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Korlátozott egér immunglobulin-nehézlánc

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(54) RESTRICTED IMMUNOGLOBULIN HEAVY CHAIN MICE

MÄUSE MIT EINGESCHRÄNKTEN SCHWEREN IMMUNGLOBULINKETTEN

SOURIS À CHAÎNE LOURDE D'IMMUNOGLOBULINE LIMITÉE

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Description

FIELD

- 5 **[0001]** Non-human animals that are genetically engineered at an immunoglobulin heavy chain variable (V) region locus (or in a transgene) to make antibodies from a restricted number of immunoglobulin heavy chain variable (V_H) segments (or a single V_H segment) and/or variants thereof. Non-human animals that have a human heavy chain variable domain derived from a single immunoglobulin heavy chain variable gene segment, e.g., human immunoglobulin V_H1-69 gene segment or human V_H1-2 gene segment. Methods for making antibody sequences in non-human animals that are
10 useful for binding pathogens, including human pathogens.

BACKGROUND

- 15 **[0002]** Non-human animals, e.g., mice, have been genetically engineered to be useful tools in methods for making antibody sequences for use in antibody-based human therapeutics. Mice with humanized variable region loci (e.g., V_H , D_H , and J_H genes, and V_L and J_L genes) are used to generate cognate heavy and light chain variable domains for use in antibody therapeutics. Other mice are available that generate fully human antibodies with cognate heavy and light chains.

- 20 **[0003]** Human antibody therapeutics are engineered based on desired characteristics with respect to certain pre-selected antigens. Humanized mice are immunized with the pre-selected antigens, and the immunized mice are used to generate antibody populations from which to identify high-affinity cognate heavy and light variable domains with desired binding characteristics. Some humanized mice, such as those having a humanization of just variable regions at endogenous mouse loci, generate populations of B cells that are similar in character and number to wild-type mouse B cell populations. As a result, an extremely large and diverse population of B cells is available in these mice from which
25 to screen antibodies, reflecting a large number of different immunoglobulin rearrangements, to identify heavy and light variable domains with the most desirable characteristics.

- [0004]** But not all antigens provoke an immune response that exhibits a very large number of rearrangements from a wide selection of variable (V) segments. That is, the human humoral immune response to certain antigens is apparently restricted. The restriction is reflected in clonal selection of B cells that express only certain V segments that bind that
30 particular antigen with sufficiently high affinity and specificity. Some such antigens are clinically significant, i.e., a number are well-known human pathogens. A presumption arises that the V segment expressed in the human immune response is a V segment that, in combination with a human D and a human J segment, is more likely to generate a useful high affinity antibody than a randomly selected V segment that has not been observed in a human antibody response to that antigen.

- 35 **[0005]** It is hypothesized that natural selection, over millennia, has selected the most efficient foundation or base from which to design a most effective weapon for neutralizing human pathogens—a clonally selected V segment. There is a need in the art for more and superior antibodies that bind and/or neutralize antigens such as the pathogens discussed above. There is a need to more rapidly generate useful sequences from selected V segments, including polymorphic and/or somatically mutated selected V segments and to more rapidly generate useful populations of B cells having
40 rearrangements of the V segments with various D and J segments, including somatically mutated versions thereof, and in particular rearrangements with unique and useful CDR3s. There is a need for biological systems, e.g., non-human animals (such as, e.g., mice, rats, rabbits, etc.) that can generate therapeutically useful antibody variable region sequences from pre-selected V segments in increased number and diversity than, e.g., can be achieved in existing modified animals. There is a need for biological systems engineered to have a committed humoral immune system for clonally
45 selecting antibody variable sequences derived from restricted, pre-selected V segments, including but not limited to cognate human heavy and light chain variable domains, useful in the manufacture of human antibody-based therapeutics against selected antigens, including certain human pathogens.

- [0006]** There is a need in the art for therapeutic antibodies that are capable of neutralizing viral antigens, e.g., HIV and HCV, including antigen-specific antibodies containing heavy chains derived from a single human variable segment,
50 and for a system that produces a diverse source of antibodies from which to select therapeutic antibody sequences. There is also a need for further methods and non-human animals for making useful antibodies, including antibodies that comprise a repertoire of heavy chains derived from a single human V_H segment and having a diverse set of CDR sequences, and including such heavy chains that express with cognate human light chain variable domains. Methods are needed for selecting CDRs for immunoglobulin-based binding proteins that provide an enhanced diversity of binding
55 proteins from which to choose, and enhanced diversity of immunoglobulin variable domains, including compositions and methods for generating somatically mutated and clonally selected immunoglobulin variable domains for use, e.g., in making human therapeutics.

SUMMARY

[0007]

In a first aspect, the invention provides a mouse whose endogenous immunoglobulin heavy chain locus is restricted in that it comprises a single human V_H gene segment, one or more human D_H gene segments, and one or more human J_H gene segments and which does not comprise a functional endogenous immunoglobulin heavy chain variable region locus; the mouse further comprising one or more human immunoglobulin V_L gene segments operably linked to one or more human J_L gene segments, wherein the single human V_H gene segment, one or more human D_H gene segments, and one or more J_H gene segments are operably linked to a non-human immunoglobulin heavy chain constant region gene, wherein the single human V_H gene segment is V_H1-69 or a polymorphic variant thereof. In a second aspect, the invention provides a cell or tissue derived from the mouse of the first aspect of the invention. In a third aspect, the invention provides a method of making a nucleic acid sequence encoding a human V_H domain comprising the steps of: (a) immunizing a mouse of the first aspect of the invention with an antigen of interest; (b) allowing said mouse to mount an immune response to the antigen of interest; and (c) obtaining an immunoglobulin V_H region nucleic acid sequence encoding a human V_H domain from said mouse. In a fourth aspect, the invention provides the use of a mouse according to the first aspect of the invention in a method of producing a nucleic acid sequence encoding a human heavy chain variable domain.

[0008] Genetically modified immunoglobulin loci are described that comprise a restricted number of different heavy chain variable region gene segments (*i.e.*, V genes, V_H genes, V_H gene segments, or V gene segments), *e.g.*, no more than one, two, or three different V genes; or no more than one V gene segment family member present, *e.g.*, in a single copy or in multiple copies and/or comprising one or more polymorphisms.

[0009] Loci are described that are capable of rearranging and forming a gene encoding a heavy chain variable domain that is derived from a V_H gene repertoire that is restricted, *e.g.*, that is a single V_H gene segment or selected from a plurality of polymorphic variants of the single V_H gene segment. Modified immunoglobulin loci include loci that comprise human immunoglobulin sequences are described, *e.g.*, a human V segment operably linked to a human or (or human/non-human chimeric) non-human immunoglobulin constant sequence (and in operable linkage with, *e.g.*, a D and/or a J segment). Modified loci that comprise multiple copies of a single V_H gene segment, including wherein one or more of the copies comprises a polymorphic variant, are described. Modified loci that comprise multiple copies of a single V_H segment, operably linked with one or more D segments and one or more J segments, operably linked to a non-human immunoglobulin constant sequence, *e.g.*, a mouse or rat sequence, are described. Non-human animals comprising such humanized loci are also described.

[0010] Non-human animals are described that have a reduced immunoglobulin heavy chain variable gene segment complexity (*i.e.*, a limited number of heavy chain variable gene segments, or a limited heavy chain variable gene repertoire), wherein the reduced immunoglobulin heavy chain variable gene segment complexity is characterized by the presence of no more than one or no more than two heavy chain variable gene segments, and wherein the heavy chain variable genes present are operably linked to a human or non-human constant region sequence.

[0011] Non-human animals are described that have a reduced immunoglobulin heavy chain variable gene segment complexity (*e.g.*, a single V_H gene segment, or a limited number of V_H gene segments that are polymorphic variants of a single V_H gene segment), wherein the reduced immunoglobulin heavy chain variable gene segment complexity is characterized by the presence of a single V_H gene segment or a plurality of V_H gene segments that are polymorphic forms of a single V_H gene segment (*e.g.*, V_H gene segments associated with high copy number and/or polymorphism in humans), and wherein the heavy chain variable genes present are operably linked to a human or non-human constant region sequence. The heavy chain variable genes present may be operably linked to one or more D and/or one or more J gene segments in the germline of the non-human animal.

[0012] Non-human animals are described that comprise an immunoglobulin heavy chain variable locus (*e.g.*, on a transgene or as an insertion or replacement at an endogenous non-human animal heavy chain variable locus) that comprises a single V_H segment operably linked to a D and/or J gene segment. The single V_H gene segment may be operably linked to one or more D and/or one or more J gene segments at the endogenous immunoglobulin heavy chain variable gene locus of the non-human animal.

[0013] Non-human animals are described that are modified at their immunoglobulin heavy chain variable region loci to delete all or substantially all (*e.g.*, all functional segments, or nearly all functional segments) endogenous immunoglobulin V_H segments and that comprise a human V_H1-69 segment (or a human V_H1-2 segment) operably linked to a D and J segment or a J segment at the endogenous immunoglobulin heavy chain variable region locus of the non-human animal.

[0014] Non-human animals are also described that are modified at their immunoglobulin heavy chain variable region loci to render the endogenous variable region loci incapable of rearranging to form a functional heavy chain comprising endogenous variable region gene segments; wherein the non-human animals comprise a single human variable gene

segment (a human V_H1-2 or a human V_H1-69 gene segment) operably linked to a D and a J segment or a J segment at the endogenous immunoglobulin heavy chain variable region locus of the non-human animal.

[0015] Non-human animals are described that comprise a restricted number (e.g., no more than one, or no more than two) of heavy chain gene segments operably linked to a human or non-human constant region sequence. In one case, the no more than one or no more than two heavy chain gene segments linked to the constant region sequence are on a transgene, e.g., are at a position other than an endogenous heavy chain locus.

[0016] Methods are described for making human immunoglobulin sequences in non-human animals. In various cases, the human immunoglobulin sequences are derived from a repertoire of immunoglobulin V sequences that consist essentially of a single human V segment, e.g., V_H1-69 or V_H1-2 , and one or more D and J segments or one or more J segments. Methods for making human immunoglobulin sequences in non-human animals, tissues, and cells are described, wherein the human immunoglobulin sequences bind a pathogen.

[0017] Methods are described for making mice characterized by a restricted immunoglobulin heavy chain locus, wherein the restriction is with respect to the number of immunoglobulin V_H gene segments. In various cases, the restriction is to one or no more than two, or a single V_H gene family member (e.g., one or more V_H alleles, variants, or polymorphic variants thereof). In various cases, the heavy chain locus further comprises one or more D_H gene segments and one or more J_H gene segments. In various cases, the V_H , D_H and J_H gene segments are human. In various cases, the V_H , D_H and J_H gene segments are operably linked to a non-human constant region (e.g., an IgM and/or an IgG). In various cases, the constant region is a mouse or rat constant region.

[0018] In one case, a method for making a mouse having a restricted immunoglobulin heavy chain locus is described, comprising introducing a nucleic acid construct as described herein into a mouse embryonic stem (ES) cell, and isolating or identifying a mouse ES cell that comprises the nucleic acid construct.

[0019] In one case, the nucleic acid construct comprises a single human V_H gene segment, one or more human D_H gene segments, and one or more human J_H gene segments. In one case, the nucleic acid construct comprises one or more site-specific recombination sites (e.g., a loxP or a Frt site).

[0020] In one case, a mouse made using a targeting vector, nucleic acid sequence, or cell as described herein is described. In various cases, the targeting vector, nucleic acid sequence or cell comprises a DNA sequence that contains a single human V_H gene segment (or polymorphic variants thereof), one or more human D_H gene segments, and one or more human J_H gene segments operably linked to a non-human constant gene.

[0021] In one case, a method for making a mouse comprising a restricted immunoglobulin heavy chain locus is described, comprising replacing a mouse immunoglobulin heavy chain locus with a human genomic sequence comprising a single human V_H gene segment (or polymorphic variants thereof), one or more human D_H gene segments, and one or more human J_H gene segments, wherein the human V_H , D_H and J_H gene segments are capable of rearranging to form a chimeric heavy chain that contains a human variable domain operably linked to a non-human constant region. In one case, the non-human constant region is a mouse or rat constant region.

[0022] In various cases, the non-human animals are rodents. In various cases, the rodents are mice and/or rats.

[0023] In one case, a modified immunoglobulin heavy chain locus is described that comprises a heavy chain V segment repertoire that is restricted with respect to the identity of the V segment, and that comprises one or more D segments and one or more J segments, or one or more J segments. In one case, the heavy chain V segment is a human segment. In one case, the one or more D segments are human D segments. In one case, the one or more J segments are human J segments. In one case, the one or more D segments and one or more J segments are human D and human J segments.

[0024] In one case, the modified locus is a non-human locus. In one case, the non-human locus is modified with at least one human immunoglobulin sequence.

[0025] In one case, the restriction is to one V segment family member. In one case, the one V segment family member is present in two or more copies. In one case, the one V segment family member is present as two or more variants (e.g., two or more polymorphic forms of the V segment family member). In one case, the one V segment is a human V segment family member. In one case, the one V segment family member is present in a number of variants as is observed in the human population with respect to that variant. In one case, the V segment family member is selected from Table 1. In one case, the V segment family member is present in a number of variants as shown, for each V segment, in a number of alleles from 1 allele to the number of alleles shown in the right column of Table 1.

[0026] In one case, the restriction is to a human V_H1-69 gene segment. In one case, the human V_H1-69 gene segment is present in two or more copies. In one case, the human V_H1-69 gene segment is present as two or more variants (e.g., two or more polymorphic forms the human V_H1-69 gene). In one case, the human V_H1-69 gene segment is present in a number of variants as is observed in the human population with respect to the human V_H1-69 gene segment. In one case, the human V_H1-69 gene segment is selected from Table 2. In one case, the human V_H1-69 gene segment is present in a number of variants as shown, for each V_H1-69 gene segment, in a number of alleles from one allele to the number of alleles shown in Table 2.

[0027] In one case, the restriction is to a human V_H1-2 gene segment. In one case, the human V_H1-2 gene segment is present in two or more copies. In one case, the human V_H1-2 gene segment is present as two or more variants (e.g.,

two or more polymorphic forms the human V_H1-2 gene). In one case, the human V_H1-2 gene segment is present in a number of variants as is observed in the human population with respect to the human V_H1-2 gene segment. In one case, the human V_H1-2 gene segment is selected from Table 3. In one case, the human V_H1-2 gene segment is present in a number of variants as shown, for each V_H1-2 gene segment, in a number of alleles from one allele to the number of alleles shown in Table 3.

[0028] In one case, a heavy chain immunoglobulin locus is described that comprises a single functional human V segment. In one case, the single functional human V segment is selected from a V_H1-2 , V_H1-3 , V_H1-8 , V_H1-18 , V_H1-24 , V_H1-45 , V_H1-46 , V_H1-58 , V_H1-69 , V_H2-5 , V_H2-26 , V_H2-70 , V_H3-7 , V_H3-9 , V_H3-11 , V_H3-13 , V_H3-15 , V_H3-16 , V_H3-20 , V_H3-21 , V_H3-23 , V_H3-30 , $V_H3-30-3$, $V_H3-30-5$, V_H3-33 , V_H3-35 , V_H3-38 , V_H3-43 , V_H3-48 , V_H3-49 , V_H3-53 , V_H3-64 , V_H3-66 , V_H3-72 , V_H3-73 , V_H3-74 , V_H4-4 , V_H4-28 , $V_H4-30-1$, $V_H4-30-2$, $V_H4-30-4$, V_H4-31 , V_H4-34 , V_H4-39 , V_H4-59 , V_H4-61 , V_H5-51 , V_H6-1 , V_H7-4-1 , and a V_H7-81 segment. In one case, the single functional human V segment is a V_H1-69 segment; in a specific case, the single functional human V segment is present in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13 polymorphic forms found in the human population. In one case, the single functional human V segment is a V_H1-2 segment; in a specific case, the single functional human V segment is present in 1, 2, 3, 4, or 5 polymorphic forms found in the human population.

[0029] In one case, the heavy chain immunoglobulin locus is a modified locus of a non-human animal. In one case, the modified non-human immunoglobulin heavy chain locus is present in the non-human animal at a position in the genome in which the corresponding unmodified non-human locus is found in the wild-type non-human animal. In one case, the modified non-human immunoglobulin heavy chain locus is present on a transgene in a non-human animal.

[0030] In one case, the single functional human V gene segment is a V_H1-69 gene segment. In one case, the V_H1-69 gene segment comprises SEQ ID NO: 34. In one case, the V_H1-69 gene segment is derived from SEQ ID NO: 34. In one case, the V_H1-69 gene segment is at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% identical to SEQ ID NO: 34.

[0031] In one case, the single functional human V gene segment is encoded by the nucleotide sequence of SEQ ID NO: 34.

[0032] In one case, the single functional human V gene segment is a V_H1-2 gene segment. In one case, the V_H1-2 gene segment comprises SEQ ID NO: 60. In one case, the V_H1-2 gene segment is derived from SEQ ID NO: 60. In one case, the V_H1-2 gene segment is at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% identical to SEQ ID NO: 60.

[0033] In one case, the single functional human V gene segment is encoded by the nucleotide sequence of SEQ ID NO: 60.

[0034] In one case, the single functional human V segment is operably linked to one or more D segments and one or more J segments, or one or more J segments. In one case, the V segment and one or more D and/or J segments are operably linked to an immunoglobulin heavy chain constant region sequence. In one case the immunoglobulin heavy chain constant region sequence is selected from a C_H1 , a hinge, a C_H2 , a C_H3 sequence, and a combination thereof. In one case, the C_H1 , hinge, C_H2 , C_H3 , or combination thereof are each non-human endogenous constant sequences. In one case, at least one of the C_H1 , hinge, C_H2 , C_H3 , or combination thereof is a human sequence. In a specific case, the C_H1 and/or hinge are human sequences.

[0035] In one case, a modified endogenous non-human immunoglobulin heavy chain locus is described, comprising a replacement of all functional V gene segments with a single human V gene segment (or a single human V gene segment present in multiple polymorphic forms or copy number), wherein the non-human immunoglobulin heavy chain locus is incapable of rearrangement to form a heavy chain variable gene that is derived from a V gene segment other than the single human V gene segment (or one of the polymorphic forms or copies).

[0036] In one case, the single human V gene segment is V_H1-69 . In one case, the single human V gene segment is V_H1-2 .

[0037] In one case, the locus comprises at least one human or non-human D_H gene segment, and one human or non-human J_H gene segment. In a specific case, the locus comprises a human D_H gene segment and a human J_H gene segment. In a specific case, the locus comprises a human J_H gene segment. In another specific case, the locus comprises a human V_H1-69 gene segment (present as a single copy or multiple copies of different polymorphic variants), all functional human D_H gene segments, and all functional human J_H gene segments. In another specific case, the locus comprises a human V_H1-2 gene segment (present as a single copy or multiple copies of different polymorphic forms), all functional human D_H gene segments, and all functional human J_H gene segments. In one case, the human V, D, and J gene segments (or V and J gene segments) are operably linked to a mouse constant region gene at an endogenous mouse heavy chain locus. In a specific case, the mouse heavy chain locus comprises a wild-type repertoire of mouse immunoglobulin constant region sequences.

[0038] In one case, a genetically modified non-human animal is described, wherein the only functional immunoglobulin heavy chain V gene segment of the non-human animal is selected from a human V_H1-2 , V_H1-3 , V_H1-8 , V_H1-18 , V_H1-24 , V_H1-45 , V_H1-46 , V_H1-58 , V_H1-69 , V_H2-5 , V_H2-26 , V_H2-70 , V_H3-7 , V_H3-9 , V_H3-11 , V_H3-13 , V_H3-15 , V_H3-16 , V_H3-20 ,

V_H3-21, V_H3-23, V_H3-30, V_H3-30-3, V_H3-30-5, V_H3-33, V_H3-35, V_H3-38, V_H3-43, V_H3-48, V_H3-49, V_H3-53, V_H3-64, V_H3-66, V_H3-72, V_H3-73, V_H3-74, V_H4-4, V_H4-28, V_H4-30-1, V_H4-30-2, V_H4-30-4, V_H4-31, V_H4-34, V_H4-39, V_H4-59, V_H4-61, V_H5-51, V_H6-1, V_H7-4-1, and V_H7-81 gene segment. In one case, the heavy chain V gene segment is a human V_H1-69 gene segment. In one case, the heavy chain V gene segment is a human V_H1-2 gene segment.

[0039] In one case, a genetically modified non-human animal is described, wherein the non-human animal comprises a single functional human V_H gene segment (present as a single copy or multiple copies of different polymorphic forms), and wherein the non-human animal is substantially incapable of forming a rearranged immunoglobulin heavy chain variable domain gene that lacks the single functional human V_H gene segment (or one of the polymorphic forms or copies).

[0040] In one case, a genetically modified non-human animal is described, wherein the only immunoglobulin heavy chain variable region expressed in the non-human animal is derived from one of a human segment selected from a human V_H1-2, V_H1-3, V_H1-8, V_H1-18, V_H1-24, V_H1-45, V_H1-46, V_H1-58, V_H1-69, V_H2-5, V_H2-26, V_H2-70, V_H3-7, V_H3-9, V_H3-11, V_H3-13, V_H3-15, V_H3-16, V_H3-20, V_H3-21, V_H3-23, V_H3-30, V_H3-30-3, V_H3-30-5, V_H3-33, V_H3-35, V_H3-38, V_H3-43, V_H3-48, V_H3-49, V_H3-53, V_H3-64, V_H3-66, V_H3-72, V_H3-73, V_H3-74, V_H4-4, V_H4-28, V_H4-30-1, V_H4-30-2, V_H4-30-4, V_H4-31, V_H4-34, V_H4-39, V_H4-59, V_H4-61, V_H5-51, V_H6-1, V_H7-4-1, and V_H7-81 gene segment. In one case, the human segment is a V_H1-69 segment. In one case, the human segment is a V_H1-2 segment. In one case, the only immunoglobulin heavy chain variable region expressed by the mouse is derived from a single V segment family member, and in one case the only immunoglobulin heavy chain variable region is derived from a polymorphic variant of the single V segment family member.

[0041] In one case, a non-human animal comprising a restricted immunoglobulin heavy chain V gene segment repertoire is described, wherein the non-human animal further comprises one or more human immunoglobulin κ light chain variable segments (V_κ). In one case, the one or more V_κ segments are operably linked to one or more human J segments. In a specific case, the J segments are human J_κ segments. In another specific case, the non-human animal does not express an immunoglobulin λ light chain. In another specific case, the non-human animal does not comprise a functional human or functional endogenous immunoglobulin λ light chain variable locus.

[0042] In one case, the non-human animal is a rodent. In one case, the rodent is a mouse.

[0043] In one case, the non-human animal comprises a replacement at the endogenous non-human immunoglobulin V_κ locus of all or substantially all functional endogenous V_κ segments with one or more functional human V_κ segments. In a further specific case, the replacement is with all or substantially all functional human immunoglobulin V_κ segments.

[0044] In one case, the non-human animal comprises a replacement at the endogenous non-human immunoglobulin V_κ locus of all or substantially all functional endogenous V_κ gene segments with human V_κ gene segments selected from V_κ4-1, V_κ5-2, V_κ7-3, V_κ2-4, V_κ1-5, V_κ1-6, V_κ3-7, V_κ1-8, V_κ1-9, V_κ2-10, V_κ3-11, V_κ1-12, V_κ1-13, V_κ2-14, V_κ3-15, V_κ1-16, V_κ1-17, V_κ2-18, V_κ2-19, V_κ3-20, V_κ6-21, V_κ1-22, V_κ1-23, V_κ2-24, V_κV_κ2-26, V_κ1-27, V_κ2-28, V_κ2-29, V_κ2-30, V_κ3-31, V_κ1-32, V_κ1-33, V_κ3-34, V_κ1-35, V_κ2-36, V_κ1-37, V_κ2-38, V_κ1-39, V_κ2-40, and a combination thereof.

[0045] In one case, the non-human animal comprises a replacement at the endogenous non-human immunoglobulin J_κ locus of all or substantially all functional endogenous non-human immunoglobulin J_κ segments with one or more functional human immunoglobulin J_κ segments. In a further specific case, the replacement is with all or substantially all functional human immunoglobulin J_κ segments.

[0046] In one case, the non-human animal comprises a replacement at the endogenous non-human immunoglobulin J_κ locus of all or substantially all functional endogenous non-human immunoglobulin J_κ gene segments with human J_κ gene segments selected from J_κ1, J_κ2, J_κ3, J_κ4, J_κ5, and a combination thereof.

[0047] In a specific case, the non-human animal comprises an immunoglobulin heavy chain variable region locus that comprises a repertoire of V segments consisting essentially of a single V segment and/or polymorphic variants thereof. In one case, the single immunoglobulin heavy chain V segment is a human V_H1-69 segment, and the non-human animal further comprises a replacement of all functional non-human D_H segments with all functional human D_H segments, and further comprises a replacement of all functional non-human J_H segments with all functional human J_H segments, and wherein the immunoglobulin heavy chain variable region locus is operably linked to a human or non-human constant region gene sequence. In a specific case, the constant region gene sequence is an endogenous non-human constant region gene sequence. In a specific case, the non-human animal rearranges segments at the non-human immunoglobulin heavy chain locus to form a gene encoding heavy chain variable region comprising a human V_H1-69 sequence, a human D_H sequence, a human J_H sequence, and a mouse constant region sequence.

[0048] In a specific case, the non-human animal comprises an immunoglobulin heavy chain variable region locus that comprises a repertoire of V segments consisting essentially of a single V segment and/or polymorphic variants thereof. In one case, the single immunoglobulin heavy chain V segment is a human V_H1-2 segment, and the non-human animal further comprises a replacement of all functional non-human D_H segments with all functional human D_H segments, and further comprises a replacement of all functional non-human J_H segments with all functional human J_H segments, and wherein the immunoglobulin heavy chain variable region locus is operably linked to a human or non-human constant region gene sequence. In a specific case, the constant region gene sequence is an endogenous non-human constant region gene sequence. In a specific case, the non-human animal rearranges segments at the non-human immunoglobulin

heavy chain locus to form a gene encoding heavy chain variable region comprising a human V_H1-2 sequence, a human D_H sequence, a human J_H sequence, and a mouse constant region sequence.

[0049] In one case, a B cell is described that comprises the rearranged gene. In a specific case, the B cell is from a mouse as described that has been immunized with an antigen of interest, and the B cell encodes an antibody that specifically binds the antigen of interest. In one case, the antigen of interest is a pathogen. In a specific case, the pathogen is selected from an influenza virus, a hepatitis virus (e.g., hepatitis B or hepatitis C virus), and a human immunodeficiency virus. In a specific case, the B cell encodes a somatically mutated, high affinity (e.g., about 10^{-9} K_D or lower) antibody comprising a human light chain variable region (e.g., a human κ light chain variable region) that specifically binds the antigen of interest.

[0050] In one case, a non-human animal comprising a restricted immunoglobulin heavy chain V segment repertoire is described, wherein the non-human animal comprises one or more human λ light chain variable ($V\lambda$) segments. In one case, the one or more human $V\lambda$ segments are operably linked to one or more human J segments. In a specific case, the J segments are human $J\lambda$ segments. In another specific case, the non-human animal does not express a κ light chain. In another specific case, the non-human animal does not comprise a functional human or non-human κ light chain variable locus.

[0051] In one case, the non-human animal comprises a replacement of all or substantially all functional non-human immunoglobulin $V\lambda$ segments with one or more functional human immunoglobulin $V\lambda$ segments. In a further specific case, the replacement is with all or substantially all functional human immunoglobulin $V\lambda$ segments.

[0052] In one case, the non-human animal comprises a replacement of all or substantially all functional non-human $V\lambda$ segments with a fragment of cluster A of the human λ light chain locus. In a specific case, the fragment of cluster A of the human λ light chain locus comprises human $V\lambda$ gene segments $V\lambda3-27$ through $V\lambda3-1$.

[0053] In one case, the non-human animal comprises a replacement of all or substantially all functional non-human $V\lambda$ segments with a fragment of cluster B of the human λ light chain locus. In a specific case, the fragment of cluster B of the human λ light chain locus comprises human $V\lambda$ gene segments $V\lambda5-52$ through $V\lambda1-40$.

[0054] In one case, the non-human animal comprises a replacement of all or substantially all functional non-human $V\lambda$ segments with a fragment of cluster A and a fragment of cluster B of the human λ light chain locus, wherein as a result of the replacement comprise human $V\lambda$ gene segments $V\lambda5-52$ through $V\lambda3-1$.

[0055] In one case, the non-human animal comprises a replacement of all or substantially all functional non-human $V\lambda$ segments with at least 12 human $V\lambda$ gene segments, at least 28 human $V\lambda$ gene segments, or at least 40 human $V\lambda$ gene segments.

[0056] In one case, the non-human animal comprises a replacement of all or substantially all functional non-human immunoglobulin $J\lambda$ gene segments with one or more functional human immunoglobulin $J\lambda$ gene segments. In a further specific case, the replacement is with all or substantially all functional human immunoglobulin $J\lambda$ gene segments. In various cases, the functional human $J\lambda$ gene segments include $J\lambda1$, $J\lambda2$, $J\lambda3$ and $J\lambda7$.

[0057] In a specific case, the non-human animal comprises an immunoglobulin heavy chain variable (V_H) region locus that comprises only a single V_H segment, wherein the single V_H segment is a human V_H1-69 segment or a human V_H1-2 segment, and further comprises a replacement of all functional non-human D_H segments with all functional human D_H segments, and further comprises a replacement of all functional non-human J_H segments with all functional human J_H segments, and wherein the V_H region locus is operably linked to a human or non-human constant region gene sequence. In a specific case, the constant region gene sequence is a non-human constant region gene sequence, e.g., an endogenous non-human constant gene sequence. In a specific case, the non-human animal rearranges segments at the non-human immunoglobulin heavy chain locus to form a gene encoding an immunoglobulin heavy chain variable region comprising a human V_H1-69 sequence (or a human V_H1-2 sequence), a human D_H sequence, a human J_H sequence, and an endogenous non-human constant region sequence.

[0058] In one case, a B cell is described that comprises the rearranged gene. In a specific case, the B cell is from a non-human animal as described that has been immunized with an antigen of interest, and the B cell encodes an antibody that specifically binds the antigen of interest. In one case, the antigen is a human protein selected from a ligand, a cell surface receptor and an intracellular protein. In one case, the antigen of interest is a pathogen. In a specific case, the pathogen is selected from an influenza virus, a hepatitis virus (e.g., hepatitis B or hepatitis C virus), and a human immunodeficiency virus. In a specific case, the B cell encodes a somatically mutated, high affinity (e.g., about 10^{-9} K_D or lower) antibody comprising a human light chain variable region (e.g., a human λ light chain variable region) that specifically binds the antigen of interest.

[0059] In one case, a non-human animal comprising a restricted immunoglobulin V_H segment repertoire is described, wherein the non-human animal comprises a human V_H1-69 segment (or a human V_H1-2 segment) on a transgene, wherein the human V_H1-69 segment is operably linked on the transgene to a human or non-human D_H segment, and/or a human or non-human J segment, and the transgene further comprises a human or non-human constant region gene, or a chimeric human/non-human constant region (e.g., a C_H1 , hinge, C_H2 , C_H3 or combination thereof wherein at least one sequence is non-human, e.g., selected from hinge, C_H2 , and C_H3 and/or hinge). In one case, the non-human animal

is a mouse or rat and the non-human D, J, and/or constant region gene is a mouse or rat gene or chimeric human/mouse or rat.

[0060] In one case, the non-human animal comprises a transgene that comprises an immunoglobulin light chain variable region locus that comprises one or more human immunoglobulin V λ gene segments and J λ gene segments, or one or more human immunoglobulin V κ gene segments and J κ gene segments, and a human immunoglobulin κ or λ light chain constant region gene, such that the transgene rearranges in the non-human animal to form a rearranged immunoglobulin κ or λ light chain gene. In various cases, the human V κ and J κ gene segments are those described herein. In various cases, the human V λ and J λ gene segments are those described herein.

[0061] In a specific case, the non-human animal comprises a transgene having an immunoglobulin heavy chain variable locus that comprises a single V segment that is a human V_H1-69 segment (or a human V_H1-2 segment), one or more human D segments, one or more human J segments, and a human constant gene operably linked to the heavy chain variable locus, such that the mouse expresses from the transgene a fully human antibody derived from the V_H1-69 segment (or the V_H1-2 segment). In one case, the non-human animal does not comprise a functional endogenous immunoglobulin heavy chain variable region locus. In a specific case, the non-human animal comprises a nonfunctional endogenous immunoglobulin heavy chain variable region locus that comprises a deletion of an endogenous non-human D_H and/or endogenous non-human J_H segment, such that the non-human animal is incapable of rearranging the endogenous immunoglobulin heavy chain variable region locus to form a rearranged non-human antibody gene. In a specific case, the non-human animal comprises a deletion of a switch sequence operably linked to an endogenous mouse heavy chain constant region. In a specific case, the switch sequence is a non-human (e.g., mouse) μ switch sequence. In another case, the non-human animal further comprises a lack of a functional endogenous light chain variable locus selected from an immunoglobulin κ locus and an immunoglobulin λ locus. In a specific case, the non-human animal comprises a deletion of a J κ and/or a J λ sequence, such that the non-human animal is incapable of rearranging an endogenous non-human immunoglobulin κ light chain and/or an endogenous non-human immunoglobulin λ light chain variable region to form a rearranged endogenous non-human immunoglobulin κ light chain and/or a rearranged endogenous non-human immunoglobulin λ light chain gene.

[0062] In one case, the non-human animal comprises a deletion of an endogenous non-human immunoglobulin κ light chain sequence that results in a functional knockout of the endogenous non-human immunoglobulin κ light chain. In one case, the non-human animal comprises a deletion of an endogenous non-human immunoglobulin λ light chain sequence that results in a functional knockout of the endogenous non-human immunoglobulin λ light chain.

[0063] In one case, the non-human animal comprises a functionally silenced endogenous immunoglobulin heavy chain variable gene locus, and comprises a restricted repertoire of human heavy chain variable gene segments (e.g., no more than one, or no more than two). In one case, the functional silencing comprises a modification of an endogenous non-human heavy chain variable gene locus selected from a deletion, an insertion, an inversion, and a combination thereof.

[0064] In one case, a rodent is described that comprises an immunoglobulin V_H repertoire derived from no more than one human V_H segment or one or more polymorphs thereof, from a D segment selected from a repertoire of one or more D segments, and from a J segment derived from a repertoire of one or more J segments. In one case, the rodent rearranges the human V_H segment, a human D segment, and a human J segment and forms a rearranged human heavy chain sequence that is operably linked to a human or a rodent constant region sequence. In one case, the human and/or rodent constant region sequence is selected from a C_H1, a hinge, a C_H2, a C_H3, and a combination thereof. In one case, the rodent expresses an immunoglobulin light chain that comprises a human variable domain, wherein the light chain is cognate with a human heavy chain domain derived from the rearranged human heavy chain sequence. In one case, the rodent does not express a polypeptide sequence selected from a non-human heavy chain variable domain, a non-human light chain variable domain, and a combination thereof.

[0065] In one case, the human V_H segment is present in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19 or more polymorphic variants, wherein each polymorphic variant is operably linked to a D and/or J segment such that each polymorphic variant is capable for rearranging and forming a rearranged heavy chain variable domain with any of the one or more D segments and any of the one or more J segments. In one case, the rodent is a mouse or a rat. In one case, the repertoire of D segments comprises two or more D segments. In one case, the repertoire of J segments comprises two or more J segments. In one case, the D and/or J segments are human segments.

[0066] In one case, a nucleic acid construct is described that comprises a sequence encoding a single human immunoglobulin V_H segment and/or polymorphic variants thereof and one or more D_H and one or more J sequences, wherein the construct comprises at least one homology arm homologous to a non-human immunoglobulin heavy chain variable locus, or a recombinase recognition site (e.g., a lox site). In one case, the V segment is a V_H1-69 segment or a V_H1-2 segment.

[0067] In one case, a nucleic acid construct is described; comprising a nucleic acid sequence encoding a single human immunoglobulin heavy chain V segment, wherein the single V_H segment is a V_H1-69 (or V_H1-2) segment. In one case, the construct comprises a site-specific recombinase recognition site. In one case, the construct comprises a first mouse homology arm upstream of the V_H1-69 (or V_H1-2) segment and a second mouse homology arm downstream of the

V_H1-69 (or V_H1-2) segment, and wherein the first mouse homology arm is homologous to a region of a mouse chromosome immediately upstream of a mouse immunoglobulin heavy chain variable region but not including a functional mouse immunoglobulin heavy chain variable segment. In one case, the construct comprises SEQ ID NO: 3. In one case, the construct comprises SEQ ID NO: 70.

[0068] In one case, the restricted single V_H segment is in a non-human animal, or the restricted V_H segment is at a non-human immunoglobulin heavy chain locus (e.g., *in situ* or in a transgene), and the non-human animal or non-human immunoglobulin heavy chain locus is selected from a mouse, rat, rabbit, pig, bovine (e.g., cow, bull, buffalo), deer, sheep, goat, chicken, cat, dog, ferret, primate (e.g., marmoset, rhesus monkey) locus or animal. In a specific case, the non-human animal or locus is a mouse or a rat locus.

[0069] In one case, a cell or tissue is described, wherein the cell or tissue is derived from a non-human animal as described herein, and comprises a restricted V_H segment repertoire. In one case, the V_H segment repertoire is restricted to a single V_H segment family member and/or polymorphic variants thereof. In a specific case, the single V_H segment is a human V_H1-69 segment or a human V_H1-2 segment. In one case, the cell or tissue is derived from spleen, lymph node or bone marrow of the non-human animal.

[0070] In one case, the cell is an ES cell. In one case, the cell is a B cell. In one case, the cell is a germ cell.

[0071] In one case, the tissue is selected from connective, muscle, nervous and epithelial tissue. In a specific case, the tissue is reproductive tissue.

[0072] In one case, the cell and/or tissue derived from a mouse as described herein are isolated for use in one or more *ex vivo* assays. In various cases, the one or more *ex vivo* assays include measurements of physical, thermal, electrical, mechanical or optical properties, a surgical procedure, measurements of interactions of different tissue types, the development of imaging techniques, or a combination thereof.

[0073] In one case, the non-human animal is a mouse.

[0074] In one case, a non-human embryo is described comprising a restricted heavy chain V_H segments as described herein. In one case, the embryo comprises an ES donor cell that comprises the restricted V_H segment, and host embryo cells.

[0075] In one case, the non-human animal is a mouse.

[0076] In one case, a non-human cell comprising a chromosome or fragment thereof of a non-human animal as described herein. In one case, the non-human cell comprises a nucleus of a non-human animal as described herein. In one case, the non-human cell comprises the chromosome or fragment thereof as the result of a nuclear transfer.

[0077] In one case, a nucleus derived from a non-human animal as described herein is described. In one case, the nucleus is from a diploid cell that is not a B cell.

[0078] In one case, a pluripotent, induced pluripotent, or totipotent cell derived from a non-human animal as described herein is described. In a specific case, the cell is a mouse embryonic stem (ES) cell.

[0079] In one case, a non-human induced pluripotent cell comprising a restricted V_H segment repertoire is described. In one case, the induced pluripotent cell is derived from a non-human animal as described herein.

[0080] In one case, a hybridoma or quadroma is described, derived from a cell of a non-human animal as described herein. In one case, the non-human animal is a mouse or rat.

[0081] In one case, a lymphocyte of a non-human animal as described herein is described. In one case, the lymphocyte is a B cell.

[0082] In one case, mouse cells and mouse embryos are described, including but not limited to ES cells, pluripotent cells, and induced pluripotent cells, that comprise genetic modifications as described herein. Cells that are XX and cells that are XY are described. Cells that comprise a nucleus containing a modification as described herein are also described, e.g., a modification introduced into a cell by pronuclear injection.

[0083] In one case, an antibody variable domain sequence made in a non-human animal as described herein is described.

[0084] In one case, a human therapeutic is described, comprising an antibody variable domain comprising a sequence derived from a non-human animal as described herein.

[0085] In one case, a method of obtaining an antibody variable region sequence from a non-human animal is described, wherein the antibody variable region sequence is derived from a human V_H1-69 segment or a V_H1-2 segment, wherein the method comprises (a) immunizing a non-human animal with an antigen of interest, wherein the non-human animal comprises a replacement at the endogenous immunoglobulin heavy chain locus of all or substantially all non-human variable segments with a single human variable segment, wherein the single human variable segment is a V_H1-69 segment or a V_H1-2 segment, and wherein the non-human animal is substantially incapable of forming a immunoglobulin heavy chain variable region sequence that is not derived from a human V_H1-69 segment or a V_H1-2 segment; (b) allowing the non-human animal to mount an immune response with respect to the antigen of interest; and, (c) identifying or isolating an immunoglobulin heavy chain variable region sequence of the non-human animal, wherein the antibody binds the antigen of interest.

[0086] In one case, the single human variable segment is a V_H1-69 segment.

[0087] In one case, the antibody variable region sequence is derived from SEQ ID NO: 34. In one case, the antibody variable region sequence is at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% identical to SEQ ID NO: 34. In one case, the antibody variable region sequence comprises SEQ ID NO: 34.

[0088] In one case, the single human variable segment is a V_H 1-2 segment.

[0089] In one case, the antibody variable region sequence is derived from SEQ ID NO: 60. In one case, the antibody variable region sequence is at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% identical to SEQ ID NO: 60. In one case, the antibody variable region sequence comprises SEQ ID NO: 60.

[0090] In one case, the immune response to the antigen is characterized by an antibody titer that is about 6×10^4 to about 5×10^5 times greater than two times background as determined in an ELISA assay. In a specific case, the antibody titer is about 1×10^5 to about 2×10^5 times greater than two times background as determined in an ELISA assay. In a specific case, the antibody titer is about 1.5×10^5 times greater than two times background as determined in an ELISA assay. In one case, the antigen is a human cell surface receptor.

[0091] In one case, a method for generating a repertoire of human antibody variable regions in a non-human animal is described, wherein the human heavy chain variable regions of the repertoire are derived from the same V_H gene family member and one of a plurality of D_H segments and one of a plurality of J_H segments, wherein the repertoire is characterized by having heavy chain immunoglobulin FR1 (framework 1), CDR1, FR2, CDR2, and FR3 sequences from a single V_H gene family member. In one case, the repertoire is further characterized by having a plurality of different CDR3 + FR4 sequences.

[0092] In one case, the single V_H gene family is selected from V_H family 1, 2, 3, 4, 5, 6, and 7. In a specific case, the single V_H gene family is V_H family 1. In one case, the single V_H gene family member is selected from V_H 1-2, V_H 1-69, V_H 2-26, V_H 2-70, and V_H 3-23. In a specific case, the single V_H gene family member is V_H 1-69. In a specific case, the single V_H gene family member is V_H 1-2.

[0093] In one case, the repertoire comprises heavy chain FR1, CDR1, FR2, CDR2 and FR3 sequences derived from a V_H 1-69 segment. In a specific case, the repertoire comprises heavy chain FR1, CDR1, FR2, CDR2 and FR3 sequences derived from SEQ ID NO: 35. In a specific case, the repertoire comprises heavy chain FR1, CDR1, FR2, CDR2 and FR3 sequences of SEQ ID NO: 35.

[0094] In one case, the repertoire comprises heavy chain FR1, CDR1, FR2, CDR2 and FR3 sequences derived from a V_H 1-2 segment. In a specific case, the repertoire comprises heavy chain FR1, CDR1, FR2, CDR2 and FR3 sequences derived from SEQ ID NO: 61. In a specific case, the repertoire comprises heavy chain FR1, CDR1, FR2, CDR2 and FR3 sequences of SEQ ID NO: 61.

[0095] In one case, a biological (*i.e.*, *in vivo*) system is described for generating a plurality of different human CDR3 sequences reflecting a plurality of rearrangements of a single human V_H gene segment with a plurality of human D and J segments, wherein the system generates human heavy chain variable domains characterized by having human FR1-CDR1-FR2-CDR2-FR3 sequences that are identical but for somatic hypermutations, wherein the heavy chain variable domains are characterized by being somatically hypermutated and derived from a single human V_H gene segment and a plurality of human D and J segments; wherein the system comprises a genetically modified non-human animal (*e.g.*, a rodent, *e.g.*, a mouse or rat) as described herein.

[0096] In one case, the single human V_H gene segment is selected from V_H 1-2, V_H 1-69, V_H 2-26, V_H 2-70, and V_H 3-23. In one case, the single human V_H gene segment is V_H 1-69. In one case, the single human V_H gene segment is V_H 1-2. In one case, the single human V_H gene segment is identified in Table 1. In one case, the single human V_H gene segment is identified in Table 2. In one case, the single human V_H gene segment is identified in Table 3.

[0097] In one case, an *in vivo* method for generating a plurality of heavy chain CDR sequences derived from rearrangements of a single human V_H gene segment with a plurality of human D and J segments is described, wherein the method generates human heavy chain variable domains characterized by having human FR1-CDR1-FR2-CDR2-FR3 sequences that are identical but for somatic hypermutations, wherein the heavy chain variable domains are characterized by being somatically hypermutated and derived from a single human V_H gene segment and a plurality of human D and J segments; wherein the system comprises a genetically modified non-human animal (*e.g.*, a rodent, *e.g.*, a mouse or rat) as described herein.

[0098] In one case, the method comprises exposing a non-human animal as described herein to an antigen of interest, allowing the non-human animal to develop an immune response to the antigen, wherein the immune response generates the plurality of heavy chain CDR sequences derived from rearrangements of the single human V_H gene segment with one of the human D and one of the human J segments, and identifying a set of heavy chain CDRs that bind the antigen. In one case, the method comprises isolating from the animal a nucleic acid sequence that encodes a human V_H domain that comprises the heavy chain CDRs.

[0099] In one case, the heavy chain CDR sequences are derived from a rearrangement of a human V_H 1-69 gene segment. In one case, the heavy chain CDR sequences are derived from a rearrangement of a human V_H 1-2 gene segment.

[0100] In one case, a method for generating a plurality of different CDR3 and FR4 sequences in a non-human animal

is described, comprising exposing a non-human animal that comprises an immunoglobulin heavy chain variable gene locus with a V_H segment repertoire restricted to a single V_H segment family member to an antigen of interest, allowing the non-human animal to develop an immune response to the antigen, wherein the immune response generates a B cell repertoire whose heavy chain variable domains are each derived from the single V_H segment family member and that comprise a plurality of different CDR3 and FR4 sequences.

[0101] In one case, the single V_H segment family member is human. In one case, the non-human animal is selected from a mouse, a rat, and a rabbit. In one case, the antigen of interest is selected from a ligand, a receptor, an intracellular protein and a secreted protein. In one case, the antigen of interest is a human pathogen as described herein.

[0102] In one case, the single human V_H gene family member is selected from V_H1-2 , V_H1-69 , V_H2-26 , V_H2-70 , and V_H3-23 . In one case, the single human V_H gene family member is V_H1-69 . In one case, the single human V_H gene family member is V_H1-2 . In one case, the single human V_H gene family member is identified in Table 1. In one case, the single human V_H gene family member is identified in Table 2. In one case, the single human V_H gene family member is identified in Table 3.

[0103] In one case, a nucleotide sequence encoding an immunoglobulin variable region made in a non-human animal as described herein is described.

[0104] In one case, an immunoglobulin heavy chain or immunoglobulin light chain variable region amino acid sequence of an antibody made in a non-human animal as described herein is described.

[0105] In one case, an immunoglobulin heavy chain or immunoglobulin light chain variable region nucleotide sequence encoding a variable region of an antibody made in a non-human animal as described herein is described.

[0106] In one case, an antibody or antigen-binding fragment thereof (e.g., Fab, F(ab)₂, scFv) made in a non-human animal as described herein is described.

[0107] In one case, a mouse having a restricted immunoglobulin heavy chain locus characterized by the presence of a single human V_H gene segment, one or more human D_H gene segments, and one or more human J_H gene segments is described, wherein the single human V_H gene segment is at an endogenous mouse locus and the V_H gene segment is operably linked to the one or more human D_H gene segments, the one or more human J_H gene segments, and to an endogenous immunoglobulin heavy chain constant gene.

[0108] In one case, the mouse further comprises a humanized immunoglobulin light chain locus comprising one or more human V_L gene segments, and one or more human J_L gene segments, wherein the human V_L gene segments and the human J_L gene segments are operably linked to a non-human immunoglobulin light chain constant region gene. In a specific case, the human V_L and J_L gene segments are at an endogenous mouse light chain locus, and wherein the non-human immunoglobulin light chain constant region gene is a mouse gene.

[0109] In one case, the humanized immunoglobulin light chain locus is on a transgene, and the constant region gene is selected from mouse, rat, and human.

[0110] In one case, the human V_L and J_L gene segments are V_K and J_K gene segments. In one case, the human V_L and J_L gene segments are V_λ and J_λ gene segments.

[0111] In one case, a non-human animal is described, wherein the non-human animal has a B cell repertoire that expresses immunoglobulin heavy chain variable domains derived from a single V segment family member. In one case, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90, or at least 95% of the B cell repertoire of the non-human animal immunoglobulin heavy chain variable domain expressed in the B cell repertoire is derived from the same V segment family member. In a specific case, the percentage is at least 90%. In one case, the B cell repertoire consists essentially of peripheral (blood) B cells. In one case, the B cell repertoire consists essentially of splenic B cells. In one case, the B cell repertoire consists essentially of bone marrow B cells. In one case, the B cell repertoire consists essentially of peripheral B cells, splenic B cells, and bone marrow B cells.

[0112] In one case, a genetically modified non-human animal is described, wherein more than 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or more than 90% of the B cells of the non-human animal that express a heavy chain immunoglobulin variable domain express a heavy chain immunoglobulin variable domain derived from a single V_H gene segment family member. In one case, at least 75% of the B cells of the non-human animal that express an immunoglobulin heavy chain variable domain express an immunoglobulin heavy chain variable domain derived from the single V_H gene segment family member. In a specific case, the percentage is at least 90%. In one case, all of the B cells that express a heavy chain domain that is derived from the single V_H gene family member.

[0113] In one case, a genetically modified mouse is described that makes an antigen-specific B cell population in response to immunization with an antigen of interest, wherein at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or more than 90%, of said antigen-specific B cell population expresses immunoglobulin heavy chains that are all derived from the same V_H gene segment. In one case, at least 75% of the antigen-specific B cell population expresses immunoglobulin heavy chains derived from the same V_H gene segment. In one case, all of the antigen-specific B cells express a heavy chain that is derived from the same V_H gene segment.

[0114] In one case, a non-human animal comprising a restricted V_H gene segment repertoire is described, wherein the restriction is to a human V_H1-69 gene segment or a V_H1-69 gene segment that is at least about 75.5%, 76.5%,

86.7%, 87.8%, 94.9%, 96.9%, 98%, or 99% identical to a $V_H1-69*01$ gene segment. In a specific case, the restricted repertoire is selected from one or more of the V_H1-69 variants of FIG. 15.

[0115] In one case, a non-human animal comprising a restricted V_H gene segment repertoire is described, wherein the restriction is to a human V_H1-2 gene segment or a V_H1-2 gene segment that is at least about 94.9%, 95.9%, 96.9%, 98%, or 99% identical to a V_H1-2 gene segment. In a specific case, the restricted repertoire is selected from one or more of the V_H1-2 variants of FIG. 18.

[0116] In one case, the non-human animal is a mouse.

[0117] In one case, the mouse exhibits an immunophenotype having a characteristic of a higher ratio of mature B cells to immature B cells as compared to a wild type mouse. In a specific case, the ratio is calculated from B cells harvested from spleen. In one case, the mouse exhibits a population of mature B cells of about 1×10^7 . In one case, the mouse exhibits a population of immature B cells of about 0.5×10^7 . In one case, the mouse exhibits a ratio of mature B cells to immature B cells in the spleen of the mouse that is about 1.5-fold to about 2-fold higher than exhibited by a wild type mouse.

[0118] In one case, the ratio is calculated from B cells harvested from bone marrow. In a specific case, the mouse exhibits a population of mature B cells of about 3×10^5 . In one case, the mouse exhibits a population of immature B cells of about 7×10^5 . In one case, the mouse exhibits a ratio of mature B cells to immature B cells in the bone marrow of the mouse that is about 3-fold, or about 3.3-fold higher than exhibited by a wild type mouse.

[0119] In one case, the mouse exhibits an immunophenotype having a characteristic of a higher number of pro B cells in the bone marrow as compared to a wild type mouse. In a specific case, the mouse exhibits a population of pro B cells in the bone marrow of the mouse that is about 2.5-fold to about 3-fold higher than exhibited in the bone marrow of a wild type mouse. In a specific case, the mouse exhibits a population of pro B cells in the bone marrow of the mouse that is about 2.75-fold higher than exhibited in the bone marrow of a wild type mouse.

[0120] In one case, the mouse exhibits an immunophenotype having a characteristic selected from the group consisting of a $CD19^+$ splenic B cell population that is about 80% of a wild-type B cell, a $CD3^+$ splenic T cell population that is about the same as a wild type mouse, and a combination thereof.

[0121] In one case, the mouse comprises a lymphocyte population whose % $CD19^+$ B cells in spleen are about the same as a wild-type mouse. In one case, the number of $CD19^+$ B cells per spleen of the mouse is at least about 50% of the number of $CD19^+$ B cells per spleen of a wild-type mouse.

[0122] In one case, the non-human animal comprises at least about 75% to about 80% of $CD19^+$ B cells in bone marrow as compared with a wild-type mouse.

[0123] In one case, the total number of $CD19^+$ bone cells per femur of the mouse is non less than about 30%, 40%, 50%, 60%, or 75% of the total number of $CD19^+$ bone marrow cells in a wild-type mouse.

[0124] In one case, the mouse expresses IgD and IgM at about the same level as observed in a wild-type mouse.

[0125] In one case, a mouse comprising a restricted human V_H segment repertoire is described, further comprising a humanized immunoglobulin light chain variable segment locus, wherein the ratio of λ to κ light chains expressed in the mouse is about the same as in a wild-type mouse.

[0126] In one case, a mouse is described, comprising a restricted immunoglobulin heavy chain locus characterized by the presence of a single V_H gene segment, one or more D_H gene segments, and one or more J_H gene segments, wherein the single V_H gene segment is a polymorphic V_H gene segment.

[0127] In one case, the polymorphic V_H gene segment is a human V_H gene segment that is associated with a high copy number in human populations. In one case, the human V_H gene segment is selected from V_H1-2 , V_H1-69 , V_H2-26 , V_H2-70 , V_H3-23 , or a polymorphic variant thereof. In a specific case, the human V_H gene segment is a V_H1-69 gene segment. In another specific case, the human V_H gene segment is a V_H1-2 gene segment.

[0128] In one case, the single V_H gene segment is operably linked to a human, mouse, or chimeric human/mouse immunoglobulin constant region gene. In a specific case, the immunoglobulin constant region gene is a mouse constant region gene. In one case, the immunoglobulin constant gene comprises a human sequence selected from a human C_H1 , a human hinge, a human C_H2 , a human C_H3 , and a combination thereof. In one case, the mouse constant gene is at an endogenous immunoglobulin heavy chain locus.

[0129] In one case, the mouse further comprises a human immunoglobulin V_L gene segment operably linked to a J gene segment and a light chain constant gene. In a specific case, the V_L gene segment and/or the J gene segment are selected from a human κ gene segment and a human λ gene segment. In one case, the V_L and/or J gene segments are human κ gene segments.

[0130] In various cases, the mouse comprises a deletion of all or substantially all endogenous V_H gene segments.

[0131] In various cases, the non-human animal comprises an inactivated endogenous heavy chain variable gene locus. In various cases, the inactivated endogenous heavy chain variable gene locus is not operably linked to an endogenous heavy chain constant region gene.

[0132] In one case, a mouse is described, wherein the mouse is characterized by the expression of serum immunoglobulin, wherein greater than 80% of the serum immunoglobulin comprises a human heavy chain variable domain and a cognate human light chain variable domain, wherein the human heavy chain variable domain is derived from a

V_H gene segment repertoire consisting essentially of a single human V_H gene segment and/or polymorphic variants thereof.

[0133] In one case, the single human V_H gene segment is a human V_H1-69 gene segment and/or polymorphic variants thereof. In one case, the single human V_H gene segment is a human V_H1-2 gene segment and/or polymorphic variants thereof.

[0134] In one case, a mouse is described, comprising, in its germline, a replacement at an endogenous immunoglobulin heavy chain locus of all or substantially all endogenous V_H gene segments with a single human V_H gene segment and/or polymorphic variants thereof. In one case, the single human V_H gene segment is a human V_H1-69 gene segment and/or polymorphic variants thereof. In one case, the single human V_H gene segment is a human V_H1-2 gene segment and/or polymorphic variants thereof.

[0135] In one case, the mouse further comprises a replacement at an endogenous immunoglobulin light chain locus of all or substantially all endogenous V_L gene segments with one or more human V_L gene segments. In a specific case, the mouse further comprises one or more human J_L gene segments operably linked to the human V_L gene segments.

[0136] In one case, use of a mouse as described herein to make an immunoglobulin variable region nucleotide sequence is described. In one case, the sequence comprises a rearranged V_H1-69 gene segment. In one case, the sequence comprises a rearranged V_H1-2 gene segment.

[0137] In one case, the immunoglobulin variable region nucleotide sequence is at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% identical with a human V_H1-69 gene segment. In a specific case, the immunoglobulin variable region nucleotide sequence is at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% identical with SEQ ID NO: 34. In various cases, the human V_H1-69 gene segment is identified from Table 2.

[0138] In one case, the immunoglobulin variable region nucleotide sequence encodes an amino acid sequence that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% identical with SEQ ID NO: 35.

[0139] In one case, the immunoglobulin variable region nucleotide sequence is at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% identical with a human V_H1-2 gene segment. In a specific case, the immunoglobulin variable region nucleotide sequence is at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% identical with SEQ ID NO: 60. In various cases, the human V_H1-2 gene segment is identified from Table 3.

[0140] In one case, the immunoglobulin variable region nucleotide sequence encodes an amino acid sequence that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% identical with SEQ ID NO: 61.

[0141] In one case, use of a mouse as described herein to make a fully human Fab or a fully human F(ab)₂ is described. In one case, the fully human Fab or fully human F(ab)₂ comprises a heavy chain variable region that comprises a rearranged human V_H1-69 gene segment. In one case, the fully human Fab or fully human F(ab)₂ comprises a heavy chain variable region that comprises a rearranged human V_H1-2 gene segment.

[0142] In one case, use of a mouse as described herein to make an immortalized cell line is described.

[0143] In one case, use of a mouse as described herein to make a hybridoma or quadroma is described.

[0144] In one case, use of a mouse as described herein to make a phage library containing human heavy chain variable regions and human light chain variable regions is described.

[0145] In one case, the human heavy chain variable regions are derived from a human V_H1-69 gene segment that comprises a sequence selected from SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56 and SEQ ID NO: 58.

[0146] In one case, the human heavy chain variable regions are derived from a human V_H1-69 gene segment that comprises a sequence selected from SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 and SEQ ID NO: 59.

[0147] In one case, the human heavy chain variable regions are all derived from a human V_H1-2 gene segment that comprises a sequence selected from SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66 and SEQ ID NO: 68.

[0148] In one case, the human heavy chain variable regions are derived from a human V_H1-2 gene segment that comprises a sequence selected from SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67 and SEQ ID NO: 69.

[0149] In one case, use of a mouse as described herein to generate a variable region sequence for making a human antibody is described, comprising (a) immunizing a mouse as described herein with an antigen of interest, (b) isolating a lymphocyte from the immunized mouse of (a), (c) exposing the lymphocyte to one or more labeled antibodies, (d) identifying a lymphocyte that is capable of binding to the antigen of interest, and (e) amplifying one or more variable region nucleic acid sequence from the lymphocyte thereby generating a variable region sequence.

[0150] In one case, the lymphocyte is derived or isolated from the spleen of the mouse. In one case, the lymphocyte is derived or isolated from a lymph node of the mouse. In one case, the lymphocyte is derived or isolated from the bone marrow of the mouse. In one case, the lymphocyte is derived or isolated from the blood of the mouse.

[0151] In one case, the labeled antibody is a fluorophore-conjugated antibody. In one case, the one or more fluorophore-conjugated antibodies are selected from an IgM, an IgG, and/or a combination thereof.

[0152] In one case, the lymphocyte is a B cell.

[0153] In one case, the one or more variable region nucleic acid sequence comprises a heavy chain variable region sequence. In one case, the one or more variable region nucleic acid sequence comprises a light chain variable region sequence. In a specific case, the light chain variable region sequence is an immunoglobulin κ light chain variable region sequence. In one case, the one or more variable region nucleic acid sequence comprises a heavy chain and a κ light chain variable region sequence.

[0154] In one case, use of a mouse as described herein to generate a heavy and a κ light chain variable region sequence for making a human antibody is described, comprising (a) immunizing a mouse as described herein with an antigen of interest, (b) isolating the spleen from the immunized mouse of (a), (c) exposing B lymphocytes from the spleen to one or more labeled antibodies, (d) identifying a B lymphocyte of (c) that is capable of binding to the antigen of interest, and (e) amplifying a heavy chain variable region nucleic acid sequence and a κ light chain variable region nucleic acid sequence from the B lymphocyte thereby generating the heavy chain and κ light chain variable region sequences.

[0155] In one case, use of a mouse as described herein to generate a heavy and a κ light chain variable region sequence for making a human antibody is described, comprising (a) immunizing a mouse as described herein with an antigen of interest, (b) isolating one or more lymph nodes from the immunized mouse of (a), (c) exposing B lymphocytes from the one or more lymph nodes to one or more labeled antibodies, (d) identifying a B lymphocyte of (c) that is capable of binding to the antigen of interest, and (e) amplifying a heavy chain variable region nucleic acid sequence and a κ light chain variable region nucleic acid sequence from the B lymphocyte thereby generating the heavy chain and κ light chain variable region sequences.

[0156] In one case, use of a mouse as described herein to generate a heavy and a κ light chain variable region sequence for making a human antibody is described, comprising (a) immunizing a mouse as described herein with an antigen of interest, (b) isolating bone marrow from the immunized mouse of (a), (c) exposing B lymphocytes from the bone marrow to one or more labeled antibodies, (d) identifying a B lymphocyte of (c) that is capable of binding to the antigen of interest, and (e) amplifying a heavy chain variable region nucleic acid sequence and a κ light chain variable region nucleic acid sequence from the B lymphocyte thereby generating the heavy chain and κ light chain variable region sequences. In various cases, the one or more labeled antibodies are selected from an IgM, an IgG, and/or a combination thereof.

[0157] In various cases, the antigen of interest is a pathogen that afflicts human subjects including, e.g., a viral antigen. Exemplary viral pathogens include, e.g., mainly those of the families of Adenoviridae, bacteria Picornaviridae, Herpesviridae, Hepadnaviridae, Flaviviridae, Retroviridae, Orthomyxoviridae, Paramyxoviridae, Papovaviridae, Polyomavirus, Rhabdoviridae, and Togaviridae. Such exemplary viruses typically range between 20-300 nanometers in length. In various cases, the antigen of interest is a viral antigen selected from a hepatitis virus (e.g., HCV, HBV, etc.), a human immunodeficiency virus (HIV), or an influenza virus (e.g., H1N1).

[0158] In various cases, use of a mouse as described herein to generate a heavy and κ light chain variable region sequence for making a human antibody is described, further comprising fusing the amplified heavy and light chain variable region sequences to human heavy and light chain constant region sequences, expressing the fused heavy and light chain sequences in a cell, and recovering the expressed heavy and light chain sequences thereby generating a human antibody.

[0159] In various cases, the human heavy chain constant regions are selected from IgM, IgD, IgA, IgE and IgG. In various specific cases, the IgG is selected from an IgG1, an IgG2, an IgG3 and an IgG4. In various cases, the human heavy chain constant region comprises a C_H1 , a hinge, a C_H2 , a C_H3 , a C_H4 , or a combination thereof. In various cases, the light chain constant region is an immunoglobulin κ constant region. In various cases, the cell is selected from a HeLa cell, a DU145 cell, a Lncap cell, a MCF-7 cell, a MDA-MB-438 cell, a PC3 cell, a T47D cell, a THP-1 cell, a U87 cell, a SHSY5Y (human neuroblastoma) cell, a Saos-2 cell, a Vero cell, a CHO cell, a GH3 cell, a PC12 cell, a human retinal cell (e.g., a PER.C6™ cell), and a MC3T3 cell. In a specific case, the cell is a CHO cell.

[0160] In one case, a method for generating a reverse-chimeric rodent-human antibody specific against an antigen of interest is described, comprising the steps of immunizing a mouse as described herein with the antigen, isolating at least one cell from the mouse producing a reverse-chimeric mouse-human antibody specific against the antigen, culturing at least one cell producing the reverse-chimeric mouse-human antibody specific against the antigen, and obtaining said antibody.

[0161] In one case, the reverse-chimeric mouse-human antibody comprises a human heavy chain variable domain fused with a mouse or rat heavy chain constant gene, and a human light chain variable domain fused with a mouse or rat or human light chain constant gene. In a specific case, the human heavy chain variable domain contains a rearranged human V_H1-69 or human V_H1-2 gene segment.

[0162] In one case, culturing at least one cell producing the reverse-chimeric rodent-human antibody specific against the antigen is performed on at least one hybridoma cell generated from the at least one cell isolated from the mouse.

[0163] In one case, the antigen of interest is a pathogen that afflicts human subjects as described herein.

[0164] In one case, a method for generating a fully human antibody specific against an antigen of interest is described,

comprising the steps of immunizing a mouse as described herein with the antigen, isolating at least one cell from the mouse producing a reverse-chimeric rodent-human antibody specific against the antigen, generating at least one cell producing a fully human antibody derived from the reverse-chimeric rodent-human antibody specific against the antigen, and culturing at least one cell producing the fully human antibody, and obtaining said fully human antibody.

[0165] In various cases, the at least one cell isolated from the mouse producing a reverse-chimeric rodent-human antibody specific against the antigen is a splenocyte or a B cell.

[0166] In various cases, the antibody is a monoclonal antibody.

[0167] In various cases, the antibody comprises a heavy chain variable domain that contains a rearranged human V_H 1-69 or human V_H 1-2 gene segment.

[0168] In various cases, immunization with the antigen of interest is carried out with protein, DNA, a combination of DNA and protein, or cells expressing the antigen. In one case, the antigen of interest is a pathogen that afflicts human subjects as described herein.

[0169] In one case, use of a mouse as described herein to make a nucleic acid sequence encoding an immunoglobulin variable region or fragment thereof is described. In one case, the nucleic acid sequence is used to make a human antibody or antigen-binding fragment thereof. In one case, the mouse is used to make an antigen-binding protein selected from an antibody, a multi-specific antibody (e.g., a bi-specific antibody), an scFv, a bi-specific scFv, a diabody, a triabody, a tetrabody, a V-NAR, a V_{HH} , a V_L , a F(ab), a F(ab)₂, a DVD (i.e., dual variable domain antigen-binding protein), a an SVD (i.e., single variable domain antigen-binding protein), or a bispecific T-cell engager (BiTE).

[0170] In one case, a method for making a human antigen-binding protein is described, comprising exposing a genetically modified non-human animal as described herein to an antigen of interest, allowing the genetically modified non-human animal to mount an immune response to the antigen, obtaining from the genetically modified non-human animal a heavy chain variable domain nucleic acid sequence encoding a human heavy chain variable domain that specifically binds the antigen of interest, cloning the heavy chain variable domain nucleic acid sequence to a human constant region sequence, and expressing in a mammalian cell an antibody comprising the human heavy chain variable domain sequence and the human constant region sequence. In one case, the mammalian cell is a CHO cell. In one case the genetically modified non-human animal comprises a human V_H gene segment repertoire that consists essentially of a single human V_H gene segment, optionally present in two or more polymorphic variants thereof, operably linked to one or more human D and/or J segments. In one case, the human V_H gene segment repertoire is at an endogenous non-human V_H segment locus. In one case, the human V_H gene segment repertoire is at a locus that is not an endogenous V_H segment locus. In one case, the human V_H gene segment rearranges with a human D segment and a human J segment to form a rearranged human VDJ gene operably linked to a constant region sequence, wherein the constant region sequence is selected from a human sequence and a rodent sequence (e.g., a mouse or rat or hamster sequence). In one case, the constant region sequence comprises a sequence selected from a C_H 1, a hinge, a C_H 2, a C_H 3, and a combination thereof; in a specific case, the constant region sequence comprises a C_H 1, a hinge, a C_H 2, and a C_H 3. In one case, the human variable domain and the constant sequence are expressed in the mammalian cell with a cognate human light chain variable domain obtained from the same mouse (e.g., sequence obtained from the same B cell as the human variable domain sequence); in one case the sequence encoding the human light chain variable domain obtained from the mouse is then fused with a sequence encoding a human light chain constant sequence, and the light chain sequence and the heavy chain sequence are expressed in the mammalian cell.

[0171] In one case, the antigen of interest is a pathogen that afflicts human subjects as described herein.

[0172] In one case, a method for making an antibody heavy chain variable domain that binds an antigen of interest is described, comprising expressing in a single cell (a) a first V_H sequence of an immunized non-human animal as described herein, wherein the first V_H sequence is fused with a C_H gene sequence; and (b) a V_L gene sequence of an immunized non-human animal as described herein, wherein the V_L gene sequence is fused with a human C_L gene sequence; maintaining the cell under conditions sufficient to express an antibody; and, isolating the antibody heavy chain variable domain. In one case, the V_L gene sequence is cognate with the first V_H sequence.

[0173] In one case, the cell comprises a second V_H gene sequence of an immunized non-human animal as described herein, wherein the second V_H gene sequence is fused with a C_H gene sequence, wherein the first V_H gene sequence encodes a V_H domain that specifically binds a first epitope, and the second V_H gene sequence encodes a V_H domain that specifically binds a second epitope, wherein the first epitope and the second epitope are not identical.

[0174] In one case, the constant region sequences are all human constant region sequences. In one case, the antigen of interest is a pathogen that afflicts human subjects as described herein.

[0175] In one case, a method for making a human bispecific antibody is described, comprising making the bispecific antibody using human variable region gene sequences of B cells of a non-human animal as described herein.

[0176] In one case, the method comprises (a) identifying a clonally selected lymphocyte of the non-human animal, wherein the non-human animal has been exposed to an antigen of interest and allowed to develop an immune response to the antigen of interest, and wherein the lymphocyte expresses an antibody that specifically binds the antigen of interest, (b) obtaining from the lymphocyte or the antibody a nucleotide sequence that encodes a human heavy chain variable

region that specifically binds the antigen of interest, and (c) employing the nucleotide sequence that encodes the human heavy chain variable region that specifically binds the antigen of interest in making the bispecific antibody. In a specific case, the human heavy chain variable region comprises a rearranged V_H1-2 or V_H1-69 gene segment.

[0177] In one case, steps (a) through (c) are performed a first time for a first antigen of interest to generate a first human heavy chain variable region sequence, and steps (a) through (c) are performed a second time for a second antigen of interest to generate a second human heavy chain variable region sequence, and wherein the first human heavy chain variable region sequence is expressed fused with a first human heavy chain constant region to form a first human heavy chain, the second human heavy chain variable region sequence is expressed fused with a second human heavy chain constant region to form a second human heavy chain, wherein the first and the second human heavy chains are expressed in the presence of a single human light chain expressed from a rearranged human V_K1-39 or a human V_K3-20 gene segment. In a specific case, the single human light chain comprises a germline sequence.

[0178] In one case, the method comprises (a) cloning heavy chain variable regions from B cells of a non-human animal as described herein which has been exposed to a first antigen of interest, and the same non-human animal, or a different non-human animal which is genetically the same and has been exposed to a second antigen of interest; and (b) expressing in a cell the heavy chain variable regions of (a) with the same heavy chain constant region and the same light chain to make a bispecific antibody.

[0179] In one case, a use of a non-human animal as described herein is described, to obtain a nucleic acid sequence that encodes a human heavy chain variable domain. In one case, the heavy chain variable domain comprises a rearranged human V_H gene segment selected from V_H1-2 and V_H1-69 .

[0180] In one case, a use of a non-human animal as described herein is described, to obtain a cell that encodes a human heavy chain variable domain. In one case, the heavy chain variable domain comprises a rearranged human V_H gene segment selected from V_H1-2 and V_H1-69 .

[0181] In one case, use of a non-human animal as described herein to make a human antibody variable domain is described. In one case, the variable domain comprises a rearranged human V_H gene segment selected from V_H1-2 and V_H1-69 .

[0182] In one case, use of a non-human animal as described herein to make a human antibody is described, comprising making the antibody using human variable region gene sequences of B cells of a non-human animal as described herein. In one case, the human antibody is a human bispecific antibody. In a specific case, the bispecific antibody comprises one heavy chain variable domain derived from a rearranged human V_H1-2 or V_H1-69 gene segment. In one case, the human variable region gene sequences comprise a rearranged human V_H1-2 or V_H1-69 gene segment.

[0183] In one case, use of a non-human animal as described herein is described to select a human immunoglobulin heavy chain variable domain. In one case, the heavy chain variable domain comprises a rearranged human V_H gene segment selected from V_H1-2 and V_H1-69 .

[0184] In one case, use of the mouse as described herein for the manufacture of a medicament (e.g., an antigen-binding protein), or for the manufacture of a sequence encoding a variable sequence of a medicament (e.g., an antigen-binding protein), for the treatment of a human disease or disorder is described. In one case, the variable sequence of a medicament comprises a polymorphic human V_H gene segment. In one case, the variable sequence of a medicament comprises a human V_H1-69 gene segment. In one case, the variable sequence of a medicament comprises a human V_H1-2 gene segment.

[0185] In one case, a nucleic acid construct encoding an immunoglobulin variable domain made in a mouse as described herein is described. In one case, the variable domain is a heavy chain variable domain. In a specific case, the heavy chain variable domain comprises a rearranged human V_H gene segment selected from V_H1-2 , V_H1-69 , V_H2-26 , V_H2-70 , or V_H3-23 . In another specific case, the heavy chain variable domain comprises a rearranged human V_H1-2 gene segment. In another specific case, the heavy chain variable domain comprises a rearranged human V_H1-69 gene segment.

[0186] In one case, the variable domain is a light chain variable domain. In a specific case, the variable domain is a κ light chain variable domain that is cognate with a human heavy chain variable domain that comprises a rearranged human V_H1-69 gene segment. In a specific case, the variable domain is a κ light chain variable domain that is cognate with a human heavy chain variable domain that comprises a rearranged human V_H1-2 gene segment.

[0187] In one case, use of a mouse as described herein to make a nucleic acid construct encoding a human immunoglobulin variable domain is described. In one case, the variable domain is a light chain variable domain. In one case, the variable domain is a κ light chain variable domain that comprises a rearranged human V_K gene segment selected from V_K4-1 , V_K5-2 , V_K7-3 , V_K2-4 , V_K1-5 , V_K1-6 , V_K3-7 , V_K1-8 , V_K1-9 , V_K2-10 , V_K3-11 , V_K1-12 , V_K1-13 , V_K2-14 , V_K3-15 , V_K1-16 , V_K1-17 , V_K2-18 , V_K2-19 , V_K3-20 , V_K6-21 , V_K1-22 , V_K1-23 , V_K2-24 , V_K3-25 , V_K2-26 , V_K1-27 , V_K2-28 , V_K2-29 , V_K2-30 , V_K3-31 , V_K1-32 , V_K1-33 , V_K3-34 , V_K1-35 , V_K2-36 , V_K1-37 , V_K2-38 , V_K1-39 , and V_K2-40 .

[0188] In one case, the variable domain is a heavy chain variable domain. In a specific case, the heavy chain variable domain comprises a rearranged human V_H gene segment selected from V_H1-2 , V_H1-69 , V_H2-26 , V_H2-70 , or V_H3-23 . In a specific case, the heavy chain variable domain comprises a rearranged human V_H1-69 gene segment. In a specific

case, the heavy chain variable domain comprises a rearranged human V_H1-2 gene segment.

[0189] In one case, use of a mouse as described herein to make a human immunoglobulin variable domain is described. In one case, the variable domain is a light chain variable domain. In one case, the variable domain is a κ light chain variable domain that comprises a rearranged human V_K gene segment selected from V_K4-1 , V_K5-2 , V_K7-3 , V_K2-4 , V_K1-5 , V_K1-6 , V_K3-7 , V_K1-8 , V_K1-9 , V_K2-10 , V_K3-11 , V_K1-12 , V_K1-13 , V_K2-14 , V_K3-15 , V_K1-16 , V_K1-17 , V_K2-18 , V_K2-19 , V_K3-20 , V_K6-21 , V_K1-22 , V_K1-23 , V_K2-24 , V_K3-25 , V_K2-26 , V_K1-27 , V_K2-28 , V_K2-29 , V_K2-30 , V_K3-31 , V_K1-32 , V_K1-33 , V_K3-34 , V_K1-35 , V_K2-36 , V_K1-37 , V_K2-38 , V_K1-39 , and V_K2-40 .

[0190] In one case, the variable domain is a heavy chain variable domain. In a specific case, the heavy chain variable domain comprises a rearranged human V_H gene segment selected from V_H1-2 , V_H1-69 , V_H2-26 , V_H2-70 , or V_H3-23 . In a specific case, the heavy chain variable domain comprises a rearranged human V_H1-69 gene segment. In a specific case, the heavy chain variable domain comprises a rearranged human V_H1-2 gene segment.

[0191] In one case, use of a non-human animal as described herein to make a nucleic acid sequence encoding a human heavy chain variable domain is described. In one case, the human heavy chain variable domain is characterized by having human FR1-CDR1-FR2-CDR2-FR3 sequences that are derived from a polymorphic human V_H gene segment. In a specific case, the human V_H gene segment is selected from a human V_H1-2 , V_H1-69 , V_H2-26 , V_H2-70 , or V_H3-23 gene segment. In one case, the human V_H gene segment is a human V_H1-69 gene segment. In one case, the human V_H gene segment is a human V_H1-2 gene segment.

[0192] In one case, a method for making a nucleic acid sequence encoding a human V_H domain is described, the method comprising immunizing a non-human animal as described herein with an antigen of interest, allowing the non-human animal to mount an immune response to the antigen of interest, and obtaining therefrom a nucleic acid sequence encoding a human V_H domain that binds the antigen of interest. In one case, the method further comprises making a nucleic acid sequence encoding a human V_L domain that is cognate with the human V_H domain, comprising isolating a B cell encoding the human V_H domain and the human V_L domain, and obtaining therefrom the sequence of the heavy and light chain variable domains. In various cases, the human V_H domain is derived from a rearranged human V_H1-69 or human V_H1-2 gene segment. In various cases, the human V_L domain is selected from a human V_K or a human V_L domain.

[0193] In one case, use of a non-human animal as described herein to make a human therapeutic is described, comprising immunizing the non-human animal with an antigen of interest, allowing the non-human animal to mount an immune response, and obtaining from the animal a nucleic acid sequence encoding an immunoglobulin variable domain that binds the antigen of interest, and employing the immunoglobulin variable domain in a human therapeutic. In one case, the variable domain is a heavy chain variable domain. In a specific case, the heavy chain variable domain is derived from a rearranged human V_H1-69 or a human V_H1-2 gene segment. In one case, the variable domain is a light chain variable domain. In a specific case, the light chain variable domain is derived from a rearranged human V_K or human V_L gene segment.

[0194] In one case, a method for making a human therapeutic is described, comprising immunizing a non-human animal as described herein with an antigen of interest, allowing the non-human animal to mount an immune response, and obtaining from the animal a nucleic acid sequence encoding an immunoglobulin variable domain that binds the antigen of interest, and employing the immunoglobulin variable domain in a human therapeutic. In one case, the variable domain is a heavy chain variable domain. In a specific case, the heavy chain variable domain is derived from a rearranged human V_H1-69 or a human V_H1-2 gene segment. In one case, the variable domain is a light chain variable domain. In a specific case, the light chain variable domain is derived from a rearranged human V_K or human V_L gene segment.

[0195] In one case, a method for making a human antigen-binding protein is described, comprising immunizing a non-human animal as described herein with an antigen of interest, allowing the animal to mount an immune response, obtaining from the mouse a nucleic acid sequence encoding an immunoglobulin variable domain that specifically binds the antigen of interest, cloning the nucleic acid sequence in a vector suitable for expression of the nucleic acid, wherein the nucleic acid sequence is cloned in frame with a nucleic acid sequence encoding a human immunoglobulin constant region or functional fragment thereof, and inserting the vector in a mammalian cell, and maintaining the cell under conditions suitable for expressing an antigen-binding protein that comprises the immunoglobulin variable domain and the immunoglobulin constant region or functional fragment thereof. In one case, the antigen-binding protein is a human antibody. In a specific case, the antibody comprises a heavy chain variable domain and a light chain variable domain obtained from a mouse as described herein. In a specific case, the antibody comprises a heavy chain variable domain obtained from a mouse as described herein. In various cases, the heavy chain variable domain is derived from a rearranged human V_H1-69 or a human V_H1-2 gene segment.

[0196] In one case, a nucleic acid sequence encoding a human antigen-binding domain made in a non-human animal as described herein is described. In one case, the nucleic acid sequence encodes a human immunoglobulin V_H domain. In one case, the nucleic acid sequence encodes a human immunoglobulin V_H domain and a cognate human V_L domain. In various cases, the human V_H domain is derived from a rearranged human V_H1-69 or a human V_H1-2 gene segment.

[0197] In one case, a method for preparation of a human antibody is described, comprising immunizing a non-human

animal as described herein with an antigen of interest, allowing the non-human animal to mount an immune response, harvesting a lymphocyte (e.g., a B cell) from the immunized animal, fusing the lymphocyte with a myeloma cell to form a hybridoma cell, obtaining from the hybridoma cell a nucleic acid sequence that encodes a human V_H domain and a human V_L domain, cloning the nucleic acid sequence in frame (i.e., in operable linkage) with a human constant region sequence to create an immunoglobulin heavy chain and an immunoglobulin light chain, and expressing the heavy and light chains in a cell capable of expressing the fully human antibody. In one case, the cell is a CHO cell. In various cases, the human V_H domain is derived from a rearranged human V_H1-69 gene segment or a human V_H1-2 gene segment.

[0198] In one case, a method for preparation of a human antibody is described, comprising immunizing a non-human animal as described herein with an antigen of interest, allowing the non-human animal to mount an immune response, harvesting a lymphocyte (e.g., a B cell) from the immunized animal, obtaining from the lymphocyte a nucleic acid sequence that encodes a human V_H domain and a human V_L domain, cloning the nucleic acid sequence in frame (i.e., in operable linkage) with a human constant region sequence to create an immunoglobulin heavy chain and an immunoglobulin light chain, and expressing the heavy and light chains in a cell capable of expressing the fully human antibody. In one case, the lymphocyte is derived from the spleen of the non-human animal. In one case, the cell is a CHO cell. In various cases, the human V_H domain is derived from a rearranged human V_H1-69 gene segment or a human V_H1-2 gene segment.

[0199] In various cases, the antigen of interest is a pathogen that afflicts human subjects as described herein. In various cases, the antigen of interest is a virus that is capable of infecting a human. Exemplary antigens that can be employed in the methods and uses described herein include microbes or microorganisms such as a virus, bacterium, prion, or fungus or any other pathogen that causes disease in humans. A person of skill, upon reading the disclosure, will appreciate those human pathogens that will be applicable for the methods and uses described herein. The various cases and cases are capable of use together, unless expressly noted otherwise or the context clearly prohibits use together.

BRIEF DESCRIPTION OF FIGURES

[0200]

FIG. 1 shows a general illustration, not to scale, of a series of targeting and molecular engineering steps employed to make a targeting vector for construction of a modified heavy chain locus containing a single human V_H1-69 gene segment, twenty-seven human D_H and six human J_H gene segments at an endogenous immunoglobulin heavy chain locus.

FIG. 2 shows a general illustration, not to scale, of a series of targeting and molecular engineering steps employed to make a targeting vector for construction of a modified heavy chain locus containing a single human V_H1-2 gene segment, twenty-seven human D_H and six human J_H gene segments at an endogenous immunoglobulin heavy chain locus.

FIG. 3 shows contour plots of splenocytes gated on single lymphocytes and stained for CD19 (B cell) and CD3 (T cell) from a wild type mouse (WT) and a mouse homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO).

FIG. 4A shows, on the left, the percent of CD19⁺ B cells in spleens harvested from wild type mice (WT) and mice homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO). On the right, the number of CD19⁺ B cells per spleen is shown for both wild type mice (WT) and mice homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO).

FIG. 4B shows, on the left, the percent of CD19⁺ B cells in bone marrow harvested from femurs of wild type mice (WT) and mice homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO). On the right, the number of CD19⁺ B cells per femur is shown for both wild type mice (WT) and mice homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO).

FIG. 5 shows contour plots of splenocytes gated on CD19⁺ B cells and stained for Igλ⁺ and Igκ⁺ expression from a wild type mouse (WT) and a mouse homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO).

FIG. 6 shows contour plots of splenocytes gated on CD19⁺ B cells and stained for immunoglobulin D (IgD) and immunoglobulin M (IgM) from a wild type mouse (WT) and a mouse homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO).

FIG. 7 shows the total number of transitional B cells (CD19⁺IgM^{hi}IgD^{int}), mature B cells (CD19⁺IgM^{int}IgD^{hi}), and the

ratio of mature to immature B cells in harvested spleens from wild type mice (WT) and mice homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO).

FIG. 8 shows contour plots of bone marrow gated on singlets stained for immunoglobulin M (IgM) and B220 from a wild type mouse (WT) and a mouse homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO).

FIG. 9 shows the total number of immature (B220^{int}IgM⁺) and mature (B220^{hi}IgM⁺) B cells in bone marrow isolated from the femurs of wild type mice (WT) and mice homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO).

FIG. 10 shows contour plots of bone marrow gated on CD19⁺ B cells and stained for ckit⁺ and CD43⁺ from a wild type mouse (WT) and a mouse homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO).

FIG. 11A shows the percent of CD19⁺ cells in populations of pro B (CD19⁺CD43⁺ckit⁺) and pre B (CD19⁺CD43⁻ckit⁻) cells in bone marrow harvested from the femurs of wild type mice (WT) and mice homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO).

FIG. 11B shows the absolute number of cells per femur in populations of pro B (CD19⁺CD43⁺ckit⁺) and pre B (CD19⁺CD43⁻ckit⁻) cells in bone marrow harvested from wild type mice (WT) and mice homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO).

FIG. 12 shows the relative mRNA expression (y-axis) in purified splenic B cells of V_H1-69-derived heavy chains in a quantitative PCR assay using a probe specific for the human V_H1-69 gene segment in mice homozygous for a replacement of the endogenous heavy chain V_H, D_H, J_H, and a replacement of the endogenous light chain V_K and J_K gene segments with human V_H, D_H, J_H, V_K and J_K gene segments (Hκ), wild type mice (WT), mice heterozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HET) and mice homozygous for a single human V_H gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus (1hV_H HO). Signals are normalized to expression of mouse Cκ.

FIG. 13 shows the nucleotide alignment of the second exon for each of thirteen reported alleles for the human V_H1-69 gene. Lower case bases indicate germline nucleotide differences among the alleles. Complementary determining regions (CDRs) are indicated with boxes around the sequence. Dashes indicate artificial gaps for proper sequence alignment. V_H1-69*01 (SEQ ID NO: 34); V_H1-69*02 (SEQ ID NO: 36); V_H1-69*03 (SEQ ID NO: 38); V_H1-69*04 (SEQ ID NO: 40); V_H1-69*05 (SEQ ID NO: 42); V_H1-69*06 (SEQ ID NO: 44); V_H1-69*07 (SEQ ID NO: 46); V_H1-69*08 (SEQ ID NO: 48); V_H1-69*09 (SEQ ID NO: 50); V_H1-69*10 (SEQ ID NO: 52); V_H1-69*11 (SEQ ID NO: 54); V_H1-69*12 (SEQ ID NO: 56); V_H1-69*13 (SEQ ID NO: 58).

FIG. 14 shows the protein alignment of the mature heavy chain variable gene sequence for each of thirteen reported alleles for the human V_H1-69 gene. Lower case amino acids indicate germline differences among the alleles. Complementary determining regions (CDRs) are indicated with boxes around the sequence. Dashes indicate artificial gaps for proper sequence alignment. V_H1-69*01 (SEQ ID NO: 35); V_H1-69*02 (SEQ ID NO: 37); V_H1-69*03 (SEQ ID NO: 39); V_H1-69*04 (SEQ ID NO: 41); V_H1-69*05 (SEQ ID NO: 43); V_H1-69*06 (SEQ ID NO: 45); V_H1-69*07 (SEQ ID NO: 47); V_H1-69*08 (SEQ ID NO: 49); V_H1-69*09 (SEQ ID NO: 51); V_H1-69*10 (SEQ ID NO: 53); V_H1-69*11 (SEQ ID NO: 55); V_H1-69*12 (SEQ ID NO: 57); V_H1-69*13 (SEQ ID NO: 59).

FIG. 15 shows a percent identity/percent similarity matrix for the aligned protein sequences of the mature variable gene for each of thirteen reported alleles for the human V_H1-69 gene. Percent identity among the V_H1-69 alleles is indicated above the shaded boxes and percent similarity is indicated below the shaded boxes. Scores for percent identity and percent similarity were scored by a ClustalW (v1.83) alignment tool using MacVector software (MacVector, Inc., North Carolina).

FIG. 16 shows the nucleotide alignment of the second exon for each of five reported alleles for the human V_H1-2 gene. Lower case bases indicate germline nucleotide differences among the alleles. Complementary determining regions (CDRs) are indicated with boxes around the sequence. Dashes indicate artificial gaps for proper sequence alignment. V_H1-2*01 (SEQ ID NO: 60); V_H1-2*02 (SEQ ID NO: 62); V_H1-2*03 (SEQ ID NO: 64); V_H1-2*04 (SEQ ID NO: 66); V_H1-2*05 (SEQ ID NO: 68).

FIG. 17 shows the protein alignment of the mature heavy chain variable gene sequence for each of five reported alleles for the human V_H1-2 gene. Lower case amino acids indicate germline differences among the alleles. Complementary determining regions (CDRs) are indicated with boxes around the sequence. Dashes indicate artificial gaps for proper sequence alignment. V_H1-2*01 (SEQ ID NO: 61); V_H1-2*02 (SEQ ID NO: 63); V_H1-2*03 (SEQ ID NO: 65); V_H1-2*04 (SEQ ID NO: 67); V_H1-2*05 (SEQ ID NO: 69).

FIG. 18 shows a percent identity/percent similarity matrix for the aligned protein sequences of the mature variable

gene for each of five reported alleles for the human V_H1-2 gene. Percent identity among the V_H1-2 alleles is indicated above the shaded boxes and percent similarity is indicated below the shaded boxes. Scores for percent identity and percent similarity were scored by a ClustalW (v1.83) alignment tool using MacVector software (MacVector, Inc., North Carolina).

FIG. 19 shows the antibody titer from mice homozygous for human heavy and human κ light chain variable gene loci ($H\kappa$; $n=4$) and mice homozygous for a single human V_H1-69 gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus ($1hV_HHO$; $n=10$) that were immunized with a human cell surface receptor (Antigen A).

FIG. 20 shows the antibody titer from mice homozygous for human heavy and human κ light chain variable gene loci ($H\kappa$; $n=5$) and mice homozygous for a single human V_H1-69 gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus ($1hV_HHO$; $n=5$) that were immunized with two different influenza vaccines.

FIG. 21 shows the percentage (y-axis) of IgM-primed heavy chains having a specified amino acid length for the V_H CDR3 region (x-axis) from mice homozygous for a single human V_H1-69 gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus and homozygous for a replacement of the endogenous κ light chain variable loci with human κ light chain variable loci that were immunized with a human cell surface receptor (Antigen A).

FIG. 22 shows the percentage (y-axis) of IgG-primed heavy chains having a specified amino acid length for the V_H CDR3 region (x-axis) from mice homozygous for a single human V_H1-69 gene segment, twenty-seven human D_H and six human J_H gene segments at the endogenous immunoglobulin heavy chain locus and homozygous for a replacement of the endogenous κ light chain variable loci with human κ light chain variable loci that were immunized with a human cell surface receptor (Antigen A).

DETAILED DESCRIPTION

[0201] This invention is not limited to particular methods, and experimental conditions described, as such methods and conditions may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular cases only, and is not intended to be limiting, since the scope of the present invention is defined by the claims.

[0202] Unless defined otherwise, all terms and phrases used herein include the meanings that the terms and phrases have attained in the art, unless the contrary is clearly indicated or clearly apparent from the context in which the term or phrase is used. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, particular methods and materials are now described.

[0203] The phrase "substantial" or "substantially" when used to refer to an amount of gene segments (e.g., "substantially all" V gene segments) includes both functional and non functional gene segments and include, in various cases, e.g., 80% or more, 85% or more, 90% or more, 95% or more, 96% or more, 97% or more, 98% or more, or 99% or more of all gene segments; in various cases, "substantially all" gene segments includes, e.g., at least 95%, 96%, 97%, 98%, or 99% of functional (i.e., non-pseudogene) gene segments.

[0204] The term "replacement" includes wherein a DNA sequence is placed into a genome of a cell in such a way as to replace a sequence within the genome with a heterologous sequence (e.g., a human sequence in a mouse), at the locus of the genomic sequence. The DNA sequence so placed may include one or more regulatory sequences that are part of source DNA used to obtain the sequence so placed (e.g., promoters, enhancers, 5'- or 3'-untranslated regions, appropriate recombination signal sequences, etc.). For example, in various cases, the replacement is a substitution of an endogenous sequence for a heterologous sequence that results in the production of a gene product from the DNA sequence so placed (comprising the heterologous sequence), but not expression of the endogenous sequence; the replacement is of an endogenous genomic sequence with a DNA sequence that encodes a protein that has a similar function as a protein encoded by the endogenous genomic sequence (e.g., the endogenous genomic sequence encodes an immunoglobulin gene or domain, and the DNA fragment encodes one or more human immunoglobulin genes or domains). In various cases, an endogenous gene or fragment thereof is replaced with a corresponding human gene or fragment thereof. A corresponding human gene or fragment thereof is a human gene or fragment that is an ortholog of, a homolog of, or is substantially identical or the same in structure and/or function, as the endogenous gene or fragment thereof that is replaced.

[0205] A precise, *in situ* replacement of six megabases of the variable regions of the mouse heavy chain immunoglobulin loci ($V_H-D_H-J_H$) with a restricted human immunoglobulin heavy chain locus was performed, while leaving the flanking mouse sequences intact and functional within the hybrid loci, including all mouse constant chain genes and locus transcriptional control regions (FIG. 1 and FIG. 2). Specifically, a single human V_H , 27 D_H , and six J_H gene segments were introduced through chimeric BAC targeting vectors into mouse ES cells using VELOCIGENE® genetic engineering technology (see, e.g., US Pat. No. 6,586,251 and Valenzuela et al., 2003, High-throughput engineering of the mouse genome coupled with high-resolution expression analysis, Nat Biotechnol 21:652-659).

Non-Human Animals With Restricted Immunoglobulin V_H Gene Segments

[0206] Non-human animals comprising immunoglobulin loci that comprise a restricted number of V_H genes, and one or more D genes and one or more J genes, are described, as are methods of making and using them. When immunized with an antigen of interest, the non-human animals generate B cell populations with antibody variable regions derived only from the restricted, pre-selected V_H gene or set of V_H genes (e.g., a pre-selected V_H gene and variants thereof). In various cases, non-human animals are described that generate B cell populations that express human antibody variable domains that are human heavy chain variable domains, along with cognate human light chain variable domains. In various cases, the non-human animals rearrange human heavy chain variable gene segments and human light chain variable gene segments from modified endogenous mouse immunoglobulin loci that comprise a replacement or insertion of the non-human unrearranged variable region sequences with human unrearranged variable region sequences.

[0207] Early work on the organization, structure, and function of the immunoglobulin genes was done in part on mice with disabled endogenous loci and engineered to have transgenic loci (randomly placed) with partial human immunoglobulin genes, e.g., a partial repertoire of human heavy chain genes linked with a human constant gene, randomly inserted into the genome, in the presence or absence of a human light chain transgene. Although these mice were somewhat less than optimal for making useful high affinity antibodies, they facilitated certain functional analyses of immunoglobulin loci. Some of these mice had as few as two or three, or even just a single, heavy chain variable gene.

[0208] Mice that express fully human immunoglobulin heavy chains derived from a single human V_H5-51 gene and 10 human D_H genes and six human J_H genes, with human μ and γ 1 constant genes, on a randomly inserted transgene (and disabled endogenous immunoglobulin loci) have been reported (Xu and Davis, 2000, Diversity in the CDR3 Region of V_H Is Sufficient for Most Antibody Specificities, *Immunity* 13:37-45). The fully human immunoglobulin heavy chains of these mice are mostly expressed with one of just two fully mouse λ light chains derived from the endogenous mouse λ light chain locus (V λ 1-J λ 1 or V λ 2-J λ 2 only), and can express no κ light chain (the mice are Ig κ ^{-/-}). These mice exhibit severely abnormal dysfunction in B cell development and antibody expression. B cell numbers are reportedly 5-10% of wild-type, IgM levels 5-10% of wild-type, and IgG1 levels are only 0.1-1% of wild-type. The observed IgM repertoire revealed highly restricted junctional diversity. The fully human heavy chains display largely identical CDR3 length across antigens, the same J_H (J_H2) usage across antigens, and an initial junctional Q residue, thus reflecting a certain lack of CDR3 diversity. The fully mouse λ light chains nearly all had a W96L substitution in J λ 1 as initial junctional residue. The mice are reportedly unable to generate any antibodies against bacterial polysaccharide. Because the human variable domains couple with mouse light chains, the utility of the human variable regions is highly limited.

[0209] Other mice that have just a single human V_H3-23 gene, human D_H and J_H genes, and mouse light chain genes have been reported, but they exhibit a limited diversity (and thus a limited usefulness) due in part to mispairing potential between human V_H and mouse V_L domains (see, e.g., Mageed et al., 2001, Rearrangement of the human heavy chain variable region gene V3-23 in transgenic mice generates antibodies reactive with a range of antigens on the basis of VHCDR3 and residues intrinsic to the heavy chain variable region, *Clin. Exp. Immunol.* 123:1-5). Similarly, mice that bear two V_H genes (3-23 and 6-1) along with human D_H and J_H genes in a transgene containing the human μ constant gene (Bruggemann et al., 1991, Human antibody production in transgenic mice: expression from 100kb of the human IgH locus, *Eur. J. Immunol.* 21:1323-1326) and express them in human IgM chains with mouse light chains may exhibit a repertoire limited by mispairing (Mackworth-Young et al., 2003, The role of antigen in the selection of the human V3-23 immunoglobulin heavy chain variable region gene, *Clin. Exp. Immunol.* 134:420-425).

[0210] Other transgenic mice that express V_H-restricted fully human heavy chains from a human transgene randomly inserted in the genome, with a limited human λ repertoire expressed from a fully human randomly inserted transgene, have also been reported (see, e.g., Taylor et al., 1992, A transgenic mouse that expresses a diversity of human sequence heavy and light chain immunoglobulins, *Nucleic Acids Res.* 20(23):6287-6295; Wagner et al., 1994, Antibodies generated from human immunoglobulin miniloci in transgenic mice, *Nucleic Acids Res.* 22(8):1389-1393). However, transgenic mice that express fully human antibodies from transgenes randomly integrated into the mouse genome, and that comprise damaged endogenous loci, are known to exhibit substantial differences in immune response as compared with wild-type mice that affect the diversity of the antibody variable domains obtainable from such mice.

[0211] Useful non-human animals that generate a diverse population of B cells that express human antibody variable domains from a restricted V_H gene repertoire and one or more D genes and one or more J genes will be capable of generating, preferably in some cases, repertoires of rearranged variable region genes that will be sufficiently diverse. In various cases, diversity includes junctional diversity, somatic hypermutation, and polymorphic diversity in V_H gene sequence (for cases where V_H genes are present in polymorphic forms). Combinatorial diversity occurs in the pairing of the V_H gene with one of a plurality of cognate human light chain variable domains (which, in various cases, comprise junctional diversity and/or somatic hypermutations).

[0212] Non-human animals comprising a restricted human V_H gene repertoire and a complete or substantially complete human V_L gene repertoire will in various cases generate populations of B cells that reflect the various sources of diversity, such as junctional diversity (e.g., VDJ, VJ joining, P additions, N additions), combinatorial diversity (e.g., cognate V_H-re-

stricted human heavy, human light), and somatic hypermutations. In cases comprising a restriction of the V_H repertoire to one human V_H gene, the one human V_H gene can be present in two or more variants. In various cases, the presence of two or more polymorphic forms of a V_H gene will enrich the diversity of the variable domains of the B cell population.

[0213] Variations in the germline sequences of gene segments (e.g., V genes) contribute to the diversity of the antibody response in humans. The relative contribution to diversity due to V gene sequence differences varies among V genes. The degree of polymorphism varies across gene families, and is reflected in a plurality of haplotypes (stretches of sequence with coinherit polymorphisms) capable of generating further diversity as observed in V_H haplotype differences between related and unrelated individuals in the human population (see, e.g., Souroujon et al., 1989, Polymorphisms in Human H Chain V Region Genes from the VHIII Gene Family, J. Immunol. 143(2):706-711). Some have suggested, based on data from particularly polymorphic human V_H gene families, that haplotype diversity in the germline is a major contributor to V_H gene heterogeneity in the human population, which is reflected in the large diversity of different germline V_H genes across the human population (see, Sasso et al., 1990, Prevalence and Polymorphism of Human VH3 Genes, J. Immunol. 145(8):2751-2757).

[0214] Although the human population displays a large diversity of haplotypes with respect to the V_H gene repertoire due to widespread polymorphism, certain polymorphisms are reflected in prevalent (i.e., conserved) alleles observed in the human population (Sasso et al., 1990). V_H polymorphism can be described in two principle forms. The first is variation arising from allelic variation associated with differences among the nucleotide sequence between alleles of the same gene segment. The second arises from the numerous duplications, insertions, and/or deletions that have occurred at the immunoglobulin heavy chain locus. This has resulted in the unique situation in which V_H genes derived by duplication from identical genes differ from their respective alleles by one or more nucleotide substitutions. This also directly influences the copy number of V_H genes at the heavy chain locus.

[0215] Polymorphic alleles of the human immunoglobulin heavy chain variable gene segments (V_H genes) have largely been the result of insertion/deletion of gene segments and single nucleotide differences within coding regions, both of which have the potential to have functional consequences on the immunoglobulin molecule. Table 1 sets forth the functional V_H genes listed by human V_H gene family and the number of identified alleles for each V_H gene in the human immunoglobulin heavy chain locus. There are some findings to suggest that polymorphic V_H genes have been implicated in susceptibility to certain diseases such as, for example, rheumatoid arthritis, whereas in other cases a linkage between V_H and disease has been less clear. This ambiguity has been attributed to the copy number and presence of various alleles in different human populations. In fact, several human V_H genes demonstrate copy number variation (e.g., V_H 1-2, V_H 1-69, V_H 2-26, V_H 2-70, and V_H 3-23). In various cases, humanized mice as described herein with restricted V_H repertoires comprise multiple polymorphic variants of an individual V_H family member (e.g., two or more polymorphic variants of V_H 1-2, V_H 1-69, V_H 2-26, V_H 2-70, or V_H 3-23, replacing all or substantially all functional mouse V_H segments at an endogenous mouse locus). In a specific case, the two or more polymorphic variants of mice described herein are in number up to and including the number indicated for the corresponding V_H family member in Table 1 (e.g., for V_H 1-69, 13 variants; for V_H 1-2, five variants; etc.).

[0216] Commonly observed variants of particular human V_H genes are known in the art. For example, one of the most complex polymorphisms in the V_H locus belongs to the V_H 1-69 gene. The human V_H 1-69 gene has 13 reported alleles (Sasso et al., 1993, A fetally expressed immunoglobulin VH1 gene belongs to a complex set of alleles, Journal of Clinical Investigation 91:2358-2367; Sasso et al., 1996, Expression of the immunoglobulin VH gene 51p1 is proportional to its germline gene copy number, Journal of Clinical Investigation 97(9):2074-2080) and exists in at least three haplotypes that carry duplications of the V_H 1-69 gene, which results in multiple copies of the V_H gene at a given locus. These polymorphic alleles include differences in the complementarity determining regions (CDRs), which may dramatically influence antigen specificity. Table 2 sets forth the reported alleles for human V_H 1-69 and the SEQ ID NOs for the DNA and protein sequences of the mature heavy chain variable regions. Table 3 sets forth the reported alleles for human V_H 1-2 genes and the SEQ ID NOs for the DNA and protein sequences of the mature heavy chain variable regions.

[0217] Representative genomic DNA and full-length protein sequences of a V_H 1-69 gene are set forth in SEQ ID NO: 1 and SEQ ID NO: 2, respectively. FIG. 13 and FIG. 14 set forth DNA and protein alignments of thirteen reported V_H 1-69 alleles, respectively. Representative DNA and protein sequences of a V_H 1-2 gene are set forth in SEQ ID NO: 60 and SEQ ID NO: 61, respectively. FIG. 16 and FIG. 17 set forth DNA and protein alignments of five reported V_H 1-2 alleles, respectively. FIG. 15 and FIG. 18 set forth a percent identity/similarity matrix for aligned protein sequences corresponding to thirteen reported human V_H 1-69 alleles and five reported human V_H 1-2 alleles, respectively. In various cases, the modified locus comprises a V_H gene selected from Table 1, present in two or more copy number, wherein the copy number includes up to and including the number of alleles shown in Table 1. In one case, the modified locus comprises a V_H 1-69 gene selected from Table 2, present in two or more copy number, wherein the copy number includes up to and including the number of alleles shown in Table 1. In one case, the modified locus comprises a V_H 1-2 gene selected from Table 3, present in two or more copy number, wherein the copy number includes up to and including the number of alleles shown in Table 1.

[0218] Although cases employing a restricted human V_H repertoire in a mouse are extensively discussed, other non-

human animals that express a restricted human V_H repertoire are also described. Such non-human animals include any of those which can be genetically modified to express a restricted human V_H repertoire as disclosed herein, including, *e.g.*, mouse, rat, rabbit, pig, bovine (*e.g.*, cow, bull, buffalo), deer, sheep, goat, chicken, cat, dog, ferret, primate (*e.g.*, marmoset, rhesus monkey), *etc.* For example, for those non-human animals for which suitable genetically modifiable ES cells are not readily available, other methods are employed to make a non-human animal comprising the genetic modification. Such methods include, *e.g.*, modifying a non-ES cell genome (*e.g.*, a fibroblast or an induced pluripotent cell) and employing nuclear transfer to transfer the modified genome to a suitable cell, *e.g.*, an oocyte, and gestating the modified cell (*e.g.*, the modified oocyte) in a non-human animal under suitable conditions to form an embryo. Methods for modifying a non-human animal genome (*e.g.*, a pig, cow, rodent, chicken, *etc.* genome) include, *e.g.*, employing a zinc finger nuclease (ZFN) or a transcription activator-like effector nuclease (TALEN) to modify a genome to include a restricted human V_H repertoire. Thus, in one case a method is described for editing a non-human animal genome to include a restricted human V_H repertoire, comprising a step of editing the genome employing a ZFN or a TALEN to include no more than one, or no more than two, human V_H gene segments (or polymorphic variants thereof), wherein the no more than one or no more than two human V_H gene segments are operably linked to an immunoglobulin constant gene sequence. In one case, the constant gene sequence is selected from a human heavy chain constant sequence and a non-human heavy chain constant sequence. In one case, the constant sequence is non-human and the no more than one or no more than two human V_H gene segments are operably linked to non-human constant gene sequence at an endogenous non-human immunoglobulin locus.

[0219] In one case, the non-human animal is a small mammal, *e.g.*, of the superfamily Dipodoidea or Muroidea. In one case, the genetically modified animal is a rodent. In one case, the rodent is selected from a mouse, a rat, and a hamster. In one case, the rodent is selected from the superfamily Muroidea. In one case, the genetically modified animal is from a family selected from Calomyscidae (*e.g.*, mouse-like hamsters), Cricetidae (*e.g.*, hamster, New World rats and mice, voles), Muridae (true mice and rats, gerbils, spiny mice, crested rats), Nesomyidae (climbing mice, rock mice, with-tailed rats, Malagasy rats and mice), Platacanthomyidae (*e.g.*, spiny dormice), and Spalacidae (*e.g.*, mole rats, bamboo rats, and zokors). In a specific case, the genetically modified rodent is selected from a true mouse or rat (family Muridae), a gerbil, a spiny mouse, and a crested rat. In one case, the genetically modified mouse is from a member of the family Muridae,

[0220] In one case, the non-human animal is a rodent that is a mouse of a C57BL strain. In one case, the C57BL strain is selected from C57BL/A, C57BL/An, C57BL/GrFa, C57BL/KaLwN, C57BL/6, C57BL/6J, C57BL/6ByJ, C57BL/6N, C57BL/6NJ, C57BL/10, C57BL/10ScSn, C57BL/10Cr, and C57BL/Ola. In another case, the mouse is a 129 strain. In one case, the 129 strain is selected from the group consisting of 129P1, 129P2, 129P3, 129X1, 129S1 (*e.g.*, 129S1/SV, 129S1/SvIm), 129S2, 129S4, 129S5, 129S9/SvEvH, 129S6 (129/SvEvTac), 129S7, 129S8, 129T1, 129T2 (see, *e.g.*, Festing et al. (1999) Revised nomenclature for strain 129 mice, Mammalian Genome 10:836, see also, Auerbach et al. (2000) Establishment and Chimera Analysis of 129/SvEv- and C57BL/6-Derived Mouse Embryonic Stem Cell Lines). In one case, the genetically modified mouse is a mix of an aforementioned 129 strain and an aforementioned C57BL strain (*e.g.*, a C57BL/6 strain). In another case, the mouse is a mix of aforementioned 129 strains, or a mix of aforementioned C57BL/6 strains. In one case, the 129 strain of the mix is a 129S6 (129/SvEvTac) strain. In another case, the mouse is a mix of a 129/SvEv- and a C57BL/6-derived strain. In a specific case, the mouse is a mix of a 129/SvEv- and a C57BL/6-derived strain as described in Auerbach et al. 2000 BioTechniques 29:1024-1032. In another case, the mouse is a BALB strain, *e.g.*, BALB/c strain. In another case, the mouse is a mix of a BALB strain (*e.g.*, BALB/c strain) and another aforementioned strain.

[0221] In one case, the non-human animal is a rat. In one case, the rat is selected from a Wistar rat, an LEA strain, a Sprague Dawley strain, a Fischer strain, F344, F6, and Dark Agouti. In one case, the rat strain is a mix of two or more of a strain selected from the group consisting of Wistar, LEA, Sprague Dawley, Fischer, F344, F6, and Dark Agouti.

Table 1

V_H Family	V_H Gene	Alleles	V_H Family	V_H Gene	Alleles
V_{H1}	1-2	5	V_{H4}	4-4	7
	1-3	2		4-28	6
	1-8	2		4-30-1	1
	1-18	3		4-30-2	5
	1-24	1		4-30-4	6
	1-45	3		4-31	10
	1-46	3		4-34	13
	1-58	2		4-39	7
	1-69	13		4-59	10

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(continued)

	V _H Family	V _H Gene	Alleles	V _H Family	V _H Gene	Alleles
5					4-61	8
	V _H 2	2-5	10			
		2-26	1	V _H 5	5-51	5
		2-70	13			
				V _H 6	6-1	2
10		3-7	3			
		3-9	2		7-4-1	5
		3-11	4	V _H 7	7-81	1
		3-13	4			
		3-15	8			
15		3-16	2			
		3-20	1			
		3-21	4			
		3-23	5			
20		3-30	19			
	V _H 3	3-30-3	2			
		3-30-5	1			
		3-33	6			
		3-35	1			
25		3-38	2			
		3-43	2			
		3-48	4			
		3-49	5			
30		3-53	4			
		3-64	5			
		3-66	4			
		3-72	2			
		3-73	2			
35		3-74	3			

Table 2

	IgHV1-69 Allele	Accession Number	SEQ ID NO: (DNA/Protein)
40	IgHV1-69*01	L22582	34/35
	IgHV1-69*02	Z27506	36/37
	IgHV1-69*03	X92340	38/39
	IgHV1-69*04	M83132	40/41
45	IgHV1-69*05	X67905	42/43
	IgHV1-69*06	L22583	44/45
	IgHV1-69*07	Z29978	46/47
	IgHV1-69*08	Z14309	48/49
50	IgHV1-69*09	Z14307	50/51
	IgHV1-69*10	Z14300	52/53
	IgHV1-69*11	Z14296	54/55
	IgHV1-69*12	Z14301	56/57
55	IgHV1-69*13	Z14214	58/59

Table 3

IgHV1-2 Allele	Accession Number	SEQ ID NO: (DNA/Protein)
IgHV1-2*01	X07448	60/61
IgHV1-2*02	X62106	62/63
IgHV1-2*03	X92208	64/65
IgHV1-2*04	Z12310	66/67
IgHV1-2*05	HM855674	68/69

Antigen-Dependent V_H Gene Usage

[0222] Antigen-dependent preferential usage of V_H genes can be exploited in the development of human therapeutics targeting clinically significant antigens. The ability to generate a repertoire of antibody variable domains using a particular V_H gene can provide a significant advantage in the search for high-affinity antibody variable domains to use in human therapeutics. Studies on naive mouse and human V_H gene usage in antibody variable domains reveal that most heavy chain variable domains are not derived from any particular single or dominantly used V_H gene. On the other hand, studies of antibody response to certain antigens reveal that in some cases a particular antibody response displays a biased usage of a particular V_H gene in the B cell repertoire following immunization.

[0223] Although the human V_H repertoire is quite diverse, by some estimates the expected frequency of usage of any given V_H gene, assuming random selection of V_H genes, is about 2% (Brezinschek et al., 1995, Analysis of the Heavy Chain Repertoire of Human Peripheral B Cells Using Single-Cell Polymerase Chain Reaction, J. Immunol. 155:190-202). But V_H usage in peripheral B cells in humans is skewed. In one study, functional V gene abundance followed the pattern V_H3 > V_H4 > V_H1 > V_H2 > V_H5 > V_H6 (Davidkova et al., 1997, Selective Usage of VH Genes in Adult Human Lymphocyte Repertoires, Scand. J. Immunol. 45:62-73). One early study estimated that V_H3 family usage frequency was about 0.65, whereas V_H1 family usage frequency was about 0.15; these and other observations suggest that the germline complexity of the human V_H repertoire is not precisely reflected in the peripheral B cell compartment in humans that have a normal germline V_H repertoire, a situation that is similar to that observed in the mouse-*i.e.*, V_H gene expression is non-stochastic (Zouali and These, 1991, Probing VH Gene-Family Utilization in Human Peripheral B Cells by In Situ Hybridization, J. Immunol. 146(8):2855-2864). According to one report, V_H gene usage in humans, from greatest to least, is V_H3 > V_H4 > V_H1 > V_H5 > V_H2 > V_H6; rearrangements in peripheral B cells reveal that V_H3 family usage is higher than to be expected based on the relative number of germline V_H3 genes (Brezinschek et al., 1995). According to another report V_H usage in humans follows the pattern V_H3 > V_H5 > V_H2 > V_H1 > V_H4 > V_H6, based on analysis of pokeweed mitogen-activated peripheral small immunocompetent B cells (Davidkova et al., 1997, Selective Usage of VH Genes in Adult Human B Lymphocyte Repertoires, Scand. J. Immunol. 45:62-73). One report asserts that among the most frequently used V_H3 family members are 3-23, 3-30 and 3-54 (Brezinschek et al., 1995). In the V_H4 family, member 4-59 and 4-4b were found relatively more frequently (*id.*), as well as 4-39 and 4-34 (Brezinschek et al., 1997, Analysis of the Human VH Gene Repertoire, J. Clin. Invest. 99(10):2488-2501). Others postulate that the activated heavy chain repertoire is skewed in favor of high V_H5 expression and lower V_H3 expression (Van Dijk-Hard and Lundkvist, 2002, Long-term kinetics of adult human antibody repertoires, Immunology 107:136-144). Other studies assert that the most commonly used V_H gene in the adult human repertoire is V_H4-59, followed by V_H3-23 and V_H3-48 (Arnaout et al., 2001, High-Resolution Description of Antibody Heavy-Chain Repertoires in Humans, PLoS ONE 6(8):108). Although usage studies are based on relatively small sample numbers and thus exhibit high variance, taken together the studies suggest that V gene expression is not purely stochastic. Indeed, studies with particular antigens have established that-in certain cases-the deck is firmly stacked against certain usages and in favor of others.

[0224] Over time, it became apparent that the observed repertoire of human heavy chain variable domains generated in response to certain antigens is highly restricted. Some antigens are associated almost exclusively with neutralizing antibodies having only certain particular V_H genes, in the sense that effective neutralizing antibodies are derived from essentially only one V_H gene. Such is the case for a number of clinically important human pathogens.

[0225] V_H1-69-derived heavy chains have been observed in a variety of antigen-specific antibody repertoires of therapeutic significance. For instance, V_H1-69 was frequently observed in heavy chain transcripts of an IgE repertoire of peripheral blood lymphocytes in young children with atopic disease (Bando et al., 2004, Characterization of VHε gene expressed in PBL from children with atopic diseases: detection of homologous VH1-69 derived transcripts from three unrelated patients, Immunology Letters 94:99-106). V_H1-69-derived heavy chains with a high degree of somatic hypermutation also occur in B cell lymphomas (Perez et al., 2009, Primary cutaneous B-cell lymphoma is associated with somatically hypermutated immunoglobulin variable genes and frequent use of VH1-69 and VH4-59 segments, British Journal of Dermatology 162:611-618), whereas some V_H1-69-derived heavy chains with essentially germline sequences (*i.e.*, little to no somatic hypermutation) have been observed among autoantibodies in patients with blood disorders (Pos

et al., 2008, VH1-69 germline encoded antibodies directed towards ADAMTS13 in patients with acquired thrombotic thrombocytopenic purpura, *Journal of Thrombosis and Haemostasis* 7:421-428).

[0226] Further, neutralizing antibodies against viral antigens such as HIV, influenza and hepatitis C (HCV) have been found to utilize germline and/or somatically mutated V_H1-69-derived sequences (Miklos et al., 2000, Salivary gland mucosa-associated lymphoid tissue lymphoma immunoglobulin VH genes show frequent use of V1-69 with distinctive CDR3 features, *Blood* 95(12):3878-3884; Kunert et al., 2004, Characterization of molecular features, antigen-binding, and in vitro properties of IgG and IgM variants of 4E10, an anti-HIV type I neutralizing monoclonal antibody, *Aids Research and Human Retroviruses* 20(7):755-762; Chan et al., 2001, VH1-69 gene is preferentially used by hepatitis C virus-associated B cell lymphomas and by normal B cells responding to the E2 viral antigen, *Blood* 97(4):1023-1026; Carbonari et al., 2005, Hepatitis C virus drives the unconstrained monoclonal expansion of VH1-69-expressing memory B cells in type II cryoglobulinemia: A model of infection-driven lymphomagenesis, *Journal of Immunology* 174:6532-6539; Wang and Palese, 2009, Universal epitopes of influenza virus hemagglutinins?, *Nature Structural & Molecular Biology* 16(3):233-234; Sui et al., 2009, Structural and functional bases for broad-spectrum neutralization of avian and human influenza A viruses, *Nature Structural & Molecular Biology* 16(3):265-273; Marasca et al., 2001, Immunoglobulin Gene Mutations and Frequent Use of VH1-69 and VH4-34 Segments in Hepatitis C Virus-Positive and Hepatitis C Virus-Negative Nodal Marginal Zone B-Cell Lymphoma, *Am. J. Pathol.* 159(1):253-261).

[0227] V_H usage bias is also observed in the humoral immune response to *Haemophilus influenzae* type b (Hib PS) in humans. Studies suggest that the V_HIII family (the V_HIIIb subfamily in particular, V_H9.1) exclusively characterizes the human humoral response to Hib PS, with diverse D and J genes (Adderson et al., 1991, Restricted Ig H Chain V Gene Usage in the Human Antibody Response to *Haemophilus influenzae* Type b Capsular Polysaccharide, *J. Immunol.* 147(5):1667-1674; Adderson et al., 1993, Restricted Immunoglobulin VH Usage and VDJ Combinations in the Human Response to *Haemophilus influenzae* Type b Capsular Polysaccharide, *J. Clin. Invest.* 91:2734-2743). Human J_H genes also display biased usage; J_H4 and J_H6 are observed at about 38-41% in peripheral B cells in humans (Brezinschek et al., 1995).

[0228] V_H usage in HIV-1-infected humans is reportedly biased against V_H3 usage and in favor of V_H1 and V_H4 gene families (Wisniewski et al., 1996, Human Antibody Variable Region Gene Usage in HIV-1 Infection, *J. Acquired Immune Deficiency Syndromes & Human Retrovirology* 11(1):31-38). However, cDNA analysis of bone marrow from affected patients' revealed significant V_H3 usage not expressed in the functional B cell repertoire, where Fabs reflecting the V_H3 usage exhibited effective *in vitro* neutralization of HIV-1 (*Id.*). It might be postulated that the humoral immune response to HIV-1 infection is possibly attenuated due to the V_H restriction; modified non-human animals as described herein (not infectable by HIV-1) might thus be useful for generating neutralizing antibody domains derived from particular V_H genes present in the genetically modified animals described herein, but derived from different V_H genes than those observed in the restricted repertoire of affected humans.

[0229] Thus, the ability to generate high affinity human antibody variable domains in V_H-restricted mice, e.g., (restricted, e.g., to a V_H3 family member and polymorph(s) thereof) immunized with HIV-1 might provide a rich resource for designing effective HIV-1-neutralizing human therapeutics by thoroughly mining the restricted (e.g., restricted to a V_H3 family member or variant(s) thereof) repertoire of such an immunized mouse.

[0230] Restriction of the human antibody response to certain pathogens may reduce the likelihood of obtaining antibody variable regions from affected humans that can serve as springboards for designing high affinity neutralizing antibodies against the pathogen. For example, the human immune response to HIV-1 infection is clonally restricted throughout HIV-1 infection and into AIDS progression (Muller et al., 1993, B-cell abnormalities in AIDS: stable and clonally restricted antibody response in HIV-1 infection, *Scand. J. Immunol.* 38:327-334; Wisniewski et al., 1996). Further, V_H genes are in general not present in all polymorphic forms in any particular individual; certain individuals in certain populations possess one variant, whereas individuals in other populations possess a different variant. Thus, the availability of a biological system that is restricted to a single V_H gene and its variants will in various embodiments provide a hitherto unexploited source of diversity for generating antibody variable regions (e.g., human heavy and light cognate domains) based on a restricted V_H gene. Thus, in one case, a genetically modified non-human animal is described that comprises a plurality of polymorphic variants of no more than one, or no more than two, human V_H gene segment family member. In one case, the no more than one, or no more than two, human V_H gene segments are operably linked to one or more human D_H gene segments, one or more human J_H gene segments, and a human or non-human constant region gene segment. In one case the constant region is at an endogenous non-human immunoglobulin constant gene locus. In one case, the non-human animal further comprises a nucleic acid sequence derived from a human V_L sequence, e.g., a rearranged or unrearranged human V_L gene segment or a rearranged human V_L/J_L sequence. In one case, the nucleic acid sequence derived from the human V_L sequence is at an endogenous non-human V_L gene locus; in one case, the nucleic acid sequence derived from the human V_L sequence is on a transgene. In a specific case, the non-human animal is incapable of expressing an immunoglobulin light chain variable domain that itself comprises an endogenous V_L or J_L gene segment, and comprises no more than one, or no more than two, light chain genes that encode rearranged human V_L domains (*i.e.*, from no more than one, or no more than two, rearranged human V_L/J_L sequences).

[0231] Genetically modified mice that express human heavy chain variable regions with restricted V_H gene segment usage are useful to generate a relatively large repertoire of functionally diverse, combinatorially diverse, and somatically mutated high affinity human immunoglobulin heavy chain variable regions from an otherwise restricted repertoire. A restricted repertoire, in one case, refers to a predetermined limitation in the number and/or identity of germline genes that results in the mouse being unable to form a rearranged heavy chain gene that is derived from any V gene other than a preselected V gene. In cases that employ a preselected V gene but not a preselected D and/or J gene, the repertoire is restricted with respect to the identity of the V gene but not the D and/or J gene (e.g., the repertoire consists essentially of no more than one, or no more than two, V_H gene segments (and/or polymorphs thereof); and a plurality of D gene segments and a plurality of J gene segments)). The identity of the preselected V gene (and any preselected D and/or J genes) is not limited to any particular V gene.

[0232] Designing a mouse so that it rearranges a single V_H gene (present as a single segment or a set of variants) with a variety of human D and J gene segments (e.g., D_H and J_H segments) provides an *in vivo* junctional diversity/combinatorial diversity/somatic hypermutation permutation machine that can be used to iterate mutations in resulting rearranged heavy chain variable region sequences (e.g., V/D/J or V/J, as the case may be). In such a mouse, the clonal selection process operates to select suitable variable regions that bind an antigen of interest that are based on a single preselected V_H gene (or variants thereof). Because the mouse's clonal selection components are dedicated to selection based on the single preselected V_H gene segment, background noise (e.g., a wide variety of non antigen-binding V_H domains derived from many germline gene segments) is largely eradicated. With judicious selection of the V_H gene segment, a relatively larger number of clonally selected, antigen-specific antibodies can be screened in a shorter period of time than with a mouse with a large diversity of V segments.

[0233] Preselecting limited repertoire and restricting a mouse to a single V segment provides a system for permuting V/D/J junctions at a rate that is in various cases higher than that observed in mice that otherwise have up to 40 or more V segments to recombine with D and J regions. Removal of other V segments frees the locus to form more V/D/J combinations for the preselected V segment than otherwise observed. The increased number of transcripts that result from the recombination of the preselected V with one of a plurality of D and one of a plurality of J segments will feed those transcripts into the clonal selection system in the form of pre-B cells, and the clonal selection system is thus dedicated to cycling B cells that express the preselected V region. In this way, more unique V region rearrangements derived from the preselected V segment can be screened by the organism than would otherwise be possible in a given amount of time.

[0234] In various cases, mice are described that enhance the junctional diversity of V/D/J recombinations for the preselected V region, because all or substantially all recombinations of the immunoglobulin heavy chain variable locus will be of the preselected V segment and the D and J segments that are placed in such mice. Therefore, the mice provide a method for generating a diversity of CDR3 segments using a base, or restricted V_H gene repertoire.

[0235] In one case, a non-human animal is described, wherein the B cell population of the non-human animal expresses immunoglobulin heavy chains that are derived from no more than one, or no more than two human V_H gene segments. In one case, each of the no more than one, or no more than two, human V_H gene segments are present in two or more polymorphic forms. In one case, the human V_H gene segment is present in three, four, five, six, seven, eight, nine, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 polymorphic forms. In one case, the non-human animal expresses a human light chain variable domain derived from a human V_L gene segment.

[0236] In one case, a method is described for generating a B cell population in a non-human animal, wherein the B cell population expresses human heavy chains derived from a single germline human V_H gene segment and two or more human D gene segments and two or more human J gene segments; the method comprising a step of immunizing a non-human animal as described herein with an antigen of interest, and allowing the non-human animal to mount an immune response to the antigen of interest, wherein the immune response comprises expressing the human heavy chains on the surface of B cells in the B cell population. In one case, the non-human animal is a rodent (e.g., a mouse or rat). In one case, the human V_H gene segment, human D_H segment, and human J_H segment are operably linked to a non-human constant region gene. In one case, the non-human animal further comprises a nucleic acid sequence encoding a human V_L domain. In one case, the nucleic acid sequence encoding the human V_L domain is linked to a non-human light chain constant region gene sequence.

[0237] In one case, a method for making a non-human animal that expresses an immunoglobulin population characterized by the immunoglobulins having heavy chains that are derived from a plurality of rearrangements of a single human V_H gene segment (or single human V_H gene family member) and one of a plurality of D_H gene segments and one of a plurality of J_H gene segments, is described. In one case, the human V_H gene segment is a human V_H1-69 gene segment. In one case, the human V_H gene segment is a human V_H1-2 gene segment.

[0238] In one case, a method is described for generating a population of human immunoglobulin heavy chain variable domains whose CDR1 and CDR2 are derived from the same germline V_H gene segment, and whose CDR3 are derived from the germline gene segment and two or more human D segments, and two or more human J segments; the method comprising immunizing a non-human animal as described herein with an antigen of interest, and allowing the non-human

animal to mount an immune response to the antigen of interest, wherein the immune response comprises expressing the human heavy chain variable domains in the context of a light chain variable domain. In one case, the non-human animal is a rodent (e.g., a mouse or rat). In one case, the human V_H gene segment, human D segment, and human J segment are operably linked to a non-human constant region gene. In one case, the non-human animal further comprises a nucleic acid sequence encoding a human V_L domain. In one case, the nucleic acid sequence encoding the human V_L domain is linked to a non-human light chain constant region gene sequence.

[0239] In one case, a genetically modified non-human animal is described, wherein the non-human animal is incapable of expressing a non-human V_H domain, and wherein each immunoglobulin heavy chain of the heavy chain population expressed in the animal comprises a human V_H domain comprising a CDR1 and a CDR2 that are identical but for one or more somatic hypermutations, and wherein the heavy chain population comprises a plurality of CDR3 sequences derived from a plurality of rearrangements with a plurality of D and J gene segments.

[0240] In one case, a biological system for generating variation in CDR3 identity and length is described, comprising a genetically modified non-human animal as described herein, wherein the non-human animal comprises no more than or no more than two human V_H gene segments, and two or more D gene segments and one or more J gene segments, wherein the non-human animal further comprises a humanized immunoglobulin light chain locus. In various cases, the non-human animal in response to immunization with an antigen of interest generates an immune response that comprises expressing an immunoglobulin heavy chain population characterized by each heavy chain having CDR1 s and CDR2s that differ only by somatic hypermutation, and CDR3s that differ by rearrangement and somatic hypermutation. In one case, the biological system is a mouse that is genetically modified as described herein. In one case, the human V_H gene segment and the human V_L gene segment are at endogenous mouse heavy and light immunoglobulin loci, respectively. In one case, one or more of the human V_H gene segment and the human V_L gene segment are on transgenes (i.e., at a locus other than an endogenous immunoglobulin locus).

EXAMPLES

[0241] The following examples are provided so as to describe to those of ordinary skill in the art how to make and use methods and compositions of the invention, and are not intended to limit the scope of what the inventors regard as their invention. Unless indicated otherwise, temperature is indicated in Celsius, and pressure is at or near atmospheric. In the foregoing Examples, when the use of kits and/reagents from various suppliers is indicated, all procedures were carried out according to manufacturer's specifications.

Example 1 Construction of Restricted Heavy Chain Loci

[0242] A uniquely engineered human heavy chain locus containing a single human V_H gene segment located upstream of all the human D_H and J_H gene segments was created by a series of homologous recombination reactions in bacterial cells (BHR) using Bacterial Artificial Chromosome (BAC) DNA. Several targeting constructs for creation of a single V_H containing heavy chain locus were constructed using VELOCIGENE® genetic engineering technology (see, e.g., US Pat. No. 6,586,251 and Valenzuela, D.M. et al. (2003) High-throughput engineering of the mouse genome coupled with high-resolution expression analysis. Nature Biotechnology 21(6): 652-659).

[0243] Construction of a Human V_H1-69 Restricted Heavy Chain Locus. Briefly, four modifications were performed using human BAC DNA to create a targeting construct containing a human V_H1-69 gene segment with all the human D_H and J_H segments (FIG. 1). In the first modification, a modified human BAC containing multiple distal (5') human V_H gene segments, including V_H1-69, an upstream hygromycin selection cassette and a 5' mouse homology arm was targeted with a second spectinomycin cassette, which also contained a modified recombination signal sequence (RSS; BHR 1, FIG. 1, top left). This modified recombination signal sequence (RSS) introduced two point mutations (T to A and G to A) in the 3' RSS region of the human V_H1-69 gene changing the RSS nonamer to the optimal consensus sequence. Thus, the first modification (BHR 1) created a human genomic fragment containing the human V_H1-69 gene segment with a modified 3' RSS, a unique AsiSI restriction site about 180 bp downstream of the RSS and a spectinomycin cassette (FIG. 1, middle left).

[0244] The second modification (BHR 2) included the use of a neomycin (Neo) cassette flanked by Frt sites to delete the hygromycin cassette and 5' human V_H gene segments upstream of the V_H1-69 gene segment. This modification was targeted 5' to the human V_H1-69 gene segment to leave intact about 8.2 kb of the promoter region of human V_H1-69 and the 5' mouse homology arm (FIG. 1, bottom left).

[0245] The third modification (BHR 3) included another spectinomycin cassette flanked by uniquely engineered 5' P1-SceI and 3' AsiSI sites targeted to a human genomic fragment containing the first three functional human V_H gene segments and all the human D_H and J_H gene segments (FIG. 1, middle right). The human genomic fragment was previously targeted with a neomycin cassette and contained 5' and 3' homology arms containing the mouse genomic sequence 5' and 3' of the endogenous heavy chain locus including the 3' intronic enhancer and the IgM gene. This

modification deleted the 5' mouse genomic sequence and human V_H gene segments, leaving about 3.3 kb of the V_H-D_H intergenic region upstream of the human D_H1-1 gene segment, all of the human D_H and J_H segments, and the 3' mouse genomic fragment containing the 3' intronic enhancer and the IgM gene (FIG. 1, bottom right).

[0246] The fourth modification was achieved by employing the unique P_I-SceI and AsiSI sites (described above) to ligate the two modified BACs from BHR 2 and BHR 3 (FIG. 1, bottom center), which yielded the final targeting construct. The final targeting construct for the creation of a modified heavy chain locus containing a single human V_H gene segment and all the human D_H and J_H gene segments in ES cells contained, from 5' to 3', a 5' homology arm containing about 20 kb of mouse genomic sequence upstream of the endogenous heavy chain locus, a 5' Frt site, a neomycin cassette, a 3' Frt site, about 8.2 kb of the human V_H1-69 promoter, the human V_H1-69 gene segment with a modified 3' RSS, 27 human D_H gene segments, six human J_H segments, and a 3' homology arm containing about 8 kb of mouse genomic sequence downstream of the mouse J_H gene segments including the 3' intronic enhancer and IgM gene (FIG. 1, bottom). The Human V_H1-69 Targeting Vector (SEQ ID NO: 3) was linearized and electroporated into mouse ES cells heterozygous for a deletion of the endogenous heavy chain locus.

[0247] Reference Example: Construction of a Human V_H1-2 Restricted Heavy Chain Locus. Using the steps described above, other polymorphic V_H gene segments in the context of mouse heavy chain constant regions are employed to construct a series of mice having a restricted number immunoglobulin heavy chain V segments (e.g., 1, 2, 3, 4, or 5), wherein the V segments are polymorphic variants of a V gene family member. Exemplary polymorphic V_H gene segments are derived from human V_H gene segments including, e.g., V_H1-2, V_H2-26, V_H2-70 and V_H3-23. Such human V_H gene segments are obtained, e.g., by de novo synthesis (e.g., Blue Heron Biotechnology, Bothell, WA) using sequences available on published databases. Thus, DNA fragments encoding each V_H gene are, in some cases, generated independently for incorporation into targeting vectors, as described herein. In this way, multiple modified immunoglobulin heavy chain loci comprising a restricted number of V_H gene segments are engineered in the context of mouse heavy chain constant regions. An exemplary targeting strategy for creating a restricted humanized heavy chain locus containing a human V_H1-2 gene segment, 27 human D_H gene segments, and six human J_H gene segments is shown in FIG. 2.

[0248] Briefly, a modified human BAC clone containing three human V_H gene segments (V_H6-1, V_H1-2, V_H1-3), 27 human D_H gene segments, and six human J_H gene segments (see USSN 13/404,075; filed 24 February 2012) is used to create a restricted humanized heavy chain locus containing a human V_H1-2 gene segment. This modified BAC clone functionally links the aforementioned human heavy chain gene segments with the mouse intronic enhancer and the IgM constant region. The restricted human V_H1-2 based heavy chain locus is achieved by two homologous recombinations using the modified human BAC clone described above.

[0249] For the first homologous recombination, 205 bp of the human V_H6-1 gene segment (from about 10 bp upstream (5') of the V_H6-1 start codon in exon 1 to about 63 bp downstream (3') of the beginning of exon 2) in the modified human BAC clone is deleted by bacterial homologous recombination using a spectinomycin (aadA) cassette flanked by unique P_I-SceI restriction sites (FIG. 2, BHR 1). This allows for subsequent removal of the aadA cassette without disrupting other human gene segments within the restricted heavy chain locus.

[0250] For the second homologous recombination, the 5' end of the modified human BAC clone including the entire human V_H1-3 gene segment and about 60 bp downstream (3') of the gene segment is deleted by homologous recombination using a hygromycin cassette containing flanking 5' AsiSI and 3' AscI restriction sites (FIG. 2, BHR 2). As described above, the spectinomycin cassette is optionally removed after confirmation of the final targeting vector including deletion of the two human V_H gene segments flanking the human V_H1-2 gene segment (FIG. 2, bottom). An exemplary human V_H1-2 targeting vector is set forth in SEQ ID NO: 70.

[0251] Employing polymorphic V_H gene segments in a restricted immunoglobulin heavy chain locus represents a novel approach for generating antibodies, populations of antibodies, and populations of B cells that express antibodies having heavy chains with diverse CDRs derived from a single human V_H gene segment. Exploiting the somatic hypermutation machinery of the host animal along with combinatorial association with rearranged human immunoglobulin light chain variable domains results in the engineering of unique heavy chains and unique V_H/V_L pairs that expand the immune repertoire of genetically modified animals and enhance their usefulness as a next generation platform for making human therapeutics, especially useful as a platform for making neutralizing antibodies specific for human pathogens.

[0252] Thus, using the strategy outlined above for incorporation of additional and/or other polymorphic V_H gene segments into the mouse immunoglobulin heavy chain locus allows for the generation of novel antibody repertoires for use in neutralizing human pathogens that might otherwise effectively evade the host immune system.

[0253] Targeted ES cells described above were used as donor ES cells and introduced into an 8-cell stage mouse embryo by the VELOCIMOUSE® method (*supra*). Mice bearing a humanized heavy chain locus containing a single human V_H gene segment, all the human D_H and J_H gene segments operably linked to the mouse immunoglobulin constant region genes were identified by genotyping using a modification of allele assay (Valenzuela *et al.*, *supra*) that detected the presence of the neomycin cassette, the human V_H gene segment and a region within the human D_H and J_H gene segments as well as endogenous heavy chain sequences. Table 4 sets forth the primers and probes used in

this assay to confirm mice harboring a restricted heavy chain locus containing a single human V_H1-69 gene segment, 27 human D_H gene segments and six human J_H gene segments.

[0254] Mice bearing an engineered heavy chain locus that contains a single human V_H gene segment can be bred to a FLPe deleter mouse strain (see, e.g., Rodriguez, C.I. et al. (2000) High-efficiency deleter mice show that FLPe is an alternative to Cre-loxP. Nature Genetics 25: 139-140) in order to remove any Frt^red neomycin cassette introduced by the targeting vector that is not removed, e.g., at the ES cell stage or in the embryo. Optionally, the neomycin cassette is retained in the mice.

[0255] Pups are genotyped and a pup heterozygous for a humanized heavy chain locus containing a single human V_H gene segment, all the human D_H and J_H segments operably linked to the endogenous mouse immunoglobulin constant genes is selected for characterizing the immunoglobulin heavy chain repertoire.

Table 4

Name (Region Detected)	Sequence (5'-3')	SEQ ID NO:
hyg (hygromycin cassette)	Forward: TCGGGCCGAT CTTAGCC	4
	Reverse: TTGACCGATT CCTTGCGG	5
	Probe: ACGAGCGGGT TCGGCCCCATT C	6
neo (neomycin cassette)	Forward: GGTGGAGAGG CTATTCGGC	7
	Reverse: GAACACGGCG GCATCAG	8
	Probe: TGGGCACAAC AGACAATCGG CTG	9
hlgH9T (human D _H - J _H genomic sequence)	Forward: TCCTCCAACG ACAGGTCCC	10
	Reverse: GATGAACTGA CGGGCACAGG	11
	Probe: TCCCTGGAAC TCTGCCCCGA CACA	12
77h3 (human V _H 1-69 gene segment)	Forward: CTCTGTGGAA AATGGTATGG AGATT	13
	Reverse: GGTAAGCATA GAAGGTGGGT ATCTTT	14
	Probe: ATAGAACTGT CATTGTGTCC AGCAATCCCA	15
mIgHA7 (mouse D _H - J _H genomic sequence)	Forward: TGGTCACCTC CAGGAGCCTC	16
	Reverse: GCTGCAGGGT GTATCAGGTG C	17
	Probe: AGTCTCTGCT TCCCCCTTGT GGCTATGAGC	18
88710T (mouse 3' V _H genomic sequence)	Forward: GATGGGAAGA GACTGGTAAC ATTTGTAC	19
	Reverse: TTCCTCTATT TCACTCTTTG AGGCTC	20
	Probe: CCTCCACTGT GTTAATGGCT GCCACAA	21
mIgHd10 (mouse 5' V _H genomic sequence)	Forward: GGTGTGCGAT GTACCCTCTG AAC	22
	Reverse: TGTGGCAGTT TAATCCAGCT TTATC	23
	Probe: CTAAAAATGC TACACCTGGG GCAAAACACC TG	24
mIgHp2 (mouse J _H genomic sequence)	Forward: GCCATGCAAG GCCAAGC	25
	Reverse: AGTTCTTGAG CCTTAGGGTG CTAG	26
	Probe: CCAGGAAAAT GCTGCCAGAG CCTG	27

Example 2 Characterization of Mice Expressing Heavy Chains Derived From a Single Human V_H Gene Segment

[0256] Mice homozygous for a single human V_H gene segment at the endogenous heavy chain locus as described in Example 1 were evaluated for expression and B cell development using flow cytometry.

[0257] Briefly, spleens and bone marrow was harvested from wild type (n=3 per group; six weeks old, male and female) and mice homozygous for a single human V_H gene segment, all human D_H and J_H gene segments operably linked to

mouse heavy chain constant regions. Red blood cells from spleens were lysed with ACK lysis buffer (Lonza Walkersville), followed by washing with complete RPMI medium.

[0258] Flow cytometry. Cells (1×10^6) were incubated with anti-mouse CD16/CD32 (2.4G2, BD PHARMINGEN™) on ice for 10 minutes, followed by labeling with the following antibody panels for 30 minutes on ice. Bone marrow panel: anti-mouse FITC-CD43 (1 B11, BioLegend), PE-ckit (2B8, BIOLEGEND®), PeCy7-IgM (II/41, EBIOSCIENCE®), PerCP-Cy5.5-IgD (11-26c.2a, BIOLEGEND®), APC-eFluor 780-B220 (RA3-6B2, EBIOSCIENCE®), APC-CD19 (MB19-1, EBIOSCIENCE®). Bone marrow and spleen panel: anti-mouse FITC-Igκ (187.1, BD Biosciences), PE-Igλ (RML-42, BIOLEGEND®), PeCy7-IgM (II/41, EBIOSCIENCE®), PerCP-Cy5.5-IgD (11-26c.2a, BIOLEGEND®), Pacific Blue-CD3 (17A2, BIOLEGEND®), APC-B220 (RA3-6B2, EBIOSCIENCE®), APC-H7-CD19 (ID3, BD Biosciences). Bone marrow: immature B cells (B220^{int}IgM⁺), mature B cells (B220^{hi}IgM⁺), pro B cells (CD19⁺ckit⁺CD43⁺), pre B cells (CD19⁺ckit⁺CD43⁻), immature Igκ⁺ B cells (B220^{int}IgM⁺Igκ⁺Igλ⁻), immature Igλ⁺ B cells (B220^{int}IgM⁺Igκ⁻Igλ⁺), mature Igκ⁺ B cells (B220^{hi}IgM⁺Igκ⁺Igλ⁻), mature Igλ⁺ B cells (B220^{hi}IgM⁺Igκ⁻Igλ⁺). Spleen: B cells (CD19⁺), mature B cells (CD19⁺IgD^{hi}IgM^{int}), transitional/immature B cells (CD19⁺IgD^{int}IgM^{hi}). Bone marrow and spleen: Igκ⁺ B cells (CD19⁺Igκ⁺Igλ⁻), Igλ⁺ B cells (CD19⁺Igκ⁻Igλ⁺).

[0259] Following staining, cells were washed and fixed in 2% formaldehyde. Data acquisition was performed on a LSRII flow cytometer and analyzed with FLOWJO™ software (Tree Star, Inc.). Results for the splenic compartment are shown in FIGs. 3, 4A and 5 - 7. Results for the bone marrow compartment are shown in FIGs. 4B and 8 - 11B.

[0260] Human V_H Expression. Expression of the human V_H1-69 gene segment was determined for mice heterozygous and homozygous for a human V_H1-69 gene segment, all human D_H and J_H gene segments operably linked to mouse heavy chain constant regions by a quantitative PCR assay using TAQMAN® probes.

[0261] Briefly, CD19⁺ B cells were purified from the spleens of groups of mice (n=3 per group) using mouse CD19 microbeads (Miltenyi Biotec) according to manufacturer's specifications. Total RNA was purified using the RNEASY™ Mini kit (Qiagen) and genomic RNA was removed using an RNase-free DNase on-column treatment (Qiagen). About 200 ng mRNA was reverse-transcribed into cDNA using the First Stand cDNA Synthesis kit (Invitrogen), followed by amplification with the TAQMAN® Universal PCR Master Mix (Applied Biosystems) using the ABI 7900 Sequence Detection System (Applied Biosystems). Unique primer/probe combinations were employed to specifically determine expression of human V_H1-69-derived heavy chains (Table 5). Relative expression was normalized to the mouse κ constant region (mCκ). The results are shown in FIG. 12.

Table 5

Name	Sequence (5'-3')	SEQ ID NO:
hlgHV1-69	Sense: AACTACGCAC AGAAGTTCCA GG	28
	Anti-sense: GCTCGTGGAT TTGTCCGC	29
	Probe: CAGAGTCACG ATTACC	30
mCκ	Sense: TGAGCAGCAC CCTCACGTT	31
	Antisense: GTGGCCTCAC AGGTATAGCT GTT	32
	Probe: ACCAAGGACG AGTATGAA	33

Example 3 Humoral Immune Response in Mice Expressing Heavy Chains Derived From a Single Human V_H Gene Segment

[0262] The humoral immune response was determined for mice homozygous for human heavy and κ light chain variable gene loci (Hκ) and mice homozygous for a single human V_H gene segment, all human D_H and J_H gene segments operably linked to mouse heavy chain constant regions (1hV_H HO) by comparative immunization using a human cell surface receptor (Antigen A).

[0263] Immunization. Serum was collected from groups of mice prior to immunization with the above antigen. Antigen (2.35 μg each) was administered in an initial priming immunization mixed with 10 μg of CpG oligonucleotide (Invivogen) and 25 μg of Adju-phos (Brenntag) as adjuvants. The immunogen was administered via footpad (f.p.) in a volume of 25 μl per mouse. Subsequently, mice were boosted via f.p. with 2.3 μg of antigen along with 10 μg CpG and 25 μg Adju-Phos as adjuvants on days 3, 6, 11, 13, 17, and 20 for a total of six boosts. Mice were bled on days 15 and 22 after the fourth and sixth boosts, respectively, and antisera were assayed for antibody titers to Antigen A.

[0264] Antibody titers were determined in sera of immunized mice using an ELISA assay. Ninety six-well microtiter plates (Thermo Scientific) were coated with Antigen A (1 μg/ml) in phosphate-buffered saline (PBS, Irvine Scientific) overnight at 40°C. The following day, plates were washed with phosphate-buffered saline containing 0.05% Tween 20 (PBS-T, Sigma-Aldrich) four times using a plate washer (Molecular Devices). Plates were then blocked with 250 μl of

1% bovine serum albumin (BSA, Sigma-Aldrich) in PBS and incubated for one hour at room temperature. The plates were then washed four times with PBS-T. Sera from immunized mice and pre-immune sera were serially diluted ten-fold in 0.1% BSA PBS-T starting at 1:100 and added to the blocked plates in duplicate and incubated for one hour at room temperature. The last two wells were left blank to be used as secondary antibody control. The plates were again washed four times with PBS-T in a plate washer. A 1:5000 dilution of goat anti-mouse IgG-Fc-Horse Radish Peroxidase (HRP, Jackson ImmunoResearch) conjugated secondary antibody was added to the plates and incubated for one hour at room temperature. Plates were again washed eight times with PBS-T and developed using TMB/H₂O₂ as substrate. The substrate was incubated for twenty minutes and the reaction stopped with 1 N H₂SO₄ (VWR). Plates were read on a spectrophotometer (Victor, Perkin Elmer) at 450 nm. Antibody titers were calculated using GRAPHPAD PRISM™ (GraphPad Software, Inc).

[0265] Serum titer was calculated as serum dilution within experimental titration range at the signal of antigen binding equivalent to two times above background. Antibody titer for the humoral immune response against a human cell surface receptor (Antigen A) is set forth in FIG. 19.

[0266] In a similar experiment, humoral immune responses were determined for mice homozygous for human heavy and κ light chain variable gene loci (H κ) and mice homozygous for a single human V_H gene segment, all human D_H and J_H gene segments operably linked to mouse heavy chain constant regions (1hV_H HO) by comparative immunization using influenza viral vaccines FLUVIRIN® (Novartis Vaccines) and FLUMIST® (MedImmune LLC).

[0267] Briefly, serum was collected from groups of mice prior to immunization with the above antigen (as described above). Mice (n=5) homozygous for a single human V_H gene segment (V_H1-69), all human D_H and J_H gene segments operably linked to mouse heavy chain constant regions (1hV_H HO) were immunized intra-nasally (*i.n.*) with FLUMIST® (live attenuated influenza vaccine) at 1/3 the normal dose/mouse. One normal dose of FLUMIST® contains 10^{6.5-7.5} FFU (fluorescent focus units) of live attenuated influenza vaccine. Therefore, each mouse was primed with 70 μ l FLUMIST® on day 1 followed by *i.n.* boost on days 3, 6, 11, 13, 17, 20 for a total of 6 boosts. No adjuvants were employed in this immunization. The mice were bled on days 15 and 22 after 4th and 6th boosts respectively and antiserum assayed for antibody titers to FLUMIST® (as described above).

[0268] In a similar manner, in immunizations with FLUVIRIN®, pre-immune serum was collected from mice prior to initiation of immunization. Mice (n=5) homozygous for a single human V_H gene segment (V_H1-69), all human D_H and J_H gene segments operably linked to mouse heavy chain constant regions (1hV_H HO) were immunized with FLUVIRIN® (trivalent inactivated influenza vaccine) via footpad (*f.p.*) with 0.75 μ g each of hemagglutinin/mouse/boost. Mice were primed on day 1 followed by *f.p.* boost on days 3, 6, 11, 13, 17, 20 for a total of 6 boosts. No adjuvants were employed in this immunization. The mice were bled on days 15 and 22 after 4th and 6th boosts respectively and antiserum assayed for antibody titers to FLUVIRIN® (as described above).

[0269] Serum titer was calculated as serum dilution within experimental titration range at the signal of antigen binding equivalent to two times above background. Antibody titer for the humoral immune response against FLUMIST® and FLUVIRIN® is set forth in FIG. 20.

[0270] As shown in this Example, antibody titers generated in 1hV_H HO mice were comparable to those generated in mice having a plurality of human V_H gene segments (H κ) for both a human cell surface receptor and a viral antigen (*e.g.*, influenza). Thus, mice having immunoglobulin heavy chain loci restricted to a single V_H gene segment are capable of mounting a robust immune response to antigen in a manner comparable to mice having immunoglobulin heavy chain loci containing a plurality of human V_H gene segments (*e.g.*, 80 V_H).

Example 4 Analysis of Antibody Gene Usage and CDR3 Length in Mice Having a Restricted Immunoglobulin Heavy Chain Locus

[0271] Splenocytes harvested from mice homozygous for a single human V_H gene segment at the endogenous heavy chain locus and homozygous for a replacement of the endogenous κ light chain variable loci with human κ light chain variable loci immunized with a human cell surface receptor (Antigen A) were analyzed for heavy and light chain gene segment usage by reverse-transcriptase polymerase chain reaction (RT-PCR) on mRNA from splenic B cells.

[0272] Briefly, spleens were harvested and homogenized in 1xPBS (Gibco) using glass slides. Cells were pelleted in a centrifuge (500xg for 5 minutes), and red blood cells were lysed in ACK Lysis buffer (Gibco) for 3 minutes. Cells were washed with 1xPBS and filtered using a 0.7 μ m cell strainer. B-cells were isolated from spleen cells using MACS magnetic positive selection for CD19 (Miltenyi Biotec). Total RNA was isolated from pelleted B-cells using the RNeasy Plus Kit (Qiagen). PolyA⁺ mRNA was isolated from total RNA using the Oligotex® Direct mRNA mini kit (Qiagen).

[0273] Double-stranded cDNA was prepared from splenic B cell mRNA by 5' RACE using the SMARTer™ Pico cDNA Synthesis Kit (Clontech) with substitution of the supplied reverse transcriptase and dNTPs with Superscript® II and dNTPs (Invitrogen). V_H and V_k antibody repertoires were amplified from the cDNA using primers specific for IgM, IgG, or Igk constant regions and the SMARTer™ 5' RACE primer (Table 6). PCR products were purified using a QIAquick® PCR Purification Kit (Qiagen). A second round of PCR was done using the same 5' RACE primer and a nested 3' primer

specific for the IgM, IgG, or Igκ constant regions (Table 7). Second round PCR products were purified using a SizeSelect™ E-Gel® system (Invitrogen). A third PCR was performed with primers that added 454 adapters and barcodes. Third round PCR products were purified using Agencourt® AMPure® XP Beads (Beckman Coulter). Purified PCR products were quantified by SYBR® qPCR using a KAPA Library Quantification Kit (KAPA Biosystems). Pooled libraries were subjected to emulsion PCR (emPCR) using a 454 GS Junior Titanium Series Lib-A emPCR Kit (Roche Diagnostics) and bidirectional sequencing using Roche 454 GS Junior instrument according to manufacturer's specifications.

[0274] Bioinformatic analysis. The 454 sequences were sorted based on the sample barcode perfect match and trimmed for quality. Sequences were annotated based on alignment of rearranged immunoglobulin sequences to human germline V(D)J segment database using local installation of Igbblast (NCBI, v2.2.25+). A sequence was marked as ambiguous and removed from analysis when multiple best hits with identical score were detected. A set of perl scripts was developed to analyze results and store data in mysql database. CDR3 region was defined between conserved C codon and FGXG motif for light and WGXX motif for heavy chains. CDR3 length was determined using only productive antibodies. From the nucleic acid sequences and predicted amino acid sequences of the antibodies, gene usage was identified for IgM-primed (15,650), IgG-primed (18,967), and Igκ-primed (26,804) sequences. Results are shown in Table 8, Table 9, FIG. 21 and FIG. 22.

[0275] Table 8 sets forth the percentage of observed human D_H and J_H gene segments used among IgM-primed (15,650 sequences) and IgG-primed (18,967 sequences) V_H1-69 derived heavy chain variable region sequences. Human D_H4-4/D_H4-11 and human D_H5-5/D_H5-18 gene segments are presented in Table 8 together due to identical sequence identity between the respective pairs of D_H gene segments. Table 9 sets forth the percentage of human V_κ and J_κ gene segments observed among light chains (26,804 sequences) cognate with V_H1-69 derived heavy chain variable regions. Percentages in Tables 8 and 9 represent rounded values and in some cases may not equal 100% when added together.

[0276] Amino acid length of the CDR3 region of IgM-primed V_H1-69-derived heavy chains is shown in FIG. 21. Amino acid length of the CDR3 region of IgG-primed V_H1-69-derived heavy chains is shown in FIG. 22.

[0277] As shown in Tables 8 and 9, mice according to the invention generate antigen-specific antibodies containing V_H1-69-derived heavy chains, which demonstrate a variety of rearrangements of a human V_H1-69 gene segment with a variety of human D_H segments and human J_H segments. Further, the antigen-specific antibodies contain cognate human light chains containing human V_κ domains resulting from a variety of rearrangements of human V_κ and J_κ gene segments.

Table 6

Primer	Sequence (5'-3')	
3' Cg1 outer	GGAAGGTGTG CACACCGCTG GAC	(SEQ ID NO: 71)
3' Cg2ac outer	GGAAGGTGTG CACACCACTG GAC	(SEQ ID NO: 72)
3' Cg2b outer	GGAAGGTGTG CACACTGCTG GAC	(SEQ ID NO: 73)
3' Cg3 outer	AGACTGTGCG CACACCGCTG GAC	(SEQ ID NO: 74)
3' mIgMCH1 outer	TCTTATCAGA CAGGGGGCTC TC	(SEQ ID NO: 75)
3' mIgκC outer	AAGAAGCACA CGACTGAGGC AC	(SEQ ID NO: 76)

Table 7

Primer	Sequence (5'-3')	
3' mIgG1/2b CH1 inner	AGTGGATAGA CWGATGGGGG TG	(SEQ ID NO: 77)
3' mIgG2a/2c CH1 inner	AGTGGATAGA CCGATGGGGC TG	(SEQ ID NO: 78)
3' mIgG3 CH1 inner	AAGGGATAGA CAGATGGGGC TG	(SEQ ID NO: 79)
3' mIgM CH1 inner	GGAAGACATT TGGGAAGGAC TG	(SEQ ID NO: 80)
3' mIgκC-2 inner	GGAAGATGGA TACAGTTGGT GC	(SEQ ID NO: 81)

Table 8

Human D _H	IgM	IgG	Human J _H	IgM	IgG
1-1	1.2	6.0	1	7.5	1.5
1-7	39.9	9.0	2	3.3	4.2
1-14	0.5	2.3	3	22.2	12.8

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(continued)

	Human D _H	IgM	IgG	Human J _H	IgM	IgG
5	1-20	2.3	1.4	4	51.5	36.4
	1-26	3.5	5.7	5	10.5	9.5
	2-2	1.1	3.2	6	4.9	29.4
	2-8	0.7	0.6			
	2-15	0.3	1.2			
10	2-21	0.7	0.3			
	3-3	6.3	5.2			
	3-9	0.6	0.6			
	3-10	0.9	10.3			
	3-16	0.9	2.0			
15	3-22	5.1	2.7			
	4-4/4-11	1.5	4.0			
	4-17	1.5	4.7			
	4-23	11.5	2.4			
20	5-12	1.1	1.8			
	5-5/5-18	1.3	3.2			
	5-24	0.3	3.3			
	6-6	1.8	4.5			
	6-13	6.1	7.4			
25	6-19	3.0	5.1			
	6-25	0.1	0.6			
	7-27	3.3	7.3			

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Table 9

	Human V _κ	% Observed	Human J _κ	% Observed
	1-5	3.4	1	28.1
	1-6	1.3	2	25.3
35	1-8	0	3	12.1
	1-9	1.3	4	22.5
	1-12	1.0	5	11.1
	1-13	0		
40	1-16	2.5		
	1-17	3.6		
	1-22	0		
	1-27	0.5		
	1-32	0		
45	1-33	14.3		
	1-35	0		
	1-37	0		
	1-39	1.6		
50	2-4	0		
	2-10	0		
	2-14	0		
	2-18	0		
	2-19	0		
55	2-23	0		
	2-24	0.7		
	2-26	0		

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(continued)

	Human V _K	% Observed	Human J _K	% Observed
5	2-28	0		
	2-29	0		
	2-30	1.9		
	2-36	0		
	2-38	0		
10	2-40	1.5		
	3-7	0		
	3-11	2.7		
	3-15	3.9		
	3-20	41.2		
15	3-25	0		
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 40 <210> 23
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 tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaaactac 180

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gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240
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10 <220>
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1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 20 25 30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
25 65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg

30 <210> 36
<211> 294
<212> DNA
<213> Homo sapiens

35 <220>
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<400> 36

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cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtat agcaaactac 180
gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240
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<220>
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<400> 37

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 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 5 20 25 30
 Thr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

 Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
 10 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 15 85 90 95
 Ala Arg

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 20 <212> DNA
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 <220>
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 cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240
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 35 <210> 39
 <211> 91
 <212> PRT
 <213> Homo sapiens

 40 <220>
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 <400> 39

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 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30
 50 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 55 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr
 85 90

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<210> 40
 <211> 296
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 <213> Homo sapiens

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 cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtat agcaaactac 180
 gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240
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<220>
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Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
			20					25					30		
Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Arg	Ile	Ile	Pro	Ile	Leu	Gly	Ile	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55				60					
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg														

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<210> 42
 <211> 294
 <212> DNA
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<220>
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<400> 42

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 cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag agtcacgatt accacggacg aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaga 294

<210> 43
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
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<400> 43

20 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30

25 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Thr Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 30 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg

35 <210> 44
 <211> 296
 <212> DNA
 <213> Homo sapiens

40 <220>
 <223> synthetic

<400> 44

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 tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag agtcacgatt accgcgacg aatccacgag cacagcctac 240
 50 atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaga 296

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 <211> 98
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      Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
          20          25          30
      Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
10     Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
          50          55          60
      Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
      65          70          75          80
      Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
15          85          90          95
      Ala Arg

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<210> 46

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20 <212> DNA

<213> Homo sapiens

<220>

<223> synthetic

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<400> 46

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      tccctatctt tggtacagca aactacgcac agaagttcca gggcagagtc acgattaccg 180
      cggacgaatc cacgagcaca gcctacatgg agctgagcag cctgagatct gag          233

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35 <211> 77

<212> PRT

<213> Homo sapiens

<220>

40 <223> synthetic

<400> 47

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      Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly
          20          25          30
      Leu Glu Trp Met Gly Arg Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr
          35          40          45
50     Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr
          50          55          60
      Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
      65          70          75

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<210> 48

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<212> DNA

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<213> Homo sapiens

<220>

<223> synthetic

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<400> 48

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      cctggacaag  ggcttgagtg  gatgggaagg  atcatcccta  tccttggtac  agcaaactac  180
      gcacagaagt  tccagggcag  agtcacgatt  accgcggaca  aatccacgag  cacagcctac  240
      atggagctga  gcagcctgag  atctgaggac  acggccgtgt  attactgtgc  gagaga      296

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<212> PRT

<213> Homo sapiens

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<223> synthetic

<400> 49

25

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      1          5          10          15
      Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
      20          25          30
30      Thr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

```

30

```

      35          40          45
      Gly Arg Ile Ile Pro Ile Leu Gly Thr Ala Asn Tyr Ala Gln Lys Phe
      50          55          60
35      Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
      65          70          75          80
      Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
      85          90          95
40      Ala Arg

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<210> 50

<211> 296

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<213> Homo sapiens

<220>

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<400> 50

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      cctggacaag  ggcttgagtg  gatgggaagg  atcatcccta  tccttggtat  agcaaactac  180
      gcacagaagt  tccagggcag  agtcacgatt  accgcggaca  aatccacgag  cacagcctac  240
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50

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Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
			20					25					30		
Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Arg	Ile	Ile	Pro	Ile	Leu	Gly	Ile	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
	50				55					60					
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr
65					70				75					80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85				90					95		
Ala	Arg														

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 <212> DNA
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<400> 52

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cctggacaag	ggcttgagtg	gatgggaggg	atcatcccta	tccttggtat	agcaaactac	180
gcacagaagt	tccagggcag	agtcacgatt	accgcggaca	aatccacgag	cacagcctac	240
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<210> 53
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <223> synthetic

<400> 53

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30
 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Gly Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg
 <210> 54
 <211> 296
 <212> DNA
 <213> Homo sapiens
 <220>
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 <400> 54
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 cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtac agcaaactac 180
 gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240
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 <210> 55
 <211> 98
 <212> PRT
 <213> Homo sapiens
 <220>
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 <400> 55
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30
 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Arg Ile Ile Pro Ile Leu Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg

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<210> 56
<211> 296
<212> DNA
<213> Homo sapiens

5

<220>
<223> synthetic

10

<400> 56

15

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cctggacaag  ggcttgagtg  gatgggaggg  atcatcccta  tctttggtac  agcaaactac  180
gcacagaagt  tccagggcag  agtcacgatt  accgcggacg  aatccacgag  cacagcctac  240
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20

<210> 57
<211> 98
<212> PRT
<213> Homo sapiens

25

<220>
<223> synthetic

<400> 57

30

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
          20          25          30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
          50          55          60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65          70          75          80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Arg
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40

<210> 58
<211> 296
<212> DNA
<213> Homo sapiens

45

<220>
<223> synthetic

50

<400> 58

55

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cctggacaag  ggcttgagtg  gatgggaggg  atcatcccta  tctttggtac  agcaaactac  180
gcacagaagt  tccagggcag  agtcacgatt  accgcggacg  aatccacgag  cacagcctac  240
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<210> 59
<211> 98
<212> PRT
<213> Homo sapiens

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<220>
<223> synthetic

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<400> 59

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25

30

35

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45

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55

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1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
			20					25					30		
Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55				60					
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
65					70				75					80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85				90					95		
Ala	Arg														

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<211> 305
<212> DNA
<213> Homo sapiens

<220>
<223> synthetic

<400> 60

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tgcgacaggc	ccctggacaa	gggcttgagt	ggatgggacg	gatcaaccct	aacagtgggtg	180
gcacaaacta	tgcacagaag	tttcagggca	gggtcaccag	taccagggac	acgtccatca	240
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cgaga						305

<210> 61
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<223> synthetic

<400> 61

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 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
 20 25 30
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Arg Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ser Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Val Val Tyr Tyr Cys
 85 90 95
 Ala Arg
 <210> 62
 <211> 307
 <212> DNA
 <213> Homo sapiens
 <220>
 <223> synthetic
 <400> 62
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 tgcgacaggc ccctggacaa gggcttgagt ggatgggatg gatcaaccct aacagtgggtg 180
 gcacaaacta tgcacagaag tttcagggca gggtcaccat gaccagggac acgtccatca 240
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 cgagaga 307
 <210> 63
 <211> 98
 <212> PRT
 <213> Homo sapiens
 <220>
 <223> synthetic
 <400> 63
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 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
 20 25 30
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg

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<210> 64
<211> 307
<212> DNA
<213> Homo sapiens

<220>
<221> variation
<222> (124)...(124)
<223> n=a, g, t, or c

<400> 64

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tgcnacaggc ccctggacaa gggcttgagt ggatgggatg gatcaaccct aacagtgggtg 180
gcacaaacta tgcacagaag tttcagggca gggtcaccat gaccagggac acgtccatca 240
gcacagccta catggagctg agcaggctga gatctgacga cacggccgtg tattactgtg 300
cgagaga 307
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<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (38)...(38)
<223> Xaa=any amino acid

<400> 65

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Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Gly	Tyr
			20					25					30		
Tyr	Met	His	Trp	Val	Xaa	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55				60					
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
65					70				75						80
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg														

<210> 66
<211> 294
<212> DNA
<213> Homo sapiens

<220>
<223> synthetic

<400> 66

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cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtgggtg cacaaactat 180
gcacagaagt ttcagggctg ggtcaccatg accagggaca cgtccatcag cacagcctac 240
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10 <210> 67
<211> 98
<212> PRT
<213> Homo sapiens

15 <220>
<223> synthetic

<400> 67

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1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30
25 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Trp Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80
30 Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg

35 <210> 68
<211> 346
<212> DNA
<213> Homo sapiens

40 <220>
<223> synthetic

<400> 68

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55 <210> 69
<211> 98
<212> PRT
<213> Homo sapiens

<220>

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<223> synthetic

<400> 69

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      1          5          10          15
      Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr

10      Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
      35          40          45
      Gly Arg Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
      50          55          60
15      Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
      65          70          75          80
      Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Val Val Tyr Tyr Cys
      85          90          95

20      Ala Arg

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<210> 70

<211> 150288

<212> DNA

25 <213> Artificial Sequence

<220>

<223> synthetic

30 <400> 70

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	ttgagagatt	tttcatacaa	tattttattct	gcaagcaaat	ttcagggatt	gaattaataa	180
5	aactgataca	gaacttcctc	tgtagggtatc	tgtgtaaaca	tcaattttctg	aatcagtgtt	240
	gtaaaatattt	tggaacacac	acacaaaatca	catttttatct	ctactttttat	ctctatttttt	300
	aaaaatgcc	aaaaaactca	ttttgtgcat	gtagcattttt	gaattcccac	catcaatgca	360
	tgatagttct	tggtttttcca	catttcataatt	gccattttatc	attatgagaa	ttgtgtgtttt	420
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45

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55

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Claims

1. A mouse whose endogenous immunoglobulin heavy chain locus is restricted in that it comprises a single human V_H gene segment, one or more human D_H gene segments, and one or more human J_H gene segments and which does not comprise a functional endogenous immunoglobulin heavy chain variable region locus; the mouse further comprising one or more human immunoglobulin V_L gene segments operably linked to one or more human J_L gene segments, wherein the single human V_H gene segment, one or more human D_H gene segments, and one or more J_H gene segments are operably linked to a non-human immunoglobulin heavy chain constant region gene, wherein the single human V_H gene segment is V_H1-69 or a polymorphic variant thereof.
2. The mouse of claim 1, wherein the mouse comprises a deletion of all endogenous V_H, D_H, and J_H gene segments.
3. The mouse of claim 1 or claim 2 wherein the single human V_H gene segment, one or more human D_H gene segments,

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and one or more human J_H gene segments replace all endogenous V_H , D_H , and J_H gene segments at an endogenous immunoglobulin heavy chain locus in the germline of said mouse.

4. The mouse of claim 3 wherein the one or more human V_L and one or more human J_L gene segments replace all endogenous V_L and J_L gene segments at an endogenous immunoglobulin light chain locus.
5. The mouse of any one of the preceding claims, wherein the one or more human V_L gene segments and/or the one or more human J_L gene segments are selected from human κ and human λ gene segments.
6. The mouse of any one of the preceding claims, wherein the one or more human immunoglobulin V_L gene segments and one or more human J_L gene segments are operably linked to a non-human light chain constant gene, for example a mouse or rat κ or λ constant region gene.
7. The mouse of any one of the preceding claims, wherein the single human V_H gene segment, one or more human D_H gene segments, and one or more J_H gene segments are operably linked to a mouse or rat immunoglobulin constant region gene.
8. The mouse of any one of the preceding claims wherein the single human V_H gene segment, one or more human D_H gene segments, and one or more J_H gene segments are operably linked to a mouse IgM constant region gene.
9. A cell or tissue derived from the mouse of any one of the preceding claims.
10. A method of making a nucleic acid sequence encoding a human V_H domain comprising the steps of: (a) immunizing a mouse of any one of the preceding claims with an antigen of interest; (b) allowing said mouse to mount an immune response to the antigen of interest; and (c) obtaining an immunoglobulin V_H region nucleic acid sequence encoding a human V_H domain from said mouse.
11. The method of claim 10, wherein the immunoglobulin V_H region nucleic acid sequence: (a) comprises a sequence at least 75% identical to SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56 or SEQ ID NO: 58; or (b) comprises SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, or a polymorphic variant thereof; or (c) encodes a protein that is at least 75% identical with SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 or SEQ ID NO: 59.
12. Use of a mouse according to any one of claims 1-8 in a method of producing a nucleic acid sequence encoding a human heavy chain variable domain.
13. Use according to claim 12, wherein the human heavy chain variable domain is **characterized by** having human FR1-CDR1-FR2-CDR2-FR3 sequences derived from a polymorphic human V_H 1-69 gene segment.
14. Use of a mouse according to any one of claims 1-8 to make a human antibody, wherein the human antibody comprises a heavy chain variable domain derived from a rearranged human V_H 1-69 gene segment, or polymorphic variant thereof, wherein the rearranged human V_H 1-69 gene segment is at least 75% identical to SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56 or SEQ ID NO: 58.

Patentansprüche

1. Eine Maus, deren endogener Locus der schweren Immunglobulinkette dadurch eingeschränkt ist, dass er ein einzelnes Gensegment von humanem V_H , ein oder mehrere Gensegmente von humanem D_H und ein oder mehrere Gensegmente von humanem J_H umfasst und der keinen funktionellen endogenen Locus der schweren Immunglobulinkette variabler Region umfasst; wobei die Maus ferner ein oder mehrere Gensegmente von humanem Immunoglobulin V_L umfasst, die operativ mit einem oder mehreren Gensegmenten von humanem J_L verknüpft sind, wobei das einzelne Gensegment von humanem V_H , das eine oder die mehreren Gensegmente von humanem D_H und das eine oder die mehreren Gensegmente J_H operativ mit einem Gen der nicht-humanen schweren Immunglobulinkette

konstanter Region verknüpft sind, wobei das einzelne humane V_H -Gensegment V_H1-69 oder eine polymorphe Variante davon ist.

2. Maus aus Anspruch 1, wobei die Maus eine Deletion von allen endogenen Gensegmenten V_H , D_H und J_H umfasst.
3. Maus aus Anspruch 1 oder Anspruch 2, wobei das einzelne Gensegment von humanem V_H , das eine oder die mehreren Gensegmente humanem D_H und das eine oder die mehreren Gensegmente von humanem J_H alle endogenen Gensegmente V_H , D_H und J_H an einem endogenen Locus der schweren Immunglobulinkette in der Keimbahn der Maus ersetzen.
4. Maus aus Anspruch 3, wobei das eine oder die mehreren humanen V_L - und das eine oder die mehreren humanen J_L -Gensegmente alle endogenen Gensegmente V_L und J_L an einem endogenen Locus der leichten Immunglobulinkette ersetzen.
5. Maus aus einem der vorhergehenden Ansprüche, wobei das eine oder die mehreren Gensegmente von humanem V_L und/oder das eine oder die mehreren Gensegmente von humanem J_L ausgewählt sind aus humanen κ - und humanen λ -Gensegmenten.
6. Maus aus einem der vorhergehenden Ansprüche, wobei das eine oder die mehreren Gensegmente von humanem Immunglobulin V_L und das eine oder die mehreren Gensegmente von humanem J_L operativ mit einem Gen der nicht-humanen leichten Immunglobulinkette konstanter Region, beispielsweise einem κ - oder λ -Gen konstanter Region von Maus oder Ratte, verknüpft sind.
7. Maus aus einem der vorhergehenden Ansprüche, wobei das einzelne Gensegment von humanem V_H , das eine oder die mehreren Gensegmente von humanem D_H und das eine oder die mehreren Gensegmente J_H operativ mit einem Immunglobulin-Gen konstanter Region von Maus oder Ratte verknüpft sind.
8. Die Maus aus einem der vorhergehenden Ansprüche, wobei das einzelne Gensegment von humanem V_H , das eine oder die mehreren Gensegmente von humanem D_H und das eine oder die mehreren Gensegmente J_H operativ mit einem IgM-Gen konstanter Region der Maus verknüpft sind.
9. Eine Zelle oder Gewebe, abgeleitet von der Maus aus einem der vorhergehenden Ansprüche.
10. Verfahren zur Herstellung einer Nucleinsäuresequenz, die für eine humane V_H -Domäne kodiert, umfassend die Schritte von: (a) Immunisieren einer Maus aus einem der vorhergehenden Ansprüche mit einem Antigen, das von Interesse ist; (b) Ermöglichen, dass die Maus eine Immunantwort auf das Antigen hervorbringt, das von Interesse ist; und (c) Gewinnen einer Nucleinsäuresequenz der Immunglobulin- V_H -Region, die für eine humane V_H -Domäne kodiert, aus der Maus.
11. Verfahren nach Anspruch 10, wobei die Nucleinsäuresequenz der Immunglobulin- V_H -Region: (a) eine Sequenz umfasst, die zu wenigstens 75 % identisch ist mit SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56 oder SEQ ID NO: 58; oder (b) SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58 oder eine polymorphe Variante davon umfasst; oder (c) für ein Protein kodiert, das zu wenigstens 75 % identisch ist mit SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 oder SEQ ID NO: 59.
12. Verwendung einer Maus nach einem der Ansprüche 1 bis 8 in einem Verfahren zur Herstellung einer Nucleinsäuresequenz, die für eine humane schwere Kette variabler Domäne kodiert.
13. Verwendung nach Anspruch 12, wobei die humane schwere Kette variabler Domäne **dadurch gekennzeichnet ist, dass** sie humane FR1-CDR1-FR2-CDR2-FR3-Sequenzen aufweist, die von einem Gensegment von polymorphem humanem V_H 1-69 abgeleitet sind.
14. Verwendung einer Maus nach einem der Ansprüche 1 bis 8, um einen humanen Antikörper herzustellen, wobei der humane Antikörper eine schwere Kette variabler Domäne umfasst, die von einem neu angeordneten Gensegment

von humanem V_H1-69 oder einer polymorphen Variante davon abgeleitet ist, wobei das neu angeordnete Gensegment von humanem V_H1-69 zu wenigstens 75 % identisch ist mit SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56 oder SEQ ID NO: 58.

5

Revendications

1. Souris dont le locus de chaîne lourde d'immunoglobuline endogène est restreint en ce qu'il comprend un seul segment de gène V_H humain, un ou plusieurs segments de gène D_H humain, et un ou plusieurs segments de gène J_H humain et qu'il ne comprend pas un locus de région variable de chaîne lourde d'immunoglobuline endogène fonctionnel ; la souris comprenant en outre un ou plusieurs segments de gène V_L humain liés de façon fonctionnelle à un ou plusieurs segments de gène J_L humain, dans laquelle le seul segment de gène V_H humain, les un ou plusieurs segments de gène D_H humain, et les un ou plusieurs segments de gène J_H sont liés de façon fonctionnelle à un gène de région constante de chaîne lourde d'immunoglobuline non humain, dans laquelle le seul segment de gène V_H humain est V_H1-69 ou l'un de ses variants polymorphes.
2. Souris selon la revendication 1, la souris comprenant une délétion de tous les segments de gène V_H, D_H et J_H endogènes.
3. Souris selon la revendication 1 ou la revendication 2, dans laquelle le seul segment de gène V_H humain, les un ou plusieurs segments de gène D_H humain, et les un ou plusieurs segments de gène J_H humain remplacent tous les segments de gène V_H, D_H et J_H endogènes au niveau d'un locus de chaîne lourde d'immunoglobuline endogène dans la lignée germinale de ladite souris.
4. Souris selon la revendication 3, dans laquelle les un ou plusieurs segments de gène V_L humain et les un ou plusieurs segments de gène J_L humain remplacent tous les segments de gène V_L et J_L endogène au niveau d'un locus de chaîne légère d'immunoglobuline endogène.
5. Souris selon l'une quelconque des revendications précédentes, dans laquelle les un ou plusieurs segments de gène V_L humain et/ou les un ou plusieurs segments de gène J_L humain sont choisis parmi des segments de gène κ humain et λ humain.
6. Souris selon l'une quelconque des revendications précédentes, dans laquelle les un ou plusieurs segments de gène V_L d'immunoglobuline humain et les un ou plusieurs segments de gène J_L humain sont liés de façon fonctionnelle à un gène de région constante de chaîne légère non humain, par exemple un gène de région constante κ ou λ de souris ou de rat.
7. Souris selon l'une quelconque des revendications précédentes, dans laquelle le seul segment de gène V_H humain, les un ou plusieurs segments de gène D_H humain, et les un ou plusieurs segments de gène J_H sont liés de façon fonctionnelle à un gène de région constante d'immunoglobuline de souris ou de rat.
8. Souris selon l'une quelconque des revendications précédentes, dans laquelle le seul segment de gène V_H humain, les un ou plusieurs segments de gène D_H humain, et les un ou plusieurs segments de gène J_H sont liés de façon fonctionnelle à un gène de région constante d'IgM de souris.
9. Cellule ou tissu dérivé de la souris selon l'une quelconque des revendications précédentes.
10. Procédé de fabrication d'une séquence d'acide nucléique codant pour un domaine V_H humain comprenant les étapes suivantes : (a) l'immunisation d'une souris selon l'une quelconque des revendications précédentes avec un antigène d'intérêt ; (b) l'étape consistant à laisser ladite souris ériger une réponse immunitaire contre l'antigène d'intérêt ; et (c) l'obtention d'une séquence d'acide nucléique de région V_H d'immunoglobuline codant pour un domaine V_H humain à partir de ladite souris.
11. Procédé selon la revendication 10, dans lequel la séquence d'acide nucléique de région V_H d'immunoglobuline : (a) comprend une séquence au moins identique à 75 % à SEQ ID NO : 34, SEQ ID NO : 36, SEQ ID NO : 38, SEQ ID NO : 40, SEQ ID NO : 42, SEQ ID NO : 44, SEQ ID NO : 46, SEQ ID NO : 48, SEQ ID NO : 50, SEQ ID NO : 52, SEQ ID NO : 54, SEQ ID NO : 56 ou SEQ ID NO : 58 ; ou (b) comprend SEQ ID NO : 34, SEQ ID NO : 36, SEQ

ID NO : 38, SEQ ID NO : 40, SEQ ID NO : 42, SEQ ID NO : 44, SEQ ID NO : 46, SEQ ID NO : 48, SEQ ID NO : 50, SEQ ID NO : 52, SEQ ID NO : 54, SEQ ID NO : 56, SEQ ID NO : 58, ou l'un de leurs variants polymorphes ; ou (c) code pour une protéine qui est au moins identique à 75 % à SEQ ID NO : 35, SEQ ID NO : 37, SEQ ID NO : 39, SEQ ID NO : 41, SEQ ID NO : 43, SEQ ID NO : 45, SEQ ID NO : 47, SEQ ID NO : 49, SEQ ID NO : 51, SEQ ID NO : 53, SEQ ID NO : 55, SEQ ID NO : 57 ou SEQ ID NO : 59.

12. Utilisation d'une souris selon l'une quelconque des revendications 1 à 8 dans un procédé de production d'une séquence d'acide nucléique codant pour un domaine variable de chaîne lourde humain.

13. Utilisation selon la revendication 12, dans laquelle le domaine variable de chaîne lourde humain est **caractérisé en ce qu'il** comporte des séquences FR1-CDR1-FR2-CDR2-FR3 humaines dérivées d'un segment de gène V_H 1-69 humain polymorphe.

14. Utilisation d'une souris selon l'une quelconque des revendications 1 à 8 pour fabriquer un anticorps humain, dans laquelle l'anticorps humain comprend un domaine variable de chaîne lourde dérivé d'un segment de gène V_H1-69 humain réarrangé, ou l'un de ses variants polymorphes, dans lequel le segment de gène V_H1-69 humain réarrangé est au moins identique à 75 % à SEQ ID NO : 34, SEQ ID NO : 36, SEQ ID NO : 38, SEQ ID NO : 40, SEQ ID NO : 42, SEQ ID NO : 44, SEQ ID NO : 46, SEQ ID NO : 48, SEQ ID NO : 50, SEQ ID NO : 52, SEQ ID NO : 54, SEQ ID NO : 56 ou SEQ ID NO : 58.

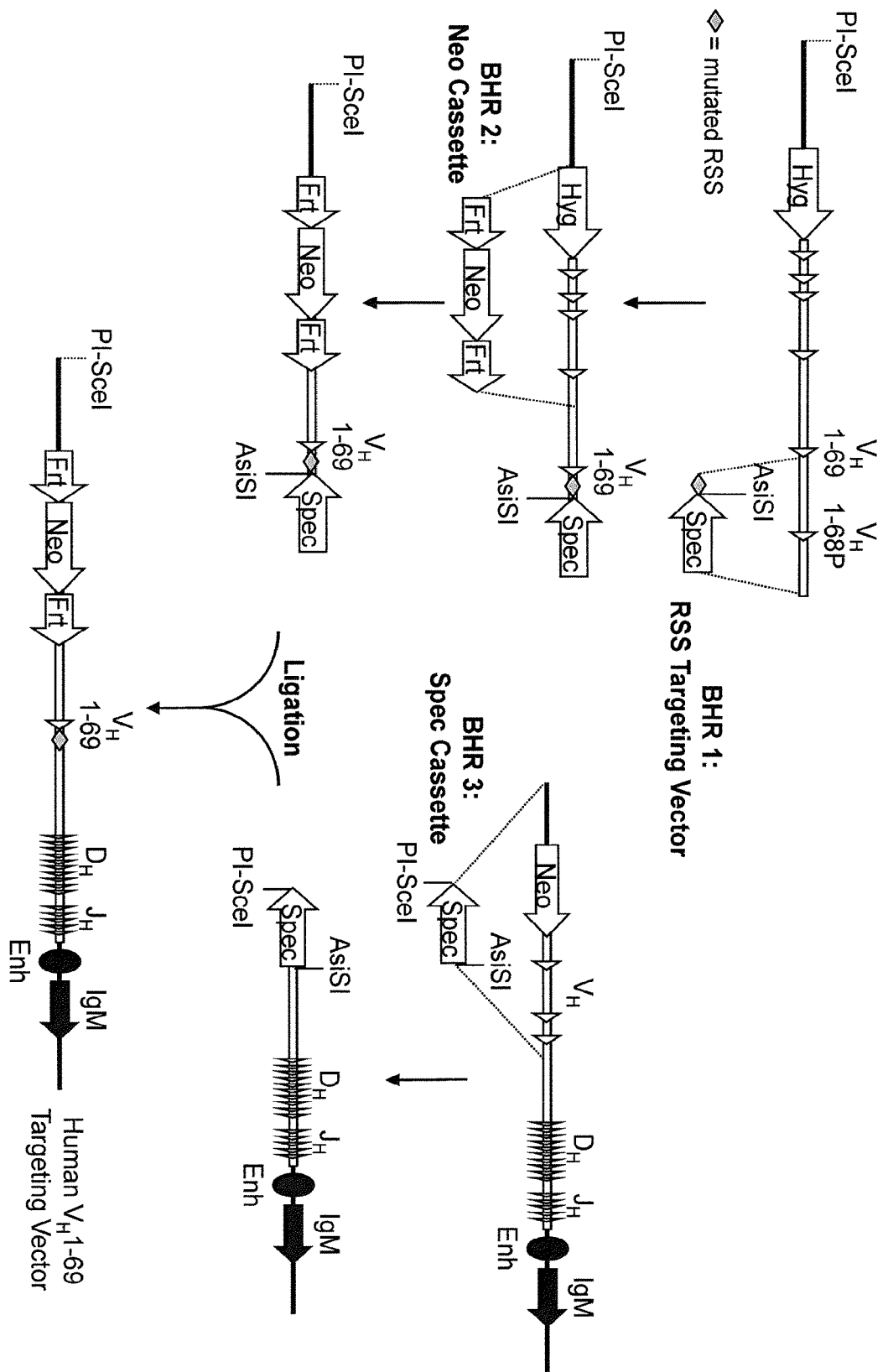


FIG. 1

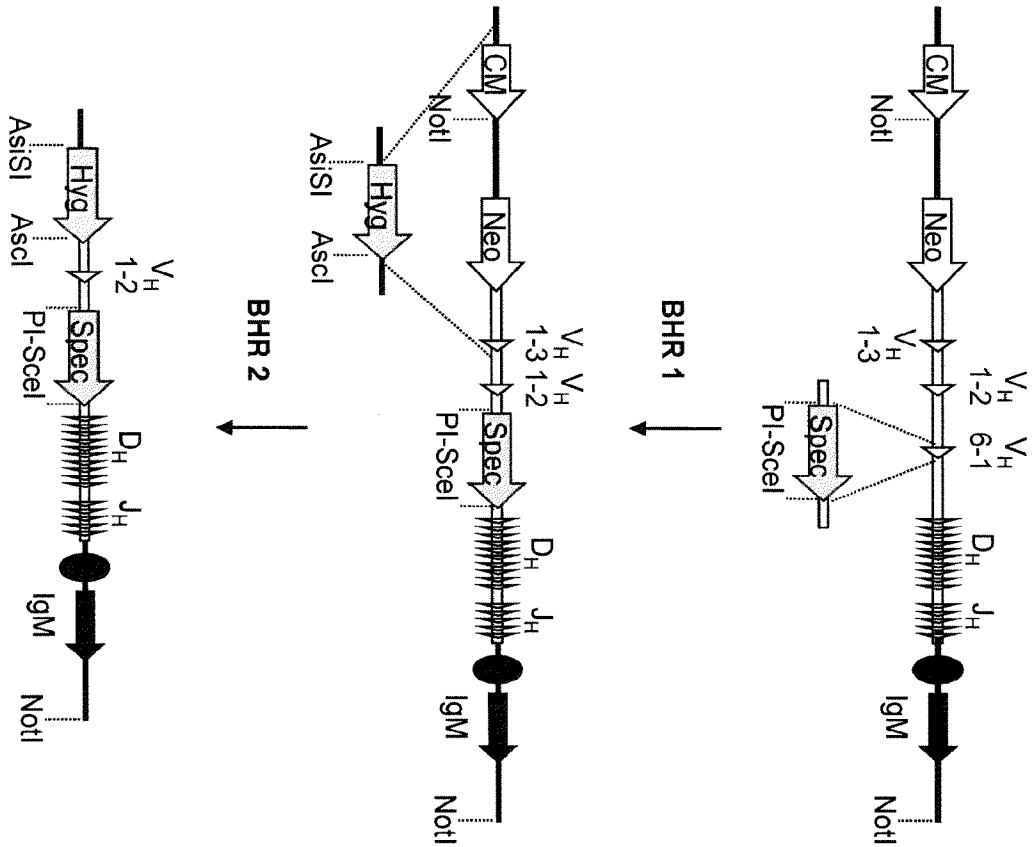


FIG. 2

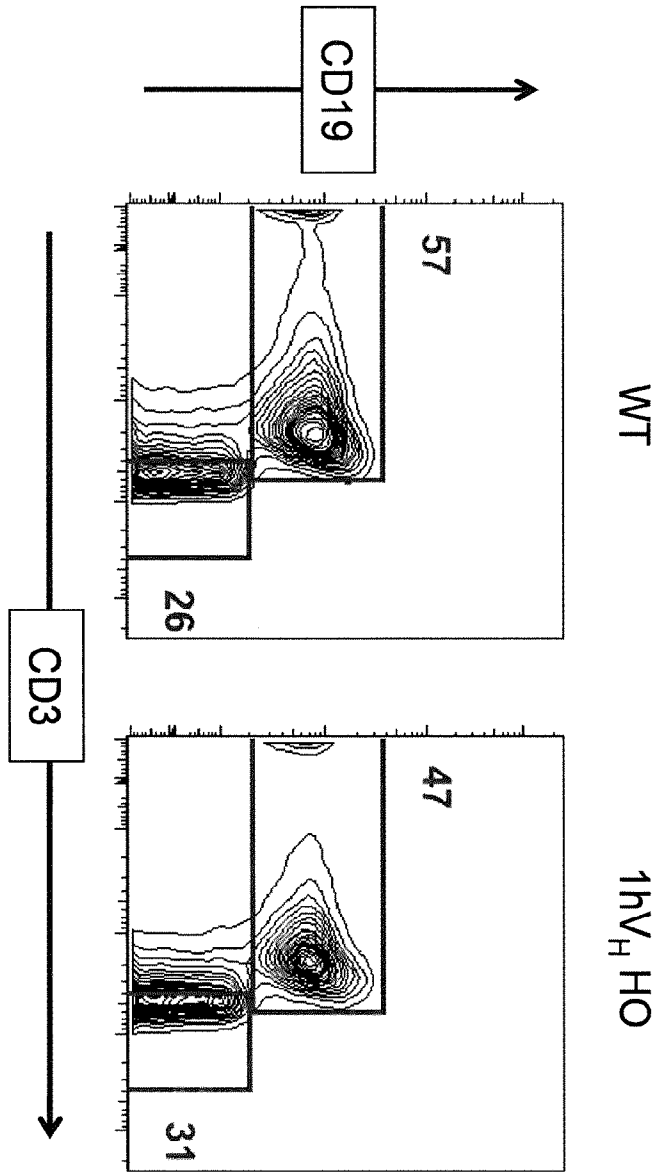
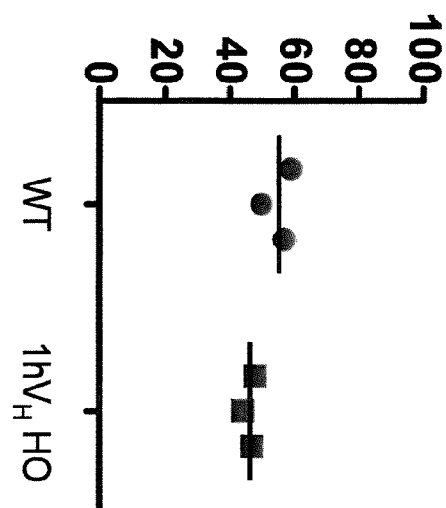


FIG. 3

% CD19⁺ B cells in spleen



CD19⁺ B cells/spleen (x10⁷)

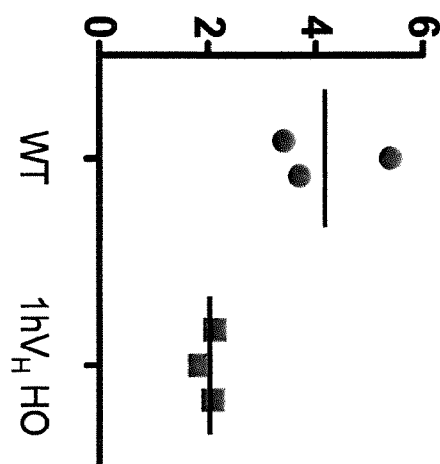
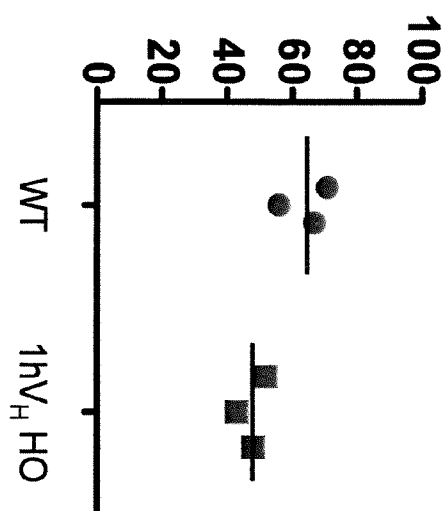


FIG. 4A

% CD19⁺ B cells in bone marrow



CD19⁺ B cells/femur (x10⁶)

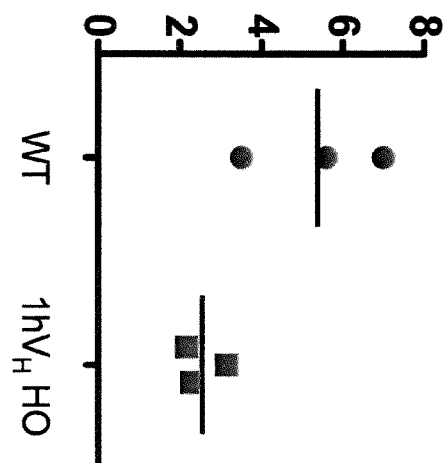


FIG. 4B

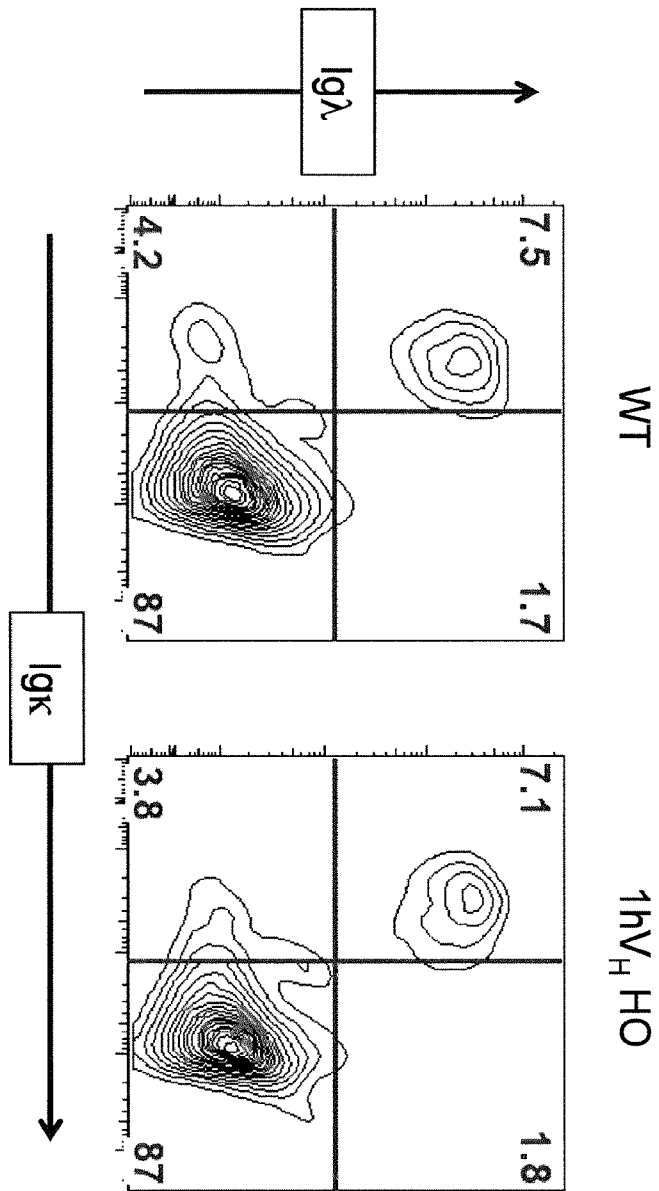


FIG. 5

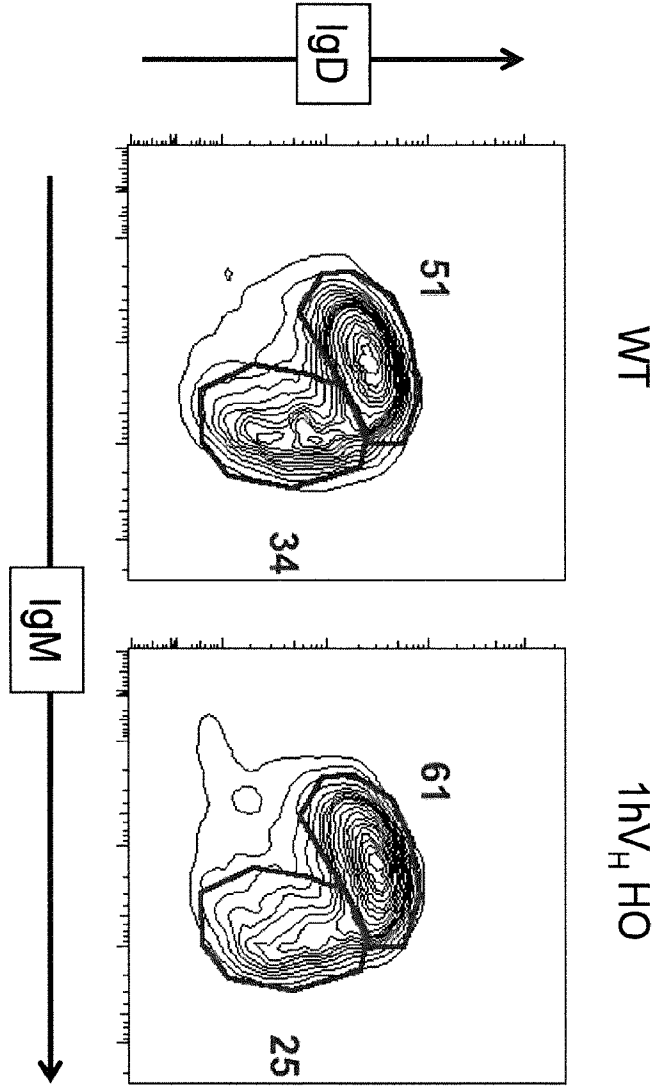


FIG. 6

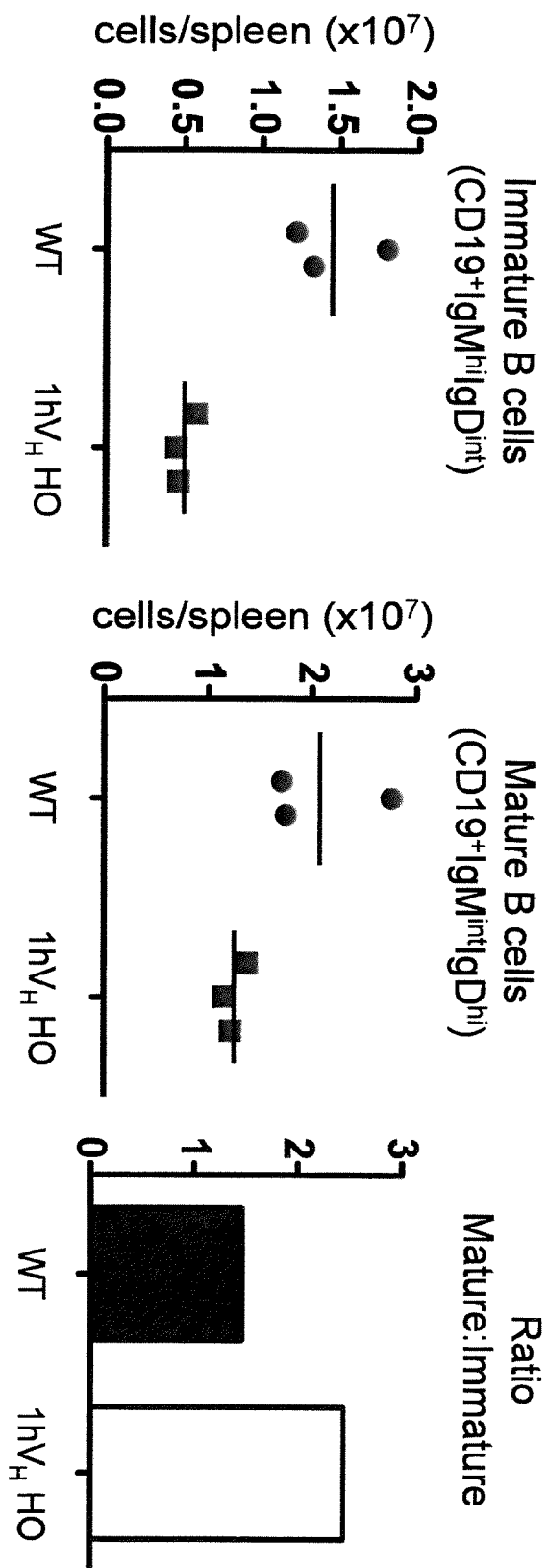


FIG. 7

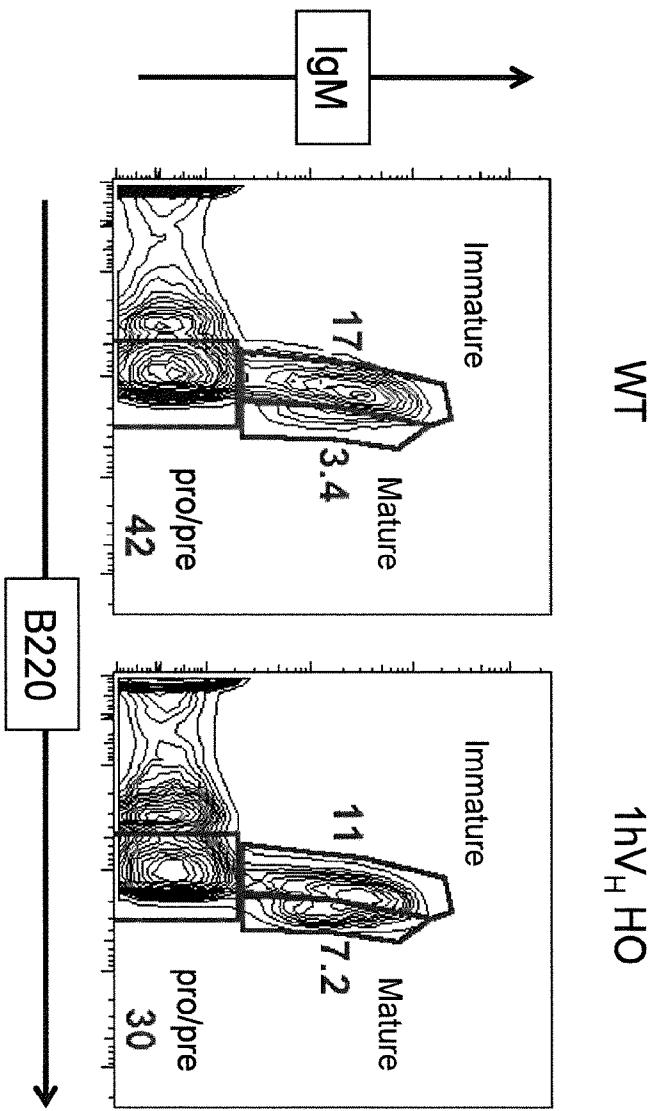


FIG. 8

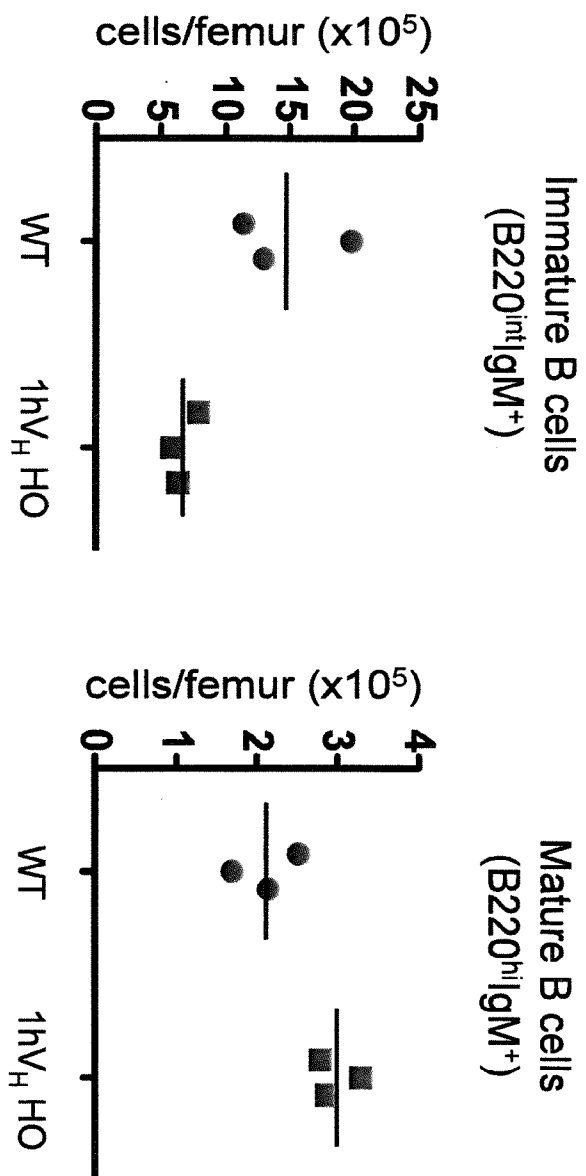


FIG. 9

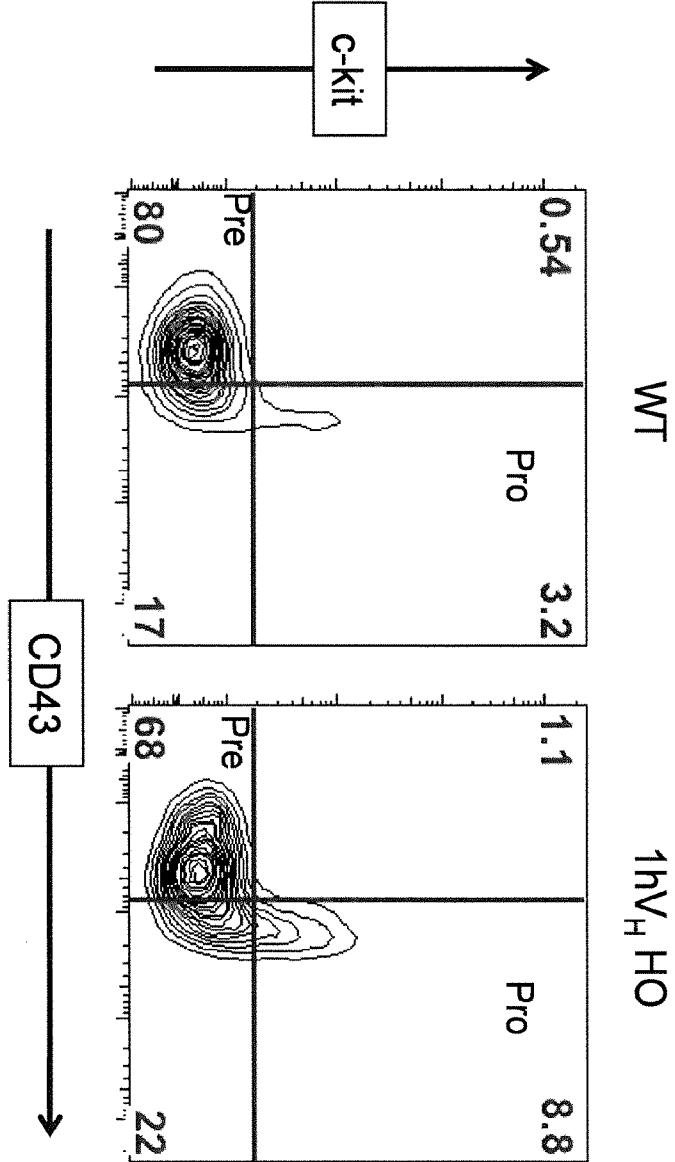


FIG. 10

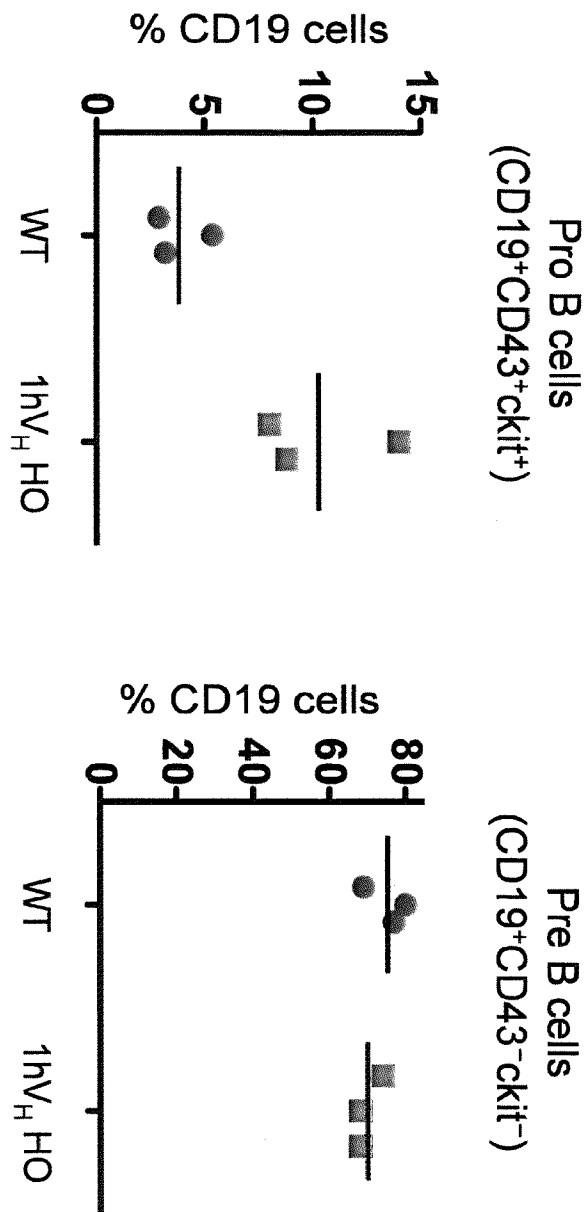


FIG. 11A

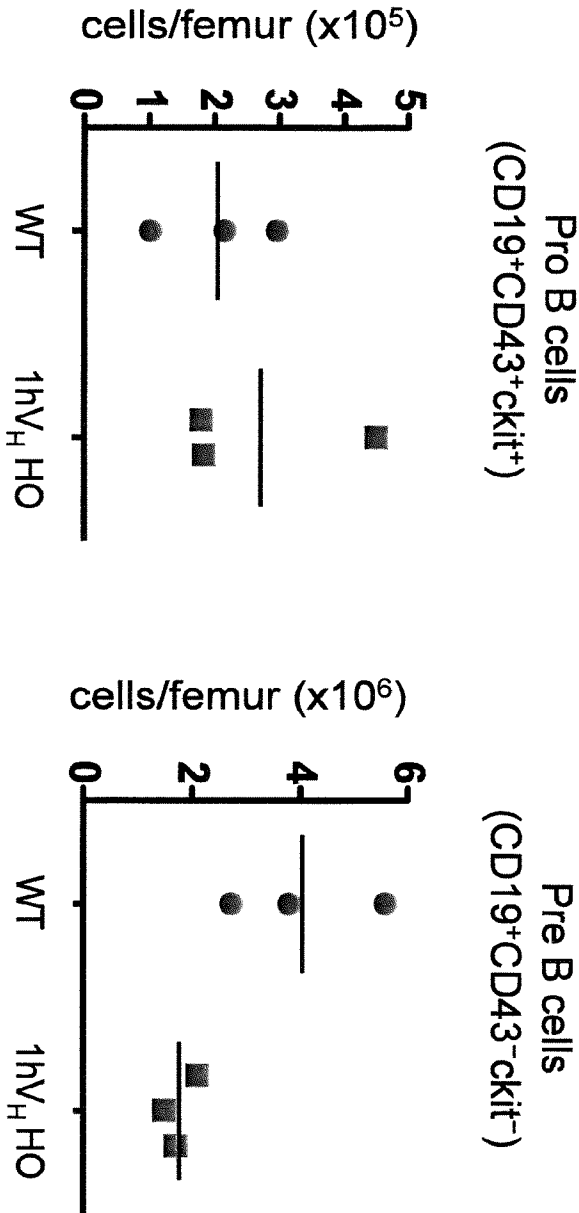


FIG. 11B

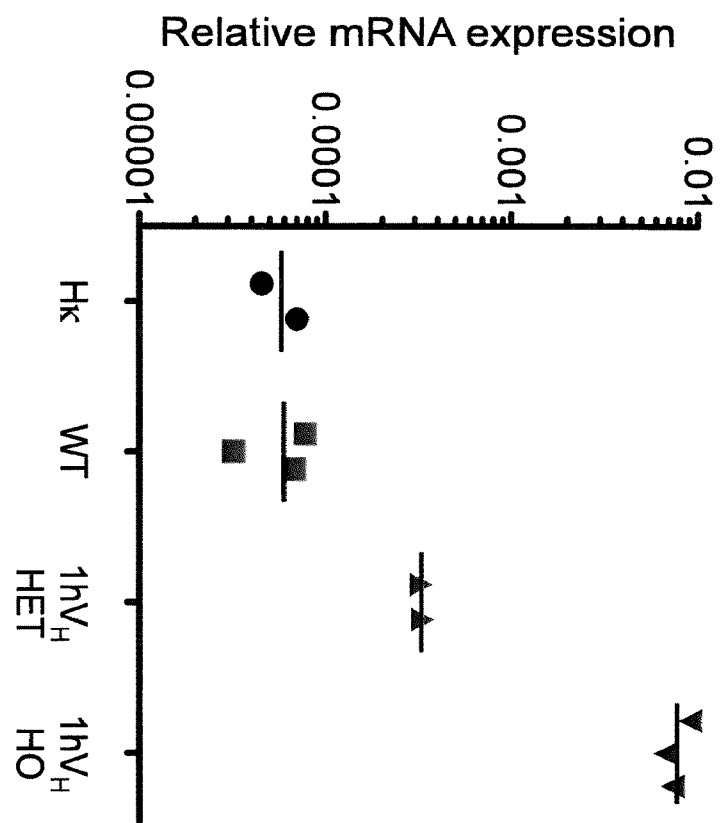


FIG. 12

	10	20	30	40	50	60	70
VH1-69*01	CAGGTgCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*02	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*03	CAGGTgCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*04	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*05	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*06	CAGGTgCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*07	-----AGAAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*08	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*09	CAGGTgCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*10	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*11	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*12	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
VH1-69*13	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCCTCGGTGAAGGTCTCCTGCAAGGCTTCT						
	80	90	100	110	120	130	140
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	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*02	ATCATCCCTATCCTTTGGTATAGCAAACTACGCACAGAAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*03	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*04	ATCATCCCTATCCTTTGGTATAGCAAACTACGCACAGAAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*05	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAAGTTCCAGGGCAGAGTCACGATTACCaCGGACGAATCC						
VH1-69*06	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*07	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*08	ATCATCCCTATCCTTTGGTACAGCAAACTACGCACAGAAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*09	ATCATCCCTATCCTTTGGTATAGCAAACTACGCACAGAAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*10	ATCATCCCTATCCTTTGGTATAGCAAACTACGCACAGAAAGTTCCAGGGCAGAGTCACGATTACCGCGGACaAATCC						
VH1-69*11	ATCATCCCTATCCTTTGGTACAGCAAACTACGCACAGAAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*12	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
VH1-69*13	ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCC						
	230	240	250	260	270	280	290
VH1-69*01	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
VH1-69*02	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA---						
VH1-69*03	ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAA						
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	AQKFQGRVTITADESTSTAYMELSSLRSED	TAVVY	CARR	
VH1-69*02	AQKFQGRVTITADKSTSTAYMELSSLRSED	TAVVY	CARR	
VH1-69*03	AQKFQGRVTITADESTSTAYMELSSLRSED	T---	---	
VH1-69*04	AQKFQGRVTITADKSTSTAYMELSSLRSED	TAVVY	CARR	
VH1-69*05	AQKFQGRVTITtDESTSTAYMELSSLRSED	TAVVY	CARR	
VH1-69*06	AQKFQGRVTITADKSTSTAYMELSSLRSED	TAVVY	CARR	
VH1-69*07	AQKFQGRVTITADESTSTAYMELSSLRSE	----	---	
VH1-69*08	AQKFQGRVTITADKSTSTAYMELSSLRSED	TAVVY	CARR	
VH1-69*09	AQKFQGRVTITADKSTSTAYMELSSLRSED	TAVVY	CARR	
VH1-69*10	AQKFQGRVTITADKSTSTAYMELSSLRSED	TAVVY	CARR	
VH1-69*11	AQKFQGRVTITADESTSTAYMELSSLRSED	TAVVY	CARR	
VH1-69*12	AQKFQGRVTITADESTSTAYMELSSLRSED	TAVVY	CARR	
VH1-69*13	AQKFQGRVTITADESTSTAYMELSSLRSED	TAVVY	CARR	
	AQKFQGRVTITADESTSTAYMELSSLRSED	TAVVY	CARR	

FIG. 14

V _H 1-69 Allele		% Identity											
		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--GCCCTGGGGCCCTCAGTGAA
 10 20 30 40 50 60 70
 VH1-2*02 GAGCCCACTCCCAAGGTG-CAGCTGGTGCAG-TCTG--GGGCTGAGGTGAAGAA--GCCCTGGGGCCCTCAGTGAA
 VH1-2*03 GAGCCCACTCCCAAGGTG-CAGCTGGTGCAG-TCTG--GGGCTGAGGTGAAGAA--GCCCTGGGGCCCTCAGTGAA
 VH1-2*04 -----CAGGTG-CAGCTGGTGCAG-TCTG--GGGCTGAGGTGAAGAA--GCCCTGGGGCCCTCAGTGAA
 VH1-2*05 GACCGtgctgcTCAgATCTCAGCctgcTCAgCTCcaTGTAgGCTGAGGTGAAGAAcGTGCCCTGGGGCCCTCAGTGAA
 GAGCCCACTCCCAAGGTGTCAgCTGGTGCAGCTCTGTGTGGGCTGAGGTGAAGAAcGTGCCCTGGGGCCCTCAGTGAA
 80 90 100 110 120 130 140 150
 VH1-2*01 GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAcCGGCTACTATTA TGCACTGG--GTGCCGA-----CAGGCCCC
 VH1-2*02 GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAcCGGCTACTATTA TGCACTGG--GTGCCGA-----CAGGCCCC
 VH1-2*03 GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAcCGGCTACTATTA TGCACTGG--GTGCCGA-----CAGGCCCC
 VH1-2*04 GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAcCGGCTACTATTA TGCACTGG--GTGCCGA-----CAGGCCCC
 VH1-2*05 cCTgCCCTG--AaCTTCTGtgcaTAgTtgTgcacCACTgtAgggtTgATCCGTCCGATCCACTCAAGCCCT
 GGTCTCTCTGCAAGGCTTCTGGATACACCTTCAcCGGCTACTATTA TGCACTGG--GTGCCGA-----CAGGCCCC
 160 170 180 190 200 210 220
 VH1-2*01 TGGACAAGGGCTTGAGTGGATGGGACGGGATCAACCCTAACAAGTGGTGGCAACAATA TGCAAGAAgTTT--CAG
 VH1-2*02 TGGACAAGGGCTTGAGTGGATGGGACGGGATCAACCCTAACAAGTGGTGGCAACAATA TGCAAGAAgTTT--CAG
 VH1-2*03 TGGACAAGGGCTTGAGTGGATGGGACGGGATCAACCCTAACAAGTGGTGGCAACAATA TGCAAGAAgTTT--CAG
 VH1-2*04 TGGACAAGGGCTTGAGTGGATGGGACGGGATCAACCCTAACAAGTGGTGGCAACAATA TGCAAGAAgTTT--CAG
 VH1-2*05 TgTcCAggGGCCTG-----TCGCAc--cCAgtgcataTAgTAgccgggtgAAggTgtatcCAGAAgCCCTTGCAg
 TGGACAAGGGCTTGAGTGGATGGGACGGGATCAACCCTAACAAGTGGTGGCAACAATA TGCAAGAAgTTT--CAG
 230 240 250 260 270 280 290 300
 VH1-2*01 GGCAGGGTCAcCAgtAACCAAGGGAACAAGTCCA--TCAGCAc-AGCCTACATGGAGCTGAGCAAGGCTGAGATCTGAC
 VH1-2*02 GGCAGGGTCAcCAATGAcCAAGGGAACAAGTCCA--TCAGCAc-AGCCTACATGGAGCTGAGCAAGGCTGAGATCTGAC
 VH1-2*03 GGCAGGGTCAcCAATGAcCAAGGGAACAAGTCCA--TCAGCAc-AGCCTACATGGAGCTGAGCAAGGCTGAGATCTGAC
 VH1-2*04 GGCAGGGTCAcCAATGAcCAAGGGAACAAGTCCA--TCAGCAc-AGCCTACATGGAGCTGAGCAAGGCTGAGATCTGAC
 VH1-2*05 GAggAcctTCAcTgAggCcccaaggCctcTtCAcCTCAgCccCAgacTgCAcc-AGCTGcAc--CTGgGA--Gtg
 GGCAGGGTCAcCAATGAcCAAGGGAACAAGTCCAAGTCCAAGTCAAGCAAGCCTACATGGAGCTGAGCAAGGCTGAGATCTGAC
 310 320 330
 VH1-2*01 GACACGGGtcGTGTATTAcTTGTGCGAGAA--
 VH1-2*02 GACACGGGtcGTGTATTAcTTGTGCGAGAGAA
 VH1-2*03 GACACGGGtcGTGTATTAcTTGTGCGAGAGAA
 VH1-2*04 GACACGGGtcGTGTATTAcTTGTGCGAGAA--
 VH1-2*05 GACAC--CtGTGgAg-AcTT-cGCGA-----
 GACACGGGtcGTGTATTAcTTGTGCGAGAGAA

FIG. 16

[illegible]

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

% Similarity

FIG. 18

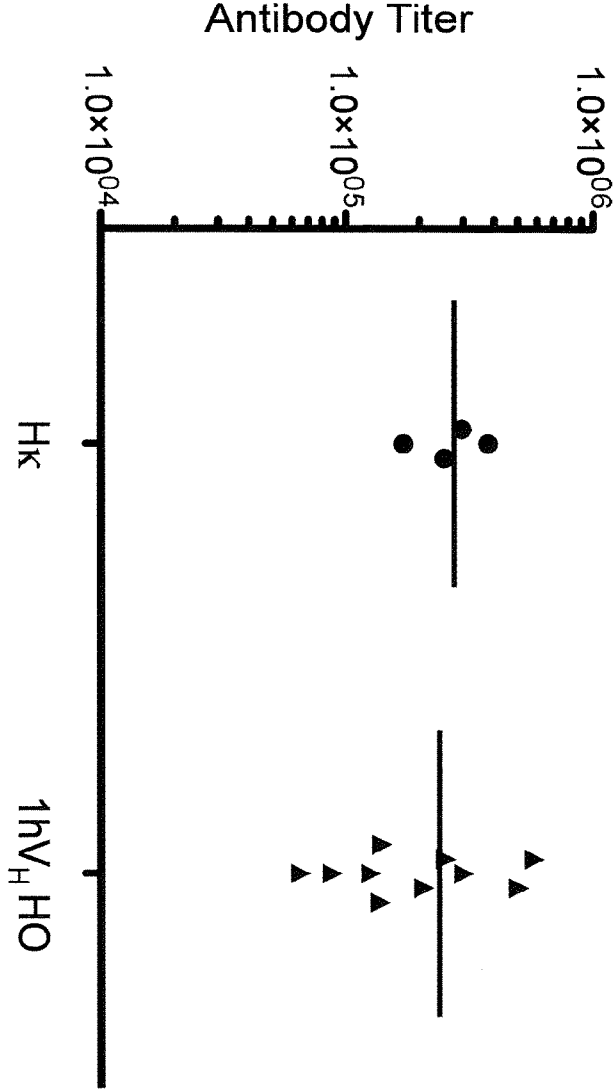


FIG. 19

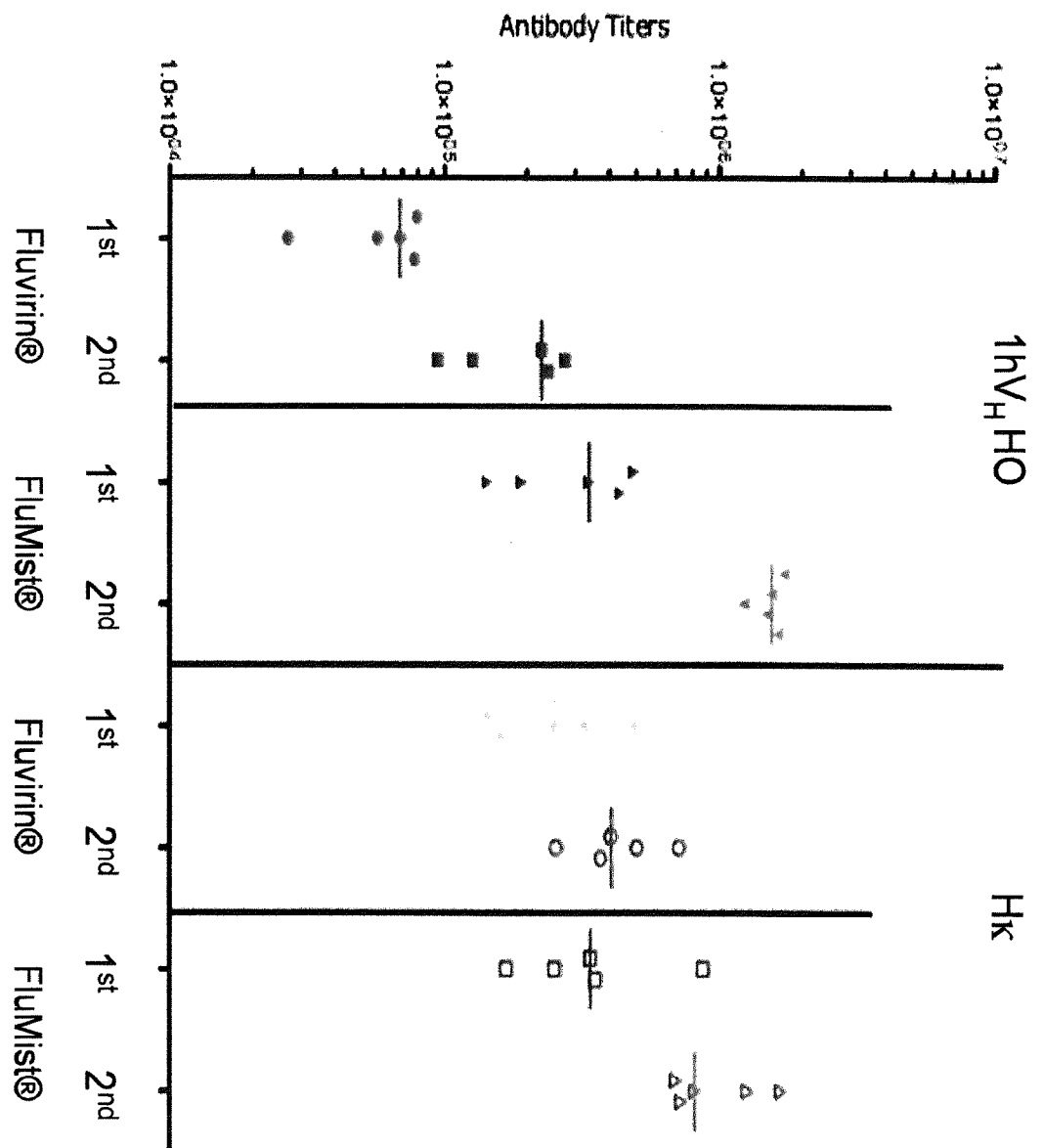


FIG. 20

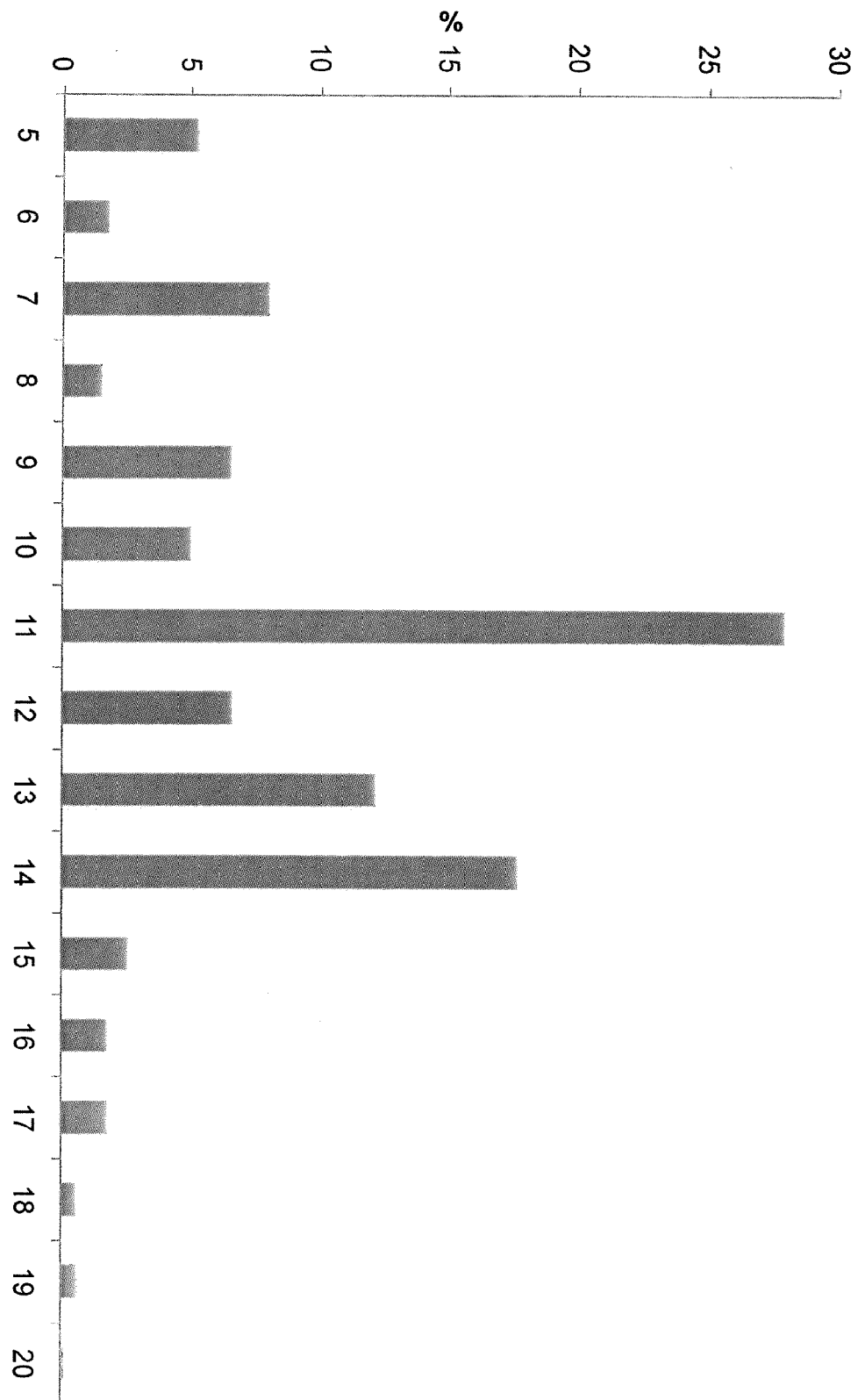


FIG. 21

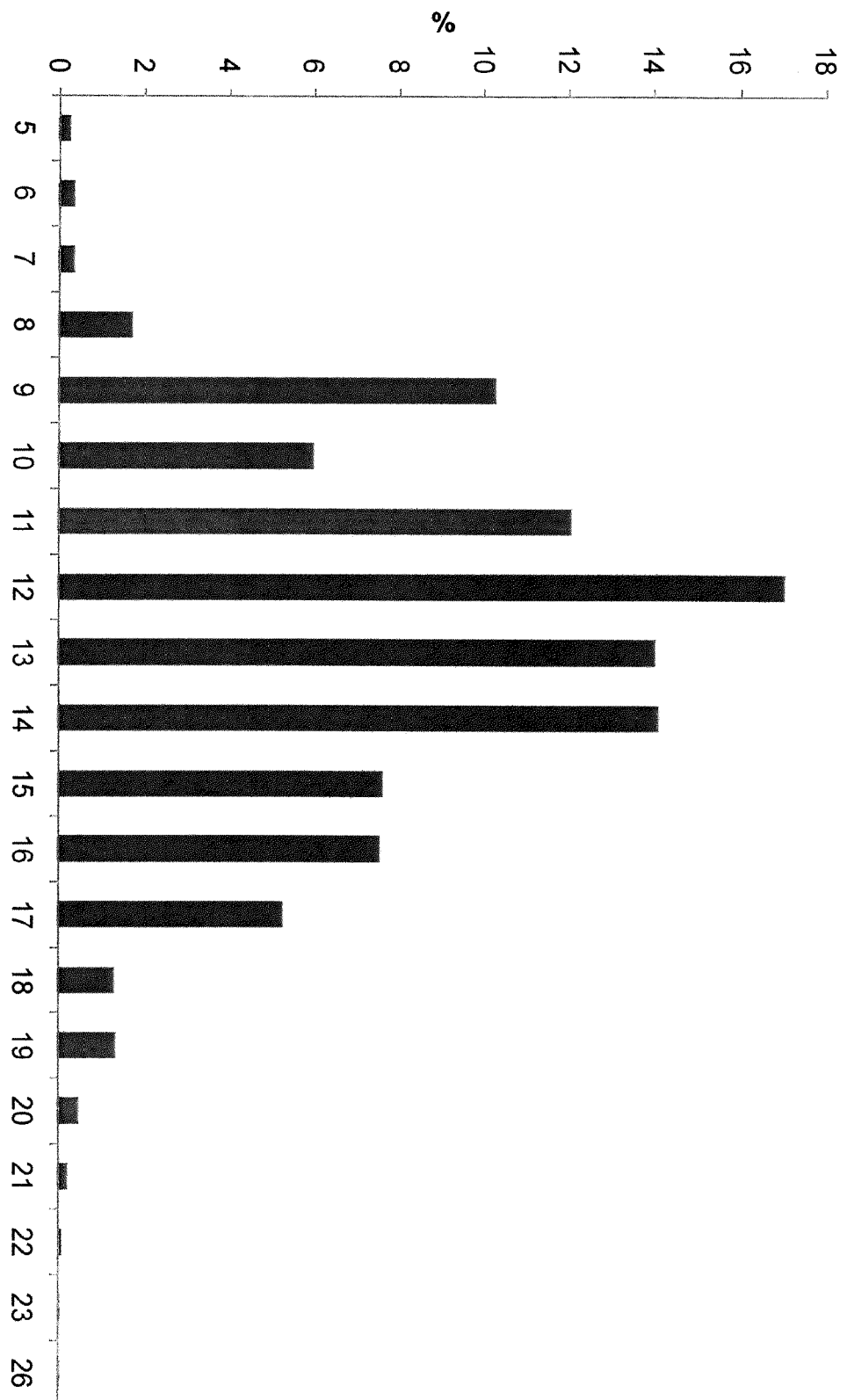


FIG. 22

REFERENCES CITED IN THE DESCRIPTION

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Non-patent literature cited in the description

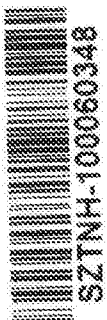
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KORLÁTOZOTT EGÉR IMMUNGLOBULIN-NEHÉZLÁNC

SZABADALMI IGÉNYPONTOK:

- 5 1. Olyan egér, amelynek endogén immunglobulin-nehézlánc lokusza úgy korlátozott, hogy tartalmaz egy humán V_H génszegmentumot, egy vagy több humán D_H génszegmentumot, egy vagy több humán J_H génszegmentumot, és amelyben a funkcionális, endogén, immunglobulin-nehézlánc nem tartalmaz variábilis régió lokuszt; az egér emellett tartalmaz egy vagy több olyan humán immunglobulin V_L génszegmentumot, amely egy vagy több
- 10 humán J_L génszegmentumhoz kapcsolódik, ahol az egyetlen humán V_H génszegmentum, egy vagy több humán D_H génszegmentum, valamint egy vagy több J_H génszegmentum olyan nem humán immunglobulin-nehézlánc konstans gén régióhoz kapcsolódik, ahol az egyetlen humán V_H génszegmentum V_H1-69 vagy annak polimorf változata.
- 15 2. Az 1. igénypontban leírt egér, ahol az egérben törölve van az összes endogén V_H , D_H és J_H génszegmentum.
3. Az 1. vagy a 2. igénypontban leírt egér, ahol az egyetlen humán V_H génszegmentum, egy vagy több humán D_H génszegmentum, valamint egy vagy több humán J_H génszegmentum
- 20 helyettesíti az összes endogén V_H , D_H és J_H génszegmentumot az említett egér csírvonalának valamelyik endogén immunglobulin-nehézlánc lokuszában.
4. A 3. igénypontban leírt egér, ahol egy vagy több humán V_L és egy vagy több humán J_L génszegmentum helyettesíti az összes endogén V_L és J_L génszegmentumot valamelyik
- 25 endogén immunglobulin-könnyűlánc lokuszban.
5. A fenti igénypontok bármelyike szerinti egér, ahol egy vagy több humán V_L génszegmentum és/vagy egy vagy több humán J_L génszegmentum humán κ és humán λ génszegmentumok közül választott.
- 30 6. A fenti igénypontok bármelyike szerinti egér, ahol egy vagy több humán immunglobulin V_L génszegmentum vagy egy vagy több humán J_L génszegmentum nem humán könnyűlánc konstans génhez kapcsolódik, például egér vagy patkány κ vagy λ konstans gén régióhoz.



7. A fenti igénypontok bármelyike szerinti egér, ahol az egyetlen humán V_H génszegmentum, egy vagy több humán D_H génszegmentum, valamint egy vagy több J_H génszegmentum egér vagy patkány immunglobulin konstans gén régiójához kapcsolódik.
- 5 8. A fenti igénypontok bármelyike szerinti egér, ahol az egyetlen humán V_H génszegmentum, egy vagy több humán D_H génszegmentum, valamint egy vagy több J_H génszegmentum egér IgM konstans gén régiójához kapcsolódik.
- 10 9. A fenti igénypontok bármelyike szerinti egérből származó sejt vagy szövet.
10. Módszer humán V_H domént kódoló nukleinsav-szekvencia létrehozására, amely a következő lépésekből áll: (a) a fenti igénypontok bármelyike szerinti egér immunizálása a vizsgált antigénnel; (b) az említett egénnél a vizsgált antigénnel szembeni immunválasz
 15 kifejllesztésének lehetővé tétele; valamint (c) az immunglobulin V_H régiójában olyan nukleinsav-szekvencia termelése, amely az említett egér humán V_H doménjét kódolja.
11. A 10. igénypontban leírt módszer, ahol a V_H immunglobulin-régiójú nukleinsav-szekvencia: (a) olyan szekvenciából áll, amely legalább 75%-ban identikus a következőkkel:
 20 SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56 vagy SEQ ID NO: 58, vagy (b) a következőkkel: SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID
 25 NO: 56, SEQ ID NO: 58, illetve annak polimorf variánsával; illetve (c) olyan fehérjét kódol, amely legalább 75%-ban identikus a következőkkel: SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 vagy SEQ ID NO: 59.
- 30 12. Az 1–8. igénypontok bármelyike szerinti egér alkalmazása olyan módszerhez, amely humán nehézlánc variábilis domént kódoló nukleinsav-szekvencia létrehozását célozza.

13. A 12. igénypontban leírt felhasználás, ahol a humán nehézlánc variábilis domént az **jellemzi**, hogy polimorf humán V_H1-69 génszegmentumokból származó humán FR1-CDR1-FR2-CDR2-FR3 szekvenciákat tartalmaz.
- 5 14. Az 1-8. igénypontok bármelyike szerinti egér alkalmazása humán antitest létrehozásához, ahol a humán antitest olyan nehézlánc variábilis domént tartalmaz, amely átrendezett humán V_H1-69 génszegmentumból vagy annak polimorf variánsából származik, ahol az átrendezett V_H1-69 génszegmentum legalább 75%-ban identikus a következőkkel: SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ
- 10 ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56 vagy SEQ ID NO: 58.