Figure 1: 1/2

Sequence of the *Archaeoglobus fulgidus* exonuclease III gene:

SEQ ID NO.: 20/21

```
          ATGCTCAAAATCGCCACCTTCAACGTAAACTCCATCAGGAGCAGACTGCACATCGTGATT
        1 ---------+---------+---------+---------+---------+---------+ 60
          TACGAGTTTTAGCGGTGGAAGTTGCATTTGAGGTAGTCCTCGTCTGACGTGTAGCACTAA

a         M  L  K  I  A  T  F  N  V  N  S  I  R  S  R  L  H  I  V  I  -

          CCGTGGCTGAAGGAGAACAAGCCTGACATTCTATGCATGCAGGAGACGAAGGTTGAGAAC
       61 ---------+---------+---------+---------+---------+---------+ 120
          GGCACCGACTTCCTCTTGTTCGGACTGTAAGATACGTACGTCCTCTGCTTCCAACTCTTG

a         P  W  L  K  E  N  K  P  D  I  L  C  M  Q  E  T  K  V  E  N  -

          AGGAAGTTTCCTGAGGCCGATTTTCACCGCATCGGCTACCACGTCGTCTTCAGCGGGAGC
      121 ---------+---------+---------+---------+---------+---------+ 180
          TCCTTCAAAGGACTCCGGCTAAAAGTGGCGTAGCCGATGGTGCAGCAGAAGTCGCCCTCG

a         R  K  F  P  E  A  D  F  H  R  I  G  Y  H  V  V  F  S  G  S  -

          AAGGGAAGGAATGGAGTGGCCATAGCTTCCCTCGAAGAGCCTGAGGATGTCAGCTTCGGT
      181 ---------+---------+---------+---------+---------+---------+ 240
          TTCCCTTCCTTACCTCACCGGTATCGAAGGGAGCTTCTCGGACTCCTACAGTCGAAGCCA

a         K  G  R  N  G  V  A  I  A  S  L  E  E  P  E  D  V  S  F  G  -

          CTCGATTCAGAGCCGAAGGACGAGGACAGGCTGATAAGGGCAAAGATAGCTGGCATAGAC
      241 ---------+---------+---------+---------+---------+---------+ 300
          GAGCTAAGTCTCGGCTTCCTGCTCCTGTCCGACTATTCCCGTTTCTATCGACCGTATCTG

a         L  D  S  E  P  K  D  E  D  R  L  I  R  A  K  I  A  G  I  D  -

          GTGATTAACACCTACGTTCCTCAGGGATTCAAAATTGACAGCGAGAAGTACCAGTACAAG
      301 ---------+---------+---------+---------+---------+---------+ 360
          CACTAATTGTGGATGCAAGGAGTCCCTAAGTTTTAACTGTCGCTCTTCATGGTCATGTTC

a         V  I  N  T  Y  V  P  Q  G  F  K  I  D  S  E  K  Y  Q  Y  K  -

          CTCCAGTGGCTTGAGAGGCTTTACCATTACCTTCAAAAAACCGTTGACTTCAGAAGCTTT
      361 ---------+---------+---------+---------+---------+---------+ 420
          GAGGTCACCGAACTCTCCGAAATGGTAATGGAAGTTTTTTGGCAACTGAAGTCTTCGAAA

a         L  Q  W  L  E  R  L  Y  H  Y  L  Q  K  T  V  D  F  R  S  F  -

          GCTGTTTGGTGTGGAGACATGAACGTTGCTCCTGAGCCAATCGACGTTCACTCCCCAGAC
      421 ---------+---------+---------+---------+---------+---------+ 480
          CGACAAACCACACCTCTGTACTTGCAACGAGGACTCGGTTAGCTGCAAGTGAGGGGTCTG

a         A  V  W  C  G  D  M  N  V  A  P  E  P  I  D  V  H  S  P  D  -

          AAGCTGAAGAACCACGTCTGCTTCCACGAGGATGCGAGAAGGGCATACAAAAAAATACTC
      481 ---------+---------+---------+---------+---------+---------+ 540
          TTCGACTTCTTGGTGCAGACGAAGGTGCTCCTACGCTCTTCCCGTATGTTTTTTTATGAG

a         K  L  K  N  H  V  C  F  H  E  D  A  R  R  A  Y  K  K  I  L  -
```

Figure 1: 2/2

```
      GAACTCGGCTTTGTTGACGTGCTGAGAAAAATACATCCCAACGAGAGAATTTACACCTTC
  541 ---------+---------+---------+---------+---------+---------+ 600
      CTTGAGCCGAAACAACTGCACGACTCTTTTTATGTAGGGTTGCTCTCTTAAATGTGGAAG

a         E  L  G  F  V  D  V  L  R  K  I  H  P  N  E  R  I  Y  T  F  -

      TACGACTACAGGGTTAAGGGAGCCATTGAGCGGGGGCTGGGATGGAGGGTTGATGCCATC
  601 ---------+---------+---------+---------+---------+---------+ 660
      ATGCTGATGTCCCAATTCCCTCGGTAACTCGCCCCCGACCCTACCTCCCAACTACGGTAG

a         Y  D  Y  R  V  K  G  A  I  E  R  G  L  G  W  R  V  D  A  I  -

      CTCGCCACCCCACCCCTCGCCGAAAGATGCGTGGACTGCTACGCAGACATCAAACCGAGG
  661 ---------+---------+---------+---------+---------+---------+ 720
      GAGCGGTGGGGTGGGGAGCGGCTTTCTACGCACCTGACGATGCGTCTGTAGTTTGGCTCC

a         L  A  T  P  P  L  A  E  R  C  V  D  C  Y  A  D  I  K  P  R  -

      CTGGCAGAAAAGCCATCCGACCACCTCCCTCTCGTTGCTGTGTTTGACGTGTAG
  721 ---------+---------+---------+---------+---------+---- 774
      GACCGTCTTTTCGGTAGGCTGGTGGAGGGAGAGCAACGACACAAACTGCACATC

a         L  A  E  K  P  S  D  H  L  P  L  V  A  V  F  D  V  *  -
```

Figure 2:

Temperature stability of *Afu* exonuclease III

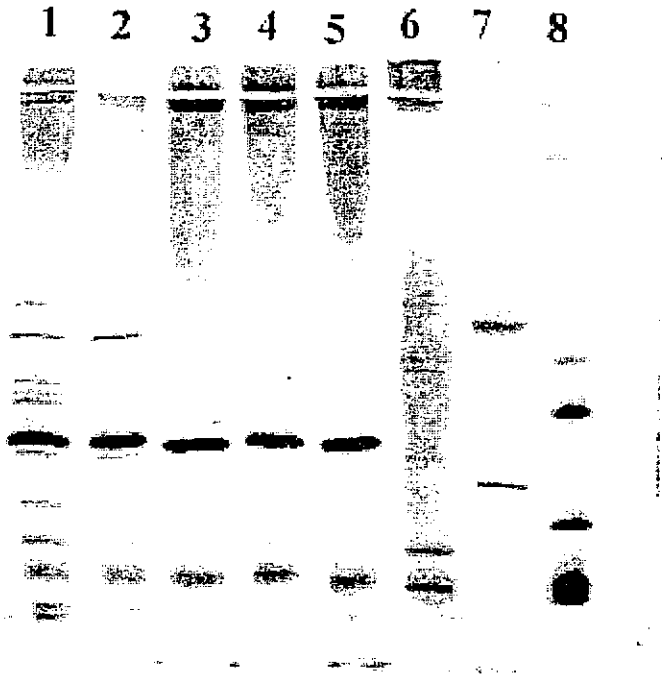


Figure 3:

Test for exonuclease III activity

1 2 3 4 5 6 7 8 9 10 11 12 13 14

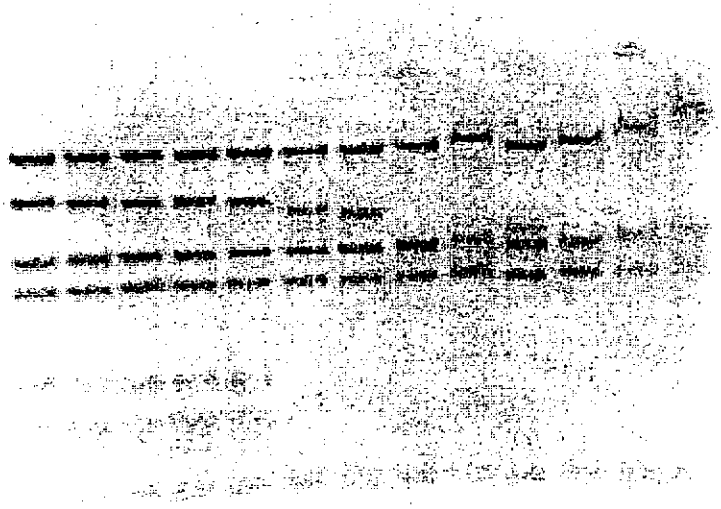


Figure 4:

Principle of the 3'-primer correction assay

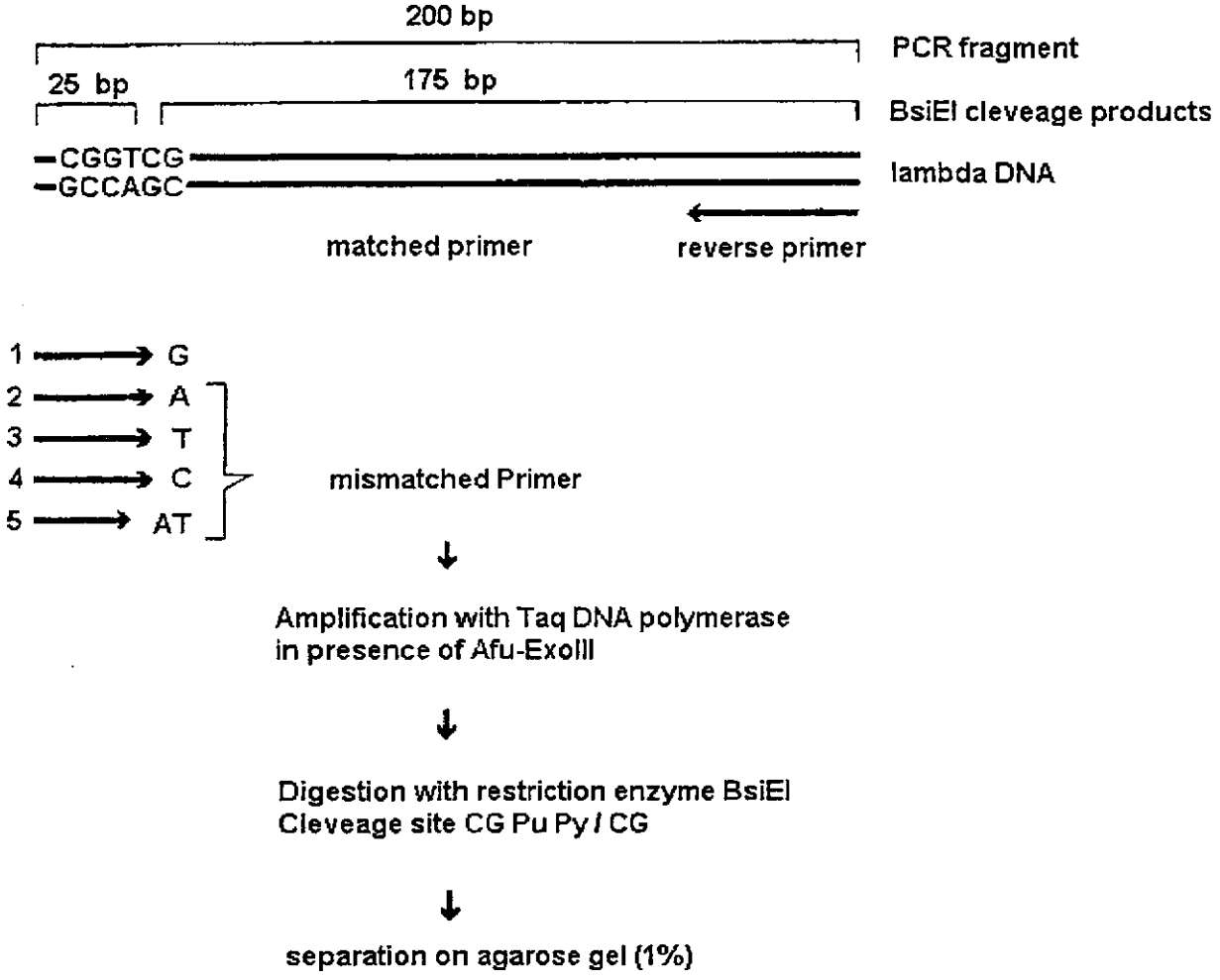


Figure 5:

Mismatched primer correction in PCR

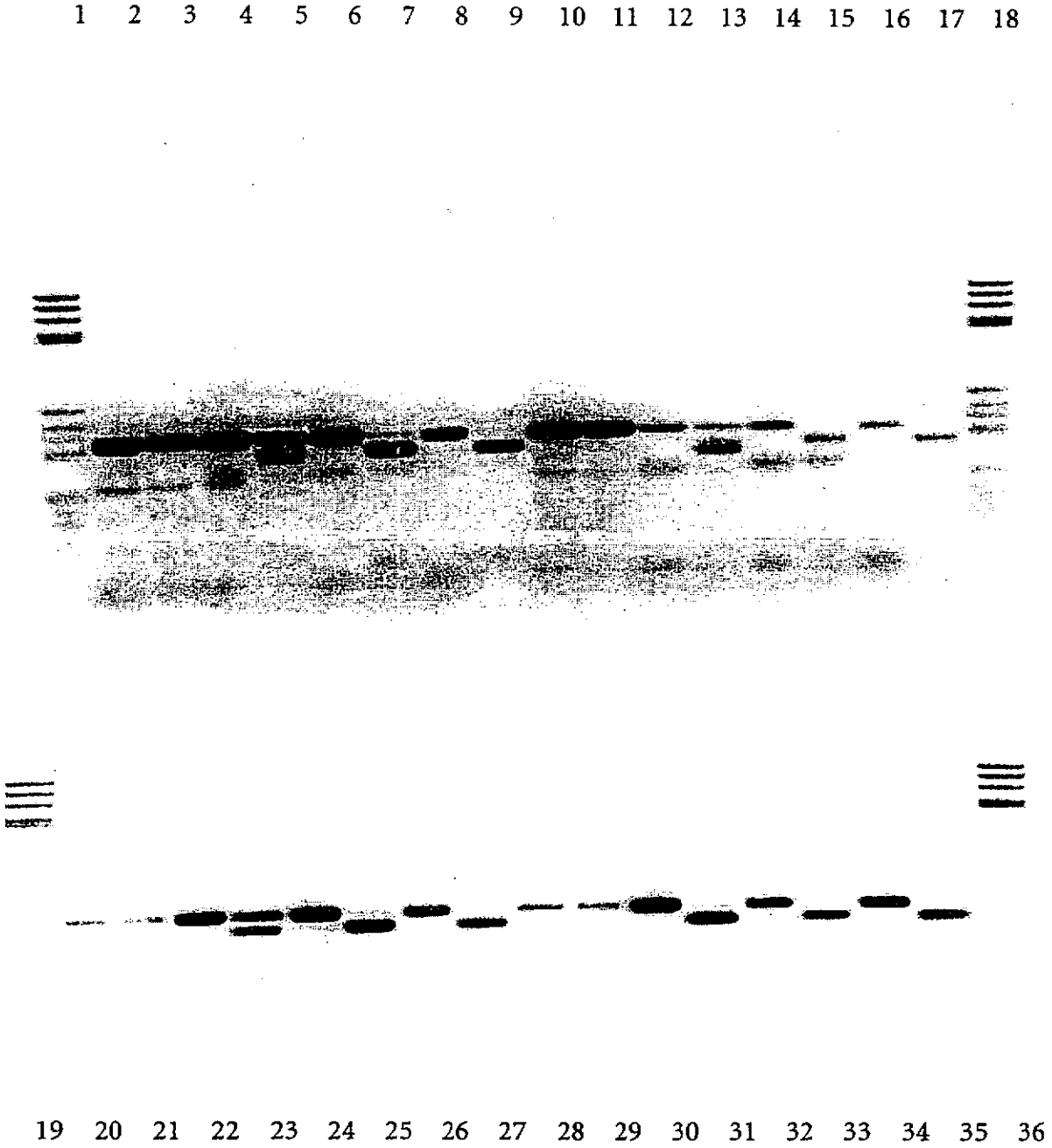


Figure 6A

Error rates of different DNA polymerases in PCR

Polymerase	Template conc. (ng)	yield (ng)	DNA duplica-tions d	blue colonies lacI$^-$	white colonies lac$^+$	total number of colonies	% lac$^-$	error rate (f_{349})
Taq Ch.	10	11650	10.2	130	2261	2391	5.4	1.57×10^{-5}
HiFi Ch.	10	11550	10.2	40	5458	5498	0.72	2.06×10^{-6}
Pwo	10	9675	9.9	17	5891	5908	0.29	8.32×10^{-7}
Taq/Exo 1	10	11550	10.2	94	4291	4385	2.14	6.10×10^{-6}
Taq/Exo 2	10	11125	10.1	146	7644	7790	1.87	5.36×10^{-6}
Taq/Exo 3	10	8500	9.7	133	8188	8321	1.6	4.74×10^{-6}
Taq/Exo 4	10	1292	7	79	7236	7315	1.08	4.44×10^{-6}
Taq/Exo 5	10	236	4.6	25	2674	2724	0.92	1.16×10^{-5} (*)

* Due to the unfavorable ratio of Taq:Exo the product yield was low. This results in an apparently low amplification efficiency d, which is an important parameter in the formula used for the calculation of the error rate.

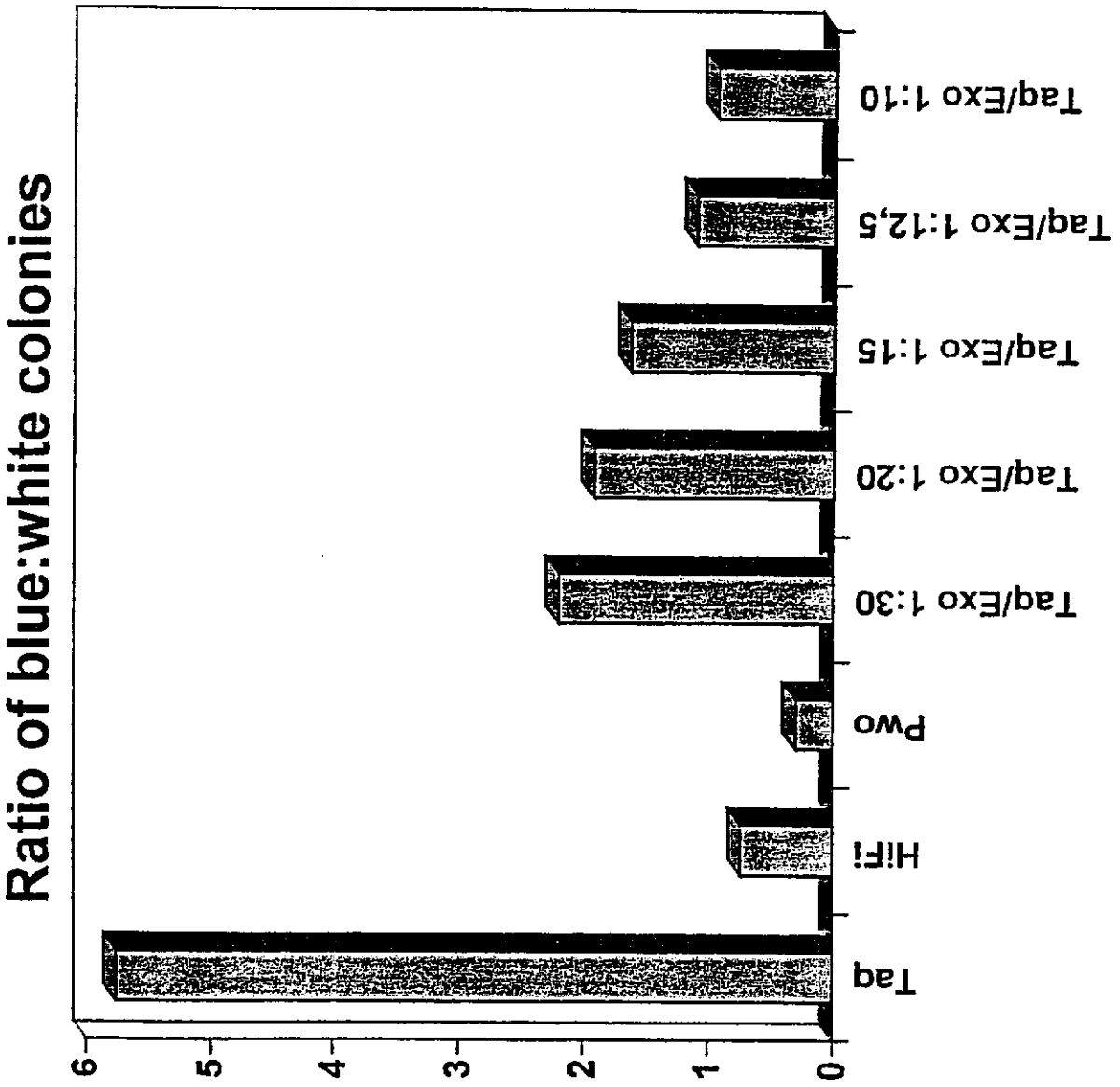

Ratio of blue:white colonies
0
1
2
3
4
5
6
Taq
HiFi
Pwo
Taq/Exo 1:30
Taq/Exo 1:20
Taq/Exo 1:15
Taq/Exo 1:12,5
Taq/Exo 1:10

Figure 6B:

Figure 7:

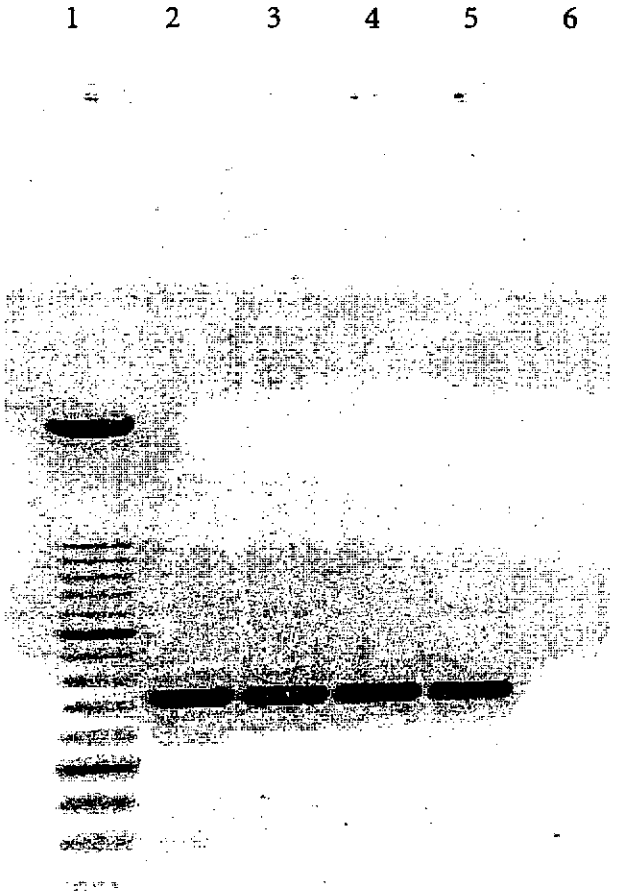


Figure 8:

UNG treatment of dUMP containing PCR products

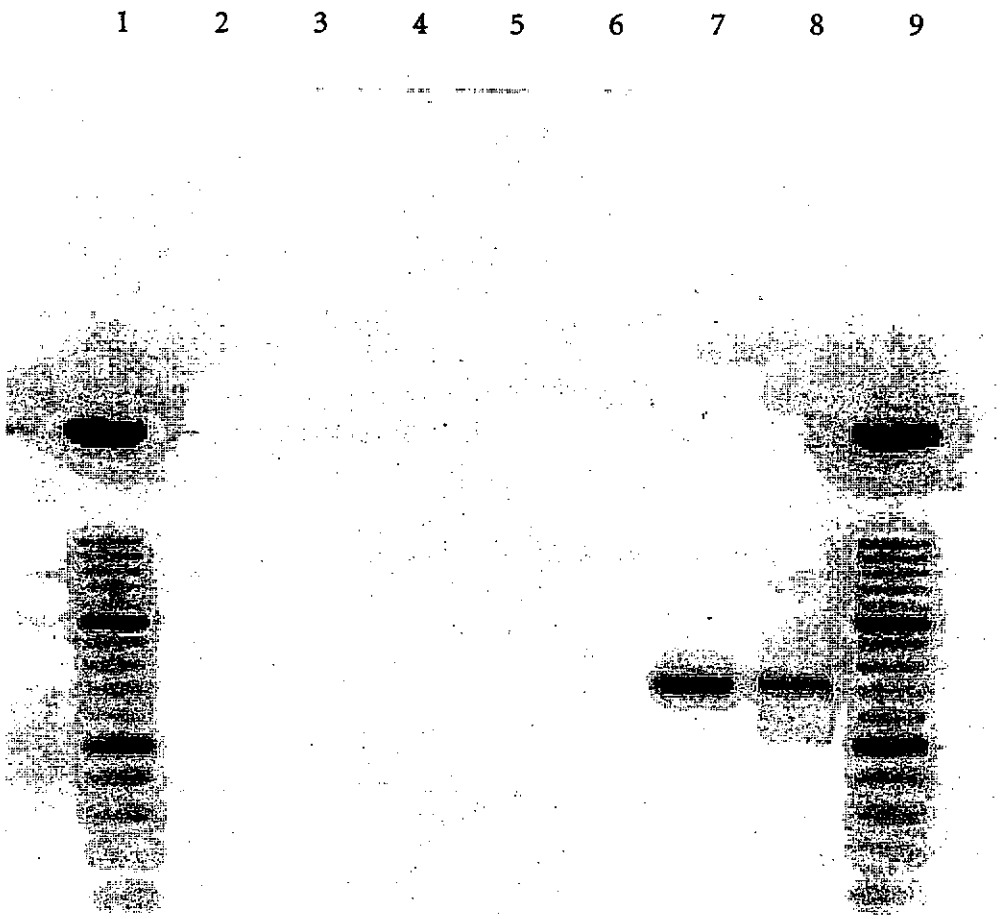


Figure 9:

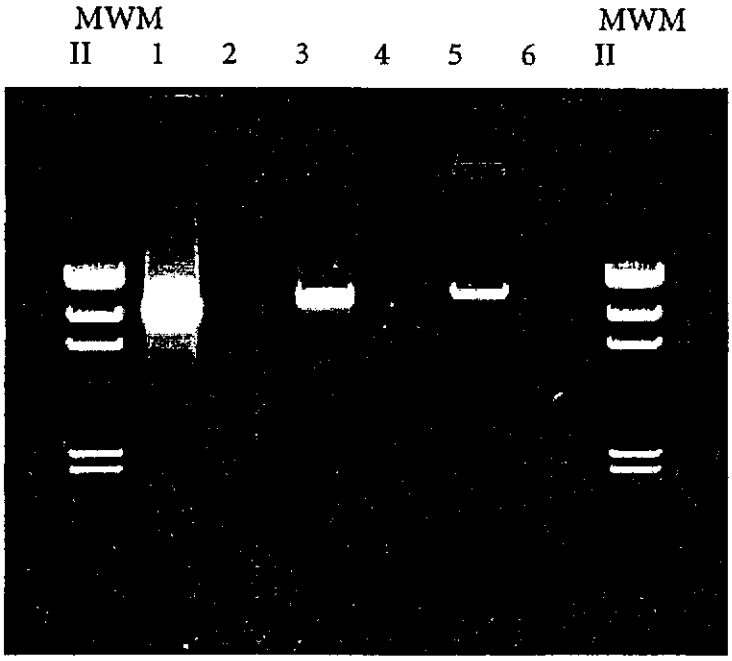


Figure 10:

1	2	3	4	5	6	7	8	9	10
MWM	1	2	3	4	5	6	7	8	MWM

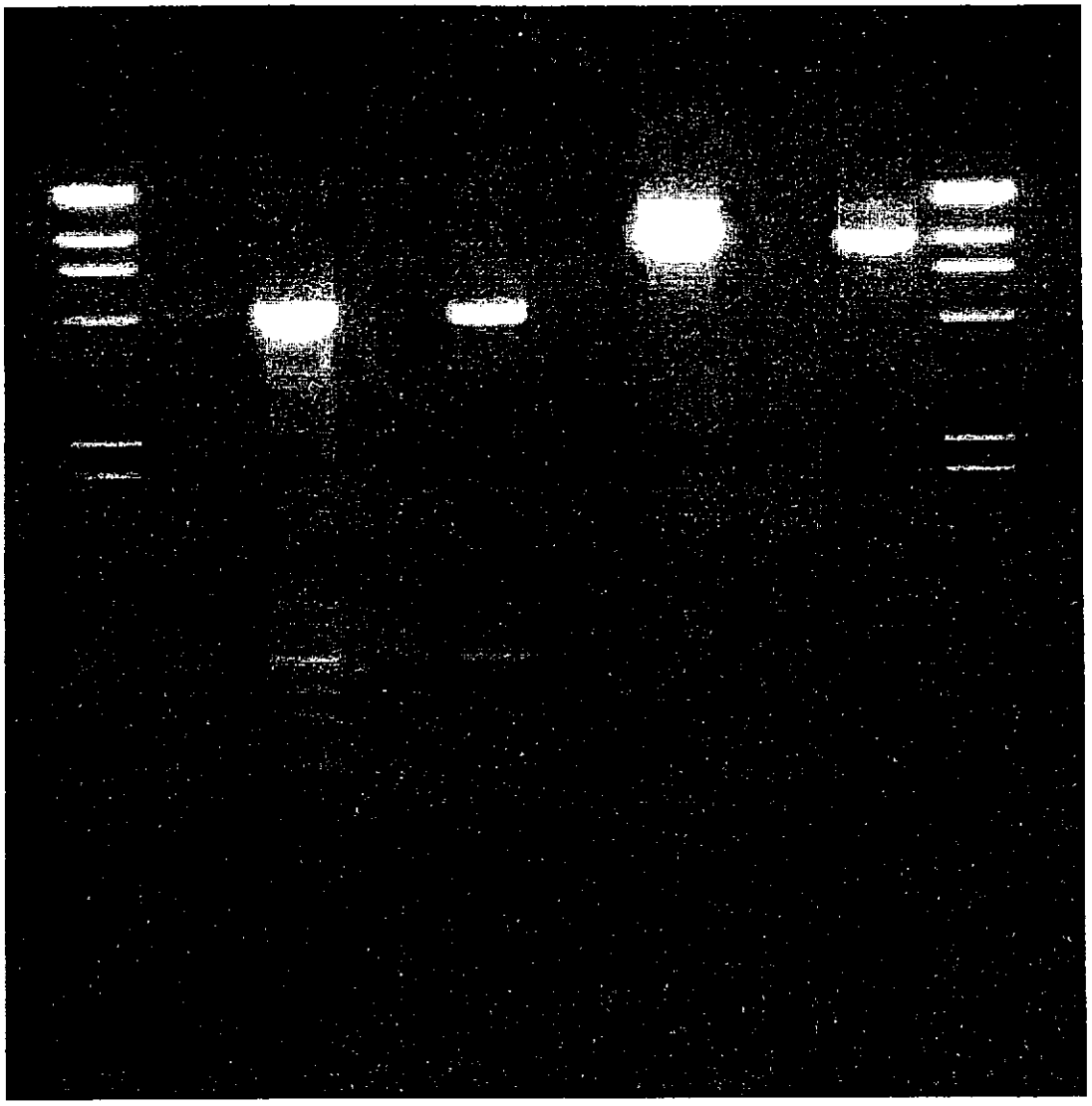


Figure 11

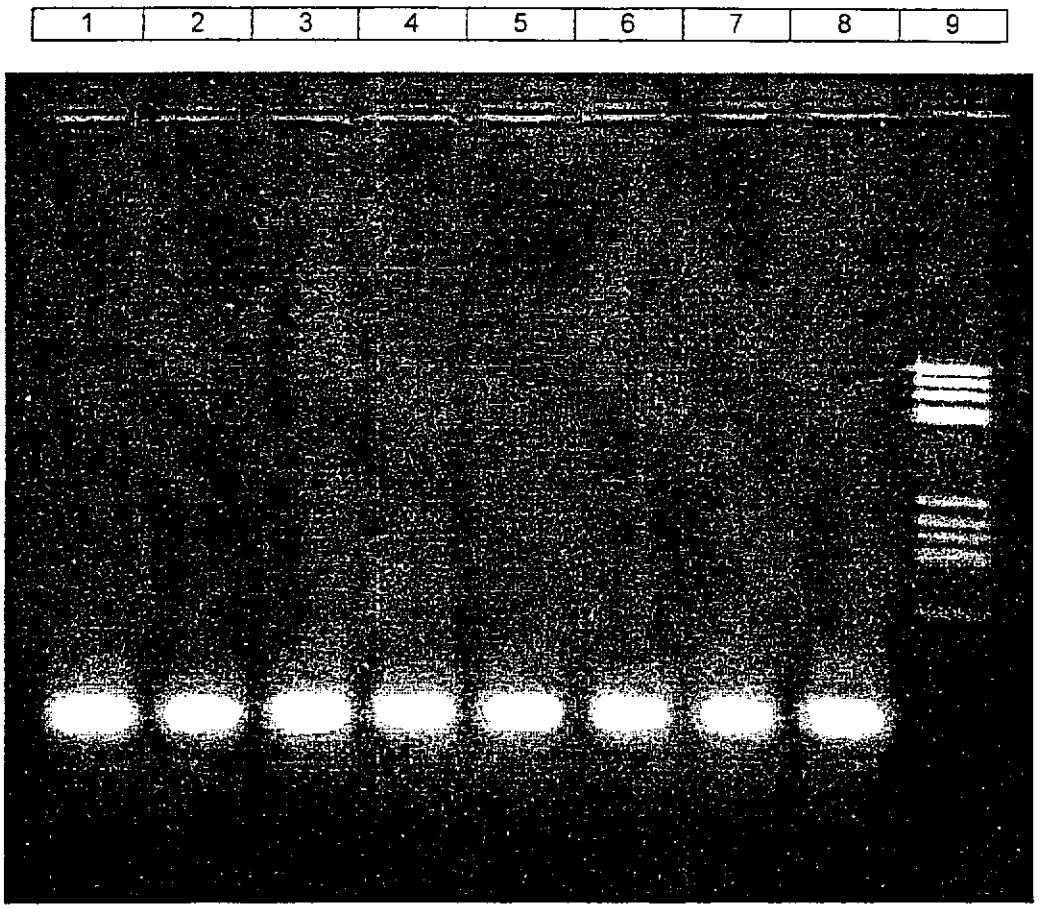


Figure 12

