

FIGURE 1

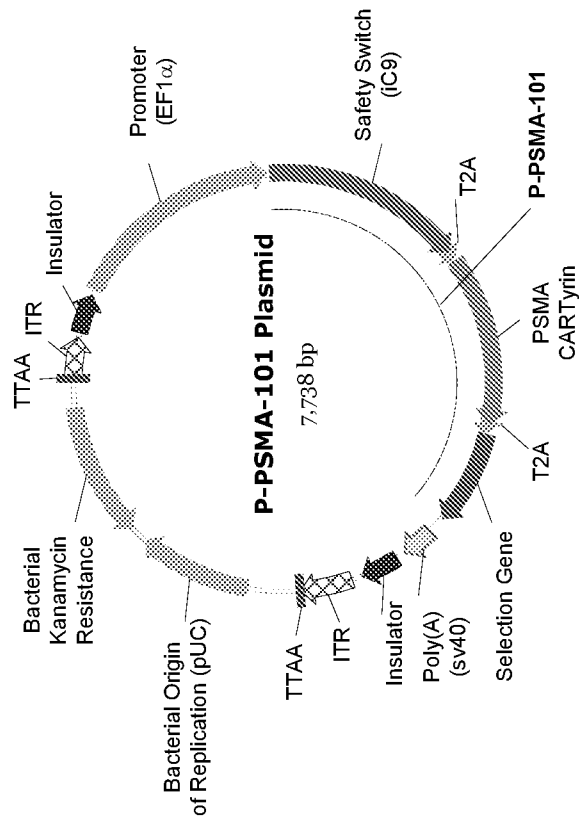


FIGURE 2

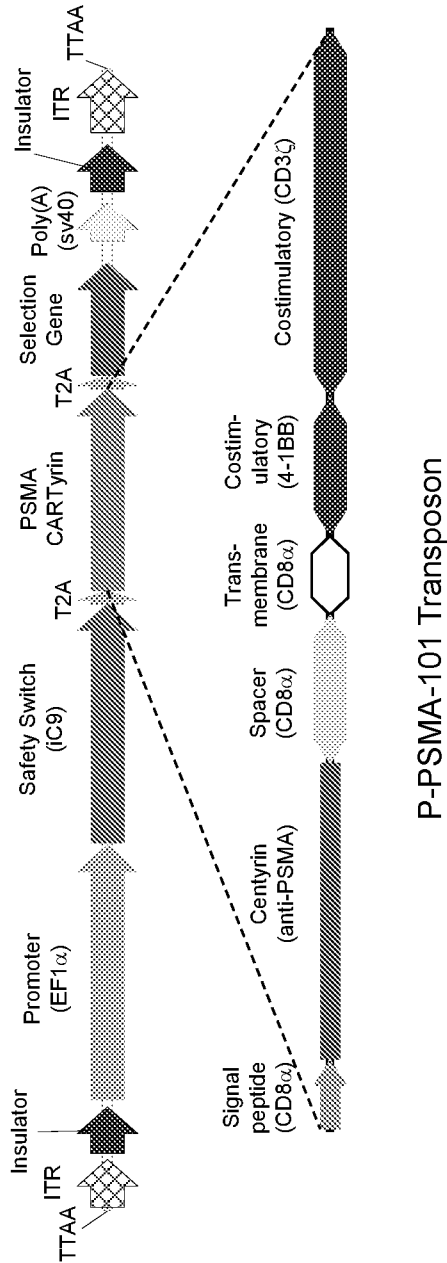


FIGURE 3A

PSMA5 CARTYRIN:
SIGNAL PEPTIDE: MALPVTALLPLALLHAARP (SEQ ID NO: 18004)
CENTYRIN (PSMA5):
MLPAPKNLVSRVTEDSARLSWDIDEQRDWFESFLIQYQSEKVGAEIVLTVPGSERSYDLTGLKPGTEYTVSIYGV
YHVYRSNPLSAIFTT (SEQ ID NO: 18000)
HINGE (CD8 α): TTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD (SEQ ID NO: 18014)
TRANSMEMBRANE (CD8 α): IYIWAFLAGTCGVLLLSLVITLYC (SEQ ID NO: 18006)
COSTIMULATORY DOMAIN #1 (4-1BB): KRGRKKLLYIFKQPFMRPVQTTQEEDGCSRCRFPFEEEEGGCEL (SEQ
ID NO: 18012)
COSTIMULATORY DOMAIN #2 (CD3 ζ):
RVKFSRSADAPAYKQGQNQLYNELNLRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQDKMAEAYSEI
GMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 18008)

P-PSMA5-101 CONSTRUCT:
MALPVTALLPLALLHAARPMLPAPKNLVSRVTEDSARLSWDIDEQRDWFESFLIQYQSEKVGAEIVLTVPGSE
RSYDLTGLKPGTEYTVSIYGVYHVYRSNPLSAIFTTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD
FACDIYIWAFLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSRCRFPFEEEEGGCELRVKFSRS
ADAPAYKQGQNQLYNELNLRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGER
RRKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 18063)

FIGURE 3B

PSMA5 CARTYRIN:
SIGNAL PEPTIDE:
ATGGCACTGCCTGTGACAGCCCTGCTGCTGCCTCTGGCCCTGCTGCTGCACGCACACGGCCC
(SEQ ID NO: 18064)
CENTYRIN (PSMA5):
ATGCTGCC TGCACCAAGAACCTGGTGGTGCTCTCGGGTGACCGAGGACTCTGCCAGACTGAGCTGGGACATC
GATGAGCAGAGGGATTGGTTCGAGAGCTTTCTGATCCAGTATCAGGAGTCCGAGAAAGTGGCGAGGGCCATC
GTCTGACAGTGCCTGGCAGCGAGCGGTCTATGACCTGACCGGCCCTGAAGCCAGGCACAGATACACCGT
GTCCATCTACGGCGTGATCACGTGTACAGGTCCAATCCTCTGTCTGCCATCTTCACCACA
(SEQ ID NO: 18001)
HINGE (CD8 α):
ACCACAACCCCTGCCCCCGAGACCTCCCACACCCCGCCCTACCATCGCGAGCCAGCCACTGTCCCTGCCGCCCT
GAGGCCTGCCGGCCCGCCCGCGGAGCAGTGACACACGCGGCCCTGGACTTTGCCCTGTGAC
(SEQ ID NO: 18065)
TRANSMEMBRANE (CD8 α):
ATCTACATATGGGCACCACCTGGCAGGAACCTGCGGCGTGCTGCTGCTGAGCCTGGTCATCACCCCTGTACTGT
(SEQ ID NO: 18066)
COSTIMULATORY DOMAIN #1 (4-1BB):
AAGAGAGGCAGGAAGAGCTGCTGTATATCTTCAAGCAGCCCTTCATGAGACCCGTGCAGACCACACAGGAG
GAGGACGGCTGCTCTTGTAGTTCCAGAGGAGGAGGAGGGAGGATGCGAGCTG (SEQ ID NO: 18067)
COSTIMULATORY DOMAIN #2 (CD3 ζ):
CGCGTGAAGTTTAGCCGGTCCGCCGATGCACCTGCATACAAAGCAGGGACAGAACCGCTGTATAACGAGCTG
AATCTGGCCCGAGAGAGAGGAGTACGAGCTGCTGGATAAGAGGGGGGGCCGGGACCCCGAGATGGGAGGCA
AGCCTCGGAGAAAGAACCCACAGGAGGGCCTGTACAAATGAGCTGCAAAAGGACAAGATGGCCGAGGCCTATT
CTGAGATCGGCATGAAGGGAGAGAGGCGCCGGGGCAAGGGACACGATGGCCTGTACCCAGGGCCTGAGCAC
CGCCACAAGGACACCTATGATGCCCTGCACATGCAGGGCCCTGCCCCCTAGTA (SEQ ID NO: 18068)

FIGURE 3C

P-PSMA5-101 CONSTRUCT:
CTGGCACTGCCTGTGACAGCCCTGCTGCCTCTGGCCCTGCTGCTGCACGCAGCACGGCCCCATGCTGCCT
GCACCAAGAACCTGGTGGTCTCGGGTGACCGAGGACTCTGCCGACTGAGCTGGGACATCGATGAGCA
GAGGATTGGTTCGAGAGCTTTCTGATCCAGTATCAGGAGTCCGAGAAAGTGGCGAGGCCATCGTGTGAC
AGTGCTGGCAGCGAGCGGTCTATGACCTGACCGGCTGAAGCCAGGCACAGTACCCGTGTCCTCTA
CGCGTGATCAGGTACAGGTCCATCTCTGTGCCATCTTCACCACAACCAACCCCTGCCCCAGA
CCTCCACACCCGCCCTACCATCGCAGCCAGCCACTGTCCCTGCGGCTGAGGCTGCCGCCGCCGC
CGCGGAGCAGTGCACACACGGGCCCTGGACTTTGCGTGTGACATCTACATATGGGCACCACTGGCAGGAA
CCTGCGCGTGTGCTGCTGAGCCTGGTCATACCCCTGTAAGAGAGGCGAGGAAAGCTGCTGTATA
TCTTCAAGCAGCCCTTCATGAGACCCGTGCAGACCACACAGGAGGAGCGTCTCTTGTAGTTCCCAG
AGGAGGAGGAGGGAGGATCGAGCTGCGCTGAAGTTTAGCCGGTCCCGCATGCCTGCATACAAGCAG
GGACAGAACCACTGTATAACGAGCTGAACTCTGGGCCGGAGAGAGGATACGACGTGCTGGATAAGAGCG
GGCCGGGACCCCGAGATGGGAGCAAGCTCGGAGAAAGAACCCACAGGAGGCTGTACAATGAGCTG
CAAAAGGACAAAGTGGCCGAGGCCTATTCTGAGATCGGCATGAAGGAGAGAGGCGCCGGGCAAGGACA
CGATGGCCTGTACGAGGCTGAGCACCGCCACAAAGGACACCTATGATGCCCTGCACATGCAGGCCCTGC
CCCCTAGA (SEQ ID NO: 18069)

FIGURE 4A

PSMA8 CARTYRIN:
SIGNAL PEPTIDE: MALPVTALLPLALLHAARP (SEQ ID NO: 18004)
CENTYRIN (PSMA8):
MLPAPKNLVSRVTEDSARLSWAIDEQRDWFESFLIQYQSEKVGAEIVLTVPGSERSYDLTGLKPGTEYTVSIYGV
YHVYRSNPLSAIFTT (SEQ ID NO: 18002)
HINGE (CD8 α): TTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD (SEQ ID NO: 18014)
TRANSMEMBRANE (CD8 α): IYIWAFLAGTCGVLLLSLVITLYC (SEQ ID NO: 18006)
COSTIMULATORY DOMAIN #1 (4-1BB): KRGRKKLLYIFKQPFMRPVQTTQEEDGCSRCRFEDEEGGCEL (SEQ
ID NO: 18012)
COSTIMULATORY DOMAIN #2 (CD3 ζ):
RVKFSRSADAPAYKQGQNLNLYNELNGRREYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQDKMAEAYSEI
GMKGERRRGKGGHDGLYQGLSTATKDYDALHMQALPPR (SEQ ID NO: 18008)

P-PSMA8-101 CONSTRUCT:
LALPVTALLPLALLHAARPMLPAPKNLVSRVTEDSARLSWAIDEQRDWFESFLIQYQSEKVGAEIVLTVPGSE
RSYDLTGLKPGTEYTVSIYGVYHVYRSNPLSAIFTTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD
FACDIYIWAFLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSRCRFEDEEGGCELRVKFSRS
ADAPAYKQGQNLNLYNELNGRREYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGER
RRKGHDGLYQGLSTATKDYDALHMQALPPR (SEQ ID NO: 18070)

FIGURE 4B

PSMA8 CARTYRIN:
SIGNAL PEPTIDE:
ATGGCACTGCCTGTGACAGCCCTGCTGCCTCTGGCCCTGCTGCTGCACGCACGGGCC
(SEQ ID NO: 18064)
CENTYRIN (PSMA8):
ATGCTGCCTGCACCAAGAACCTGGTGGTCTCGGGTACCAGAGACTTCCAGACTGAGCTGGGCCATC
GACGAGCAGAGGGATTGGTCGAGAGCTTTCTGATCCAGTATCAGGAGTCCGAGAAAGTGGCGAGGCCATC
GTGCTGACAGTCCCTGGCAGCGCGGTCTTGA TCTGACCGCCCTGAAGCCAGGCACAGGTACACCGT
GTCCATCTACGGCGGTGTATCAGGTGTACAGGTCCAATCCTCTGCTGCCATCTTCAACACA
(SEQ ID NO: 18003)
HINGE (CD8_α):
ACCACAACCCCTGCCCCCAGACCTCCACACCCGCCCTACCATCGCAGCCACTGTCCCTGCGGCCT
GAGCCTGCCGGCCCGCCCGGGGAGCAGTGCACACACGGGGCCTGGACTTTGCCTGTGAC
(SEQ ID NO: 18065)
TRANSMEMBRANE (CD8_α):
ATCTACATATGGGCACCACTGGCAGGAACCTGCGGCGTGTGCTGCTGAGCCTGGTCAACCCGTACTGT
(SEQ ID NO: 18066)
COSTIMULATORY DOMAIN #1 (4-1BB):
AAGAGAGGCAGGAAGCTGTGTATATCTTCAAGCAGCCCTTCATGAGACCCGTGCAGACCACACAGGAG
GAGGACGGCTGCTTTGTAGGTTCCAGAGAGGAGGAGGGAGGATGCGAGCTG (SEQ ID NO: 18067)
COSTIMULATORY DOMAIN #2 (CD3_ζ):
CGCGTGAAGTTAGCCGGTCCGCCGATGCACCTGCATACAAGCAGGACAGAACCAAGCTGTATAACGAGCTG
AATCTGGCCCGGAGAGAGGAGTACGACGTGCTGGATAAGAGCGGGGCCCGGACCCCGAGATGGGAGGCA
AGCCTCGGAGAAAGAACCCACAGGAGGCCCTGTACAAATGAGCTGCAAAAGGACAAAGATGGCCGAGGCCTATT
CTGAGATCGGCATGAAGGGAGAGAGCGCCCGGGCAAGGACACGATGGCCTGTACCAAGGGCCTGAGCAC
CGCCACAAAGGACACCTATGATGCCCTGCACATGCAGGCCCTGCCCCCTAGA (SEQ ID NO: 18068)

FIGURE 4C

P-PSMA8-101 CONSTRUCT:
CTGGCACTGCCTGTGACAGCCCTGCTGCCTCTGGCCCTGCTGCTGCACGCAGCACGGCCCCATGCTGCCT
GCACCAAGAACCTGGTGTCTCGGGTGACCGAGGACTCTGCCGACTGAGCTGGGCCATCGACGAGCA
GAGGATTGGTTCGAGAGCTTTCTGATCCAGTATCAGAGTCCGAGAAAGTGGCGAGGCCATCGTGTGAC
AGTGCTGGCAGCGAGCGGTCTATGATCTGACCGGCTGAAGCCAGGCACAGTACACCGTGTCCATCTA
CGCGTGATCAGGTACAGGTCCATCTCTGTCTGCCATCTTCAACCACCAACCAACCCCTGCCCCGAGA
CCTCCACACCCGCCCTACCATCGCAGCCAGCCACTGTCCCTGCGGCTGAGGCTGCCGGCCCGCCG
CGCGGAGCAGTGCACACACGGGCTGGACTTTGCCCTGTGACATCTACATATGGGCACCACTGGCAGGAA
CCTGCGCGTGTGCTGTGAGCCTGGTCATACCCCTGTACTGTAAGAGAGGCAGGAAGAGCTGCTGTATA
TCTTCAAGCAGCCCTTCATGAGACCCGTGCAGACCACACAGGAGGAGCGTCTCTTGTAGTTCCCAG
AGGAGGAGGAGGGAGGATCGAGCTGCCTGTAAGTTTAGCCGGTCCCGCATGCCTGCATACAAGCAG
GGACAGAACCACTGTATAACGAGCTGAACTCTGGCCCGGAGAGAGGAGTACGACGTGCTGGATAAGAGCG
GGCCCGGACCCCGAGATGGGAGCAAGCTCGGAGAAAGAACCCACAGAGGGCTGTACAATGAGCTG
CAAAAGGACAAAGATGGCCGAGGCTATTCTGAGATCGGCATGAAGGAGAGAGGCGCCGGGCAAGGACA
CGATGGCCTGTACGAGGCTGAGCACCCGCCACAAAGGACACCTATGATGCCCTGCACATGCAGGCCCTGC
CCCTAGA (SEQ ID NO: 18071)

FIGURE 5

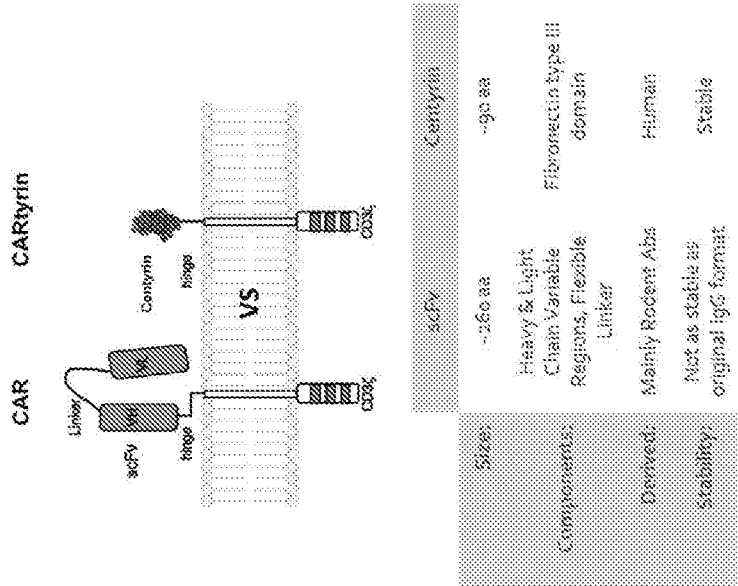
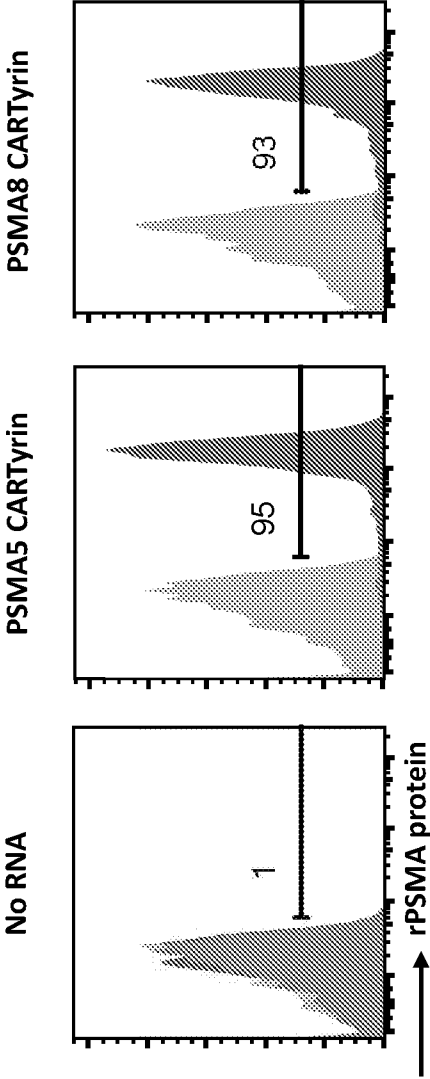
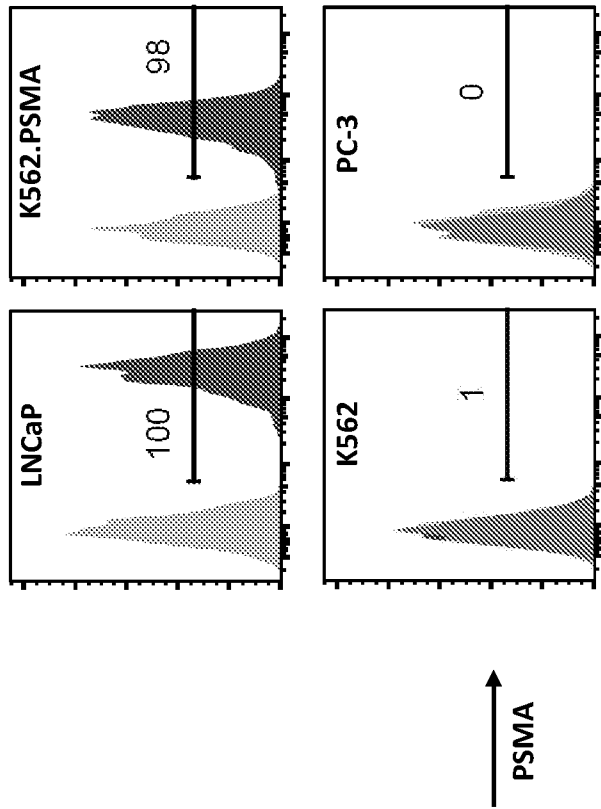


FIGURE 6A



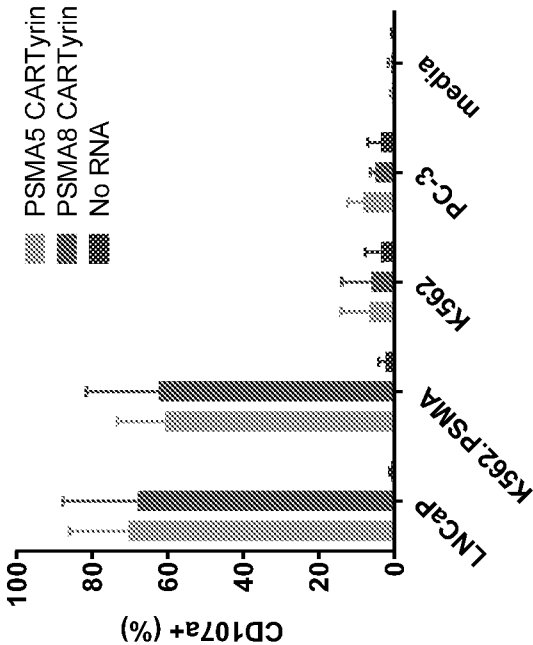
A) PSMA CARTyrin surface expression 24 hours post mRNA transfection of human pan T cells

FIGURE 6B



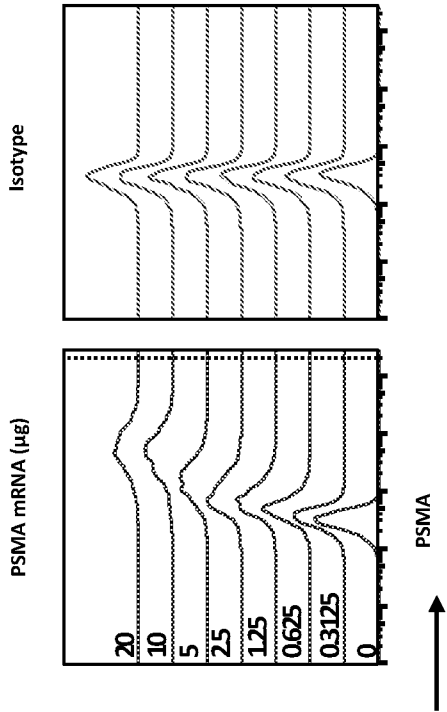
B) Expression of PSMA protein on tumor cell lines. Gray histogram represents the isotype control

FIGURE 6C



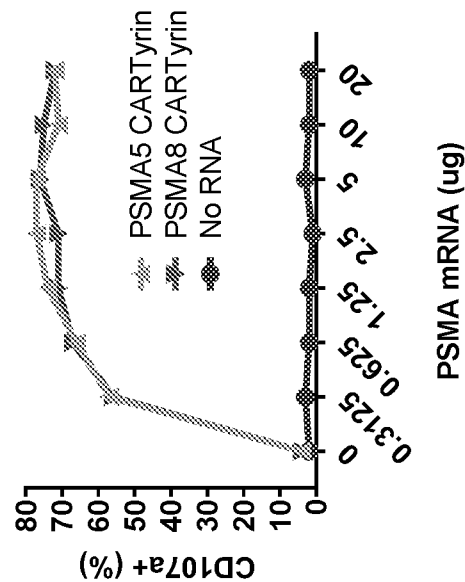
C) Degranulation of RNA-electroporated PSMA CARTyrin T cells against PSMA+ tumor cell lines

FIGURE 6D



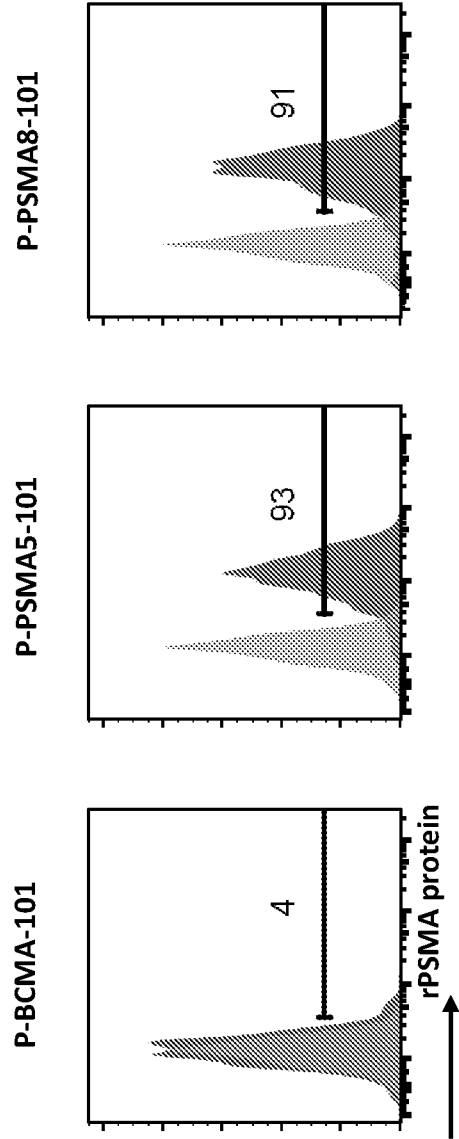
D) PSMA surface expression following transfection of K562 using various amounts of PSMA mRNA

FIGURE 6E



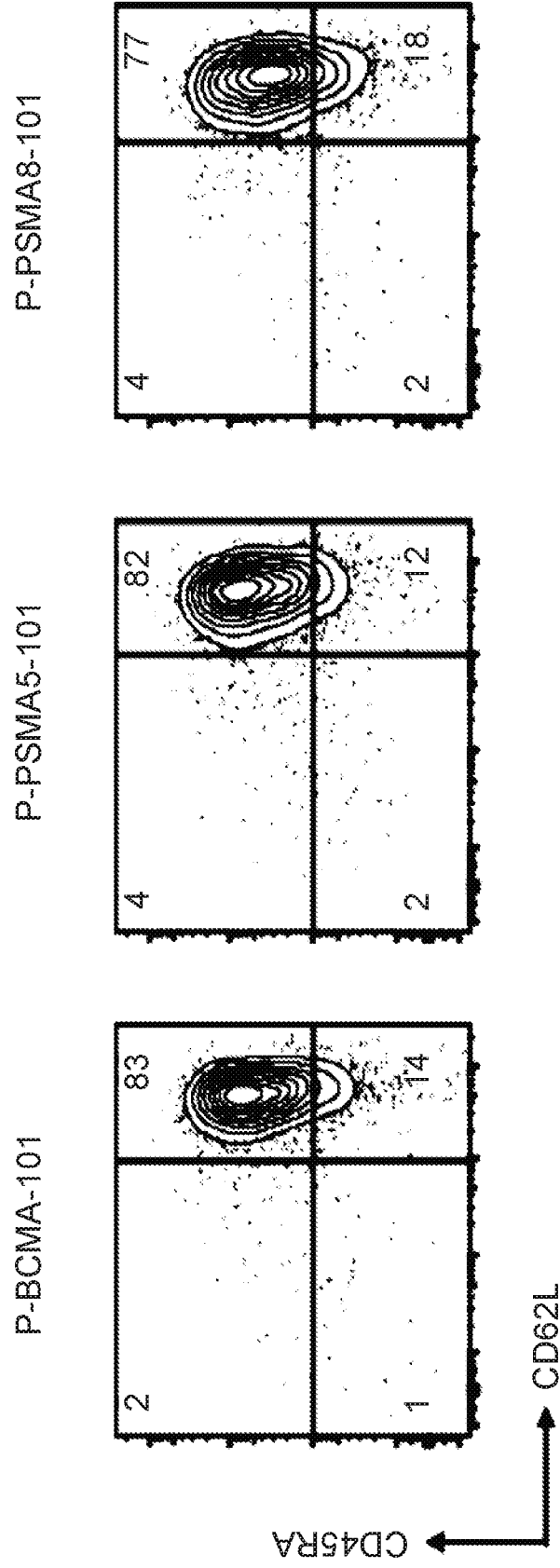
E) Degranulation of RNA-electroporated PSMA CARTyrin T cells against K562 expressing various amounts of PSMA protein

FIGURE 7A



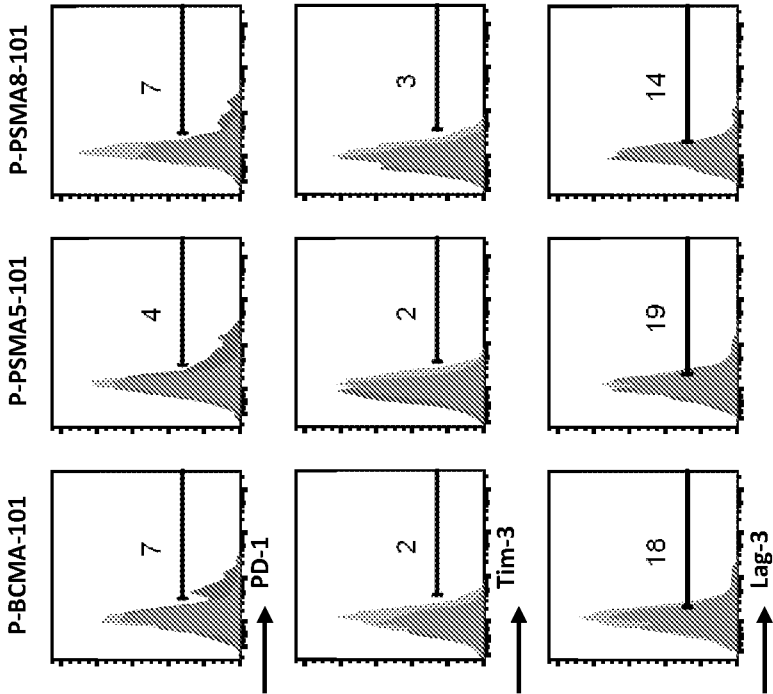
A) P-PSMA-101 T cells bind cognate recombinant soluble PSMA antigen

FIGURE 7B



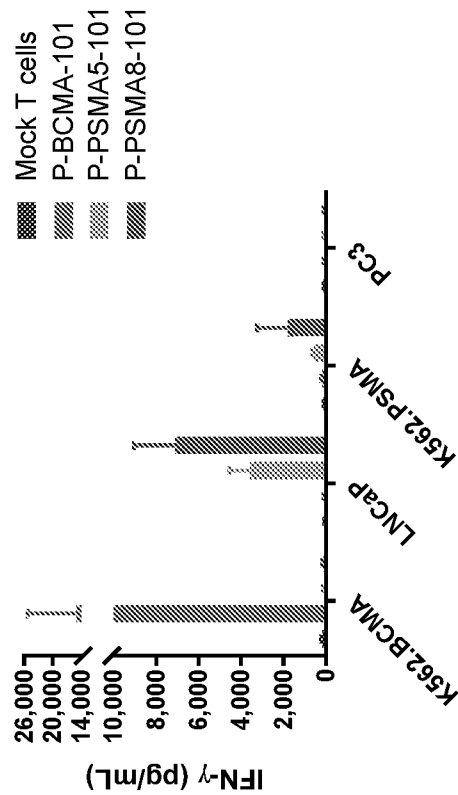
B) Phenotypic analysis of memory T cell markers

FIGURE 7C



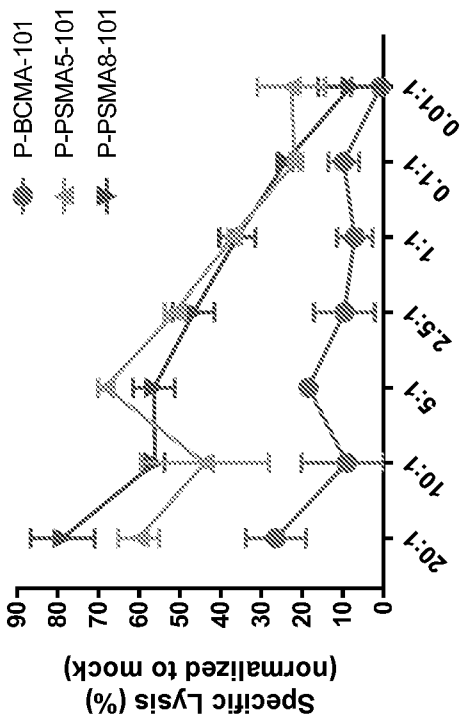
C) Phenotypic analysis of activation/exhaustion markers where CD4+ (purple) and CD8+ (gray) cells are displayed

FIGURE 7D



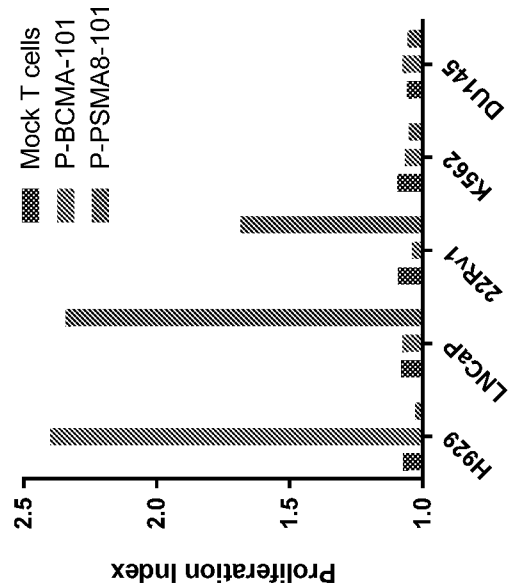
D) IFN- γ secretion of P-PSMA-101 against PSMA⁺ cell lines
K562.PSMA and LNCaP

FIGURE 7E



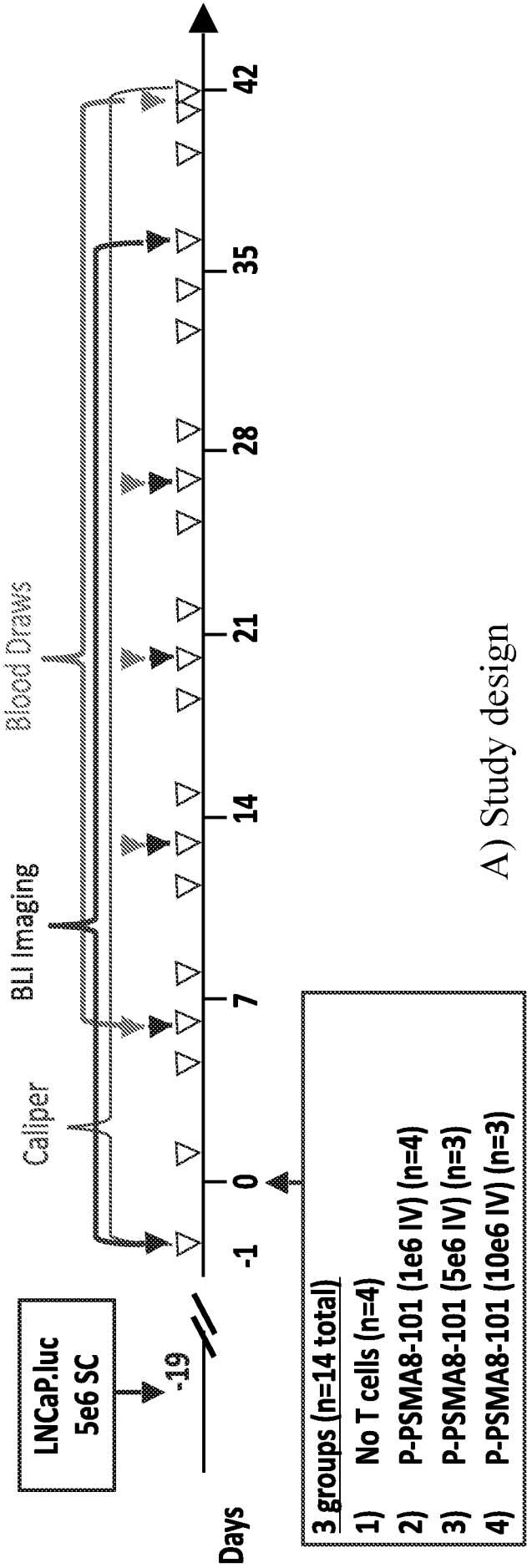
E) Killing of PSMA⁺ LNCaP by P-PSMA-101 or control P-BCMA-101 at the indicated effector to target ratios

FIGURE 7F



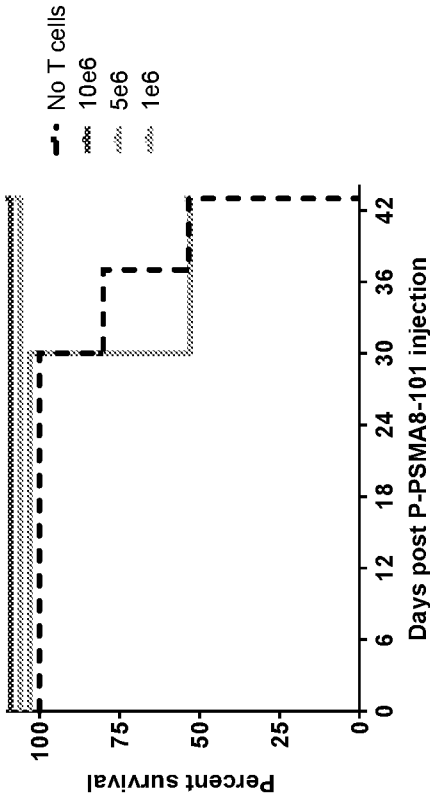
F) Proliferation of P-PSMA-101 against cell lines H929 (PSMA⁺/BCMA⁺), LNCaP (PSMA⁺/BCMA⁻), 22Rv1 (PSMA⁺/BCMA⁻), K562 (PSMA⁻/BCMA⁻), and DU145 (PSMA⁻/BCMA⁻)

FIGURE 8A



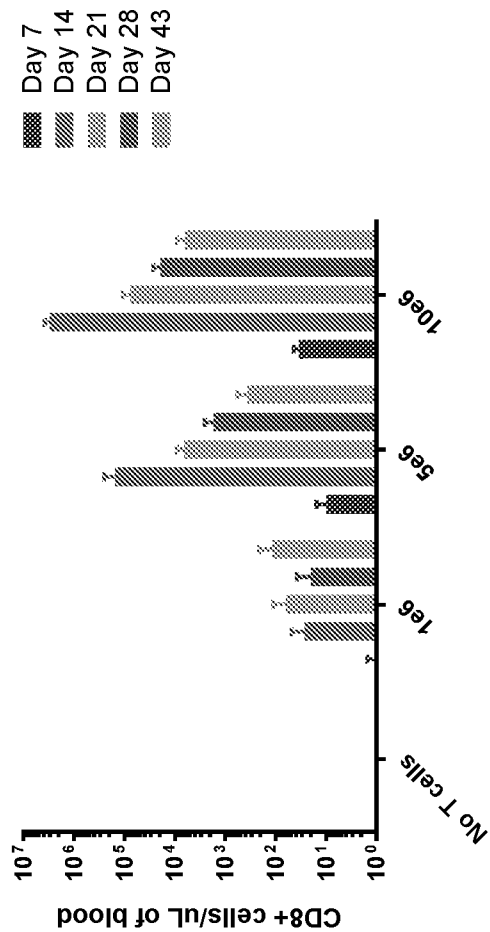
A) Study design

FIGURE 8B



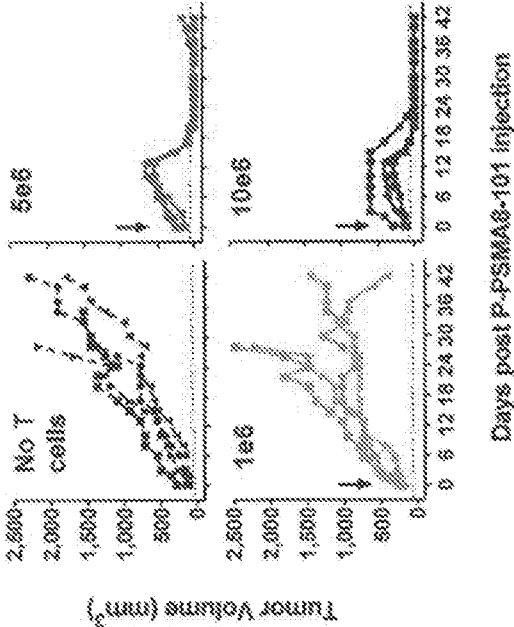
B) Survival data

FIGURE 8C



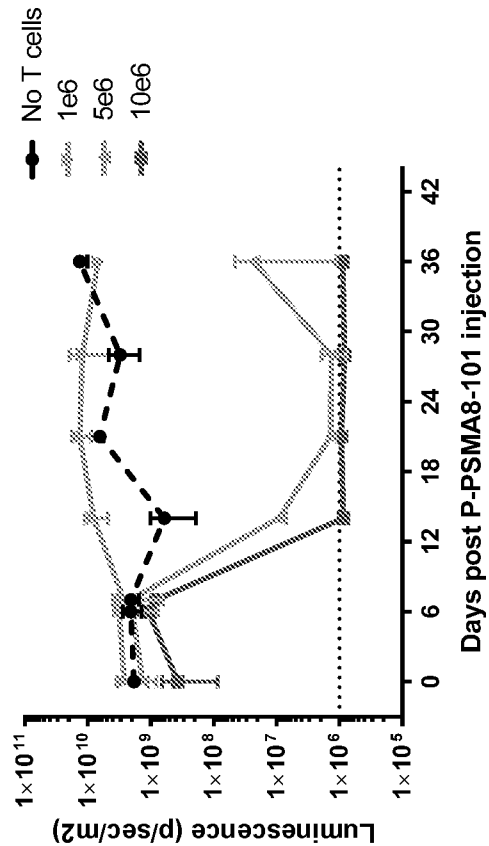
C) Enumeration of CD8+ T cells per microliter of peripheral blood

FIGURE 8D



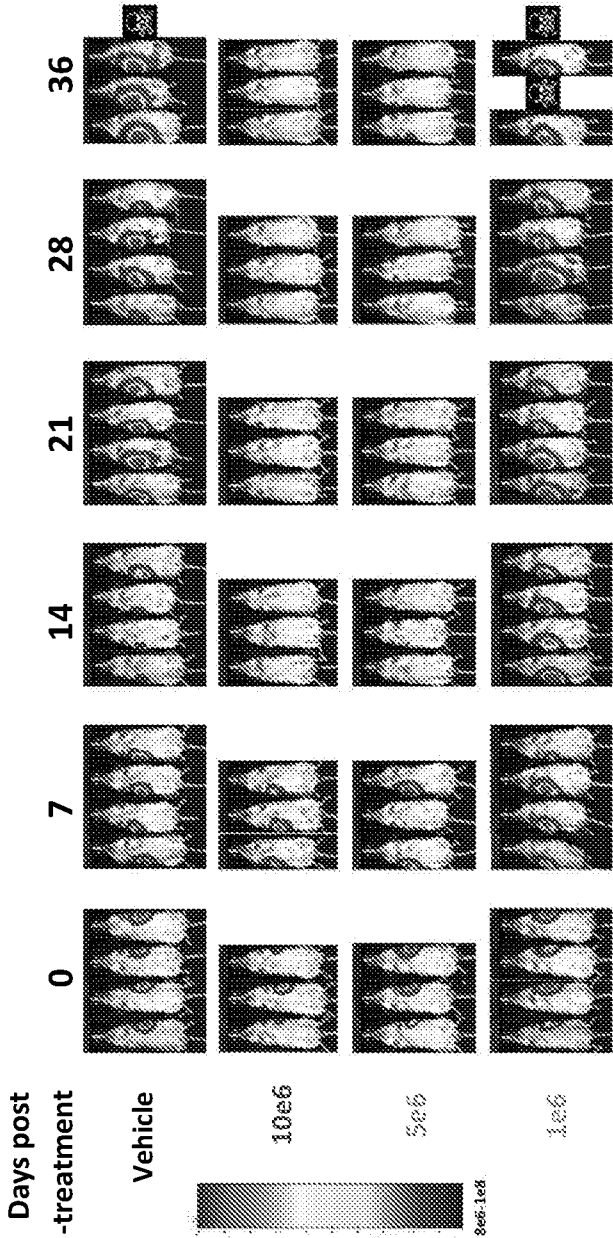
D) Tumor burden by caliper measurement

FIGURE 8E



E) Tumor burden by BLI (imaging quantified)

FIGURE 8F



F) Tumor burden by BLI (imaging)

FIGURE 9A

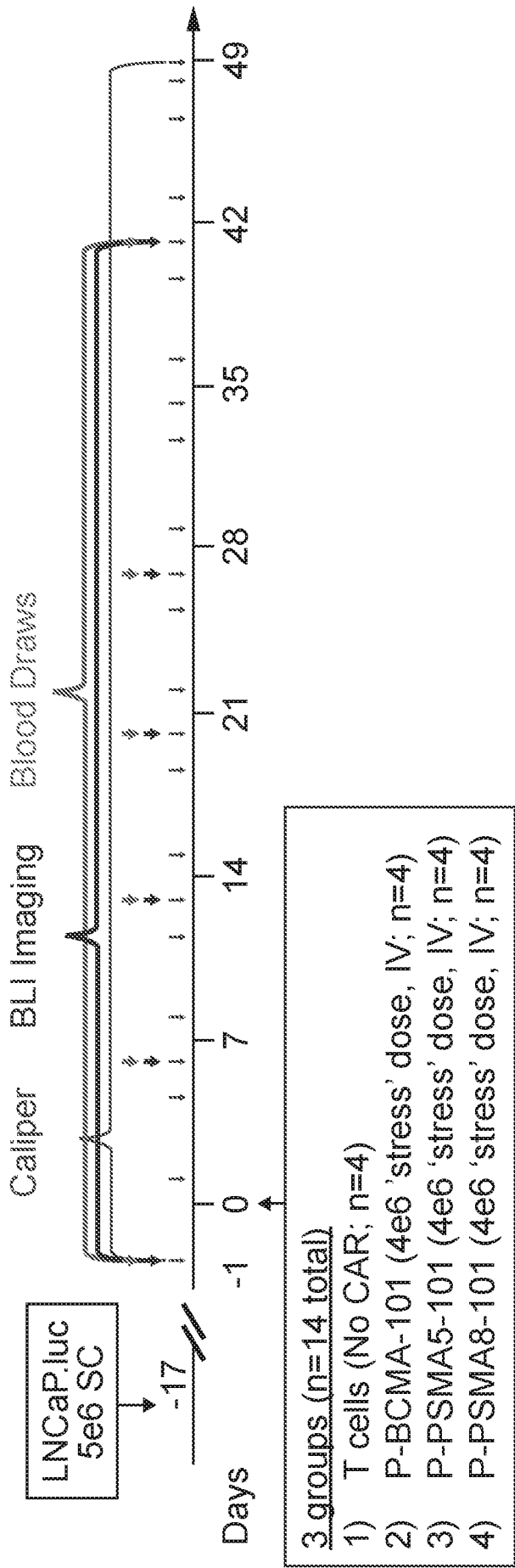
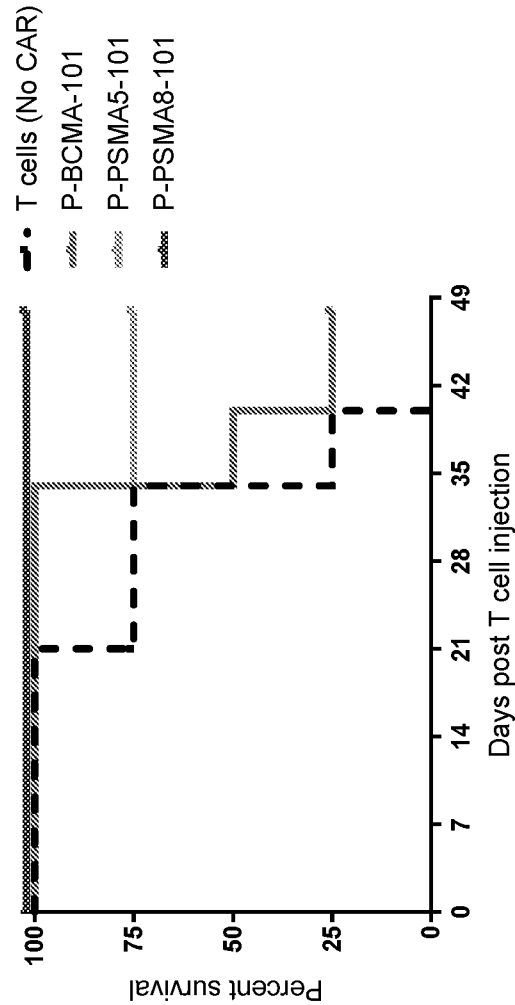
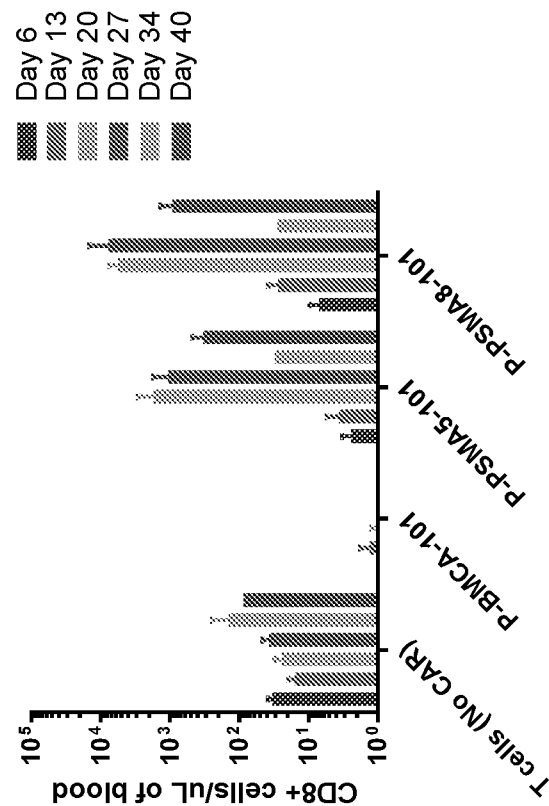


FIGURE 9B



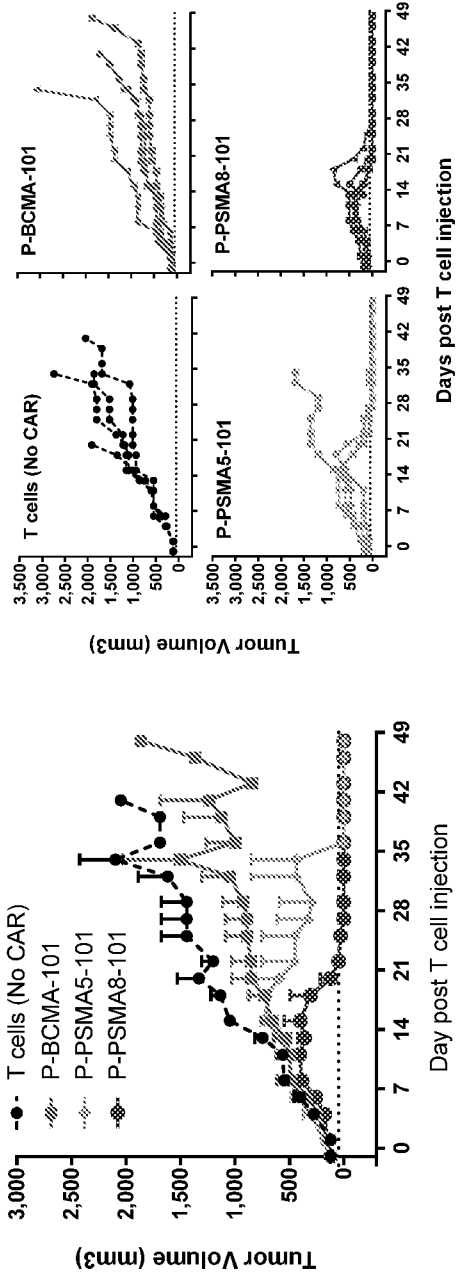
B) Survival data

FIGURE 9C



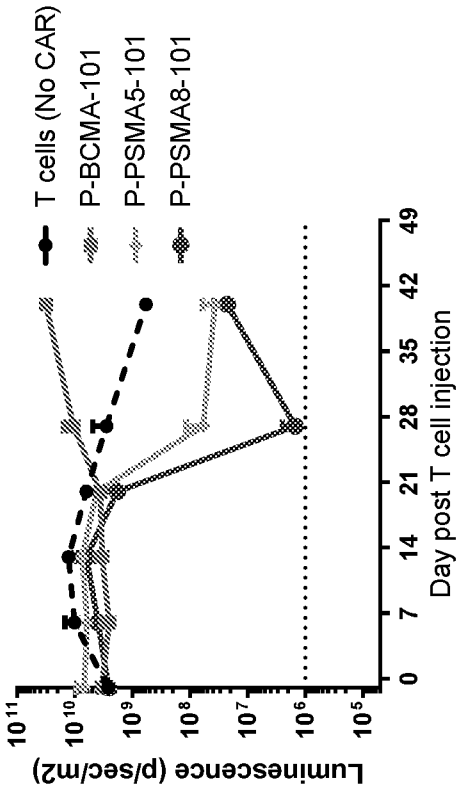
C) Enumeration of CD8+ T cells per microliter of peripheral blood

FIGURE 9D



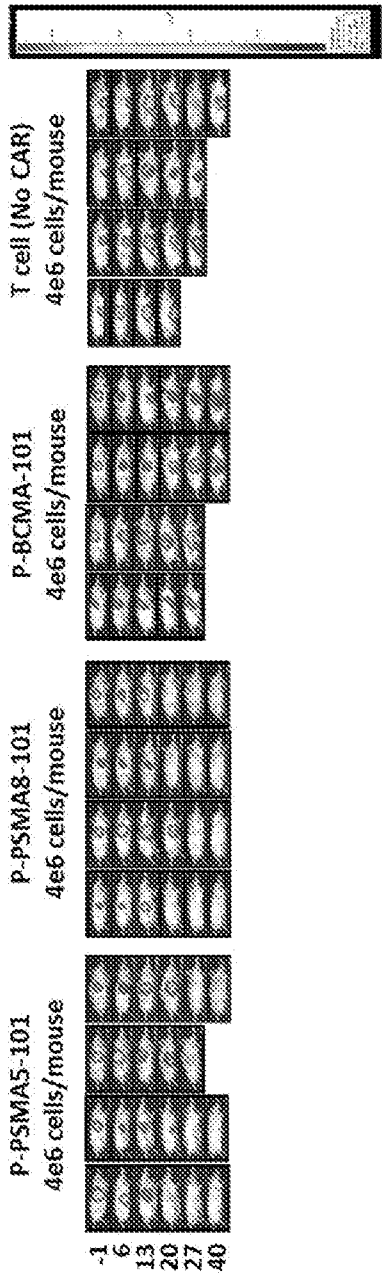
D) Tumor burden by caliper measurement

FIGURE 9E



E) Tumor burden by BLI (imaging quantified)

FIGURE 9F



F) Tumor burden by BLI (imaging)

iC9/AP1903 Safety Switch Day 12

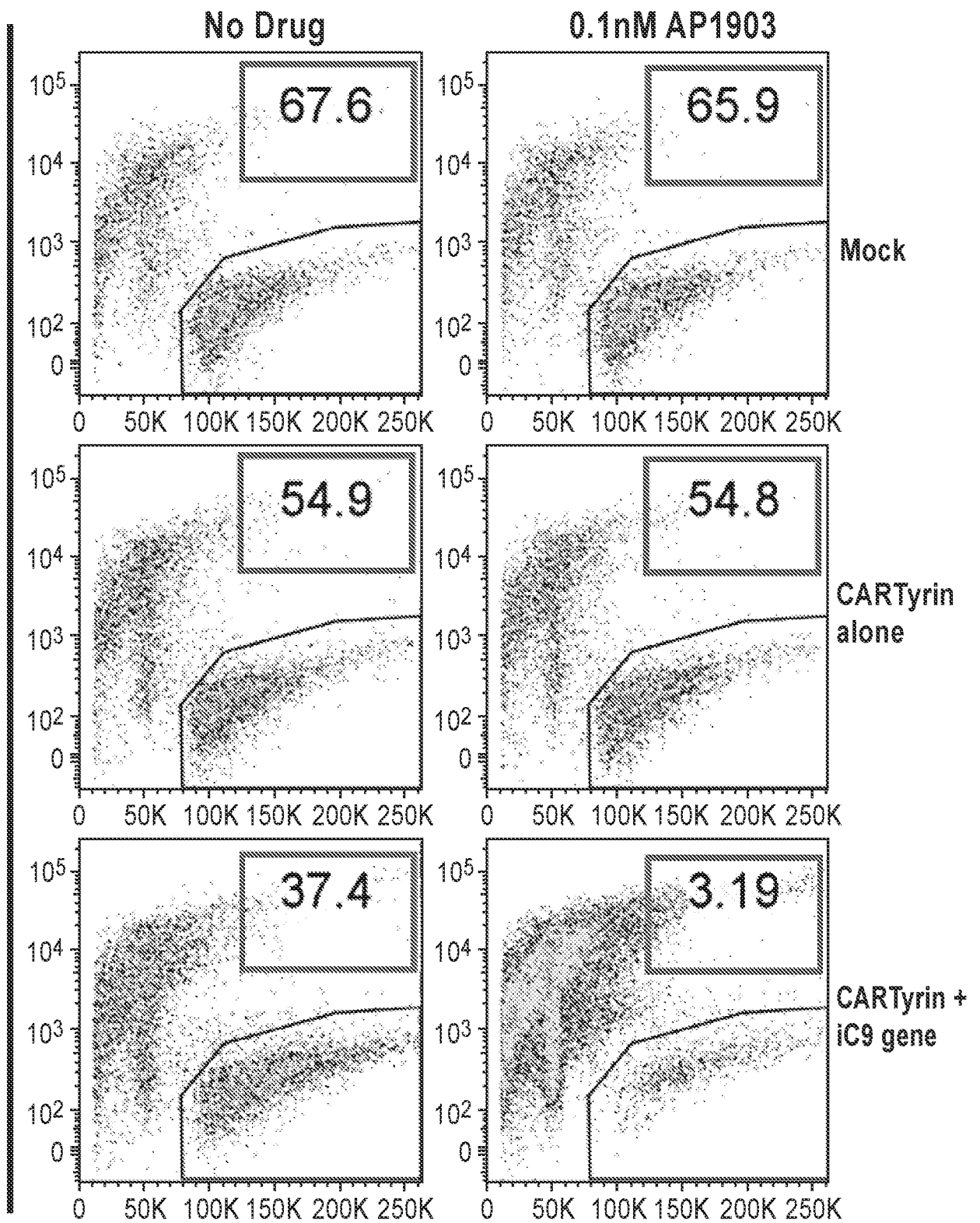


FIGURE 10

CARTyrin

iC9/AP1903 Safety Switch Day 12

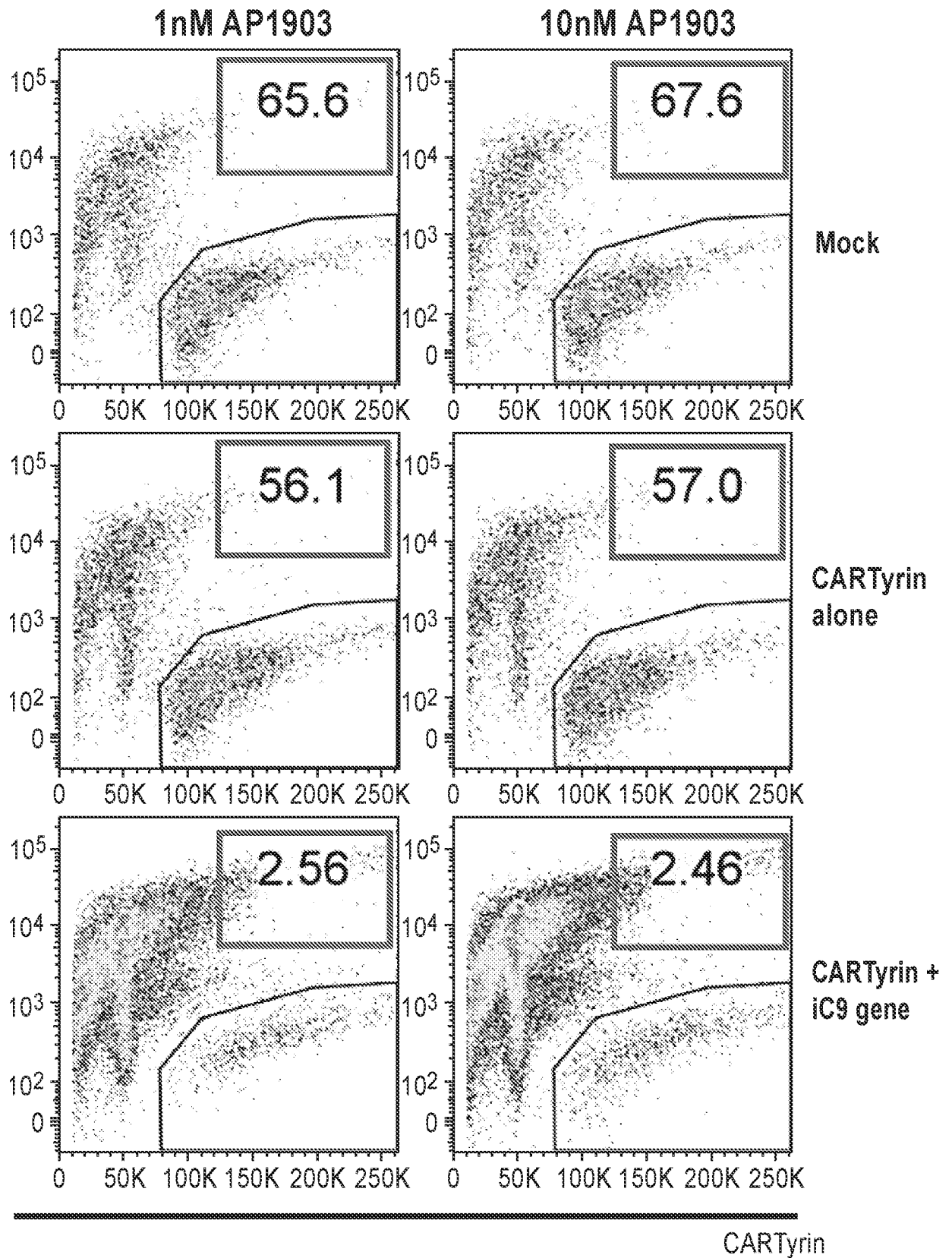
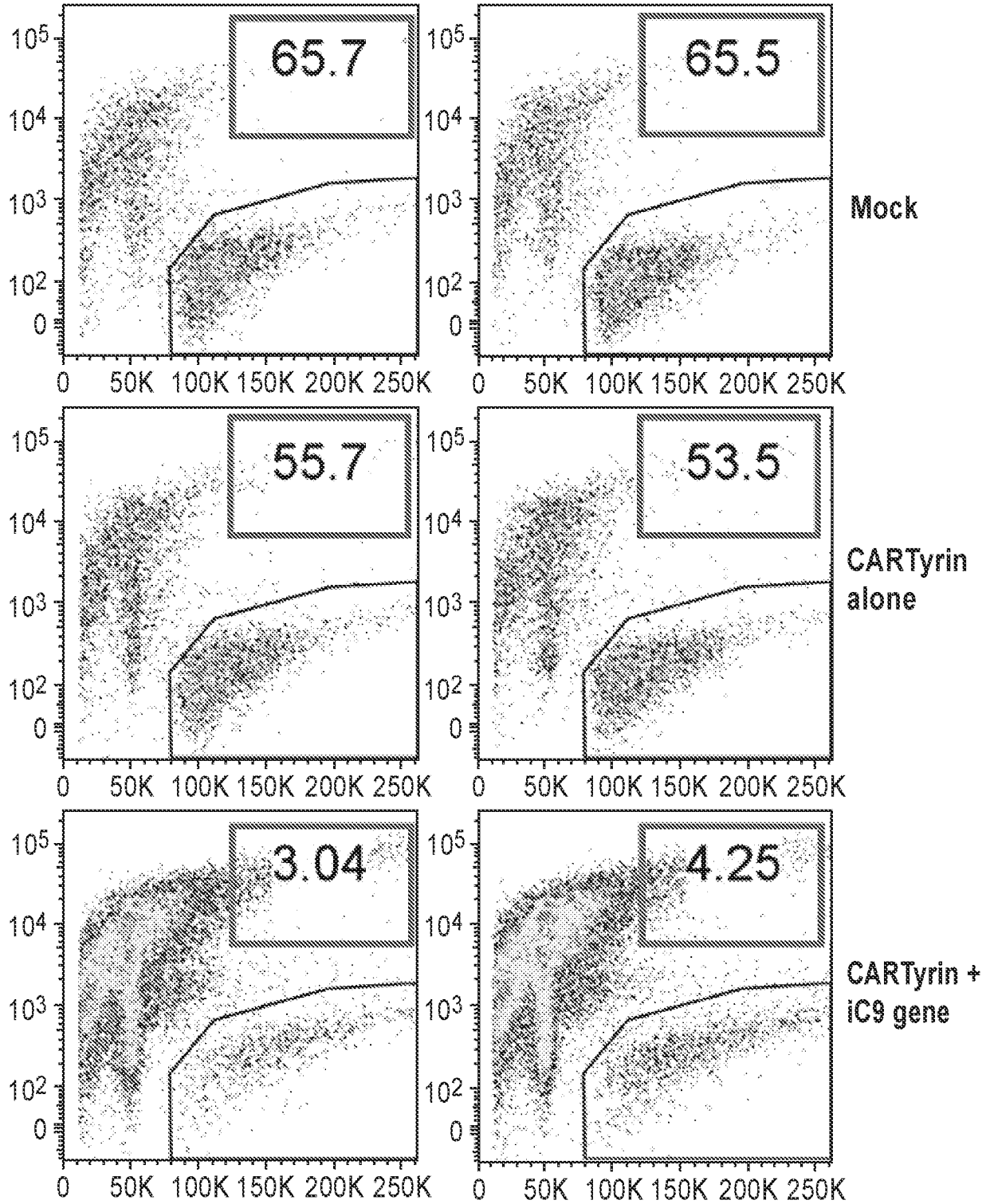


FIGURE 10 (cont.)

iC9/AP1903 Safety Switch Day 12

100nM AP1903

1000nM AP1903



CARTyrin

FIGURE 10 (cont.)

iC9/AP1903 Safety Switch Day 12

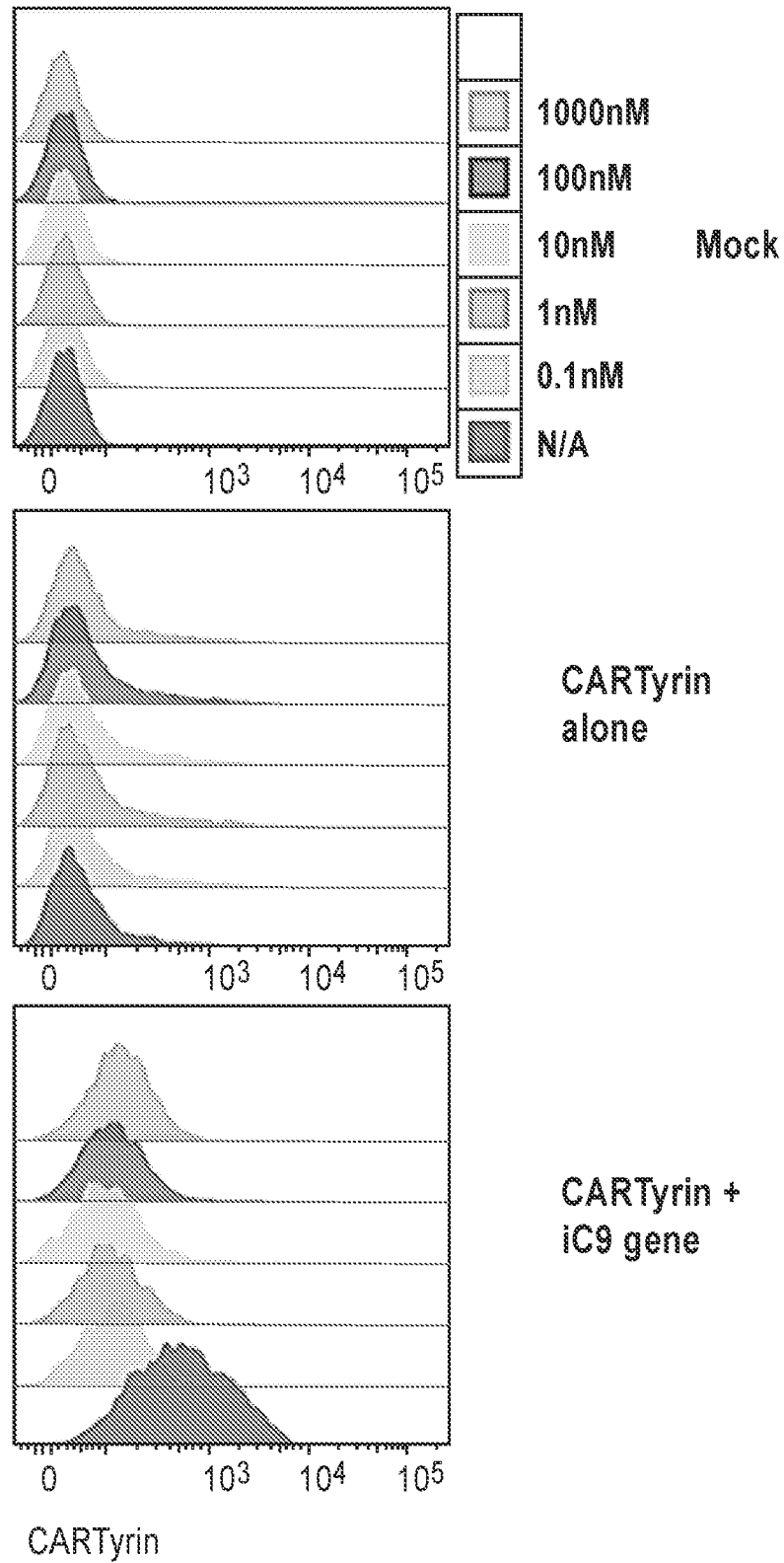


FIGURE 10 (cont.)

iC9/AP1903 Safety Switch Day 19

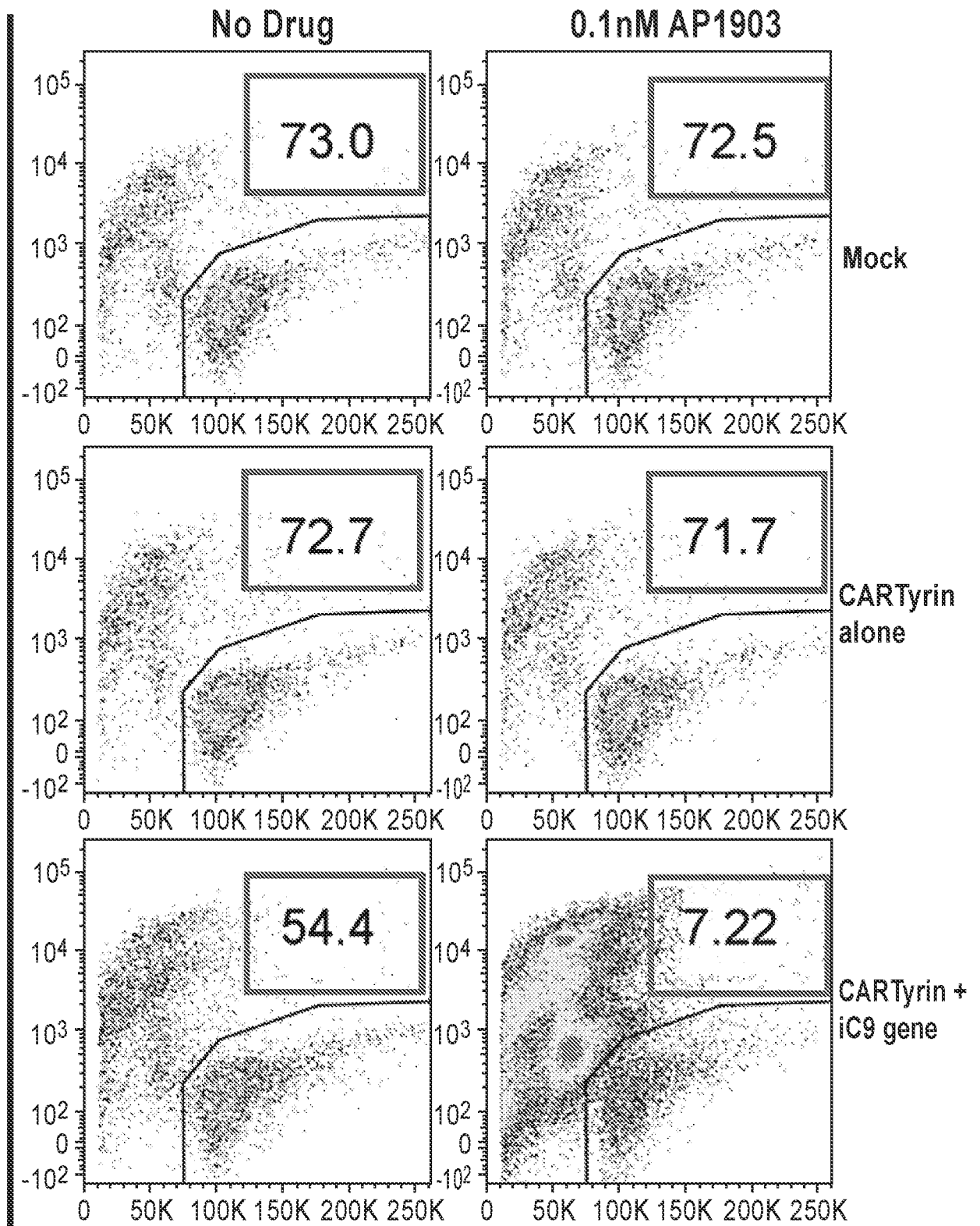


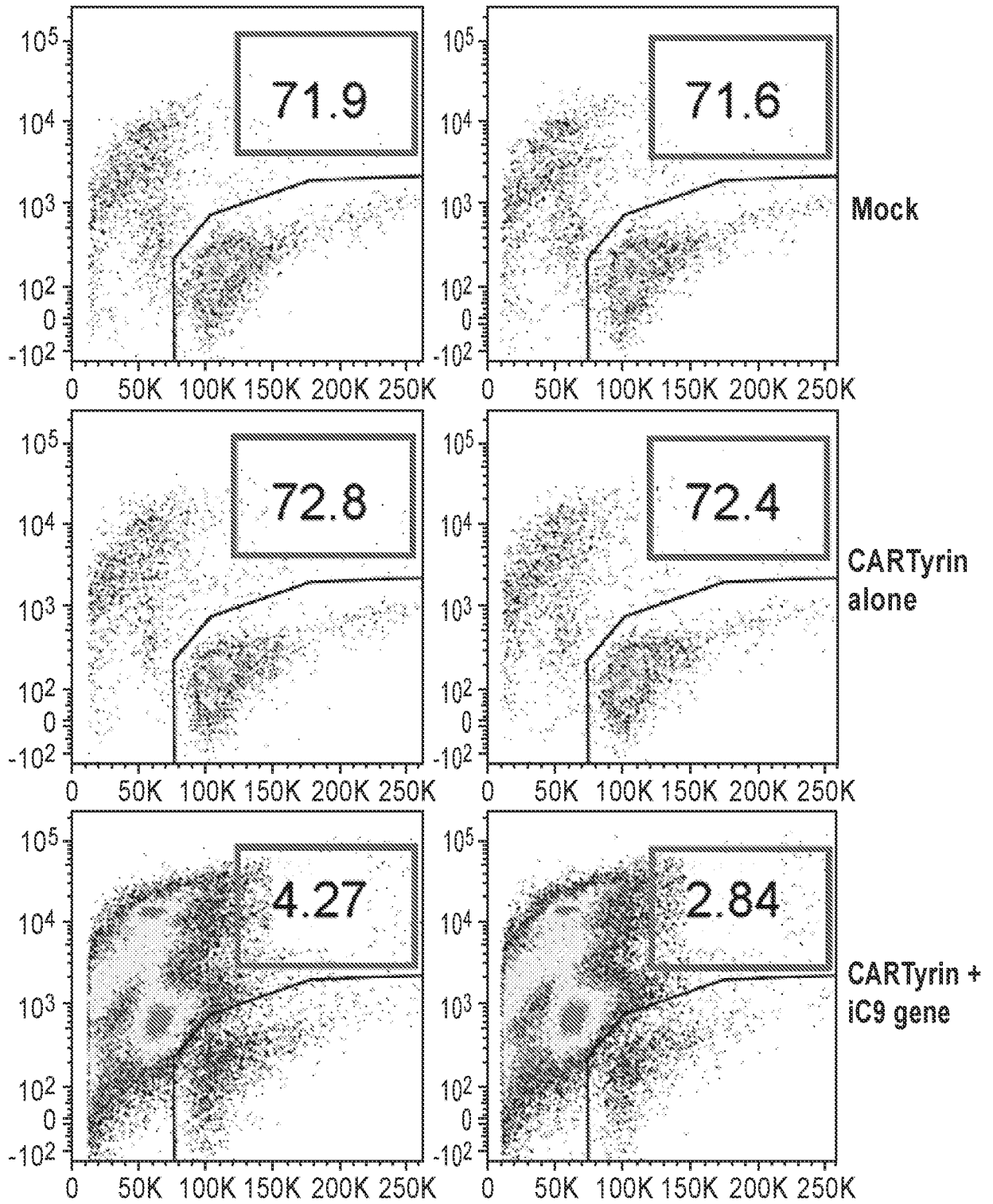
FIGURE 11

CARTyrin

iC9/AP1903 Safety Switch Day 19

1nM AP1903

10nM AP1903



CARTyrin

FIGURE 11 (cont.)

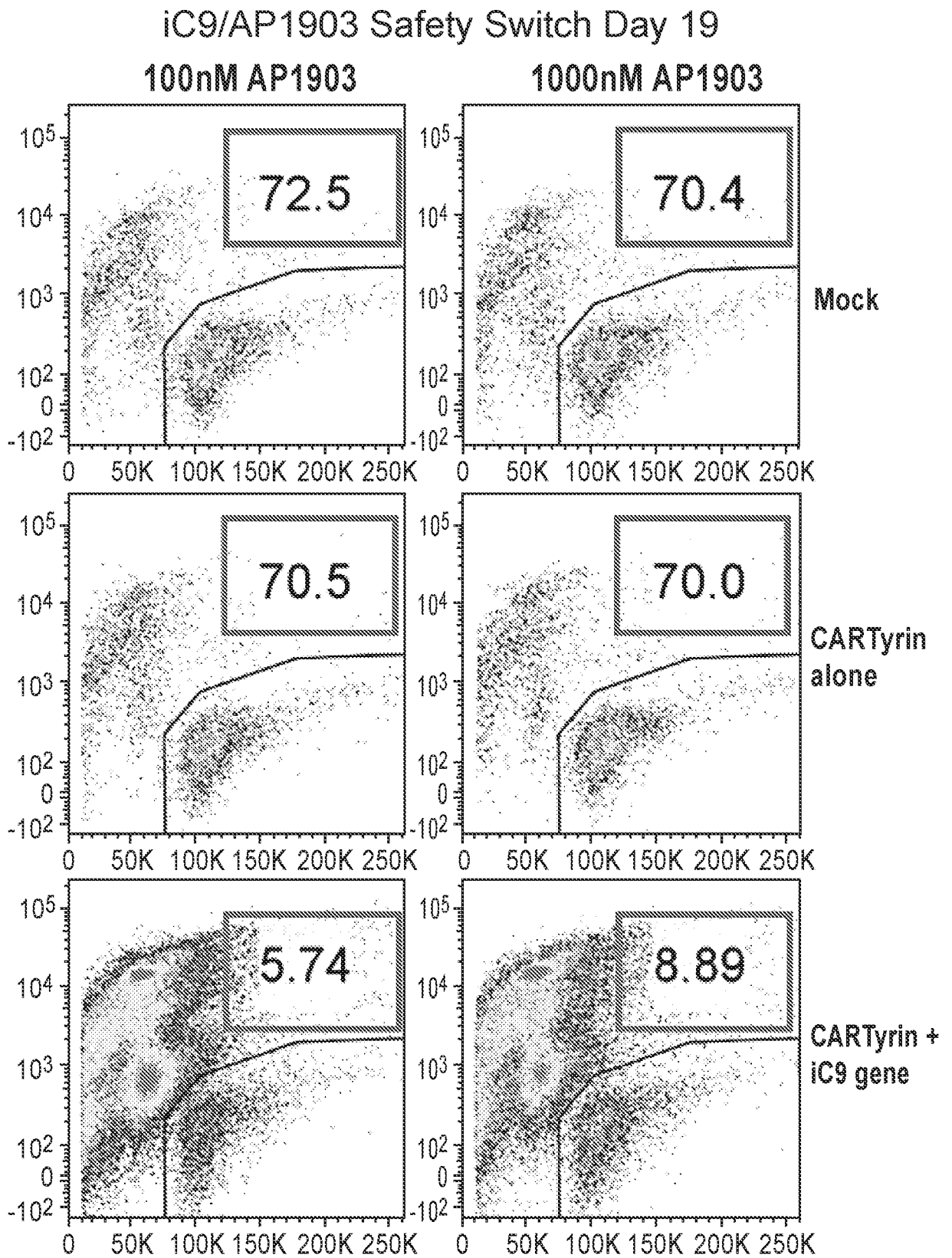


FIGURE 11 (cont.)

CARTyrin

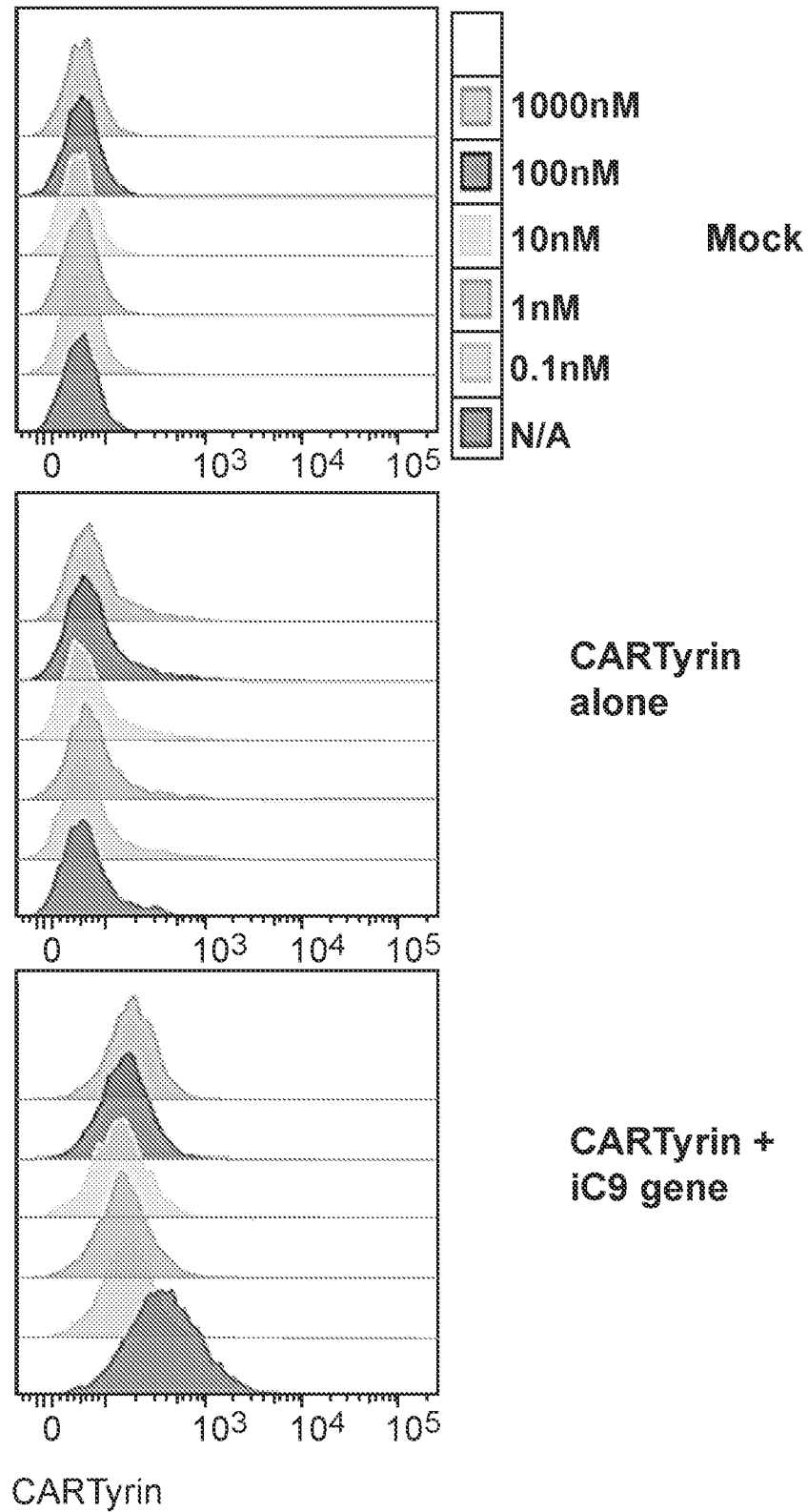
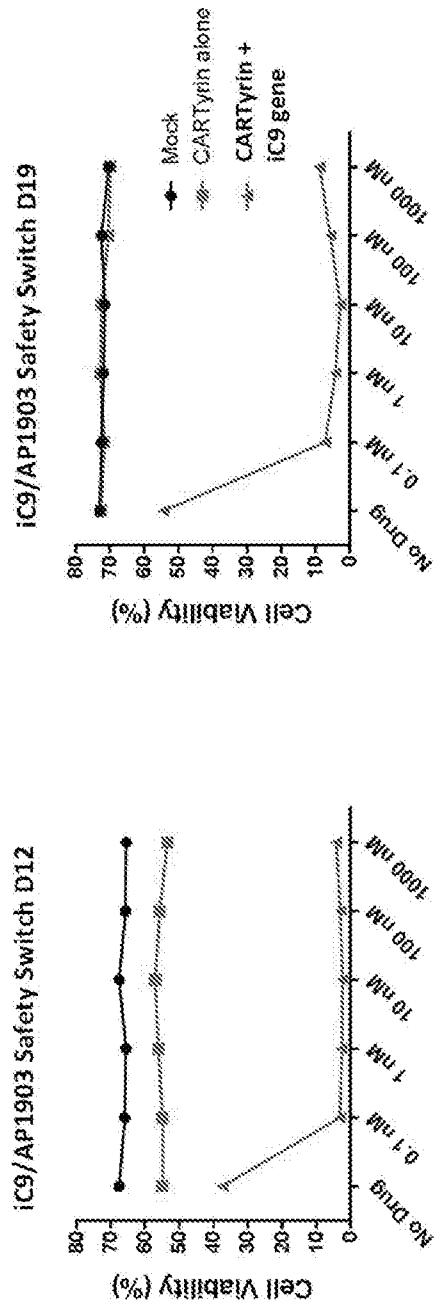


FIGURE 11 (cont.)

FIGURE 12

ic9/AP1903 Safety Switch Summary



>95% of the CARTyrin⁺ T cells expressing the ic9 safety switch were eliminated within 24 hours

FIGURE 13

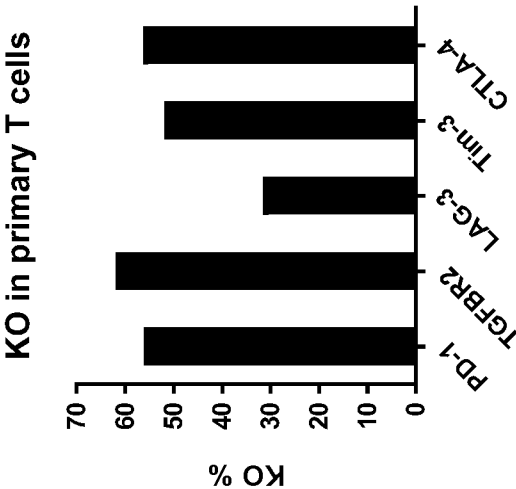


FIGURE 14

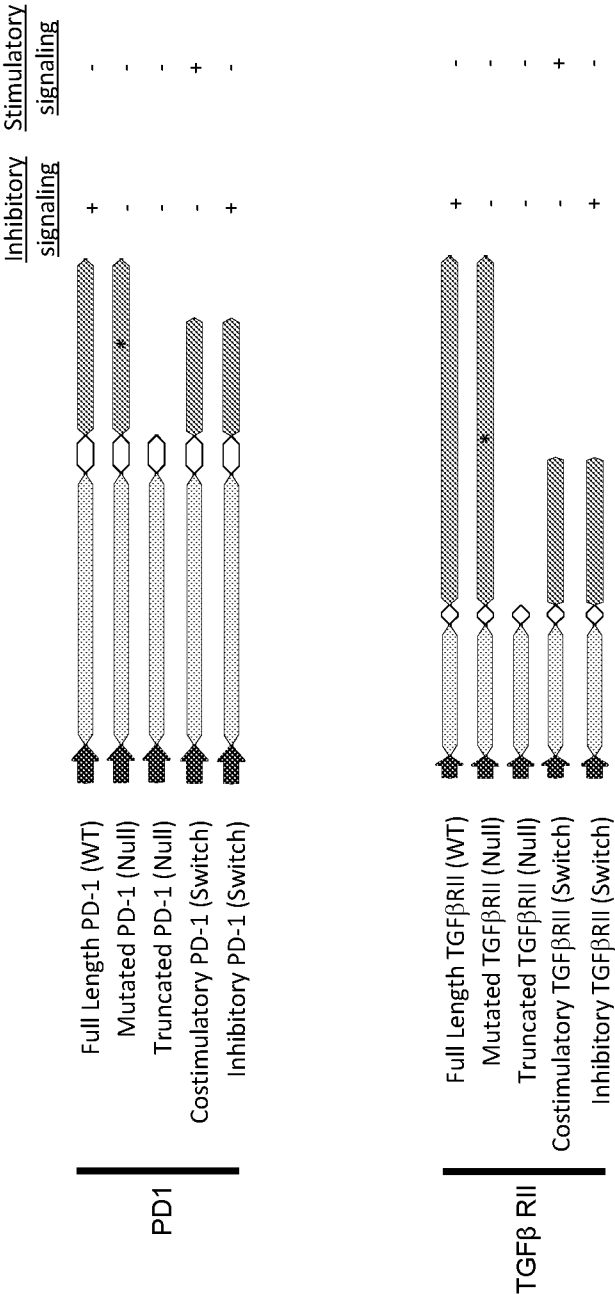


FIGURE 15A

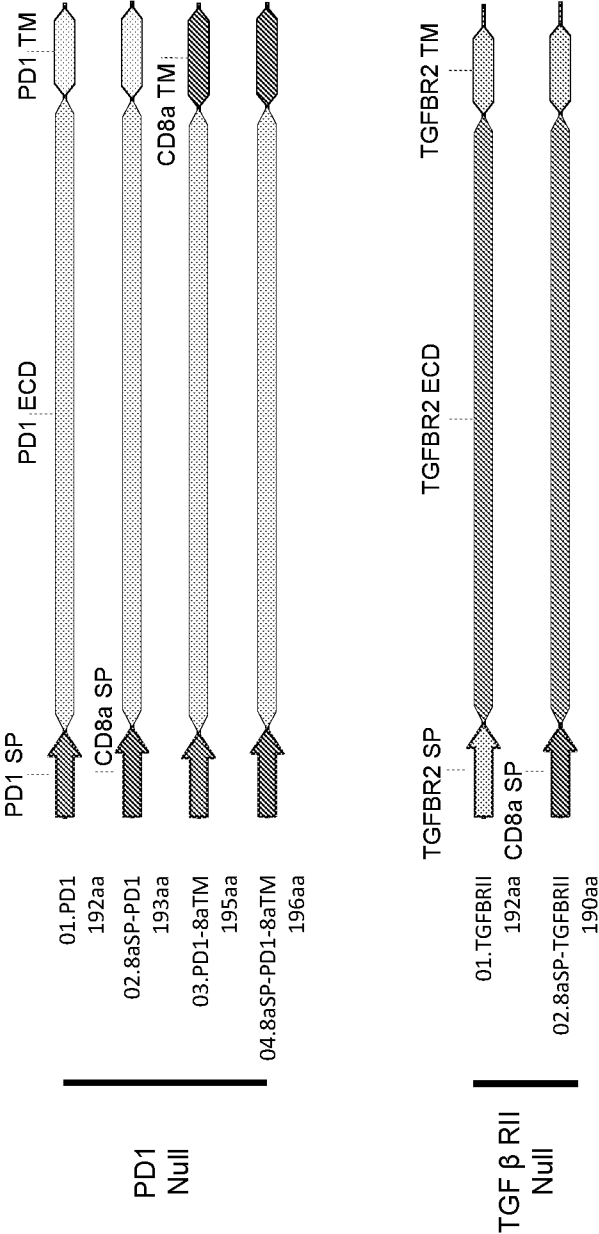


FIGURE 15B

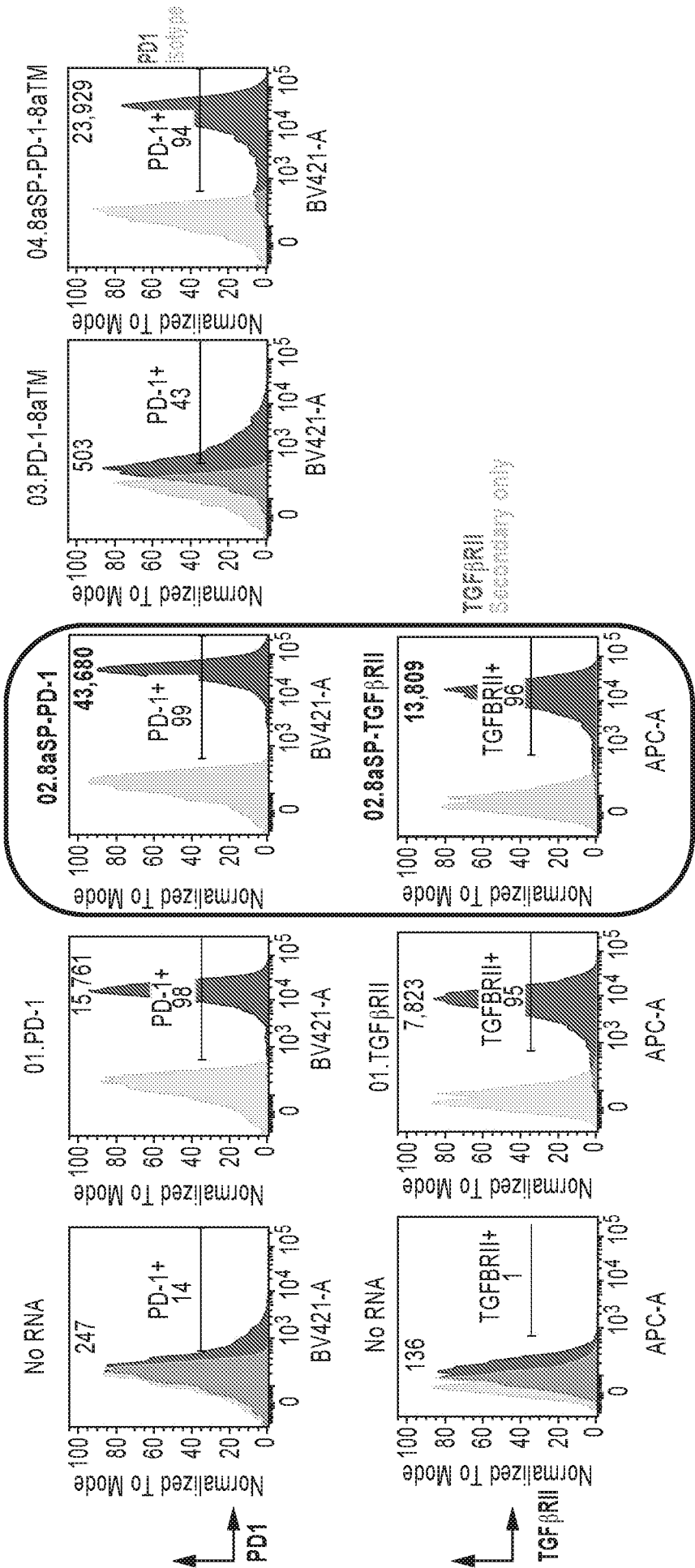
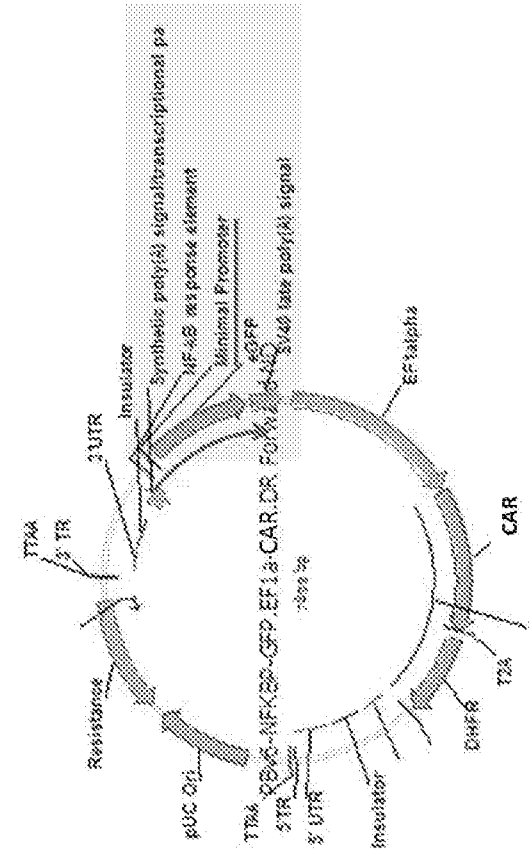
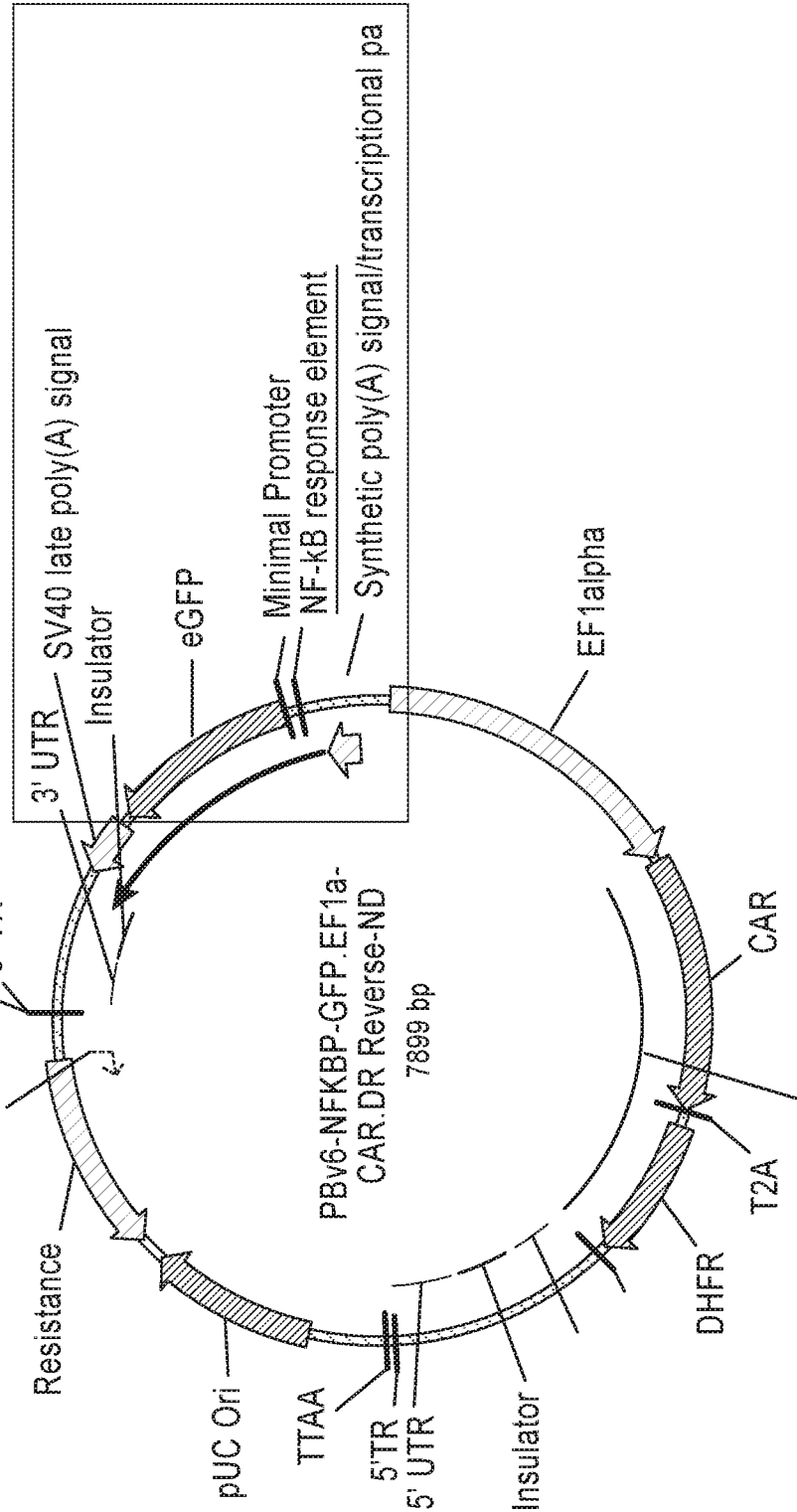


FIGURE 16A



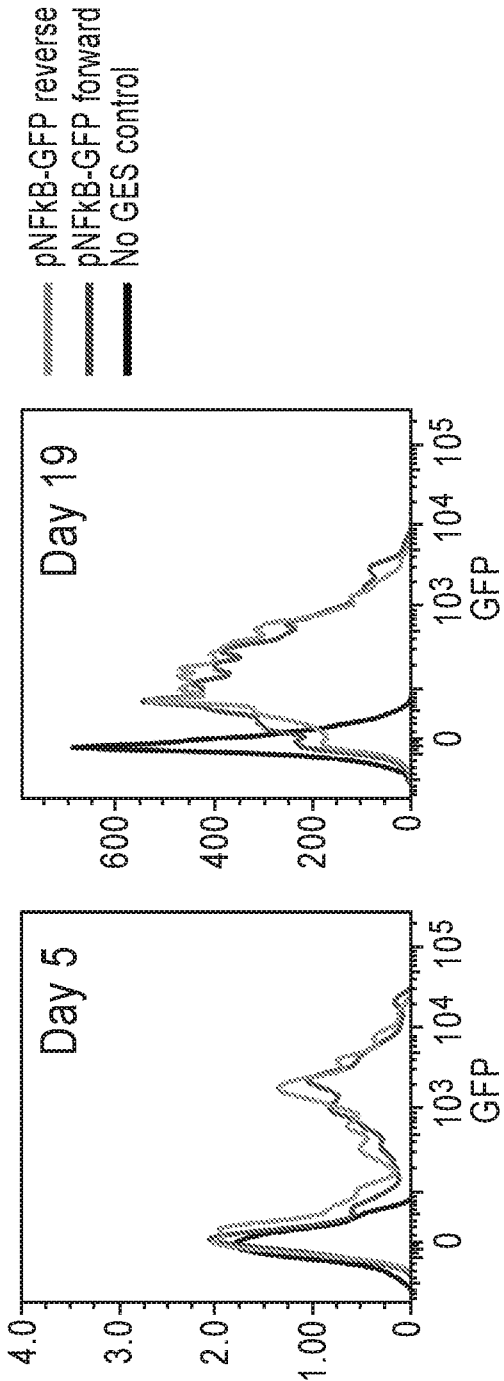
pNFkB-GFP & EF1α-CAR in the same direction

FIGURE 16B



pNFkB-GFP & EF1a-CAR in the opposite direction

FIGURE 17



- At Day 5-post T cell activation (Day 5), T cells are proliferating and are highly stimulated; GFP expression is strong since NFkB activity is high
- By Day 19, T cells are almost fully resting; GFP expression is significantly lower than Day 5 (~1/8 MFI), since NFkB activity is low
- GFP expression is still observed at Day 19, which may due to the long half life of GFP protein (~30hr), or, basal level of NFkB activity through TCR, CAR, cytokine, growth factor, etc...

FIGURE 18

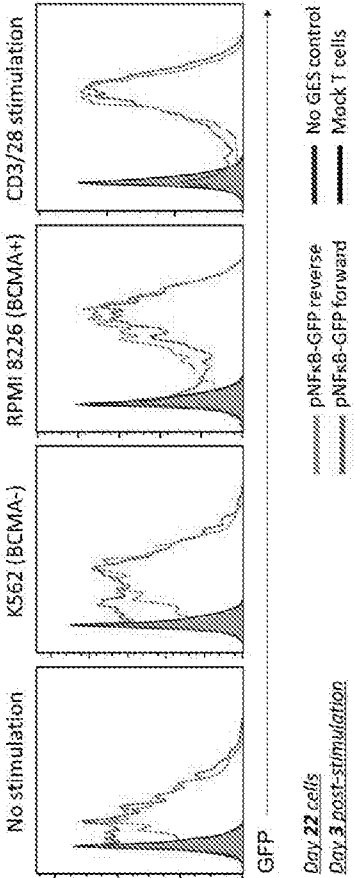
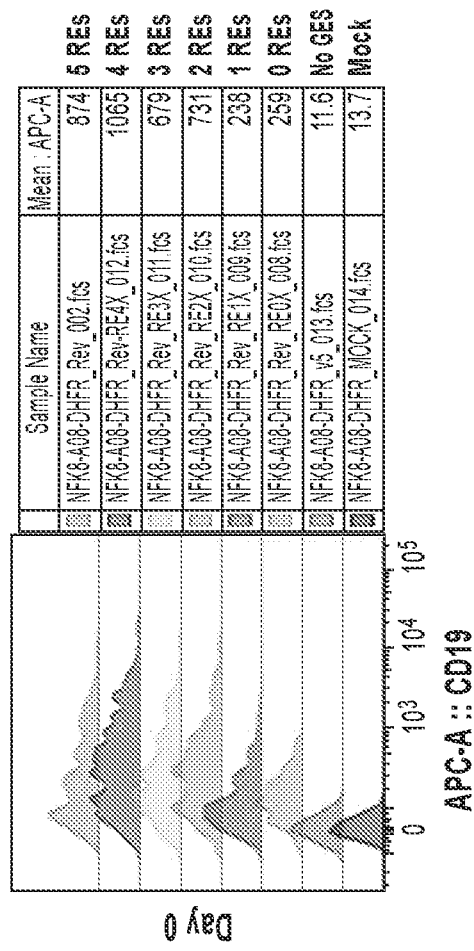


FIGURE 19 CD4+ T Cells



CD8+ T Cells

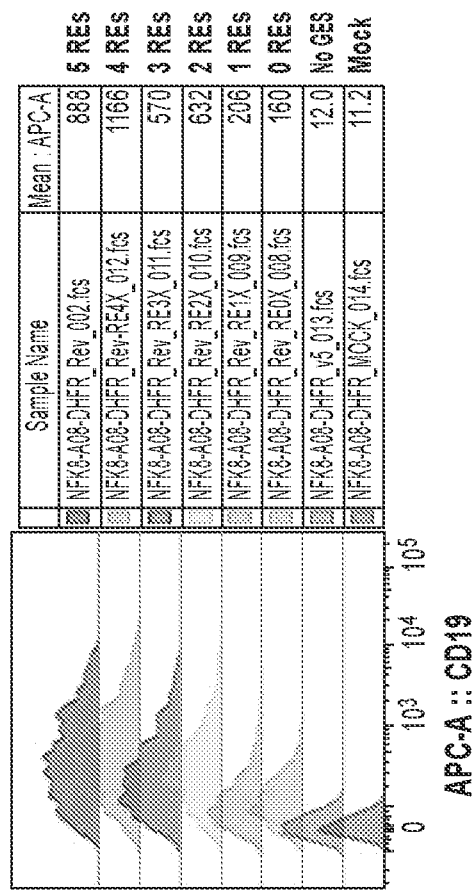
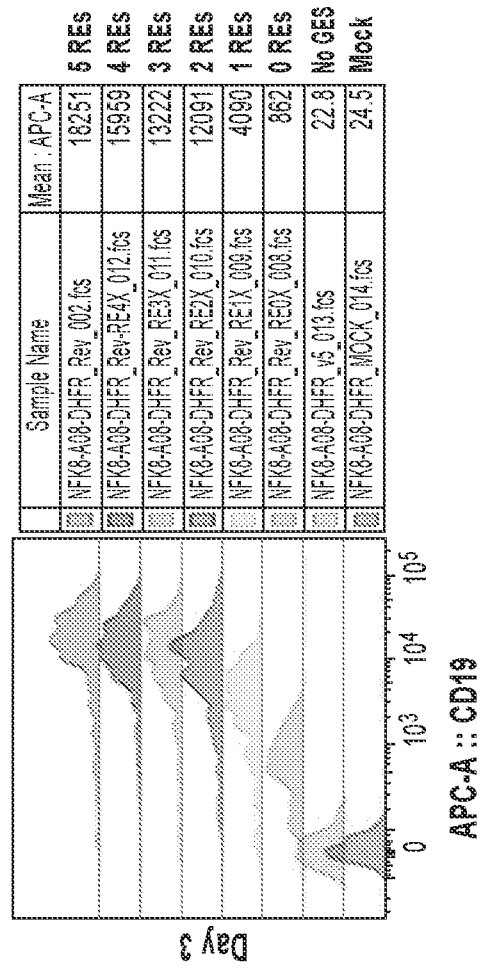
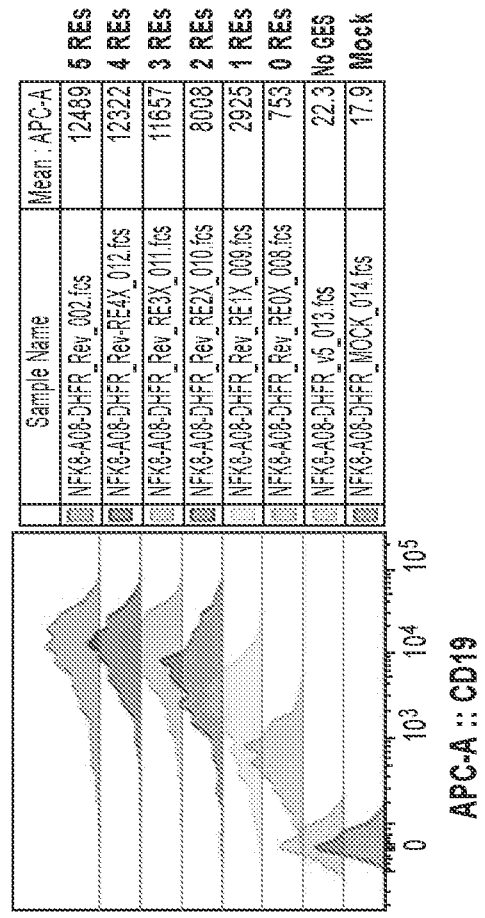
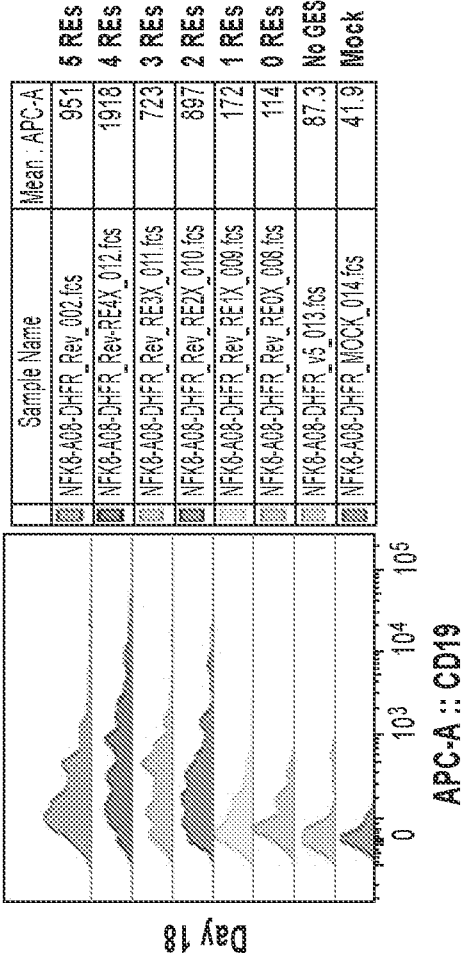


FIGURE 19 (cont.)

CD4+ T Cells



CD8+ T Cells

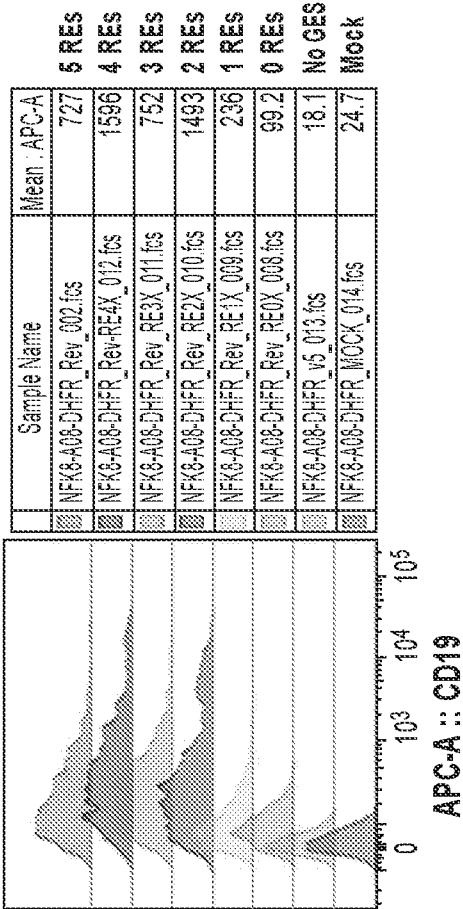


FIGURE 19 (cont.)

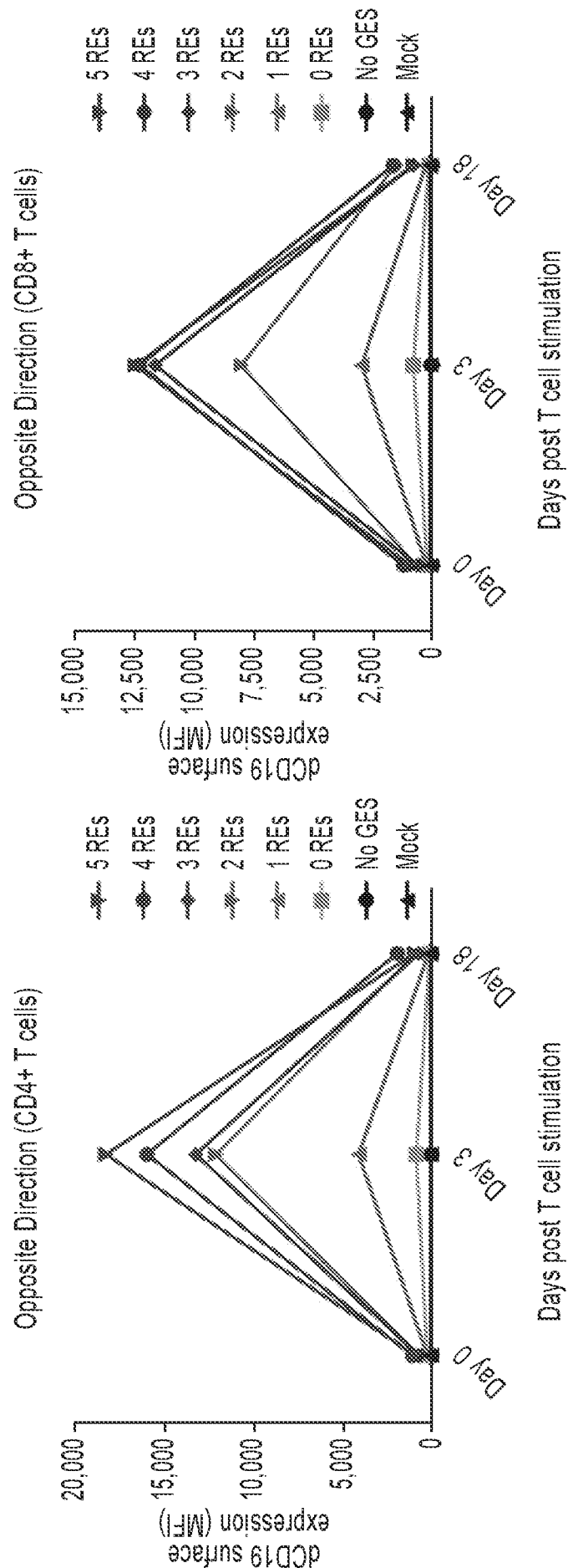


FIGURE 20

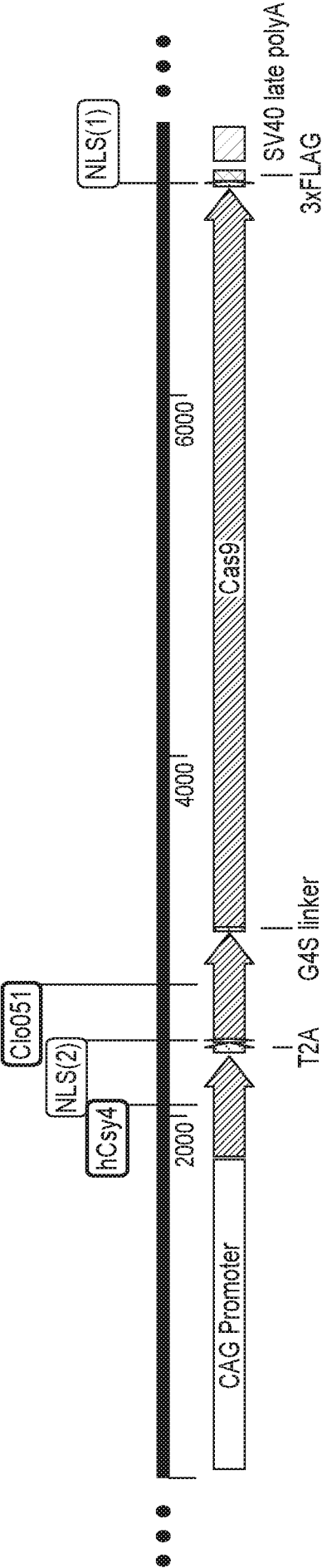
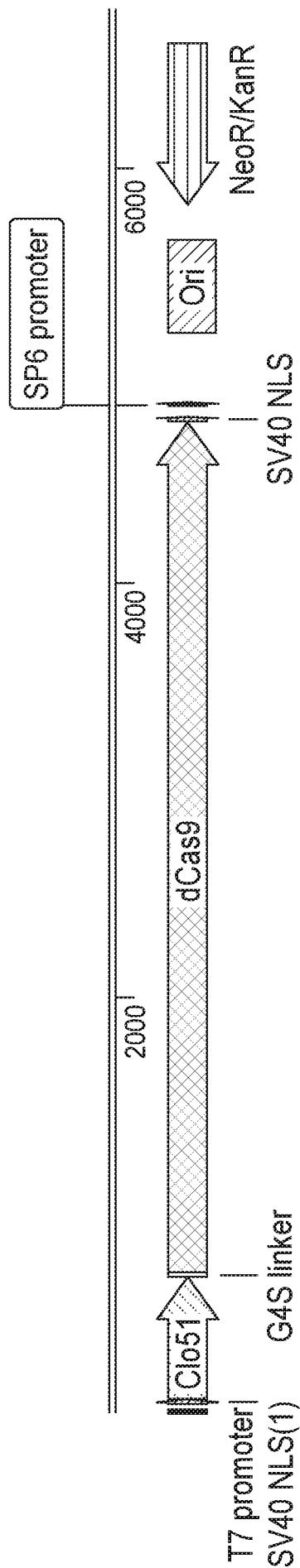


FIGURE 21



pRT1-Clo51-dCas9 Double NLS
6767 bp

FIGURE 22

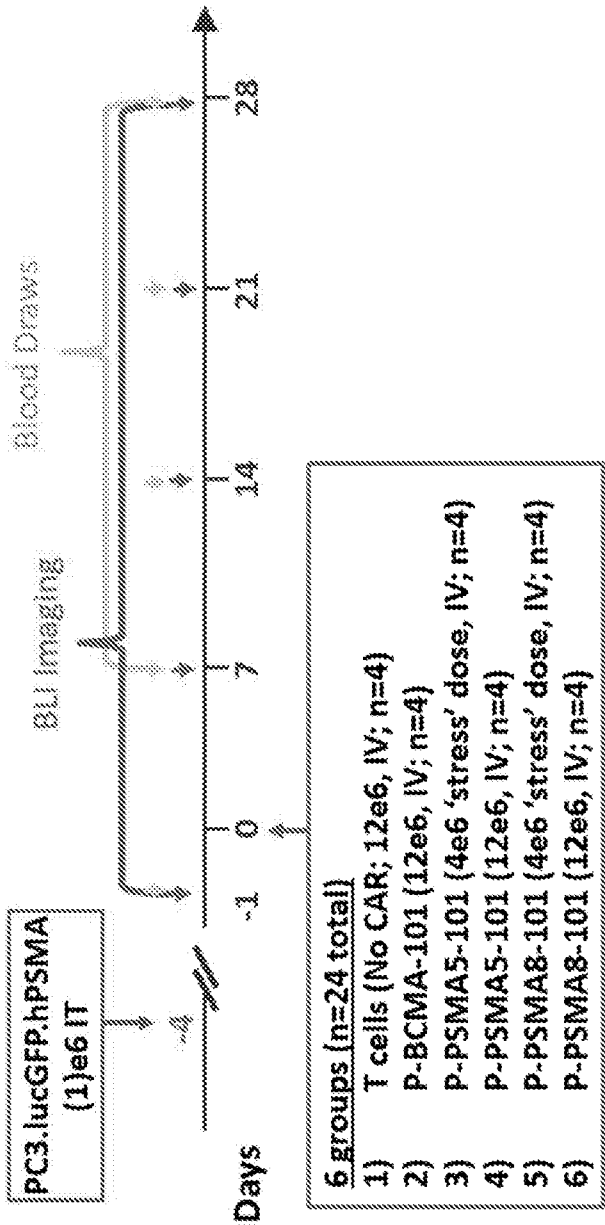


FIGURE 23

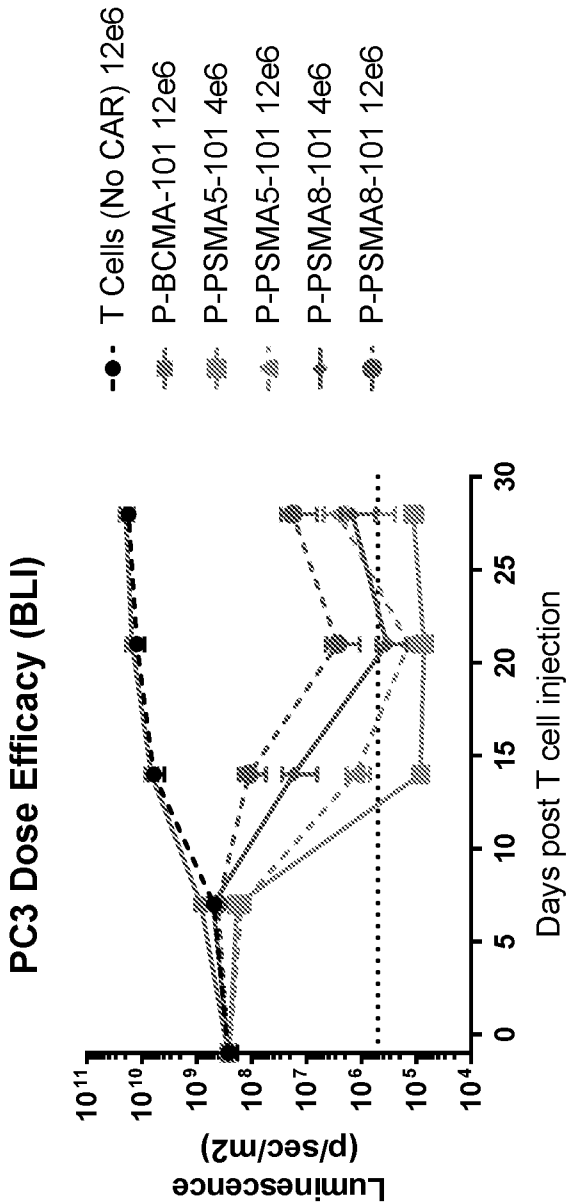


FIGURE 24

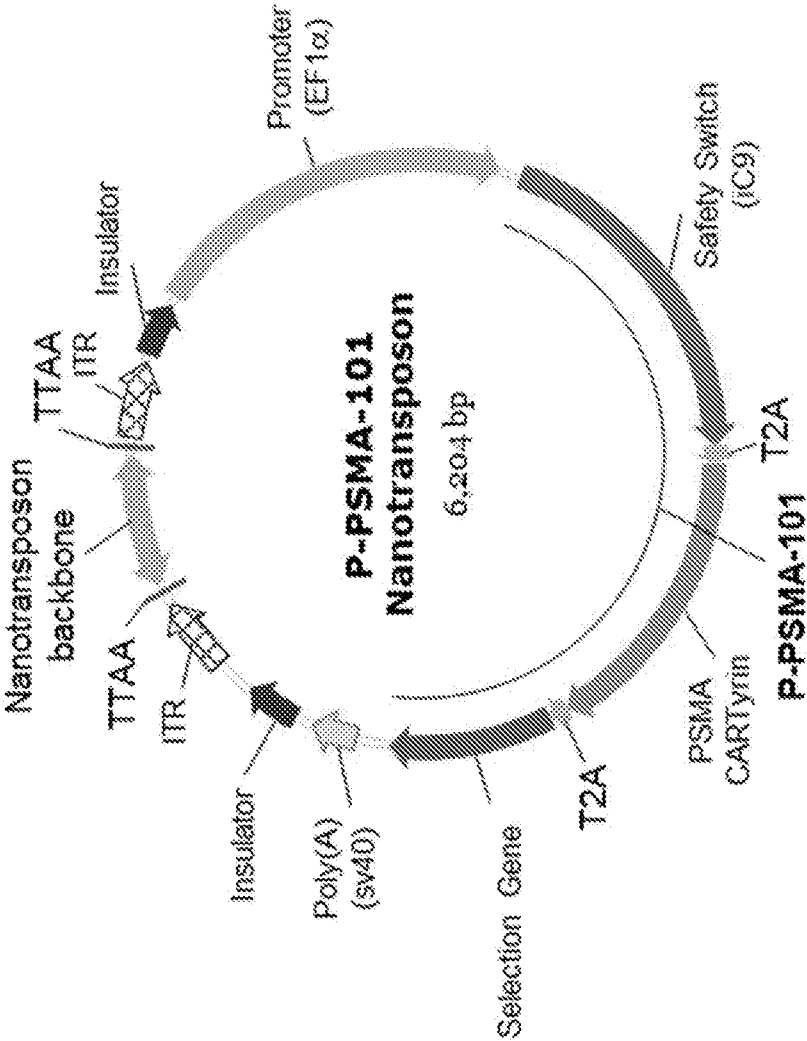


FIGURE 25

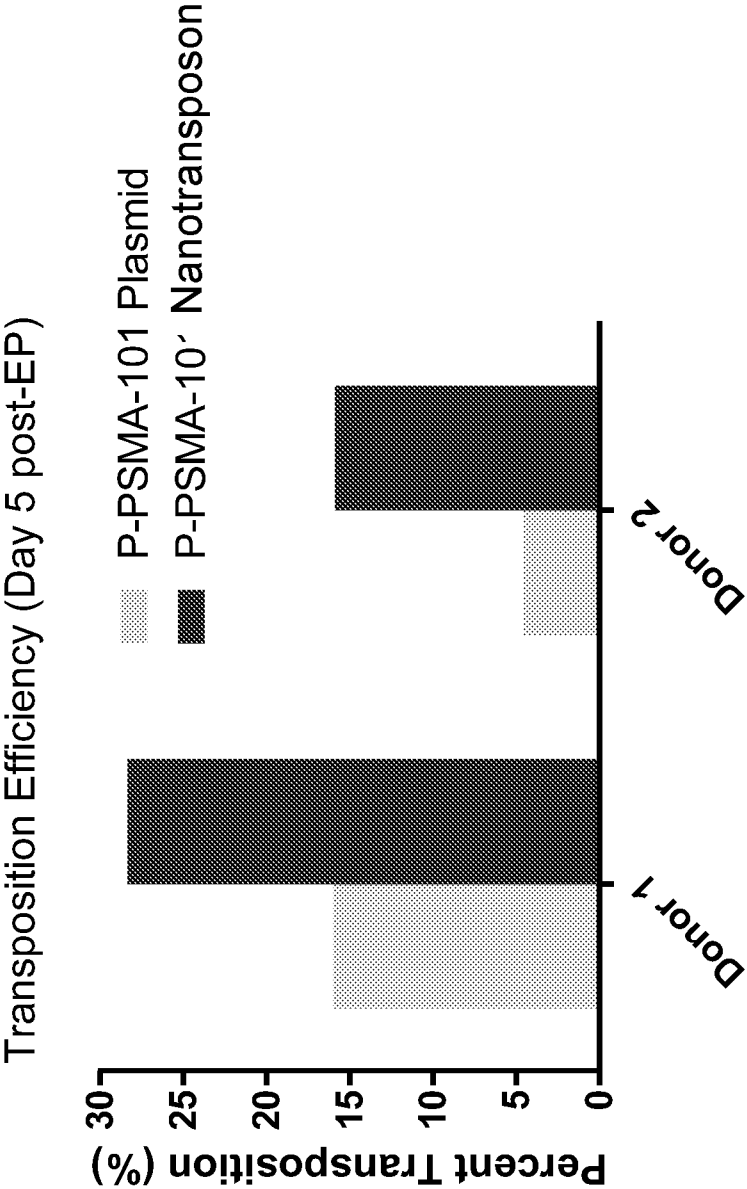


FIGURE 26

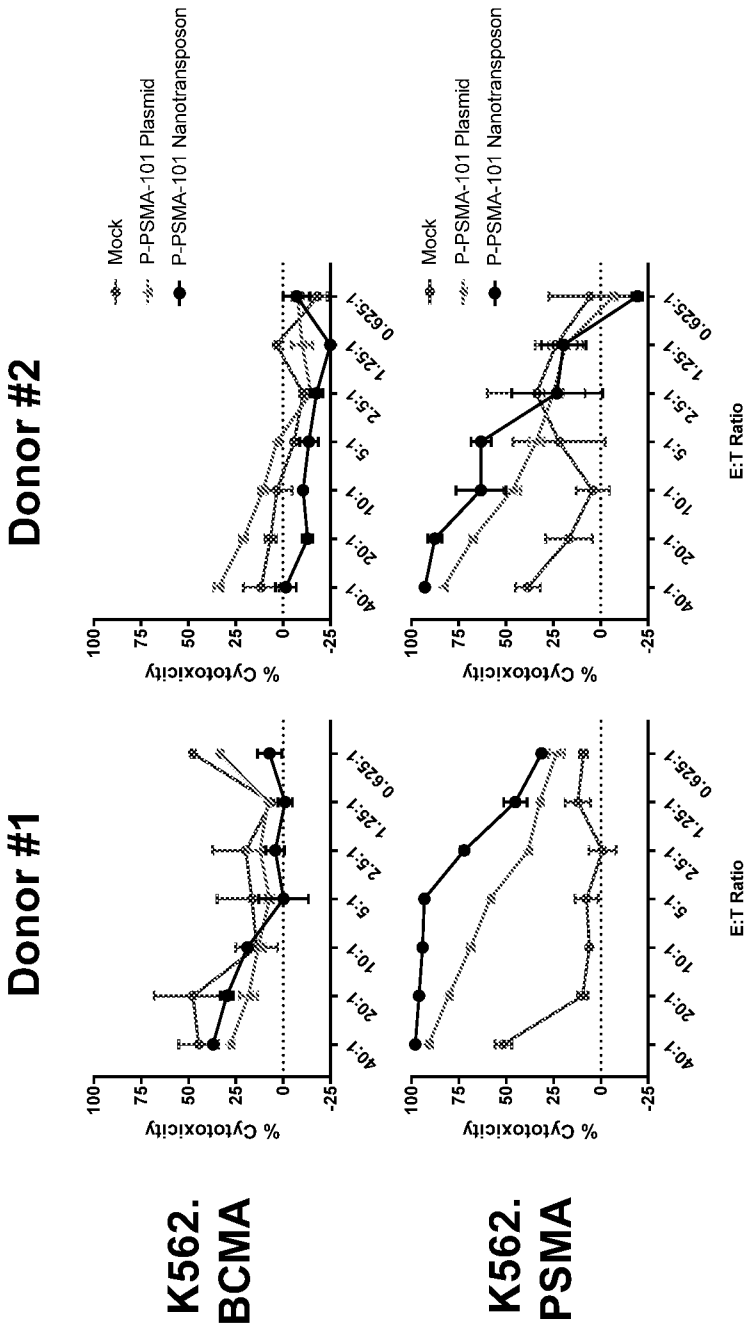


FIGURE 27

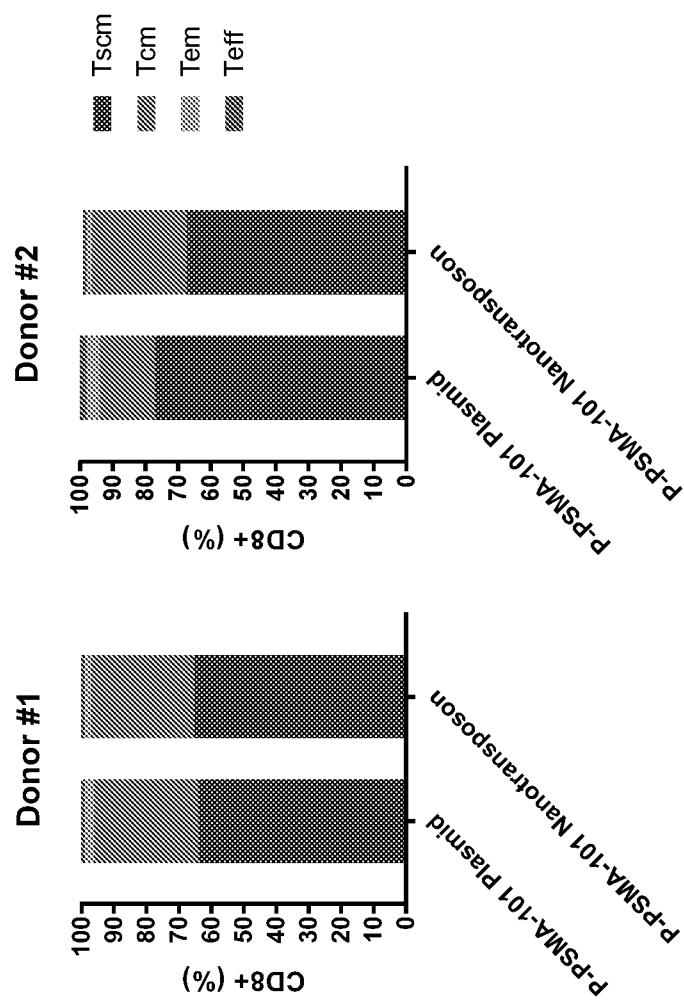


FIGURE 28

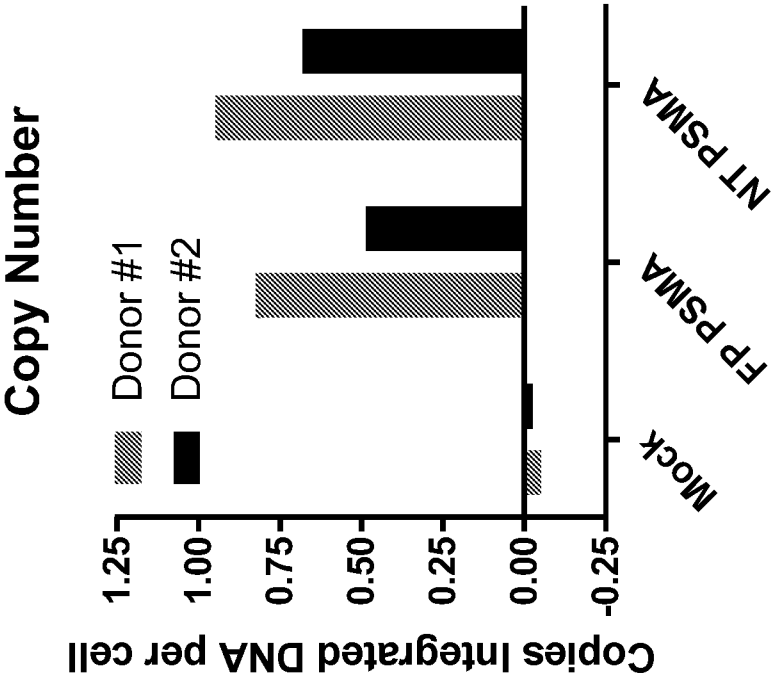
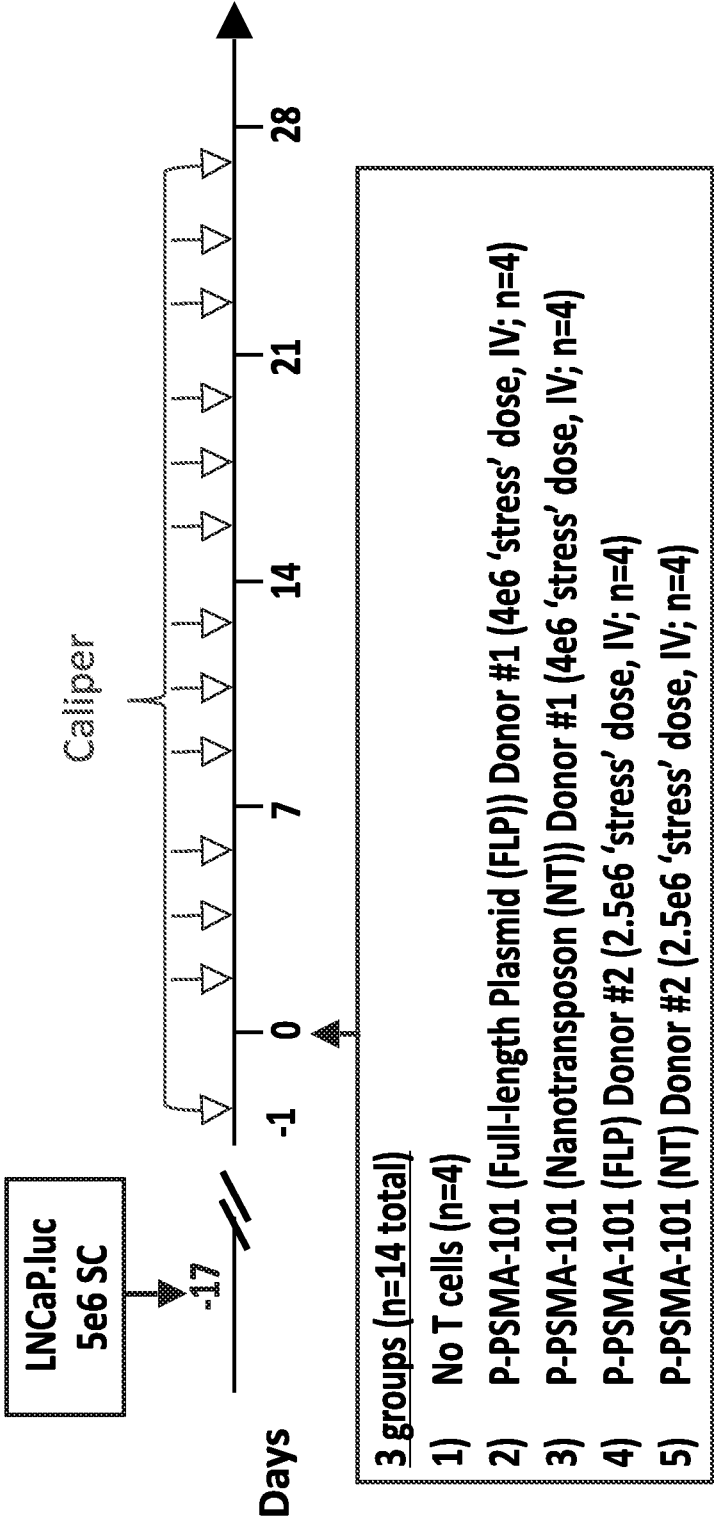
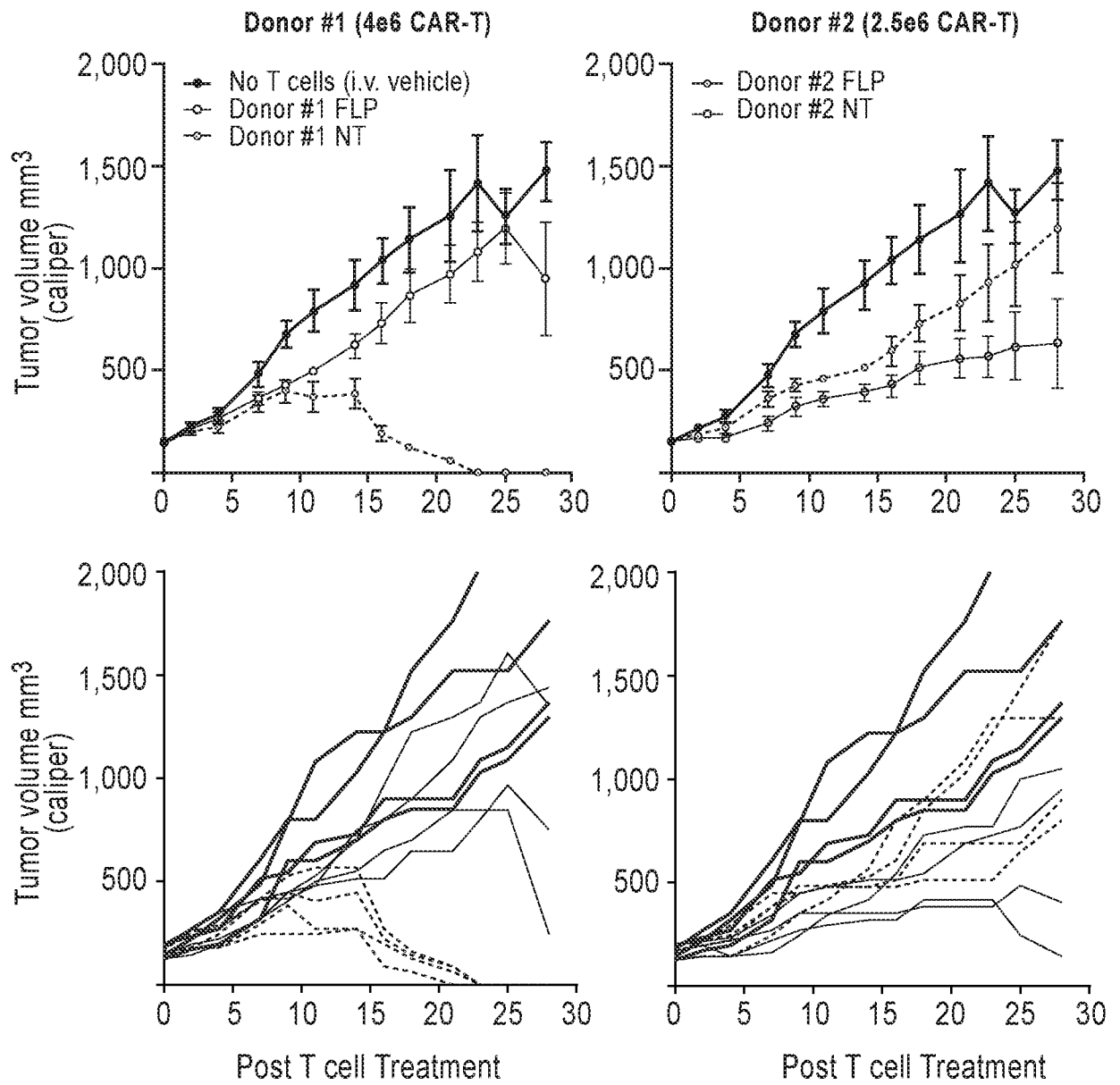


FIGURE 29A



A) Study design



B) Caliper Measurements

FIGURE 29B

FIGURE 30

T-cell receptor (TCR) and co-receptors CD28 and CD2

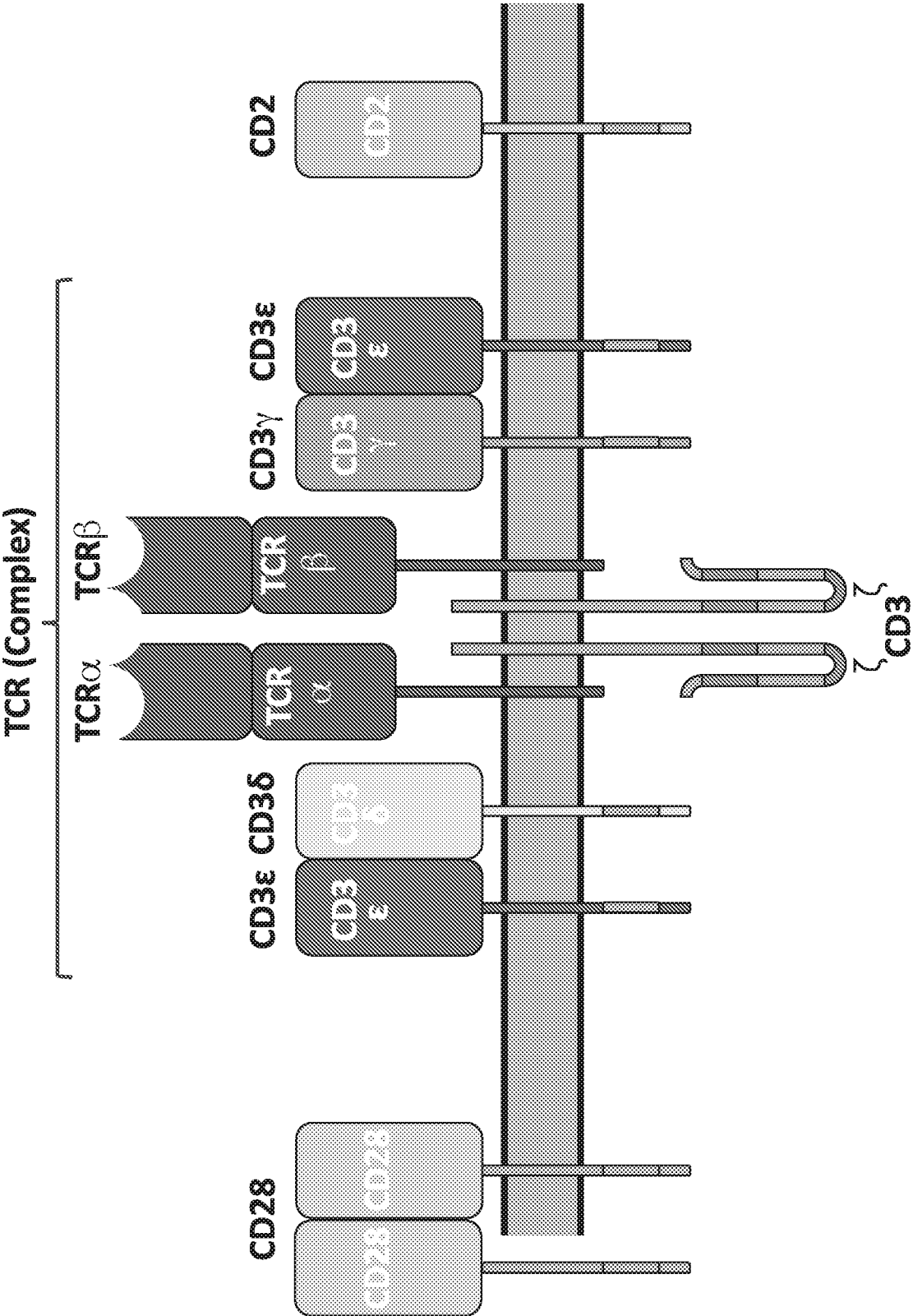


FIGURE 31

Primary and secondary co-stimulation is delivered to T-cell via binding of agonist mAbs (anti-CD3, anti-CD28, and anti-CD2)

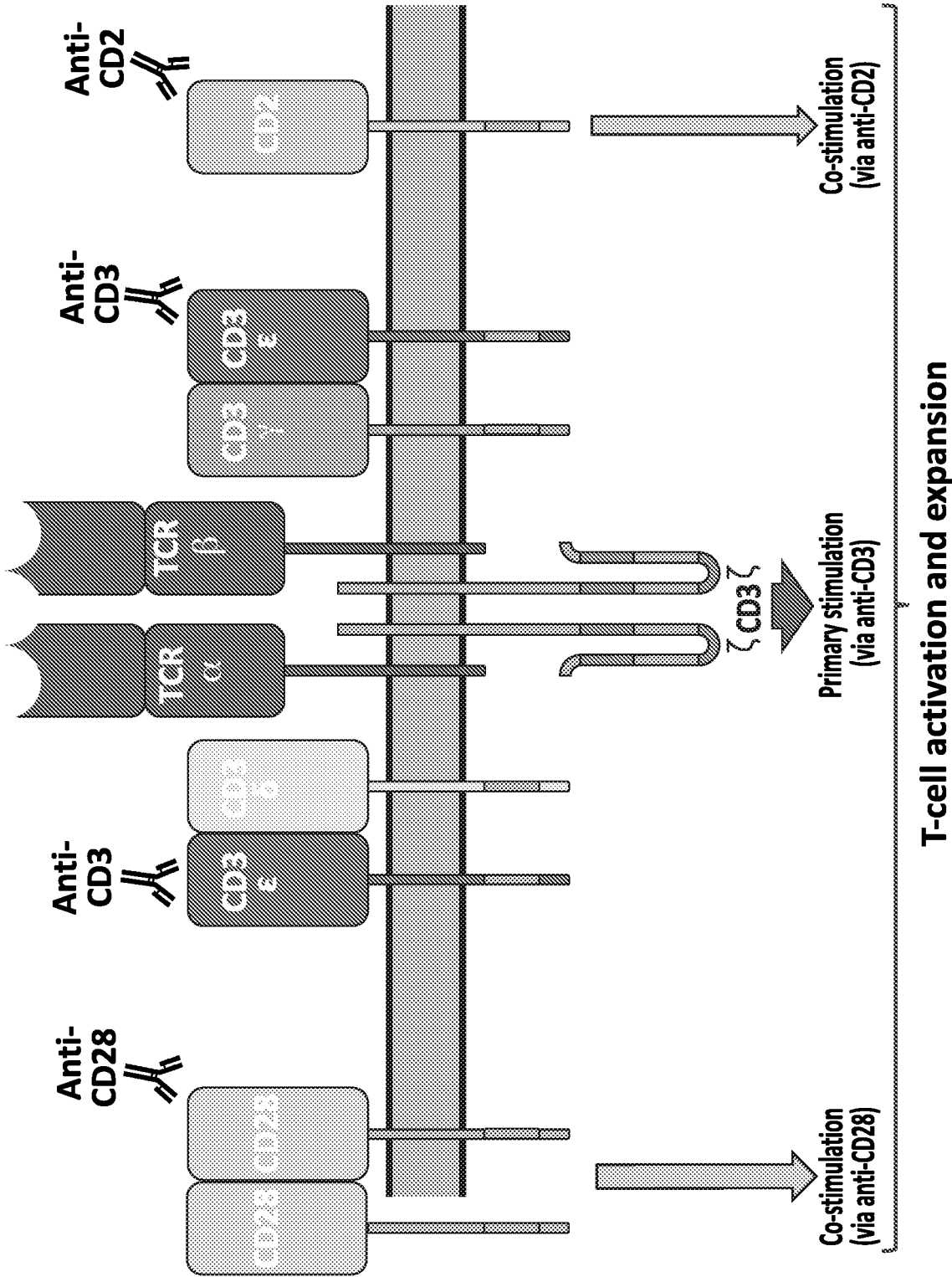


FIGURE 32

Enhanced stimulation by expression of Chimeric Stimulatory Receptors (CSR)s

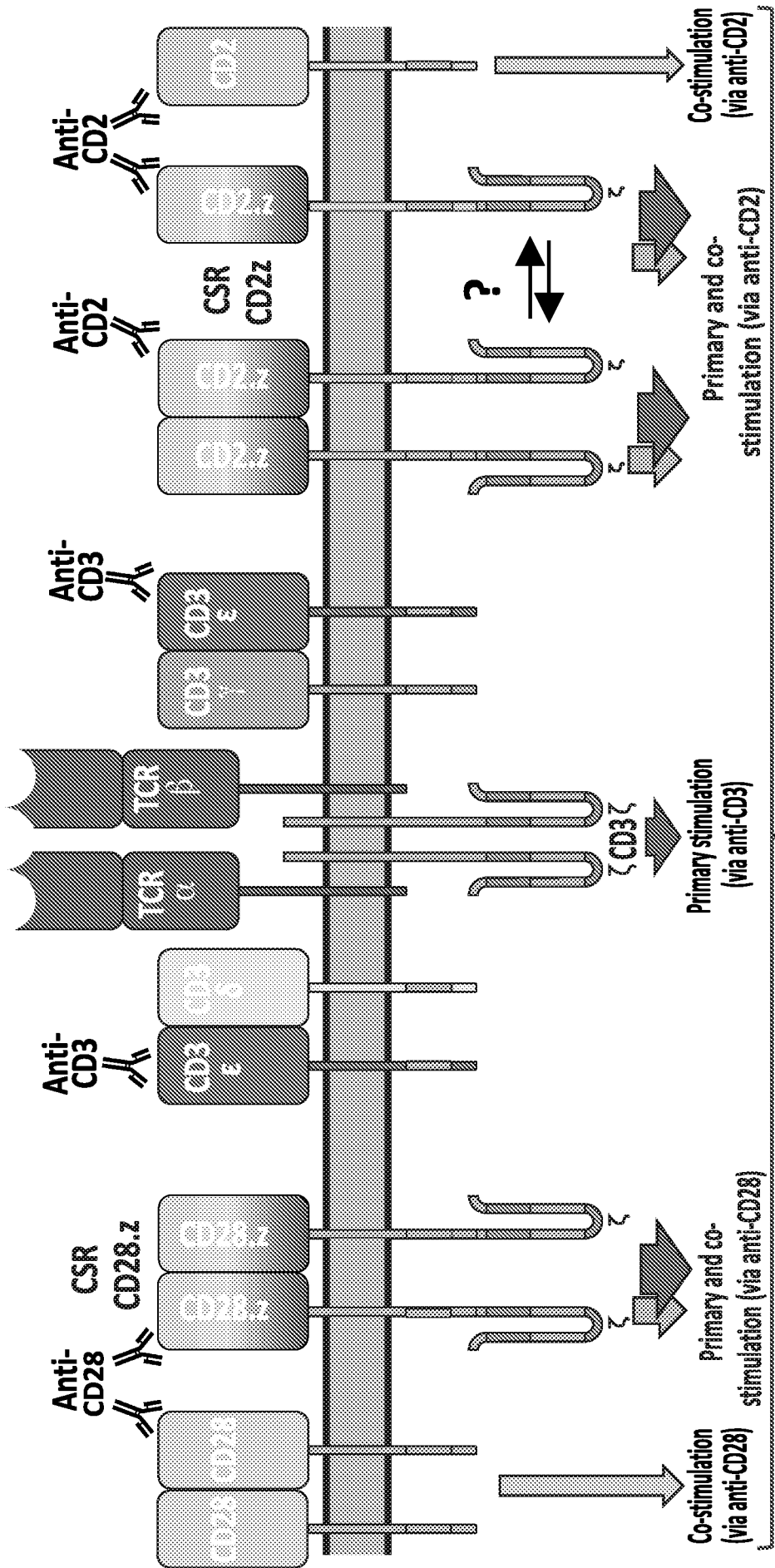


FIGURE 33A

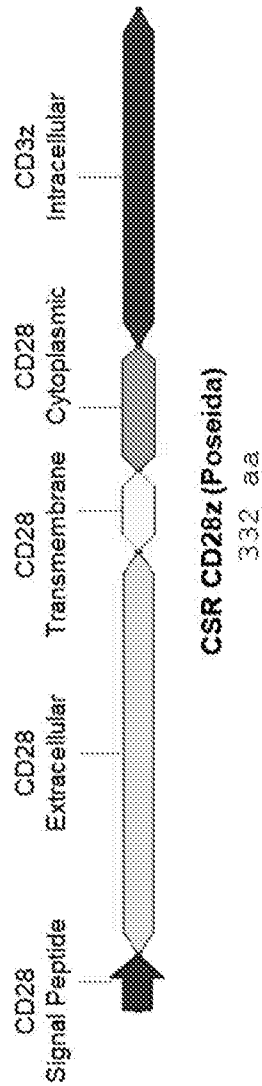


FIGURE 33B

MLRLLALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASHKGLDSAVE
VCVVYGNYSQQLQVYSKTGFNC DGKLGNESVTFYLQNLVYNQTDIYFCKIEVMYPPPYLDN
EKSNGTIIHVKGKHLCPSP LFPGPSKPFWVLVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHS
DYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRR
EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHG
LYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 17910)

FIGURE 33C

ATGCTGAGACTGCTGCTGGCCCTGAATCTGTTCCCCAGCATCCAAGTGACCGGCAACAAGA
TCCTGGTCAAGCAGAGCCCTATGCTGGTGGCCTACGACACGCCGTGAACCTGAGCTGCAA
GTACAGCTACAACCTGTTACGACAGAGAGTCCGGCCAGCCTGCACAAAGGACTGGATTCT
GCTGTGGAAGTGTGCGTGGTACGGCAACTACAGCCAGCAGCTGCAGGTCTACAGCAAG
ACCGGCTTCAACTGCGACGGCAAGCTGGGCAATGAGAGCGTGACCTTCTACCTGCAAAACC
TGACGTGAACCAAGACCGACATCTATTTCTGCAAGATCGAAGTGATGTAACCGCCTCCTTAC
CTGGACAACGAGAAGTCCAACGGCACCATCATCCACGTGAAGGGCAAGCACCTGTGTCCTT
CTCCACTGTTCCCGGACCTAGCAAGCCTTTCTGGGTGCTCGTTGTTGTTGGCGCGTGCTG
GCCTGTTATAGCCTGCTGGTTACAGTGGCCTTCATCATCTTTTGGTCCGAAGCAAGCGGA
GCCGGCTGCTGCACAGCGACTACATGAACATGACCCCTAGACGGCCCGGACCAACAGAA
AGCACTACCAGCCTTACGCTCCTCTAGAGACTTCGCCGCCTACCGGTCCAGAGTGAAGTTC
TCCAGATCCGCGATGCTCCCGCCTATAAGCAGGGCCAGAACCCAGCTGTACAACGAGCTGA
ACCTGGGGAGAAAGAGAAGAGTACGATGTGCTGGACAAGCGGAGAGGCAGAGATCCTGAG
ATGGGCGGCAAGCCAGACGGAAGAATCCTCAAGAGGGCCTGTACAATGAACTGCAGAAA
GACAAGATGGCCGAGGCCTACAGCGAGATCGGAATGAAGGGCGAGCGCAGAAGAGGCA
AGGGACACGATGGACTGTACCAAGGGCCTGAGCACCCGCCAACCAAGGATACCTATGATGCCC
TGCACATGCAGGGCCCTGCCTCCAAGA (SEQ ID NO: 17911)

FIGURE 34A

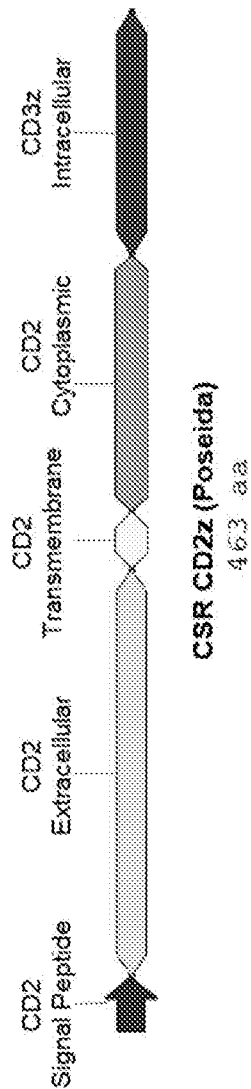


FIGURE 34B

MSFPCKFVASFLLIFNVSSKGAVSKEITNALETWGALGQDINLDIPSFQMSDDIDDIIKWEKT
SDKKKIAQFRKEKETFKEDTYKLFKNGTLKIKHLKTDDQDIYKVSIIYDTKGKNVLEKIFDLKI
QERSKPKISWTCINTTLTCEVMNGTDPELNLYQDGKHLKLSQRVITHKWTTSLSAKFKCT
AGNKVSKESSVEPVSCPEKGLDIYLIIGICGGGSLLMVFALLVFYITKRKKQRRRRNDEELET
RAHRVATEERGRKPHQIPASTPQNPAATSQHPPPPGRHRSQAPSHRPPPGHVRVQHQPQK
RPPAPSGTQVHQQKGPPLPRPRVQPKPPHGAENSLSPSSNRVKFSRSADAPAYKQGQN
QLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMK
GERRRGKGDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 17912)

FIGURE 34C

ATGAGCTTCCCTTGCAAGTTCGTGGCCAGCTTCTGTCTGATCTTCAACGTGTCTCTAAGGGCGCC
GTGTCCAAAGAGATCACAAACGCCCTGGAAACCTGGGAGCCCTCGGCCAGGATATTAAACCTGG
ACATCCCAGCTTCAGATGAGCGACGACATCGATGACATCAAGTGGGAGAAAAACCCAGCGACAA
GAAGAAGATCGCCAGTTCGGAAAGAGAAAGAGACATTCAAAGAGAAAGGACACCTACAAGCT
GTTCAAGAACGGCACCTGAAGATCAAGCACCTGAAACCGACGACGACGACATCTATAAGGTG
TCCATCTACGACACCAAGGGCAAGAACGTGCTGGAAAAGATCTTCGACCTCAAGATCCTCAAGAGCG
GGTGTCCAAAGCCTAAGATCAGCTGGACCTGCATCAACACCACACTGACCTGCGAAGTGATGAACG
GCACAGACCCGAGCTGAACCTGTACCAGGATGGCAAAACACCTGAAGCTGAGCCAGCGCGTGAT
CACCCAAAGTGGACAAAGCCTGAGCGCAAGTTCAAGTGCAACCGCCGGAACAAAGTGCT
AAAGAGTCCAGCTCGAGCCCGTGTCTTGCCTGAAAAAGGACTGGACATCTACCTGATCATCGG
CATCTGTGGCGGGGAGCCTGCTGATGGTGTCTGTGGCTGCTGTGTCTACATCACCAAGC
GGAAGAAGCAGCGGAGCAGACGGAACGACGAGGAACCTGGAACACACGGGCCCATAGAGTGCC
ACCGAGGAAAGAGGCAGAAAGCCCCACCAGATCCAGCCAGCACACCCAGAAATCCTGCCACCTC
TCAACACCTCCACCTCCACCTGGACACAGATCTCAGGCCCCATCTCAGACCTCCACCACCTGG
TCATCGGGTGCAGCACCAAGCCTCAGAAAAAGACCTCCTGCTCCTAGCGGCACACAGGTGCACCAAGC
AAAAAGGACCTCCACTGCCCTCGCCTAGAGTGCAGCTAAACCTCCTCATGGCGCCGCTGAGAAC
AGCTGTCTCCAAGCAGCAACAGAGTGAAGTTCAGCCGACGCGCCGATGCTCCTGCCTATAAGCA
GGACAGAACCAAGCTGTCAACGAGCTGAATCTGGGGCGCAGAGAGATCGATGTGTGGA
CAAGCGAGAGGCAGAGATCCTGAGATGGCGGCAAGCCAGACGGAAGAAATCCTCAAGAGGG
CCTGTATAATGAGCTGCAGAAAGACAAGATGGCCGAGGCCTACAGCGAGATCGGAATGAAGGG
CGAGCGCAGAAGAGGCAAGGGACACGATGGACTGTATCAGGGCCTGAGCACCGCCCAAGGA
TACCTATGATGCCCTGCACATGCAGGGCCCTGCCTCCAAGA (SEQ ID NO: 17913)

FIGURE 35

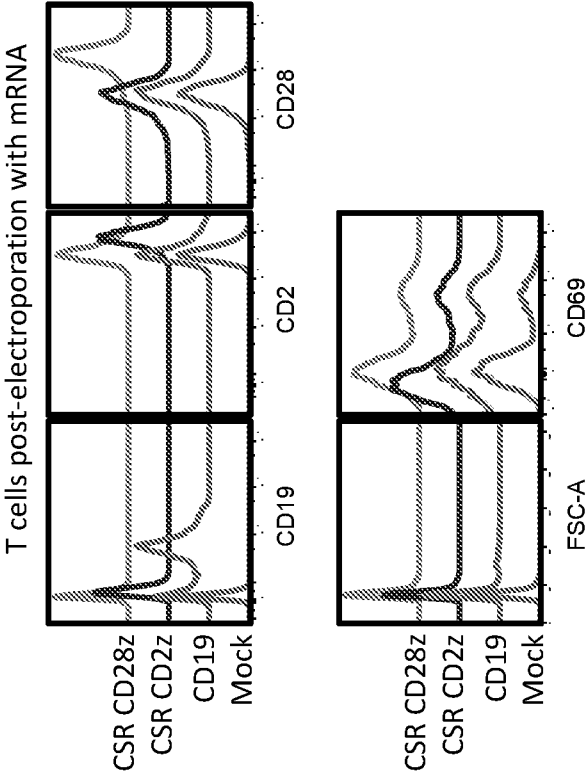


FIGURE 36

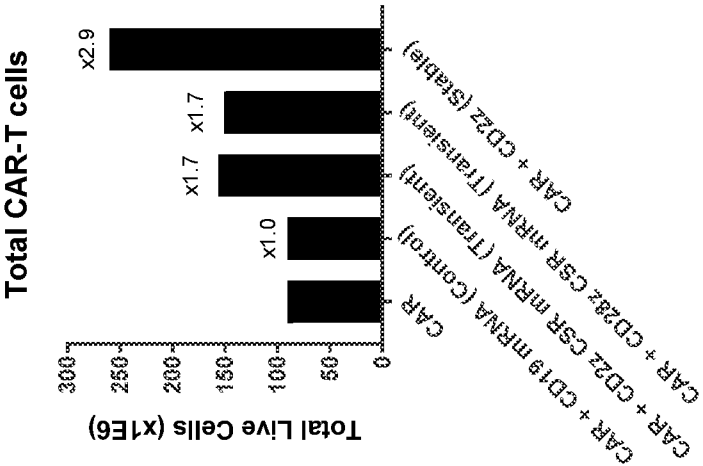


FIGURE 37

