



FIG. 1

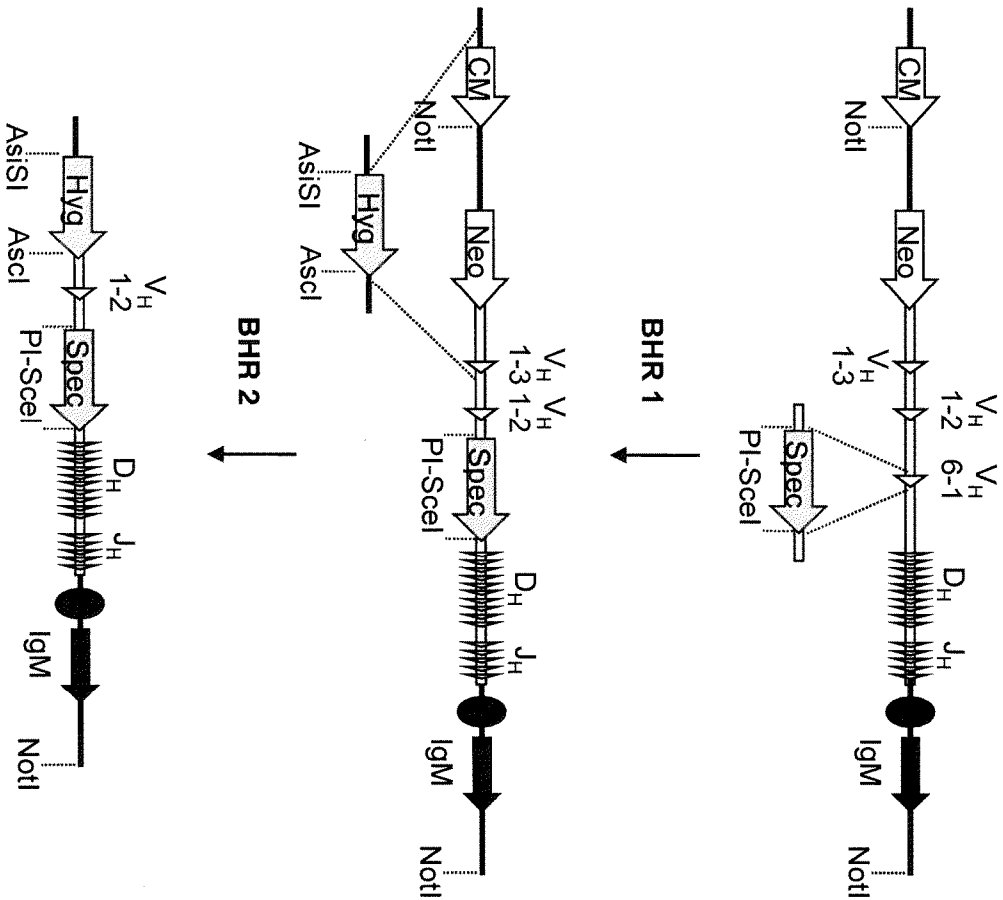


FIG. 2

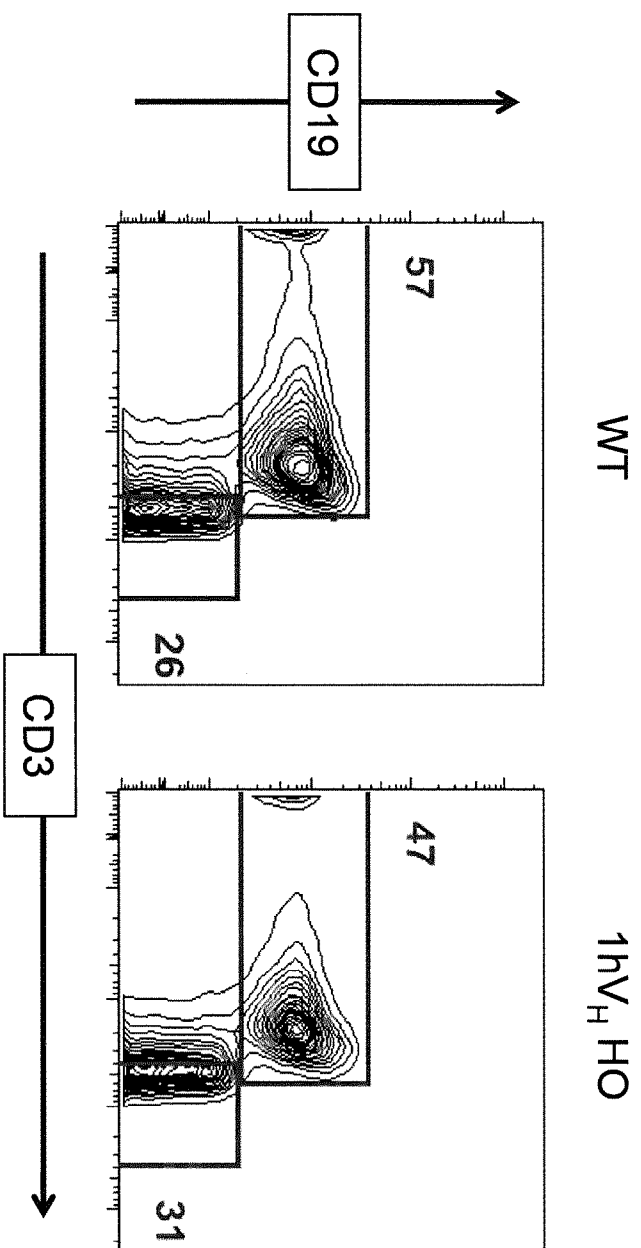
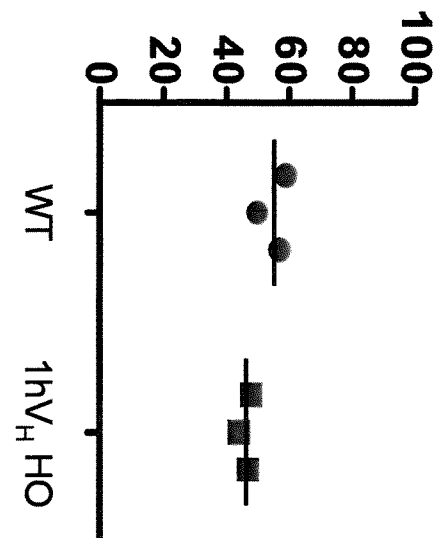


FIG. 3

% CD19⁺ B cells in spleen



CD19⁺ B cells/spleen ($\times 10^7$)

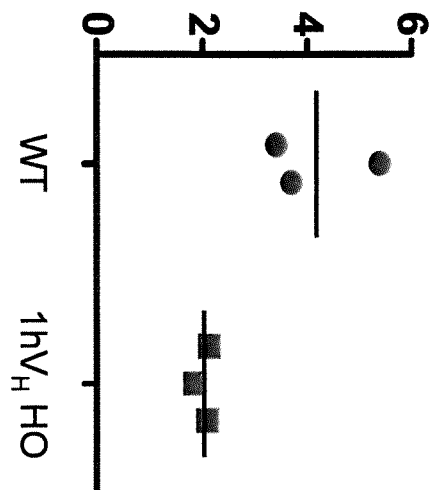
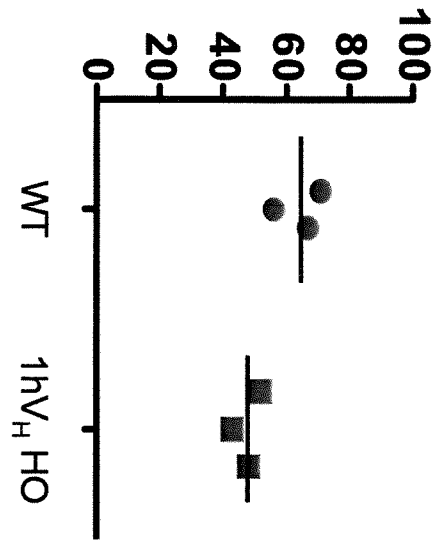


FIG. 4A

% CD19⁺ B cells in bone marrow



CD19⁺ B cells/femur (x10⁶)

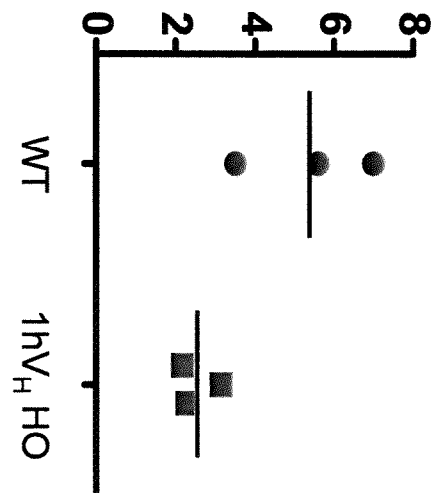


FIG. 4B

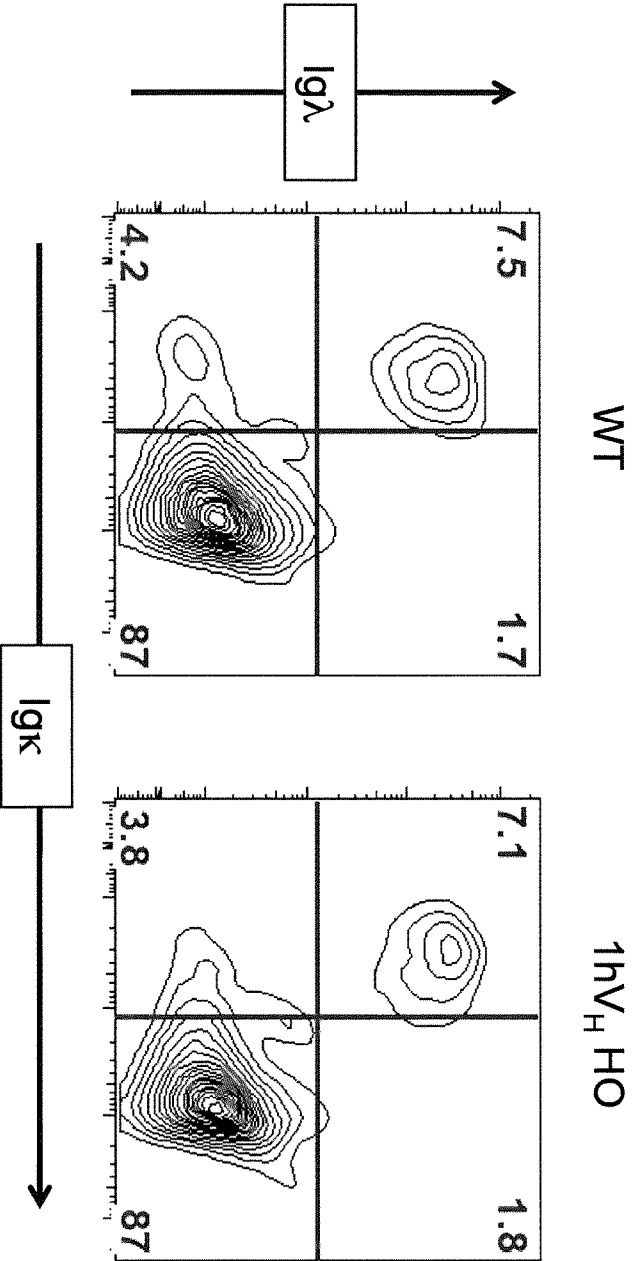


FIG. 5

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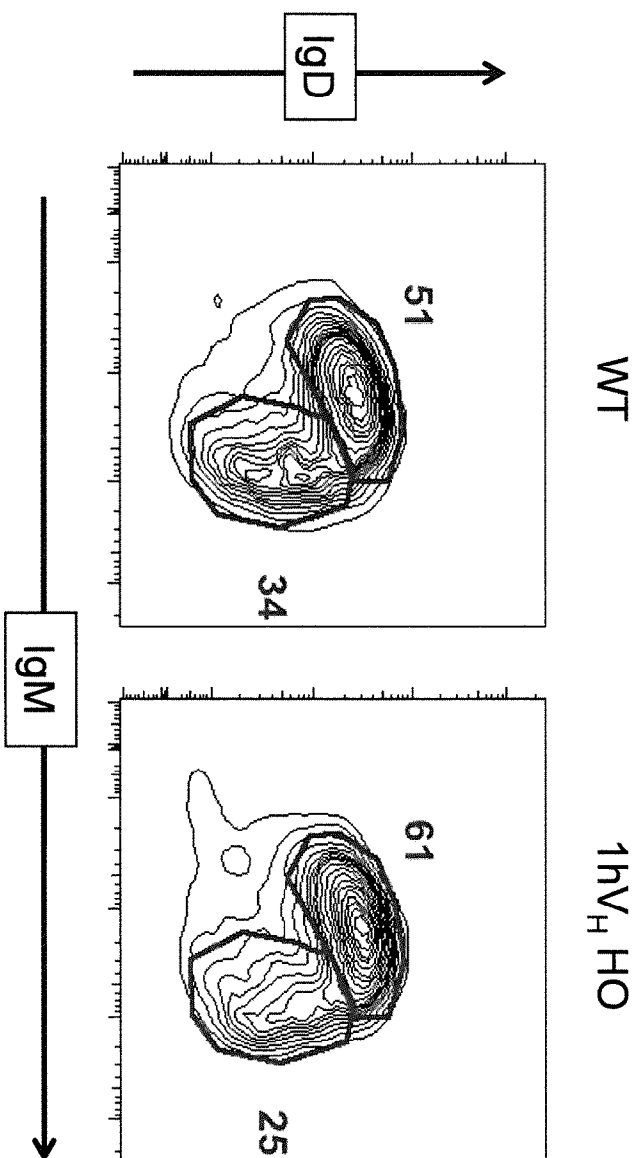


FIG. 6

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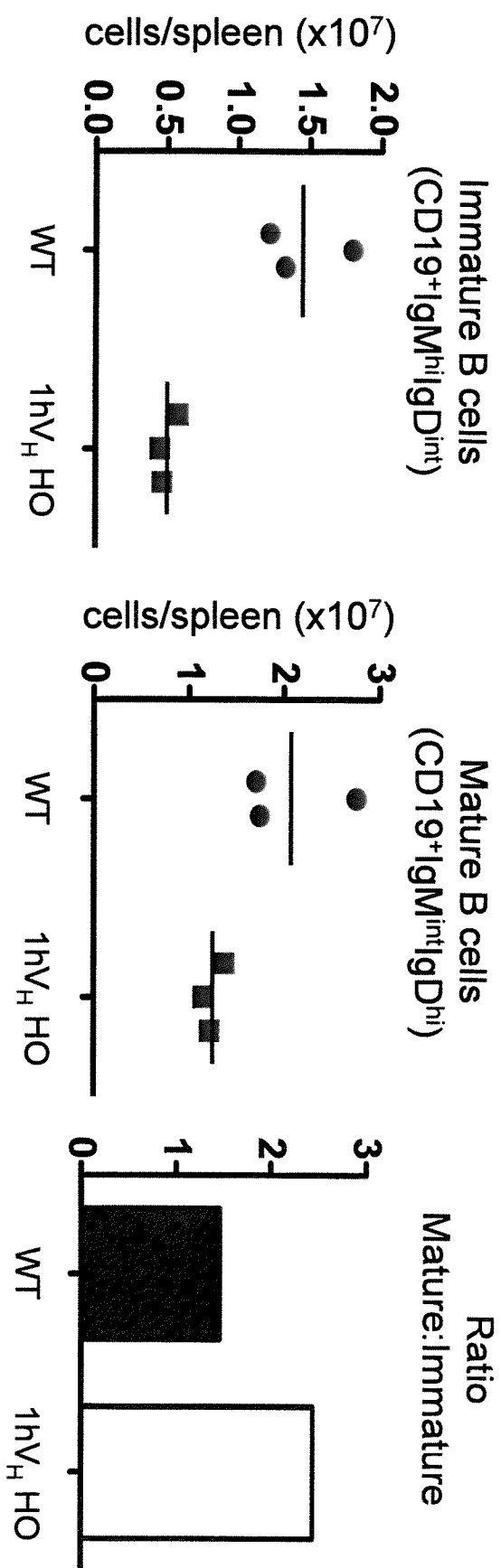


FIG. 7

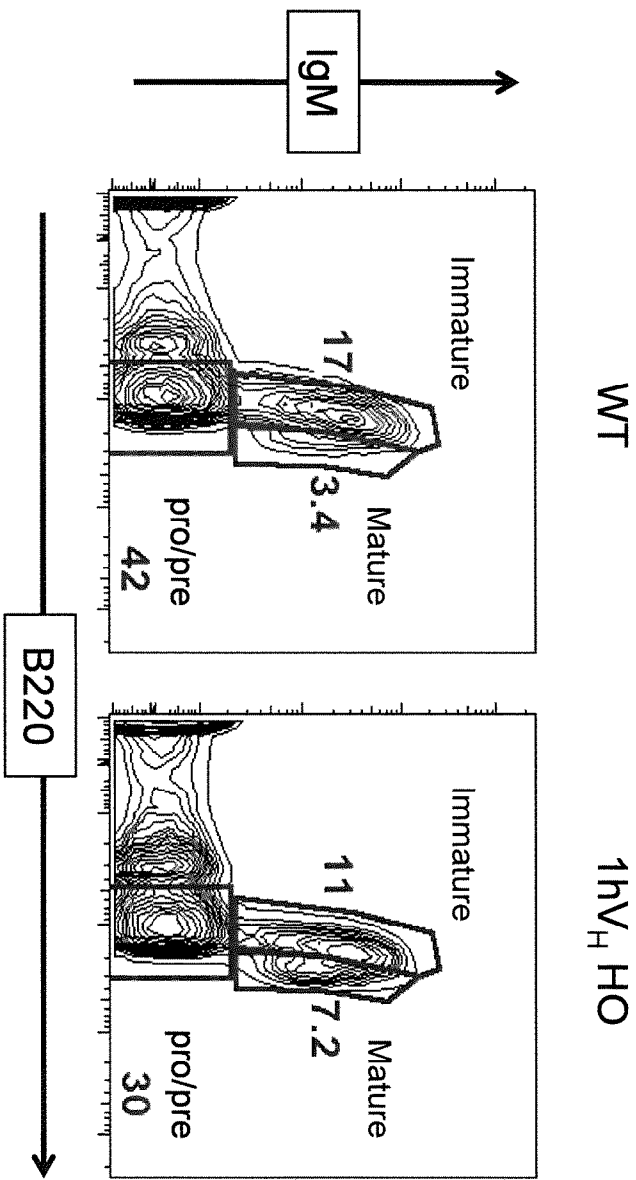


FIG. 8

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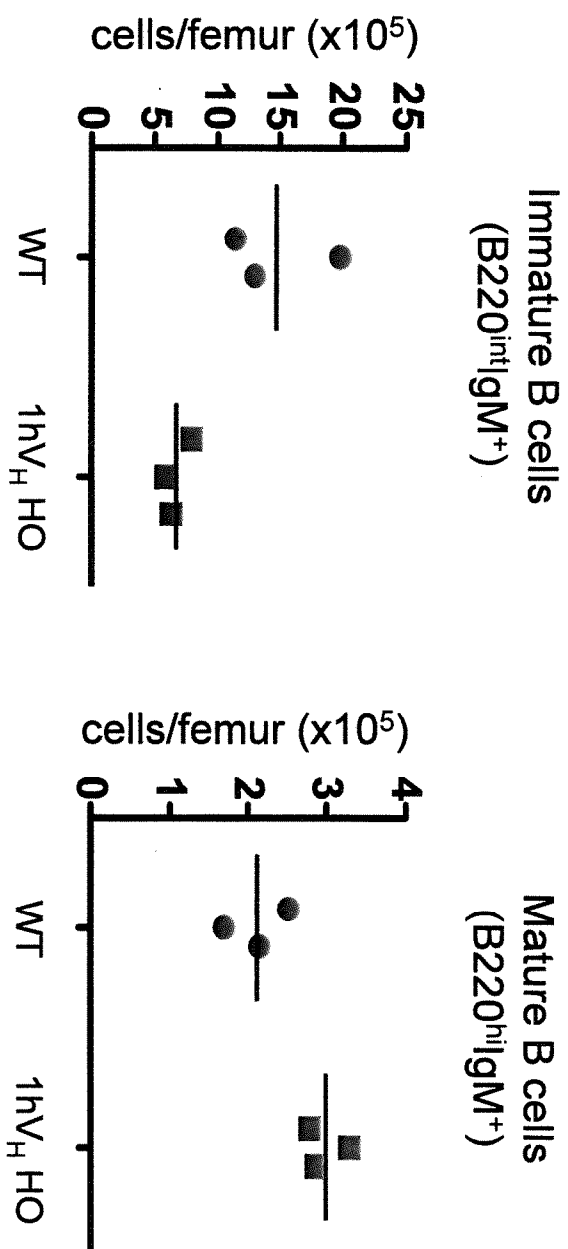


FIG. 9

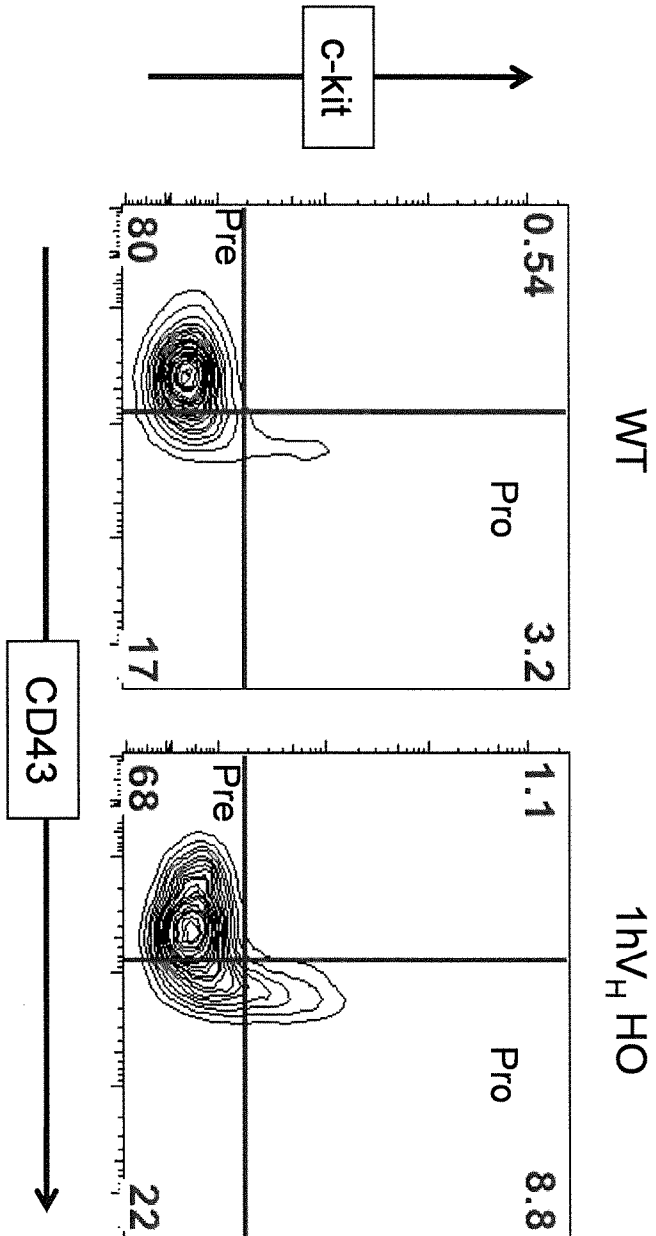


FIG. 10

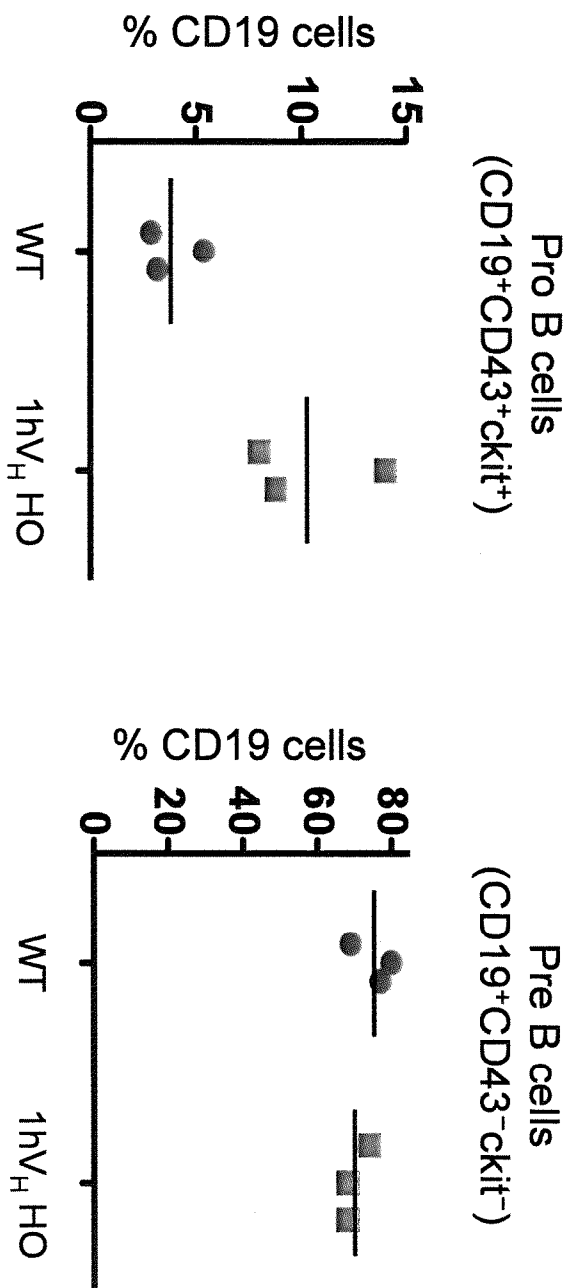


FIG. 11A

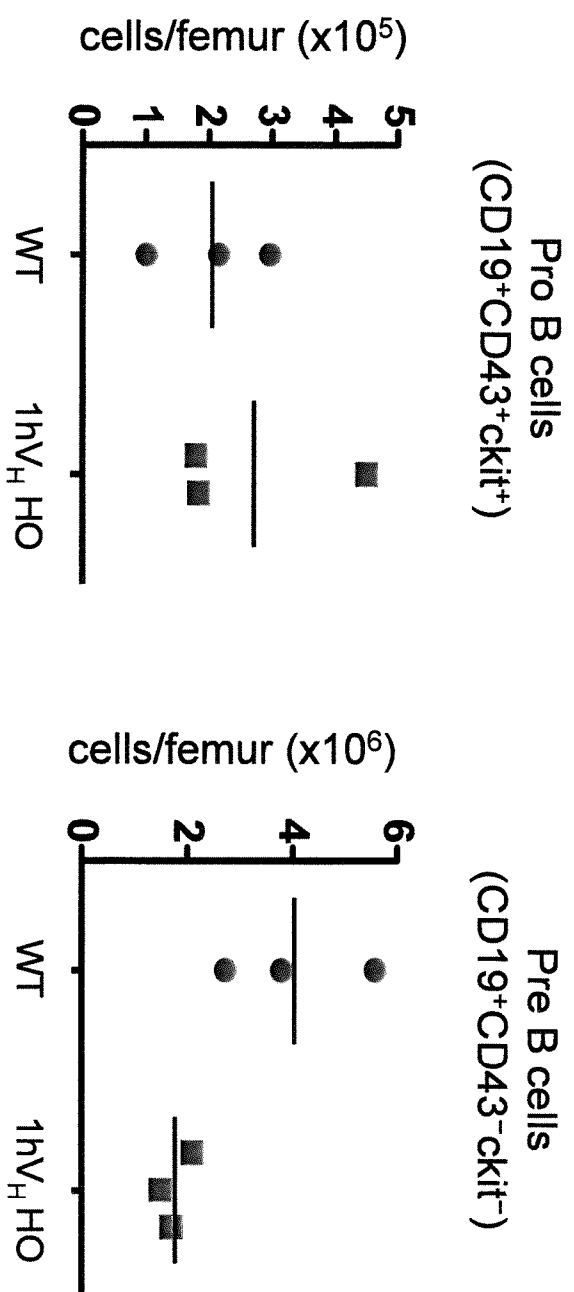


FIG. 11B

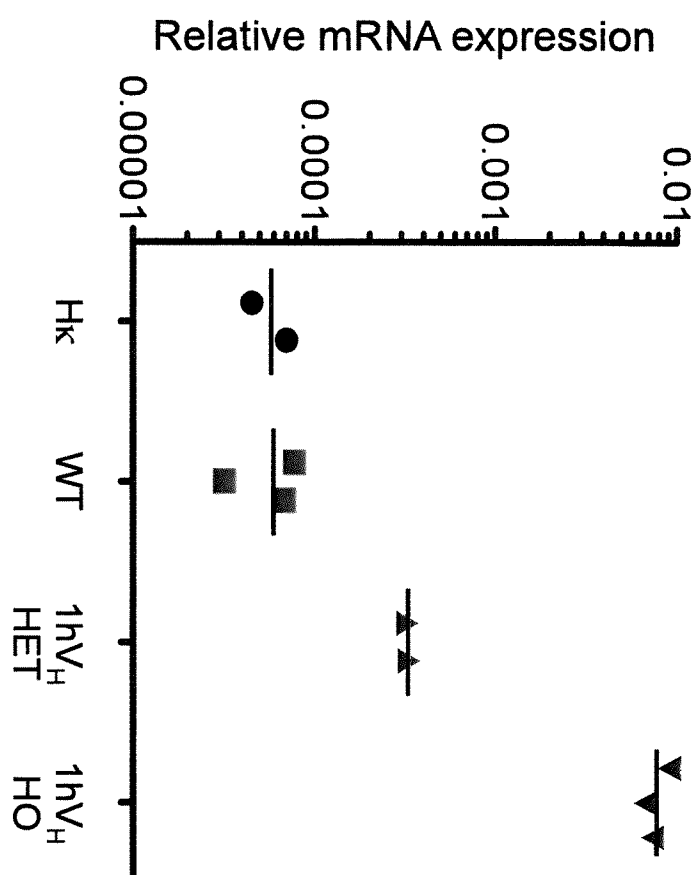


FIG. 12

	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	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC	aGTGAAGGTCTCCTGCAAGGCTTCT					
VH1-69*11	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*12	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*13	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC	aGTGAAGGTCTCCTGCAAGGCTTCT					

	80	90	100	110	120	130	140	150
VH1-69*01	GGAGGCACCTTCAGCAGCTATGCTAT	ATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAGGG						
VH1-69*02	GGAGGCACCTTCAGCAGCTATaCTAT	ATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAaGG						
VH1-69*03	GGAGGCACCTTCAGCAGCTATGCTAT	ATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAGGG						
VH1-69*04	GGAGGCACCTTCAGCAGCTATGCTAT	ATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAaGG						
VH1-69*05	GGAGGCACCTTCAGCAGCTATGCTAT	ATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAGGG						
VH1-69*06	GGAGGCACCTTCAGCAGCTATGCTAT	ATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAGGG						
VH1-69*07	GGAGGCACCTTCAGCAGCTATGCTAT	ATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAaGG						
VH1-69*08	GGAGGCACCTTCAGCAGCTATaCTAT	ATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAaGG						
VH1-69*09	GGAGGCACCTTCAGCAGCTATGCTAT	ATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAaGG						
VH1-69*10	GGAGGCACCTTCAGCAGCTATGCTAT	ATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAGGG						
VH1-69*11	GGAGGCACCTTCAGCAGCTATGCTAT	ATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAaGG						
VH1-69*12	GGAGGCACCTTCAGCAGCTATGCTAT	ATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAGGG						
VH1-69*13	GGAGGCACCTTCAGCAGCTATGCTAT	ATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAGGG						

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

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

FIG. 13

[illegible]

FIG. 14

% Identity													
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

FIG. 15

```

VH1-2*01  GAGCCCACTCCCAAGGTG-CAGCTGGTGCAG-TCTG---GGGCTGAGGTGAAGAA--GCTGGGGGCTCAGTGA
10
VH1-2*02  GAGCCCACTCCCAAGGTG-CAGCTGGTGCAG-TCTG---GGGCTGAGGTGAAGAA--GCTGGGGGCTCAGTGA
30
VH1-2*03  GAGCCCACTCCCAAGGTG-CAGCTGGTGCAG-TCTG---GGGCTGAGGTGAAGAA--GCTGGGGGCTCAGTGA
50
VH1-2*04  -----CAGGTG-CAGCTGGTGCAG-TCTG---GGGCTGAGGTGAAGAA--GCTGGGGGCTCAGTGA
70
VH1-2*05  GACCGTgtcgtcAGatcTCAgCctgcTCAgCTcCATgTAgGcGTgtGAtgAGGTGAAGAAcGTGCCTGGGGCCTCAgTGA
100
GAGCCCACTCCCAAGGTGTCAgCCTGGTGCAGCTCTGTGTGGGCTGAGGTGAAGAAcGTGCCTGGGGCCTCAgTGA
120
VH1-2*01  GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAcCGGCTACTATATGCACTGG---GTGCGA-----CAGGCCCC
80
VH1-2*02  GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAcCGGCTACTATATGCACTGG---GTGCGA-----CAGGCCCC
90
VH1-2*03  GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAcCGGCTACTATATGCACTGG---GTGCGA-----CAGGCCCC
100
VH1-2*04  GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAcCGGCTACTATATGCACTGG---GTGCGA-----CAGGCCCC
110
VH1-2*05  cCTgcccTG--AaaCTTCTGtgCAtAgTtTgtgCcaCcaCTgttAgggtTgATCCGTccCATCCACTCAgGCCc
120
GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAcCGGCTACTATATGCACTGG---GTGCGA-----CAGGCCCC
130
VH1-2*01  TGGACAAGGGCTTGAGTGGATGGGAcGGATCAAcCCTAAcAGTGGTGGCAcAAcTATGcAcAGAAgTTT--cAG
160
VH1-2*02  TGGACAAGGGCTTGAGTGGATGGGATGGGATGGATCAAcCCTAAcAGTGGTGGCAcAAcTATGcAcAGAAgTTT--cAG
170
VH1-2*03  TGGACAAGGGCTTGAGTGGATGGGATGGGATCAAcCCTAAcAGTGGTGGCAcAAcTATGcAcAGAAgTTT--cAG
180
VH1-2*04  TGGACAAGGGCTTGAGTGGATGGGATGGGATCAAcCCTAAcAGTGGTGGCAcAAcTATGcAcAGAAgTTT--cAG
190
VH1-2*05  TgtccAgggGcCTG---TcGcAc--cCagtgCatAtAgTAgccGgtgAAAggtgtatccAGAAgCCTTgCAg
200
TGGACAAGGGCTTGAGTGGATGGGATGGGATCAAcCCTAAcAGTGGTGGCAcAAcTATGcAcAGAAgTTTgCAg
210
VH1-2*01  230
VH1-2*02  240
VH1-2*03  250
VH1-2*04  260
VH1-2*05  270
VH1-2*01  GGCAGGGTCAcCAgtACCAAGGGAcAcGTCCA--TCAgCAc-AgCCTACATGGAGcTGAAGcAGGCTGAGATCTGA
280
VH1-2*02  GGCAGGGTCAcCAATGAcCAAGGGAcAcGTCCA--TCAgCAc-AgCCTACATGGAGcTGAAGcAGGCTGAGATCTGA
290
VH1-2*03  GGCAGGGTCAcCAATGAcCAAGGGAcAcGTCCA--TCAgCAc-AgCCTACATGGAGcTGAAGcAGGCTGAGATCTGA
300
VH1-2*04  GGCtGGGTCAcCAATGAcCAAGGGAcAcGTCCA--TCAgCAc-AgCCTACATGGAGcTGAAGcAGGCTGAGATCTGA
310
VH1-2*05  GAgAcctTCAcTgAggCcCcaGgtctcTtCAcCTCAgCcCcaGacctgCAcc-AgCTGcAc--CTGgGA--Gtg
320
GGCAGGGTCAcCAATGAcCAAGGGAcAcGTCCAcCTCAgCAcCAgCcCTACATGGAGcTGAAGcAGGCTGAGATCTGA
330
VH1-2*01  GACACGGtCGTGtATTAcCTGGTGGAGAA--
VH1-2*02  GACACGGcCGTGtATTAcCTGGTGGAGAA--
VH1-2*03  GACACGGcCGTGtATTAcCTGGTGGAGAA--
VH1-2*04  GACACGGcCGTGtATTAcCTGGTGGAGAA--
VH1-2*05  GACAC--cTgTgAg-AcCT--cGCGA-----
GACACGGcCGTGtATTAcCTGGTGGAGAA

```

FIG. 16

	10	20	30	40	50
VH1-2*01	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 r		
VH1-2*02	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*03	Q V Q L V Q S G A E V K K 1 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		
VH1-2*04	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*05	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 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		
VH1-2*01	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 Y C A R				
VH1-2*02	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 Y C A R				
VH1-2*03	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 Y C A R				
VH1-2*04	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 Y C A R				
VH1-2*05	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 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 Y C A 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

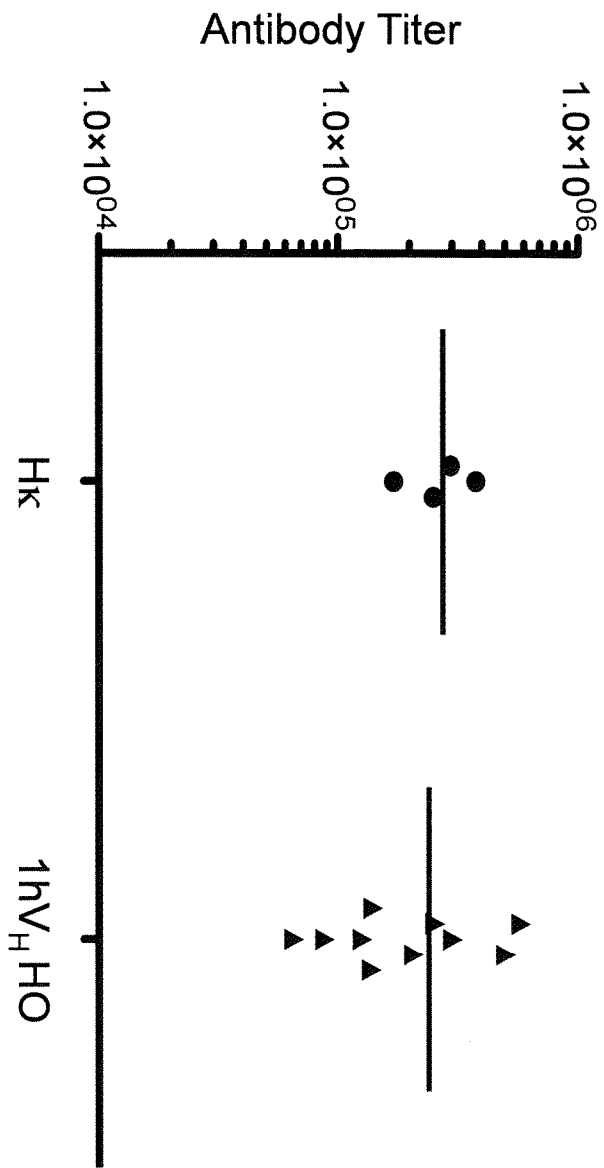


FIG. 19

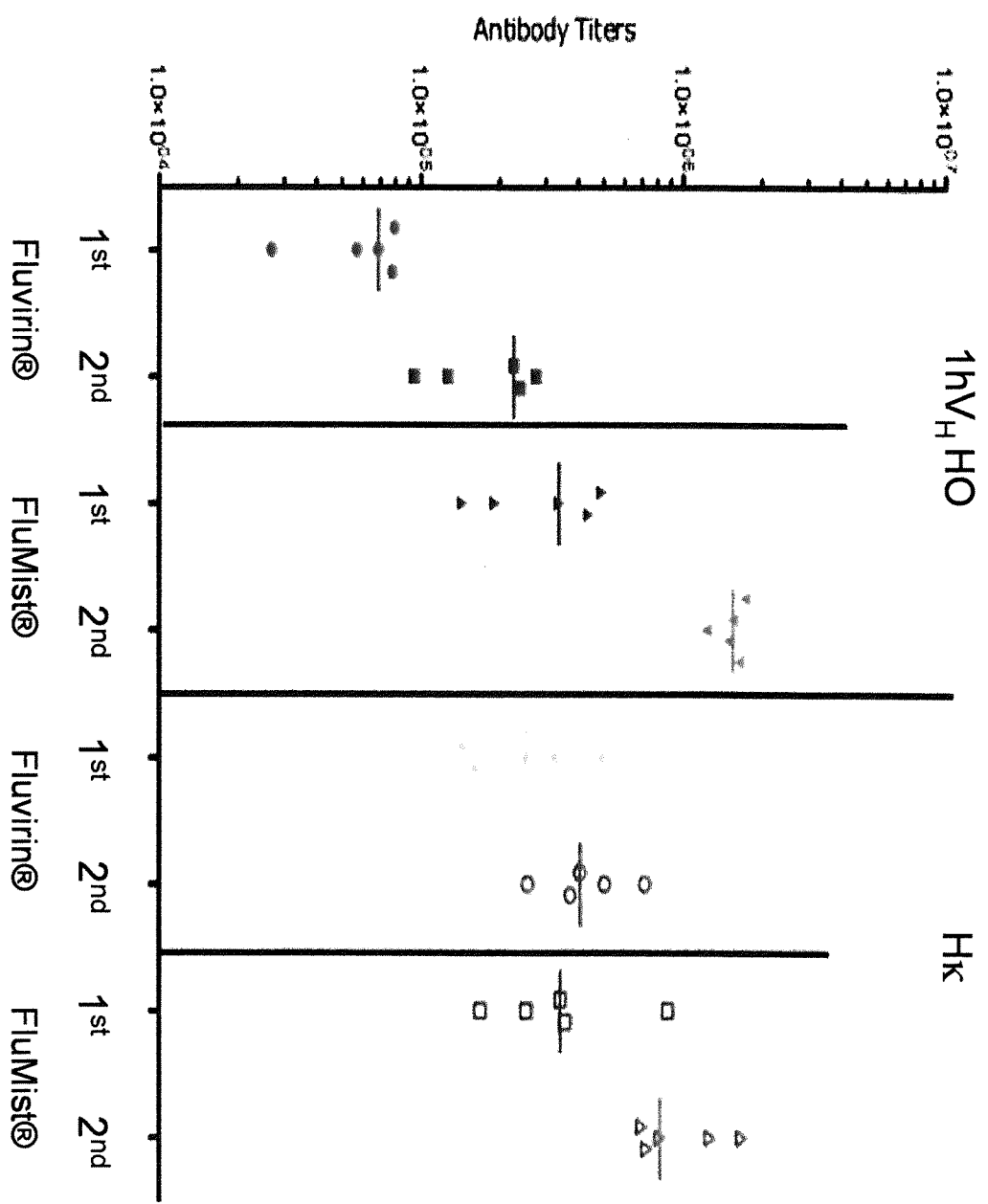


FIG. 20

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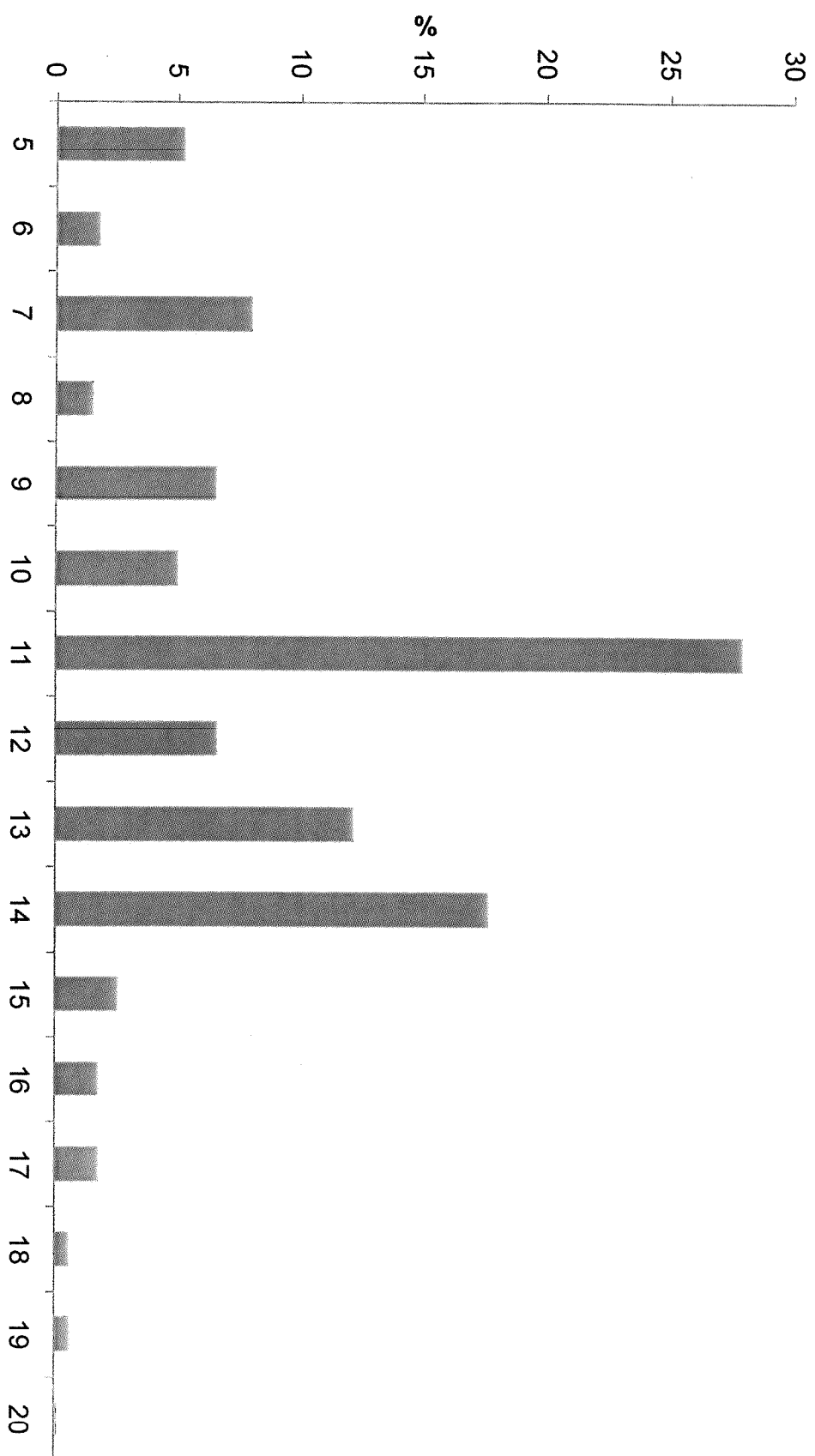


FIG. 21

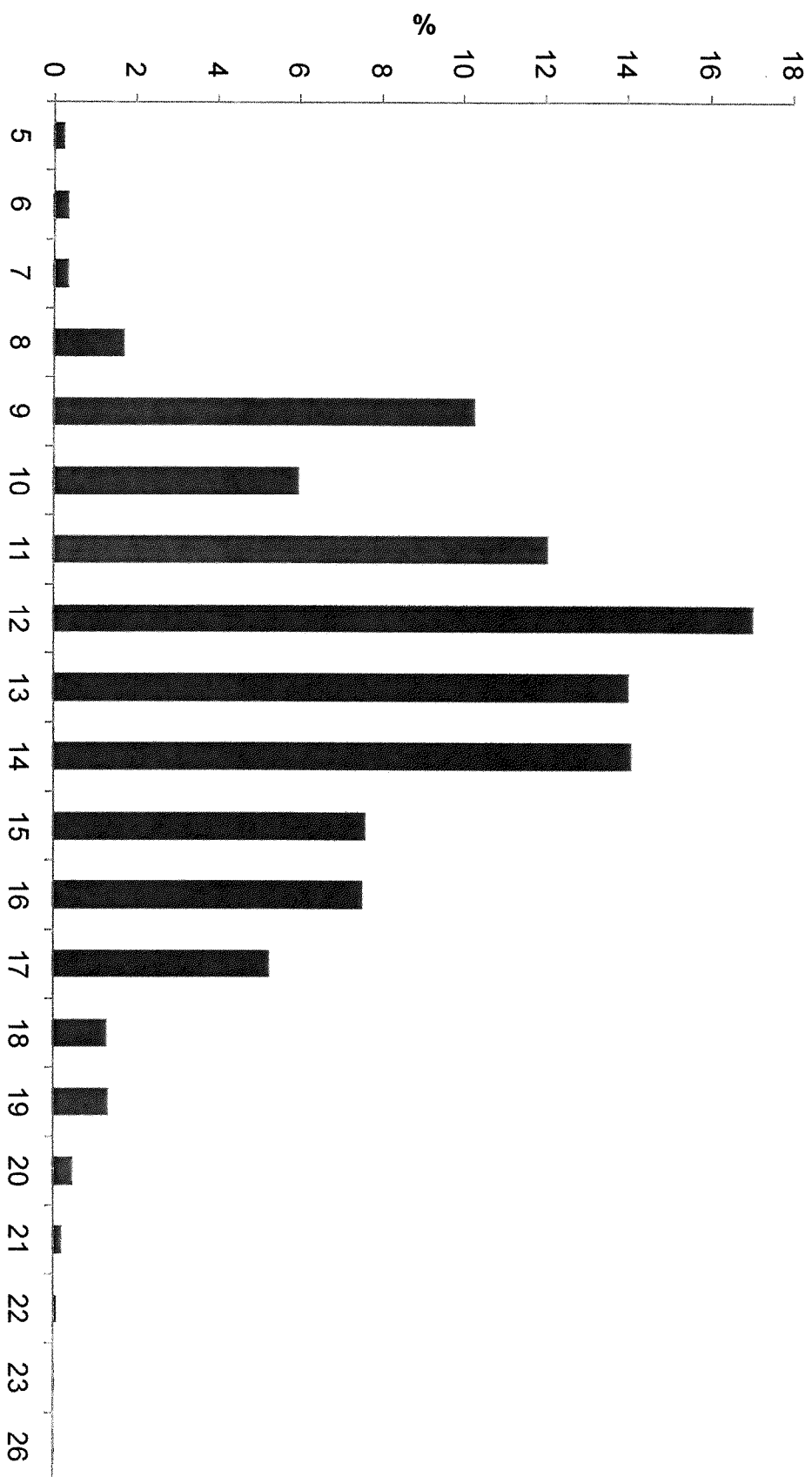


FIG. 22