

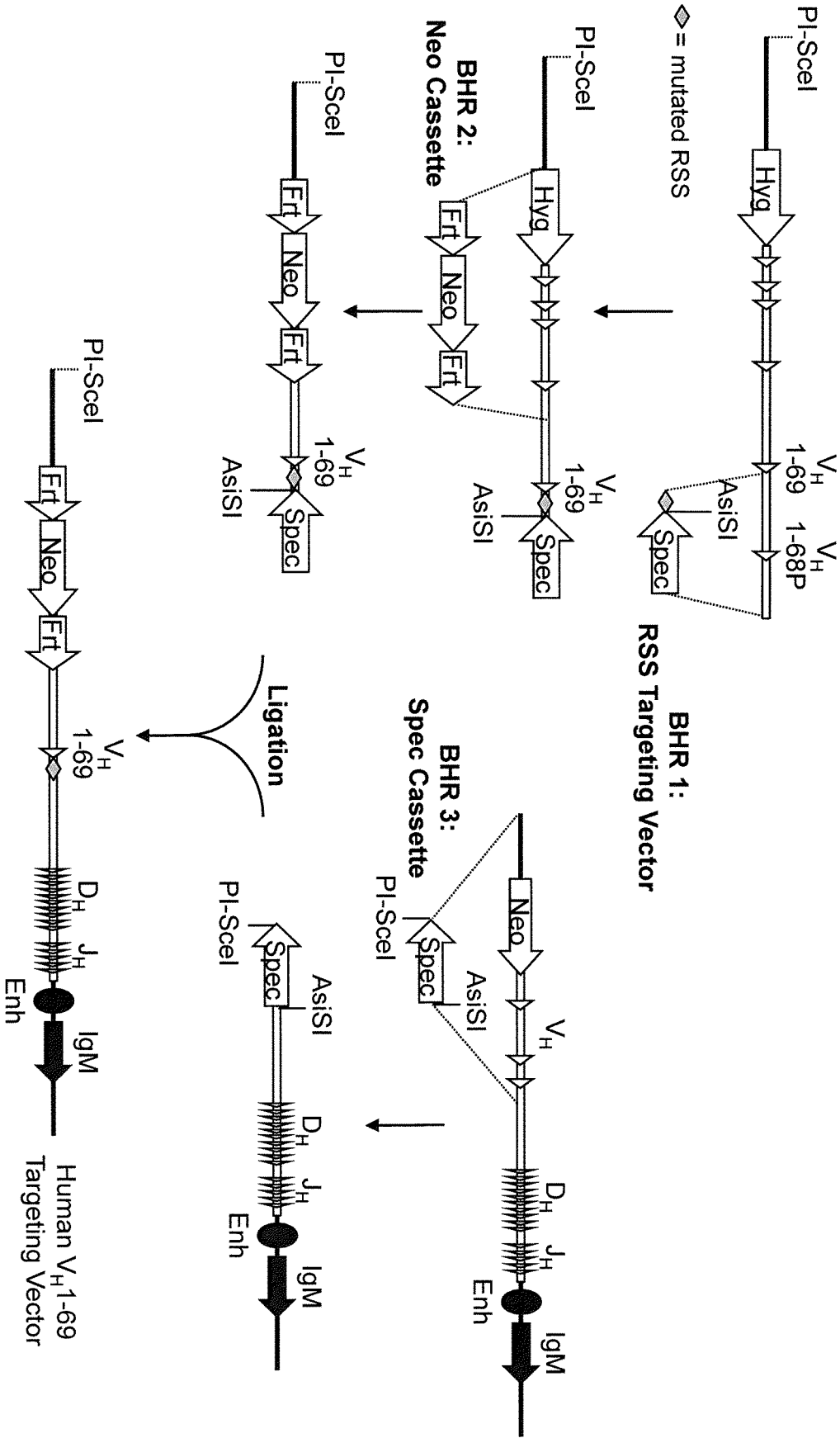


FIG. 1

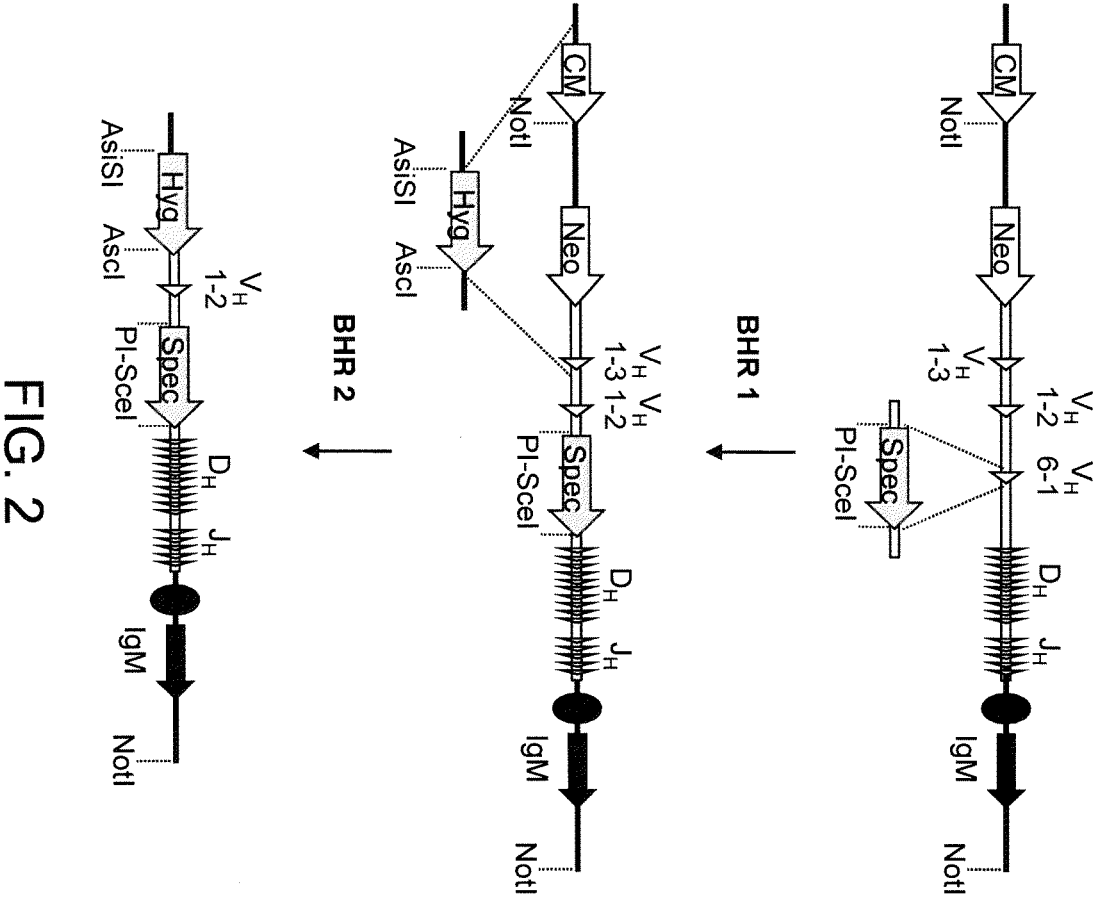


FIG. 2

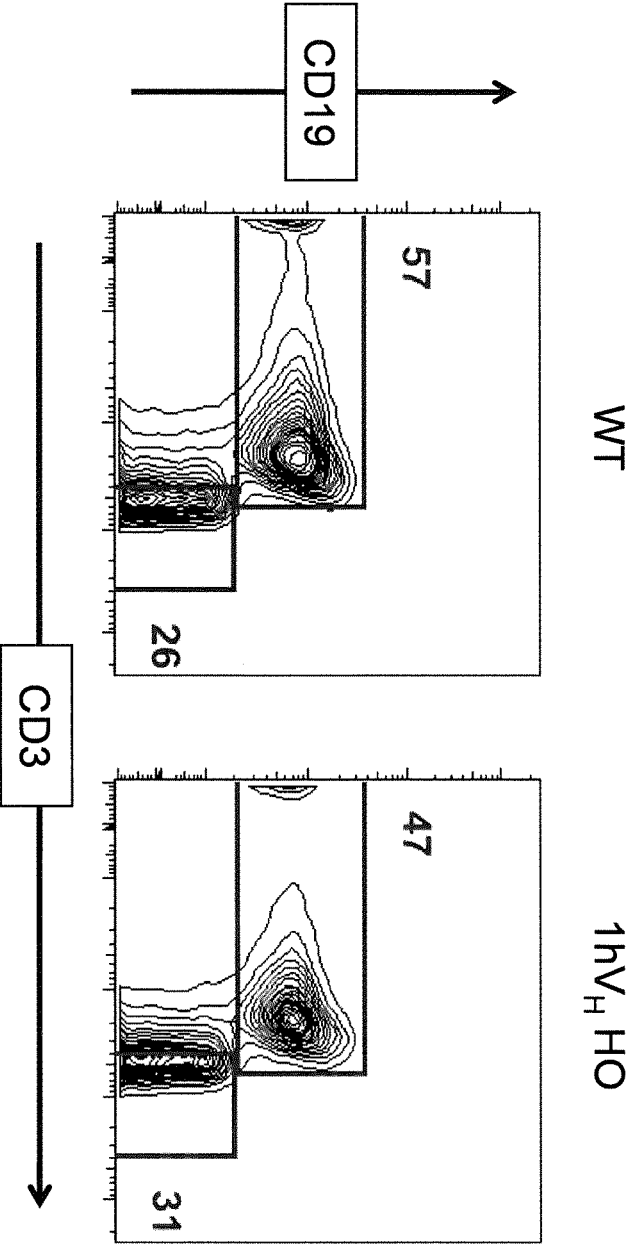


FIG. 3

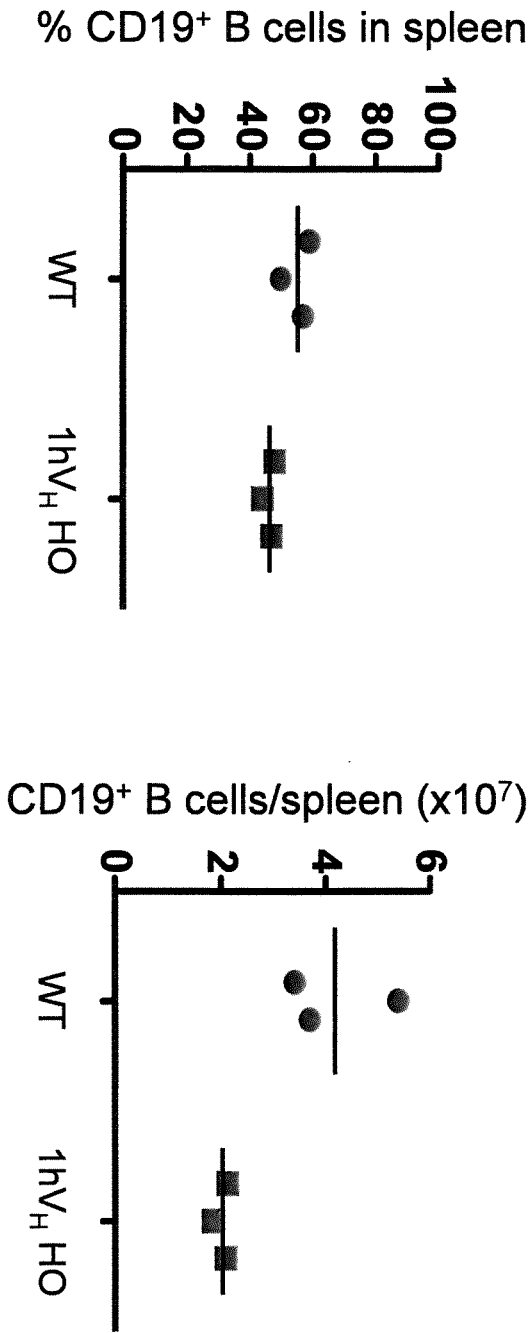
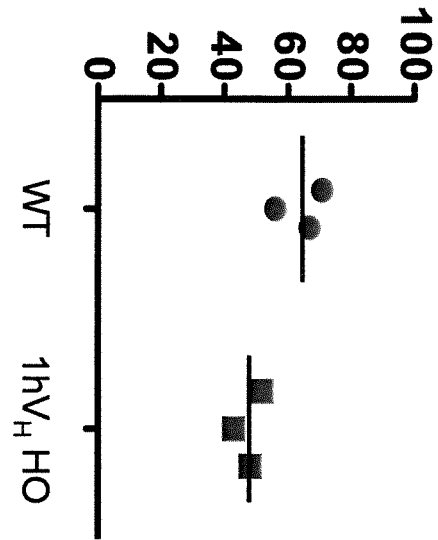


FIG. 4A

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% CD19⁺ B cells in bone marrow



CD19⁺ B cells/femur (x10⁶)

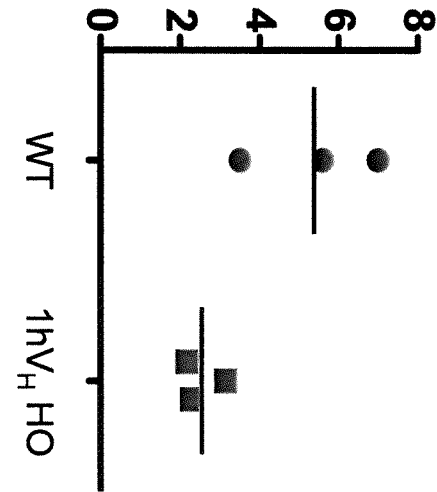


FIG. 4B

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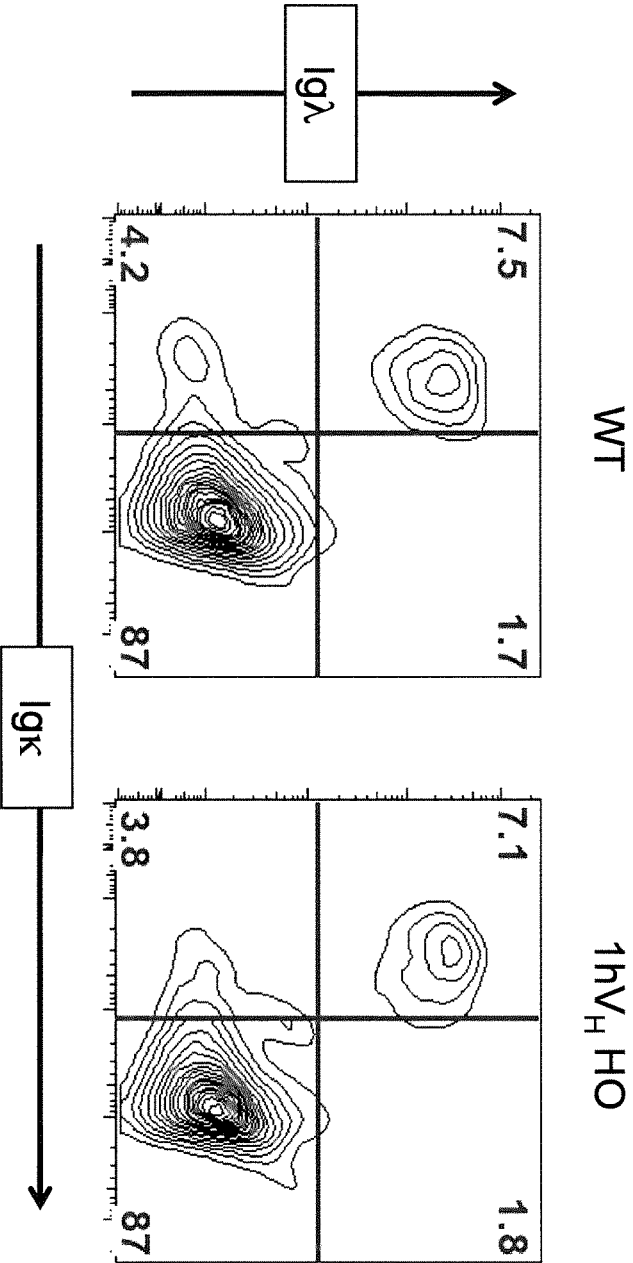


FIG. 5

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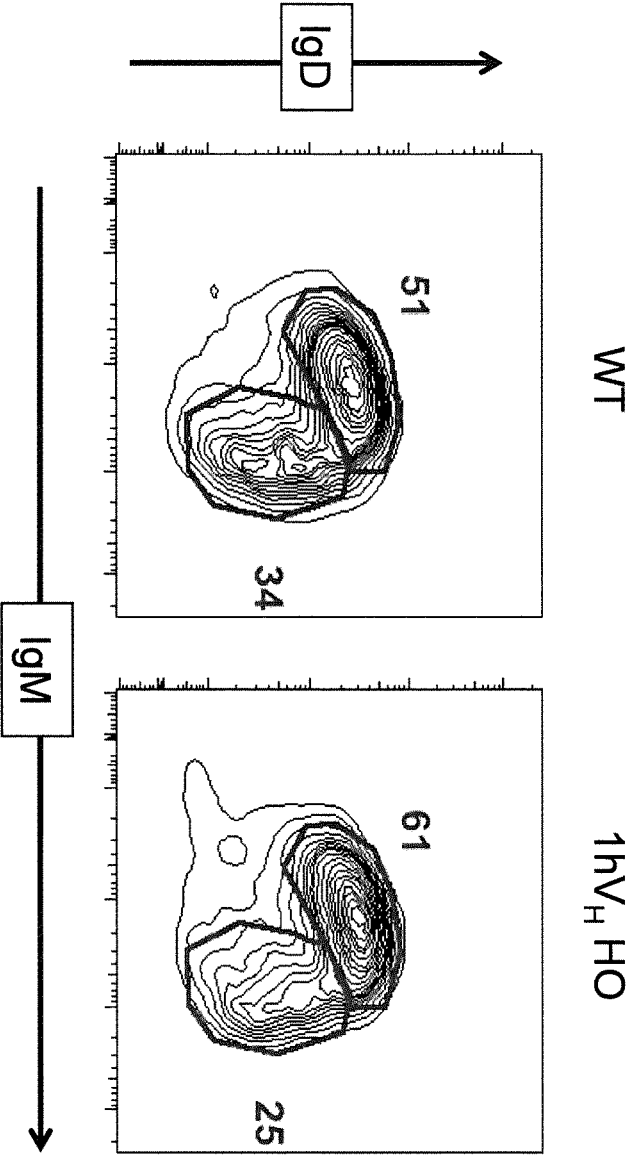


FIG. 6

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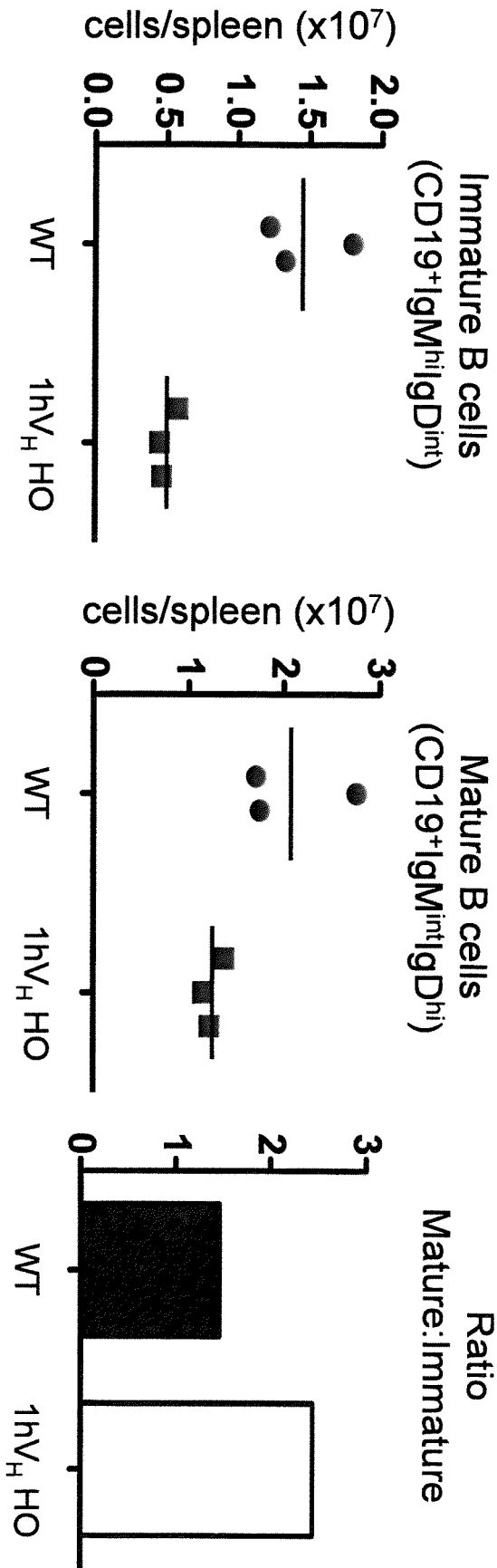


FIG. 7

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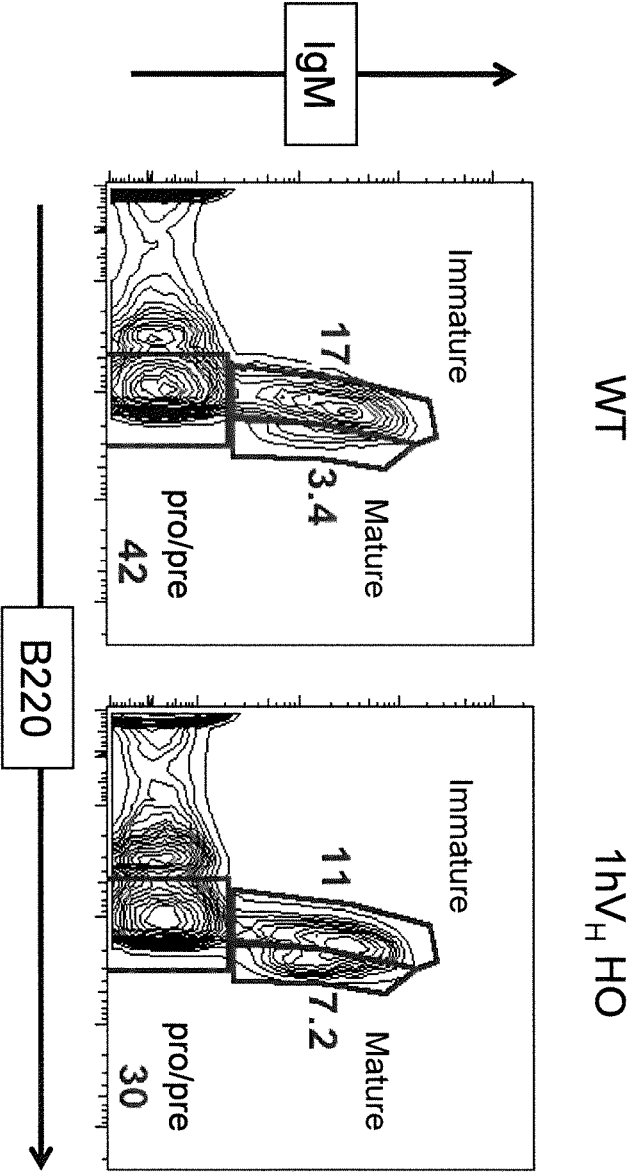


FIG. 8

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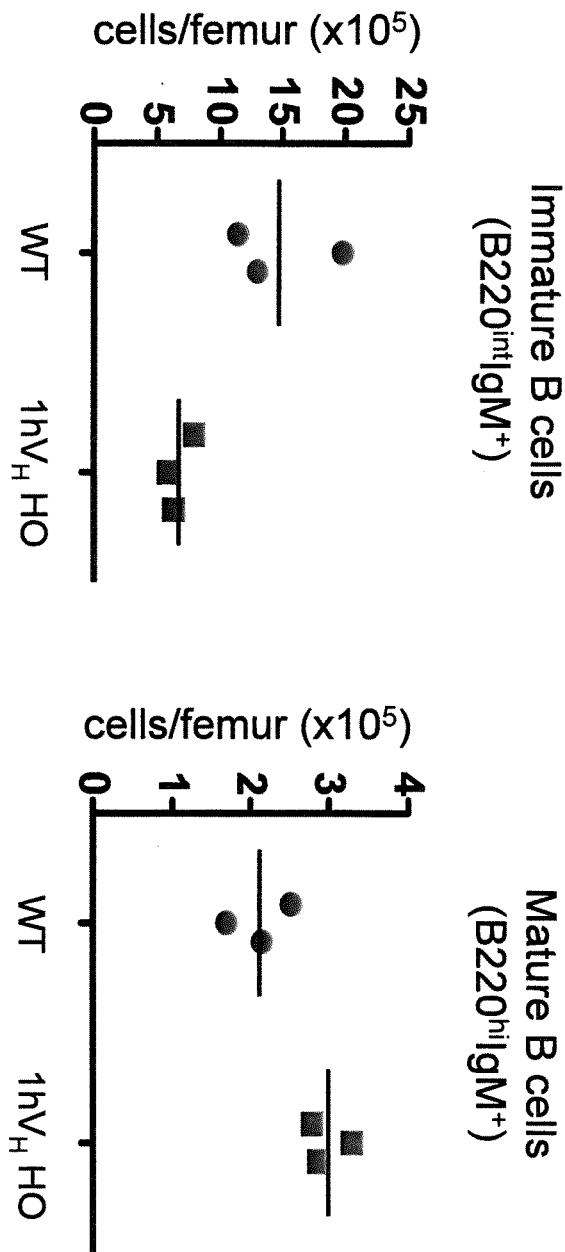


FIG. 9

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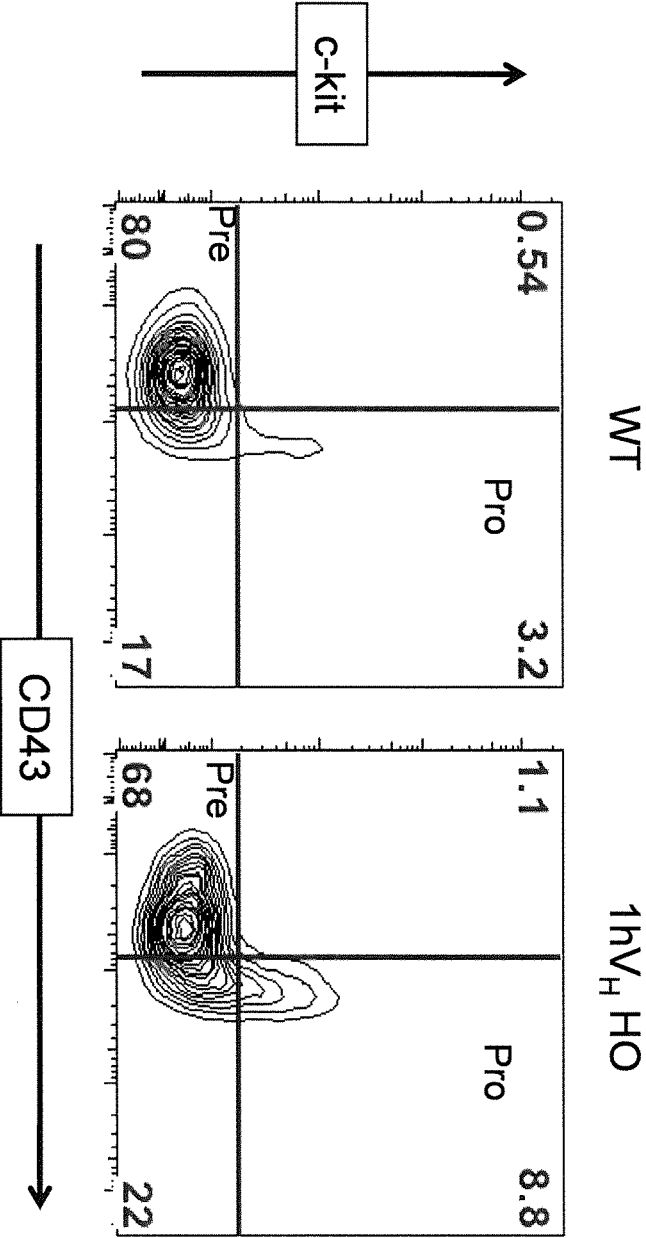


FIG. 10

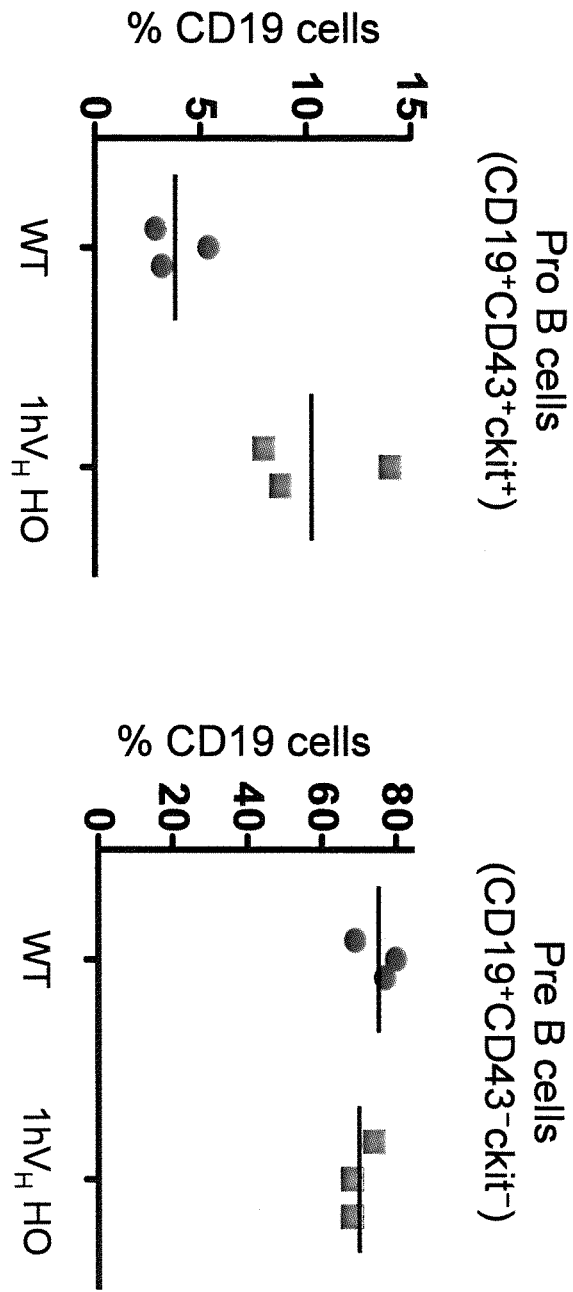


FIG. 11A

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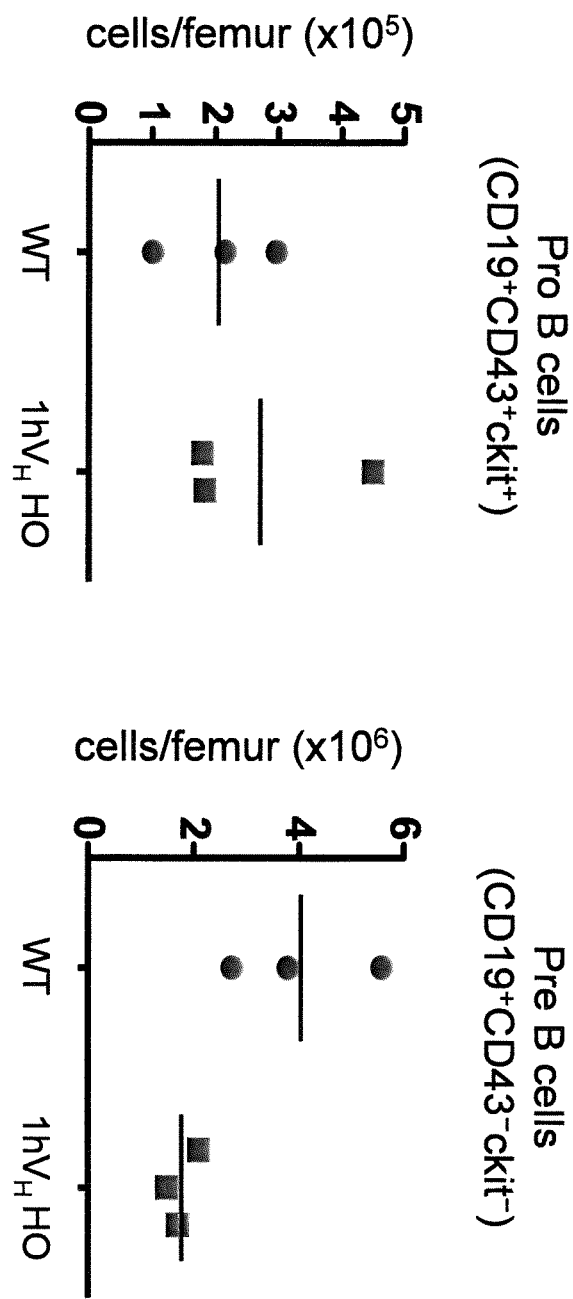


FIG. 11B

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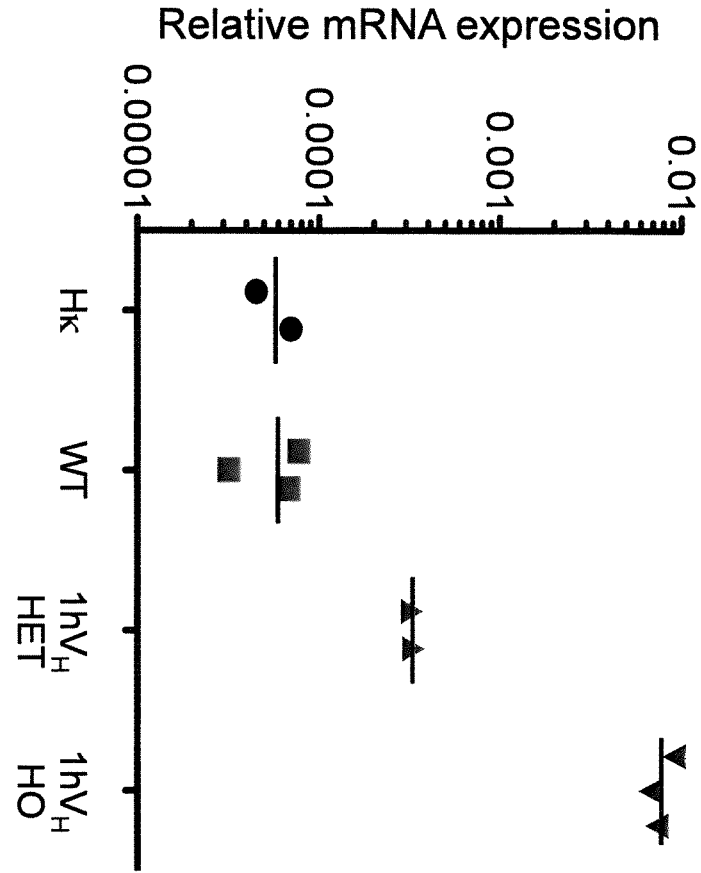


FIG. 12

	10	20	30	40	50	60	70
VH1-69*01	CAGGTgCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*02	CAGGTCCAGCTGGTGCaaTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*03	CAGGTgCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*04	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*05	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*06	CAGGTgCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*07	-----AGAAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*08	CAGGTCCAGCTGGTGCaaTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*09	CAGGTgCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*10	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCaGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*11	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*12	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*13	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCaGTGAAGGTCTCCTGCAAGGCTTCT						

	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	ATCATCCCTATCCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*02	ATCATCCCTATCCTTTGGTAtAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*03	ATCATCCCTATCCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*04	ATCATCCCTATCCTTTGGTAtAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*05	ATCATCCCTATCCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCaCGGACGAATCC						
VH1-69*06	ATCATCCCTATCCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*07	ATCATCCCTATCCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*08	ATCATCCCTATCCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*09	ATCATCCCTATCCTTTGGTAtAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*10	ATCATCCCTATCCTTTGGTAtAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*11	ATCATCCCTATCCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*12	ATCATCCCTATCCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*13	ATCATCCCTATCCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						

	230	240	250	260	270	280	290
VH1-69*01	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*02	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA---						
VH1-69*03	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAtGACACGGC-----						
VH1-69*04	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*05	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA---						
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. 13

	70	80	90	100
VH1-69*01	AQKFQGRVT	ITADEST	STAYMEL	SSLRSED
VH1-69*02	AQKFQGRVT	ITADKST	STAYMEL	SSLRSED
VH1-69*03	AQKFQGRVT	ITADEST	STAYMEL	SSLRSED
VH1-69*04	AQKFQGRVT	ITADKST	STAYMEL	SSLRSED
VH1-69*05	AQKFQGRVT	ITADEST	STAYMEL	SSLRSED
VH1-69*06	AQKFQGRVT	ITADKST	STAYMEL	SSLRSED
VH1-69*07	AQKFQGRVT	ITADEST	STAYMEL	SSLRSED
VH1-69*08	AQKFQGRVT	ITADKST	STAYMEL	SSLRSED
VH1-69*09	AQKFQGRVT	ITADKST	STAYMEL	SSLRSED
VH1-69*10	AQKFQGRVT	ITADKST	STAYMEL	SSLRSED
VH1-69*11	AQKFQGRVT	ITADEST	STAYMEL	SSLRSED
VH1-69*12	AQKFQGRVT	ITADEST	STAYMEL	SSLRSED
VH1-69*13	AQKFQGRVT	ITADEST	STAYMEL	SSLRSED

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

% Similarity

% Identity

FIG. 15

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VH1-2*01  GAGCCCACTCCCAAGGTG-CAGCTGGTGCAG-TCTG---GGCTGAGGTGAAGAA--GCTGGGGCCCTCAGTGAA
              10              20              30              40              50              60              70
VH1-2*02  GAGCCCACTCCCAAGGTG-CAGCTGGTGCAG-TCTG---GGCTGAGGTGAAGAA--GCTGGGGCCCTCAGTGAA
VH1-2*03  GAGCCCACTCCCAAGGTG-CAGCTGGTGCAG-TCTG---GGCTGAGGTGAAGAA--GCTGGGGCCCTCAGTGAA
VH1-2*04  -----CAGGTG-CAGCTGGTGCAG-TCTG---GGCTGAGGTGAAGAA--GCTGGGGCCCTCAGTGAA
VH1-2*05  GACCGTgtcgtcAgaatctCAGCctgcctCAGCTccatGtagGctGctGatgAagAACGTGCCCTGGGGCCCTCAGTGAA
              GAGCCCACTCCCAAGGTGTCAGCTGGTGCAGCTCTGTGTGGGCTGAGGTGAAGAA
VH1-2*01  GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAACCGGCTACTATATGCACTGG---GTGCCA-----CAGGCCCC
              80              90              100              110              120              130              140              150
VH1-2*02  GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAACCGGCTACTATATGCACTGG---GTGCCA-----CAGGCCCC
VH1-2*03  GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAACCGGCTACTATATGCACTGG---GTGCCA-----CAGGCCCC
VH1-2*04  GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAACCGGCTACTATATGCACTGG---GTGCCA-----CAGGCCCC
VH1-2*05  cctgccctg--AaaCTTCTGtgcaTAgTtTgtgCcaCcaCTgtTtagggtTgattCCctCCatCCACTCAagCCct
              GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAACCGGCTACTATATGCACTGGTCCGTCCGTCCGATCCACTCAGGCC
VH1-2*01  TGGACAAGGGCTTGAAGTGGATGGGAcGGATTCAAcCCTAAACAGTGGTGGCAcAACTATGcACAGAAgTTT--CAG
              160              170              180              190              200              210              220
VH1-2*02  TGGACAAGGGCTTGAAGTGGATGGGAcGGATTCAAcCCTAAACAGTGGTGGCAcAACTATGcACAGAAgTTT--CAG
VH1-2*03  TGGACAAGGGCTTGAAGTGGATGGGAcGGATTCAAcCCTAAACAGTGGTGGCAcAACTATGcACAGAAgTTT--CAG
VH1-2*04  TGGACAAGGGCTTGAAGTGGATGGGAcGGATTCAAcCCTAAACAGTGGTGGCAcAACTATGcACAGAAgTTT--CAG
VH1-2*05  TgtccaGggGcCTG---TccGAc---ccAgTgcatAtAGTAgccGgtgAAAggtgtatccAGAAgCCTTGGCAg
              TGGACAAGGGCTTGAAGTGGATGGGAcGGATTCAAcCCTAAACAGTGGTGGCAcAACTATGcACAGAAgTTTGGCAg
VH1-2*01  GGCAGGGTCAcCAgtACCAAGGGAcAcGTCCA--TCAgCAc-AGcCTTACATGGAGcCTGAAGcAGGCTGAATCTGAc
              230              240              250              260              270              280              290              300
VH1-2*02  GGCAGGGTCAcCAgtACCAAGGGAcAcGTCCA--TCAgCAc-AGcCTTACATGGAGcCTGAAGcAGGCTGAATCTGAc
VH1-2*03  GGCAGGGTCAcCAgtACCAAGGGAcAcGTCCA--TCAgCAc-AGcCTTACATGGAGcCTGAAGcAGGCTGAATCTGAc
VH1-2*04  GGCtGGGTCAcCAgtACCAAGGGAcAcGTCCA--TCAgCAc-AGcCTTACATGGAGcCTGAAGcAGGCTGAATCTGAc
VH1-2*05  GAgAcctTCAcTgagGcCccagGcttcttCAcCTCAgCccCAgCCTTACATGGAGcCTGAAGcAGGCTGAATCTGAc
              GGCAGGGTCAcCAgtACCAAGGGAcAcGTCCAcCTCAgCAcCAgCCTTACATGGAGcCTGAAGcAGGCTGAATCTGAc
VH1-2*01  GACACGGGtCGTGtATTAcCTGTGCGAGAA---
              310              320              330
VH1-2*02  GACACGGGcCGTGtATTAcCTGTGCGAGAGAA
VH1-2*03  GACACGGGcCGTGtATTAcCTGTGCGAGAGAA
VH1-2*04  GACACGGGcCGTGtATTAcCTGTGCGAGAGAA
VH1-2*05  GACAC---cTGTgAg-AcCT--CGCGA-----
              GACACGGGcCGTGtATTAcCTGTGCGAGAGAA

```

FIG. 16

	60	70	80	90
VH1-2*01	I N P N S G G T	N Y A Q K F Q G R V T	S I S T A Y M E L S R L R	S D D T V V Y Y C A R R
VH1-2*02	I N P N S G G T	N Y A Q K F Q G R V T	S I S T A Y M E L S R L R	S D D T A V Y Y C A R R
VH1-2*03	I N P N S G G T	N Y A Q K F Q G R V T	S I S T A Y M E L S R L R	S D D T A V Y Y C A R R
VH1-2*04	I N P N S G G T	N Y A Q K F Q G W V T	S I S T A Y M E L S R L R	S D D T A V Y Y C A R R
VH1-2*05	I N P N S G G T	N Y A Q K F Q G R V T	S I S T A Y M E L S R L R	S D D T V V Y Y C A R R
	I N P N S G G T	N Y A Q K F Q G R V T	S I S T A Y M E L S R L R	S D D T A V Y Y C A R R

FIG. 17

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

FIG. 18

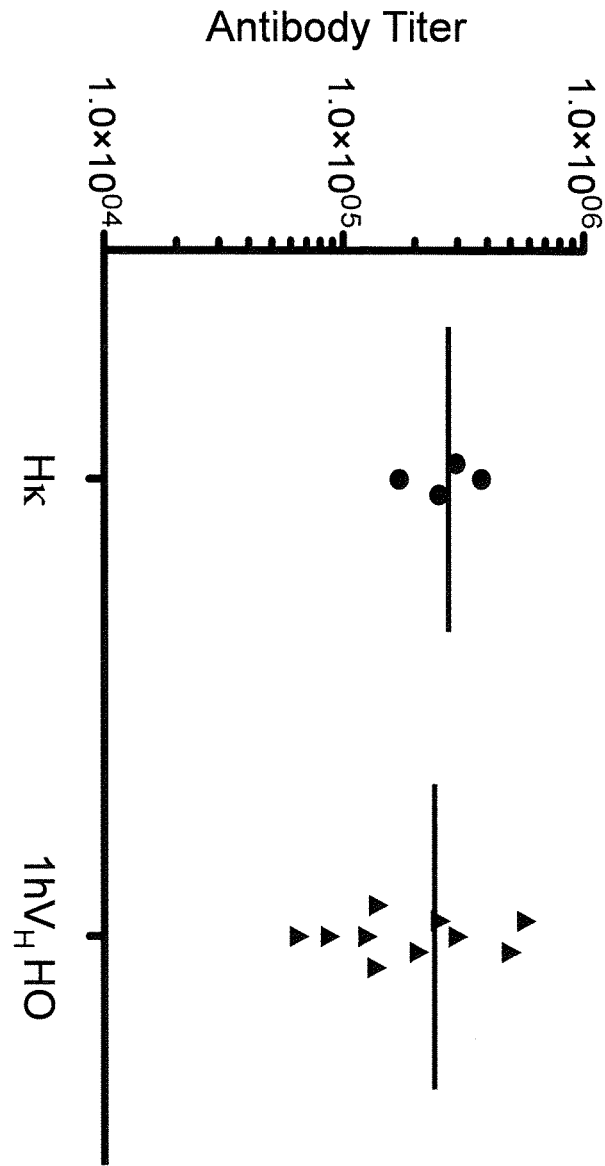


FIG. 19

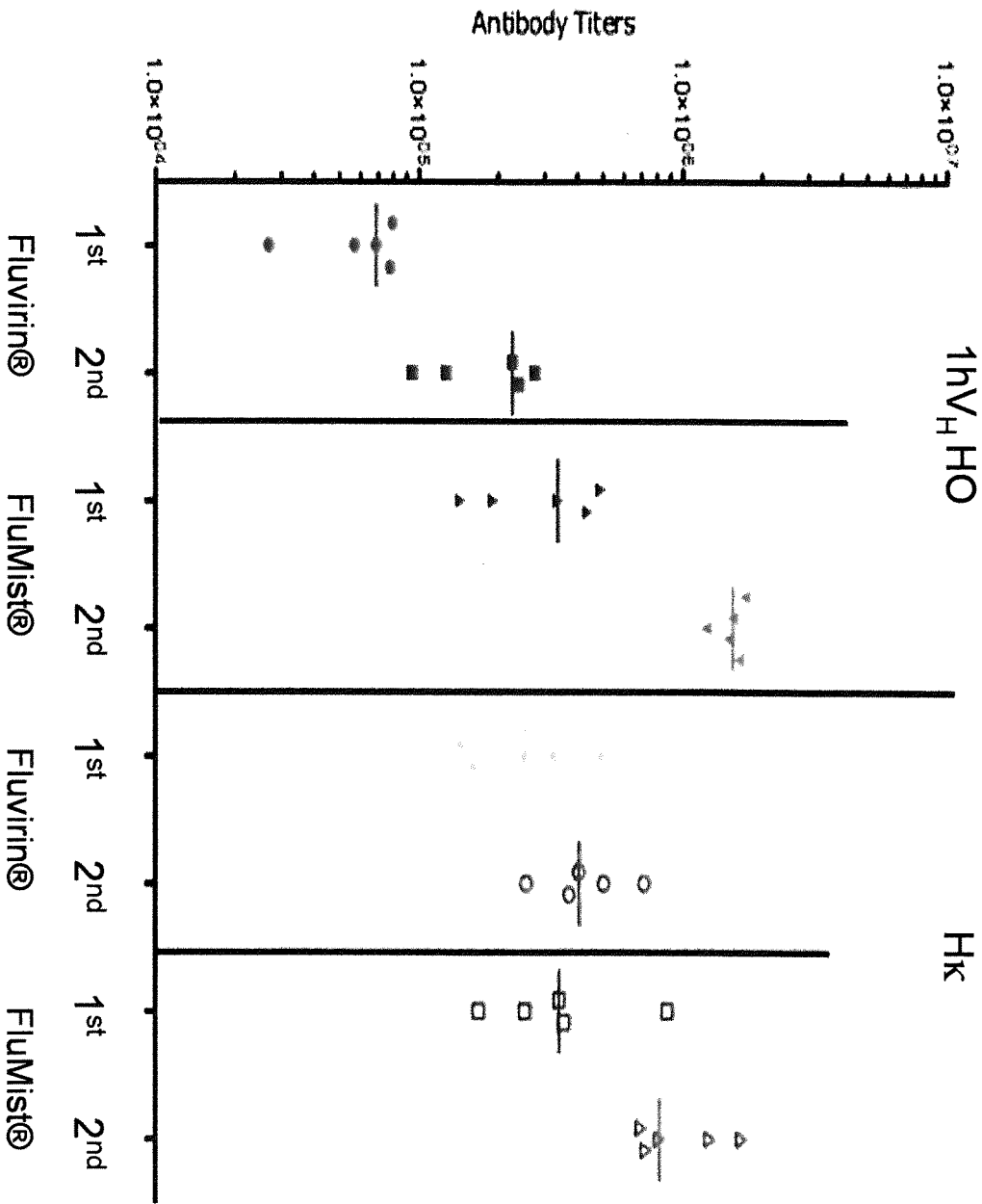


FIG. 20

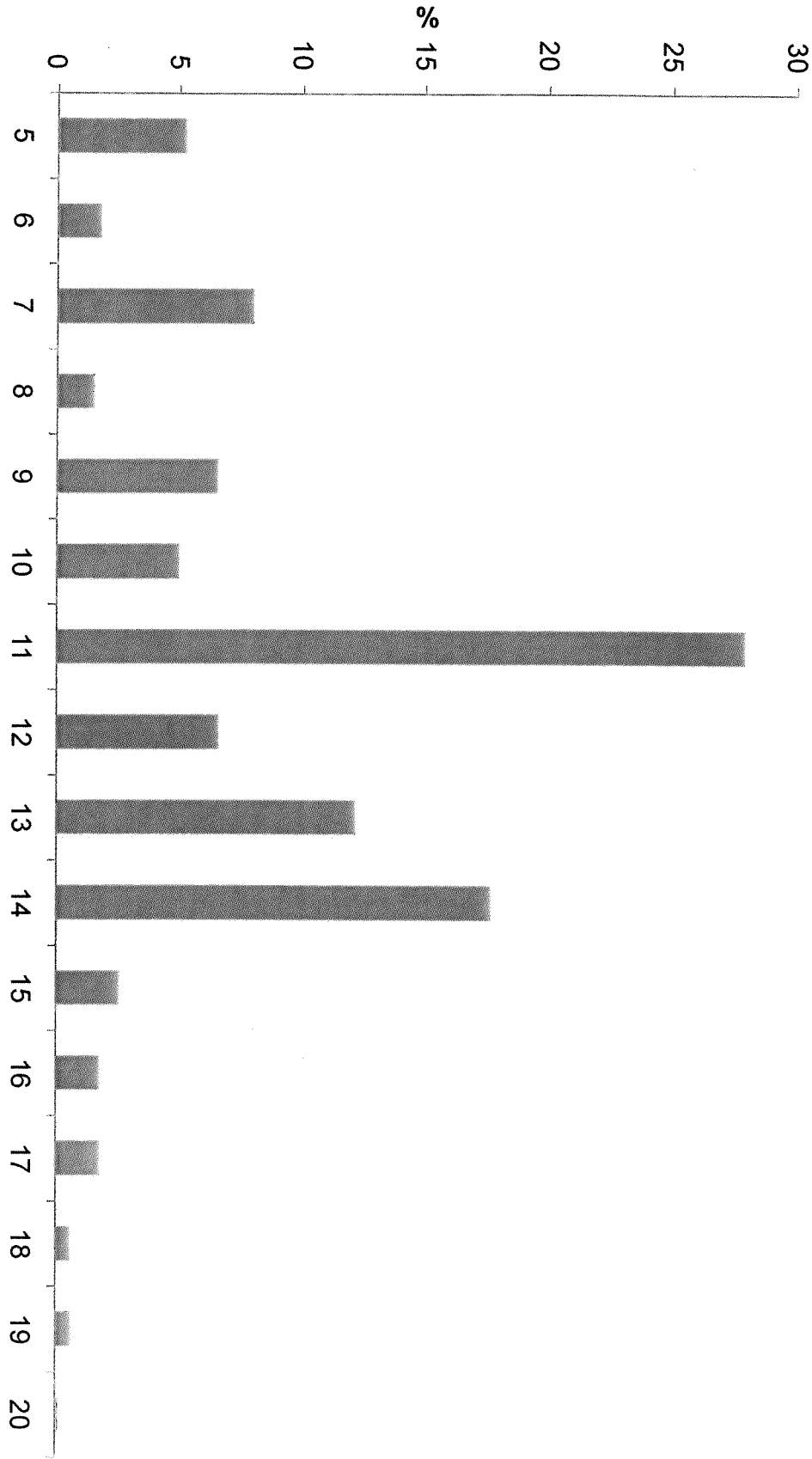


FIG. 21

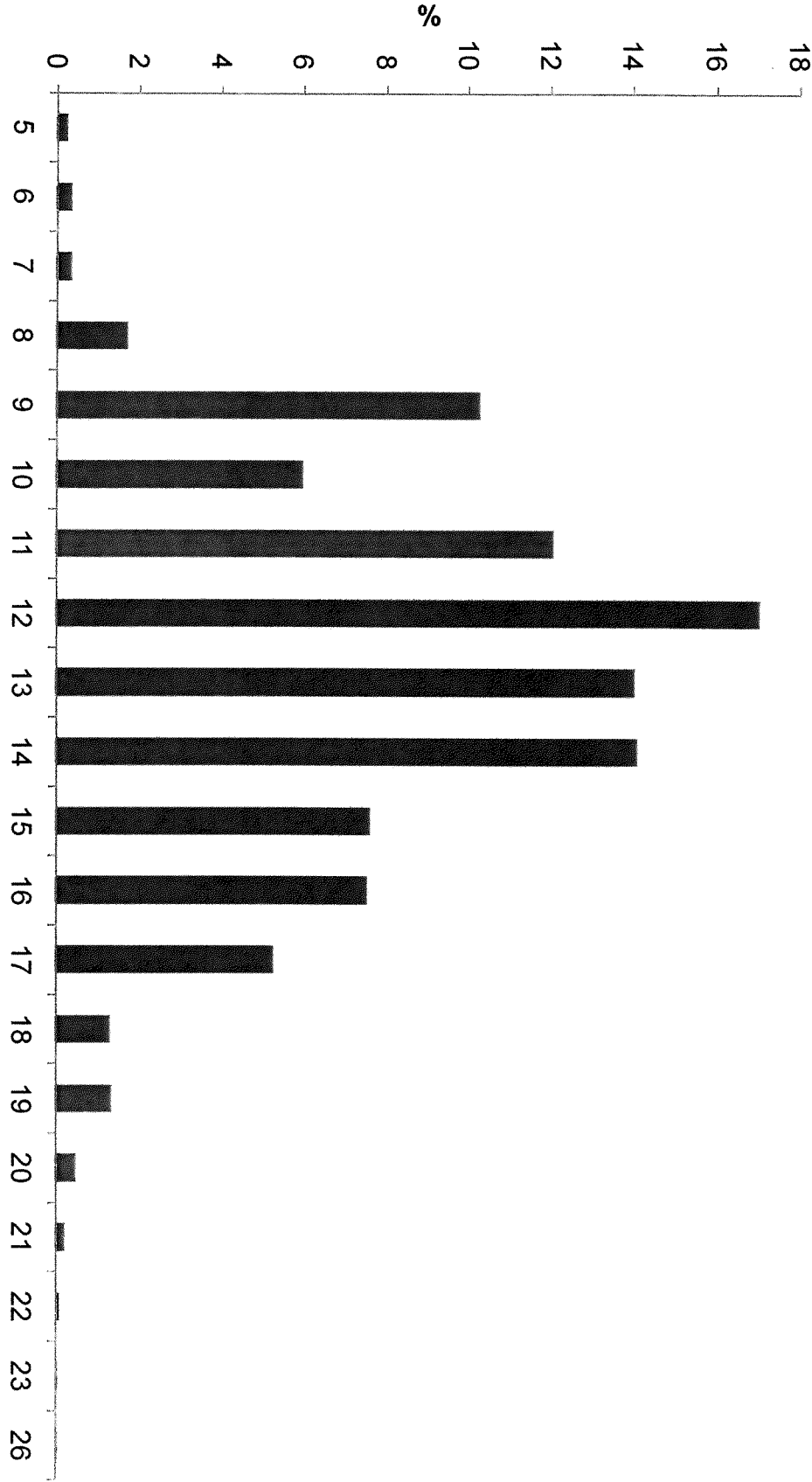


FIG. 22