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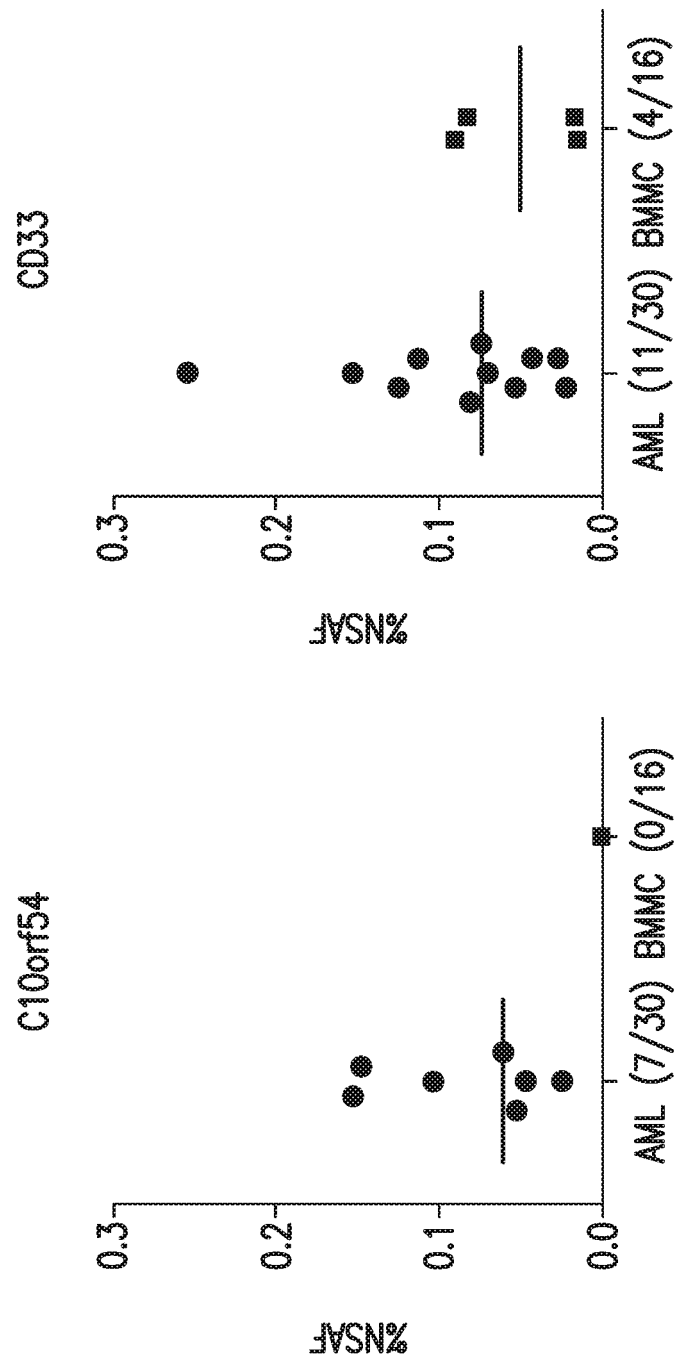


FIG. 1A

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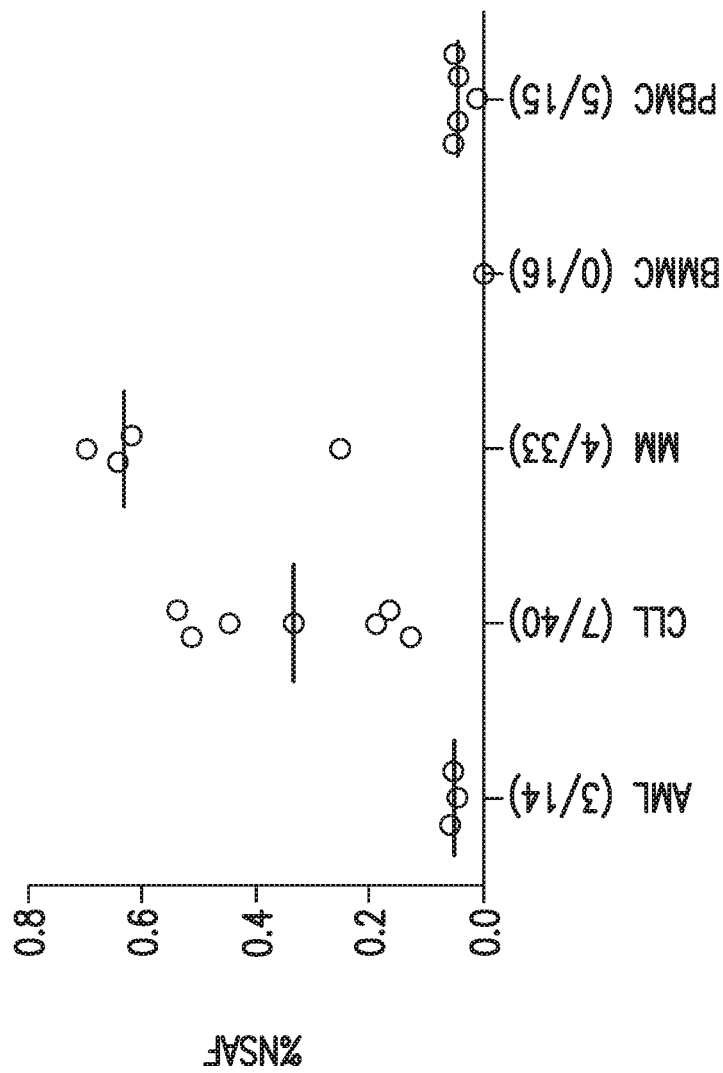


FIG. 1B

	CD13 ⁺ /CD33 ⁺				CD34 ⁺ /CD33 ⁺				CD34 ⁺ /CD33 ⁻			
	Incidence*	Pos, [%]	Fold MFI		Incidence*	Pos, [%]	Fold MFI		Incidence*	Pos, [%]	Fold MFI	
C100RF54												
AML	18/23 (3 relapses)	31	48.6		10/21 (3 relapses)	41	50.9		9/21 (3 relapses)	25	8.5	
BMNC	3/3	75	28.1		1/3	31	0.9		0/3	1.5	0.5	

FIG. 2

huVH1

Potential humanized sequence based on IMGT IGHV1-18 acceptor framework (method 1)
QVQLVQSGAEVKKPGASVKCKAS **GYFTSYGIS** WVRQAPGQGLEWMG **WISAYNGNTNYAQKLG** RVITMTDTSISTAYMELSLRSDDTAVYYCAR

Joining region

IMGT J00256|IGHJ4*01|YFDYWQGLTVTVSS

seq	10	20	30	40	50	60	70	80	90
	b b b	b b b	b b b	b i i	i i b b	b b	i b	b b b	b b b
76E1	EVQLVQSGAEVKKPGASVKISCKAS	GYSTGYNNN	WVKQSNKGKSLIEWIG	NIDPYDYTSYNLKFKD	KATLTVDKSSSTAYMQLKSLTSEDSAVYYCAT				
	* * *	* * *	* * *	* * *	* * *	* * *	* * *	* * *	*

huVH1a	QVQLVQSGAEVKKPGASVKVSKAS	GYSTGYNNN	WVRQAPGQGLEWMG	NIDPYDYTSYNLKFKD	RVITMTDTSISTAYMELSLRSDDTAVYYCAR				
	I	Q	S	I	E	Q	A	L	V
		S			S	S			
		D		A	A	D			
		A		A					

AbM	10	20	30	40	50	60	70	80	90
huVH1b	QVQLVQSGAEVKKPGASVKVSKAS	GYSTGYNNN	WVRQAPGQGLEWMG	NIDPYDYTSYAKLQ	RVITMTDTSISTAYMELSLRSDDTAVYYCAR				
	I	Q	S	I	E	F	A	L	V
		S			S				
		D		A					
		A							

seq	100	110
	ib	i b b b
76E1	STMITPFDY	WGQGTLTVTVSS
	**	
huVH1a	STMITPFDY	WGQGTLTVTVSS
	L	L
AbM	100a	110
huVH1b	STMITPFDY	WGQGTLTVTVSS
	L	L

- (1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international Immunogenetics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isocapsartate formation or Asp-Pro (DP) bond cleavage.

FIG. 3A

huVH3

Potential humanized sequence based on IMGT IGHV3-48 acceptor framework (method 2)
EVQLVESGGGLVQPGGSLRLSCAAS **GFTFSSYSIN** WVRQAPGKGLEWVS **YSSSSSTIYADSVKG** RFTISRDNAKNSLYQMNSLRAEDTAVYYCAR

Joining region

IMGT J00256|IGHJ4*01|YFDYWGQTLVTVSS

seq	10	20	30	40	50	60	70	80	90
	b b b	b b b	b b b	b i i	i i b b	i b	b b b	b b b	b b i b
76E1	EVQL	QS	GP	EL	EP	KG	AS	VK	IS
	EVQL	QS	GP	EL	EP	KG	AS	VK	IS
huVH3a	EVQL	VES	GGGL	VQ	PGG	SLRL	S	CAAS	
	Q	V I	Q	S	IG	E	Q	A L V K	S A M L
									I
AbM	10	20	30	40	50	60	70	80	90
huVH3b	EVQL	VES	GGGL	VQ	PGG	SLRL	S	CAAS	
	Q	V I	Q	S	IG	E	Q	A L V K	S A M L
									I

seq 100 110

76E1	STMITPFDY	WGQGT	TLVT	VSS
huVH3a	STMITPFDY	WGQGT	TLVT	VSS
AbM	100a	110		
huVH3b	STMITPFDY	WGQGT	TLVT	VSS

FIG. 3B

- (1) CDR sequences noted in bold.
- (2) Human germline and joining sequences from IMGT® the international Immunogenetics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
- (3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
- (4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
- (5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
- (6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
- (7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isocapsartate formation or Asp-Pro (DP) bond cleavage.

huVH1

Potential humanized sequence based on IMGT IGHV1-18 acceptor framework (method 1)

QVQLVQSGAEVKKPGASVKCKAS **GYTFSYGIS** WVRQAPGQGLEWMG **WISAYNGNTNYAQKLQG** RVTMTDTSTSTAYMELRSLRSDDTAVYYCAR

Joining region

IMGT 00256|IGHJ4*01|YFDYWGQGLTVTVSS

seq 10 20 30 40 50 60 70 80 90
b b b b b b b b i b b b b b b b b b
141A QVQLQSGAELMKPGASVKISCKAT **GYTFSRYWIE** WKQRPQHGLEWIG **EILPGSGSTNYNEKFKG** KATFTADTSSNTAYMQLSSLTSEDSAVYYCAG
* ** * * * * * * * * * * * * * * * *
huVH1a QVQLVQSGAEVKKPGASVKVCKAS **GYTFSRYWIE** WVRQAPGQGLEWMG **EILPGSGSTNYNEKFKG** RVTMTDTSTSTAYMELRSLRSDDTAVYYCAR
M I I Q Q A F A N G

AbM 10 20 30 40 50 a 60 70 abc 80 90
QVQLVQSGAEVKKPGASVKVCKAS **GYTFSRYWIE** WVRQAPGQGLEWMG **EILPGSGSTNYAQKLQG** RVTMTDTSTSTAYMELRSLRSDDTAVYYCAR
M I I Q S D A F A N G

seq 100 110 120
i b i b b b
141A **EEVDGYPWF**CGY WGQGLTVTVSA

huVH1a **EEVDGYPWF**CGY WGQGLTVTVSS
E S A

AbM 100abcd 110
huVH1b **EEVDGYPWF**CGY WGQGLTVTVSS
E S A

- (1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImmunoGenetics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
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(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isooaspartate formation or Asp-Pro (DP) bond cleavage.

seq	10	20	30	40	50	60	70	80	90
141A	b b b	b b b b	b b	b b i i	i i b b	i b	b b b	b b b	b b i b
	QVQLQQSGAELMKPCASVKISCKAT	GYTFSRYWIE	WVKQRPCHGLEWIG	EILPCSGSTINYEKFKG	KATFTADTSSNTAYMQLSSLISED	SAVYYCAG			
	* * * * *	* * * * *	* * *	* * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
huVH3a	EVQLVESGGGLVQPGGSLRLS	CAAS	GYTFSRYWIE	WVRQAPGKGLEWVS	EILPCSGSTINYEKFKG	RFTISRDNAKNSLYQMNSLRAED	IAVYYCAR		
	Q M V I		IG	Q Q	A F A I	A M L			

	10	20	30	40	50	60	70	80	90
AbM									
huVH3b	EVQLVESGGGLVQPGGSLRLS	CAAS	GYFSRYWIE	WYRQAPKGLEWVS	EILPGCGSTIN	YADSVKG	RTISRDNAKNSLYLQMN	SLRAEDIAVYYCAR	
	Q	M	V	I	IG	Q	F	A	F
						S	A	I	A
						D			
						A			
seq	100	110	120						
	ib	i	b	b	b				
41A	EEVIVNAPVQIEGAY	WQACTIVTUSA							

huVH3a	EEVDGYPWF^Y	WCQGLTVTSS	
	E		
	S		
	A		
AbM	100abcd	110	
huVH3b	EEVDGYPWF^Y	WCQGLTVTSS	
	E		
	S		
	A		

* (1) CDR sequences noted in bold.
 (2) Human germline and joining sequences from IMGT® the international ImmunoGenetics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
 (3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
 (4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
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 (6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
 (7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isocarpate formation or Asp-Pro (DP) bond cleavage.

huVH1

Potential humanized sequence based on IMGT IGHV1-18 acceptor framework (method 1)
QVQLVQSGAEVKKPGASVKCKAS **GYFTSYGIS** WVRQAPGQGLEWMG **WISAYNGNTNYACKLQG** RVTMTIDTSTAYMELRSLRSDDTAVYYCAR

Joining region

IMGT J00256|IGHJ4*01|YFDYWGQTLVTSS

seq	10	20	30	40	50	60	70	80	90
	b b b	b b b	b b b	b i i	i i b b	b b	b b b	b b b	b b b
175A	QVQLQSGAELMKPGASVKISCKAT	GYTFSTHWIE	WVKQRPQGHGLEWIG	EILPGSGSTSYNEKFKG	KATFTADTSSNTAYMQLSSLTSEDSAVYYCAR				
	*	**	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*
huVH1a	QVQLVQSGAEVKKPGASVKVSKAS	GYTFSTHWIE	WVRQAPGQGLEWMG	EILPGSGSTSYNEKFKG	RVTMTIDTSTAYMELRSLRSDDTAVYYCAR				
	I		I			Q	A F A		

AbM	10	20	30	40	50	60	70	80	90
huVH1b	QVQLVQSGAEVKKPGASVKVSKAS	GYTFSTHWIE	WVRQAPGQGLEWMG	EILPGSGSTSYAQKLQG	RVTMTIDTSTAYMELRSLRSDDTAVYYCAR				
		I		I		F	A F A		

seq	100	110
	ib	i b b b
175A	WLLYYAYNDY	WGQGTSLVTSS
		*
huVH1a	WLLYYAYNDY	WGQGTSLVTSS
AbM	100ab	110
huVH1b	WLLYYAYNDY	WGQGTSLVTSS

- (1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImmunoGenetics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isospartate formation or Asp-Pro (DP) bond cleavage.

FIG. 5A

huVH3

Potential humanized sequence based on IMGT IGHV3-48 acceptor framework (method 2)
EVQLVESGGGLVQPGGSLRLSCAAS **GYTFSSYN** WVRQAPGKGLEWVS **YISSSSTIYADSVKG** RFTISRDNKNSLYLQMNSLRAEDTAVYYCAR

Joining region
IMGT J00256|IGHJ4*01|YFDYWGQTLVTSS

seq	10	20	30	40	50	60	70	80	90
	b b b	b b b	b b b	b i i	i i b b	b b b	b b b	b b b	b b b
175A	QVQLQQSGAELMKPGASVKISCKAT	GYTFSTHWIE	WVKQRPQGHGLEWIG	EILPGSGSTSYNEKFKG	KATFTADTSSNTAYMQLSSLTSEDSAVYYCAR				
	* * * * *	* * * * *	* * *						
huVH3a	EVQLVESGGGLVQPGGSLRLSCAAS	GYTFSTHWIE	WVRQAPGKGLEWVS	<u>EILPGSGSTSYNEKFKG</u>	RFTISRDNKNSLYLQMNSLRAEDTAVYYCAR				
	Q	V I	<u>IG</u>	Q	A F A I	A M L			

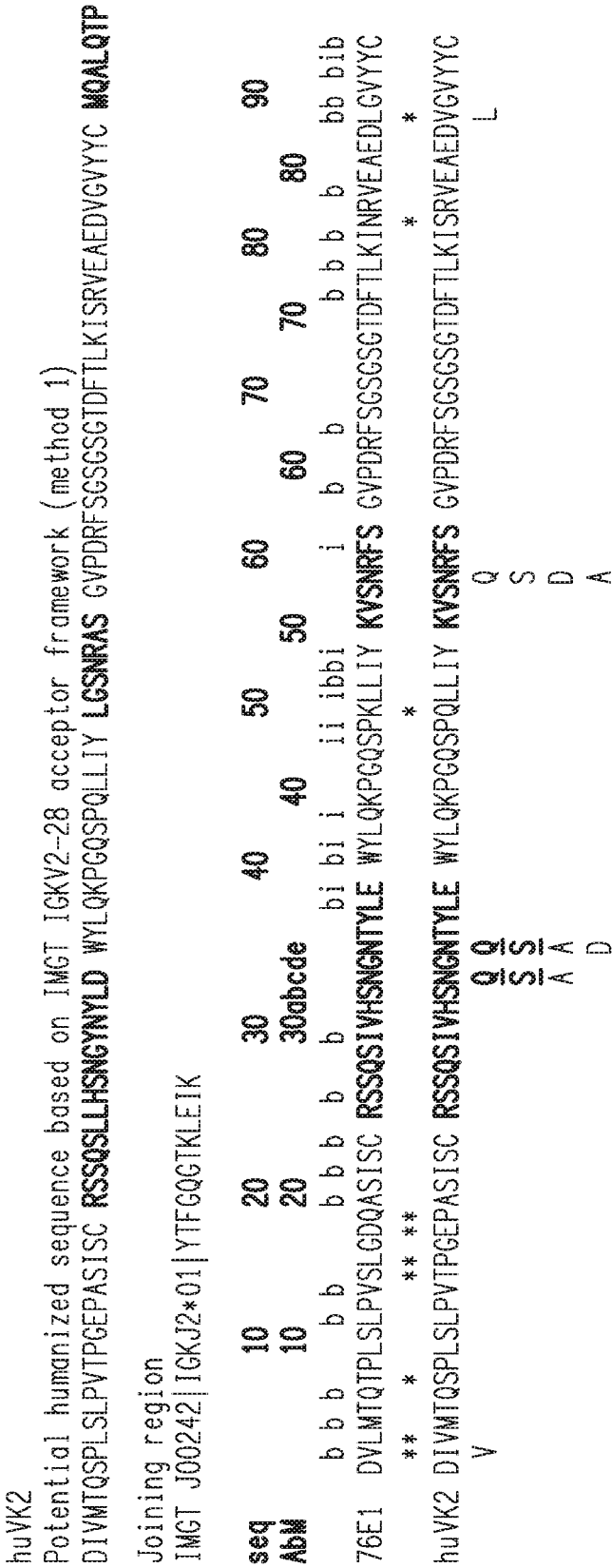
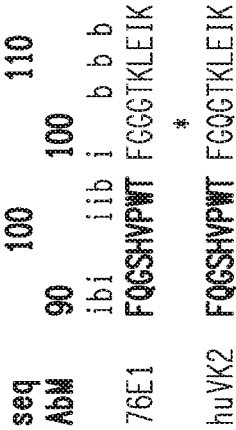
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AbM	10	20	30	40	50	60	70	80	90
huVH3b	EVQLVESGGGLVQPGGSLRLSCAAS	GYTFSTHWIE	WVRQAPGKGLEWVS	<u>EILPGSGSTSYADSVKG</u>	RFTISRDNKNSLYLQMNSLRAEDTAVYYCAR				
	Q	V I	<u>IG</u>	F	A F A I	A M L			

seq	100	110
	ib	i b b b
175A	WLLYYAYNDY WGQGTSLVTSS	*
huVH3a	WLLYYAYNDY WGQGTSLVTSS	
AbM	100ab	110
huVH3b	WLLYYAYNDY WGQGTSLVTSS	

- (1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international Immunogenetics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isospartate formation or Asp-Pro (DP) bond cleavage.

FIG. 5B



- (1) CDR sequences noted in bold.
- (2) Human germline and joining sequences from IMGT® the international Immunogenetics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
- (3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
- (4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
- (5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
- (6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
- (7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isocarpate formation or Asp-Pro (DP) bond cleavage.

FIG. 6A

huVK1
Potential humanized sequence based on IMGT IGKV1-39 acceptor framework (method 2)
DIQMTQSPSSLSASVGRVTITC **RASQISSYLN** WYQKPGKAPKLLIY **AASSLQS** GVPDRFSGSGCTDFTLTISSLQPEDFATYYC **QQSYSTP**

Joining region
IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30abcde	40	50	60	70	80	
	b b b	b b b	b b b	b i b i	i i i b b i	i b b	b b b	b b b	b b b
76E1	DVLM	IQTP	LSPL	VS	LG	DA	SIC	RSSQSI	VH SGNTYLE
	**	*	*	*	*	*	*	*	*
	**	*	*	*	*	*	*	*	*
huVK1	DIQMTQSPSSLSASVGRVTITC	RSSQSI	VH SGNTYLE	WYQKPGKAPKLLIY	KVSNRFS	GVPDRFSGSGCTDFTLTISSLQPEDFATYYC			
	V	V	A	S	Q	V	LG		

seq	100	110
AbM	90	100
	ibi	iib i b b b
76E1	FGGSHVPWT	FGG GTKLEIK
	*	
huVK1	FGGSHVPWT	FGG GTKLEIK

- (1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international Immunogenetics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isooxalate formation or Asp-Pro (DP) bond cleavage.

FIG. 6B

huVK3
Potential humanized sequence based on IMGT IGKV3-20 acceptor framework (method 1)
EIVLTQSPGTLSPGERATLSC **RASQVSSSYLA** WYQKPGQAPRLIIY **CASSRAT** GIPDRFSGSGCTDFTLTISRLEPEDFAVYYC **QQYGSSP**

Joining region
IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

seq	10	20	30	40	50	60	70	80
AbM	10	20	34	40	50	60	70	80
141A	b b b	b b b	b b b	i i i b b	i b b	b b b	b b b	b b b
	b b b	b b b	b b b	i i i b b	i b b	b b b	b b b	b b b
141A	QIVLSQSPAILSAPGEKVTMT	C RASSLSYMH	WYQKPGCSSPKWIY	ATSNLAS	GVPARFSGSGCTSYSLTISRVEAEDAATYYC			
	* * *	* * *	* * *	* * *	* * *	* * *	* * *	* * *
huVK3	EIVLTQSPGTLSPGERATLSC	RASSLSYMH	WYQKPGQAPRLIIY	ATSNLAS	GIPDRFSGSGCTDFTLTISRLEPEDFAVYYC			
	A	V M	S P W	Q V	Y V			

seq	90	100
AbM	90	100
141A	ibi iib i	b b b
	QQWSSNPYT	FGGGTKLEIK
	*	
huVK3	QQWSSNPYT	FGGGTKLEIK
	Q	
	S	
	A	

- (1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international Immunogenetics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isospartate formation or Asp-Pro (DP) bond cleavage.

FIG. 7A

huVK1
Potential humanized sequence based on IMGT IGKV1-39 acceptor framework (method 2)
DIQMTQSPSSLSASVGRVTITC **RASQISSYLN** WYQKPGKAPKLLIY **AASSLQS** GVPFRFSGSGCTDFTLTISLQPEDFATYYC **QQSYSTP**

Joining region
IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

seq	10	20	30	40	50	60	70	80
AbM	10	20	34	40	50	60	70	80
141A	b b b	b b b	b b i i	i i i b b i	i b b	b b b b	b b b	b b i b
	QIVLSQSPAILSAPGEKVTMTC	RASSLSYMH	WYQKPGCSSPKWIY	ATSNLAS	GVPARFSGSGCTSYSLTISRVEAEDAATYYC			
	* * * *	* * * *	* * *	* * *	* * * *			
huVK1	DIQMTQSPSSLSASVGRVTITC	RASSLSYMH	WYQKPGKAPKLLIY	ATSNLAS	GVPFRFSGSGCTDFTLTISLQPEDFATYYC			
	L	M	S	P W	Q	Y	V	

seq	90	100
AbM	90	100
141A	ibi iib i	b b b
	QQWSSNPYT	FGGGTKLEIK
	*	
huVK1	QQWSSNPYT	FGGGTKLEIK
	Q	
	S	
	A	

- (1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImmunoGenetics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isooxalate formation or Asp-Pro (DP) bond cleavage.

FIG. 7B

huVK1
Potential humanized sequence based on IMGT IGV1-39 acceptor framework (method 2)
DIQMTQSPSSLSASVGRVTITC **RASQISSYLN** WYQKPGKAPKLLIY **AASSLOS** GVPSRFGSGSGTDFTLTISSLQPEDFATYYC **QQSYSTP**

Joining region
IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30abcde	40	50	60	70	80	
	b b b	b b b	b b b	b i b i	i i i b b i	i b b	b b b	b b b	b b b
175A	DVLMITQIPLSLPVSLGDAISCS	RSSQSI VHSGNTYLE	WYQKPGKAPKLLIY	KLSNRFS	GVPSRFGSGSGTDFTLTKISRVEAEDLGYYC				
	** * * * *	** * *							
huVK1	DIQMTQSPSSLSASVGRVTITC	RSSQSI VHSGNTYLE	WYQKPGKAPKLLIY	KLSNRFS	GVPSRFGSGSGTDFTLTISSLQPEDFATYYC				
	V	V	A	S	Q	V	LG		
				<u>Q</u> <u>Q</u>					
				<u>S</u> <u>S</u>	S				
				A A	D				
					A				

seq	100	110
AbM	90	100
	i b i	i b b
175A	FQGSIFPYT FGQGTKLEIK	
	*	
huVK1	FQGSIFPYT FGQGTKLEIK	

- (1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international Immunogenetics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isooxalate formation or Asp-Pro (DP) bond cleavage.

FIG. 8B

76E1 VH
EVQLLQSGPELEKPGASVKISCKAS**GYSF****AAAAAAAAAWVKQSNK**SL**EWIGAI****AAAAAAAAAAAAAAAA**AKATLTVDKSSSTAYMQLKSLTSEDSAVYYC
ATA**AAAAAFDY**WGQGTLLTVSS (SEQ ID NO: 1143)
human subgroup I

141A VH
QVQLQQSGAELMKPGASVKISCKAT**GYTF****AAAAAAAAAWVKQRP**GH**LEWIGAI****AAAAAAAAAAAAAAAA**AKATFTADTSSNTAYMQLSSLTSEDSAVYYC
AG**AAAAAAAAAAAAAAAA**WGQGTLLTVSA (SEQ ID NO: 1144)
human subgroup I

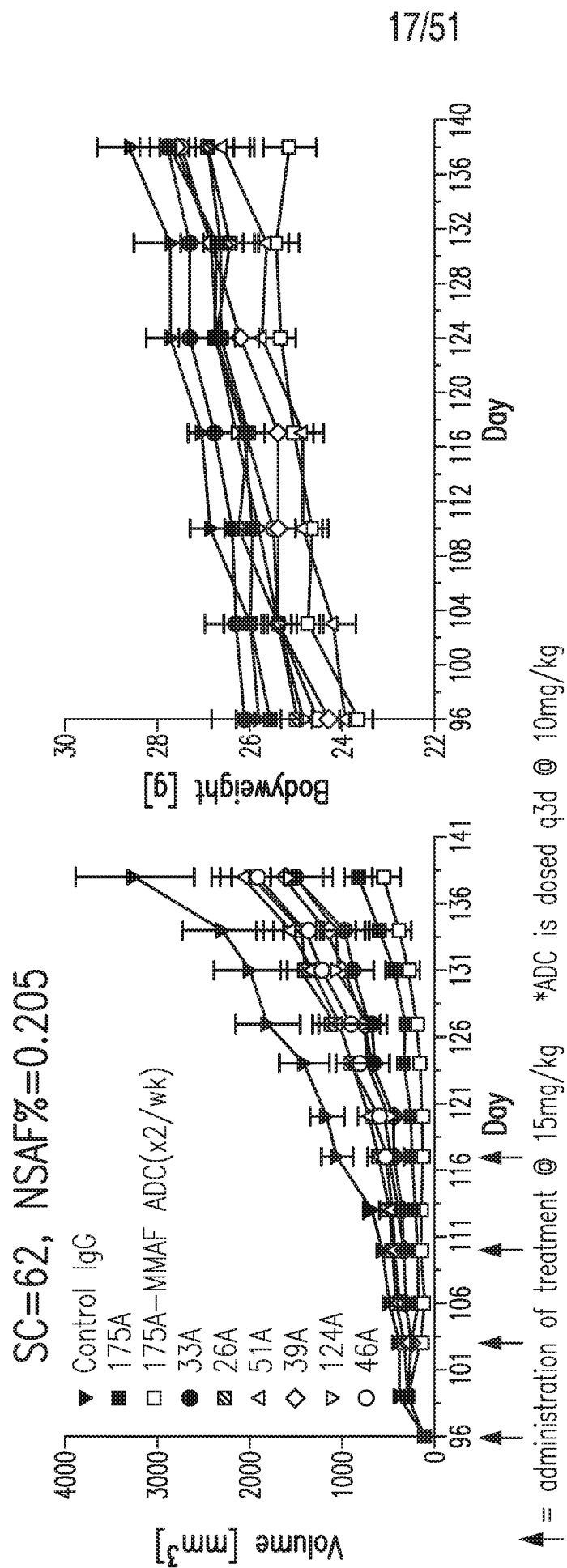
175A VH
QVQLQQSGAELMKPGASVKISCKAT**GYTF****AAAAAAAAAWVKQRP**GH**LEWIGAI****AAAAAAAAAAAAAAAA**AKATFTADTSSNTAYMQLSSLTSEDSAVYYC
AR**AAAAAYANDY**WGQGTSTVTVSS (SEQ ID NO: 1145)
human subgroup I

76E1 VL
DVLMTQTPLSLPVSLGDQASIS**CRSSQ****AAAAAAAAAWLQKPGQSPKLLIY****AAAAAAAAAGVPDR**FGSGSGTDFTLKINRVEAEDLGYY**CAQA**
AAPATFGGGTKLEIK (SEQ ID NO: 1146)
human kappa II

141A VL
QIVLSQSPAILSAPGEKVT**MTCR****AS****AAAAAAAAAWYQKPGSSPKWII****YAA**N**LA**SGV**PAR**FGSGSGTSYSLTISRVEAEDAATYY**CCQ****AAAA**PAT
FGGGTKLEIK (SEQ ID NO: 1147)
human kappa III

175A VL
DVLMTQTPLSLPVSLGDQASIS**CRSSQ****AAAAAAAAAWLQKPGQSPKLLIY****AAAAAAAAAGVPDR**FGSGSGTDFTLKISRVEAEDLGYY**CAQA**
AAPATFGGGTKLEIK (SEQ ID NO: 1148)
human kappa II

FIG. 9



Kasumi-3 NOD	Control IgG2a	175A	175A- MMAF	33A	26A	51A	39A	124A	46A
Volume±SD	3255±1704	833±429	555±511	1514±1156	1982±997	1668±638	2039±1102	1305±674	1925±791
TGI	-	-77	-86	-55	-41	-51	-39	-62	-42
p-Value	-	0.0088	0.0050	0.0447	0.1154	0.0507	0.1370	0.0363	0.0937

FIG. 10

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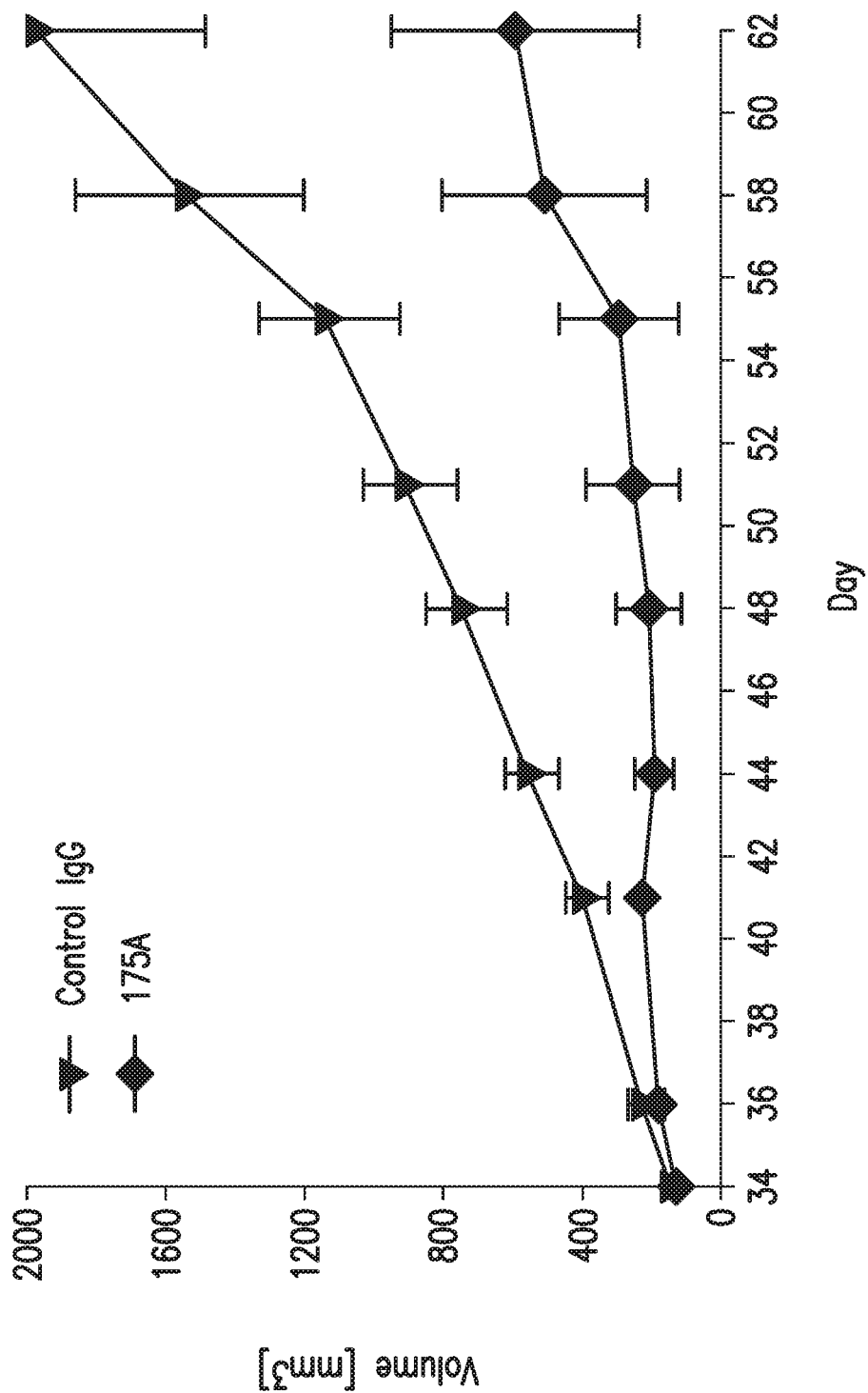


FIG. 11

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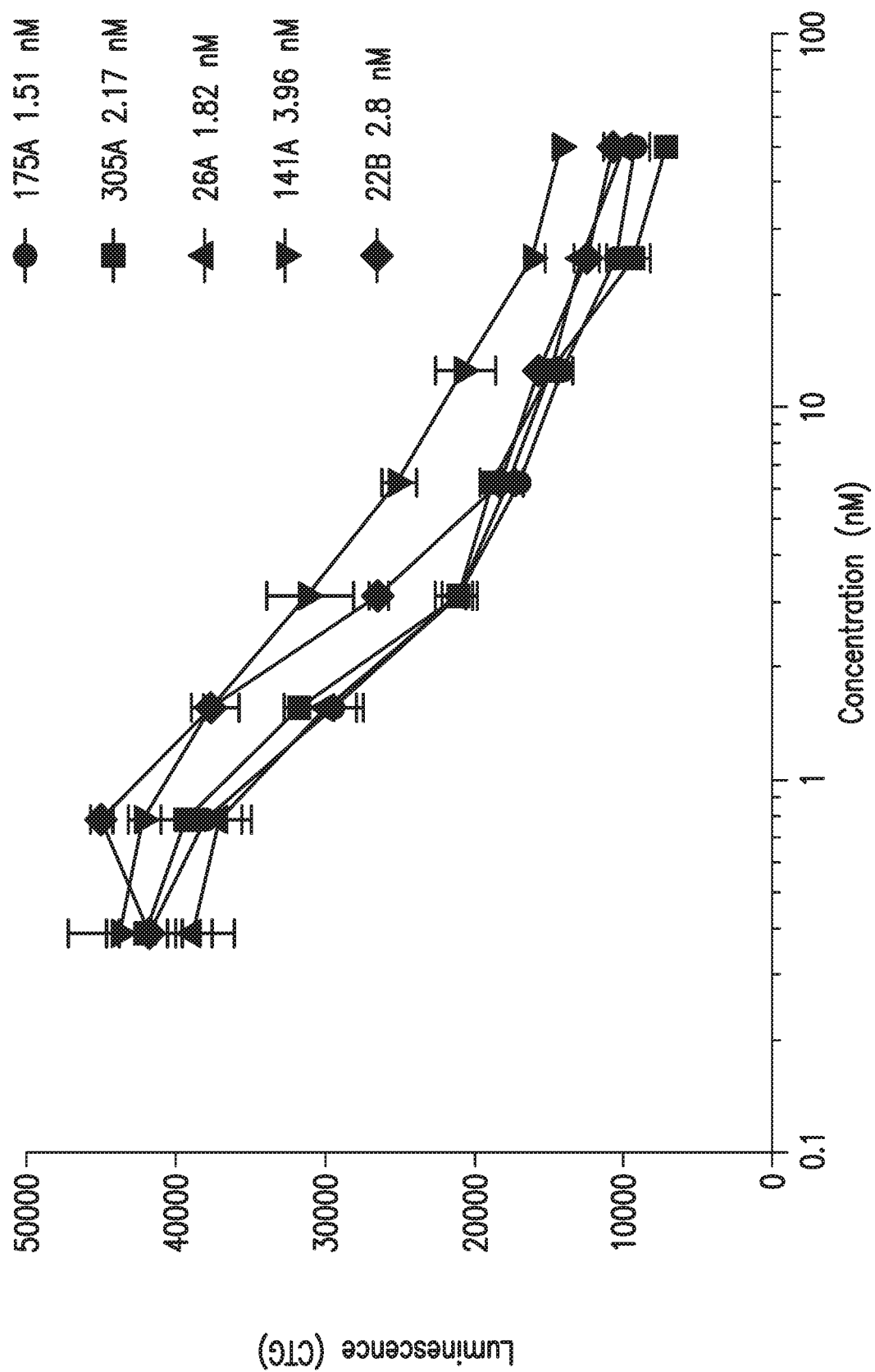


FIG. 12

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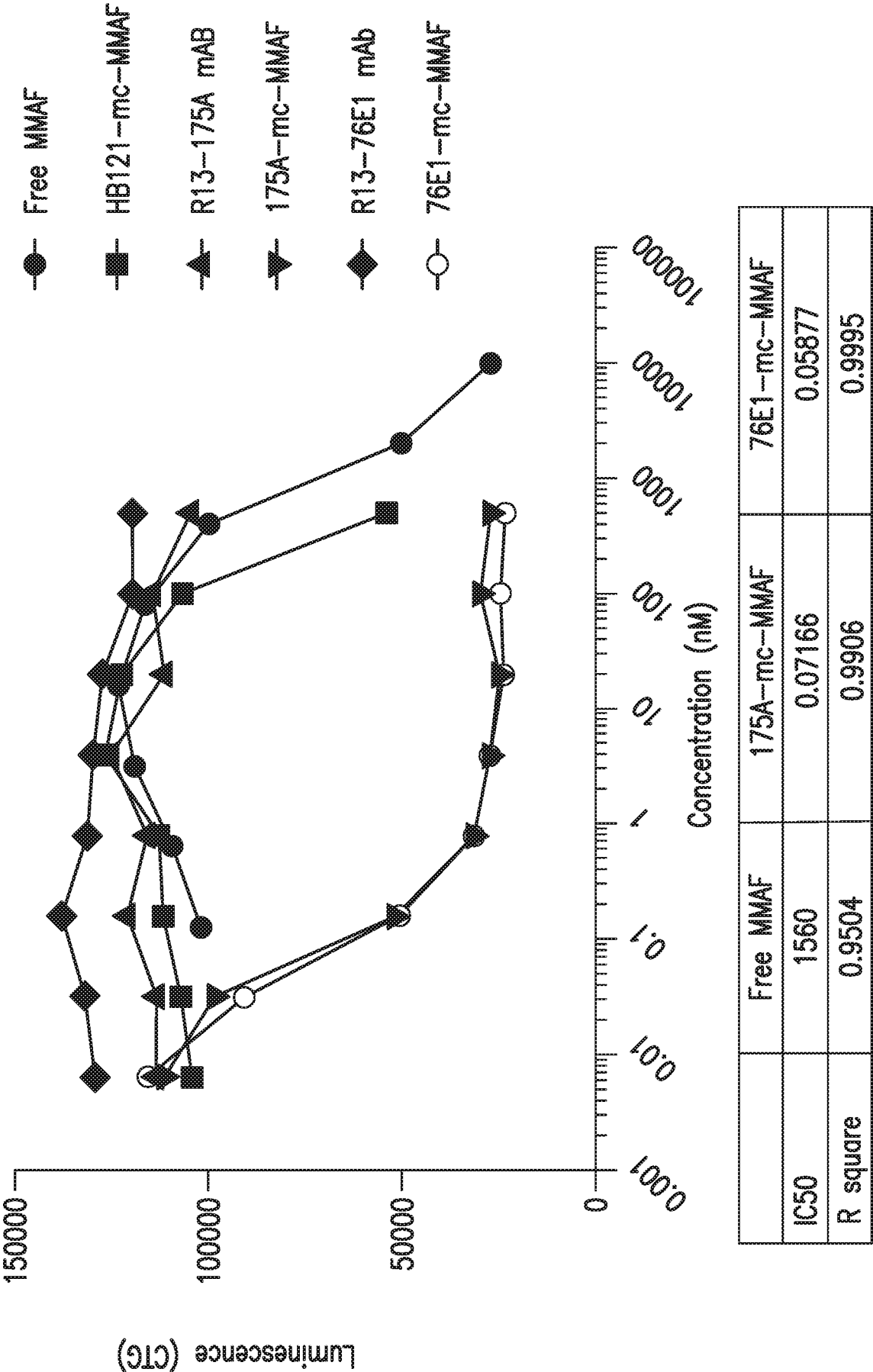


FIG. 13

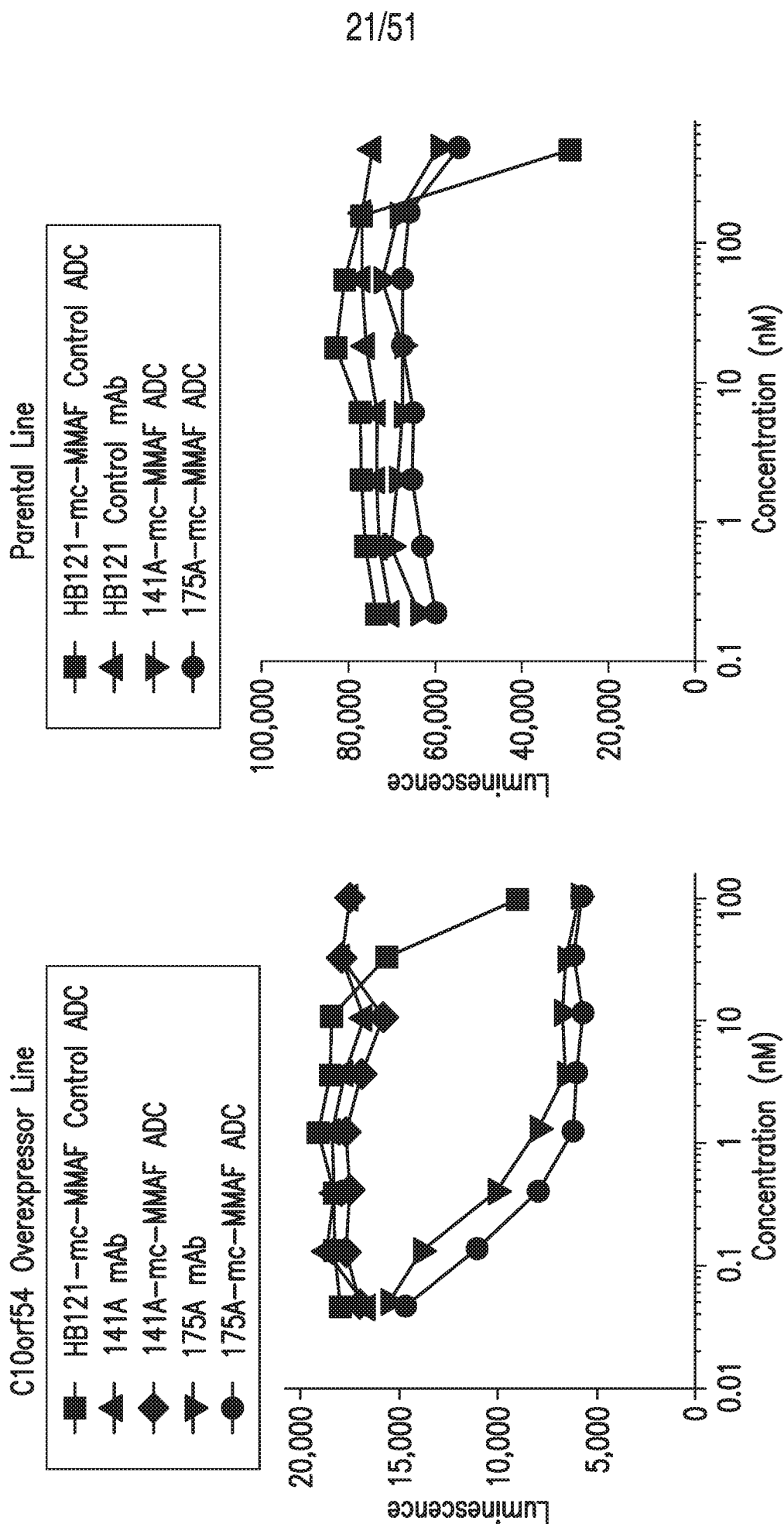


FIG. 14

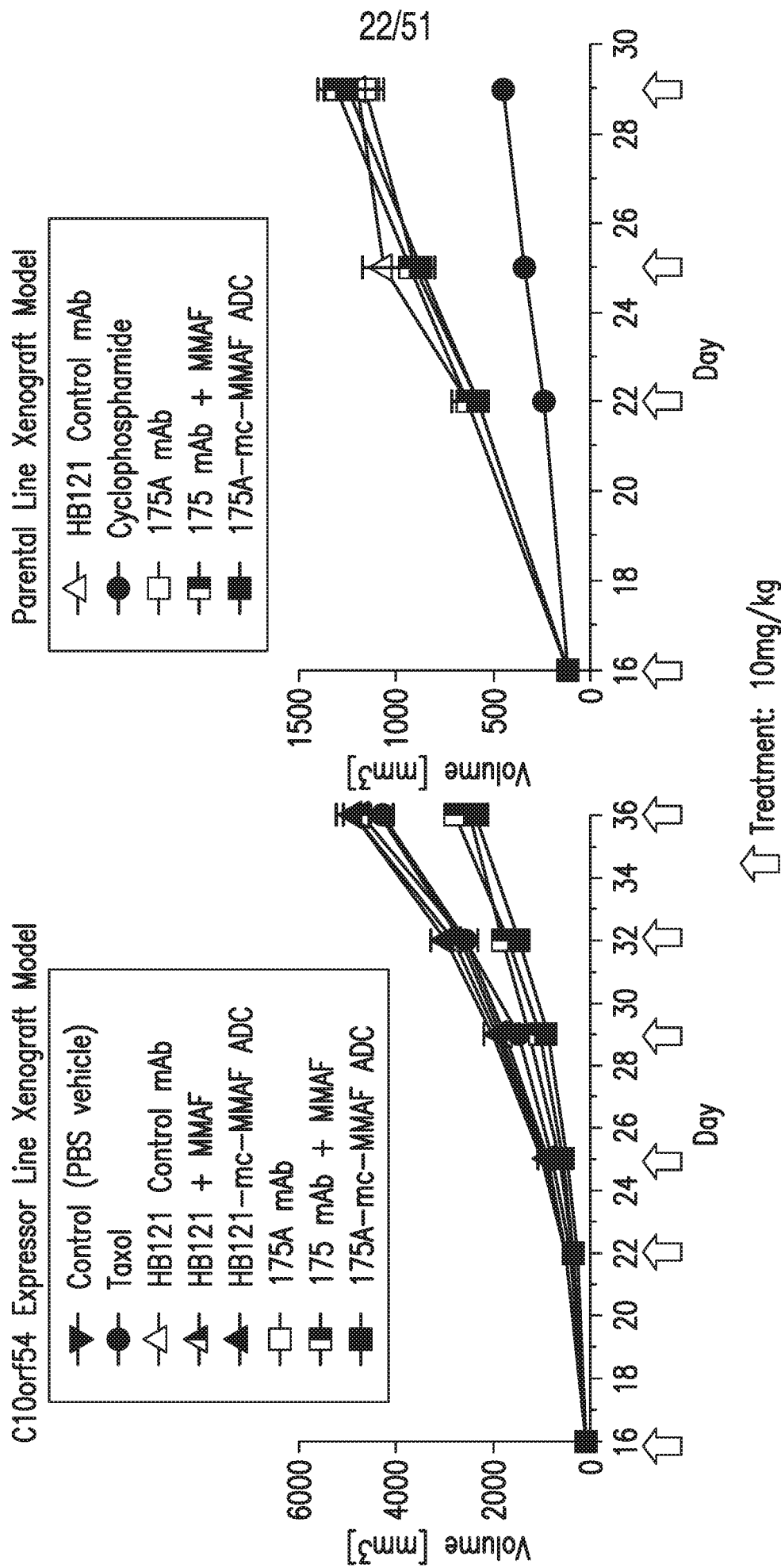


FIG. 15

R13 VH									
R13-3610-76E1 MGWTWIFILILSVTTGVHS									
R13-3610-141A MEWTWVFLFLLSVTAGVHS									
R13-3610-175A MEWTWVFLFLLSVTAGVHS									
Kabat	1	10	22	31-35	40	50-0-60-65			
AbM	1	10	22	26-35	40	50-0-58 65			
Chothia	1	10	22	26-32	40	0-55 65			
Contact	1	10	22	30-35	40	47-0-58 65			
IMGT	1	23	27-38	41	56-65	74			
76E1 EVQLQQSGPELEKPGASVKISCKAS GYSFTGYNMN WVKQSNKGSLEWIG NIDPYDYTSYNLKFQD									
141A QVQLQQSGAELMKPGASVKISCKAT GYTFERYWIE WVKQRPCHGLEWIG EILPGSGSTINYEKFKG									
175A QVQLQQSGAELMKPGASVKISCKAT GYTFSTHWIE WVKQRPCHGLEWIG EILPGSGSTSYNEKFKG									
Kabat	70	80	abc	90	95-100-102	110			
AbM	70	80	abc	90	95-100-102	110			
Chothia	70	80	abc	90	96-100-101	110			
Contact	70	80	abc	90	93-100-101	110			
IMGT	75	89	105-117						
76E1 KATLTVDKSSSTAYMQLSLTSEDSAVYYCAT STMITP---FDY WGQGTTLTVSS									
141A KATFTADTSSNTAYMQLSSLTSEDSAVYYCAG EEVYDGYPWFGY WGQGTILVTVSA									
175A KATFTADTSSNTAYMQLSSLTSEDSAVYYCAR WLLYYA---MDY WGQGTSTVTSS									

FIG. 16A

R13-3610-76E1 MKLPVRLVLVFWIPASS
R13-3610-141A MDFQVQIFSLLISASVMSRG
R13-3610-175A MKLPVRLVLVFWIPASS

Kabat	1	10	20	24-27abcd	34	40	50-56
AbM	1	10	20	24	30abcd	40	50-56
Chothia	1	10	20	26	30abcd-32	40	50-
Contact	1	10	20	30abcd	36	40	46-55
IMGT	1		23	27	38	41	56-65 69

76E1 DVLMQTPLSLPVS LGDQASISC RSSQSIVHSNGNTYLE WYLQKPGQSPKLLIY KVSNRFS
141A QIVLSQSPAILSASPGKEKVTMT C RASSL-----SYMH WYQKPGSSPKPIY ATSNLAS
175A DVLMQTPLSLPVS LGDQASISC RSSQSIVHSNGNTYLE WYLQKPGQSPKLLIY KLSNRFS

Antibody	60	70	80	89—97
Kabat	60	70	80	89—97
AbM	60	70	80	89—97
Chothia	60	70	80	91—96
Contact	60	70	80	89—96
IMGT	70	89	105—117	
76E1	GVPDRFSGSGTDFTLKINRVEAEDLGVYYC FQGSHPWT FGGGTKLEIK			
141A	GVPARFSGSGTSVSLTISRVEADAATYYC QQWSSNPYT FGGGTKLEIK			
175A	GVPDRFSGSGTDFTLKISRVEAEDLGVYYC FQGSHPYT FGGGTKLEIK			

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R13 VL													
AbM	1	10	20	24	30abcd	34	40	50	56				
hu141A	EIVLTQSPGTLSPGERATLSC RASSL-----SYMH WYQKPGQAPRPWIY ATSNLAS												
hu76E1	DIVMTQSPSLPVTGPASISC RSSQSI VHSNGNTYLE WYLQKPGQSPQLLIY KVSNRFS												
hu175A	DIVMTQSPSLPVTGPASISC RSSQSI VHSNGNTYLE WYLQKPGQSPQLLIY KLSNRFS												
consen	<i>DIVMTQSPSLPVTGPASISC RSSQSIVHSNGNTYLE WYLQKPGQSPQLLIY KVSNRFS</i>												
	<i>V</i>												
	<i>L</i>												
AbM	60	70	80	89	97								
hu141A	GIPDRFSGSGTDYTLTISRLEPEDFAVYYC QQWSSNPYT FGQGTKLEIK (SEQ ID NO: 1139)												
hu76E1	GVPDRFSGSGTDFTLKISRVEAEDVGVYYC FGQSHVPWT FGQGTKLEIK (SEQ ID NO: 1140)												
hu175A	GVPDRFSGSGTDFTLKISRVEAEDVGVYYC FGQSHFPYT FGQGTKLEIK (SEQ ID NO: 1141)												
consen	<i>GVPDRFSGSGTDFTLKISRVEAEDVGVYYC FGQSHXPYT FGQGTKLEIK (SEQ ID NO: 1142)</i>												
	<i>V W</i>												
	<i>F Y</i>												

FIG. 17B

VH Domains									
AbM#	10	20	26	30	35	40	50	a	65
5B	QVQLQQSGAELVRPGSVKISCKG	GYTFD-YGMH	WVKQSHAKSLEWIG	IIDTYGDAYNQKFKG					
46A	QVQLQQAGGELVRPGSVKISCKG	GYTFD-YGMH	WVKQSHAKSLEWIG	IINTYYGDATYNQKFKG					
97A	QVQLQQSGAELVRPGSVKISCKG	GYTFD-YGMH	WVKQSHAKSLEWIG	VIDTYGDASNQKFKG					
128A	QVQLQQSGAELVRPGSVKISCKG	GYTFD-YGMH	WVKQSHAKSLEWIG	LIDTYGDATYNHFKG					
146C	QVQLQQSGAELVRPGSVKISCKG	GYTFD-YGMH	WVKQSHAKSLEWIG	LIDTYGDATYNHFKG					
208A	QVQLQQSGAELVRPGSVKISCKG	GYTFD-YGMH	WVKQSHAKSLEWIG	VIDTYGDAGYNQKFKG					
consensus			GYTFD-YGMH					*I*TYYGDA**N*KFKG	
215A	EVQLQQSGPELVKPGASMKISCKAS	GFSFTG-YTMN	WVKQSHGKNLEWIG	LISPYNGGTSYNQKFKG					
26A	EVQLQQSGPELVKPGASMKISCKAS	GFSFTG-YTMN	WVKQSHVKNLEWIG	LISPYNGGTSYNQKFKG					
164A	EVQLQQSGPELEKPGASVKISCKAS	GYSFTG-YNMN	WVKQSNQKSLEWIG	NIDPYYGASYNQKFKG					
230A	EVQLQQSGPELEKPGASVKISCKAS	GYSFTG-SNMN	WVKQNNQKSLEWIG	NIDPYGYTTYNQKFKG					
76E1	EVQLQQSGPELEKPGASVKISCKAS	GYSFTG-YNMN	WVKQSNQKSLEWIG	NIDPYDYTSYNLKFKD					
53A	EVQLQQSGPELVKPGASVKMSCKAS	GYTFTS-YFMH	WVKQKPGGLEWIG	YIYPYNDGTYNEKFKG					
259A	EVQLQQSGPELVKPGASVKMSCKAS	GYTFTS-YFMH	WVKQKPGGLEWIG	YIYPYNDGTYNEKFKG					
consensus			GYTFTS-YFMH					YIYPYNDGTYNEKFKG	
33A	QVQLQQSGAELMKPGASVKISCKAT	GYTFSS-YWIE	WVKQRPBGHLEWIG	EILPGSGSTSYNEKFKG					
39A	QVQLQQSGAELMKPGASVKISCKAT	GYTFSS-NWIE	WVKQRPBGHLEWIG	EILPGSGSTSYNEKFKG					
124A	QVQLQQSGAELMKPGASVKISCKAT	GYTFSS-NWIE	WVKQRPBGHLEWIG	EILPGSGSTSYNEKFKG					
175A	QVQLQQSGAELMKPGASVKISCKAT	GYTFST-HWIE	WVKQRPBGHLEWIG	EILPGSGSTSYNEKFKG					
321D	QVQLQQSGAELMKPGAAVKISCKAT	GYTFSS-HWIE	WVKQRPBGHLEWIG	EILPGSGSTDYNEKFKG					
consensus			GYTFSS-HWIE					EILPGSGST*YNEKFKG	
141A	QVQLQQSGAELMKPGASVKISCKAT	GYTFSR-YWIE	WVKQRPBGHLEWIG	EILPGSGSTNYNEKFKG					
51A	QVQLQQSGAELMKPGASVKISCKAT	GYTFSR-YWIE	WVKQRPBGHLEWIG	EILPGSGSTNYNEKFKG					
consensus			GYTFSR-YWIE					EILPGSGSTNYNEKFKG	
353A	EVKLLESGGLVQPGGSLKLSAAS	GFDFSR-YWMN	WVRQAPGKGLEWIG	EINPDSSTINYTPSLKD					
305A	DVQLQESGPGLVKPSQSLSLTCSVT	CYSITSGYYWN	WIRQFPGNKLEWIG	YIS-YDGSNNYNPSSLKN					

FIG. 18A

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AbM#	70	80	abc	90	95	100	102	110
5B	KATMTVDKSSSTAYMELARLTSED	SAIYYCAR	RAGNAM	-----	DY	WGQGTSVT	VS	
46A	KATMTVDKSSSTAYMELARLTSED	SAIYYCAR	RAGTAM	-----	DY	WGQGTSVT	VS	
97A	KATMTVDKSSSTAYMELARLTSED	SAIYYCAR	RAGNAM	-----	DY	WGQGTSVT	VS	
128A	KATMTVDKSSRTAYMELARLTSED	SAIYYCAR	RAGNAM	-----	DY	WGQGTSVT	AS	
146C	KATMTVDKSSRTAYMELARLTSED	SAIYYCAR	RAGNAM	-----	DY	WGQGTSVT	AS	
208A	KATMTVDKSSSTAYMELARLTSED	SAIYYCAR	RAGNAM	-----	DY	WGQGTSVT	VS	
consensus			RAGNAM	-----	DY			
215A	KATLTVDKSSSTAYMELLSLTSED	SAVYYCAR	RAYGYAM	-----	DY	WGQGTSVT	VS	
26A	KATLTVDKSSSTAYMELLSLTSED	SAVYYCAR	RAYGYAM	-----	DY	WGQGTSVT	VS	
164A	KATLTVDKSSSTAYMQLKSLTSED	SAVYYCTR	SNYGYGYF	-----	DV	WGAGTTVT	VS	
230A	KATLTVDKSSSTAYMQLKSLTSED	SAVYYCAR	DYDYGALGYF	-----	DV	WGAGTTVT	VS	
76E1	KATLTVDKSSSTAYMQLKSLTSED	SAVYYCAT	STMITPF	-----	DY	WGQGTTLT	VS	
53A	KATLTSDKSSSTAYMELSSLTSED	SAVYYCAR	FDYDTL	-----	RY	WGQGTTLT	VS	
259A	KATLTSDKSSSTAYMDLSSLTSED	SAVYYCAR	FDYDTL	-----	RY	WGQGTTLT	VS	
consensus			FDYDTL	-----	RY			
33A	KATFTADTSSNTAYMQLSGLTSED	SAVYYCAR	WLLYYYAM	-----	VY	WGQGTSVT	VS	
39A	KATFTADTSSNTAYMQLSSLTSED	SAVYYCAR	WLLYYYAM	-----	DY	WGQGTSVT	VS	
124A	KATFTADTSSNTAYMQLSSLTSED	SAVYYCAR	WLLYYYAM	-----	DF	WGQGTSVT	VS	
175A	KATFTADTSSNTAYMQLSSLTSED	SAVYYCAR	WLLYYYAM	-----	DY	WGQGTSVT	VS	
321D	KATFTADTSSNTAYMQLSSLTSED	SAVYYCAR	WLLYYYAM	-----	DY	WGQGTSVT	VS	
consensus			WLLYYYAM	-----	DY			
141A	KATFTADTSSNTAYMQLSSLTSED	SAVYYCAG	EEVYDGYPF	-----	GY	WGQGTILT	VS	
51A	KATFTADTSSNTAYMQLSSLTSED	SAVYYCAS	EEVYDGYPF	-----	GY	WGQGTILT	VS	
consensus			EEVYDGYPF	-----	GY			
353A	KFIISRDNKNTLYLQNSKVRYED	TALYYCAR	PGEIYYGSYWFAY			WGQGTILT	VS	
305A	RISITRDTSKNQFFLKLNSVT	TEDTATYYCAR	RHDYLSF	-----	AY	WGQGTILT	VS	

FIG. 18B

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VL Domains		10	20	24	30	34	40	50	56
AbM#									
5B	NIVMTQPKFLLVSAGDRVITTC	KASQSVS	NDVA	WYQKPGQSPKLLIY	YASNRYT				
46A	SIVMTQPKFLLVSAGDRVITTC	KASQSVS	NDVA	WYQKPGQSPKLLIY	YASNRYT				
97A	SIVMTQPKFLLVSAGDRVAITC	KASQSVS	NDVA	WYQKPGQSPKLLIY	YASNRYT				
128A	NIAMTQPKFLLVSAGDRVITTC	KASQSVS	NDIA	WYQKPGQSPKLLIY	YASNRYT				
146C	NIAMTQPKFLLVSAGDRVITTC	KASQSVS	NDIA	WYQKPGQSPKLLIY	YASNRYT				
208A	SIVMTQPKFLLVSAGDRVITTC	KASQSVS	NDVA	WYQKPGQSPKLLIY	YASNRYT				
consensus		KASQSVS	ND*A		YASNRYT				
215A	QIVLTQSPAIMASPGKEKVTMTTC	SASSSVS	YMF	WYQKPGSSPRLLIY	DTSNLAS				
26A	QIVLTQSPAIMASPGKEKVTMTTC	SASSSVS	YMY	WYQKPGSSPRLLIY	DTSNLAS				
164A-1	NIMMTQSPSSLAVSAGEKVTMTSC	KSSQSVLYSSNQKNYLA	WYQKPGQSPKLLIY	WASTRES					
164A-2	ENVLTQSPAIMAASPGKEKVTMTTC	SASSSVS	SNLH	WYQKSGTSTKFWIY	RTSNLAS				
230A	DVVMITQPLSLPVLGDQASISC	RSSQSLVHSNGN-TYLH	WYQKPGQSPKLLIY	KVSNRFS					
76E1	DVLMITQPLSLPVLGDQASISC	RSSQSLVHSNGN-TYLE	WYQKPGQSPKLLIY	KVSNRFS					
53A	DVVLITQPLSLPWNIGDQASISC	KSTKSLNSDGF-TYLD	WYQKPGQSPKLLIY	LVSNRFS					
259A	DVVLITQPLSLPWNIGDQASISC	KSTKSLNSDGF-TYLD	WYQKPGQSPKLLIY	LISNRFS					
consensus		KSTKSLNSDGF-TYLD		L*SNRFS					
33A	DVLMITQPLSLPVLGDQASISC	RSSQSLVHSNGN-TYLE	WYQKPGQSPKLLIY	KVSNRFS					
39A	DVLMITQPLSLPVLGDQASISC	RSSQSLVHSNGN-TYLE	WYQKPGQSPKLLIY	KVSNRFS					
124A	DVLMITQPLSLPVLGDQASISC	RSSQSLVHSNGN-TYLE	WYQKPGQSPKLLIY	KVSNRFS					
175A	DVLMITQPLSLPVLGDQASISC	RSSQSLVHSNGN-TYLE	WYQKPGQSPKLLIY	KVSNRFS					
321D	DVLMITQPLSLPVLGDQASISC	RSSQSLVHSNGN-TYLE	WYQKPGQSPKLLIY	KVSNRFS					
consensus		RSSQSLVH*NGN-TYLE		K*SNRFS					
141A	QIVLSQSPAILSASPGKEKVTMTTC	RASSSL	SYMH	WYQKPGSSPKPWIIY	ATSNLAS				
51A	QIVLSQSPAILSASPGKEKVTMTTC	RASSSL	SYMH	WYQKPGSSPKPWIIY	ATSNLAS				
consensus		RASSSL	SYMH		ATSNLAS				
353A	DIVLTQSPASLAVSLGQRATITSC	RASESVEYYGT-SLMQ	WFQKPGQPPKLLIY	AASNVES					
305A	DIVLTQSPASLAVSLGQRATITSC	KASQSDYDGD-SYMN	WYQKPGQPPKLLIY	AASNLES					

FIG. 18C

AbM#	60	70	80	89	97
5B	GVPDRFTGCGYGTDFITISTVQAE	DLAVYFC	QDDYSSPRT	FGG	TKLEIK
46A	GVPDRFTGCGYGTDFITISTVQAE	DLAVYFC	QDDYSSPRT	FGG	TKLEIK
97A	GVPDRFTGCGYGTDFITISTVQAE	DLAVYFC	QDDYSSPRT	FGG	TKLEIK
128A	GVPDRFTGCGYGTDFITISTVQAE	DLAVYFC	QDDYSSPRT	FGG	TKLEIK
146C	GVPDRFTGCGYGTDFITISTVQAE	DLAVYFC	QDDYSSPRT	FGG	TKLEIK
208A	GVPDRFTGCGYGTDFITISTVQAE	DLAVYFC	QDDYSSPRT	FGG	TKLEIK
consensus			QDDY*SPRT		
215A	GVPLRFSCGSGTISLTISRMEAE	DAATYYC	QQWSSYPFT	FCG	TKLEIK
26A	GVPLRFSCGSGTISLTISRMEAE	DAATYYC	QQWSSYPFT	FCG	TKLEIK
164A-1	GVPDRFTGCGSGIDFTILTISSVQAE	DLAVYFC	HQFLSS-YT	FGG	TKLEMK
164A-2	EVPAFSCGSGTISLTISRMEAE	DAATYYC	QQWSSYPRT	FGG	TKLEIK
230A	GVPDRFSCGSGIDFTILKISRVEAE	DLGVYFC	SQSTHVPYT	FGG	TKLEIK
76E1	GVPDRFSCGSGIDFTILKINRVEAE	DLGVYFC	FQGSHPVPT	FGG	TKLEIK
53A	GVPDRFSCGSGIDFTILKISRVEAE	DLGVYFC	FQSNYFPWT	FGG	TKLEIK
259A	GVPDRFSCGSGIDFTILKISRVEAE	DLGVYFC	FQSNYFPWT	FGG	TKLEIK
consensus			FQSNYFPWT		
33A	GVPDRFSGSGIDFTILKISRVEAE	DLGVYFC	FQGSHPVYT	FGG	TKLEIK
39A	GVPDRFSGSGIDFTILKISRVEAE	DLGVYFC	FQGSHPVYT	FGG	TKLEIK
124A	GVPDRFSGSGIDFTILKISRVEAE	DLGVYFC	FQGSHPVYT	FGG	TKLEIK
175A	GVPDRFSGSGIDFTILKISRVEAE	DLGVYFC	FQGSHPVYT	FGG	TKLEIK
321D	GVPDRFSGSGIDFTILKITRVEAE	DLGVYFC	FQGSHPVPT	FGG	TKLEIK
consensus			FQGSHPVPT		
141A	GVPARFSGSGTISLTISRVEAE	DAATYYC	QQWSSNPYT	FGG	TKLEIK
51A	GVPARFSGSGTISLTISRVEAE	DAATYYC	QQWSSNPYT	FGG	TKLEIK
consensus			QQWSSNPYT		
353A	RVPARFSGSGIDFSLNIHPVEED	DIAMVFC	QQSRKDPWT	FGG	TKLEIK
305A	GIPARFSGSGIDFTILNIHPVEEE	DAATYYC	QQSDEDPYT	FGG	TKLEIK

FIG. 18D

mAb	Human VH Germline	Human VL Germline	Paratope Bin
5B	IGHV1-46	IGKV1-39	1
46A	IGHV1-46	IGKV1-39	1
97A	IGHV1-46	IGKV1-39	1
128A	IGHV1-46	IGKV1-39	1
146C	IGHV1-46	IGKV1-39	1
208A	IGHV1-46	IGKV1-39	1
215A	IGHV1-46	IGKV3-11	2
26A	IGHV1-46	IGKV3-11	3
164A	IGHV1-46	IGKV4-1	4
		IGKV3D-20	4
230A	IGHV1-46	IGKV2-30	5
76E1	IGHV1-46	IGKV2-30	6
	IGHV1-18	IGKV2-28	
53A	IGHV1-46	IGKV2-29	7
259A	IGHV1-46	IGKV2-29	7
33A	IGHV1-46	IGKV2-30	8
39A	IGHV1-46	IGKV2-30	8
124A	IGHV1-46	IGKV2-30	8
175A	IGHV1-46	IGKV2-30	8
	IGHV1-18	IGKV2-28	
321D	IGHV1-46	IGKV2-30	8
141A	IGHV1-46	IGKV3-20	9
	IGHV1-18	IGKV3-20	
51A	IGHV1-46	IGKV3-20	9
353A	IGHV3-74	IGKV1-39	10
305A	IGHV4-61	IGKV1-39	11

FIG. 19

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Human VH germline sequences

IGHV1-18*01
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWI SAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYC
AR

IGHV1-46*01
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVVRQAPGQGLEWMGI INPSGGSTSYAQKFQGRVTMTTRDTSTSTVYMELSSLRSED TAVYYC
AR

IGHV3-74*01
EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYMMHWVRQAPGKGLVWVSRINSDGSSTSYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYC
AR

IGHV4-61*01
QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGSYYWSWIRQPPCKGLEWIGYIYYSGSTNYPNPSLKSRVTISVDTSKNQFSLKLSSTVAADTAVYY
CAR

FIG. 20A

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Human VL kappa germline sequences

IGKV1-39*01
 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPP

IGKV2-28*01
 DIVMTQSPPLSPVTPGEPASISCRSSQSLHNSNGYNLDWYLQKPGQSPQQLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYCMQALQTPP

IGKV2-29*02
 DIVMTQTPLSLSVTPCQPASISCKSSQSLHSDGKTYLYWYLQKPGQSPQQLIYEVSSRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCMQGIHLPP

IGKV2-30*02
 DVVMTQSPPLSPVTLGQPASISCRSSQSLVHSDGNTYLNWFQQRPGQSPRRLIYKVSNRDSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYCMQGTHWPP

IGKV3-11*01
 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRTGIPARFSGSGSGTDFTLTISLLEPEDFVYYCQQRSNWPP

IGKV3-20*01
 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFVYYCQYCGSSPP

IGKV3D-20*01
 EIVLTQSPATLSLSPGERATLSCGASQSVSSYLAWYQQKPGAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFVYYCQYCGSSPP

IGKV4-1*01
 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVDPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQYYSTPP

FIG. 20B

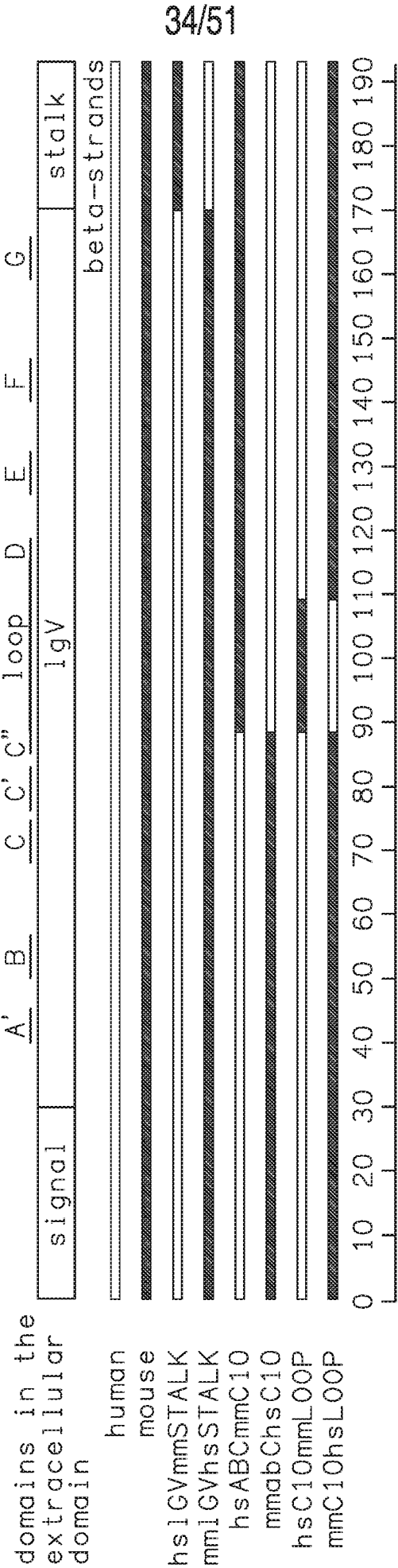


FIG. 21A

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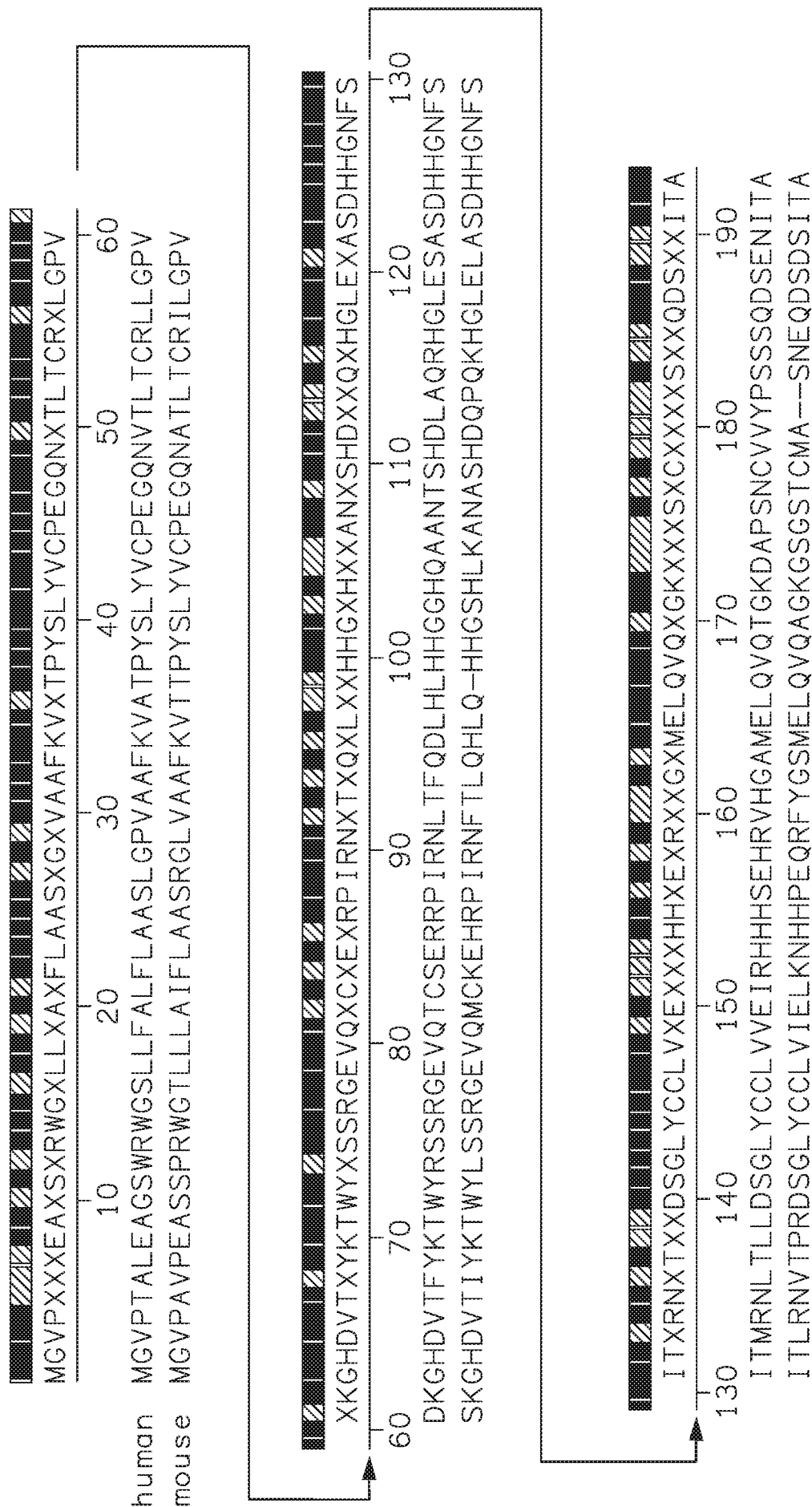


FIG. 21A CONTINUED

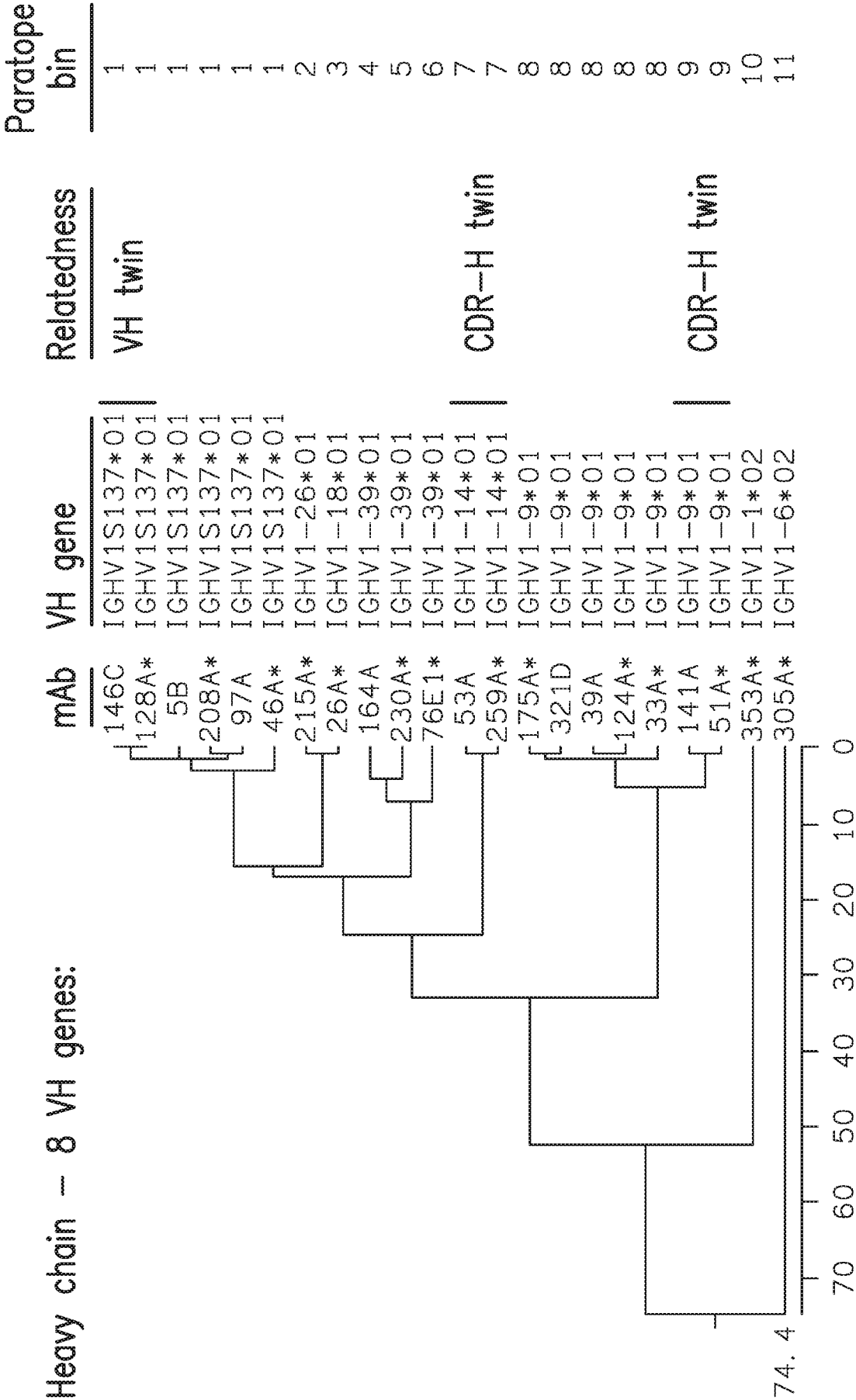


FIG. 21B

Paratope bin	Flow cluster
1	a
1	a
1	a
1	a
1	tbd
1	a
2	b
3	a
4	a
5	a
6	b
7	b
7	b
8	c
8	a
8	b
8	b
8	a
9	d
9	d
10	e
11	f

Flow cluster – chimeric and full-length constructs with at least 10% staining relative to human:

a: hslGVmmSTALK, mmABChsC10, mmC10hsLOOP

b: hslGVmmSTALK, mmABChsC10

c: hslGVmmSTALK

d: hslGVmmSTALK, mmABChsC10, hsC10mmLOOP

e: hslGVmmSTALK, mmABChsC10, hsC10mmLOOP, rat

f: hslGVmmSTALK, hsABCmmC10, hsC10mmLOOP

Note: all mAbs stain full-length human & full-length cyno

tbd: to be determined

FIG. 21B continued

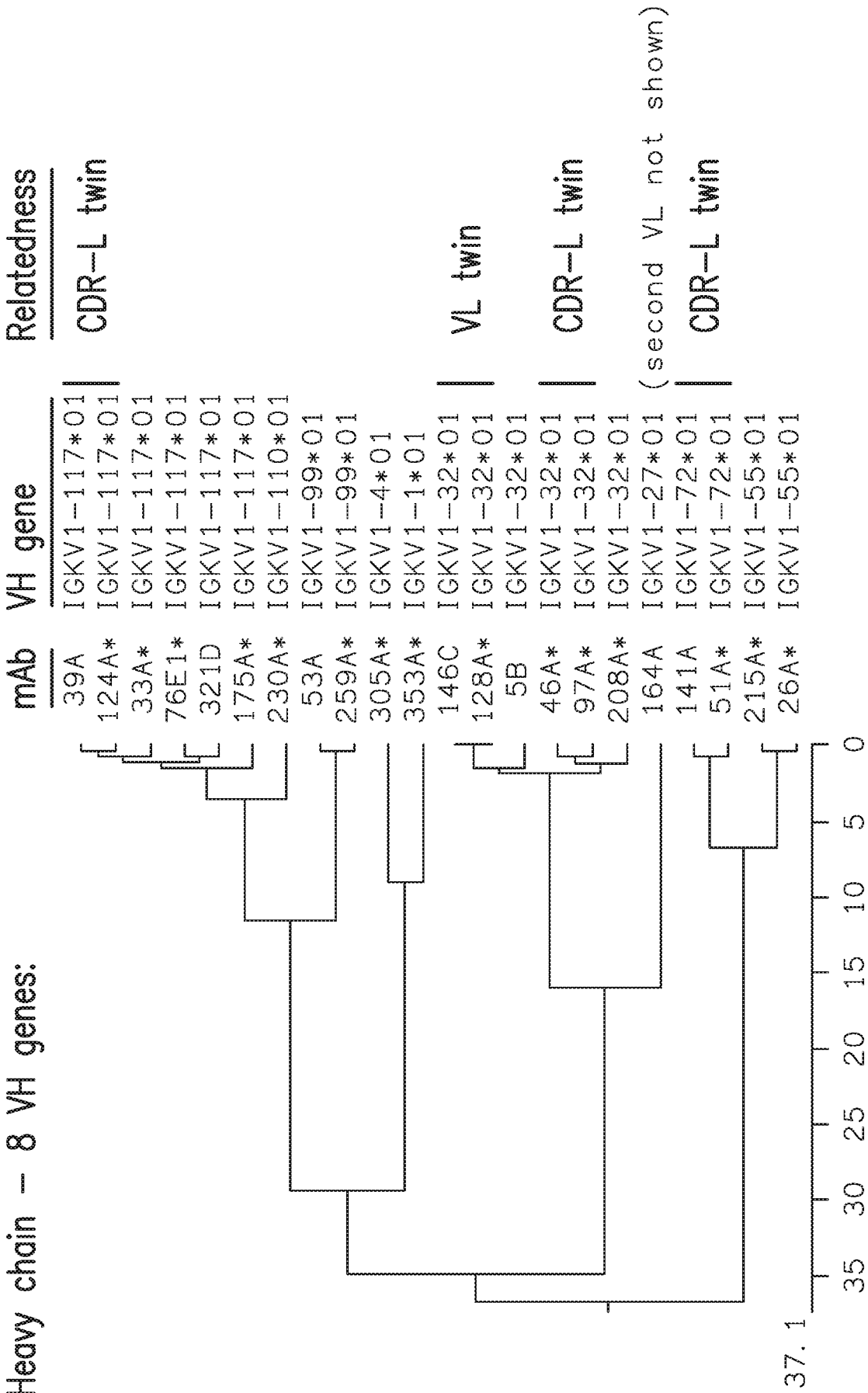


FIG. 21B continued

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework (AbM CDR definition)
 IGHV1-46*01 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYMHWRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTTRDTSTSTVYMELSSLRSED¹TAVYYCAR
 Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLTVTVSS

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30	40	50	60	70	80	90
26A	b b b	p b b	b b	b i i	i i b b	i b	b b b	b b b	b b b
	EVQLQQSGPELVKPGASMKISCKAS	GFSFTG YTMN	WVKQSHVKNLEWIG	LISPYNGG TS	YNQKFQGRVTMTTRDTSTSTVYMELSSLRSED ¹ TAVYYCAR				
	* * *	* * *	* * * * *	*					
1-46*01	QVQLVQSGAEVKKPGASVKVSCKAS	GYFTSYMH	WVRQAPGQGLEWMG	IINPSGGST	YAQKFQGRVTMTTRDTSTSTVYMELSSLRSED ¹ TAVYYCAR				
h26AH1	QVQLVQSGAEVKKPGASVKVSCKAS	GFSFTG YTMN	WVRQAPGQGLEWMG	LISPYNGG TS	YAQKFQGRVTMTTRDTSTSTVYMELSSLRSED ¹ TAVYYCAR				
h26AH2	QVQLVQSGAEVKKPGASVKISCKAS	GFSFTG YTMN	WVRQAPGQGLEWIG	LISPYNGG TS	YAQKFQGRATLTVDKSTSTAYMELSSLRSED ¹ TAVYYCAR				
h26AH3	QVQLVQSGAEVKKPGASVKISCKAS	GFSFTG YTMN	WVRQAPGQGLEWIG	LISPYNGG TS	YAQKFQGRATLTVDKSTSTAYMELSSLRSED ¹ TAVYYCAR				
	V	M		#					

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seq	100	110
AbM	100	110
26A	b i b b	
	RAYGYAMDY	WGQGTSLTVTVSS
		*
h26AH1	RAYGYAMDY	WGQGTSLTVTVSS
h26AH2	RAYGYAMDY	WGQGTSLTVTVSS
h26AH3	RAYGYAMDY	WGQGTSLTVTVSS

- (1) CDR sequences noted in bold. CDR definitions are AbM definition from website www.bioinf.org.uk/abs/.
- (2) Human germline and joining sequences from IMGT® the international ImmunoGenetics® information system www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
- (3) Residue numbering shown as sequential (seq) or according to Chothia from website www.bioinf.org.uk/abs/ (AbM).
- (4) "b" notes buried sidechain; "p" notes partially buried; "i" notes sidechain at interface between VH and VL domains.
- (5) Sequence differences between human and murine germlines noted by asterisk (*).
- (6) Potential changes in CDR sequences noted below each CDR sequence. These may prevent asparagine (N) deamidation.

FIG. 22A

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Potential humanized sequence based on IMGT IGKV3-11*01 acceptor framework (AbM CDR definition)
 IGHV3-11*01 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRAIGIPARFSGSGGTDFLTIISSLEPEDFAVYQCQRSNWPP
 Joining region IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

seq	10	20	30	40	50	60	70	80
AbM	10	20	30	40	50	60	70	80
26A	b b b	b b b	b b b	b b b	i i i b b i	b b b	b b b	b b b b b
	QIVLTQSPA	IMSA	SPGEKVT	MTCSASSSVS--YMY	WYQKPGSSPRLIIY	DTSN	LAS	GVPLRFSGSGGT
	*	** *	** *	** *	** *	** *	** *	** *
IGKV3-11	EIVLTQSPATLSLSPGERATLSC	RASQSVSSYLA	WYQKPGQAPRLIIY	DASNRA	TGIPARFSGSGGT	DFLTII	ISSLEPEDFAVY	YC
h26AL1	EIVLTQSPATLSLSPGERATLSC	SASSSVS--YMY	WYQKPGQAPRLIIY	DTSN	LAS	GVPLRFSGSGGT	DFLTII	ISSLEPEDFAVY
h26AL2	EIVLTQSPATLSLSPGERVTMSC	SASSSVS--YMY	WYQKPGQAPRLIIY	DTSN	LAS	GVPLRFSGSGGT	DFLTII	ISSLEPEDFAVY
h26AH3	EIVLTQSPATMSASPGERV	TMSC	SASSSVS--YMY	WYQKPGQAPRLIIY	DTSN	LAS	GVPLRFSGSGGT	DFLTII

seq	90	100
AbM	90	100
26A	i b i i b	i b b b
	QQWSSYPFT	FGSGTKLEIK
	*	
IGKV3-11	QQRSNWPP	
h26AL1	QQWSSYPFT	FGSGTKLEIK
h26AL2	QQWSSYPFT	FGSGTKLEIK
h26AL3	QQWSSYPFT	FGSGTKLEIK

- (1) CDR sequences noted in bold. CDR definitions are AbM definition from website www.bioinf.org.uk/abs/.
- (2) Human germline and joining sequences from IMGT® the international ImmunoGenetics® information system www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
- (3) Residue numbering shown as sequential (seq) or according to Chothia from website www.bioinf.org.uk/abs/ (AbM).
- (4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
- (5) Sequence differences between human and murine germlines noted by asterisk (*).
- (6) Potential additional mutations in frameworks are noted below sequence.
- (7) Potential changes in CDR sequences noted below each CDR sequence.

FIG. 22B

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Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework (AbM CDR definition)
IGHV1-46*01 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYYMHVWRQAPGQGLEWMGIINPSGCGSTSYAQKFQGRVTMTTRDTSTVYMELSSLRSEDTAVYYCAR
Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLVTVSS

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30	40	50	60	70	80	90
128A	b b b	p b b b b	b b b	b i i	i i b b	i b	b b b b	b b b b	b i b i b b
	QVQLVQSGAEVKKPGASVKISCKGS	GYTFDYG	GMH	WVKQSHAKSLEWIG	LIDTYYG	DAT	YNHKFKGKATMTVDKSSRTAYMELARLTSEDS	AIYYCAR	

1-46*01 QVQLVQSGAEVKKPGASVKVSCKAS GYTFSTYYMH VWRQAPGQGLEWMG IINPSGCGSTSYAQKFQGRVTMTTRDTSTVYMELSSLRSEDTAVYYCAR
h128AH1 QVQLVQSGAEVKKPGASVKVSCKAS GYTFDYG GMH VWRQAPGQGLEWMG LIDTYYG DAT YAQKFQGRCTMTTRDTSTVYMELSSLRSEDTAVYYCAR
h128AH2 QVQLVQSGAEVKKPGASVKISCKGS GYTFDYG GMH VWRQAPGQGLEWIG LIDTYYG DAT YAQKFQGRATMTVDSTSTAYMELSSLRSEDTAVYYCAR
h128AH3 QVQLVQSGAEVKKPGASVKISCKGS GYTFDYG GMH VWRQAPGQGLEWIG LIDTYYG DAT YAQKFQGRATMTVDKSTSTAYMELSSLRSEDTAVYYCAR

seq	100	110
AbM	100	110
128A	RAGNAMDY	WGQGTSVTASS
		* *
h128AH1	RAGNAMDY	WGQGTSVTASS
h128AH2	RAGNAMDY	WGQGLVTVSS
h128AH3	RAGNAMDY	WGQGLVTVSS

- (1) CDR sequences noted in bold. CDR definitions are AbM definition from website www.bioinf.org.uk/abs/.
- (2) Human germline and joining sequences from IMGT® the international ImmunoGenetics® information system www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
- (3) Residue numbering shown as sequential (seq) or according to Chothia from website www.bioinf.org.uk/abs/ (AbM).
- (4) "b" notes buried sidechain; "p" notes partially buried; "i" notes sidechain at interface between VH and VL domains.
- (5) Sequence differences between human and murine germlines noted by asterisk (*).
- (6) Potential additional mutations in frameworks are noted below sequence.

FIG. 23A

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Potential humanized sequence based on IMGT ICKV1-39*01 acceptor framework (AbM CDR definition)
 ICKV1-39*01 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGSGTDFLTITSSLPEDFATYYCQQSYSTPP
 Joining region IMGT J00242|ICKJ2*01|YTFGGGTKLEIK

seq	10	20	30	40	50	60	70	80
AbM	10	20	30	40	50	60	70	80
128A	b b b	b b b	b b b	b b b	i i i	b b b	b b b	b b b
	NIAMTQTPKFLLSAGDRVTITC	KASQSVSNDIA	WYQKPGKAPKLLIY	YASNRYT	GVPDRFTGSGYGTDFLTITSSLPEDFATYYC			
	* * *	* * *	* * *	* * *	* * *	* * *	* * *	* * *
ICKV1-39	DIQMTQSPSSLSASVGDRVTITC	RASQSISSYLN	WYQKPGKAPKLLIY	AASSLQS	GVPSRFSGSGTDFLTITSSLPEDFATYYC			
h128AL1	DIQMTQSPSSLSASVGDRVTITC	KASQSVSNDIA	WYQKPGKAPKLLIY	YASNRYT	GVPSRFSGSGTDFLTITSSLPEDFATYYC			
h128AL2	DIQMTQSPSSLSASVGDRVTITC	KASQSVSNDIA	WYQKPGKAPKLLIY	YASNRYT	GVPSRFSGSGTDFLTITSSLPEDFATYYC			
h128AL3	DIQMTQSPSSLSASVGDRVTITC	KASQSVSNDIA	WYQKPGKAPKLLIY	YASNRYT	GVPSRFSGSGTDFLTITSSLPEDFATYYC			

seq	90	100
AbM	90	100
128A	ibi iib i	b b b
	QQDYSSPRT	FGGGTKLEIK
		*
ICKV1-39	QQSYSTPP	
h128AL1	QQDYSSPRT	FGGGTKLEIK
h128AL2	QQDYSSPRT	FGGGTKLEIK
h128AL3	QQDYSSPRT	FGGGTKLEIK

- (1) CDR sequences noted in bold. CDR definitions are AbM definition from website www.bioinf.org.uk/abs/.
- (2) Human germline and joining sequences from IMGT® the international ImmunoGenetics® information system www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
- (3) Residue numbering shown as sequential (seq) or according to Chothia from website www.bioinf.org.uk/abs/ (AbM).
- (4) "b" notes sidechain at interface between VH and VL domains.
- (5) Sequence differences between human and murine germlines noted by asterisk (*).
- (6) Potential additional mutations in frameworks are noted below sequence.
- (7) Potential changes in CDR sequences noted below each CDR sequence. These may prevent asparagine (N) deamidation.

FIG. 23B

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework (AbM CDR definition)
 IGHV1-46*01 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYMHVWRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTDSTSTVYMELSSLRSEDTAVYYCAR
 Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLVTVSS

	10	20	30	40	50	60	70	80	90
seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30	40	50	60	70	80	90
124A	b b b	p b b b	b b b	b i i	i i b b	i b	b b b x	b b b	b i b b b
	QVQLVQSGAEVKKPGASVKISCKAT	GYTFSSNWIE	WVKQRP	GHG	LEWMG	EILP	GGSGSTS	YNEKF	KGKATFTADTSSNTAYMQLSLTSEDS
	*	**	*	*	*	*	*	*	*
1-46*01	QVQLVQSGAEVKKPGASVKVCKAS	GYTFTSYMH	WVRQAP	CGQ	GLEWMG	IINP	SGSGSTS	YAKFQ	GRVTMTDSTSTVYMELSSLRSEDTAVYYCAR
h124AH1	QVQLVQSGAEVKKPGASVKVCKAS	GYTFSSNWIE	WVRQAP	CGQ	GLEWMG	EILP	GGSGSTS	YAKFQ	GRVTMTDSTSTVYMELSSLRSEDTAVYYCAR
h124AH2	QVQLVQSGAEVKKPGASVKISCKAS	GYTFSSNWIE	WVRQAP	CGQ	GLEWMG	EILP	GGSGSTS	YAKFQ	GRATFTADTSTAYMELSSLRSEDTAVYYCAR

	100	110	110
seq	100	110	110
AbM	100	110	110
124A	WLLYYAMDF	WGQGT	SVTVSS
h124AH1	WLLYYAMDF	WGQGT	ILVTVSS
h124AH2	WLLYYAMDF	WGQGT	ILVTVSS

- (1) CDR sequences noted in bold. CDR definitions are AbM definition from website www.bioinf.org.uk/abs/.
- (2) Human germline and joining sequences from IMGT® the international ImmunoGenetics® information system www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
- (3) Residue numbering shown as sequential (seq) or according to Chothia from website www.bioinf.org.uk/abs/ (AbM).
- (4) "b" notes buried sidechain; "p" notes partially buried; "i" notes sidechain at interface between VH and VL domains.
- (5) Sequence differences between human and murine germlines noted by asterisk (*).
- (6) Potential changes in CDR sequences noted below each CDR sequence. These may prevent asparagine (N) deamidation.

FIG. 24A

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Potential humanized sequence based on IMGT IGV2-30*01 acceptor framework (AbM CDR definition)
 IGV2-30*01 DVVMTQSPVLSPLVTLGQPASISCRSSQSLVSDGNTYLNWFQRPQSPRRLLIYKVSNRDVGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCMQGTHWPP
 Joining region IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

	10	20	30	40	50	60	70	80	90
seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30	40	50	60	70	80	90
124A	b b b	b b b	b b b	b b b	i i i	b b b	b b b	b b b	b b b
	DVLTQTPLSLPVS	LGQASISC	RSSQSI	VHNGNTYLE	WYQKPGQSPKLLIY	KVSNRFS	GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC		
	*	*	*	*	*	*	*	*	*
IGKV2-30	DVMTQSPVLSPLVTLGQPASISC	RSSQSLVSDGNTYLN	WFQRPQSPRRLLIY	KVSNRDS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC				
h124AL1	DVMTQSPVLSPLVTLGQPASISC	RSSQSI	VHNGNTYLE	WYQKPGQSPKLLIY	KVSNRFS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC			
h124AL2	DVMTQSPVLSPLVTLGQPASISC	RSSQSI	VHNGNTYLE	WYQKPGQSPKLLIY	KVSNRFS	GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC			

	90	100	110
seq	90	100	110
AbM	90	100	110
124A	ibi iib	i b b	b b
	FGSHVPYT	FGGTKLEIK	*
IGKV2-30	MQGTHWPP		
h124AL1	FGSHVPYT	FGGTKLEIK	
h124AL2	FGSHVPYT	FGGTKLEIK	

- (1) CDR sequences noted in bold. CDR definitions are AbM definition from website www.bioinf.org.uk/abs/.
- (2) Human germline and joining sequences from IMGT® the international ImmunoGenetics® information system www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
- (3) Residue numbering shown as sequential (seq) or according to Chothia from website www.bioinf.org.uk/abs/ (AbM).
- (4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
- (5) Sequence differences between human and murine germlines noted by asterisk (*).
- (6) Potential additional mutations in frameworks are noted below sequence.
- (7) Potential changes in CDR sequences noted below each CDR sequence. These may prevent asparagine (N) deamidation or isoaspartate formation (DG).

FIG. 24B

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Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework (AbM CDR definition)
IGHV1-46*01 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYMHWRAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLSRSED TAVYYCAR
Joining region IMGT J00256|IGHJ4*01|YFDYWGQGITLVTVSS

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30	40	50	60	70	80	90
259A	b b b	p b b b	b b b	b i i	i i b b	b b	b b b	b b b	b i b i b b
	EVQLQSGPELVKPGASVKMSCKAS	GYFTSYFMH	WVKQKPGQGLEWIG	YIYPYNDG	YNEKFKGKATLTSDKSSSTAYMDLSSLTSED	SAVYYCAR			
1-46*01	QVQLVQSGAEVKKPGASVKVSCKAS	GYFTSYFMH	WVRQAPGQGLEWVG	IINPSGGST	YAKFQGRVTMTRDTSTSTVYMELSSLSRSED	TAVYYCAR			
h259AH1	QVQLVQSGAEVKKPGASVKVSCKAS	GYFTSYFMH	WVRQAPGQGLEWVG	YIYPYNDG	YAKFQGRVTMTRDTSTSTVYMELSSLSRSED	TAVYYCAR			
h259AH2	QVQLVQSGAEVKKPGASVKMSCKAS	GYFTSYFMH	WVRQAPGQGLEWIG	YIYPYNDG	YAKFQGRATLTSDTSTSTAYMELSSLSRSED	TAVYYCAR			
h259AH3	QVQLVQSGAEVKKPGASVKMSCKAS	GYFTSYFMH	WVRQAPGQGLEWIG	YIYPYNDG	YAKFQGRATLTSDKSTSTAYMELSSLSRSED	TAVYYCAR			

seq	100	110
AbM	100	110
259A	b i b b b	
	FDYDILRY	WGQGITLVTVSS
h259AH1	FDYDILRY	WGQGITLVTVSS
h259AH2	FDYDILRY	WGQGITLVTVSS
h259AH3	FDYDILRY	WGQGITLVTVSS

- (1) CDR sequences noted in bold. CDR definitions are AbM definition from website www.bioinf.org.uk/abs/.
- (2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics® information system www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
- (3) Residue numbering shown as sequential (seq) or according to Chothia from website www.bioinf.org.uk/abs/ (AbM).
- (4) "b" notes buried sidechain; "p" notes partially buried; "i" notes sidechain at interface between VH and VL domains.
- (5) Sequence differences between human and murine germlines noted by asterisk (*).
- (6) Potential additional mutations in frameworks are noted below sequence.
- (7) Potential changes in CDR sequences noted below each CDR sequence. These may prevent asparagine (N) deamidation or isoaspartate formation (DG).

FIG. 25A

Potential humanized sequence based on IMGT IGV2-28*01 acceptor framework (AbM CDR definition)
IGKV2-28*01 DIVMTQSP¹SLPVTGPGEPAISCRSSQSL²LHSGNYLDWYLQKPGQSP³QLLIYLG⁴SNRASGVPDRFSGSGGTDF⁵TLKISRVEAEDVG⁶VYCMQALQTPP
Joining region IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30abcde	40	50	60	70	80	90
259A	b b b	b b b	b b b	b i i i	i i i b b i	b b b	b b b	b b b	b b b
	DVLTQTPLSLP	VNIQDQASISC	KSTKSLNSDGF	TYLD WYLQKPGQSP	QLLIY LISNRFS	GVPDRFSGSGGTDF	TLKISRVEAED	LG	VVYC

IGKV2-28	DIVMTQSP ¹ SLPVTGPGEPAISCRSSQSL ² LHSGNYLDWYLQKPGQSP ³ QLLIYLG ⁴ SNRASGVPDRFSGSGGTDF ⁵ TLKISRVEAEDVG ⁶ VYCMQALQTPP
h259AL1	DIVMTQSP ¹ SLPVTGPGEPAISCR KSTKSLNSDGF TYLDWYLQKPGQSP ³ QLLIY LISNRFS GVPDRFSGSGGTDF ⁵ TLKISRVEAEDVG ⁶ VYCMQALQTPP
h259AL1	DIVLTQSP ¹ SLPVTGPGEPAISCR KSTKSLNSDGF TYLDWYLQKPGQSP ³ QLLIY LISNRFS GVPDRFSGSGGTDF ⁵ TLKISRVEAEDVG ⁶ VYCMQALQTPP

seq	100	110
AbM	90	100
259A	i b i i b i	b b b
	FQSNYFPWT	FGGGTKLEIK

IGKV2-28	MQALQTPP
h259AL1	FQSNYFPWT
h259AH2	FQSNYFPWT

- (1) CDR sequences noted in bold. CDR definitions are AbM definition from website www.bioinf.org.uk/abs/.
- (2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics® information system www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
- (3) Residue numbering shown as sequential (seq) or according to Chothia from website www.bioinf.org.uk/abs/ (AbM).
- (4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
- (5) Sequence differences between human and murine germlines noted by asterisk (*).
- (6) Potential additional mutations in frameworks are noted below sequence.
- (7) Potential changes in CDR sequences noted below each CDR sequence. These may prevent asparagine (N) deamidation or isoaspartate formation (DG).

FIG. 25B

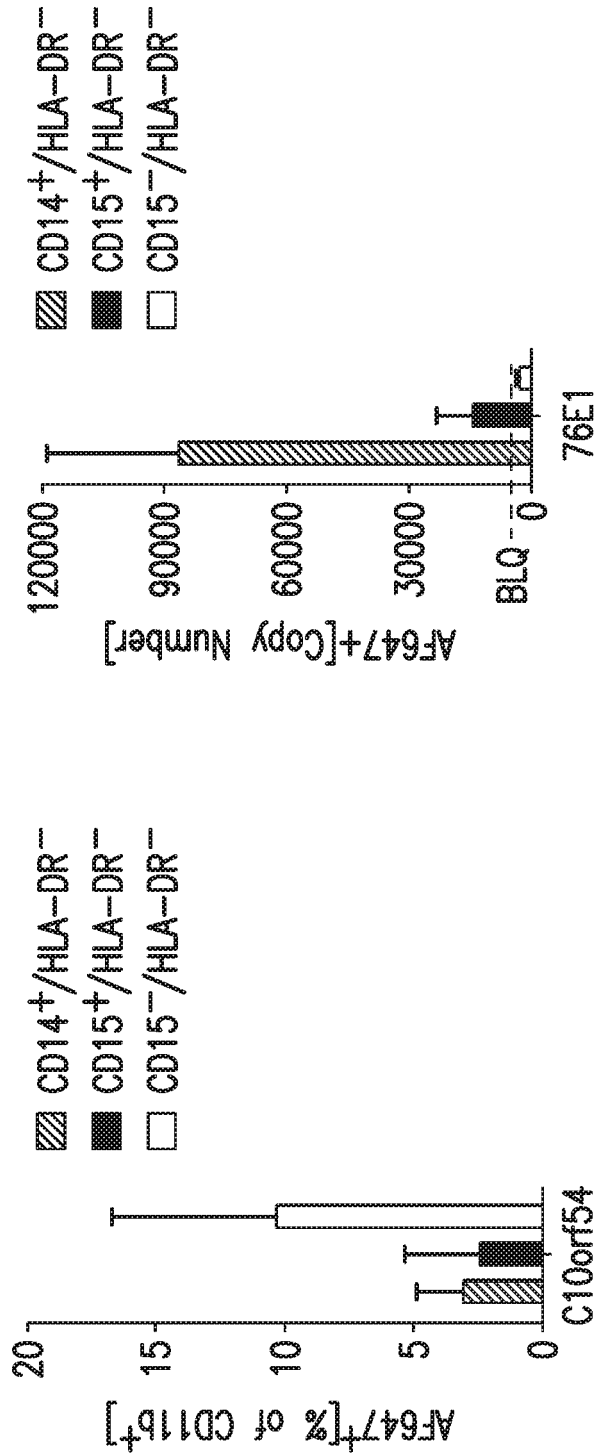


FIG. 26B

FIG. 26A

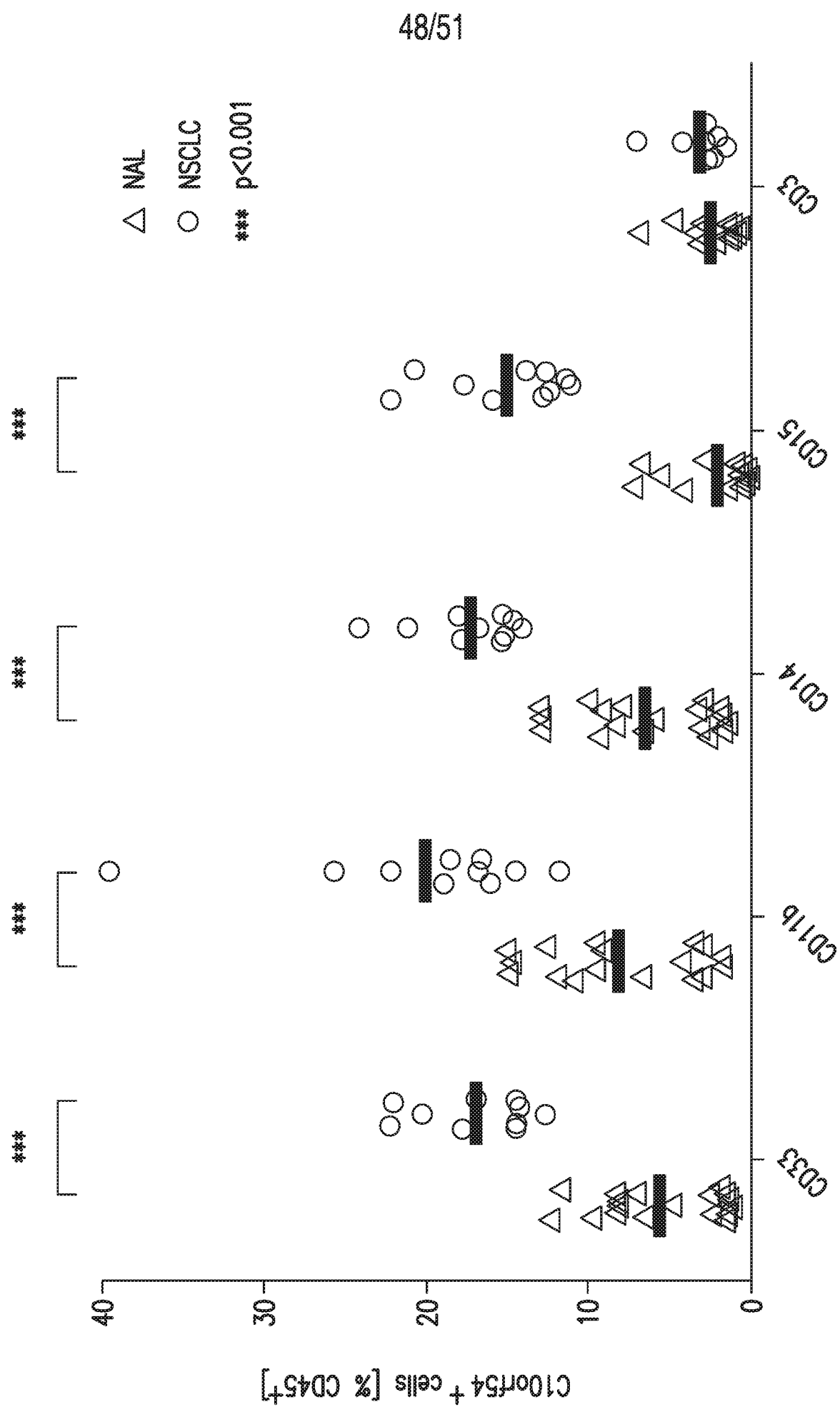


FIG. 27

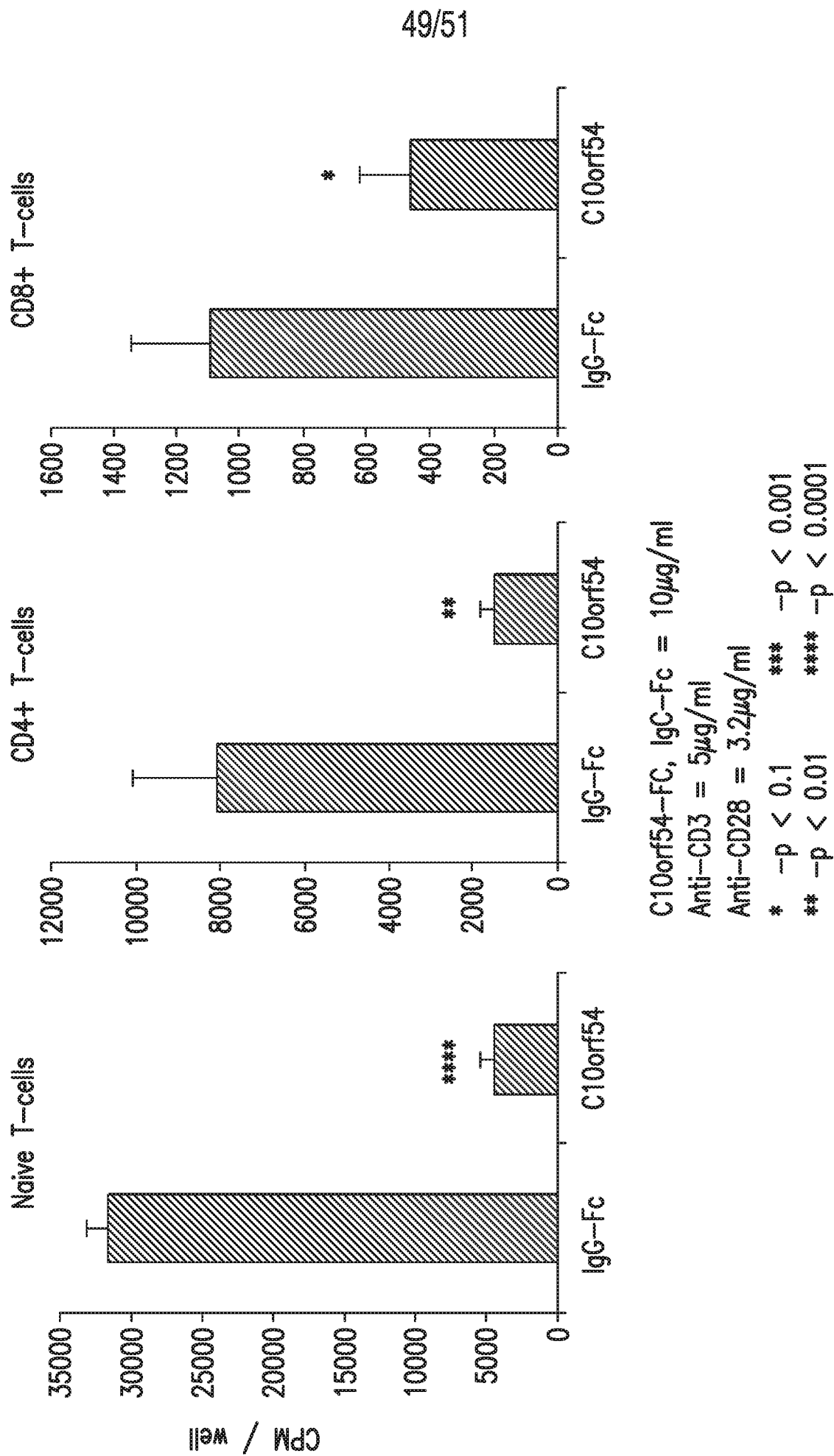


FIG. 28

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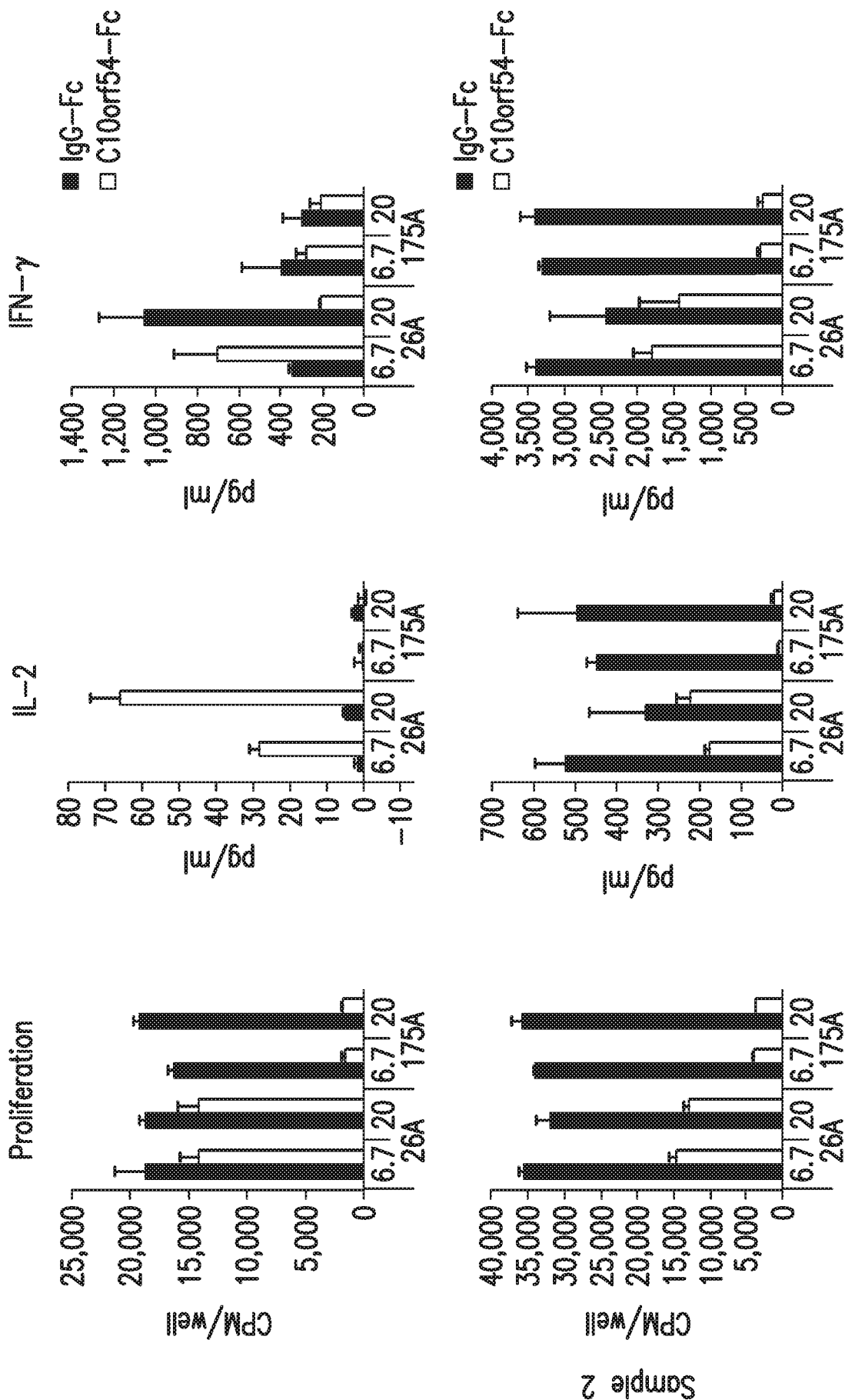


FIG. 29

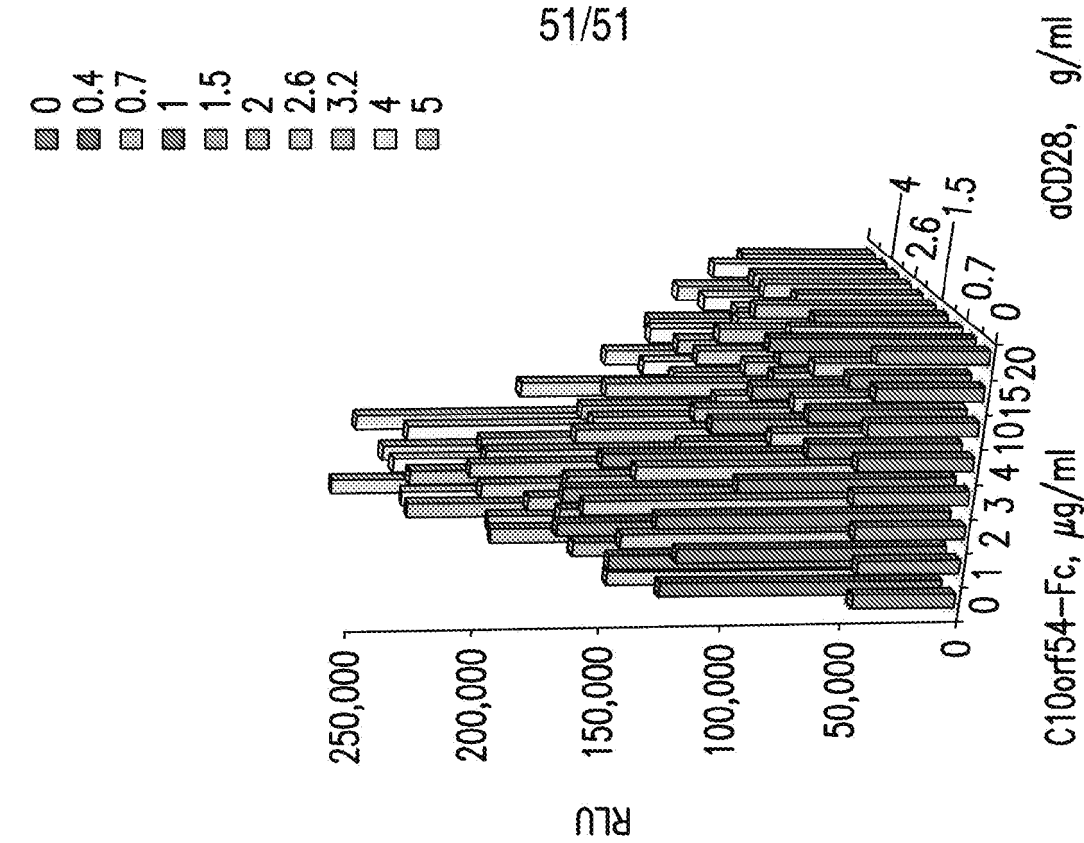


FIG. 30C

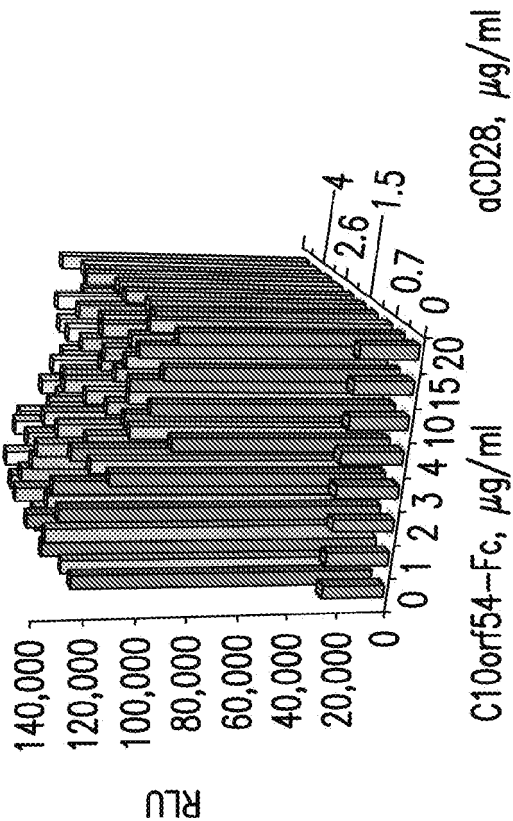


FIG. 30A

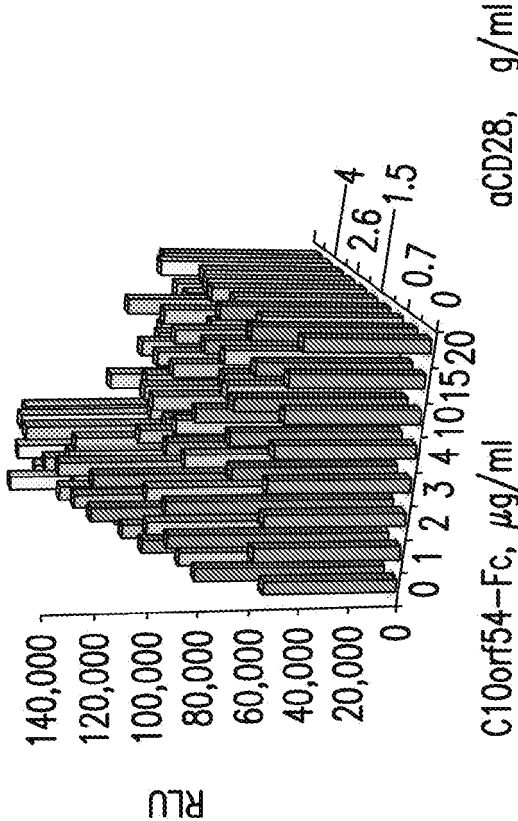


FIG. 30B