

Fig. 1

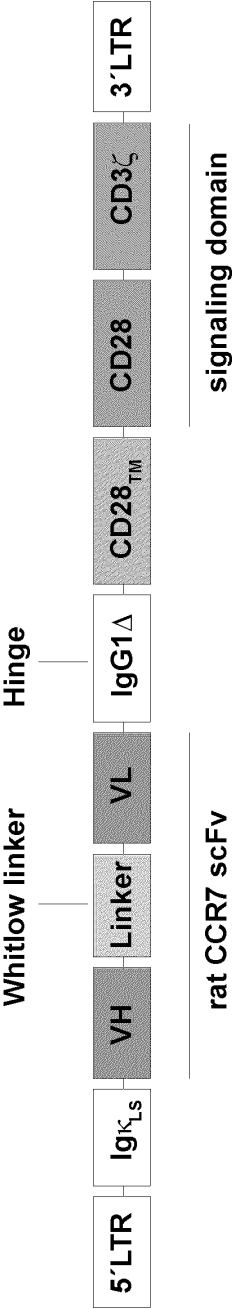


Fig. 2

ID	Leader	scFV	Order	Linker	Spacer	Trans- membrane domain	Co- stimulatory domain	Activation domain
M5	Igk	Rat(r)	VH-VL	Whitlow	IgG1Δ	CD28	CD28	CD3ζ
M8	Igk	Partially humanized (ph)	VH-VL	Whitlow	IgG1Δ	CD28	CD28	CD3ζ
M9	Igk	Fully humanized (fh)	VH-VL	Whitlow	IgG1Δ	CD28	CD28	CD3ζ
M17	Igk	rVH-fhVL	VH-VL	Whitlow	IgG1Δ	CD28	CD28	CD3ζ
M18	Igk	fhVH-rVL	VH-VL	Whitlow	IgG1Δ	CD28	CD28	CD3ζ
M19	Igk	rVH-phVL	VH-VL	Whitlow	IgG1Δ	CD28	CD28	CD3ζ
M20	Igk	phVH-rVL	VH-VL	Whitlow	IgG1Δ	CD28	CD28	CD3ζ
M28	Igk	rVH-phVL(T14P)	VH-VL	Whitlow	IgG1Δ	CD28	CD28	CD3ζ
M29	Igk	rVH-phVL(S22T)	VH-VL	Whitlow	IgG1Δ	CD28	CD28	CD3ζ
M30	Igk	rVH-phVL(D40N)	VH-VL	Whitlow	IgG1Δ	CD28	CD28	CD3ζ
M31	Igk	rVH-phVL(K45R)	VH-VL	Whitlow	IgG1Δ	CD28	CD28	CD3ζ

HV

				<-----FR1-IMGT-----><-----CDR1-IM
	A V Q L V E S G G L V Q P K E S L K I S C A A S G F T F S			
Query_1	GCGTGCAGCTTGTTGAGTCGTGGTGAGGATTTGGTGACCTAAGGAGTCATTGAATAATCTCATGTGCAGCCTCTGGATTCACCTTCAGT	90		
IGHV10-5*01	.G.....	90		
V	A V Q L V E S G G L V Q P K E S L K I S C A A S G F T F S			
	GT-----><-----FR2-IMGT-----><-----CDR2-IMGT----->			
	N A A M Y W V R Q A P G K G L E W V A R I R T K P N N F A T	180		
Query_1	AAATGCTGCCATGTACTGGGTCCGCCAGGCTCCAGGAAGGGTCTGGAATGGGTTCGCAATAAGAACAATAAACCTTAATAATTTTGCAACA	180		
IGHV10-5*01	A.....			
V	N A A M Y W V R Q A P G K G L E W V A R I R T K P N N Y A T			
	<-----FR3-IMGT----->			
	Y Y A D S V K G R F T I S R D D S K S M V Y L Q M D K L K T	270		
Query_1	TATTATGCTGACTCAGTGAAGGACAGATTCACCATCTCCAGAGATGATTCAAAAGCATGGTCTACCTACAAATGGATTAAGTTGAAGAACT	270		
IGHV10-5*01	T.....C.....			
V	Y Y A D S V K G R F T I S R D D S K S M V Y L Q M D N L K T			
	<-----CDR3-IMGT-----><-----FR4-IMGT----->			
	E D T A M Y Y C T A G K D Y F A Y W G Q G T L V T V S S	355		
Query_1	GAGGACACAGCCATGTATTATTGTACAGCTGGGAAGGATTACTTTTGCTTACTGGGCGCAAGGCACCTCTGGTCACCTGCTCTTCAG	355		
IGHV10-5*01	C.....	299		
V	E D T A M Y Y C T A			
D	IGHD1-6*01	15		20
I	IGHJ3*01	9		51

Fig. 3 (cont.)
B

VL

V	97.7%	(292/299)	Query_1 IGKV2S6*01	1	1	D I V M T Q G A L P N P V P S G E S A S I T C Q S S K S L L GATATTGTGATGACCCAGGTGCACTCCCAATCCTGTCCTTGAGAGTCAGCTTCCATCCAGTCAGTAGCAAGAGTCTGCTGT.....A D I V M T Q G A L P N P V P S G E S A S I T C Q S S K S L L
V	97.7%	(292/299)	Query_1 IGKV2S6*01	91	91	CDR1-IMGT<><<FR1-IMGT<><<FR2-IMGT<><<CDR2-IMGT<><< F S D G K T Y L N W Y L Q R P G Q S P Q F L I Y W M S T R A TTCAGCGATGGCAAGACATCTGAATTGGTATCTGCAGAGGCCAGCAGCTCTCCTCAGTTCCTGATCTATTGGATGTCTACCGTGCA CA....A..... H S N G K T Y L N W Y L Q R P G Q S P Q F L I Y W M S T R A
V	97.7%	(292/299)	Query_1 IGKV2S6*01	181	181	FR3-IMGT<><<FR4-IMGT<><< S G V S D R F S G S G S G T D F T L K I S R V E A E D V G V TCAGGAGTCTCAGACAGGTTCAGTGGCAGTGGTTCAGGAACAGATTTACACTGAAATCAGTAGAGTGGAGCTGAGGATGTGGGTGTG S G V S D R F S G S G S G T D F T L K I S R V E A E D V G V
V	97.7%	(292/299)	Query_1 IGKV2S6*01	271	271	CDR3-IMGT<><<FR3-IMGT<><<FR4-IMGT<><< Y Y C Q Q F L E F P F T F G S G T K L E I K TATTACTGCAGCAATTTCTAGAGTTCCATTCCAGTTCGGCTCAGGGACGAAGTTGGAAATAAACGA..... Y Y C Q Q D L E F P
J	100.0%	(38/38)	IGKJ4*01	1	38	

Fig. 4

Sequence ID: Query_273963 Length: 354 Number of Matches: 1
Range 1: 1 to 351

Score	Expect	Identities	Gaps	Strand	Frame
282 bits(312)	1e-80()	273/351(78%)	0/351(0%)	Plus/Plus	
Original 1	GCCGTGCAGCTTGTGAGTCTGGTGGAGGATTGGTGCAGCCCTAAGGAGTCATTGAAAAATC				60
CO 1	 GCCGTGCAGCTGGTGGAACTCTGGCGGAGGACTGGTGCAGCCCTAAAGAGAGCCCTGAAGATC				60
Original 61	TCATGTGCAGCCTCTGGATTCCACCTTCAGTAATGCTGCCATGTACTGGGTCGCCCAGGCT				120
CO 61	 AGCTGTGCCGCCAGCGGCTTCACTTTAGCAAAGCCGCTATGTACTGGTCCGACAGGCC				120
Original 121	CCAGGAAAGGTCTGGAAATGGGTGCTCGCATAAAGAACTAAACCTAATAATTTTGCAACA				180
CO 121	 CCTGGAAAAGGCCCTGGAATGGGTGCCCCGGATCAGGACCAAGCCTAACAACTTCGCCACC				180
Original 181	TATTATGCTGACTCAGTGAAAGGCAGATTACCATCTCCAGAGATGATTCAAAAAGCATG				240
CO 181	 TACTACGCCGACAGCGTGAAGGGCAGATTACCATCAGCCGGGACGACAGCAAGAGCATG				240
Original 241	GTCTACCTACAAATGGATAAGTTGAAAACCTGAGGACACAGCCATGTATTATTGTACAGCT				300
CO 241	 GTGTACCTGCAGATGGACAAGCTGAAAACCCGAGGACACCCGCTATGTACTACTGCACCGCC				300
Original 301	GGGAAGGATTACTTTGCTTACTGGGGCCAAAGGCACCTCTGGTCACTGTCTCT				351
CO 301	 GGCAAGGACTACTTCGCCCTATTGGGGACAGGGCACCCCTGGTCACAGTGCTT				351

Fig. 5

Sequence ID: Query_31653 Length: 339 Number of Matches: 1
Range 1: 1 to 335

Score	Expect	Identities	Gaps	Strand	Frame
271 bits(300)	2e-770	261/335(78%)	0/335(0%)	Plus/Plus	
Original	1	GATATTGTGATGACCCAGGGTGCACTCCCAATCCTGTCCCTTCTGGAGAGTCAGCTTCC			60
CO	1	GATATCGTGATGACACAGGGCGCTCTGCCCAA+CTGTGCTTCTGGCGAGAGCGCCTCT			60
Original	61	ATCACCTGCCAGTCTAGCAAGAGTCTGCTGTTCAGCGATGGCAAGACATACTTGAATTGG			120
CO	61	ATCACCTGTACAGAGCAGCAAGTCCCTGCTGTTACGCGACGGCAAGACCTACCTGAACCTGG			120
Original	121	TATCTGCAGAGGCCAGGACAGTCTCTCAGTTCCTGATCTATTGGATGTCTACCCGTGCA			180
CO	121	+ATCTGCAGAGGCCCGGACAGAGCCCTCAGTTCCTGATCTACTGGATGAGCACCAAGAGCC			180
Original	181	TCAGGAGTCTCAGACAGGTTTCAGTGGCAGTGGTCAGGAACAGATTTTCACACTGAAAAATC			240
CO	181	AGCGGCGTGTCCGATAGATTTTCTGGCAGCGGCTCCGGCACCGACTTACCCCTGAAGATT			240
Original	241	AGTAGAGTGGAGGCTGAGGATGTGGGTGTATTACTGTCAGCAAATTTCTAGAGTTTCCA			300
CO	241	AGCAGAGTGGAAAGCCGAGGACGTGGGCGTGTACTATTGCCAGCAGTTCCTGGAGTTCCTCA			300
Original	301	TTCACGTTTCGGCTCAGGGACGAAGTTGGAAATAAA			335
CO	301	TTTCACTTTCGGCAGGGCCACCAAGCTGGAAATCAA			335

Fig. 6

Sequence ID: ACS95849.1 Length: 122 Number of Matches: 1

Range 1: 2 to 121 GenPept Graphics

Score	Expect	Method	Identities	Positives	Gaps
188 bits(478)	3e-62	Compositional matrix adjust.	93/120(78%)	103/120(85%)	3/120(2%)
Query 1	VQLVESGGGLVQPKESLKISCAASGFTFSNAAMYWVRQAPGKGLEWVARIRTKPNNFATY	60			
	VQLVESGGGLVQP SLK+SCAASGFTFS +AM+WVRQA GKGLEWV RIR+K N++AT				
Sbjct 2	VQLVESGGGLVQPGGSLKLSCAASGFTFSGSAMHWRQASGKGLEWVGRIIRSKANSYATA	61			
Query 61	YADSVKGRFTISRDDSKSMVYLQMDKLKTEDTAMYYC-TAGKD--YFAYWGQGTLLTVSS	117			
	YA SVKGRFTISRDDSK+ YLQM+ LKTEDTA+YYC T G D +F YWGQGTLLTVSS				
Sbjct 62	YAASVKGRFTISRDDSKNTAYLQMNLSLKTEDTAVYYCTTCGGDCSHFGYWGQGTLLTVSS	121			

Fig. 7

Sequence ID: QAV55361.1 Length: 112 Number of Matches: 1

Range 1: 1 to 112 [GenPept](#) [Graphics](#)

Score	Expect	Method	Identities	Positives	Gaps
174 bits(442)	6e-57	Compositional matrix adjust.	87/112(78%)	94/112(83%)	0/112(0%)
Query 1	DIVMTQ	GALPNPVP	GESASITCQSSKSLLFSDGKTYLNWYLQRP	QSPQFLIYWM	STRA 60
	DIVMTQ L PV	GE ASI+C+SS+SLL SDG YL+WYLQRP	QSPQ LIY S RA		
Sbjct 1	DIVMTQ	SPLSLPVT	PGEPASISCRSSQSLHSDGYNYL	DWYLQRP	QSPQLLIYLSIRA 60
Query 61	SGVSDR	FRFSGSGT	DFTLTKISRVEAEDVG	VYCCQFLEFP	FTFGSGTKLEIK 112
	SGVSDR	FRFSGSGT	DFTLTKISRVEAEDVG	VYCC Q L+ P	FTFG GTK++IK
Sbjct 61	SGVSDR	FRFSGSGT	DFTLTKISRVEAEDVG	VYCCMQALQ	TPFTFGPKVDIK 112

Fig. 8

IMGT labels	V-REGION	FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT	
Nb of positions including IMGT gaps (AA)	104 (106)	26	12	17	10	39	0 (2)	
Nb of AA	97 (99)	24	8	17	10	38	0 (2)	
Nb of identical AA	77 (78)	21	6	14	6	30	0 (1)	
Nb of AA changes	20 (21)	3	2	3	4	8	0 (1)	
AA changes	Very similar	(+ + +)	1	0	0	0	0	
	Similar	(+ + -)	0	0	0	0	1	0
		(+ - +)	0	0	0	1	1	0
	Dissimilar	(+ - -)	0	0	2	0	1	0
		(- + -)	0	1	1	1	0	0
		(- - +)	0	0	0	0	0	0
	Very dissimilar	(- - -)	2	1	0	2	5	0 (1)

Fig. 9

IMGT labels	V-REGION	FR1-IMGT	CDR1-IMGT	FR2-IMGT	CDR2-IMGT	FR3-IMGT	CDR3-IMGT		
Nb of positions including IMGT gaps (AA)	110 (111)	26	12	17	10	39	6 (7)		
Nb of AA	99 (100)	26	11	17	3	36	6 (7)		
Nb of identical AA	77 (78)	17	8	14	1	34	3 (4)		
Nb of AA changes	22	9	3	3	2	2	3		
AA changes	Very similar	(+ + +)	2	0	0	1	0	0	1
		(+ + -)	3	1	0	0	1	0	0
	Similar	(+ - +)	1	1	0	0	0	0	0
		(+ - -)	10	5	2	1	0	2	0
	Dissimilar	(- + -)	0	0	0	0	0	0	0
		(- - +)	0	0	0	0	0	0	0
	Very dissimilar	(- - -)	6	2	1	0	1	0	2

Fig. 10

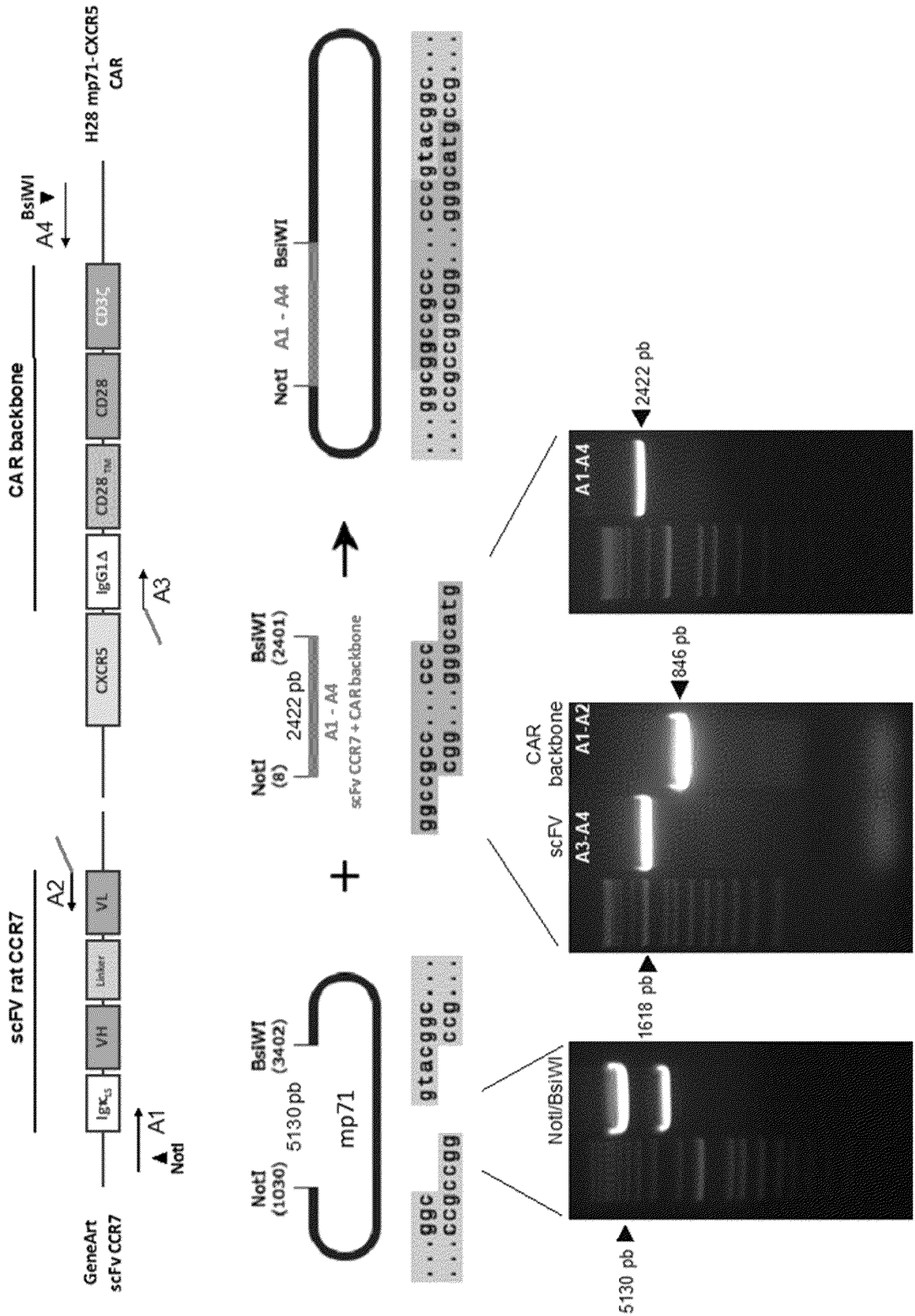


Fig. 11

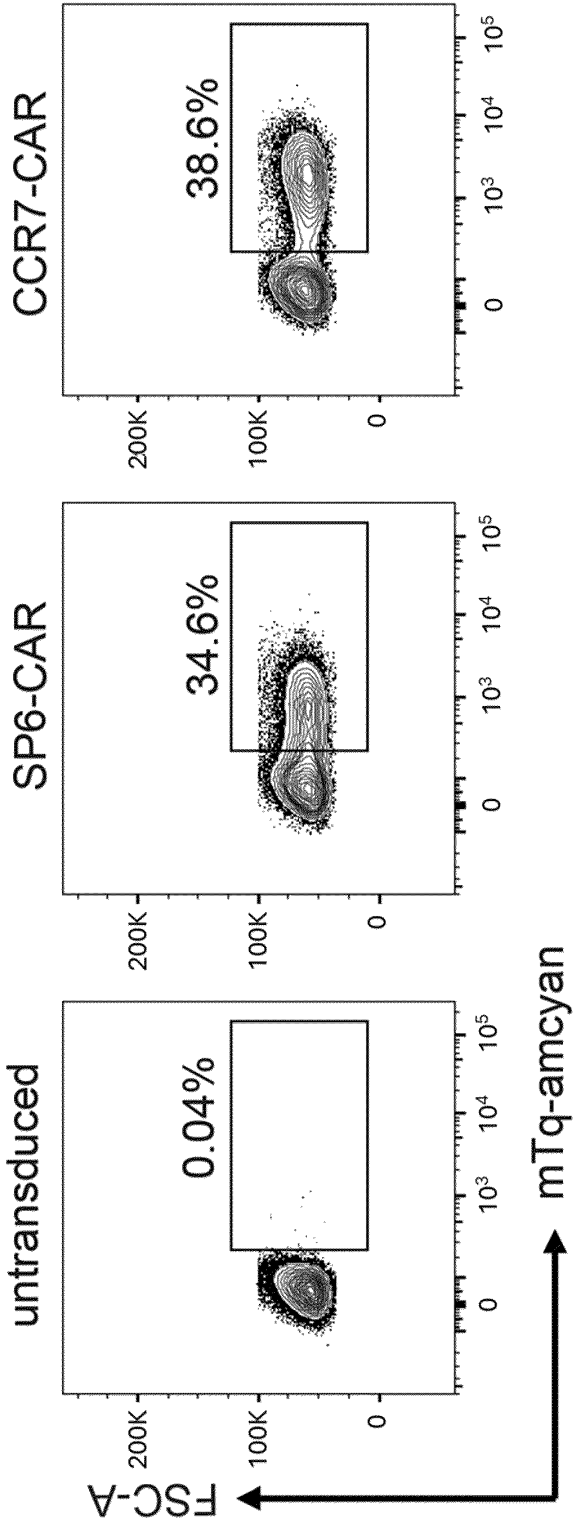


Fig. 12

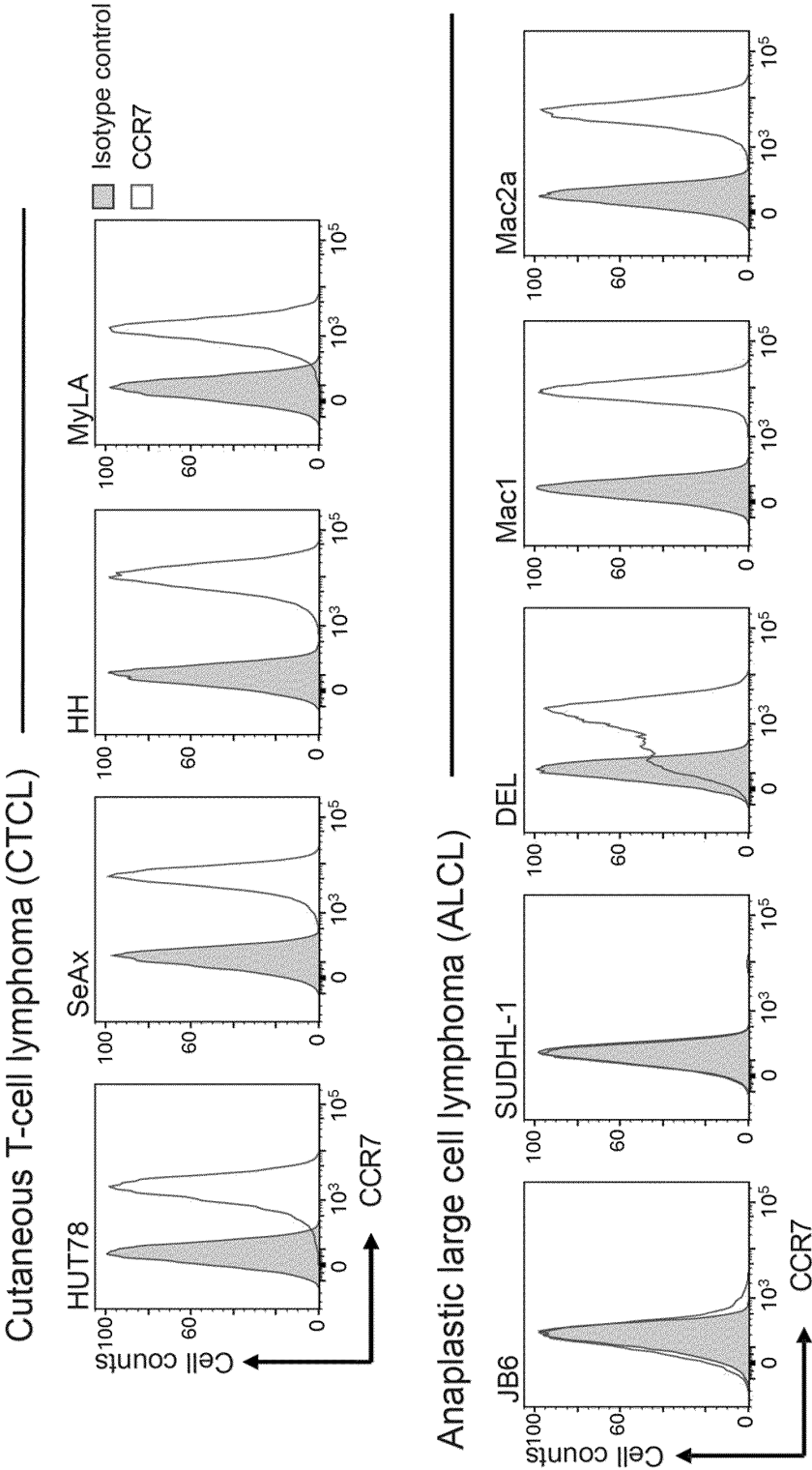


Fig. 13

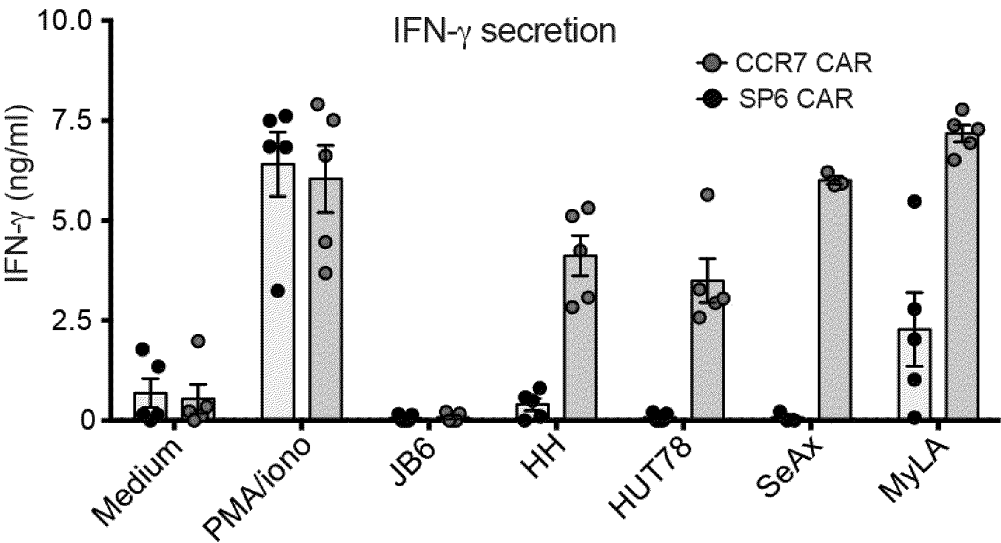


Fig. 14

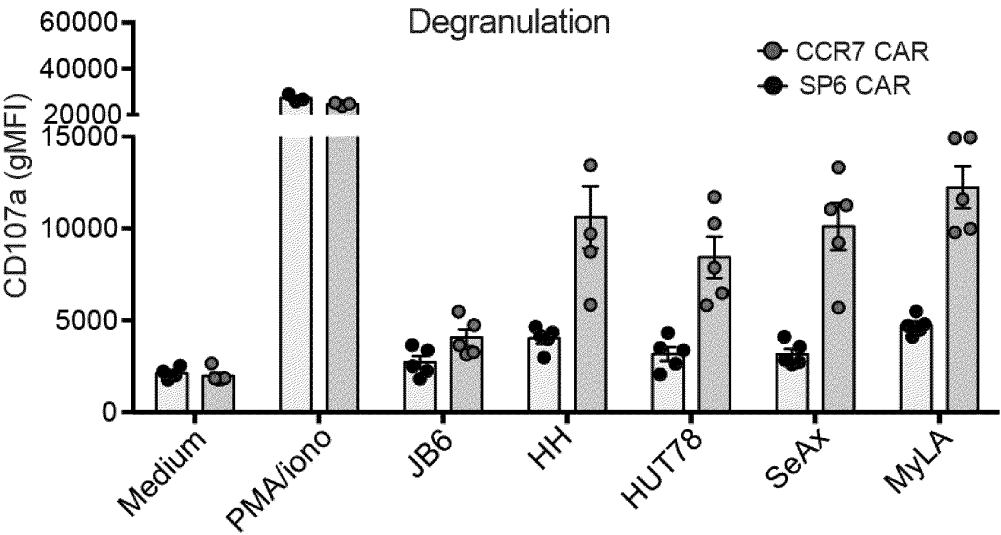


Fig. 15

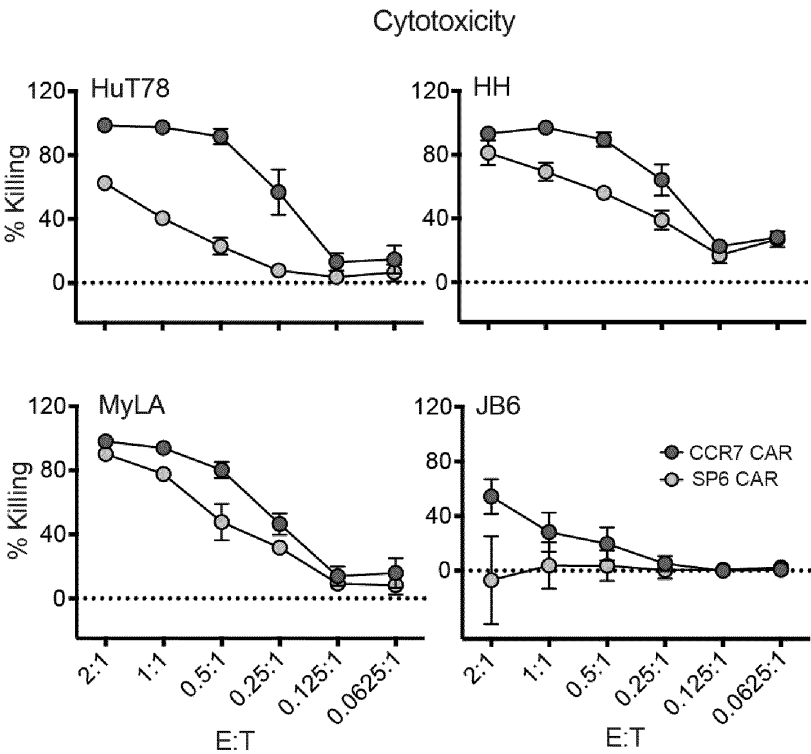


Fig. 16

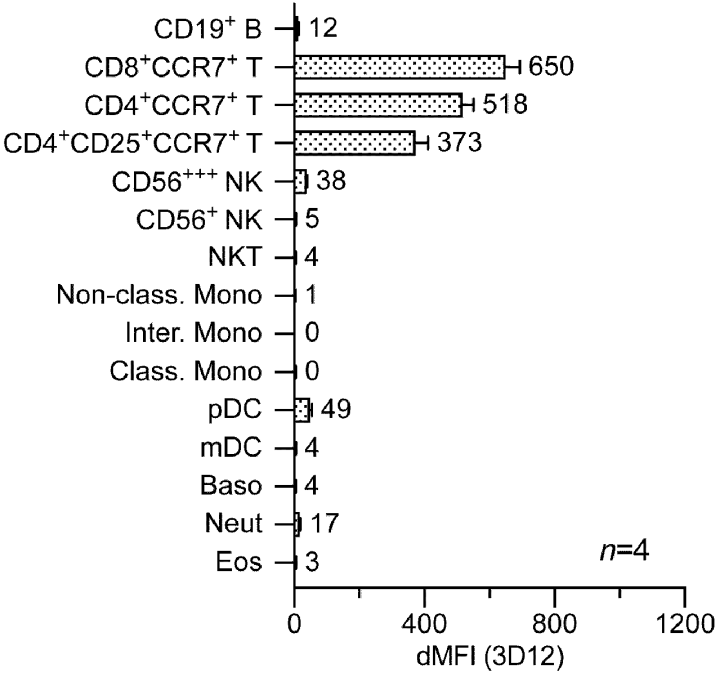


Fig. 17

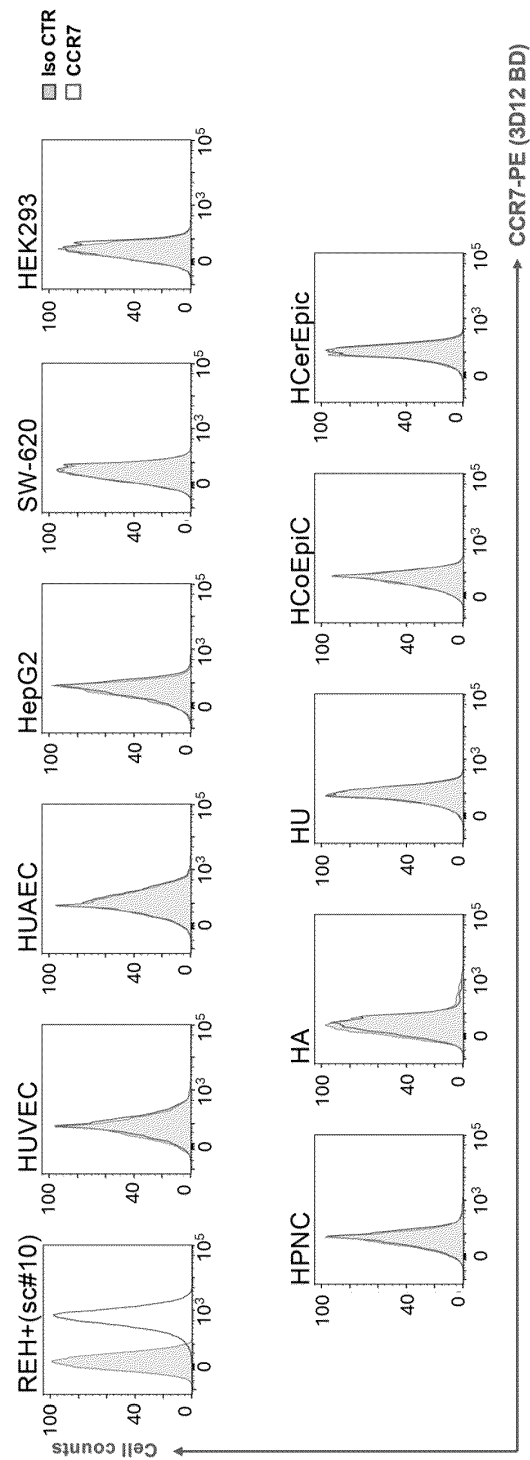


Fig. 18

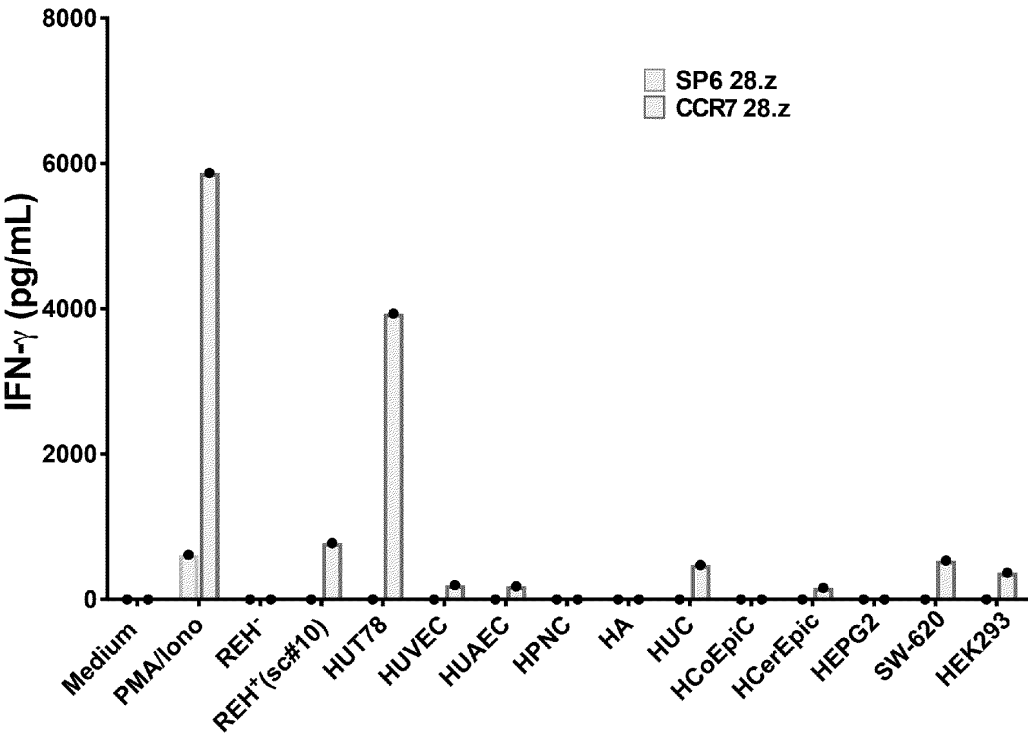


Fig. 19

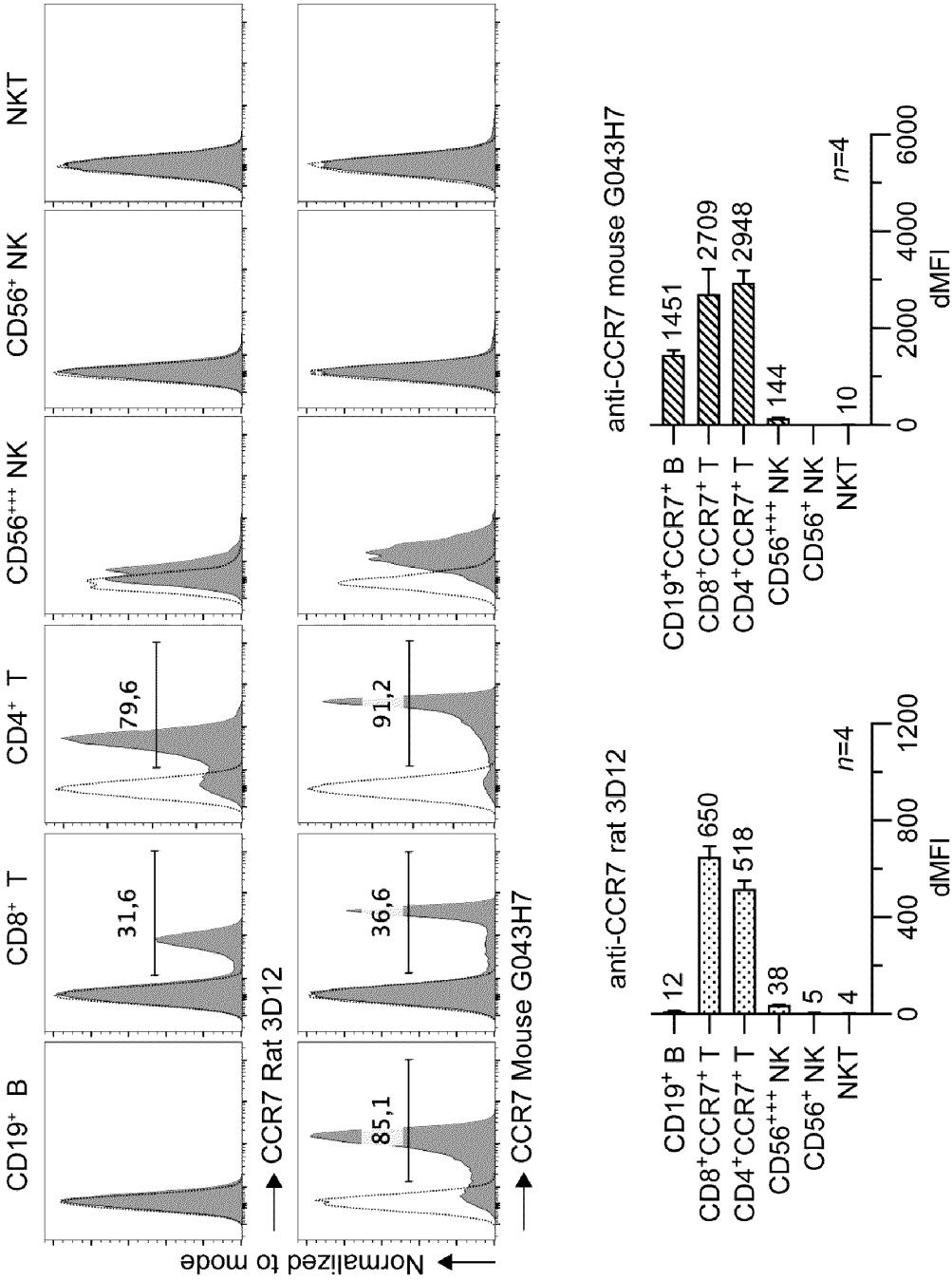


Fig. 20

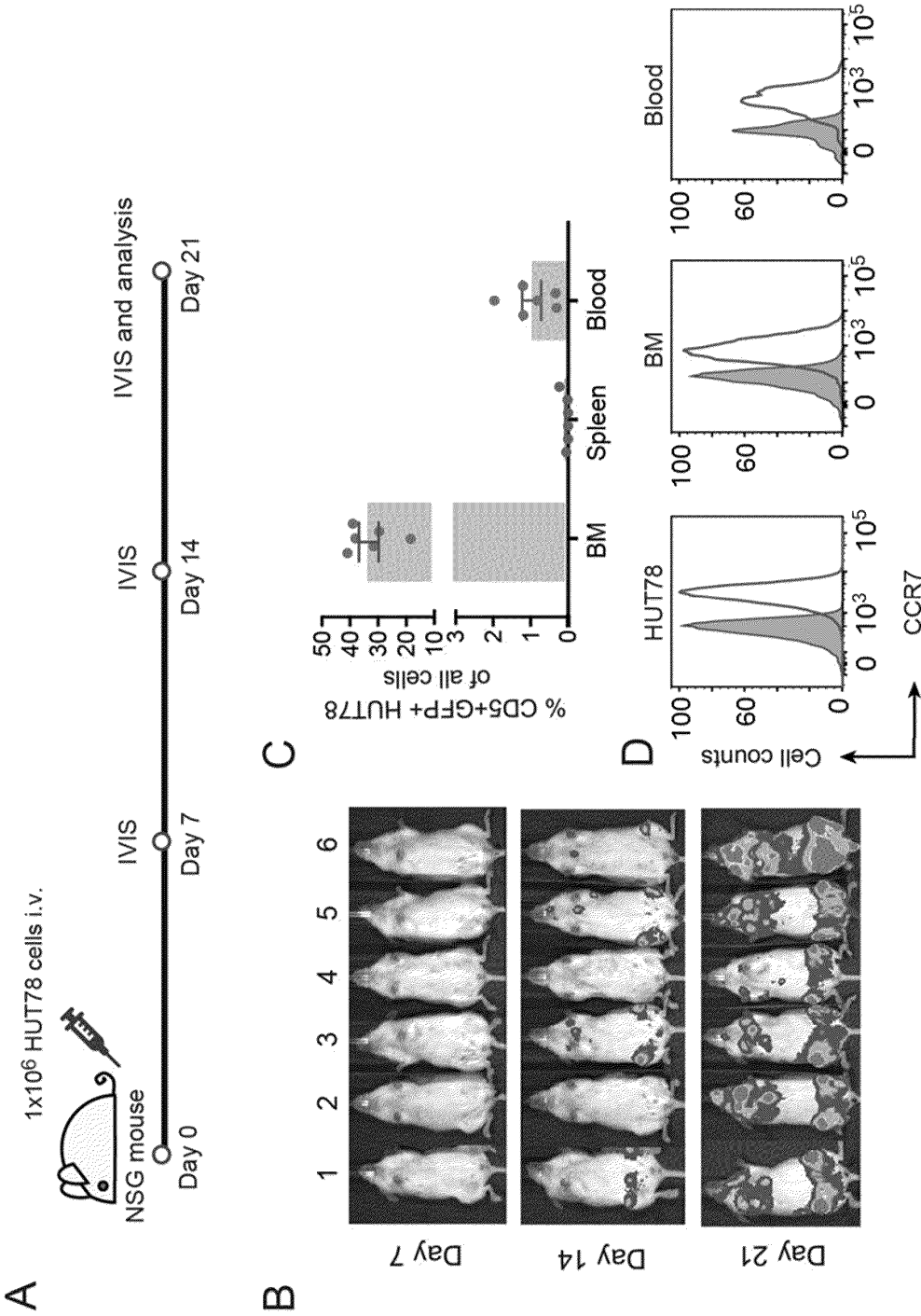


Fig. 21

