

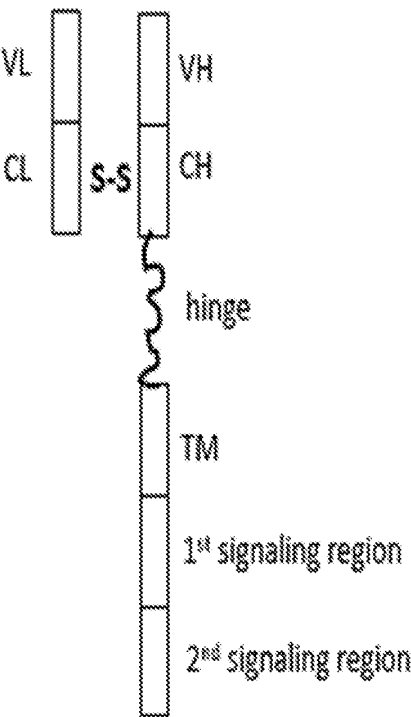


FIG. 1A

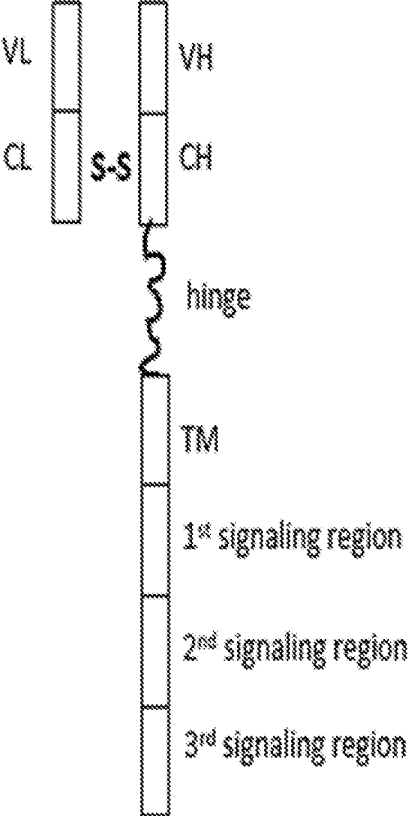


FIG. 1B

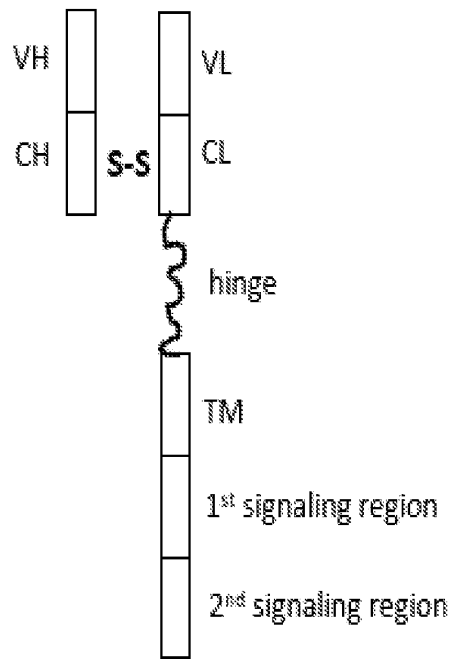


FIG. 2A

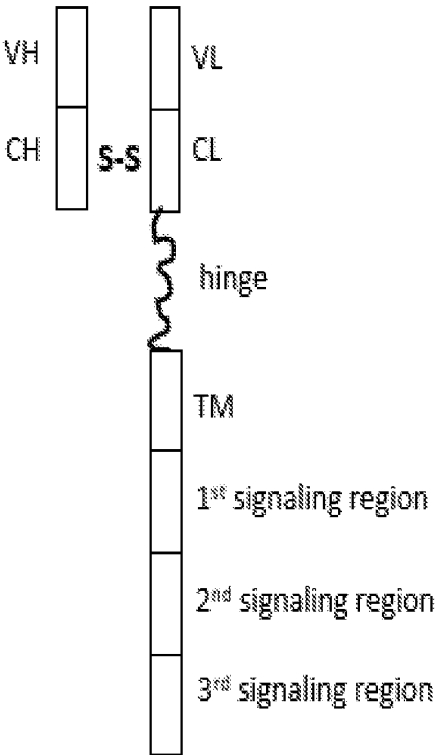


FIG. 2B

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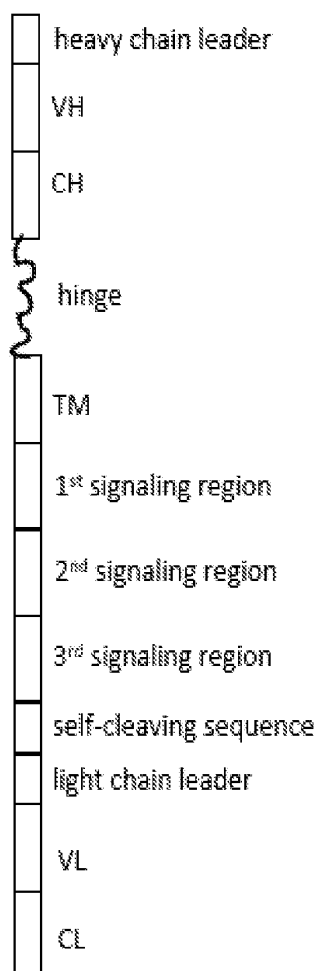


FIG. 3A

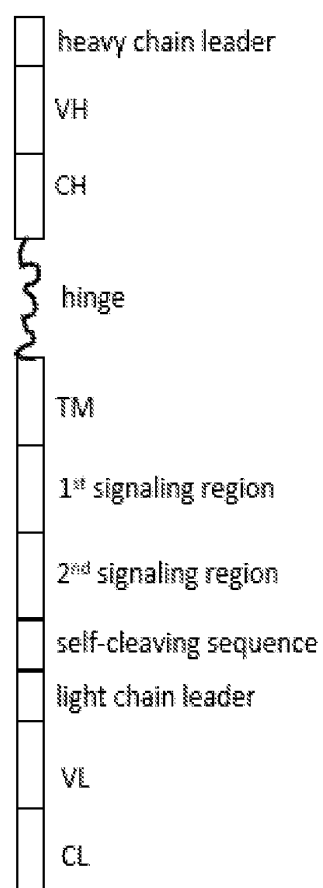


FIG. 3B

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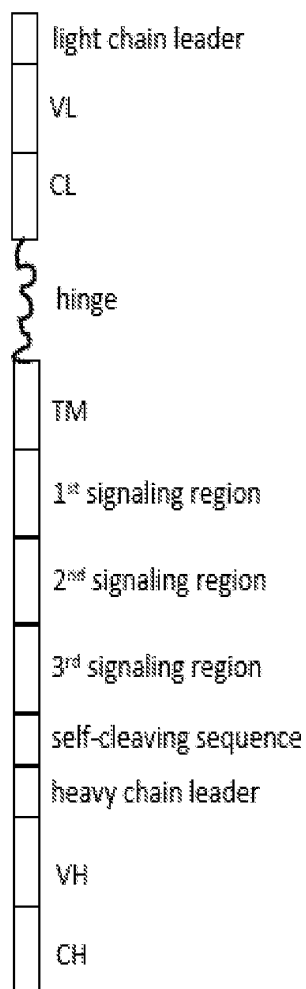


FIG. 4A

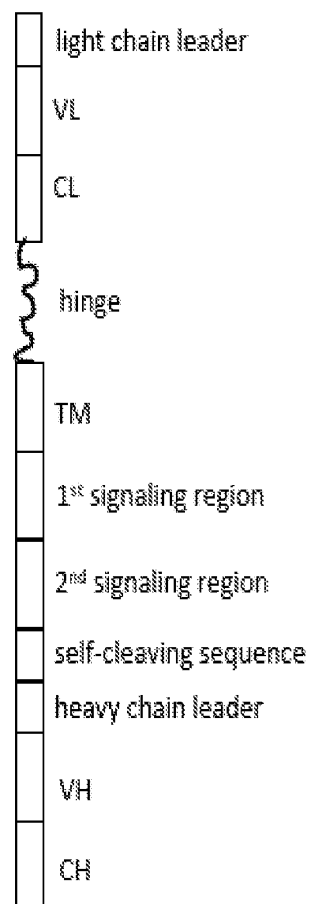


FIG. 4B

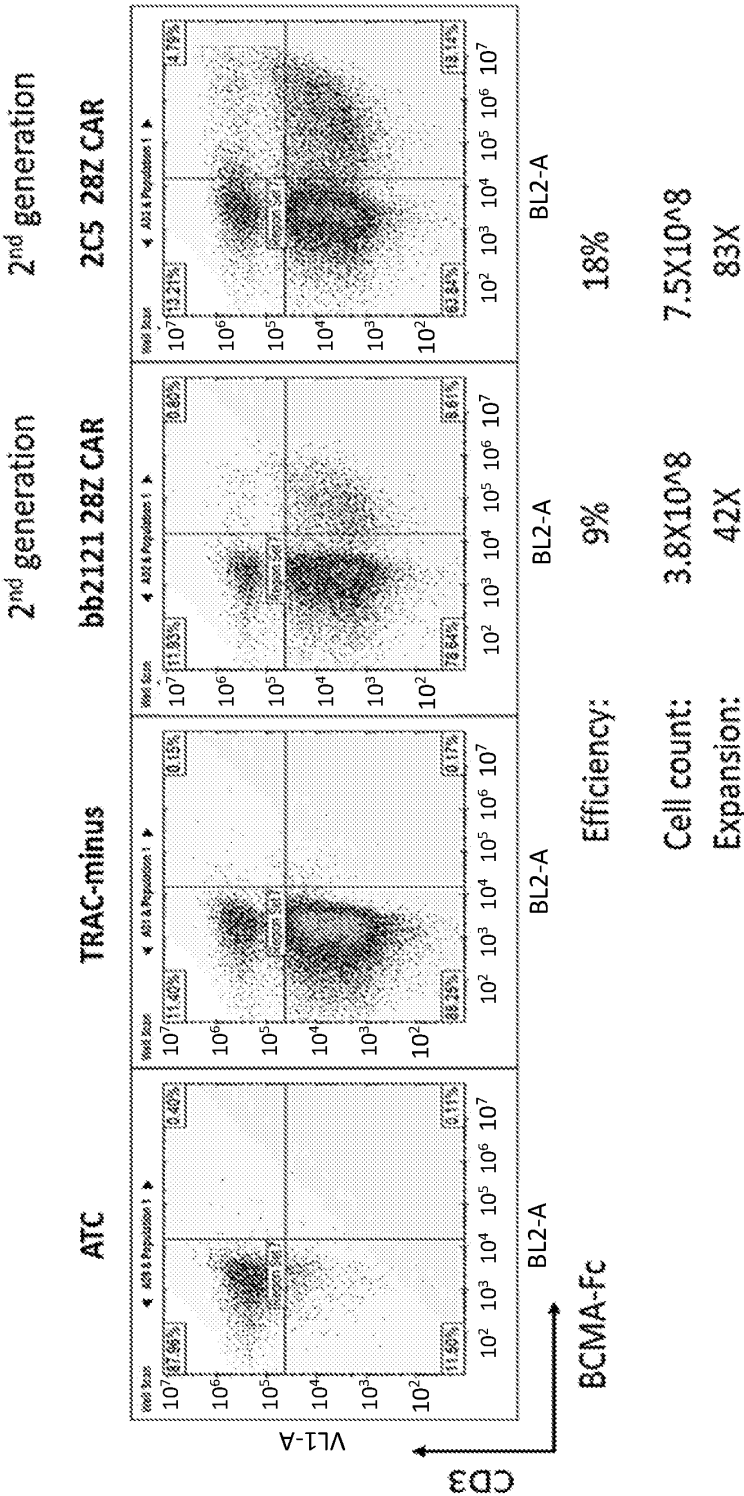


FIG. 5A

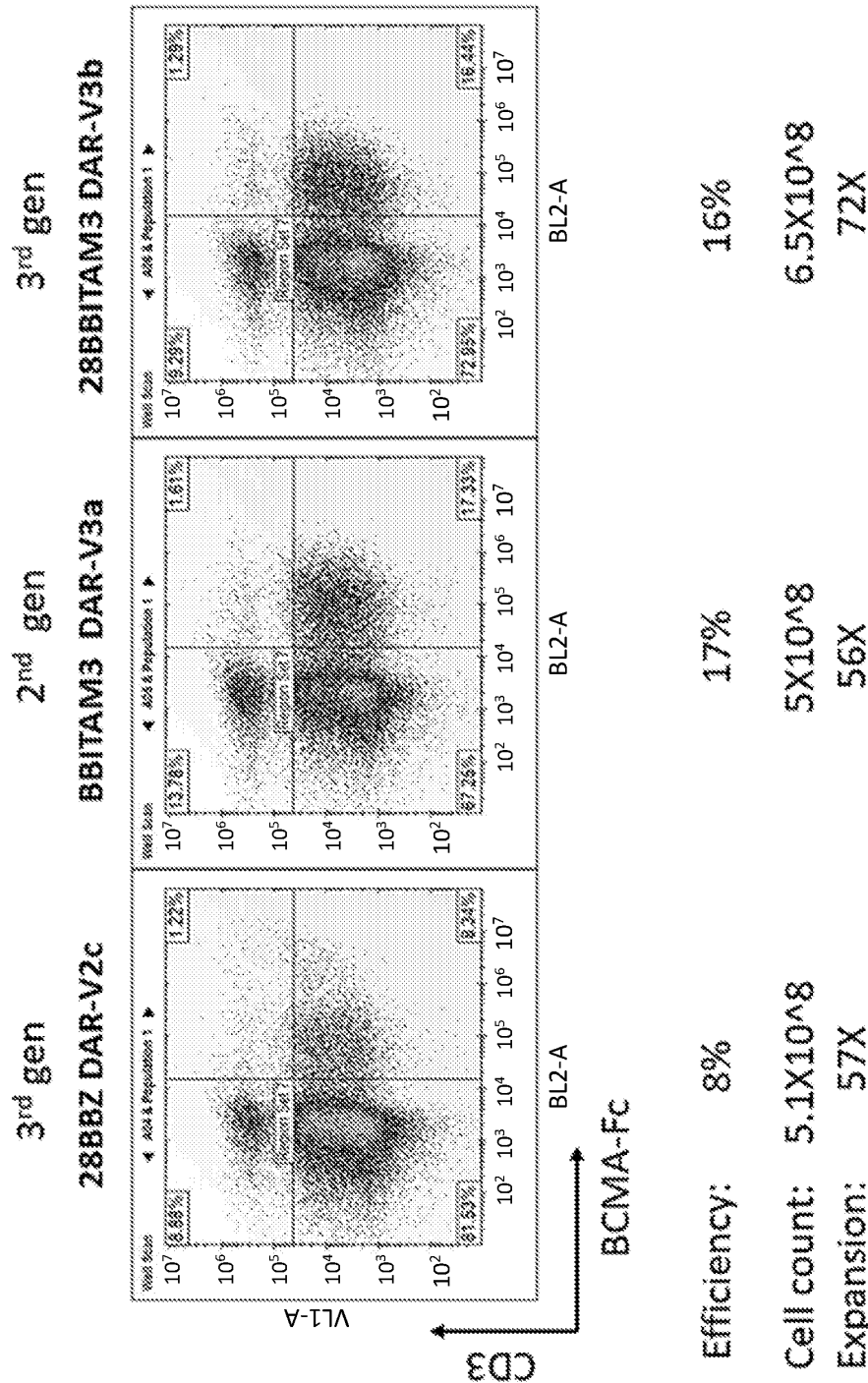


FIG. 5B

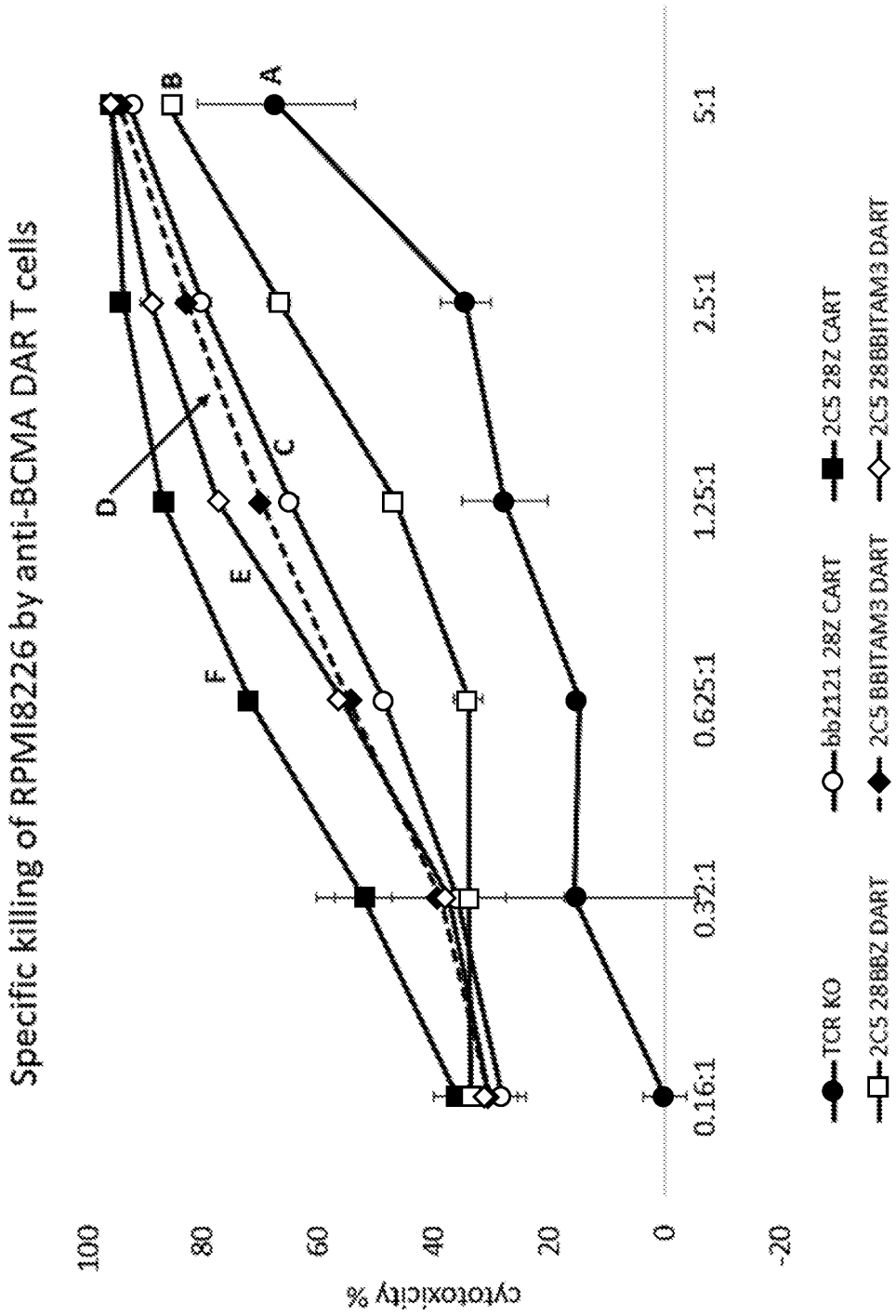


FIG. 6

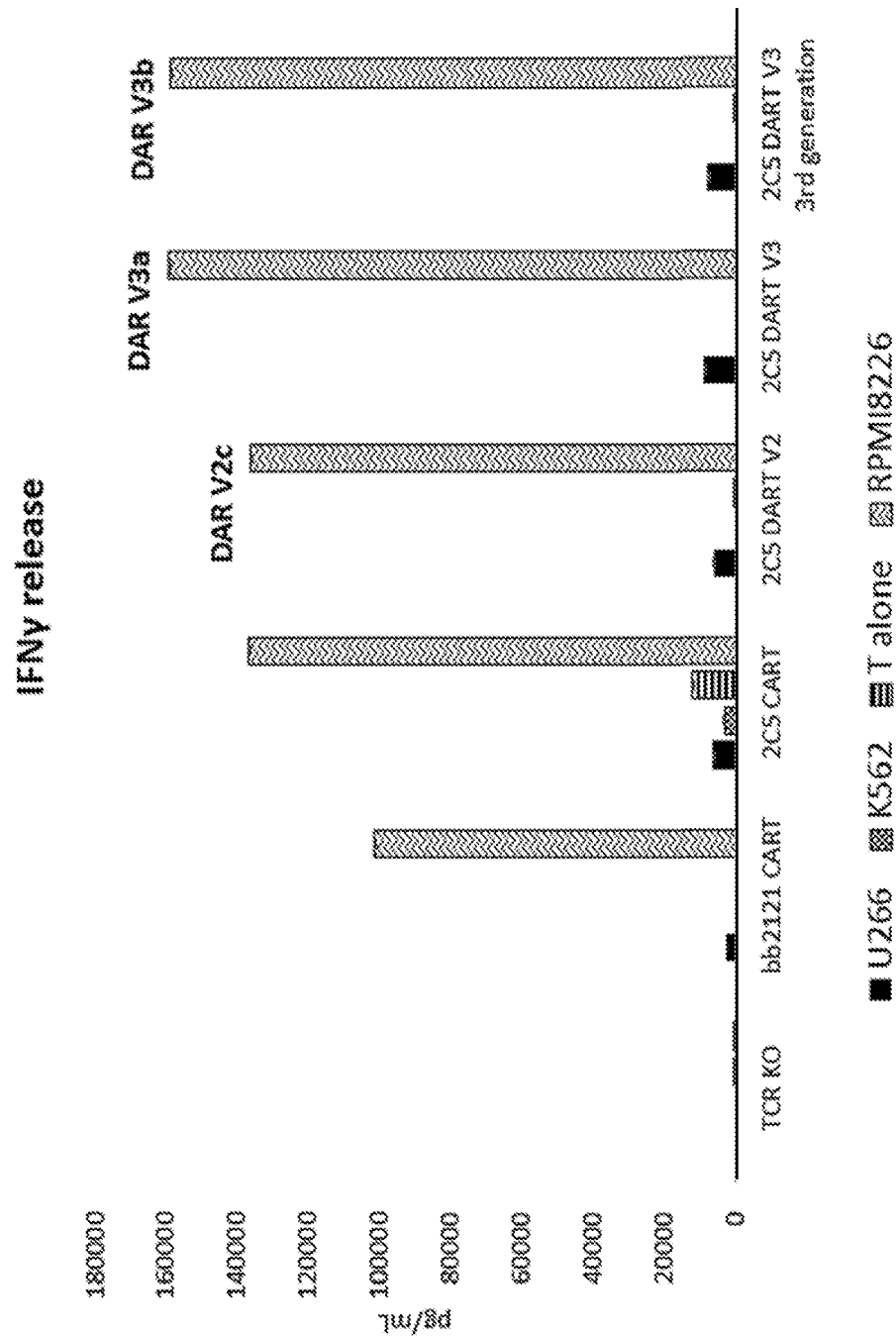


FIG. 7A

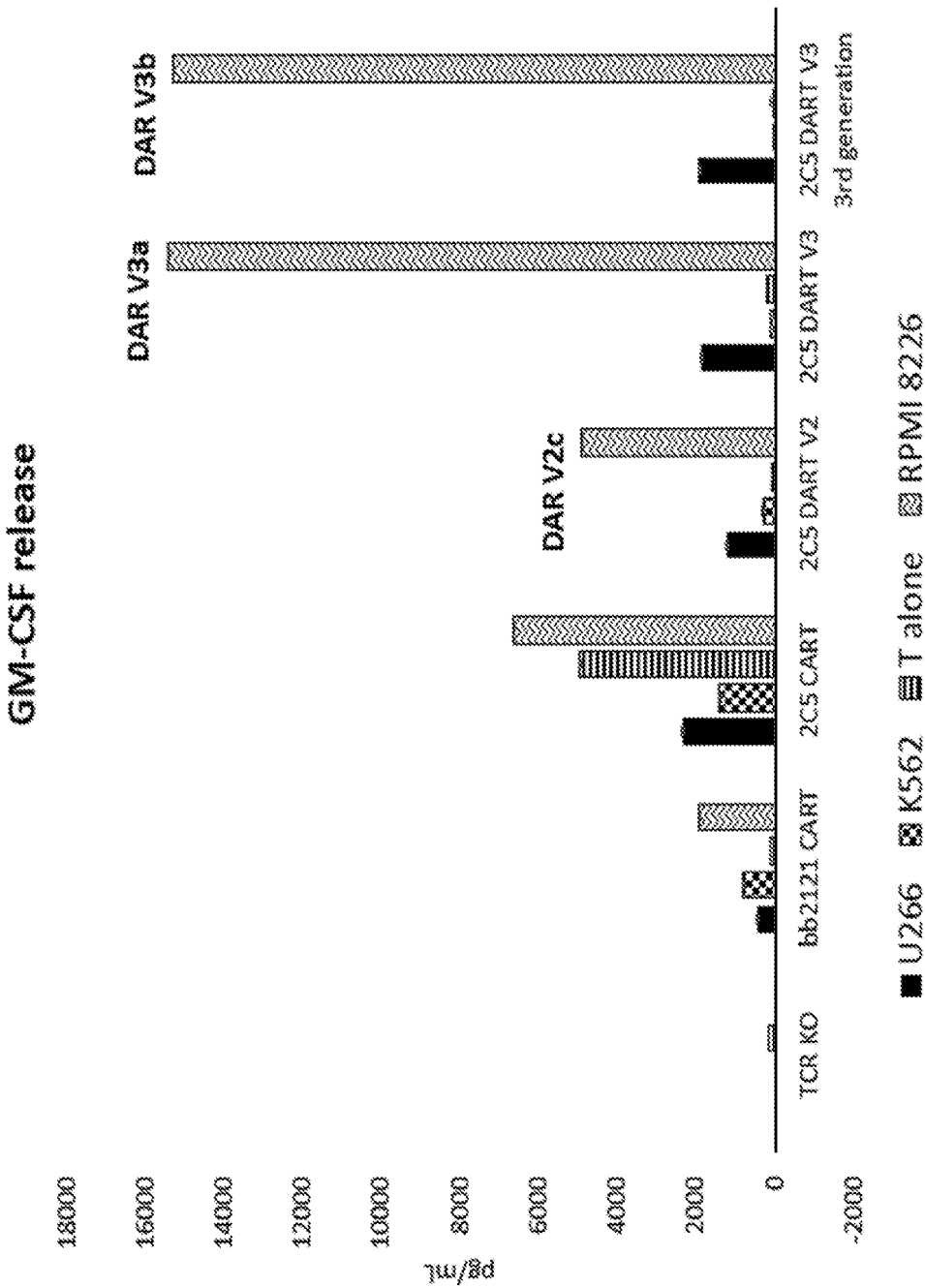


FIG. 7B

TRAC-MINUS

T only

U266

RPMI8226

K562

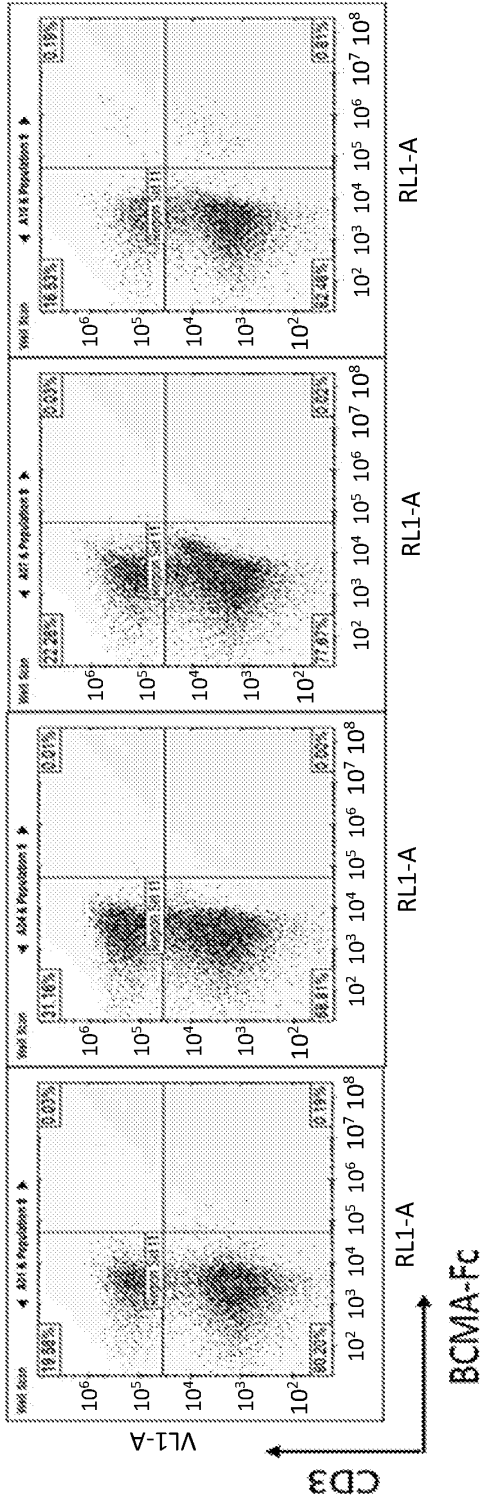
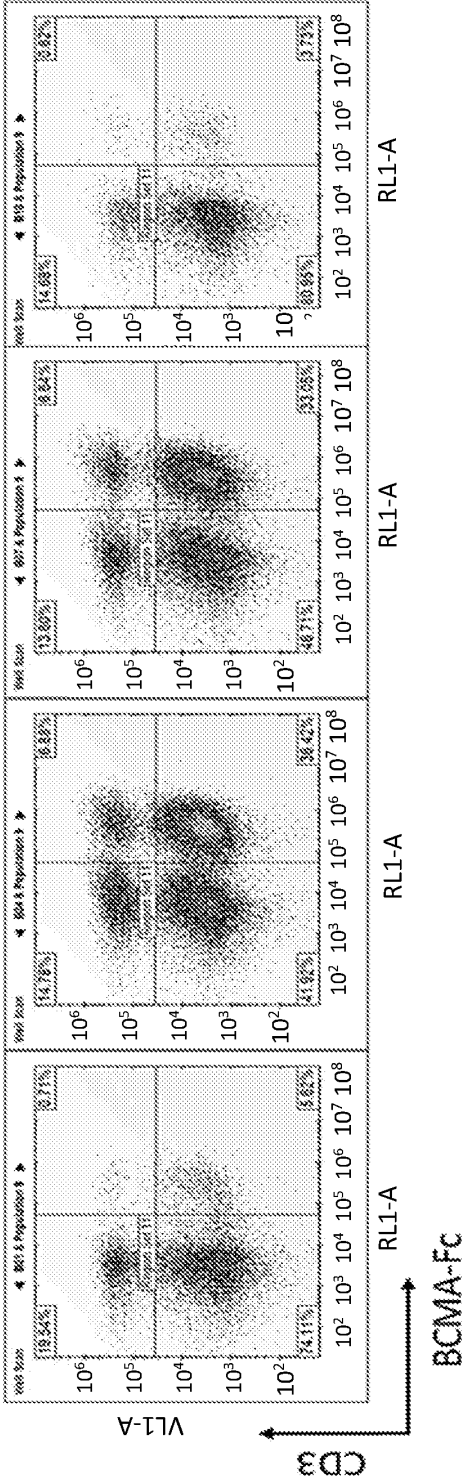


FIG. 8A

bb2121 28Z CAR
2nd generation

K562 RPMI8226 U266 T only



6% 36% 33% 4%

FIG. 8B

2C5 28Z CAR
2nd generation

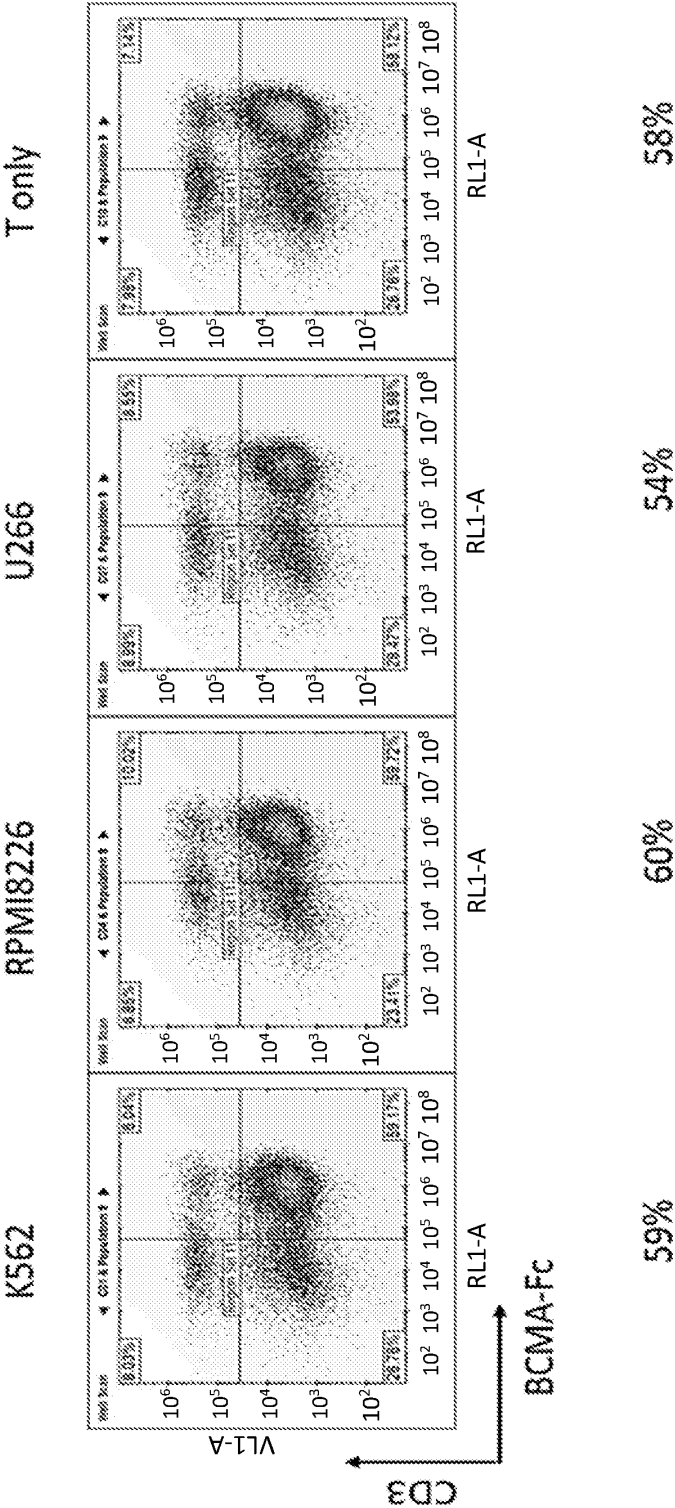


FIG. 8C

2C5 28BBZ DAR V2c

3rd generation

T only

U266

RPMI8226

K562

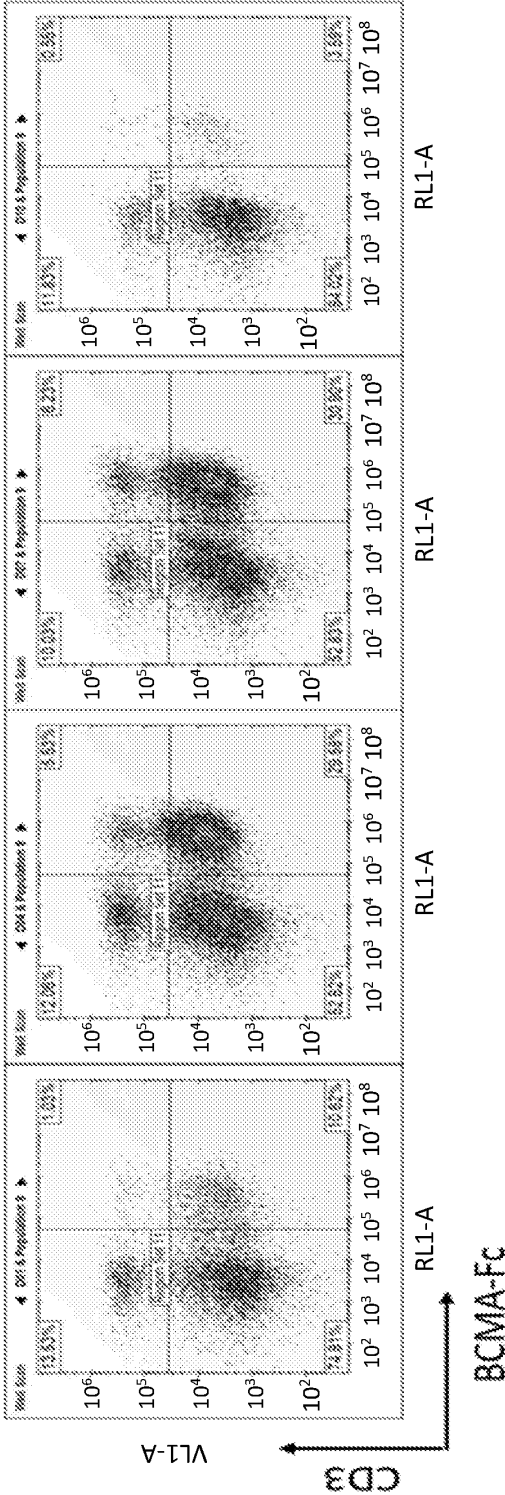


FIG. 8D

Clonal expansion of anti-BCMA DAR T cells three days after co-culture

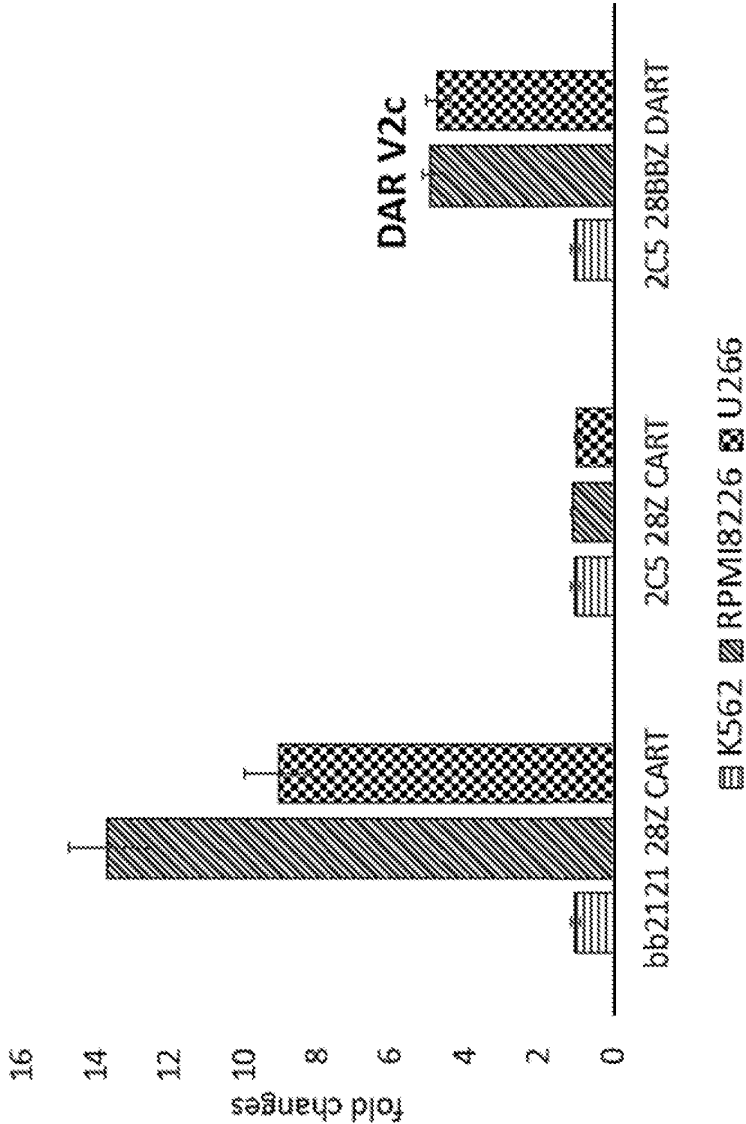


FIG. 9

TRAC-MINUS

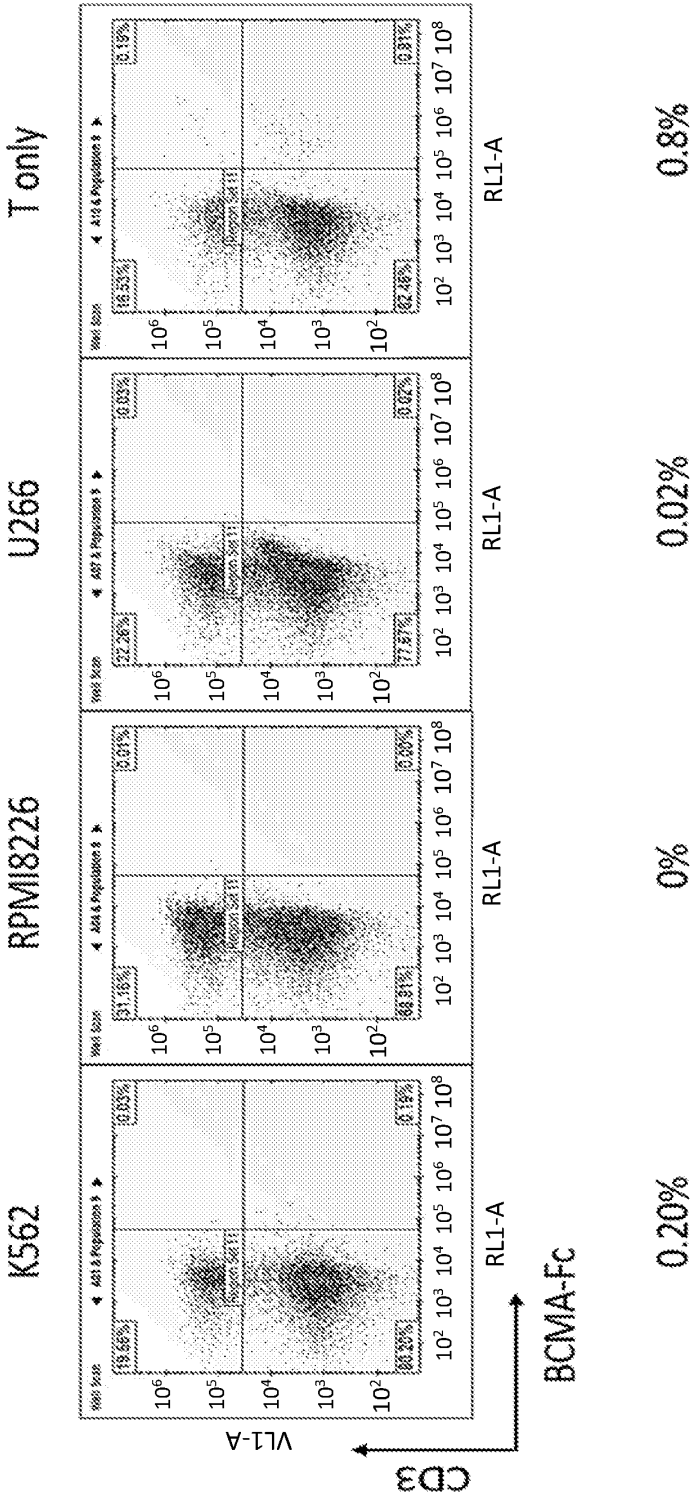


FIG. 10A

bb2121 28Z CAR
2nd generation

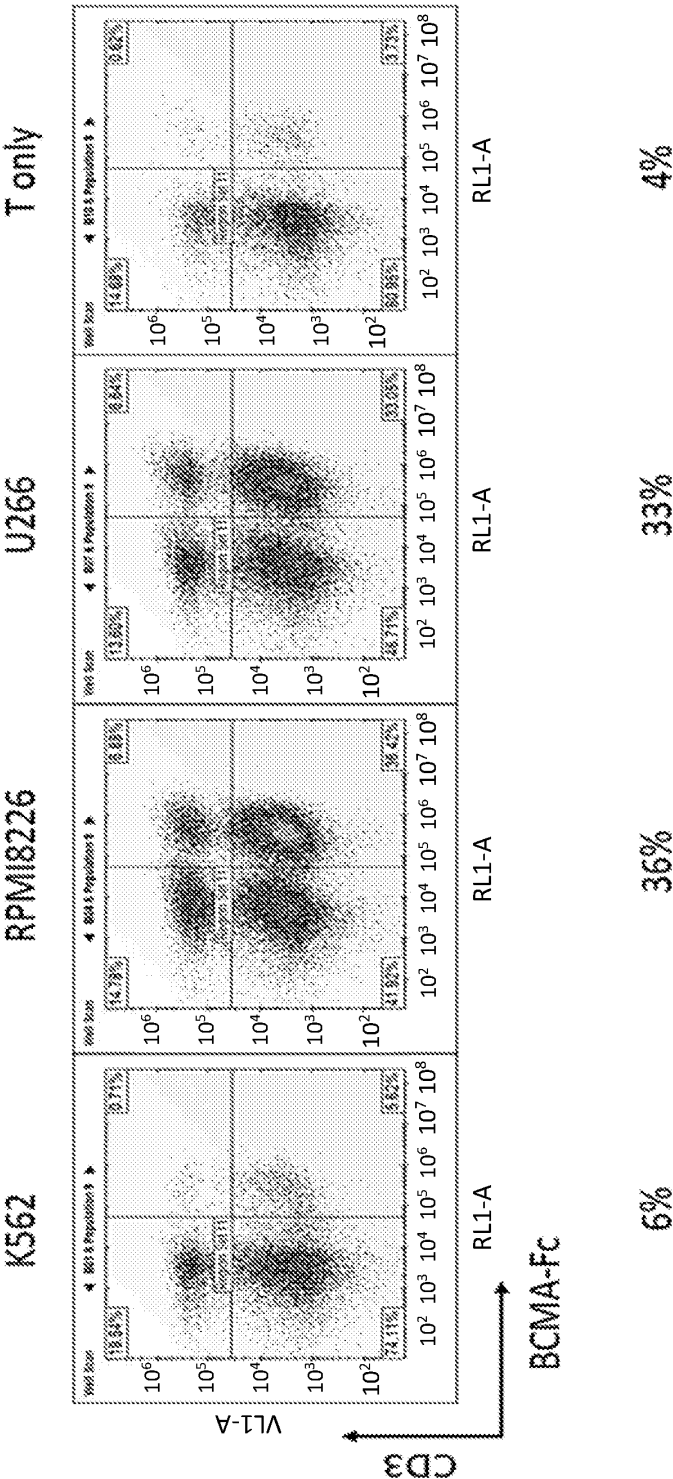


FIG. 10B

2C5 BBZ DAR V2a
2nd generation

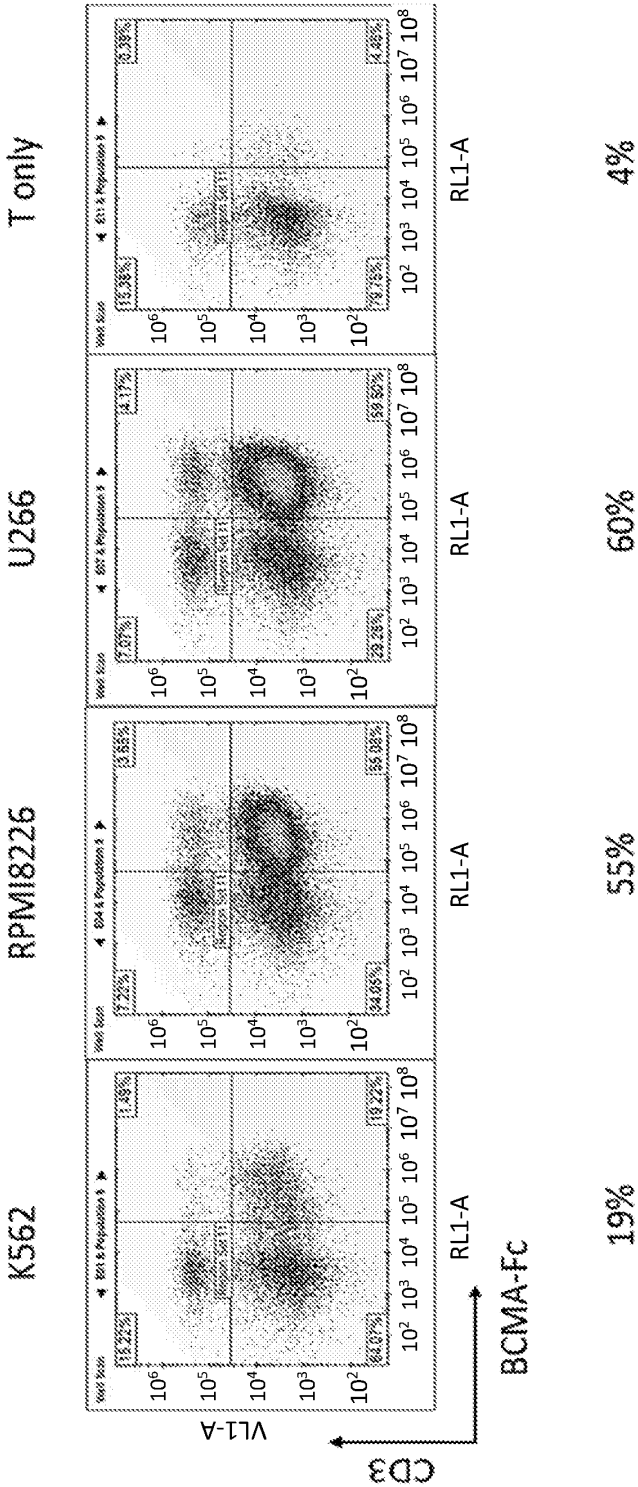


FIG. 10C

28BBZ DAR V2c
3rd generation

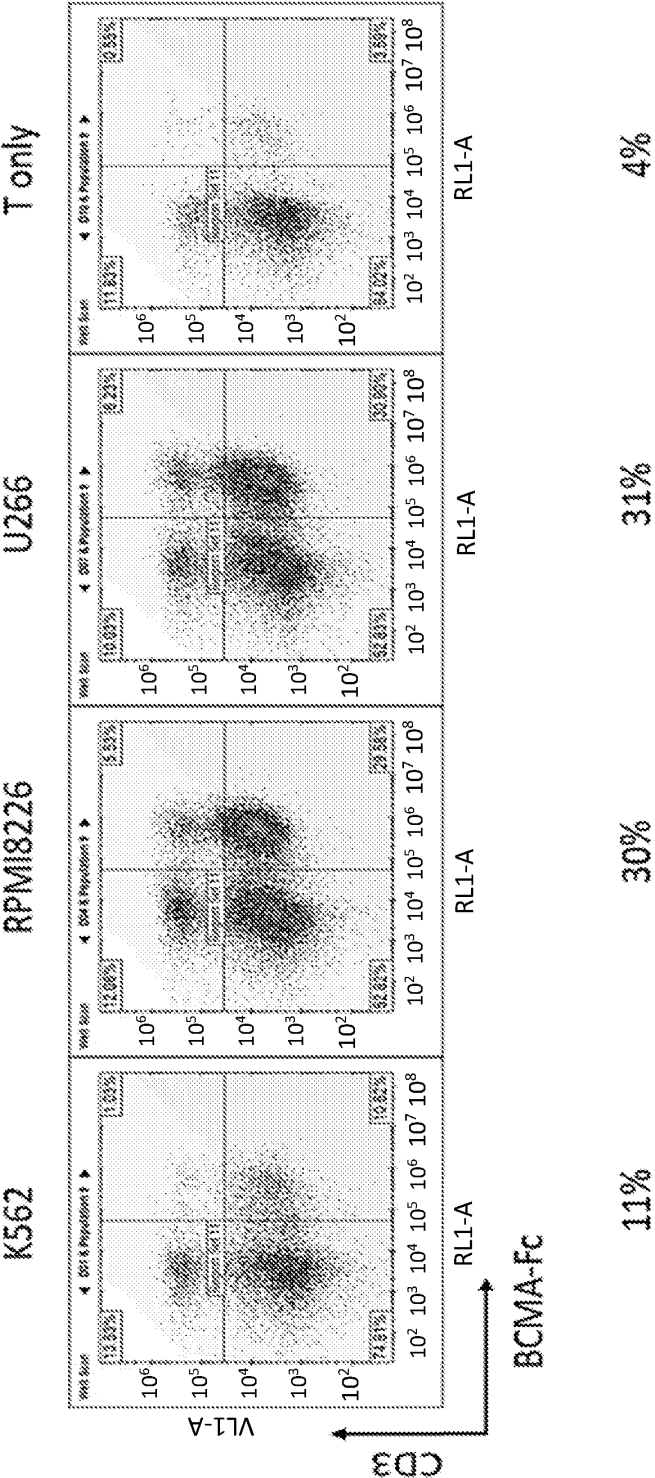


FIG. 10D

BBITAM3 DAR V3a
2nd generation

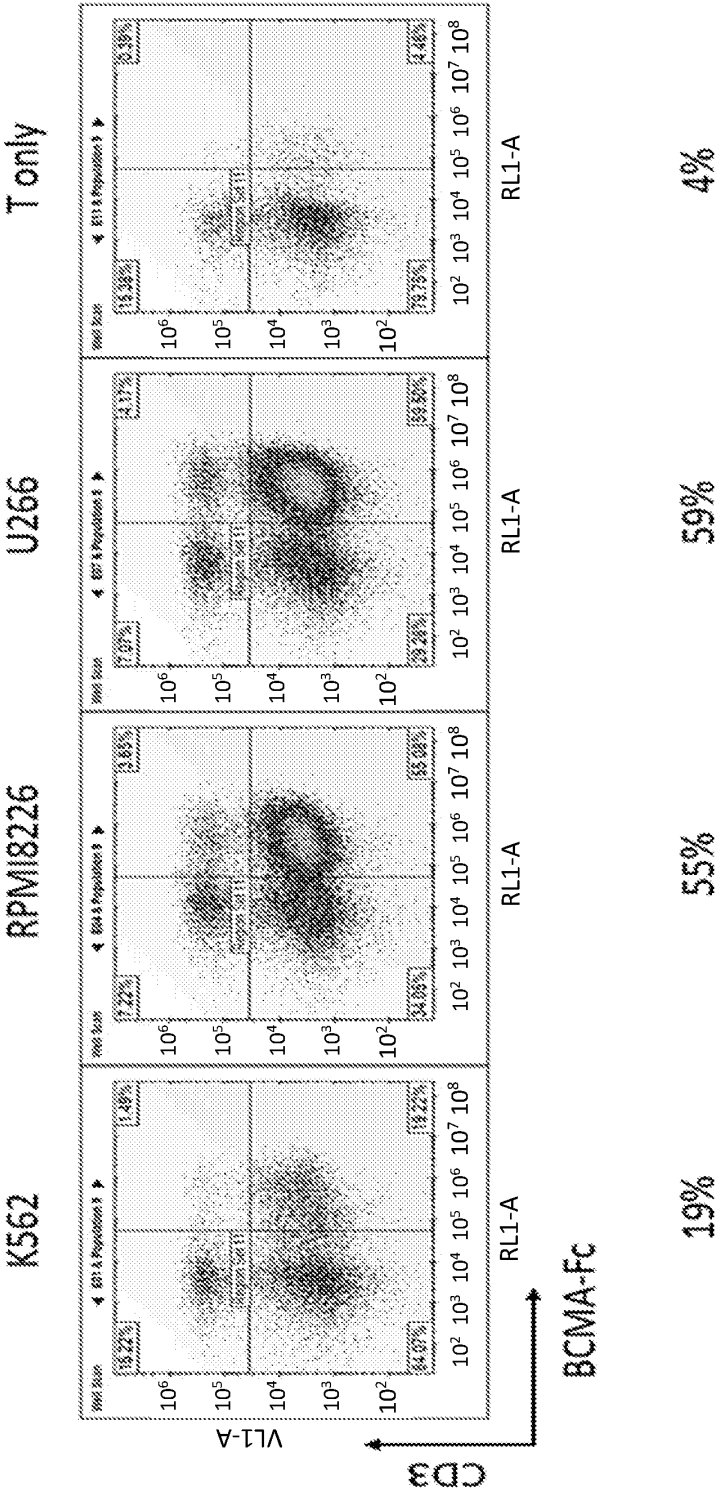


FIG. 10E

28BBITAM3 DAR V3b
3rd generation

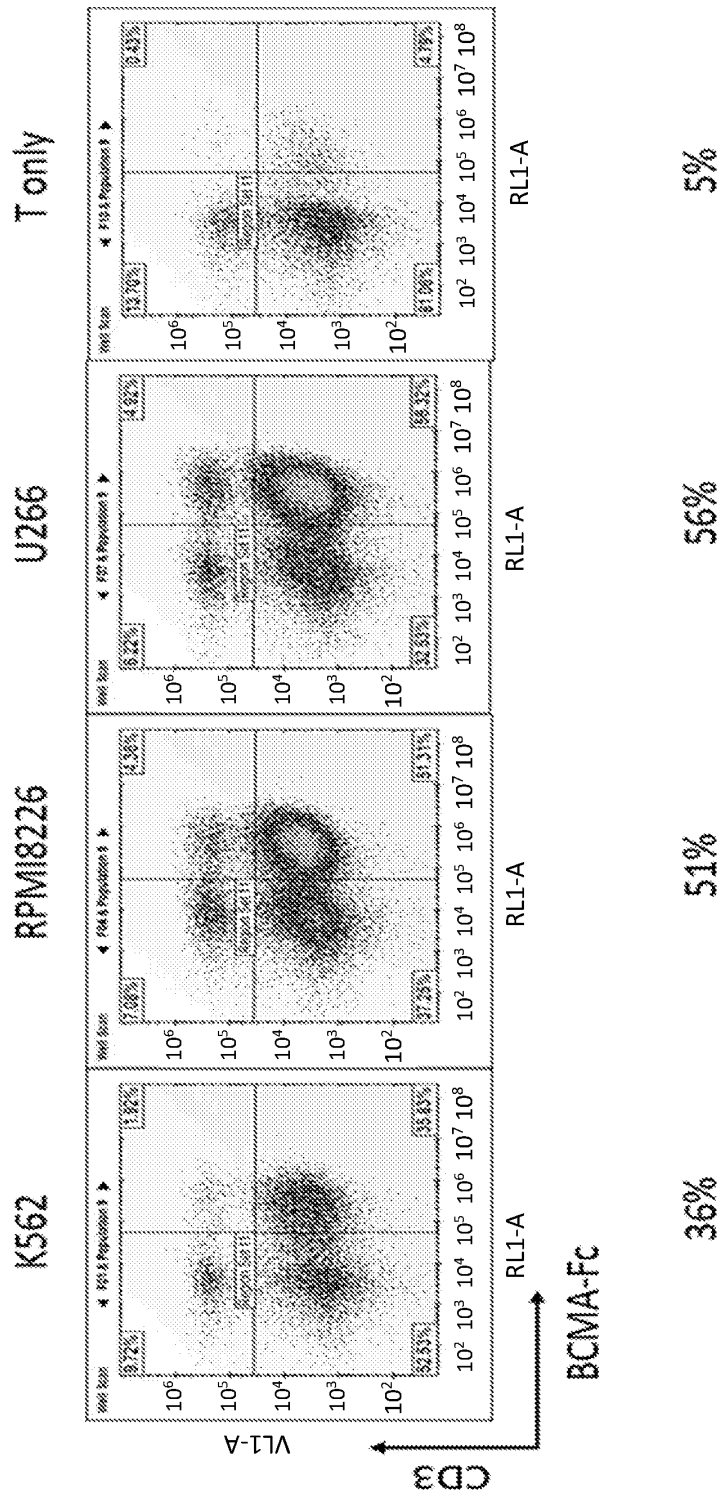


FIG. 10F

Clonal expansion of anti-BCMA CAR or DAR
3 days after co-culture

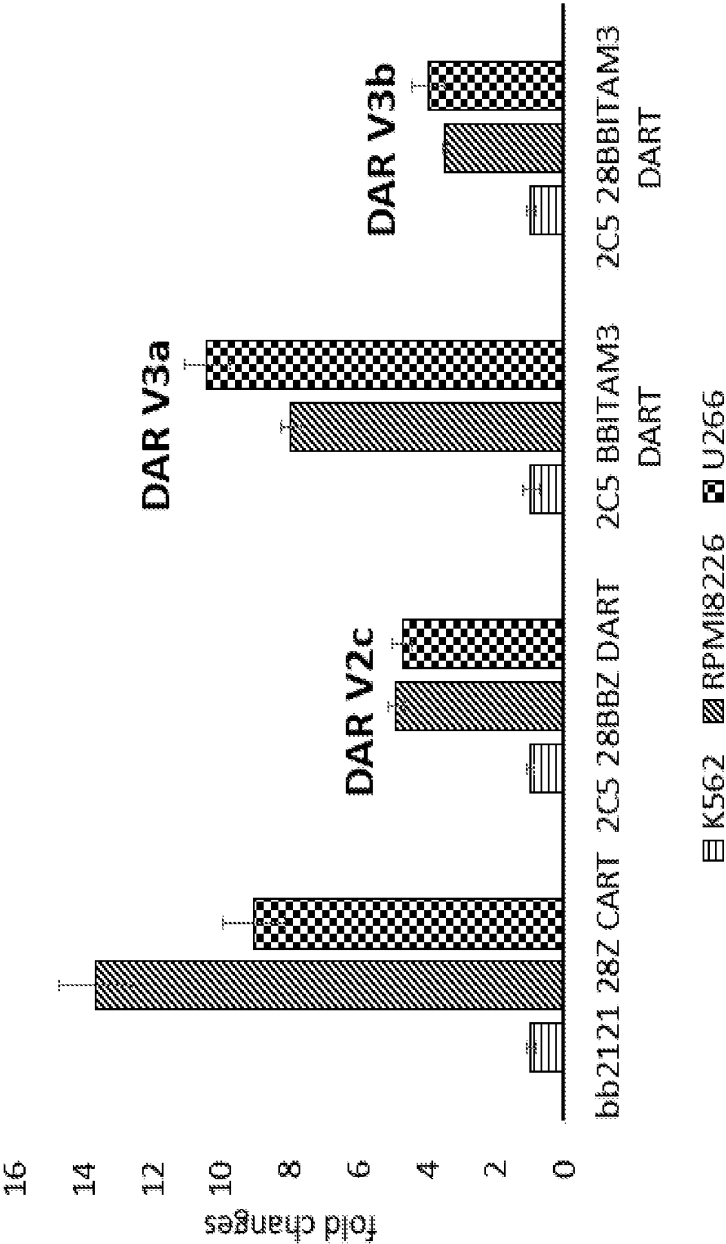


FIG. 11

Specific killing of RPMI8226 by anti-BCMA DART cells

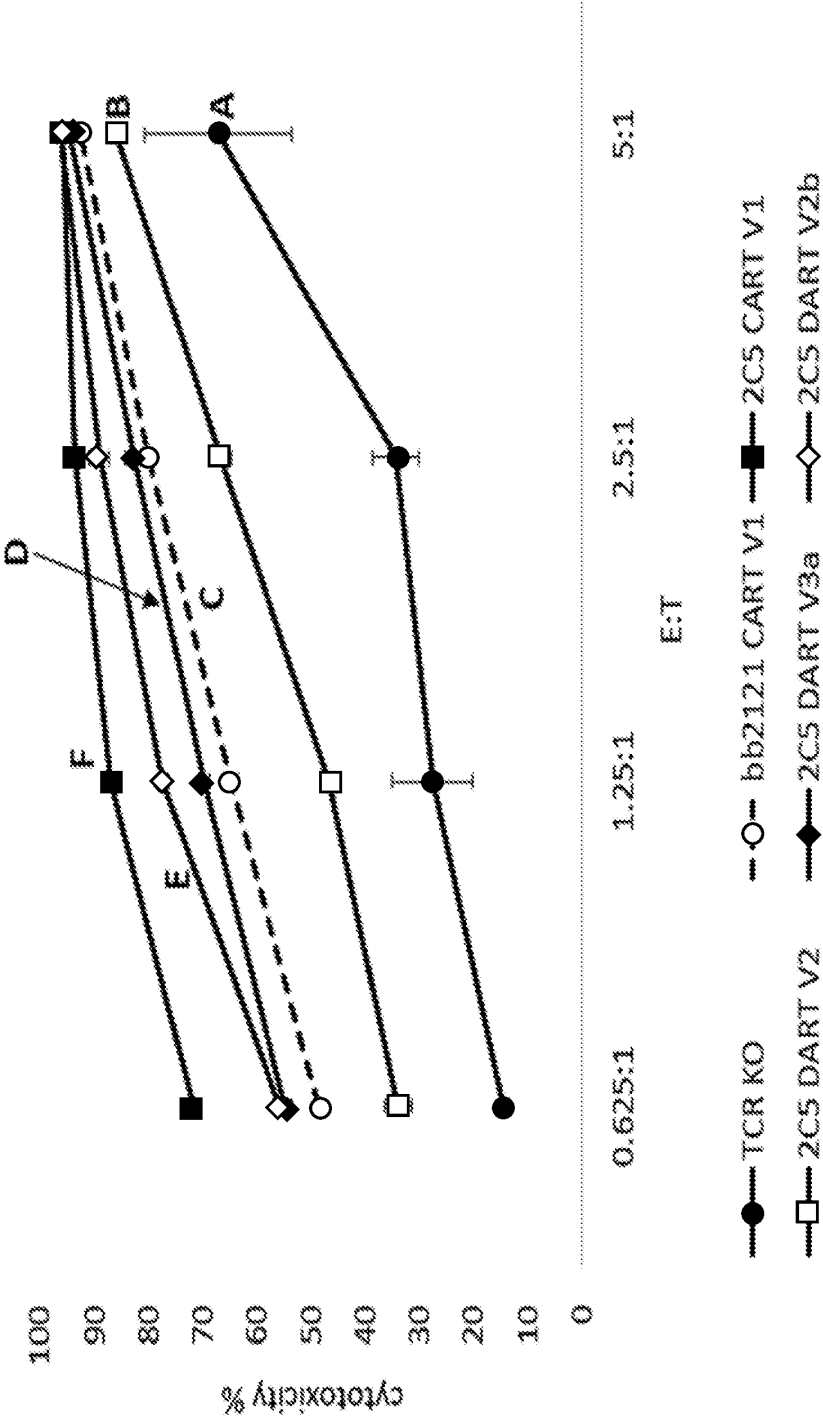


FIG. 12

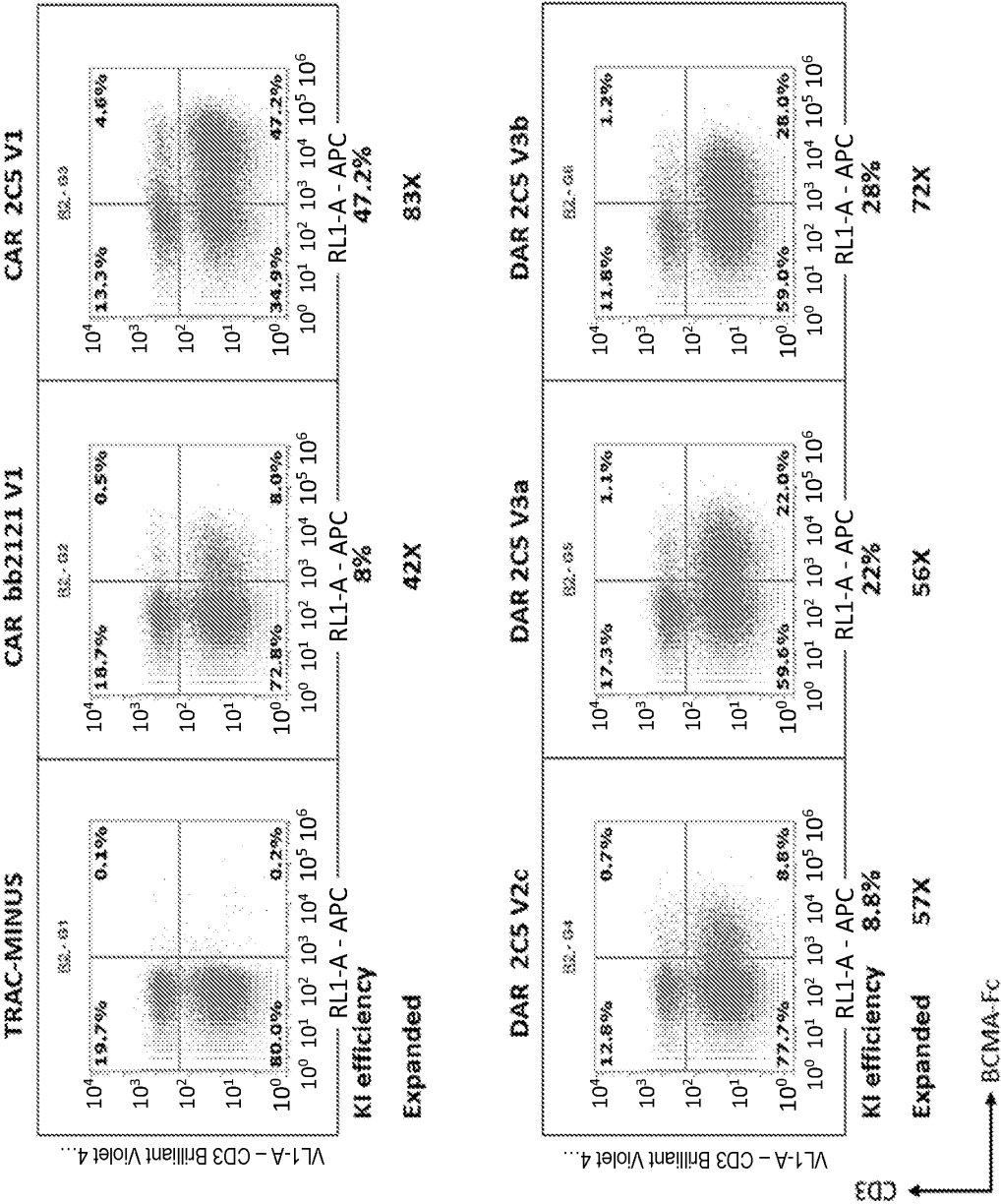


FIG. 13A

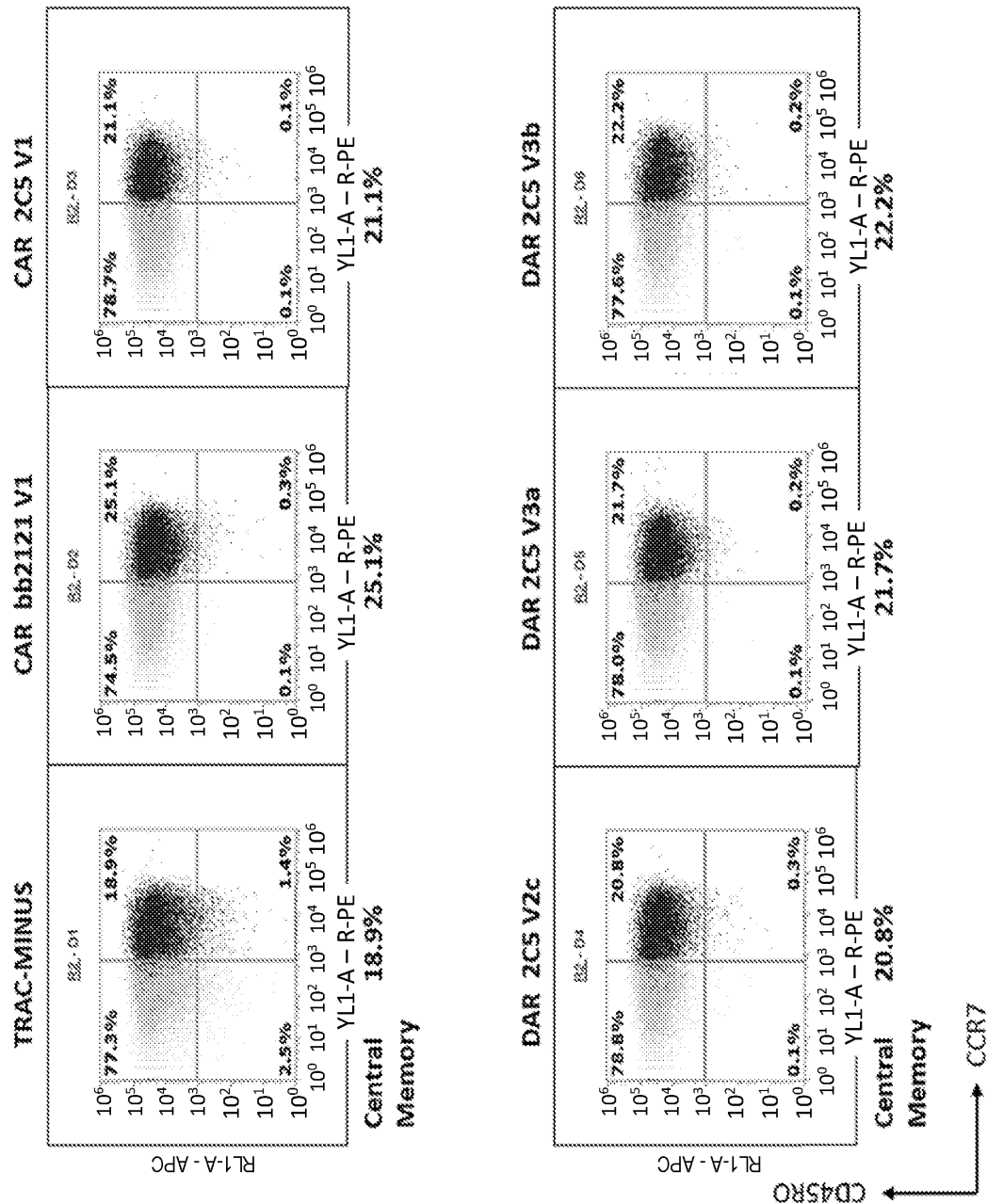


FIG. 13B

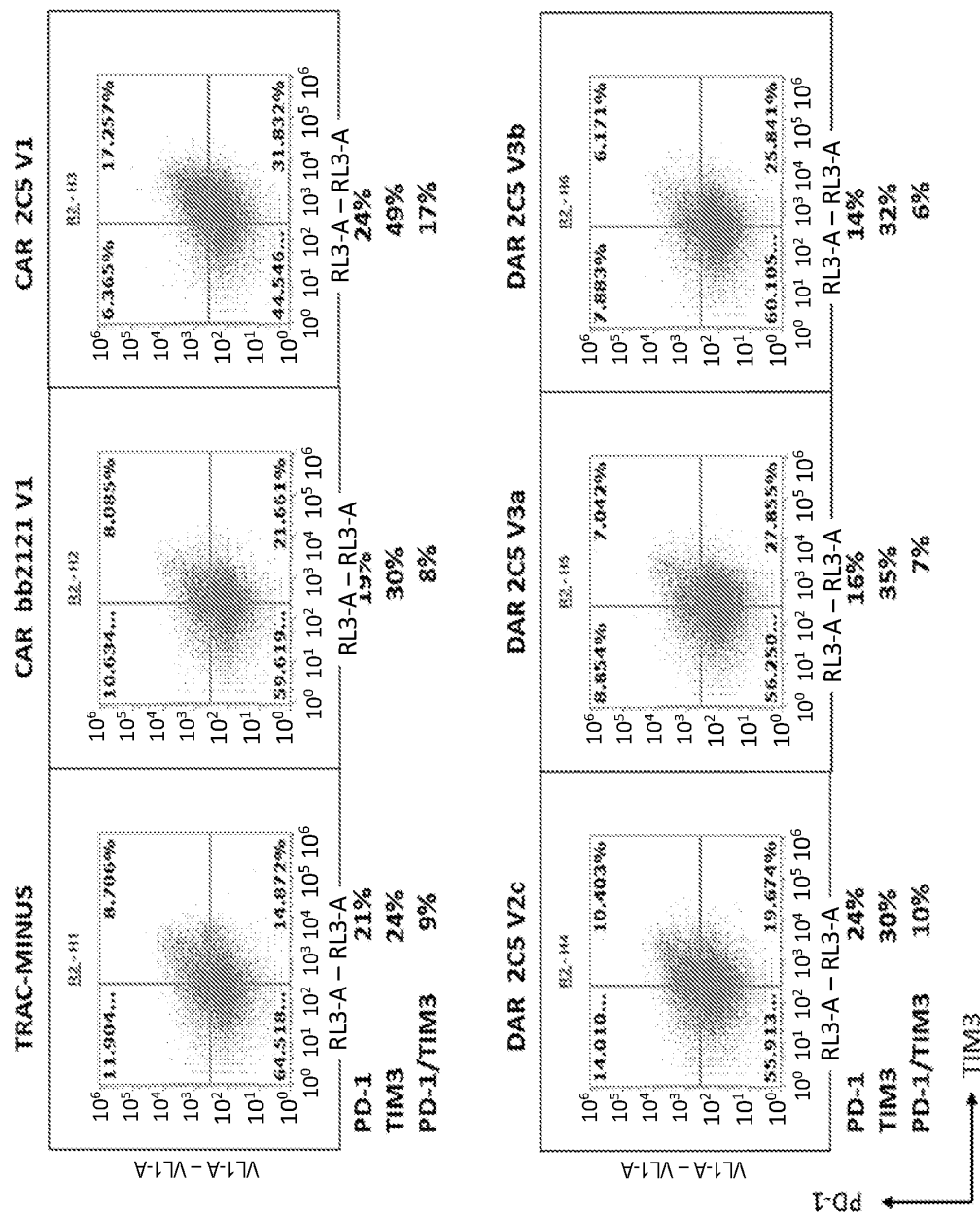
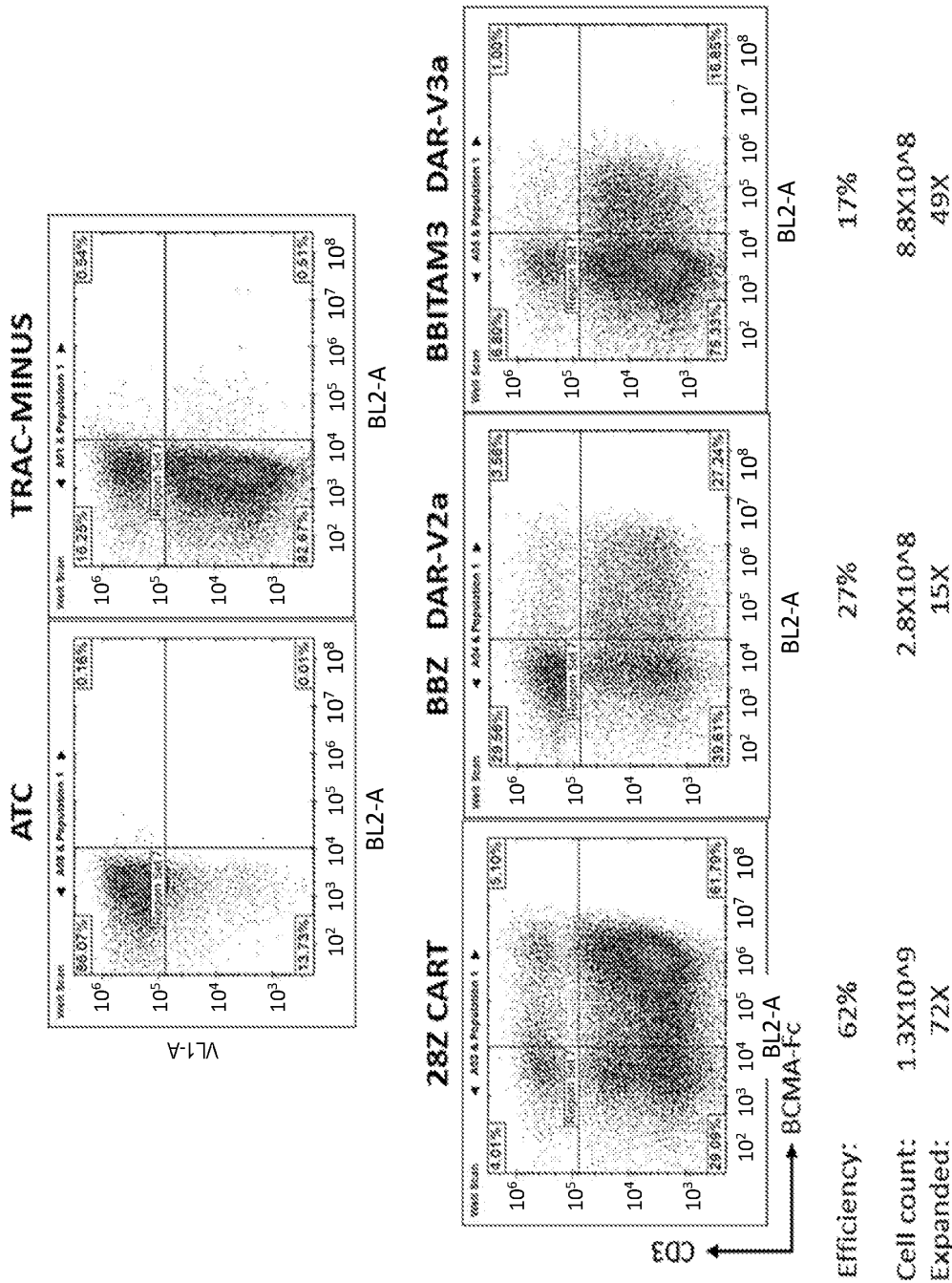


FIG. 13C



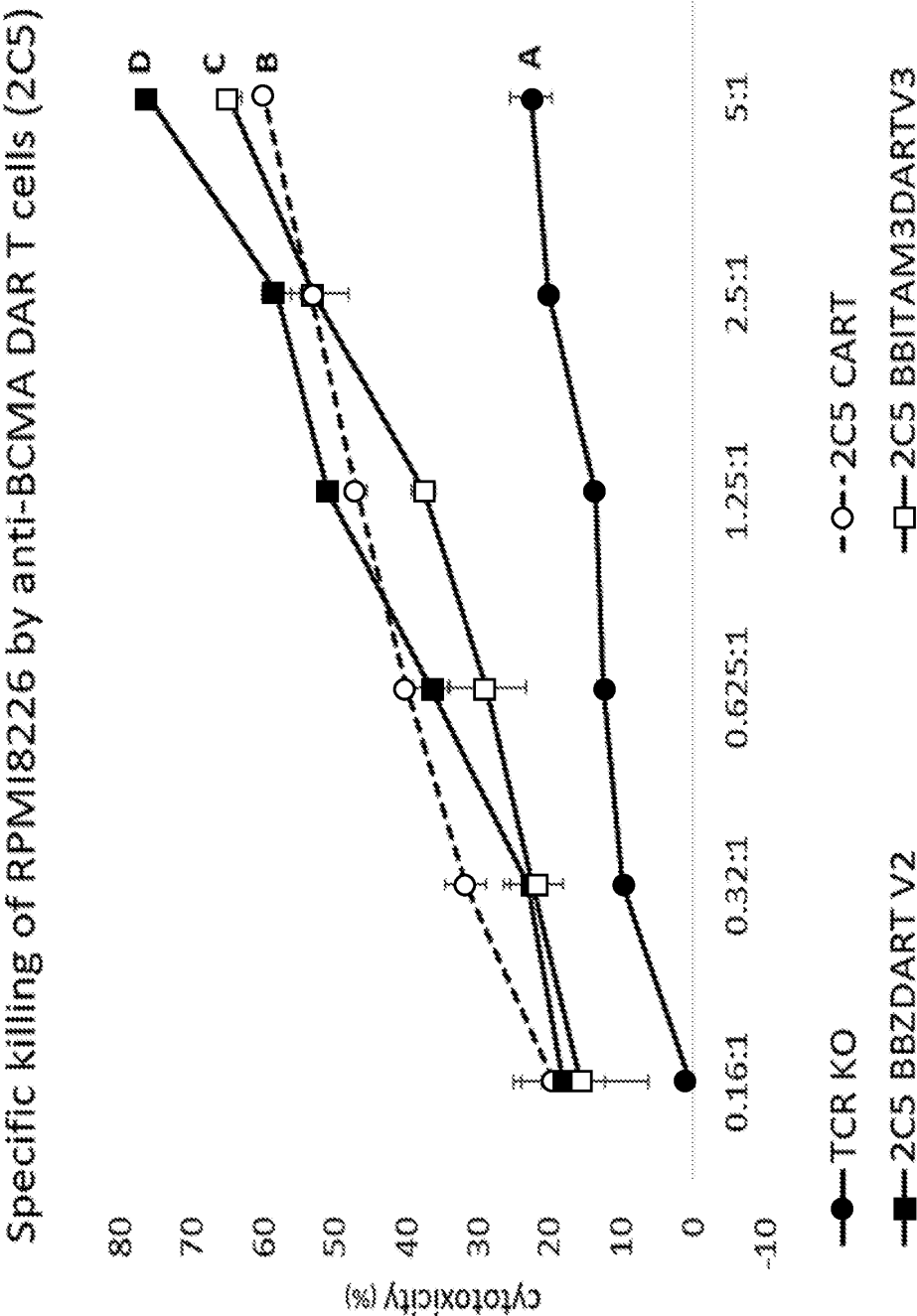


FIG. 15

TRAC-minus

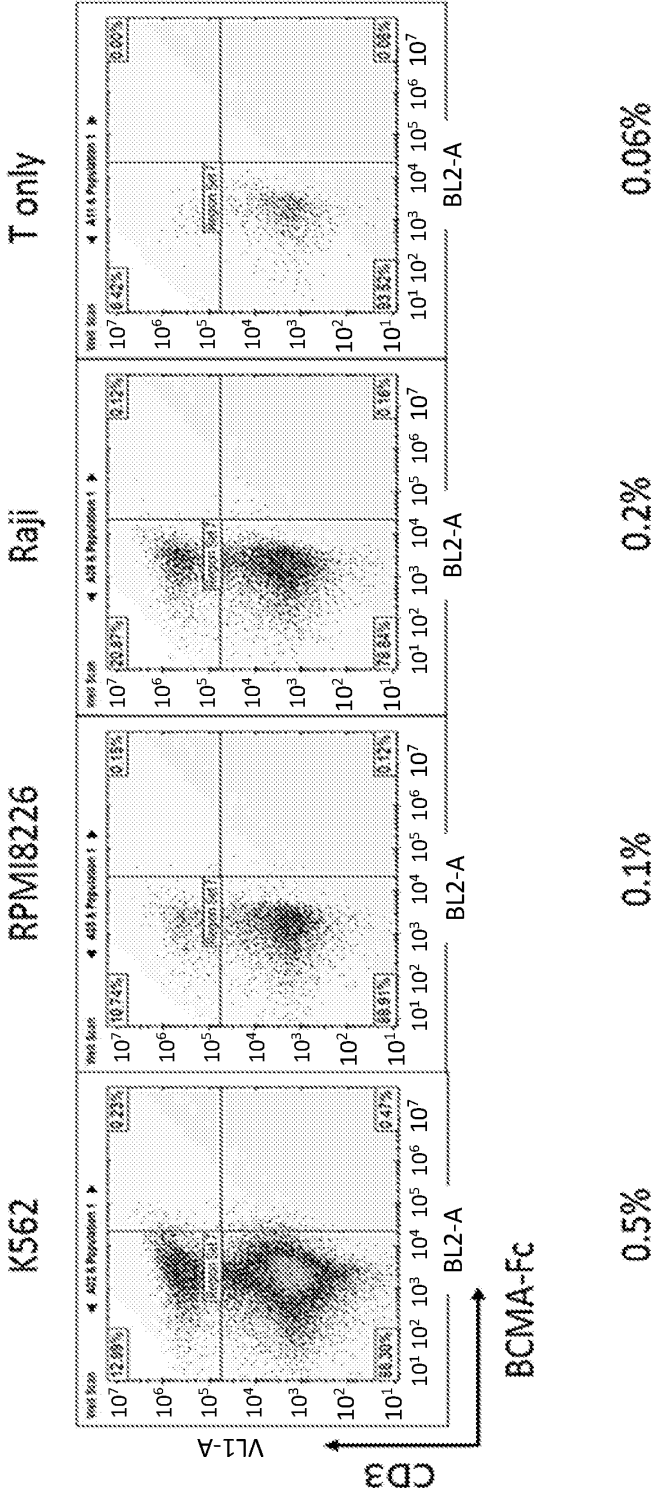


FIG. 16A

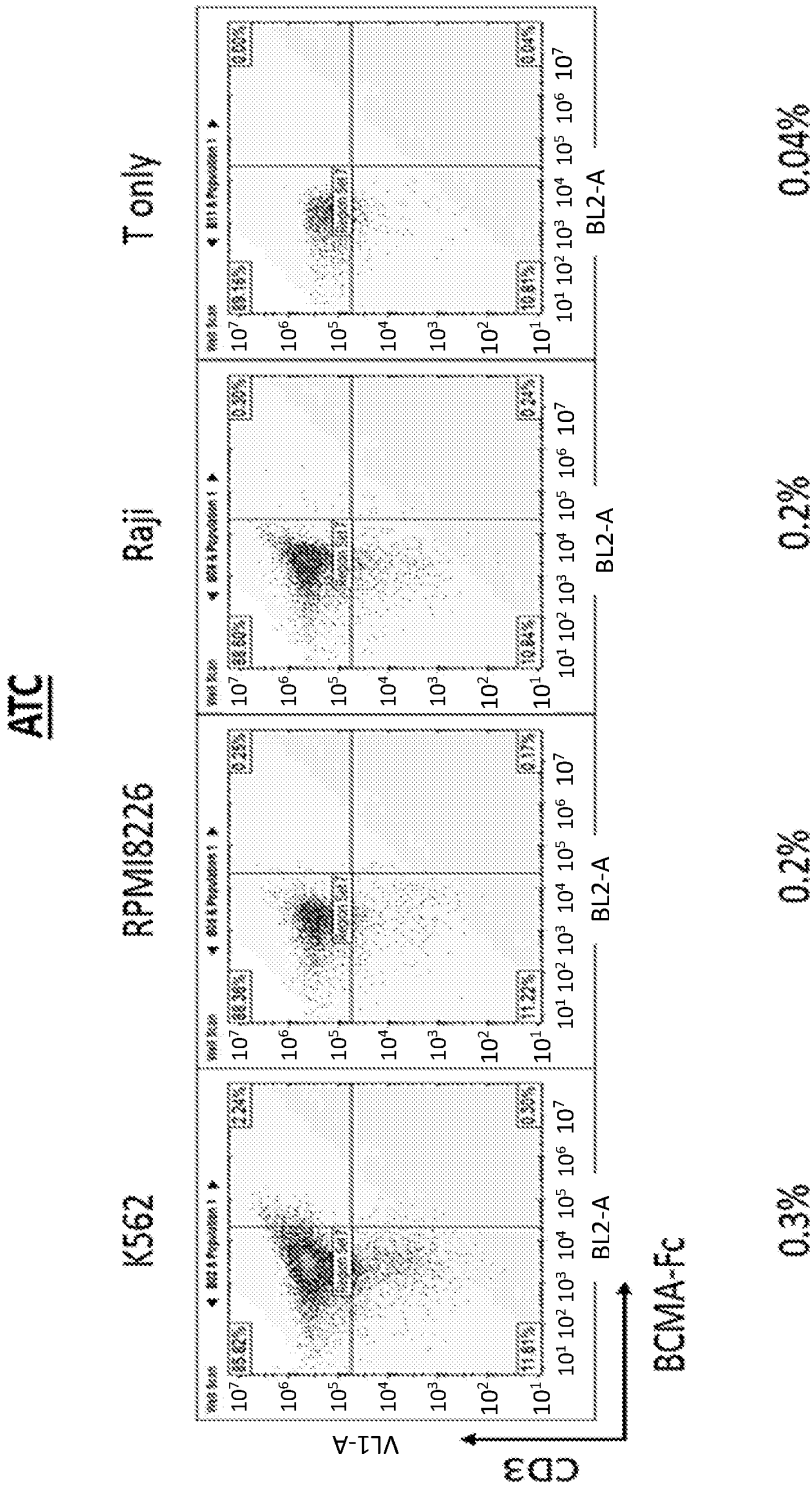


FIG. 16B

28Z CAR

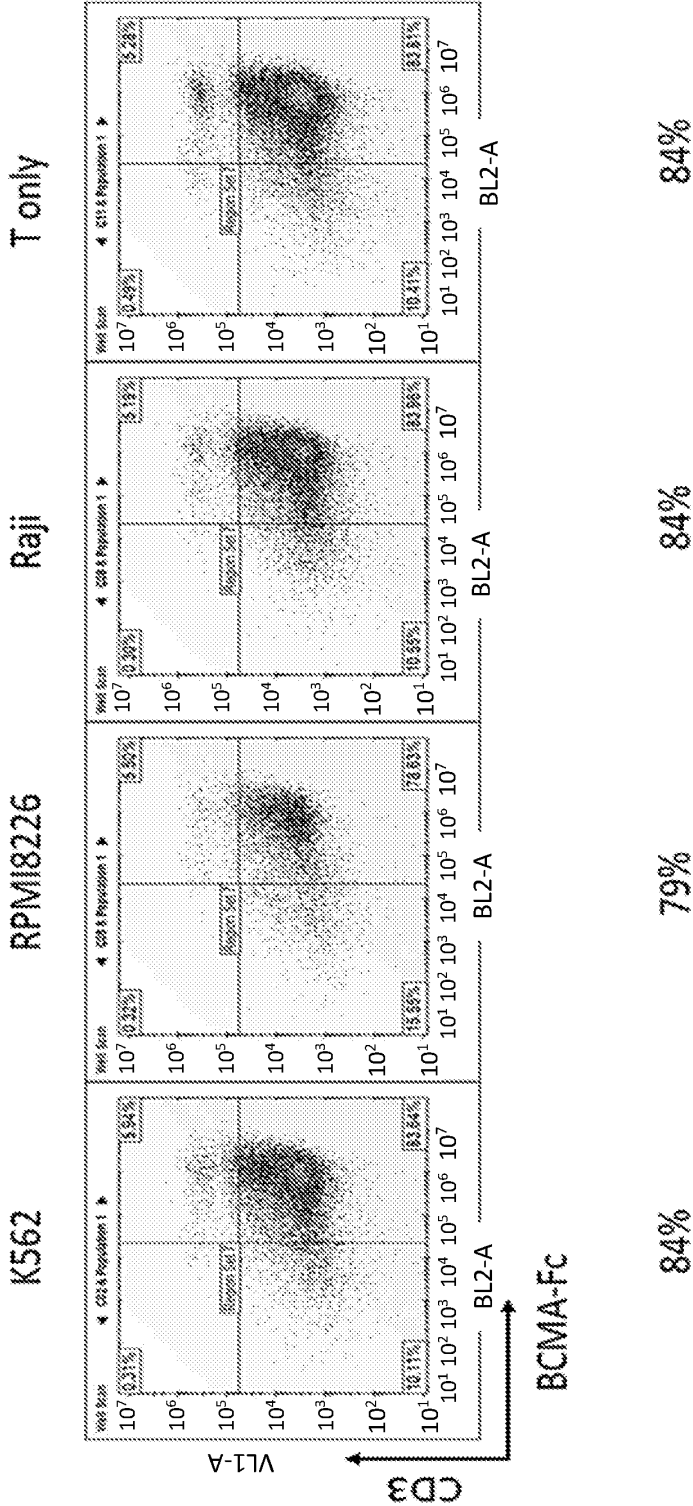


FIG. 16C

BBZ DAR V2a

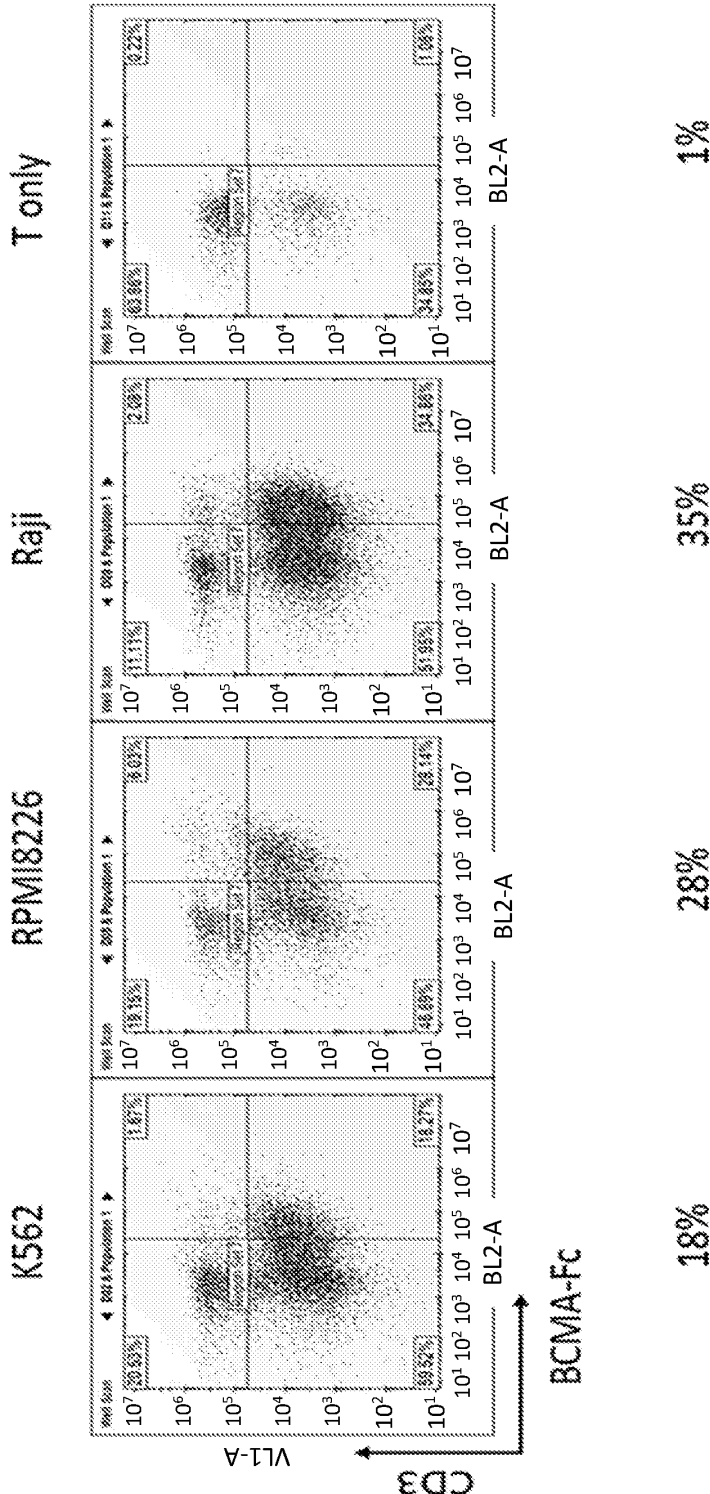


FIG. 16D

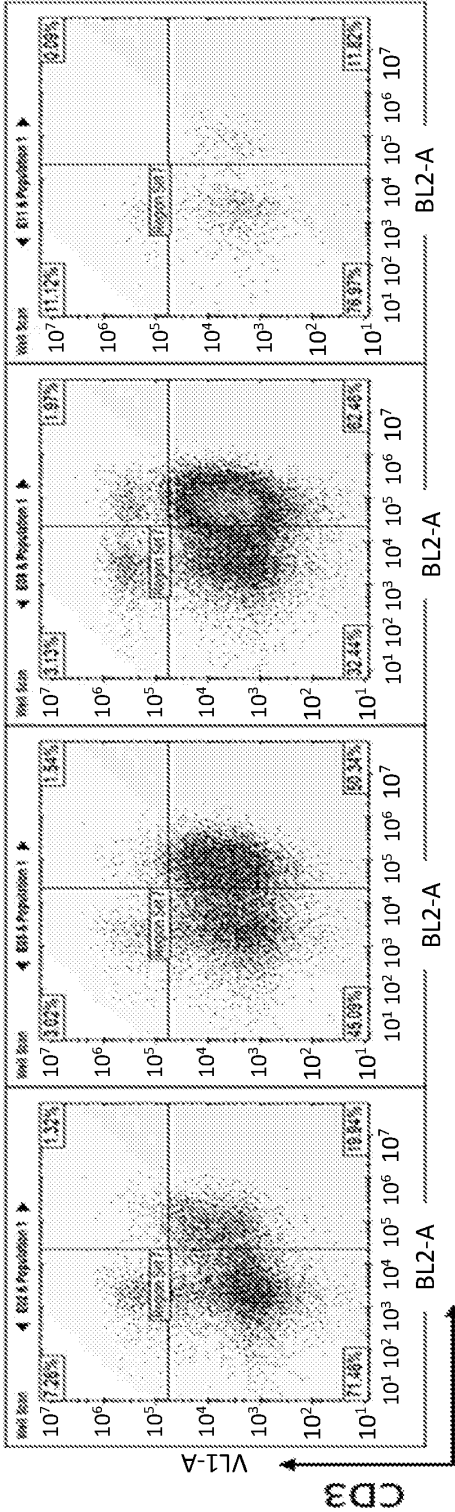
BBITAM3 DAR V3a

T only

Raji

RPMI8226

K562



BCMA-Fc

20%

50%

62%

12%

FIG. 16E

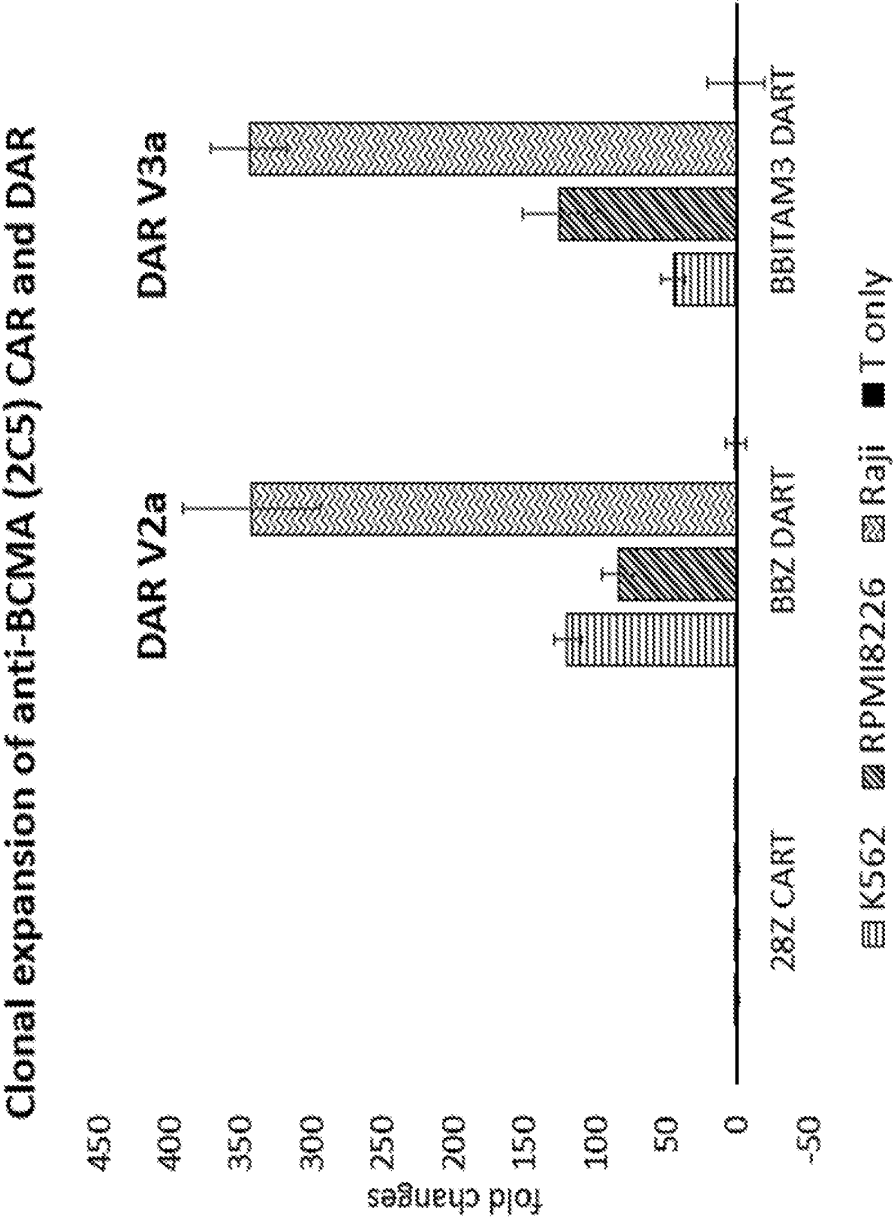


FIG. 17

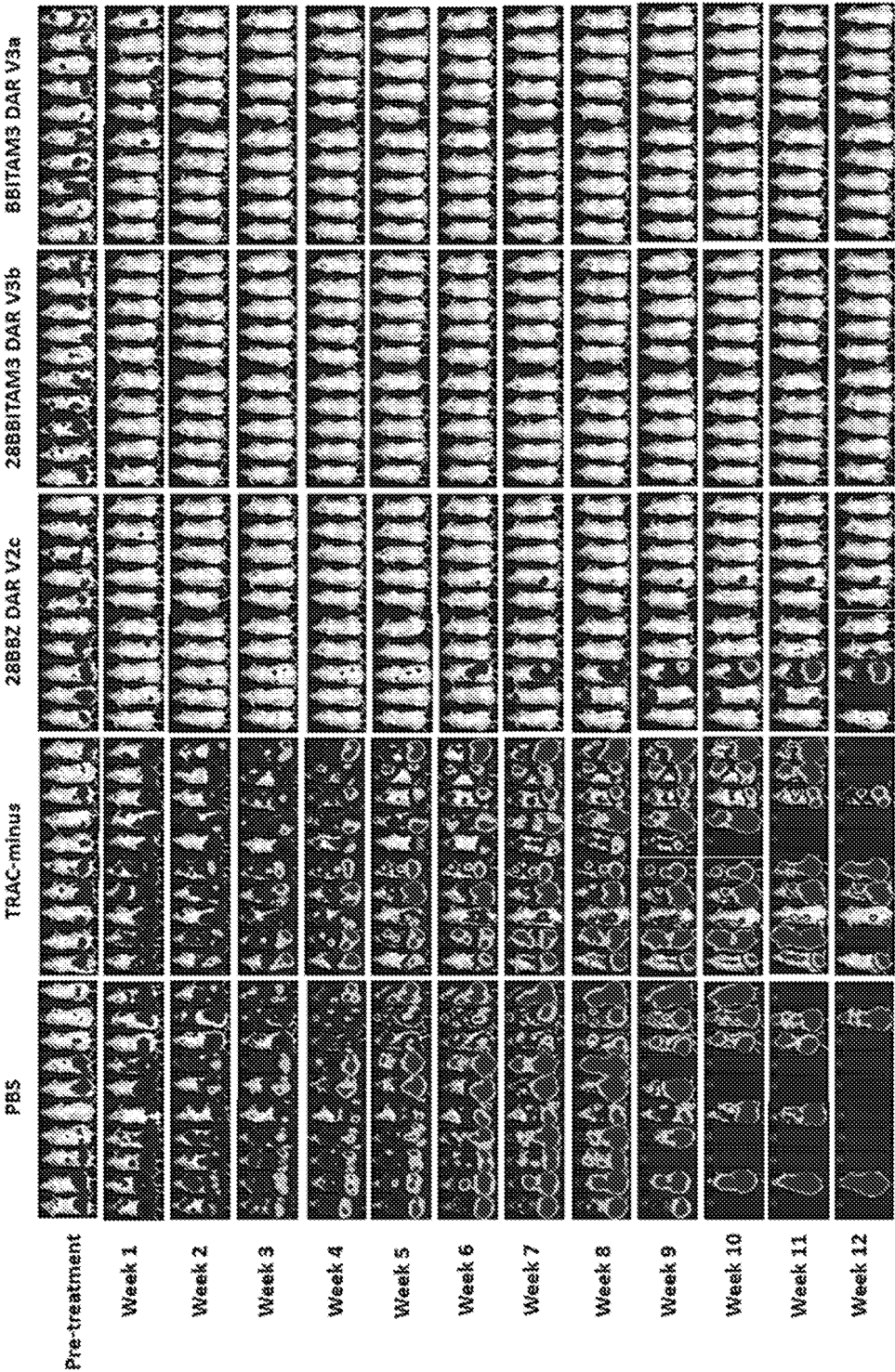


FIG. 18A

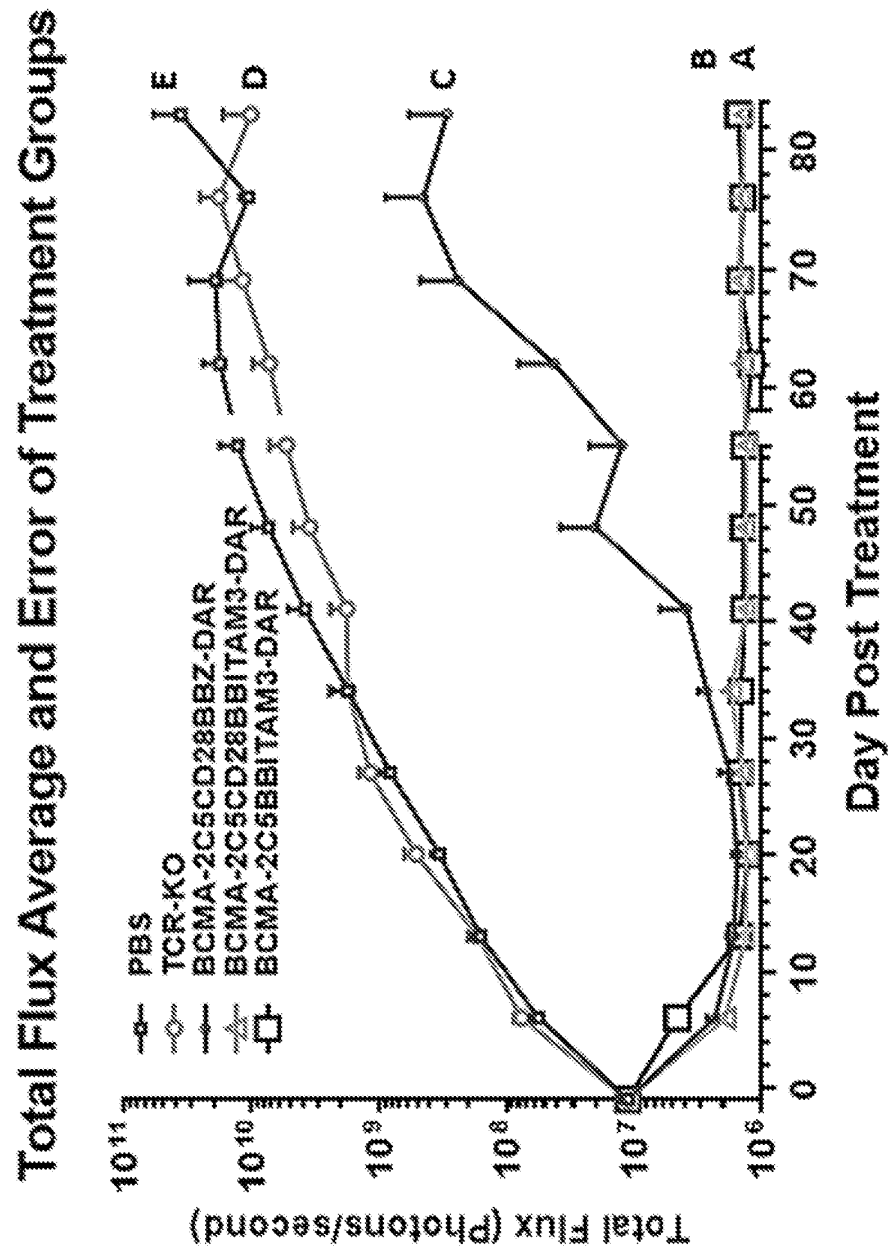


FIG. 18B

Tumor Growth Inhibition Index		Day 0	Week 1	Week 2	Week 3	Week 4	Week 5	Week 6	Week 7	Week 8
V2c	PBS	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
	TCR-KO	-0.55%	-36.31%	-5.90%	-51.38%	-44.95%	0.43%	52.558%	52.376%	58.379%
	BCMA-2C5CD28BBZ-DAR	-0.63%	95.84%	98.98%	99.54%	99.84%	99.88%	99.912%	99.733%	99.906%
	BCMA-2C5CD28BBITAM3-DAR	-0.52%	96.54%	99.17%	99.61%	99.89%	99.93%	99.979%	99.989%	99.994%
V3a	BCMA-2C5BBITAM3-DAR	-0.01%	91.82%	99.07%	99.62%	99.88%	99.95%	99.977%	99.988%	99.993%

FIG. 18C

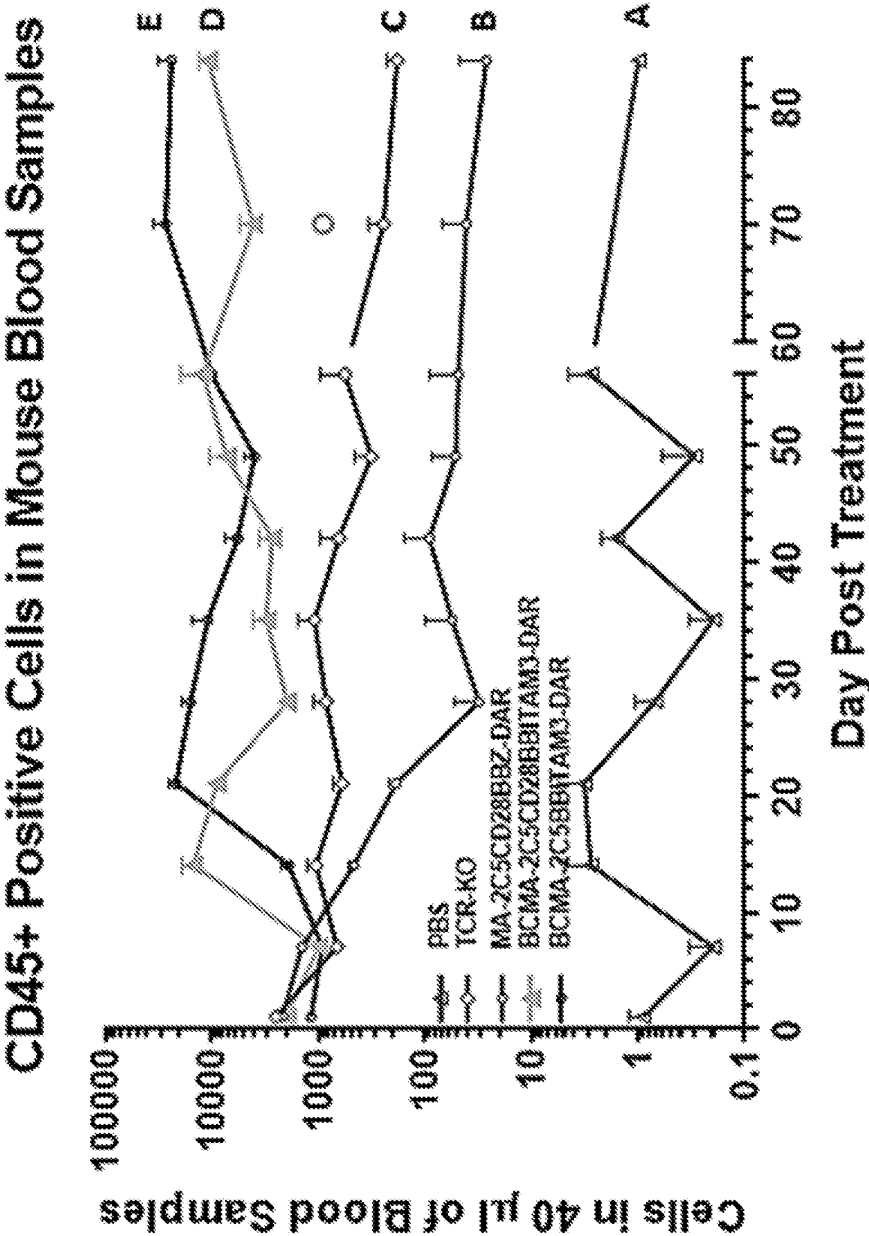


FIG. 18D

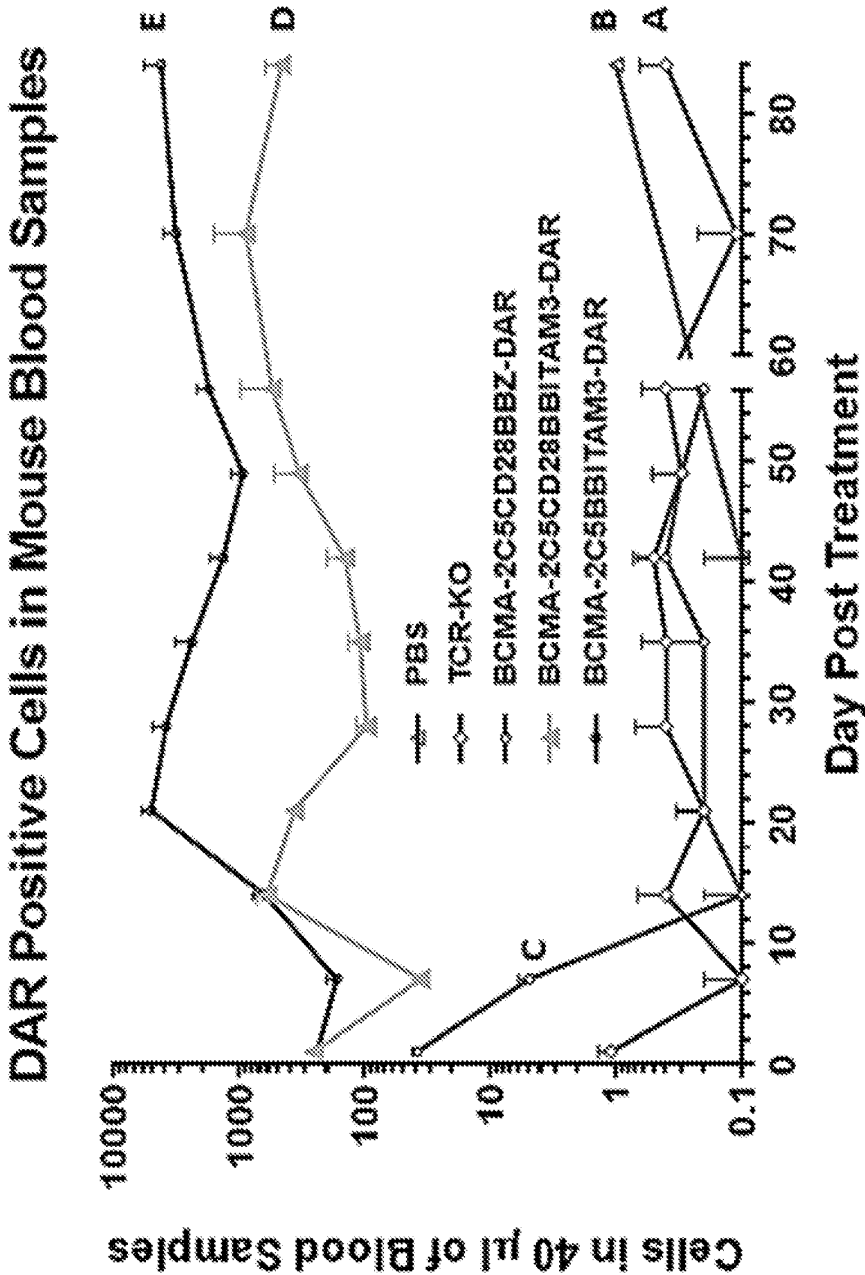


FIG. 18E

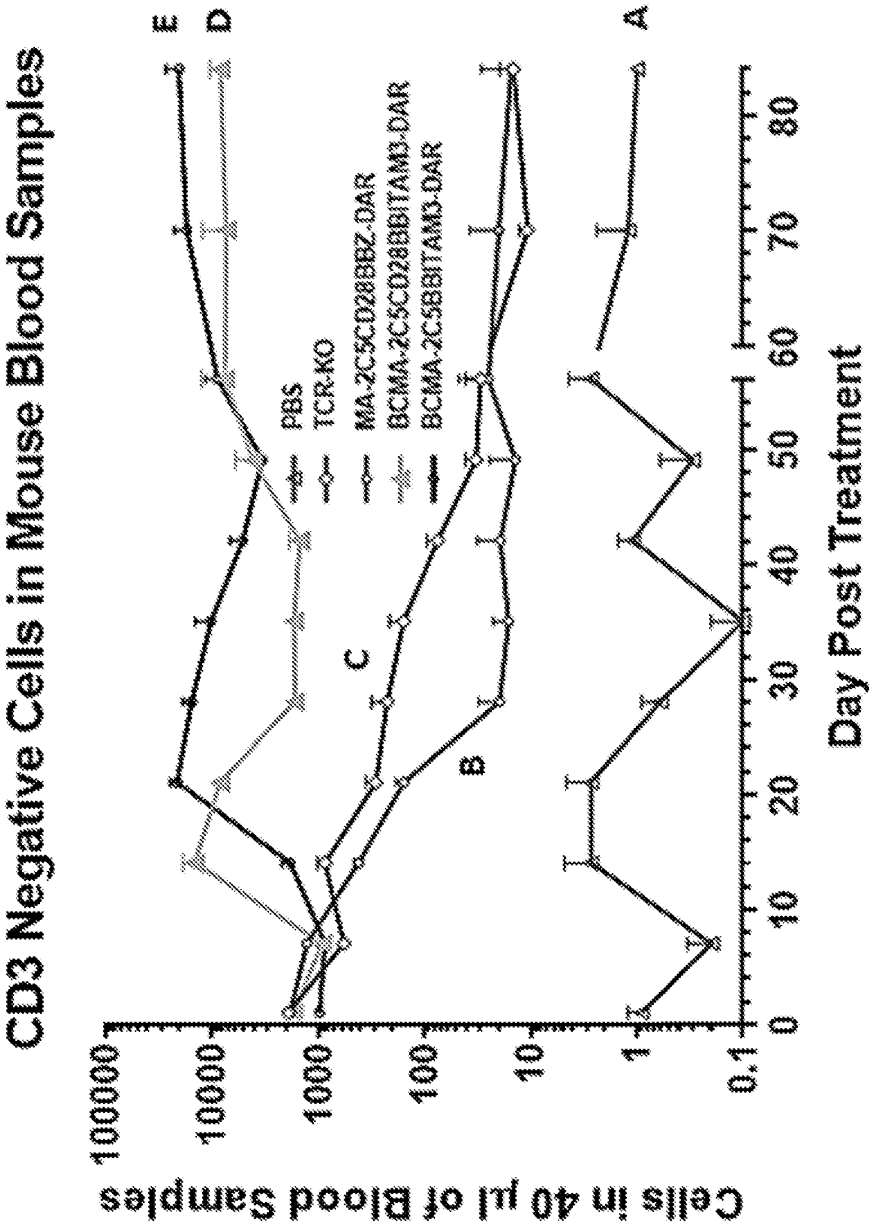


FIG. 18F

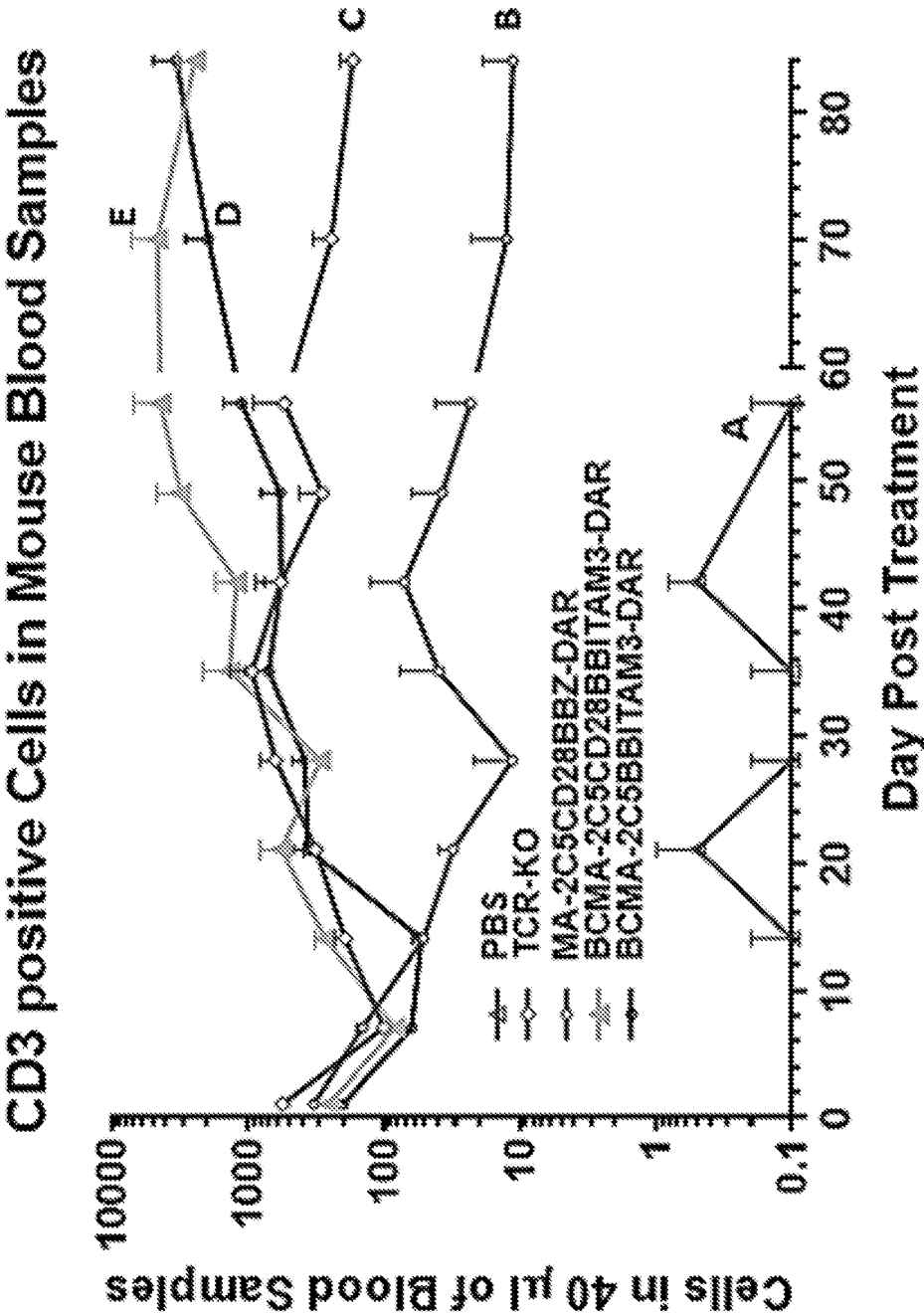


FIG. 18G

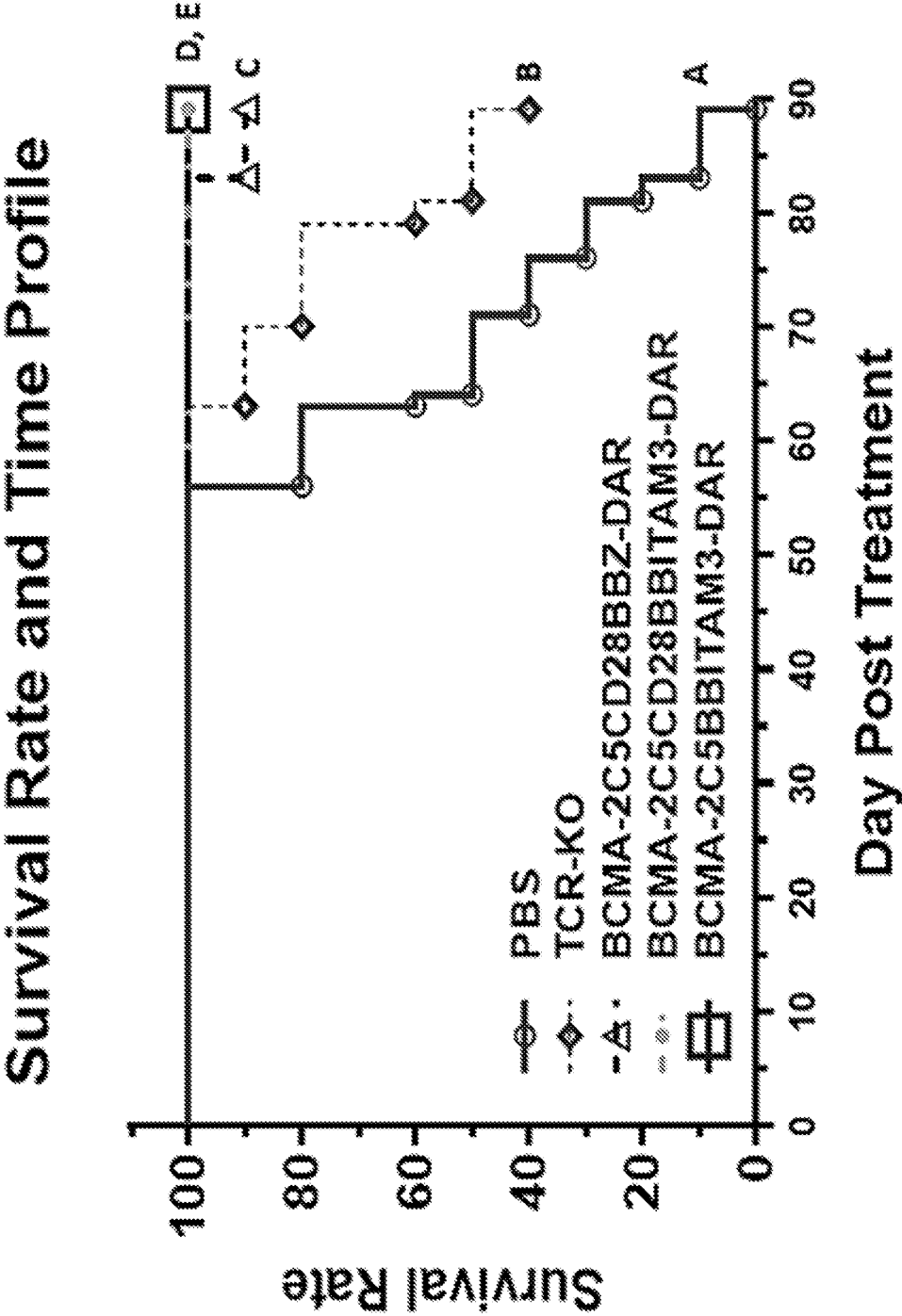


FIG. 18H

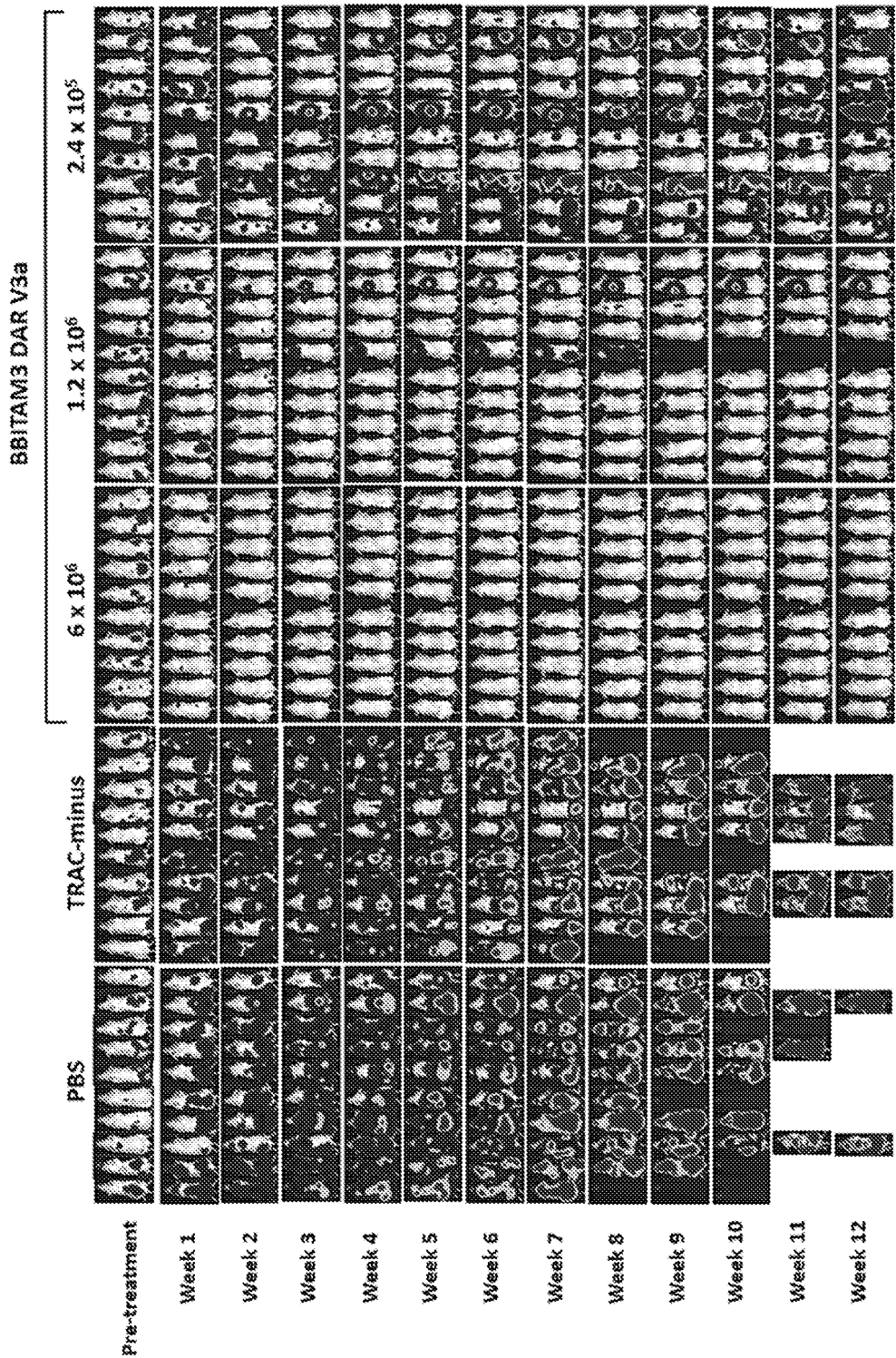


FIG. 19A

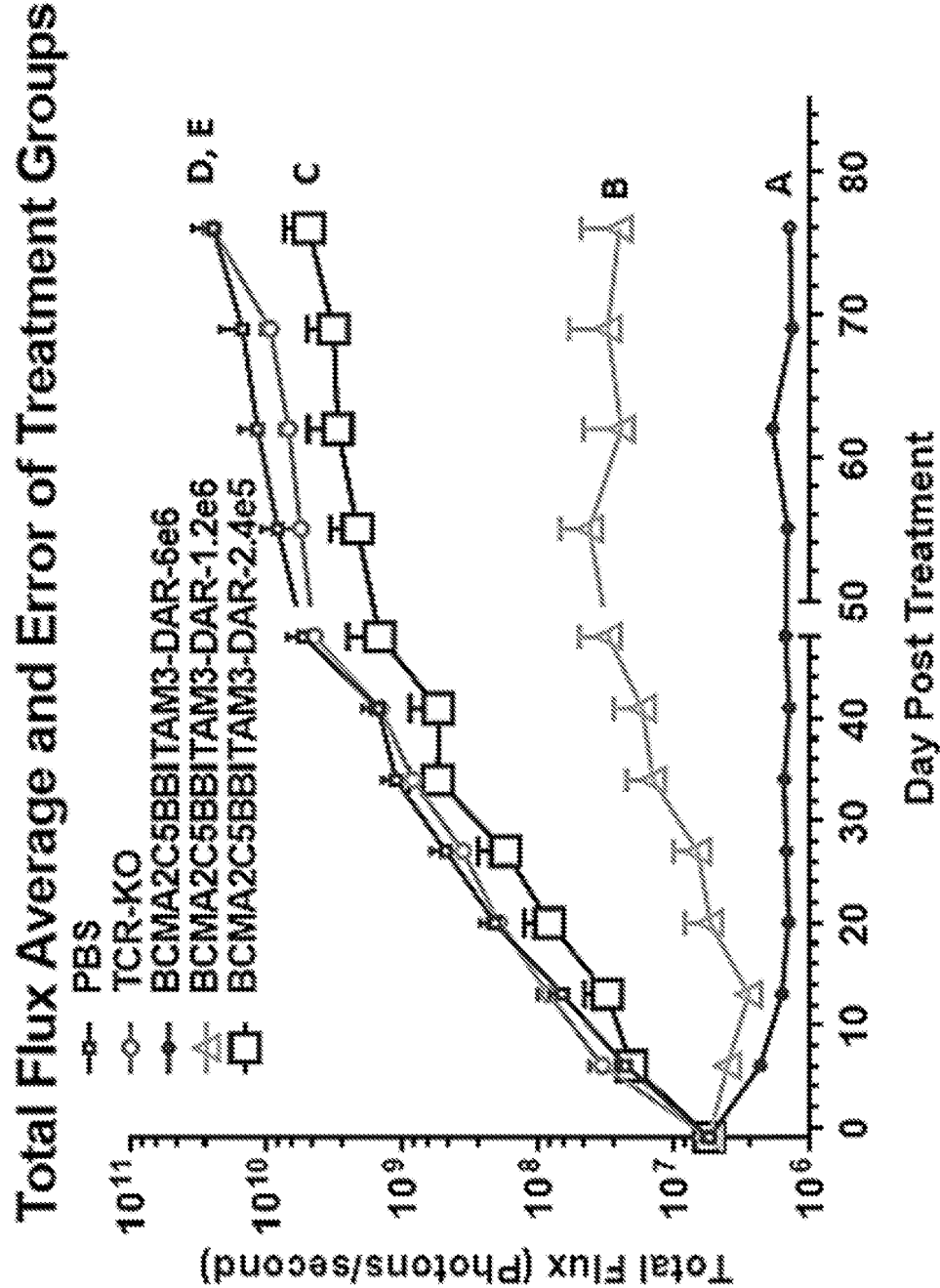


FIG. 19B

	Tumor Growth Inhibition Index	Day 0	Week 1	Week 2	Week 3	Week 4	Week 5	Week 6	Week 7
	PBS	0.0%	0.00%	0.00%	0.0%	0.000%	0.000%	0.000%	0.000%
	TCR-KO	0.2%	-48.86%	-24.92%	6.1%	25.036%	24.615%	3.120%	17.450%
V3a	BCMA2C5BBITA M3-DAR-9e6	0.2%	89.69%	97.60%	99.3%	99.793%	99.906%	99.939%	99.981%
V3a	BCMA2C5BBITA M3-DAR-1.2e6	0.3%	82.11%	95.78%	97.4%	98.705%	98.763%	98.887%	99.444%
V3a	BCMA2C5BBITA M3-DAR-2.4e5	0.3%	9.14%	53.86%	60.3%	63.450%	50.493%	63.780%	72.561%

FIG. 19C

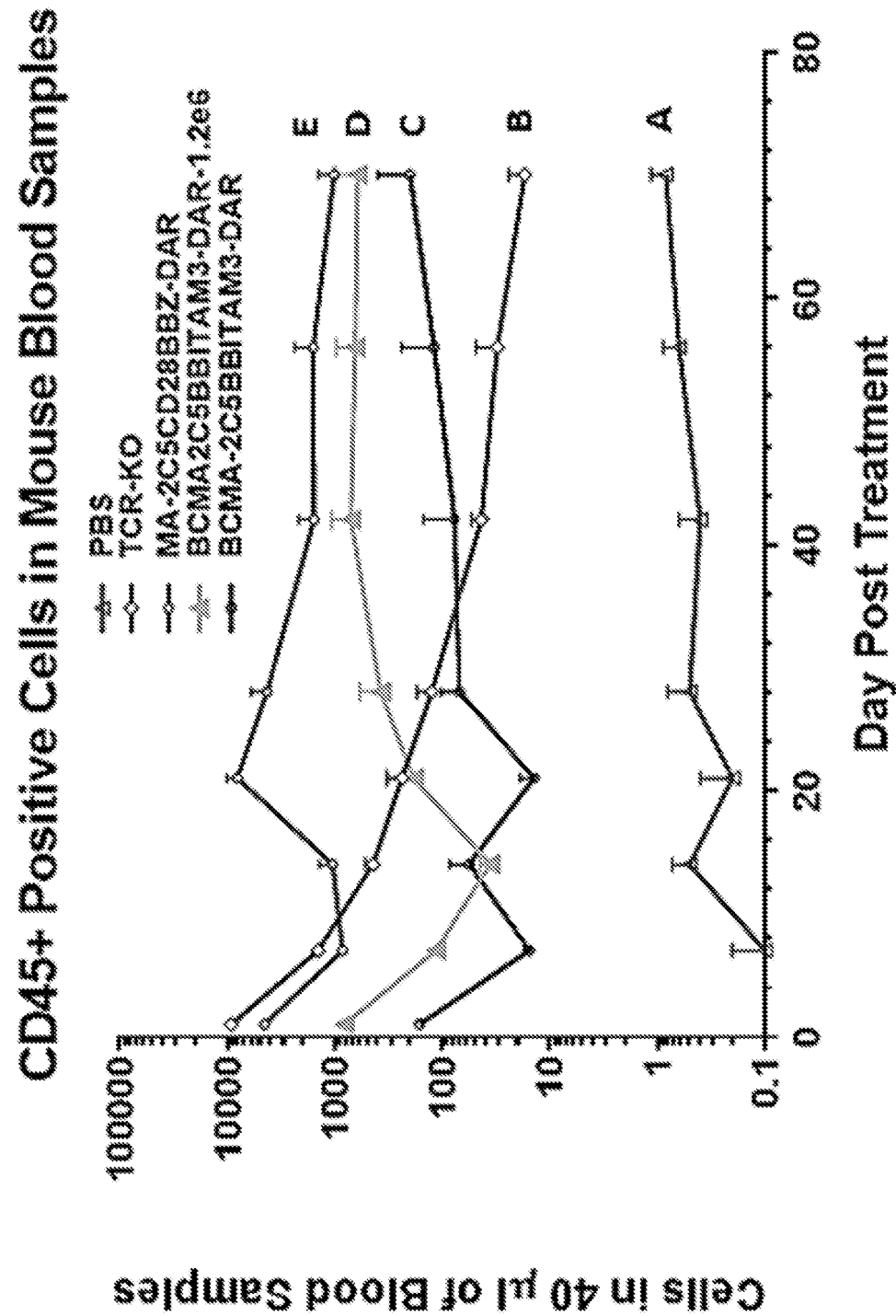


FIG. 19D

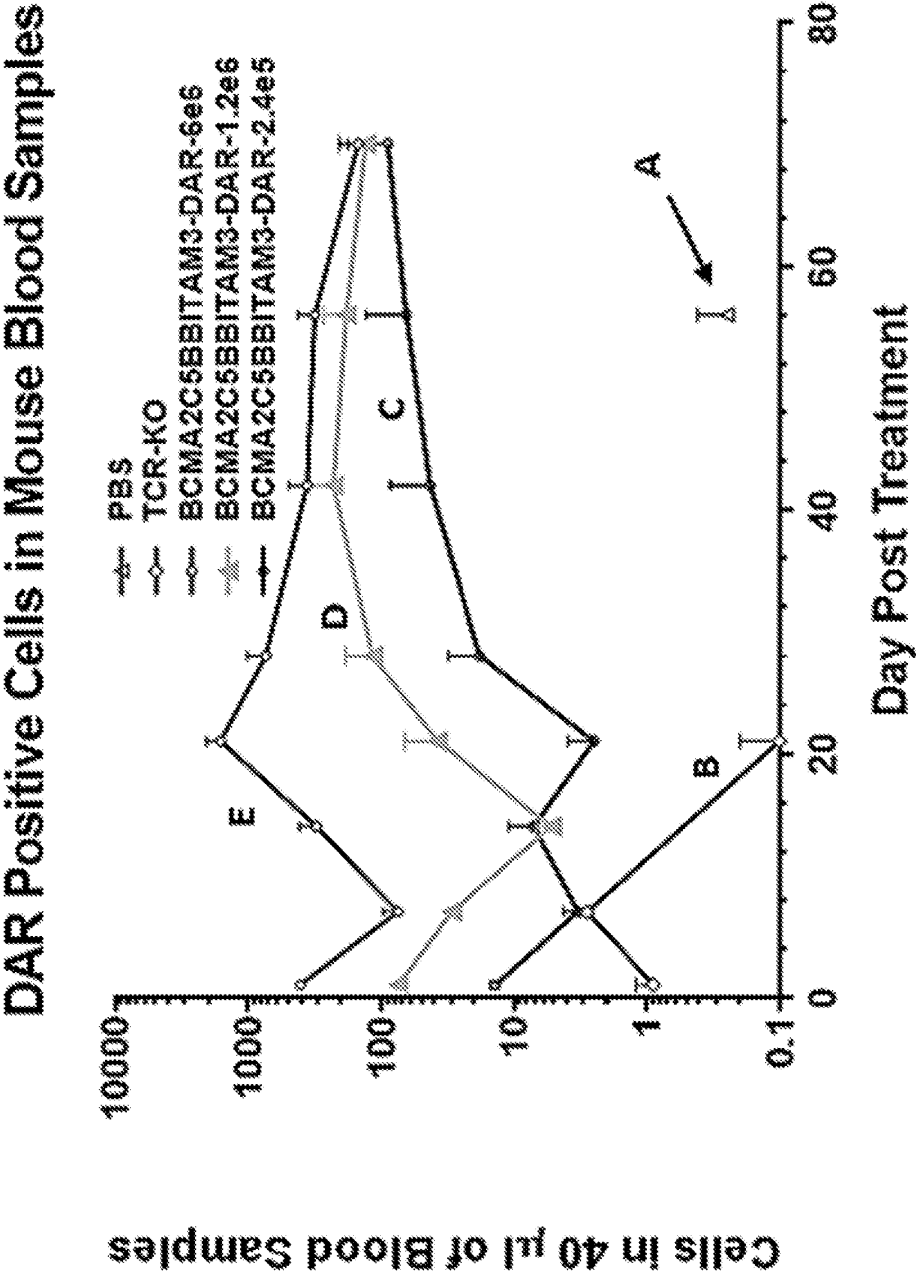


FIG. 19E

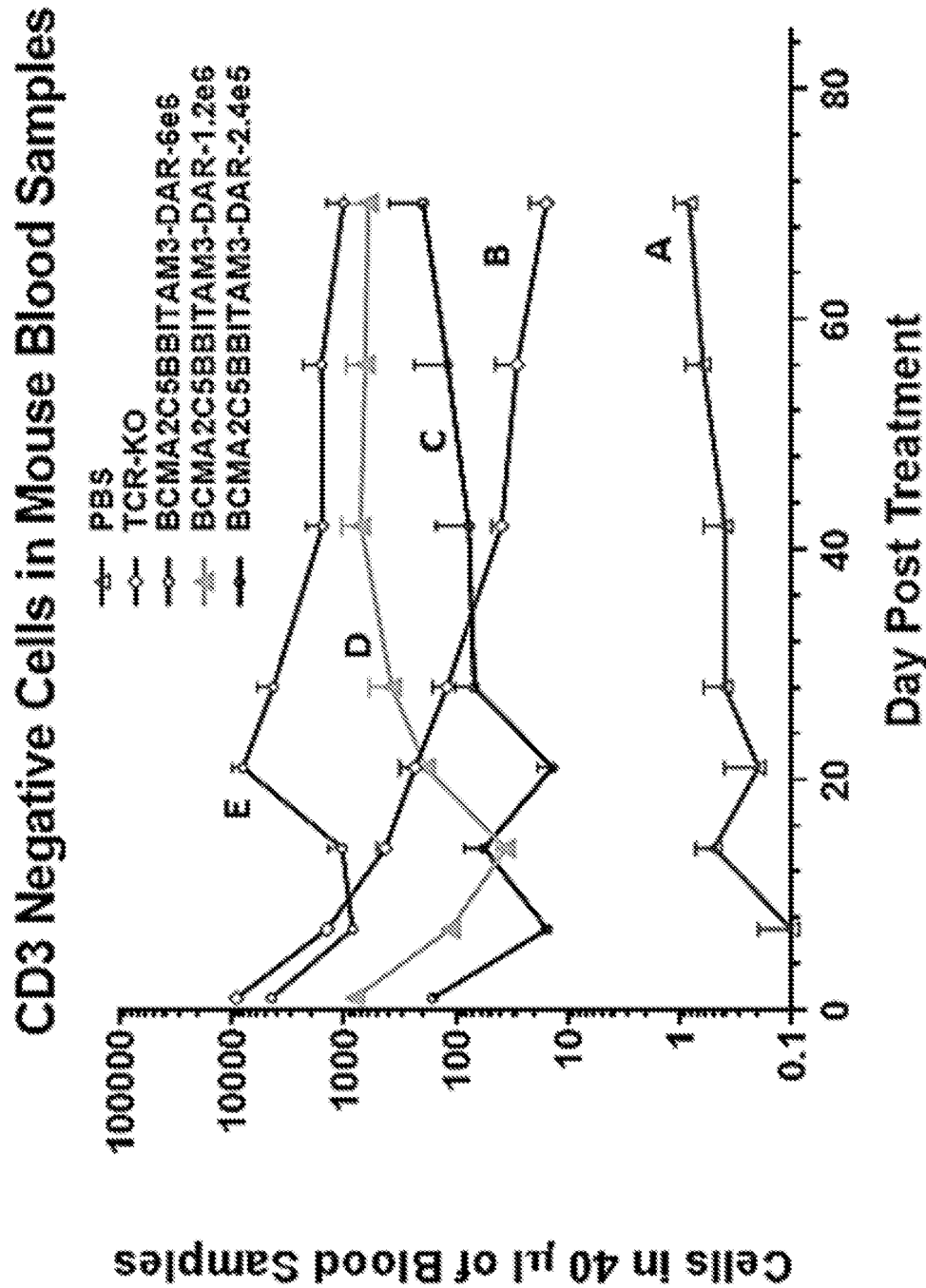


FIG. 19F

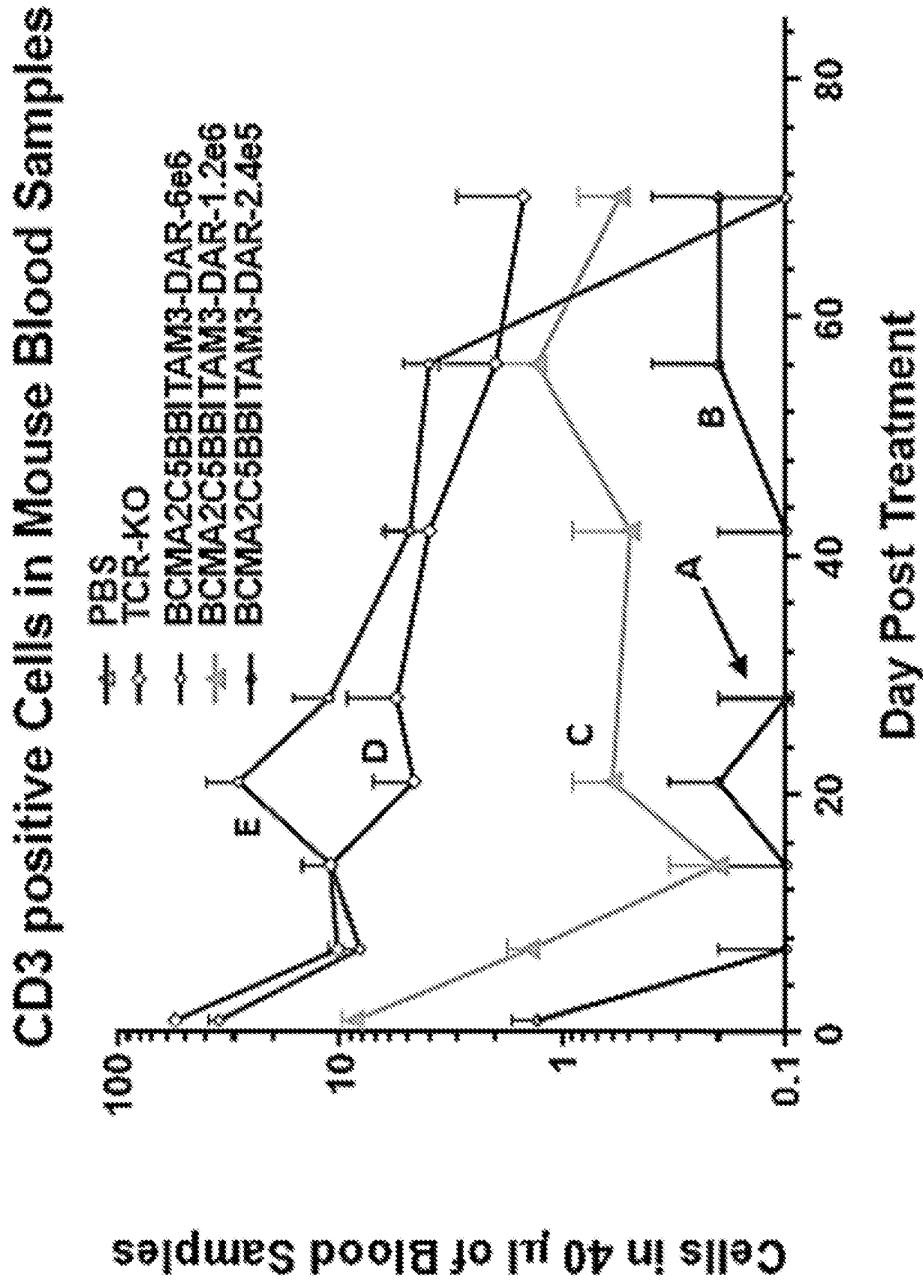


FIG. 19G

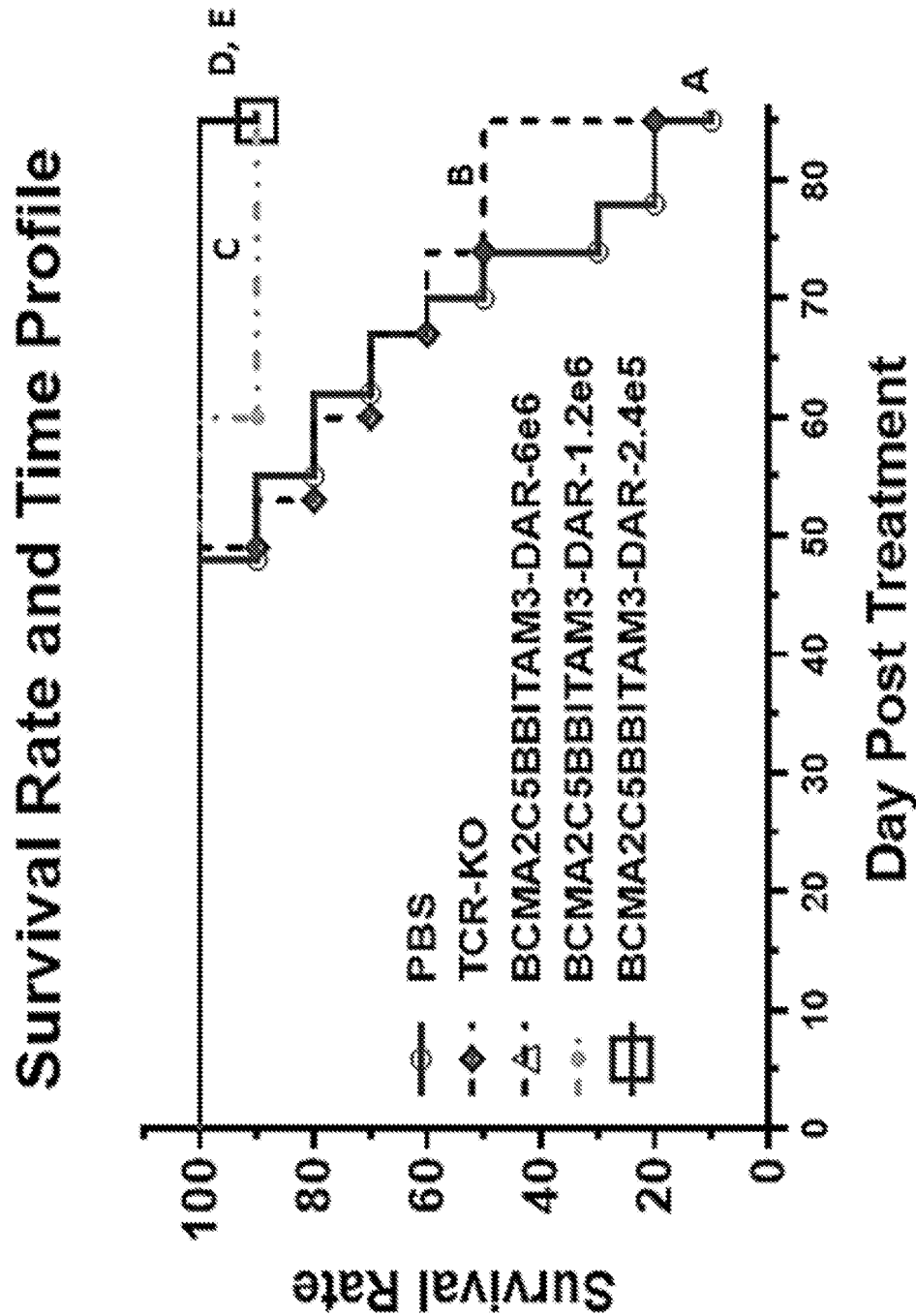


FIG. 19H

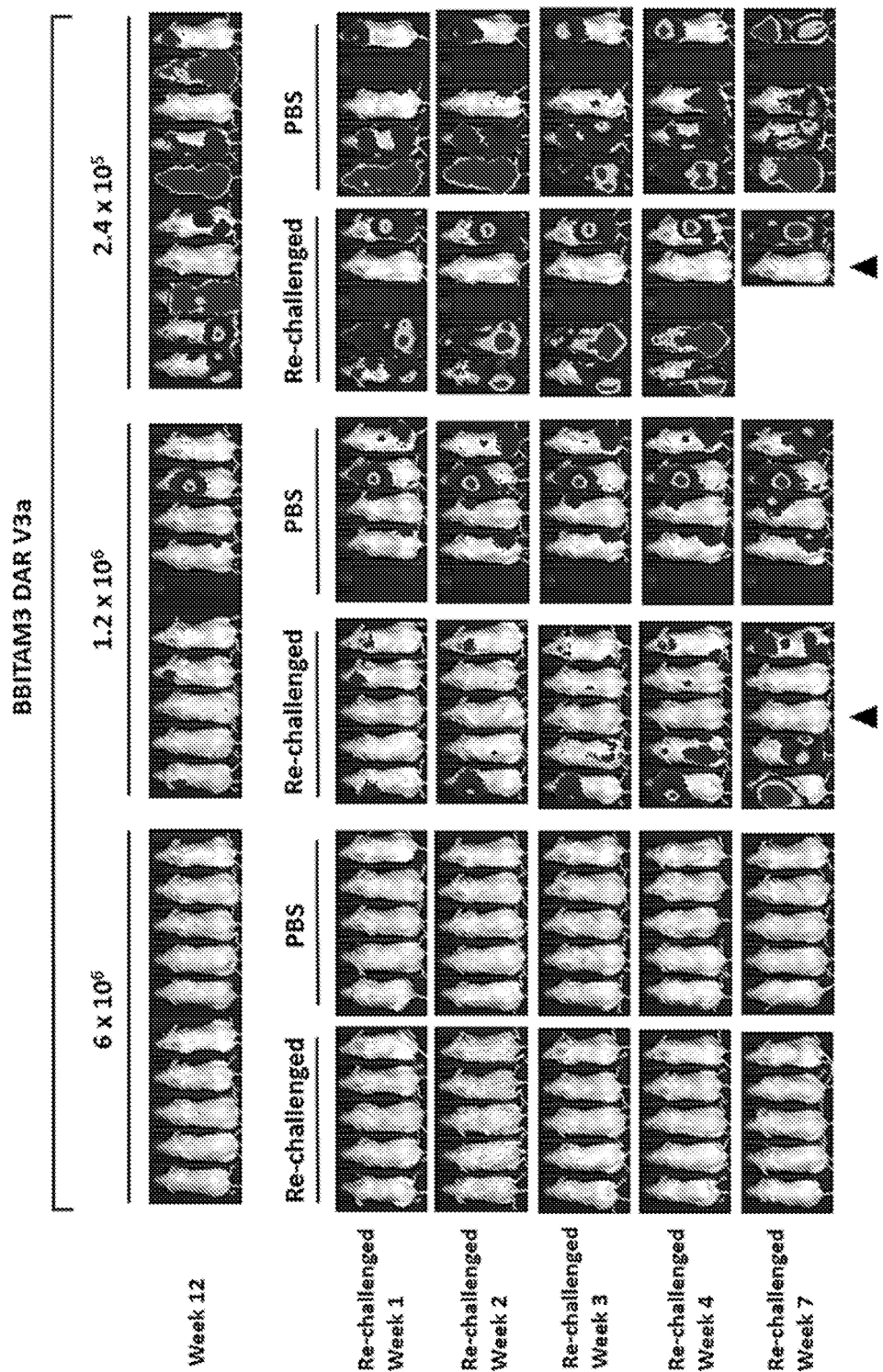


FIG. 20A

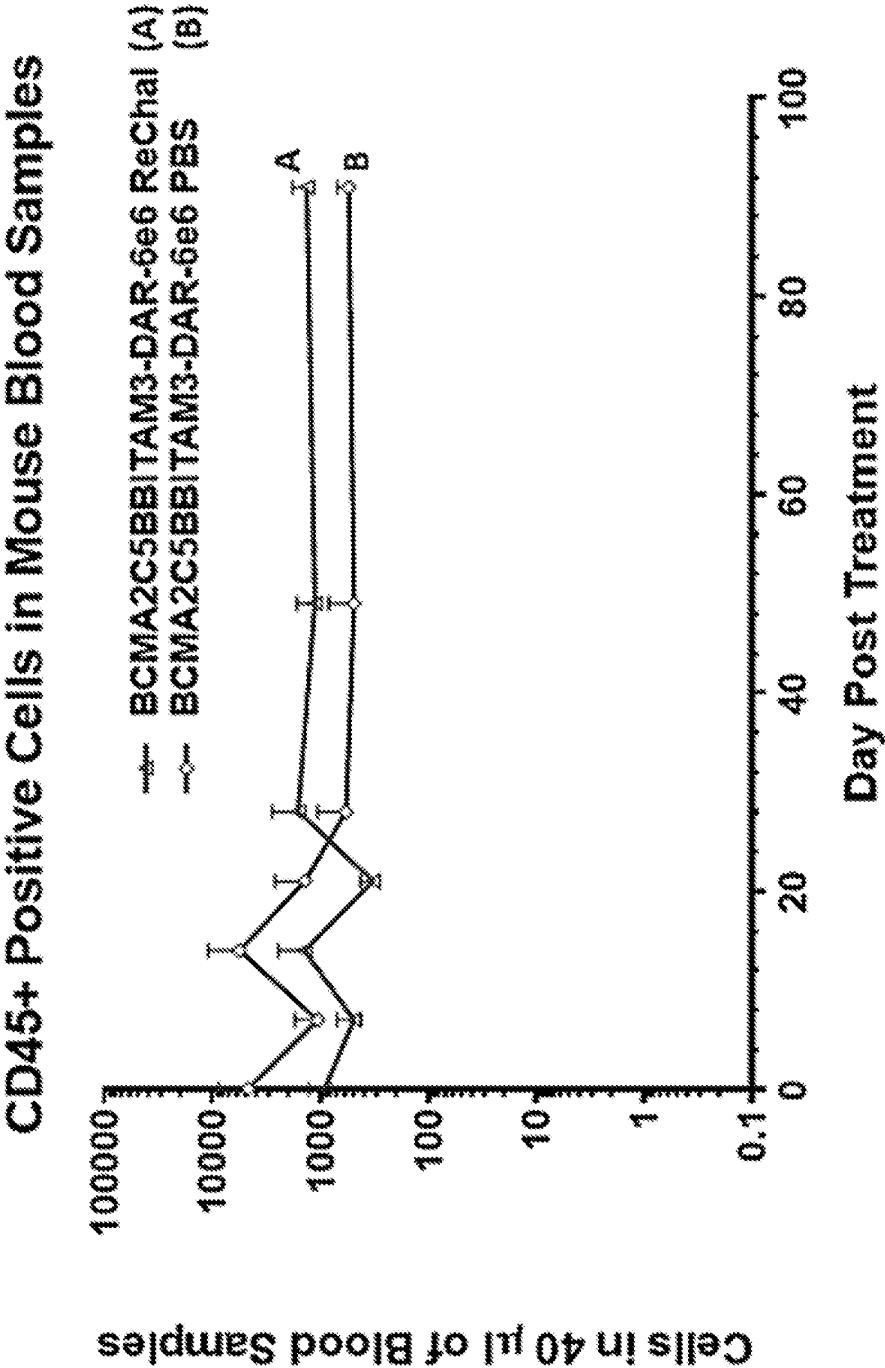


FIG. 20B

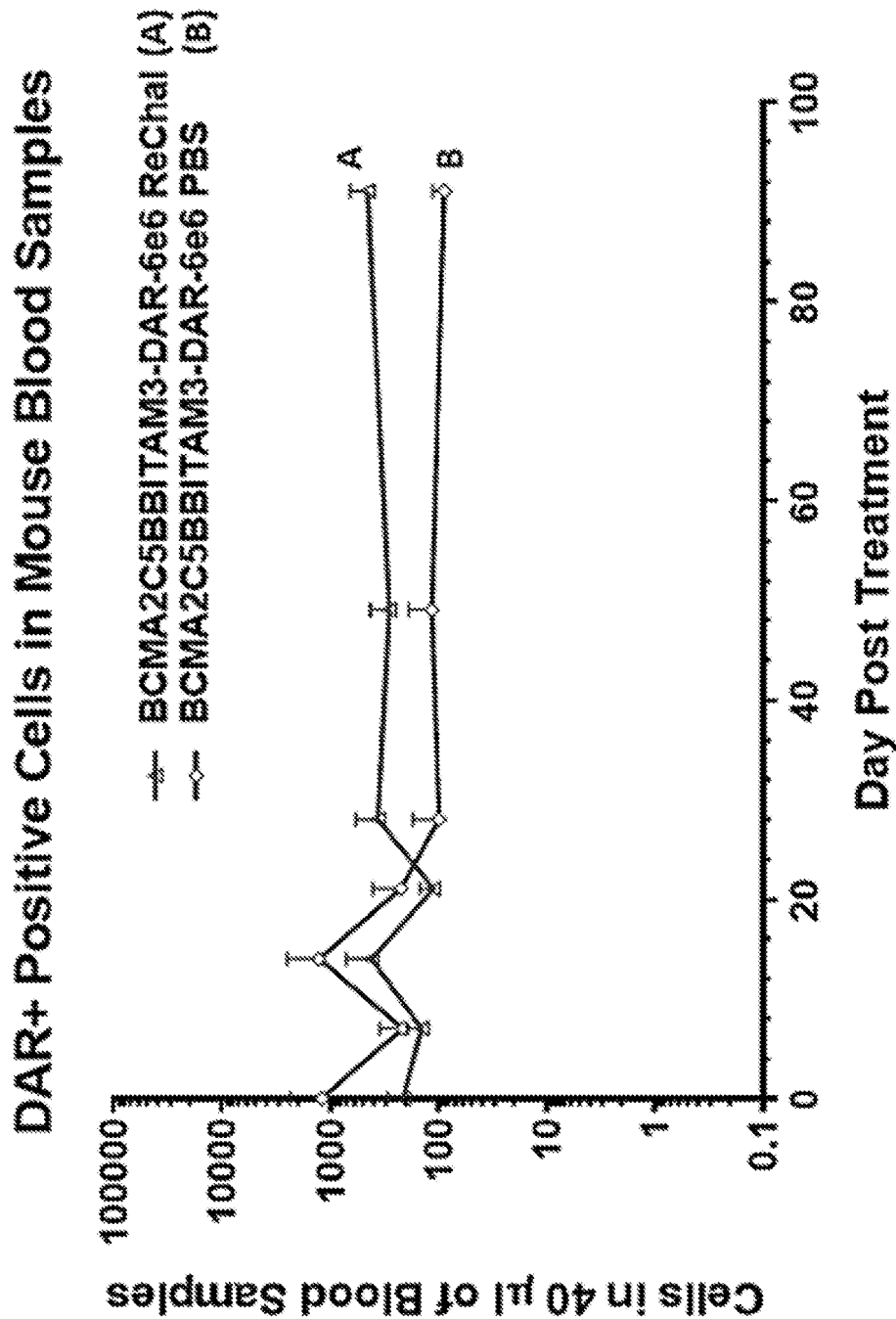


FIG. 20C

Wild type human BCMA antigen SEQ ID NO:1
MLQMAGQCSQNEYFD¹SL²LHACIP³Q⁴LRCSNT⁵P⁶PL⁷TCQRYCNASVTNSVKG⁸TNA

Mutant-1 human BCMA antigen SEQ ID NO:2
MLQMAGQCSQNEYFD¹S²GGHACIP³Q⁴LRCSNT⁵P⁶PL⁷TCQRYCNASVTNSVKG⁸TNA

Mutant-2 human BCMA antigen SEQ ID NO:3
MLQMAGQCSQNEYFD¹SL²LHACIP³Q⁴LRCSNPP⁵GTCQRYCNASVTNSVKG⁸TNA

Human APRIL antigen SEQ ID NO:4
MPASSPFL¹LAPK²PPGNMGGPV³REPAL⁴SV⁵ALWLS⁶GAAL⁷GAVACAMALL⁸TQ⁹TELQ¹⁰SLRR¹¹EVSR¹²LQ¹³TG¹⁴GGPSQ¹⁵NGEGYP¹⁶WQSL¹⁷PEQ¹⁸SSD¹⁹
ALEAWENGERSR²⁰KRR²¹AVL²²TQ²³K²⁴Q²⁵HS²⁶VL²⁷HL²⁸VPIN²⁹ATSK³⁰DDSD³¹VE³²VMWQ³³PALRRGR³⁴GLQA³⁵QGY³⁶GVRI³⁷QDAGV³⁸LLYSQ³⁹VL⁴⁰FQ⁴¹DV⁴²TF⁴³TM⁴⁴
GQVVSREGQGR⁴⁵QETL⁴⁶FR⁴⁷CIR⁴⁸SMP⁴⁹SH⁵⁰PD⁵¹RAYNS⁵²CYSAG⁵³V⁵⁴FHL⁵⁵HQ⁵⁶DI⁵⁷LS⁵⁸VI⁵⁹IP⁶⁰R⁶¹AK⁶²LN⁶³LS⁶⁴PH⁶⁵GT⁶⁶FL⁶⁷GF⁶⁸V⁶⁹KL⁷⁰

Human BAFF antigen SEQ ID NO:5
MDDSTEREQ¹SR²LTS³CL⁴KK⁵RE⁶MK⁷LKE⁸CVS⁹IL¹⁰PR¹¹KES¹²PS¹³VR¹⁴SS¹⁵KD¹⁶GK¹⁷LLA¹⁸AT¹⁹LL²⁰ALL²¹SC²²CL²³TV²⁴VS²⁵FY²⁶Q²⁷VAAL²⁸QGD²⁹DLAS³⁰LRAEL³¹Q³²HH³³AE³⁴
KL³⁵PAGAGAPKAG³⁶LEAP³⁷AV³⁸TAG³⁹LKI⁴⁰FE⁴¹PPAP⁴²GEGNSS⁴³QNS⁴⁴RN⁴⁵KRA⁴⁶VQ⁴⁷GPEET⁴⁸VTQ⁴⁹DCL⁵⁰Q⁵¹LIAD⁵²SET⁵³PTIQ⁵⁴KGSY⁵⁵TF⁵⁶VPW⁵⁷LLS⁵⁸FK⁵⁹RGSAL⁶⁰
EEKEN⁶¹KIL⁶²VKET⁶³GY⁶⁴FFI⁶⁵YG⁶⁶QVLY⁶⁷TD⁶⁸KTYAM⁶⁹GHLI⁷⁰Q⁷¹RK⁷²KV⁷³HV⁷⁴FG⁷⁵DEL⁷⁶SL⁷⁷VT⁷⁸LF⁷⁹RCI⁸⁰Q⁸¹NMPET⁸²LP⁸³NNSCYSAGIA⁸⁴KLEEG⁸⁵DEL⁸⁶QLAIP⁸⁷REN⁸⁸
AQISLDGDV⁸⁹TF⁹⁰FGALK⁹¹LL⁹²

FIG. 21

Anti-BCMA-2C5 heavy chain variable region SEQ ID NO:6
EVQLVESGGGLVKPFGSLRLSCAASGFTSTTAWMSVVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLK
TEDTAVYYCAKGGGTGYGWGGTTTVVSS

Anti-BCMA-2C5 heavy chain constant region SEQ ID NO:7
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKP
SNTKVDKRVPEPKSCDKTHT

Anti-BCMA-2C5 light chain variable region SEQ ID NO:8
QSALTQPAVSVSGSPGQSVTISCTGTSSAHGGHYVSWYQQHPGKAPKLMICYDVSNRPSGVSNRFGSKSGNTASLTISGLQAEDEADYY
CGSYTSSSGSYVFGTGTKLTVL

Anti-BCMA-BC7A light chain variable region SEQ ID NO:9
SYVLTQPAVSVSGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMICYDVSNRPSGVSNRFGSKSGNTASLTISGLQAEDEADYY
CGSYTSSSGSYVFGTGTKLTVL

Anti-BCMA-BC7A (variant QSVLT - lambda) light chain variable region SEQ ID NO:10
QSVLTQPAVSVSGSPGQSVTISCTGTSSAHGGHYVSWYQQHPGKAPKLMICYDVSNRPSGVSNRFGSKSGNTASLTISGLQAEDEADYY
CGSYTSSSGSYVFGTGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAA
SSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

Anti-BCMA-2C5 light chain constant region SEQ ID NO:11
GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQV
THEGSTVEKTVAPTECS

FIG. 22

Anti-BCMA-2E1 heavy chain variable region

SEQ ID NO:12

EVQLVESGGGLVKPGGSLRLSCAAAGFTSSTAWMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLK
TETAAYYCAKGGGTGYGWGQGTTVTSS

Anti-BCMA-2E1 light chain variable region

SEQ ID NO:13

QSALTQPAASVSGSPGQSVTISCTGTSSDGGGHTYVSWYQQHPGKAPKLMICYDVSNRPSWVSNRFSGSKSGNTASLTISGLQAEDEADYY
CGSYTSSSGSYVFGTGTKLTVL

Anti-BCMA-BC4C9 heavy chain variable region

SEQ ID NO:14

EVQLVQSGAEVKKPGASVKVSKAFGYTFTSYDINWVRQATQGLEWGMNPNPNSGNTGYAQKFQGRVTMTNRNTSISTAYMELSSLRSE
DTAVYYCASGLGEWGQGTLLVTVSS

Anti-BCMA-BC4C9 light chain variable region

SEQ ID NO:15

QSVLTQPAASVSGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMICYDVSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYY
CISYSSSTFYVFGTGTKVTVL

Anti-BCMA-BC5C4 heavy chain variable region

SEQ ID NO:16

EVQLVESGGGLVQPGRSLRLSCAAAGFTTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIQYADSVKGRFTISRDNAKNSLYLQMNSLRAE
DTAVYYCATIDNVAFHSWGQGTLLVTVSS

Anti-BCMA-BC5C4 light chain variable region

SEQ ID NO:17

QSVLTQPPASGSPGQSVTISCTGTSSDIGYNYVSWYQQHPGKAPKLIIYEVSNRPSGVSDRFSGSKSGNTASLTISGLQAEDEADYY
CSSYTDNGALVVFGGGTGKLTVL

FIG. 23

Anti-BCMA-BC6G8 heavy chain variable region

SEQ ID NO:18

QVQLQQSGPGLVKPSQTLTSLTCAISGDSVSSNSVGWHWIRQSPSRGLEWLGRTYYRSNFATDYAASVRGRMTINADTSTNQISLHLNSLTPEDTAVYYCTRDWYGVDYDFWGQGGLTVTVSS

Anti-BCMA-BC6G8 light chain variable region

SEQ ID NO:19

SYELMQPPSVSVAPGKTARI TCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHLVVFEGGKLTIVL

Anti-BCMA-2D11 heavy chain variable region

SEQ ID NO:20

EVQLVESGGGLVKPGGSLRLSCAASGFTSSTAAMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCAKGGGTGYGWGQGTTTVTVSS

Anti-BCMA-2D11 light chain variable region

SEQ ID NO:21

SYELTQPASVSGSPGQSVTISCTGTSSVVGHDYVSWYQQHPGKAPKLMIIYDVSNRPSGVSNRFGSKSGNTASLTISGLQAEDEADYYCGSYTSSGGSYVFGTGTKVTVL

Anti-BCMA-2G2 heavy chain variable region

SEQ ID NO:22

EVQLVESGGGLVKPGGSLRLSCAASGFTSSTAAMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCAKGGGTGYGWGQGTTTVTVSS

Anti-BCMA-2G2 light chain variable region

SEQ ID NO:23

QSVLTQPASVSGSPGQSVTISCTGTSSSVGGRQYVSWYQQHPGKAPKLMIIYDVSNRPSGVSNRFGSKSGNTASLTISGLQAEDEADYYCGSYTSSGGSYVFGTGTKLTIVL

FIG. 24

Anti-BCMA-2D8 heavy chain variable region

SEQ ID NO:24

EVQLVESGGGLVKPGGSLRLSCAASGFTSSTAWMSWVRQAPGKGLWVGRIKSKSDGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLK
TEDTAVYYCAKGGGTGYGWGQGTTVTVSS

Anti-BCMA-2D8 light chain variable region

SEQ ID NO:25

QSVLTQPASVSGSPGQSVTISCTGTSSSIGDSYYVSWYQQHPGKAPKLMICYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYY
CGSYTSSSGSYVFGTGTTLTVL

Anti-BCMA-2E8 heavy chain variable region

SEQ ID NO:26

EVQLVESGGGLVKPGGSLRLSCAASGFTSSTAWMSWVRQAPGKGLWVGRIKSKSDGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLK
TEDTAVYYCAKGGGTGYGWGQGTTVTVSS

Anti-BCMA-2E8 light chain variable region

SEQ ID NO:27

QSVLTQPASVSGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMICYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYY
CGSLRSNGDYVFGTGTTLTVL

FIG. 25

Anti-BCMA Bluebird (bb2121) heavy chain variable region SEQ ID NO:28
QIQLVQSGPELKKPGETVKISCKASGYTFDDYSINWVKRAPGKGLKWMGWINTETREPAYAYDFRGRFAFSLETSASTAYLQINNLYE
DTATYFCALDYSYAMDYWGQGTTLTVSS

Anti-BCMA Bluebird (bb2121) heavy chain constant region SEQ ID NO:29
ASTKGPSTVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKP
SNTKVDKRVPEPKSCDKTHT

Anti-BCMA Bluebird (bb2121) light chain variable region SEQ ID NO:30
DIVLTQSPASLAMSGLGKRATISCRASESVSVIGAHLIHWYQQKPGQPPKLLIYLASNLETGVPARFSGSGSGTDFTLTIDPVEEDDAI
YSCLQSRIFRPRTFGGGTKLEIK

Anti-BCMA Bluebird (bb2121) light chain constant region SEQ ID NO:31
RTVAAPSVFIFPPSDEQLKSGTASVWCCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEV
THQGLSSPVTKSFNRGEC

FIG. 26

CAR GS linker SEQ ID NO:32
GGGSGGGGGGGGS

CAR bb2121 linker SEQ ID NO:33
GSTSGGKPGSGEGS

CD8 hinge SEQ ID NO:34
AKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAPR

CD28 hinge SEQ ID NO:35
KIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLPFGPSKP

CD8 hinge + CD28 hinge (long hinge) SEQ ID NO:36
AKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAPRKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLPFGPSKP

CD28 transmembrane SEQ ID NO:37
FWVLVVGGLACYSLLVTVAFIIFWV

CD8 transmembrane SEQ ID NO:38
IYIWAPLAGTCGVLLLSLVITLY

4-1BB transmembrane SEQ ID NO:39
IISFFIALTSTALLFLLFFLTIRFSWV

CD3zeta transmembrane SEQ ID NO:40
LCYLLDGILFIYGVILTALFL

FIG. 27

4-1BB co-stimulatory sequence

SEQ ID NO:41

KRGRKKLLYIFKQPFMRPVQTQEEEDGCSCRFPEEEEGGCEL

CD28 co-stimulatory sequence

SEQ ID NO:42

RSKRSRLLHSDYMNMTPRRPGPTRKKHYQPYAPPRDFAAYRS

OX40 co-stimulatory sequence

SEQ ID NO:43

ALYLLRRDQRLPPDAHKPPFGGSGFRTPIQEEQADAHSTIAKI

CD3zeta ITAM 1, 2, 3

SEQ ID NO:44

RVKFSSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP
EMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGK
GHDGLYQGLSTATKDTYDALHMQALPPR

CD3zeta ITAM 1

SEQ ID NO:45

RVKFSSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR

CD3zeta ITAM 2

SEQ ID NO:46

RVKFSSRSADRGDRDP
EMGGKPRRKNPQEGLYNELQDKMAEAYSEIGM

CD3zeta ITAM 3

SEQ ID NO:47

RVKFSSRSADKGERRRRGK
GHDGLYQGLSTATKDTYDALHMQALPPR

FIG. 28

DAR V1 intracellular domain SEQ ID NO:48
RSKRSRLLSHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGK
PRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

DAR V2a intracellular domain SEQ ID NO:49
KRGKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG
KPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

DAR V2b and CAR (28Z) intracellular domain SEQ ID NO:50
RSKRSRLLSHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGK
PRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

DAR V2c intracellular domain SEQ ID NO:51
KRGKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRSKRSLLSHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSR
SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGGHDGLYQGLST
ATKDTYDALHMQALPPR

DAR V3a and V4 intracellular domain SEQ ID NO:52
KRGKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

DAR V3b intracellular domain SEQ ID NO:53
KRGKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRSKRSLLSHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSR
SADKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

FIG. 29

DAR V3c intracellular domain SEQ ID NO:87

RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

DAR V2c-alt intracellular domain SEQ ID NO:88

RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEGGGCELRVKFSR
SADAPAYQQGQNQLYNEINLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGGHDGLYQGLST
ATKDTYDALHMQALPPR

DAR V3b-alt intracellular domain SEQ ID NO:89

RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEGGGCELRVKFSR
SADKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

FIG. 30

Heavy chain leader sequence SEQ ID NO:54
MEWSWFLFFLSVTITGVHS

Light chain leader sequence SEQ ID NO:55
MSVPTQVLGLLLLWLTDAAC

Alternative leader sequence SEQ ID NO:56
MALPVTALLPLALLHAARE

T2A self-cleaving sequence SEQ ID NO:57
GSGEGRGSLITCGDVEENPGP

P2A self-cleaving sequence SEQ ID NO:58
GSGATNFSLLKQAGDVEENPGP

E2A self-cleaving sequence SEQ ID NO:59
GSGQCTNYALLKLAGDVEENPGP

F2A self-cleaving sequence SEQ ID NO:60
GSGVKQTLNFDLLKLAGDVEENPGP

FIG. 31

CAR 28Z BCMA-2C5 SEQ ID NO:61

MEWSWVFLFFLSVTTGVHSQVQLVESGGGLVKPGGSLRLSCAASGFTSTTAWMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRF
TISRDDSKNTLFLQMNSLKTEDTAVYCAKGGGTGYGWGGTLVTSSGGGGGGGGSSYVLTQPASVSGSPGQSVTISCTGTS
SAHGHHYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCGSYTSSGSYVFGTGTCLTLVLAKPPT
TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAPRKIEVMYPPPYLDNEKSNGTI IHVKGKHLCPSPLPFGPSKPFWVLV
VGGVLACYSLLVTVAFI IFWVRSKRSLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLG
RREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR

CAR 28Z BCMA-bb2121 SEQ ID NO:62

MEWSWVFLFFLSVTTGVHSDIVLTQSPASLAMSGLKRATISCRASESVSIVGAHLIHWYQQKPGQPPKLLIYIASNIETGVPARFSGSG
SGDTFTLTIDPVEEDDAIYSCLOSRIFPRTFGGGTKLEIKGSTSGSKPGSGEGSQIQLVQSGPELKKPGETVKISCKASGYTFTDYS
INWVKRAPGKGLKWMGWINTETREPAYAYDFRGRFAFSLETSASTAYLQINNLYEDTATYFCALDYSYAMDYWGQGTTLTVSSAKPPT
TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAPRKIEVMYPPPYLDNEKSNGTI IHVKGKHLCPSPLPFGPSKPFWVLV
VGGVLACYSLLVTVAFI IFWVRSKRSLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLG
RREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR

FIG. 32

DAR V1 BCMA-2C5 precursor SEQ ID NO:63

MEWSWVFLFFLSVTTGVHSEVQLVESGGGLVKPGGSLRLSCAASGFTSSTAWMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRF
TISRDDSKNTLFLQMNLSLKTEDTAVYCAKGGGTGYGWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKTHTAKPTTTTPAPRPPTPAPTIASQP
LSLRPEACRPAAGGAVHTRGLDFAPRKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLPFGPSKPFWVLVVGGVLACYSLLVTVAFI
IFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNEINLGRREEYDVLDKRRGRDPE
MGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQLPPR**GS****GEGRGSL****LT****CGDVEENPCP**
MSVPTQVLGLLLLWLTDARCSYVLTQPASVSGSPGQSVTISCTGTSSAHGGHYVSWYQQHPGKAPKLMICYDVSNRPSGVSNRFGSGKS
GNTASLTIISGLQAEDEADYYCGSYTSSGSYVFGTGKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSP
VKAGVETTTTPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS

DAR V1 BCMA-2C5 1st polypeptide SEQ ID NO:64

EVQLVESGGGLVKPGGSLRLSCAASGFTSSTAWMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRFTISRDDSKNTLFLQMNLSLK
TEDTAVYCAKGGGTGYGWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKTHTAKPTTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR
GLDFAPRKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLPFGPSKPFWVLVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMT
TPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ
KDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQLPPR

DAR V1 BCMA-2C5 2nd polypeptide SEQ ID NO:65

SYVLTQPASVSGSPGQSVTISCTGTSSAHGGHYVSWYQQHPGKAPKLMICYDVSNRPSGVSNRFGSGKSGNTASLTIISGLQAEDEADYY
CGSYTSSGSYVFGTGKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQNNKYAA
SSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS

FIG. 33

DAR V2a BCMA-2C5 precursor SEQ ID NO:66

MEWSWVFLFFLSVTITGVHSEVQLVESGGGLVKPGGSLRLSCAASGFTSSTAWMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRF
TISRDDSKNTLFLQMNSLKTEDTAVYICAKGGGTGYGWGQGTTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTKIEVMYPPPYLDNEKSNGTIIH
VKGKHLCPSPLPFGPSKPFFWLVVVGVLACYSLLVTVAFII FWVKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFPEEEEEGGCELRV
KFSRSADAPAYQQGQNQLYNELNLGRRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQ
GLSTATKDTYDALHMQALPPRGSEGRGSLLTCGDVEENPGFPMSVPTQVLGLLLLLWLTDARCSYVLTQPASVSGSPGQSVTISCTGTSS
AHGHHYVSWYQQHPGKAPKLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYCGSYTSSGSYVFGTGTKLTVLGQPKAA
PSVTLPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSQCQVTHEGST
VEKTVAPTECS

DAR V2a BCMA-2C5 1st polypeptide SEQ ID NO:67

EVQLVESGGGLVKPGGSLRLSCAASGFTSSTAWMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLK
TEDTAVYICAKGGGTGYGWGQGTTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWSGALTSGVHTFPAVLQSS
GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLPFGPSKPF
WVLVVGVLACYSLLVTVAFII FWVKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYQQGQNQLY
NELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALP
PR

DAR V2a BCMA-2C5 2nd polypeptide SEQ ID NO:68

SYVLTQPASVSGSPGQSVTISCTGTSSAHGHHYVSWYQQHPGKAPKLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADY
CGSYTSSGSYVFGTGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAA
SSYLSLTPEQWKSHRSYSQCQVTHEGSTVEKTVAPTECS

FIG. 34

DAR V2b BCMA-2C5 precursor SEQ ID NO:69

MEWSWVFLFFLSVTTGVHSEVQLVESGGGLVKPGGSLRLSCAASGFTSSTAWMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRF
TISRDDSKNTLFLQMNLSLKTEDTAVYCAKGGGTGYGWGGTQTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKTHTKIEVMYPPPYLDNEKSNGTIIH
VKGKHLCPSPFLFPGPSKPFWVLVVGGLVACYSLLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVK
FSRSADAPAYQQGQNQLYNELNLRREEYDLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMGERRRRGKGGHDGLYQG
LSTATKDTYDALHMQALPPRGS~~EG~~RGSLTTCGDVEENPGFMSVPTQVLGLLLLLWLTDARCSYVLTQPASVSGSPGQSVTISCTGTSSA
HGHHYVSWYQQHPGKAPKLMIIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCGSYTSSGSYVFGTGTCLTVLGQPKAAP
SVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETITTPSKQNNKYAASSYLSLTPEQWKSHRSYSYCQVTHEGSTV
EKTVAPTecs

DAR V2b BCMA-2C5 1st polypeptide SEQ ID NO:70

EVQLVESGGGLVKPGGSLRLSCAASGFTSSTAWMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRFTISRDDSKNTLFLQMNLSLK
TEDTAVYCAKGGGTGYGWGGTQTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQSS
GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKTHTKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPF
WVLVVGGLVACYSLLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYN
ELNLRREEYDLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPP
R

DAR V2b BCMA-2C5 2nd polypeptide SEQ ID NO:71

SYVLTQPASVSGSPGQSVTISCTGTSSAHGGHYVSWYQQHPGKAPKLMIIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYY
CGSYTSSGSYVFGTGTCLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETITTPSKQNNKYAA
SSYLSLTPEQWKSHRSYSYCQVTHEGSTVEKTVAPTECS

FIG. 35

DAR V2c BCMA-2C5 precursor SEQ ID NO:72

MEWSWVFLFFLSVTITGVHSEVQLVESGGGLVKPGGSLRLSCAASGFTSSTAWMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRF
TISRDDSKNTLFLQMNSLKTEDTAVYCAKGGGTGYGWGQGTTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTTVSW
NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQYICNVNHKPSNTKVDKRVEPKSCDKTHHTKIEVMYPPPYLDNEKSNGTIIH
VKGKHLCPSPLPFGPSKPFFWLVVVGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSKRG
RKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPR
RKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGKGHDGLYQGLSTATKDTYDALHMQALPPR**GS****EG****RG****SL****L****TCGDV****EE****NP****G****P****M****S****V****P****T****Q**
VLGLLLWLTDARCSYVLTQPASVSGSPGQSVTISCTGTSSAHGGHYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASL
TISGLQAEDEADYYCGSYTSSGSYVFGTGTKLTVLGQPKAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE
TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

DAR V2c BCMA-2C5 1st polypeptide SEQ ID NO:73

EVQLVESGGGLVKPGGSLRLSCAASGFTSSTAWMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLK
TEDTAVYCAKGGGTGYGWGQGTTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNSGALTSGVHTFPAVLQSS
GLYSLSSVTVPSSSLGTQYICNVNHKPSNTKVDKRVEPKSCDKTHHTKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLPFGPSKPF
WVLVVGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSKRGKKLLIYIFKQPFMRPVQTT
QEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAE
AYSEIGMKGERRRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

DAR V2c BCMA-2C5 2nd polypeptide SEQ ID NO:74

SYVLTQPASVSGSPGQSVTISCTGTSSAHGGHYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYY
CGSYTSSGSYVFGTGTKLTVLGQPKAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAA
SSYSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

FIG. 36

DAR V3a BCMA-2C5 precursor SEQ ID NO:75

MEWSVFLFFLSVTTGVHSEVQLVESGGGLVKPGGSLRLSCAASGFTSSTAAMSWVRQAPGKGLWVGRIKSKSDGGTTDYAAPVKGRF
TISRDDSKNTLFLQMNSLKTEDTAVYYCAKGGGTGYGWGQTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSW
NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKHTHTKIEVMYPPPYLDNEKSNGTIIH
VKGKHLCPSPFLFPGPSKPFWVLLVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFEEEEGGCELRV
KFSRADKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR**GSGEGRGSLLT**TCGDVEENPCEPMSVPTQVLGLLLLLWLTDAKCSYVLT
QPASVSGSPGQSVTISCTGTSSAHGGHYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYCGSYT
SSGSYVFGTGTKLTVLGQPKAAPSVTLFPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNNNKYAASSYLS
LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS

DAR V3a BCMA-2C5 1st polypeptide SEQ ID NO:76

EVQLVESGGGLVKPGGSLRLSCAASGFTSSTAAMSWVRQAPGKGLWVGRIKSKSDGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLK
TEDTAVYYCAKGGGTGYGWGQTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNGALTSGVHTFPAVLQSS
GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKHTHTKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPF
WVLLVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFEEEEGGCELRVKFSRADKGERRRGKGDG
LYQGLSTATKDTYDALHMQALPPR

DAR V3a BCMA-2C5 2nd polypeptide SEQ ID NO:77

SYVLTQPASVSGSPGQSVTISCTGTSSAHGGHYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADY
CGSYTSSGSYVFGTGTKLTVLGQPKAAPSVTLFPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNNNKYAA
SSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCS

FIG. 37

DAR V3b BCMA-2C5 precursor SEQ ID NO:78

MEWSWFLFFLSVTTGVHSEVQLVESGGGLVKPGGSLRLSCAASGFTSTAWMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRF
TISRDDSKNTLFLQMNSLKTEDTAVYYCAKGGGTGYGWGQGTTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSW
NSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKTHHTKIEVMYPPPYLDNEKSNGTIIH
VKGKHLCPSPLEFPGPSKPFWVLVVVGVLACYSLLLVTVAFIIFWVRSKRSLRLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSKRG
RKLLYIFKQPFMRPVQTTQEEDGCSRCRFEEEEGGCELRVKFSRSDKGERRRGKHDGLYQGLSTATKDTYDALHMQALPPR**GSCEG**
RGSLLTCGDVEENPGPMSVPTQVLGLLLLLWLTDA RCSYVLTQPASVSGSPGQSVTISCTGTSSAHGGHYVSWYQQHPGKAPKLMIIDV
SNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCGSYTSSGSYVFGTGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD
FYPGA VTVAWKADSSPVKAGVETTTTPSKQSNNKYAAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

DAR V3b BCMA-2C5 1st polypeptide SEQ ID NO:79

EVQLVESGGGLVKPGGSLRLSCAASGFTSTAWMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLK
TEDTAVYYCAKGGGTGYGWGQGTTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKTHHTKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLEFPGPSKPF
WVLVVVGVLACYSLLLVTVAFIIFWVRSKRSLRLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTT
QEEDGCSRCRFEEEEGGCELRVKFSRSDKGERRRGKHDGLYQGLSTATKDTYDALHMQALPPR

DAR V3b BCMA-2C5 2nd polypeptide SEQ ID NO:80

SYVLTQPASVSGSPGQSVTISCTGTSSAHGGHYVSWYQQHPGKAPKLMIIDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYY
CGSYTSSGSYVFGTGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNNKYAA
SSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

FIG. 38

DAR V4 BCMA-2C5 precursor SEQ ID NO:81
MEWSWFLFLSVTTGVHSEVQLVESGGGLVKPGGSLRLSCAASGFTSTAMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRF
TISRDDSKNTLFLQMNSLKTEDTAVYYCAKGGGTGYGWGGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSW
NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKTHTFWLVVVGVLACYSLLVTVA
FIIFWVKRGRKKLLYIFKQPFMRPVQTQEEEDGCSCRFPEEEEGGCELRVKFSRADKGERRRGKGGHDGLYQGLSTATKDTYDALHMQAL
PPR**GSCEGRGSLLT****TCGDVEENP**GPMSVPTQVLGLLLLLWLTDA RCSYVLTQPASVSGSPGQSVTISCTGTSSAHGGHYVSWYQQHPGKA
PKLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCGSYTSSGSYVFGTGTCLTLVGQPKAAPSVTLFPPSSEELQANKA
TLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

DAR V4 BCMA-2C5 1st polypeptide SEQ ID NO:82
EVQLVESGGGLVKPGGSLRLSCAASGFTSTAMSWVRQAPGKGLEWVGRIKSKSDGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLK
TEDTAVYYCAKGGGTGYGWGGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKTHTFWLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQ
PMPVQTTQEEEDGCSCRFPEEEEGGCELRVKFSRADKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

DAR V4 BCMA-2C5 2nd polypeptide SEQ ID NO:83
SYVLTQPASVSGSPGQSVTISCTGTSSAHGGHYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYY
CGSYTSSGSYVFGTGTCLTLVGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNNKYAA
SSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

FIG. 39

DAR V2a BCMA-bb2121 precursor SEQ ID NO:84

MEWSWFLFFLSVTGVSQIQLVQSGPELKKPGETVKISCKASGYTFTDYSINWVKRAPGKGLKMWGINTEPREPAYAYDFRGRFAF
SLETSASTAYLQINNLLKYEDTATYFCALDYSYAMDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWSWN
SGALITSGVHTFFPAVLQSSGLYSLSSVTVPSSSLGTQYICNVNHKPSNTKVDKRVKPKSCDKTHTKIEVMYPPPYLDNEKSNGTIIHV
KGKHLCPSPLPFGPSKPFWLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTQEEEDGCSCRFEEEEGGCELRVK
FSRSADAPAYQQQNQLYNELNLGRREYDVLDRRGRDPPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMGERRRRGKGGHDGLYQG
LSTATKDTYDALHMQALPFRGSGEGRGSLLTCDVEENP GPMVSVP TQVLGLLLLLWLT DARC DI VLTQSPASLAMS LGKRATISCRASES
VSVIGAHLIHWYQQKPGQPPKLLIYLASNLETGVPARFSGSGGTFTLTIDPVEEDDVAIYSCLOSRIFPRTFGGGTKLEIKRTVAAP
SVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

DAR V2a BCMA-bb2121 1st polypeptide SEQ ID NO:85

QIQLVQSGPELKKPGETVKISCKASGYTFTDYSINWVKRAPGKGLKMWGINTEPREPAYAYDFRGRFAFSLETSASTAYLQINNLLKYE
DTATYFCALDYSYAMDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPAVLQSSG
LYSLSSVTVPSSSLGTQYICNVNHKPSNTKVDKRVKPKSCDKTHTKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLPFGPSKPFW
VLVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTQEEEDGCSCRFEEEEGGCELRVKFSRSADAPAYQQQNQLYN
ELNLGRREYDVLDRRGRDPPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPP
R

DAR V2a BCMA-bb2121 2nd polypeptide SEQ ID NO:86

DIVLTQSPASLAMS LGKRATISCRASESVSVIGAHLIHWYQQKPGQPPKLLIYLASNLETGVPARFSGSGGTFTLTIDPVEEDVAI
YSCLOSRIFPRTFGGGTKLEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS
LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIG. 40