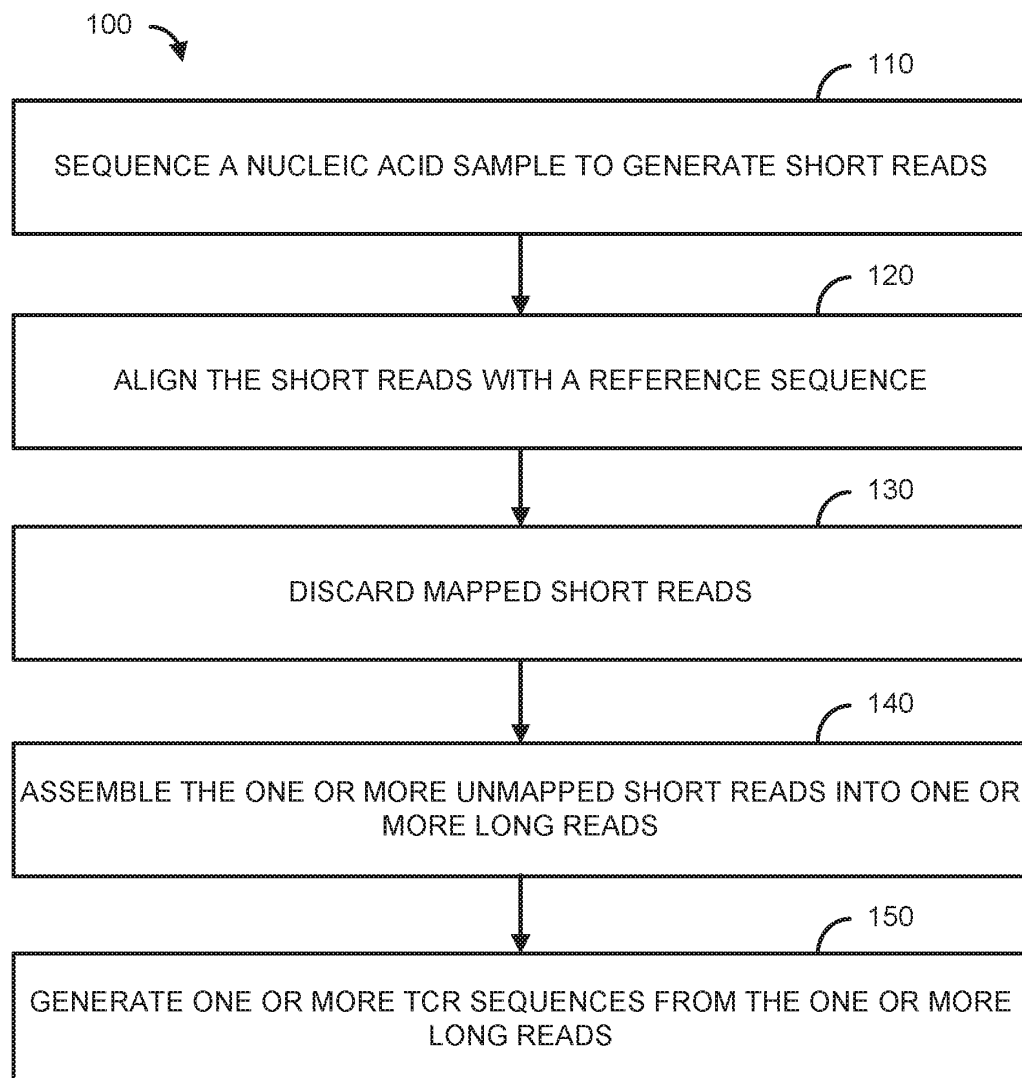


FIG. 1



CDR3	Tumor										Tumor bearing spleen									
	aG1TR+aPD1					aPD1					aG1TR					aPD1				
	11 day		8 day		Isotype	11 day		8 day		Isotype	11 day		8 day		Isotype	11 day		8 day		Isotype
	11 day	8 day	11 day	8 day		11 day	8 day	11 day	8 day		11 day	8 day	11 day	8 day		11 day	8 day	11 day	8 day	
TCR Sequence 1	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 2	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 3	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 4	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 5	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 6	3	0	1	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0
TCR Sequence 7	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 8	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 9	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 10	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 11	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 12	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 13	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 14	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 15	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 16	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 17	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 18	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 19	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 20	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCR Sequence 21	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
TCR Sequence 22	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
TCR Sequence 23	0	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0	0	0
% of cells with the same clones (n>=3)	31.9% (43/141)	0% (0/81)	26.7% (32/120)	4.8% (3/63)	20.3% (16/79)	0% (0/127)	5.7% (6/105)	6.4% (3/47)	0% (0/127)	5.7% (6/105)	0% (0/113)	0% (0/78)	0% (0/72)	0% (0/86)	0% (0/46)	0% (0/42)	0% (0/128)	0% (0/31)	0% (0/31)	0% (0/31)

FIG. 2

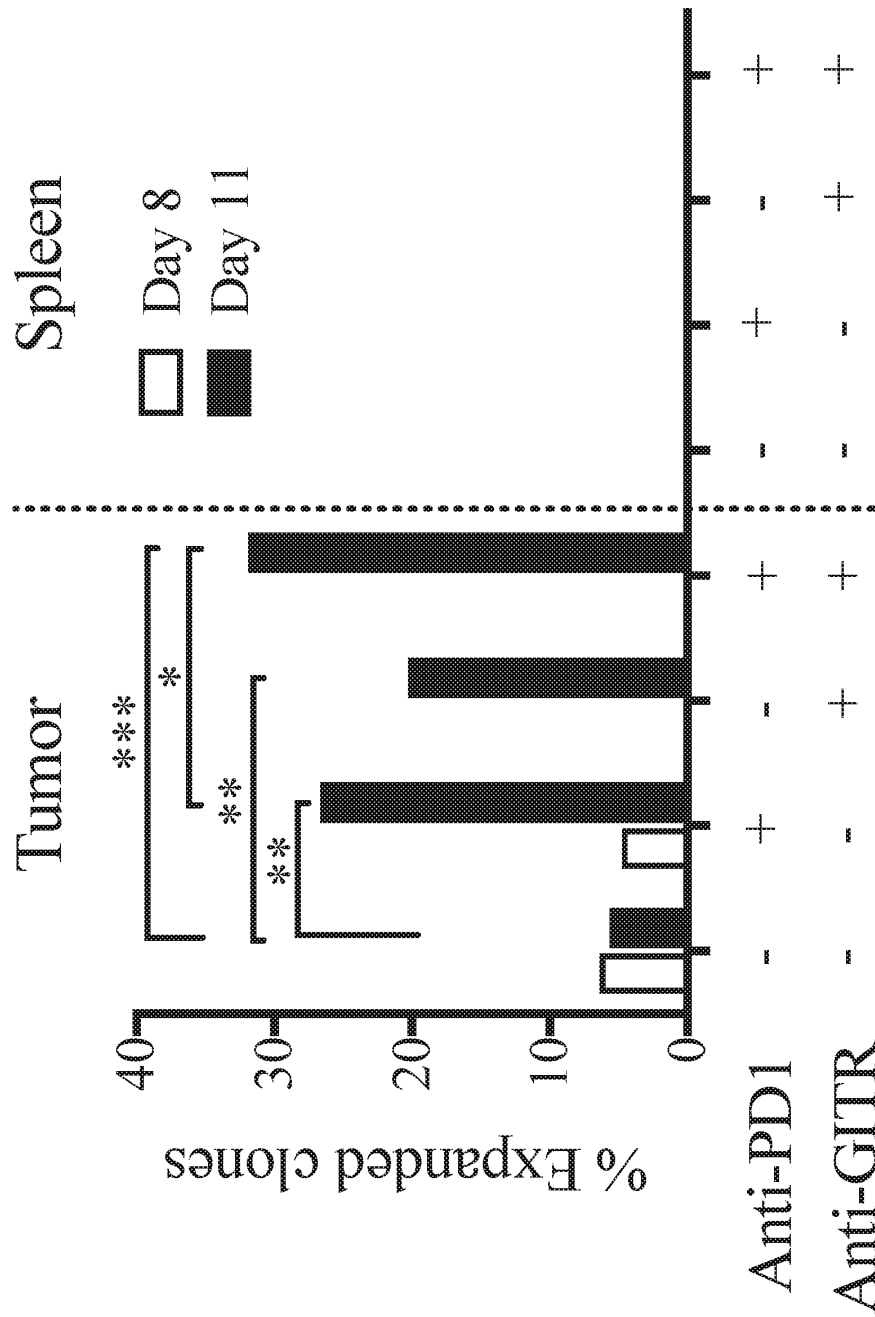
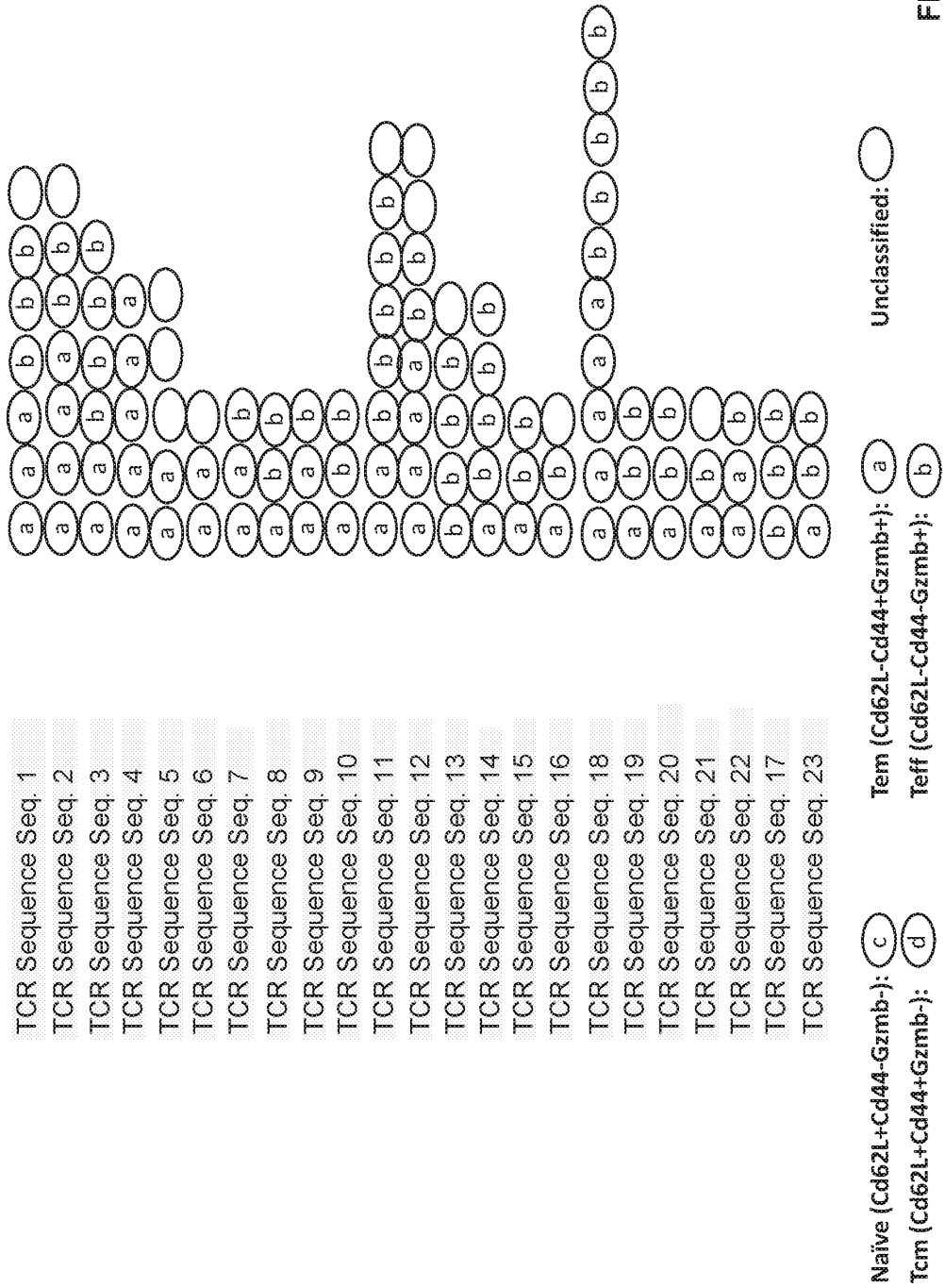


FIG. 3



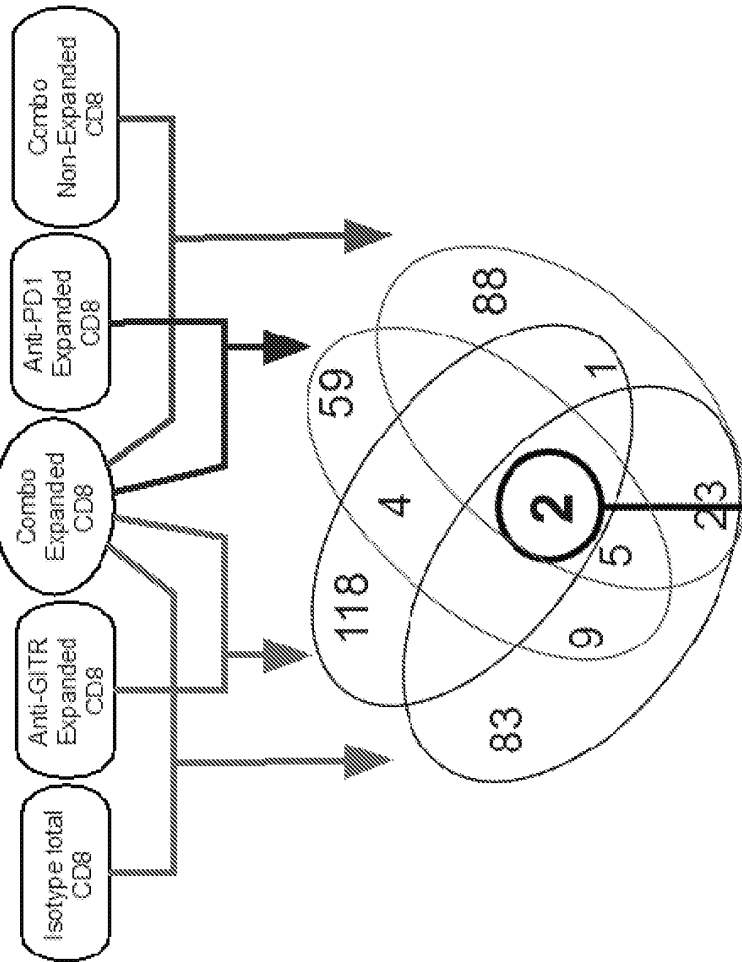
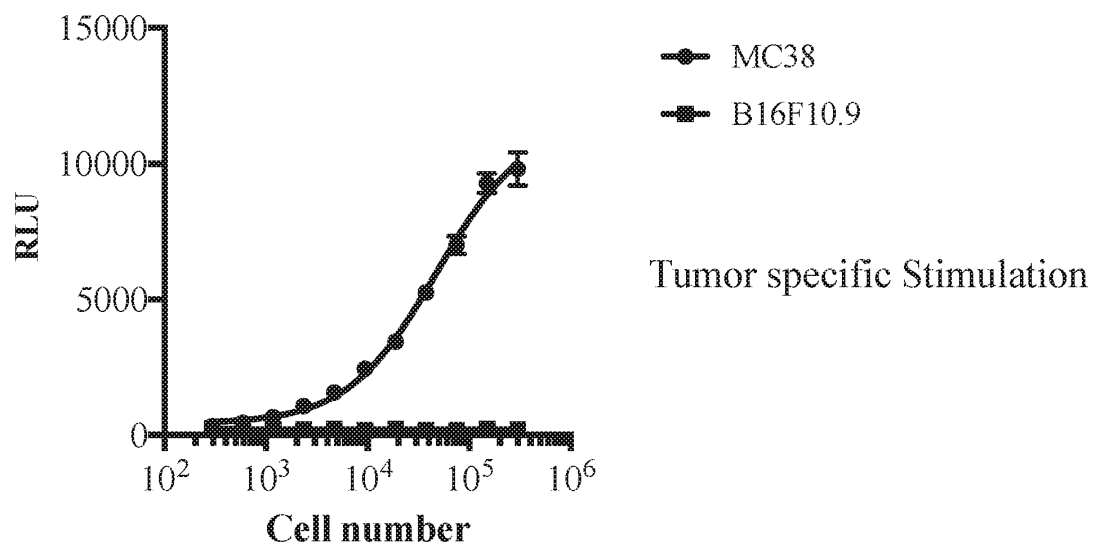


FIG. 5

	Combo expanded vs Isotype	Combo expanded vs Non-expanded	Combo expanded vs anti-GITR expanded	Combo expanded vs anti-PD1 expanded
CD226	10.7	5.0	9.2	6.5
Pde4d	4.8	3.6	6.9	4.9

FIG. 6A



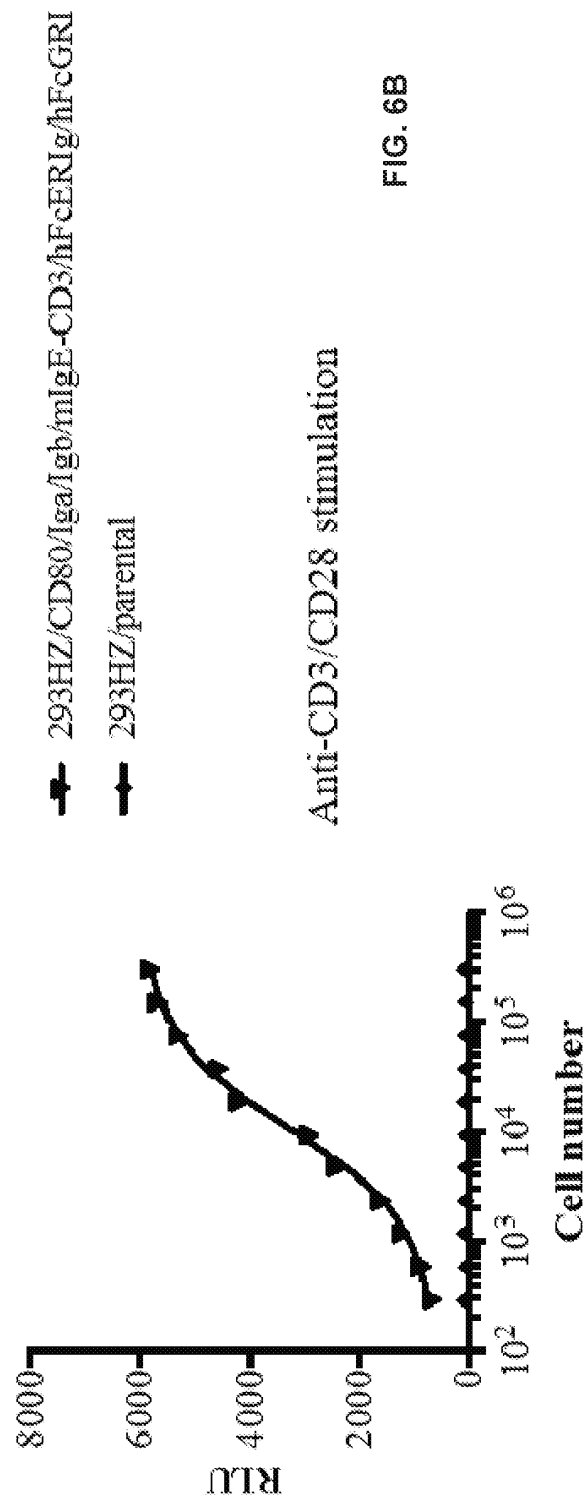
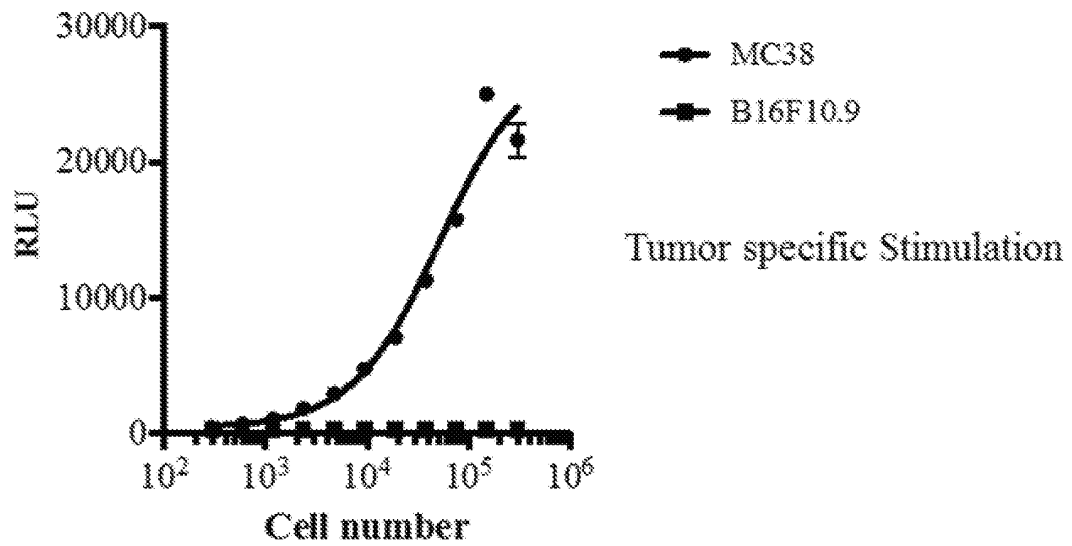


FIG. 6B

FIG. 6C



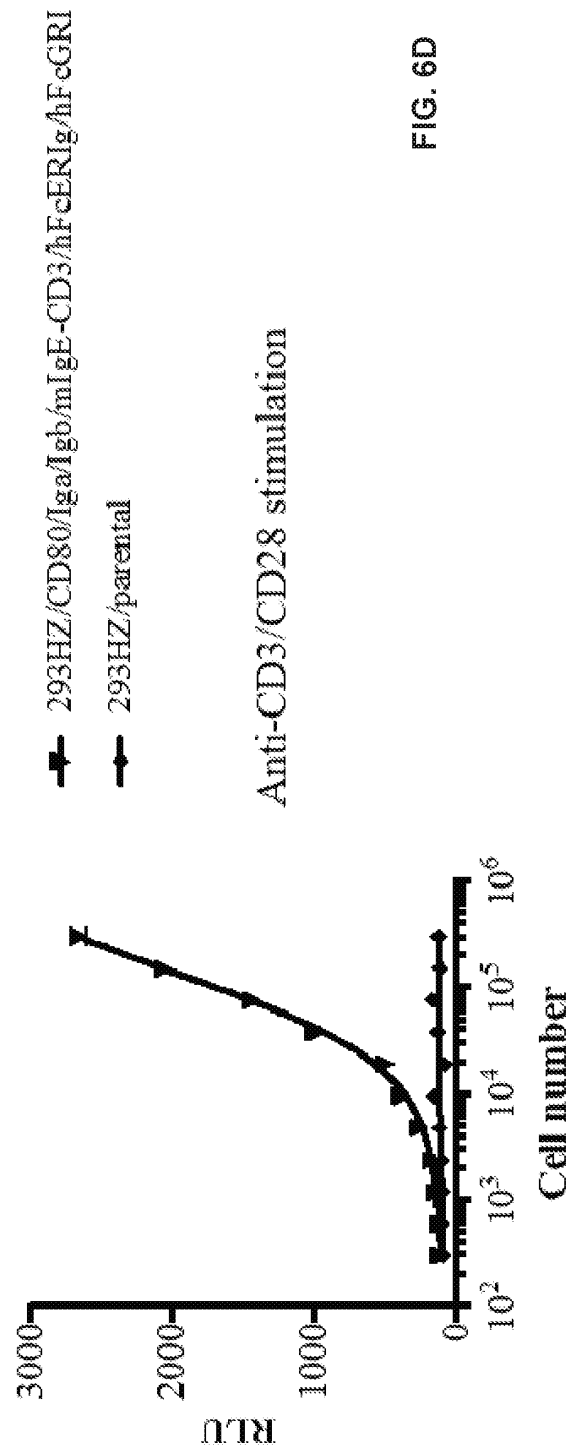
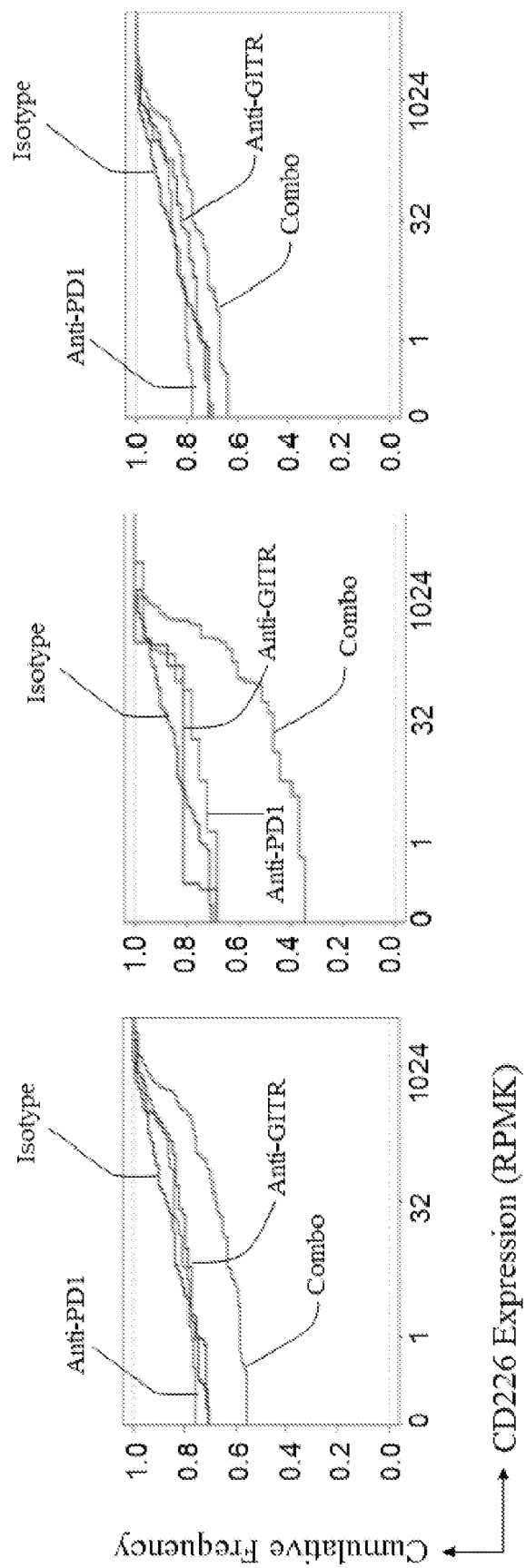


FIG. 6D

FIG. 7A



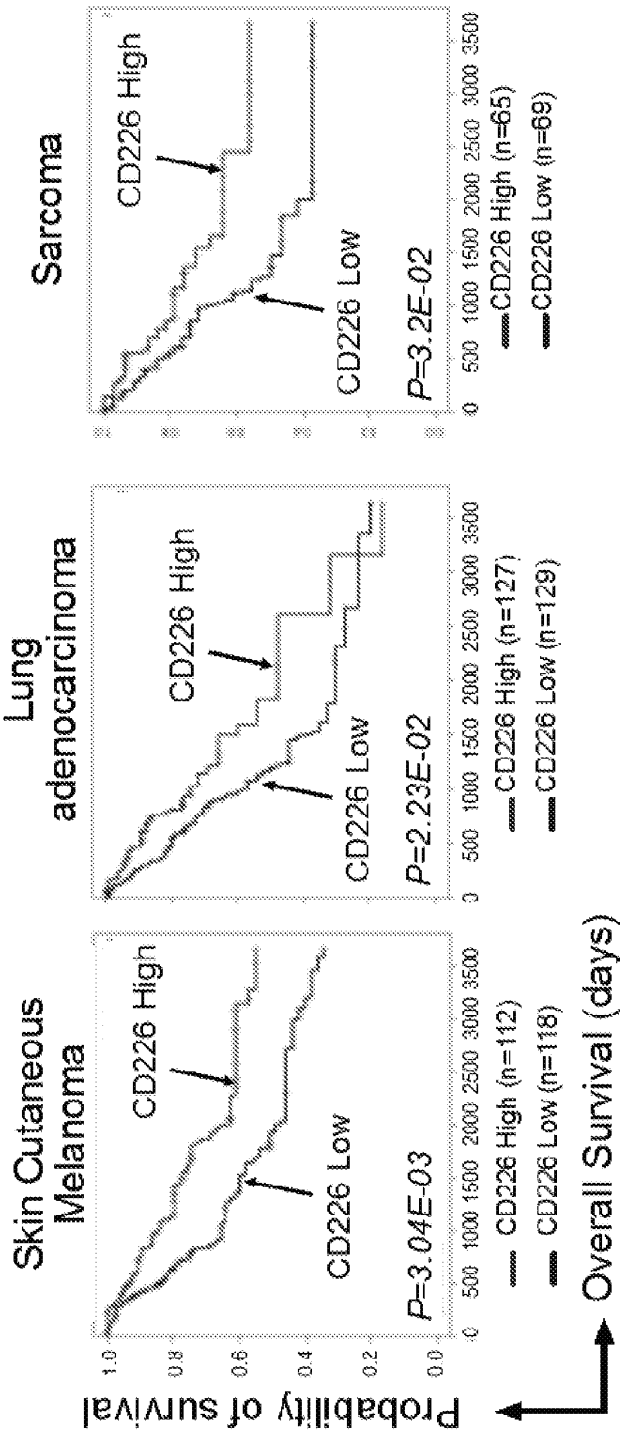


FIG. 7B

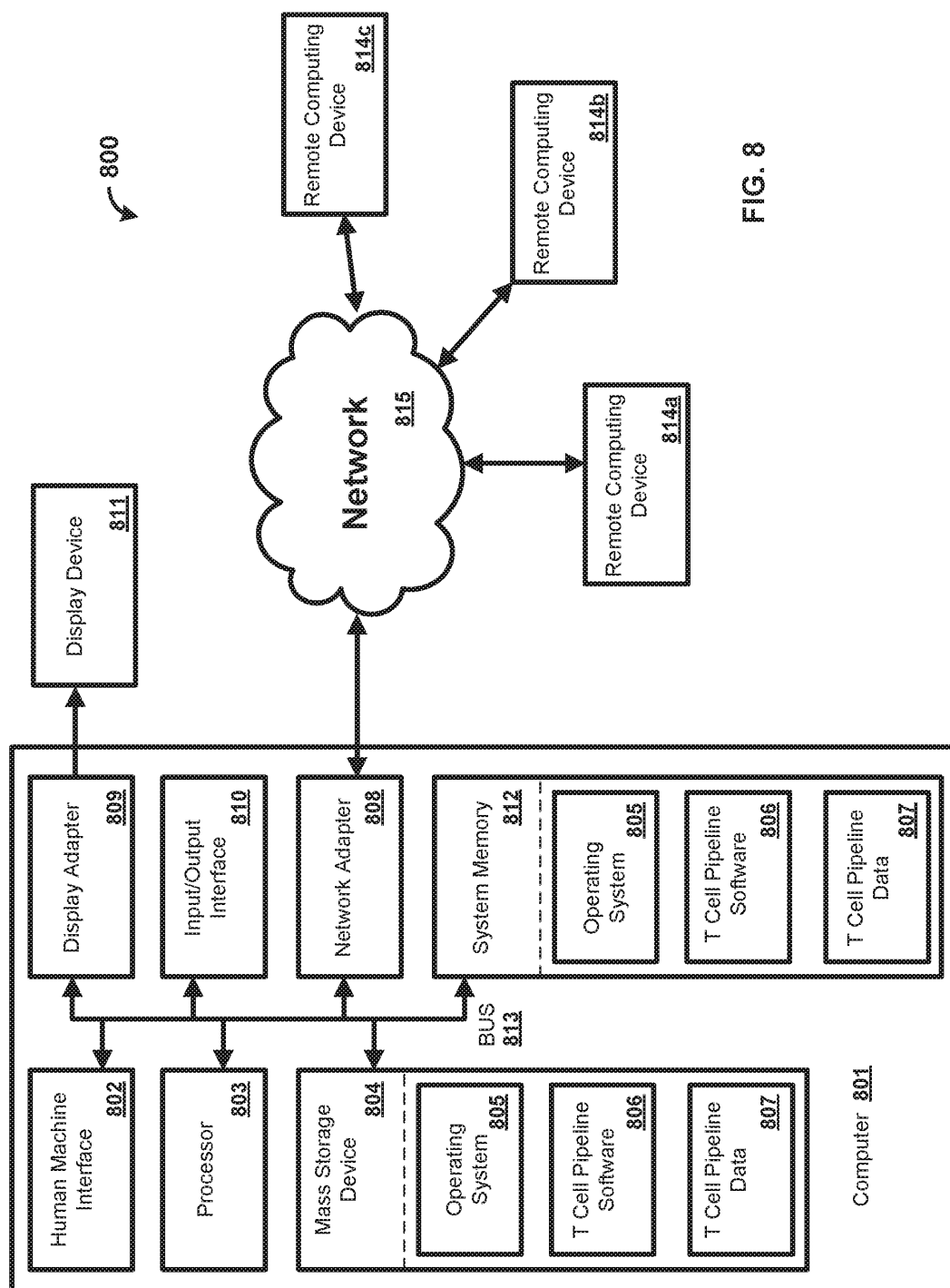
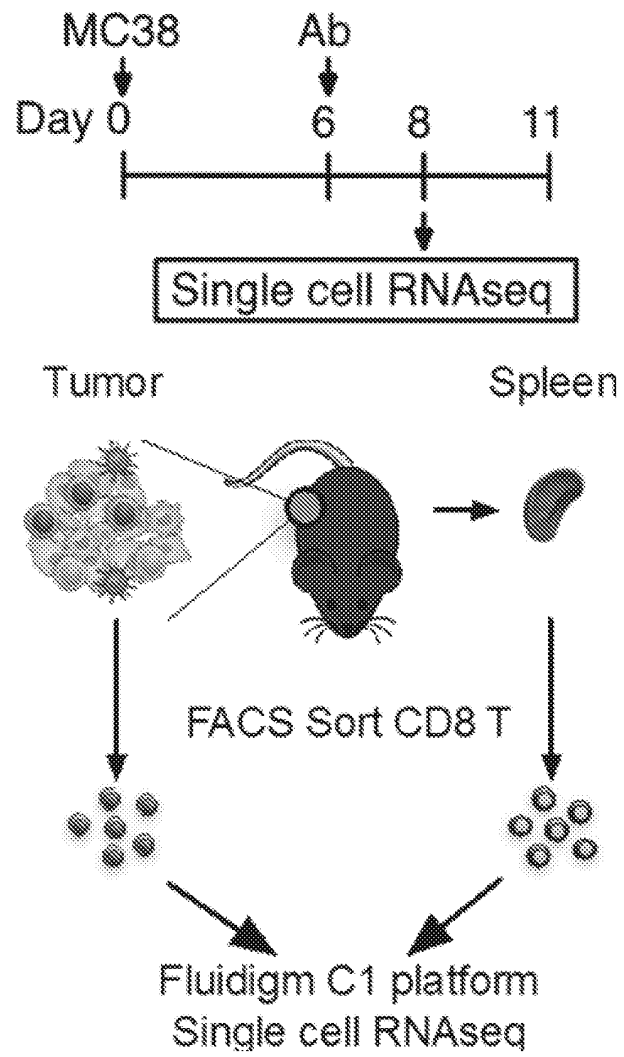


FIG. 8

FIG. 9A



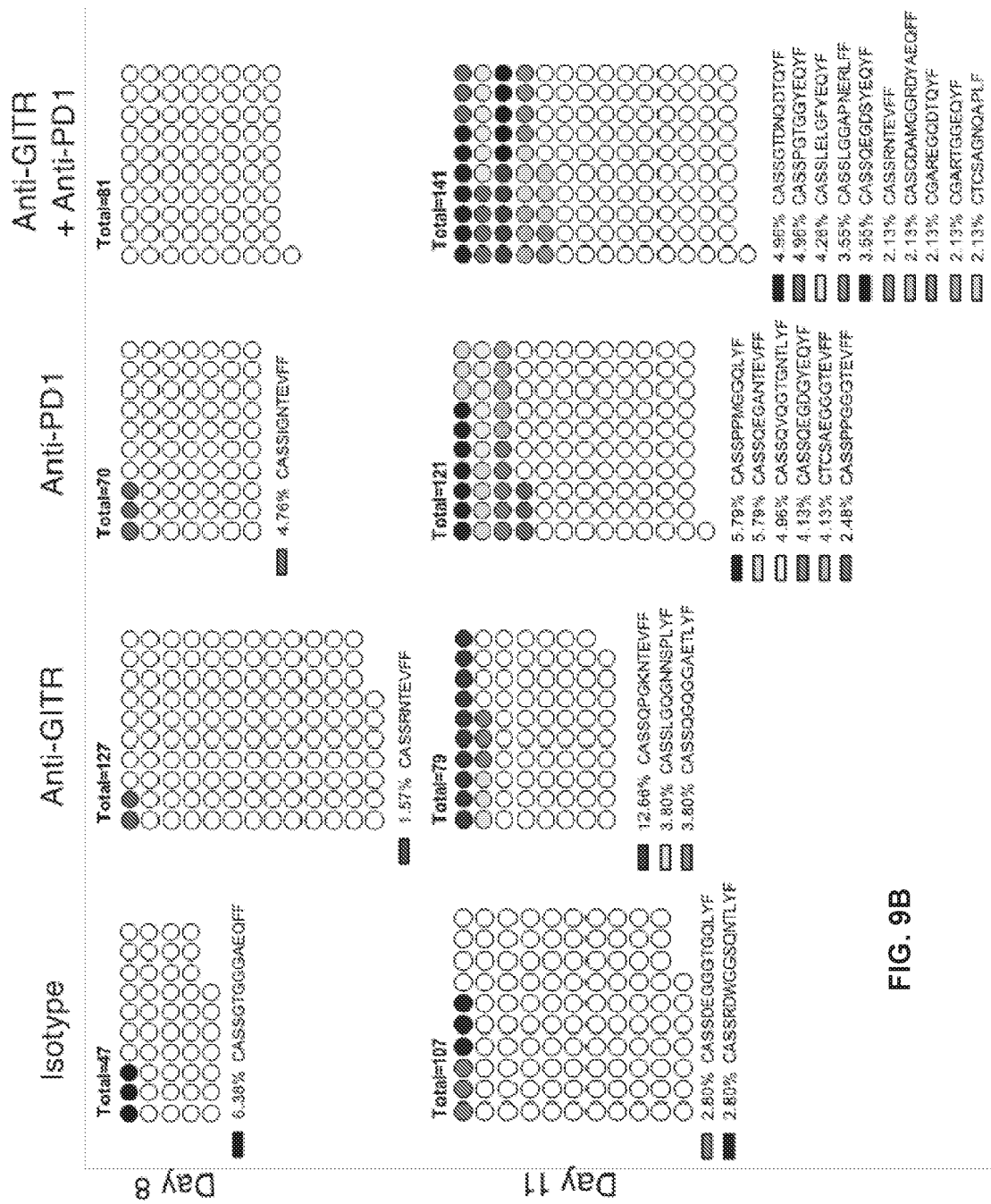


FIG. 9B

FIG. 9C

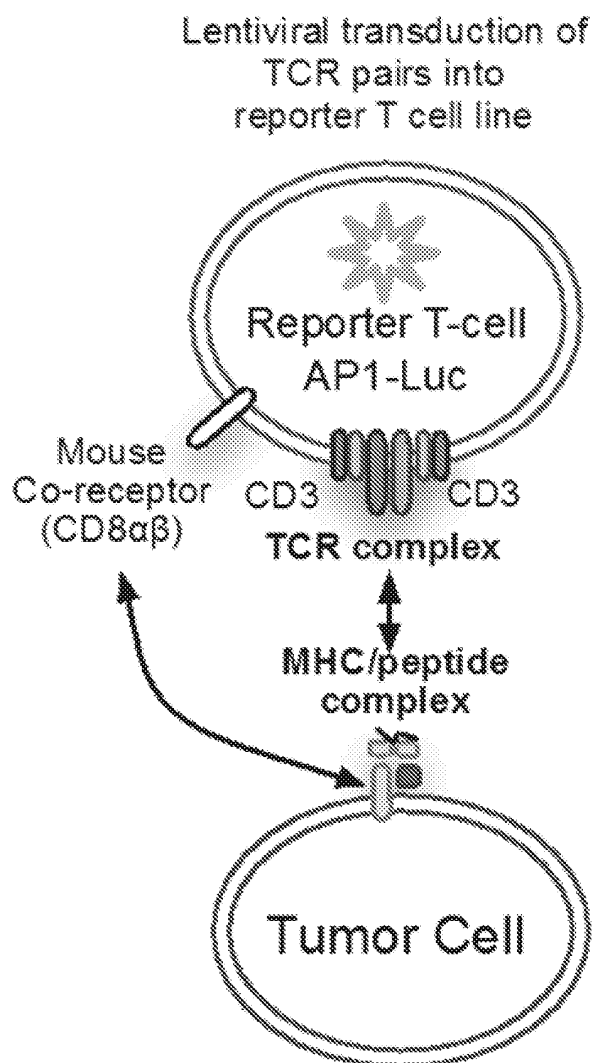


FIG. 9D

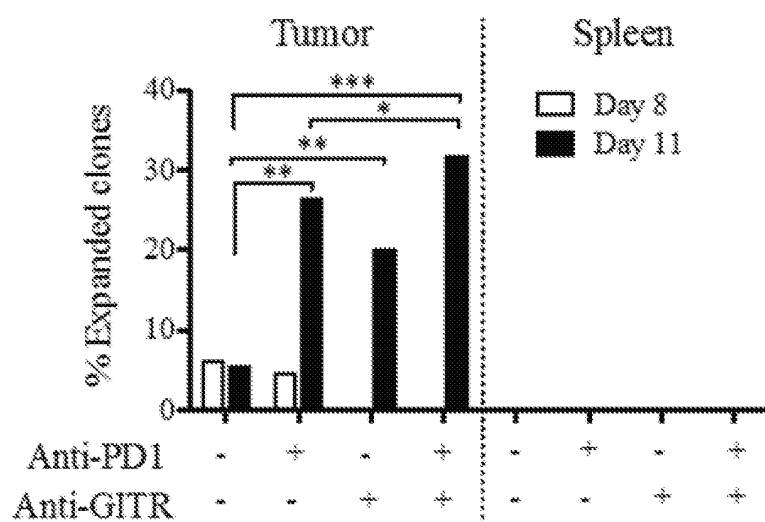
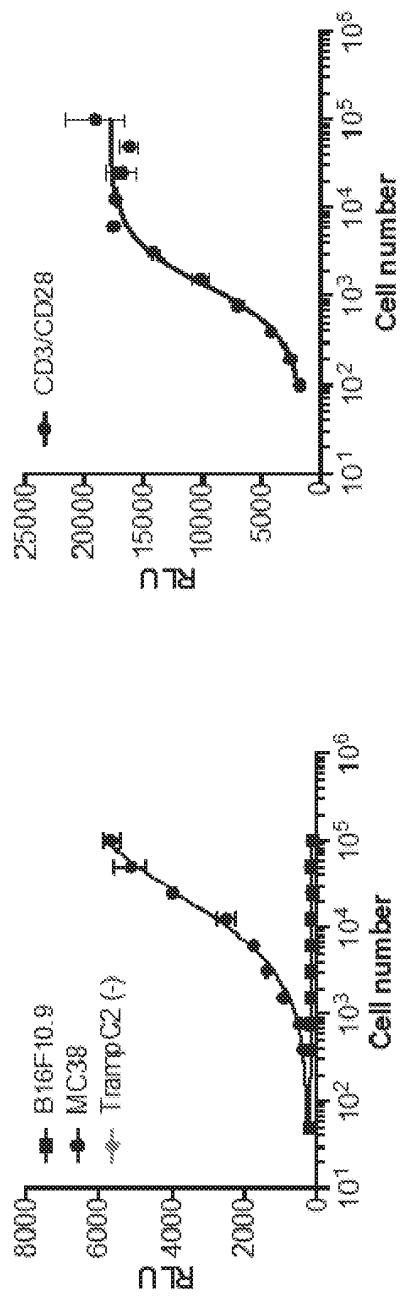


FIG. 9E



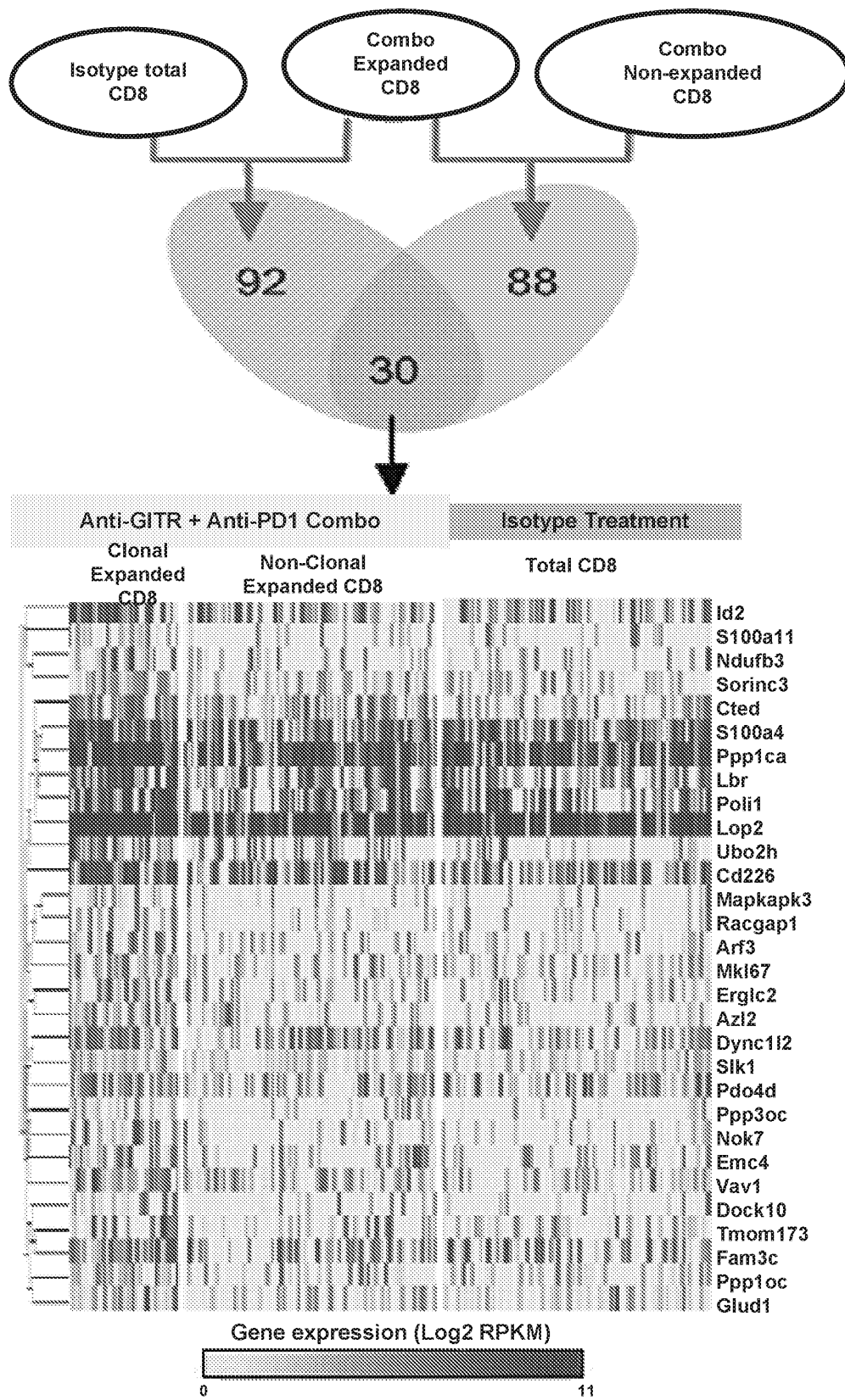
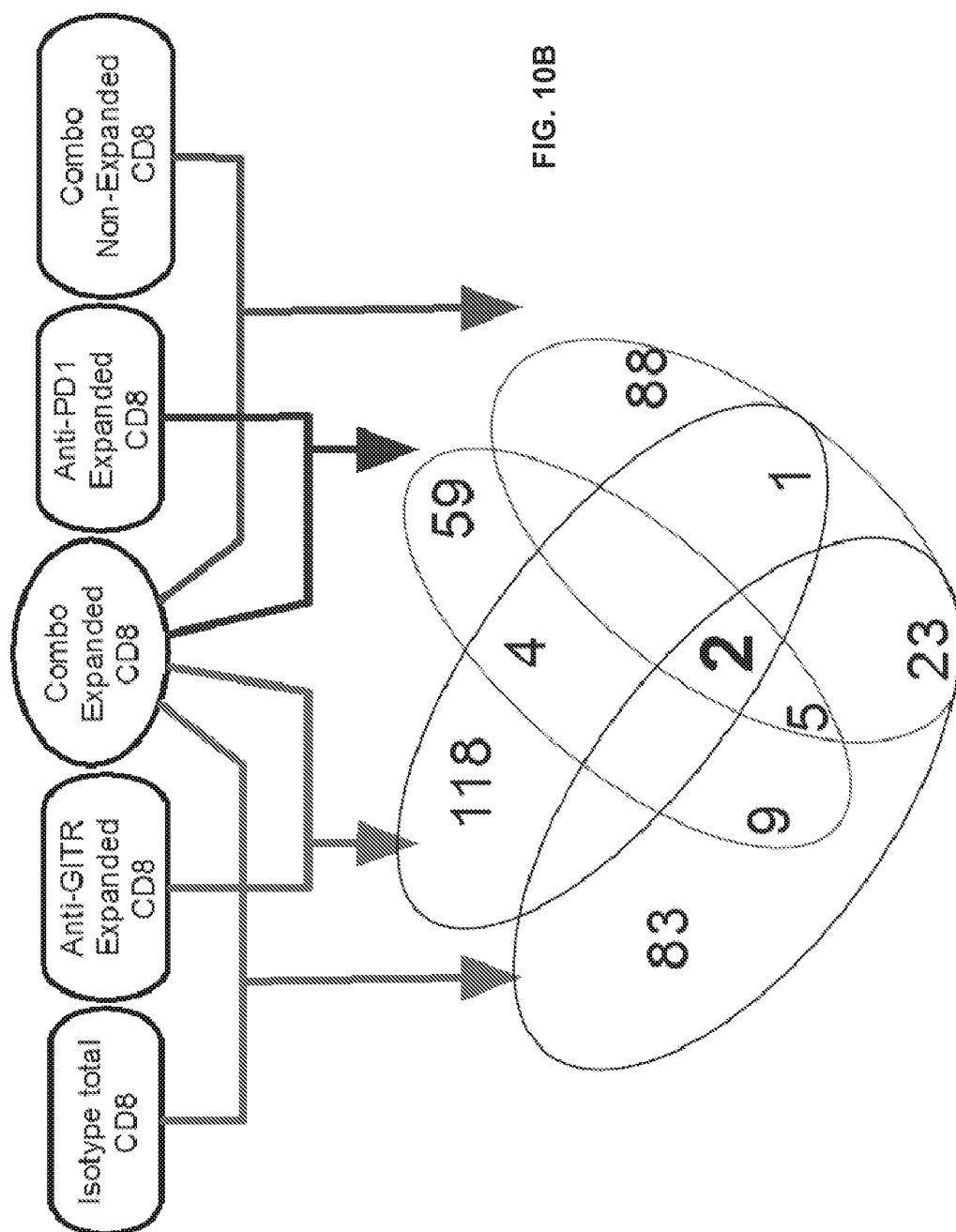


FIG. 10A



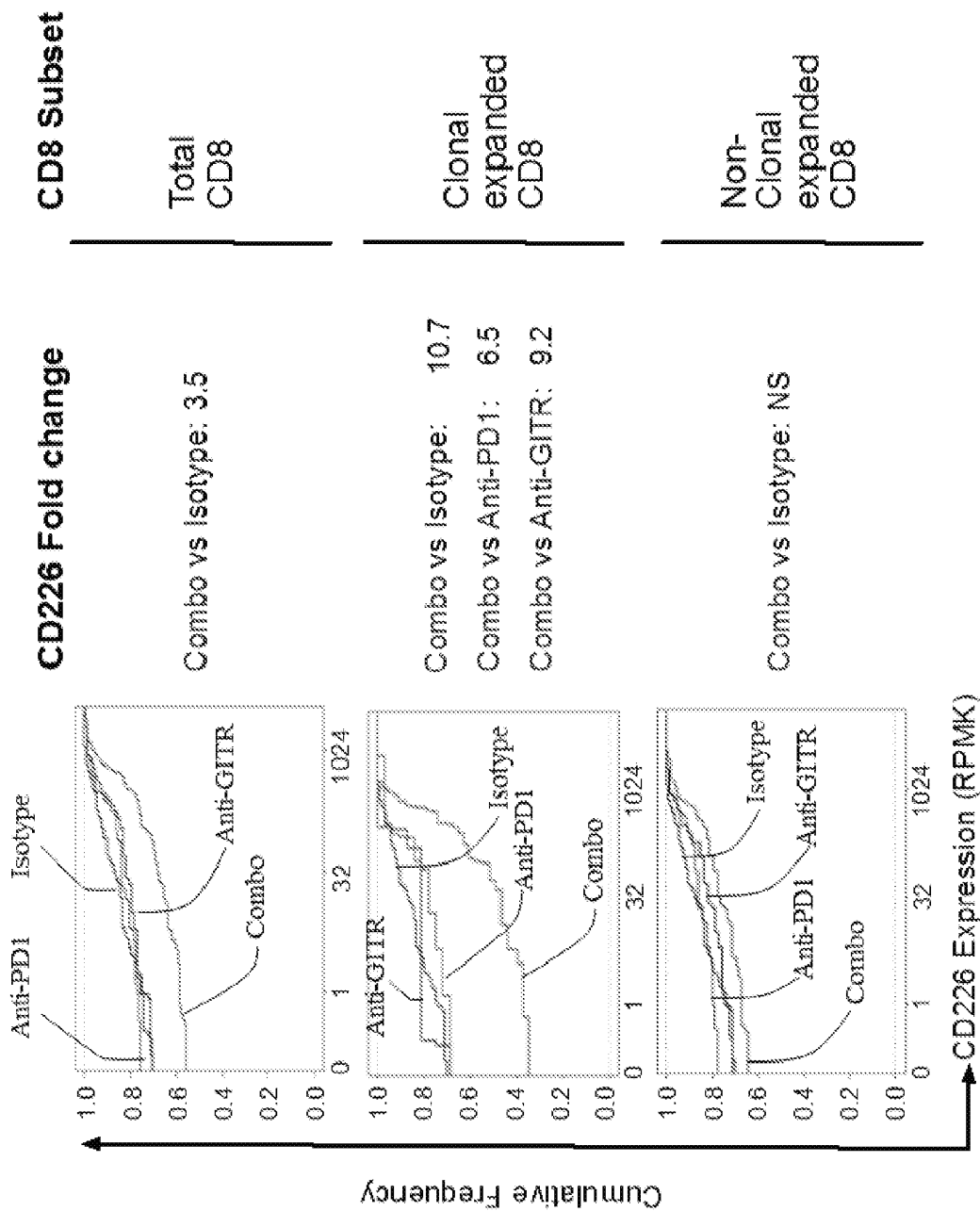


FIG. 10C

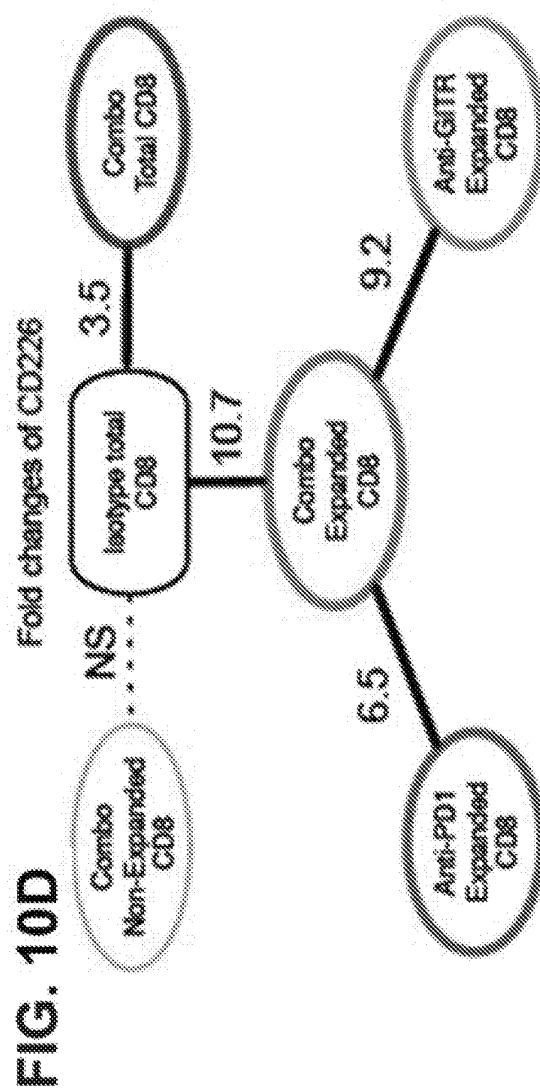


Figure 3: CD226 expression in spleen and tumor cells.

Flow Cytometry Analysis:

- Left Plot:** CD4 vs CD8. The CD8⁺ population is gated for further analysis.
- Right Plot:** OVA-Pentamer vs CD8. The CD8⁺ population is divided into OVA-specific CD8 (black) and Non-specific CD8 (hatched).

Bar Graphs (CD226 MFI):

Spleen:

Cell Type	CD226 MFI (approx.)
Non-specific CD8	2000
OVA-specific CD8	2200
Non-specific CD8	2500
OVA-specific CD8	2800
Non-specific CD8	3000
OVA-specific CD8	3500
Non-specific CD8	4000
OVA-specific CD8	4500
Non-specific CD8	5000
OVA-specific CD8	5500

Tumor:

Cell Type	CD226 MFI (approx.)
Non-specific CD8	1500
OVA-specific CD8	1800
Non-specific CD8	2000
OVA-specific CD8	2200
Non-specific CD8	2500
OVA-specific CD8	2800
Non-specific CD8	3000
OVA-specific CD8	3500
Non-specific CD8	4000
OVA-specific CD8	4500

Legend:

- Total CD8 (white)
- Non-specific CD8 (hatched)
- OVA-specific CD8 (black)

FIG. 11B

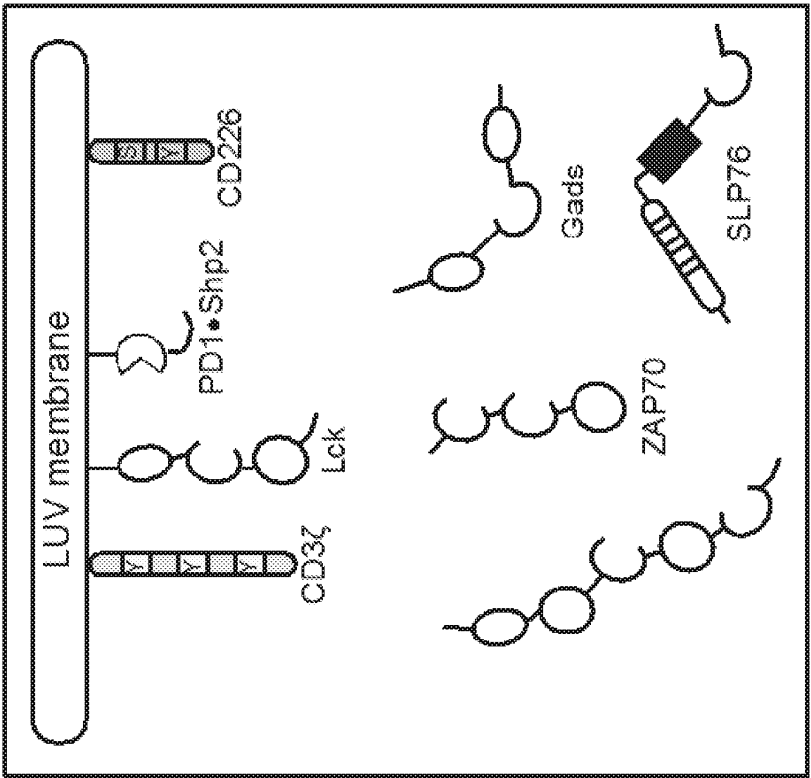
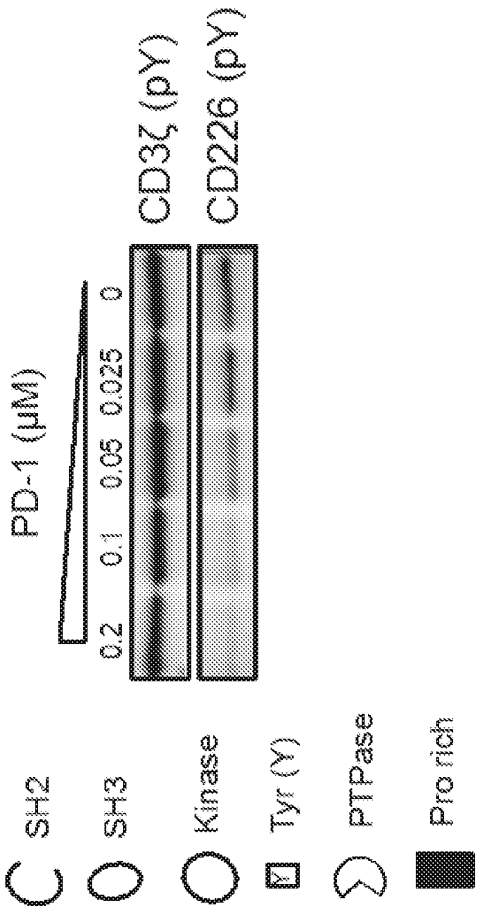


FIG. 11C



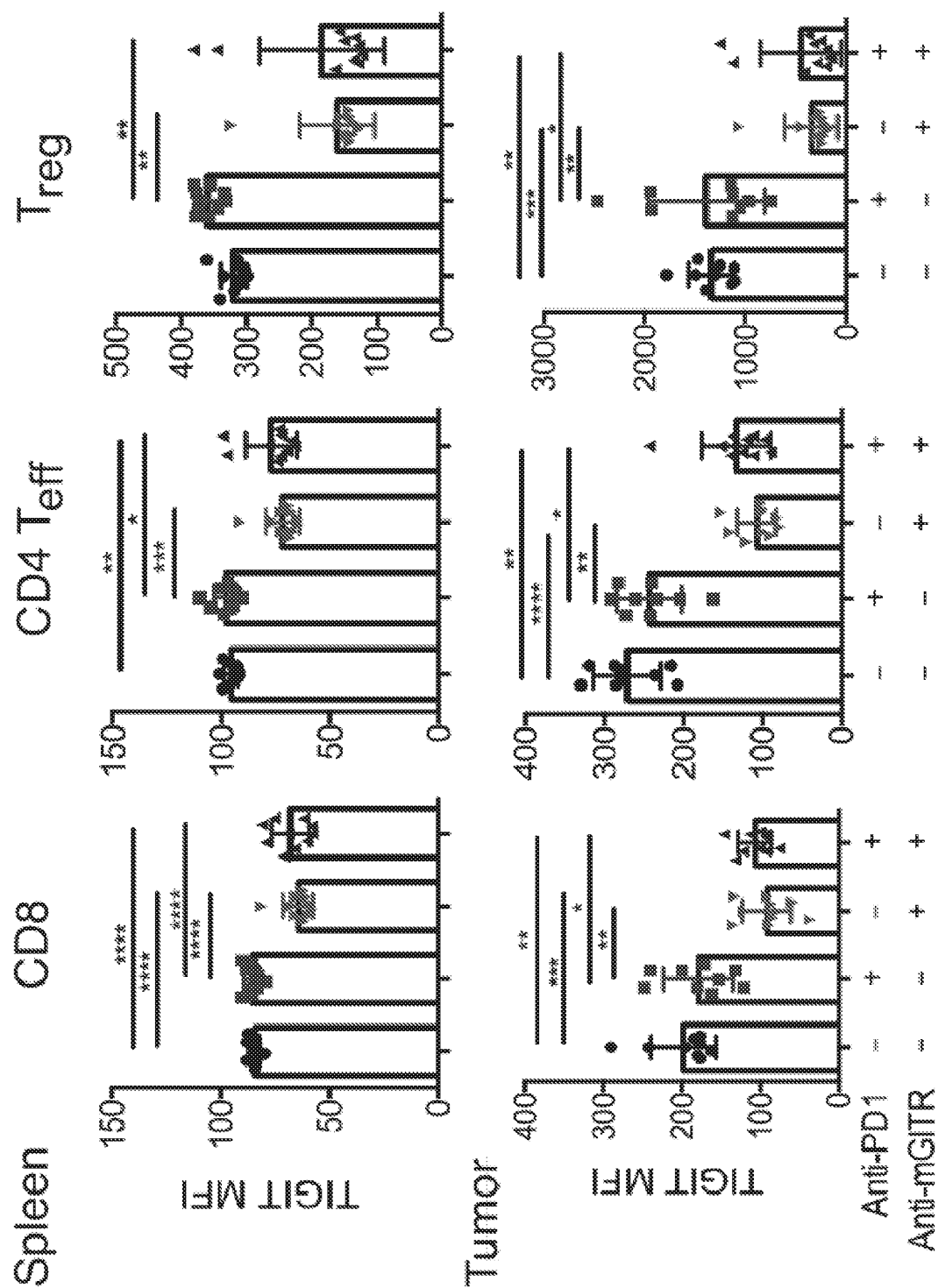


FIG. 11D

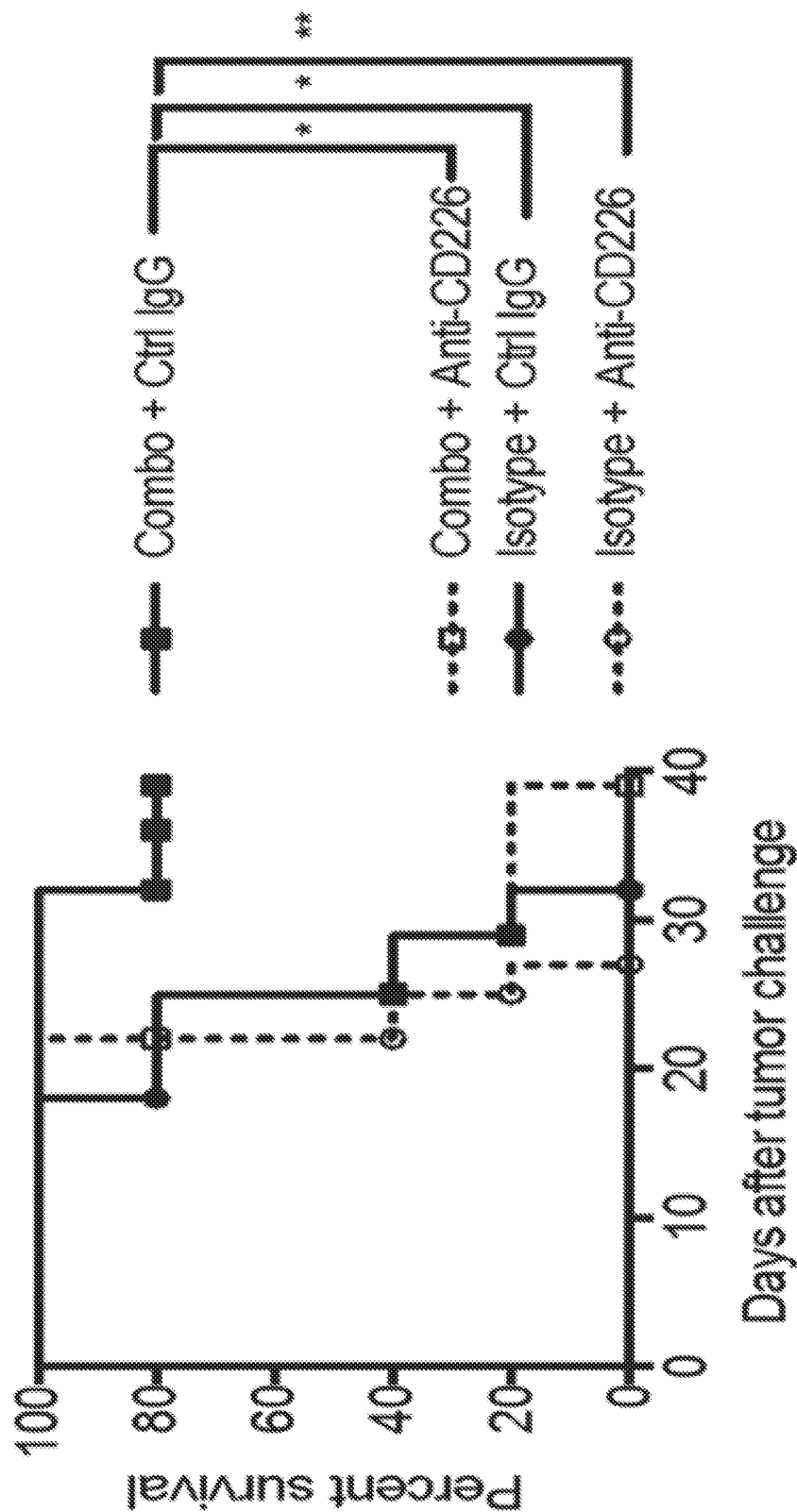


FIG. 12A

FIG. 12B

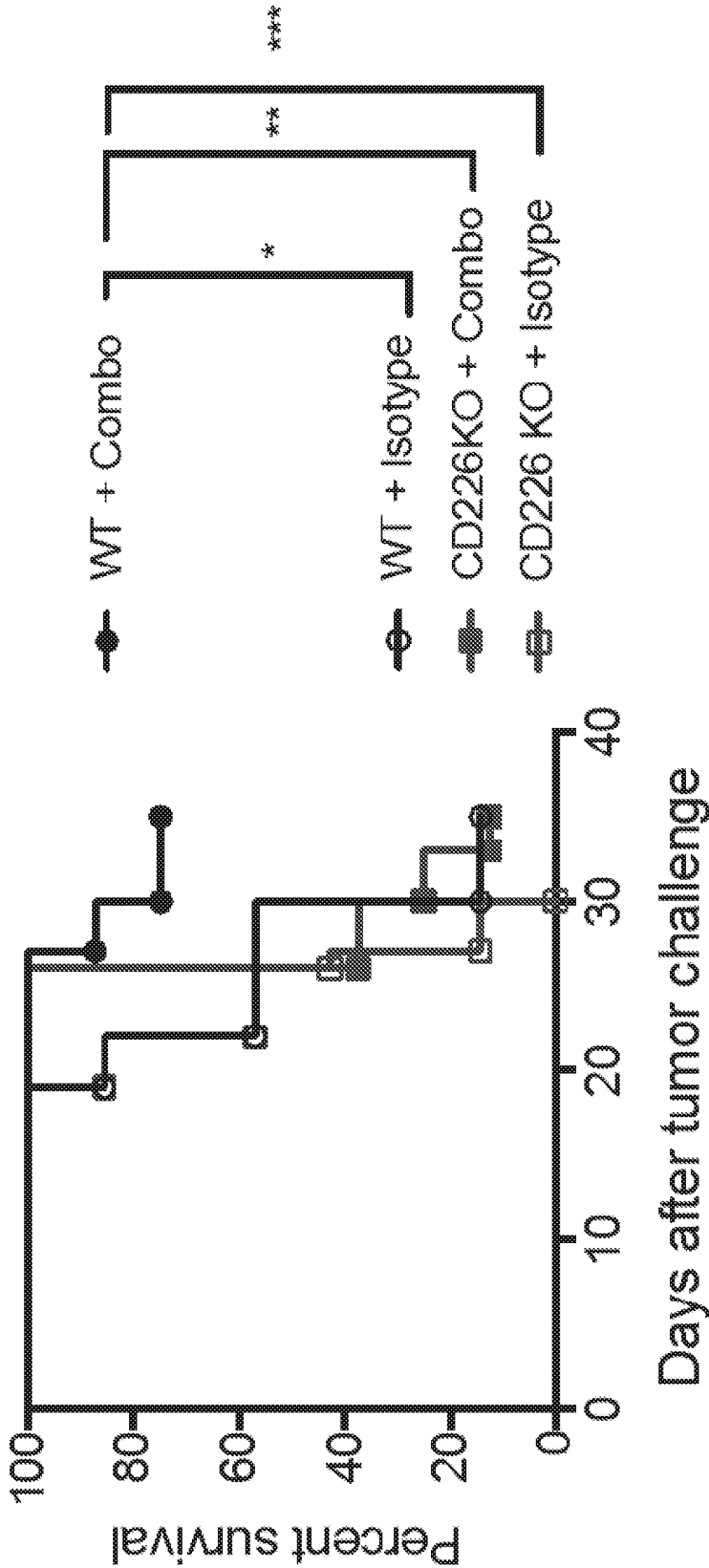


FIG. 12C

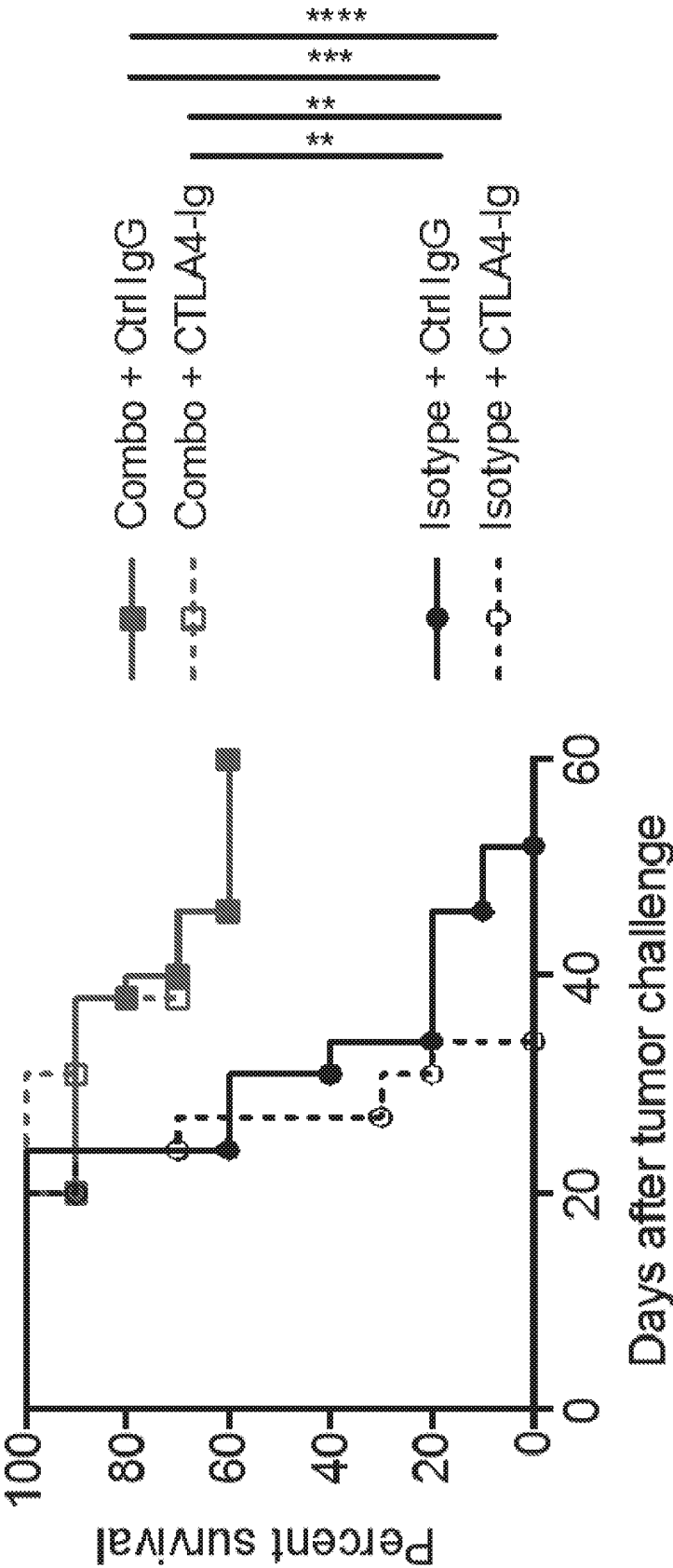


FIG. 12D

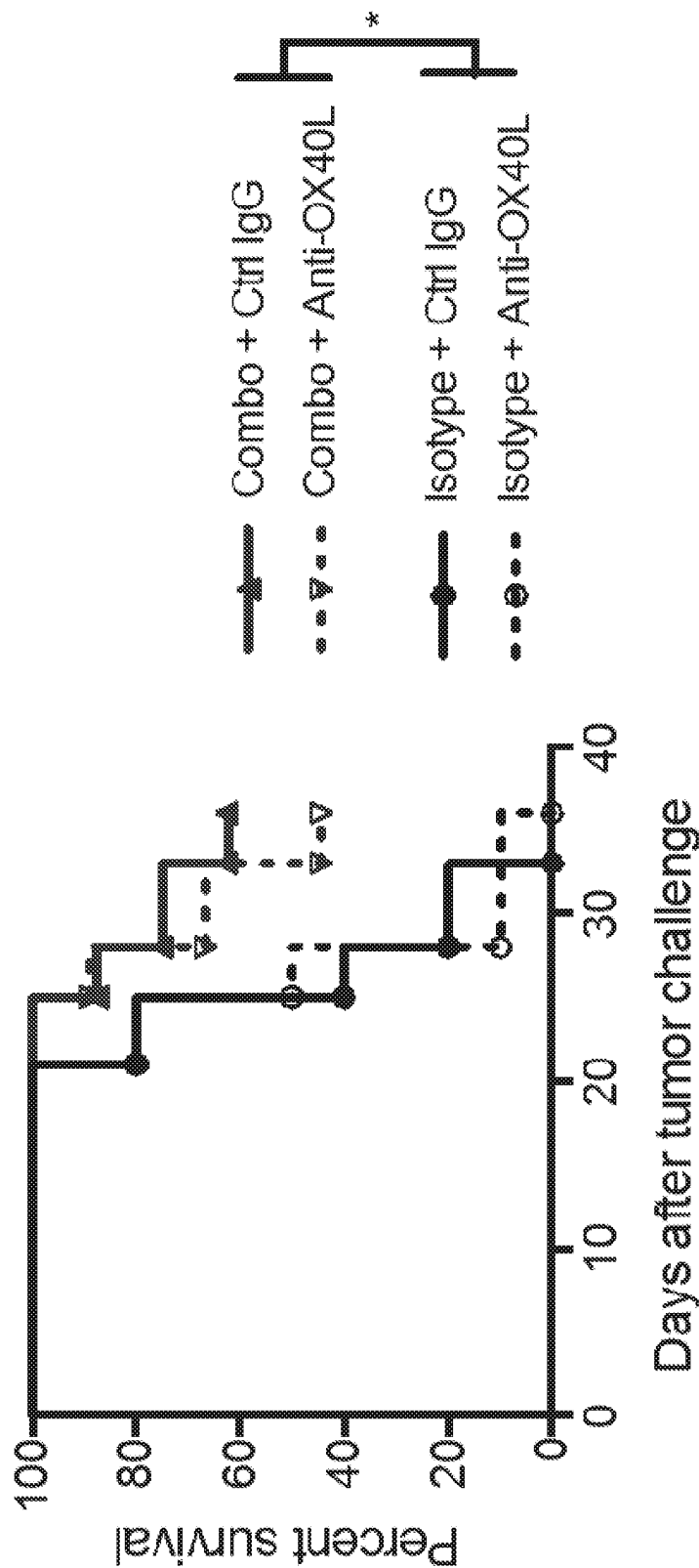


FIG. 12E

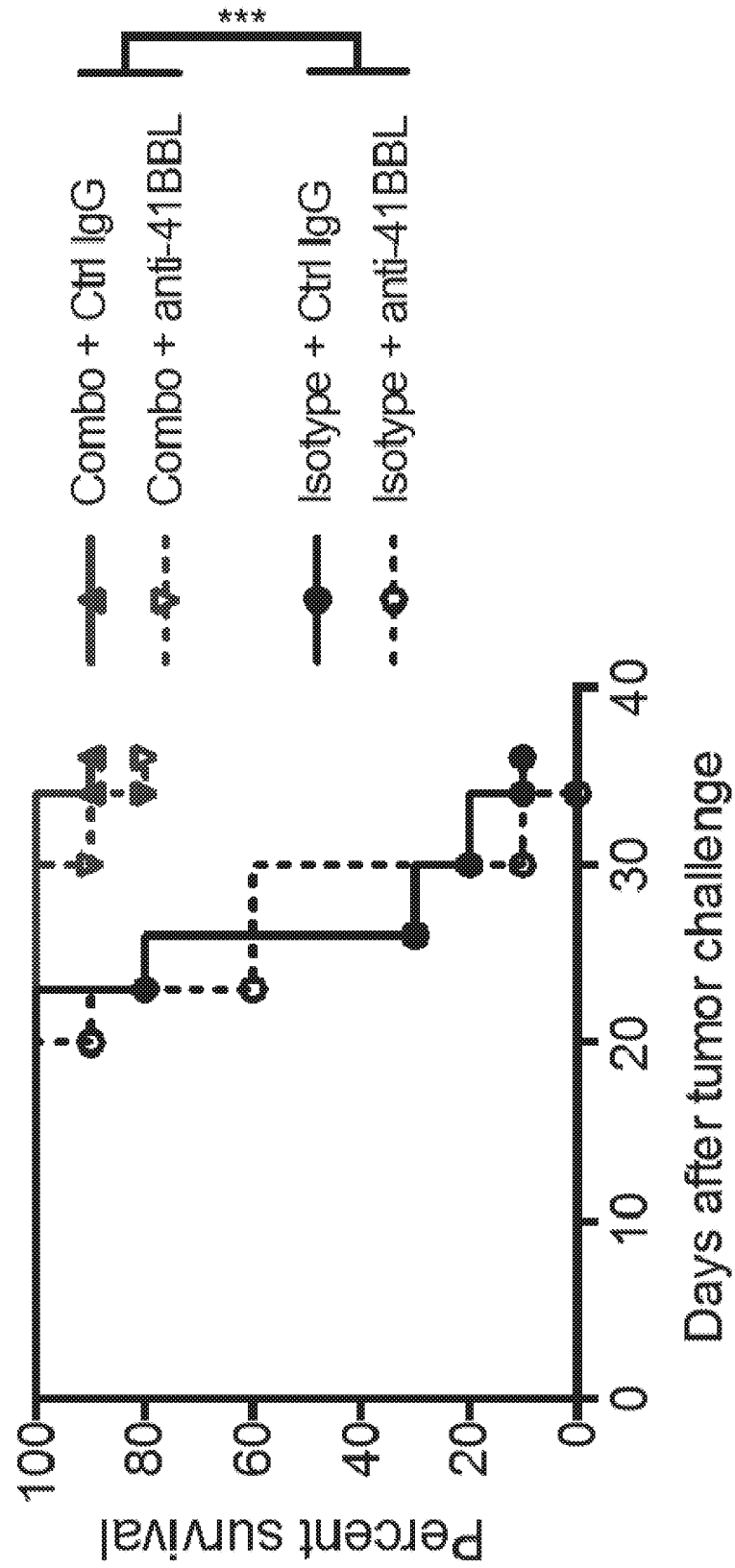


FIG. 12F

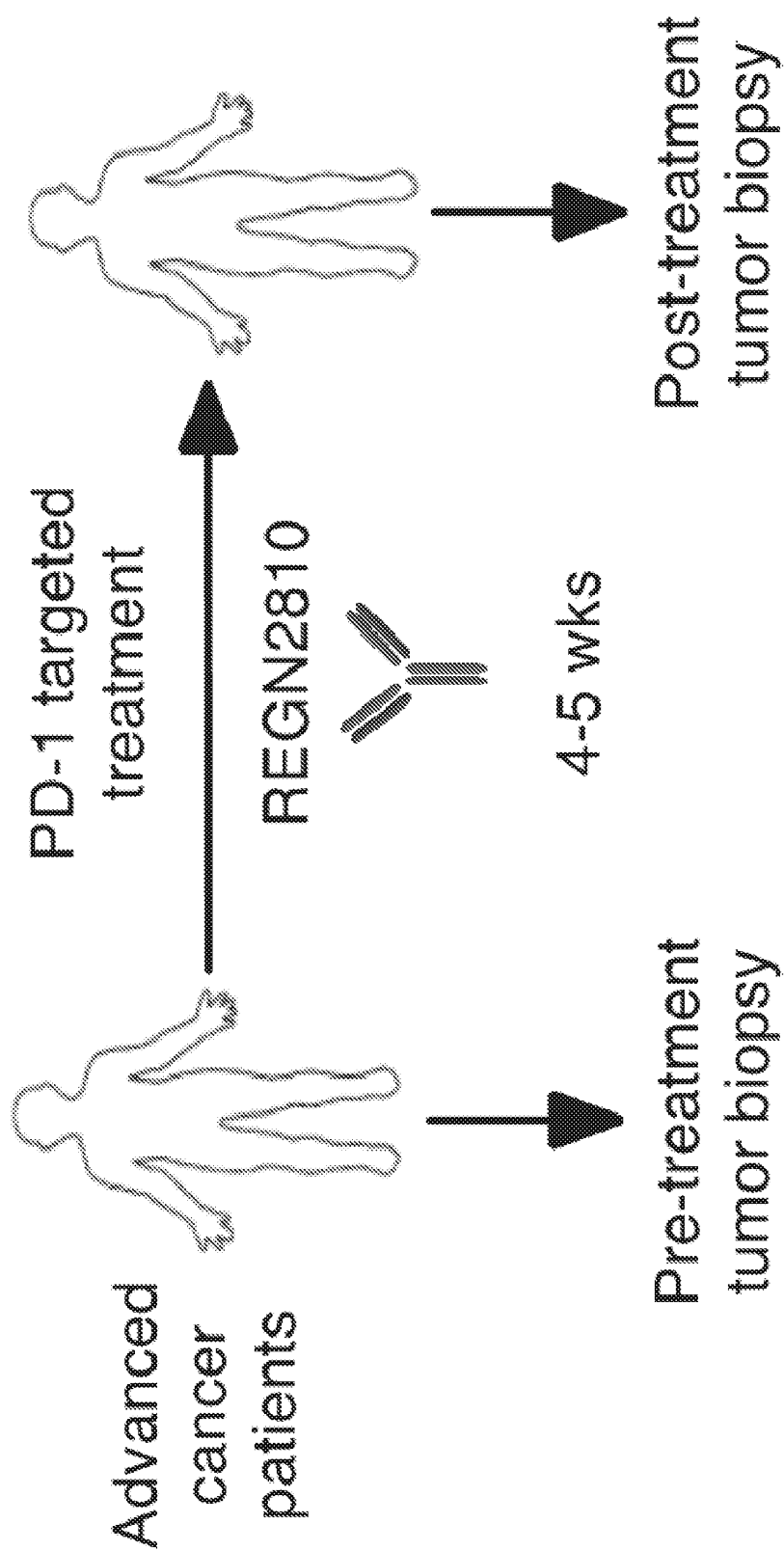


FIG. 12G

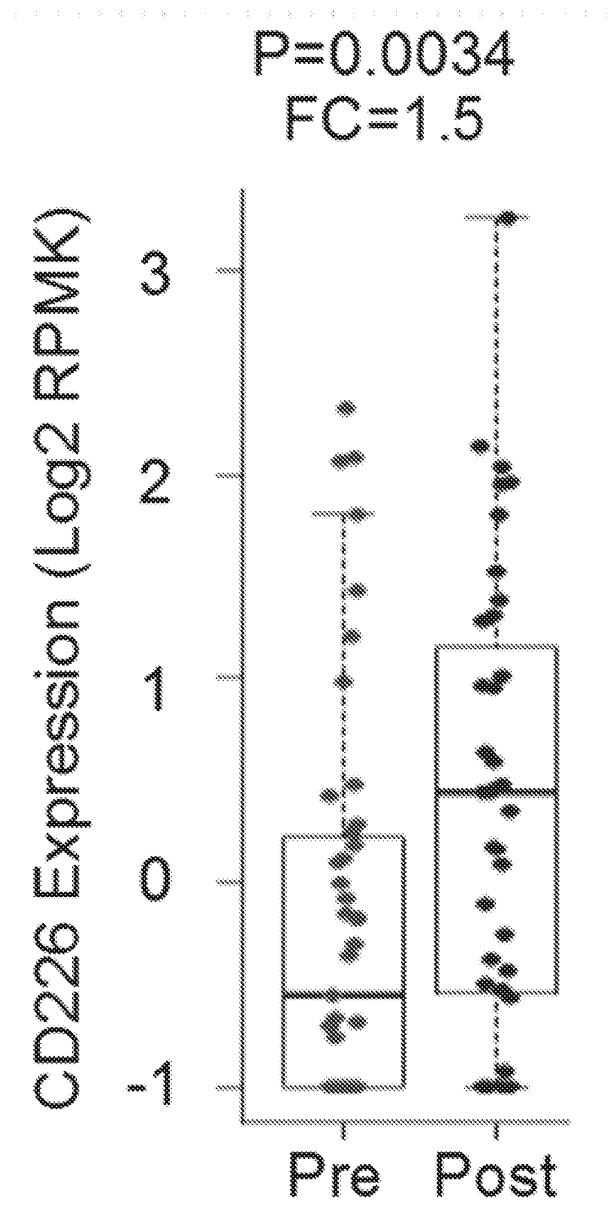


FIG. 12H

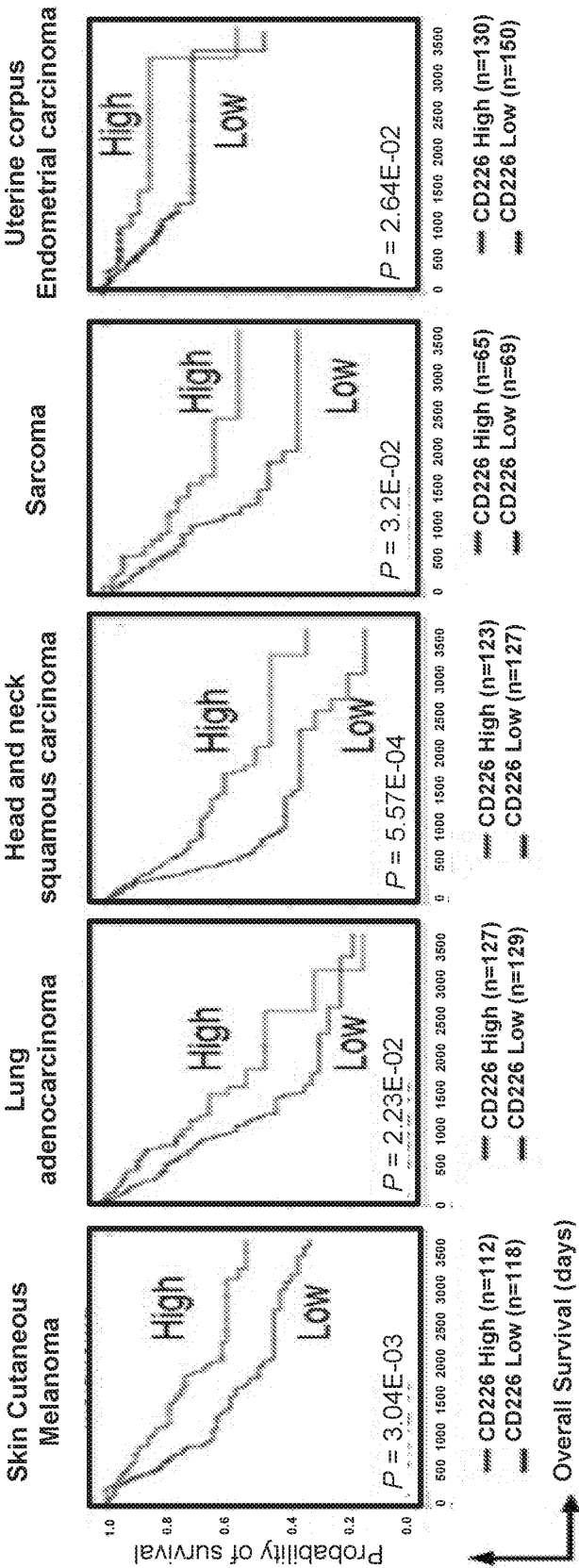


FIG. 13

Sample ID	Description	Species	Sample type	MitTCR	TCRklass	rpsTCR	Input reads (passed QC>=25)
Renca	kidney tumor cell line	mouse	negative control	23	0	0	44,906,248
B16F1	melanoma tumor cell line	mouse	negative control	76	0	0	39,305,839
Colon26	Colon tumor cell line	mouse	negative control	22	1	0	39,233,756
MC38	colon tumor cell line	mouse	negative control	99	1	0	48,661,267
T-ALL_neg1	Spleen from Rag1/2 KO mouse	mouse	negative control	17	1	0	39,068,155
T-ALL_neg2	Spleen from Rag1/2 KO mouse	mouse	negative control	51	0	0	39,469,692
NeuProgCell	Neural progenitor cell line	human	negative control	123	0	0	37,684,399
LHCN-M2	Skeletal myoblast cell line	human	negative control	77	0	0	36,639,557

FIG. 14

TCR type	Total	CDR3 detected by our pipeline	Detection rate of our pipeline	Detection rate reported by Han A. et al.
TRB-CDR3	1,379	1,186	86.0%	92%
TRA-CDR3	1,379	1,078	78.2%	87%
TRA&B-CDR3	1,379	1,009	73.1%	82%

FIG. 15

Treatment	Pathway	p Value
Anti-PD1 + Anti-GITR	Adaptive immune response	1.50E-08
	Cell cycle	5.80E-07
	Metabolism of lipids and lipoproteins	3.00E-04
Anti-PD1	Lymphocyte activation	2.30E-05
	Gene targets for miR-124u (T cell activation)	1.80E-05
	Jak-STAT signaling pathway	3.00E-04
Anti-GITR	Glucose metabolism	8.20E-10
	Protein metabolism	7.50E-08
	The citric acid cycle and respiratory electron transport	3.90E-06

FIG. 16A

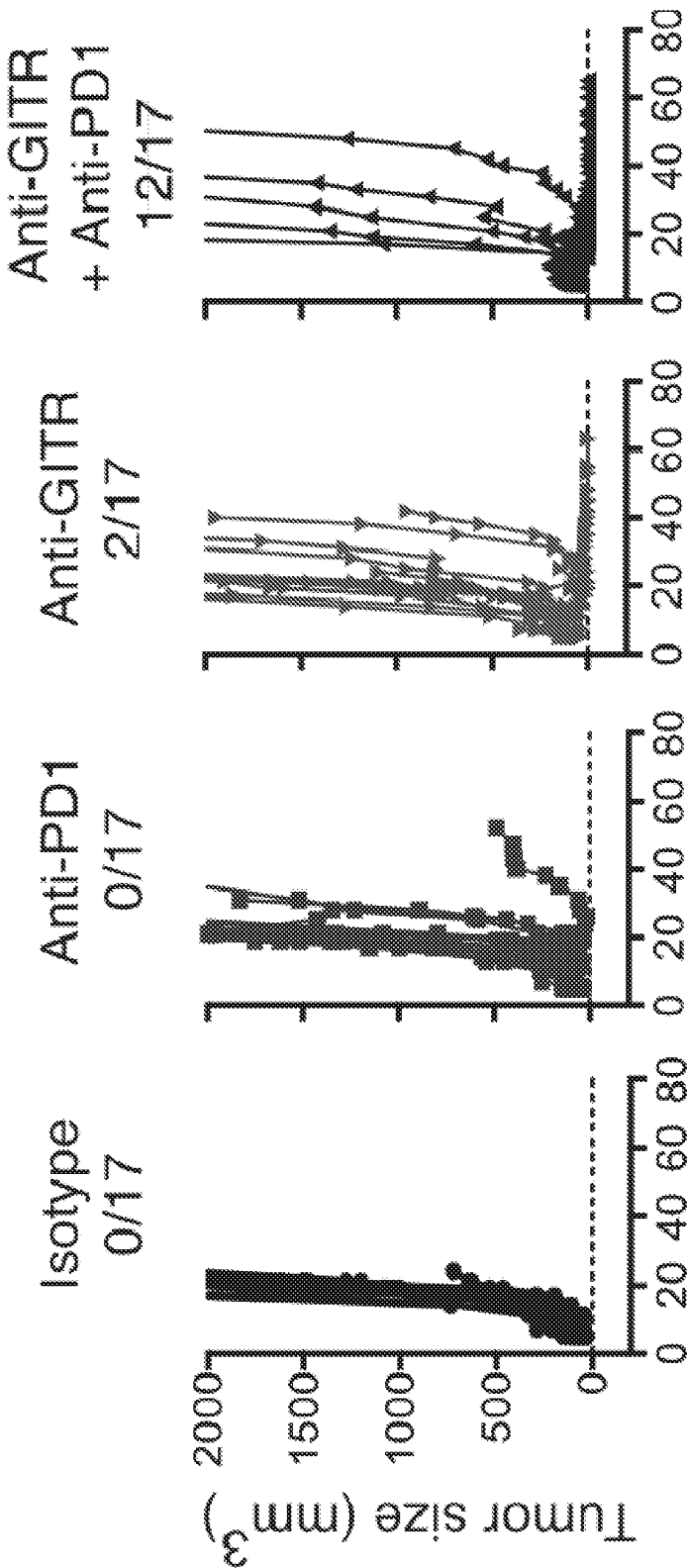
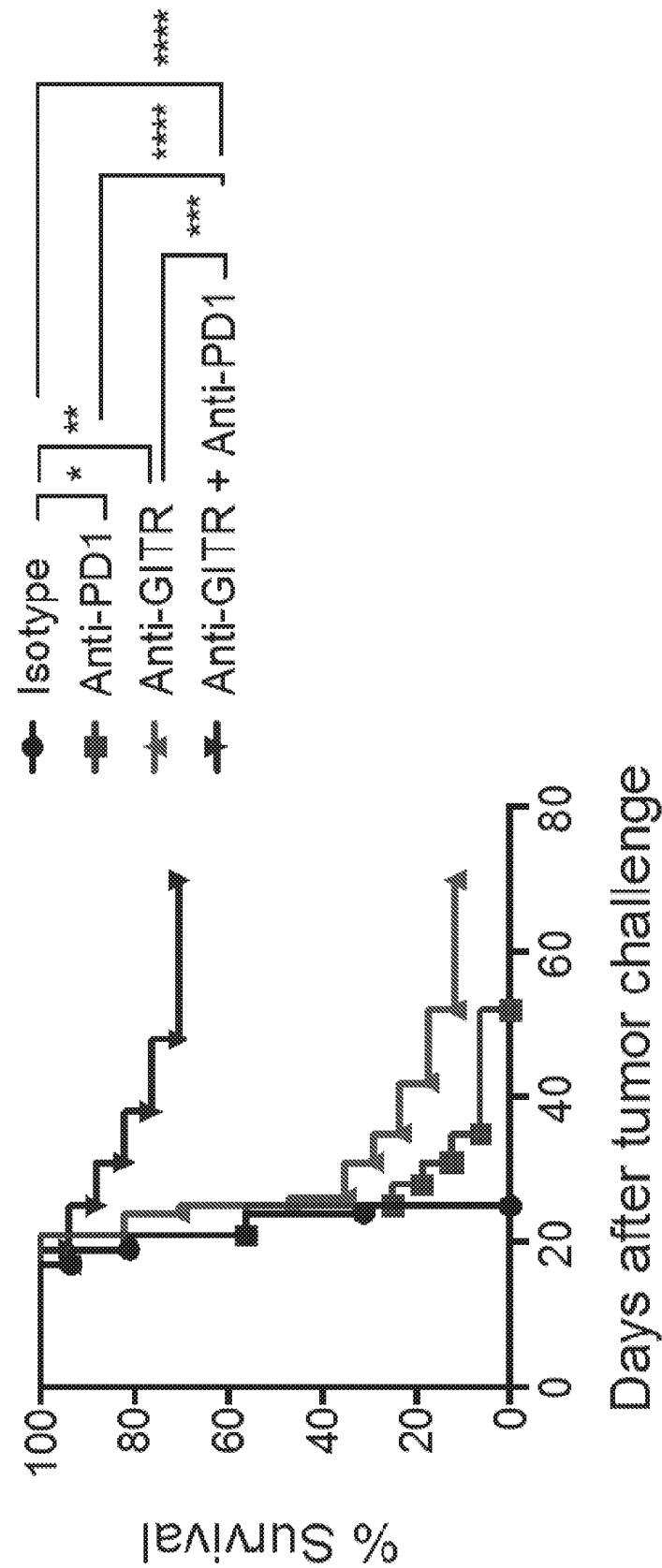


FIG. 16B



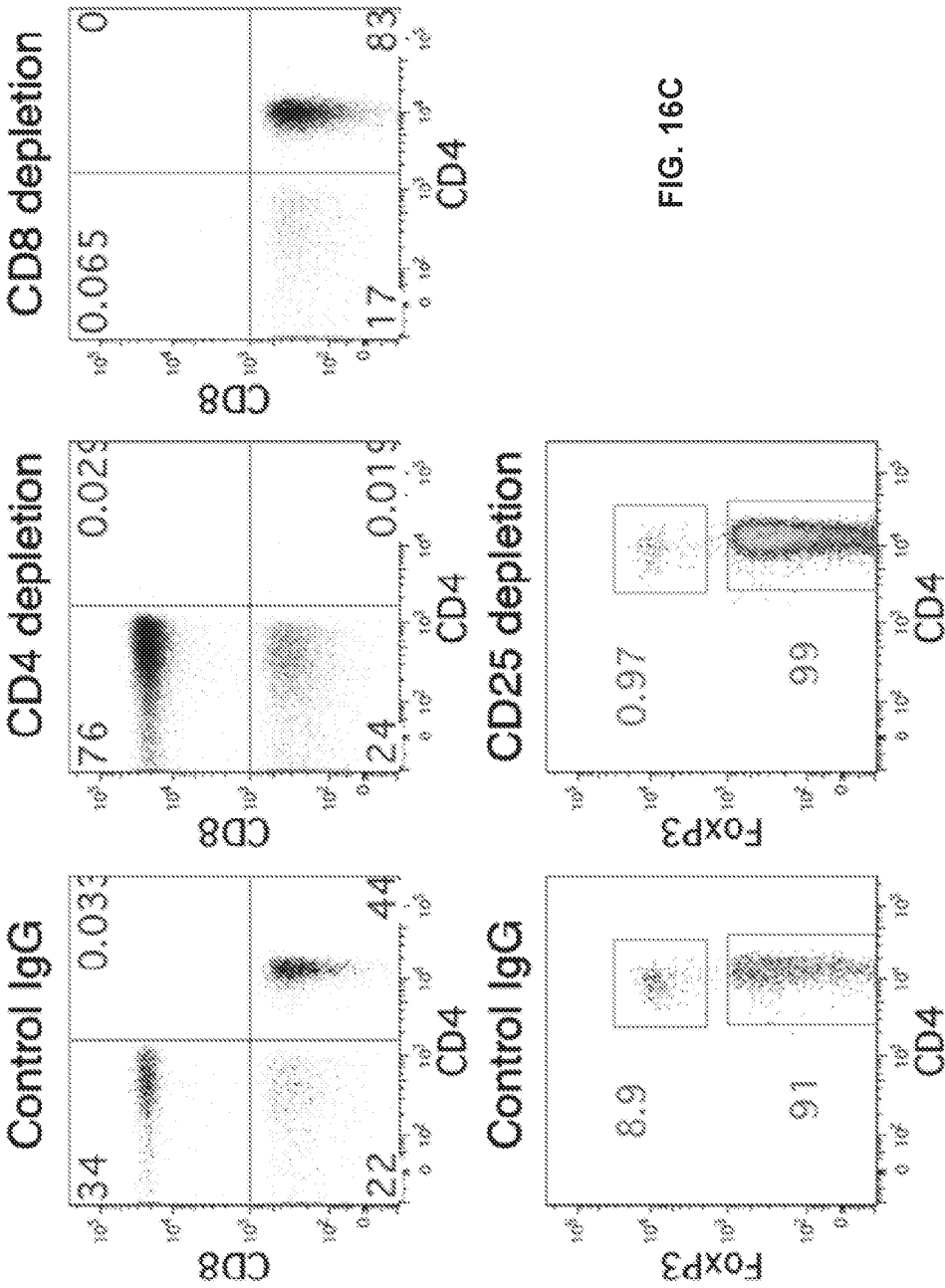


FIG. 16C

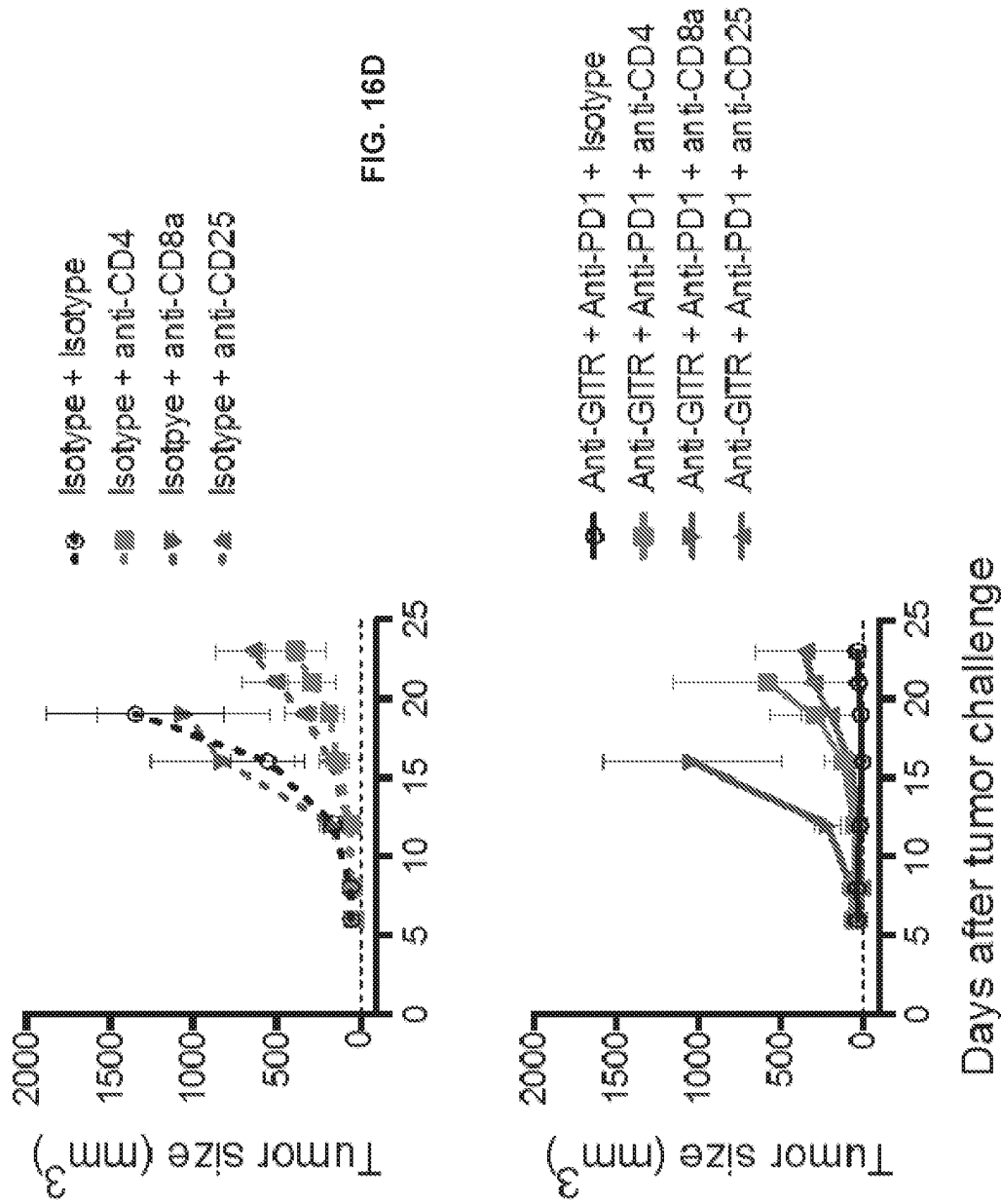


FIG. 16E

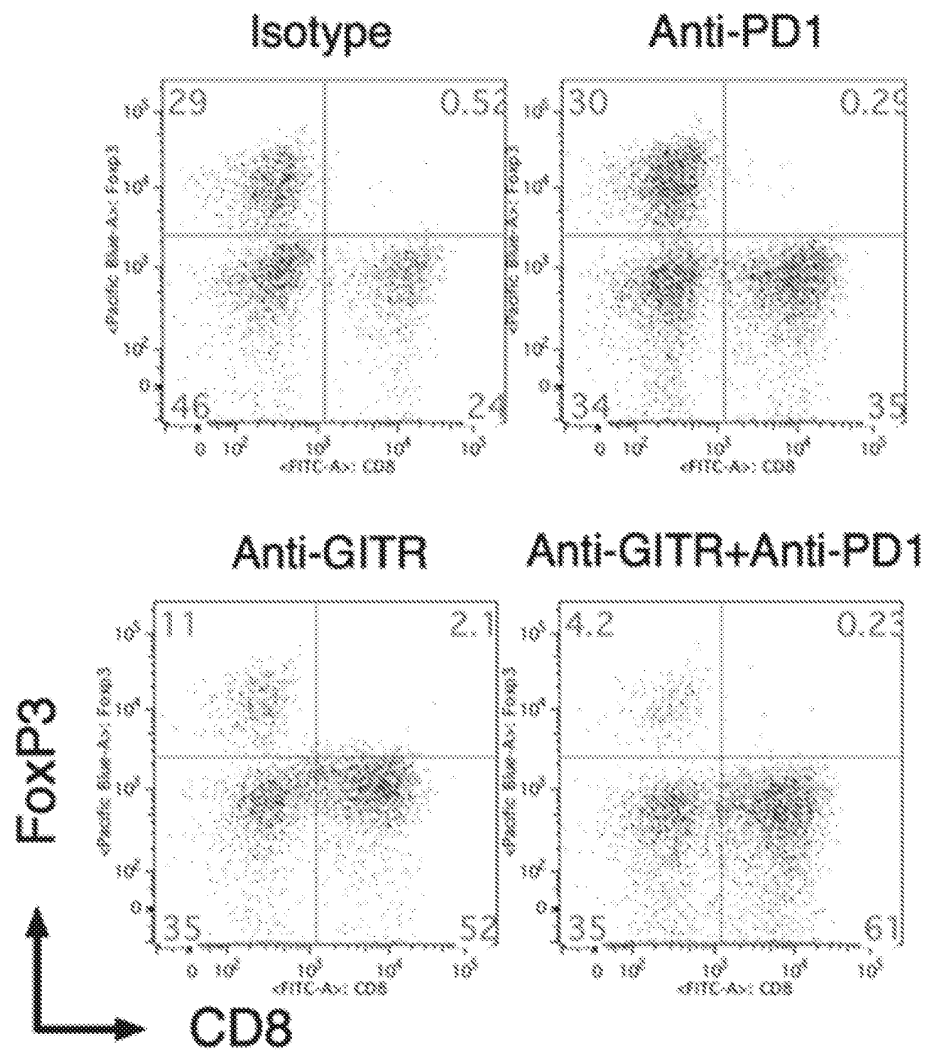
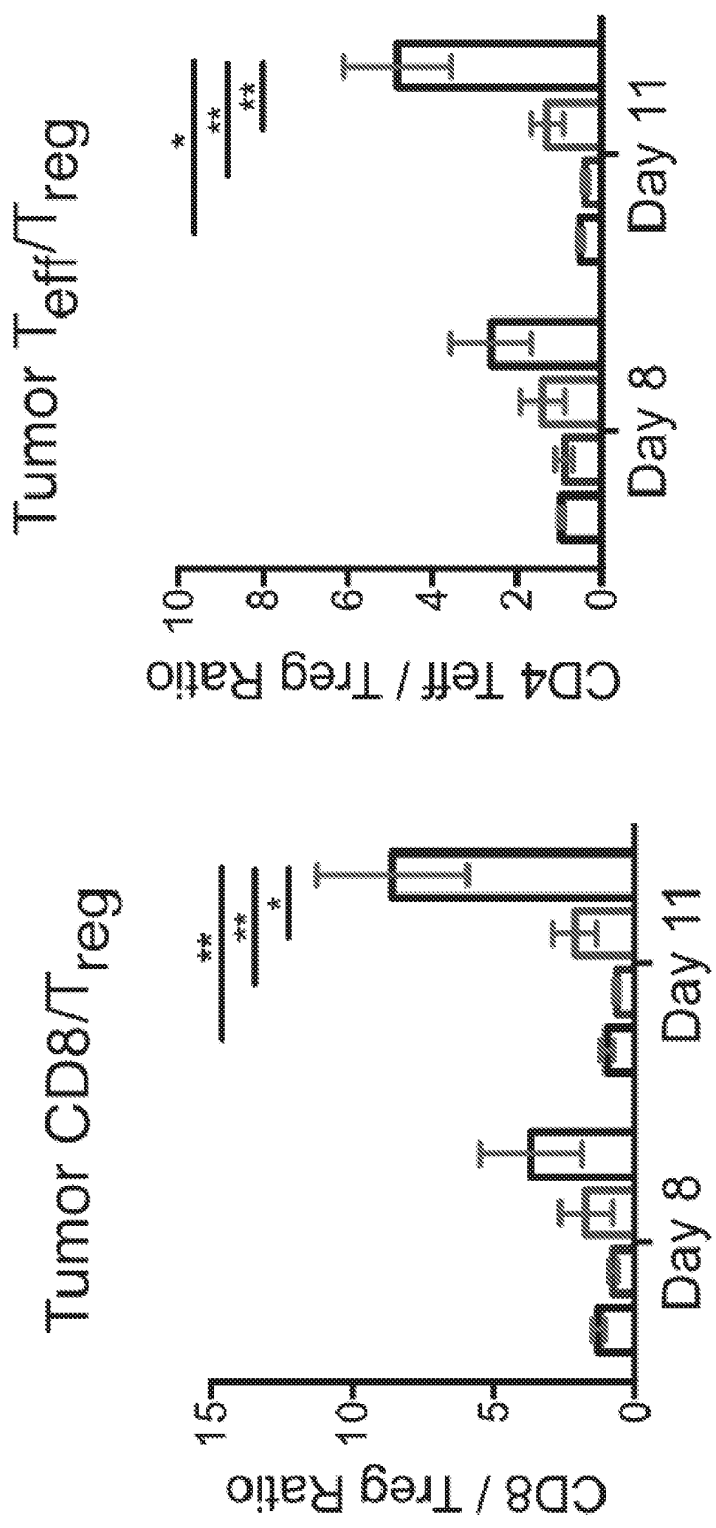


FIG. 16F



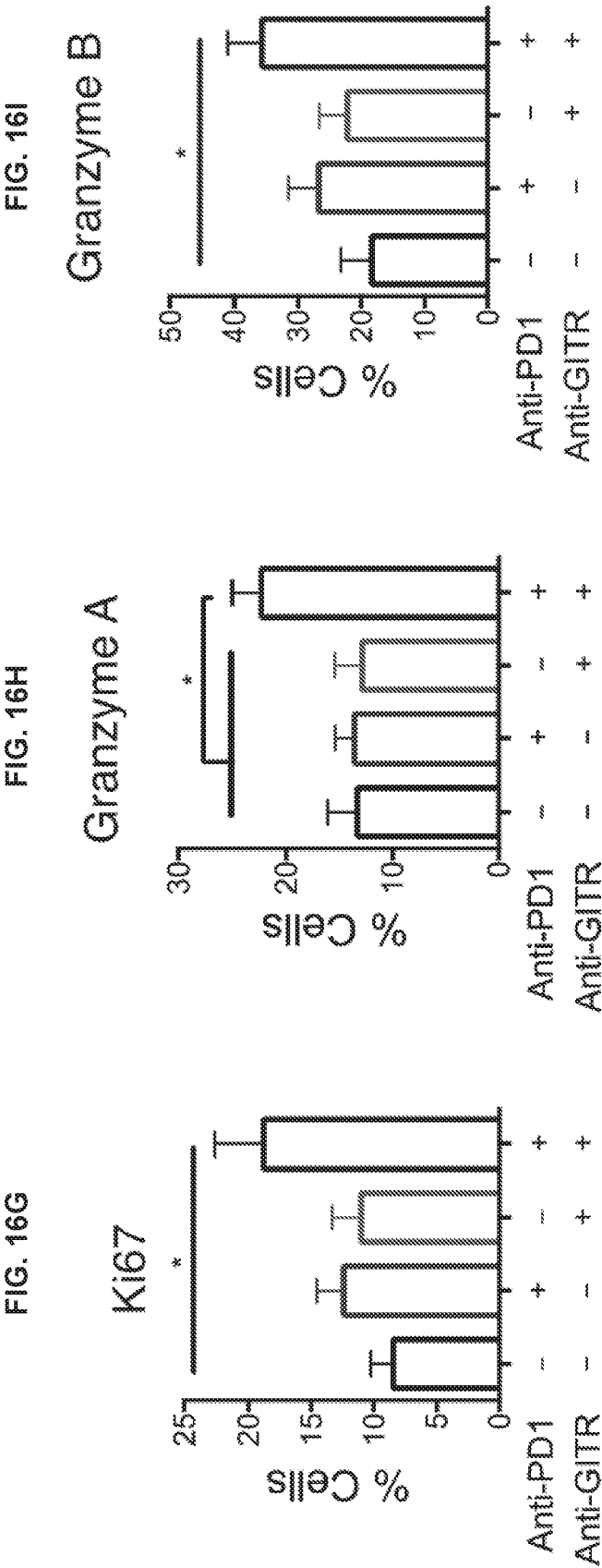


FIG. 16J

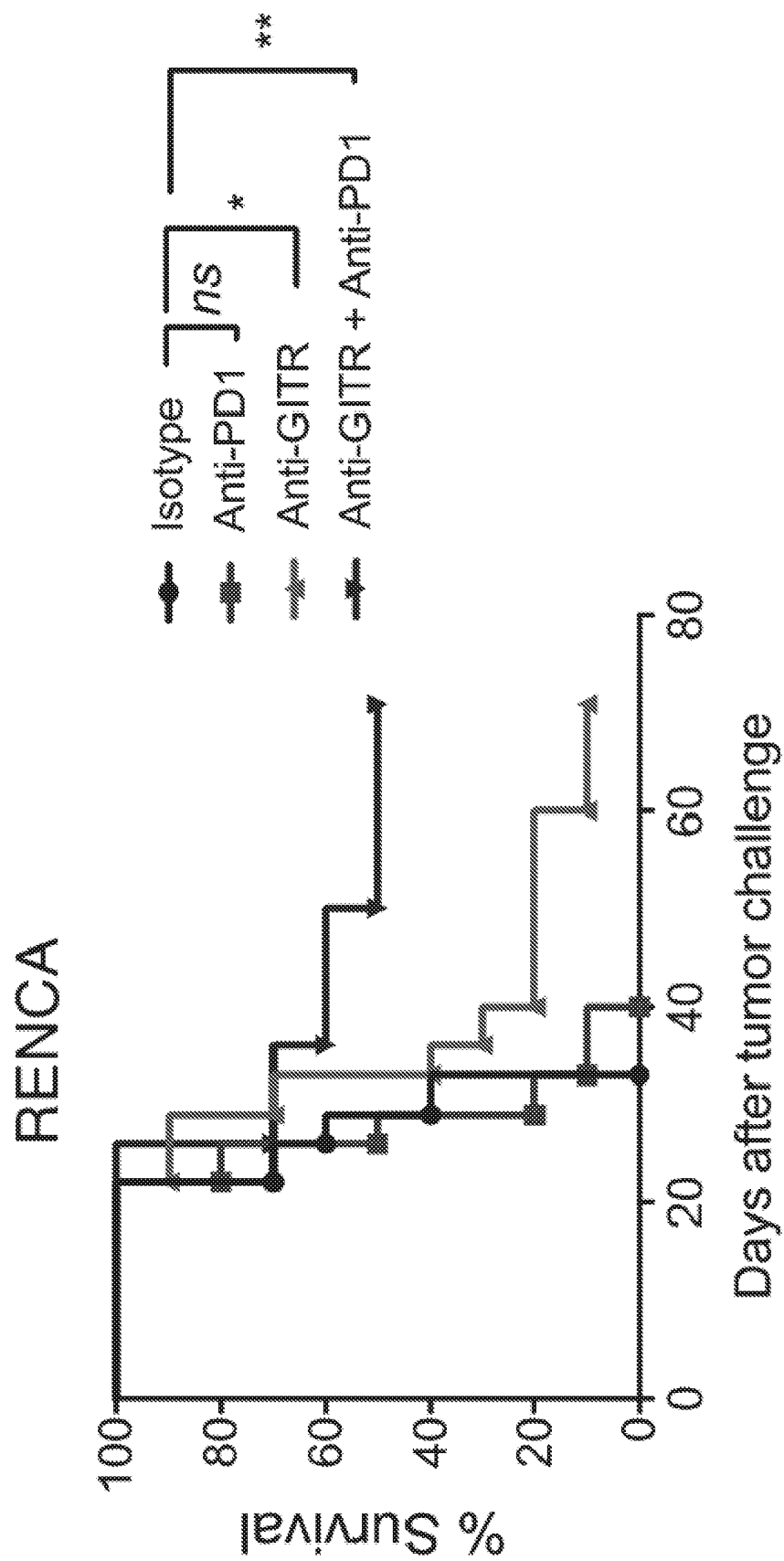
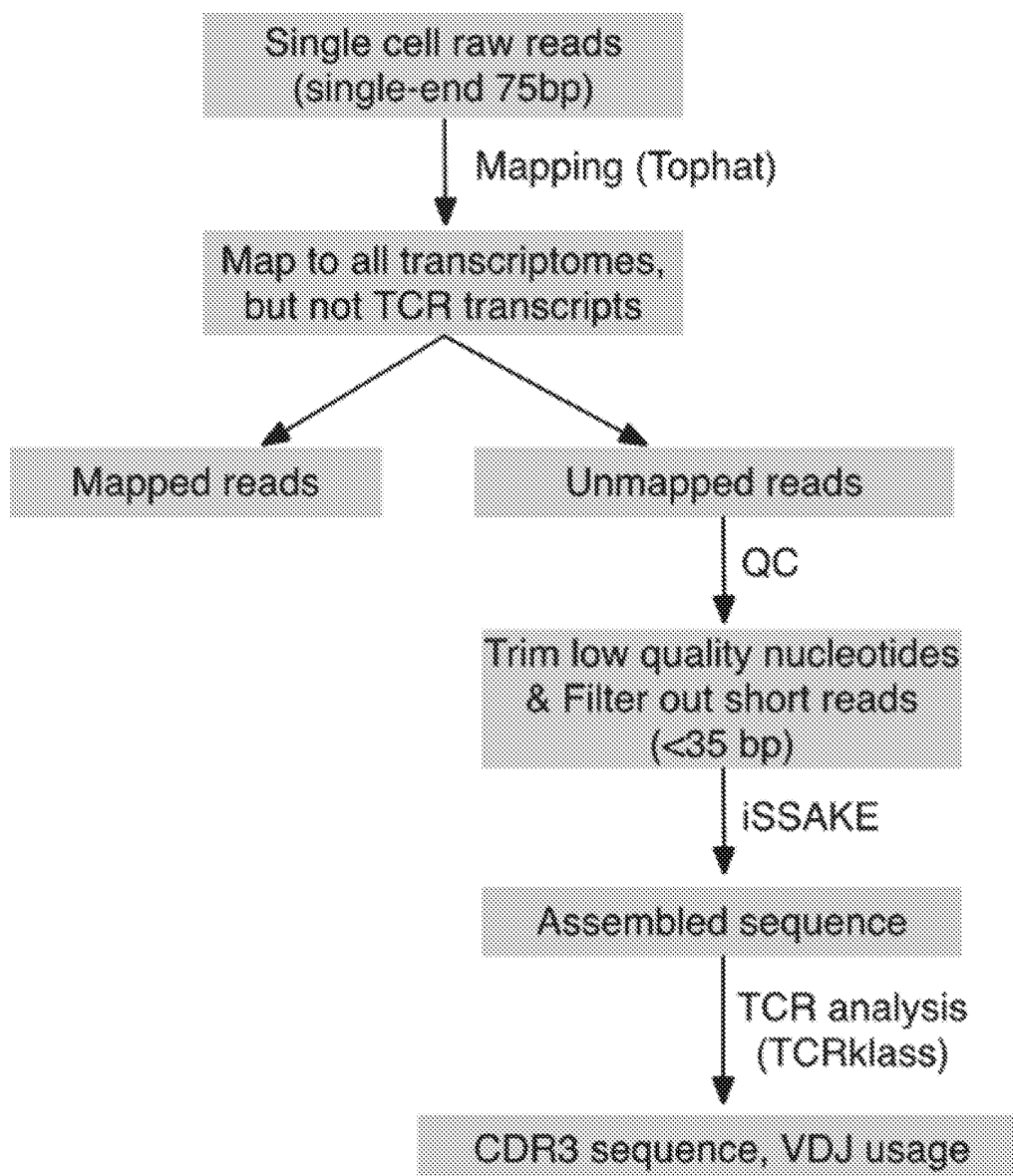


FIG. 17



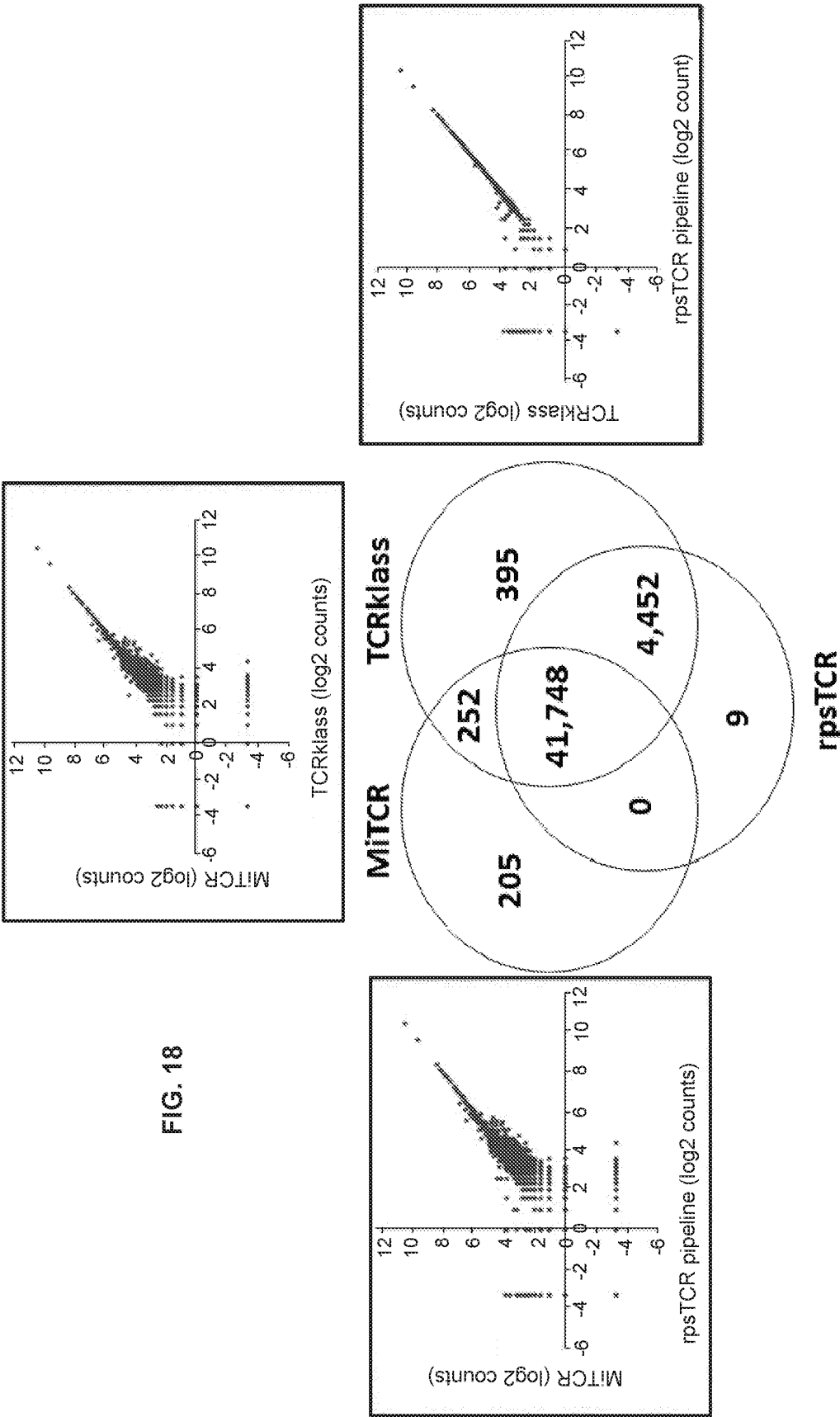
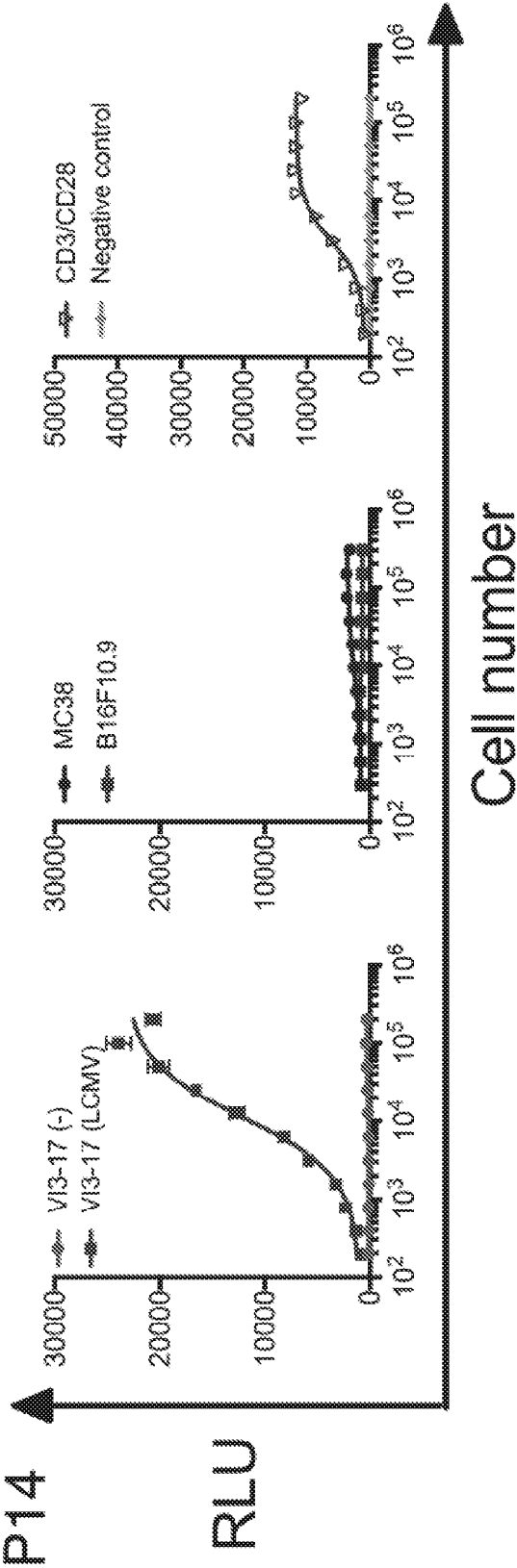


FIG. 19



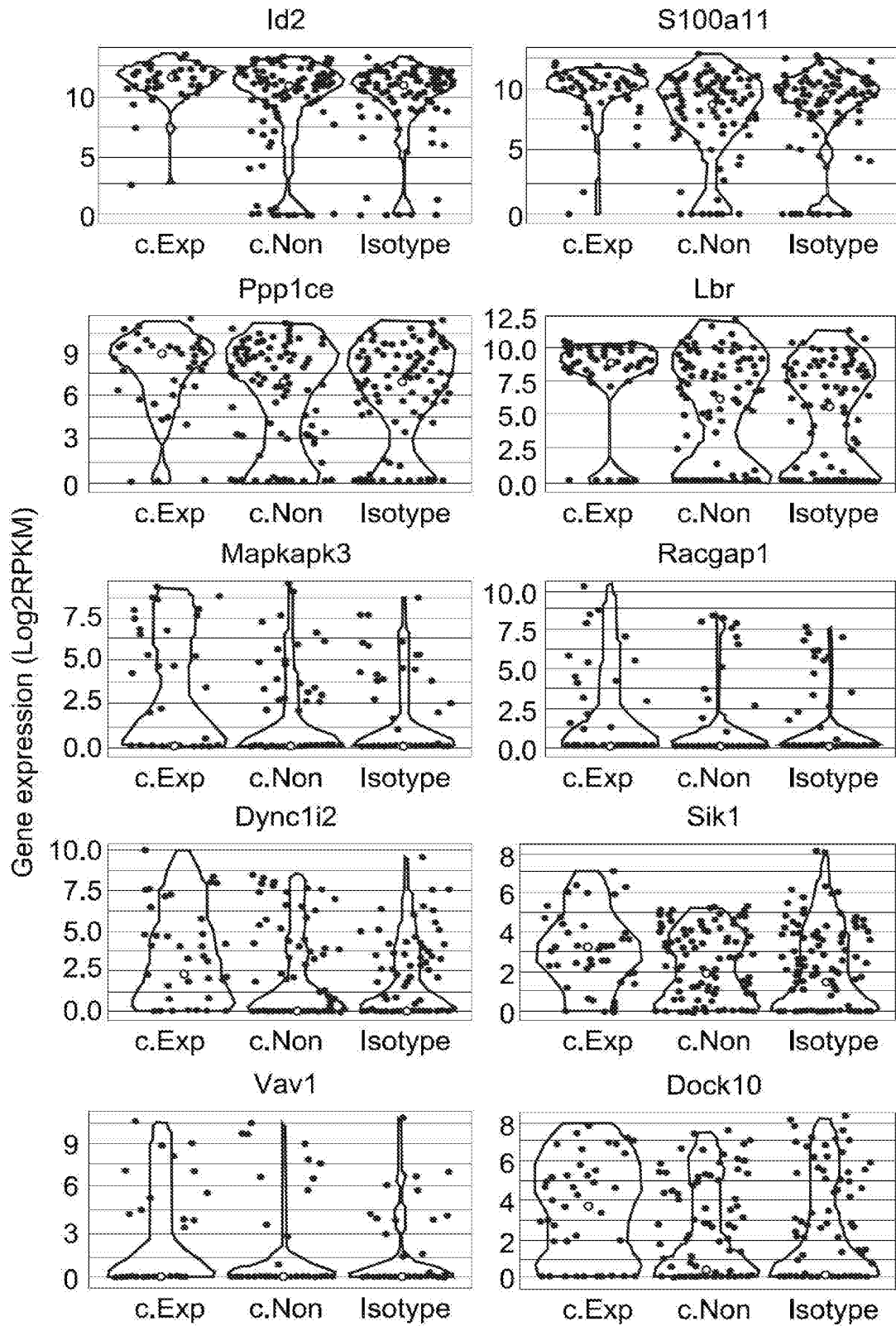


FIG. 20

SUBSTITUTE SHEET (RULE 26)

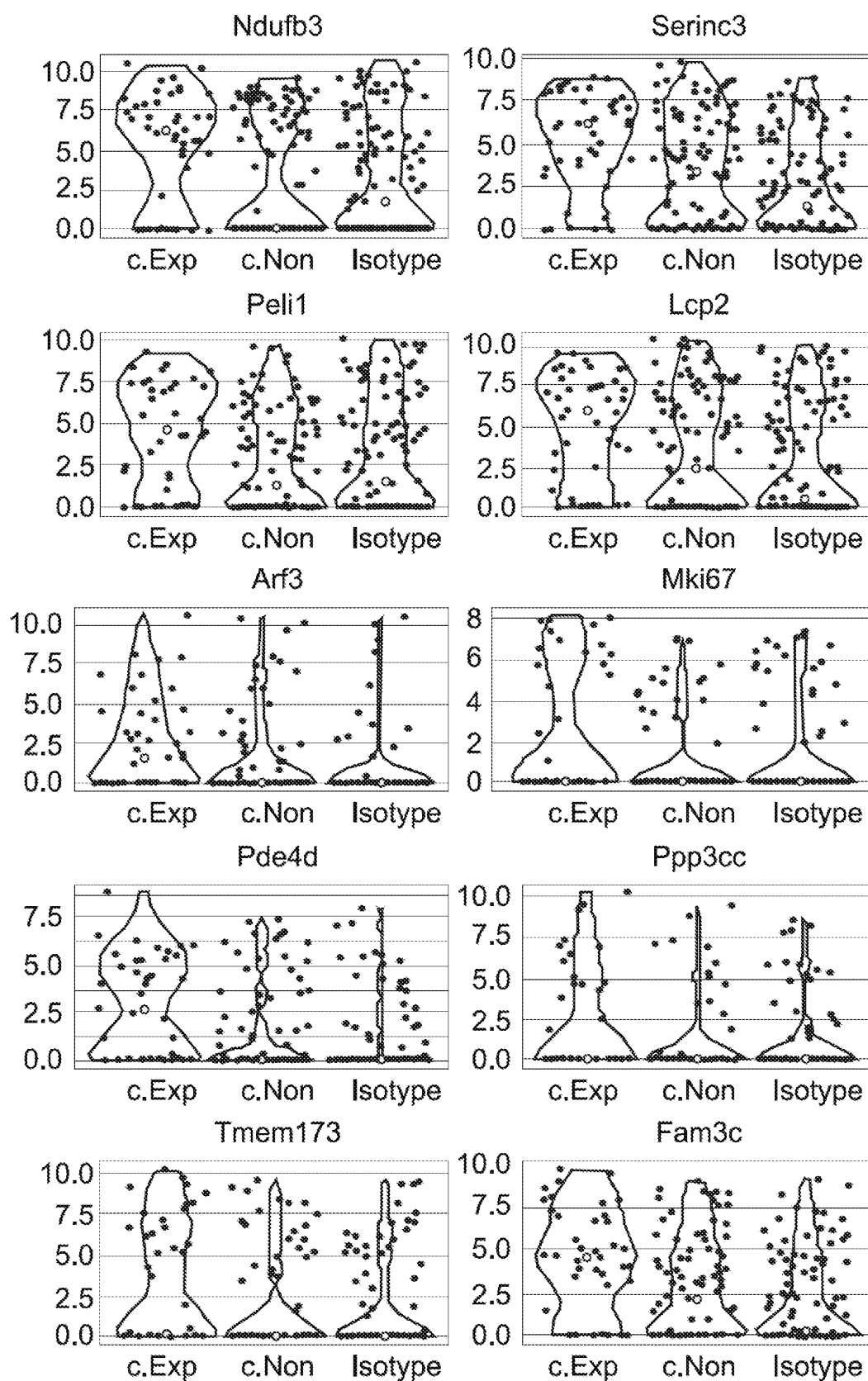


FIG. 20 Cont'd

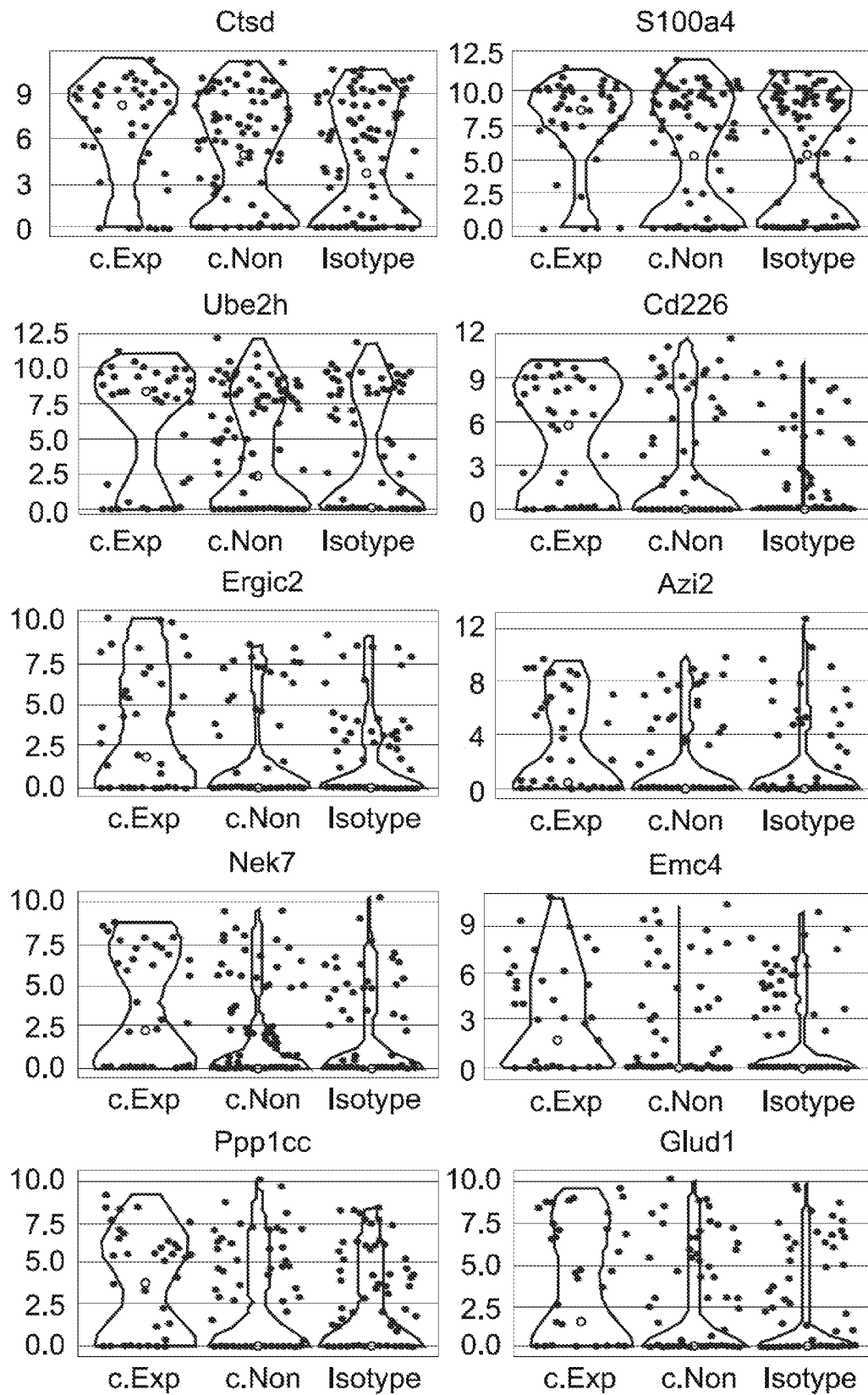
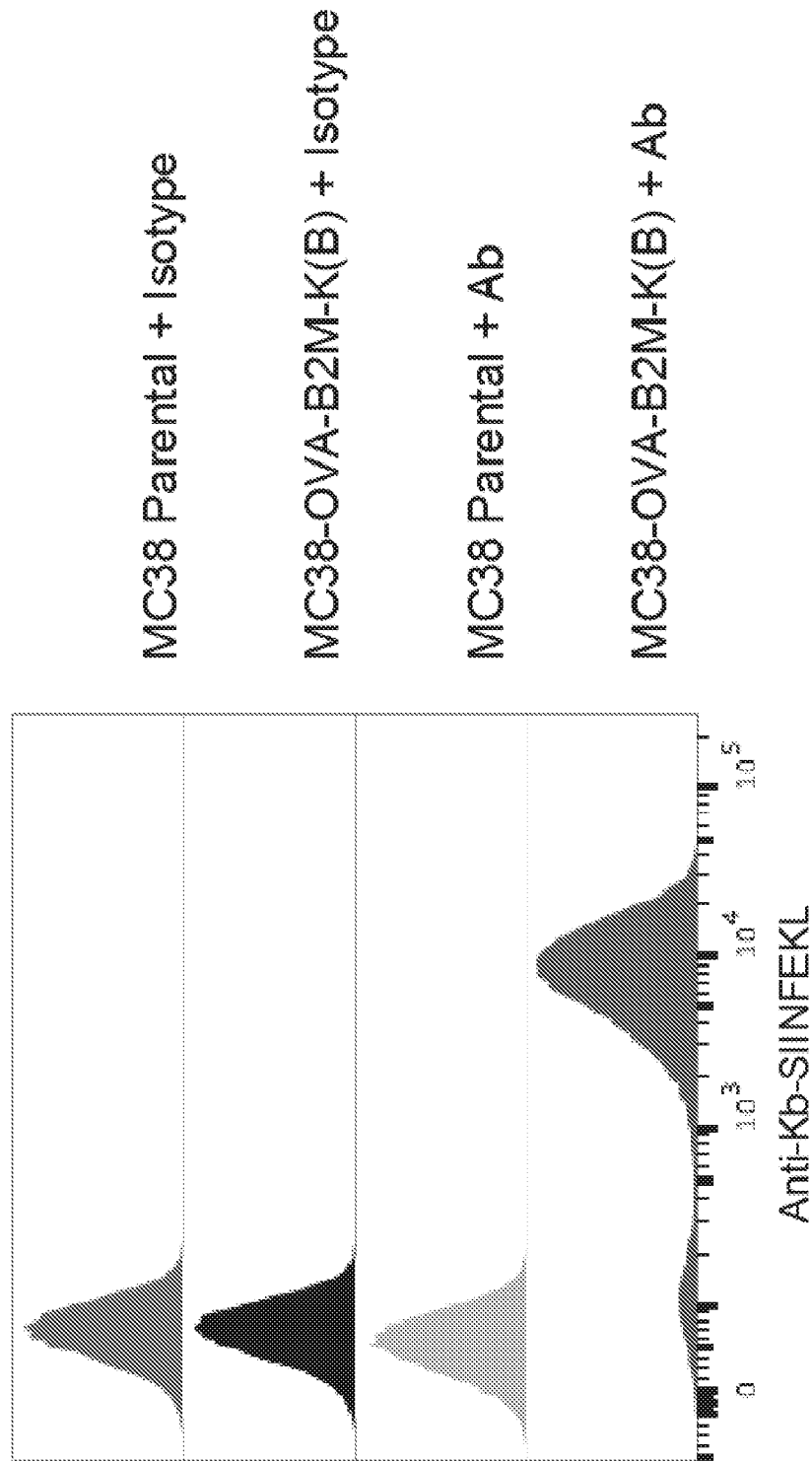


FIG. 20 Cont'd

SUBSTITUTE SHEET (RULE 26)

FIG. 21A



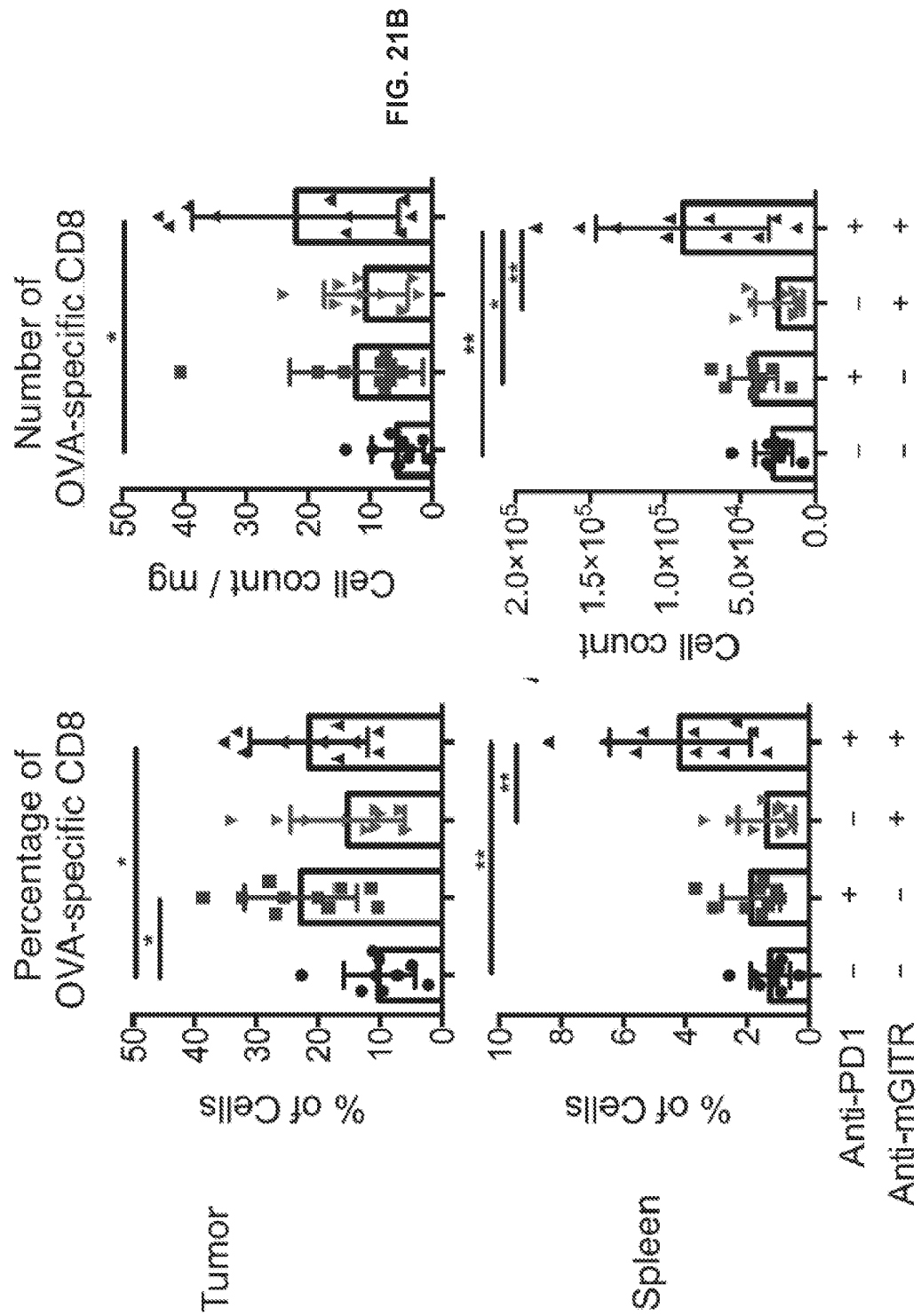


FIG. 21C

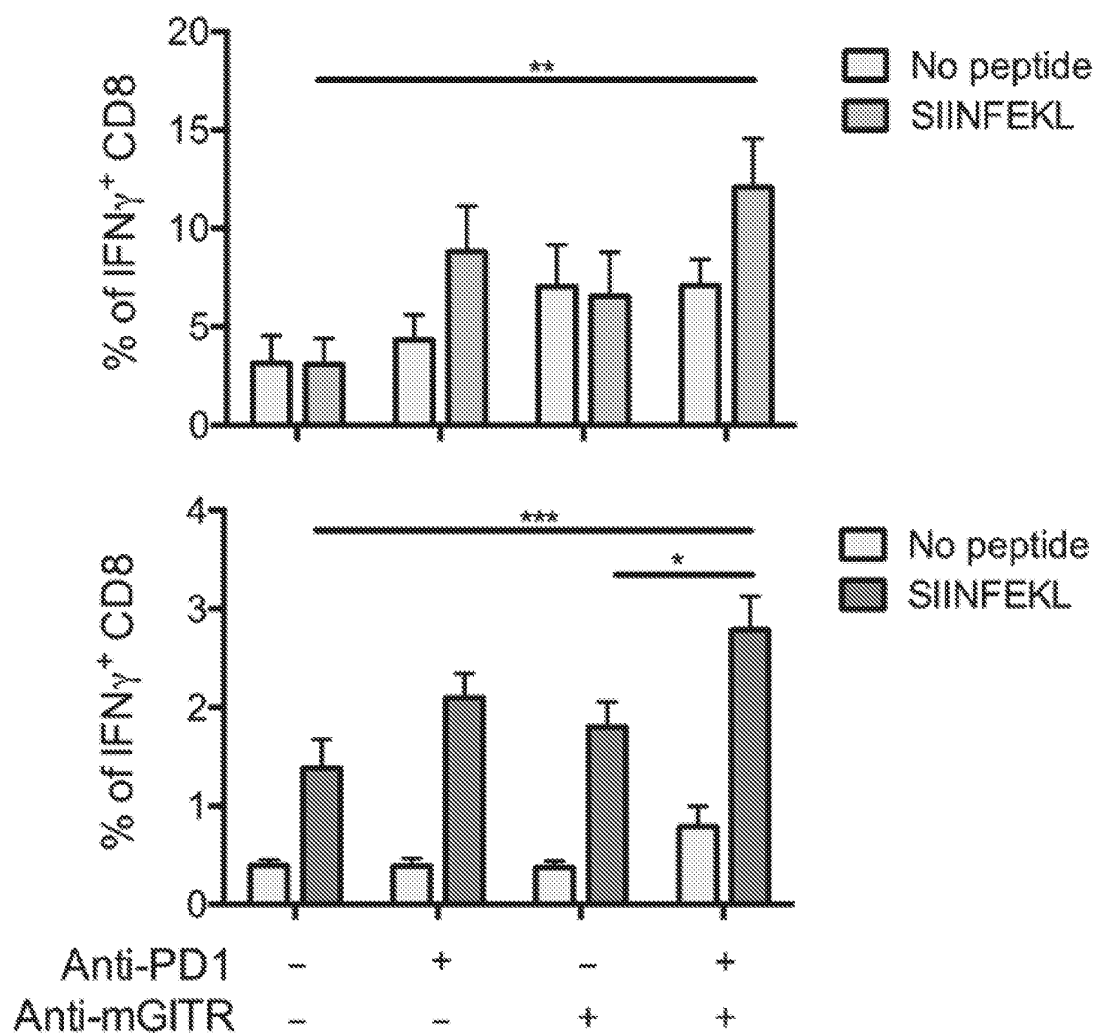


FIG. 22A

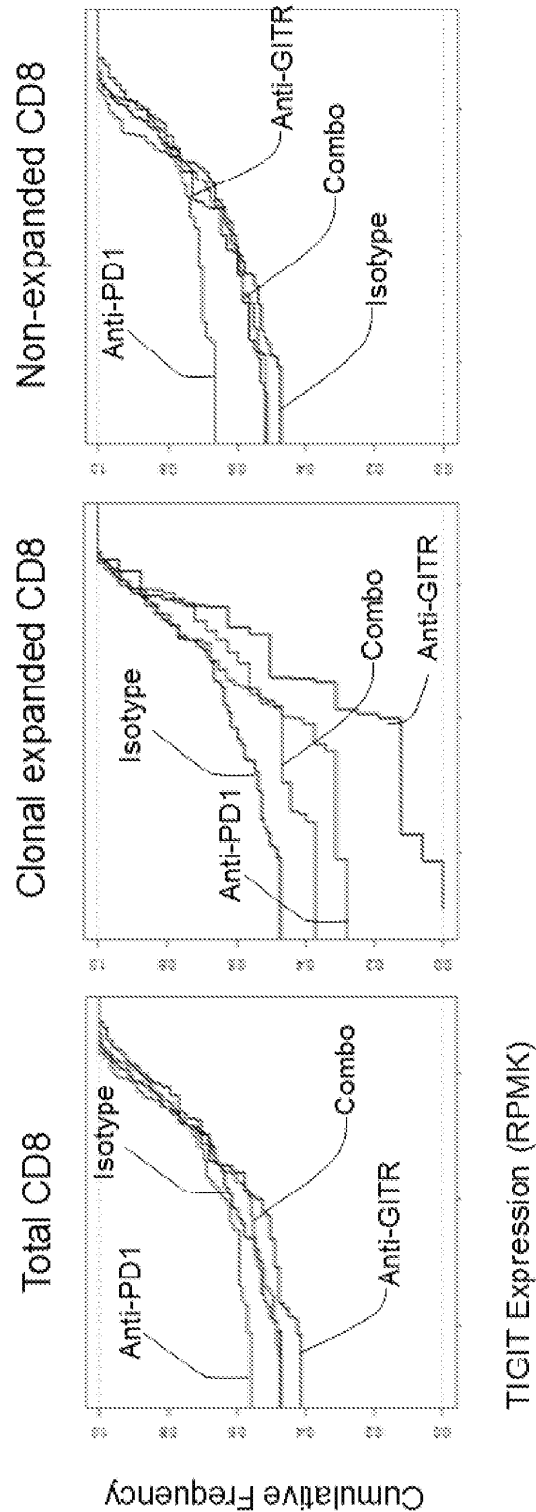


FIG. 22B

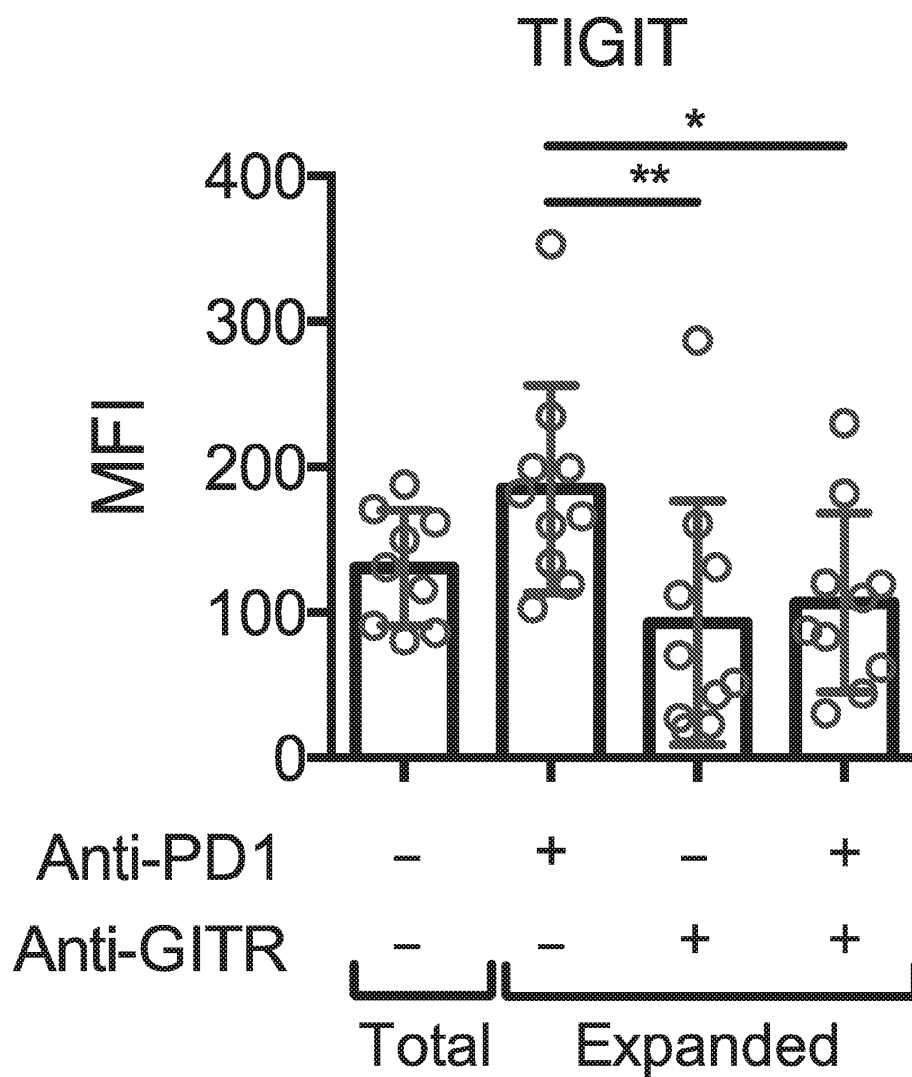


FIG. 22C

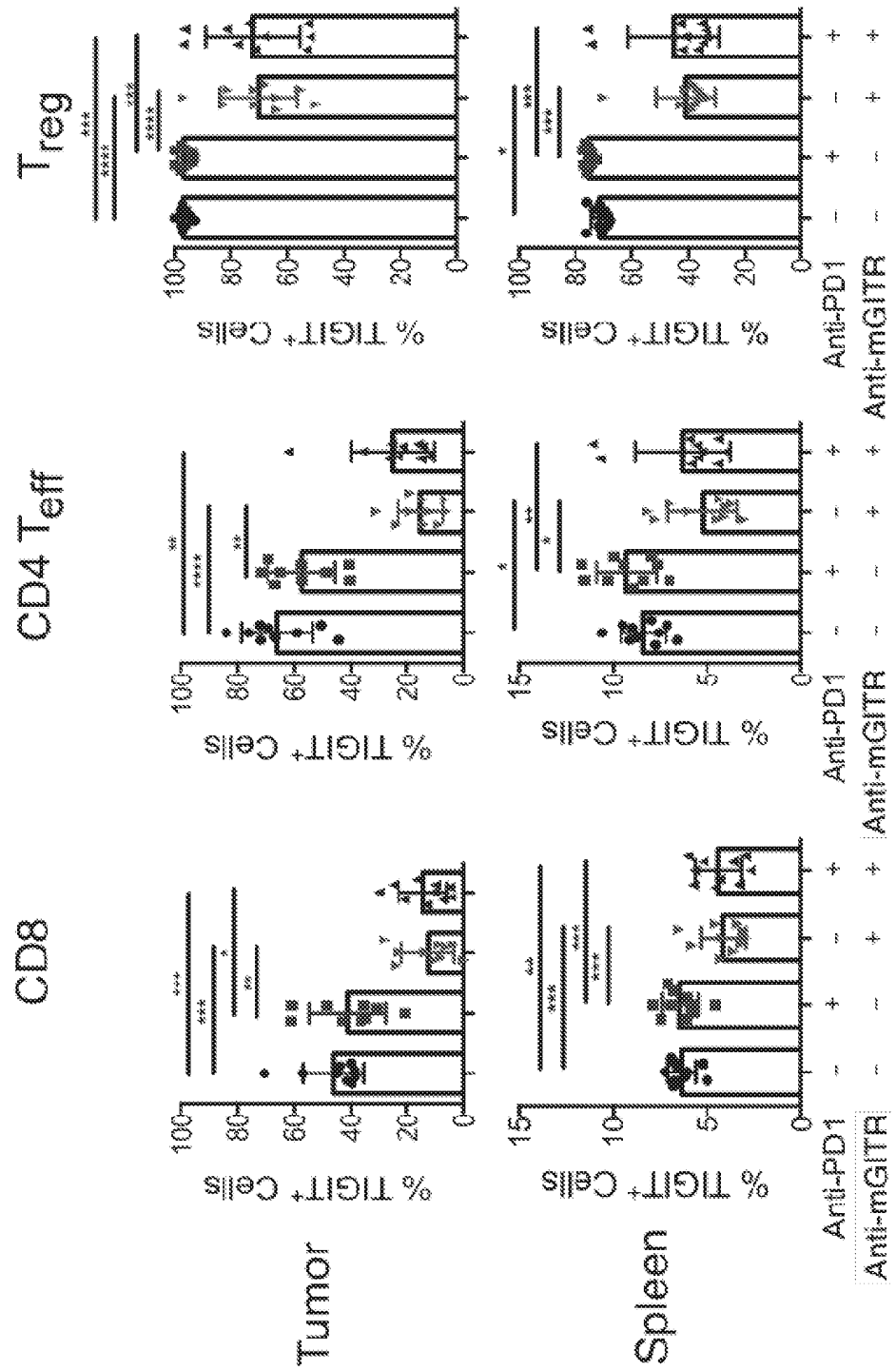
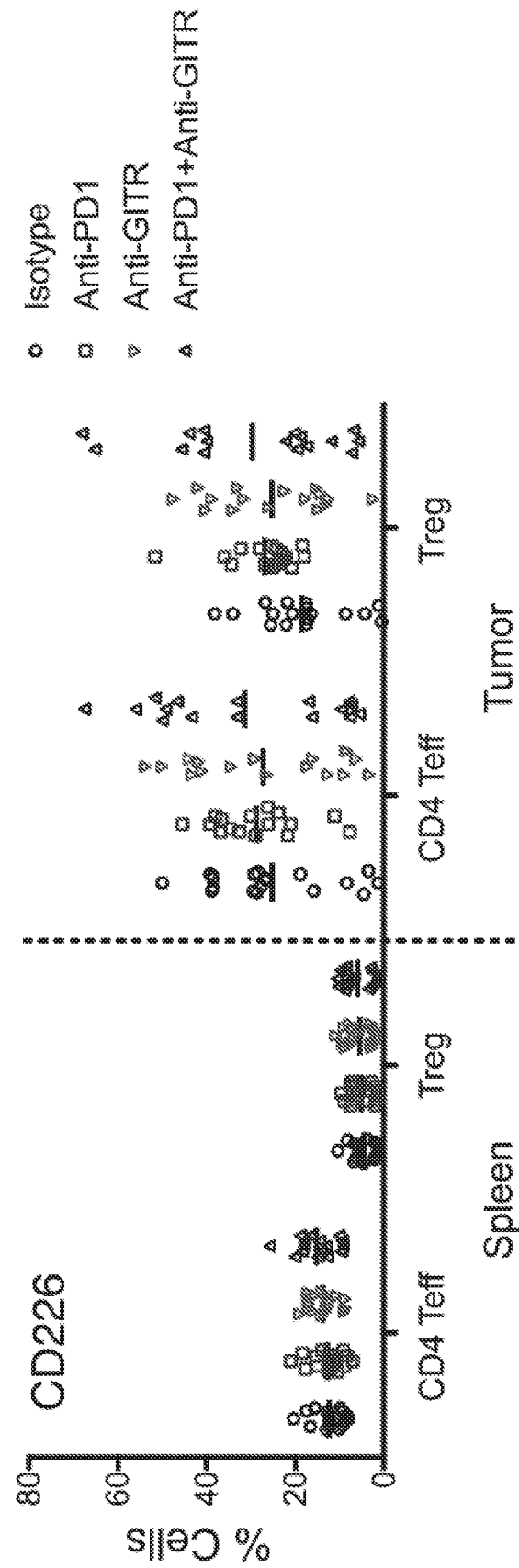


FIG. 22D



The diagram illustrates the pTZ19 vector, a circular plasmid with a total size of 72K. The map is marked with positions from 4K to 72K. Key features include an ATG start codon at 8K, a Deletion (754 bp) region from 32K to 60K, and a STOP codon at 72K. An inset shows the deletion region with a cassette containing an ATG start codon and a STOP codon.

Cd226 knockout, contains eGFP-Neo self-deleting cassette

Cd226 knockout, cassette deleted, eGFP and LoxP site remain

FIG. 23B

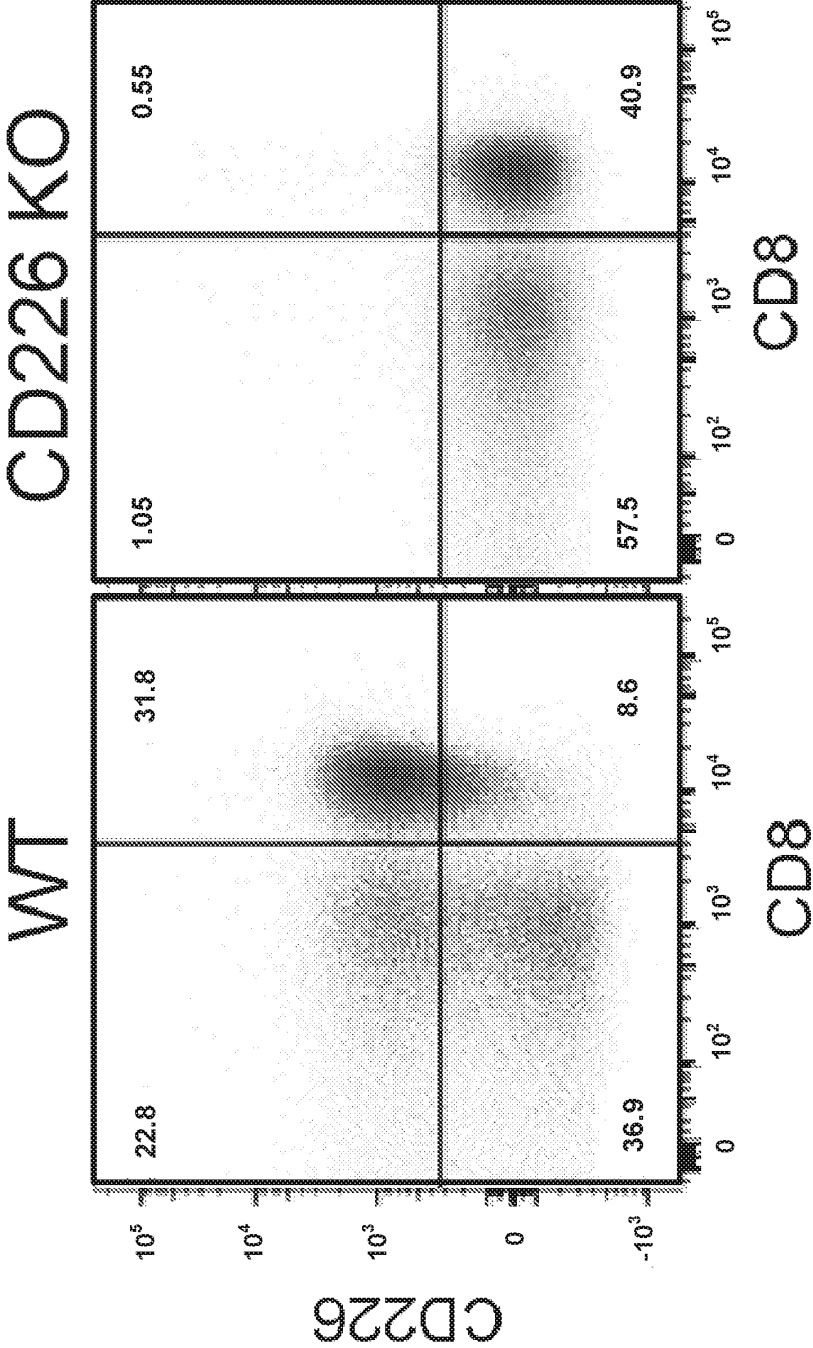
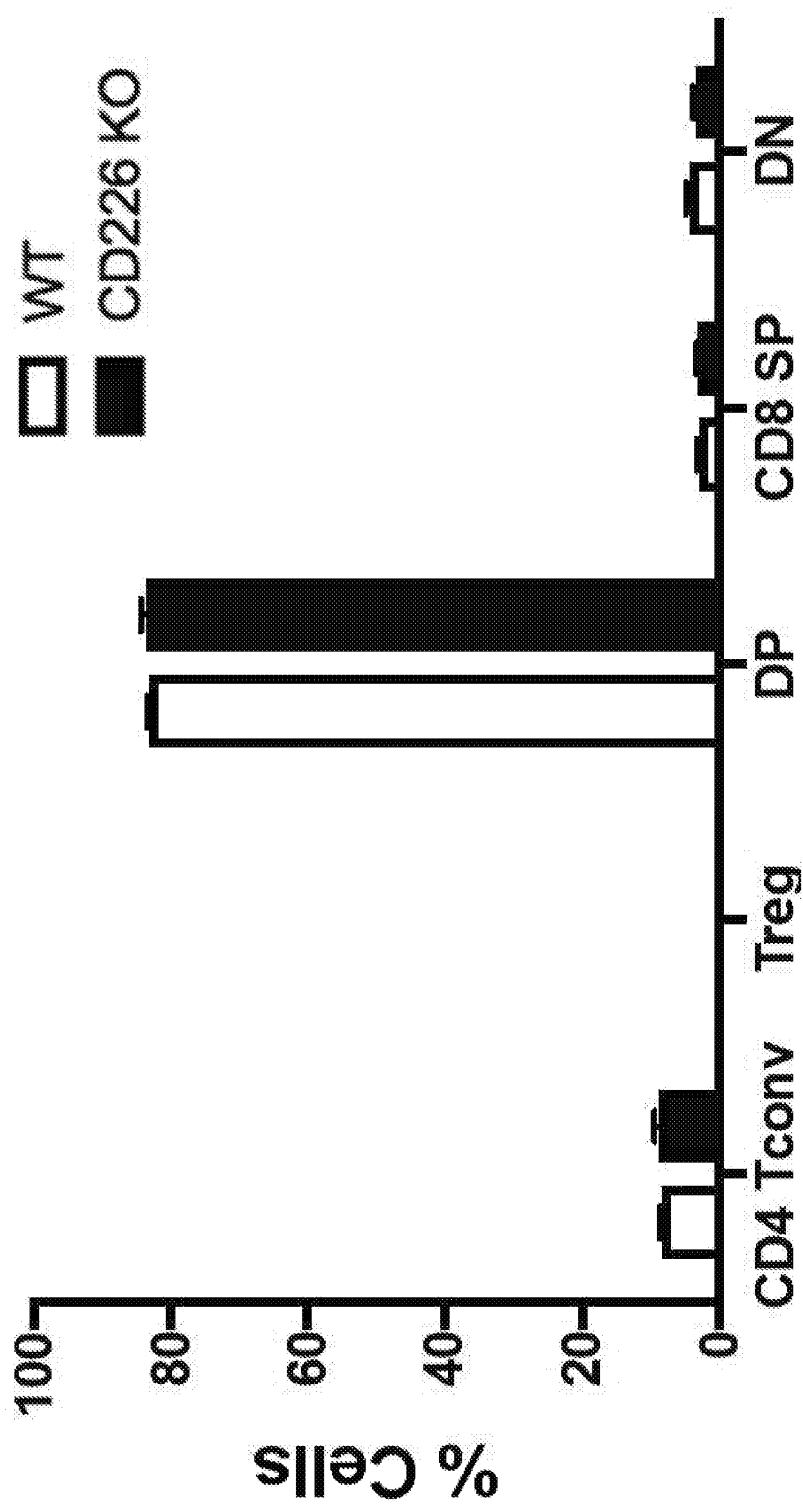


FIG. 23C



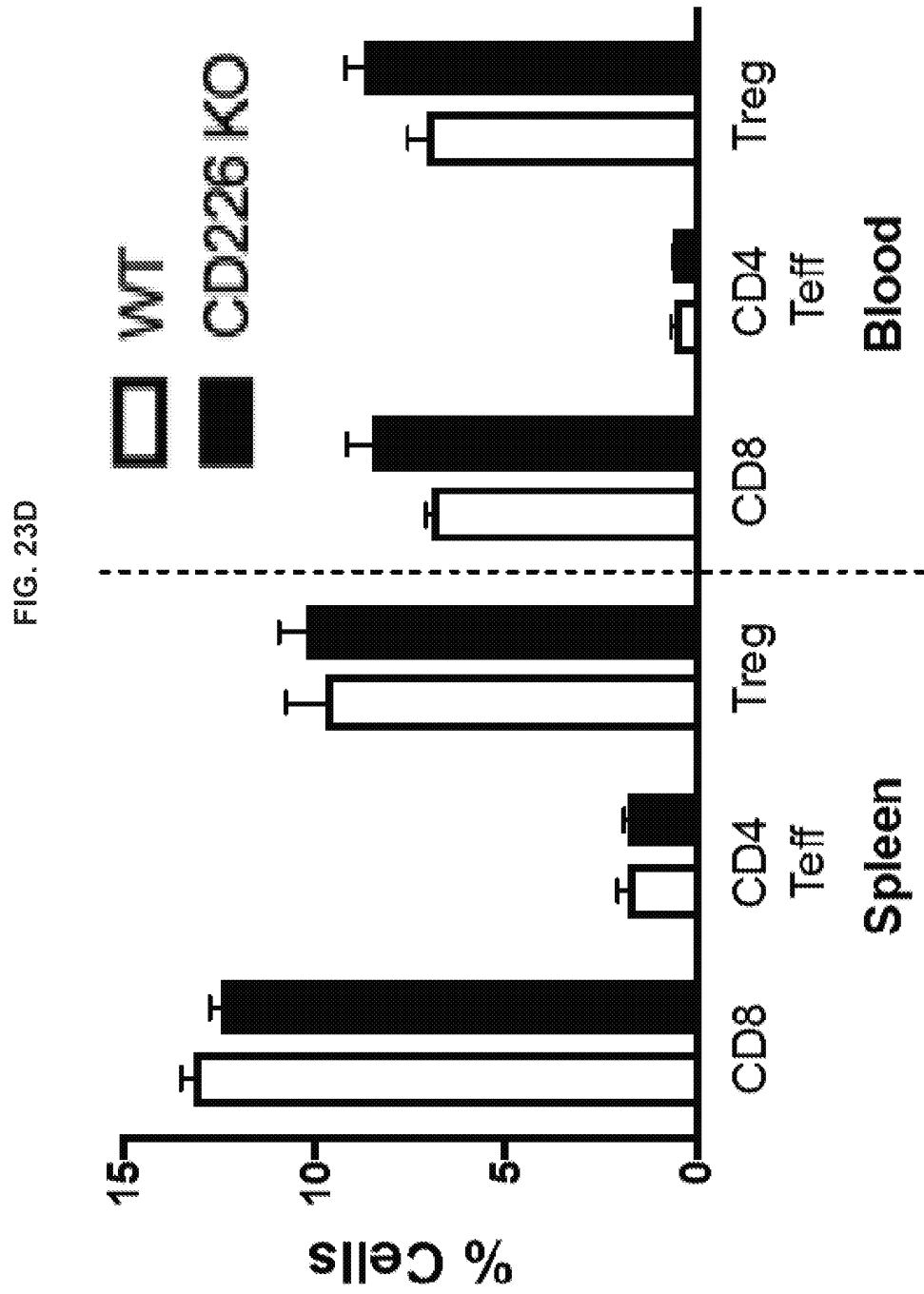


FIG. 23E

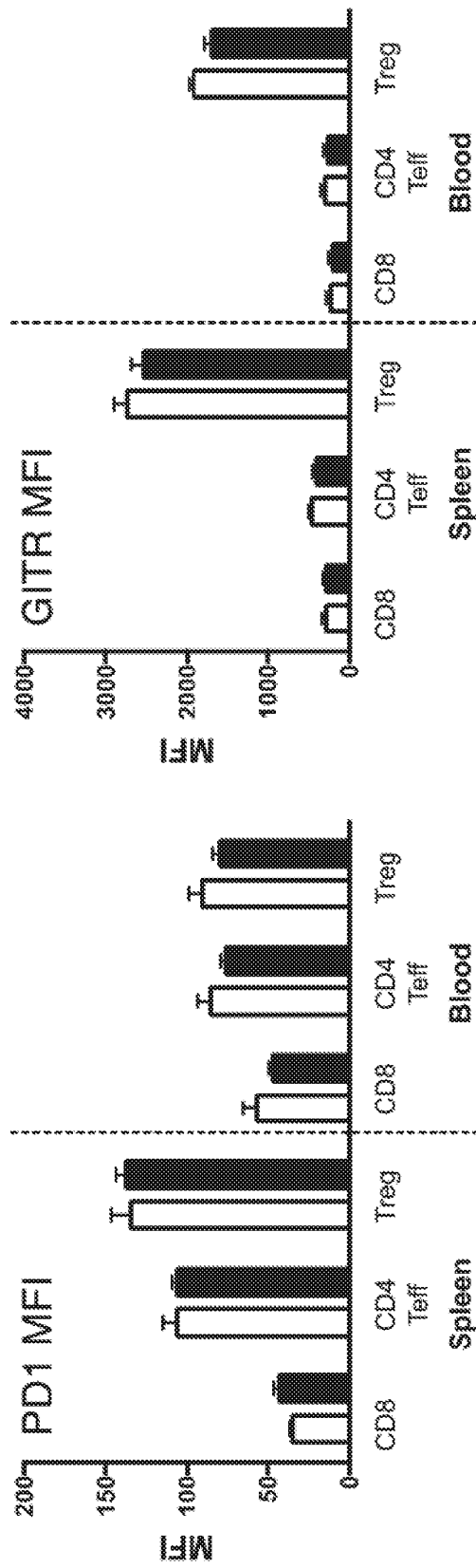


FIG. 23F

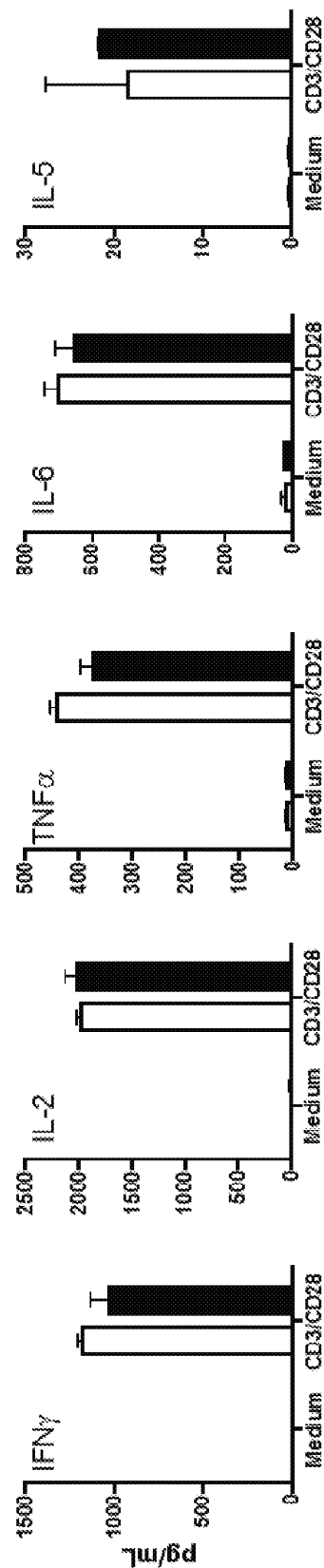


FIG. 24A

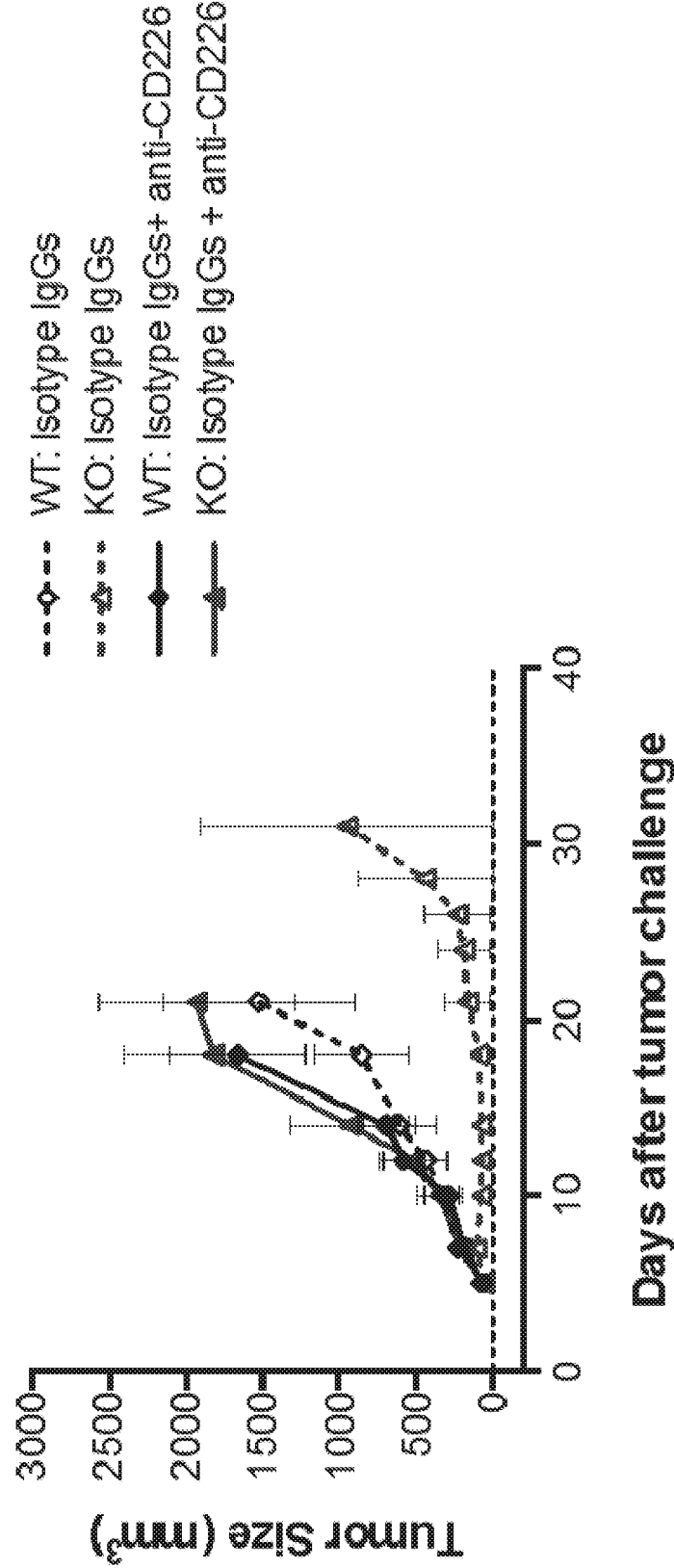
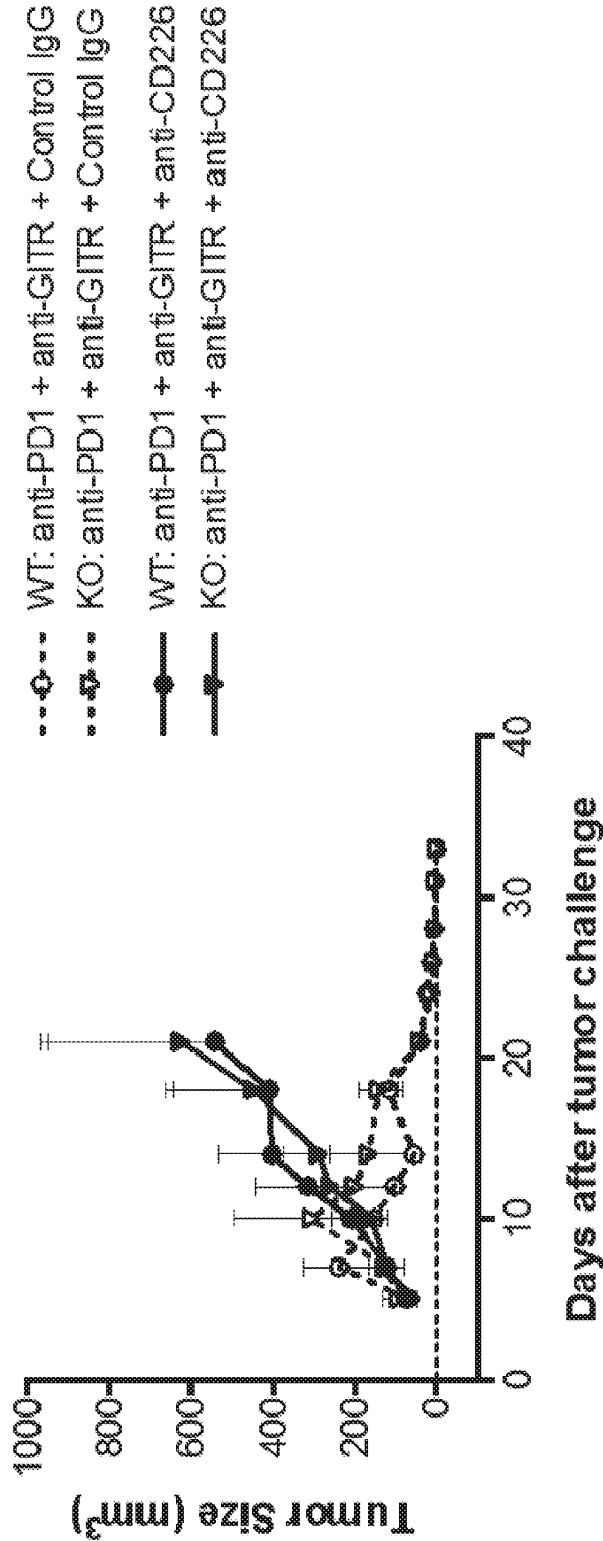


FIG. 24B



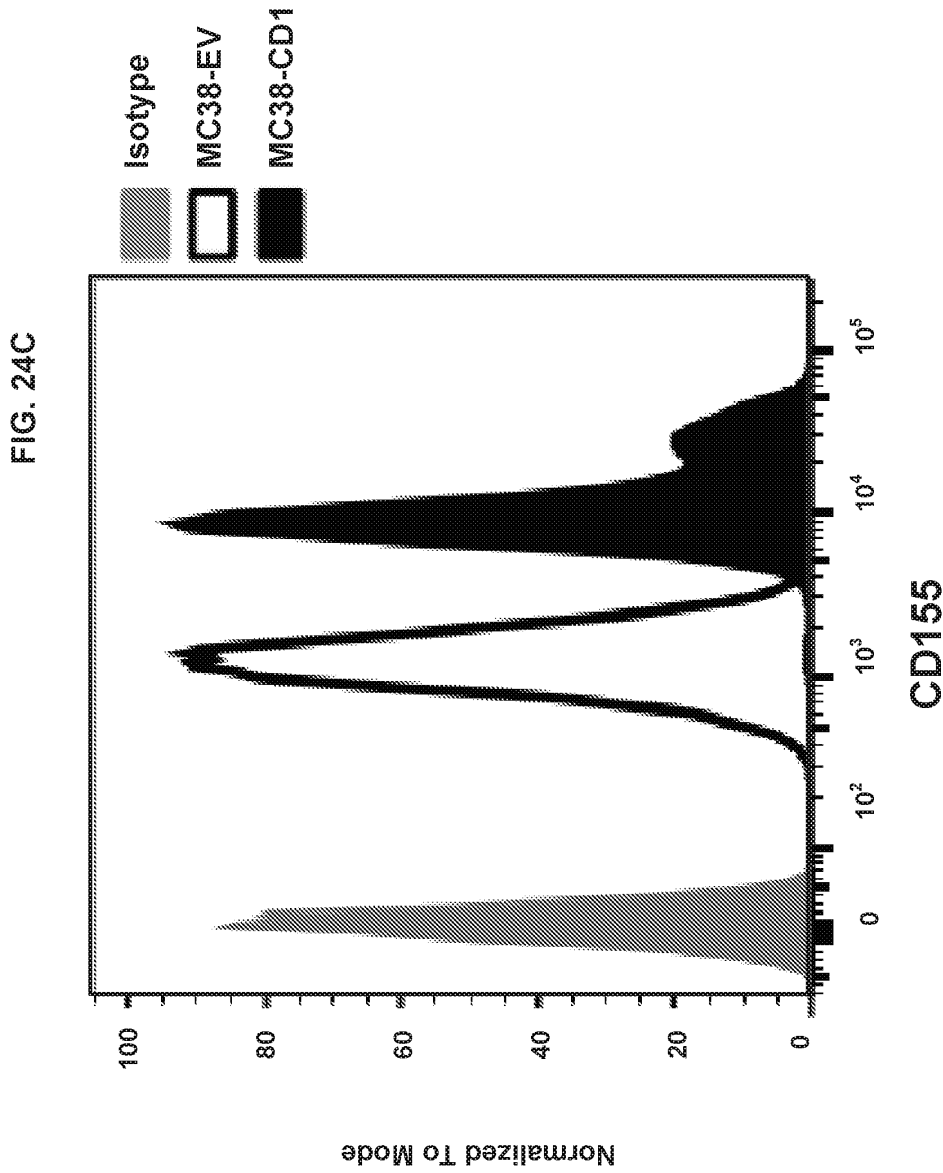
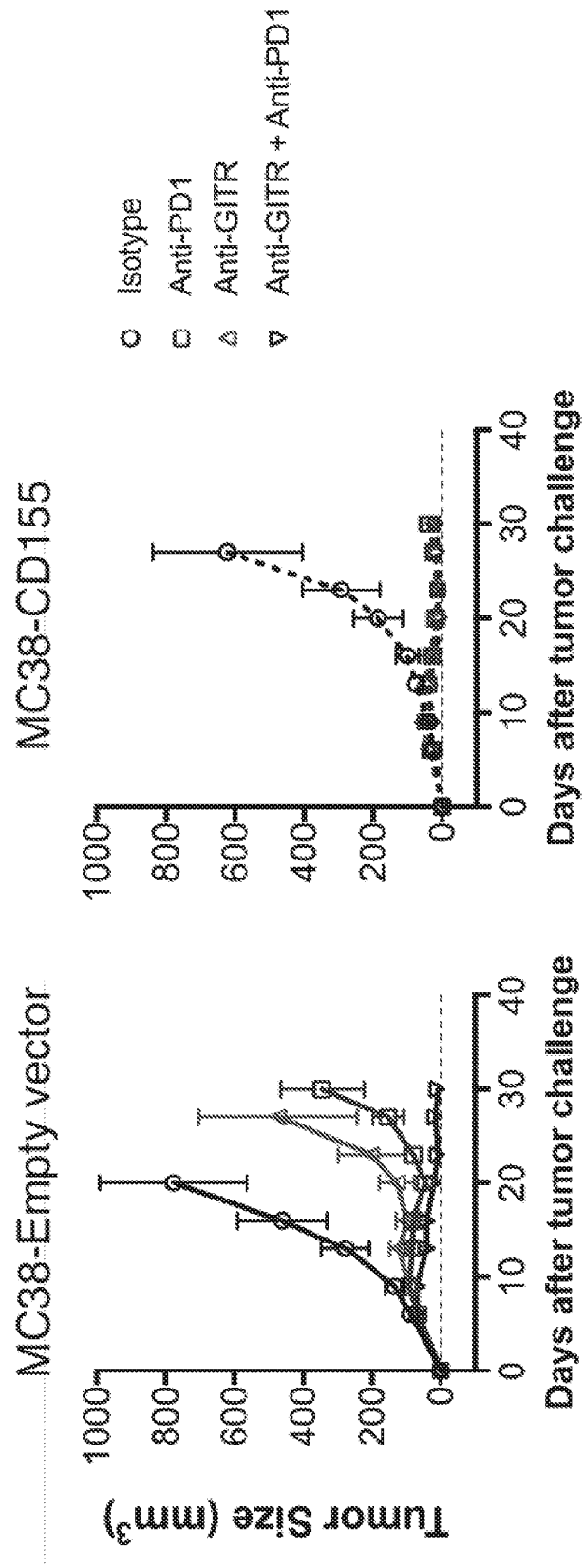


FIG. 24D



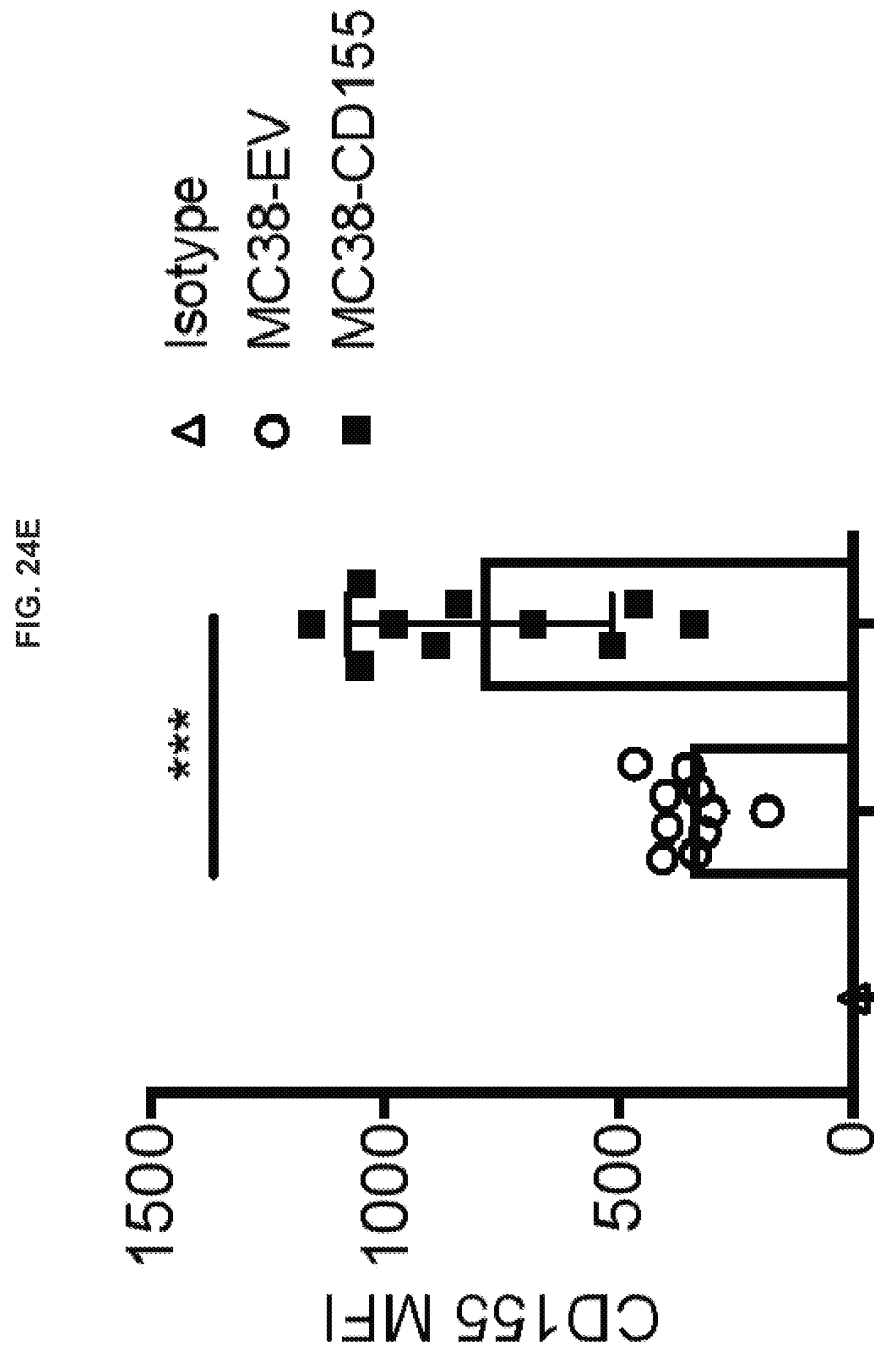


FIG. 24F

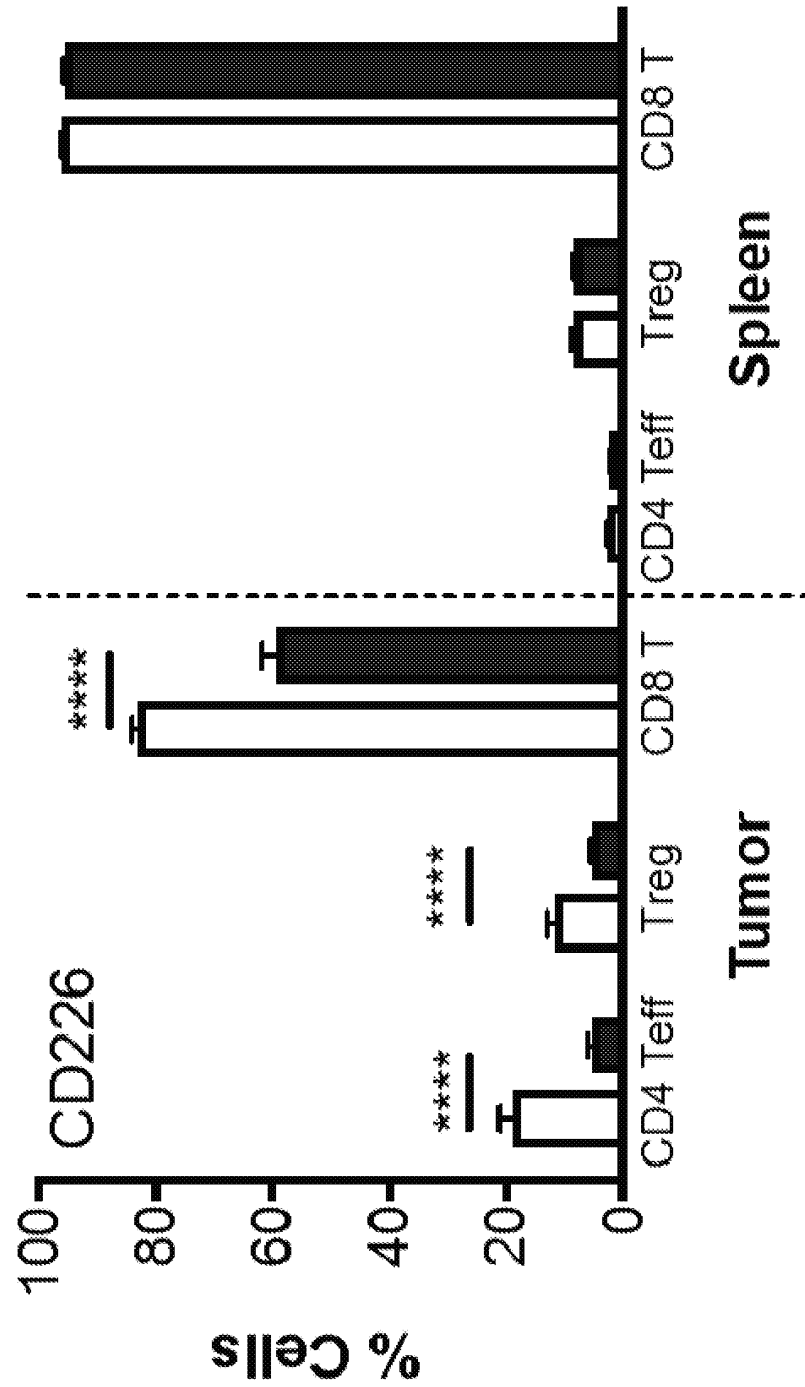
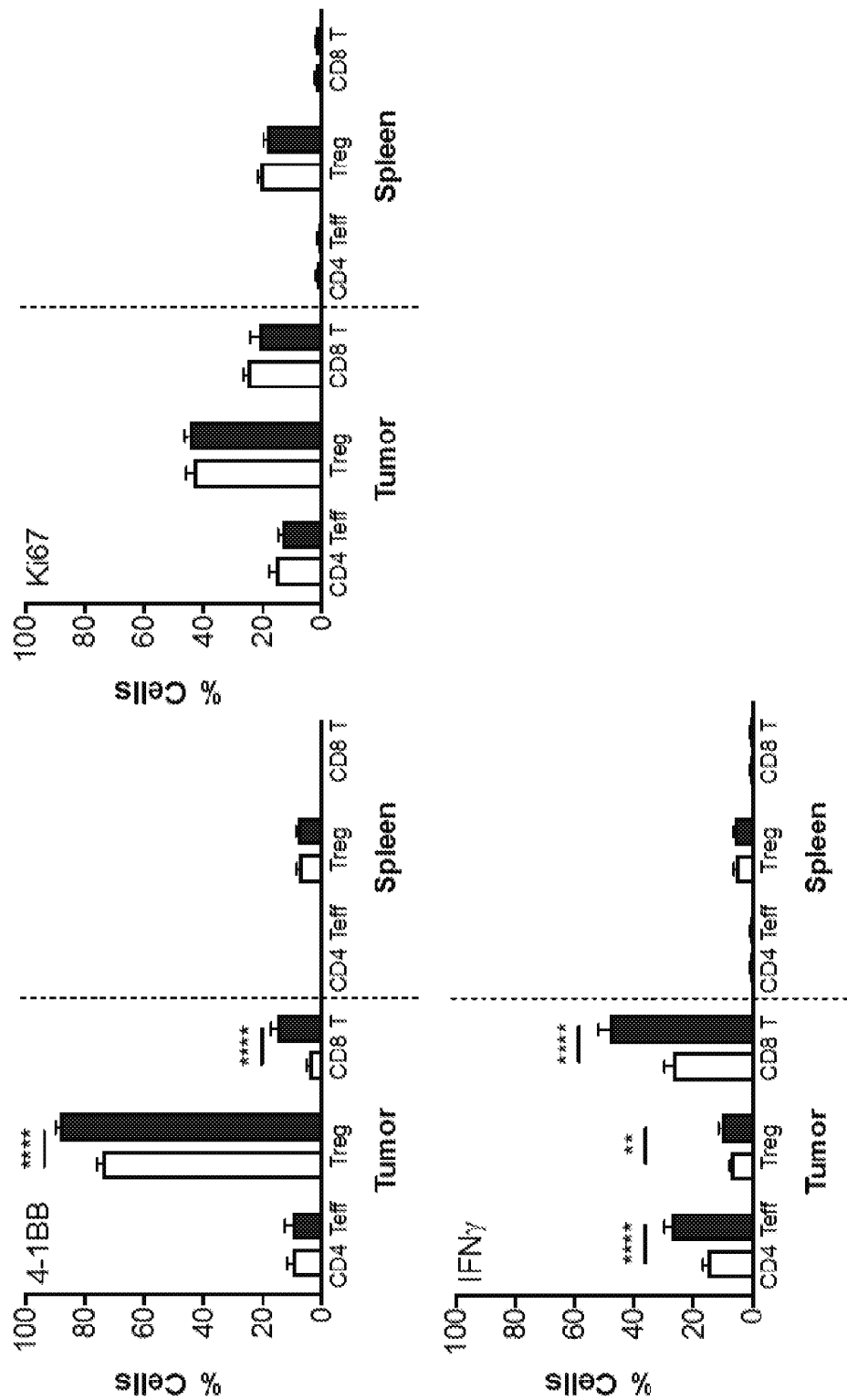
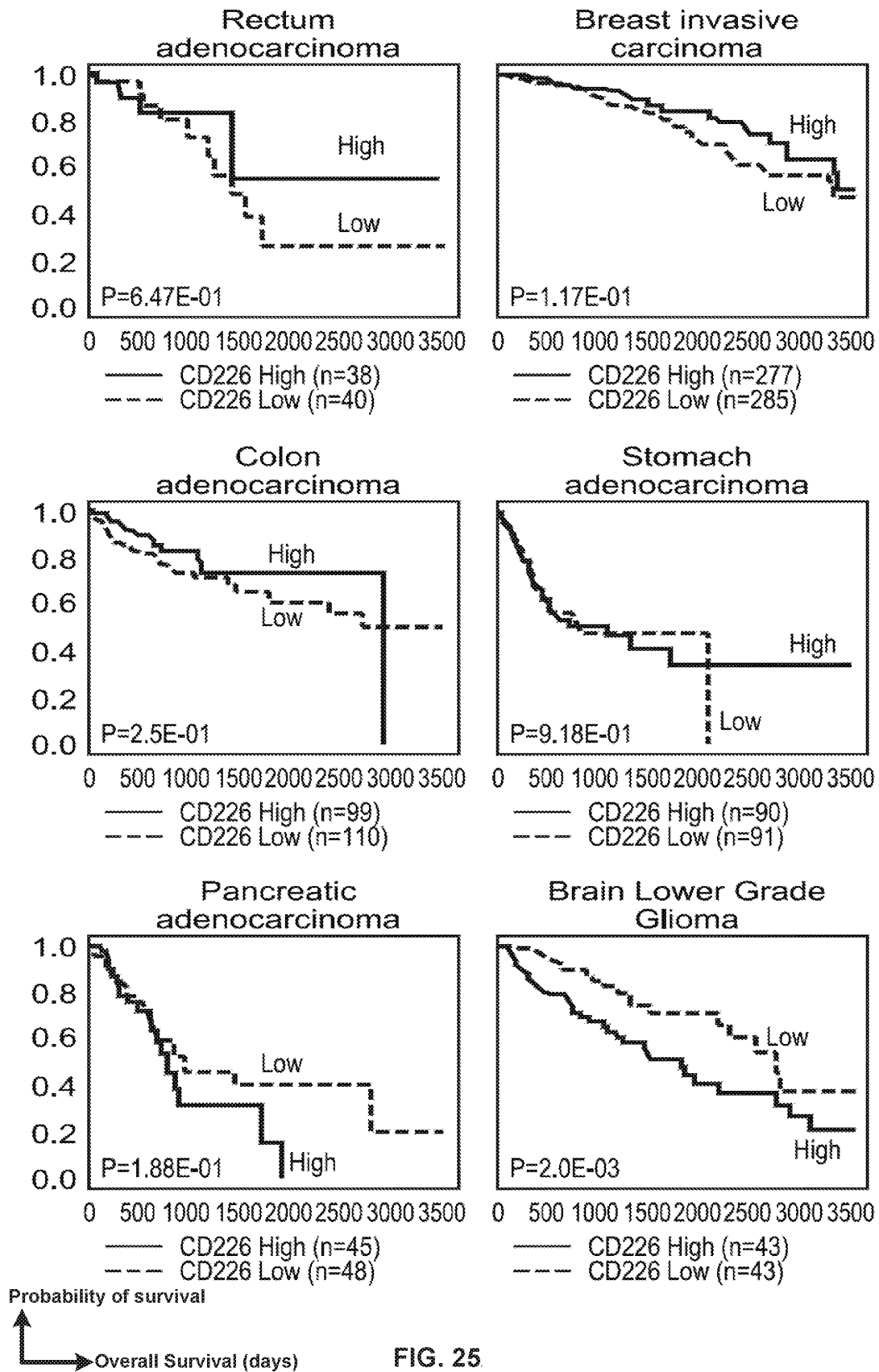


FIG. 24G





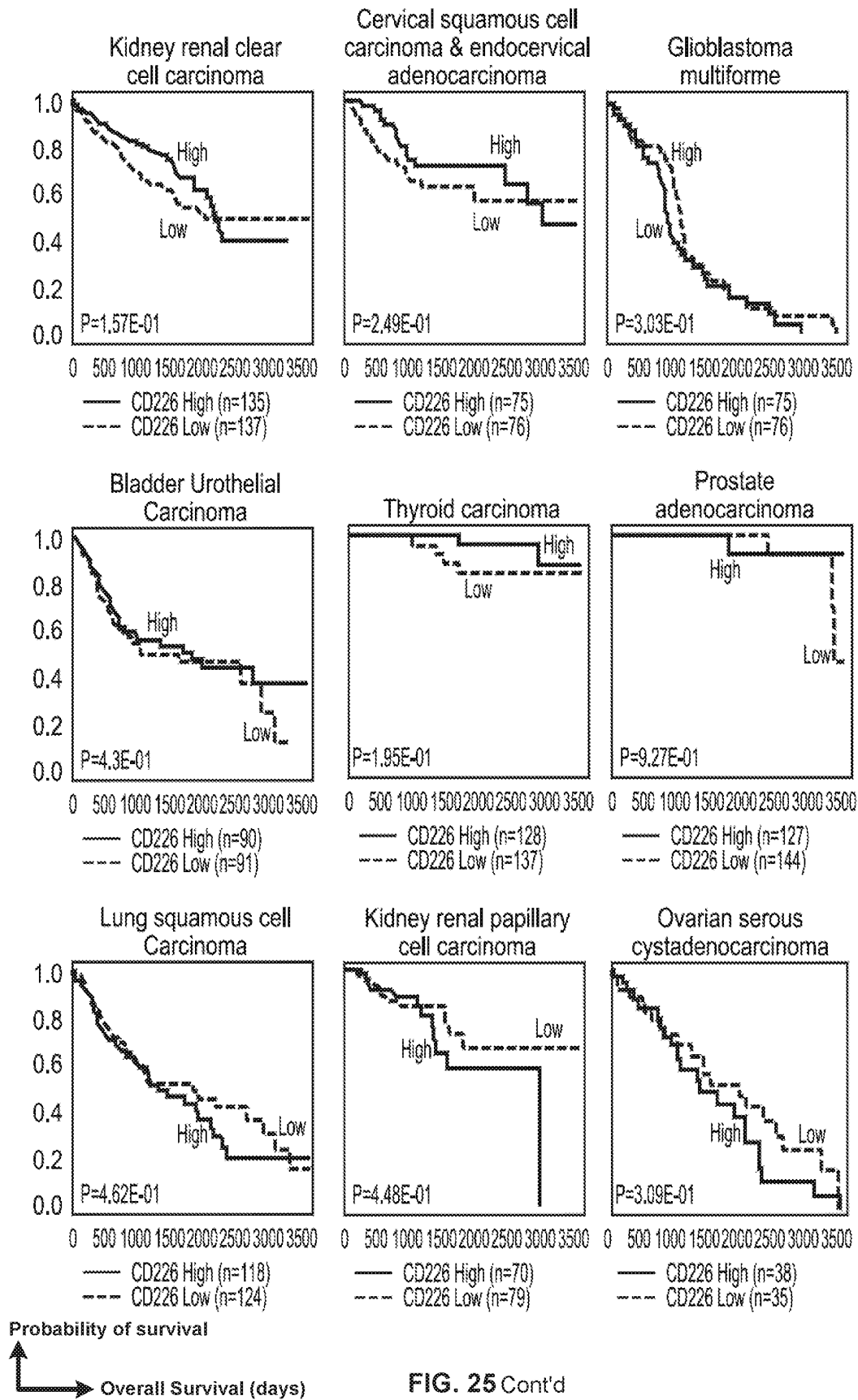


FIG. 25 Cont'd

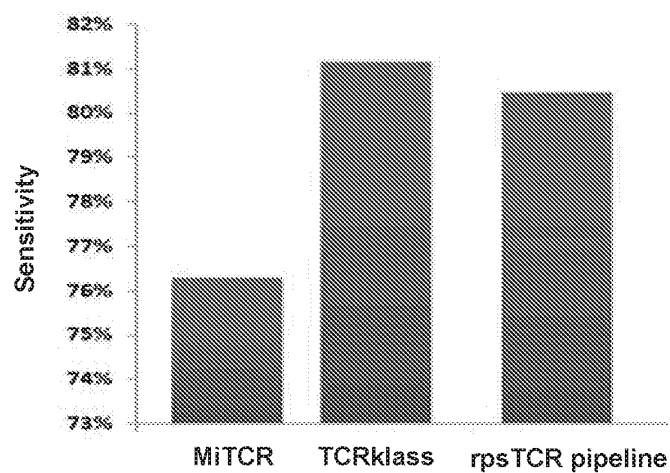
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RT primers	TCRα	5' - GCAGGTGAAGCTTGCTGGTTGCT - 3' (SEQ ID NO:25)
	TCRβ	5' - CGAGGGTAGCCTTTTGTGTTTGC - 3' (SEQ ID NO:26)
1st round PCR primers	TCRα	5' - ACACTCTTCCCTACACGACGCTCTTCCGATCT TCAAAGTCGGTGAACAGGCAGAG - 3' (SEQ ID NO:27)
	TCRβ	5' - ACACTCTTCCCTACACGACGCTCTTCCGATCT GACCTGGGTGGAGTCACATTTCTC - 3' (SEQ ID NO:28)
	PE2-PIIA	5' - GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT AAGCAGTGGTATCAACGCAGAGT - 3' (SEQ ID NO:29)
	Forward	5' - AATGATACGGCGACCACCGAGATCTACACXXXXXX ACACTCTTCCCTACACGACGCTCTTCCGATCT - 3' (SEQ ID NO:30)
2nd round PCR Primers	Reverse	5' - CAAGCAGAAGACGGCATACGAGATXXXXXX GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT - 3' (SEQ ID NO:31)

FIG. 26

FIG. 27

Sample ID	Species	Sample type	MiTCR	TCRklass	rpsTCR pipeline	Input reads (passed QC>=25)
M620343	mouse	negative control	23	0	0	44,906,248
M620295	mouse	negative control	76	0	0	39,305,839
M620279	mouse	negative control	22	1	0	39,233,756
M620274	mouse	negative control	99	1	0	48,661,267
M620272	mouse	negative control	5	0	0	32,426,335
M620270	mouse	negative control	22	0	0	46,609,234
T-ALL_neg1-40M	mouse	negative control	17	1	0	39,068,155
T-ALL_neg2-40M	mouse	negative control	51	0	0	39,469,692
NeuProgCell-40M	human	negative control	123	0	0	37,684,399
LHCN-M2-40M	human	negative control	77	0	0	36,639,557
VI-next-mouse-T cell	mouse	positive control	128,956	137,156	135,980	169,009



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FIG. 28

PCT/US2017/065649

Top CDR3s found by MiTCR	CDR3	VI-next			MP-50bp-500M		
		MiTCR	TCRklass	rpsTCR	MiTCR	TCRklass	rpsTCR
	CATSNYLGYF	0	0	0	63	0	0
	CARHYF	0	0	0	63	0	0
	CAFFYWLF	0	0	0	62	0	0
	CGAGSFQHF	0	0	0	39	0	0
	CARDSIF	0	0	0	21	0	0
	CARGRRITIF	0	0	0	15	0	0
	CARHDLYF	0	0	0	15	0	0
	CARHGIF	0	0	0	15	0	0
	CAKDRGTIF	0	0	0	14	0	0
	CARGPRGIF	0	0	0	13	0	0
Top CDR3s found by TCRklass	CDR3	VI-next			MP-50bp-500M		
		MiTCR	TCRklass	rpsTCR	MiTCR	TCRklass	rpsTCR
	CASSPDADTQYF	0	0	0	3	3	0
	CGAGTTETLYF	27	27	27	3	2	2
	CASSDVRDTEVFF	178	174	174	2	2	0
	CASSDLGEDTQYF	39	44	44	2	2	1
	CTCSASAETLYF	35	30	29	2	2	1
	CASSQEARNYAEQFF	21	21	21	2	2	0
	CASSLGNYAEQFF	8	8	8	2	2	1
	CASGDRYAEQFF	7	7	7	2	2	0
	CASGDGGGNTLYF	5	5	5	2	2	2
	CASSVGGQDTQYF	2	0	2	2	2	0
Top CDR3s found by rps TCR pipeline	CDR3	VI-next			MP-50bp-500M		
		MiTCR	TCRklass	rpsTCR	MiTCR	TCRklass	rpsTCR
	CASSSPGQGAREQYF	1423	1383	1374	3	0	21
	CTCSAGQKAETLYF	805	788	773	1	1	9
	CASSQDWGGDEQYF	287	277	274	1	1	7
	CASSPGQISNERLFF	0	0	0	0	0	5
	CTCSADWGAETLYF	266	265	260	2	1	4
	CASSPGQLQNTLYF	103	102	102	0	0	4
	CASSGRDRGLGNTLYF	77	76	75	0	0	4
	CAKTENSDYTF	18	18	18	4	1	4
	CASSVTGEGNTLYF	18	18	18	0	0	4
	CASRRHLSYEQYF	8	8	8	3	0	4

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FIG. 29

CDR3		VI-Next data (301bp)			
	Rank	MITCR	TCRklass	rps TCR pipeline	
CASSSPGQGAREQYF	1	1423	1383	1374	
CTCSAGQKAETLYF	2	805	788	773	
CTCSAERASAETLYF	3	337	330	326	
CASSRDWGASAETLYF	4	329	323	323	
CASSQDWGGDEQYF	5	287	277	274	
CTCSADWGAETLYF	6	266	265	260	
CASGDAPGTNSDYFT	7	237	231	231	
CASSDGTGDYAEQFF	8	224	217	217	
CASSDGGKANERLFF	9	215	211	211	
CTCSADGRGNIAEQFF	10	190	189	188	

CDR3		MP-50BP-MITCR				
	10M	50m	100m	200m	500m	
CASSSPGQGAREQYF	0	0	0	1	3(rank 15)	
CTCSAGQKAETLYF	0	0	0	0	1	
CTCSAERASAETLYF	0	0	0	0	1	
CASSRDWGASAETLYF	0	0	0	0	0	
CASSQDWGGDEQYF	0	0	0	1	1	
CTCSADWGAETLYF	0	0	0	0	2	
CASGDAPGTNSDYFT	0	0	0	0	0	
CASSDGTGDYAEQFF	0	0	0	1	1	
CASSDGGKANERLFF	0	0	0	0	0	
CTCSADGRGNIAEQFF	0	0	0	0	0	

CDR3		MP-50bp-TCRklass				
	10M	50m	100m	200m	500m	
CASSSPGQGAREQYF	0	0	0	0	0	
CTCSAGQKAETLYF	0	0	0	0	1	
CTCSAERASAETLYF	0	0	0	0	0	
CASSRDWGASAETLYF	0	0	0	0	0	
CASSQDWGGDEQYF	0	0	0	1	1	
CTCSADWGAETLYF	0	0	0	0	1	
CASGDAPGTNSDYFT	0	0	0	0	0	
CASSDGTGDYAEQFF	0	0	0	1	1	
CASSDGGKANERLFF	0	0	0	0	0	
CTCSADGRGNIAEQFF	0	0	0	0	0	

CDR3		MP-50bp-rpsTCR pipeline				
	10M	50m	100m	200m	500m	
CASSSPGQGAREQYF	1	2	5(rank 1)	9(rank 1)	21(rank 1)	
CTCSAGQKAETLYF	0	0	3(rank 2)	4(rank 2)	9(rank 2)	
CTCSAERASAETLYF	0	0	0	1	1	
CASSRDWGASAETLYF	0	0	0	0	1	
CASSQDWGGDEQYF	0	0	0	2	7(rank 3)	
CTCSADWGAETLYF	0	0	1	1	4(rank 5)	
CASGDAPGTNSDYFT	0	0	0	2	2	
CASSDGTGDYAEQFF	0	0	0	0	2	
CASSDGGKANERLFF	0	0	0	0	0	
CTCSADGRGNIAEQFF	0	0	0	0	0	

Top CDR3s found by MiTCR	CDR3	VI-next			MP-100bp-200M		
		MiTCR	TCRklass	rpsTCR	MiTCR	TCRklass	rpsTCR
	CATSNYLGYF	0	0	0	106	0	0
	CARHYF	0	0	0	85	0	0
	CAFFYWLF	0	0	0	83	0	0
	CGAGSFQHF	0	0	0	60	0	0
	CARGRRITIF	0	0	0	49	0	0
	CAKDGGVTIF	0	0	0	33	0	0
	CARDSIF	0	0	0	31	0	0
	CARGPRGIF	0	0	0	31	0	0
	CARHDLYYF	0	0	0	25	0	0
	CASSFKDKRMQDVNF	0	0	0	24	0	0
Top CDR3s found by TCRklass	CDR3	VI-next			MP-100bp-200M		
		MiTCR	TCRklass	rpsTCR	MiTCR	TCRklass	rpsTCR
	CASLQYF	0	0	0	0	99	0
	CASGGKKTSTAFF	0	0	0	0	97	0
	CASSSPGQGAREQYF	1423	1383	1374	23	18	13
	CASRRGIGNTLFY	87	86	86	9	8	8
	CTCSAGQKAETLYF	805	788	773	8	5	7
	CASRRHLSYEQYF	8	8	8	6	5	6
	CASGDAPGTNSDYTF	237	231	231	6	4	4
	CASSQDWGGDEQYF	287	277	274	4	4	4
	CASSGRDRGLGNTLYF	77	76	75	4	4	4
	CGARDRGSNTLYF	1	1	1	4	4	7
Top CDR3s found by rps TCR pipeline	CDR3	VI-next			MP-100bp-200M		
		MiTCR	TCRklass	rpsTCR	MiTCR	TCRklass	rpsTCR
	CASSSPGQGAREQYF	1423	1383	1374	23	18	13
	CASRRGIGNTLFY	87	86	86	9	8	8
	CTCSAGQKAETLYF	805	788	773	8	5	7
	CGARDRGSNTLYF	1	1	1	4	4	7
	CASRRHLSYEQYF	8	8	8	6	5	6
	CASSQDPWGVEQYF	2	2	2	3	3	5
	CASGDAPGTNSDYTF	237	231	231	6	4	4
	CASSQDWGGDEQYF	287	277	274	4	4	4
	CASSGRDRGLGNTLYF	77	76	75	4	4	4
	CASSDHSSAETLYF	78	77	77	3	3	4

FIG. 31

CDR3	10-Short data [001ba]		MAP-100bp-ABTCR					MAP-100bp-TCRdelta					MAP-100bp-rp51 C8 pipeline				
	Rank	ABTCR	TCRdelta	100M	100M	200M	500M	100M	500M	100M	500M	100M	500M	100M	500M	100M	500M
CASSPQQAIEQFF	1	1423	1395	3 (rank 12)	9 (rank 4)	24 (rank 6)	22 (rank 11)	33 (rank 10)	3 (rank 10)	6 (rank 8)	3 (rank 8)	3 (rank 10)	5 (rank 12)	3 (rank 12)	5 (rank 12)	3 (rank 12)	5 (rank 12)
CTSAAGQAETLVF	2	809	786	0 (rank 11)	0 (rank 11)	4 (rank 13)	0 (rank 20)	23 (rank 26)	0	0	0	2 (rank 4)	0 (rank 12)	0 (rank 12)	0 (rank 12)	0 (rank 12)	0 (rank 12)
CTSAEPASAEITLVF	3	337	335	0	0	0	1 (rank 23)	9 (rank 35)	0	0	0	0	0	0	0	0	0
CASSRWGASAEITLVF	4	329	327	0	0	0	1	5 (rank 39)	0	0	0	0	0	0	0	0	0
CASSQDWGGEGQVF	5	387	377	0	0	0	1 (rank 24)	8 (rank 35)	0	0	0	0	0	0	0	0	0
CTSAZWGAETLVF	6	266	263	0	0	0	2	7 (rank 37)	0	0	0	0	0	0	0	0	0
CASSGDAFPTNSQVTF	7	277	231	0	0	0	2 (rank 22)	6 (rank 39)	0	0	0	0	0	0	0	0	0
CASSDGTGZAEQVF	8	324	317	0	0	0	2 (rank 24)	9 (rank 35)	0	0	0	0	0	0	0	0	0
CASSDGGKAEITLVF	9	213	211	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTSAAGRNVAEQVF	10	196	189	0	0	0	0	1	0	0	0	0	0	0	0	0	0

FIG. 32

CDR3	# of cells	Single cell sequencing (75bp)			Bulk RNA sequencing (80bp)		
		MITCR	TCRklass	rpsTCR	MITCR	TCRklass	rpsTCR
CASSPTGYNSPLYF	4	495	465	982	242	302	512
CASSQVQGS AETLYF	5	142	138	646	200	189	394
CASSGTGGNQDTQYF	1	495	408	595	0	0	0
CASGDAGTGN YAEQFF	1	282	247	399	32	26	29
CASSLRTGYNSPLYF	3	206	202	294	123	141	114
CASRLGGDQNTLYF	3	292	151	291	82	53	131
CASKTGGEQYF	1	297	140	285	154	93	75
CASSEGDTLYF	1	370	307	229	46	38	18
CASSPGTFNQDTQYF	3	113	78	195	45	23	36
CASASWTGDEQYF	1	110	49	144	0	0	0
CASSLPGSQNTLYF	1	98	61	140	0	0	0
CASSRDWAQDTQYF	2	127	81	128	141	125	169
CASSDNWGAGEQYF	1	161	107	99	5	5	2
CASSSGTASDTQYF	1	41	30	36	0	0	0
CASSQTRDWG YEQYF	1	33	17	75	28	18	70
CTCSGGLGGLEQYF	1	66	34	74	10	6	9
CASSLGTGGIEQYF	1	56	32	54	4	4	5
CASSLSDSNQDTQYF	1	52	47	50	0	0	0
CASSERGGGRDTQYF	1	49	34	46	0	0	0
CTCSAVREGNSPLYF	1	41	34	46	6	5	4
CASSLTGVSNERLFF	1	74	63	42	0	0	0
CASSRQLNSDYTF	2	50	46	35	129	114	96
CASSLRQGSNTEVFF	1	34	32	34	40	23	20
CASSQNRDISAETLYF	1	22	23	34	77	76	117
CASSWTANTEVFF	1	72	42	30	0	0	0
CASSLRDWGQDTQYF	1	26	19	28	39	27	39
CASSHWGGTTGQLYF	1	28	27	21	0	0	0
CASSYSKGS AETLYF	1	17	17	17	0	0	0
CAVSMINYNVLYF	1	0	1	17	0	6	13
CASSDQQYEQYF	1	10	7	14	0	0	0
CASSQRTGQNTLYF	1	12	9	6	0	0	0
CASSQEGPGQLYF	1	8	7	5	39	35	27
CASTGQGYNSPLYF	1	0	1	1	0	0	0
CGANSQQLAVFF	1	5	0	0	0	0	0
CSFIYF	1	4	0	0	3	0	0
CAARGYNQGLIF	1	3	0	0	0	0	0