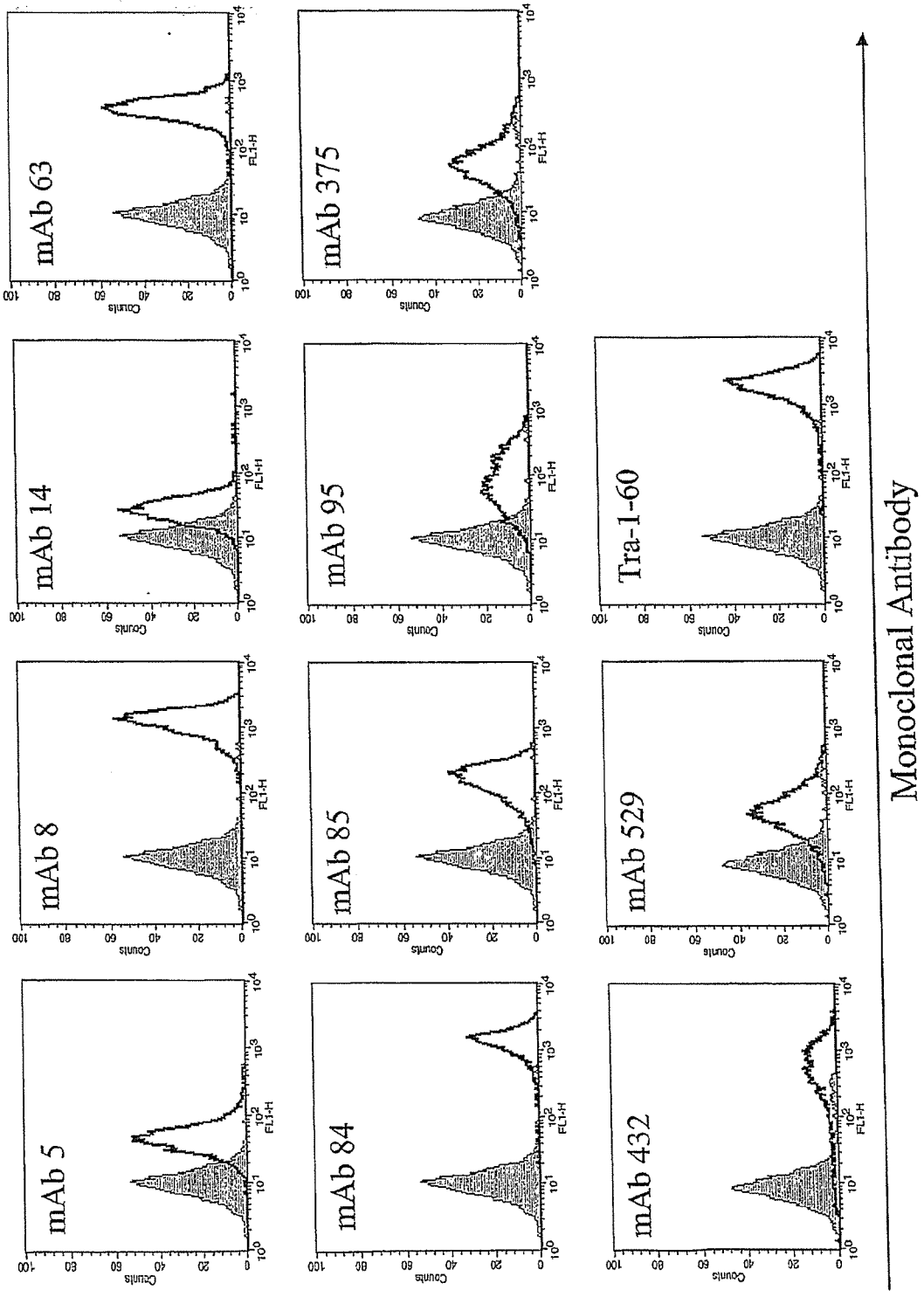

mAb 63
mAb 375
mAb 14
mAb 95
Tra-1-60
mAb 8
mAb 85
mAb 529
mAb 5
mAb 84
mAb 432
Count
Monoclonal Antibody

FIGURE 1

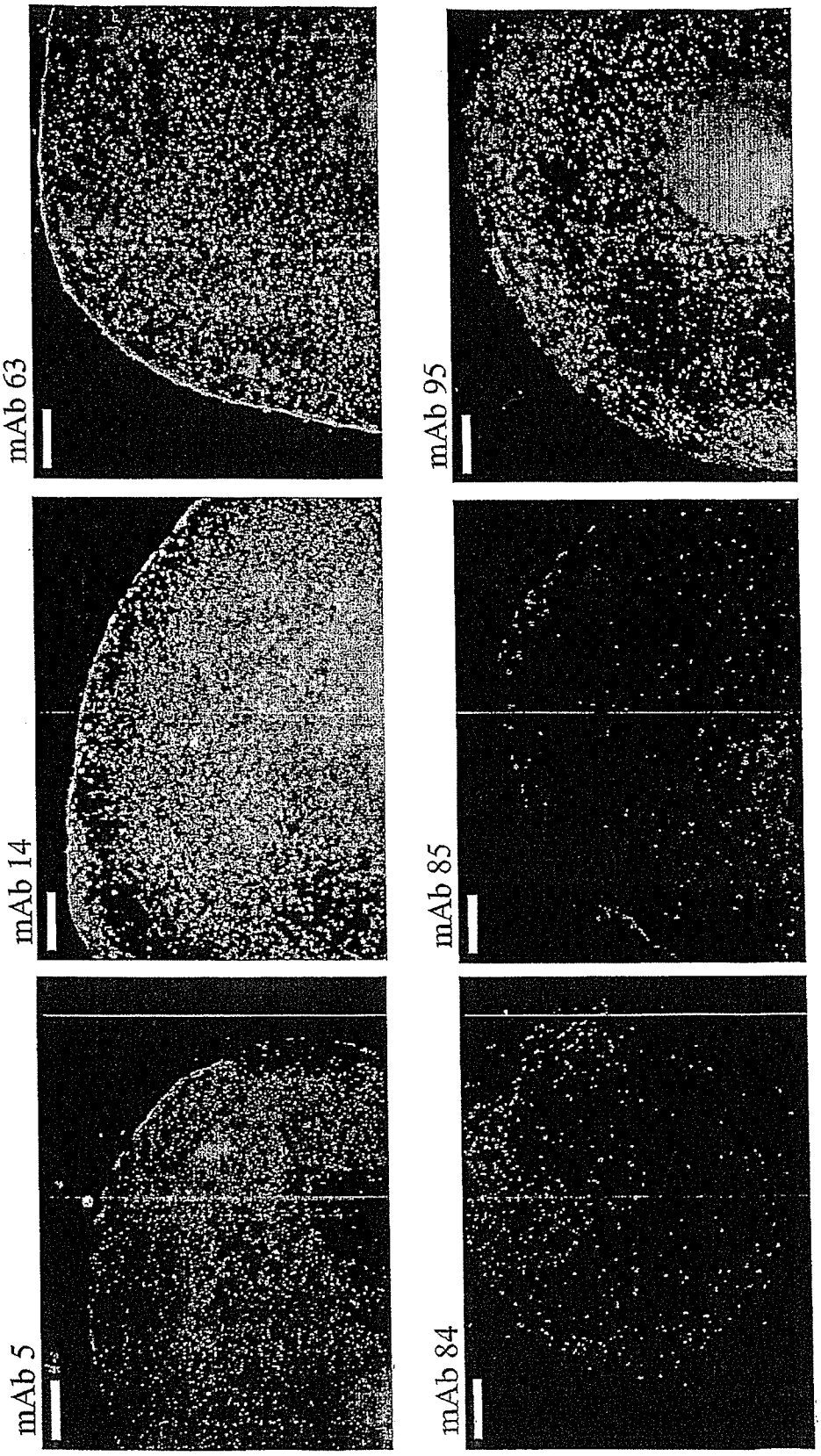


figure 2

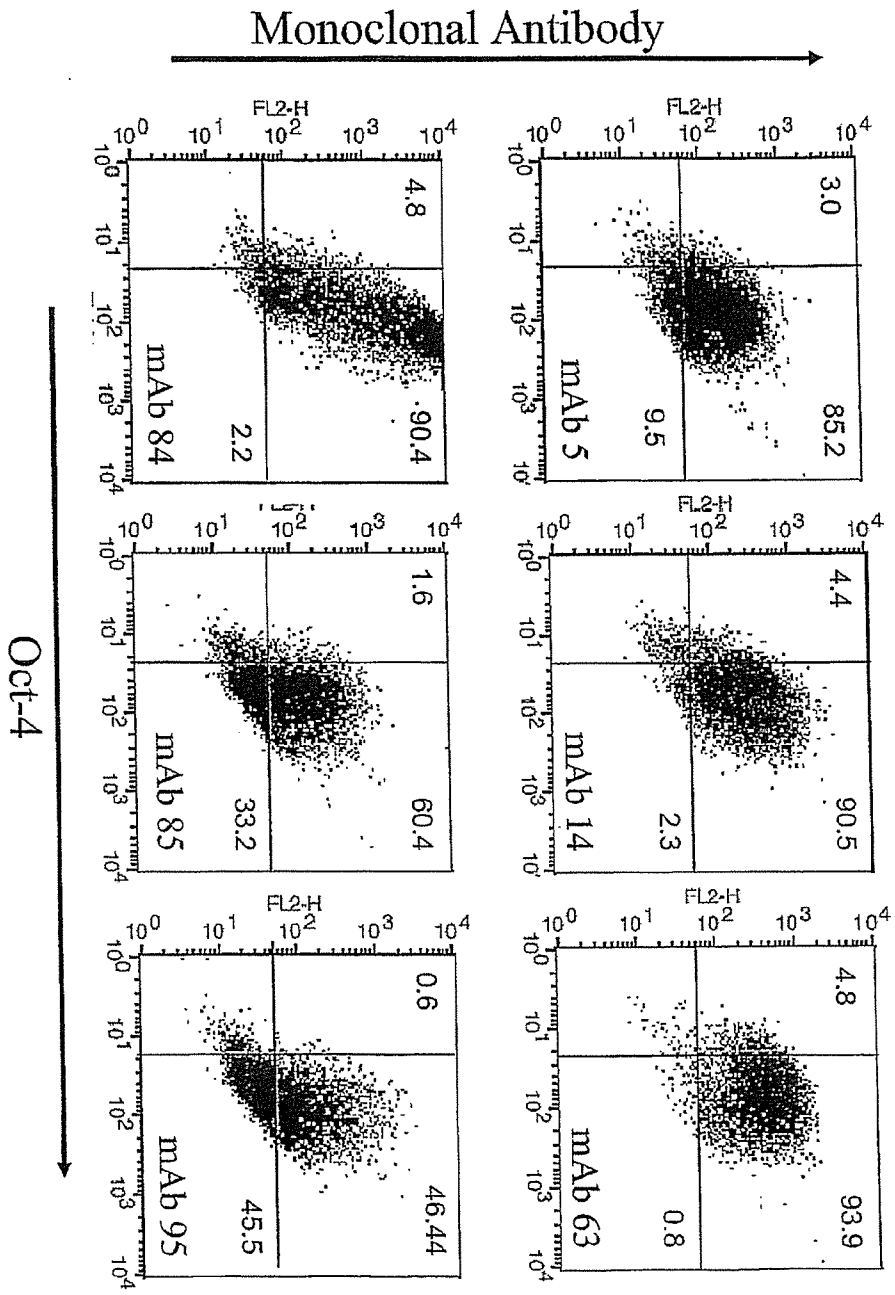

Monoclonal Antibody
Oct-4
FL2-H
mAb 84
4.8
90.4
2.2
mAb 5
3.0
85.2
9.5
mAb 85
1.6
60.4
33.2
mAb 14
4.4
90.5
2.3
mAb 95
0.6
46.44
45.5
mAb 63
4.8
93.9
0.8

FIGURE 3

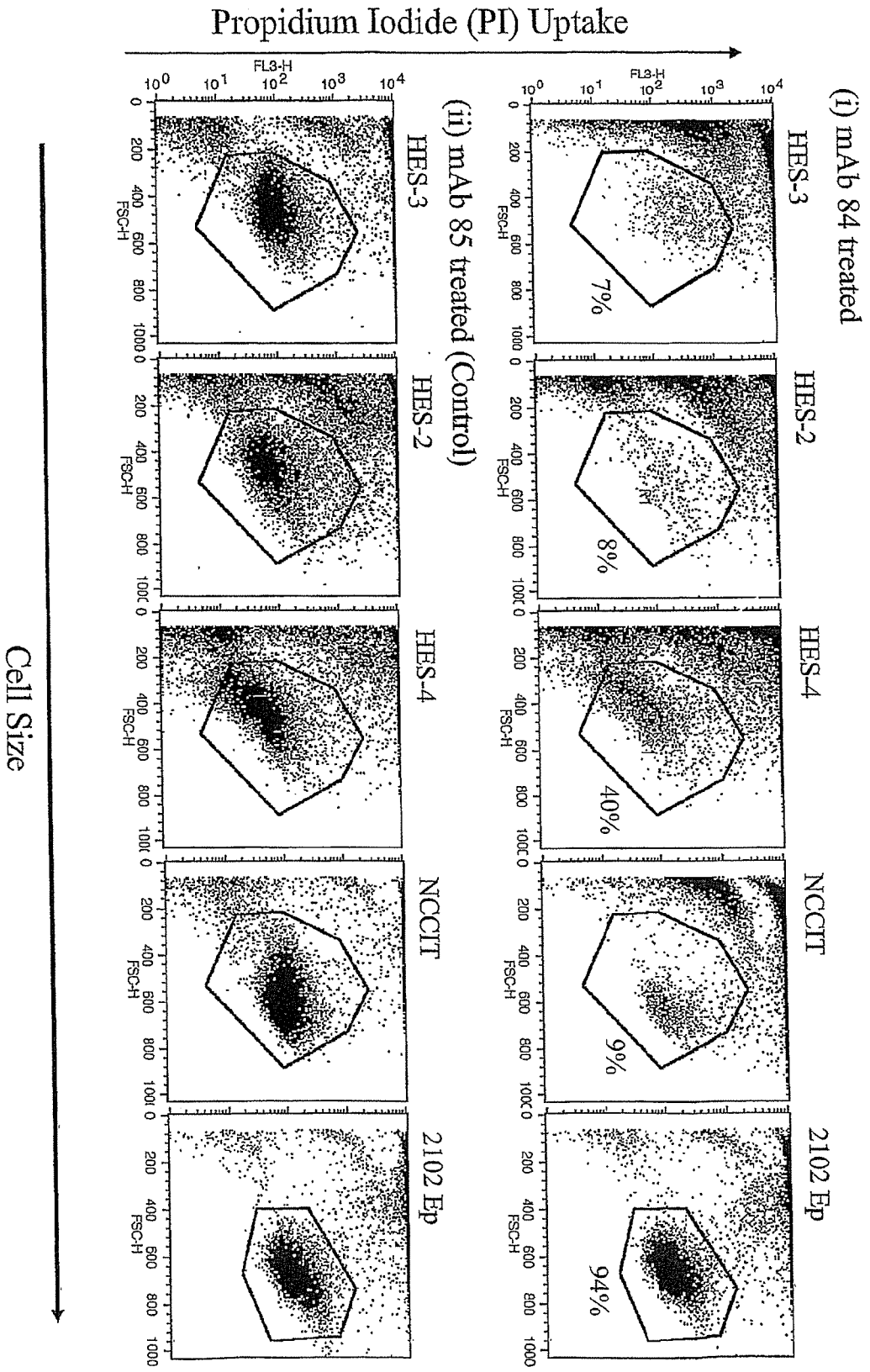

Propidium Iodide (PI) Uptake
Cell Size
(i) mAb 84 treated
(ii) mAb 85 treated (Control)
HES-3
HES-2
HES-4
NCCIT
2102 Ep
7%
8%
40%
9%
94%
FL3-H
FSC-H

FIGURE 4

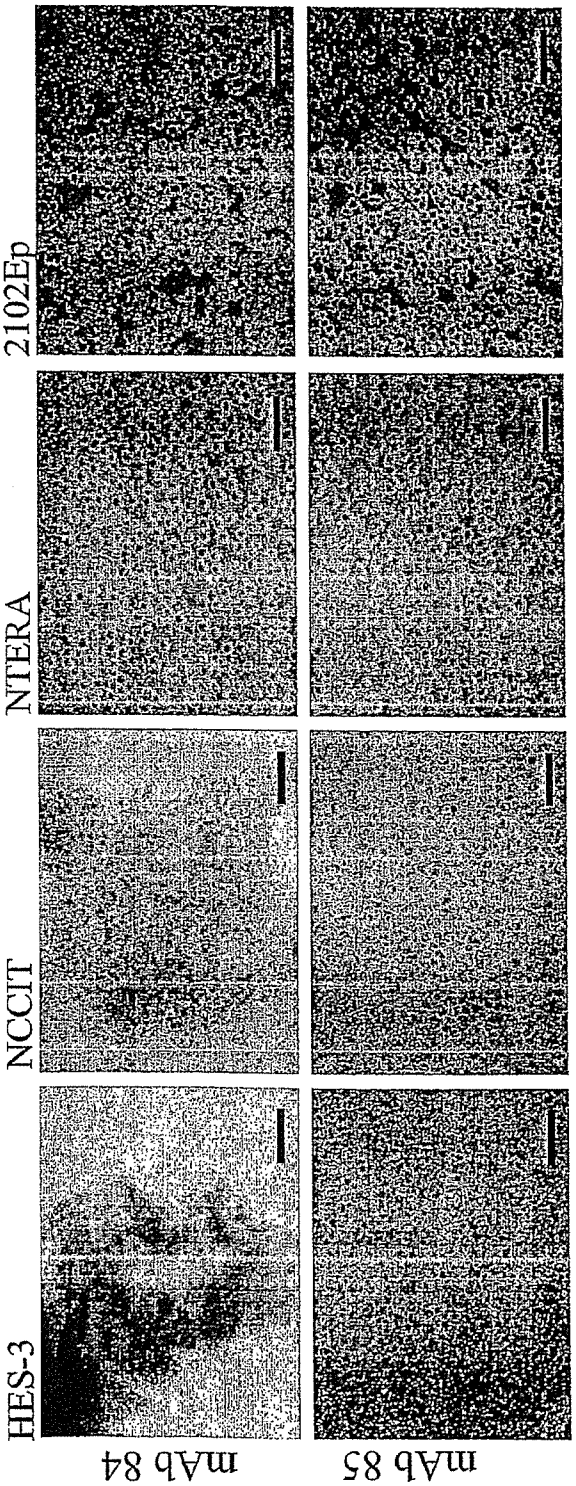


FIGURE 5

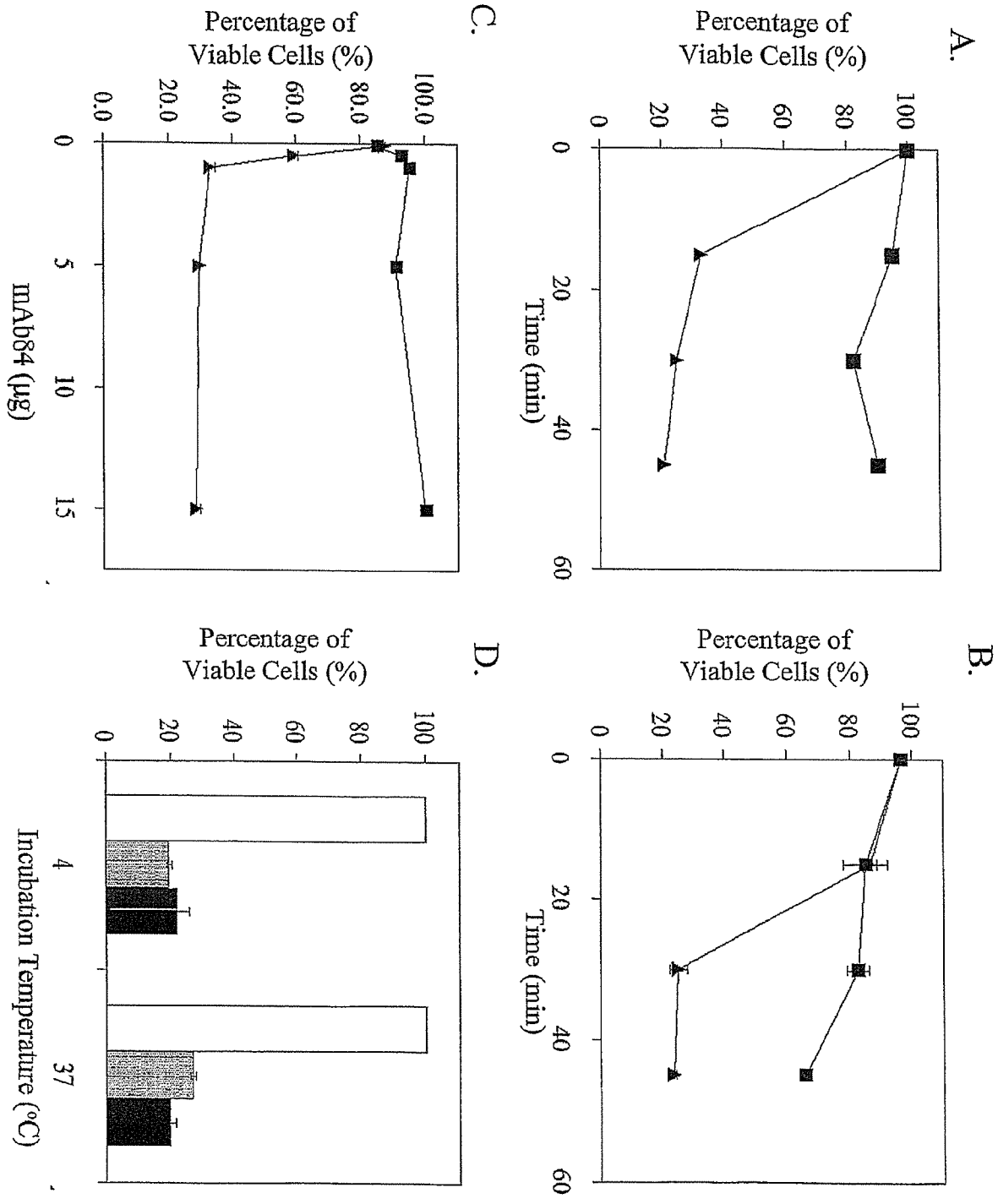

A.
Percentage of Viable Cells (%)
0
20
40
60
80
100
0
20
40
60
Time (min)
B.
Percentage of Viable Cells (%)
0
20
40
60
80
100
0
20
40
60
Time (min)
C.
Percentage of Viable Cells (%)
0.0
20.0
40.0
60.0
80.0
100.0
0
5
10
15
mAb84 (µg)
D.
Percentage of Viable Cells (%)
0
20
40
60
80
100
4
37
Incubation Temperature (°C)

FIGURE 6

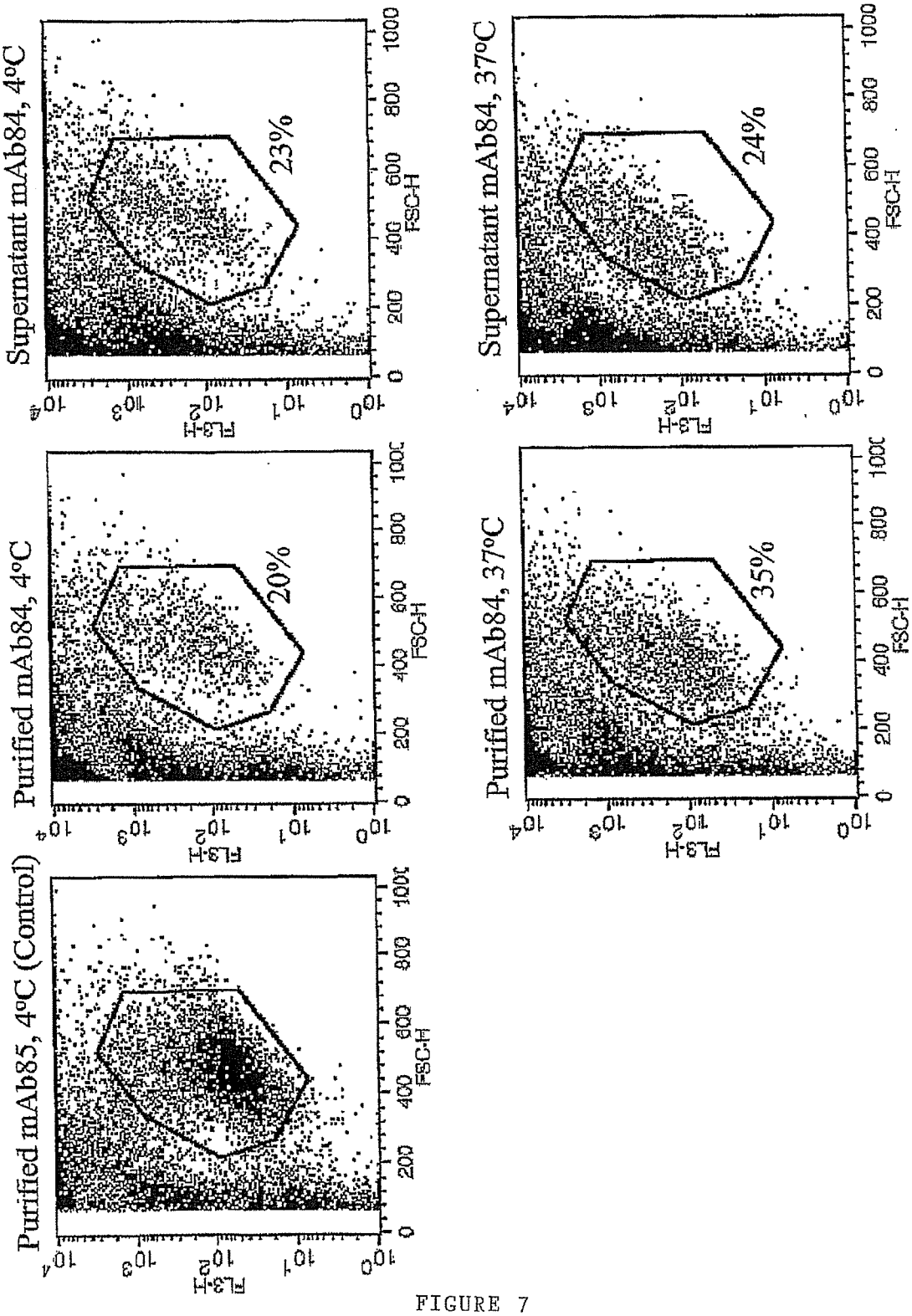

Supernatant mAb84, 4°C
23%
Purified mAb84, 4°C
20%
Purified mAb85, 4°C (Control)
Supernatant mAb84, 37°C
24%
Purified mAb84, 37°C
35%
FL3-H
FSC-H
R1

FIGURE 7

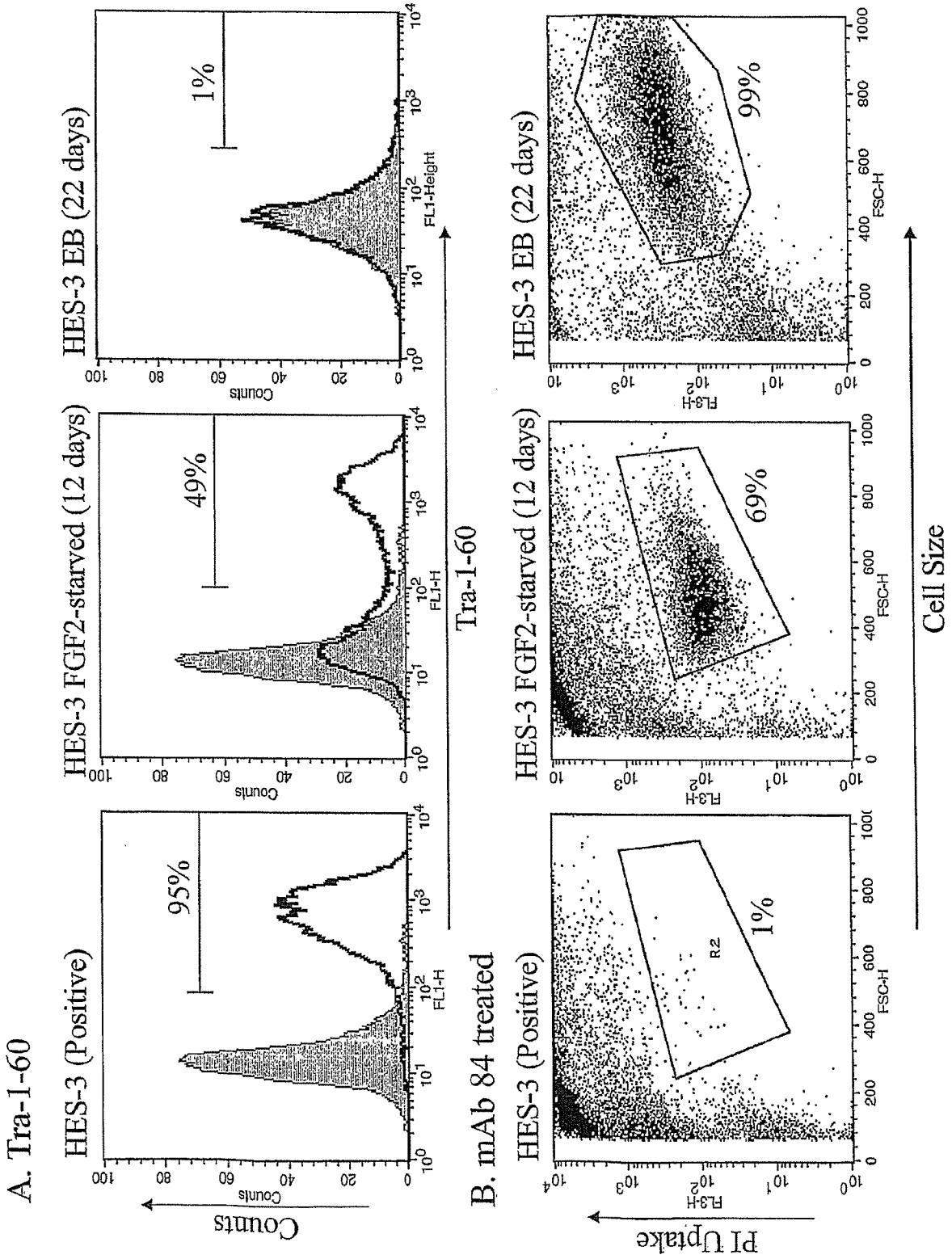

A. Tra-1-60
HES-3 (Positive)
95%
HES-3 FGF2-starved (12 days)
49%
HES-3 EB (22 days)
1%
Counts
FL1-H
FL1-Height
Tra-1-60
B. mAb 84 treated
HES-3 (Positive)
R2
1%
HES-3 FGF2-starved (12 days)
69%
HES-3 EB (22 days)
99%
PI Uptake
FL3-H
FSC-H
Cell Size

FIGURE 8

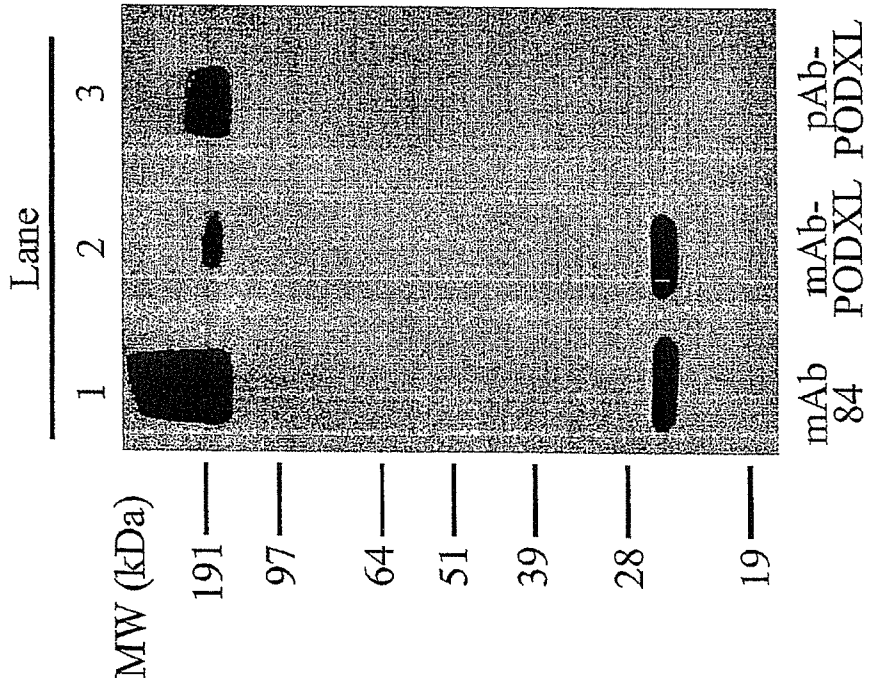


FIGURE 9A

(O00592) Podocalyxin-like protein 1 precursor

```
  1  MRCALALSAL LLLLSTPPLL PSSPSPSPSP SPSQNATQTT TDSSNKTAPT
 51  PASSVTIMAT DTAQQSTVPT SKANEILASV KATTLGVSSD SPGTTTLAQQ
101  VSGPVNTTVA RGGGSGNPTT TIESPKSTKS ADTTTVATST ATAKPNTTSS
151  QNGAEDTTNS GGKSSHSVTT DLTSTKAEHL TTPHPTSPLS PRQPTLTHPV
201  ATPTSSGHDH LMKISSSSST VAIPGYTFTS PGMTTTLPSS VISQRTQQTS
251  SQMPASSTAP SSQETVQPTS PATALRTPTL PETMSSSPTA ASTTHRYPKT
301  PSPTVAHESN WAKCEDLETQ TQSEKQLVLN LTGNTLCAGG ASDEKLISLI
351  CRAVKATFNP AQDKCGIRLA SVPGSQTVVV KEITIHTKLP AKDVYERLKD
401  KWDELKEAGV SDMKLGDQGP PEEAEDRFSM PLIITIVCMA SFLLLVAALY
451  GCCHQRLSQR KDQQRLTEEL QTVENGYHDN PTLEVMETSS EMQEKKVVSL
501  NGELGDSWIV PLDNLTKDDL DEEEDTHL
```

FIGURE 9B

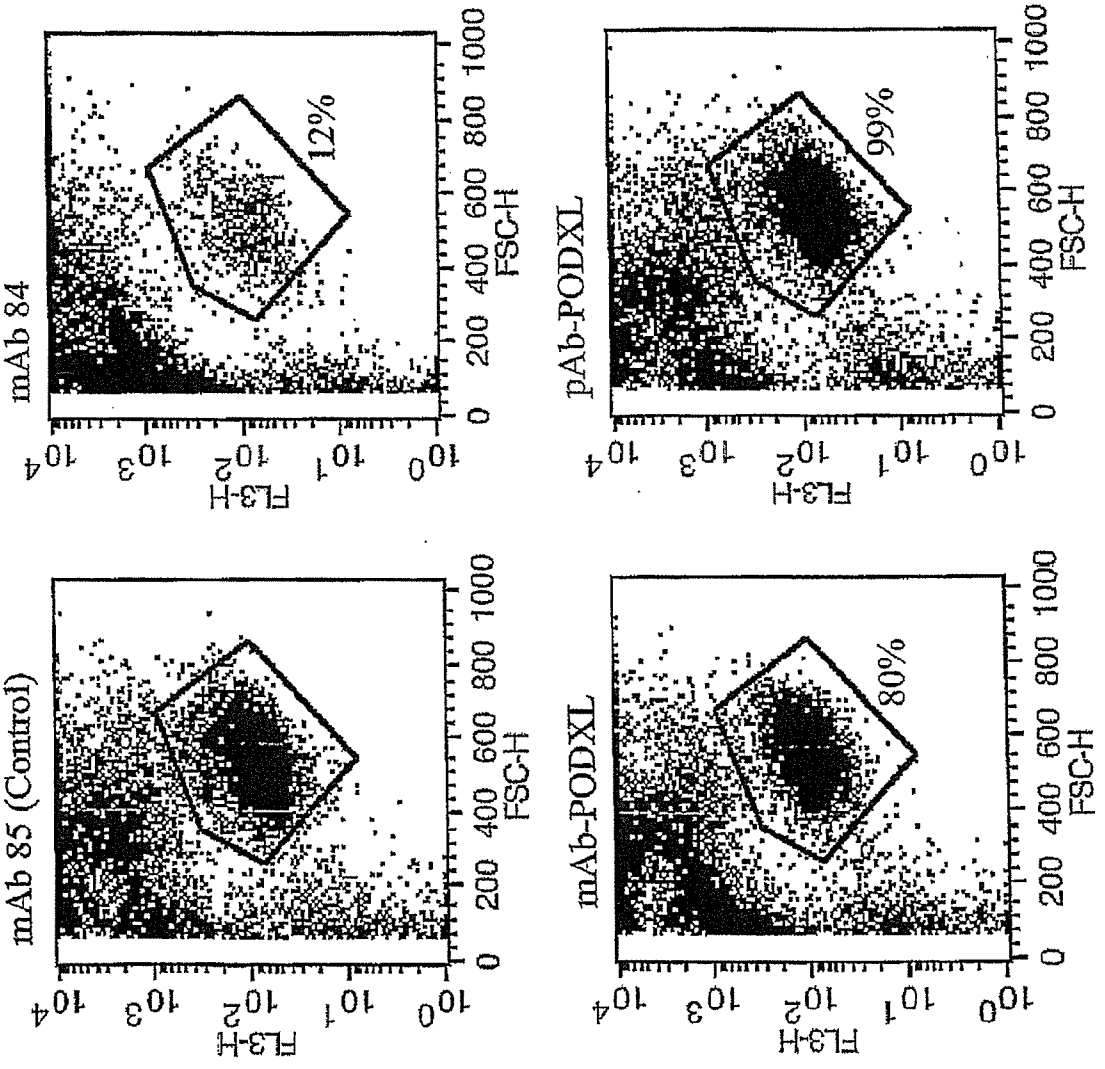

mAb 84
12%
pAb-PODXL
99%
mAb 85 (Control)
mAb-PODXL
80%
FL3-H
FSC-H
0
200
400
600
800
1000
10^0
10^1
10^2
10^3
10^4

FIGURE 10A

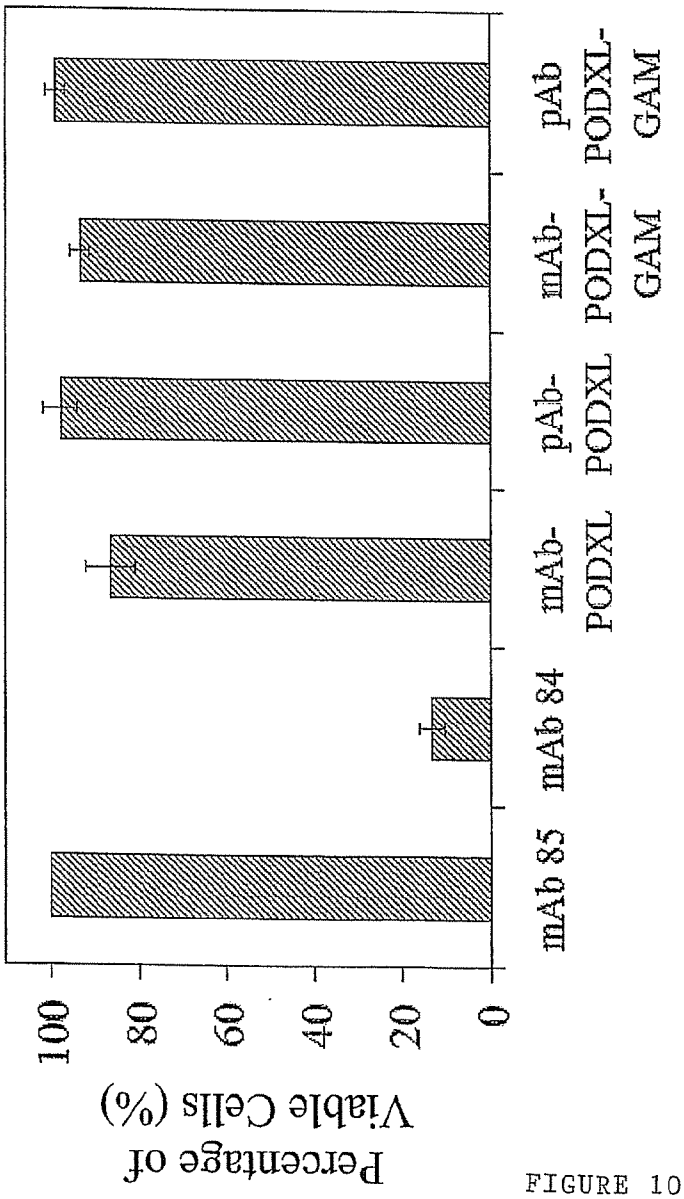

Percentage of Viable Cells (%)
100
80
60
40
20
0
mAb 85
mAb 84
mAb-PODXL
pAb-PODXL
mAb-PODXL-GAM
pAb PODXL-GAM

FIGURE 10B

mAb 84 VL

The amino acids not underlined correspond to framework regions and underlined corresponds to CDRs.

```
1        ACGCCAGCTATTTAGGTGACACTATAGAATACTCAAGCTATGCATCCAACGCGTTGGGAG

61       CTCTCCCATATGGTCGACCTGCAGGCGGCCGCACTAGTGATTGACATTGAGCTCACCCAG
1                                                    D  I  E  L  T  Q

121      TCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGC
7         S  P  A  I  M  S  A  S  P  G  E  K  V  T  M  T  C  S  A  S

181      TCAAGTGTAAATTACATGTACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAGACTCCTG
27        S  S  V  N  Y  M  Y  W  Y  Q  Q  K  P  G  S  S  P  R  L  L

241      ATTTATGACACATCCAACCTGGCTTCTGGAGTCCCTGTTCGCTTCAGTGGCAGTGGGTCT
47        I  Y  D  T  S  N  L  A  S  G  V  P  V  R  F  S  G  S  G  S

301      GGGACCTCTTACTCTCTCACAATCAGCCGAATGGAGGCTGAAGATGCTGCCACTTATTAC
67        G  T  S  Y  S  L  T  I  S  R  M  E  A  E  D  A  A  T  Y  Y

361      TGCCAGCAGTGGAGTAGTTACCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA
87        C  Q  Q  W  S  S  Y  P  Y  T  F  G  G  G  T  K  L  E  I  K

421      CGGAATCCCGCGGCCATGGCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCTATAG
107       R

481      TGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGG
541      CGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGA
601      AGAGGCGCGCACCGATCGCCCTTCTCAACAGTTGCGCAGCCTGAATAGCGAATAGACGCG
661      CCCTGTAGCGGCGCATTATGCGCGGCGGGGTGTGGTGGTTACGCGCAGCGTGACCGCTAC
721      ACTTGTCAGCGCCCTAGCGCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTC
781      GCCGGCTTGCTCGTCAGG
```

Based on V Base and Kabat Numbering
NOT UNDERLINED: Framework
underlined: CDR

FIGURE 11

mAb 84 VH

The amino acids not underlined correspond to framework regions and underlined corresponds to CDRs.

```
1         AGACGGCCAGTGATTGTATACGACTCACTATAGGGCGAATTGGGCCCGACGTCGCATGCT

61        CCCGGCCGCCATGGCCGCGGGATTCAGGTGCAGCTGCAGCAGTCAGGAGGAGGCTTGGTG
1                                 Q  V  Q  L  Q  Q  S  G  G  G  L  V

121       CAACCTGGAGGATCCATGAAACTCTCCTGTGTTGCCTCTGGATTCACTTTCAGTAACTAC
13         Q  P  G  G  S  M  K  L  S  C  V  A  S  G  F  T  F  S  N  Y

181       TGGATGAACTGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGA
33         W  M  N  W  V  R  Q  S  P  E  K  G  L  E  W  V  A  E  I  R

241       TTGAAATCTAATAATTATGCAACACATTATGCGGAGTCTGTGAAAGGGAGGTTCACCATC
53         L  K  S  N  N  Y  A  T  H  Y  A  E  S  V  K  G  R  F  T  I

301       TCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATGAACAACTTAAGAGCTGAAGAC
73         S  R  D  D  S  K  S  S  V  Y  L  Q  M  N  N  L  R  A  E  D

361       ACTGGCATTTATTACTGTACGGGGGAGAGGGCCTGGGGCCAAGGGACCACGGTCACCGTC
93         T  G  I  Y  Y  C  T  G  E  R  A  W  G  Q  G  T  T  V  T  V

421       TCCTCAAATCACTAGTGCGGCCGCCTGCAGGTCGACCATATGGGAGAGCTCCCAACGCGT
113        S  S

481       TGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCA
541       TAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGA
601       AGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTG
661       CGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGC
721       CAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCGCTTCT
```

Based on V Base and Kabat Numbering
Not Underlined: Framework
Underlined: CDR

FIGURE 12