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	Stop	SEQ ID NO.	Hydrophilic	SEQ ID NO.	Hydrophobic	SEQ ID NO.
D1-1	VQLER	8	YNWND	45	GTTGT	88
HD1-1	VPLAR	9	YHWHD	46	GTTGT	88
D1-7	V*LEL	-	YNWNY	47	GITGT	89
HD1-7	VSLAL	10	YHWHY	48	GITGT	89
D1-20	V*LER	-	YNWND	45	GITGT	89
HD1-20	VSLAR	11	YHWHD	46	GITGT	89
D1-26	V*WELL	12	YSGSY	49	GIVGAT	90
HD1-26	VSWEPL	13	YHGSY	50	GIMGAT	91
D2-2*02	RIL**YQLLY	14	GYCSSTSCYT	51	DIVVPAAI	92
HD2-2*02	RTL*SYQLPY	15	GHCSHTSOHT	52	DIVVPAAI	93
D2-8*01	RILY*WCMLY	16, 17	GYCTNGVCYT	53	DIVLMVYAI	94
HD2-8*01	RTLYSWCMPY	18	GHCTHGVCHT	54	DIVLMVYAI	94
D2-15	RIL*WW*LLL	-	GYCSGGSCYS	55	DIVVVAAT	95
HD2-15	RTL*SW*LPL	-	GHCSHGSCHS	56	DIVVVAAT	96
D2-21*02	SILWW*LLF	19	AYCGDCYS	57	HIVVTAI	97
HD2-21*02	STLWWSLPL	20	AHCGHCHS	58	HIVVTAI	97
D3-3*01	VLRFLEWLLY	21	YYDFWSGYT	59	ITIFGWII	98
HD3-3*01	VSPFLEWSLY	22	YHFWSGHYT	60	ITIFGWII	98
D3-9	VLRYFDWLL*	23	YYDILTGYN	61	ITIF*LVII	99, 100
HD3-9	VSPYFDWSL*	24	YHHILTGHYN	62	ITIF*LVII	99, 100
D3-10*01	VLLWFGELL*	25	YYGSGSYN	63	ITMVRGVII	101
HD3-10*01	VSPWFGESE*	26	YHGSAGSHYN	64	ITMVRGVII	101
D3-16*02	VL*LRLGELSLY	27	YYDYVWGSYRYT	65	IMITFGGVVI	102
HD3-16*02	VS*SRLGESSLY	28	YHDHVVWGSYRYT	66	IMITFGGVVI	102
D3-22	VLL***WLLL	29	YYDSSSGYNY	67	ITMIVVIT	103
HD3-22	VSL***WLLL	30, 31	YHYHSSGHYNY	68	ITIVVIT	104
D4-4	*LQ*L	-	DYSNY	69	TTVT	105
HD4-4	*PQSL	32	DHSHY	70	TTVT	105
D4-11p	*LQ*L	-	DYSNY	69	TTVT	105

FIG. 1A

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	Stop	SEQ ID NO.	Hydrophilic	SEQ ID NO.	Hydrophobic	SEQ ID NO.
HD4-11p	*PQSL	32	DHSY	70	TTVT	105
D4-17	*LR*L	-	DYGDY	71	TTVT	105
HD4-17	*PRSL	33	DHGHY	72	TTVT	105
D4-23p	*LRW*L	-	DYGGNS	73	TTVT	106
HD4-23p	*PRWSL	34	DHGGHS	74	TTVT	106
D5-5	WIQLWL	35	GYSGY	75	VDTAMV	107
HD5-5	WTQPWL	36	GSHGY	76	VDTAMV	107
D5-12	WI*WLRL	37	GYSGYDY	77	VDIVATI	108
HD5-12	WT*WPPL	38	GSHGHY	78	VDIVATI	108
D5-18	WIQLWL	35	GYSGY	75	VDTAMV	107
HD5-18	WTQPWL	36	GSHGY	76	VDTAMV	107
D5-24p	*RWLQL	39	RDGYNY	79	VEMATI	109
HD5-24p	*TWPL	40	RHGHY	80	VDMATI	110
D6-6	V*QLV	-	EYSSS	81	SIAAR	111
HD6-6	A*PLV	-	ESHSS	82	SIATR	112
D6-13	V*QQLV	41	GYSSSWY	83	GIAAG	113
HD6-13	A*PQLV	42	GSHSWY	84	GIATAG	114
D6-19	V*QWL	43	GYSSGWY	85	GIAVAG	115
HD6-19	A*PWL	44	GSHGWY	86	GIAAG	116
D6-25	V*QRL	-	GYSSGY	87	GIAA	117
HD6-25	A*PRL	-	GSHGY	76	GIATA	118

FIG. 1B

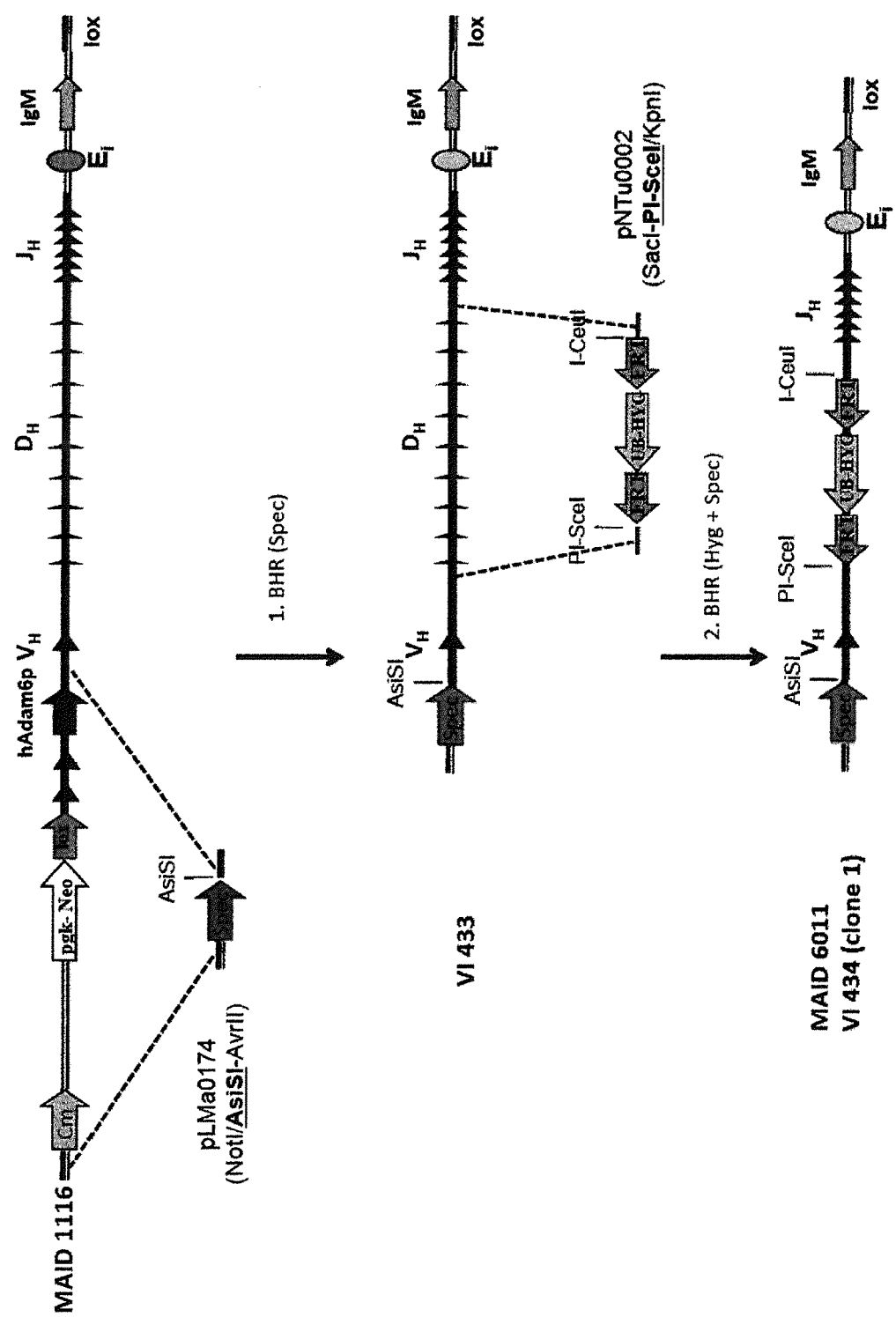


FIG. 2

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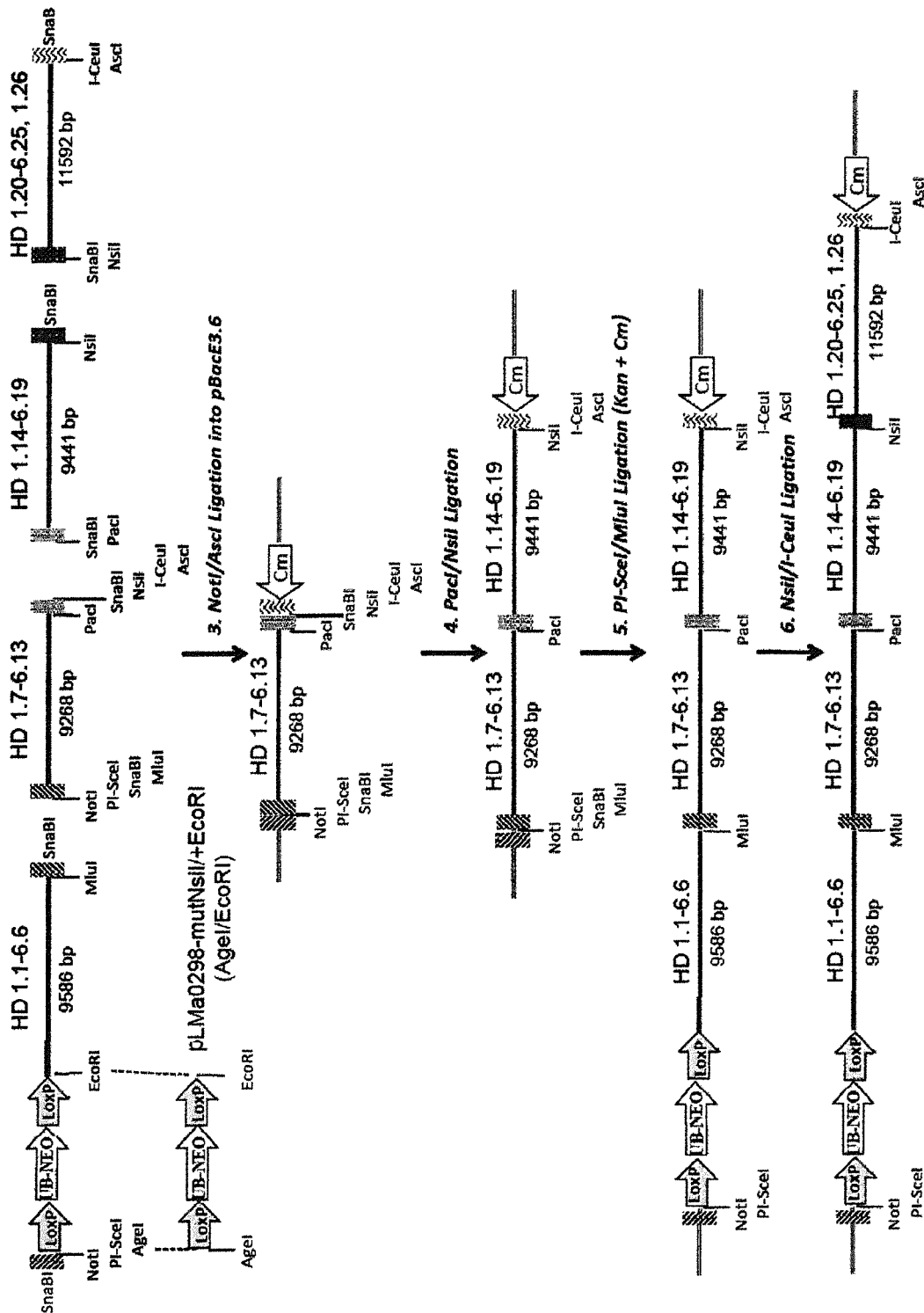


FIG. 3

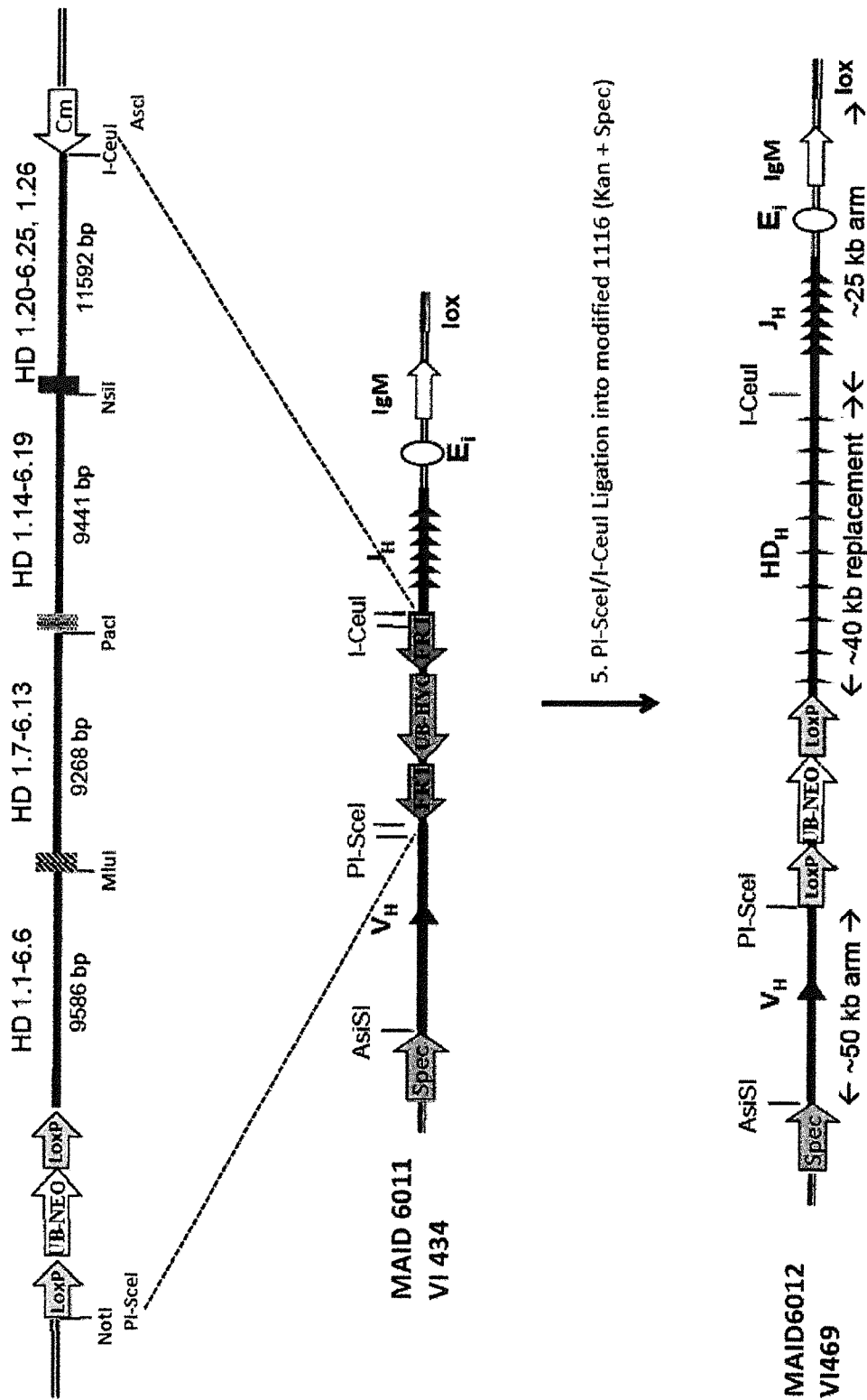


FIG. 4

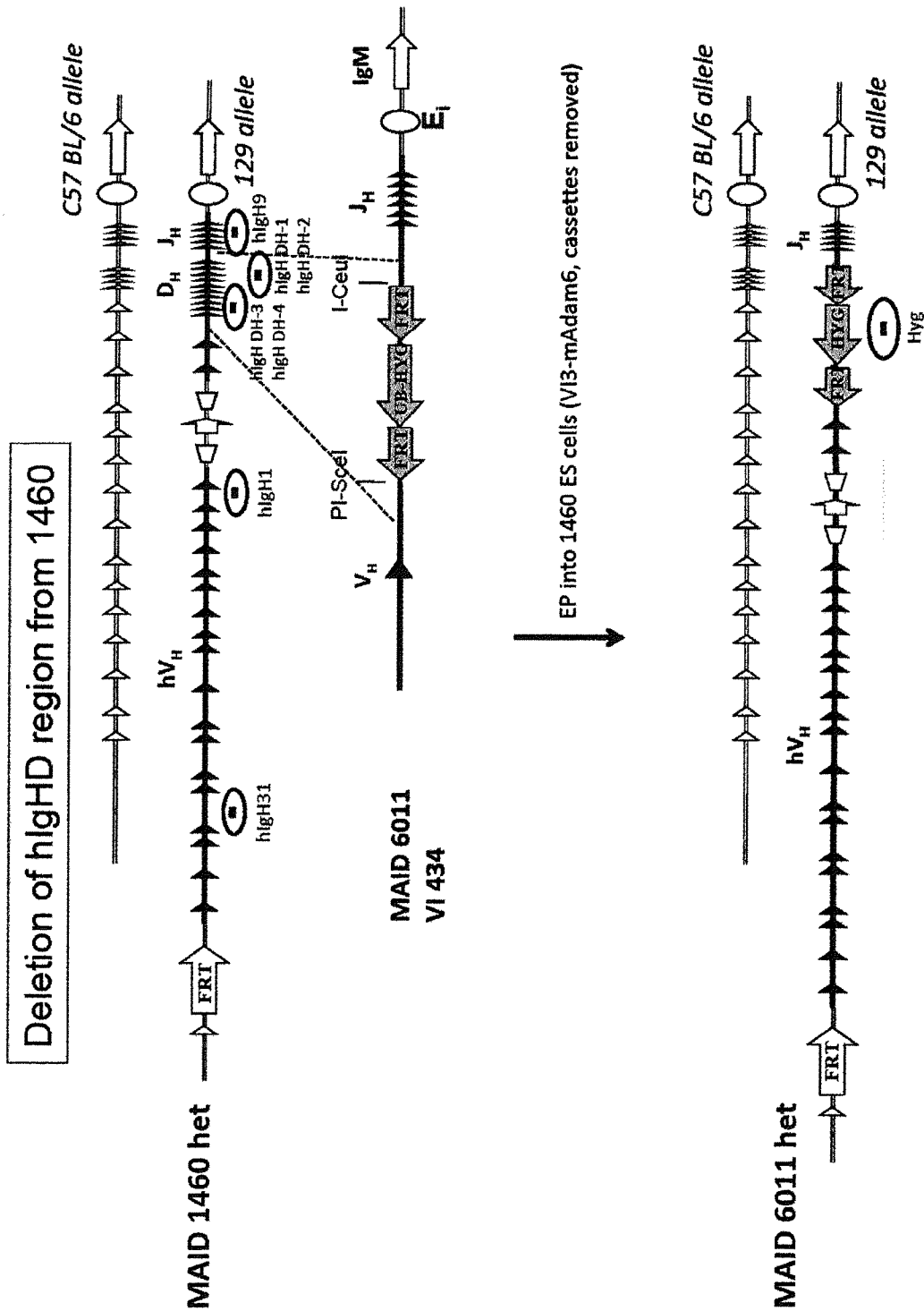


FIG. 5

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Probes for MAID 6011 (deletion of hlgH DH segments in MAID1460)						
Name	Forward Primer	Probe	Reverse Primer	Type	Label	Location
hlgH DH-1	CGGGTCACTGCCATTCTG (SEQ ID NO: 119)	TCTGCATTGCTCCAGCGC (SEQ ID NO: 120)	TCTGGCGCATGAACCCCAAT (SEQ ID NO: 121)	LOA	FAM- BHQ 1	hlgH D segments
hlgH DH-2	GTGCAGGGGAGGACCTTCT G (SEQ ID NO: 122)	AGTCACCAAGCACAGAGCCCTGAC (SEQ ID NO: 123)	GCCAGGGAGTTGCCCTAGTG (SEQ ID NO: 124)	LOA	FAM- BHQ 1	hlgH D segments
hlgH DH-3	GTGGCCCACTTCCCTTCT (SEQ ID NO: 125)	CAGCTGGAACCCACCATGACCT (SEQ ID NO: 126)	GACCTGCCCTCGGATGACA (SEQ ID NO: 127)	LOA	FAM- BHQ 1	hlgH D segments
hlgH DH-4	TGGCCAGAACTGACCTTAC (SEQ ID NO: 128)	ACCGACAAGAGTCCTCAGG (SEQ ID NO: 129)	GGAGTCGGCTCTGGATGTG (SEQ ID NO: 130)	LOA	BHQ- plus	hlgH D segments
hyg	TGCGGCCGATCTTAGCC (SEQ ID NO: 131)	ACGAGCGGGTTCGGCCCATTC (SEQ ID NO: 132)	TTGACCGATTCTTGCGG (SEQ ID NO: 133)	GOA	FA- BHQ 1	
hlgH1	CAGTCCCGTTGATCCAGCC (SEQ ID NO: 134)	CCCATCAGGGATTGTATCTCTGT GGACG (SEQ ID NO: 135)	GGATATGCAGCACTGTGCCAC (SEQ ID NO: 136)	AR		hlgH
hlgH9	TCCTCCAACGACAGGTCCC (SEQ ID NO: 137)	TCCCTGGAACCTCTGCCCGACACA (SEQ ID NO: 138)	GATGAACTGACGGGCACAGG (SEQ ID NO: 139)	AR		hlgH
hlgH31	ATCACACTCATCCCATCCCC (SEQ ID NO: 140)	CCCTTCCCTAAGTACCACAGAGTGG GCTC (SEQ ID NO: 141)	CACAGGGAAGCAGGAACTGC (SEQ ID NO: 142)	AR		hlgH

FIG. 6

Insertion of HD_H (His-substituted) hlgH D_H region

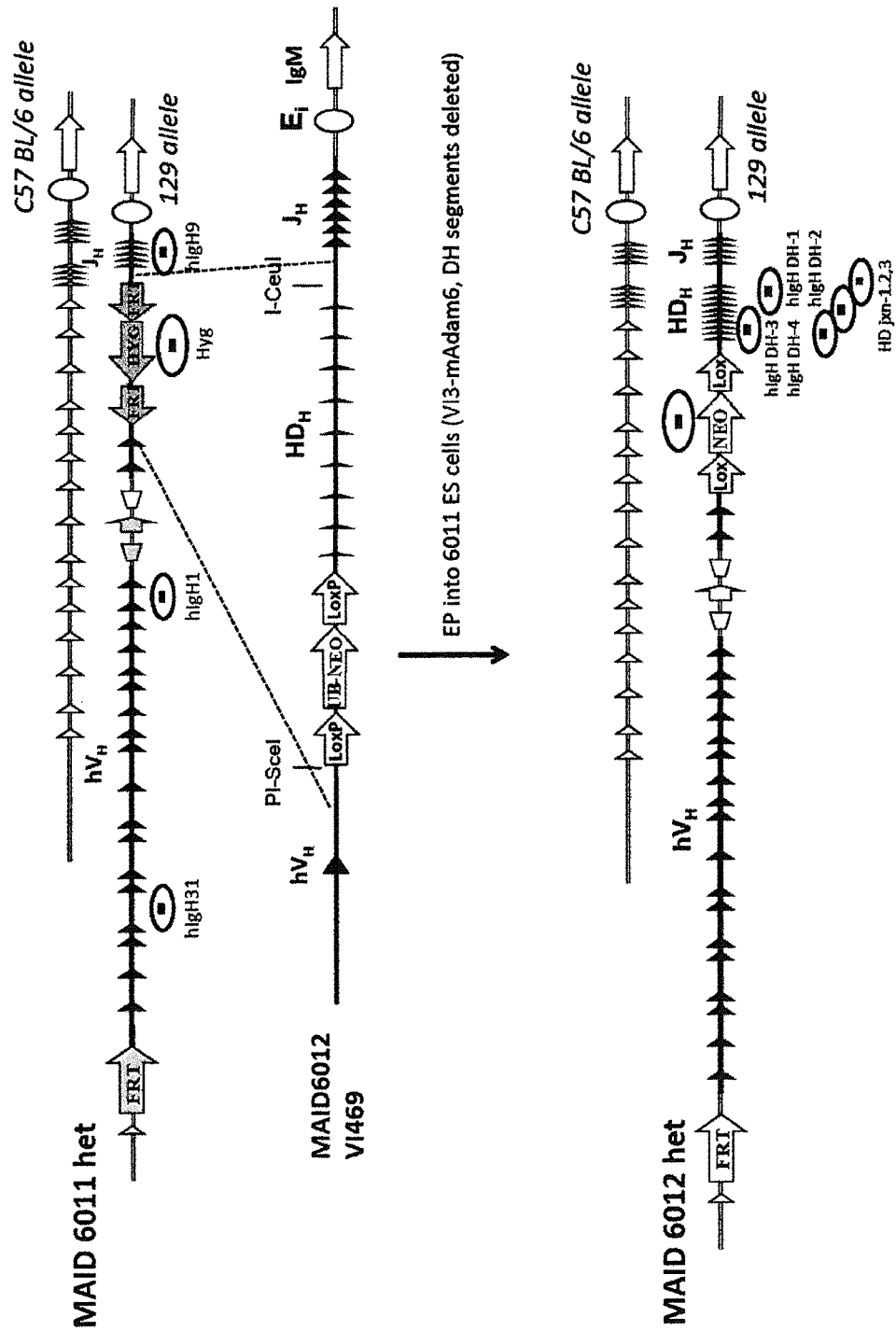


FIG. 7

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Probes for MAID 6012 (insertion of HD, His-substituted high DH segments)						
Name	Forward Primer	Probe	Reverse Primer	Type	Label	Location
hys	TGCGCCGATCTTAGCC (SEQ ID NO: 131)	ACGAGCGGTTCGGCCCATTC (SEQ ID NO: 132)	TTGACCGATTCTTGCGG (SEQ ID NO: 133)	LOA	FAM- BHQ1	
HD jxn-1	GGAGCCAGGACGACACA (SEQ ID NO: 143)	TGGGCTCGTAGTTTGACGT (SEQ ID NO: 144)	GGGACTTCTTACCCACA CTTCA (SEQ ID NO: 145)	GOA	MGB	Synthetic linker-1 in HD segments
HD jxn-2	GGTCCCGAGCACTCTTAATAAA C (SEQ ID NO: 146)	CCTCGAATGGAATAC (SEQ ID NO: 147)	GGGAGAGCAACCATTCG TTGT (SEQ ID NO: 148)	GOA	MGB	Synthetic linker-2 in HD segments
HD jxn-3	CCGAGCACCGATGCATCTA (SEQ ID NO: 149)	CGCAGTCATGTAATGC (SEQ ID NO: 150)	GGGAGGCGAACTGACTG TCA (SEQ ID NO: 151)	GOA	MGB	Synthetic linker-3 in HD segments
high DH-1	CGGGTCACTGCCATTCTG (SEQ ID NO: 119)	TCTGCATTCGCTCCAGCGC (SEQ ID NO: 120)	TCTGCGGCATGAACCCAA T (SEQ ID NO: 121)	GOA	FAM- BHQ1	high D segments
high DH-2	GTGAGGGAGGACCTTCTG (SEQ ID NO: 122)	AGTACCAAGCACAGAGCCCTGA C (SEQ ID NO: 123)	GCCAGGGAGTTGCCTAG TG (SEQ ID NO: 124)	GOA	FAM- BHQ1	high D segments
high DH-3	GTGGCCCACTTCCCTTCCT (SEQ ID NO: 125)	CAGCTGGAACCCACCATGACCT (SEQ ID NO: 126)	GACCTGCTCGGATGACA (SEQ ID NO: 127)	GOA	FAM- BHQ1	high D segments
high DH-4	TGGCCAGAACTGACCCCTAC (SEQ ID NO: 128)	ACCGACAAGAGTCCCTCAGG (SEQ ID NO: 129)	GGAGTCGGCTCTGGATGTG (SEQ ID NO: 130)	GOA	BHQ- plus	high D segments
neo	GGTGGAGAGGCTATTTCGGC (SEQ ID NO: 152)	TGGGCACAACAGACAATCGGCTG (SEQ ID NO: 153)	GAACACGCGGCATCAG (SEQ ID NO: 154)	GOA	FAM- BHQ1	
highH1	CAGTCCCCTTGATCCAGCC (SEQ ID NO: 134)	CCCATCAGGGATTTGTATCTC TGTGGACG (SEQ ID NO: 135)	GGATATGCAGCACTGTGCC AC (SEQ ID NO: 136)	AR		high
highH9	TCCTCCAACGACAGGTCCC (SEQ ID NO: 137)	TCCCTGGAACTCTGCCCCGACACA (SEQ ID NO: 138)	GATGAACTGACGGGCACA GG (SEQ ID NO: 139)	AR		high
highH31	ATCACACTCATCCCATCCCC (SEQ ID NO: 140)	CCCTTCCCTAAGTACCACAGAGTG GGCTC (SEQ ID NO: 141)	CACAGGGAAGCAGGAAGT GC (SEQ ID NO: 142)	AR		high

FIG. 8

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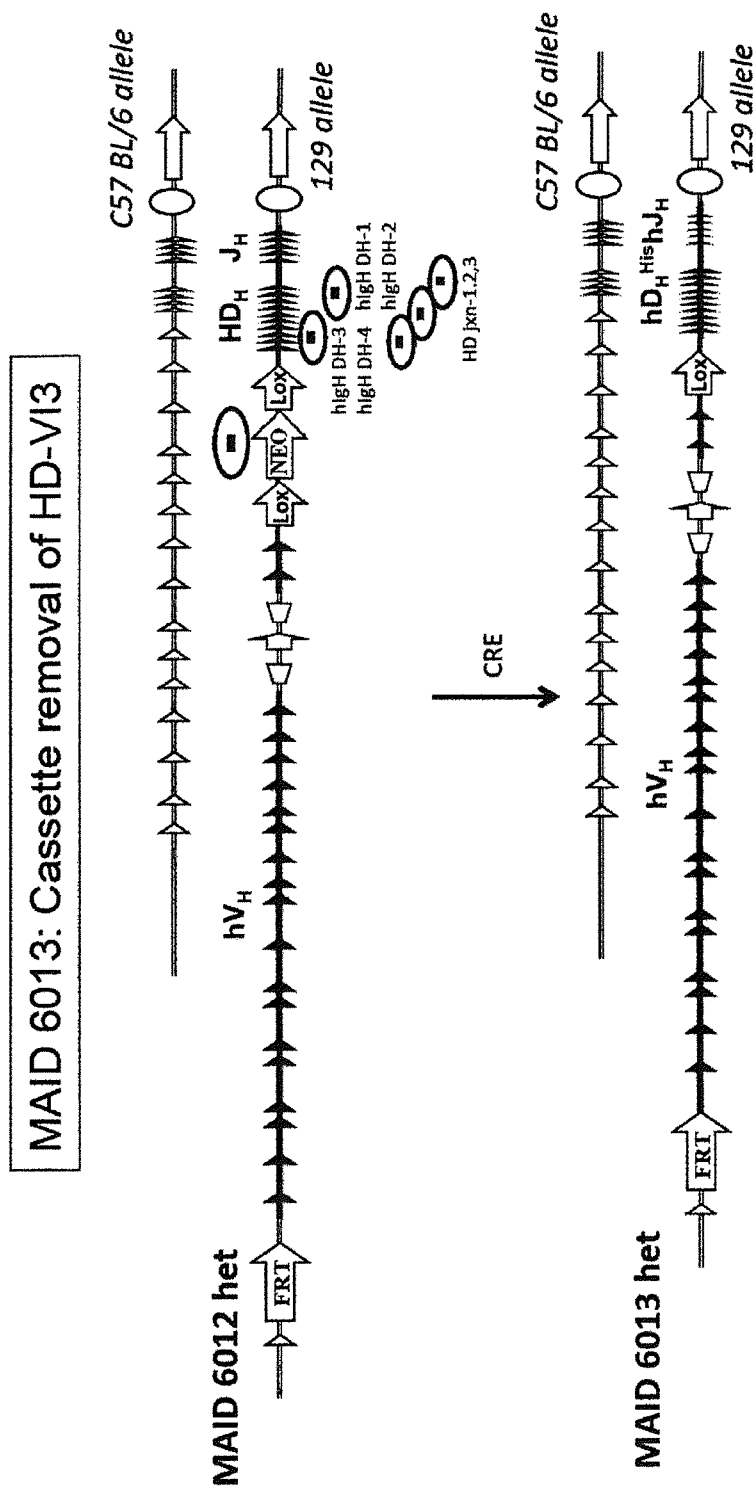


FIG. 9

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Human D Gene Segment	Direct 5'-3' Orientation	SEQ ID NO.	Inverted Orientation	SEQ ID NO.
IGHD1-1 X97051, IGHD1-1*01	ggtaaacctggaacgac G T T G T V Q L E R Y N W N D	155 88 8 45	gtcgtccagttgtacc V V P V V S F Q L Y R S S C T	206 207 208 209
IGHD1-7 X13972, IGHD1-7*01	ggtaataactggaactac G I T G T V * L E L Y N W N Y	156 89 - 47	gtagtccagttatacc V V P V I * F Q L Y S S S Y T	210 211 212 213
IGHD 1-20 X13972, IGHD1- 14*01	ggtaataaccggaaccac G I T G T V * P E P Y N R N H	157 89 - 158	gtgtccggttatacc V V P V I W F R L Y G S G Y T	214 211 215 216
IGHD 1-20 X97501, IGHD1- 20*01	ggtaataactggaacgac G I T G T V * L E R Y N W N D	159 89 - 45	gtcgtccagttatacc V V P V I S F Q L Y R S S Y T	217 211 208 218
IGHD1-26 X97501, IGHD1- 26*01	ggtaatactggagctactac G I V G A T V * W E L L Y S G S Y Y	160 90 12 49	gtagtagctccactatacc V V A P T I * * L P L Y S S S H Y T	219 220 221 222
IGHD2-2 J00232, IGHD2-2*01	aggatattgtagtagtaccagctgctatgcc R I L * * Y Q L L C G Y C S S T S C Y A D I V V V P A M	161 162 163 164	ggcatagcagctggtactactacaatacct G I A A G T T T I S A * Q L V L L Q Y P H S S W Y Y N I	223 224 225 226

FIG. 10A

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Human D Gene Segment	Direct 5'-3' Orientation	SEQ ID NO.	Inverted Orientation	SEQ ID NO.
X97051, IGHD2-2*02	aggatattgtagtagtaccagctgctatacc R I L * * Y Q L L Y G Y C S S T S C Y T D I V V V P A A I	165 14 51 92	ggatagcagctggtagtactacaataatcct G I A A G T T T I S V * Q L V L L Q Y P Y S S W Y Y Y N I	227 224 225 226
	tggaattgtagtagtaccagctgctatgcc W I L * * Y Q L L C G Y C S S T S C Y A D I V V V P A A M	166 167 168 169	ggcatagcagctggtagtactacaataatcca G I A A G T T T I S A * Q L V L L Q Y P H S S W Y Y Y N I	228 224 225 226
X13972, IGHD2-8*01	aggatattgtagtagtaccagctgctatacc R I L Y * W C M L Y G Y C T N G V C Y T D I V L M V Y A I	170 16, 17 53 94	ggatagcatcacccattagtaacaatcct G I A Y T I S T I S V * H T P L V Q Y P Y S I H H * Y N I	229 230 231 232
	agatattgtagtagtaccagctgctatacc R I L Y W W C M L Y G Y C T G G V C Y T D I V L V V Y A I	171 172 173 174	ggatagcatcacccattagtaacaatcct G I A Y T T S T I S V * H T P P V Q Y L Y S I H H Q Y N I	233 234 235 236
J00234, IGHD2-8*02	aggatattgtagtagtaccagctgctatacc R I L * W W * L L L G Y C S G G S C Y S D I V V V V A A T	175 - 55 95	ggagtagcagctaccaccaciacaaatcct G V A A T T T T I S E * Q L P P L Q Y P S S S Y H H Y N I	237 238 239 240
	agcatattggtagtagtaccagctgctatcc S I L W W * L L F A Y C G G D C Y S H I V V V I A I	176 19 57 177	ggaatagcaatcacccacacaaatgct G I A I T T T I C E * Q S P P Q Y A N S N H H H N M	241 242 243 244
X97051, IGHD2-21*02	agcatattggtagtagtaccagctgctatcc S I L W W * L L F A Y C G G D C Y S H I V V V T A I	178 19 57 97	ggaatagcagctaccaccacacaaatgct G I A V T T T I C E * Q S P P Q Y A N S S H H H N M	245 246 247 248

FIG. 10B

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Human D Gene Segment	Direct 5'-3' Orientation	SEQ ID NO.	Inverted Orientation	SEQ ID NO.
IGHD3-3	X13972, IGHD3-3*01	179	ggataataaccactcaaaaatcgtaataac	249
		21	G I I T T P K I V I	250
		59	V * * P L Q K S * Y	251
		98	Y N N H S K N R N	252
IGHD3-9	X93618, IGHD3-3*02	180	ggataataaccactcaaaaatcgtaataac	253
		181	G I I T T P K M L I	254
		182	V * * P L Q K C * Y	255
		183	Y N N H S K N A N	256
IGHD3-10	X13972, IGHD3-9*01	184	gtataataaccagtcacaaatcgtaataac	257
		23	V I I T S Q N I V I	258
		61	L * * P V K I S * Y	259
		99, 100	Y N N Q S K Y R N	260
IGHD3-16	X13972, IGHD3-10*01	185	gtataataacccccgaaccatagtaataac	261
		25	V I I T P R T I V I	262
		63	L * * L P E P * * Y	263
		101	Y N N S P N H S N	264
IGHD3-22	X93615, IGHD3-10*02	186	gtataataacccccgaaccatagtaataac	265
		187	V I I T P R T * * Y	266
		188	L * * L P E H S N	267
		189	Y N N S P N I V I	268
IGHD3-16	X93614, IGHD3-16*01	190	ggataagcataactcccccaaacgtaataataac	269
		191	G I S I T P P N V I I I	270
		192	V * A * L P Q T * S * Y	271
		193	Y K H N S P K R N H N	272
IGHD3-22	X93616, IGHD3-22*01	194	gtataataaccactacatagtaataac	273
		29	V V I T T T I I V I	274
		67	* * * P L L S * * Y	275
		103	S N N H Y Y H S N	276

FIG. 10C

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Human D Gene Segment	Direct 5'-3' Orientation	SEQ ID NO.	Inverted Orientation	SEQ ID NO.
IGHD4-4	X13972, IGHD4-4*01	195	gtagtactgtagtca	277
		-	V V T V V	278
		69	* L L * S	-
		105	S Y C S	279
IGHD4-11	X13972, IGHD4-11*01	195	gtagtactgtagtca	277
		-	V V T V V	278
		69	* L L * S	-
		105	S Y C S	279
IGHD4-17	X97501, IGHD4-17*01	196	gtagtaccgtagtca	280
		-	V V T V V	278
		71	* S P * S	-
		105	S H R S	281
IGHD4-23	X97051, IGHD4-23*01	197	ggagtaccaccgtagtca	282
		-	G V T T V V	283
		73	E L P P * S	284
		106	S Y H R S	285
IGHD5-5	X13972, IGHD5-5*01	198	gtaaccatagctgtagccac	286
		107	V T I A V S	287
		35	* P * L Y P	-
		75	N H S C I H	288
IGHD5-12	X13972, IGHD5-12*01	199	gtaatcgtagccactatccac	289
		108	V I V A T I S	290
		37	* S * P L Y P	291
		77	N R S H Y I H	292
IGHD5-18	X97051, IGHD5-18*01	198	gtaaccatagctgtagccac	286
		107	V T I A V S	287
		35	* P * L Y P	-
		75	N H S C I H	288

FIG. 10D

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Human D Gene Segment	Direct 5'-3' Orientation	SEQ ID NO.	Inverted Orientation	SEQ ID NO.
IGHD5-24	X97051, IGHD5- 24*01 gtagataggctacaattac V E M A T I * R W L Q L R D G Y N Y	200	gtaattgtagccatctctac V I V A I S * L * P S L N C S H L Y	293
		110		294
		39		-
		79		295
IGHD6-6	X13972, IGHD6-6*01 gagtatagcagctgtctc E Y S S S S S I A A R V * Q L V	201	ggacgagctgtctactc G R A A I L D E L L Y T S C Y T	296
		81		297
		112		298
		-		299
IGHD6-13	X13972, IGHD6- 13*01 gggtatagcagcagctgtac G Y S S S W Y G I A A A G V * Q Q L V	202	gtaccagctgtctataccc V P A A A I P Y Q L L L Y T S C C Y T	300
		83		301
		114		302
		41		303
IGHD6-19	X97051, IGHD6- 19*01 gggtatagcagtggtgtac G Y S S G W Y G I A V A G V * Q W L V	203	gtaccagccactgtataccc V P A T A I P Y Q P L L Y T S H C Y T	304
		85		305
		116		306
		44		307
IGHD6-25	X97051, IGHD6- 25*01 gggtatagcagcgggtac G Y S S G Y G I A A A V * Q R L	204	gtagccgtgtctataccc V A A A I P * P L L Y S R C Y T	308
		87		309
		116		310
		-		311
IGHD7-27	J00256, IGHD7- 27*01 ctaactgggga L T G * L G N W G	205	tccccagttag S P V P Q L P S *	312
		-		-
		-		-
		-		-

FIG. 10E

Antibody Sequence 1

1c1|Query_1_reversed
IGHV4-34*01

<-----FWR1-----><-----CDR1
Q V Q L Q Q W G A G L L K P S D T L S L T C A V Y G G S F S
CAGTGCAGCTACAGCGGGGCGCAGACTGTTGAGCTTCGGATACCTGTCCCTCACCGCGCTCTATGGTGCGTCTTCAGT
.....G.....
Q V Q L Q Q W G A G L L K P S E T L S L T C A V Y G G S F S
-----FWR2-----><-----CDR2-----><
G Y Y W S W I R Q P P G K G L E W I G E I N H S G S T N Y N
GGTTACTGAGCTGGATCCCGCAGCCCGCAGGGGCTGGAGTGGGAAATCAATCATAGTGGAAAGCCCAACTACAC
.....G.....
G Y Y W S W I R Q P P G K G L E W I G E I N H S G S T N Y N
-----FWR3-----
P S L K S R V T I S V D T S K N Q F S L K L S S V T A A D T
CCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCTCCAGACCTGCTGTGACCCGCGGACACG
.....
P S L K S R V T I S V D T S K N Q F S L K L S S V T A A D T
----->
A V Y Y C A G H S H G W Y Y Y Y Y G M D V W G Q G T T V T V
CCTGTATTACTGTCCGGGCATATCCATGGCTGGTACTACTACTACGGTATGGAGCTCTGGGGCCAGGACCCACGGTCCACCGTC
.....
A V Y Y C A (SEQ ID NO:314)
----->
S S (SEQ ID NO:313)
TCCTCA 473 (SEQ ID NO:312)
..... 62

D gene segment	Hydrophilic	SEQ ID NO.
D6-19	GYSSGWY	85
HD6-19	GSHGWY	86

FIG. 11

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D gene segment	Hydrophilic	SEQ ID NO.
D4-17	DYGDY	71
HD4-17	DHGHY	72

FIG. 12

D gene segment	Hydrophilic	SEQ ID NO.
D6-13	GYSSSWY	83
HD6-13	GHSHSWY	84

FIG. 13

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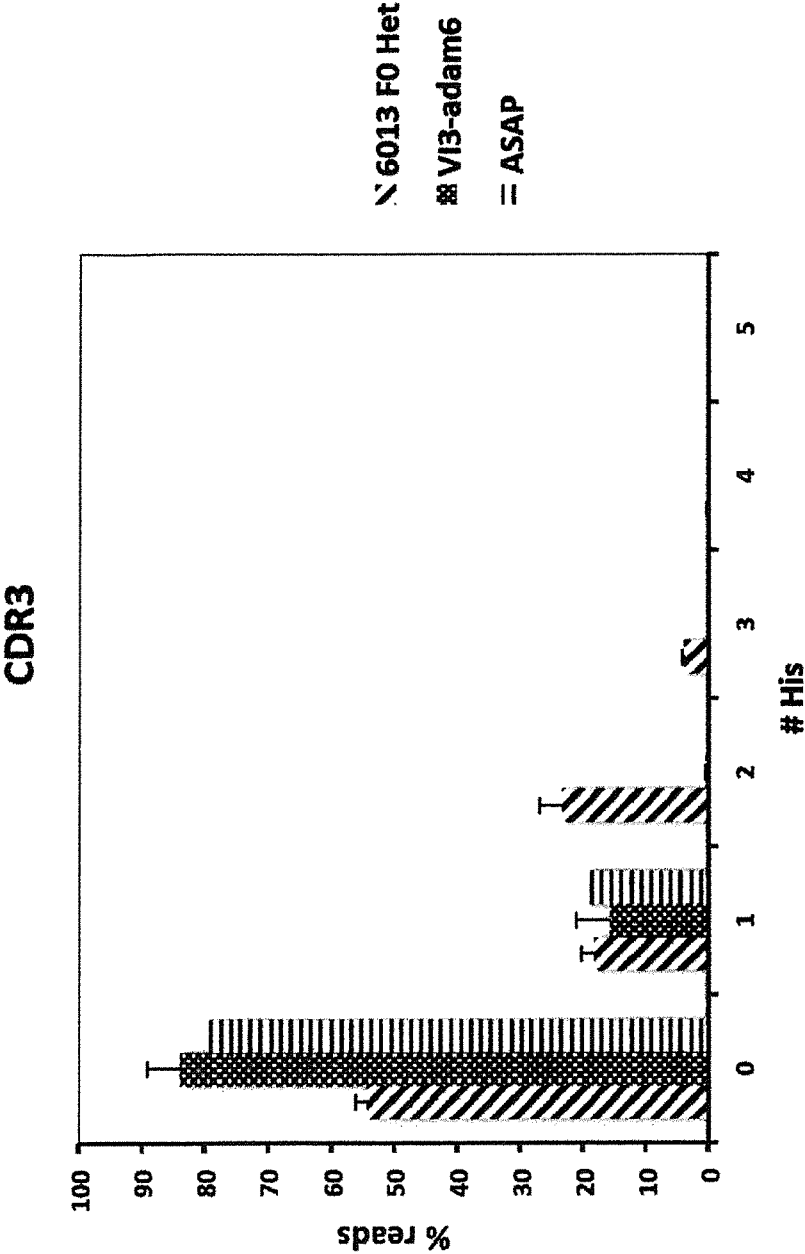


FIG. 14

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IGKV1-39*01	-----FR1-IMGT----- CDR1 -----FR2-IMGT----- C -----	SEQ ID NO:325
A	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS	
B	F...T H I....V...YT....	
C	A.....I.NF.....G.YN.....	
D	 HN NN.....H.....N.....	
E	A.....T.N.....	
F	N.D.....	
G	A.L.....N.N.....N.D.....	
H	A.....N.N.. H D.F.....	
I	A.L.....	
J	A.....	
K	A.L.....M.....	
IGKV1-39*01	-----FR3-IMGT----- CDR3-	
A	RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST-P-----	
B	...A.....T....NI..FTFGPGTKVDIKR	
C	Y...T.H...GN.....SMYTFGQGTQLEIKR	
D	 H I..ITFGQGTRLEIKR	
E	 H I..ITFGQGTRLEIKR	
F	T.H..... H ITFGQGTRLEIKR	
G	T..... H ITFGQGTRLEIKR	
H	P.ITFGQGTRVEIKR	
I	...K..... I H.ITFGQGTKEIKR	
J	 H .IP.ITFGQGTRLEIK.	
K	T.....R..... H ..P.ITFGQGTKEIKR	

FIG. 15

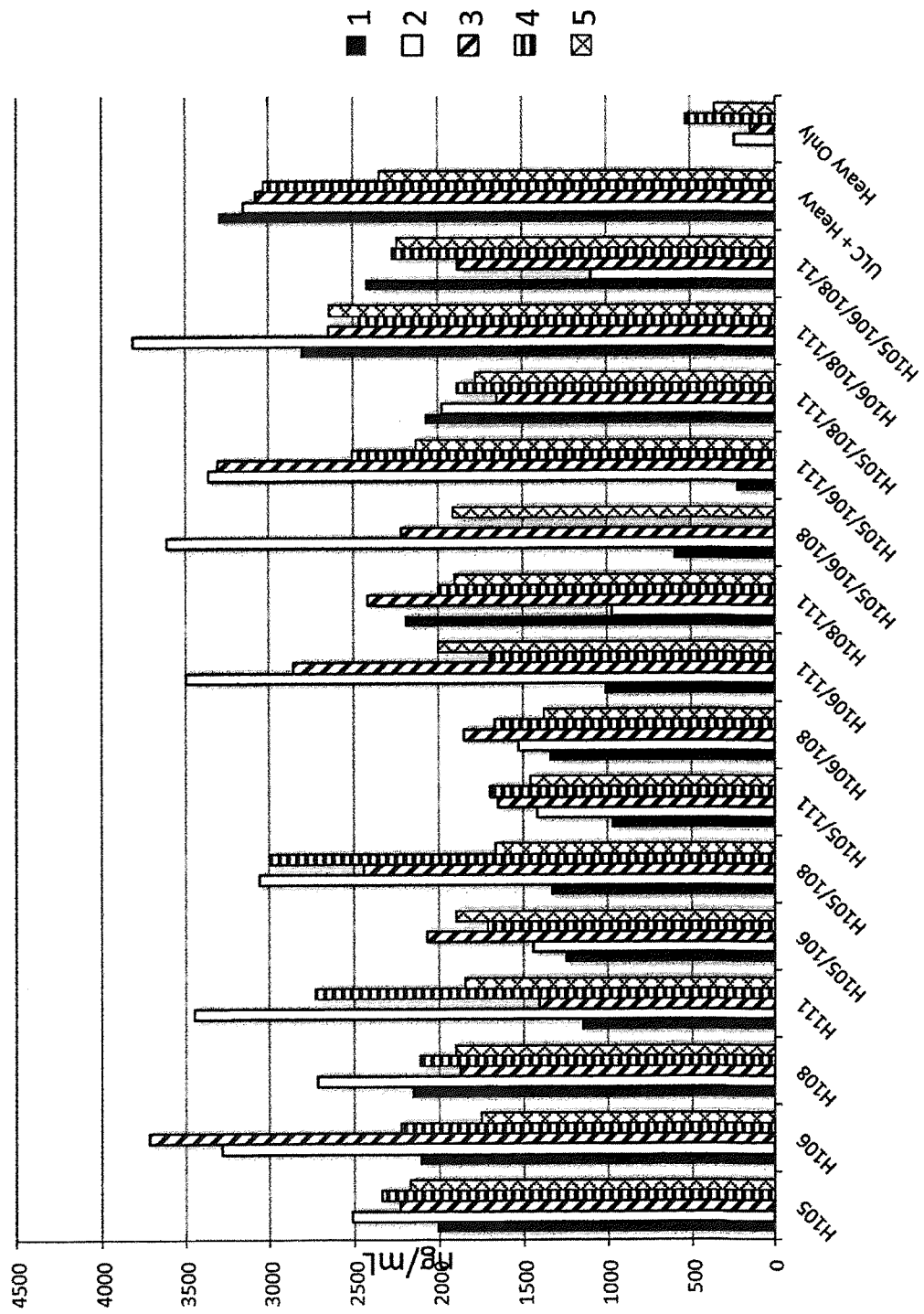


FIG. 17

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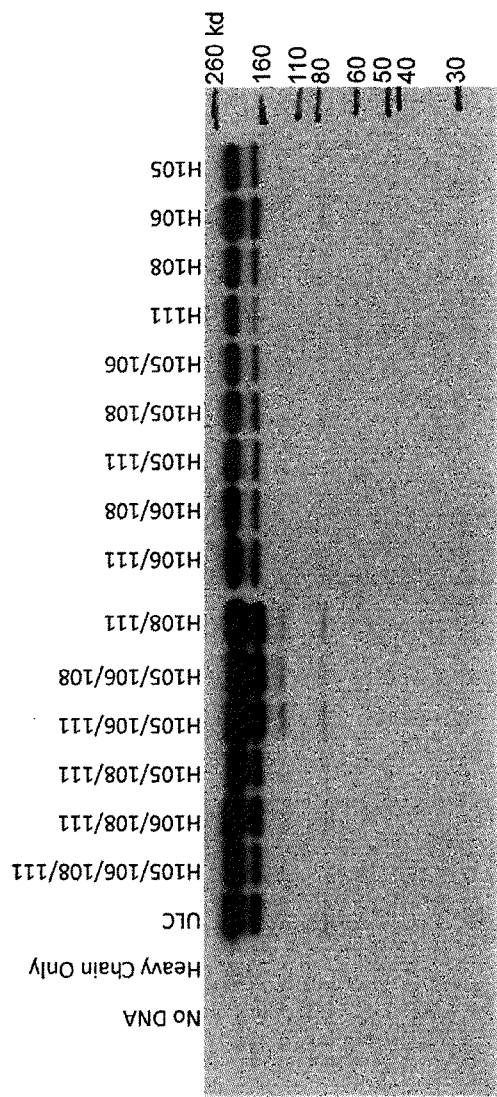


FIG. 18

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HC	Vk mut	Kinetics at pH 7.2					Kinetics at pH 5.75					low/neutral pH				
		mAb capture level (RU)	100nM Antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	% (min)	mAb capture level (RU)	100nM antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	% (min)	ka	kd	KD
H4H6006	H105	44	11	4.25E+05	1.18E-03	2.77E-09	10	32	5	1.27E+06	2.05E-03	1.61E-09	6	3.0	1.7	0.6
	H106	46	12	4.42E+05	9.32E-04	2.11E-09	12	27	4	1.56E+06	1.72E-03	1.10E-09	7	3.5	1.8	0.5
	H108	46	12	4.51E+05	9.02E-04	2.00E-09	13	33	5	1.15E+06	1.47E-03	1.28E-09	8	2.5	1.6	0.6
	H111	47	13	3.86E+05	9.54E-04	2.47E-09	12	36	5	8.81E+05	1.52E-03	1.73E-09	8	2.3	1.6	0.7
	H105	16	1	NB	NB	NB	NB	6	-4	NB	NB	NB	NB			
	H105	40	11	4.83E+05	8.73E-04	1.81E-09	13	30	4	1.54E+06	1.26E-03	8.20E-10	9	3.2	1.4	0.5
	H105	22	4	3.81E+05	1.32E-03	3.45E-09	9	16	-2	NB	NB	NB	NB			
	H106	51	15	4.87E+05	7.60E-04	1.56E-09	15	40	8	1.16E+06	1.04E-03	8.96E-10	11	2.4	1.4	0.6
	H106	38	9	3.94E+05	9.00E-04	2.28E-09	13	29	2	1.55E+06	1.60E-03	1.03E-09	7	3.9	1.8	0.5
	H108	51	14	3.98E+05	8.29E-04	2.08E-09	14	40	6	8.42E+05	1.19E-03	1.42E-09	10	2.1	1.4	0.7
	H105	14	1	NB	NB	NB	NB	9	-5	NB	NB	NB	NB			
	H105	15	1	NB	NB	NB	NB	10	-5	NB	NB	NB	NB			
	H105	17	2	4.38E+05	9.60E-04	2.19E-09	12	12	-5	NB	NB	NB	NB			
	H10	40	10	3.72E+05	7.42E-04	2.00E-09	16	30	2	NB	NB	NB	NB			
	H105	15	1	NB	NB	NB	NB	9	-6	NB	NB	NB	NB			
	L-39 UIC	72	22	3.90E+05	1.18E-03	3.03E-09	10	56	11	7.89E+05	1.84E-03	2.39E-09	6	2.0	1.6	0.8

FIG. 19A

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HC	V _k mut	Kinetics at pH 7.2						Kinetics at pH 5.75						low/neutral pH		
		mAb capture level (RU)	100nM Antigen bound (RU)	k _a (1/Ms)	k _d (1/s)	KD (nM)	% (min)	mAb capture level (RU)	100nM antigen bound (RU)	k _a (1/Ms)	k _d (1/s)	KD (nM)	% (min)	k _a	k _d	KD
H4H6008	H105	79	21	3.47E+05	1.09E-03	3.15E-09	11	62	8	5.15E+05	3.54E-03	6.87E-09	3	1.5	3.2	2.2
	H106	60	13	3.19E+05	1.92E-03	6.02E-09	6	48	2	1.92E+06	2.48E-02	1.29E-08	0	6.0	12.9	2.1
	H108	84	20	2.89E+05	2.66E-03	9.17E-09	4	1	-5	NB	NB	NB	NB	1.5	5.1	3.4
	H111	77	19	3.28E+05	1.54E-03	4.69E-09	8	60	5	4.96E+05	7.85E-03	1.58E-08	1	1.5	5.1	3.4
	H105	30	4	3.39E+05	9.91E-04	2.92E-09	12	-1	-7	NB	NB	NB	NB			
	H105	77	20	3.16E+05	1.40E-03	4.45E-09	8	62	6	4.76E+05	5.41E-03	1.14E-08	2	1.5	3.9	2.6
	H105	44	11	3.51E+05	4.10E-04	1.17E-09	28	34	0	NB	NB	NB	NB			
	H106	81	18	2.99E+05	2.20E-03	7.34E-09	5	66	4	3.87E+05	1.16E-02	3.01E-08	1	1.3	5.3	4.1
	H106	87	19	3.05E+05	1.64E-03	5.38E-09	7	73	5	4.34E+05	6.96E-03	1.60E-08	2	1.4	4.2	3.0
	H108	85	22	3.42E+05	1.63E-03	4.76E-09	7	70	5	3.94E+05	8.00E-03	2.03E-08	1	1.2	4.9	4.3
	H105	29	4	3.53E+05	9.63E-04	2.73E-09	12	24	-5	NB	NB	NB	NB			
	H105	32	5	2.87E+05	9.83E-04	3.43E-09	12	26	-5	NB	NB	NB	NB			
	H105	39	9	3.47E+05	3.26E-04	9.38E-10	35	32	-2	NB	NB	NB	NB			
	H106	57	11	2.72E+05	1.63E-03	5.99E-09	7	46	-1	NB	NB	NB	NB			
	H105	36	6	2.93E+05	1.05E-03	3.58E-09	11	29	-5	NB	NB	NB	NB			
	H105	128	33	3.02E+05	1.86E-03	6.15E-09	6	103	13	3.24E+05	5.67E-03	1.75E-08	2	1.1	3.1	2.8
	UIC															

FIG. 19B

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HC	Vk mut	Kinetics at pH 7.2						Kinetics at pH 5.75						low/neutral pH		
		mAb capture level (RU)	100nM Antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t½ (min)	mAb capture level (RU)	100nM antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t½ (min)	ka	kd	KD
H4H3046	H105	73	0	NB	NB	NB	NB	62	-8	NB	NB	NB	NB			
	H106	64	0	NB	NB	NB	NB	54	-9	NB	NB	NB	NB			
	H108	75	1	NB	NB	NB	NB	64	-8	NB	NB	NB	NB			
	H111	73	0	NB	NB	NB	NB	62	-9	NB	NB	NB	NB			
	H105	45	0	NB	NB	NB	NB	38	-9	NB	NB	NB	NB			
	H106															
	H105	65	0	NB	NB	NB	NB	56	-9	NB	NB	NB	NB			
	H108															
	H105	34	0	NB	NB	NB	NB	27	-9	NB	NB	NB	NB			
	H111															
	H106	77	0	NB	NB	NB	NB	67	-9	NB	NB	NB	NB			
	H108															
	H106	75	0	NB	NB	NB	NB	67	-9	NB	NB	NB	NB			
	H111															
	H108	66	0	NB	NB	NB	NB	56	-9	NB	NB	NB	NB			
	H111															
	H105	54	0	NB	NB	NB	NB	46	-9	NB	NB	NB	NB			
	H106															
	H108	47	0	NB	NB	NB	NB	41	-9	NB	NB	NB	NB			
	H111															
	H105	37	0	NB	NB	NB	NB	31	-9	NB	NB	NB	NB			
	H108															
	H111															
	H106	69	0	NB	NB	NB	NB	59	-9	NB	NB	NB	NB			
	H108															
	H111															
	H105	54	0	NB	NB	NB	NB	49	-9	NB	NB	NB	NB			
	H106															
	H108															
	H111															
	1-39 ULC	97	0	NB	NB	NB	NB	88	-9	NB	NB	NB	NB			

FIG. 19C

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HC	Vk mut	Kinetics at pH 7.2						Kinetics at pH 5.75						low/neutral pH		
		mAb capture level (RU)	100nM Antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t½ (min)	mAb capture level (RU)	100nM antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t½ (min)	ka	kd	KD
HAH2964	H105	327	23	1.43E+05	8.40E-03	5.89E-08	1	318	2	IC	IC	IC	IC			
	H106	303	26	9.67E+04	3.40E-03	3.52E-08	3	289	11	9.48E+04	2.08E-02	2.20E-07	1	1.0	6.1	6.3
	H108	287	29	1.37E+05	2.46E-03	1.80E-08	5	268	12	7.69E+04	1.32E-02	1.71E-07	1	0.6	5.4	9.5
	H111	311	21	1.31E+05	6.83E-03	5.20E-08	2	292	0	NB	NB	NB	NB			
	H105	285	17	9.65E+04	6.20E-03	6.43E-08	2	262	-3	NB	NB	NB	NB			
	H106															
	H105	271	21	1.23E+05	9.82E-03	7.99E-08	1	262	-3	NB	NB	NB	NB			
	H108	221	11	2.37E+05	2.11E-02	8.88E-08	1	216	-6	NB	NB	NB	NB			
	H105	344	28	1.04E+05	6.66E-03	6.38E-08	2	316	3	IC	IC	IC	IC			
	H106	341	25	1.16E+05	9.09E-03	7.81E-08	1	321	2	IC	IC	IC	IC			
	H108	300	20	9.64E+04	1.01E-02	1.05E-07	1	274	-4	NB	NB	NB	NB			
	H105	269	10	1.31E+05	2.52E-02	1.93E-07	0	243	-8	NB	NB	NB	NB			
	H106	286	5	6.34E+04	5.06E-02	7.99E-07	0	265	-9	NB	NB	NB	NB			
	H108	309	13	3.26E+05	3.47E-02	1.06E-07	0	279	-8	NB	NB	NB	NB			
	H105	315	9	1.55E+05	5.89E-02	3.81E-07	0	279	-8	NB	NB	NB	NB			
	H106	260	0	NB	NB	NB	NB	238	-10	NB	NB	NB	NB			
	H108	386	32	1.30E+05	2.05E-03	1.58E-08	6	362	17	7.58E+04	7.97E-03	1.05E-07	1	0.6	3.9	6.6
	1-39 ULC															

FIG. 19D

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HC	V _k mut	Kinetics at pH 7.2						Kinetics at pH 5.75						low/neutral pH		
		mAb capture level (RU)	100nM Antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t% (min)	mAb capture level (RU)	100nM antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t% (min)	ka	kd	KD
H4H3010	H105	52	8	1.06E+05	7.43E-04	7.04E-09	16	43	-1	NB	NB	NB	NB			
	H106	50	9	1.26E+05	3.54E-04	2.82E-09	33	40	0	NB	NB	NB	NB			
	H108	50	8	9.29E+04	2.43E-04	2.62E-09	48	42	-1	NB	NB	NB	NB			
	H111	55	11	1.53E+05	1.66E-04	1.09E-09	69	48	2	IC	IC	IC	IC			
	H105	55	10	1.31E+05	5.18E-04	3.94E-09	22	45	1	NB	NB	NB	NB			
	H106	48	8	8.96E+04	4.58E-04	5.12E-09	25	41	-1	NB	NB	NB	NB			
	H108	38	6	8.85E+04	1.64E-04	1.85E-09	70	32	-3	NB	NB	NB	NB			
	H111	59	11	1.06E+05	1.61E-04	1.52E-09	72	52	2	4.79E+05	1.00E-06	2.09E-12	11550	4.5	0.0	0.0
	H106	76	7	6.81E+04	5.23E-04	7.68E-09	22	72	0	NB	NB	NB	NB			
	H108	58	11	1.17E+05	9.26E-05	7.92E-10	125	52	2	IC	IC	IC	IC			
	H111	67	13	1.11E+05	3.17E-04	2.86E-09	36	58	4	IC	IC	IC	IC			
	H105	70	8	6.45E+04	9.94E-04	1.54E-08	12	57	-1	NB	NB	NB	NB			
	H106	49	8	8.52E+04	1.10E-04	1.29E-09	105	44	-1	NB	NB	NB	NB			
	H108	54	3	1.02E+04	1.46E-03	1.44E-07	8	46	-5	NB	NB	NB	NB			
	H111	70	6	7.28E+04	5.55E-03	7.61E-08	2	62	-5	NB	NB	NB	NB			
	H105	83	15	1.02E+05	1.79E-04	1.77E-09	64	77	7	2.11E+05	1.00E-06	4.74E-12	11550	2.1	0.0	0.0
	1-39															
	ULC															

FIG. 19E

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HC	Vk mut	Kinetics at pH 7.2						Kinetics at pH 5.75						low/neutral pH		
		mAb capture level (RU)	100nM Antigen bound (RU)	ka (1/Ms)	Kd (M)	t½ (min)	mAb capture level (RU)	100nM antigen bound (RU)	ka (1/Ms)	Kd (M)	t½ (min)	ka	Kd			
H4H3029	H105	71	8	1.41E+05	2.96E-04	39	60	-3	NB	NB	NB					
	H106	72	8	1.50E+05	2.39E-04	48	64	-2	NB	NB	NB					
	H108	68	7	1.19E+05	7.97E-05	145	61	-2	NB	NB	NB					
	H111	69	8	1.50E+05	1.78E-04	65	63	-2	NB	NB	NB					
	H105	88	10	1.60E+05	2.45E-04	47	77	0	NB	NB	NB					
	H106															
	H105	67	8	1.45E+05	1.14E-04	102	59	-3	NB	NB	NB					
	H108															
	H105	13	0	NB	NB	NB	14	-11	NB	NB	NB					
	H106															
	H108	92	10	1.34E+05	1.34E-04	86	82	0	NB	NB	NB					
	H106															
	H108	85	5	5.82E+04	1.10E-03	10	78	-4	NB	NB	NB					
	H105	62	7	1.48E+05	1.73E-04	67	55	-4	NB	NB	NB					
	H106															
	H108	85	10	1.36E+05	1.97E-04	59	75	0	NB	NB	NB					
	H105															
	H106	78	6	1.35E+05	2.18E-03	5	70	-4	NB	NB	NB					
	H108															
	H105	55	6	1.50E+05	2.48E-04	47	48	-5	NB	NB	NB					
	H106															
	H108	73	4	8.60E+04	1.59E-03	7	66	-6	NB	NB	NB					
	H105															
	H106	95	7	1.19E+05	6.71E-03	2	85	-6	NB	NB	NB					
	H108															
	H105															
	H106	108	12	1.34E+05	1.65E-04	70	98	2	IC	IC	IC					
	H108															
	1-39 UIC															

FIG. 19F

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HC	Vk mut	Kinetics at pH 7.2						Kinetics at pH 5.75						low/neutral pH		
		mAb capture level (RU)	100nM Antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t% (min)	mAb capture level (RU)	100nM antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t% (min)	ka	kd	KD
H4HS978	H105	44	7	3.88E+05	5.73E-03	1.48E-08	2	41	-5	NB	NB	NB	NB			
	H106	36	7	3.15E+05	3.03E-03	9.62E-09	4	34	-5	NB	NB	NB	NB			
	H108	38	8	3.18E+05	9.61E-04	3.02E-09	12	32	-4	NB	NB	NB	NB			
	H111	43	8	3.13E+05	2.32E-03	7.40E-09	5	40	-5	NB	NB	NB	NB			
	H105	33	4	2.69E+05	5.41E-03	2.01E-08	2	29	-9	NB	NB	NB	NB			
	H105	34	7	2.13E+05	2.15E-03	1.01E-08	5	30	-7	NB	NB	NB	NB			
	H105	32	5	3.47E+05	6.27E-03	1.81E-08	2	30	-8	NB	NB	NB	NB			
	H106	50	10	3.67E+05	3.09E-03	8.42E-09	4	46	-4	NB	NB	NB	NB			
	H106	62	12	2.88E+05	4.47E-03	1.55E-08	3	56	-2	NB	NB	NB	NB			
	H108	45	9	3.22E+05	2.05E-03	6.37E-09	6	43	-4	NB	NB	NB	NB			
	H105	36	5	3.57E+05	7.48E-03	2.10E-08	2	35	-8	NB	NB	NB	NB			
	H105	39	7	3.37E+05	8.35E-03	2.48E-08	1	35	-6	NB	NB	NB	NB			
	H105	29	4	2.94E+05	4.52E-03	1.54E-08	3	28	-8	NB	NB	NB	NB			
	H106	41	7	3.12E+05	6.37E-03	2.04E-08	2	39	-6	NB	NB	NB	NB			
	H105	50	9	2.97E+05	6.83E-03	2.30E-08	2	45	-5	NB	NB	NB	NB			
	1-39	74	16	2.92E+05	1.73E-03	5.91E-09	7	67	3	1.20E+06	9.67E-03	8.05E-09	1	4.1	5.6	1.4
	ULC															

FIG. 19G

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HC	Vk mut	Kinetics at pH 7.2						Kinetics at pH 5.75						low/neutral pH		
		mAb capture level (RU)	100nM Antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	% (min)	mAb capture level (RU)	100nM antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	% (min)	ka	kd	KD
H4H5981	H105	121	24	3.04E+05	8.81E-03	2.90E-08	1	112	7	4.47E+05	6.21E-02	1.39E-07	0	1.5	7.1	4.8
	H106	113	29	2.41E+05	2.99E-03	1.24E-08	4	103	10	6.84E+05	1.89E-02	2.76E-08	1	2.8	6.3	2.2
	H108	114	31	3.09E+05	2.83E-03	9.16E-09	4	104	11	5.06E+05	1.33E-02	2.63E-08	1	1.6	4.7	2.9
	H111	104	26	3.45E+05	3.98E-03	1.15E-08	3	96	4	4.54E+05	6.26E-02	1.38E-07	0	1.3	15.8	12.0
	H105	109	26	2.39E+05	3.10E-03	1.29E-08	4	103	9	5.00E+05	1.77E-02	3.53E-08	1	2.1	5.7	2.7
	H105	109	27	2.91E+05	4.48E-03	1.54E-08	3	97	7	1.00E+06	9.77E-02	9.76E-08	0	3.4	21.8	6.3
	H105	85	16	2.62E+05	7.59E-03	2.90E-08	2	80	-1	NB	NB	NB	NB			
	H106	121	33	2.33E+05	2.71E-03	1.16E-08	4	115	14	3.88E+05	1.19E-02	3.07E-08	1	1.7	4.4	2.6
	H106	117	32	2.29E+05	2.28E-03	9.97E-09	5	113	13	3.71E+05	8.88E-03	2.40E-08	1	1.6	3.9	2.4
	H108	93	24	3.39E+05	4.04E-03	1.19E-08	3	87	3	4.54E+05	5.11E-02	1.12E-07	0	1.3	12.7	9.4
	H105	94	25	2.24E+05	1.23E-03	5.47E-09	9	85	8	4.94E+05	3.02E-03	6.12E-09	4	2.2	2.5	1.1
	H105	111	24	2.31E+05	4.65E-03	2.01E-08	2	100	4	1.94E+05	8.05E-02	4.15E-07	0	0.8	17.3	20.6
	H105	83	21	2.60E+05	5.20E-03	2.00E-08	2	79	1	NB	NB	NB	NB			
	H106	100	28	2.11E+05	2.23E-03	1.05E-08	5	93	6	4.26E+05	1.83E-02	4.29E-08	1	2.0	8.2	4.1
	H105	104	24	2.46E+05	5.05E-03	2.05E-08	2	98	2	IC	IC	IC	IC			
	H105	133	34	2.80E+05	3.40E-03	1.22E-08	3	124	13	4.29E+05	1.42E-02	3.30E-08	1	1.5	4.2	2.7
	1-39 ULC															

FIG. 19H

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HC	Vk mut	Kinetics at pH 7.2						Kinetics at pH 5.75						low/neutral pH		
		mAb capture level (RU)	100nM Antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t% (min)	mAb capture level (RU)	100nM antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t% (min)	ka	kd	KD
669999H4H5	H105	87	8	5.04E+04	1.18E-03	2.34E-08	10	78	-5	NB	NB	NB	NB			
	H106	72	7	1.04E+05	6.40E-04	6.17E-09	18	66	-7	NB	NB	NB	NB			
	H108	77	6	3.47E+04	1.47E-03	4.23E-08	8	72	-8	NB	NB	NB	NB			
	H111	77	6	1.39E+05	4.59E-03	3.31E-08	3	71	-8	NB	NB	NB	NB			
	H105	85	8	9.95E+04	3.69E-04	3.71E-09	31	77	-6	NB	NB	NB	NB			
	H105	71	6	2.60E+03	8.63E-04	3.32E-07	13	63	-7	NB	NB	NB	NB			
	H105	51	3	9.81E+03	7.03E-03	7.16E-07	2	47	-10	NB	NB	NB	NB			
	H106	80	6	4.81E+04	4.78E-04	9.94E-09	24	71	-10	NB	NB	NB	NB			
	H106	91	9	3.28E+04	6.44E-04	1.96E-08	18	85	-6	NB	NB	NB	NB			
	H108	70	6	3.98E+04	2.01E-03	5.05E-08	6	65	-9	NB	NB	NB	NB			
	H105	79	5	4.95E+04	5.53E-04	1.12E-08	21	74	-10	NB	NB	NB	NB			
	H105	74	8	1.92E+04	4.59E-04	2.39E-08	25	68	-6	NB	NB	NB	NB			
	H105	56	4	1.03E+03	4.18E-03	4.04E-06	3	52	-10	NB	NB	NB	NB			
	H106	74	5	8.96E+03	1.66E-03	1.86E-07	7	66	-9	NB	NB	NB	NB			
	H105	79	7	1.73E+04	9.49E-04	5.50E-08	12	75	-9	NB	NB	NB	NB			
	1-39 ULC	110	10	5.01E+05	4.02E-03	8.02E-09	3	100	-5	NB	NB	NB	NB			

FIG. 19I

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HC	Vk mut	Kinetics at pH 7.2						Kinetics at pH 5.75						low/neutral pH		
		mAb capture level (RU)	100nM Antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t½ (min)	mAb capture level (RU)	100nM antigen bound (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t½ (min)	ka	kd	KD
H4H6011	H105	150	22	1.15E+05	3.17E-04	2.77E-09	36	147	6	7.61E+04	1.00E-06	1.31E-11	11550	0.7	0.0	0.0
	H106	127	17	8.73E+04	3.46E-04	3.96E-09	33	119	2	4.89E+04	1.00E-06	2.05E-11	11550	0.6	0.0	0.0
	H108	124	15	7.56E+04	5.90E-04	7.80E-09	20	112	-4	NB	NB	NB	NB			
	H111	135	17	1.08E+05	5.59E-04	5.19E-09	21	128	0	NB	NB	NB	NB			
	H105	130	18	1.03E+05	3.91E-04	3.81E-09	30	123	3	1.89E+05	2.33E-04	1.23E-09	49	1.8	0.6	0.3
	H106	117	16	9.29E+04	5.24E-04	5.64E-09	22	110	-2	NB	NB	NB	NB			
	H108	109	16	1.06E+05	4.39E-04	4.15E-09	26	105	0	NB	NB	NB	NB			
	H105	105	8	6.95E+04	4.86E-04	7.00E-09	24	100	-8	NB	NB	NB	NB			
	H106	171	16	3.07E+05	1.44E-03	4.69E-09	8	163	0	NB	NB	NB	NB			
	H108	133	16	9.17E+04	6.20E-04	6.76E-09	19	126	-3	NB	NB	NB	NB			
	H111	135	10	6.11E+04	6.93E-04	1.13E-08	17	132	-8	NB	NB	NB	NB			
	H105	117	12	6.52E+04	8.99E-04	1.38E-08	13	111	-3	NB	NB	NB	NB			
	H106	129	16	9.95E+04	5.82E-04	5.85E-09	20	121	-3	NB	NB	NB	NB			
	H108	124	11	2.36E+04	8.53E-04	3.62E-08	14	118	-6	NB	NB	NB	NB			
	H111	144	14	3.65E+04	9.51E-04	2.60E-08	12	140	-6	NB	NB	NB	NB			
	1-39 ULC	198	25	1.13E+05	4.36E-04	3.85E-09	27	181	6	6.02E+04	2.02E-04	3.36E-09	57	0.5	0.5	0.9
	Buffer	2	1	NB	NB	NB	NB	-2	-11	NB	NB	NB	NB			
	Buffer	3	1	NB	NB	NB	NB	0	-10	NB	NB	NB	NB			

FIG. 19J

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Heavy Chain	Light Chain Mutant	Kinetics at pH 7.4						Kinetics at pH 5.75						Ratio of low pH / neutral pH		
		mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	ka	kd	KD
1	H105	488	47.2	3.52E+05	9.30E-03	2.64E-08	1.2	378	37.8	4.24E+05	1.38E-02	3.24E-08	0.8	1.2	1.5	1.2
	H106	620	73.7	3.22E+05	3.67E-03	1.14E-08	3.1	505	65.4	3.66E+05	4.86E-03	1.33E-08	2.4	1.1	1.3	1.2
	H108	648	99.0	3.17E+05	2.07E-03	6.54E-09	5.6	496	80.7	3.59E+05	3.02E-03	8.41E-09	3.8	1.1	1.5	1.3
	H111	669	81.0	3.01E+05	3.81E-03	1.27E-08	3.0	536	62.8	3.32E+05	5.41E-03	1.63E-08	2.1	1.1	1.4	1.3
	H105/106	492	55.6	3.74E+05	6.44E-03	1.72E-08	1.8	404	45.7	4.30E+05	1.01E-02	2.34E-08	1.1	1.2	1.6	1.4
	H105/108	538	75.2	3.28E+05	4.17E-03	1.27E-08	2.8	416	56.3	3.87E+05	7.43E-03	1.92E-08	1.6	1.2	1.8	1.5
	H105/111	501	44.6	3.44E+05	9.77E-03	2.84E-08	1.2	402	31.9	4.06E+05	1.70E-02	4.19E-08	0.7	1.2	1.7	1.5
	H106/108	494	64.9	3.36E+05	4.14E-03	1.23E-08	2.8	407	43.0	4.07E+05	1.17E-02	2.86E-08	1.0	1.2	2.8	2.3
	H106/111	536	78.2	3.09E+05	3.10E-03	1.00E-08	3.7	423	61.4	3.62E+05	4.68E-03	1.29E-08	2.5	1.2	1.5	1.3
	H108/111	584	78.5	3.11E+05	3.80E-03	1.22E-08	3.0	473	59.0	3.50E+05	6.13E-03	1.75E-08	1.9	1.1	1.6	1.4
	H105/106/108	442	51.2	3.72E+05	6.38E-03	1.71E-08	1.8	370	28.4	4.26E+05	2.13E-02	5.00E-08	0.5	1.1	3.3	2.9
	H105/106/111	473	62.8	3.40E+05	4.55E-03	1.34E-08	2.5	378	47.6	4.07E+05	7.42E-03	1.82E-08	1.6	1.2	1.6	1.4
	H105/108/111	433	49.5	3.57E+05	7.42E-03	2.08E-08	1.6	354	31.3	4.09E+05	1.73E-02	4.23E-08	0.7	1.1	2.3	2.0
	H106/108/111	491	66.6	3.44E+05	3.82E-03	1.11E-08	3.0	415	43.3	3.91E+05	1.06E-02	2.72E-08	1.1	1.1	2.8	2.5
	H105/106/108/111	454	57.9	3.51E+05	5.77E-03	1.64E-08	2.0	368	36.8	4.06E+05	1.35E-02	3.32E-08	0.9	1.2	2.3	2.0
	ULC + Heavy	586	76.0	3.16E+05	3.85E-03	1.22E-08	3.0	483	66.5	3.45E+05	4.58E-03	1.33E-08	2.5	1.1	1.2	1.1
Heavy only		141	-1.3	NB	NB	NB	NB	107	-6.7	NB	NB	NB	NB	Negative Control		
No DNA		60	-1.5	NB	NB	NB	NB	26	-7.2	NB	NB	NB	NB			

FIG. 20A

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Heavy Chain	Light Chain Mutant	Kinetics at pH 7.4						Kinetics at pH 5.75						Ratio of low pH / neutral pH		
		mAb capture d (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	mAb capture d (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	ka	kd	KD
	H105	720	33.7	1.02E+05	9.10E-04	8.89E-09	12.7	595	0.3	NB	NB	NB	NB	No binding at Low pH		
	H106	735	32.9	9.11E+04	4.47E-04	4.91E-09	25.8	623	4.3	2.27E+04	6.41E-03	2.82E-07	1.8	0.2	14.3	57.4
	H108	728	32.2	8.48E+04	2.67E-04	3.14E-09	43.3	598	3.6	1.16E+03	3.41E-03	2.93E-06	3.4	0.0	12.8	933.1
	H111	802	42.4	1.17E+05	1.15E-04	9.88E-10	100.3	670	14.1	3.01E+04	7.08E-04	2.35E-08	16.3	0.3	6.1	23.8
	H105/106	570	24.9	8.51E+04	2.92E-04	3.43E-09	39.5	484	2.4	1.14E+04	6.47E-03	5.69E-07	1.8	0.1	22.1	165.9
	H105/108	723	28.4	8.73E+04	1.30E-03	1.49E-08	8.9	603	-2.6	NB	NB	NB	NB	No binding at Low pH		
	H105/111	627	28.5	8.82E+04	3.60E-04	4.08E-09	32.1	519	2.3	1.02E+04	1.30E-02	1.27E-06	0.9	0.1	36.2	311.3
	H106/108	550	21.1	6.75E+04	9.12E-04	1.35E-08	12.7	470	-1.9	NB	NB	NB	NB	No binding at Low pH		
	H106/111	808	32.7	9.01E+04	6.78E-04	7.52E-09	17.0	678	0.9	NB	NB	NB	NB	No binding at Low pH		
	H108/111	801	40.5	1.17E+05	9.80E-05	8.40E-10	117.8	676	10.6	1.87E+04	5.84E-04	3.12E-08	19.8	0.2	6.0	37.1
	H105/106/108	409	13.0	8.21E+04	4.29E-04	5.22E-09	26.9	345	-4.4	NB	NB	NB	NB	No binding at Low pH		
	H105/106/111	767	9.3	4.84E+04	1.25E-03	2.58E-08	9.3	645	-6.1	NB	NB	NB	NB	No binding at Low pH		
	H105/108/111	578	24.5	8.99E+04	2.87E-04	3.19E-09	40.2	479	-0.7	NB	NB	NB	NB	No binding at Low pH		
	H106/108/111	765	15.1	5.04E+04	1.65E-03	3.27E-08	7.0	661	-5.9	NB	NB	NB	NB	No binding at Low pH		
	H105/106/108/111	723	0.3	NB	NB	NB	NB	611	-7.0	NB	NB	NB	NB	No binding at either pH tested		
	ULC + Heavy only	781	39.8	1.13E+05	1.78E-04	1.57E-09	64.9	665	11.7	2.04E+04	1.22E-03	6.00E-08	9.4	0.2	6.9	38.2
	No DNA	63	-2.1	NB	NB	NB	NB	35	-6.4	NB	NB	NB	NB	Negative Control		

FIG. 20B

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Heavy Chain	Light Chain Mutant	Kinetics at pH 7.4						Kinetics at pH 5.75						Ratio of low pH / neutral pH		
		mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	ka	kd	KD
3	H105	574	12.4	5.64E+04	1.21E-03	2.15E-08	9.5	496	0.1	NB	NB	NB	NB	No binding	No binding	Low pH
	H106	662	16.1	7.37E+04	5.36E-04	7.27E-09	21.5	584	3.0	3.00E+04	4.79E-03	1.58E-07	2.4	0.4	8.9	21.7
	H108	518	12.3	4.82E+04	2.15E-04	4.46E-09	53.7	440	2.2	3.70E+04	1.25E-03	3.40E-08	9.3	0.8	5.8	7.6
	H111	480	9.1	1.82E+04	4.16E-04	2.28E-08	27.7	406	0.4	NB	NB	NB	NB	No binding	No binding	Low pH
	H105/106	487	7.4	1.82E+04	7.45E-03	4.10E-07	1.6	423	-4.1	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH	No binding	Low pH
	H105/108	548	11.8	3.25E+04	5.25E-04	1.62E-08	22.0	468	0.0	NB	NB	NB	NB	No binding	No binding	Low pH
	H105/111	504	7.9	1.06E+04	1.66E-03	1.57E-07	7.0	430	-1.6	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH	No binding	Low pH
	H106/108	487	10.7	6.64E+04	2.91E-04	4.38E-09	39.7	424	-4.2	NB	NB	NB	NB	No binding	No binding	Low pH
	H106/111	563	10.5	2.75E+04	3.71E-04	1.35E-08	31.2	482	-1.9	NB	NB	NB	NB	No binding	No binding	Low pH
	H108/111	528	10.1	1.10E+04	8.01E-05	7.27E-09	144.2	449	-0.5	NB	NB	NB	NB	No binding	No binding	Low pH
	H105/106/108	470	6.4	2.64E+04	5.40E-03	2.04E-07	2.1	412	-5.3	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH	No binding	Low pH
	H105/106/111	539	0.8	NB	NB	NB	NB	462	-5.6	NB	NB	NB	NB	No binding at either pH tested	No binding	Low pH
	H105/108/111	419	6.5	1.76E+04	4.01E-04	2.27E-08	28.8	354	-3.8	NB	NB	NB	NB	No binding	No binding	Low pH
	H106/108/111	509	3.3	5.47E+04	9.07E-04	1.66E-08	12.7	443	-5.9	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH	No binding	Low pH
	H105/106/108/111	450	-1.1	NB	NB	NB	NB	382	-6.4	NB	NB	NB	NB	No binding at either pH tested	No binding	Low pH
	ULC + Heavy	688	16.9	3.54E+04	3.57E-04	1.01E-08	32.3	598	5.0	1.16E+04	1.76E-03	1.52E-07	6.6	0.3	4.9	15.0
	Heavy only	152	-1.6	NB	NB	NB	NB	127	-5.4	NB	NB	NB	NB	Negative Control		
	No DNA	54	-1.7	NB	NB	NB	NB	30	-5.6	NB	NB	NB	NB			

FIG. 20C

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Heavy Chain	Light Chain Mutant	Kinetics at pH 7.4						Kinetics at pH 5.75						Ratio of low pH / neutral pH		
		mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/MS)	kd (1/s)	KD (M)	t _{1/2} (min)	mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/MS)	kd (1/s)	KD (M)	t _{1/2} (min)	ka	kd	KD
4	H105	598	4.9	2.80E+04	1.38E-03	4.91E-08	8.4	512	-0.2	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H106	569	7.1	1.49E+04	9.67E-04	6.49E-08	11.9	494	1.2	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H108	587	6.3	2.25E+04	2.02E-03	8.96E-08	5.7	500	-0.9	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H111	606	5.6	3.46E+04	2.19E-03	6.33E-08	5.3	521	-0.9	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/106	517	3.1	2.00E+04	2.05E-03	1.03E-07	5.6	460	-1.1	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/108	581	2.5	1.61E+05	2.30E-03	1.43E-08	5.0	506	-2.7	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/111	575	3.8	1.01E+04	1.70E-03	1.68E-07	6.8	504	-2.0	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H106/108	498	2.5	4.01E+04	6.07E-04	1.51E-08	19.0	447	-3.9	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H106/111	587	3.0	7.85E+04	9.20E-04	1.17E-08	12.6	509	-2.6	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H108/111	599	4.0	9.68E+04	2.02E-03	2.09E-08	5.7	528	-2.6	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/106/108	64	-1.7	NB	NB	NB	NB	46	-5.4	NB	NB	NB	NB	No binding at either pH tested		
	H105/106/111	561	1.1	NB	NB	NB	NB	493	-2.8	NB	NB	NB	NB	No binding at either pH tested		
	H105/108/111	521	2.7	7.66E+04	1.29E-03	1.68E-08	9.0	461	-3.2	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H106/108/111	577	1.3	NB	NB	NB	NB	514	-4.2	NB	NB	NB	NB	No binding at either pH tested		
	H105/106/108/111	554	0.6	NB	NB	NB	NB	495	-4.8	NB	NB	NB	NB	No binding at either pH tested		
	ULC + Heavy	585	7.4	5.69E+04	2.01E-03	3.53E-08	5.7	527	1.9	NB	NB	NB	NB	No binding at Low pH		
	Heavy only	187	-2.4	NB	NB	NB	NB	161	-5.4	NB	NB	NB	NB	No binding at Low pH		
	No DNA	49	-2.6	NB	NB	NB	NB	25	-5.6	NB	NB	NB	NB	Negative Control		

FIG. 20D

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Heavy Chain	Light Chain Mutant	Kinetics at pH 7.4						Kinetics at pH 5.75						Ratio of low pH / neutral pH		
		mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	ka	kd	KD
5	H105	522	3.2	5.05E+04	9.48E-03	1.88E-07	1.2	463	-4.3	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H106	496	0.3	NB	NB	NB	NB	437	-5.2	NB	NB	NB	NB	No binding at either pH tested		
	H108	475	-0.1	NB	NB	NB	NB	415	-5.7	NB	NB	NB	NB	No binding at either pH tested		
	H111	523	1.6	NB	NB	NB	NB	463	-4.7	NB	NB	NB	NB	No binding at either pH tested		
	H105/106	534	-0.6	NB	NB	NB	NB	472	-5.5	NB	NB	NB	NB	No binding at either pH tested		
	H105/108	499	2.0	5.80E+04	1.16E-02	1.99E-07	1.0	433	-5.5	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/111	489	0.1	NB	NB	NB	NB	426	-4.7	NB	NB	NB	NB	No binding at either pH tested		
	H106/108	441	-0.5	NB	NB	NB	NB	386	-4.2	NB	NB	NB	NB	No binding at either pH tested		
	H106/111	529	-0.8	NB	NB	NB	NB	461	-6.3	NB	NB	NB	NB	No binding at either pH tested		
	H108/111	495	4.1	1.73E+05	1.06E-02	6.11E-08	1.1	435	-4.0	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/106/108	505	-1.1	NB	NB	NB	NB	444	-5.5	NB	NB	NB	NB	No binding at either pH tested		
	H105/106/111	499	-1.7	NB	NB	NB	NB	438	-5.8	NB	NB	NB	NB	No binding at either pH tested		
	H105/108/111	436	0.8	NB	NB	NB	NB	388	-3.7	NB	NB	NB	NB	No binding at either pH tested		
	H106/108/111	539	-1.4	NB	NB	NB	NB	477	-4.0	NB	NB	NB	NB	No binding at either pH tested		
	H105/106/108/111	556	-1.6	NB	NB	NB	NB	490	-4.4	NB	NB	NB	NB	No binding at either pH tested		
	ULC + Heavy	516	0.6	NB	NB	NB	NB	451	-5.0	NB	NB	NB	NB	No binding at either pH tested		
	Heavy only	144	-1.3	NB	NB	NB	NB	122	-5.7	NB	NB	NB	NB	No binding at either pH tested		
	No DNA	47	-1.4	NB	NB	NB	NB	25	-5.8	NB	NB	NB	NB	Negative Control		

FIG. 20E

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V_H	V_K	K_D at pH7.4 (nM)	K_D at pH5.75 (nM)	$T_{1/2}$ at pH7.4 (min)	$T_{1/2}$ at pH5.75 (min)
2	Parental ULC	1.6	60	65	9.4
2	ULC (His105,106)	3.4	570	39	1.8
2	ULC (His105,111)	4.1	1270	32	0.9
2	ULC (His105,108,111)	3.2	NB	40	NB
2	ULC (His105,106,108)	5.2	NB	27	NB
3	Parental ULC	10.1	152	32	6.6
3	ULC (His106,108)	4.4	NB	40	NB
3	ULC (His108,111)	7.3	NB	144	NB
6	Parental ULC	3.0	2.4	10	6
6	ULC (His105,111)	3.5	NB	9	NB
6	ULC (His106, 108,111)	2.0	NB	16	NB

FIG. 21

Site-directed mutagenesis primers for Histidine substitutions in CDR3 of Universal Light Chain of hVK1-39JK5

Primer name	Sequence	%GC	N	%mismatch	Tm
GERMLINE hVH1-39/JK5	CAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGATCACCTTCGGC				
1633-H106/108/111 F	CCTTACTACTGTCAACATAGT C ACAGTACCC A TCCGATCACCTTCG	47.0	45	6.7	79.0
1633-H105/106/108/111 F	CAACTTACTACTGTCA CCA TAGT C ACAGTACCC A TCCGATCACCTTCGGC	50.0	50	8.0	80.5
1633-H106/108/111 R	CGAAGGTGATCGGA T GGGTACTGT G ACT A TATGTTGACAGTAGTAAG	47.0	45	6.7	79.0
1633-H105/106/108/111 R	GCCGAAGGTGATCGGA T GGGTACTGT G ACT A TATGTTGACAGTAGTAAGTTG	50.0	50	8.0	80.5

Primer	SEQ ID NO
GERMLINE hVK1-39/JK5	405
1633-H106/108/111 F	358
1633-H105/106/108/111 F	359
1633-H106/108/111 R	360
1633-H105/106/108/111 R	361

FIG. 22

Construction of VK1-39 HULC LTVECs

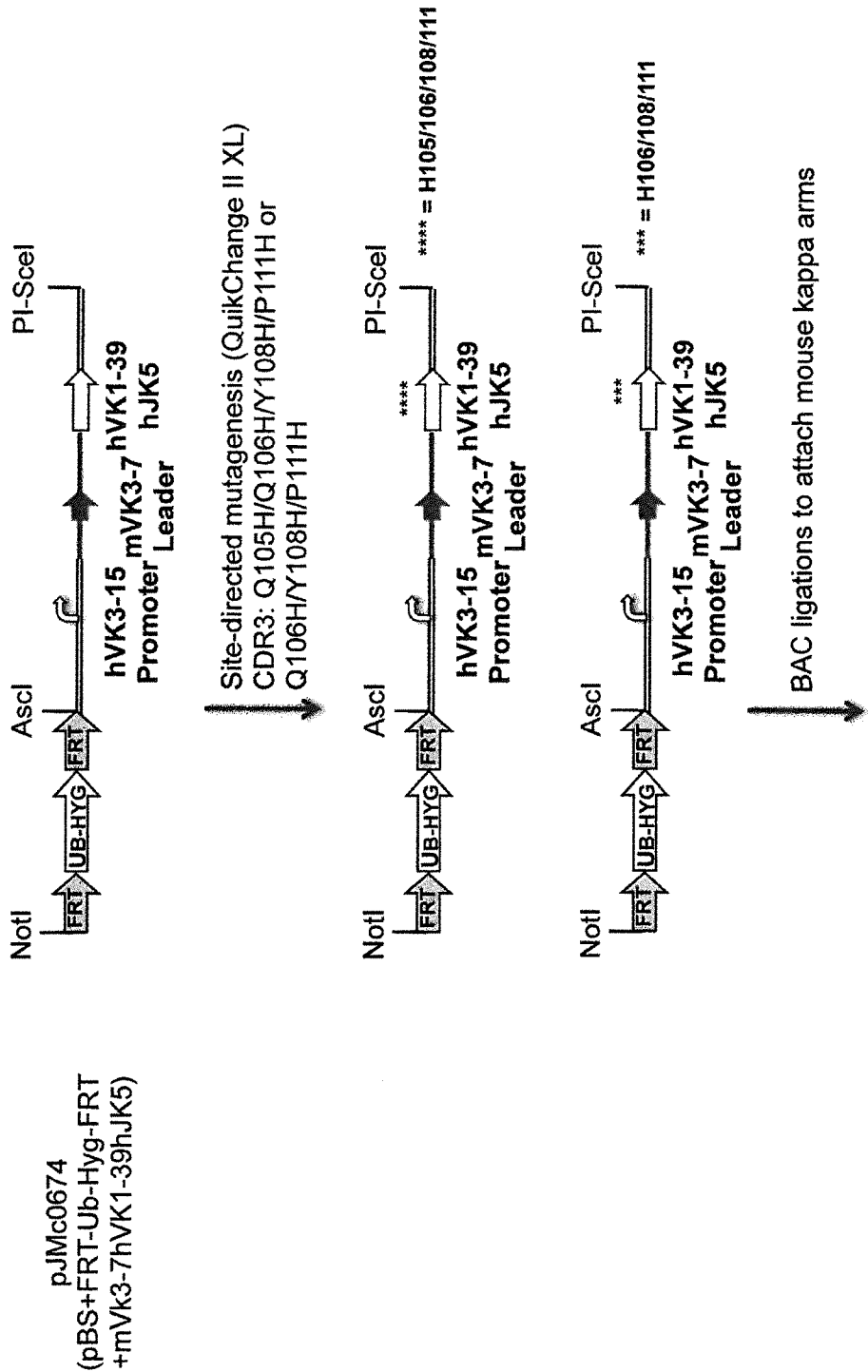
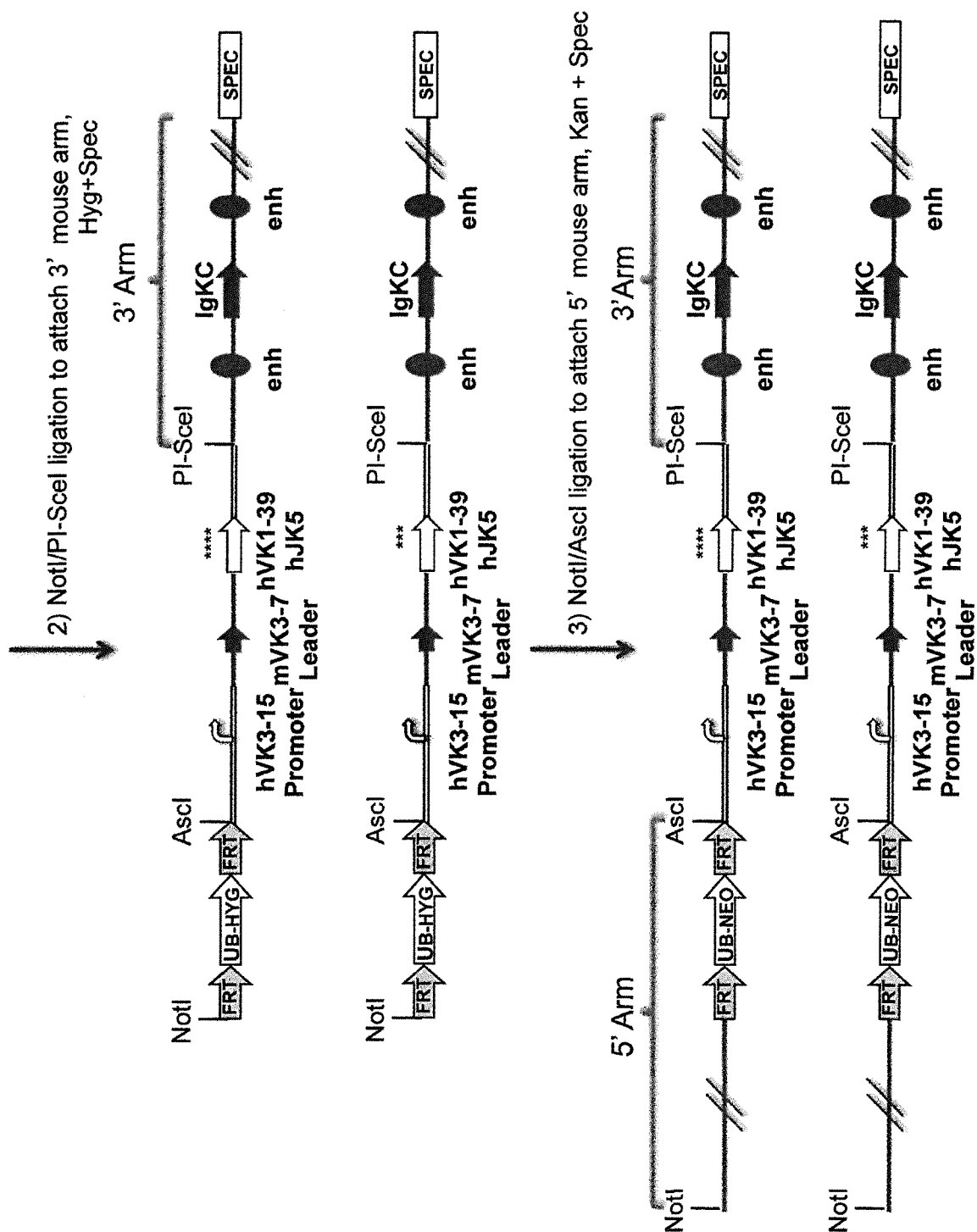


FIG. 23A

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(ULC-H105/106/108/111)

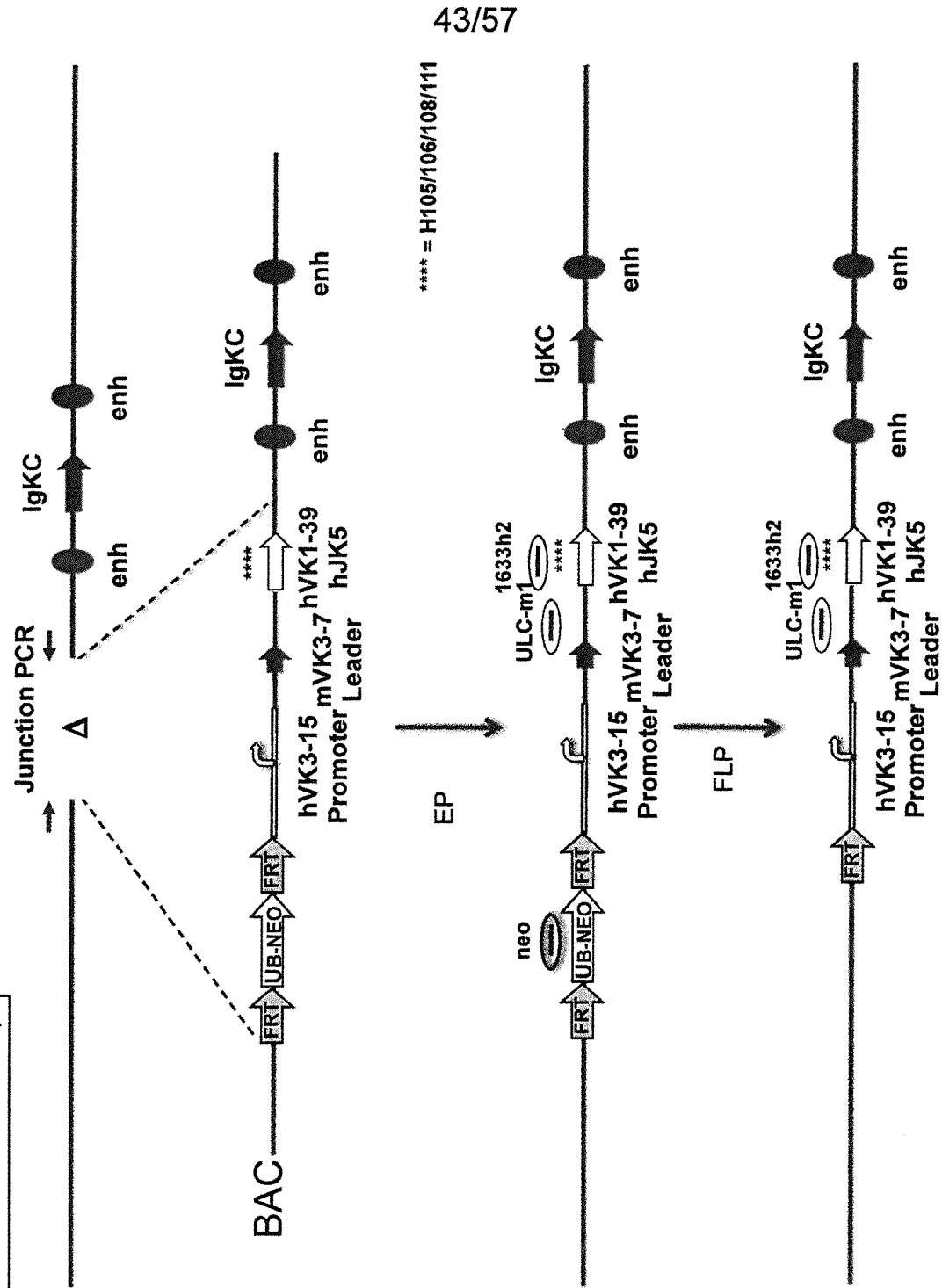


FIG. 23C

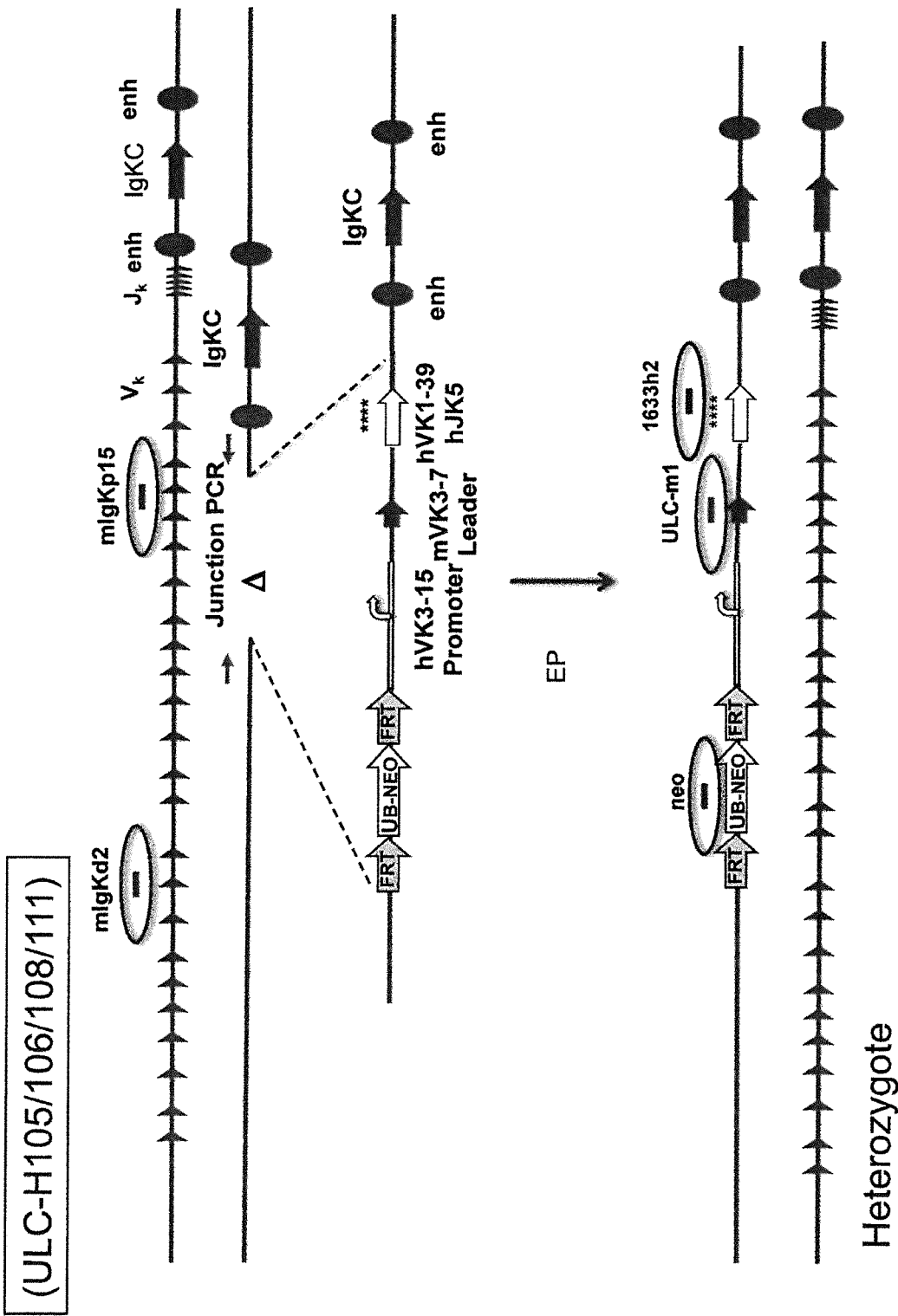


FIG. 23D

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(ULC-H106/108/111)

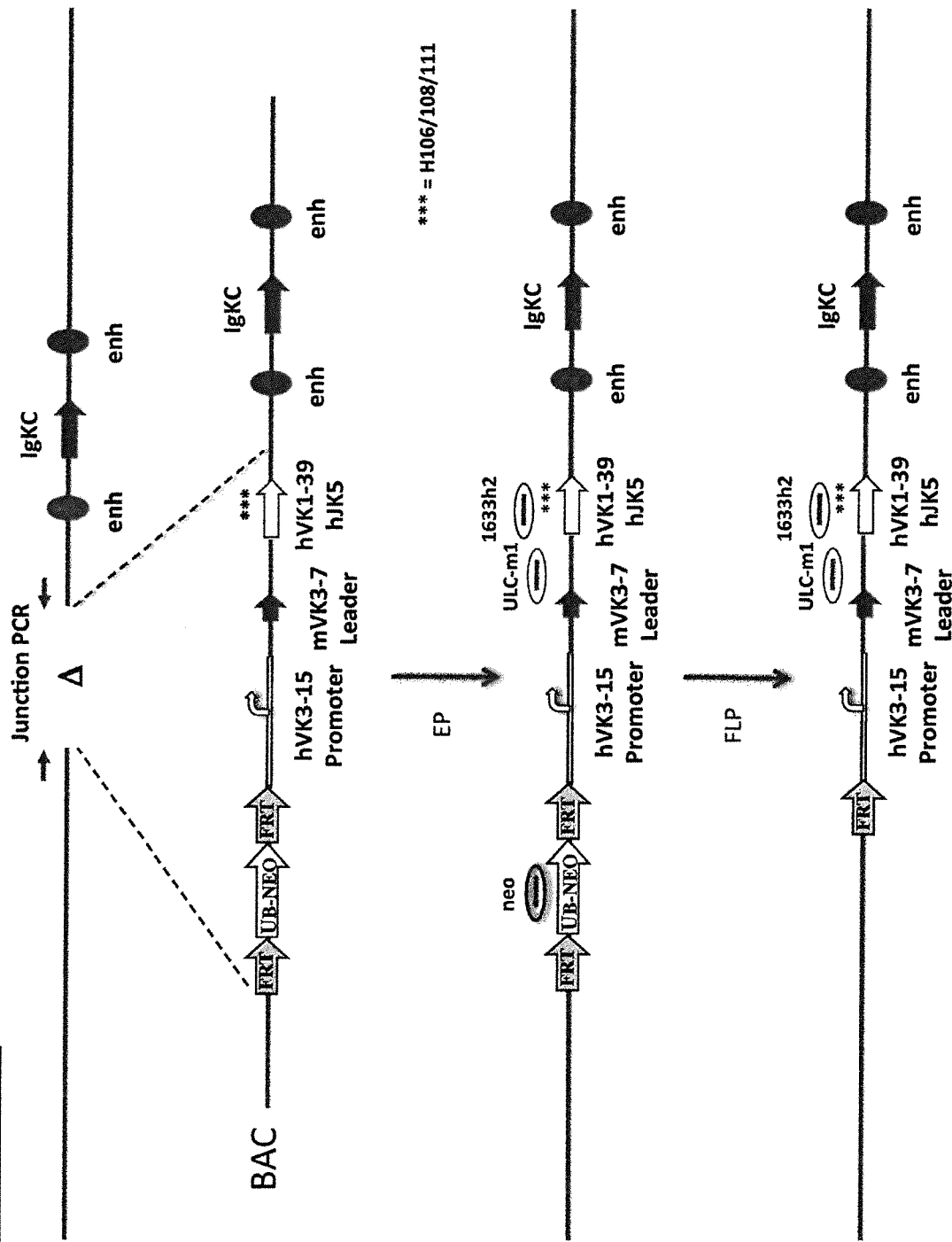


FIG. 23E

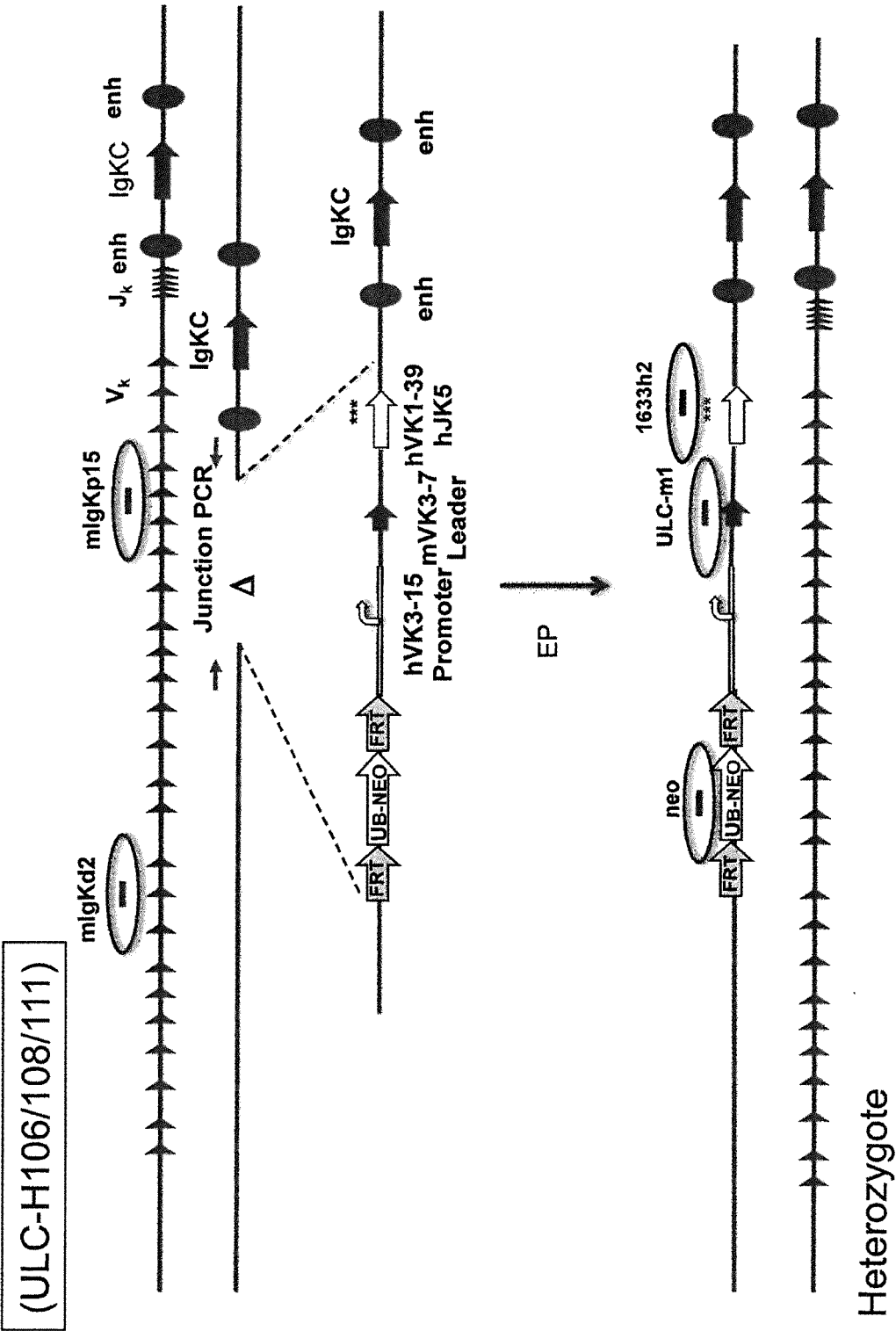


FIG. 23F

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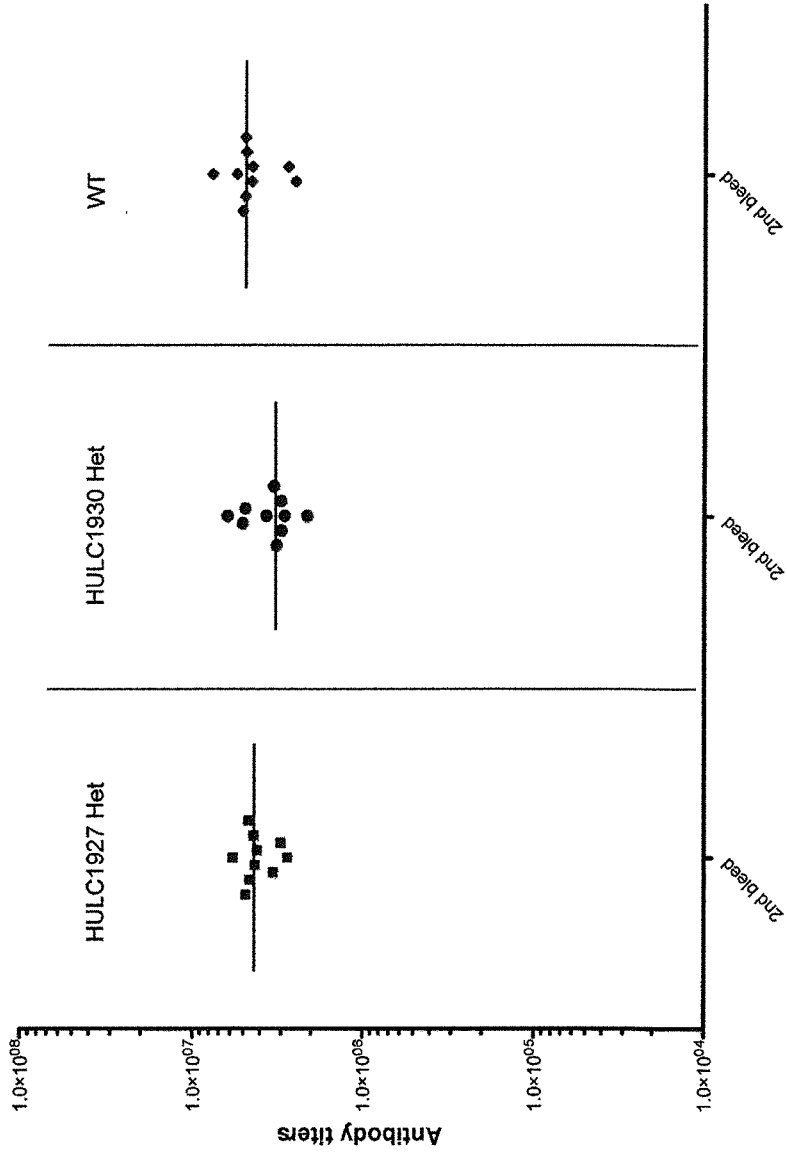


FIG. 24

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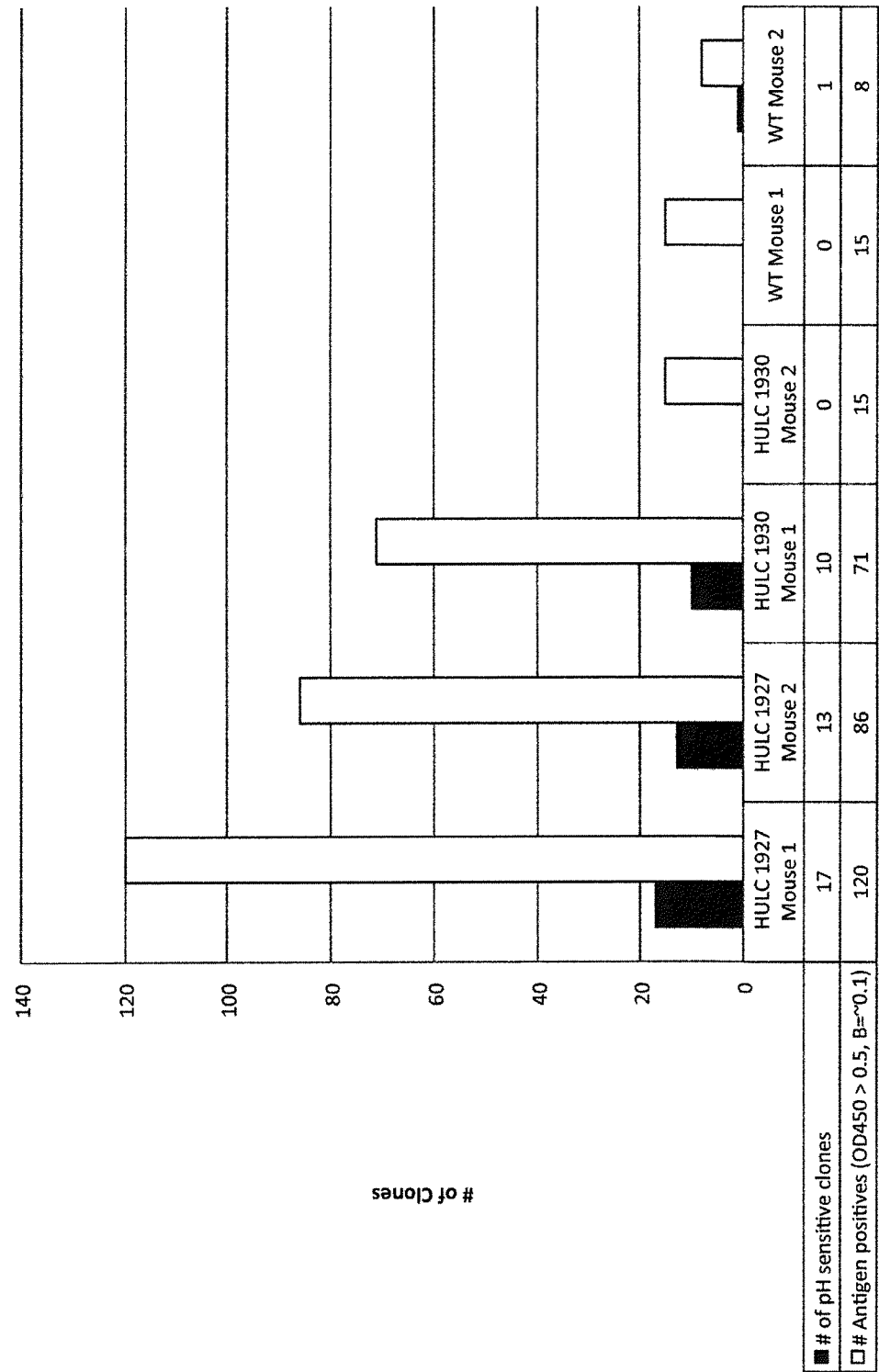


FIG. 25

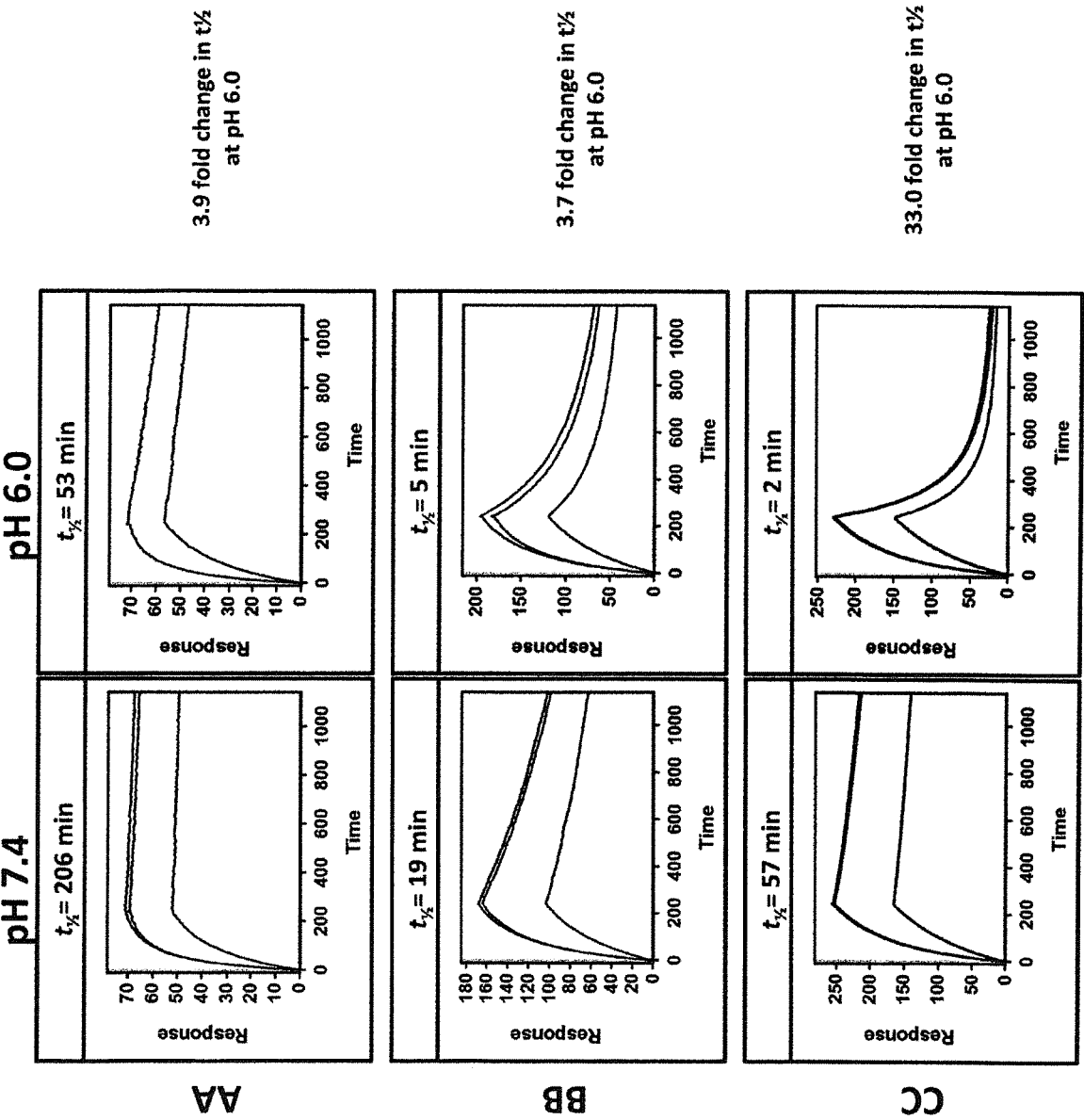


FIG. 26A

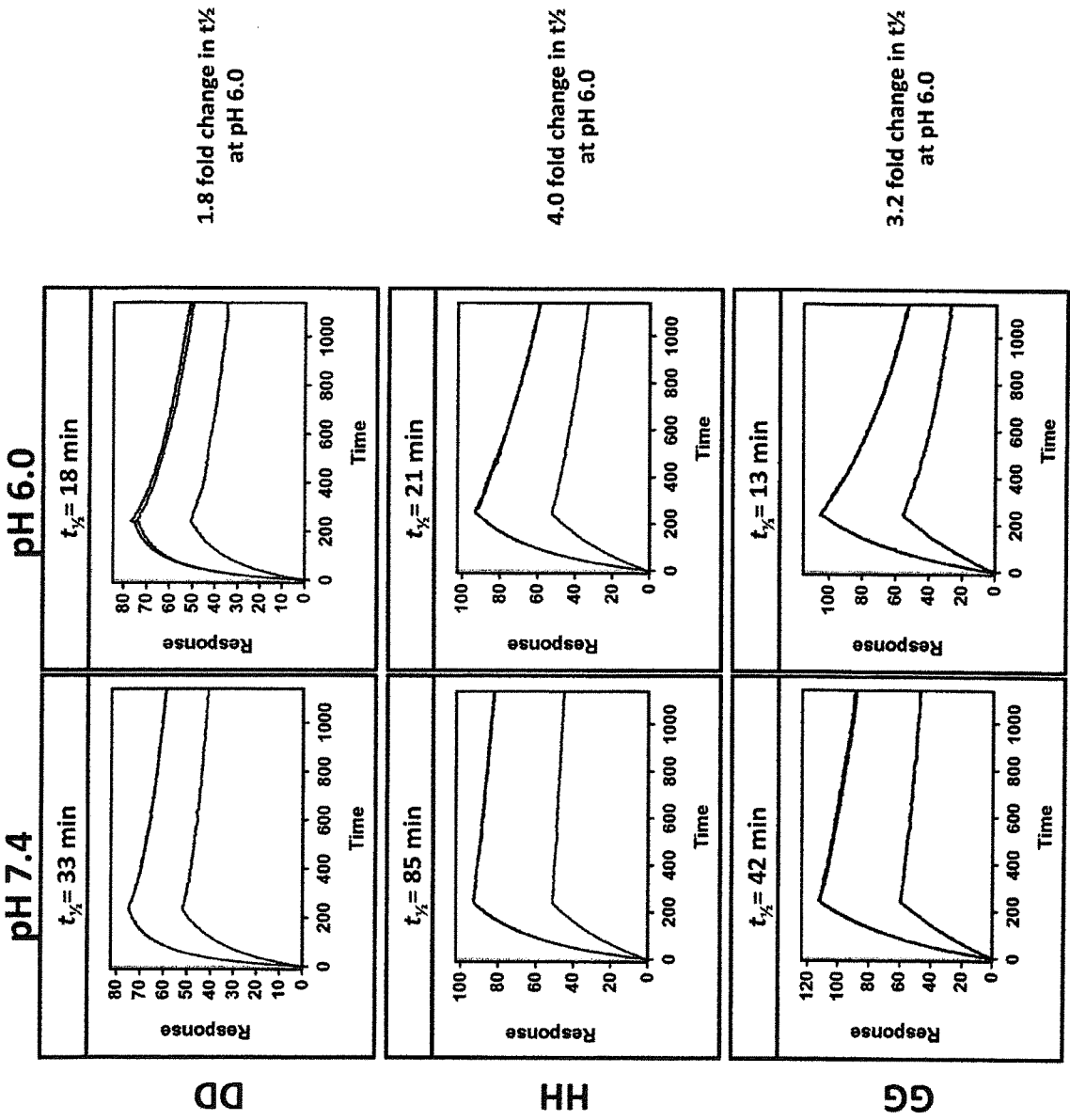


FIG. 26B

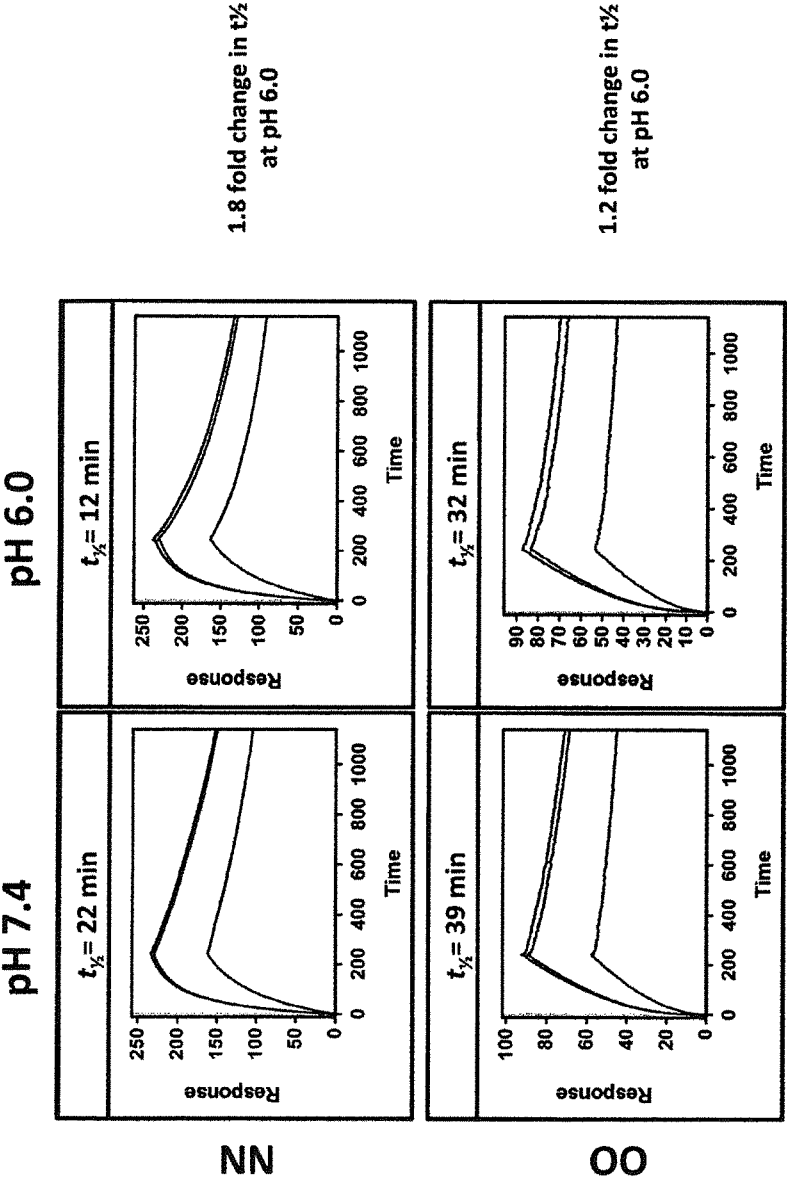


FIG. 26C

	105	106	107	108	109	110	111	
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	CAG	CAG	TAT	GGT	AGC	TCA	CCT	SEQ. ID NO:398
H105/106/107/109	H	H	H	G	H	S	P	SEQ. ID NO:401
	CAT	CAC	CAT	GGT	CAC	TCA	CCT	SEQ. ID NO:400
H105/106/109	H	H	Y	G	H	S	P	SEQ. ID NO:403
	CAT	CAC	TAT	GGT	CAC	TCA	CCT	SEQ. ID NO:402

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FIG. 27

Site-directed mutagenesis primers for Histidine substitutions in CDR3 of VK3-20JK1 ULC plasmid

Primer name	Sequence	%GC	N	mismatches	Tm
GERMLINE hVK3-20	GATTTTCAGTGTATTACTCTCAGCAGTATGGTAGCTCACCTTGGACGTTCCGGC				
hVK3-20 (H105/106/107/109) F	GATTTTCAGTGTATTACTCTCAGCAGTATGGTAGCTCACCTTGGACGTTCCGGC	48	54	5	79.5
hVK3-20 (H105/106/107/109) R	GCCGAACGTCCAAAGTGAGTGACCATGGTGATGACAGTAATACACTGCAAAATC	48	54	5	79.5
hVK3-20 (H105/106/109) F	GCAGTGTATTACTCTCAGTCACTATGGTCACTCACCTTGGACGTTCCGG	49	47	4	78.7
hVK3-20 (H105/106/109) R	CCGAACGTCCAAGTGAGTGACCATAGTGATGACAGTAATACACTGC	49	47	4	79.7

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Primer	SEQ ID NO
GERMLINE hVK3-20/JK1	384
hVK3-20 H105/106/107/109 F	385
hVK3-20 H105/106/107/109 R	386
hVK3-20 H105/106/109 F	387
hVK3-20 H105/106/109 R	388

FIG. 28

Construction of VK3-20 HULC LTVECs

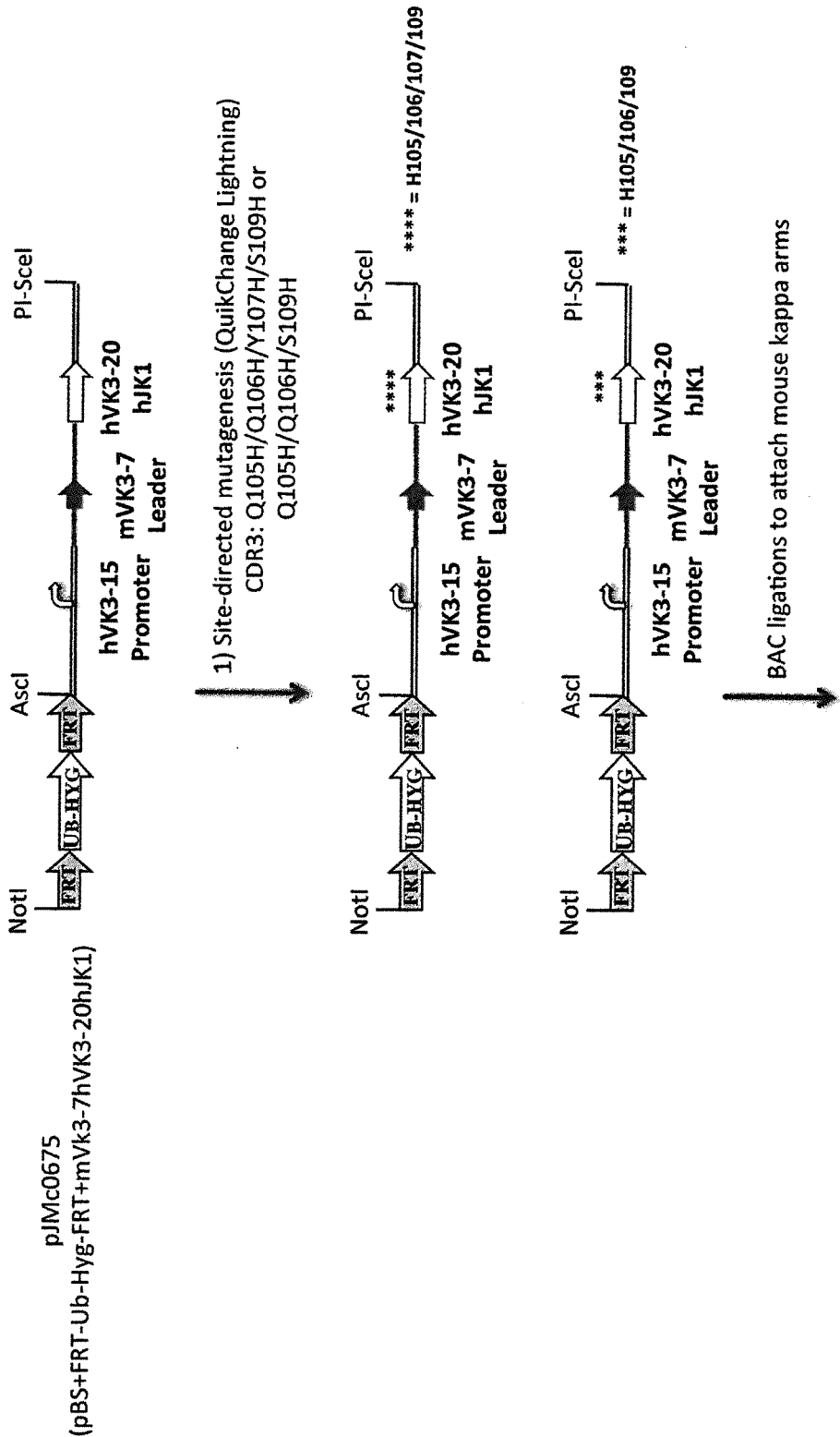
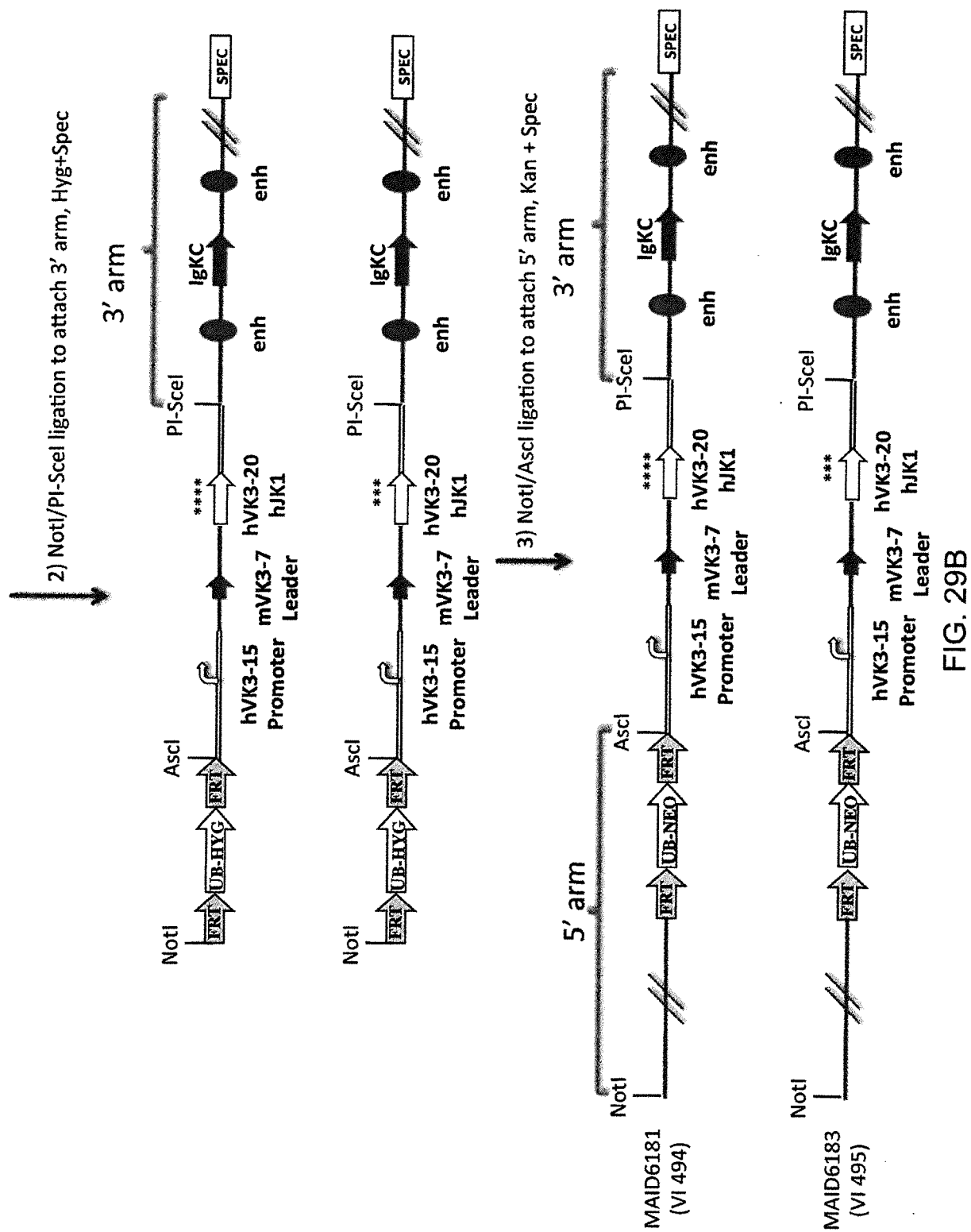


FIG. 29A



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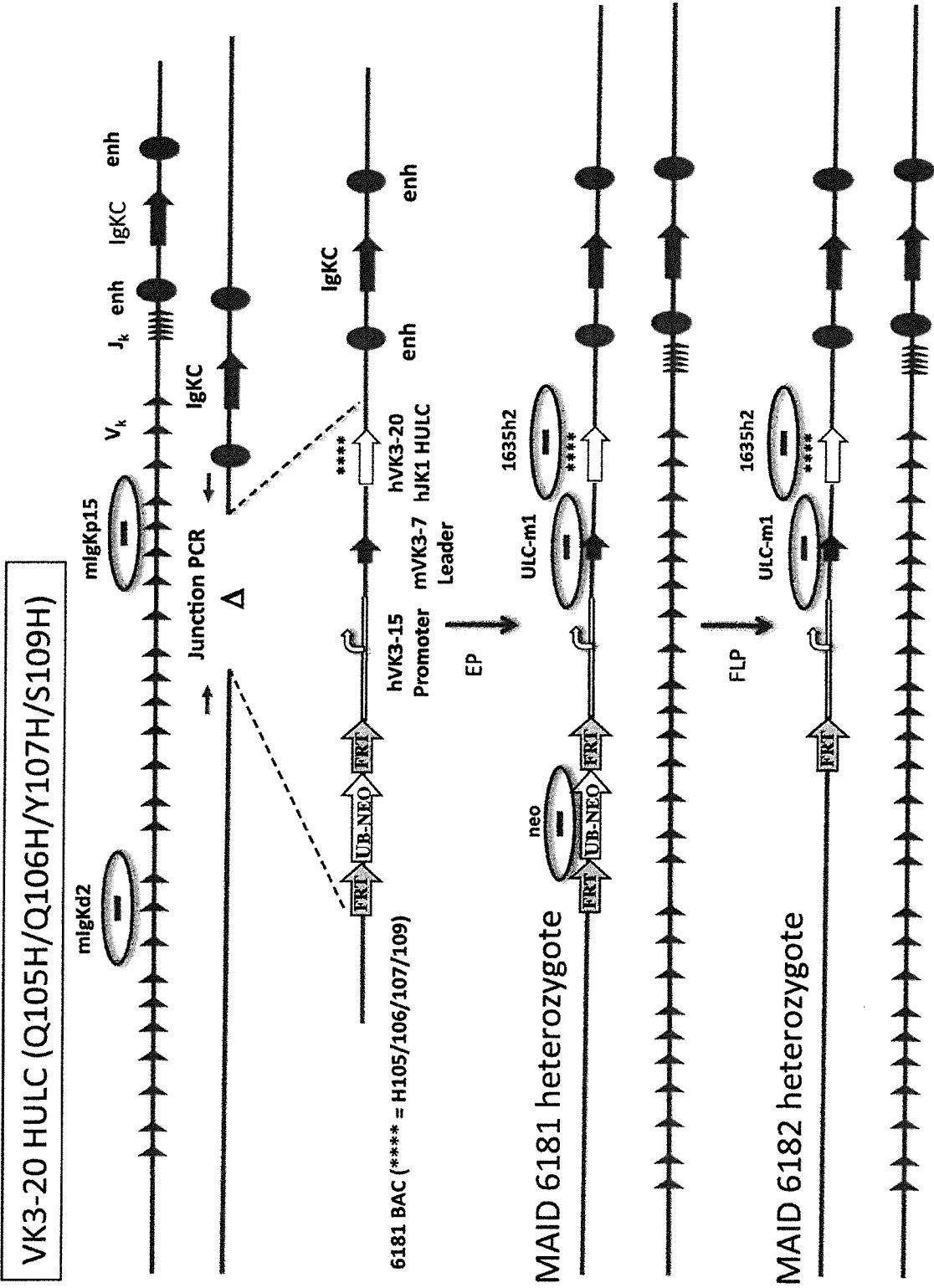


FIG. 29C

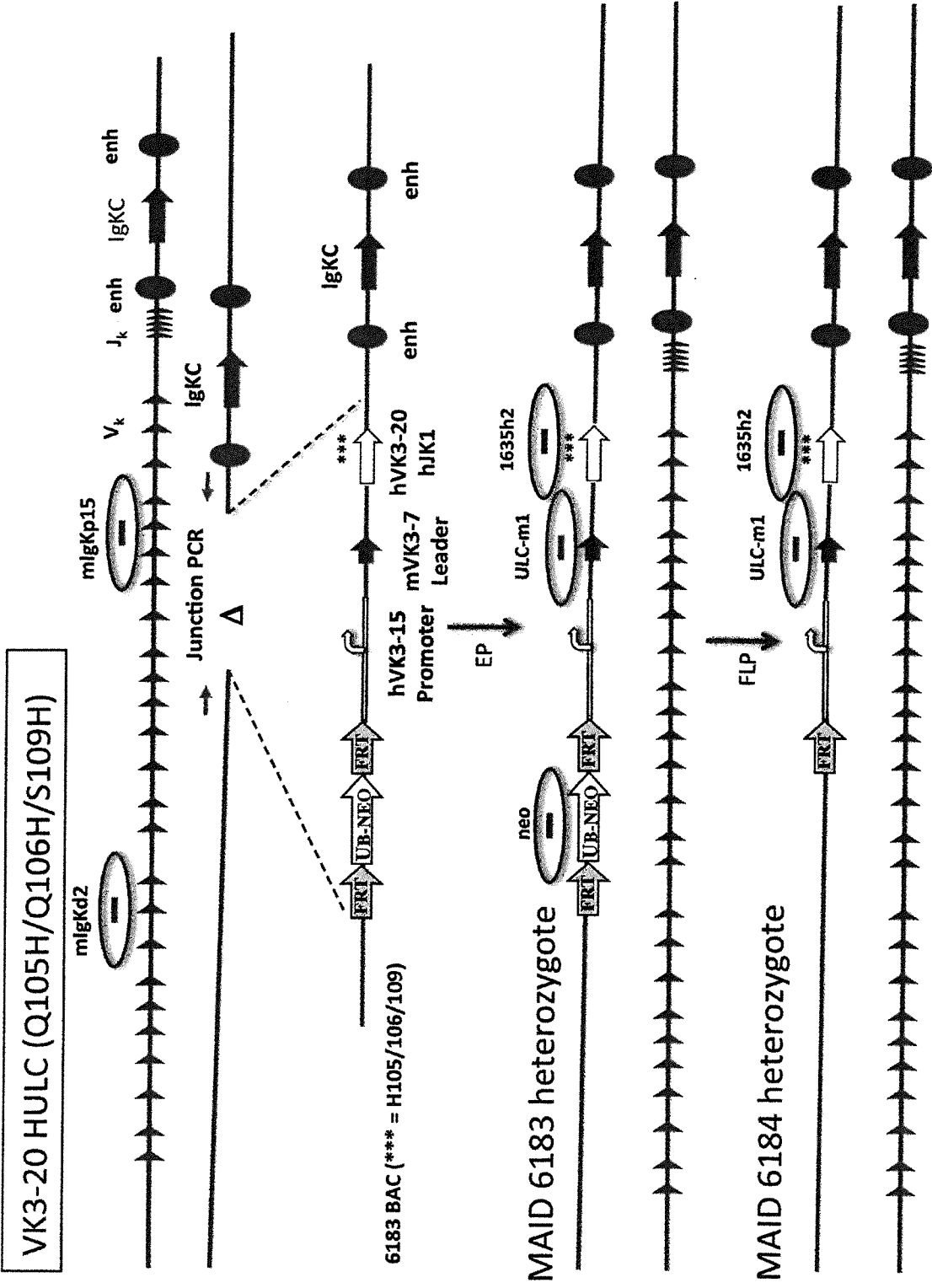


FIG. 29D

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Macdonald, Lynn
Martin, Joel
Murphy, Andrew J.

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<130> 1900A-WO

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<151> 2012-03-16

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<151> 2012-03-20

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<400> 9

Val Pro Leu Ala Arg
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<220>
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<210> 13
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Val Ser Trp Glu Pro Leu
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<210> 305
<211> 7
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<220>
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<400> 305

Val Pro Ala Thr Ala Ile Pro
1 5

<210> 306
<211> 6
<212> PRT
<213> Unknown

<220>
<223> Mamma1

<400> 306

Tyr Gln Pro Leu Leu Tyr
1 5

<210> 307
<211> 6
<212> PRT
<213> Unknown

<220>
<223> Mamma1

<400> 307

Thr Ser His Cys Tyr Thr
1 5

<210> 308
<211> 18
<212> DNA
<213> Unknown

<220>
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18

<210> 309
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<220>

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<223> Mammal

<400> 309

Val Ala Ala Ala Ile Pro
1 5

<210> 310

<211> 4

<212> PRT

<213> Unknown

<220>

<223> Mammal

<400> 310

Pro Leu Leu Tyr
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<210> 311

<211> 5

<212> PRT

<213> Unknown

<220>

<223> Mammal

<400> 311

Ser Arg Cys Tyr Thr
1 5

<210> 312

<211> 366

<212> DNA

<213> Homo sapiens

<400> 312

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acctgcgctg tctatggtgg gtccttcagt ggttactact ggagctggat ccgccagccc	120
ccaggggaagg ggctggagtg gattggggaa atcaatcata gtggaagcac caactacaac	180
ccgtccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg	240
aagctgagct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcggg gcatagccat	300
ggctggtact actactacta cggtatggac gtctggggcc aagggaccac ggtcaccgtc	360
tcctca	366

<210> 313

<211> 122

<212> PRT

<213> Homo sapiens

<400> 313

Gln val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Asp
1 5 10 15

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Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Gly His Ser His Gly Trp Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 314
<211> 96
<212> PRT
<213> Homo sapiens

<400> 314

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

<210> 315
<211> 355
<212> DNA
<213> Homo sapiens

<400> 315

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acctgcactg tctctggtgg ctccatcagc agtggtggtt actactggag ctggatccgc 120

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cagcaccag ggaagggcct ggagtggatt gggtagatct attacagtgg gagcacctac 180
tacaaccgt ccctcaagag tcgagttacc atatcagtag acacgtctaa gaaccagttc 240
tccctgaagc tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgaggggg 300
gaccacggtc actacgacta ctggggccag ggaaccctgg tcaccgtctc ctcag 355

<210> 316
<211> 118
<212> PRT
<213> Homo sapiens

<400> 316

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Gly Asp His Gly His Tyr Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 317
<211> 98
<212> PRT
<213> Homo sapiens

<400> 317

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

1900A-WO_SEQ_ST25
 Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
 65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95

Cys Ala

<210> 318
 <211> 370
 <212> DNA
 <213> Homo sapiens

<400> 318
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 cagcccccag ggaaggggct ggagtggatt gggagtatct attatagtgg gagcacctac 180
 tacaaccctg ccctcaagag tcgagtcacc atatccgtag acacgtccaa gaaccagttc 240
 tccctgaagc tgagctctgt gaccgccgca gacacggctg tgtattactg tgcgagacat 300
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 gtctcctcag 370

<210> 319
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 319
 Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
 20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
 65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95

1900A-WO_SEQ_ST25
 Cys Ala Arg His Glu Gly His Ser His Leu Asn Trp Phe Asp Pro Trp
 100 105 110

Gly Gln Gly Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 320
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 320

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
 20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
 65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95

Cys Ala Arg

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<220>
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22

<210> 322
 <211> 22
 <212> DNA
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<220>
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<400> 322
 ggaagacatt tgggaaggac tg

22

<210> 323

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<211> 4
<212> PRT
<213> Unknown

<220>
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<220>
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<222> (3)..(3)
<223> wherein the "Xaa" represents any amino acid

<400> 323

Phe Gly Xaa Gly
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<210> 324
<211> 4
<212> PRT
<213> Unknown

<220>
<223> Mammal

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> wherein the "Xaa" represents any amino acid

<400> 324

Trp Gly Xaa Gly
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<211> 95
<212> PRT
<213> Artificial

<220>
<223> Synthetic

<400> 325

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro
85 90 95

<210> 326
<211> 21
<212> DNA
<213> Artificial

<220>
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<220>
<221> CDS
<222> (1)..(21)

<400> 326
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Gln Gln Ser Tyr Ser Thr Pro
1 5

21

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<211> 7
<212> PRT
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<220>
<223> Synthetic Construct

<400> 327
Gln Gln Ser Tyr Ser Thr Pro
1 5

<210> 328
<211> 21
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<220>
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<220>
<221> CDS
<222> (1)..(21)

<400> 328
cac cat agc cac agc acc cac
His His Ser His Ser Thr His
1 5

21

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<211> 7
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<220>
<223> Synthetic Construct

<400> 329
His His Ser His Ser Thr His

1

5

<210> 330
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<220>
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 <222> (1)..(21)

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 His Gln Ser Tyr Ser Thr Pro
 1 5

21

<210> 331
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<220>
 <223> Synthetic Construct

<400> 331
 His Gln Ser Tyr Ser Thr Pro
 1 5

<210> 332
 <211> 21
 <212> DNA
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<220>
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 <222> (1)..(21)

<400> 332
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 Gln His Ser Tyr Ser Thr Pro
 1 5

21

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<400> 333
 Gln His Ser Tyr Ser Thr Pro
 1 5

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 <222> (1)..(21)

<400> 334
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 Gln Gln Ser His Ser Thr Pro
 1 5

21

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<220>
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<400> 335
 Gln Gln Ser His Ser Thr Pro
 1 5

<210> 336
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<220>
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 cag cag agc tac agc acc cac
 Gln Gln Ser Tyr Ser Thr His
 1 5

21

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<220>
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<400> 337
 Gln Gln Ser Tyr Ser Thr His
 1 5

<210> 338

<211> 21
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 <213> Artificial

<220>
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 <222> (1)..(21)

<400> 338
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 His His Ser Tyr Ser Thr Pro
 1 5

21

<210> 339
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<400> 339

His His Ser Tyr Ser Thr Pro
 1 5

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<400> 340
 cac cag agc cac agc acc ccc
 His Gln Ser His Ser Thr Pro
 1 5

21

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<400> 341

His Gln Ser His Ser Thr Pro
 1 5

<210> 342
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<213> Artificial

<220>

<223> Synthetic

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<221> CDS

<222> (1)..(21)

<400> 342

cac cag agc tac agc acc cac
His Gln Ser Tyr Ser Thr His
1 5

21

<210> 343

<211> 7

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<223> Synthetic Construct

<400> 343

His Gln Ser Tyr Ser Thr His
1 5

<210> 344

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1)..(21)

<400> 344

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Gln His Ser His Ser Thr Pro
1 5

21

<210> 345

<211> 7

<212> PRT

<213> Artificial

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<223> Synthetic Construct

<400> 345

Gln His Ser His Ser Thr Pro
1 5

<210> 346

<211> 21

<212> DNA

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<220>
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<220>
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<222> (1)..(21)

<400> 346
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Gln His Ser Tyr Ser Thr His
1 5

21

<210> 347
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<400> 347
Gln His Ser Tyr Ser Thr His
1 5

<210> 348
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<220>
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<220>
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<222> (1)..(21)

<400> 348
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Gln Gln Ser His Ser Thr His
1 5

21

<210> 349
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 349
Gln Gln Ser His Ser Thr His
1 5

<210> 350
<211> 21
<212> DNA
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<220>
<223> Synthetic

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<220>
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 <222> (1)..(21)

<400> 350
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 His His Ser His Ser Thr Pro
 1 5

21

<210> 351
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<220>
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 His His Ser His Ser Thr Pro
 1 5

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<220>
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 <222> (1)..(21)

<400> 352
 cac cat agc tac agc acc cac
 His His Ser Tyr Ser Thr His
 1 5

21

<210> 353
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 His His Ser Tyr Ser Thr His
 1 5

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1900A-WO_SEQ_ST25

<220>
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<400> 354
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 His Gln Ser His Ser Thr His
 1 5

21

<210> 355
 <211> 7
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<220>
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<400> 355
 His Gln Ser His Ser Thr His
 1 5

<210> 356
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic

<220>
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 <222> (1)..(21)

<400> 356
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 Gln His Ser His Ser Thr His
 1 5

21

<210> 357
 <211> 7
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 <213> Artificial

<220>
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<400> 357
 Gln His Ser His Ser Thr His
 1 5

<210> 358
 <211> 45
 <212> DNA
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<220>
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<400> 358
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45

1900A-WO_SEQ_ST25

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 <220>
 <223> Synthetic

 <400> 359
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 <400> 360
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 <212> DNA
 <213> Artificial

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 <400> 361
 gccgaaggtg atcggatggg tactgtgact atggtgacag tagtaagttg 50

 <210> 362
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 <213> Artificial

 <220>
 <223> Synthetic

 <400> 362
 tgggcacaac agacaatcgg ctg 23

 <210> 363
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 <220>
 <223> Synthetic

 <400> 363
 ggtggagagg ctattcggc 19

 <210> 364
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1900A-WO_SEQ_ST25

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<210> 368 <211> 26 <212> DNA <213> Artificial	
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<210> 369 <211> 21 <212> DNA <213> Artificial	
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 ggccacattc catgggttc 19

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 gcaaacaaaa accactggcc 20

<210> 373
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 <212> DNA
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 ctgttcctct aaaactggac tccacagtaa atggaaa 37

<210> 374
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<210> 375
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 cacagcttgt gcagcctcc 19

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<210> 376
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 <220>
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 <400> 376
 agaagaagcc tgtactacag catccgtttt acagtca 37

 <210> 377
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 <220>
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 <400> 377
 accatagtca cagtaccca 19

 <210> 378
 <211> 23
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 <400> 378
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 <400> 379
 cccttggccg aagtgat 18

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 <400> 380
 atagtcacag tacccatcc 19

 <210> 381
 <211> 23
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 <220>
 <223> Synthetic

1900A-WO_SEQ_ST25

<400> 381
agtctgcaac ctgaagattt tgc 23

<210> 382
<211> 18
<212> DNA
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<220>
<223> Synthetic

<400> 382
cccttggccg aagtgat 18

<210> 383
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<220>
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<400> 383
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 384
<211> 54
<212> DNA
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<220>
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<400> 384
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<210> 385

1900A-WO_SEQ_ST25

<211> 54
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 <210> 386
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 <212> DNA
 <213> Artificial

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 <400> 386
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 <400> 388
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 <400> 389
 aaagagccac cctctcctgc aggg 24

 <210> 390
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 <212> DNA
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tccaggcacc ctgtctttg	1900A-WO_SEQ_ST25	19	
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

1900A-WO_SEQ_ST25

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
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Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
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