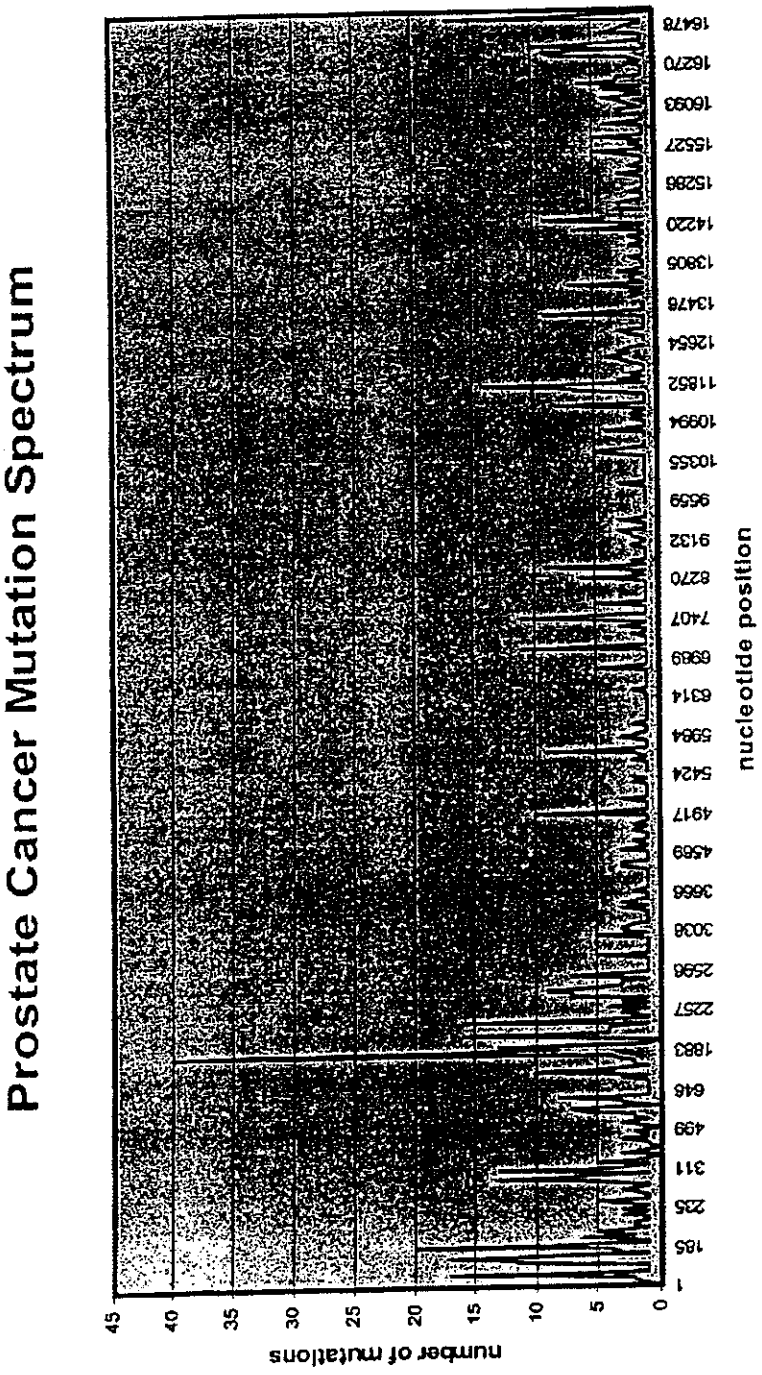

Prostate Cancer Mutation Spectrum
number of mutations
0
5
10
15
20
25
30
35
40
45
nucleotide position
1
185
235
311
499
646
1883
2257
2596
3038
3666
4569
4917
5424
5984
6314
6989
7407
8270
9132
9659
10355
10994
11852
12654
13476
13805
14220
15286
15527
16093
16270
16478

Figure 1

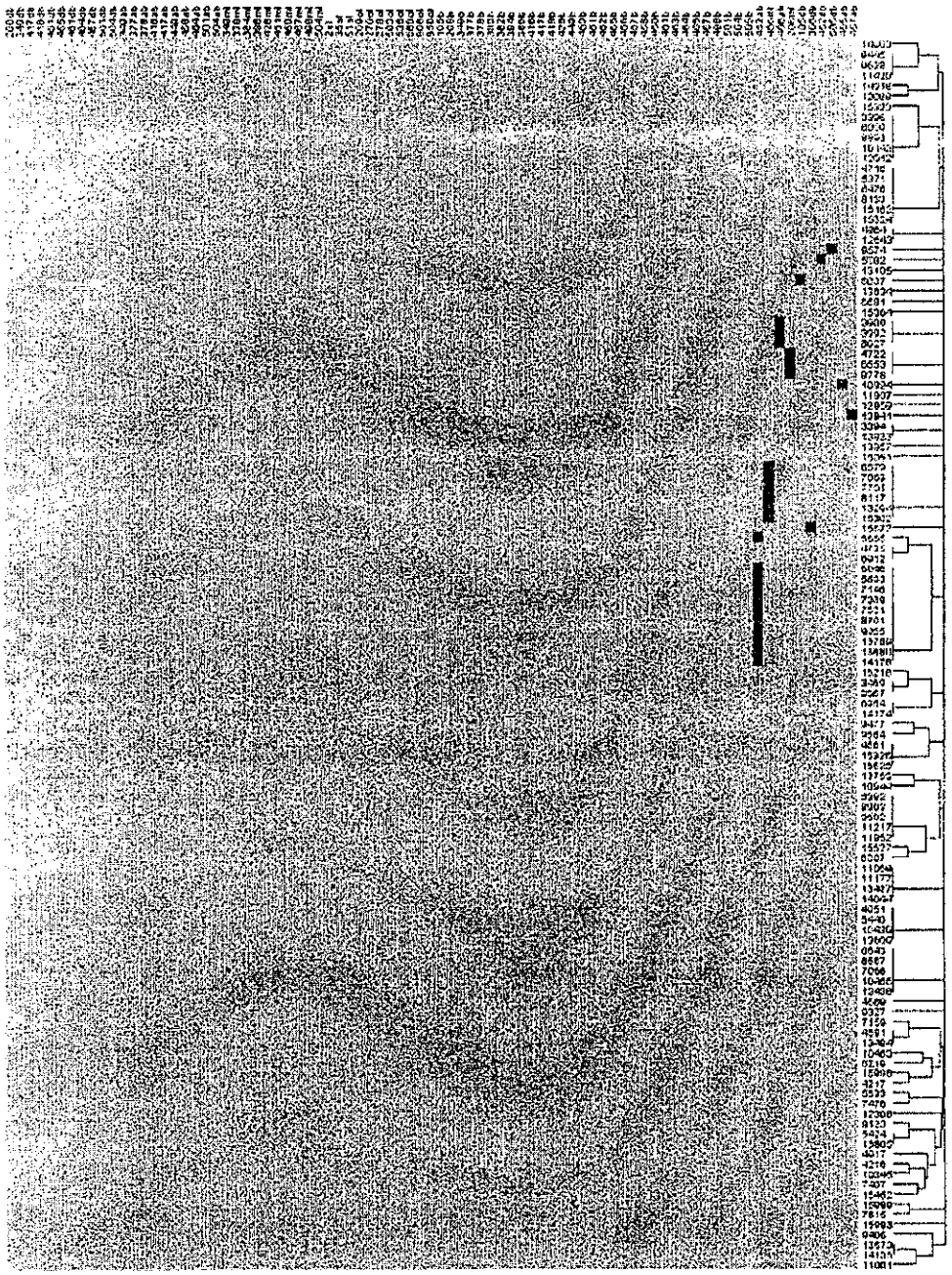


Figure 2

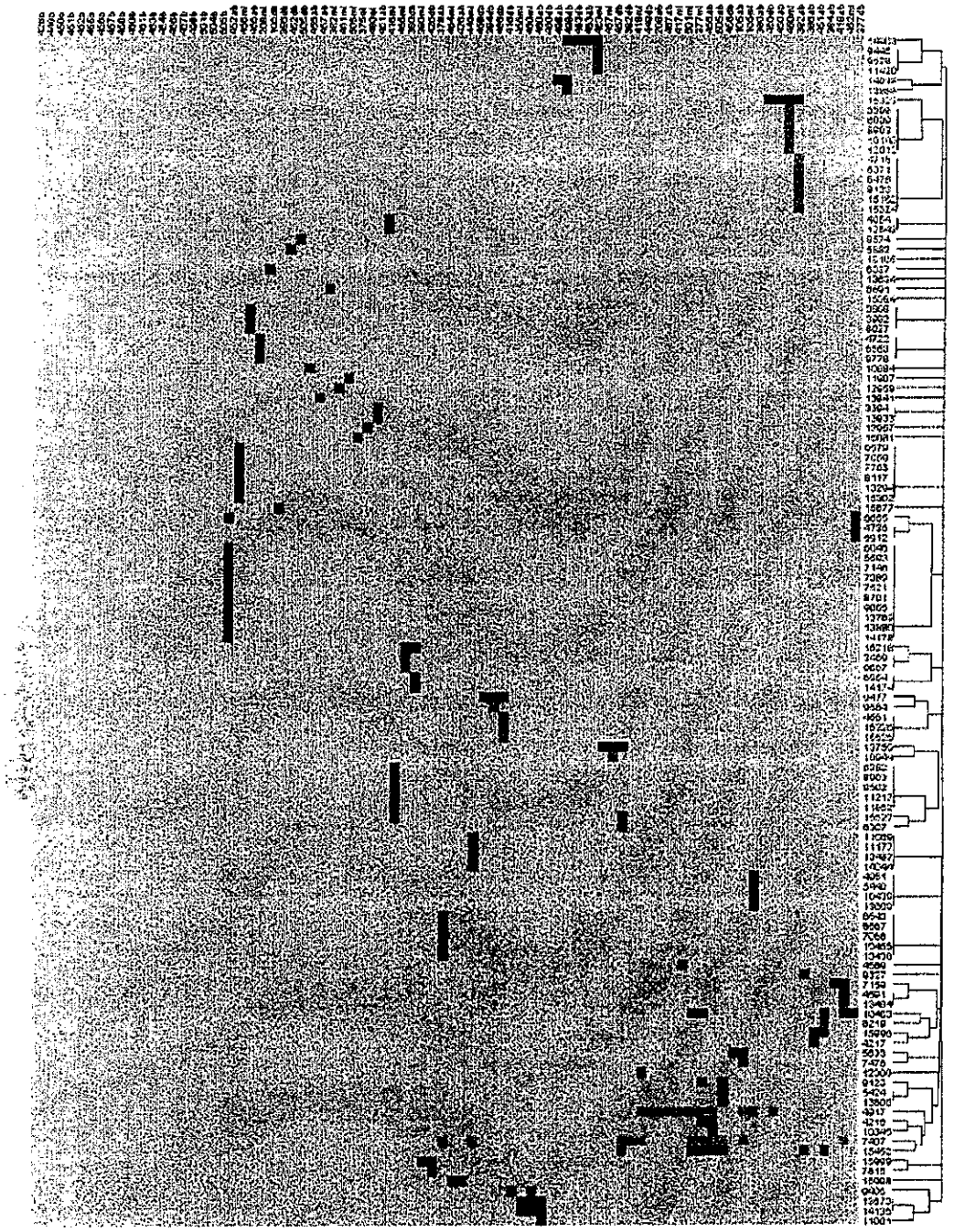


Figure 3

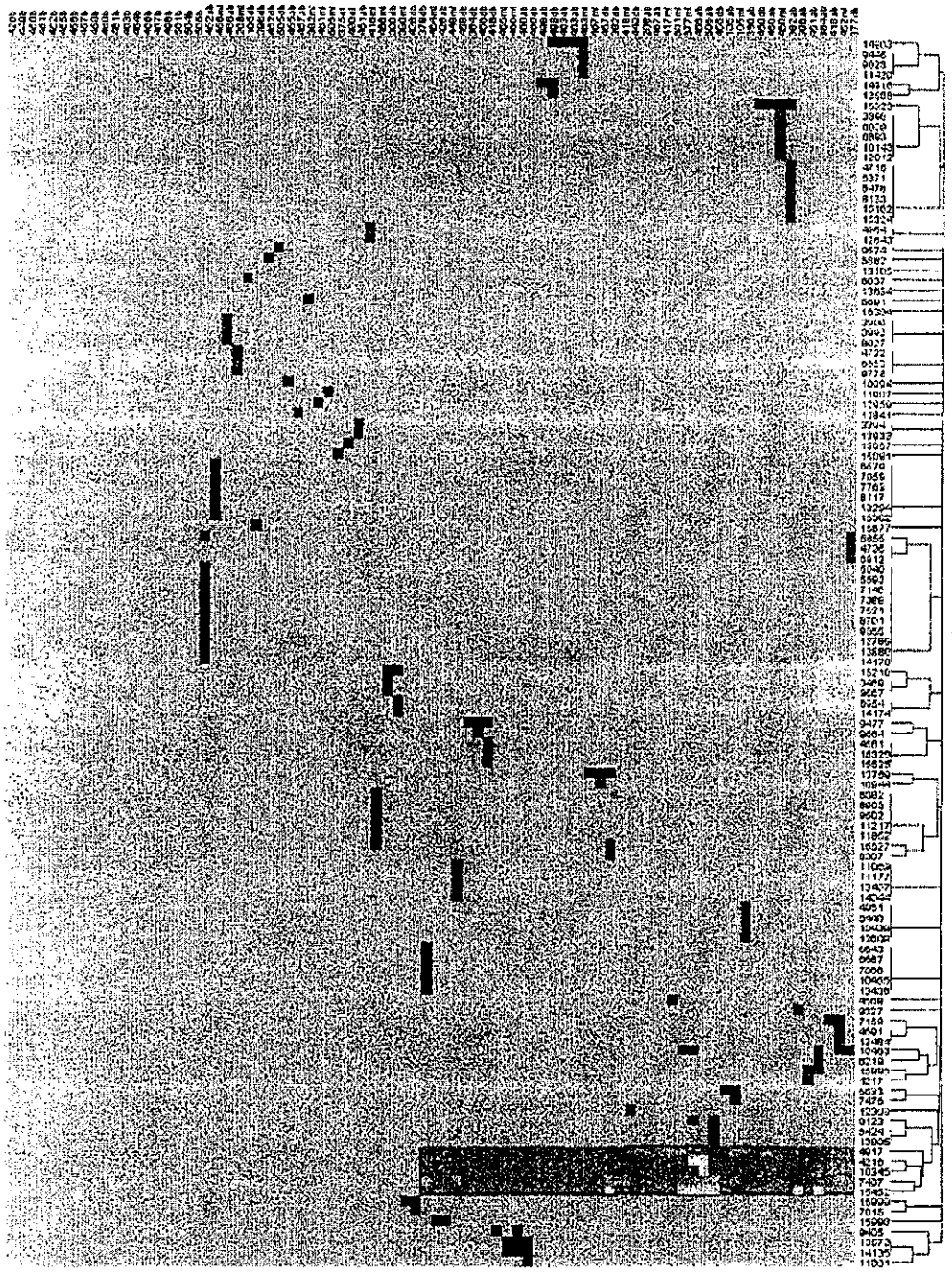


Figure 4

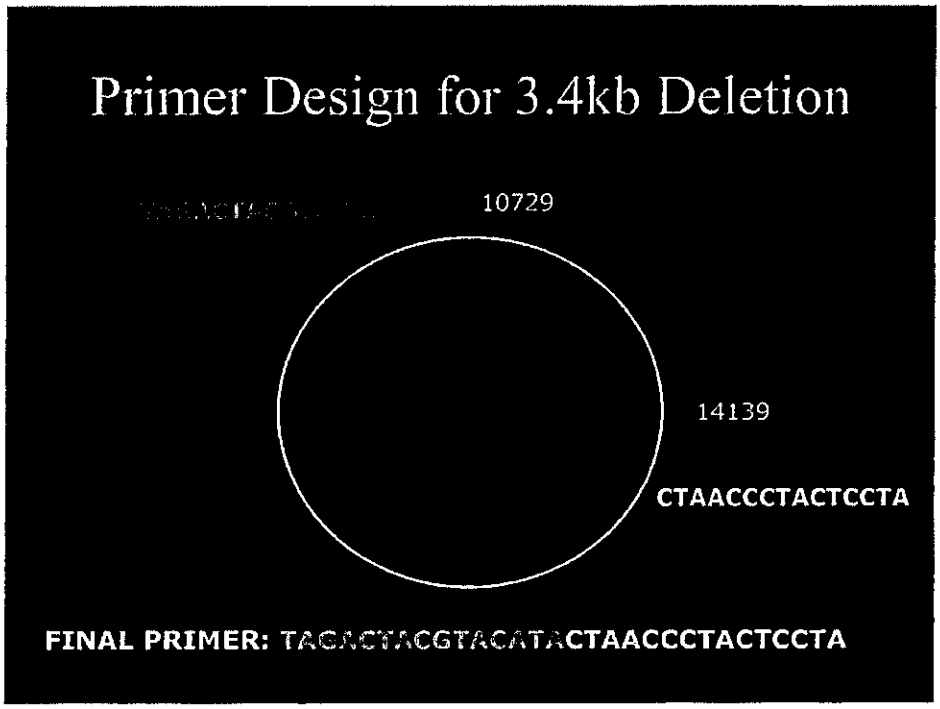

Primer Design for 3.4kb Deletion
10729
14139
CTAACCCTACTCCTA
FINAL PRIMER: TAGACTACGTACATACTAACCCTACTCCTA

Figure 5

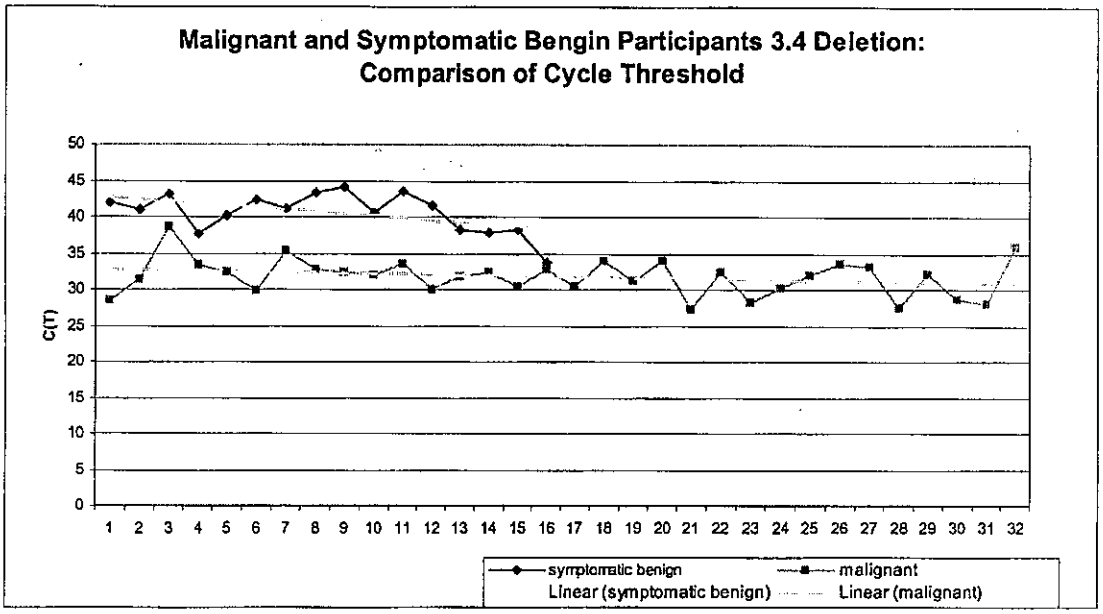

Malignant and Symptomatic Bengin Participants 3.4 Deletion:
Comparison of Cycle Threshold
C(T)
50
45
40
35
30
25
20
15
10
5
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32
symptomatic benign
malignant
Linear (symptomatic benign)
Linear (malignant)

Figure 6

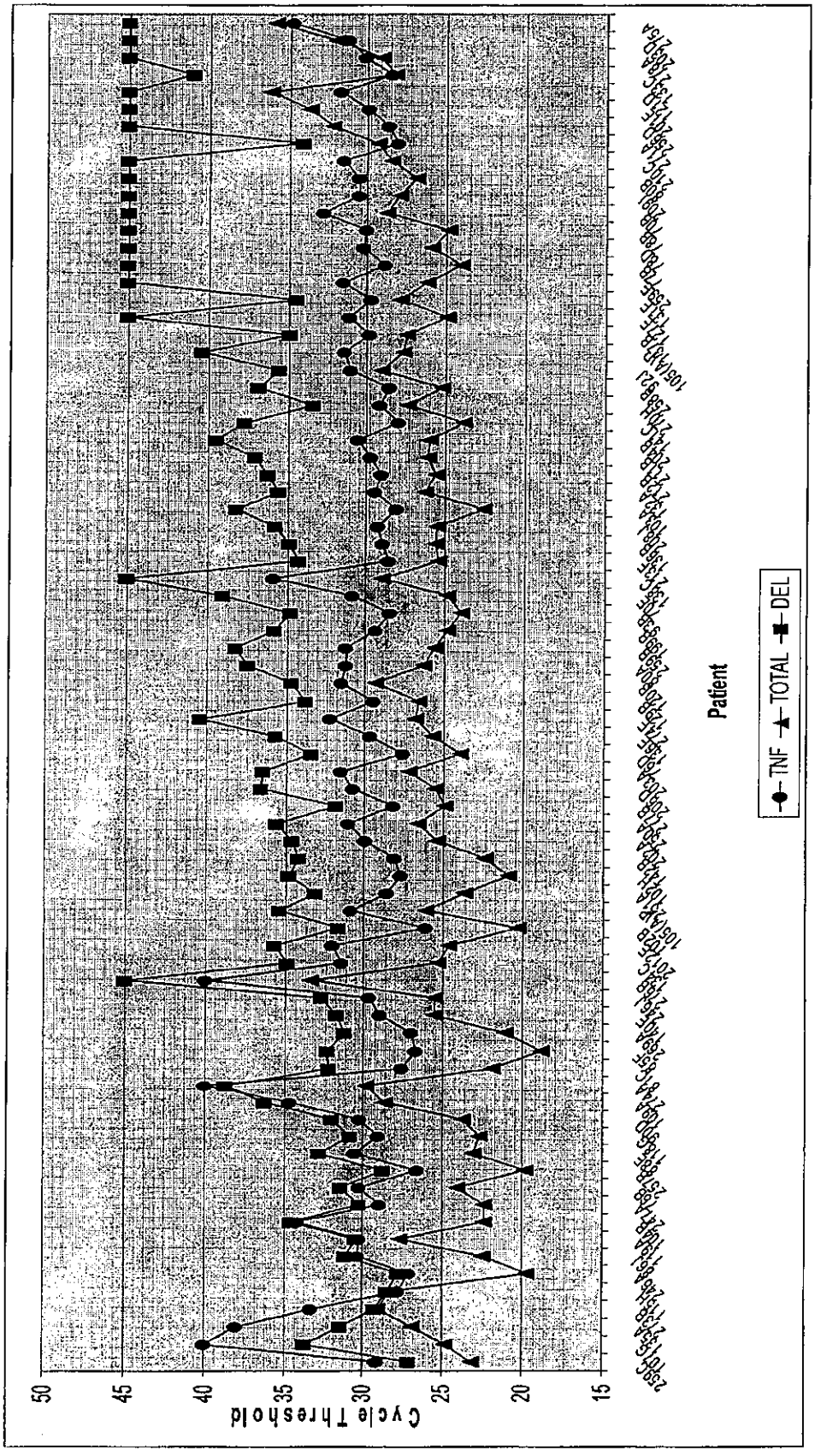


Figure 7

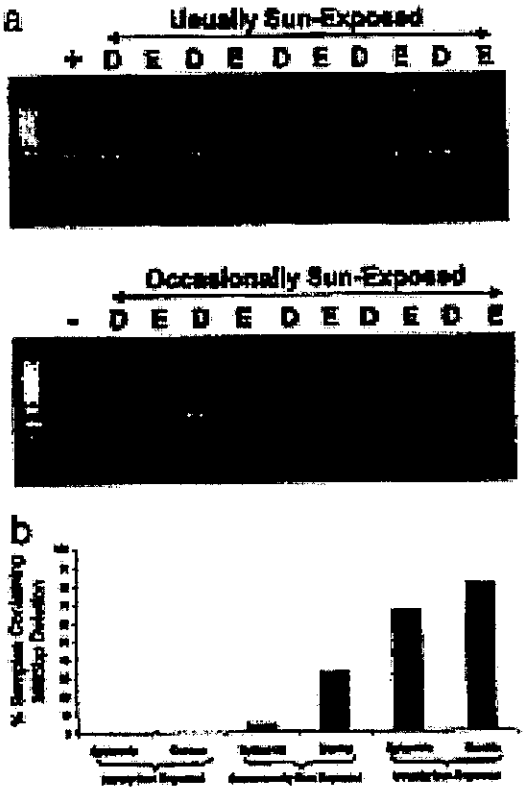

a
Usually Sun-Exposed
+ D E D E D E D E D E
Occasionally Sun-Exposed
- D E D E D E D E D E
b

Figure 8:

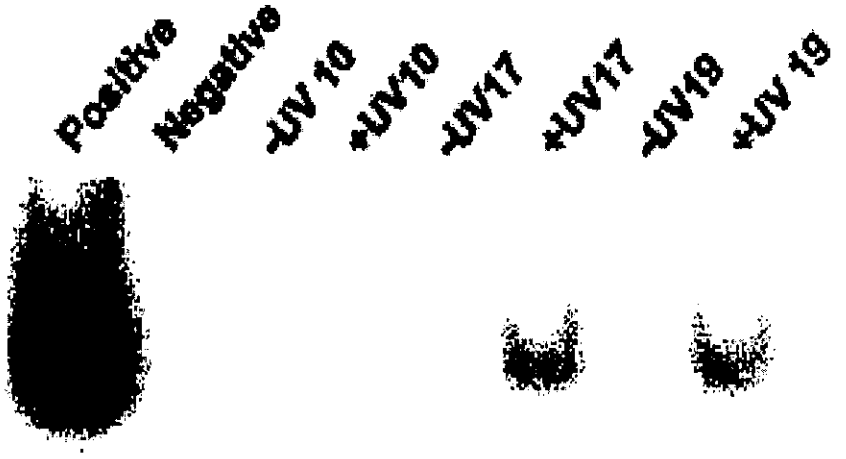


Figure 9:

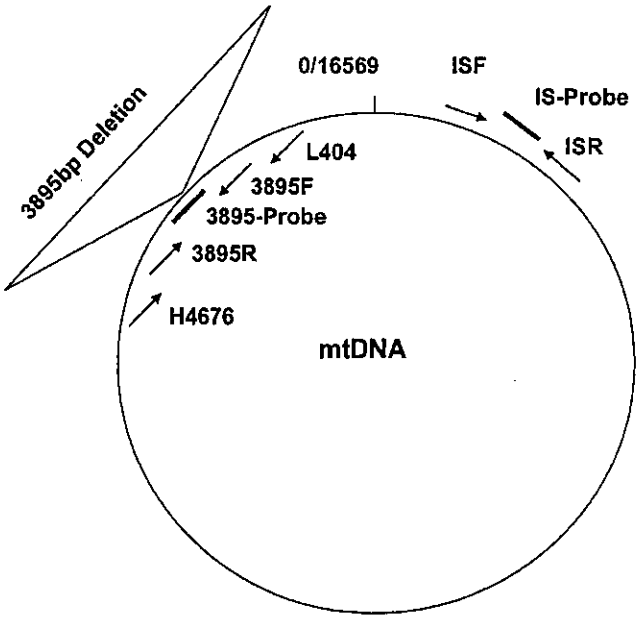

0/16569
ISF
IS-Probe
ISR
L404
3895F
3895-Probe
3895R
H4676
3895bp Deletion
mtDNA

Figure 10

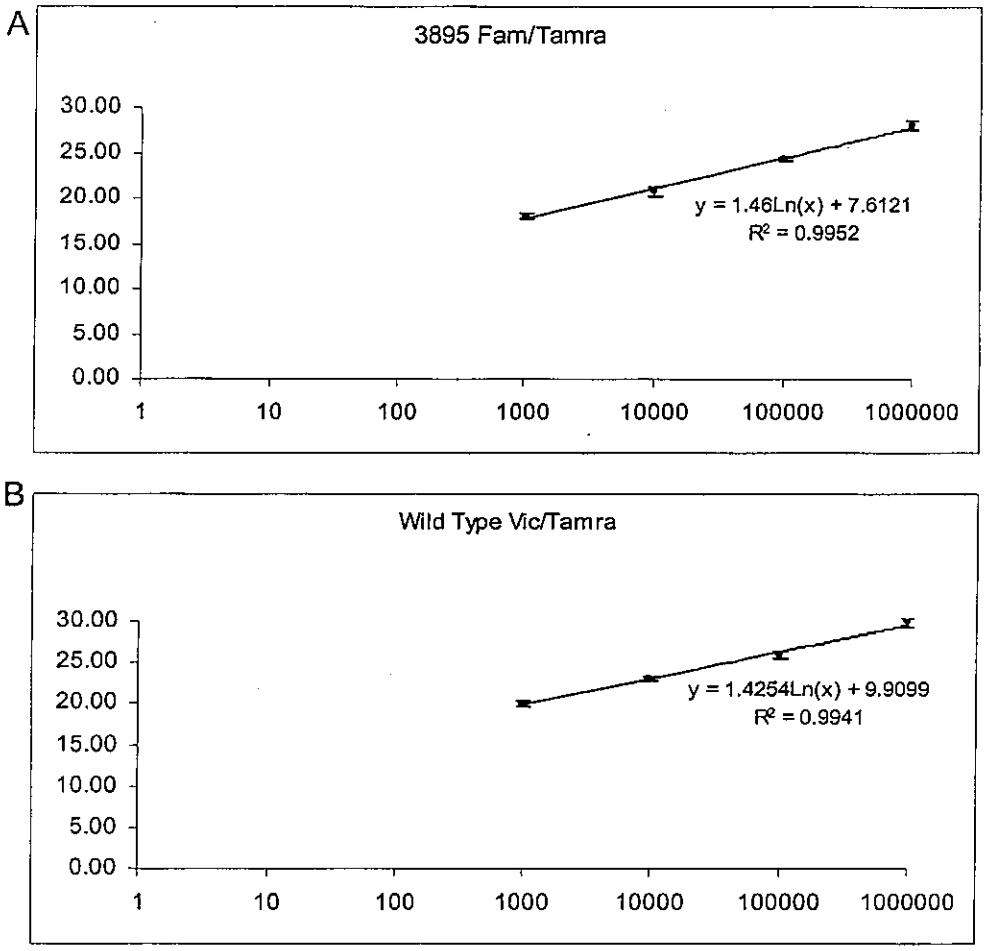

A
3895 Fam/Tamra
30.00
25.00
20.00
15.00
10.00
5.00
0.00
1
10
100
1000
10000
100000
1000000
y = 1.46Ln(x) + 7.6121
R² = 0.9952
B
Wild Type Vic/Tamra
30.00
25.00
20.00
15.00
10.00
5.00
0.00
1
10
100
1000
10000
100000
1000000
y = 1.4254Ln(x) + 9.9099
R² = 0.9941

Figure 11

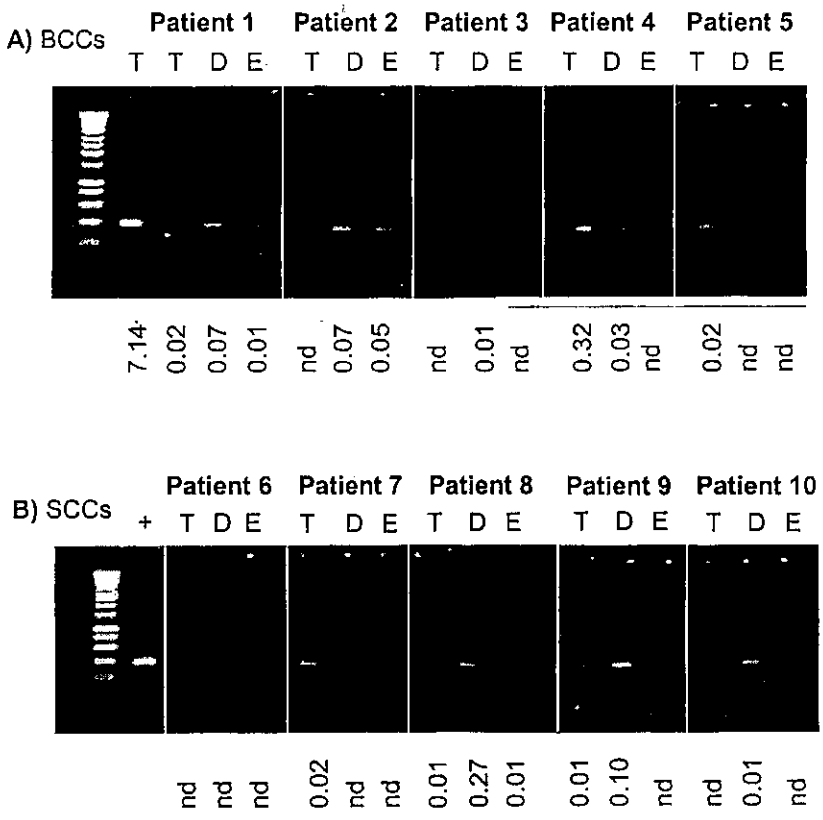
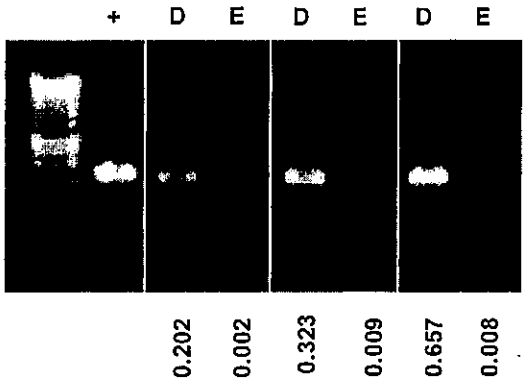

A) BCCs
Patient 1
Patient 2
Patient 3
Patient 4
Patient 5
T T D E T D E T D E T D E T D E
7.14 0.02 0.07 0.01 nd 0.07 0.05 nd 0.01 nd 0.32 0.03 nd 0.02 nd nd
B) SCCs
Patient 6
Patient 7
Patient 8
Patient 9
Patient 10
+ T D E T D E T D E T D E T D E
nd nd nd 0.02 nd nd 0.01 0.27 0.01 0.01 0.10 nd nd 0.01 nd

Figure 12

A) Usually Sun Exposed



B) Occasionally Sun Exposed

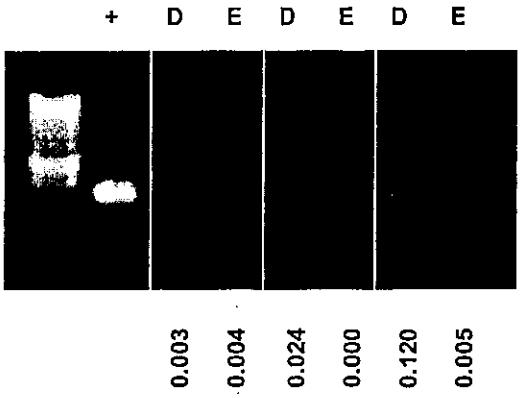


Figure 13

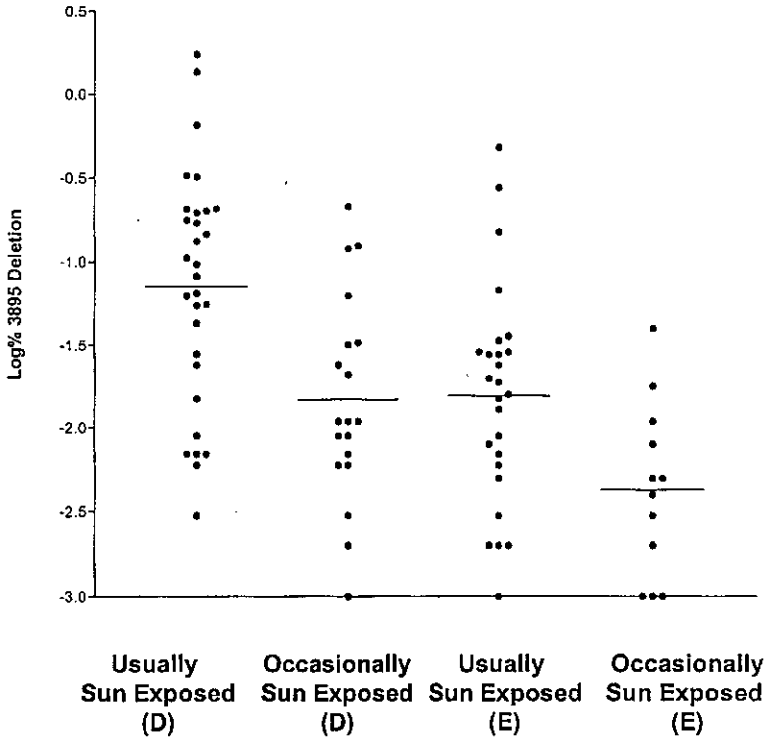

0.5
0.0
-0.5
-1.0
-1.5
-2.0
-2.5
-3.0
Log% 3895 Deletion
Usually Sun Exposed (D)
Occasionally Sun Exposed (D)
Usually Sun Exposed (E)
Occasionally Sun Exposed (E)

Figure 14

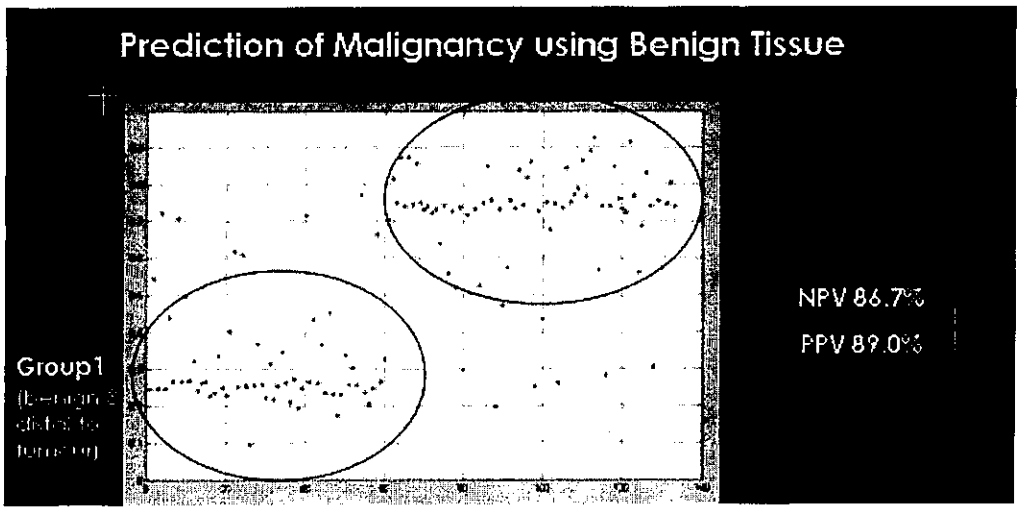

Prediction of Malignancy using Benign Tissue
NPV 86.7%
PPV 89.0%
Group1

Figure 15