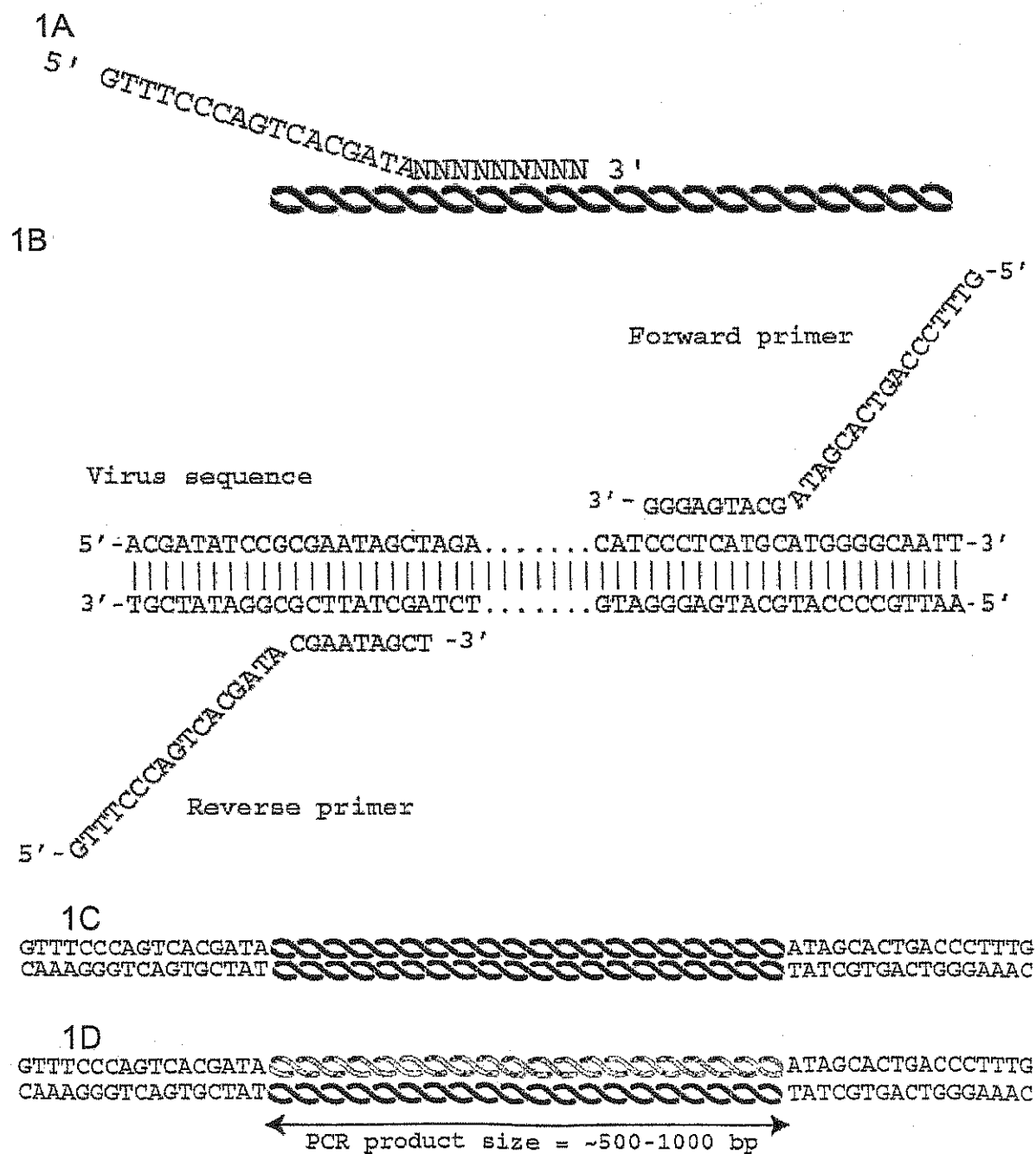


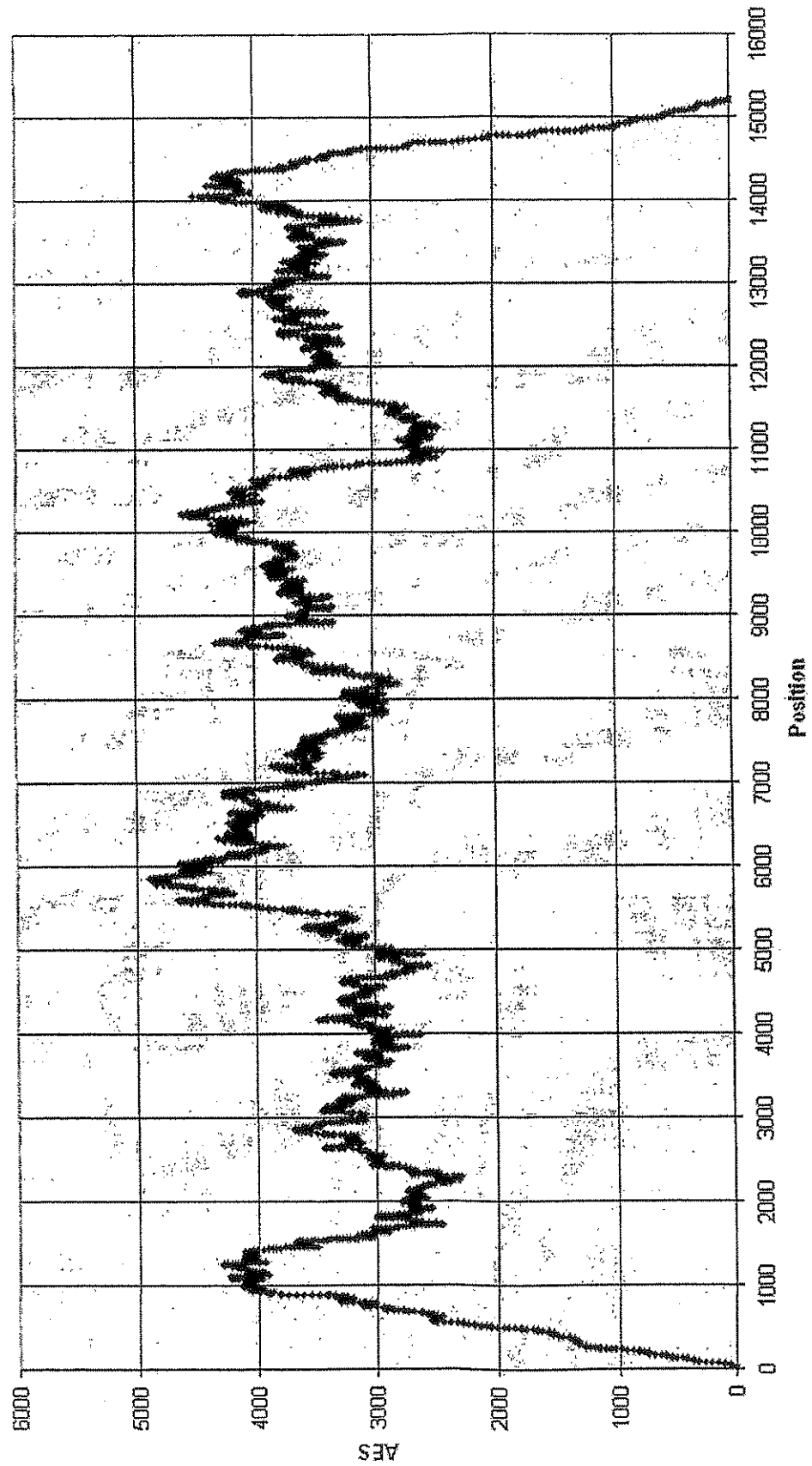
1/20

FIGURE 1

2/20

FIGURE 2

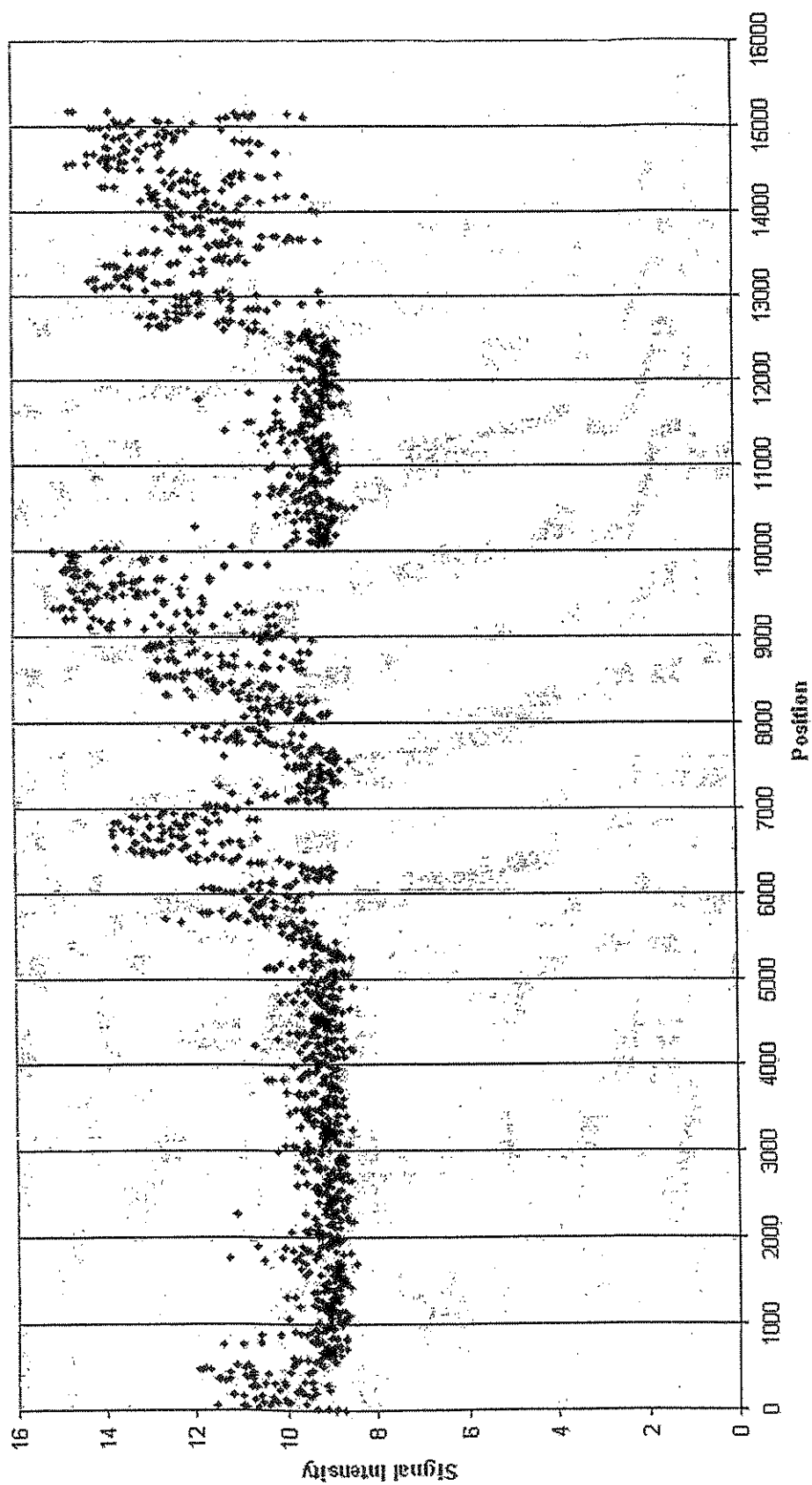
Amplification Efficiency Map (RSV)



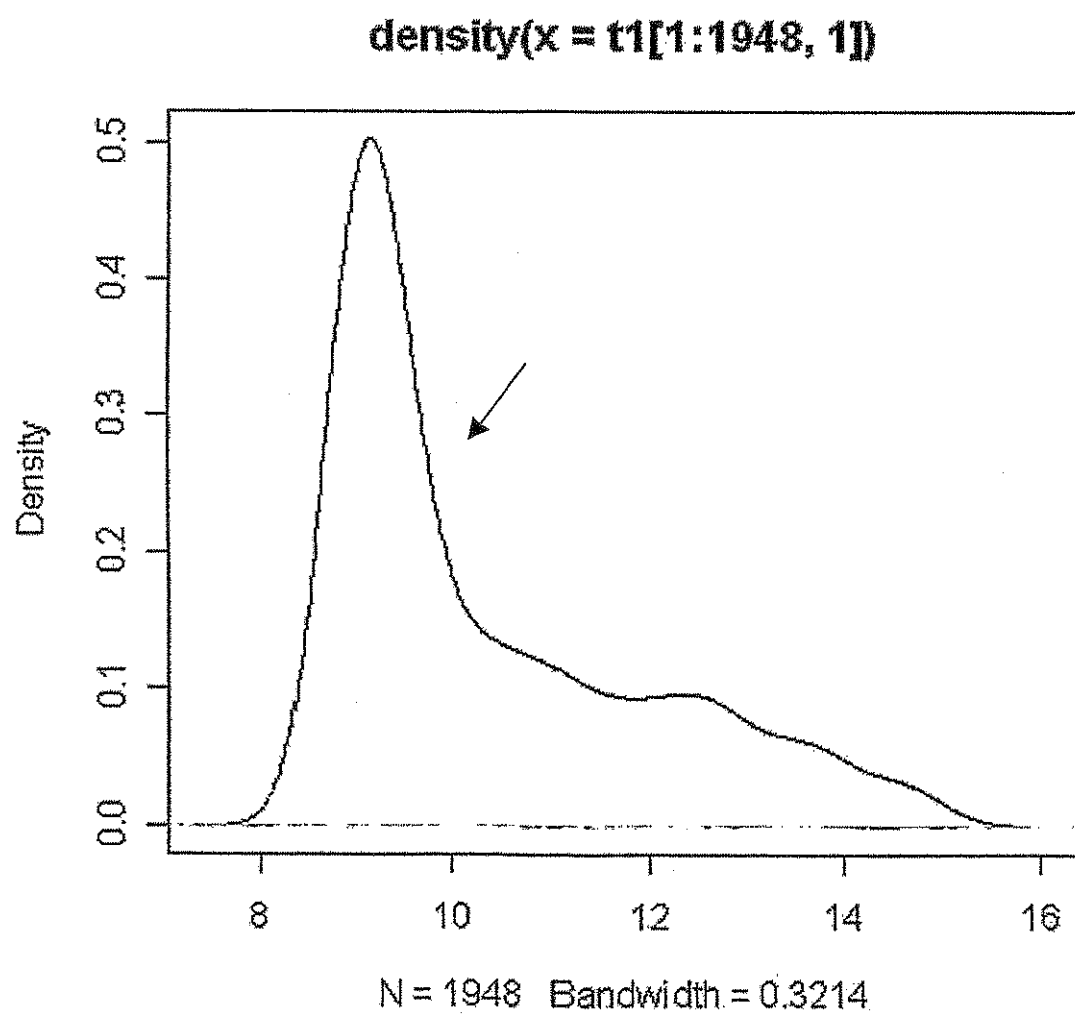
3/20

FIGURE 3

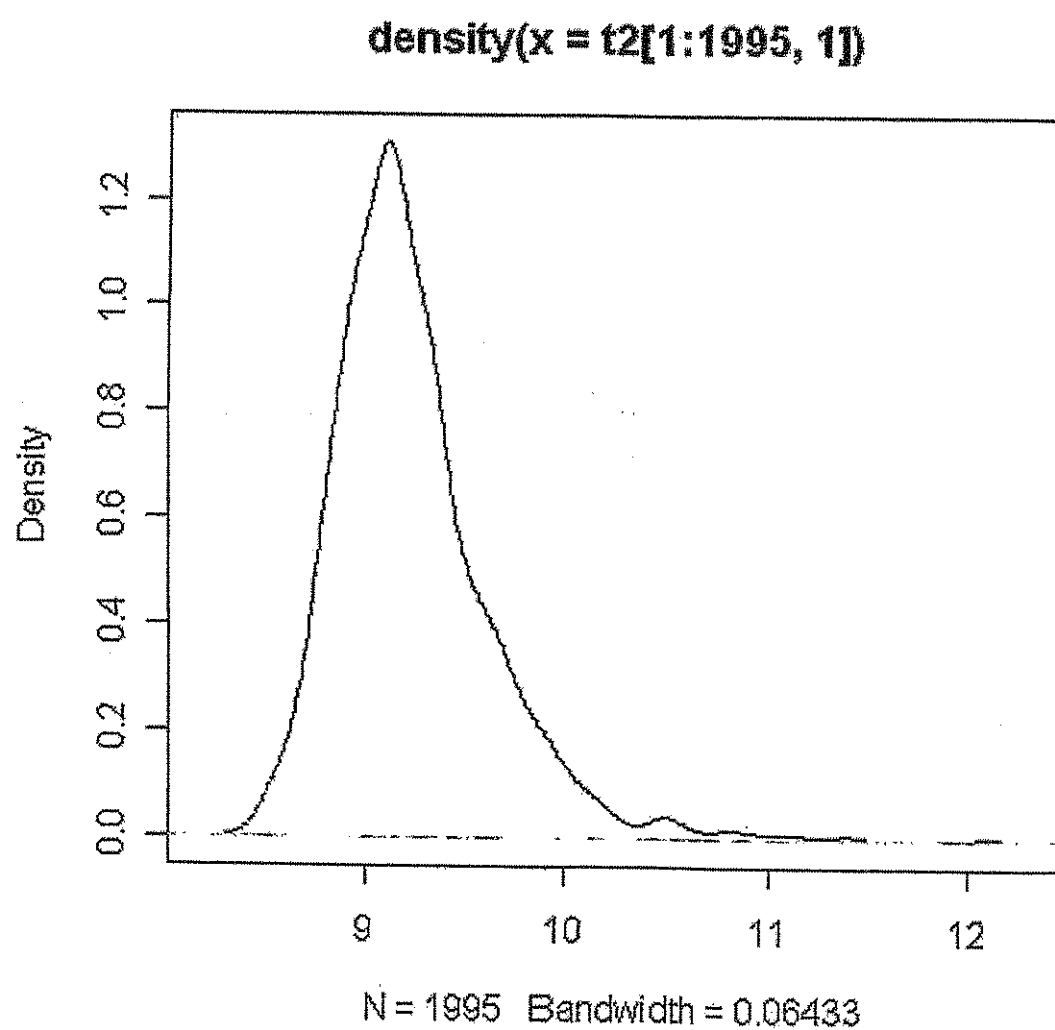
RSV Signal Intensity Map



4/20

FIGURE 4A

5/20

FIGURE 4B

6/20

FIGURE 5

Given PDC data D with virus set V and probe set P ,

Let $V' = \Phi$

For every $v_a \in V$,

- Compute one-tailed t-test with significance level 0.05 of probes in v_a

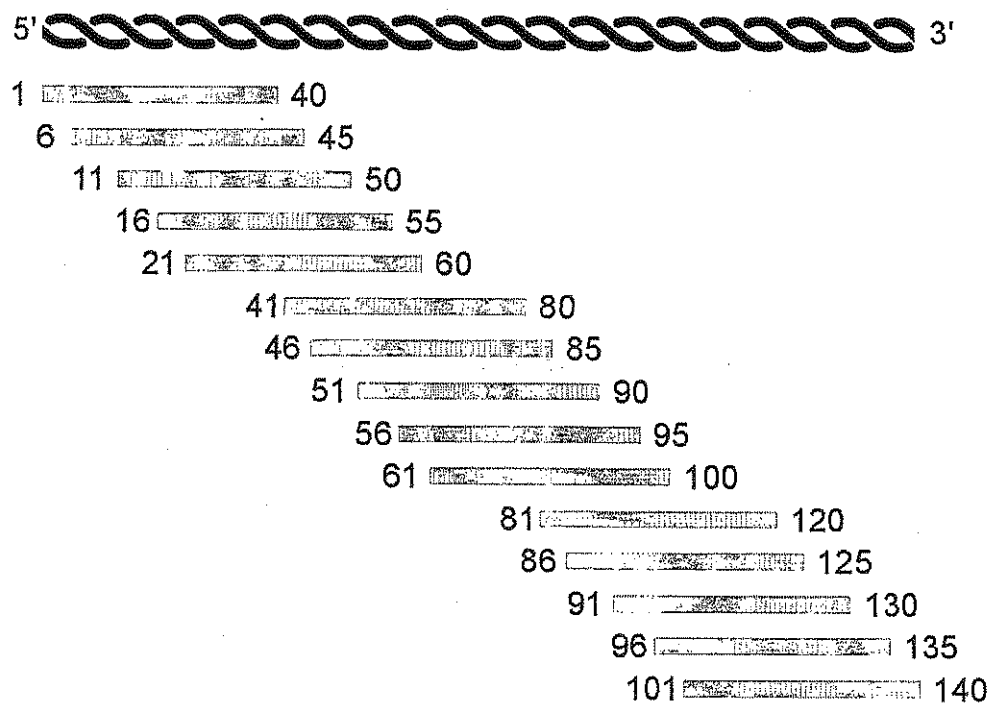
If(p -value of $t_a < 0.05$)

- Accept if $KL(P_a \| P) \geq 0.1$; $V' = V' \cup \{v_a\}$
- Reject otherwise;

Reject otherwise;

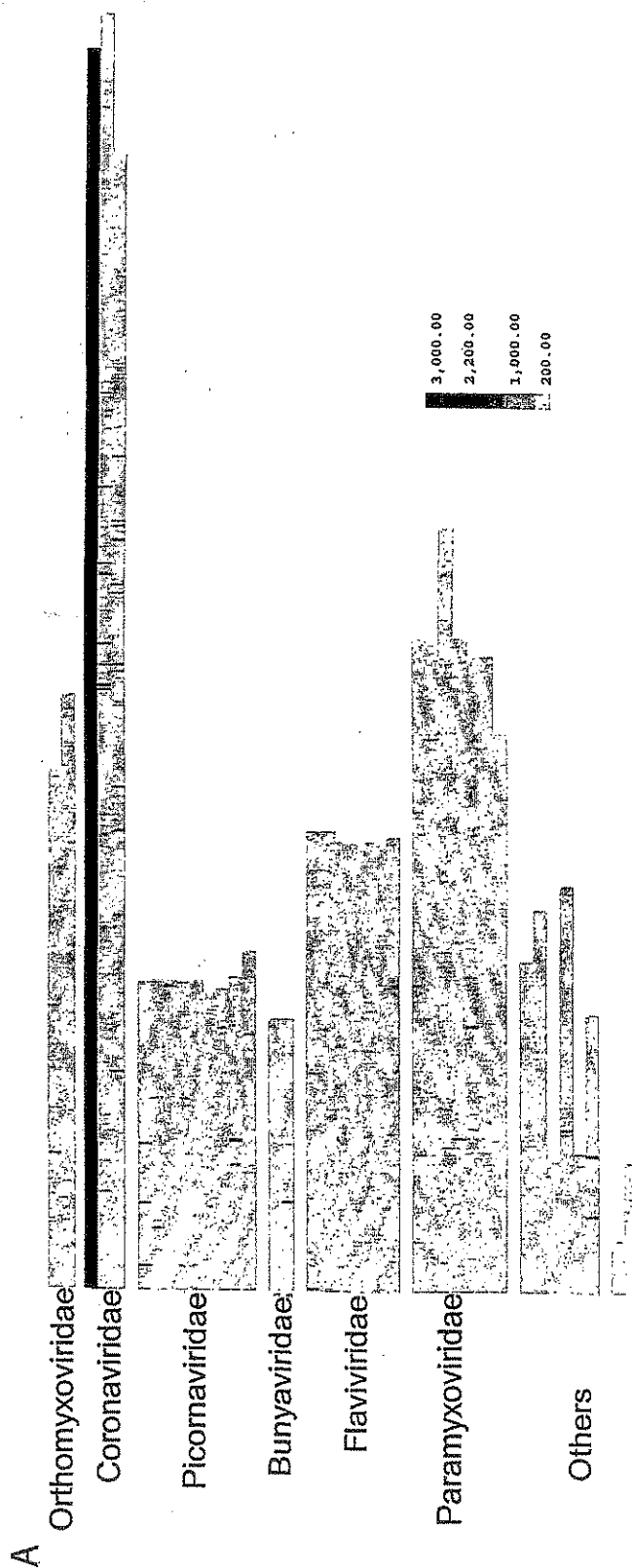
Return V'

7/20

FIGURE 6

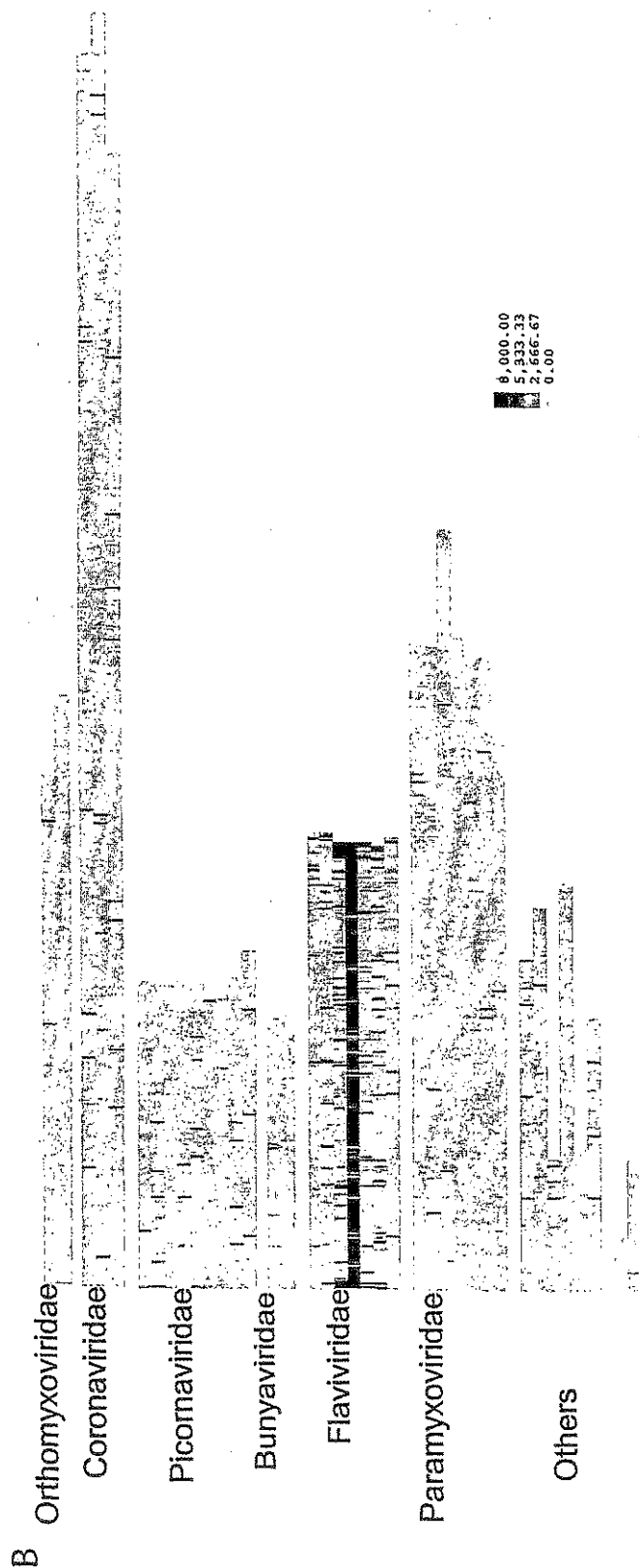
8/20

FIGURE 7A



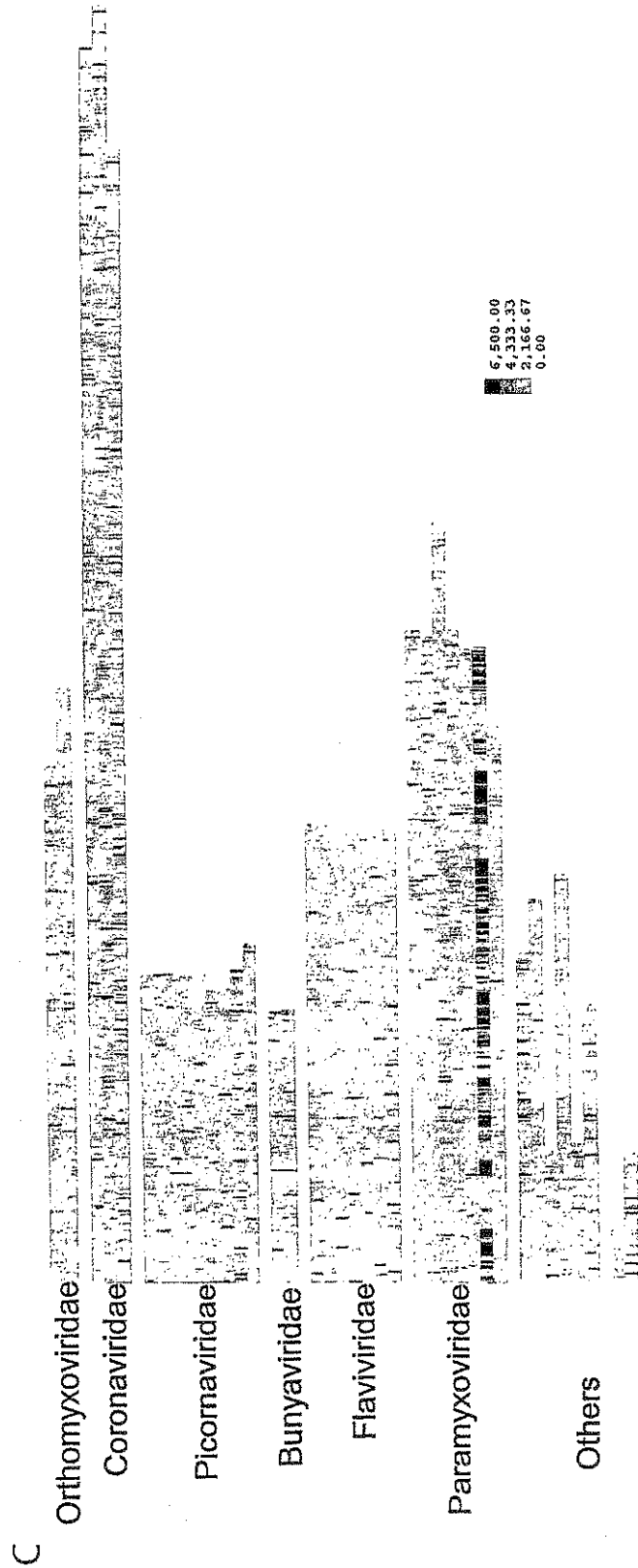
9/20

FIGURE 7B



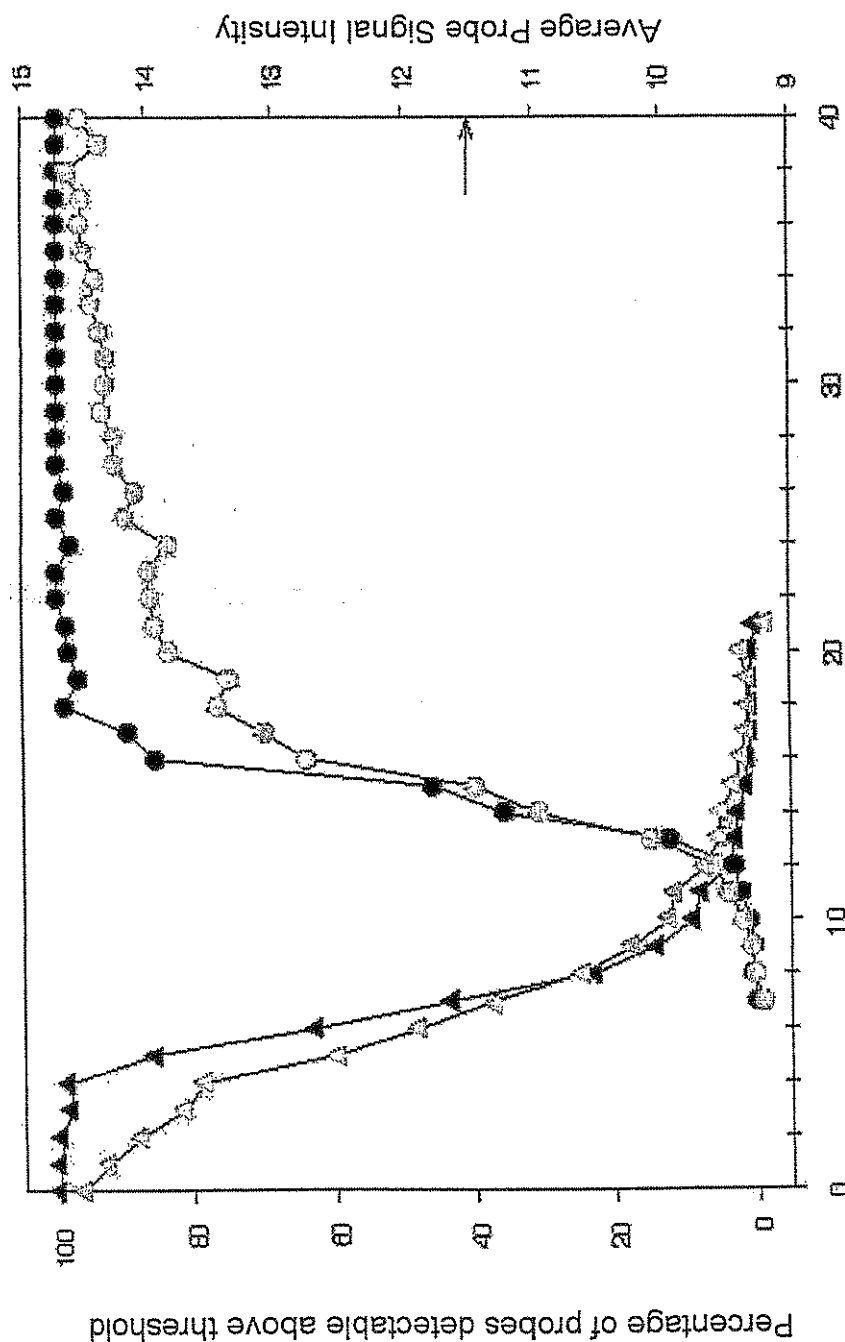
10/20

FIGURE 7C



11/20

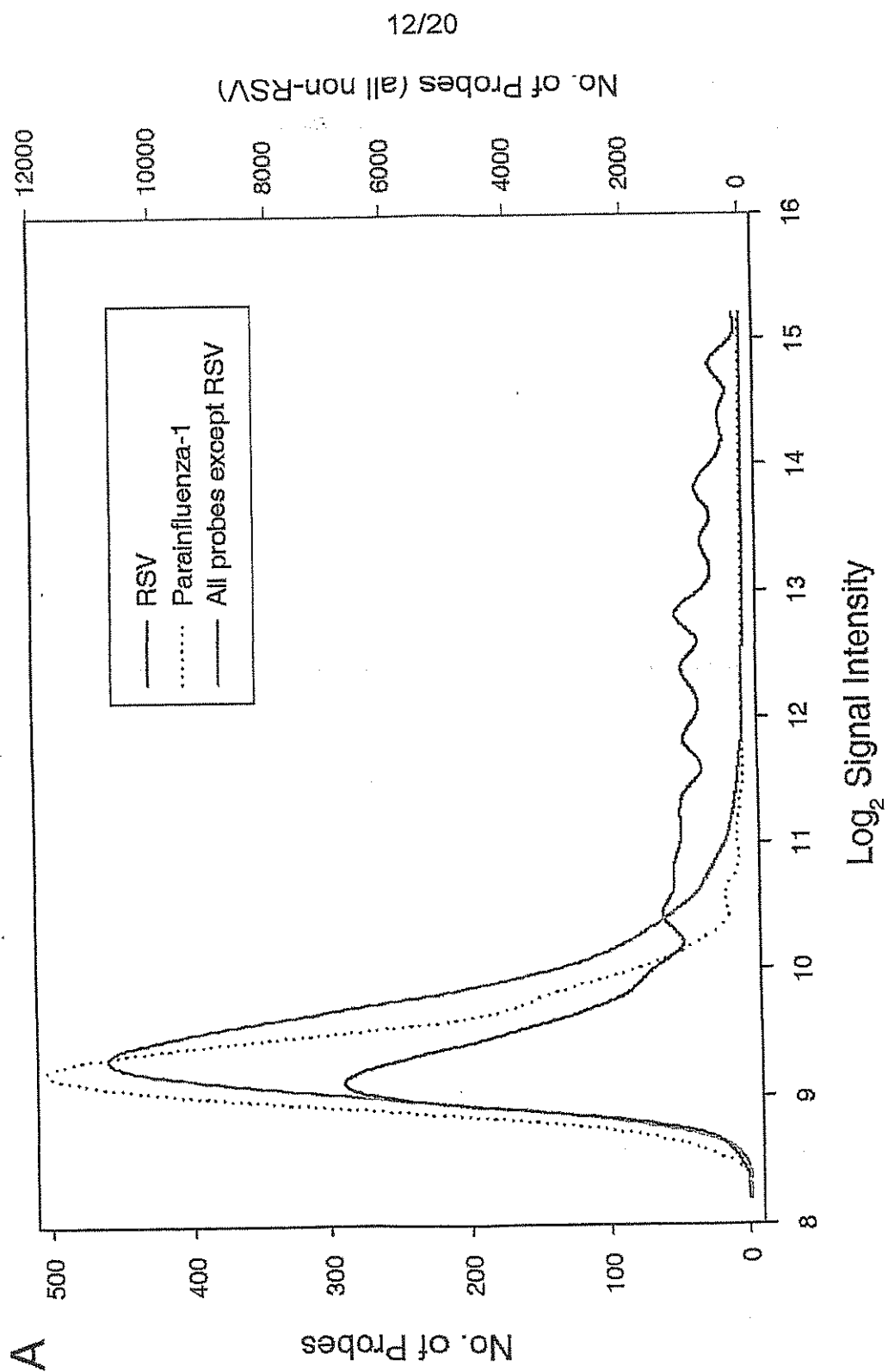
FIGURE 8



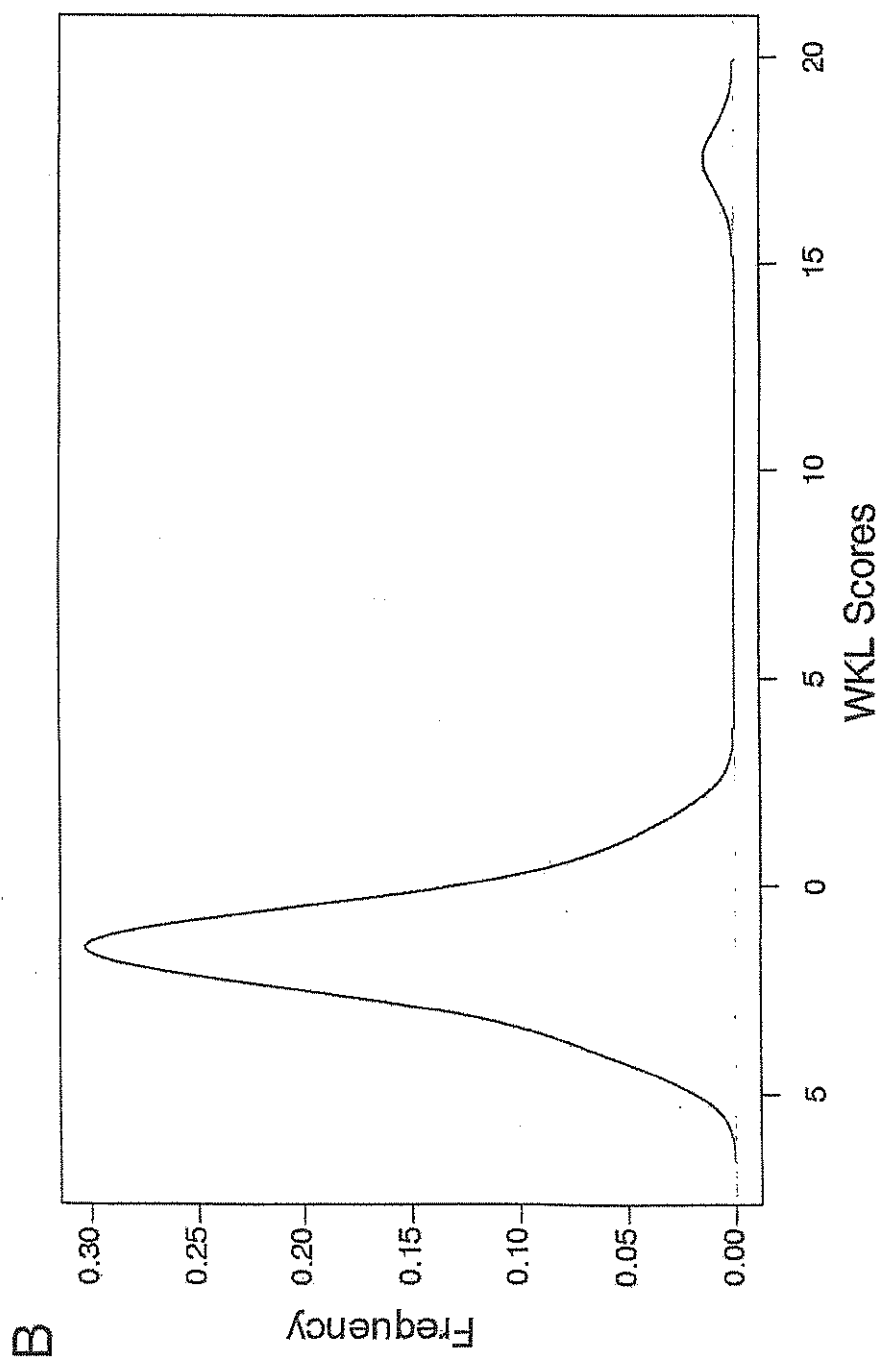
HD or MCM scores relative to Hawaii Dengue type 1

- Probe Hamming Distance (HD)
- Probe Maximum Contiguous Match (MCM)
- Average Probe Signal Intensity vs Probe HD
- Average Probe Signal Intensity vs Probe MCM
- Probe detection threshold
- Optimal HD/MCM threshold

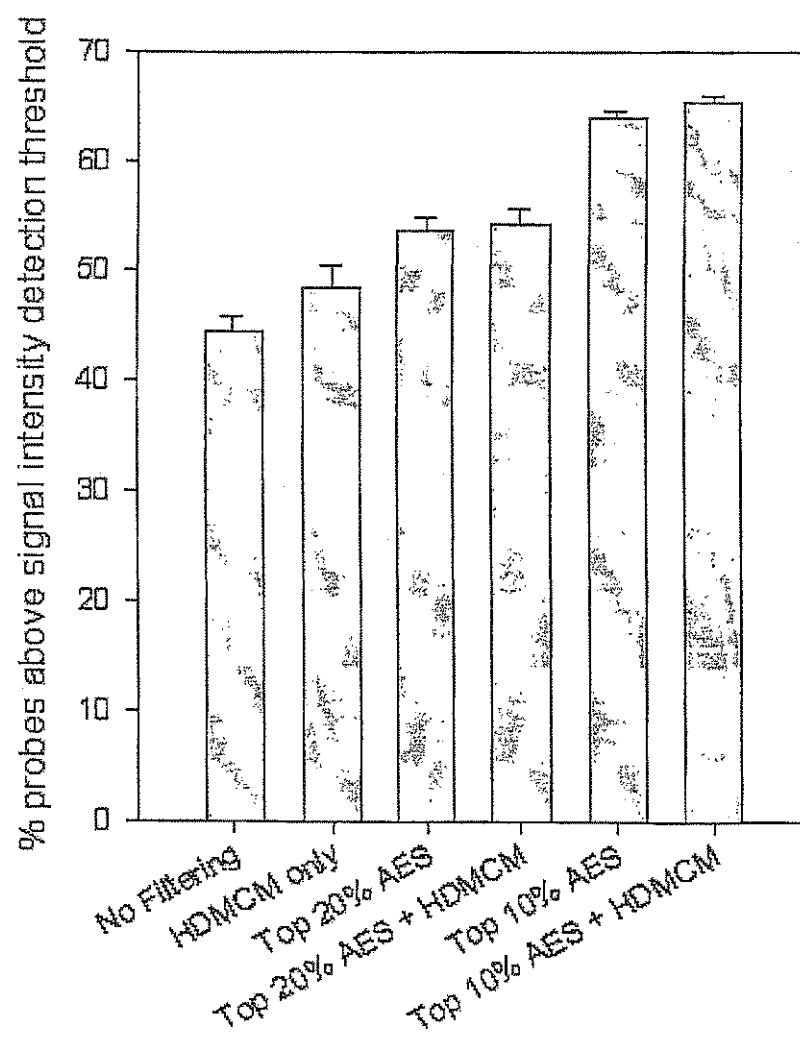
FIGURE 9A



13/20

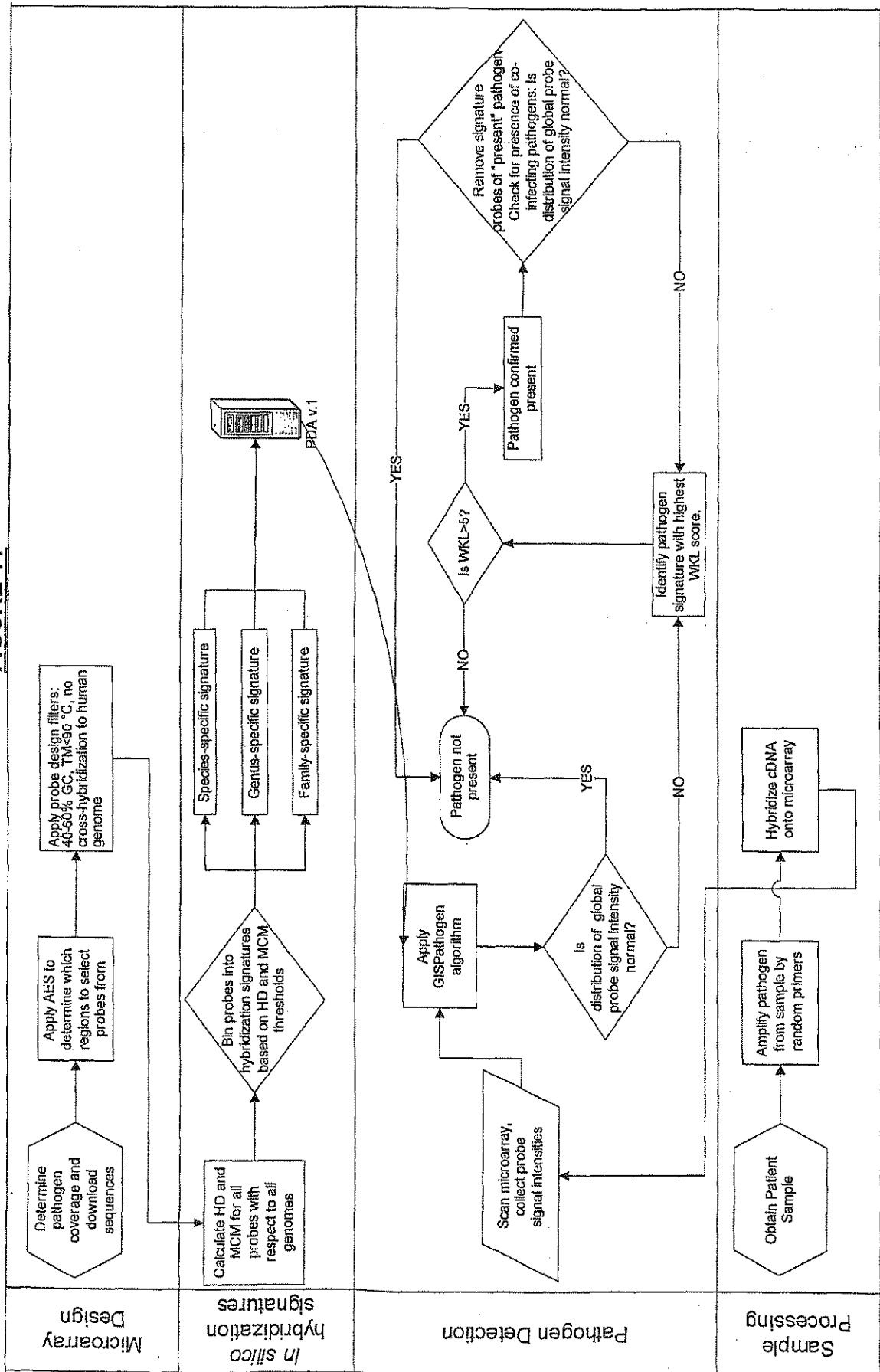
FIGURE 9B

14/20

FIGURE 10

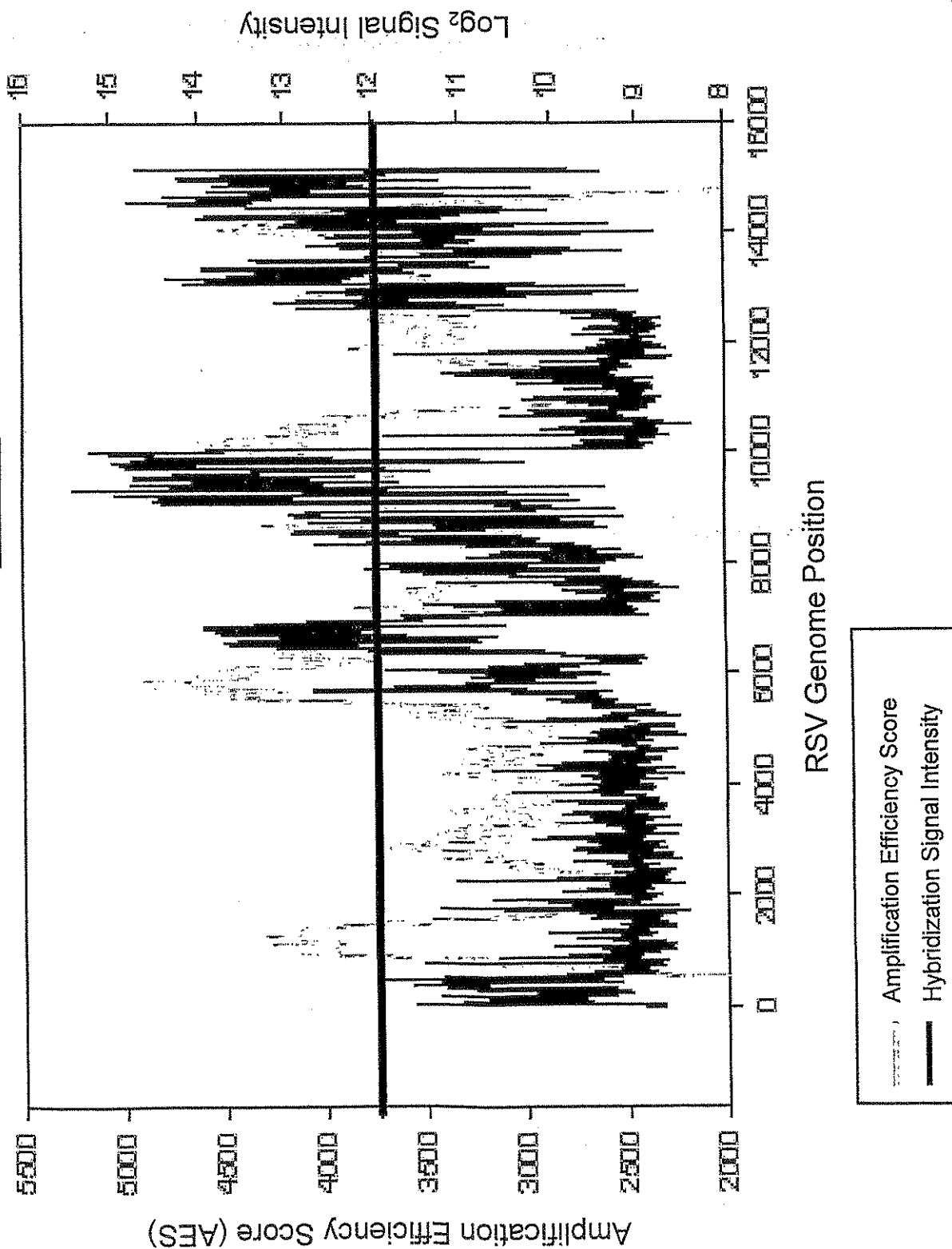
15/20

FIGURE 11



16/20

FIGURE 12



17/20

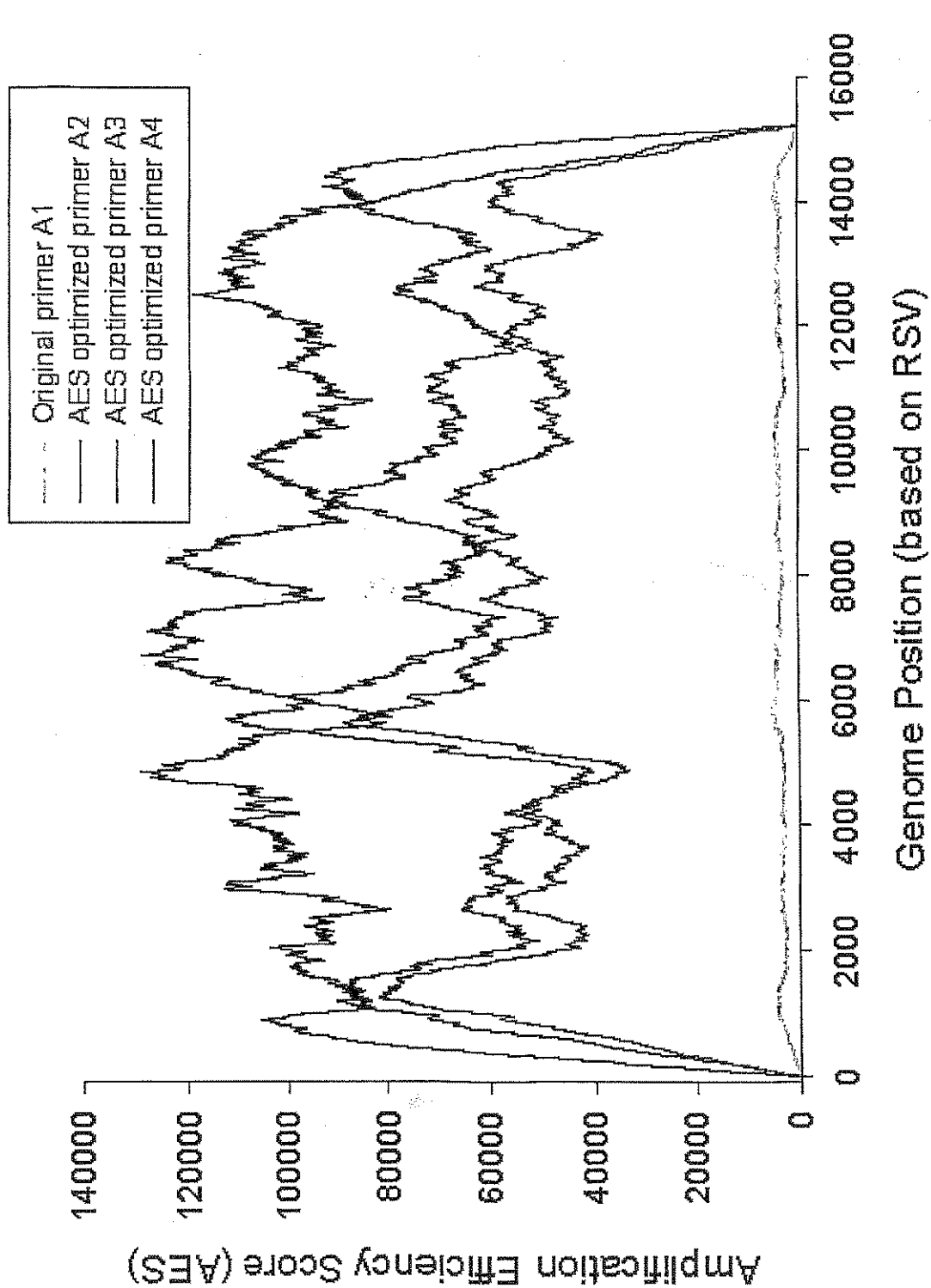
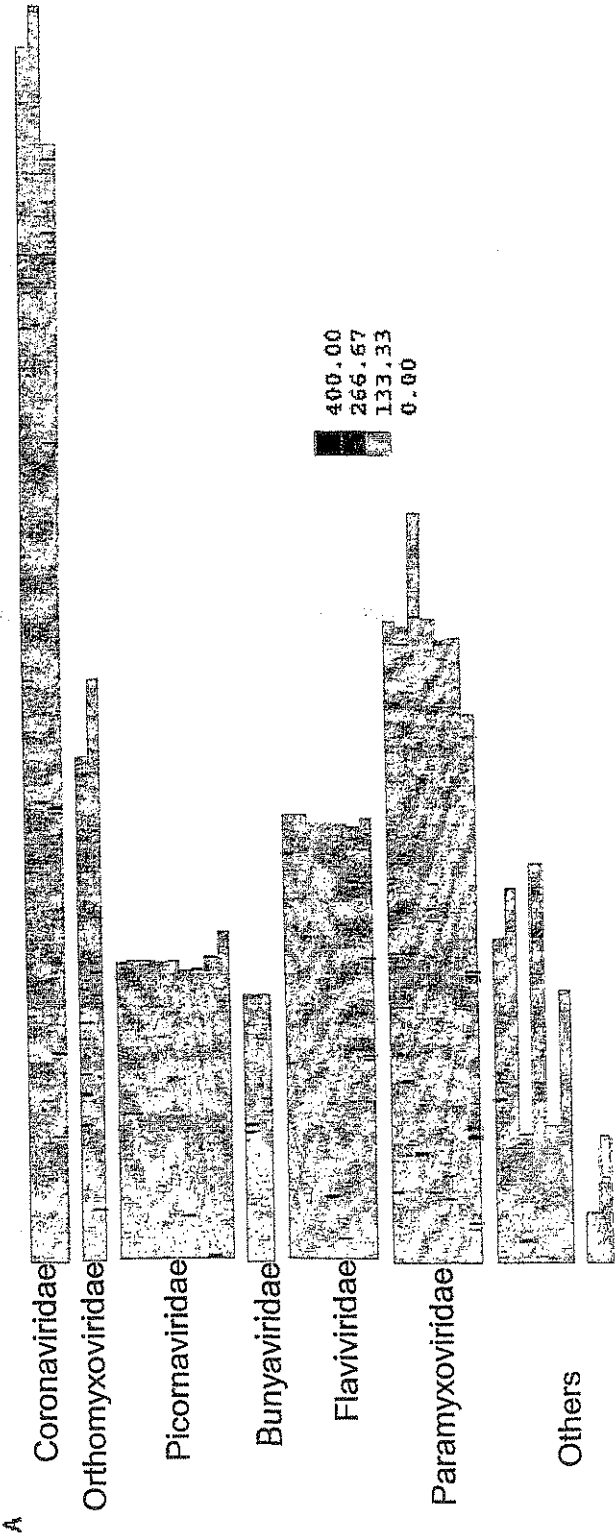
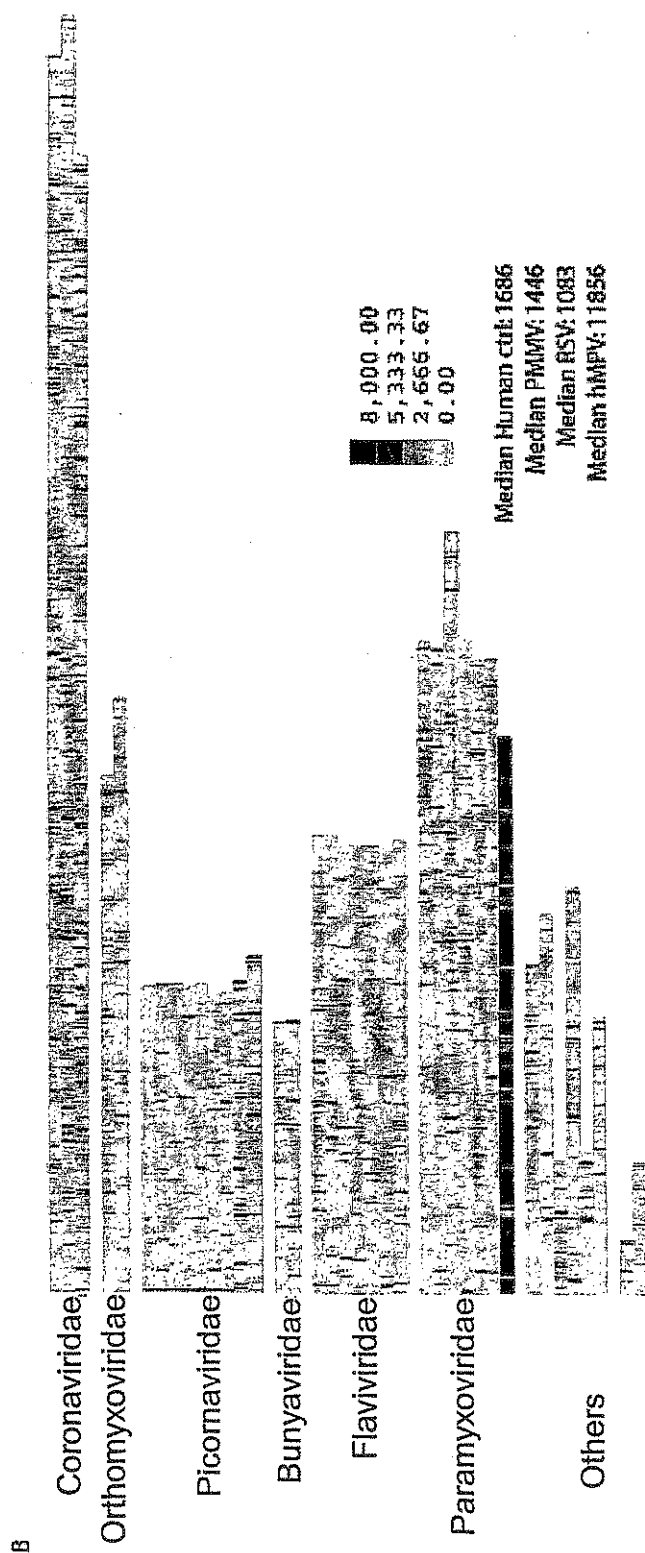
FIGURE 13

FIGURE 14A



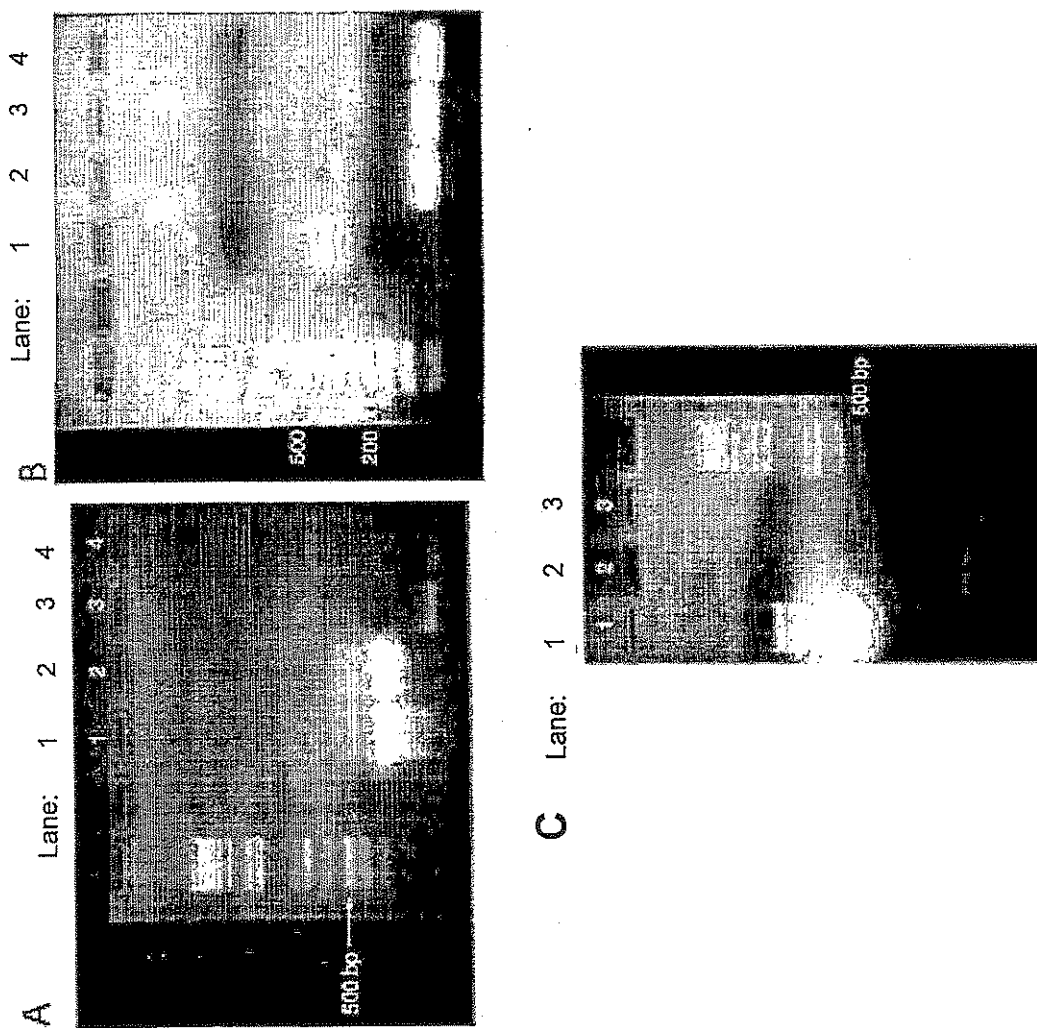
19/20

FIGURE 14B



20/20

FIGURE 15(A,B,C)



SEQUENCE LISTING

<110> Agency for Science, Technology and Research

<120> Method and/or apparatus of oligonucleotide design and/or of nucleic acid detection

<130> FP3143

<140> 11/202,023

<141> 2005-08-12

<160> 13

<170> PatentIn version 3.3

<210> 1

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Forward and/or reverse random primer (Figure 1A)

<220>

<221> misc feature

<222> (18) . . (26)

<223> n is a, c, g, or t

<400> 1

gtttcccagt cacgatannn nnnnnn

26

<210> 2

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Random forward primer (Figure 1B)

<400> 2

gtttcccagt cacgatagca tgaggg

26

<210> 3

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Random reverse primer (Figure 1B)

<400> 3

gtttcccagt cacgatacga atagct

26

<210> 4

<211> 22

<212> DNA
<213> Artificial

<220>
<223> Fragment of virus sequence (upper leftmost strand of virus sequence in Figure 1B)

<400> 4
acgatatccg cgaatagcta ga 22

<210> 5
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Fragment of virus sequence (upper rightmost strand of virus sequence in Figure 1B)

<400> 5
catccctcat gcatggggca att 23

<210> 6
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Fragment of virus sequence (lower leftmost strand of virus sequence in Figure 1B)

<400> 6
tgctataggc gcttatcgat ct 22

<210> 7
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Fragment of virus sequence (lower rightmost strand of virus sequence in Figure 1B)

<400> 7
gtagggagta cgtaccccgt taa 23

<210> 8
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Random Primer Tag (top strand Figure 1C and 1D)

<400> 8
gtttcccagt cacgata 17

<210> 9
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Random Primer Tag (bottom strand Figure 1C and 1D)

<400> 9
caaagggtca gtgctat 17

<210> 10
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer A1 (Figure 13)

<400> 10
gtttcccagt cacgata 17

<210> 11
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer A2 (Figure 13)

<400> 11
gatgagggaa gatgggg 17

<210> 12
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer A3 (Figure 13)

<400> 12
ctcatgcacg acccaaa 17

<210> 13
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer A4 (Figure 13)

<400> 13
agatccattc caccoca 17