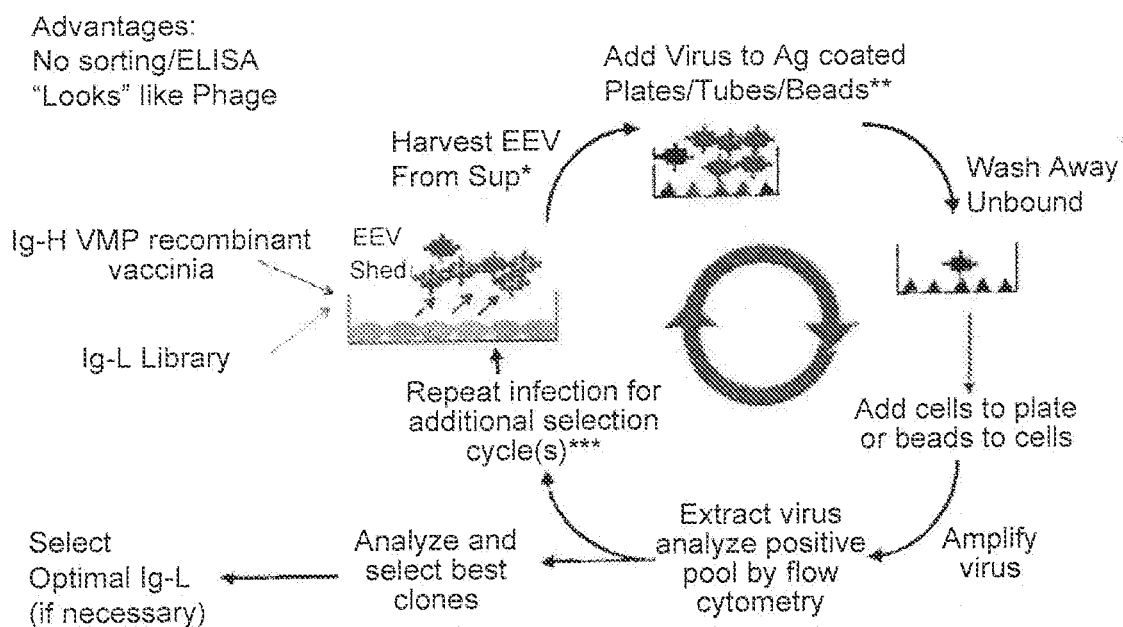


"pJEM1"

AAAAAATGAAAATAAATACAAAGGTTCTTGAGGGTTGTGTTAAATTGAAAGCGAGAAATAATCATAAAT
TCCATGGGATGGAGCTGTATCACTCTCTTCTTGGTAGCAACAGCTACAG**GCGCGC**ACTCCGAGATCCAG
CTGGTGCAGAGCGGCCCTGAGCTGAAGCAGCCTGGCGAGACCGTGAGGATCAGCTGCAAGGCCAGCGGC
TACACCTTCACCAACTACGGCATGAAGTGGGTGAAGCAGGCCCTGGCAAGGGCCTGAAGTGGATGGGC
TGGATCAACACCTACACCGGCGAGCCTACCTACGCCGCCGACTTCAAGAGGAGGTTACCTTCAGCCTG
GAGACCAGCGCCAGCACCGCCACCTGCAGATCAGCAACCTGAAGAACGACGACACCGCCACCTACTTC
TGCGCCAAGTACCCTCACTACTACGGCAGCAGCCACCGGTACTTCGACGTGTGGGGCGCCGGC**ACCACG**
GTCACCGTCTCCTCAGCCTCCACCAAGGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
TCTGGGGGCGACAGCGGCCCTGGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGG
AACTCAGGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCC
CTCAGCAGCGTCTGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAC
AAGCCCAGCAACACCAAGGTGGACAAGAAAGTTACATCAACTACAAATGACACTGATAAAGTAGATTAT
GAAGAATACTCCACAGAGTTGATTGTAAACACAGATAGTGAATCGACTATAGACATAATACTATCTGGA
TCTACACATTACCGGAAACTAGTTCTAAGAAACCTGATTATATAGATAATTCTAATTGCTCGTCGGTA
TTCGAAATCGCGACTCCGGAACCAATTACTGATAATGTAGAAGATCATACAGACACCGTCACATACACT
AGTGATAGCATTAATACAGTAAGTGCATCATCTGGAGAATCCACAACAGACGAGACTCCGGAACCAATT
ACTGATAAAGAAGATCATACAGTTACAGACACTGTCTCATACACTACAGTAAGTACATCATCTGGAATT
GTCACTACTAAATCAACCACCGATGATGCGGATCTTATGATACGTACAATGATAATGATACAGTACCA
CCAATACTGTAGGCGGTAGTACAACCTCTATTAGCAATTATAAAACCAAGGACTTTGTAGAAATATTT
GGTATTACCGCATTAAATTATATTGTGCGCCGTGGCAATTTCTGTATTACATATTATATATAATAAAA
CGTTACAGTAAACACAAACAGAGAACAAGTCTAG
(SEQ ID NO: 1)

Double underline – H5 promoter
Single underline – Leader peptide
Squiggly underline – Representative Heavy Variable region
Bold underline – IgG CH1 domain
No underline – Vaccinia A56R
Bold italics – BssHII and BstEII variable gene cloning site

FIG. 1



*For IMV: Harvest cells, homogenize, spin out debris and proceed

**Depletion step could be used

***Could add cell sorting as final step

FIG. 2

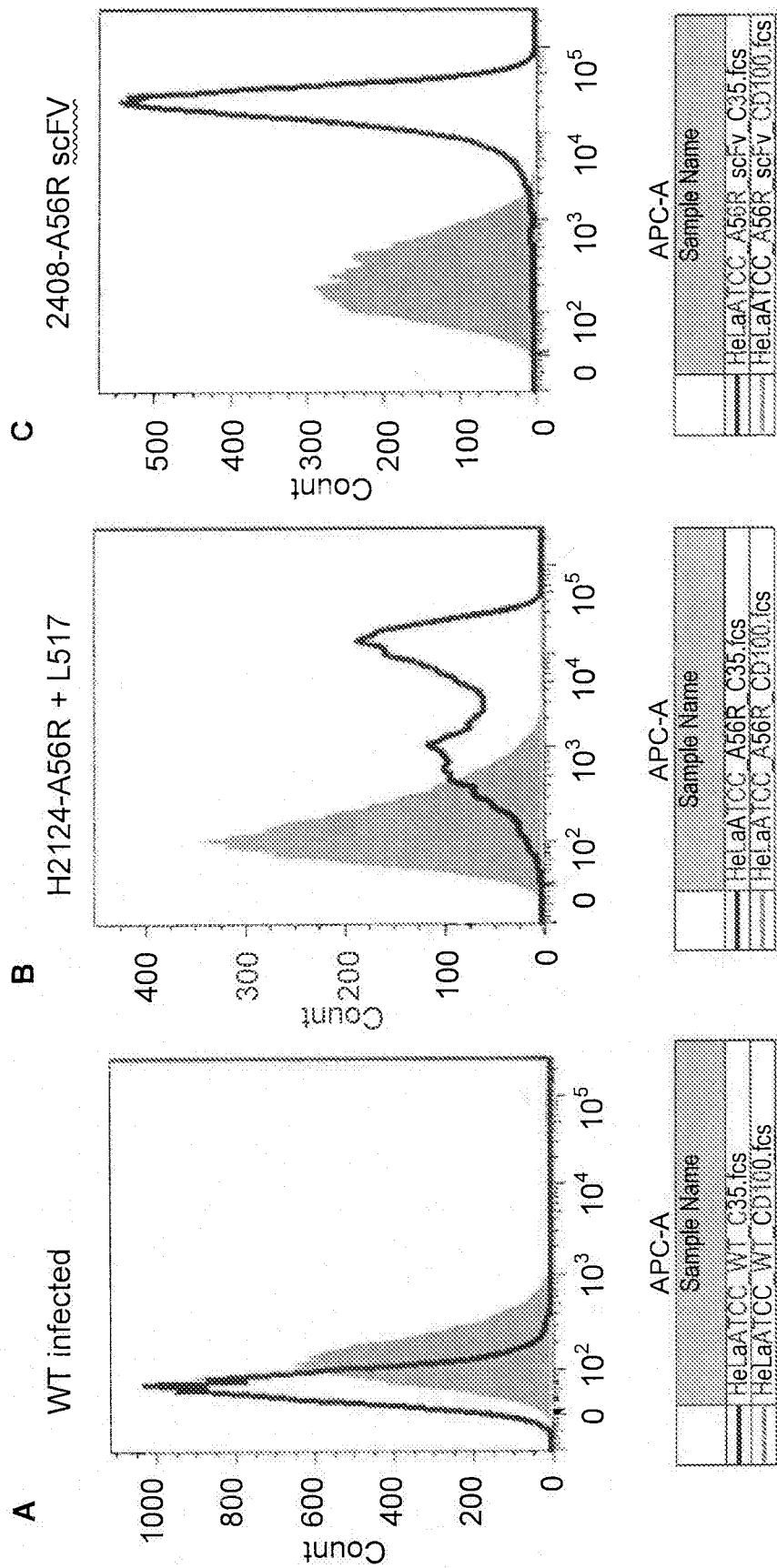
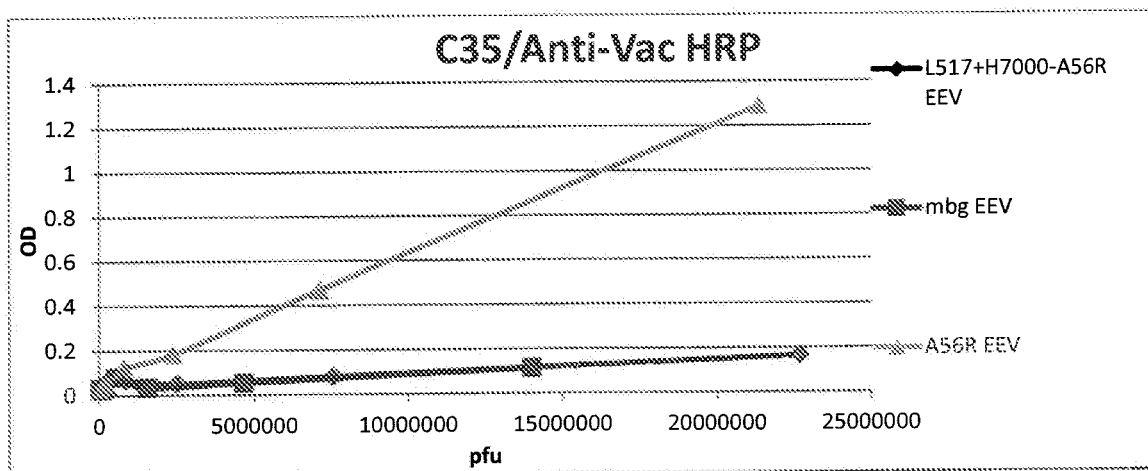


FIG. 3

A



B

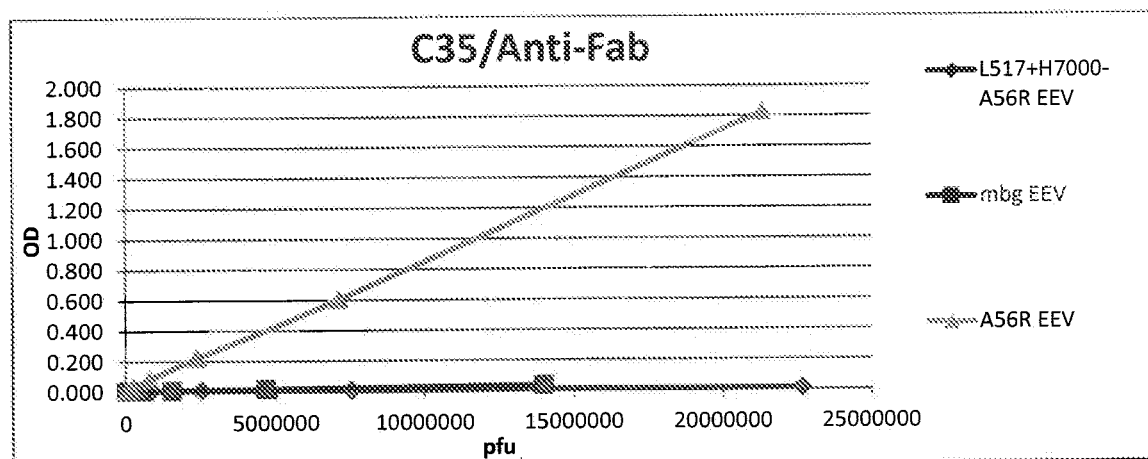


FIGURE 4

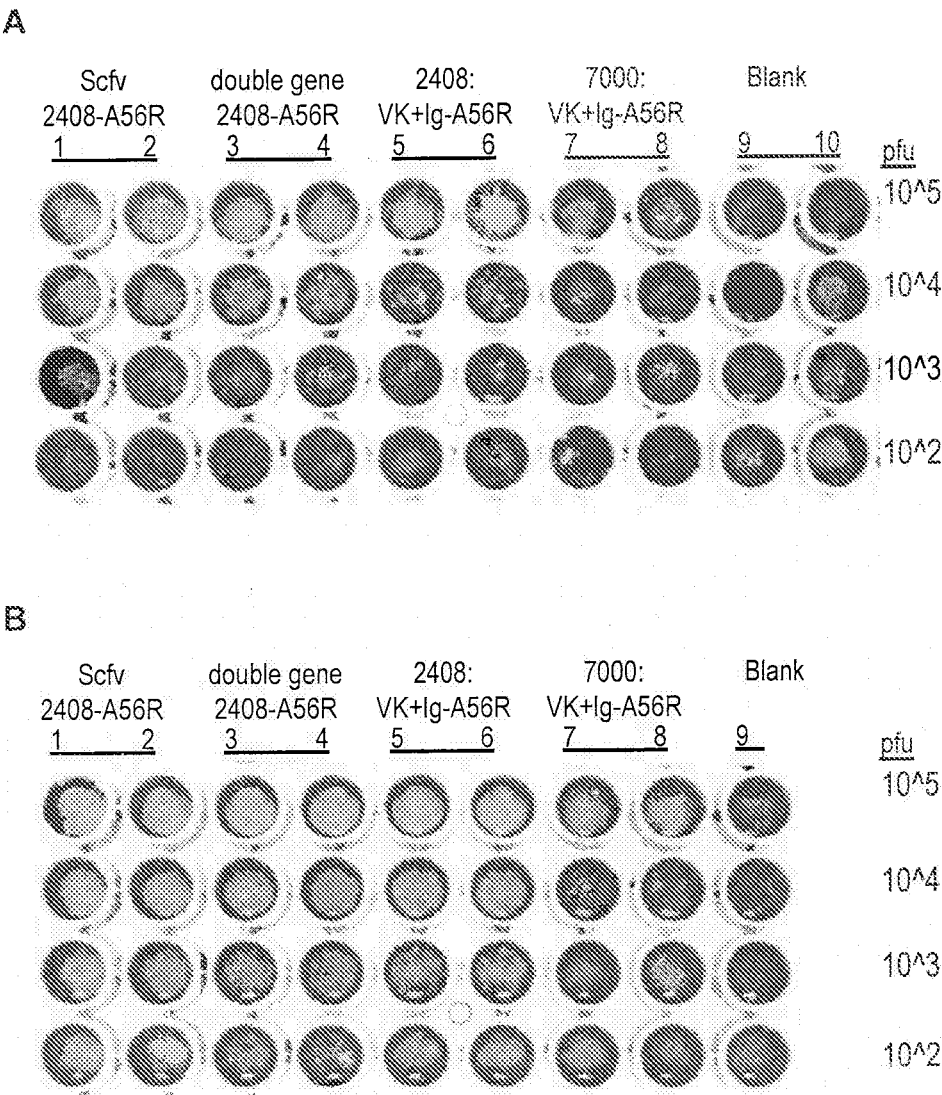


FIG. 5

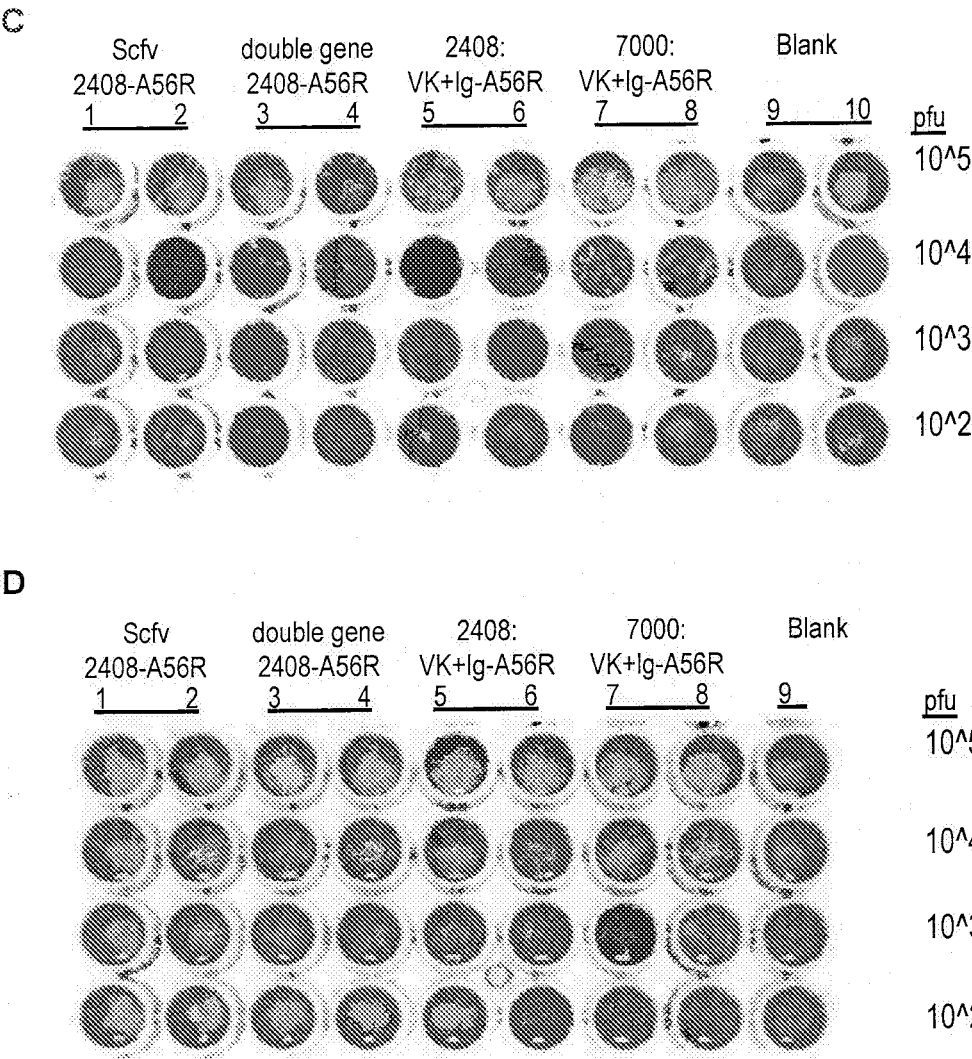


FIG. 5
(Continued)

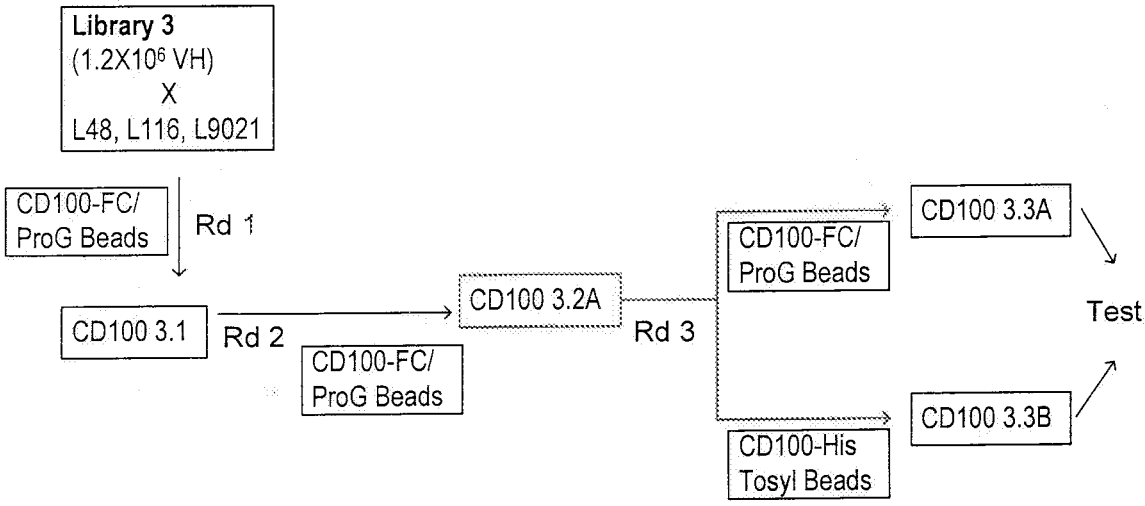


FIG. 6

Alignment:

>VH3-11

Identities = 81/98 (82%), Positives = 88/98 (89%)

C. 20: 1 EVQLVESGGGLVKPGGSLRLSCAASFFITDYYLSWIRQAPGKPEWISYISSYSRYIN 60
+VQLVESGGGLVKPGGSLRLSCAASGF F+DYY+SWIRQAPGKG EW+SYISS Y
VH311: 1 QVQLVESGGGLVKPGGSLRLSCAASGFIFSDYYNENIRQAPGKLEWYSYISSSSSTIY 60
C. 20: 61 ADSVKGRFTIISRDNTIRNSIYLQMNIIRVEDTAVYYCAR 98 (SEQ ID NO: 19)
ADSVKGRFTIISRDN +NS+YLOMH+LR EDTAVYYCAR
VH311: 61 ADSVKGRFTIISRDNARNISLYLQMNIIRAEEDTAVYYCAR 98

FIG. 7

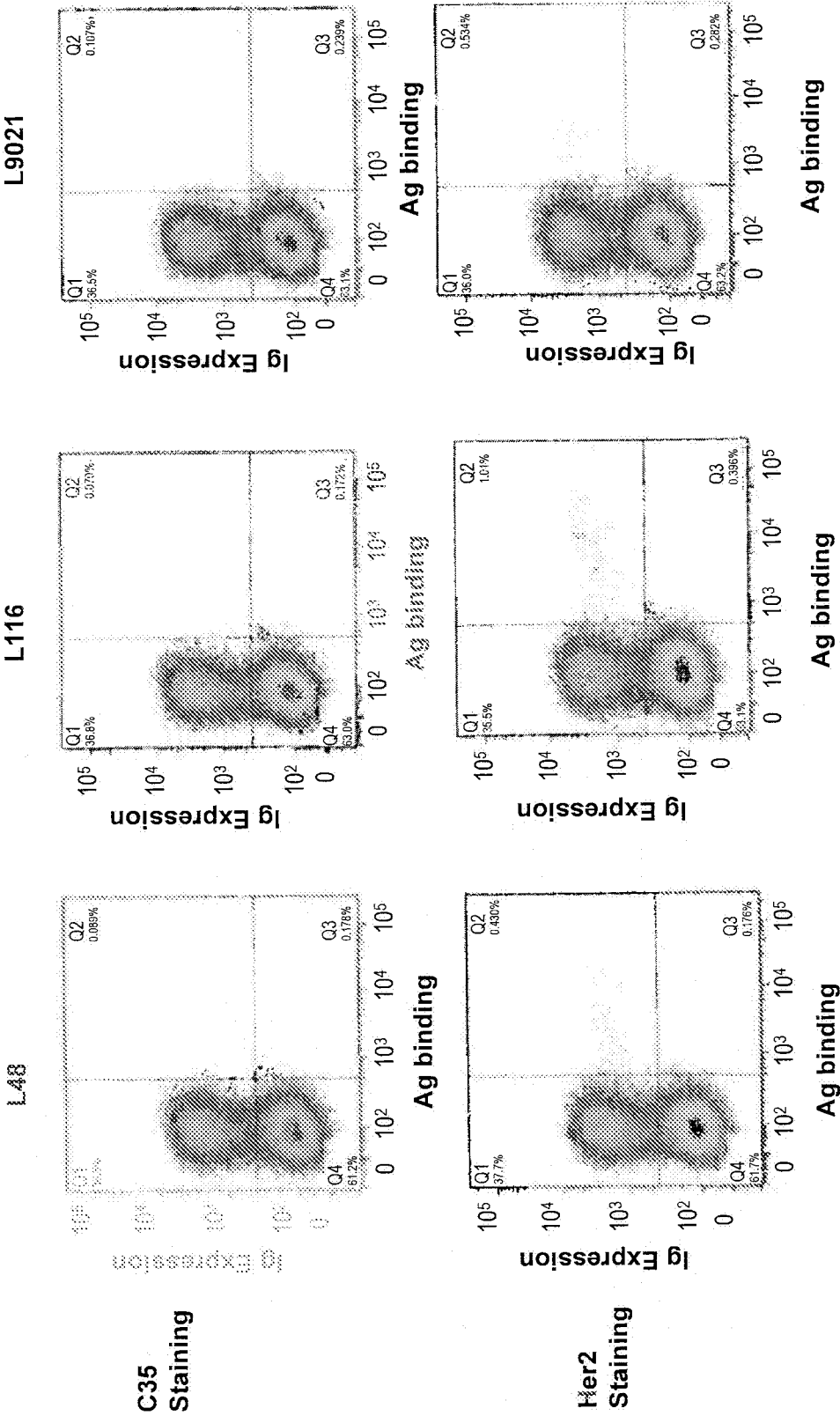


FIG. 8

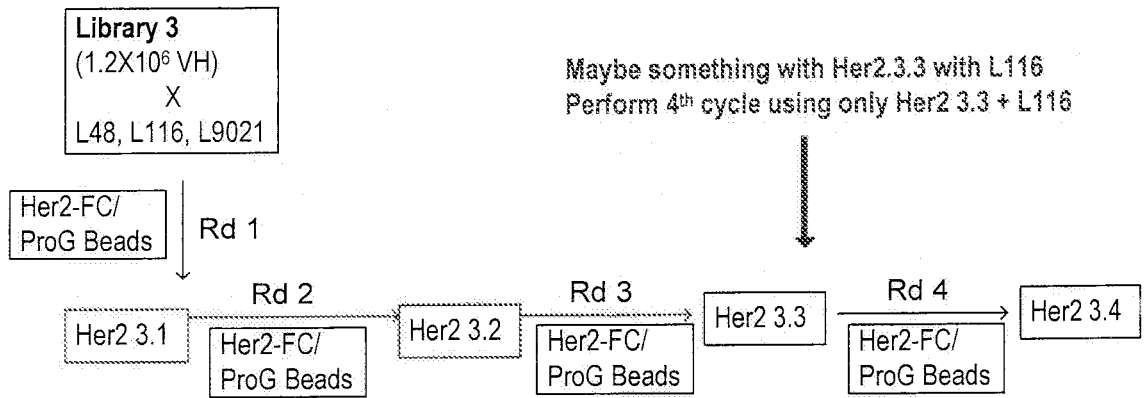


FIG. 9

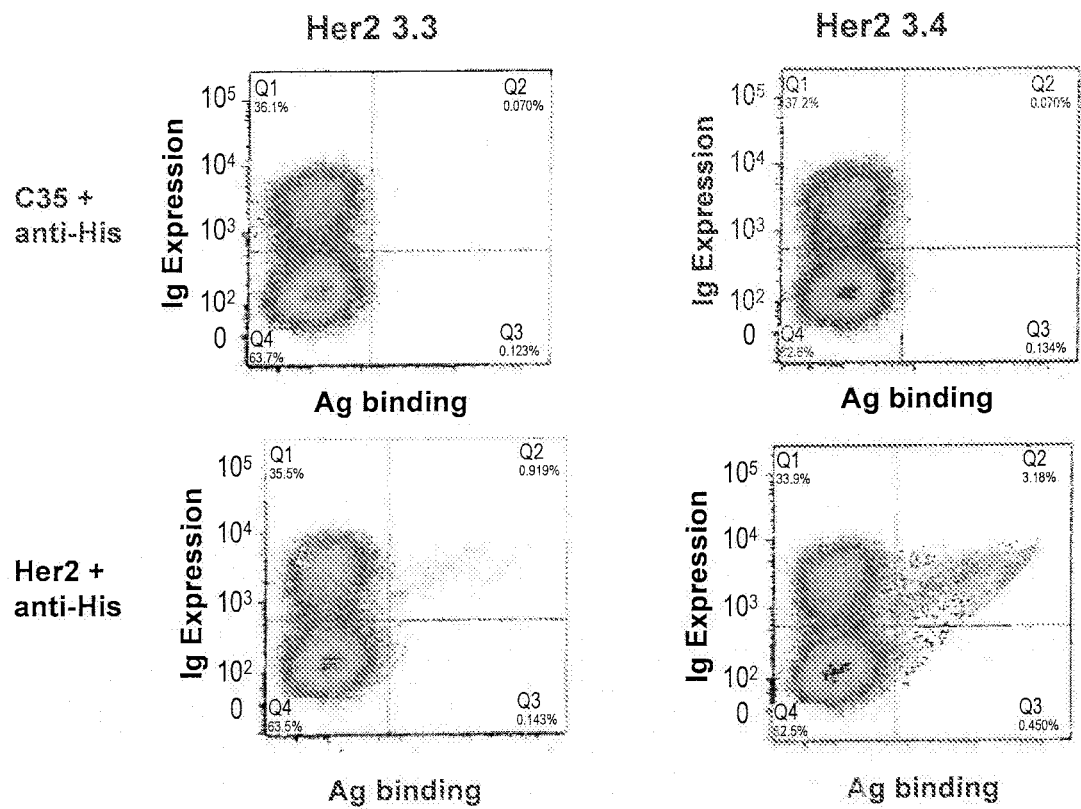


FIG. 10

Her2 B10 clone Sequence

EVQLLESGGGFVQPGGSLRLSCAASGFAFNYYALSWVRQAPGRGLKWVSAISPDGD
YIYYADSVKGRFIFSRDNSRNMLSLQMTSLGAEDTALYYCARQNNVRDGAVAGPLD
HWGQGTTLVT

>IGHV3-23*01

Identities = 77/98 (78%), Positives = 85/98 (86%)

B10 : 1 EVQLLESGGGFVQPGGSLRLSCAASGFAFNYYALSWVRQAPGRGLKWVSAISPDGDYIYY 60
EVQLLESGGG VQPGGSRLRLSCAASGF F++YA+SWVRQAPG+GL+WVSAIS G YY
VH323: 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGGSGSTYY 60

B10 : 61 ADSVKGRFIFSRDNSRNMLSLQMTSLGAEDTALYYCAR 98 (SEQ ID NO:20)
ADSVKGRF SRDNS+N L LQM SL AEDTA+YYCA+
VH323: 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK 98

FIGURE 11

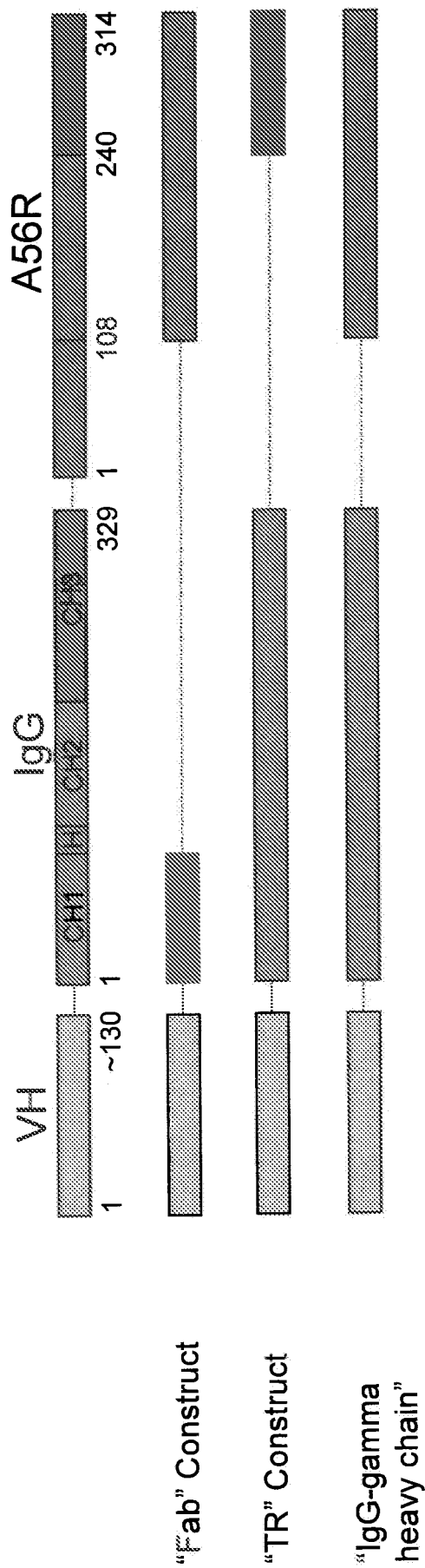


FIG. 12

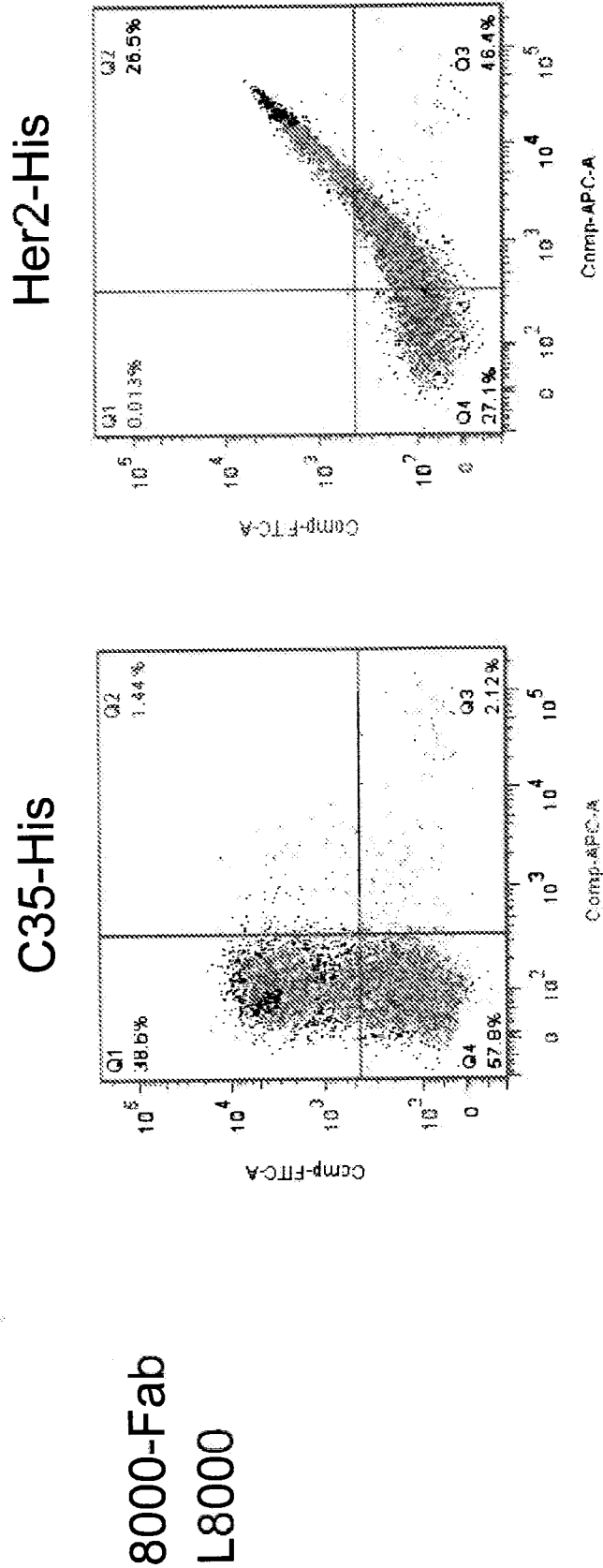
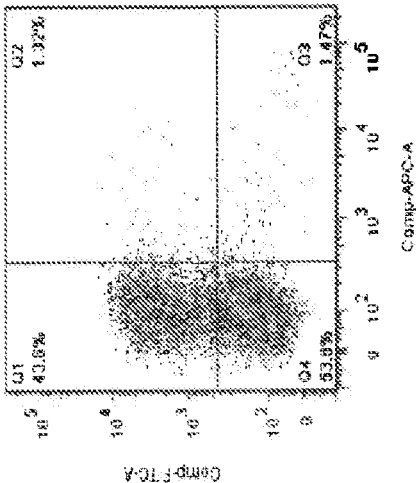
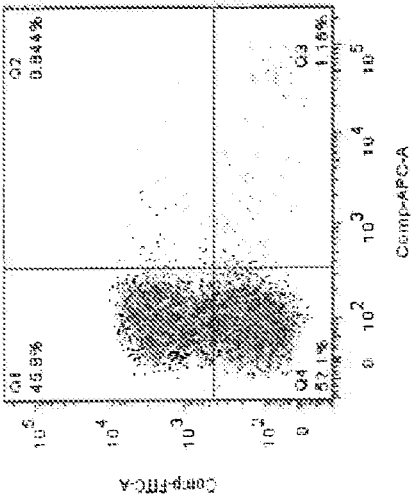
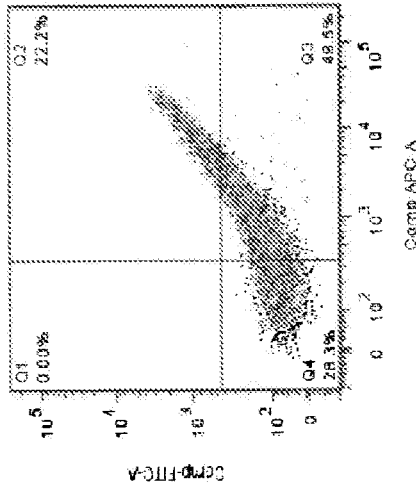
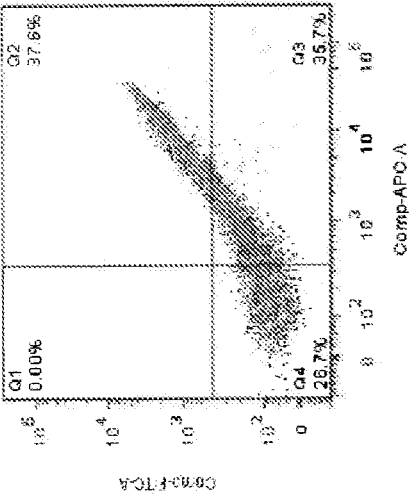


FIG. 13

C35-His



Her2-His



A. 8000-IgG
L8000

B. 8000-TR
L8000

FIG. 14

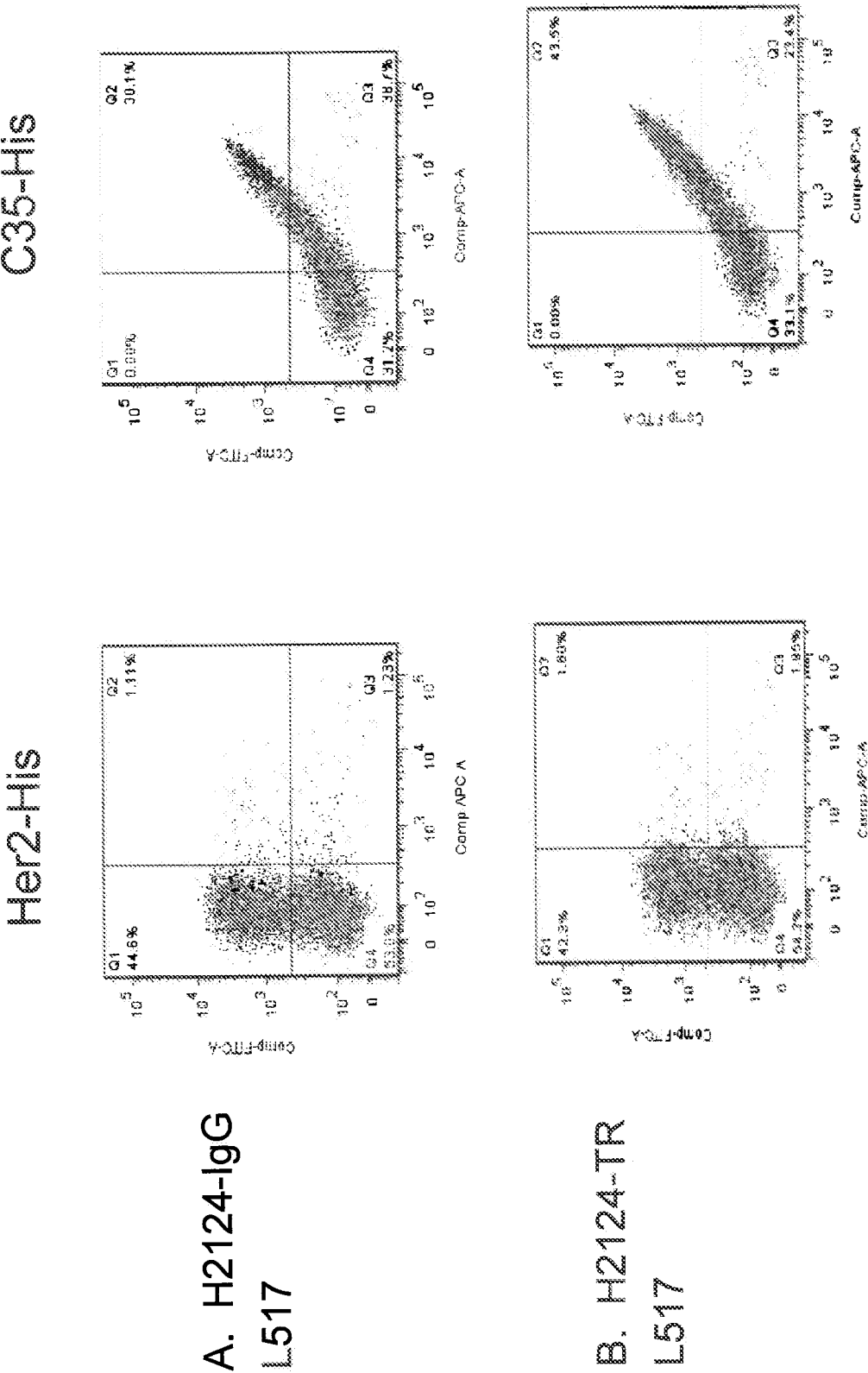
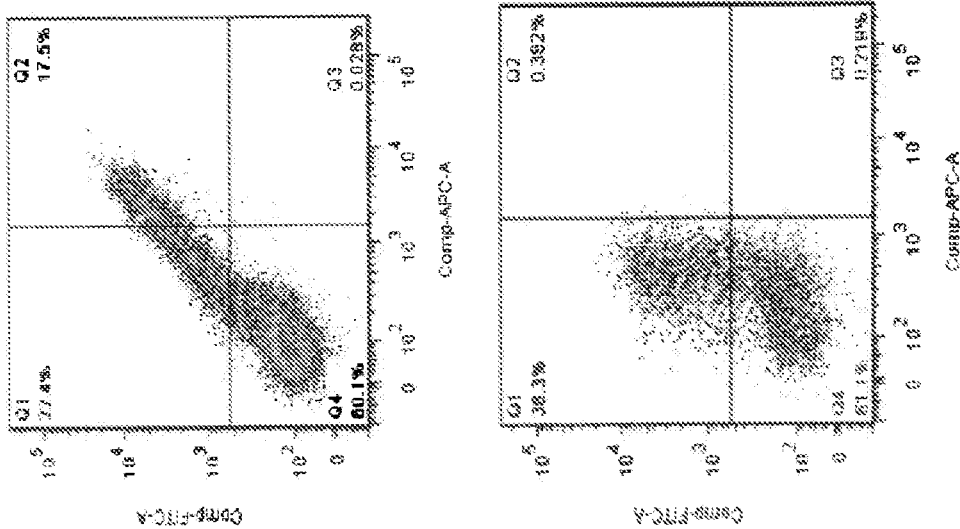
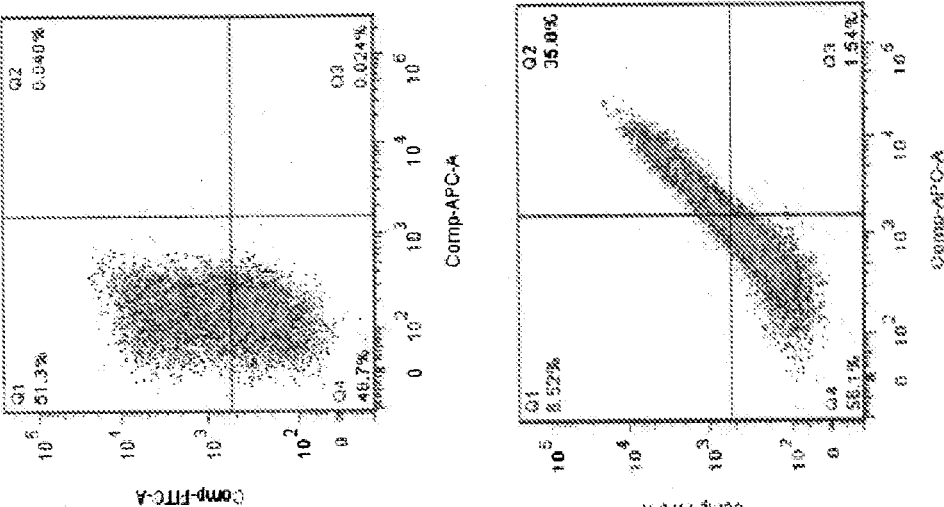


FIG. 15

B. 8000



A. 2368



Her2
Staining

CD100
Staining

FIG. 16

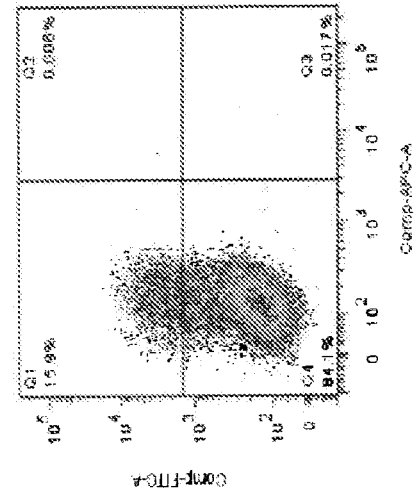
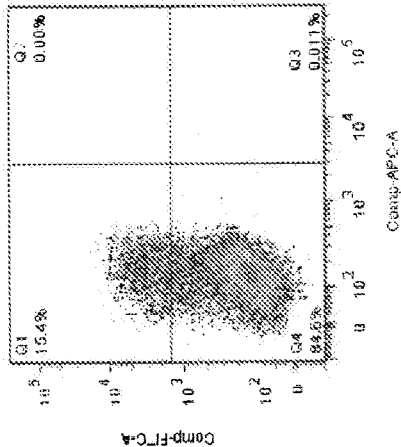
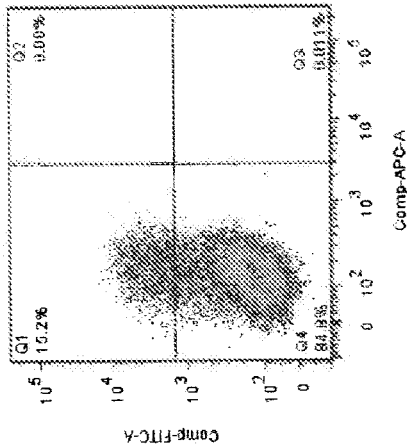
C. L9021

B. L151

A. L223

Her2
Staining

CD100
Staining



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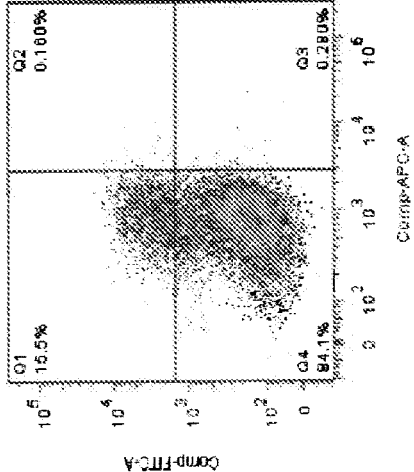
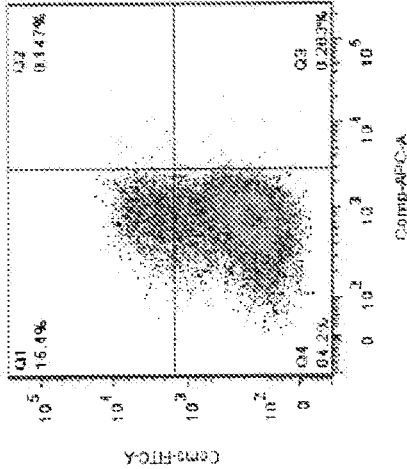
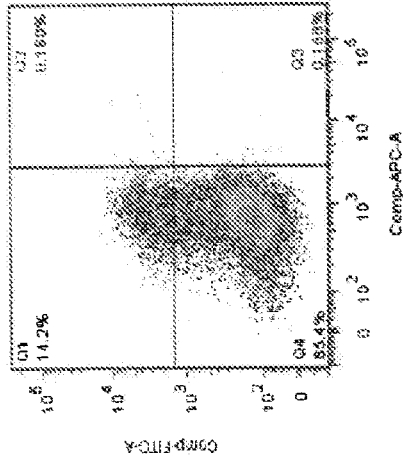
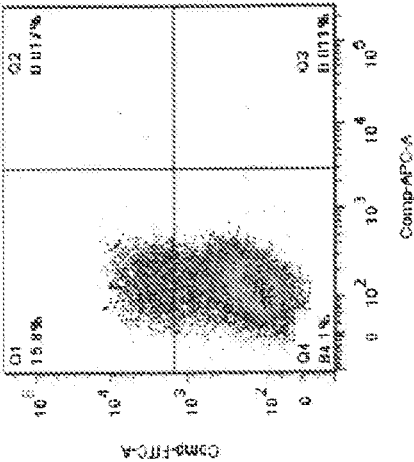
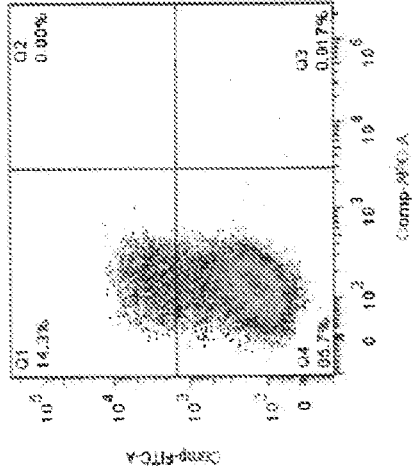


FIG. 17

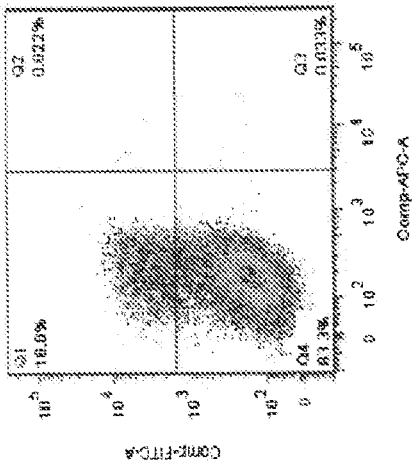
C. L122



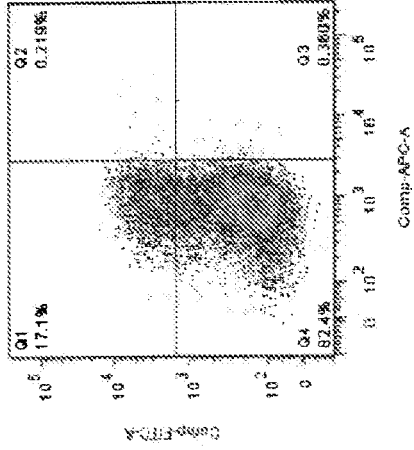
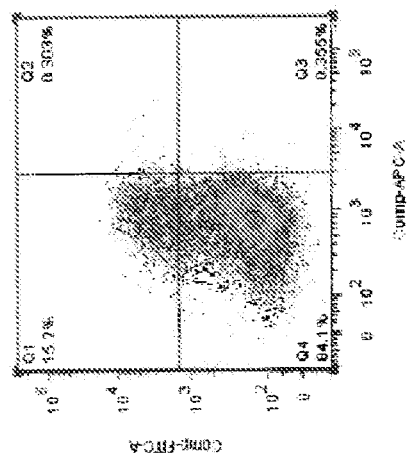
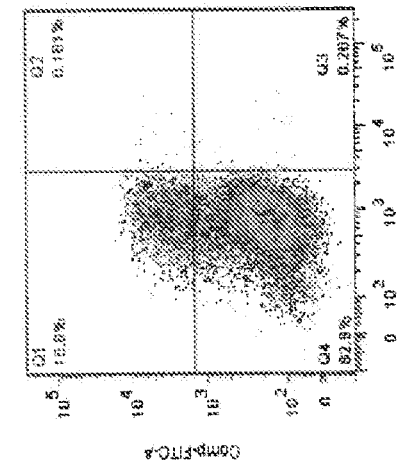
B. L7110



A. L48



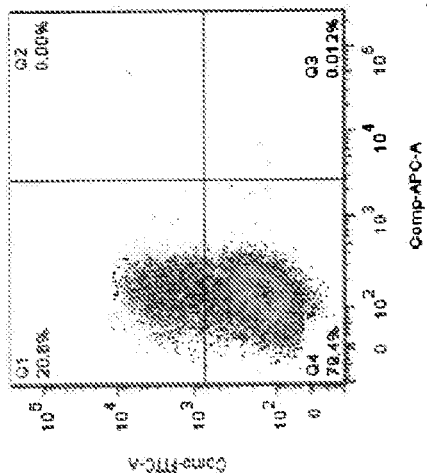
Her2
Staining



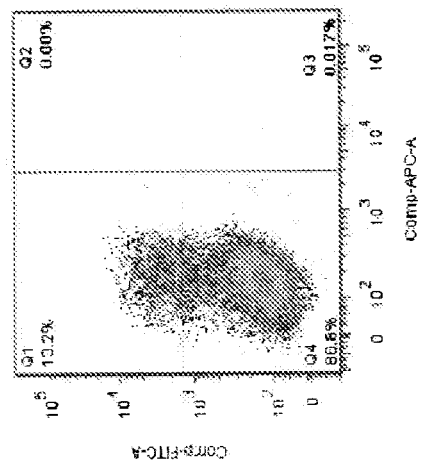
CD100
Staining

FIG. 18

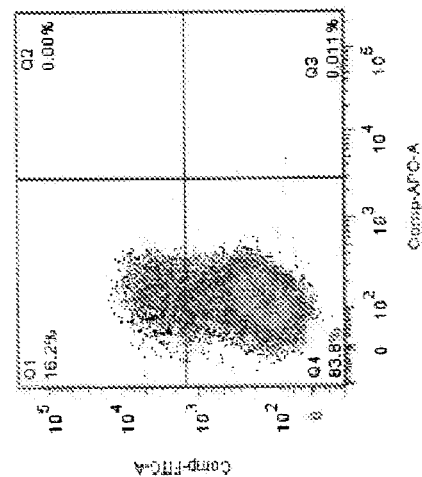
C. L3-1



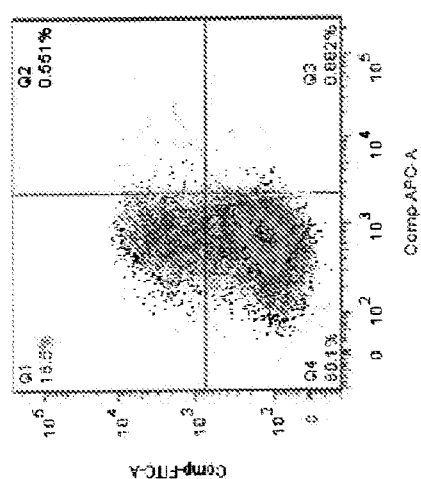
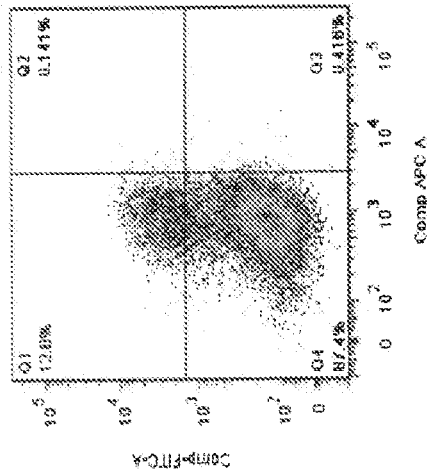
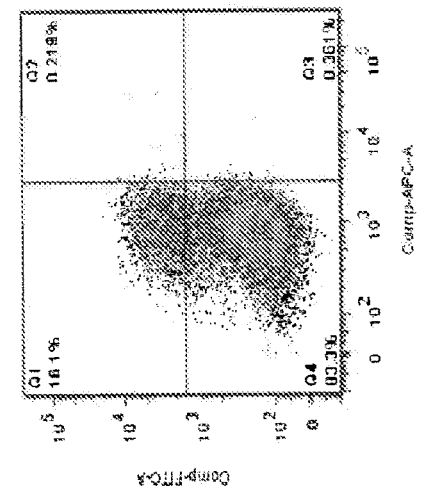
B. L214



A. L116



Her2
Staining



CD100
Staining

FIG. 19

C. L9021

B. L151

A. L223

Her2
Staining

CD100
Staining

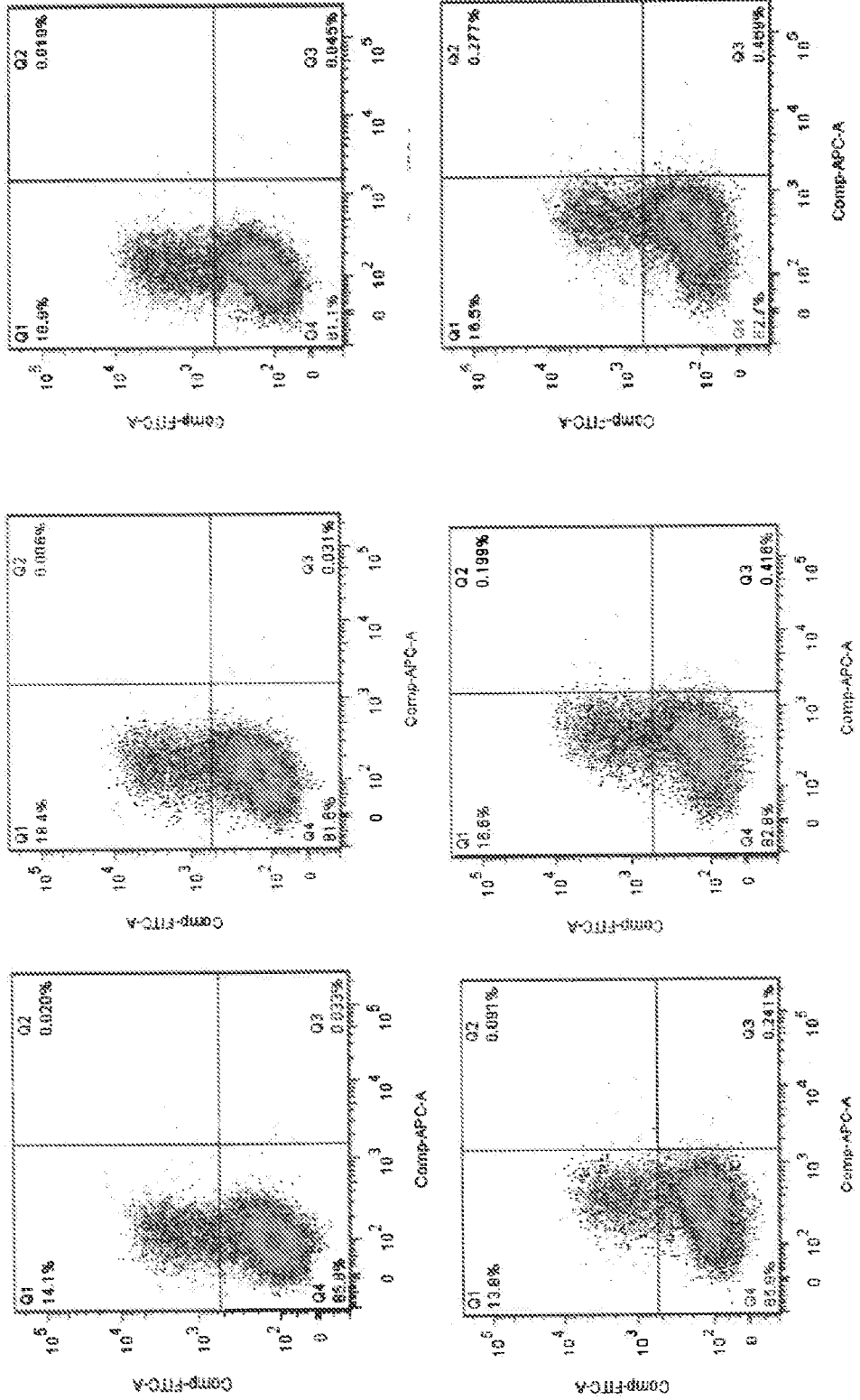


FIG. 20

C. L122

B. L7110

A. L48

Her2
Staining

CD100
Staining

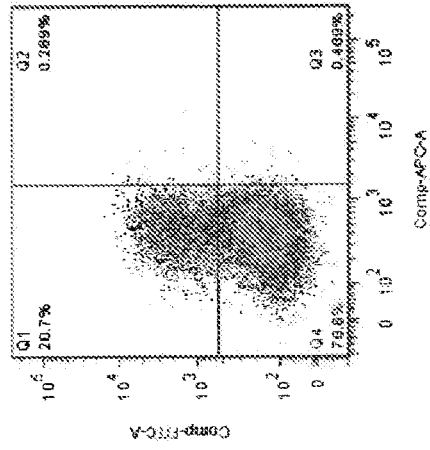
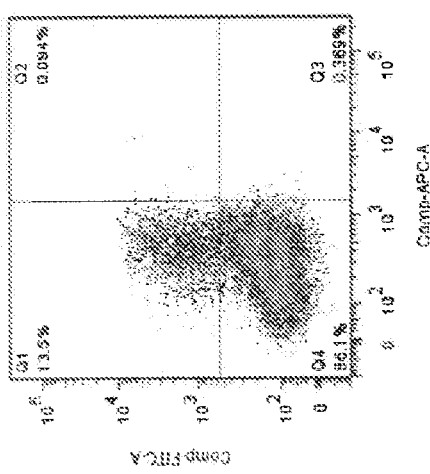
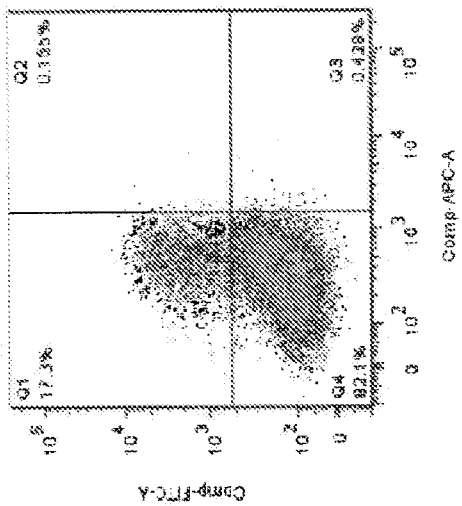
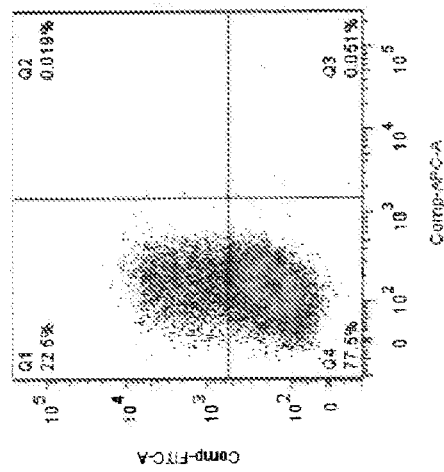
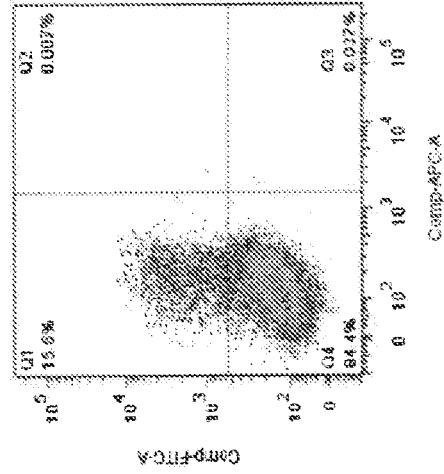
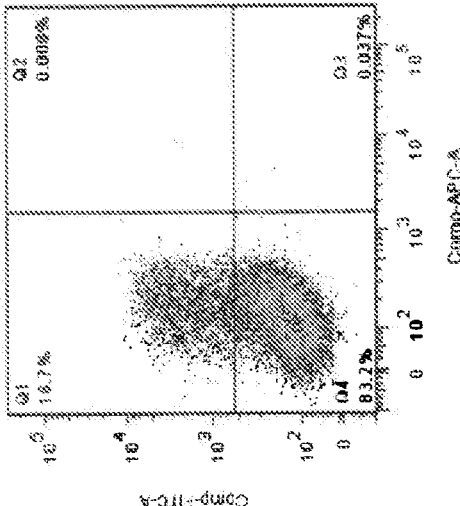
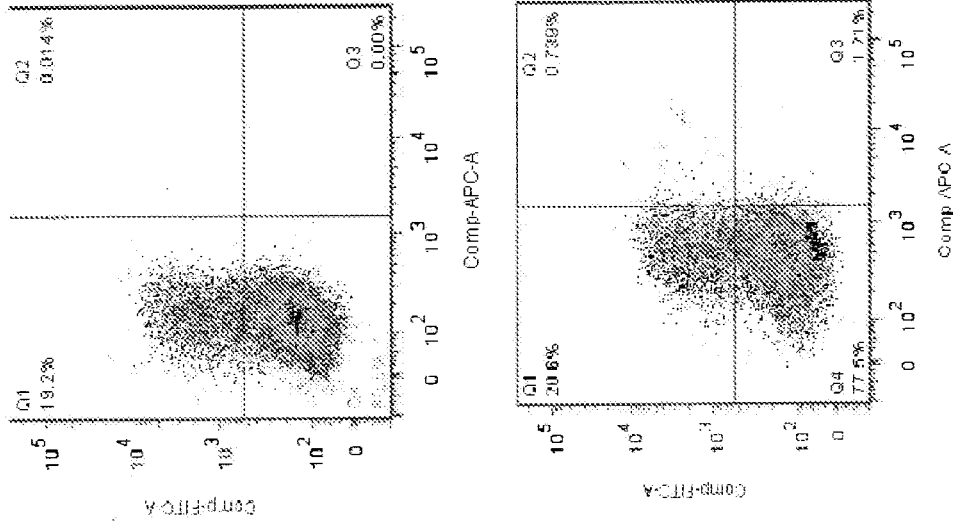
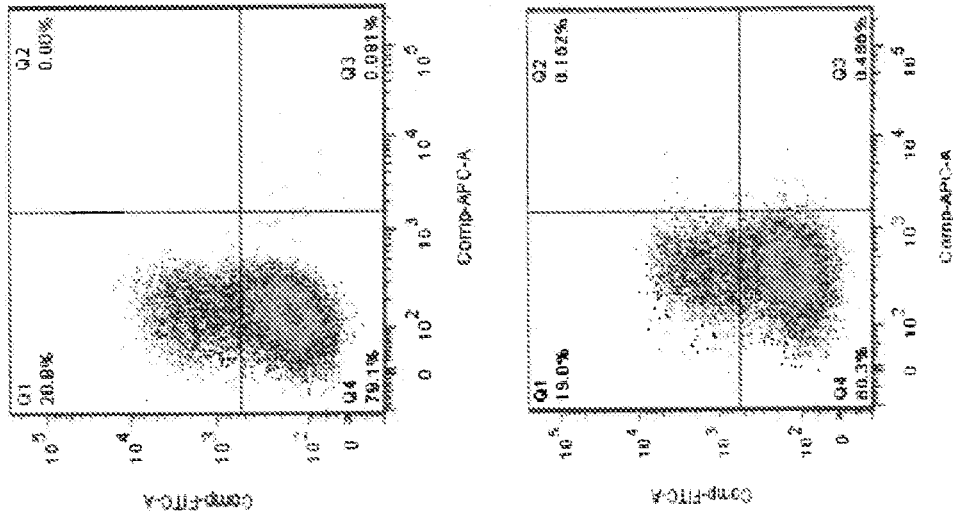


FIG. 21

C. L3-1



B. L214



A. L116

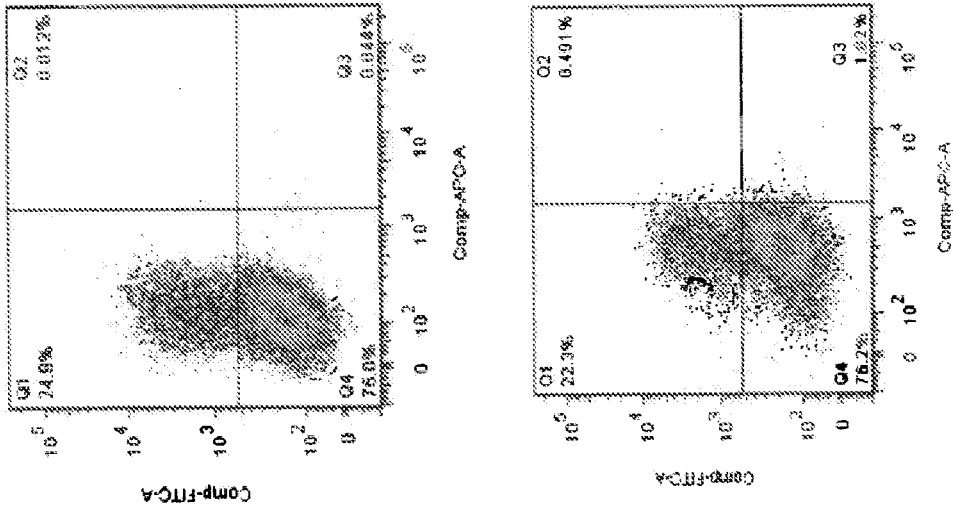


FIG. 22

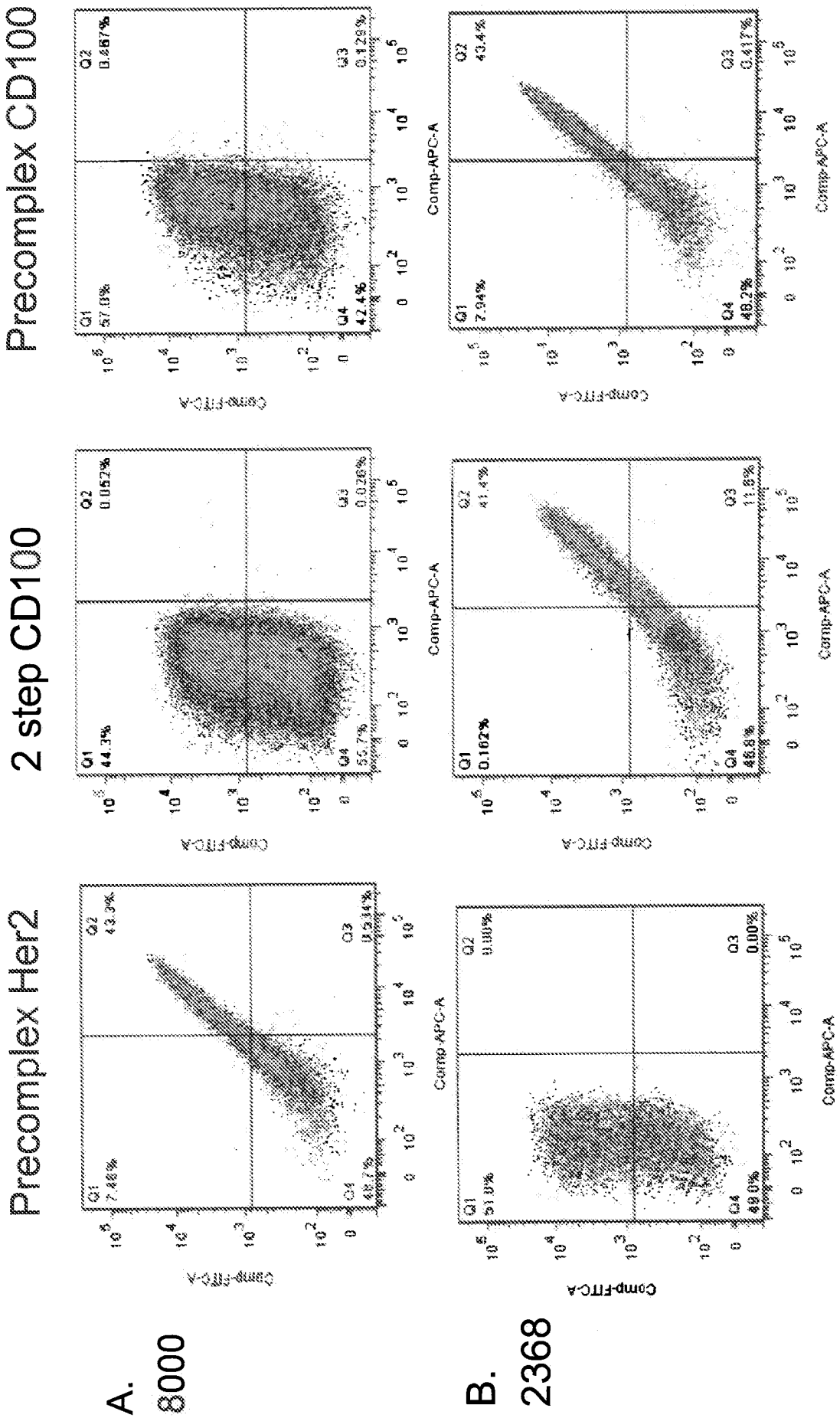


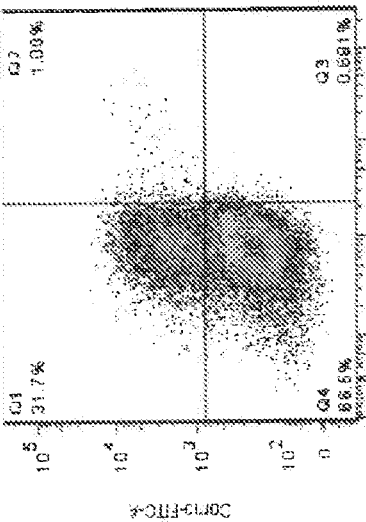
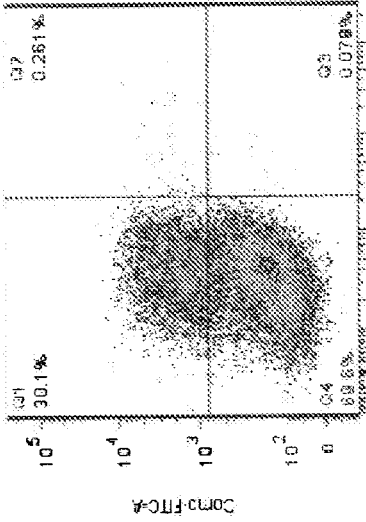
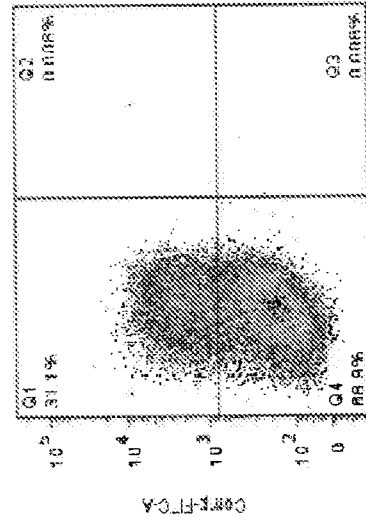
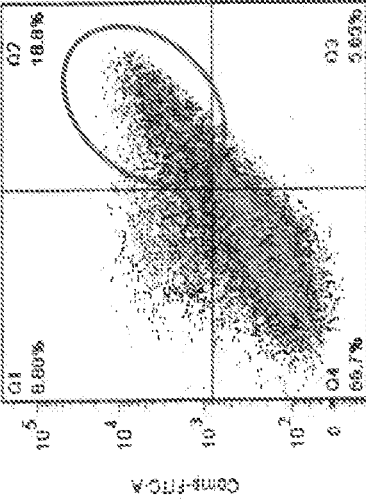
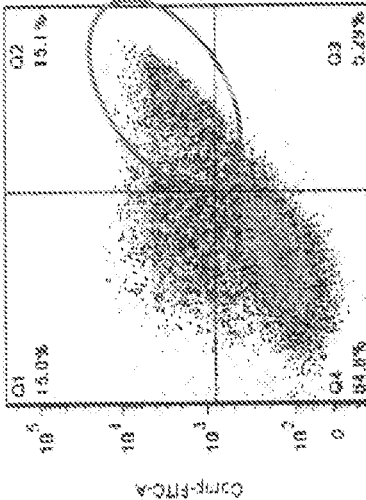
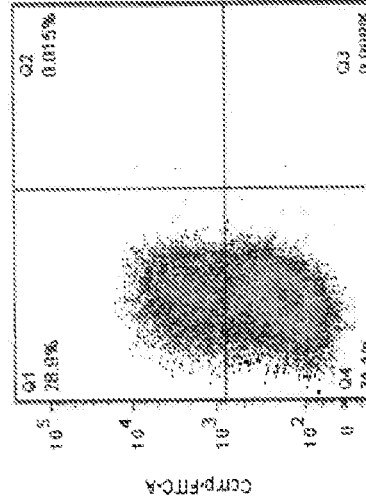
FIG. 23

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Precomplex CD100

2 step CD100

Precomplex Her2



Comp-APC-A

Comp-APC-A

Comp-APC-A

FIG. 24

A. CD100
Lib 10.3
pre-sorted
Tosyl
selected

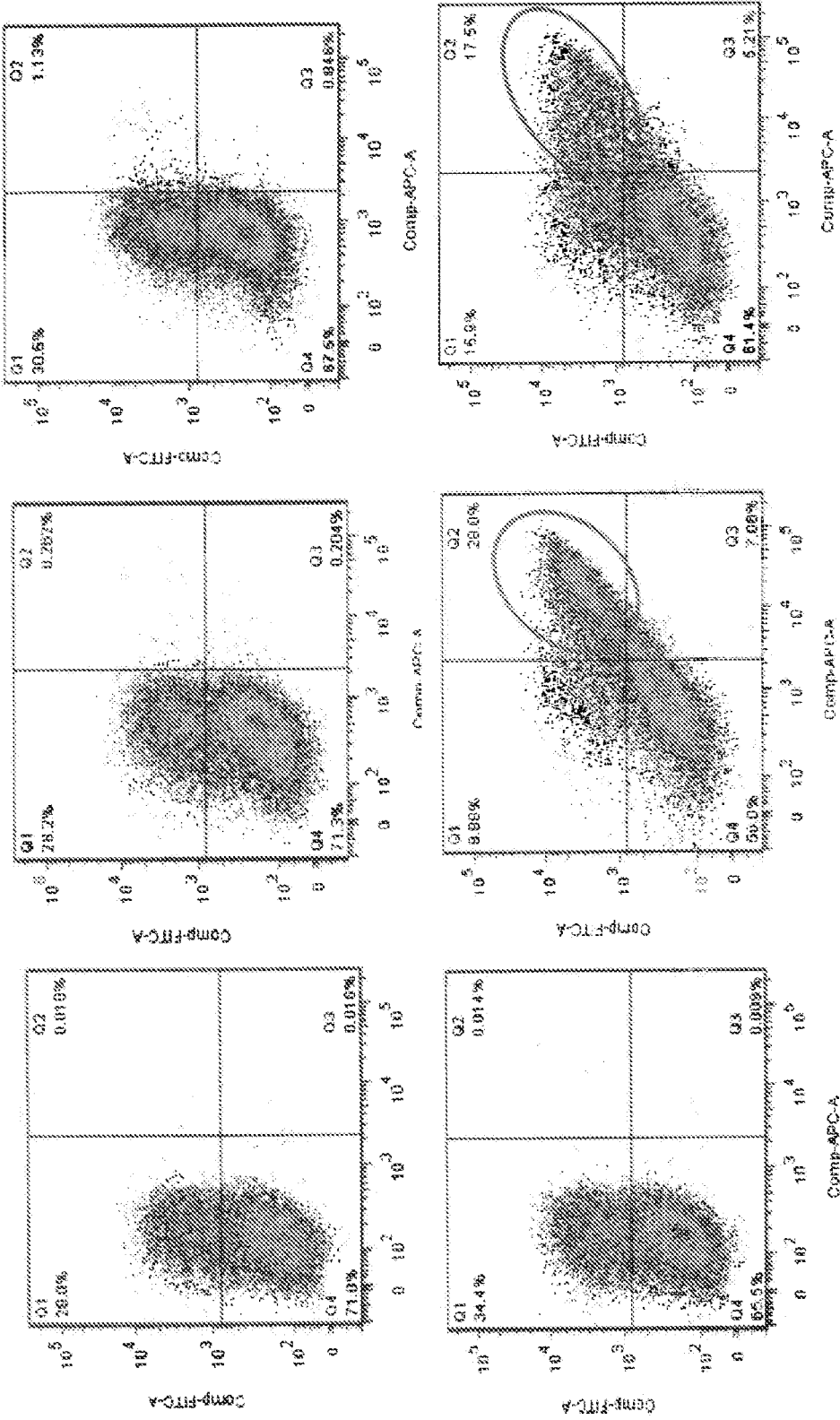
B. CD100
Lib 10.3
sorted
Tosyl
selected

A. CD100
Lib 10.3
pre-sorted
ProtG
selected

Precomplex Her2

2 step CD100

Precomplex CD100



B. CD100
Lib 10.3
sorted
ProtG
selected

FIG. 25

- mAb 2050 VH5-51 synthetic
- mAb 2063 VH3-30 naïve
- mAb 2110 VH3-7 naïve
- Specific to native CD100 on Jurkat cells with low binding to background on BxPC3

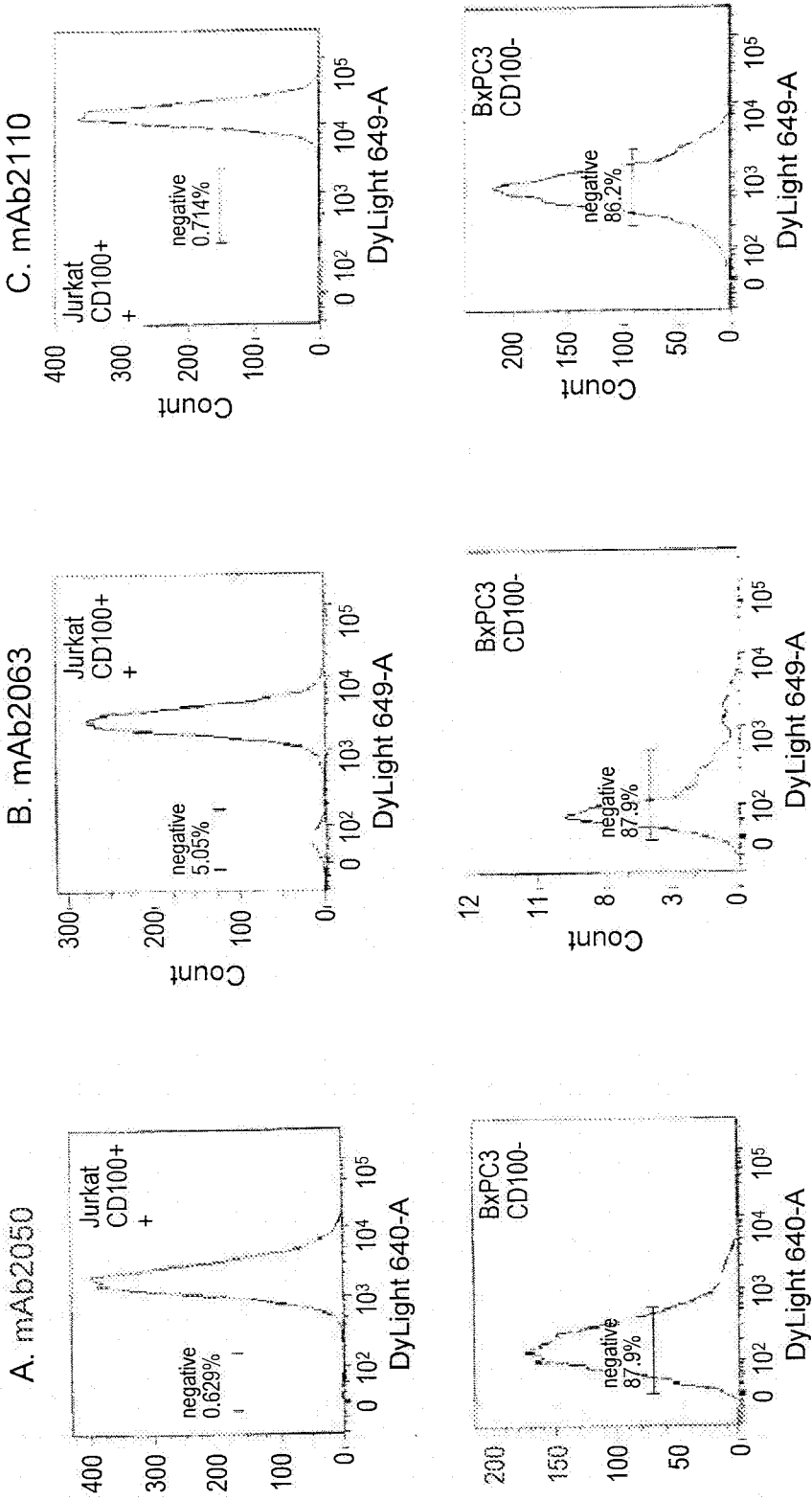


FIG. 26

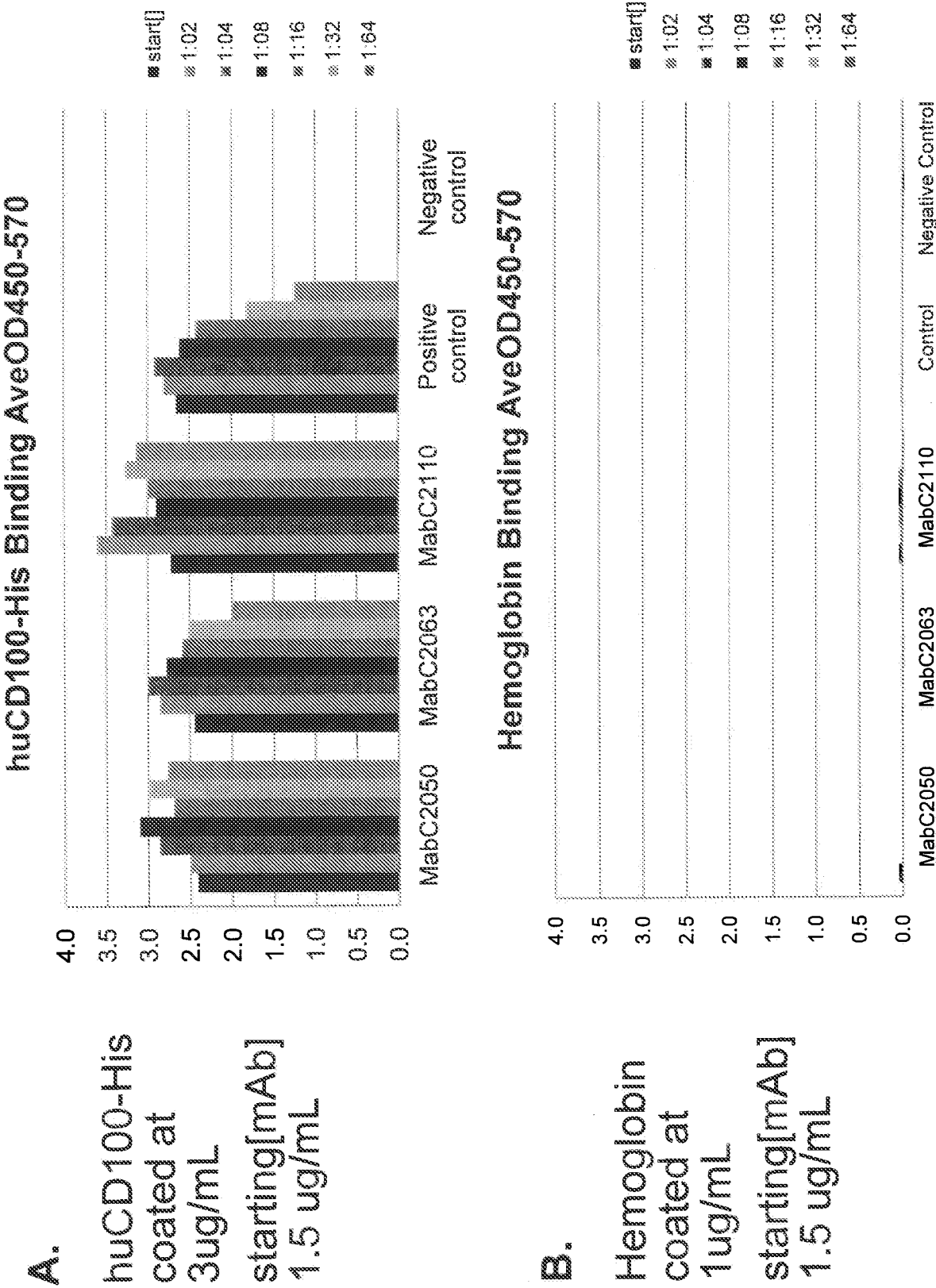


FIG. 27

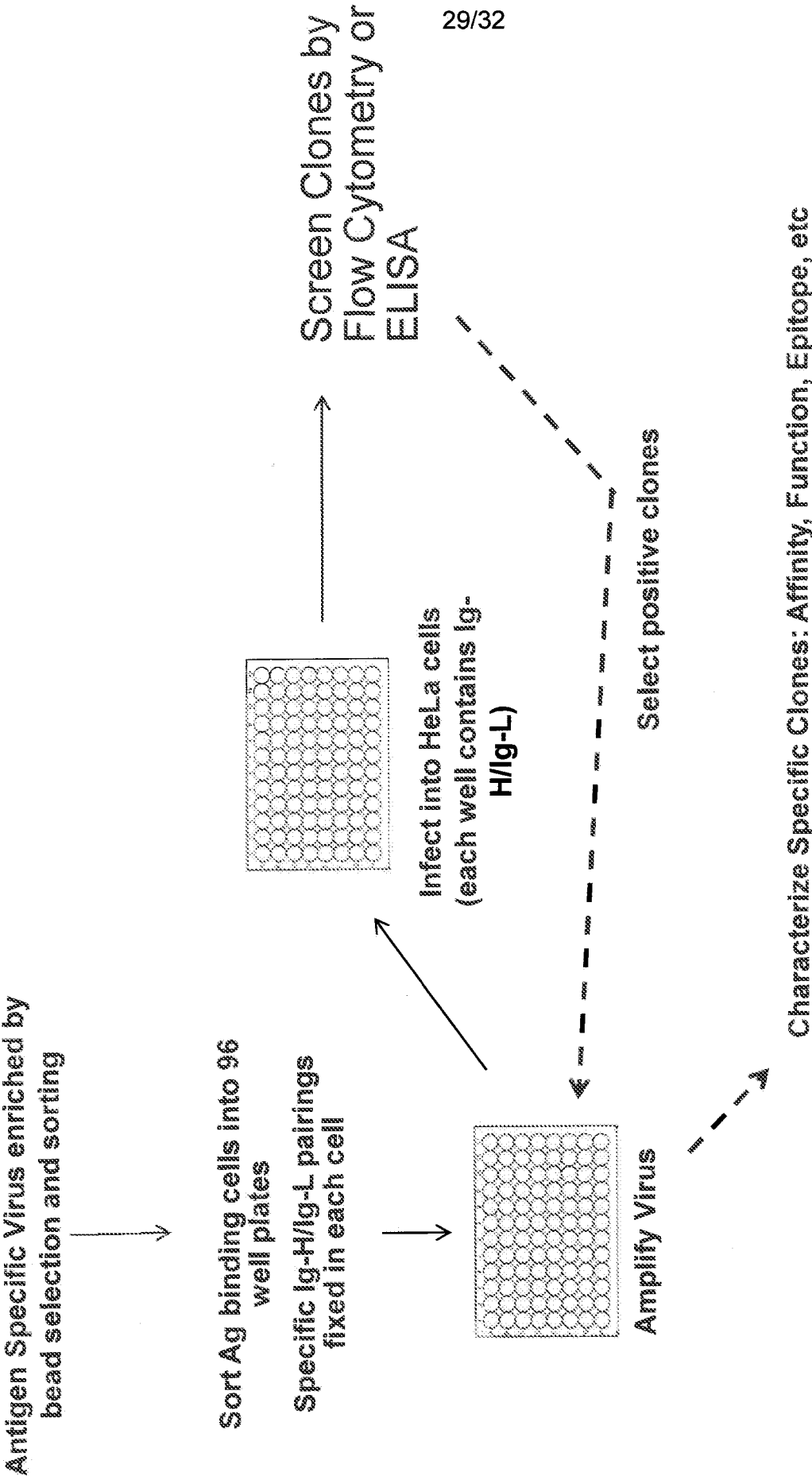
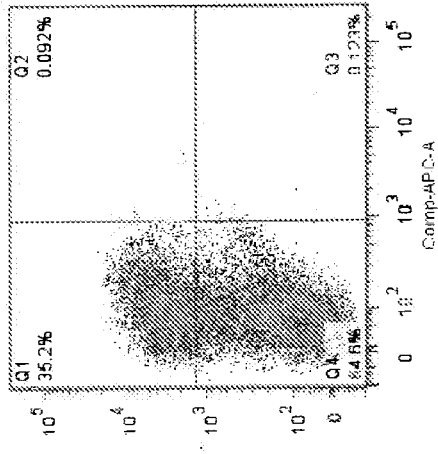
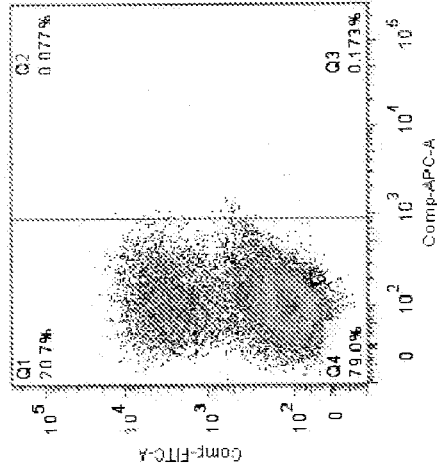


FIG. 28

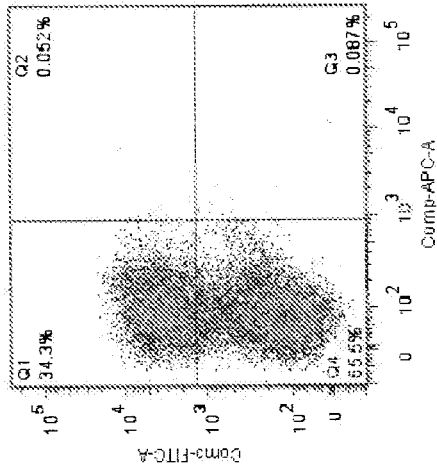
C. 3.H2



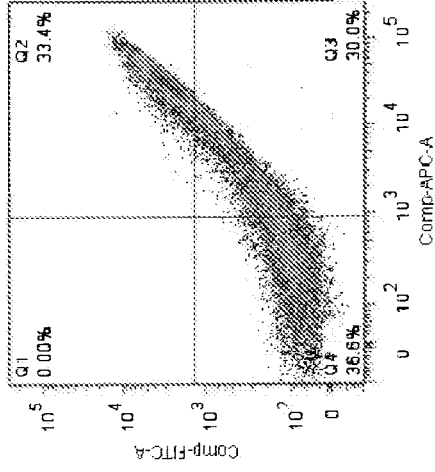
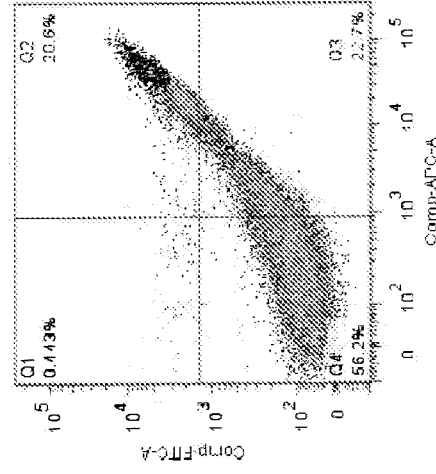
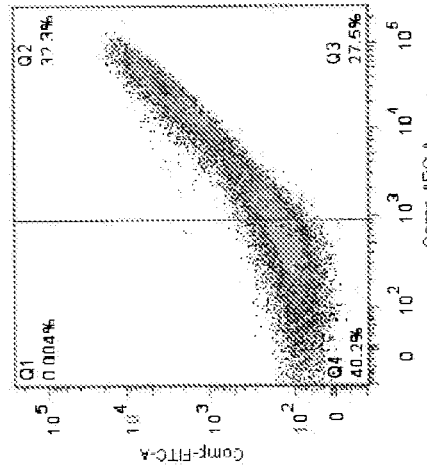
B. 3.D8



A. 3.D5



C35
Staining



Her2
Staining

FIG. 29

Her2 Binding Specificity

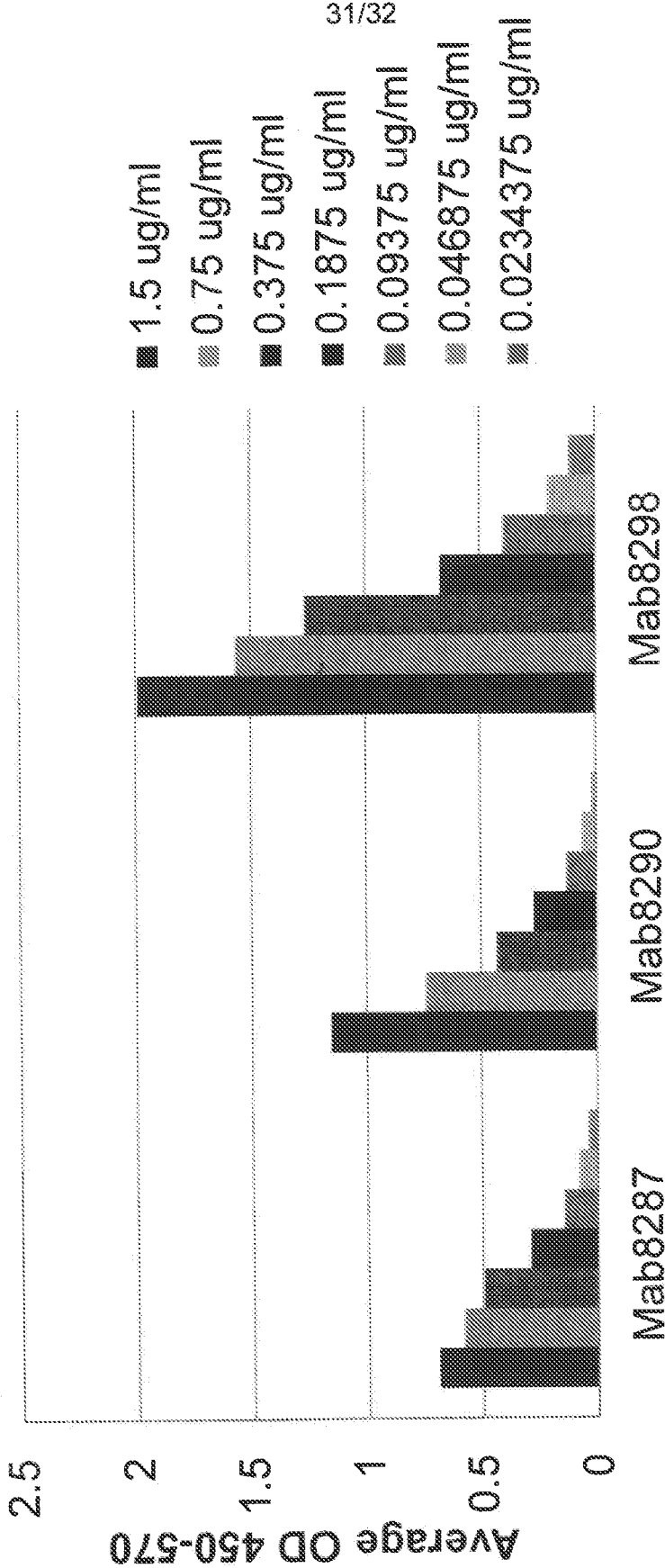


FIG. 30

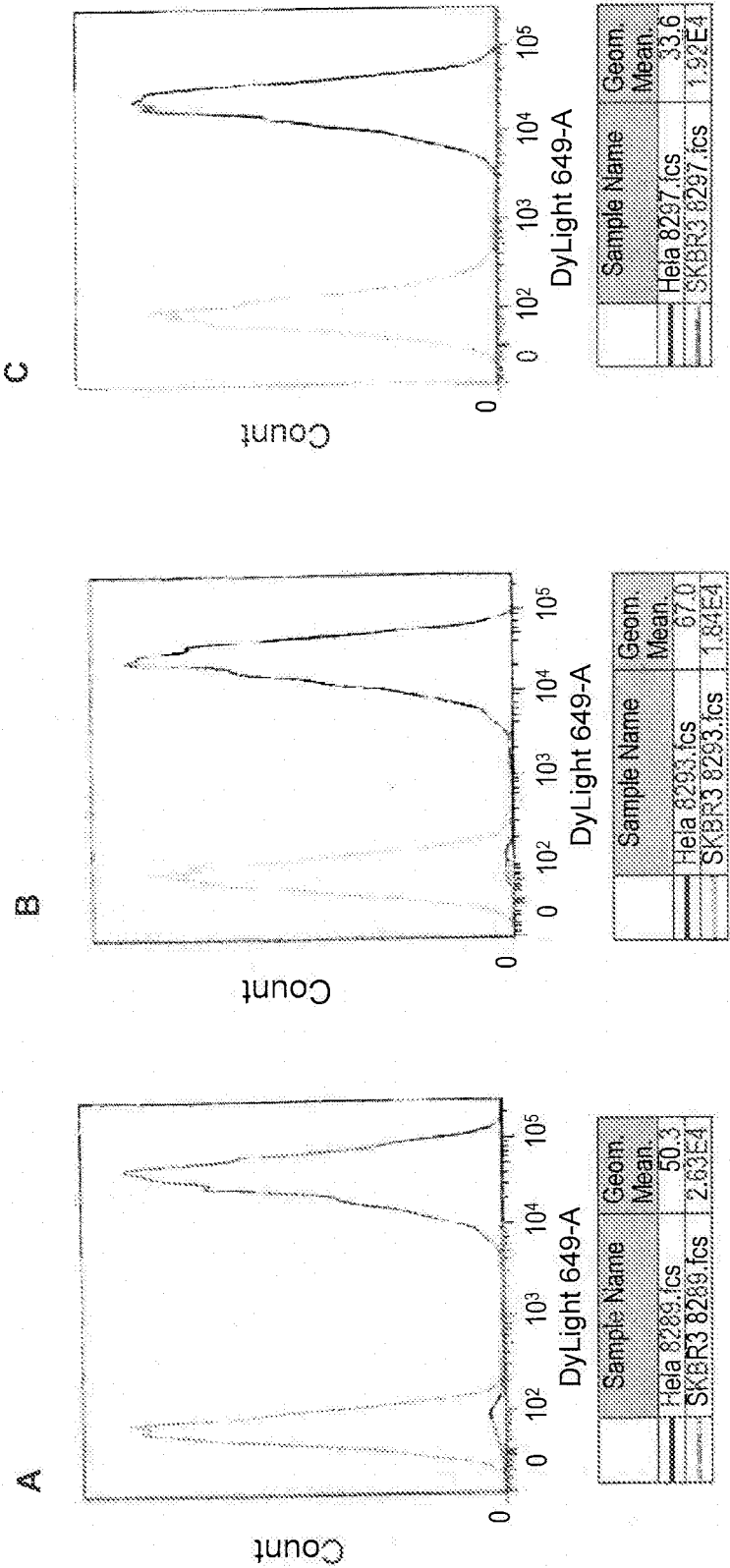


FIG. 31