

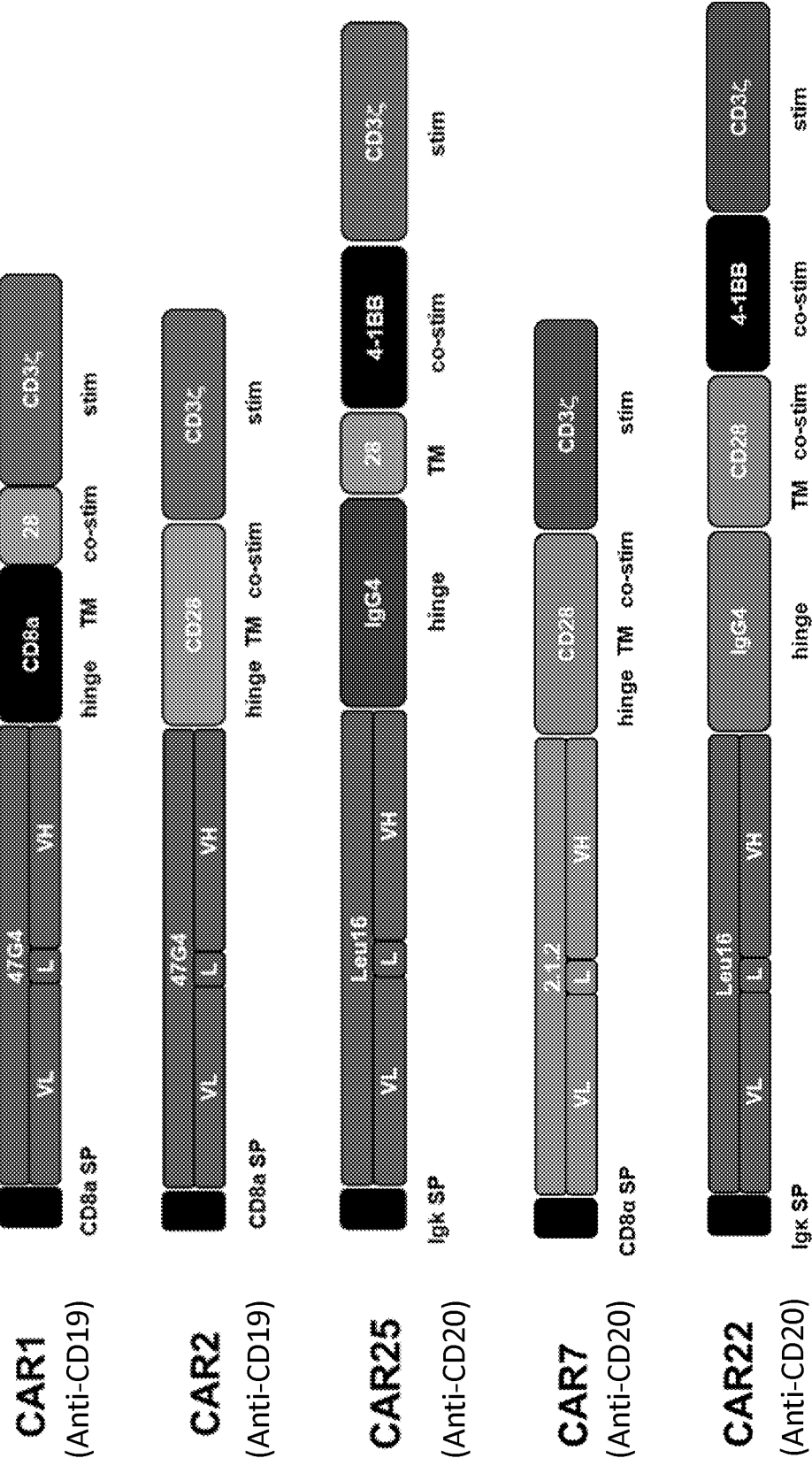


FIG. 1

SEQ ID NO.	CAR construct	Amino acid sequence (CAR + SP)	Note
1	CAR1	MALPVTALLPLALLLHAARPEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSRFTFGPGTKVDIKGSTSGSGKPGSGEGSTKGQVQLVQSGAEVKKPGSSVKVCKDSSGTFSSYAISWVRQAPGQGLEWMGGIPIFGTTNYAQQFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREAVAADWLDPWGQGTLLTVSSFPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAFLAGTCGVLLLSLVITLYCNHRNRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR	Length (whole): 502 Length (CAR): 481 Diff: 21 Source: Genebank QHQ73568.1
2	CAR2	MALPVTALLPLALLLHAARPEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSRFTFGPGTKVDIKGSTSGSGKPGSGEGSTKGQVQLVQSGAEVKKPGSSVKVCKDSSGTFSSYAISWVRQAPGQGLEWMGGIPIFGTTNYAQQFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREAVAADWLDPWGQGTLLTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFPGPSKPFVVLVVGGLACYSLLTVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR	Length (whole): 485 Length (CAR): 464 Diff: 21 Source: Genebank QHQ73565.1
3	CAR25	METDTLLLWVLLLWVPGSTGDIVLTQSPAILSASPGEKVTMTCRASSSVNYMDWYQQKPGSSPKPWIYATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWFSNPPTFGGGTKLEIKGSTSGGGSGGGSGGGGSSEVQLQQSGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGQGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSADYYCARSNYYGSSYWFVDVWGAGTTVTVSSESKYGPCCPPCPAPEFDGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLKMFVVLVVGGLACYSLLTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTQEEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR	Length (whole): 677 Length (CAR): 657 Diff: 20

FIG. 2A

SEQ ID NO.	CAR construct	Amino acid sequence (CAR + SP)	Note
74	CAR7	MALPVTALLLPLALLLHAARPDIVMTQTPHSSPVTLGQPASISCRSS QSLVSRDGNTYLSWLQQRPGQPPRLIYKISNRFSGVPNRFSGSG AGTDFTLKISRVKAEDVGYYCMQATQFPLTFGQGTRLEIKGGGG SGGGSGGGGSEVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWI GWVRQMPGKGLEWMGIIYPGDS DTRYSPSFQGGQVTISADKSIST AYLQWSSLKASDTAMYYCARQGD FWSGYGGMDVWGGQTTVT VSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFPGPSKPFWVL VVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGP TRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAE AYSEIGMKGERRRRGKGHDLGLYQGLSTATKDTYDALHMQALPPR	Length (whole): 489 Length (CAR): 468 Diff: 21
75	CAR22	METDTLLLWVLLLWVPGSTGDIVLTQSPAILSASPGEKVTMTCRAS SSVNYMDWYQKKPGSSPKWIYATSNLASGVPARFSGSGSGTSY SLTISRVEAEDAATYYCQQWFSNPPTFGGGTKLEIKGSTSGGGSG GGSGGGGSSEVQLQQSGAELVKPGASVKMSCKASGYTFTSYNM HWVKQTPGQGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSST AYMQLSSLTSEDSADYYCARSNYYGSSYWFFDVWGAGTTTVSSL DESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL PSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSL SLSLGKMFVVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRGGHSDY MNMTPRRPGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPF MRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQDKMAEAYSEIGMKGERRRRGKGHDLGLYQGLSTATKDTYDALH MQALPPR	Length (whole): 720 Length (CAR): 700 Diff: 20

FIG. 2A (cont'd)

SEQ ID NO.	CAR construct	Amino acid sequence (mature CAR)
4	CAR1	EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGASS RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSRFTFGPGTKVDIK GSTSGSGKPGSGEGSTKGQVQLVQSGAEVKKPGSSVKVSCDKSGGTFSSYAIS WVRQAPGQGLEWMGGIIPFGTTNYAQQFQGRVTITADESTSTAYMELSSL RSEDTAVYYCAREAVAADWLDPWGQGTLTVSSFPVFLPAKPTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSL VITLYCNHRNRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYD ALHMQALPPR
5	CAR2	EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGASS RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSRFTFGPGTKVDIK GSTSGSGKPGSGEGSTKGQVQLVQSGAEVKKPGSSVKVSCDKSGGTFSSYAIS WVRQAPGQGLEWMGGIIPFGTTNYAQQFQGRVTITADESTSTAYMELSSL RSEDTAVYYCAREAVAADWLDPWGQGTLTVSSIEVMYPPPYLDNEKSNGTI IHVKGKHLCPSPFPGPSKPFVWLTVVGGVLACYSLLVTVAFIIFWVRSKRSRL LHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
6	CAR25	DIVLTQSPAILSASPGEKVTMTCRASSSVNYMDWYQKKPGSSPKPWYATSNL ASGVPARFSGSGSGTSYSTISRVEAEDAATYYCQQWSFNPTFGGGTKLEIK GSTSGGGSGGGSGGGGSSEVQLQQSGAELVKPGASVKMSCKASGYTFTSY NMHWVKQTPGQGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQ LSSLTSEDSADYYCARSNYYGSSYWFFDVWGAGTTTVTVSSESKYGPCCPPCPA PEFDGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK TISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYT QKSLSLSLGKMFVWLTVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFM RPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM KGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

FIG. 2B

SEQ ID NO.	CAR construct	Amino acid sequence (Mature CAR)
76	CAR7	DIVMTQTPHSSPVTLGQPASISCRSSQSLVSRDGNTYLSWLQQRPGQPPRLIY KISNRFSGVPNRFSGSGAGTDFTLKISRVKAEDVGYYCMQATQFPLTFGQGT RLEIKGGGGSGGGGSGGGGSEVQLVQSGAEVKKPGESLKISCKGSGYSFTSYW IGWVRQMPGKGLEWMGIIYPGDS DTRYSPSFQGQVTISADKSISTAYLQWSSL KASDTAMYYCARQGD FWSGYGGMDVWGQGT TTVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSP LFPGPSKPFWVLVVGGVLACYSLLVTVAFIIFWVRSK RSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQ QGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
77	CAR22	DIVLTQSPAILSASPGEKVTMTCRASSSVNYMDWYQKKPGSSPKPWYATSNL ASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQWFSNPPTFGGGTKLEIKG STSGGGSGGGGSGGGGSSEVQLQQSGAELVKPGASVKMSCKASGYTFTSYNM HWVKQTPGQGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLT SEDSADYYCARSNYGSSYWFFDVWGAGTTTVTVSSLDESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHN AKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK GQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSL GKMFVVLVVVGGVLACYSLLVTVAFIIFWVRSKRSGHSDYMNMTPRRPG PTRKHYPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRPE EEEGGCELRVKFSRSADAPAYQGQNQLYNELNLGRREEYDVL DKRRGRDPE MGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGK GHDGLYQGLST ATKDTYDALHMQALPPR

FIG. 2B (cont'd)

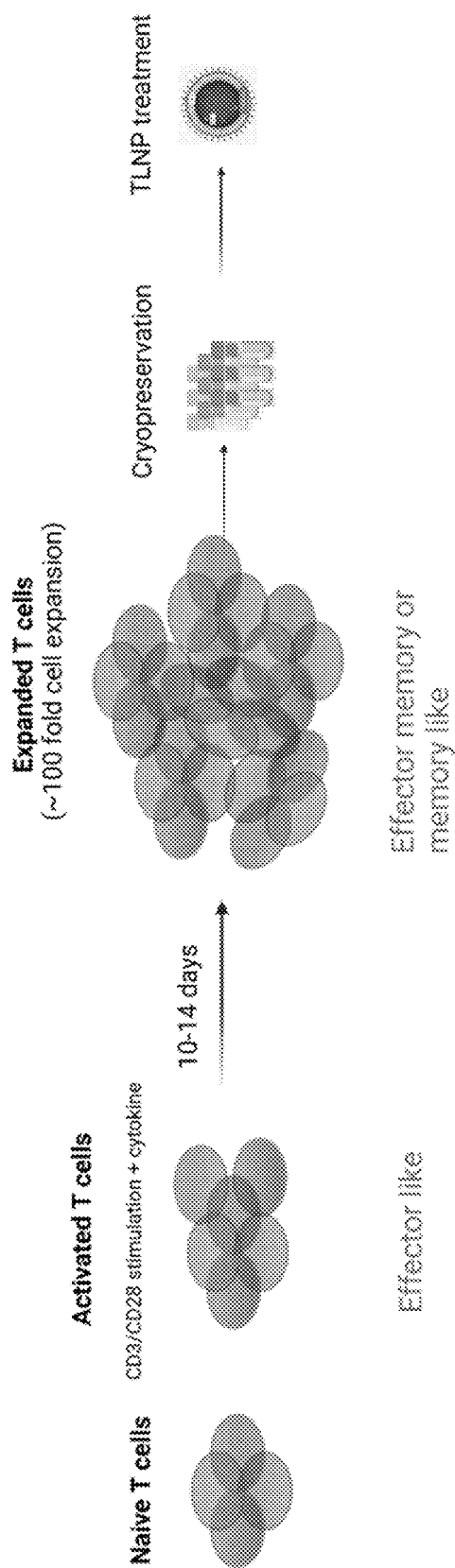
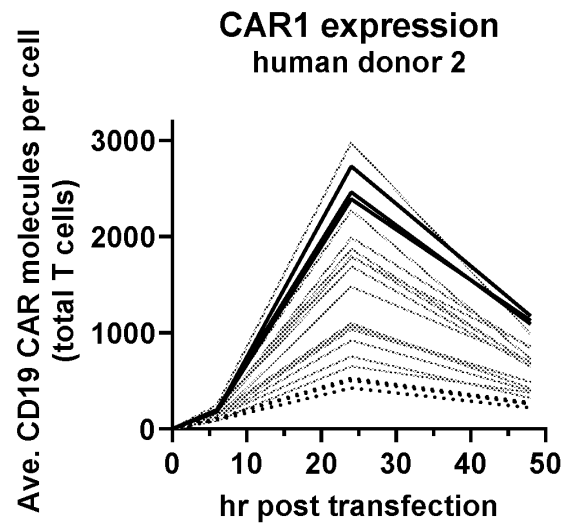
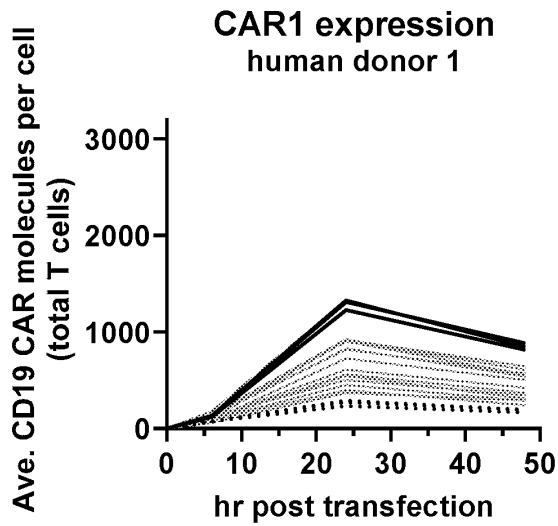
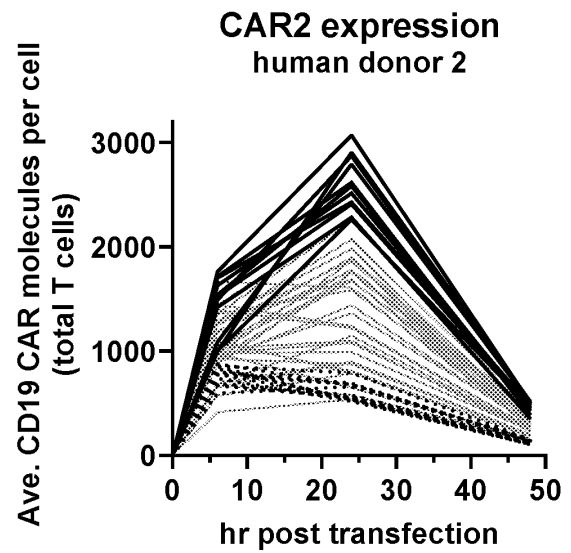
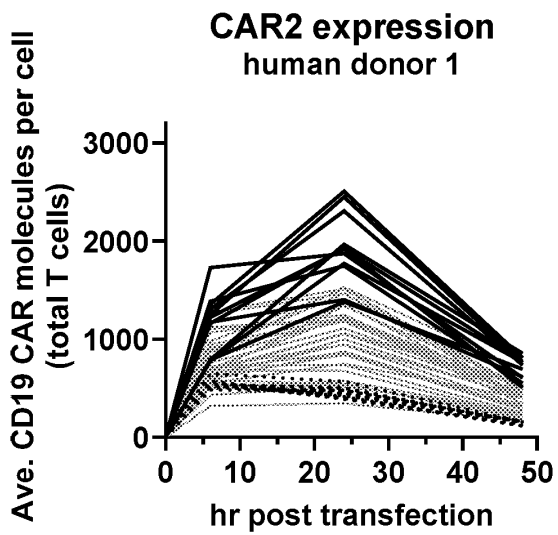


FIG. 3A

Expanded T cells**CAR1****CAR2****FIG. 3B**

SEQ ID NO:	RM	5' UTR	ORF encoded CAR-Codon optimization strategy (OPT)	3' UTR	Round 2 Tier	Round 3 Tier
111	RM_61117	TEV	CAR1-OPT6 single stop	XBG (no BsrGI)	3	3
112	RM_61118	TEV	CAR2-OPT6 single stop	XBG (no BsrGI)	3	3
113	RM_61321	mHBB	CAR1-OPT4	PNLIP	1	1
114	RM_61324	mHBB	CAR1-OPT4	RPS3A	1	1
115	RM_61326	mHBB	CAR1-OPT4	RPS3A-PNLIP	1	1
116	RM_61329	CPA1	CAR1-OPT4	CPA1	2	2
117	RM_61330	DEFA3	CAR1-OPT4	DEFA3	2	1
118	RM_61334	CD8a	CAR1-OPT4	hHBA1	3	3
119	RM_61340	synthetic	CAR1-OPT4	hHBA1	2	2
120	RM_61341	HBA	CAR1-OPT4	AES-mtRNR1	2	2
121	RM_61347	mHBB	CAR1-OPT4	hHBA1	2	1
122	RM_61348	hAlb	CAR1-OPT4	hHBA1	2	2
123	RM_61349	mHBB	CAR1-OPT4	hHBA1-3x miR122 bs	1	1
124	RM_61350	TEV	CAR1-OPT7	XBG	2	1
125	RM_61351	TEV	CAR1-OPT5	XBG	2	2
126	RM_61352	TEV	CAR1-OPT3	XBG	3	3
127	RM_61353	TEV	CAR1-OPT2	XBG	3	2
128	RM_61355	mHBB	CAR2-OPT4	hHBA1	1	1
129	RM_61356	hAlb	CAR2-OPT4	hHBA1	2	1
130	RM_61357	mHBB	CAR2-OPT4	hHBA1-3x miR122 bs	1	1
131	RM_61358	TEV	CAR2-OPT7	XBG	2	1
132	RM_61359	TEV	CAR1-OPT4	XBG	2	2
133	RM_61360	TEV	CAR2-OPT4	XBG	2	2
134	RM_61362	TEV	CAR1-OPT6 double stop	XBG	3	3
135	RM_61363	TEV	CAR2-OPT6 triple stops	XBG	3	3
136	RM_61378	eIF4G aptamer x1	CAR1-OPT4	hHBA1	2	1
137	RM_61379	aptamer control	CAR1-OPT4	hHBA1	2	1
138	RM_61411	TEV	CAR2-OPT1	XBG	2	2

FIG. 3C

SEQ ID NO:	RM	5' UTR	ORF encoded CAR-Codon optimization strategy (OPT)	3' UTR	Round 2 Tier	Round 3 Tier
139	RM_61449	TEV	CAR2-OPT2	XBG	2	3
140	RM_61450	TEV	CAR2-OPT3	XBG	2	3
141	RM_61451	mHBB	CAR2-OPT2	hHBA1	2	2
142	RM_61452	mHBB	CAR2-OPT3	hHBA1	2	2
143	RM_61453	synthetic	CAR2-OPT4	hHBA1	2	2
144	RM_61454	HBA	CAR2-OPT4	AES-mtRNR1	2	2
145	RM_61455	DEFA3	CAR2-OPT4	DEFA3	2	1
146	RM_61456	CPA1	CAR2-OPT4	CPA1	2	2
147	RM_61457	CD8a	CAR2-OPT4	hHBA1	3	2
148	RM_61458	eIF4G aptamer x1	CAR2-OPT4	hHBA1	2	1
149	RM_61459	aptamer control	CAR2-OPT4	hHBA1	2	2
150	RM_61460	mHBB	CAR2-OPT4	RPS3A	2	2
151	RM_61461	mHBB	CAR2-OPT4	PNLIP-RPS3A	1	1
152	RM_61462	DEFA3	CAR2-OPT2	DEFA3	2	2
153	RM_61463	CPA1	CAR2-OPT2	CPA1	2	3
154	RM_61464	CD8a	CAR2-OPT2	hHBA1	3	3
155	RM_61465	eIF4G aptamer x1	CAR2-OPT2	hHBA1	2	2
156	RM_61466	aptamer control	CAR2-OPT2	hHBA1	2	2
157	RM_61467	mHBB	CAR2-OPT2	RPS3A	2	2
158	RM_61468	mHBB	CAR2-OPT2	PNLIP-RPS3A	2	2
159	RM_61482	mHBB	CAR2-OPT1	hHBA1	1	1
160	RM_61483	DEFA3	CAR2-OPT1	DEFA3	1	1
161	RM_61484	CPA1	CAR2-OPT1	CPA1	2	2
162	RM_61485	CD8a	CAR2-OPT1	hHBA1	2	2
163	RM_61486	eIF4G aptamer x1	CAR2-OPT1	hHBA1	1	1
164	RM_61487	aptamer control	CAR2-OPT1	hHBA1	1	1

FIG. 3C (cont'ed)

SEQ ID NO:	RM	5' UTR	ORF encoded CAR-Codon optimization strategy (OPT)	3' UTR	Round 2 Tier	Round 3 Tier
165	RM_61488	mHBB	CAR2-OPT1	RPS3A	1	1
166	RM_61489	mHBB	CAR2-OPT1	PNLIP-RPS3A	1	1
167	RM_61501	TEV	CAR2-OPT5	XBG	2	2
168	RM_61512	TEV	CAR2-OPT6 double stops	XBG	3	3
169	RM_61513	mHBB	CAR2-OPT6 double stops	hHBA1	3	3
170	RM_61514	DEFA3	CAR2-OPT6 double stops	DEFA3	3	3
171	RM_61515	CPA1	CAR2-OPT6 double stops	CPA1	2	2
172	RM_61516	CD8a	CAR2-OPT6 double stops	hHBA1	3	3
173	RM_61517	eIF4G aptamer x1	CAR2-OPT6 double stops	hHBA1	3	3
174	RM_61518	aptamer control	CAR2-OPT6 double stops	hHBA1	3	3
175	RM_61519	mHBB	CAR2-OPT6 double stops	RPS3A	3	3
176	RM_61520	mHBB	CAR2-OPT6 double stops	PNLIP-RPS3A	3	3

FIG. 3C (cont'ed)

CAR1 - Human Donor 1

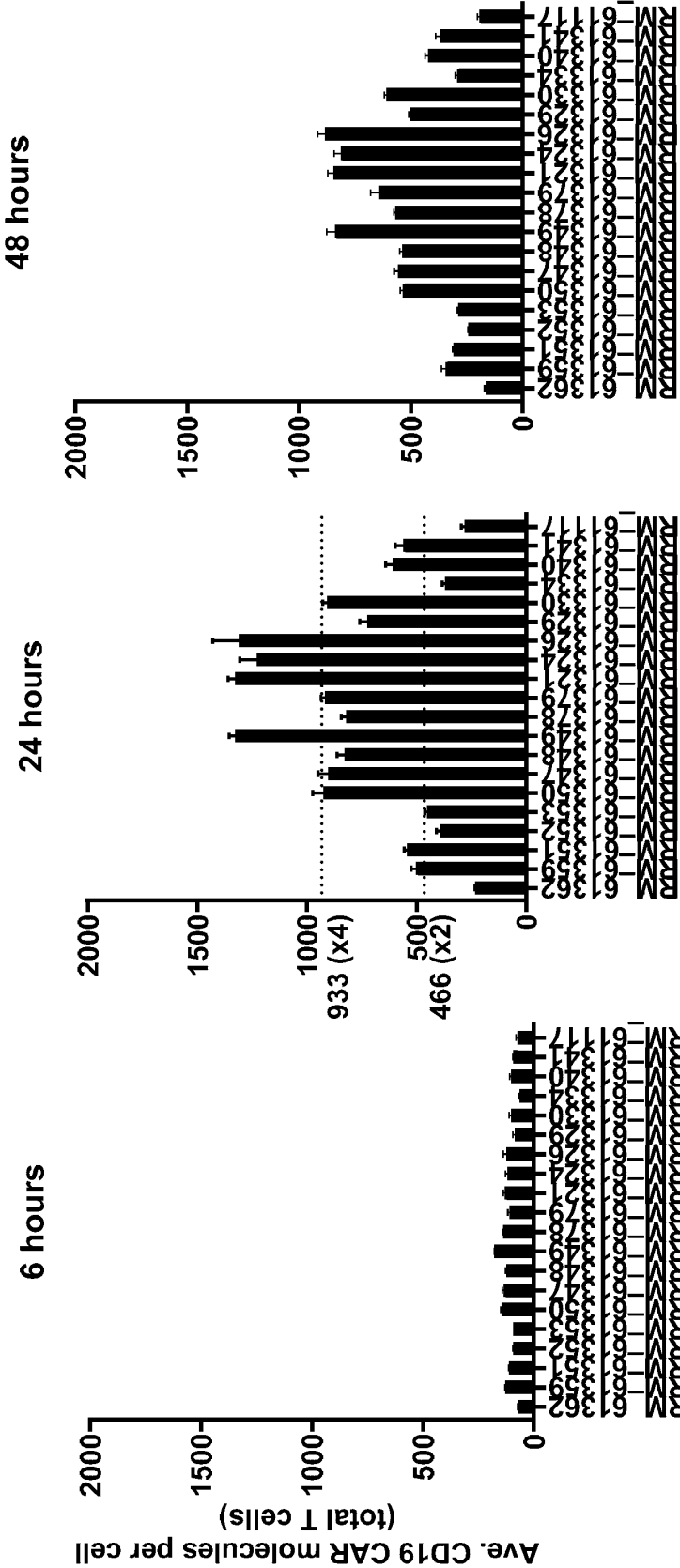


FIG. 3D

FIG. 3E

FIG. 3F

CAR1 - Human Donor 2

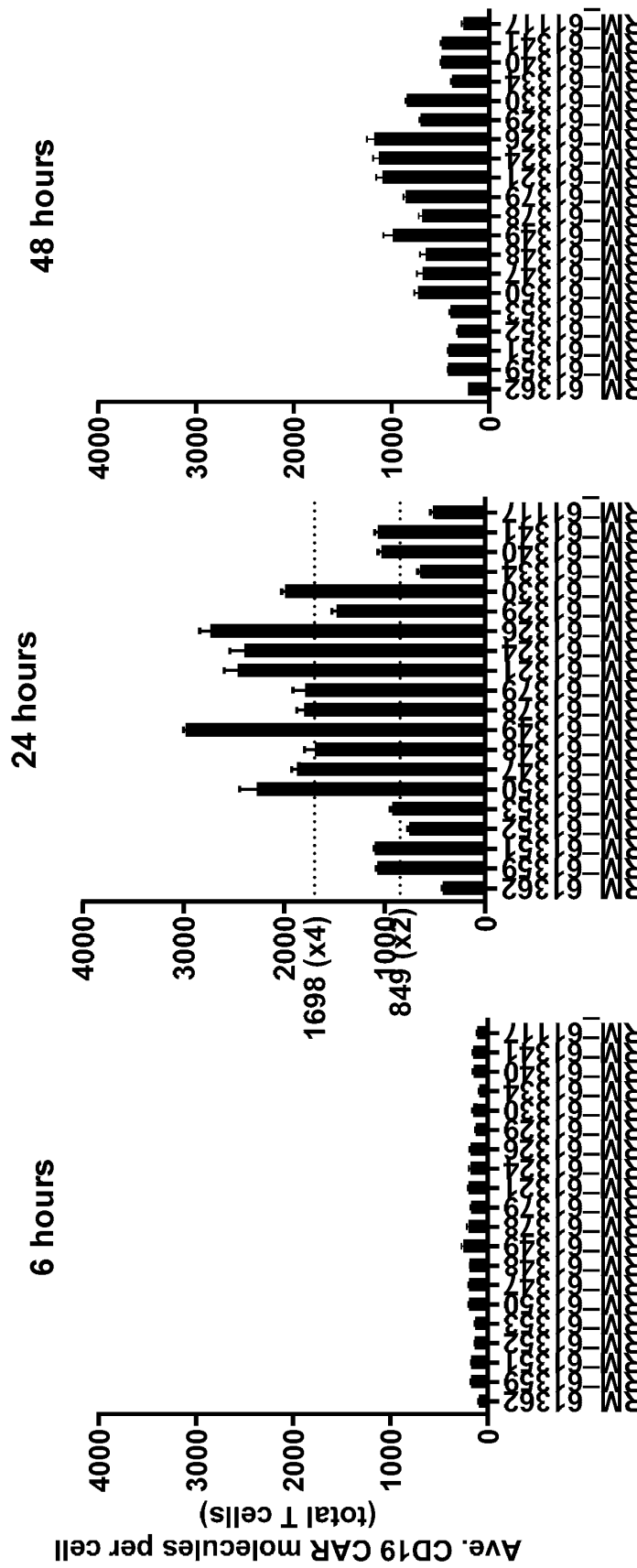


FIG. 3G

FIG. 3H

FIG. 31

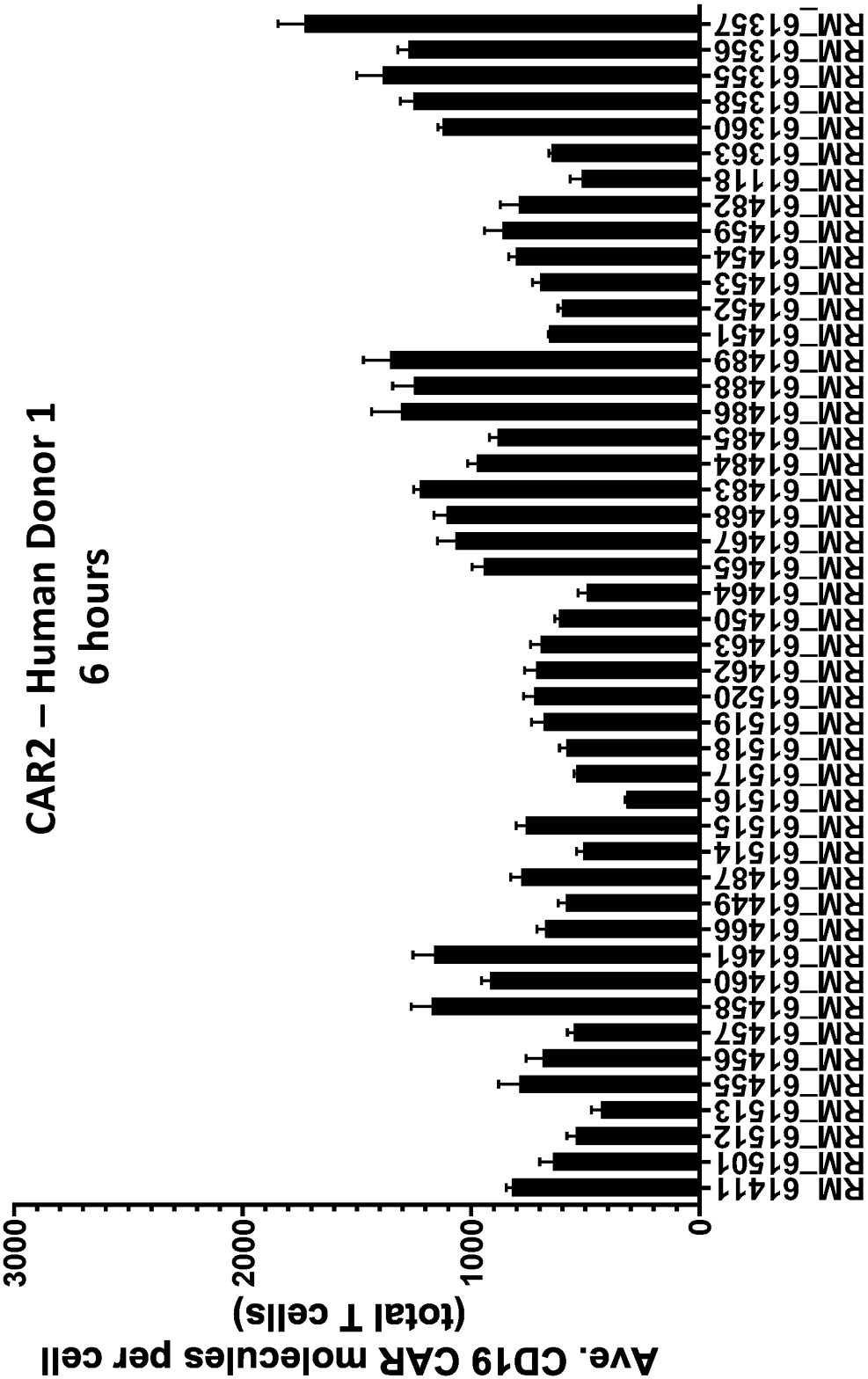


FIG. 3J

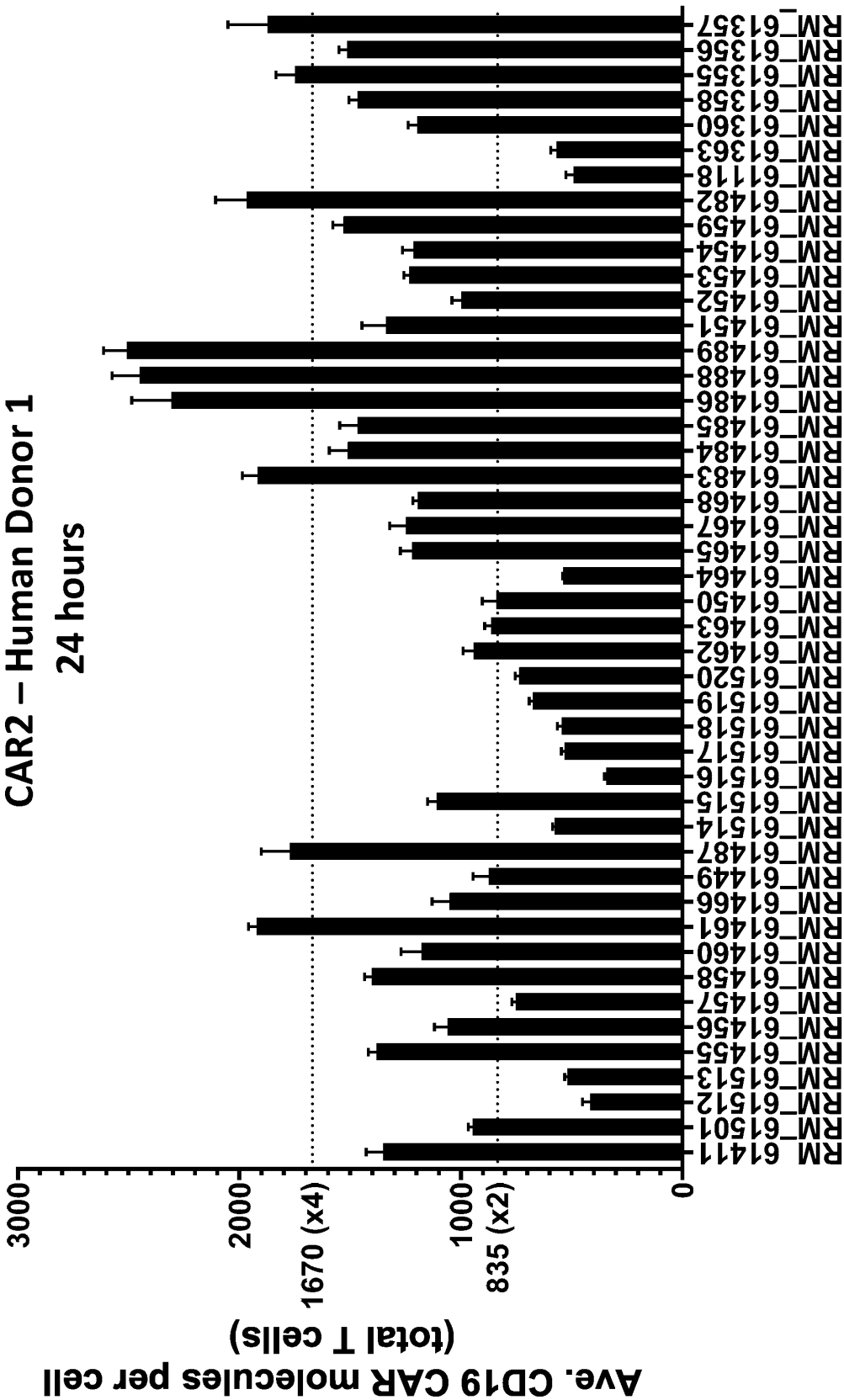


FIG. 3K

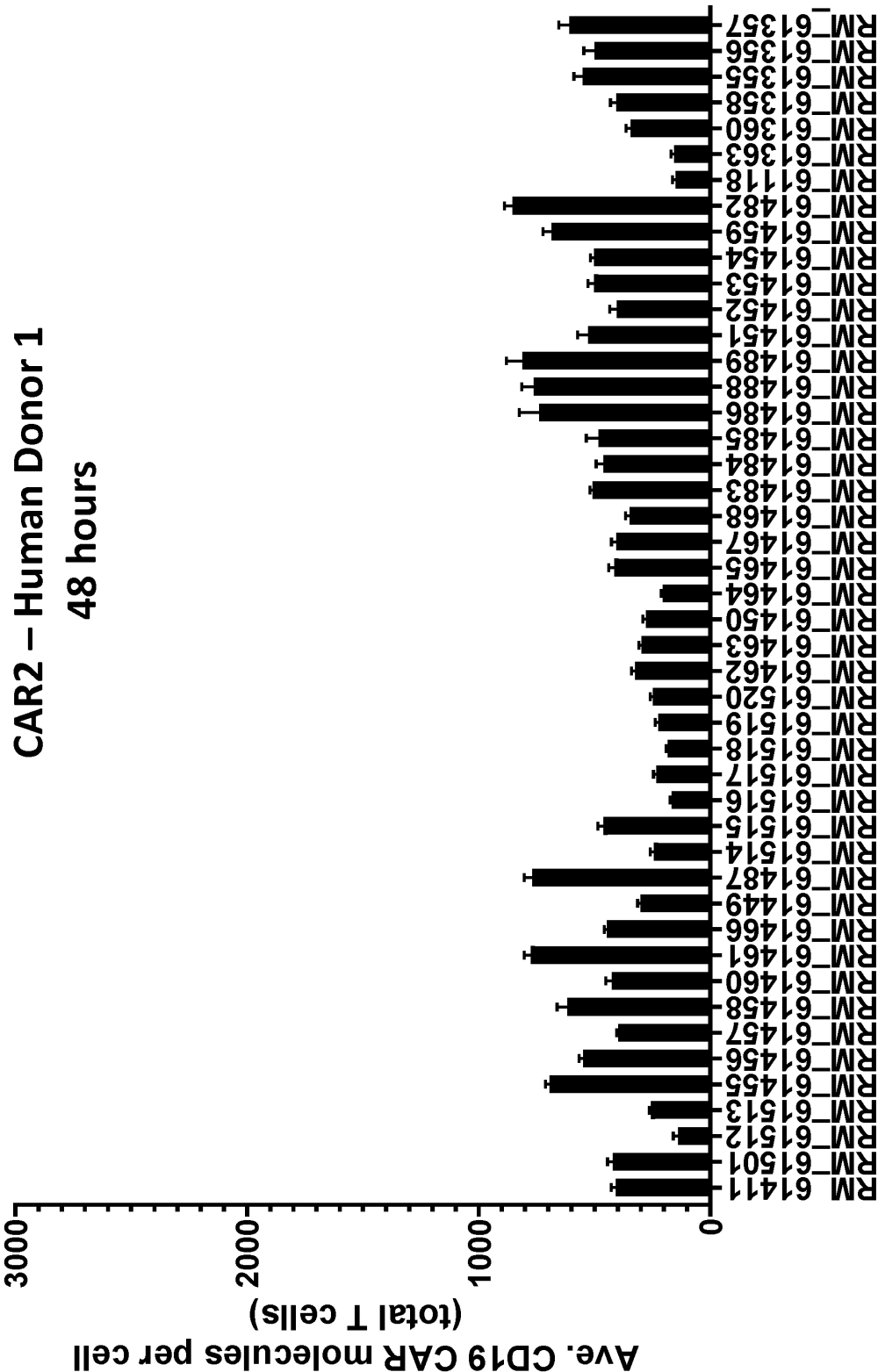


FIG. 3L

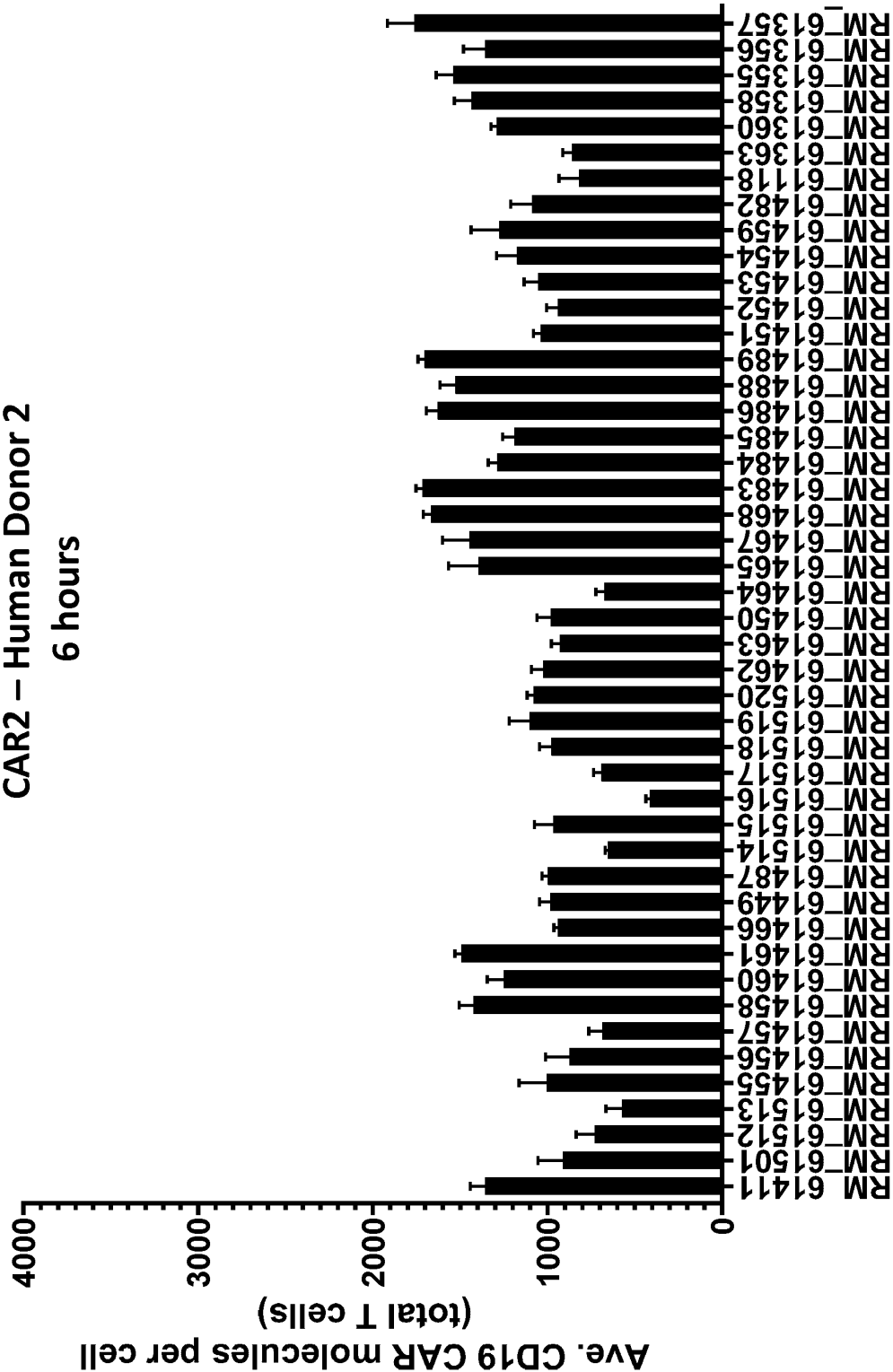


FIG. 3M

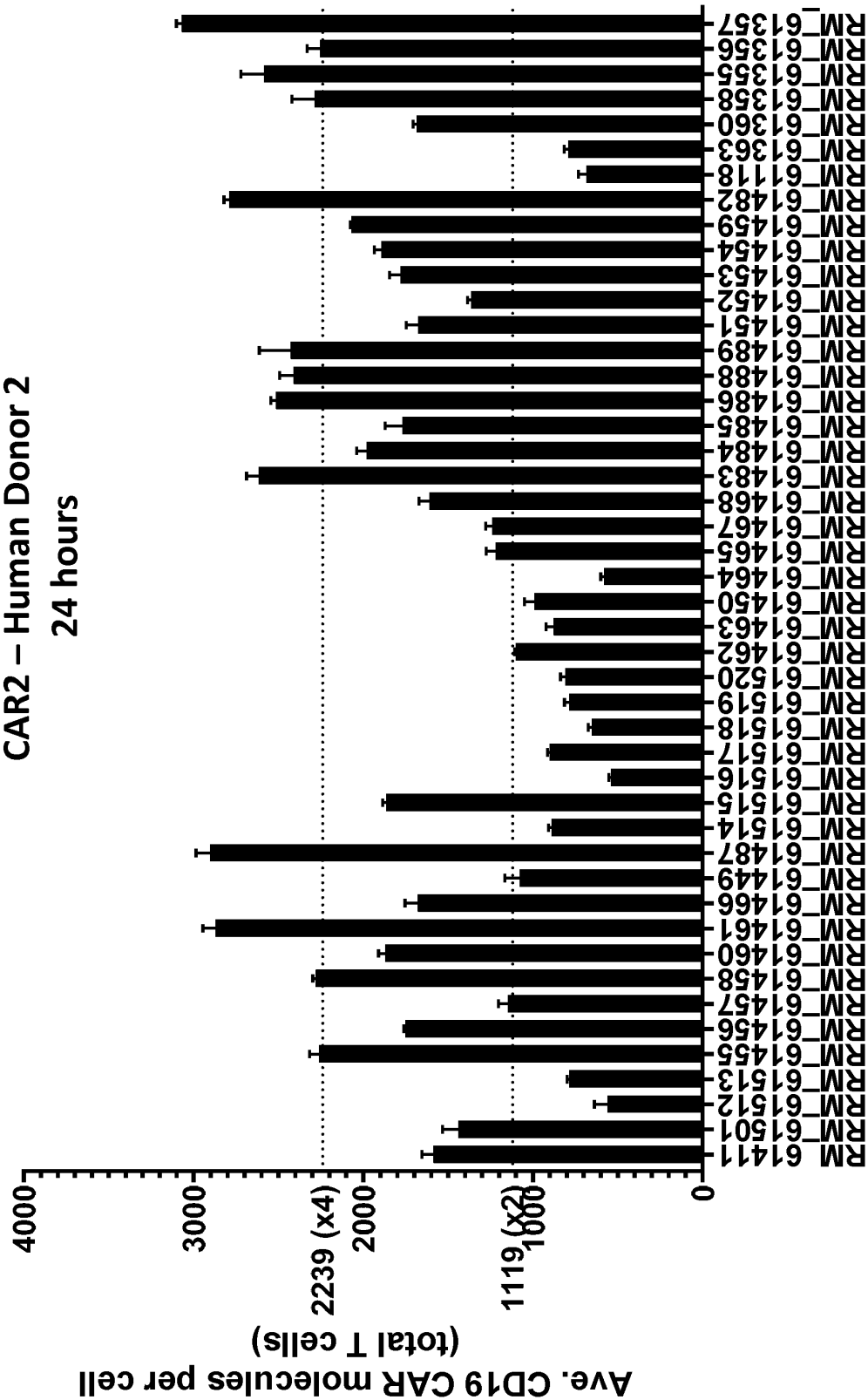


FIG. 3N

CAR2 – Human Donor 2
48 hours



FIG. 30

Expanded T cells from human donor 1

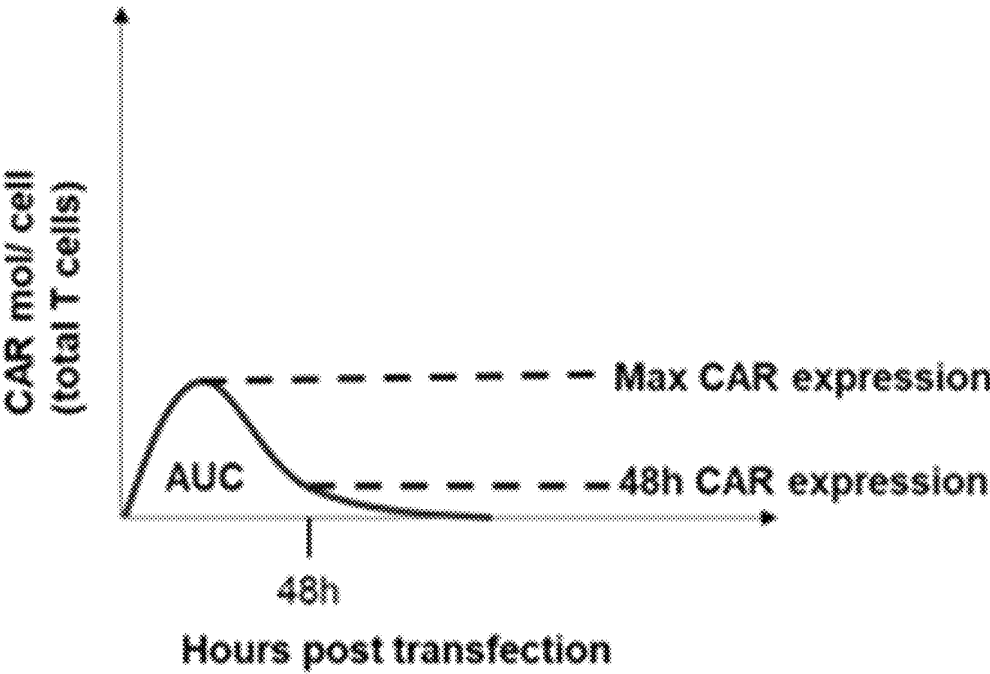


FIG. 4A

Expanded T cells from human donor 1

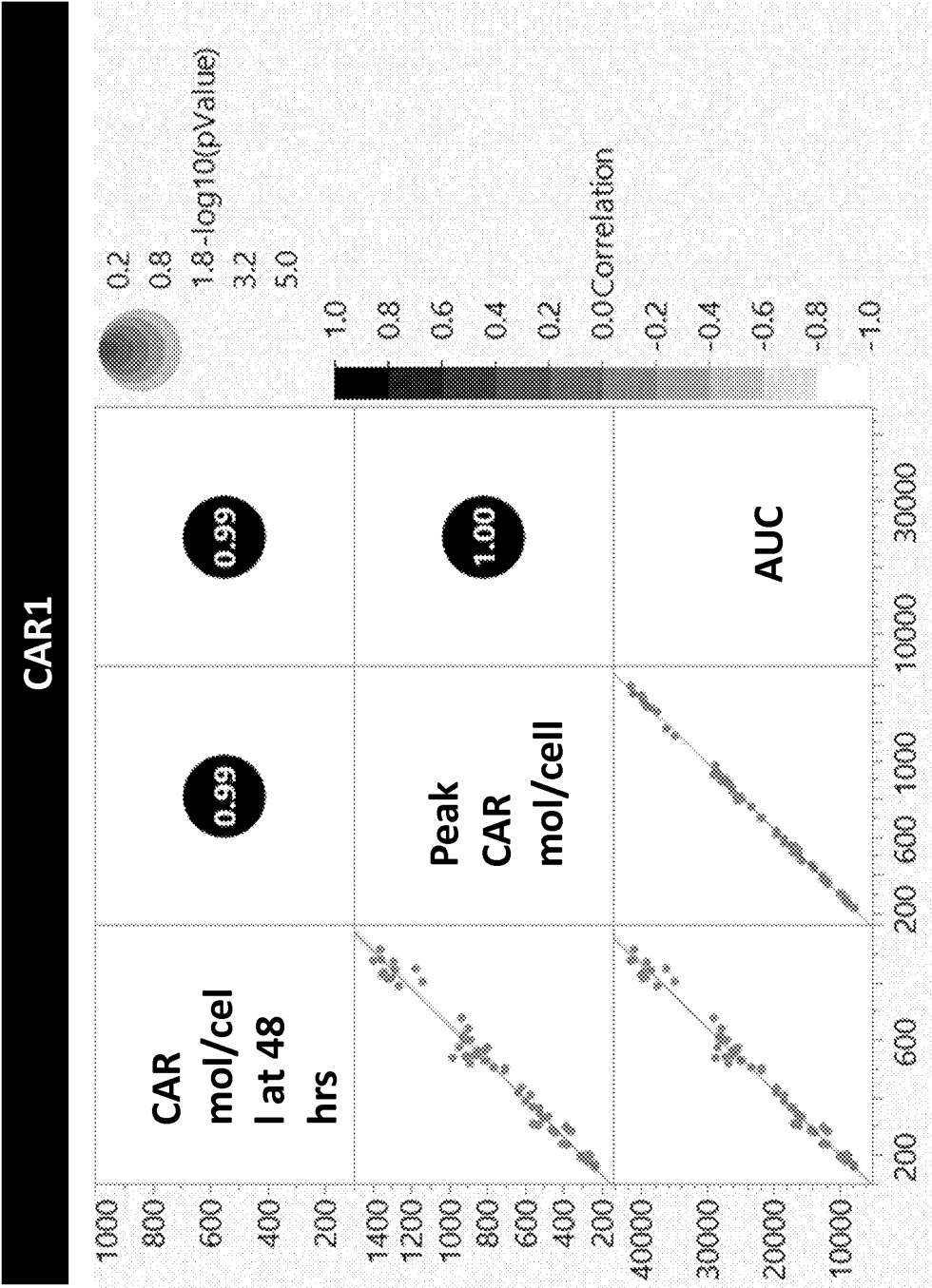


FIG. 4B

Expanded T cells from human donor 1

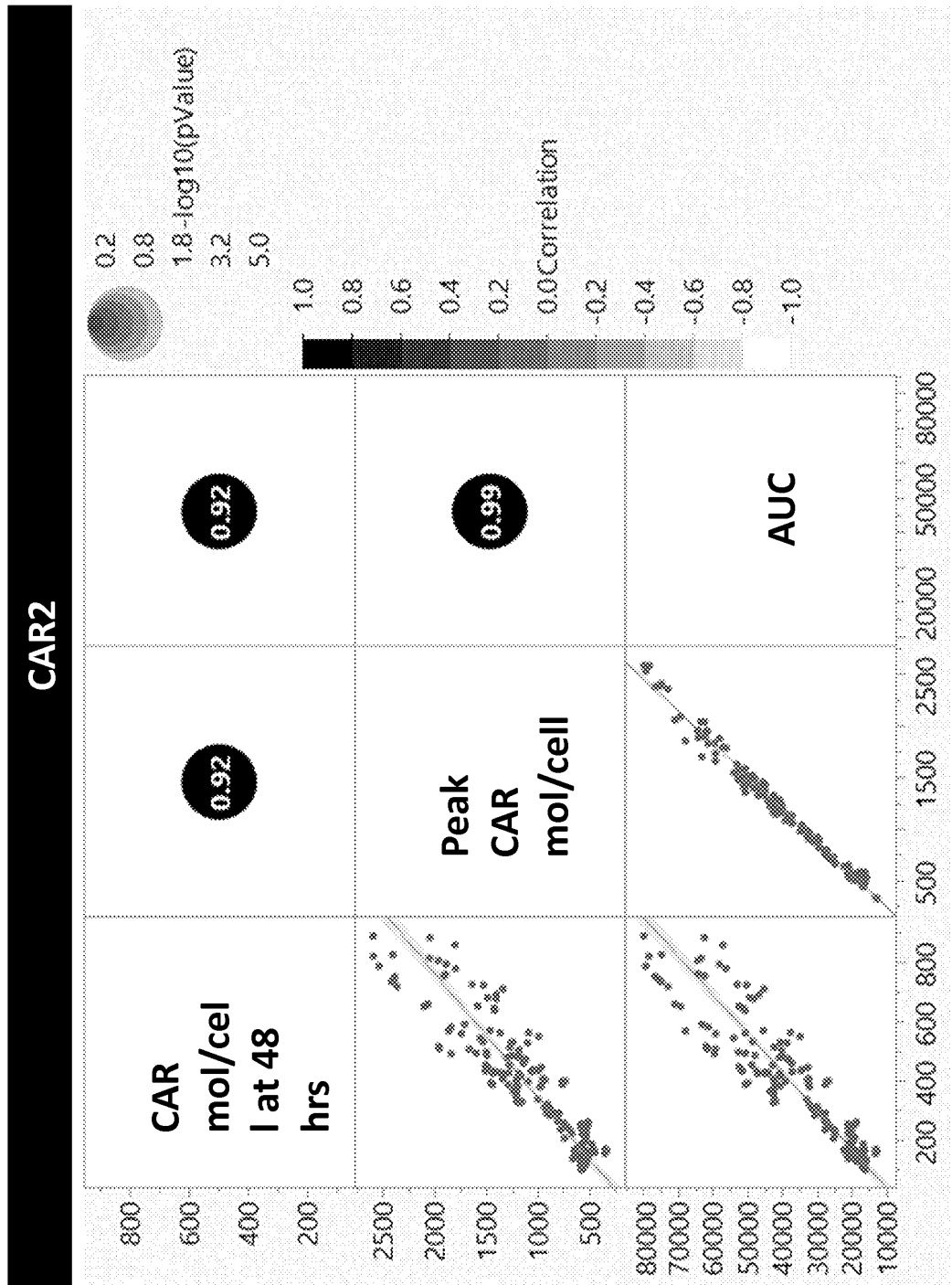
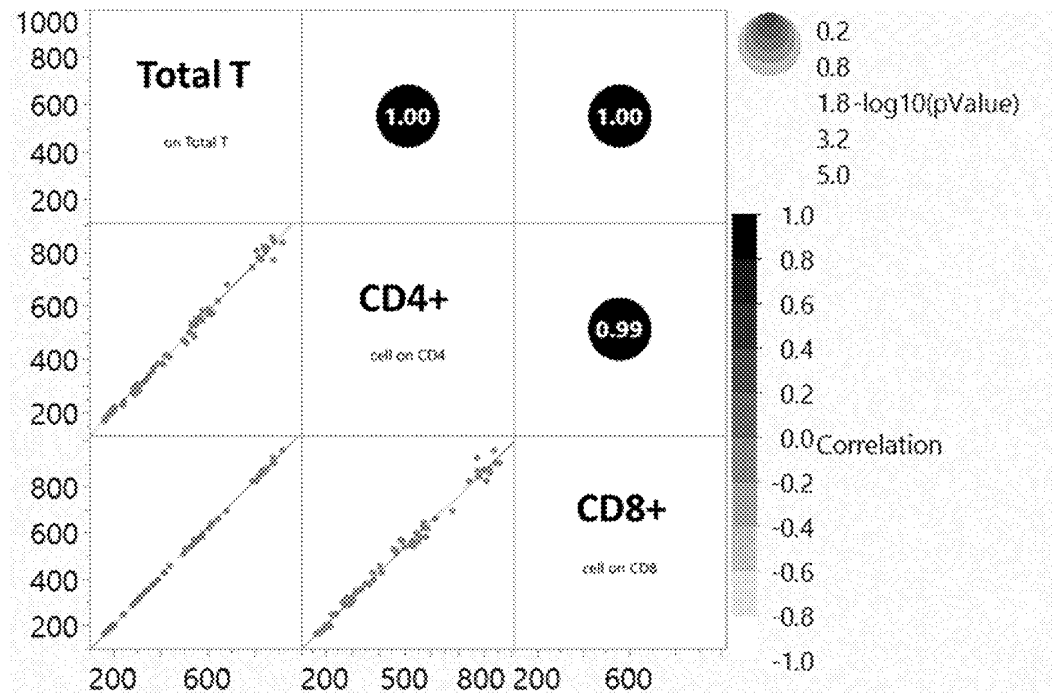


FIG. 4C

Expanded T cells from human donor 1

CAR1 mol/cell @48h



CAR2 mol/cell @48h

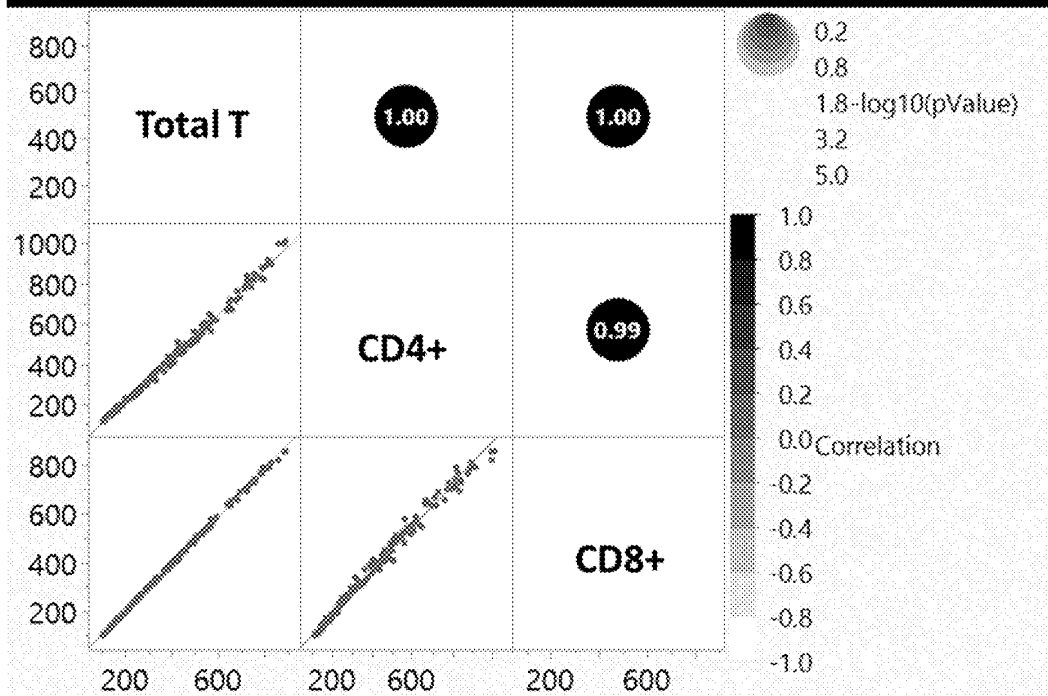
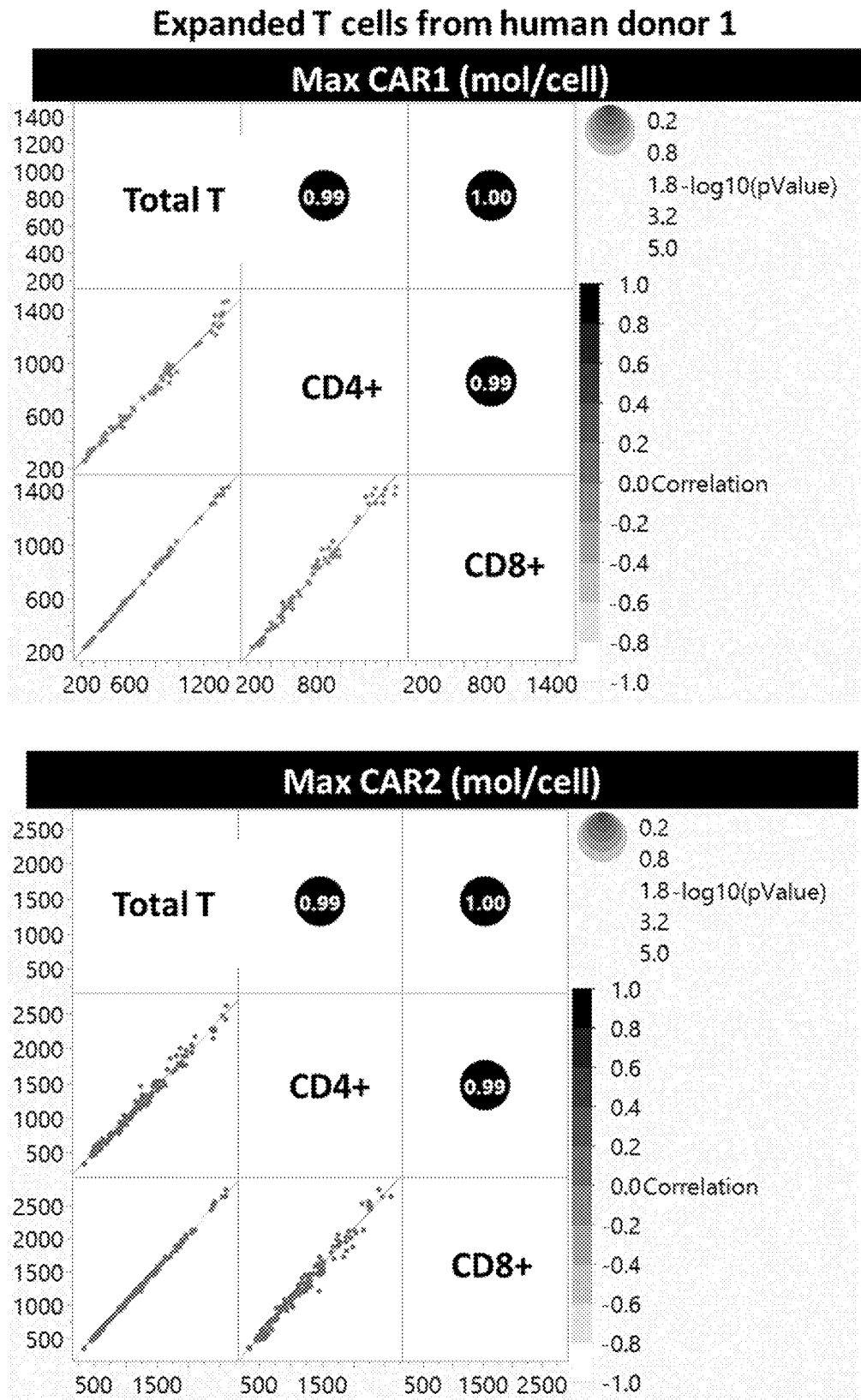


FIG. 4D

**FIG. 4E**

Expanded T cells from human donor 1

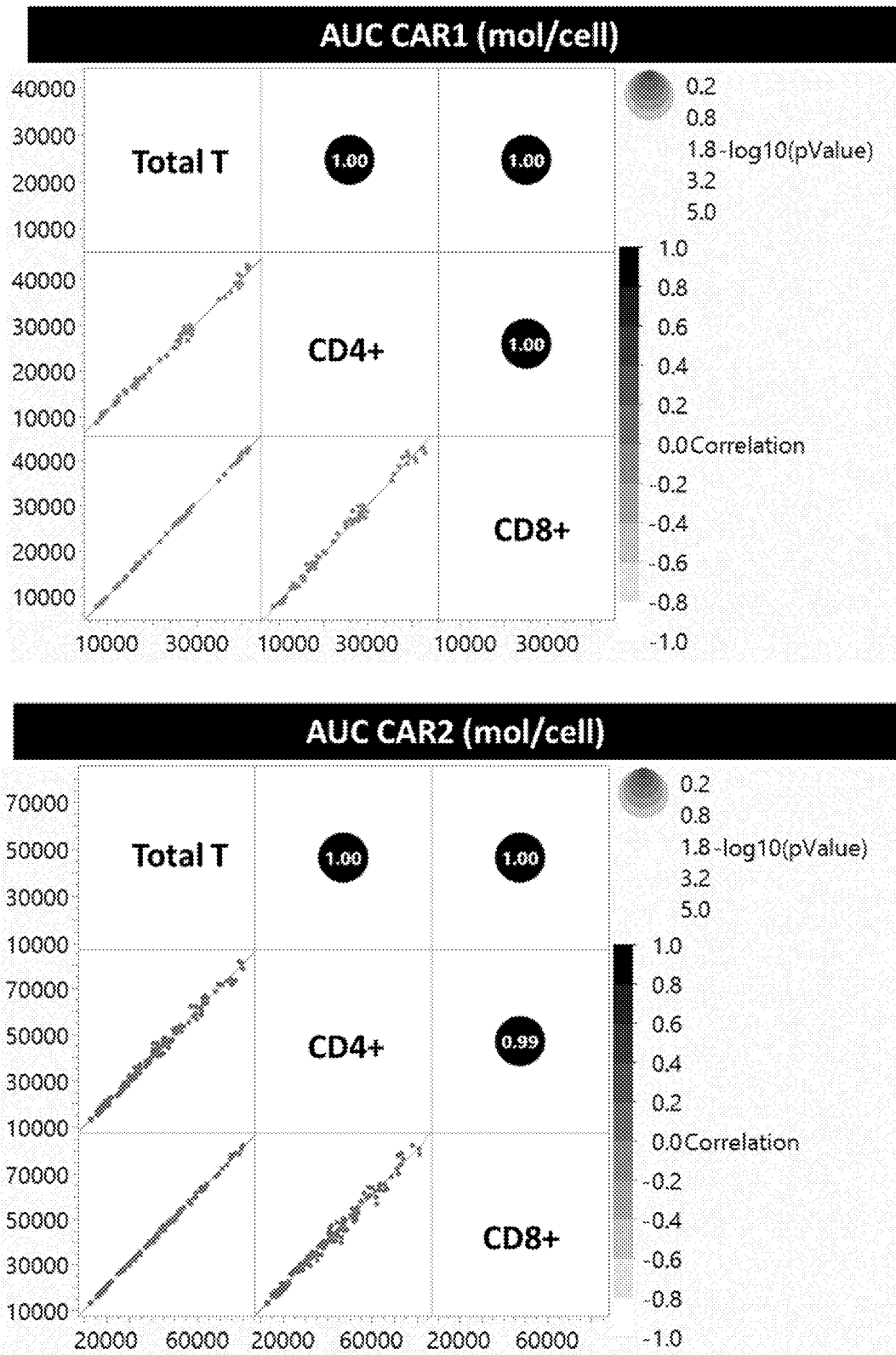
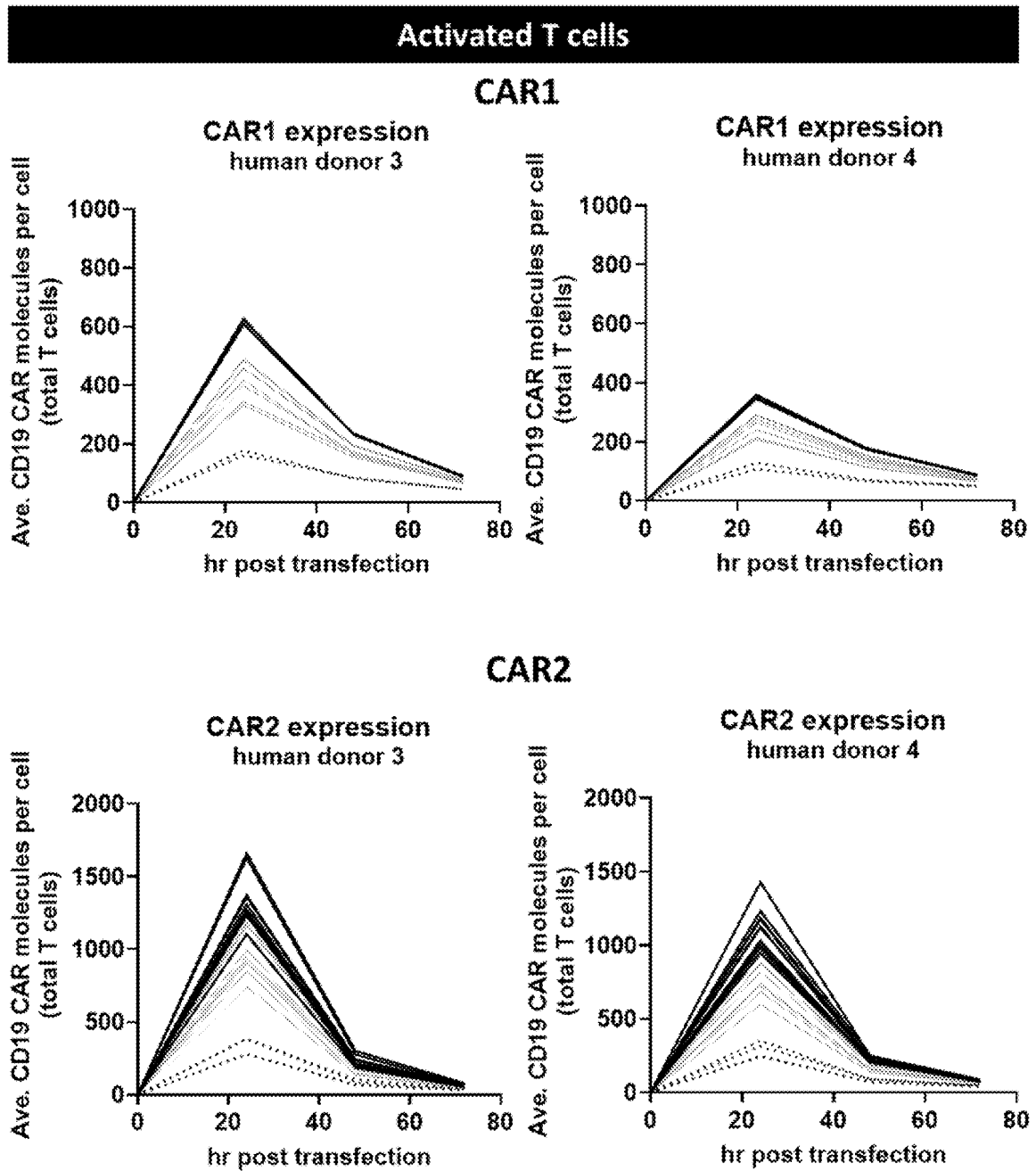


FIG. 4F

**FIG. 5A**

CAR1 – Human Donor 3

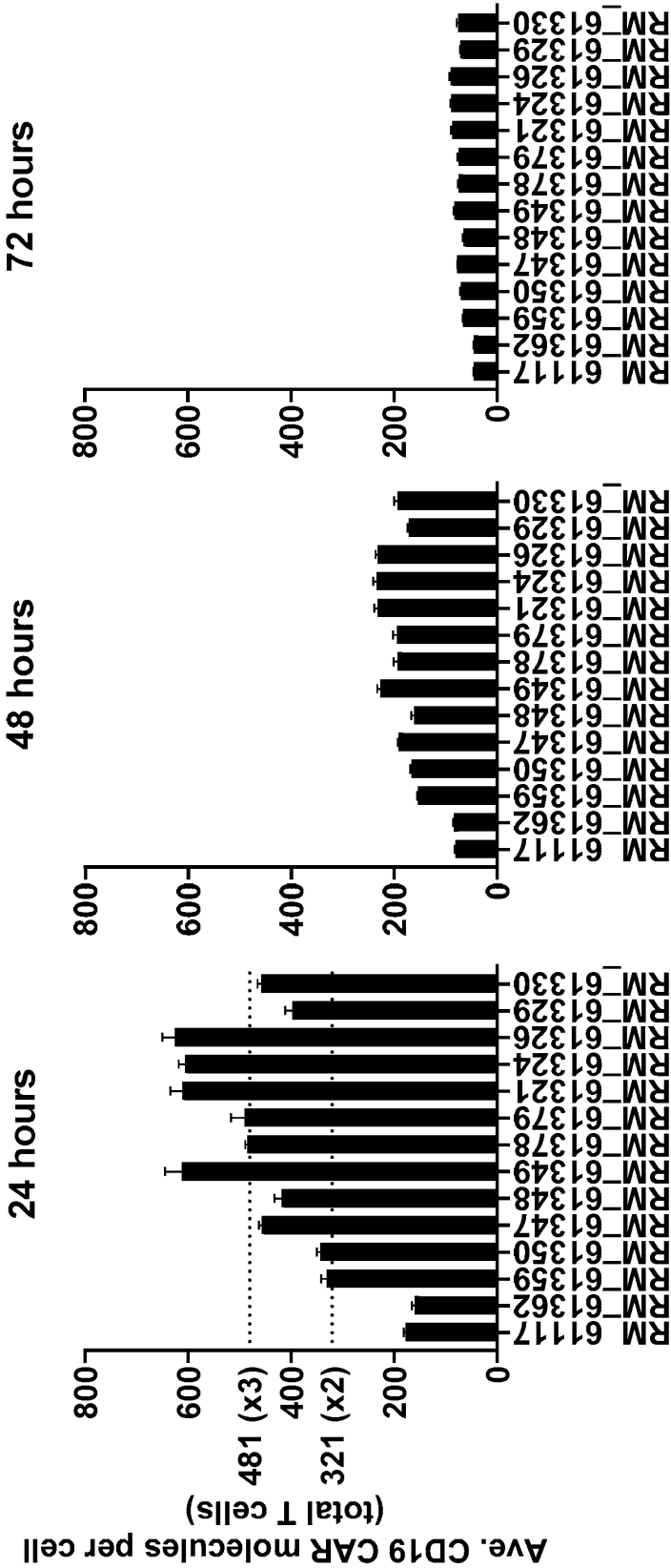


FIG. 5B

FIG. 5C

FIG. 5D

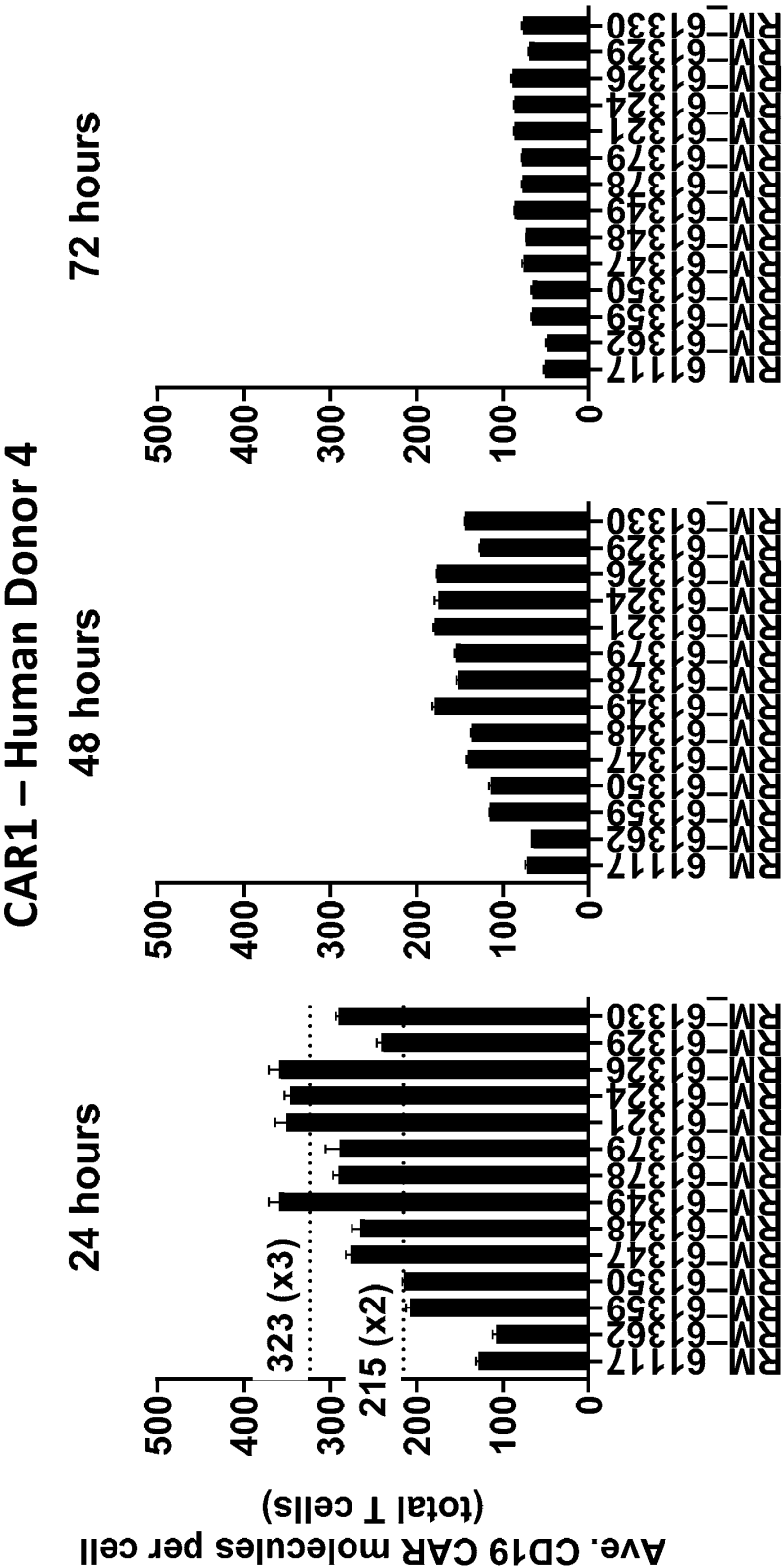


FIG. 5G

FIG. 5F

FIG. 5E

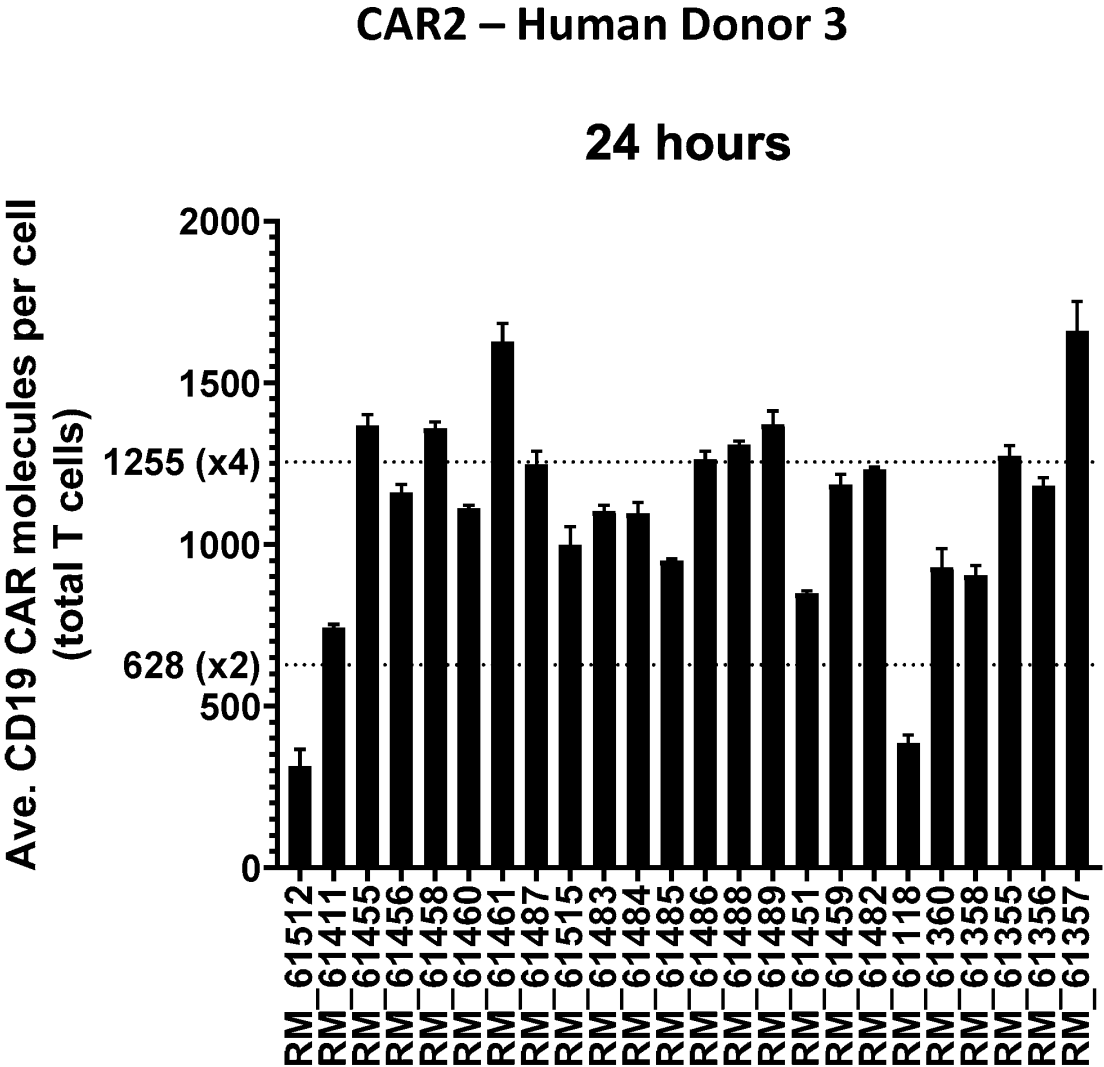


FIG. 5H

CAR2 – Human Donor 3

48 hours

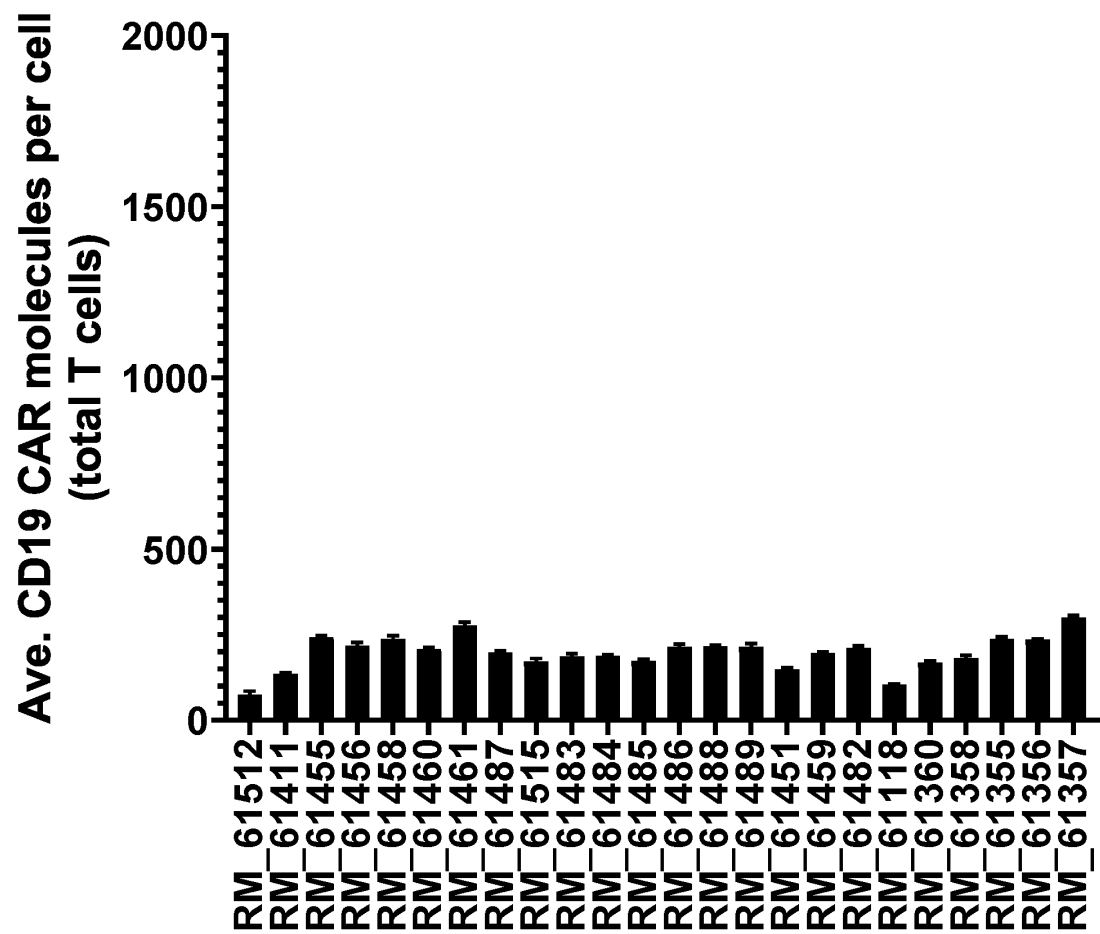


FIG. 5I

CAR2 – Human Donor 3
72 hours

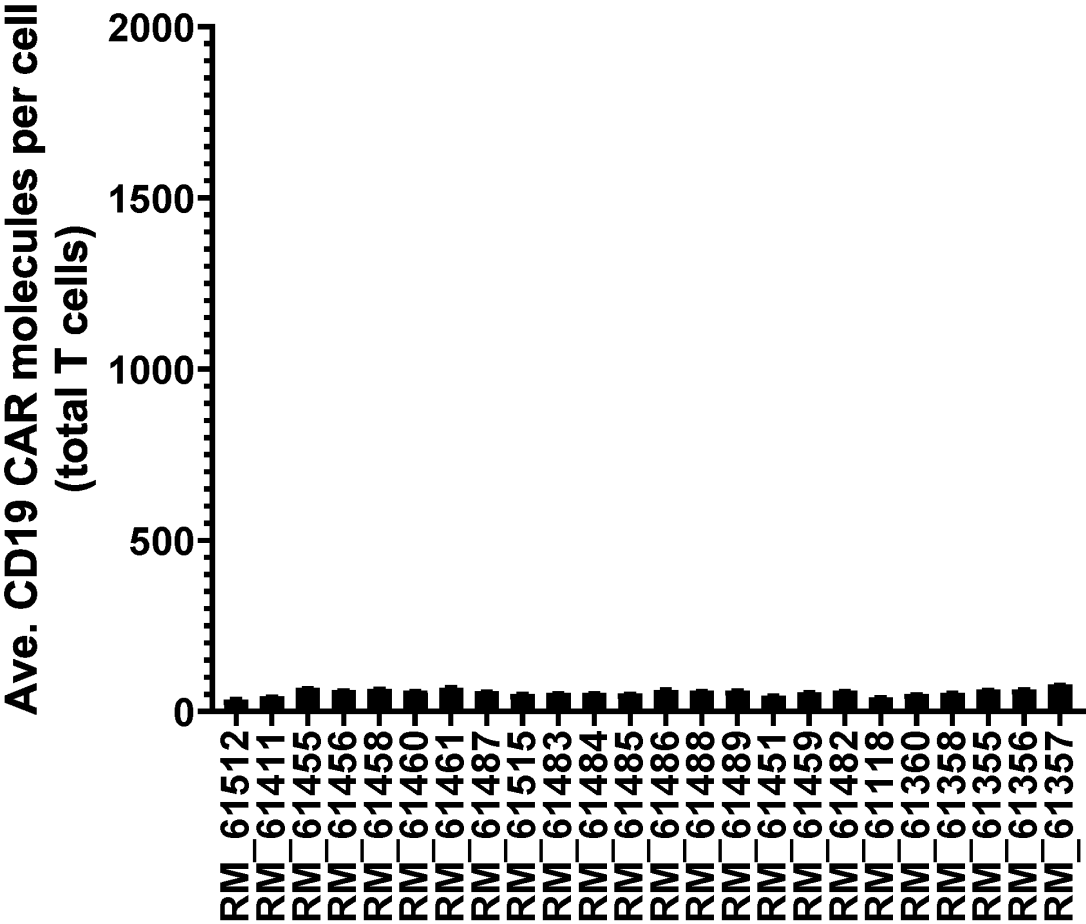


FIG. 5J

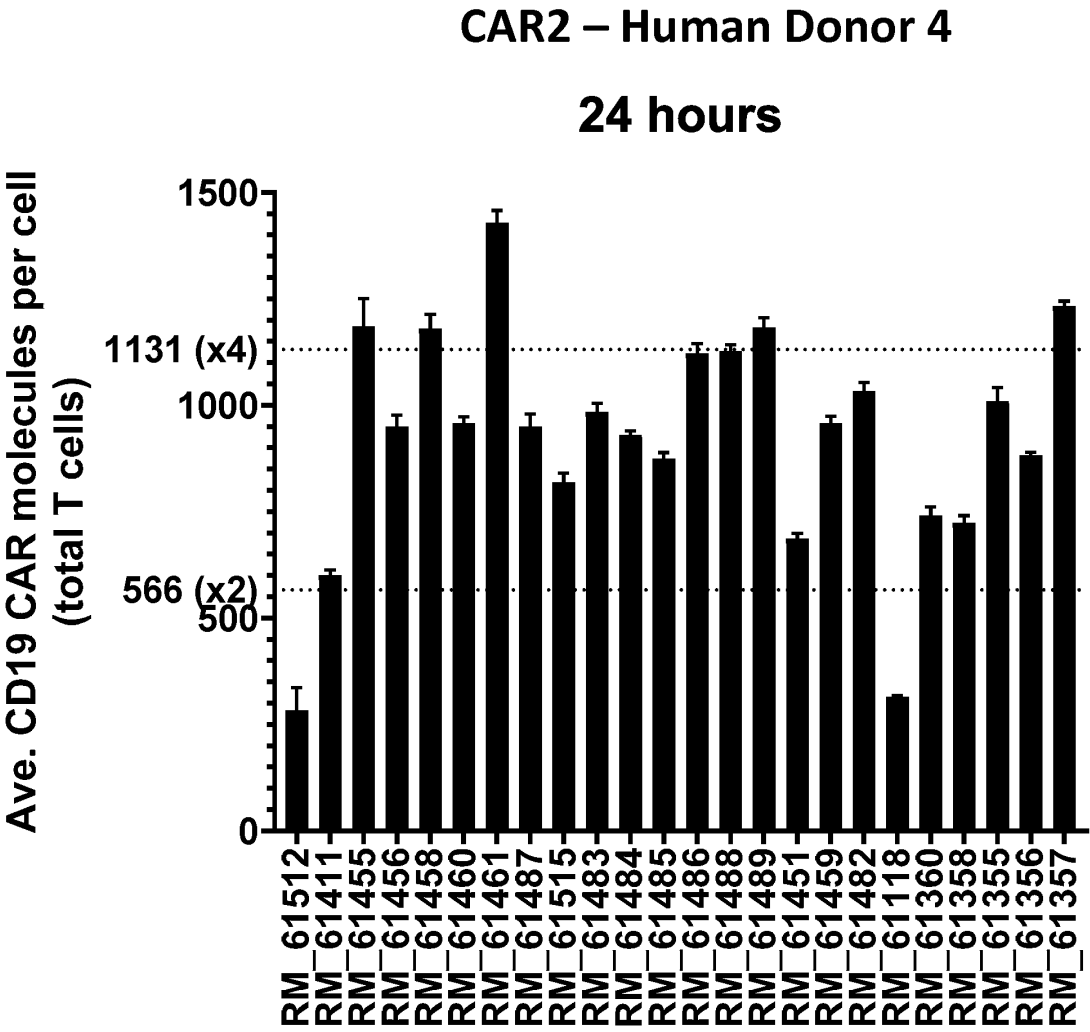


FIG. 5K

CAR2 – Human Donor 4

48 hours

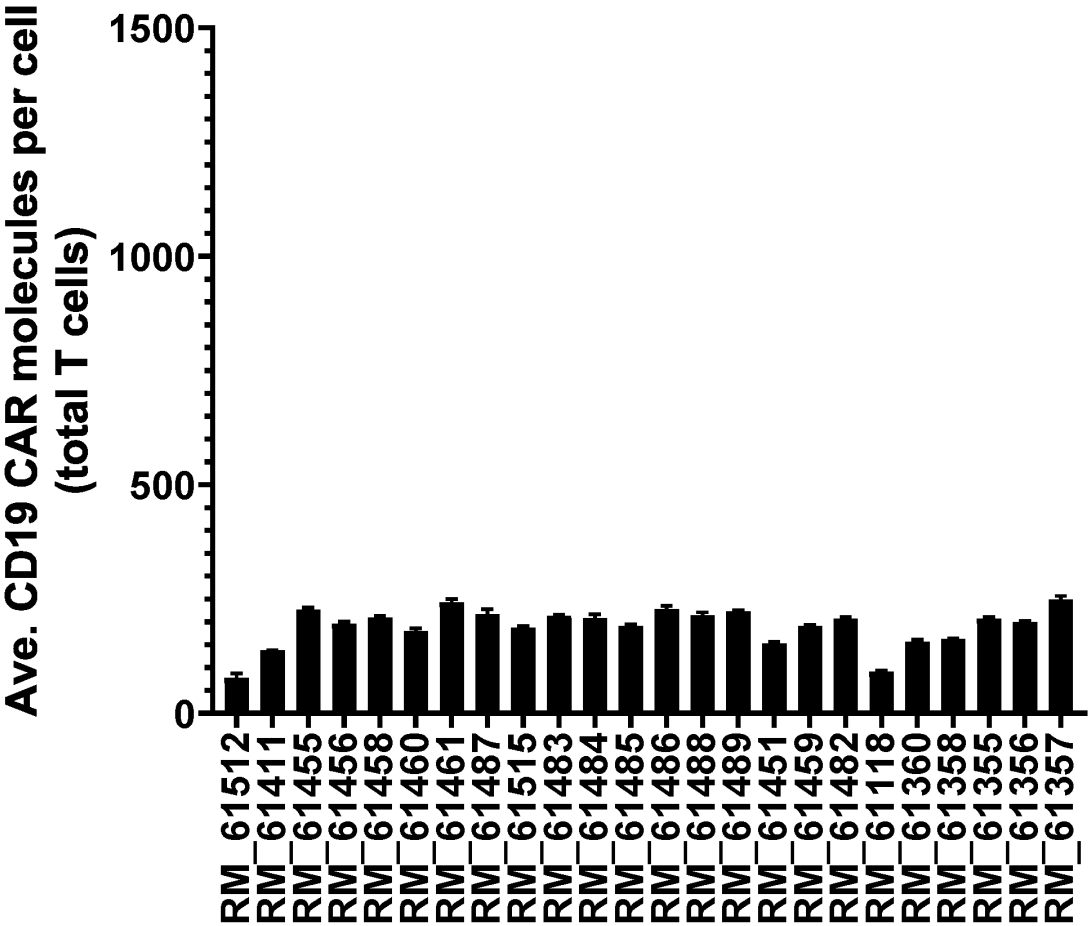


FIG. 5L

CAR2 – Human Donor 4

72 hours

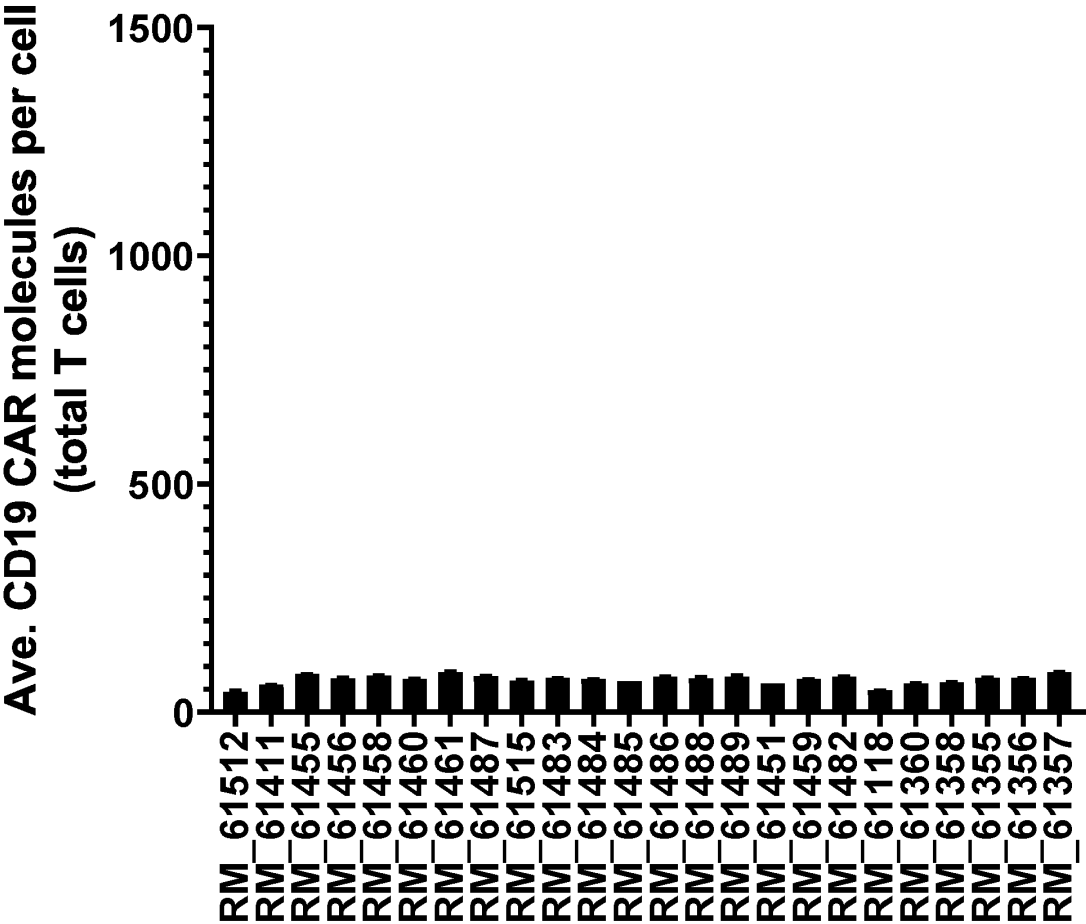


FIG. 5M

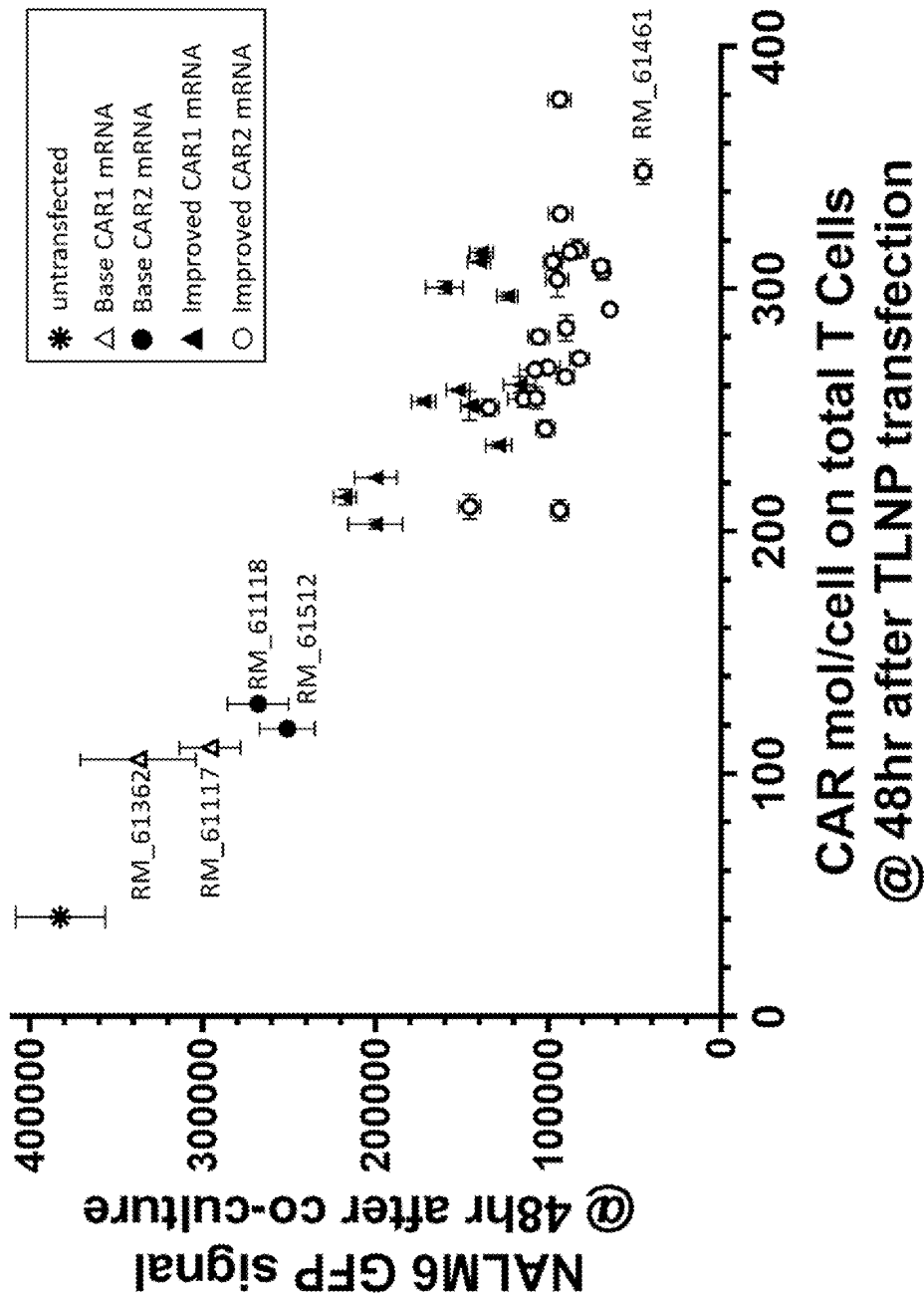
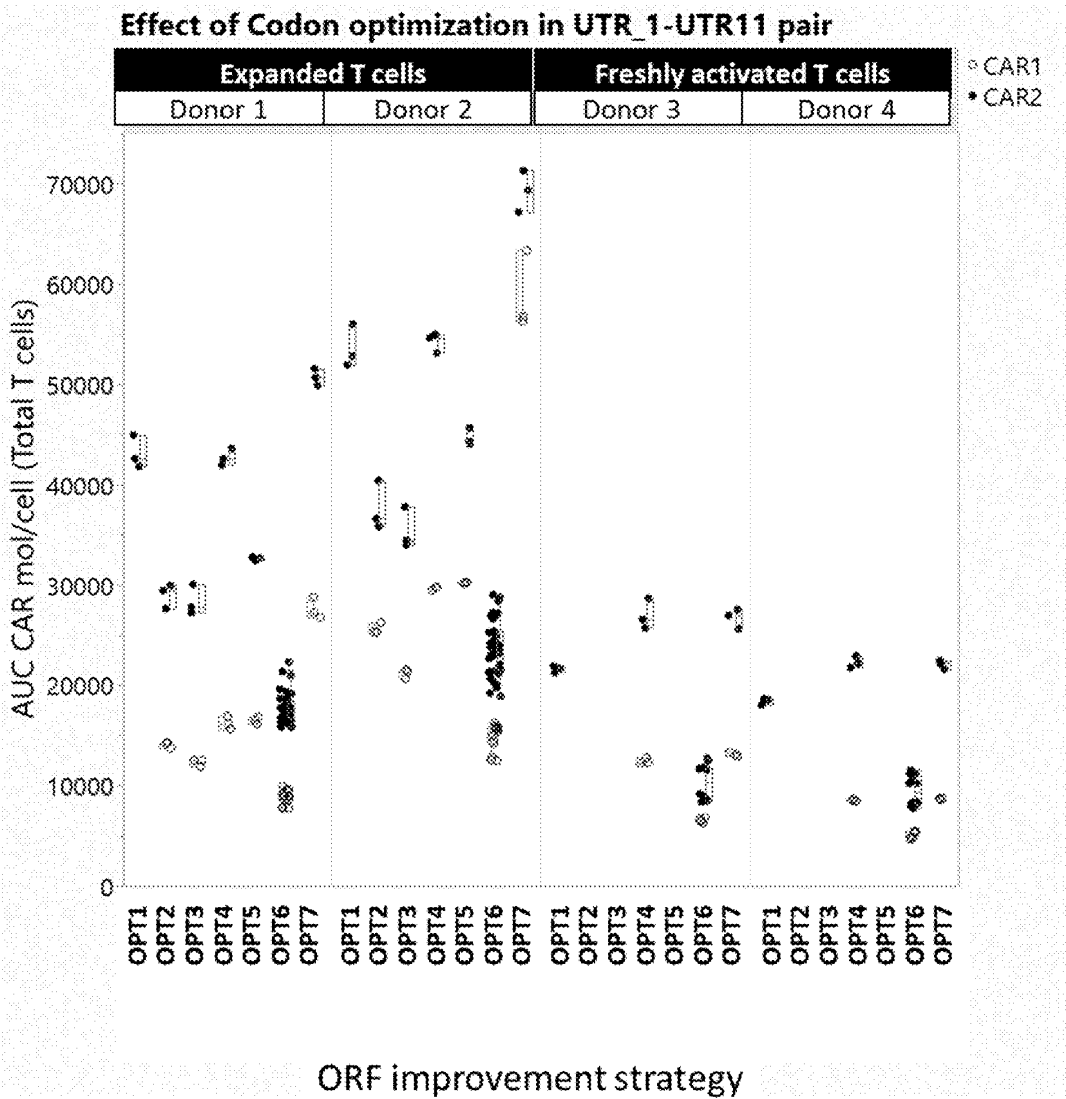
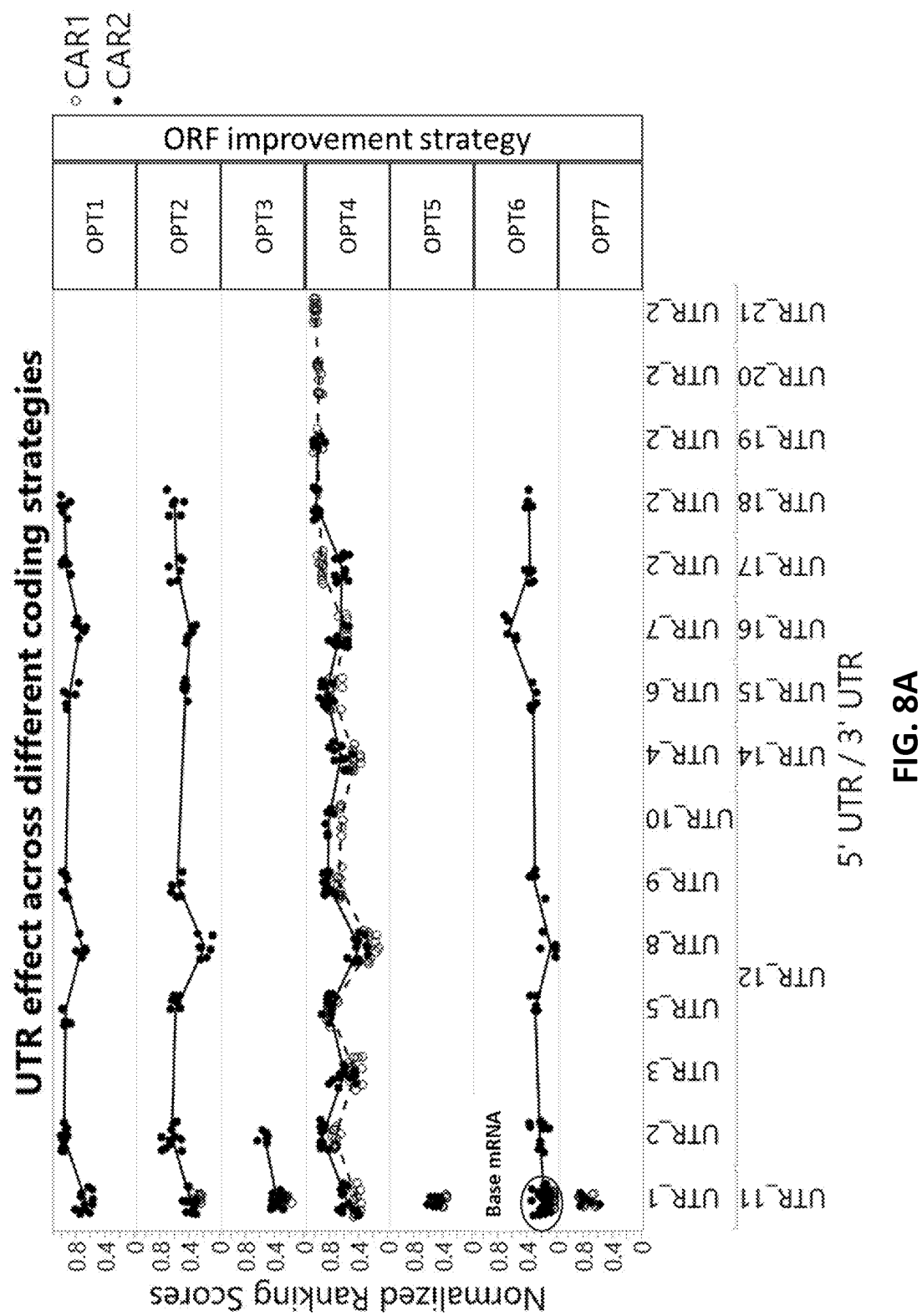


FIG. 6



UTR combination	UTR combination code
TEV_XBG	UTR_1 & UTR_11

FIG. 7



UTR combination	UTR combination code
TEV_XBG	UTR_1 & UTR_11
mHBB_PNLIP	UTR_2 & UTR_20
mHBB_RPS3A	UTR_2 & UTR_17
mHBB_RPS3A-PNLIP	UTR_2 & UTR_21
CPA1_CPA1	UTR_7 & UTR_16
DEFA3_DEFA3	UTR_6 & UTR_15
CD8a_hHBA1	UTR_8 & UTR_12
synthetic_hHBA1	UTR_3 & UTR_12
HBA_AES-mtRNR1	UTR_4 & UTR_14
mHBB_hHBA1	UTR_2 & UTR_12
hAlb_hHBA1	UTR_10 & UTR_12
mHBB_hHBA1-3x miR122 bs	UTR_2 & UTR_19
eIF4G aptamer x1_hHBA1	UTR_9 & UTR_12
aptamer control_hHBA1	UTR_5 & UTR_12
mHBB_PNLIP-RPS3A	UTR_2 & UTR_18

FIG. 8A (cont'ed)

UTR No. (FIG. 8A)	5' UTR (abbrev.)	SEQ ID NO.	Whole 5' UTR seq (whole 5' UTR length)	SEQ ID NO.	Core 5' UTR sequence (core 5' UTR length)
2	mouse hemoglobin subunit beta (mHBB)	11	AGCAUAAAAGUCACAUUU GCUUCUGACAUAGUUGUG UUGACUCACAACCCAGAA ACAGACAUCGAAUUCGCUG CCACC (79)	21	UCACAUUUGCUUCU GACAUAGUUGUGUU GACUCACAACCCAG AAACAGACAUC (54)
7	Carboxypeptidase A1 (CPA1)	12	AGCAUAAAAGCUCGGUCCU GGGAGGGUUUAAAAGCCA GGGGGCCGUCUCGACCUCA GUCUGACCUUCCCUCCCGG CAGCAGCGAAUUCGCUGCC ACC (97)	22	CUCGGUCCUGGGAG GGUUUAAAAGCCAG GGGGCCGUCUCGACC UCAGUCUGACCUUCC CUCCCGGCAGCAGC (72)
6	Defensin alpha 3 (DEFA3)	13	AGCAUAAAAGGGCUGCUCC UUGCUAUAGAAGACCUGG GACAGAGGACUGCUGUCU GCCUCUCUGGUCACCCUG CCUAGCUAGAGGAUCUGU GACCCCAGCCGAAUUCGCU GCCACC (117)	23	GGCUGCUCCUUGC UAGAAGACCUGGGAC AGAGGACUGCUGUC UGCCUCUCUGGUCA CCCUGCCUAGCUAGA GGAUCUGUGACCCCA GCC (92)
10	albumin (hAlb)	14	AGCAUAAAAGCUAGCUUU UCUCUUCUGUCAACCCAC ACGCCUUUGGCACAGAAUU CGCUGCCACC (66)	24	CUAGCUUUUCUCUUC UGUCAACCCACACG CCUUUGGCACA (41)
4	hemoglobin subunit alpha 1 (HBA)	15	AGCAUAAAAGACUAGUAU UCUUCUGGUCCCCACAGAC UCAGAGAGAACCCGAAUUC GCUGCCACC (65)	25	ACUAGUAUUCUUCU GGUCCCCACAGACUC AGAGAGAACCC (40)
9	single copy of aptamer for translation initiation factor 4G (eIF4G aptamer x1)	16	AGCAUAAAAGACUCACUAU UUGUUUUCGCGCCCAGUU GCAAAAAGUGUCGUAAUU GACUAAGAAUUCGCUGCCA CC (76)	26	ACUCACUAUUUGUU UUCGCGCCCAGUUGC AAAAAGUGUCGUAAU UGACUAA (51)

FIG. 8B

UTR No. (FIG. 8A)	5' UTR (abbrev.)	SEQ ID NO.	Whole 5' UTR seq (whole 5' UTR length)	SEQ ID NO.	Core 5' UTR sequence (core 5' UTR length)
5	sequence randomized - eIF4G aptamer (aptamer control)	17	AGCAUAAAAGGCUUCU AGCAAUAGGCUAUAAU UCUUCAUCGUGUUGUA ACAAGCGAACUCUGAA UUCGCUGCCACC (76)	27	GCUUCUAGCAAUAGGCU AUAAUUCUUCAUCGUG UUGUAACAAGCGAACUC U (51)
3	synthetic 5' UTR sequence (Synthetic)	18	AGCAUAAAAGAAUAA GAGAGAAAAGAAGAGU AAGAAGAAAUUAAGA CCCCGGCGCCGAAUUCG CUGCCACC (73)	28	AAAUAGAGAGAAAAGA AGAGUAAGAAGAAAUAU AAGACCCCGCGGCC (48)
1	Tobacco Etch Virus (TEV)	19	AGCAUAAAAGUCUCAAC ACAACAUAUACAAAACA AACGAAUCUCAAGCAAU CAAGCAUUCUACUUCU AUUGCAGCAAUUUAAA UCAUUUCUUUUAAAAGC AAAAGCAAUUUUCUGA AAAUUUUCACCAUUUA CGAACGAUAGCGAAUU CGCUGCCACC (157)	29	UCUCAACACAACAUUA CAAAACAAACGAAUCUC AAGCAAUCAAGCAUUCU ACUUCUAUUGCAGCAAU UUAAAUCAUUUCUUUU AAAGCAAAAGCAAUUUU CUGAAAAUUUUCACCAU UUACGAACGAUAGC (132)
8	CD8 alpha (CD8a)	20	AGCAUAAAAGAACUUU CCCCCUCGGCGCCCCA CCGGCUCGCGCGGCCU CCCCUCGCGCCCGAGCU UCGAGCCAAGCAGCGUC CUGGGGAGCGGUCGA AUUCGCUGCCACC (113)	30	AACUUUCCCCCUCGGC GCCCCACCGGCUCCCGC CGCCUCCCCUCGCGCCG AGCUUCGAGCCAAGCAG CGUCCUGGGGAGCGCG UC (88)
	common 5' end 10-nt sequence	7	AGCAUAAAAG		
	common 3' end 15-nt sequence	8	GAAUUCGCUGCCACC		

FIG. 8B (cont'ed)

UTR No. (FIG. 8A)	3' UTR (abbrev.)	SEQ ID NO.	Whole 3' UTR seq (whole 3' UTR length)	SEQ ID NO.	Core 3' UTR sequence (core 3' UTR length)
20	Pancreatic triacylglycerol lipase (PNLIP)	31	AGGAUCCGAGACUACUG UUAUUUGACCAUGAAU UGACUUCUAAUAAAAUC UAGUGGUGAUGCUGUAC A (69)	41	GAGACUACUGUUAUU UGACCAUGAAUUGA CUUCUAAUAAAAUCU AGUGGUGAUGC (56)
17	ribosomal protein S3A (RPS3A)	32	AGGAUCCAGUUCAGACU UCAAAUAGUGGCCAAUA AAAAGUGCUAUUUGUGA UGGUUUGCUUCUGUGU ACA (70)	42	AGUUCAGACUCAA UAGUGGCCAAUAAA AGUGCUAUUUGUGA UGGUUUGCUUCUG (57)
21	ribosomal protein S3A- Pancreatic triacylglycerol lipase (RPS3A- PNLIP)	33	AGGAUCCAGUUCAGACU UCAAAUAGUGGCCAAUA AAAAGUGCUAUUUGUGA UGGUUUGCUUCUGGAGA CUACUGUUAUUUGACCA AUGAAUUGACUUCUAAU AAAAUCUAGUGGUGAUG CUGUACA (126)	43	AGUUCAGACUCAA UAGUGGCCAAUAAA AGUGCUAUUUGUGA UGGUUUGCUUCUGG AGACUACUGUUAUUU GACCAUGAAUUGAC UUCUAAUAAAAUCU GUGGUGAUGC (113)
18	Pancreatic triacylglycerol lipase- ribosomal protein S3A (PNLIP-RPS3A)	34	AGGAUCCGAGACUACUG UUAUUUGACCAUGAAU UGACUUCUAAUAAAAUC UAGUGGUGAUGCAGUUC AGACUUCAAUAGUGGC AAAUAAAAAGUGCUAUU UGUGAUGGUUUGCUUC UGUGUACA (126)	44	GAGACUACUGUUAUU UGACCAUGAAUUGA CUUCUAAUAAAAUCU AGUGGUGAUGCAGU UCAGACUUCAAUAG UGGCAAUAAAAAGU GCUAUUUGUGAUGG UUUGCUUCUG (113)
12	hemoglobin subunit alpha 1 (hHBA1)	35	AGGAUCCGCGGAGCCU CGGUGGCCAUGCUUCU GCCCCUUGGGCCUCCCC CAGCCCCUCCUCCCCUUC CUGCACCCGUACCCCGU GGUCUUUGAAUAAAGUC UGAGUGGGCGGCAUGUA CA (124)	45	GCUGGAGCCUCGGUG GCCAUGCUUCUUGCC CCUUGGGCCUCCCCC AGCCCCUCCUCCCCU CCUGCACCCGUACCC CGUGGUCUUUGAAU AAAGUCUGAGUGGGC GGCA (111)

FIG. 8C

UTR No. (FIG. 8A)	3' UTR (abbrev.)	SEQ ID NO.	Whole 3' UTR seq (whole 3' UTR length)	SEQ ID NO.	Core 3' UTR sequence (core 3' UTR length)
19	hemoglobin subunit alpha 1 with 3 copies of miR-122 binding sites (hHBA1-3x miR122 bs)	36	AGGAUCCCAAACACCAUUG UCACACUCCAGCUGGAGCC UCGGUGGCCAUGCUCUUCU GCCCCUUGGGCCCCAAACAC CAUUGUCACACUCCAUCCC CCCAGCCCCUCCUCCCCUUC CUGCACC CGUACCCCCAAA CACCAUUGUCACACUCCAG UGGUCUUUGAAUAAAGUC UGAGUGGGCGGCAUGUAC A (190)	46	CAAACACCAUUGUCACA CUCCAGCUGGAGCCUCG GUGGCCAUGCUCUUCUUG CCCCUUGGGCCCCAAACA CCAUUGUCACACUCCA CCCCCAGCCCCUCCUCC CCUUCCUGCACC CGUAC CCCCCAAACACCAUUGU CACACUCCAGUGGUCUU UGAAUAAAGUCUGAGU GGGCGGCA (177)
16	Carboxypeptidase A1 (CPA1)	37	AGGAUCCGCUGACCCUUUG ACACCCUUCUUGUCCUCCU CUCUGGCCCCAUCCAGGCA ACCAAUAAAGUUUGAGUG UACCAGGAACAGAAUCCUG GGGCUUGCUGUACA (109)	47	GCUGACCCUUUGACACC CUUCUUGUCCUCCUCUC UGGCCCAUCCAGGCAA CCAAUAAAGUUUGAGU GUACCAGGAACAGAAUC CUGGGGCUUGC (96)
15	Defensin alpha 3 (DEFA3)	38	AGGAUCCGCUUGCAGAAAA AGAAAAAUGAGCUAAAAU UUGC UUUGAGAGCUACAG GGAAUUGCUAUUACUCCUG UACCUUCUGCUCAAUUUCC UUUCCUCAUCUCAAUAAA UGCCUUGUUACAAGAUGU ACA (134)	48	GCUUGCAGAAAAAGAAA AAUGAGCUAAAAUUUG CUUUGAGAGCUACAGG GAAUUGCUAUUACUCCU GUACCUUCUGCUCAAUU UCCUUUCCUCAUCUCAA AUAAAUGCCUUGUUACA AGA (121)
14	amino-terminal enhancer of split-mitochondrially encoded 12S rRNA (AES-mtRNR1)	39	AGGAUCCUGGUACUGCAU GCACGCAUAGCUAGCUGCC CCUUUCCCGUCCUGGGUAC CCCGAGUCUCCCCGACCUC GGGUCCCAGGUAUGCUCUCC ACCUCCACCUGCCCCACUCA CCACCUCUGCUAGUUCAG ACACCUCCAAGCACGCAGC AAUGCAGCUAAAACGCUU AGCCUAGCCACCCCCACG GGAAACAGCAGUGAUUAA CUUUAGCAAUAAACGAAAG UUUAACUAAGCUAUACUAA CCCCAGGGUUGGUCAAUUU CGUGCCAGCCACACCCUGG AUGUACA (296)	49	CUGGUACUGCAUGCACG CAAUGCUAGCUGCCCCU UUCCCGUCCUGGGUACC CCGAGUCUCCCCGACC UCGGGUCCCAGGUAUGC UCCACCUCCACCUGCC CACUACCACCUUCUGCU AGUCCAGACACCUCCC AAGCACGCAGCAAUGCA GCUAAAACGCUUAGCC UAGCCACACCCCCACGG GAAACAGCAGUGAUUAA CCUUUAGCAAUAAACGA AAGUUUAACUAAGCUAU ACUAACCCCAGGGUUGG UCAAUUUCGUGCCAGCC ACACCCUGGA (283)

FIG. 8C (cont'ed)

UTR No. (FIG. 8A)	3' UTR (abbrev.)	SEQ ID NO.	Whole 3' UTR seq (whole 3' UTR length)	SEQ ID NO.	Core 3' UTR sequence (core 3' UTR length)
11	Xenopus beta globin (XBG)	40	AGGAUCCAGUGACU GACUAGGAUCUGGU UACCACUAAACCAGC CUCAAGAACACCCGA AUGGAGUCUCUAAG CUACAUAUACCAAC UUACACUUACAAAA UGUUGUCCCCCAAA AUGUAGCCAUUCGU AUCUGCUCUAAUA AAAAGAAAGUUUCU UCACAUUCUGUACA (171)	50	GGUUACCACUAAACC AGCCUCAAGAACACC CGAAUGGAGUCUCUA AGCUACAUAUACCA ACUUACACUUACAAA AUGUUGUCCCCCAAA AUGUAGCCAUUCGUA UCUGCUCUAAUAAA AAGAAAGUUUCUUC CAUUC (140)
11	Xenopus beta globin - no BsrGI (XBG-no BsrGI)	51	GGAUCCAGUGACUG ACUAGGAUCUGGUU ACCACUAAACCAGCC UCAAGAACACCCGA AUGGAGUCUCUAAG CUACAUAUACCAAC UUACACUUACAAAA UGUUGUCCCCCAAA AUGUAGCCAUUCGU AUCUGCUCUAAUA AAAAGAAAGUUUCU UCACAUUC (164)	50	GGUUACCACUAAACC AGCCUCAAGAACACC CGAAUGGAGUCUCUA AGCUACAUAUACCA ACUUACACUUACAAA AUGUUGUCCCCCAAA AUGUAGCCAUUCGUA UCUGCUCUAAUAAA AAGAAAGUUUCUUC CAUUC (140)
	common 5' end 7-nt sequence	9	AGGAUCC		
	common 3' end 6-nt sequence	10	UGUACA		

FIG. 8C (cont'ed)

CAR1 mean rank sum score of Screening in Examples 2 and 3 in freshly activated human T cells.

normalized to the highest rank sum in each column								
	R4	R4	R4	R4	R4	R4	R5	R4-5
RM	AUC CAR mol/cell on Total T at 48 hrs R4	CAR mol/cell on Total T at 48 hrs R 4	Max CAR mol/cell on Total T at 48 hrs R4	AUC CAR mol/cell on Total T at 48 hrs R4	CAR mol/cell on Total T at 48 hrs R 4	Max CAR mol/cell on Total T at 48 hrs R4	CAR mol/cell on Total T at 48 hrs R 5	average rank Normaliz ed
RM_61326	1.000	0.974	1.000	1.000	0.893	1.000	0.927	0.970
RM_61321	0.939	0.969	0.935	0.922	1.000	0.918	1.000	0.955
RM_61349	0.930	0.882	0.944	0.991	0.987	1.000	0.797	0.933
RM_61324	0.939	1.000	0.913	0.862	0.880	0.874	0.837	0.901
RM_61379	0.704	0.668	0.701	0.690	0.742	0.636	0.553	0.671
RM_61378	0.713	0.646	0.727	0.698	0.674	0.675	0.545	0.668
RM_61330	0.574	0.651	0.563	0.629	0.592	0.693	0.634	0.619
RM_61347	0.565	0.603	0.554	0.517	0.515	0.515	0.659	0.561
RM_61348	0.409	0.293	0.433	0.440	0.438	0.468	0.415	0.413
RM_61329	0.400	0.445	0.372	0.362	0.361	0.364	0.341	0.378
RM_61350	0.287	0.349	0.277	0.276	0.236	0.286	0.268	0.283
RM_61359	0.209	0.223	0.216	0.216	0.253	0.208	0.195	0.217
RM_61117	0.130	0.061	0.130	0.129	0.129	0.130	0.122	0.119
RM_61362	0.052	0.122	0.052	0.052	0.052	0.052	0.049	0.061

FIG. 9A

CAR2 mean rank sum score of Screening in Examples 2 and 3 in freshly activated human T cells.

RM	normalized to the highest rank sum in each column							R4-5 average rank Normalized
	R4	R4	R4	R4	R4	R4	R5	
	AUC CAR mol/cell on Total T R4	CAR mol/cell on Total T at 48 hrs R 4	Max CAR mol/cell on Total T R4	AUC CAR mol/cell on Total T R4	CAR mol/cell on Total T at 48 hrs R 4	Max CAR mol/cell on Total T R4	CAR mol/cell on Total T at 48 hrs R 5	
RM_61357	1.000	1.000	1.000	0.948	1.000	0.948	1.000	0.985
RM_61461	0.978	0.961	0.996	1.000	0.978	1.000	0.958	0.982
RM_61455	0.900	0.900	0.899	0.900	0.895	0.883	0.915	0.899
RM_61458	0.891	0.853	0.894	0.874	0.690	0.883	0.829	0.845
RM_61489	0.873	0.680	0.903	0.887	0.847	0.887	0.815	0.842
RM_61488	0.803	0.693	0.815	0.779	0.753	0.792	0.739	0.768
RM_61486	0.725	0.673	0.733	0.792	0.891	0.788	0.716	0.760
RM_61355	0.777	0.857	0.762	0.680	0.642	0.684	0.770	0.739
RM_61482	0.677	0.647	0.689	0.710	0.631	0.710	0.570	0.662
RM_61487	0.659	0.519	0.698	0.589	0.766	0.541	0.622	0.628
RM_61356	0.633	0.844	0.590	0.407	0.528	0.403	0.723	0.590
RM_61456	0.563	0.703	0.559	0.528	0.496	0.550	0.549	0.564
RM_61483	0.441	0.429	0.465	0.654	0.751	0.636	0.387	0.538
RM_61459	0.568	0.494	0.597	0.545	0.437	0.563	0.420	0.518
RM_61460	0.493	0.617	0.474	0.511	0.345	0.558	0.484	0.497
RM_61484	0.441	0.437	0.449	0.511	0.659	0.485	0.430	0.487
RM_61485	0.336	0.316	0.341	0.385	0.437	0.390	0.207	0.345
RM_61515	0.354	0.307	0.363	0.338	0.397	0.338	0.289	0.341
RM_61358	0.288	0.372	0.280	0.273	0.299	0.268	0.263	0.292
RM_61360	0.306	0.294	0.311	0.286	0.251	0.290	0.286	0.289
RM_61451	0.223	0.221	0.225	0.221	0.236	0.221	0.136	0.212
RM_61411	0.183	0.182	0.185	0.182	0.183	0.182	0.131	0.176
RM_61118	0.131	0.143	0.132	0.104	0.127	0.104	0.070	0.116
RM_61512	0.070	0.065	0.070	0.078	0.071	0.078	0.028	0.066

FIG. 9B

RM	MEAN_CAR mol/cell on Total T at 48hr after tLNP transfection	CAR mol/cel Standard error	Nalm6 GFP @ 48hr after co- culture	GFP standard error	CAR2 expression rel. to the base	CAR1 expression rel. to the base	residual Nalm6 cells
RM_61411	208.6	4.16	93427	5179	1.8		24%
RM_61512	118.5	0.62	251144	16048	1.0		66%
RM_61455	330.9	2.51	93025	6690	2.8		24%
RM_61456	280.2	2.96	105550	6075	2.4		28%
RM_61458	316.4	3.83	83283	6450	2.7		22%
RM_61460	271.1	2.17	81816	5745	2.3		21%
RM_61461	348.3	5.03	45109	4827	2.9		12%
RM_61487	291.4	1.92	64324	3184	2.5		17%
RM_61515	254.5	3.45	114029	9204	2.1		30%
RM_61483	263.5	1.09	90047	4993	2.2		24%
RM_61484	267.5	2.01	100206	7097	2.3		26%
RM_61485	242.2	3.45	101787	5594	2.0		27%
RM_61486	307.0	3.32	68479	4166	2.6		18%
RM_61488	309.1	2.26	69423	4785	2.6		18%
RM_61489	314.9	2.90	87411	9658	2.7		23%
RM_61451	210.0	5.02	145354	6203	1.8		38%
RM_61459	266.4	2.37	107773	9099	2.2		28%
RM_61482	283.8	5.33	89588	4511	2.4		23%
RM_61118	128.7	0.95	267936	17639	1.1		70%
RM_61362	105.8	0.61	337273	33433		1.0	88%
RM_61359	202.9	1.88	199995	15760		1.9	52%
RM_61350	214.1	3.21	217705	6634		2.0	57%
RM_61347	260.3	3.31	116500	9291		2.5	30%
RM_61348	235.4	1.25	128716	7499		2.2	34%
RM_61349	296.9	1.58	123664	6070		2.8	32%
RM_61378	253.5	1.30	172136	6985		2.4	45%
RM_61379	251.7	5.97	145870	4822		2.4	38%
RM_61321	315.0	1.58	138777	6739		3.0	36%
RM_61324	300.5	2.51	160090	10914		2.8	42%
RM_61326	311.0	0.36	139901	6644		2.9	37%
RM_61329	222.0	0.36	199761	12157		2.1	52%
RM_61330	258.2	0.63	152237	6957	2.2		40%
RM_61360	254.9	4.34	106953	4751	2.2		28%
RM_61358	250.9	3.56	134392	5959	2.1		35%
RM_61355	311.0	3.46	97396	5124	2.6		25%
RM_61356	303.8	7.12	94786	6568	2.6		25%
RM_61357	378.1	3.10	93462	6568	3.2		24%
RM_61117	110.6	0.95	295687	17676		1.0	77%
untransfect ed	40.9	0.39	382317	25895		0.4	100%

FIG. 10

CAR expression on human CD8+ T cells at 24 hours post
transfection via CD8-targeted LNP

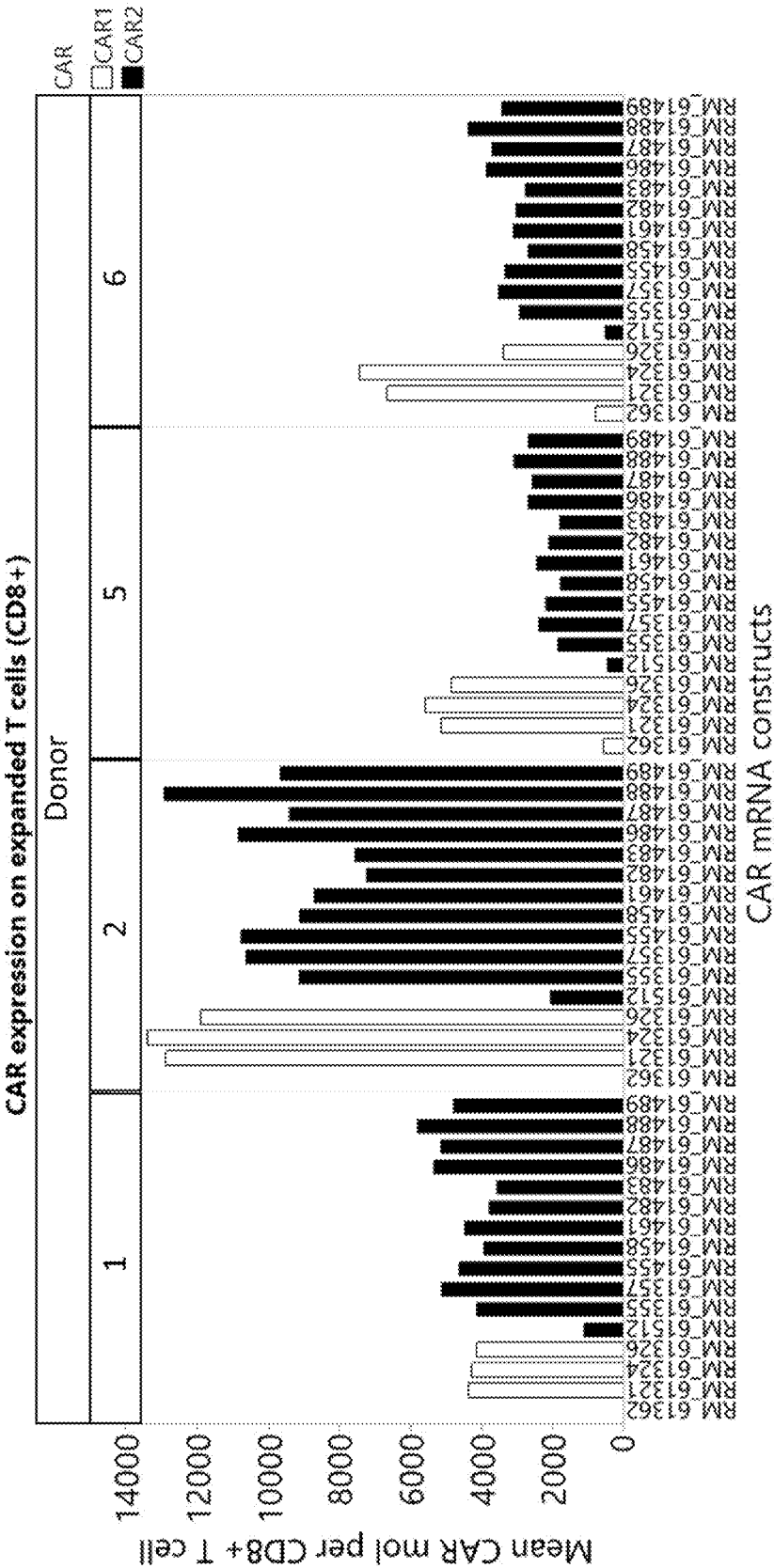


FIG. 11A

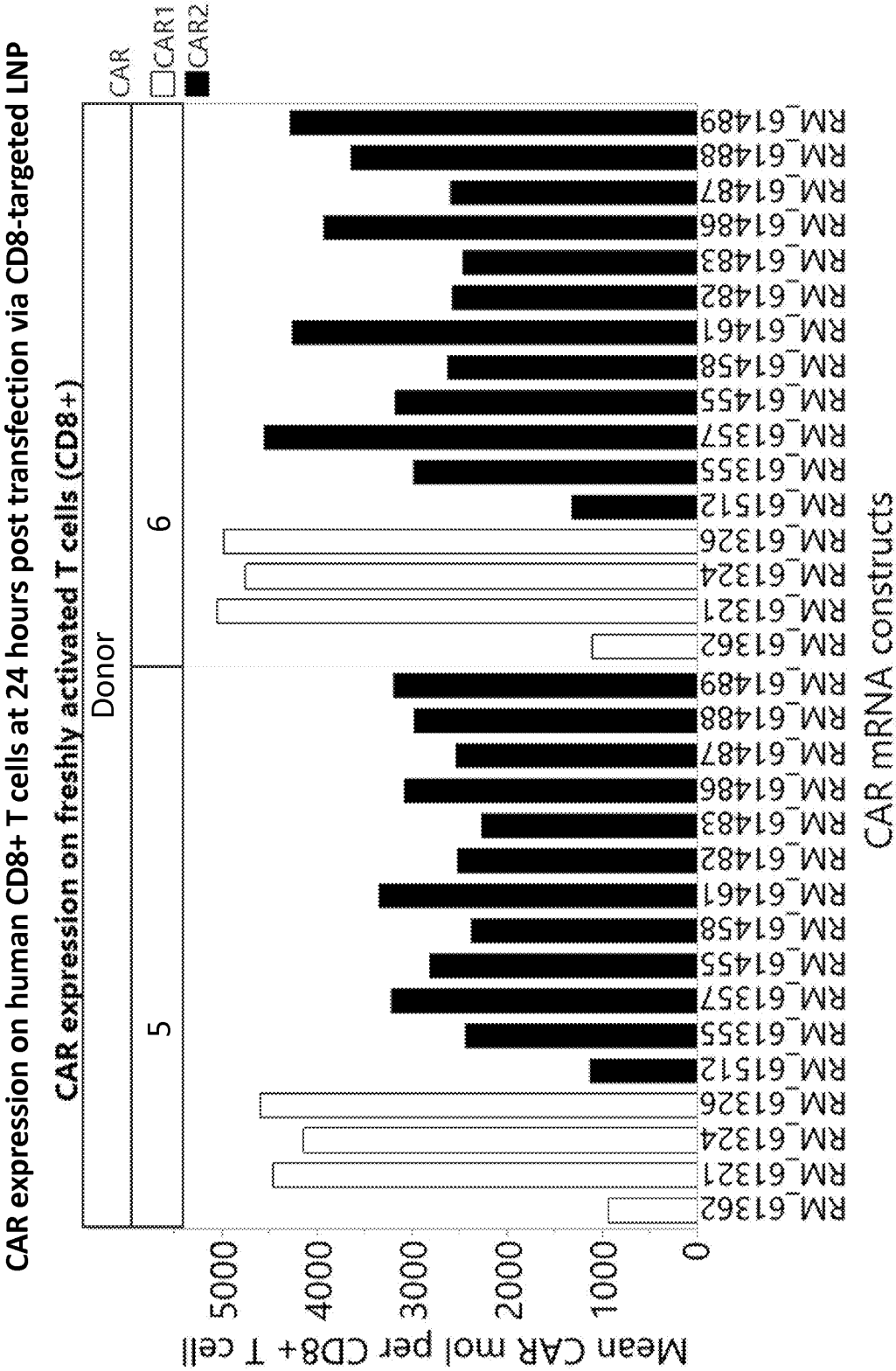


FIG. 11B

CAR expression on human CD8+ T cells at 24 hours post transfection via CD8-targeted LNP

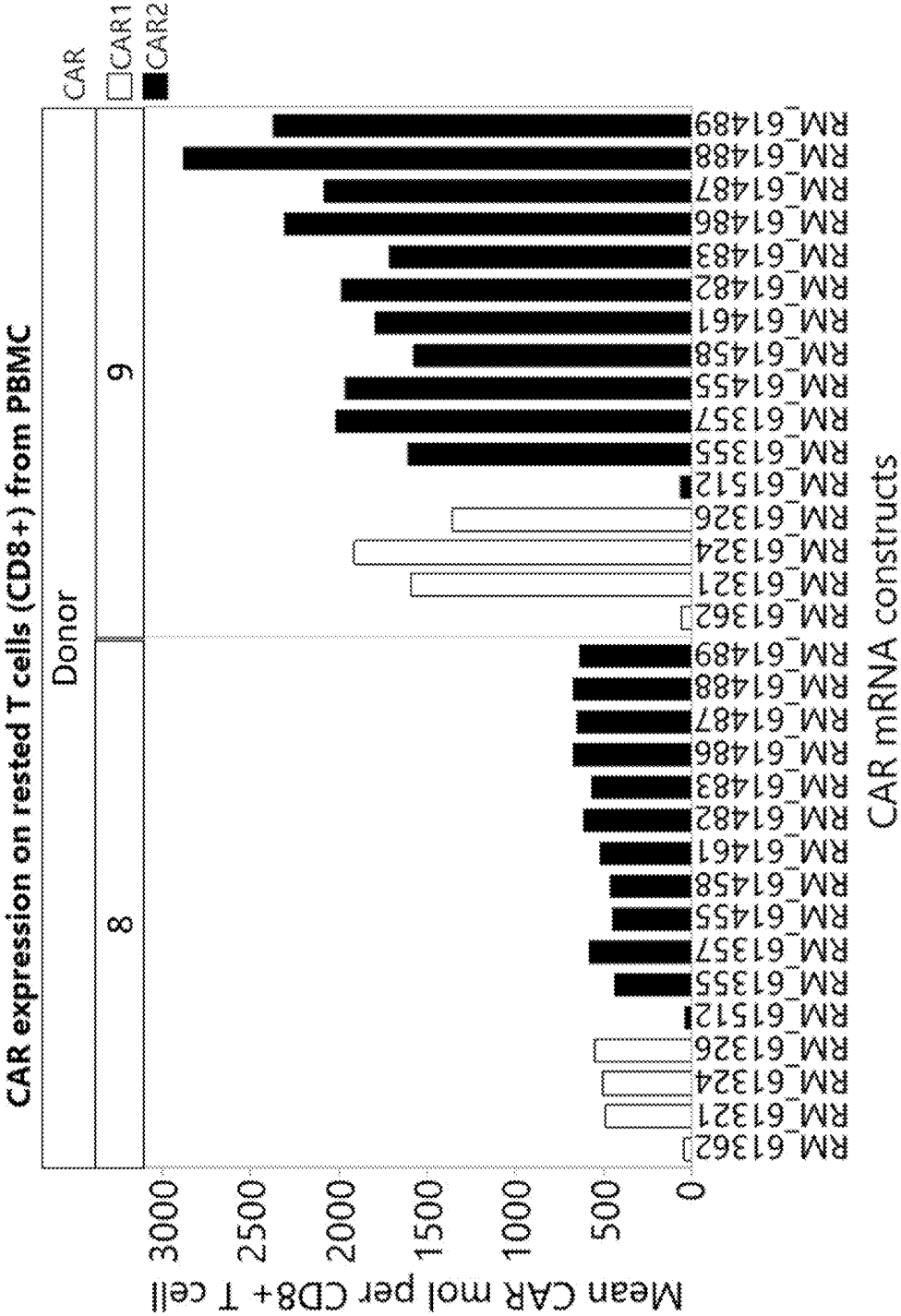


FIG. 11C

10 μ g dose

Pan T cells

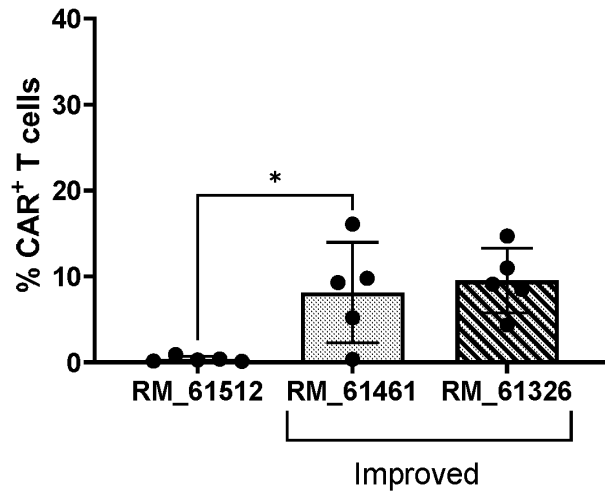
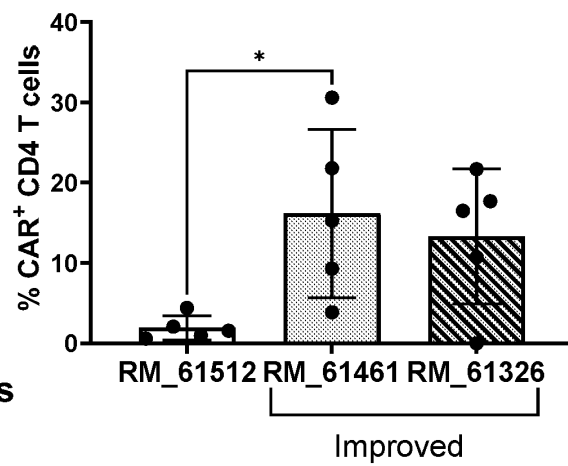
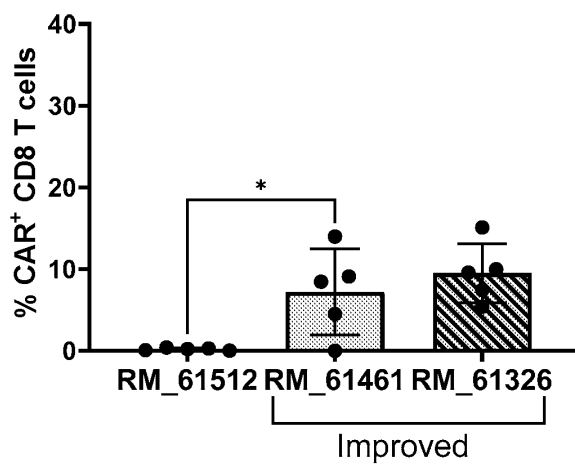
CD4⁺ T cellsCD8⁺ T cells

FIG. 12

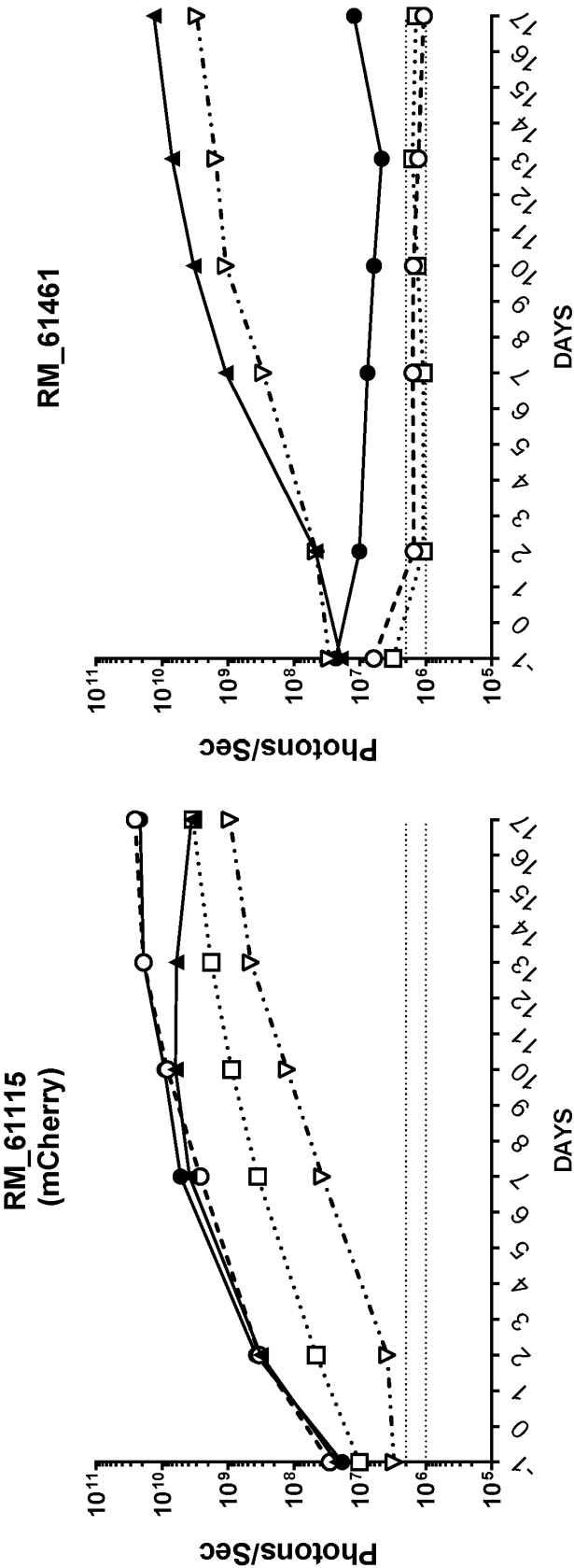


FIG. 13

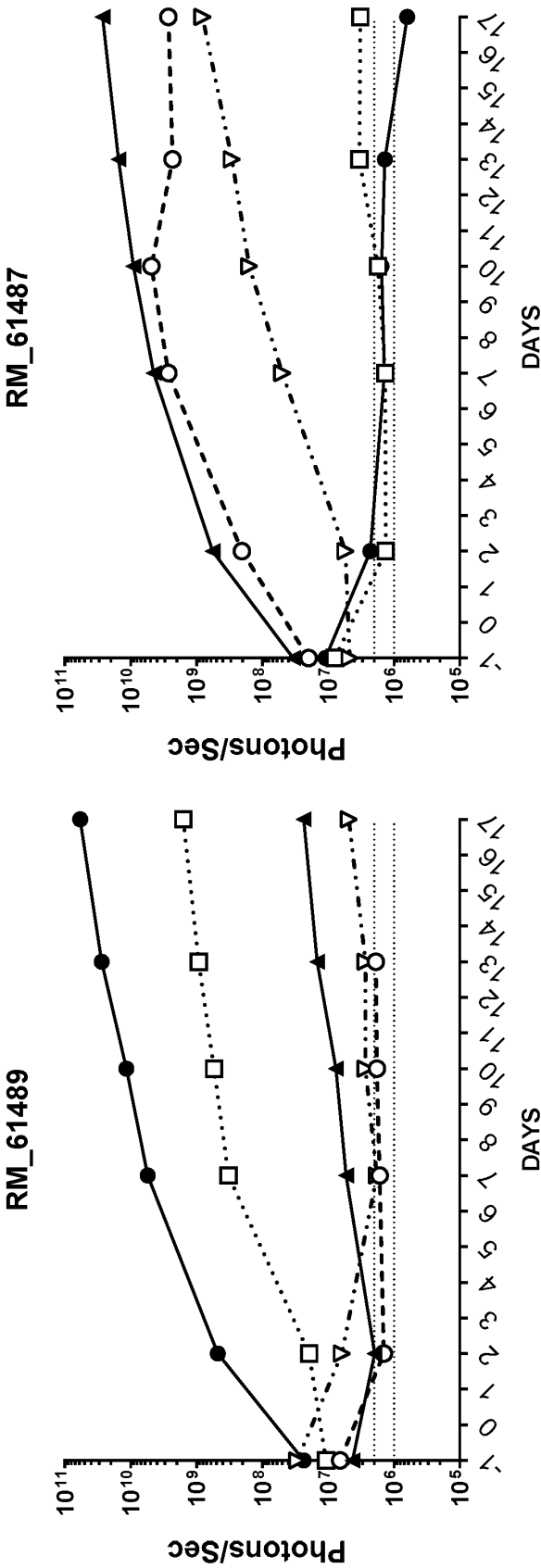


FIG. 13 (cont'ed)

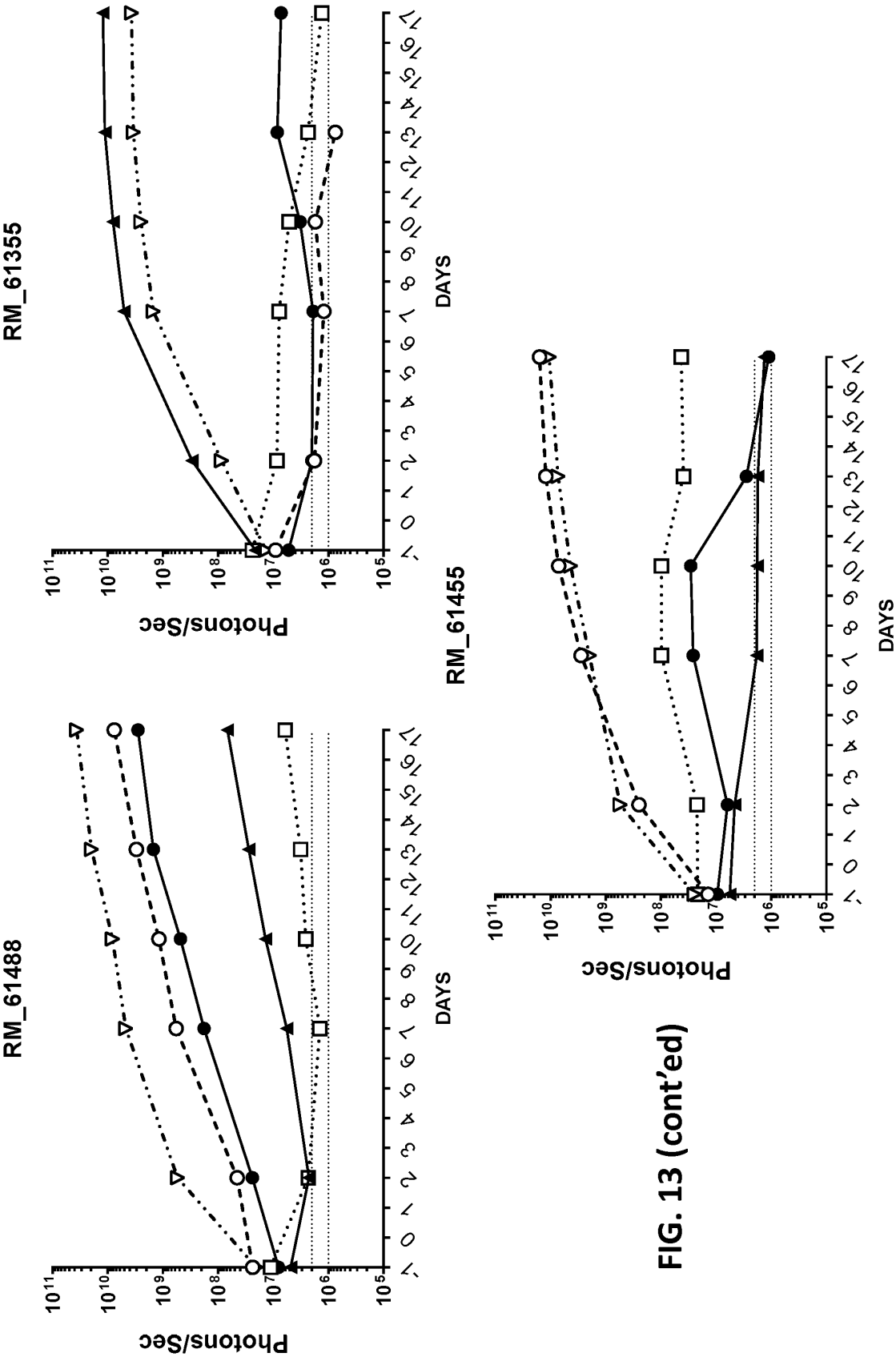


FIG. 13 (cont'ed)

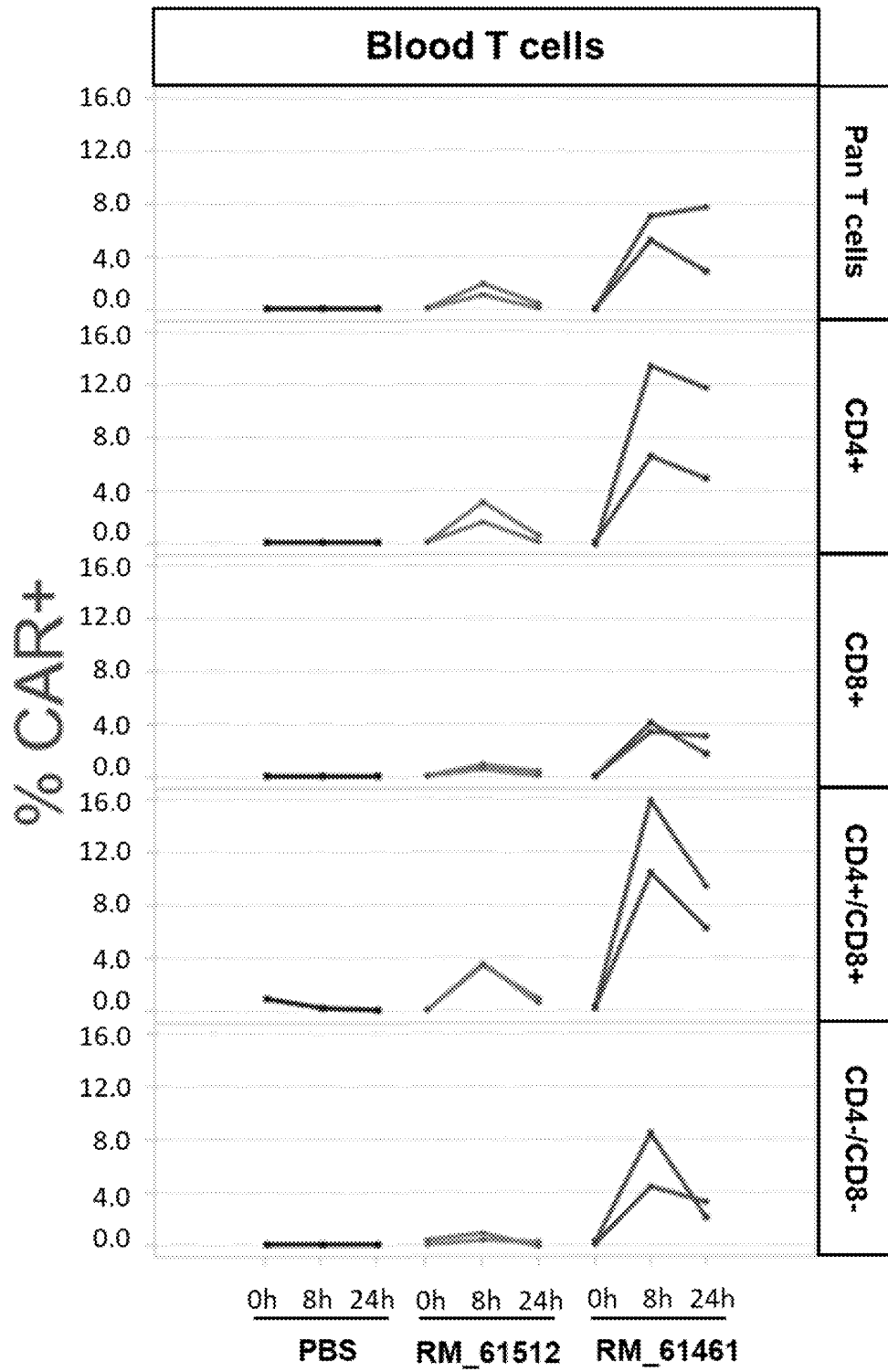
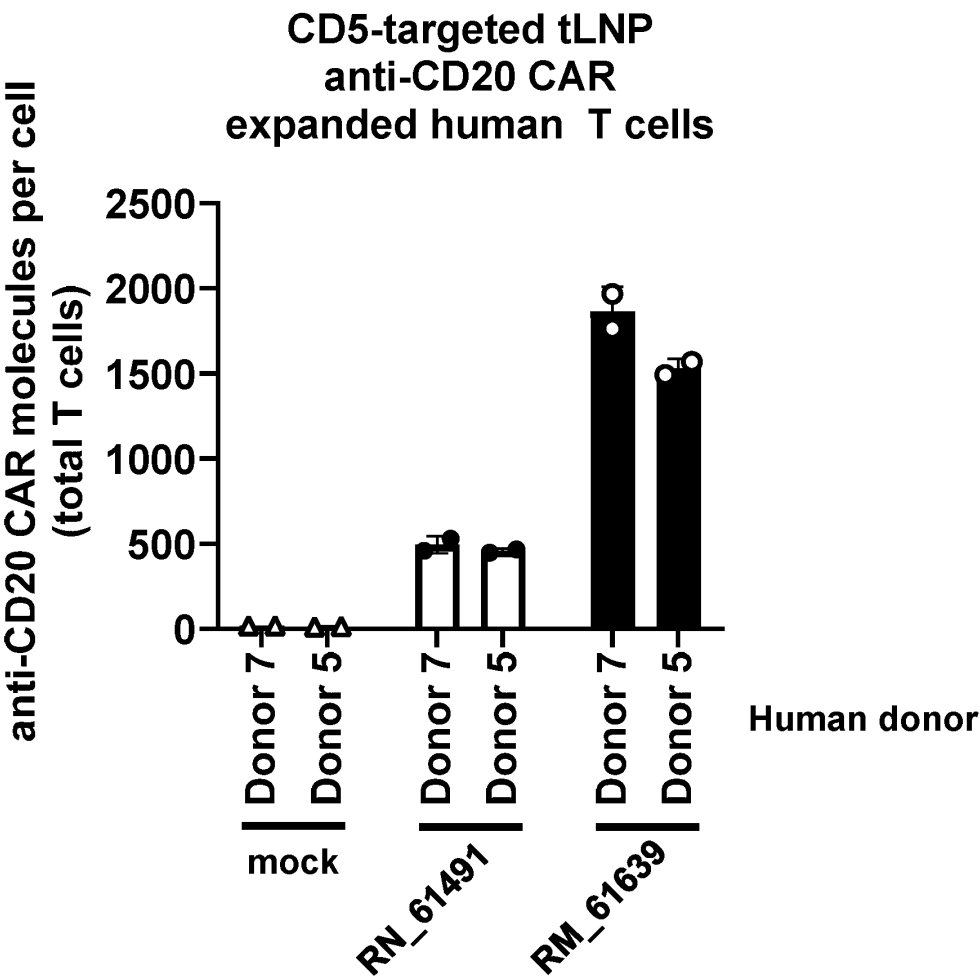


FIG. 14



SEQ ID NO	RM	5' UTR	ORF encoded CAR-Codon optimization method (OPT)	3' UTR
177	RM_61491	TEV	CAR25-OPT6	XBG
178	RM_61639	mHBB	CAR25-OPT4	PNLIP-RPS3A

FIG. 15

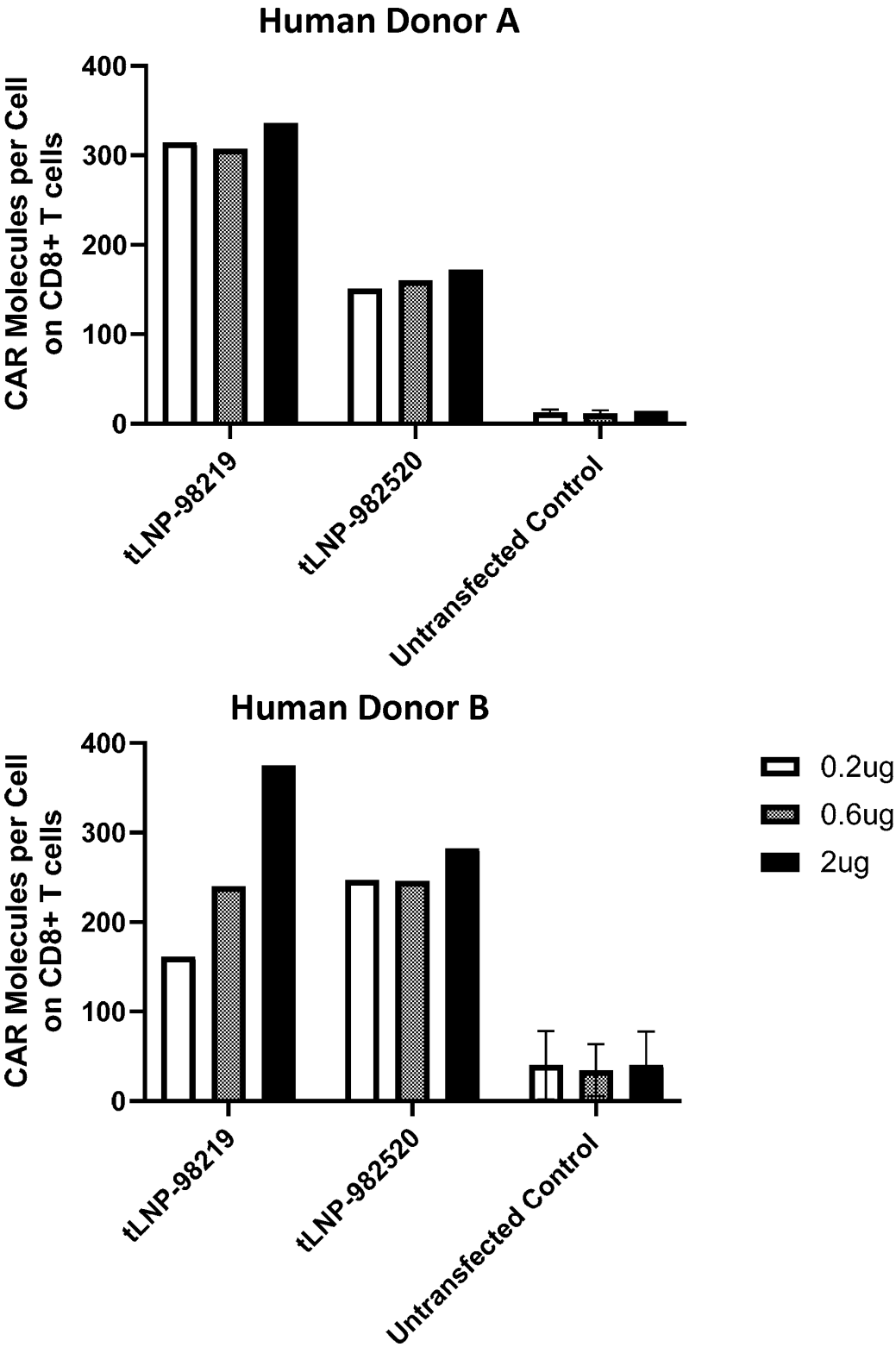


FIG. 16A

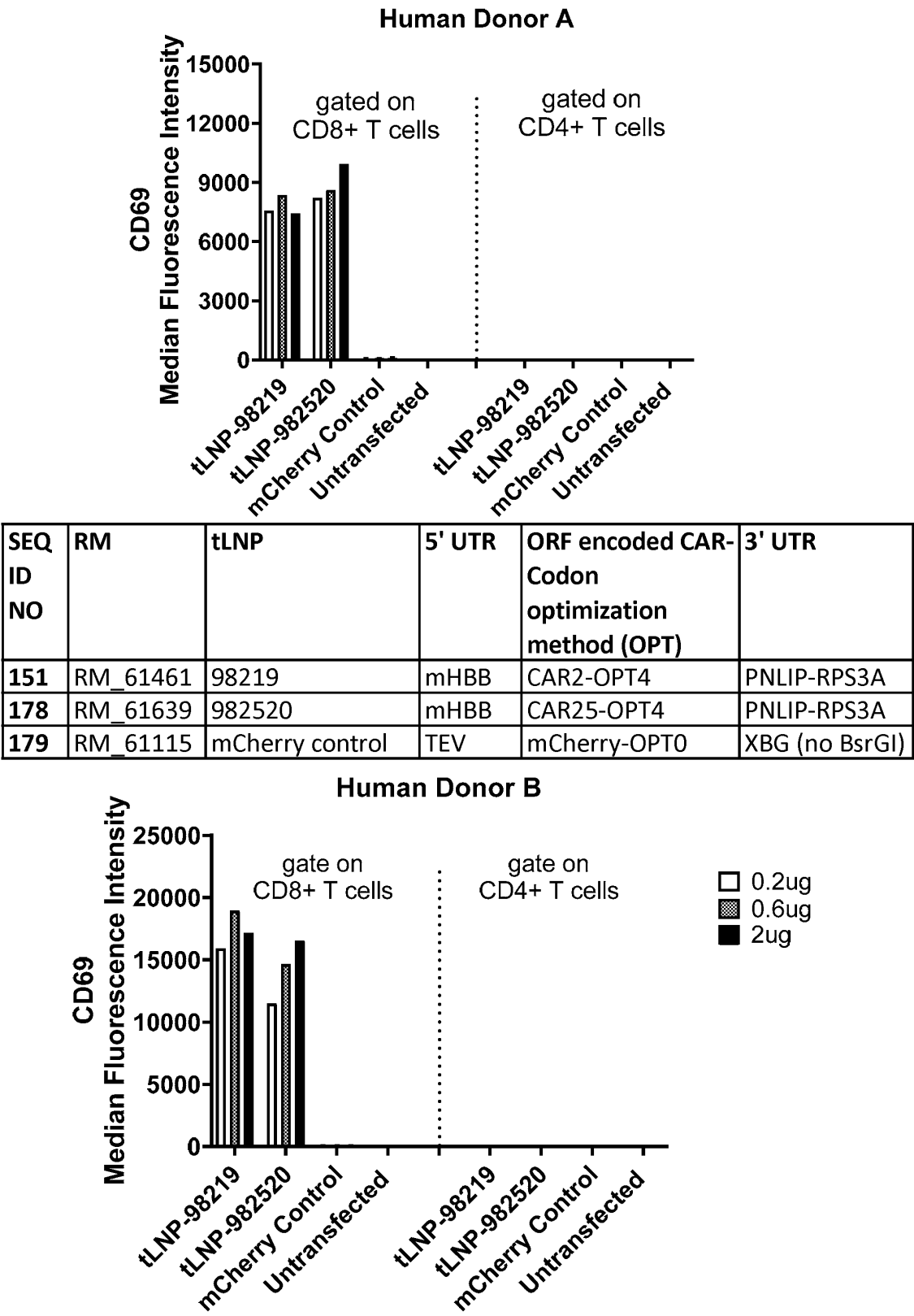
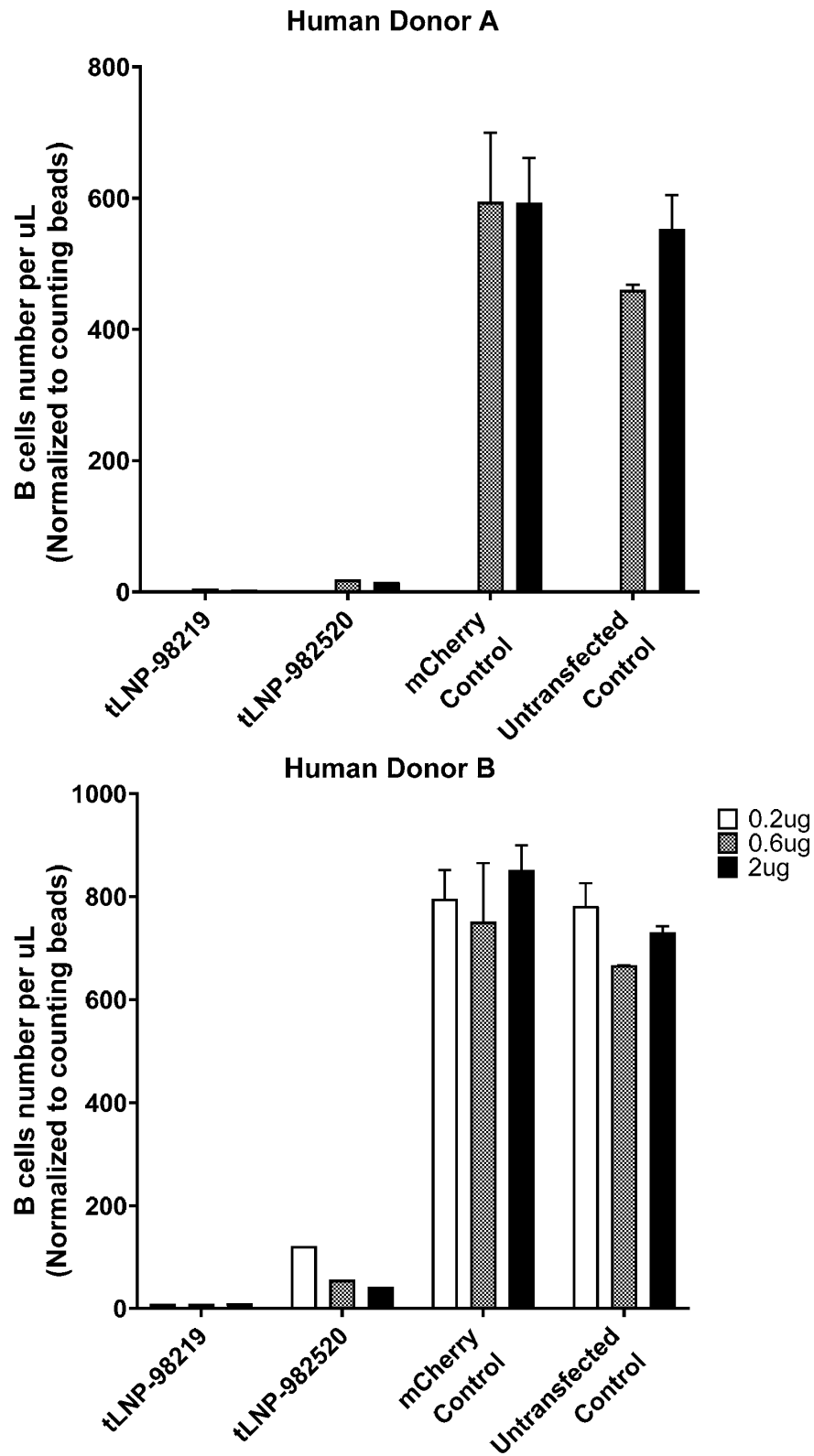
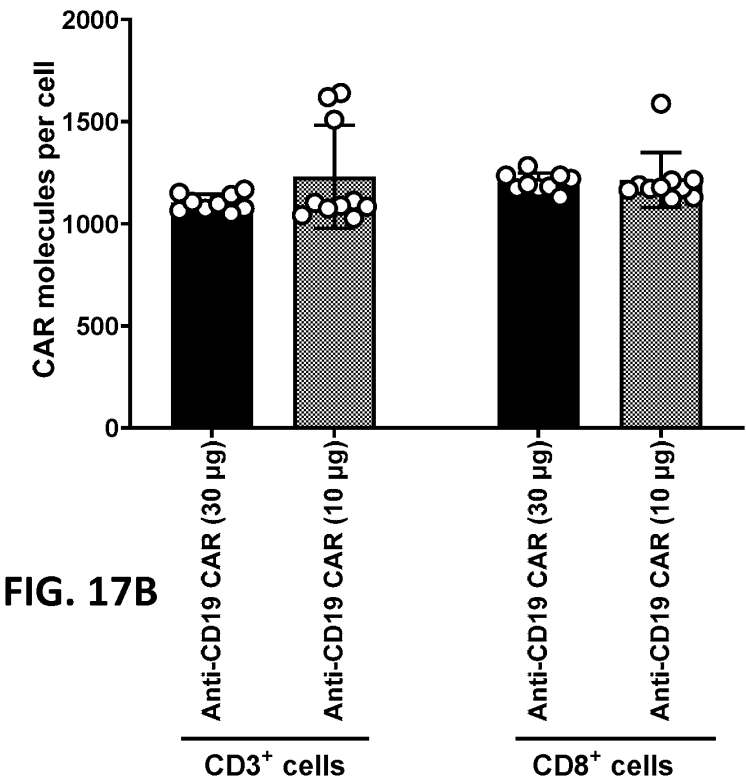
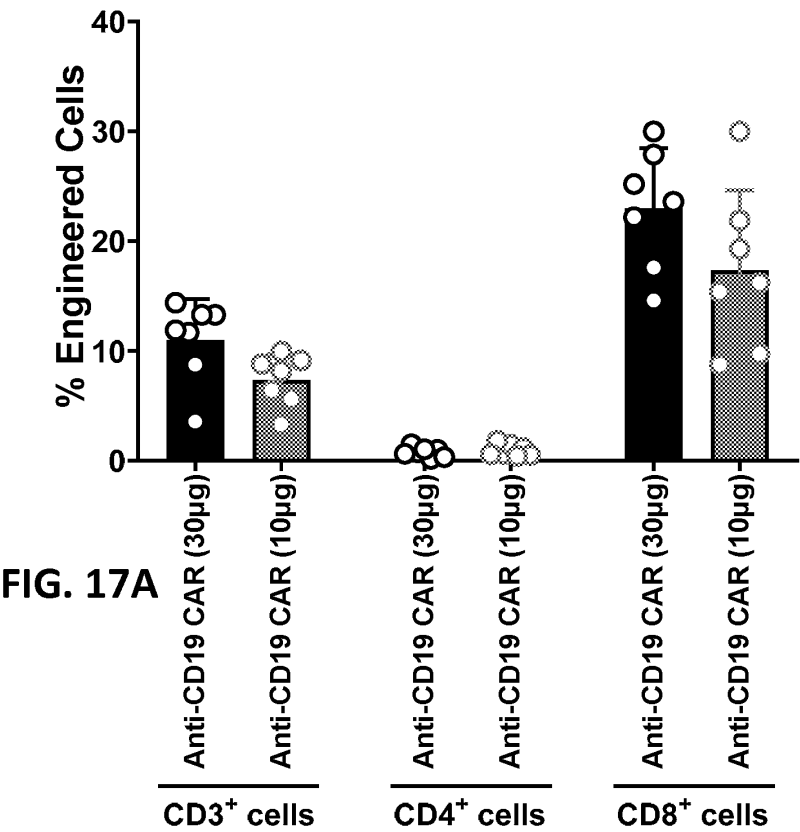


FIG. 16B

**FIG. 16C**



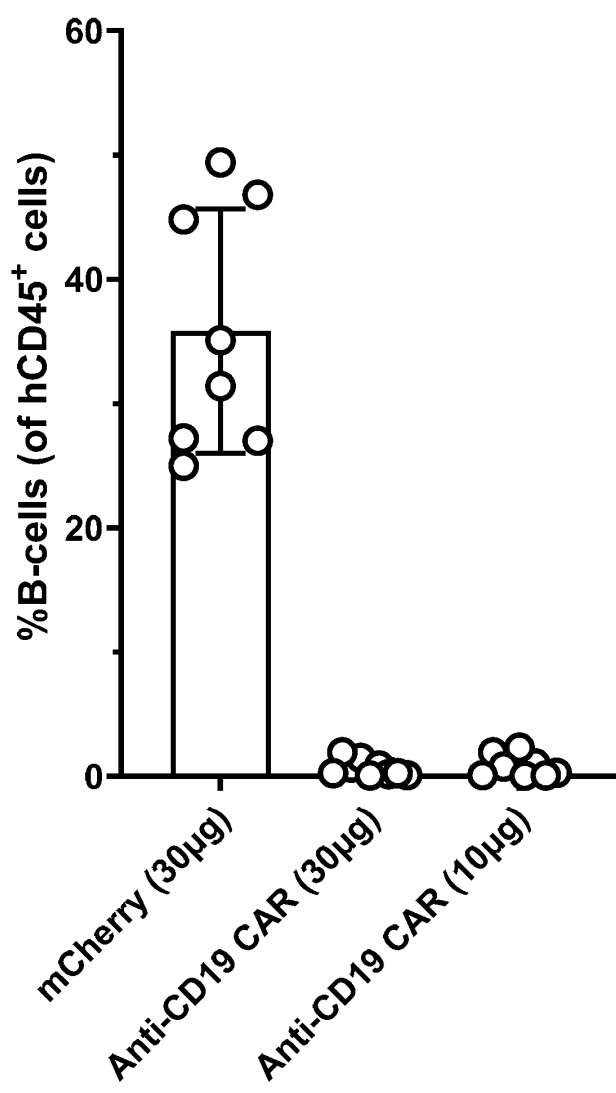


FIG. 17C

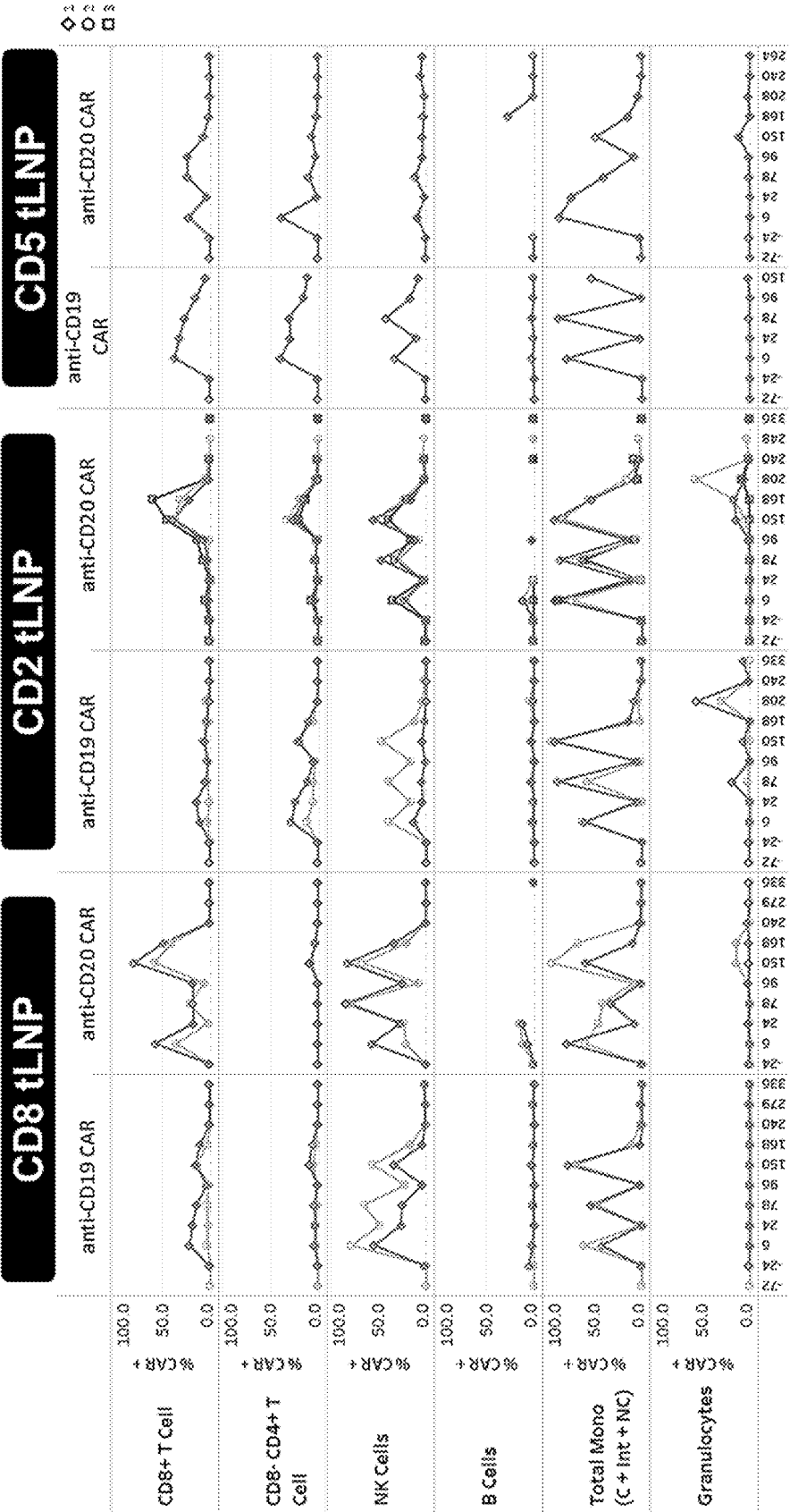


FIG. 18A

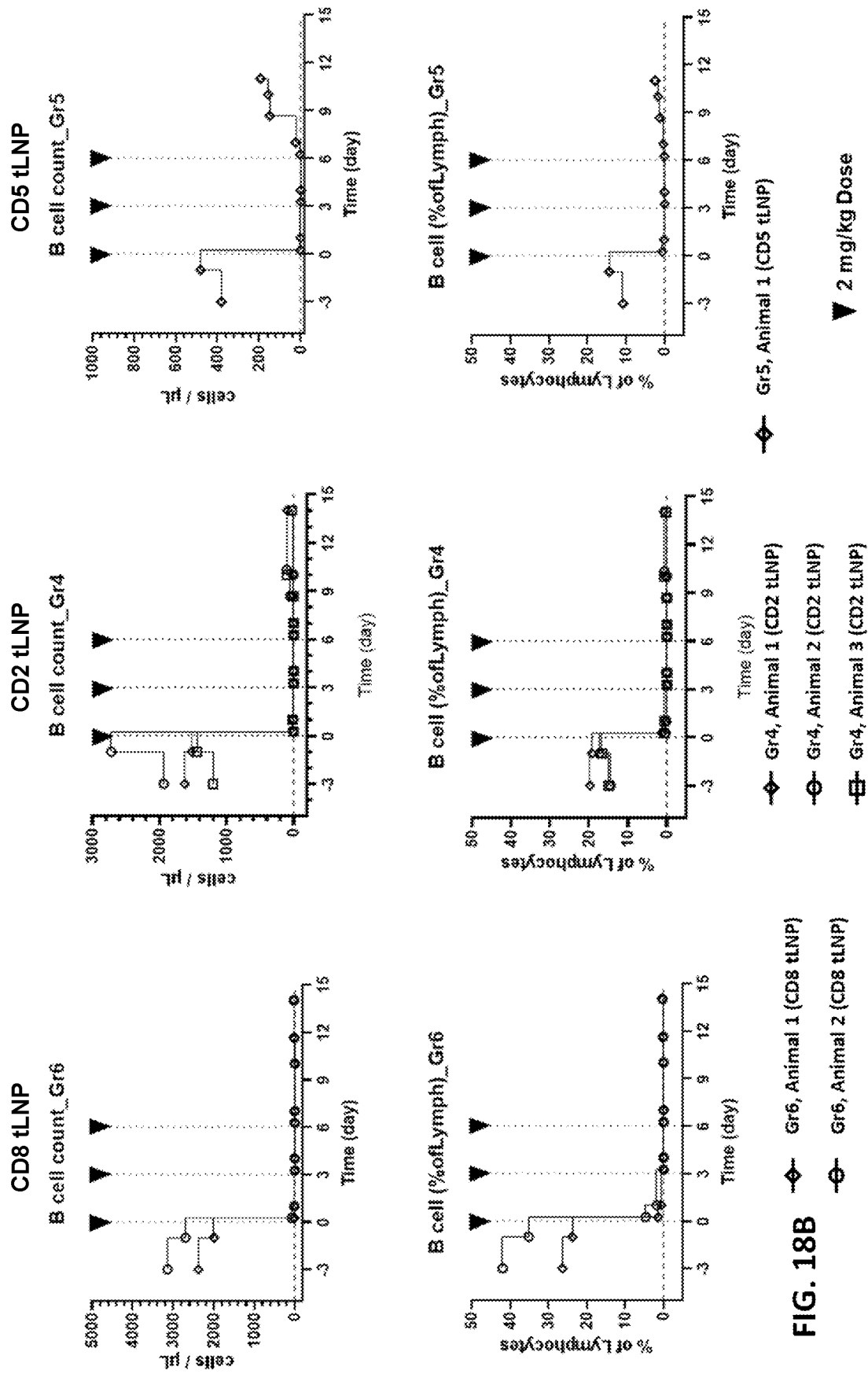


FIG. 18B

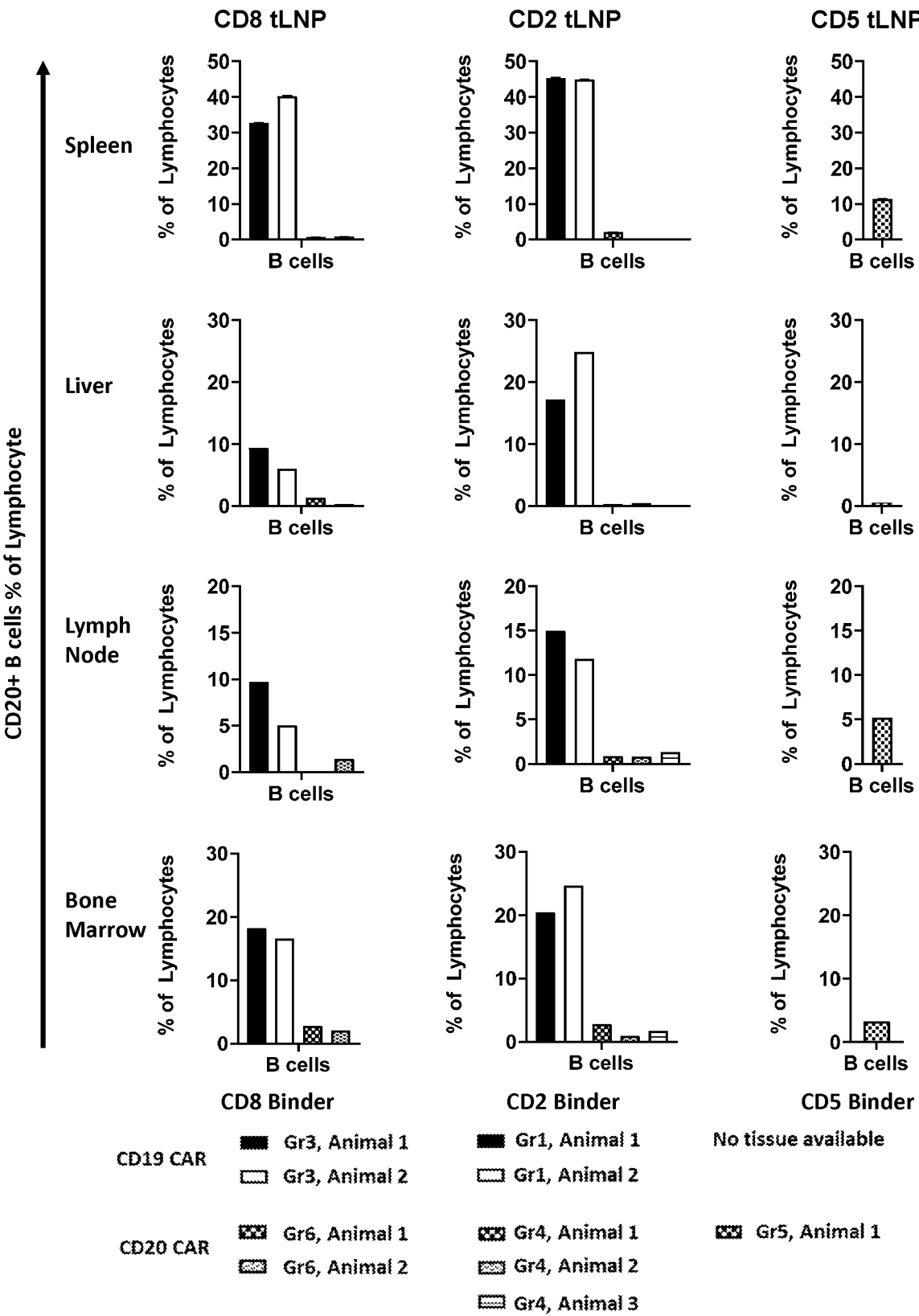


FIG. 18C

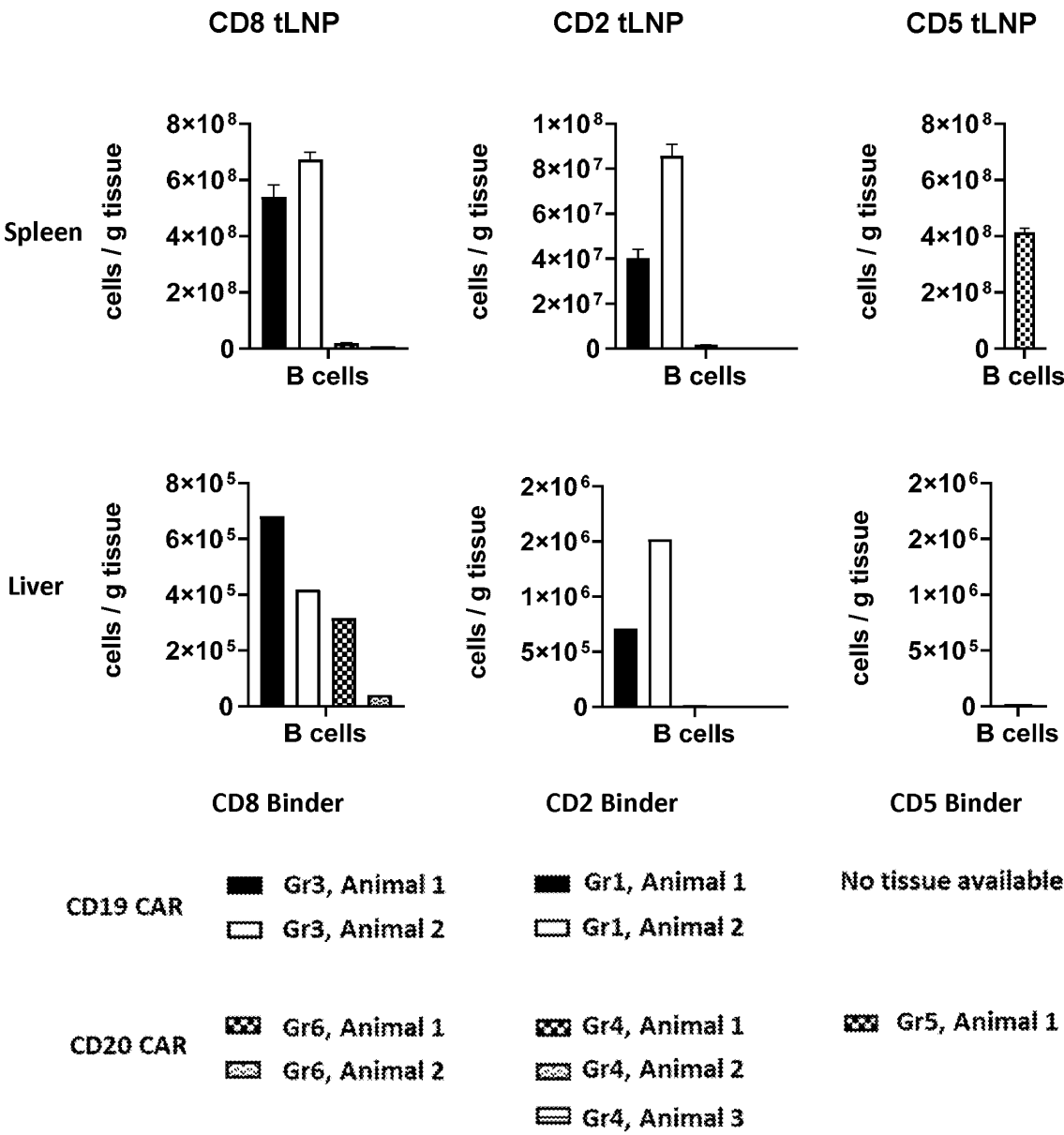
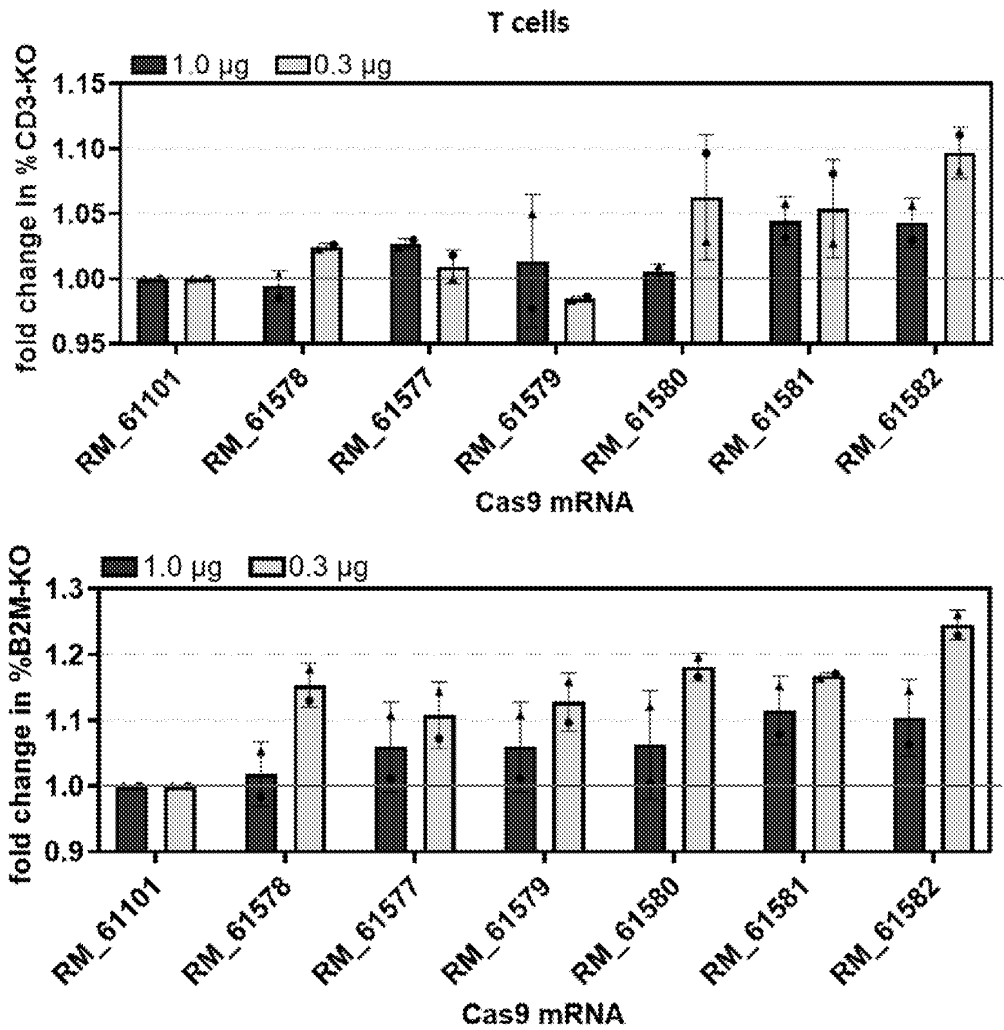


FIG. 18D



RM	SEQ ID NO	5' UTR	ORF encoded Cas9-Codon optimization method (OPT)	3' UTR
RM_61101	306	TEV	Cas9-OPT8	XBG
RM_61577	307	mHBB	Cas9'-OPT8	PNLIP-RPS3A
RM_61578	308	mHBB	Cas9'-OPT8	hHBA1
RM_61579	309	mHBB	Cas9-OPT2	PNLIP-RPS3A
RM_61580	310	mHBB	Cas9-OPT2	hHBA1
RM_61581	311	mHBB	Cas9-OPT4	PNLIP-RPS3A
RM_61582	312	mHBB	Cas9-OPT4	hHBA1

Cas9': Cas9 with two silent mutations to remove BspQI restriction sites.

FIG. 19A

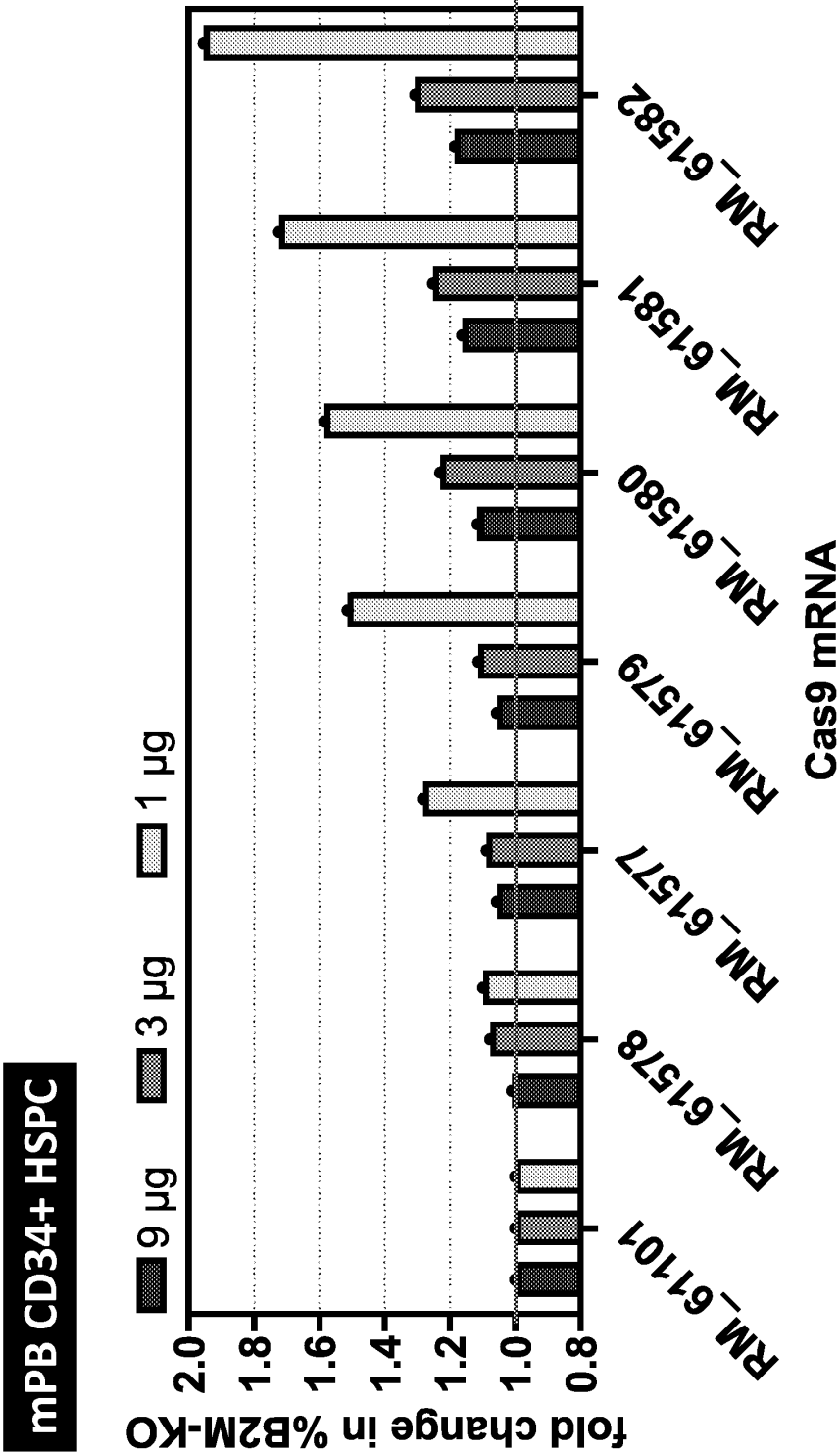
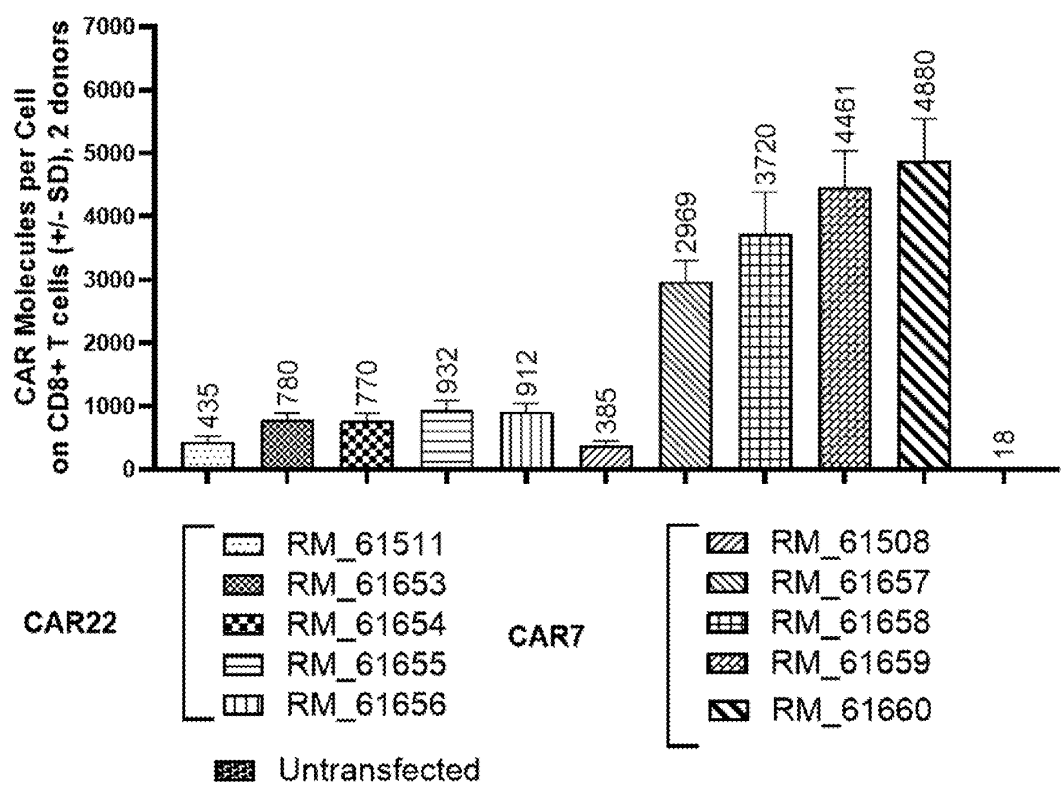


FIG. 19B



SEQ ID NO	RM	5' UTR	ORF encoded CAR-Codon optimization method (OPT)	3' UTR
315	RM_61511	TEV	CAR22-OPT8	XBG
316	RM_61653	mHBB	CAR22-OPT4	PNLIP-RPS3A
317	RM_61654	mHBB	CAR22-OPT4	hHBA1-3x miR122 bs
318	RM_61655	mHBB	CAR22-OPT0	PNLIP-RPS3A
319	RM_61656	mHBB	CAR22-OPT0	hHBA1-3x miR122 bs
320	RM_61508	TEV	CAR7-OPT6	XBG
321	RM_61657	mHBB	CAR7-OPT4	PNLIP-RPS3A
322	RM_61658	mHBB	CAR7-OPT4	hHBA1-3x miR122 bs
323	RM_61659	mHBB	CAR7-OPT0	PNLIP-RPS3A
324	RM_61660	mHBB	CAR7-OPT0	hHBA1-3x miR122 bs

FIG. 20

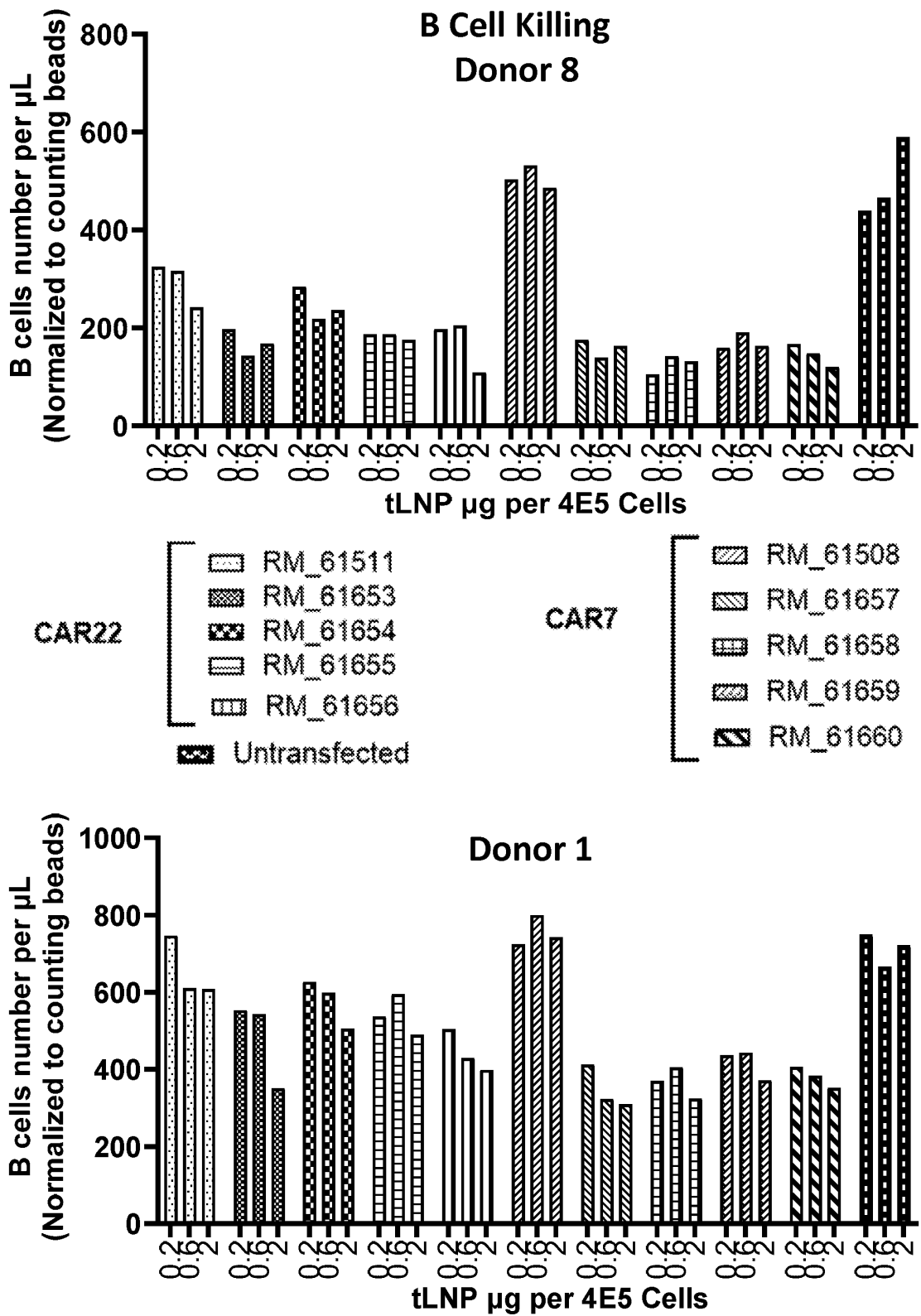


FIG. 21A

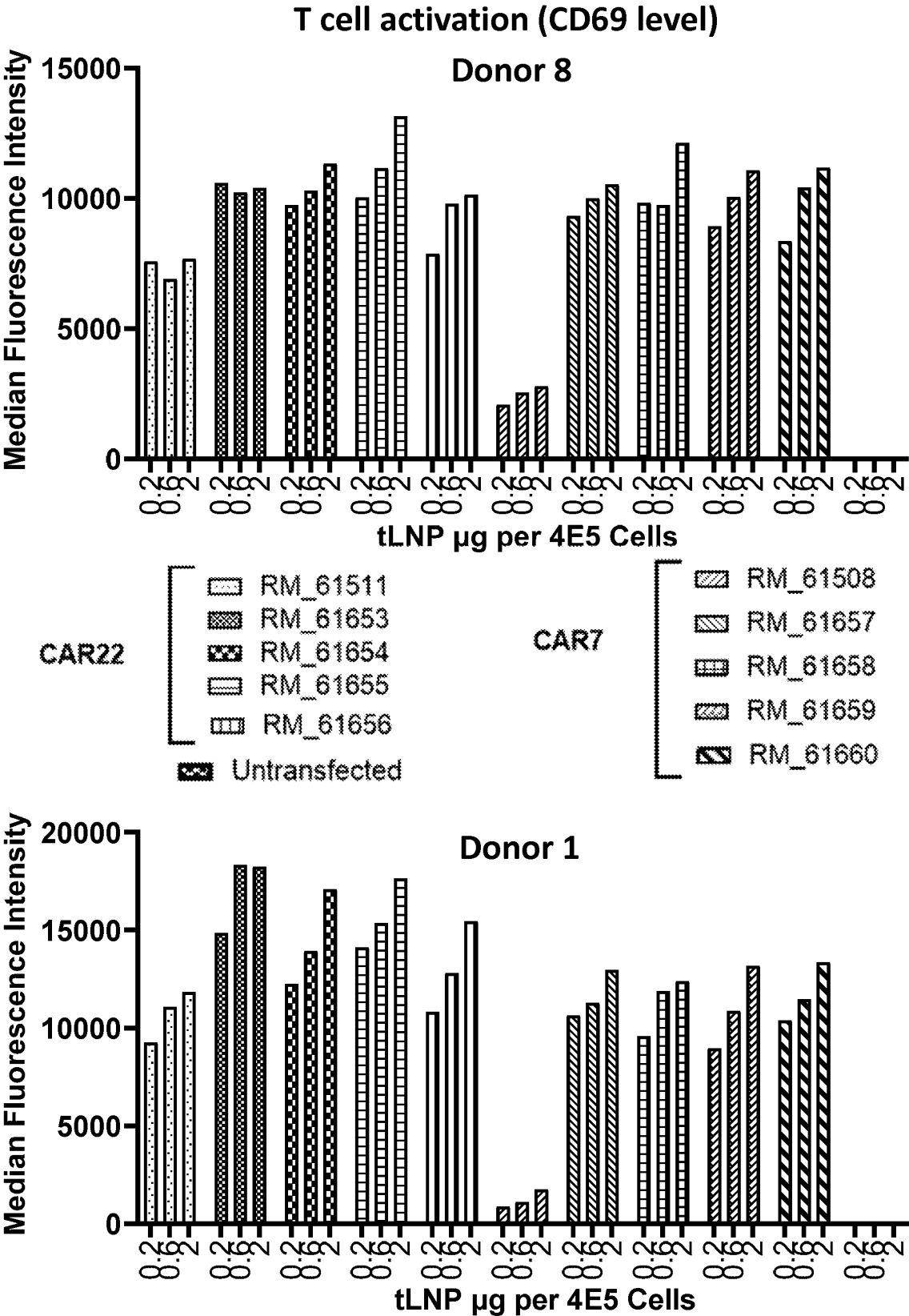
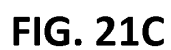


FIG. 21B



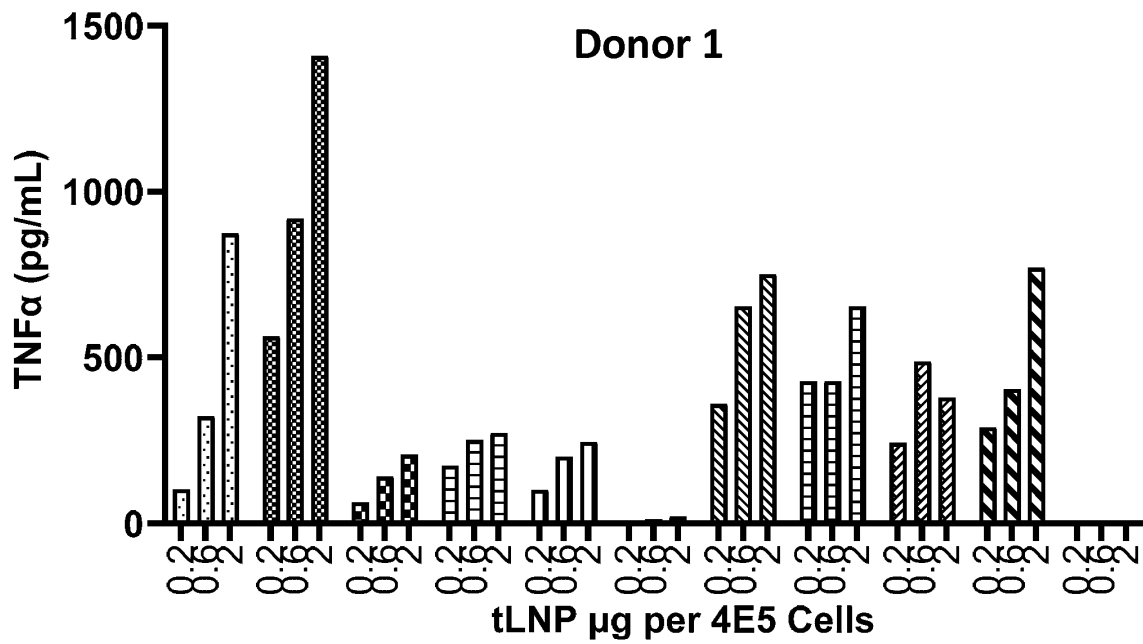


FIG. 21D

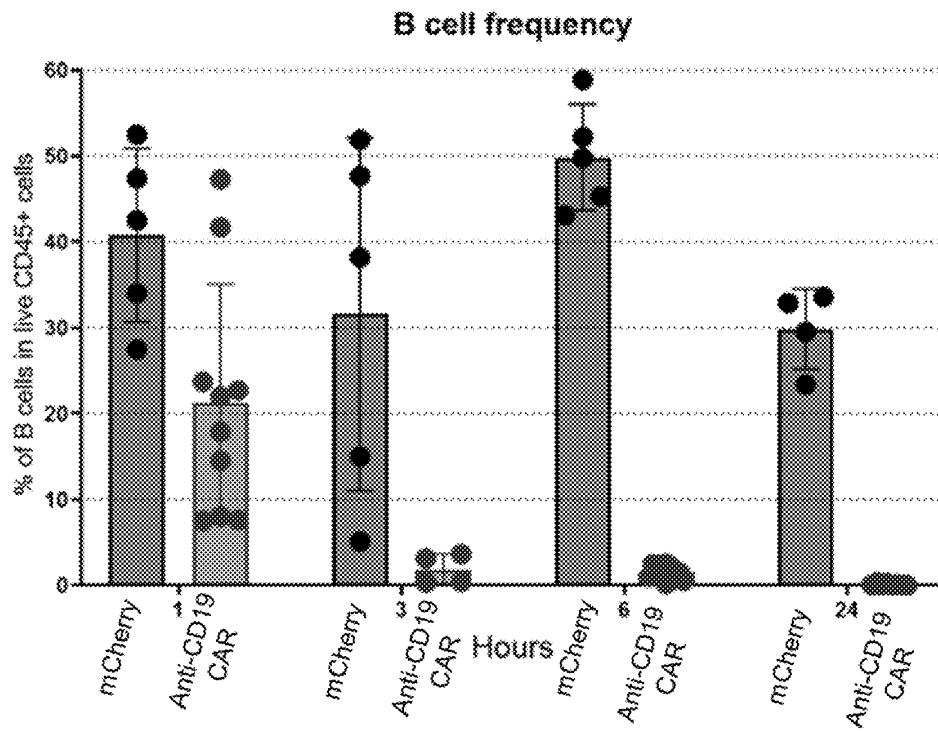


FIG. 22A

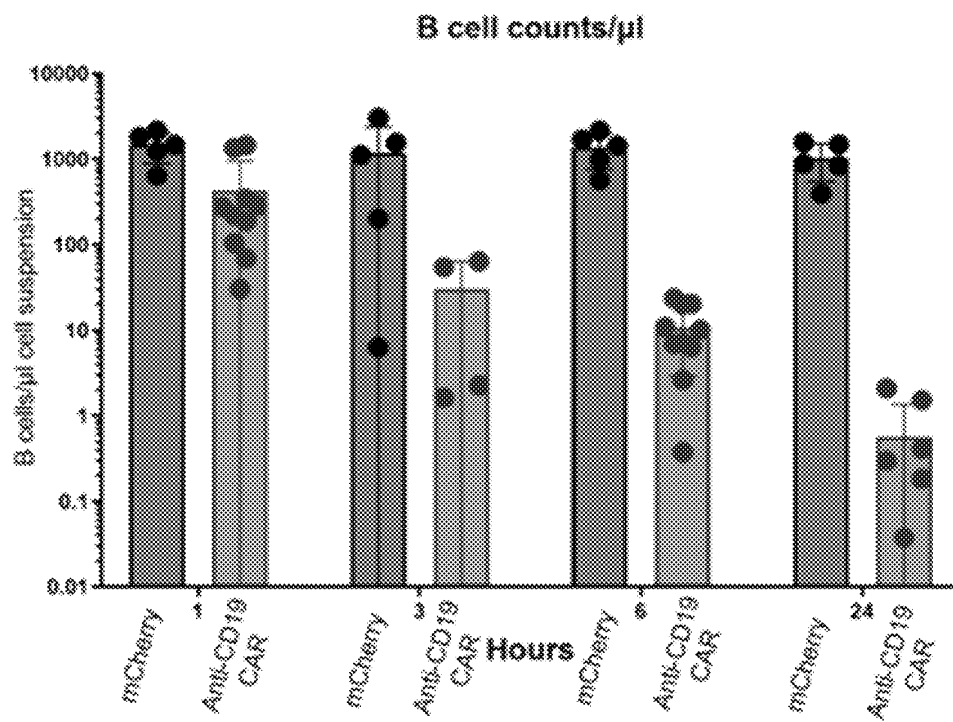


FIG. 22B

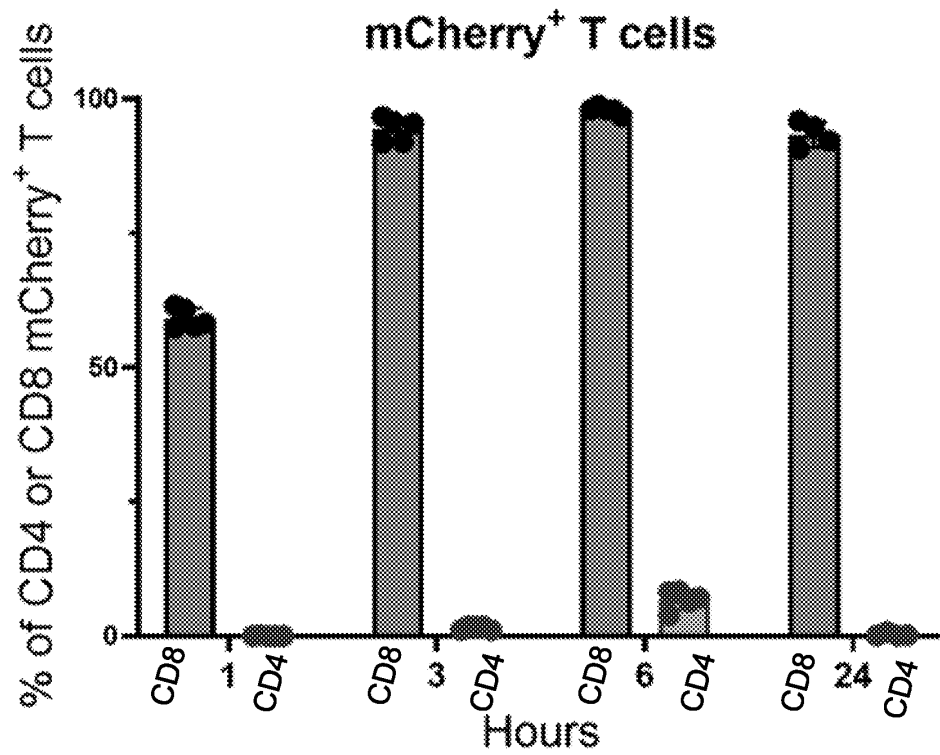


FIG. 23A

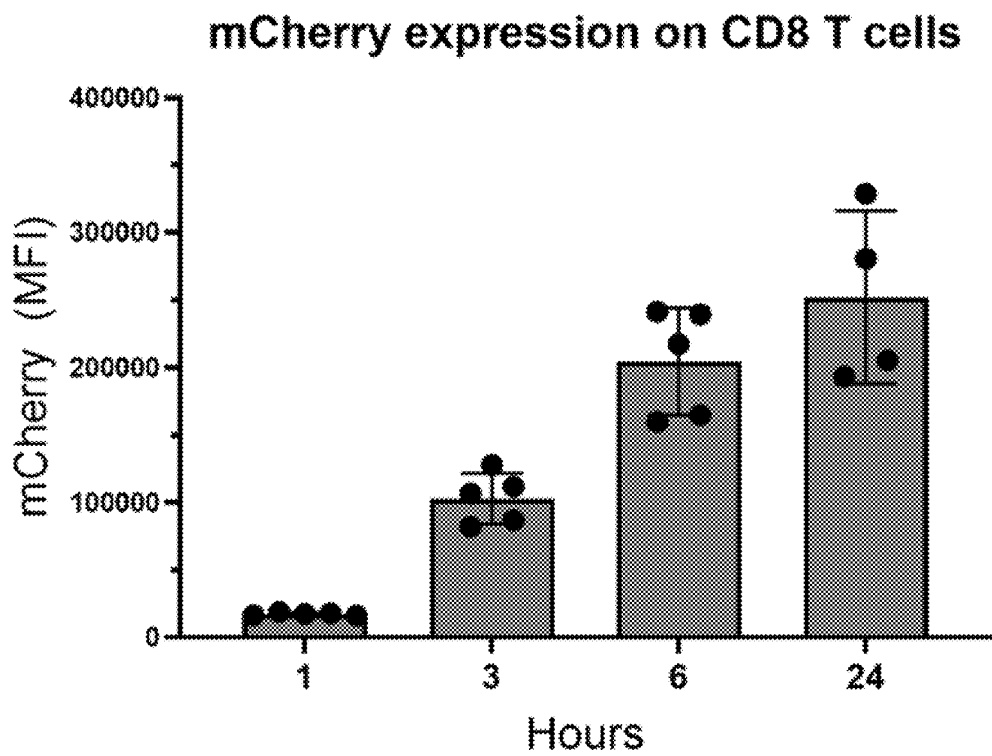


FIG. 23B

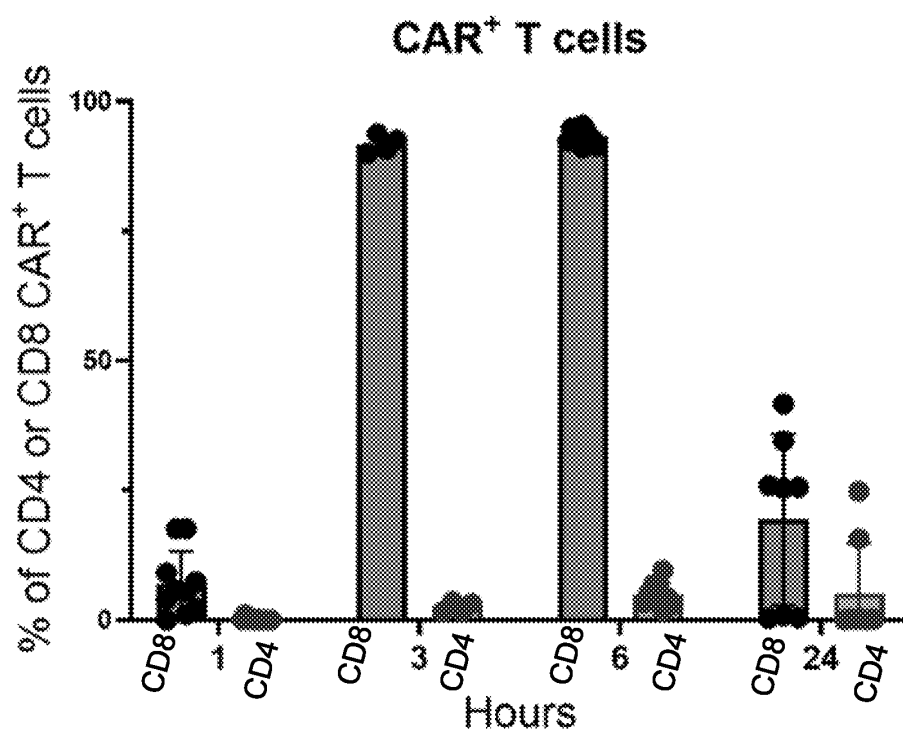


FIG. 23C

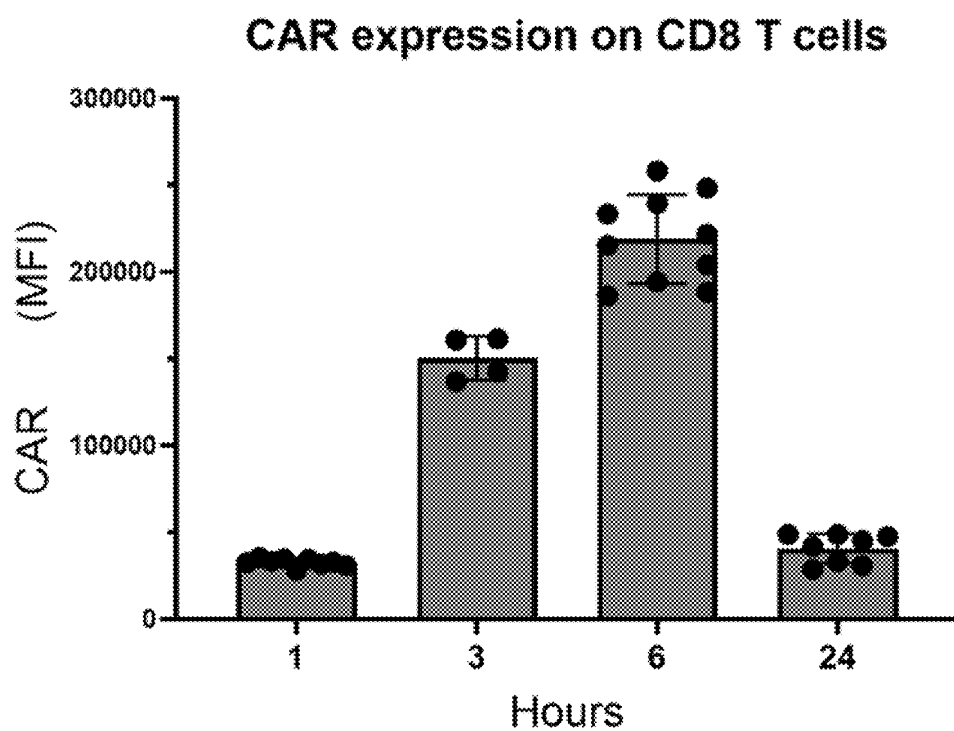
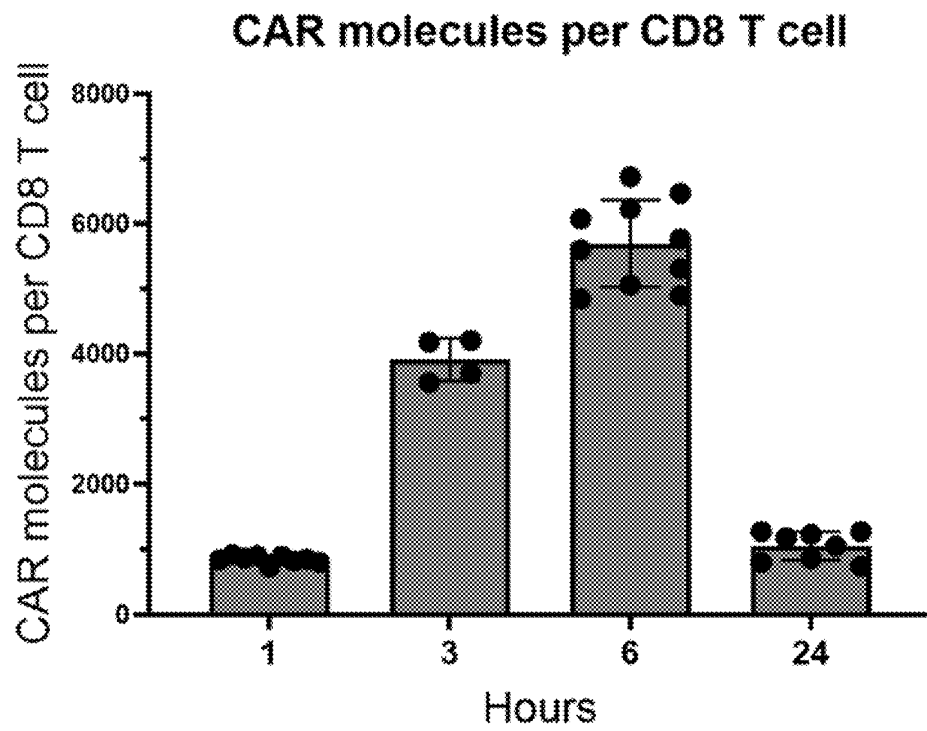
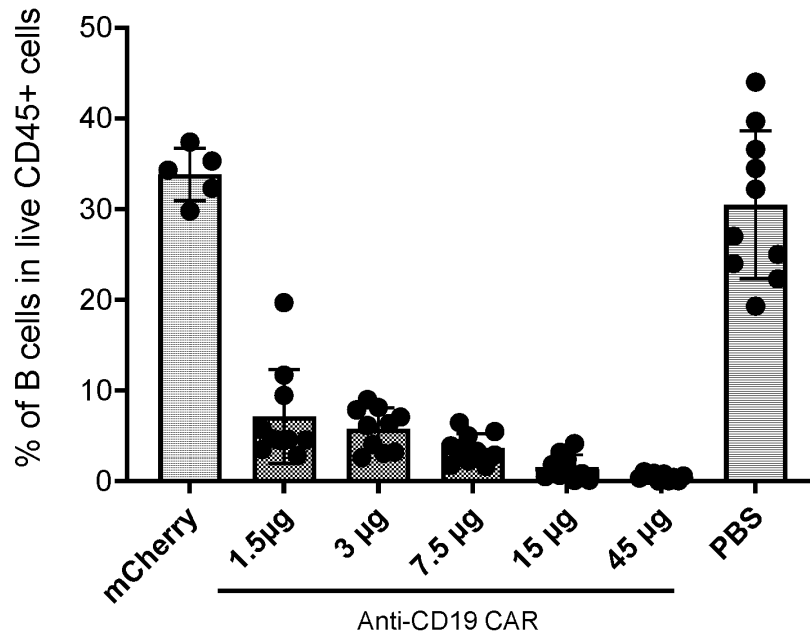
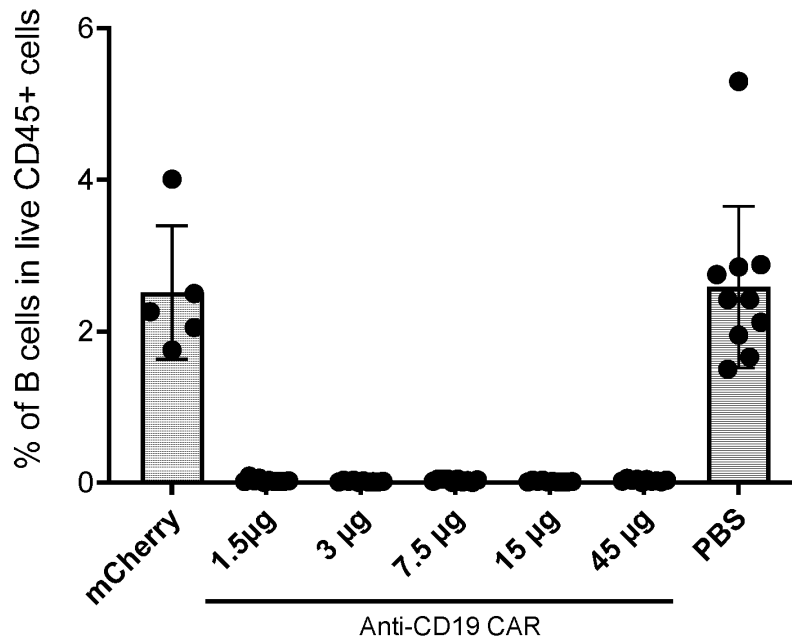
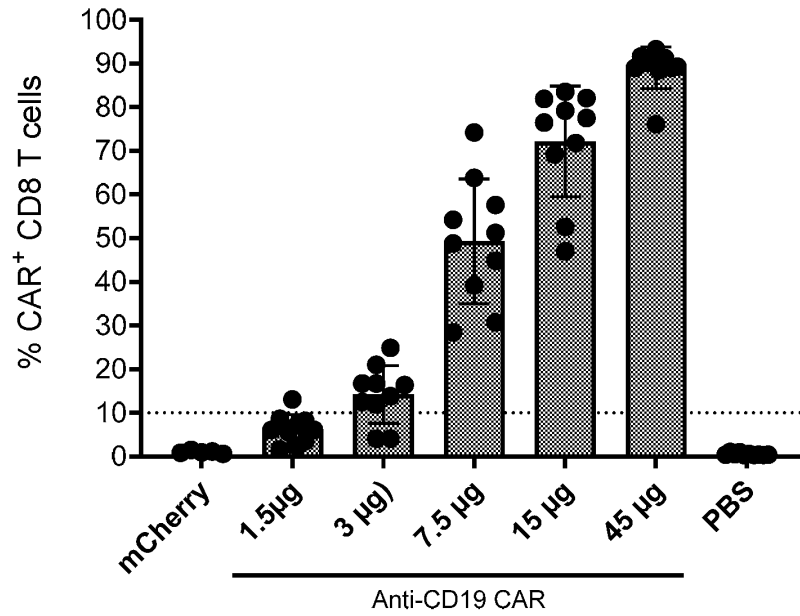


FIG. 23D

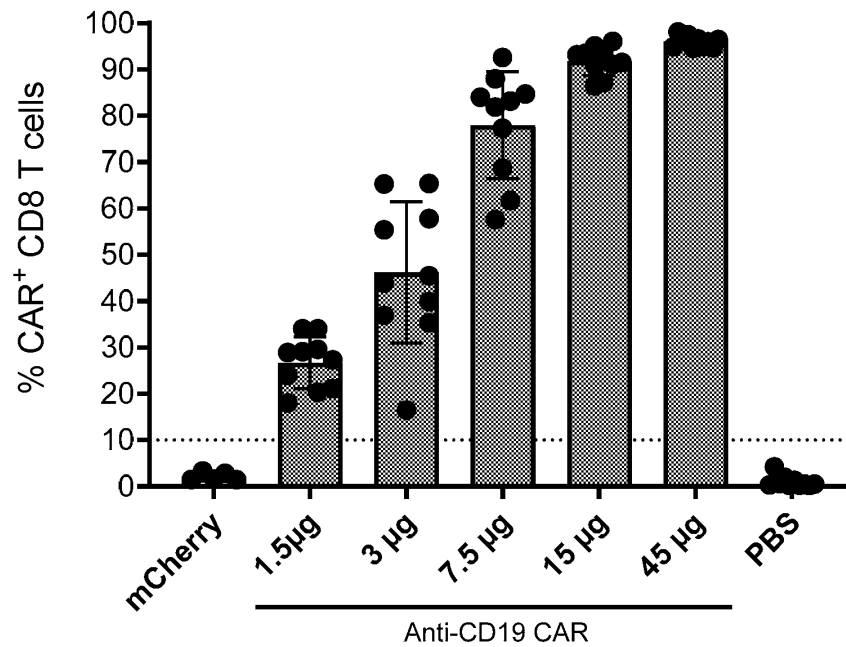
**FIG. 23E**

B cell frequencies (Spleen)**B cell frequencies (Blood)****FIG. 24A**

CAR expression in spleen



CAR expression in blood

**FIG. 24B**

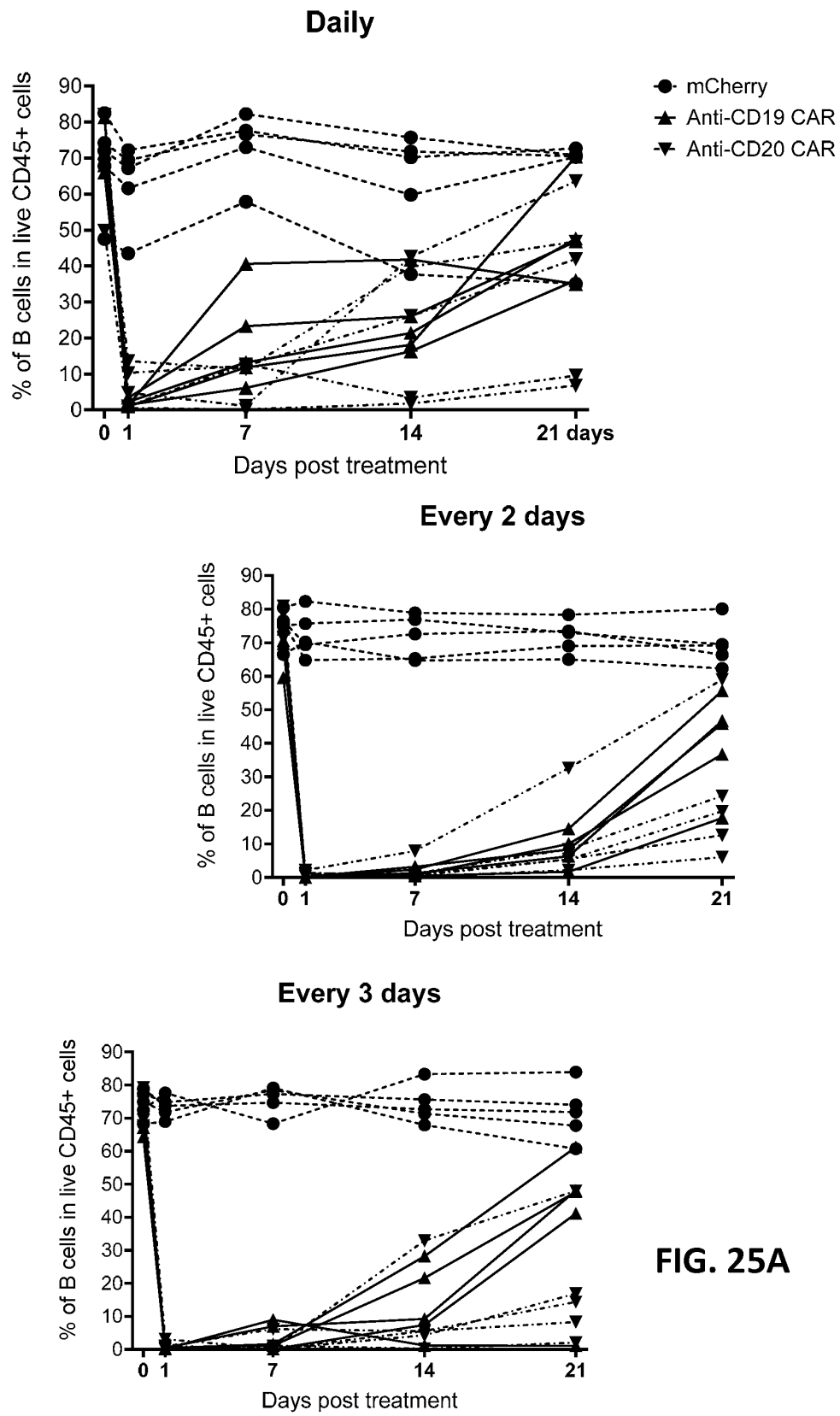


FIG. 25A

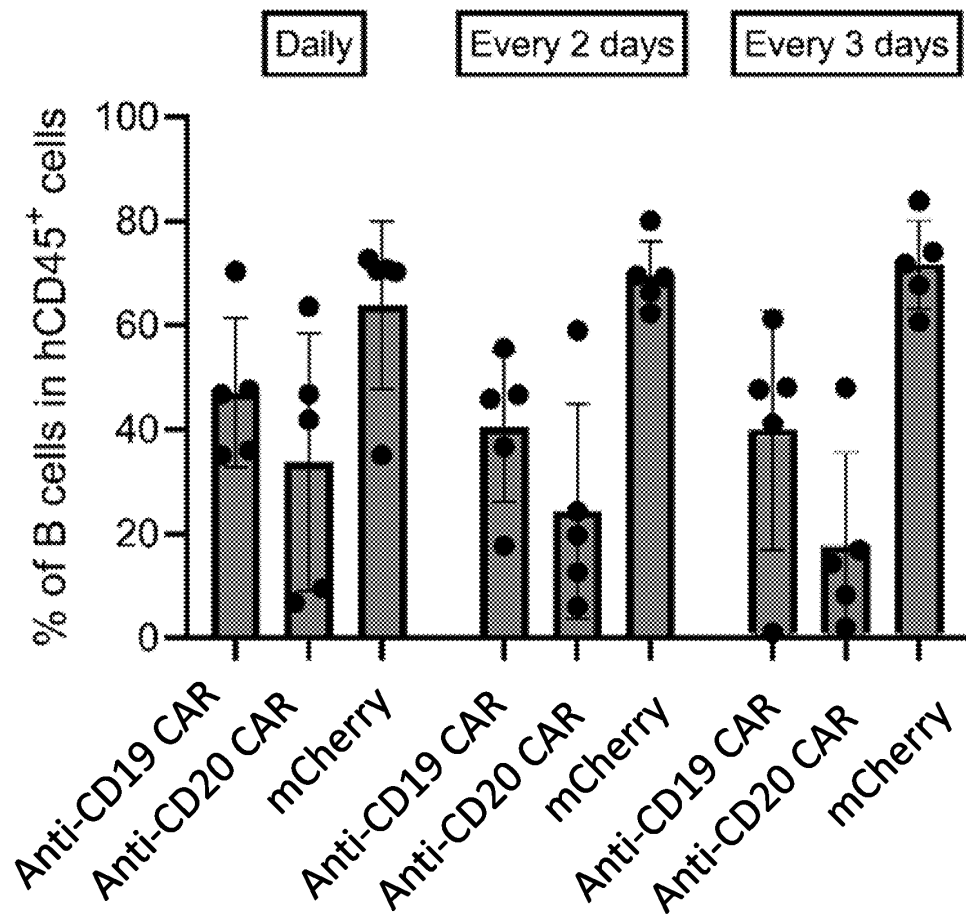


FIG. 25B

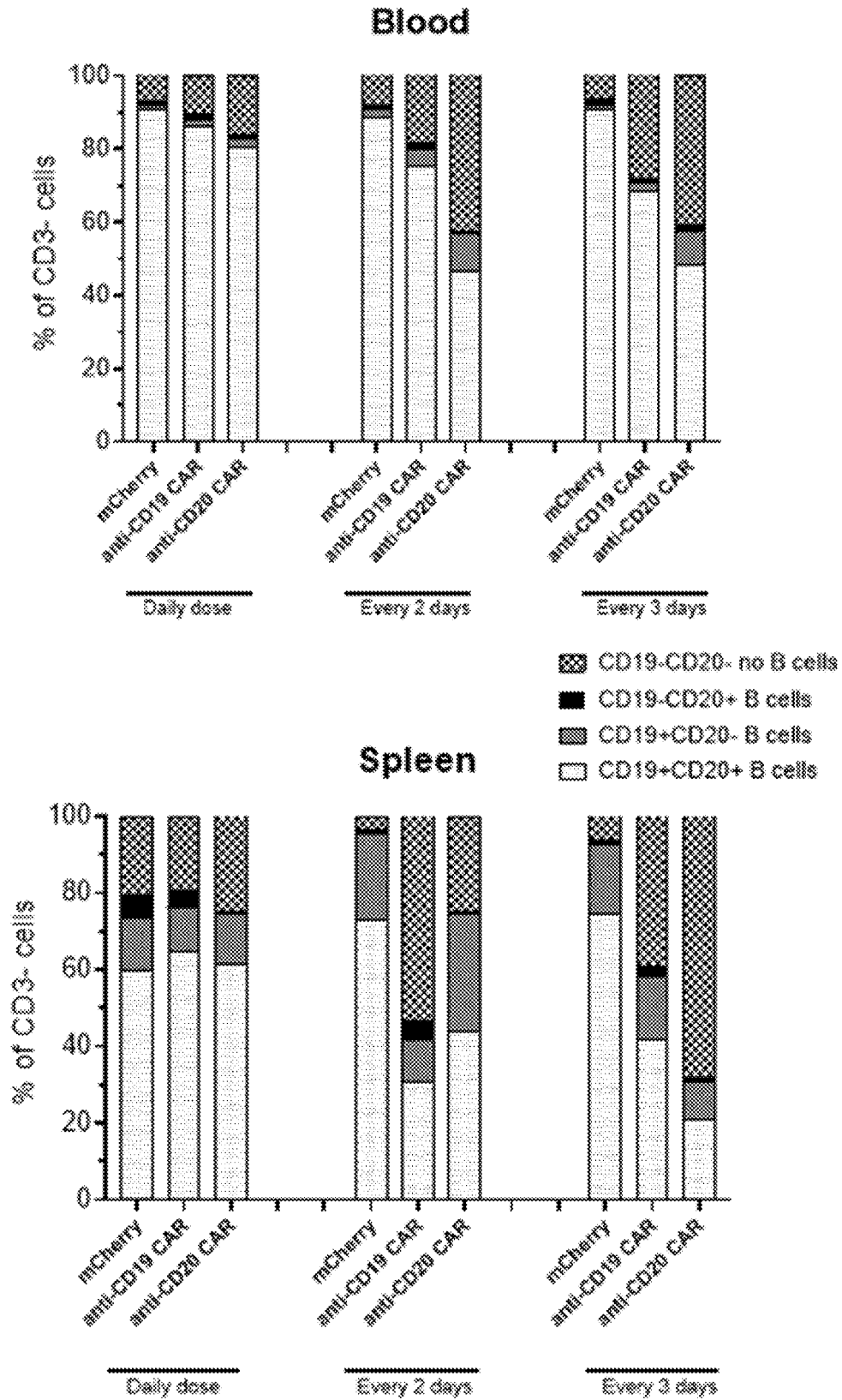


FIG. 26

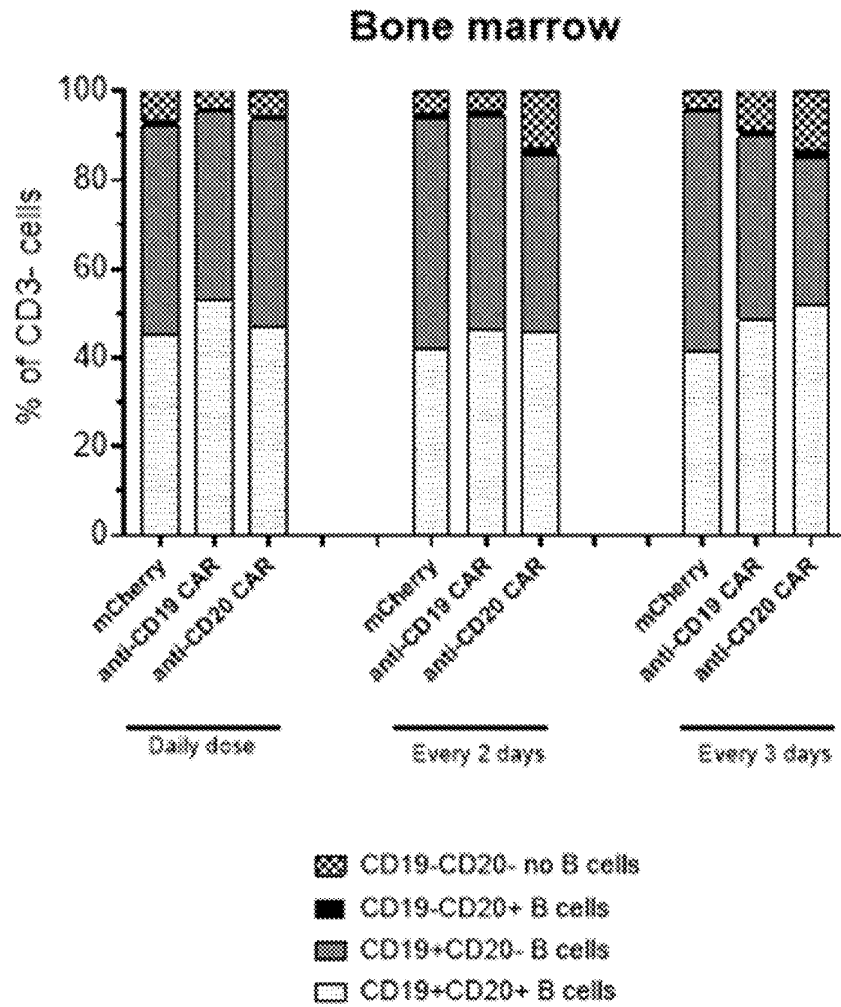
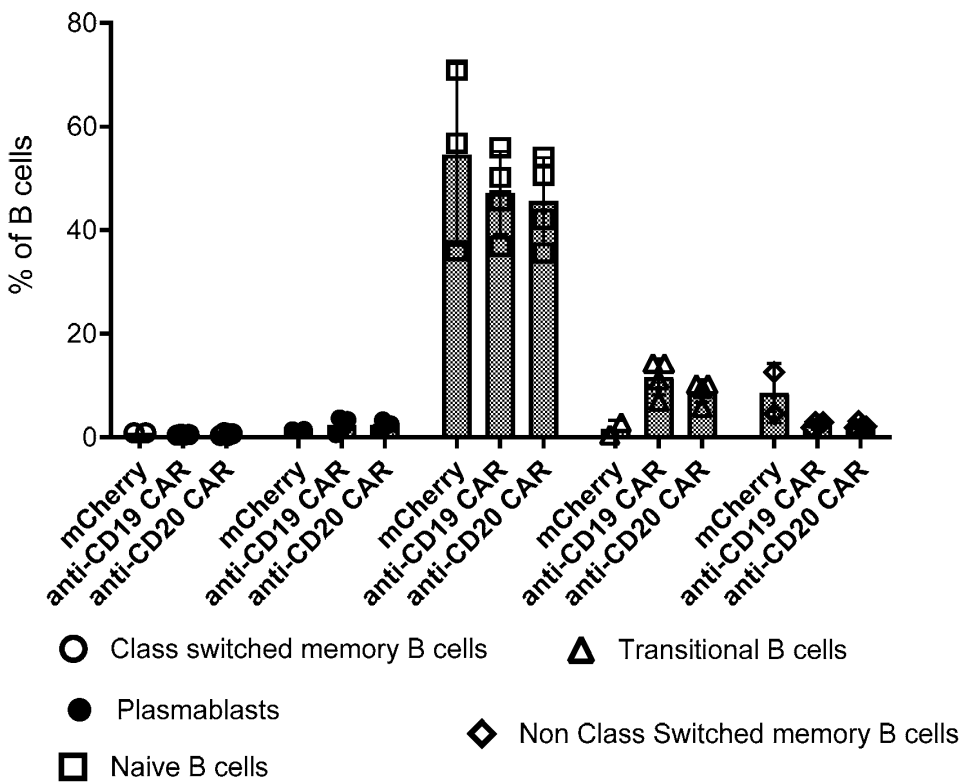


FIG. 26 (CONT'D)

Spleen - Daily



Spleen - Every 2 days

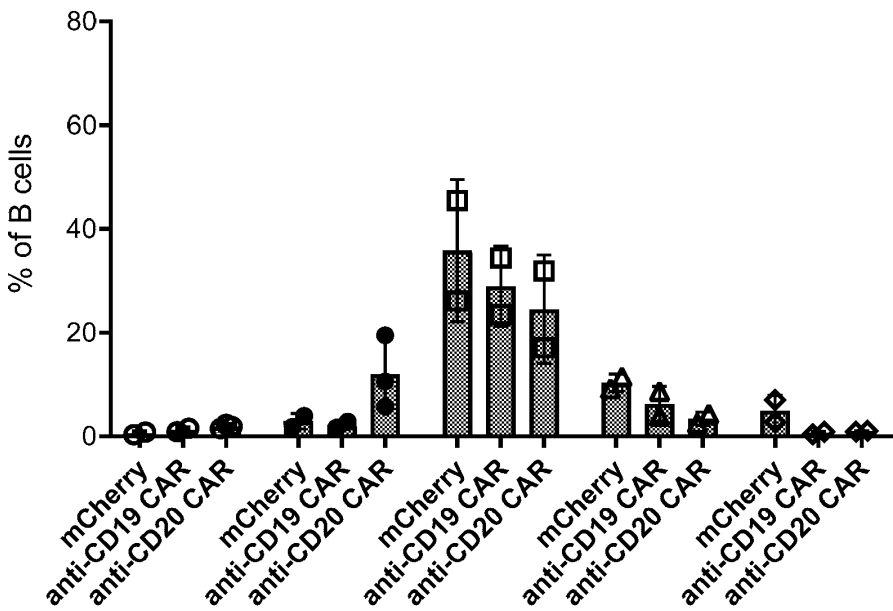


FIG. 27A

Spleen - Every 3 days

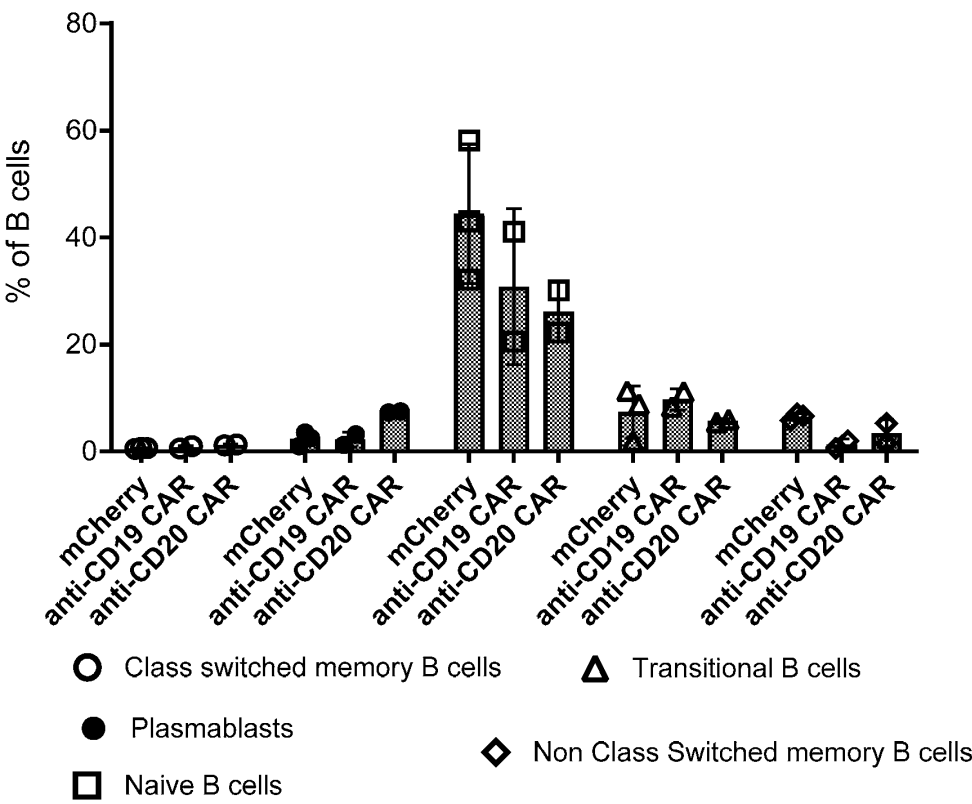


FIG. 27A (CONT'D)

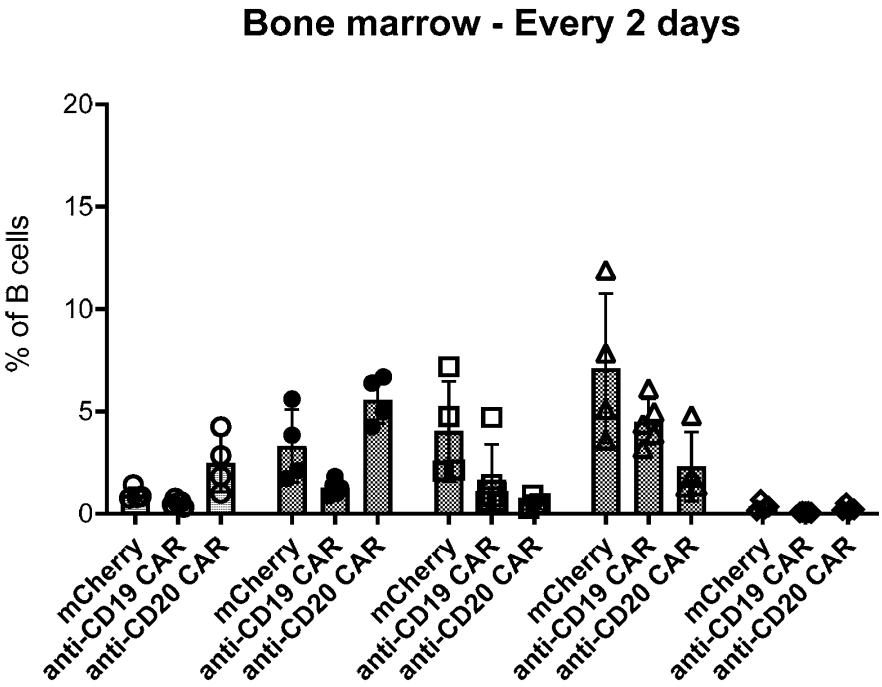
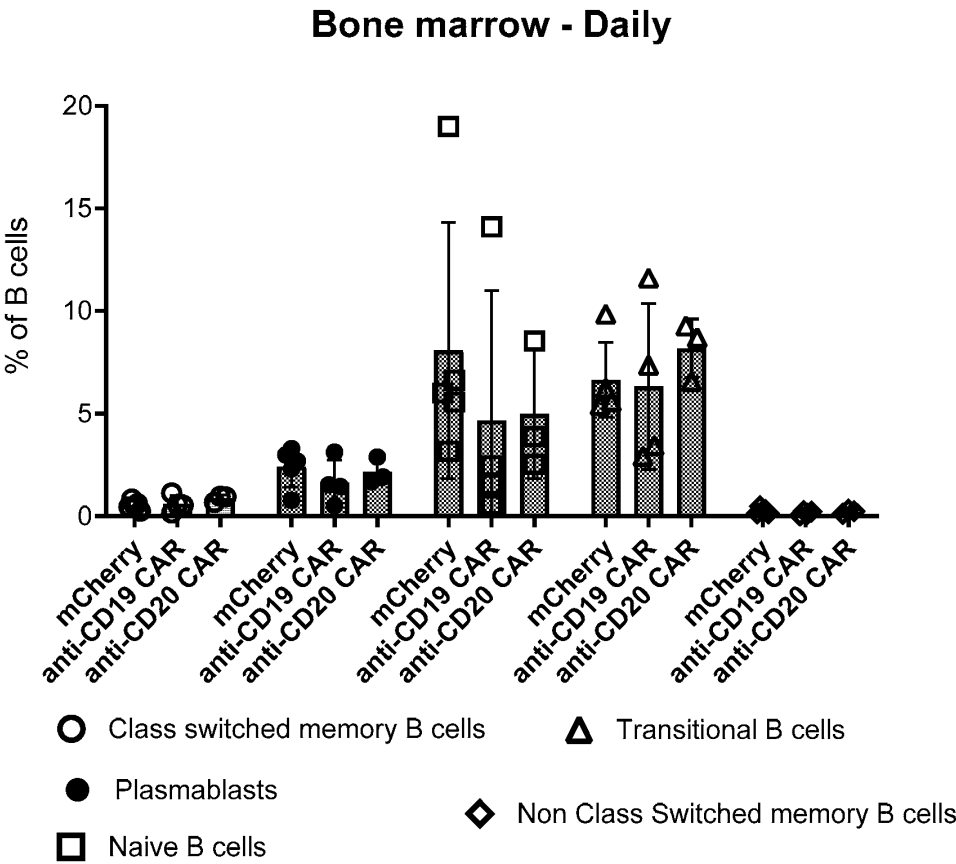


FIG. 27B

Bone marrow - Every 3 days

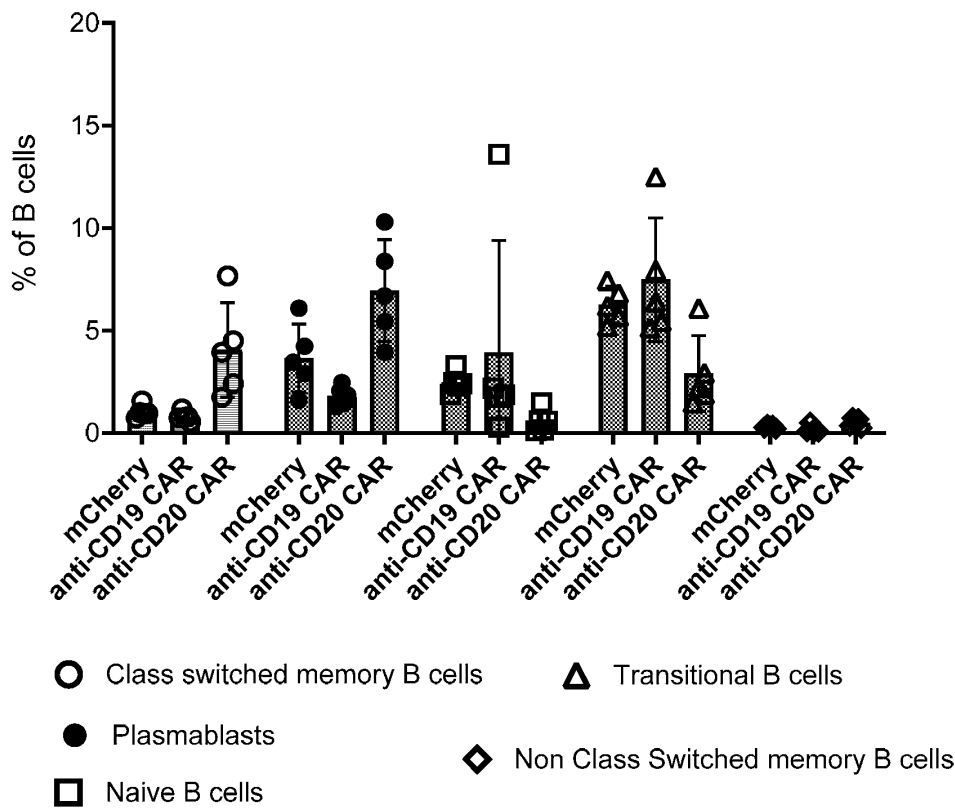


FIG. 27B (CONT'D)

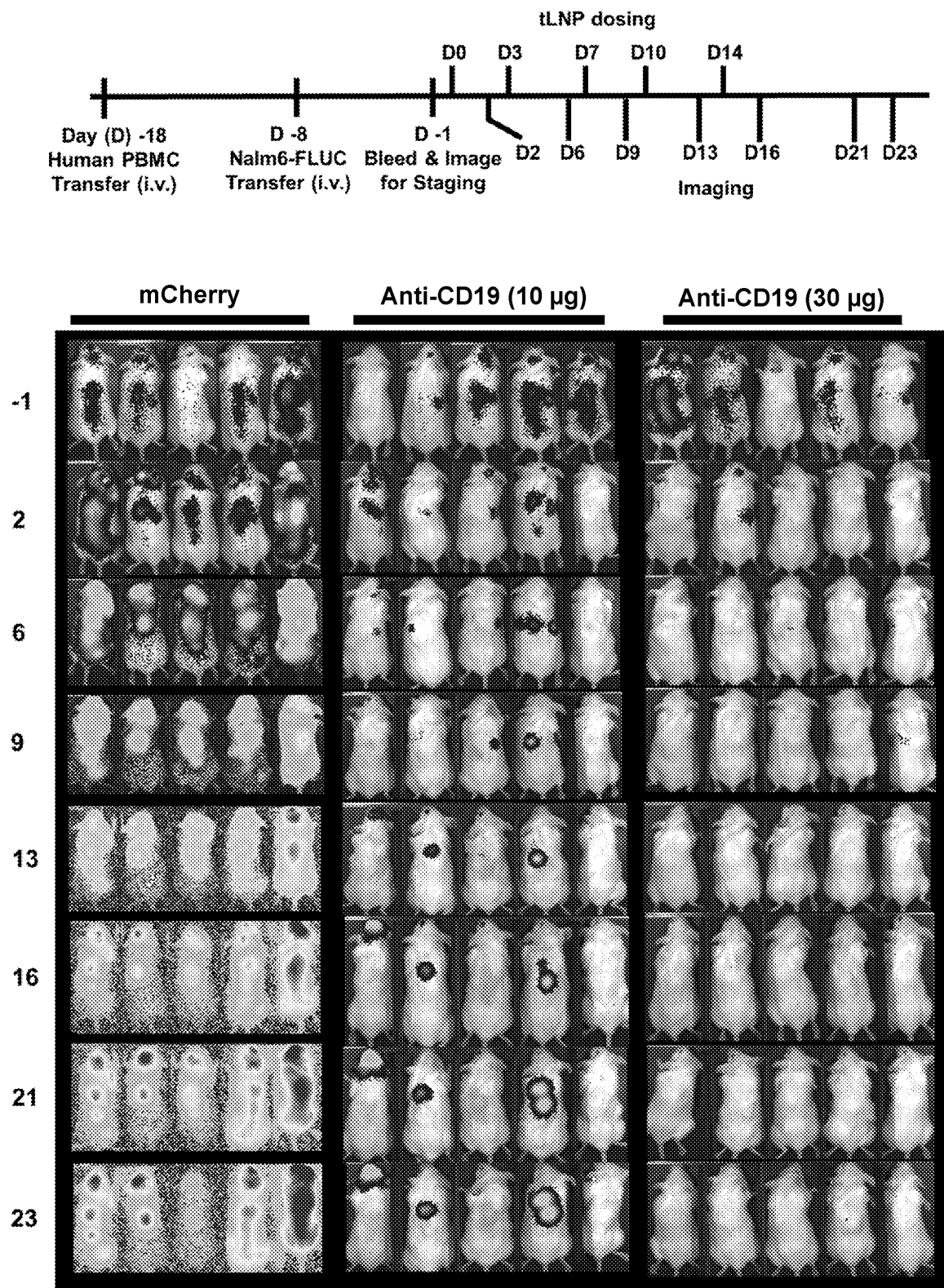


FIG. 28