

FIGURE 1

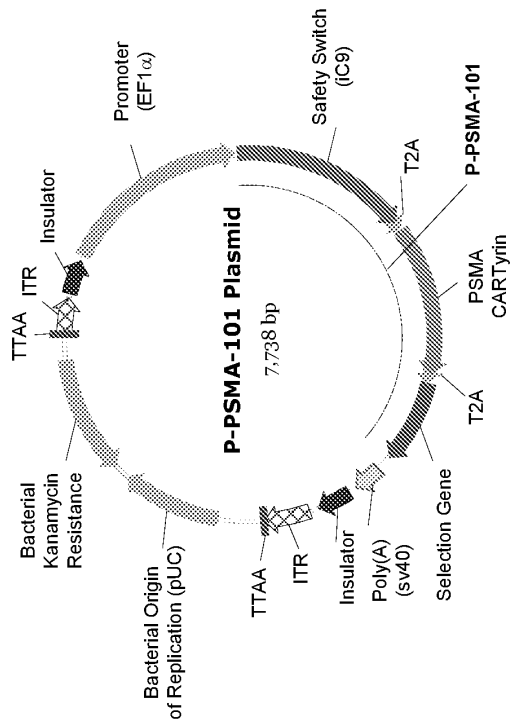


FIGURE 2

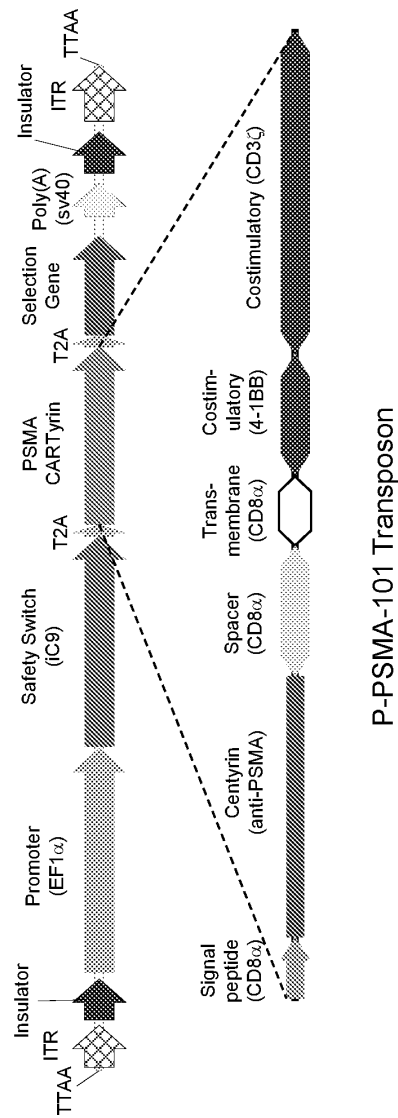


FIGURE 3A

PSMA5 CARTYRIN:
SIGNAL PEPTIDE: MALPVTALLPLALLHAARP (SEQ ID NO: 18004)
CENTYRIN (PSMA5):
MLPAPKNLVVSRVTEDSARLSWDIDEQRDWFESLIQYQSEKVGAEIVLTPGSERSYDLTGLKPGTEYTVSYGV
YHVYRSNPLSAIFTT (SEQ ID NO: 18000)
HINGE (CD8 α): TTPAPRPPTPAPTIASQPLSLRPEACRPAAAGGAVHTRGLDFACD (SEQ ID NO: 18014)
TRANSMEMBRANE (CD8 α): IYWAPLAGTCGVLLSLVITLYC (SEQ ID NO: 18006)
COSTIMULATORY DOMAIN #1 (4-1BB): KRGRKLLYIFKQPFMRPVQTTQEEDGCSRCRFPPEEEGGCEL (SEQ
ID NO: 18012)
COSTIMULATORY DOMAIN #2 (CD3 ζ):
RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPFMGGKPRRKNPQEGLYNELQDKMAEAYSEI
GMKGERRRGKHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 18008)

P-PSMA5-101 CONSTRUCT:
MALPVTALLPLALLHAARPMLPAPKNLVVSRVTEDSARLSWDIDEQRDWFESLIQYQSEKVGAEIVLTPGSE
RSYDLTGLKPGTEYTVSYGVYHVYRSNPLSAIFTTTPAPRPPTPAPTIASQPLSLRPEACRPAAAGGAVHTRGLD
FACDIYWAPLAGTCGVLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSRCRFPPEEEGGCELRVKFSRS
ADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPFMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGER
RRKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 18063)

PSMA5 CARTYRIN:

SIGNAL PEPTIDE:
ATGGCACTGCCTGTGACAGCCCTGCTGCTGCCTCTGCCCTGCTGCTGACGCACGACGCGCC
(SEQ ID NO: 18064)

CENTYRIN (PSMA5):
 ATATCTGCCTCGACCAAGAAACCTGGTGGTCTCGGTTGACCGAGGACTTGCACGACTGAGCTGGGACATC
 ATATCTGACGACGAGGATTTCTGAGAGCTTTCTGATCCAGTATCAGAGTCCGAGAAAGTGGCGGAGGCATC
 GTGCTGACATGTCCTGGCAGGACGGTCTTATCACTCGACCGGCTGAAGCCAGGCACAGGTACACCGT
 GTGCATCTACGGGTGATCATCGTGTACAGGTCCAACTCTGTCTGCCATCTTCCACCACA
 (SEQ ID NO: 18001)

HINGE (CD8₂):
GAGGCCTGCGGCCCCGCCGGGAGCAGTGCACACACGGGGCTGGACTTGGCTGTGAC
(SEQ ID NO: 18065)

TRANSMEMBRANE (CD8 α):
ATCTACATATGGGACCACTGGCAGAACCTGCGGCTGCTGCTGCTGAGCCTGGTCATCACCCCTGACTGT
(SEQ ID NO: 18066)

COSTIMULATORY DOMAIN #1 (4-1BB):
GAGAGAGAGCGAAGAAAGCTGCTGTATATCTTCAAGCAGCCCTTATGAGACCCGTGCAGACCACACAGGAG
GAGACCGGCTCTCTTGTAGGCTCCCAAGCAGGAGGAGGAGGATTCGAGCTG (SEQ ID NO: 18067)

COSTIMULATORY DOMAIN #2 (CD3):
 CCGGTGTGAAGTTTACGCGGTGCGCGATGCACTGCATCAACAGAGGACAGAACCAAGCTGTATAACGAGCTG
 CAGGCTGCGAGGAGGAGGAGTACGATGCTGGATAAGAGCGGGGCGGGACCCGCGAGATGGGAGGCA
 AGGCTCGAGAAAGAACCCACAGAGGCGCTGTACAATGAGCTGCAAAAGACAAAGATGCCGAGGCGCTATT
 CTGAGATCGGCATGAAGGAGAGAGCGCGCGGGCAAGGGACACATGGCTGTACCAAGGCGGCTGAGGAC
 CGCCACAAAGAGCACGCTATTGATGCCCTGCATATGCAATGCAAGCGCCCTGCCCCCTGA (SEQ ID NO: 18068)

FIGURE 3C

P-PSMA5-101 CONSTRUCT:
CTGGCACTGCCTGTGACAGCCCTGCTGCTGCCTCTGGCCCTGCTGCTGCACGACGACGCGCCCATGCTGCCT
GCACCAAGAACCTGGTGTCTCGGTGACCGAGGACTCTGCCAGACTGAGCTGGGACATCGATGAGCA
GAGGATTGGTTGAGAGCTTCTGATCCAGTATCAGGAGTCCGAGAAAGTGGCGAGGCCATCGTGTGAC
AGTCCCTGGCAGCGAGCGTCTATGACCTGACCGGCTGAAGCCAGGCACAGAGTACCGTGTCCATCTA
CGCGTGTATCACGTGTACAGGTCCAATCTCTGTCTGCCATCTTACCCAAACCCACCCCTGCCCCCA
CTCCCAACCCGCCCTACCATCGGAGCCGCCACTGTCCCTGCGGCTGAGGCTGCGGCGCCGCGC
CGCGGAGCAGTGCACACGCGGCTGGACTTTGCCCTGTGACATCTACATATGGGCACCACTGGCAGGAA
CCTGCGGCTGCTGCTGAGCCTGGTCAACCCCTGTAAGAGAGGAGGAGGAGCTGCTGTATA
TCTTCAAGCAGCCCTTCAAGAGCCCGTGCAGACACACAGGAGGAGGAGCGGCTGCTCTTTAGGTTCCAG
AGGAGGAGGAGGAGATGCGAGCTGCGGTGAAGTTTAGCCGGTCCGCCGATGCACCTGCATACAAGCAG
GGACAGAAACAGCTGTATAACGAGCTGAATCTGGCCCGGAGAGGAGTACGACGTGCTGGATAAGAGCG
GGCCCGGACCCCGAGATGGAGGCAAGCTCGGAGAAAGAACCCAGAGGAGGCCGTGTACAATGAGCTG
CAAAGGACAAGATGCCGAGGCTATTCTGAGATCGGCATGAAGGAGAGAGCGGCCCGGGCAAGGACA
CGATGGCTGTACCCAGGCTGAGCACCGCCACAAGGACACCTATGATGCCCTGCACATGCAGGCCCTGC
CCCCTAGA (SEQ ID NO: 18069)

FIGURE 4A

PSMA8 CARTYRIN:
SIGNAL PEPTIDE: MALPVTALLPLALLHAARP (SEQ ID NO: 18004)
CENTYRIN (PSMA8):
MLPAPKNLVVSRVTEDSARLSWAIDEQRDWFESFLIQYQSEKVGAEIVLTPGSESYDLTGLKPGTEYTVSYGV
YHVYRSNPLSAIFTT (SEQ ID NO: 18002)
HINGE (CD8 α): TTPAPRPPTPAPTIASQPLSLRPEACRPAAAGGAVHTRGLDFACD (SEQ ID NO: 18014)
TRANSMEMBRANE (CD8 α): IYWAPLAGTCGVLLSLVITLYC (SEQ ID NO: 18006)
COSTIMULATORY DOMAIN #1 (4-1BB): KRGRKKLLYIFKQPFMRPVQTTQEEDGCSRCRFPPEEEGGCEL (SEQ
ID NO: 18012)
COSTIMULATORY DOMAIN #2 (CD3 ζ):
RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPFMGGKPRRKNPQEGLYNELQDKMAEAYSEI
GMKGERRRGKHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 18008)

P-PSMA8-101 CONSTRUCT:
LALPVTALLPLALLHAARPMILPAPKNLVVSRVTEDSARLSWAIDEQRDWFESFLIQYQSEKVGAEIVLTPGSE
RSYDLTGLKPGTEYTVSYGVYHVYRSNPLSAIFTTTPAPRPPTPAPTIASQPLSLRPEACRPAAAGGAVHTRGLD
FACDIYWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSRCRFPPEEEGGCELRVKFSRS
ADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPFMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGER
RRKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 18070)

FIGURE 4B

PSMA8 CARTYRIN:
SIGNAL PEPTIDE:
ATGGCACTGCCTGTGACAGCCCTGCTGCTGCCTCTGGCCCTGCTGCTGCACGACACGGCCCC
(SEQ ID NO: 18064)
CENTYRIN (PSMA8):
ATGCTGCCGTGCACCAAGAACCTGGTGGTGTCTCGGGTGACCGAGGACTCTGCCAGACTGAGCTGGGCCATC
GACGAGCAGAGGATTGGTTTCGAGAGCTTTCTGATCCAGTATCAGAGTCCGAGAAAGTGGCGAGGCCATC
GTGCTGACAGTGCCTGGCAGCGAGCGGTCTATGATCTGACCGCCTGAAGCCAGGCACAGAGTACACCGT
GTCCATCTACGGCGTGATCACGTGTACAGGTCCAAATCCTCTGCTTGCCATCTTCACCACA
(SEQ ID NO: 18003)
HINGE (CD8_α):
ACCAACCCCTGCCCCAGACCTCCCAACCCGCCCTACCATCGCAGCCAGCCACTGTCCCTGCGGCCT
GAGCCTGCCCGCCCGCCCGCGGAGCAGTGCACACACGGGGCCTGGACTTTGCCCTGTGAC
(SEQ ID NO: 18065)
TRANSMEMBRANE (CD8_α):
ATCTACATATGGGCACCACTGGCAGGAACCTGCGCGGTGCTGCTGAGCCTGGTCAATCACCCTGTACTGT
(SEQ ID NO: 18066)
COSTIMULATORY DOMAIN #1 (4-1BB):
AAGAGAGGCAGGAAGAAGCTGCTGTATATCTTCAAGCAGCCCTTCAATGAGACCCGTGCAGACACACAGGAG
GAGGACCGCTGCTCTGTAGTTCCCAAGAGGAGGAGGAGGAGTCCGAGCTG (SEQ ID NO: 18067)
COSTIMULATORY DOMAIN #2 (CD3_ζ):
CGCGTGAAGTTTAGCCGGTCCCGCATGCACCTGCATACAAGCAGGGAGACAGACCAGCTGTATAACGAGCTG
AATCTGGGCGGAGAGAGGAGTACGACGTGCTGGATAAGAGCGGGGCCCGGACCCCGAGATGGAGGCA
AGCCTCGGAGAAAGAACCCACAGGAGGCGCTGTACAATGAGCTGCAAAAGGACAAGATGGCCGAGGCCATT
CTGAGTCGGCATGAAGGAGAGAGGCGCCGGGCAAGGGACACGATGGCCTGTACCAAGGCCCTGAGCAC
CGCCACAAAGGACACCTATGATGCCCTGCACATGCAGGCCCTGCCCCCTAGA (SEQ ID NO: 18068)

FIGURE 4C

P-PSMA8-101 CONSTRUCT:
CTGGCACTGCCTGTGACAGCCCTGCTGCTGCCTCTGGCCCTGCTGCTGCACGCAGCACGGCCCATGCTGCCT
GCACCAAGAACCTGGTGTCTCGGTGACCGAGGACTCTGCCAGACTGAGCTGGGCCATCGACGAGCA
GAGGATTGGTTGAGAGCTTCTGATCCAGTATCAGGAGTCCGAGAAAGTGGCGAGGCCCATCGTGTGAC
AGTCCCTGGCAGCGAGCGTCTATGATCTGACCCGGCTGAAGCCAGGCACAGTACACCGTGTCCATCTA
CGGCGTGTATCACGTGTACAGGTCCAATCCTCTGTCTGCCATCTTACCCAAACCCACCCCTGCCCCAGA
CCTCCACACCCGCCCTACCATCGCAGCCAGCCACTGTCCCTGCGGCTGAGGCTGCGGCCCTGCCGCGCGC
CGCGGAGCAGTGCACACAGCGGCCCTGGACTTTGCCCTGTGACATCTACATATGGGCACCACTGGCAGGAA
CCTGCGCGTGTGCTGCTGAGCCTGGTCTATCACCCCTGTAAGAGAGGCAAGAGCTGCTGTATA
TCTTCAAGCAGCCCTTCAAGAGCCCGTGCAGACACACAGGAGGAGCGGCTGCTCTTTGAGGTTCCAG
AGGAGGAGGAGGAGGATGCGAGCTGCGGTGAAGTTTAGCCGGTCCGCCGATGCACCTGCATACAAGCAG
GGACAGAACCAAGCTGTATACGAGCTGAATCTGGGCCGGAAGAGGAGTACGACGTGCTGGATAAGAGCG
GGCCCGGACCCCGAGATGGAGGCAAGCTCGGAGAAAGAACCCAGAGGAGGCCGTGTACAATGAGCTG
CAAAGGACAAGATGCCGAGGCCTATTCTGAGATCGGCATGAAGGAGAGAGCGCCCGGGCAAGGGACA
CGATGGCTGTACCCAGGCTGAGCACCGCCACAAAGGACACCTATGATGCCCTGCACATGCAGGCCCTGC
CCCCTAGA (SEQ ID NO: 18071)

FIGURE 5

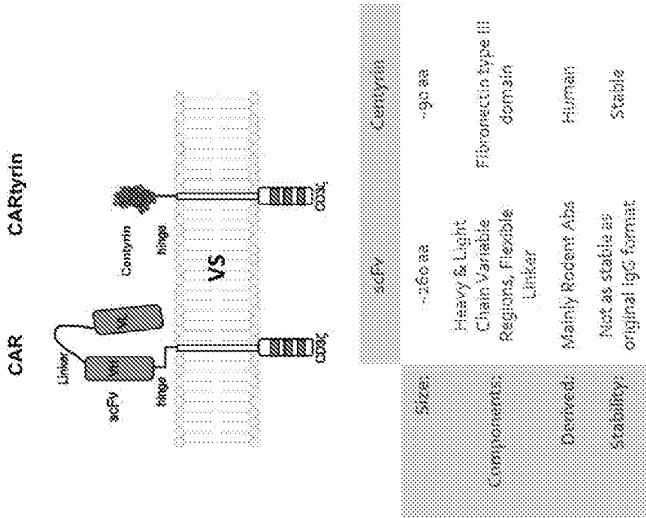
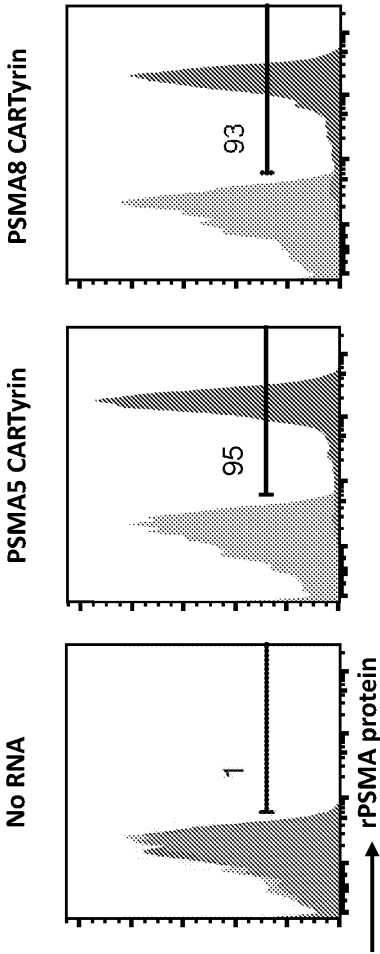
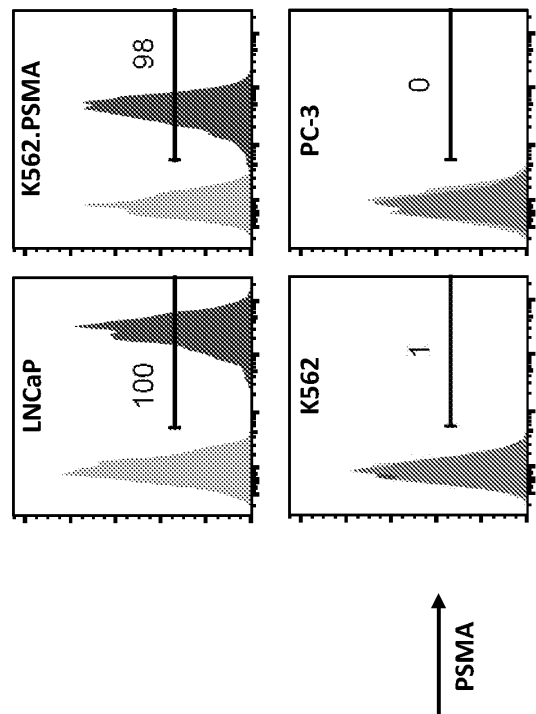


FIGURE 6A



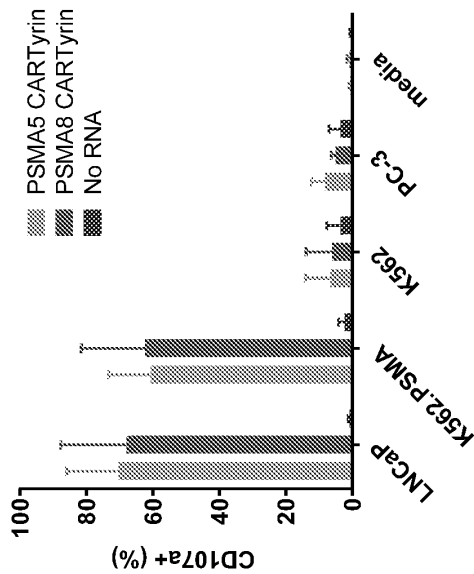
A) PSMA CARTyrin surface expression 24 hours post mRNA transfection of human pan T cells

FIGURE 6B



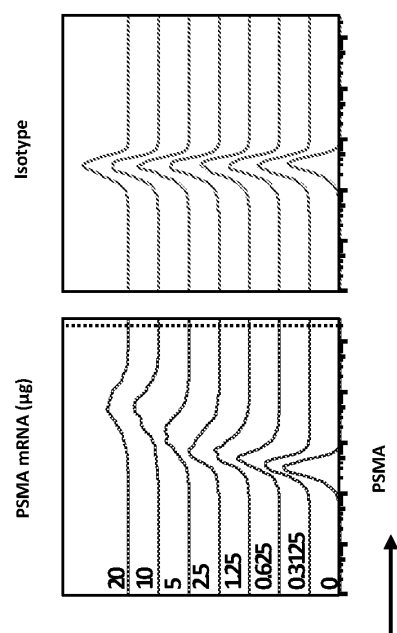
B) Expression of PSMA protein on tumor cell lines. Gray histogram represents the isotype control

FIGURE 6C



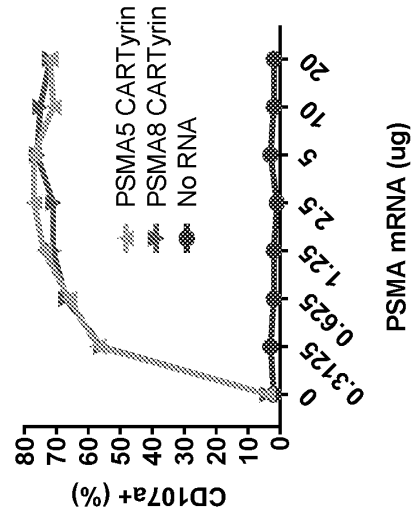
C) Degranulation of RNA-electroporated PSMA CARTyrin T cells against PSMA+ tumor cell lines

FIGURE 6D



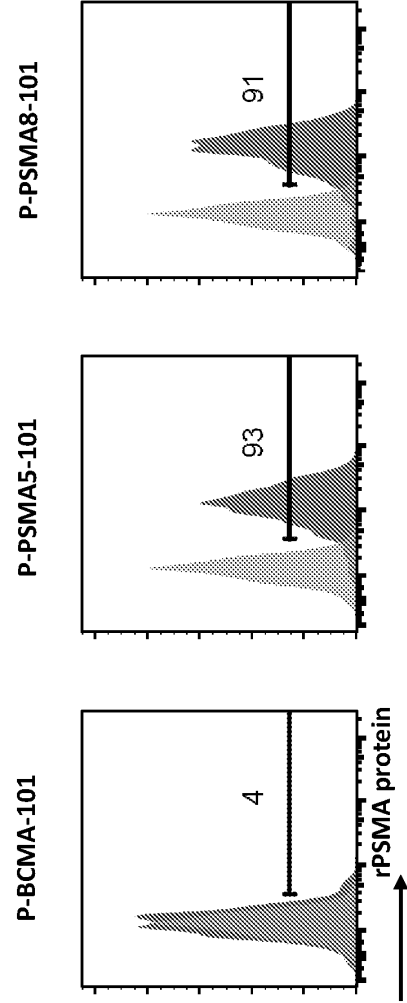
D) PSMA surface expression following transfection of K562 using various amounts of PSMA mRNA

FIGURE 6E



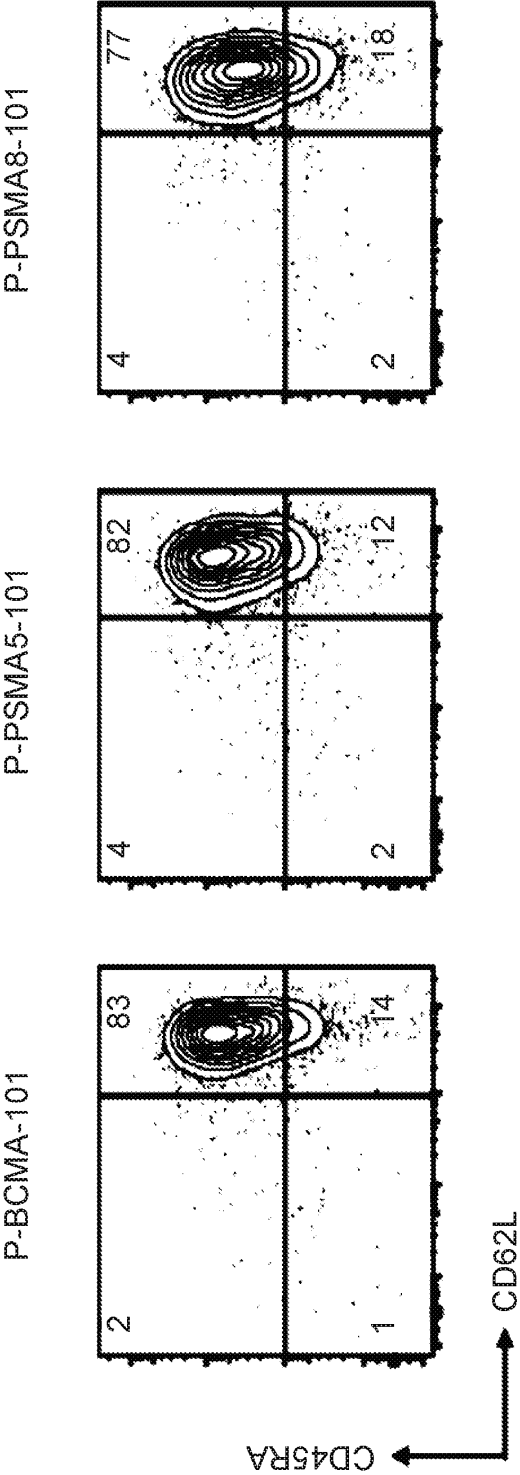
E) Degranulation of RNA-electroporated PSMA CARTyrin T cells against K562 expressing various amounts of PSMA protein

FIGURE 7A



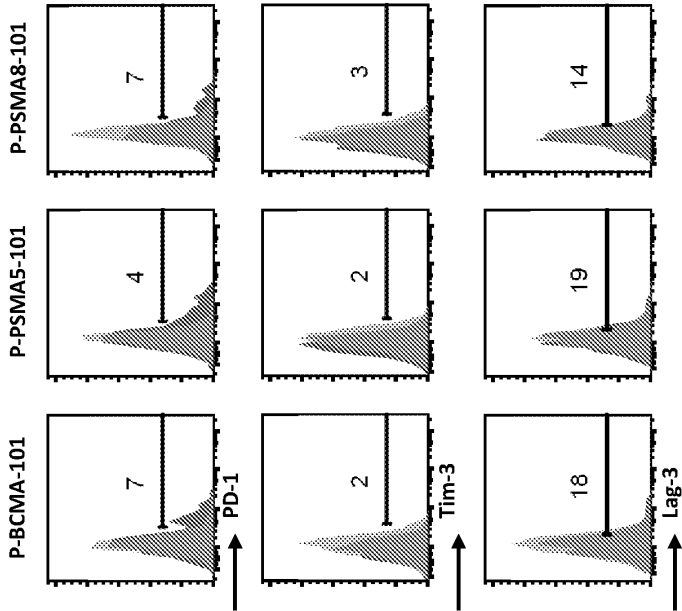
A) P-PSMA-101 T cells bind cognate recombinant soluble PSMA antigen

FIGURE 7B



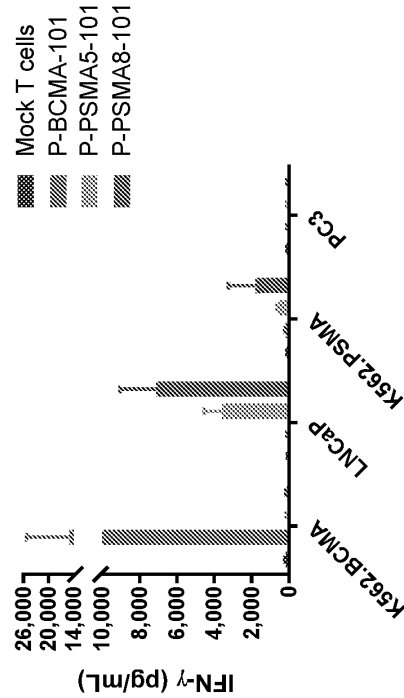
B) Phenotypic analysis of memory T cell markers

FIGURE 7C



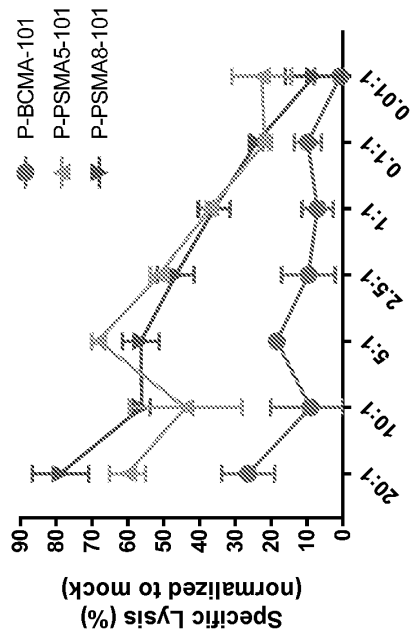
C) Phenotypic analysis of activation/exhaustion markers where CD4+ (purple) and CD8+ (gray) cells are displayed

FIGURE 7D



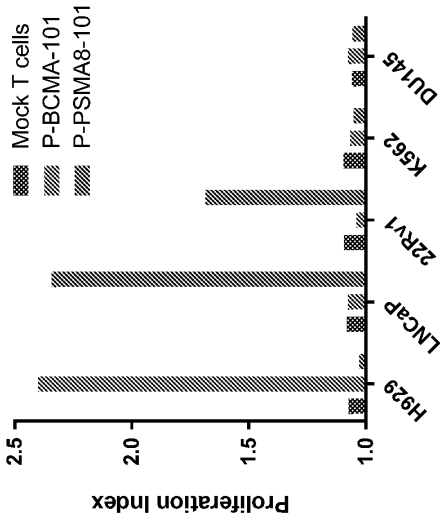
D) IFN- γ secretion of P-PSMA-101 against PSMA⁺ cell lines
K562.PSMA and LNCaP

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

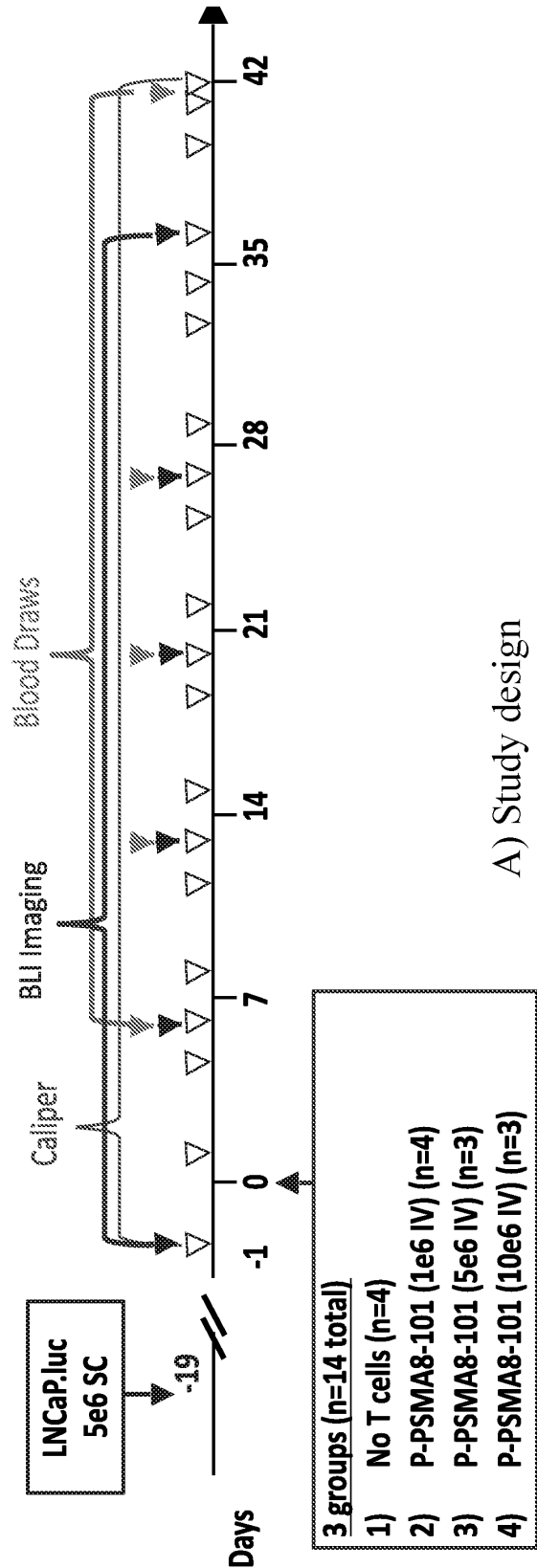
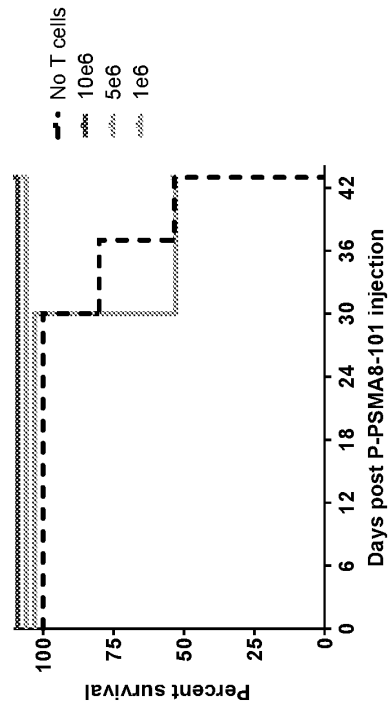
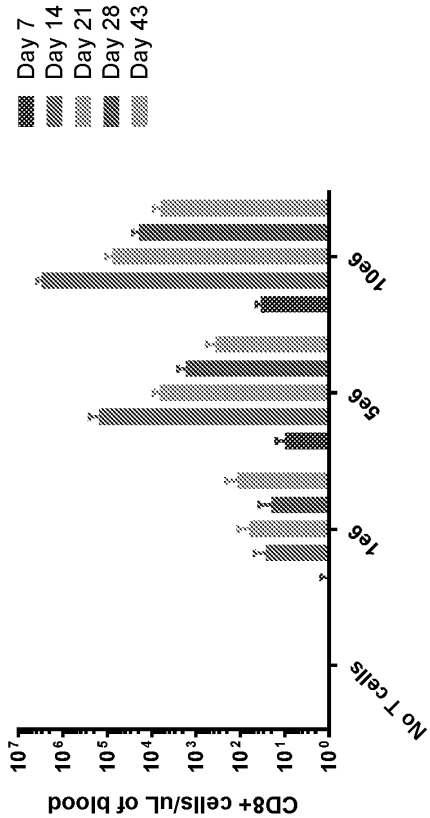


FIGURE 8B



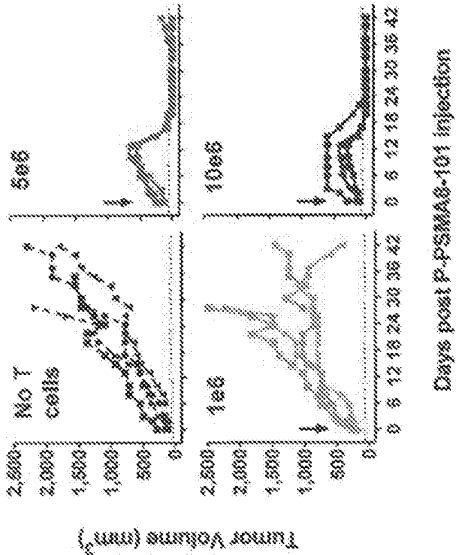
B) Survival data

FIGURE 8C



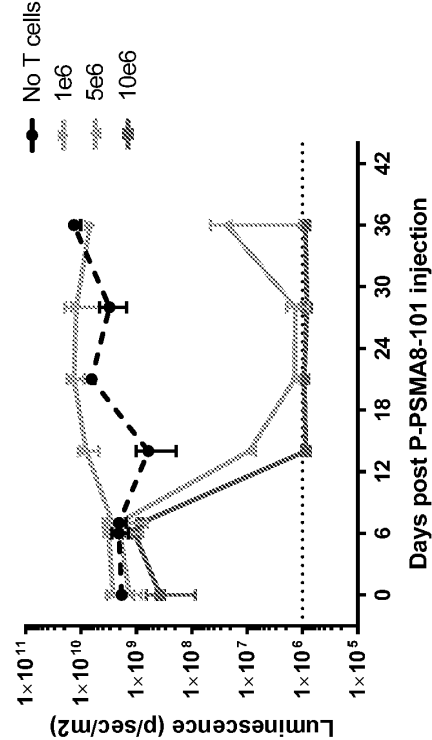
C) Enumeration of CD8+ T cells per microliter of peripheral blood

FIGURE 8D



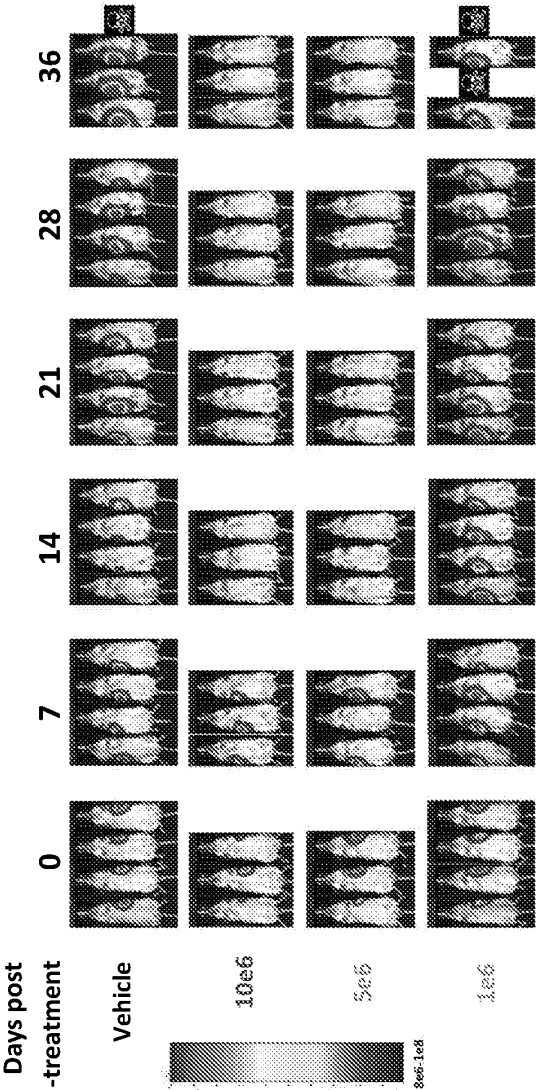
D) Tumor burden by caliper measurement

FIGURE 8E



E) Tumor burden by BLI (imaging quantified)

FIGURE 8F



F) Tumor burden by BLI (imaging)

FIGURE 9A

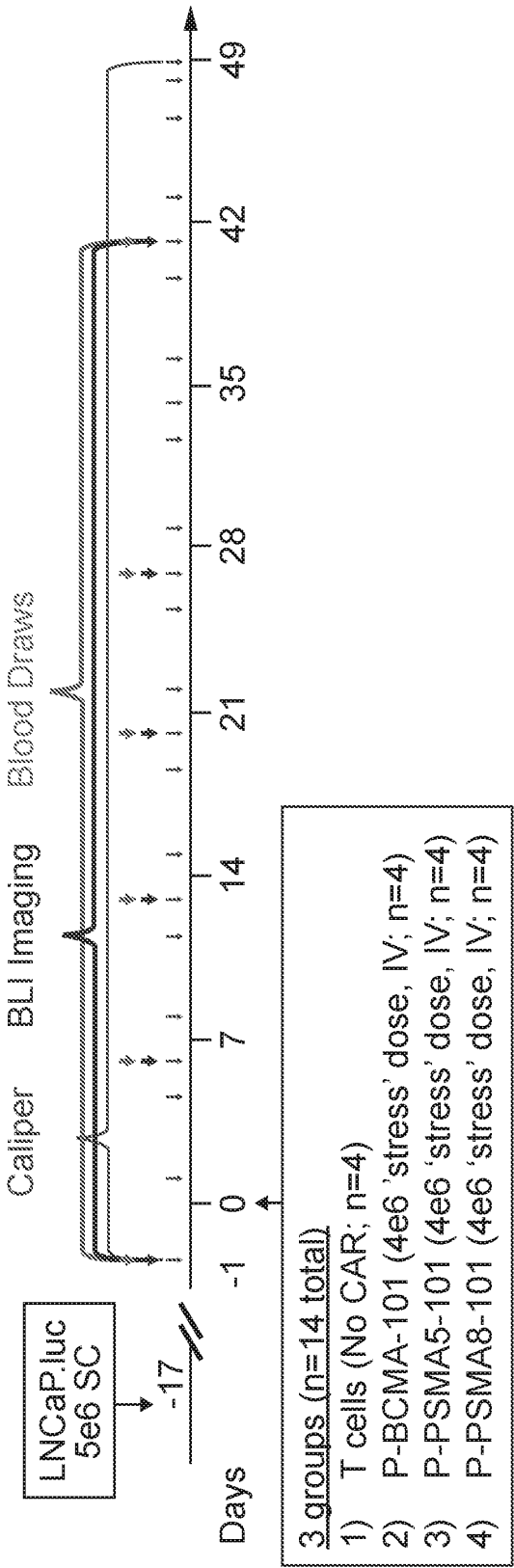


FIGURE 9B

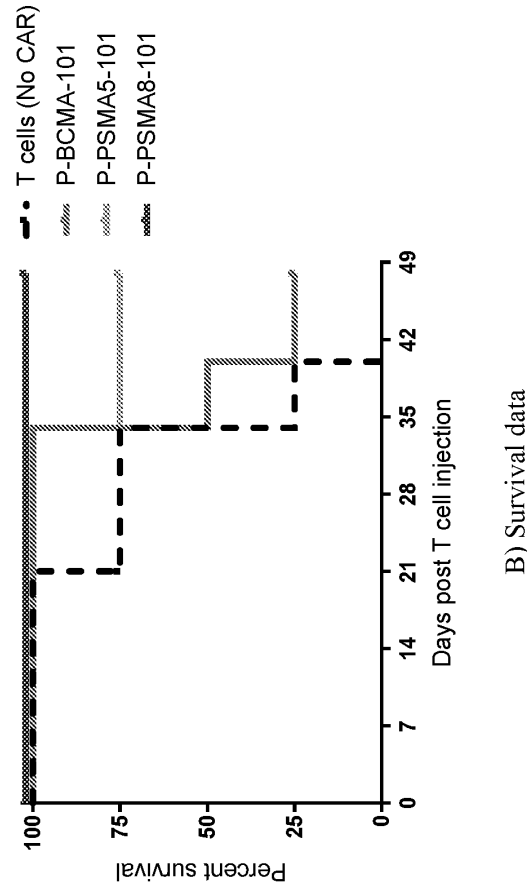
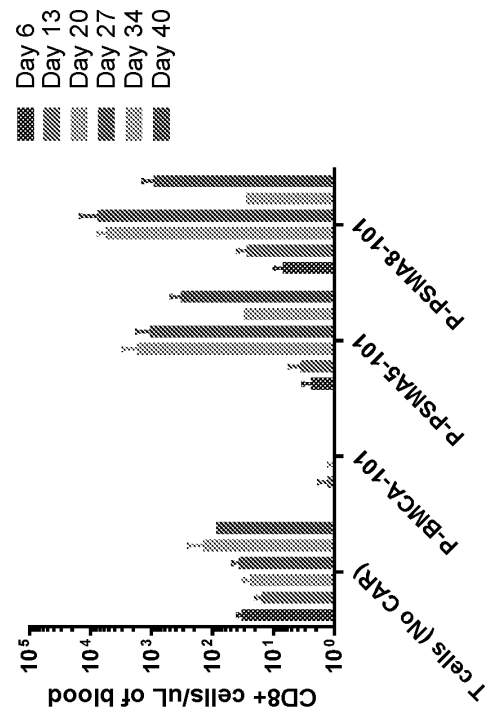
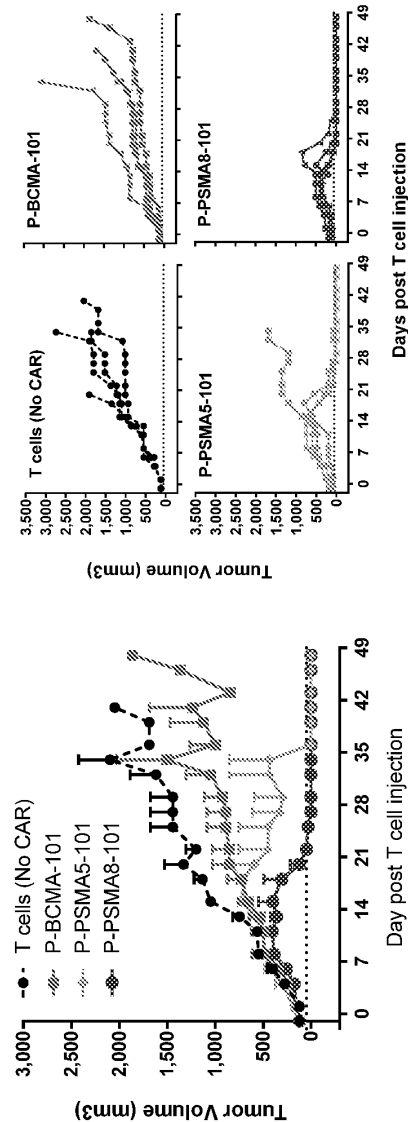


FIGURE 9C



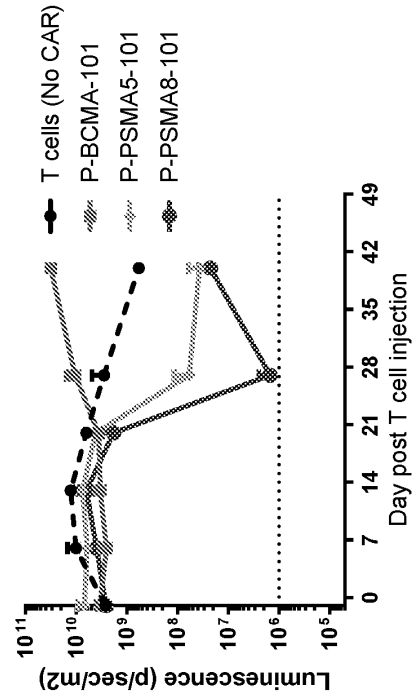
C) Enumeration of CD8+ T cells per microliter of peripheral blood

FIGURE 9D



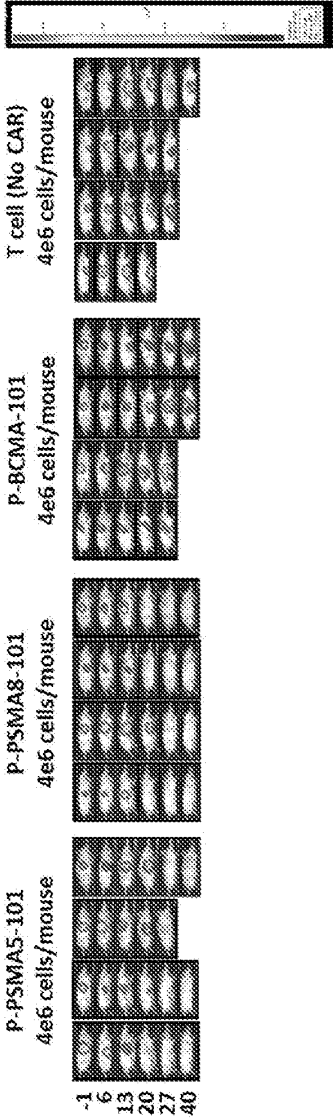
D) Tumor burden by caliper measurement

FIGURE 9E

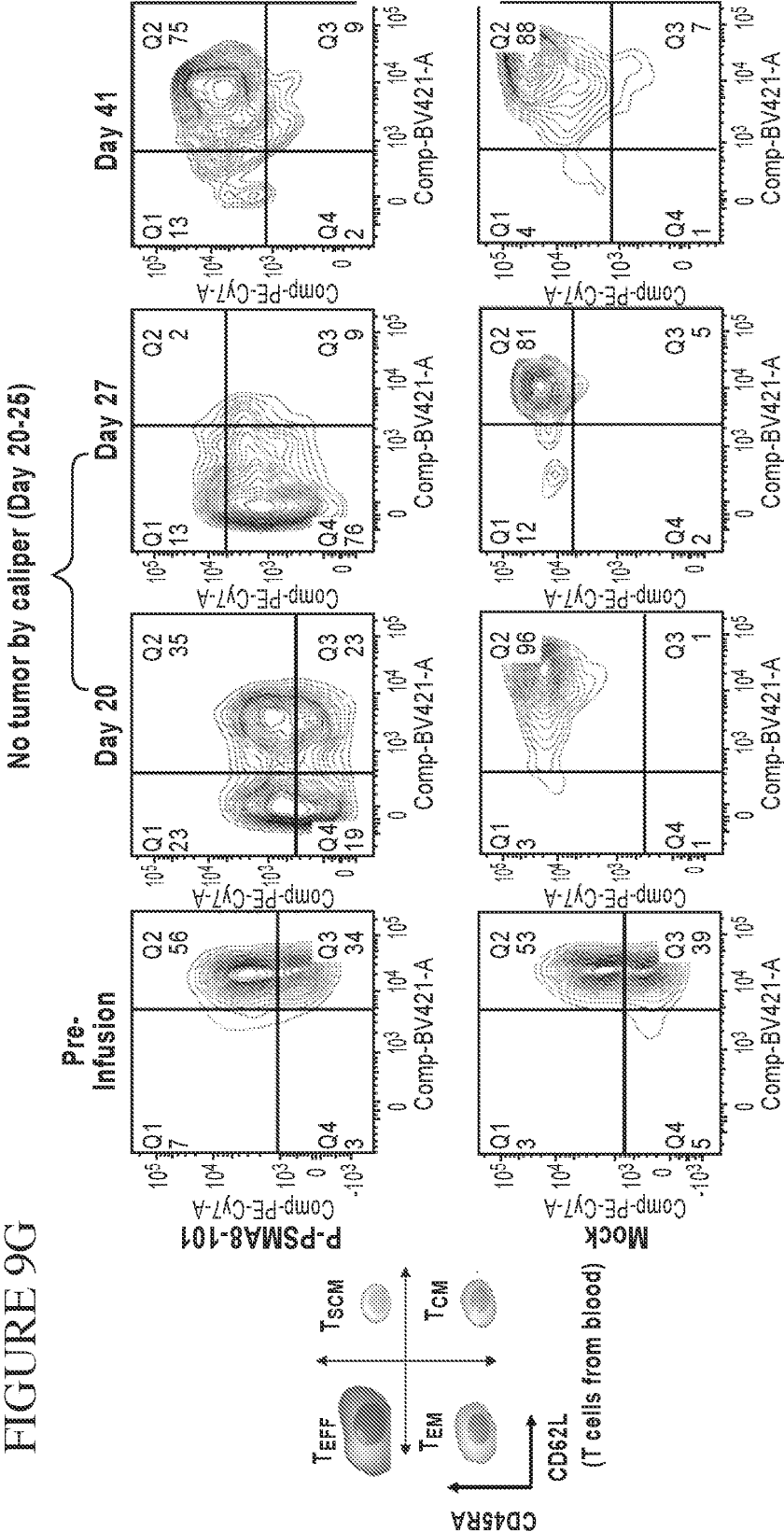


E) Tumor burden by BLI (imaging quantified)

FIGURE 9F



F) Tumor burden by BLI (imaging)



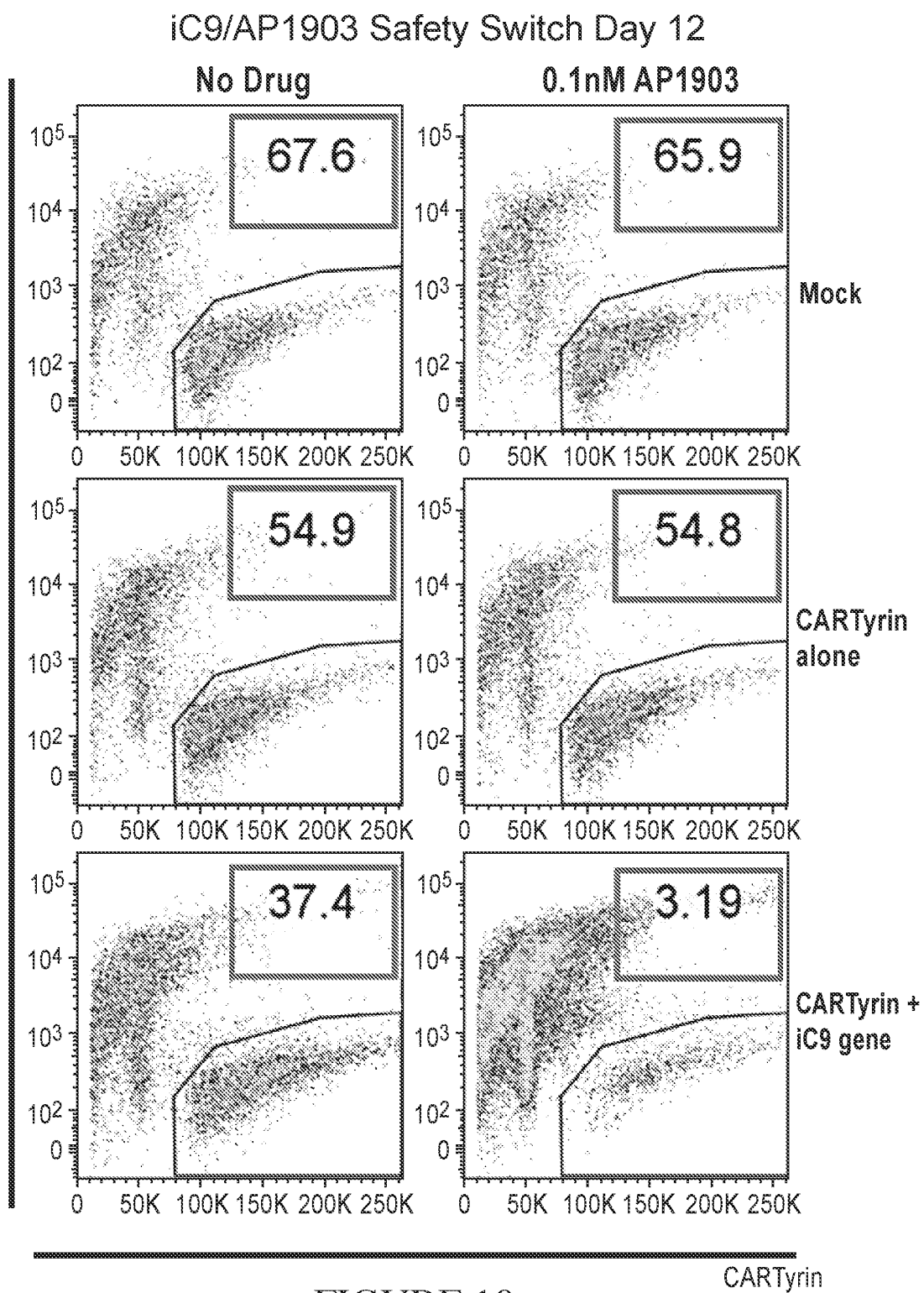


FIGURE 10

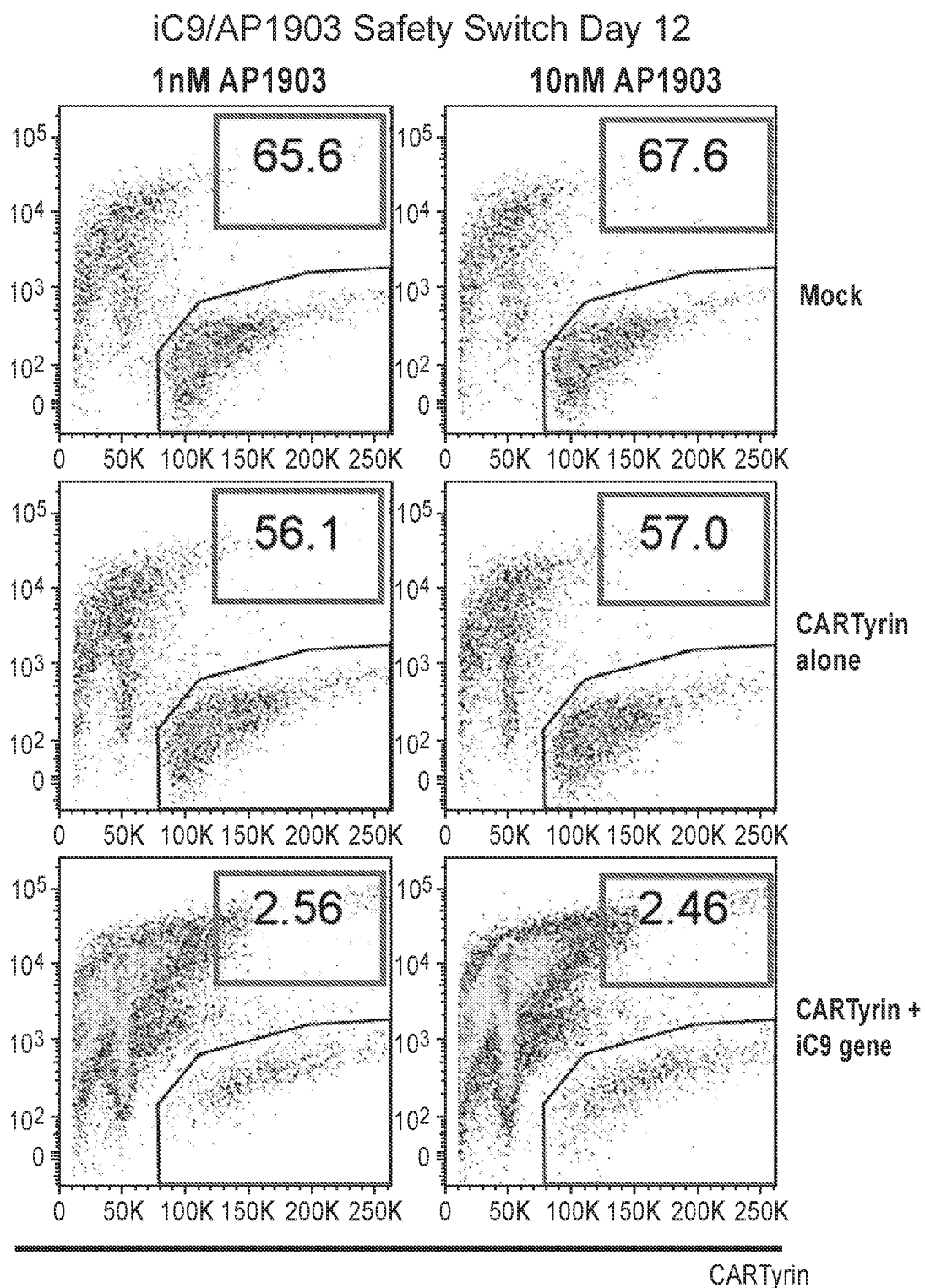


FIGURE 10 (cont.)

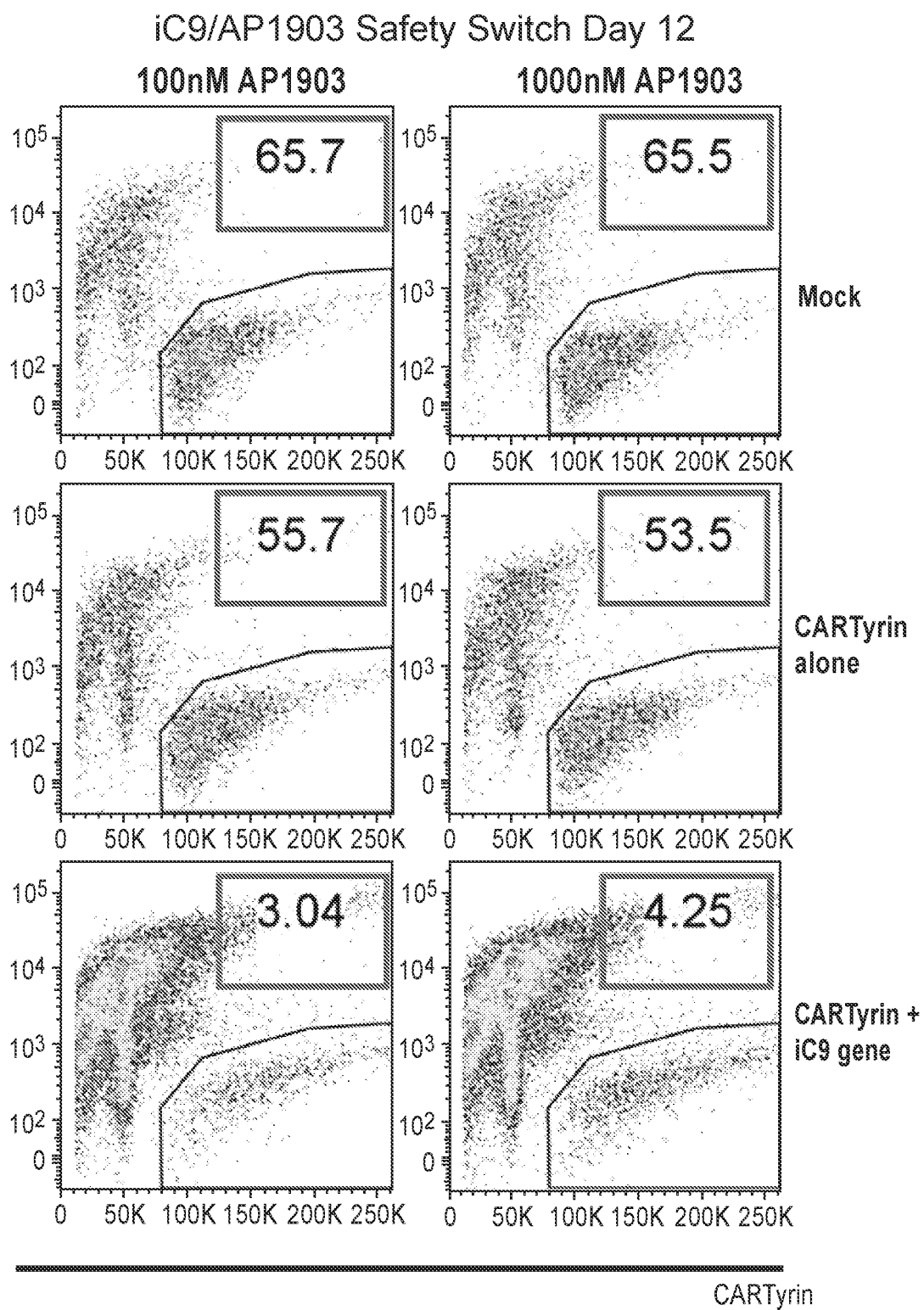


FIGURE 10 (cont.)

iC9/AP1903 Safety Switch Day 12

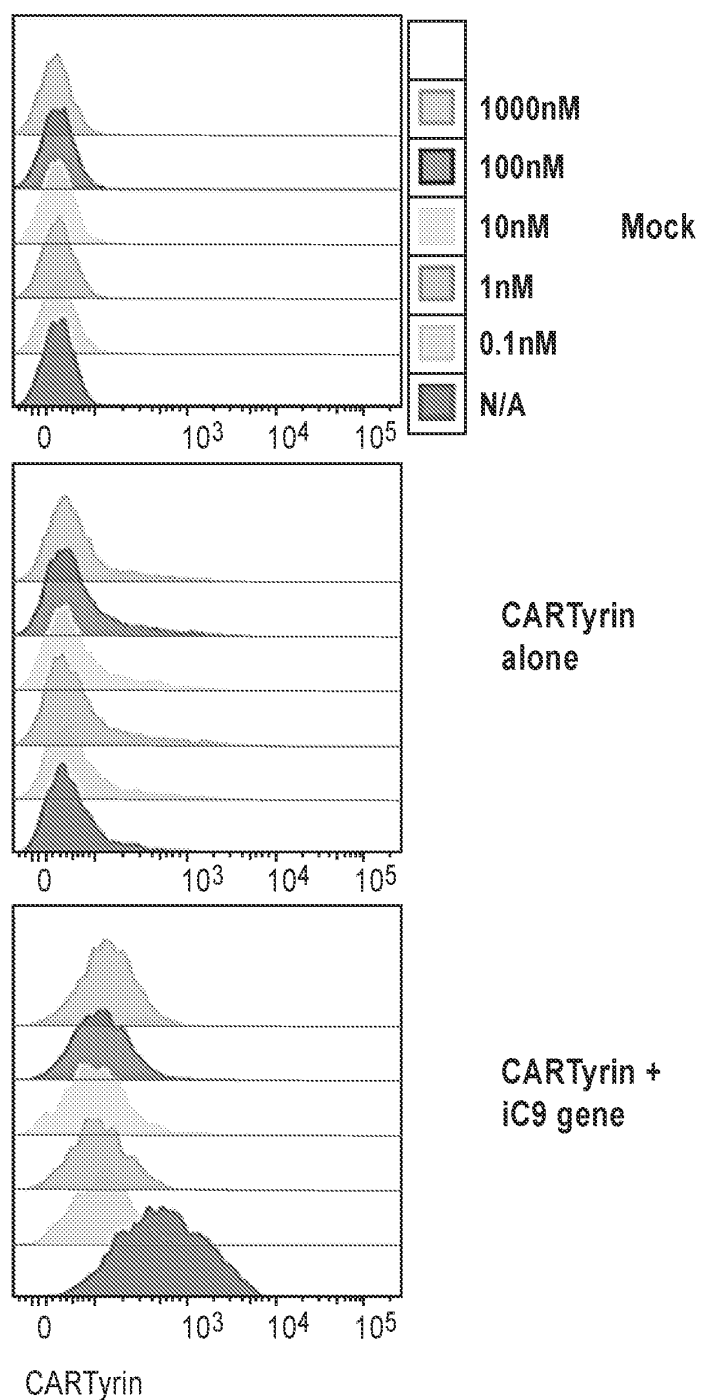


FIGURE 10 (cont.)

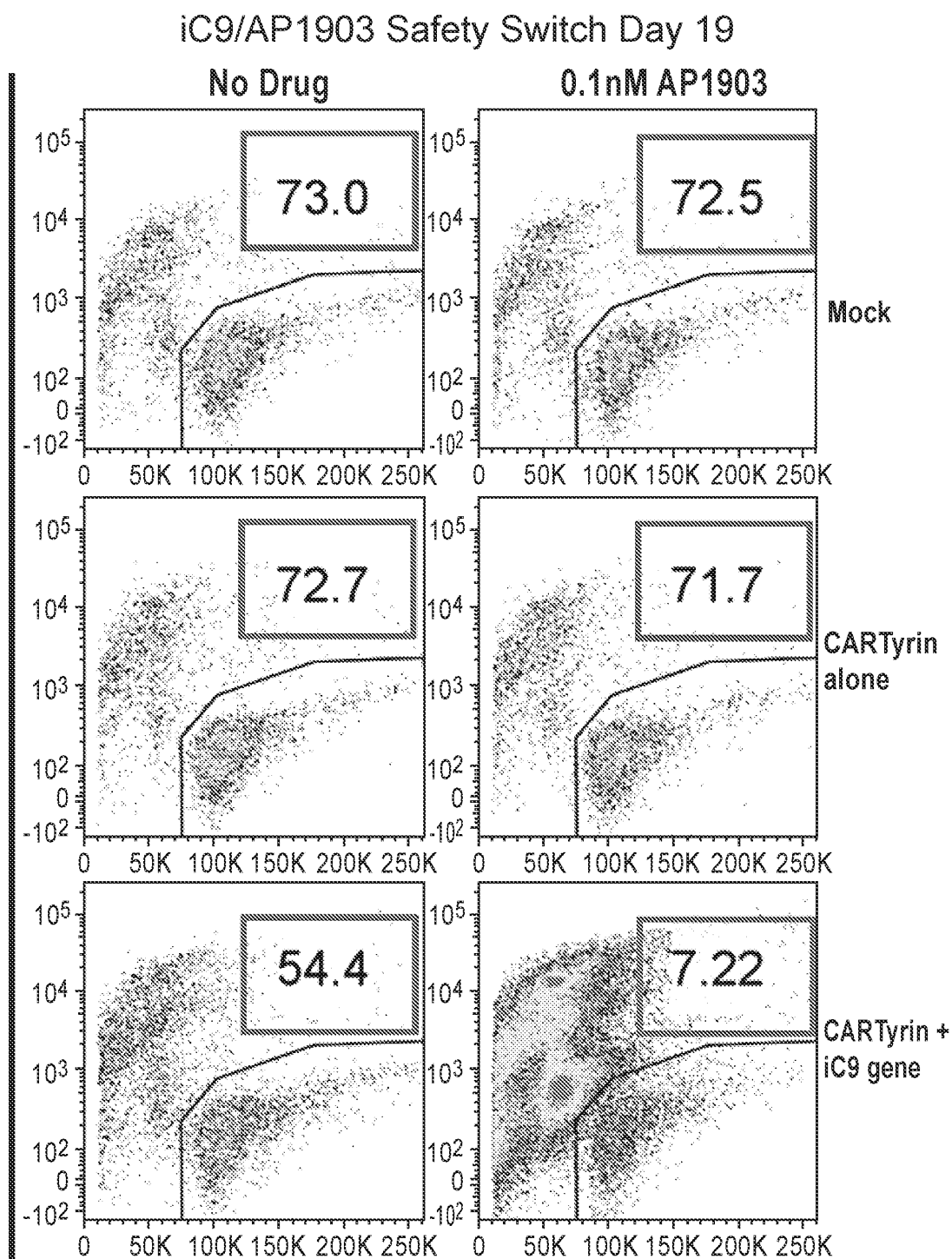


FIGURE 11

CARTyrin

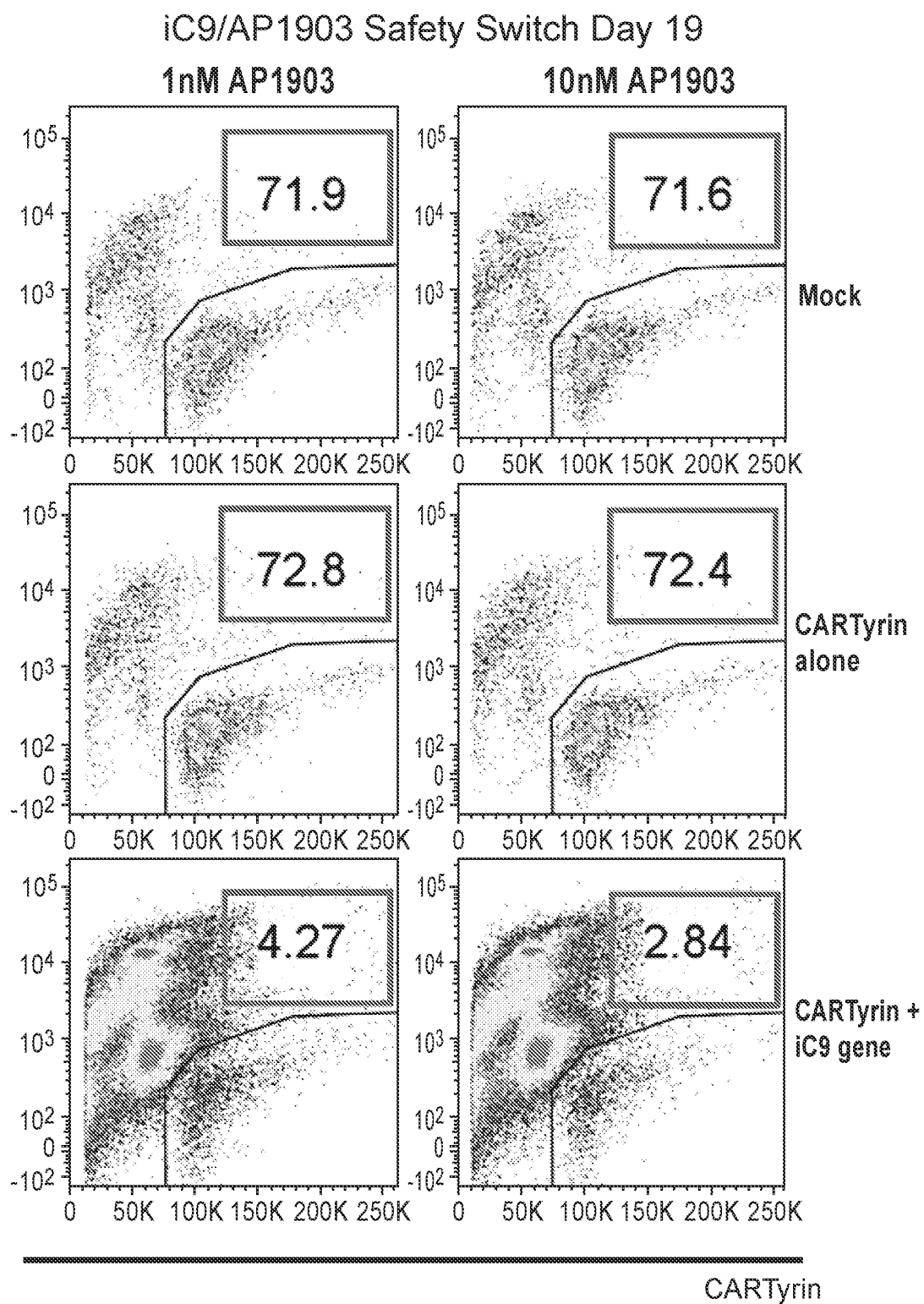


FIGURE 11 (cont.)

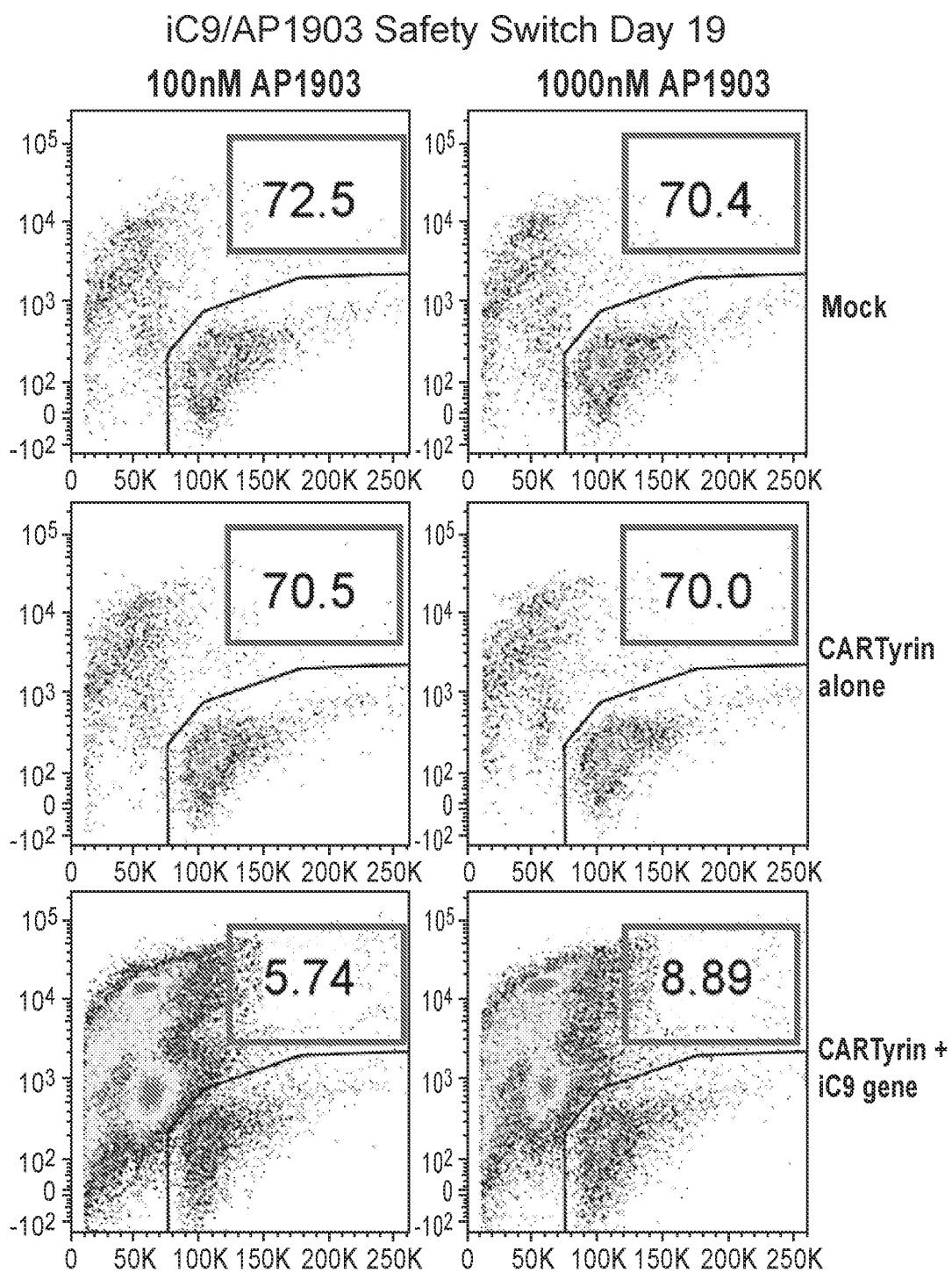


FIGURE 11 (cont.)

CARTyrin

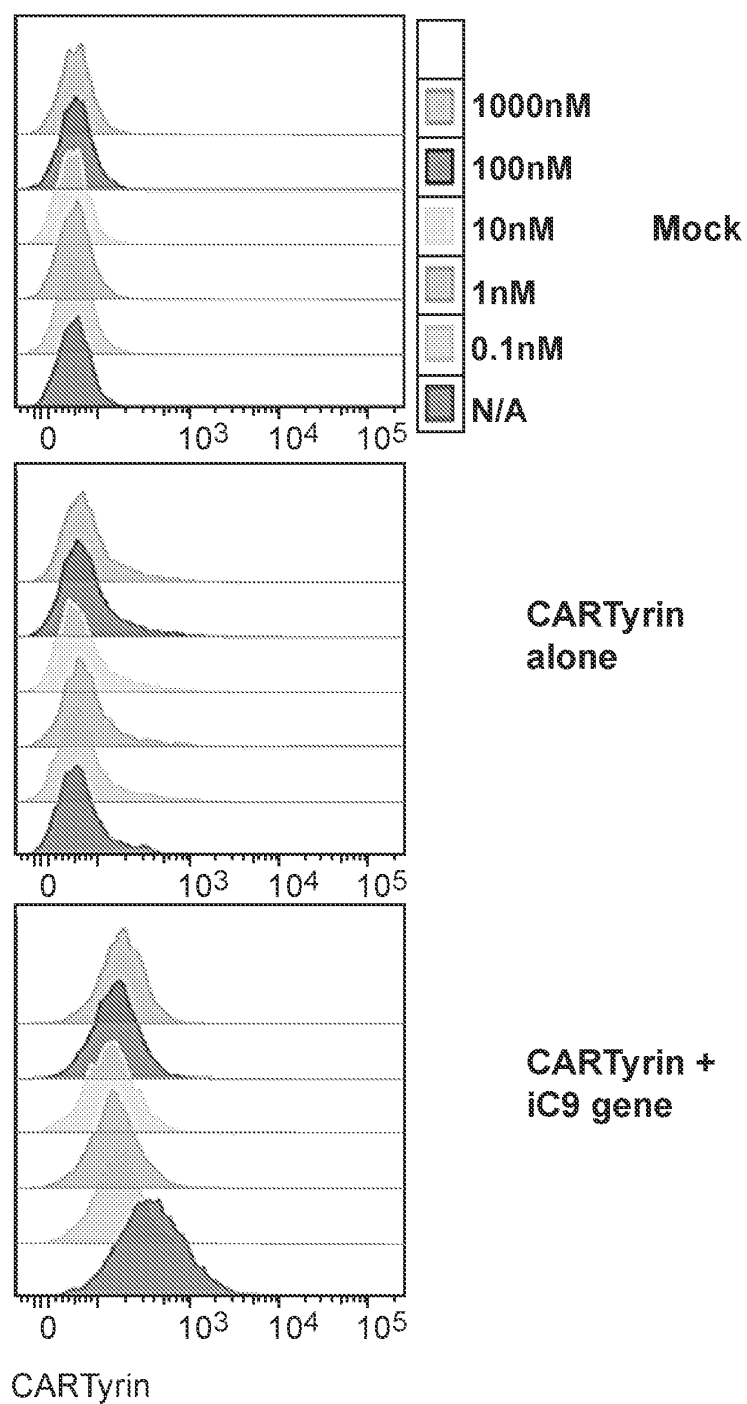
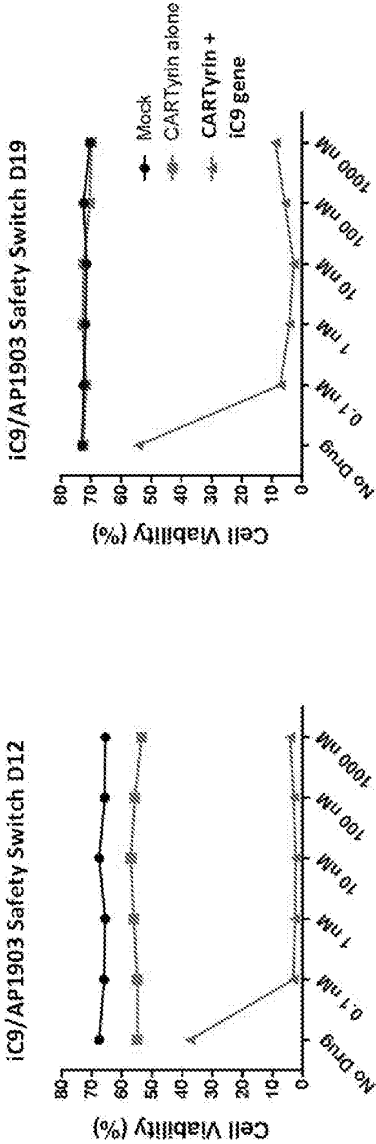


FIGURE 11 (cont.)

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

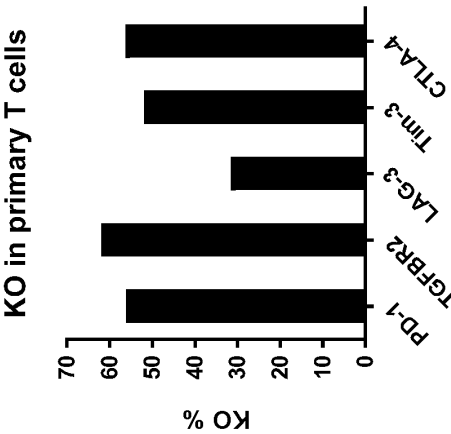


FIGURE 14

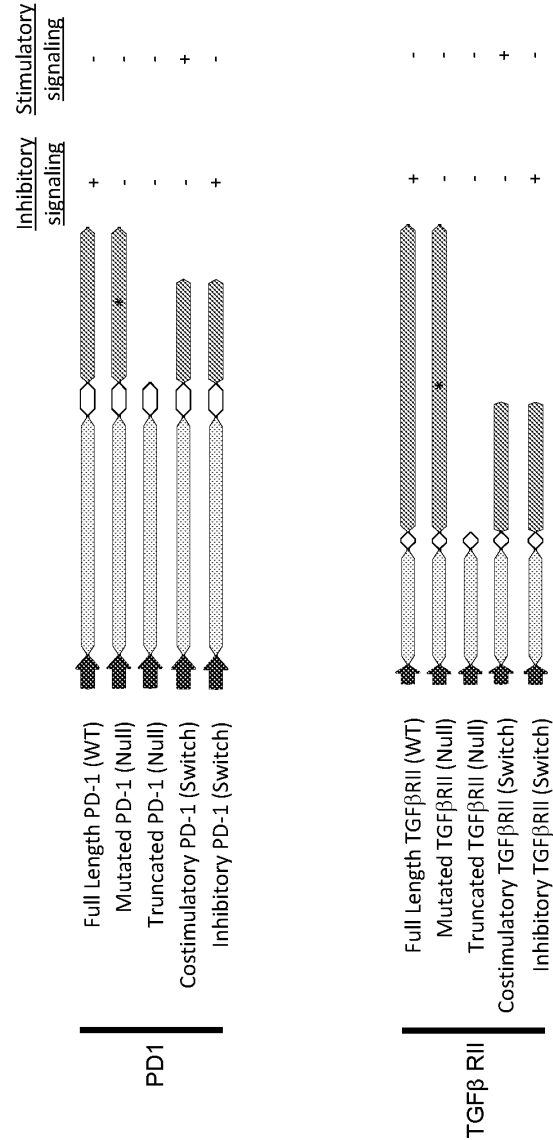


FIGURE 15A

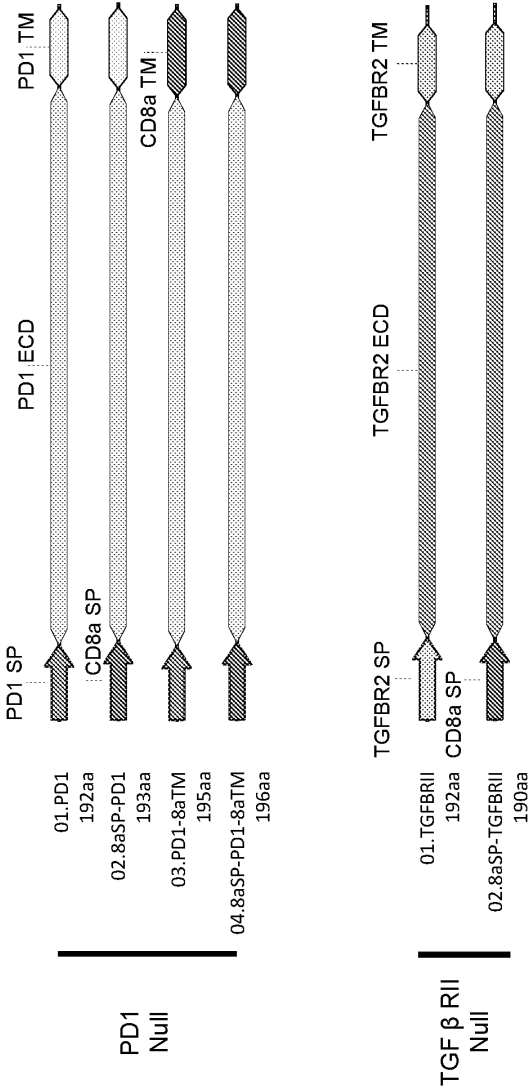


FIGURE 15B

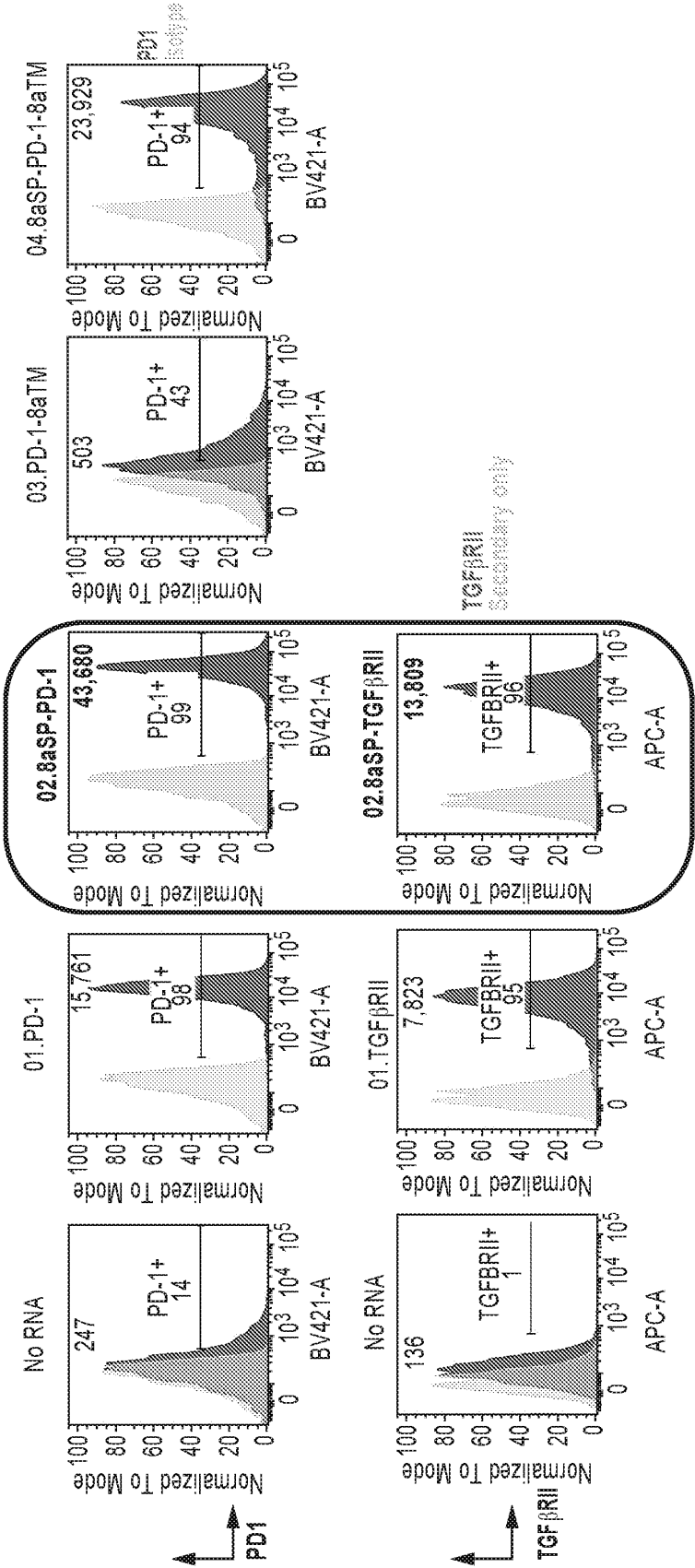
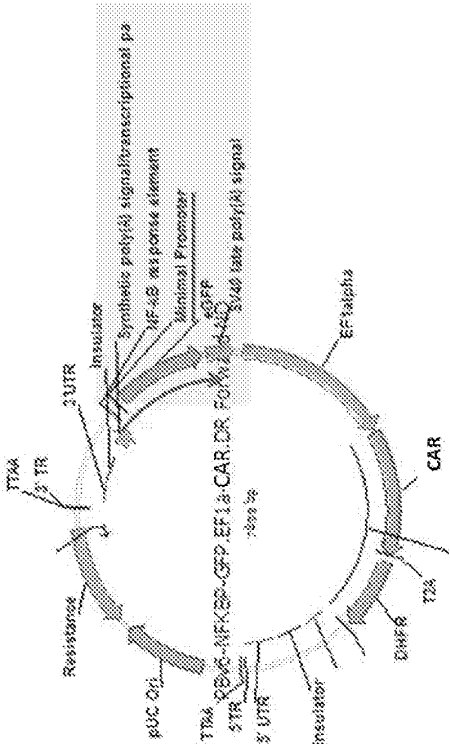
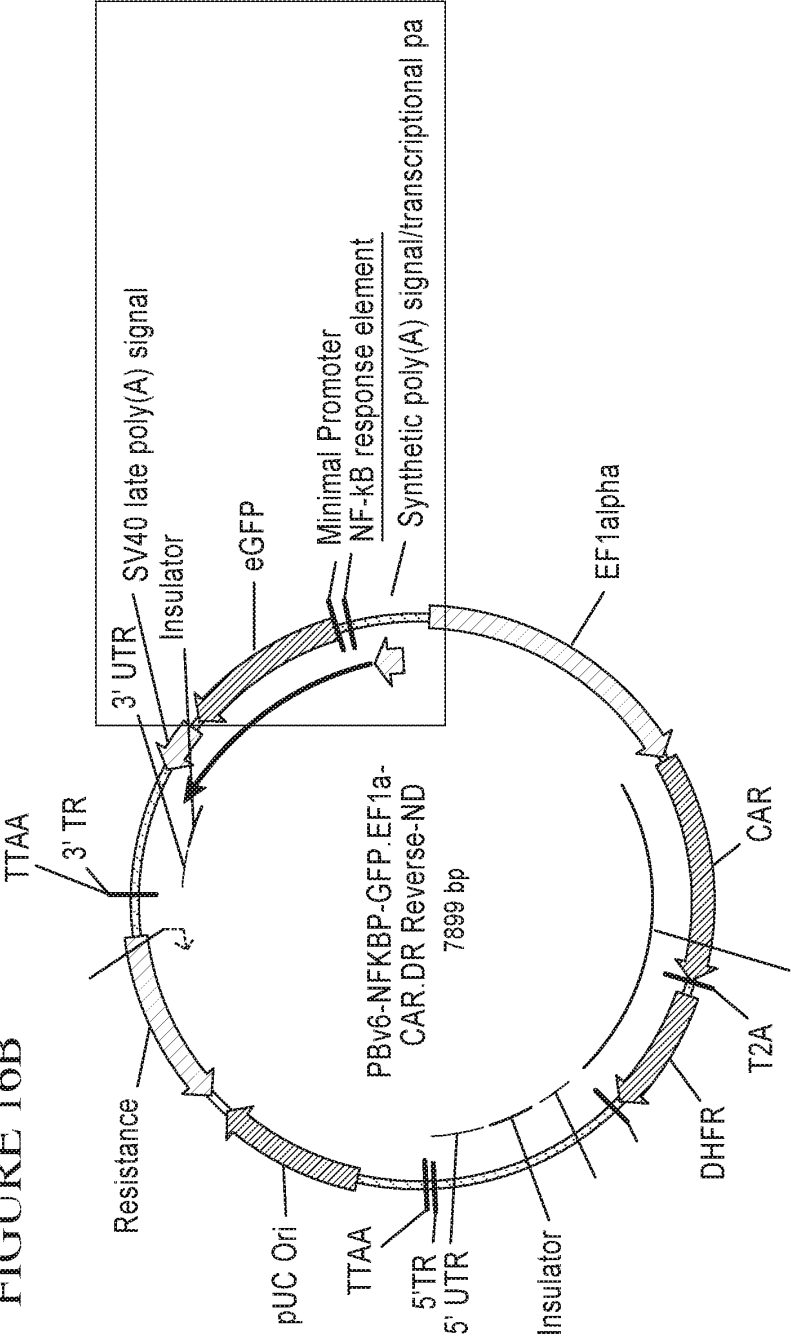


FIGURE 16A



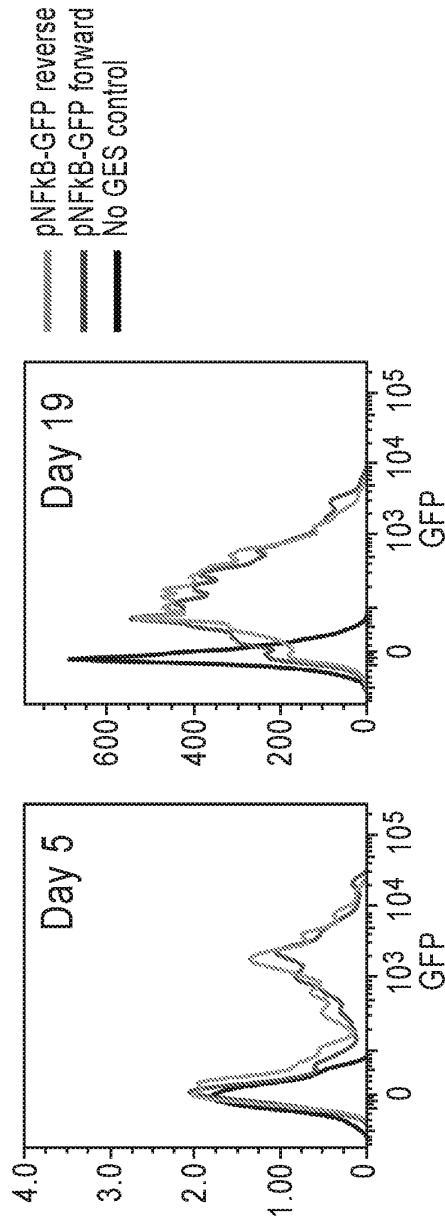
pNFKB-GFP & EF1α-CAR in the same direction

FIGURE 16B



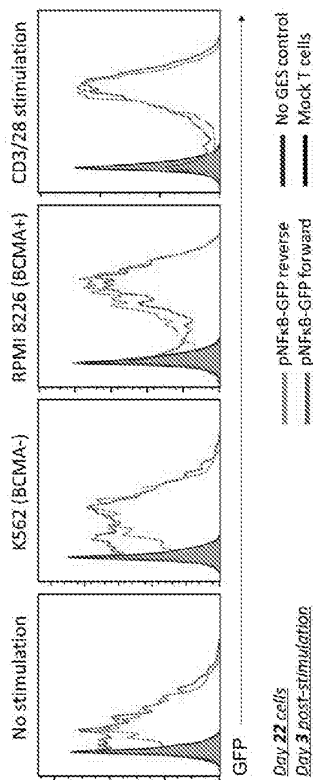
pNFKB-GFP & EF1a-CAR in the opposite direction

FIGURE 17

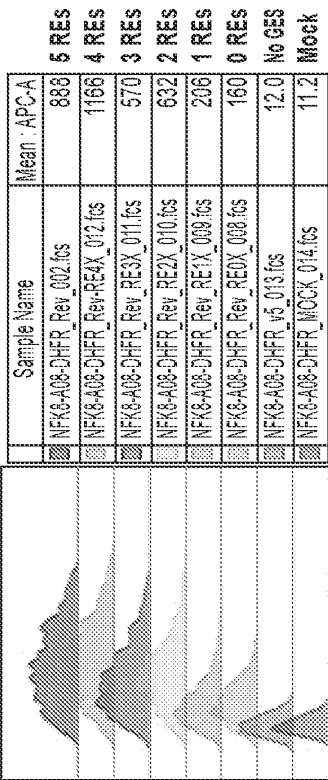


- At Day 5-post T cell activation (Day 5), T cells are proliferating and are highly stimulated; GFP expression is strong since NFkB activity is high
- By Day 19, T cells are almost fully resting; GFP expression is significantly lower than Day 5 (~1/8 MFI), since NFkB activity is low
- GFP expression is still observed at Day 19, which may be 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

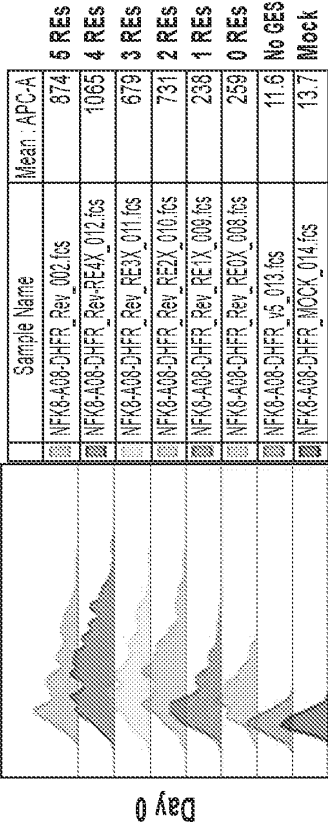


CD8+ T Cells

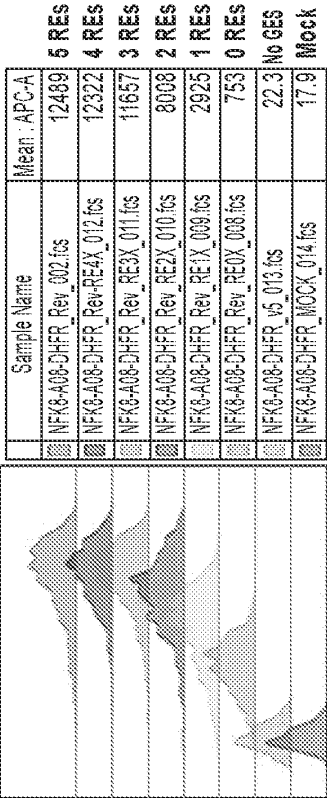


APC-A :: CD19

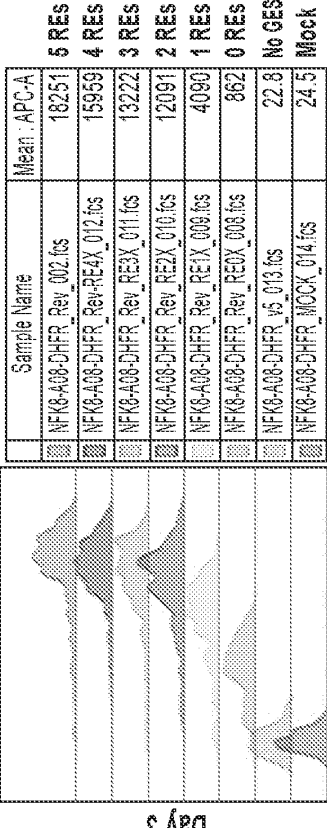
CD4+ T Cells



APC-A :: CD19



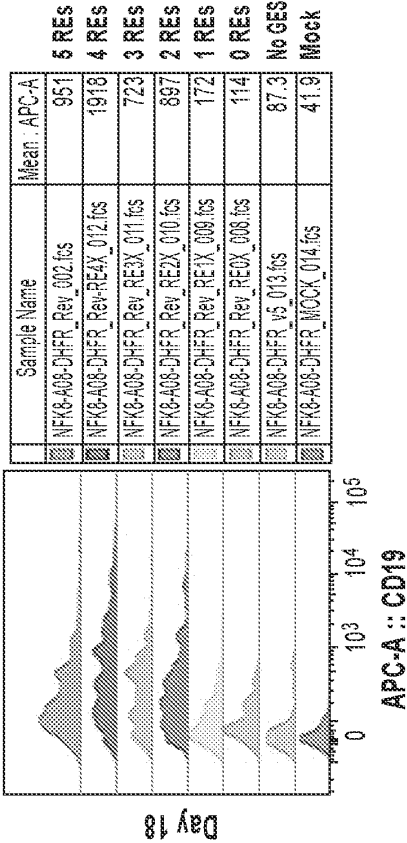
APC-A :: CD19



APC-A :: CD19

FIGURE 19 (cont.)

CD4+ T Cells



CD8+ T Cells

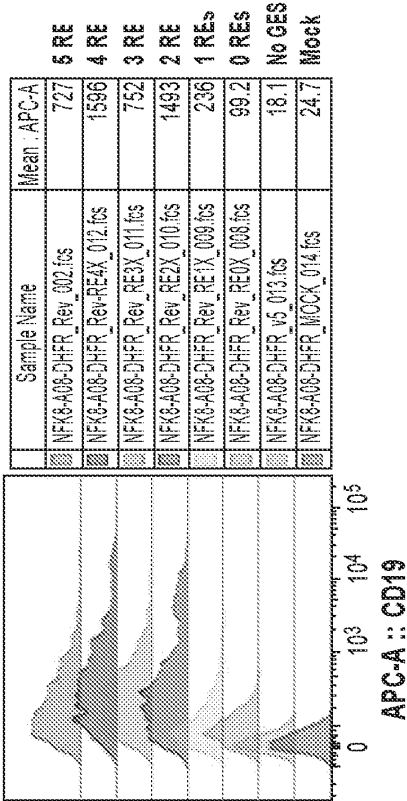


FIGURE 19 (cont.)

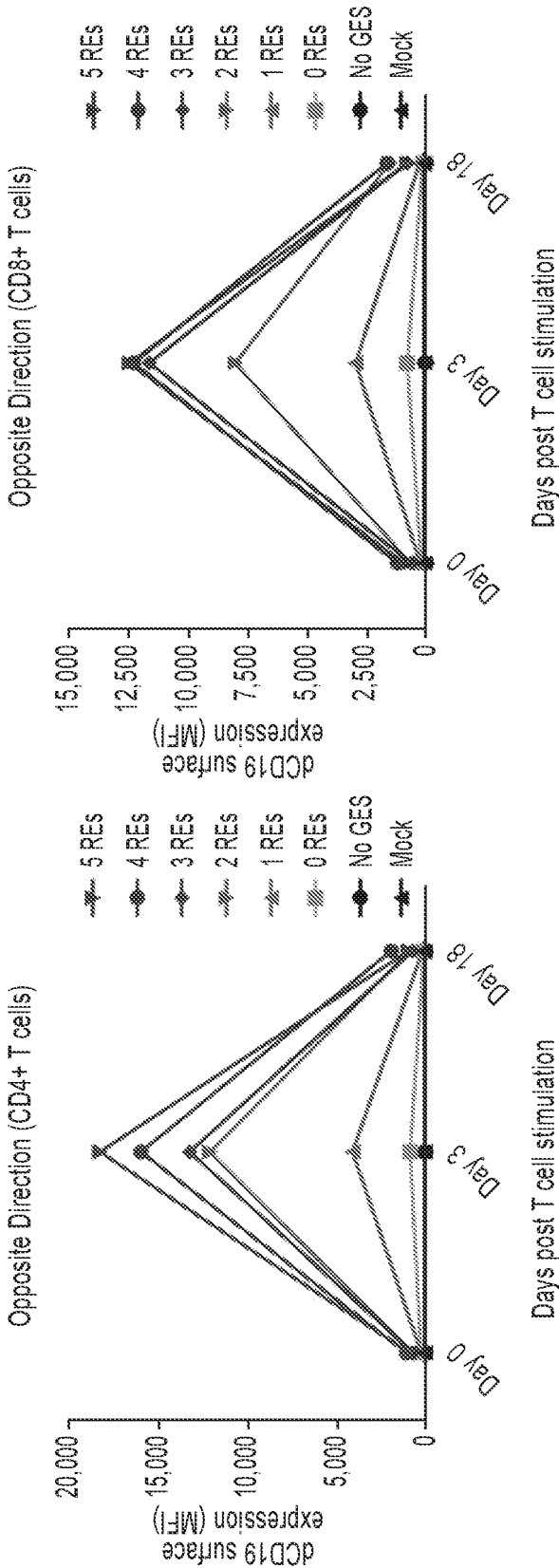


FIGURE 20

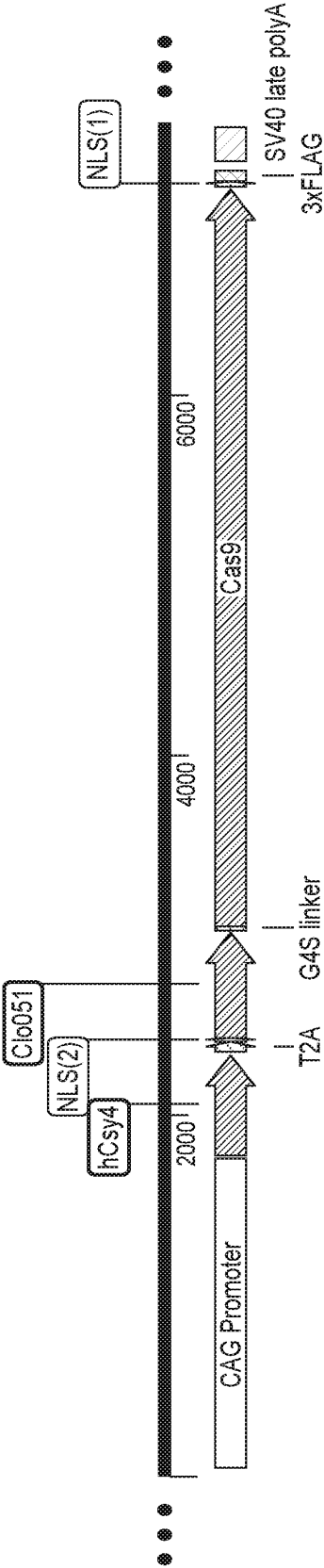
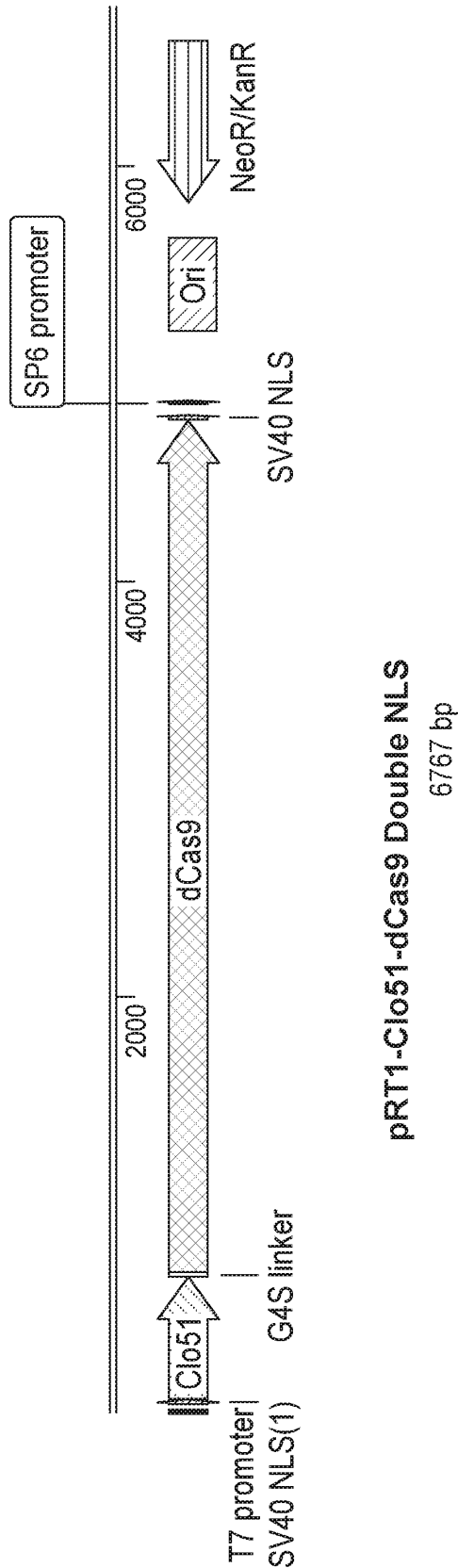


FIGURE 21



pRT1-Cio51-dCas9 Double NLS

6767 bp

FIGURE 22

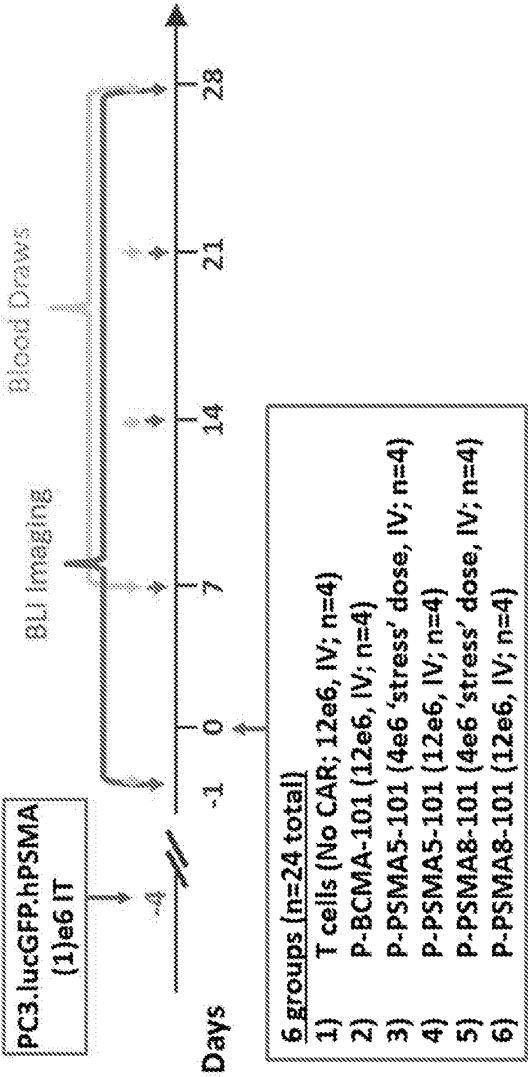


FIGURE 23

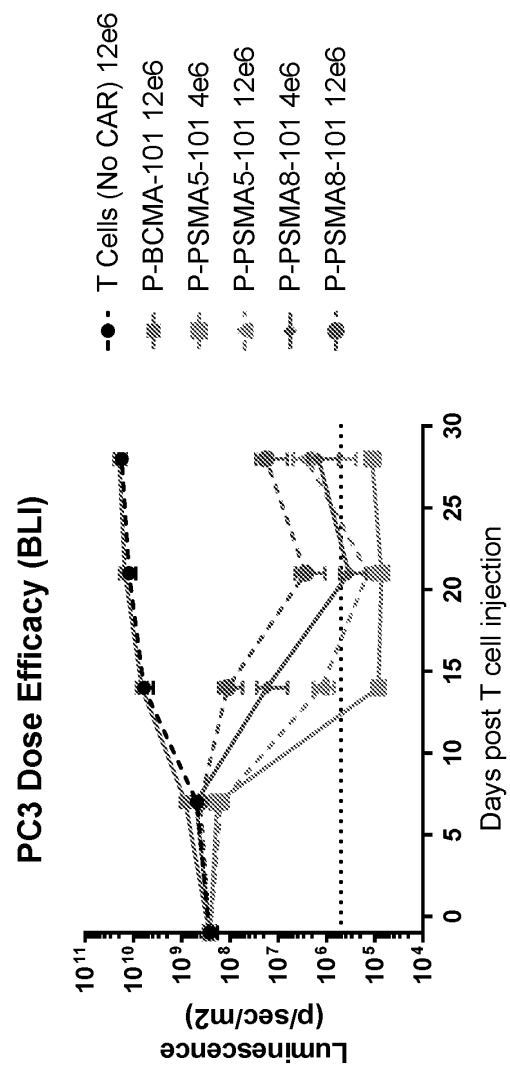


FIGURE 24

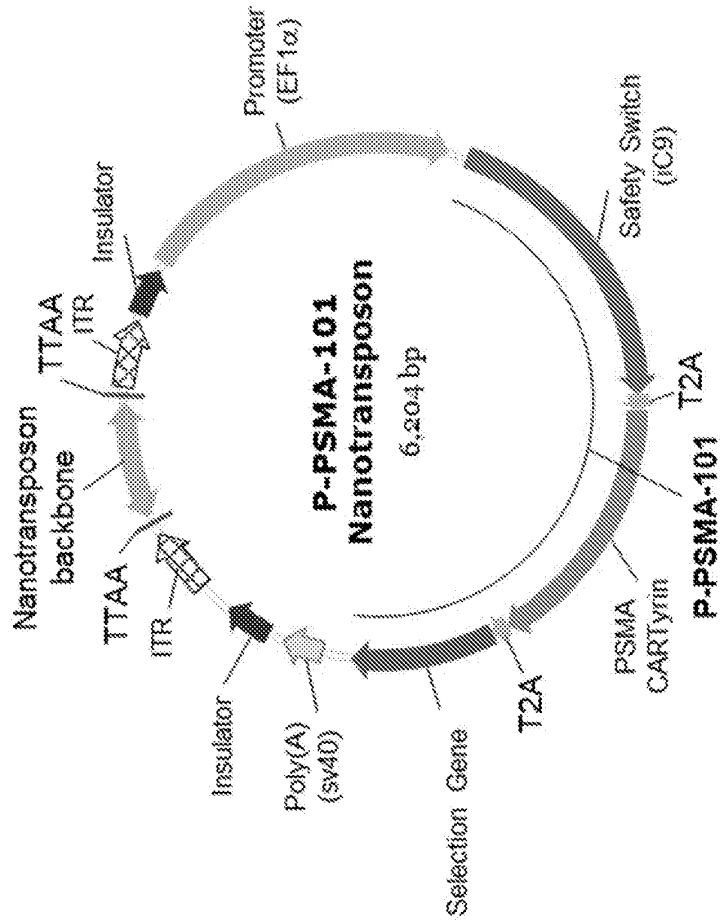


FIGURE 25

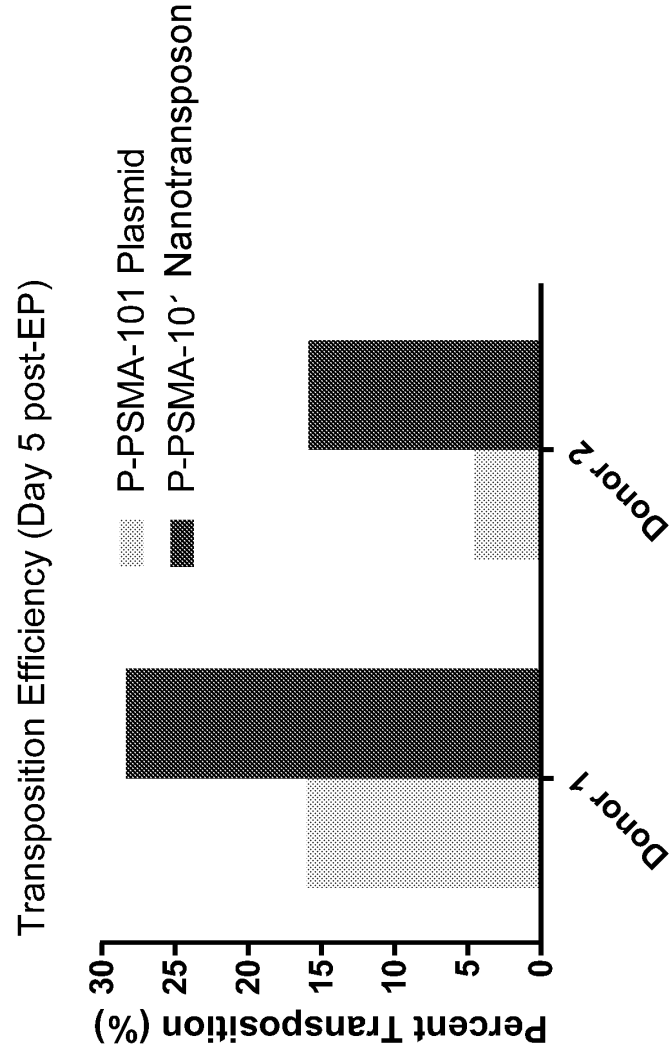


FIGURE 26

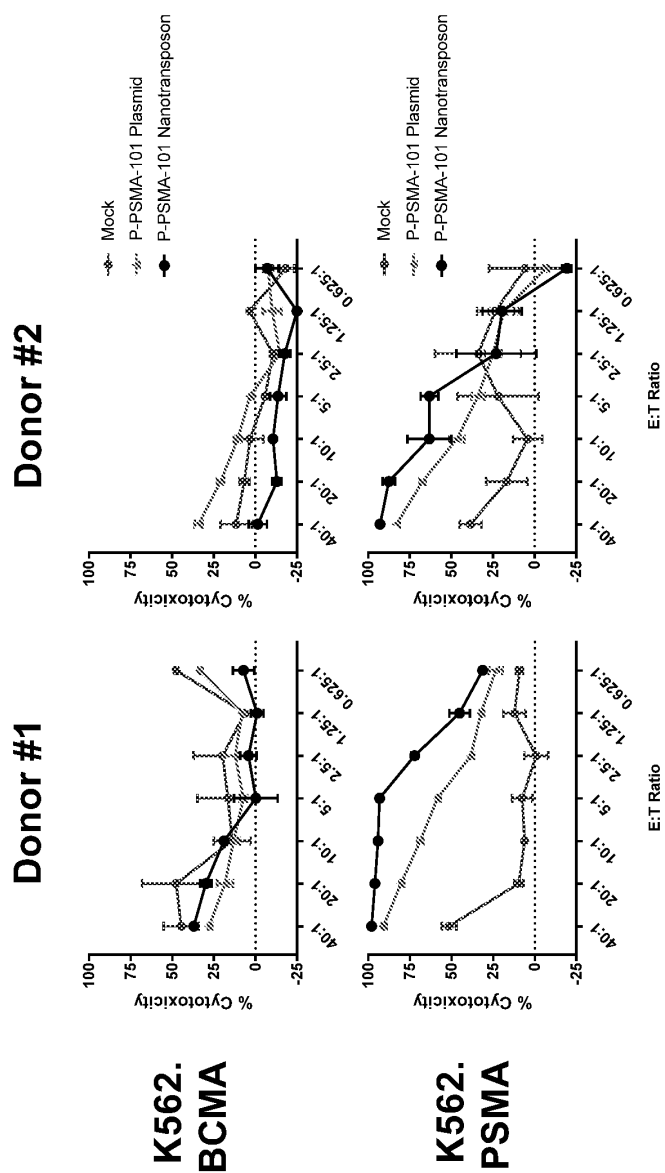


FIGURE 27

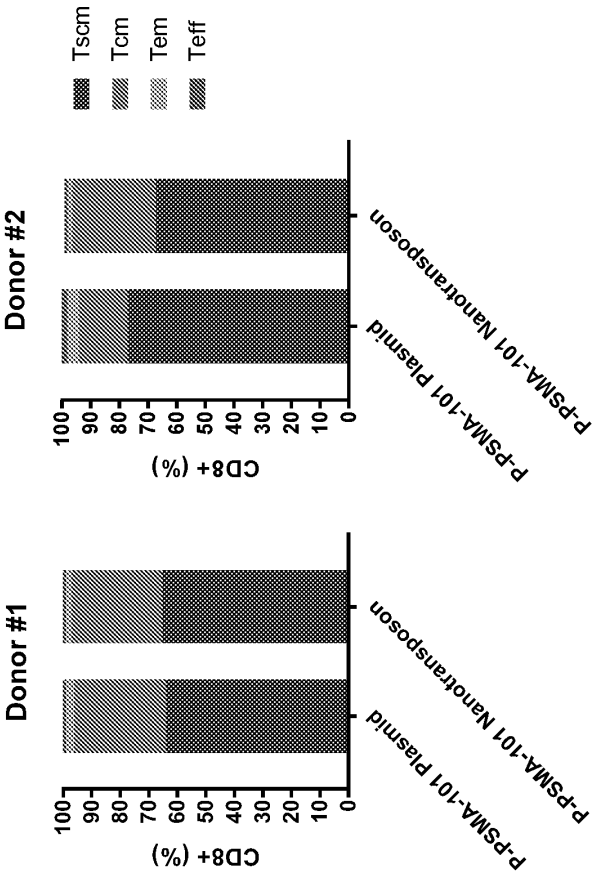


FIGURE 28

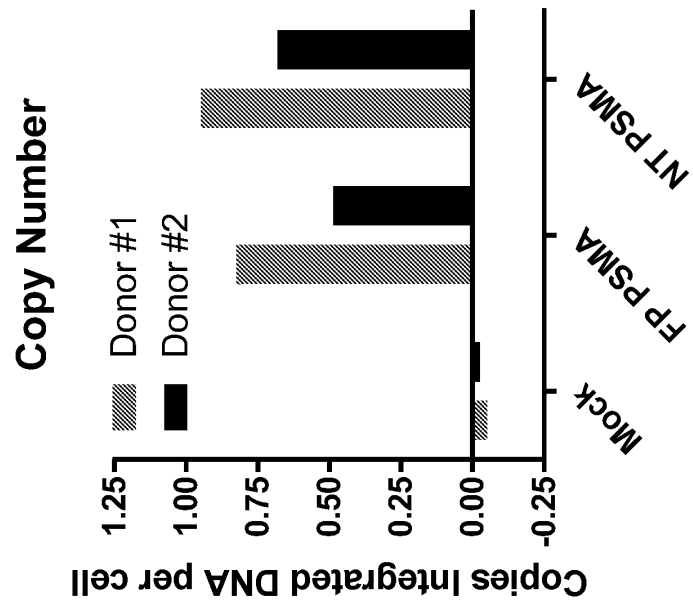
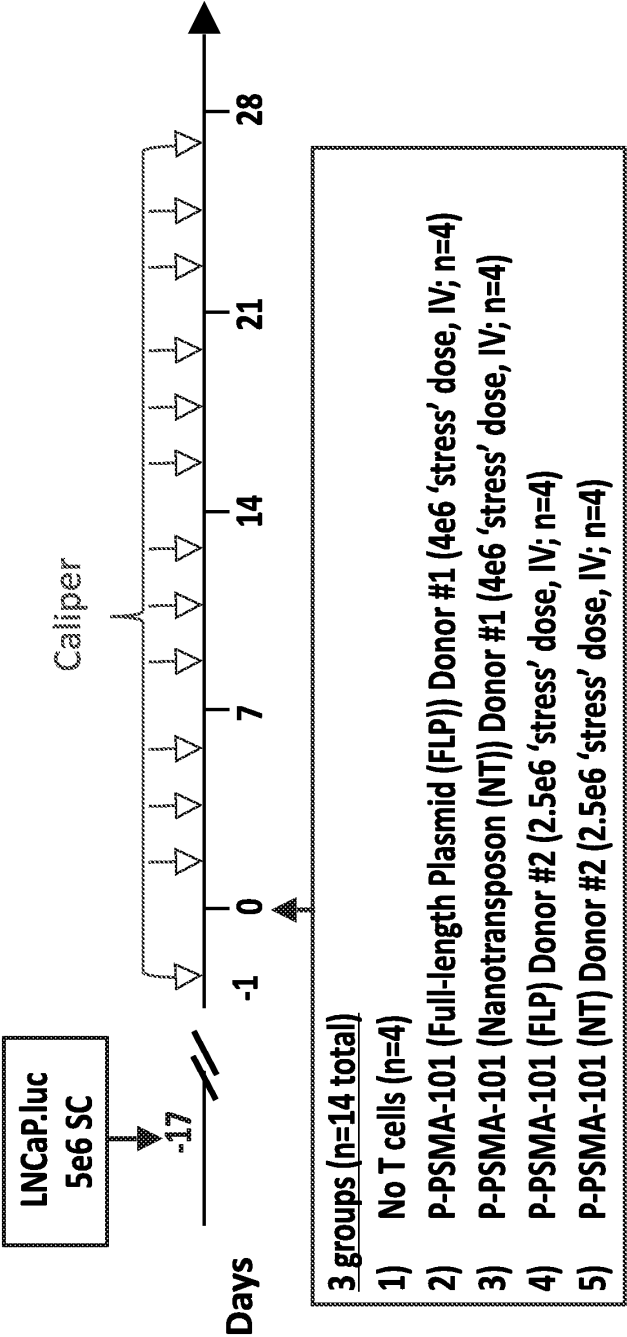
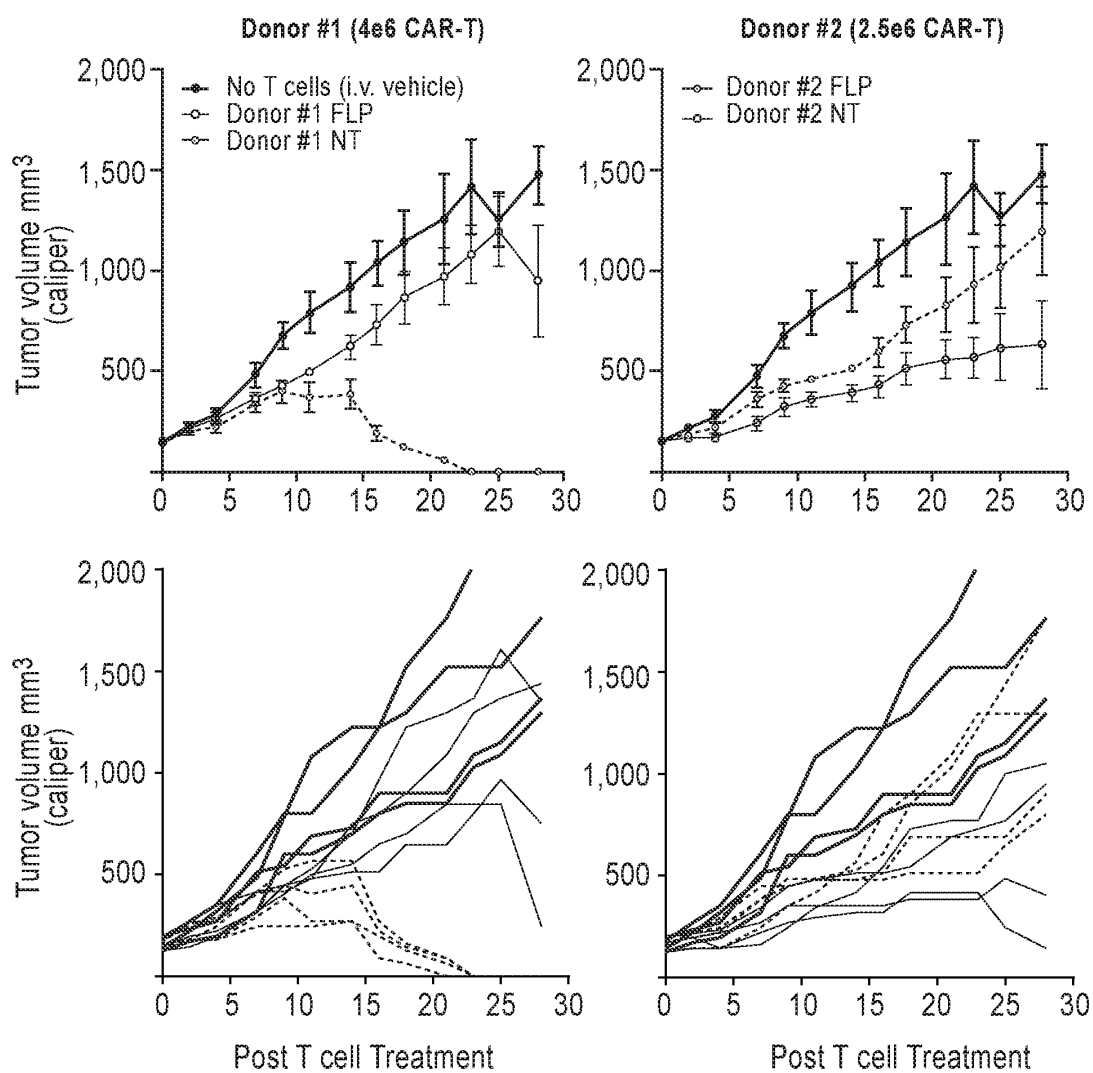


FIGURE 29A



A) Study design

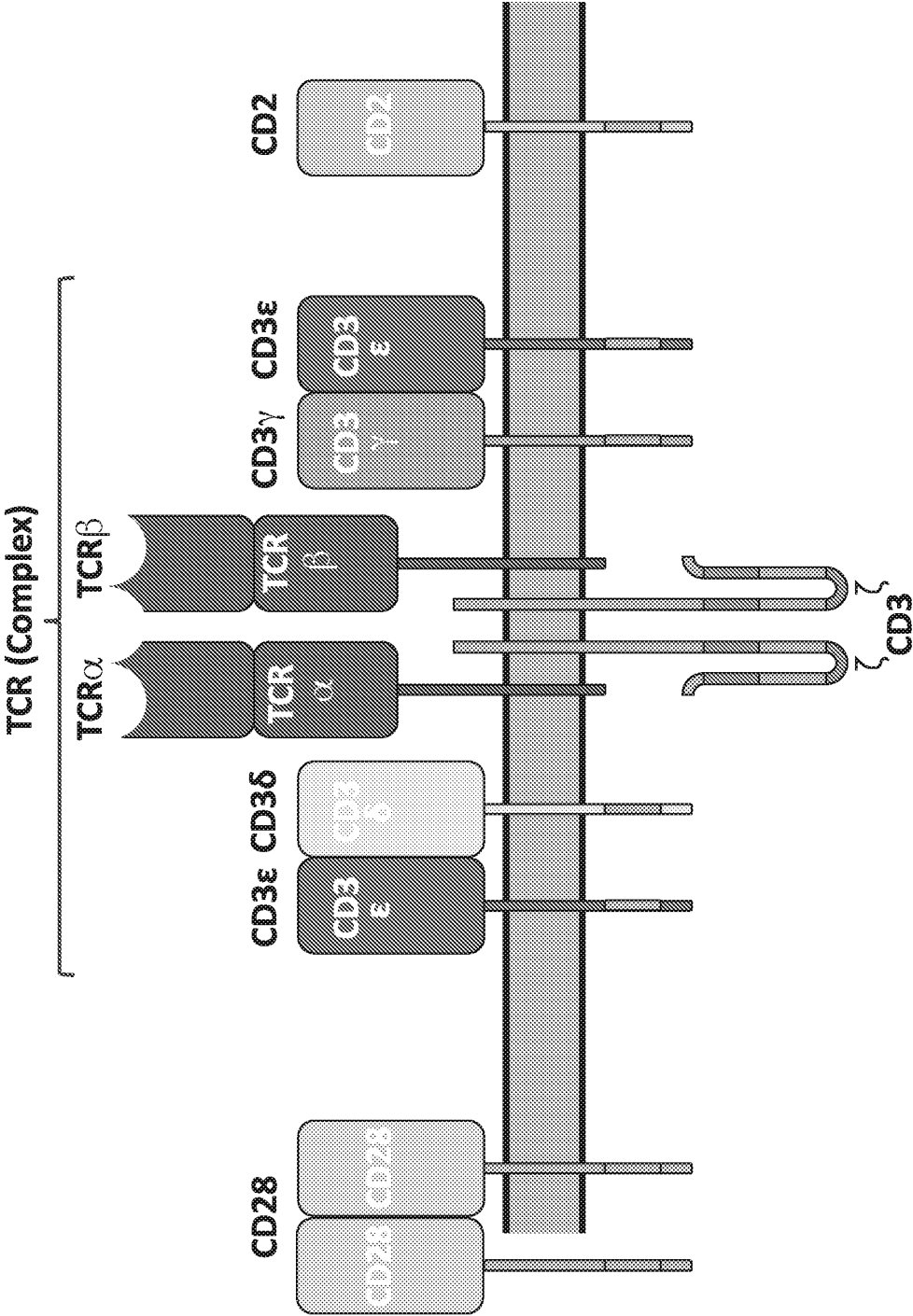


B) Caliper Measurements

FIGURE 29B

FIGURE 30

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



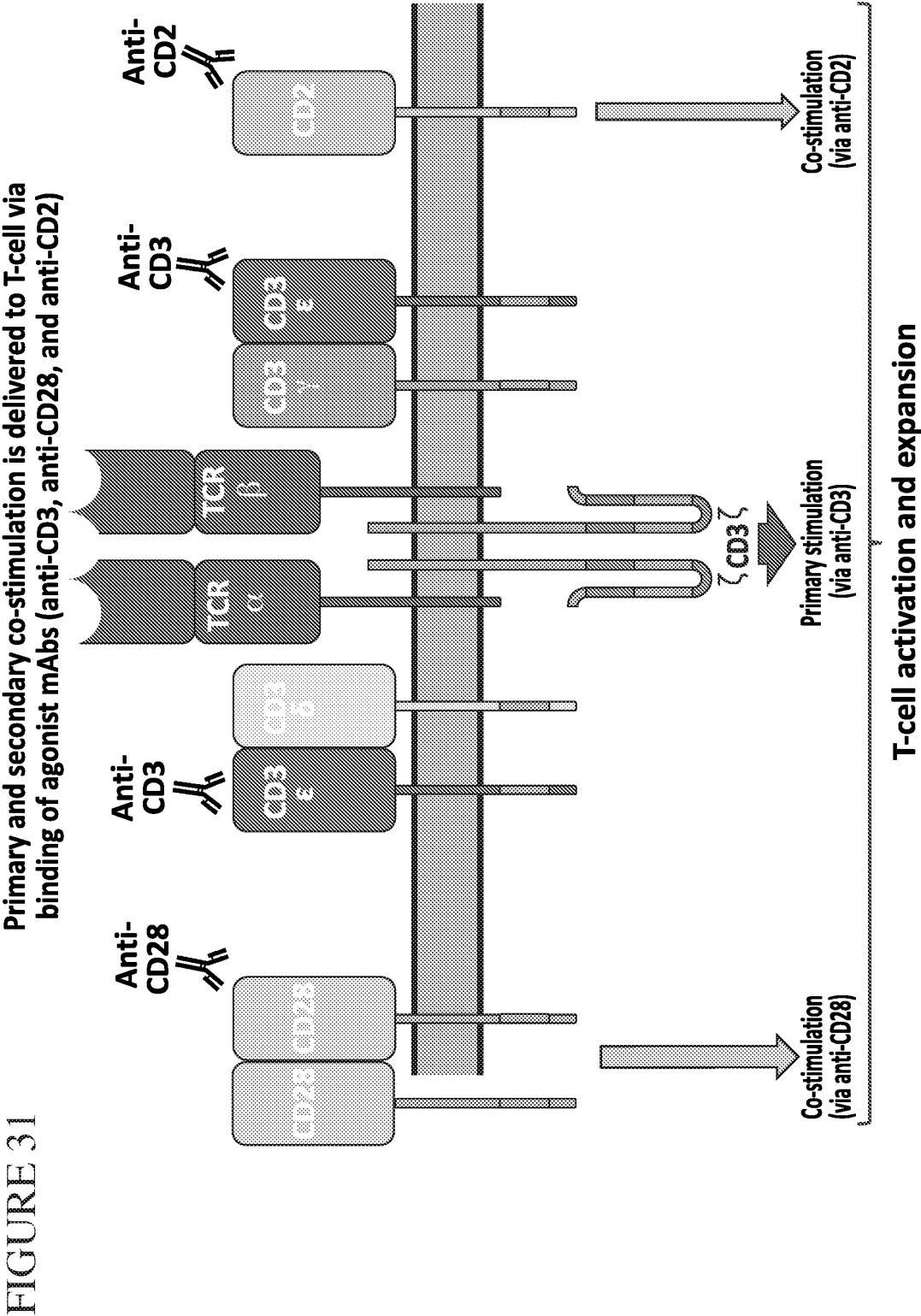
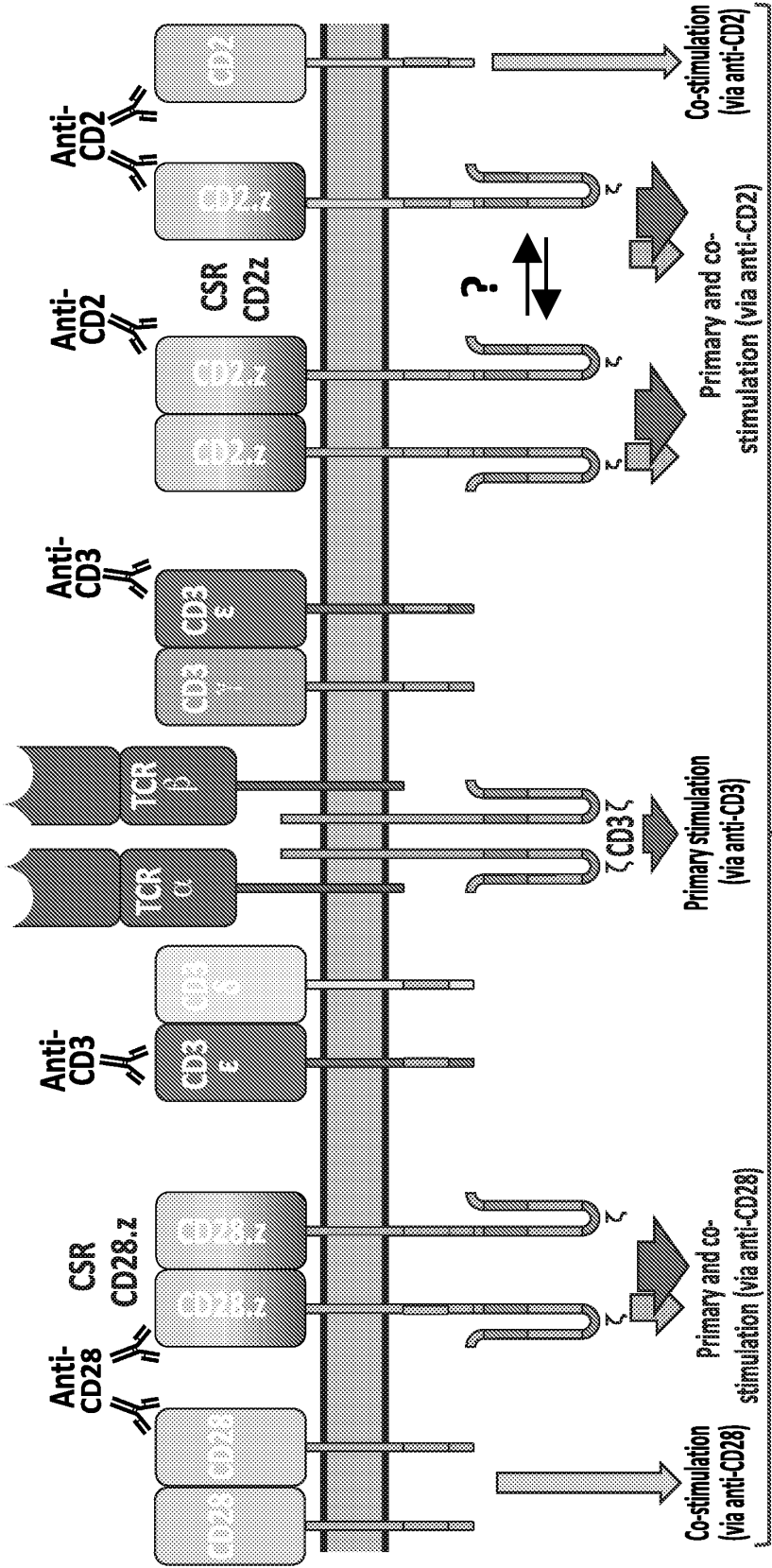


FIGURE 32

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



ENHANCED T-cell activation and expansion

FIGURE 33A

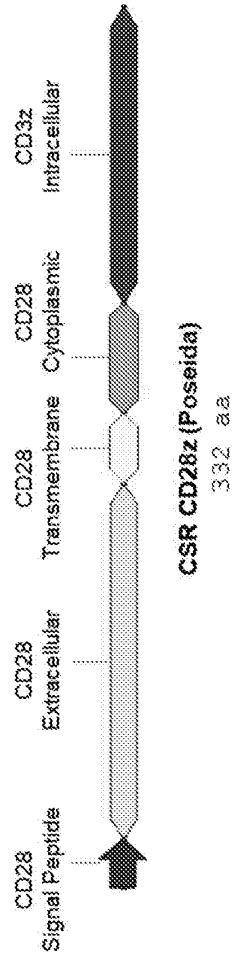


FIGURE 33B

MLRLLALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRSLHKGLDSAVE
VCVVYGNYSQQLQVYSKTGFNCDCGKLGNESTFYLQNLVYNQTDIYFCKIEVMYPPPYLDN
EKSNGTIIHVKGKHLCPSPLPFGPSKPFWVLLVWGGVLACYSLLVTVAFIIFWVRSKRSRLHS
DYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRR
EEYDVLDKRRGRDPGPGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDG
LYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 17910)

FIGURE 33C

ATGCTGAGACTGCTGGCCCTGAATCTGTTCCCAAGCATCCAAAGTGACCGGCAACAAGA
TCCTGGTCAAGCAGAGCCCTATGCTGGTGGCTACGACAACGCCGTGAACCTGAGCTGCAA
GTACAGCTACAACTGTTACAGCAGAGAGTCCGGGCCAGCTGCACAAGGACTGGATTCT
GCTGTGGAAGTGTGCGTGTACGGCAACTACAGCCAGAGCTGCAGGTCTACAGCAAG
ACCGGCTTCAACTGCGACGGCAAGCTGGGCAATGAGAGCGTGACCTTACCTGCAAAACC
TGTACGTGAACCAAGACCATCTATTCTGCAAGATCGAAGTGATGACCCGCTCCTTAC
CTGGACAACGAGAAGTCCACGGCACCATCATCCACGTGAAGGGCAAGCACCTGTGTCTT
CTCCACTGTTCCCCGGACTAGCAAGCCTTCTGGGTGCTCGTTGTTGGCGCGTGCTG
GCCTGTTATAGCTGCTGGTTACAGTGGCCTTCATCATCTTTTGGGTCCGAAGCAAGCGGA
GCCGGCTGCTGCACAGCGACTACATGAACATGACCCCTAGACGGGCCGAGCAACAGTTT
AGCACTACCAAGCCTACGCTCTCCTAGAGACTTCGCCGCTACCGGTCCAGAGTGAAGTTC
TCCAGATCCGCCGATGCTCCCGCTATAAGCAGGGGCCAGAACCAAGCTGTACAACGAGCTGA
ACCTGGGGAGAAGAGAAGTACGATGTGCTGGACAAGCGGAGAGGCAGAGATCCTGAG
ATGGGCGGCAAGCCAGACGGAAGAATCCTCAAGAGGGCCTGTACAATGAAGTGCAGAAA
GACAAGATGGCCGAGGCTACAGCGAGATCGGAATGAAGGGCGAGCGCAGAGAGGCA
AGGGACACGATGGACTGTACCAAGGGCCTGAGCACCGCCACCAAGGATACCTATGATGCC
TGCACATGCAGGGCCTGCCTCCAAGA (SEQ ID NO: 17911)

FIGURE 34A

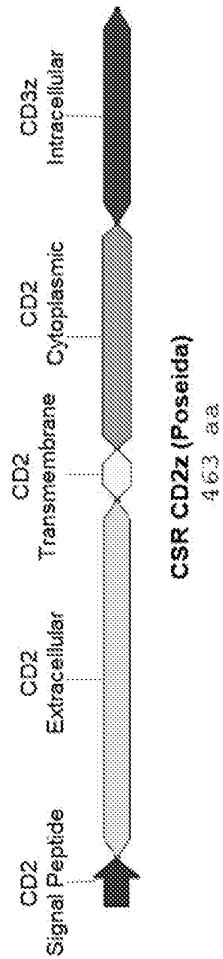


FIGURE 34B

MSFPCKFVASFLLIIFNVSSKGAVSKEITNALETWGALGQDINLDIPSFQMSDDIDDIKWEKT
SDKKIAQFRKEKETFEKEDTYKLFKNGLTKIKHLKTDQDIYKVSIDTKGKNVLEKIFDLKI
QERVSKPKISWTCINTTLTCEVMNGTDPENLYQDGKHLKLSQRVITHKWTTSLSAKFKCT
AGNKVSKESSVEPVSCPEKGLDIYLIIGICGGGSLLMVFALLVYITKRKKQSRNRNDEELET
RAHRVATEERGRKPHQIPASTPQNPAQSHPHPPGHRHQAPSHRPPPGHVRVQHQPQK
RPPAPSGTQVHQKGPPLPRPRVQPKPPHGAENSLSPSSNRVKFSRSADAPAYKQGGQN
QLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMIK
GERRRGKGDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 17912)

FIGURE 34C

ATGAGCTTCCCTGCAAGTTCGTGGCCAGCTTCCTGCTGATCTTCAACGTGTCTCTAAGGGGCC
GTGTCCAAAGAGATCAAAACGCCCTGAAACCTGGGAGCCCTCGGCCAGGATATTAACCTGG
ACATCCCCAGCTTCCAGATGAGCGACGACATCGATGACATCAAGTGGGAGAAAACCCAGCGACAA
GAAGAAGATCGCCAGTTCGGAAAGAGAAAGAGACATTCAAAGAGAAAGGACACCTACAAGCT
GTTCAAGAACGGCACCTGAAGATCAAGCACCTGAAACCCGACGACGAGGACATCTATAAGGTG
TCCATCTACGACACCAAGGGCAAGACGTGCTGGAAAAAGATCTTCGACCTCAAGATCCAAGAGCG
GGTGTCCAAGCCTAAGATCAGCTGGACCTGCATCAACACCCACACTGACCTGCGAAGTGATGAACG
GCACAGACCCCGAGCTGAACCTGTACCAGGATGGCAAAACACCTGAAGCTGAGCCAGCGCGTGAT
CACCCACAAGTGGACAACAAGCCTGAGCGCCAAGTTCAAGTGCACCGCCGGAACAAAGTGCT
AAAGAGTCCAGCGTCGAGCCCGTGTCTGCCCTGAAAAAGGACTGGACATCTACCTGATCATCGG
CATCTGTGGCGGGAAGCCTGCTGATGGTGTCTGTGGCTCTGCTGGTGTCTACATCAACCAAGC
GGAAGAACGAGCGGAGCAGACGGAACGACGAGGAATCGAAACACACGGGCCCATAGAGTGGCC
ACCGAGGAAAAGGCGAGAAAGCCCAACAGATTCAGCCAGCACACCCAGAAATCCTGCCACCTC
TCAACACCTCCACCTCCAGCTGGACACAGATCTCAGGCCCATCTCAGACCTCCACACCTGG
TCATCGGTGCAGCACGCTCAGAAAAGACCTCTGCTCTAGCGGCACACAGGTGCACAGC
AAAAGGACCTCCTGCTGCTGCTGAGTGCAGCTAAACCTCTCATGGCGCCGCTGAGAAC
AGCTGTCTCCAAGCAGCAACAGAGTGAAGTTCAGCCGACGCGCGGATGCTCCTGCCTATAAGCA
GGGACAGAACCCAGCTGTACAACGAGCTGAATCTGGGCGCAGAGAGAGTACGATGTGCTGGA
CAAGCGGAGAGGAGAGATCTGAGATGGGCGCAAGCCAGACGGAAGAAATCCTCAAGAGGG
CCTGTATATGAGCTGCAGAAAGACAAAGATGGCCGAGGCTACAGCGAGATCGGAATGAAGGG
CGAGCGCAGAAAGGCAAGGACACGATGGACTGTATCAGGCGCTGAGCACCGCCACCCCAAGGA
TACCTATGATGCCCTGCACATGCAGGCCCTGCCTCCAAGA (SEQ ID NO: 17913)

FIGURE 35

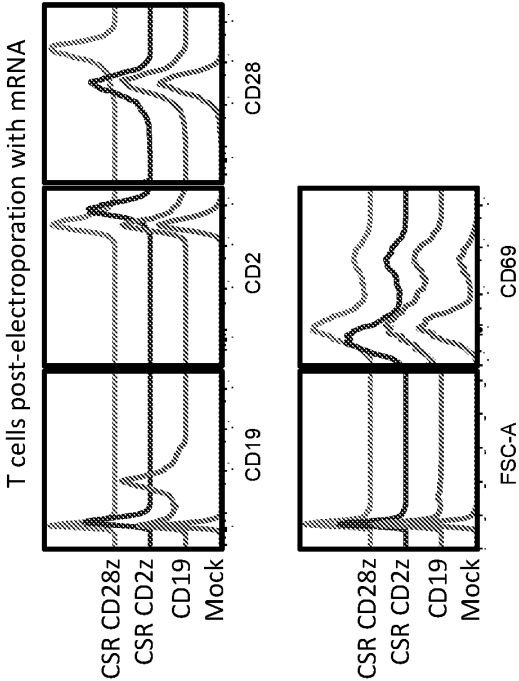


FIGURE 36

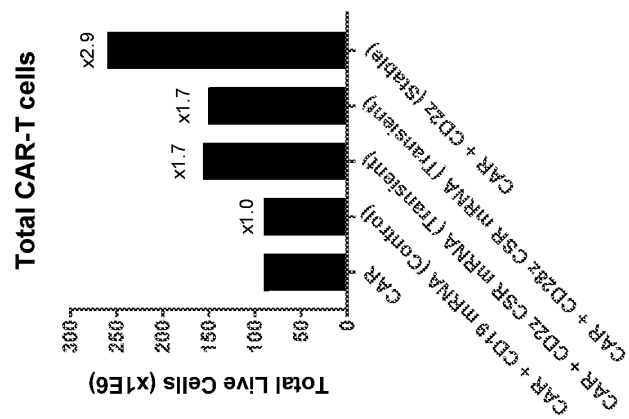


FIGURE 37

