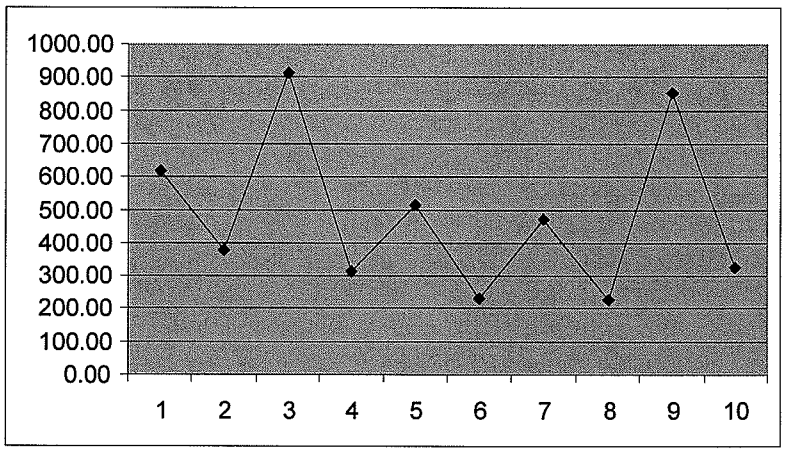


FIG 1

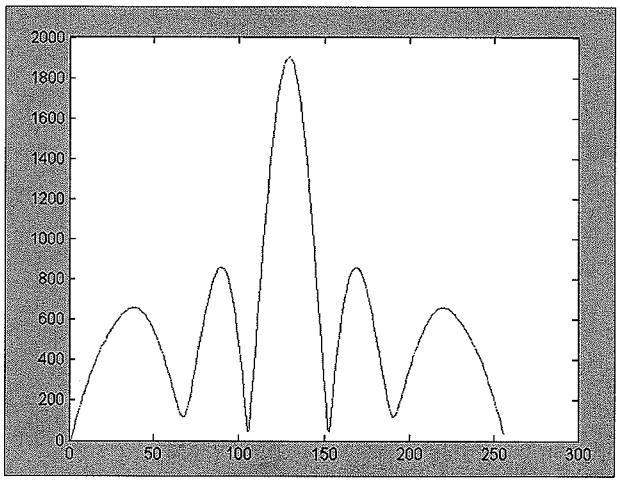


FIG 2a

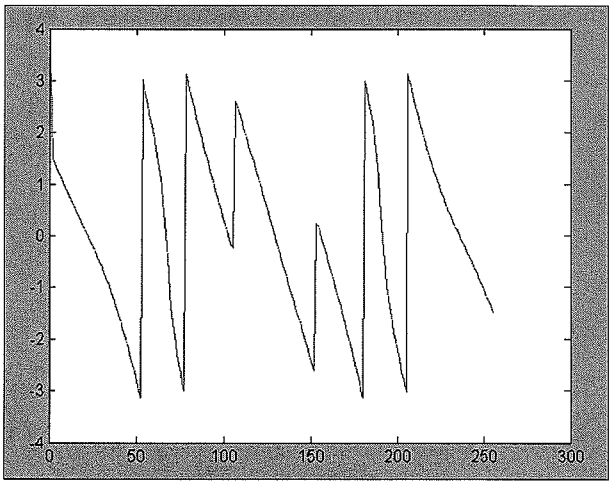


FIG 2b

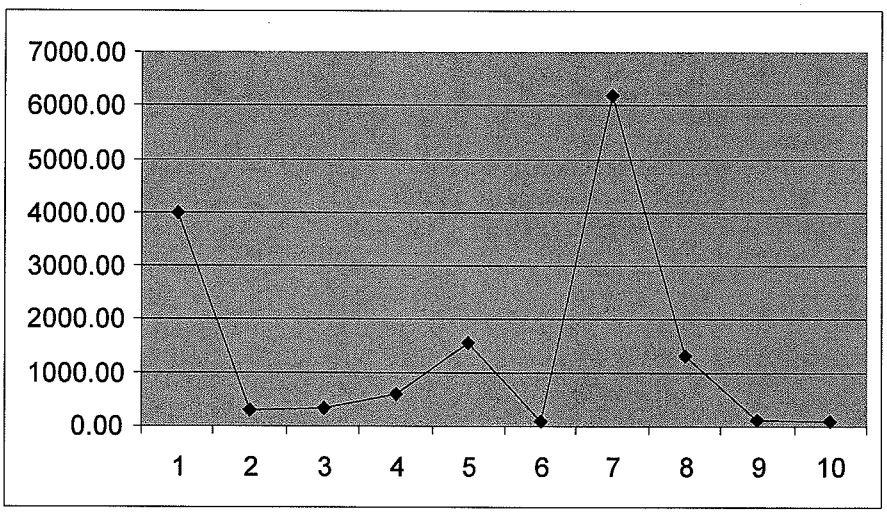

7000.00
6000.00
5000.00
4000.00
3000.00
2000.00
1000.00
0.00
1
2
3
4
5
6
7
8
9
10

FIG 3

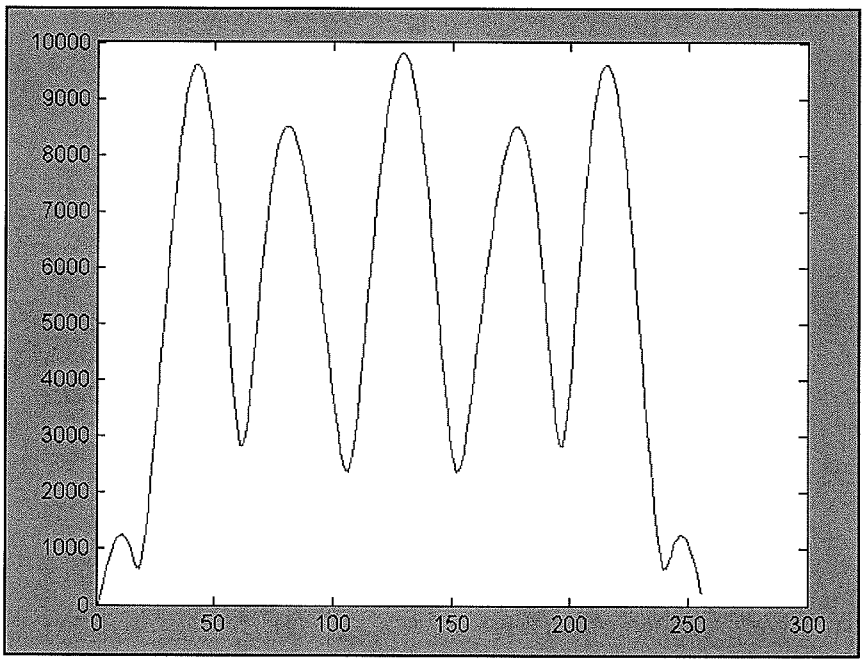

10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
300

FIG 4

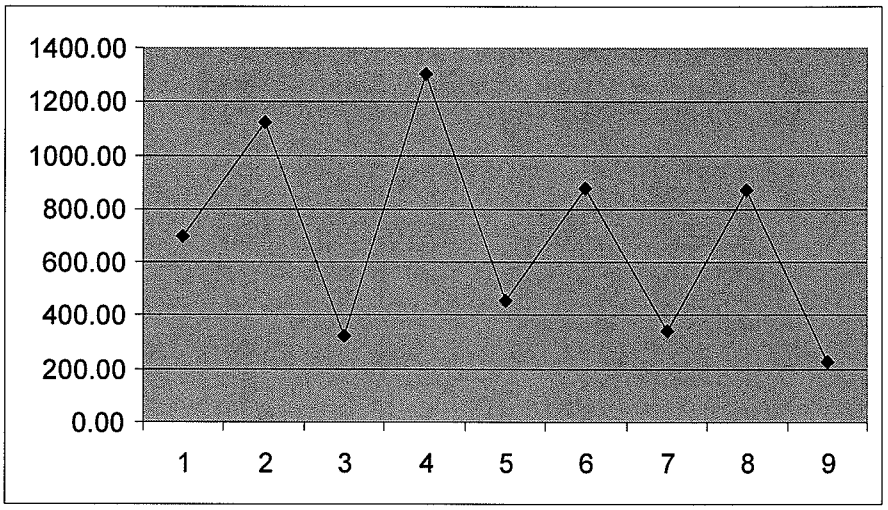


FIG 5

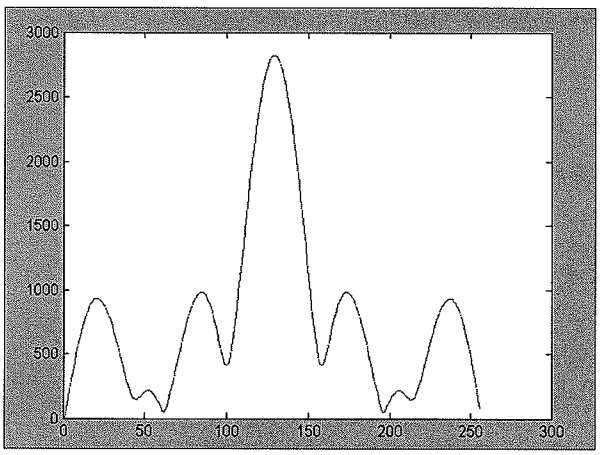


FIG 6a

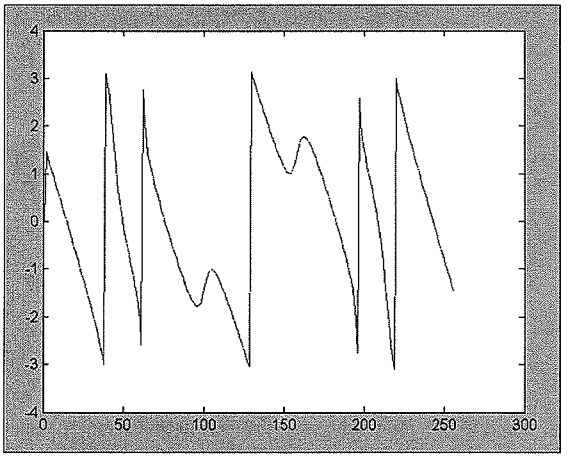


FIG 6b

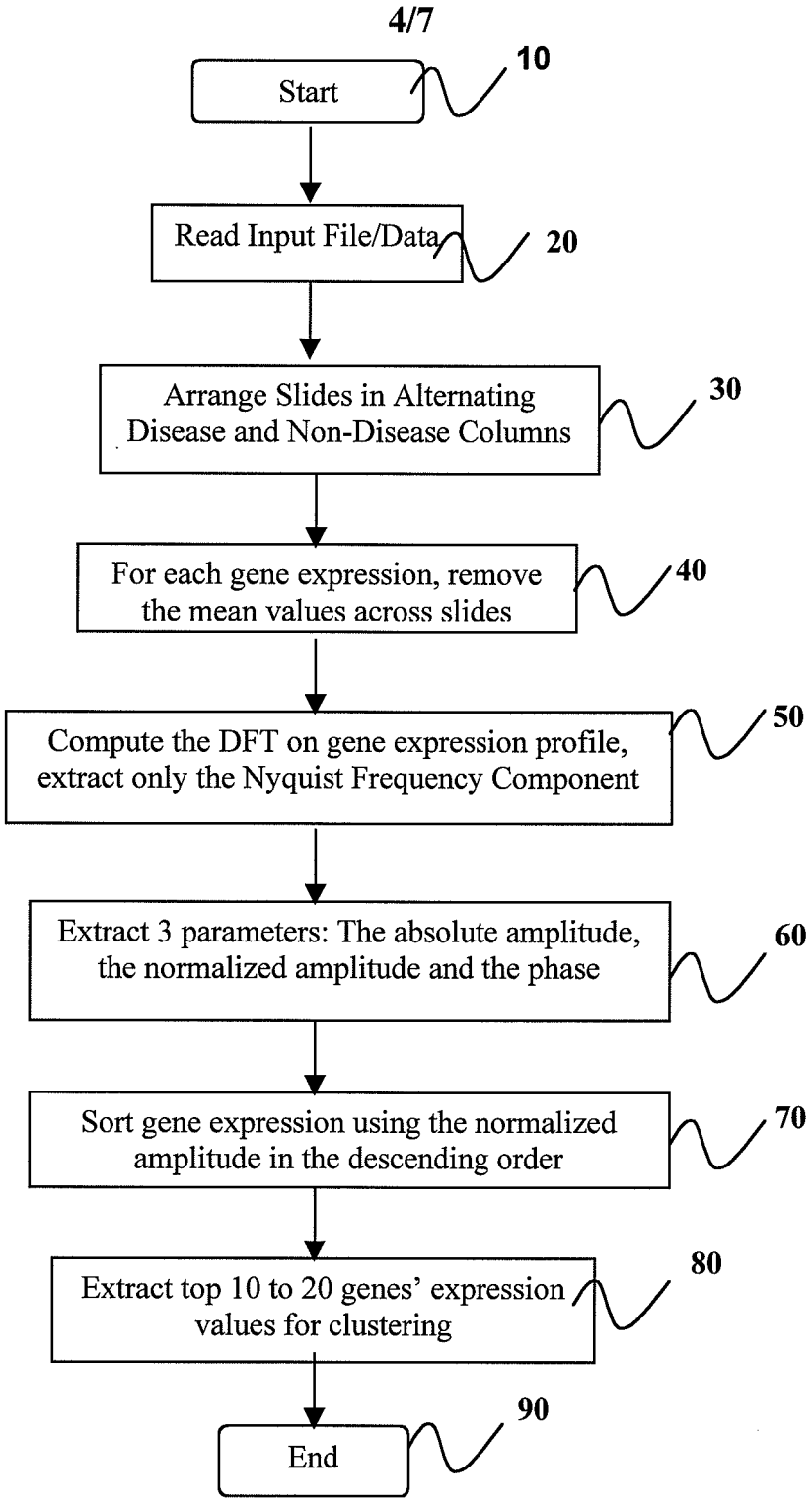

Start
10
Read Input File/Data
20
Arrange Slides in Alternating Disease and Non-Disease Columns
30
For each gene expression, remove the mean values across slides
40
Compute the DFT on gene expression profile, extract only the Nyquist Frequency Component
50
Extract 3 parameters: The absolute amplitude, the normalized amplitude and the phase
60
Sort gene expression using the normalized amplitude in the descending order
70
Extract top 10 to 20 genes' expression values for clustering
80
End
90

FIG 7

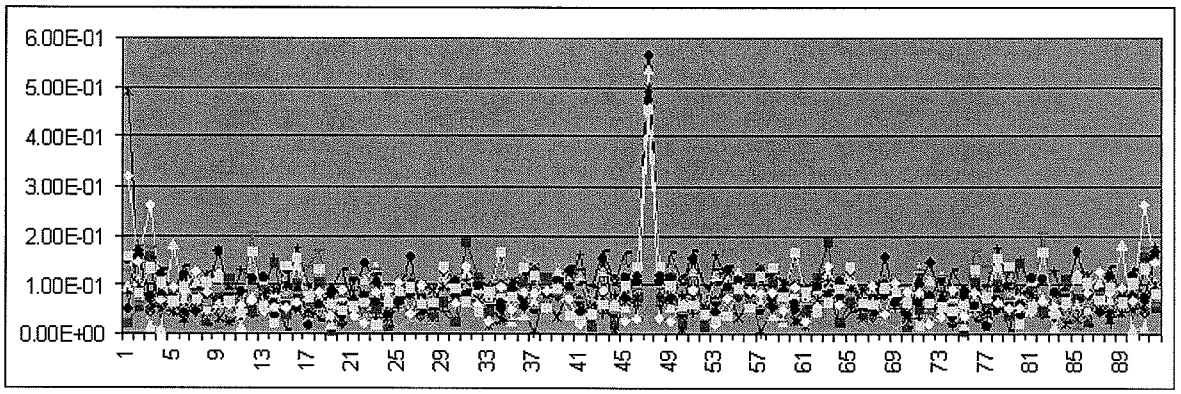

6.00E-01
5.00E-01
4.00E-01
3.00E-01
2.00E-01
1.00E-01
0.00E+00
1
5
9
13
17
21
25
29
33
37
41
45
49
53
57
61
65
69
73
77
81
85
89

FIG 8a

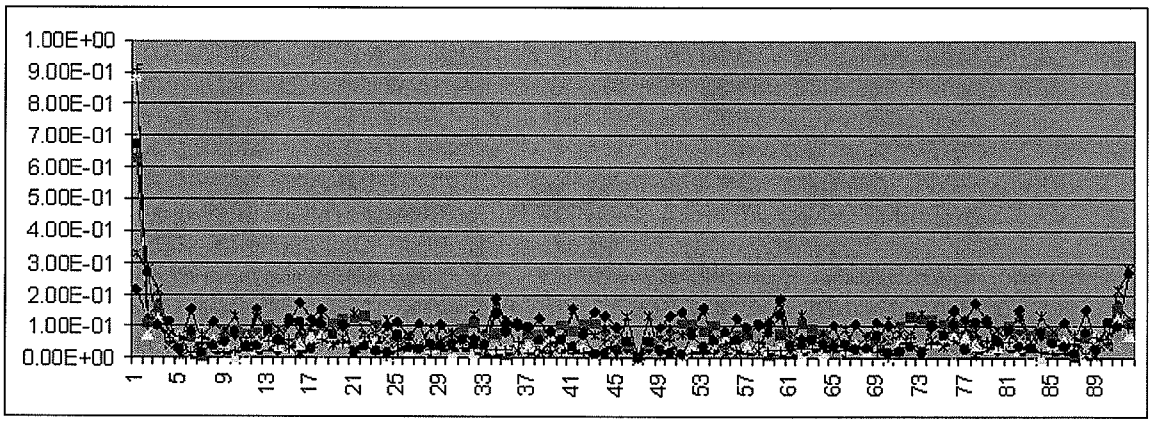

1.00E+00
9.00E-01
8.00E-01
7.00E-01
6.00E-01
5.00E-01
4.00E-01
3.00E-01
2.00E-01
1.00E-01
0.00E+00
1
5
9
13
17
21
25
29
33
37
41
45
49
53
57
61
65
69
73
77
81
85
89

FIG 8b

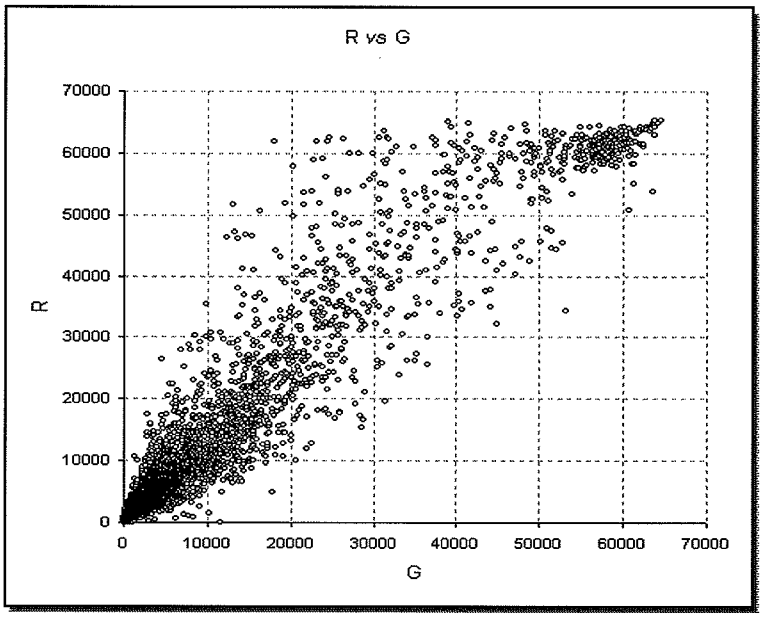

R vs G
70000
60000
50000
40000
30000
20000
10000
0
R
0
10000
20000
30000
40000
50000
60000
70000
G

FIG 9a

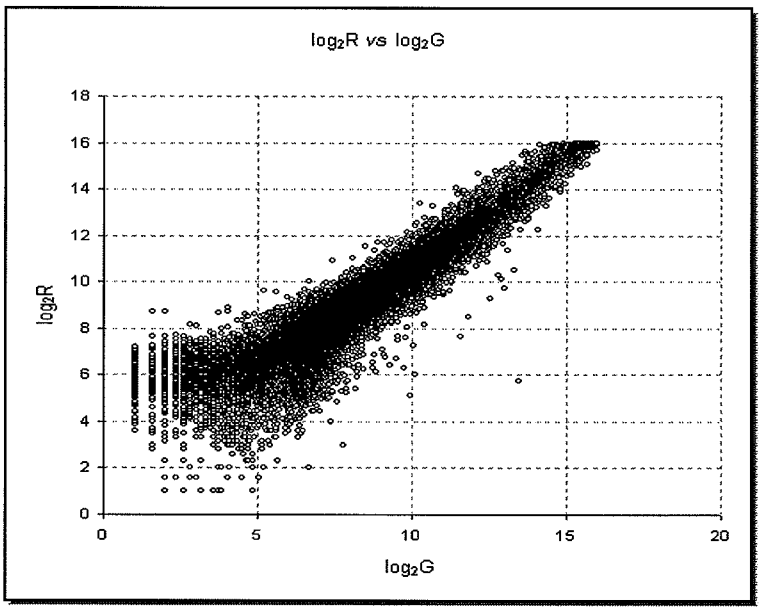

log2R vs log2G
18
16
14
12
10
8
6
4
2
0
log2R
0
5
10
15
20
log2G

FIG 9b

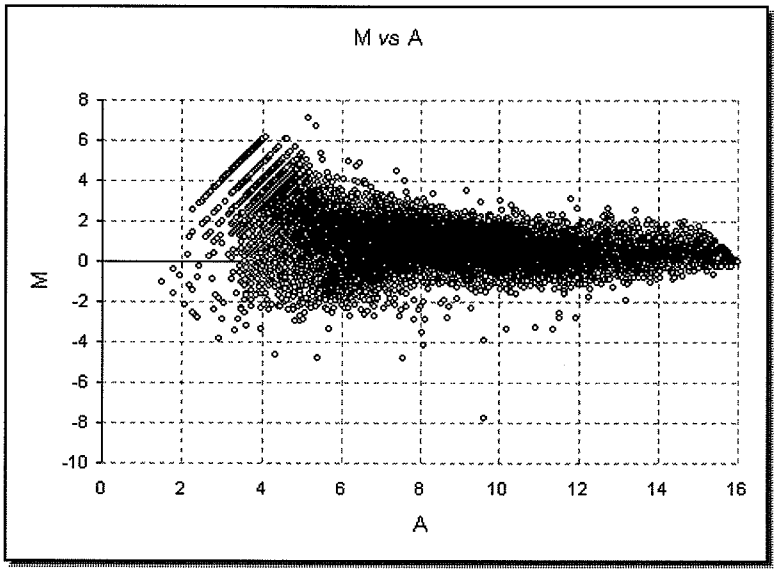

M vs A
M
A
8
6
4
2
0
-2
-4
-6
-8
-10
0
2
4
6
8
10
12
14
16

FIG 9c

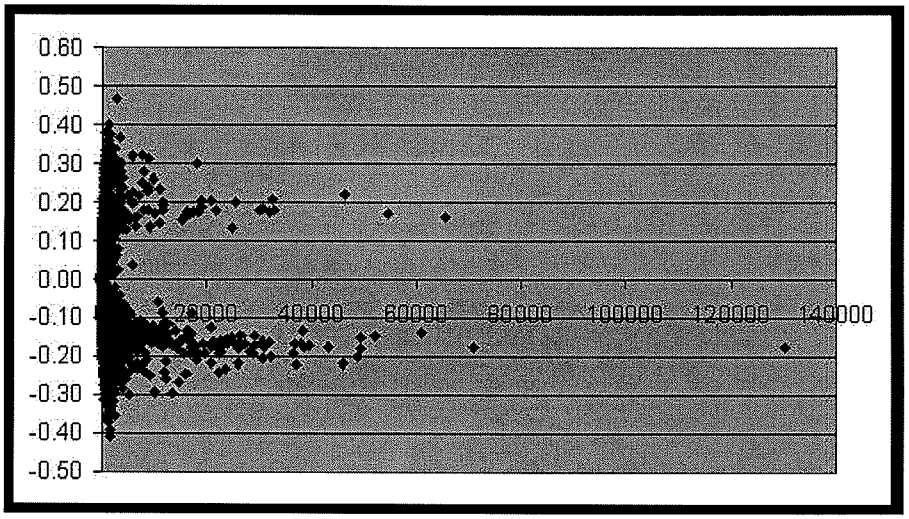

0.60
0.50
0.40
0.30
0.20
0.10
0.00
-0.10
-0.20
-0.30
-0.40
-0.50
20000
40000
60000
80000
100000
120000
140000

FIG 10