

1 1/85 45

```

mu11B6_VH DVQLQESGPGGLVKPSQSLSLTCTVTGNSITSDYAWNWIROFPGNR
hu11B6_VH QVQLQESGPGGLVKPSDTLSLTCAVSGNSITSDYAWNWIROPPGKG
KL2B357_VH QVQLQESGPGGLVKPSOTLSLTCTVSGNSITSDYAWNWIROFPGKG
KL2B358_VH QVQLQESGPGGLVKPSOTLSLTCTVSGNSITSDYAWNWIROPPGKG
KL2B359_VH QVQLQESGPGGLVKPSOTLSLTCTVSGNSITSDYAWNWIROFPGKR
KL2B360_VH QVQLQESGPGGLVKPSOTLSLTCTVSGNSITSDYAWNWIROFPGKG
HCF3 QVQLQESGPGGLVKPSDTLSLTCAVSGNSITSDYAWNWIROFPGKG
HCG5 QVQLQESGPGGLVKPSDTLSLTCAVSGNSITSDYAWNWIROFPGKG
Aln *****:*****:*****:*****

```

46 90

```

mu11B6_VH LEWMGYISYSGSTTYSPSLKSRFSITRDTSKNQFFLQLNSVTED
hu11B6_VH LEWMGYISYSGSTTYNPSLKSRTMSRDTSKNQFSLKLSSVTAVD
KL2B357_VH LEWMGYISYSGSTTYNPSLKSRTISRDTSKNQFSLKLSSVTAAD
KL2B358_VH LEWMGYISYSGSTTYNPSLKSRTISRDTSKNQFSLKLSSVTAAD
KL2B359_VH LEWMGYISYSGSTTYNPSLKSRTISRDTSKNQFSLKLSSVTAAD
KL2B360_VH LEWMGYISYSGSTTYNPSLKSRTISRDTSKNQFSLKLSSVTAAD
HCF3 LEWMGYISYSGSTTYNPSLKSRTISRDTSKNQFSLKLSSVTPVD
HCG5 LEWMGYISYSGSTTYNPSLKSRTISRDTSKNQFSLKLSSVTPVD
Aln ***:*****.*****.:*****:*****.***.

```

91 117

```

mu11B6_VH TATYFCATGYYYGSGFWGQGTTLVTVSS
hu11B6_VH TAVYYCATGYYYGSGFWGQGTTLVTVSS
KL2B357_VH TAVYYCATGYYYGSGFWGQGTTLVTVSS
KL2B358_VH TAVYYCATGYYYGSGFWGQGTTLVTVSS
KL2B359_VH TAVYYCATGYYYGSGFWGQGTTLVTVSS
KL2B360_VH TAVYYCATGYYYGSGFWGQGTTLVTVSS
HCF3 TAVYYCATGYYYGSGFWGQGTTLVTVSS
HCG5 TAVYYCATGYYYGSGFWGQGTTLVTVSS
Aln **.*****

```

VH consensus sequence (SEQ ID NO: 75)

QVQLQESGPGGLVKPS~~X₁~~TL~~X₂~~SLTCAVSGNSITSDYAWNWIRO~~X₃~~PGK~~X₄~~LEWMGYISYSGSTTYNPSLKSRT~~X₅~~ISRDTSKNQFSLKLSSVT~~X₆~~~~X₇~~~~X₈~~DTAVYYCATGYYYGSGFWGQGTTLVTVSS

X₁ is D or Q; X₅ is I or M;
X₂ is A or T; X₆ is I or M;
X₃ is P or F; X₇ is A or P; or
X₄ is G or R; X₈ is V or A.

FIG. 1

VL consensus sequence (SEQ ID NO: 74)

X₁IVLTQSPX₂X₃LX₄X₅SX₆GERATX₇X₈CX₉ASESVEYFGTSLMHWYQQKPGQPPX₁₀LLIYAASNX₁₁
ESGX₁₂FX₁₃RFSGSGSGTDFTLTIX₁₄SLX₁₅X₁₆QX₁₇EDX₁₈X₁₉VYX₂₀COQTRKVPYTFGX₂₁GTX₂₂EIK

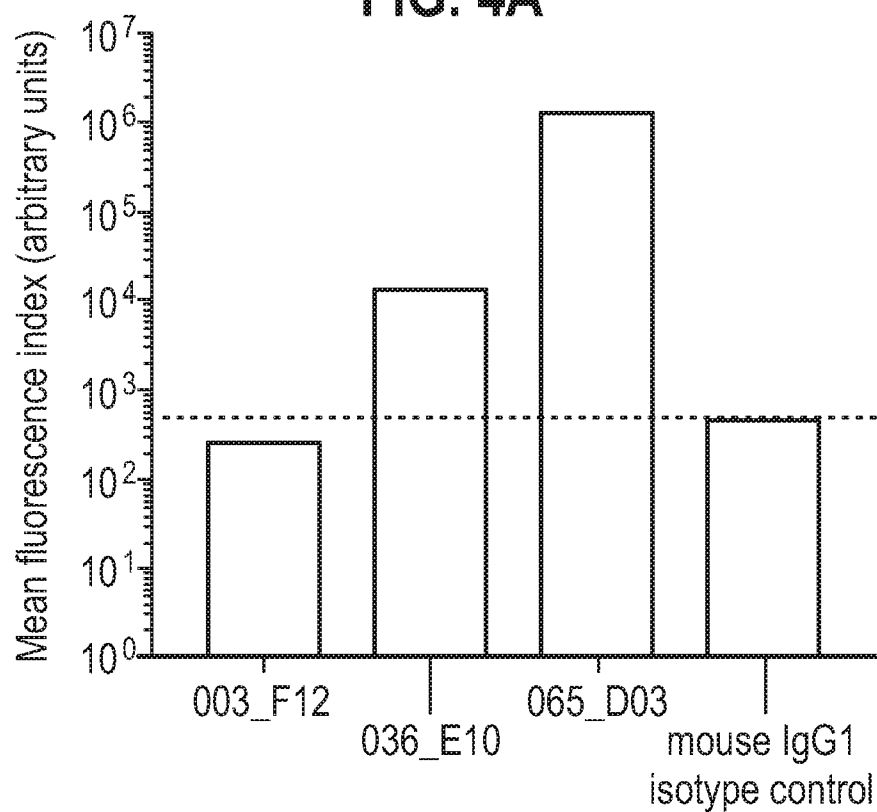
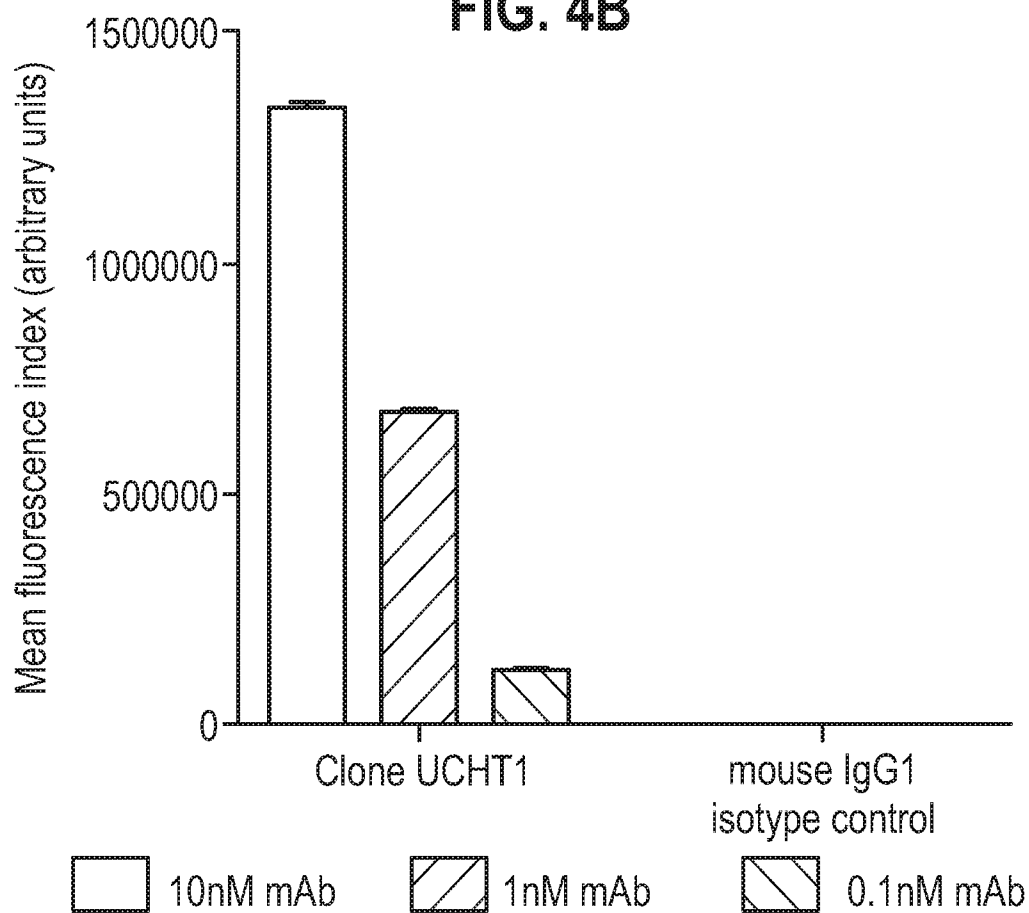
SUBSTITUTE SHEET (RULE 26)

3 / 85

FIG. 3

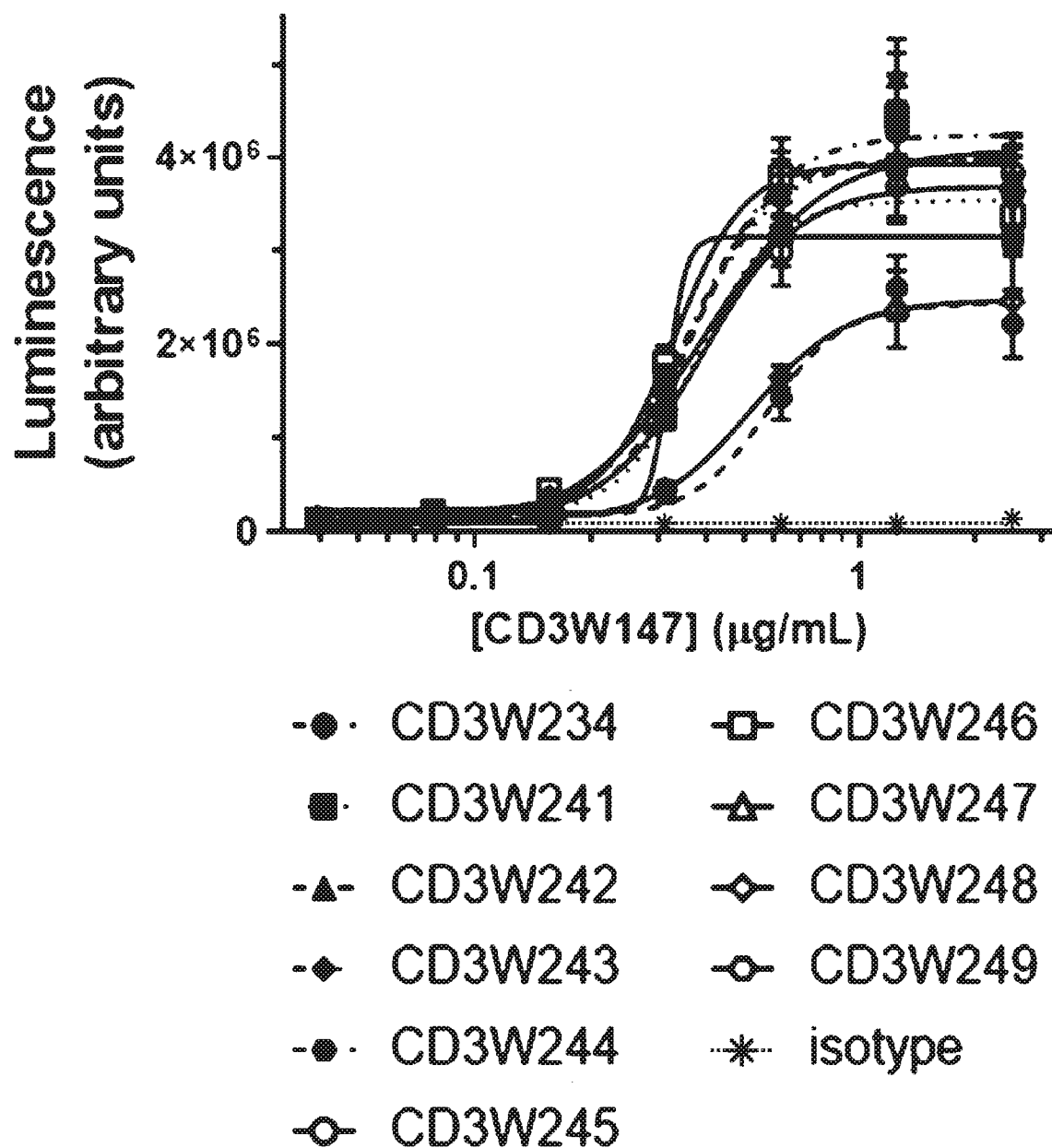
	1		50
h11B6	VPLIEGRIVGGWE	CEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCL	
KL2B494	VPLIEGRIVGGWE	CEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCL	
KL2B467	VPLIEGRIVGGWE	CEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCL	
KL2B30	VPLIEGRIVGGWE	CEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCL	
KL2B413	VPLIEGRIVGGWE	CEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCL	
KL2B53	VPLIEGRIVGGWE	CEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCL	
	51		100
h11B6	KKNSQVWLGRHNL	FEPEDTGQRPVSHSFPHPLYNMSLLKHQSLRPDEDS	
KL2B494	KKNSQVWLGRHNL	FEPEDTGQRPVSHSFPHPLYNMSLLKHQSLRPDEDS	
KL2B467	KKNSQVWLGRHNL	FEPEDTGQRPVSHSFPHPLYNMSLLKHQSLRPDEDS	
KL2B30	KKNSQVWLGRHNL	FEPEDTGQRPVSHSFPHPLYNMSLLKHQSLRPDEDS	
KL2B413	KKNSQVWLGRHNL	FEPEDTGQRPVSHSFPHPLYNMSLLKHQSLRPDEDS	
KL2B53	KKNSQVWLGRHNL	FEPEDTGQRPVSHSFPHPLYNMSLLKHQSLRPDEDS	
	101		150
h11B6	SHDLMLLRLSEPAKITD	VVKVLGLPTQEPALGTTTCYASGWGSIEPEEFLLR	
KL2B494	SHDLMLLRLSEPAKITD	VVKVLGLPTQEPALGTTTCYASGWGSIEPEEFLLR	
KL2B467	SHDLMLLRLSEPAKITD	VVKVLGLPTQEPALGTTTCYASGWGSIEPEEFLLR	
KL2B30	SHDLMLLRLSEPAKITD	VVKVLGLPTQEPALGTTTCYASGWGSIEPEEFLLR	
KL2B413	SHDLMLLRLSEPAKITD	VVKVLGLPTQEPALGTTTCYASGWGSIEPEEFLLR	
KL2B53	SHDLMLLRLSEPAKITD	VVKVLGLPTQEPALGTTTCYASGWGSIEPEEFLLR	
	151		200
h11B6	PRSLQCVSLHLLSNDM	CARAYSEKVTEFMLCAGLWTGGKDTCCGDSGGPL	
KL2B494	PRSLQCVSLHLLSNDM	CARAYSEKVTEFMLCAGLWTGGKDTCCGDSGGPL	
KL2B467	PRSLQCVSLHLLSNDM	CARAYSEKVTEFMLCAGLWTGGKDTCCGDSGGPL	
KL2B30	PRSLQCVSLHLLSNDM	CARAYSEKVTEFMLCAGLWTGGKDTCCGDSGGPL	
KL2B413	PRSLQCVSLHLLSNDM	CARAYSEKVTEFMLCAGLWTGGKDTCCGDSGGPL	
KL2B53	PRSLQCVSLHLLSNDM	CARAYSEKVTEFMLCAGLWTGGKDTCCGDSGGPL	
	201		244
H11B6	VCNGVLQGITSWGPEPCALPEKPAVYTKVVHYR	KWIKDTIAANP	
KL2B494	VCNGVLQGITSWGPEPCALPEKPAVYTKVVHYR	KWIKDTIAANP	
KL2B467	VCNGVLQGITSWGPEPCALPEKPAVYTKVVHYR	KWIKDTIAANP	
KL2B30	VCNGVLQGITSWGPEPCALPEKPAVYTKVVHYR	KWIKDTIAANP	
KL2B413	VCNGVLQGITSWGPEPCALPEKPAVYTKVVHYR	KWIKDTIAANP	
KL2B53	VCNGVLQGITSWGPEPCALPEKPAVYTKVVHYR	KWIKDTIAANP	

4 / 85

FIG. 4A**FIG. 4B**

5 / 85

FIG. 5



VL consensus sequence (SEQ ID NO: genus:157)

wherein

SUBSTITUTE SHEET (RULE 26)

8 / 85

FIG. 8A

E:T=3:1

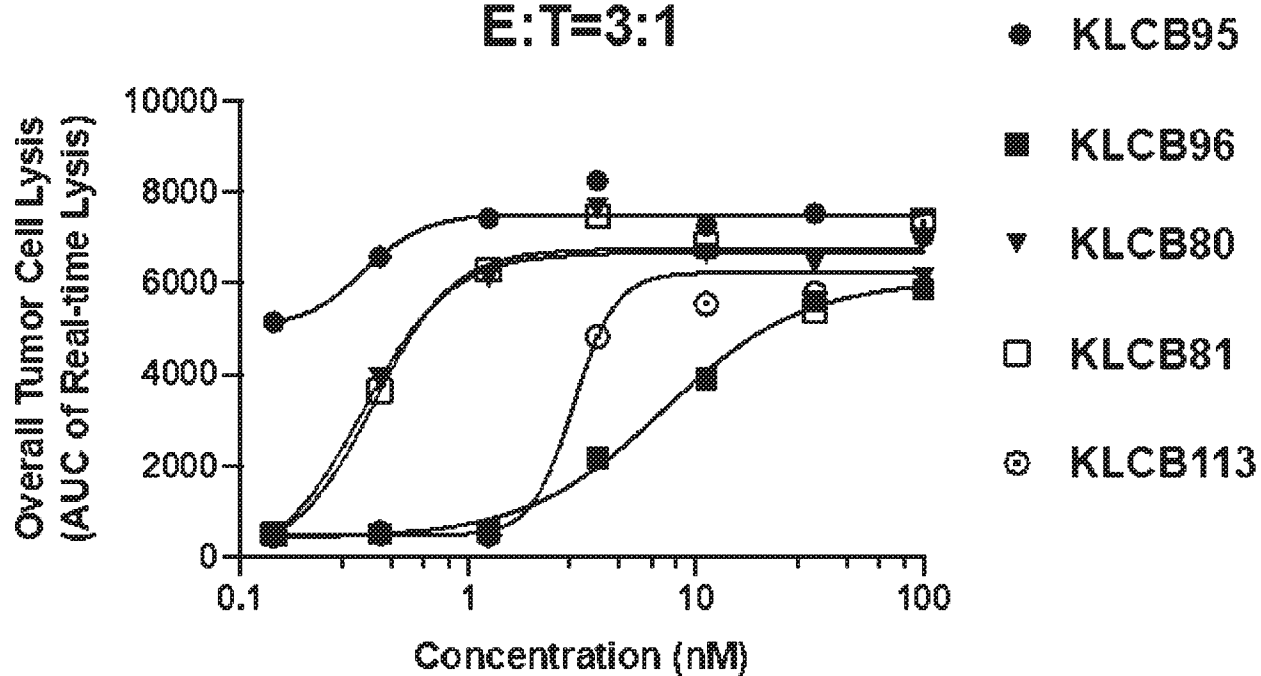
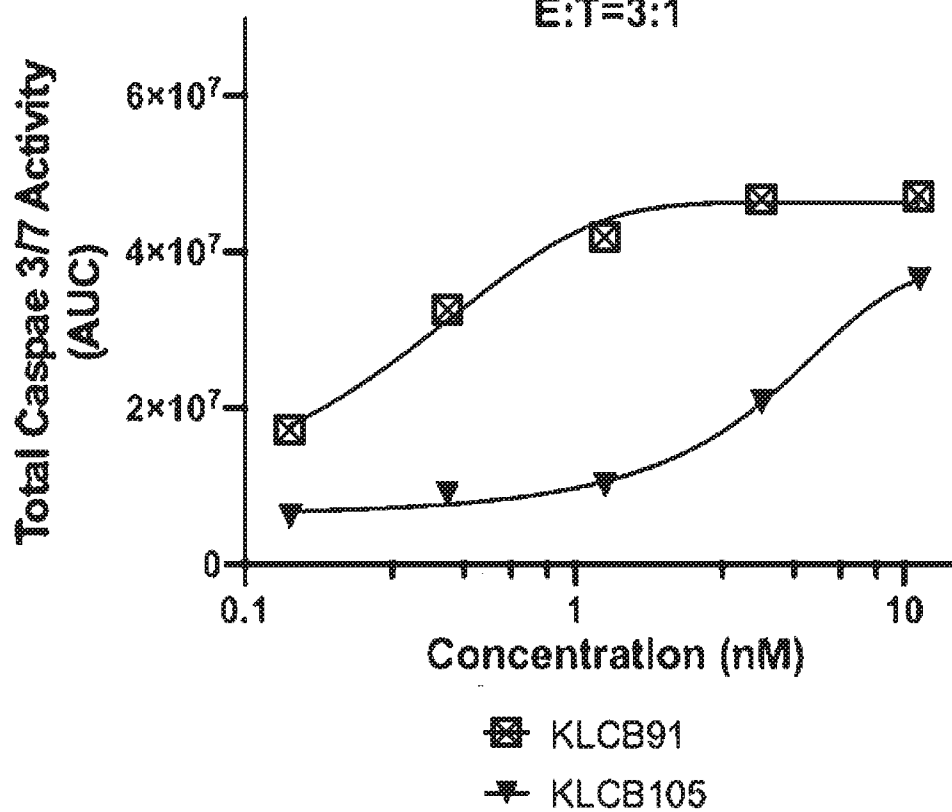


FIG. 8B

E:T=3:1



9 / 85

FIG. 9A

T Cell Activation

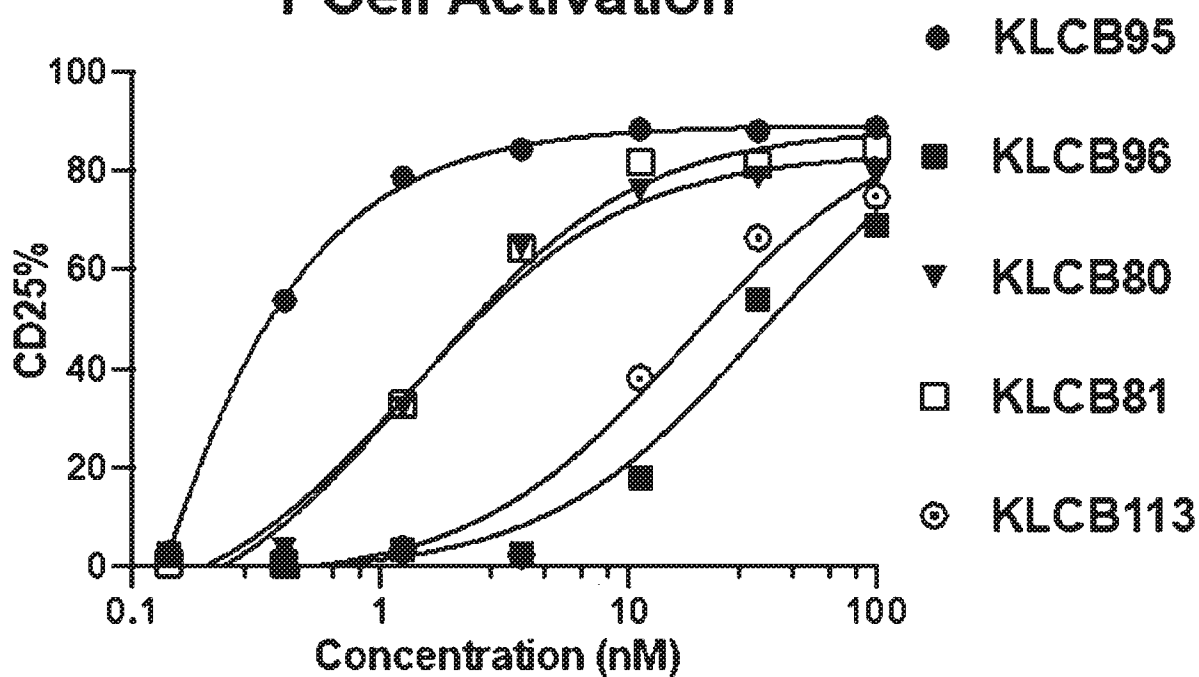
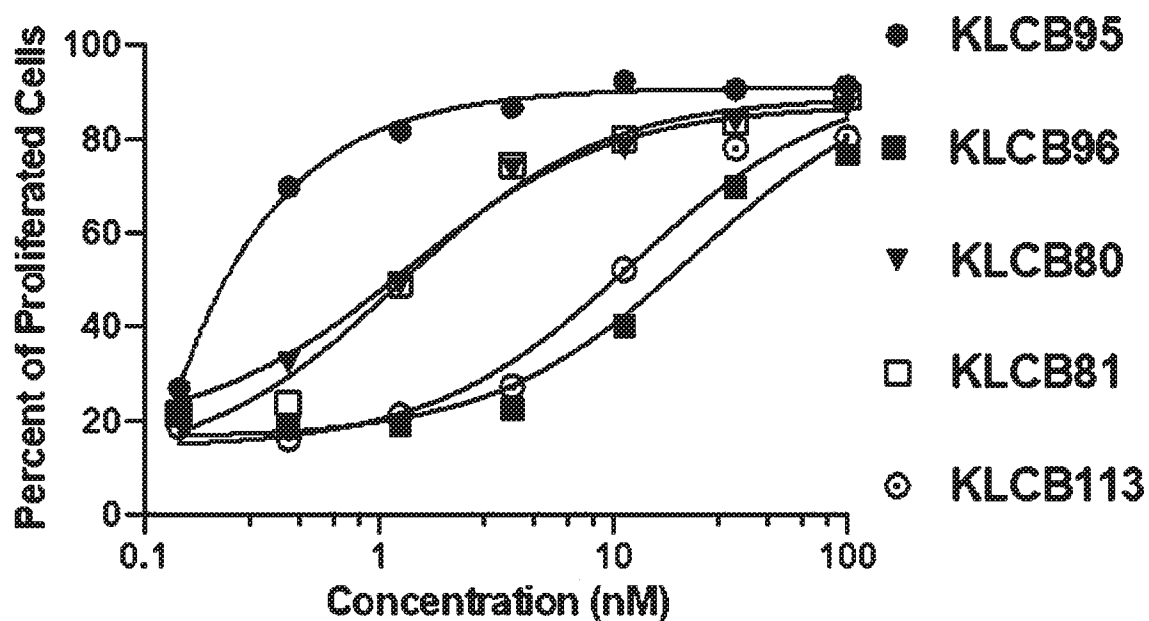


FIG. 9B

Proliferation



10 / 85

FIG. 10A
IFN- γ Release

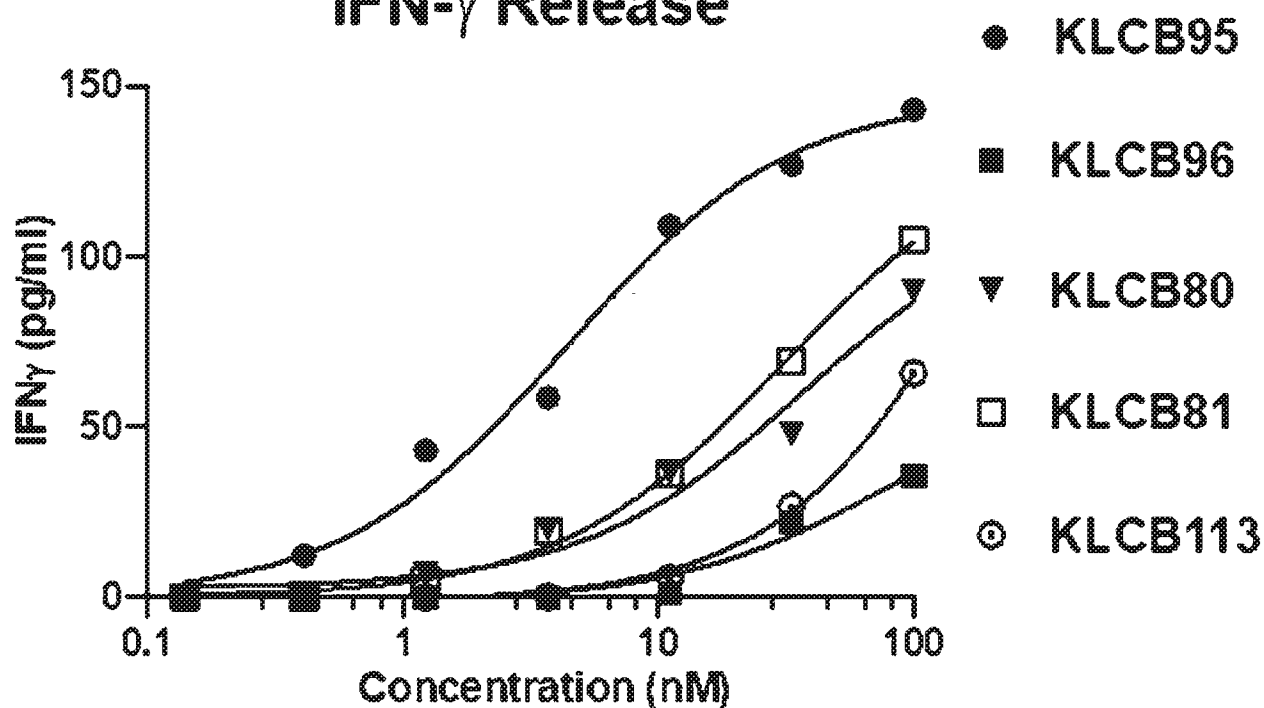
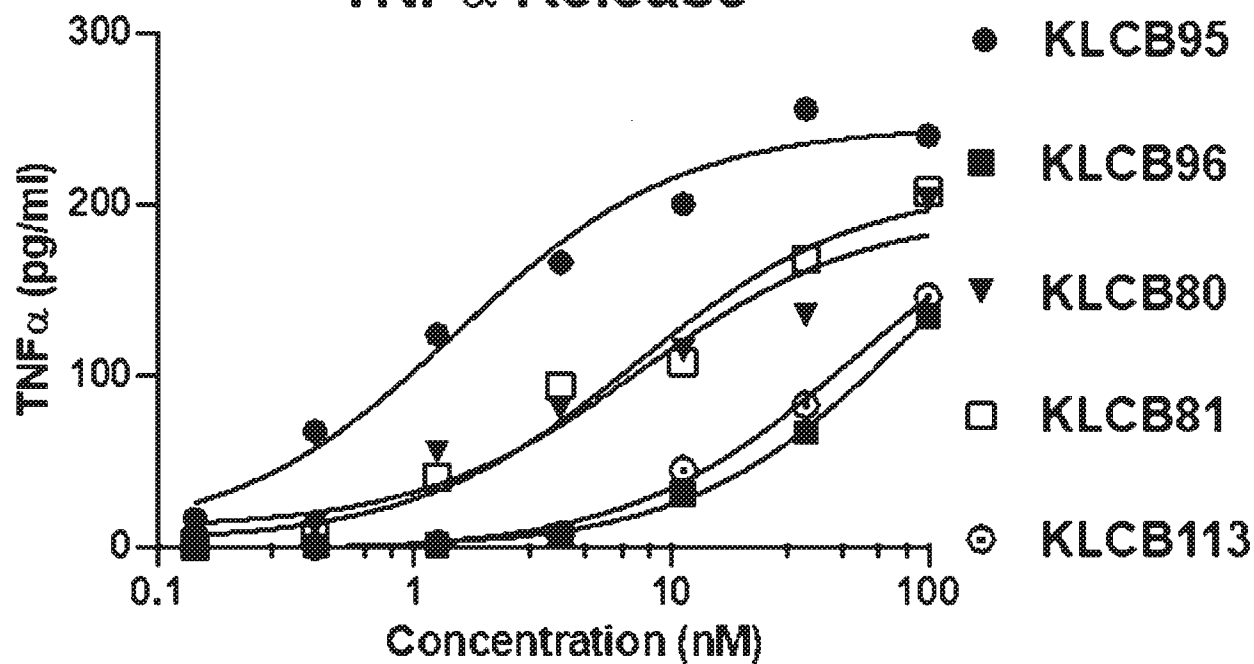


FIG. 10B
TNF α Release



11 / 85

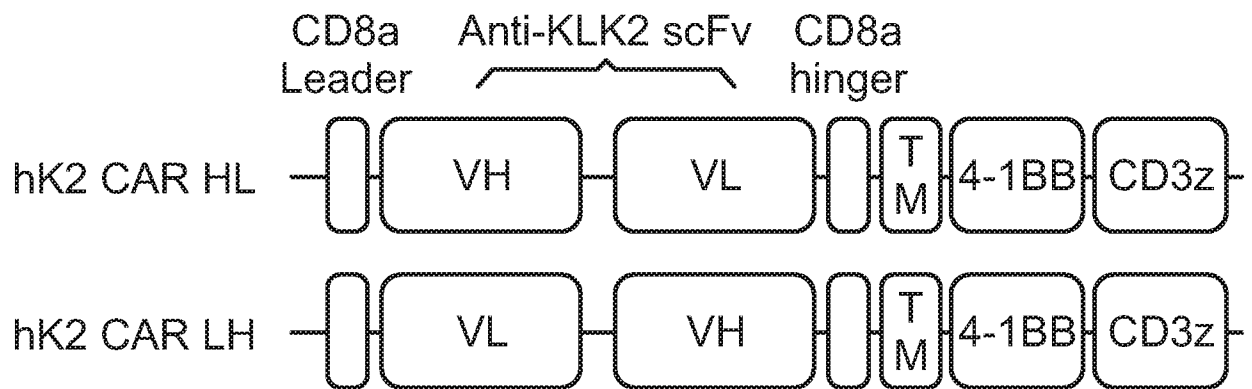
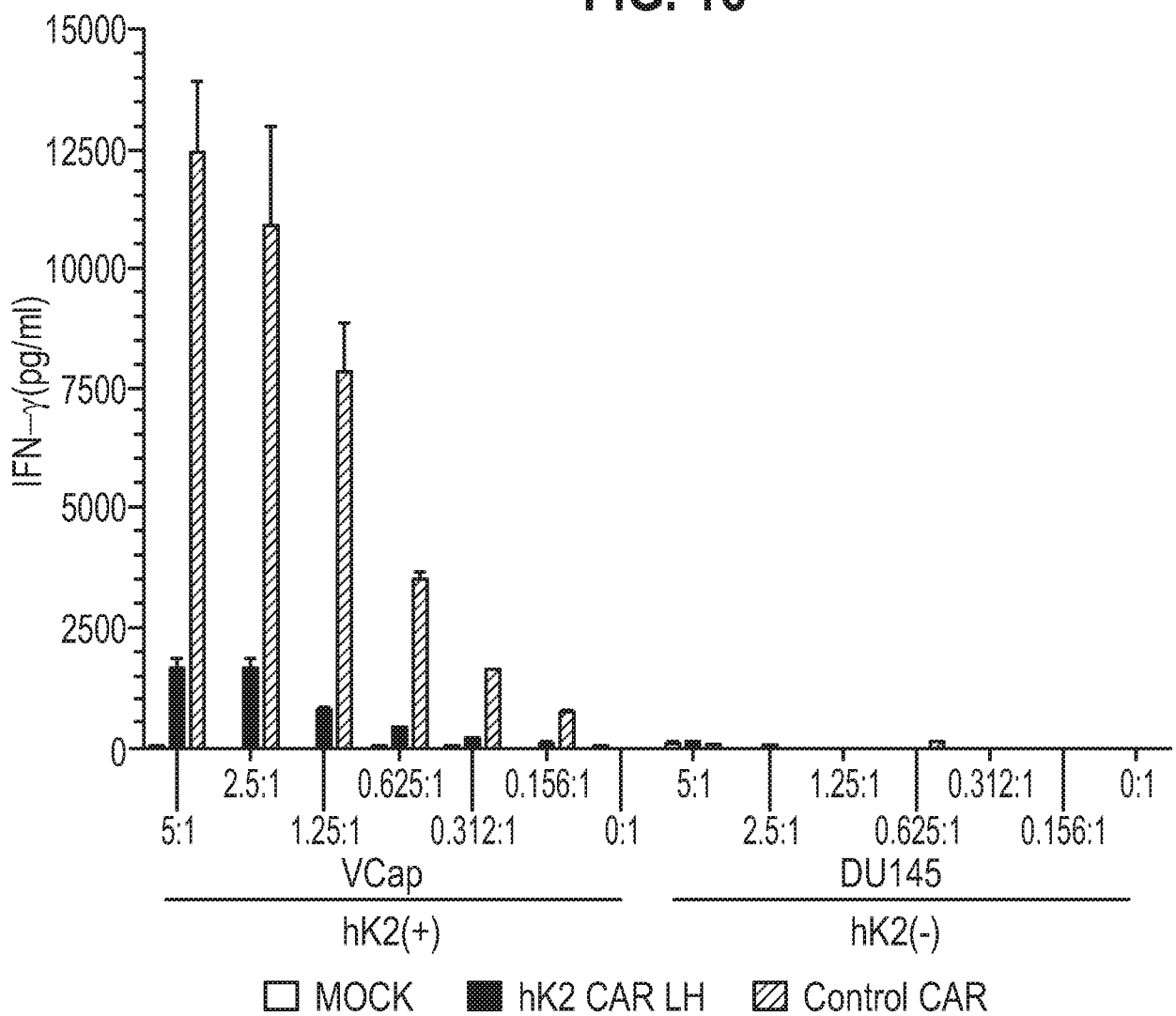
FIG. 11**FIG. 16**

FIG. 12A

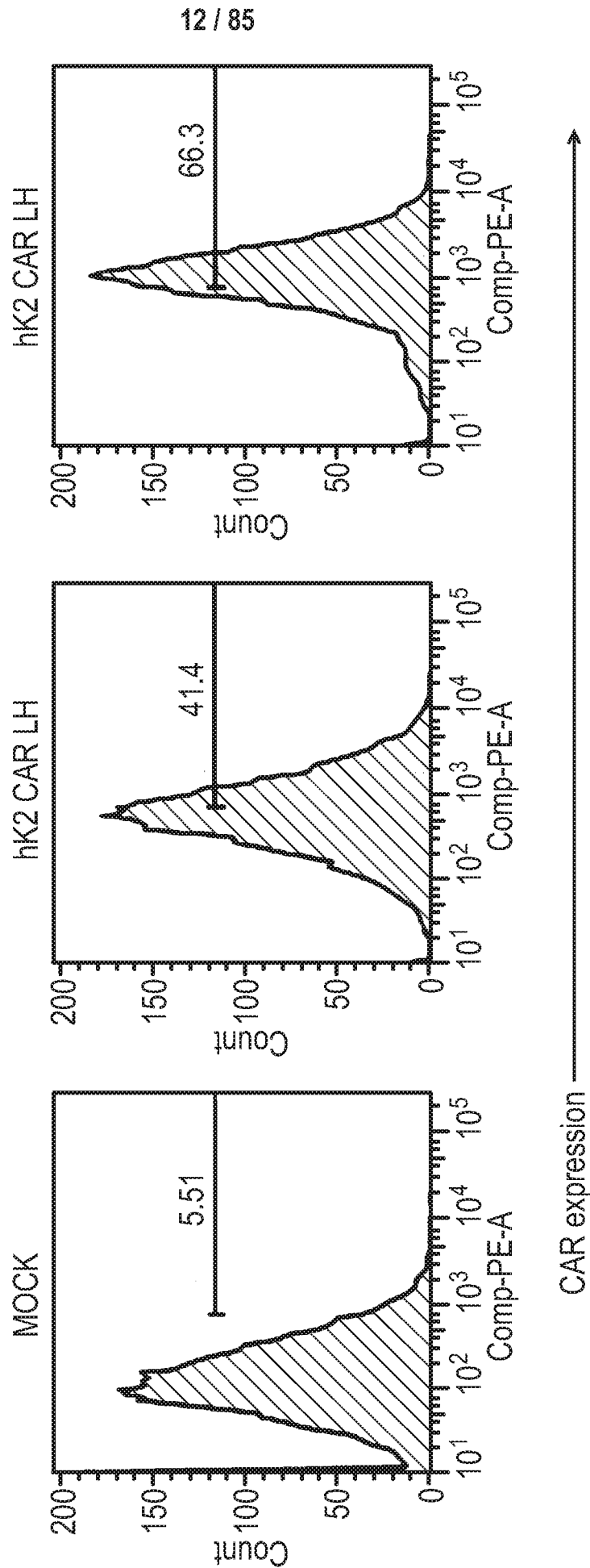
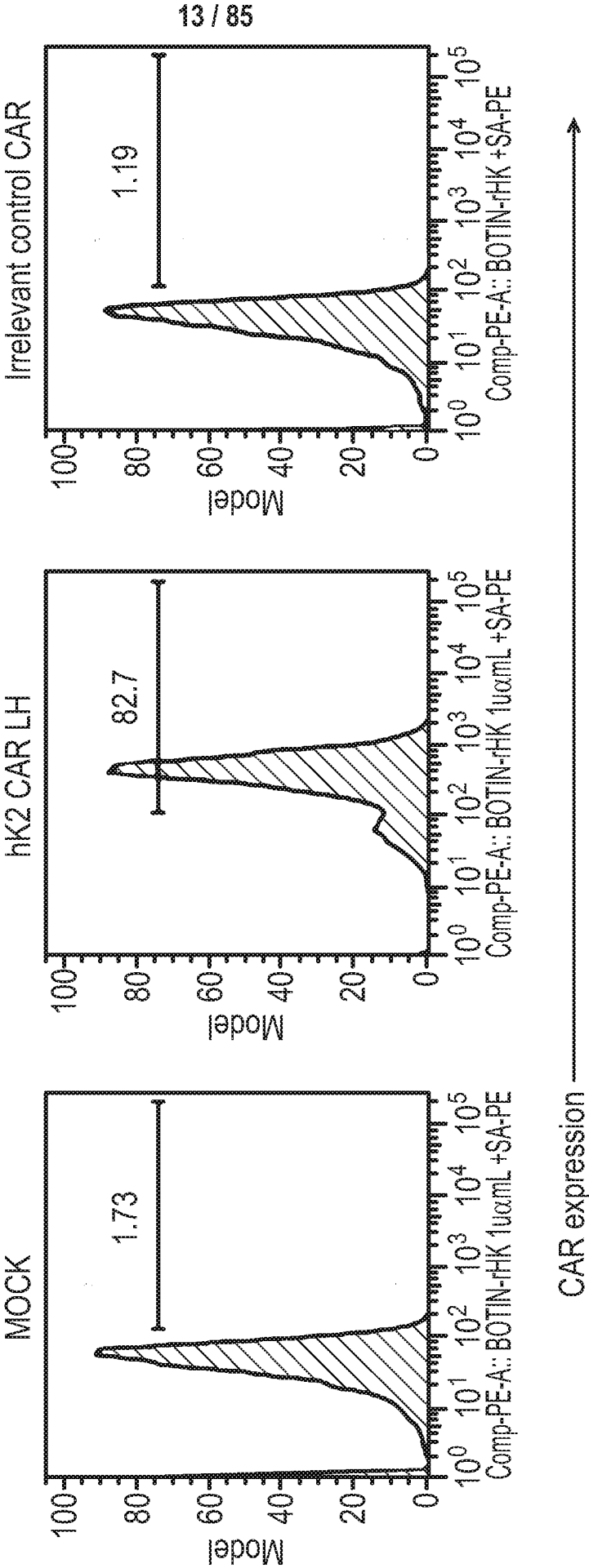
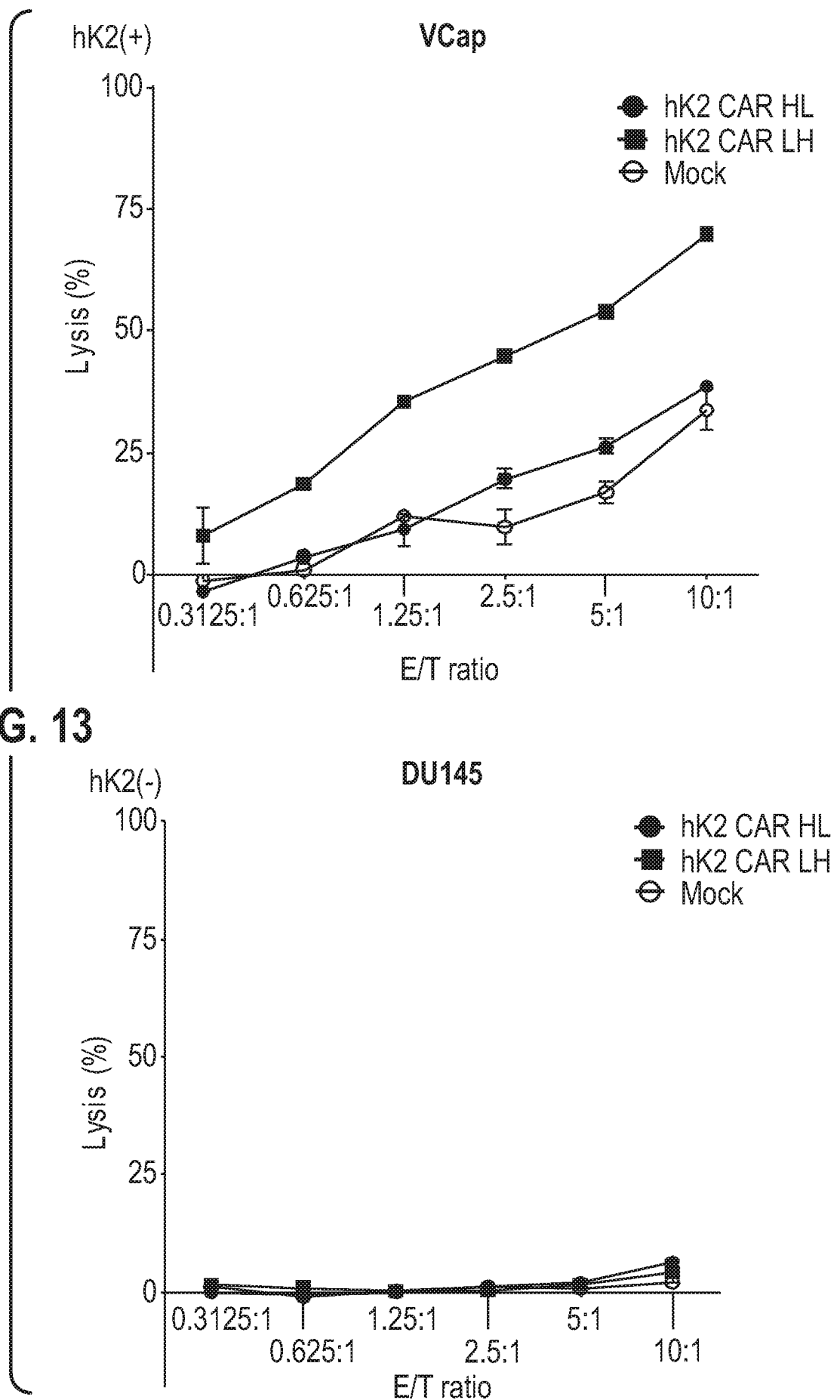


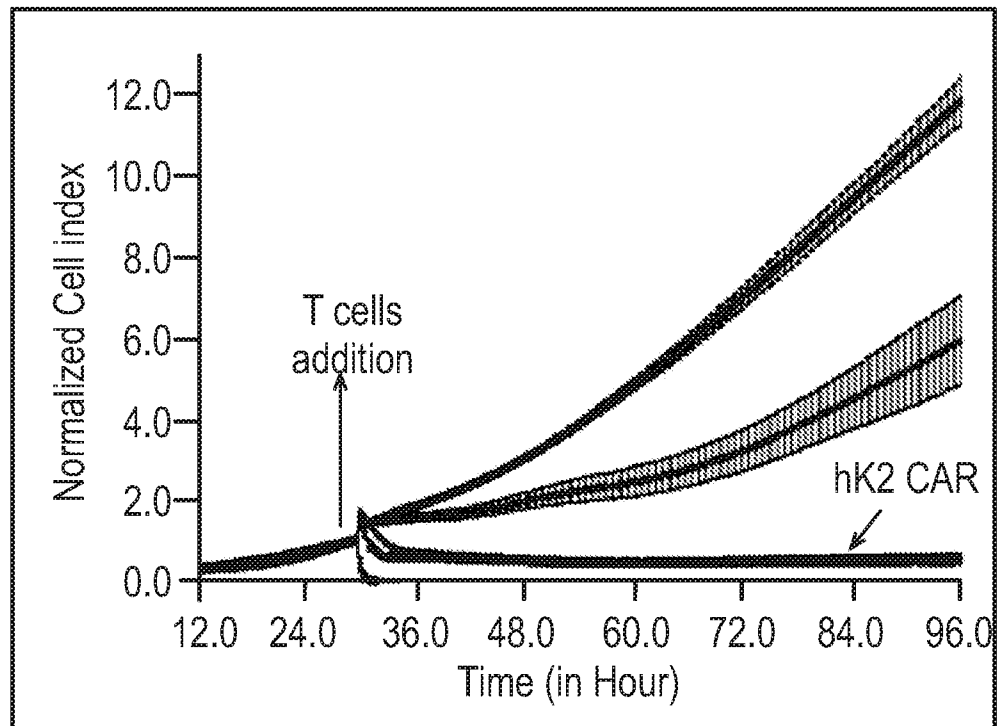
FIG. 12B



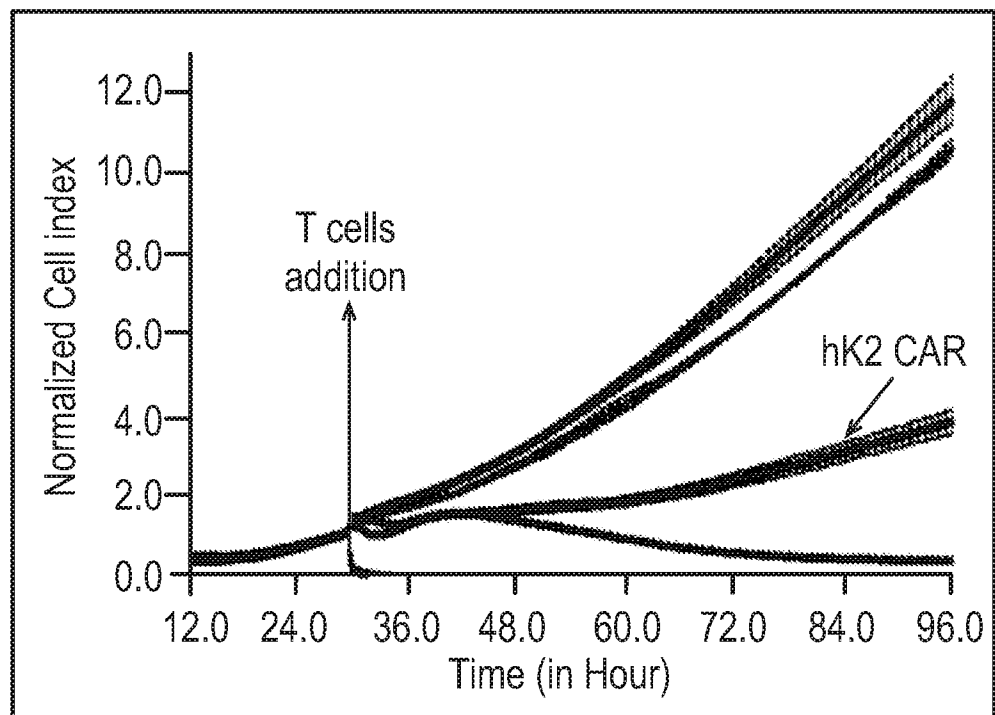
14 / 85



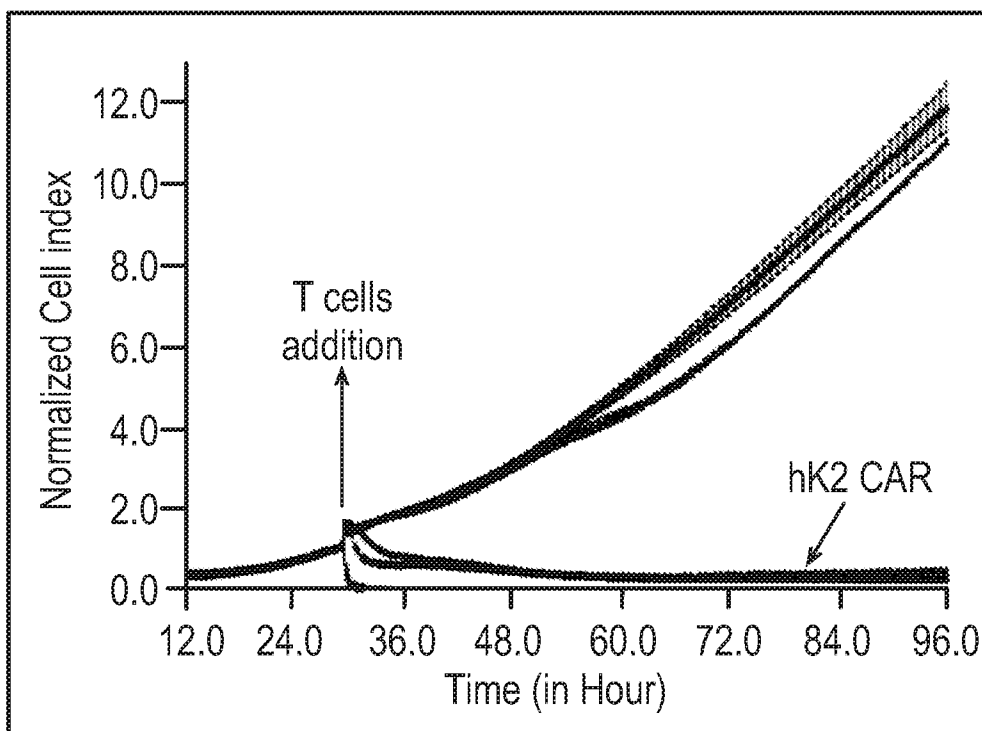
15 / 85

FIG. 14**5:1**

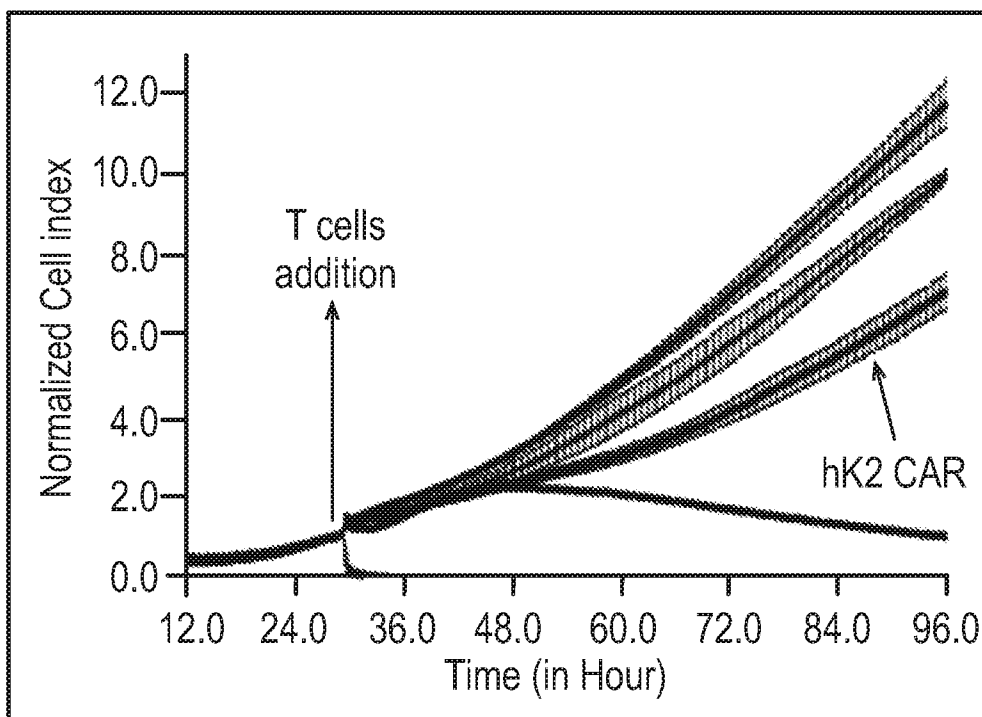
VCap

0.625:1

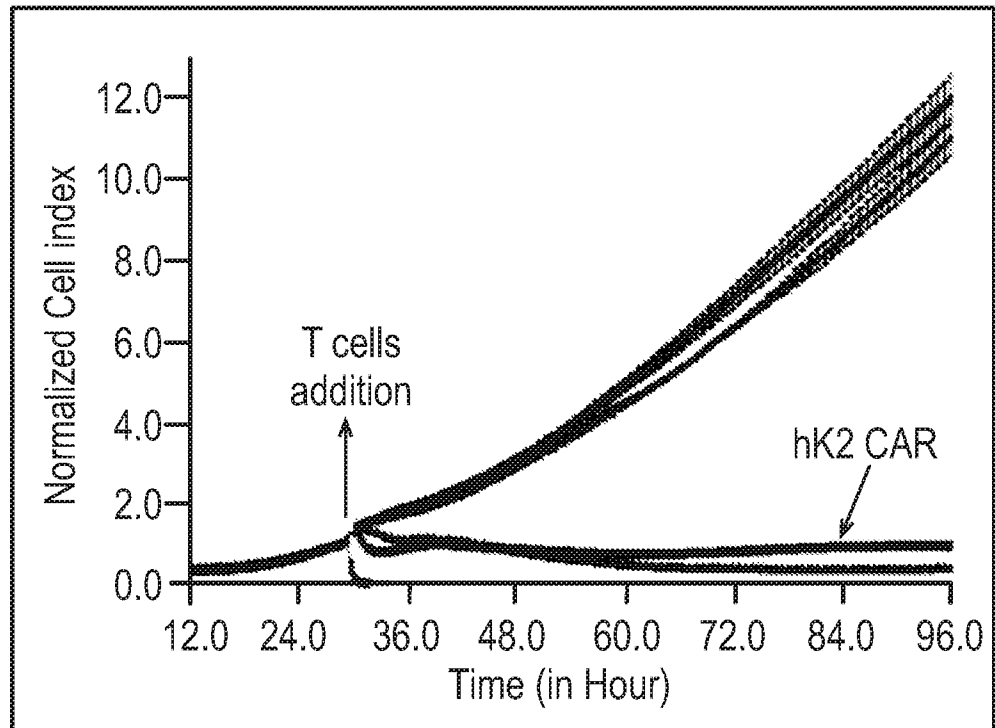
16 / 85

FIG. 14(contd)**25:1**

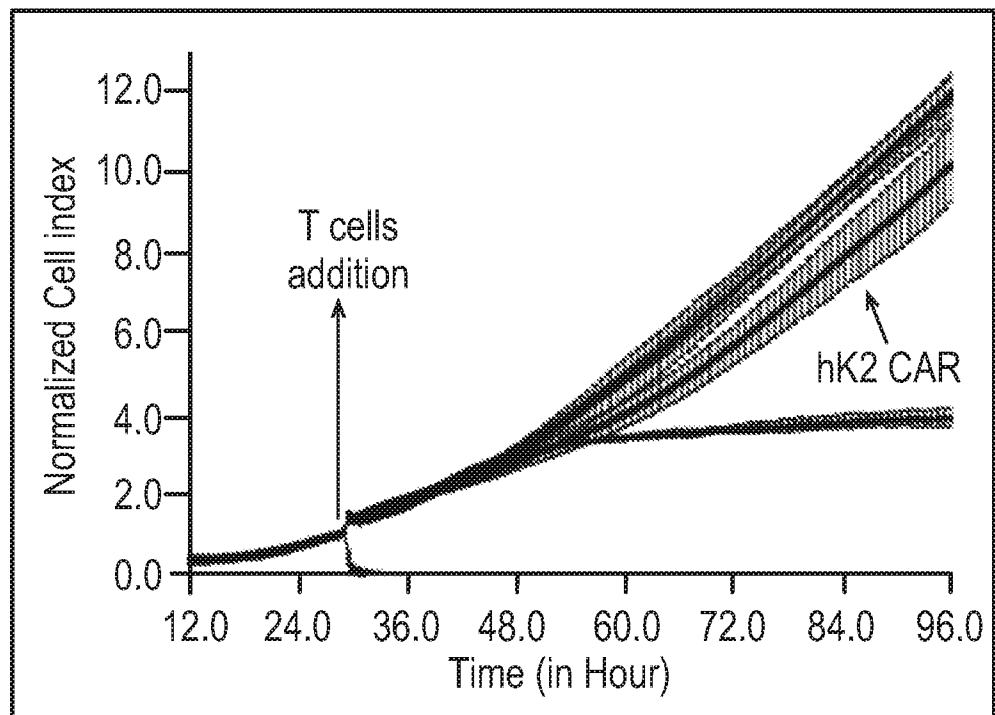
VCap

0.312:1

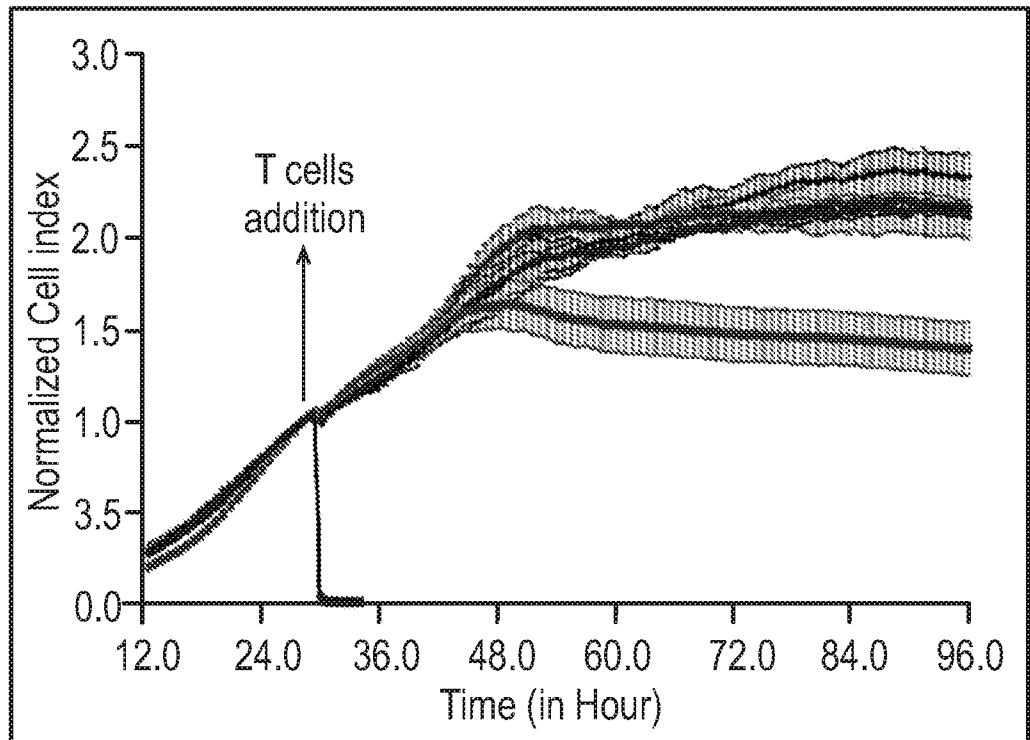
17 / 85

FIG. 14(contd)**1.25:1**

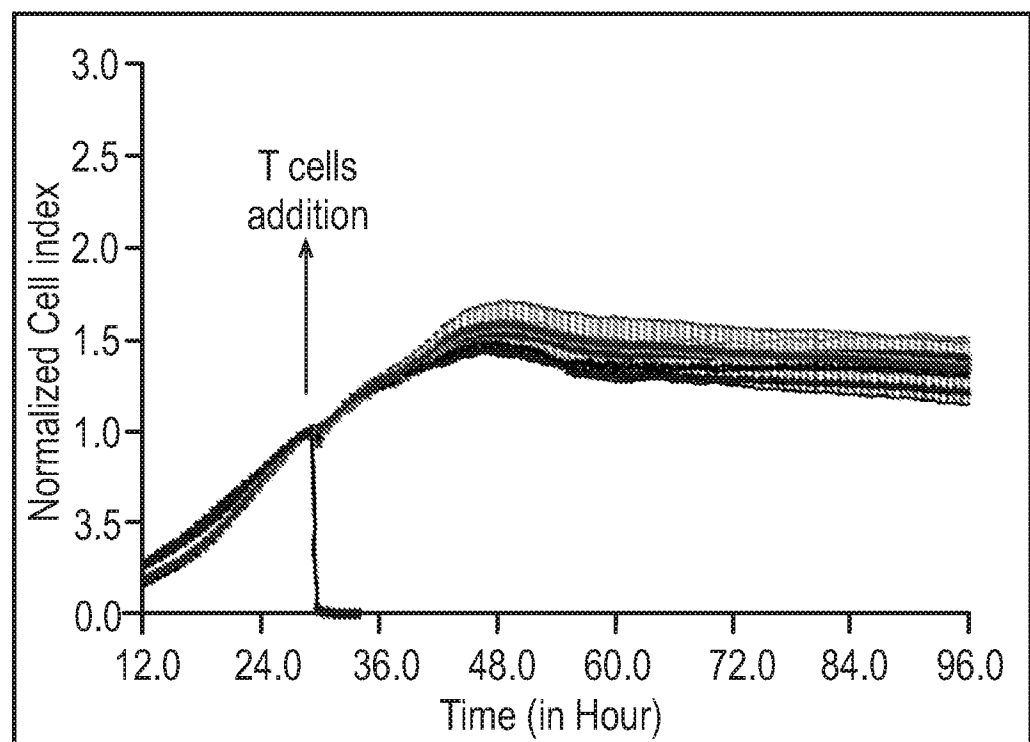
VCap

0.156:1

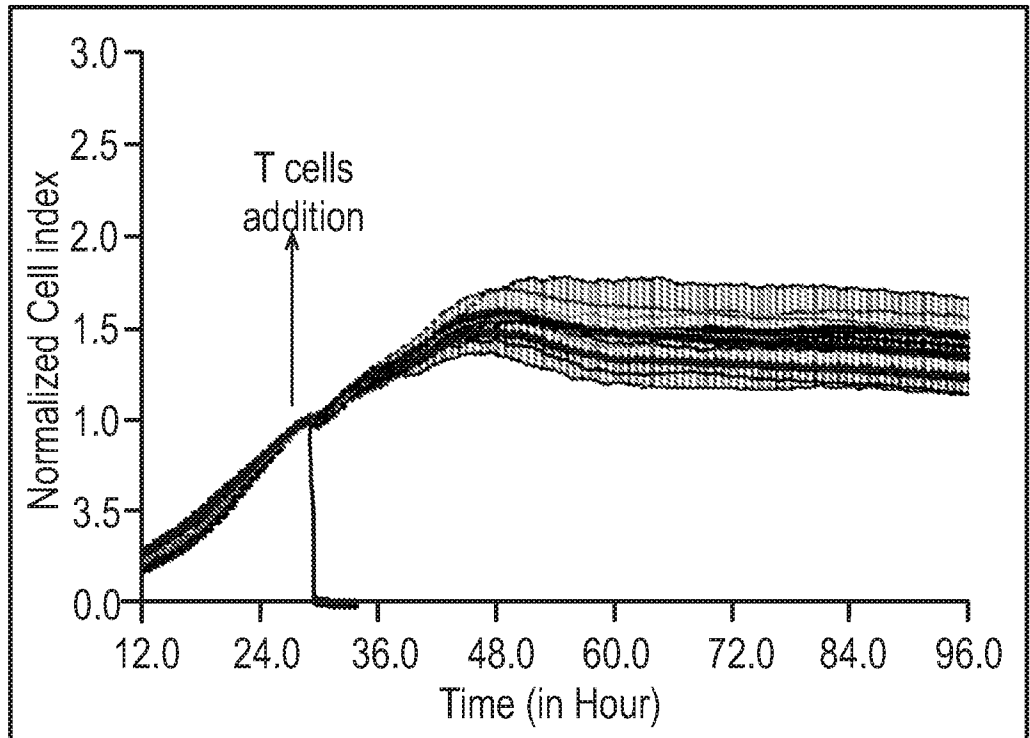
18 / 85

FIG. 15**5:1**

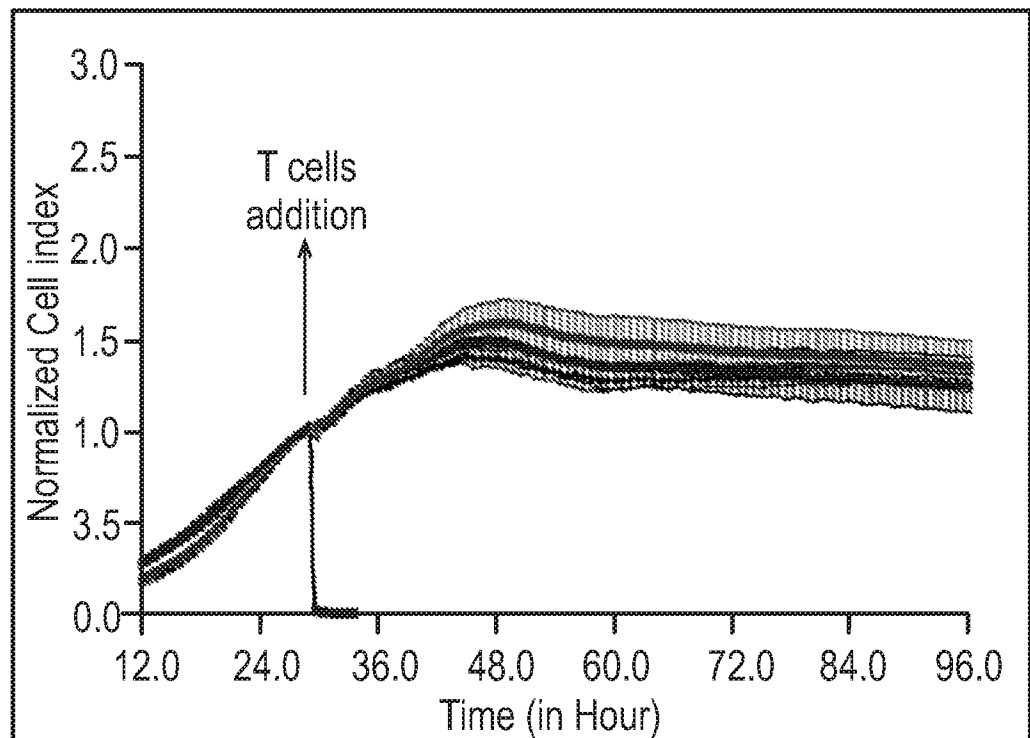
DU145

0.625:1

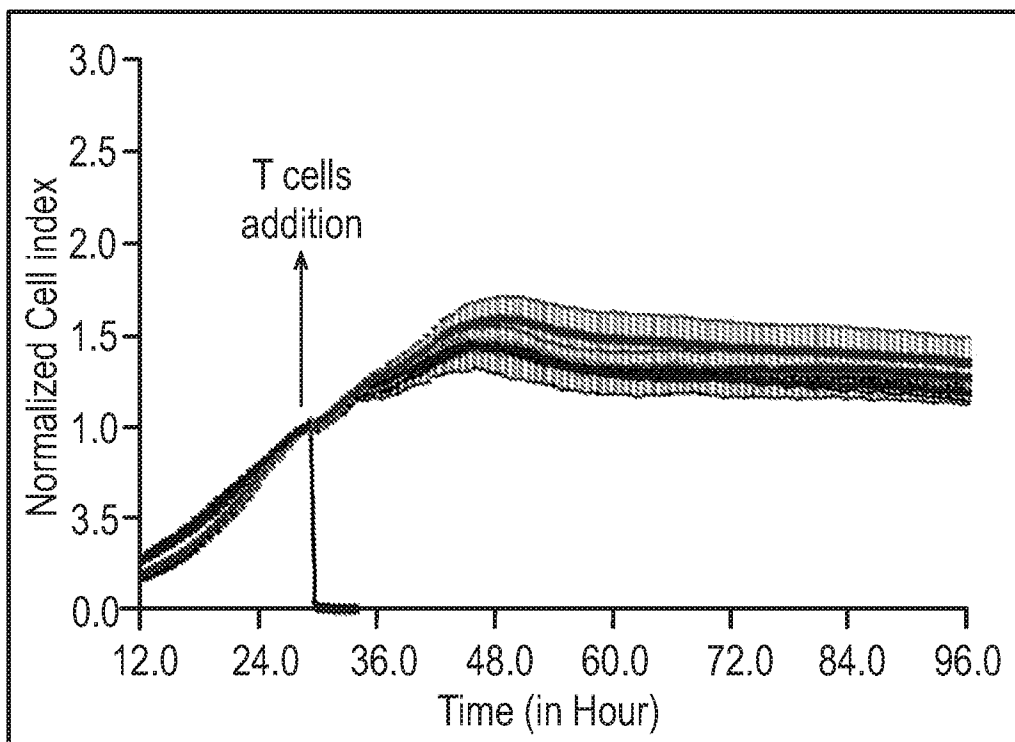
19 / 85

FIG. 15(contd)**2.5:1**

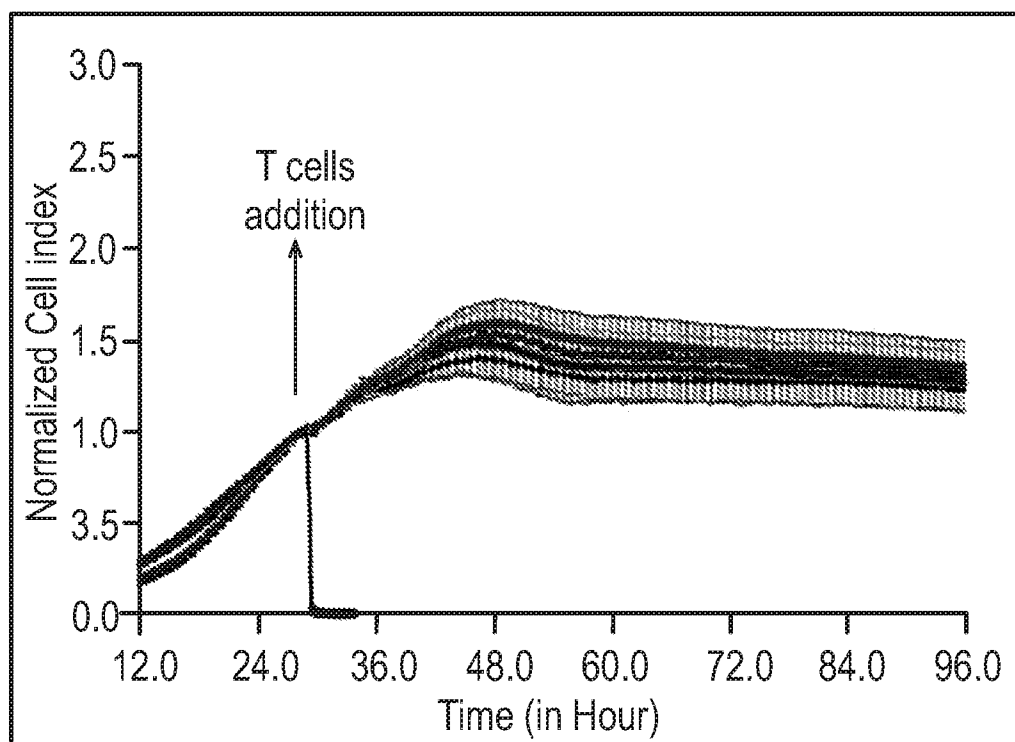
DU145

0.312:1

20 / 85

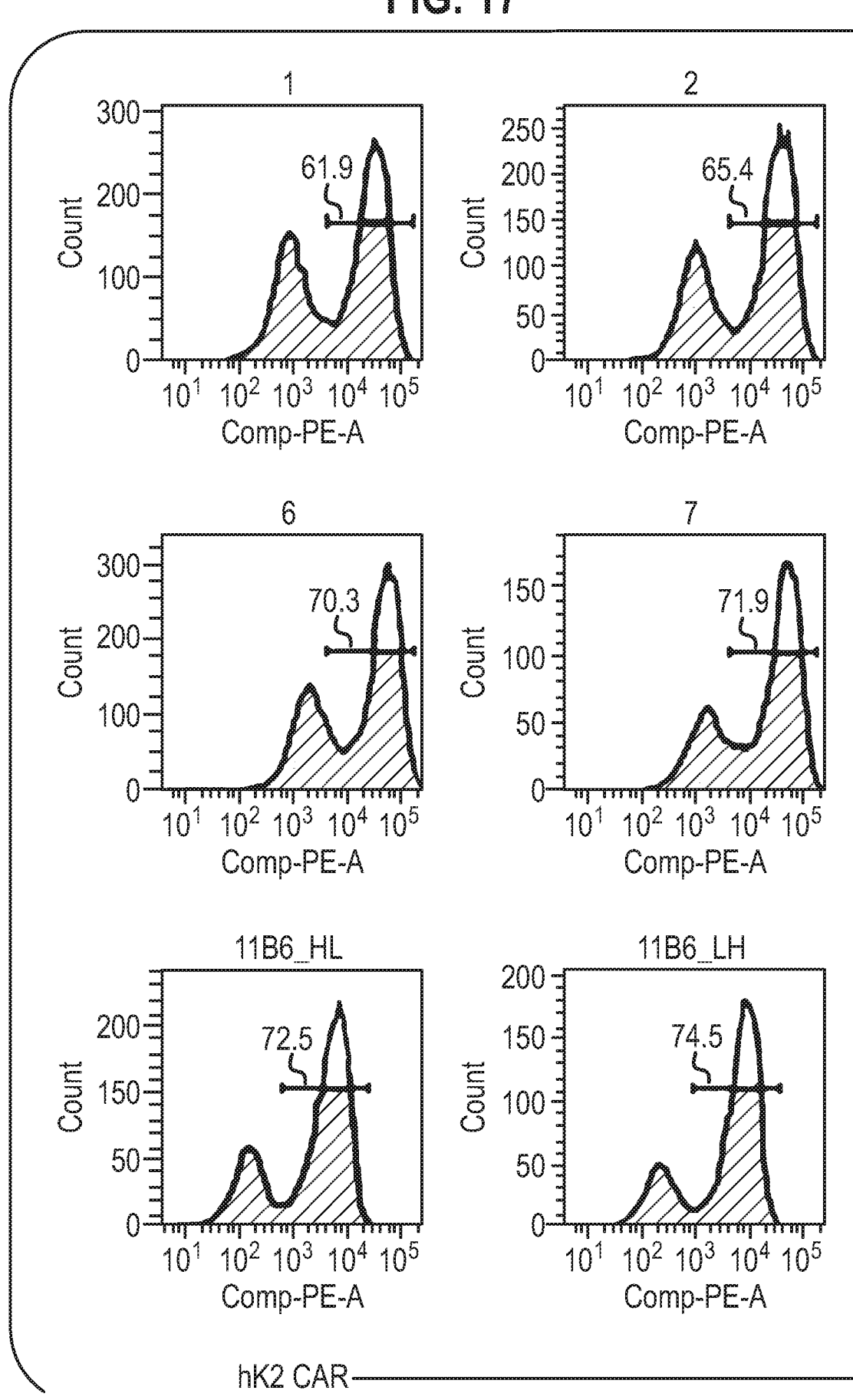
FIG. 15(contd)**1.25:1**

DU145

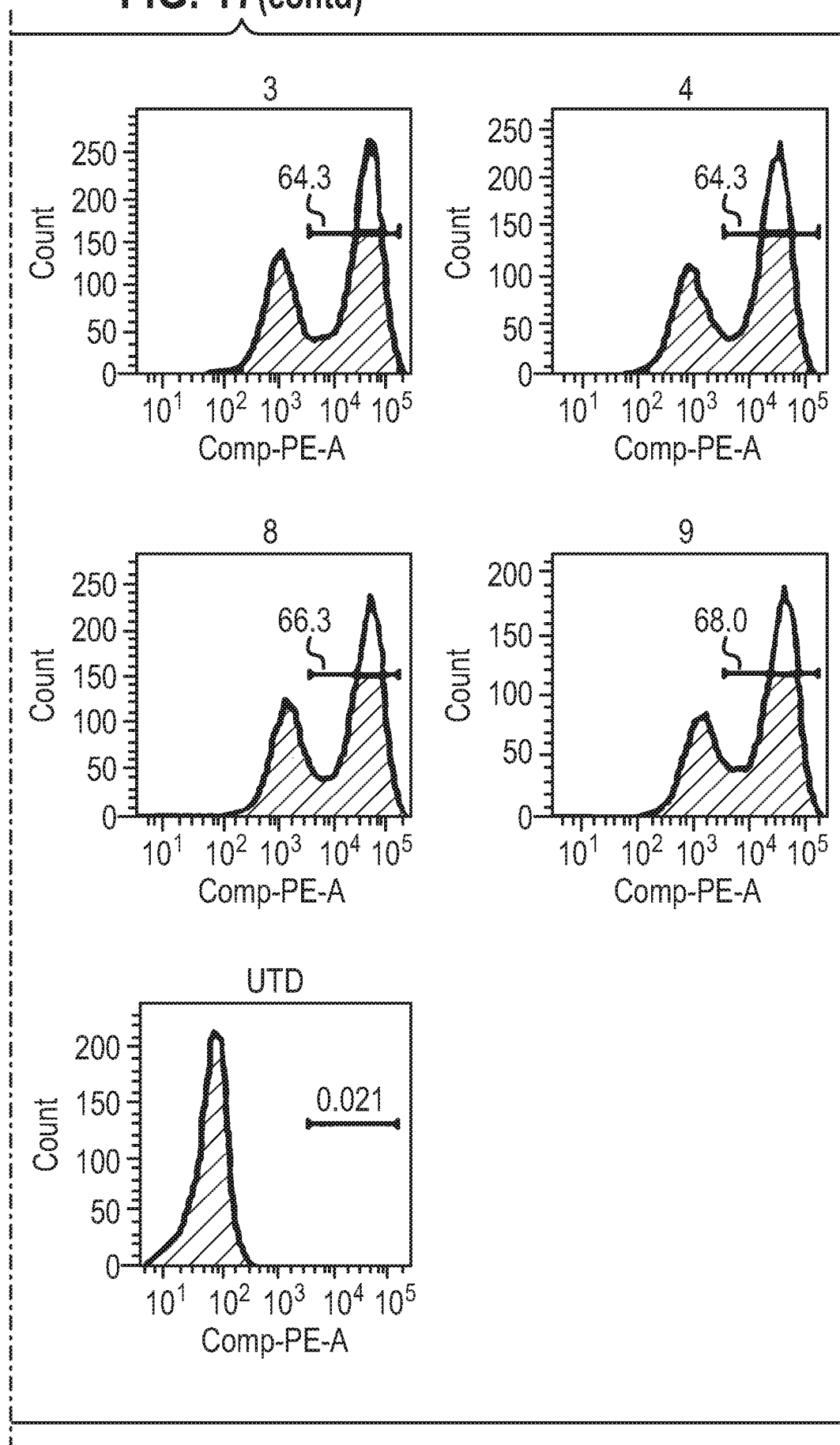
0.156:1

21 / 85

FIG. 17



22 / 85

FIG. 17(contd)

23 / 85

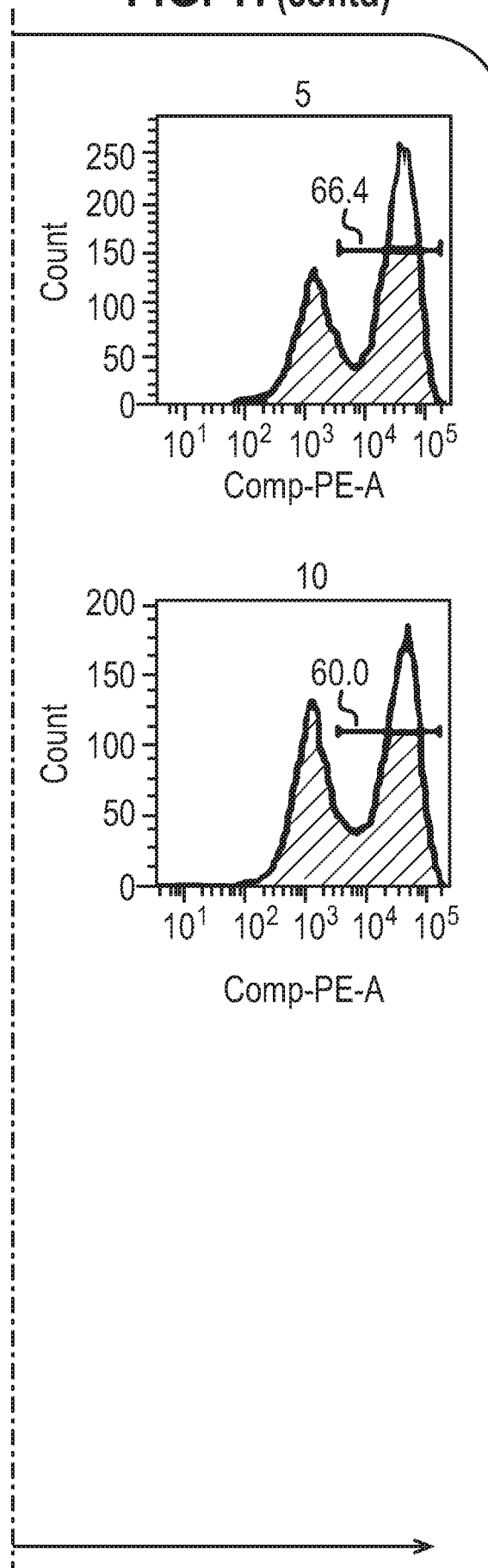
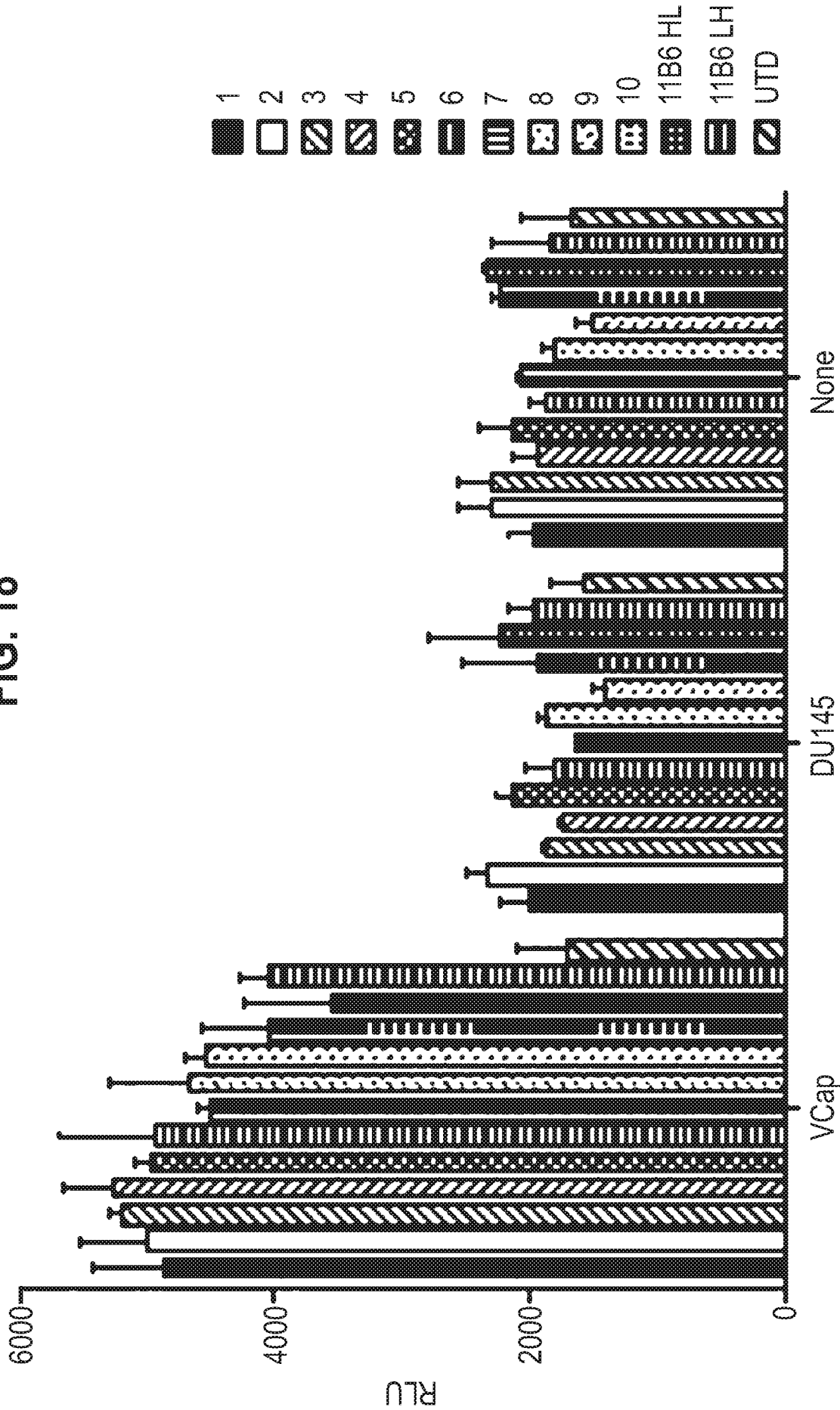
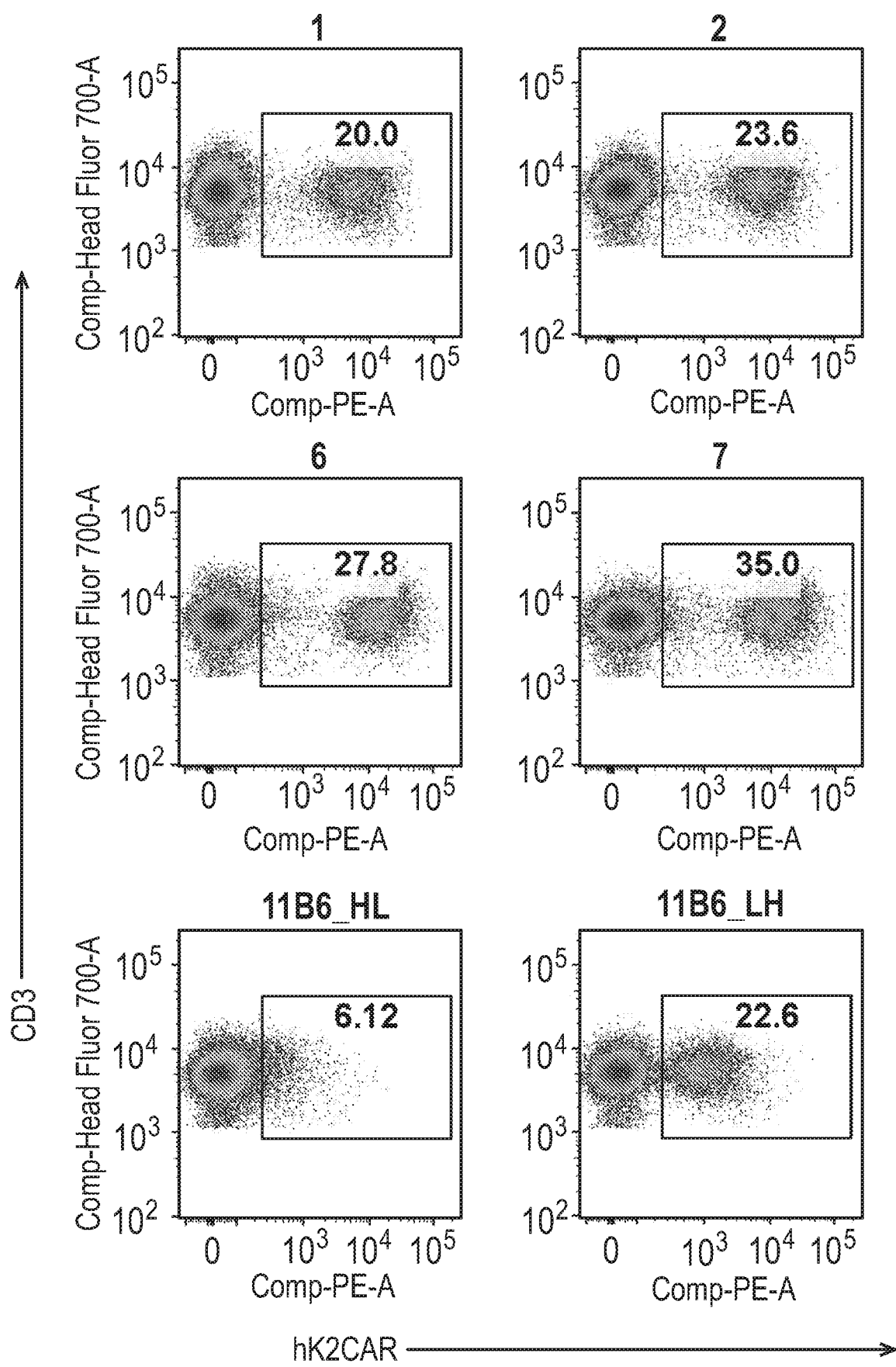
FIG. 17(contd)

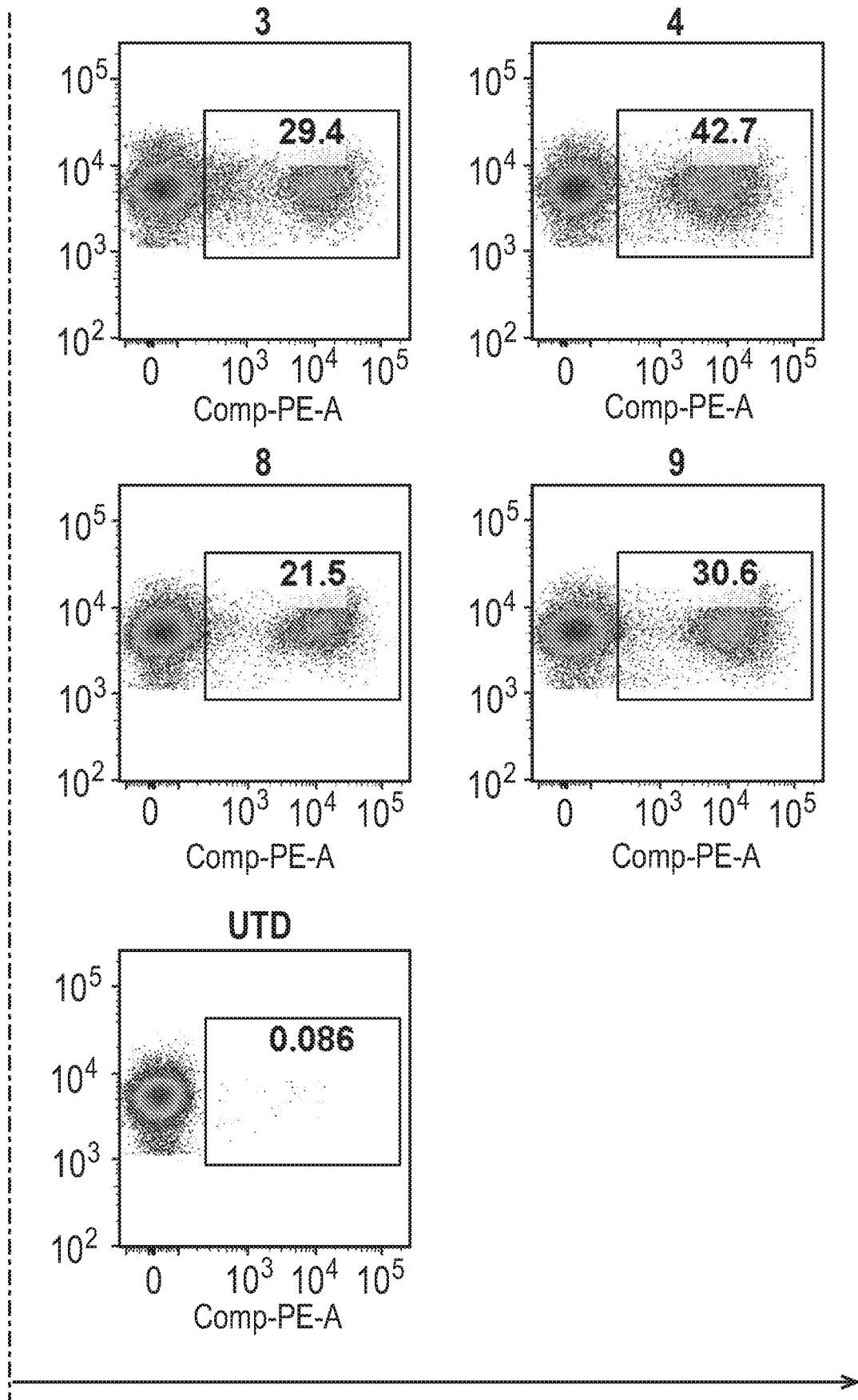
FIG. 18



25 / 85

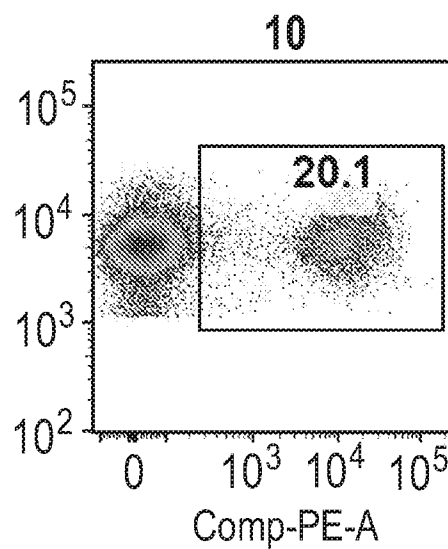
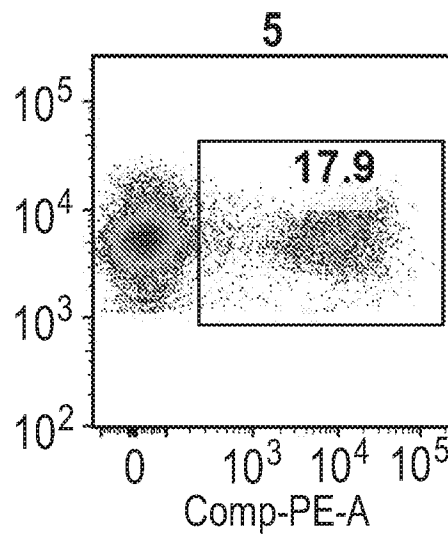
FIG. 19

26 / 85

FIG. 19(contd)

27 / 85

FIG. 19(contd)



→ hK2CAR

28 / 85

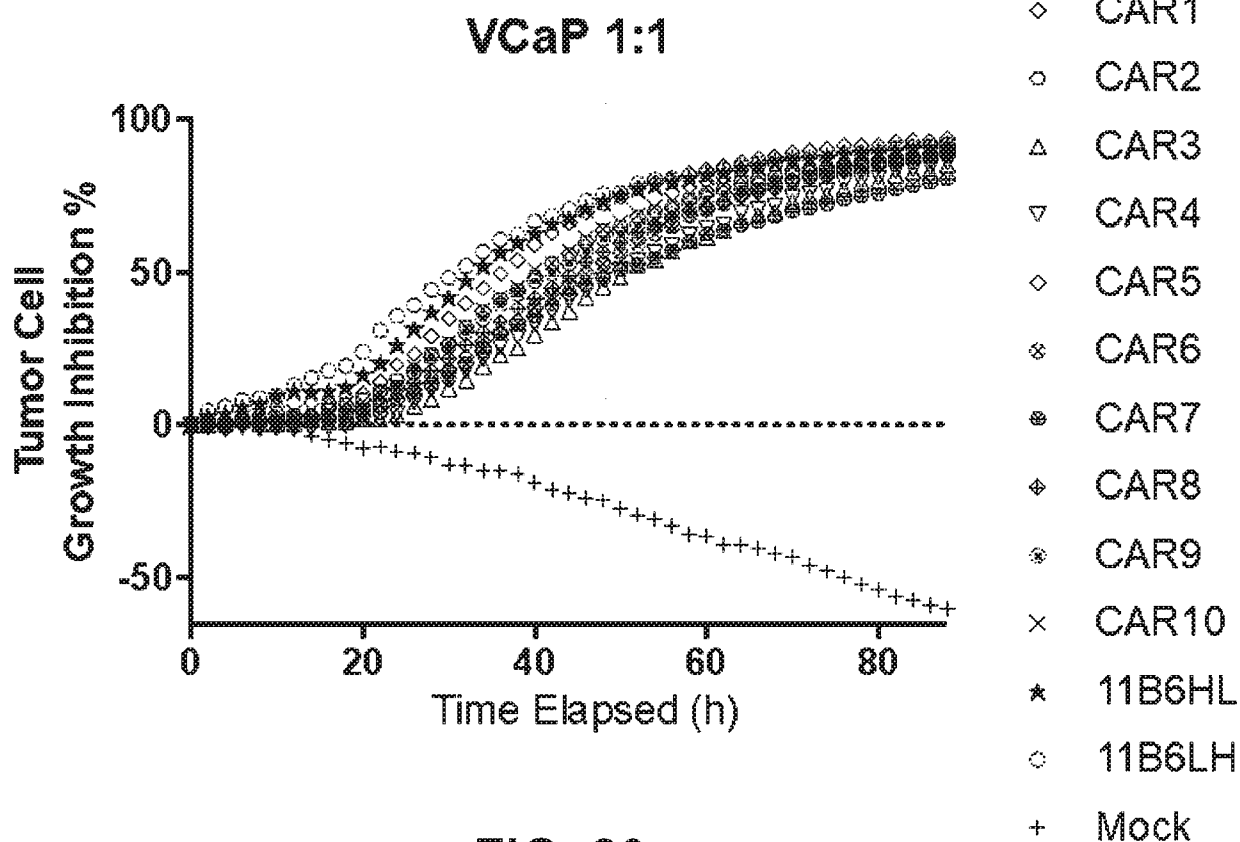
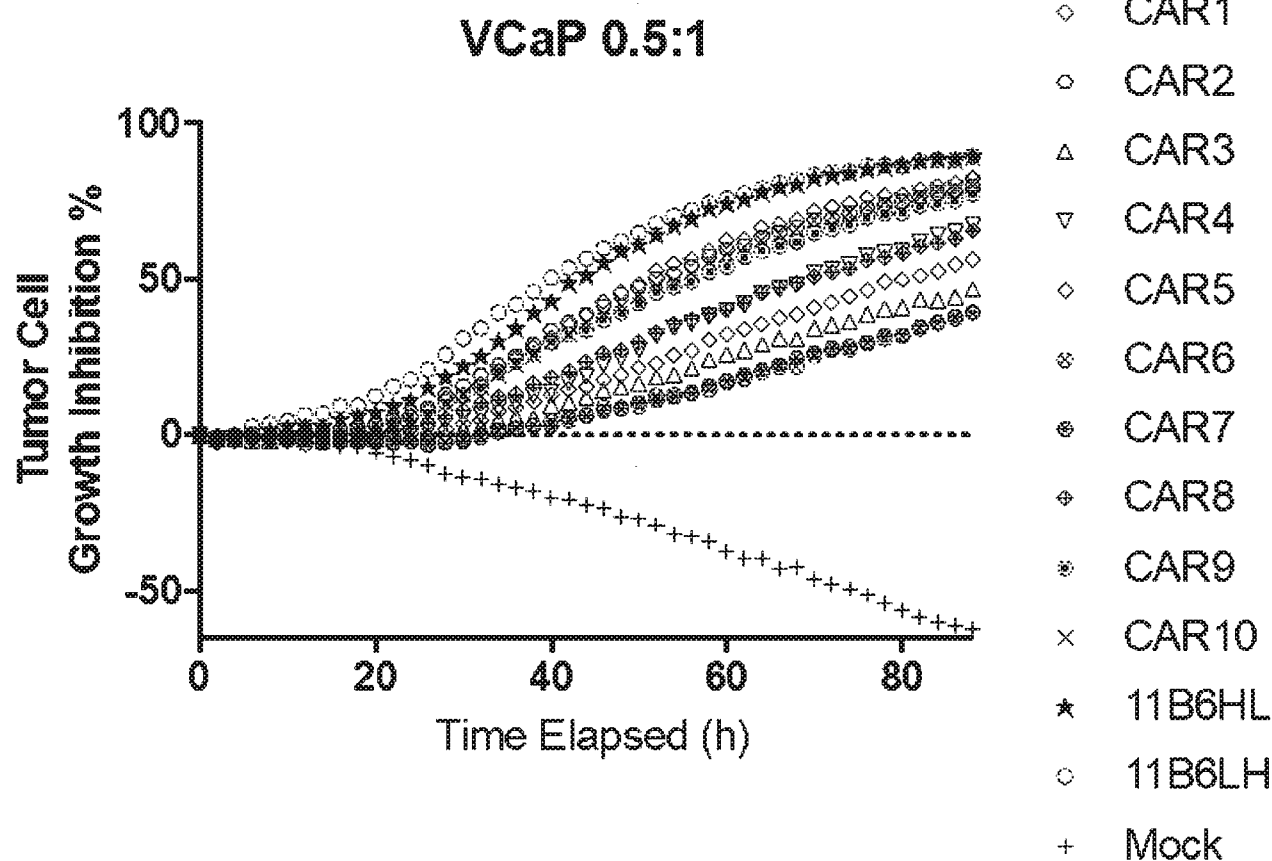


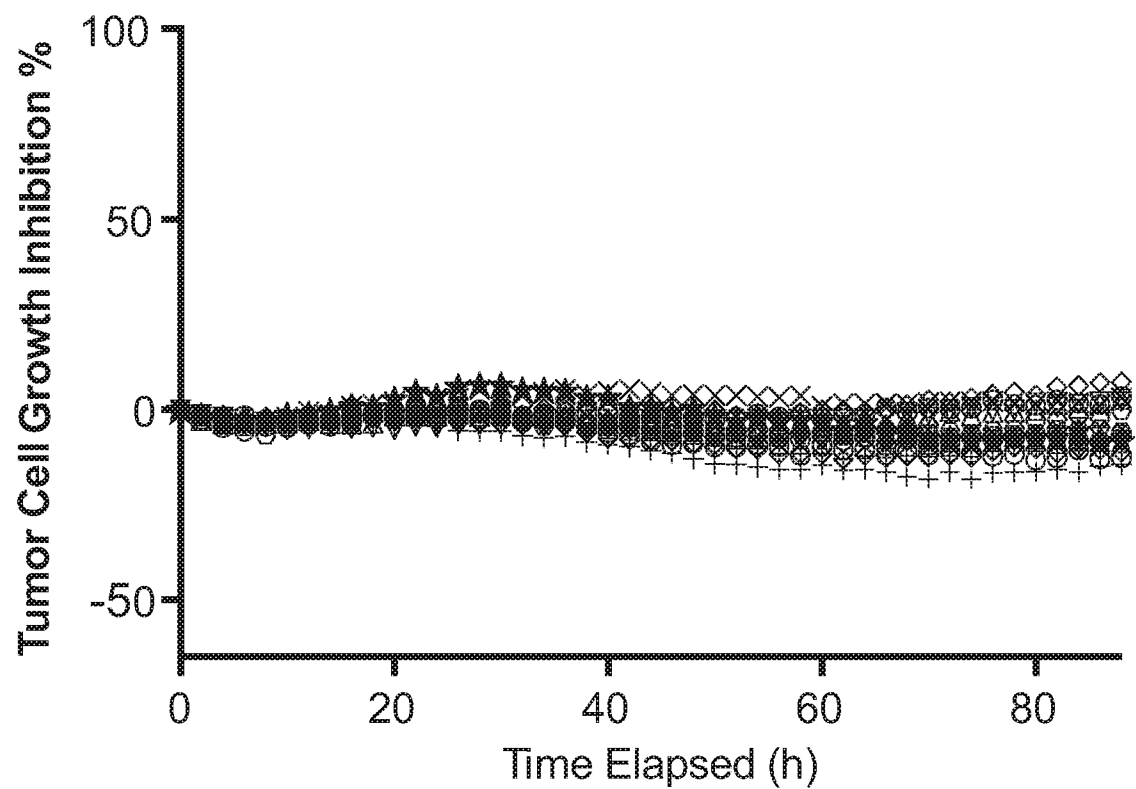
FIG. 20



29 / 85

FIG. 21

PC3 1:1



- | | | | |
|---|------|---|--------|
| ◇ | CAR1 | ⊕ | CAR8 |
| ○ | CAR2 | ⊗ | CAR9 |
| △ | CAR3 | × | CAR10 |
| ▽ | CAR4 | ★ | 11B6HL |
| ◇ | CAR5 | ○ | 11B6LH |
| ⊗ | CAR6 | + | Mock |
| ⊕ | CAR7 | | |

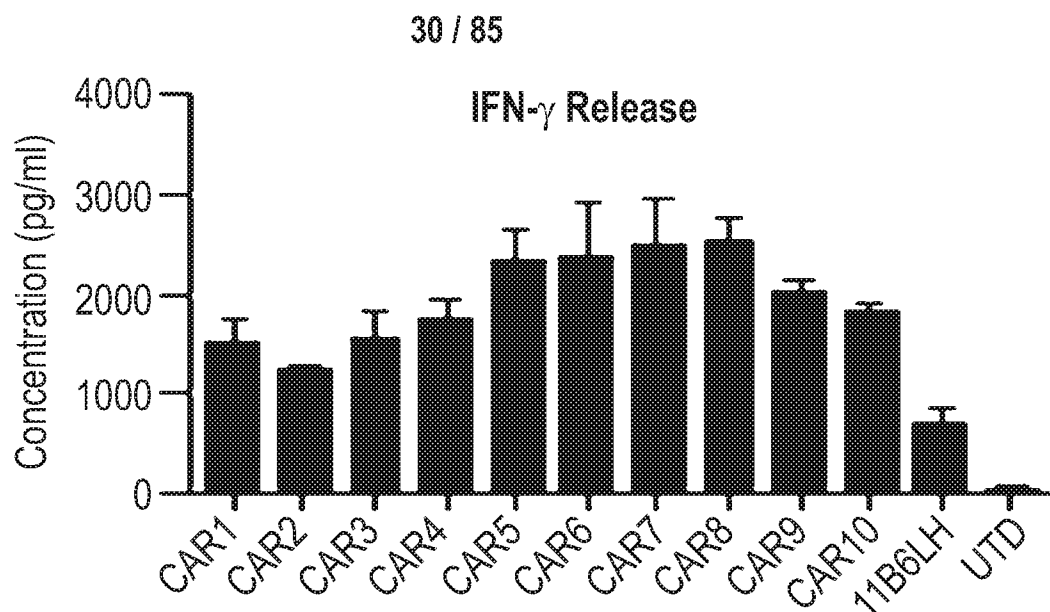
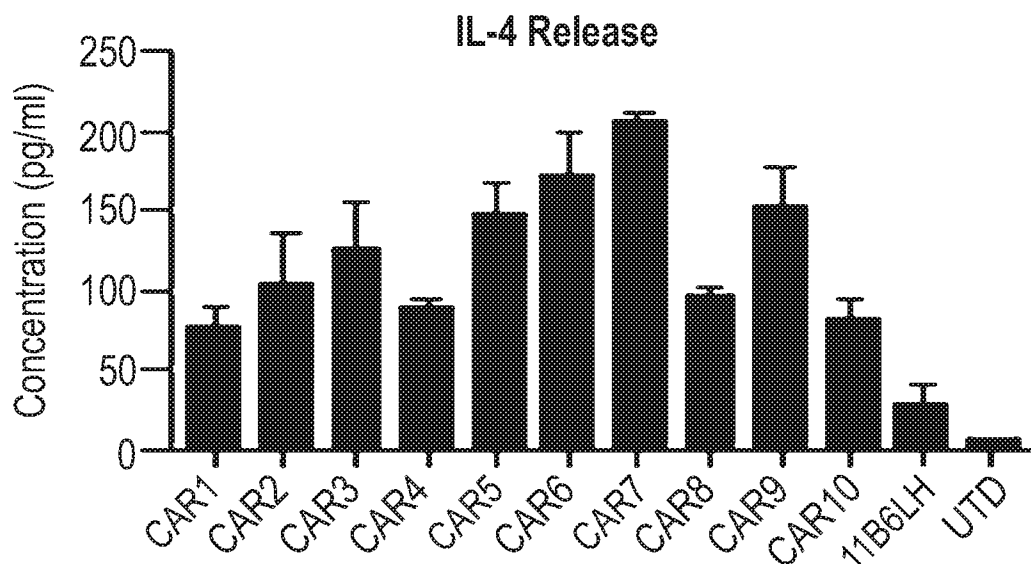
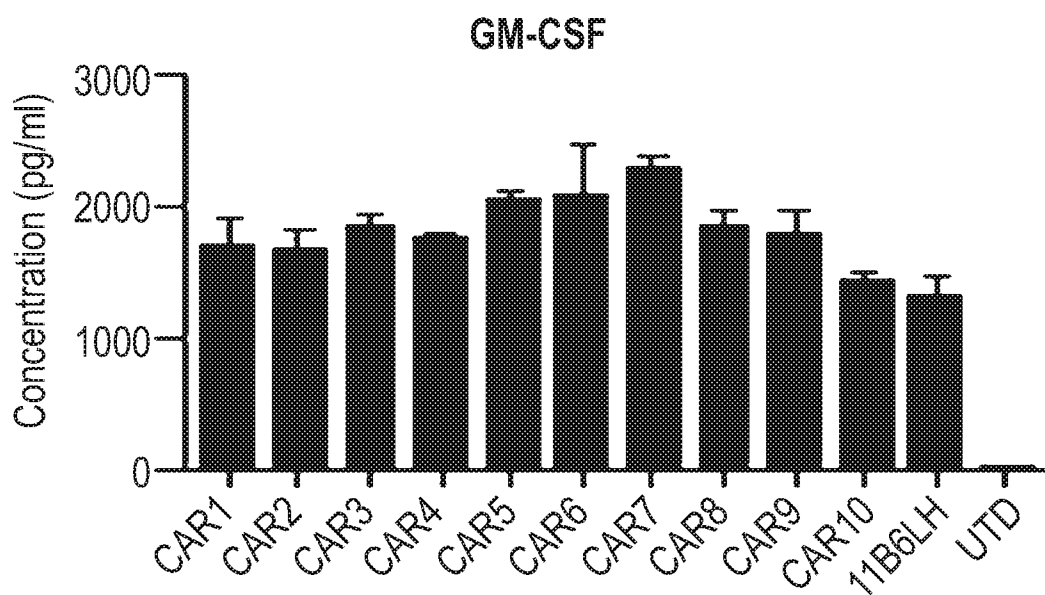


FIG. 22



31 / 85

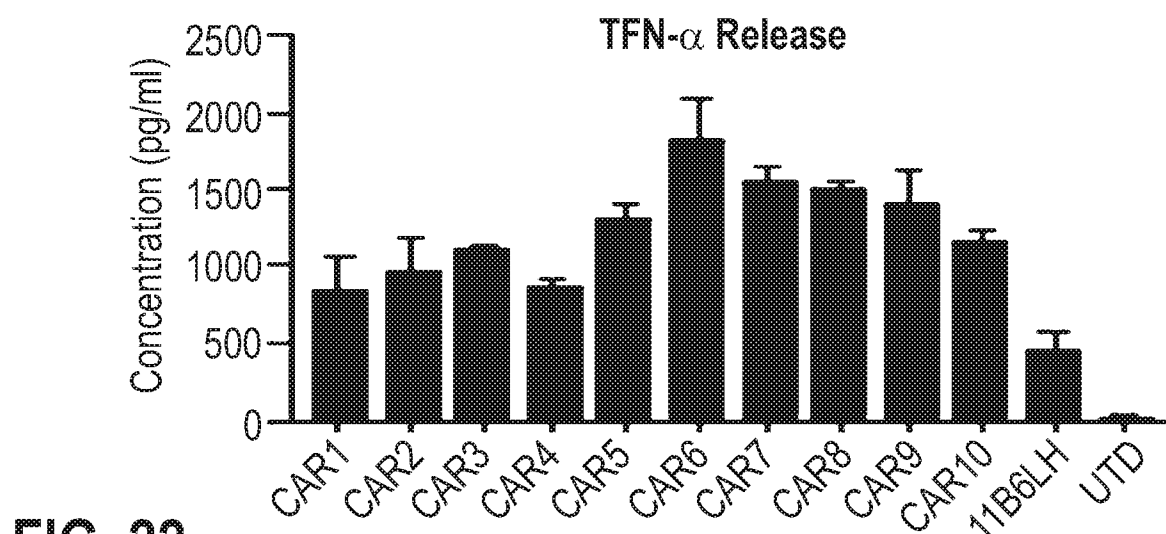
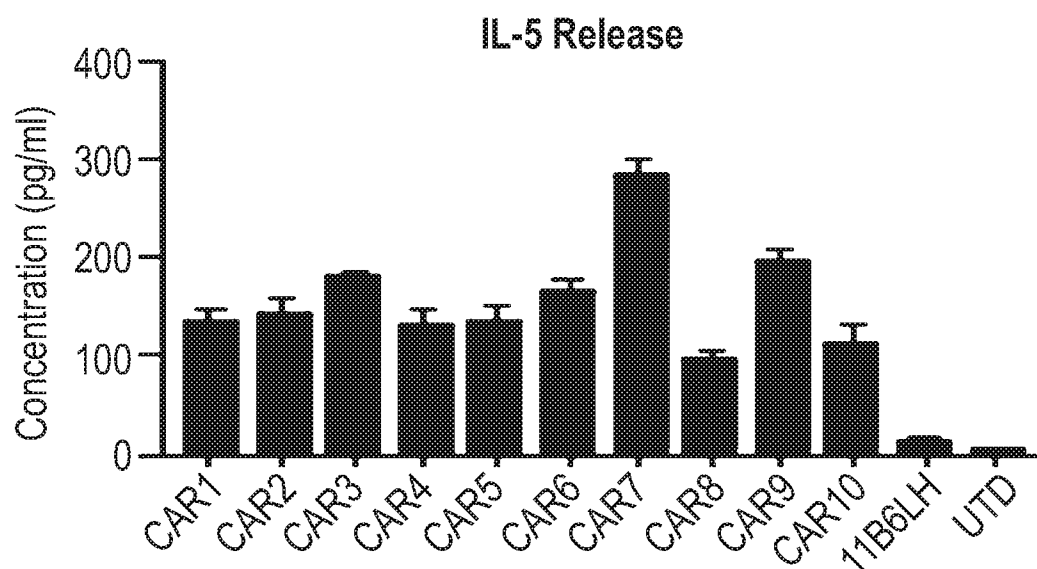
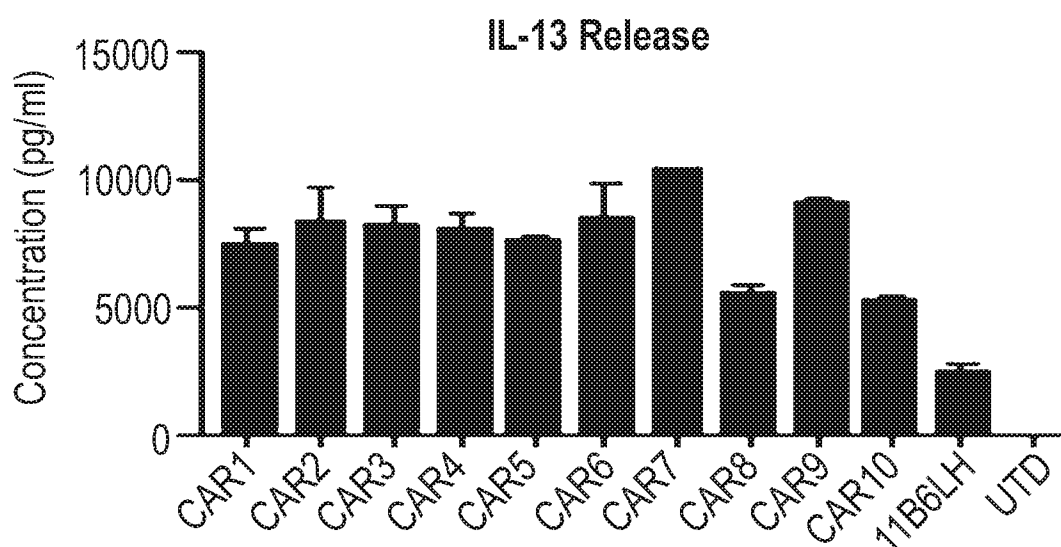


FIG. 22
(contd)



32 / 85

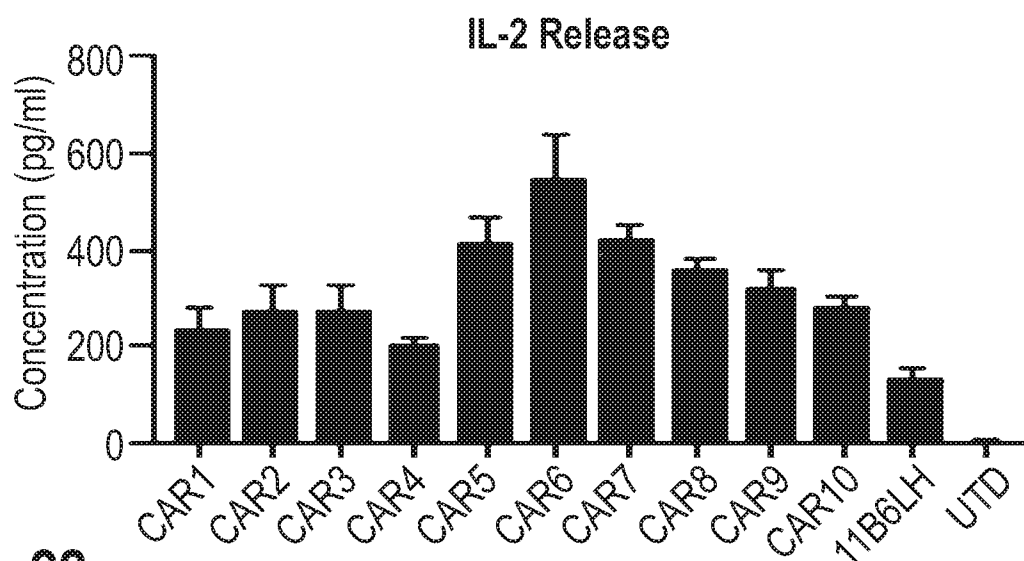


FIG. 22
(contd)

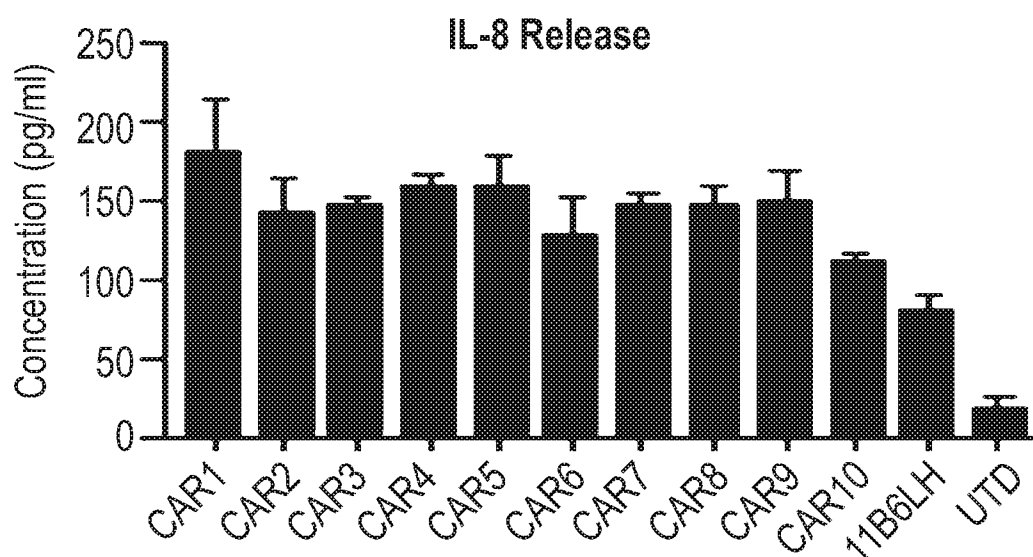
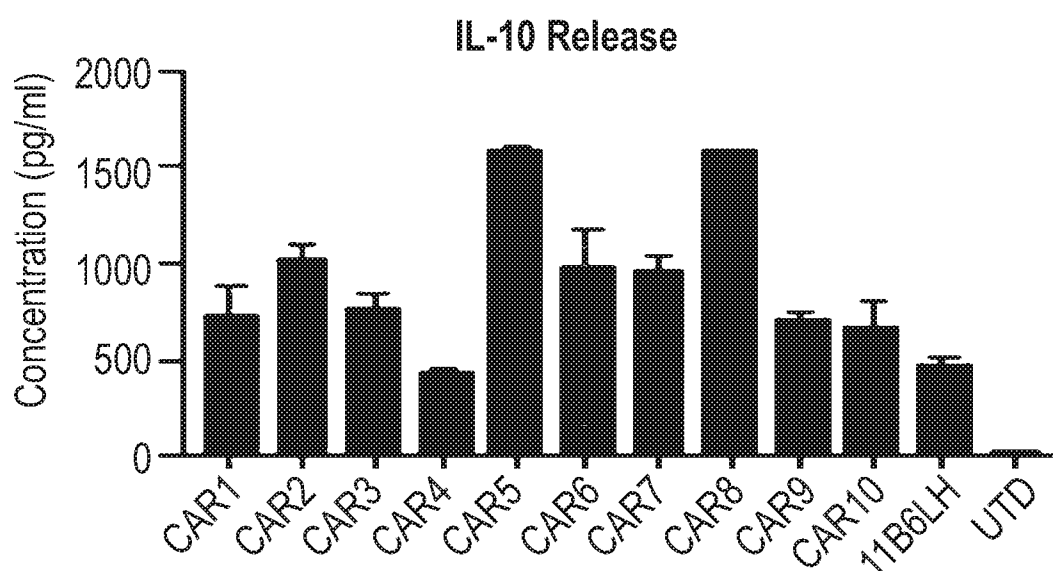
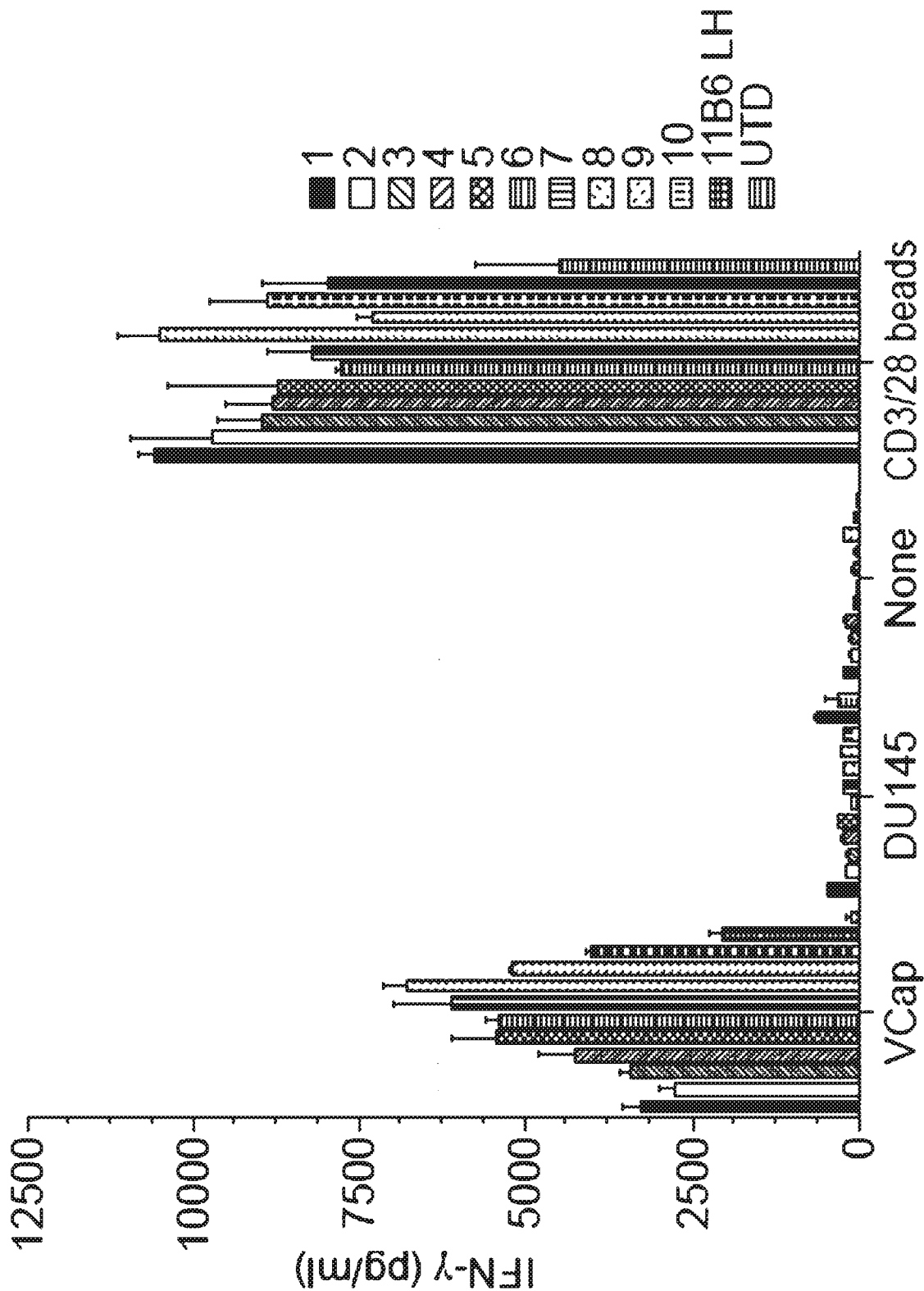
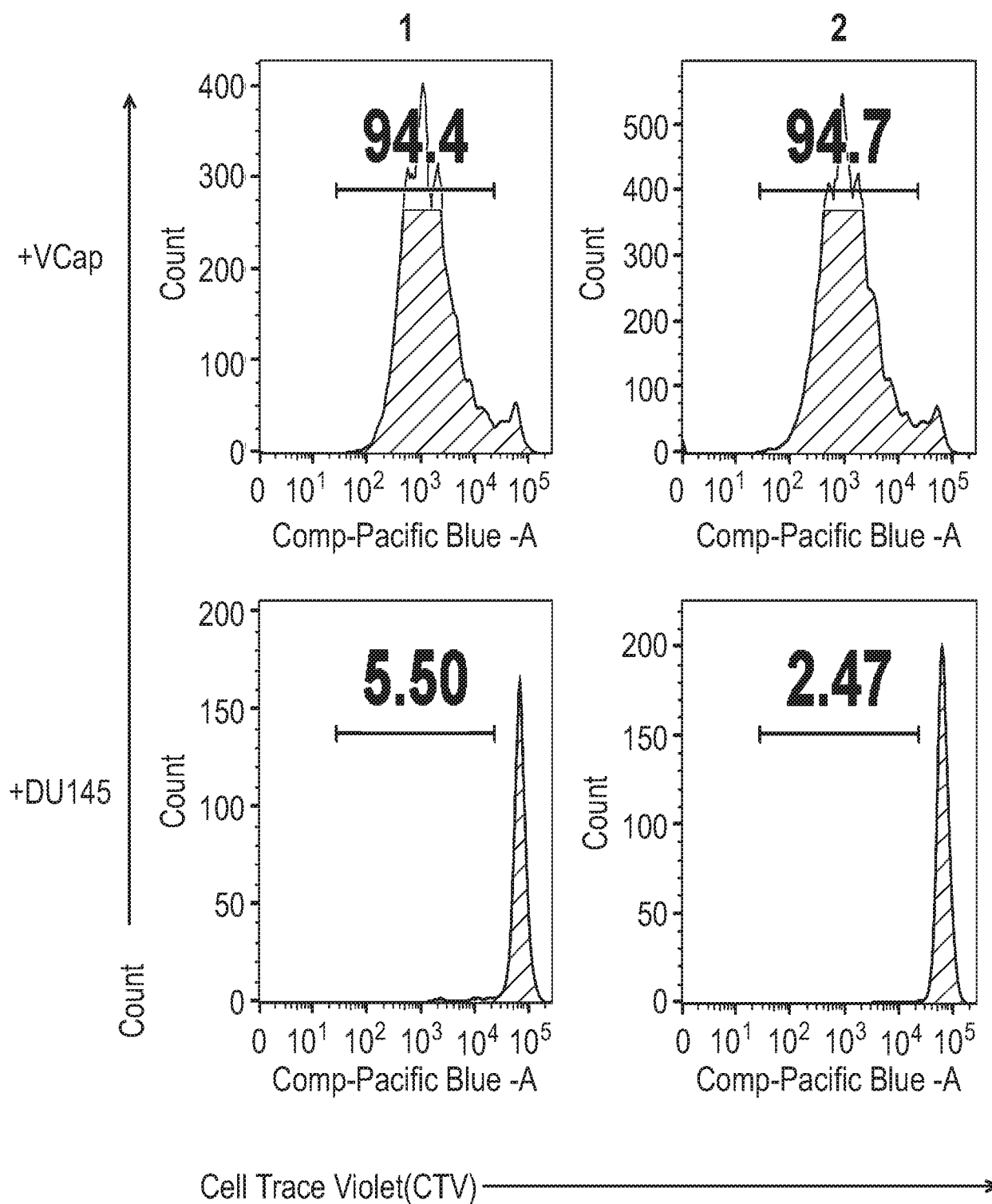


FIG. 23



34 / 85

FIG. 24A



35 / 85

FIG. 24A(contd)

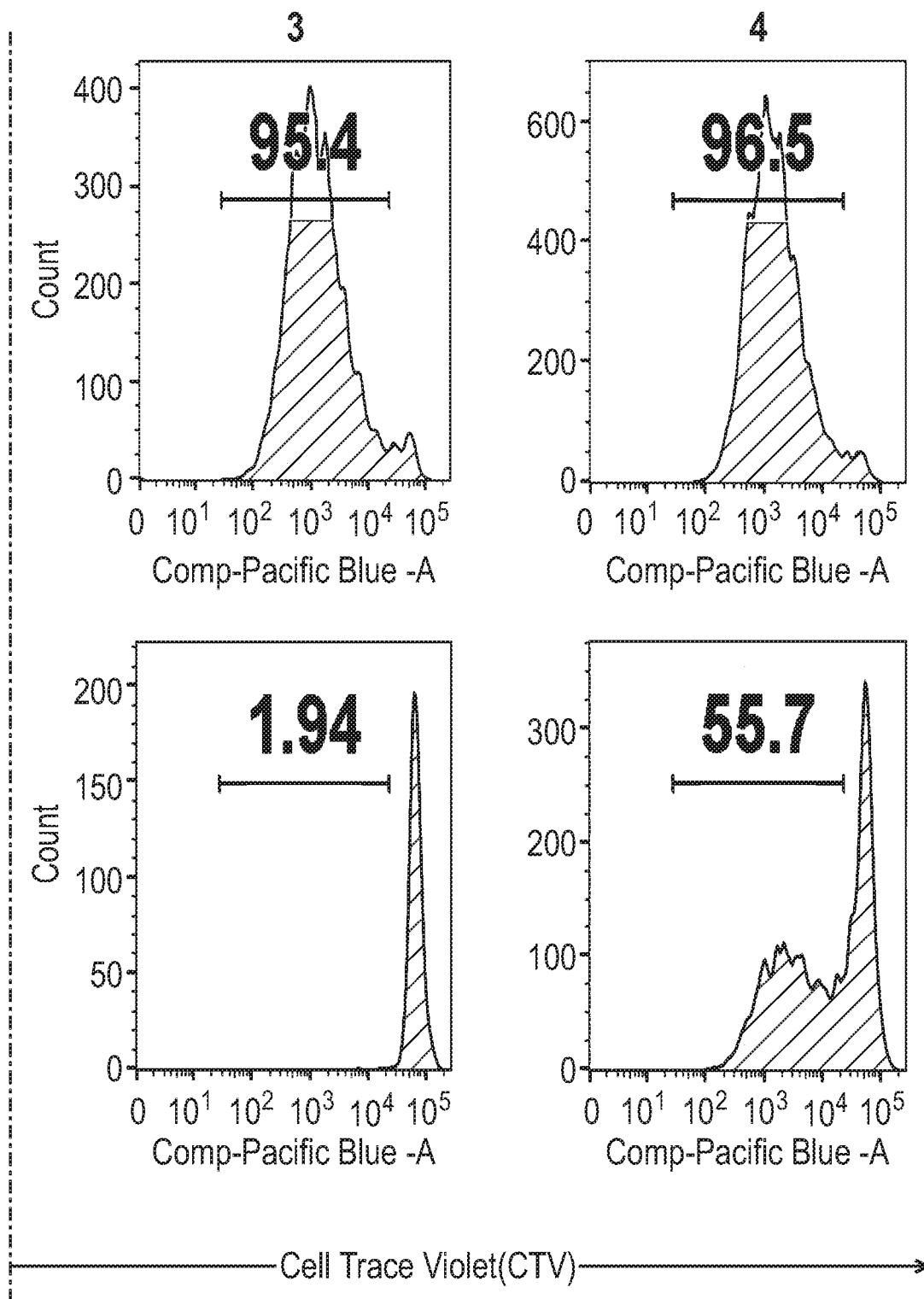
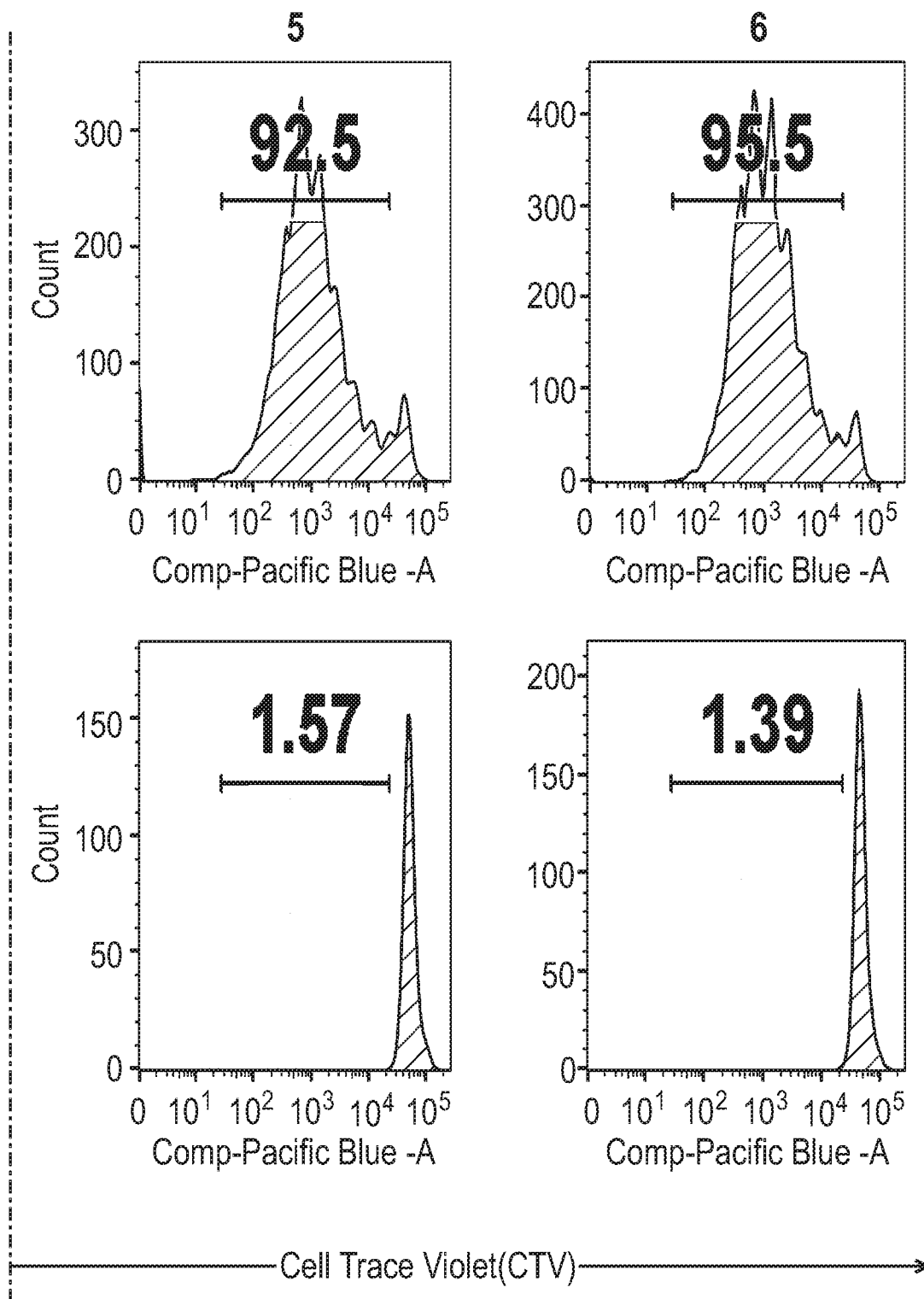
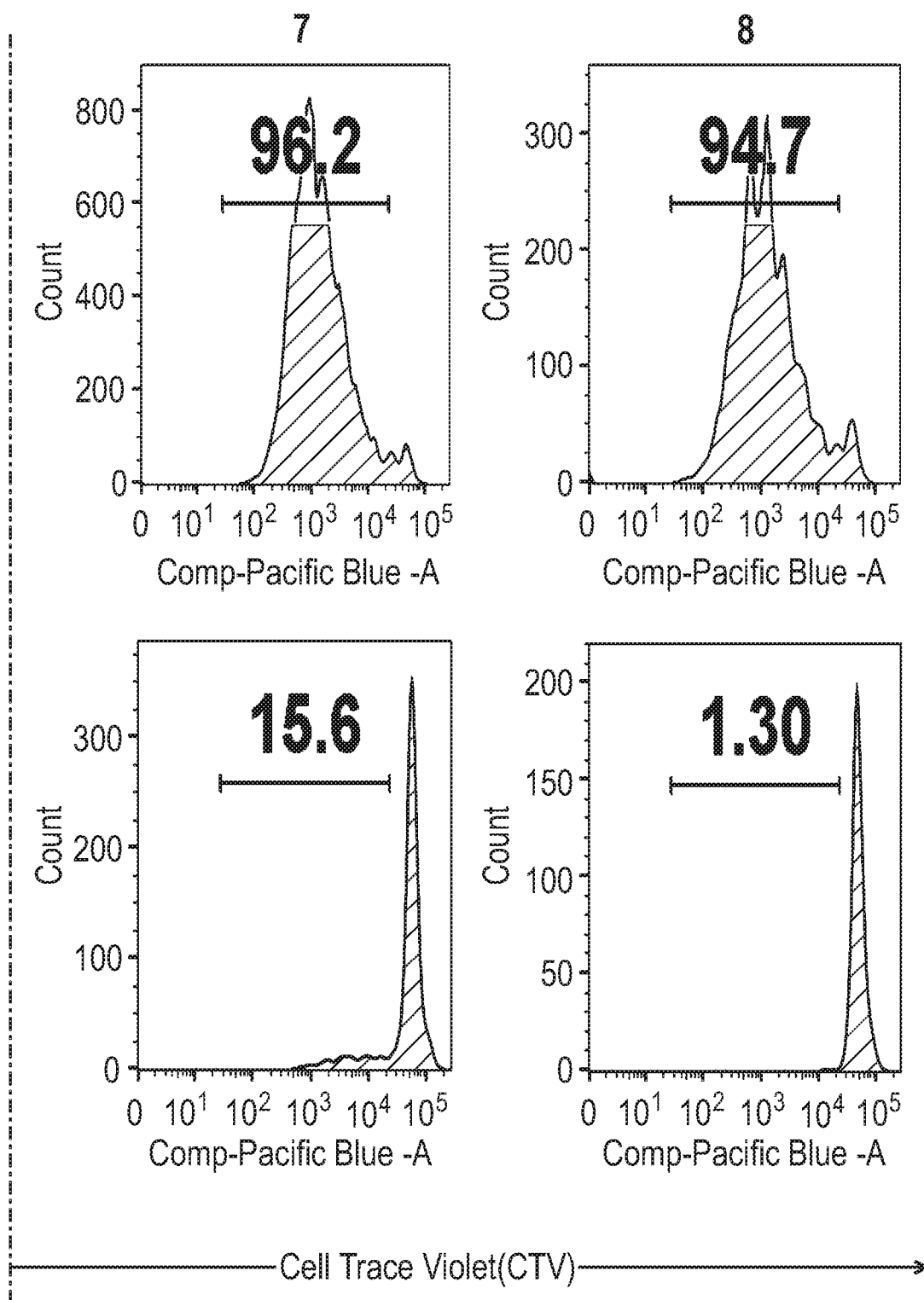


FIG. 24A(contd)



37 / 85

FIG. 24A(contd)



38 / 85

FIG. 24A(contd)

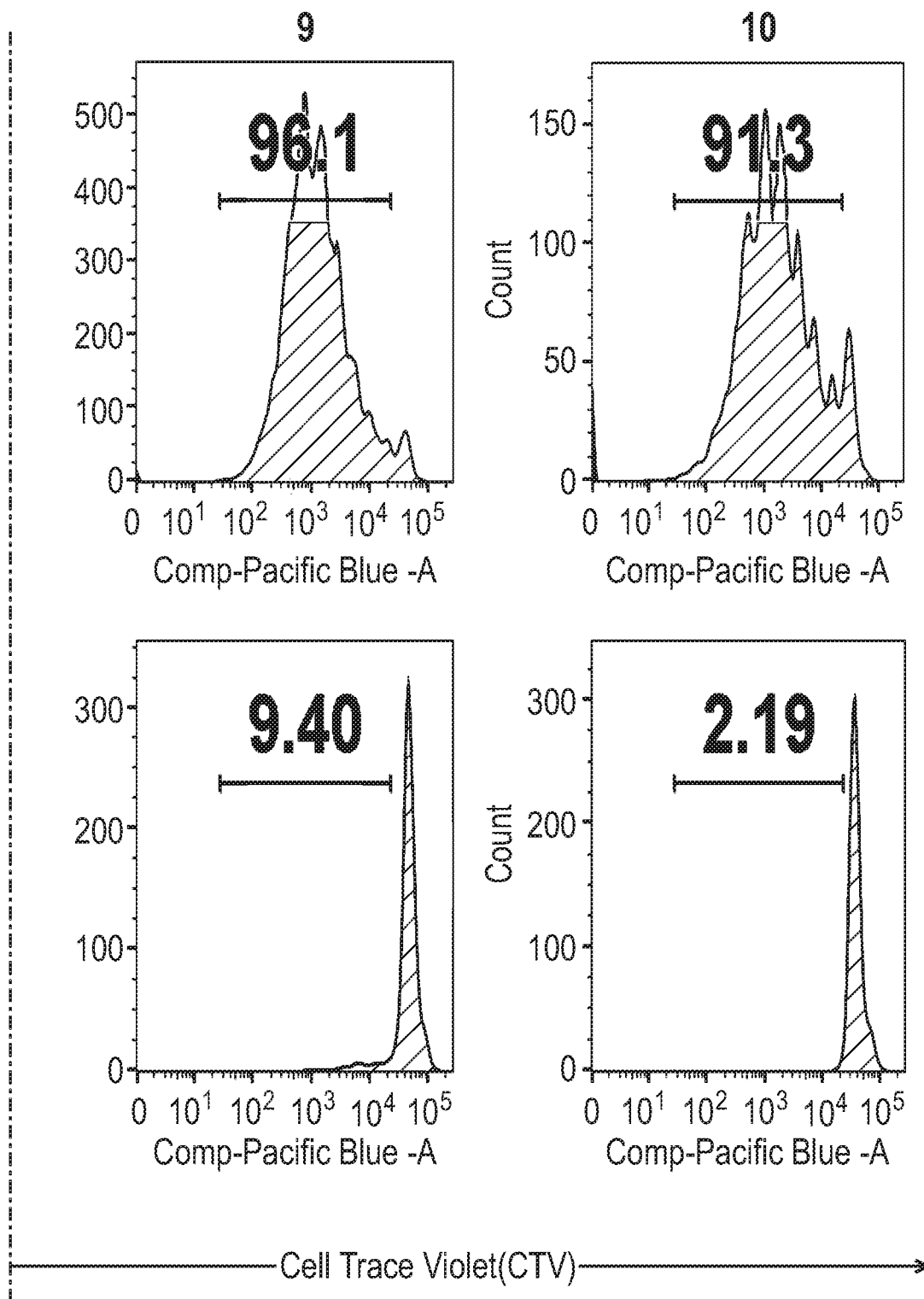
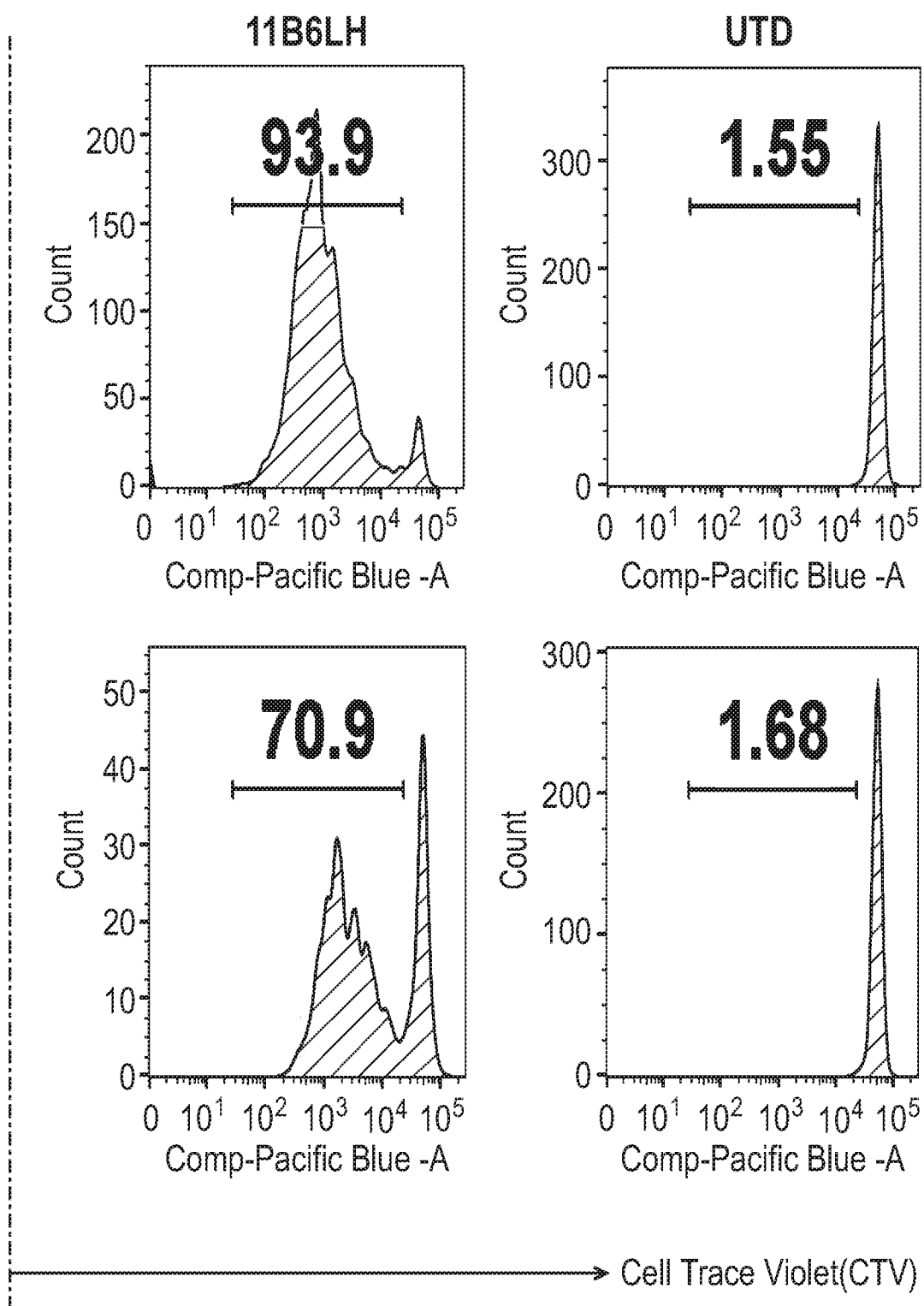
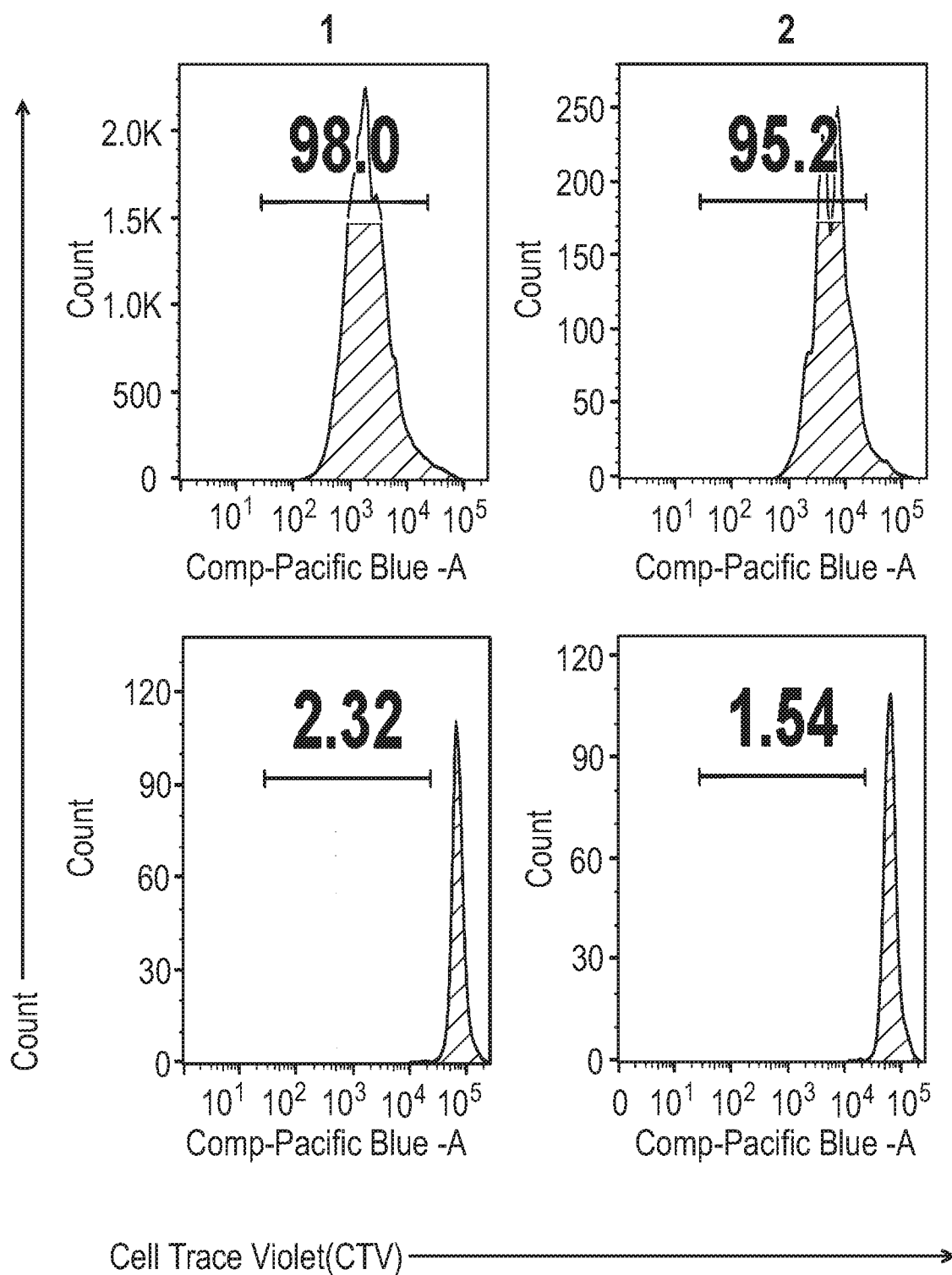


FIG. 24A(contd)



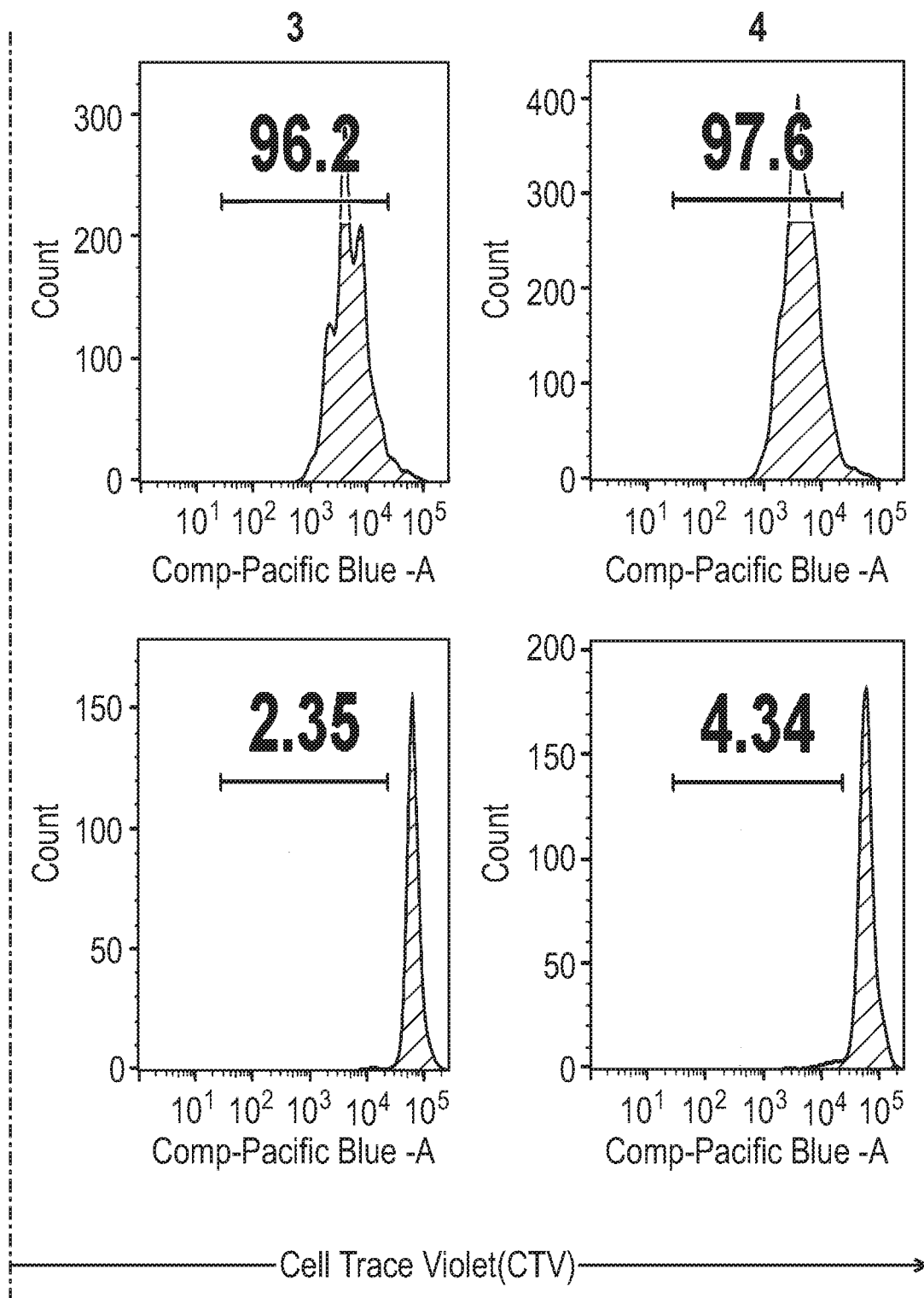
40 / 85

FIG. 24B

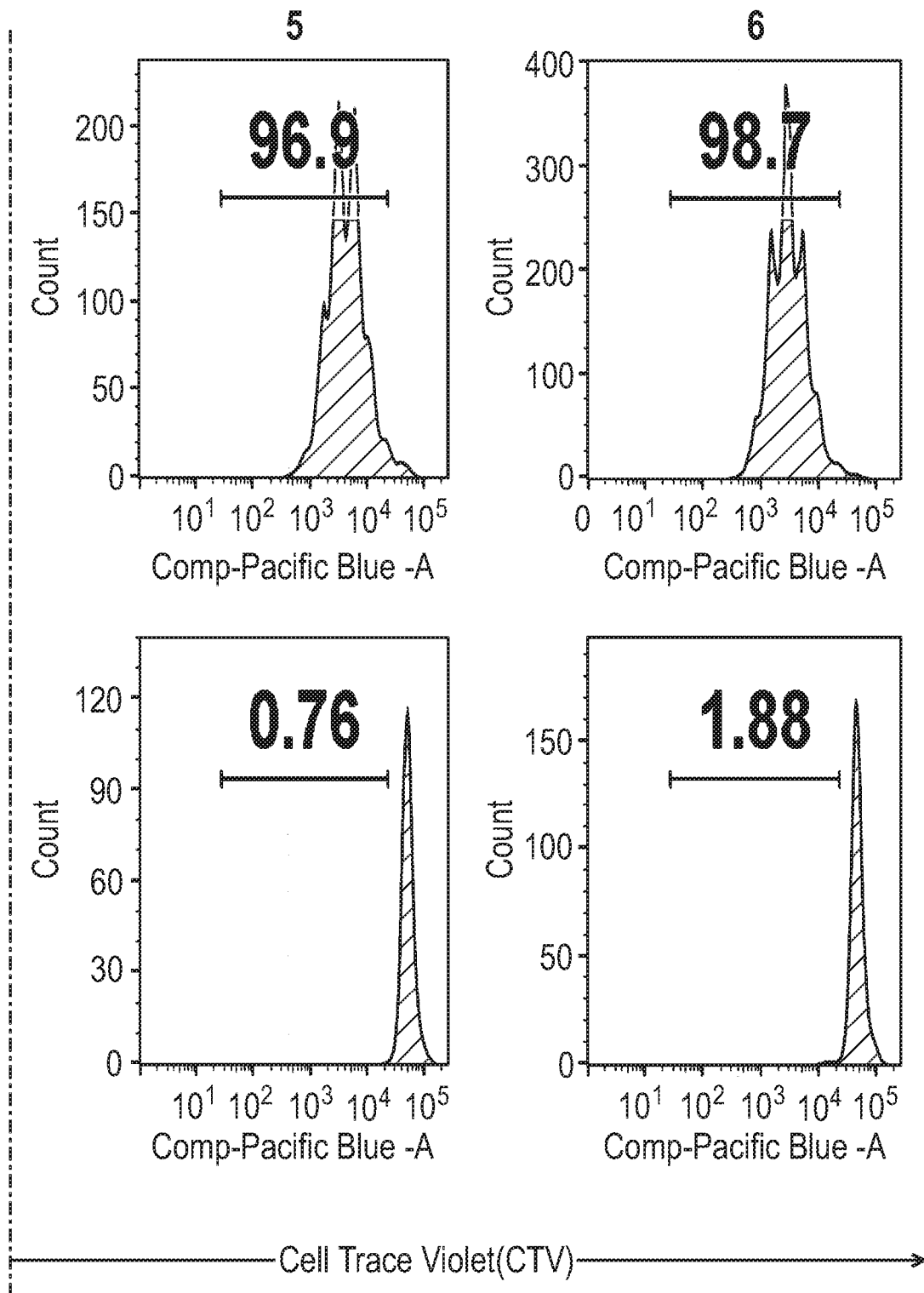


41 / 85

FIG. 24B(contd)

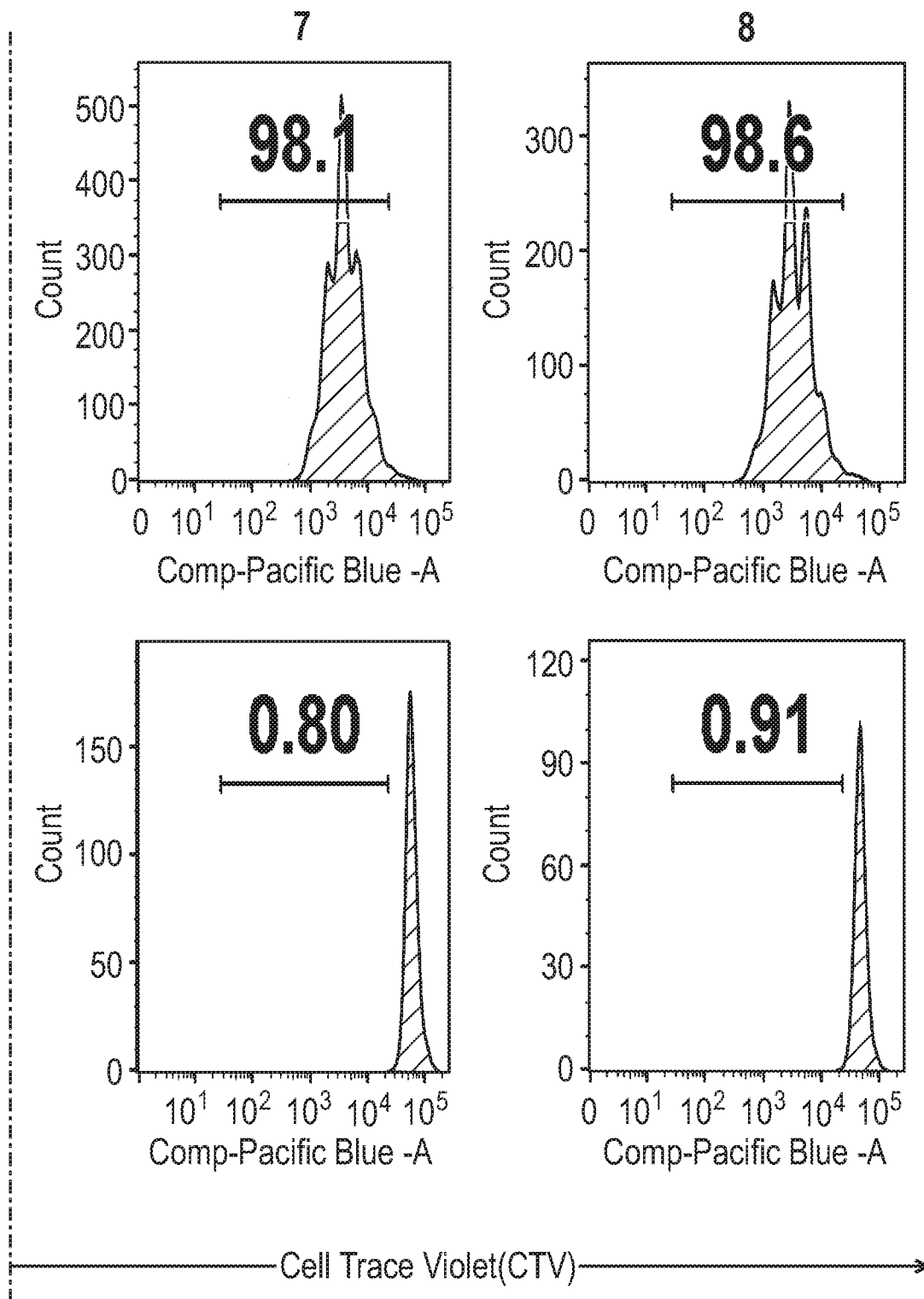


42 / 85

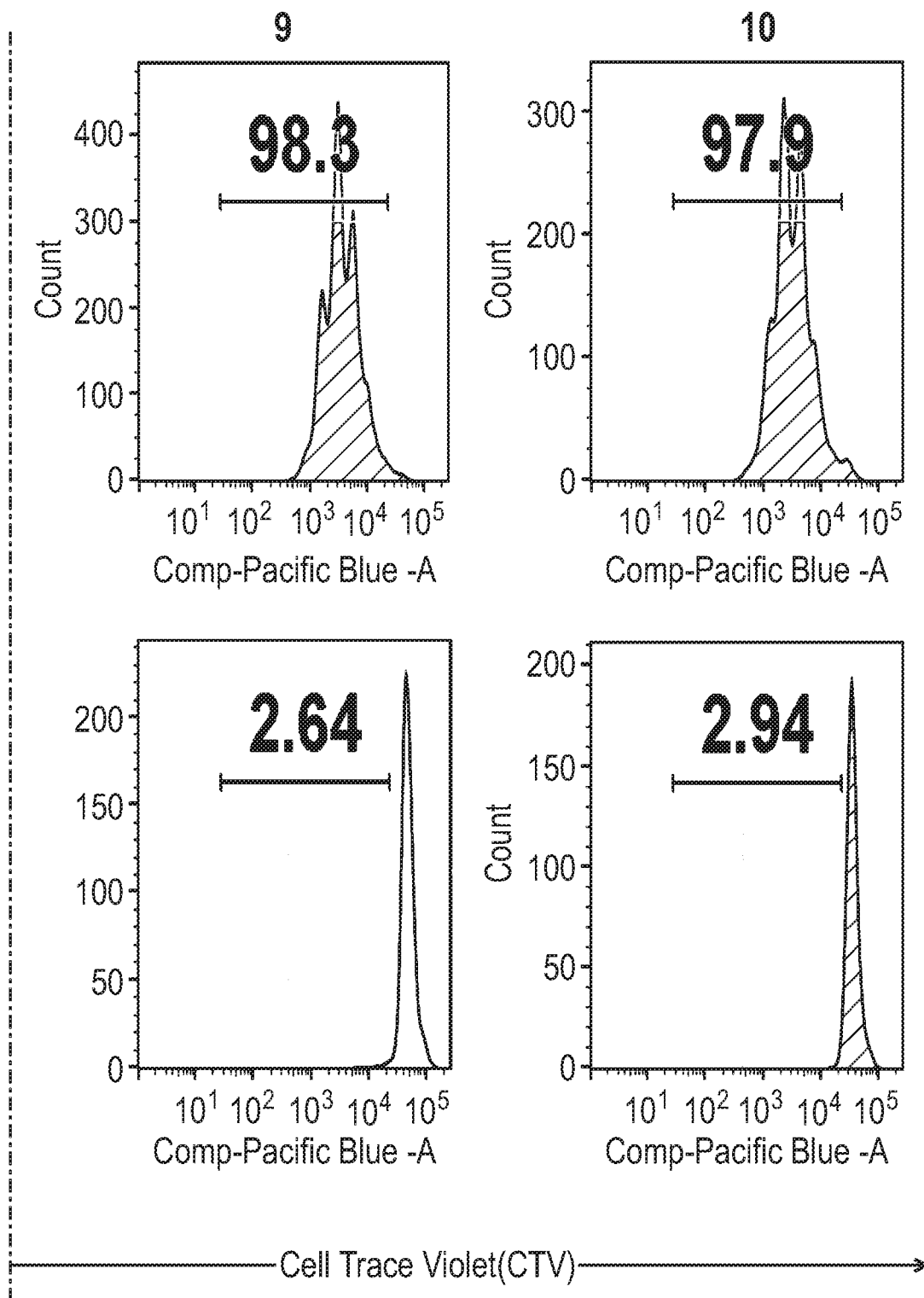
FIG. 24B(contd)

43 / 85

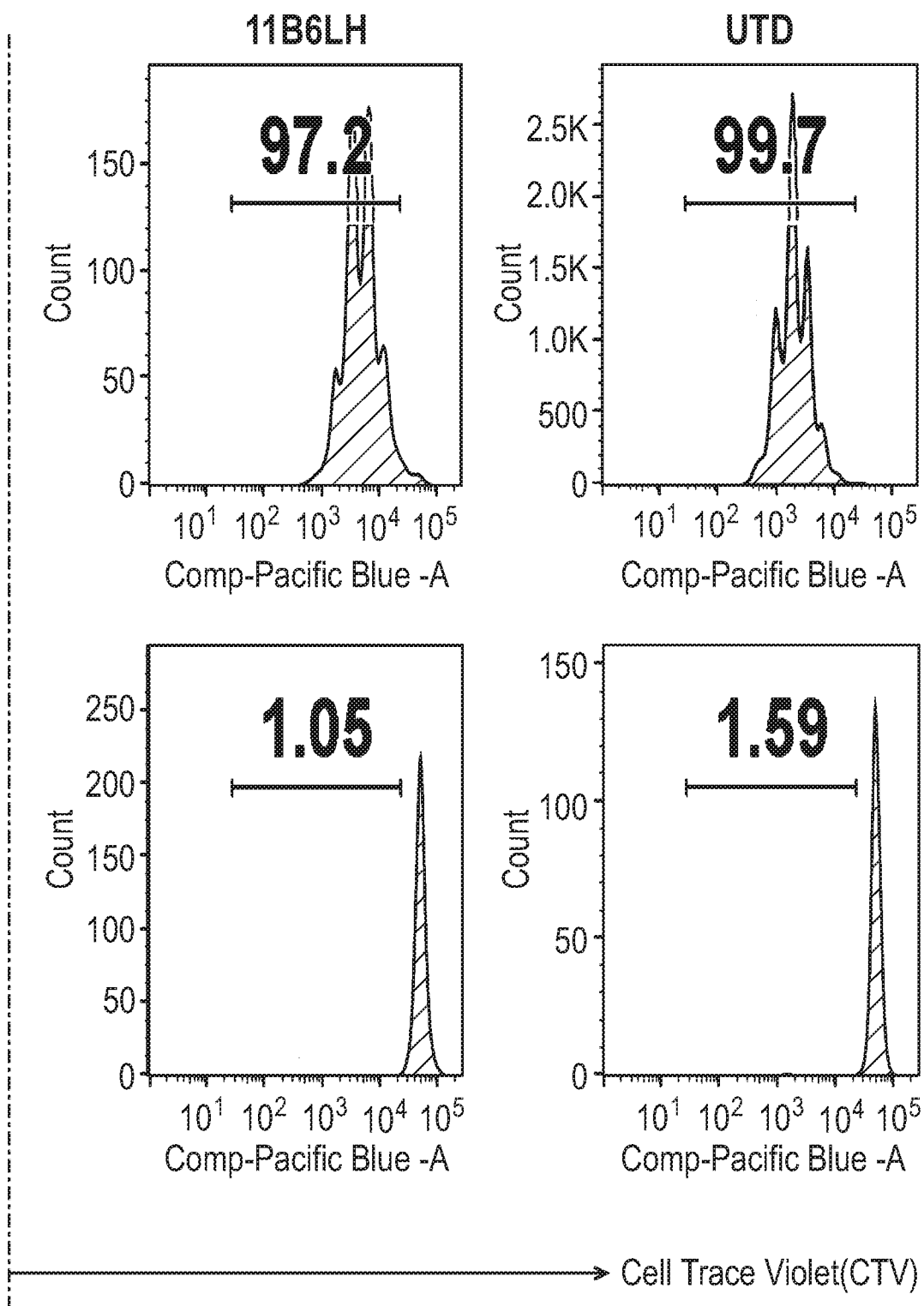
FIG. 24B(contd)

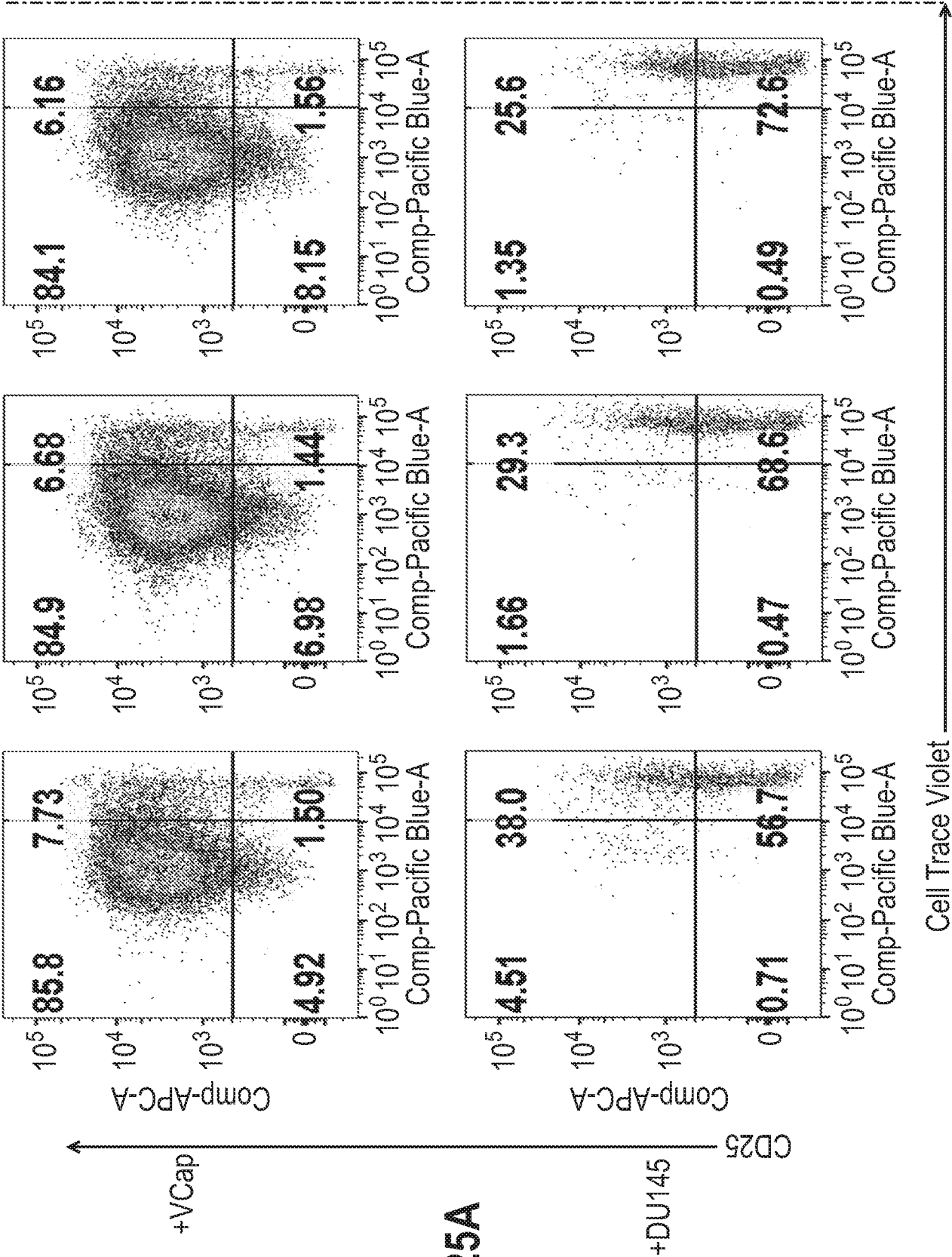


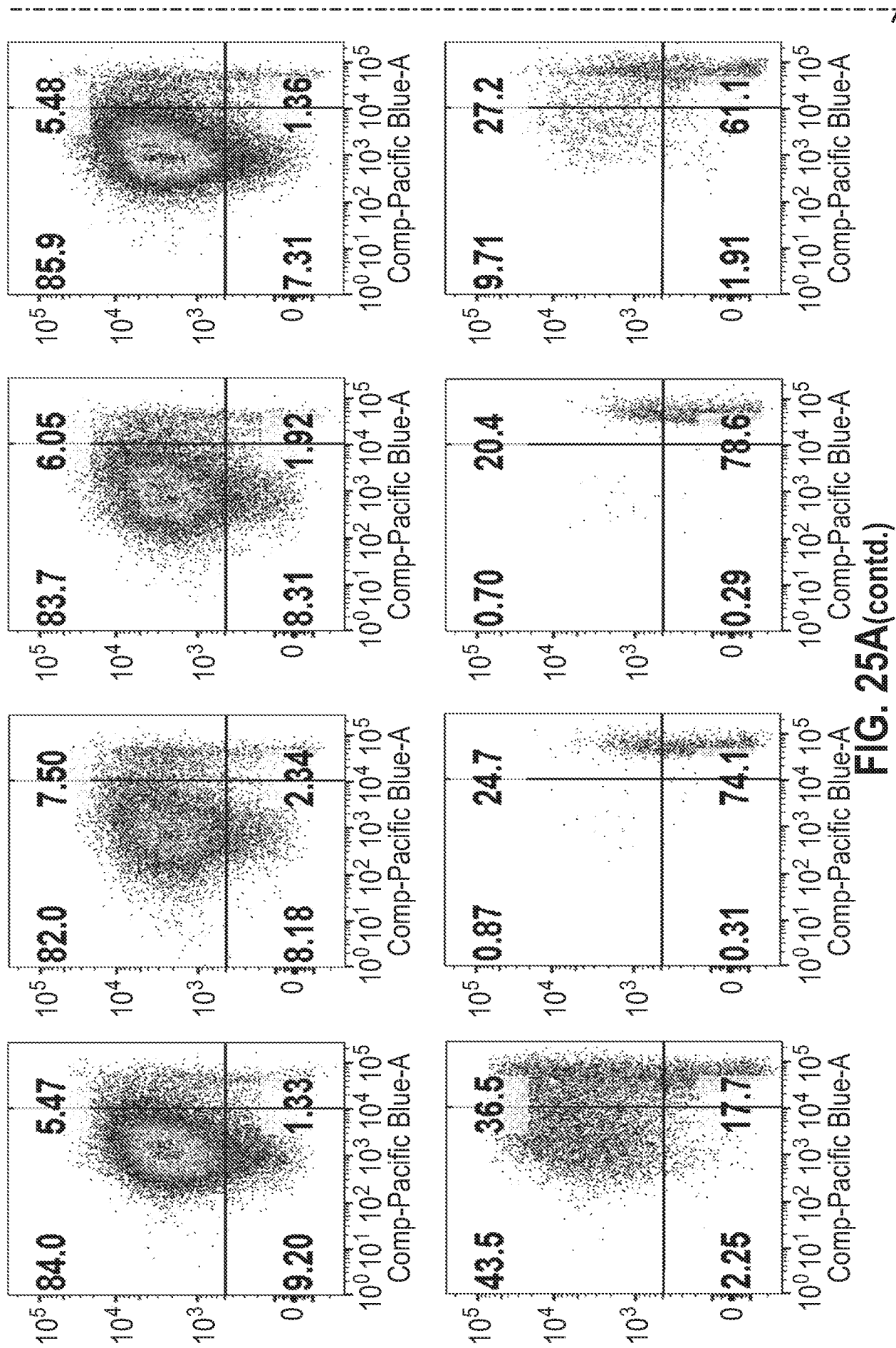
44 / 85

FIG. 24B(contd)

45 / 85

FIG. 24B(contd)





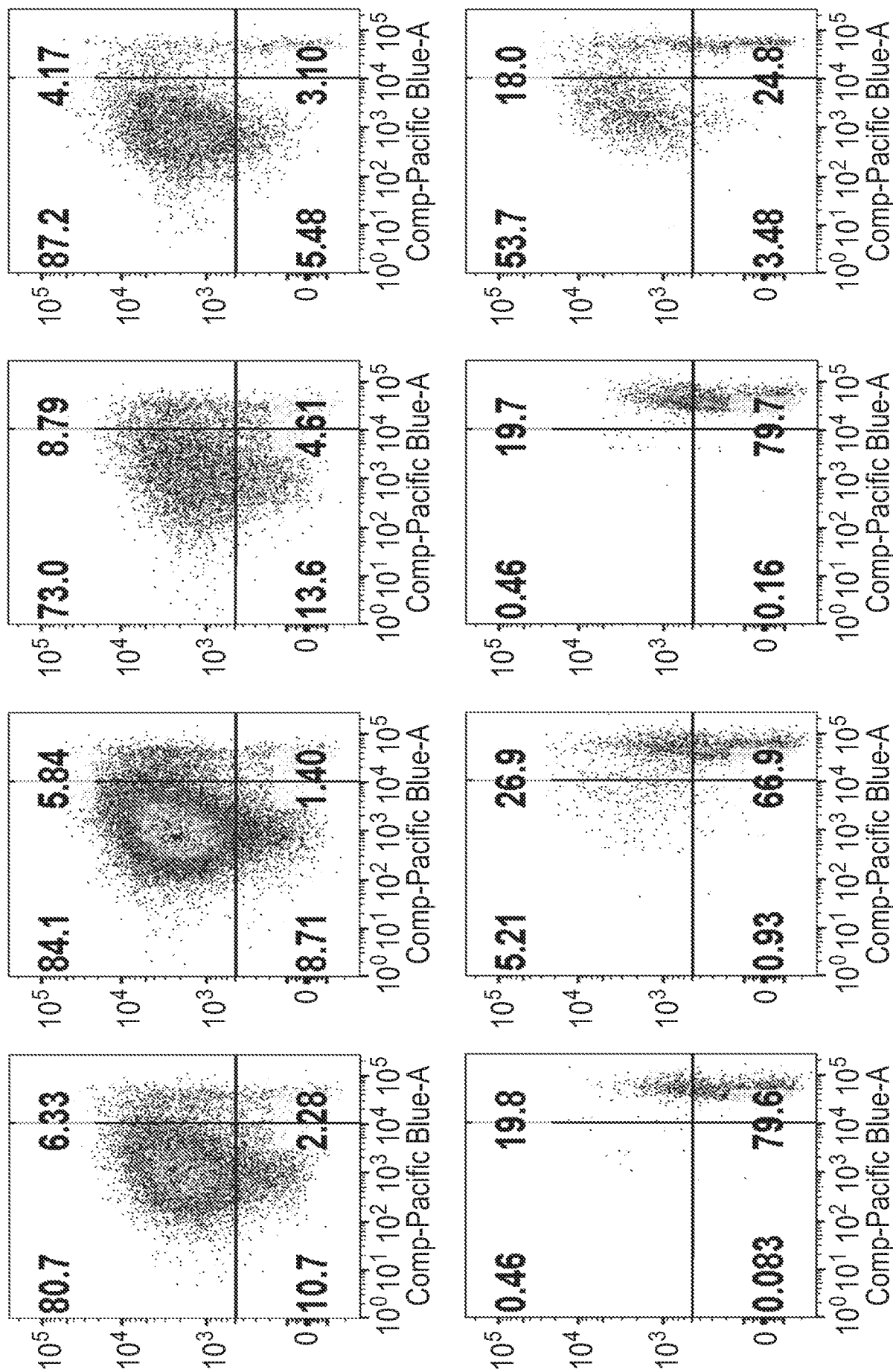
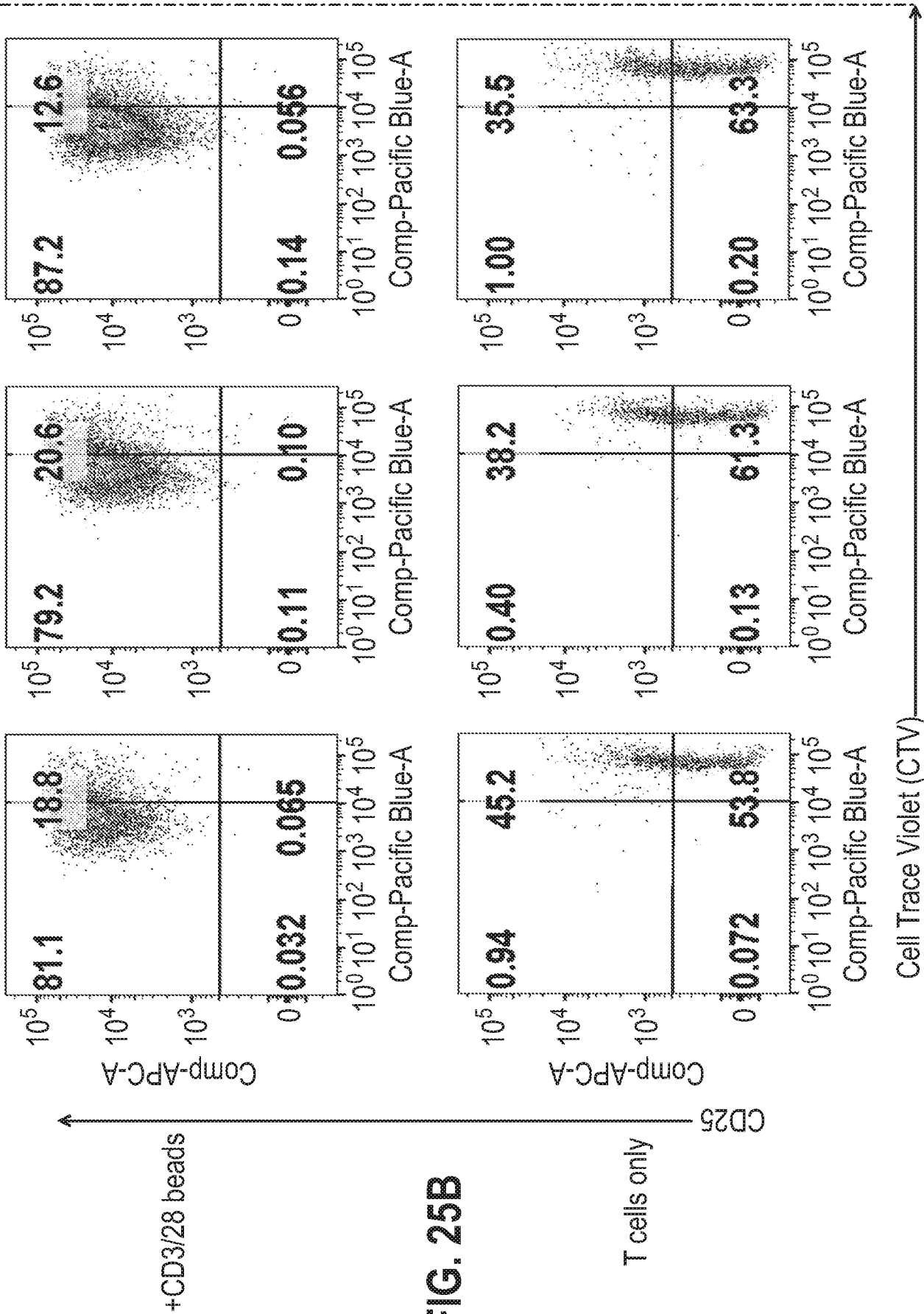


FIG. 25A(contd.)



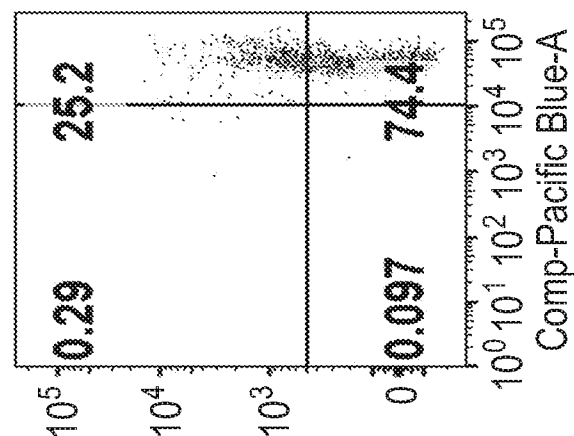
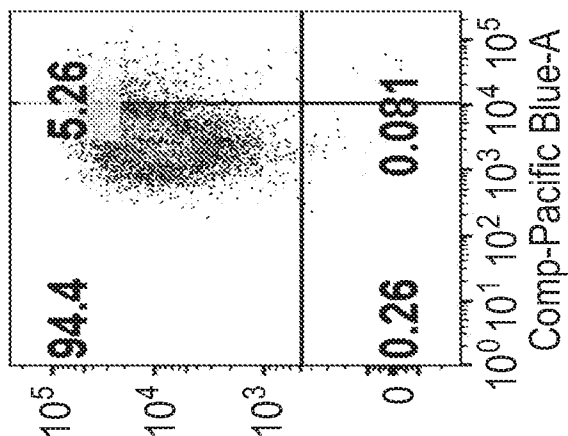
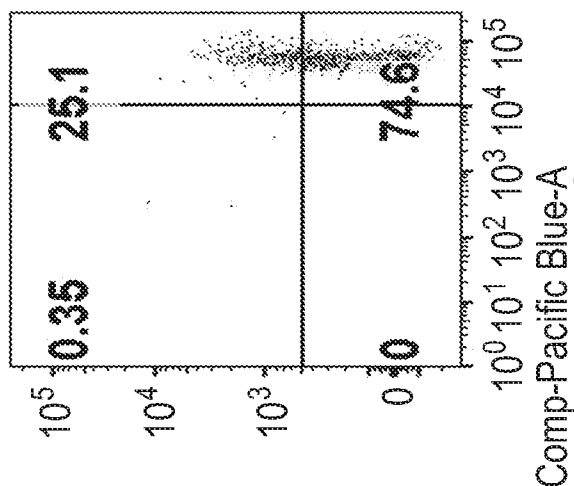
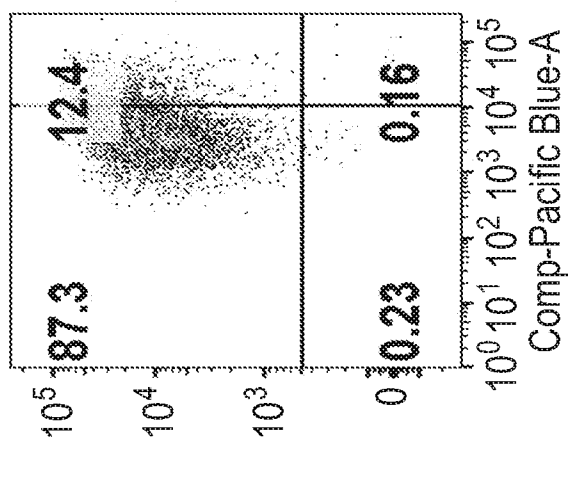
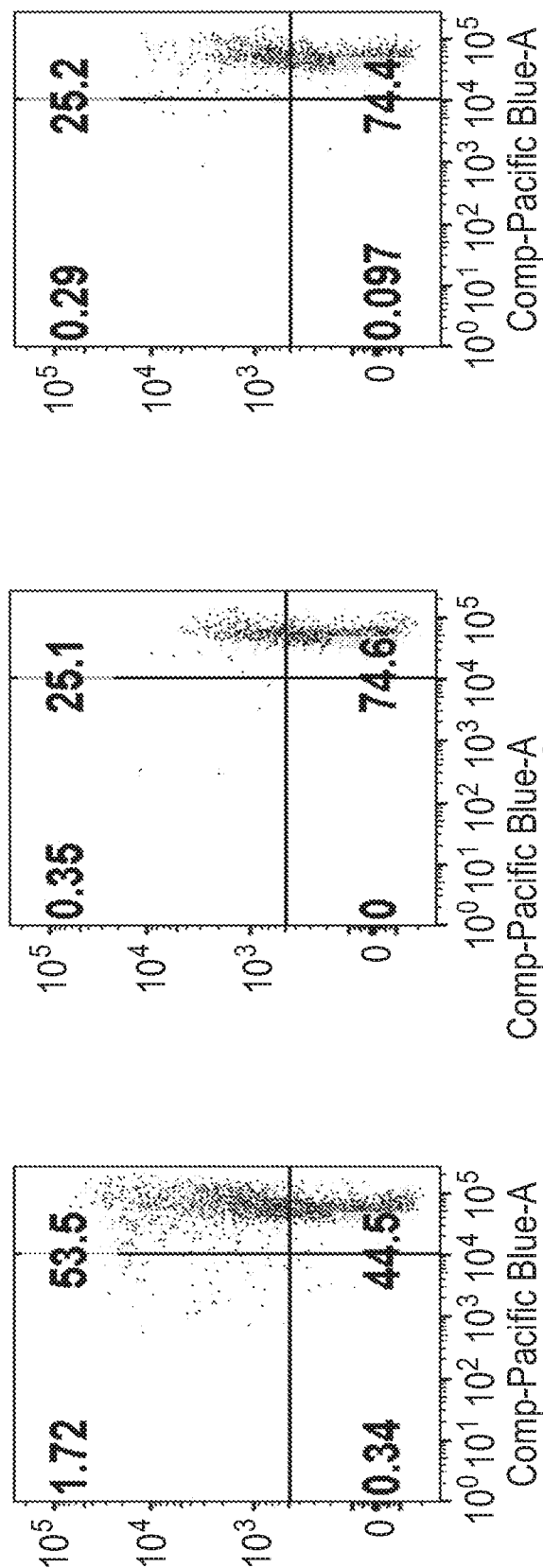
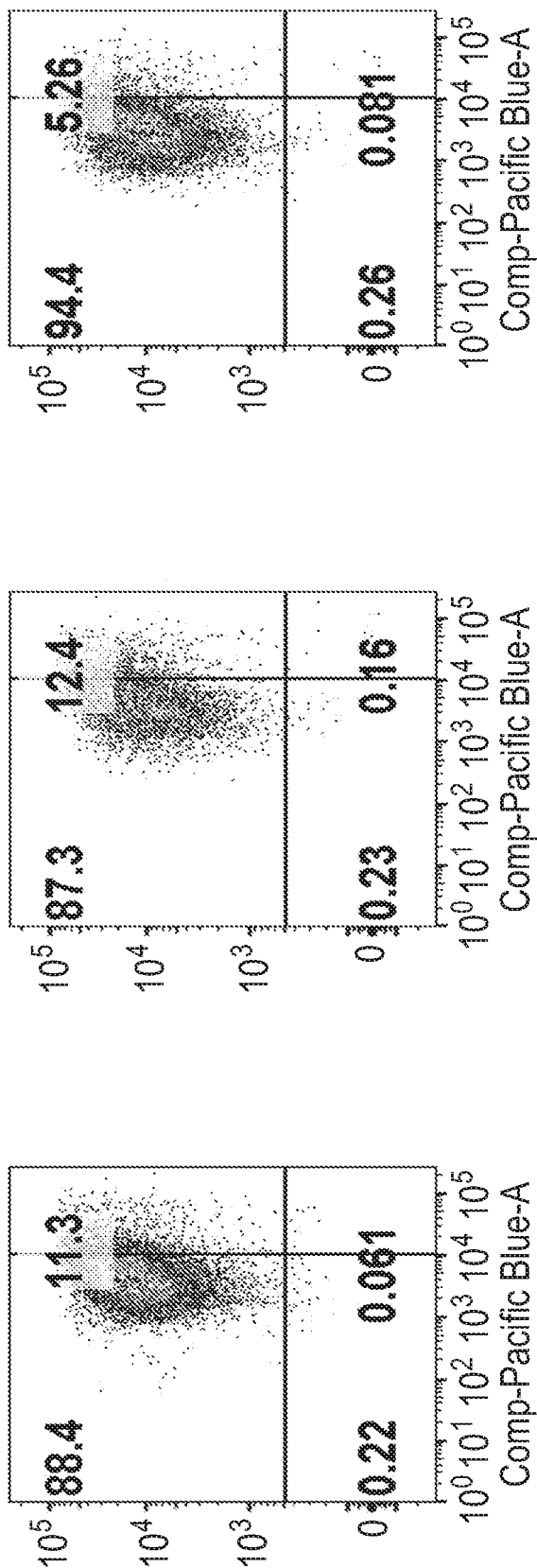


FIG. 25B(contd.)

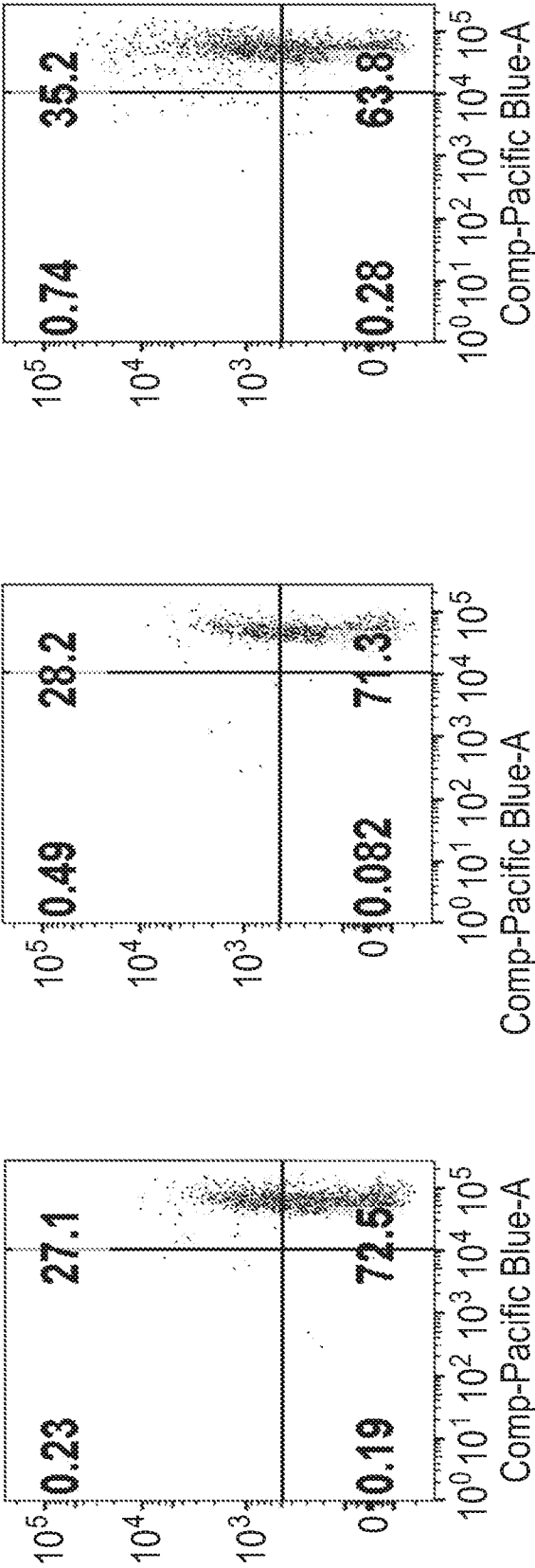
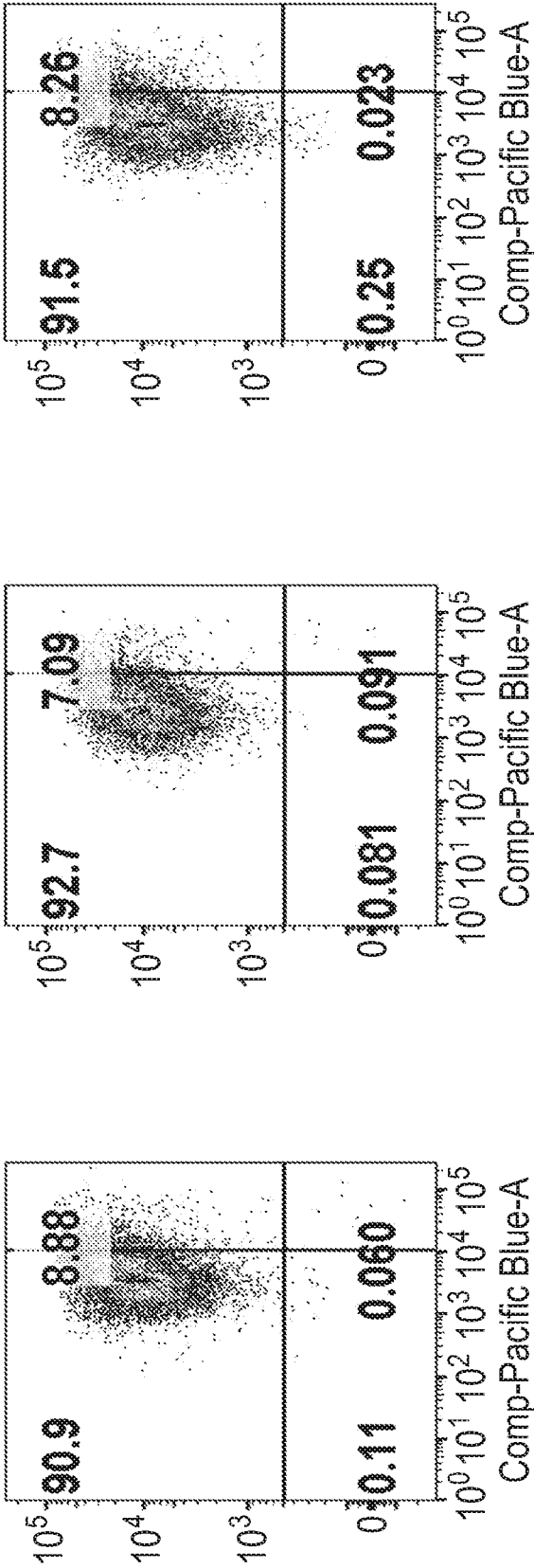


FIG. 25B(contd.)

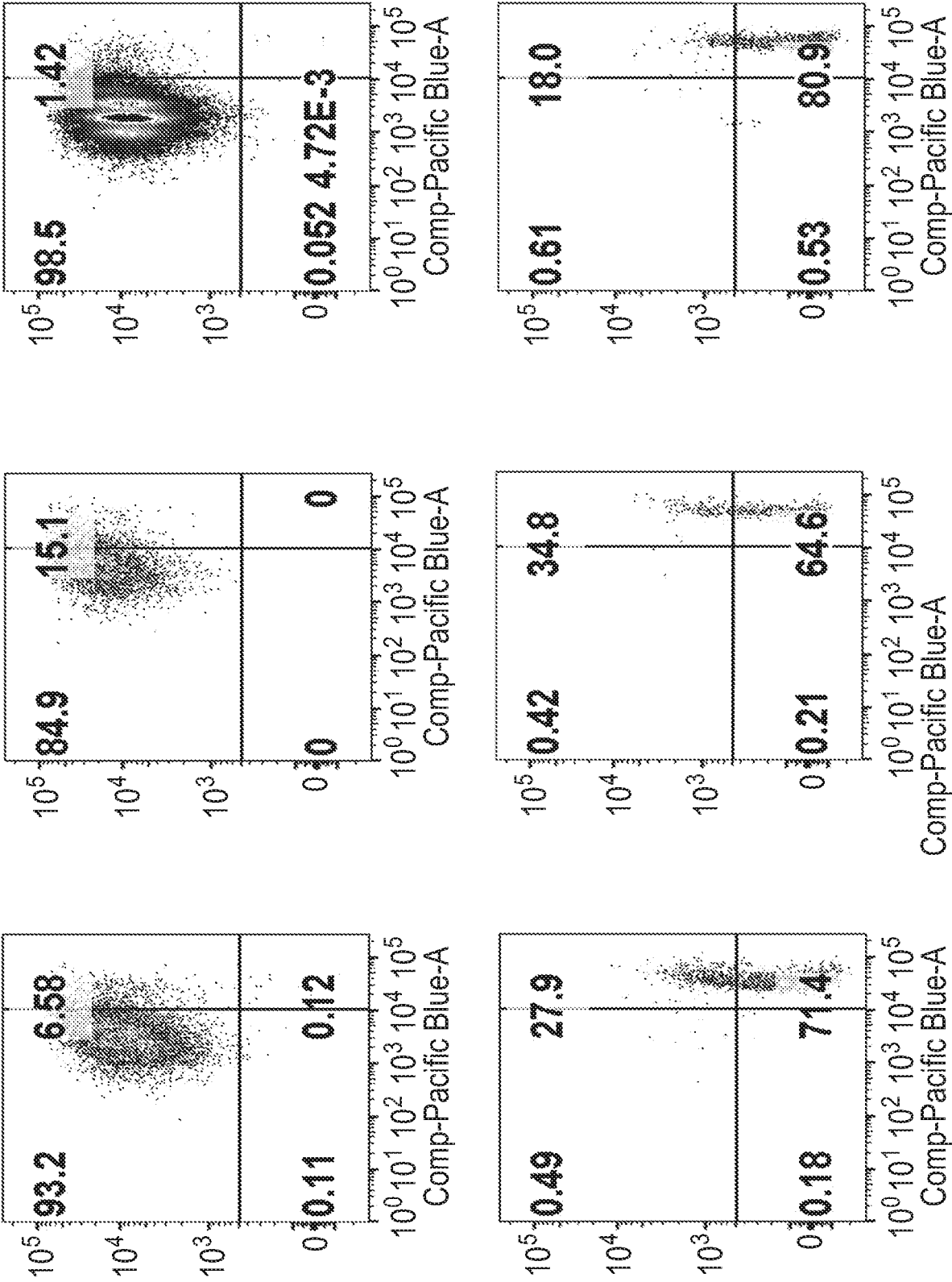


FIG. 25B
(contd.)

FIG. 26

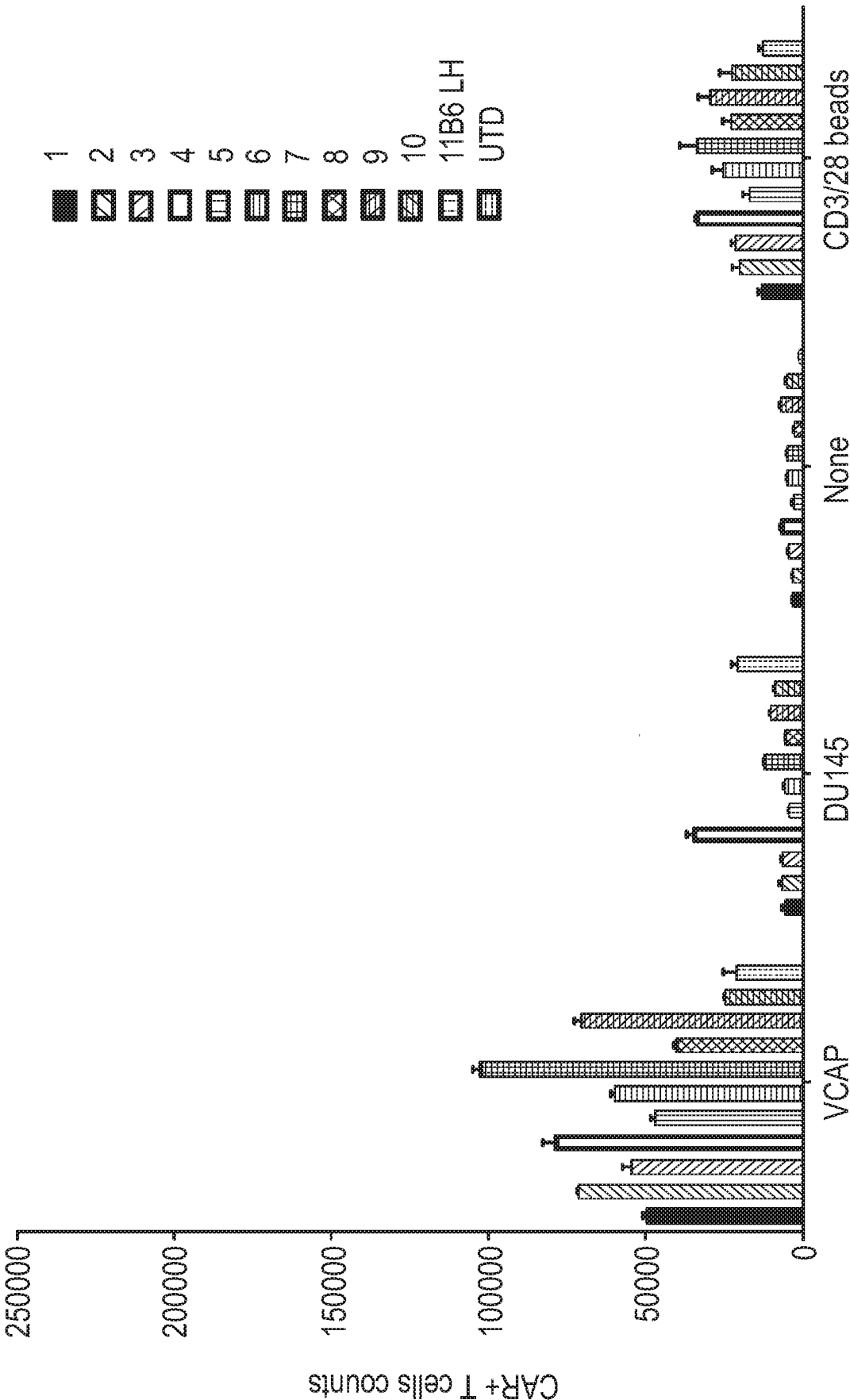


FIG. 27

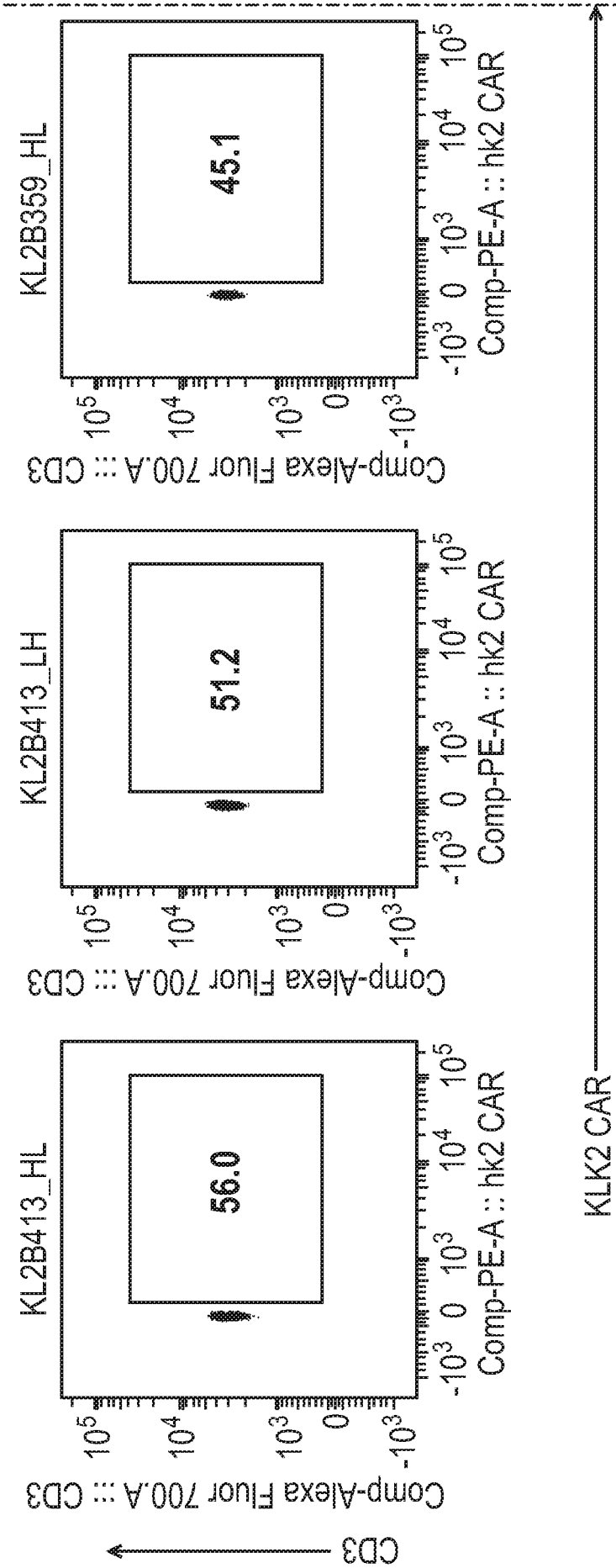


FIG. 27(contd)

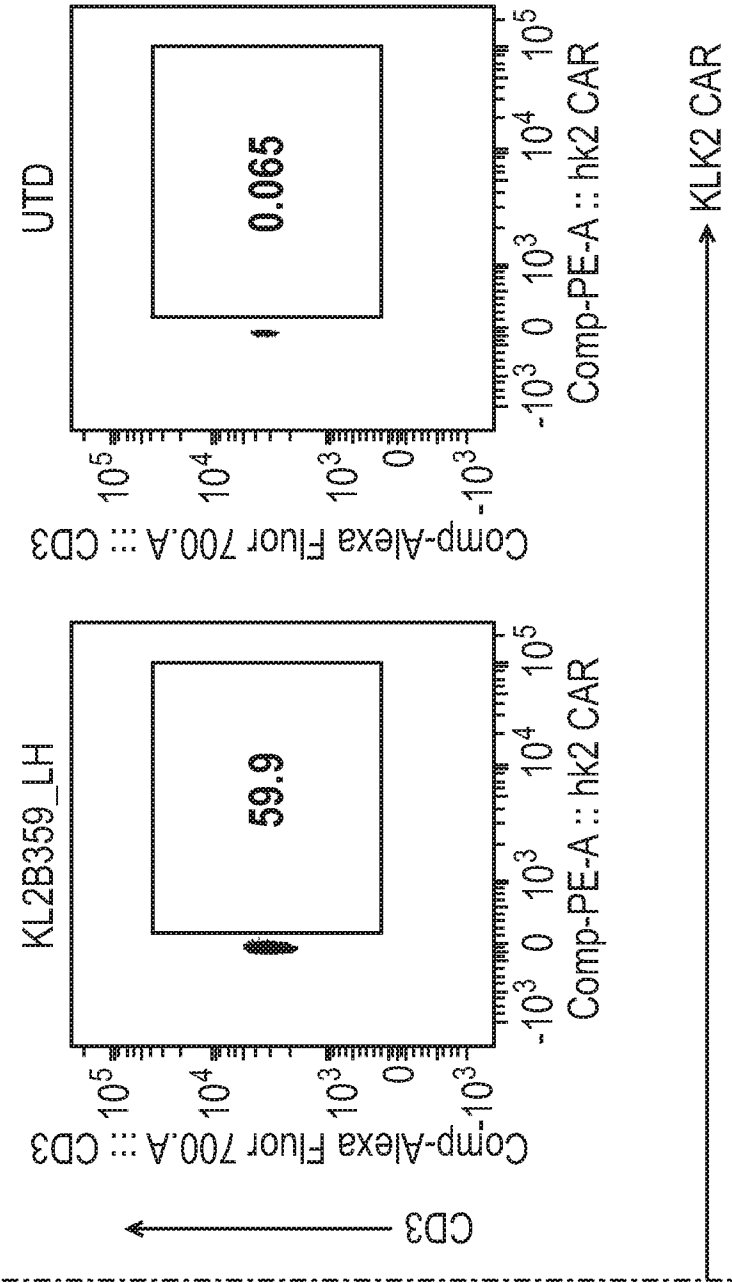


FIG. 28

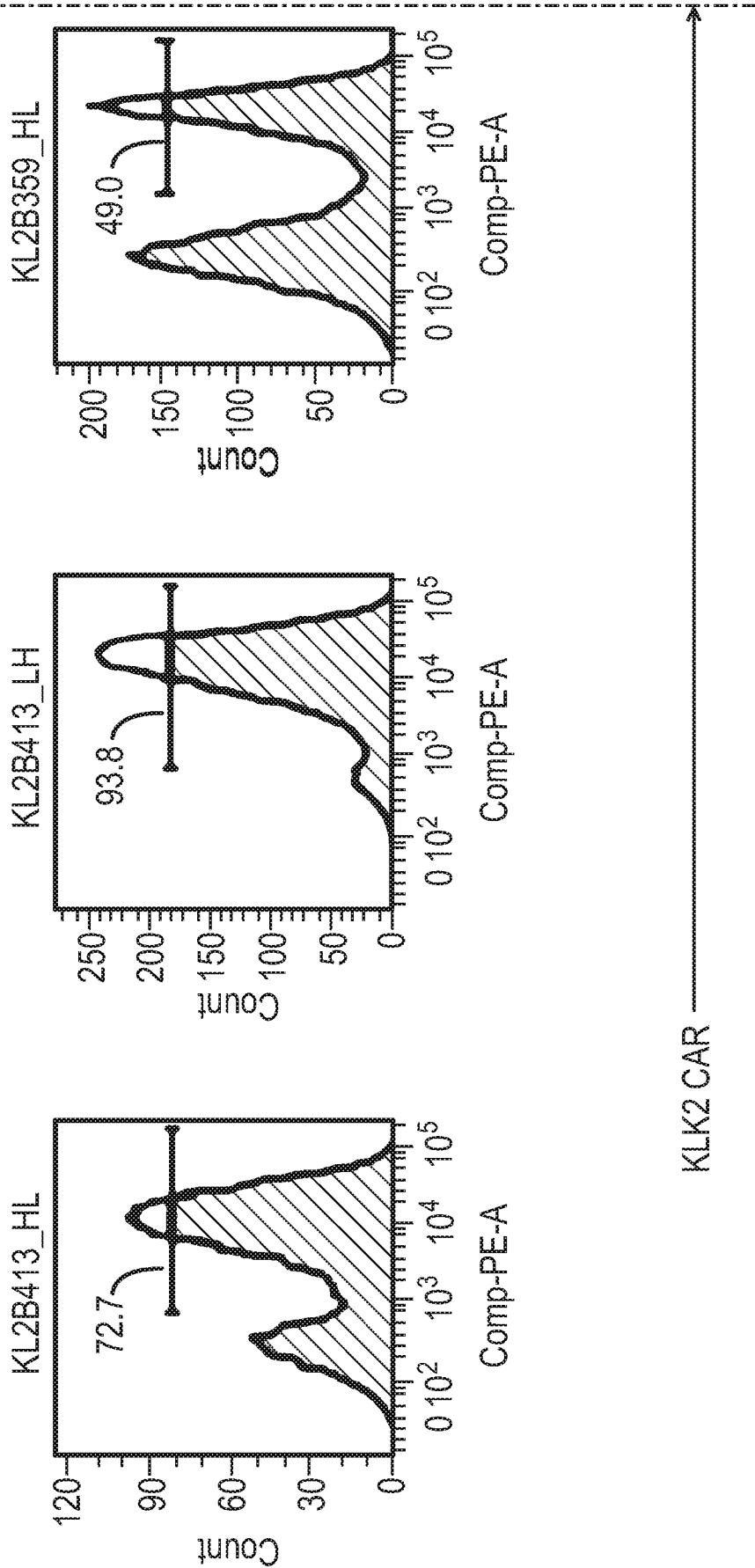


FIG. 28(contd)

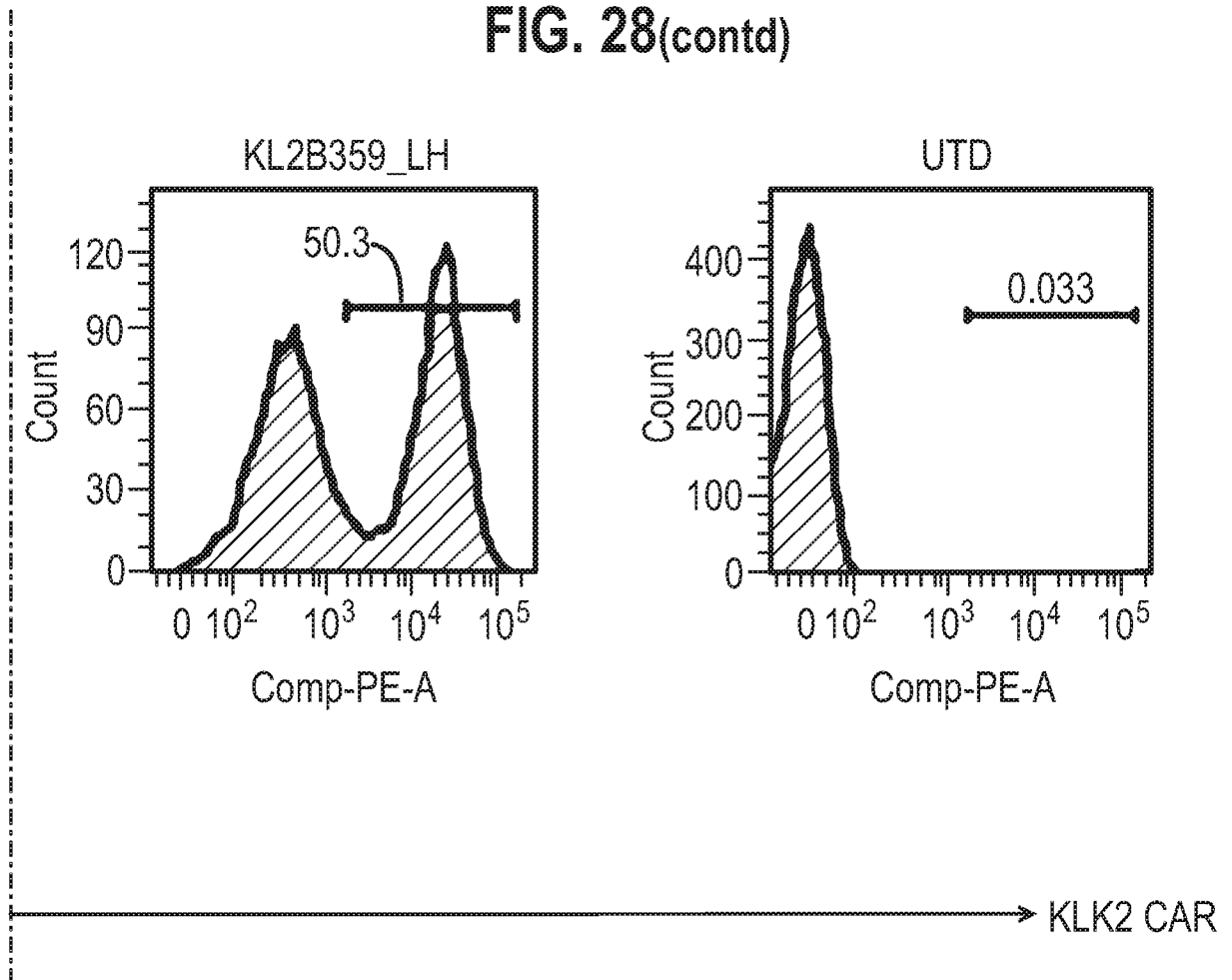
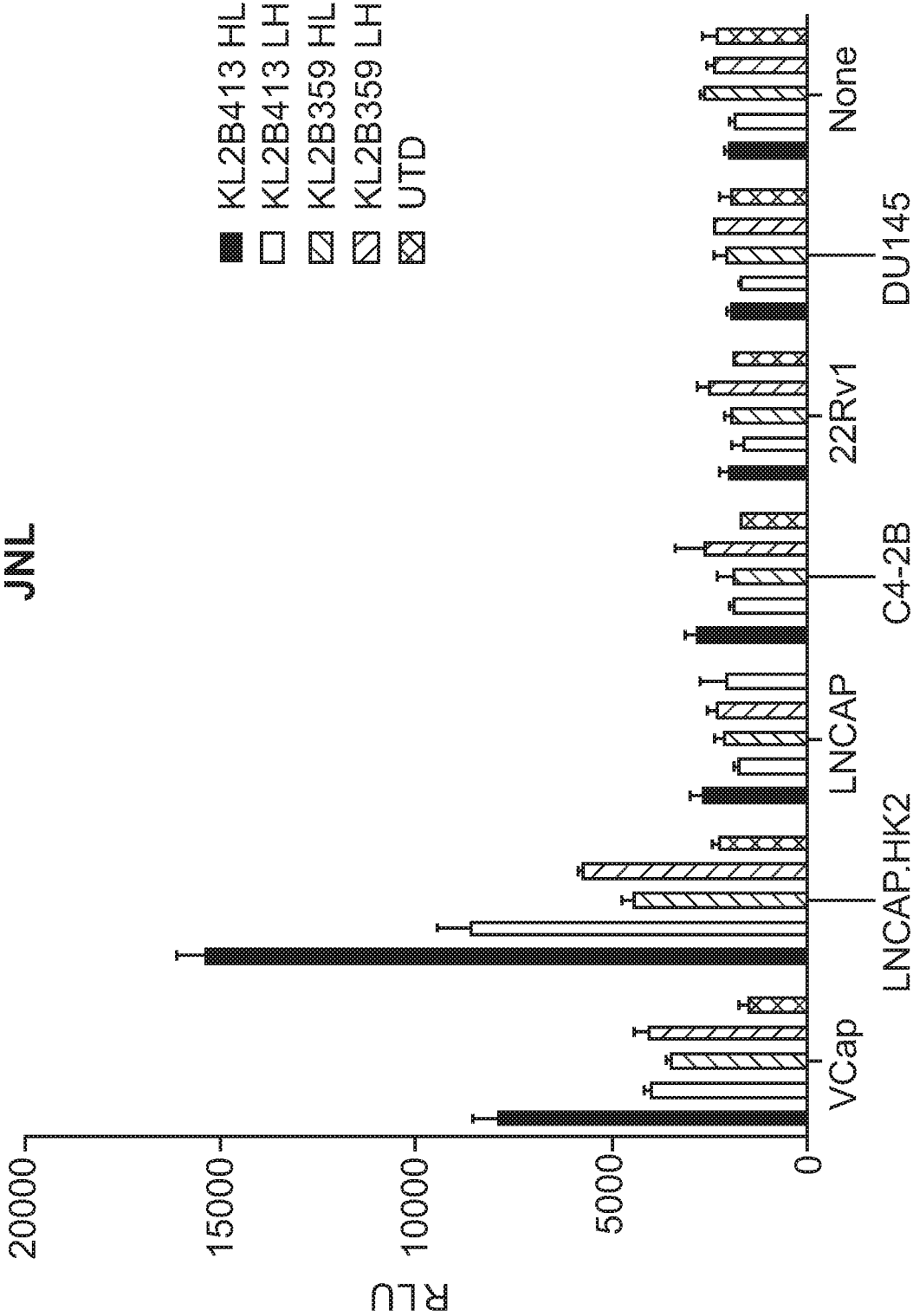


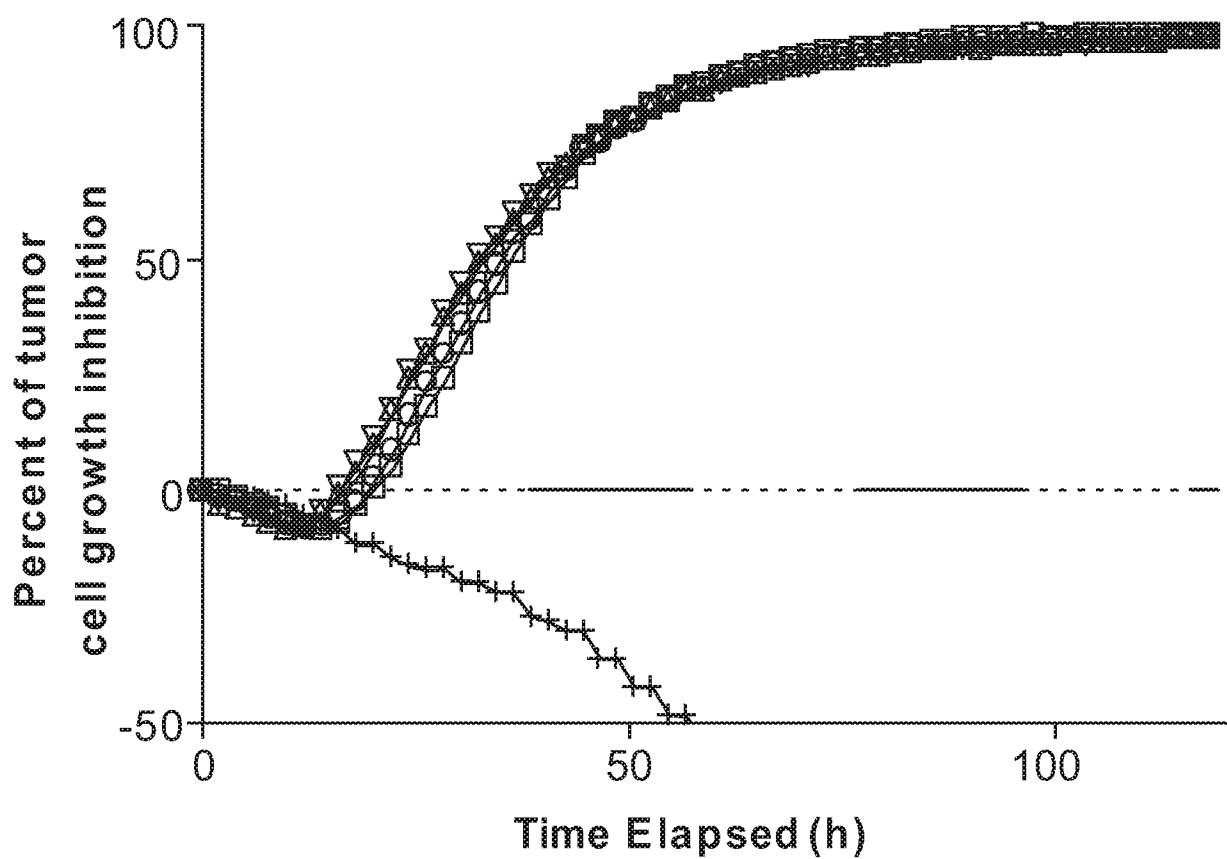
FIG. 29



59 / 85

FIG. 30

VCaP E:T=1:1



—○— B413HL

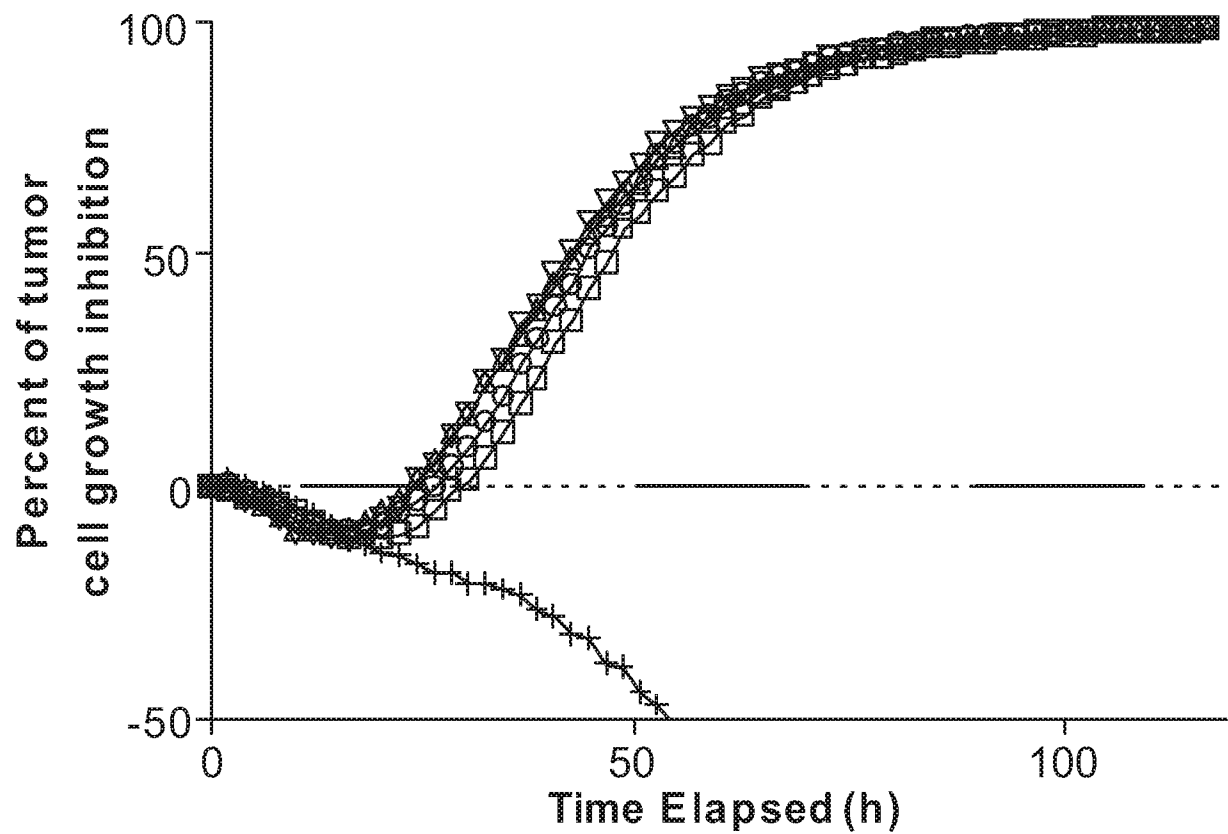
—□— B413LH

—△— B359HL

—▽— B359LH

—+— Mock UTD

60 / 85

FIG. 30(contd)**VCaP E:T=0.5:1**

- B413HL
- B413LH
- △— B359HL
- ▽— B359LH
- +— Mock UTD

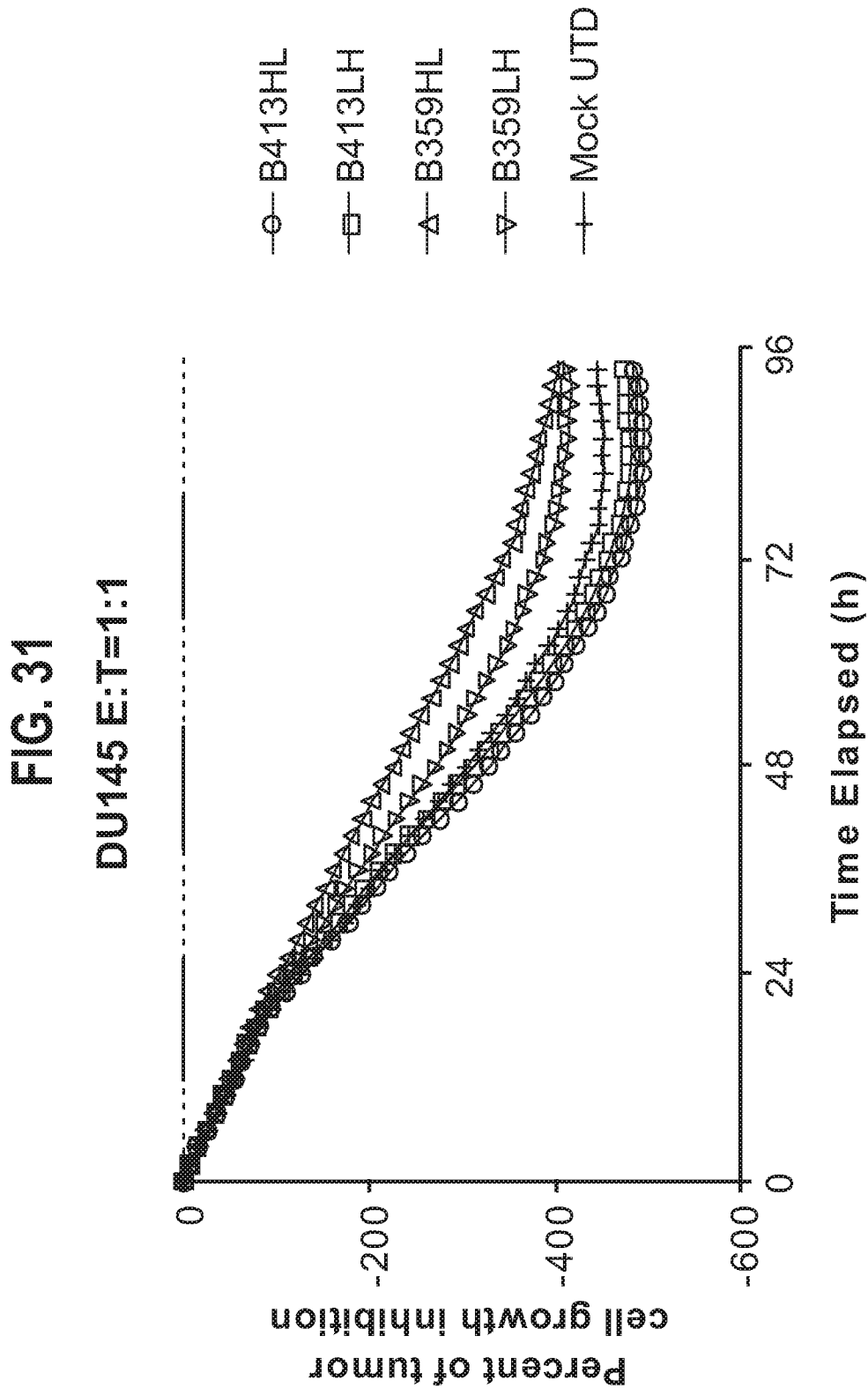


FIG. 32

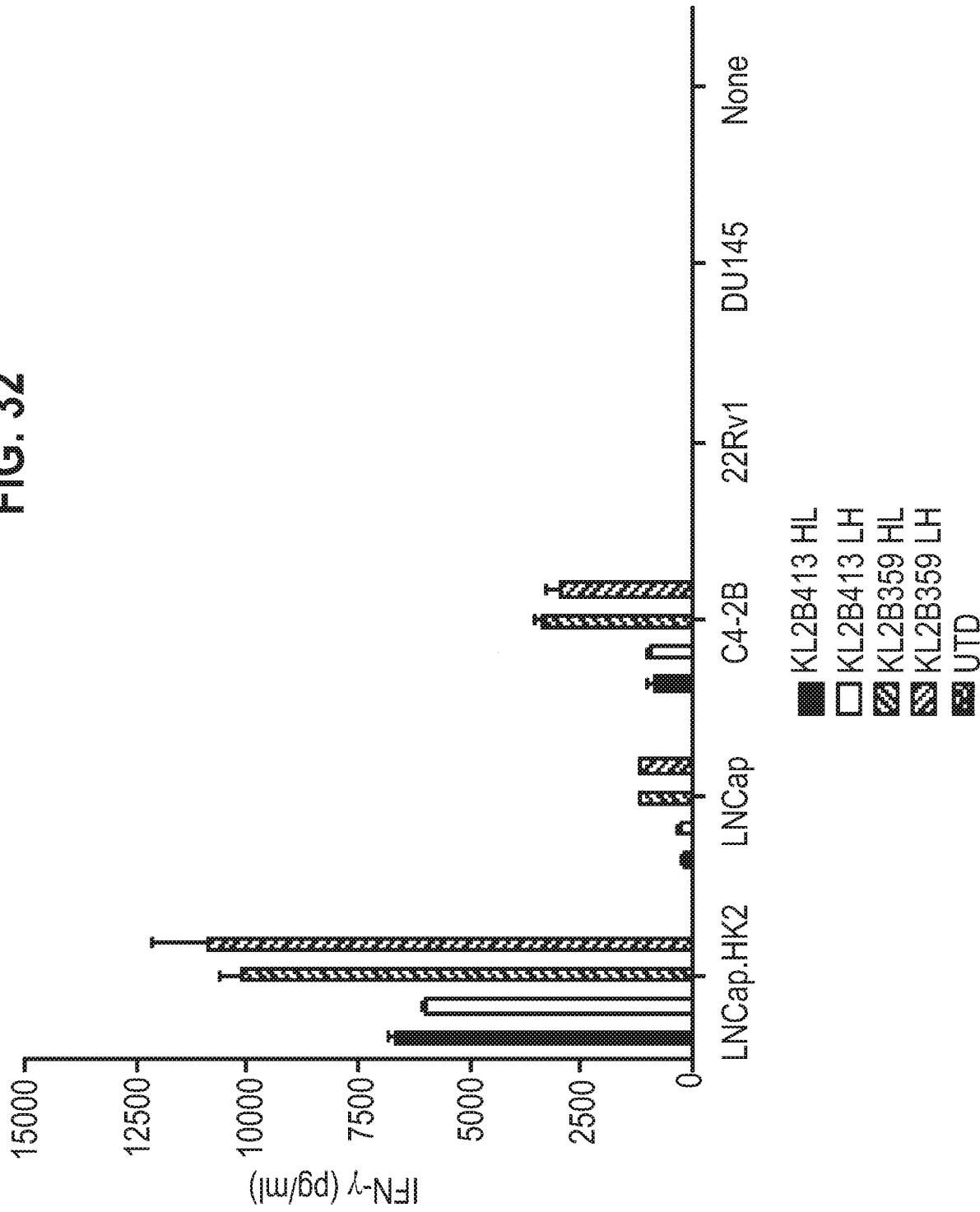
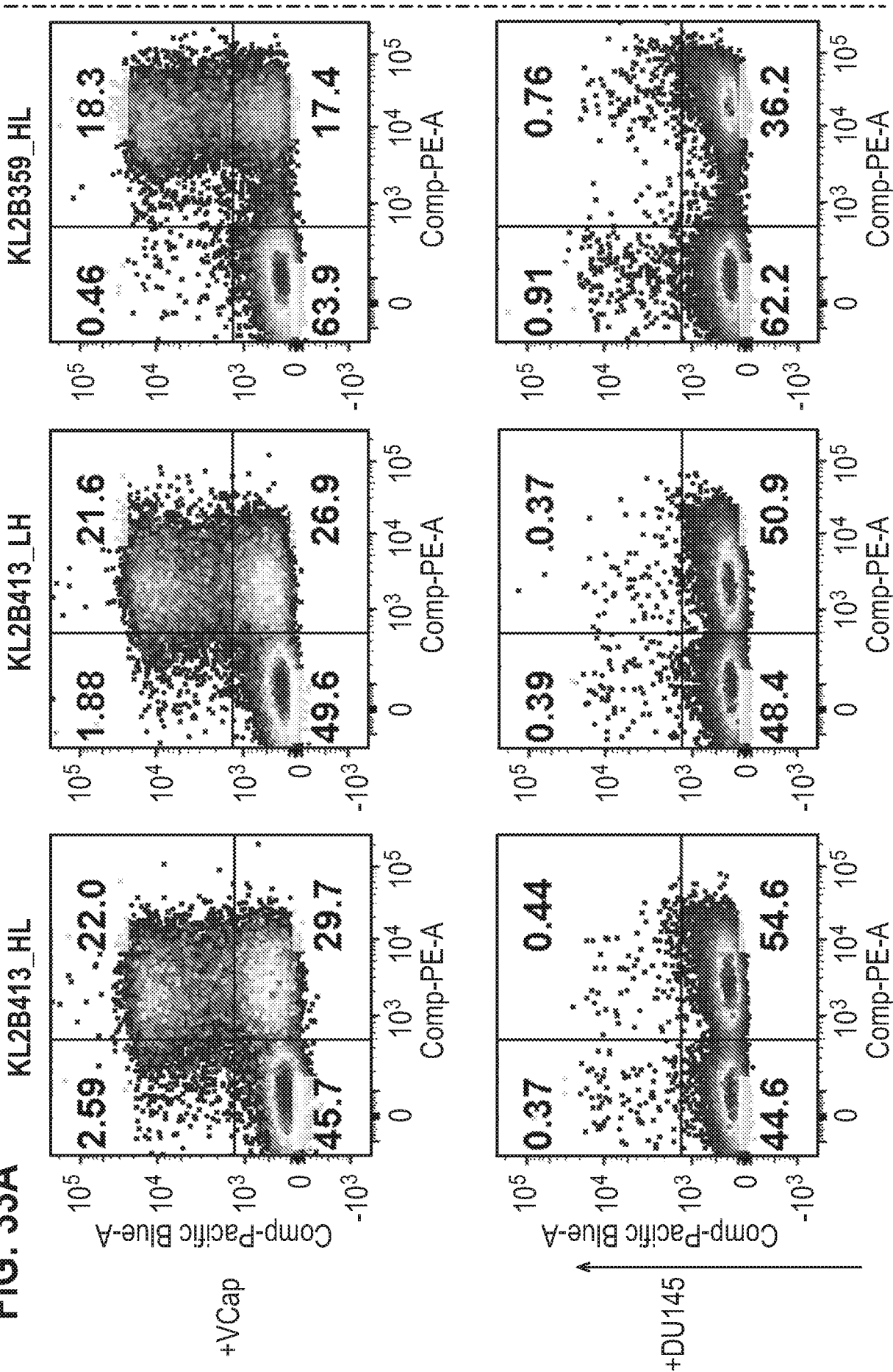


FIG. 33A



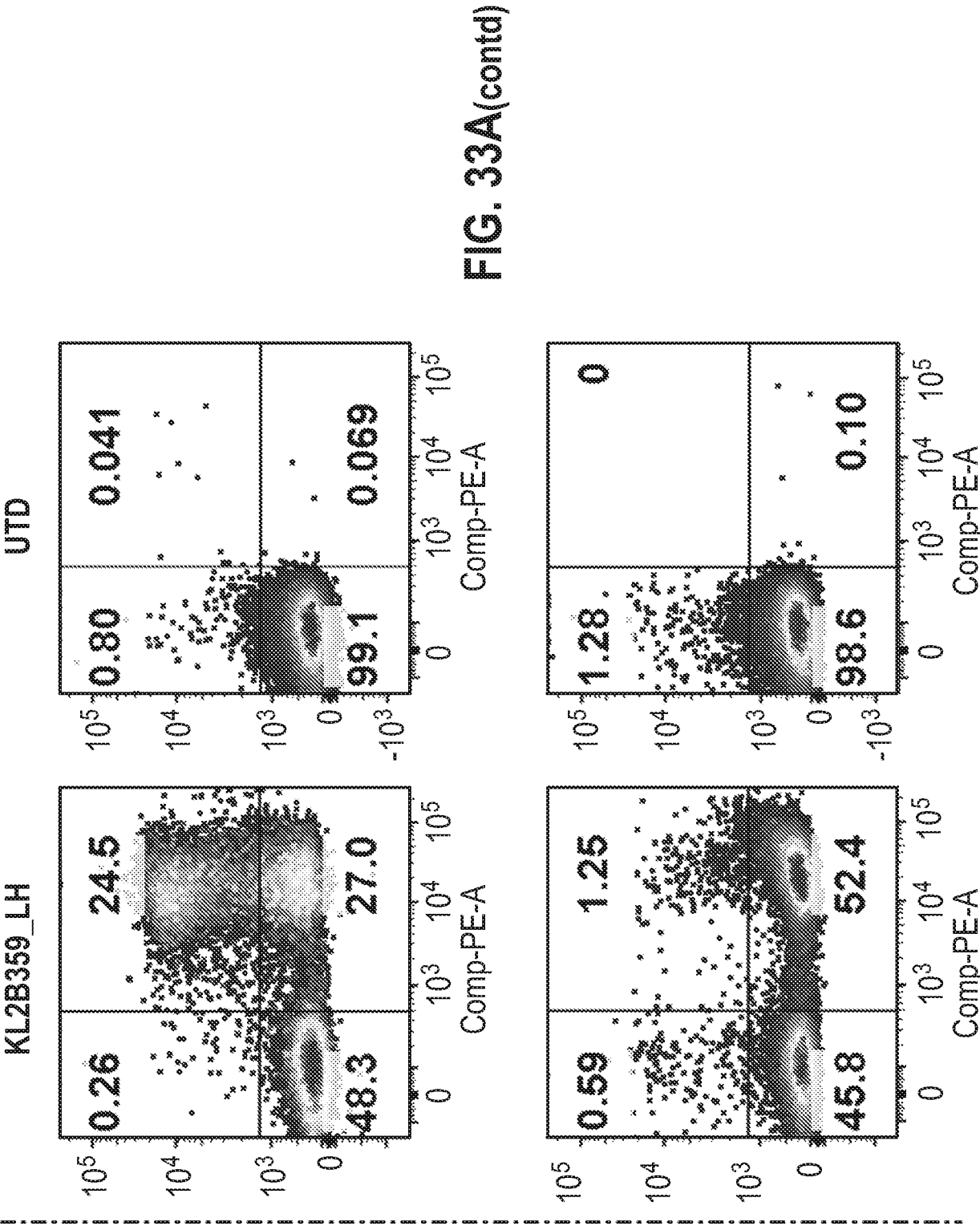
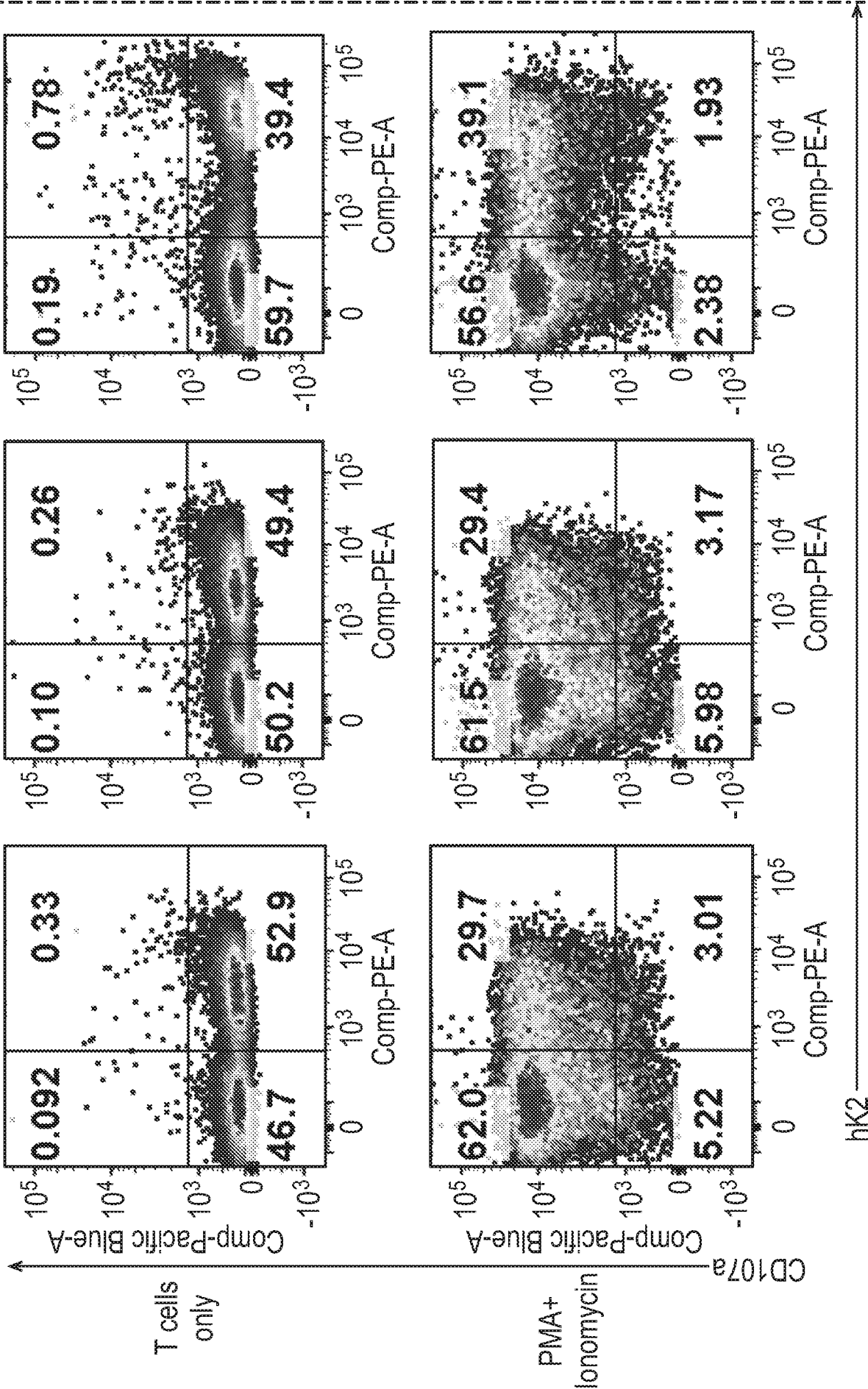
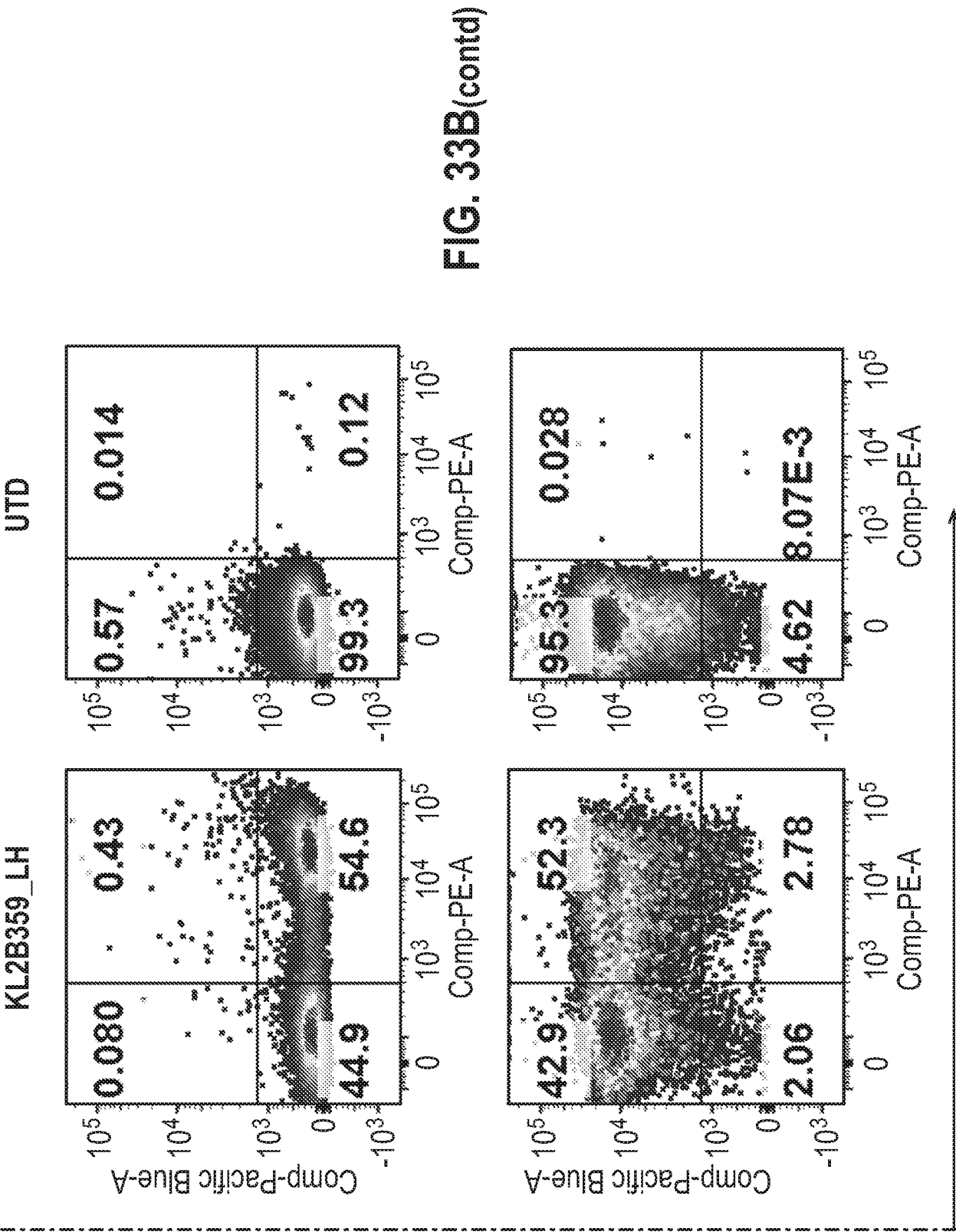


FIG. 33B





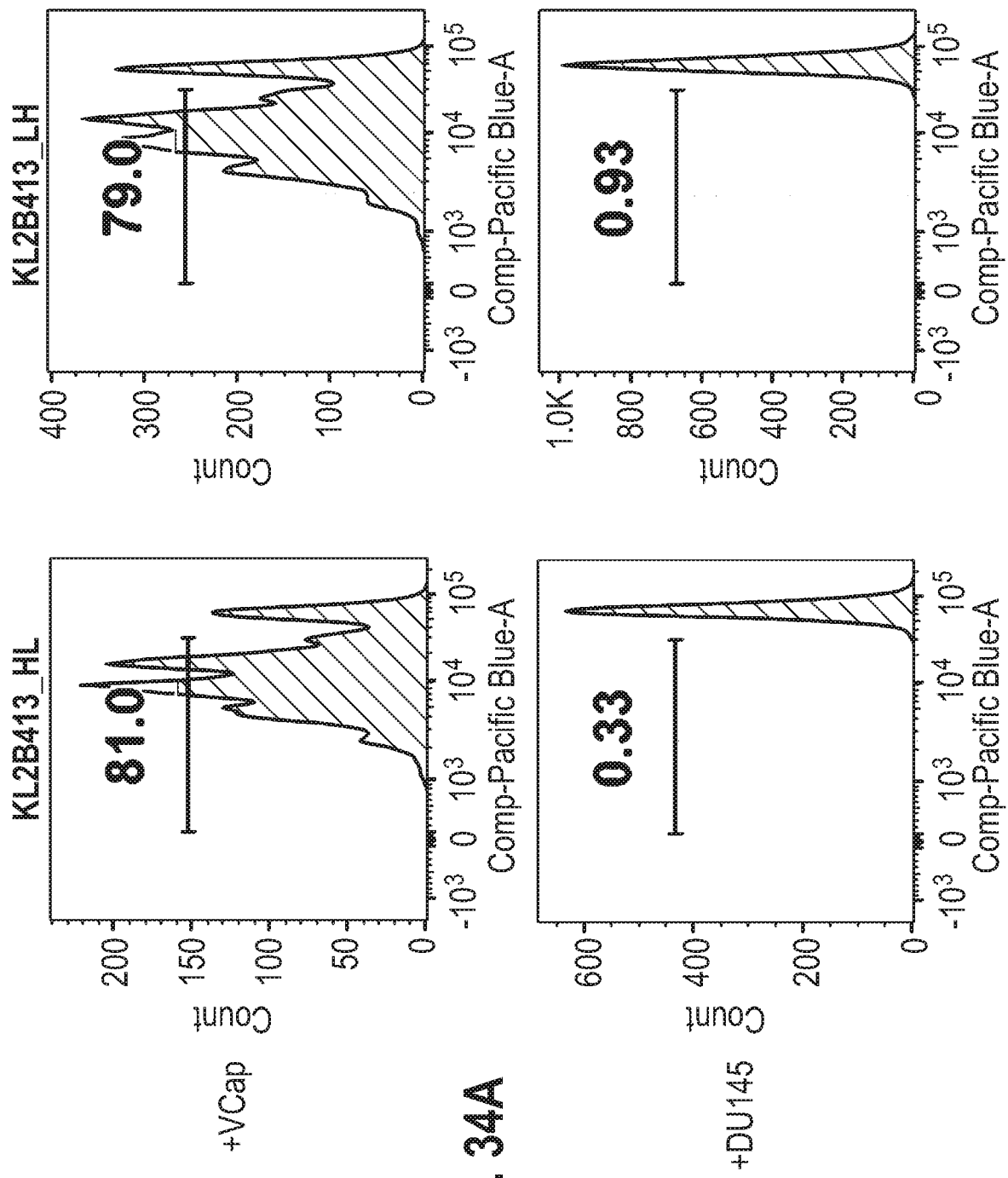
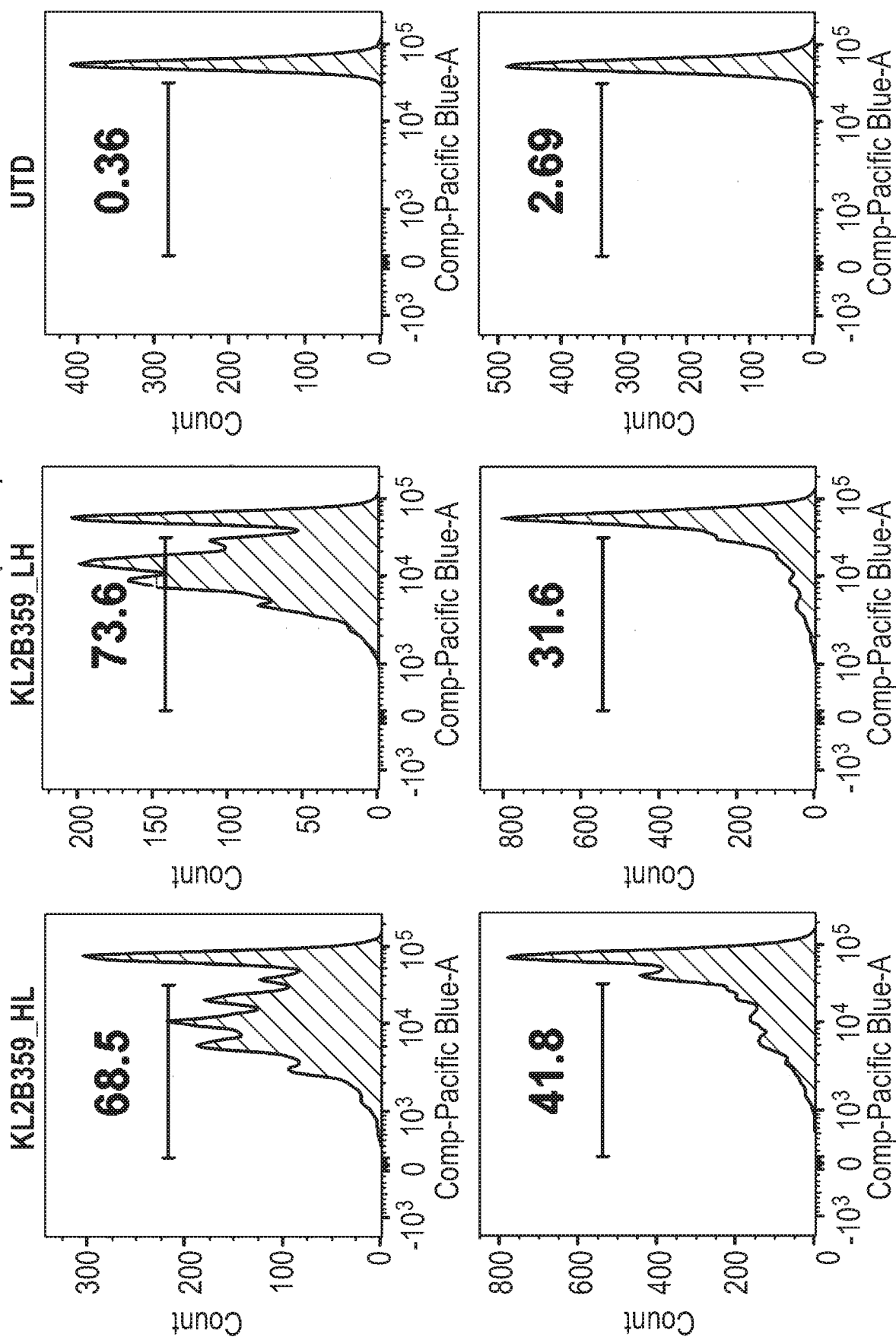


FIG. 34A

FIG. 34A(contd)



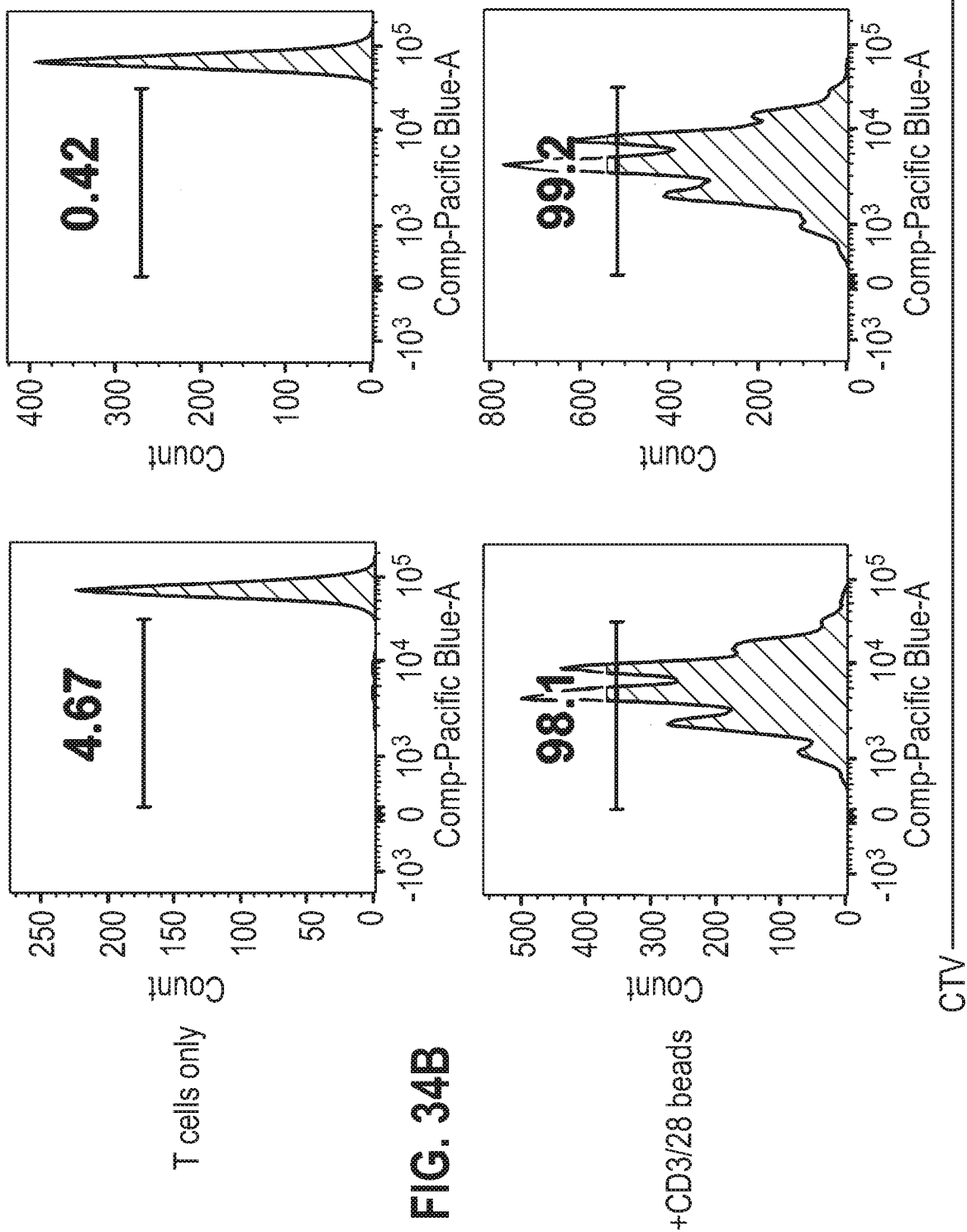


FIG. 34B

FIG. 34B(contd)

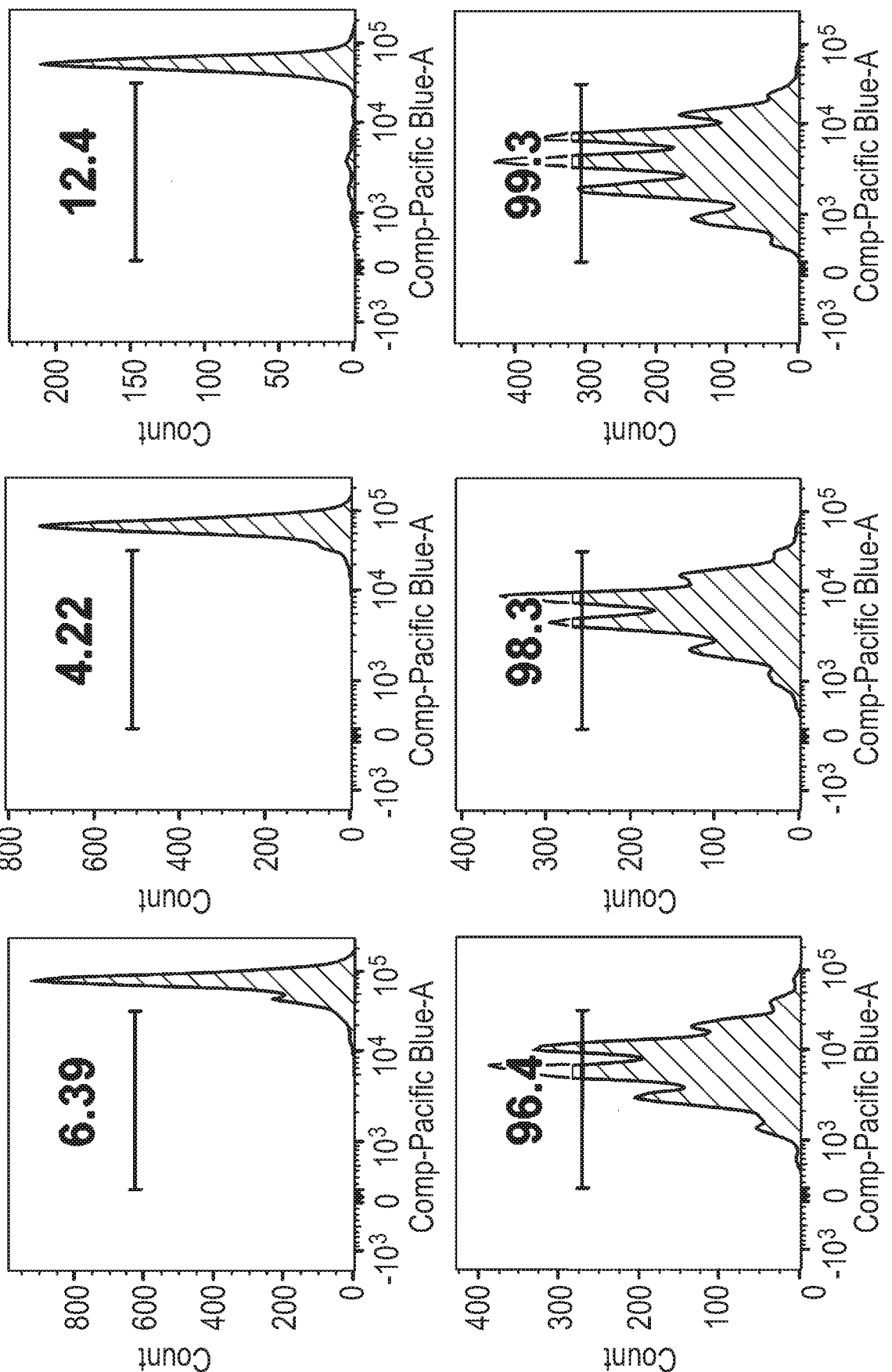


FIG. 35

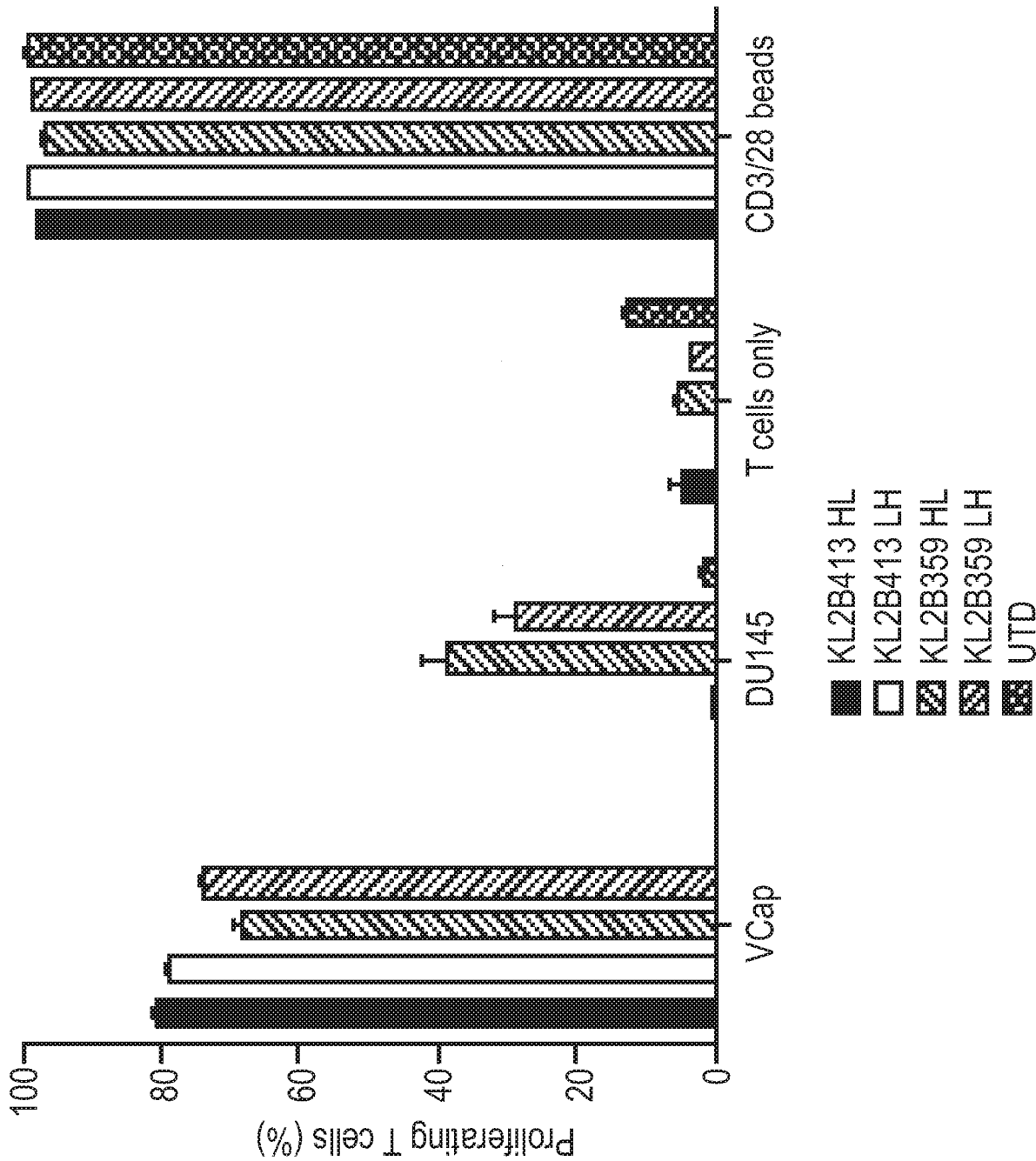
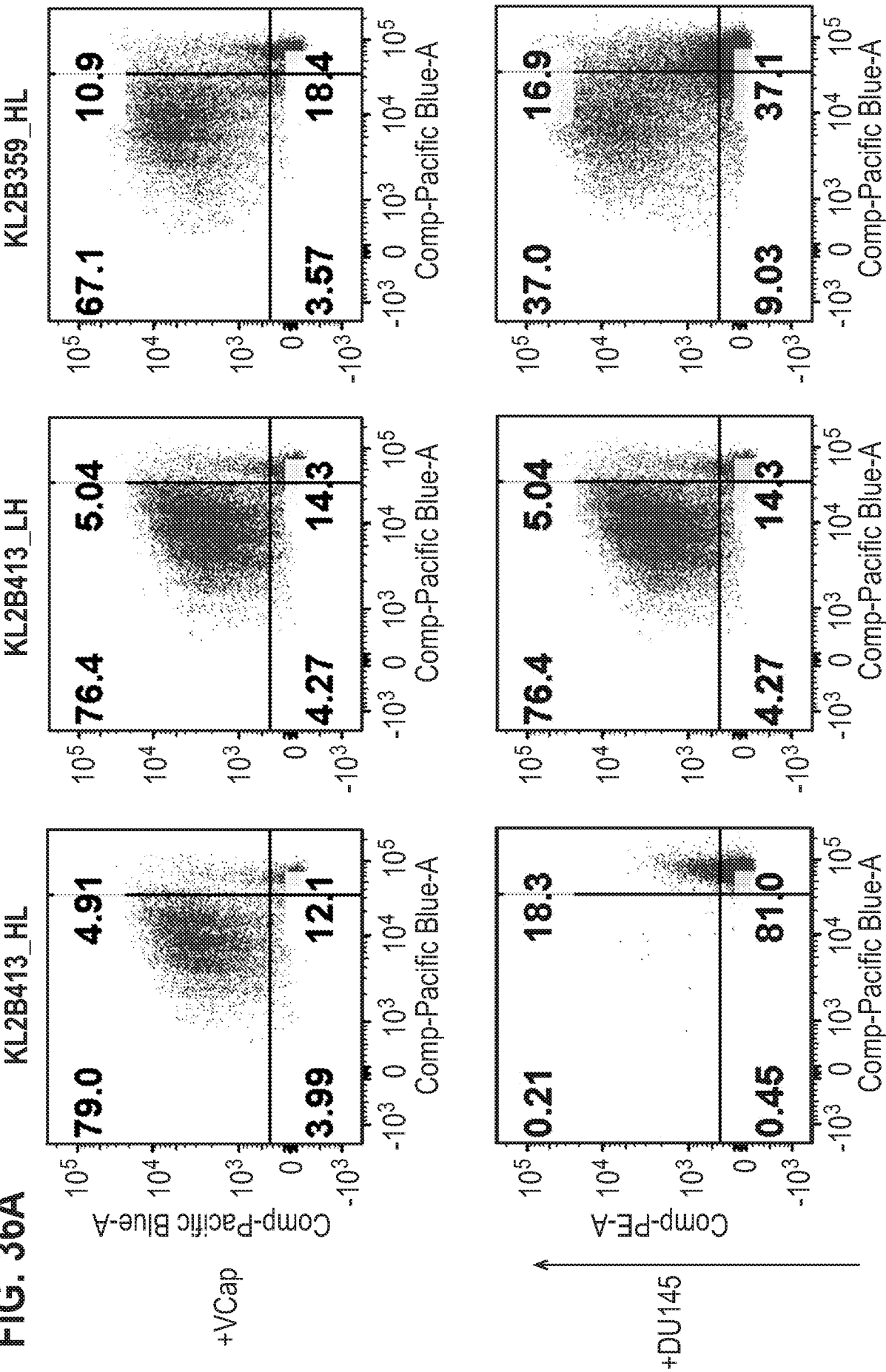


FIG. 36A



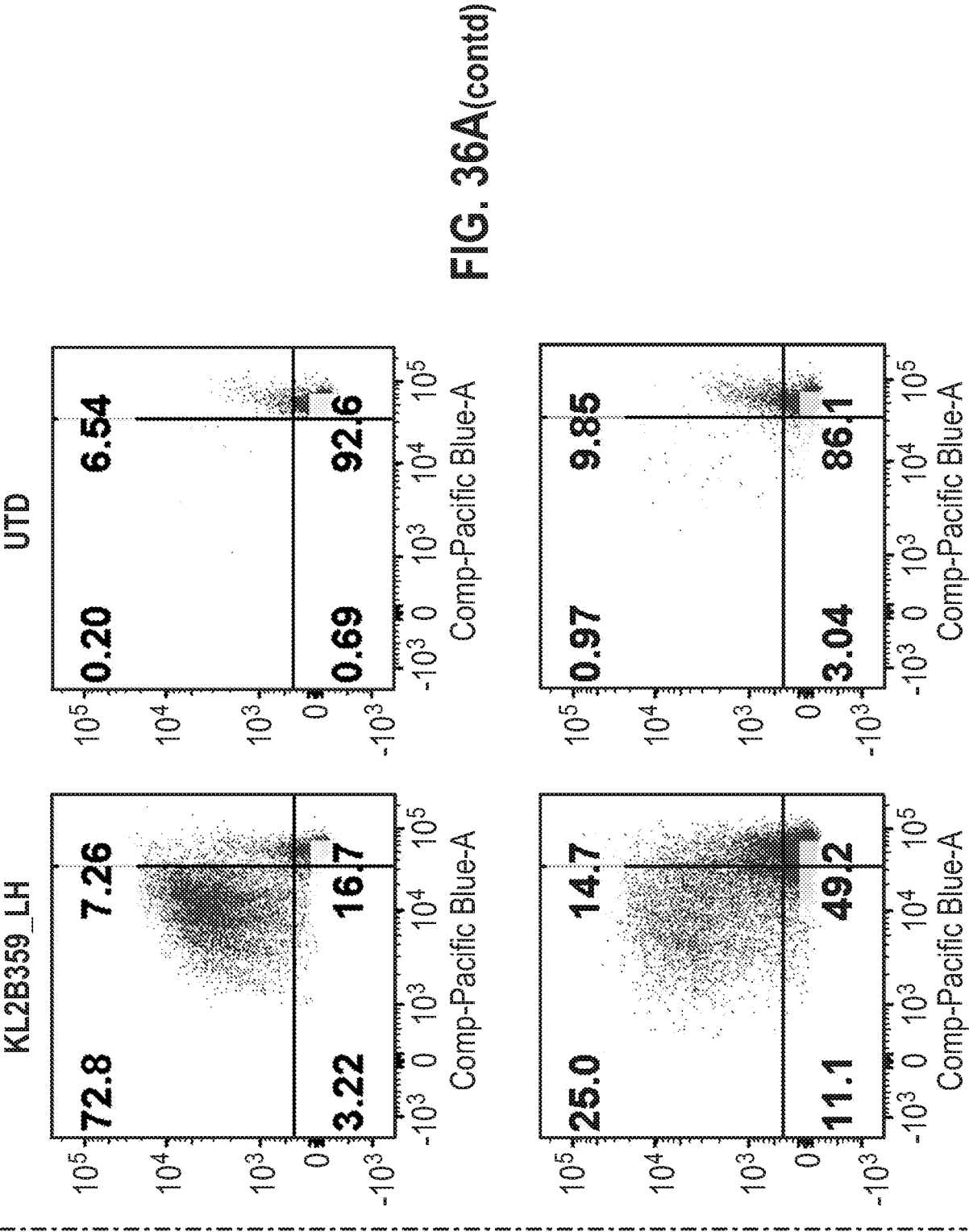
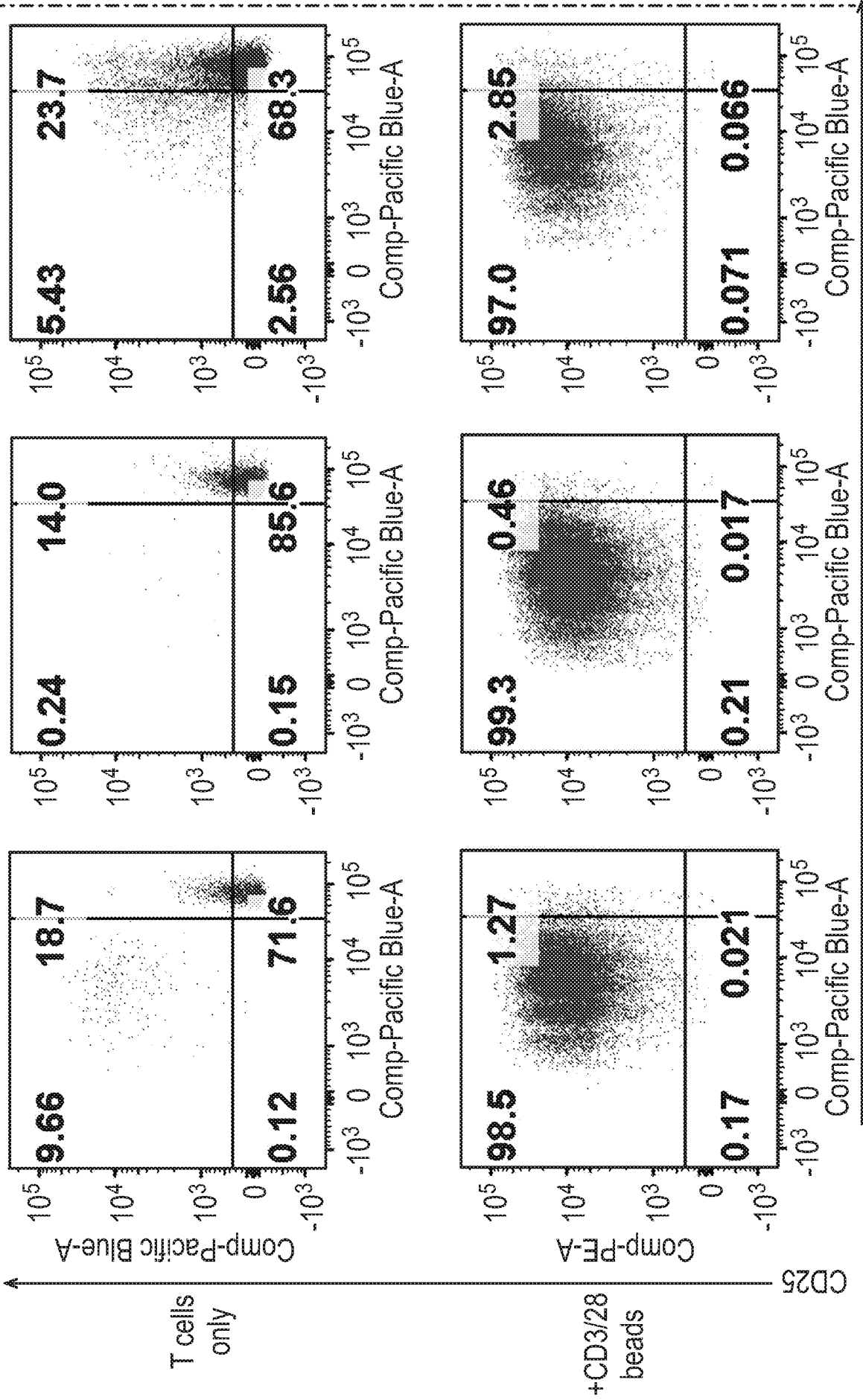


FIG. 36B



75 / 85

FIG. 36B(contd)

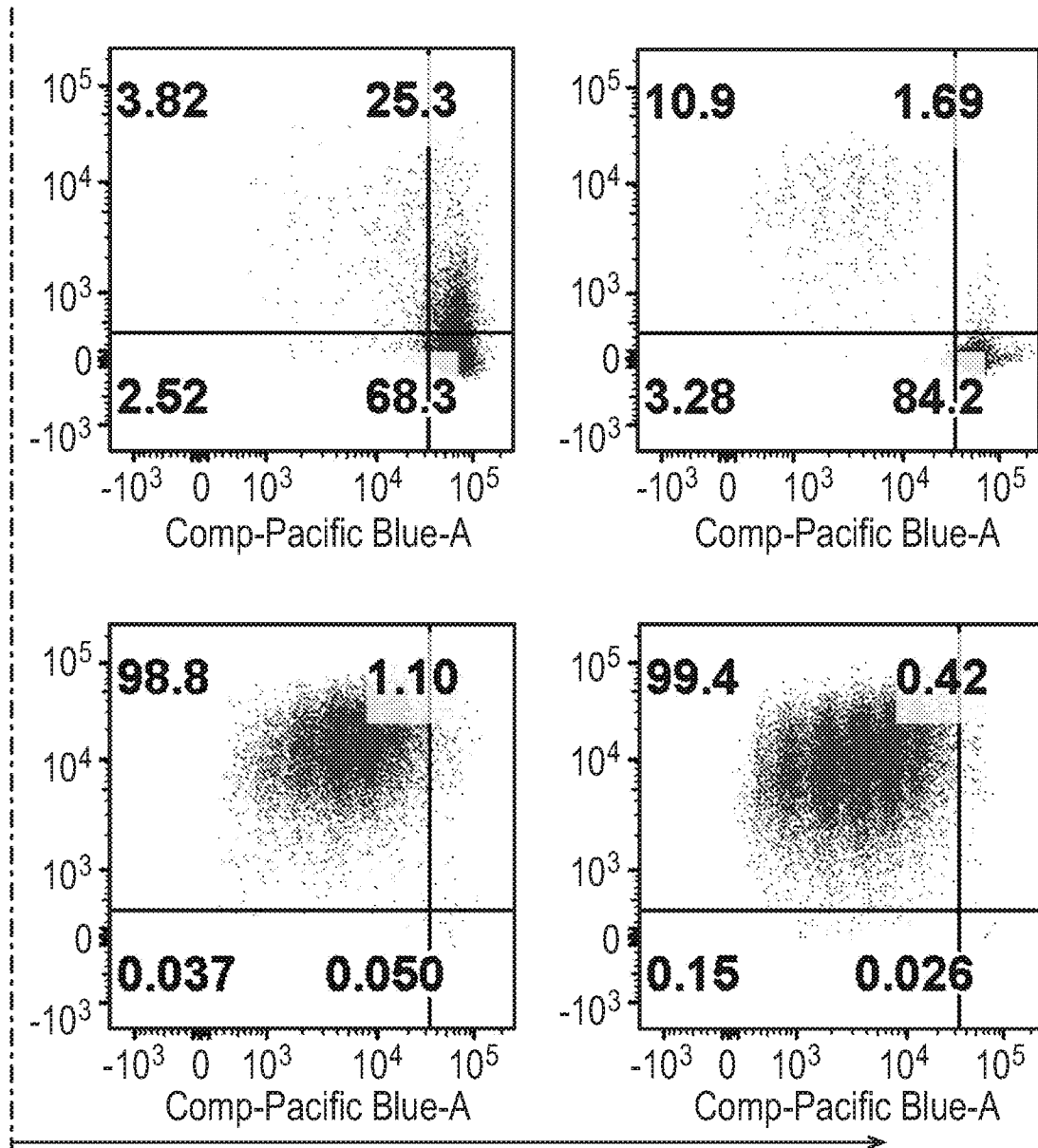
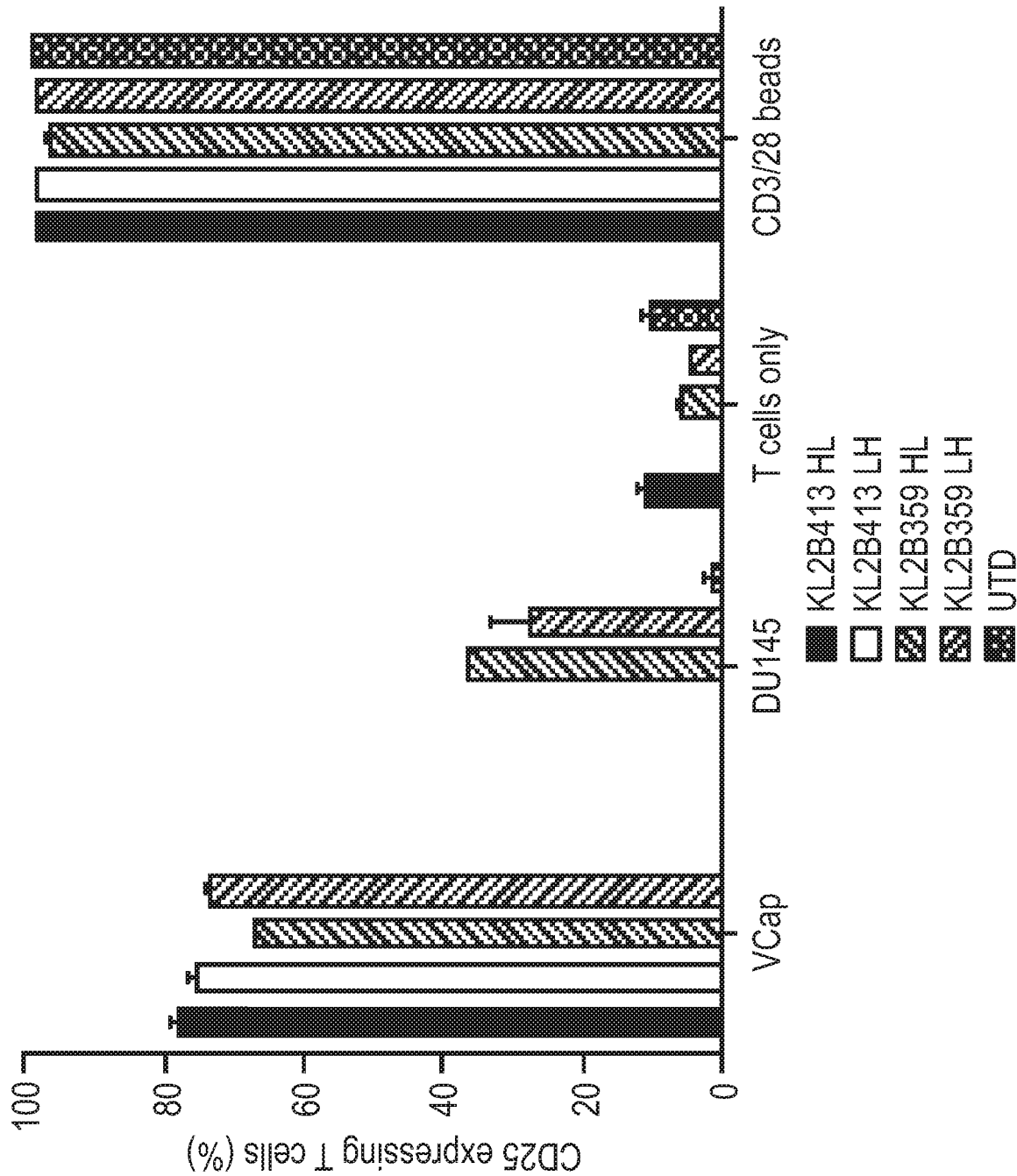


FIG. 37



77 / 85

FIG. 38A**Sequence of KL2B494 (Heavy Chain)**

QVQLVESGGG LVQPGGSLRL SCAAS**GGTTS** **HYAM**SWVRQA PGKGLEWVST
 IGGSGGSTYY **ADSVKGRFTI** SRDNSKNTLY LQMNSLRAED **TAVYYCAKPH**
WWWVALYD **QMDVWGQGT**M VTVSSASTKG PSVFPLAPSS KSTSGGTAAL
 GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS
 LGTQTYICNV NHKPSNTKVD KKVEPKSCDK THTCPPCPAP EAAGGPSVFL
 FPPKPKDTLM ISRTPEVTCV VVSVSHEDPE VKFNWYVDGV EVHNAKTKPR
 EEQYNSTYRV VSVLTVLHQD WLNKEYKCK VSNKALPAPI EKTISKAKGQ
 PREPQVYTL PPSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK
 TTPPVLDSDG SFFLYSKLTV DKSRWQQGNV FSCSVMEAL HNHYTQKSLS
 LSPGK

Sequence of KL2B494 (Light chain)

SSELTPPPSV SVAPGQTARI TCGGNNIGSK **SVHWYQQKPG** QAPVLVV**YDD**
SDRPSCLPER FSGSNSGNTA TLTISRVEAG DEADYYCQVW DSSSDHVVFQ
 GGTKLTVLGQ PKAAPSVTLF PPSSEELQAN KATLVCLISD FYPGAVTVAW
 KADSSPVKAG VETTTPSKQS NNKYAASSYL SLTPEQWKSH RSYSCQVTHE
 GSTVEKTVAP TECS

78 / 85

FIG. 38B**Sequence of KL2B467 (Heavy chain)**

QVQLVESGGG VVQPGRLRL SCAASG**FTFS** **Y**YGMHWVRQA PGKGLEWVAF
 ISYDGSNKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAHLP
 YS**GSYMAFDY** WGQGTQVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV
 KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSV TVPSSSLGTQ
 TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPEAAG GPSVFLFPPK
 PKDTLMISRT PEVTCVVVSV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY
 NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP
 QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTTP
 VLDS DGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG
 K

Sequence of KL2B467 (Light chain)

QSVLTQPPSV SVAPGQTASI TC**GGDNIGSK** **SV**HWYQQKPG QAPVLVVY**DN**
SDRPSGIPER FSGSNSGTTA TLTISRVEAG DEADYYCQVW DSSSDHPVVF
 GGGTKVTVLG QPKAAPSVTL FPPSSEELQA NKATLVCLIS DFYPGAVTVA
 WKADSSPVKA GVETTTPSKQ SNNKYAASSY LSLTPEQWKS HRSYSCQVTH
 EGSTVEKTVA PTECS

79 / 85

FIG. 38C**Sequence of hu11B6 (Heavy chain)**

QVQLQESGPG LVKPSDTLSL TCAVS~~GNSIT~~ ~~SDY~~AWNWIRQ PPGKGLEWIG
YISYSGSTTY NPSLKSRVTM SRDTSKNQFS LKLSSVTAVD TAVYYCATGY
YYGSGFWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
 PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVTVPS SSLGTQTYIC
 NVNHNKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
 LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
 RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
 LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS
 DGSFFLYSKL TVDKSRWQQG NVFSCSVME ALHNHYTQKS LSLSPGK

Sequence of hu11B6 (Light chain)

DIVLTQSPDS LAVSLGERAT INCKASESVE YFGTSLMHWY QOKPGQPPKL
LIYAASNRES GVPDRFSGSG SGTDFTLTIS SLQAEDVAVY YCQOTRKVPY
TFGQGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVCLL NNFYPREAKV
 QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLKADY EKHKVYACEV
 THQGLSSPVT KSFNRGEC

80 / 85

FIG. 38D**Sequence of KL2B413 (Heavy chain)**

EVQLVESGGG LVQPGGSLRL SCAAS**GF**TS SYWMTWVRQP PGKGLEWVAN
IKQDGSERYF VDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYC**ARDQ**
NYDILTGHYG MDVWGQGTTV TVSSASTKGP SVFPLAPCSR STSESTAALG
 CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL
 GTKTYTCNVD HKPSNTKVDK RVESKYGPPC PPCPAPEAAG GPSVFLFPPK
 PKDTLMISRT PEVTCVVVDV SQEDPEVQFN WYVDGVEVHN AKTKPREEQF
 NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK GLPSSIEKTI SKAKGQPREP
 QVYTLPPSQE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTTP
 VLDS DGSFFL YSRLTVDKSR WQEGNVFSCS VMHEALHNHY TQKSLSLSLG
 K

Sequence of KL2B413 (Light chain)

EIVLTQSPSF LSASVGDRVT ITCRASQGIS SYLSWYQQKP GKAPKLLIYA
TSTLQSGVPS RFSGSGSGTE FTLTISSLQP EDFATYYCQQ LNSYPRTFGQ
 GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV
 DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYEKHK VYACEVTHQG
 LSSPVTKSFN RGEC

81 / 85

FIG. 38E

Sequence of KL2B30 Fab of KLCB80 bispecific (heavy chain)

QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYWSWIRQP PGKGLEWIGY
IYYSGSTNYN PSLKSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCAGTW
EGVWTFNYY GMDVWGQGT VTVSSASTKG PSVFPLAPSS KSTSGGTAAL
GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS
LGTQTYICNV NHKPSNTKVD KKVEPKSCDK THTCPPCPAP EAAGGPSVFL
FPPKPKDTLM ISRTPEVTCV VVSVSHEDPE VKFNWYVDGV EVHNAKTKPR
EEQYNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ
PREPQVYVLP PSREEMTKNQ VSLCLVKGF YPSDIAVEWE SNGQPENNYL
TWPPVLDSDG SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS
LSPG

Sequence of KL2B30 Fab of KLCB80 bispecific (light chain)

DIQMTQSPSF LSASVGDRVT ITCRASOGIS SYLAWYQQKP GKAPKFLIVA
ASTLOSGVPS RFGSGSGTE FTLTISSLQP EDFATYYCQQ LNSYPLTFGG
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV
DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYEKHK VYACEVTHQG
LSSPVTKSFN RGEC

82 / 85

FIG. 38F

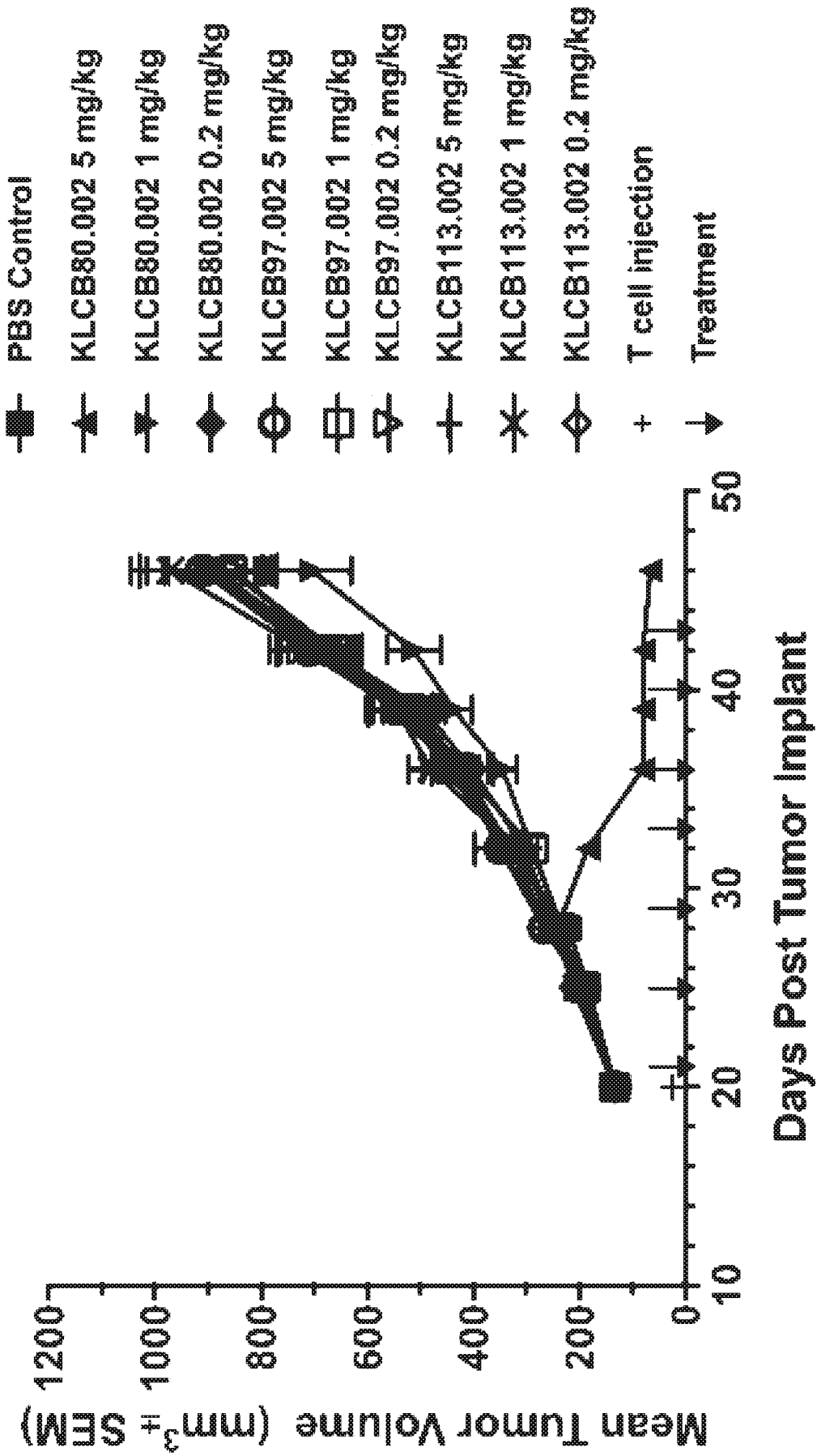
Sequence of KL2B353 Fab of KLCB113 bispecific (heavy chain)

EVQLVESGGG VVQPGRSLRL SCVASGFTFS SYDIHWVRQA PGKGLEWVAI
ISYDGSKKDY TDSVKGRFTI SRDNSKNTLY LQMDSLRVED SAVYSCARES
GNSHYYYYGM DVWGQGTMTV VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEA AGGPSVFLEP
PKPKDTLMIS RTPEVTCVTV SVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYVLPSS REEMTKNQVS LLCLVKGFYP SDIAVEWESN GPENNYLTW
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS
PG

Sequence of KL2B353 Fab of KLCB113 bispecific (heavy chain)

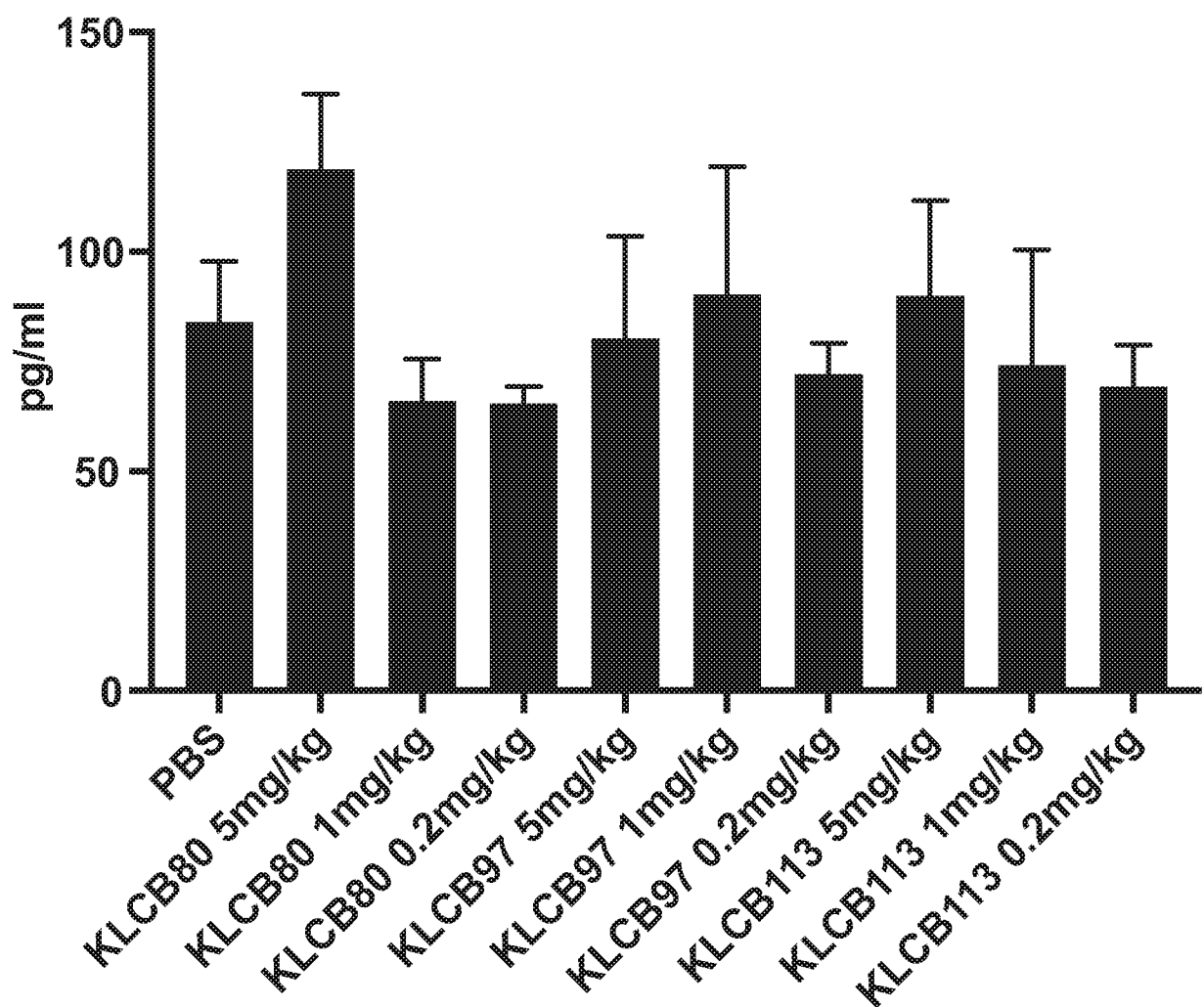
DIVMTQSPSS LSASVGDRVT ITCRASQDIS NYLAWYQQKP GKVPKFLIYA
ASTLHSGVPS RFSGSGSGTD FTLTISSLQP EDVATYYCQK YNSAPYTFGQ
GTRLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV
DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYEKHK VYACEVTHQG
LSSPVTKSFN RGEK

FIG. 39A
KLK2xCD3 Redictors in vCaP



84 / 85

FIG. 39B

IFN- γ 6h

85 / 85

FIG. 39B(contd)

