGAGTGGGCGACGTCGACCGGGGCGGTATACTGGCACCTGCGGAAGAAAGCTGGAGACACT | 890 |
| KF386164.1 | GGAACCCGGAGATGTTGACCGTGCCGTCTATTGGCACCTCAAGAAGTTTGC GGGGCACTGCC | 894 |
| JX402858.1 | GGAACCTGGAGATGTTGACCGTGCCGTTTATTGGCACCTCAAGAAGTTTGC TGGAACTGCC | 893 |
| KY315689.1 | GGAACCTGGAGATGTTGACCGTGCTGTTTACTGGCACCTCAAGAAGTTTGC TG GAAATGCT | 833 |
| JN189992.2 | GGAGTTGGAGATGTTGACCGTGCCGTCTACTGGCACCTCAAGAAGTTTGC TG GCCACCGCT | 893 |
| GU592791.1 | GGAACCTGGAGATGTTGACCGTGCTGTTTATTGGCACCTCAAGAAGTTTGC TG GAAATGCT | 878 |
| AF499774.1 | GGAACCTGGAGATGTTGACCGTGCTGTTTATTGGCACCTCAAGAAGTTTGC TG GAAATGCT | 867 |
| MG637439.1 | GGAACCTGGAGATGTTGACCGTGCTGTTTACTGGCACCTCAAGAAGTTTGC TG GAAATGCT | 893 |
| KU705815.1 | GGAACCTGGAGATGTTGATCGTGCTGTTTATTGGCACCTCAAGAAGTTTGC TG GAAATGCT | 877 |
| AF245004.1 | GGAACCTGGAGATGTTGACCGTGCTGTTTACTGGCACCTCAAGAAGTTTGC TG GAAATGCT | 881 |
| JF412263.1 | GGAACCTGGAGATGTTGATCGAGCTGTCTATGGGCACCTCAAGAAGTTTGC TG GAAATGCT | 893 |
| MN309752.1 | GGAACCTGGAGATGTTGATCGAGCTGTCTATTGGGCACCTCAAGAAGTTTGC TG GAAATGCT | 893 |
| KM588181.1 | GGAACCTGGAGATGTTGATCGTGCTGTTTATTGGCACCTCAAGAAGTTTGC TG GAAATGCT | 890 |
| FJ789784.1 | GGAACCTGGAGATGTTGACCGTGCTGTTTACTGGCACCTCAAGAAGTTTGC TG GAAATGCT | 893 |
| AF245003.1 | GGAACCTGGAGATGTTGACCGTGCTGTTTACTGGCACCTCAAGAAGTTTGC TG GAAATGCT | 881 |
| NC_008041.1 | GGAACCTGGAGATGTTGACCGTGCTGTTTATTGGCACCTCAAGAAGTTTGC TG GAAATGCT | 893 |
| AY744705.1 | GGAACCTGGAGATGTTGACCGTGCTGTTTACTGGCACCTCAAGAAGTTTGC TG GAAATGCT *** ** * * * * * * * * * * * * * * | 893 |
| KY354702.2 | CAGGTACCTGCTGGGTACTTTGACTGGGGACTGTGGGATGACTTCAACAAGACATTCACA | 950 |
| KF386164.1 | GCCACACCGGMTGGCTGGTTTCGCTGGGGCATCTGGGACAACCTTCAACAAAACATTTACC | 954 |
| JX402858.1 | ACCACACCTGCAGGTGTGGTTTCGCTGGGGCGCTCTGGGACAACCTTAAACAAAACGTTTACA | 893 |
| KY315689.1 | AGCACACCTGCAGGCTGGTTTCGCTGGGGCATCTGGGACAACCTTCAACAAGACGTTTACA | 953 |
| JN189992.2 | GCCACACCTGCAGGCTGGTTTCGCTGGGGCATCTGGGACAACCTTCAACAAAACGTTTACA | 953 |
| GU592791.1 | GGCACACCTGCAGGCTGGTTTCGCTGGGGCATCTGGGACAACCTTCAACAAGACGTTTCGCA | 938 |
| AF499774.1 | AGCACACCTGCAGGCTGGTTTCGCTGGGGCATCTGGGACAACCTTCAACAAGACGTTTACA | 927 |
| MG637439.1 | GGCACACCTGCAGGCTGGTTTCGCTGGGGCATCTGGGACAACCTTCAACAAGACGTTTACA | 953 |
| KU705815.1 | GGCACACCTGCAGGCTGGTTTCGCTGGGGCATCTGGGACAACCTTCAACAAGACGTTTACA | 937 |
| AF245004.1 | GGCACACCTGCAGGCTGGTTTCGCTGGGGCATCTGGGACAACCTTCAACAAGACGTTTACA | 941 |
| JF412263.1 | GGCACACCTGCAGGCTGGTTTCGCTGGGGCATCTGGGACAACCTTCAACAAGACGTTTACA | 953 |
| MN309752.1 | GGCACACCTGCAGGCTGGTTTCGCTGGGGCATCTGGGACAACCTTCAACAAGACGTTTACA | 953 |
| KM588181.1 | GGCACACCTGCAGGCTGGTTTCGCTGGGGCATCTGGGACAACCTTCAACA | |

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KY354702.2   GTTGGGGCGCCTACTACTCCGACCAGCAACCACGGCAAATCTTGCTGCCGGCTGGCAGC   1010
KF386164.1   GACGGTATCGCTTACTATTCTGACGAGCAGCCACGCCAGATCCTGCTCCCGGTAGGCACT   1014
JX402858.1   GATGGCGTTGCTTACTACCCTGACGAGCAGCCTCGTCAAATCTCCTGCCCGTTGGCACT   953
KY315689.1   GATGGCGTTGCTTACTACCCTGATGAGCAGCCTCGTCAAATCCTGCTGCCTGTTGGCACT   1013
JN189992.2   GATGGCGTTGCTTACTACTCTGATGAGCAGCCTCGTCAAATCCTCCTGCCTGTTGGCACT   1013
GU592791.1   GATGCCGTTGGCTACTACTCTGATGCGCAGCCTCGTCAAATCCTGCTGCTGTTGGCCACT   998
AF499774.1   GATGGCGTTGCCTACTACTCTGATGAGCAGCCCCGTCAAATCCTGCTGCCTGTTGGCACT   987
MG637439.1   GATGGCGTTGCTTACTACTCTGATGAGCAGCCCCGTCAAATCCTGCTGCCTGTTGGCACT   1013
KU705815.1   GATGGCGTTGCCTACTACTCTGATGAGCAGCCCCGTCAAATCCTGCTGCCTGTTGGCACT   997
AF245004.1   GATGGCGTTGCCTACTACTCTGATGAGCAGCCCCGTCAAATCCTGCTGCCTGTTGGCACT   1001
JF412263.1   GATGGCGTTGCCTACTACTCTGATGAGCAGCCCCGTCAAATCCTGCTGCCTGTTGGCACT   1013
MN309752.1   GATGGCGTTGCCTACTACTCTGATGAGCAGCCCCGTCAAATCCTGCTGCCTGTTGGCACT   1013
KM588181.1   GATGGCGTTGCCTACTACTCTGATGAGCAGCCCCGTCAAATCCTGCTGCCTGTTGGCACT   1010
FJ789784.1   GATGGCGTTGCTTACTACTCTGATGAGCAGCCTCGTCAAATCCTGCTGCCTGTTGGCACT   1013
AF245003.1   GATGGCGTTGCCTACTACTCTGATGAGCAGCCCCGTCAAATCCTGCTGCCTGTTGGCACT   1001
NC_008041.1  GATGGCGTTGCCTACTACTCTGATGAGCAGCCTCGTCAAATCCTGCTGCCTGTTGGCACT   1013
AY744705.1   GATGGCGTTGCCTACTACTCTGATGAGCAGCCCCGTCAAATCCTGCTGCCTGTTGGCACT   1013
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Conventional PCR reverse primer: ATCCGGTTCCCTAGTGC
KY354702.2   CTCTTCACCCGTGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1070
KF386164.1   ACCTTCACCAAGGTCGATGCGGGAACCTAACCGGGTCAATCCGGAATCCCTAGTGC   1074
JX402858.1   GTCTGCACCAGGGTTGATTTCGGAACCTAACCGGGTCAATCCGGAATCCCTAGTGC   1013
KY315689.1   GTCTGCACCAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1073
JN189992.2   GTCTGCACCAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1073
GU592791.1   GTCTGCATAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1058
AF499774.1   GTCTGCATCAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1047
MG637439.1   GTCTGCACCAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1073
KU705815.1   GTCTGCACCAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1057
AF245004.1   GTCTGCACCAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1061
JF412263.1   GTCTGCACCAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1073
MN309752.1   GTCTGCACCAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1073
KM588181.1   GTCTGCACCAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1070
FJ789784.1   GTCTGCACCAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1073
AF245003.1   GTCTGCACCAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1061
NC_008041.1  GTCTGCACCAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1073
AY744705.1   GTCTGCACCAGGGTTGACTCGGAAAACTAACCGGGTCAATCCGGAATCCCTAGTGC   1073
**  **  *  **  **  ***  *****  *****  *****  *****
KY354702.2   TGGATGACCAATTTGAGAAATTGATTATGGCACTAACCACTATCAAAATT-----   1120
KF386164.1   TTGATGACCAATTTGAACAATTAATTAATGCACTAAGTATTATAACTAATGAAATACAAA   1134
JX402858.1   TTGATGACCAATTTGAACAATTTGATTAAAGCACTAACATATATAAATGAAGAAATACAAA   1073
KY315689.1   TTGATGACCAATTTGAACAATTTGATTAAAGCACTAACAAATATAAATAAAGAAATACAAA   1133
JN189992.2   TTGATGACCAATTTGAACAATTTGATTAAAGCACTAACAAACATAAACAAGAAATACAAA   1133
GU592791.1   TTGATGACCAATTTGAACAATTTGATTAAAGCACTAACAAATATAAATAAAGAAATACAAA   1118
AF499774.1   TTGATGACCAATTTGAACAATTTGATTAAAGCACTAACAAACATAAATAAAGAAATACAAA   1107
MG637439.1   TTGATGACCAATTTGAACAATTTGATTAAAGCACTAACAAATATAAATAAAGAAATACAAA   1133
KU705815.1   TTGATGACCAATTTGAACAATTTGATTAAAGCACTAACAAATATAAATAAAGAAATACAAA   1117
AF245004.1   TTGATGACCAATTTGAACAATTTGATTAAAGCACTAACGAACATAAATAAAGAAATACAAA   1121
JF412263.1   TTGATGACCAATTTGAACAATTTGATTAAAGCACTAAAGAATATAAATAAAGAAATACAAA   1133
MN309752.1   TTGATGACCAATTTGAACAATTTGATTAAAGCACTAACAAATATAAATAAAGAAATACAAA   1133
KM588181.1   TTGATGACCAATTTGAACAATTTGATTAAAGCACTAACAAATATAAATAAAGAAATACAAA   1130
FJ789784.1   TTGATGACCAATTTGAACAATTTGATTAAAGCACTAACAAACATAAATAAAGAAATACAAA   1133
AF245003.1   TTGATGACCAATTTGAACAATTTGATTAAAGCACTAACAAATATAAATAAAGAAATACAAA   1121
NC_008041.1  TTGATGACCAATTTGAACAATTTGATTAAAGCACTAACAAATATAAATAAAGAAATACAAA   1133
AY744705.1   TTGATGACCAATTCGAACAATTTGATTAAAGCACTAACAAATATAAATAAAGAAATACAAA   1133
*  *****  *  **  *  *  *  *  *  *  *  *  *  *  *
KY354702.2   -----GAAATTGACAATAACAAGAGCGAAATTGAAGCTATCGCTAACAAATTAA   1169
KF386164.1   TAAACAAAACCGAAATTGGCAAGAATAAGAGCGAAATTGACGCTATCGCCACTAAATTAA   1194
JX402858.1   CAAACAAAATTGAAATTGGAAGAAGACAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1133
KY315689.1   CAAACAAAACCGAAATTGGAAGAAGATAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1193
JN189992.2   CAAACAAAACCGAAATTGGAAGAAGATAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1193
GU592791.1   CAAACAAAACCGAAATTGGAAGAAGATAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1178
AF499774.1   CAAACAAAACCGAAATTGGAAGAAGATAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1167
MG637439.1   CAAACAAAACCGAAATTGGAAGAAGACAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1193
KU705815.1   CAAACAAAACCGAAATTGGAAGAAGATAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1177
AF245004.1   CAAACAAAACCGAAATTGGAAGAAGATAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1181
JF412263.1   CAAACAAAACCGAAATTGGAAGAAGATAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1193
MN309752.1   CAAACAAAACCGAAATTGGAAGAAGATAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1193
KM588181.1   CAAACAAAACCGAAATTGGAAGAAGATAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1190
FJ789784.1   CAAACAAAACCGAAATTGGAAGAAGATAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1193
AF245003.1   CAAACAAAACCGAAATTGGAAGAAGATAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1181
NC_008041.1  CAAACAAAACCGAAATTGGAAGAAGATAGAAGCGAAATTGAATCACTCGCTAGCAAATTAA   1193
AY744705.1   CAAACAAAACCGAAATTGGAAGAAGATAGAAGCGAAATTGAACCACTCGCTAGCAAATTAA   1193
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| | | |
|-------------|---|------|
| KY354702.2 | ACGACAAAGCACCCAAAGAGGGTTCGATTGCTATTGTTGGTACCATTGACGGCGTACCTG | 1229 |
| KF386164.1 | AAGACAAAGCCCCCAAGGAGGTGCTATTGCTATTGTTGGTACCATTGACGGCGTACCGG | 1254 |
| JX402858.1 | ACGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGATGGCGTACCGG | 1193 |
| KY315689.1 | ACGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGACGGCGTACCGG | 1253 |
| JN189992.2 | ATGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGACGGCGTACCGG | 1253 |
| GU592791.1 | ACGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGACGGCGTACCGG | 1238 |
| AF499774.1 | ACGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGACGGCGTACCGG | 1227 |
| MG637439.1 | ATGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGACGGCGTACCGG | 1253 |
| KU705815.1 | ACGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGACGGCGTACCGG | 1237 |
| AF245004.1 | ACGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGCACCCTTGACGGCGTACCGG | 1241 |
| JF412263.1 | ACGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGACGGCGTACCGG | 1253 |
| MN309752.1 | ACGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGACGGCGTACCGG | 1253 |
| KM588181.1 | ACGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGACGGCGTACCGG | 1250 |
| FJ789784.1 | ACGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGACGGCGTACCGG | 1253 |
| AF245003.1 | ATGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGACGGCGTACCGG | 1241 |
| NC_008041.1 | ACGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGACGGCGTACCGG | 1253 |
| AY744705.1 | ATGACAAAGCACCCAAAGGAGGTGCGATTGCTATTGTTGGTACCCTTGACGGCGTACCGG | 1253 |
| | * | |
| KY354702.2 | GAACAGTTGACGGCGCTTACCTCGCCGAATCTGTCTAGCGTGCTTGATACGGTGCCAGCT | 1289 |
| KF386164.1 | CTACGGTTGACGGCCTTTACACGGCCACACCCGTGCCGCGTGCTTAATAGGGTGCCAGCT | 1314 |
| JX402858.1 | CTACGCTCGACGGCCTTTATACGGCTGGAGACGTGCCGCGTGCTTGATTGGGTGCCAGTG | 1253 |
| KY315689.1 | CTACGCTTGAAGGCCTATACACGGCTTGAAGCGCGCCGCGTGTCTGTGCACAGGCTAAAT | 1313 |
| JN189992.2 | CTACGCTCGAAGGCCTATATACGGCTGGAAGCGCGCCGCGTGCTTGATTGGGTGCCAGTG | 1313 |
| GU592791.1 | CTACGCTTGAAGGCCTATACACGGCTTGAAGCGCGCCGCGTGCTTAATTGGGTGCCAGTG | 1298 |
| AF499774.1 | CT- CGCTTGAAGGCCTATACACGGCTGGAAGCGCGCCGCGTGCTTAATTGGGTGCCAGTG | 1286 |
| MG637439.1 | CTACGCTTGAAGGCCTATATACGGCTGGAAGCGCGCCGCGTGCTTGATTGGGTGCCAGTG | 1313 |
| KU705815.1 | CTACGCTTGAAGGCCTATACACGGCTGGAAGCGCGCCGCGTGCTTAATTGGGTGCCAGTG | 1297 |
| AF245004.1 | CCACGCTTGAAGGCCTATATACGGCTGGAAGCGCGCCGCGTGCTTAATTGGGTGCCAGTG | 1301 |
| JF412263.1 | CTACGCTTGAAGGCCTATACACGGCTGGAAGCGCGCCGCGTGCTTAATTGGGTGCCAGTG | 1313 |
| MN309752.1 | CTACGCTTGAAGGCCTATACACGGCTGGAAGCGCGCCGCGTGCTTAATTGGGTGCCAGTG | 1313 |
| KM588181.1 | CTACGCTTGAAGGCCTATACACGGCTGGAAGCGCGCCGCGTGCTTAATTGGGTGCCAGTG | 1310 |
| FJ789784.1 | CTACGCTTGAAGGCCTATACACGGCTGGAAGCGCGCCGCGTGCTTAATTGGGTGCCAGTG | 1313 |
| AF245003.1 | CTACGCTTGAAGGCCTGTATACACGGCTGGAAGCGCGCCGCGTGCTTAATTGGGTGCCAGTG | 1301 |
| NC_008041.1 | CTACGCTTGAAGGCCTATACACGGCTGGAAGCGCGCCGCGTGCTTAATTGGGTGCCAGTG | 1313 |
| AY744705.1 | CTACGCTTGAAGGCCTATACACGGCTGGAAGCGCGCCGCGTGCTTAATTGGGTGCCAGTG | 1313 |
| | * | |
| KY354702.2 | TTACCAAGTCTTGTCCAAACGCCGAGGATTTCCTCTTTGGGCATGTTGGGTTACCGTTAGC | 1349 |
| KF386164.1 | TTACCAAGTTCGTATCCACGCCGAGGATTTCCTCCCTTTGG-GCATGTTGGGTTACCGTACGC | 1373 |
| JX402858.1 | GTACCAATTCGTATCCACGCCGAGGATTTCCTCTTTG-GGCTGTTGGGTTACCGTTAGC | 1312 |
| KY315689.1 | GTCTGTACACAGGCTAAAACAGTGTTCCTCCAGCA-----TGTTCCGTGTTACGATGCC | 1366 |
| JN189992.2 | GTACCAAGTTCGTATTCAACGCCGATGAAATCCCTCTTTG-GGCTGTTGGGTTACCGTCAGC | 1372 |
| GU592791.1 | GTACCAAGTTCGTATCCAAACGCCGAGGAAGTCCCTCTTTG-GGCTGTTGGGTTACCGTTAGC | 1357 |
| AF499774.1 | GTACCAAGTTCGTATCCAAACGCCGAGGAAGTCCCTCTTTG-GGCTGTTGGGTTACCGTTAGC | 1345 |
| MG637439.1 | GTACCAAGTTCGTATCCACG-CCGAGGAATTCCTCTTTG-GGCTGTTGGGTTACCGTTAGC | 1371 |
| KU705815.1 | GTACCAAGTTCGTATCCAAACGCCGAGGAATTCCTCTTTG-GGA----- | 1338 |
| AF245004.1 | GTACCAAGTTCGTATCCAAACGCCGAGGAAGTCCCTCTTTG-GGCTGTTGGGTTACCGTTAGC | 1360 |
| JF412263.1 | GTACCAAGTTCGTATCCAAACGCCGAGGAATTCCTCTTTG-GGCTGTTGGGTTACCGTTAGC | 1372 |
| MN309752.1 | GTACCAAGTTCGTATCCAAACGCCGAGGAATTCCTCTTTG-GGCTGTTGGGTTACCGTTAGC | 1372 |
| KM588181.1 | GTACCAAGTTCGTATCCAAACGCCGAGGATCCCTCTTTG-GGCTGTTGGGTTACCGTTAGC | 1369 |
| FJ789784.1 | GTACCAAGTTCGTATCCAAACGCCGAGGAAGTCCCTCTTTG-GGCTGTTGGGTTACCGTTAGC | 1372 |
| AF245003.1 | GTACCAAGTTCGTATCCAAACGCCGAGGAAGTCCCTCTTTG-GGCTGTTGGGTTACCGTTAGC | 1360 |
| NC_008041.1 | GTACCAAGTTCGTATCCAAACGCCGAGGAAGTCCCTCTTTG-GGCTGTTGGGTTACCGTTAGC | 1372 |
| AY744705.1 | GTACCAAGTTCGTATCCAAACGCCGAGGAAGTCCCTCTTTG-GGCTGTTGGGTTACCGTTAGC | 1372 |
| | * | |
| KY354702.2 | TCCGCGCAGTGAGCACCACCG-----CCATGTGGTTAAATGGCCGCTGATCG----- | 1396 |
| KF386164.1 | TCCACGTATCGAGCGCCACCGCCA-----TGTTGGCTAAATGGCCGCTGATCGCTACCCA | 1427 |
| JX402858.1 | TCCGCGCAGTGAGCACCACCG----- | 1333 |
| KY315689.1 | AAGGCACACACCAGCCGAAATCGCTGACGCAAGTGCAAACTTGGCCATGCCAAGGCACAC | 1426 |
| JN189992.2 | TCCGCGCA-----GTGAGCACCAC-CGCCATGTGGTTAAATGGCCGCTGATC-G----- | 1419 |
| GU592791.1 | TCCGCGTA-----GTGAGCACCAC-CGCCATGTGGTTAAANNNGCCCCNNGNCT-A----- | 1404 |
| AF499774.1 | TCCGCGCA-----GGGAGCACCAC-CGC----- | 1367 |
| MG637439.1 | TCCGCGCA-----GTGAGCACCAC-CGCCATGTGGTTAAATGGCCGCTGATC-G----- | 1418 |
| KU705815.1 | ----- | 1338 |
| AF245004.1 | TCCGCGCA-----GTGAGCACCAC-CGCCATGTGGT----- | 1390 |
| JF412263.1 | TCCGCGCA-----GTGAGCACCAC-CGCCATGTGGTTAAATGGCCGCTGATC-G----- | 1419 |
| MN309752.1 | TCCGCGCA-----GTGAGCACCAC-CGCCATGTGGTTAAATGGCCGCTGATC-G----- | 1419 |
| KM588181.1 | TCCGCGCA-----GTGAGCACCAC-CGCCATGCGGTTAAATGGCCGCTGATC-G----- | 1416 |
| FJ789784.1 | TCCGCGCA-----GTGAGCACCAC-CGCCATGTGGTTAAATGGCCGCTGATC-G----- | 1419 |
| AF245003.1 | TCCGCGCA-----GTGAGCACCAC-CGCCATGTGGT----- | 1390 |
| NC_008041.1 | TCCGCGTA-----GTGAGCACCAC-CGCCATGTGGTTAAATGGCCGCTGATC-G----- | 1419 |
| AY744705.1 | TCCGCGCA-----GTGAGCACCAC-CGCCATGTGGTTAAATGGCCGCTGATC-G----- | 1419 |

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| KY354702.2 | ----- | 1396 |
| KF386164.1 | TTTCGGC----- | 1434 |
| JX402858.1 | ----- | 1333 |
| KY315689.1 | ACCAGCCGAAATCGCTGACGCAGTGCAAACTTGGCCGCAAGTTCCGCTGAGCTGGTTGA | 1486 |
| JN189992.2 | --CTTCTCAACTCGGC----- | 1433 |
| GU592791.1 | ----- | 1404 |
| AF499774.1 | ----- | 1367 |
| MG637439.1 | --CTTCTCAACTCGGC----- | 1432 |
| KU705815.1 | ----- | 1338 |
| AF245004.1 | ----- | 1390 |
| JF412263.1 | --CTTCTCAACTCGGCG----- | 1434 |
| MN309752.1 | --CTTCTCAACTCGGCG----- | 1434 |
| KM588181.1 | --CTTCTCAACTCTGC----- | 1430 |
| FJ789784.1 | --CTTCTCAACTCGGC----- | 1433 |
| AF245003.1 | ----- | 1390 |
| NC_008041.1 | --CTTCTCAACTCGGCG----- | 1434 |
| AY744705.1 | --CTTCTCAACTGTGGTT----- | 1435 |
| | | |
| KY354702.2 | ----- | 1396 |
| KF386164.1 | ----- | 1434 |
| JX402858.1 | ----- | 1333 |
| KY315689.1 | AACTGACTGTGCTTAATTGGGTGCCAGTGGTACCAGTCGTATCCACCGTGCCAAGGCACA | 1546 |
| JN189992.2 | ----- | 1433 |
| GU592791.1 | ----- | 1404 |
| AF499774.1 | ----- | 1367 |
| MG637439.1 | ----- | 1432 |
| KU705815.1 | ----- | 1338 |
| AF245004.1 | ----- | 1390 |
| JF412263.1 | ----- | 1434 |
| MN309752.1 | ----- | 1434 |
| KM588181.1 | ----- | 1430 |
| FJ789784.1 | ----- | 1433 |
| AF245003.1 | ----- | 1390 |
| NC_008041.1 | ----- | 1434 |
| AY744705.1 | ----- | 1435 |
| | | |
| KY354702.2 | ----- | 1396 |
| KF386164.1 | ----- | 1434 |
| JX402858.1 | ----- | 1333 |
| KY315689.1 | CACCAGCCGAAATCGCTGACGCAGTGCAAACTTGGCCATGCCAAGGCACACACCAGCCG | 1606 |
| JN189992.2 | ----- | 1433 |
| GU592791.1 | ----- | 1404 |
| AF499774.1 | ----- | 1367 |
| MG637439.1 | ----- | 1432 |
| KU705815.1 | ----- | 1338 |
| AF245004.1 | ----- | 1390 |
| JF412263.1 | ----- | 1434 |
| MN309752.1 | ----- | 1434 |
| KM588181.1 | ----- | 1430 |
| FJ789784.1 | ----- | 1433 |
| AF245003.1 | ----- | 1390 |
| NC_008041.1 | ----- | 1434 |
| AY744705.1 | ----- | 1435 |
| | | |
| KY354702.2 | ----- | 1396 |
| KF386164.1 | ----- | 1434 |
| JX402858.1 | ----- | 1333 |
| KY315689.1 | AAATCGCTGACGCAGTGCAAACTTGGCCGCAACCGAGGAGTCCCTCTTTGGGCTGTTGG | 1666 |
| JN189992.2 | ----- | 1433 |
| GU592791.1 | ----- | 1404 |
| AF499774.1 | ----- | 1367 |
| MG637439.1 | ----- | 1432 |
| KU705815.1 | ----- | 1338 |
| AF245004.1 | ----- | 1390 |
| JF412263.1 | ----- | 1434 |
| MN309752.1 | ----- | 1434 |
| KM588181.1 | ----- | 1430 |
| FJ789784.1 | ----- | 1433 |
| AF245003.1 | ----- | 1390 |
| NC_008041.1 | ----- | 1434 |
| AY744705.1 | ----- | 1435 |
| | | |
| KY354702.2 | ----- | 1396 |

| | | |
|-------------|---|------|
| KF386164.1 | ----- | 1434 |
| JX402858.1 | ----- | 1333 |
| KY315689.1 | ATTACCGTTAGCTCCGCGCAGTGAGCACACCGCCATGTGGTTAAATGGCCACTGATCGC | 1726 |
| JN189992.2 | ----- | 1433 |
| GU592791.1 | ----- | 1404 |
| AF499774.1 | ----- | 1367 |
| MG637439.1 | ----- | 1432 |
| KU705815.1 | ----- | 1338 |
| AF245004.1 | ----- | 1390 |
| JF412263.1 | ----- | 1434 |
| MN309752.1 | ----- | 1434 |
| KM588181.1 | ----- | 1430 |
| FJ789784.1 | ----- | 1433 |
| AF245003.1 | ----- | 1390 |
| NC_008041.1 | ----- | 1434 |
| AY744705.1 | ----- | 1435 |

| | | |
|-------------|---------------|------|
| KY354702.2 | ----- | 1396 |
| KF386164.1 | ----- | 1434 |
| JX402858.1 | ----- | 1333 |
| KY315689.1 | TTTTCTACTCGGC | 1739 |
| JN189992.2 | ----- | 1433 |
| GU592791.1 | ----- | 1404 |
| AF499774.1 | ----- | 1367 |
| MG637439.1 | ----- | 1432 |
| KU705815.1 | ----- | 1338 |
| AF245004.1 | ----- | 1390 |
| JF412263.1 | ----- | 1434 |
| MN309752.1 | ----- | 1434 |
| KM588181.1 | ----- | 1430 |
| FJ789784.1 | ----- | 1433 |
| AF245003.1 | ----- | 1390 |
| NC_008041.1 | ----- | 1434 |
| AY744705.1 | ----- | 1435 |

Figure S3. Sequences of the RNA1 and RNA2 fragments of the NNV isolate from this study.

| | |
|---|-----|
| RNA1 fragment amplified in this study | bp |
| GATGAGTTCACCTATGATGGTCAAAGCGTGTTCAAAGAAAGAAGCATACAACGCCCCAAAT | 60 |
| TACCCAGGAACATTTCAACCGTTCCGCACACCCAAAACGTCAAGTTGTCCAGCTACACC | 120 |
| TACGCTTTCAAAGCCAGTGTTCTCCAGCATGTTCCGTGGTACATGCCAACGCACACCCCA | 180 |
| GCGGAAATCGCTGACGCAGTGCAAAACTTGGCCGCAAGTTCCTGAGCTGGTTGAAACT | 240 |
| GACTACAGCAAGTTCGATGGCATTCTTGCGCTTTATGCGTGAGTGCGTCGAATTTGCC | 300 |
| ATCTATAAGCGCTGGGTTACCTGGACCACTTGCCAGAGTTAACAACCTTATTGGCTAAT | 360 |
| GAGATCCAAGCAGCTGCTGTTACACGACTGGGCATCAAGTATGATCCTGATTGCAGTCGC | 420 |
| CTCAGTGGTTCTGCTCTCACGACAGACGGAAACAGCATTGCTAATGCGTTCGTCTCATA | 480 |
| CTTGCTGGTCGCATGGCTGGCATGGATGATGATGAAGCTTGGTCTTGGATCGGCATTGTC | 540 |
| TACGGTGATGATGGGCTCCGATCTGGTAATGTTTCAAATGAGCTCCTCACCACACTGCT | 600 |
| TCTTCCCTCGGCTTTGATTTGAAAATAGTGAATCGCGCGCCACGTGGCTCTCCAGTGACA | 660 |
| TTTCTGTCTCGAGTATACCTCGATCCTTGGTCCTCACCAGGCTTCCGTGCAGTCGCCATTA | 720 |
| AGAACATTATTGAAATTGCACACCACCTGTGATACCCAGTCAGAGATTGACGACATTG | 778 |

| | |
|---|-----|
| RNA2 fragment amplified in this study | bp |
| CCAAGGCCCGCGAATCCGCAACCTCGTCGACGTGCTAACAATCGTCGGCGTAGTAATCGC | 60 |
| ACTGACGCACCTGTGTCCAAGGCCTCGACCGTAACCTGGATTTGGACGTGGGACCAATGAC | 120 |
| GTCCATCTCTCAGGTATGTCGAGAATCTCCAGGCCGTCTCCAGCCGGGACAGGAACA | 180 |
| GACGGATACGTTGTTGTTGACGCAACCATCGTCCCCGACCTCCTGCCACGACTGGGACAC | 240 |
| GCTGCTAGAATCTTCCAGCGATACGCTGTTGAAACACTGGAGTTTGAATTCAGCCAATG | 300 |
| TGCCCCGCAAAACACGGGCGGTGGTTACGTTGCTGGCTTCTGCCTGATCCAACGACAAC | 360 |
| GATCACACCTTCGACGCACTTCAAGCAACTCGTGGTGCAGTCGTTGCCAAATGGTGGGAA | 420 |
| AGCAGAACAGTCCGACCGCAGTTCACTCGCACGCTCCTCTGGACCTCGTCGGGAAAGGAG | 480 |
| CAGCGTCTTACATCACCTGGTCGGCTGATACTCCTGTGTGTCGGCAACAACACTGACGTG | 540 |
| GTTAACGTGTGCGGTGCTGTGTCGCTGGAGTGTTGCGACTGAGCGTTCCGTCTCTGAAACA | 600 |
| CCTGAAGAGACCACCGCTCCCATCATGACACAAGGTCCCCTGTACAATGATTCCCTCGCT | 660 |
| GCAACTGACTTCAAGTCCATCCTCCTAGGATCTACAGCACTGGACATTGCTCCTGACGGA | 720 |
| GCAATCTTCCAGCTGGACCGTCCGTTGTCCATTGACTACAACCTTGAGTTGGAGATGTT | 780 |
| GACCGTGCCGTCTACTGGCACCTCAAGAAGTTTGCTGGCACCGCTGCCACACCTGCAGGC | 840 |
| TGGTTTCGCTGGGGCATCTGGGACAACCTCAACAAAACGTTACAGATGGCGTTGCTTAC | 900 |
| TACTCCGATCAGCAGCCTCGTCAAATCCTGCTGCCTGTTGGCACTGTCTGCACAGGGGT | 960 |
| TGACTCGGAAAATAACCGGGTCATCC | 987 |

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