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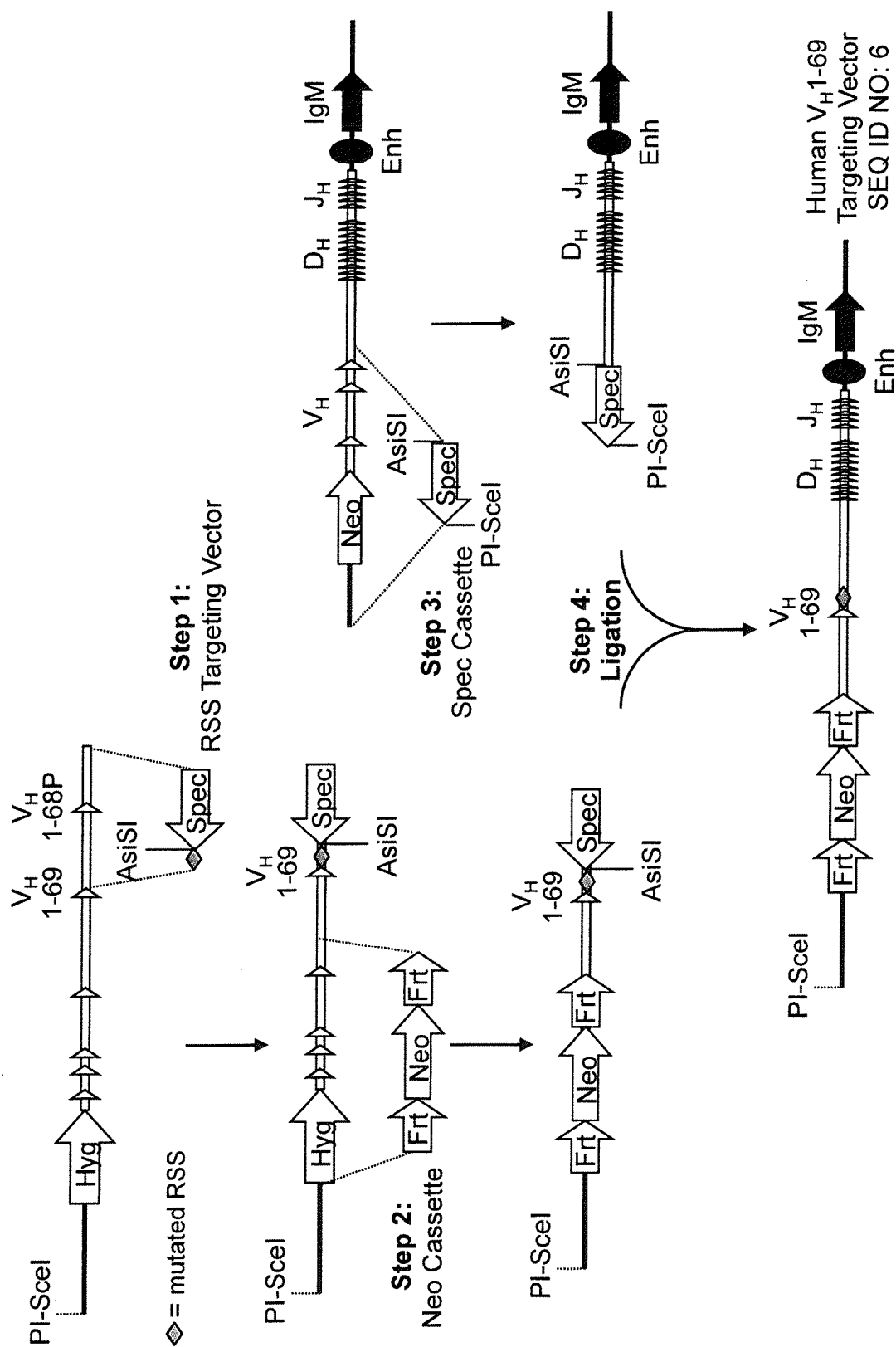


FIG. 1

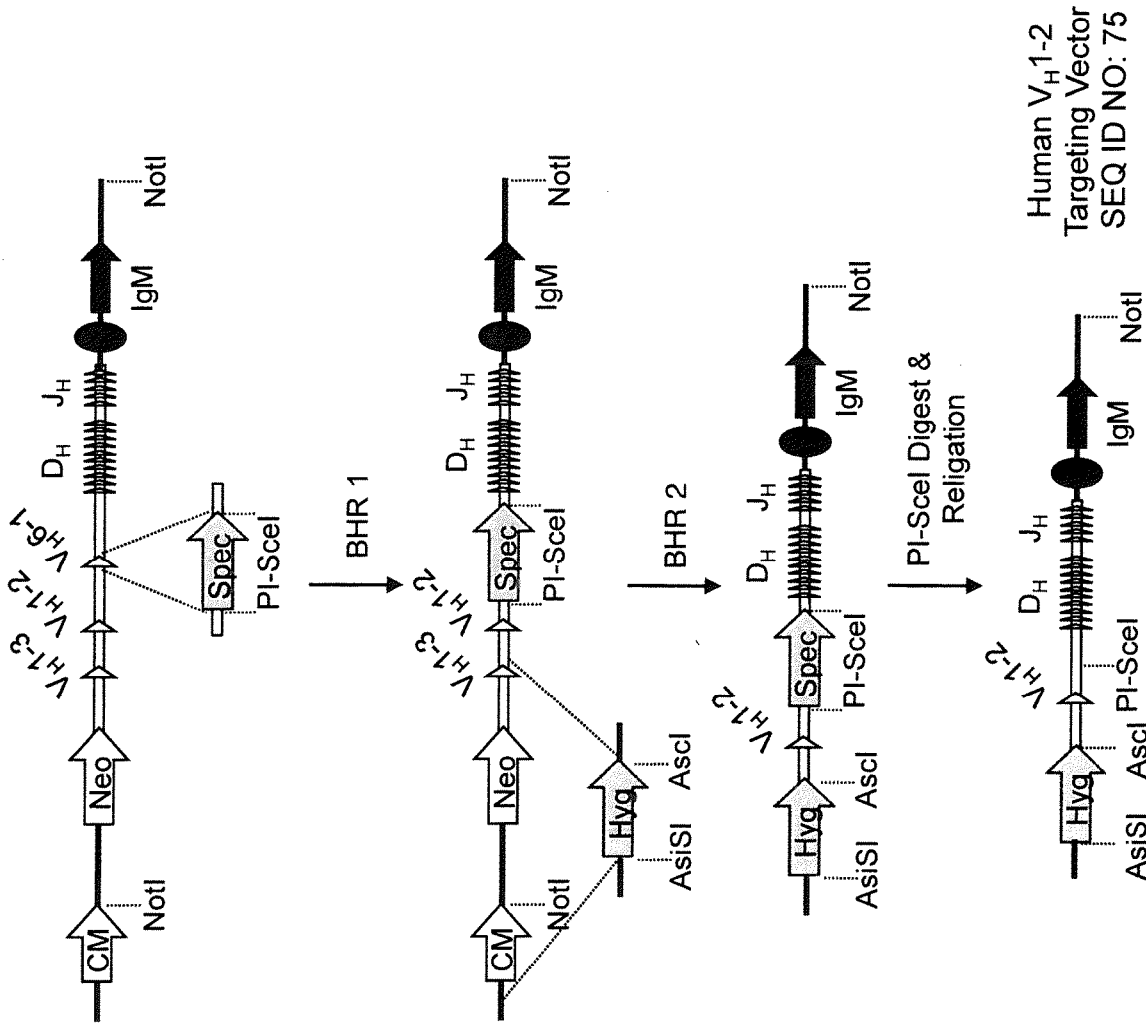


FIG. 2

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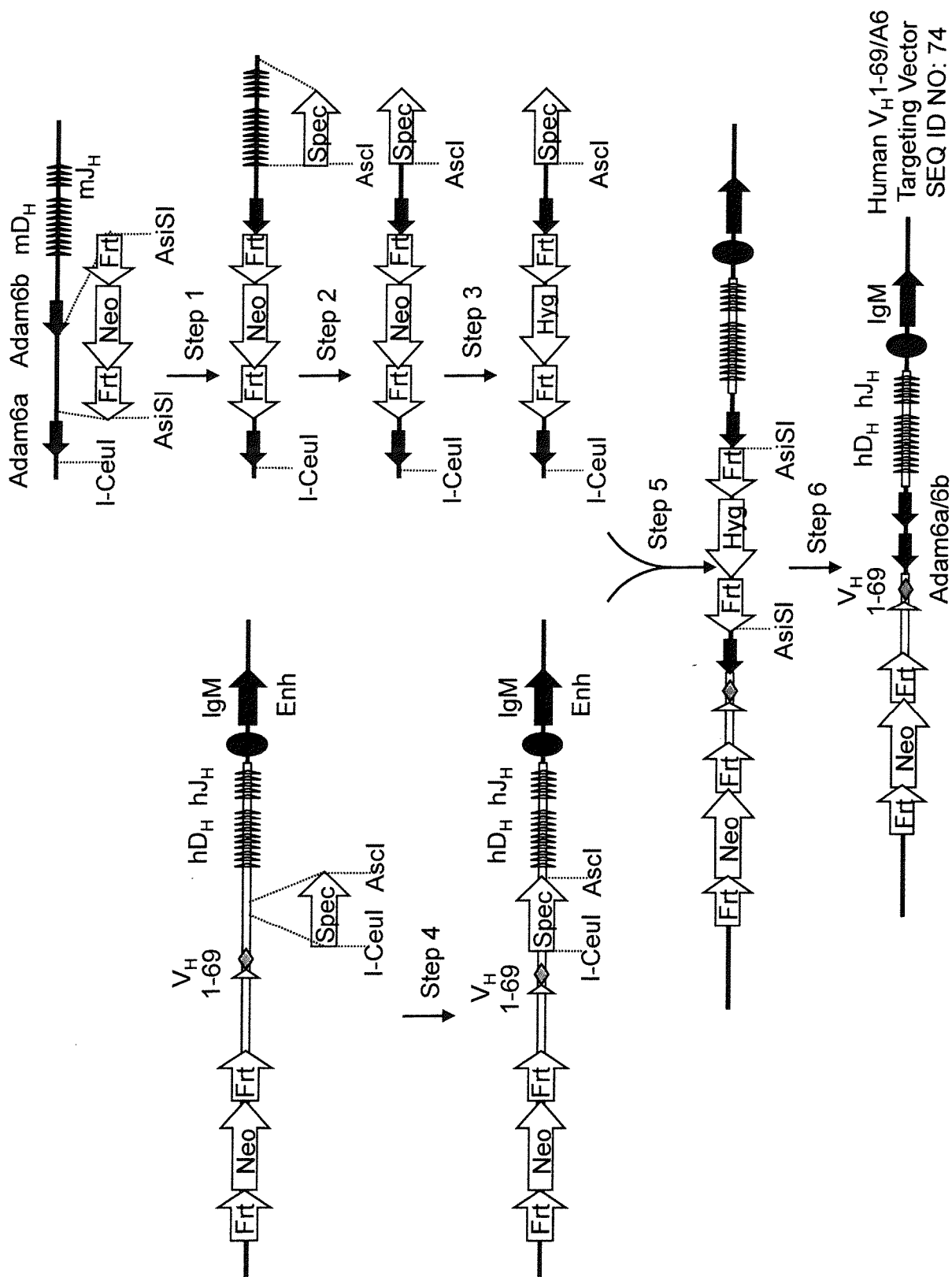


FIG. 3

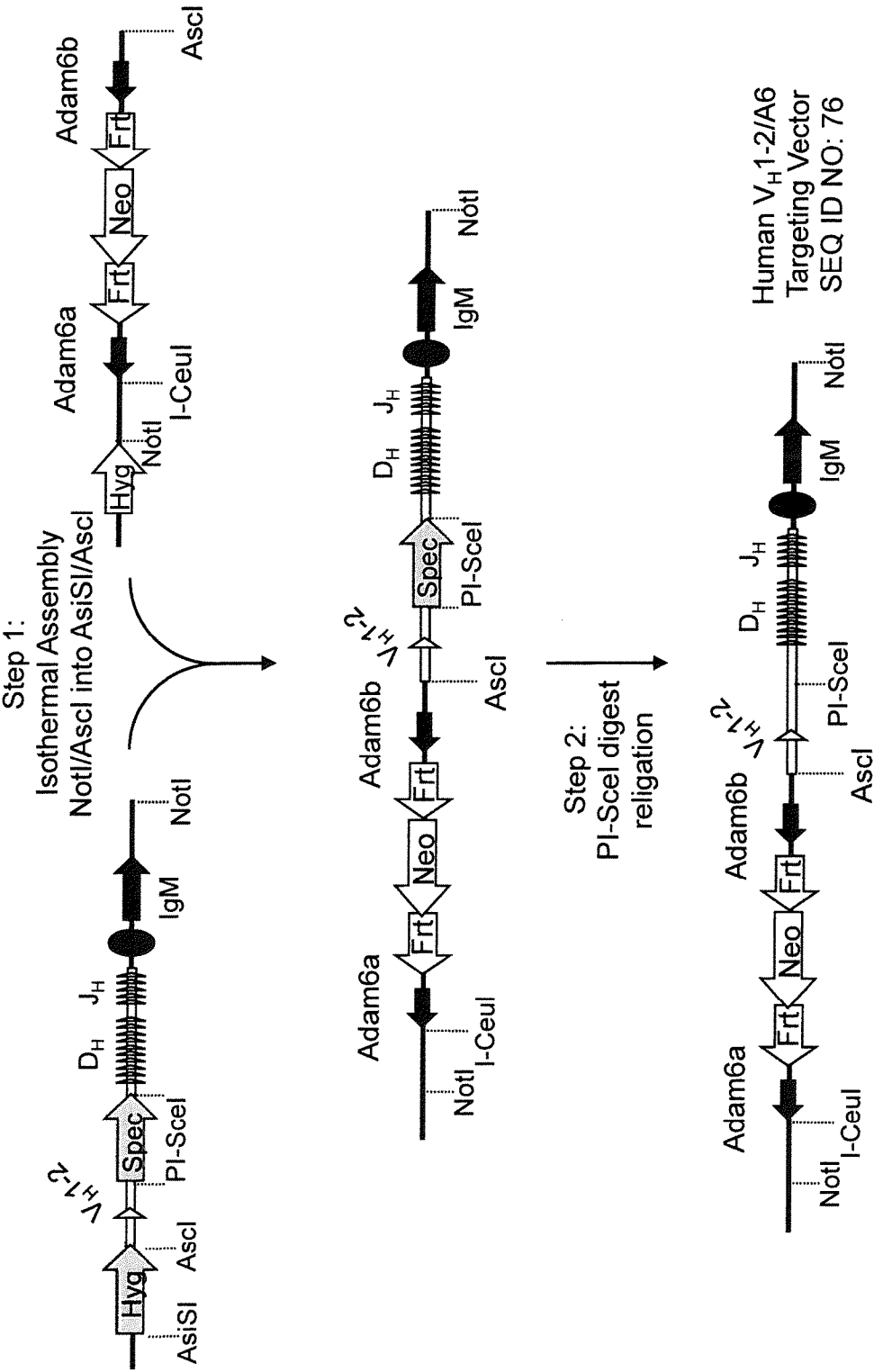


FIG. 4

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	10	20	30	40	50	60	70
VH1-69*01	CAGGTg	CAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT					
VH1-69*02	CAGGTCCAGCTGGTGC	AaTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT					
VH1-69*03	CAGGTg	CAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT					
VH1-69*04	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*05	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*06	CAGGTg	CAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT					
VH1-69*07	-----	-----	-----	-----	-----	-----	-----
VH1-69*08	CAGGTCCAGCTGGTGC	AaTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT					
VH1-69*09	CAGGTg	CAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT					
VH1-69*10	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCaGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*11	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*12	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCaGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*13	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCaGTGAAGGTCTCCTGCAAGGCTTCT						
	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						

	80	90	100	110	120	130	140	150
VH1-69*01	GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG							
VH1-69*02	GGAGGCACCTTCAGCAGCTATaCTATCAGCTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAaGG							
VH1-69*03	GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG							
VH1-69*04	GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAaGG							
VH1-69*05	GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG							
VH1-69*06	GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG							
VH1-69*07	GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAaGG							
VH1-69*08	GGAGGCACCTTCAGCAGCTATaCTATCAGCTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAaGG							
VH1-69*09	GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAaGG							
VH1-69*10	GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG							
VH1-69*11	GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAaGG							
VH1-69*12	GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG							
VH1-69*13	GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG							

	160	170	180	190	200	210	220
VH1-69*01	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*02	ATCATCCCTATCCTTTGGTAtAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*03	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*04	ATCATCCCTATCCTTTGGTAtAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*05	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCaCGGACGAATCC						
VH1-69*06	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*07	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*08	ATCATCCCTATCCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*09	ATCATCCCTATCCTTTGGTAtAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*10	ATCATCCCTATCCTTTGGTAtAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*11	ATCATCCCTATCCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*12	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*13	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						

	230	240	250	260	270	280	290
VH1-69*01	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*02	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*03	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*04	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*05	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*06	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*07	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*08	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*09	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*10	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*11	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*12	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*13	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						

FIG. 5

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VH1-69*01	QVQLVQSGAEVKKPGSSSVKVSCKASG	30	40	50	60
VH1-69*02	QVQLVQSGAEVKKPGSSSVKVSCKASG	30	40	50	60
VH1-69*03	QVQLVQSGAEVKKPGSSSVKVSCKASG	30	40	50	60
VH1-69*04	QVQLVQSGAEVKKPGSSSVKVSCKASG	30	40	50	60
VH1-69*05	QVQLVQSGAEVKKPGSSSVKVSCKASG	30	40	50	60
VH1-69*06	QVQLVQSGAEVKKPGSSSVKVSCKASG	30	40	50	60
VH1-69*07	-----KPGSSSVKVSCKASG	30	40	50	60
VH1-69*08	QVQLVQSGAEVKKPGSSSVKVSCKASG	30	40	50	60
VH1-69*09	QVQLVQSGAEVKKPGSSSVKVSCKASG	30	40	50	60
VH1-69*10	QVQLVQSGAEVKKPGSSSVKVSCKASG	30	40	50	60
VH1-69*11	QVQLVQSGAEVKKPGSSSVKVSCKASG	30	40	50	60
VH1-69*12	QVQLVQSGAEVKKPGSSSVKVSCKASG	30	40	50	60
VH1-69*13	QVQLVQSGAEVKKPGSSSVKVSCKASG	30	40	50	60

VH1-69*01	AQKFQGRVTITADESTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*02	AQKFQGRVTITADkSTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*03	AQKFQGRVTITADESTSTAYMELSSLRSDDT	70	80	90	100
VH1-69*04	AQKFQGRVTITADkSTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*05	AQKFQGRVTITtDESTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*06	AQKFQGRVTITADkSTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*07	AQKFQGRVTITADESTSTAYMELSSLRSE	70	80	90	100
VH1-69*08	AQKFQGRVTITADkSTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*09	AQKFQGRVTITADkSTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*10	AQKFQGRVTITADkSTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*11	AQKFQGRVTITADESTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*12	AQKFQGRVTITADESTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*13	AQKFQGRVTITADESTSTAYMELSSLRSEDTAVY	70	80	90	100

FIG. 6

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% IDENTITY													
V _H 1-69 Allele	V _H 1-69*01	V _H 1-69*02	V _H 1-69*03	V _H 1-69*04	V _H 1-69*05	V _H 1-69*06	V _H 1-69*07	V _H 1-69*08	V _H 1-69*09	V _H 1-69*10	V _H 1-69*11	V _H 1-69*12	V _H 1-69*13
V _H 1-69*01	100	94.9	91.8	95.9	99	99	77.6	95.9	95.9	96.9	98	100	100
V _H 1-69*02	95.9	100	86.7	99	93.9	95.9	74.5	99	99	98	96.9	94.9	94.9
V _H 1-69*03	92.9	88.8	100	87.8	90.8	90.8	82.4	87.8	87.8	88.8	89.8	91.8	91.8
V _H 1-69*04	95.9	100	88.8	100	94.9	96.9	75.5	98	100	99	98	95.9	95.9
V _H 1-69*05	100	95.9	92.9	95.9	100	98	76.5	94.9	94.9	95.9	96.9	99	99
V _H 1-69*06	99.0	96.9	91.8	96.9	99	100	76.5	96.9	96.9	98	96.9	99	99
V _H 1-69*07	77.6	75.5	83.5	75.5	77.6	76.5	100	75.5	75.5	74.5	77.6	77.6	77.6
V _H 1-69*08	96.9	99	89.8	99	96.9	98	76.5	100	98	96.9	98	95.9	95.9
V _H 1-69*09	95.9	100	88.8	100	95.9	96.9	75.5	99	100	99	98	95.9	95.9
V _H 1-69*10	96.9	99	89.8	99	96.9	98	74.5	98	99	100	96.9	96.9	96.9
V _H 1-69*11	98	98	90.8	98	98	96.9	77.6	99	98	96.9	100	98	98
V _H 1-69*12	100	95.9	92.9	95.9	100	99	77.6	96.9	95.9	96.9	98	100	100
V _H 1-69*13	100	95.9	92.9	95.9	100	99.0	77.6	96.9	95.9	96.9	98	100	100
% SIMILARITY													

FIG. 7

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VH1-2*01 VH1-2*02 VH1-2*03 VH1-2*04 VH1-2*05	10					20					30					40					50																														
	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S	V	K	V	S	C	K	A	S	G	Y	T	F	T	G	Y	Y	M	H	W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	I	r
	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S	V	K	V	S	C	K	A	S	G	Y	T	F	T	G	Y	Y	M	H	W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	W	
	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S	V	K	V	S	C	K	A	S	G	Y	T	F	T	G	Y	Y	M	H	W	V	x	Q	A	P	G	Q	G	L	E	W	M	G	W	
	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S	V	K	V	S	C	K	A	S	G	Y	T	F	T	G	Y	Y	M	H	W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	W	
VH1-2*01 VH1-2*02 VH1-2*03 VH1-2*04 VH1-2*05	60					70					80					90																																			
	I	N	P	N	S	G	G	T	N	Y	A	Q	K	F	Q	G	R	V	T	s	T	R	D	T	S	I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	V	V	Y	C	A	R				
	I	N	P	N	S	G	G	T	N	Y	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	A	V	Y	C	A	R				
	I	N	P	N	S	G	G	T	N	Y	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	A	V	Y	C	A	R				
	I	N	P	N	S	G	G	T	N	Y	A	Q	K	F	Q	G	w	V	T	M	T	R	D	T	S	I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	A	V	Y	C	A	R				
VH1-2*01 VH1-2*02 VH1-2*03 VH1-2*04 VH1-2*05	60					70					80					90																																			
	I	N	P	N	S	G	G	T	N	Y	A	Q	K	F	Q	G	R	V	T	s	T	R	D	T	S	I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	V	V	Y	C	A	R				
	I	N	P	N	S	G	G	T	N	Y	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	A	V	Y	C	A	R				
	I	N	P	N	S	G	G	T	N	Y	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	A	V	Y	C	A	R				
	I	N	P	N	S	G	G	T	N	Y	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	V	V	Y	C	A	R				
VH1-2*01 VH1-2*02 VH1-2*03 VH1-2*04 VH1-2*05	60					70					80					90																																			
	I	N	P	N	S	G	G	T	N	Y	A	Q	K	F	Q	G	R	V	T	s	T	R	D	T	S	I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	V	V	Y	C	A	R				
	I	N	P	N	S	G	G	T	N	Y	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	A	V	Y	C	A	R				
	I	N	P	N	S	G	G	T	N	Y	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	A	V	Y	C	A	R				
	I	N	P	N	S	G	G	T	N	Y	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	Y	M	E	L	S	R	L	R	S	D	D	T	V	V	Y	C	A	R				

FIG. 9

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% IDENTITY						
V _H 1-2 Allele	V _H 1-2*01	V _H 1-2*02	V _H 1-2*03	V _H 1-2*04	V _H 1-2*05	
V _H 1-2*01	100	96.9	94.9	95.9	99.0	
V _H 1-2*02	96.9	100	98.0	99.0	98.0	
V _H 1-2*03	94.9	98.0	100	96.9	95.9	
V _H 1-2*04	95.9	99.0	96.9	100	96.9	
V _H 1-2*05	99.0	98.0	95.9	96.9	100	
% SIMILARITY						

FIG. 10