

	Stop	SEQ ID NO.	Hydrophilic	SEQ ID NO.	Hydrophobic	SEQ ID NO.
D1-1	VQLER	8	YNWND		GTTGT	88
HD1-1	VPLAR	9	YHWHD		GTTGT	88
D1-7	V*LEL	-	YNWNY		GITGT	89
HD1-7	VSLAL	10	YHWHY		GITGT	89
D1-20	V*LER	-	YNWND		GITGT	89
HD1-20	VSLAR	11	YHWHD		GITGT	89
D1-26	V*WELL	12	YSGSY		GIVGAT	90
HD1-26	VSWEPL	13	YHGSHY		GIMGAT	91
D2-2*02	RIL**YQLLY	14	GYCSSTSCYT	51	DIVVPAAL	92
HD2-2*02	RTL*SYQLPY	15	GHCSHTSCHT	52	DIVVPAAL	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	AYCGGDCYS	57	HIVVTAI	97
HD2-21*02	STLWWSLPF	20	AHCGGHCHS	58	HIVVTAI	97
D3-3*01	VLRFEWLLY	21	YYDFWSGYT	59	ITIFGVII	98
HD3-3*01	VSPFLEWSLY	22	YHFWSGHYT	60	ITIFGVII	98
D3-9	VLRYPDWLL*	23	YYDILTGYN	61	ITIF*LVII	99, 100
HD3-9	VSPYFDWSL*	24	YHHILTGYN	62	ITIF*LVII	99, 100
D3-10*01	VLLWFGEII*	25	YYGSGSYN	63	ITMVRGVII	101
HD3-10*01	VSPWFGEISL*	26	YHHGSGSHYN	64	ITMVRGVII	101
D3-16*02	VL*LRLGELSLY	27	YYDYVWGSYRYT	65	IMITFGGVVI	102
HD3-16*02	VS*SRLGESSLY	28	YHDHVGSHRYT	66	IMITFGGVVI	102
D3-22	VLL***WLLL	29	YYDSSGYYY	67	ITMIVVIT	103
HD3-22	VSLS**WSLL	30, 31	YHYHSSGHYY	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

	Stop	SEQ ID NO.	Hydrophilic	SEQ ID NO.	Hydrophobic	SEQ ID NO.
HD4-11p	*PQSL	32	DHSHY	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	GYSYGY	75	VDTAMV	107
HD5-5	WTQPWL	36	GHSYGY	76	VDTAMV	107
D5-12	WI*WLRL	37	GYSYDY	77	VDIVATI	108
HD5-12	WT*WPPL	38	GHSYHY	78	VDIVATI	108
D5-18	WIQLWL	35	GYSYGY	75	VDTAMV	107
HD5-18	WTQPWL	36	GHSYGY	76	VDTAMV	107
D5-24p	*RWLQL	39	RDGYNY	79	VEMATI	109
HD5-24p	*TWPPL	40	RHGHY	80	VDMATI	110
D6-6	V*QLV	-	EYSSSS	81	SIAAR	111
HD6-6	A*PLV	-	ESHSS	82	SIATR	112
D6-13	V*QQLV	41	GYSSSWY	83	GIAAAG	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	GIAAA	117
HD6-25	A*PRL	-	GSHGY	76	GIATA	118

FIG. 1B

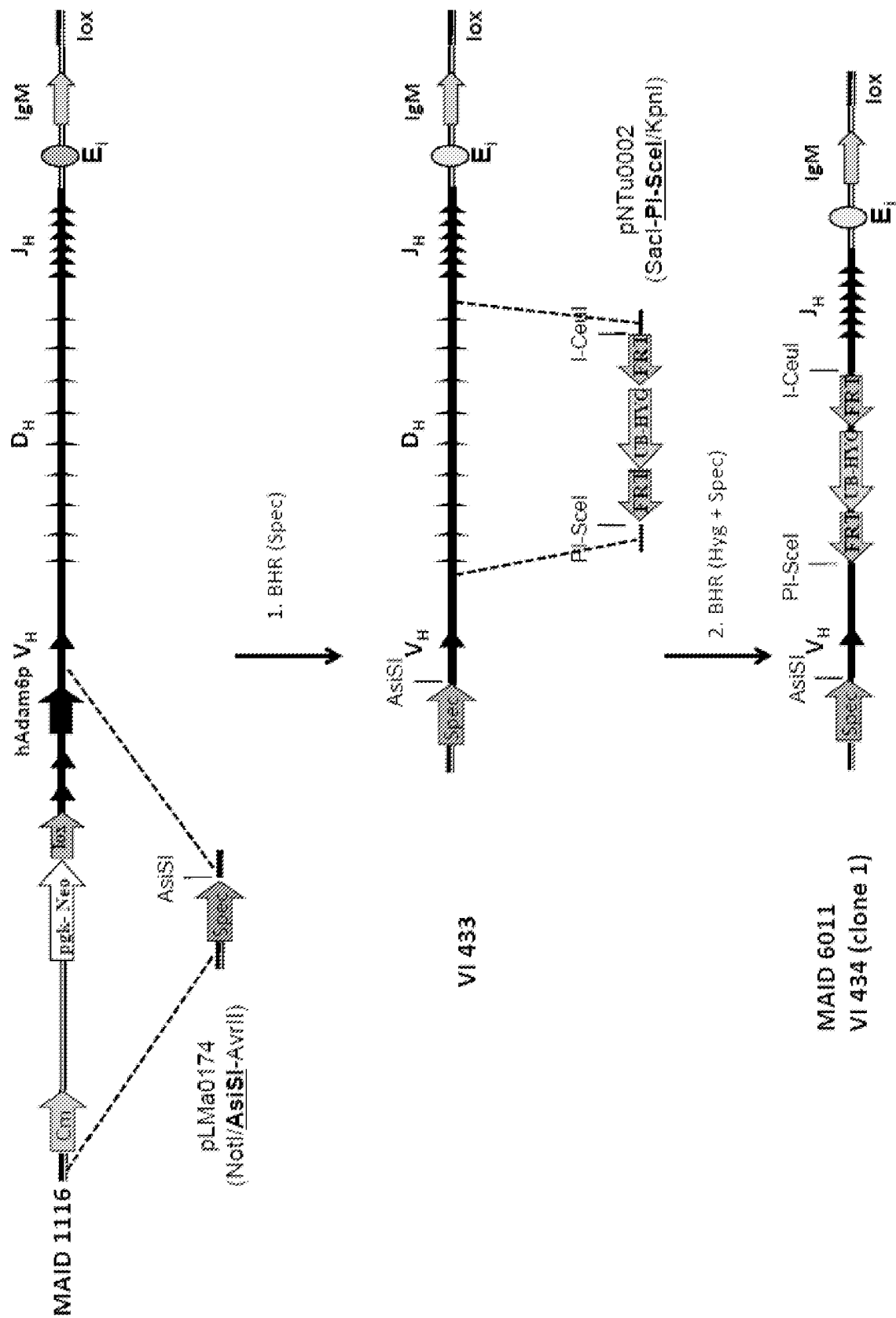


FIG. 2

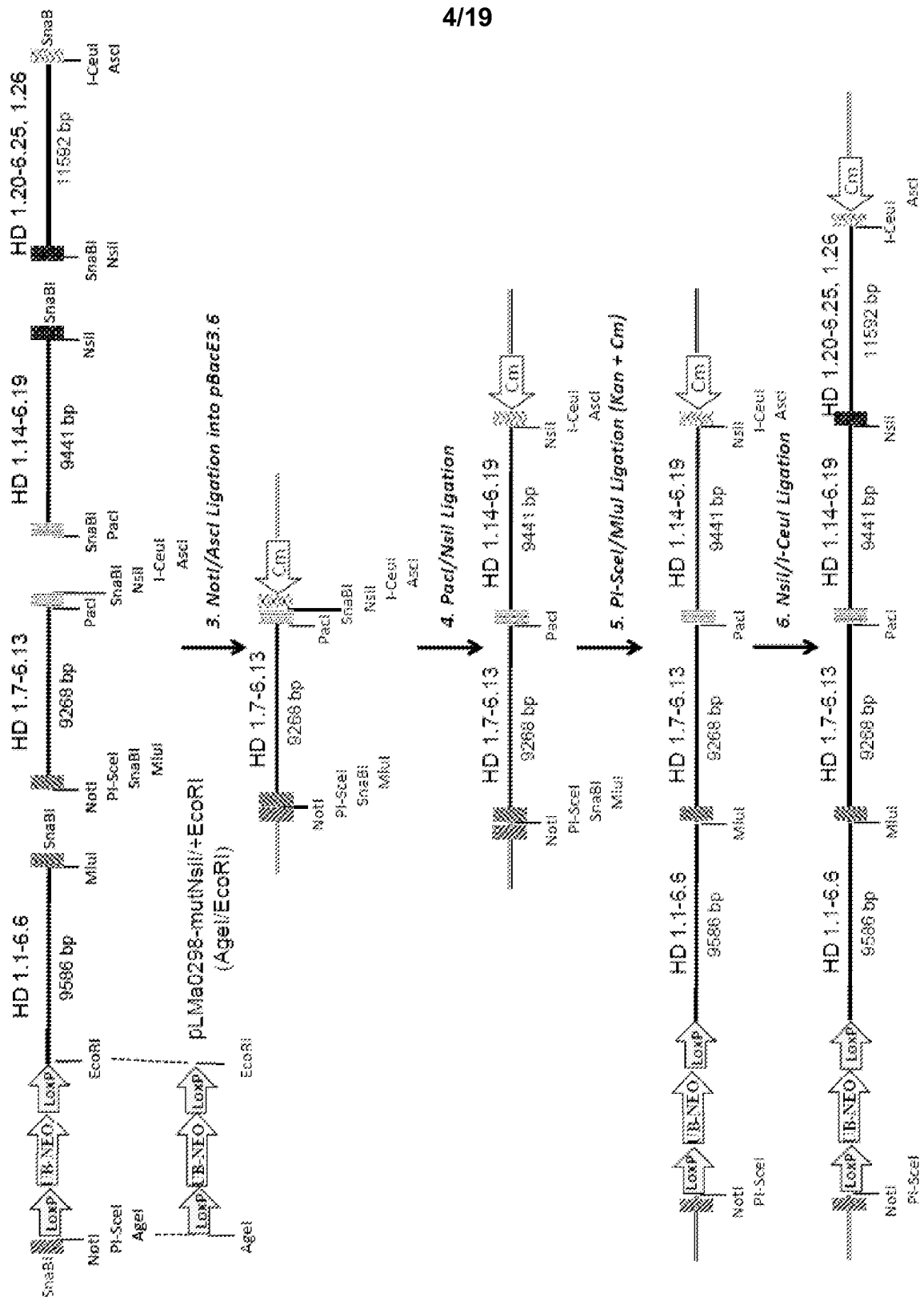


FIG. 3

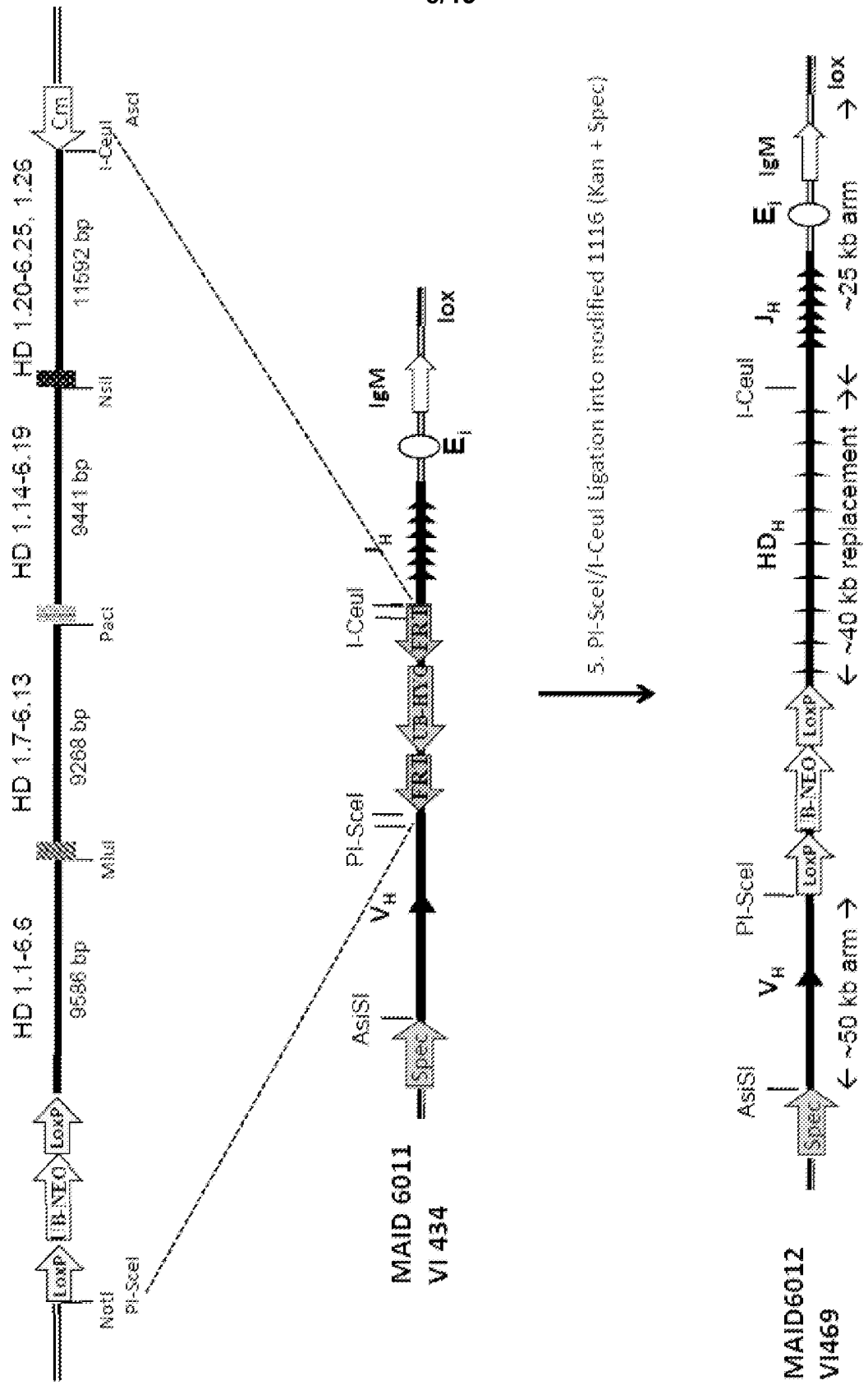


FIG. 4

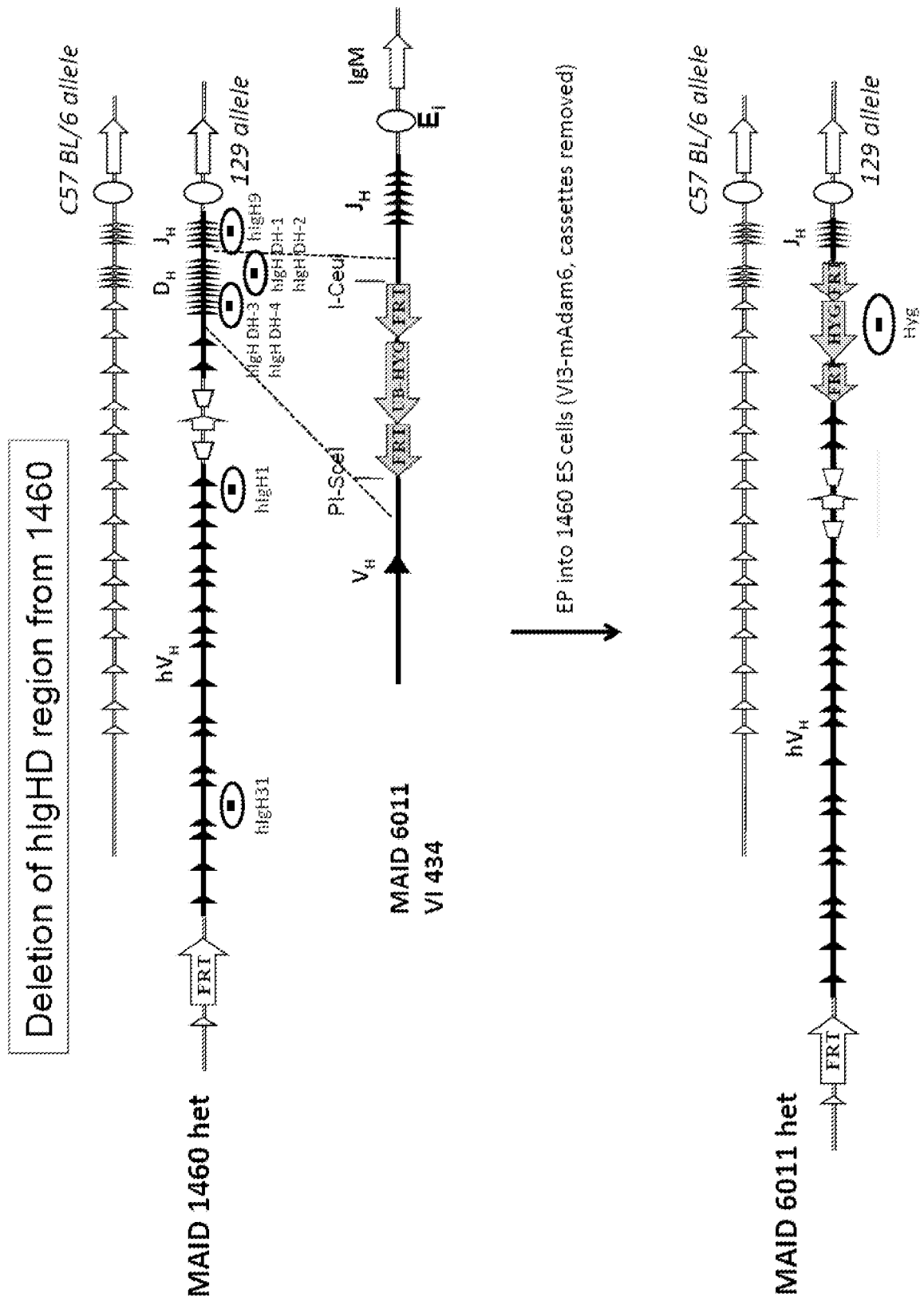


FIG. 5

7/19

Probes for MAID 6011 (deletion of high DH segments in MAID1460)						
Name	Forward Primer	Probe	Reverse Primer	Type	Label	Location
high DH-1	CGGGTCACTGCCATTCTG (SEQ ID NO: 119)	TCTGCAATCGCTCCAGCGC (SEQ ID NO: 120)	TCTGCGGCAIGAACCCAAI (SEQ ID NO: 121)	LOA	FAM- BHQ 1	high D segments
high DH-2	GTGCAGGGAGGACCTTCT G (SEQ ID NO: 122)	AGTCACCAAGCACAGAGCCCTGAC (SEQ ID NO: 123)	GCCAGGGAGTTGCCCTAGTG (SEQ ID NO: 124)	LOA	FAM- BHQ 1	high D segments
high DH-3	GTGGCCCACTTCCCTTCT (SEQ ID NO: 125)	CAGCTGGAACCCACCAIACCT (SEQ ID NO: 126)	GACCTGCCCTCGGATGACA (SEQ ID NO: 127)	LOA	FAM- BHQ 1	high D segments
high DH-4	TGGCCAGAACTGACCTTAC (SEQ ID NO: 128)	ACCGACAAGAGTCCCTCAGG (SEQ ID NO: 129)	GGAGTCGGCTCTGGATGTG (SEQ ID NO: 130)	LOA	BHQ- plus	high D segments
hvs	TGCGGCCGATCTTAGCC (SEQ ID NO: 131)	ACGAGCGGGTTCGGCCCATTC (SEQ ID NO: 132)	TTGACCGATTCTTGCGG (SEQ ID NO: 133)	GOA	FA- BHQ 1	
high1	CAGTCCCGTTGATCCAGCC (SEQ ID NO: 134)	CCCATCAGGGATTTGTATCTCTGT GGACG (SEQ ID NO: 135)	GGATATGCAGCACTGTGCCAC (SEQ ID NO: 136)	AR		high
high9	TCCTCCAACGACAGGTCCC (SEQ ID NO: 137)	TCCCTGGAACTCTGCCCCGACACA (SEQ ID NO: 138)	GATGAACGACGGGCACAGG (SEQ ID NO: 139)	AR		high
high31	ATCACACTCATCCCATCCCC (SEQ ID NO: 140)	CCCTTCCCTAAGTACCACAGAGTGG GCTC (SEQ ID NO: 141)	CACAGGGAAGCAGGAAGTGC (SEQ ID NO: 142)	AR		high

FIG. 6

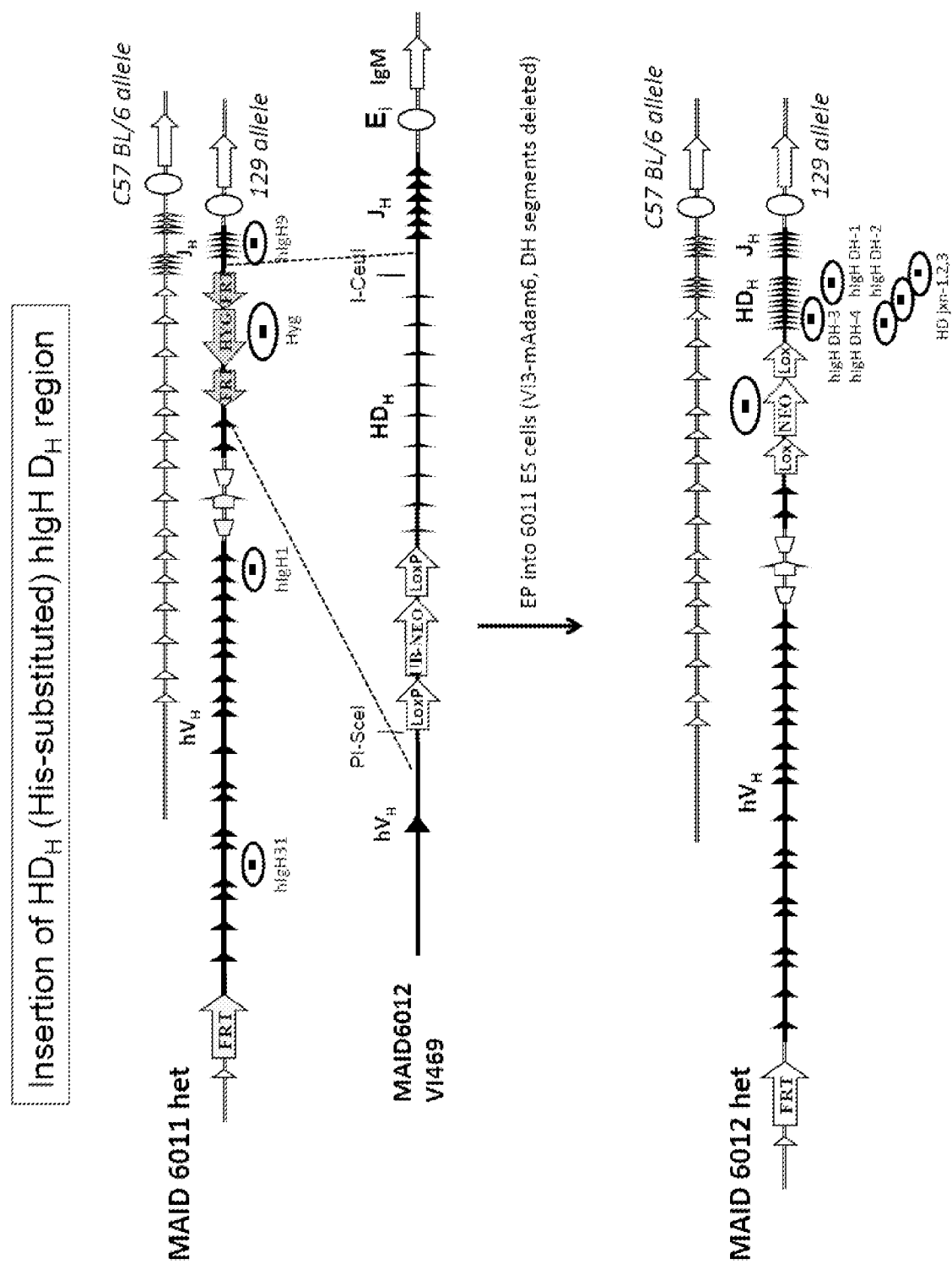


FIG. 7

9/19

Probes for MAID 6012 (insertion of HD, His-substituted hlgH DH segments)						
Name	Forward Primer	Probe	Reverse Primer	Type	Label	Location
hyg	TGCGGCGGATCTTAGCC (SEQ ID NO: 131)	ACGAGCGGGTTCGGCCCATTC (SEQ ID NO: 132)	TTGACCGATTCCTTGCGG (SEQ ID NO: 133)	LOA	FAM- BHQ1	
HD jxn-1	GGAGCCAGGCGGACACACA (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	GGTCCCGAGCACTCTTAATTAAA C (SEQ ID NO: 146)	CTCGAATGGAACTAC (SEQ ID NO: 147)	GGGAGAGCAACCAATCG TTGT (SEQ ID NO: 148)	GOA	MGB	Synthetic linker-2 in HD segments
HD jxn-3	CCGAGCACCGATGCACTCA (SEQ ID NO: 149)	CGCAGTCATGTAATGC (SEQ ID NO: 150)	GGGAGGCGAACTGACTG TCA (SEQ ID NO: 151)	GOA	MGB	Synthetic linker-3 in HD segments
hlgH DH-1	CGGGTCACTGCCATTCTG (SEQ ID NO: 119)	TCTGCATTGCTCCAGCGC (SEQ ID NO: 120)	TCTGCGGCATGAACCCAA T (SEQ ID NO: 121)	GOA	FAM- BHQ1	hlgH D segments
hlgH DH-2	GTGAGGGGAGGACCTTCTG (SEQ ID NO: 122)	AGTCACCAAGCACAGAGCCCTGA C (SEQ ID NO: 123)	GCCAGGAGTTGCCTAG TG (SEQ ID NO: 124)	GOA	FAM- BHQ1	hlgH D segments
hlgH DH-3	GTGGCCCACTTCCTTCCT (SEQ ID NO: 125)	CAGCTGGAACCCACCATGACCT (SEQ ID NO: 126)	GACCTGCCTCGGATGACA (SEQ ID NO: 127)	GOA	FAM- BHQ1	hlgH D segments
hlgH DH-4	TGGCCAGAACTGACCCTAC (SEQ ID NO: 128)	ACCGACAAGAGTCCCTCAGG (SEQ ID NO: 129)	GGAGTCGGCTCTGGATGTG (SEQ ID NO: 130)	GOA	BHQ- plus	hlgH D segments
neo	GGTGGAGAGGCTATTCCGGC (SEQ ID NO: 152)	TGGGCACAACAGACAATCGGCTG (SEQ ID NO: 153)	GAACACGGCGGCATCAG (SEQ ID NO: 154)	GOA	FAM- BHQ1	
hlgH1	CAGTCCGTTGATCCAGCC (SEQ ID NO: 134)	CCCATCAGGGATTGTATCTC TGTTGAGC (SEQ ID NO: 135)	GGATATGCAGCACTGTGCC AC (SEQ ID NO: 136)	AR		hlgH
hlgH9	TCCTCCAAACGACAGGTCCC (SEQ ID NO: 137)	TCCCTGGAACTCTGCCCGACACA (SEQ ID NO: 138)	GATGAACATGACGGGCACA GG (SEQ ID NO: 139)	AR		hlgH
hlgH31	ATCACACTCATCCCATCCCC (SEQ ID NO: 140)	CCCTCCCTAAGTACCACAGAGTG GGCTC (SEQ ID NO: 141)	CACAGGGAAGCAGGAAC GC (SEQ ID NO: 142)	AR		hlgH

FIG. 8

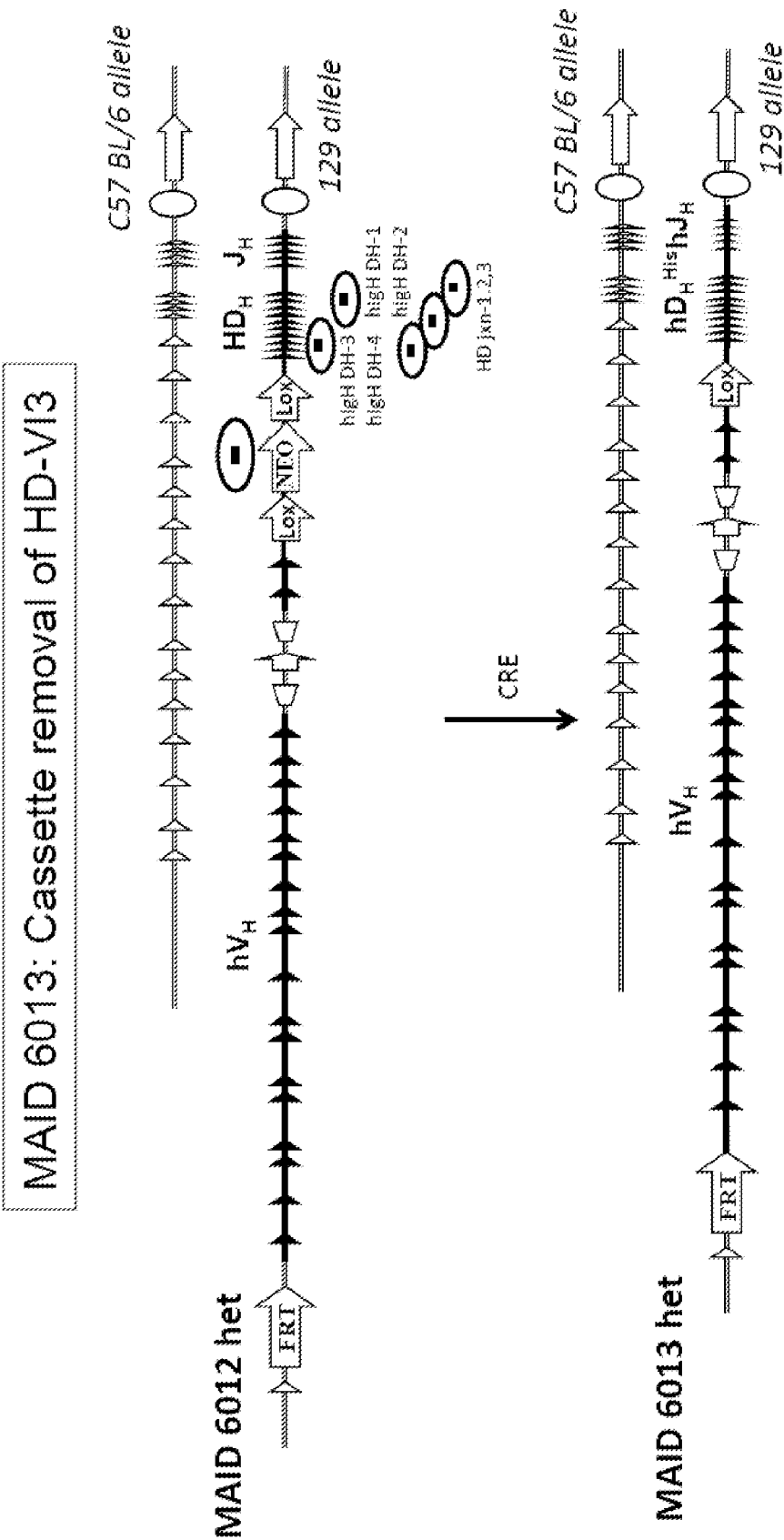


FIG. 9

11/19

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

FIG. 10A

12/19

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	ggtagcagctggtagtactacaatactct 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
M35648, IGHD2-2*03	tggatattgtagtagtaccagctgctatgcc 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	ggtagcagctggtagtactacaataatcca 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	aggatattgtactaaiggtgtagtctatacc 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	ggtagcagctggtagtactacaatactct 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
J000233, IGHD2-8*02	aagatattgtactgggtgtagtctatacc 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	ggtagcagctggtagtactacaataatctt 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- 15*01	aggatattgtagtgggtgtagtctatcc 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	ggtagcagctgaccaccactacaatactct G V A A T T T T I S E * Q L P P L Q Y P S S Y H H Y N I	237 238 239 240
J00235, IGHD2- 21*01	agcatattgtgggtgtagtctatcc 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	ggaatagcaatcaccaccacaataatgct 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	agcatattgtgggtgtagtctatcc 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	ggaatagcagtcaccaccacaataatgct 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

13/19

Human D Gene Segment	Direct 5'-3' Orientation	SEQ ID NO.	Inverted Orientation	SEQ ID NO.
IGHD3-3	X13972, IGHD3-3*01 gtattacgattttggagtggtattatacc V L R F L E W L L Y Y Y D F W S G Y Y T I T I F G V V I I	179	ggtaataaaccaccccaaaatcgtaatac G I I T T P K I V I V * * P L Q K S * Y Y N N H S K N R N	249
		21		250
		59		251
		98		252
IGHD3-9	X13972, IGHD3-9*01 gtattacgattttggagtggtattatacc V L R Y F D W L L * Y Y D I L T G Y Y N I T I F * L V I I	180	ggtaataaaccaccccaaaatcgtaatac G I I T T P K M L I V * * P L Q K C * Y Y N N H S K N A N	253
		181		254
		182		255
		183		256
IGHD3-10	X13972, IGHD3-10*01 gtattacgattttggagtggtattatacc V L R Y F D W L L * Y Y D I L T G Y Y N I T I F * L V I I	184	gtataataaaccagtcacaaatcgtaatac V I I T S Q N I V I L * * P V K I S * Y Y N N Q S K Y R N	257
		23		258
		61		259
		99, 100		260
IGHD3-16	X13972, IGHD3-16*01 gtattacgattttggagtggtattatacc V L L W F G E L L * Y Y Y G S G S Y Y N I T M V R G V I I	185	gtataataaaccaccccaaaatcgtaatac V I I T P R T I V I L * * L P E P * * Y Y N N S P N H S N	261
		25		262
		63		263
		101		264
IGHD3-22	X93615, IGHD3-22*01 gtattacgattttggagtggtattatacc V L L C S G S Y Y N Y Y Y V R G V I I I T M F G R L L *	186	gtataataaaccaccccaaaatcgtaatac V I I T P R T * * Y L * * L P E H S N Y N N S P N I V I	265
		187		266
		188		267
		189		268
IGHD3-15	X93614, IGHD3-15*01 gtattacgattttggagtggtattatacc V L * L R L G E L C L Y Y Y D Y V W G S Y A Y T I M I T F G G V M L I	190	ggtaataaaccaccccaaaatcgtaatac G I S I T P P N V I I V * A * L P Q T * S * Y Y K H N S P K R N H N	269
		191		270
		192		271
		193		272
IGHD3-22	X93616, IGHD3-22*01 gtattacgattttggagtggtattatacc V L L * * * W L L L Y Y Y D S S G Y Y Y I T M I V V V I T	194	gtagtaataaaccaccccaaaatcgtaatac V V I T T T I I V I * * * P L L S * * Y S N N H Y Y H S N	273
		29		274
		67		275
		103		276

FIG. 10C

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

FIG. 10D

15/19

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

FIG. 10E

Antibody Sequence 1

[illegible]

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

FIG. 11

Antibody Sequence 2

[illegible]

FIG. 12

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

Antibody Sequence 3

[illegible]

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

FIG. 13

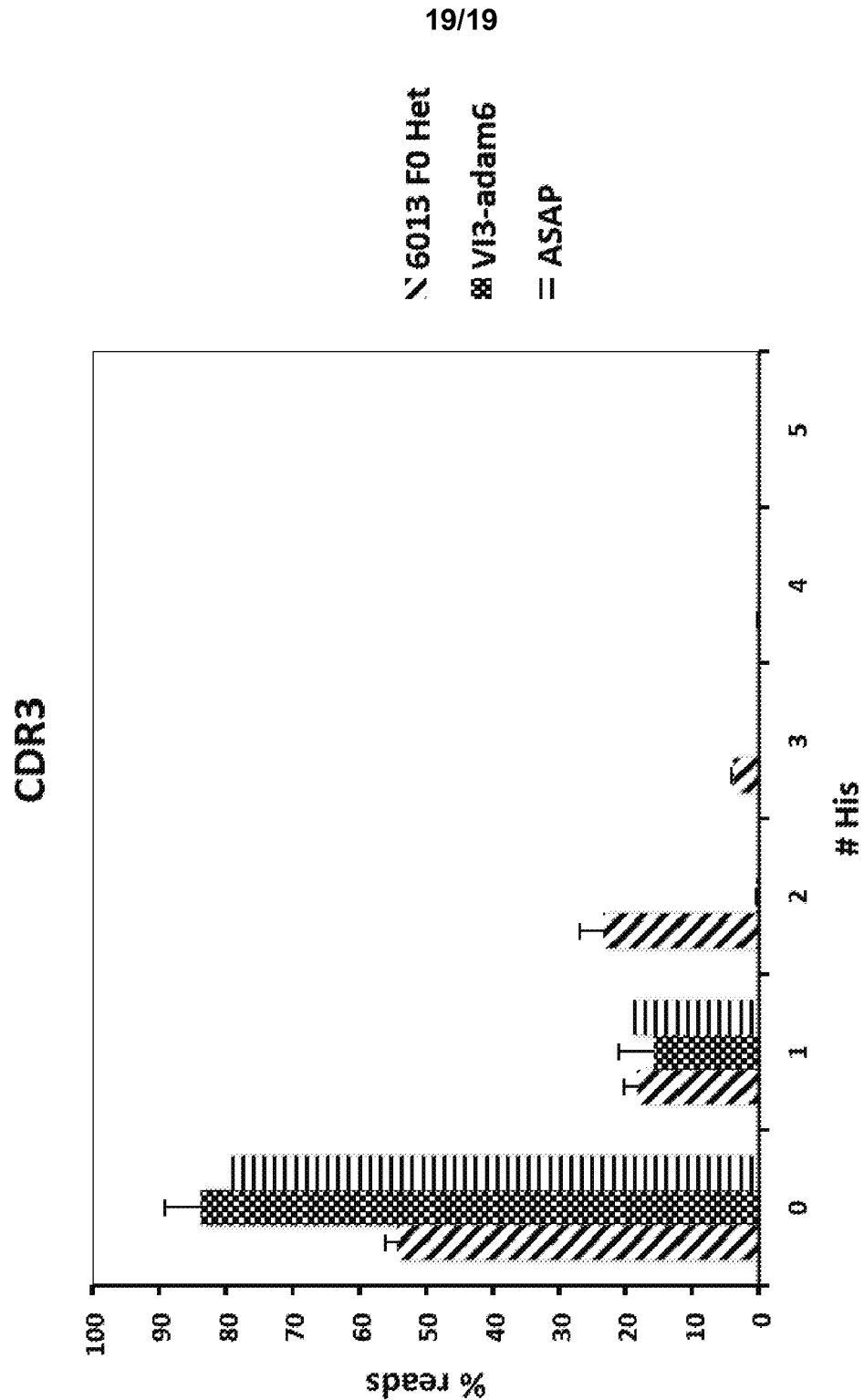


FIG. 14