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APPENDIXES

Appendix A

Bacterial Growth Media and Plant Nutrient Solutions

Preparation of all bacterial growth media and plant nutrient solutions are as described by Somasegaran and Hoben (1994) unless otherwise stated.

Yeast Extract Mannitol Broth (YMB)

Mannitol	10.0 g
K_2HPO_4	0.5 g
$MgSO_4.7H_2O$	0.2 g
NaCl	0.1 g
Yeast extract	0.5 g
Deionized water	1.0 g

pH of medium was adjusted to 6.8 with 0.1 N NaOH. The medium was autoclaved at 121°C for 15 min.

Yeast Extract Mannitol Agar (YMA)

YMB	1 liter
Agar	15 g

Agar was added to 1 liter of YMB. The solution was shaken to suspend the agar then autoclaved at 121°C for 15 min. After autoclaving, the medium was shaken to ensure even mixing of melted agar with medium before pouring onto petri dishes and left to solidify.

YMA with Congo Red

Congo Red stock solution : 250 mg of Congo Red dissolved in 100 ml of deionized water. 10 ml of Congo Red stock solution were added to 1 liter of YMA. The final Congo Red concentration was 25 $\mu g.ml^{-1}$. The medium was autoclaved at 121°C for 15 min.

N-free Nutrient Solutions

Stock Solutions	Chemicals	g/liter
1	$CaCl_2.2H_2O$	294.1
2	KH_2PO_4	136.1
3	$FeC_6H_5O_7.3H_2O$	6.7
	$MgSO_4.7H_2O$	123.3
	K_2SO_4	87.0
	$MnSO_4.H_2O$	0.338
4	H_3BO_3	0.247
	$ZnSO_4.7H_2O$	0.288
	$CuSO_4.5H_2O$	0.100
	$CoSO_4.7H_2O$	0.056
	$Na_2\ MoO_2.7\ H_2O$	0.048

Warm water was used to prepare stock solutions to get the ferric-citrate into solution. Ten liters of full-strength plant culture solution were prepared as follows :

- To 5 liters of water, add 5 ml of each stock solution and mix.
- Dilute to 10 liters by adding another 5 liters of water.
- Adjust pH to either 5.0 or 6.8 with 1 N HCl
- For positive control treatment, 0.05% KNO_3 was added to give final N concentation of 70 ppm.

Appendix B

Chemicals and Solutions

1. Solutions for DNA extraction (Gibco BRL)

Saline-EDTA solution

15 mM NaCl, 10 mM EDTA, pH 8.0

0.9 g NaCl, 0.29 g EDTA were added to distilled water. The final volume was made to 100 ml. 0.1 N NaOH was used to adjust pH to 8.0 before autoclaving at $121^{\circ}C$ for 15 min.

DNAzol

DNAzol solution (Gibco BRL) was used according to manufacturer's instruction.

2. Solutions for SDS-PAGE (Bio-rad)

Stock solutions

A. Acrylamide/bis (30%T, 2.67%C)

87.6 g acrylamide (29.2 g/100 ml)

2.4 g N'N'-bis-methylene-acrylamide (0.8 g/100 ml)

Make to 300 ml with deionized water. Filter and store at $4^{\circ}C$ in the dark (30 days maximum).

B. 1.5 M Tris-HCl, pH 8.8

27.23 g Tris base (18.15 g/100 ml)

80 ml deionized water

Adjust to pH 8.8 with 6N HCl. Make to 150 ml with deionized water and store at $4^{\circ}C$

C. 0.5 M Tris-HCl, pH 6.8

6 g Tris base

60 ml deionized water

Adjust to pH 6.8 with 6N HCl. Make to 100 ml with deionized water and store at 4°C

D. 10% SDS

Dissolve 10 g SDS in 90 ml water with gentle stirring and bring to 100 ml with ddH_2O

E. Sample buffer (SDS reducing buffer) (store at room temperature)

Deionized water	3.8 ml
0.5 M Tris-HCl, pH 6.8	1.0 ml
Glycerol	0.8 ml
10% (w/v) SDS	1.6 ml
2-mercaptoethanol	0.4 ml
1% (w/v) bromophenol blue	0.4 ml

Dilute the sample at least 1:4 with sample buffer, and heat at 95°C for 4 minutes

F. 5X electrode (running buffer), pH 8.3

Tris base	9.0 g	(15 g/l)
Glycine	43.2 g	(72 g/l)
SDS	3.0 g	(5 g/l)

Make to 600 ml with deionized water.

Store at 4°C. Warm to room temperature before use if precipitation occurs. Dilute 60 ml 5X stock with 240 ml deionized water for one electrophoretic run.

G. 10% Ammonium persulfate

One milliliter of aqueous 10% (w/v) Ammonium persulfate stock solution was prepared and stored at 4°C. Ammonium persulfate decomposes slowly, and fresh solutions were prepared weekly.

Appendix C

Raw Data

1. Figures 5.1-5.6, 5.7-5.12, 5.13-5.18 showed 16S rDNA sequences of strains S172, S173 and S174 respectively.

2. Comparisons of 16S rDNA sequences of isolates S172, S173, and S174 with data in GenBank using the BLAST program (NCBI).

3. Duncan's Mutiple Range Test (Glover & Mitchell, 1998)

Duncan's Mutiple Range Test was performed as follows :

1.Means of plant dry weight were placed in order of magnitide.

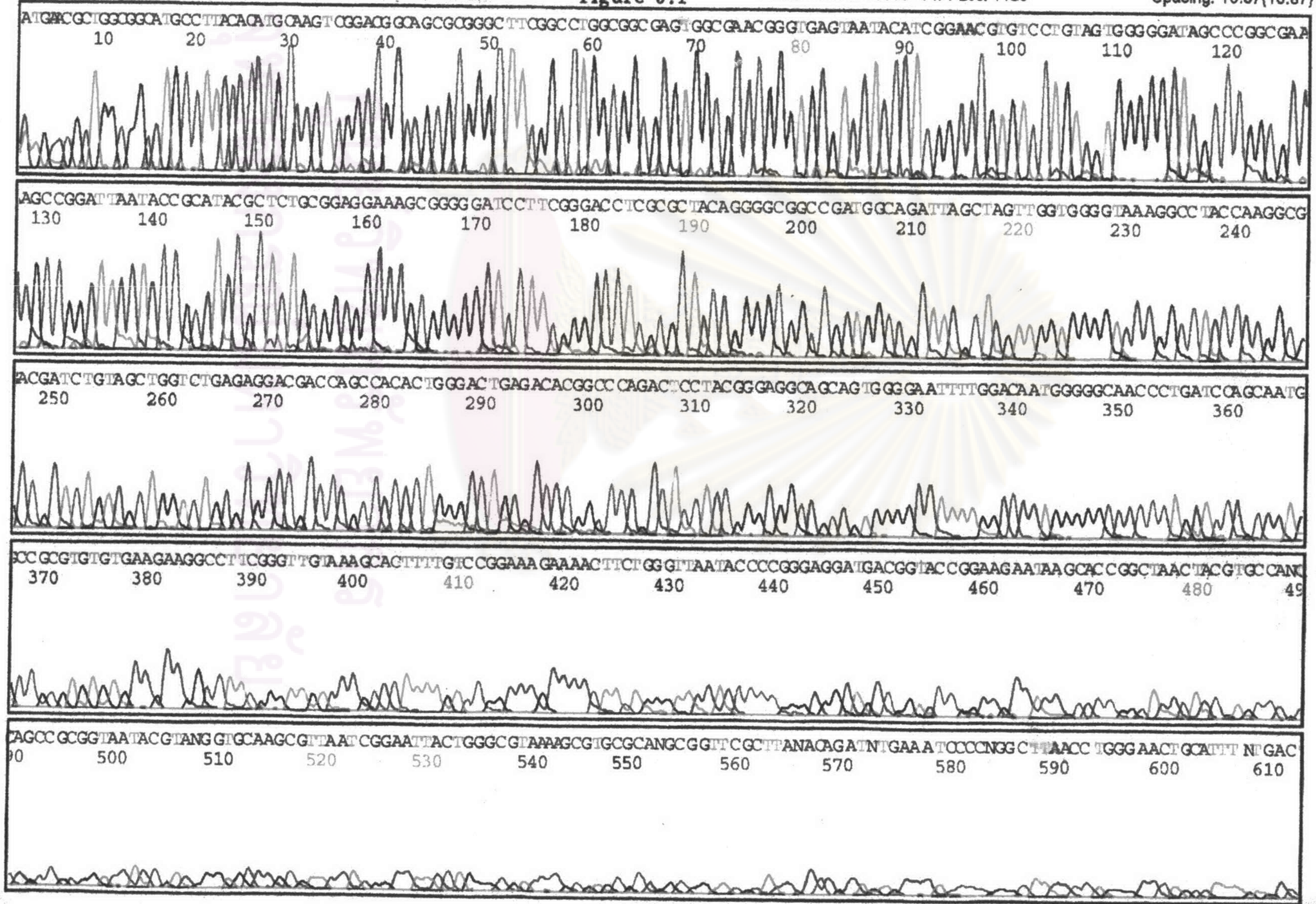
2.The standard error of the means was calculated .

3.The values of r_{α} (p, f) were obtained from Duncan's table.

4.Any two means that were "p" apart and which differed by more than R_p were declared to be significantly different.

ABI PRISM™ | Model 377 Version 3.4 ABI100 Version 3.2 | 08•PCR ProductS172/forward27 PCR ProductS172/forward27f Lane 8 | SQ....4703.... | Signal G:340 A:147 T:69 C:178 DT {BD Set Any-Primer} BD Matrix Std.Jan31,01. Points 1189 to 10616 Pk 1 Loc: 1189 | Page...2...of...2... Page 1 of 2 Thu, Oct 11, 2001 07:53 Wed, Oct 10, 2001 16:17 Spacing: 10.87{10.87}

Figure 5.1



ABI PRISM™

Model 377
Version 3.4
ABI100
Version 3.2

35•S172/1241f

S172/1241f
Lane 35

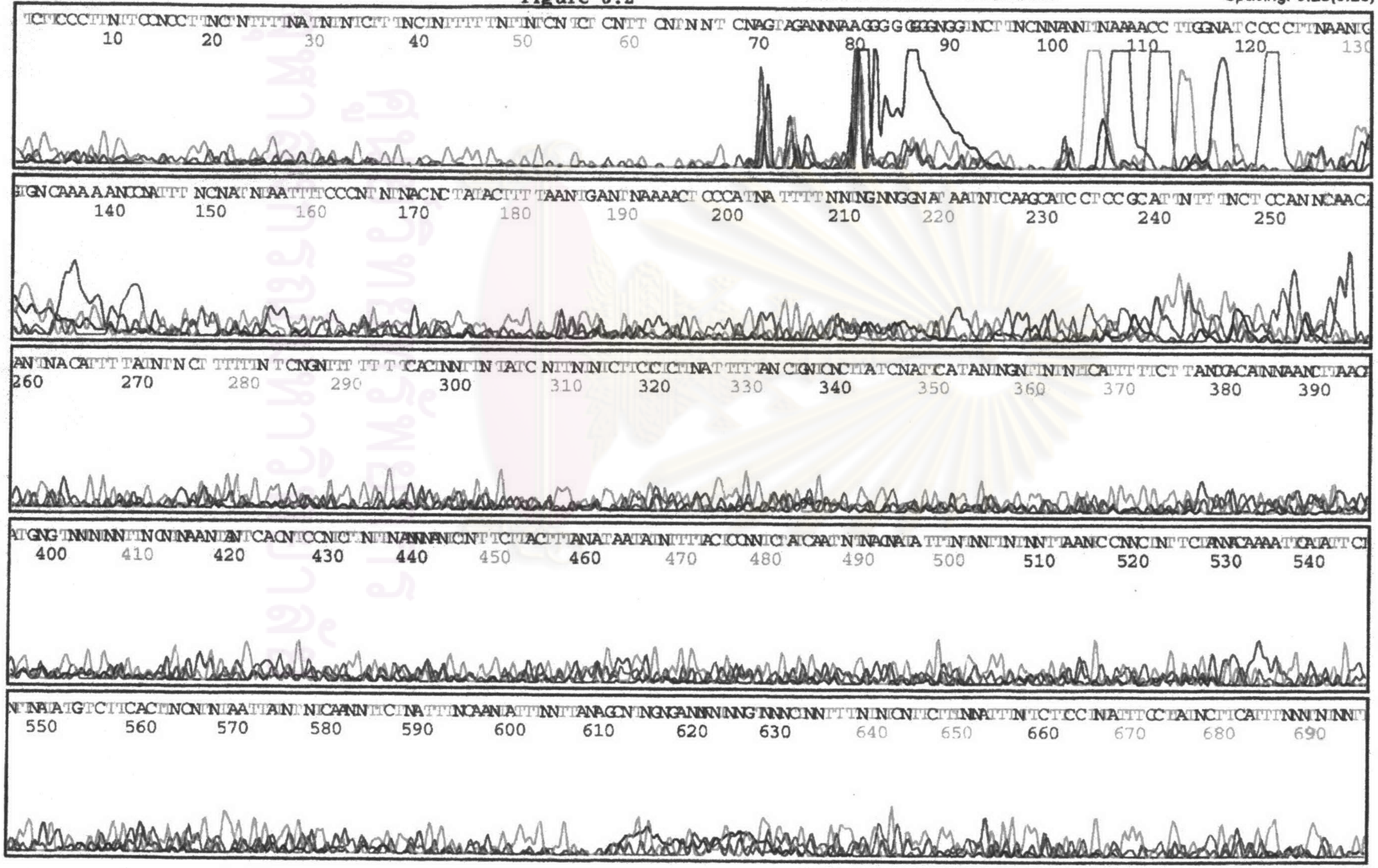
SQ. 5356

Signal G:15 A:10 T:10 C:14
DT {BD Set Any-Primer}
BD Matrix Std.Jan31,01.
Points 300 to 10616 Pk 1 Loc: 300

Page 2 of 2

Page 1 of 2
Sun, Dec 02, 2001 09:08
Sat, Dec 01, 2001 16:38
Spacing: 9.28(9.28)

Figure 5.2



ABI PRISM™

Model 377
Version 3.4
ABI100
Version 3.2

11•S172/343r

S172/343r
Lane 11

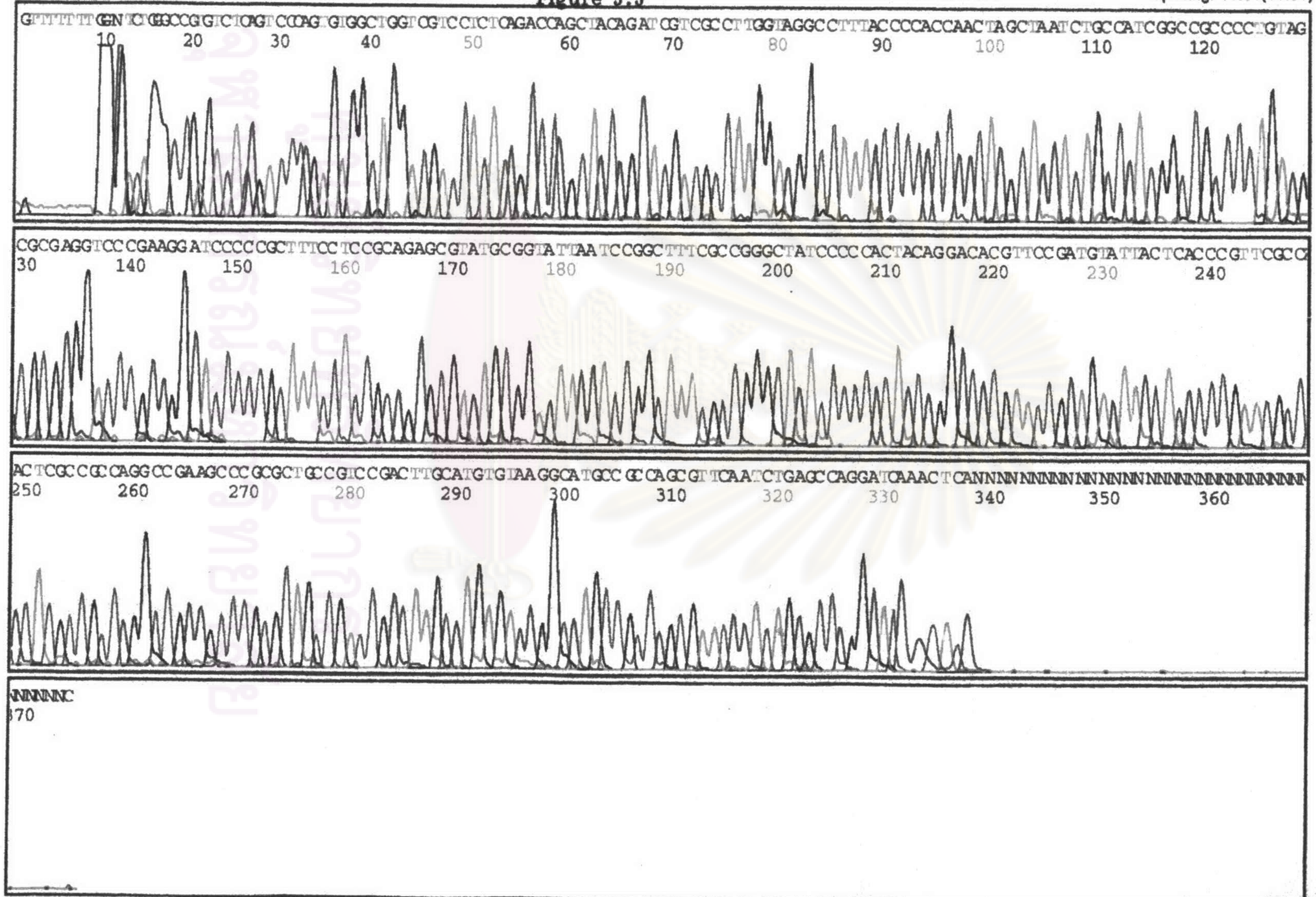
SQ....S355....

Signal G:339 A:196 T:152 C:392
DT (BD Set Any-Primer)
BD Matrix Std.Jan31,01.
Points 973 to 5000 Pk 1 Loc: 973

Page...2...of...2...

Page 1 of 1
Sat, Dec 01, 2001 08:46
Fri, Nov 30, 2001 15:59
Spacing: 11.01(11.01)

Figure 5.3



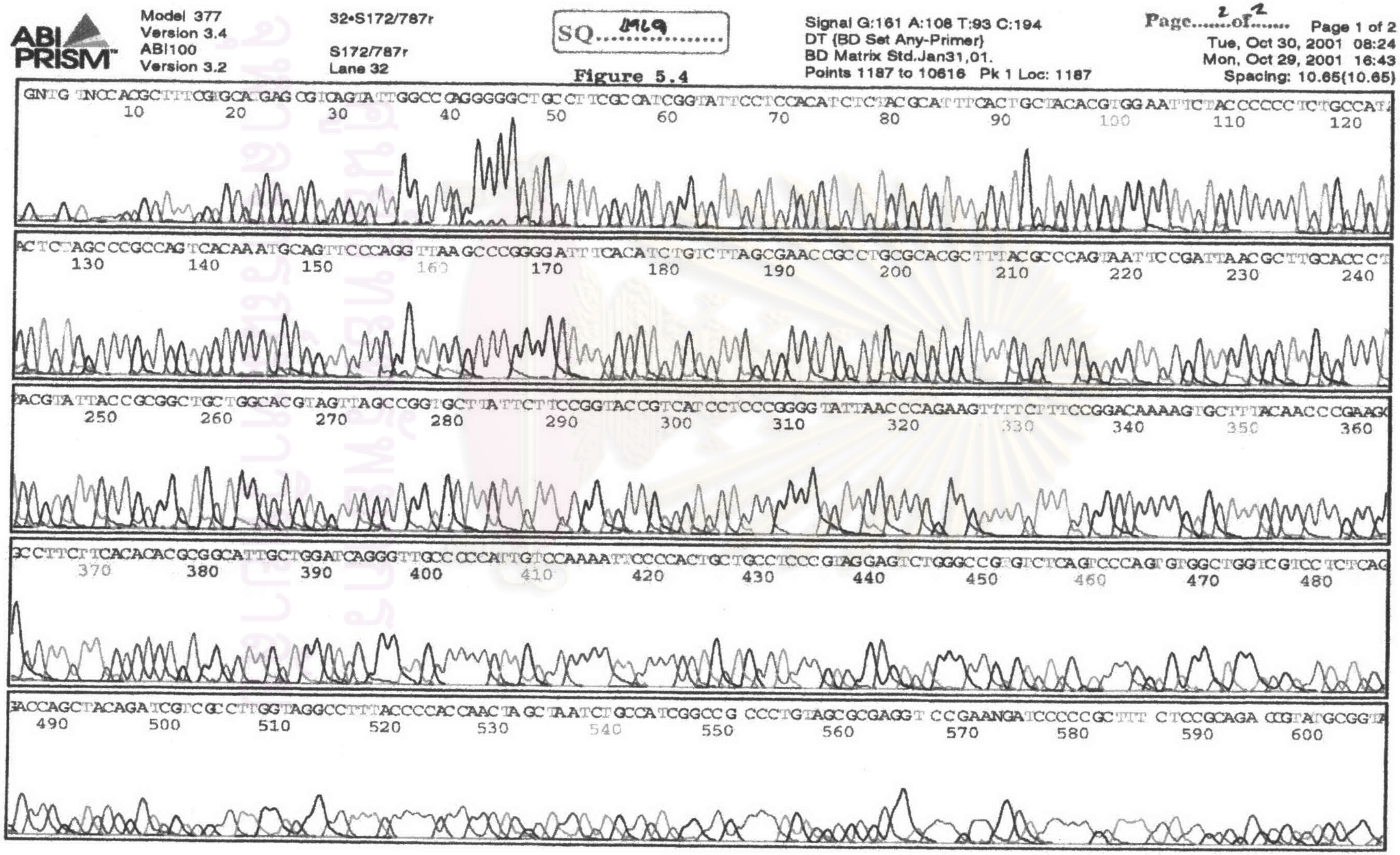

ABI PRISM
Model 377
Version 3.4
ABI100
Version 3.2
32•S172/787r
S172/787r
Lane 32
SQ. MLQ
Signal G:161 A:108 T:93 C:194
DT (BD Set Any-Primer)
BD Matrix Std.Jan31,01.
Points 1187 to 10616 Pk 1 Loc: 1187
Page 2 of 2
Page 1 of 2
Tue, Oct 30, 2001 08:24
Mon, Oct 29, 2001 16:43
Spacing: 10.65(10.65)

Figure 5.4

ABI PRISM

Model 377
Version 3.4
ABI100
Version 3.2

35•S172/1100r

S172/1100r
Lane 35

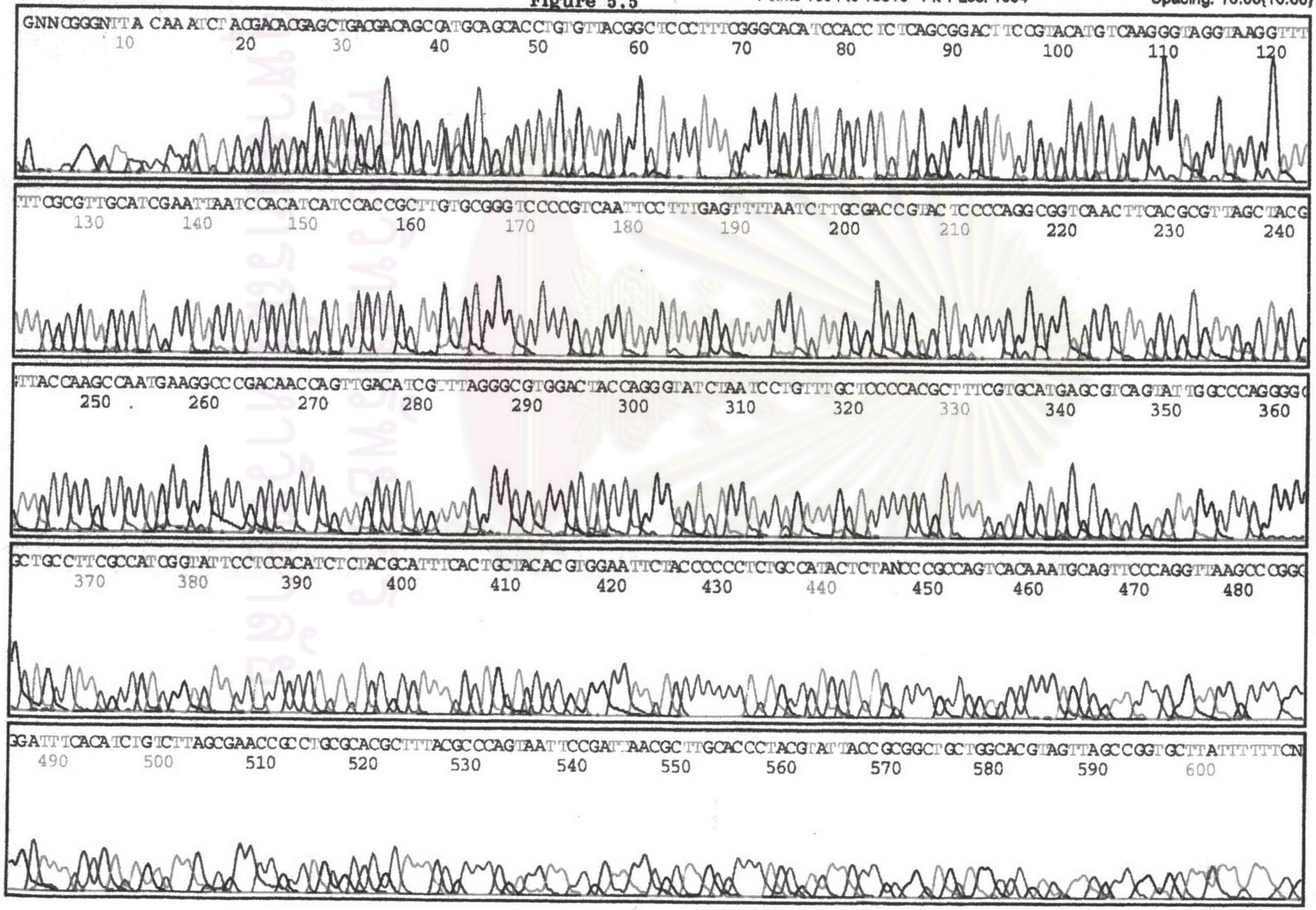
SQ. 0970

Signal G:205 A:124 T:98 C:206
DT {BD Set Any-Primer}
BD Matrix Std.Jan31.01.
Points 1004 to 10616 Pk 1 Loc: 1004

Page 2 of 2

Page 1 of 2
Tue, Oct 30, 2001 08:26
Mon, Oct 29, 2001 16:43
Spacing: 10.66(10.66)

Figure 5.5



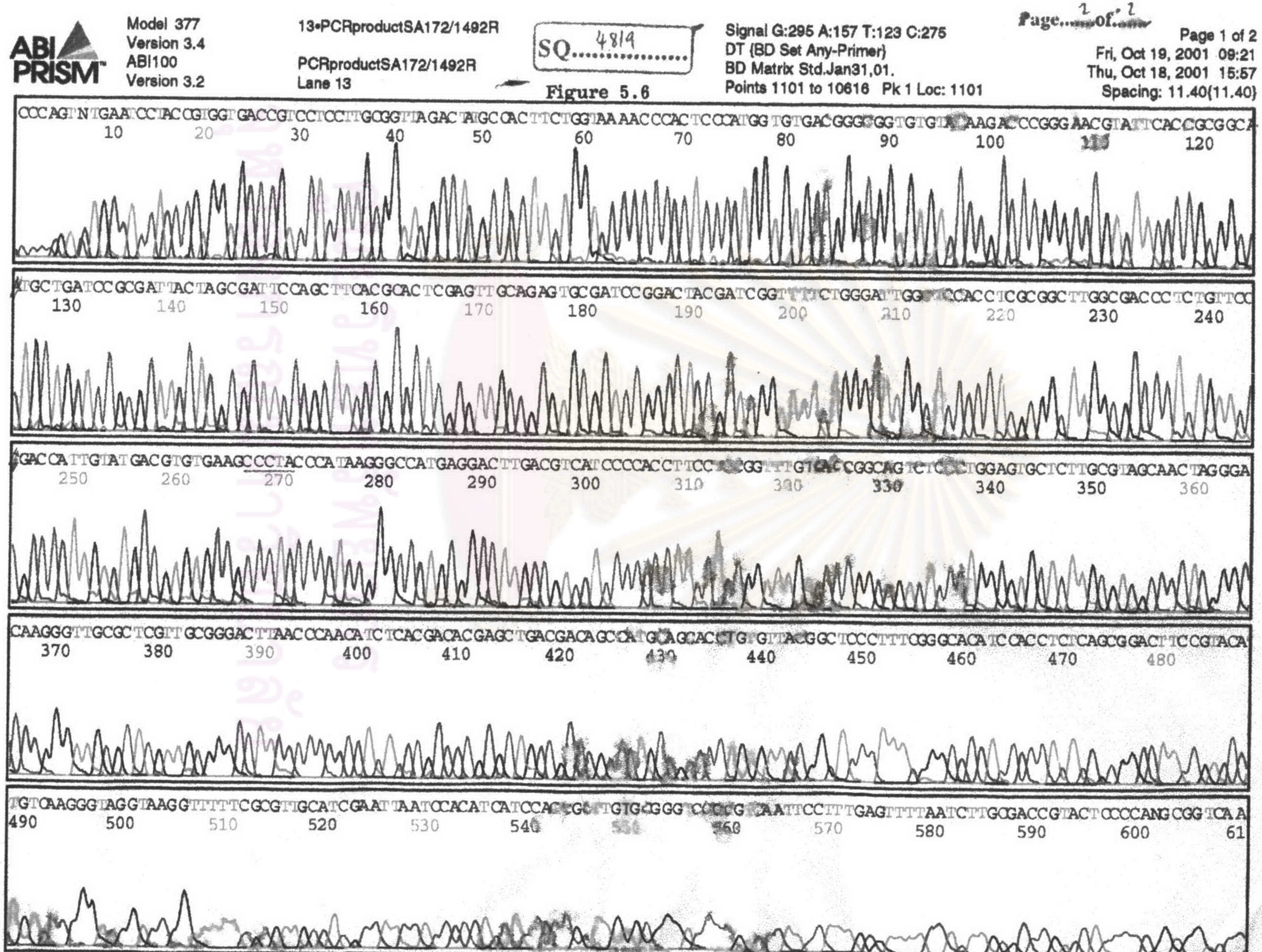

ABI PRISM
Model 377
Version 3.4
ABI100
Version 3.2
13•PCRproductSA172/1492R
PCRproductSA172/1492R
Lane 13
SQ 4814
Signal G:295 A:157 T:123 C:275
DT {BD Set Any-Primer}
BD Matrix Std.Jan31,01.
Points 1101 to 10616 Pk 1 Loc: 1101
Page 1 of 2
Fri, Oct 19, 2001 09:21
Thu, Oct 18, 2001 15:57
Spacing: 11.40{11.40}

Figure 5.6

ABI PRISM

Model 377
Version 3.4
ABI100
Version 3.2

09•PCR ProductS173/forward27

PCR ProductS173/forward27f
Lane 9

SQ. 4505

Signal G:116 A:54 T:30 C:60
DT {BD Set Any-Primer}
BD Matrix Std.Jan31,01.
Points 1001 to 10616 Pk 1 Loc: 1001

Page 1 of 2
Thu, Oct 11, 2001 07:53
Wed, Oct 10, 2001 16:17
Spacing: 10.82{10.82}

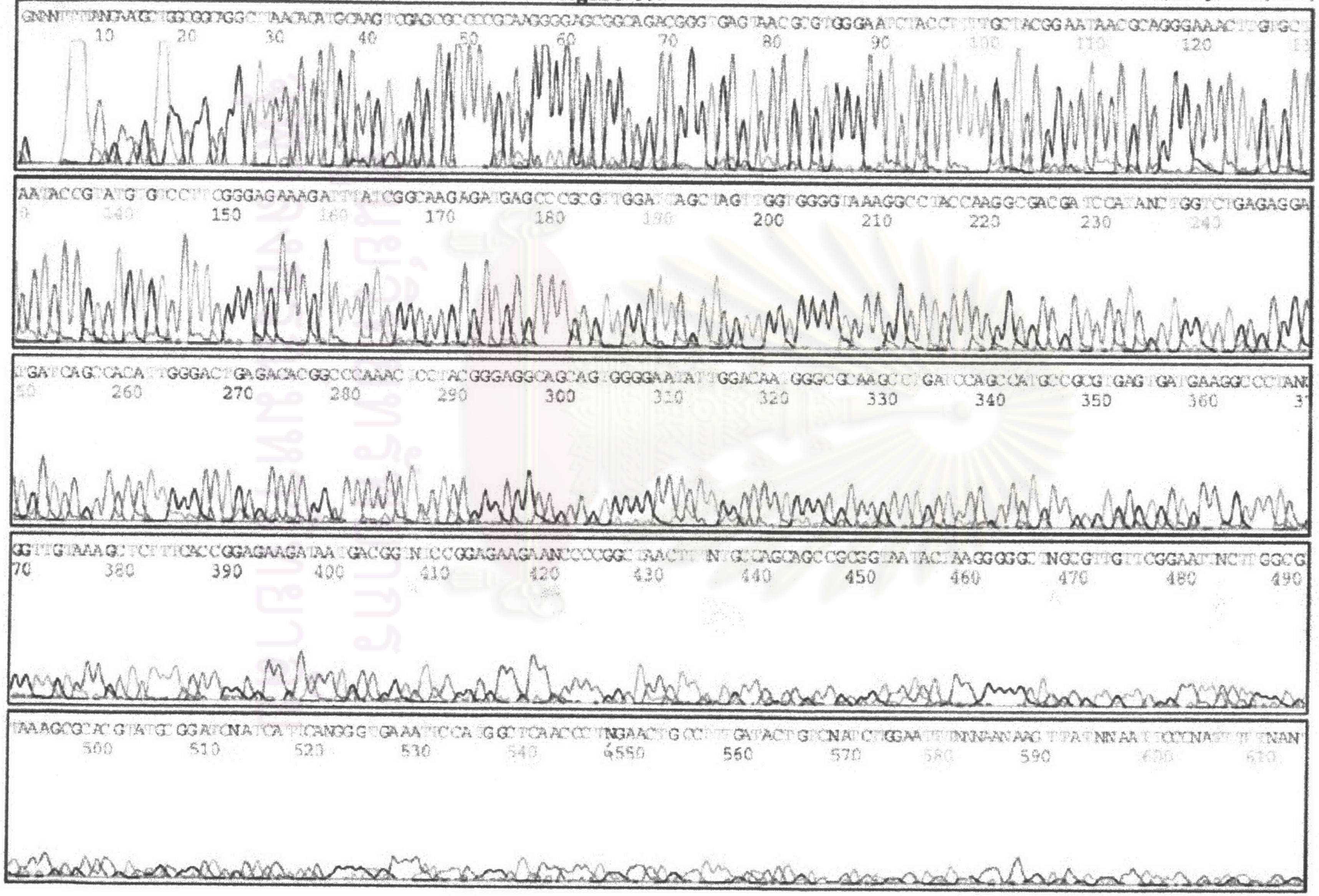


Figure 5.7

ABI PRISM™

Model 377
Version 3.4
ABI100
Version 3.2

14•S173/1241f

S173/1241f
Lane 14

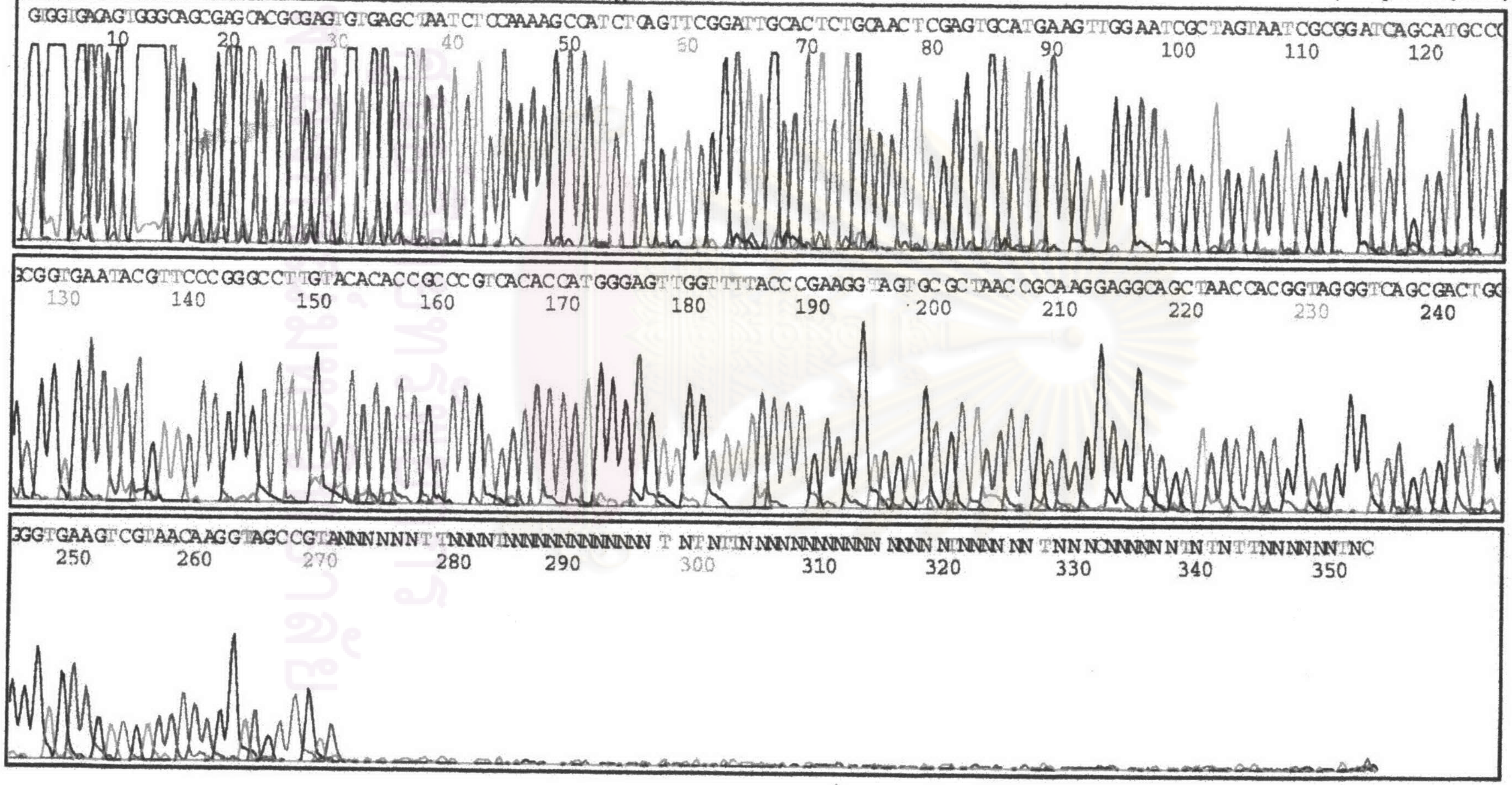
SQ. 5358

Signal G:241 A:131 T:71 C:169
DT {BD Set Any-Primer}
BD Matrix Std.Jan31,01.
Points 1147 to 5000 Pk 1 Loc: 1147

Page 2 of 2

Page 1 of 1
Sat, Dec 01, 2001 08:47
Fri, Nov 30, 2001 15:59
Spacing: 11.07{11.07}

Figure 5.8



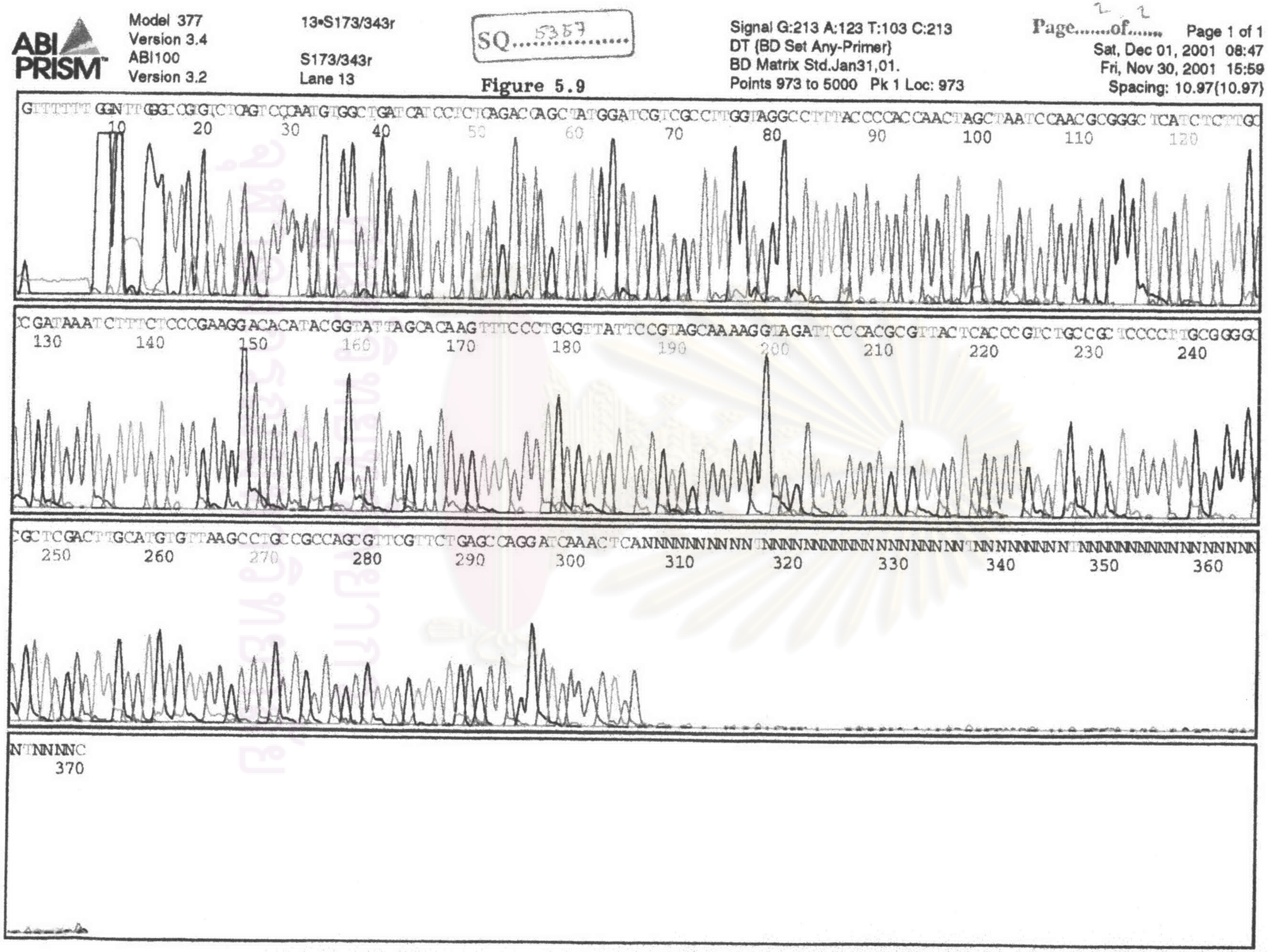

ABI PRISM
Model 377
Version 3.4
ABI100
Version 3.2
13•S173/343r
S173/343r
Lane 13
SQ...5357
Signal G:213 A:123 T:103 C:213
DT {BD Set Any-Primer}
BD Matrix Std.Jan31,01.
Points 973 to 5000 Pk 1 Loc: 973
Page...2...of...2
Page 1 of 1
Sat, Dec 01, 2001 08:47
Fri, Nov 30, 2001 15:59
Spacing: 10.97{10.97}

Figure 5.9

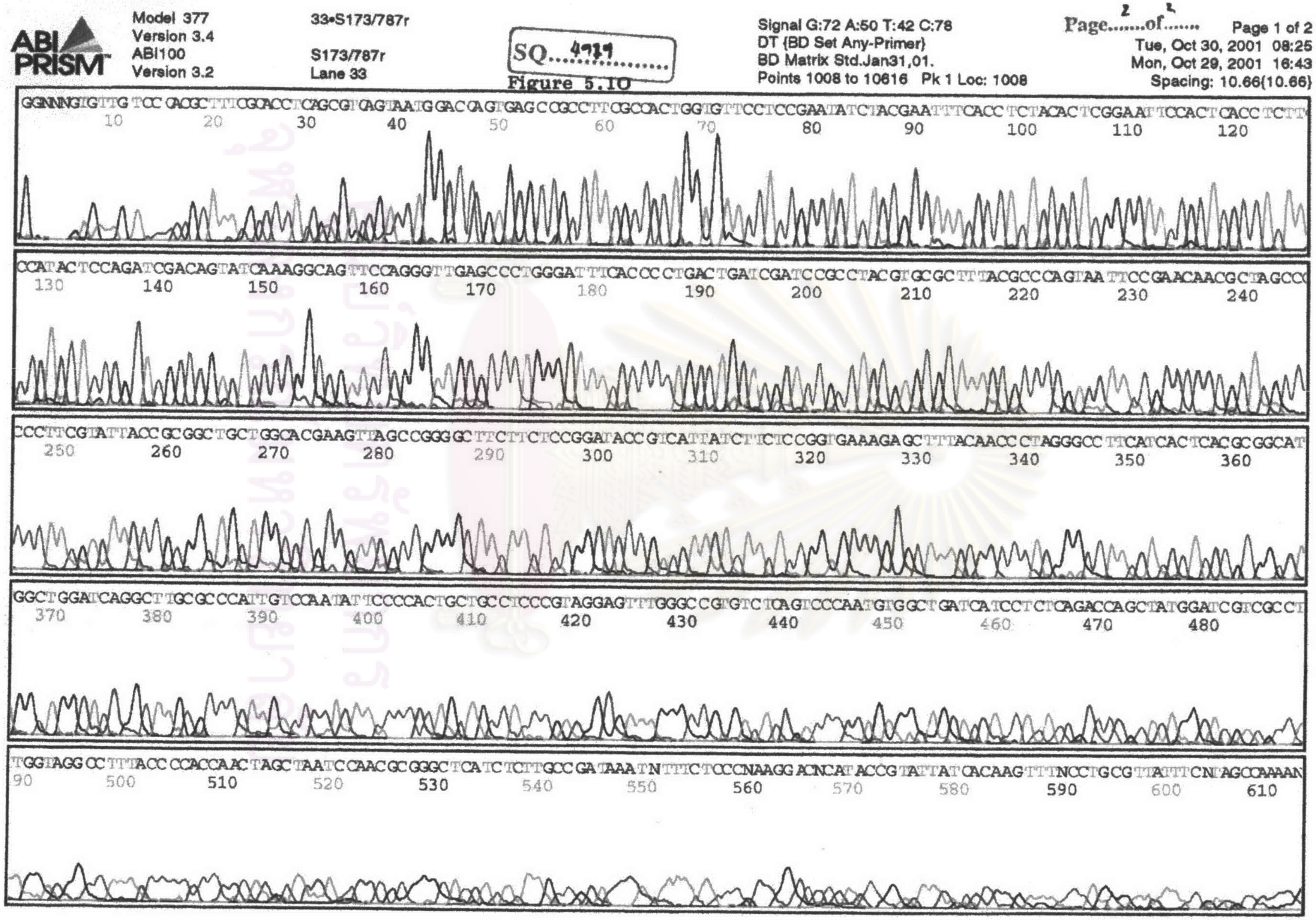

ABI PRISM
Model 377
Version 3.4
ABI100
Version 3.2
33•S173/787r
S173/787r
Lane 33
SQ....4717.........
Signal G:72 A:50 T:42 C:78
DT {BD Set Any-Primer}
BD Matrix Std.Jan31,01.
Points 1008 to 10616 Pk 1 Loc: 1008
Page...2...of...2...
Page 1 of 2
Tue, Oct 30, 2001 08:25
Mon, Oct 29, 2001 16:43
Spacing: 10.66(10.66)

Figure 5.10

ABI PRISM™

Model 377
Version 3.4
ABI100
Version 3.2

36•S173/1100r

S173/1100r
Lane 36

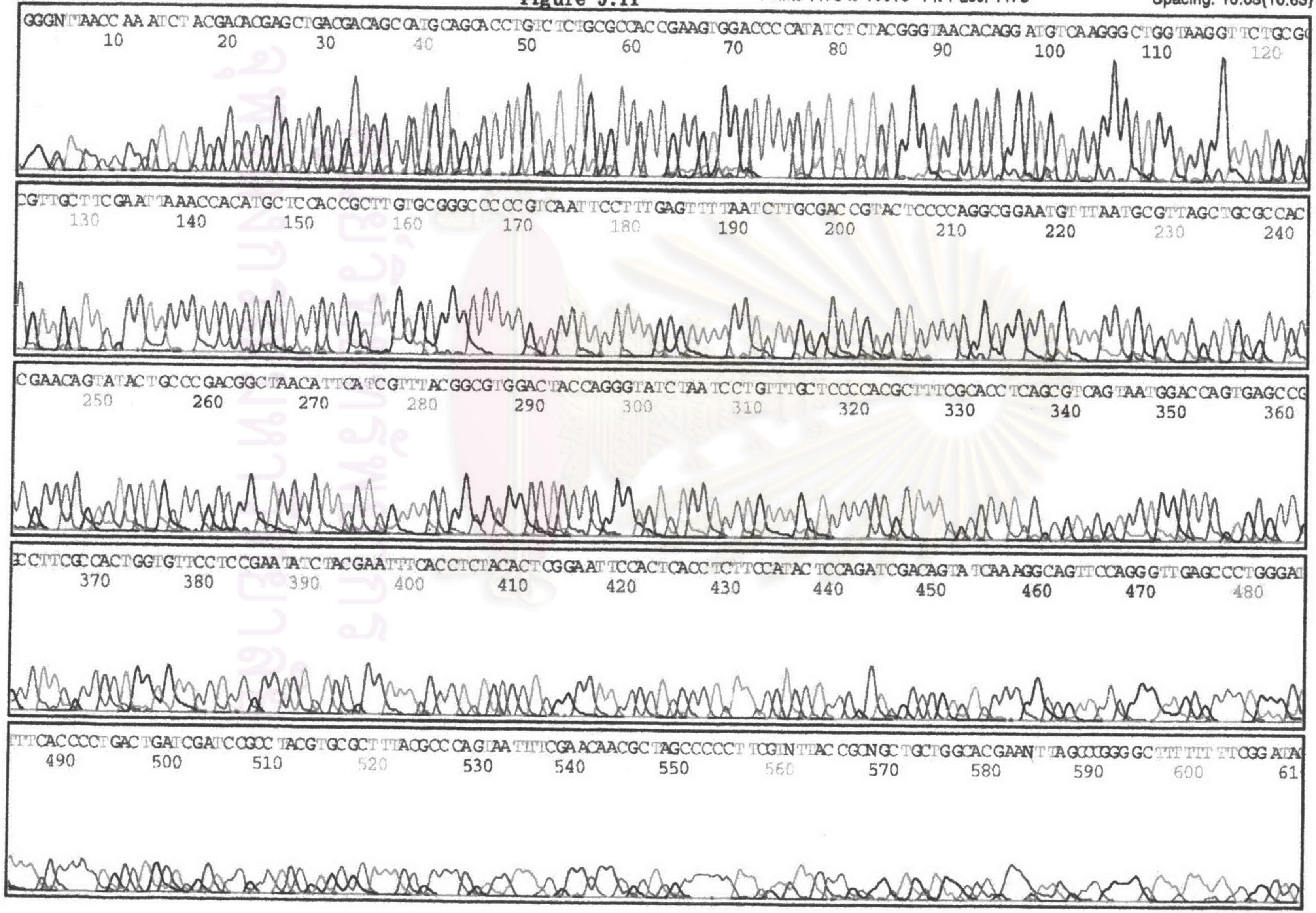
SQ......4912.........

Signal G:121 A:79 T:57 C:123
DT (BD Set Any-Primer)
BD Matrix Std.Jan31,01.
Points 1173 to 10616 Pk 1 Loc: 1173

Page...1...of...1...

Page 1 of 2
Tue, Oct 30, 2001 08:26
Mon, Oct 29, 2001 16:43
Spacing: 10.63(10.63)

Figure 5.11



ABI PRISM™

Model 377
Version 3.4
ABI100
Version 3.2

14•PCRproductS173/1492R

PCRproductS173/1492R
Lane 14

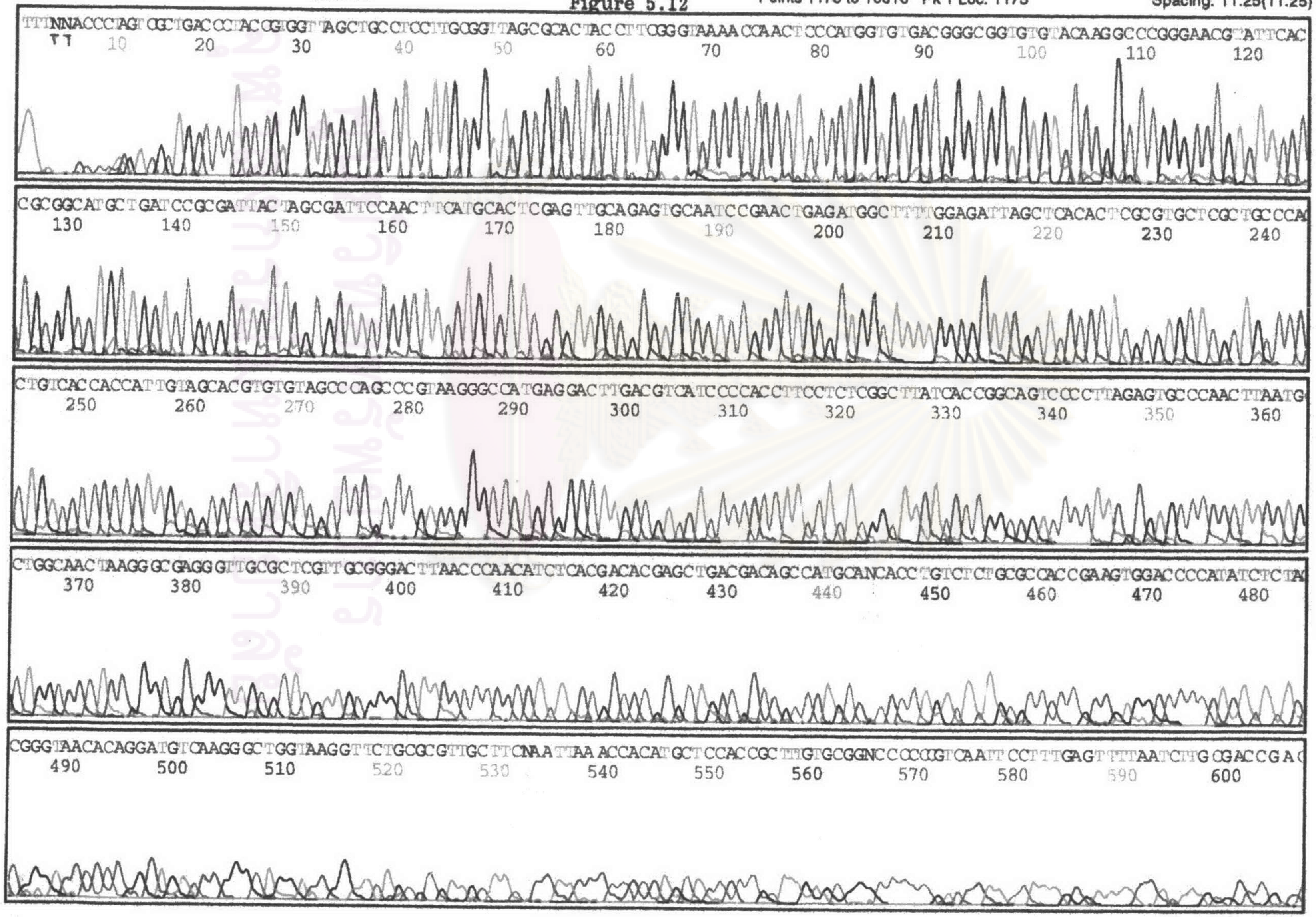
SQ....4820....

Signal G:145 A:78 T:60 C:128
DT {BD Set Any-Primer}
BD Matrix Std.Jan31,01.
Points 1173 to 10616 Pk 1 Loc: 1173

Page...2...of...2...

Page 1 of 2
Fri, Oct 19, 2001 09:21
Thu, Oct 18, 2001 15:57
Spacing: 11.25(11.25)

Figure 5.12



ABI PRISM

Model 377
Version 3.4
ABI100
Version 3.2

25•S174/27f

S174/27f
Lane 25

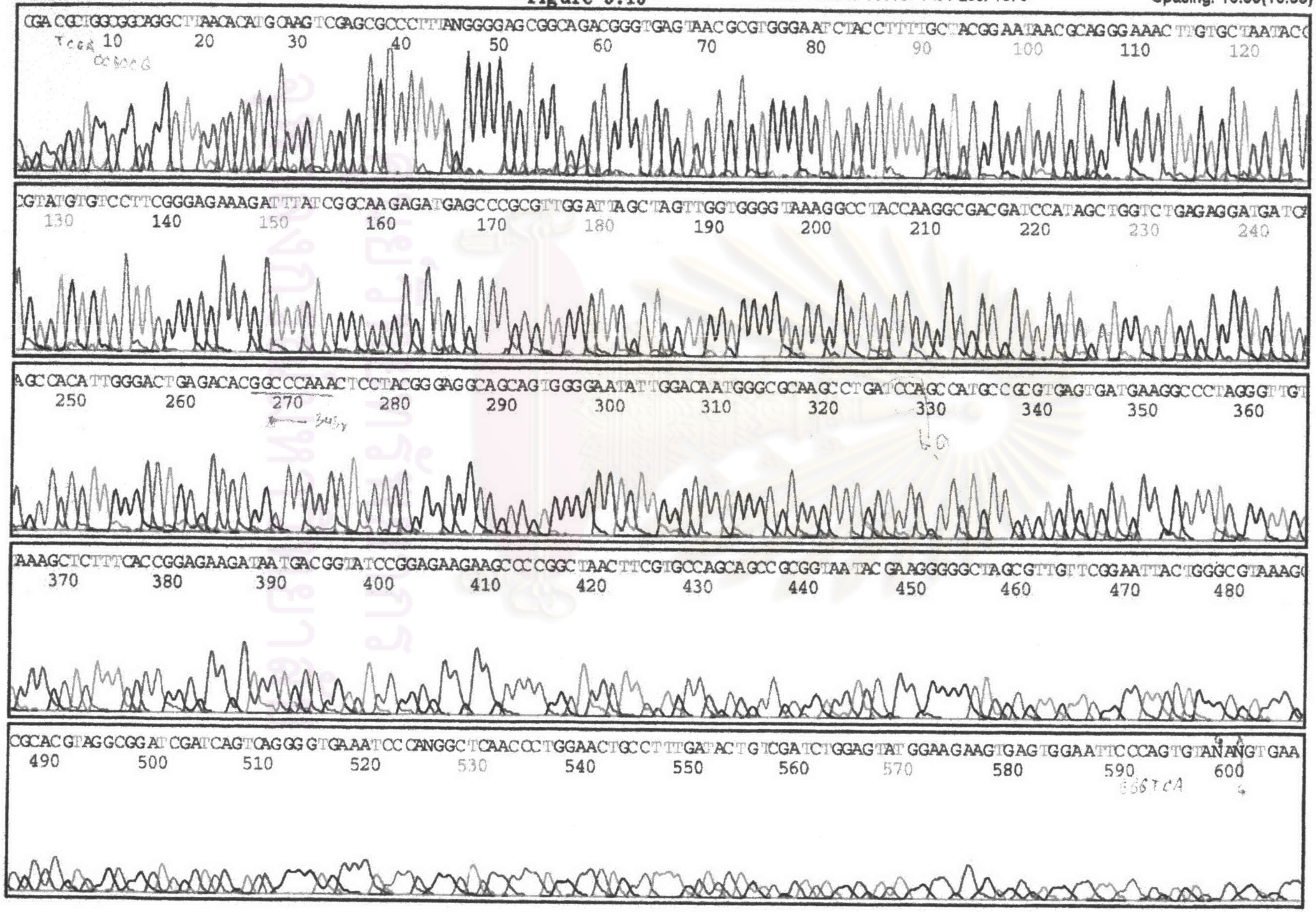
SQ......5204......

Figure 5.13

Signal G:314 A:163 T:73 C:161
DT {BD Set Any-Primer}
BD Matrix Std.Jan31,01.
Points 1079 to 10616 Pk 1 Loc: 1079

Page...2...of...2...

Page 1 of 2
Sun, Nov 25, 2001 18:07
Fri, Nov 23, 2001 16:03
Spacing: 10.99(10.99)



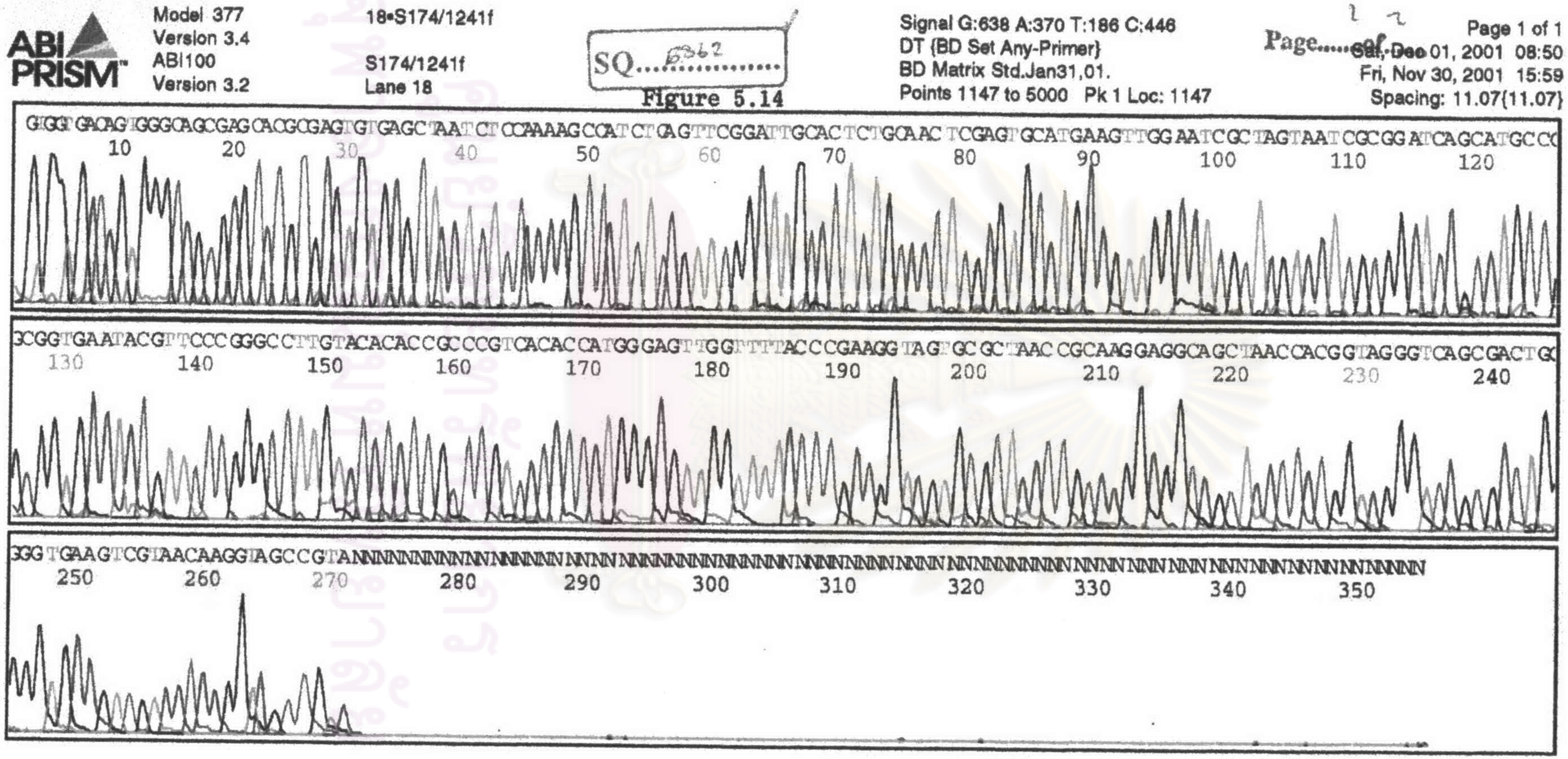

ABI PRISM
Model 377
Version 3.4
ABI100
Version 3.2
18•S174/1241f
S174/1241f
Lane 18
SQ.......
Signal G:638 A:370 T:186 C:446
DT {BD Set Any-Primer}
BD Matrix Std.Jan31,01.
Points 1147 to 5000 Pk 1 Loc: 1147
Page 1 of 1
Sat, Dec 01, 2001 08:50
Fri, Nov 30, 2001 15:59
Spacing: 11.07{11.07}
Page......of......

Figure 5.14

ABI PRISM™

Model 377
Version 3.4
ABI100
Version 3.2

17•S174/343r

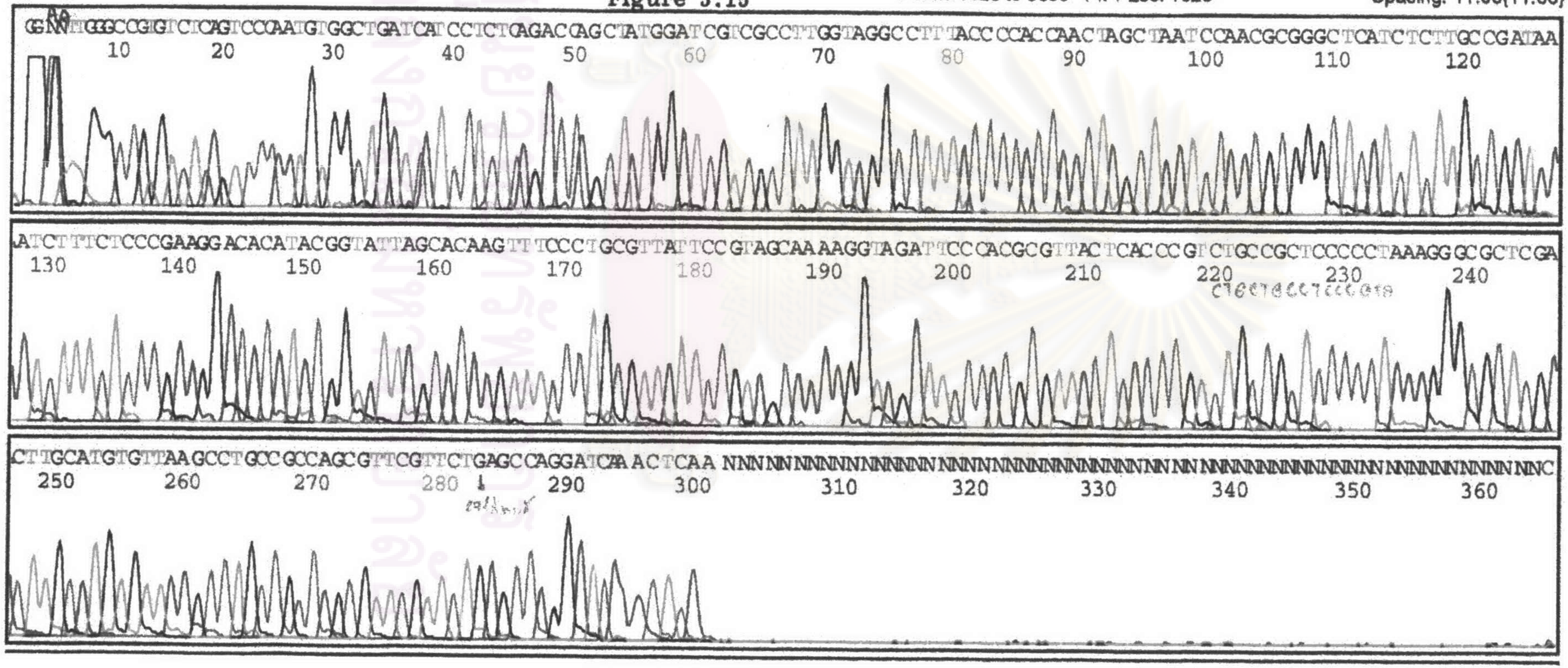
S174/343r
Lane 17

SQ......

Signal G:288 A:185 T:136 C:259
DT {BD Set Any-Primer}
BD Matrix Std.Jan31,01.
Points 1028 to 5000 Pk 1 Loc: 1028

Page 1 of 1
Sat, Dec 01, 2001 08:50
Fri, Nov 30, 2001 15:59
Spacing: 11.06{11.06}

Figure 5.15



ABI PRISM

Model 377
Version 3.4
ABI100
Version 3.2

15•S174/787r

S174/787r
Lane 15

SQ. 5359

Signal G:196 A:139 T:117 C:245
DT {BD Set Any-Primer}
BD Matrix Std.Jan31,01.
Points 971 to 10616 Pk 1 Loc: 971

Page 2 of 2

Page 1 of 2
Sat, Dec 01, 2001 08:31
Fri, Nov 30, 2001 15:59
Spacing: 10.98{10.98}

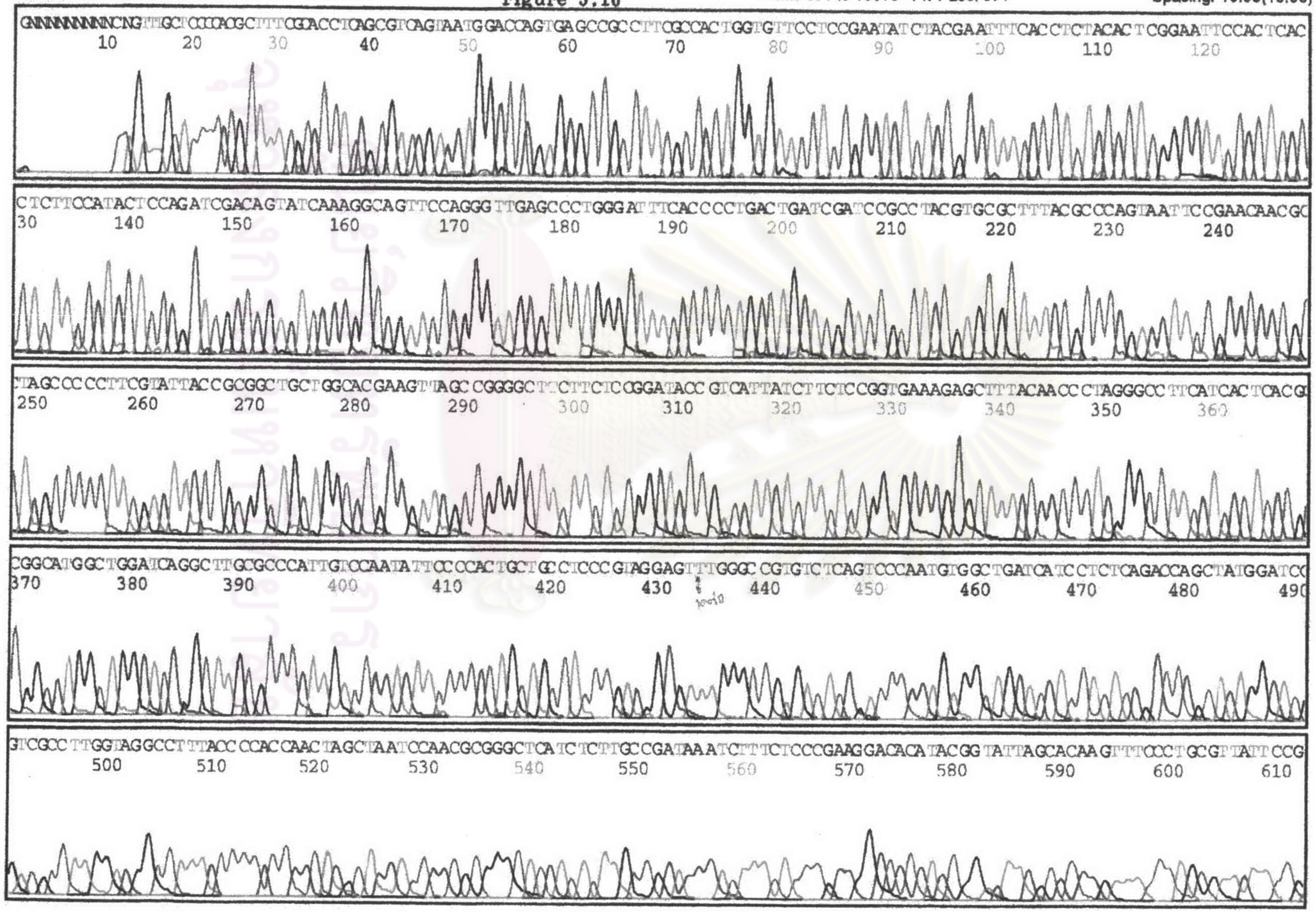


Figure 5.16

ABI PRISM™

Model 377
Version 3.4
ABI100
Version 3.2

16•S174/1100r

S174/1100r
Lane 16

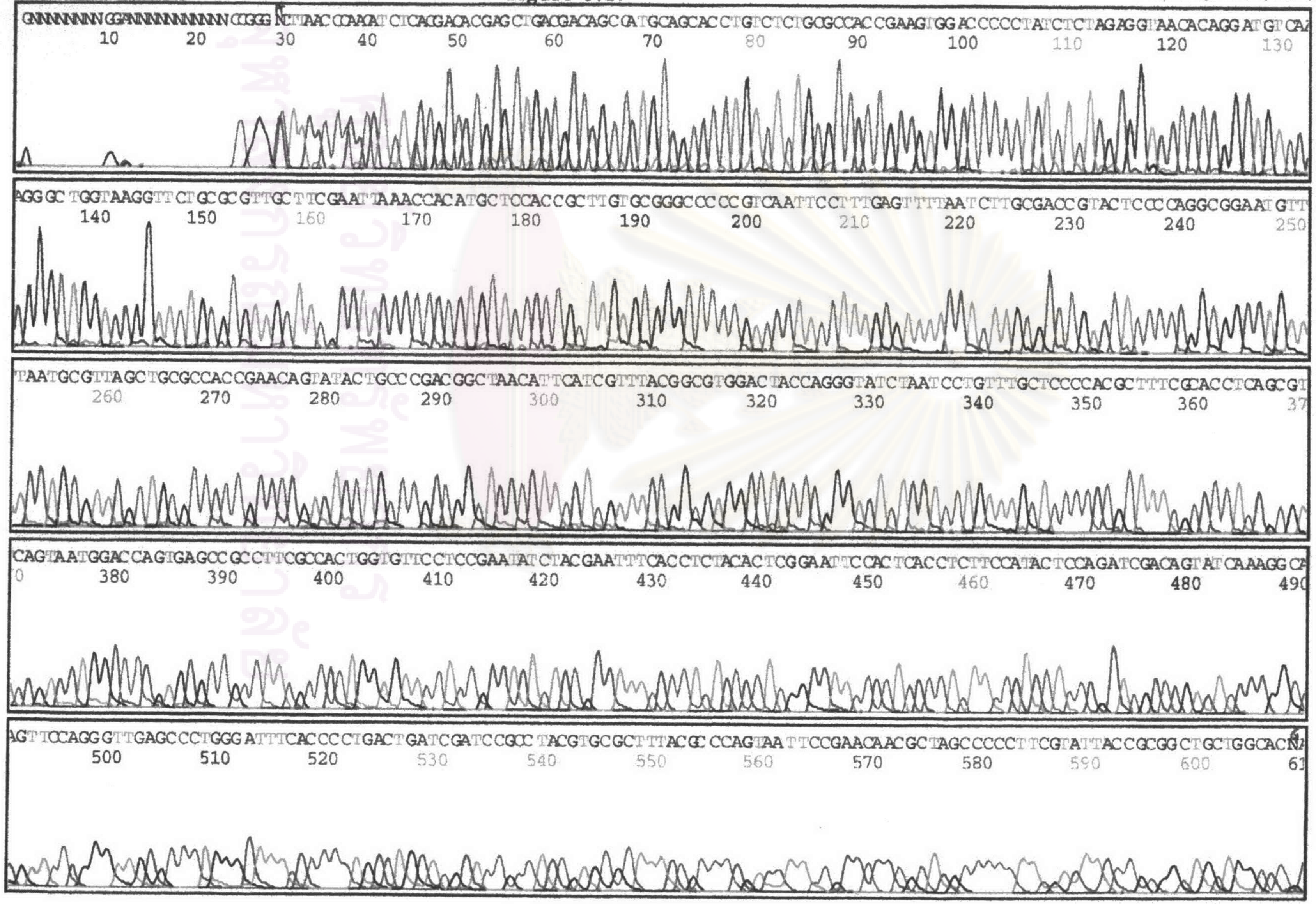
SQ.....8360.....

Signal G:389 A:281 T:204 C:476
DT {BD Set Any-Primer}
BD Matrix Std.Jan31,01.
Points 970 to 10616 Pk 1 Loc: 970

Page...2...of...2...

Page 1 of 2
Sat, Dec 01, 2001 08:31
Fri, Nov 30, 2001 15:59
Spacing: 10.84{10.84}

Figure 5.17



ABI PRISM™

Model 377
Version 3.4
ABI100
Version 3.2

26•S174/1492r

S174/1492r
Lane 26

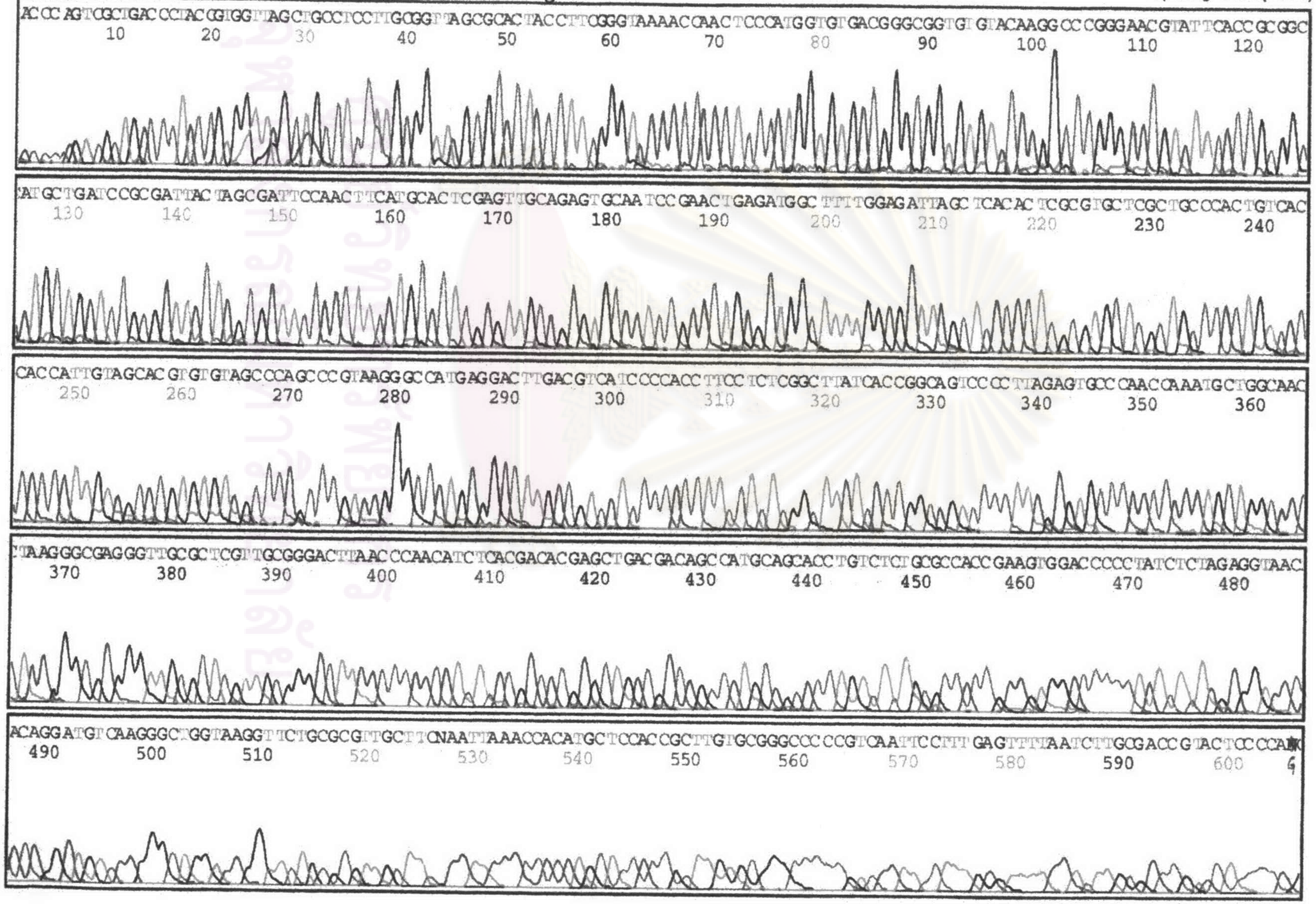
SQ......5205......

Signal G:343 A:190 T:129 C:299
DT {BD Set Any-Primer}
BD Matrix Std.Jan31,01.
Points 1192 to 10616 Pk 1 Loc: 1192

Page....2....of....2....

Page 1 of 2
Sun, Nov 25, 2001 18:07
Fri, Nov 23, 2001 16:03
Spacing: 11.00{11.00}

Figure 5.18



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                                                              Score    E
Sequences producing significant alignments:                  (bits) Value

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gi|3273471|gb|U96940.1|U96940  Burkholderia graminis 16S rib...  1053   0.0
gi|3273470|gb|U96939.1|U96939  Burkholderia graminis 16S rib...  1053   0.0
gi|9280413|gb|AF247493.1|AF247493  Burkholderia sp. C4.7 16S...  1045   0.0
gi|17863929|gb|AF448046.1|AF448046  Burkholderia sp. SOD-7 1...  1039   0.0
gi|2623537|gb|U91570.1|BCU91570  Burkholderia caryophylli 16...  1031   0.0
gi|17863928|gb|AF448045.1|AF448045  Burkholderia sp. SOD-6 1...  1013   0.0
gi|21070363|gb|AF508806.1|  Burkholderia sp. TNFYE-5 16S rib...  1005   0.0
gi|18249661|dbj|AB066231.1|  Burkholderia sp. PJ310 gene for...  1001   0.0
gi|12718590|emb|AJ292643.1|UEU292643  uncultured eubacterium...   997   0.0

                                 Alignments
>gi|3273472|gb|U96941.1|U96941  Burkholderia graminis 16S ribosomal RNA gene, partial
sequence
          Length = 1584

 Score = 1053 bits (531), Expect = 0.0
 Identities = 534/535 (99%)
 Strand = Plus / Minus


Query: 524  acgacacgagctgacgacagccatgcagcacctgtgttacggctccctttcgggcacatc 583
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1025 acgacacgagctgacgacagccatgcagcacctgtgttacggctccctttcgggcacatc 966


Query: 584  cacctctcagcggacttccgtacatgtcaagggtaggtaaggtttttcgcgttgcatcga 643
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 965  cacctctcagcggacttccgtacatgtcaagggtaggtaaggtttttcgcgttgcatcga 906


Query: 644  attaatccacatcatccaccgcttgtgcgggtccccgtcaattcctttgagttttaatct 703
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 905  attaatccacatcatccaccgcttgtgcgggtccccgtcaattcctttgagttttaatct 846


Query: 704  tgcgaccgtactccccaggcggtcaacttcacgcgttagctacgttaccaagccaatgaa 763
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 845  tgcgaccgtactccccaggcggtcaacttcacgcgttagctacgttaccaagccaatgaa 786


Query: 764  ggcccgacaaccagttgacatcgtttagggcgtggactaccagggtatctaatcctgttt 823
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 785  ggcccgacaaccagttgacatcgtttagggcgtggactaccagggtatctaatcctgttt 726
```

```
Query: 824  gctccccacgctttcgtgcatgagcgtcagtattggcccaggggctgccttcgccatcg 883
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 725  gctccccacgctttcgtgcatgagcgtcagtattggcccaggggctgccttcgccatcg 666

Query: 884  gtattcctccacatctctacgcatttcactgctacacgtggaattctacccccctctgcc 943
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 665  gtattcctccacatctctacgcatttcactgctacacgtggaattctacccccctctgcc 606

Query: 944  atactctatcccgccagtcacaaatgcagttcccaggttaagcccggggatttcacatct 1003
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 605  atactctagcccgccagtcacaaatgcagttcccaggttaagcccggggatttcacatct 546

Query: 1004 gtcttagcgaaccgcctgcgcacgctttacgcccagtaattccgattaacgcttg 1058
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 545  gtcttagcgaaccgcctgcgcacgctttacgcccagtaattccgattaacgcttg 491
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Strand = Plus / Minus

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 490 caccctacgtattaccgcggctgctggcacgtagttagccggtgcttattcttccggtac 431

Query: 61  cgtcatcctcccggggtattaacccagaagttttctttccggacaaaagtgctttacaac 120
           ||||||||  || || ||||| ||  |  |||||||||||||||||||||||||||||||
Sbjct: 430 cgtcatcccgcccggatattagccaggcggttttctttccggacaaaagtgctttacaac 371

Query: 121 ccgaaggccttcttcacacacgcggcattgctggatcagggttgcccccattgtccaaaa 180
           |||||||||||||||||||||||||||||||||||||||| |||| ||||||||||||||
Sbjct: 370 ccgaaggccttcttcacacacgcggcattgctggatcaggcttgcgcccattgtccaaaa 311

Query: 181 ttccccactgctgcctcccgtaggagtctgggccgtgtctcagtcccagtgtggctggtc 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 310 ttccccactgctgcctcccgtaggagtctgggccgtgtctcagtcccagtgtggctggtc 251

Query: 241 gtcctctcagaccagctacagatcgtcgccttggtaggcctttaccccaccaactagcta 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 250 gtcctctcagaccagctacagatcgtcgccttggtaggcctttaccccaccaactagcta 191
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```
Query: 301 atctgccatcggccgcccctgtagcgcgaggtcccgaaggatcccccgctttcctccgca 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 190 atctgccatcggccgcccctgtagcgcgaggtcccgaaggatcccccgctttcctccgca 131

Query: 361 gagcgtatgcggtattaatccggctttcgccgggctatccccactacaggacacgttcc 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 130 gagcgtatgcggtattaatccggctttcgccgggctatccccactacaggacacgttcc 71

Query: 421 gatgtattactcaacccgttcgccactcgccgccagg 457
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Sbjct: 70  gatgtattactc-acccgttcgccactcgccaccagg 35
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Score = 753 bits (380), Expect = 0.0
Identities = 387/388 (99%), Gaps = 1/388 (0%)
Strand = Plus / Minus

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            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct: 1421 tgaatcctaccgtggtgaccgtcctccttgcggttagacta-gccacttctggtaaaacc 1363

Query: 1117 cactcccatggtgtgacgggcggtgtgtacaagacccgggaacgtattcaccgcggcatg 1176
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1362 cactcccatggtgtgacgggcggtgtgtacaagacccgggaacgtattcaccgcggcatg 1303

Query: 1177 ctgatccgcgattactagcgattccagcttcacgcactcgagttgcagagtgcgatccgg 1236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1302 ctgatccgcgattactagcgattccagcttcacgcactcgagttgcagagtgcgatccgg 1243

Query: 1237 actacgatcggttttctgggattggctccacctcgcggcttggcgaccctctgttccgac 1296
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Sbjct: 1242 actacgatcggttttctgggattggctccacctcgcggcttggcgaccctctgttccgac 1183

Query: 1297 cattgtatgacgtgtgaagccctacccataagggccatgaggacttgacgtcatccccac 1356
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1182 cattgtatgacgtgtgaagccctacccataagggccatgaggacttgacgtcatccccac 1123

Query: 1357 cttcctccggtttgtcaccggcagtctccctggagtgctcttgcgtagcaactagggaca 1416
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sequences producing significant alignments:	Score (bits)	E Value
gi|28894114|gb|AY206687.1| Rhizobium rhizogenes strain 163C...	2658	0.0
gi|464144|dbj|D14504.1|ATU16SRDJ Rhizobium sp. K-Ag-3 gene ...	2654	0.0
gi|27261750|gb|AY166841.1| Rhizobium tropici UPRM8033 16S r...	2637	0.0
gi|1055273|gb|U38469.1|RTU38469 Rhizobium tropici 16S ribos...	2619	0.0
gi|28849772|gb|AF514802.1| Rhizobium sp. ORS217 16S ribosom...	2615	0.0
gi|464139|dbj|D14505.1|ATU16SRDK Rhizobium sp. Ch-Ag-4 gene...	2615	0.0
gi|464142|dbj|D14501.1|ATU16SRDG Rhizobium rhizogenes gene ...	2615	0.0
gi|464203|dbj|D11344.1|RHM16SRDC Rhizobium tropici gene for...	2609	0.0
gi|28849771|gb|AF514801.1| Rhizobium sp. ORS214 16S ribosom...	2605	0.0
gi|296410|emb|X67224.1|AR16SRRNA A.rhizogenes (LMG 152) gen...	2605	0.0

Alignments

>gi|28894114|gb|AY206687.1| Rhizobium rhizogenes strain 163C 16S ribosomal RNA, partial sequence
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Score = 2658 bits (1341), Expect = 0.0
Identities = 1421/1444 (98%), Gaps = 4/1444 (0%)
Strand = Plus / Minus

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Sbjct: 1446 tacggctaccttgttacgacttcaccccagtcgctgaccctaccgtggttagctgcctcc 1387

Query: 61   ttgcggttagcgcactaccttcgggtaaaaccaactcccatggtgtgacgggcggtgtgt 120
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Sbjct: 1386 ttgcggttagcgcactaccttcgggtaaaaccaactcccatggtgtgacgggcggtgtgt 1327

Query: 121  acaaggcccgggaacgtattcaccgcggcatgctgatccgcgattactagcgattccaac 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1326 acaaggcccgggaacgtattcaccgcggcatgctgatccgcgattactagcgattccaac 1267

Query: 181  ttcatgcactcgagttgcagagtgcaatccgaactgagatggcttttggagattagctca 240
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Sbjct: 1266 ttcatgcactcgagttgcagagtgcaatccgaactgagatggcttttggagattagctca 1207

Query: 241  cactcgcgtgctcgctgcccactgtcaccaccattgtagcacgtgtgtagcccagcccgt 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1206 cactcgcgtgctcgctgcccactgtcaccaccattgtagcacgtgtgtagcccagcccgt 1147

Query: 301  aagggccatgaggacttgacgtcatccccaccttcctctcggcttatcaccggcagtccc 360
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Sbjct: 1146 aagggccatgaggacttgacgtcatccccaccttcctctcggcttatcaccggcagtccc 1087
```

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Query: 361  cttagagtgcccaacttaatgctggcaactaagggcgagggttgcgctcgttgcggggat 420
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Sbjct: 1086 cttagagtgcccaactgaatgctggcaactaagggcgagggttgcgctcgttgcgggact 1027

Query: 421  taaccaaa--tct-acgacacgagctgacgacagccatgcagcacctgtctctgcgccac 477
            ||||| ||  ||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1026 taacccaacatctcacgacacgagctgacgacagccatgcagcacctgtctctgcgccac 967

Query: 478  cgaagtggaccccatatctctacgggtaacacaggatgtcaagggctggtaaggttctgc 537
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 966  cgaagtggaccccatatctctacgggtaacacaggatgtcaagggctggtaaggttctgc 907

Query: 538  gcgttgcttcgaattaaaccacatgctccaccgcttgtgcgggcccccgtcaattccttt 597
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 906  gcgttgcttcgaattaaaccacatgctccaccgcttgtgcgggcccccgtcaattccttt 847

Query: 598  gagttttaatcttgcgaccgtactccccaggcggaatgtttaatgcgttagctgcgccac 657
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Sbjct: 846  gagttttaatcttgcgaccgtactccccaggcggaatgtttaatgcgttagctgcgccac 787

Query: 658  cgaacagtatactgcccgacggctaacattcatcgtttacggcgtggactaccagggtat 717
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 786  cgaacagtatactgcccgacggctaacattcatcgtttacggcgtggactaccagggtat 727

Query: 718  ctaatcctgtgttgtccc-acgctttcgcacctcagcgtcagtaatggaccagtgagccg 776
            |||||||||| |  |||| |||||||||||||||||||||||||||||||||||||||||
Sbjct: 726  ctaatcctgtttgctccccacgctttcgcacctcagcgtcagtaatggaccagtgagccg 667

Query: 777  ccttcgccactggtgttcctccgaatatctacgaatttcacctctacactcggaattcca 836
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 666  ccttcgccactggtgttcctccgaatatctacgaatttcacctctacactcggaattcca 607

Query: 837  ctcacctcttccatactccagatcgacagtatcaaaggcagttccagggttgagccctgg 896
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 606  ctcacctcttccatactccagatcgacagtatcaaaggcagttccagggttgagccctgg 547

Query: 897  gatttcacccctgactgatcgatccgcctacgtgcgctttacgcccagtaattccgaaca 956
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Sbjct: 546  gatttcacccctgactgatcgatccgcctacgtgcgctttacgcccagtaattccgaaca 487

Query: 957  acgctagcccccttagtattaccgcggctgctggcaaaaagttagccggggattcttctc 1016
            |||||||||||||| |||||||||||||||||||||  ||||||||||||| ||||||||
Sbjct: 486  acgctagcccccttcgtattaccgcggctgctggcacgaagttagccggggcttcttctc 427
```

```
Query: 1017 cggataccgtcattatcttctccggtgaaagagctttacaaccatagggccttcatcact 1076
            ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct: 426  cggataccgtcattatcttctccggtgaaagagctttacaaccctagggccttcatcact 367

Query: 1077 cacgcggcatggctggatcaggcttgcgcccattgtccaatattccccactgctgcctcc 1136
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 366  cacgcggcatggctggatcaggcttgcgcccattgtccaatattccccactgctgcctcc 307

Query: 1137 cgtaggagtttgggccgtgtctcagtcccaatgtggctgatcatcctctcagaccagcta 1196
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 306  cgtaggagtttgggccgtgtctcagtcccaatgtggctgatcatcctctcagaccagcta 247

Query: 1197 tggatcgtcgccttggtaggcctttaccccaccaactagctaatccaacgcgggctcatc 1256
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 246  tggatcgtcgccttggtaggcctttaccccaccaactagctaatccaacgcgggctcatc 187

Query: 1257 tcttgccgataaatctttctcccgaaggacacatacggtattagcacaagtttccctgcg 1316
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 186  ctttcccgataaatctttctcccgaaggacacatacggtattagcacaagtttccctgcg 127

Query: 1317 ttattccgtagcaaaaggtagattcccacgcgttactcacccgtctgccgctccccttgc 1376
            ||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126  ttattccgtagaaaagggtagattcccacgcgttactcacccgtctgccgctccccttgc 67

Query: 1377 ggggcgctcgacttgcatgtgttaagcctgccgccagcgttcgttctgagccaggatcaa 1436
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 66   ggggcgctcgacttgcatgtgttaagcctgccgccagcgttcgttctgagccaggatcaa 7

Query: 1437 actc 1440
            ||||
Sbjct: 6    actc 3
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Query= gi|174| (1277 letters)

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                                                     Score    E
Sequences producing significant alignments:          (bits) Value

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gi|27261750|gb|AY166841.1|  Rhizobium tropici UPRM8033 16S r...  1735   0.0
gi|21898743|gb|AY117623.1|  Rhizobium tropici strain PRF34 1...  1735   0.0
gi|9837365|gb|AF286362.1|  Rhizobium sp. PRY71 16S ribosomal...  1735   0.0
gi|14029734|gb|AF364856.1|AF364856  Rhizobium sp. L28 115D 1...  1735   0.0
gi|3724150|emb|Z94806.1|RSPZ94806  Rhizobium genosp. Q 16S r...  1733   0.0
gi|28894114|gb|AY206687.1|  Rhizobium rhizogenes strain 163C...  1725   0.0
gi|1055273|gb|U38469.1|RTU38469  Rhizobium tropici 16S ribos...  1725   0.0
gi|286266|dbj|D12798.1|RHM16SRRNG  Rhizobium tropici 16S rRN...  1725   0.0
gi|296479|emb|X67233.1|RL16SRRN  R.leguminosarum (LMG 9518) ...  1715   0.0
```

Alignments

```
>gi|464144|dbj|D14504.1|ATU16SRDJ  Rhizobium sp. K-Ag-3 gene for 16S rRNA, complete
sequence
          Length = 1468

 Score = 1752 bits (884), Expect = 0.0
 Identities = 971/1002 (96%)
 Strand = Plus / Minus


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Query: 1232 gttaagcctgccgccagcgttcgttctgagccaggatcaaac 1273
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Score = 539 bits (272), Expect = e-150
Identities = 272/272 (100%)
Strand = Plus / Minus

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Sbjct: 1202 cactcgcgtgctcgctgcccactgtcaccacc 1171
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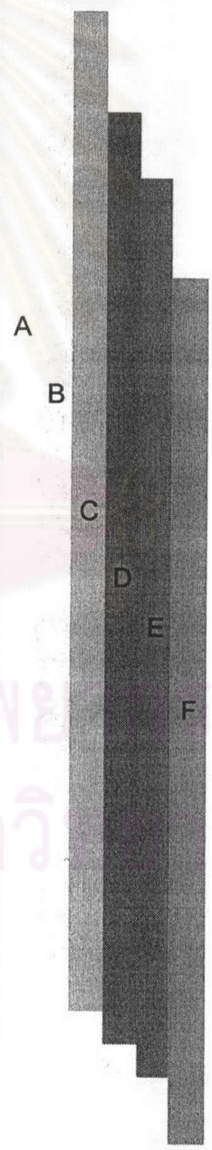
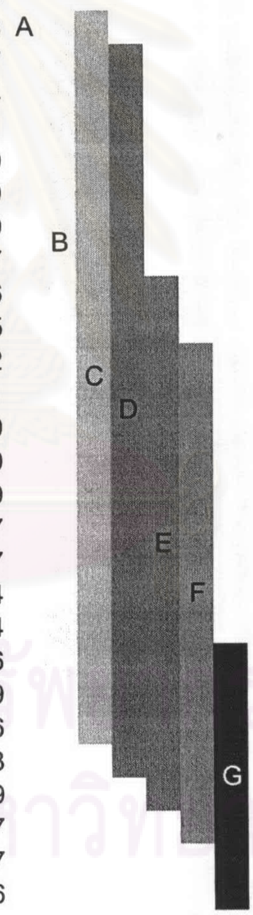
Data for table 4.1 Duncan's Multiple Range Test for plant dry weight when each of *Bradyrhizobium japonicum* strains S76, S78, S162, S178 was inoculated onto germinating seeds of soybean *Glycine max* cv. SJ 4, SJ 5, CM 2, CM 60, ST 1, ST 2, ST 3 in Leonard jars with nitrogen-free medium pH 5.0 for 28 days.

p	r	R	mean
2	2.86	0.91	2.24
3	3.01	0.96	2.21
4	3.10	0.99	2.17
5	3.17	1.01	2.16
6	3.22	1.02	2.12
7	3.27	1.04	2.11
8	3.30	1.05	2.10
9	3.33	1.06	1.93
10	3.35	1.07	1.92
11	3.35	1.07	1.92
12	3.35	1.07	1.91
13	3.35	1.07	1.89
14	3.35	1.07	1.79
15	3.35	1.07	1.75
16	3.47	1.10	1.74
17	3.47	1.10	1.72
18	3.47	1.10	1.67
19	3.47	1.10	1.62
20	3.47	1.10	1.62
21	3.47	1.10	1.55
22	3.47	1.10	1.52
23	3.47	1.10	1.50
24	3.47	1.10	1.50
25	3.47	1.10	1.50
26	3.47	1.10	1.48
27	3.47	1.10	1.43
28	3.47	1.10	1.40
29	3.47	1.10	1.40
30	3.47	1.10	1.37
31	3.47	1.10	1.36
32	3.47	1.10	1.31
33	3.47	1.10	1.31
34	3.47	1.10	1.21
35	3.47	1.10	1.18
36	3.47	1.10	1.18
37	3.47	1.10	1.12
38	3.47	1.10	1.09
39	3.47	1.10	0.89
40	3.47	1.10	0.79
41	3.47	1.10	0.76
42	3.47	1.10	0.68
			0.61



Data for table 4.3 Duncan's Multiple Range Test for plant dry weight when each of *Burkholderia* sp. S172, *Sinorhizobium fredii* S173, S174 was inoculated onto germinating seeds of soybean *Glycine max* cv. SJ 4, SJ 5, CM 2, CM 60, ST 1, ST 2, ST 3 in Leonard jars with nitrogen-free medium pH 5.0 for 28 days.

p	r	R	mean
2	2.89	0.74	2.38
3	3.04	0.78	2.00
4	3.13	0.80	1.95
5	3.20	0.82	1.92
6	3.25	0.84	1.90
7	3.29	0.85	1.83
8	3.32	0.85	1.79
9	3.35	0.86	1.75
10	3.37	0.87	1.68
11	3.39	0.87	1.67
12	3.41	0.88	1.64
13	3.42	0.88	1.61
14	3.43	0.88	1.60
15	3.44	0.88	1.59
16	3.45	0.89	1.59
17	3.45	0.89	1.57
18	3.46	0.89	1.56
19	3.47	0.89	1.45
20	3.47	0.89	1.42
21	3.47	0.89	1.41
22	3.47	0.89	1.40
23	3.47	0.89	1.40
24	3.47	0.89	1.39
25	3.47	0.89	1.37
26	3.47	0.89	1.37
27	3.47	0.89	1.34
28	3.47	0.89	1.34
29	3.47	0.89	1.16
30	3.47	0.89	0.89
31	3.47	0.89	0.86
32	3.47	0.89	0.83
33	3.47	0.89	0.69
34	3.47	0.89	0.57
35	3.47	0.89	0.47
			0.46



Data for table 4.4 Duncan's Multiple Range Test for plant dry weight when each of *Burkholderia* sp. S172, *Sinorhizobium fredii* S173, S174 was inoculated onto germinating seeds of soybean *Glycine max* cv. SJ 4, SJ 5, CM 2, CM 60, ST 1, ST 2, ST 3 in Leonard jars with nitrogen-free medium pH 6.8 for 28 days.

p	r	R	mean
2	2.89	0.7196	0.53
3	3.04	0.757	0.59
4	3.13	0.7794	0.69
5	3.20	0.7968	0.79
6	3.25	0.81	0.87
7	3.29	0.8192	0.88
8	3.32	0.8267	0.91
9	3.35	0.8342	1.25
10	3.37	0.8391	1.29
11	3.39	0.8441	1.3
12	3.41	0.8491	1.34
13	3.42	0.8516	1.36
14	3.43	0.8541	1.37
15	3.44	0.8566	1.37
16	3.45	0.8591	1.4
17	3.45	0.8591	1.42
18	3.46	0.8615	1.42
19	3.47	0.864	1.57
20	3.47	0.864	1.57
21	3.47	0.864	1.57
22	3.47	0.864	1.6
23	3.47	0.864	1.62
24	3.47	0.864	1.62
25	3.47	0.864	1.65
26	3.47	0.864	1.67
27	3.47	0.864	1.69
28	3.47	0.864	1.72
29	3.47	0.864	1.74
30	3.47	0.864	1.79
31	3.47	0.864	1.83
32	3.47	0.864	1.89
33	3.47	0.864	1.95
34	3.47	0.864	2.06
35	3.47	0.864	2.25
			2.17

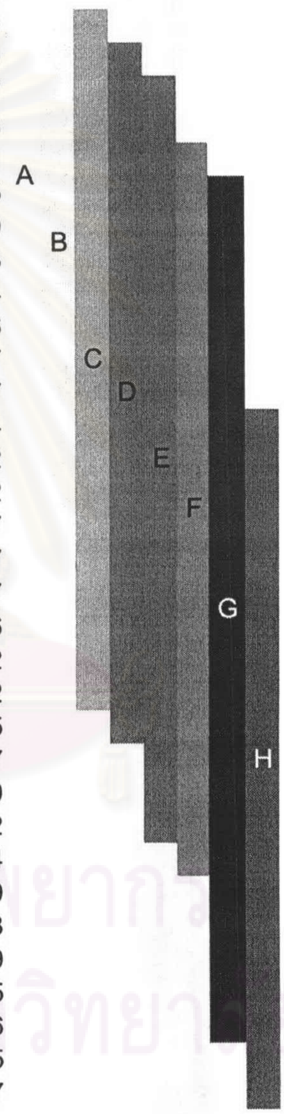


Table A9. Critical values for Duncan's multiple range test

The body of the table represents $D_{\square,(r,v)}$ the critical value for Duncan's multiple range test for significance level α, *v* degrees of freedom and range *r*.

Example: The *D* value to compare two means on the 4-range at α = 0.05 with 10 degrees of freedom is 3.37

v	α	*Range of sample means* 2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	α	*v*
1	.100	8.929	8.929	8.929	8.929	8.929	8.929	8.929	8.929	8.929	8.929	8.929	8.929	8.929	8.929	8.929	8.929	8.929	8.929	8.929	.100	1
1	.050	17.97	17.97	17.97	17.97	17.97	17.97	17.97	17.97	17.97	17.97	17.97	17.97	17.97	17.97	17.97	17.97	17.97	17.97	17.97	.050	1
1	.010	89.98	89.98	89.98	89.98	89.98	89.98	89.98	89.98	89.98	89.98	89.98	89.98	89.98	89.98	89.98	89.98	89.98	89.98	89.98	.010	1
2	.100	4.129	4.129	4.129	4.129	4.129	4.129	4.129	4.129	4.129	4.129	4.129	4.129	4.129	4.129	4.129	4.129	4.129	4.129	4.129	.100	2
2	.050	6.085	6.085	6.085	6.085	6.085	6.085	6.085	6.085	6.085	6.085	6.085	6.085	6.085	6.085	6.085	6.085	6.085	6.085	6.085	.050	2
2	.010	14.03	14.03	14.03	14.03	14.03	14.03	14.03	14.03	14.03	14.03	14.03	14.03	14.03	14.03	14.03	14.03	14.03	14.03	14.03	.010	2
3	.100	3.328	3.330	3.330	3.330	3.330	3.330	3.330	3.330	3.330	3.330	3.330	3.330	3.330	3.330	3.330	3.330	3.330	3.330	3.330	.100	3
3	.050	4.501	4.516	4.516	4.516	4.516	4.516	4.516	4.516	4.516	4.516	4.516	4.516	4.516	4.516	4.516	4.516	4.516	4.516	4.516	.050	3
3	.010	8.260	8.321	8.321	8.321	8.321	8.321	8.321	8.321	8.321	8.321	8.321	8.321	8.321	8.321	8.321	8.321	8.321	8.321	8.321	.010	3
4	.100	3.015	3.074	3.081	3.081	3.081	3.081	3.081	3.081	3.081	3.081	3.081	3.081	3.081	3.081	3.081	3.081	3.081	3.081	3.081	.100	4
4	.050	3.927	4.012	4.033	4.033	4.033	4.033	4.033	4.033	4.033	4.033	4.033	4.033	4.033	4.033	4.033	4.033	4.033	4.033	4.033	.050	4
4	.010	6.511	6.677	6.740	6.756	6.756	6.756	6.756	6.756	6.756	6.756	6.756	6.756	6.756	6.756	6.756	6.756	6.756	6.756	6.756	.010	4
5	.100	2.850	2.934	2.964	2.969	2.969	2.969	2.969	2.969	2.969	2.969	2.969	2.969	2.969	2.969	2.969	2.969	2.969	2.969	2.969	.100	5
5	.050	3.635	3.749	3.796	3.814	3.814	3.814	3.814	3.814	3.814	3.814	3.814	3.814	3.814	3.814	3.814	3.814	3.814	3.814	3.814	.050	5
5	.010	5.702	5.893	5.989	6.040	6.065	6.074	6.074	6.074	6.074	6.074	6.074	6.074	6.074	6.074	6.074	6.074	6.074	6.074	6.074	.010	5
6	.100	2.748	2.846	2.890	2.907	2.911	2.911	2.911	2.911	2.911	2.911	2.911	2.911	2.911	2.911	2.911	2.911	2.911	2.911	2.911	.100	6
6	.050	3.460	3.586	3.649	3.680	3.694	3.697	3.697	3.697	3.697	3.697	3.697	3.697	3.697	3.697	3.697	3.697	3.697	3.697	3.697	.050	6
6	.010	5.243	5.439	5.549	5.615	5.655	5.680	5.694	5.701	5.703	5.703	5.703	5.703	5.703	5.703	5.703	5.703	5.703	5.703	5.703	.010	6
7	.100	2.679	2.785	2.838	2.864	2.876	2.878	2.878	2.878	2.878	2.878	2.878	2.878	2.878	2.878	2.878	2.878	2.878	2.878	2.878	.100	7
7	.050	3.344	3.477	3.548	3.588	3.611	3.622	3.625	3.625	3.625	3.625	3.625	3.625	3.625	3.625	3.625	3.625	3.625	3.625	3.625	.050	7
7	.010	4.948	5.145	5.260	5.333	5.383	5.416	5.439	5.454	5.464	5.470	5.472	5.472	5.472	5.472	5.472	5.472	5.472	5.472	5.472	.010	7
8	.100	2.630	2.741	2.800	2.832	2.849	2.857	2.858	2.858	2.858	2.858	2.858	2.858	2.858	2.858	2.858	2.858	2.858	2.858	2.858	.100	8
8	.050	3.261	3.398	3.475	3.521	3.549	3.566	3.575	3.579	3.579	3.579	3.579	3.579	3.579	3.579	3.579	3.579	3.579	3.579	3.579	.050	8
8	.010	4.745	4.939	5.056	5.134	5.189	5.227	5.256	5.276	5.291	5.302	5.309	5.313	5.316	5.317	5.317	5.317	5.317	5.317	5.317	.010	8
9	.100	2.592	2.708	2.771	2.808	2.829	2.840	2.845	2.846	2.846	2.846	2.846	2.846	2.846	2.846	2.846	2.846	2.846	2.846	2.846	.100	9
9	.050	3.199	3.339	3.420	3.470	3.502	3.523	3.536	3.544	3.547	3.547	3.547	3.547	3.547	3.547	3.547	3.547	3.547	3.547	3.547	.050	9
9	.010	4.595	4.787	4.906	4.986	5.043	5.086	5.117	5.142	5.160	5.174	5.185	5.193	5.199	5.202	5.205	5.206	5.206	5.206	5.206	.010	9
10	.100	2.563	2.682	2.748	2.788	2.813	2.827	2.835	2.839	2.839	2.839	2.839	2.839	2.839	2.839	2.839	2.839	2.839	2.839	2.839	.100	10
10	.050	3.151	3.293	3.376	3.430	3.465	3.489	3.505	3.516	3.522	3.525	3.525	3.525	3.525	3.525	3.525	3.525	3.525	3.525	3.525	.050	10
10	.010	4.482	4.671	4.789	4.871	4.931	4.975	5.010	5.036	5.058	5.074	5.087	5.098	5.106	5.112	5.117	5.120	5.122	5.123	5.124	.010	10
11	.100	2.540	2.660	2.729	2.772	2.799	2.817	2.827	2.833	2.835	2.835	2.835	2.835	2.835	2.835	2.835	2.835	2.835	2.835	2.835	.100	11
11	.050	3.113	3.256	3.341	3.397	3.435	3.462	3.480	3.493	3.501	3.506	3.509	3.510	3.510	3.510	3.510	3.510	3.510	3.510	3.510	.050	11
11	.010	4.392	4.579	4.697	4.780	4.841	4.887	4.923	4.952	4.975	4.994	5.009	5.021	5.031	5.039	5.045	5.050	5.054	5.057	5.059	.010	11

Calculated with the `ProbMc` function of The SAS System, Vs. 6.12.

Table A9. Critical values for Duncan's multiple range test (Continued ...)

ν	α	Range of sample means 2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	α	ν
12	.100	2.521	2.643	2.714	2.759	2.788	2.808	2.820	2.828	2.832	2.833	2.833	2.833	2.833	2.833	2.833	2.833	2.833	2.833	2.833	.100	12
12	.050	3.081	3.225	3.312	3.370	3.410	3.439	3.459	3.474	3.484	3.491	3.495	3.498	3.498	3.498	3.498	3.498	3.498	3.498	3.498	.050	12
12	.010	4.320	4.504	4.622	4.705	4.765	4.812	4.850	4.882	4.907	4.927	4.944	4.957	4.969	4.978	4.986	4.993	4.998	5.002	5.005	.010	12
13	.100	2.504	2.628	2.701	2.748	2.779	2.800	2.814	2.824	2.829	2.832	2.832	2.832	2.832	2.832	2.832	2.832	2.832	2.832	2.832	.100	13
13	.050	3.055	3.200	3.288	3.348	3.389	3.419	3.441	3.458	3.470	3.478	3.484	3.488	3.490	3.490	3.490	3.490	3.490	3.490	3.490	.050	13
13	.010	4.261	4.442	4.560	4.643	4.706	4.754	4.793	4.824	4.850	4.871	4.889	4.904	4.917	4.927	4.936	4.944	4.950	4.955	4.960	.010	13
14	.100	2.491	2.616	2.689	2.739	2.771	2.794	2.810	2.820	2.827	2.831	2.833	2.833	2.833	2.833	2.833	2.833	2.833	2.833	2.833	.100	14
14	.050	3.033	3.178	3.268	3.328	3.371	3.402	3.426	3.444	3.457	3.467	3.474	3.479	3.482	3.484	3.484	3.484	3.484	3.484	3.484	.050	14
14	.010	4.210	4.390	4.508	4.591	4.654	4.703	4.743	4.775	4.802	4.824	4.843	4.859	4.872	4.884	4.894	4.902	4.909	4.916	4.921	.010	14
15	.100	2.479	2.605	2.681	2.730	2.764	2.788	2.805	2.817	2.825	2.830	2.833	2.834	2.834	2.834	2.834	2.834	2.834	2.834	2.834	.100	15
15	.050	3.014	3.160	3.250	3.312	3.356	3.389	3.413	3.432	3.446	3.457	3.465	3.471	3.476	3.478	3.480	3.480	3.480	3.480	3.480	.050	15
15	.010	4.167	4.346	4.463	4.547	4.610	4.660	4.700	4.733	4.760	4.783	4.803	4.820	4.834	4.846	4.857	4.866	4.874	4.881	4.887	.010	15
16	.100	2.469	2.596	2.672	2.723	2.759	2.784	2.802	2.814	2.824	2.830	2.833	2.835	2.836	2.836	2.836	2.836	2.836	2.836	2.836	.100	16
16	.050	2.998	3.144	3.235	3.297	3.343	3.376	3.402	3.422	3.437	3.449	3.458	3.465	3.470	3.473	3.476	3.477	3.477	3.477	3.477	.050	16
16	.010	4.131	4.308	4.425	4.508	4.572	4.622	4.662	4.696	4.724	4.748	4.768	4.785	4.800	4.813	4.825	4.835	4.843	4.851	4.858	.010	16
17	.100	2.460	2.587	2.665	2.717	2.753	2.779	2.798	2.812	2.822	2.829	2.834	2.837	2.838	2.838	2.838	2.838	2.838	2.838	2.838	.100	17
17	.050	2.984	3.130	3.222	3.285	3.331	3.365	3.392	3.412	3.429	3.441	3.451	3.459	3.465	3.469	3.472	3.474	3.475	3.475	3.475	.050	17
17	.010	4.099	4.275	4.391	4.474	4.538	4.589	4.630	4.664	4.692	4.717	4.737	4.755	4.771	4.785	4.797	4.807	4.816	4.824	4.832	.010	17
18	.100	2.452	2.580	2.659	2.711	2.749	2.776	2.795	2.810	2.821	2.829	2.834	2.838	2.840	2.840	2.840	2.840	2.840	2.840	2.840	.100	18
18	.050	2.971	3.117	3.210	3.274	3.320	3.356	3.383	3.404	3.421	3.435	3.445	3.454	3.460	3.465	3.469	3.472	3.473	3.474	3.474	.050	18
18	.010	4.071	4.246	4.361	4.445	4.509	4.559	4.601	4.635	4.664	4.689	4.710	4.729	4.745	4.759	4.771	4.782	4.792	4.801	4.808	.010	18
19	.100	2.445	2.574	2.653	2.706	2.744	2.772	2.793	2.808	2.820	2.828	2.834	2.839	2.841	2.843	2.843	2.843	2.843	2.843	2.843	.100	19
19	.050	2.960	3.106	3.199	3.264	3.311	3.347	3.375	3.397	3.415	3.429	3.440	3.449	3.456	3.462	3.466	3.469	3.472	3.473	3.474	.050	19
19	.010	4.046	4.220	4.335	4.418	4.483	4.533	4.575	4.610	4.639	4.664	4.686	4.705	4.722	4.736	4.749	4.760	4.771	4.780	4.788	.010	19
20	.100	2.439	2.568	2.648	2.702	2.741	2.769	2.791	2.807	2.819	2.828	2.835	2.839	2.843	2.845	2.845	2.845	2.845	2.845	2.845	.100	20
20	.050	2.950	3.097	3.190	3.255	3.303	3.339	3.368	3.390	3.409	3.423	3.435	3.445	3.452	3.459	3.463	3.467	3.470	3.472	3.473	.050	20
20	.010	4.024	4.197	4.312	4.395	4.459	4.510	4.552	4.587	4.617	4.642	4.664	4.684	4.701	4.716	4.729	4.741	4.751	4.761	4.769	.010	20
25	.100	2.416	2.546	2.628	2.685	2.726	2.758	2.782	2.800	2.815	2.827	2.836	2.843	2.849	2.853	2.856	2.858	2.859	2.860	2.860	.100	25
25	.050	2.913	3.059	3.154	3.221	3.271	3.310	3.341	3.366	3.386	3.403	3.417	3.429	3.439	3.447	3.454	3.459	3.464	3.468	3.471	.050	25
25	.010	3.942	4.112	4.224	4.307	4.371	4.423	4.466	4.502	4.532	4.559	4.582	4.603	4.621	4.638	4.652	4.665	4.677	4.688	4.698	.010	25
30	.100	2.400	2.532	2.615	2.674	2.717	2.750	2.776	2.796	2.813	2.826	2.837	2.846	2.853	2.859	2.863	2.867	2.869	2.871	2.873	.100	30
30	.050	2.888	3.035	3.131	3.199	3.250	3.290	3.322	3.349	3.371	3.389	3.405	3.418	3.429	3.439	3.447	3.454	3.460	3.466	3.470	.050	30
30	.010	3.889	4.056	4.168	4.250	4.314	4.366	4.409	4.445	4.477	4.504	4.528	4.550	4.569	4.586	4.601	4.615	4.628	4.640	4.650	.010	30
50	.100	2.370	2.504	2.590	2.652	2.698	2.735	2.764	2.788	2.808	2.825	2.839	2.851	2.862	2.871	2.879	2.885	2.891	2.896	2.901	.100	50
50	.050	2.841	2.988	3.084	3.154	3.208	3.251	3.286	3.315	3.340	3.362	3.380	3.396	3.410	3.423	3.434	3.444	3.453	3.461	3.468	.050	50
50	.010	3.787	3.948	4.057	4.138	4.202	4.254	4.297	4.335	4.367	4.395	4.421	4.443	4.464	4.482	4.499	4.515	4.529	4.542	4.554	.010	50
60	.100	2.363	2.497	2.584	2.646	2.693	2.731	2.761	2.786	2.807	2.825	2.840	2.853	2.864	2.874	2.883	2.890	2.897	2.903	2.908	.100	60
60	.050	2.829	2.976	3.073	3.143	3.198	3.241	3.277	3.307	3.333	3.355	3.374	3.391	3.406	3.419	3.431	3.441	3.451	3.460	3.468	.050	60
60	.010	3.762	3.922	4.031	4.111	4.174	4.226	4.270	4.307	4.340	4.368	4.394	4.417	4.437	4.456	4.474	4.489	4.504	4.518	4.530	.010	60
100	.100	2.348	2.483	2.571	2.635	2.684	2.723	2.755	2.782	2.805	2.824	2.841	2.856	2.869	2.881	2.891	2.901	2.909	2.917	2.924	.100	100
100	.050	2.806	2.953	3.050	3.122	3.177	3.222	3.259	3.290	3.317	3.341	3.361	3.380	3.396	3.411	3.424	3.436	3.447	3.457	3.467	.050	100
100	.010	3.714	3.871	3.978	4.057	4.120	4.172	4.215	4.253	4.286	4.315	4.341	4.364	4.385	4.405	4.422	4.439	4.454	4.468	4.482	.010	100

BIOGRAPHY

Miss Patima Permpoonpattana was born on April 25, 1978. She obtained a Bachelor of Science Degree in Biotechnology from King Mongkut's Institute of Technology Lardkrabang, Bangkok, Thailand, in 2000.

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