

JRC GMO-Amplicons BLAST (PROTEIN CODING SEQUENCES)

Query= AHAS_Arabidopsis_thaliana_-_X51514.1	3
Query= barnase_Bacillus_amyloliquefaciens_-_X12871.1	3
Query= barstar_Bacillus_amyloliquefaciens_-_X15545.1	3
Query= bar_Streptomyces_hygroscopicus_-_X05822.1	3
Query= bla_Escherichia_coli_UMN026_-_NC_011751.1	5
Query= bxn_Klebsiella_pneumoniae_-_J03196.1	5
Query= CMV_CP_Cucumber_mosaic_virus_-_NC_001440.1	6
Query= cp4epsps_Glycine_max_-_AB209952.1	6
Query= cpTi_Vigna_unguiculata_-_AJ271752.1	8
Query= cry1A.105_synthetic_construct_-_FB707511.1	8
Query= cry1Ab_synthetic_construct_-_AX392802.1	11
Query= cry1Ac_Bacillus_thuringiensis_-_U89872.1	15
Query= cry1F_Bacillus_thuringiensis_-_EU679501.1	16
Query= cry2Ab2_Bacillus_thuringiensis_serovar_kurstaki_-_JN415485.1	16
Query= cry3A_Bacillus_thuringiensis_serovar_tenebrionis_-_EU332160.1	16
Query= cry3Bb1_Bacillus_thuringiensis_-_M89794.1	16
Query= gat4621_Bacillus_licheniformis_WX-02_-_CP012110.1	16
Query= gox_Ochrobactrum_sp._G-1_-_GU214711.1	17
Query= GUS_Escherichia_coli_-_M14641.1	17
Query= manA_Escherichia_coli_-_M15380.1	17
Query= nptII_Escherichia_coli_-_V00618.1	17
Query= pat-STRVR_Streptomyces_viridochromogenes_-_M22827.1	44
Query= PG_Solanum_lycopersicum_-_M37304.1	46
Query= PLRVrep_Potato_leafroll_virus_-_NC_001747.1	47

Query= vip3A(a)_Bacillus_thuringiensis_-_L48811.1 48

Query= AHAS_Arabidopsis_thaliana_-X51514.1

Length=2365

	Score	E
	(Bits)	Value
Sequences producing significant alignments:		
lcl Amplicon_410 non-redundant amplicon of 4 matches	75.2	5e-15

[>lcl|Amplicon_410 non-redundant amplicon of 4 matches](#)

Length=88

Score = 75.2 bits (82), Expect = 5e-15

Identities = 41/41 (100%), Gaps = 0/41 (0%)

Strand=Plus/Plus

Query 1651 AACAGAAGTTTCCGTTGAGCTTTAAGACGTTTGGGGAAGCT 1691

|||||

Sbjct 1 AACAGAAGTTTCCGTTGAGCTTTAAGACGTTTGGGGAAGCT 41

Lambda K H

0.634 0.408 0.912

Gapped

Lambda K H

0.625 0.410 0.780

Effective search space used: 224934928

Query= barnase_Bacillus_amyloliquefaciens_-X12871.1

Length=429

***** No hits found *****

Lambda K H

0.634 0.408 0.912

Gapped

Lambda K H

0.625 0.410 0.780

Effective search space used: 40040600

Query= barstar_Bacillus_amyloliquefaciens_-X15545.1

Length=474

***** No hits found *****

***** No hits found *****

Lambda K H

0.634 0.408 0.912

Gapped

Lambda K H

0.625 0.410 0.780

Effective search space used: 44435300

Query= bar_Streptomyces_hygroscopicus_-X05822.1

Length=835

	Score	E
	(Bits)	Value
Sequences producing significant alignments:		
lcl Amplicon_17 non-redundant amplicon of 1781 matches	125	1e-30
lcl Amplicon_619 non-redundant amplicon of 2 matches	120	5e-29
lcl Amplicon_586 non-redundant amplicon of 13 matches	120	5e-29
lcl Amplicon_123 non-redundant amplicon of 50 matches	120	5e-29
lcl Amplicon_642 non-redundant amplicon of 3 matches	120	5e-29
lcl Amplicon_552 non-redundant amplicon of 1 matches	111	2e-26
lcl Amplicon_15 non-redundant amplicon of 1787 matches	109	9e-26
lcl Amplicon_618 non-redundant amplicon of 2 matches	104	4e-24
lcl Amplicon_122 non-redundant amplicon of 50 matches	104	4e-24
lcl Amplicon_551 non-redundant amplicon of 1 matches	91.5	2e-20
lcl Amplicon_574 non-redundant amplicon of 8 matches	89.7	8e-20
lcl Amplicon_185 non-redundant amplicon of 33 matches	75.2	2e-15
lcl Amplicon_422 non-redundant amplicon of 3 matches	66.2	9e-13

[>lcl|Amplicon_17 non-redundant amplicon of 1781 matches](#)

Length=69

Score = 125 bits (138), Expect = 1e-30

Identities = 69/69 (100%), Gaps = 0/69 (0%)

Strand=Plus/Plus

Query 231 CGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGAGGAACCGCA 290

|||||

Sbjct 1 CGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGAGGAACCGCA 60

Query 291 GGAGTGGAC 299

|||||

Sbjct 61 GGAGTGGAC 69

[>lcl|Amplicon_619_non-redundant_amplicon_of_2_matches](#) Length=69

Score = 120 bits (132), Expect = 5e-29
Identities = 68/69 (99%), Gaps = 0/69 (0%)
Strand=Plus/Plus

Query 231 CGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCA 290
|
Sbjct 1 CGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCA 60
Query 291 GGAGTGGAC 299
|
Sbjct 61 GGAGTAGAC 69
|

[>lcl|Amplicon_586_non-redundant_amplicon_of_13_matches](#)

Length=69
Score = 120 bits (132), Expect = 5e-29
Identities = 68/69 (99%), Gaps = 0/69 (0%)
Strand=Plus/Plus

Query 231 CGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCA 290
|
Sbjct 1 CGTCAACCACTACATCCAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCA 60
Query 291 GGAGTGGAC 299
|
Sbjct 61 GGAGTGGAC 69

[>lcl|Amplicon_123_non-redundant_amplicon_of_50_matches](#)

Length=69
Score = 120 bits (132), Expect = 5e-29
Identities = 68/69 (99%), Gaps = 0/69 (0%)
Strand=Plus/Plus

Query 231 CGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCA 290
|
Sbjct 1 CGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCA 60
Query 291 GGAGTGGAC 299
|
Sbjct 61 GGACTGGAC 69

[>lcl|Amplicon_642_non-redundant_amplicon_of_3_matches](#)

Length=69
Score = 120 bits (132), Expect = 5e-29
Identities = 68/69 (99%), Gaps = 0/69 (0%)
Strand=Plus/Plus

Query 231 CGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCA 290
|
Sbjct 1 CGTCAACCACTACACCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCA 60
Query 291 GGAGTGGAC 299
|
Sbjct 61 GGAGTGGAC 69

[>lcl|Amplicon_552_non-redundant_amplicon_of_1_matches](#)

Length=69
Score = 111 bits (122), Expect = 2e-26
Identities = 66/69 (96%), Gaps = 0/69 (0%)
Strand=Plus/Plus

Query 231 CGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCA 290
|
Sbjct 1 CGTCAACCACTACATCGAGACAAGCACTGTCAACTTCCGTACCGAGCCTCAGGAACCTCA 60
Query 291 GGAGTGGAC 299
|
Sbjct 61 GGAGTGGAC 69

[>lcl|Amplicon_15_non-redundant_amplicon_of_1787_matches](#)

Length=60

[>lcl|Amplicon_15_non-redundant_amplicon_of_1787_matches](#)

Length=60
Score = 109 bits (120), Expect = 9e-26
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 250 ACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCAGGAGTGGACGGACGACCTC 309
|
Sbjct 1 ACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCAGGAGTGGACGGACGACCTC 60

[>lcl|Amplicon_618_non-redundant_amplicon_of_2_matches](#) Length=60

Score = 104 bits (114), Expect = 4e-24
Identities = 59/60 (98%), Gaps = 0/60 (0%)

Strand=Plus/Plus
 Query 250 ACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCAGGAGTGGACGGACGACCTC 309
 |||
 Sbjct 1 ACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCAGGAGTAGACGGACGACCTC 60
[>lcl|Amplicon 122 non-redundant amplicon of 50 matches](#)
 Length=60
 Score = 104 bits (114), Expect = 4e-24
 Identities = 59/60 (98%), Gaps = 0/60 (0%)
 Strand=Plus/Plus
 Query 250 ACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCAGGAGTGGACGGACGACCTC 309
 |||
 Sbjct 1 ACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCAGGACTGGACGGACGACCTC 60
[>lcl|Amplicon 551 non-redundant amplicon of 1 matches](#)
 Length=60
 Score = 91.5 bits (100), Expect = 2e-20
 Identities = 56/60 (93%), Gaps = 0/60 (0%)
 Strand=Plus/Plus
 Query 250 ACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCAGGAGTGGACGGACGACCTC 309
 |||
 Sbjct 1 ACAAGCACTGTCAACTTCCGTACCGAGCCTCAGGAACCTCAGGAGTGGACCGACGACCTC 60
[>lcl|Amplicon 574 non-redundant amplicon of 8 matches](#) Length=57
 Score = 89.7 bits (98), Expect = 8e-20
 Identities = 57/60 (95%), Gaps = 3/60 (5%)
 Strand=Plus/Plus
 Query 250 ACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCAGGAGTGGACGGACGACCTC 309
 |||
 Sbjct 1 ACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAA--GCAGGAGTGGACGGACGACCTC 57
[>lcl|Amplicon 185 non-redundant amplicon of 33 matches](#)
 Length=60
 Score = 75.2 bits (82), Expect = 2e-15
 Identities = 52/59 (88%), Gaps = 0/59 (0%)
 Strand=Plus/Plus
 Query 250 ACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCAGGAGTGGACGGACGACCT 308
 ||
 Query 250 ACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCAGGAGTGGACGGACGACCT 308
 ||
 Sbjct 1 ACGAGCACGGTCAACTTCCGTACCGAGCCGCAGACTCCGCAGGAGTGGATCGACGACCT 59
[>lcl|Amplicon 422 non-redundant amplicon of 3 matches](#) Length=63
 Score = 66.2 bits (72), Expect = 9e-13
 Identities = 52/62 (84%), Gaps = 3/62 (5%)
 Strand=Plus/Plus
 Query 250 ACAAGCACGGTCAACTTCCGTACCGAG---CCGCAGGAACCGCAGGAGTGGACGGACGAC 306
 ||
 Sbjct 1 ACGAGCACGGTCAACTTCCGTACCGAGGAGCCGCAGACTCCGCAGGAGTGGATCGACGAC 60
 Query 307 CT 308
 ||
 Sbjct 61 CT 62
 Lambda K H
 0.634 0.408 0.912
 Gapped
 Lambda K H
 0.625 0.410 0.780
 Effective search space used: 78900965

Query= bla_Escherichia_coli_UMN026_-_NC_011751.1

Length=861
 ***** No hits found *****
 Lambda K H
 0.634 0.408 0.912
 Gapped
 Lambda K H
 0.625 0.410 0.780
 Effective search space used: 81418051

Query= bxn_Klebsiella_pneumoniae_-_J03196.1

Length=1212
 ***** No hits found *****
 Lambda K H
 0.634 0.408 0.912

Gapped
 Lambda K H
 0.634 0.408 0.912

Gapped
 Lambda K H
 0.625 0.410 0.780

Effective search space used: 115398712

Query= CMV_CP_Cucumber_mosaic_virus_-_NC_001440.1

Length=657

	Score	E
	(Bits)	Value
Sequences producing significant alignments:		
lcl Amplicon_602 non-redundant amplicon of 2 matches	<u>84.2</u>	3e-18

>[lcl|Amplicon_602 non-redundant amplicon of 2 matches](#)

Length=220

Score = 84.2 bits (92), Expect = 3e-18
 Identities = 48/49 (98%), Gaps = 0/49 (0%)

Strand=Plus/Plus

```

Query 1 ATGGACAAATCTGAATCAACCAGTGCTGGTCGTAACCGTCGACGTCGTC 49
      |||
Sbjct 159 ATGGACAAATCTGAATCAACCAGTGCTGGTCGTAACCATCGACGTCGTC 207
Lambda K H
0.634 0.408 0.912
    
```

Gapped
 Lambda K H
 0.625 0.410 0.780

Effective search space used: 62307080

Query= cp4epsps_Glycine_max_-_AB209952.1

Length=1584

	Score	E
	(Bits)	Value
Sequences producing significant alignments:		
lcl Amplicon_28 non-redundant amplicon of 30 matches	<u>219</u>	1e-58
lcl Amplicon_392 non-redundant amplicon of 3 matches	<u>214</u>	5e-57
lcl Amplicon_61 non-redundant amplicon of 127 matches	<u>196</u>	1e-51
lcl Amplicon_388 non-redundant amplicon of 3 matches	<u>194</u>	5e-51
lcl Amplicon_366 non-redundant amplicon of 3 matches	<u>176</u>	1e-45
lcl Amplicon_29 non-redundant amplicon of 33 matches	<u>159</u>	1e-40
lcl Amplicon_112 non-redundant amplicon of 116 matches	<u>136</u>	1e-33
lcl Amplicon_304 non-redundant amplicon of 3 matches	<u>132</u>	1e-32
lcl Amplicon_87 non-redundant amplicon of 13 matches	<u>125</u>	2e-30
lcl Amplicon_367 non-redundant amplicon of 3 matches	<u>116</u>	1e-27
lcl Amplicon_545 non-redundant amplicon of 12 matches	<u>64.4</u>	6e-12

>[lcl|Amplicon_28 non-redundant amplicon of 30 matches](#)

Length=121

Score = 219 bits (242), Expect = 1e-58
 Identities = 121/121 (100%), Gaps = 0/121 (0%)
 Strand=Plus/Plus
 Score = 219 bits (242), Expect = 1e-58
 Identities = 121/121 (100%), Gaps = 0/121 (0%)

Strand=Plus/Plus

```

Query 182 CCTTTAGGATTTTCAGCATCAGTGGCTACAGCCTGCATGCTTCACGGTGCAAGCAGCCGGC 241
      |||
Sbjct 1 CCTTTAGGATTTTCAGCATCAGTGGCTACAGCCTGCATGCTTCACGGTGCAAGCAGCCGGC 60
Query 242 CCGCAACCGCCC GCAAATCCTCTGGCCTTTCCGGAACCGTCCGCATTC CCGGCGACAAGT 301
      |||
Sbjct 61 CCGCAACCGCCC GCAAATCCTCTGGCCTTTCCGGAACCGTCCGCATTC CCGGCGACAAGT 120
Query 302 C 302
      |
Sbjct 121 C 121
    
```

>[lcl|Amplicon_392 non-redundant amplicon of 3 matches](#)

Length=121

Score = 214 bits (236), Expect = 5e-57
 Identities = 120/121 (99%), Gaps = 0/121 (0%)

Strand=Plus/Plus

```

Query 182 CCTTTAGGATTTTCAGCATCAGTGGCTACAGCCTGCATGCTTCACGGTGCAAGCAGCCGGC 241
      ||
Sbjct 1 CCCTTAGGATTTTCAGCATCAGTGGCTACAGCCTGCATGCTTCACGGTGCAAGCAGCCGGC 60
Query 242 CCGCAACCGCCC GCAAATCCTCTGGCCTTTCCGGAACCGTCCGCATTC CCGGCGACAAGT 301
    
```

```

|||||
Sbjct 61 CCGCAACCGCCCGCAAATCCTCTGGCCTTTCCGGAACCGTCCGCATTCCCGGCGACAAGT 120
Query 302 C 302
|
Sbjct 121 C 121
>lcl|Amplicon 61 non-redundant amplicon of 127 matches
Length=108
Score = 196 bits (216), Expect = 1e-51
Identities = 108/108 (100%), Gaps = 0/108 (0%)
Strand=Plus/Plus
Query 215 GCATGCTTCACGGTGCAAGCAGCCGGCCCGCAACCGCCCGCAAATCCTCTGGCCTTTCCG 274
|||||
Sbjct 1 GCATGCTTCACGGTGCAAGCAGCCGGCCCGCAACCGCCCGCAAATCCTCTGGCCTTTCCG 60
Query 275 GAACCGTCCGCATTCCCGGCGACAAGTCGATCTCCACCGGTCCTTCA 322
|||||
Sbjct 61 GAACCGTCCGCATTCCCGGCGACAAGTCGATCTCCACCGGTCCTTCA 108
>lcl|Amplicon 388 non-redundant amplicon of 3 matches
Length=108
Score = 194 bits (214), Expect = 5e-51
Identities = 107/107 (100%), Gaps = 0/107 (0%)
Strand=Plus/Plus
Query 216 CATGCTTCACGGTGCAAGCAGCCGGCCCGCAACCGCCCGCAAATCCTCTGGCCTTTCCGG 275
|||||
Sbjct 2 CATGCTTCACGGTGCAAGCAGCCGGCCCGCAACCGCCCGCAAATCCTCTGGCCTTTCCGG 61
Query 276 AACCGTCCGCATTCCCGGCGACAAGTCGATCTCCACCGGTCCTTCA 322
|||||
Sbjct 62 AACCGTCCGCATTCCCGGCGACAAGTCGATCTCCACCGGTCCTTCA 108
>lcl|Amplicon 366 non-redundant amplicon of 3 matches
Length=142
>lcl|Amplicon 366 non-redundant amplicon of 3 matches
Length=142
Score = 176 bits (194), Expect = 1e-45
Identities = 121/142 (85%), Gaps = 21/142 (15%)
Strand=Plus/Plus
Query 182 CCTTTAGGATTTT CAGCATCAGTGGCTACAGC-----CTGCATGC 220
|||||
Sbjct 1 CCTTTAGGATTTT CAGCATCAGTGGCTACAGCGACGTT CAGAATTC CGTGTA ACTGCATGC 60
Query 221 TTCACGGTGCAAGCAGCCGGCCCGCAACCGCCCGCAAATCCTCTGGCCTTTCCGGAACCG 280
|||||
Sbjct 61 TTCACGGTGCAAGCAGCCGGCCCGCAACCGCCCGCAAATCCTCTGGCCTTTCCGGAACCG 120
Query 281 TCCGCATTCCCGGCGACAAGTC 302
|||||
Sbjct 121 TCCGCATTCCCGGCGACAAGTC 142
>lcl|Amplicon 29 non-redundant amplicon of 33 matches Length=88
Score = 159 bits (176), Expect = 1e-40
Identities = 88/88 (100%), Gaps = 0/88 (0%)
Strand=Plus/Plus
Query 188 GGATTTT CAGCATCAGTGGCTACAGCCTGCATGCTT CACGGTGCAAGCAGCCGGCCCGCAA 247
|||||
Sbjct 1 GGATTTT CAGCATCAGTGGCTACAGCCTGCATGCTT CACGGTGCAAGCAGCCGGCCCGCAA 60
Query 248 CCGCCCGCAAATCCTCTGGCCTTTCCGG 275
|||||
Sbjct 61 CCGCCCGCAAATCCTCTGGCCTTTCCGG 88
>lcl|Amplicon 112 non-redundant amplicon of 116 matches
Length=108
Score = 136 bits (150), Expect = 1e-33
Identities = 95/108 (88%), Gaps = 0/108 (0%)
Strand=Plus/Plus
Query 215 GCATGCTTCACGGTGCAAGCAGCCGGCCCGCAACCGCCCGCAAATCCTCTGGCCTTTCCG 274
|||||
Sbjct 1 GCATGCTTCACGGTGCAAGCAGCCGTCCAGCAACTGCTCGTAAGTCCCTCTGGTCTTTCTG 60
Query 275 GAACCGTCCGCATTCCCGGCGACAAGTCGATCTCCACCGGTCCTTCA 322
|||||
Sbjct 61 GAACCGTCCGTATTCCAGGTGACAAGTCTATCTCCACAGGTCCTTCA 108
>lcl|Amplicon 304 non-redundant amplicon of 3 matches
Length=108
Score = 132 bits (146), Expect = 1e-32
Identities = 93/106 (88%), Gaps = 0/106 (0%)
Strand=Plus/Plus

```


lcl Amplicon_177	non-redundant amplicon of 20 matches	<u>87.8</u>	1e-18
lcl Amplicon_446	non-redundant amplicon of 2 matches	<u>86.0</u>	4e-18
lcl Amplicon_96	non-redundant amplicon of 7 matches	<u>82.4</u>	5e-17
lcl Amplicon_603	non-redundant amplicon of 8 matches	<u>64.4</u>	1e-11
lcl Amplicon_168	non-redundant amplicon of 21 matches	<u>62.6</u>	5e-11

>[lcl|Amplicon 335 non-redundant amplicon of 3 matches](#)

Length=212

Score = 170 bits (188), Expect = 1e-43
Identities = 106/114 (93%), Gaps = 0/114 (0%)

Strand=Plus/Plus

```

Query 1 ATGGACAACAACCCAAACATCAACGAGTGCATCCCGTACAACCTGCCTCAGCAACCCCTGAG 60
      |||
Sbjct 84 ATGGACAACAACCCCAACATCAACGAGTGCATCCCGTACAACCTGCCTGAGCAACCCCGAG 143
Query 61 GTCGAGGTGCTCGGCGGTGAGCGCATCGAGACCGGTTACACCCCATCGACATC 114
      |||
Sbjct 144 GTGGAGGTGCTGGGCGGCGAGCGCATCGAGACCGGCTACACCCCATCGACATC 197

```

>[lcl|Amplicon 5 non-redundant amplicon of 285 matches](#)

Length=129

Score = 165 bits (182), Expect = 5e-42
Identities = 114/129 (88%), Gaps = 0/129 (0%)

Strand=Plus/Plus

```

Query 103 CCCATCGACATCTCCCTCTCCCTCACGCAGTTCCTGCTCAGCGAGTTCGTGCCAGGCGCT 162
      |||
Sbjct 1 CCCATCGACATCAGCCTGAGCCTGACCCAGTTCCTGCTGAGCGAGTTCGTGCCCGGCGCC 60
Query 163 GGCTTCGTCTCTGGGCTCGTGGACATCATCTGGGGCATCTTTGGCCCCCTCCAGTGGGAC 222
      |||
Sbjct 61 GGCTTCGTGCTGGGCTGGTGGACATCATCTGGGGCATCTTCGGCCCCAGCCAGTGGGAC 120
Query 223 GCCTTCCTG 231
      |||
Sbjct 61 GGCTTCGTGCTGGGCTGGTGGACATCATCTGGGGCATCTTCGGCCCCAGCCAGTGGGAC 120
Query 223 GCCTTCCTG 231
      |||
Sbjct 121 GCCTTCCTG 129

```

>[lcl|Amplicon 553 non-redundant amplicon of 1 matches](#)

Length=129

Score = 152 bits (168), Expect = 3e-38
Identities = 111/129 (86%), Gaps = 0/129 (0%)

Strand=Plus/Plus

```

Query 103 CCCATCGACATCTCCCTCTCCCTCACGCAGTTCCTGCTCAGCGAGTTCGTGCCAGGCGCT 162
      |||
Sbjct 1 CCGATTGACATCAGCCTGAGCCTGACCCAGTTCCTGCTGAGCGAGTTCGTGCCGGGCGCC 60
Query 163 GGCTTCGTCTCTGGGCTCGTGGACATCATCTGGGGCATCTTTGGCCCCCTCCAGTGGGAC 222
      |||
Sbjct 61 GGCTTCGTGCTGGGCTGGTGGACATCATCTGGGGCATCTTCGGCCGAGCCAGTGGGAC 120
Query 223 GCCTTCCTG 231
      |||
Sbjct 121 GCCTTCCTG 129

```

>[lcl|Amplicon 176 non-redundant amplicon of 20 matches](#)

Length=129

Score = 152 bits (168), Expect = 3e-38
Identities = 111/129 (86%), Gaps = 0/129 (0%)

Strand=Plus/Plus

```

Query 103 CCCATCGACATCTCCCTCTCCCTCACGCAGTTCCTGCTCAGCGAGTTCGTGCCAGGCGCT 162
      |||
Sbjct 1 CCCATCGACATCAGCCTGAGCCTGACCCAGTTCCTGCTGAGCGAGTTCGTGCCTGGTGCT 60
Query 163 GGCTTCGTCTCTGGGCTCGTGGACATCATCTGGGGCATCTTTGGCCCCCTCCAGTGGGAC 222
      |||
Sbjct 61 GGCTTCGTGCTGGGACTAGTGGACATCATCTGGGGCATCTTCGGTCCCAGCCAGTGGGAT 120
Query 223 GCCTTCCTG 231
      |||
Sbjct 121 GCCTTCCTG 129

```

>[lcl|Amplicon 72 non-redundant amplicon of 36 matches](#) Length=73

Score = 132 bits (146), Expect = 3e-32
Identities = 73/73 (100%), Gaps = 0/73 (0%)

Strand=Plus/Minus

```

Query 91 ACCGGTTACACCCCATCGACATCTCCCTCTCCCTCACGCAGTTCCTGCTCAGCGAGTTC 150
      |||
Sbjct 73 ACCGGTTACACCCCATCGACATCTCCCTCTCCCTCACGCAGTTCCTGCTCAGCGAGTTC 14
Query 151 GTGCCAGGCGCTG 163

```

```

|||||
Sbjct 13 GTGCCAGGCGCTG 1
>lcl|Amplicon 256 non-redundant amplicon of 19 matches
Length=73
Score = 123 bits (136), Expect = 2e-29
Identities = 71/73 (97%), Gaps = 0/73 (0%)
Strand=Plus/Minus
Score = 123 bits (136), Expect = 2e-29
Identities = 71/73 (97%), Gaps = 0/73 (0%)
Strand=Plus/Minus

```

```

Query 91 ACCGGTTACACCCCCATCGACATCTCCCTCTCCCTCACGCAGTTCCTGCTCAGCGAGTTC 150
|||||
Sbjct 73 ACCGGTTACTCCCATCGACATCTCCCTCTCCCTCACGCAGTTCCTGCTCAGCGAGTTC 14
Query 151 GTGCCAGGCGCTG 163
|||||

```

```

Sbjct 13 GTGCCAGGTGCTG 1
>lcl|Amplicon 40 non-redundant amplicon of 223 matches
Length=73
Score = 96.9 bits (106), Expect = 2e-21
Identities = 65/73 (89%), Gaps = 0/73 (0%)
Strand=Plus/Minus

```

```

Query 91 ACCGGTTACACCCCCATCGACATCTCCCTCTCCCTCACGCAGTTCCTGCTCAGCGAGTTC 150
|||||
Sbjct 73 ACCGGTTACTCCCATCGACATCTCCTTGCTCCTTGACACAGTTTCTGCTCAGCGAGTTC 14
Query 151 GTGCCAGGCGCTG 163
|||||

```

```

Sbjct 13 GTGCCAGGTGCTG 1
>lcl|Amplicon 395 non-redundant amplicon of 14 matches
Length=73

```

```

Score = 96.9 bits (106), Expect = 2e-21
Identities = 65/73 (89%), Gaps = 0/73 (0%)
Strand=Plus/Minus

```

```

Query 91 ACCGGTTACACCCCCATCGACATCTCCCTCTCCCTCACGCAGTTCCTGCTCAGCGAGTTC 150
|||||
Sbjct 73 ACCGGTTACTCCCATCGACATCTCCTTGCTCCTTGACACAGTTTCTGCTCAGCGAGTTC 14
Query 151 GTGCCAGGCGCTG 163
|||||

```

```

Sbjct 13 GTGCCAGGAGCTG 1
>lcl|Amplicon 496 non-redundant amplicon of 1 matches
Length=74

```

```

Score = 89.7 bits (98), Expect = 3e-19
Identities = 64/74 (86%), Gaps = 0/74 (0%)
Strand=Plus/Plus

```

```

Query 382 GAGGAGATGCGCATCCAGTTCAACGACATGAACAGCGCCCTGACCACCGCCATCCCCTC 441
|||||
Sbjct 1 GAGGAGATGCGTATTCAATTCAACGATATGAACAGCGCCTTGACCACAGCTATCCCATTG 60
Query 442 TTCGCCGTCCAGAA 455
|||||

```

```

Sbjct 61 TTCGCAGTCCAGAA 74
>lcl|Amplicon 41 non-redundant amplicon of 214 matches
Length=74

```

```

Score = 89.7 bits (98), Expect = 3e-19
Identities = 64/74 (86%), Gaps = 0/74 (0%)
Strand=Plus/Plus

```

```

Query 382 GAGGAGATGCGCATCCAGTTCAACGACATGAACAGCGCCCTGACCACCGCCATCCCCTC 441
|||||
Sbjct 1 GAGGAAATGCGTATTCAATTCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATTG 60
Query 382 GAGGAGATGCGCATCCAGTTCAACGACATGAACAGCGCCCTGACCACCGCCATCCCCTC 441
|||||

```

```

Sbjct 1 GAGGAAATGCGTATTCAATTCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATTG 60
Query 442 TTCGCCGTCCAGAA 455
|||||

```

```

Sbjct 61 TTCGCAGTCCAGAA 74
>lcl|Amplicon 170 non-redundant amplicon of 26 matches
Length=127

```

```

Score = 87.8 bits (96), Expect = 1e-18
Identities = 71/86 (83%), Gaps = 0/86 (0%)
Strand=Plus/Plus

```

```

Query 1 ATGGACAACAACCCAAACATCAACGAGTGCATCCCGTACAACAGCCTCAGCAACCCTGAG 60

```

```

Sbjct 40  |||...||| 99
Query 61  GTCGAGGTGCTCGGCCGGTGAGCGCAT 86
Sbjct 100 GTTGAAGTACTTGGTGGGAGAACGCAT 125
>lcl|Amplicon 177 non-redundant amplicon of 20 matches
Length=73

```

```

Score = 87.8 bits (96), Expect = 1e-18
Identities = 63/73 (86%), Gaps = 0/73 (0%)
Strand=Plus/Minus
Query 91  ACCGGTTACACCCCCATCGACATCTCCCTCTCCCTCACGCAGTTCCTGCTCAGCGAGTTC 150
Sbjct 73  ACCGGTTACACCCCCATCGACATCAGCCTGAGCCTGACCCAGTTCCTGCTGAGCGAGTTC 14
Query 151 GTGCCAGGCGCTG 163

```

```

Sbjct 13  GTGCCTGGTGCTG 1
>lcl|Amplicon 446 non-redundant amplicon of 2 matches Length=74
Score = 86.0 bits (94), Expect = 4e-18
Identities = 62/72 (86%), Gaps = 0/72 (0%)
Strand=Plus/Plus
Query 384 GGAGATGCGCATCCAGTTCACGACATGAACAGCGCCCTGACCACCGCCATCCCCTCTT 443
Sbjct 3  GGAAATGCGTATTCAATTCACGACATGAACAGCGCCTTGACCACAGCTATCCCATTGTT 62
Query 444 CGCCGTCCAGAA 455
Sbjct 63  CGCAGTCCAGAA 74

```

```

>lcl|Amplicon 96 non-redundant amplicon of 7 matches Length=72
Score = 82.4 bits (90), Expect = 5e-17
Identities = 45/45 (100%), Gaps = 0/45 (0%)
Strand=Plus/Plus
Query 2643 AGCAGAGAAGAAGTGGAGGGACAAACGTGAGAAACTCGAATGGGA 2687
Sbjct 28  AGCAGAGAAGAAGTGGAGGGACAAACGTGAGAAACTCGAATGGGA 72
Sbjct 28  AGCAGAGAAGAAGTGGAGGGACAAACGTGAGAAACTCGAATGGGA 72

```

```

>lcl|Amplicon 603 non-redundant amplicon of 8 matches
Length=83
Score = 64.4 bits (70), Expect = 1e-11
Identities = 44/50 (88%), Gaps = 0/50 (0%)
Strand=Plus/Plus
Query 1795 ATCGACAGGTTTGAATTGATTCCAGTTACTGCAACCCTCGAGGCTGAGTA 1844
Sbjct 17  ATCGACAGATTTCGAGTTTCATTCAGTTACTGCAACACTCGAGGCTGAATA 66

```

```

>lcl|Amplicon 168 non-redundant amplicon of 21 matches
Length=113
Score = 62.6 bits (68), Expect = 5e-11
Identities = 34/34 (100%), Gaps = 0/34 (0%)
Strand=Plus/Plus
Query 1  ATGGACAACAACCCAAACATCAACGAGTGCATCC 34
Sbjct 80  ATGGACAACAACCCAAACATCAACGAGTGCATCC 113
Lambda K H
0.634 0.408 0.912
Gapped
Lambda K H
0.625 0.410 0.780
Effective search space used: 337114506

```

Query= cry1Ab_synthetic_construct_-_AX392802.1
Length=3582

Sequences producing significant alignments:	Score (Bits)	E Value
lcl Amplicon_335 non-redundant amplicon of 3 matches	<u>233</u>	1e-62
lcl Amplicon_5 non-redundant amplicon of 285 matches	<u>233</u>	1e-62
lcl Amplicon_553 non-redundant amplicon of 1 matches	<u>215</u>	4e-57
lcl Amplicon_176 non-redundant amplicon of 20 matches	<u>201</u>	8e-53
lcl Amplicon_331 non-redundant amplicon of 7 matches	<u>163</u>	2e-41
lcl Amplicon_177 non-redundant amplicon of 20 matches	<u>114</u>	9e-27
lcl Amplicon_747 non-redundant amplicon of 2 matches	<u>113</u>	3e-26
lcl Amplicon_169 non-redundant amplicon of 10 matches	<u>113</u>	3e-26

lcl Amplicon_368	non-redundant amplicon of 3 matches	<u>107</u>	1e-24
lcl Amplicon_170	non-redundant amplicon of 26 matches	<u>87.8</u>	1e-18
lcl Amplicon_496	non-redundant amplicon of 1 matches	<u>84.2</u>	1e-17
lcl Amplicon_72	non-redundant amplicon of 36 matches	<u>84.2</u>	1e-17
lcl Amplicon_41	non-redundant amplicon of 214 matches	<u>84.2</u>	1e-17
lcl Amplicon_446	non-redundant amplicon of 2 matches	<u>80.6</u>	2e-16
lcl Amplicon_256	non-redundant amplicon of 19 matches	<u>75.2</u>	8e-15
lcl Amplicon_40	non-redundant amplicon of 223 matches	<u>69.8</u>	3e-13
lcl Amplicon_395	non-redundant amplicon of 14 matches	<u>69.8</u>	3e-13

>[lcl|Amplicon_335 non-redundant amplicon of 3 matches](#)

Length=212

Score = 233 bits (258), Expect = 1e-62
 Identities = 129/129 (100%), Gaps = 0/129 (0%)
 Score = 233 bits (258), Expect = 1e-62
 Identities = 129/129 (100%), Gaps = 0/129 (0%)
 Strand=Plus/Plus

```

Query 1 ATGGACAACAACCCCAACATCAACGAGTGCATCCCCTACAACCTGCCTGAGCAACCCCGAG 60
      |||
Sbjct 84 ATGGACAACAACCCCAACATCAACGAGTGCATCCCCTACAACCTGCCTGAGCAACCCCGAG 143
Query 61 GTGGAGGTGCTGGGCGGCGAGCGCATCGAGACCGGCTACACCCCATCGACATCAGCCTG 120
      |||
Sbjct 144 GTGGAGGTGCTGGGCGGCGAGCGCATCGAGACCGGCTACACCCCATCGACATCAGCCTG 203
Query 121 AGCCTGACC 129
      |||
Sbjct 204 AGCCTGACC 212
  
```

>[lcl|Amplicon_5 non-redundant amplicon of 285 matches](#)

Length=129

Score = 233 bits (258), Expect = 1e-62
 Identities = 129/129 (100%), Gaps = 0/129 (0%)
 Strand=Plus/Plus

```

Query 103 CCCATCGACATCAGCCTGAGCCTGACCCAGTTCCTGCTGAGCGAGTTCGTGCCCGGCGCC 162
      |||
Sbjct 1 CCCATCGACATCAGCCTGAGCCTGACCCAGTTCCTGCTGAGCGAGTTCGTGCCCGGCGCC 60
Query 163 GGCTTCGTGCTGGGCCTGGTGGACATCATCTGGGGCATCTTCGGCCCCAGCCAGTGGGAC 222
      |||
Sbjct 61 GGCTTCGTGCTGGGCCTGGTGGACATCATCTGGGGCATCTTCGGCCCCAGCCAGTGGGAC 120
Query 223 GCCTTCCTG 231
      |||
Sbjct 121 GCCTTCCTG 129
  
```

>[lcl|Amplicon_553 non-redundant amplicon of 1 matches](#)

Length=129

Score = 215 bits (238), Expect = 4e-57
 Identities = 125/129 (97%), Gaps = 0/129 (0%)
 Strand=Plus/Plus

```

Query 103 CCCATCGACATCAGCCTGAGCCTGACCCAGTTCCTGCTGAGCGAGTTCGTGCCCGGCGCC 162
      |||
Sbjct 1 CCGATTGACATCAGCCTGAGCCTGACCCAGTTCCTGCTGAGCGAGTTCGTGCCCGGCGCC 60
Query 163 GGCTTCGTGCTGGGCCTGGTGGACATCATCTGGGGCATCTTCGGCCCCAGCCAGTGGGAC 222
      |||
Sbjct 61 GGCTTCGTGCTGGGCCTGGTGGACATCATCTGGGGCATCTTCGGCCCCAGCCAGTGGGAC 120
Query 223 GCCTTCCTG 231
      |||
Sbjct 121 GCCTTCCTG 129
  
```

>[lcl|Amplicon_176 non-redundant amplicon of 20 matches](#)

Length=129

Score = 201 bits (222), Expect = 8e-53
 Identities = 122/129 (95%), Gaps = 0/129 (0%)
 Strand=Plus/Plus

```

Query 103 CCCATCGACATCAGCCTGAGCCTGACCCAGTTCCTGCTGAGCGAGTTCGTGCCCGGCGCC 162
      |||
Sbjct 1 CCCATCGACATCAGCCTGAGCCTGACCCAGTTCCTGCTGAGCGAGTTCGTGCCCGGCGCC 60
Query 163 GGCTTCGTGCTGGGCCTGGTGGACATCATCTGGGGCATCTTCGGCCCCAGCCAGTGGGAC 222
      |||
Sbjct 1 CCCATCGACATCAGCCTGAGCCTGACCCAGTTCCTGCTGAGCGAGTTCGTGCCCGGCGCC 60
Query 163 GGCTTCGTGCTGGGCCTGGTGGACATCATCTGGGGCATCTTCGGCCCCAGCCAGTGGGAC 222
      |||
Sbjct 61 GGCTTCGTGCTGGGACTAGTGGACATCATCTGGGGCATCTTCGGTCCCAGCCAGTGGGAT 120
Query 223 GCCTTCCTG 231
      |||
  
```



```

          ||||| || ||
Sbjct 64 GCAGTCCAGAA 74
>lcl|Amplicon 41 non-redundant amplicon of 214 matches
Length=74
  Score = 66.2 bits (72), Expect = 5e-12
  Identities = 59/74 (80%), Gaps = 0/74 (0%)
  Strand=Plus/Plus
Query 769 GAAGAGATGCGTATTCAATTCAATGACATGAACAGTGCCCTTACAACCGCTATTCTCTT 828
          || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1 GAGGAAATGCGTATTCAATTCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATTG 60
Query 829 TTTGCAGTTCAAAA 842
          || ||||| || ||
Sbjct 61 TTCGCAGTCCAGAA 74
Lambda K H
  0.634 0.408 0.912
Gapped
Lambda K H
  0.625 0.410 0.780
Effective search space used: 395289628
Effective search space used: 395289628

```

Query= cry1F_Bacillus_thuringiensis_-EU679501.1

```

Length=3525
***** No hits found *****
Lambda K H
  0.634 0.408 0.912
Gapped
Lambda K H
  0.625 0.410 0.780
Effective search space used: 336250848

```

Query= cry2Ab2_Bacillus_thuringiensis_serovar_kurstaki_-JN415485.1

```

Length=1902
***** No hits found *****
Lambda K H
  0.634 0.408 0.912
Gapped
Lambda K H
  0.625 0.410 0.780
Effective search space used: 180504522

```

Query= cry3A_Bacillus_thuringiensis_serovar_tenebrionis_-EU332160.1

```

Length=1952
***** No hits found *****
Lambda K H
  0.634 0.408 0.912
Gapped
Lambda K H
  0.625 0.410 0.780
Effective search space used: 185302622

```

Query= cry3Bb1_Bacillus_thuringiensis_-M89794.1

```

Length=2277
***** No hits found *****
Lambda K H
  0.634 0.408 0.912
Gapped
Lambda K H
  0.625 0.410 0.780
Effective search space used: 216490272

```

Query= gat4621_Bacillus_licheniformis_WX-02_-CP012110.1

```

Length=441
***** No hits found *****
Lambda K H
  0.634 0.408 0.912
Gapped
Lambda K H
  0.625 0.410 0.780
Effective search space used: 41212520

```


Query= gox_Ochrobactrum_sp._G-1_-_GU214711.1

Length=1296

***** No hits found *****

Lambda	K	H
0.634	0.408	0.912

Gapped

Lambda	K	H
0.625	0.410	0.780

Effective search space used: 123530836

Query= GUS_Escherichia_coli_-_M14641.1

Length=7742

***** No hits found *****

***** No hits found *****

Lambda	K	H
0.634	0.408	0.912

Gapped

Lambda	K	H
0.625	0.410	0.780

Effective search space used: 734272360

Query= manA_Escherichia_coli_-_M15380.1

Length=1604

***** No hits found *****

Lambda	K	H
0.634	0.408	0.912

Gapped

Lambda	K	H
0.625	0.410	0.780

Effective search space used: 153348624

Query= nptII_Escherichia_coli_-_V00618.1

Length=1300

Sequences producing significant alignments:

	Score (Bits)	E Value
lcl Amplicon_6 non-redundant amplicon of 57587 matches	<u>389</u>	1e-109
lcl Amplicon_113 non-redundant amplicon of 5 matches	<u>385</u>	1e-108
lcl Amplicon_55 non-redundant amplicon of 814 matches	<u>385</u>	1e-108
lcl Amplicon_604 non-redundant amplicon of 1 matches	<u>383</u>	4e-108
lcl Amplicon_262 non-redundant amplicon of 8 matches	<u>383</u>	4e-108
lcl Amplicon_402 non-redundant amplicon of 9 matches	<u>383</u>	4e-108
lcl Amplicon_769 non-redundant amplicon of 1 matches	<u>383</u>	4e-108
lcl Amplicon_745 non-redundant amplicon of 2 matches	<u>383</u>	4e-108
lcl Amplicon_436 non-redundant amplicon of 3 matches	<u>383</u>	4e-108
lcl Amplicon_580 non-redundant amplicon of 3 matches	<u>383</u>	4e-108
lcl Amplicon_590 non-redundant amplicon of 2 matches	<u>383</u>	4e-108
lcl Amplicon_573 non-redundant amplicon of 1 matches	<u>383</u>	4e-108
lcl Amplicon_571 non-redundant amplicon of 1 matches	<u>383</u>	4e-108
lcl Amplicon_75 non-redundant amplicon of 5 matches	<u>383</u>	4e-108
lcl Amplicon_534 non-redundant amplicon of 22 matches	<u>383</u>	4e-108
lcl Amplicon_516 non-redundant amplicon of 4 matches	<u>383</u>	4e-108
lcl Amplicon_274 non-redundant amplicon of 5 matches	<u>383</u>	4e-108
lcl Amplicon_280 non-redundant amplicon of 6 matches	<u>383</u>	4e-108
lcl Amplicon_195 non-redundant amplicon of 156 matches	<u>383</u>	4e-108
lcl Amplicon_62 non-redundant amplicon of 186 matches	<u>383</u>	4e-108
lcl Amplicon_343 non-redundant amplicon of 5 matches	<u>383</u>	4e-108
lcl Amplicon_342 non-redundant amplicon of 8 matches	<u>383</u>	4e-108
lcl Amplicon_34 non-redundant amplicon of 41 matches	<u>383</u>	4e-108
lcl Amplicon_241 non-redundant amplicon of 20 matches	<u>383</u>	4e-108
lcl Amplicon_20 non-redundant amplicon of 179 matches	<u>383</u>	4e-108
lcl Amplicon_788 non-redundant amplicon of 1 matches	<u>381</u>	1e-107
lcl Amplicon_34 non-redundant amplicon of 41 matches	<u>383</u>	4e-108
lcl Amplicon_241 non-redundant amplicon of 20 matches	<u>383</u>	4e-108
lcl Amplicon_20 non-redundant amplicon of 179 matches	<u>383</u>	4e-108
lcl Amplicon_788 non-redundant amplicon of 1 matches	<u>381</u>	1e-107
lcl Amplicon_628 non-redundant amplicon of 1 matches	<u>381</u>	1e-107
lcl Amplicon_294 non-redundant amplicon of 8 matches	<u>379</u>	5e-107
lcl Amplicon_386 non-redundant amplicon of 3 matches	<u>379</u>	5e-107
lcl Amplicon_384 non-redundant amplicon of 3 matches	<u>379</u>	5e-107
lcl Amplicon_432 non-redundant amplicon of 8 matches	<u>379</u>	5e-107
lcl Amplicon_413 non-redundant amplicon of 14 matches	<u>379</u>	5e-107
lcl Amplicon_401 non-redundant amplicon of 2 matches	<u>304</u>	3e-84

lcl Amplicon_775	non-redundant	amplicon	of 1 matches	379	5e-107
lcl Amplicon_638	non-redundant	amplicon	of 1 matches	379	5e-107
lcl Amplicon_637	non-redundant	amplicon	of 1 matches	379	5e-107
lcl Amplicon_636	non-redundant	amplicon	of 1 matches	379	5e-107
lcl Amplicon_635	non-redundant	amplicon	of 2 matches	379	5e-107
lcl Amplicon_633	non-redundant	amplicon	of 1 matches	379	5e-107
lcl Amplicon_627	non-redundant	amplicon	of 3 matches	379	5e-107
lcl Amplicon_400	non-redundant	amplicon	of 3 matches	379	5e-107
lcl Amplicon_282	non-redundant	amplicon	of 18 matches	379	5e-107
lcl Amplicon_570	non-redundant	amplicon	of 1 matches	379	5e-107
lcl Amplicon_568	non-redundant	amplicon	of 1 matches	379	5e-107
lcl Amplicon_566	non-redundant	amplicon	of 1 matches	379	5e-107
lcl Amplicon_347	non-redundant	amplicon	of 6 matches	379	5e-107
lcl Amplicon_393	non-redundant	amplicon	of 3 matches	379	5e-107
lcl Amplicon_444	non-redundant	amplicon	of 2 matches	378	2e-106
lcl Amplicon_754	non-redundant	amplicon	of 1 matches	378	2e-106
lcl Amplicon_309	non-redundant	amplicon	of 7 matches	378	2e-106
lcl Amplicon_345	non-redundant	amplicon	of 3 matches	376	6e-106
lcl Amplicon_407	non-redundant	amplicon	of 3 matches	376	6e-106
lcl Amplicon_610	non-redundant	amplicon	of 1 matches	374	2e-105
lcl Amplicon_536	non-redundant	amplicon	of 1 matches	374	2e-105
lcl Amplicon_356	non-redundant	amplicon	of 3 matches	374	2e-105
lcl Amplicon_221	non-redundant	amplicon	of 8 matches	374	2e-105
lcl Amplicon_767	non-redundant	amplicon	of 1 matches	370	3e-104
lcl Amplicon_480	non-redundant	amplicon	of 3 matches	370	3e-104
lcl Amplicon_423	non-redundant	amplicon	of 7 matches	370	3e-104
lcl Amplicon_784	non-redundant	amplicon	of 1 matches	367	3e-103
lcl Amplicon_63	non-redundant	amplicon	of 9 matches	365	1e-102
lcl Amplicon_770	non-redundant	amplicon	of 1 matches	361	1e-101
lcl Amplicon_8	non-redundant	amplicon	of 150 matches	361	1e-101
lcl Amplicon_765	non-redundant	amplicon	of 1 matches	349	9e-98
lcl Amplicon_136	non-redundant	amplicon	of 17 matches	347	3e-97
lcl Amplicon_160	non-redundant	amplicon	of 7 matches	343	4e-96
lcl Amplicon_786	non-redundant	amplicon	of 1 matches	334	2e-93
lcl Amplicon_756	non-redundant	amplicon	of 1 matches	329	8e-92
lcl Amplicon_7	non-redundant	amplicon	of 58045 matches	313	6e-87
lcl Amplicon_763	non-redundant	amplicon	of 1 matches	309	8e-86
lcl Amplicon_752	non-redundant	amplicon	of 1 matches	309	8e-86
lcl Amplicon_114	non-redundant	amplicon	of 5 matches	309	8e-86
lcl Amplicon_433	non-redundant	amplicon	of 8 matches	307	3e-85
lcl Amplicon_746	non-redundant	amplicon	of 2 matches	307	3e-85
lcl Amplicon_639	non-redundant	amplicon	of 1 matches	307	3e-85
lcl Amplicon_437	non-redundant	amplicon	of 3 matches	307	3e-85
lcl Amplicon_634	non-redundant	amplicon	of 1 matches	307	3e-85
lcl Amplicon_611	non-redundant	amplicon	of 1 matches	307	3e-85
lcl Amplicon_572	non-redundant	amplicon	of 1 matches	307	3e-85
lcl Amplicon_535	non-redundant	amplicon	of 22 matches	307	3e-85
lcl Amplicon_517	non-redundant	amplicon	of 4 matches	307	3e-85
lcl Amplicon_275	non-redundant	amplicon	of 5 matches	307	3e-85
lcl Amplicon_281	non-redundant	amplicon	of 6 matches	307	3e-85
lcl Amplicon_172	non-redundant	amplicon	of 47 matches	307	3e-85
lcl Amplicon_196	non-redundant	amplicon	of 156 matches	307	3e-85
lcl Amplicon_414	non-redundant	amplicon	of 14 matches	307	3e-85
lcl Amplicon_344	non-redundant	amplicon	of 5 matches	307	3e-85
lcl Amplicon_348	non-redundant	amplicon	of 8 matches	307	3e-85
lcl Amplicon_35	non-redundant	amplicon	of 41 matches	307	3e-85
lcl Amplicon_242	non-redundant	amplicon	of 11 matches	307	3e-85
lcl Amplicon_21	non-redundant	amplicon	of 187 matches	307	3e-85
lcl Amplicon_776	non-redundant	amplicon	of 1 matches	306	9e-85
lcl Amplicon_768	non-redundant	amplicon	of 1 matches	306	9e-85
lcl Amplicon_21	non-redundant	amplicon	of 187 matches	307	3e-85
lcl Amplicon_776	non-redundant	amplicon	of 1 matches	306	9e-85
lcl Amplicon_768	non-redundant	amplicon	of 1 matches	306	9e-85
lcl Amplicon_401	non-redundant	amplicon	of 3 matches	304	3e-84
lcl Amplicon_387	non-redundant	amplicon	of 3 matches	304	3e-84
lcl Amplicon_385	non-redundant	amplicon	of 3 matches	304	3e-84
lcl Amplicon_581	non-redundant	amplicon	of 3 matches	304	3e-84
lcl Amplicon_569	non-redundant	amplicon	of 1 matches	304	3e-84
lcl Amplicon_567	non-redundant	amplicon	of 1 matches	304	3e-84
lcl Amplicon_283	non-redundant	amplicon	of 18 matches	304	3e-84
lcl Amplicon_295	non-redundant	amplicon	of 8 matches	304	3e-84

lcl Amplicon_394	non-redundant	amplicon of 3 matches	<u>304</u>	3e-84
lcl Amplicon_445	non-redundant	amplicon of 2 matches	<u>302</u>	1e-83
lcl Amplicon_357	non-redundant	amplicon of 3 matches	<u>302</u>	1e-83
lcl Amplicon_757	non-redundant	amplicon of 1 matches	<u>298</u>	1e-82
lcl Amplicon_537	non-redundant	amplicon of 1 matches	<u>298</u>	1e-82
lcl Amplicon_771	non-redundant	amplicon of 1 matches	<u>297</u>	5e-82
lcl Amplicon_471	non-redundant	amplicon of 1 matches	<u>297</u>	5e-82
lcl Amplicon_424	non-redundant	amplicon of 7 matches	<u>295</u>	2e-81
lcl Amplicon_764	non-redundant	amplicon of 1 matches	<u>293</u>	6e-81
lcl Amplicon_787	non-redundant	amplicon of 1 matches	<u>289</u>	7e-80
lcl Amplicon_773	non-redundant	amplicon of 1 matches	<u>289</u>	7e-80
lcl Amplicon_64	non-redundant	amplicon of 9 matches	<u>289</u>	7e-80
lcl Amplicon_161	non-redundant	amplicon of 7 matches	<u>277</u>	4e-76
lcl Amplicon_137	non-redundant	amplicon of 17 matches	<u>273</u>	5e-75
lcl Amplicon_650	non-redundant	amplicon of 1 matches	<u>262</u>	1e-71
lcl Amplicon_472	non-redundant	amplicon of 1 matches	<u>244</u>	3e-66
lcl Amplicon_783	non-redundant	amplicon of 1 matches	<u>241</u>	3e-65
lcl Amplicon_755	non-redundant	amplicon of 1 matches	<u>219</u>	1e-58
lcl Amplicon_186	non-redundant	amplicon of 4 matches	<u>208</u>	2e-55
lcl Amplicon_778	non-redundant	amplicon of 1 matches	<u>197</u>	3e-52
lcl Amplicon_779	non-redundant	amplicon of 1 matches	<u>174</u>	4e-45
lcl Amplicon_753	non-redundant	amplicon of 1 matches	<u>163</u>	7e-42
lcl Amplicon_421	non-redundant	amplicon of 4 matches	<u>161</u>	2e-41
lcl Amplicon_777	non-redundant	amplicon of 1 matches	<u>152</u>	1e-38
lcl Amplicon_772	non-redundant	amplicon of 1 matches	<u>150</u>	4e-38

>[lcl|Amplicon 6 non-redundant amplicon of 57587 matches](#)

Length=215

Score = 389 bits (430), Expect = 1e-109

Identities = 215/215 (100%), Gaps = 0/215 (0%)

Strand=Plus/Plus

```

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
          |||
Sbjct 1   CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
          |||
Sbjct 61   CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
          |||
Sbjct 121  GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
          |||
Sbjct 181  TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215
    
```

>[lcl|Amplicon 113 non-redundant amplicon of 5 matches](#)

Length=215

Score = 385 bits (426), Expect = 1e-108

Identities = 214/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

```

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
          |||
Sbjct 1   CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
          |||
Sbjct 61   CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
          |||
Sbjct 121  GTACTCGRATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
          |||
Sbjct 181  TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215
    
```

>[lcl|Amplicon 55 non-redundant amplicon of 814 matches](#)

Length=215

Score = 385 bits (426), Expect = 1e-108

Identities = 213/213 (100%), Gaps = 0/213 (0%)

Strand=Plus/Plus

```

Query 466 CACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACG 525
          |||
Sbjct 3   CACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACG 62
    
```

Query 526 CTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGT 585
 |||
 Sbjct 63 CTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGT 122
 Query 586 ACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTC 645
 |||
 Sbjct 123 ACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTC 182
 Query 646 GCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 183 GCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon_604 non-redundant amplicon of 1 matches](#)

Length=215

Score = 383 bits (424), Expect = 4e-108

Identities = 214/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGGAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon_262 non-redundant amplicon of 8 matches](#)

Length=215

>[lcl|Amplicon_262 non-redundant amplicon of 8 matches](#)

Length=215

Score = 383 bits (424), Expect = 4e-108

Identities = 214/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCACGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon_402 non-redundant amplicon of 9 matches](#)

Length=215

Score = 383 bits (424), Expect = 4e-108

Identities = 214/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon_769 non-redundant amplicon of 1 matches](#)

Length=215

Score = 383 bits (424), Expect = 4e-108

Identities = 212/212 (100%), Gaps = 0/212 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523

>lcl|Amplicon 590 non-redundant amplicon of 2 matches

Length=215

Score = 383 bits (424), Expect = 4e-108

Identities = 214/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>lcl|Amplicon 573 non-redundant amplicon of 1 matches

Length=215

Score = 383 bits (424), Expect = 4e-108

Identities = 214/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
Sbjct 181 CCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>lcl|Amplicon 571 non-redundant amplicon of 1 matches

Length=215

Score = 383 bits (424), Expect = 4e-108

Identities = 214/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>lcl|Amplicon 75 non-redundant amplicon of 5 matches

Length=215

Score = 383 bits (424), Expect = 4e-108

Identities = 214/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678

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Sbjct 181 TCGCGCCAGCCGAACTGTTCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 215
>lcl|Amplicon 534 non-redundant amplicon of 22 matches
Length=215
Score = 383 bits (424), Expect = 4e-108
Identities = 214/215 (99%), Gaps = 0/215 (0%)
Strand=Plus/Plus
Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 523
|||||
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|||||
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
|
Sbjct 121 GCACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAACTGTTCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 678
|||||

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Sbjct 181 TCGCGCCAGCCGAACTGTTCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 215
>lcl|Amplicon 516 non-redundant amplicon of 4 matches
Length=215
Score = 383 bits (424), Expect = 4e-108
Identities = 214/215 (99%), Gaps = 0/215 (0%)
Strand=Plus/Plus
Score = 383 bits (424), Expect = 4e-108
Identities = 214/215 (99%), Gaps = 0/215 (0%)
Strand=Plus/Plus
Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 523
|||||
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|||||
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
|
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAACTGTTCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 678
|||||

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Sbjct 181 TCGCGCCAGCCGAACTGTTCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 215
>lcl|Amplicon 274 non-redundant amplicon of 5 matches
Length=215
Score = 383 bits (424), Expect = 4e-108
Identities = 214/215 (99%), Gaps = 0/215 (0%)
Strand=Plus/Plus
Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 523
|||||
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|||||
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
|
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATCATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAACTGTTCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 678
|||||

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Sbjct 181 TCGCGCCAGCCGAACTGTTCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 215
>lcl|Amplicon 280 non-redundant amplicon of 6 matches
Length=215
Score = 383 bits (424), Expect = 4e-108
Identities = 214/215 (99%), Gaps = 0/215 (0%)
Strand=Plus/Plus
Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 523
|||||
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|||||
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCYC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643

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|||||
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 678
|||||
Sbjct 181 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 215
>lcl|Amplicon_195 non-redundant amplicon of 156 matches
Sbjct 181 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 215
>lcl|Amplicon_195 non-redundant amplicon of 156 matches
Length=215
Score = 383 bits (424), Expect = 4e-108
Identities = 214/215 (99%), Gaps = 0/215 (0%)
Strand=Plus/Plus
Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
|||||
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|||||
Sbjct 61 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGGGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
|||||
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 678
|||||
Sbjct 181 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 215
>lcl|Amplicon_62 non-redundant amplicon of 186 matches
Length=215
Score = 383 bits (424), Expect = 4e-108
Identities = 214/215 (99%), Gaps = 0/215 (0%)
Strand=Plus/Plus
Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
|||||
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|||||
Sbjct 61 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
|||||
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAACATCAGGGGC 180
Query 644 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 678
|||||
Sbjct 181 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 215
>lcl|Amplicon_343 non-redundant amplicon of 5 matches
Length=215
Score = 383 bits (424), Expect = 4e-108
Identities = 214/215 (99%), Gaps = 0/215 (0%)
Strand=Plus/Plus
Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
|||||
Sbjct 1 CTCATCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|||||
Sbjct 61 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
|||||
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 678
|||||
Sbjct 181 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 215
>lcl|Amplicon_342 non-redundant amplicon of 8 matches
Length=215
Score = 383 bits (424), Expect = 4e-108
Identities = 214/215 (99%), Gaps = 0/215 (0%)
Strand=Plus/Plus
Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
|||||

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Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAGGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon_34 non-redundant amplicon of 41 matches](#)

Length=215

Score = 383 bits (424), Expect = 4e-108
 Identities = 214/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGGAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon_241 non-redundant amplicon of 20 matches](#)

Length=215

Score = 383 bits (424), Expect = 4e-108
 Identities = 214/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCAATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon_20 non-redundant amplicon of 179 matches](#)

Length=215

Score = 383 bits (424), Expect = 4e-108
 Identities = 214/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCGCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon_788 non-redundant amplicon of 1 matches](#)

Length=216

Score = 381 bits (422), Expect = 1e-107
 Identities = 215/216 (99%), Gaps = 1/216 (0%)

Strand=Plus/Plus
 Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCA-GGGG 642
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGG 180
 Query 643 CTCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 CTCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 216
[>lcl|Amplicon 628 non-redundant amplicon of 1 matches](#)

Length=215
 Score = 381 bits (422), Expect = 1e-107
 Identities = 213/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus
 Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAACCGAAGTTCGCCANGCTCAAGGCG 215

[>lcl|Amplicon 294 non-redundant amplicon of 8 matches](#)

Length=215
 Score = 379 bits (420), Expect = 5e-107
 Identities = 213/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus
 Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTGTCCATCATGGCTGATGCAATACGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

[>lcl|Amplicon 386 non-redundant amplicon of 3 matches](#)

Length=215
 Score = 379 bits (420), Expect = 5e-107
 Identities = 213/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus
 Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTACACATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

[>lcl|Amplicon 384 non-redundant amplicon of 3 matches](#)

Length=215

Score = 379 bits (420), Expect = 5e-107
>[lcl|Amplicon 384 non-redundant amplicon of 3 matches](#)

Length=215

Score = 379 bits (420), Expect = 5e-107
Identities = 213/215 (99%), Gaps = 0/215 (0%)
Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
|
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
|
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATTGGGATGATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 678
|
Sbjct 181 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon 432 non-redundant amplicon of 8 matches](#)

Length=215

Score = 379 bits (420), Expect = 5e-107
Identities = 213/215 (99%), Gaps = 0/215 (0%)
Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
|
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
|
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTCTCGATCAGGATGATCTGGACGAAGAACATCAGGGGC 180
Query 644 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 678
|
Sbjct 181 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon 413 non-redundant amplicon of 14 matches](#)

Length=215

Score = 379 bits (420), Expect = 5e-107
Identities = 213/215 (99%), Gaps = 0/215 (0%)
Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
|
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|
Sbjct 61 CGCTTGATCCGGCTACATGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
|
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAGGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 678
|
Sbjct 181 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 215
Query 644 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 678
|
Sbjct 181 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon 775 non-redundant amplicon of 1 matches](#)

Length=215

Score = 379 bits (420), Expect = 5e-107
Identities = 214/215 (99%), Gaps = 1/215 (0%)
Strand=Plus/Plus

Query 465 TCACCTTGCTCC-TGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
|
Sbjct 1 TCACCTTGCTCCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
|

Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215
 >[lcl|Amplicon 638 non-redundant amplicon of 1 matches](#)
 Length=215
 Score = 379 bits (420), Expect = 5e-107
 Identities = 213/215 (99%), Gaps = 0/215 (0%)
 Strand=Plus/Plus
 Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGTTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCAGGACGAAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon 637 non-redundant amplicon of 1 matches](#)
 Length=215
 Score = 379 bits (420), Expect = 5e-107
 Identities = 212/213 (99%), Gaps = 0/213 (0%)
 Strand=Plus/Plus
 Query 466 CACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACG 525
 |||
 Sbjct 3 CACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCAGCTGCATACG 62
 Query 526 CTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGT 585
 |||
 Sbjct 63 CTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGT 122
 Query 586 ACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTC 645
 |||
 Sbjct 123 ACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTC 182
 Query 586 ACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTC 645
 |||
 Sbjct 123 ACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTC 182
 Query 646 GCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 183 GCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon 636 non-redundant amplicon of 1 matches](#)
 Length=215
 Score = 379 bits (420), Expect = 5e-107
 Identities = 212/213 (99%), Gaps = 0/213 (0%)
 Strand=Plus/Plus
 Query 466 CACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACG 525
 |||
 Sbjct 3 CACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACG 62
 Query 526 CTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGT 585
 |||
 Sbjct 63 CTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGT 122
 Query 586 ACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTC 645
 |||
 Sbjct 123 ACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGGCGAAGAGCATCAGGGGCTC 182
 Query 646 GCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 183 GCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon 635 non-redundant amplicon of 2 matches](#)
 Length=215
 Score = 379 bits (420), Expect = 5e-107
 Identities = 212/213 (99%), Gaps = 0/213 (0%)
 Strand=Plus/Plus
 Query 466 CACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACG 525
 |||
 Sbjct 3 CACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACG 62
 Query 526 CTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGT 585
 |||

Sbjct 63 CTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGT 122
 Query 586 ACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTC 645
 |||
 Sbjct 123 ACTCGGATGGAAGCCGGTCTTGTGCGATCAAGATGATCTGGACGAAGAGCATCAGGGGCTC 182
 Query 646 GCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 183 GCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon 633 non-redundant amplicon of 1 matches](#)

Length=215

Score = 379 bits (420), Expect = 5e-107
 Identities = 213/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GFACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GFACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon 627 non-redundant amplicon of 3 matches](#)

Length=215

Score = 379 bits (420), Expect = 5e-107
 Identities = 213/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GFACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GFACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAGGAACATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCG 215

>[lcl|Amplicon 400 non-redundant amplicon of 3 matches](#)

Length=214

Score = 379 bits (420), Expect = 5e-107
 Identities = 214/215 (99%), Gaps = 1/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GFACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTA-TCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 179
 Query 644 TCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 180 TCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCG 214

>[lcl|Amplicon 282 non-redundant amplicon of 18 matches](#)

Length=214

Score = 379 bits (420), Expect = 5e-107
 Identities = 214/215 (99%), Gaps = 1/215 (0%)

Strand=Plus/Plus

Identities = 214/215 (99%), Gaps = 1/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523

```

Sbjct 1 |CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA| 60
Query 524 |CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC| 583
Sbjct 61 |CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCG-GCGAGCAC| 119
Query 584 |GTA|CTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC| 643
Sbjct 120 |GTA|CTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC| 179
Query 644 |TCGCGCCAGCCGA|ACTGTTTCGCCAGGCTCAAGGCG 678
Sbjct 180 |TCGCGCCAGCCGA|ACTGTTTCGCCAGGCTCAAGGCG 214

```

>[lcl|Amplicon 570 non-redundant amplicon of 1 matches](#)

Length=215

Score = 379 bits (420), Expect = 5e-107

Identities = 213/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

```

Query 464 |CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA| 523
Sbjct 1 |CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA| 60
Query 524 |CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC| 583
Sbjct 61 |CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC| 120
Query 584 |GTA|CTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC| 643
Sbjct 121 |GTA|CTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC| 180
Query 644 |TCGCGCCAGCCGA|ACTGTTTCGCCAGGCTCAAGGCG 678
Sbjct 181 |TCGCGCCAGCCGA|ACTGTTTCGCCAGGCTCAAGGCG 215

```

>[lcl|Amplicon 568 non-redundant amplicon of 1 matches](#)

Length=215

Score = 379 bits (420), Expect = 5e-107

Identities = 213/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

```

Query 464 |CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA| 523
Sbjct 1 |CTCACCTTGCTCCTGCCGAGAAAAGTACCCATCATGGCTGATGCAATGCGGCGGCTGCATA| 60
Query 524 |CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC| 583
Sbjct 61 |CGCTTGATCCGGCTACCTGCCCATTCACCACCAAGCGAAACATCGCATCGAGCGAGCAC| 120
Query 584 |GTA|CTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC| 643
Sbjct 121 |GTA|CTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC| 180
Query 644 |TCGCGCCAGCCGA|ACTGTTTCGCCAGGCTCAAGGCG 678
Sbjct 181 |TCGCGCCAGCCGA|ACTGTTTCGCCAGGCTCAAGGCG 215

```

>[lcl|Amplicon 566 non-redundant amplicon of 1 matches](#)

Length=215

>[lcl|Amplicon 566 non-redundant amplicon of 1 matches](#)

Length=215

Score = 379 bits (420), Expect = 5e-107

Identities = 213/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

```

Query 464 |CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA| 523
Sbjct 1 |CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA| 60
Query 524 |CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC| 583
Sbjct 61 |CGCTTGATCCGGCTACCTGCCCATTCGTCACCAAGCGAAACATCGCATCGAGCGAGCAC| 120
Query 584 |GTA|CTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC| 643
Sbjct 121 |GTA|CTCAGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC| 180
Query 644 |TCGCGCCAGCCGA|ACTGTTTCGCCAGGCTCAAGGCG 678
Sbjct 181 |TCGCGCCAGCCGA|ACTGTTTCGCCAGGCTCAAGGCG 215

```

>[lcl|Amplicon 347 non-redundant amplicon of 6 matches](#)

Length=215

Score = 379 bits (420), Expect = 5e-107

Identities = 213/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus
 Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215
[>lcl|Amplicon 393 non-redundant amplicon of 3 matches](#)

Length=214
 Score = 379 bits (420), Expect = 5e-107
 Identities = 214/215 (99%), Gaps = 1/215 (0%)

Strand=Plus/Plus
 Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGG-CTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 179
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGG-CTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 179
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 180 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 214

[>lcl|Amplicon 444 non-redundant amplicon of 2 matches](#)
 Length=218

Score = 378 bits (418), Expect = 2e-106
 Identities = 215/218 (99%), Gaps = 3/218 (1%)

Strand=Plus/Plus
 Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTAT---CCATCATGGCTGATGCAATGCGGCGGCTGC 520
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATTATCCATCATGGCTGATGCAATGCGGCGGCTGC 60
 Query 521 ATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAG 580
 |||
 Sbjct 61 ATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAG 120
 Query 581 CACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGG 640
 |||
 Sbjct 121 CACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGG 180
 Query 641 GGCTCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 GGCTCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 218

[>lcl|Amplicon 754 non-redundant amplicon of 1 matches](#)
 Length=215

Score = 378 bits (418), Expect = 2e-106
 Identities = 211/212 (99%), Gaps = 0/212 (0%)

Strand=Plus/Plus
 Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAAGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAG 675
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAG 212

[>lcl|Amplicon 309 non-redundant amplicon of 7 matches](#)

Length=216

Score = 378 bits (418), Expect = 2e-106

Identities = 213/214 (99%), Gaps = 1/214 (0%)

Strand=Plus/Plus

Query 466 CACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACG 525
 |||
 Sbjct 3 CACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACG 62
 Query 526 CTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGT 585
 |||
 Sbjct 63 CTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGT 122
 Query 586 ACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTC 645
 |||
 Sbjct 63 CTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGT 122
 Query 586 ACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTC 645
 |||
 Sbjct 123 ACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTC 182
 Query 646 GCGCCAGCCG-AACTGTTCCGCCAGGCTCAAGGCG 678
 |||

Sbjct 183 GCGCCAGCCGAAACTGTTCCGCCAGGCTCAAGGCG 216
>lcl|Amplicon 345 non-redundant amplicon of 3 matches

Length=214

Score = 376 bits (416), Expect = 6e-106

Identities = 213/215 (99%), Gaps = 1/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTAAACCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCA-GGGC 179
 Query 644 TCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 180 TCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCG 214

>lcl|Amplicon 407 non-redundant amplicon of 3 matches

Length=214

Score = 376 bits (416), Expect = 6e-106

Identities = 212/213 (99%), Gaps = 1/213 (0%)

Strand=Plus/Plus

Query 466 CACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACG 525
 |||
 Sbjct 3 CACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACG 62
 Query 526 CTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGT 585
 |||
 Sbjct 63 CTTGATCCGGCTACCTGCCCATTCGACCACCA-GCGAAACATCGCATCGAGCGAGCACGT 121
 Query 586 ACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTC 645
 |||
 Sbjct 122 ACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTC 181
 Query 646 GCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 182 GCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCG 214

>lcl|Amplicon 610 non-redundant amplicon of 1 matches

Length=215

Score = 374 bits (414), Expect = 2e-105

Identities = 212/215 (99%), Gaps = 0/215 (0%)

Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643


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|||||
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAAGGGC 180
Query 644 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 678
|||||
Sbjct 181 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAAGCG 215
>lcl|Amplicon 536 non-redundant amplicon of 1 matches
Length=215
Score = 374 bits (414), Expect = 2e-105
Identities = 214/216 (99%), Gaps = 2/216 (1%)
Strand=Plus/Plus
Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTG-ATGCAATGCGGCGGCTGCAT 522
|||||
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCA-GGCTGAATGCAATGCGGCGGCTGCAT 59
Query 523 ACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCA 582
|||||
Sbjct 60 ACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCA 119
Query 583 CGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGG 642
|||||
Sbjct 120 CGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGG 179
Query 643 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 678
|||||
Sbjct 180 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 215
>lcl|Amplicon 356 non-redundant amplicon of 3 matches
Length=215
Score = 374 bits (414), Expect = 2e-105
Identities = 212/215 (99%), Gaps = 0/215 (0%)
Strand=Plus/Plus
Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
|||||
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGTTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|||||
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGG 643
|||||
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATTTGGACGAAGAGCATCAGGGG 180
Query 644 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCG 678
|||||
Sbjct 181 TCGCGCCAGCCGAATGTTCGCCAGGCTCAAGGCG 215
>lcl|Amplicon 221 non-redundant amplicon of 8 matches
Length=214
Score = 374 bits (414), Expect = 2e-105
Identities = 212/214 (99%), Gaps = 1/214 (0%)
Length=214
Score = 374 bits (414), Expect = 2e-105
Identities = 212/214 (99%), Gaps = 1/214 (0%)
Strand=Plus/Plus
Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
||| |||||
Sbjct 1 CTCGCCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|||||
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGG 643
|||||
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGAC-AAGAGCATCAGGGG 179
Query 644 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGC 677
|||||
Sbjct 180 TCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGC 213
>lcl|Amplicon 767 non-redundant amplicon of 1 matches
Length=214
Score = 370 bits (410), Expect = 3e-104
Identities = 212/215 (99%), Gaps = 1/215 (0%)
Strand=Plus/Plus
Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
|||||
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583

```

```

|||||
Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
|||||
Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCA-GATGATCTGGACGAAAAGCATCAAGGGC 179
Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
|||||
Sbjct 180 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 214

```

>[lcl|Amplicon_480 non-redundant amplicon of 3 matches](#)

Length=215

Score = 370 bits (410), Expect = 3e-104

Identities = 211/215 (98%), Gaps = 0/215 (0%)

Strand=Plus/Plus

```

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523

```

```

|||||
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|||||

```

```

Sbjct 61 CGCTTGACCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
|||||

```

```

Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTTGACCAGGATGACCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
|||||

```

```

Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

```

```

Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

```

```

>lcl|Amplicon\_423 non-redundant amplicon of 7 matches

```

Length=215

Score = 370 bits (410), Expect = 3e-104

Identities = 211/215 (98%), Gaps = 0/215 (0%)

Strand=Plus/Plus

```

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523

```

```

|||||
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
|||||

```

```

Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGAGGAGGAAGCGAAACATCGCATCGAGCGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
|||||

```

```

Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
|||||

```

```

Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

```

```

>lcl|Amplicon\_784 non-redundant amplicon of 1 matches

```

Length=217

Score = 367 bits (406), Expect = 3e-103

Identities = 213/217 (98%), Gaps = 2/217 (1%)

Strand=Plus/Plus

```

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTAT-CCATCAT-GGCTGATGCAATGCGGCGGCTGCA 521

```

```

|||||
Sbjct 1 CTCACCTTGCTCTTGCCGAGAAAAGTATTCCATCATTGGCTGATGCAATGCGGCGGCTGCA 60
Query 522 TACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGC 581
|||||

```

```

Sbjct 61 TACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGC 120
Query 582 ACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGG 641
|||||

```

```

Sbjct 121 ACGTACTCGGATGGAAGCCGGTCTTTTCGATCAGGATGATCTGGACGAAGAGCATCAGGG 180
Query 642 GCTCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
|||||

```

```

Sbjct 181 GCTCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 217

```

```

>lcl|Amplicon\_63 non-redundant amplicon of 9 matches

```

Length=215

Score = 365 bits (404), Expect = 1e-102

Identities = 210/215 (98%), Gaps = 0/215 (0%)

Strand=Plus/Plus

```

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523

```

```

|||||

```

Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCCTGGCTGACGCACTGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGCTGGAAGCCGGTCTTGTGCGATCAGGACGATCTGGACGAAGAGCATCAGGGGC 180
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGCTGGAAGCCGGTCTTGTGCGATCAGGACGATCTGGACGAAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||

Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215
[>lcl|Amplicon 770 non-redundant amplicon of 1 matches](#)

Length=215
 Score = 361 bits (400), Expect = 1e-101
 Identities = 209/215 (97%), Gaps = 0/215 (0%)
 Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 180
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 181 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

[>lcl|Amplicon 8 non-redundant amplicon of 150 matches](#)

Length=209
 Score = 361 bits (400), Expect = 1e-101
 Identities = 209/215 (97%), Gaps = 6/215 (3%)
 Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |||
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 583
 |||
 Sbjct 61 CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 120
 Query 584 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
 |||
 Sbjct 121 GTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATC-----AAGAGCATCAGGGGC 174
 Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 175 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 209

[>lcl|Amplicon 765 non-redundant amplicon of 1 matches](#)

Length=212
 Score = 349 bits (386), Expect = 9e-98
 Identities = 210/216 (97%), Gaps = 4/216 (2%)
 Strand=Plus/Plus

Query 463 TCTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCAT 522
 |||
 Sbjct 1 TCTCAC-TTGCTCTTGCCGAGAA-GTATCCATCATGGCTGATGCAATGCGGCG-CTGCAT 57
 Query 523 ACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCA 582
 |||
 Query 523 ACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCA 582
 |||
 Sbjct 58 ACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAA-CATCGCATCGAGCGAGCA 116
 Query 583 CGTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGG 642
 |||
 Sbjct 117 CGTACTCGGATGGAAGCCGGTCTTTTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGG 176
 Query 643 CTCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
 |||
 Sbjct 177 CTCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 212

[>lcl|Amplicon 136 non-redundant amplicon of 17 matches](#)

Length=205
 Sbjct 58 ACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAA-CATCGCATCGAGCGAGCA 116

Score = 347 bits (384), Expect = 3e-97
Identities = 205/215 (95%), Gaps = 10/215 (5%)
Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGGAGCAC 583
Sbjct 61 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
Sbjct 121 GTACTCGGATGGAAG-----CGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 170
Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
Sbjct 171 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 205

>lcl|Amplicon 160 non-redundant amplicon of 7 matches

Length=215

Score = 343 bits (380), Expect = 4e-96
Identities = 206/214 (96%), Gaps = 2/214 (1%)
Strand=Plus/Plus

Query 466 CACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACG 525
Sbjct 3 CACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATCGGGCGGCTCGATACG 62
Query 526 CTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGGAGCACGT 585
Sbjct 63 CTTGATCCGGCTACCTGCCATTCG-CCACCAAGCGAAACATCGCATCGAGCGGAGCACGT 121
Query 586 ACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC-T 644
Sbjct 122 ACTCGGATGGAAGCCGGTCTAGTCGATCAGGATGATCTGGACGAAGAGCATCAGGCGCGT 181
Query 645 CGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 678
Sbjct 182 CGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCG 215

>lcl|Amplicon 786 non-redundant amplicon of 1 matches

Length=217

Score = 334 bits (370), Expect = 2e-93
Identities = 210/220 (95%), Gaps = 6/220 (3%)
Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGGAGCAC 583
Sbjct 61 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGGAGCAC 120
Query 584 GTACTC-GGATGGAAGCCGG--TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGG 640
Sbjct 121 GTACTCGGGATGGAAGCCGGTCTTGGTCGATCAGGATGATCTGGACGAAAAGCATCAAG 180
Query 641 GGCTCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCGCG 680
Sbjct 181 GGCTCGCG-CAGCCGAACGTTCG-CAGGCTCAA-GCGCG 217

>lcl|Amplicon 756 non-redundant amplicon of 1 matches

Length=210

Score = 329 bits (364), Expect = 8e-92
Identities = 205/212 (97%), Gaps = 6/212 (3%)
Strand=Plus/Plus

Query 464 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
Query 524 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGGAGCAC 583
Sbjct 61 CGCTTGATCCGGCTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGGAGCAC 120
Query 584 GTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC 643
Sbjct 121 GTACTCGGATGG-AGCCGGTCTTGTTCGATCA-GATGATCTGGACG-AGAGCATCA-GGGC 176
Query 644 TCGCGCCAGCCGAACGTTCGCCAGGCTCAAG 675
Sbjct 177 TCGCGCCAGTCG-ACTGTTGCCA-GCTCAAG 206

>[lcl|Amplicon 7 non-redundant amplicon of 58045 matches](#)

Length=173
 Score = 313 bits (346), Expect = 6e-87
 Identities = 173/173 (100%), Gaps = 0/173 (0%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 173

>[lcl|Amplicon 763 non-redundant amplicon of 1 matches](#)

Length=212
 Score = 309 bits (342), Expect = 8e-86
 Identities = 208/221 (94%), Gaps = 11/221 (5%)
 Strand=Plus/Plus
 Score = 309 bits (342), Expect = 8e-86
 Identities = 208/221 (94%), Gaps = 11/221 (5%)
 Strand=Plus/Plus
 Query 464 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 523
 |
 Sbjct 1 CTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA 60
 Query 524 CGCTTGATCC-GGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCA 582
 |
 Sbjct 61 CGCTTGATCCGGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCA 120
 Query 583 CGTACTCGGATGGAAG-CCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGG 641
 |
 Sbjct 121 CGTACTCGGATGGAAGCCGGTCTTGTCGATCA-GATGATCTGGACG-AGAGCATCA-TG 177
 Query 642 GCTCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCGCGCA 682
 |
 Sbjct 178 GCTCGCGCCAGC--GACTG-TCGCCA-GCTCA--GCGCGCA 212

>[lcl|Amplicon 752 non-redundant amplicon of 1 matches](#)

Length=173
 Score = 309 bits (342), Expect = 8e-86
 Identities = 171/171 (100%), Gaps = 0/171 (0%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGA 620
 |
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGA 171

>[lcl|Amplicon 114 non-redundant amplicon of 5 matches](#)

Length=173
 Score = 309 bits (342), Expect = 8e-86
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |
 Sbjct 121 CATCGAGCGAGCACGTACTCGRATGGAAGCCGGTCTTGTCGATCAGGATGATC 173

>[lcl|Amplicon 433 non-redundant amplicon of 8 matches](#)

Length=173
 Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |

Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 173

>[lcl|Amplicon_746 non-redundant amplicon of 2 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTACATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 173

>[lcl|Amplicon_639 non-redundant amplicon of 1 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGTTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 173

>[lcl|Amplicon_437 non-redundant amplicon of 3 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCGTTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCGTTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 173

>[lcl|Amplicon_634 non-redundant amplicon of 1 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCGAGCATAACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||

Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 173
[>lcl|Amplicon 611 non-redundant amplicon of 1 matches](#)
 Length=173
 Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATACAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 173
[>lcl|Amplicon 572 non-redundant amplicon of 1 matches](#)
 Length=173
 Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 173
[>lcl|Amplicon 535 non-redundant amplicon of 22 matches](#)
 Length=173
[>lcl|Amplicon 535 non-redundant amplicon of 22 matches](#)
 Length=173
 Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGCACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 173
[>lcl|Amplicon 517 non-redundant amplicon of 4 matches](#)
 Length=173
 Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 173
[>lcl|Amplicon 275 non-redundant amplicon of 5 matches](#)
 Length=173
 Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||

Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 622
 |||

Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATCATC 173

>[lcl|Amplicon 281 non-redundant amplicon of 6 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)

Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||

Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60 Query

450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||

Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60

Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||

Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120

Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 622
 |||

Sbjct 121 CATCGAGCGAGCYCGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 173

>[lcl|Amplicon 172 non-redundant amplicon of 47 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)

Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||

Sbjct 1 GGATCTCCTGTCATCCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60

Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||

Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120

Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 622
 |||

Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 173

>[lcl|Amplicon 196 non-redundant amplicon of 156 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)

Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||

Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60

Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||

Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120

Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 622
 |||

Sbjct 121 CATCGAGCGGGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 173

>[lcl|Amplicon 414 non-redundant amplicon of 14 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85
 Identities = 172/173 (99%), Gaps = 0/173 (0%)

Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||

Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60

Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||

Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACATGCCCATTCGACCACCAAGCGAAACATCG 120

Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 622
 |||

Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACATGCCCATTCGACCACCAAGCGAAACATCG 120

Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 622
 |||

Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 173

>[lcl|Amplicon 344 non-redundant amplicon of 5 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85

Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 173

>[lcl|Amplicon 348 non-redundant amplicon of 8 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85

Identities = 172/173 (99%), Gaps = 0/173 (0%)

Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAGGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 173

>[lcl|Amplicon 35 non-redundant amplicon of 41 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85

Identities = 172/173 (99%), Gaps = 0/173 (0%)

Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGGACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 173

>[lcl|Amplicon 242 non-redundant amplicon of 11 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85

>[lcl|Amplicon 242 non-redundant amplicon of 11 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85

Identities = 172/173 (99%), Gaps = 0/173 (0%)

Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 173

>[lcl|Amplicon 21 non-redundant amplicon of 187 matches](#)

Length=173

Score = 307 bits (340), Expect = 3e-85

Identities = 172/173 (99%), Gaps = 0/173 (0%)

Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCGCCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||

Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 173
[>lcl|Amplicon 776 non-redundant amplicon of 1 matches](#)
 Length=174
 Score = 306 bits (338), Expect = 9e-85
 Identities = 173/174 (99%), Gaps = 1/174 (1%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCC-TGCCGAGAAAGTATCCATCATGGCTGATGCAA 508
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCCTGCCGAGAAAGTATCCATCATGGCTGATGCAA 60
 Query 509 TCGCGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATC 568
 |||
 Sbjct 61 TCGCGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATC 120
 Query 569 GCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 622
 |||
 Sbjct 121 GCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 174
[>lcl|Amplicon 768 non-redundant amplicon of 1 matches](#)
 Length=173
 Score = 306 bits (338), Expect = 9e-85
 Identities = 173/174 (99%), Gaps = 1/174 (1%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCT 623
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCA-GATGATCT 173
[>lcl|Amplicon 401 non-redundant amplicon of 3 matches](#)
 Length=172
 Score = 304 bits (336), Expect = 3e-84
 Identities = 172/173 (99%), Gaps = 1/173 (1%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTA-TCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 172
[>lcl|Amplicon 387 non-redundant amplicon of 3 matches](#)
 Length=173
 Score = 304 bits (336), Expect = 3e-84
 Identities = 171/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTACACATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC 173
[>lcl|Amplicon 385 non-redundant amplicon of 3 matches](#)
 Length=173
 Score = 304 bits (336), Expect = 3e-84
 Identities = 171/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60

Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATTGGGATGATC 173

>[lcl|Amplicon_581 non-redundant amplicon of 3 matches](#)

Length=173

Score = 304 bits (336), Expect = 3e-84
 Identities = 171/173 (99%), Gaps = 0/173 (0%)

Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGACCTCCTGTCATCTCACCTTGCCCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 173

>[lcl|Amplicon_569 non-redundant amplicon of 1 matches](#)

Length=173

Score = 304 bits (336), Expect = 3e-84
 Identities = 171/173 (99%), Gaps = 0/173 (0%)

Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 173

>[lcl|Amplicon_567 non-redundant amplicon of 1 matches](#)

Length=173

Score = 304 bits (336), Expect = 3e-84
 Identities = 171/173 (99%), Gaps = 0/173 (0%)

Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 173

>[lcl|Amplicon_283 non-redundant amplicon of 18 matches](#)

Length=172

Score = 304 bits (336), Expect = 3e-84

>[lcl|Amplicon_283 non-redundant amplicon of 18 matches](#)

Length=172

Score = 304 bits (336), Expect = 3e-84
 Identities = 172/173 (99%), Gaps = 1/173 (1%)

Strand=Plus/Plus

Query 450 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCG-GCAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 172

>[lcl|Amplicon_295 non-redundant amplicon of 8 matches](#)

Length=173

Score = 304 bits (336), Expect = 3e-84
 Identities = 171/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus
 Query 450 GGATCTCCTGTTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAAT 509
 |||
 Sbjct 1 GGATCTCCTGTTCATCTCACCTTGCTCCTGCCGAGAAAGTGTCCATCATGGCTGATGCAAT 60
 Query 510 GCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 569
 |||
 Sbjct 61 ACGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCG 120
 Query 570 CATCGAGCGAGCAGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 622
 |||
 Sbjct 121 CATCGAGCGAGCAGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC 173
 Lambda K H
 0.634 0.408 0.912
 Gapped
 Lambda K H
 0.625 0.410 0.780
 Effective search space used: 123918080

Query= pat-STRVR_Streptomyces_viridochromogenes_- _M22827.1

Length=1312

Sequences producing significant alignments:	Score (Bits)	E Value
lcl Amplicon_185 non-redundant amplicon of 33 matches	109	1e-25
lcl Amplicon_422 non-redundant amplicon of 3 matches	98.7	2e-22
lcl Amplicon_17 non-redundant amplicon of 1781 matches	96.9	9e-22
lcl Amplicon_619 non-redundant amplicon of 2 matches	91.5	4e-20
lcl Amplicon_586 non-redundant amplicon of 13 matches	91.5	4e-20
lcl Amplicon_123 non-redundant amplicon of 50 matches	91.5	4e-20
lcl Amplicon_642 non-redundant amplicon of 3 matches	91.5	4e-20
lcl Amplicon_552 non-redundant amplicon of 1 matches	82.4	2e-17
lcl Amplicon_15 non-redundant amplicon of 1787 matches	75.2	3e-15
lcl Amplicon_618 non-redundant amplicon of 2 matches	71.6	3e-14
lcl Amplicon_122 non-redundant amplicon of 50 matches	71.6	3e-14
lcl Amplicon_551 non-redundant amplicon of 1 matches	66.2	1e-12
lcl Amplicon_15 non-redundant amplicon of 1787 matches	75.2	3e-15
lcl Amplicon_618 non-redundant amplicon of 2 matches	71.6	3e-14
lcl Amplicon_122 non-redundant amplicon of 50 matches	71.6	3e-14
lcl Amplicon_551 non-redundant amplicon of 1 matches	66.2	1e-12
lcl Amplicon_574 non-redundant amplicon of 8 matches	60.8	6e-11

>[lcl|Amplicon 185 non-redundant amplicon of 33 matches](#)

Length=60

Score = 109 bits (120), Expect = 1e-25
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus
 Query 348 ACGAGCACGGTCAACTTCCGTACGGAGCCGAGACTCCGCAGGAGTGGATCGACGACCTG 407
 |||
 Sbjct 1 ACGAGCACGGTCAACTTCCGTACGGAGCCGAGACTCCGCAGGAGTGGATCGACGACCTG 60

>[lcl|Amplicon 422 non-redundant amplicon of 3 matches](#) Length=63

Score = 98.7 bits (108), Expect = 2e-22
 Identities = 60/63 (95%), Gaps = 3/63 (5%)
 Strand=Plus/Plus
 Query 348 ACGAGCACGGTCAACTTCCGTACGGAG---CCGCAGACTCCGCAGGAGTGGATCGACGAC 404
 |||
 Sbjct 1 ACGAGCACGGTCAACTTCCGTACGGAGGAGCCGAGACTCCGCAGGAGTGGATCGACGAC 60
 Query 405 CTG 407
 |||

Sbjct 61 CTG 63

>[lcl|Amplicon 17 non-redundant amplicon of 1781 matches](#) Length=69

Score = 96.9 bits (106), Expect = 9e-22
 Identities = 62/68 (91%), Gaps = 0/68 (0%)
 Strand=Plus/Plus
 Query 329 CGTCAATCACTACATCGAGACGAGCAGGTCACCTTCCGTACGGAGCCGAGACTCCGCA 388
 |||
 Sbjct 1 CGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGAGGAACCGCA 60
 Query 389 GGAGTGGGA 396
 |||

Sbjct 61 GGAGTGGGA 68

>[lcl|Amplicon 619 non-redundant amplicon of 2 matches](#) Length=69

Score = 91.5 bits (100), Expect = 4e-20

Identities = 61/68 (90%), Gaps = 0/68 (0%)
Strand=Plus/Plus
Query 329 CGTCAATCACTACATCGAGACGAGCACGGTCAACTTCCGTACGGAGCCGCAGACTCCGCA 388
||||| ||||||||||||||| ||||||||||||||||||| ||||||||| |||||
Sbjct 1 CGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCA 60
Query 389 GGAGTGGA 396
||||| ||
Sbjct 61 GGAGTAGA 68
[>lcl|Amplicon_586 non-redundant amplicon of 13 matches](#)
Length=69
Score = 91.5 bits (100), Expect = 4e-20
[>lcl|Amplicon_586 non-redundant amplicon of 13 matches](#)
Length=69
Score = 91.5 bits (100), Expect = 4e-20
Identities = 61/68 (90%), Gaps = 0/68 (0%)
Strand=Plus/Plus
Query 329 CGTCAATCACTACATCGAGACGAGCACGGTCAACTTCCGTACGGAGCCGCAGACTCCGCA 388
||||| ||||||||| ||||| ||||||||||||||||||| ||||||||| |||||
Sbjct 1 CGTCAACCACTACATCCAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCA 60
Query 389 GGAGTGGA 396
|||||||
Sbjct 61 GGAGTGGA 68
[>lcl|Amplicon_123 non-redundant amplicon of 50 matches](#)
Length=69
Score = 91.5 bits (100), Expect = 4e-20
Identities = 61/68 (90%), Gaps = 0/68 (0%)
Strand=Plus/Plus
Query 329 CGTCAATCACTACATCGAGACGAGCACGGTCAACTTCCGTACGGAGCCGCAGACTCCGCA 388
||||| ||||||||||||||| ||||||||||||||||||| ||||||||| |||||
Sbjct 1 CGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCA 60
Query 389 GGAGTGGA 396
||| |||||
Sbjct 61 GGACTGGA 68
[>lcl|Amplicon_642 non-redundant amplicon of 3 matches](#)
Length=69
Score = 91.5 bits (100), Expect = 4e-20
Identities = 61/68 (90%), Gaps = 0/68 (0%)
Strand=Plus/Plus
Query 329 CGTCAATCACTACATCGAGACGAGCACGGTCAACTTCCGTACGGAGCCGCAGACTCCGCA 388
||||| ||||||||| ||||||| ||||||||||||||||||| ||||||||| |||||
Sbjct 1 CGTCAACCACTACACCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCA 60
Query 389 GGAGTGGA 396
|||||||
Sbjct 61 GGAGTGGA 68
[>lcl|Amplicon_552 non-redundant amplicon of 1 matches](#) Length=69
Score = 82.4 bits (90), Expect = 2e-17
Identities = 59/68 (87%), Gaps = 0/68 (0%)
Strand=Plus/Plus
Query 329 CGTCAATCACTACATCGAGACGAGCACGGTCAACTTCCGTACGGAGCCGCAGACTCCGCA 388
||||| ||||||||||||||| ||||| ||||||||||||||||||| ||||| ||| || ||
Sbjct 1 CGTCAACCACTACATCGAGACAAGCACTGTCAACTTCCGTACCGAGCCTCAGGAACCTCA 60
Query 389 GGAGTGGA 396
|||||||
Sbjct 61 GGAGTGGA 68
[>lcl|Amplicon_15 non-redundant amplicon of 1787 matches](#)
Length=60
Score = 75.2 bits (82), Expect = 3e-15
Identities = 52/59 (88%), Gaps = 0/59 (0%)
Strand=Plus/Plus
Score = 75.2 bits (82), Expect = 3e-15
Identities = 52/59 (88%), Gaps = 0/59 (0%)
Strand=Plus/Plus
Query 348 ACGAGCACGGTCAACTTCCGTACGGAGCCGCAGACTCCGAGGAGTGGATCGACGACCT 406
|| ||||||||||||||||||| ||||||||| ||||||||||||||| |||||||||
Sbjct 1 ACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGAGGAGTGGACGACGACCT 59
[>lcl|Amplicon_618 non-redundant amplicon of 2 matches](#) Length=60
Score = 71.6 bits (78), Expect = 3e-14
Identities = 51/59 (86%), Gaps = 0/59 (0%)

Strand=Plus/Plus

Query 348 ACGAGCACGGTCAACTTCCGTACGGAGCCGAGACTCCGCAGGAGTGGATCGACGACCT 406
|| |||
Sbjct 1 ACAAGCACGGTCAACTTCCGTACCGAGCCGAGGAACCGCAGGAGTAGACGGACGACCT 59

>lcl|Amplicon 122 non-redundant amplicon of 50 matches

Length=60

Score = 71.6 bits (78), Expect = 3e-14
Identities = 51/59 (86%), Gaps = 0/59 (0%)
Strand=Plus/Plus

Query 348 ACGAGCACGGTCAACTTCCGTACGGAGCCGAGACTCCGCAGGAGTGGATCGACGACCT 406
|| |||
Sbjct 1 ACAAGCACGGTCAACTTCCGTACCGAGCCGAGGAACCGCAGGACTGGACGGACGACCT 59

>lcl|Amplicon 551 non-redundant amplicon of 1 matches

Length=60

Score = 66.2 bits (72), Expect = 1e-12
Identities = 50/59 (85%), Gaps = 0/59 (0%)
Strand=Plus/Plus

Query 348 ACGAGCACGGTCAACTTCCGTACGGAGCCGAGACTCCGCAGGAGTGGATCGACGACCT 406
|| |||
Sbjct 1 ACAAGCACTGTCAACTTCCGTACCGAGCCTCAGGAACCTCAGGAGTGGACCGACGACCT 59

>lcl|Amplicon 574 non-redundant amplicon of 8 matches Length=57

Score = 60.8 bits (66), Expect = 6e-11
Identities = 50/59 (85%), Gaps = 3/59 (5%)
Strand=Plus/Plus

Query 348 ACGAGCACGGTCAACTTCCGTACGGAGCCGAGACTCCGCAGGAGTGGATCGACGACCT 406
|| |||
Sbjct 1 ACAAGCACGGTCAACTTCCGTAC-GAGCCGAG--GAAGCAGGAGTGGACGGACGACCT 56

Lambda K H
0.634 0.408 0.912

Gapped

Lambda K H
0.625 0.410 0.780

Effective search space used: 125079812

Query= PG_Solanum_lycopersicum_-M37304.1

Length=7456

Table with 3 columns: Sequences producing significant alignments, Score (Bits), and E Value. Rows include lcl|Amplicon_134, lcl|Amplicon_135, and lcl|Amplicon_744.

>lcl|Amplicon 134 non-redundant amplicon of 16 matches

Length=384

Score = 693 bits (768), Expect = 0.0
Identities = 384/384 (100%), Gaps = 0/384 (0%)
Strand=Plus/Plus

Query 3333 GGATCCTTAGAAGCATCTAGTAAAATTTTCAGACTACAAAGATAGAAGGCTTTGGATTGCT 3392
Sbjct 1 GGATCCTTAGAAGCATCTAGTAAAATTTTCAGACTACAAAGATAGAAGGCTTTGGATTGCT 60
Query 3393 TTTGATAGTGTTCAAAATTTAGTTGTTGGAGGAGGAGGAACATCAATGGCAATGGACAA 3452
Sbjct 61 TTTGATAGTGTTCAAAATTTAGTTGTTGGAGGAGGAGGAACATCAATGGCAATGGACAA 120
Query 3453 GTATGGTGGCCAAGTCTTGCAAATAAATAAATCACTGGTAATTTTATAACCTTGCTTA 3512
Sbjct 121 GTATGGTGGCCAAGTCTTGCAAATAAATAAATCACTGGTAATTTTATAACCTTGCTTA 180
Query 3513 TAAGTTTTACGCTATGTTGCTCGAATTTCTTAAACTTGTTCCTAAAGATATTATATATTTG 3572
Sbjct 181 TAAGTTTTACGCTATGTTGCTCGAATTTCTTAAACTTGTTCCTAAAGATATTATATATTTG 240
Query 3573 AAGGAGGTGTCACAAATGCATCACATTTTTAGAGATTCCGACCAATATTAGTTTTATGTA 3632
Sbjct 241 AAGGAGGTGTCACAAATGCATCACATTTTTAGAGATTCCGACCAATATTAGTTTTATGTA 300
Query 3633 ATCTAATTTTCAGAGCATCTTGCCTTGACTGATCATTGTTACCCcttttttcttCATG 3692
Sbjct 301 ATCTAATTTTCAGAGCATCTTGCCTTGACTGATCATTGTTACCCcttttttcttCATG 360
Query 3693 CAGCCATGCAGGGATGCACCAACG 3716
Sbjct 361 CAGCCATGCAGGGATGCACCAACG 384

>lcl|Amplicon 135 non-redundant amplicon of 5 matches

Length=384

Score = 688 bits (762), Expect = 0.0
Identities = 383/384 (99%), Gaps = 0/384 (0%)
Strand=Plus/Plus

Query 3333 GGATCCTTAGAAGCATCTAGTAAAATTTTCAGACTACAAAGATAGAAGGCTTTGGATTGCT 3392
Sbjct 1 GGATCCTTAGAAGCATCTAGTAAAATTTTCAGACTACAAAGATAGAAGGCTTTGGATTGCT 60
Query 3393 TTTGATAGTGTTCAAATTTAGTTGTTGGAGGAGGAGGAACATCAATGGCAATGGACAA 3452
Sbjct 61 TTTGATAGTGTTCAAATTTAGTTGTTGGAGGAGGAGGAACATCAATGGCAATAGACAA 120
Query 3453 GTATGGTGGCCAAGTTCTTGCAAATAAATAAATCACTGGTAAATTTATAACCTTGCTTA 3512
Sbjct 121 GTATGGTGGCCAAGTTCTTGCAAATAAATAAATCACTGGTAAATTTATAACCTTGCTTA 180
Query 3513 TAAGTTTTACGCTATGTTGCTCGAATTCTTTAAACTTGTTCCTAAAGATATTATATATTTG 3572
Sbjct 121 GTATGGTGGCCAAGTTCTTGCAAATAAATAAATCACTGGTAAATTTATAACCTTGCTTA 180
Query 3513 TAAGTTTTACGCTATGTTGCTCGAATTCTTTAAACTTGTTCCTAAAGATATTATATATTTG 3572
Sbjct 181 TAAGTTTTACGCTATGTTGCTCGAATTCTTTAAACTTGTTCCTAAAGATATTATATATTTG 240
Query 3573 AAGGAGGTGTCACAAATGCATCACATTTTGTAGAGATTCCGACCAATATTAGTTTTATGTA 3632
Sbjct 241 AAGGAGGTGTCACAAATGCATCACATTTTGTAGAGATTCCGACCAATATTAGTTTTATGTA 300
Query 3633 ATCTAATTTTCAGAGCATCTTTCGCTTGTACTGATCATTGTTACCCtttttttCCTTCATG 3692
Sbjct 301 ATCTAATTTTCAGAGCATCTTTCGCTTGTACTGATCATTGTTACCCTTTTTTTCTTCATG 360
Query 3693 CAGCCATGCAGGGATGCACCAACG 3716
Sbjct 361 CAGCCATGCAGGGATGCACCAACG 384

>lcl|Amplicon_744_non-redundant_amplicon_of_1_matches

Length=389

Score = 607 bits (672), Expect = 1e-174
Identities = 370/390 (95%), Gaps = 7/390 (2%)
Strand=Plus/Plus

Query 3333 GGATCCTTAGAAGCATCTAGTAAAATTTTCAGACTACAAAGATAGAAGGCTTTGGATTGCT 3392
Sbjct 1 GGATCCTTAGAAGCATCTAGTAAAATTTTCAGACTACAAAGATAGAAGGCTTTGGATTGCT 60
Query 3393 TTTGATAGTGTTCAAATTTAGTTGTTGGAGGAGGAGGAACATCAATGGCAATGGACAA 3452
Sbjct 61 TTTGATAGTGTTCAAATTTAGTTGTTGGAGGAGGAGGAACATCAATGGCAATGGACAA 120
Query 3453 GTATGGTGGCCAAGTTCTTGCAAATAAATAAATCACTGGTAAATTTATAACCTTGCTTA 3512
Sbjct 121 GTATGGTGGCCACGTTCTTGCAAATAAATAAATCACTGGTAAATTTATAACCTTGCTTA 180
Query 3513 TAAGTTTTACGCTATGTTGCTCGAATTCTTTAA-----ACTGTTCTAAAGATATTATAT 3567
Sbjct 181 TAAGTTTTACACTATATTGCTCGGATTTTTTAAATTATATTTGTTCTAAAGATAATGTAT 240
Query 3568 ATTTGAAGGAGGTGTCACAAATGC-ATCACATTTTGTAGAGATTCCGACCAATATTAGTTT 3626
Sbjct 241 ATTTGAAGGAGGTGTCACAAATGCAATCACATTTTGTAGAGATTTCGAGCAATATTAGTTT 300
Query 3627 TATGTAATCTAATTTTCAGAGCATCTTTCGCTTGTACTGATCATTGTTACCCtttttttC 3686
Sbjct 301 TATGTGATCTGATTTTCAGAGCATCTTTCGCTTGTACTGATCATTGTTA-CCTTTTTTTTC 359
Query 3687 TTCATGCAGCCATGCAGGGATGCACCAACG 3716
Sbjct 360 TTCATGCAGCCATGCAGGGATGCACCAACG 389

Lambda K H
0.634 0.408 0.912

Gapped

Lambda K H
0.625 0.410 0.780

Effective search space used: 707070042

Query= PLRVrep_Potato_leafroll_virus_-_NC_001747.1

Length=5987

***** No hits found *****

Lambda K H
0.634 0.408 0.912

Gapped

Lambda K H
0.625 0.410 0.780

Effective search space used: 567349045

Query= vip3A(a)_Bacillus_thuringiensis_-_L48811.1

Length=4483

***** No hits found *****

Lambda	K	H
0.634	0.408	0.913

Gapped

Lambda	K	H
0.625	0.410	0.780

Effective search space used: 424299093

Database: GMOMETHODS non redundant amplicon set
849 sequences; 113,791 total letters

Database: GMOMETHODS non redundant amplicon set

Posted date: Apr 20, 2016 9:31 AM

Number of letters in database: 113,791

Number of sequences in database: 849

Matrix: blastn matrix 2 -3

Gap Penalties: Existence: 5, Extension: 2

Reference:

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.