

APPENDIX A
RECIPE FOR CTAB BUFFER

CTAB Extraction Buffer (100mL)

2g	CTAB
2g	PVP
8g	NaCl
50mL	dH ₂ O
5mL	0.5M EDTA

Autoclave and add 10ml 1M Trise base.

Top up dH₂O to 100mL.

Store at room temperature.

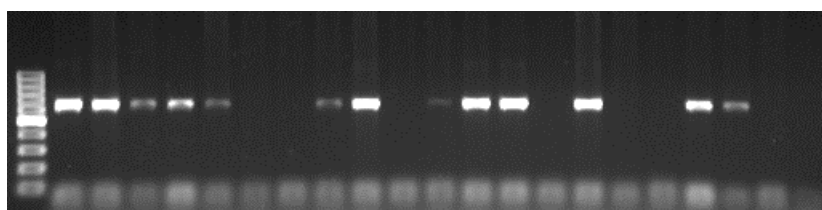
APPENDIX B

PCR AMPLIFICATION OF DNA SAMPLES OBTAINED FROM T2 PLANTS

PCR screening of A1.1 (A), A5.2 (B), A7.4 (C1,C2), A8.5 (D), and A9.2 (E1,E2) lines with *Gus* linker primers. Lane M: GeneRuler™ 100bp DNA Ladder (Fermentas, Canada); Lane -ve: Control negative (no DNA sample).

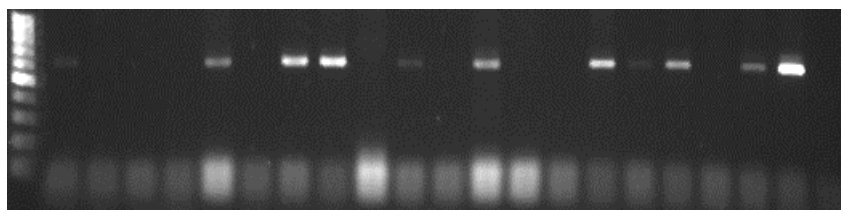
A)

M 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 -ve



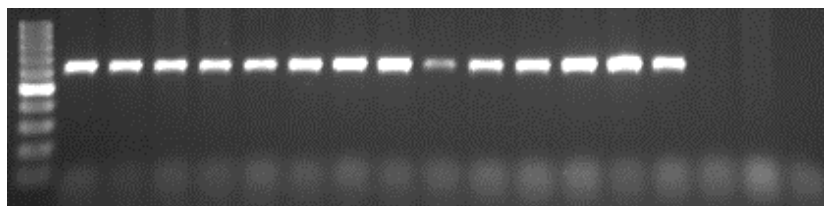
B)

M 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 -ve



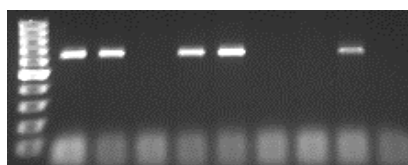
C1)

M 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 -ve



C2)

M 17 18 19 20 21 22 23 24 -ve



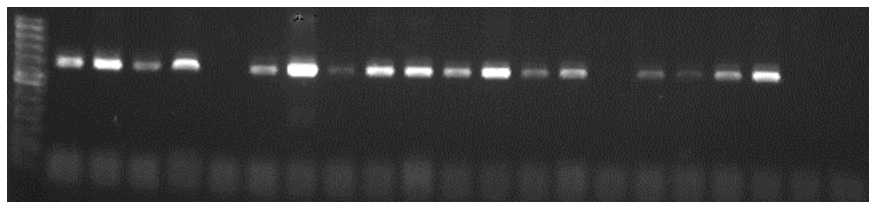
APPENDIX B

PCR AMPLIFICATION OF DNA SAMPLES OBTAINED FROM T2 PLANTS

PCR screening of A1.1 (A), A5.2 (B), A7.4 (C1,C2), A8.5 (D), and A9.2 (E1,E2) lines with *Gus* linker primers. Lane M: GeneRuler™ 100bp DNA Ladder (Fermentas, Canada); Lane -ve: Control negative (no DNA sample).

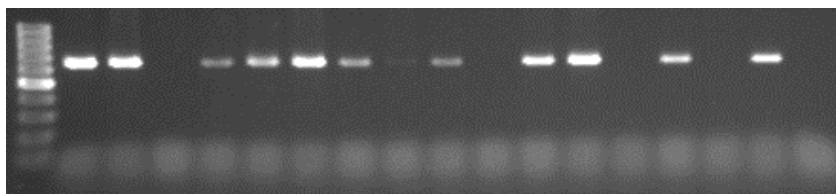
D)

M 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 -ve



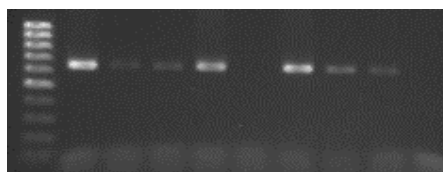
E1)

M 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 -ve



E2)

M 17 18 19 20 21 22 23 24 -ve



APPENDIX C

SEQUENCING ANALYSIS OF *GUS* SEQUENCES

```
>lcl|15057 A1_1 Full length sequence
Length=639

Score = 1133 bits (1256), Expect = 0.0
Identities = 636/639 (99%), Gaps = 3/639 (0%)
Strand=Plus/Plus

Query 1 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 60
      |||
Sbjct 1 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 60

Query 61 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 120
      |||
Sbjct 61 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 120

Query 121 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTC 180
      |||
Sbjct 121 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTC 180

Query 181 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTAC 240
      |||
Sbjct 181 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTAC 240

Query 241 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 300
      |||
Sbjct 241 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 300

Query 301 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 360
      |||
Sbjct 301 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 360

Query 361 ACCCGTCCGCAA-GTGCACGGGAATATTT--CGCCACTGGCGGAAGCAACGCGTAAACTC 417
      |||
Sbjct 361 ACCCGTCCGCAAAGGTGCACGGGAATATTTTCGCGCCACTGGCGGAAGCAACGCGTAAACTC 420

Query 418 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACC 477
      |||
Sbjct 421 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACC 480

Query 478 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 537
      |||
Sbjct 481 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 540

Query 538 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 597
      |||
Sbjct 541 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 600

Query 598 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 636
      |||
Sbjct 601 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 639
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APPENDIX C

SEQUENCING ANALYSIS OF GUS SEQUENCES

>lcl|56587 A2_2 Full length sequence
Length=642

Score = 1160 bits (628), Expect = 0.0
Identities = 636/639 (99%), Gaps = 3/639 (0%)
Strand=Plus/Plus

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Query 1 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 60
      |||
Sbjct 3 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 62

Query 61 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 120
      |||
Sbjct 63 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 122

Query 121 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAACTGCTGCTGTC 180
      |||
Sbjct 123 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAACTGCTGCTGTC 182

Query 181 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTAC 240
      |||
Sbjct 183 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTAC 242

Query 241 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 300
      |||
Sbjct 243 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 302

Query 301 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 360
      |||
Sbjct 303 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 362

Query 361 ACCCGTCCGCAA-GTGCACGGGAATATTT--CGCCACTGGCGGAAGCAACGCGTAAACTC 417
      |||
Sbjct 363 ACCCGTCCGCAAGGTGCACGGGAATATTTTCGCGCCACTGGCGGAAGCAACGCGTAAACTC 422

Query 418 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACC 477
      |||
Sbjct 423 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACC 482

Query 478 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 537
      |||
Sbjct 483 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 542

Query 538 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 597
      |||
Sbjct 543 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 602

Query 598 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 636
      |||
Sbjct 603 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 641
```

APPENDIX C

SEQUENCING ANALYSIS OF GUS SEQUENCES

>lcl|3461 A3_2 Full length sequence
Length=625

Score = 1125 bits (609), Expect = 0.0
Identities = 619/623 (99%), Gaps = 3/623 (0%)
Strand=Plus/Plus

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Query 2 ATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGCTGATGGTGCACGACCACG 61
      |
Sbjct 2 ATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGCTGATGGTGCACGACCACG 61

Query 62 CATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAAG 121
      |
Sbjct 62 CATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAAG 121

Query 122 AGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTCC 181
      |
Sbjct 122 AGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTCC 181

Query 182 GCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTACA 241
      |
Sbjct 182 GCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTACA 241

Query 242 GCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTGA 301
      |
Sbjct 242 GCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTGA 301

Query 302 TAGCGCGTGACAAAAACCACCCAAGCGTGGTGTATGTGGAGTATTGCCAACGAACCGGATA 361
      |
Sbjct 302 TAGCGCGTGACAAAAACCACCCAAGCGTGGTGTATGTGGAGTATTGCCAACGAACCGGATA 361

Query 362 CCCGTCCGCAA-GTGACGGGAATATTT--CGCCACTGGCGGAAGCAACGCGTAAACTCG 418
      |
Sbjct 362 CCCGTCCGCAAGGTGACGGGAATATTTTCGCGCCACTGGCGGAAGCAACGCGTAAACTCG 421

Query 419 ACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACCA 478
      |
Sbjct 422 ACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACCA 481

Query 479 TCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCG 538
      |
Sbjct 482 TCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCG 541

Query 539 GCGATTTGGAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAAC 598
      |
Sbjct 542 GCGATTTGGAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAAC 601

Query 599 TGCATCAGCCGATTATCATCACC 621
      |
Sbjct 602 TGCATCAGCCGATTATCATCACC 624
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APPENDIX C

SEQUENCING ANALYSIS OF GUS SEQUENCES

```
>lcl|44357 A5_2 Full length sequence
Length=633

Score = 1079 bits (584), Expect = 0.0
Identities = 623/639 (97%), Gaps = 13/639 (2%)
Strand=Plus/Plus

Query 1 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 60
      |||
Sbjct 3 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACG---AC 59

Query 61 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 120
      |
Sbjct 60 -C-----GACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 112

Query 121 GAGATGCTCGACTGGGACAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTC 180
      |||
Sbjct 113 GAGATGCTCGACTGGGACAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTC 172

Query 181 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTAC 240
      |||
Sbjct 173 GGCTTTCAGCTGTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTAC 232

Query 241 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 300
      |||
Sbjct 233 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 292

Query 301 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 360
      |||
Sbjct 293 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 352

Query 361 ACCCGTCCGCAA-GTGCACGGGAATATTT--CGCCACTGGCGGAAGCAACGCGTAAACTC 417
      |||
Sbjct 353 ACCCGTCCGCAAAGGTGCACGGGAATATTTTCGCGCCACTGGCGGAAGCAACGCGTAAACTC 412

Query 418 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACC 477
      |||
Sbjct 413 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACC 472

Query 478 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 537
      |||
Sbjct 473 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 532

Query 538 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 597
      |||
Sbjct 533 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 592

Query 598 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 636
      |||
Sbjct 593 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 631
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APPENDIX C

SEQUENCING ANALYSIS OF GUS SEQUENCES

>lcl|1425 A6_6 Full length sequence
Length=642

Score = 1160 bits (628), Expect = 0.0
Identities = 636/639 (99%), Gaps = 3/639 (0%)
Strand=Plus/Plus

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Query 1 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 60
      |||
Sbjct 2 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 61

Query 61 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 120
      |||
Sbjct 62 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 121

Query 121 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTC 180
      |||
Sbjct 122 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTC 181

Query 181 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTAC 240
      |||
Sbjct 182 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTAC 241

Query 241 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 300
      |||
Sbjct 242 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 301

Query 301 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 360
      |||
Sbjct 302 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 361

Query 361 ACCCGTCCGCAA-GTGCACGGGAATATTT--CGCCACTGGCGGAAGCAACGCGTAAACTC 417
      |||
Sbjct 362 ACCCGTCCGCAAAGGTGCACGGGAATATTTTCGCGCCACTGGCGGAAGCAACGCGTAAACTC 421

Query 418 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACC 477
      |||
Sbjct 422 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACC 481

Query 478 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 537
      |||
Sbjct 482 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 541

Query 538 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 597
      |||
Sbjct 542 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 601

Query 598 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 636
      |||
Sbjct 602 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 640
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APPENDIX C

SEQUENCING ANALYSIS OF GUS SEQUENCES

>lcl|45083 A7_4 Full length sequence
Length=640

Score = 1158 bits (627), Expect = 0.0
Identities = 635/638 (99%), Gaps = 3/638 (0%)
Strand=Plus/Plus

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Query 2 ATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGCTGATGGTGCACGACCACG 61
|||||
Sbjct 1 ATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGCTGATGGTGCACGACCACG 60

Query 62 CATTAATGGACTGGATTGGGGCCAACCTCCTACCGTACCTCGCATTACCCTTACGCTGAAG 121
|||||
Sbjct 61 CATTAATGGACTGGATTGGGGCCAACCTCCTACCGTACCTCGCATTACCCTTACGCTGAAG 120

Query 122 AGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTCTG 181
|||||
Sbjct 121 AGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTCTG 180

Query 182 GCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTACA 241
|||||
Sbjct 181 GCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTACA 240

Query 242 GCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTGA 301
|||||
Sbjct 241 GCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTGA 300

Query 302 TAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGATA 361
|||||
Sbjct 301 TAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGATA 360

Query 362 CCCGTCCGCAA-GTGCACGGGAATATTT--CGCCACTGGCGGAAGCAACGCGTAAACTCG 418
|||||
Sbjct 361 CCCGTCCGCAAGGTGCACGGGAATATTTTCGCGCCACTGGCGGAAGCAACGCGTAAACTCG 420

Query 419 ACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACCA 478
|||||
Sbjct 421 ACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACCA 480

Query 479 TCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCG 538
|||||
Sbjct 481 TCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCG 540

Query 539 GCGATTTGGAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAAC 598
|||||
Sbjct 541 GCGATTTGGAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAAC 600

Query 599 TGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 636
|||||
Sbjct 601 TGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 638
```

APPENDIX C

SEQUENCING ANALYSIS OF GUS SEQUENCES

>lcl|33489 A8_5 Full length sequence
Length=639

Score = 1158 bits (627), Expect = 0.0
Identities = 635/638 (99%), Gaps = 3/638 (0%)
Strand=Plus/Plus

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Query 2 ATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGCTGATGGTGCACGACCACG 61
|
Sbjct 1 ATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGCTGATGGTGCACGACCACG 60

Query 62 CATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAAG 121
|
Sbjct 61 CATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAAG 120

Query 122 AGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTCC 181
|
Sbjct 121 AGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTCC 180

Query 182 GCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTACA 241
|
Sbjct 181 GCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTACA 240

Query 242 GCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTGA 301
|
Sbjct 241 GCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTGA 300

Query 302 TAGCGCGTGACAAAAACCACCCAAGCGTGGTGTGATGTGGAGTATTGCCAACGAACCGGATA 361
|
Sbjct 301 TAGCGCGTGACAAAAACCACCCAAGCGTGGTGTGATGTGGAGTATTGCCAACGAACCGGATA 360

Query 362 CCCGTCCGCAA-GTGACGGGAATATTT--CGCCACTGGCGGAAGCAACGCGTAAACTCG 418
|
Sbjct 361 CCCGTCCGCAAGGTGCACGGGAATATTTTCGCGCCACTGGCGGAAGCAACGCGTAAACTCG 420

Query 419 ACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACCA 478
|
Sbjct 421 ACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACCA 480

Query 479 TCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCG 538
|
Sbjct 481 TCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCG 540

Query 539 GCGATTTGGAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAAC 598
|
Sbjct 541 GCGATTTGGAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAAC 600

Query 599 TGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 636
|
Sbjct 601 TGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 638
```

APPENDIX C

SEQUENCING ANALYSIS OF GUS SEQUENCES

>lcl|6513 A9_3 Full length sequence
Length=640

Score = 1158 bits (627), Expect = 0.0
Identities = 635/638 (99%), Gaps = 3/638 (0%)
Strand=Plus/Plus

```
Query 2 ATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGCTGATGGTGCACGACCACG 61
|||||
Sbjct 1 ATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGCTGATGGTGCACGACCACG 60

Query 62 CATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAAG 121
|||||
Sbjct 61 CATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAAG 120

Query 122 AGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTATTGATGAAACTGCTGCTGTCTG 181
|||||
Sbjct 121 AGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTATTGATGAAACTGCTGCTGTCTG 180

Query 182 GCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTACA 241
|||||
Sbjct 181 GCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTACA 240

Query 242 GCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTGA 301
|||||
Sbjct 241 GCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTGA 300

Query 302 TAGCGCGTGACAAAAACCACCCAAGCGTGGTGTGAGTATTGCCAACGAACCGGATA 361
|||||
Sbjct 301 TAGCGCGTGACAAAAACCACCCAAGCGTGGTGTGAGTATTGCCAACGAACCGGATA 360

Query 362 CCCGTCCGCAA-GTGCACGGGAATATTT--CGCCACTGGCGGAAGCAACGCGTAAACTCG 418
|||||
Sbjct 361 CCCGTCCGCAAGGTGCACGGGAATATTTTCGCGCCACTGGCGGAAGCAACGCGTAAACTCG 420

Query 419 ACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACCA 478
|||||
Sbjct 421 ACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACCA 480

Query 479 TCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCG 538
|||||
Sbjct 481 TCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCG 540

Query 539 GCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAAC 598
|||||
Sbjct 541 GCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAAC 600

Query 599 TGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 636
|||||
Sbjct 601 TGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 638
```

APPENDIX C

SEQUENCING ANALYSIS OF *GUS* SEQUENCES

>lcl|19619 A1_1_2 Full length sequence
Length=442

Score = 695 bits (376), Expect = 0.0
Identities = 414/431 (96%), Gaps = 7/431 (2%)
Strand=Plus/Plus

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Query 35  ATAACGTGCT-GATGGTGCACGACCACGCATTAATGGACTG-GATTGGGGCCAACCTCCTA 92
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 13  ATAACGGGCTGGATGGTG-ACGACCACGCATTAATGGACTGCGATTGGGGCCAACCTCCTA 71

Query 93  CCGTAC-CTCGCATTACCCTTACGCTGAAGAGATGCTCGACTGGGCAGATGAACATGGCA 151
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 72  CCGCCCTCTCGCATTACCCTTACGCTGAAGAGATGCTCGCCTGGGCAGATGAACATGGCA 131

Query 152 TC GTGGTGATTGATGAAACTGCTGCTGCTCGGCTTTAACCTCTCTTTAGGCATTGGTTTCG 211
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 132 TC GTGCCGATTGATGAAACTGCTGCTGCTCGGCTTTACCTCTCTTTAGGCATTGGTTTCG 191

Query 212  AAGCGGGCAACAAGCCGAAAGAAGTACAGCGAAGAGGCAGTCAACGGGGAAACTCAGC 271
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 192  AAGCGGGCAACAAGCCGAAAGAAGTACAGCGAAGAGGCAGTCAACGGGGAAACTCAGC 251

Query 272  AAGCGCACTTACAGGCGATTAAAGAGCTGATAGCGCGTGACAAAAACCAACCAAGCGTGG 331
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 252  AAGCGCACTTACAGGCGATTAAAGAGCTGATAGCGCGTGACAAAAACCAACCAAGCTTGG 311

Query 332  TGATGTGGAGTATTGCCAACGAACCGGATACCCGTCCGCAAG-TGCACGGGAATATTTTCG 390
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 312  TGATGTGGAGTATTGCCAACGAACCGGATACCCGTCCGCAAGGTGCATGGGAATATTTTCG 371

Query 391  C-C-ACTGGCGGAAGCAACGCGTAAACTCGACCCGACGCGTCCGATCACCTGCGTCAATG 448
      | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 372  CGCCACTGGCGGAAGCAACGCGTAAACTCGACCCGACGCGTCCGATCACCTGCGTCAATG 431

Query 449  TAATGTTCTGC 459
      ||||| |||||
Sbjct 432  TAATGTTCTGC 442
```

APPENDIX C

SEQUENCING ANALYSIS OF GUS SEQUENCES

>lcl|49995 A2_2_9 Full length sequence
Length=580

Score = 1038 bits (562), Expect = 0.0
Identities = 572/576 (99%), Gaps = 3/576 (1%)
Strand=Plus/Plus

```
Query 1 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 60
      |||
Sbjct 5 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 64

Query 61 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 120
      |||
Sbjct 65 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 124

Query 121 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTC 180
      |||
Sbjct 125 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTC 184

Query 181 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTAC 240
      |||
Sbjct 185 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTAC 244

Query 241 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 300
      |||
Sbjct 245 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 304

Query 301 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 360
      |||
Sbjct 305 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 364

Query 361 ACCCGTCCGCAAG-TGCACGGGAATATTTTCGC-C-ACTGGCGGAAGCAACGCGTAAACTC 417
      |||
Sbjct 365 ACCCGTCCGCAAGGTGCACGGGAATATTTTCGCGCCACTGGCGGAAGCAACGCGTAAACTC 424

Query 418 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATAACC 477
      |||
Sbjct 425 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATAACC 484

Query 478 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 537
      |||
Sbjct 485 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 544

Query 538 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAA 573
      ||
Sbjct 545 GGGGATTTGAAACGGCAGAGAAGGTACTGGAAAAA 580
```

APPENDIX C

SEQUENCING ANALYSIS OF *GUS* SEQUENCES

>lcl|63487 A3_2_6 Full length sequence

Length=640

Score = 1133 bits (1256), Expect = 0.0
Identities = 636/639 (99%), Gaps = 3/639 (0%)
Strand=Plus/Plus

```
Query 1 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 60
      |||
Sbjct 2 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 61

Query 61 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 120
      |||
Sbjct 62 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 121

Query 121 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAACTGCTGCTGTC 180
      |||
Sbjct 122 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAACTGCTGCTGTC 181

Query 181 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTAC 240
      |||
Sbjct 182 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTAC 241

Query 241 AGCGAAGAGGCAGTCAACGGGGAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 300
      |||
Sbjct 242 AGCGAAGAGGCAGTCAACGGGGAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 301

Query 301 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 360
      |||
Sbjct 302 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 361

Query 361 ACCCGTCCGCAA-GTGCACGGGAATATTT--CGCCACTGGCGGAAGCAACGCGTAAACTC 417
      |||
Sbjct 362 ACCCGTCCGCAAAGGTGCACGGGAATATTTTCGCGCCACTGGCGGAAGCAACGCGTAAACTC 421

Query 418 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATAACC 477
      |||
Sbjct 422 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATAACC 481

Query 478 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 537
      |||
Sbjct 482 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 541

Query 538 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 597
      |||
Sbjct 542 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 601

Query 598 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 636
      |||
Sbjct 602 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 640
```

APPENDIX C

SEQUENCING ANALYSIS OF *GUS* SEQUENCES

>lcl|42739 A5_2_8 Full length sequence

Length=644

Score = 1160 bits (628), Expect = 0.0
Identities = 636/639 (99%), Gaps = 3/639 (0%)
Strand=Plus/Plus

```
Query 1 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 60
      |||
Sbjct 2 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 61

Query 61 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 120
      |||
Sbjct 62 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 121

Query 121 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAACTGCTGCTGTC 180
      |||
Sbjct 122 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAACTGCTGCTGTC 181

Query 181 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTAC 240
      |||
Sbjct 182 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTAC 241

Query 241 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 300
      |||
Sbjct 242 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 301

Query 301 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 360
      |||
Sbjct 302 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 361

Query 361 ACCCGTCCGCAA-GTGCACGGGAATATTT--CGCCACTGGCGGAAGCAACGCGTAAACTC 417
      |||
Sbjct 362 ACCCGTCCGCAAGGTGCACGGGAATATTTTCGCGCCACTGGCGGAAGCAACGCGTAAACTC 421

Query 418 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATAACC 477
      |||
Sbjct 422 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATAACC 481

Query 478 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 537
      |||
Sbjct 482 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 541

Query 538 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 597
      |||
Sbjct 542 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 601

Query 598 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 636
      |||
Sbjct 602 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGAT 640
```

APPENDIX C

SEQUENCING ANALYSIS OF *GUS* SEQUENCES

>lcl|7013 A7_4_13 Full length sequence
Length=578

Score = 1031 bits (558), Expect = 0.0
Identities = 571/578 (99%), Gaps = 3/578 (1%)
Strand=Plus/Plus

```
Query 2 ATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGCTGATGGTGCACGACCAG 61
|||||
Sbjct 1 ATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGCTGATGGTGCACGACCAG 60

Query 62 CATTAATGGACTGGATTGGGGCCAACCTCCTACCGTACCTCGCATTACCCTTACGCTGAAG 121
|||||
Sbjct 61 CATTAATGGACTGGATTGGGGCCAACCTCCTACCGTACCTCGCATTACCCTTACGCTGAAG 120

Query 122 AGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTCTG 181
|||||
Sbjct 121 AGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTCTG 180

Query 182 GCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTACA 241
|||||
Sbjct 181 GCTTTAACCTGTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAACTGTACA 240

Query 242 GCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTGA 301
|||||
Sbjct 241 GCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTGA 300

Query 302 TAGCGCGTGACAAAAACCACCCAAGCGTGGTGTGAGTATTGCCAACGAACCGGATA 361
|||||
Sbjct 301 TAGCGCGTGACAAAAACCACCCAAGCGNGGTGTGAGTATTGCCAACGAACCGGATA 360

Query 362 CCCGTCCGCAAG-TGCACGGGAATATTTTCGC-C-ACTGGCGGAAGCAACGCGTAAACTCG 418
|||||
Sbjct 361 CCCGTCCGCAAGGTGCACGGGAATATTTTCGC-C-ACTGGCGGAAGCAACGCGTAAACTCG 420

Query 419 ACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACCA 478
|||||
Sbjct 421 ACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACCA 480

Query 479 TCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCG 538
|||
Sbjct 481 TCANCNATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCG 540

Query 539 GCGATTTGGAACGGCAGAGAAGGTACTGGAAAAAGAA 576
|||||
Sbjct 541 GCGATTTGGAACGGCAGAGAAGGTACTGGAAAAAGAA 578
```


APPENDIX C

SEQUENCING ANALYSIS OF *GUS* SEQUENCES

>lcl|28673 A8_5_15 Full length sequence

Length=639

Score = 1158 bits (627), Expect = 0.0
Identities = 635/638 (99%), Gaps = 3/638 (0%)
Strand=Plus/Plus

```
Query 1 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 60
      |||
Sbjct 2 CATGAAGATGCGGACTTACGTGGCAAAGGATTTCGATAACGTGCTGATGGTGCACGACCAC 61

Query 61 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 120
      |||
Sbjct 62 GCATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAA 121

Query 121 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAACTGCTGCTGTC 180
      |||
Sbjct 122 GAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAACTGCTGCTGTC 181

Query 181 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTAC 240
      |||
Sbjct 182 GGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTAC 241

Query 241 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 300
      |||
Sbjct 242 AGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTG 301

Query 301 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 360
      |||
Sbjct 302 ATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGAT 361

Query 361 ACCCGTCCGCAA-GTGCACGGGAATATTT--CGCCACTGGCGGAAGCAACGCGTAAACTC 417
      |||
Sbjct 362 ACCCGTCCGCAAGGTGCACGGGAATATTTTCGCGCCACTGGCGGAAGCAACGCGTAAACTC 421

Query 418 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATAACC 477
      |||
Sbjct 422 GACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATAACC 481

Query 478 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 537
      |||
Sbjct 482 ATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGC 541

Query 538 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 597
      |||
Sbjct 542 GGCGATTTGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAA 601

Query 598 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGA 635
      |||
Sbjct 602 CTGCATCAGCCGATTATCATCACCGAATACGGCGTGGA 639
```

APPENDIX C

SEQUENCING ANALYSIS OF GUS SEQUENCES

>lcl|35133 A9_2_2 Full length sequence
Length=637

Score = 1146 bits (620), Expect = 0.0
Identities = 632/637 (99%), Gaps = 3/637 (0%)
Strand=Plus/Plus

```
Query 2 ATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGCTGATGGTGCACGACCACG 61
|
Sbjct 1 ATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGCTGATGGTGCACGACCACG 60

Query 62 CATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAAG 121
|
Sbjct 61 CATTAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAAG 120

Query 122 AGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTCTG 181
|
Sbjct 121 AGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTCTG 180

Query 182 GCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTACA 241
|
Sbjct 181 GCTTTCACCTGTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTACA 240

Query 242 GCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTGA 301
|
Sbjct 241 GCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTGA 300

Query 302 TAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGATA 361
|
Sbjct 301 TAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAACCGGATA 360

Query 362 CCCGTCGCAA-GTGACGGGAATATTT--CGCCACTGGCGGAAGCAACGCGTAAACTCG 418
|
Sbjct 361 CCCGTCGCAAAGGTGCACGGGAATATTTTCGCGCCACTGGCGGAAGCAACGCGTAAACTCG 420

Query 419 ACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACCA 478
|
Sbjct 421 ACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACCA 480

Query 479 TCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCG 538
|
Sbjct 481 TCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCG 540

Query 539 GCGATTTGAAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAAC 598
|
Sbjct 541 GCGATTTGAAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAAC 600

Query 599 TGCATCAGCCGATTATCATCACCGAATACGGCGTGGA 635
|
Sbjct 601 TGCATCAGCCGATTATCATCACCGAATACGGCGTGGA 637
```

APPENDIX D

RESTRICTION SUMMARY RESULTS

Results for linear 636 residue sequence "Gus Linker probe" starting "catgaagatg"

Site:	Positions:
AatI agg cct	none
AatII gacgt c	none
Acc16I tgc gca	none
AccII cg cg	307, 409, 427
AccIII t ccgga	none
AclI aa cgtt	none
AcvI cac gtg	none
AfaI gt ac	97, 239, 564
AfeI agc gct	none
AflII c ttaag	none
AgeI a ccggt	none
AhlI a ctagt	none
Alw441 g tgcac	50, 374
AluI ag ct	298
Aor51HI agc gct	none
ApaI gggcc c	none
ApaLI g tgcac	50, 374
AscI gg cgcgcc	none
AseI at taat	65
Asp718I g gtacc	none
AsuII tt cgaa	210
AvaI c ycgrg	none
AviII tgc gca	none
AvrII c ctagg	none
Ball tgg cca	none
BamHI g gatcc	none
BanIII at cgat	none
BbeI ggcgc c	none
BbrPI cac gtg	none
BbuI gcatg c	none
BcuI a ctagt	none
BclI t gatca	none
BfaI c tag	none

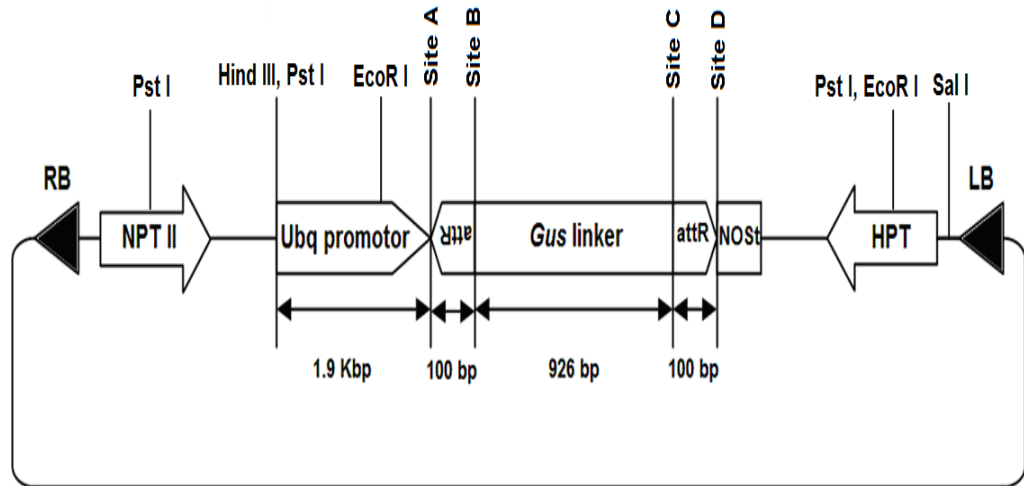
BfrI c ttaag	none
BfrBI atg cat	none
BglII a gatct	none
BlnI c ctagg	none
BseCI at cgat	none
BsePI g cgcgc	none
BseX3I c ggccg	none
BshTI a ccggt	none
Bsp1407I t gtaca	237
Bsp19I c catgg	none
BspDI at cgat	none
BspEI t ccgga	none
BsrGI t gtaca	237
BssHII g cgcgc	none
BstUI cg cg	307, 409, 427
ClaI at cgat	none
DpnII gatc	432, 484
DraI ttt aaa	none
EagI c ggccg	none
EcoRI glaattc	none
EcoRV gat atc	none
EgeI ggc gcc	none
FseI ggccgg cc	none
FspI tgc gca	none
HaeIII gg cc	83, 584
HincII gty rac	256
HindIII a agctt	none
HinfI g antc	30
HpaI gtt aac	none
HpaII c cgg	356
KasI g cgcgc	none
KpnI ggtac c	none
MboI gatc	432, 484
MfeI c aattg	none
MluI a cgcgt	407, 425
MscI tgg cca	none
MseI t taa	65, 186, 291
MspI c cgg	356
NaeI gcc ggc	none

NarI gg cgcc	none
NcoI c catgg	none
NdeI ca tatg	none
NdeII gatc	432, 484
NgoMIV g ccggc	none
NheI g ctagc	none
NlaIII catg	5, 149
NotI gc ggccgc	none
NruI tcg cga	none
NsiI atgca t	none
PacI ttaat taa	none
PciI a catgt	none
PhoI gg cc	83, 584
PmeI gttt aaac	none
PmlI cac gtg	none
PsiI tta taa	none
PstI ctgca g	none
PvuI cgat cg	none
PvuII cag ctg	none
RsaI gt ac	97, 239, 564
SacI gagct c	none
SacII ccgc gg	none
SalI g tcgac	none
SbfI cctgca gg	none
ScaI agt act	none
SfoI ggc gcc	none
SmaI ccc ggg	none
SnaBI tac gta	none
SpeI a ctagt	none
SphI gcatg c	none
SspI aat att	385
SstI gagct c	none
SstII ccgc gg	none
StuI agg cct	none
SwaI attt aat	none
TaqI t cga	33, 129, 210, 417
TliI c tcgag	none
VspI at taat	65
XbaI t ctaga	none

XhoI c tcgag	none
XmaI c ccggg	none

APPENDIX E

SCHEMATIC MAP OF PANDA VECTOR



(Miki and Shimamoto, 2004)

APPENDIX F

POLLEN TUBE GERMINATION PERCENTAGE OF PLANTS AT DIFFERENT TIME INTERVALS AFTER ANTHOR DEHISCENCE

Plants	0 min	15 min	30 min	45 min	60 min	75 min
A1.1 (Transgenic)	63.4	37.6	11.2	3.40	1.30	0
A2.4 (Transgenic)	59	33	15.60	4.80	1.40	0
A3.7 (Transgenic)	61.70	32	9.30	2	0	0
Ci3 (Non-transgenic)	58.80	35.50	12.70	3.50	1.20	0
Ci6 (Non-transgenic)	60.40	39.40	12.80	3.20	0	0
Ci8 (Non-transgenic)	62.50	29.40	15.60	5	2.10	0