

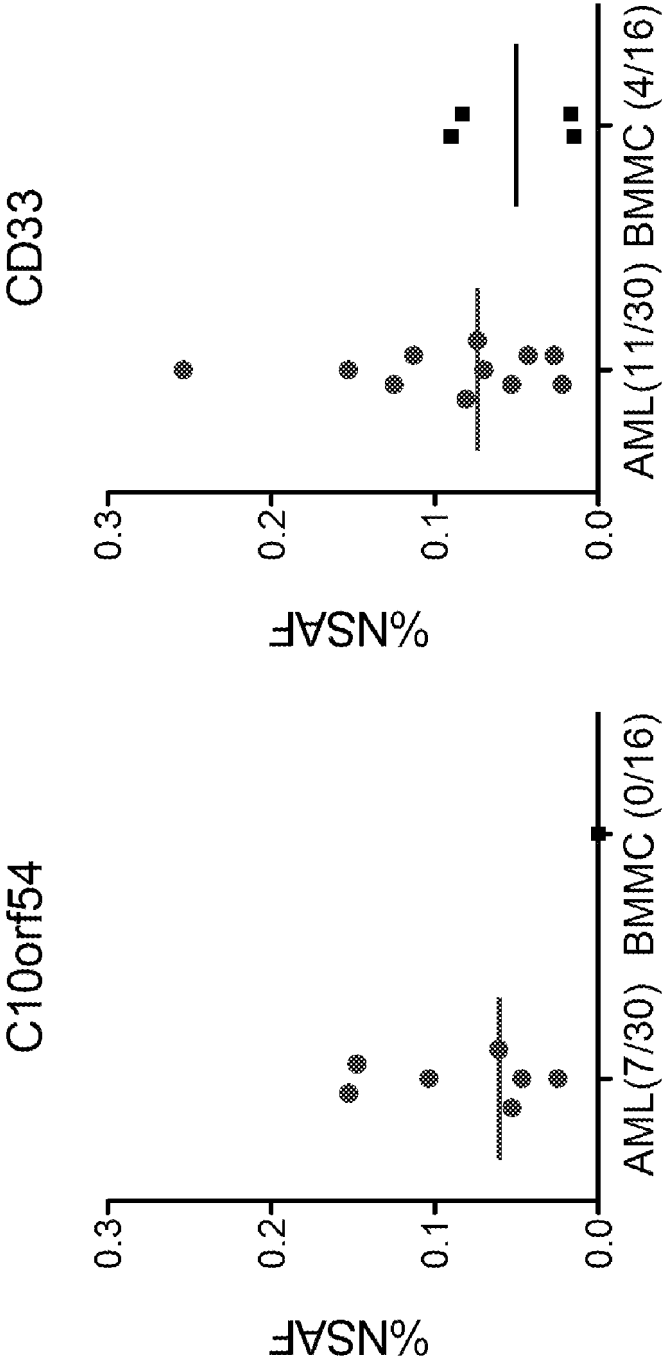


FIG. 1A

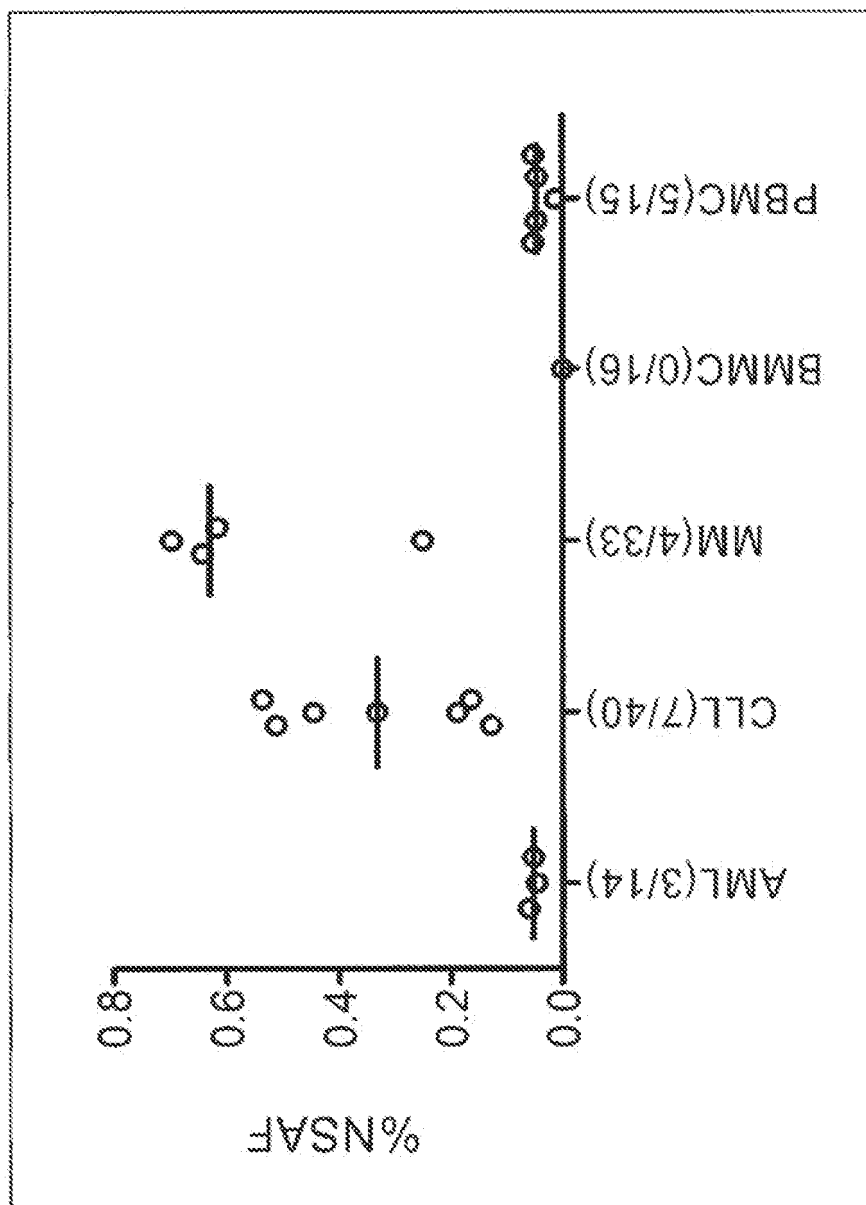


FIG. 1B

	CD13 ⁺ /CD33 ⁺				CD34 ⁺ /CD33 ⁺				CD34 ⁺ /CD33 ⁻			
	Incidence [*]	Pos, [%]	Fold MFI		Incidence [*]	Pos, [%]	Fold MFI		Incidence [*]	Pos, [%]	Fold MFI	
C10ORF54												
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

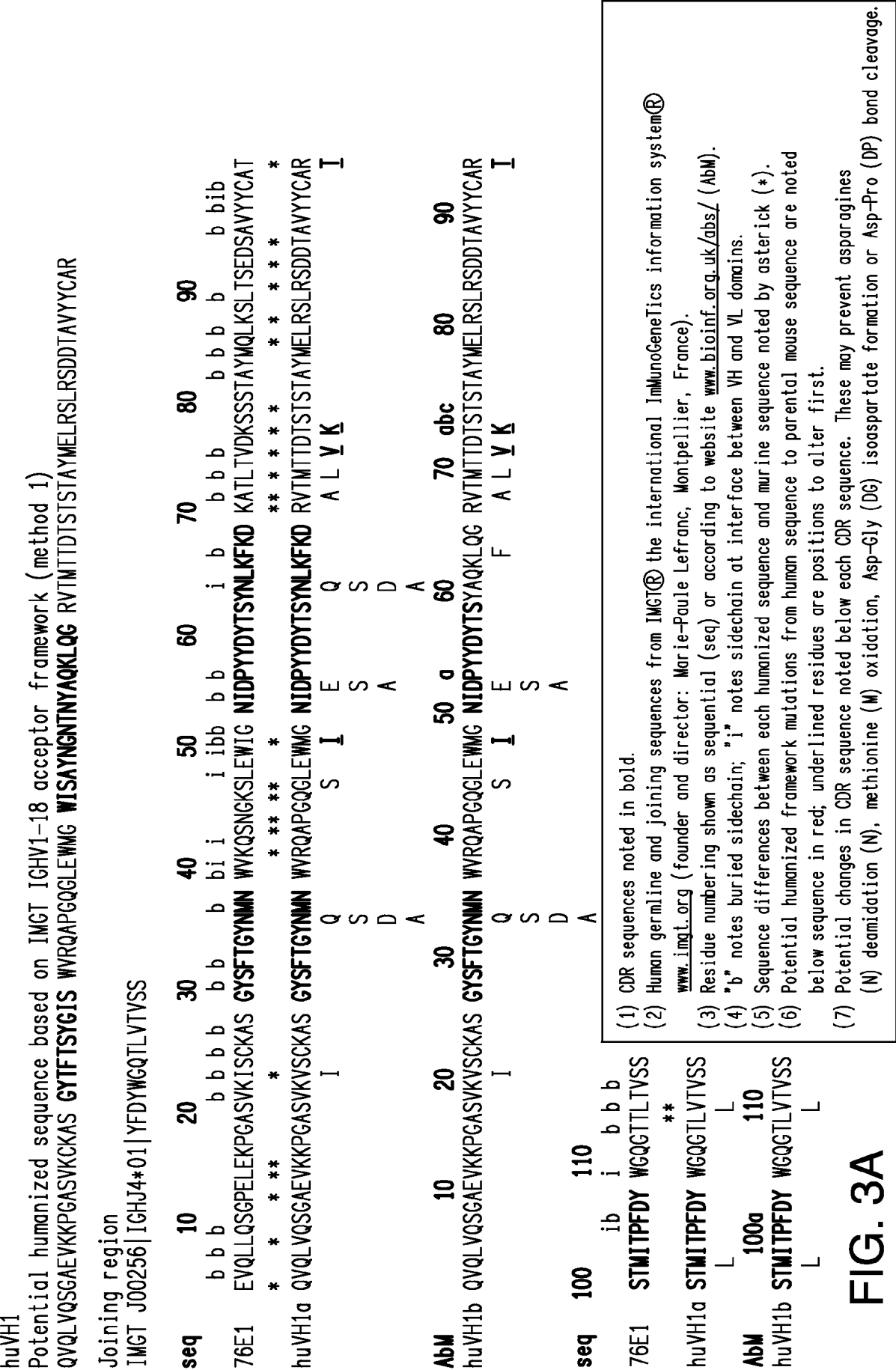


FIG. 3B

huVH3

Potential humanized sequence based on IMGT IGHV3-48 acceptor framework (method 2)

EVQLVESGGGLVQPGGSLRLSCAAS **G**FTFSY**S****M** WVRQAPGKGLEWVS **Y**ISSSS**T**IYAD**S**VKG RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR

Joining region

IMGT J00256|IGHJ4*01|YFDYWGQTLVTVSS

FIG. 4B

seq	10	20	30	40	50	60	70	80	90
	b b b	b b b b	b b b b	b b i i	i b b b	i b b b b	b b b b	b b b b	b b i b
141A	QVQLQQSGAELMKPGASVKISCKAT	G YTF S RY W IE WKQRPGHGLEWIG	E IL P GS G ST N Y N E K FG	KATFTADTSSNTAYMQLSSLTSEDS	SAVYYCAG				
	* * *	* * *	* * *	* * *	* * *	* * *	* * *	* * *	* * *
huVH3a	EVQLVESGGGLVQPGGSLRLSCAAS	G YTF S RY W IE WVRQAPGKGLEWVS	E IL P GS G ST N Y N E K FG	RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR					
	Q M V I		<u>I</u> G	Q Q	A F A I	A M L			G
				S S					
				D D					
				A A					

AbM	10	20	30	40	50	60	70	80	90
huVH3b	EVQLVESGGGLVQPGGSLRLSCAAS	G YTF S RY W IE WVRQAPGKGLEWVS	E IL P GS G ST N Y N E K FG	RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR					
	Q M V I		<u>I</u> G	Q F	A F A I	A M L			G
seq	100	110	120						
	ib i b b b			S					
141A	EEVDGYPWFY	WGQGLVTVSA		A					

huVH3a **E**EVVDGYPWFY WGQGLVTVSS

AbM **100abcd** **110**

huVH3b **E**EVVDGYPWFY WGQGLVTVSS

(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 asterisk (*).

(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.

FIG. 5A

huVH3
Potential humanized sequence based on IMGT IGHV3-48 acceptor framework (method 2)
EVQLVESGGGLVQPGGSLRLSCAAS **GTFFSSYMN** WVRQAPGKGLEWVS **YISSSSSTIYADSVKG** RFTISRDNKNSLYQMNSLRAEDTAVYYCAR

Joining region
IMGT J00256|IGHJ4*01|YFDYWGQTLVTVSS

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

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

seq	100	110
175A	WLLYYYANDY WGQGTSVT VSS	WGQGTSVT VSS
huVH3a	WLLYYYANDY WGQGTL VTVSS	WGQGTL VTVSS
AbM	100ab	110
huVH3b	WLLYYYANDY WGQGTL VTVSS	WGQGTL VTVSS

- (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) isooaspartate formation or Asp-Pro (DP) bond cleavage.

FIG. 5B

huVK2
Potential humanized sequence based on IMGT IGKV2-28 acceptor framework (method 1)
DIVMTQSP^{LS}LPVTPGEPASISC **RSSQSLHSNGNYLD** WYLQKPGQSP^{QL}LIY **LGSNRAS** GVPDRFSGSGGTDFTLKISRVEAEDVGYYC **MQALQTP**
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	DVLMTQTPLSLPVSLGDAQSISC	RSSQSIVHSNGNTYLE	WYLQKPGQSP ^{QL} LIY	KVSNRFS	GVPDRFSGSGGTDFTLKISRVEAEDLGYYC				
	** *	** **	*	*	*	*	*	*	*
huVK2	DIVMTQSP ^{LS} LPVTPGEPASISC	RSSQSIVHSNGNTYLE	WYLQKPGQSP ^{QL} LIY	KVSNRFS	GVPDRFSGSGGTDFTLKISRVEAEDVGYYC				
	V								L
			Q Q			Q			
			S S			S			
			D D			D			
			A			A			

seq	100	110
AbM	90	100
	i b i	i b b
76E1	FGQSHVPWT	FGGGTKLEIK
	*	
huVK2	FGQSHVPWT	FGGGTKLEIK

(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) isooaspartate formation or Asp-Pro (DP) bond cleavage.

FIG. 6A

huVK1
Potential humanized sequence based on IMGT IGKV1-39 acceptor framework (method 2)
DIQMTQSPSSLASVGDRTTTC **RASQSISSYLN** WYQQKPKAPKLLIY **AASSLQS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC **QQSYSTP**
Joining region
IMGT J00242|IGKJ2*01|YTFGGQGTKLEIK

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	DVLMTQTPLSLPVSLGDAQSISC	RSSQSIVHSNGNTYLE	WYLQKPGQSPKLLIY	KVSNRFS	GVPSRFSGSGSGTDFTLKINRVEAEDLGYYC				
	** * * *	** * *				*		* * * * *	** *
huVK1	DIQMTQSPSSLASVGDRTTTC	RSSQSIVHSNGNTYLE	WYQQKPKAPKLLIY	KVSNRFS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC				
	V	V	A	S	Q	S	V	LG	
			Q Q			S			
			S S			D			
			A A			A			
			D						

seq	100	110
AbM	90	100
	ibi iib i	b b b
76E1	FGCSHPWT	FGGQTKLEIK
	*	
huVK1	FGCSHPWT	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 (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) isoaspartate formation or Asp-Pro (DP) bond cleavage.

FIG. 6B

huVK3
Potential humanized sequence based on IMGT IGV3-20 acceptor framework (method 1)
EIVLTQSPGTLSPGERATLSC **RASQVSSSYLA** WYQQKPGQAPRLIIY **GASSRAT** GIPDRFSGSGGTDFLTISRLEPEDFAVYYC **QQYGSSP**
Joining region
IMGT J00242|IGKJ2*01|YTFGGQTKLEIK

seq	10	20	30	40	50	60	70	80
AbM	10	20	34	40	50	60	70	80
	b b b	b b b	b b b	i i i b b i	i b b	b b b	b b b	b b b
141A	QIVLSQSPAILSASPGKVTMTC RASSLSLYMH WYQQKPGSSPKPWIIY ATSNLAS GVPARFSGSGGTSLTISRVEAEDAATYYC							
	* * *	* * *	** **	** **	** **	***	* * *	* * *
huVK3	EIVLTQSPGTLSPGERATLSC RASSLSLYMH WYQQKPGQAPRLIIY ATSNLAS GIPDRFSGSGGTDFLTISRLEPEDFAVYYC							
	A	V M	S	P W	Q	V	Y	V

seq	90	100
AbM	90	100
	ibi iib i	b b b
141A	QQWSSNPYT FCGGCKLEIK	
	*	
huVK3	QQWSSNPYT FCGGCKLEIK	
	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 [\(5\) 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 \(DG\) isoaspartate formation or Asp-Pro \(DP\) bond cleavage.](http://www.bioinf.org.uk/abs/>(AbM).</div><div>(4))
- FIG. 7A
- SUBSTITUTE SHEET (RULE 26)

huVK1
Potential humanized sequence based on IMGT IGV1-39 acceptor framework (method 2)
DIQMTQSPSSLSASVGDRVTITC **RASQSISSYLN** WYQQKPKAPKLLIY **AASSLQS** GVPSTRFSGSGGTDFLTISSLQPEDFATYYC **QQSYSTP**
Joining region
IMGT J00242|IGKJ2*01|YTFGGQTKLEIK

seq	10	20	30	40	50	60	70	80
AbM	10	20	34	40	50	60	70	80
	b b b	b b b	b b b	i i i	b b b	b b b	b b b	b b b
141A	QIVLSQSPAILSASPGEKVTITC RASSLSYMH WYQQKPGSSPKPWIY ATSNLAS GVPARFSGSGTSLTISRVEAEDAATYYC							
	* * * *	* * * *	* * *	* * *	*	***	***	*
huVK1	DIQMTQSPSSLSASVGDRVTITC RASSLSYMH WYQQKPKAPKLLIY ATSNLAS GVPSTRFSGSGGTDFLTISSLQPEDFATYYC							
	L	M	S	P	W	Q	Y	V

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

FIG. 7B

- (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 [\(5\) 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 \(DG\) isoaspartate formation or Asp-Pro \(DP\) bond cleavage.](http://www.bioinf.org.uk/abs/>(AbM).</div><div>(4))
- SUBSTITUTE SHEET (RULE 26)

huVK2
Potential humanized sequence based on IMGT IGKV2-28 acceptor framework (method 1)
DIVMTQSP^{LS}LPVTPGEPASISC **RSSQSLHSNGNYLD** WYLQKPGQSP^{QL}LIY **LGSNRAS** GVPDRFSGSGGTDFTLKISRVEAEDVG^{YY}YC **MQALQTP**

Joining region
IMGT J00242|IGKJ2*01|YTFGGQTKLEIK

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30abcde	40	50	60	70	80	90
	b b 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
175A	DVLMTQTPLSLPVSLGDAQSISC	RSSQSI VHSNGNTYLE	WYLQKPGQSP ^{QL} LIY	KL SNRFS	GVPDRFSGSGGTDFTLKISRVEAEDLG ^{YY} YC				
	** *	** **		*					*
huVK2	DIVMTQSP ^{LS} LPVTPGEPASISC	RSSQSI VHSNGNTYLE	WYLQKPGQSP ^{QL} LIY	KL SNRFS	GVPDRFSGSGGTDFTLKISRVEAEDVG ^{YY} YC				L
	V		<u>Q</u> <u>Q</u>		Q				
			<u>S</u> <u>S</u>		S				
			A A		D				
			D		A				

seq 100 110
AbM 90 100
ibi iib i b b b
175A **FQGS**HFPYT FCGGTKLEIK
*
huVK2 **FQGS**HFPYT FCGGTKLEIK

- (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 sequences 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) isoaspartate formation or Asp-Pro (DP) bond cleavage.

FIG. 8A

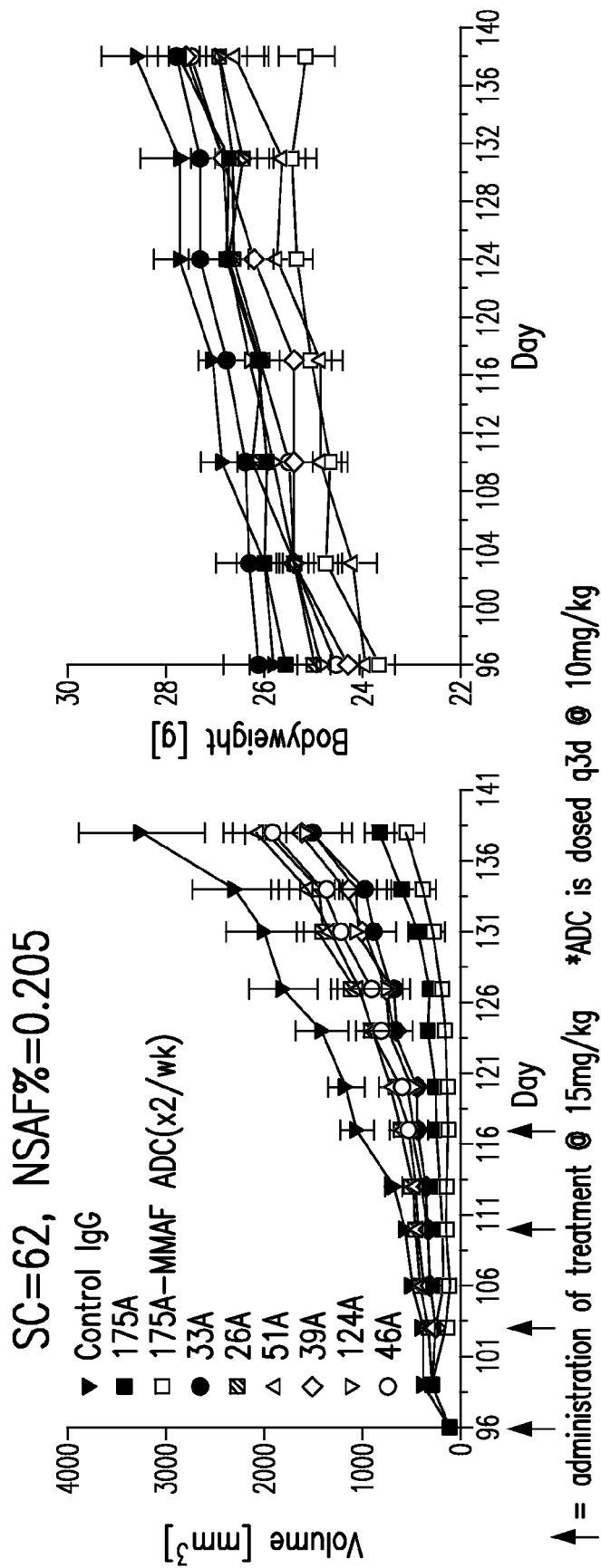
huVK1
Potential humanized sequence based on IMGT IGV1-39 acceptor framework (method 2)
DIQMTQSPSSLSASVGRVTITC **RASQSISSYLN** WYQQKPKAPKLLIY **AASSLQS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC **QQSYSTP**
Joining region
IMGT J00242|IGKJ2*01|YTFGGQTKLEIK

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30abcde	40	50	60	70	80	90
	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	DVLMTQTPLSLPVSLGDAQIS	C	RSSQSI VH SN GYLE	WY	QKPKAPKLLIY	KL SNRFS	GV	PSRFSGSGSGTDFTL	KISRVEAEDLG
	**	*	*	*	*	*	*	*	*
	**	*	*	*	*	*	*	*	*
huVK1	DIQMTQSPSSLSASVGRVTITC		RSSQSI VH SN GYLE	WY	QKPKAPKLLIY	KL SNRFS	GV	PSRFSGSGSGTDFTL	TISSLQPEDFATYYC
	V	V	A		S	Q		V	LG
			Q Q			S			
			S S			S			
			A A			D			
			D			A			

seq	100	110
AbM	90	100
	i b i	i b b
175A	FQGS HFPYT	FGCGTKLEIK
	*	
huVK1	FQGS HFPYT	FGCGTKLEIK

- (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 sequences 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) isoaspartate formation or Asp-Pro (DP) bond cleavage.

FIG. 8B



Kasumi-3 NOD	Control IgG _{2a}	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

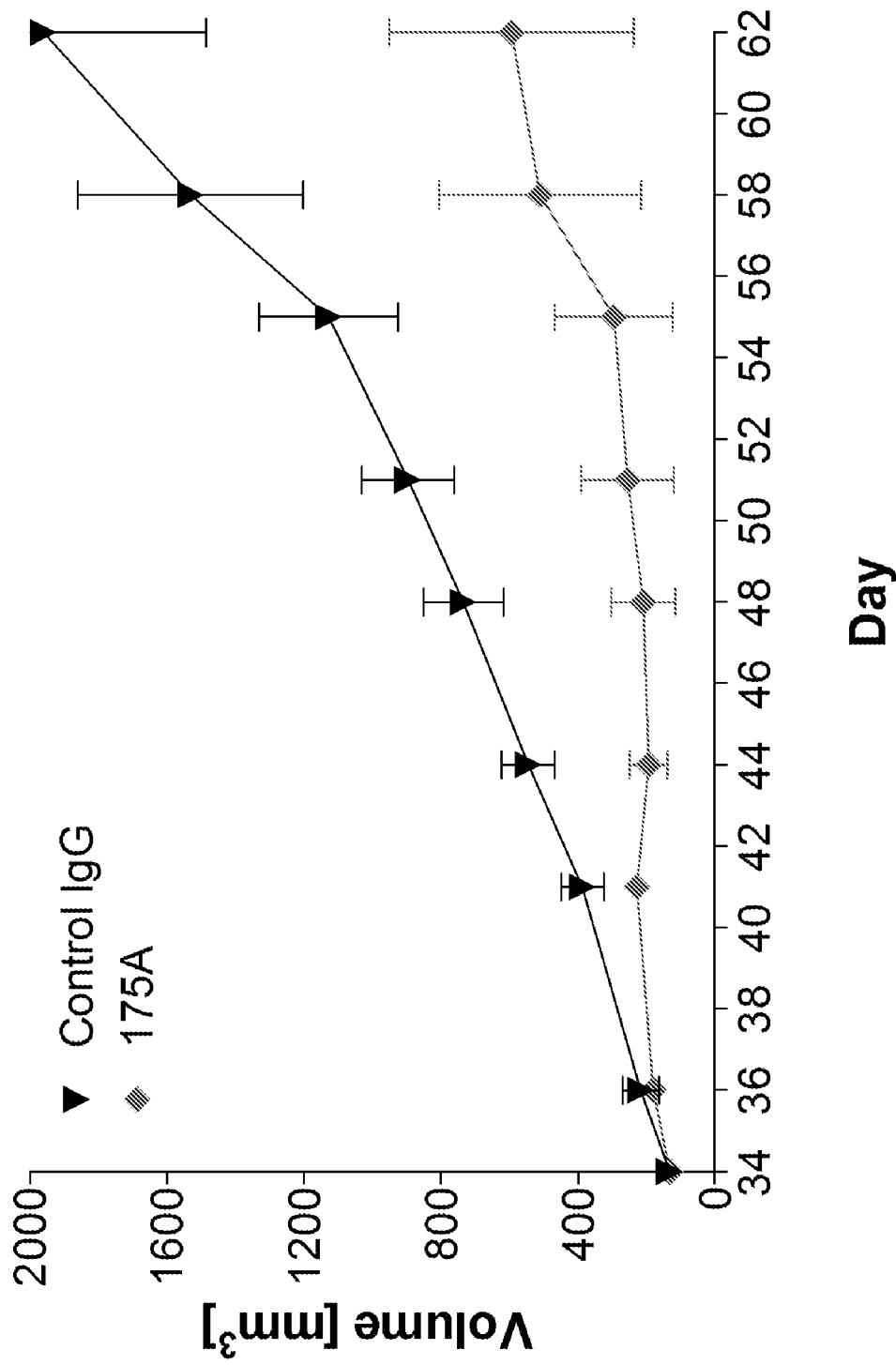


FIG. 11

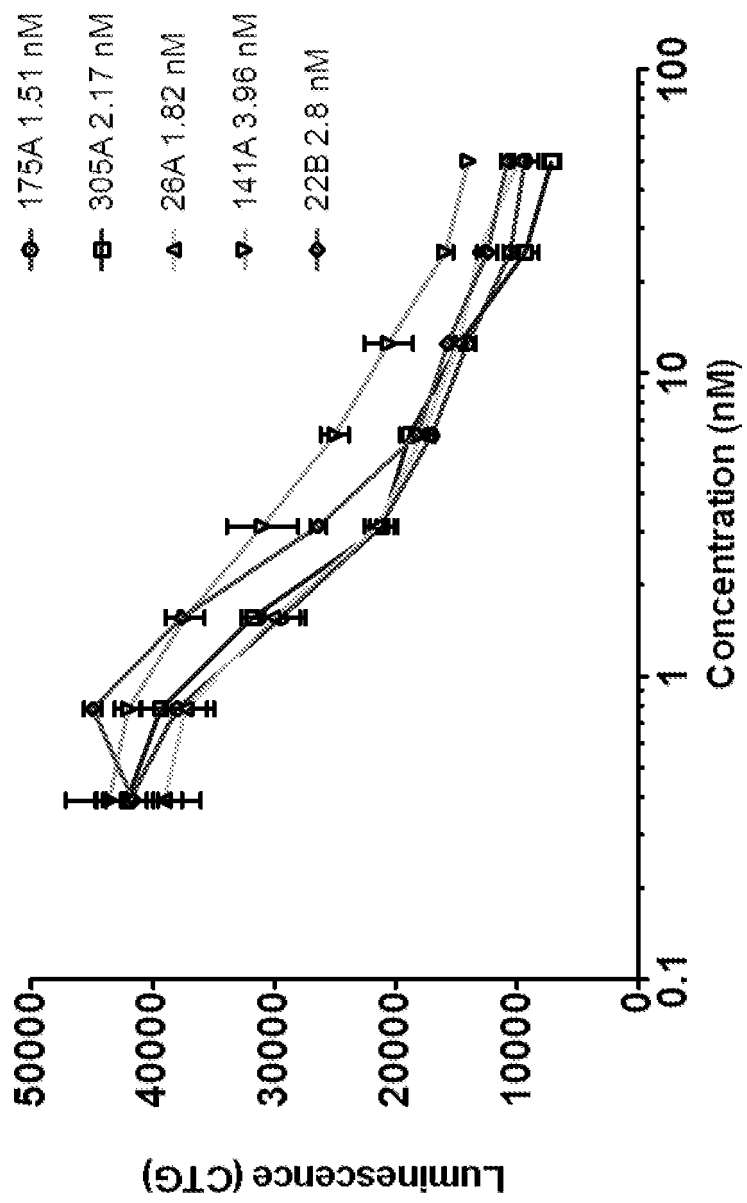
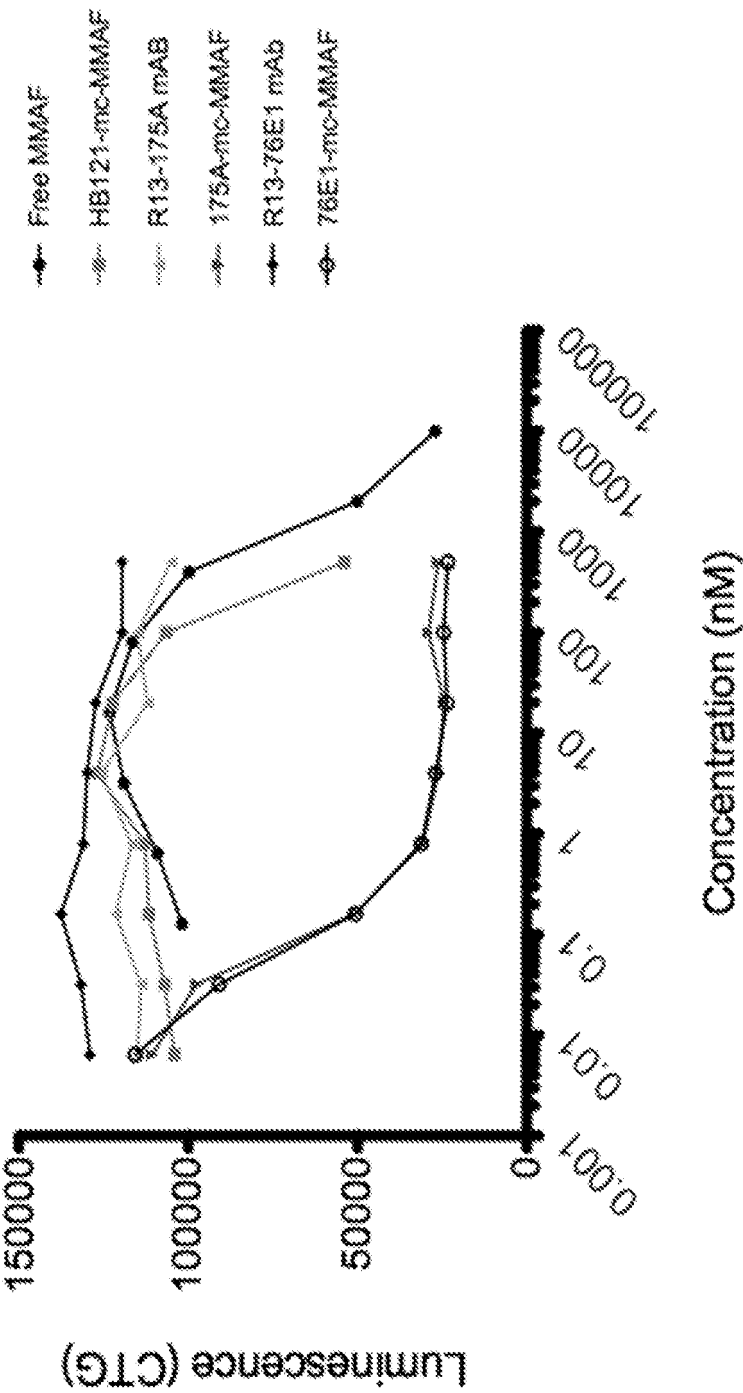


FIG. 12



	Free MMAF	175A-mc-MMAF	76E1-mc-MMAF
IC50	1560	0.07166	0.05877
R square	0.9504	0.9906	0.9995

FIG. 13

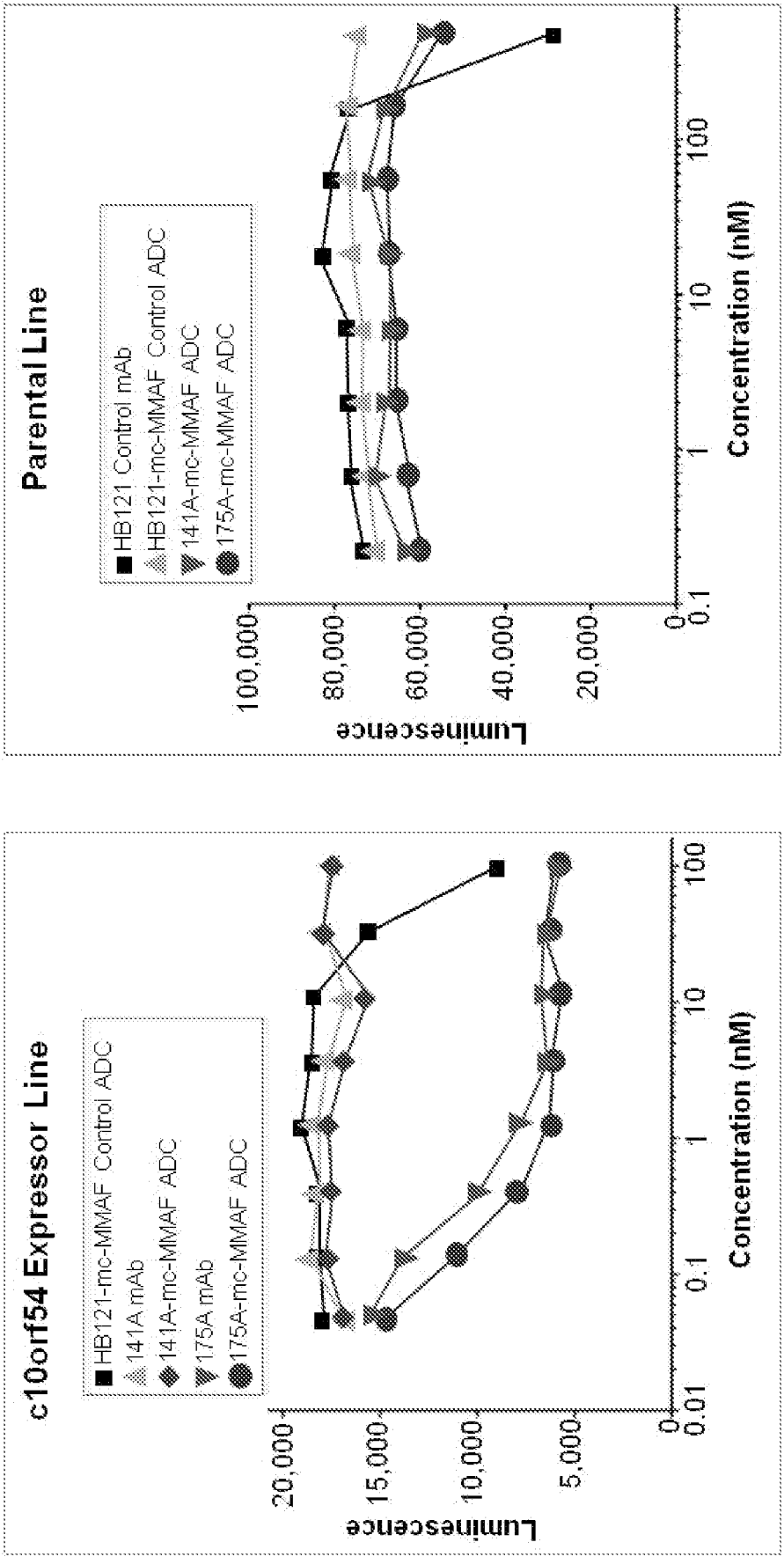


FIG. 14

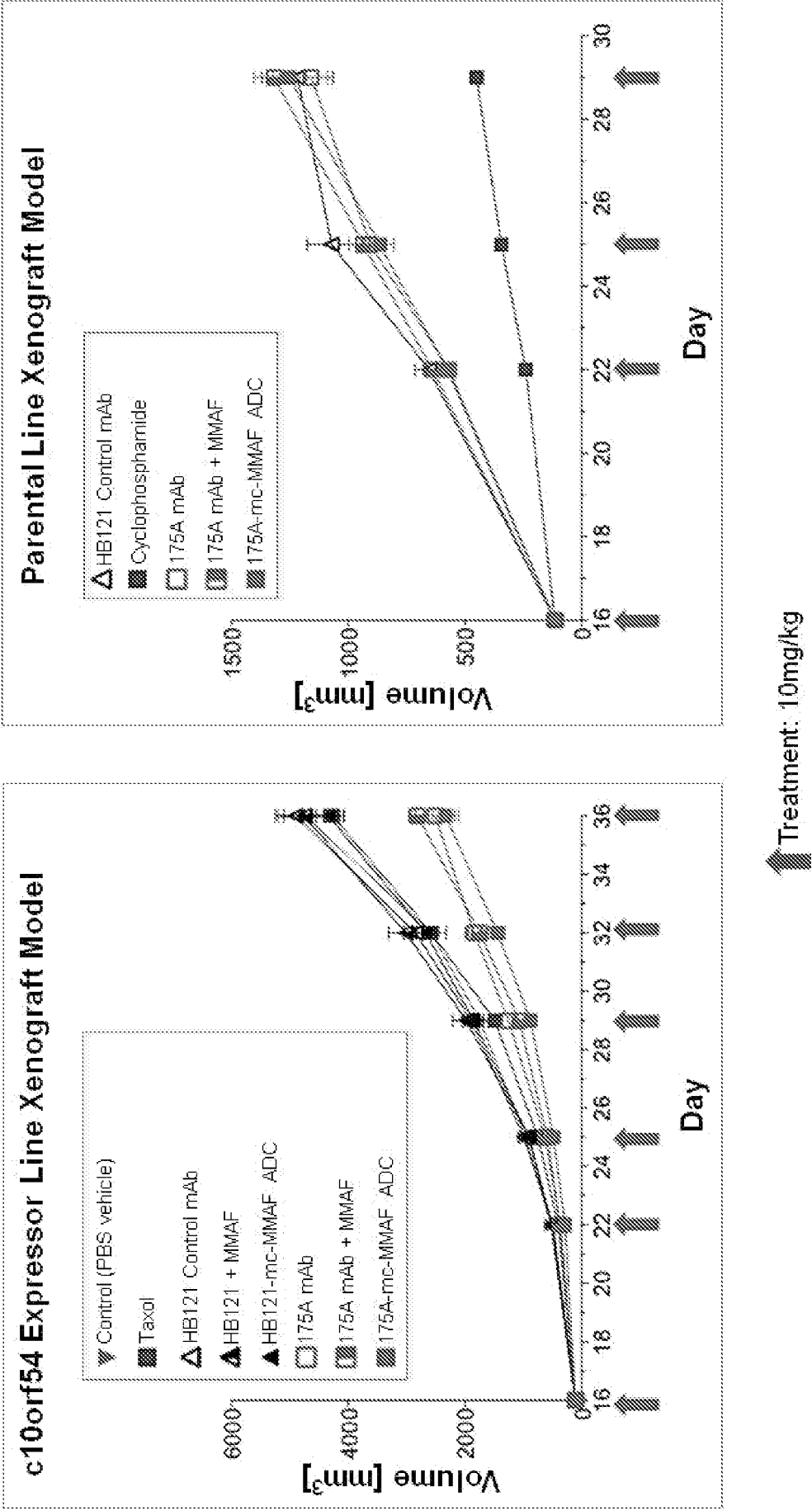


FIG. 15

R13 VH

R13-3610-76E1 MGWTWIFILLSVTTGVHS
R13-3610-141A MEWTWVFLFLSVTAGVHS
R13-3610-175A MEWTWVFLFLSVTAGVHS

Kabat	1	10	22	31--35	40	50--a-----60----	65
AbM	1	10	22	26-----35	40	50--a-----58	65
Chothia	1	10	22	26-----32	40	a-55	65
Contact	1	10	22	30----35	40	47-----a-----58	65
IMGT	1		23	27-----38	41	56-----65	74

76E1 EVQLLQSGPELEKPGASVKISCKAS GYSFTGYNMN WVKQSNKGKSLWIG NIDPYYDYTSYNLKFKD
141A QVQLQQSGAELMKPGASVKISCKAT GYTFSTRYWIE WVKQRPFGHGLEWIG EILPGSGSTNYNEKFKG
175A QVQLQQSGAELMKPGASVKISCKAT GYTFSTHWIE WVKQRPFGHGLEWIG 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 KATLTVDKSSSTAYMQLKSLTSEDSAVYYCAT STMITP---FDY WQQGTLTVSS
141A KATFTADTSSNTAYMQLSSLTSEDSAVYYCAG EEVYDGYPWFGY WQQGTLVTVSA
175A KATFTADTSSNTAYMQLSSLTSEDSAVYYCAR WLLYYA--MDY WQQGTSVTVSS

FIG. 16A

R13 VL

R13-3610-76E1 MKLPVRLLVLMFWIPASSS
R13-3610-141A MDFQVQIFSFLLISASVIMSRG
R13-3610-175A MKLPVRLLVLMFWIPASSS

Kabat	1	10	20	24-27abcd-----34	40	50-----56
AbM	1	10	20	24-----30abcd---34	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 DVLMTQTPLSLPVSIGDQASISC RSSQSIIVHSNGNTYLE WYLQKPGQSPKLLIY KVSNRFS
141A QIVLSQSPAILSASPGKVTMT C RASSL-----SYMH WYQQKPGSSPKPWIY ATSNLAS
175A DVLMTQTPLSLPVSIGDQASISC RSSQSIIVHSNGNTYLE WYLQKPGQSPKLLIY KLSNRFS

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 GVPDRFSGSGGTDFTLKINRVEAEDLGVIYC FQGSHPWT FGGGTKLEIK
141A GVPARFSGSGGTSYSLTISRVEAEDAATYIC QQWSSNPYT FGGGTKLEIK
175A GVPDRFSGSGGTDFTLKISRVEAEDLGVIYC FQGSHPYT FGGGTKLEIK

FIG. 16B

R13 VH

AbM	1	10	22	26-----35	40	50--a-----58	65
hu76E1	QVQLVQSGAEVKKPGASVKVCKAS	GYSFTGYNMN	WVRQAPGQGLEWIG	NIDPYDYTSYNLFKFD			
hu141A	QVQLVQSGAEVKKPGASVKVCKAS	GYTFSRYWIE	WVRQAPGQGLEWIG	EILPGSGSTNYNEKFKG			
hu175A	QVQLVQSGAEVKKPGASVKVCKAS	GYTFSSTHWIE	WVRQAPGQGLEWIG	EILPGSGSTSYNEKFKG			
consen	QVQLVQSGAEVKKPGASVKVCKAS	GYTFSXXWIE	WVRQAPGQGLEWIG	EILPGSGSTXYNEKFKG			
		RY		N			
		TH		S			

AbM

hu76E1

hu141A

hu175A

consen

70	80	abc	90	95--100---102	110		
RVTMTVDKSTSTAYMELRLSRSDDDTAVYYCAT	STMITP---	FDY	WGQGT	LVTVSS	(SEQ ID NO: 1135)		
RVTMTADTSTSTAYMELRLSRSDDDTAVYYCAG	EEVYDGYPWFGY	WGQGT	LVTVSS	(SEQ ID NO: 1136)			
RVTMTADTSTSTAYMELRLSRSDDDTAVYYCAR	WLLYYA--MDY	WGQGT	LVTVSS	(SEQ ID NO: 1137)			
RVTMTADTSTSTAYMELRLSRSDDDTAVYYCAR	xxxxxxxxxxXY	WGQGT	LVTVSS	(SEQ ID NO: 1138)			
	MG						
	FD						

FIG. 17A

R13 VL

AbM	1	10	20	24-----30abcd---34	40	50-----56
hu141A	EIVLTQSPGTLSLSPGERATLSC	RASSSL-----SYMH	WYQQKPGQAPRPWIY	ATSNLAS		
hu76E1	DIVMTQSPPLSLPVTTPGEPASISC	RSSQSIVHSNGNTYLE	WYLQKPGQSPQLLIY	KVSNRFS		
hu175A	DIVMTQSPPLSLPVTTPGEPASISC	RSSQSIVHSNGNTYLE	WYLQKPGQSPQLLIY	KLSNRFS		
consen	DIVMTQSPPLSLPVTTPGEPASISC	RSSQSIVHSNGNTYLE	WYLQKPGQSPQLLIY	KXSNRFS		

V
L

AbM	60	70	80	89-----97		
hu141A	GIPDRFSGSGTDYTLTISRLEPEDFAVYYC	QQWSSNPYT	FGQGTKLEIK	(SEQ ID NO: 1139)		
hu76E1	GVPDRFSGSGTDFTLKISRVEAEDVGVYYC	FQGSHPVPT	FGQGTKLEIK	(SEQ ID NO: 1140)		
hu175A	GVPDRFSGSGTDFTLKISRVEAEDVGVYYC	FQGSHPPT	FGQGTKLEIK	(SEQ ID NO: 1141)		
consen	GVPDRFSGSGTDFTLKISRVEAEDVGVYYC	FQGSHPPT	FGQGTKLEIK	(SEQ ID NO: 1142)		

V W
F Y

FIG. 17B