

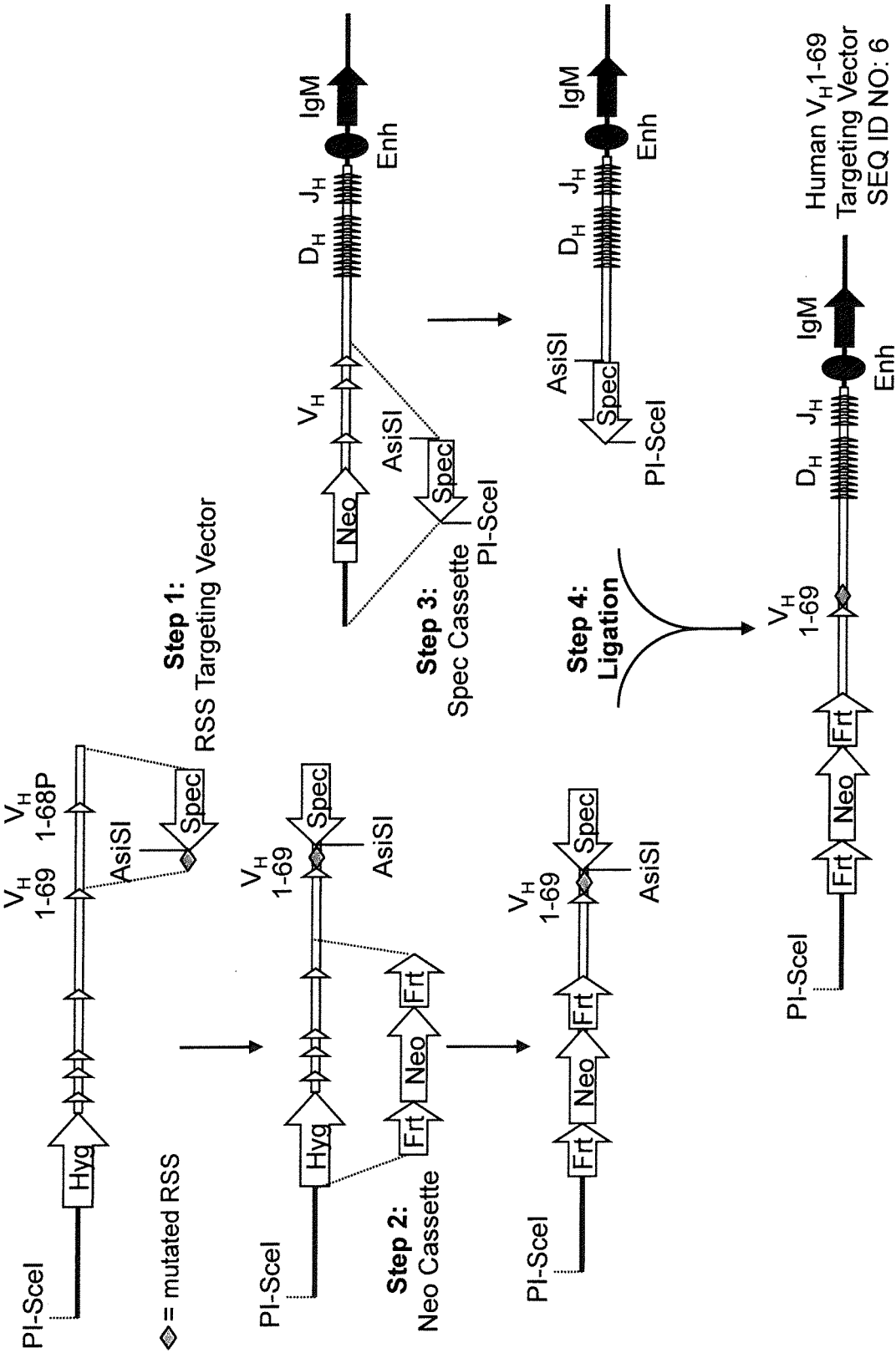


FIG. 1

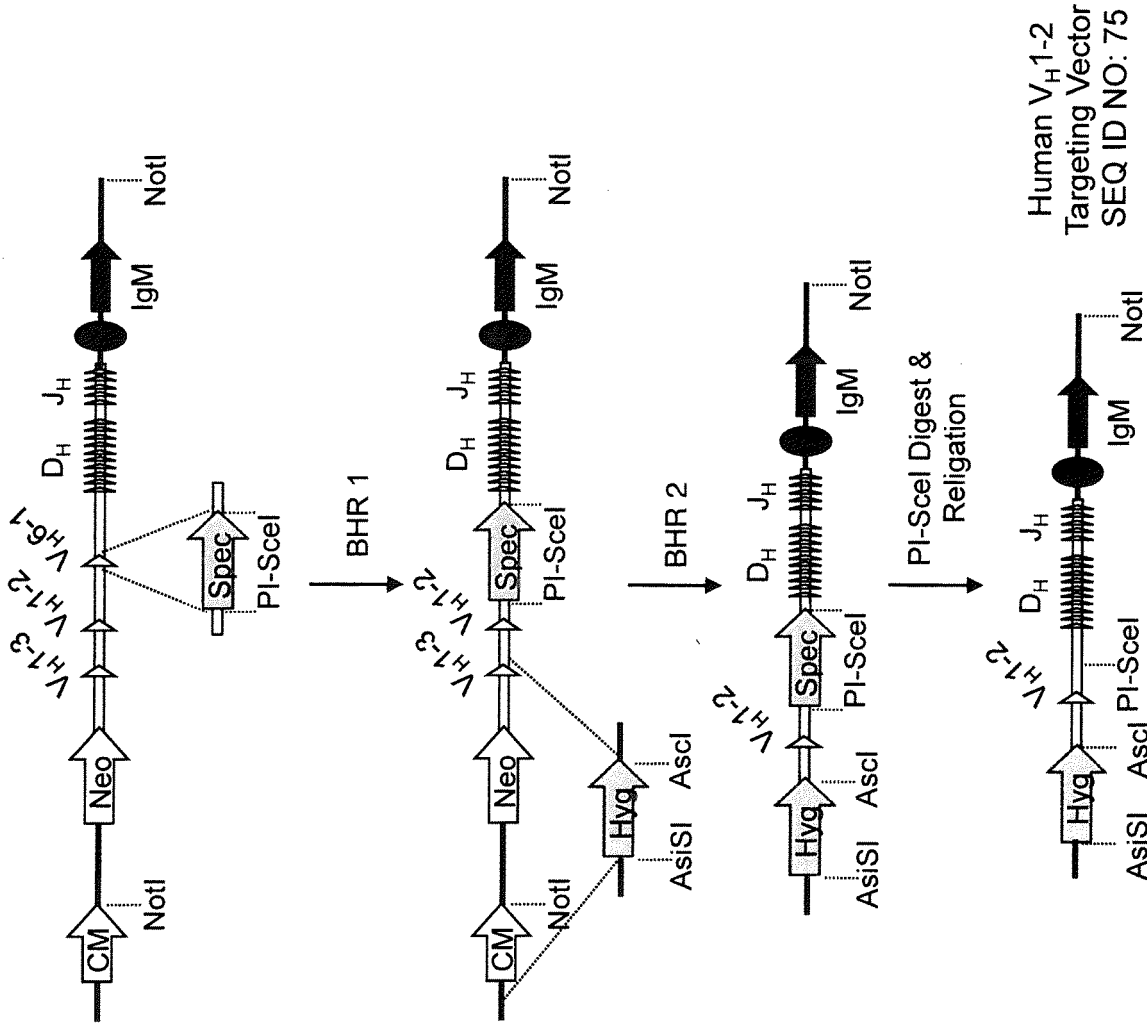


FIG. 2

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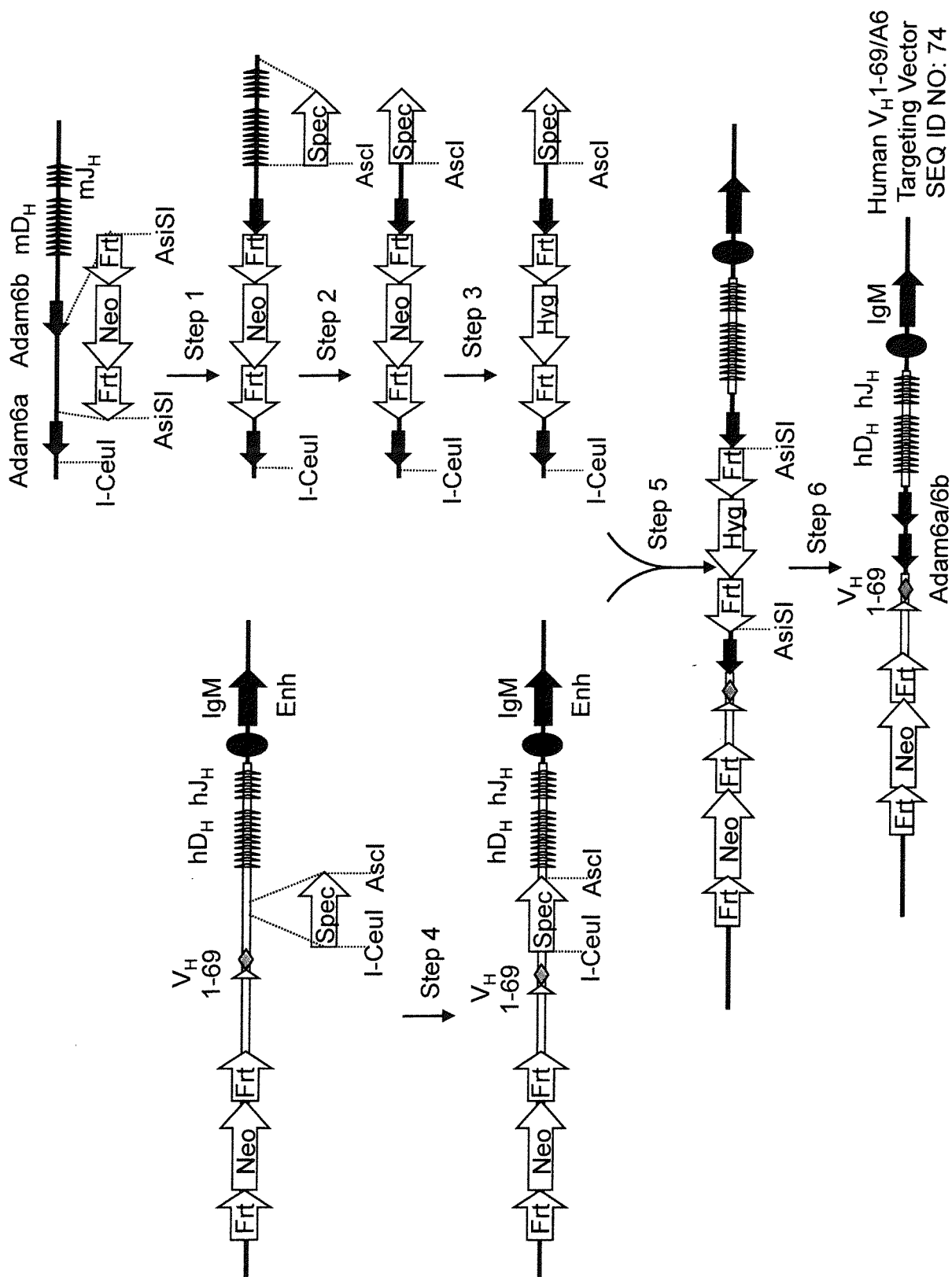


FIG. 3

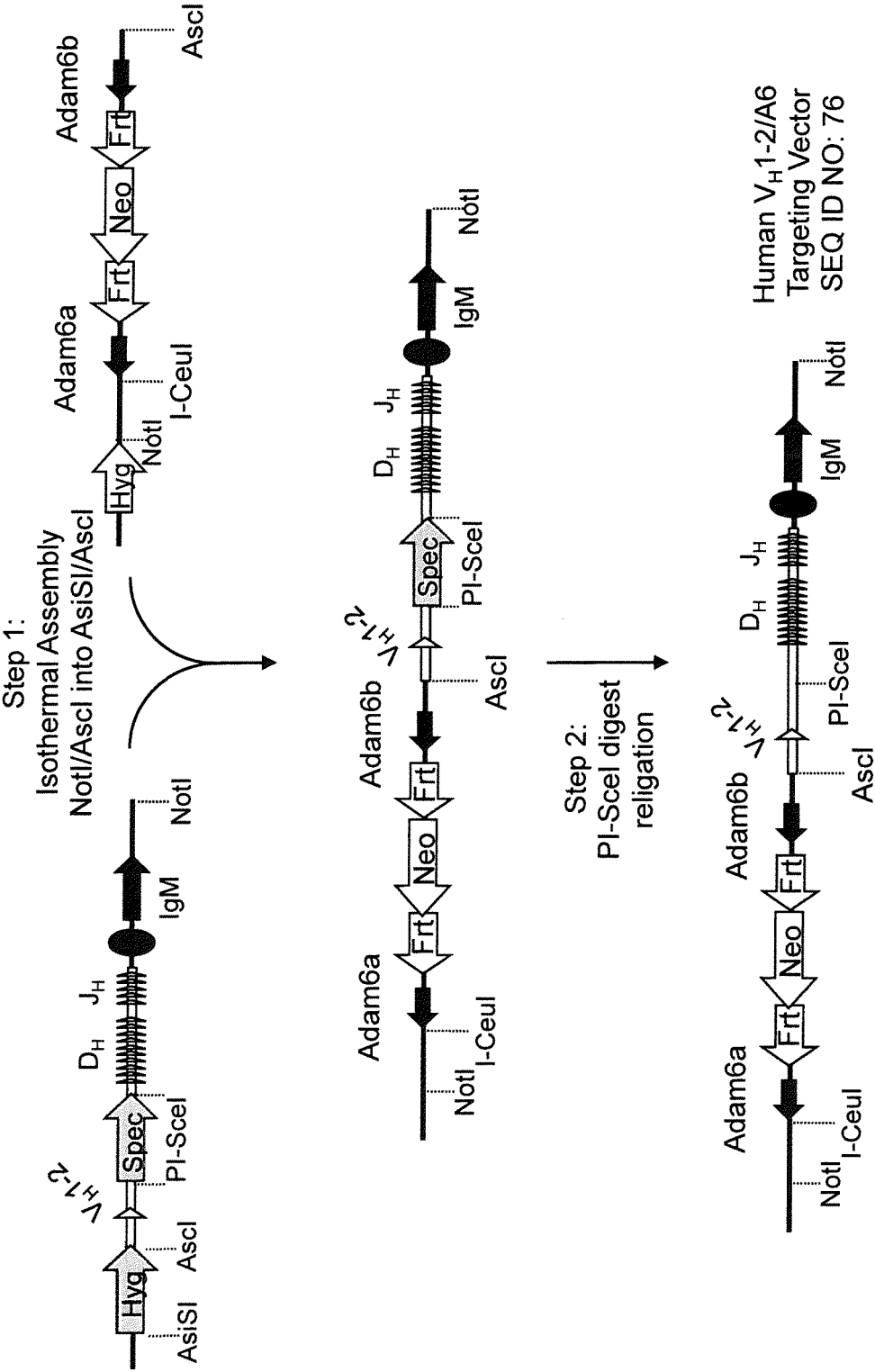


FIG. 4

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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	-----	-----AGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT					
VH1-69*08	CAGGTCCAGCTGGTGC	AaTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT					
VH1-69*09	CAGGTg	CAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT					
VH1-69*10	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCaGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*11	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*12	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*13	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCaGTGAAGGTCTCCTGCAAGGCTTCT						
	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						

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

	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	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAA---						
VH1-69*03	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAtGACACGGC-----						
VH1-69*04	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*05	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAA---						
VH1-69*06	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*07	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAG-----						
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	QVQLVQSGAEVKKPKPGSSSVKVSCKASG	30	40	50	60
VH1-69*02	QVQLVQSGAEVKKPKPGSSSVKVSCKASG	30	40	50	60
VH1-69*03	QVQLVQSGAEVKKPKPGSSSVKVSCKASG	30	40	50	60
VH1-69*04	QVQLVQSGAEVKKPKPGSSSVKVSCKASG	30	40	50	60
VH1-69*05	QVQLVQSGAEVKKPKPGSSSVKVSCKASG	30	40	50	60
VH1-69*06	QVQLVQSGAEVKKPKPGSSSVKVSCKASG	30	40	50	60
VH1-69*07	-----KPGSSSVKVSCKASG	30	40	50	60
VH1-69*08	QVQLVQSGAEVKKPKPGSSSVKVSCKASG	30	40	50	60
VH1-69*09	QVQLVQSGAEVKKPKPGSSSVKVSCKASG	30	40	50	60
VH1-69*10	QVQLVQSGAEVKKPKPGSSSVKVSCKASG	30	40	50	60
VH1-69*11	QVQLVQSGAEVKKPKPGSSSVKVSCKASG	30	40	50	60
VH1-69*12	QVQLVQSGAEVKKPKPGSSSVKVSCKASG	30	40	50	60
VH1-69*13	QVQLVQSGAEVKKPKPGSSSVKVSCKASG	30	40	50	60
	QVQLVQSGAEVKKPKPGSSSVKVSCKASG	30	40	50	60
VH1-69*01	AQKFQGRVTITADESTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*02	AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*03	AQKFQGRVTITADESTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*04	AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*05	AQKFQGRVTITADESTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*06	AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVY	70	80	90	100
VH1-69*07	AQKFQGRVTITADESTSTAYMELSSLRSEDTAVY	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
	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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10      20      30      40      50      60      70
VH1-2*01 GAGCCCACTCCAGGTG-CAGCTGGTGCAG-TCTG--GGGCTGAGGTGAAGAA--GCGCTGGGGCCCTCAGTGAA
VH1-2*02 GAGCCCACTCCAGGTG-CAGCTGGTGCAG-TCTG--GGGCTGAGGTGAAGAA--GCGCTGGGGCCCTCAGTGAA
VH1-2*03 GAGCCCACTCCAGGTG-CAGCTGGTGCAG-TCTG--GGGCTGAGGTGAAGAA--GCGTGGGGCCCTCAGTGAA
VH1-2*04 -----CAGGTG-CAGCTGGTGCAG-TCTG--GGGCTGAGGTGAAGAA--GCGTGGGGCCCTCAGTGAA
VH1-2*05 GAcCgtgtcgtcAGAtcCAGCctGctCAGCTcCaTGTaGGCTGtGCTGaTgCAGTgTcCctGGtCatgGTGAc
GAGCCCACTCCAGGTGTCAGCTGGTGCAGCTCTGTGTGGCTGAGGTGAAGAACGTGCGCTGGGGCCCTCAGTGAA

100      110      120      130      140      150
VH1-2*01 GGTCTCTCTGCAAGGCTTCTGGATAcAcAcCTTcAcCGGCTAcTATATGCACTGG--GTGCGA-----CAGGCCCC
VH1-2*02 GGTCTCTCTGCAAGGCTTCTGGATAcAcAcCTTcAcCGGCTAcTATATGCACTGG--GTGCGA-----CAGGCCCC
VH1-2*03 GGTCTCTCTGCAAGGCTTCTGGATAcAcAcCTTcAcCGGCTAcTATATGCACTGG--GTGCGA-----CAGGCCCC
VH1-2*04 GGTCTCTCTGCAAGGCTTCTGGATAcAcAcCTTcAcCGGCTAcTATATGCACTGG--GTGCGA-----CAGGCCCC
VH1-2*05 cCTgcCCTG--AaaCTTCTGtgCAtaGtTtGtgCcCaCcaCTGTtaGggtTgaTcCGTccCaTCCAcTCAaGccCt
GGTCTCTCTGCAAGGCTTCTGGATAcAcAcCTTcAcCGGCTAcTATATGCACTGGTCCGTGCGATCCAcTCAAGGCCCC

160      170      180      190      200      210      220
VH1-2*01 TGGACAAGGGCTTGAGTGGATGGGAcGGATCAACCCTAAcAGTGGTGGCAcAAAcTATGcCAcAGAAgTtT--CAG
VH1-2*02 TGGACAAGGGCTTGAGTGGATGGGAcGGATCAACCCTAAcAGTGGTGGCAcAAAcTATGcCAcAGAAgTtT--CAG
VH1-2*03 TGGACAAGGGCTTGAGTGGATGGGAcGGATCAACCCTAAcAGTGGTGGCAcAAAcTATGcCAcAGAAgTtT--CAG
VH1-2*04 TGGACAAGGGCTTGAGTGGATGGGAcGGATCAACCCTAAcAGTGGTGGCAcAAAcTATGcCAcAGAAgTtT--CAG
VH1-2*05 TgtcCAgGGCCtG-----TcGCAc--cCAgtgCataAtAGTAgccGgtgAAAggtgtatccAGAAgCctTGcAG
TGGACAAGGGCTTGAGTGGATGGGAcGGATCAACCCTAAcAGTGGTGGCAcAAAcTATGcCAcAGAAgTtTtTGcAG

230      240      250      260      270      280      290      300
VH1-2*01 GGCAGGGTCAcCAgtACcAGGGAcACGTCCA--TCAGCAc-AGCCCTAcATGGAGCTGAGcAGGCTGAGATCTGAc
VH1-2*02 GGCAGGGTCAcCAgtACcAGGGAcACGTCCA--TCAGCAc-AGCCCTAcATGGAGCTGAGcAGGCTGAGATCTGAc
VH1-2*03 GGCAGGGTCAcCAgtACcAGGGAcACGTCCA--TCAGCAc-AGCCCTAcATGGAGCTGAGcAGGCTGAGATCTGAc
VH1-2*04 GGCtGGGTCAcCAgtACcAGGGAcACGTCCA--TCAGCAc-AGCCCTAcATGGAGCTGAGcAGGCTGAGATCTGAc
VH1-2*05 GaGacctCAcTgaGgCccagGcttctcTcCAcCTcAGcCCcAGAcTgCAcc-AGCTGcAc--CTGgGA--Gt9
GGCAGGGTCAcCAgtACcAGGGAcACGTCCAcCTcAGcCCcAGcCTAcATGGAGCTGAGcAGGCTGAGATCTGAc

310      320      330
VH1-2*01 GAcACGgtCGTGTATTAcTTGTGCGAGAGAA--
VH1-2*02 GAcACGgtCGTGTATTAcTTGTGCGAGAGAA
VH1-2*03 GAcACGgtCGTGTATTAcTTGTGCGAGAGAA
VH1-2*04 GAcACGgtCGTGTATTAcTTGTGCGAGAGAA
VH1-2*05 GAcAc--cTGTGgAg-AcCT-cGCGA-----
GAcACGgtCGTGTATTAcTTGTGCGAGAGAA

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FIG. 8

VH1-2*01 VH1-2*02 VH1-2*03 VH1-2*04 VH1-2*05	10	20	30	40	50
	QVQLVQSGAEVKKPGASVKVSCKASSGYTFTGYVMHWVRQAPGQGLEWMG r				
	QVQLVQSGAEVKKPGASVKVSCKASSGYTFTGYVMHWVRQAPGQGLEWMG W				
	QVQLVQSGAEVKK1GASVKVSCKASSGYTFTGYVMHWV xQA PGQGLEWMG W				
	QVQLVQSGAEVKKPGASVKVSCKASSGYTFTGYVMHWVRQAPGQGLEWMG W				
VH1-2*01 VH1-2*02 VH1-2*03 VH1-2*04 VH1-2*05	60	70	80	90	
	INPN SGGTNYAQKFQGRVTS TRDTSISTAYMEELSR LRSDDT VVY C AR				
	INPN SGGTNYAQKFQGRVTMTTRDTSISTAYMEELSR LRSDDT A VY C AR				
	INPN SGGTNYAQKFQGRVTMTTRDTSISTAYMEELSR LRSDDT A VY C AR				
	INPN SGGTNYAQKFQGWVTMTTRDTSISTAYMEELSR LRSDDT A VY C AR				
VH1-2*01 VH1-2*02 VH1-2*03 VH1-2*04 VH1-2*05	10	20	30	40	50
	QVQLVQSGAEVKKPGASVKVSCKASSGYTFTGYVMHWVRQAPGQGLEWMG r				
	QVQLVQSGAEVKKPGASVKVSCKASSGYTFTGYVMHWVRQAPGQGLEWMG W				
	QVQLVQSGAEVKK1GASVKVSCKASSGYTFTGYVMHWV xQA PGQGLEWMG W				
	QVQLVQSGAEVKKPGASVKVSCKASSGYTFTGYVMHWVRQAPGQGLEWMG W				
VH1-2*01 VH1-2*02 VH1-2*03 VH1-2*04 VH1-2*05	60	70	80	90	
	INPN SGGTNYAQKFQGRVTS TRDTSISTAYMEELSR LRSDDT VVY C AR				
	INPN SGGTNYAQKFQGRVTMTTRDTSISTAYMEELSR LRSDDT A VY C AR				
	INPN SGGTNYAQKFQGRVTMTTRDTSISTAYMEELSR LRSDDT A VY C AR				
	INPN SGGTNYAQKFQGWVTMTTRDTSISTAYMEELSR LRSDDT A VY C AR				

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