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Common light chain mouse.

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A genetically modified mouse is provided, wherein the mouse expresses an immunoglobulin light chain repertoire characterized by a limited number of light chain variable domains. Mice are provided that express just one or a few immunoglobulin light chain variable domains from a limited repertoire in their germline. Methods for making bispecific antibodies having universal light chains using mice as described herein, including human light chain variable regions, are provided. Methods for making human variable regions suitable for use in multispecific binding proteins, e.g., bispecific antibodies, and host cells are provided. Bispecific antibodies capable of binding first and second antigens are provided, wherein the first and second antigens are separate epitopes of a single protein or separate epitopes on two different proteins are provided.

COMMON LIGHT CHAIN MOUSE

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims benefit under 35 U.S.C. § 119(e) of U.S. Patent
5 Application Serial No. 13/798,310, filed March 13, 2013, which application is hereby
incorporated by reference in its entirety.

SEQUENCE LISTING

[0002] The present application makes reference to a sequence listing submitted in
10 electronic form as an ascii .txt file named "2010794-0549_ST25" on March 13, 2014. The
.txt file was generated on March 11, 2014 and is 18 kb in size.

FIELD

[0003] A genetically modified mouse is provided that expresses antibodies having a
15 common human variable/mouse constant light chain associated with diverse human
variable/mouse constant heavy chains. A method for making a human bispecific antibody
from human variable region gene sequences of B cells of the mouse is provided.

BACKGROUND

20 [0004] Antibodies typically comprise a homodimeric heavy chain component, wherein
each heavy chain monomer is associated with an identical light chain. Antibodies having a
heterodimeric heavy chain component (*e.g.*, bispecific antibodies) are desirable as therapeutic
antibodies. But making bispecific antibodies having a suitable light chain component that
can satisfactorily associate with each of the heavy chains of a bispecific antibody has proved
25 problematic.

[0005] In one approach, a light chain might be selected by surveying usage statistics for
all light chain variable domains, identifying the most frequently employed light chain in
human antibodies, and pairing that light chain *in vitro* with the two heavy chains of differing
specificity.

30 [0006] In another approach, a light chain might be selected by observing light chain
sequences in a phage display library (*e.g.*, a phage display library comprising human light
chain variable region sequences, *e.g.*, a human scFv library) and selecting the most

commonly used light chain variable region from the library. The light chain can then be tested on the two different heavy chains of interest.

[0007] In another approach, a light chain might be selected by assaying a phage display library of light chain variable sequences using the heavy chain variable sequences of both heavy chains of interest as probes. A light chain that associates with both heavy chain variable sequences might be selected as a light chain for the heavy chains.

[0008] In another approach, a candidate light chain might be aligned with the heavy chains' cognate light chains, and modifications are made in the light chain to more closely match sequence characteristics common to the cognate light chains of both heavy chains. If the chances of immunogenicity need to be minimized, the modifications preferably result in sequences that are present in known human light chain sequences, such that proteolytic processing is unlikely to generate a T cell epitope based on parameters and methods known in the art for assessing the likelihood of immunogenicity (*i.e., in silico* as well as wet assays).

[0009] All of the above approaches rely on *in vitro* methods that subsume a number of *a priori* restraints, *e.g.*, sequence identity, ability to associate with specific pre-selected heavy chains, *etc.* There is a need in the art for compositions and methods that do not rely on manipulating *in vitro* conditions, but that instead employ more biologically sensible approaches to making human epitope-binding proteins that include a common light chain.

SUMMARY

[0010] Genetically modified mice that express human immunoglobulin heavy and light chain variable domains, wherein the mice have a limited light chain variable repertoire, are provided. A biological system for generating a human light chain variable domain that associates and expresses with a diverse repertoire of affinity-matured human heavy chain variable domains is provided. Methods for making binding proteins comprising immunoglobulin variable domains are provided, comprising immunizing mice that have a limited immunoglobulin light chain repertoire with an antigen of interest, and employing an immunoglobulin variable region gene sequence of the mouse in a binding protein that specifically binds the antigen of interest. Methods include methods for making human immunoglobulin heavy chain variable domains suitable for use in making multi-specific antigen-binding proteins.

[0011] Genetically engineered mice are provided that select suitable affinity-matured human immunoglobulin heavy chain variable domains derived from a repertoire of unarranged human heavy chain variable region gene segments, wherein the affinity-matured human heavy chain variable domains associate and express with a single human light chain variable domain derived from one human light chain variable region gene segment. Genetically engineered mice that present a choice of two human light chain variable region gene segments are also provided. In various aspects, the one or two gene segments include human V κ 1-39 and human V κ 3-20.

[0012] Genetically engineered mice are provided that express a limited repertoire of human light chain variable domains, or a single human light chain variable domain, from a limited repertoire of human light chain variable region gene segments. The mice are genetically engineered to include a single unarranged human light chain variable region gene segment (or two human light chain variable region gene segments) that rearranges to form a rearranged human light chain variable region gene (or two rearranged light chain variable region genes) that express a single light chain (or that express either or both of two light chains). The rearranged human light chain variable domains are capable of pairing with a plurality of affinity-matured human heavy chains selected by the mice, wherein the heavy chain variable regions specifically bind different epitopes.

[0013] Genetically engineered mice are provided that express a limited repertoire of human light chain variable domains, or a single human light chain variable domain, from a limited repertoire of human light chain variable region sequences. The mice are genetically engineered to include a single V/J human light chain sequence (or two V/J sequences) that express a variable region of a single light chain (or that express either or both of two variable regions). A light chain comprising the variable sequence is capable of pairing with a plurality of affinity-matured human heavy chains clonally selected by the mice, wherein the heavy chain variable regions specifically bind different epitopes.

[0014] In one aspect, a genetically modified mouse is provided that comprises a single human immunoglobulin light chain variable (V_L) region gene segment that is capable of rearranging with a human J gene segment (selected from one or a plurality of J_L segments) and encoding a human V_L domain of an immunoglobulin light chain. In another aspect, the mouse comprises no more than two human V_L gene segments, each of which is capable of rearranging with a human J gene segment (selected from one or a plurality of J_L segments) and encoding a human V_L domain of an immunoglobulin light chain.

[0015] In one embodiment, the single human V_L gene segment is operably linked to a human J_L gene segment selected from Jκ1, Jκ2, Jκ3, Jκ4, and Jκ5, wherein the single human V_L gene segment is capable of rearranging to form a sequence encoding a light chain variable region gene with any of the one or more human J_L gene segments.

- 5 **[0016]** In one embodiment, the genetically modified mouse comprises an immunoglobulin light chain locus that does not comprise an endogenous mouse V_L gene segment that is capable of rearranging to form an immunoglobulin light chain gene, wherein the V_L locus comprises a single human V_L gene segment that is capable of rearranging to encode a V_L region of a light chain gene. In a specific embodiment, the human V_L gene segment is a human Vκ1-39Jκ5 gene segment or a human Vκ3-20Jκ1 gene segment. In one embodiment, the genetically modified mouse comprises a V_L locus that does not comprise an endogenous mouse V_L gene segment that is capable of rearranging to form an immunoglobulin light chain gene, wherein the V_L locus comprises no more than two human V_L gene segments that are capable of rearranging to encode a V_L region of a light chain gene.
- 10 In a specific embodiment, the no more than 2 human V_L gene segments are a human Vκ1-39Jκ5 gene segment and a human Vκ3-20Jκ1 gene segment.

- [0017]** In one aspect, a genetically modified mouse is provided that comprises a single rearranged (V/J) human immunoglobulin light chain variable (V_L) region (*i.e.*, a V_L/J_L region) that encodes a human V_L domain of an immunoglobulin light chain. In another aspect, the mouse comprises no more than two rearranged human V_L regions that are capable of encoding a human V_L domain of an immunoglobulin light chain.
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- [0018]** In one embodiment, the V_L region is a rearranged human Vκ1-39/J sequence or a rearranged human Vκ3-20/J sequence. In one embodiment, the human J_L segment of the rearranged V_L/J_L sequence is selected from Jκ1, Jκ2, Jκ3, Jκ4, and Jκ5. In a specific embodiment, the V_L region is a human Vκ1-39Jκ5 sequence or a human Vκ3-20Jκ1 sequence. In a specific embodiment, the mouse has both a human Vκ1-39Jκ5 sequence and a human Vκ3-20Jκ1 sequence.
- 25

- [0019]** In one embodiment, the human V_L gene segment is operably linked to a human or mouse leader sequence. In one embodiment, the leader sequence is a mouse leader sequence. In a specific embodiment, the mouse leader sequence is a mouse Vκ3-7 leader sequence. In a specific embodiment, the leader sequence is operably linked to an unrearranged human V_L gene segment. In a specific embodiment, the leader sequence is operably linked to a rearranged human V_L/J_L sequence.
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[0020] In one embodiment, the V_L gene segment is operably linked to an immunoglobulin promoter sequence. In one embodiment, the promoter sequence is a human promoter sequence. In a specific embodiment, the human immunoglobulin promoter is a human $V\kappa 3-15$ promoter. In a specific embodiment, the promoter is operably linked to an unarranged human V_L gene segment. In a specific embodiment, the promoter is operably linked to a rearranged human V_L/J_L sequence.

[0021] In one embodiment, the light chain locus comprises a leader sequence flanked 5' (with respect to transcriptional direction of a V_L gene segment) with a human immunoglobulin promoter and flanked 3' with a human V_L gene segment that rearranges with a human J segment and encodes a V_L domain of a reverse chimeric light chain comprising an endogenous mouse light chain constant region (C_L). In a specific embodiment, the V_L gene segment is at the mouse $V\kappa$ locus, and the mouse C_L is a mouse $C\kappa$.

[0022] In one embodiment, the light chain locus comprises a leader sequence flanked 5' (with respect to transcriptional direction of a V_L gene segment) with a human immunoglobulin promoter and flanked 3' with a rearranged human V_L region (V_L/J_L sequence) and encodes a V_L domain of a reverse chimeric light chain comprising an endogenous mouse light chain constant region (C_L). In a specific embodiment, the rearranged human V_L/J_L sequence is at the mouse kappa (κ) locus, and the mouse C_L is a mouse $C\kappa$.

[0023] In one embodiment, the V_L locus of the modified mouse is a κ light chain locus, and the κ light chain locus comprises a mouse κ intronic enhancer, a mouse κ 3' enhancer, or both an intronic enhancer and a 3' enhancer.

[0024] In one embodiment, the mouse comprises a nonfunctional immunoglobulin lambda (λ) light chain locus. In a specific embodiment, the λ light chain locus comprises a deletion of one or more sequences of the locus, wherein the one or more deletions renders the λ light chain locus incapable of rearranging to form a light chain gene. In another embodiment, all or substantially all of the V_L gene segments of the λ light chain locus are deleted.

[0025] In one embodiment, mouse makes a light chain that comprises a somatically mutated V_L domain derived from a human V_L gene segment. In one embodiment, the light chain comprises a somatically mutated V_L domain derived from a human V_L gene segment, and a mouse $C\kappa$ region. In one embodiment, the mouse does not express a λ light chain.

[0026] In one embodiment, the genetically modified mouse is capable of somatically hypermutating the human V_L region sequence. In a specific embodiment, the mouse comprises a cell that comprises a rearranged immunoglobulin light chain gene derived from a human V_L gene segment that is capable of rearranging and encoding a V_L domain, and the rearranged immunoglobulin light chain gene comprises a somatically mutated V_L domain.

[0027] In one embodiment, the mouse comprises a cell that expresses a light chain comprising a somatically mutated human V_L domain linked to a mouse C_k , wherein the light chain associates with a heavy chain comprising a somatically mutated V_H domain derived from a human V_H gene segment and wherein the heavy chain comprises a mouse heavy chain constant region (C_H). In a specific embodiment, the heavy chain comprises a mouse C_{H1} , a mouse hinge, a mouse C_{H2} , and a mouse C_{H3} . In a specific embodiment, the heavy chain comprises a human C_{H1} , a hinge, a mouse C_{H2} , and a mouse C_{H3} .

[0028] In one embodiment, the mouse comprises a replacement of endogenous mouse V_H gene segments with one or more human V_H gene segments, wherein the human V_H gene segments are operably linked to a mouse C_H region gene, such that the mouse rearranges the human V_H gene segments and expresses a reverse chimeric immunoglobulin heavy chain that comprises a human V_H domain and a mouse C_H . In one embodiment, 90-100% of unrearranged mouse V_H gene segments are replaced with at least one unrearranged human V_H gene segment. In a specific embodiment, all or substantially all of the endogenous mouse V_H gene segments are replaced with at least one unrearranged human V_H gene segment. In one embodiment, the replacement is with at least 19, at least 39, or at least 80 or 81 unrearranged human V_H gene segments. In one embodiment, the replacement is with at least 12 functional unrearranged human V_H gene segments, at least 25 functional unrearranged human V_H gene segments, or at least 43 functional unrearranged human V_H gene segments. In one embodiment, the mouse comprises a replacement of all mouse D_H and J_H segments with at least one unrearranged human D_H segment and at least one unrearranged human J_H segment. In one embodiment, the at least one unrearranged human D_H segment is selected from 1-1, D_{H1-7} , 1-26, 2-8, 2-15, 3-3, 3-10, 3-16, 3-22, 5-5, 5-12, 6-6, 6-13, 7-27, and a combination thereof. In another embodiment, the at least one unrearranged human D_H segment is selected from D_{H7-27} , D_{H1-26} , D_{H6-25} , D_{H5-24} , D_{H4-23} , D_{H3-22} , D_{H2-21} , D_{H1-20} , D_{H6-19} , D_{H5-18} , D_{H4-17} , D_{H3-16} , D_{H2-15} , D_{H1-14} , D_{H6-13} , D_{H5-12} , D_{H4-11} , D_{H3-10} , D_{H3-9} , D_{H2-8} , D_{H1-7} , D_{H6-6} , D_{H5-5} , D_{H4-4} , D_{H3-3} , D_{H2-2} , D_{H1-1} , and a combination thereof. In one embodiment, the at least one unrearranged human J_H segment is selected from 1, 2, 3, 4, 5, 6, and a

combination thereof. In a specific embodiment, the one or more human V_H gene segment is selected from a 1-2, 1-8, 1-24, 1-69, 2-5, 3-7, 3-9, 3-11, 3-13, 3-15, 3-20, 3-23, 3-30, 3-33, 3-48, 3-53, 4-31, 4-39, 4-59, 5-51, a 6-1 human V_H gene segment, and a combination thereof.

In another specific embodiment the one or more human V_H gene segment is selected from V_H6-1 , V_H1-2 , V_H1-3 , V_H2-5 , V_H3-7 , V_H1-8 , V_H3-9 , V_H3-11 , V_H3-13 , V_H3-15 , V_H1-18 , V_H3-20 , V_H3-21 , V_H3-23 , V_H1-24 , V_H2-26 , V_H4-28 , V_H3-30 , V_H4-31 , V_H3-33 , V_H4-34 , V_H4-39 , V_H3-43 , V_H1-46 , V_H3-48 , V_H3-49 , V_H5-51 , V_H3-53 , V_H1-58 , V_H4-59 , V_H4-61 , V_H3-64 , V_H3-66 , V_H1-69 , V_H2-70 , V_H3-72 , V_H3-73 , and a combination thereof. In one embodiment, the mouse comprises a replacement of all or substantially all of the endogenous mouse V_H gene segments and all of the mouse D_H and J_H segments with all or substantially all human V_H , D_H , and J_H segments. In one embodiment, the mouse comprises a complete repertoire of human heavy chain V, D, and J segments. In one embodiment, the mouse comprises a B cell that expresses a binding protein that specifically binds an antigen of interest, wherein the binding protein comprises a light chain derived from a human $V_{\kappa}1-39/J_{\kappa}5$ rearrangement or a human $V_{\kappa}3-20/J_{\kappa}1$ rearrangement, and wherein the cell comprises a rearranged immunoglobulin heavy chain gene derived from a rearrangement of human V_H gene segments selected from a 1-69, 2-5, 3-13, 3-23, 3-30, 3-33, 3-53, 4-39, 4-59, and 5-51 gene segment. In one embodiment, the one or more human V_H gene segments are rearranged with a human heavy chain J_H gene segment selected from 1, 2, 3, 4, 5, and 6. In one embodiment, the one or more human V_H and J_H gene segments are rearranged with a human D_H gene segment selected from 1-1, 1-7, 1-26, 2-8, 2-15, 3-3, 3-10, 3-16, 3-22, 5-5, 5-12, 6-6, 6-13, and 7-27. In a specific embodiment, the light chain gene has 1, 2, 3, 4, or 5 or more somatic hypermutations.

[0029] In one embodiment, the mouse comprises a B cell that comprises a rearranged immunoglobulin heavy chain variable region gene sequence comprising a $V_H/D_H/J_H$ region selected from 2-5/6-6/1, 2-5/3-22/1, 3-13/6-6/5, 3-23/2-8/4, 3-23/3-3/4, 3-23/3-10/4, 3-23/6-6/4, 3-23/7-27/4, 3-30/1-1/4, 3-30/1-7/4, 3-30/3-3/3, 3-30/3-3/4, 3-30/3-22/5, 3-30/5-5/2, 3-30/5-12/4, 3-30/6-6/1, 3-30/6-6/3, 3-30/6-6/4, 3-30/6-6/5, 3-30/6-13/4, 3-30/7-27/4, 3-30/7-27/5, 3-30/7-27/6, 3-33/1-7/4, 3-33/2-15/4, 4-39/1-26/3, 4-59/3-16/3, 4-59/3-16/4, 4-59/3-22/3, 5-51/3-16/6, 5-51/5-5/3, 5-51/6-13/5, 3-53/1-1/4, 1-69/6-6/5, and 1-69/6-13/4. In a specific embodiment, the B cell expresses a binding protein comprising a human immunoglobulin heavy chain variable region fused with a mouse heavy chain constant

region, and a human immunoglobulin light chain variable region fused with a mouse light chain constant region.

[0030] In one embodiment, the rearranged human V_L region is a human $V_{\kappa 1-39J\kappa 5}$ sequence, and the mouse expresses a reverse chimeric light chain comprising (i) a V_L domain
 5 derived from the human V_L/J_L sequence and (ii) a mouse C_L ; wherein the light chain is associated with a reverse chimeric heavy chain comprising (i) a mouse C_H and (ii) a somatically mutated human V_H domain derived from a human V_H gene segment selected from a 1-2, 1-8, 1-24, 1-69, 2-5, 3-7, 3-9, 3-11, 3-13, 3-15, 3-20, 3-23, 3-30, 3-33, 3-48, 3-53, 4-31, 4-39, 4-59, 5-51, a 6-1 human V_H gene segment, and a combination thereof. In one
 10 embodiment, the mouse expresses a light chain that is somatically mutated. In one embodiment the C_L is a mouse C_{κ} . In a specific embodiment, the human V_H gene segment is selected from a 2-5, 3-13, 3-23, 3-30, 4-59, 5-51, and 1-69 gene segment. In a specific embodiment, the somatically mutated human V_H domain comprises a sequence derived from a D_H segment selected from 1-1, 1-7, 2-8, 3-3, 3-10, 3-16, 3-22, 5-5, 5-12, 6-6, 6-13, and 7-
 15 27. In a specific embodiment, the somatically mutated human V_H domain comprises a sequence derived from a J_H segment selected from 1, 2, 3, 4, 5, and 6. In a specific embodiment, the somatically mutated human V_H domain is encoded by a rearranged human $V_H/D_H/J_H$ sequence selected from 2-5/6-6/1, 2-5/3-22/1, 3-13/6-6/5, 3-23/2-8/4, 3-23/3-3/4, 3-23/3-10/4, 3-23/6-6/4, 3-23/7-27/4, 3-30/1-1/4, 3-30/1-7/4, 3-30/3-3/4, 3-30/3-22/5, 3-30/5-
 20 5/2, 3-30/5-12/4, 3-30/6-6/1, 3-30/6-6/3, 3-30/6-6/4, 3-30/6-6/5, 3-30/6-13/4, 3-30/7-27/4, 3-30/7-27/5, 3-30/7-27/6, 4-59/3-16/3, 4-59/3-16/4, 4-59/3-22/3, 5-51/5-5/3, 1-69/6-6/5, and 1-69/6-13/4.

[0031] In one embodiment, the rearranged human V_L region is a human $V_{\kappa 3-20J\kappa 1}$ sequence, and the mouse expresses a reverse chimeric light chain comprising (i) a V_L domain
 25 derived from the rearranged human V_L/J_L sequence, and (ii) a mouse C_L ; wherein the light chain is associated with a reverse chimeric heavy chain comprising (i) a mouse C_H , and (ii) a somatically mutated human V_H derived from a human V_H gene segment selected from a 1-2, 1-8, 1-24, 1-69, 2-5, 3-7, 3-9, 3-11, 3-13, 3-15, 3-20, 3-23, 3-30, 3-33, 3-48, 3-53, 4-31, 4-39, 4-59, 5-51, a 6-1 human V_H gene segment, and a combination thereof. In one embodiment,
 30 the mouse expresses a light chain that is somatically mutated. In one embodiment the C_L is a mouse C_{κ} . In a specific embodiment, the human V_H gene segment is selected from a 3-30, 3-33, 3-53, 4-39, and 5-51 gene segment. In a specific embodiment, the somatically mutated human V_H domain comprises a sequence derived from a D_H segment selected from 1-1, 1-7,

1-26, 2-15, 3-3, 3-16, and 6-13. In a specific embodiment, the somatically mutated human V_H domain comprises a sequence derived from a J_H segment selected from 3, 4, 5, and 6. In a specific embodiment, the somatically mutated human V_H domain is encoded by a rearranged human V_H/D_H/J_H sequence selected from 3-30/1-1/4, 3-30/3-3/3, 3-33/1-7/4, 3-33/2-15/4, 4-39/1-26/3, 5-51/3-16/6, 5-51/6-13/5, and 3-53/1-1/4.

[0032] In one embodiment, the mouse comprises both a rearranged human V_κ1-39J_κ5 sequence and a rearranged human V_κ3-20J_κ1 sequence, and the mouse expresses a reverse chimeric light chain comprising (i) a V_L domain derived from the human V_κ1-39J_κ5 sequence or the human V_κ3-20J_κ1 sequence, and (ii) a mouse C_L; wherein the light chain is associated with a reverse chimeric heavy chain comprising (i) a mouse C_H, and (ii) a somatically mutated human V_H derived from a human V_H gene segment selected from a 1-2, 1-8, 1-24, 1-69, 2-5, 3-7, 3-9, 3-11, 3-13, 3-15, 3-20, 3-23, 3-30, 3-33, 3-48, 3-53, 4-31, 4-39, 4-59, 5-51, a 6-1 human V_H gene segment, and a combination thereof. In one embodiment, the mouse expresses a light chain that is somatically mutated. In one embodiment the C_L is a mouse C_κ.

[0033] In one embodiment, provided herein is a mouse that expresses a single rearranged human immunoglobulin light chain variable (V_L) region derived from a rearranged germline variable region sequence that comprises a human V_L gene segment derived from a human V_κ3-20 gene segment and a human immunoglobulin heavy chain variable (V_H) region cognate with said V_L region wherein the V_H region comprises a human V_H segment derived from a segment selected from V_H6-1, V_H1-2, V_H1-3, V_H2-5, V_H3-7, V_H1-8, V_H3-9, V_H3-11, V_H3-13, V_H3-15, V_H1-18, V_H3-20, V_H3-21, V_H3-23, V_H1-24, V_H2-26, V_H4-28, V_H3-30, V_H4-31, V_H3-33, V_H4-34, V_H4-39, V_H3-43, V_H1-46, V_H3-48, V_H3-49, V_H5-51, V_H3-53, V_H1-58, V_H4-59, V_H4-61, V_H3-64, V_H3-66, V_H1-69, V_H2-70, V_H3-72, and V_H3-73. In one embodiment, the V_H region comprises a human V_H segment derived from a segment selected from V_H1-2, V_H1-3, V_H2-5, V_H3-7, V_H1-8, V_H3-9, V_H3-13, V_H3-15, V_H3-20, V_H3-21, V_H3-23, V_H1-24, V_H2-26, V_H4-28, V_H4-31, V_H4-34, V_H3-43, V_H1-46, V_H3-48, V_H3-49, V_H1-58, V_H4-61, V_H3-64, V_H3-66, V_H3-72, and V_H3-73. In one embodiment, the human V_H segment is derived from V_H3-49, V_H4-61, V_H4-28, or V_H3-66. In one embodiment, the human V_H region in the mouse comprises a human J_H segment derived from J_H1, J_H2, J_H3, J_H4, or J_H5. In one embodiment, the human V_H region further comprises a D_H segment derived from D_H7-27, D_H1-26, D_H6-25, D_H5-24, D_H4-23, D_H3-22, D_H2-21, D_H1-20, D_H6-19, D_H5-18, D_H4-17, D_H3-16, D_H2-15, D_H1-14, D_H6-13, D_H5-12, D_H4-11, D_H3-10, D_H3-9, D_H2-8, D_H1-7, D_H6-6,

D_H5-5, D_H4-4, D_H3-3, D_H2-2, or D_H1-1. In one embodiment, the human V_H region is operably linked to human, rat, or mouse immunoglobulin heavy chain constant (C_H) region, e.g., a mouse C_H region. In one aspect, the human V_H region is expressed from an endogenous immunoglobulin heavy chain locus. In one embodiment, such mouse comprises
5 the human V_L region that comprises a human J_κ gene segment derived from a human J_κ1 gene segment. In one embodiment, the human V_κ3-20 gene segment is present in rearrangement with the human J_κ1 gene segment in the mouse germline. In one aspect, the mouse lacks a mouse V_L and/or J_L segments. In one aspect, the human V_L region in the mouse is operably linked to a human, rat, or mouse immunoglobulin light chain constant (C_L)
10 region, e.g., a mouse C_L region. In one aspect, the human V_L region is expressed from an endogenous mouse immunoglobulin light chain locus. In one embodiment, the mouse expresses an antibody comprising the regions described herein in response to an antigen of interest.

[0034] In another embodiment, provided herein is a mouse that expresses a single
15 rearranged human immunoglobulin light chain variable (V_L) region derived from a rearranged germline variable region sequence that comprises a human V_L gene segment derived from a human V_κ1-39 gene segment and a human immunoglobulin heavy chain variable (V_H) region cognate with said V_L region wherein the V_H region comprises a human V_H segment derived from a segment selected from V_H6-1, V_H1-2, V_H1-3, V_H2-5, V_H3-7,
20 V_H1-8, V_H3-9, V_H3-11, V_H3-13, V_H3-15, V_H1-18, V_H3-20, V_H3-21, V_H3-23, V_H1-24, V_H2-26, V_H4-28, V_H3-30, V_H4-31, V_H3-33, V_H4-34, V_H4-39, V_H3-43, V_H1-46, V_H3-48, V_H3-49, V_H5-51, V_H3-53, V_H1-58, V_H4-59, V_H4-61, V_H3-64, V_H3-66, V_H1-69, V_H2-70, V_H3-72, and V_H3-73. In one embodiment, the V_H region comprises a human V_H segment derived from a segment selected from V_H1-2, V_H1-3, V_H3-7, V_H1-8, V_H3-11, V_H3-21, V_H3-23, V_H1-24, V_H2-
25 26, V_H4-28, V_H3-33, V_H3-43, V_H1-46, V_H3-49, V_H1-58, V_H4-61, V_H3-66, V_H2-70, V_H3-72, and V_H3-73. In one embodiment, the human V_H segment is derived from V_H3-49, V_H4-61, V_H4-28, or V_H3-66. In one embodiment, the human V_H region in the mouse comprises a human J_H segment derived from J_H1, J_H2, J_H3, J_H4, or J_H5. In one embodiment, the human V_H region further comprises a D_H segment derived from D_H7-27, D_H1-26, D_H6-25, D_H5-24,
30 D_H4-23, D_H3-22, D_H2-21, D_H1-20, D_H6-19, D_H5-18, D_H4-17, D_H3-16, D_H2-15, D_H1-14, D_H6-13, D_H5-12, D_H4-11, D_H3-10, D_H3-9, D_H2-8, D_H1-7, D_H6-6, D_H5-5, D_H4-4, D_H3-3, D_H2-2, or D_H1-1. In one embodiment, the human V_H region is operably linked to human, rat, or mouse immunoglobulin heavy chain constant (C_H) region, e.g., a mouse C_H region. In one aspect,

the human V_H region is expressed from an endogenous immunoglobulin heavy chain locus. In one embodiment, such mouse comprises the human V_L region that comprises a human J_κ gene segment derived from a human J_κ5 gene segment. In one embodiment, the human V_κ1-39 gene segment is present in rearrangement with the human J_κ5 gene segment in the mouse germline. In one aspect, the mouse lacks a mouse V_L and/or J_L segments. In one aspect, the human V_L region in the mouse is operably linked to a human, rat, or mouse immunoglobulin light chain constant (C_L) region, e.g., a mouse C_L region. In one aspect, the human V_L region is expressed from an endogenous mouse immunoglobulin light chain locus. In one embodiment, the mouse expresses an antibody comprising the regions described herein in response to an antigen of interest.

[0035] In yet another embodiment, provided herein is a mouse that expresses a single rearranged human immunoglobulin V_L region that is derived from a human rearranged germline V_κ3-20/J_κ1 sequence and a human immunoglobulin V_H region cognate with the human immunoglobulin V_L region wherein the human immunoglobulin V_H region is derived from a human V_H/D_H/J_H gene segment rearrangement selected from rearrangements listed in Table 25. Also provided herein is a mouse that expresses a single rearranged human immunoglobulin V_L region that is derived from a human rearranged germline V_κ1-39/J_κ5 sequence and a human immunoglobulin V_H region cognate with the human immunoglobulin V_L region wherein the human immunoglobulin V_H region is derived from a human V_H/D_H/J_H gene segment rearrangements selected from rearrangements listed in Table 26.

[0036] In one embodiment, 90-100% of the endogenous unrearranged mouse V_H gene segments are replaced with at least one unrearranged human V_H gene segment. In a specific embodiment, all or substantially all of the endogenous unrearranged mouse V_H gene segments are replaced with at least one unrearranged human V_H gene segment. In one embodiment, the replacement is with at least 18, at least 39, at least 80, or 81 unrearranged human V_H gene segments. In one embodiment, the replacement is with at least 12 functional unrearranged human V_H gene segments, at least 25 functional unrearranged human V_H gene segments, or at least 43 unrearranged human V_H gene segments.

[0037] In one embodiment, the genetically modified mouse is a C57BL strain, in a specific embodiment selected from C57BL/A, C57BL/An, C57BL/GrFa, C57BL/KaLwN, C57BL/6, C57BL/6J, C57BL/6ByJ, C57BL/6NJ, C57BL/10, C57BL/10ScSn, C57BL/10Cr, and C57BL/Ola. In a specific embodiment, the genetically modified mouse is a mix of an aforementioned 129 strain and an aforementioned C57BL/6 strain. In another specific

embodiment, the mouse is a mix of aforementioned 129 strains, or a mix of aforementioned BL/6 strains. In a specific embodiment, the 129 strain of the mix is a 129S6 (129/SvEvTac) strain.

[0038] In one embodiment, the mouse expresses a reverse chimeric antibody comprising a light chain that comprises a mouse C κ and a somatically mutated human V_L domain derived from a rearranged human V κ 1-39J κ 5 sequence or a rearranged human V κ 3-20J κ 1 sequence, and a heavy chain that comprises a mouse C_H and a somatically mutated human V_H domain derived from a human V_H gene segment selected from a 1-2, 1-8, 1-24, 1-69, 2-5, 3-7, 3-9, 3-11, 3-13, 3-15, 3-20, 3-23, 3-30, 3-33, 3-48, 3-53, 4-31, 4-39, 4-59, 5-51, and a 6-1 human V_H gene segment, wherein the mouse does not express a fully mouse antibody and does not express a fully human antibody. In another embodiment, the mouse expresses a reverse chimeric antibody comprising a mouse C κ and a somatically mutated human V_L domain derived from a rearranged human V κ 1-39J κ 5 sequence or a rearranged human V κ 3-20J κ 1 sequence, and a heavy chain that comprises a mouse C_H and a somatically mutated human V_H domain derived from a human V_H gene segment selected from V_H6-1, V_H1-2, V_H1-3, V_H2-5, V_H3-7, V_H1-8, V_H3-9, V_H3-11, V_H3-13, V_H3-15, V_H1-18, V_H3-20, V_H3-21, V_H3-23, V_H1-24, V_H2-26, V_H4-28, V_H3-30, V_H4-31, V_H3-33, V_H4-34, V_H4-39, V_H3-43, V_H1-46, V_H3-48, V_H3-49, V_H5-51, V_H3-53, V_H1-58, V_H4-59, V_H4-61, V_H3-64, V_H3-66, V_H1-69, V_H2-70, V_H3-72, and V_H3-73 segment, wherein the mouse does not express a fully mouse antibody and does not express a fully human antibody. In one embodiment the mouse comprises a κ light chain locus that comprises a replacement of endogenous mouse κ light chain gene segments with the rearranged human V κ 1-39J κ 5 sequence or the rearranged human V κ 3-20J κ 1 sequence, and comprises a replacement of all or substantially all endogenous mouse V_H gene segments with a complete or substantially complete repertoire of human V_H gene segments.

[0039] In one aspect, a population of antigen-specific antibodies derived from a mouse as described herein is provided, wherein the antibodies comprise a light chain gene derived from a human V κ 1-39/J κ 5 rearrangement or a human V κ 3-20/J κ 1 rearrangement, and wherein the antibodies comprise a rearranged immunoglobulin heavy chain gene derived from a rearrangement of a human V_H gene segment selected from a 1-2, 1-3, 1-8, 1-18, 1-24, 1-46, 1-58, 1-69, 2-5, 2-26, 2-70, 3-7, 3-9, 3-11, 3-13, 3-15, 3-16, 3-20, 3-21, 3-23, 3-30, 3-33, 3-43, 3-48, 3-53, 3-64, 3-72, 3-73, 4-31, 4-34, 4-39, 4-59, 5-51, and a 6-1 human V_H gene segment. In one embodiment, the one or more human V_H gene segments are rearranged with

a human heavy chain J_H gene segment selected from 1, 2, 3, 4, 5, and 6. In a specific embodiment, the light chain has 1, 2, 3, 4, or 5 or more somatic hypermutations.

[0040] In one embodiment, the light chain has 1, 2, 3, or 4 somatic hypermutations. In one embodiment, the light chain gene has 1 or 2 mutations. In various embodiments, the light chain gene is capable of incurring multiple mutations along its sequence.

[0041] In one embodiment, the light chain is derived from a human V κ 1-39/J κ 5 rearrangement and the light chain has at least one or no more than four somatic hypermutations. In one embodiment, the light chain comprises at least two somatic hypermutations. In one embodiment, the light chain comprises at least three somatic hypermutations. In one embodiment, the light chain comprises at least four somatic hypermutations. In a specific embodiment, the mutations are present in one or more framework regions (FWs) of the light chain. In a specific embodiment, the mutations are present in one or more complementarity determining regions (CDRs) of the light chain. In a specific embodiment, the mutations are present in one or more FWs and/or one or more CDRs of the light chain. In various embodiments, the framework regions are selected from framework 1 (FW1), framework 2 (FW2), framework 3 (FW3), and/or a combination thereof. In various embodiments, the CDRs are selected from CDR1, CDR2, CDR3, and/or a combination thereof.

[0042] In one embodiment, the heavy chain comprises at least one mutation in one or more FWs or one or more CDRs. In one embodiment, the heavy chain comprises at least one mutation in one or more FWs and one or more CDRs. In one embodiment, the heavy chain comprises at least two mutations in one or more FWs and one or more CDRs. In one embodiment, the heavy chain comprises at least three mutations in one or more FWs and one or more CDRs. In one embodiment, the heavy chain comprises at least four mutations in one or more FWs and one or more CDRs. In one embodiment, the heavy chain comprises at least five or more than five mutations in one or more FWs and one or more CDRs; in a specific embodiment, the heavy chain comprises at least five or more than five mutations in two FWs; in a specific embodiment, the heavy chain comprises at least five or more than five mutations in one FW and one CDR.

[0043] In one embodiment, the light chain is derived from a human V κ 1-39/J κ 5 rearrangement and about 9% of the V κ 1-39/J κ 5-derived light chains have at least one mutation present in FW1; in one embodiment, at least 9% of the light chains comprise one mutation present in FW1. In one embodiment, the light chain is derived from a human V κ 1-

39/Jκ5 rearrangement and about 25% of the Vκ1-39/Jκ5-derived light chains have at least one or no more than two mutations present in CDR1; in one embodiment, at least 19% of the light chains have one mutation present in CDR1; in one embodiment, at least 5% of the light chains have two mutations present in CDR1.

5 [0044] In one embodiment, the light chain is derived from a human Vκ1-39/Jκ5 rearrangement and about 20% of the Vκ1-39/Jκ5-derived light chains have at least one or no more than three mutations present in FW2; in one embodiment, at least 17% of the light chains have one mutation present in FW2; in one embodiment, at least 1% of the light chains have two mutations present in FW2; in one embodiment, at least 1% of the light chains have
10 three mutations present in FW2.

[0045] In one embodiment, the light chain is derived from a human Vκ1-39/Jκ5 rearrangement and about 10% of the Vκ1-39/Jκ5-derived light chains have at least one or no more than two mutations present in CDR2; in one embodiment, at least 10% of the light chains have one mutation present in CDR2; in one embodiment, at least 1% of the light
15 chains have two mutations present in CDR2.

[0046] In one embodiment, the light chain is derived from a human Vκ1-39/Jκ5 rearrangement and about 29% of the Vκ1-39/Jκ5-derived light chains have at least one or no more than four mutations present in FW3; in one embodiment, at least 21% of the light chains have one mutation present in FW3; in one embodiment, at least 5% of the light chains
20 have two mutations present in FW3; in one embodiment, at least 2% of the light chains have three mutations present in FW3; in one embodiment, at least 2% of the light chains have four mutations present in FW3.

[0047] In one embodiment, the light chain is derived from a human Vκ1-39/Jκ5 rearrangement and about 37% of the Vκ1-39/Jκ5-derived light chains have at least one or no
25 more than four mutations present in CDR3; in one embodiment, at least 27% of the light chains have one mutation present in CDR3; in one embodiment, at least 8% of the light chains have two mutations present in CDR3; in one embodiment, at least 1% of the light chains have three mutations present in CDR3; in one embodiment, at least 1% of the light chains have four mutations present in CDR3.

30 [0048] In one embodiment, a population of antigen-specific antibodies derived from a mouse as described herein is provided, wherein the antibodies comprise a light chain derived from a human Vκ1-39/Jκ5 rearrangement and about 9% of the Vκ1-39/Jκ5-derived light chains have one or more mutations present in FW1, about 25% of the Vκ1-39/Jκ5-derived

light chains have one or more mutations present in CDR1, about 20% of the V κ 1-39/J κ 5-derived light chains have one or more mutations present in FW2, about 10% of the V κ 1-39/J κ 5-derived light chains have one or more mutations present in CDR2, about 29% of the V κ 1-39/J κ 5-derived light chains have one or more mutations present in FW3, and about 37% of the V κ 1-39/J κ 5-derived light chains have one or more mutations present in CDR3.

[0049] In one embodiment, the light chain is derived from a human V κ 1-39/J κ 5 rearrangement and about 35% of the heavy chains have at least one mutation present in FW1; in one embodiment, at least 25% of the heavy chains have one mutation present in FW1; in one embodiment, at least 9 % of the heavy chains have two mutations present in FW1; in one embodiment, at least 1% of the heavy chains have three mutations present in FW1; in one embodiment, at least 1% of the heavy chains have more than five mutations present in FW1.

[0050] In one embodiment, the light chain is derived from a human V κ 1-39/J κ 5 rearrangement and about 92% of the heavy chains have at least one or no more than four mutations present in CDR1; in one embodiment, at least 92% of the heavy chains have at least one, at least two, at least three, or at least four mutations present in CDR1; in one embodiment, at least 26% of the heavy chains have one mutation present in CDR1; in one embodiment, at least 44% of the heavy chains have two mutations present in CDR1; in one embodiment, at least 19% of the heavy chains have three mutations present in CDR1; in one embodiment, at least 3% of the heavy chains have four mutations present in CDR1.

[0051] In one embodiment, the light chain is derived from a human V κ 1-39/J κ 5 rearrangement and about 66% of the heavy chains have at least one or no more than three mutations present in FW2; in one embodiment, at least 66% of the heavy chains have at least one, at least two, or at least three mutations present in FW2; in one embodiment, at least 35% of the heavy chains have one mutation present in FW2; in one embodiment, at least 23% of the heavy chains have two mutations present in FW2; in one embodiment, at least 8% of the heavy chains have three mutations present in FW2.

[0052] In one embodiment, the light chain is derived from a human V κ 1-39/J κ 5 rearrangement and about 70% of the heavy chains have at least one or no more than four mutations present in CDR2; in one embodiment, at least 70% of the heavy chains have at least two, at least three, or at least four mutations present in CDR2; in one embodiment, at least 34% have one mutation present in CDR2; in one embodiment, at least 20% of the heavy chains have two mutations present in CDR2; in one embodiment, at least 12% of the heavy

chains have three mutations present in CDR2; in one embodiment, at least 5% of the heavy chains have four mutations present in CDR2.

[0053] In one embodiment, the light chain is derived from a human V κ 1-39/J κ 5 rearrangement and about 91% of the heavy chains have at least one or up to five or more mutations present in FW3; in one embodiment, at least 91% of the heavy chains have at least two, at least three, at least four, or at least five or more mutations present in FW3; in one embodiment, at least 19% of the heavy chains have one mutation present in FW3; in one embodiment, at least 33% of the heavy chains have two mutations present in FW3; in one embodiment, at least 22% of the heavy chains have three mutations present in FW3; in one embodiment, at least 11% of the heavy chains have four mutations present in FW3; in one embodiment, at least 7% of the heavy chains have five or more mutations present in FW3.

[0054] In one embodiment, the light chain is derived from a human V κ 1-39/J κ 5 rearrangement and about 63% of the heavy chains have at least one or no more than two mutations present in CDR3; in one embodiment, at least 63% of the heavy chains have at one mutation present in CDR3; in one embodiment, at least 54% of the heavy chains have one mutation present in CDR3; in one embodiment, at least 9% of the heavy chains have two mutations present in CDR3.

[0055] In one embodiment, a population of antigen-specific antibodies derived from a mouse as described herein is provided, wherein the antibodies comprise a light chain derived from a human V κ 1-39/J κ 5 rearrangement and at least 35% of the heavy chains have one or more mutations present in FW1, about 92% of the heavy chains have one or more mutations present in CDR1, about 66% of the heavy chains have one or more mutations present in FW2, about 70% of the heavy chains have one or more mutations present in CDR2, about 91% of the heavy chains have one or more mutations present in FW3, and about 63% of the heavy chains have one or more mutations present in CDR3.

[0056] In one embodiment, the light chain is derived from a human V κ 3-20/J κ 1 rearrangement and the light chain gene has at least one or no more than two somatic hypermutations; in one embodiment, the light chain gene has at least two, at least three, at least four or more somatic hypermutations. In a specific embodiment, the mutations are present in one or more framework regions of the light chain. In a specific embodiment, the mutations are present in one or more CDR regions of the light chain. In a specific embodiment, the mutations are present in one or more framework regions and/or one or more CDR regions of the light chain. In various embodiments, the framework regions are selected

from framework 1 (FW1), framework 2 (FW2), framework 3 (FW3), and/or a combination thereof.

[0057] In one embodiment, the light chain is derived from a human V κ 3-20/J κ 1 rearrangement and about 10% of the V κ 3-20/J κ 1-derived light chains have at least one mutation present in FW1; in one embodiment, at least 10% of the light chains have one mutation in FW1.

[0058] In one embodiment, the light chain is derived from a human V κ 3-20/J κ 1 rearrangement and about 53% of the V κ 3-20/J κ 1-derived light chains have at least one or no more than two mutations present in CDR1; in one embodiment, at least 27% of the light chains have one or more mutations in CDR1; in one embodiment, about 54% of the light chains have one or two mutations present in CDR1.

[0059] In one embodiment, the light chain is derived from a human V κ 3-20/J κ 1 rearrangement and about 6% of the V κ 3-20/J κ 1-derived light chains have at least one or no more than two mutations present in FW2; in one embodiment, at least 6% of light chains have at least one mutation present in FW2; in one embodiment, at least 3% of the light chains have one mutation present in FW2; in one embodiment, at least 3% of the light chains have two mutations present in FW2.

[0060] In one embodiment, the light chain is derived from a human V κ 3-20/J κ 1 rearrangement and at least about 3% of the V κ 3-20/J κ 1-derived light chains have at least one mutation present in CDR2; in one embodiment, at least 3% of the light chains have one mutation in CDR2.

[0061] In one embodiment, the light chain is derived from a human V κ 3-20/J κ 1 rearrangement and about 17% or more of the V κ 3-20/J κ 1-derived light chains have at least one or no more than two mutations present in FW3; in one embodiment, at least 20% of the light chain have one mutation present in FW3; in one embodiment, at least 17% of the light chains have two mutations present in FW3.

[0062] In one embodiment, the light chain is derived from a human V κ 3-20/J κ 1 rearrangement and at least 43% of the V κ 3-20/J κ 1-derived light chains have at least one mutation present in CDR3; in one embodiment, at least 43% of the light chains have one mutation in CDR3.

[0063] In one embodiment, a population of antigen-specific antibodies derived from a mouse as described herein is provided, wherein the antibodies comprise a light chain derived

from a human V κ 3-20/J κ 1 rearrangement and about 10% of the V κ 3-20/J κ 1-derived light chains have one or more mutations present in at least, about 53% of the V κ 3-20/J κ 1-derived light chains have one or more mutations present in CDR1, about 6% of the V κ 3-20/J κ 1-derived light chains have one or more mutations present in FW2, about 3% of the V κ 3-20/J κ 1-derived light chains have one or more mutations present in CDR2, about 37% of the V κ 3-20/J κ 1-derived light chains have one or more mutations present in FW3, and about 43% of the V κ 3-20/J κ 1-derived light chains have one or more mutations present in CDR3.

[0064] In one embodiment, the light chain is derived from a human V κ 3-20/J κ 1 rearrangement and about 43% of the heavy chains have at least one or no more than two mutations present in FW1; in one embodiment, at least 41% of the heavy chains have at least one mutation present in FW1; in one embodiment, about 41% of the heavy chains have one mutation present in FW1; in one embodiment, about 2% of the heavy chains have two mutations present in FW1.

[0065] In one embodiment, the light chain is derived from a human V κ 3-20/J κ 1 rearrangement and about 92% of the heavy chains have at least one or no more than four mutations present in CDR1; in one embodiment, at least 43% of heavy chains have at least one mutation present in CDR1; in one embodiment, at least 25% of heavy chains have at least two mutations present in CDR1; in one embodiment, at least 15% of heavy chains have at least 3 mutations present in CDR1; in one embodiment, at least 10% of heavy chains have 4 or more mutations present in CDR1.

[0066] In one embodiment, the light chain is derived from a human V κ 3-20/J κ 1 rearrangement and about 46% of the heavy chains have at least one or no more than three mutations present in FW2; in one embodiment, at least 34% of heavy chains have at least one mutation present in FW2; in one embodiment, at least 10% of heavy chains have two or more mutations present in FW2; in one embodiment, at least 2% of heavy chains have three or more mutations present in FW2.

[0067] In one embodiment, the light chain is derived from a human V κ 3-20/J κ 1 rearrangement and about 84% of the heavy chains have at least one or up to five or more than five mutations present in CDR2; in one embodiment, at least 39% of the heavy chains have one or more mutations present in CDR2; in one embodiment, at least 18% of the heavy chains have two or more mutations present in CDR2; in one embodiment, at least 21% of the heavy chains have three or more mutations present in CDR2; in one embodiment, at least 3%

of the heavy chains have four or more mutations present in CDR2; in one embodiment, at least 2% of the heavy chains have five or more mutations present in CDR2.

[0068] In one embodiment, the light chain is derived from a human V κ 3-20/J κ 1 rearrangement and about 92% of the heavy chains have at least one or up to five or more than
 5 five mutations present in FW3; in one embodiment, at least 21% of the light chains have at least one mutation present in FW3; in one embodiment, at least 20% of heavy chains have at least two mutations present in FW3; in one embodiment, at least 13% of the heavy chains have at least three mutations present in FW3; in one embodiment, at least 20% of the heavy chains have at least four mutations in FW3; in one embodiment, at least 18% of the heavy
 10 chains have at least 5 mutations in FW3.

[0069] In one embodiment, the light chain is derived from a human V κ 3-20/J κ 1 rearrangement and about 7% of the heavy chains have at least one mutation present in CDR3; in one embodiment, about 7% of the heavy chains have one mutation in CDR3.

[0070] In one embodiment, a population of antigen-specific antibodies derived from a
 15 mouse as described herein is provided, wherein the antibodies comprise a light chain derived from a human V κ 3-20/J κ 1 rearrangement and about 43% of the heavy chains have one or more mutations present in FW1, about 92% of the heavy chains have one or more mutations present in CDR1, about 46% of the heavy chains have one or more mutations present in FW2, about 84% of the heavy chains have one or more mutations present in CDR2, about 92% of
 20 the heavy chains have one or more mutations present in FW3, and about 7% of the heavy chains have one or more mutations present in CDR3.

[0071] In one aspect, a mouse that expresses an immunoglobulin light chain from a rearranged immunoglobulin light chain sequence is provided, wherein the rearranged immunoglobulin light chain sequence is present in the germline of the mouse, wherein the
 25 immunoglobulin light chain comprises a human variable sequence. In one embodiment, the germline of the mouse comprises a rearranged immunoglobulin light chain sequence that is derived from the same V segment and the same J segment as all non-surrogate light chain sequences present in every B cell of the mouse that comprises a rearranged light chain sequence.

[0072] In one embodiment, the germline of the mouse lacks a functional unrearranged immunoglobulin light chain V gene segment. In one embodiment, the germline of the mouse lacks a functional unrearranged immunoglobulin light chain J gene segment.

[0073] In one embodiment, the germline of the mouse comprises no more than one, no more than two, or no more than three rearranged (V/J) light chain sequences.

[0074] In one embodiment, the rearranged V/J sequence comprises a κ light chain sequence. In a specific embodiment, the κ light chain sequence is a human κ light chain sequence. In a specific embodiment, the κ light chain sequence is selected from a human V κ 1-39/J sequence, a human V κ 3-20/J sequence, and a combination thereof. In a specific embodiment, the κ light chain sequence is a human V κ 1-39/J κ 5 sequence. In a specific embodiment, the κ light chain sequence is a human V κ 3-20/J κ 1 sequence.

[0075] In one embodiment, the mouse further comprises in its germline a sequence selected from a mouse κ intronic enhancer 5' with respect to the rearranged immunoglobulin light chain sequence, a mouse κ 3' enhancer, and a combination thereof.

[0076] In one embodiment, the mouse comprises an unrearranged human V_H gene segment, an unrearranged human D_H gene segment, and an unrearranged human J_H gene segment, wherein said V_H, D_H, and J_H gene segments are capable of rearranging to form an immunoglobulin heavy chain variable gene sequence operably linked to a heavy chain constant gene sequence. In one embodiment, the mouse comprises a plurality of human V_H, D_H, and J_H gene segments. In a specific embodiment, the human V_H, D_H, and J_H gene segments replace endogenous mouse V_H, D_H, and J_H gene segments at the endogenous mouse immunoglobulin heavy chain locus. In a specific embodiment, the mouse comprises a replacement of all or substantially all functional mouse V_H, D_H, and J_H gene segments with all or substantially all functional human V_H, D_H, and J_H gene segments.

[0077] In one embodiment, the mouse expresses an immunoglobulin light chain that comprises a mouse constant sequence. In one embodiment, the mouse expresses an immunoglobulin light chain that comprises a human constant sequence.

[0078] In one embodiment, the mouse expresses an immunoglobulin heavy chain that comprises a mouse sequence selected from a C_H1 sequence, a hinge sequence, a C_H2 sequence, a C_H3 sequence, and a combination thereof.

[0079] In one embodiment, the mouse expresses an immunoglobulin heavy chain that comprises a human sequence selected from a C_H1 sequence, a hinge sequence, a C_H2 sequence, a C_H3 sequence, and a combination thereof.

[0080] In one embodiment, the rearranged immunoglobulin light chain sequence in the germline of the mouse is at an endogenous mouse immunoglobulin light chain locus. In a specific embodiment, the rearranged immunoglobulin light chain sequence in the germline of

the mouse replaces all or substantially all mouse light chain V and J sequences at the endogenous mouse immunoglobulin light chain locus.

[0081] In one aspect, a mouse is provided that comprises a B cell population characterized by each B cell that comprises a non-surrogate light chain sequence comprises a rearranged light chain gene that is derived from a single human V segment and a single human J segment, wherein the only light chain variable sequence in the germline of the mouse is a rearranged sequence derived from the single human V segment and the single human J segment, and wherein each B cell that comprises the rearranged light chain gene further comprises a gene encoding a cognate human heavy chain variable domain, and wherein the rearranged light chain gene comprises at least one, at least two, at least three, or at least four somatic hypermutations.

[0082] In one aspect, a pluripotent, induced pluripotent, or totipotent cell derived from a mouse as described herein is provided. In a specific embodiment, the cell is a mouse embryonic stem (ES) cell.

[0083] In one aspect, a tissue derived from a mouse as described herein is provided. In one embodiment, the tissue is derived from spleen, lymph node or bone marrow of a mouse as described herein.

[0084] In one aspect, a nucleus derived from a mouse as described herein is provided. In one embodiment, the nucleus is from a diploid cell that is not a B cell.

[0085] In one aspect, a mouse cell is provided that is isolated from a mouse as described herein. In one embodiment, the cell is an ES cell. In one embodiment, the cell is a lymphocyte. In one embodiment, the lymphocyte is a B cell. In one embodiment, the B cell expresses a chimeric heavy chain comprising a variable domain derived from a human gene segment; and a light chain derived from a rearranged human V κ 1-39/J sequence, rearranged human V κ 3-20/J sequence, or a combination thereof; wherein the heavy chain variable domain is fused to a mouse constant region and the light chain variable domain is fused to a mouse or a human constant region.

[0086] In one aspect, a hybridoma is provided, wherein the hybridoma is made with a B cell of a mouse as described herein. In a specific embodiment, the B cell is from a mouse as described herein that has been immunized with an immunogen comprising an epitope of interest, and the B cell expresses a binding protein that binds the epitope of interest, the binding protein has a somatically mutated human V_H domain and a mouse C_H, and has a

human V_L domain derived from a rearranged human V_κ1-39J_κ5 or a rearranged human V_κ3-20J_κ1 and a mouse C_L.

[0087] In one aspect, a mouse embryo is provided, wherein the embryo comprises a donor ES cell that is derived from a mouse as described herein.

5 **[0088]** In one aspect, a targeting vector is provided, comprising, from 5' to 3' in transcriptional direction with reference to the sequences of the 5' and 3' mouse homology arms of the vector, a 5' mouse homology arm, a human or mouse immunoglobulin promoter, a human or mouse leader sequence, and a human V_L region selected from a rearranged human V_κ1-39J_κ5 or a rearranged human V_κ3-20J_κ1, and a 3' mouse homology arm. In one
10 embodiment, the 5' and 3' homology arms target the vector to a sequence 5' with respect to an enhancer sequence that is present 5' and proximal to the mouse C_κ gene. In one embodiment, the promoter is a human immunoglobulin variable region gene segment promoter. In a specific embodiment, the promoter is a human V_κ3-15 promoter. In one embodiment, the leader sequence is a mouse leader sequence. In a specific embodiment, the
15 mouse leader sequence is a mouse V_κ3-7 leader sequence.

[0089] In one aspect, a targeting vector is provided as described above, but in place of the 5' mouse homology arm the human or mouse promoter is flanked 5' with a site-specific recombinase recognition site (SRRS), and in place of the 3' mouse homology arm the human V_L region is flanked 3' with an SRRS.

20 **[0090]** In one aspect, a reverse chimeric antibody made by a mouse as described herein, wherein the reverse chimeric antibody comprises a light chain comprising a human V_L and a mouse C_L, and a heavy chain comprising a human V_H and a mouse C_H.

[0091] In one aspect, a method for making an antibody is provided, comprising
25 expressing in a single cell (a) a first V_H gene sequence of an immunized mouse as described herein fused with a human C_H gene sequence; (b) a V_L gene sequence of an immunized mouse as described herein fused with a human C_L gene sequence; and, (c) maintaining the cell under conditions sufficient to express a fully human antibody, and isolating the antibody. In one embodiment, the cell comprises a second V_H gene sequence of a second immunized mouse as described herein fused with a human C_H gene sequence, the first V_H gene sequence
30 encodes a V_H domain that recognizes a first epitope, and the second V_H gene sequence encodes a V_H domain that recognizes a second epitope, wherein the first epitope and the second epitope are not identical.

[0092] In one aspect, a method for making an epitope-binding protein is provided, comprising exposing a mouse as described herein with an immunogen that comprises an epitope of interest, maintaining the mouse under conditions sufficient for the mouse to generate an immunoglobulin molecule that specifically binds the epitope of interest, and isolating the immunoglobulin molecule that specifically binds the epitope of interest; wherein the epitope-binding protein comprises a heavy chain that comprises a somatically mutated human V_H and a mouse C_H , associated with a light chain comprising a mouse C_L and a human V_L derived from a rearranged human $V\kappa 1$ -39J $\kappa 5$ or a rearranged human $V\kappa 3$ -20J $\kappa 1$.

[0093] In one aspect, a cell that expresses an epitope-binding protein is provided, wherein the cell comprises: (a) a human nucleotide sequence encoding a human V_L domain that is derived from a rearranged human $V\kappa 1$ -39J $\kappa 5$ or a rearranged human $V\kappa 3$ -20J $\kappa 1$, wherein the human nucleotide sequence is fused (directly or through a linker) to a human immunoglobulin light chain constant domain cDNA sequence (*e.g.*, a human κ constant domain DNA sequence); and, (b) a first human V_H nucleotide sequence encoding a human V_H domain derived from a first human V_H nucleotide sequence, wherein the first human V_H nucleotide sequence is fused (directly or through a linker) to a human immunoglobulin heavy chain constant domain cDNA sequence; wherein the epitope-binding protein recognizes a first epitope. In one embodiment, the epitope-binding protein binds the first epitope with a dissociation constant of lower than 10^{-6} M, lower than 10^{-8} M, lower than 10^{-9} M, lower than 10^{-10} M, lower than 10^{-11} M, or lower than 10^{-12} M.

[0094] In one embodiment, the cell comprises a second human nucleotide sequence encoding a second human V_H domain, wherein the second human sequence is fused (directly or through a linker) to a human immunoglobulin heavy chain constant domain cDNA sequence, and wherein the second human V_H domain does not specifically recognize the first epitope (*e.g.*, displays a dissociation constant of, *e.g.*, 10^{-6} M, 10^{-5} M, 10^{-4} M, or higher), and wherein the epitope-binding protein recognizes the first epitope and the second epitope, and wherein the first and the second immunoglobulin heavy chains each associate with an identical light chain of (a).

[0095] In one embodiment, the second V_H domain binds the second epitope with a dissociation constant that is lower than 10^{-6} M, lower than 10^{-7} M, lower than 10^{-8} M, lower than 10^{-9} M, lower than 10^{-10} M, lower than 10^{-11} M, or lower than 10^{-12} M.

[0096] In one embodiment, the epitope-binding protein comprises a first immunoglobulin heavy chain and a second immunoglobulin heavy chain, each associated with an identical

light chain derived from a rearranged human V_L region selected from a human V_κ1-39J_κ5 or a human V_κ3-20J_κ1, wherein the first immunoglobulin heavy chain binds a first epitope with a dissociation constant in the nanomolar to picomolar range, the second immunoglobulin heavy chain binds a second epitope with a dissociation constant in the nanomolar to picomolar range, the first epitope and the second epitope are not identical, the first immunoglobulin heavy chain does not bind the second epitope or binds the second epitope with a dissociation constant weaker than the micromolar range (*e.g.*, the millimolar range), the second immunoglobulin heavy chain does not bind the first epitope or binds the first epitope with a dissociation constant weaker than the micromolar range (*e.g.*, the millimolar range), and one or more of the V_L, the V_H of the first immunoglobulin heavy chain, and the V_H of the second immunoglobulin heavy chain, are somatically mutated.

[0097] In one embodiment, the first immunoglobulin heavy chain comprises a protein A-binding residue, and the second immunoglobulin heavy chain lacks the protein A-binding residue.

[0098] In one embodiment, the cell is selected from CHO, COS, 293, HeLa, and a retinal cell expressing a viral nucleic acid sequence (*e.g.*, a PERC.6™ cell).

[0099] In one aspect, a reverse chimeric antibody is provided, comprising a human V_H and a mouse heavy chain constant domain, a human V_L and a mouse light chain constant domain, wherein the antibody is made by a process that comprises immunizing a mouse as described herein with an immunogen comprising an epitope, and the antibody specifically binds the epitope of the immunogen with which the mouse was immunized. In one embodiment, the V_L domain is somatically mutated. In one embodiment the V_H domain is somatically mutated. In one embodiment, both the V_L domain and the V_H domain are somatically mutated. In one embodiment, the V_L is linked to a mouse C_κ domain.

[00100] In one aspect, a mouse is provided, comprising human V_H gene segments replacing all or substantially all mouse V_H gene segments at the endogenous mouse heavy chain locus; no more than one or two rearranged human light chain V_L/J_L sequences selected from a rearranged V_κ1-39/J and a rearranged V_κ3-20/J or a combination thereof, replacing all mouse light chain gene segments; wherein the human heavy chain variable gene segments are linked to a mouse constant gene, and the rearranged human light chain sequences are linked to a human or mouse constant gene.

[00101] In one aspect, a mouse ES cell comprising a replacement of all or substantially all mouse heavy chain variable gene segments with human heavy chain variable gene segments,

and no more than one or two rearranged human light chain V_L/J_L sequences, wherein the human heavy chain variable gene segments are linked to a mouse immunoglobulin heavy chain constant gene, and the rearranged human light chain V_L/J_L sequences are linked to a mouse or human immunoglobulin light chain constant gene. In a specific embodiment, the light chain constant gene is a mouse constant gene.

[00102] In one aspect, an antigen-binding protein made by a mouse as described herein is provided. In a specific embodiment, the antigen-binding protein comprises a human immunoglobulin heavy chain variable region fused with a mouse constant region, and a human immunoglobulin light chain variable region derived from a $V_{\kappa}1-39$ gene segment or a $V_{\kappa}3-20$ gene segment, wherein the light chain constant region is a mouse constant region.

[00103] In one aspect, a fully human antigen-binding protein made from an immunoglobulin variable region gene sequence from a mouse as described herein is provided, wherein the antigen-binding protein comprises a fully human heavy chain comprising a human variable region derived from a sequence of a mouse as described herein, and a fully human light chain comprising a $V_{\kappa}1-39$ or a $V_{\kappa}3-20$. In one embodiment, the light chain variable region comprises one to five somatic mutations. In one embodiment, the light chain variable region is a cognate light chain variable region that is paired in a B cell of the mouse with the heavy chain variable region.

[00104] In one embodiment, the fully human antigen-binding protein comprises a first heavy chain and a second heavy chain, wherein the first heavy chain and the second heavy chain comprise non-identical variable regions independently derived from a mouse as described herein, and wherein each of the first and second heavy chains express from a host cell associated with a human light chain derived from a $V_{\kappa}1-39$ gene segment or a $V_{\kappa}3-20$ gene segment. In one embodiment, the first heavy chain comprises a first heavy chain variable region that specifically binds a first epitope of a first antigen, and the second heavy chain comprises a second heavy chain variable region that specifically binds a second epitope of a second antigen. In a specific embodiment, the first antigen and the second antigen are different. In a specific embodiment, the first antigen and the second antigen are the same, and the first epitope and the second epitope are not identical; in a specific embodiment, binding of the first epitope by a first molecule of the binding protein does not block binding of the second epitope by a second molecule of the binding protein.

[00105] In one aspect, a fully human binding protein derived from a human immunoglobulin sequence of a mouse as described herein comprises a first immunoglobulin

heavy chain and a second immunoglobulin heavy chain, wherein the first immunoglobulin heavy chain comprises a first variable region that is not identical to a variable region of the second immunoglobulin heavy chain, and wherein the first immunoglobulin heavy chain comprises a wild type protein A binding determinant, and the second heavy chain lacks a wild type protein A binding determinant. In one embodiment, the first immunoglobulin heavy chain binds protein A under isolation conditions, and the second immunoglobulin heavy chain does not bind protein A or binds protein A at least 10-fold, a hundred-fold, or a thousand-fold weaker than the first immunoglobulin heavy chain binds protein A under isolation conditions. In a specific embodiment, the first and the second heavy chains are IgG1 isotypes, wherein the second heavy chain comprises a modification selected from 95R (EU 435R), 96F (EU 436F), and a combination thereof, and wherein the first heavy chain lacks such modification.

[00106] In one aspect, a method for making a bispecific antigen-binding protein is provided, comprising exposing a first mouse as described herein to a first antigen of interest that comprises a first epitope, exposing a second mouse as described herein to a second antigen of interest that comprises a second epitope, allowing the first and the second mouse to each mount immune responses to the antigens of interest, identifying in the first mouse a first human heavy chain variable region that binds the first epitope of the first antigen of interest, identifying in the second mouse a second human heavy chain variable region that binds the second epitope of the second antigen of interest, making a first fully human heavy chain gene that encodes a first heavy chain that binds the first epitope of the first antigen of interest, making a second fully human heavy chain gene that encodes a second heavy chain that binds the second epitope of the second antigen of interest, expressing the first heavy chain and the second heavy chain in a cell that expresses a single fully human light chain derived from a human V κ 1-39 or a human V κ 3-20 gene segment to form a bispecific antigen-binding protein, and isolating the bispecific antigen-binding protein.

[00107] In one embodiment, the first antigen and the second antigen are not identical.

[00108] In one embodiment, the first antigen and the second antigen are identical, and the first epitope and the second epitope are not identical. In one embodiment, binding of the first heavy chain variable region to the first epitope does not block binding of the second heavy chain variable region to the second epitope.

[00109] In one embodiment, the human light chain when paired with the first heavy chain specifically binds the first epitope of the first antigen and when paired the second heavy chain specifically binds the second epitope of the second antigen.

[00110] In one embodiment, the first antigen is selected from a soluble antigen and a cell surface antigen (*e.g.*, a tumor antigen), and the second antigen comprises a cell surface receptor. In a specific embodiment, the cell surface receptor is an immunoglobulin receptor. In a specific embodiment, the immunoglobulin receptor is an Fc receptor. In one embodiment, the first antigen and the second antigen are the same cell surface receptor, and binding of the first heavy chain to the first epitope does not block binding of the second heavy chain to the second epitope.

[00111] In one embodiment, the light chain variable domain of the light chain comprises 2 to 5 somatic mutations. In one embodiment, the light chain variable domain is a somatically mutated cognate light chain expressed in a B cell of the first or the second immunized mouse with either the first or the second heavy chain variable domain. In one embodiment, the light chain of the cell comprises a germline sequence.

[00112] In one embodiment, the first fully human heavy chain bears an amino acid modification that reduces its affinity to protein A, and the second fully human heavy chain does not comprise a modification that reduces its affinity to protein A.

[00113] In one aspect, a method of preparing a bispecific antibody that specifically binds to a first and a second antigen is provided, wherein the method comprises (a) identifying a first nucleic acid sequence that encodes a first human heavy chain variable (V_H) domain that is specific for the first antigen; (b) identifying a second nucleic acid sequence that encodes a second human heavy chain variable (V_H) domain that is specific for the second antigen; (c) providing a third nucleic acid sequence that encodes a human light chain variable (V_L) region which, when paired with the V_H region of (a) specifically binds the first antigen, and when paired with the V_H region of (b) specifically binds to the second antigen; (d) culturing a host cell comprising the first, second, and third nucleic acid sequences to allow expression of the first and second human V_H regions and the human V_L region to form the bispecific antibody; and (d) recovering said bispecific antibody. In various aspects, the first and second antigens are different from one another. In various aspects the first and second nucleic acid sequences are isolated from an immunized mouse that expresses a human immunoglobulin V_L region from a rearranged immunoglobulin light chain sequence, wherein the rearranged immunoglobulin sequence is in the germline of the mouse.

[00114] In one embodiment, the human V_L region is derived from a rearranged human light chain sequence comprising a human V_κ1-39 gene segment or a human V_κ3-20 gene segment. In a specific embodiment, the rearranged human light chain sequence is a germline sequence (*i.e.*, does not comprise a somatic hypermutation within the V gene segment sequence).

[00115] In one embodiment, the third nucleic acid sequence is isolated from a mouse that expresses a human immunoglobulin V_L region from a rearranged immunoglobulin light chain sequence in the germline of the mouse. In one embodiment, the rearranged immunoglobulin light chain sequence comprises a human V_κ1-39 or human V_κ3-20 gene segment. In a specific embodiment, the rearranged immunoglobulin light chain sequence comprises a human V_κ1-39 gene segment. In one embodiment, the human immunoglobulin V_L region is expressed from a modified endogenous immunoglobulin light chain locus.

[00116] In one embodiment, the first and second antigens are present on one molecule. In one embodiment, the first and second antigens are present on different molecules. In various embodiments, the first or second nucleic acid sequence comprises a modification that reduces the affinity of the encoded heavy chain to protein A.

[00117] In one embodiment, the first or second nucleic acid sequences comprise a rearranged human heavy chain variable region sequence comprising a human heavy chain gene segment selected from V_H1-2, V_H1-3, V_H1-8, V_H1-18, V_H1-24, 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_H3-20, V_H3-21, V_H3-23, V_H3-30, V_H3-33, 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_H4-28, V_H4-31, V_H4-34, V_H4-39, V_H4-59, V_H4-61, V_H5-51, and V_H6-1. In one specific embodiment, the heavy chain gene segment is V_H2-5, V_H3-23 or V_H3-30. In another specific embodiment, the heavy chain gene segment is V_H3-49, V_H4-61, V_H4-28, or V_H3-66.

[00118] In one aspect, a method of preparing a bispecific antibody that specifically binds to a first and a second antigen is provided, wherein the method comprises (a) identifying a first nucleic acid sequence that encodes a first human heavy chain variable (V_H) domain that is specific for the first antigen; (b) identifying a second nucleic acid sequence that encodes a second human heavy chain variable (V_H) domain that is specific for the second antigen; (c) providing a third nucleic acid sequence that encodes a human light chain variable (V_L) region derived from a human V_κ1-39 or human V_κ3-20 gene segment which, when paired with the V_H region of (a) specifically binds the first antigen, and when paired with the V_H region of (b) specifically binds to the second antigen; (d) culturing a host cell comprising the first,

second, and third nucleic acid sequences to allow expression of the first and second human V_H regions and the human V_L region to form the bispecific antibody; and (d) recovering said bispecific antibody. In various aspects, the first and second antigens are different from one another. In various aspects, the first and second nucleic acid sequences are isolated from an immunized mouse that expresses a human immunoglobulin V_L region from a rearranged immunoglobulin sequence that is derived from a human V κ 1-39 or human V κ 3-20 gene segment, wherein the rearranged human V κ 1-39 or V κ 3-30 gene segment is in the germline of the mouse.

[00119] In one embodiment, the third nucleic acid sequence is a germline sequence (*i.e.*, does not comprise a somatic hypermutation within the V gene segment sequence). In one embodiment, the third nucleic acid sequence is isolated from the mouse that expresses a human immunoglobulin V_L region derived from a human V κ 1-39 or human V κ 3-20 gene segment from a rearranged immunoglobulin light chain sequence in the germline of the mouse. In a specific embodiment, the third nucleic acid sequence comprises two to five somatic hypermutations in a complementary determining region (CDR) and/or a framework region (FWR). In one embodiment, the human immunoglobulin V_L region is expressed from a modified endogenous immunoglobulin light chain locus.

[00120] In one embodiment, the first and second antigens are present on one molecule. In one embodiment, the first and second antigens are present on different molecules. In one embodiment, the first or second nucleic acid sequence comprises a modification that reduces the affinity of the encoded heavy chain to protein A.

[00121] In one embodiment, the first or second nucleic acid sequences comprise a rearranged human heavy chain variable region sequence comprising a human heavy chain gene segment selected from V_H1-2, V_H1-3, V_H1-8, V_H1-18, V_H1-24, 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_H3-20, V_H3-21, V_H3-23, V_H3-30, V_H3-33, 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_H4-28, V_H4-31, V_H4-34, V_H4-39, V_H4-59, V_H4-61, V_H5-51, and V_H6-1. In one specific embodiment, the heavy chain gene segment is V_H2-5, V_H3-23 or V_H3-30. In another specific embodiment, the heavy chain gene segment is V_H3-49, V_H4-61, V_H4-28, or V_H3-66.

[00122] In one aspect, a method for making a bispecific antibody is provided, comprising exposing a mouse as described herein to an antigen of interest, allowing the mouse to mount an immune response to the antigen of interest, identifying a first human heavy chain variable region that binds a first epitope of the antigen of interest, identifying a second human heavy

chain variable region that binds a second epitope of the antigen of interest, making a first fully human heavy chain gene that encodes the first heavy chain that binds the first epitope of the antigen of interest, making a second fully human heavy chain gene that encodes a second heavy chain that binds the second epitope of the antigen of interest, expressing the first heavy chain and the second heavy chain in a cell that expresses a single fully human light chain derived from a human V κ 1-39 or a human V κ 3-20 gene segment to form a bispecific antibody, and isolating the bispecific antigen-binding protein.

[00123] In one embodiment, the first epitope and the second epitope are not identical. In one embodiment, binding of the first heavy chain variable region to the first epitope does not block binding of the second heavy chain variable region to the second epitope. In one embodiment, the first and second heavy chains are capable of binding the first and second epitopes simultaneously.

[00124] In one embodiment, the bispecific antibody binds the first and second epitopes simultaneously. In one embodiment, the bispecific antibody binds the first epitope and second epitope independently.

[00125] In one embodiment, the binding response of the bispecific antibody to the antigen is about 2-fold higher than the binding response of the first heavy chain variable region to the antigen. In one embodiment, the binding response of the bispecific antibody to the antigen is about 2-fold higher than the binding response of the second heavy chain variable region to the antigen. In one embodiment, the binding response of the bispecific antibody to the antigen is about the same as, or about equal to, the binding response of the first heavy chain variable region and or the second heavy chain variable region to the antigen.

[00126] In one embodiment, the antigen is selected from a soluble antigen, a cell surface antigen (*e.g.*, a tumor antigen) and a cell surface receptor. In a specific embodiment, the cell surface receptor is an immunoglobulin receptor. In a specific embodiment, the immunoglobulin receptor is an Fc receptor.

[00127] In one embodiment, the light chain variable domain of the light chain comprises 2 to 5 somatic mutations. In one embodiment, the light chain variable domain is a somatically mutated cognate light chain expressed in a B cell of the immunized mouse with either the first or the second heavy chain variable domain.

[00128] In one embodiment, the first fully human heavy chain bears an amino acid modification that reduces its affinity to protein A, and the second fully human heavy chain does not comprise a modification that reduces its affinity to protein A.

[00129] In various embodiments, methods for making bispecific antibodies are enhanced by employing a common light chain to pair with each heavy chain variable regions of the bispecific antibodies. In various embodiments, employing a common light chain as described herein reduces the number of inappropriate species of immunoglobulins lacking bispecificity as compared to employing original cognate light chains. In various embodiments, the heavy chain variable regions of the bispecific antibodies are identified from monospecific antibodies comprising a common light chain. In various embodiments, the heavy chain variable regions of the bispecific antibodies comprise human heavy chain variable gene segments that are rearranged *in vivo* within mouse B cells that have been previously engineered to express a limited human light chain repertoire, or a single human light chain, cognate with human heavy chains and, in response to exposure with an antigen of interest, generate a chimeric antibody repertoire containing a plurality of human heavy chain variable regions that are cognate with one or one of two possible human light chain variable regions, wherein the chimeric antibodies are specific for the antigen of interest.

[00130] In various aspects, a method of preparing a bispecific antibody is provided, the bispecific antibody comprising 1) a first polypeptide and a second polypeptide, wherein the first and second polypeptides each include a multimerization domain (*e.g.*, an immunoglobulin Fc domain) allowing the first and second polypeptides to form a dimer, and the multimerization domains promote stable interaction between first and second polypeptides, and wherein one of the multimerization domains bears an amino acid modification that reduces its affinity to protein A and the other multimerization domain lacks the modification, 2) a binding domain in each of the first and second polypeptide, each binding domain comprising a variable heavy chain and a variable light chain, wherein the variable light chain of the first polypeptide and the variable light chain of the second polypeptide have a common amino acid sequence, which common sequence has an amino acid sequence identity to an original light chain of each of the polypeptides of at least 80%, of at least 85%, preferably at least 90%, more preferably at least 95% and most preferably 100% sequence identity. In various embodiments, the variable light chain is derived from a human V κ 1-39 or a human V κ 3-20 gene segment. In various embodiments, the variable light chain is a rearranged human light chain sequence. In various embodiments, the variable light chain is isolated from a mouse as described herein.

[00131] In various embodiments, the method comprises the steps of (i) culturing a host cell comprising a nucleic acid encoding the first polypeptide, the second polypeptide, and the

common light chain, wherein the nucleic acid is expressed; and (ii) recovering the bispecific antibody from the host cell culture; in one embodiment, the nucleic acid encoding the first polypeptide or the nucleic acid encoding the second polypeptide, bears an amino acid modification that reduces its affinity to protein A. In one embodiment, the nucleic acid encoding the first polypeptide, the second polypeptide, and the common light chain is present in a single vector or in separate vectors. In one embodiment, the host cell is used to make a bispecific antibody according to the preceding paragraph.

[00132] In one aspect, a method of preparing a bispecific antibody is provided, comprising (a) selecting a first nucleic acid encoding a first human heavy chain variable region isolated from a mouse as described herein; (b) selecting a second nucleic acid encoding a second human heavy chain variable region isolated from the same or separate mouse as described herein; (c) providing a third nucleic acid encoding a human light chain variable region isolated from a mouse as described herein or derived from a rearranged human light chain variable region as described herein; (c) introducing into a host cell the first, second and third nucleic acids and culturing the host cell so that expression of the first, second and third nucleic acid occurs; and (d) recovering the bispecific antibody formed from the cell culture.

[00133] In one embodiment, the first and second human heavy chain variable regions are somatically mutated. In a specific embodiment, the first and second human heavy chain variable regions are independently derived from a rearranged human V_H gene segment selected from 1-2, 1-3, 1-8, 1-18, 1-24, 1-46, 1-58, 1-69, 2-5, 2-26, 2-70, 3-7, 3-9, 3-11, 3-13, 3-15, 3-16, 3-20, 3-21, 3-23, 3-30, 3-33, 3-43, 3-48, 3-49, 3-53, 3-64, 3-66, 3-72, 3-73, 4-28, 4-31, 4-34, 4-39, 4-59, 4-61, 5-51, and a 6-1 human V_H gene segment. In one embodiment, the first and second human heavy chain variable regions are independently derived from a rearranged human V_H gene segment selected from 2-5, 3-30 and 3-23. In one embodiment, the first human heavy chain variable region is derived from a human V_{H2-5} gene segment and the second human heavy chain variable region is derived from a human V_{H3-30} gene segment. In one embodiment, the first human heavy chain variable region is derived from a human V_{H3-30} gene segment and the second human heavy chain variable region is derived from a human V_{H3-23} gene segment. In one embodiment, the first human heavy chain variable region is derived from a human V_{H3-23} gene segment and the second human heavy chain variable region is derived from a human V_{H3-30} gene segment.

[00134] In one embodiment, the first or second nucleic acid is modified prior to step (c), wherein the first or second nucleic acid is modified such that it has a reduced affinity to protein A.

[00135] In one embodiment, the third nucleic acid is isolated from a mouse as described herein. In one embodiment, the third nucleic acid comprises 2 to 5 somatic mutations. In one embodiment, the third nucleic acid encodes a human light chain variable region derived from a human V κ 1-39 gene segment. In one embodiment, the third nucleic acid encodes a human light chain variable region derived from a human V κ 3-20 gene segment.

[00136] In one embodiment, the third nucleic acid is derived from a rearranged human light chain variable region. In one embodiment, the rearranged human light chain variable region comprises a sequence derived from a human V κ 1-39 gene segment or a human V κ 3-20 gene segment. In one embodiment, the rearranged human light chain variable region comprises a germline human V κ 1-39 sequence (*i.e.*, does not comprise a somatic hypermutation within the V gene segment sequence). In one embodiment, the rearranged human light chain variable region comprises a germline human V κ 3-20 sequence.

[00137] In various embodiments, a method of preparing a bispecific antibody that incorporates a first human heavy chain comprising a variable domain derived from a modified mouse that lacks a rearranged human light chain sequence in its germline is provided, wherein the first human heavy chain is paired with a cognate human light chain that comprises a rearranged human light chain variable region derived from a human V κ 1-39 or a human V κ 3-20 gene segment. In various embodiments, a second human heavy chain with a different specificity from the first human heavy chain is identified from an immunized mouse as described herein. Nucleic acids encoding the two heavy chains and the common light chain are introduced into a host cell as described in the preceding paragraphs so that expression of all three chains occurs and the bispecific antibody is recovered from the cell culture.

[00138] In one embodiment, the mouse is immunized with the same antigen used to generate the first human heavy chain variable domain. In one embodiment, the mouse is immunized with a different antigen used to generate the first human heavy chain variable domain.

[00139] In one aspect, a method of selecting human heavy chains that can pair with a single human light chain to make a bispecific antibody is provided, including nucleic acids that encode the bispecific antibody and a host cell comprising the nucleic acids.

[00140] In one aspect, a method of increasing the amount of a desired bispecific antibody in a cell culture over undesired products such as monospecific antibodies is provided, wherein one of the heavy chains of the bispecific antibody is modified to reduce its affinity to protein A.

- 5 **[00141]** In one aspect, an isolated host cell is provided, wherein the host cell comprises (a) a first nucleic acid sequence encoding a first human heavy chain variable region that binds a first antigen, wherein the first nucleic acid sequence is isolated from a mouse immunized with the first antigen that expresses a human immunoglobulin V_L region from a rearranged immunoglobulin light chain sequence in the germline of the mouse; (b) a second nucleic acid
10 sequence encoding a second human heavy chain variable region that binds a second antigen, wherein the second nucleic acid sequence is isolated from a mouse immunized with the second antigen that expresses a human immunoglobulin V_L region from a rearranged immunoglobulin light chain sequence in the germline of the mouse; (c) a third nucleic acid
15 chain variable region of (a) specifically binds the first antigen, and when paired with the heavy chain variable region of (b) specifically binds to the second antigen.

[00142] In various aspects, the first and second antigens are different from one another. In various aspects, the expression of the first, second and third nucleic acid sequences leads to the formation of a bispecific antibody that specifically binds to the first and second antigens.

- 20 **[00143]** In one embodiment, the human V_L region is derived from a rearranged human light chain sequence comprising a human V_κ1-39 gene segment or a human V_κ3-20 gene segment. In a specific embodiment, the rearranged human light chain sequence is a germline sequence (*i.e.*, does not comprise a somatic hypermutation within the variable domain). In one embodiment, the third nucleic acid sequence is isolated from a mouse that expresses a
25 human immunoglobulin V_L region from a rearranged immunoglobulin light chain sequence, wherein the rearranged human light chain sequence is present in the germline of the mouse. In one embodiment, the rearranged immunoglobulin light chain sequence comprises a human V_κ1-39 gene segment or a human V_κ3-20 gene segment. In a specific embodiment, the human V_κ1-39 gene segment or human V_κ3-20 gene segment comprises at least one somatic
30 hypermutation in a complementary determining region (CDR) or framework region (FWR). In a specific embodiment, the first, second and third nucleic acid sequences are isolated from a mouse that expresses a human immunoglobulin V_L region derived from a human V_κ1-39 or human V_κ3-20 gene segment from a rearranged immunoglobulin light chain sequence,

wherein the rearranged immunoglobulin light chain sequence is present in the germline of the mouse.

[00144] In various embodiments, the mouse does not contain an endogenous light chain variable region gene segment that is capable of rearranging to form an immunoglobulin light chain.

[00145] In one embodiment, the human immunoglobulin V_L region is expressed from a modified endogenous immunoglobulin light chain locus. In one embodiment, the first and second antigens are present on one molecule. In one embodiment, the first and second antigens are present on different molecules. In one embodiment, the first or second nucleic acid sequence comprises a modification that reduces the affinity of the encoded heavy chain to protein A.

[00146] In one embodiment, the first or second nucleic acid sequences comprise a rearranged human heavy chain variable region sequence comprising a human heavy chain gene segment selected from V_{H1-2} , V_{H1-3} , V_{H1-8} , V_{H1-18} , V_{H1-24} , 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_{H3-20} , V_{H3-21} , V_{H3-23} , V_{H3-30} , V_{H3-33} , 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_{H4-28} , V_{H4-31} , V_{H4-34} , V_{H4-39} , V_{H4-59} , V_{H4-61} , V_{H5-51} , and V_{H6-1} . In a specific embodiment, the heavy chain gene segment is V_{H2-5} , V_{H3-23} or V_{H3-30} .

[00147] In one aspect, an antibody or a bispecific antibody comprising a human heavy chain variable domain made in accordance with the invention is provided. In another aspect, use of a mouse as described herein to make a fully human antibody or a fully human bispecific antibody is provided.

[00148] In one aspect, a genetically modified mouse, embryo, or cell described herein comprises a κ light chain locus that retains endogenous regulatory or control elements, *e.g.*, a mouse κ intronic enhancer, a mouse κ 3' enhancer, or both an intronic enhancer and a 3' enhancer, wherein the regulatory or control elements facilitate somatic mutation and affinity maturation of an expressed sequence of the κ light chain locus.

[00149] In one aspect, a mouse is provided that comprises a B cell population characterized by having immunoglobulin light chains derived from no more than one, or no more than two, rearranged or unrearranged immunoglobulin light chain V and J gene segments, wherein the mouse exhibits a $\kappa:\lambda$ light chain ratio that is about the same as a mouse that comprises a wild type complement of immunoglobulin light chain V and J gene segments.

[00150] In one embodiment, the immunoglobulin light chains are derived from no more than one, or no more than two, rearranged immunoglobulin light chain V and J gene segments. In a specific embodiment, the light chains are derived from no more than one rearranged immunoglobulin light chain V and J gene segments.

- 5 **[00151]** In one aspect, a mouse as described herein is provided that expresses an immunoglobulin light chain derived from no more than one, or no more than two, human V κ /J κ sequences, wherein the mouse comprises a replacement of all or substantially all endogenous mouse heavy chain variable region gene segments with one or more human heavy chain variable region gene segments, and the mouse exhibits a ratio of (a) CD19⁺ B cells that express an immunoglobulin having a λ light chain, to (b) CD19⁺ B cells that express an immunoglobulin having a κ light chain, of about 1 to about 20.

- [00152]** In one embodiment, the mouse expresses a single κ light chain derived from a human V κ 1-39J κ 5 sequence, and the ratio of CD19⁺ B cells that express an immunoglobulin having a λ light chain to CD19⁺ B cells that express an immunoglobulin having a κ light chain is about 1 to about 20; in one embodiment, the ratio is about 1 to at least about 66; in a specific embodiment, the ratio is about 1 to 66.

- [00153]** In one embodiment, the mouse expresses a single κ light chain derived from a human V κ 3-20J κ 5 sequence, and the ratio of CD19⁺ B cells that express an immunoglobulin having a λ light chain to CD19⁺ B cells that express an immunoglobulin having a κ light chain is about 1 to about 20; in one embodiment, the ratio is about 1 to about 21. In specific embodiments, the ratio is 1 to 20, or 1 to 21.

- [00154]** In one aspect, a genetically modified mouse is provided that expresses a single rearranged κ light chain, wherein the mouse comprises a functional λ light chain locus, and wherein the mouse expresses a B cell population that comprises Ig κ ⁺ cells that express a κ light chain derived from the same single rearranged κ light chain. In one embodiment, the percent of Ig κ ⁺Ig λ ⁺ B cells in the mouse is about the same as in a wild type mouse. In a specific embodiment, the percent of Ig κ ⁺Ig λ ⁺ B cells in the mouse is about 2 to about 6 percent. In a specific embodiment, the percent of Ig κ ⁺Ig λ ⁺ B cells in a mouse wherein the single rearranged κ light chain is derived from a V κ 1-39J κ 5 sequence is about 2 to about 3; in a specific embodiment, the percent is about 2.6. In a specific embodiment, the percent of Ig κ ⁺Ig λ ⁺ B cells in a mouse wherein the single rearranged κ light chain is derived from a V κ 3-20J κ 1 sequence is about 4 to about 8; in a specific embodiment, the percent is about 6.

[00155] In one aspect, a genetically modified mouse is provided, wherein the mouse expresses a single rearranged κ light chain derived from a human $V\kappa$ and $J\kappa$ gene segment, wherein the mouse expresses a B cell population that comprises a single κ light chain derived from the single rearranged κ light chain sequence, wherein the genetically modified mouse has not been rendered resistant to somatic hypermutations. In one embodiment, at least 90% of the κ light chains expressed on a B cell of the mouse exhibit from at least one to about five somatic hypermutations.

[00156] In one aspect, a genetically modified mouse is provided that is modified to express a single κ light chain derived from no more than one, or no more than two, rearranged κ light chain sequences, wherein the mouse exhibits a κ light chain usage that is about two-fold or more, at least about three-fold or more, or at least about four-fold or more greater than the κ light chain usage exhibited by a wild type mouse, or greater than the κ light chain usage exhibited by a mouse of the same strain that comprises a wild type repertoire of κ light chain gene segments. In a specific embodiment, the mouse expresses the single κ light chain from no more than one rearranged κ light chain sequence. In a more specific embodiment, the rearranged κ light chain sequence is selected from a $V\kappa 1-39J\kappa 5$ and $V\kappa 3-20J\kappa 1$ sequence. In one embodiment, the rearranged κ light chain sequence is a $V\kappa 1-39J\kappa 5$ sequence. In one embodiment, the rearranged κ light chain sequence is a $V\kappa 3-20J\kappa 1$ sequence.

[00157] In one aspect, a genetically modified mouse is provided that expresses a single κ light chain derived from no more than one, or no more than two, rearranged κ light chain sequences, wherein the mouse exhibits a κ light chain usage that is about 100-fold or more, at least about 200-fold or more, at least about 300-fold or more, at least about 400-fold or more, at least about 500-fold or more, at least about 600-fold or more, at least about 700-fold or more, at least about 800-fold or more, at least about 900-fold or more, at least about 1000-fold or more greater than the same κ light chain usage exhibited by a mouse bearing a complete or substantially complete human κ light chain locus. In a specific embodiment, the mouse bearing a complete or substantially complete human κ light chain locus lacks a functional unrearranged mouse κ light chain sequence. In a specific embodiment, the mouse expresses the single κ light chain from no more than one rearranged κ light chain sequence. In one embodiment, the mouse comprises one copy of a rearranged κ light chain sequence (*e.g.*, a heterozygote). In one embodiment, the mouse comprises two copies of a rearranged κ light chain sequence (*e.g.*, a homozygote). In a more specific embodiment, the rearranged κ

light chain sequence is selected from a V κ 1-39J κ 5 and V κ 3-20J κ 1 sequence. In one embodiment, the rearranged κ light chain sequence is a V κ 1-39J κ 5 sequence. In one embodiment, the rearranged κ light chain sequence is a V κ 3-20J κ 1 sequence.

[00158] In one aspect, a genetically modified mouse is provided that expresses a single light chain derived from no more than one, or no more than two, rearranged light chain sequences, wherein the light chain in the genetically modified mouse exhibits a level of expression that is at least 10-fold to about 1,000-fold, 100-fold to about 1,000-fold, 200-fold to about 1,000-fold, 300-fold to about 1,000-fold, 400-fold to about 1,000-fold, 500-fold to about 1,000-fold, 600-fold to about 1,000-fold, 700-fold to about 1,000-fold, 800-fold to about 1,000-fold, or 900-fold to about 1,000-fold higher than expression of the same rearranged light chain exhibited by a mouse bearing a complete or substantially complete light chain locus. In one embodiment, the light chain comprises a human sequence. In a specific embodiment, the human sequence is a κ sequence. In one embodiment, the human sequence is a λ sequence. In one embodiment, the light chain is a fully human light chain.

[00159] In one embodiment, the level of expression is characterized by quantitating mRNA of transcribed light chain sequence, and comparing it to transcribed light chain sequence of a mouse bearing a complete or substantially complete light chain locus.

[00160] In one aspect, a genetically modified mouse is provided that expresses a single κ light chain derived from no more than one, or no more than two, rearranged κ light chain sequences, wherein the mouse, upon immunization with antigen, exhibits a serum titer that is comparable to a wild type mouse immunized with the same antigen. In a specific embodiment, the mouse expresses a single κ light chain from no more than one rearranged κ light chain sequence. In one embodiment, the serum titer is characterized as total immunoglobulin. In a specific embodiment, the serum titer is characterized as IgM specific titer. In a specific embodiment, the serum titer is characterized as IgG specific titer. In a more specific embodiment, the rearranged κ light chain sequence is selected from a V κ 1-39J κ 5 and V κ 3-20J κ 1 sequence. In one embodiment, the rearranged κ light chain sequence is a V κ 1-39J κ 5 sequence. In one embodiment, the rearranged κ light chain sequence is a V κ 3-20J κ 1 sequence.

[00161] In one aspect, a genetically modified mouse is provided that expresses a population of antigen-specific antibodies, wherein all of the immunoglobulin light chains of the population of antigen-specific antibodies comprise a human light chain variable (V_L) region derived from the same single human V_L gene segment and the immunoglobulin heavy

chains comprise a human heavy chain variable (V_H) region derived from one of a plurality of human V_H gene segments.

[00162] In various embodiments, the human V_H gene segments are selected from V_{H1-2} , V_{H1-3} , V_{H1-8} , V_{H1-18} , V_{H1-24} , V_{H1-46} , V_{H1-58} , V_{H1-69} , V_{H2-5} , V_{H2-26} , V_{H2-70} , V_{H3-7} ,
 5 V_{H3-9} , V_{H3-11} , V_{H3-13} , V_{H3-15} , V_{H3-20} , V_{H3-21} , V_{H3-23} , V_{H3-30} , V_{H3-33} , 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_{H4-28} , V_{H4-31} , V_{H4-34} , V_{H4-39} , V_{H4-59} , V_{H4-61} , V_{H5-51} , and V_{H6-1} .

[00163] In various embodiments, same single human V_L gene segment is selected from a human $V_{\kappa 1-39}$ gene segment and a human $V_{\kappa 3-20}$ gene segment. In various embodiments,
 10 all of the immunoglobulin light chains comprise a human light chain J (J_L) gene segment selected from a J_{κ} and a J_{λ} gene segment. In a specific embodiment, the human J_L gene segment is selected from a human $J_{\kappa 1}$ and a $J_{\kappa 5}$ gene segment. In various embodiments, the mouse lacks a sequence selected from a mouse immunoglobulin V_L gene segment, a mouse immunoglobulin J_L gene segment, and a combination thereof. In various embodiments, the
 15 human V_L region is operably linked to a human, mouse, or rat immunoglobulin light chain constant (C_L) region. In a specific embodiment, the human V_L region is operably linked to a mouse C_{κ} region. In a specific embodiment, the human V_L region is operably linked to a rat C_{κ} region.

[00164] In various embodiments, the human V_L region is expressed from an endogenous
 20 immunoglobulin light chain locus. In various embodiments, the human V_H region is operably linked to a human, mouse, or rat immunoglobulin heavy chain constant (C_H) region. In various embodiments the (C_H) region comprises a human sequence selected from a C_{H1} , a hinge, a C_{H2} , a C_{H3} , a C_{H4} , and/or a combination thereof. In various embodiments, the human V_H region is expressed from an endogenous immunoglobulin heavy chain locus.

[00165] In one aspect, a genetically modified mouse is provided that expresses a plurality
 25 of immunoglobulin heavy chains associated with a single light chain. In one embodiment, the heavy chain comprises a human sequence. In various embodiments, the human sequence is selected from a variable sequence, a C_{H1} , a hinge, a C_{H2} , a C_{H3} , and a combination thereof. In one embodiment, the single light chain comprises a human sequence. In various
 30 embodiments, the human sequence is selected from a variable sequence, a constant sequence, and a combination thereof. In one embodiment, the mouse comprises a disabled endogenous immunoglobulin locus and expresses the heavy chain and/or the light chain from a transgene or extrachromosomal episome. In one embodiment, the mouse comprises a replacement at an

endogenous mouse locus of some or all endogenous mouse heavy chain gene segments (*i.e.*, V, D, J), and/or some or all endogenous mouse heavy chain constant sequences (*e.g.*, C_H1, hinge, C_H2, C_H3, or a combination thereof), and/or some or all endogenous mouse light chain sequences (*e.g.*, V, J, constant, or a combination thereof), with one or more human

5 immunoglobulin sequences.

[00166] In one aspect, a mouse suitable for making antibodies that have the same light chain is provided, wherein all or substantially all antibodies made in the mouse are expressed with the same light chain. In one embodiment, the light chain is expressed from an endogenous light chain locus.

10 **[00167]** In one aspect, a method for making a light chain for a human antibody is provided, comprising obtaining from a mouse as described herein a light chain sequence and a heavy chain sequence, and employing the light chain sequence and the heavy chain sequence in making a human antibody. In one embodiment, the human antibody is a bispecific antibody.

15 **[00168]** In one aspect, a method for identifying a human heavy chain variable domain that is capable of binding an antigen of interest with an engineered light chain as described herein is provided, wherein the method comprises providing a heavy chain variable domain derived from a first antibody that is capable of binding the antigen, repairing the heavy chain variable domain with a germline light chain sequence and transfecting a cell so that each are
20 expressed to form a second antibody, exposing the second antibody to the antigen, and measuring binding of the second antibody to the antigen.

[00169] In one embodiment, the light chain of the first antibody comprises a human V κ 1-39 sequence. In one embodiment, the light chain of the first antibody comprises a human V κ 3-20 sequence. In one embodiment, the germline light chain sequence comprises a human
25 V κ 1-39 or V κ 3-20 sequence. In various embodiments, binding of the second antibody to the antigen is determined by comparison of binding of the first antibody to the antigen.

[00170] Any of the embodiments and aspects described herein can be used in conjunction with one another, unless otherwise indicated or apparent from the context. Other
30 embodiments will become apparent to those skilled in the art from a review of the ensuing description.

BRIEF DESCRIPTION OF FIGURES

[00171] **FIG. 1** illustrates a targeting strategy for replacing endogenous mouse immunoglobulin light chain variable region gene segments with a human V κ 1-39J κ 5 gene region.

5 **[00172]** **FIG. 2** illustrates a targeting strategy for replacing endogenous mouse immunoglobulin light chain variable region gene segments with a human V κ 3-20J κ 1 gene region.

[00173] **FIG. 3** illustrates a targeting strategy for replacing endogenous mouse immunoglobulin light chain variable region gene segments with a human VpreB/J λ 5 gene region.

[00174] **FIG. 4** shows the percent of CD19⁺ B cells (y-axis) from peripheral blood for wild type mice (WT), mice homozygous for an engineered human rearranged V κ 1-39J κ 5 light chain region (V κ 1-39J κ 5 HO) and mice homozygous for an engineered human rearranged V κ 3-20J κ 1 light chain region (V κ 3-20J κ 1 HO).

15 **[00175]** **FIG. 5A** shows the relative mRNA expression (y-axis) of a V κ 1-39-derived light chain in a quantitative PCR assay using probes specific for the junction of an engineered human rearranged V κ 1-39J κ 5 light chain region (V κ 1-39J κ 5 Junction Probe) and the human V κ 1-39 gene segment (V κ 1-39 Probe) in a mouse homozygous for a replacement of the endogenous V κ and J κ gene segments with human V κ and J κ gene segments (H κ), a wild type mouse (WT), and a mouse heterozygous for an engineered human rearranged V κ 1-39J κ 5 light chain region (V κ 1-39J κ 5 HET). Signals are normalized to expression of mouse C κ . N.D.: not detected.

25 **[00176]** **FIG. 5B** shows the relative mRNA expression (y-axis) of a V κ 1-39-derived light chain in a quantitative PCR assay using probes specific for the junction of an engineered human rearranged V κ 1-39J κ 5 light chain region (V κ 1-39J κ 5 Junction Probe) and the human V κ 1-39 gene segment (V κ 1-39 Probe) in a mouse homozygous for a replacement of the endogenous V κ and J κ gene segments with human V κ and J κ gene segments (H κ), a wild type mouse (WT), and a mouse homozygous for an engineered human rearranged V κ 1-39J κ 5 light chain region (V κ 1-39J κ 5 HO). Signals are normalized to expression of mouse C κ .

30 **[00177]** **FIG. 5C** shows the relative mRNA expression (y-axis) of a V κ 3-20-derived light chain in a quantitative PCR assay using probes specific for the junction of an engineered human rearranged V κ 3-20J κ 1 light chain region (V κ 3-20J κ 1 Junction Probe) and the human

V κ 3-20 gene segment (V κ 3-20 Probe) in a mouse homozygous for a replacement of the endogenous V κ and J κ gene segments with human V κ and J κ gene segments (H κ), a wild type mouse (WT), and a mouse heterozygous (HET) and homozygous (HO) for an engineered human rearranged V κ 3-20J κ 1 light chain region. Signals are normalized to expression of mouse C κ .

[00178] FIG. 6A shows IgM (left) and IgG (right) titer in wild type (WT; N=2) and mice homozygous for an engineered human rearranged V κ 1-39J κ 5 light chain region (V κ 1-39J κ 5 HO; N=2) immunized with β -galactosidase.

[00179] FIG. 6B shows total immunoglobulin (IgM, IgG, IgA) titer in wild type (WT; N=5) and mice homozygous for an engineered human rearranged V κ 3-20J κ 1 light chain region (V κ 3-20J κ 1 HO; N=5) immunized with β -galactosidase.

[00180] FIG. 7A shows a schematic of monospecific antibodies (Parent-1 and Parent-2) and a bispecific antibody (Bispecific) constructed from heavy chain variable regions from each parent monospecific antibody. A common light chain variable region (darkened) is indicated in the bispecific antibody.

[00181] FIG. 7B shows a schematic for the binding characteristics of two parent monoclonal antibodies (Parent-1 and Parent-2) for an antigen of interest, as well as the binding characteristic of a bispecific antibody constructed from pairing the heavy chain variable regions from each monospecific parent antibody with a common light chain. The capability of the bispecific antibody to bind to two distinct epitopes of the antigen of interest either separately (bottom left) or simultaneously (bottom right) is indicated.

[00182] FIG. 8 shows a bar graph of the binding of 300nM bispecific (darkened bars) and monospecific (striped and gray bars) antibodies to a captured monomeric Antigen E surface in BIACORE™ units (RU). Monoclonal parent-1 antibody (P1 Ab), monoclonal parent-2 (P2 Ab) and bispecific antibodies (BsAb) are indicated.

DETAILED DESCRIPTION

[00183] 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 embodiments only, and is not intended to be limiting, since the scope of the present invention is defined by the claims.

[00184] 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. All publications mentioned are hereby incorporated by reference in their entirety.

5 **[00185]** The term "antibody", as used herein, includes immunoglobulin molecules comprising four polypeptide chains, two heavy (H) chains and two light (L) chains interconnected by disulfide bonds. Each heavy chain comprises a heavy chain variable (V_H) region and a heavy chain constant region (C_H). The heavy chain constant region comprises three domains, C_{H1} , C_{H2} and C_{H3} . Each light chain comprises a light chain variable (V_L)
 10 region and a light chain constant region (C_L). The V_H and V_L regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each V_H and V_L comprises three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4 (heavy
 15 chain CDRs may be abbreviated as HCDR1, HCDR2 and HCDR3; light chain CDRs may be abbreviated as LCDR1, LCDR2 and LCDR3. The term "high affinity" antibody refers to an antibody that has a K_D with respect to its target epitope about of 10^{-9} M or lower (*e.g.*, about 1×10^{-9} M, 1×10^{-10} M, 1×10^{-11} M, or about 1×10^{-12} M). In one embodiment, K_D is measured by surface plasmon resonance, *e.g.*, BIACORE™; in another embodiment, K_D is
 20 measured by ELISA.

[00186] The phrase "bispecific antibody" includes an antibody capable of selectively binding two or more epitopes. Bispecific antibodies include fragments of two different monoclonal antibodies (FIG. 7A) and generally comprise two nonidentical heavy chains derived from the two different monoclonal antibodies, with each heavy chain specifically
 25 binding a different epitope—either on two different molecules (*e.g.*, different epitopes on two different immunogens; see FIG. 7B, bottom left) or on the same molecule (*e.g.*, different epitopes on the same immunogen; see FIG. 7B, bottom right). If a bispecific antibody is capable of selectively binding two different epitopes (a first epitope and a second epitope), the affinity of the first heavy chain for the first epitope will generally be at least one to two or
 30 three or four or more orders of magnitude lower than the affinity of the first heavy chain for the second epitope, and vice versa. Epitopes specifically bound by the bispecific antibody can be on the same or a different target (*e.g.*, on the same or a different protein; see FIG. 7B). Exemplary bispecific antibodies include those with a first heavy chain specific for a tumor

antigen and a second heavy chain specific for a cytotoxic marker, *e.g.*, an Fc receptor (*e.g.*, FcγRI, FcγRII, FcγRIII, etc.) or a T cell marker (*e.g.*, CD3, CD28, etc.). Further, the second heavy chain variable region can be substituted with a heavy chain variable region having a different desired specificity. For example, a bispecific antibody with a first heavy chain specific for a tumor antigen and a second heavy chain specific for a toxin can be paired so as to deliver a toxin (*e.g.*, saporin, vinca alkaloid, *etc.*) to a tumor cell. Other exemplary bispecific antibodies include those with a first heavy chain specific for an activating receptor (*e.g.*, B cell receptor, FcγRI, FcγRIIA, FcγRIIIA, FcαRI, T cell receptor, *etc.*) and a second heavy chain specific for an inhibitory receptor (*e.g.*, FcγRIIB, CD5, CD22, CD72, CD300a, *etc.*). Such bispecific antibodies can be constructed for therapeutic conditions associated with cell activation (*e.g.* allergy and asthma). Bispecific antibodies can be made, for example, by combining heavy chains that recognize different epitopes of the same or different immunogen (FIG. 7B). For example, nucleic acid sequences encoding heavy chain variable sequences that recognize different epitopes of the same or different immunogen can be fused to nucleic acid sequences encoding the same or different heavy chain constant regions, and such sequences can be expressed in a cell that expresses an immunoglobulin light chain. A typical bispecific antibody has two heavy chains each having three heavy chain CDRs, followed by (N-terminal to C-terminal) a C_H1 domain, a hinge, a C_H2 domain, and a C_H3 domain, and an immunoglobulin light chain that either does not confer epitope-binding specificity but that can associate with each heavy chain, or that can associate with each heavy chain and that can bind one or more of the epitopes bound by the heavy chain epitope-binding regions, or that can associate with each heavy chain and enable binding of one or both of the heavy chains to one or both epitopes.

[00187] The term “cell” includes any cell that is suitable for expressing a recombinant nucleic acid sequence. Cells include those of prokaryotes and eukaryotes (single-cell or multiple-cell), bacterial cells (*e.g.*, strains of *E. coli*, *Bacillus spp.*, *Streptomyces spp.*, *etc.*), mycobacteria cells, fungal cells, yeast cells (*e.g.*, *S. cerevisiae*, *S. pombe*, *P. pastoris*, *P. methanolica*, *etc.*), plant cells, insect cells (*e.g.*, SF-9, SF-21, baculovirus-infected insect cells, *Trichoplusia ni*, *etc.*), non-human animal cells, human cells, or cell fusions such as, for example, hybridomas or quadromas. In some embodiments, the cell is a human, monkey, ape, hamster, rat, or mouse cell. In some embodiments, the cell is eukaryotic and is selected from the following cells: CHO (*e.g.*, CHO K1, DXB-11 CHO, Veggie-CHO), COS (*e.g.*, COS-7), retinal cell, Vero, CV1, kidney (*e.g.*, HEK293, 293 EBNA, MSR 293, MDCK, HaK,

BHK), HeLa, HepG2, WI38, MRC 5, Colo205, HB 8065, HL-60, (*e.g.*, BHK21), Jurkat, Daudi, A431 (epidermal), CV-1, U937, 3T3, L cell, C127 cell, SP2/0, NS-0, MMT 060562, Sertoli cell, BRL 3A cell, HT1080 cell, myeloma cell, tumor cell, and a cell line derived from an aforementioned cell. In some embodiments, the cell comprises one or more viral genes, *e.g.*, a retinal cell that expresses a viral gene (*e.g.*, a PER.C6™ cell).

[00188] The phrase “complementarity determining region,” or the term “CDR,” includes an amino acid sequence encoded by a nucleic acid sequence of an organism’s immunoglobulin genes that normally (*i.e.*, in a wild type animal) appears between two framework regions in a variable region of a light or a heavy chain of an immunoglobulin molecule (*e.g.*, an antibody or a T cell receptor). A CDR can be encoded by, for example, a germline sequence or a rearranged or unrearranged sequence, and, for example, by a naive or a mature B cell or a T cell. A CDR can be somatically mutated (*e.g.*, vary from a sequence encoded in an animal’s germline), humanized, and/or modified with amino acid substitutions, additions, or deletions. In some circumstances (*e.g.*, for a CDR3), CDRs can be encoded by two or more sequences (*e.g.*, germline sequences) that are not contiguous (*e.g.*, in an unrearranged nucleic acid sequence) but are contiguous in a B cell nucleic acid sequence, *e.g.*, as the result of splicing or connecting the sequences (*e.g.*, V-D-J recombination to form a heavy chain CDR3).

[00189] The term “conservative,” when used to describe a conservative amino acid substitution, includes substitution of an amino acid residue by another amino acid residue having a side chain R group with similar chemical properties (*e.g.*, charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of interest of a protein, for example, the ability of a variable region to specifically bind a target epitope with a desired affinity. Examples of groups of amino acids that have side chains with similar chemical properties include aliphatic side chains such as glycine, alanine, valine, leucine, and isoleucine; aliphatic-hydroxyl side chains such as serine and threonine; amide-containing side chains such as asparagine and glutamine; aromatic side chains such as phenylalanine, tyrosine, and tryptophan; basic side chains such as lysine, arginine, and histidine; acidic side chains such as aspartic acid and glutamic acid; and, sulfur-containing side chains such as cysteine and methionine. Conservative amino acids substitution groups include, for example, valine/leucine/isoleucine, phenylalanine/tyrosine, lysine/arginine, alanine/valine, glutamate/aspartate, and asparagine/glutamine. In some embodiments, a conservative amino acid substitution can be substitution of any native residue

in a protein with alanine, as used in, for example, alanine scanning mutagenesis. In some embodiments, a conservative substitution is made that has a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet *et al.* (1992) Exhaustive Matching of the Entire Protein Sequence Database, Science 256:1443-45, hereby incorporated by reference. In some

5 embodiments, the substitution is a moderately conservative substitution wherein the substitution has a nonnegative value in the PAM250 log-likelihood matrix.

[00190] In some embodiments, residue positions in an immunoglobulin light chain or heavy chain differ by one or more conservative amino acid substitutions. In some embodiments, residue positions in an immunoglobulin light chain or functional fragment

10 thereof (*e.g.*, a fragment that allows expression and secretion from, *e.g.*, a B cell) are not identical to a light chain whose amino acid sequence is listed herein, but differs by one or more conservative amino acid substitutions.

[00191] The phrase “epitope-binding protein” includes a protein having at least one CDR and that is capable of selectively recognizing an epitope, *e.g.*, is capable of binding an epitope

15 with a K_D that is at about one micromolar or lower (*e.g.*, a K_D that is about 1×10^{-6} M, 1×10^{-7} M, 1×10^{-8} M, 1×10^{-9} M, 1×10^{-10} M, 1×10^{-11} M, or about 1×10^{-12} M). Therapeutic epitope-binding proteins (*e.g.*, therapeutic antibodies) frequently require a K_D that is in the nanomolar or the picomolar range.

[00192] The phrase “functional fragment” includes fragments of epitope-binding proteins

20 that can be expressed, secreted, and specifically bind to an epitope with a K_D in the micromolar, nanomolar, or picomolar range. Specific recognition includes having a K_D that is at least in the micromolar range, the nanomolar range, or the picomolar range.

[00193] The term “germline” includes reference to an immunoglobulin nucleic acid sequence in a non-somatically mutated cell, *e.g.*, a non-somatically mutated B cell or pre-B

25 cell or hematopoietic cell.

[00194] The phrase “heavy chain,” or “immunoglobulin heavy chain” includes an immunoglobulin heavy chain constant region sequence from any organism. Heavy chain variable domains include three heavy chain CDRs and four FR regions, unless otherwise specified. Fragments of heavy chains include CDRs, CDRs and FRs, and combinations

30 thereof. A typical heavy chain has, following the variable domain (from N-terminal to C-terminal), a C_H1 domain, a hinge, a C_H2 domain, and a C_H3 domain. A functional fragment of a heavy chain includes a fragment that is capable of specifically recognizing an epitope

(*e.g.*, recognizing the epitope with a K_D in the micromolar, nanomolar, or picomolar range), that is capable of expressing and secreting from a cell, and that comprises at least one CDR.

[00195] The term “identity” when used in connection with sequence includes identity as determined by a number of different algorithms known in the art that can be used to measure

nucleotide and/or amino acid sequence identity. In some embodiments described herein, identities are determined using a ClustalW v. 1.83 (slow) alignment employing an open gap penalty of 10.0, an extend gap penalty of 0.1, and using a Gonnet similarity matrix

(MACVECTOR™ 10.0.2, MacVector Inc., 2008). The length of the sequences compared with respect to identity of sequences will depend upon the particular sequences, but in the

case of a light chain constant domain, the length should contain sequence of sufficient length to fold into a light chain constant domain that is capable of self-association to form a

canonical light chain constant domain, *e.g.*, capable of forming two beta sheets comprising beta strands and capable of interacting with at least one C_H1 domain of a human or a mouse.

In the case of a C_H1 domain, the length of sequence should contain sequence of sufficient

length to fold into a C_H1 domain that is capable of forming two beta sheets comprising beta strands and capable of interacting with at least one light chain constant domain of a mouse or a human.

[00196] The phrase “immunoglobulin molecule” includes two immunoglobulin heavy chains and two immunoglobulin light chains. The heavy chains may be identical or different, and the light chains may be identical or different.

[00197] The phrase “light chain” includes an immunoglobulin light chain sequence from any organism, and unless otherwise specified includes human κ and λ light chains and a VpreB, as well as surrogate light chains. Light chain variable (V_L) domains typically include three light chain CDRs and four framework (FR) regions, unless otherwise specified.

Generally, a full-length light chain includes, from amino terminus to carboxyl terminus, a V_L domain that includes FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4, and a light chain constant domain. Light chains include those, *e.g.*, that do not selectively bind either a first or a second epitope selectively bound by the epitope-binding protein in which they appear. Light chains also include those that bind and recognize, or assist the heavy chain with binding and

recognizing, one or more epitopes selectively bound by the epitope-binding protein in which they appear. Common light chains are those derived from a rearranged human $V\kappa1$ -39J $\kappa5$ sequence or a rearranged human $V\kappa3$ -20J $\kappa1$ sequence, and include somatically mutated (*e.g.*, affinity matured) versions.

[00198] The phrase “micromolar range” is intended to mean 1-999 micromolar; the phrase “nanomolar range” is intended to mean 1-999 nanomolar; the phrase “picomolar range” is intended to mean 1-999 picomolar.

[00199] The phrase “somatically mutated” includes reference to a nucleic acid sequence from a B cell that has undergone class-switching, wherein the nucleic acid sequence of an immunoglobulin variable region (*e.g.*, a heavy chain variable domain or including a heavy chain CDR or FR sequence) in the class-switched B cell is not identical to the nucleic acid sequence in the B cell prior to class-switching, such as, for example, a difference in a CDR or framework nucleic acid sequence between a B cell that has not undergone class-switching and a B cell that has undergone class-switching. “Somatically mutated” includes reference to nucleic acid sequences from affinity-matured B cells that are not identical to corresponding immunoglobulin variable region sequences in B cells that are not affinity-matured (*i.e.*, sequences in the genome of germline cells). The phrase “somatically mutated” also includes reference to an immunoglobulin variable region nucleic acid sequence from a B cell after exposure of the B cell to an epitope of interest, wherein the nucleic acid sequence differs from the corresponding nucleic acid sequence prior to exposure of the B cell to the epitope of interest. The phrase “somatically mutated” refers to sequences from antibodies that have been generated in an animal, *e.g.*, a mouse having human immunoglobulin variable region nucleic acid sequences, in response to an immunogen challenge, and that result from the selection processes inherently operative in such an animal.

[00200] The term “unrearranged,” with reference to a nucleic acid sequence, includes nucleic acid sequences that exist in the germline of an animal cell.

[00201] The phrase “variable domain” includes an amino acid sequence of an immunoglobulin light or heavy chain (modified as desired) that comprises the following amino acid regions, in sequence from N-terminal to C-terminal (unless otherwise indicated): FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4.

Universal Light Chain

[00202] Prior efforts to make useful multispecific epitope-binding proteins, *e.g.*, bispecific antibodies, have been hindered by variety of problems that frequently share a common paradigm: *in vitro* selection or manipulation of sequences to rationally engineer, or to engineer through trial-and-error, a suitable format for pairing a heterodimeric bispecific human immunoglobulin. Unfortunately, most if not all of the *in vitro* engineering approaches

provide largely *ad hoc* fixes that are suitable, if at all, for individual molecules. On the other hand, *in vivo* methods for employing complex organisms to select appropriate pairings that are capable of leading to human therapeutics have not been realized.

[00203] Generally, native mouse sequences are frequently not a good source for human

5 therapeutic sequences. For at least that reason, generating mouse heavy chain immunoglobulin variable regions that pair with a common human light chain is of limited practical utility. More *in vitro* engineering efforts would be expended in a trial-and-error process to try to humanize the mouse heavy chain variable sequences while hoping to retain epitope specificity and affinity while maintaining the ability to couple with the common
10 human light chain, with uncertain outcome. At the end of such a process, the final product may maintain some of the specificity and affinity, and associate with the common light chain, but ultimately immunogenicity in a human would likely remain a profound risk.

[00204] Therefore, a suitable mouse for making human therapeutics would include a suitably large repertoire of human heavy chain variable region gene segments in place of
15 endogenous mouse heavy chain variable region gene segments. The human heavy chain variable region gene segments should be able to rearrange and recombine with an endogenous mouse heavy chain constant domain to form a reverse chimeric heavy chain (*i.e.*, a heavy chain comprising a human variable domain and a mouse constant region). The heavy chain should be capable of class switching and somatic hypermutation so that a suitably large
20 repertoire of heavy chain variable domains are available for the mouse to select one that can associate with the limited repertoire of human light chain variable regions.

[00205] A mouse that selects a common light chain for a plurality of heavy chains has a practical utility. In various embodiments, antibodies that express in a mouse that can only express a common light chain will have heavy chains that can associate and express with an
25 identical or substantially identical light chain. This is particularly useful in making bispecific antibodies. For example, such a mouse can be immunized with a first immunogen to generate a B cell that expresses an antibody that specifically binds a first epitope. The mouse (or a mouse genetically the same) can be immunized with a second immunogen to generate a B cell that expresses an antibody that specifically binds the second epitope. Variable heavy
30 regions can be cloned from the B cells and expressed with the same heavy chain constant region and the same light chain in a cell to make a bispecific antibody, wherein the heavy chain component of the bispecific antibody has been selected by a mouse to associate and express with the light chain component.

[00206] The inventors have engineered a mouse for generating immunoglobulin light chains that will suitably pair with a rather diverse family of heavy chains, including heavy chains whose variable regions depart from germline sequences, *e.g.*, affinity matured or somatically mutated variable regions. In various embodiments, the mouse is devised to pair

5 human light chain variable domains with human heavy chain variable domains that comprise somatic mutations, thus enabling a route to high affinity binding proteins suitable for use as human therapeutics.

[00207] The genetically engineered mouse, through the long and complex process of antibody selection within an organism, makes biologically appropriate choices in pairing a

10 diverse collection of human heavy chain variable domains with a limited number of human light chain options. In order to achieve this, the mouse is engineered to present a limited number of human light chain variable domain options in conjunction with a wide diversity of human heavy chain variable domain options. Upon challenge with an immunogen, the mouse maximizes the number of solutions in its repertoire to develop an antibody to the immunogen,

15 limited largely or solely by the number of light chain options in its repertoire. In various embodiments, this includes allowing the mouse to achieve suitable and compatible somatic mutations of the light chain variable domain that will nonetheless be compatible with a relatively large variety of human heavy chain variable domains, including in particular somatically mutated human heavy chain variable domains.

[00208] To achieve a limited repertoire of light chain options, the mouse is engineered to render nonfunctional or substantially nonfunctional its ability to make, or rearrange, a native mouse light chain variable domain. This can be achieved, *e.g.*, by deleting the mouse's light chain variable region gene segments. The endogenous mouse locus can then be modified by an exogenous suitable human light chain variable region gene segment of choice, operably

25 linked to the endogenous mouse light chain constant domain, in a manner such that the exogenous human variable region gene segments can combine with the endogenous mouse light chain constant region gene and form a rearranged reverse chimeric light chain gene (human variable, mouse constant). In various embodiments, the light chain variable region is capable of being somatically mutated. In various embodiments, to maximize ability of the

30 light chain variable region to acquire somatic mutations, the appropriate enhancer(s) is retained in the mouse. For example, in modifying a mouse κ light chain locus to replace endogenous mouse κ light chain gene segments with human κ light chain gene segments, the

mouse κ intronic enhancer and mouse κ 3' enhancer are functionally maintained, or undisturbed.

[00209] A genetically engineered mouse is provided that expresses a limited repertoire of reverse chimeric (human variable, mouse constant) light chains associated with a diversity of reverse chimeric (human variable, mouse constant) heavy chains. In various embodiments, the endogenous mouse κ light chain gene segments are deleted and replaced with a single (or two) rearranged human light chain region, operably linked to the endogenous mouse C κ gene. In embodiments for maximizing somatic hypermutation of the rearranged human light chain region, the mouse κ intronic enhancer and the mouse κ 3' enhancer are maintained. In various embodiments, the mouse also comprises a nonfunctional λ light chain locus, or a deletion thereof or a deletion that renders the locus unable to make a λ light chain.

[00210] A genetically engineered mouse is provided that, in various embodiments, comprises a light chain variable region locus lacking endogenous mouse light chain V_L and J_L gene segments and comprising a rearranged human light chain variable region, in one embodiment a rearranged human V_L/J_L sequence, operably linked to a mouse constant region, wherein the locus is capable of undergoing somatic hypermutation, and wherein the locus expresses a light chain comprising the human V_L/J_L sequence linked to a mouse constant region. Thus, in various embodiments, the locus comprises a mouse κ 3' enhancer, which is correlated with a normal, or wild type, level of somatic hypermutation.

[00211] The genetically engineered mouse in various embodiments when immunized with an antigen of interest generates B cells that exhibit a diversity of rearrangements of human immunoglobulin heavy chain variable regions that express and function with one or with two rearranged light chains, including embodiments where the one or two light chains comprise human light chain variable regions that comprise, *e.g.*, 1 to 5 somatic mutations. In various embodiments, the human light chains so expressed are capable of associating and expressing with any human immunoglobulin heavy chain variable region expressed in the mouse.

Epitope-binding Proteins Binding More Than One Epitope

[00212] The compositions and methods of described herein can be used to make binding proteins that bind more than one epitope with high affinity, *e.g.*, bispecific antibodies. Advantages of the invention include the ability to select suitably high binding (*e.g.*, affinity matured) heavy chain immunoglobulin chains each of which will associate with a single light chain.

[00213] Several techniques for making bispecific antibody fragments from recombinant cell culture have been reported. However, synthesis and expression of bispecific binding proteins has been problematic, in part due to issues associated with identifying a suitable light chain that can associate and express with two different heavy chains, and in part due to isolation issues. In various embodiments, compositions and methods described herein provide the advantage of full length bispecific antibodies that do not require special modification(s) to maintain traditional immunoglobulin structure by increasing stability/interaction of the components (FIG. 7A). In various embodiments, such modification(s) has proven cumbersome and served as an obstacle to development of bispecific antibody technology and their potential use in treating for human disease. Thus, in various embodiments, through providing a natural immunoglobulin structure (*i.e.*, full length) having the added property of multiple specificities, full length bispecific antibodies maintain their critical effector functions that previous bispecific fragments lack, and further provide therapeutics that demonstrate the important pharmacokinetic parameter of a longer half-life.

[00214] The methods and compositions described herein allow for a genetically modified mouse to select, through otherwise natural processes, a suitable light chain that can associate and express with more than one heavy chain, including heavy chains that are somatically mutated (*e.g.*, affinity matured). Human V_L and V_H sequences from suitable B cells of immunized mice as described herein that express affinity matured antibodies having reverse chimeric heavy chains (*i.e.*, human variable and mouse constant) can be identified and cloned in frame in an expression vector with a suitable human constant region gene sequence (*e.g.*, a human IgG1). Two such constructs can be prepared, wherein each construct encodes a human heavy chain variable domain that binds a different epitope. One of the human V_{LS} (*e.g.*, human $V_{\kappa 1-39J_{\kappa 5}}$ or human $V_{\kappa 3-20J_{\kappa 1}}$), in germline sequence or from a B cell wherein the sequence has been somatically mutated, can be fused in frame to a suitable human constant region gene (*e.g.*, a human κ constant gene). These three fully human heavy and light constructs can be placed in a suitable cell for expression. The cell will express two major species: a homodimeric heavy chain with the identical light chain, and a heterodimeric heavy chain with the identical light chain. To allow for a facile separation of these major species, one of the heavy chains is modified to omit a Protein A-binding determinant, resulting in a differential affinity of a homodimeric binding protein from a heterodimeric binding protein. Compositions and methods that address this issue are described in USSN 12/832,838, filed 25 June 2010, entitled "Readily Isolated Bispecific Antibodies with Native

Immunoglobulin Format,” published as US 2010/0331527A1, hereby incorporated by reference.

[00215] In one aspect, an epitope-binding protein as described herein is provided, wherein human V_L and V_H sequences are derived from mice described herein that have been immunized with an antigen comprising an epitope of interest.

[00216] In one embodiment, an epitope-binding protein is provided that comprises a first and a second polypeptide, the first polypeptide comprising, from N-terminal to C-terminal, a first epitope-binding region that selectively binds a first epitope, followed by a constant region that comprises a first C_H3 region of a human IgG selected from IgG1, IgG2, IgG4, and a combination thereof; and, a second polypeptide comprising, from N-terminal to C-terminal, a second epitope-binding region that selectively binds a second epitope, followed by a constant region that comprises a second C_H3 region of a human IgG selected from IgG1, IgG2, IgG4, and a combination thereof, wherein the second C_H3 region comprises a modification that reduces or eliminates binding of the second C_H3 domain to protein A.

[00217] In one embodiment, the second C_H3 region comprises an H95R modification (by IMGT exon numbering; H435R by EU numbering). In another embodiment, the second C_H3 region further comprises a Y96F modification (IMGT; Y436F by EU).

[00218] In one embodiment, the second C_H3 region is from a modified human IgG1, and further comprises a modification selected from the group consisting of D16E, L18M, N44S, K52N, V57M, and V82I (IMGT; D356E, L358M, N384S, K392N, V397M, and V422I by EU).

[00219] In one embodiment, the second C_H3 region is from a modified human IgG2, and further comprises a modification selected from the group consisting of N44S, K52N, and V82I (IMGT; N384S, K392N, and V422I by EU).

[00220] In one embodiment, the second C_H3 region is from a modified human IgG4, and further comprises a modification selected from the group consisting of Q15R, N44S, K52N, V57M, R69K, E79Q, and V82I (IMGT; Q355R, N384S, K392N, V397M, R409K, E419Q, and V422I by EU).

[00221] One method for making an epitope-binding protein that binds more than one epitope is to immunize a first mouse in accordance with the invention with an antigen that comprises a first epitope of interest, wherein the mouse comprises an endogenous immunoglobulin light chain variable region locus that does not contain an endogenous mouse V_L that is capable of rearranging and forming a light chain, wherein at the endogenous mouse

immunoglobulin light chain variable region locus is a single rearranged human V_L region operably linked to the mouse endogenous light chain constant region gene, and the rearranged human V_L region is selected from a human V_κ1-39J_κ5 and a human V_κ3-20J_κ1, and the endogenous mouse V_H gene segments have been replaced in whole or in part with human V_H gene segments, such that immunoglobulin heavy chains made by the mouse are solely or substantially heavy chains that comprise human variable domains and mouse constant domains. When immunized, such a mouse will make a reverse chimeric antibody, comprising only one of two human light chain variable domains (*e.g.*, one of human V_κ1-39J_κ5 or human V_κ3-20J_κ1). Once a B cell is identified that encodes a V_H that binds the epitope of interest, the nucleotide sequence of the V_H (and, optionally, the V_L) can be retrieved (*e.g.*, by PCR) and cloned into an expression construct in frame with a suitable human immunoglobulin constant domain. This process can be repeated to identify a second V_H domain that binds a second epitope, and a second V_H gene sequence can be retrieved and cloned into an expression vector in frame to a second suitable immunoglobulin constant domain. The first and the second immunoglobulin constant domains can be the same or different isotype, and one of the immunoglobulin constant domains (but not the other) can be modified as described herein or in US 2010/0331527A1, and epitope-binding protein can be expressed in a suitable cell and isolated based on its differential affinity for Protein A as compared to a homodimeric epitope-binding protein, *e.g.*, as described in US 2010/0331527A1.

[00222] In one embodiment, a method for making a bispecific epitope-binding protein is provided, comprising identifying a first affinity-matured (*e.g.*, comprising one or more somatic hypermutations) human V_H nucleotide sequence (V_H1) from a mouse as described herein, identifying a second affinity-matured (*e.g.*, comprising one or more somatic hypermutations) human V_H nucleotide sequence (V_H2) from a mouse as described herein, cloning V_H1 in frame with a human heavy chain lacking a Protein A-determinant modification as described in US 2010/0331527A1 to form heavy chain 1 (HC1), cloning V_H2 in frame with a human heavy chain comprising a Protein A-determinant as described in US 2010/0331527A1 to form heavy chain 2 (HC2), introducing an expression vector comprising HC1 and the same or a different expression vector comprising HC2 into a cell, wherein the cell also expresses a human immunoglobulin light chain that comprises a human V_κ1-39/human J_κ5 or a human V_κ3-20/human J_κ1 fused to a human light chain constant domain, allowing the cell to express a bispecific epitope-binding protein comprising a V_H

domain encoded by V_{H1} and a V_H domain encoded by V_{H2} , and isolating the bispecific epitope-binding protein based on its differential ability to bind Protein A as compared with a monospecific homodimeric epitope-binding protein. In a specific embodiment, HC1 is an IgG1, and HC2 is an IgG1 that comprises the modification H95R (IMGT; H435R by EU) and further comprises the modification Y96F (IMGT; Y436F by EU). In one embodiment, the V_H domain encoded by V_{H1} , the V_H domain encoded by V_{H2} , or both, are somatically mutated.

Human V_H Genes That Express with a Common Human V_L

[00223] A variety of human variable regions from affinity-matured antibodies raised against four different antigens were expressed with either their cognate light chain, or at least one of a human light chain selected from human $V_{\kappa 1-39/J\kappa 5}$, human $V_{\kappa 3-20/J\kappa 1}$, or human $V_{preB/J\lambda 5}$ (see Example 1). For antibodies to each of the antigens, somatically mutated high affinity heavy chains from different gene families paired successfully with rearranged human germline $V_{\kappa 1-39/J\kappa 5}$ and $V_{\kappa 3-20/J\kappa 1}$ regions and were secreted from cells expressing the heavy and light chains. For $V_{\kappa 1-39/J\kappa 5}$ and $V_{\kappa 3-20/J\kappa 1}$, V_H domains derived from the following human V_H gene families expressed favorably: 1-2, 1-8, 1-24, 2-5, 3-7, 3-9, 3-11, 3-13, 3-15, 3-20, 3-23, 3-30, 3-33, 3-48, 4-31, 4-39, 4-59, 5-51, and 6-1. Thus, a mouse that is engineered to express a limited repertoire of human V_L domains from one or both of $V_{\kappa 1-39/J\kappa 5}$ and $V_{\kappa 3-20/J\kappa 1}$ will generate a diverse population of somatically mutated human V_H domains from a V_H locus modified to replace mouse V_H gene segments with human V_H gene segments.

[00224] Mice genetically engineered to express reverse chimeric (human variable, mouse constant) immunoglobulin heavy chains associated with a single rearranged light chain (*e.g.*, a $V_{\kappa 1-39/J}$ or a $V_{\kappa 3-20/J}$), when immunized with an antigen of interest, generated B cells that comprised a diversity of human V_H rearrangements and expressed a diversity of high-affinity antigen-specific antibodies with diverse properties with respect to their ability to block binding of the antigen to its ligand, and with respect to their ability to bind variants of the antigen (see Examples 5-10 and 12).

[00225] Thus, the mice and methods described herein are useful in making and selecting human immunoglobulin heavy chain variable domains, including somatically mutated human heavy chain variable domains, that result from a diversity of rearrangements, that exhibit a wide variety of affinities (including exhibiting a K_D of about a nanomolar or less), a wide

variety of specificities (including binding to different epitopes of the same antigen), and that associate and express with the same or substantially the same human immunoglobulin light chain variable region.

5 **Fully Human Bispecific Antibodies Having a Common Light Chain**

- [00226] As a first step in various embodiments, the first and second nucleic acid sequences that each encode human heavy chain variable domains (and any additional nucleic acid sequences forming the bispecific antibody) are selected from parent monoclonal antibodies having desired characteristics such as, for example, capable of binding different epitopes (see 10 FIGs. 7A and 7B), having different affinities, *etc.* Normally, the nucleic acid sequences encoding the human heavy chain variable domains are isolated from immunized mice, as described herein, to allow for fusing with human heavy chain constant regions to be suitable for human administration. Further modifications to the sequence(s) can be made by introducing mutations that add additional functionality to the bispecific antibody can be 15 achieved, which include, for example, increasing serum half-life (*e.g.*, see U.S. 7,217,797) and/or increasing antibody-dependent cell-mediated cytotoxicity (*e.g.*, see U.S. 6,737,056). Introducing mutations into the constant regions of antibodies is known in the art. Additionally, part of the bispecific antibody can be made recombinantly in cell culture and other part(s) of the molecule can be made by those techniques mentioned above.
- 20 [00227] Several techniques for the producing antibodies have been described. For example, in various embodiments chimeric antibodies are produced in mice as described herein. Antibodies can be isolated directly from B cells of an immunized mouse (*e.g.*, see U.S. 2007/0280945A1) and/or the B cells of the immunized mouse can be used to make hybridomas (Kohler and Milstein, 1975, *Nature* 256:495-497). DNA encoding the antibodies 25 (human heavy and/or light chains) from mice as described herein is readily isolated and sequenced using conventional techniques. Hybridoma and/or B cells of derived from mice as described herein serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the 30 recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the murine sequences.

[00228] In various embodiments, following isolation of the DNA and selection of the first and second nucleic acid sequences that encode the first and second human heavy chain variable domains having the desired specificities/affinities, and a third nucleic acid sequence that encodes a human light chain domain (a germline rearranged sequence or a light chain sequence isolated from a mouse as described herein), the three nucleic acid sequences encoding the molecules are expressed to form the bispecific antibody using recombinant techniques which are widely available in the art. Often, the expression system of choice will involve a mammalian cell expression vector and host so that the bispecific antibody is appropriately glycosylated (*e.g.*, in the case of bispecific antibodies comprising antibody domains which are glycosylated). However, the molecules can also be produced in the prokaryotic expression systems. Normally, the host cell will be transformed with DNA encoding both the first human heavy chain variable domain, the second human heavy chain variable domain, the human light chain domain on a single vector or independent vectors. However, it is possible to express the first human heavy chain variable domain, second human heavy chain variable domain, and human light chain domain (the bispecific antibody components) in independent expression systems and couple the expressed polypeptides *in vitro*. In various embodiments, the human light chain domain comprises a germline sequence. In various embodiments, the human light chain domain comprises no more than one, no more than two, no more than three, no more than four, or no more than five somatic hypermutations with the light chain variable sequence of the light chain domain.

[00229] In various embodiments, the nucleic acid(s) (*e.g.*, cDNA or genomic DNA) encoding the two heavy chains and single human light chain is inserted into a replicable vector for further cloning (amplification of the DNA) and/or for expression. Many vectors are available, and generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Each component may be selected individually or based on a host cell choice or other criteria determined experimentally. Several examples of each component are known in the art.

[00230] Expression and cloning vectors usually contain a promoter that is recognized by the host organism and is operably linked to the nucleic acid sequences that encode each or all the components of the bispecific antibody. A large number of promoters recognized by a variety of potential host cells are well known. These promoters are operably linked to

bispecific antibody-encoding DNA by removing the promoter from the source DNA by restriction enzyme digestion and inserting the isolated promoter sequence into the vector.

[00231] Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) may also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding the bispecific antibody components. Suitable expression vectors for various embodiments include those that provide for the transient expression in mammalian cells of DNA encoding the bispecific antibody. In general, transient expression involves the use of an expression vector that is able to replicate efficiently in a host cell, such that the host cell accumulates many copies of the expression vector and, in turn, synthesizes high levels of a desired polypeptide encoded by the expression vector. Transient expression systems, comprising a suitable expression vector and a host cell, allow for the convenient positive identification of polypeptides encoded by cloned DNAs, as well as for the rapid screening of bispecific antibodies having desired binding specificities/affinities or the desired gel migration characteristics relative to the parental antibodies having homodimers of the first or second human heavy chain variable domains.

[00232] In various embodiments, once the DNA encoding the components of the bispecific antibody are assembled into the desired vector(s) as described above, they are introduced into a suitable host cell for expression and recovery. Transfecting host cells can be accomplished using standard techniques known in the art appropriate to the host cell selected (*e.g.*, electroporation, nuclear microinjection, bacterial protoplast fusion with intact cells, or polycations, *e.g.*, polybrene, polyornithine, *etc.*).

[00233] A host cell is chosen, in various embodiments, that best suits the expression vector containing the components and allows for the most efficient and favorable production of the bispecific antibody species. Exemplary host cells for expression include those of prokaryotes and eukaryotes (single-cell or multiple-cell), bacterial cells (*e.g.*, strains of *E. coli*, *Bacillus spp.*, *Streptomyces spp.*, *etc.*), mycobacteria cells, fungal cells, yeast cells (*e.g.*, *S. cerevisiae*, *S. pombe*, *P. pastoris*, *P. methanolica*, *etc.*), plant cells, insect cells (*e.g.*, SF-9, SF-21, baculovirus-infected insect cells, *Trichoplusia ni*, *etc.*), non-human animal cells, human cells, or cell fusions such as, for example, hybridomas or quadromas. In various embodiments, the

cell is a human, monkey, ape, hamster, rat, or mouse cell. In various embodiments, the cell is eukaryotic cell selected from CHO (*e.g.*, CHO K1, DXB-11 CHO, Veggie-CHO), COS (*e.g.*, COS-7), retinal cell, Vero, CV1, kidney (*e.g.*, HEK293, 293 EBNA, MSR 293, MDCK, HaK, BHK), HeLa, HepG2, WI38, MRC 5, Colo205, HB 8065, HL-60, (*e.g.*, BHK21), Jurkat, Daudi, A431 (epidermal), CV-1, U937, 3T3, L cell, C127 cell, SP2/0, NS-0, MMT 060562, Sertoli cell, BRL 3A cell, HT1080 cell, myeloma cell, tumor cell, and a cell line derived from an aforementioned cell. In various embodiments, the cell comprises one or more viral genes, *e.g.* a retinal cell that expresses a viral gene (*e.g.*, a PER.C6™ cell).

[00234] Mammalian host cells used to produce the bispecific antibody may be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), Sigma), RPMI-1640 (Sigma), and Dulbeccols Modified Eagle's Medium ((DMEM), Sigma) are suitable for culturing the host cells. Media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleosides (such as adenosine and thymidine), antibiotics (such as GENTAMYCIN™), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other supplements may also be included at appropriate concentrations as known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are, in various embodiments, those previously used with the host cell selected for expression, and will be apparent to those skilled in the art.

[00235] The bispecific antibody is in various embodiments recovered from the culture medium as a secreted polypeptide, although it also may be recovered from host cell lysate when directly produced without a secretory signal. If the bispecific antibody is membrane-bound, it can be released from the membrane using a suitable detergent solution (*e.g.*, Triton-X 100). Preferably, the bispecific antibodies described herein involves the use of a first immunoglobulin C_H3 domain and a second immunoglobulin C_H3 domain, wherein the first and second immunoglobulin C_H3 domains differ from one another by at least one amino acid, and wherein at least one amino acid difference reduces binding of the bispecific antibody to Protein A as compared to a bi-specific antibody lacking the amino acid difference (see U.S. 2010/0331527A1; herein incorporated by reference). In one embodiment, the first immunoglobulin C_H3 domain binds Protein A and the second immunoglobulin C_H3 domain contains a mutation that reduces or abolishes Protein A binding such as an H95R

modification (by IMGT exon numbering; H435R by EU numbering). The second C_H3 may further comprise a Y96F modification (by IMGT; Y436F by EU). Further modifications that may be found within the second C_H3 include: D16E, L18M, N44S, K52N, V57M, and V82I (by IMGT; D356E, L358M, N384S, K392N, V397M, and V422I by EU) in the case of IgG1 antibodies; N44S, K52N, and V82I (IMGT; N384S, K392N, and V422I by EU) in the case of IgG2 antibodies; and Q15R, N44S, K52N, V57M, R69K, E79Q, and V82I (by IMGT; Q355R, N384S, K392N, V397M, R409K, E419Q, and V422I by EU) in the case of IgG4 antibodies. Variations on the bi-specific antibody format described above are contemplated within the scope of the present invention.

[00236] Because of the dual nature of bispecific antibodies (*i.e.*, may be specific for different epitopes of one polypeptide or may contain antigen-binding domains specific for more than one target polypeptide, see FIG. 7B; see also, *e.g.*, Tutt *et al.*, 1991, *J. Immunol.* 147:60-69; Kufer *et al.*, 2004, *Trends Biotechnol.* 22:238-244), they offer many useful advantages for therapeutic application. For example, the bispecific antibodies can be used for redirected cytotoxicity (*e.g.*, to kill tumor cells), as a vaccine adjuvant, for delivering thrombolytic agents to clots, for converting enzyme activated prodrugs at a target site (*e.g.*, a tumor), for treating infectious diseases, targeting immune complexes to cell surface receptors, or for delivering immunotoxins to tumor cells.

[00237] The bispecific antibodies described herein can also be used in several therapeutic and non-therapeutic and/or diagnostic assay methods, such as, enzyme immunoassays, two-site immunoassays, *in vitro* or *in vivo* immunodiagnosis of various diseases (*e.g.*, cancer), competitive binding assays, direct and indirect sandwich assays, and immunoprecipitation assays. Other uses for the bispecific antibodies will be apparent to those skilled in the art.

[00238] 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. Efforts have been made to ensure accuracy with respect to numbers used (*e.g.*, amounts, temperature, *etc.*) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is average molecular weight, temperature is indicated in Celsius, and pressure is at or near atmospheric.

EXAMPLES

[00239] 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. Efforts have been made to ensure accuracy with respect to numbers used (*e.g.*, amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, temperature is indicated in Celsius, pressure is at or near atmospheric, parts are by parts by weight, and molecular weight is average molecular weight.

10 Example 1

Identification of Human V_H Regions That Associate with Selected Human V_L Regions

[00240] An *in vitro* expression system was constructed to determine if a single rearranged human germline light chain could be co-expressed with human heavy chains from antigen specific human antibodies.

15 [00241] Methods for generating human antibodies in genetically modified mice are known (see *e.g.*, US 6,596,541, Regeneron Pharmaceuticals, VELOCIMMUNE®). The VELOCIMMUNE® technology involves generation of a genetically modified mouse having a genome comprising human heavy and light chain variable regions operably linked to endogenous mouse constant region loci such that the mouse produces an antibody comprising
20 a human variable region and a mouse constant region in response to antigenic stimulation. The DNA encoding the variable regions of the heavy and light chains of the antibodies produced from a VELOCIMMUNE® mouse are fully human. Initially, high affinity chimeric antibodies are isolated having a human variable region and a mouse constant region. As described below, the antibodies are characterized and selected for desirable
25 characteristics, including affinity, selectivity, epitope, *etc.* The mouse constant regions are replaced with a desired human constant region to generate a fully human antibody containing a non-IgM isotype, for example, wild type or modified IgG1, IgG2, IgG3 or IgG4. While the constant region selected may vary according to specific use, high affinity antigen-binding and target specificity characteristics reside in the variable region.

30 [00242] A VELOCIMMUNE® mouse was immunized with a growth factor that promotes angiogenesis (Antigen C) and antigen-specific human antibodies were isolated and sequenced for V gene usage using standard techniques recognized in the art. Selected antibodies were cloned onto human heavy and light chain constant regions and 69 heavy chains were selected

for pairing with one of three human light chains: (1) the cognate κ light chain linked to a human κ constant region, (2) a rearranged human germline V κ 1-39J κ 5 linked to a human κ constant region, or (3) a rearranged human germline V κ 3-20J κ 1 linked to a human κ constant region. Each heavy chain and light chain pair were co-transfected in CHO-K1 cells using standard techniques. Presence of antibody in the supernatant was detected by anti-human IgG in an ELISA assay. Antibody titer (ng/ml) was determined for each heavy chain/light chain pair and titers with the different rearranged germline light chains were compared to the titers obtained with the parental antibody molecule (*i.e.*, heavy chain paired with cognate light chain) and percent of native titer was calculated (Table 1). V_H: Heavy chain variable gene. ND: no expression detected under current experimental conditions.

Table 1

V _H	Antibody Titer (ng/mL)			Percent of Native Titer	
	Cognate LC	V κ 1-39J κ 5	V κ 3-20J κ 1	V κ 1-39J κ 5	V κ 3-20J κ 1
3-15	63	23	11	36.2	17.5
1-2	103	53	ND	51.1	-
3-23	83	60	23	72.0	27.5
3-33	15	77	ND	499.4	-
4-31	22	69	17	309.4	76.7
3-7	53	35	28	65.2	53.1
-	22	32	19	148.8	89.3
1-24	3	13	ND	455.2	-
3-33	1	47	ND	5266.7	-
3-33	58	37	ND	63.1	-
-	110	67	18	60.6	16.5
3-23	127	123	21	96.5	16.3
3-33	28	16	2	57.7	7.1

3-23	32	50	38	157.1	119.4
-	18	45	18	254.3	101.7
3-9	1	30	23	2508.3	1900.0
3-11	12	26	6	225.9	48.3
1-8	16	ND	13	-	81.8
3-33	54	81	10	150.7	19.1
-	34	9	ND	25.9	-
3-20	7	14	54	203.0	809.0
3-33	19	38	ND	200.5	-
3-11	48	ND	203	-	423.6
-	11	23	8	212.7	74.5
3-33	168	138	182	82.0	108.2
3-20	117	67	100	57.5	86.1
3-23	86	61	132	70.7	154.1
3-33	20	12	33	60.9	165.3
4-31	69	92	52	133.8	75.0
3-23	87	78	62	89.5	71.2
1-2	31	82	51	263.0	164.6
3-23	53	93	151	175.4	285.4
-	11	8	17	75.7	151.4
3-33	114	36	27	31.6	23.4
3-15	73	39	44	53.7	59.6
3-33	1	34	16	5600.0	2683.3
3-9	58	112	57	192.9	97.6
3-33	67	20	105	30.1	157.0
3-33	34	21	24	62.7	70.4
3-20	10	49	91	478.4	888.2
3-33	66	32	25	48.6	38.2
3-23	17	59	56	342.7	329.8

-	58	108	19	184.4	32.9
-	68	54	20	79.4	29.9
3-33	42	35	32	83.3	75.4
-	29	19	13	67.1	43.9
3-9	24	34	29	137.3	118.4
3-30/33	17	33	7	195.2	43.1
3-7	25	70	74	284.6	301.6
3-33	87	127	ND	145.1	-
6-1	28	56	ND	201.8	-
3-33	56	39	20	69.9	36.1
3-33	10	53	1	520.6	6.9
3-33	20	67	10	337.2	52.3
3-33	11	36	18	316.8	158.4
3-23	12	42	32	356.8	272.9
3-33	66	95	15	143.6	22.5
3-15	55	68	ND	123.1	-
-	32	68	3	210.9	10.6
1-8	28	48	ND	170.9	-
3-33	124	192	21	154.3	17.0
3-33	0	113	ND	56550.0	-
3-33	10	157	1	1505.8	12.5
3-33	6	86	15	1385.5	243.5
3-23	70	115	22	163.5	31.0
3-7	71	117	21	164.6	29.6
3-33	82	100	47	122.7	57.1
3-7	124	161	41	130.0	33.5

[00243] In a similar experiment, VELOCIMMUNE® mice were immunized with several different antigens and selected heavy chains of antigen specific human antibodies were tested for their ability to pair with different rearranged human germline light chains (as described

above). The antigens used in this experiment included an enzyme involved in cholesterol homeostasis (Antigen A), a serum hormone involved in regulating glucose homeostasis (Antigen B), a growth factor that promotes angiogenesis (Antigen C) and a cell-surface receptor (Antigen D). Antigen specific antibodies were isolated from mice of each immunization group and the heavy chain and light chain variable regions were cloned and sequenced. From the sequence of the heavy and light chains, V gene usage was determined and selected heavy chains were paired with either their cognate light chain or a rearranged human germline V κ 1-39J κ 5 region. Each heavy/light chain pair was co-transfected in CHO-K1 cells and the presence of antibody in the supernatant was detected by anti-human IgG in an ELISA assay. Antibody titer ($\mu\text{g/ml}$) was determined for each heavy chain/light chain pairing and titers with the different rearranged human germline light chains were compared to the titers obtained with the parental antibody molecule (*i.e.*, heavy chain paired with cognate light chain) and percent of native titer was calculated (Table 2). V_H: Heavy chain variable gene. V κ : κ light chain variable gene. ND: no expression detected under current experimental conditions.

Table 2

Antigen	Antibody	V _H	V κ	Titer ($\mu\text{g/ml}$)			Percent of Native Titer
				V _H Alone	V _H + V κ	V _H + V κ 1-39J κ 5	
A	320	1-18	2-30	0.3	3.1	2.0	66
	321	2-5	2-28	0.4	0.4	1.9	448
	334	2-5	2-28	0.4	2.7	2.0	73
	313	3-13	3-15	0.5	0.7	4.5	670
	316	3-23	4-1	0.3	0.2	4.1	2174
	315	3-30	4-1	0.3	0.2	3.2	1327
	318	4-59	1-17	0.3	4.6	4.0	86
B	257	3-13	1-5	0.4	3.1	3.2	104
	283	3-13	1-5	0.4	5.4	3.7	69
	637	3-13	1-5	0.4	4.3	3.0	70

	638	3-13	1-5	0.4	4.1	3.3	82
	624	3-23	1-17	0.3	5.0	3.9	79
	284	3-30	1-17	0.3	4.6	3.4	75
	653	3-33	1-17	0.3	4.3	0.3	7
	268	4-34	1-27	0.3	5.5	3.8	69
	633	4-34	1-27	0.6	6.9	3.0	44
C	730	3-7	1-5	0.3	1.1	2.8	249
	728	3-7	1-5	0.3	2.0	3.2	157
	691	3-9	3-20	0.3	2.8	3.1	109
	749	3-33	3-15	0.3	3.8	2.3	62
	750	3-33	1-16	0.3	3.0	2.8	92
	724	3-33	1-17	0.3	2.3	3.4	151
	706	3-33	1-16	0.3	3.6	3.0	84
	744	1-18	1-12	0.4	5.1	3.0	59
	696	3-11	1-16	0.4	3.0	2.9	97
	685	3-13	3-20	0.3	0.5	3.4	734
	732	3-15	1-17	0.3	4.5	3.2	72
	694	3-15	1-5	0.4	5.2	2.9	55
	743	3-23	1-12	0.3	3.2	0.3	10
	742	3-23	2-28	0.4	4.2	3.1	74
	693	3-23	1-12	0.5	4.2	4.0	94
D	136	3-23	2-28	0.4	5.0	2.7	55
	155	3-30	1-16	0.4	1.0	2.2	221
	163	3-30	1-16	0.3	0.6	3.0	506
	171	3-30	1-16	0.3	1.0	2.8	295
	145	3-43	1-5	0.4	4.4	2.9	65
	49	3-48	3-11	0.3	1.7	2.6	155
	51	3-48	1-39	0.1	1.9	0.1	4
	159	3-7	6-21	0.4	3.9	3.6	92
	169	3-7	6-21	0.3	1.3	3.1	235

	134	3-9	1-5	0.4	5.0	2.9	58
	141	4-31	1-33	2.4	4.2	2.6	63
	142	4-31	1-33	0.4	4.2	2.8	67

[00244] The results obtained from these experiments demonstrate that somatically mutated, high affinity heavy chains from different gene families are able to pair with rearranged human germline V κ 1-39J κ 5 and V κ 3-20J κ 1 regions and be secreted from the cell as a normal antibody molecule. As shown in Table 1, antibody titer was increased for about 61% (42 of 69) heavy chains when paired with the rearranged human V κ 1-39J κ 5 light chain and about 29% (20 of 69) heavy chains when paired with the rearranged human V κ 3-20J κ 1 light chain as compared to the cognate light chain of the parental antibody. For about 20% (14 of 69) of the heavy chains, both rearranged human germline light chains conferred an increase in expression as compared to the cognate light chain of the parental antibody. As shown in Table 2, the rearranged human germline V κ 1-39J κ 5 region conferred an increase in expression of several heavy chains specific for a range of different classes of antigens as compared to the cognate light chain for the parental antibodies. Antibody titer was increased by more than two-fold for about 35% (15/43) of the heavy chains as compared to the cognate light chain of the parental antibodies. For two heavy chains (315 and 316), the increase was greater than ten-fold as compared to the parental antibody. Within all the heavy chains that showed increase expression relative to the cognate light chain of the parental antibody, family three (V_H3) heavy chains are over represented in comparison to other heavy chain variable region gene families. This demonstrates a favorable relationship of human V_H3 heavy chains to pair with rearranged human germline V κ 1-39J κ 5 and V κ 3-20J κ 1 light chains.

Example 2

Generation of a Rearranged Human Germline Light Chain Locus

[00245] Various rearranged human germline light chain targeting vectors were made using VELOCIGENE® 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, Nature Biotech. 21(6): 652-659) to modify mouse genomic Bacterial Artificial Chromosome (BAC) clones 302g12 and 254m04 (Invitrogen). Using these two BAC clones, genomic constructs were engineered to contain a single rearranged human germline light

chain region and inserted into an endogenous κ light chain locus that was previously modified to delete the endogenous κ variable and joining gene segments.

[00246] Construction of Rearranged Human Germline Light Chain Targeting

Vectors. Three different rearranged human germline light chain regions were made using standard molecular biology techniques recognized in the art. The human variable gene segments used for constructing these three regions included rearranged human V κ 1-39J κ 5 sequence, a rearranged human V κ 3-20J κ 1 sequence and a rearranged human VpreBJ λ 5 sequence.

[00247] A DNA segment containing exon 1 (encoding the leader peptide) and intron 1 of the mouse V κ 3-7 gene was made by de novo DNA synthesis (Integrated DNA Technologies). Part of the 5' untranslated region up to a naturally occurring BlnI restriction enzyme site was included. Exons of human V κ 1-39 and V κ 3-20 genes were PCR amplified from human genomic BAC libraries. The forward primers had a 5' extension containing the splice acceptor site of intron 1 of the mouse V κ 3-7 gene. The reverse primer used for PCR of the human V κ 1-39 sequence included an extension encoding human J κ 5, whereas the reverse primer used for PCR of the human V κ 3-20 sequence included an extension encoding human J κ 1. The human VpreBJ λ 5 sequence was made by de novo DNA synthesis (Integrated DNA Technologies). A portion of the human J κ -C κ intron including the splice donor site was PCR amplified from plasmid pBS-296-HA18-PISceI. The forward PCR primer included an extension encoding part of either a human J κ 5, J κ 1, or J λ 5 sequence. The reverse primer included a PI-SceI site, which was previously engineered into the intron.

[00248] The mouse V κ 3-7 exon1/intron 1, human variable light chain exons, and human J κ -C κ intron fragments were sewn together by overlap extension PCR, digested with BlnI and PI-SceI, and ligated into plasmid pBS-296-HA18-PISceI, which contained the promoter from the human V κ 3-15 variable gene segment. A loxed hygromycin cassette within plasmid pBS-296-HA18-PISceI was replaced with a FRTed hygromycin cassette flanked by NotI and AscI sites. The NotI/PI-SceI fragment of this plasmid was ligated into modified mouse BAC 254m04, which contained part of the mouse J κ -C κ intron, the mouse C κ exon, and about 75 kb of genomic sequence downstream of the mouse κ locus, which provided a 3' homology arm for homologous recombination in mouse ES cells. The NotI/AscI fragment of this BAC was then ligated into modified mouse BAC 302g12, which contained a FRTed neomycin

cassette and about 23 kb of genomic sequence upstream of the endogenous κ locus for homologous recombination in mouse ES cells.

[00249] Rearranged Human Germline V κ 1-39J κ 5 Targeting Vector (FIG. 1).

Restriction enzyme sites were introduced at the 5' and 3' ends of an engineered light chain insert for cloning into a targeting vector: an *Asc*I site at the 5' end and a *PI-Sce*I site at the 3' end. Within the 5' *Asc*I site and the 3' *PI-Sce*I site the targeting construct from 5' to 3' included a 5' homology arm containing sequence 5' to the endogenous mouse κ light chain locus obtained from mouse BAC clone 302g12, a FRTed neomycin resistance gene, an genomic sequence including the human V κ 3-15 promoter, a leader sequence of the mouse V κ 3-7 variable gene segment, an intron sequence of the mouse V κ 3-7 variable gene segment, an open reading frame of a rearranged human germline V κ 1-39J κ 5 region, a genomic sequence containing a portion of the human J κ -C κ intron, and a 3' homology arm containing sequence 3' of the endogenous mouse J κ 5 gene segment obtained from mouse BAC clone 254m04 (Figure 1, middle). Genes and/or sequences upstream of the endogenous mouse κ light chain locus and downstream of the most 3' J κ gene segment (*e.g.*, the endogenous 3' enhancer) were unmodified by the targeting construct (see Figure 1). The sequence of the engineered human V κ 1-39J κ 5 locus is shown in SEQ ID NO: 1.

[00250] Targeted insertion of the rearranged human germline V κ 1-39J κ 5 region into BAC DNA was confirmed by polymerase chain reaction (PCR) using primers located at sequences within the rearranged human germline light chain region. Briefly, the intron sequence 3' to the mouse V κ 3-7 leader sequence was confirmed with primers ULC-m1F (AGGTGAGGGT ACAGATAAGT GTTATGAG; SEQ ID NO: 2) and ULC-m1R (TGACAAATGC CCTAATTATA GTGATCA; SEQ ID NO: 3). The open reading frame of the rearranged human germline V κ 1-39J κ 5 region was confirmed with primers 1633-h2F (GGGCAAGTCA GAGCATTAGC A; SEQ ID NO: 4) and 1633-h2R (TGCAAAGTGG ATGCAGCATA G; SEQ ID NO: 5). The neomycin cassette was confirmed with primers neoF (GGTGGAGAGG CTATTCGGC; SEQ ID NO: 6) and neoR (GAACACGGCG GCATCAG; SEQ ID NO: 7). Targeted BAC DNA was then used to electroporate mouse ES cells to create modified ES cells for generating chimeric mice that express a rearranged human germline V κ 1-39J κ 5 region.

[00251] Positive ES cell clones were confirmed by TAQMANTM screening and karyotyping using probes specific for the engineered V κ 1-39J κ 5 light chain region inserted

into the endogenous locus. Briefly, probe neoP (TGGGCACAAC AGACAATCGG CTG; SEQ ID NO:8) which binds within the neomycin marker gene, probe ULC-m1P (CCATTATGAT GCTCCATGCC TCTCTGTTC; SEQ ID NO: 9) which binds within the intron sequence 3' to the mouse V κ 3-7 leader sequence, and probe 1633h2P

5 (ATCAGCAGAA ACCAGGGAAA GCCCCT; SEQ ID NO: 10) which binds within the rearranged human germline V κ 1-39J κ 5 open reading frame. Positive ES cell clones were then used to implant female mice to give rise to a litter of pups expressing the germline V κ 1-39J κ 5 light chain region.

[00252] Alternatively, ES cells bearing the rearranged human germline V κ 1-39J κ 5 light
10 chain region are transfected with a construct that expresses FLP in order to remove the FRTed neomycin cassette introduced by the targeting construct. Optionally, the neomycin cassette is removed by breeding to mice that express FLP recombinase (*e.g.*, US 6,774,279). Optionally, the neomycin cassette is retained in the mice.

[00253] **Rearranged Human Germline V κ 3-20J κ 1 Targeting Vector (FIG. 2).** In a
15 similar fashion, an engineered light chain locus expressing a rearranged human germline V κ 3-20J κ 1 region was made using a targeting construct including, from 5' to 3', a 5' homology arm containing sequence 5' to the endogenous mouse κ light chain locus obtained from mouse BAC clone 302g12, a FRTed neomycin resistance gene, a genomic sequence including the human V κ 3-15 promoter, a leader sequence of the mouse V κ 3-7 variable gene
20 segment, an intron sequence of the mouse V κ 3-7 variable gene segment, an open reading frame of a rearranged human germline V κ 3-20J κ 1 region, a genomic sequence containing a portion of the human J κ -C κ intron, and a 3' homology arm containing sequence 3' of the endogenous mouse J κ 5 gene segment obtained from mouse BAC clone 254m04 (Figure 2, middle). The sequence of the engineered human V κ 3-20J κ 1 locus is shown in SEQ ID NO:
25 11.

[00254] Targeted insertion of the rearranged human germline V κ 3-20J κ 1 region into BAC
DNA was confirmed by polymerase chain reaction (PCR) using primers located at sequences within the rearranged human germline V κ 3-20J κ 1 light chain region. Briefly, the intron
sequence 3' to the mouse V κ 3-7 leader sequence was confirmed with primers ULC-m1F
30 (SEQ ID NO: 2) and ULC-m1R (SEQ ID NO: 3). The open reading frame of the rearranged human germline V κ 3-20J κ 1 region was confirmed with primers 1635-h2F (TCCAGGCACC CTGTCTTTG; SEQ ID NO: 12) and 1635-h2R (AAGTAGCTGC TGCTAACACT

CTGACT; SEQ ID NO: 13). The neomycin cassette was confirmed with primers neoF (SEQ ID NO: 6) and neoR (SEQ ID NO: 7). Targeted BAC DNA was then used to electroporate mouse ES cells to create modified ES cells for generating chimeric mice that express the rearranged human germline V κ 3-20J κ 1 light chain.

5 **[00255]** Positive ES cell clones were confirmed by TAQMAN™ screening and karyotyping using probes specific for the engineered V κ 3-20J κ 1 light chain region inserted into the endogenous κ light chain locus. Briefly, probe neoP (SEQ ID NO:8) which binds within the neomycin marker gene, probe ULC-m1P (SEQ ID NO: 9) which binds within the mouse V κ 3-7 leader sequence, and probe 1635h2P (AAAGAGCCAC CCTCTCCTGC
10 AGGG; SEQ ID NO: 14) which binds within the human V κ 3-20J κ 1 open reading frame. Positive ES cell clones were then used to implant female mice. A litter of pups expressing the human germline V κ 3-20J κ 1 light chain region.

[00256] Alternatively, ES cells bearing human germline V κ 3-20J κ 1 light chain region can be transfected with a construct that expresses FLP in order to remove the FRTed neomycin
15 cassette introduced by the targeting construct. Optionally, the neomycin cassette may be removed by breeding to mice that express FLP recombinase (*e.g.*, US 6,774,279). Optionally, the neomycin cassette is retained in the mice.

[00257] Rearranged Human Germline VpreBJ λ 5 Targeting Vector (FIG. 3). In a similar fashion, an engineered light chain locus expressing a rearranged human germline
20 VpreBJ λ 5 region was made using a targeting construct including, from 5' to 3', a 5' homology arm containing sequence 5' to the endogenous mouse κ light chain locus obtained from mouse BAC clone 302g12, a FRTed neomycin resistance gene, a genomic sequence including the human V κ 3-15 promoter, a leader sequence of the mouse V κ 3-7 variable gene segment, an intron sequence of the mouse V κ 3-7 variable gene segment, an open reading
25 frame of a rearranged human germline VpreBJ λ 5 region, a genomic sequence containing a portion of the human J κ -C κ intron, and a 3' homology arm containing sequence 3' of the endogenous mouse J κ 5 gene segment obtained from mouse BAC clone 254m04 (Figure 3, middle). The sequence of the engineered human VpreBJ λ 5 locus is shown in SEQ ID NO: 15.

30 **[00258]** Targeted insertion of the rearranged human germline VpreBJ λ 5 region into BAC DNA was confirmed by polymerase chain reaction (PCR) using primers located at sequences within the rearranged human germline VpreBJ λ 5 region light chain region. Briefly, the

intron sequence 3' to the mouse V κ 3-7 leader sequence was confirmed with primers ULC-m1F (SEQ ID NO: 2) and ULC-m1R (SEQ ID NO: 3). The open reading frame of the rearranged human germline VpreBJ λ 5 region was confirmed with primers 1616-h1F (TGTCCTCGGC CCTTGGA; SEQ ID NO: 16) and 1616-h1R (CCGATGTCAT GGTCGTTTCCT; SEQ ID NO: 17). The neomycin cassette was confirmed with primers neoF (SEQ ID NO: 6) and neoR (SEQ ID NO: 7). Targeted BAC DNA was then used to electroporate mouse ES cells to create modified ES cells for generating chimeric mice that express the rearranged human germline VpreBJ λ 5 light chain.

[00259] Positive ES cell clones are confirmed by TAQMAN™ screening and karyotyping using probes specific for the engineered VpreBJ λ 5 light chain region inserted into the endogenous κ light chain locus. Briefly, probe neoP (SEQ ID NO:8), which binds within the neomycin marker gene, probe ULC-m1P (SEQ ID NO: 9), which binds within the mouse IgV κ 3-7 leader sequence, and probe 1616h1P (ACAATCCGCC TCACCTGCAC CCT; SEQ ID NO: 18) which binds within the human VpreBJ λ 5 open reading frame. Positive ES cell clones are then used to implant female mice to give rise to a litter of pups expressing a germline light chain region.

[00260] Alternatively, ES cells bearing the rearranged human germline VpreBJ λ 5 light chain region are transfected with a construct that expresses FLP in order to remove the FRTed neomycin cassette introduced by the targeting construct. Optionally, the neomycin cassette is removed by breeding to mice that express FLP recombinase (*e.g.*, US 6,774,279). Optionally, the neomycin cassette is retained in the mice.

Example 3

Generation of Mice expressing a single rearranged human light chain

[00261] Targeted ES cells described above were used as donor ES cells and introduced into an 8-cell stage mouse embryo by the VELOCIMOUSE® method (see, *e.g.*, US Pat. No. 7,294,754 and Poueymirou *et al.* (2007) F0 generation mice that are essentially fully derived from the donor gene-targeted ES cells allowing immediate phenotypic analyses Nature Biotech. 25(1): 91-99. VELOCIMICE® independently bearing an engineered human germline V κ 1-39J κ 5 light chain region, a V κ 3-20J κ 1 light chain region or a VpreBJ λ 5 light chain region are identified by genotyping using a modification of allele assay (Valenzuela *et al.*, *supra*) that detects the presence of the unique rearranged human germline light chain region.

[00262] Pups are genotyped and a pup heterozygous or homozygous for the unique rearranged human germline light chain region are selected for characterizing expression of the rearranged human germline light chain region.

[00263] Flow Cytometry. Expression of the rearranged human light chain region in the

5 normal antibody repertoire of common light chain mice was validated by analysis of immunoglobulin κ and λ expression in splenocytes and peripheral blood of common light chain mice. Cell suspensions from harvested spleens and peripheral blood of wild type (n=5), V κ 1-39J κ 5 common light chain heterozygote (n=3), V κ 1-39J κ 5 common light chain homozygote (n=3), V κ 3-20J κ 1 common light chain heterozygote (n=2), and V κ 3-20J κ 1
10 common light chain homozygote (n=2) mice were made using standard methods and stained with CD19⁺, Ig λ ⁺ and Ig κ ⁺ using fluorescently labeled antibodies (BD Pharmingen).

[00264] Briefly, 1×10^6 cells were incubated with anti-mouse CD16/CD32 (clone 2.4G2, BD Pharmingen) on ice for 10 minutes, followed by labeling with the following antibody cocktail for 30 minutes on ice: APC conjugated anti-mouse CD19 (clone 1D3, BD

15 Pharmingen), PerCP-Cy5.5 conjugated anti-mouse CD3 (clone 17A2, BioLegend), FITC conjugated anti-mouse Ig $\square$ (clone 187.1, BD Pharmingen), PE conjugated anti-mouse Ig λ (clone RML-42, BioLegend). Following staining, cells were washed and fixed in 2% formaldehyde. Data acquisition was performed on an LSRII flow cytometer and analyzed with FlowJo. Gating: total B cells (CD19⁺CD3⁻), Ig κ ⁺ B cells (Ig κ ⁺Ig λ ⁻CD19⁺CD3⁻), Ig λ ⁺ B
20 cells (Ig κ ⁻Ig λ ⁺CD19⁺CD3⁻). Data gathered from blood and splenocyte samples demonstrated similar results. Table 3 sets forth the percent positive CD19⁺ B cells from peripheral blood of one representative mouse from each group that are Ig λ ⁺, Ig κ ⁺, or Ig λ ⁺Ig κ ⁺. Percent of CD19⁺ B cells in peripheral blood from wild type (WT) and mice homozygous for either the V κ 1-39J κ 5 or V κ 3-20J κ 1 common light chain are shown in FIG. 4.

Table 3

Mouse	CD19 ⁺ B cells		
	Ig λ ⁺	Ig κ ⁺	Ig λ ⁺ Ig κ ⁺
Wild type	4.8	93	0.53
V κ 1-39J κ 5	1.4	93	2.6
V κ 3-20J κ 1	4.2	88	6

[00265] Common Light Chain Expression. Expression of each common light chain (V κ 1-39J κ 5 and V κ 3-20J κ 1) was analyzed in heterozygous and homozygous mice using a quantitative PCR assay (*e.g.* TAQMAN™).

[00266] Briefly, CD19⁺ B cells were purified from the spleens of wild type, mice

- 5 homozygous for a replacement of the mouse heavy chain and κ light chain variable region loci with corresponding human heavy chain and κ light chain variable region loci (H κ), as well as mice homozygous and heterozygous for each rearranged human light chain region (V κ 1-39J κ 5 or V κ 3-20J κ 1) using mouse CD19 Microbeads (Miltenyi Biotec) according to manufacturer's specifications. Total RNA was purified from CD19⁺ B cells using RNeasy
- 10 Mini kit (Qiagen) according to manufacturer's specifications and genomic RNA was removed using an RNase-free DNase on-column treatment (Qiagen). 200 ng mRNA was reverse-transcribed into cDNA using the First Stand cDNA Synthesis kit (Invitrogen) and the resulting cDNA was amplified with the Taqman Universal PCR Master Mix (Applied Biosystems). All reactions were performed using the ABI 7900 Sequence Detection System
- 15 (Applied Biosystems) using primers and Taqman MGB probes spanning (1) the V κ -J κ junction for both common light chains, (2) the V κ gene alone (*i.e.* V κ 1-39 and V κ 3-20), and (3) the mouse C κ region. Table 4 sets forth the sequences of the primers and probes employed for this assay. Relative expression was normalized to expression of the mouse C κ region. Results are shown in FIG. 5A, 5B and 5C.

20

Table 4

Region	Primer/Probe Description (5'-3')	SEQ ID NOs:
V κ 1-39J κ 5 Junction	(Sense) AGCAGTCTGC AACCTGAAGA TTT	19
	(Anti-sense) GTTTAATCTC CAGTCGTGTC	20
	CCTT	21
	(Probe) CCTCCGATCA CCTTC	
V κ 1-39	(Sense) AAACCAGGGA AAGCCCCTAA	22
	(Anti-sense) ATGGGACCCC ACTTTGCA	23
	(Probe) CTCCTGATCT ATGCTGCAT	24

V κ 3-20J κ 1 Junction	(Sense) CAGCAGACTG GAGCCTGAAG A	25
	(Anti-sense) TGATTTCCAC CTTGGTCCCT T	26
	(Probe) TAGCTCACCT TGGACGTT	27
V κ 3-20	(Sense) CTCCTCATCT ATGGTGCATC CA	28
	(Anti-sense) GACCCACTGC CACTGAACCT	29
	(Probe) CCACTGGCAT CCC	30
Mouse C κ	(Sense) TGAGCAGCAC CCTCACGTT	31
	(Anti-sense) GTGGCCTCAC AGGTATAGCT GTT	32
	(Probe) ACCAAGGACG AGTATGAA	33

[00267] Antigen Specific Common Light Chain Antibodies. Common light chain mice bearing either a V κ 1-39J κ 5 or V κ 3-20J κ 1 common light chain at the endogenous mouse κ light chain locus were immunized with β -galactosidase and antibody titer was measured.

- 5 **[00268]** Briefly, β -galactosidase (Sigma) was emulsified in titermax adjuvant (Sigma), as per manufacturers directions. Wild type (n=7), V κ 1-39J κ 5 common light chain homozygotes (n=2) and V κ 3-20J κ 1 common light chain homozygotes (n=5) were immunized by subcutaneous injection with 100 μ g β -galactosidase/Titermax. Mice were boosted by subcutaneous injection two times, 3 weeks apart, with 50 μ g β -galactosidase/Titermax.
- 10 After the second boost, blood was collected from anaesthetized mice using a retro-orbital bleed into serum separator tubes (BD Biosciences) as per manufacturer's directions. To measure anti- β -galactosidase IgM or IgG antibodies, ELISA plates (Nunc) were coated with 1 μ g/mL β -galactosidase overnight at 4°C. Excess antigen was washed off before blocking with PBS with 1% BSA for one hour at room temperature. Serial dilutions of serum were
- 15 added to the plates and incubated for one hour at room temperature before washing. Plates were then incubated with HRP conjugated anti-IgM (Southern Biotech) or anti-IgG (Southern Biotech) for one hour at room temperature. Following another wash, plates were developed with TMB substrate (BD Biosciences). Reactions were stopped with 1N sulfuric acid and OD₄₅₀ was read using a Victor X5 Plate Reader (Perkin Elmer). Data was analyzed with
- 20 GraphPad Prism and signal was calculated as the dilution of serum that is two times above background. Results are shown in FIG. 6A and 6B.

[00269] As shown in this Example, the ratio of κ/λ B cells in both the splenic and peripheral compartments of V κ 1-39J κ 5 and V κ 3-20J κ 1 common light chain mice

demonstrated a near wild type pattern (Table 3 and FIG. 4). VpreBJ λ 5 common light chain mice, however, demonstrated fewer peripheral B cells, of which about 1-2% express the engineered human light chain region (data not shown). The expression levels of the V κ 1-39J κ 5 and V κ 3-20J κ 1 rearranged human light chain regions from the endogenous κ light chain locus were elevated in comparison to an endogenous κ light chain locus containing a complete replacement of mouse V κ and J κ gene segments with human V κ and J κ gene segments (FIG. 5A, 5B and 5C). The expression levels of the VpreBJ λ 5 rearranged human light chain region demonstrated similar high expression from the endogenous κ light chain locus in both heterozygous and homozygous mice (data not shown). This demonstrates that in direct competition with the mouse λ , κ , or both endogenous light chain loci, a single rearranged human V_L/J_L sequence can yield better than wild type level expression from the endogenous κ light chain locus and give rise to normal splenic and blood B cell frequency. Further, the presence of an engineered κ light chain locus having either a human V κ 1-39J κ 5 or human V κ 3-20J κ 1 sequence was well tolerated by the mice and appear to function in wild type fashion by representing a substantial portion of the light chain repertoire in the humoral component of the immune response (FIG 6A and 6B).

Example 4

Breeding of mice expressing a single rearranged human germline light chain

[00270] This Example describes several other genetically modified mouse strains that can be bred to any one of the common light chain mice described herein to create multiple genetically modified mouse strains harboring multiple genetically modified immunoglobulin loci.

[00271] Endogenous Ig λ Knockout (KO). To optimize the usage of the engineered light chain locus, mice bearing one of the rearranged human germline light chain regions are bred to another mouse containing a deletion in the endogenous λ light chain locus. In this manner, the progeny obtained will express, as their only light chain, the rearranged human germline light chain region as described in Example 2. Breeding is performed by standard techniques recognized in the art and, alternatively, by a commercial breeder (*e.g.*, The Jackson Laboratory). Mouse strains bearing an engineered light chain locus and a deletion of the endogenous λ light chain locus are screened for presence of the unique light chain region and absence of endogenous mouse λ light chains.

[00272] Humanized Endogenous Heavy Chain Locus. Mice bearing an engineered human germline light chain locus are bred with mice that contain a replacement of the endogenous mouse heavy chain variable gene locus with the human heavy chain variable gene locus (see US 6,596,541; the VELOCIMMUNE® mouse, Regeneron Pharmaceuticals, Inc.). The VELOCIMMUNE® mouse comprises a genome comprising human heavy chain variable regions operably linked to endogenous mouse constant region loci such that the mouse produces antibodies comprising a human heavy chain variable region and a mouse heavy chain constant region in response to antigenic stimulation. The DNA encoding the variable regions of the heavy chains of the antibodies is isolated and operably linked to DNA encoding the human heavy chain constant regions. The DNA is then expressed in a cell capable of expressing the fully human heavy chain of the antibody.

[00273] Mice bearing a replacement of the endogenous mouse V_H locus with the human V_H locus and a single rearranged human germline V_L region at the endogenous κ light chain locus are obtained. Reverse chimeric antibodies containing somatically mutated heavy chains (human V_H and mouse C_H) with a single human light chain (human V_L and mouse C_L) are obtained upon immunization with an antigen of interest. V_H and V_L nucleotide sequences of B cells expressing the antibodies are identified and fully human antibodies are made by fusion the V_H and V_L nucleotide sequences to human C_H and C_L nucleotide sequences in a suitable expression system.

Example 5

Generation of Antibodies from Mice Expressing Human Heavy Chains and a Rearranged Human Germline Light Chain Region

[00274] After breeding mice that contain the engineered human light chain region to various desired strains containing modifications and deletions of other endogenous Ig loci (as described in Example 4), selected mice can be immunized with an antigen of interest.

[00275] Generally, a VELOCIMMUNE® mouse containing one of the single rearranged human germline light chain regions is challenged with an antigen, and lymphatic cells (such as B-cells) are recovered from serum of the animals. The lymphatic cells are fused with a myeloma cell line to prepare immortal hybridoma cell lines, and such hybridoma cell lines are screened and selected to identify hybridoma cell lines that produce antibodies containing human heavy chain variables and a rearranged human germline light chains which are specific to the antigen used for immunization. DNA encoding the variable regions of the

heavy chains and the light chain are isolated and linked to desirable isotypic constant regions of the heavy chain and light chain. Due to the presence of the endogenous mouse sequences and any additional cis-acting elements present in the endogenous locus, the single light chain of each antibody may be somatically mutated. This adds additional diversity to the antigen-specific repertoire comprising a single light chain and diverse heavy chain sequences. The resulting cloned antibody sequences are subsequently expressed in a cell, such as a CHO cell. Alternatively, DNA encoding the antigen-specific chimeric antibodies or the variable domains of the light and heavy chains are identified directly from antigen-specific lymphocytes.

10 **[00276]** Initially, high affinity chimeric antibodies are isolated having a human variable region and a mouse constant region. As described above, the antibodies are characterized and selected for desirable characteristics, including affinity, selectivity, epitope, *etc.* The mouse constant regions are replaced with a desired human constant region to generate the fully human antibody containing a somatically mutated human heavy chain and a single light chain
15 derived from a rearranged human germline light chain region of the invention. Suitable human constant regions include, for example wild type or modified IgG1 or IgG4.

[00277] Separate cohorts of VELOCIMMUNE® mice containing a replacement of the endogenous mouse heavy chain locus with human V_H, D_H, and J_H gene segments and a replacement of the endogenous mouse κ light chain locus with either the engineered germline
20 Vκ1-39Jκ5 human light chain region or the engineered germline Vκ3-20Jκ1 human light chain region (described above) were immunized with a human cell-surface receptor protein (Antigen E). Antigen E is administered directly onto the hind footpad of mice with six consecutive injections every 3-4 days. Two to three micrograms of Antigen E are mixed with 10 μg of CpG oligonucleotide (Cat # tlr1-modn - ODN1826 oligonucleotide; InVivogen, San
25 Diego, CA) and 25 μg of Adju-Phos (Aluminum phosphate gel adjuvant, Cat# H-71639-250; Brenntag Biosector, Frederikssund, Denmark) prior to injection. A total of six injections are given prior to the final antigen recall, which is given 3-5 days prior to sacrifice. Bleeds after the 4th and 6th injection are collected and the antibody immune response is monitored by a standard antigen-specific immunoassay.

30 **[00278]** When a desired immune response is achieved splenocytes are harvested and fused with mouse myeloma cells to preserve their viability and form hybridoma cell lines. The hybridoma cell lines are screened and selected to identify cell lines that produce Antigen E-specific common light chain antibodies. Using this technique several anti-Antigen E-specific

common light chain antibodies (*i.e.*, antibodies possessing human heavy chain variable domains, the same human light chain variable domain, and mouse constant domains) are obtained.

[00279] Alternatively, anti-Antigen E common light chain antibodies are isolated directly from antigen-positive B cells without fusion to myeloma cells, as described in U.S. 2007/0280945A1, herein specifically incorporated by reference in its entirety. Using this method, several fully human anti-Antigen E common light chain antibodies (*i.e.*, antibodies possessing human heavy chain variable domains, either an engineered human V κ 1-39J κ 5 light chain or an engineered human V κ 3-20J κ 1 light chain region, and human constant domains) were obtained.

[00280] The biological properties of the exemplary anti-Antigen E common light chain antibodies generated in accordance with the methods of this Example are described in detail in the sections set forth below.

Example 6

Heavy Chain Gene Segment Usage in Antigen-Specific Common Light Chain Antibodies

[00281] To analyze the structure of the human anti-Antigen E common light chain antibodies produced, nucleic acids encoding heavy chain antibody variable regions were cloned and sequenced. From the nucleic acid sequences and predicted amino acid sequences of the antibodies, gene usage was identified for the heavy chain variable region (HCVR) of selected common light chain antibodies obtained from immunized VELOCIMMUNE® mice containing either the engineered human V κ 1-39J κ 5 light chain or engineered human V κ 3-20J κ 1 light chain region. Results are shown in Tables 5 and 6, which demonstrate that mice according to the invention generate antigen-specific common light chain antibodies from a variety of human heavy chain gene segments, due to a variety of rearrangements, when employing either a mouse that expresses a light chain from only a human V κ 1-39- or a human V κ 3-20-derived light chain. Human V_H gene segments of the 2, 3, 4, and 5 families rearranged with a variety of human D_H segments and human J_H segments to yield antigen-specific antibodies.

Table 5

VK1-39Jk5							
Common Light Chain Antibodies							
Antibody	HCVR			Antibody	HCVR		
	V _H	D _H	J _H		V _H	D _H	J _H
2952	2-5	6-6	1	6030	3-30	6-6	5
5978	2-5	6-6	1	6032	3-30	6-6	5
5981	2-5	3-22	1	2985	3-30	6-13	4
6027	3-13	6-6	5	2997	3-30	6-13	4
3022	3-23	3-10	4	3011	3-30	6-13	4
3028	3-23	3-3	4	3047	3-30	6-13	4
5999	3-23	6-6	4	5982	3-30	6-13	4
6009	3-23	2-8	4	6002	3-30	6-13	4
6011	3-23	7-27	4	6003	3-30	6-13	4
5980	3-30	1-1	4	6012	3-30	6-13	4
3014	3-30	1-7	4	6013	3-30	6-13	4
3015	3-30	1-7	4	6014	3-30	6-13	4
3023	3-30	1-7	4	6015	3-30	6-13	4
3024	3-30	1-7	4	6016	3-30	6-13	4
3032	3-30	1-7	4	6017	3-30	6-13	4
6024	3-30	1-7	4	6020	3-30	6-13	4
6025	3-30	1-7	4	6034	3-30	6-13	4
6031	3-30	1-7	4	2948	3-30	7-27	4
6007	3-30	3-3	4	2987	3-30	7-27	4
2982	3-30	3-22	5	2996	3-30	7-27	4
6001	3-30	3-22	5	3005	3-30	7-27	4
6005	3-30	3-22	5	3012	3-30	7-27	4
6035	3-30	5-5	2	3020	3-30	7-27	4

3013	3-30	5-12	4
3042	3-30	5-12	4
2955	3-30	6-6	1
3043	3-30	6-6	3
3018	3-30	6-6	4
2949	3-30	6-6	5
2950	3-30	6-6	5
2954	3-30	6-6	5
2978	3-30	6-6	5
3016	3-30	6-6	5
3017	3-30	6-6	5
3033	3-30	6-6	5
3041	3-30	6-6	5
5979	3-30	6-6	5
5998	3-30	6-6	5
6004	3-30	6-6	5
6010	3-30	6-6	5
6019	3-30	6-6	5
6021	3-30	6-6	5
6022	3-30	6-6	5
6023	3-30	6-6	5

3021	3-30	7-27	4
3025	3-30	7-27	4
3030	3-30	7-27	4
3036	3-30	7-27	4
5997	3-30	7-27	4
6033	3-30	7-27	4
3004	3-30	7-27	5
6028	3-30	7-27	6
3010	4-59	3-16	3
3019	4-59	3-16	3
6018	4-59	3-16	3
6026	4-59	3-16	3
6029	4-59	3-16	3
6036	4-59	3-16	3
6037	4-59	3-16	3
2964	4-59	3-22	3
3027	4-59	3-16	4
3046	5-51	5-5	3
6000	1-69	6-13	4
6006	1-69	6-6	5
6008	1-69	6-13	4

Table 6

Vκ3-20Jκ1							
Common Light Chain Antibodies							
Antibody	HCVR			Antibody	HCVR		
	V _H	D _H	J _H		V _H	D _H	J _H
5989	3-30	3-3	3	5992	4-39	1-26	3
5994	3-33	1-7	4	2975	5-51	6-13	5
5985	3-33	2-15	4	2972	5-51	3-16	6
5987	3-33	2-15	4	5986	5-51	3-16	6
5995	3-33	2-15	4	5993	5-51	3-16	6
2968	4-39	1-26	3	5996	5-51	3-16	6
5988	4-39	1-26	3	5984	3-53	1-1	4
5990	4-39	1-26	3				

Example 7**Determination of Blocking Ability of Antigen-Specific Common Light Chain Antibodies by LUMINEX™ Assay**

5 **[00282]** Ninety-eight human common light chain antibodies raised against Antigen E were tested for their ability to block binding of Antigen E's natural ligand (Ligand Y) to Antigen E in a bead-based assay.

[00283] The extracellular domain (ECD) of Antigen E was conjugated to two myc epitope tags and a 6X histidine tag (Antigen E-mmH) and amine-coupled to carboxylated
 10 microspheres at a concentration of 20 µg/mL in MES buffer. The mixture was incubated for two hours at room temperature followed by bead deactivation with 1M Tris pH 8.0 followed by washing in PBS with 0.05% (v/v) Tween-20. The beads were then blocked with PBS (Irvine Scientific, Santa Ana, CA) containing 2% (w/v) BSA (Sigma-Aldrich Corp., St. Louis, MO). In a 96-well filter plate, supernatants containing Antigen E-specific common
 15 light chain antibodies were diluted 1:15 in buffer. A negative control containing a mock supernatant with the same media components as for the antibody supernatant was prepared. Antigen E-labeled beads were added to the supernatants and incubated overnight at 4°C. Biotinylated-Ligand Y protein was added to a final concentration of 0.06 nM and incubated

for two hours at room temperature. Detection of biotinylated-Ligand Y bound to Antigen E-myc-myc-6His labeled beads was determined with R-Phycoerythrin conjugated to Streptavidin (Moss Inc, Pasadena, MD) followed by measurement in a LUMINEX™ flow cytometry-based analyzer. Background Mean Fluorescence Intensity (MFI) of a sample without Ligand Y was subtracted from all samples. Percent blocking was calculated by division of the background-subtracted MFI of each sample by the adjusted negative control value, multiplying by 100 and subtracting the resulting value from 100.

[00284] In a similar experiment, the same 98 human common light chain antibodies raised against Antigen E were tested for their ability to block binding of Antigen E to Ligand Y-labeled beads.

[00285] Briefly, Ligand Y was amine-coupled to carboxylated microspheres at a concentration of 20 µg/mL diluted in MES buffer. The mixture and incubated two hours at room temperature followed by deactivation of beads with 1M Tris pH 8 then washing in PBS with 0.05% (v/v) Tween-20. The beads were then blocked with PBS (Irvine Scientific, Santa Ana, CA) containing 2% (w/v) BSA (Sigma-Aldrich Corp., St. Louis, MO). In a 96-well filter plate, supernatants containing Antigen E-specific common light chain antibodies were diluted 1:15 in buffer. A negative control containing a mock supernatant with the same media components as for the antibody supernatant was prepared. A biotinylated-Antigen E-mmH was added to a final concentration of 0.42 nM and incubated overnight at 4°C. Ligand Y-labeled beads were then added to the antibody/Antigen E mixture and incubated for two hours at room temperature. Detection of biotinylated-Antigen E-mmH bound to Ligand Y-beads was determined with R-Phycoerythrin conjugated to Streptavidin (Moss Inc, Pasadena, MD) followed by measurement in a LUMINEX™ flow cytometry-based analyzer.

Background Mean Fluorescence Intensity (MFI) of a sample without Antigen E was subtracted from all samples. Percent blocking was calculated by division of the background-subtracted MFI of each sample by the adjusted negative control value, multiplying by 100 and subtracting the resulting value from 100.

[00286] Tables 7 and 8 show the percent blocking for all 98 anti-Antigen E common light chain antibodies tested in both LUMINEX™ assays. ND: not determined under current experimental conditions.

Table 7

Vκ1-39Jκ5		
Common Light Chain Antibodies		
Antibody	% Blocking of Antigen E-Labeled Beads	% Blocking of Antigen E In Solution
2948	81.1	47.8
2948G	38.6	ND
2949	97.6	78.8
2949G	97.1	73.7
2950	96.2	81.9
2950G	89.8	31.4
2952	96.1	74.3
2952G	93.5	39.9
2954	93.7	70.1
2954G	91.7	30.1
2955	75.8	30.0
2955G	71.8	ND
2964	92.1	31.4
2964G	94.6	43.0
2978	98.0	95.1
2978G	13.9	94.1
2982	92.8	78.5
2982G	41.9	52.4
2985	39.5	31.2
2985G	2.0	5.0
2987	81.7	67.8
2987G	26.6	29.3
2996	87.3	55.3
2996G	95.9	38.4

2997	93.4	70.6
2997G	9.7	7.5
3004	79.0	48.4
3004G	60.3	40.7
3005	97.4	93.5
3005G	77.5	75.6
3010	98.0	82.6
3010G	97.9	81.0
3011	87.4	42.8
3011G	83.5	41.7
3012	91.0	60.8
3012G	52.4	16.8
3013	80.3	65.8
3013G	17.5	15.4
3014	63.4	20.7
3014G	74.4	28.5
3015	89.1	55.7
3015G	58.8	17.3
3016	97.1	81.6
3016G	93.1	66.4
3017	94.8	70.2
3017G	87.9	40.8
3018	85.4	54.0
3018G	26.1	12.7
3019	99.3	92.4
3019G	99.3	88.1
3020	96.7	90.3
3020G	85.2	41.5
3021	74.5	26.1

3021G	81.1	27.4
3022	65.2	17.6
3022G	67.2	9.1
3023	71.4	28.5
3023G	73.8	29.7
3024	73.9	32.6
3024G	89.0	10.0
3025	70.7	15.6
3025G	76.7	24.3
3027	96.2	61.6
3027G	98.6	75.3
3028	92.4	29.0
3028G	87.3	28.8
3030	6.0	10.6
3030G	41.3	14.2
3032	76.5	31.4
3032G	17.7	11.0
3033	98.2	86.1
3033G	93.6	64.0
3036	74.7	32.7
3036G	90.1	51.2
3041	95.3	75.9
3041G	92.4	51.6
3042	88.1	73.3
3042G	60.9	25.2
3043	90.8	65.8
3043G	92.8	60.3

Table 8

Vκ3-20Jκ1		
Common Light Chain Antibodies		
Antibody	% Blocking of Antigen E-Labeled Beads	% Blocking of Antigen E In Solution
2968	97.1	73.3
2968G	67.1	14.6
2969	51.7	20.3
2969G	37.2	16.5
2970	92.2	34.2
2970G	92.7	27.2
2971	23.4	11.6
2971G	18.8	18.9
2972	67.1	38.8
2972G	64.5	39.2
2973	77.7	27.0
2973G	51.1	20.7
2974	57.8	12.4
2974G	69.9	17.6
2975	49.4	18.2
2975G	32.0	19.5
2976	1.0	1.0
2976G	50.4	20.4

[00287] In the first LUMINEX™ experiment described above, 80 common light chain antibodies containing the Vκ1-39Jκ5 engineered light chain were tested for their ability to block Ligand Y binding to Antigen E-labeled beads. Of these 80 common light chain

5 antibodies, 68 demonstrated >50% blocking, while 12 demonstrated <50% blocking (6 at 25-50% blocking and 6 at <25% blocking). For the 18 common light chain antibodies

containing the V κ 3-20J κ 1 engineered light chain, 12 demonstrated >50% blocking, while 6 demonstrated <50% blocking (3 at 25-50% blocking and 3 at <25% blocking) of Ligand Y binding to Antigen E-labeled beads.

[00288] In the second LUMINEX™ experiment described above, the same 80 common light chain antibodies containing the V κ 1-39J κ 5 engineered light chain were tested for their ability to block binding of Antigen E to Ligand Y-labeled beads. Of these 80 common light chain antibodies, 36 demonstrated >50% blocking, while 44 demonstrated <50% blocking (27 at 25-50% blocking and 17 at <25% blocking). For the 18 common light chain antibodies containing the V κ 3-20J κ 1 engineered light chain, 1 demonstrated >50% blocking, while 17 demonstrated <50% blocking (5 at 25-50% blocking and 12 at <25% blocking) of Antigen E binding to Ligand Y-labeled beads.

[00289] The data of Tables 7 and 8 establish that the rearrangements described in Tables 5 and 6 generated anti-Antigen E-specific common light chain antibodies that blocked binding of Ligand Y to its cognate receptor Antigen E with varying degrees of efficacy, which is consistent with the anti-Antigen E common light chain antibodies of Tables 5 and 6 comprising antibodies with overlapping and non-overlapping epitope specificity with respect to Antigen E.

Example 8

Determination of Blocking Ability of Antigen-Specific Common Light Chain Antibodies by ELISA

[00290] Human common light chain antibodies raised against Antigen E were tested for their ability to block Antigen E binding to a Ligand Y-coated surface in an ELISA assay.

[00291] Ligand Y was coated onto 96-well plates at a concentration of 2 μ g/mL diluted in PBS and incubated overnight followed by washing four times in PBS with 0.05% Tween-20. The plate was then blocked with PBS (Irvine Scientific, Santa Ana, CA) containing 0.5% (w/v) BSA (Sigma-Aldrich Corp., St. Louis, MO) for one hour at room temperature. In a separate plate, supernatants containing anti-Antigen E common light chain antibodies were diluted 1:10 in buffer. A mock supernatant with the same components of the antibodies was used as a negative control. Antigen E-mmH (described above) was added to a final concentration of 0.150 nM and incubated for one hour at room temperature. The antibody/Antigen E-mmH mixture was then added to the plate containing Ligand Y and incubated for one hour at room temperature. Detection of Antigen E-mmH bound to Ligand

Y was determined with Horse-Radish Peroxidase (HRP) conjugated to anti-Penta-His antibody (Qiagen, Valencia, CA) and developed by standard colorimetric response using tetramethylbenzidine (TMB) substrate (BD Biosciences, San Jose, CA) neutralized by sulfuric acid. Absorbance was read at OD450 for 0.1 sec. Background absorbance of a sample without Antigen E was subtracted from all samples. Percent blocking was calculated by division of the background-subtracted MFI of each sample by the adjusted negative control value, multiplying by 100 and subtracting the resulting value from 100.

[00292] Tables 9 and 10 show the percent blocking for all 98 anti-Antigen E common light chain antibodies tested in the ELISA assay. ND: not determined under current experimental conditions.

Table 9

Vκ1-39Jκ5			
Common Light Chain Antibodies			
Antibody	% Blocking of Antigen E In Solution	Antibody	% Blocking of Antigen E In Solution
2948	21.8	3015	23.7
2948G	22.9	3015G	10.2
2949	79.5	3016	78.1
2949G	71.5	3016G	37.4
2950	80.4	3017	61.6
2950G	30.9	3017G	25.2
2952	66.9	3018	40.6
2952G	47.3	3018G	14.5
2954	55.9	3019	94.6
2954G	44.7	3019G	92.3
2955	12.1	3020	80.8
2955G	25.6	3020G	ND
2964	34.8	3021	7.6
2964G	47.7	3021G	20.7

2978	90.0	3022	2.4
2978G	90.2	3022G	15.0
2982	59.0	3023	9.1
2982G	20.4	3023G	19.2
2985	10.5	3024	7.5
2985G	ND	3024G	15.2
2987	31.4	3025	ND
2987G	ND	3025G	13.9
2996	29.3	3027	61.4
2996G	ND	3027G	82.7
2997	48.7	3028	40.3
2997G	ND	3028G	12.3
3004	16.7	3030	ND
3004G	3.5	3030G	9.5
3005	87.2	3032	ND
3005G	54.3	3032G	13.1
3010	74.5	3033	77.1
3010G	84.6	3033G	32.9
3011	19.4	3036	17.6
3011G	ND	3036G	24.6
3012	45.0	3041	59.3
3012G	12.6	3041G	30.7
3013	39.0	3042	39.9
3013G	9.6	3042G	16.1
3014	5.2	3043	57.4
3014G	17.1	3043G	46.1

Table 10

Vκ3-20Jκ1 Common Light Chain Antibodies			
Antibody	% Blocking of Antigen E In Solution	Antibody	% Blocking of Antigen E In Solution
2968	68.9	2972G	35.7
2968G	15.2	2973	20.7
2969	10.1	2973G	23.1
2969G	23.6	2974	ND
2970	34.3	2974G	22.0
2970G	41.3	2975	8.7
2971	6.3	2975G	19.2
2971G	27.1	2976	4.6
2972	9.6	2976G	26.7

[00293] As described in this Example, of the 80 common light chain antibodies containing the Vκ1-39Jκ5 engineered light chain tested for their ability to block Antigen E binding to a Ligand Y-coated surface, 22 demonstrated >50% blocking, while 58 demonstrated <50% blocking (20 at 25-50% blocking and 38 at <25% blocking). For the 18 common light chain antibodies containing the Vκ3-20Jκ1 engineered light chain, one demonstrated >50% blocking, while 17 demonstrated <50% blocking (5 at 25-50% blocking and 12 at <25% blocking) of Antigen E binding to a Ligand Y-coated surface.

[00294] These results are also consistent with the Antigen E-specific common light chain antibody pool comprising antibodies with overlapping and non-overlapping epitope specificity with respect to Antigen E.

Example 9

BIACORE™ Affinity Determination for Antigen-Specific Common Light Chain

Antibodies

[00295] Equilibrium dissociation constants (K_D) for selected antibody supernatants were determined by SPR (Surface Plasmon Resonance) using a BIACORE™ T100 instrument (GE Healthcare). All data was obtained using HBS-EP (10mM Hepes, 150mM NaCl, 0.3mM EDTA, 0.05% Surfactant P20, pH 7.4) as both the running and sample buffers, at 25°C.

- 5 Antibodies were captured from crude supernatant samples on a CM5 sensor chip surface previously derivatized with a high density of anti-human Fc antibodies using standard amine coupling chemistry. During the capture step, supernatants were injected across the anti-human Fc surface at a flow rate of 3 μ L/min, for a total of 3 minutes. The capture step was followed by an injection of either running buffer or analyte at a concentration of 100 nM for
- 10 2 minutes at a flow rate of 35 μ L/min. Dissociation of antigen from the captured antibody was monitored for 6 minutes. The captured antibody was removed by a brief injection of 10 mM glycine, pH 1.5. All sensorgrams were double referenced by subtracting sensorgrams from buffer injections from the analyte sensorgrams, thereby removing artifacts caused by dissociation of the antibody from the capture surface. Binding data for each antibody was fit
- 15 to a 1:1 binding model with mass transport using BIAcore T100 Evaluation software v2.1. Results are shown in Tables 11 and 12.

Table 11

Vk1-39Jk5					
Common Light Chain Antibodies					
Antibody	100 nM Antigen E		Antibody	100 nM Antigen E	
	K_D (nM)	$T_{1/2}$ (min)		K_D (nM)	$T_{1/2}$ (min)
2948	8.83	28	3015	29.1	11
2948G	95.0	1	3015G	65.9	0
2949	3.57	18	3016	4.99	17
2949G	6.37	9	3016G	18.9	4
2950	4.91	17	3017	9.83	8
2950G	13.6	5	3017G	55.4	2
2952	6.25	7	3018	11.3	36
2952G	7.16	4	3018G	32.5	3

2954	2.37	24	3019	1.54	59
2954G	5.30	9	3019G	2.29	42
2955	14.4	6	3020	5.41	39
2955G	12.0	4	3020G	41.9	6
2964	14.8	6	3021	50.1	6
2964G	13.0	9	3021G	26.8	4
2978	1.91	49	3022	25.7	17
2978G	1.80	58	3022G	20.8	12
2982	6.41	19	3023	263	9
2982G	16.3	9	3023G	103	5
2985	64.4	9	3024	58.8	7
2985G	2.44	8	3024G	7.09	10
2987	21.0	11	3025	35.2	6
2987G	37.6	4	3025G	42.5	8
2996	10.8	9	3027	7.15	6
2996G	24.0	2	3027G	4.24	18
2997	7.75	19	3028	6.89	37
2997G	151	1	3028G	7.23	22
3004	46.5	14	3030	46.2	7
3004G	1.93	91	3030G	128	3
3005	2.35	108	3032	53.2	9
3005G	6.96	27	3032G	13.0	1
3010	4.13	26	3033	4.61	17
3010G	2.10	49	3033G	12.0	5
3011	59.1	5	3036	284	12
3011G	41.7	5	3036G	18.2	10
3012	9.71	20	3041	6.90	12
3012G	89.9	2	3041G	22.9	2
3013	20.2	20	3042	9.46	34

3013G	13.2	4	3042G	85.5	3
3014	213	4	3043	9.26	29
3014G	36.8	3	3043G	13.1	22

Table 12V κ 3-20J κ 1

Common Light Chain Antibodies

Antibody	100 nM Antigen E		Antibody	100 nM Antigen E	
	K _D (nM)	T _{1/2} (min)		K _D (nM)	T _{1/2} (min)
2968	5.50	8	2973	5.35	39
2968G	305	0	2973G	11.0	44
2969	34.9	2	2974	256	0
2969G	181	1	2974G	138	0
2970G	12.3	3	2975	38.0	2
2971G	32.8	22	2975G	134	1
2972	6.02	13	2976	6.73	10
2972G	74.6	26	2976G	656	8

[00296] The binding affinities of common light chain antibodies comprising the rearrangements shown in Tables 5 and 6 vary, with nearly all exhibiting a K_D in the nanomolar range. The affinity data is consistent with the common light chain antibodies resulting from the combinatorial association of rearranged variable domains described in Tables 5 and 6 being high-affinity, clonally selected, and somatically mutated. Coupled with data previously shown, the common light chain antibodies described in Tables 5 and 6 comprise a collection of diverse, high-affinity antibodies that exhibit specificity for one or more epitopes on Antigen E.

Example 10**Determination of Binding Specificities of Antigen-Specific Common Light Chain**

Antibodies by LUMINEX™ Assay

[00297] Selected anti-Antigen E common light chain antibodies were tested for their ability to bind to the ECD of Antigen E and Antigen E ECD variants, including the cynomolgous monkey ortholog (*Mf* Antigen E), which differs from the human protein in approximately 10% of its amino acid residues; a deletion mutant of Antigen E lacking the last 10 amino acids from the C-terminal end of the ECD (Antigen E- Δ CT); and two mutants containing an alanine substitution at suspected locations of interaction with Ligand Y (Antigen E-Ala1 and AntigenE-Ala2). The Antigen E proteins were produced in CHO cells and each contained a myc-myc-His C-terminal tag.

[00298] For the binding studies, Antigen E ECD protein or variant protein (described above) from 1 mL of culture medium was captured by incubation for 2 hr at room temperature with 1×10^6 microsphere (LUMINEX™) beads covalently coated with an anti-myc monoclonal antibody (MAb 9E10, hybridoma cell line CRL-1729™; ATCC, Manassas, VA). The beads were then washed with PBS before use. Supernatants containing anti-

Antigen E common light chain antibodies were diluted 1:4 in buffer and added to 96-well filter plates. A mock supernatant with no antibody was used as negative control. The beads containing the captured Antigen E proteins were then added to the antibody samples (3000 beads per well) and incubated overnight at 4°C. The following day, the sample beads were washed and the bound common light chain antibody was detected with a R-phycoerythrin-conjugated anti-human IgG antibody. The fluorescence intensity of the beads (approximately 100 beads counted for each antibody sample binding to each Antigen E protein) was measured with a LUMINEX™ flow cytometry-based analyzer, and the median fluorescence intensity (MFI) for at least 100 counted beads per bead/antibody interaction was recorded. Results are shown in Tables 13 and 14.

Table 13

Vκ1-39Jκ5 Common Light Chain Antibodies					
Antibody	Mean Fluorescence Intensity (MFI)				
	Antigen E- ECD	Antigen E- Δ CT	Antigen E- Ala1	Antigen E- Ala2	<i>Mf</i> Antigen E
2948	1503	2746	4953	3579	1648

2948G	537	662	2581	2150	863
2949	3706	4345	8169	5678	5142
2949G	3403	3318	7918	5826	5514
2950	3296	4292	7756	5171	4749
2950G	2521	2408	7532	5079	3455
2952	3384	1619	1269	168	911
2952G	3358	1001	108	55	244
2954	2808	3815	7114	5039	3396
2954G	2643	2711	7620	5406	3499
2955	1310	2472	4738	3765	1637
2955G	1324	1802	4910	3755	1623
2964	5108	1125	4185	346	44
2964G	4999	729	4646	534	91
2978	6986	2800	14542	10674	8049
2978G	5464	3295	11652	8026	6452
2982	4955	2388	13200	9490	6772
2982G	3222	2013	8672	6509	4949
2985	1358	832	4986	3892	1669
2985G	43	43	128	244	116
2987	3117	1674	7646	5944	2546
2987G	3068	1537	9202	6004	4744
2996	4666	1917	12875	9046	6459
2996G	2752	1736	8742	6150	4873
2997	5164	2159	12167	8361	5922
2997G	658	356	3392	2325	1020
3004	2794	1397	8542	6268	3083
3004G	2753	1508	8267	5808	4345
3005	5683	2221	12900	9864	5868
3005G	4344	2732	10669	7125	5880

3010	4829	1617	2642	3887	44
3010G	3685	1097	2540	3022	51
3011	2859	2015	7855	5513	3863
3011G	2005	1072	6194	4041	3181
3012	3233	2221	8543	5637	3307
3012G	968	378	3115	2261	1198
3013	2343	1791	6715	4810	2528
3013G	327	144	1333	1225	370
3014	1225	1089	5436	3621	1718
3014G	1585	851	5178	3705	2411
3015	3202	2068	8262	5554	3796
3015G	1243	531	4246	2643	1611
3016	4220	2543	8920	5999	5666
3016G	2519	1277	6344	4288	4091
3017	3545	2553	8700	5547	5098
3017G	1972	1081	5763	3825	3038
3018	2339	1971	6140	4515	2293
3018G	254	118	978	1020	345
3019	5235	1882	7108	4249	54
3019G	4090	1270	4769	3474	214
3020	3883	3107	8591	6602	4420
3020G	2165	1209	6489	4295	2912
3021	1961	1472	6872	4641	2742
3021G	2091	1005	6430	3988	2935
3022	2418	793	7523	2679	36
3022G	2189	831	6182	3051	132
3023	1692	1411	5788	3898	2054
3023G	1770	825	5702	3677	2648
3024	1819	1467	6179	4557	2450

3024G	100	87	268	433	131
3025	1853	1233	6413	4337	2581
3025G	1782	791	5773	3871	2717
3027	4131	1018	582	2510	22
3027G	3492	814	1933	2596	42
3028	4361	2545	9884	5639	975
3028G	2835	1398	7124	3885	597
3030	463	277	1266	1130	391
3030G	943	302	3420	2570	1186
3032	2083	1496	6594	4402	2405
3032G	295	106	814	902	292
3033	4409	2774	8971	6331	5825
3033G	2499	1234	6745	4174	4210
3036	1755	1362	6137	4041	1987
3036G	2313	1073	6387	4243	3173
3041	3674	2655	8629	5837	4082
3041G	2519	1265	6468	4274	3320
3042	2653	2137	7277	5124	3325
3042G	1117	463	4205	2762	1519
3043	3036	2128	7607	5532	3366
3043G	2293	1319	6573	4403	3228

Table 14

Vκ3-20Jκ1 Common Light Chain Antibodies					
Antibody	Mean Fluorescence Intensity (MFI)				
	Antigen E- ECD	Antigen E- ΔCT	Antigen E- Ala1	Antigen E- Ala2	<i>Mf</i> Antigen E
2968	6559	3454	14662	3388	29

2968G	2149	375	9109	129	22
2969	2014	1857	7509	5671	3021
2969G	1347	610	6133	4942	2513
2970	5518	1324	14214	607	32
2970G	4683	599	12321	506	31
2971	501	490	2506	2017	754
2971G	578	265	2457	2062	724
2972	2164	2158	8408	6409	3166
2972G	1730	992	6364	4602	2146
2973	3527	1148	3967	44	84
2973G	1294	276	1603	28	44
2974	1766	722	8821	241	19
2974G	2036	228	8172	135	26
2975	1990	1476	8669	6134	2468
2975G	890	315	4194	3987	1376
2976	147	140	996	1079	181
2976G	1365	460	6024	3929	1625

[00299] The anti-Antigen E common light chain antibody supernatants exhibited high specific binding to the beads linked to Antigen E-ECD. For these beads, the negative control mock supernatant resulted in negligible signal (<10 MFI) when combined with the Antigen E-ECD bead sample, whereas the supernatants containing anti-Antigen E common light chain antibodies exhibited strong binding signal (average MFI of 2627 for 98 antibody supernatants; MFI > 500 for 91/98 antibody samples).

[00300] As a measure of the ability of the selected anti-Antigen E common light chain antibodies to identify different epitopes on the ECD of Antigen E, the relative binding of the antibodies to the variants were determined. All four Antigen E variants were captured to the anti-myc LUMINEX™ beads as described above for the native Antigen E-ECD binding studies, and the relative binding ratios ($MFI_{\text{variant}}/MFI_{\text{Antigen E-ECD}}$) were determined. For 98 tested common light chain antibody supernatants shown in Tables 12 and 13, the average ratios ($MFI_{\text{variant}}/MFI_{\text{Antigen E-ECD}}$) differed for each variant, likely reflecting different capture

amounts of proteins on the beads (average ratios of 0.61, 2.9, 2.0, and 1.0 for Antigen E-ΔCT, Antigen E-Ala1, Antigen E-Ala2, and *Mf* Antigen E, respectively). For each protein variant, the binding for a subset of the 98 tested common light chain antibodies showed greatly reduced binding, indicating sensitivity to the mutation that characterized a given variant. For example, 19 of the common light chain antibody samples bound to the *Mf* Antigen E with $MFI_{\text{variant}}/MFI_{\text{Antigen E-ECD}}$ of <8%. Since many in this group include high or moderately high affinity antibodies (5 with $K_D < 5\text{nM}$, 15 with $K_D < 50\text{ nM}$), it is likely that the lower signal for this group results from sensitivity to the sequence (epitope) differences between native Antigen E-ECD and a given variant rather than from lower affinities.

[00301] These data establish that the common light chain antibodies described in Tables 5 and 6 represent a diverse group of Antigen-E-specific common light chain antibodies that specifically recognize more than one epitope on Antigen E.

Example 11

Light Chain Shuffling in Common Light Chain Antibodies

[00302] Heavy chains of selected antigen-specific common light chain antibodies were tested for binding to Antigen E after repairing the heavy chains with either a germline Vκ1-39Jκ5 or a germline Vκ3-20Jκ1 engineered light chain (as described in Example 1).

[00303] Briefly, 247 heavy chains of Antigen E-specific common light chain antibodies (Vκ1-39Jκ5 and Vκ3-20Jκ1) were transfected with either a germline Vκ1-39 or a germline Vκ3-20 engineered light chain and rescreened for binding to Antigen E by a LUMINEX™ assay (as described in Example 7 and Example 10). Binding to Antigen E was confirmed by BIACORE™ (as described in Example 9). The results are shown in Table 15.

[00304] As shown in this Example, twenty-eight common light chain antibodies specific for Antigen E were capable of binding to Antigen E when repaired with a germline form of the light chain.

Table 15

Original Light Chain	Repaired Light Chain	No. Tested	No. Confirmed Binders
1-39	1-39	198	23
3-20	3-20	49	5

Example 12**Heavy Chain Gene Usage and Somatic Hypermutation Frequency in Common Light Chain Antibodies**

5 [00305] Heavy and light chain sequences (>6000) of antibodies raised in
 VELCOIMMUNE® mice (*e.g.*, US 6,596,541 and US 7,105,348) were compiled with heavy
 and light chain sequences (>600) of common light chain antibodies obtained by a multi-
 antigen immunization scheme employing the engineered light chain mice (described above)
 to compare heavy chain gene segment usage and somatic hypermutation frequencies of the
 10 antibody chains.

[00306] **Heavy Chain Gene Usage.** Heavy and light chain sequences obtained from
 VELOCIMMUNE® mice containing a replacement of the endogenous mouse heavy chain
 locus with human V_H, D_H, and J_H gene segments and a replacement of the endogenous mouse
 κ light chain locus with either the engineered germline Vκ1-39Jκ5 human light chain region
 15 or the engineered germline Vκ3-20Jκ1 human light chain region (as described in Example 2)
 immunized with a human cell-surface receptor (Antigen E), a heterodimer of two human cell-
 surface glycoproteins (Antigen F), a human cytokine receptor (Antigen G) and a human
 tumor differentiation antigen (Antigen H) were analyzed for heavy chain gene segment usage
 and V_H and J_H gene segments were recorded. Results are shown in Tables 16 – 18.

20 Percentages in Tables 16 – 18 represent rounded values and in some cases may not equal
 100% when added together.

[00307] Table 16 sets forth the percent heavy chain family usage for antibodies from
 VELCOIMMUNE® mice (VI), antibodies from VELCOIMMUNE® mice having a cognate
 Vκ1-39 light chain (VI – Vκ1-39), antibodies from Vκ1-39 engineered light chain mice
 25 (Vκ1-39), antibodies from VELCOIMMUNE® mice having a cognate Vκ3-20 light chain
 (VI – Vκ3-20), and antibodies from Vκ3-20 engineered light chain mice (Vκ3-20). Table 17
 sets forth the percent V_H and J_H gene usage for antibodies from VELCOIMMUNE® mice
 (VI), antibodies from VELCOIMMUNE® mice having a cognate Vκ1-39 light chain (VI –
 Vκ1-39), antibodies from Vκ1-39 engineered light chain mice (Vκ1-39), antibodies from
 30 VELCOIMMUNE® mice having a cognate Vκ3-20 light chain (VI – Vκ3-20), and
 antibodies from Vκ3-20 engineered light chain mice (Vκ3-20). Table 18 sets forth the
 percent V_H gene usage for antibodies from Vκ1-39 engineered light chain mice (Vκ1-39
 Mice) from each immunization group (Antigens E, F, G and H) and the percent V_H gene

usage for antibodies from Vκ3-20 engineered light chain mice (Vκ3-20 Mice) from selected immunization groups (Antigens E and G).

[00308] As shown in this Example, heavy chain gene usage for antigens tested in Vκ1-39Jκ5-engineered light chain mice was characterized by a preponderance of V_H family III subgroups (V_H3-7, V_H3-9, V_H3-11, V_H3-13, V_H3-20, V_H3-23, V_H3-30, V_H3-33 and V_H3-48). Notable usage of other V_H family subgroups was characterized by usage of V_H1-18, V_H1-69, V_H2-5, V_H4-59 and V_H6-1. For antigens tested in Vκ3-20Jκ1 engineered light chain mice, heavy chain gene usage was characterized by a preponderance of V_H family III, V_H family IV and V_H family V subgroups (V_H3-11, V_H3-30, V_H3-33, V_H4-39, V_H4-59 and V_H5-51). Notable usage of other V_H family subgroups was characterized by usage of V_H1-18, V_H1-69, V_H2-70 and V_H6-1.

[00309] Somatic Hypermutation Frequency. Heavy and light chains from antibodies raised in VELCOIMMUNE® mice and the engineered light chain mice (described above) were aligned to germline sequences according to the heavy and light chain gene usage demonstrated for each heavy and/or light chain. Amino acid changes for each framework region (FW) and complementarity determining region (CDR) for both heavy and light chain of each sequence were calculated. Results are shown in Tables 19 – 22. Percentages in Tables 21 – 24 represent rounded values and in some cases may not equal 100% when added together.

[00310] Table 19 sets forth the number of amino acid (AA) changes observed in each FW and CDR region of heavy chains of antibodies from VELCOIMMUNE® mice, heavy chains of antibodies from Vκ1-39 engineered light chain mice (Vκ1-39 Mice) and heavy chains of antibodies from Vκ3-20 engineered light chain mice (Vκ3-20 Mice). Table 20 sets forth the number of amino acid (AA) changes observed in each FW and CDR region of light chains of antibodies from VELCOIMMUNE® mice, the light chain of antibodies from Vκ1-39 engineered mice (Vκ1-39 Mice) and the light chain of antibodies from Vκ3-20 engineered mice (Vκ3-20 Mice). Table 21 sets forth the number of amino acid (AA) changes observed in each FW and CDR region of heavy chains of antibodies from Vκ1-39 engineered light chain mice (Vκ1-39 Mice) for selected immunization groups (Antigens E, F and H). Table 22 sets forth the number of amino acid (AA) changes observed in each FW and CDR region of heavy chains of antibodies from Vκ3-20 engineered light chain mice (Vκ3-20 Mice) for selected immunization groups (Antigens E and G).

Table 16

V _H Family	VI	VI – V _K 1-39	V _K 1-39	VI – V _K 3-20	V _K 3-20
1	9.0	14.8	3.3	7.1	4.9
2	2.2	1.8	4.6	0	1.6
3	77.8	69.8	77.3	61.4	29.5
4	8.4	8.3	11.2	27.1	39.3
5	0.9	0	0.7	4.3	23.0
6	1.7	5.3	3.0	0	1.6

Table 17

V _H Gene	VI	VI – V _K 1-39	V _K 1-39	VI – V _K 3-20	V _K 3-20
1-2	3.9	8.3	0	2.9	0
1-3	0	0	0	0	0
1-8	1.3	0.6	0	1.4	0
1-18	3.0	0.6	1.3	2.1	1.6
1-24	0.4	3.6	0	0.7	0
1-46	0.1	0	0	0	0
1-58	0	0	0	0	0
1-69	0.3	1.8	2.0	0	3.3
2-5	1.9	0	4.6	0	0
2-26	0.2	1.8	0.0	0	0
2-70	0.1	0	0	0	1.6
3-7	3.0	14.8	0	1.4	0
3-9	8.5	3.6	29.6	16.4	0
3-11	5.4	10.7	0	7.1	1.6
3-13	3.2	1.8	0.7	2.1	0
3-15	4.0	4.7	0.3	0.7	0

3-20	1.0	0.6	0.3	5.0	0
3-21	0.8	0.6	0	2.1	0
3-23	20.4	8.9	3.3	8.6	0
3-30	17.6	4.1	35.2	12.9	1.6
3-33	12.6	14.8	0	5.0	26.2
3-43	0.2	0.6	0	0	0
3-48	0.8	1.2	7.2	0	0
3-53	0.3	3.6	0.3	0	0
3-64	0	0	0.3	0	0
3-72	0	0	0	0	0
3-73	0	0	0	0	0
4-31	2.7	0	0.7	8.6	0
4-34	1.8	0.6	0.3	14.3	0
4-39	1.6	0.6	3.0	2.1	14.8
4-59	2.3	7.1	7.2	2.1	24.6
5-51	0.9	0	0.7	4.3	23.0
6-1	1.7	5.3	3.0	0	1.6

J_H Gene VI VI – Vκ1-39 Vκ1-39 VI – Vκ3-20 Vκ3-20

1	1.5	1.2	7.1	0	0
2	4.5	2.4	0.7	5.0	26.9
3	10.5	16.6	13.1	13.6	26.9
4	44.0	34.3	32.3	50.7	9.6
5	9.6	10.1	16.8	7.9	1.9
6	29.7	35.5	30.0	22.9	34.6

Table 18

V _H Gene	Vκ1-39 Mice	Vκ3-20 Mice
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	Antigen E	Antigen F	Antigen G	Antigen H	Antigen E	Antigen G
1-2	0	0	0	0	0	0
1-3	0	0	0	0	0	0
1-8	0	0	0	0	0	0
1-18	0	0	0	8.3	0	3.1
1-24	0	0	0	0	0	0
1-46	0	0	0	0	0	0
1-58	0	0	0	0	0	0
1-69	2.9	0	25.0	0	0	6.3
2-5	8.2	0	0	0	0	0
2-26	0	0	0	0	0	0
2-70	0	0	0	0	0	3.1
3-7	0	0	0	0	0	0
3-9	1.2	98.8	0	14.6	0	0
3-11	0	0	0	0	0	3.1
3-13	0.6	0	25.0	0	0	0
3-15	0	1.2	0	0	0	0
3-20	0	0	25.0	0	0	0
3-21	0	0	0	0	0	0
3-23	4.1	0	25.0	4.2	0	0
3-30	62.9	0	0	0	3.4	0
3-33	0	0	0	0	13.8	37.5
3-43	0	0	0	0	0	0
3-48	0.6	0	0	43.8	0	0
3-53	1.6	0	0	0	0	0
3-64	1.6	0	0	0	0	0
3-72	0	0	0	0	0	0
3-73	0	0	0	0	0	0
4-31	0	0	0	4.2	0	0

4-34	0	0	0	2.1	0	0
4-39	5.3	0	0	0	31.0	0
4-59	11.8	0	0	4.2	3.4	43.8
5-51	1.2	0	0	0	48.3	0
6-1	0	0	0	18.8	0	3.1

Table 19

Heavy Chains of Antibodies from VELCOIMMUNE® Mice

AA Changes

	FW1	CDR1	FW2	CDR2	FW3	CDR3
0	63	32	36	26	12	82
1	23	32	41	31	22	17
2	9	25	17	23	27	1
3	4	10	5	16	13	0
4	0	1	1	3	12	0
>5	1	0	0	1	14	0

Heavy Chains of Antibodies from Vκ1-39 Mice

AA Changes

	FW1	CDR1	FW2	CDR2	FW3	CDR3
0	65	8	34	30	9	37
1	25	26	35	34	19	54
2	9	44	23	20	33	9
3	1	19	8	12	22	0
4	0	3	0	5	11	0
>5	1	0	0	0	7	0

Heavy Chains of Antibodies from Vκ3-20 Mice

AA Changes

	FW1	CDR1	FW2	CDR2	FW3	CDR3
0	57	8	54	16	8	93

1	41	43	34	39	21	7
2	2	25	10	18	20	0
3	0	15	2	21	13	0
4	0	10	0	3	20	0
>5	0	0	0	2	18	0

Table 20

Light Chains of Antibodies from VELCOIMMUNE® Mice

AA Changes

	FW1	CDR1	FW2	CDR2	FW3	CDR3
0	65	24	49	60	33	23
1	24	20	34	31	27	38
2	9	27	16	9	18	28
3	1	20	1	0	14	7
4	0	7	0	0	4	3
>5	1	1	0	0	3	0

Light Chains of Antibodies from Vκ1-39 Mice

AA Changes

	FW1	CDR1	FW2	CDR2	FW3	CDR3
0	91	75	80	90	71	63
1	9	19	17	10	21	27
2	0	5	1	1	5	8
3	0	0	1	0	2	1
4	0	0	0	0	2	1
>5	0	0	0	0	0	0

Light Chains of Antibodies from Vκ3-20 Mice

AA Changes

	FW1	CDR1	FW2	CDR2	FW3	CDR3
0	90	47	93	97	63	57

1	10	27	3	3	20	43
2	0	27	3	0	17	0
3	0	0	0	0	0	0
4	0	0	0	0	0	0
>5	0	0	0	0	0	0

Table 21

# AA Changes	Heavy Chains of Anti-Antigen E Antibodies from Vκ1-39 Mice					
	FW1	CDR1	FW2	CDR2	FW3	CDR3
0	75	8	49	41	14	36
1	21	25	33	35	25	52
2	4	43	14	18	28	12
3	0	20	4	5	16	0
4	0	5	0	1	12	0
>5	1	0	0	0	5	0

# AA Changes	Heavy Chains of Anti-Antigen F Antibodies from Vκ1-39 Mice					
	FW1	CDR1	FW2	CDR2	FW3	CDR3
0	52	0	6	6	2	15
1	35	24	32	35	15	78
2	11	59	46	22	49	7
3	0	17	16	24	29	0
4	0	0	0	12	4	0
>5	1	0	0	0	1	0

AA Changes Heavy Chains of Anti-Antigen H Antibodies from Vκ1-39 Mice

	FW1	CDR1	FW2	CDR2	FW3	CDR3
0	54	21	29	33	4	77
1	17	35	50	27	6	23
2	23	21	15	21	25	0
3	6	21	4	15	27	0
4	0	2	2	2	15	0
>5	0	0	0	2	23	0

Table 22

# AA Changes	Heavy Chains of Anti-Antigen E Antibodies from Vκ3-20 Mice					
	FW1	CDR1	FW2	CDR2	FW3	CDR3
0	79	17	62	24	17	90
1	21	28	34	55	31	10
2	0	28	3	21	24	0
3	0	14	0	0	10	0
4	0	14	0	0	3	0
>5	0	0	0	0	14	0

# AA Changes	Heavy Chains of Anti-Antigen G Antibodies from Vκ3-20 Mice					
	FW1	CDR1	FW2	CDR2	FW3	CDR3
0	38	0	47	9	0	97
1	59	56	34	25	13	3
2	3	22	16	16	16	0
3	0	16	3	41	16	0
4	0	6	0	6	34	0
>5	0	0	0	3	22	0

Example 13**Analysis of Heavy Chain Variable Region Segment Usage in Mice Having Universal Light Chain**

[00311] Splenocytes harvested from mice homozygous for a universal light chain (V κ 1-39J κ 5 or V κ 3-20J κ 1) at the endogenous light chain locus and homozygous for replacement of the endogenous heavy chain V_H region with human heavy chain V_H region were analyzed for heavy chain variable region segment usage of their IgM antibodies. One V κ 3-20J κ 1 and three V κ 1-39J κ 5 mice were used for analysis.

[00312] 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).

[00313] Double-stranded cDNA was prepared from splenic B cell mRNA by 5' RACE using the SMARTer Pico cDNA Synthesis Kit (Clontech). The Clontech reverse transcriptase and dNTPs were substituted with Superscript II and dNTPs from Invitrogen. V_H antibody repertoires were amplified from the cDNA using primers specific for IgM constant region (3' mIgM CH1 outer; SEQ ID NO:34: TCTTATCAGACAGGGGGCTCTC) and the SMARTer 5' RACE primer. PCR products were cleaned up 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 constant region (3' mIgM CH1 inner; SEQ ID NO:35: GGAAGACATTTGGGAAGGACTG). 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 the 454 GS Junior Titanium Series Lib-A emPCR Kit (Roche Diagnostics) and bidirectional sequencing using Roche 454 GS Junior instrument according to the manufacturer's protocols.

[00314] For 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 Ig sequences to human germline V, D and J segments database using local installation of igblast (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

5 was defined between conserved C codon and WGXXG motif for heavy chains. Heavy chain V, D, J segment gene usage for a V κ 3-20J κ 1 universal light chain mouse is shown in Table 23; and for V κ 1-39J κ 5 universal light chain mice is shown in Table 24 (with %IgM signifying a proportion of particular V, D, and J from total reads analyzed). Usage of various rearranged variable regions (VDJ segments; showing productive rearrangements only) for

10 V κ 3-20J κ 1 universal light chain mouse is shown in Table 25, and for V κ 1-39J κ 5 universal light chain mice is shown in Table 26 (with % values signifying proportion of reads with a particular VDJ from the total population of productive rearrangements). D_H5-5 and D_H5-18 regions have the same nucleic acid sequence, so their % usage in Tables below is combined, and indicated as “D_H5-18” only. D_H4-4 and D_H4-11 regions have the same nucleic acid

15 sequence, so their % usage in Tables below is combined and indicated as “D_H4-11” only. The data in Tables 23, 25 and 26 is representative data from one mouse each, the data in Table 24 is representative data from three mice.

Table 23

Human V _H		Human D _H		Human J _H	
V _H Segment	% IgM	D _H Segment	% IgM	J _H Segment	% IgM
6-1	7.2	7-27	9.83	1	1.65
1-2	4.32	1-26	9.28	2	6.83
1-3	0.2	6-25	0.59	3	13.1
2-5	0.39	5-24	2.71	4	46.96
3-7	2.41	4-23	1.5	5	7.35
1-8	6.59	3-22	1.26	6	22.95
3-9	0.89	2-21	0.93		
3-11	0.93	1-20	2.99		
3-13	0.59	6-19	2.39		
3-15	1.54	5-18	3.9		
1-18	5.36	4-17	1.63		
3-20	0.26	3-16	2		
3-21	3.43	2-15	0.91		
3-23	3.67	1-14	0.63		
1-24	1.65	6-13	10.41		
2-26	0.39	5-12	1.78		
4-28	0.28	4-11	3.3		
3-30	0.95	3-10	5.62		
4-31	4.06	3-9	2.32		
3-33	2.8	2-8	1.17		
4-34	8.18	1-7	14.14		
4-39	22.17	6-6	9.91		
3-43	1.41	3-3	4.9		
1-46	0.41	2-2	2.47		
3-48	1.15	1-1	3.43		
3-49	0.26				
5-51	2.62				

Human V _H		Human D _H		Human J _H	
V _H Segment	% IgM	D _H Segment	% IgM	J _H Segment	% IgM
3-53	1.04				
1-58	0.5				
4-59	11.21				
4-61	0.02				
3-64	0.15				
3-66	0.04				
1-69	1.93				
2-70	0.63				
3-72	0.13				
3-73	0.04				

Table 24

Human V _H			Human D _H			Human J _H		
V _H Segment	% IgM	Std Dev	D _H Segment	% IgM	Std Dev	J _H Segment	% IgM	Std Dev
6-1	3.3	1.59	7-27	6.0	0.75	1	1.9	0.5
1-2	1.5	1.17	1-26	9.0	0.69	2	3.3	0.7
1-3	0.6	0.46	6-25	0.8	0.69	3	10.8	0.9
2-5	3.2	1.42	5-24	4.4	0.95	4	51.9	4.0
3-7	6.5	2.16	4-23	1.3	0.44	5	7.6	0.4
1-8	3.8	1.11	3-22	1.2	0.39	6	20.2	2.2
3-9	2.4	0.33	2-21	1.6	0.85			
3-11	1.5	0.51	1-20	3.2	0.66			
3-13	3.7	1.12	6-19	2.7	0.22			
3-15	3.4	1.00	5-18	4.1	1.75			
1-18	6.5	1.41	4-17	1.5	0.43			
3-20	0.6	0.27	3-16	1.6	0.20			
3-21	4.6	0.86	2-15	1.1	0.28			

Human V _H			Human D _H			Human J _H		
V _H Segment	% IgM	Std Dev	D _H Segment	% IgM	Std Dev	J _H Segment	% IgM	Std Dev
3-23	7.5	1.24	1-14	1.6	0.25			
1-24	0.4	0.17	6-13	9.1	0.66			
2-26	3.1	2.98	5-12	2.9	0.49			
4-28	0.4	0.52	4-11	3.7	0.87			
3-30	2.0	0.69	3-10	5.9	1.57			
4-31	1.4	0.30	3-9	1.8	0.46			
3-33	4.7	0.42	2-8	1.1	0.20			
4-34	5.9	3.42	1-7	15.1	0.64			
4-39	5.2	1.11	6-6	9.7	1.49			
3-43	0.9	0.45	3-3	3.6	0.95			
1-46	0.4	0.05	2-2	3.5	1.39			
3-48	4.6	1.38	1-1	3.7	0.56			
3-49	0.2	0.09						
5-51	1.2	0.91						
3-53	1.1	0.70						
1-58	0.1	0.05						
4-59	8.4	1.68						
4-61	0.1	0.08						
3-64	1.1	0.68						
3-66	0.1	0.05						
1-69	1.5	0.52						
2-70	5.1	3.73						
3-72	0.4	0.36						
3-73	0.2							

Table 25

Human V _H	Human J _H	Human D _H	%
IGHV4-39	IGHJ4	IGHD1-26	2.04
IGHV4-39	IGHJ6	IGHD7-27	1.69
IGHV4-39	IGHJ4	IGHD7-27	1.65
IGHV4-39	IGHJ4	IGHD6-6	1.48
IGHV3-7	IGHJ4	IGHD2-2	1.39
IGHV4-59	IGHJ4	IGHD6-6	1.22
IGHV4-39	IGHJ2	IGHD6-13	1.13
IGHV4-39	IGHJ4	IGHD6-13	1.13
IGHV4-39	IGHJ4	IGHD3-10	1.04
IGHV4-39	IGHJ4	IGHD1-1	0.95
IGHV1-8	IGHJ6	IGHD1-7	0.91
IGHV4-59	IGHJ4	IGHD6-13	0.87
IGHV4-39	IGHJ4	IGHD1-7	0.82
IGHV1-18	IGHJ3	IGHD7-27	0.78
IGHV4-39	IGHJ4	IGHD6-19	0.78
IGHV1-2	IGHJ2	IGHD6-13	0.74
IGHV4-31	IGHJ3	IGHD7-27	0.74
IGHV4-59	IGHJ6	IGHD6-6	0.69
IGHV3-43	IGHJ6	IGHD6-13	0.65
IGHV4-39	IGHJ4	IGHD3-3	0.65
IGHV1-8	IGHJ4	IGHD1-7	0.61
IGHV4-34	IGHJ6	IGHD6-6	0.61
IGHV1-8	IGHJ6	IGHD6-13	0.56
IGHV4-39	IGHJ3	IGHD1-26	0.56
IGHV4-59	IGHJ6	IGHD1-7	0.56
IGHV5-51	IGHJ6	IGHD1-7	0.56
IGHV1-2	IGHJ4	IGHD2-2	0.52
IGHV4-39	IGHJ4	IGHD5-18	0.52

Human V _H	Human J _H	Human D _H	%
IGHV4-59	IGHJ4	IGHD3-10	0.52
IGHV6-1	IGHJ4	IGHD1-7	0.52
IGHV6-1	IGHJ4	IGHD7-27	0.52
IGHV1-2	IGHJ4	IGHD1-26	0.48
IGHV3-11	IGHJ3	IGHD1-20	0.48
IGHV4-31	IGHJ4	IGHD7-27	0.48
IGHV4-34	IGHJ6	IGHD1-7	0.48
IGHV4-39	IGHJ4	IGHD3-9	0.48
IGHV4-39	IGHJ6	IGHD1-7	0.48
IGHV4-59	IGHJ4	IGHD1-7	0.48
IGHV4-59	IGHJ6	IGHD1-26	0.48
IGHV4-59	IGHJ6	IGHD3-10	0.48
IGHV1-18	IGHJ4	IGHD1-7	0.43
IGHV1-8	IGHJ4	IGHD3-3	0.43
IGHV3-7	IGHJ4	IGHD6-6	0.43
IGHV4-39	IGHJ4	IGHD3-16	0.43
IGHV4-59	IGHJ4	IGHD1-26	0.43
IGHV6-1	IGHJ4	IGHD1-26	0.43
IGHV1-2	IGHJ4	IGHD6-13	0.39
IGHV4-34	IGHJ4	IGHD6-6	0.39
IGHV4-39	IGHJ3	IGHD6-6	0.39
IGHV4-59	IGHJ3	IGHD7-27	0.39
IGHV6-1	IGHJ4	IGHD1-1	0.39
IGHV6-1	IGHJ4	IGHD3-22	0.39
IGHV1-18	IGHJ4	IGHD1-26	0.35
IGHV1-69	IGHJ4	IGHD6-6	0.35
IGHV3-21	IGHJ4	IGHD6-6	0.35
IGHV4-28	IGHJ4	IGHD1-20	0.35

Human V _H	Human J _H	Human D _H	%
IGHV4-39	IGHJ5	IGHD1-7	0.35
IGHV4-59	IGHJ4	IGHD5-18	0.35
IGHV6-1	IGHJ4	IGHD6-13	0.35
IGHV1-2	IGHJ4	IGHD1-7	0.30
IGHV3-21	IGHJ6	IGHD3-10	0.30
IGHV3-23	IGHJ4	IGHD6-13	0.30
IGHV3-43	IGHJ6	IGHD3-3	0.30
IGHV4-34	IGHJ4	IGHD1-7	0.30
IGHV4-34	IGHJ5	IGHD3-3	0.30
IGHV4-34	IGHJ6	IGHD6-19	0.30
IGHV4-59	IGHJ3	IGHD5-18	0.30
IGHV4-59	IGHJ6	IGHD6-13	0.30
IGHV5-51	IGHJ5	IGHD6-19	0.30
IGHV1-18	IGHJ4	IGHD6-13	0.26
IGHV1-2	IGHJ3	IGHD7-27	0.26
IGHV1-2	IGHJ4	IGHD1-1	0.26
IGHV1-8	IGHJ4	IGHD6-6	0.26
IGHV1-8	IGHJ4	IGHD7-27	0.26
IGHV1-8	IGHJ6	IGHD6-6	0.26
IGHV3-23	IGHJ4	IGHD7-27	0.26
IGHV4-31	IGHJ3	IGHD3-10	0.26
IGHV4-34	IGHJ4	IGHD3-3	0.26
IGHV4-34	IGHJ6	IGHD6-13	0.26
IGHV4-39	IGHJ2	IGHD2-8	0.26
IGHV4-39	IGHJ4	IGHD4-17	0.26
IGHV4-39	IGHJ5	IGHD5-18	0.26
IGHV4-59	IGHJ3	IGHD1-7	0.26
IGHV4-59	IGHJ6	IGHD3-3	0.26

Human V _H	Human J _H	Human D _H	%
IGHV6-1	IGHJ3	IGHD1-7	0.26
IGHV6-1	IGHJ3	IGHD7-27	0.26
IGHV6-1	IGHJ4	IGHD2-21	0.26
IGHV6-1	IGHJ4	IGHD3-16	0.26
IGHV1-18	IGHJ4	IGHD1-20	0.22
IGHV1-18	IGHJ4	IGHD2-2	0.22
IGHV1-69	IGHJ4	IGHD1-26	0.22
IGHV1-8	IGHJ4	IGHD1-20	0.22
IGHV1-8	IGHJ4	IGHD1-26	0.22
IGHV1-8	IGHJ6	IGHD1-20	0.22
IGHV3-21	IGHJ4	IGHD1-7	0.22
IGHV3-23	IGHJ4	IGHD1-26	0.22
IGHV4-34	IGHJ4	IGHD1-26	0.22
IGHV4-34	IGHJ4	IGHD7-27	0.22
IGHV4-34	IGHJ5	IGHD6-6	0.22
IGHV4-39	IGHJ3	IGHD1-7	0.22
IGHV4-39	IGHJ3	IGHD3-16	0.22
IGHV4-39	IGHJ4	IGHD2-15	0.22
IGHV4-39	IGHJ5	IGHD7-27	0.22
IGHV4-59	IGHJ3	IGHD6-6	0.22
IGHV4-59	IGHJ4	IGHD3-3	0.22
IGHV4-59	IGHJ4	IGHD3-9	0.22
IGHV4-59	IGHJ6	IGHD5-12	0.22
IGHV4-59	IGHJ6	IGHD5-18	0.22
IGHV5-51	IGHJ4	IGHD6-6	0.22
IGHV5-51	IGHJ5	IGHD3-3	0.22
IGHV6-1	IGHJ3	IGHD1-26	0.22
IGHV6-1	IGHJ5	IGHD1-26	0.22

Human V _H	Human J _H	Human D _H	%
IGHV1-18	IGHJ4	IGHD7-27	0.17
IGHV1-18	IGHJ6	IGHD1-7	0.17
IGHV1-2	IGHJ4	IGHD5-18	0.17
IGHV1-24	IGHJ4	IGHD1-7	0.17
IGHV1-58	IGHJ3	IGHD7-27	0.17
IGHV1-8	IGHJ6	IGHD1-26	0.17
IGHV3-11	IGHJ4	IGHD7-27	0.17
IGHV3-15	IGHJ4	IGHD1-7	0.17
IGHV3-21	IGHJ4	IGHD3-10	0.17
IGHV3-23	IGHJ2	IGHD6-6	0.17
IGHV3-23	IGHJ4	IGHD1-20	0.17
IGHV3-23	IGHJ4	IGHD3-10	0.17
IGHV3-23	IGHJ4	IGHD6-19	0.17
IGHV3-23	IGHJ4	IGHD6-6	0.17
IGHV3-33	IGHJ4	IGHD6-6	0.17
IGHV3-43	IGHJ6	IGHD3-22	0.17
IGHV3-53	IGHJ2	IGHD1-7	0.17
IGHV3-53	IGHJ4	IGHD5-18	0.17
IGHV3-7	IGHJ4	IGHD7-27	0.17
IGHV3-9	IGHJ4	IGHD1-26	0.17
IGHV4-31	IGHJ3	IGHD1-1	0.17
IGHV4-31	IGHJ6	IGHD3-3	0.17
IGHV4-34	IGHJ2	IGHD1-7	0.17
IGHV4-34	IGHJ3	IGHD1-7	0.17
IGHV4-34	IGHJ4	IGHD2-15	0.17
IGHV4-34	IGHJ4	IGHD3-10	0.17
IGHV4-34	IGHJ4	IGHD6-13	0.17
IGHV4-34	IGHJ6	IGHD2-2	0.17

Human V _H	Human J _H	Human D _H	%
IGHV4-34	IGHJ6	IGHD3-10	0.17
IGHV4-39	IGHJ2	IGHD7-27	0.17
IGHV4-39	IGHJ4	IGHD6-25	0.17
IGHV4-39	IGHJ5	IGHD1-26	0.17
IGHV4-39	IGHJ5	IGHD3-16	0.17
IGHV4-39	IGHJ6	IGHD1-1	0.17
IGHV4-39	IGHJ6	IGHD1-26	0.17
IGHV4-59	IGHJ4	IGHD5-12	0.17
IGHV4-59	IGHJ5	IGHD1-7	0.17
IGHV4-59	IGHJ6	IGHD2-2	0.17
IGHV4-59	IGHJ6	IGHD7-27	0.17
IGHV5-51	IGHJ6	IGHD2-2	0.17
IGHV6-1	IGHJ3	IGHD6-19	0.17
IGHV6-1	IGHJ4	IGHD6-6	0.17
IGHV6-1	IGHJ6	IGHD1-26	0.17
IGHV1-18	IGHJ4	IGHD5-12	0.13
IGHV1-18	IGHJ4	IGHD5-18	0.13
IGHV1-18	IGHJ5	IGHD1-7	0.13
IGHV1-2	IGHJ4	IGHD3-3	0.13
IGHV1-2	IGHJ4	IGHD6-6	0.13
IGHV1-2	IGHJ4	IGHD7-27	0.13
IGHV1-2	IGHJ6	IGHD1-26	0.13
IGHV1-24	IGHJ5	IGHD1-7	0.13
IGHV1-24	IGHJ6	IGHD1-1	0.13
IGHV1-69	IGHJ4	IGHD7-27	0.13
IGHV1-8	IGHJ4	IGHD3-10	0.13
IGHV1-8	IGHJ4	IGHD6-13	0.13
IGHV1-8	IGHJ5	IGHD6-13	0.13

Human V _H	Human J _H	Human D _H	%
IGHV1-8	IGHJ6	IGHD1-1	0.13
IGHV1-8	IGHJ6	IGHD3-10	0.13
IGHV2-5	IGHJ4	IGHD1-20	0.13
IGHV2-70	IGHJ4	IGHD1-7	0.13
IGHV3-15	IGHJ4	IGHD1-20	0.13
IGHV3-21	IGHJ6	IGHD3-3	0.13
IGHV3-21	IGHJ6	IGHD4-17	0.13
IGHV3-23	IGHJ4	IGHD1-7	0.13
IGHV3-23	IGHJ4	IGHD2-2	0.13
IGHV3-23	IGHJ4	IGHD3-3	0.13
IGHV3-23	IGHJ6	IGHD1-1	0.13
IGHV3-23	IGHJ6	IGHD1-26	0.13
IGHV3-30	IGHJ4	IGHD5-18	0.13
IGHV3-33	IGHJ4	IGHD7-27	0.13
IGHV3-43	IGHJ6	IGHD5-18	0.13
IGHV3-53	IGHJ4	IGHD3-10	0.13
IGHV3-53	IGHJ4	IGHD6-6	0.13
IGHV3-7	IGHJ4	IGHD1-26	0.13
IGHV3-7	IGHJ4	IGHD6-13	0.13
IGHV4-31	IGHJ4	IGHD1-26	0.13
IGHV4-34	IGHJ2	IGHD6-13	0.13
IGHV4-34	IGHJ2	IGHD7-27	0.13
IGHV4-34	IGHJ3	IGHD1-26	0.13
IGHV4-34	IGHJ4	IGHD1-1	0.13
IGHV4-34	IGHJ4	IGHD5-18	0.13
IGHV4-34	IGHJ5	IGHD1-26	0.13
IGHV4-34	IGHJ5	IGHD6-13	0.13
IGHV4-34	IGHJ6	IGHD1-26	0.13

Human V _H	Human J _H	Human D _H	%
IGHV4-39	IGHJ2	IGHD2-2	0.13
IGHV4-39	IGHJ3	IGHD2-2	0.13
IGHV4-39	IGHJ4	IGHD2-8	0.13
IGHV4-39	IGHJ4	IGHD3-22	0.13
IGHV4-39	IGHJ6	IGHD6-6	0.13
IGHV4-59	IGHJ2	IGHD6-13	0.13
IGHV4-59	IGHJ2	IGHD6-6	0.13
IGHV4-59	IGHJ3	IGHD6-13	0.13
IGHV4-59	IGHJ4	IGHD7-27	0.13
IGHV4-59	IGHJ6	IGHD1-1	0.13
IGHV4-59	IGHJ6	IGHD2-15	0.13
IGHV5-51	IGHJ4	IGHD1-26	0.13
IGHV5-51	IGHJ4	IGHD1-7	0.13
IGHV5-51	IGHJ6	IGHD6-13	0.13
IGHV5-51	IGHJ6	IGHD6-6	0.13
IGHV6-1	IGHJ1	IGHD6-13	0.13
IGHV6-1	IGHJ4	IGHD1-20	0.13
IGHV6-1	IGHJ4	IGHD2-15	0.13
IGHV6-1	IGHJ4	IGHD2-2	0.13
IGHV6-1	IGHJ4	IGHD3-10	0.13
IGHV6-1	IGHJ4	IGHD4-17	0.13
IGHV6-1	IGHJ4	IGHD5-18	0.13
IGHV6-1	IGHJ4	IGHD6-19	0.13
IGHV1-18	IGHJ3	IGHD1-26	0.09
IGHV1-18	IGHJ3	IGHD1-7	0.09
IGHV1-18	IGHJ3	IGHD6-6	0.09
IGHV1-18	IGHJ4	IGHD1-1	0.09
IGHV1-18	IGHJ4	IGHD3-16	0.09

Human V _H	Human J _H	Human D _H	%
IGHV1-18	IGHJ4	IGHD6-19	0.09
IGHV1-18	IGHJ4	IGHD6-6	0.09
IGHV1-18	IGHJ6	IGHD3-9	0.09
IGHV1-18	IGHJ6	IGHD6-6	0.09
IGHV1-18	IGHJ6	IGHD3-10	0.09
IGHV1-2	IGHJ3	IGHD1-7	0.09
IGHV1-2	IGHJ3	IGHD6-6	0.09
IGHV1-2	IGHJ4	IGHD1-20	0.09
IGHV1-2	IGHJ4	IGHD5-12	0.09
IGHV1-2	IGHJ5	IGHD6-6	0.09
IGHV1-24	IGHJ4	IGHD1-26	0.09
IGHV1-24	IGHJ4	IGHD3-9	0.09
IGHV1-46	IGHJ4	IGHD3-16	0.09
IGHV1-46	IGHJ6	IGHD3-10	0.09
IGHV1-58	IGHJ4	IGHD1-26	0.09
IGHV1-69	IGHJ3	IGHD1-7	0.09
IGHV1-69	IGHJ4	IGHD6-13	0.09
IGHV1-69	IGHJ6	IGHD6-6	0.09
IGHV1-8	IGHJ4	IGHD3-16	0.09
IGHV1-8	IGHJ4	IGHD5-18	0.09
IGHV1-8	IGHJ5	IGHD1-7	0.09
IGHV1-8	IGHJ5	IGHD6-19	0.09
IGHV1-8	IGHJ6	IGHD3-3	0.09
IGHV1-8	IGHJ6	IGHD5-12	0.09
IGHV2-26	IGHJ4	IGHD1-26	0.09
IGHV2-5	IGHJ4	IGHD5-18	0.09
IGHV2-70	IGHJ4	IGHD1-20	0.09
IGHV2-70	IGHJ4	IGHD5-18	0.09

Human V _H	Human J _H	Human D _H	%
IGHV2-70	IGHJ4	IGHD6-13	0.09
IGHV3-13	IGHJ5	IGHD1-20	0.09
IGHV3-13	IGHJ6	IGHD6-6	0.09
IGHV3-15	IGHJ3	IGHD7-27	0.09
IGHV3-15	IGHJ4	IGHD6-13	0.09
IGHV3-15	IGHJ6	IGHD6-6	0.09
IGHV3-21	IGHJ1	IGHD6-6	0.09
IGHV3-21	IGHJ2	IGHD2-21	0.09
IGHV3-21	IGHJ3	IGHD1-20	0.09
IGHV3-21	IGHJ4	IGHD1-1	0.09
IGHV3-21	IGHJ4	IGHD1-26	0.09
IGHV3-21	IGHJ4	IGHD1-7	0.09
IGHV3-23	IGHJ4	IGHD1-1	0.09
IGHV3-23	IGHJ4	IGHD5-18	0.09
IGHV3-23	IGHJ5	IGHD1-20	0.09
IGHV3-23	IGHJ6	IGHD3-3	0.09
IGHV3-33	IGHJ4	IGHD4-17	0.09
IGHV3-33	IGHJ4	IGHD5-12	0.09
IGHV3-33	IGHJ4	IGHD6-13	0.09
IGHV3-33	IGHJ6	IGHD6-6	0.09
IGHV3-43	IGHJ6	IGHD1-26	0.09
IGHV3-48	IGHJ1	IGHD3-10	0.09
IGHV3-48	IGHJ3	IGHD7-27	0.09
IGHV3-48	IGHJ4	IGHD5-18	0.09
IGHV3-53	IGHJ2	IGHD6-6	0.09
IGHV3-53	IGHJ6	IGHD1-26	0.09
IGHV3-64	IGHJ4	IGHD7-27	0.09
IGHV3-7	IGHJ4	IGHD1-1	0.09

Human V _H	Human J _H	Human D _H	%
IGHV3-7	IGHJ4	IGHD2-15	0.09
IGHV3-7	IGHJ4	IGHD3-10	0.09
IGHV3-7	IGHJ4	IGHD3-16	0.09
IGHV3-7	IGHJ5	IGHD1-26	0.09
IGHV3-9	IGHJ6	IGHD6-6	0.09
IGHV4-28	IGHJ4	IGHD6-6	0.09
IGHV4-31	IGHJ4	IGHD3-3	0.09
IGHV4-31	IGHJ4	IGHD6-19	0.09
IGHV4-34	IGHJ2	IGHD3-16	0.09
IGHV4-34	IGHJ3	IGHD3-16	0.09
IGHV4-34	IGHJ3	IGHD5-12	0.09
IGHV4-34	IGHJ3	IGHD6-13	0.09
IGHV4-34	IGHJ3	IGHD6-6	0.09
IGHV4-34	IGHJ3	IGHD7-27	0.09
IGHV4-34	IGHJ4	IGHD3-16	0.09
IGHV4-34	IGHJ4	IGHD5-12	0.09
IGHV4-34	IGHJ4	IGHD6-19	0.09
IGHV4-34	IGHJ5	IGHD2-2	0.09
IGHV4-34	IGHJ5	IGHD3-10	0.09
IGHV4-34	IGHJ5	IGHD5-18	0.09
IGHV4-34	IGHJ5	IGHD6-19	0.09
IGHV4-39	IGHJ1	IGHD6-6	0.09
IGHV4-39	IGHJ3	IGHD1-1	0.09
IGHV4-39	IGHJ3	IGHD2-21	0.09
IGHV4-39	IGHJ3	IGHD3-22	0.09
IGHV4-39	IGHJ3	IGHD6-13	0.09
IGHV4-39	IGHJ3	IGHD7-27	0.09
IGHV4-39	IGHJ4	IGHD1-20	0.09

Human V _H	Human J _H	Human D _H	%
IGHV4-39	IGHJ4	IGHD2-21	0.09
IGHV4-39	IGHJ4	IGHD5-12	0.09
IGHV4-39	IGHJ5	IGHD1-20	0.09
IGHV4-39	IGHJ5	IGHD2-8	0.09
IGHV4-39	IGHJ5	IGHD3-10	0.09
IGHV4-39	IGHJ5	IGHD3-3	0.09
IGHV4-39	IGHJ5	IGHD6-19	0.09
IGHV4-39	IGHJ5	IGHD6-6	0.09
IGHV4-39	IGHJ6	IGHD2-15	0.09
IGHV4-39	IGHJ6	IGHD3-9	0.09
IGHV4-39	IGHJ6	IGHD6-13	0.09
IGHV4-59	IGHJ1	IGHD3-9	0.09
IGHV4-59	IGHJ3	IGHD1-1	0.09
IGHV4-59	IGHJ3	IGHD3-9	0.09
IGHV4-59	IGHJ3	IGHD4-17	0.09
IGHV4-59	IGHJ4	IGHD2-15	0.09
IGHV4-59	IGHJ4	IGHD2-2	0.09
IGHV4-59	IGHJ4	IGHD2-8	0.09
IGHV4-59	IGHJ4	IGHD3-16	0.09
IGHV4-59	IGHJ4	IGHD3-22	0.09
IGHV4-59	IGHJ5	IGHD1-26	0.09
IGHV4-59	IGHJ5	IGHD6-13	0.09
IGHV4-59	IGHJ5	IGHD6-6	0.09
IGHV4-59	IGHJ6	IGHD6-19	0.09
IGHV4-59	IGHJ6	IGHD3-10	0.09
IGHV5-51	IGHJ4	IGHD3-10	0.09
IGHV5-51	IGHJ4	IGHD7-27	0.09
IGHV5-51	IGHJ6	IGHD5-12	0.09

Human V _H	Human J _H	Human D _H	%
IGHV6-1	IGHJ2	IGHD1-7	0.09
IGHV6-1	IGHJ2	IGHD2-2	0.09
IGHV6-1	IGHJ3	IGHD2-8	0.09
IGHV6-1	IGHJ3	IGHD3-10	0.09
IGHV6-1	IGHJ5	IGHD3-9	0.09
IGHV6-1	IGHJ5	IGHD6-6	0.09
IGHV1-18	IGHJ2	IGHD1-1	0.04
IGHV1-18	IGHJ2	IGHD1-26	0.04
IGHV1-18	IGHJ2	IGHD6-6	0.04
IGHV1-18	IGHJ3	IGHD2-15	0.04
IGHV1-18	IGHJ3	IGHD3-16	0.04
IGHV1-18	IGHJ4	IGHD3-3	0.04
IGHV1-18	IGHJ4	IGHD3-9	0.04
IGHV1-18	IGHJ4	IGHD4-17	0.04
IGHV1-18	IGHJ5	IGHD1-26	0.04
IGHV1-18	IGHJ5	IGHD2-2	0.04
IGHV1-18	IGHJ5	IGHD6-6	0.04
IGHV1-18	IGHJ6	IGHD1-26	0.04
IGHV1-18	IGHJ6	IGHD2-2	0.04
IGHV1-18	IGHJ6	IGHD3-10	0.04
IGHV1-18	IGHJ6	IGHD3-22	0.04
IGHV1-18	IGHJ6	IGHD5-18	0.04
IGHV1-18	IGHJ6	IGHD6-13	0.04
IGHV1-18	IGHJ6	IGHD6-19	0.04
IGHV1-18	IGHJ6	IGHD1-7	0.04
IGHV1-18	IGHJ6	IGHD3-3	0.04
IGHV1-2	IGHJ1	IGHD1-7	0.04
IGHV1-2	IGHJ1	IGHD6-13	0.04

Human V _H	Human J _H	Human D _H	%
IGHV1-2	IGHJ2	IGHD3-10	0.04
IGHV1-2	IGHJ2	IGHD6-6	0.04
IGHV1-2	IGHJ3	IGHD1-26	0.04
IGHV1-2	IGHJ3	IGHD2-21	0.04
IGHV1-2	IGHJ3	IGHD3-10	0.04
IGHV1-2	IGHJ4	IGHD2-15	0.04
IGHV1-2	IGHJ4	IGHD3-10	0.04
IGHV1-2	IGHJ4	IGHD3-16	0.04
IGHV1-2	IGHJ4	IGHD3-22	0.04
IGHV1-2	IGHJ4	IGHD3-9	0.04
IGHV1-2	IGHJ4	IGHD4-17	0.04
IGHV1-2	IGHJ4	IGHD6-25	0.04
IGHV1-2	IGHJ6	IGHD2-15	0.04
IGHV1-2	IGHJ6	IGHD5-12	0.04
IGHV1-2	IGHJ6	IGHD5-18	0.04
IGHV1-2	IGHJ6	IGHD6-13	0.04
IGHV1-2	IGHJ6	IGHD6-6	0.04
IGHV1-2	IGHJ6	IGHD3-10	0.04
IGHV1-2	IGHJ4	IGHD3-16	0.04
IGHV1-24	IGHJ2	IGHD3-10	0.04
IGHV1-24	IGHJ2	IGHD1-7	0.04
IGHV1-24	IGHJ3	IGHD1-7	0.04
IGHV1-24	IGHJ3	IGHD6-6	0.04
IGHV1-24	IGHJ4	IGHD2-2	0.04
IGHV1-24	IGHJ4	IGHD2-21	0.04
IGHV1-24	IGHJ4	IGHD3-10	0.04
IGHV1-24	IGHJ4	IGHD3-16	0.04
IGHV1-24	IGHJ4	IGHD5-12	0.04

Human V _H	Human J _H	Human D _H	%
IGHV1-24	IGHJ4	IGHD5-18	0.04
IGHV1-24	IGHJ4	IGHD6-6	0.04
IGHV1-24	IGHJ5	IGHD1-1	0.04
IGHV1-24	IGHJ6	IGHD1-26	0.04
IGHV1-24	IGHJ6	IGHD1-7	0.04
IGHV1-24	IGHJ6	IGHD2-8	0.04
IGHV1-24	IGHJ6	IGHD7-27	0.04
IGHV1-3	IGHJ4	IGHD1-7	0.04
IGHV1-46	IGHJ4	IGHD1-7	0.04
IGHV1-46	IGHJ4	IGHD5-18	0.04
IGHV1-46	IGHJ4	IGHD6-6	0.04
IGHV1-46	IGHJ5	IGHD6-6	0.04
IGHV1-46	IGHJ6	IGHD3-22	0.04
IGHV1-58	IGHJ2	IGHD1-26	0.04
IGHV1-58	IGHJ3	IGHD6-13	0.04
IGHV1-58	IGHJ4	IGHD1-1	0.04
IGHV1-58	IGHJ4	IGHD6-19	0.04
IGHV1-58	IGHJ4	IGHD6-6	0.04
IGHV1-69	IGHJ3	IGHD3-9	0.04
IGHV1-69	IGHJ3	IGHD6-13	0.04
IGHV1-69	IGHJ3	IGHD6-6	0.04
IGHV1-69	IGHJ4	IGHD1-20	0.04
IGHV1-69	IGHJ4	IGHD1-7	0.04
IGHV1-69	IGHJ4	IGHD2-2	0.04
IGHV1-69	IGHJ4	IGHD3-10	0.04
IGHV1-69	IGHJ4	IGHD4-17	0.04
IGHV1-69	IGHJ5	IGHD1-26	0.04
IGHV1-69	IGHJ5	IGHD1-7	0.04

Human V _H	Human J _H	Human D _H	%
IGHV1-69	IGHJ5	IGHD3-10	0.04
IGHV1-69	IGHJ5	IGHD5-12	0.04
IGHV1-69	IGHJ5	IGHD6-13	0.04
IGHV1-69	IGHJ5	IGHD6-6	0.04
IGHV1-69	IGHJ6	IGHD1-20	0.04
IGHV1-69	IGHJ6	IGHD1-26	0.04
IGHV1-69	IGHJ6	IGHD1-7	0.04
IGHV1-69	IGHJ6	IGHD2-15	0.04
IGHV1-69	IGHJ6	IGHD7-27	0.04
IGHV1-69	IGHJ6	IGHD6-25	0.04
IGHV1-8	IGHJ1	IGHD6-13	0.04
IGHV1-8	IGHJ2	IGHD1-20	0.04
IGHV1-8	IGHJ2	IGHD1-7	0.04
IGHV1-8	IGHJ3	IGHD1-26	0.04
IGHV1-8	IGHJ3	IGHD1-7	0.04
IGHV1-8	IGHJ3	IGHD5-18	0.04
IGHV1-8	IGHJ3	IGHD6-6	0.04
IGHV1-8	IGHJ4	IGHD3-9	0.04
IGHV1-8	IGHJ4	IGHD5-12	0.04
IGHV1-8	IGHJ4	IGHD6-25	0.04
IGHV1-8	IGHJ5	IGHD1-20	0.04
IGHV1-8	IGHJ5	IGHD1-26	0.04
IGHV1-8	IGHJ5	IGHD5-12	0.04
IGHV1-8	IGHJ5	IGHD6-6	0.04
IGHV1-8	IGHJ6	IGHD2-21	0.04
IGHV1-8	IGHJ6	IGHD3-9	0.04
IGHV1-8	IGHJ6	IGHD5-18	0.04
IGHV2-26	IGHJ3	IGHD1-26	0.04

Human V _H	Human J _H	Human D _H	%
IGHV2-26	IGHJ4	IGHD1-1	0.04
IGHV2-26	IGHJ4	IGHD6-13	0.04
IGHV2-26	IGHJ6	IGHD1-20	0.04
IGHV2-26	IGHJ6	IGHD1-26	0.04
IGHV2-5	IGHJ2	IGHD6-6	0.04
IGHV2-5	IGHJ4	IGHD5-12	0.04
IGHV2-5	IGHJ4	IGHD6-13	0.04
IGHV2-5	IGHJ4	IGHD7-27	0.04
IGHV2-5	IGHJ5	IGHD3-10	0.04
IGHV2-5	IGHJ5	IGHD6-25	0.04
IGHV2-5	IGHJ6	IGHD3-9	0.04
IGHV2-70	IGHJ1	IGHD3-10	0.04
IGHV2-70	IGHJ2	IGHD7-27	0.04
IGHV2-70	IGHJ4	IGHD3-10	0.04
IGHV2-70	IGHJ4	IGHD7-27	0.04
IGHV2-70	IGHJ6	IGHD1-26	0.04
IGHV2-70	IGHJ6	IGHD1-7	0.04
IGHV2-70	IGHJ6	IGHD2-15	0.04
IGHV2-70	IGHJ6	IGHD3-22	0.04
IGHV2-70	IGHJ6	IGHD5-12	0.04
IGHV2-70	IGHJ6	IGHD6-13	0.04
IGHV2-70	IGHJ6	IGHD6-6	0.04
IGHV2-70	IGHJ6	IGHD7-27	0.04
IGHV3-11	IGHJ3	IGHD6-6	0.04
IGHV3-11	IGHJ4	IGHD1-26	0.04
IGHV3-11	IGHJ4	IGHD1-7	0.04
IGHV3-11	IGHJ4	IGHD2-21	0.04
IGHV3-11	IGHJ4	IGHD3-10	0.04

Human V _H	Human J _H	Human D _H	%
IGHV3-11	IGHJ4	IGHD6-13	0.04
IGHV3-11	IGHJ4	IGHD6-6	0.04
IGHV3-11	IGHJ6	IGHD1-7	0.04
IGHV3-13	IGHJ2	IGHD3-22	0.04
IGHV3-13	IGHJ3	IGHD1-1	0.04
IGHV3-13	IGHJ3	IGHD2-2	0.04
IGHV3-13	IGHJ4	IGHD6-13	0.04
IGHV3-15	IGHJ1	IGHD1-7	0.04
IGHV3-15	IGHJ1	IGHD6-19	0.04
IGHV3-15	IGHJ2	IGHD1-26	0.04
IGHV3-15	IGHJ4	IGHD1-1	0.04
IGHV3-15	IGHJ4	IGHD1-26	0.04
IGHV3-15	IGHJ4	IGHD2-2	0.04
IGHV3-15	IGHJ4	IGHD2-21	0.04
IGHV3-15	IGHJ4	IGHD2-8	0.04
IGHV3-15	IGHJ4	IGHD3-10	0.04
IGHV3-15	IGHJ4	IGHD3-16	0.04
IGHV3-15	IGHJ4	IGHD3-22	0.04
IGHV3-15	IGHJ4	IGHD3-3	0.04
IGHV3-15	IGHJ4	IGHD6-19	0.04
IGHV3-15	IGHJ4	IGHD7-27	0.04
IGHV3-15	IGHJ4	IGHD1-26	0.04
IGHV3-15	IGHJ5	IGHD1-1	0.04
IGHV3-15	IGHJ5	IGHD1-26	0.04
IGHV3-15	IGHJ5	IGHD1-7	0.04
IGHV3-20	IGHJ3	IGHD1-20	0.04
IGHV3-20	IGHJ4	IGHD1-20	0.04
IGHV3-20	IGHJ4	IGHD1-26	0.04

Human V _H	Human J _H	Human D _H	%
IGHV3-20	IGHJ6	IGHD5-12	0.04
IGHV3-21	IGHJ1	IGHD6-6	0.04
IGHV3-21	IGHJ2	IGHD5-18	0.04
IGHV3-21	IGHJ3	IGHD1-26	0.04
IGHV3-21	IGHJ3	IGHD2-2	0.04
IGHV3-21	IGHJ3	IGHD2-8	0.04
IGHV3-21	IGHJ3	IGHD3-10	0.04
IGHV3-21	IGHJ3	IGHD7-27	0.04
IGHV3-21	IGHJ4	IGHD1-20	0.04
IGHV3-21	IGHJ4	IGHD2-2	0.04
IGHV3-21	IGHJ4	IGHD5-12	0.04
IGHV3-21	IGHJ4	IGHD6-19	0.04
IGHV3-21	IGHJ4	IGHD6-25	0.04
IGHV3-21	IGHJ4	IGHD7-27	0.04
IGHV3-21	IGHJ4	IGHD1-20	0.04
IGHV3-21	IGHJ5	IGHD2-15	0.04
IGHV3-21	IGHJ6	IGHD1-1	0.04
IGHV3-21	IGHJ6	IGHD1-20	0.04
IGHV3-21	IGHJ6	IGHD1-7	0.04
IGHV3-21	IGHJ6	IGHD2-2	0.04
IGHV3-21	IGHJ6	IGHD5-12	0.04
IGHV3-21	IGHJ6	IGHD6-13	0.04
IGHV3-21	IGHJ6	IGHD6-6	0.04
IGHV3-23	IGHJ1	IGHD1-20	0.04
IGHV3-23	IGHJ1	IGHD2-2	0.04
IGHV3-23	IGHJ1	IGHD1-1	0.04
IGHV3-23	IGHJ3	IGHD2-21	0.04
IGHV3-23	IGHJ3	IGHD3-3	0.04

Human V _H	Human J _H	Human D _H	%
IGHV3-23	IGHJ3	IGHD6-6	0.04
IGHV3-23	IGHJ4	IGHD2-15	0.04
IGHV3-23	IGHJ4	IGHD2-8	0.04
IGHV3-23	IGHJ4	IGHD3-16	0.04
IGHV3-23	IGHJ4	IGHD4-17	0.04
IGHV3-23	IGHJ4	IGHD5-12	0.04
IGHV3-23	IGHJ4	IGHD1-7	0.04
IGHV3-23	IGHJ5	IGHD1-7	0.04
IGHV3-23	IGHJ5	IGHD3-10	0.04
IGHV3-23	IGHJ5	IGHD4-17	0.04
IGHV3-23	IGHJ5	IGHD1-7	0.04
IGHV3-23	IGHJ5	IGHD6-13	0.04
IGHV3-23	IGHJ6	IGHD1-20	0.04
IGHV3-23	IGHJ6	IGHD3-10	0.04
IGHV3-23	IGHJ6	IGHD3-16	0.04
IGHV3-23	IGHJ6	IGHD3-22	0.04
IGHV3-23	IGHJ6	IGHD6-6	0.04
IGHV3-30	IGHJ4	IGHD1-1	0.04
IGHV3-30	IGHJ4	IGHD1-26	0.04
IGHV3-30	IGHJ4	IGHD2-2	0.04
IGHV3-30	IGHJ4	IGHD3-10	0.04
IGHV3-30	IGHJ4	IGHD4-17	0.04
IGHV3-30	IGHJ4	IGHD7-27	0.04
IGHV3-30	IGHJ6	IGHD5-18	0.04
IGHV3-33	IGHJ3	IGHD1-1	0.04
IGHV3-33	IGHJ3	IGHD1-20	0.04
IGHV3-33	IGHJ3	IGHD6-13	0.04
IGHV3-33	IGHJ3	IGHD6-19	0.04

Human V _H	Human J _H	Human D _H	%
IGHV3-33	IGHJ3	IGHD6-6	0.04
IGHV3-33	IGHJ3	IGHD1-20	0.04
IGHV3-33	IGHJ4	IGHD1-20	0.04
IGHV3-33	IGHJ4	IGHD1-26	0.04
IGHV3-33	IGHJ4	IGHD3-10	0.04
IGHV3-33	IGHJ4	IGHD3-22	0.04
IGHV3-33	IGHJ4	IGHD3-3	0.04
IGHV3-33	IGHJ4	IGHD5-18	0.04
IGHV3-33	IGHJ4	IGHD6-19	0.04
IGHV3-33	IGHJ4	IGHD4-17	0.04
IGHV3-33	IGHJ4	IGHD6-25	0.04
IGHV3-33	IGHJ5	IGHD4-17	0.04
IGHV3-33	IGHJ5	IGHD6-6	0.04
IGHV3-33	IGHJ5	IGHD7-27	0.04
IGHV3-33	IGHJ6	IGHD1-1	0.04
IGHV3-33	IGHJ6	IGHD1-7	0.04
IGHV3-33	IGHJ6	IGHD3-10	0.04
IGHV3-33	IGHJ6	IGHD6-13	0.04
IGHV3-33	IGHJ6	IGHD7-27	0.04
IGHV3-33	IGHJ6	IGHD5-12	0.04
IGHV3-33	IGHJ6	IGHD6-19	0.04
IGHV3-43	IGHJ4	IGHD6-13	0.04
IGHV3-43	IGHJ6	IGHD2-2	0.04
IGHV3-43	IGHJ6	IGHD3-9	0.04
IGHV3-43	IGHJ6	IGHD6-6	0.04
IGHV3-48	IGHJ2	IGHD6-6	0.04
IGHV3-48	IGHJ3	IGHD2-8	0.04
IGHV3-48	IGHJ3	IGHD6-13	0.04

Human V _H	Human J _H	Human D _H	%
IGHV3-48	IGHJ4	IGHD1-26	0.04
IGHV3-48	IGHJ4	IGHD4-17	0.04
IGHV3-48	IGHJ4	IGHD6-19	0.04
IGHV3-48	IGHJ5	IGHD1-26	0.04
IGHV3-48	IGHJ5	IGHD5-18	0.04
IGHV3-48	IGHJ6	IGHD1-20	0.04
IGHV3-48	IGHJ6	IGHD1-26	0.04
IGHV3-48	IGHJ6	IGHD2-2	0.04
IGHV3-48	IGHJ6	IGHD3-16	0.04
IGHV3-48	IGHJ6	IGHD6-6	0.04
IGHV3-48	IGHJ6	IGHD2-2	0.04
IGHV3-49	IGHJ4	IGHD1-7	0.04
IGHV3-49	IGHJ4	IGHD3-16	0.04
IGHV3-49	IGHJ4	IGHD3-9	0.04
IGHV3-49	IGHJ4	IGHD6-13	0.04
IGHV3-49	IGHJ4	IGHD7-27	0.04
IGHV3-49	IGHJ5	IGHD5-12	0.04
IGHV3-49	IGHJ6	IGHD1-26	0.04
IGHV3-49	IGHJ6	IGHD2-2	0.04
IGHV3-53	IGHJ1	IGHD6-13	0.04
IGHV3-53	IGHJ1	IGHD6-13	0.04
IGHV3-53	IGHJ2	IGHD3-3	0.04
IGHV3-53	IGHJ2	IGHD7-27	0.04
IGHV3-53	IGHJ3	IGHD1-26	0.04
IGHV3-53	IGHJ3	IGHD2-2	0.04
IGHV3-53	IGHJ3	IGHD6-6	0.04
IGHV3-53	IGHJ4	IGHD1-26	0.04
IGHV3-53	IGHJ4	IGHD2-2	0.04

Human V _H	Human J _H	Human D _H	%
IGHV3-53	IGHJ4	IGHD3-3	0.04
IGHV3-53	IGHJ4	IGHD6-13	0.04
IGHV3-53	IGHJ4	IGHD7-27	0.04
IGHV3-53	IGHJ5	IGHD6-6	0.04
IGHV3-53	IGHJ6	IGHD1-1	0.04
IGHV3-53	IGHJ6	IGHD7-27	0.04
IGHV3-53	IGHJ6	IGHD6-13	0.04
IGHV3-64	IGHJ3	IGHD3-16	0.04
IGHV3-64	IGHJ4	IGHD6-6	0.04
IGHV3-64	IGHJ6	IGHD6-6	0.04
IGHV3-66	IGHJ4	IGHD6-19	0.04
IGHV3-7	IGHJ3	IGHD7-27	0.04
IGHV3-7	IGHJ4	IGHD2-21	0.04
IGHV3-7	IGHJ4	IGHD2-8	0.04
IGHV3-7	IGHJ4	IGHD4-17	0.04
IGHV3-7	IGHJ5	IGHD2-8	0.04
IGHV3-7	IGHJ6	IGHD3-3	0.04
IGHV3-7	IGHJ6	IGHD6-6	0.04
IGHV3-72	IGHJ3	IGHD1-7	0.04
IGHV3-72	IGHJ4	IGHD3-3	0.04
IGHV3-72	IGHJ4	IGHD6-13	0.04
IGHV3-72	IGHJ4	IGHD6-25	0.04
IGHV3-72	IGHJ4	IGHD7-27	0.04
IGHV3-73	IGHJ4	IGHD1-26	0.04
IGHV3-9	IGHJ1	IGHD3-10	0.04
IGHV3-9	IGHJ1	IGHD3-22	0.04
IGHV3-9	IGHJ2	IGHD1-26	0.04
IGHV3-9	IGHJ3	IGHD1-26	0.04

Human V _H	Human J _H	Human D _H	%
IGHV3-9	IGHJ3	IGHD5-18	0.04
IGHV3-9	IGHJ4	IGHD1-7	0.04
IGHV3-9	IGHJ4	IGHD3-3	0.04
IGHV3-9	IGHJ4	IGHD3-9	0.04
IGHV3-9	IGHJ4	IGHD5-12	0.04
IGHV3-9	IGHJ4	IGHD7-27	0.04
IGHV3-9	IGHJ5	IGHD1-1	0.04
IGHV3-9	IGHJ5	IGHD1-7	0.04
IGHV3-9	IGHJ6	IGHD1-26	0.04
IGHV3-9	IGHJ6	IGHD3-10	0.04
IGHV3-9	IGHJ6	IGHD3-22	0.04
IGHV3-9	IGHJ6	IGHD7-27	0.04
IGHV4-28	IGHJ4	IGHD6-13	0.04
IGHV4-31	IGHJ1	IGHD6-13	0.04
IGHV4-31	IGHJ2	IGHD7-27	0.04
IGHV4-31	IGHJ3	IGHD1-26	0.04
IGHV4-31	IGHJ3	IGHD1-7	0.04
IGHV4-31	IGHJ3	IGHD2-15	0.04
IGHV4-31	IGHJ3	IGHD2-2	0.04
IGHV4-31	IGHJ3	IGHD2-21	0.04
IGHV4-31	IGHJ3	IGHD3-16	0.04
IGHV4-31	IGHJ3	IGHD3-3	0.04
IGHV4-31	IGHJ3	IGHD3-9	0.04
IGHV4-31	IGHJ4	IGHD1-7	0.04
IGHV4-31	IGHJ4	IGHD3-10	0.04
IGHV4-31	IGHJ4	IGHD3-9	0.04
IGHV4-31	IGHJ4	IGHD4-17	0.04
IGHV4-31	IGHJ4	IGHD5-18	0.04

Human V _H	Human J _H	Human D _H	%
IGHV4-31	IGHJ4	IGHD6-13	0.04
IGHV4-31	IGHJ4	IGHD6-6	0.04
IGHV4-31	IGHJ5	IGHD3-3	0.04
IGHV4-31	IGHJ6	IGHD2-2	0.04
IGHV4-31	IGHJ6	IGHD5-18	0.04
IGHV4-31	IGHJ6	IGHD6-13	0.04
IGHV4-31	IGHJ6	IGHD6-6	0.04
IGHV4-31	IGHJ6	IGHD7-27	0.04
IGHV4-34	IGHJ1	IGHD4-17	0.04
IGHV4-34	IGHJ1	IGHD6-6	0.04
IGHV4-34	IGHJ2	IGHD1-1	0.04
IGHV4-34	IGHJ2	IGHD1-20	0.04
IGHV4-34	IGHJ2	IGHD3-3	0.04
IGHV4-34	IGHJ2	IGHD4-17	0.04
IGHV4-34	IGHJ2	IGHD5-12	0.04
IGHV4-34	IGHJ2	IGHD6-19	0.04
IGHV4-34	IGHJ2	IGHD6-6	0.04
IGHV4-34	IGHJ3	IGHD1-1	0.04
IGHV4-34	IGHJ3	IGHD2-2	0.04
IGHV4-34	IGHJ3	IGHD3-3	0.04
IGHV4-34	IGHJ3	IGHD3-9	0.04
IGHV4-34	IGHJ4	IGHD2-2	0.04
IGHV4-34	IGHJ4	IGHD2-8	0.04
IGHV4-34	IGHJ4	IGHD3-22	0.04
IGHV4-34	IGHJ4	IGHD4-17	0.04
IGHV4-34	IGHJ5	IGHD1-7	0.04
IGHV4-34	IGHJ5	IGHD2-15	0.04
IGHV4-34	IGHJ5	IGHD2-8	0.04

Human V _H	Human J _H	Human D _H	%
IGHV4-34	IGHJ5	IGHD3-9	0.04
IGHV4-34	IGHJ5	IGHD5-12	0.04
IGHV4-34	IGHJ5	IGHD7-27	0.04
IGHV4-34	IGHJ6	IGHD1-1	0.04
IGHV4-34	IGHJ6	IGHD1-20	0.04
IGHV4-34	IGHJ6	IGHD2-8	0.04
IGHV4-34	IGHJ6	IGHD3-22	0.04
IGHV4-34	IGHJ6	IGHD3-3	0.04
IGHV4-34	IGHJ6	IGHD3-9	0.04
IGHV4-34	IGHJ6	IGHD5-12	0.04
IGHV4-34	IGHJ6	IGHD5-18	0.04
IGHV4-34	IGHJ6	IGHD7-27	0.04
IGHV4-34	IGHJ6	IGHD3-3	0.04
IGHV4-39	IGHJ1	IGHD1-7	0.04
IGHV4-39	IGHJ1	IGHD3-10	0.04
IGHV4-39	IGHJ1	IGHD4-17	0.04
IGHV4-39	IGHJ1	IGHD6-13	0.04
IGHV4-39	IGHJ1	IGHD5-18	0.04
IGHV4-39	IGHJ2	IGHD1-26	0.04
IGHV4-39	IGHJ2	IGHD2-15	0.04
IGHV4-39	IGHJ2	IGHD3-10	0.04
IGHV4-39	IGHJ2	IGHD5-12	0.04
IGHV4-39	IGHJ2	IGHD6-19	0.04
IGHV4-39	IGHJ2	IGHD6-6	0.04
IGHV4-39	IGHJ2	IGHD2-8	0.04
IGHV4-39	IGHJ3	IGHD1-20	0.04
IGHV4-39	IGHJ3	IGHD2-15	0.04
IGHV4-39	IGHJ3	IGHD2-8	0.04

Human V _H	Human J _H	Human D _H	%
IGHV4-39	IGHJ3	IGHD3-10	0.04
IGHV4-39	IGHJ3	IGHD3-9	0.04
IGHV4-39	IGHJ3	IGHD4-17	0.04
IGHV4-39	IGHJ3	IGHD3-10	0.04
IGHV4-39	IGHJ4	IGHD2-2	0.04
IGHV4-39	IGHJ4	IGHD1-26	0.04
IGHV4-39	IGHJ5	IGHD1-1	0.04
IGHV4-39	IGHJ5	IGHD2-21	0.04
IGHV4-39	IGHJ5	IGHD4-17	0.04
IGHV4-39	IGHJ5	IGHD6-13	0.04
IGHV4-39	IGHJ6	IGHD1-20	0.04
IGHV4-39	IGHJ6	IGHD2-21	0.04
IGHV4-39	IGHJ6	IGHD3-10	0.04
IGHV4-39	IGHJ6	IGHD3-16	0.04
IGHV4-39	IGHJ6	IGHD4-17	0.04
IGHV4-39	IGHJ6	IGHD5-12	0.04
IGHV4-39	IGHJ6	IGHD6-13	0.04
IGHV4-59	IGHJ1	IGHD3-9	0.04
IGHV4-59	IGHJ1	IGHD5-12	0.04
IGHV4-59	IGHJ2	IGHD1-20	0.04
IGHV4-59	IGHJ2	IGHD1-7	0.04
IGHV4-59	IGHJ2	IGHD2-21	0.04
IGHV4-59	IGHJ2	IGHD3-10	0.04
IGHV4-59	IGHJ2	IGHD3-22	0.04
IGHV4-59	IGHJ2	IGHD3-9	0.04
IGHV4-59	IGHJ2	IGHD6-19	0.04
IGHV4-59	IGHJ2	IGHD7-27	0.04
IGHV4-59	IGHJ3	IGHD1-26	0.04

Human V _H	Human J _H	Human D _H	%
IGHV4-59	IGHJ3	IGHD3-10	0.04
IGHV4-59	IGHJ3	IGHD3-16	0.04
IGHV4-59	IGHJ3	IGHD5-12	0.04
IGHV4-59	IGHJ4	IGHD1-20	0.04
IGHV4-59	IGHJ4	IGHD2-21	0.04
IGHV4-59	IGHJ4	IGHD4-17	0.04
IGHV4-59	IGHJ4	IGHD6-25	0.04
IGHV4-59	IGHJ5	IGHD2-2	0.04
IGHV4-59	IGHJ5	IGHD2-21	0.04
IGHV4-59	IGHJ5	IGHD3-10	0.04
IGHV4-59	IGHJ5	IGHD3-3	0.04
IGHV4-59	IGHJ5	IGHD5-18	0.04
IGHV4-59	IGHJ5	IGHD6-25	0.04
IGHV4-59	IGHJ5	IGHD3-16	0.04
IGHV4-59	IGHJ5	IGHD3-3	0.04
IGHV4-59	IGHJ5	IGHD6-13	0.04
IGHV4-59	IGHJ6	IGHD1-20	0.04
IGHV4-59	IGHJ6	IGHD2-21	0.04
IGHV4-59	IGHJ6	IGHD2-8	0.04
IGHV4-59	IGHJ6	IGHD3-16	0.04
IGHV4-59	IGHJ6	IGHD4-17	0.04
IGHV5-51	IGHJ1	IGHD6-13	0.04
IGHV5-51	IGHJ2	IGHD6-13	0.04
IGHV5-51	IGHJ4	IGHD2-15	0.04
IGHV5-51	IGHJ4	IGHD2-21	0.04
IGHV5-51	IGHJ4	IGHD3-16	0.04
IGHV5-51	IGHJ4	IGHD3-9	0.04
IGHV5-51	IGHJ4	IGHD5-18	0.04

Human V _H	Human J _H	Human D _H	%
IGHV5-51	IGHJ4	IGHD6-13	0.04
IGHV5-51	IGHJ4	IGHD6-19	0.04
IGHV5-51	IGHJ5	IGHD1-7	0.04
IGHV5-51	IGHJ6	IGHD3-16	0.04
IGHV5-51	IGHJ6	IGHD5-18	0.04
IGHV5-51	IGHJ6	IGHD7-27	0.04
IGHV5-51	IGHJ6	IGHD6-6	0.04
IGHV6-1	IGHJ1	IGHD1-26	0.04
IGHV6-1	IGHJ1	IGHD1-7	0.04
IGHV6-1	IGHJ1	IGHD2-15	0.04
IGHV6-1	IGHJ2	IGHD1-1	0.04
IGHV6-1	IGHJ2	IGHD6-19	0.04
IGHV6-1	IGHJ2	IGHD6-6	0.04
IGHV6-1	IGHJ2	IGHD7-27	0.04
IGHV6-1	IGHJ3	IGHD2-2	0.04
IGHV6-1	IGHJ3	IGHD3-16	0.04
IGHV6-1	IGHJ3	IGHD3-3	0.04
IGHV6-1	IGHJ3	IGHD4-17	0.04
IGHV6-1	IGHJ3	IGHD6-13	0.04
IGHV6-1	IGHJ3	IGHD6-25	0.04
IGHV6-1	IGHJ3	IGHD6-6	0.04
IGHV6-1	IGHJ4	IGHD2-8	0.04
IGHV6-1	IGHJ4	IGHD5-12	0.04
IGHV6-1	IGHJ5	IGHD1-1	0.04
IGHV6-1	IGHJ5	IGHD1-20	0.04
IGHV6-1	IGHJ5	IGHD1-7	0.04
IGHV6-1	IGHJ5	IGHD2-8	0.04
IGHV6-1	IGHJ5	IGHD3-3	0.04

Human V _H	Human J _H	Human D _H	%
IGHV6-1	IGHJ5	IGHD6-13	0.04
IGHV6-1	IGHJ5	IGHD6-19	0.04
IGHV6-1	IGHJ5	IGHD7-27	0.04
IGHV6-1	IGHJ5	IGHD1-7	0.04
IGHV6-1	IGHJ6	IGHD1-1	0.04
IGHV6-1	IGHJ6	IGHD1-20	0.04
IGHV6-1	IGHJ6	IGHD1-7	0.04
IGHV6-1	IGHJ6	IGHD3-16	0.04
IGHV6-1	IGHJ6	IGHD6-19	0.04
IGHV6-1	IGHJ6	IGHD7-27	0.04
IGHV6-1	IGHJ6	IGHD2-8	0.04

Table 26

uman V _H	Human J _H	Human D _H	%
IGHV2-70	IGHJ3	IGHD3-10	5.05
IGHV4-59	IGHJ4	IGHD1-26	3.07
IGHV2-26	IGHJ4	IGHD3-9	2.44
IGHV4-28	IGHJ4	IGHD1-26	2.38
IGHV1-18	IGHJ6	IGHD1-26	1.64
IGHV2-5	IGHJ4	IGHD1-7	1.55
IGHV1-18	IGHJ3	IGHD4-17	1.49
IGHV4-59	IGHJ4	IGHD6-6	1.49
IGHV3-33	IGHJ4	IGHD6-6	1.38
IGHV1-69	IGHJ4	IGHD6-13	1.26
IGHV3-64	IGHJ4	IGHD1-7	1.23
IGHV4-39	IGHJ4	IGHD3-10	1.21
IGHV3-23	IGHJ4	IGHD1-26	1.18
IGHV1-18	IGHJ4	IGHD6-6	0.98
IGHV3-23	IGHJ4	IGHD1-7	0.98
IGHV3-11	IGHJ4	IGHD5-18	0.95
IGHV1-18	IGHJ6	IGHD6-19	0.92
IGHV2-5	IGHJ4	IGHD6-19	0.92
IGHV3-15	IGHJ4	IGHD7-27	0.92
IGHV4-34	IGHJ6	IGHD6-13	0.92
IGHV4-59	IGHJ4	IGHD7-27	0.92
IGHV1-18	IGHJ6	IGHD3-9	0.89
IGHV2-26	IGHJ4	IGHD1-26	0.89
IGHV1-18	IGHJ3	IGHD7-27	0.86
IGHV4-59	IGHJ6	IGHD3-3	0.80
IGHV3-33	IGHJ6	IGHD6-6	0.78
IGHV3-7	IGHJ4	IGHD6-13	0.78
IGHV3-7	IGHJ6	IGHD6-19	0.78
IGHV1-18	IGHJ4	IGHD1-7	0.72

uman V _H	Human J _H	Human D _H	%
IGHV1-69	IGHJ6	IGHD5-12	0.72
IGHV3-72	IGHJ6	IGHD6-6	0.72
IGHV4-34	IGHJ3	IGHD6-6	0.72
IGHV3-21	IGHJ6	IGHD2-8	0.69
IGHV3-30	IGHJ4	IGHD3-22	0.69
IGHV3-33	IGHJ4	IGHD1-7	0.69
IGHV6-1	IGHJ4	IGHD1-26	0.69
IGHV4-59	IGHJ4	IGHD6-13	0.66
IGHV1-8	IGHJ4	IGHD1-26	0.63
IGHV3-13	IGHJ4	IGHD3-10	0.63
IGHV2-70	IGHJ4	IGHD1-26	0.60
IGHV3-33	IGHJ5	IGHD1-1	0.60
IGHV1-18	IGHJ4	IGHD1-26	0.57
IGHV1-8	IGHJ6	IGHD1-7	0.57
IGHV1-8	IGHJ4	IGHD3-10	0.55
IGHV3-15	IGHJ5	IGHD1-20	0.55
IGHV3-23	IGHJ6	IGHD6-13	0.55
IGHV3-33	IGHJ2	IGHD3-10	0.55
IGHV2-70	IGHJ5	IGHD3-10	0.52
IGHV3-15	IGHJ6	IGHD6-6	0.52
IGHV3-21	IGHJ6	IGHD4-17	0.52
IGHV1-18	IGHJ6	IGHD6-13	0.46
IGHV1-8	IGHJ4	IGHD1-26	0.46
IGHV3-13	IGHJ4	IGHD6-25	0.46
IGHV3-23	IGHJ4	IGHD6-13	0.46
IGHV4-39	IGHJ4	IGHD1-7	0.46
IGHV1-18	IGHJ4	IGHD2-2	0.43
IGHV2-26	IGHJ5	IGHD3-3	0.43
IGHV3-13	IGHJ4	IGHD4-17	0.43
IGHV3-13	IGHJ6	IGHD3-10	0.43

uman V _H	Human J _H	Human D _H	%
IGHV4-34	IGHJ6	IGHD1-26	0.43
IGHV4-59	IGHJ6	IGHD4-17	0.43
IGHV1-18	IGHJ6	IGHD3-22	0.40
IGHV1-46	IGHJ4	IGHD6-13	0.40
IGHV1-8	IGHJ6	IGHD2-2	0.40
IGHV1-8	IGHJ3	IGHD3-9	0.40
IGHV3-13	IGHJ4	IGHD1-7	0.40
IGHV3-33	IGHJ2	IGHD6-6	0.40
IGHV3-48	IGHJ4	IGHD1-7	0.40
IGHV4-39	IGHJ4	IGHD5-12	0.40
IGHV4-59	IGHJ6	IGHD3-22	0.40
IGHV1-8	IGHJ6	IGHD3-3	0.37
IGHV2-5	IGHJ3	IGHD6-6	0.37
IGHV3-43	IGHJ4	IGHD6-6	0.37
IGHV4-39	IGHJ4	IGHD6-19	0.37
IGHV4-59	IGHJ4	IGHD1-1	0.37
IGHV2-26	IGHJ4	IGHD3-16	0.34
IGHV2-70	IGHJ3	IGHD7-27	0.34
IGHV3-15	IGHJ1	IGHD6-6	0.34
IGHV3-23	IGHJ4	IGHD3-9	0.34
IGHV3-23	IGHJ4	IGHD6-6	0.34
IGHV3-53	IGHJ5	IGHD6-6	0.34
IGHV3-64	IGHJ2	IGHD1-1	0.34
IGHV3-11	IGHJ4	IGHD3-10	0.32
IGHV3-13	IGHJ4	IGHD3-16	0.32
IGHV3-13	IGHJ4	IGHD6-6	0.32
IGHV3-33	IGHJ4	IGHD1-26	0.32
IGHV3-9	IGHJ3	IGHD1-7	0.32
IGHV3-9	IGHJ5	IGHD1-26	0.32
IGHV4-34	IGHJ4	IGHD3-16	0.32

uman V _H	Human J _H	Human D _H	%
IGHV4-39	IGHJ4	IGHD2-8	0.32
IGHV4-59	IGHJ4	IGHD3-3	0.32
IGHV2-26	IGHJ3	IGHD3-22	0.29
IGHV2-5	IGHJ4	IGHD6-6	0.29
IGHV2-70	IGHJ5	IGHD4-17	0.29
IGHV3-13	IGHJ4	IGHD1-1	0.29
IGHV3-13	IGHJ4	IGHD1-26	0.29
IGHV3-13	IGHJ6	IGHD5-18	0.29
IGHV3-7	IGHJ5	IGHD6-19	0.29
IGHV4-39	IGHJ5	IGHD6-13	0.29
IGHV1-69	IGHJ6	IGHD3-22	0.26
IGHV1-8	IGHJ3	IGHD5-18	0.26
IGHV2-26	IGHJ2	IGHD7-27	0.26
IGHV2-5	IGHJ3	IGHD1-1	0.26
IGHV2-5	IGHJ4	IGHD1-26	0.26
IGHV3-13	IGHJ3	IGHD3-22	0.26
IGHV3-15	IGHJ4	IGHD6-13	0.26
IGHV3-21	IGHJ6	IGHD1-7	0.26
IGHV3-48	IGHJ4	IGHD6-13	0.26
IGHV3-9	IGHJ6	IGHD1-26	0.26
IGHV4-39	IGHJ4	IGHD1-26	0.26
IGHV1-18	IGHJ2	IGHD3-10	0.23
IGHV1-8	IGHJ4	IGHD2-8	0.23
IGHV2-5	IGHJ4	IGHD4-17	0.23
IGHV2-70	IGHJ4	IGHD1-7	0.23
IGHV2-70	IGHJ4	IGHD6-6	0.23
IGHV3-15	IGHJ4	IGHD1-26	0.23
IGHV3-15	IGHJ4	IGHD1-7	0.23
IGHV3-23	IGHJ5	IGHD3-9	0.23
IGHV3-23	IGHJ6	IGHD6-6	0.23

uman V _H	Human J _H	Human D _H	%
IGHV3-30	IGHJ3	IGHD3-16	0.23
IGHV3-48	IGHJ3	IGHD7-27	0.23
IGHV3-48	IGHJ4	IGHD3-9	0.23
IGHV3-64	IGHJ6	IGHD6-6	0.23
IGHV3-7	IGHJ3	IGHD6-13	0.23
IGHV3-7	IGHJ4	IGHD6-6	0.23
IGHV4-31	IGHJ4	IGHD1-26	0.23
IGHV4-31	IGHJ6	IGHD6-6	0.23
IGHV4-39	IGHJ3	IGHD1-7	0.23
IGHV4-59	IGHJ4	IGHD2-15	0.23
IGHV1-18	IGHJ5	IGHD1-7	0.20
IGHV1-18	IGHJ5	IGHD3-3	0.20
IGHV1-2	IGHJ4	IGHD3-3	0.20
IGHV1-24	IGHJ4	IGHD5-18	0.20
IGHV1-8	IGHJ4	IGHD7-27	0.20
IGHV1-8	IGHJ6	IGHD3-3	0.20
IGHV2-5	IGHJ5	IGHD3-10	0.20
IGHV3-23	IGHJ2	IGHD6-6	0.20
IGHV3-23	IGHJ3	IGHD1-26	0.20
IGHV3-23	IGHJ5	IGHD1-7	0.20
IGHV3-33	IGHJ4	IGHD6-13	0.20
IGHV3-7	IGHJ5	IGHD5-18	0.20
IGHV3-9	IGHJ6	IGHD6-6	0.20
IGHV4-28	IGHJ3	IGHD2-15	0.20
IGHV4-34	IGHJ4	IGHD1-7	0.20
IGHV4-39	IGHJ4	IGHD7-27	0.20
IGHV4-59	IGHJ3	IGHD1-1	0.20
IGHV1-58	IGHJ6	IGHD6-13	0.17
IGHV1-69	IGHJ5	IGHD3-10	0.17
IGHV2-26	IGHJ4	IGHD1-7	0.17

uman V _H	Human J _H	Human D _H	%
IGHV2-5	IGHJ4	IGHD2-2	0.17
IGHV2-70	IGHJ3	IGHD1-20	0.17
IGHV2-70	IGHJ5	IGHD6-13	0.17
IGHV3-23	IGHJ6	IGHD7-27	0.17
IGHV3-7	IGHJ3	IGHD2-2	0.17
IGHV3-7	IGHJ4	IGHD1-7	0.17
IGHV3-9	IGHJ3	IGHD6-6	0.17
IGHV3-9	IGHJ4	IGHD6-19	0.17
IGHV3-9	IGHJ5	IGHD1-7	0.17
IGHV4-34	IGHJ4	IGHD3-3	0.17
IGHV4-59	IGHJ4	IGHD1-7	0.17
IGHV1-69	IGHJ6	IGHD7-27	0.14
IGHV1-8	IGHJ1	IGHD6-6	0.14
IGHV1-8	IGHJ4	IGHD1-20	0.14
IGHV1-8	IGHJ4	IGHD3-3	0.14
IGHV2-5	IGHJ4	IGHD1-20	0.14
IGHV2-70	IGHJ5	IGHD1-26	0.14
IGHV3-13	IGHJ4	IGHD6-13	0.14
IGHV3-21	IGHJ2	IGHD3-22	0.14
IGHV3-23	IGHJ3	IGHD3-16	0.14
IGHV3-23	IGHJ3	IGHD3-9	0.14
IGHV3-23	IGHJ4	IGHD5-18	0.14
IGHV3-48	IGHJ4	IGHD1-26	0.14
IGHV3-48	IGHJ4	IGHD3-10	0.14
IGHV3-48	IGHJ6	IGHD3-9	0.14
IGHV3-7	IGHJ4	IGHD6-6	0.14
IGHV3-7	IGHJ5	IGHD2-21	0.14
IGHV3-9	IGHJ6	IGHD3-10	0.14
IGHV4-34	IGHJ4	IGHD6-6	0.14
IGHV4-34	IGHJ4	IGHD7-27	0.14

uman V _H	Human J _H	Human D _H	%
IGHV4-34	IGHJ6	IGHD3-10	0.14
IGHV4-39	IGHJ2	IGHD7-27	0.14
IGHV4-39	IGHJ4	IGHD6-6	0.14
IGHV4-59	IGHJ3	IGHD4-17	0.14
IGHV4-59	IGHJ4	IGHD3-9	0.14
IGHV4-59	IGHJ5	IGHD6-13	0.14
IGHV4-59	IGHJ6	IGHD3-10	0.14
IGHV6-1	IGHJ4	IGHD1-1	0.14
IGHV1-18	IGHJ5	IGHD6-13	0.11
IGHV1-2	IGHJ5	IGHD1-7	0.11
IGHV2-26	IGHJ4	IGHD7-27	0.11
IGHV2-5	IGHJ4	IGHD1-1	0.11
IGHV2-70	IGHJ3	IGHD2-2	0.11
IGHV2-70	IGHJ4	IGHD2-8	0.11
IGHV2-70	IGHJ5	IGHD6-6	0.11
IGHV3-13	IGHJ4	IGHD1-20	0.11
IGHV3-15	IGHJ4	IGHD3-22	0.11
IGHV3-21	IGHJ4	IGHD1-26	0.11
IGHV3-23	IGHJ3	IGHD1-20	0.11
IGHV3-23	IGHJ4	IGHD4-17	0.11
IGHV3-23	IGHJ4	IGHD5-12	0.11
IGHV3-23	IGHJ6	IGHD2-2	0.11
IGHV3-30	IGHJ4	IGHD1-7	0.11
IGHV3-30	IGHJ6	IGHD3-10	0.11
IGHV3-48	IGHJ4	IGHD1-1	0.11
IGHV3-49	IGHJ2	IGHD3-10	0.11
IGHV3-9	IGHJ4	IGHD5-18	0.11
IGHV4-59	IGHJ3	IGHD1-7	0.11
IGHV4-59	IGHJ6	IGHD1-26	0.11
IGHV6-1	IGHJ5	IGHD1-20	0.11

uman V _H	Human J _H	Human D _H	%
IGHV1-18	IGHJ4	IGHD5-18	0.09
IGHV1-18	IGHJ6	IGHD6-6	0.09
IGHV2-26	IGHJ3	IGHD6-13	0.09
IGHV2-5	IGHJ6	IGHD6-13	0.09
IGHV2-70	IGHJ4	IGHD2-15	0.09
IGHV2-70	IGHJ4	IGHD3-3	0.09
IGHV3-11	IGHJ6	IGHD1-7	0.09
IGHV3-15	IGHJ3	IGHD1-7	0.09
IGHV3-15	IGHJ4	IGHD3-3	0.09
IGHV3-21	IGHJ4	IGHD7-27	0.09
IGHV3-21	IGHJ6	IGHD1-20	0.09
IGHV3-21	IGHJ6	IGHD3-10	0.09
IGHV3-23	IGHJ3	IGHD7-27	0.09
IGHV3-23	IGHJ4	IGHD3-3	0.09
IGHV3-23	IGHJ5	IGHD1-26	0.09
IGHV3-23	IGHJ5	IGHD7-27	0.09
IGHV3-30	IGHJ4	IGHD2-15	0.09
IGHV3-30	IGHJ4	IGHD6-6	0.09
IGHV3-33	IGHJ4	IGHD1-1	0.09
IGHV3-33	IGHJ4	IGHD3-22	0.09
IGHV3-48	IGHJ3	IGHD6-13	0.09
IGHV3-48	IGHJ4	IGHD5-12	0.09
IGHV3-7	IGHJ4	IGHD1-20	0.09
IGHV3-7	IGHJ4	IGHD1-26	0.09
IGHV4-34	IGHJ4	IGHD1-26	0.09
IGHV4-34	IGHJ4	IGHD3-10	0.09
IGHV4-39	IGHJ2	IGHD4-17	0.09
IGHV4-39	IGHJ2	IGHD5-12	0.09
IGHV4-39	IGHJ4	IGHD2-15	0.09
IGHV4-59	IGHJ3	IGHD3-16	0.09

uman V _H	Human J _H	Human D _H	%
IGHV4-59	IGHJ3	IGHD7-27	0.09
IGHV4-59	IGHJ4	IGHD3-10	0.09
IGHV4-59	IGHJ4	IGHD5-18	0.09
IGHV1-18	IGHJ4	IGHD3-10	0.06
IGHV1-24	IGHJ4	IGHD1-26	0.06
IGHV1-69	IGHJ4	IGHD6-6	0.06
IGHV1-69	IGHJ5	IGHD3-9	0.06
IGHV1-8	IGHJ4	IGHD1-1	0.06
IGHV1-8	IGHJ4	IGHD1-7	0.06
IGHV1-8	IGHJ4	IGHD3-3	0.06
IGHV1-8	IGHJ5	IGHD6-13	0.06
IGHV1-8	IGHJ6	IGHD3-10	0.06
IGHV2-26	IGHJ3	IGHD1-26	0.06
IGHV2-26	IGHJ5	IGHD5-12	0.06
IGHV2-5	IGHJ3	IGHD3-3	0.06
IGHV2-5	IGHJ3	IGHD5-12	0.06
IGHV2-5	IGHJ4	IGHD2-21	0.06
IGHV2-5	IGHJ5	IGHD5-18	0.06
IGHV2-5	IGHJ6	IGHD3-3	0.06
IGHV2-5	IGHJ6	IGHD7-27	0.06
IGHV2-70	IGHJ4	IGHD6-13	0.06
IGHV3-11	IGHJ3	IGHD1-26	0.06
IGHV3-13	IGHJ2	IGHD1-7	0.06
IGHV3-13	IGHJ5	IGHD5-18	0.06
IGHV3-15	IGHJ5	IGHD6-6	0.06
IGHV3-15	IGHJ6	IGHD6-13	0.06
IGHV3-20	IGHJ4	IGHD6-13	0.06
IGHV3-20	IGHJ6	IGHD4-17	0.06
IGHV3-21	IGHJ6	IGHD2-2	0.06
IGHV3-21	IGHJ6	IGHD6-6	0.06

uman V _H	Human J _H	Human D _H	%
IGHV3-23	IGHJ3	IGHD6-6	0.06
IGHV3-23	IGHJ5	IGHD2-2	0.06
IGHV3-23	IGHJ5	IGHD3-16	0.06
IGHV3-30	IGHJ5	IGHD1-7	0.06
IGHV3-33	IGHJ4	IGHD3-3	0.06
IGHV3-43	IGHJ6	IGHD3-10	0.06
IGHV3-43	IGHJ6	IGHD6-13	0.06
IGHV3-48	IGHJ4	IGHD7-27	0.06
IGHV3-49	IGHJ5	IGHD6-6	0.06
IGHV3-64	IGHJ4	IGHD2-2	0.06
IGHV3-72	IGHJ4	IGHD1-26	0.06
IGHV4-34	IGHJ1	IGHD6-6	0.06
IGHV4-34	IGHJ3	IGHD3-16	0.06
IGHV4-34	IGHJ3	IGHD4-17	0.06
IGHV4-34	IGHJ4	IGHD6-19	0.06
IGHV4-39	IGHJ3	IGHD7-27	0.06
IGHV4-39	IGHJ4	IGHD2-2	0.06
IGHV4-39	IGHJ4	IGHD6-13	0.06
IGHV4-39	IGHJ5	IGHD6-6	0.06
IGHV4-39	IGHJ6	IGHD1-26	0.06
IGHV4-59	IGHJ2	IGHD6-13	0.06
IGHV4-59	IGHJ3	IGHD1-26	0.06
IGHV4-59	IGHJ5	IGHD5-12	0.06
IGHV4-59	IGHJ5	IGHD5-18	0.06
IGHV4-59	IGHJ5	IGHD7-27	0.06
IGHV4-59	IGHJ6	IGHD7-27	0.06
IGHV4-59	IGHJ6	IGHD1-7	0.06
IGHV5-51	IGHJ6	IGHD2-2	0.06
IGHV6-1	IGHJ1	IGHD6-13	0.06
IGHV6-1	IGHJ3	IGHD7-27	0.06

uman V _H	Human J _H	Human D _H	%
IGHV6-1	IGHJ4	IGHD1-7	0.06
IGHV1-18	IGHJ3	IGHD1-20	0.03
IGHV1-18	IGHJ3	IGHD1-7	0.03
IGHV1-18	IGHJ3	IGHD5-12	0.03
IGHV1-18	IGHJ4	IGHD1-1	0.03
IGHV1-18	IGHJ4	IGHD2-15	0.03
IGHV1-18	IGHJ4	IGHD2-8	0.03
IGHV1-18	IGHJ4	IGHD6-13	0.03
IGHV1-18	IGHJ4	IGHD7-27	0.03
IGHV1-18	IGHJ5	IGHD1-20	0.03
IGHV1-2	IGHJ3	IGHD1-1	0.03
IGHV1-2	IGHJ4	IGHD1-7	0.03
IGHV1-24	IGHJ3	IGHD6-6	0.03
IGHV1-24	IGHJ4	IGHD4-17	0.03
IGHV1-58	IGHJ4	IGHD6-6	0.03
IGHV1-69	IGHJ4	IGHD3-3	0.03
IGHV1-8	IGHJ4	IGHD6-19	0.03
IGHV1-8	IGHJ6	IGHD3-22	0.03
IGHV2-26	IGHJ3	IGHD1-1	0.03
IGHV2-26	IGHJ3	IGHD6-6	0.03
IGHV2-26	IGHJ4	IGHD1-1	0.03
IGHV2-26	IGHJ4	IGHD5-12	0.03
IGHV2-26	IGHJ4	IGHD5-18	0.03
IGHV2-26	IGHJ4	IGHD6-6	0.03
IGHV2-26	IGHJ5	IGHD6-6	0.03
IGHV2-26	IGHJ6	IGHD3-16	0.03
IGHV2-5	IGHJ3	IGHD5-18	0.03
IGHV2-5	IGHJ4	IGHD3-22	0.03
IGHV2-5	IGHJ4	IGHD3-3	0.03
IGHV2-5	IGHJ4	IGHD5-18	0.03

uman V _H	Human J _H	Human D _H	%
IGHV2-5	IGHJ4	IGHD6-13	0.03
IGHV2-5	IGHJ6	IGHD1-7	0.03
IGHV2-5	IGHJ6	IGHD6-6	0.03
IGHV2-70	IGHJ3	IGHD1-7	0.03
IGHV2-70	IGHJ4	IGHD1-1	0.03
IGHV2-70	IGHJ4	IGHD5-12	0.03
IGHV3-11	IGHJ3	IGHD1-1	0.03
IGHV3-11	IGHJ4	IGHD2-2	0.03
IGHV3-11	IGHJ4	IGHD3-10	0.03
IGHV3-13	IGHJ2	IGHD3-22	0.03
IGHV3-13	IGHJ4	IGHD2-21	0.03
IGHV3-13	IGHJ4	IGHD2-8	0.03
IGHV3-13	IGHJ6	IGHD2-15	0.03
IGHV3-15	IGHJ4	IGHD1-1	0.03
IGHV3-15	IGHJ4	IGHD2-21	0.03
IGHV3-15	IGHJ4	IGHD3-16	0.03
IGHV3-15	IGHJ4	IGHD4-17	0.03
IGHV3-15	IGHJ5	IGHD2-2	0.03
IGHV3-15	IGHJ6	IGHD1-1	0.03
IGHV3-15	IGHJ6	IGHD3-3	0.03
IGHV3-20	IGHJ4	IGHD1-26	0.03
IGHV3-20	IGHJ4	IGHD1-7	0.03
IGHV3-21	IGHJ3	IGHD5-12	0.03
IGHV3-21	IGHJ4	IGHD2-15	0.03
IGHV3-21	IGHJ4	IGHD6-13	0.03
IGHV3-21	IGHJ4	IGHD6-6	0.03
IGHV3-21	IGHJ6	IGHD6-13	0.03
IGHV3-23	IGHJ4	IGHD2-8	0.03
IGHV3-23	IGHJ4	IGHD6-19	0.03
IGHV3-23	IGHJ6	IGHD1-7	0.03

uman V _H	Human J _H	Human D _H	%
IGHV3-23	IGHJ6	IGHD3-3	0.03
IGHV3-23	IGHJ6	IGHD4-17	0.03
IGHV3-30	IGHJ4	IGHD1-26	0.03
IGHV3-30	IGHJ4	IGHD3-10	0.03
IGHV3-30	IGHJ4	IGHD6-13	0.03
IGHV3-33	IGHJ2	IGHD7-27	0.03
IGHV3-33	IGHJ3	IGHD6-6	0.03
IGHV3-33	IGHJ4	IGHD1-20	0.03
IGHV3-33	IGHJ4	IGHD2-15	0.03
IGHV3-33	IGHJ4	IGHD3-16	0.03
IGHV3-33	IGHJ5	IGHD1-26	0.03
IGHV3-33	IGHJ5	IGHD6-6	0.03
IGHV3-33	IGHJ6	IGHD1-20	0.03
IGHV3-33	IGHJ6	IGHD3-22	0.03
IGHV3-33	IGHJ6	IGHD3-9	0.03
IGHV3-48	IGHJ3	IGHD1-26	0.03
IGHV3-48	IGHJ3	IGHD5-12	0.03
IGHV3-48	IGHJ3	IGHD6-6	0.03
IGHV3-48	IGHJ4	IGHD6-6	0.03
IGHV3-48	IGHJ5	IGHD3-22	0.03
IGHV3-53	IGHJ2	IGHD7-27	0.03
IGHV3-53	IGHJ4	IGHD5-18	0.03
IGHV3-53	IGHJ6	IGHD2-15	0.03
IGHV3-64	IGHJ3	IGHD1-7	0.03
IGHV3-7	IGHJ1	IGHD3-3	0.03
IGHV3-7	IGHJ2	IGHD3-3	0.03
IGHV3-7	IGHJ4	IGHD4-17	0.03
IGHV3-7	IGHJ5	IGHD1-7	0.03
IGHV3-7	IGHJ5	IGHD2-8	0.03
IGHV3-72	IGHJ3	IGHD6-6	0.03

uman V _H	Human J _H	Human D _H	%
IGHV3-72	IGHJ4	IGHD1-20	0.03
IGHV3-9	IGHJ3	IGHD1-26	0.03
IGHV3-9	IGHJ4	IGHD1-26	0.03
IGHV3-9	IGHJ4	IGHD3-3	0.03
IGHV3-9	IGHJ4	IGHD6-6	0.03
IGHV3-9	IGHJ4	IGHD7-27	0.03
IGHV3-9	IGHJ6	IGHD1-7	0.03
IGHV4-31	IGHJ2	IGHD7-27	0.03
IGHV4-31	IGHJ4	IGHD6-6	0.03
IGHV4-31	IGHJ6	IGHD3-10	0.03
IGHV4-34	IGHJ1	IGHD1-26	0.03
IGHV4-34	IGHJ2	IGHD6-6	0.03
IGHV4-34	IGHJ2	IGHD7-27	0.03
IGHV4-34	IGHJ3	IGHD1-1	0.03
IGHV4-34	IGHJ3	IGHD1-20	0.03
IGHV4-34	IGHJ3	IGHD1-7	0.03
IGHV4-34	IGHJ4	IGHD2-15	0.03
IGHV4-34	IGHJ4	IGHD5-18	0.03
IGHV4-34	IGHJ5	IGHD1-1	0.03
IGHV4-34	IGHJ5	IGHD1-7	0.03
IGHV4-34	IGHJ5	IGHD2-2	0.03
IGHV4-34	IGHJ5	IGHD6-13	0.03
IGHV4-34	IGHJ5	IGHD6-6	0.03
IGHV4-34	IGHJ6	IGHD1-7	0.03
IGHV4-34	IGHJ6	IGHD2-2	0.03
IGHV4-34	IGHJ6	IGHD3-22	0.03
IGHV4-39	IGHJ2	IGHD6-6	0.03
IGHV4-39	IGHJ3	IGHD1-26	0.03
IGHV4-39	IGHJ3	IGHD6-6	0.03
IGHV4-39	IGHJ4	IGHD3-16	0.03

uman V _H	Human J _H	Human D _H	%
IGHV4-39	IGHJ5	IGHD1-7	0.03
IGHV4-59	IGHJ1	IGHD3-10	0.03
IGHV4-59	IGHJ2	IGHD1-7	0.03
IGHV4-59	IGHJ2	IGHD5-18	0.03
IGHV4-59	IGHJ3	IGHD2-15	0.03
IGHV4-59	IGHJ3	IGHD3-10	0.03
IGHV4-59	IGHJ3	IGHD3-22	0.03
IGHV4-59	IGHJ3	IGHD6-6	0.03
IGHV4-59	IGHJ4	IGHD3-16	0.03
IGHV4-59	IGHJ4	IGHD3-22	0.03
IGHV4-59	IGHJ6	IGHD1-20	0.03
IGHV4-59	IGHJ6	IGHD6-13	0.03
IGHV4-59	IGHJ6	IGHD6-6	0.03
IGHV4-59	IGHJ4	IGHD3-3	0.03
IGHV5-51	IGHJ4	IGHD2-21	0.03
IGHV5-51	IGHJ5	IGHD1-26	0.03
IGHV5-51	IGHJ6	IGHD3-3	0.03
IGHV6-1	IGHJ3	IGHD1-1	0.03
IGHV6-1	IGHJ4	IGHD2-21	0.03
IGHV6-1	IGHJ4	IGHD5-18	0.03
IGHV6-1	IGHJ4	IGHD7-27	0.03
IGHV6-1	IGHJ5	IGHD1-1	0.03
IGHV6-1	IGHJ6	IGHD1-26	0.03
IGHV6-1	IGHJ6	IGHD4-17	0.03
IGHV6-1	IGHJ6	IGHD6-6	0.03

Example 14**Binding Affinity of Bispecific Antibodies Having Universal Light Chains**

[00315] Fully human bispecific antibodies were constructed from cloned human heavy chain variable regions of selected monospecific anti-Antigen E common light chain antibodies (described in Example 5) using standard recombinant DNA techniques known in the art. Table 27 sets forth the pairing of human heavy chains (HC-1 and HC-2) from selected parental monospecific antibodies, each pair employed with a germline rearranged human V κ 1-39/J κ 1 light chain for construction of each bispecific antibody.

[00316] Binding of bispecific or parental monospecific anti-Antigen E antibodies to the extracellular domain (ECD) of Antigen E was determined using a real-time surface plasmon resonance biosensor assay on a BIACORE™ 2000 instrument (GE Healthcare). A CM5 BIACORE™ sensor surface derivatized with anti-c-myc-specific monoclonal antibody (Clone# 9E10) using EDC-NHS chemistry was used to capture the C-terminal myc-myc-hexahistidine tagged ECD of Antigen E (AntigenE-mmh). Around 190 RUs of AntigenE-mmh was captured on the BIACORE™ sensor surface, followed by the injection of 300nM and 50nM concentrations of different bispecific or parental monospecific anti-Antigen E antibodies at a flow rate of 50 μ l/min. The experiment was performed at 25°C in HBST running buffer (0.01M HEPES pH 7.4, 0.15M NaCl, 3mM EDTA, 0.05% v/v Surfactant P20). The amount of antibody binding to AntigenE-mmh surface at 300nM concentration was recorded three seconds before the end of antibody injection and plotted.

[00317] Table 28 and FIG. 8 set forth the binding responses (BIACORE™ units; RU) observed for each bispecific antibody (BsAb) and monospecific parental antibody (PAb-1, PAb-2). Since each antibody was injected under saturating conditions over an identical AntigenE-mmh surface, the binding response reflects the binding stoichiometry for each antibody binding to the antigen capture surface.

[00318] As shown in this Example, the observed binding response for each bispecific antibody was approximately 2-fold greater than the binding response for each parental monospecific antibody (Table 28 and FIG. 8), demonstrating functional construction of bispecific antibodies using heavy chains of antigen-specific monoclonal antibodies and a common light chain where each Fab arm in the bispecific antibody molecule binds simultaneously to distinct epitopes on the extracellular domain of a cell surface receptor (Antigen E; see FIG. 7B, bottom left).

Table 27

Bispecific Antibody	Parent HC-1	Parent HC-2
3108	2952	2978
3109	2978	3022
3111	2952	3005
3112	3022	3005

Table 28

Bispecific Antibody	Binding Response (RU)		
	PAb-1	PAb-2	BsAb
3108	236	229	485
3109	236	197	408
3111	202	229	435
3112	202	197	345

Numbered Further Aspects of the Disclosure

The following represent numbered further aspects of the invention but do not at present represent claims.

- 5 (1) A mouse that expresses a single rearranged human immunoglobulin light chain variable (V_L) region derived from a rearranged germline variable region sequence that comprises a human V_L gene segment derived from a human $V_{\kappa 3-20}$ gene segment and
a human immunoglobulin heavy chain variable (V_H) region cognate with said V_L region wherein the V_H region comprises a human V_H segment derived from a segment
10 selected from V_{H6-1} , V_{H1-2} , V_{H1-3} , V_{H2-5} , V_{H3-7} , V_{H1-8} , V_{H3-9} , V_{H3-11} , V_{H3-13} , V_{H3-15} , V_{H1-18} , V_{H3-20} , V_{H3-21} , V_{H3-23} , V_{H1-24} , V_{H2-26} , V_{H4-28} , V_{H3-30} , V_{H4-31} , V_{H3-33} , V_{H4-34} , V_{H4-39} , V_{H3-43} , V_{H1-46} , V_{H3-48} , V_{H3-49} , V_{H5-51} , V_{H3-53} , V_{H1-58} , V_{H4-59} , V_{H4-61} , V_{H3-64} , V_{H3-66} , V_{H1-69} , V_{H2-70} , V_{H3-72} , and V_{H3-73} .
- (2) The mouse of (1), wherein the V_H region comprises a human V_H segment derived from
15 a segment selected from V_{H1-2} , V_{H1-3} , V_{H2-5} , V_{H3-7} , V_{H1-8} , V_{H3-9} , V_{H3-13} , V_{H3-15} , V_{H3-20} , V_{H3-21} , V_{H3-23} , V_{H1-24} , V_{H2-26} , V_{H4-28} , V_{H4-31} , V_{H4-34} , V_{H3-43} , V_{H1-46} , V_{H3-48} , V_{H3-49} , V_{H1-58} , V_{H4-61} , V_{H3-64} , V_{H3-66} , V_{H3-72} , and V_{H3-73} .
- (3) The mouse of (2), wherein the human V_H segment is derived from V_{H3-49} , V_{H4-28} , V_{H4-61} , or V_{H3-66} .
- 20 (4) The mouse of (1), wherein the human V_L region further comprises a human J_{κ} gene segment derived from a human $J_{\kappa 1}$ gene segment.
- (5) The mouse of (4), wherein the human $V_{\kappa 3-20}$ gene segment is present in rearrangement with the human $J_{\kappa 1}$ gene segment in the mouse germline.
- (6) The mouse of (1), wherein the mouse lacks a mouse immunoglobulin V_L and/or J_L
25 segment(s).
- (7) The mouse of (1), wherein the human V_L region is operably linked to a human, rat, or mouse immunoglobulin light chain constant (C_L) region.
- (8) The mouse of (1), wherein the human V_L region is expressed from an endogenous mouse immunoglobulin light chain locus.
- 30 (9) The mouse of (1), wherein the human V_H region further comprises a human J_H segment derived from J_{H1} , J_{H2} , J_{H3} , J_{H4} , or J_{H5} .
- (10) The mouse of (1), wherein the human V_H region further comprises a D_H segment derived from D_{H7-27} , D_{H1-26} , D_{H6-25} , D_{H5-24} , D_{H4-23} , D_{H3-22} , D_{H2-21} , D_{H1-20} , D_{H6-19} ,

D_H5-18, D_H4-17, D_H3-16, D_H2-15, D_H1-14, D_H6-13, D_H5-12, D_H4-11, D_H3-10, D_H3-9, D_H2-8, D_H1-7, D_H6-6, D_H5-5, D_H4-4, D_H3-3, D_H2-2, or D_H1-1.

(11) The mouse of (1), wherein the human V_H region is operably linked to human, rat, or mouse immunoglobulin heavy chain constant (C_H) region.

5 (12) The mouse of (1), wherein the human V_H region is expressed from an endogenous immunoglobulin heavy chain locus.

(13) A mouse that expresses a single rearranged human immunoglobulin V_L region that is derived from a human rearranged germline V_κ3-20/J_κ1 sequence and a human

immunoglobulin V_H region cognate with the human immunoglobulin V_L region wherein the
10 human immunoglobulin V_H region is derived from a human V_H/D_H/J_H gene segment rearrangement selected from rearrangements listed in Table 25.

(14) A mouse that expresses

a single rearranged human immunoglobulin light chain variable (V_L) region derived from a rearranged germline variable region sequence that comprises a human V_L gene

15 segment derived from a human V_κ1-39 gene segment and

a human immunoglobulin heavy chain variable (V_H) region cognate with said V_L region wherein the V_H region comprises a human V_H segment derived from a segment selected from V_H6-1, V_H1-2, V_H1-3, V_H2-5, V_H3-7, V_H1-8, V_H3-9, V_H3-11, V_H3-13, V_H3-15, V_H1-18, V_H3-20, V_H3-21, V_H3-23, V_H1-24, V_H2-26, V_H4-28, V_H3-30, V_H4-31, V_H3-33, V_H4-
20 34, V_H4-39, V_H3-43, V_H1-46, V_H3-48, V_H3-49, V_H5-51, V_H3-53, V_H1-58, V_H4-59, V_H4-61, V_H3-64, V_H3-66, V_H1-69, V_H2-70, V_H3-72, and V_H3-73.

(15) The mouse of (14), wherein the V_H region comprises a human V_H segment derived from a segment selected from V_H1-2, V_H1-3, V_H3-7, V_H1-8, V_H3-11, V_H3-21, V_H3-23, V_H1-24, V_H2-26, V_H4-28, V_H3-33, V_H3-43, V_H1-46, V_H3-49, V_H1-58, V_H4-61, V_H3-66, V_H2-70,
25 V_H3-72, and V_H3-73.

(16) The mouse of (15), wherein the human V_H segment is derived from V_H3-49, V_H4-61, V_H4-28, or V_H3-66.

(17) The mouse of (14), wherein the human V_L region further comprises a human J_κ gene segment derived from a human J_κ5 gene segment.

30 (18) The mouse of (17), wherein the human V_κ1-39 gene segment is present in rearrangement with the human J_κ5 gene segment in the mouse germline.

(19) The mouse of (14), wherein the mouse lacks a mouse immunoglobulin V_L and/or J_L segment(s).

(20) The mouse of (14), wherein the human V_L region is operably linked to a human, rat, or mouse immunoglobulin light chain constant (C_L) region.

(21) The mouse of (14), wherein the human V_L region is expressed from an endogenous mouse immunoglobulin light chain locus.

5 (22) The mouse of (14), wherein the human V_H region further comprises a human J_H segment derived from J_H1, J_H2, J_H3, J_H4, or J_H5.

(23) The mouse of (14), wherein the human V_H region further comprises a D_H segment derived from D_H7-27, D_H1-26, D_H6-25, D_H5-24, D_H4-23, D_H3-22, D_H2-21, D_H1-20, D_H6-19, D_H5-18, D_H4-17, D_H3-16, D_H2-15, D_H1-14, D_H6-13, D_H5-12, D_H4-11, D_H3-10, D_H3-9, D_H2-10, D_H1-7, D_H6-6, D_H5-5, D_H4-4, D_H3-3, D_H2-2, or D_H1-1.

(24) The mouse of (14), wherein the human V_H region is operably linked to human, rat, or mouse immunoglobulin heavy chain constant (C_H) region.

(25) The mouse of (14), wherein the human V_H region is expressed from an endogenous immunoglobulin heavy chain locus.

15 (26) A mouse that expresses a single rearranged human immunoglobulin V_L region that is derived from a human rearranged germline Vκ1-39/Jκ5 gene segment and a human immunoglobulin V_H region cognate with the human immunoglobulin V_L region wherein the human immunoglobulin V_H region is derived from a human V_H/D_H/J_H gene segment rearrangement selected from rearrangements listed in Table 26.

Additional numbered further Aspects of the Disclosure

The following represent additional numbered further aspects of the invention but do not at present represent claims.

5 (27) A method of making a fully human bispecific antibody comprising:

a) expressing a first human heavy chain comprising a first human variable region that is found in B cells of a genetically engineered mouse, which mouse:

10 i) has a germline genome that is homozygous or heterozygous for a universal kappa light chain gene consisting of a human germline V_κ gene segment rearranged to a human germline J_κ gene segments operably linked with a C_κ gene segment; and also includes unrearranged human V_H gene segments operably linked with a C_H gene segment; and

15 ii) includes B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human V_H gene segments, wherein the rearranged human V_H gene segments include each of V_H6-1, V_H1-2, V_H1-3, V_H2-5, V_H3-7, V_H1-8, V_H3-9, V_H3-11, V_H3-13, V_H3-15, V_H1-18, V_H3-20, V_H3-21, V_H3-23, V_H1-24, V_H2-26, V_H4-28, V_H3-30, V_H4-31, V_H3-33, V_H4-34, V_H4-39, V_H3-43, V_H1-46, V_H3-48, V_H3-49, V_H5-51, V_H3-53, V_H1-58, V_H4-59, V_H4-61, V_H3-64, V_H3-66, V_H1-69, V_H2-70, 20 V_H3-72, V_H3-73; and

b) pairing the expressed first human heavy chain with a human light chain and with a second human heavy chain that also binds to the human light chain.

(28) The method of (27), wherein the rearranged human germline V_κ and J_κ gene segments are operably linked with a mouse C_κ gene segment or a rat C_κ gene segment.

25 (29) The method of (27) or (28), wherein the unrearranged human V_H gene segments are operatively linked with a mouse C_H gene segment or a rat C_H gene segment.

(30) The method of any one of (27) to (29), wherein the second human heavy chain 30 comprises a second human variable region that is also found in B cells of the genetically engineered mouse.

(31) The method of any one of (27) to (30), wherein the human germline V κ gene segment is a V κ 1-39 or V κ 3-20 gene segment.

(32) The method of any one of (27) to (31), wherein the universal kappa light chain consists of human germline V κ 1-39 rearranged to human germline J κ 5 or human V κ 3-20 rearranged to human J κ 1.

(33) The method of any one of (27) to (32), wherein the mouse:

(i) has a germline that includes unrearranged human D_H gene segments operatively linked with both the human V_H gene segments and the mouse C_H gene segment; and

(ii) includes B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human D_H gene segments, wherein the rearranged human D_H gene segments include each of D_H7-27, D_H1-26, D_H6-25, D_H5-24, D_H4-23, D_H3-22, D_H2-21, D_H1-20, D_H6-19, D_H5-18, D_H4-17, D_H3-16, D_H2-15, D_H1-14, D_H6-13, D_H5-12, D_H4-11, D_H3-10, D_H3-9, D_H2-8, D_H1-7, D_H6-6, D_H5-5, D_H4-4, D_H3-3, D_H2-2, D_H1-1.

(34) The method of (33), wherein the mouse has a germline that includes unrearranged human J_H gene segments operatively linked with the human V_H gene segments and the human D_H gene segments, and thereby with the mouse C_H gene segments.

(35) The method of (34), wherein the rearranged human germline V κ gene segment is a V κ 1-39 gene segment and the mouse includes B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human V_H, J_H, and D_H gene segments as set forth in Table 26.

(36) The method of (34), wherein the rearranged human germline V κ gene segment is a V κ 3-20 gene segment and the mouse includes B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human V_H, J_H, and D_H gene segments as set forth in Table 25.

(37) The method of any one of (27) to (36), wherein the first human variable region is encoded by a rearranged V_H3-49, V_H4-28, V_H4-61, or V_H3-66 derived gene segment.

(38) The method of any one of (27) to (37), wherein the only kappa light chain expressed by the B cells is encoded by the universal kappa light chain gene or by a somatically mutated variant thereof.

5 (39) The method of any one of (27) to (38), wherein the only light chain expressed by the B cells is encoded by the universal kappa light chain gene or by a somatically mutated variant thereof.

(40) The method of any one of (27) to (39), wherein the unrearranged human V_H gene
10 segments replace endogenous mouse V_H gene segments.

(41) A bispecific antibody produced according to the method of any one of (27) to (40).

(42) A method of identifying a human immunoglobulin heavy chain variable region useful in
15 the production of bi-specific antibodies, the method comprising a step of:

identifying the human immunoglobulin heavy chain variable region as expressed in B cells of a genetically engineered mouse, which mouse:

i) has a germline genome that is homozygous or heterozygous for a universal kappa light chain gene consisting of a human germline V_K gene segment rearranged
20 to a human germline J_K gene segment operably linked with a C_K gene segment; and also includes unrearranged human V_H gene segments operably linked with a C_H gene segment; and

ii) includes B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human V_H gene segments, wherein the rearranged human
25 V_H gene segments include each of V_{H6-1} , V_{H1-2} , V_{H1-3} , V_{H2-5} , V_{H3-7} , V_{H1-8} , V_{H3-9} , V_{H3-11} , V_{H3-13} , V_{H3-15} , V_{H1-18} , V_{H3-20} , V_{H3-21} , V_{H3-23} , V_{H1-24} , V_{H2-26} , V_{H4-28} , V_{H3-30} , V_{H4-31} , V_{H3-33} , V_{H4-34} , V_{H4-39} , V_{H3-43} , V_{H1-46} , V_{H3-48} , V_{H3-49} , V_{H5-51} , V_{H3-53} , V_{H1-58} , V_{H4-59} , V_{H4-61} , V_{H3-64} , V_{H3-66} , V_{H1-69} , V_{H2-70} , V_{H3-72} , V_{H3-73} .

30 (43) The method of (42), wherein the rearranged human germline V_K and J_K gene segments are operably linked with a mouse C_K gene segment or a rat C_K gene segment.

(44) The method of (42) or (43), wherein the unrearranged human V_H gene segments are operatively linked with a mouse C_H gene segment or a rat C_H gene segment.

(45) The method of any one of (42) to (44), wherein the human germline V_K gene segment is
5 a V_{K1-39} or V_{K3-20} gene segment.

(46) The method of any one of (42) to (45), wherein the universal kappa light chain consists of human germline V_{K1-39} rearranged to human germline J_{K5} or human V_{K3-20} rearranged to human J_{K1} .

10

(47) The method of any one of (42) to (46), wherein the mouse:

(i) has a germline that includes unrearranged human D_H gene segments operatively linked with both the human V_H gene segments and the mouse C_H gene segment; and

(ii) includes B cells, pre-immunization, that express heavy chain genes arising from
15 rearrangement of the human D_H gene segments, wherein the rearranged human D_H gene segments include each of D_{H7-27} , D_{H1-26} , D_{H6-25} , D_{H5-24} , D_{H4-23} , D_{H3-22} , D_{H2-21} , D_{H1-20} , D_{H6-19} , D_{H5-18} , D_{H4-17} , D_{H3-16} , D_{H2-15} , D_{H1-14} , D_{H6-13} , D_{H5-12} , D_{H4-11} , D_{H3-10} , D_{H3-9} , D_{H2-8} , D_{H1-7} , D_{H6-6} , D_{H5-5} , D_{H4-4} , D_{H3-3} , D_{H2-2} , D_{H1-1} .

20 (48) The method of (47), wherein the mouse has a germline that includes unrearranged human J_H gene segments operatively linked with the human V_H gene segments and the human D_H gene segments, and thereby with the mouse C_H gene segments.

(49) The method of (48), wherein the rearranged human germline V_K gene segment is a
25 V_{K1-39} gene segment and the mouse includes B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human V_H , J_H , and D_H gene segments as set forth in Table 26.

(50) The method of (48), wherein the rearranged human germline V_K gene segment is a
30 V_{K3-20} gene segment and the mouse includes B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human V_H , J_H , and D_H gene segments as set forth in Table 25.

(51) The method of any one of (42) to (50), wherein the first human variable region is encoded by a rearranged V_H3-49, V_H4-28, V_H4-61, or V_H3-66 derived gene segment.

5 (52) The method of any one of (42) to (51), wherein the only kappa light chain expressed by the B cells is encoded by the universal kappa light chain gene or by a somatically mutated variant thereof.

10 (53) The method of any one of (42) to (52), wherein the only light chain expressed by the B cells is encoded by the universal kappa light chain gene or by a somatically mutated variant thereof.

(54) The method of any one of (42) to (53), wherein the unrearranged human V_H gene segments replace endogenous mouse V_H gene segments.

15 (55) A method of making a product that is an antigen-binding protein comprising:
(a) identifying a human immunoglobulin heavy chain variable region as expressed in B cells of a genetically engineered mouse, which mouse:

20 i) has a germline genome that is homozygous or heterozygous for a universal kappa light chain gene consisting of rearranged human germline V_κ and J_κ gene segments; and also includes unrearranged human V_H gene segments; and

25 ii) includes B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human V_H gene segments, wherein the rearranged human V_H gene segments include each of V_H6-1, V_H1-2, V_H1-3, V_H2-5, V_H3-7, V_H1-8, V_H3-9, V_H3-11, V_H3-13, V_H3-15, V_H1-18, V_H3-20, V_H3-21, V_H3-23, V_H1-24, V_H2-26, V_H4-28, V_H3-30, V_H4-31, V_H3-33, V_H4-34, V_H4-39, V_H3-43, V_H1-46, V_H3-48, V_H3-49, V_H5-51, V_H3-53, V_H1-58, V_H4-59, V_H4,

30 where the heavy chain variable region identified is derived from one of V_H6-1, V_H1-2, V_H1-3, V_H2-5, V_H3-7, V_H1-8, V_H3-9, V_H3-11, V_H3-13, V_H3-15, V_H1-18, V_H3-20, V_H3-21, V_H3-23, V_H1-24, V_H2-26, V_H4-28, V_H3-30, V_H4-31, V_H3-33, V_H4-34, V_H4-39, V_H3-43, V_H1-46, V_H3-48, V_H3-49, V_H5-51, V_H3-53, V_H1-58, V_H4-59, V_H4

(b) expressing a heavy chain comprising the human heavy chain variable region identified and a human heavy chain constant region with a light chain comprising a light

chain variable region selected from V κ 1-39/J κ and V κ 3-20/J κ and a human light chain constant region.

5 (56) The method of (55), wherein the rearranged human germline V κ and J κ gene segments are operably linked with a mouse C κ gene segment or a rat C κ gene segment.

(57) The method of (55) or (56), wherein the unrearranged human V H gene segments are operatively linked with a mouse C H gene segment or a rat C H gene segment.

10 (58) The method of any one of (55) to (57), wherein the human germline V κ gene segment is a V κ 1-39 or V κ 3-20 gene segment.

(59) The method of any one of (55) to (58), wherein the universal kappa light chain consists of human germline V κ 1-39 rearranged to human germline J κ 5 or human V κ 3-20 rearranged
15 to human J κ 1.

(60) The method of any one of (55) to (58), wherein the mouse:

(i) has a germline that includes unrearranged human D H gene segments operatively linked with both the human V H gene segments and the mouse C H gene segment; and

20 (ii) includes B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human D H gene segments, wherein the rearranged human D H gene segments include each of D H 7-27, D H 1-26, D H 6-25, D H 5-24, D H 4-23, D H 3-22, D H 2-21, D H 1-20, D H 6-19, D H 5-18, D H 4-17, D H 3-16, D H 2-15, D H 1-14, D H 6-13, D H 5-12, D H 4-11, D H 3-10, D H 3-9, D H 2-8, D H 1-7, D H 6-6, D H 5-5, D H 4-4, D H 3-3, D H 2-2, D H 1-1.

25

(61) The method of (60), wherein the mouse has a germline that includes unrearranged human J H gene segments operatively linked with the human V H gene segments and the human D H gene segments, and thereby with the mouse C H gene segments.

30 (62) The method of (61), wherein the rearranged human germline V κ gene segment is a V κ 1-39 gene segment and the mouse includes B cells, pre-immunization, that express heavy

chain genes arising from rearrangement of the human V_H , J_H , and D_H gene segments as set forth in Table 26.

(63) The method of (61), wherein the rearranged human germline V_K gene segment is a V_{K3-20} gene segment and the mouse includes B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human V_H , J_H , and D_H gene segments as set forth in Table 25.

(64) The method of any one of (55) to (63), wherein the first human variable region is encoded by a rearranged V_{H3-49} , V_{H4-28} , V_{H4-61} , or V_{H3-66} derived gene segment.

(65) The method of any one of (55) to (64), wherein the only kappa light chain expressed by the B cells is encoded by the universal kappa light chain gene or by a somatically mutated variant thereof.

(66) The method of any one of (55) to (65), wherein the only light chain expressed by the B cells is encoded by the universal kappa light chain gene or by a somatically mutated variant thereof.

(67) The method of any one of (55) to (66), wherein the unrearranged human V_H gene segments replace endogenous mouse V_H gene segments.

(68) A bispecific antibody produced according to the method of any one of (55) to (67).

(69) A method for making a bispecific antigen-binding protein, comprising:

(a) exposing a first genetically modified mouse to a first antigen of interest that comprises a first epitope;

(b) exposing a second genetically modified mouse, which is the same or different mouse, to a second antigen of interest that comprises a second epitope;

(c) allowing the first and the second mouse to each mount immune responses to the antigens of interest, identifying in the first mouse a first human heavy chain variable region that binds the first epitope of the first antigen of interest, identifying in the second mouse a second human heavy chain variable region that binds the second epitope of the second

antigen of interest, making a first fully human heavy chain gene that encodes a first heavy chain that binds the first epitope of the first antigen of interest, making a second fully human heavy chain gene that encodes a second heavy chain that binds the second epitope of the second antigen of interest, expressing the first heavy chain and the second heavy chain in a cell that expresses a single fully human light chain derived from a human V κ 1-39/J or a human V κ 3-20/J gene segment to form a bispecific antigen-binding protein, and isolating the bispecific antigen-binding protein,

the first and second mice expressing human immunoglobulin heavy and light chain variable domains, where:

(i) the mice express an immunoglobulin light chain variable domain repertoire consisting of a single human light chain variable domain which is expressed from a rearranged human V κ 1-39/J gene or a human V κ 3-20/J gene; and

(ii) the mice include B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human V_H gene segments, wherein the rearranged human V_H gene segments include each of V_H6-1, V_H1-2, V_H1-3, V_H2-5, V_H3-7, V_H1-8, V_H3-9, V_H3-11, V_H3-13, V_H3-15, V_H1-18, V_H3-20, V_H3-21, V_H3-23, V_H1-24, V_H2-26, V_H4-28, V_H3-30, V_H4-31, V_H3-33, V_H4-34, V_H4-39, V_H3-43, V_H1-46, V_H3-48, V_H3-49, V_H5-51, V_H3-53, V_H1-58, V_H4-59, V_H4-61, V_H3-64, V_H3-66, V_H1-69, V_H2-70, V_H3-72, V_H3-73.

(70) The method of (69), wherein the rearranged human V κ 1-39/J gene or a human V κ 3-20/J gene are operably linked with a mouse C κ gene segment or a rat C κ gene segment.

(71) The method of (69) or (70), wherein the rearranged human V κ 1-39/J gene is or a human V κ 1-39/J κ 5 or the rearranged human V κ 3-20/J is human V κ 3-20/J κ 1.

(72) The method of any one of (69) to (71), wherein the mouse:

(i) has a germline that includes unrearranged human D_H gene segments operatively linked with both human V_H gene segments and a mouse C_H gene segment; and

(ii) includes B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human D_H gene segments, wherein the rearranged human D_H gene segments include each of D_H7-27, D_H1-26, D_H6-25, D_H5-24, D_H4-23, D_H3-22, D_H2-21, D_H1-20, D_H6-19, D_H5-18, D_H4-17, D_H3-16, D_H2-15, D_H1-14, D_H6-13, D_H5-12, D_H4-11, D_H3-10, D_H3-9, D_H2-8, D_H1-7, D_H6-6, D_H5-5, D_H4-4, D_H3-3, D_H2-2, D_H1-1.

(73) The method of (72), wherein the mouse has a germline that includes unrearranged human J_H gene segments operatively linked with the human V_H gene segments and the human D_H gene segments, and thereby with the mouse C_H gene segments.

(74) The method of (73), wherein the rearranged human germline V_κ gene segment is a V_κ1-39/J gene segment and the mouse includes B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human V_H, J_H, and D_H gene segments as set forth in Table 26.

(75) The method of (72), wherein the rearranged human germline V_κ gene segment is a V_κ3-20/J gene segment and the mouse includes B cells, pre-immunization, that express heavy chain genes arising from rearrangement of the human V_H, J_H, and D_H gene segments as set forth in Table 25.

(76) The method of any one of (69) to (75), wherein the first human variable region is encoded by a rearranged V_H3-49, V_H4-28, V_H4-61, or V_H3-66 derived gene segment.

(77) The method of any one of (69) to (76), wherein the unrearranged human V_H gene segments replace endogenous mouse V_H gene segments.

(78) A bispecific antibody produced according to the method of any one of (69) to (77).

Conclusies

1. Een gastheercel omvattende:

(a) een eerste nucleïnezuur sequentie coderend voor een eerste humane

5 immunoglobuline zware keten welke aan een eerste antigen bindt, waarbij de eerste humane immunoglobuline zware keten een sequentie omvat van een eerste variabele domein van de humane zware keten welke gecodeerd wordt door een nucleotide sequentie verkregen uit van een eerste muis welke geïmmuniseerd is met het eerste antigen;

10 (b) een tweede nucleïnezuur sequentie coderend voor een tweede humane immunoglobuline zware keten welke aan een tweede antigen bindt, waarbij de tweede humane immunoglobuline zware keten een sequentie omvat van een tweede variabele domein van de humane zware keten welke gecodeerd wordt door een nucleotide sequentie verkregen uit een tweede muis welke geïmmuniseerd is met het tweede antigen;

15

waarbij de eerste en de tweede muis beide tot expressie brengen (i) een variabel domein van de humane immunoglobuline lichte keten welke gecodeerd wordt door een enkel herrangschikt variabel gebied van de humane immunoglobuline lichte keten gen sequentie afkomstig van dezelfde herrangschikte humane V κ 1-39/J κ sequentie welke aanwezig is in de

20 kiembaan van de muis, waarbij de herrangschikte humane V κ 1-39/J κ sequentie een humaan kiembaan V κ 1-39 gen segment en een humaan kiembaan J κ gen segment omvat , welke herrangschikte V κ 1-39/J κ sequentie operabel gekoppeld is aan een constant gebied van de immunoglobuline lichte keten sequentie, en (ii) een meervoud van variabele domeinen van de humane immunoglobuline zware keten; en

25

(c) een derde nucleïnezuur sequentie coderend voor een humane immunoglobuline lichte keten omvattende een enkel herrangschikt variabel gebied van de humane immunoglobuline lichte keten gen sequentie afkomstig van dezelfde herrangschikte humane V κ 1-39/J κ sequentie;

30

waarbij ten minste één van de eerste of de tweede variabele domeinen van het humane immunoglobuline afkomstig is van een herrangschikt humaan V_H/D/J_H gebied geselecteerd uit

de groep bestaande uit de herrangschikkingen zoals beschreven in tabellen 29 en 30

hieronder:

5

Tabel 29

Humaan V_H	Humaan J_H	Humaan D_H
IGHV2-70	IGHJ3	IGHD3-10
IGHV4-59	IGHJ4	IGHD1-26
IGHV2-26	IGHJ4	IGHD3-9
IGHV4-28	IGHJ4	IGHD1-26
IGHV1-18	IGHJ6	IGHD1-26
IGHV2-5	IGHJ4	IGHD1-7
IGHV1-18	IGHJ3	IGHD4-17
IGHV4-59	IGHJ4	IGHD6-6
IGHV3-33	IGHJ4	IGHD6-6
IGHV1-69	IGHJ4	IGHD6-13
IGHV3-64	IGHJ4	IGHD1-7
IGHV4-39	IGHJ4	IGHD3-10
IGHV3-23	IGHJ4	IGHD1-26
IGHV1-18	IGHJ4	IGHD6-6
IGHV3-23	IGHJ4	IGHD1-7
IGHV3-11	IGHJ4	IGHD5-18
IGHV1-18	IGHJ6	IGHD6-19
IGHV2-5	IGHJ4	IGHD6-19
IGHV3-15	IGHJ4	IGHD7-27
IGHV4-34	IGHJ6	IGHD6-13
IGHV4-59	IGHJ4	IGHD7-27
IGHV1-18	IGHJ6	IGHD3-9
IGHV2-26	IGHJ4	IGHD1-26
IGHV1-18	IGHJ3	IGHD7-27
IGHV4-59	IGHJ6	IGHD3-3
IGHV3-33	IGHJ6	IGHD6-6
IGHV3-7	IGHJ4	IGHD6-13
IGHV3-7	IGHJ6	IGHD6-19
IGHV1-18	IGHJ4	IGHD1-7
IGHV1-69	IGHJ6	IGHD5-12
IGHV3-72	IGHJ6	IGHD6-6
IGHV4-34	IGHJ3	IGHD6-6
IGHV3-21	IGHJ6	IGHD2-8

Humaan V_H	Humaan J_H	Humaan D_H
IGHV3-30	IGHJ4	IGHD3-22
IGHV3-33	IGHJ4	IGHD1-7
IGHV6-1	IGHJ4	IGHD1-26
IGHV4-59	IGHJ4	IGHD6-13
IGHV1-8	IGHJ4	IGHD1-26
IGHV3-13	IGHJ4	IGHD3-10
IGHV2-70	IGHJ4	IGHD1-26
IGHV3-33	IGHJ5	IGHD1-1
IGHV1-18	IGHJ4	IGHD1-26
IGHV1-8	IGHJ6	IGHD1-7
IGHV1-8	IGHJ4	IGHD3-10
IGHV3-15	IGHJ5	IGHD1-20
IGHV3-23	IGHJ6	IGHD6-13
IGHV3-33	IGHJ2	IGHD3-10
IGHV2-70	IGHJ5	IGHD3-10
IGHV3-15	IGHJ6	IGHD6-6
IGHV3-21	IGHJ6	IGHD4-17
IGHV1-18	IGHJ6	IGHD6-13
IGHV1-8	IGHJ4	IGHD1-26
IGHV3-13	IGHJ4	IGHD6-25
IGHV3-23	IGHJ4	IGHD6-13
IGHV4-39	IGHJ4	IGHD1-7
IGHV1-18	IGHJ4	IGHD2-2
IGHV2-26	IGHJ5	IGHD3-3
IGHV3-13	IGHJ4	IGHD4-17
IGHV3-13	IGHJ6	IGHD3-10
IGHV4-34	IGHJ6	IGHD1-26
IGHV4-59	IGHJ6	IGHD4-17
IGHV1-18	IGHJ6	IGHD3-22
IGHV1-46	IGHJ4	IGHD6-13
IGHV1-8	IGHJ6	IGHD2-2
IGHV1-8	IGHJ3	IGHD3-9
IGHV3-13	IGHJ4	IGHD1-7

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-33	IGHJ2	IGHD6-6
IGHV3-48	IGHJ4	IGHD1-7
IGHV4-39	IGHJ4	IGHD5-12
IGHV4-59	IGHJ6	IGHD3-22
IGHV1-8	IGHJ6	IGHD3-3
IGHV2-5	IGHJ3	IGHD6-6
IGHV3-43	IGHJ4	IGHD6-6
IGHV4-39	IGHJ4	IGHD6-19
IGHV4-59	IGHJ4	IGHD1-1
IGHV2-26	IGHJ4	IGHD3-16
IGHV2-70	IGHJ3	IGHD7-27
IGHV3-15	IGHJ1	IGHD6-6
IGHV3-23	IGHJ4	IGHD3-9
IGHV3-53	IGHJ5	IGHD6-6
IGHV3-64	IGHJ2	IGHD1-1
IGHV3-11	IGHJ4	IGHD3-10
IGHV3-13	IGHJ4	IGHD3-16
IGHV3-13	IGHJ4	IGHD6-6
IGHV3-33	IGHJ4	IGHD1-26
IGHV3-9	IGHJ3	IGHD1-7
IGHV3-9	IGHJ5	IGHD1-26
IGHV4-34	IGHJ4	IGHD3-16
IGHV4-39	IGHJ4	IGHD2-8
IGHV4-59	IGHJ4	IGHD3-3
IGHV2-26	IGHJ3	IGHD3-22
IGHV2-5	IGHJ4	IGHD6-6
IGHV2-70	IGHJ5	IGHD4-17
IGHV3-13	IGHJ4	IGHD1-1
IGHV3-13	IGHJ4	IGHD1-26
IGHV3-13	IGHJ6	IGHD5-18
IGHV3-7	IGHJ5	IGHD6-19
IGHV4-39	IGHJ5	IGHD6-13
IGHV1-69	IGHJ6	IGHD3-22
IGHV1-8	IGHJ3	IGHD5-18
IGHV2-26	IGHJ2	IGHD7-27
IGHV2-5	IGHJ3	IGHD1-1
IGHV2-5	IGHJ4	IGHD1-26
IGHV3-13	IGHJ3	IGHD3-22
IGHV3-15	IGHJ4	IGHD6-13
IGHV3-21	IGHJ6	IGHD1-7
IGHV3-48	IGHJ4	IGHD6-13
IGHV3-9	IGHJ6	IGHD1-26

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-39	IGHJ4	IGHD1-26
IGHV1-18	IGHJ2	IGHD3-10
IGHV1-8	IGHJ4	IGHD2-8
IGHV2-5	IGHJ4	IGHD4-17
IGHV2-70	IGHJ4	IGHD1-7
IGHV2-70	IGHJ4	IGHD6-6
IGHV3-15	IGHJ4	IGHD1-26
IGHV3-15	IGHJ4	IGHD1-7
IGHV3-23	IGHJ5	IGHD3-9
IGHV3-23	IGHJ6	IGHD6-6
IGHV3-30	IGHJ3	IGHD3-16
IGHV3-48	IGHJ3	IGHD7-27
IGHV3-48	IGHJ4	IGHD3-9
IGHV3-64	IGHJ6	IGHD6-6
IGHV3-7	IGHJ3	IGHD6-13
IGHV3-7	IGHJ4	IGHD6-6
IGHV4-31	IGHJ4	IGHD1-26
IGHV4-31	IGHJ6	IGHD6-6
IGHV4-39	IGHJ3	IGHD1-7
IGHV4-59	IGHJ4	IGHD2-15
IGHV1-18	IGHJ5	IGHD1-7
IGHV1-18	IGHJ5	IGHD3-3
IGHV1-2	IGHJ4	IGHD3-3
IGHV1-24	IGHJ4	IGHD5-18
IGHV1-8	IGHJ4	IGHD7-27
IGHV1-8	IGHJ6	IGHD3-3
IGHV2-5	IGHJ5	IGHD3-10
IGHV3-23	IGHJ2	IGHD6-6
IGHV3-23	IGHJ3	IGHD1-26
IGHV3-23	IGHJ5	IGHD1-7
IGHV3-33	IGHJ4	IGHD6-13
IGHV3-7	IGHJ5	IGHD5-18
IGHV3-9	IGHJ6	IGHD6-6
IGHV4-28	IGHJ3	IGHD2-15
IGHV4-34	IGHJ4	IGHD1-7
IGHV4-39	IGHJ4	IGHD7-27
IGHV4-59	IGHJ3	IGHD1-1
IGHV1-58	IGHJ6	IGHD6-13
IGHV1-69	IGHJ5	IGHD3-10
IGHV2-26	IGHJ4	IGHD1-7
IGHV2-5	IGHJ4	IGHD2-2
IGHV2-70	IGHJ3	IGHD1-20

Humaan V _H	Humaan J _H	Humaan D _H
IGHV2-70	IGHJ5	IGHD6-13
IGHV3-23	IGHJ6	IGHD7-27
IGHV3-7	IGHJ3	IGHD2-2
IGHV3-7	IGHJ4	IGHD1-7
IGHV3-9	IGHJ3	IGHD6-6
IGHV3-9	IGHJ4	IGHD6-19
IGHV3-9	IGHJ5	IGHD1-7
IGHV4-34	IGHJ4	IGHD3-3
IGHV4-59	IGHJ4	IGHD1-7
IGHV1-69	IGHJ6	IGHD7-27
IGHV1-8	IGHJ1	IGHD6-6
IGHV1-8	IGHJ4	IGHD1-20
IGHV1-8	IGHJ4	IGHD3-3
IGHV2-5	IGHJ4	IGHD1-20
IGHV2-70	IGHJ5	IGHD1-26
IGHV3-13	IGHJ4	IGHD6-13
IGHV3-21	IGHJ2	IGHD3-22
IGHV3-23	IGHJ3	IGHD3-16
IGHV3-23	IGHJ3	IGHD3-9
IGHV3-23	IGHJ4	IGHD5-18
IGHV3-48	IGHJ4	IGHD1-26
IGHV3-48	IGHJ4	IGHD3-10
IGHV3-48	IGHJ6	IGHD3-9
IGHV3-7	IGHJ4	IGHD6-6
IGHV3-7	IGHJ5	IGHD2-21
IGHV3-9	IGHJ6	IGHD3-10
IGHV4-34	IGHJ4	IGHD6-6
IGHV4-34	IGHJ4	IGHD7-27
IGHV4-34	IGHJ6	IGHD3-10
IGHV4-39	IGHJ2	IGHD7-27
IGHV4-39	IGHJ4	IGHD6-6
IGHV4-59	IGHJ3	IGHD4-17
IGHV4-59	IGHJ4	IGHD3-9
IGHV4-59	IGHJ5	IGHD6-13
IGHV4-59	IGHJ6	IGHD3-10
IGHV6-1	IGHJ4	IGHD1-1
IGHV1-18	IGHJ5	IGHD6-13
IGHV1-2	IGHJ5	IGHD1-7
IGHV2-26	IGHJ4	IGHD7-27
IGHV2-5	IGHJ4	IGHD1-1
IGHV2-70	IGHJ3	IGHD2-2
IGHV2-70	IGHJ4	IGHD2-8

Humaan V _H	Humaan J _H	Humaan D _H
IGHV2-70	IGHJ5	IGHD6-6
IGHV3-13	IGHJ4	IGHD1-20
IGHV3-15	IGHJ4	IGHD3-22
IGHV3-21	IGHJ4	IGHD1-26
IGHV3-23	IGHJ3	IGHD1-20
IGHV3-23	IGHJ4	IGHD4-17
IGHV3-23	IGHJ4	IGHD5-12
IGHV3-23	IGHJ6	IGHD2-2
IGHV3-30	IGHJ6	IGHD3-10
IGHV3-48	IGHJ4	IGHD1-1
IGHV3-49	IGHJ2	IGHD3-10
IGHV3-9	IGHJ4	IGHD5-18
IGHV4-59	IGHJ3	IGHD1-7
IGHV4-59	IGHJ6	IGHD1-26
IGHV6-1	IGHJ5	IGHD1-20
IGHV1-18	IGHJ4	IGHD5-18
IGHV1-18	IGHJ6	IGHD6-6
IGHV2-26	IGHJ3	IGHD6-13
IGHV2-5	IGHJ6	IGHD6-13
IGHV2-70	IGHJ4	IGHD2-15
IGHV2-70	IGHJ4	IGHD3-3
IGHV3-11	IGHJ6	IGHD1-7
IGHV3-15	IGHJ3	IGHD1-7
IGHV3-15	IGHJ4	IGHD3-3
IGHV3-21	IGHJ4	IGHD7-27
IGHV3-21	IGHJ6	IGHD1-20
IGHV3-21	IGHJ6	IGHD3-10
IGHV3-23	IGHJ3	IGHD7-27
IGHV3-23	IGHJ5	IGHD1-26
IGHV3-23	IGHJ5	IGHD7-27
IGHV3-30	IGHJ4	IGHD2-15
IGHV3-33	IGHJ4	IGHD1-1
IGHV3-33	IGHJ4	IGHD3-22
IGHV3-48	IGHJ3	IGHD6-13
IGHV3-48	IGHJ4	IGHD5-12
IGHV3-7	IGHJ4	IGHD1-20
IGHV3-7	IGHJ4	IGHD1-26
IGHV4-34	IGHJ4	IGHD1-26
IGHV4-34	IGHJ4	IGHD3-10
IGHV4-39	IGHJ2	IGHD4-17
IGHV4-39	IGHJ2	IGHD5-12
IGHV4-39	IGHJ4	IGHD2-15

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-59	IGHJ3	IGHD7-27
IGHV4-59	IGHJ4	IGHD3-10
IGHV4-59	IGHJ4	IGHD5-18
IGHV1-18	IGHJ4	IGHD3-10
IGHV1-24	IGHJ4	IGHD1-26
IGHV1-69	IGHJ4	IGHD6-6
IGHV1-69	IGHJ5	IGHD3-9
IGHV1-8	IGHJ4	IGHD1-1
IGHV1-8	IGHJ4	IGHD1-7
IGHV1-8	IGHJ4	IGHD3-3
IGHV1-8	IGHJ5	IGHD6-13
IGHV1-8	IGHJ6	IGHD3-10
IGHV2-26	IGHJ3	IGHD1-26
IGHV2-26	IGHJ5	IGHD5-12
IGHV2-5	IGHJ3	IGHD3-3
IGHV2-5	IGHJ3	IGHD5-12
IGHV2-5	IGHJ4	IGHD2-21
IGHV2-5	IGHJ5	IGHD5-18
IGHV2-5	IGHJ6	IGHD3-3
IGHV2-5	IGHJ6	IGHD7-27
IGHV2-70	IGHJ4	IGHD6-13
IGHV3-11	IGHJ3	IGHD1-26
IGHV3-13	IGHJ2	IGHD1-7
IGHV3-13	IGHJ5	IGHD5-18
IGHV3-15	IGHJ5	IGHD6-6
IGHV3-15	IGHJ6	IGHD6-13
IGHV3-20	IGHJ4	IGHD6-13
IGHV3-20	IGHJ6	IGHD4-17
IGHV3-21	IGHJ6	IGHD2-2
IGHV3-21	IGHJ6	IGHD6-6
IGHV3-23	IGHJ3	IGHD6-6
IGHV3-23	IGHJ5	IGHD2-2
IGHV3-23	IGHJ5	IGHD3-16
IGHV3-30	IGHJ5	IGHD1-7
IGHV3-33	IGHJ4	IGHD3-3
IGHV3-43	IGHJ6	IGHD3-10
IGHV3-43	IGHJ6	IGHD6-13
IGHV3-48	IGHJ4	IGHD7-27
IGHV3-49	IGHJ5	IGHD6-6
IGHV3-64	IGHJ4	IGHD2-2
IGHV3-72	IGHJ4	IGHD1-26
IGHV4-34	IGHJ1	IGHD6-6

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-34	IGHJ3	IGHD3-16
IGHV4-34	IGHJ3	IGHD4-17
IGHV4-34	IGHJ4	IGHD6-19
IGHV4-39	IGHJ3	IGHD7-27
IGHV4-39	IGHJ4	IGHD2-2
IGHV4-39	IGHJ4	IGHD6-13
IGHV4-39	IGHJ5	IGHD6-6
IGHV4-39	IGHJ6	IGHD1-26
IGHV4-59	IGHJ2	IGHD6-13
IGHV4-59	IGHJ3	IGHD1-26
IGHV4-59	IGHJ5	IGHD5-12
IGHV4-59	IGHJ5	IGHD5-18
IGHV4-59	IGHJ5	IGHD7-27
IGHV4-59	IGHJ6	IGHD7-27
IGHV4-59	IGHJ6	IGHD1-7
IGHV5-51	IGHJ6	IGHD2-2
IGHV6-1	IGHJ1	IGHD6-13
IGHV6-1	IGHJ3	IGHD7-27
IGHV6-1	IGHJ4	IGHD1-7
IGHV1-18	IGHJ3	IGHD1-20
IGHV1-18	IGHJ3	IGHD1-7
IGHV1-18	IGHJ3	IGHD5-12
IGHV1-18	IGHJ4	IGHD1-1
IGHV1-18	IGHJ4	IGHD2-15
IGHV1-18	IGHJ4	IGHD2-8
IGHV1-18	IGHJ4	IGHD6-13
IGHV1-18	IGHJ4	IGHD7-27
IGHV1-18	IGHJ5	IGHD1-20
IGHV1-2	IGHJ3	IGHD1-1
IGHV1-2	IGHJ4	IGHD1-7
IGHV1-24	IGHJ3	IGHD6-6
IGHV1-24	IGHJ4	IGHD4-17
IGHV1-58	IGHJ4	IGHD6-6
IGHV1-69	IGHJ4	IGHD3-3
IGHV1-8	IGHJ4	IGHD6-19
IGHV1-8	IGHJ6	IGHD3-22
IGHV2-26	IGHJ3	IGHD1-1
IGHV2-26	IGHJ3	IGHD6-6
IGHV2-26	IGHJ4	IGHD1-1
IGHV2-26	IGHJ4	IGHD5-12
IGHV2-26	IGHJ4	IGHD5-18
IGHV2-26	IGHJ4	IGHD6-6

Humaan V _H	Humaan J _H	Humaan D _H
IGHV2-26	IGHJ5	IGHD6-6
IGHV2-26	IGHJ6	IGHD3-16
IGHV2-5	IGHJ3	IGHD5-18
IGHV2-5	IGHJ4	IGHD3-22
IGHV2-5	IGHJ4	IGHD3-3
IGHV2-5	IGHJ4	IGHD5-18
IGHV2-5	IGHJ4	IGHD6-13
IGHV2-5	IGHJ6	IGHD1-7
IGHV2-5	IGHJ6	IGHD6-6
IGHV2-70	IGHJ3	IGHD1-7
IGHV2-70	IGHJ4	IGHD1-1
IGHV2-70	IGHJ4	IGHD5-12
IGHV3-11	IGHJ3	IGHD1-1
IGHV3-11	IGHJ4	IGHD2-2
IGHV3-11	IGHJ4	IGHD3-10
IGHV3-13	IGHJ2	IGHD3-22
IGHV3-13	IGHJ4	IGHD2-21
IGHV3-13	IGHJ4	IGHD2-8
IGHV3-13	IGHJ6	IGHD2-15
IGHV3-15	IGHJ4	IGHD1-1
IGHV3-15	IGHJ4	IGHD2-21
IGHV3-15	IGHJ4	IGHD3-16
IGHV3-15	IGHJ4	IGHD4-17
IGHV3-15	IGHJ5	IGHD2-2
IGHV3-15	IGHJ6	IGHD1-1
IGHV3-15	IGHJ6	IGHD3-3
IGHV3-20	IGHJ4	IGHD1-26
IGHV3-20	IGHJ4	IGHD1-7
IGHV3-21	IGHJ3	IGHD5-12
IGHV3-21	IGHJ4	IGHD2-15
IGHV3-21	IGHJ4	IGHD6-13
IGHV3-21	IGHJ4	IGHD6-6
IGHV3-21	IGHJ6	IGHD6-13
IGHV3-23	IGHJ4	IGHD2-8
IGHV3-23	IGHJ4	IGHD6-19
IGHV3-23	IGHJ6	IGHD1-7
IGHV3-23	IGHJ6	IGHD3-3
IGHV3-23	IGHJ6	IGHD4-17
IGHV3-30	IGHJ4	IGHD1-26
IGHV3-30	IGHJ4	IGHD3-10
IGHV3-33	IGHJ2	IGHD7-27
IGHV3-33	IGHJ3	IGHD6-6

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-33	IGHJ4	IGHD1-20
IGHV3-33	IGHJ4	IGHD2-15
IGHV3-33	IGHJ4	IGHD3-16
IGHV3-33	IGHJ5	IGHD1-26
IGHV3-33	IGHJ5	IGHD6-6
IGHV3-33	IGHJ6	IGHD1-20
IGHV3-33	IGHJ6	IGHD3-22
IGHV3-33	IGHJ6	IGHD3-9
IGHV3-48	IGHJ3	IGHD1-26
IGHV3-48	IGHJ3	IGHD5-12
IGHV3-48	IGHJ3	IGHD6-6
IGHV3-48	IGHJ4	IGHD6-6
IGHV3-48	IGHJ5	IGHD3-22
IGHV3-53	IGHJ2	IGHD7-27
IGHV3-53	IGHJ4	IGHD5-18
IGHV3-53	IGHJ6	IGHD2-15
IGHV3-64	IGHJ3	IGHD1-7
IGHV3-7	IGHJ1	IGHD3-3
IGHV3-7	IGHJ2	IGHD3-3
IGHV3-7	IGHJ4	IGHD4-17
IGHV3-7	IGHJ5	IGHD1-7
IGHV3-7	IGHJ5	IGHD2-8
IGHV3-72	IGHJ3	IGHD6-6
IGHV3-72	IGHJ4	IGHD1-20
IGHV3-9	IGHJ3	IGHD1-26
IGHV3-9	IGHJ4	IGHD1-26
IGHV3-9	IGHJ4	IGHD3-3
IGHV3-9	IGHJ4	IGHD6-6
IGHV3-9	IGHJ4	IGHD7-27
IGHV3-9	IGHJ6	IGHD1-7
IGHV4-31	IGHJ2	IGHD7-27
IGHV4-31	IGHJ4	IGHD6-6
IGHV4-31	IGHJ6	IGHD3-10
IGHV4-34	IGHJ1	IGHD1-26
IGHV4-34	IGHJ2	IGHD6-6
IGHV4-34	IGHJ2	IGHD7-27
IGHV4-34	IGHJ3	IGHD1-1
IGHV4-34	IGHJ3	IGHD1-20
IGHV4-34	IGHJ3	IGHD1-7
IGHV4-34	IGHJ4	IGHD2-15
IGHV4-34	IGHJ4	IGHD5-18
IGHV4-34	IGHJ5	IGHD1-1

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-34	IGHJ5	IGHD1-7
IGHV4-34	IGHJ5	IGHD2-2
IGHV4-34	IGHJ5	IGHD6-13
IGHV4-34	IGHJ5	IGHD6-6
IGHV4-34	IGHJ6	IGHD1-7
IGHV4-34	IGHJ6	IGHD2-2
IGHV4-34	IGHJ6	IGHD3-22
IGHV4-39	IGHJ2	IGHD6-6
IGHV4-39	IGHJ3	IGHD1-26
IGHV4-39	IGHJ3	IGHD6-6
IGHV4-39	IGHJ4	IGHD3-16
IGHV4-39	IGHJ5	IGHD1-7
IGHV4-59	IGHJ1	IGHD3-10
IGHV4-59	IGHJ2	IGHD1-7
IGHV4-59	IGHJ2	IGHD5-18
IGHV4-59	IGHJ3	IGHD2-15
IGHV4-59	IGHJ3	IGHD3-10
IGHV4-59	IGHJ3	IGHD6-6
IGHV4-59	IGHJ4	IGHD3-16

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-59	IGHJ4	IGHD3-22
IGHV4-59	IGHJ6	IGHD1-20
IGHV4-59	IGHJ6	IGHD6-13
IGHV4-59	IGHJ6	IGHD6-6
IGHV4-59	IGHJ4	IGHD3-3
IGHV5-51	IGHJ4	IGHD2-21
IGHV5-51	IGHJ5	IGHD1-26
IGHV5-51	IGHJ6	IGHD3-3
IGHV6-1	IGHJ3	IGHD1-1
IGHV6-1	IGHJ4	IGHD2-21
IGHV6-1	IGHJ4	IGHD5-18
IGHV6-1	IGHJ4	IGHD7-27
IGHV6-1	IGHJ5	IGHD1-1
IGHV6-1	IGHJ6	IGHD1-26
IGHV6-1	IGHJ6	IGHD4-17
IGHV6-1	IGHJ6	IGHD6-6

Tabel 30

5

Humaan V _H	Humaan J _H	Humaan D _H
IGHV2-5	IGHJ4	IGHD1-7
IGHV3-33	IGHJ4	IGHD6-6
IGHV4-39	IGHJ4	IGHD3-10
IGHV3-23	IGHJ4	IGHD1-26
IGHV3-23	IGHJ4	IGHD1-7
IGHV2-5	IGHJ4	IGHD6-19
IGHV3-15	IGHJ4	IGHD7-27
IGHV4-59	IGHJ4	IGHD7-27
IGHV4-59	IGHJ6	IGHD3-3
IGHV3-33	IGHJ6	IGHD6-6
IGHV1-69	IGHJ6	IGHD5-12
IGHV3-21	IGHJ6	IGHD2-8
IGHV3-30	IGHJ4	IGHD3-22
IGHV4-59	IGHJ4	IGHD6-13
IGHV3-33	IGHJ5	IGHD1-1
IGHV3-15	IGHJ5	IGHD1-20
IGHV3-23	IGHJ6	IGHD6-13
IGHV3-33	IGHJ2	IGHD3-10

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-15	IGHJ6	IGHD6-6
IGHV3-21	IGHJ6	IGHD4-17
IGHV3-23	IGHJ4	IGHD6-13
IGHV4-39	IGHJ4	IGHD1-7
IGHV4-59	IGHJ6	IGHD4-17
IGHV3-33	IGHJ2	IGHD6-6
IGHV4-39	IGHJ4	IGHD5-12
IGHV4-59	IGHJ6	IGHD3-22
IGHV2-5	IGHJ3	IGHD6-6
IGHV4-39	IGHJ4	IGHD6-19
IGHV4-59	IGHJ4	IGHD1-1
IGHV3-15	IGHJ1	IGHD6-6
IGHV3-23	IGHJ4	IGHD3-9
IGHV3-33	IGHJ4	IGHD1-26
IGHV4-39	IGHJ4	IGHD2-8
IGHV4-59	IGHJ4	IGHD3-3
IGHV2-5	IGHJ4	IGHD6-6
IGHV4-39	IGHJ5	IGHD6-13

Humaan V _H	Humaan J _H	Humaan D _H
IGHV1-69	IGHJ6	IGHD3-22
IGHV2-5	IGHJ3	IGHD1-1
IGHV2-5	IGHJ4	IGHD1-26
IGHV3-15	IGHJ4	IGHD6-13
IGHV3-21	IGHJ6	IGHD1-7
IGHV4-39	IGHJ4	IGHD1-26
IGHV2-5	IGHJ4	IGHD4-17
IGHV3-15	IGHJ4	IGHD1-26
IGHV3-15	IGHJ4	IGHD1-7
IGHV3-23	IGHJ5	IGHD3-9
IGHV3-23	IGHJ6	IGHD6-6
IGHV3-30	IGHJ3	IGHD3-16
IGHV4-39	IGHJ3	IGHD1-7
IGHV4-59	IGHJ4	IGHD2-15
IGHV1-24	IGHJ4	IGHD5-18
IGHV2-5	IGHJ5	IGHD3-10
IGHV3-23	IGHJ2	IGHD6-6
IGHV3-23	IGHJ3	IGHD1-26
IGHV3-23	IGHJ5	IGHD1-7
IGHV3-33	IGHJ4	IGHD6-13
IGHV4-39	IGHJ4	IGHD7-27
IGHV4-59	IGHJ3	IGHD1-1
IGHV1-69	IGHJ5	IGHD3-10
IGHV2-5	IGHJ4	IGHD2-2
IGHV3-23	IGHJ6	IGHD7-27
IGHV4-59	IGHJ4	IGHD1-7
IGHV1-69	IGHJ6	IGHD7-27
IGHV2-5	IGHJ4	IGHD1-20
IGHV3-21	IGHJ2	IGHD3-22
IGHV3-23	IGHJ3	IGHD3-16
IGHV3-23	IGHJ3	IGHD3-9
IGHV3-23	IGHJ4	IGHD5-18
IGHV4-39	IGHJ2	IGHD7-27
IGHV4-39	IGHJ4	IGHD6-6
IGHV4-59	IGHJ3	IGHD4-17
IGHV4-59	IGHJ4	IGHD3-9
IGHV4-59	IGHJ5	IGHD6-13
IGHV4-59	IGHJ6	IGHD3-10
IGHV2-5	IGHJ4	IGHD1-1
IGHV3-15	IGHJ4	IGHD3-22
IGHV3-21	IGHJ4	IGHD1-26
IGHV3-23	IGHJ3	IGHD1-20

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-23	IGHJ4	IGHD4-17
IGHV3-23	IGHJ4	IGHD5-12
IGHV3-23	IGHJ6	IGHD2-2
IGHV3-30	IGHJ6	IGHD3-10
IGHV4-59	IGHJ3	IGHD1-7
IGHV4-59	IGHJ6	IGHD1-26
IGHV2-5	IGHJ6	IGHD6-13
IGHV3-15	IGHJ3	IGHD1-7
IGHV3-15	IGHJ4	IGHD3-3
IGHV3-21	IGHJ4	IGHD7-27
IGHV3-21	IGHJ6	IGHD1-20
IGHV3-21	IGHJ6	IGHD3-10
IGHV3-23	IGHJ3	IGHD7-27
IGHV3-23	IGHJ5	IGHD1-26
IGHV3-23	IGHJ5	IGHD7-27
IGHV3-30	IGHJ4	IGHD2-15
IGHV3-33	IGHJ4	IGHD1-1
IGHV3-33	IGHJ4	IGHD3-22
IGHV4-39	IGHJ2	IGHD4-17
IGHV4-39	IGHJ2	IGHD5-12
IGHV4-39	IGHJ4	IGHD2-15
IGHV4-59	IGHJ3	IGHD7-27
IGHV4-59	IGHJ4	IGHD3-10
IGHV4-59	IGHJ4	IGHD5-18
IGHV1-24	IGHJ4	IGHD1-26
IGHV1-69	IGHJ4	IGHD6-6
IGHV1-69	IGHJ5	IGHD3-9
IGHV2-5	IGHJ3	IGHD3-3
IGHV2-5	IGHJ3	IGHD5-12
IGHV2-5	IGHJ4	IGHD2-21
IGHV2-5	IGHJ5	IGHD5-18
IGHV2-5	IGHJ6	IGHD3-3
IGHV2-5	IGHJ6	IGHD7-27
IGHV3-15	IGHJ5	IGHD6-6
IGHV3-15	IGHJ6	IGHD6-13
IGHV3-21	IGHJ6	IGHD2-2
IGHV3-21	IGHJ6	IGHD6-6
IGHV3-23	IGHJ3	IGHD6-6
IGHV3-23	IGHJ5	IGHD2-2
IGHV3-23	IGHJ5	IGHD3-16
IGHV3-30	IGHJ5	IGHD1-7
IGHV3-33	IGHJ4	IGHD3-3

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-39	IGHJ3	IGHD7-27
IGHV4-39	IGHJ4	IGHD2-2
IGHV4-39	IGHJ4	IGHD6-13
IGHV4-39	IGHJ5	IGHD6-6
IGHV4-39	IGHJ6	IGHD1-26
IGHV4-59	IGHJ2	IGHD6-13
IGHV4-59	IGHJ3	IGHD1-26
IGHV4-59	IGHJ5	IGHD5-12
IGHV4-59	IGHJ5	IGHD5-18
IGHV4-59	IGHJ5	IGHD7-27
IGHV4-59	IGHJ6	IGHD7-27
IGHV4-59	IGHJ6	IGHD1-7
IGHV5-51	IGHJ6	IGHD2-2
IGHV1-24	IGHJ3	IGHD6-6
IGHV1-24	IGHJ4	IGHD4-17
IGHV1-69	IGHJ4	IGHD3-3
IGHV2-5	IGHJ3	IGHD5-18
IGHV2-5	IGHJ4	IGHD3-22
IGHV2-5	IGHJ4	IGHD3-3
IGHV2-5	IGHJ4	IGHD5-18
IGHV2-5	IGHJ4	IGHD6-13
IGHV2-5	IGHJ6	IGHD1-7
IGHV2-5	IGHJ6	IGHD6-6
IGHV3-15	IGHJ4	IGHD1-1
IGHV3-15	IGHJ4	IGHD2-21
IGHV3-15	IGHJ4	IGHD3-16
IGHV3-15	IGHJ4	IGHD4-17
IGHV3-15	IGHJ5	IGHD2-2
IGHV3-15	IGHJ6	IGHD1-1
IGHV3-15	IGHJ6	IGHD3-3
IGHV3-21	IGHJ3	IGHD5-12
IGHV3-21	IGHJ4	IGHD2-15
IGHV3-21	IGHJ4	IGHD6-13
IGHV3-21	IGHJ4	IGHD6-6
IGHV3-21	IGHJ6	IGHD6-13
IGHV3-23	IGHJ4	IGHD6-19

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-23	IGHJ6	IGHD1-7
IGHV3-23	IGHJ6	IGHD3-3
IGHV3-23	IGHJ6	IGHD4-17
IGHV3-30	IGHJ4	IGHD1-26
IGHV3-30	IGHJ4	IGHD3-10
IGHV3-33	IGHJ2	IGHD7-27
IGHV3-33	IGHJ3	IGHD6-6
IGHV3-33	IGHJ4	IGHD1-20
IGHV3-33	IGHJ4	IGHD3-16
IGHV3-33	IGHJ5	IGHD1-26
IGHV3-33	IGHJ5	IGHD6-6
IGHV3-33	IGHJ6	IGHD1-20
IGHV3-33	IGHJ6	IGHD3-22
IGHV3-33	IGHJ6	IGHD3-9
IGHV4-39	IGHJ2	IGHD6-6
IGHV4-39	IGHJ3	IGHD6-6
IGHV4-39	IGHJ4	IGHD3-16
IGHV4-39	IGHJ5	IGHD1-7
IGHV4-59	IGHJ1	IGHD3-10
IGHV4-59	IGHJ2	IGHD1-7
IGHV4-59	IGHJ2	IGHD5-18
IGHV4-59	IGHJ3	IGHD2-15
IGHV4-59	IGHJ3	IGHD3-10
IGHV4-59	IGHJ3	IGHD6-6
IGHV4-59	IGHJ4	IGHD3-22
IGHV4-59	IGHJ6	IGHD1-20
IGHV4-59	IGHJ6	IGHD6-13
IGHV4-59	IGHJ6	IGHD6-6
IGHV4-59	IGHJ4	IGHD3-3
IGHV5-51	IGHJ4	IGHD2-21
IGHV5-51	IGHJ5	IGHD1-26
IGHV5-51	IGHJ6	IGHD3-3

- 5 waarbij de gastheercel de eerste, de tweede en de derde nucleïnezuur sequenties tot expressie brengt, daarbij een bispecifiek antigeen-bindend eiwit vormend welke het eerste en het tweede antigeen bindt.

2. De gastheercel volgens conclusie 1 waarbij de eerste muis en de tweede muis dezelfde muis of verschillende muizen zijn.
3. De gastheercel volgens conclusie 1 of 2, waarbij het humane kiembaan J segment J κ 5 is.
4. De gastheercel volgens een der conclusies 1-3, waarbij de muis geen endogene κ immunoglobuline lichte keten variabel gen segment heeft welke in staat is te herrangschikken om zodoende een gen te vormen welke codeert voor een variabel domein van de immunoglobuline lichte keten.
5. De gastheercel volgens een der conclusies 1-4, waarbij het eerste en het tweede antigeen:
 - twee verschillende antigenen zijn; of
 - hetzelfde antigeen zijn en de eerste en de tweede humane immunoglobuline zware ketens twee verschillende epitopen van hetzelfde antigeen binden.
6. De gastheercel volgens een der conclusies 1-5, waarbij:
 - de kiembaan van de eerste muis of tweede muis een humaan V_H gen segment omvat geselecteerd uit V_H3-49, V_H3-66, V_H4-28, en/of V_H4-61.
7. De gastheercel volgens een der conclusies 1-6, waarbij:
 - het variabele domein van de humane immunoglobuline zware keten van het eerste of de tweede zware keten afkomstig is van een humaan V_H gen segment geselecteerd uit V_H3-49, V_H3-66, V_H4-28 en/of V_H4-61.
8. De gastheercel volgens conclusie 5, waarbij de eerste en tweede antigenen hetzelfde antigeen zijn en de bindingsreactie van het bispecifieke antigeen-bindend eiwit met het genoemde zelfde antigeen ten minste tweemaal zo hoog is dan de bindingsreactie van een monospecifiek antigeen-bindend eiwit welke alleen het eerste humane immunoglobuline zware keten omvat en/of een monospecifiek antigeen-bindend eiwit welke alleen het tweede humane immunoglobuline zware keten omvat.

9. De gastheercel volgens een der conclusies 1-8, waarbij de eerste of de tweede humane immunoglobuline zware keten van het bispecifieke antigeen-bindend eiwit, maar niet beide, een aminozuur modificatie omvat welke haar affiniteit voor Eiwit A reduceert.

5 10. De gastheercel volgens conclusie 9, waarbij de modificatie geselecteerd is uit 95R (EUR 435R), 96F (EUR 436F), of een combinatie hiervan.

11. De gastheercel volgens een der conclusies 1-10, waarbij in de eerste en tweede muis het constante gebied van de immunoglobuline lichte keten sequentie een humane, muis of rat
10 sequentie is en/of de murine C_H is een muis of rat C_H.

12. Een bispecifiek antigeen-bindend eiwit welke tot expressie gebracht wordt door een gastheercel volgens een der conclusies 1-11.

15 13. Werkwijze voor het genereren van een gastheercel voor gebruik in het maken van een bispecifieke antilichamen omvattende de volgende stappen:

(a) verkrijgen van een eerste nucleïnezuur sequentie coderend voor een eerste variabele gebied van de humane immuoglobuline zware keten afkomstig van een B cel van
20 een eerste genetisch gemodificeerde muis welke geïmmuniseerd is met een eerste antigeen van belang welke een eerste epitoom omvat, welke eerste muis:

(i) een kiembaan omvat welke homozygoot of heterozygoot is voor een enkel herrangschikt variabel gebied van de humane immunoglobuline lichte keten gen
25 sequentie afkomstig van een herrangschikte humane V_κ1-39/J_κ sequentie, waarbij de herrangschikte humane V_κ1-39/J_κ sequentie een humane kiembaan V_κ1-39 gen segment omvat en een humane kiembaan J_κ segment, waarbij de herrangschikte humane V_κ1-39/J_κ sequentie operabel gekoppeld is aan een constant gebied van de immunoglobuline lichte keten sequentie; en

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(ii) een kiembaan omvat die niet herrangschikte humane V_H gen segmenten, humane D gen segmenten en humane J_H gen segmenten heeft, waarbij de

niet herrangschikte humane V_H gen segmenten operabel gekoppeld zijn aan een murine C_H gebied; en

(iii) een populatie van B cellen omvat waarbij elke B cel van deze populatie een variabel domein van de humane immunoglobuline lichte keten tot expressie brengt welke afkomstig is van de herrangschikte humane $V\kappa 1-39/J\kappa$ sequentie en waarbij de B cel populatie ten minste één B cel omvat welke een variabel domein van de humane immunoglobuline zware keten tot expressie brengt welke afkomstig is van een herrangschikt humaan $V_H/D/J_H$ gebied.

(b) verkrijgen van een tweede nucleïnezuur sequentie coderend voor een tweede variabele gebied van de humane immuoglobuline zware keten afkomstig van een B cel van een tweede genetisch gemodificeerde muis welke geïmmuniseerd is met een tweede antigeen van belang welke een tweede epitoop omvat, welke tweede muis:

(i) een kiembaan omvat welke homozygoot of heterozygoot is voor hetzelfde enkele herrangschikte variabel gebied van de humane immunoglobuline lichte keten gen sequentie als in de eerste muis, welke afkomstig is van dezelfde herrangschikte humane $V\kappa 1-39/J\kappa$ sequentie als in de eerste muis, waarbij de herrangschikte humane $V\kappa 1-39/J\kappa$ sequentie het humane kiembaan $V\kappa 1-39$ gen segment omvat en het humane kiembaan $J\kappa$ segment, waarbij de herrangschikte humane $V\kappa 1-39/J\kappa$ sequentie operabel gekoppeld is aan een constant gebied van de immunoglobuline lichte keten sequentie;

(ii) een kiembaan omvat die niet herrangschikte humane V_H gen segmenten, humane D gen segmenten en humane J_H gen segmenten heeft, waarbij de niet herrangschikte humane V_H gen segmenten operabel gekoppeld zijn aan een murine C_H gebied; en

(iii) een populatie van B cellen omvat waarbij elke B cel van deze populatie een variabel domein van de humane immunoglobuline lichte keten tot expressie brengt welke afkomstig is uit de herrangschikte humane $V\kappa 1-39/J\kappa$ sequentie en waarbij de B cel populatie ten minste één B cel omvat welke een variabel domein van de humane

immunoglobuline zware keten tot expressie brengt welke afkomstig is uit een herrangschikt humaan $V_H/D/J_H$ gebied.

(c) verkrijgen van een derde nucleïnezuur sequentie omvattende deze enkele

5 herrangschikte variabele gebied van de humane immunoglobulin lichte keten gen sequentie afkomstig van een humane $V_{\kappa 1-39}/J_{\kappa}$ sequentie welke aanwezig is in de kiembaan van de eerste en de tweede muis; en

(d) introduceren in een gastheercel van de eerste, tweede en derde nucleïnezuur

10 sequenties en kweken van de gastheercel zodat de eerste, tweede en derde nucleïnezuur sequenties tot expressie komen, daarbij vormend een bispecifiek antigeen-bindend eiwit welke bindt aan het eerste en de tweede epitopen van het eerste en het tweede antigeen van belang,

15 waarbij ten minste één van de eerste of de tweede domeinen van de humane immunoglobuline zware keten verkregen is door een herrangschikking geselecteerd uit de groep bestaande uit de herrangschikkingen zoals uiteengezet in Tabel 29 en Tabel 30 hieronder:

20

Tabel 29

Humaan V_H	Humaan J_H	Humaan D_H
IGHV2-70	IGHJ3	IGHD3-10
IGHV4-59	IGHJ4	IGHD1-26
IGHV2-26	IGHJ4	IGHD3-9
IGHV4-28	IGHJ4	IGHD1-26
IGHV1-18	IGHJ6	IGHD1-26
IGHV2-5	IGHJ4	IGHD1-7
IGHV1-18	IGHJ3	IGHD4-17
IGHV4-59	IGHJ4	IGHD6-6
IGHV3-33	IGHJ4	IGHD6-6
IGHV1-69	IGHJ4	IGHD6-13
IGHV3-64	IGHJ4	IGHD1-7
IGHV4-39	IGHJ4	IGHD3-10
IGHV3-23	IGHJ4	IGHD1-26
IGHV1-18	IGHJ4	IGHD6-6

Humaan V_H	Humaan J_H	Humaan D_H
IGHV3-23	IGHJ4	IGHD1-7
IGHV3-11	IGHJ4	IGHD5-18
IGHV1-18	IGHJ6	IGHD6-19
IGHV2-5	IGHJ4	IGHD6-19
IGHV3-15	IGHJ4	IGHD7-27
IGHV4-34	IGHJ6	IGHD6-13
IGHV4-59	IGHJ4	IGHD7-27
IGHV1-18	IGHJ6	IGHD3-9
IGHV2-26	IGHJ4	IGHD1-26
IGHV1-18	IGHJ3	IGHD7-27
IGHV4-59	IGHJ6	IGHD3-3
IGHV3-33	IGHJ6	IGHD6-6
IGHV3-7	IGHJ4	IGHD6-13
IGHV3-7	IGHJ6	IGHD6-19

Humaan V _H	Humaan J _H	Humaan D _H
IGHV1-18	IGHJ4	IGHD1-7
IGHV1-69	IGHJ6	IGHD5-12
IGHV3-72	IGHJ6	IGHD6-6
IGHV4-34	IGHJ3	IGHD6-6
IGHV3-21	IGHJ6	IGHD2-8
IGHV3-30	IGHJ4	IGHD3-22
IGHV3-33	IGHJ4	IGHD1-7
IGHV6-1	IGHJ4	IGHD1-26
IGHV4-59	IGHJ4	IGHD6-13
IGHV1-8	IGHJ4	IGHD1-26
IGHV3-13	IGHJ4	IGHD3-10
IGHV2-70	IGHJ4	IGHD1-26
IGHV3-33	IGHJ5	IGHD1-1
IGHV1-18	IGHJ4	IGHD1-26
IGHV1-8	IGHJ6	IGHD1-7
IGHV1-8	IGHJ4	IGHD3-10
IGHV3-15	IGHJ5	IGHD1-20
IGHV3-23	IGHJ6	IGHD6-13
IGHV3-33	IGHJ2	IGHD3-10
IGHV2-70	IGHJ5	IGHD3-10
IGHV3-15	IGHJ6	IGHD6-6
IGHV3-21	IGHJ6	IGHD4-17
IGHV1-18	IGHJ6	IGHD6-13
IGHV1-8	IGHJ4	IGHD1-26
IGHV3-13	IGHJ4	IGHD6-25
IGHV3-23	IGHJ4	IGHD6-13
IGHV4-39	IGHJ4	IGHD1-7
IGHV1-18	IGHJ4	IGHD2-2
IGHV2-26	IGHJ5	IGHD3-3
IGHV3-13	IGHJ4	IGHD4-17
IGHV3-13	IGHJ6	IGHD3-10
IGHV4-34	IGHJ6	IGHD1-26
IGHV4-59	IGHJ6	IGHD4-17
IGHV1-18	IGHJ6	IGHD3-22
IGHV1-46	IGHJ4	IGHD6-13
IGHV1-8	IGHJ6	IGHD2-2
IGHV1-8	IGHJ3	IGHD3-9
IGHV3-13	IGHJ4	IGHD1-7
IGHV3-33	IGHJ2	IGHD6-6
IGHV3-48	IGHJ4	IGHD1-7
IGHV4-39	IGHJ4	IGHD5-12
IGHV4-59	IGHJ6	IGHD3-22

Humaan V _H	Humaan J _H	Humaan D _H
IGHV1-8	IGHJ6	IGHD3-3
IGHV2-5	IGHJ3	IGHD6-6
IGHV3-43	IGHJ4	IGHD6-6
IGHV4-39	IGHJ4	IGHD6-19
IGHV4-59	IGHJ4	IGHD1-1
IGHV2-26	IGHJ4	IGHD3-16
IGHV2-70	IGHJ3	IGHD7-27
IGHV3-15	IGHJ1	IGHD6-6
IGHV3-23	IGHJ4	IGHD3-9
IGHV3-53	IGHJ5	IGHD6-6
IGHV3-64	IGHJ2	IGHD1-1
IGHV3-11	IGHJ4	IGHD3-10
IGHV3-13	IGHJ4	IGHD3-16
IGHV3-13	IGHJ4	IGHD6-6
IGHV3-33	IGHJ4	IGHD1-26
IGHV3-9	IGHJ3	IGHD1-7
IGHV3-9	IGHJ5	IGHD1-26
IGHV4-34	IGHJ4	IGHD3-16
IGHV4-39	IGHJ4	IGHD2-8
IGHV4-59	IGHJ4	IGHD3-3
IGHV2-26	IGHJ3	IGHD3-22
IGHV2-5	IGHJ4	IGHD6-6
IGHV2-70	IGHJ5	IGHD4-17
IGHV3-13	IGHJ4	IGHD1-1
IGHV3-13	IGHJ4	IGHD1-26
IGHV3-13	IGHJ6	IGHD5-18
IGHV3-7	IGHJ5	IGHD6-19
IGHV4-39	IGHJ5	IGHD6-13
IGHV1-69	IGHJ6	IGHD3-22
IGHV1-8	IGHJ3	IGHD5-18
IGHV2-26	IGHJ2	IGHD7-27
IGHV2-5	IGHJ3	IGHD1-1
IGHV2-5	IGHJ4	IGHD1-26
IGHV3-13	IGHJ3	IGHD3-22
IGHV3-15	IGHJ4	IGHD6-13
IGHV3-21	IGHJ6	IGHD1-7
IGHV3-48	IGHJ4	IGHD6-13
IGHV3-9	IGHJ6	IGHD1-26
IGHV4-39	IGHJ4	IGHD1-26
IGHV1-18	IGHJ2	IGHD3-10
IGHV1-8	IGHJ4	IGHD2-8
IGHV2-5	IGHJ4	IGHD4-17

Humaan V _H	Humaan J _H	Humaan D _H
IGHV2-70	IGHJ4	IGHD1-7
IGHV2-70	IGHJ4	IGHD6-6
IGHV3-15	IGHJ4	IGHD1-26
IGHV3-15	IGHJ4	IGHD1-7
IGHV3-23	IGHJ5	IGHD3-9
IGHV3-23	IGHJ6	IGHD6-6
IGHV3-30	IGHJ3	IGHD3-16
IGHV3-48	IGHJ3	IGHD7-27
IGHV3-48	IGHJ4	IGHD3-9
IGHV3-64	IGHJ6	IGHD6-6
IGHV3-7	IGHJ3	IGHD6-13
IGHV3-7	IGHJ4	IGHD6-6
IGHV4-31	IGHJ4	IGHD1-26
IGHV4-31	IGHJ6	IGHD6-6
IGHV4-39	IGHJ3	IGHD1-7
IGHV4-59	IGHJ4	IGHD2-15
IGHV1-18	IGHJ5	IGHD1-7
IGHV1-18	IGHJ5	IGHD3-3
IGHV1-2	IGHJ4	IGHD3-3
IGHV1-24	IGHJ4	IGHD5-18
IGHV1-8	IGHJ4	IGHD7-27
IGHV1-8	IGHJ6	IGHD3-3
IGHV2-5	IGHJ5	IGHD3-10
IGHV3-23	IGHJ2	IGHD6-6
IGHV3-23	IGHJ3	IGHD1-26
IGHV3-23	IGHJ5	IGHD1-7
IGHV3-33	IGHJ4	IGHD6-13
IGHV3-7	IGHJ5	IGHD5-18
IGHV3-9	IGHJ6	IGHD6-6
IGHV4-28	IGHJ3	IGHD2-15
IGHV4-34	IGHJ4	IGHD1-7
IGHV4-39	IGHJ4	IGHD7-27
IGHV4-59	IGHJ3	IGHD1-1
IGHV1-58	IGHJ6	IGHD6-13
IGHV1-69	IGHJ5	IGHD3-10
IGHV2-26	IGHJ4	IGHD1-7
IGHV2-5	IGHJ4	IGHD2-2
IGHV2-70	IGHJ3	IGHD1-20
IGHV2-70	IGHJ5	IGHD6-13
IGHV3-23	IGHJ6	IGHD7-27
IGHV3-7	IGHJ3	IGHD2-2
IGHV3-7	IGHJ4	IGHD1-7

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-9	IGHJ3	IGHD6-6
IGHV3-9	IGHJ4	IGHD6-19
IGHV3-9	IGHJ5	IGHD1-7
IGHV4-34	IGHJ4	IGHD3-3
IGHV4-59	IGHJ4	IGHD1-7
IGHV1-69	IGHJ6	IGHD7-27
IGHV1-8	IGHJ1	IGHD6-6
IGHV1-8	IGHJ4	IGHD1-20
IGHV1-8	IGHJ4	IGHD3-3
IGHV2-5	IGHJ4	IGHD1-20
IGHV2-70	IGHJ5	IGHD1-26
IGHV3-13	IGHJ4	IGHD6-13
IGHV3-21	IGHJ2	IGHD3-22
IGHV3-23	IGHJ3	IGHD3-16
IGHV3-23	IGHJ3	IGHD3-9
IGHV3-23	IGHJ4	IGHD5-18
IGHV3-48	IGHJ4	IGHD1-26
IGHV3-48	IGHJ4	IGHD3-10
IGHV3-48	IGHJ6	IGHD3-9
IGHV3-7	IGHJ4	IGHD6-6
IGHV3-7	IGHJ5	IGHD2-21
IGHV3-9	IGHJ6	IGHD3-10
IGHV4-34	IGHJ4	IGHD6-6
IGHV4-34	IGHJ4	IGHD7-27
IGHV4-34	IGHJ6	IGHD3-10
IGHV4-39	IGHJ2	IGHD7-27
IGHV4-39	IGHJ4	IGHD6-6
IGHV4-59	IGHJ3	IGHD4-17
IGHV4-59	IGHJ4	IGHD3-9
IGHV4-59	IGHJ5	IGHD6-13
IGHV4-59	IGHJ6	IGHD3-10
IGHV6-1	IGHJ4	IGHD1-1
IGHV1-18	IGHJ5	IGHD6-13
IGHV1-2	IGHJ5	IGHD1-7
IGHV2-26	IGHJ4	IGHD7-27
IGHV2-5	IGHJ4	IGHD1-1
IGHV2-70	IGHJ3	IGHD2-2
IGHV2-70	IGHJ4	IGHD2-8
IGHV2-70	IGHJ5	IGHD6-6
IGHV3-13	IGHJ4	IGHD1-20
IGHV3-15	IGHJ4	IGHD3-22
IGHV3-21	IGHJ4	IGHD1-26

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-23	IGHJ3	IGHD1-20
IGHV3-23	IGHJ4	IGHD4-17
IGHV3-23	IGHJ4	IGHD5-12
IGHV3-23	IGHJ6	IGHD2-2
IGHV3-30	IGHJ6	IGHD3-10
IGHV3-48	IGHJ4	IGHD1-1
IGHV3-49	IGHJ2	IGHD3-10
IGHV3-9	IGHJ4	IGHD5-18
IGHV4-59	IGHJ3	IGHD1-7
IGHV4-59	IGHJ6	IGHD1-26
IGHV6-1	IGHJ5	IGHD1-20
IGHV1-18	IGHJ4	IGHD5-18
IGHV1-18	IGHJ6	IGHD6-6
IGHV2-26	IGHJ3	IGHD6-13
IGHV2-5	IGHJ6	IGHD6-13
IGHV2-70	IGHJ4	IGHD2-15
IGHV2-70	IGHJ4	IGHD3-3
IGHV3-11	IGHJ6	IGHD1-7
IGHV3-15	IGHJ3	IGHD1-7
IGHV3-15	IGHJ4	IGHD3-3
IGHV3-21	IGHJ4	IGHD7-27
IGHV3-21	IGHJ6	IGHD1-20
IGHV3-21	IGHJ6	IGHD3-10
IGHV3-23	IGHJ3	IGHD7-27
IGHV3-23	IGHJ5	IGHD1-26
IGHV3-23	IGHJ5	IGHD7-27
IGHV3-30	IGHJ4	IGHD2-15
IGHV3-33	IGHJ4	IGHD1-1
IGHV3-33	IGHJ4	IGHD3-22
IGHV3-48	IGHJ3	IGHD6-13
IGHV3-48	IGHJ4	IGHD5-12
IGHV3-7	IGHJ4	IGHD1-20
IGHV3-7	IGHJ4	IGHD1-26
IGHV4-34	IGHJ4	IGHD1-26
IGHV4-34	IGHJ4	IGHD3-10
IGHV4-39	IGHJ2	IGHD4-17
IGHV4-39	IGHJ2	IGHD5-12
IGHV4-39	IGHJ4	IGHD2-15
IGHV4-59	IGHJ3	IGHD7-27
IGHV4-59	IGHJ4	IGHD3-10
IGHV4-59	IGHJ4	IGHD5-18
IGHV1-18	IGHJ4	IGHD3-10

Humaan V _H	Humaan J _H	Humaan D _H
IGHV1-24	IGHJ4	IGHD1-26
IGHV1-69	IGHJ4	IGHD6-6
IGHV1-69	IGHJ5	IGHD3-9
IGHV1-8	IGHJ4	IGHD1-1
IGHV1-8	IGHJ4	IGHD1-7
IGHV1-8	IGHJ4	IGHD3-3
IGHV1-8	IGHJ5	IGHD6-13
IGHV1-8	IGHJ6	IGHD3-10
IGHV2-26	IGHJ3	IGHD1-26
IGHV2-26	IGHJ5	IGHD5-12
IGHV2-5	IGHJ3	IGHD3-3
IGHV2-5	IGHJ3	IGHD5-12
IGHV2-5	IGHJ4	IGHD2-21
IGHV2-5	IGHJ5	IGHD5-18
IGHV2-5	IGHJ6	IGHD3-3
IGHV2-5	IGHJ6	IGHD7-27
IGHV2-70	IGHJ4	IGHD6-13
IGHV3-11	IGHJ3	IGHD1-26
IGHV3-13	IGHJ2	IGHD1-7
IGHV3-13	IGHJ5	IGHD5-18
IGHV3-15	IGHJ5	IGHD6-6
IGHV3-15	IGHJ6	IGHD6-13
IGHV3-20	IGHJ4	IGHD6-13
IGHV3-20	IGHJ6	IGHD4-17
IGHV3-21	IGHJ6	IGHD2-2
IGHV3-21	IGHJ6	IGHD6-6
IGHV3-23	IGHJ3	IGHD6-6
IGHV3-23	IGHJ5	IGHD2-2
IGHV3-23	IGHJ5	IGHD3-16
IGHV3-30	IGHJ5	IGHD1-7
IGHV3-33	IGHJ4	IGHD3-3
IGHV3-43	IGHJ6	IGHD3-10
IGHV3-43	IGHJ6	IGHD6-13
IGHV3-48	IGHJ4	IGHD7-27
IGHV3-49	IGHJ5	IGHD6-6
IGHV3-64	IGHJ4	IGHD2-2
IGHV3-72	IGHJ4	IGHD1-26
IGHV4-34	IGHJ1	IGHD6-6
IGHV4-34	IGHJ3	IGHD3-16
IGHV4-34	IGHJ3	IGHD4-17
IGHV4-34	IGHJ4	IGHD6-19
IGHV4-39	IGHJ3	IGHD7-27

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-39	IGHJ4	IGHD2-2
IGHV4-39	IGHJ4	IGHD6-13
IGHV4-39	IGHJ5	IGHD6-6
IGHV4-39	IGHJ6	IGHD1-26
IGHV4-59	IGHJ2	IGHD6-13
IGHV4-59	IGHJ3	IGHD1-26
IGHV4-59	IGHJ5	IGHD5-12
IGHV4-59	IGHJ5	IGHD5-18
IGHV4-59	IGHJ5	IGHD7-27
IGHV4-59	IGHJ6	IGHD7-27
IGHV4-59	IGHJ6	IGHD1-7
IGHV5-51	IGHJ6	IGHD2-2
IGHV6-1	IGHJ1	IGHD6-13
IGHV6-1	IGHJ3	IGHD7-27
IGHV6-1	IGHJ4	IGHD1-7
IGHV1-18	IGHJ3	IGHD1-20
IGHV1-18	IGHJ3	IGHD1-7
IGHV1-18	IGHJ3	IGHD5-12
IGHV1-18	IGHJ4	IGHD1-1
IGHV1-18	IGHJ4	IGHD2-15
IGHV1-18	IGHJ4	IGHD2-8
IGHV1-18	IGHJ4	IGHD6-13
IGHV1-18	IGHJ4	IGHD7-27
IGHV1-18	IGHJ5	IGHD1-20
IGHV1-2	IGHJ3	IGHD1-1
IGHV1-2	IGHJ4	IGHD1-7
IGHV1-24	IGHJ3	IGHD6-6
IGHV1-24	IGHJ4	IGHD4-17
IGHV1-58	IGHJ4	IGHD6-6
IGHV1-69	IGHJ4	IGHD3-3
IGHV1-8	IGHJ4	IGHD6-19
IGHV1-8	IGHJ6	IGHD3-22
IGHV2-26	IGHJ3	IGHD1-1
IGHV2-26	IGHJ3	IGHD6-6
IGHV2-26	IGHJ4	IGHD1-1
IGHV2-26	IGHJ4	IGHD5-12
IGHV2-26	IGHJ4	IGHD5-18
IGHV2-26	IGHJ4	IGHD6-6
IGHV2-26	IGHJ5	IGHD6-6
IGHV2-26	IGHJ6	IGHD3-16
IGHV2-5	IGHJ3	IGHD5-18
IGHV2-5	IGHJ4	IGHD3-22

Humaan V _H	Humaan J _H	Humaan D _H
IGHV2-5	IGHJ4	IGHD3-3
IGHV2-5	IGHJ4	IGHD5-18
IGHV2-5	IGHJ4	IGHD6-13
IGHV2-5	IGHJ6	IGHD1-7
IGHV2-5	IGHJ6	IGHD6-6
IGHV2-70	IGHJ3	IGHD1-7
IGHV2-70	IGHJ4	IGHD1-1
IGHV2-70	IGHJ4	IGHD5-12
IGHV3-11	IGHJ3	IGHD1-1
IGHV3-11	IGHJ4	IGHD2-2
IGHV3-11	IGHJ4	IGHD3-10
IGHV3-13	IGHJ2	IGHD3-22
IGHV3-13	IGHJ4	IGHD2-21
IGHV3-13	IGHJ4	IGHD2-8
IGHV3-13	IGHJ6	IGHD2-15
IGHV3-15	IGHJ4	IGHD1-1
IGHV3-15	IGHJ4	IGHD2-21
IGHV3-15	IGHJ4	IGHD3-16
IGHV3-15	IGHJ4	IGHD4-17
IGHV3-15	IGHJ5	IGHD2-2
IGHV3-15	IGHJ6	IGHD1-1
IGHV3-15	IGHJ6	IGHD3-3
IGHV3-20	IGHJ4	IGHD1-26
IGHV3-20	IGHJ4	IGHD1-7
IGHV3-21	IGHJ3	IGHD5-12
IGHV3-21	IGHJ4	IGHD2-15
IGHV3-21	IGHJ4	IGHD6-13
IGHV3-21	IGHJ4	IGHD6-6
IGHV3-21	IGHJ6	IGHD6-13
IGHV3-23	IGHJ4	IGHD2-8
IGHV3-23	IGHJ4	IGHD6-19
IGHV3-23	IGHJ6	IGHD1-7
IGHV3-23	IGHJ6	IGHD3-3
IGHV3-23	IGHJ6	IGHD4-17
IGHV3-30	IGHJ4	IGHD1-26
IGHV3-30	IGHJ4	IGHD3-10
IGHV3-33	IGHJ2	IGHD7-27
IGHV3-33	IGHJ3	IGHD6-6
IGHV3-33	IGHJ4	IGHD1-20
IGHV3-33	IGHJ4	IGHD2-15
IGHV3-33	IGHJ4	IGHD3-16
IGHV3-33	IGHJ5	IGHD1-26

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-33	IGHJ5	IGHD6-6
IGHV3-33	IGHJ6	IGHD1-20
IGHV3-33	IGHJ6	IGHD3-22
IGHV3-33	IGHJ6	IGHD3-9
IGHV3-48	IGHJ3	IGHD1-26
IGHV3-48	IGHJ3	IGHD5-12
IGHV3-48	IGHJ3	IGHD6-6
IGHV3-48	IGHJ4	IGHD6-6
IGHV3-48	IGHJ5	IGHD3-22
IGHV3-53	IGHJ2	IGHD7-27
IGHV3-53	IGHJ4	IGHD5-18
IGHV3-53	IGHJ6	IGHD2-15
IGHV3-64	IGHJ3	IGHD1-7
IGHV3-7	IGHJ1	IGHD3-3
IGHV3-7	IGHJ2	IGHD3-3
IGHV3-7	IGHJ4	IGHD4-17
IGHV3-7	IGHJ5	IGHD1-7
IGHV3-7	IGHJ5	IGHD2-8
IGHV3-72	IGHJ3	IGHD6-6
IGHV3-72	IGHJ4	IGHD1-20
IGHV3-9	IGHJ3	IGHD1-26
IGHV3-9	IGHJ4	IGHD1-26
IGHV3-9	IGHJ4	IGHD3-3
IGHV3-9	IGHJ4	IGHD6-6
IGHV3-9	IGHJ4	IGHD7-27
IGHV3-9	IGHJ6	IGHD1-7
IGHV4-31	IGHJ2	IGHD7-27
IGHV4-31	IGHJ4	IGHD6-6
IGHV4-31	IGHJ6	IGHD3-10
IGHV4-34	IGHJ1	IGHD1-26
IGHV4-34	IGHJ2	IGHD6-6
IGHV4-34	IGHJ2	IGHD7-27
IGHV4-34	IGHJ3	IGHD1-1
IGHV4-34	IGHJ3	IGHD1-20
IGHV4-34	IGHJ3	IGHD1-7
IGHV4-34	IGHJ4	IGHD2-15
IGHV4-34	IGHJ4	IGHD5-18
IGHV4-34	IGHJ5	IGHD1-1

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-34	IGHJ5	IGHD1-7
IGHV4-34	IGHJ5	IGHD2-2
IGHV4-34	IGHJ5	IGHD6-13
IGHV4-34	IGHJ5	IGHD6-6
IGHV4-34	IGHJ6	IGHD1-7
IGHV4-34	IGHJ6	IGHD2-2
IGHV4-34	IGHJ6	IGHD3-22
IGHV4-39	IGHJ2	IGHD6-6
IGHV4-39	IGHJ3	IGHD1-26
IGHV4-39	IGHJ3	IGHD6-6
IGHV4-39	IGHJ4	IGHD3-16
IGHV4-39	IGHJ5	IGHD1-7
IGHV4-59	IGHJ1	IGHD3-10
IGHV4-59	IGHJ2	IGHD1-7
IGHV4-59	IGHJ2	IGHD5-18
IGHV4-59	IGHJ3	IGHD2-15
IGHV4-59	IGHJ3	IGHD3-10
IGHV4-59	IGHJ3	IGHD6-6
IGHV4-59	IGHJ4	IGHD3-16
IGHV4-59	IGHJ4	IGHD3-22
IGHV4-59	IGHJ6	IGHD1-20
IGHV4-59	IGHJ6	IGHD6-13
IGHV4-59	IGHJ6	IGHD6-6
IGHV4-59	IGHJ4	IGHD3-3
IGHV5-51	IGHJ4	IGHD2-21
IGHV5-51	IGHJ5	IGHD1-26
IGHV5-51	IGHJ6	IGHD3-3
IGHV6-1	IGHJ3	IGHD1-1
IGHV6-1	IGHJ4	IGHD2-21
IGHV6-1	IGHJ4	IGHD5-18
IGHV6-1	IGHJ4	IGHD7-27
IGHV6-1	IGHJ5	IGHD1-1
IGHV6-1	IGHJ6	IGHD1-26
IGHV6-1	IGHJ6	IGHD4-17
IGHV6-1	IGHJ6	IGHD6-6

Tabel 30

Humaan V_H	Humaan J_H	Humaan D_H
IGHV2-5	IGHJ4	IGHD1-7
IGHV3-33	IGHJ4	IGHD6-6
IGHV4-39	IGHJ4	IGHD3-10
IGHV3-23	IGHJ4	IGHD1-26
IGHV3-23	IGHJ4	IGHD1-7
IGHV2-5	IGHJ4	IGHD6-19
IGHV3-15	IGHJ4	IGHD7-27
IGHV4-59	IGHJ4	IGHD7-27
IGHV4-59	IGHJ6	IGHD3-3
IGHV3-33	IGHJ6	IGHD6-6
IGHV1-69	IGHJ6	IGHD5-12
IGHV3-21	IGHJ6	IGHD2-8
IGHV3-30	IGHJ4	IGHD3-22
IGHV4-59	IGHJ4	IGHD6-13
IGHV3-33	IGHJ5	IGHD1-1
IGHV3-15	IGHJ5	IGHD1-20
IGHV3-23	IGHJ6	IGHD6-13
IGHV3-33	IGHJ2	IGHD3-10
IGHV3-15	IGHJ6	IGHD6-6
IGHV3-21	IGHJ6	IGHD4-17
IGHV3-23	IGHJ4	IGHD6-13
IGHV4-39	IGHJ4	IGHD1-7
IGHV4-59	IGHJ6	IGHD4-17
IGHV3-33	IGHJ2	IGHD6-6
IGHV4-39	IGHJ4	IGHD5-12
IGHV4-59	IGHJ6	IGHD3-22
IGHV2-5	IGHJ3	IGHD6-6
IGHV4-39	IGHJ4	IGHD6-19
IGHV4-59	IGHJ4	IGHD1-1
IGHV3-15	IGHJ1	IGHD6-6
IGHV3-23	IGHJ4	IGHD3-9
IGHV3-33	IGHJ4	IGHD1-26
IGHV4-39	IGHJ4	IGHD2-8
IGHV4-59	IGHJ4	IGHD3-3
IGHV2-5	IGHJ4	IGHD6-6
IGHV4-39	IGHJ5	IGHD6-13
IGHV1-69	IGHJ6	IGHD3-22
IGHV2-5	IGHJ3	IGHD1-1
IGHV2-5	IGHJ4	IGHD1-26
IGHV3-15	IGHJ4	IGHD6-13

Humaan V_H	Humaan J_H	Humaan D_H
IGHV3-21	IGHJ6	IGHD1-7
IGHV4-39	IGHJ4	IGHD1-26
IGHV2-5	IGHJ4	IGHD4-17
IGHV3-15	IGHJ4	IGHD1-26
IGHV3-15	IGHJ4	IGHD1-7
IGHV3-23	IGHJ5	IGHD3-9
IGHV3-23	IGHJ6	IGHD6-6
IGHV3-30	IGHJ3	IGHD3-16
IGHV4-39	IGHJ3	IGHD1-7
IGHV4-59	IGHJ4	IGHD2-15
IGHV1-24	IGHJ4	IGHD5-18
IGHV2-5	IGHJ5	IGHD3-10
IGHV3-23	IGHJ2	IGHD6-6
IGHV3-23	IGHJ3	IGHD1-26
IGHV3-23	IGHJ5	IGHD1-7
IGHV3-33	IGHJ4	IGHD6-13
IGHV4-39	IGHJ4	IGHD7-27
IGHV4-59	IGHJ3	IGHD1-1
IGHV1-69	IGHJ5	IGHD3-10
IGHV2-5	IGHJ4	IGHD2-2
IGHV3-23	IGHJ6	IGHD7-27
IGHV4-59	IGHJ4	IGHD1-7
IGHV1-69	IGHJ6	IGHD7-27
IGHV2-5	IGHJ4	IGHD1-20
IGHV3-21	IGHJ2	IGHD3-22
IGHV3-23	IGHJ3	IGHD3-16
IGHV3-23	IGHJ3	IGHD3-9
IGHV3-23	IGHJ4	IGHD5-18
IGHV4-39	IGHJ2	IGHD7-27
IGHV4-39	IGHJ4	IGHD6-6
IGHV4-59	IGHJ3	IGHD4-17
IGHV4-59	IGHJ4	IGHD3-9
IGHV4-59	IGHJ5	IGHD6-13
IGHV4-59	IGHJ6	IGHD3-10
IGHV2-5	IGHJ4	IGHD1-1
IGHV3-15	IGHJ4	IGHD3-22
IGHV3-21	IGHJ4	IGHD1-26
IGHV3-23	IGHJ3	IGHD1-20
IGHV3-23	IGHJ4	IGHD4-17
IGHV3-23	IGHJ4	IGHD5-12

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-23	IGHJ6	IGHD2-2
IGHV3-30	IGHJ6	IGHD3-10
IGHV4-59	IGHJ3	IGHD1-7
IGHV4-59	IGHJ6	IGHD1-26
IGHV2-5	IGHJ6	IGHD6-13
IGHV3-15	IGHJ3	IGHD1-7
IGHV3-15	IGHJ4	IGHD3-3
IGHV3-21	IGHJ4	IGHD7-27
IGHV3-21	IGHJ6	IGHD1-20
IGHV3-21	IGHJ6	IGHD3-10
IGHV3-23	IGHJ3	IGHD7-27
IGHV3-23	IGHJ5	IGHD1-26
IGHV3-23	IGHJ5	IGHD7-27
IGHV3-30	IGHJ4	IGHD2-15
IGHV3-33	IGHJ4	IGHD1-1
IGHV3-33	IGHJ4	IGHD3-22
IGHV4-39	IGHJ2	IGHD4-17
IGHV4-39	IGHJ2	IGHD5-12
IGHV4-39	IGHJ4	IGHD2-15
IGHV4-59	IGHJ3	IGHD7-27
IGHV4-59	IGHJ4	IGHD3-10
IGHV4-59	IGHJ4	IGHD5-18
IGHV1-24	IGHJ4	IGHD1-26
IGHV1-69	IGHJ4	IGHD6-6
IGHV1-69	IGHJ5	IGHD3-9
IGHV2-5	IGHJ3	IGHD3-3
IGHV2-5	IGHJ3	IGHD5-12
IGHV2-5	IGHJ4	IGHD2-21
IGHV2-5	IGHJ5	IGHD5-18
IGHV2-5	IGHJ6	IGHD3-3
IGHV2-5	IGHJ6	IGHD7-27
IGHV3-15	IGHJ5	IGHD6-6
IGHV3-15	IGHJ6	IGHD6-13
IGHV3-21	IGHJ6	IGHD2-2
IGHV3-21	IGHJ6	IGHD6-6
IGHV3-23	IGHJ3	IGHD6-6
IGHV3-23	IGHJ5	IGHD2-2
IGHV3-23	IGHJ5	IGHD3-16
IGHV3-30	IGHJ5	IGHD1-7
IGHV3-33	IGHJ4	IGHD3-3
IGHV4-39	IGHJ3	IGHD7-27
IGHV4-39	IGHJ4	IGHD2-2

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-39	IGHJ4	IGHD6-13
IGHV4-39	IGHJ5	IGHD6-6
IGHV4-39	IGHJ6	IGHD1-26
IGHV4-59	IGHJ2	IGHD6-13
IGHV4-59	IGHJ3	IGHD1-26
IGHV4-59	IGHJ5	IGHD5-12
IGHV4-59	IGHJ5	IGHD5-18
IGHV4-59	IGHJ5	IGHD7-27
IGHV4-59	IGHJ6	IGHD7-27
IGHV4-59	IGHJ6	IGHD1-7
IGHV5-51	IGHJ6	IGHD2-2
IGHV1-24	IGHJ3	IGHD6-6
IGHV1-24	IGHJ4	IGHD4-17
IGHV1-69	IGHJ4	IGHD3-3
IGHV2-5	IGHJ3	IGHD5-18
IGHV2-5	IGHJ4	IGHD3-22
IGHV2-5	IGHJ4	IGHD3-3
IGHV2-5	IGHJ4	IGHD5-18
IGHV2-5	IGHJ4	IGHD6-13
IGHV2-5	IGHJ6	IGHD1-7
IGHV2-5	IGHJ6	IGHD6-6
IGHV3-15	IGHJ4	IGHD1-1
IGHV3-15	IGHJ4	IGHD2-21
IGHV3-15	IGHJ4	IGHD3-16
IGHV3-15	IGHJ4	IGHD4-17
IGHV3-15	IGHJ5	IGHD2-2
IGHV3-15	IGHJ6	IGHD1-1
IGHV3-15	IGHJ6	IGHD3-3
IGHV3-21	IGHJ3	IGHD5-12
IGHV3-21	IGHJ4	IGHD2-15
IGHV3-21	IGHJ4	IGHD6-13
IGHV3-21	IGHJ4	IGHD6-6
IGHV3-21	IGHJ6	IGHD6-13
IGHV3-23	IGHJ4	IGHD6-19
IGHV3-23	IGHJ6	IGHD1-7
IGHV3-23	IGHJ6	IGHD3-3
IGHV3-23	IGHJ6	IGHD4-17
IGHV3-30	IGHJ4	IGHD1-26
IGHV3-30	IGHJ4	IGHD3-10
IGHV3-33	IGHJ2	IGHD7-27
IGHV3-33	IGHJ3	IGHD6-6
IGHV3-33	IGHJ4	IGHD1-20

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-33	IGHJ4	IGHD3-16
IGHV3-33	IGHJ5	IGHD1-26
IGHV3-33	IGHJ5	IGHD6-6
IGHV3-33	IGHJ6	IGHD1-20
IGHV3-33	IGHJ6	IGHD3-22
IGHV3-33	IGHJ6	IGHD3-9
IGHV4-39	IGHJ2	IGHD6-6
IGHV4-39	IGHJ3	IGHD6-6
IGHV4-39	IGHJ4	IGHD3-16
IGHV4-39	IGHJ5	IGHD1-7
IGHV4-59	IGHJ1	IGHD3-10
IGHV4-59	IGHJ2	IGHD1-7
IGHV4-59	IGHJ2	IGHD5-18
IGHV4-59	IGHJ3	IGHD2-15

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-59	IGHJ3	IGHD3-10
IGHV4-59	IGHJ3	IGHD6-6
IGHV4-59	IGHJ4	IGHD3-22
IGHV4-59	IGHJ6	IGHD1-20
IGHV4-59	IGHJ6	IGHD6-13
IGHV4-59	IGHJ6	IGHD6-6
IGHV4-59	IGHJ4	IGHD3-3
IGHV5-51	IGHJ4	IGHD2-21
IGHV5-51	IGHJ5	IGHD1-26
IGHV5-51	IGHJ6	IGHD3-3

5 14. Werkwijze voor het vervaardigen van een bispecifiek antigeen-bindend eiwit
omvattende:

(a) tot expressie brengen van een eerste variabel domein van de humane
immunoglobuline zware keten welke gecodeerd wordt door een eerste variabel gebied van de
humane immunoglobuline zware keten afkomstig van een B cel van een eerste genetische
10 gemanipuleerde muis welke geïmmuniseerd is met een eerste antigeen van belang welke een
eerste epitoop omvat, welke eerste muis:

(i) een kiembaan omvat welke homozygoot of heterozygoot is voor een
enkel herrangschikt variabel gebied van de humane immunoglobuline lichte keten gen
15 sequentie, welke is afkomstig van een herrangschikte humane V κ 1-39/J κ sequentie,
waarbij de herrangschikte humane V κ 1-39/J κ sequentie een humane kiembaan V κ 1-39
gen segment en een humane kiembaan J κ segment omvat, welke herrangschikte
humane V κ 1-39/J κ sequentie operabel gekoppeld is aan een constant gebied van de
immunoglobuline lichte keten sequentie;

20

(ii) een kiembaan omvat welke niet herrangschikte humane V_H gen
segmenten, humane D gen segmenten en humane J_H gen segmenten heeft, welke niet

herrangschikte humane V_H gen segmenten operabel gekoppeld zijn aan een murine C_H gebied;

5 (iii) een populatie van B cellen omvat waarbij elke B cel in de populatie een variabel domein van de humane immunoglobuline lichte keten tot expressie brengt welke afkomstig is van de herrangschikte humane $V_{\kappa 1-39/J\kappa}$ sequentie en waarbij de B cel populatie ten minste één B cel omvat welke een variabel domein van de humane immunoglobuline zware keten tot expressie brengt;

10 (b) tot expressie brengen van een tweede variabele domein van de humane immunoglobuline zware keten welke gecodeerd wordt door een tweede variabel gebied van de humane immunoglobuline zware keten afkomstig van een B cel van een tweede genetische gemanipuleerde muis welke geïmmuniseerd is met een tweede antigeen van belang welke een tweede epitoom omvat, welke tweede muis:

15

(i) een kiembaan omvat welke homozygoot of heterozygoot is voor een enkele herrangschikte variabel gebied van de humane immunoglobuline lichte keten gen sequentie welke afkomstig is van dezelfde herrangschikte humane $V_{\kappa 1-39/J\kappa}$ sequentie als in de eerste muis, waarbij de herrangschikte humane $V_{\kappa 1-39/J\kappa}$ sequentie het humane kiembaan $V_{\kappa 1-39}$ gen segment en het humane $J\kappa$ segment omvat, welke herrangschikte humane $V_{\kappa 1-39/J\kappa}$ sequentie operabel gekoppeld is aan een constant gebied van een immunoglobuline lichte keten sequentie;

20

(ii) een kiembaan omvat welke niet herrangschikte humane V_H gen segmenten, humane D gen segmenten en humane J_H gen segmenten heeft, welke niet herrangschikte humane V_H gen segmenten operabel gekoppeld zijn aan een murine C_H gebied;

25

(iii) een populatie van B cellen omvat waarbij elke B cel in de populatie een variabel domein van de immunoglobuline lichte keten tot expressie brengt welke afkomstig is van de herrangschikte humane $V_{\kappa 1-39/J\kappa}$ sequentie en waarbij de B cel populatie ten minste één B cel omvat welke een variabel domein van de humane immunoglobuline zware keten tot expressie brengt; en

30

(c) koppelen van de tot expressie gebrachte eerste humane immunoglobuline zware keten welke het variabele domein omvat welke gecodeerd wordt door de eerste variabele gebied van de humane immunoglobuline zware keten met een enkele humane lichte keten en met de tot expressie gebrachte tweede humane immunoglobuline zware keten welke ook gekoppeld wordt met de enkele humane immunoglobuline lichte keten, de tweede humane immunoglobuline zware keten omvattende een variabel domein gecodeerd door een tweede variabele gebied van de humane immunoglobuline zware keten, zodoende genererend een bispecifiek antigeen-bindend eiwit,

waarbij ten minste één van de eerste of de tweede humane immunoglobuline zware ketens afkomstig is uit een herrangschikking gekozen uit de groep bestaande uit de herrangschikkingen zoals genoemd in Tabellen 29 en 30 hieronder:

Tabel 29

Humaan V _H	Humaan J _H	Humaan D _H
IGHV2-70	IGHJ3	IGHD3-10
IGHV4-59	IGHJ4	IGHD1-26
IGHV2-26	IGHJ4	IGHD3-9
IGHV4-28	IGHJ4	IGHD1-26
IGHV1-18	IGHJ6	IGHD1-26
IGHV2-5	IGHJ4	IGHD1-7
IGHV1-18	IGHJ3	IGHD4-17
IGHV4-59	IGHJ4	IGHD6-6
IGHV3-33	IGHJ4	IGHD6-6
IGHV1-69	IGHJ4	IGHD6-13
IGHV3-64	IGHJ4	IGHD1-7
IGHV4-39	IGHJ4	IGHD3-10
IGHV3-23	IGHJ4	IGHD1-26
IGHV1-18	IGHJ4	IGHD6-6
IGHV3-23	IGHJ4	IGHD1-7
IGHV3-11	IGHJ4	IGHD5-18
IGHV1-18	IGHJ6	IGHD6-19
IGHV2-5	IGHJ4	IGHD6-19
IGHV3-15	IGHJ4	IGHD7-27
IGHV4-34	IGHJ6	IGHD6-13
IGHV4-59	IGHJ4	IGHD7-27

Humaan V _H	Humaan J _H	Humaan D _H
IGHV1-18	IGHJ6	IGHD3-9
IGHV2-26	IGHJ4	IGHD1-26
IGHV1-18	IGHJ3	IGHD7-27
IGHV4-59	IGHJ6	IGHD3-3
IGHV3-33	IGHJ6	IGHD6-6
IGHV3-7	IGHJ4	IGHD6-13
IGHV3-7	IGHJ6	IGHD6-19
IGHV1-18	IGHJ4	IGHD1-7
IGHV1-69	IGHJ6	IGHD5-12
IGHV3-72	IGHJ6	IGHD6-6
IGHV4-34	IGHJ3	IGHD6-6
IGHV3-21	IGHJ6	IGHD2-8
IGHV3-30	IGHJ4	IGHD3-22
IGHV3-33	IGHJ4	IGHD1-7
IGHV6-1	IGHJ4	IGHD1-26
IGHV4-59	IGHJ4	IGHD6-13
IGHV1-8	IGHJ4	IGHD1-26
IGHV3-13	IGHJ4	IGHD3-10
IGHV2-70	IGHJ4	IGHD1-26
IGHV3-33	IGHJ5	IGHD1-1
IGHV1-18	IGHJ4	IGHD1-26

Humaan V _H	Humaan J _H	Humaan D _H
IGHV1-8	IGHJ6	IGHD1-7
IGHV1-8	IGHJ4	IGHD3-10
IGHV3-15	IGHJ5	IGHD1-20
IGHV3-23	IGHJ6	IGHD6-13
IGHV3-33	IGHJ2	IGHD3-10
IGHV2-70	IGHJ5	IGHD3-10
IGHV3-15	IGHJ6	IGHD6-6
IGHV3-21	IGHJ6	IGHD4-17
IGHV1-18	IGHJ6	IGHD6-13
IGHV1-8	IGHJ4	IGHD1-26
IGHV3-13	IGHJ4	IGHD6-25
IGHV3-23	IGHJ4	IGHD6-13
IGHV4-39	IGHJ4	IGHD1-7
IGHV1-18	IGHJ4	IGHD2-2
IGHV2-26	IGHJ5	IGHD3-3
IGHV3-13	IGHJ4	IGHD4-17
IGHV3-13	IGHJ6	IGHD3-10
IGHV4-34	IGHJ6	IGHD1-26
IGHV4-59	IGHJ6	IGHD4-17
IGHV1-18	IGHJ6	IGHD3-22
IGHV1-46	IGHJ4	IGHD6-13
IGHV1-8	IGHJ6	IGHD2-2
IGHV1-8	IGHJ3	IGHD3-9
IGHV3-13	IGHJ4	IGHD1-7
IGHV3-33	IGHJ2	IGHD6-6
IGHV3-48	IGHJ4	IGHD1-7
IGHV4-39	IGHJ4	IGHD5-12
IGHV4-59	IGHJ6	IGHD3-22
IGHV1-8	IGHJ6	IGHD3-3
IGHV2-5	IGHJ3	IGHD6-6
IGHV3-43	IGHJ4	IGHD6-6
IGHV4-39	IGHJ4	IGHD6-19
IGHV4-59	IGHJ4	IGHD1-1
IGHV2-26	IGHJ4	IGHD3-16
IGHV2-70	IGHJ3	IGHD7-27
IGHV3-15	IGHJ1	IGHD6-6
IGHV3-23	IGHJ4	IGHD3-9
IGHV3-53	IGHJ5	IGHD6-6
IGHV3-64	IGHJ2	IGHD1-1
IGHV3-11	IGHJ4	IGHD3-10
IGHV3-13	IGHJ4	IGHD3-16
IGHV3-13	IGHJ4	IGHD6-6

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-33	IGHJ4	IGHD1-26
IGHV3-9	IGHJ3	IGHD1-7
IGHV3-9	IGHJ5	IGHD1-26
IGHV4-34	IGHJ4	IGHD3-16
IGHV4-39	IGHJ4	IGHD2-8
IGHV4-59	IGHJ4	IGHD3-3
IGHV2-26	IGHJ3	IGHD3-22
IGHV2-5	IGHJ4	IGHD6-6
IGHV2-70	IGHJ5	IGHD4-17
IGHV3-13	IGHJ4	IGHD1-1
IGHV3-13	IGHJ4	IGHD1-26
IGHV3-13	IGHJ6	IGHD5-18
IGHV3-7	IGHJ5	IGHD6-19
IGHV4-39	IGHJ5	IGHD6-13
IGHV1-69	IGHJ6	IGHD3-22
IGHV1-8	IGHJ3	IGHD5-18
IGHV2-26	IGHJ2	IGHD7-27
IGHV2-5	IGHJ3	IGHD1-1
IGHV2-5	IGHJ4	IGHD1-26
IGHV3-13	IGHJ3	IGHD3-22
IGHV3-15	IGHJ4	IGHD6-13
IGHV3-21	IGHJ6	IGHD1-7
IGHV3-48	IGHJ4	IGHD6-13
IGHV3-9	IGHJ6	IGHD1-26
IGHV4-39	IGHJ4	IGHD1-26
IGHV1-18	IGHJ2	IGHD3-10
IGHV1-8	IGHJ4	IGHD2-8
IGHV2-5	IGHJ4	IGHD4-17
IGHV2-70	IGHJ4	IGHD1-7
IGHV2-70	IGHJ4	IGHD6-6
IGHV3-15	IGHJ4	IGHD1-26
IGHV3-15	IGHJ4	IGHD1-7
IGHV3-23	IGHJ5	IGHD3-9
IGHV3-23	IGHJ6	IGHD6-6
IGHV3-30	IGHJ3	IGHD3-16
IGHV3-48	IGHJ3	IGHD7-27
IGHV3-48	IGHJ4	IGHD3-9
IGHV3-64	IGHJ6	IGHD6-6
IGHV3-7	IGHJ3	IGHD6-13
IGHV3-7	IGHJ4	IGHD6-6
IGHV4-31	IGHJ4	IGHD1-26
IGHV4-31	IGHJ6	IGHD6-6

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-39	IGHJ3	IGHD1-7
IGHV4-59	IGHJ4	IGHD2-15
IGHV1-18	IGHJ5	IGHD1-7
IGHV1-18	IGHJ5	IGHD3-3
IGHV1-2	IGHJ4	IGHD3-3
IGHV1-24	IGHJ4	IGHD5-18
IGHV1-8	IGHJ4	IGHD7-27
IGHV1-8	IGHJ6	IGHD3-3
IGHV2-5	IGHJ5	IGHD3-10
IGHV3-23	IGHJ2	IGHD6-6
IGHV3-23	IGHJ3	IGHD1-26
IGHV3-23	IGHJ5	IGHD1-7
IGHV3-33	IGHJ4	IGHD6-13
IGHV3-7	IGHJ5	IGHD5-18
IGHV3-9	IGHJ6	IGHD6-6
IGHV4-28	IGHJ3	IGHD2-15
IGHV4-34	IGHJ4	IGHD1-7
IGHV4-39	IGHJ4	IGHD7-27
IGHV4-59	IGHJ3	IGHD1-1
IGHV1-58	IGHJ6	IGHD6-13
IGHV1-69	IGHJ5	IGHD3-10
IGHV2-26	IGHJ4	IGHD1-7
IGHV2-5	IGHJ4	IGHD2-2
IGHV2-70	IGHJ3	IGHD1-20
IGHV2-70	IGHJ5	IGHD6-13
IGHV3-23	IGHJ6	IGHD7-27
IGHV3-7	IGHJ3	IGHD2-2
IGHV3-7	IGHJ4	IGHD1-7
IGHV3-9	IGHJ3	IGHD6-6
IGHV3-9	IGHJ4	IGHD6-19
IGHV3-9	IGHJ5	IGHD1-7
IGHV4-34	IGHJ4	IGHD3-3
IGHV4-59	IGHJ4	IGHD1-7
IGHV1-69	IGHJ6	IGHD7-27
IGHV1-8	IGHJ1	IGHD6-6
IGHV1-8	IGHJ4	IGHD1-20
IGHV1-8	IGHJ4	IGHD3-3
IGHV2-5	IGHJ4	IGHD1-20
IGHV2-70	IGHJ5	IGHD1-26
IGHV3-13	IGHJ4	IGHD6-13
IGHV3-21	IGHJ2	IGHD3-22
IGHV3-23	IGHJ3	IGHD3-16

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-23	IGHJ3	IGHD3-9
IGHV3-23	IGHJ4	IGHD5-18
IGHV3-48	IGHJ4	IGHD1-26
IGHV3-48	IGHJ4	IGHD3-10
IGHV3-48	IGHJ6	IGHD3-9
IGHV3-7	IGHJ4	IGHD6-6
IGHV3-7	IGHJ5	IGHD2-21
IGHV3-9	IGHJ6	IGHD3-10
IGHV4-34	IGHJ4	IGHD6-6
IGHV4-34	IGHJ4	IGHD7-27
IGHV4-34	IGHJ6	IGHD3-10
IGHV4-39	IGHJ2	IGHD7-27
IGHV4-39	IGHJ4	IGHD6-6
IGHV4-59	IGHJ3	IGHD4-17
IGHV4-59	IGHJ4	IGHD3-9
IGHV4-59	IGHJ5	IGHD6-13
IGHV4-59	IGHJ6	IGHD3-10
IGHV6-1	IGHJ4	IGHD1-1
IGHV1-18	IGHJ5	IGHD6-13
IGHV1-2	IGHJ5	IGHD1-7
IGHV2-26	IGHJ4	IGHD7-27
IGHV2-5	IGHJ4	IGHD1-1
IGHV2-70	IGHJ3	IGHD2-2
IGHV2-70	IGHJ4	IGHD2-8
IGHV2-70	IGHJ5	IGHD6-6
IGHV3-13	IGHJ4	IGHD1-20
IGHV3-15	IGHJ4	IGHD3-22
IGHV3-21	IGHJ4	IGHD1-26
IGHV3-23	IGHJ3	IGHD1-20
IGHV3-23	IGHJ4	IGHD4-17
IGHV3-23	IGHJ4	IGHD5-12
IGHV3-23	IGHJ6	IGHD2-2
IGHV3-30	IGHJ6	IGHD3-10
IGHV3-48	IGHJ4	IGHD1-1
IGHV3-49	IGHJ2	IGHD3-10
IGHV3-9	IGHJ4	IGHD5-18
IGHV4-59	IGHJ3	IGHD1-7
IGHV4-59	IGHJ6	IGHD1-26
IGHV6-1	IGHJ5	IGHD1-20
IGHV1-18	IGHJ4	IGHD5-18
IGHV1-18	IGHJ6	IGHD6-6
IGHV2-26	IGHJ3	IGHD6-13

Humaan V _H	Humaan J _H	Humaan D _H
IGHV2-5	IGHJ6	IGHD6-13
IGHV2-70	IGHJ4	IGHD2-15
IGHV2-70	IGHJ4	IGHD3-3
IGHV3-11	IGHJ6	IGHD1-7
IGHV3-15	IGHJ3	IGHD1-7
IGHV3-15	IGHJ4	IGHD3-3
IGHV3-21	IGHJ4	IGHD7-27
IGHV3-21	IGHJ6	IGHD1-20
IGHV3-21	IGHJ6	IGHD3-10
IGHV3-23	IGHJ3	IGHD7-27
IGHV3-23	IGHJ5	IGHD1-26
IGHV3-23	IGHJ5	IGHD7-27
IGHV3-30	IGHJ4	IGHD2-15
IGHV3-33	IGHJ4	IGHD1-1
IGHV3-33	IGHJ4	IGHD3-22
IGHV3-48	IGHJ3	IGHD6-13
IGHV3-48	IGHJ4	IGHD5-12
IGHV3-7	IGHJ4	IGHD1-20
IGHV3-7	IGHJ4	IGHD1-26
IGHV4-34	IGHJ4	IGHD1-26
IGHV4-34	IGHJ4	IGHD3-10
IGHV4-39	IGHJ2	IGHD4-17
IGHV4-39	IGHJ2	IGHD5-12
IGHV4-39	IGHJ4	IGHD2-15
IGHV4-59	IGHJ3	IGHD7-27
IGHV4-59	IGHJ4	IGHD3-10
IGHV4-59	IGHJ4	IGHD5-18
IGHV1-18	IGHJ4	IGHD3-10
IGHV1-24	IGHJ4	IGHD1-26
IGHV1-69	IGHJ4	IGHD6-6
IGHV1-69	IGHJ5	IGHD3-9
IGHV1-8	IGHJ4	IGHD1-1
IGHV1-8	IGHJ4	IGHD1-7
IGHV1-8	IGHJ4	IGHD3-3
IGHV1-8	IGHJ5	IGHD6-13
IGHV1-8	IGHJ6	IGHD3-10
IGHV2-26	IGHJ3	IGHD1-26
IGHV2-26	IGHJ5	IGHD5-12
IGHV2-5	IGHJ3	IGHD3-3
IGHV2-5	IGHJ3	IGHD5-12
IGHV2-5	IGHJ4	IGHD2-21
IGHV2-5	IGHJ5	IGHD5-18

Humaan V _H	Humaan J _H	Humaan D _H
IGHV2-5	IGHJ6	IGHD3-3
IGHV2-5	IGHJ6	IGHD7-27
IGHV2-70	IGHJ4	IGHD6-13
IGHV3-11	IGHJ3	IGHD1-26
IGHV3-13	IGHJ2	IGHD1-7
IGHV3-13	IGHJ5	IGHD5-18
IGHV3-15	IGHJ5	IGHD6-6
IGHV3-15	IGHJ6	IGHD6-13
IGHV3-20	IGHJ4	IGHD6-13
IGHV3-20	IGHJ6	IGHD4-17
IGHV3-21	IGHJ6	IGHD2-2
IGHV3-21	IGHJ6	IGHD6-6
IGHV3-23	IGHJ3	IGHD6-6
IGHV3-23	IGHJ5	IGHD2-2
IGHV3-23	IGHJ5	IGHD3-16
IGHV3-30	IGHJ5	IGHD1-7
IGHV3-33	IGHJ4	IGHD3-3
IGHV3-43	IGHJ6	IGHD3-10
IGHV3-43	IGHJ6	IGHD6-13
IGHV3-48	IGHJ4	IGHD7-27
IGHV3-49	IGHJ5	IGHD6-6
IGHV3-64	IGHJ4	IGHD2-2
IGHV3-72	IGHJ4	IGHD1-26
IGHV4-34	IGHJ1	IGHD6-6
IGHV4-34	IGHJ3	IGHD3-16
IGHV4-34	IGHJ3	IGHD4-17
IGHV4-34	IGHJ4	IGHD6-19
IGHV4-39	IGHJ3	IGHD7-27
IGHV4-39	IGHJ4	IGHD2-2
IGHV4-39	IGHJ4	IGHD6-13
IGHV4-39	IGHJ5	IGHD6-6
IGHV4-39	IGHJ6	IGHD1-26
IGHV4-59	IGHJ2	IGHD6-13
IGHV4-59	IGHJ3	IGHD1-26
IGHV4-59	IGHJ5	IGHD5-12
IGHV4-59	IGHJ5	IGHD5-18
IGHV4-59	IGHJ5	IGHD7-27
IGHV4-59	IGHJ6	IGHD7-27
IGHV4-59	IGHJ6	IGHD1-7
IGHV5-51	IGHJ6	IGHD2-2
IGHV6-1	IGHJ1	IGHD6-13
IGHV6-1	IGHJ3	IGHD7-27

Humaan V _H	Humaan J _H	Humaan D _H
IGHV6-1	IGHJ4	IGHD1-7
IGHV1-18	IGHJ3	IGHD1-20
IGHV1-18	IGHJ3	IGHD1-7
IGHV1-18	IGHJ3	IGHD5-12
IGHV1-18	IGHJ4	IGHD1-1
IGHV1-18	IGHJ4	IGHD2-15
IGHV1-18	IGHJ4	IGHD2-8
IGHV1-18	IGHJ4	IGHD6-13
IGHV1-18	IGHJ4	IGHD7-27
IGHV1-18	IGHJ5	IGHD1-20
IGHV1-2	IGHJ3	IGHD1-1
IGHV1-2	IGHJ4	IGHD1-7
IGHV1-24	IGHJ3	IGHD6-6
IGHV1-24	IGHJ4	IGHD4-17
IGHV1-58	IGHJ4	IGHD6-6
IGHV1-69	IGHJ4	IGHD3-3
IGHV1-8	IGHJ4	IGHD6-19
IGHV1-8	IGHJ6	IGHD3-22
IGHV2-26	IGHJ3	IGHD1-1
IGHV2-26	IGHJ3	IGHD6-6
IGHV2-26	IGHJ4	IGHD1-1
IGHV2-26	IGHJ4	IGHD5-12
IGHV2-26	IGHJ4	IGHD5-18
IGHV2-26	IGHJ4	IGHD6-6
IGHV2-26	IGHJ5	IGHD6-6
IGHV2-26	IGHJ6	IGHD3-16
IGHV2-5	IGHJ3	IGHD5-18
IGHV2-5	IGHJ4	IGHD3-22
IGHV2-5	IGHJ4	IGHD3-3
IGHV2-5	IGHJ4	IGHD5-18
IGHV2-5	IGHJ4	IGHD6-13
IGHV2-5	IGHJ6	IGHD1-7
IGHV2-5	IGHJ6	IGHD6-6
IGHV2-70	IGHJ3	IGHD1-7
IGHV2-70	IGHJ4	IGHD1-1
IGHV2-70	IGHJ4	IGHD5-12
IGHV3-11	IGHJ3	IGHD1-1
IGHV3-11	IGHJ4	IGHD2-2
IGHV3-11	IGHJ4	IGHD3-10
IGHV3-13	IGHJ2	IGHD3-22
IGHV3-13	IGHJ4	IGHD2-21
IGHV3-13	IGHJ4	IGHD2-8

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-13	IGHJ6	IGHD2-15
IGHV3-15	IGHJ4	IGHD1-1
IGHV3-15	IGHJ4	IGHD2-21
IGHV3-15	IGHJ4	IGHD3-16
IGHV3-15	IGHJ4	IGHD4-17
IGHV3-15	IGHJ5	IGHD2-2
IGHV3-15	IGHJ6	IGHD1-1
IGHV3-15	IGHJ6	IGHD3-3
IGHV3-20	IGHJ4	IGHD1-26
IGHV3-20	IGHJ4	IGHD1-7
IGHV3-21	IGHJ3	IGHD5-12
IGHV3-21	IGHJ4	IGHD2-15
IGHV3-21	IGHJ4	IGHD6-13
IGHV3-21	IGHJ4	IGHD6-6
IGHV3-21	IGHJ6	IGHD6-13
IGHV3-23	IGHJ4	IGHD2-8
IGHV3-23	IGHJ4	IGHD6-19
IGHV3-23	IGHJ6	IGHD1-7
IGHV3-23	IGHJ6	IGHD3-3
IGHV3-23	IGHJ6	IGHD4-17
IGHV3-30	IGHJ4	IGHD1-26
IGHV3-30	IGHJ4	IGHD3-10
IGHV3-33	IGHJ2	IGHD7-27
IGHV3-33	IGHJ3	IGHD6-6
IGHV3-33	IGHJ4	IGHD1-20
IGHV3-33	IGHJ4	IGHD2-15
IGHV3-33	IGHJ4	IGHD3-16
IGHV3-33	IGHJ5	IGHD1-26
IGHV3-33	IGHJ5	IGHD6-6
IGHV3-33	IGHJ6	IGHD1-20
IGHV3-33	IGHJ6	IGHD3-22
IGHV3-33	IGHJ6	IGHD3-9
IGHV3-48	IGHJ3	IGHD1-26
IGHV3-48	IGHJ3	IGHD5-12
IGHV3-48	IGHJ3	IGHD6-6
IGHV3-48	IGHJ4	IGHD6-6
IGHV3-48	IGHJ5	IGHD3-22
IGHV3-53	IGHJ2	IGHD7-27
IGHV3-53	IGHJ4	IGHD5-18
IGHV3-53	IGHJ6	IGHD2-15
IGHV3-64	IGHJ3	IGHD1-7
IGHV3-7	IGHJ1	IGHD3-3

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-7	IGHJ2	IGHD3-3
IGHV3-7	IGHJ4	IGHD4-17
IGHV3-7	IGHJ5	IGHD1-7
IGHV3-7	IGHJ5	IGHD2-8
IGHV3-72	IGHJ3	IGHD6-6
IGHV3-72	IGHJ4	IGHD1-20
IGHV3-9	IGHJ3	IGHD1-26
IGHV3-9	IGHJ4	IGHD1-26
IGHV3-9	IGHJ4	IGHD3-3
IGHV3-9	IGHJ4	IGHD6-6
IGHV3-9	IGHJ4	IGHD7-27
IGHV3-9	IGHJ6	IGHD1-7
IGHV4-31	IGHJ2	IGHD7-27
IGHV4-31	IGHJ4	IGHD6-6
IGHV4-31	IGHJ6	IGHD3-10
IGHV4-34	IGHJ1	IGHD1-26
IGHV4-34	IGHJ2	IGHD6-6
IGHV4-34	IGHJ2	IGHD7-27
IGHV4-34	IGHJ3	IGHD1-1
IGHV4-34	IGHJ3	IGHD1-20
IGHV4-34	IGHJ3	IGHD1-7
IGHV4-34	IGHJ4	IGHD2-15
IGHV4-34	IGHJ4	IGHD5-18
IGHV4-34	IGHJ5	IGHD1-1
IGHV4-34	IGHJ5	IGHD1-7
IGHV4-34	IGHJ5	IGHD2-2
IGHV4-34	IGHJ5	IGHD6-13
IGHV4-34	IGHJ5	IGHD6-6
IGHV4-34	IGHJ6	IGHD1-7
IGHV4-34	IGHJ6	IGHD2-2
IGHV4-34	IGHJ6	IGHD3-22

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-39	IGHJ2	IGHD6-6
IGHV4-39	IGHJ3	IGHD1-26
IGHV4-39	IGHJ3	IGHD6-6
IGHV4-39	IGHJ4	IGHD3-16
IGHV4-39	IGHJ5	IGHD1-7
IGHV4-59	IGHJ1	IGHD3-10
IGHV4-59	IGHJ2	IGHD1-7
IGHV4-59	IGHJ2	IGHD5-18
IGHV4-59	IGHJ3	IGHD2-15
IGHV4-59	IGHJ3	IGHD3-10
IGHV4-59	IGHJ3	IGHD6-6
IGHV4-59	IGHJ4	IGHD3-16
IGHV4-59	IGHJ4	IGHD3-22
IGHV4-59	IGHJ6	IGHD1-20
IGHV4-59	IGHJ6	IGHD6-13
IGHV4-59	IGHJ6	IGHD6-6
IGHV4-59	IGHJ4	IGHD3-3
IGHV5-51	IGHJ4	IGHD2-21
IGHV5-51	IGHJ5	IGHD1-26
IGHV5-51	IGHJ6	IGHD3-3
IGHV6-1	IGHJ3	IGHD1-1
IGHV6-1	IGHJ4	IGHD2-21
IGHV6-1	IGHJ4	IGHD5-18
IGHV6-1	IGHJ4	IGHD7-27
IGHV6-1	IGHJ5	IGHD1-1
IGHV6-1	IGHJ6	IGHD1-26
IGHV6-1	IGHJ6	IGHD4-17
IGHV6-1	IGHJ6	IGHD6-6

Tabel 30

Humaan V _H	Humaan J _H	Humaan D _H
IGHV2-5	IGHJ4	IGHD1-7
IGHV3-33	IGHJ4	IGHD6-6
IGHV4-39	IGHJ4	IGHD3-10
IGHV3-23	IGHJ4	IGHD1-26
IGHV3-23	IGHJ4	IGHD1-7
IGHV2-5	IGHJ4	IGHD6-19
IGHV3-15	IGHJ4	IGHD7-27

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-59	IGHJ4	IGHD7-27
IGHV4-59	IGHJ6	IGHD3-3
IGHV3-33	IGHJ6	IGHD6-6
IGHV1-69	IGHJ6	IGHD5-12
IGHV3-21	IGHJ6	IGHD2-8
IGHV3-30	IGHJ4	IGHD3-22
IGHV4-59	IGHJ4	IGHD6-13

Humaan V _H	Humaan J _H	Humaan D _H
IGHV3-33	IGHJ5	IGHD1-1
IGHV3-15	IGHJ5	IGHD1-20
IGHV3-23	IGHJ6	IGHD6-13
IGHV3-33	IGHJ2	IGHD3-10
IGHV3-15	IGHJ6	IGHD6-6
IGHV3-21	IGHJ6	IGHD4-17
IGHV3-23	IGHJ4	IGHD6-13
IGHV4-39	IGHJ4	IGHD1-7
IGHV4-59	IGHJ6	IGHD4-17
IGHV3-33	IGHJ2	IGHD6-6
IGHV4-39	IGHJ4	IGHD5-12
IGHV4-59	IGHJ6	IGHD3-22
IGHV2-5	IGHJ3	IGHD6-6
IGHV4-39	IGHJ4	IGHD6-19
IGHV4-59	IGHJ4	IGHD1-1
IGHV3-15	IGHJ1	IGHD6-6
IGHV3-23	IGHJ4	IGHD3-9
IGHV3-33	IGHJ4	IGHD1-26
IGHV4-39	IGHJ4	IGHD2-8
IGHV4-59	IGHJ4	IGHD3-3
IGHV2-5	IGHJ4	IGHD6-6
IGHV4-39	IGHJ5	IGHD6-13
IGHV1-69	IGHJ6	IGHD3-22
IGHV2-5	IGHJ3	IGHD1-1
IGHV2-5	IGHJ4	IGHD1-26
IGHV3-15	IGHJ4	IGHD6-13
IGHV3-21	IGHJ6	IGHD1-7
IGHV4-39	IGHJ4	IGHD1-26
IGHV2-5	IGHJ4	IGHD4-17
IGHV3-15	IGHJ4	IGHD1-26
IGHV3-15	IGHJ4	IGHD1-7
IGHV3-23	IGHJ5	IGHD3-9
IGHV3-23	IGHJ6	IGHD6-6
IGHV3-30	IGHJ3	IGHD3-16
IGHV4-39	IGHJ3	IGHD1-7
IGHV4-59	IGHJ4	IGHD2-15
IGHV1-24	IGHJ4	IGHD5-18
IGHV2-5	IGHJ5	IGHD3-10
IGHV3-23	IGHJ2	IGHD6-6
IGHV3-23	IGHJ3	IGHD1-26
IGHV3-23	IGHJ5	IGHD1-7
IGHV3-33	IGHJ4	IGHD6-13

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-39	IGHJ4	IGHD7-27
IGHV4-59	IGHJ3	IGHD1-1
IGHV1-69	IGHJ5	IGHD3-10
IGHV2-5	IGHJ4	IGHD2-2
IGHV3-23	IGHJ6	IGHD7-27
IGHV4-59	IGHJ4	IGHD1-7
IGHV1-69	IGHJ6	IGHD7-27
IGHV2-5	IGHJ4	IGHD1-20
IGHV3-21	IGHJ2	IGHD3-22
IGHV3-23	IGHJ3	IGHD3-16
IGHV3-23	IGHJ3	IGHD3-9
IGHV3-23	IGHJ4	IGHD5-18
IGHV4-39	IGHJ2	IGHD7-27
IGHV4-39	IGHJ4	IGHD6-6
IGHV4-59	IGHJ3	IGHD4-17
IGHV4-59	IGHJ4	IGHD3-9
IGHV4-59	IGHJ5	IGHD6-13
IGHV4-59	IGHJ6	IGHD3-10
IGHV2-5	IGHJ4	IGHD1-1
IGHV3-15	IGHJ4	IGHD3-22
IGHV3-21	IGHJ4	IGHD1-26
IGHV3-23	IGHJ3	IGHD1-20
IGHV3-23	IGHJ4	IGHD4-17
IGHV3-23	IGHJ6	IGHD2-2
IGHV3-30	IGHJ6	IGHD3-10
IGHV4-59	IGHJ3	IGHD1-7
IGHV4-59	IGHJ6	IGHD1-26
IGHV2-5	IGHJ6	IGHD6-13
IGHV3-15	IGHJ3	IGHD1-7
IGHV3-15	IGHJ4	IGHD3-3
IGHV3-21	IGHJ4	IGHD7-27
IGHV3-21	IGHJ6	IGHD1-20
IGHV3-21	IGHJ6	IGHD3-10
IGHV3-23	IGHJ3	IGHD7-27
IGHV3-23	IGHJ5	IGHD1-26
IGHV3-23	IGHJ5	IGHD7-27
IGHV3-30	IGHJ4	IGHD2-15
IGHV3-33	IGHJ4	IGHD1-1
IGHV3-33	IGHJ4	IGHD3-22
IGHV4-39	IGHJ2	IGHD4-17
IGHV4-39	IGHJ2	IGHD5-12

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-39	IGHJ4	IGHD2-15
IGHV4-59	IGHJ3	IGHD7-27
IGHV4-59	IGHJ4	IGHD3-10
IGHV4-59	IGHJ4	IGHD5-18
IGHV1-24	IGHJ4	IGHD1-26
IGHV1-69	IGHJ4	IGHD6-6
IGHV1-69	IGHJ5	IGHD3-9
IGHV2-5	IGHJ3	IGHD3-3
IGHV2-5	IGHJ3	IGHD5-12
IGHV2-5	IGHJ4	IGHD2-21
IGHV2-5	IGHJ5	IGHD5-18
IGHV2-5	IGHJ6	IGHD3-3
IGHV2-5	IGHJ6	IGHD7-27
IGHV3-15	IGHJ5	IGHD6-6
IGHV3-15	IGHJ6	IGHD6-13
IGHV3-21	IGHJ6	IGHD2-2
IGHV3-21	IGHJ6	IGHD6-6
IGHV3-23	IGHJ3	IGHD6-6
IGHV3-23	IGHJ5	IGHD2-2
IGHV3-23	IGHJ5	IGHD3-16
IGHV3-30	IGHJ5	IGHD1-7
IGHV3-33	IGHJ4	IGHD3-3
IGHV4-39	IGHJ3	IGHD7-27
IGHV4-39	IGHJ4	IGHD2-2
IGHV4-39	IGHJ4	IGHD6-13
IGHV4-39	IGHJ5	IGHD6-6
IGHV4-39	IGHJ6	IGHD1-26
IGHV4-59	IGHJ2	IGHD6-13
IGHV4-59	IGHJ3	IGHD1-26
IGHV4-59	IGHJ5	IGHD5-12
IGHV4-59	IGHJ5	IGHD5-18
IGHV4-59	IGHJ5	IGHD7-27
IGHV4-59	IGHJ6	IGHD7-27
IGHV4-59	IGHJ6	IGHD1-7
IGHV5-51	IGHJ6	IGHD2-2
IGHV1-24	IGHJ3	IGHD6-6
IGHV1-24	IGHJ4	IGHD4-17
IGHV1-69	IGHJ4	IGHD3-3
IGHV2-5	IGHJ3	IGHD5-18
IGHV2-5	IGHJ4	IGHD3-22
IGHV2-5	IGHJ4	IGHD3-3
IGHV2-5	IGHJ4	IGHD5-18

Humaan V _H	Humaan J _H	Humaan D _H
IGHV2-5	IGHJ4	IGHD6-13
IGHV2-5	IGHJ6	IGHD1-7
IGHV2-5	IGHJ6	IGHD6-6
IGHV3-15	IGHJ4	IGHD1-1
IGHV3-15	IGHJ4	IGHD2-21
IGHV3-15	IGHJ4	IGHD3-16
IGHV3-15	IGHJ4	IGHD4-17
IGHV3-15	IGHJ5	IGHD2-2
IGHV3-15	IGHJ6	IGHD1-1
IGHV3-15	IGHJ6	IGHD3-3
IGHV3-21	IGHJ3	IGHD5-12
IGHV3-21	IGHJ4	IGHD2-15
IGHV3-21	IGHJ4	IGHD6-13
IGHV3-21	IGHJ4	IGHD6-6
IGHV3-21	IGHJ6	IGHD6-13
IGHV3-23	IGHJ4	IGHD6-19
IGHV3-23	IGHJ6	IGHD1-7
IGHV3-23	IGHJ6	IGHD3-3
IGHV3-23	IGHJ6	IGHD4-17
IGHV3-30	IGHJ4	IGHD1-26
IGHV3-30	IGHJ4	IGHD3-10
IGHV3-33	IGHJ2	IGHD7-27
IGHV3-33	IGHJ3	IGHD6-6
IGHV3-33	IGHJ4	IGHD1-20
IGHV3-33	IGHJ4	IGHD3-16
IGHV3-33	IGHJ5	IGHD1-26
IGHV3-33	IGHJ5	IGHD6-6
IGHV3-33	IGHJ6	IGHD1-20
IGHV3-33	IGHJ6	IGHD3-22
IGHV3-33	IGHJ6	IGHD3-9
IGHV4-39	IGHJ2	IGHD6-6
IGHV4-39	IGHJ3	IGHD6-6
IGHV4-39	IGHJ4	IGHD3-16
IGHV4-39	IGHJ5	IGHD1-7
IGHV4-59	IGHJ1	IGHD3-10
IGHV4-59	IGHJ2	IGHD1-7
IGHV4-59	IGHJ2	IGHD5-18
IGHV4-59	IGHJ3	IGHD2-15
IGHV4-59	IGHJ3	IGHD3-10
IGHV4-59	IGHJ3	IGHD6-6
IGHV4-59	IGHJ4	IGHD3-22
IGHV4-59	IGHJ4	IGHD3-22
IGHV4-59	IGHJ6	IGHD1-20

Humaan V _H	Humaan J _H	Humaan D _H
IGHV4-59	IGHJ6	IGHD6-13
IGHV4-59	IGHJ6	IGHD6-6
IGHV4-59	IGHJ4	IGHD3-3
IGHV5-51	IGHJ4	IGHD2-21

Humaan V _H	Humaan J _H	Humaan D _H
IGHV5-51	IGHJ5	IGHD1-26
IGHV5-51	IGHJ6	IGHD3-3

15. De werkwijze volgens conclusie 13 of 14 waarbij de eerste muis en de tweede muis
5 dezelfde muis of verschillende muizen zijn.
16. De werkwijze volgens een der conclusies 13-15, waarbij het humane kiembaan J
segment Jk5 is.
- 10 17. De werkwijze volgens een der conclusies 13-16, waarbij dezelfde of verschillende
muizen geen endogeen variabel gebied van de κ immunoglobuline lichte keten gen segment
bevatten welke in staat is te herrangschikken om zodoende een gen te vormen welke codeert
voor een variabel domein van de immunoglobuline lichte keten.
- 15 18. De werkwijze volgens een der conclusies 13-17, waarbij de eerste en de tweede
antigenen:
twee verschillende antigenen zijn; of
hetzelfde antigeen zijn en de eerste en de tweede humane immunoglobuline zware
ketens aan verschillende epitopen op hetzelfde antigeen binden.
- 20 19. De werkwijze volgens een der conclusies 13-18, waarbij:
de kiembaan van de eerste muis of de tweede muis een humaan V_H gen segment heeft
geselecteerd uit V_H3-49, V_H3-66, V_H4-28 en/of V_H4-61.
- 25 20. De werkwijze volgens een der conclusies 13-19, waarbij:
het humane variabel domein van de immunoglobuline zware keten van het eerste of
tweede zware keten is afkomstig van een humaan V_H gen segment geselecteerd uit V_H3-49,
V_H3-66, V_H4-28 en/of V_H4-61.

21. De werkwijze volgens conclusie 18, waarbij de eerste en tweede antigenen hetzelfde antigeen zijn en de bindingsreactie van het bispecifieke antigeen-bindend eiwit met het zelfde antigeen ten minste tweemaal zo groot is als de bindingsreactie van een monospecifiek antigeen-bindend eiwit welke alleen de eerste humane immunoglobuline zware keten en/of
5 een monospecifiek antigeen-bindend eiwit welke alleen de tweede humane immunoglobuline zware keten omvat.
22. De werkwijze volgens een der conclusies 13-21, waarbij het eerste of het tweede humane immunoglobuline zware keten van het bispecifieke antigeen-bindend eiwit, maar niet
10 beide, een aminozuur modificatie heeft welke haar affiniteit voor Eiwit A reduceert.
23. De werkwijze volgens conclusie 22, waarbij de modificatie is geselecteerd uit 95R (EUR 435R), 96F (EUR 436F) of een combinatie hiervan.
- 15 24. De werkwijze volgens een der conclusies 13-23, waarbij in de eerste en de tweede muis het constante gebied van de immunoglobuline lichte keten sequentie een humane, muis of rat sequentie is, en/of het murine C_H is muis of rat C_H.
25. Een gastheercel vervaardigd volgens de methode van conclusie 13.
20
26. Een bispecifiek antigeen-bindend eiwit vervaardigd met de gastheercel volgens conclusie 25.
27. Een bispecifiek antigeen-bindend eiwit vervaardigd volgens de werkwijze volgens een
25 der conclusies 14-24.

Fig. 1

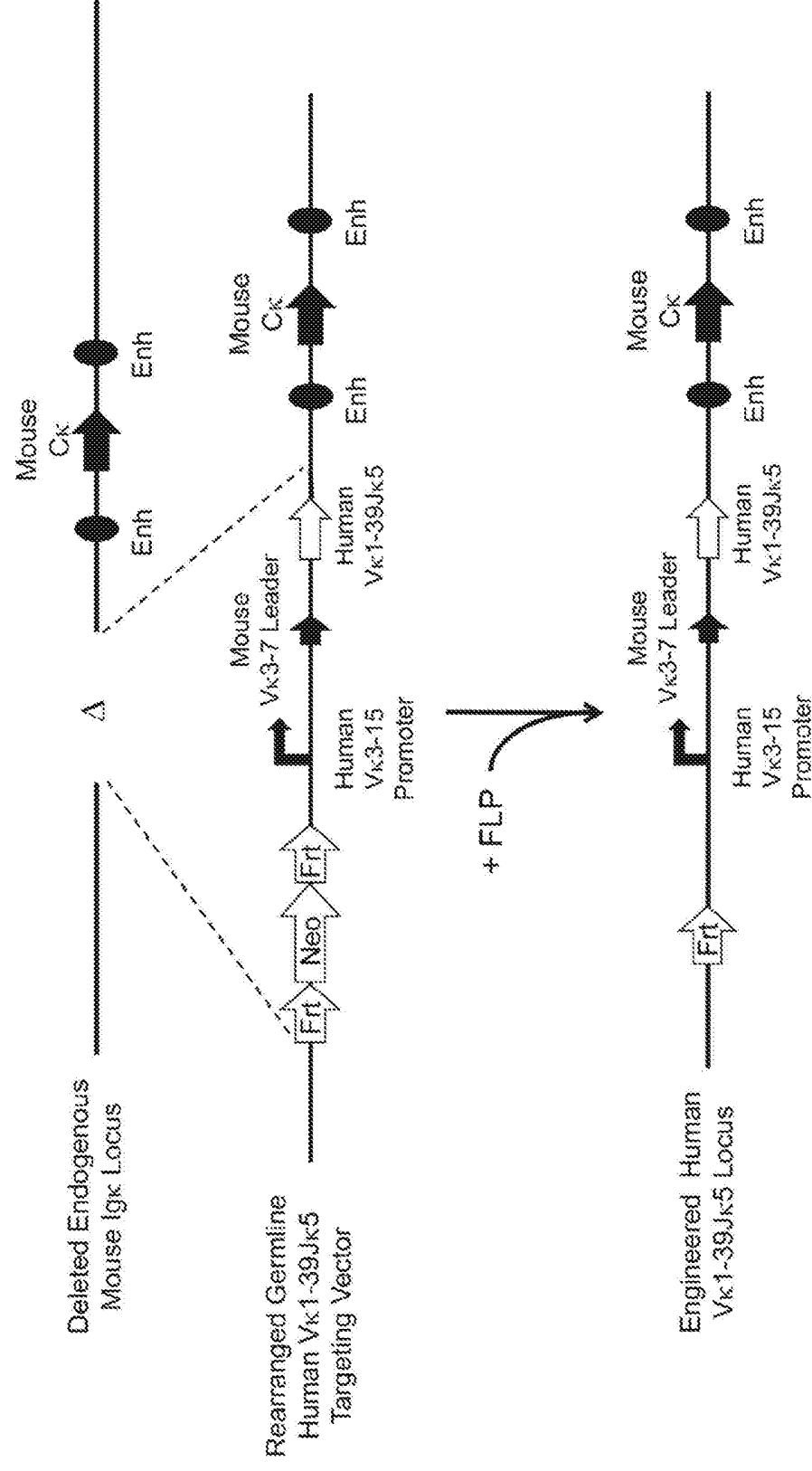


Fig. 2

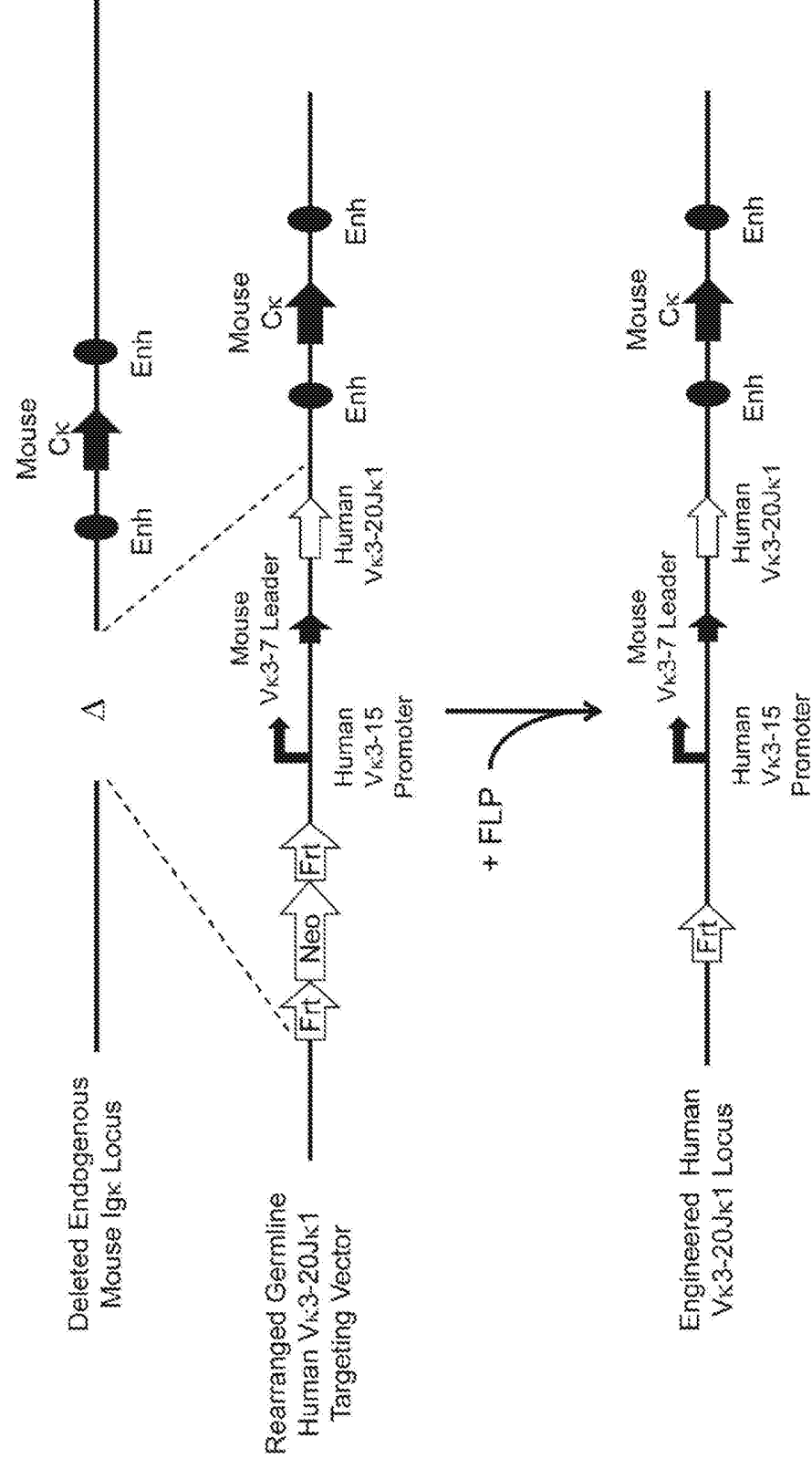


Fig. 3

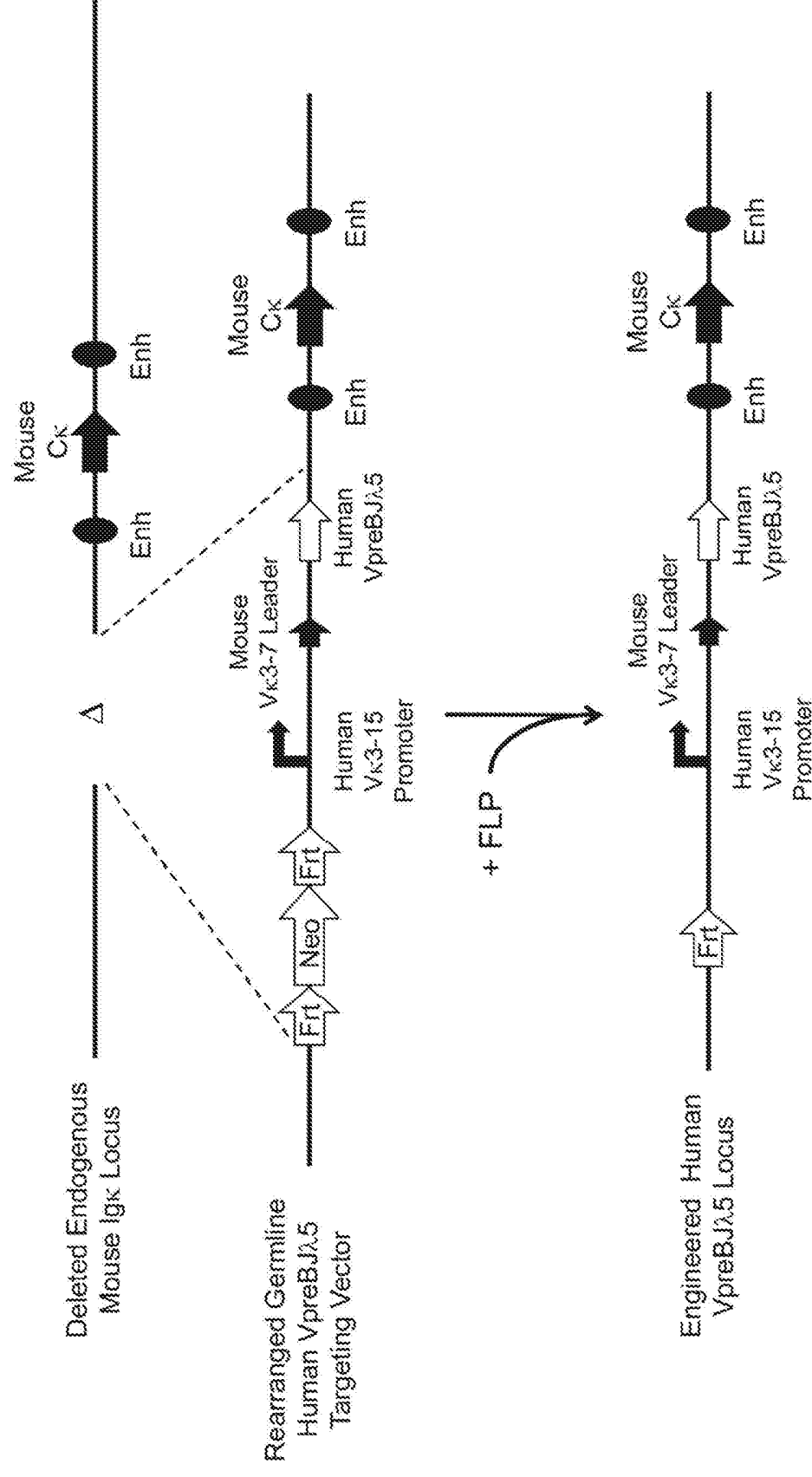


Fig. 4

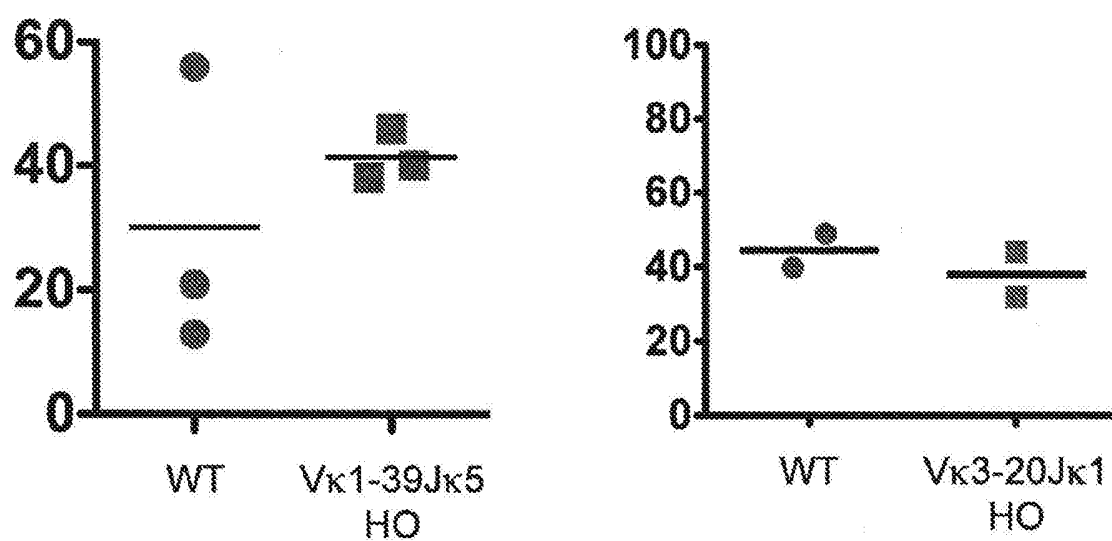


Fig. 5a

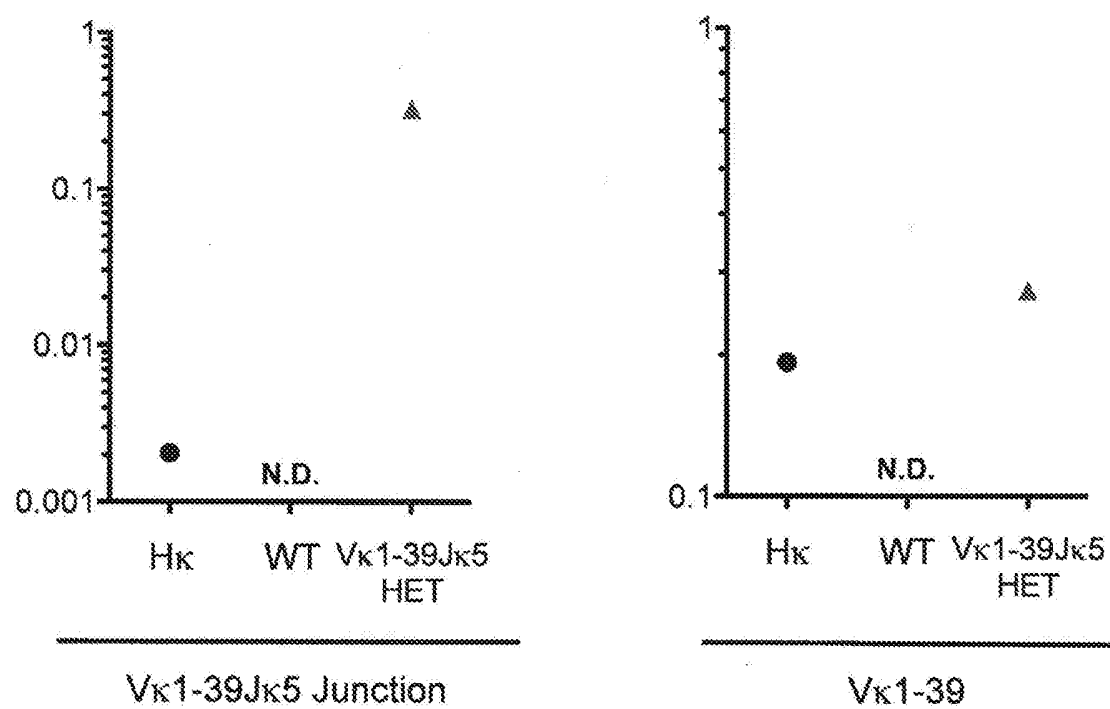


Fig. 5b

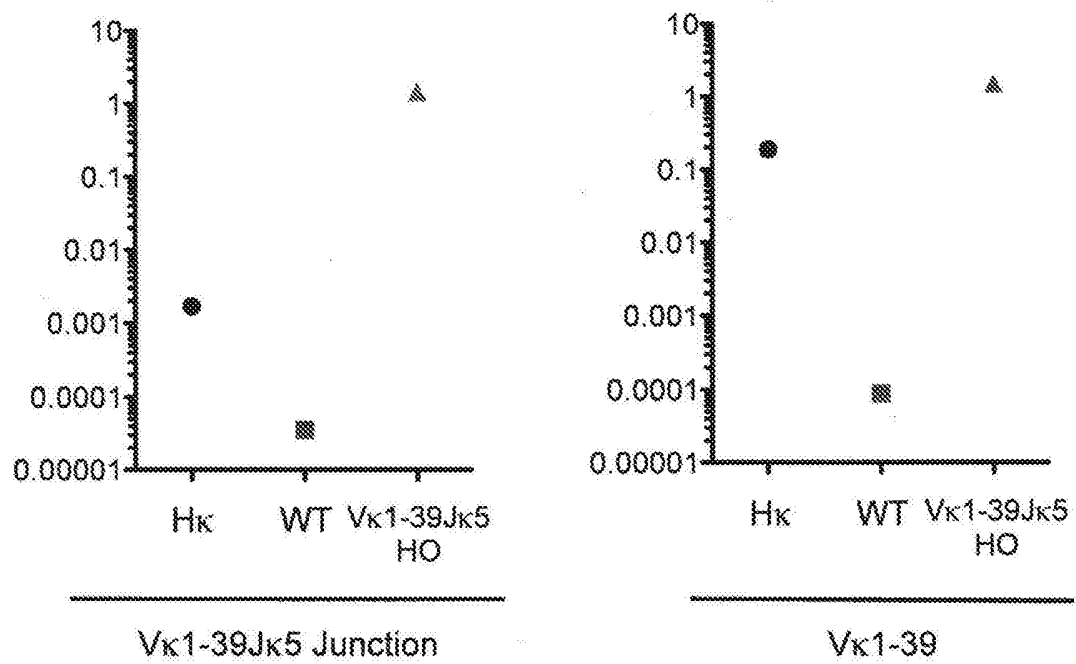


Fig. 5c

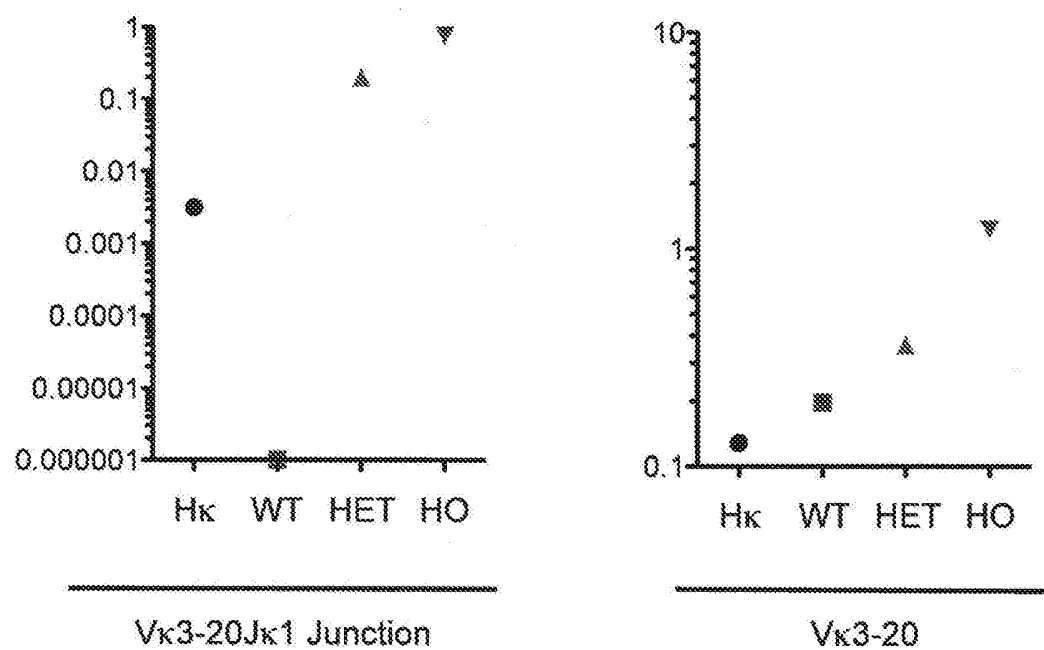


Fig. 6a

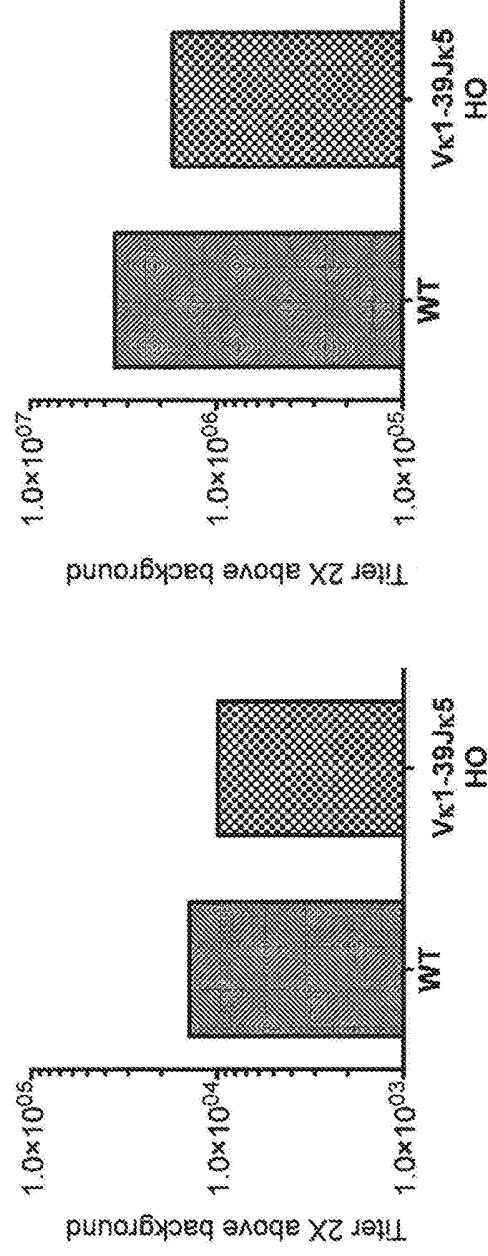


Fig. 6b

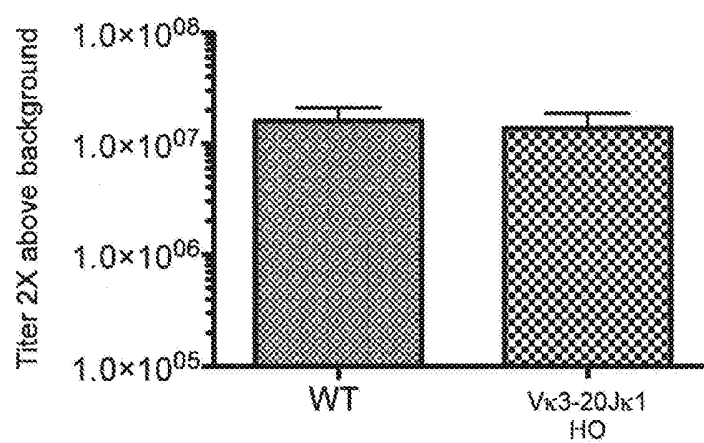


Fig. 7a

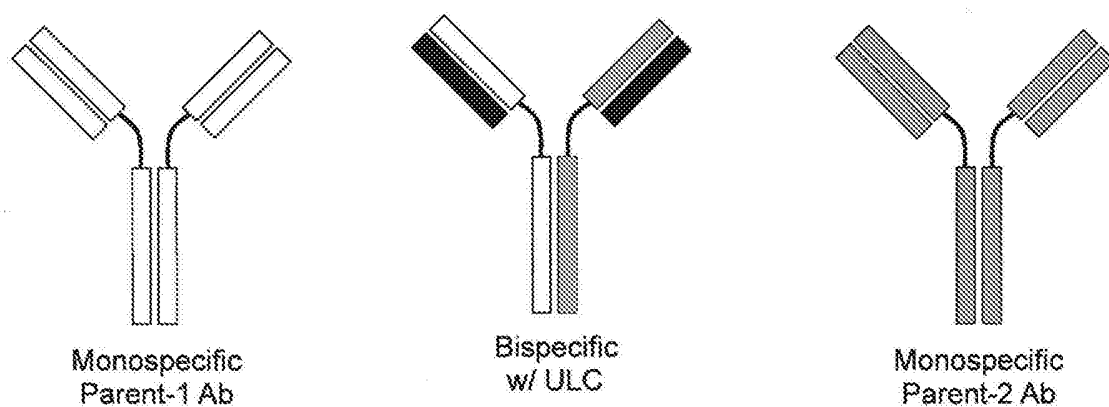


Fig. 7b

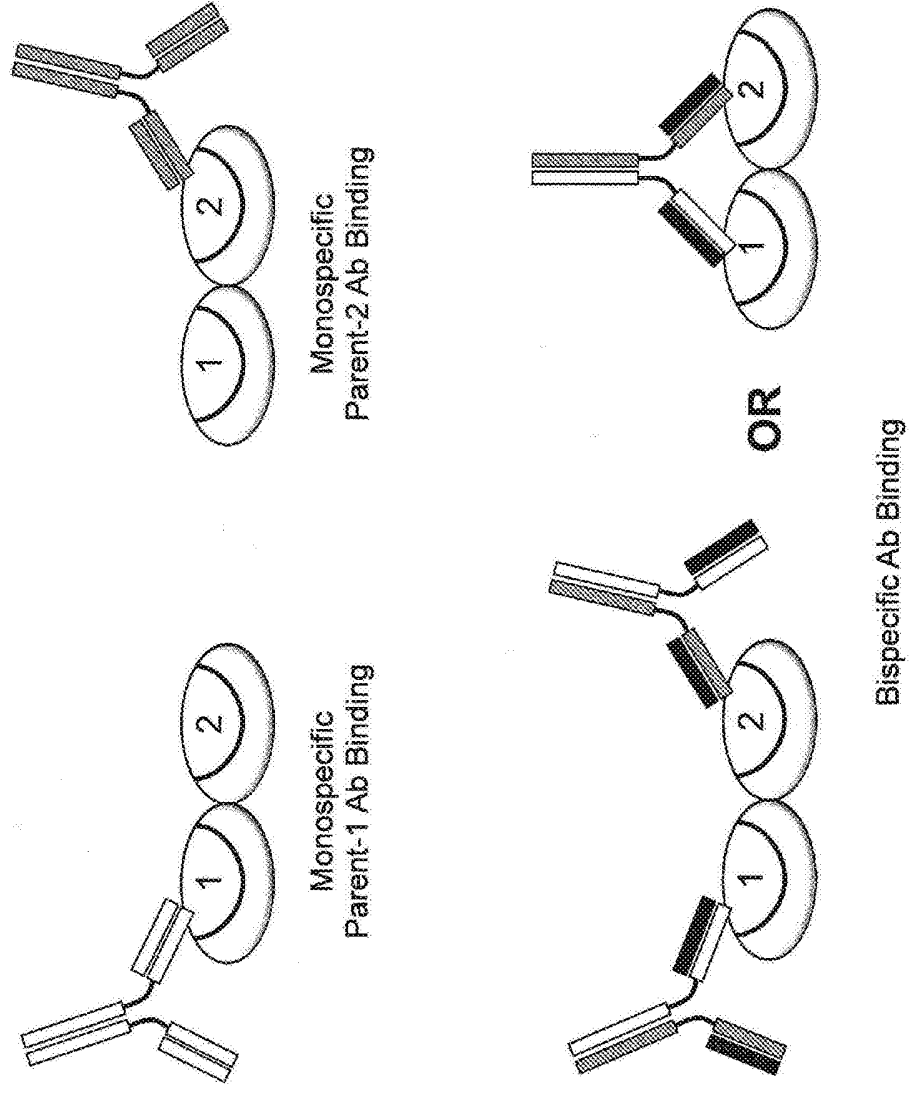
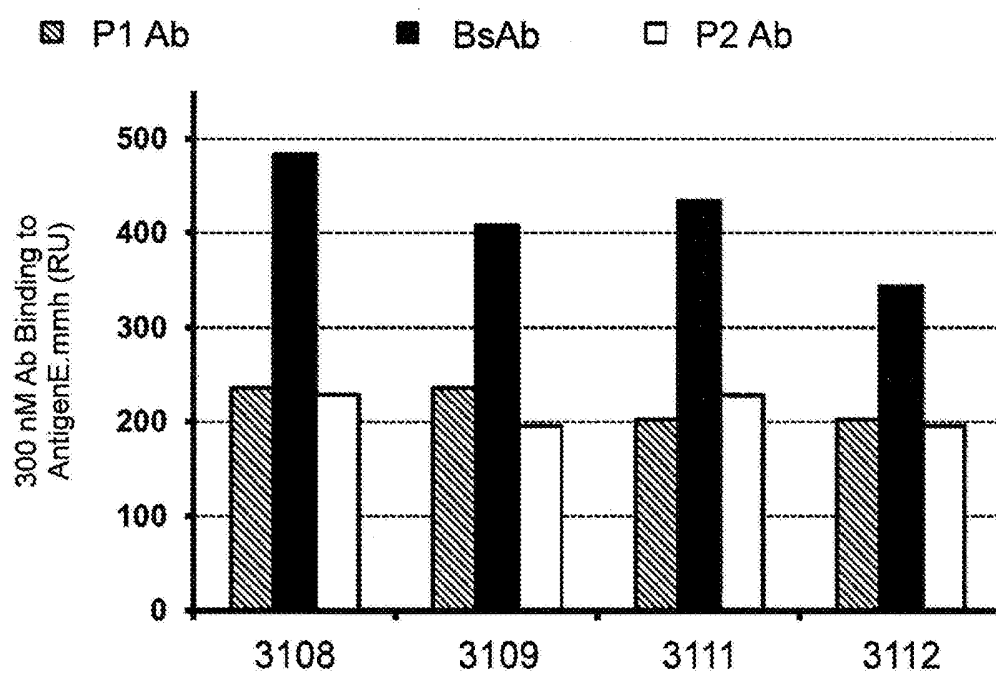


Fig. 8



ABSTRACT

A genetically modified mouse is provided, wherein the mouse expresses an immunoglobulin light chain repertoire characterized by a limited number of light chain variable domains. Mice are provided that express just one or a few immunoglobulin light chain variable domains from a limited repertoire in their germline. Methods for making bispecific antibodies having universal light chains using mice as described herein, including human light chain variable regions, are provided. Methods for making human variable regions suitable for use in multispecific binding proteins, *e.g.*, bispecific antibodies, and host cells are provided. Bispecific antibodies capable of binding first and second antigens are provided, wherein the first and second antigens are separate epitopes of a single protein or separate epitopes on two different proteins are provided.



ONDERZOEKSRAPPORT

BETREFFENDE HET RESULTAAT VAN HET ONDERZOEK NAAR DE STAND VAN DE TECHNIEK

RELEVANTE LITERATUUR			
Categorie ¹	Literatuur met, voor zover nodig, aanduiding van speciaal van belang zijnde tekstgedeelten of figuren.	Van belang voor conclusie(s) nr.	Classificatie (IPC)
X	US 2013/045492 A1 (BABB ROBERT [US] ET AL) 21 februari 2013 (2013-02-21)	1-10, 12-24, 26-37, 39-42,52	INV. C07K16/00 C07K16/46 A01K67/027
Y	* alineas [0088], [0103], [0220]; tabel 5 *	11,25, 38,43-51	C12N15/85

X	US 2012/192300 A1 (BABB ROBERT [US] ET AL) 26 juli 2012 (2012-07-26)	1-10, 12-24, 26-37, 39-42,52	
Y	* alineas [0088], [0103], [0181]; tabel 5 *	11,25, 38,43-51	

X	US 2012/021409 A1 (MCWHIRTER JOHN [US] ET AL) 26 januari 2012 (2012-01-26)	1-10, 12-24, 26-37, 39-42,52	
Y	* alineas [0017], [0027] - [0029], [0140] *	11,25, 38,43-51	

X	US 2011/195454 A1 (MCWHIRTER JOHN [US] ET AL) 11 augustus 2011 (2011-08-11)	1-10, 12-24, 26-37, 39-42,52	Onderzochte gebieden van de techniek
Y	* het gehele document *	11,25, 38,43-51	C07K A01K C12N

		-/--	
Indien gewijzigde conclusies zijn ingediend, heeft dit rapport betrekking op de conclusies ingediend op:			
Plaats van onderzoek: München		Datum waarop het onderzoek werd voltooid: 11 juli 2014	Bevoegd ambtenaar: van Heusden, Miranda
¹ CATEGORIE VAN DE VERMELDE LITERATUUR			
X: de conclusie wordt als niet nieuw of niet inventief beschouwd ten opzichte van deze literatuur		T: na de indieningsdatum of de voorrangedatum gepubliceerde literatuur die niet bezwarend is voor de octrooiaanvraag, maar wordt vermeld ter verheldering van de theorie of het principe dat ten grondslag ligt aan de uitvinding	
Y: de conclusie wordt als niet inventief beschouwd ten opzichte van de combinatie van deze literatuur met andere geciteerde literatuur van dezelfde categorie, waarbij de combinatie voor de vakman voor de hand liggend wordt geacht		E: eerdere octrooi(aanvraag), gepubliceerd op of na de indieningsdatum, waarin dezelfde uitvinding wordt beschreven	
A: niet tot de categorie X of Y behorende literatuur die de stand van de techniek beschrijft		D: in de octrooiaanvraag vermeld	
O: niet-schriftelijke stand van de techniek		L: om andere redenen vermelde literatuur	
P: tussen de voorrangedatum en de indieningsdatum gepubliceerde literatuur		S: lid van dezelfde octrooifamilie of overeenkomstige octrooipublicatie	

2

EOB FORM 02 83 (P0414B)

RELEVANTE LITERATUUR		
Categorie ¹	Literatuur met, voor zover nodig, aanduiding van speciaal van belang zijnde tekstgedeelten of figuren.	Van belang voor conclusie(s) nr:
Y	Marie-Paule Lefranc ET AL: "Nomenclature of the Human Immunoglobulin Genes" In: "Current Protocols in Immunology", 1 mei 2001 (2001-05-01), John Wiley & Sons, Inc., Hoboken, NJ, USA, XP055055079, ISBN: 978-0-47-114273-7 DOI: 10.1002/0471142735.ima01ps40, * het gehele document *	11,25, 38,43-51
X,P	WO 2013/134263 A1 (REGENERON PHARMA [US]) 12 september 2013 (2013-09-12)	1-10, 12-24, 26-37, 39-42,52
Y,P	* het gehele document *	11,25, 38,43-51
X,P	WO 2013/184761 A1 (REGENERON PHARMA [US]) 12 december 2013 (2013-12-12)	1-10, 12-24, 26-37, 39-42,52
Y,P	* het gehele document *	11,25, 38,43-51
A	WO 2004/009618 A2 (CRUCCELL HOLLAND BV [NL]; VAN BERKEL PATRICK HENDRIKUS C [NL]; BRUS RON) 29 januari 2004 (2004-01-29) * het gehele document *	1-52

2

EOB FORM 02.83 (P0414C)

¹ CATEGORIE VAN DE VERMELDE LITERATUUR

X: de conclusie wordt als niet nieuw of niet inventief beschouwd ten opzichte van deze literatuur
 Y: de conclusie wordt als niet inventief beschouwd ten opzichte van de combinatie van deze literatuur met andere geciteerde literatuur van dezelfde categorie, waarbij de combinatie voor de vakman voor de hand liggend wordt geacht
 A: niet tot de categorie X of Y behorende literatuur die de stand van de techniek beschrijft
 O: niet-schriftelijke stand van de techniek
 P: tussen de voorrangsdatum en de indieningsdatum gepubliceerde literatuur

T: na de indieningsdatum of de voorrangsdatum gepubliceerde literatuur die niet bezwarend is voor de octrooiaanvraag, maar wordt vermeld ter verheldering van de theorie of het principe dat ten grondslag ligt aan de uitvinding
 E: eerdere octrooi(aanvraag), gepubliceerd op of na de indieningsdatum, waarin dezelfde uitvinding wordt beschreven
 D: in de octrooiaanvraag vermeld
 L: om andere redenen vermelde literatuur
 &: lid van dezelfde octrooifamilie of overeenkomstige octrooipublicatie

**AANHANGSEL BEHORENDE BIJ HET RAPPORT BETREFFENDE
HET ONDERZOEK NAAR DE STAND VAN DE TECHNIEK,
UITGEVOERD IN DE OCTROOIAANVRAGE NR.**

NO 138927
NL 2012424

Het aanhangsel bevat een opgave van elders gepubliceerde octrooiaanvragen of octrooien (zogenaaamde leden van dezelfde octrooifamilie), die overeenkomen met octrooischriften genoemd in het rapport.

De opgave is samengesteld aan de hand van gegevens uit het computerbestand van het Europees Octrooibureau per

De juistheid en volledigheid van deze opgave wordt noch door het Europees Octrooibureau, noch door het Bureau voor de Industriële eigendom gegarandeerd; de gegevens worden verstrekt voor informatiedoeleinden.

11-07-2014

In het rapport genoemd octrooigeschrift	Datum van publicatie	Overeenkomend(e) geschrift(en)	Datum van publicatie
US 2013045492 A1	21-02-2013	GEEN	
US 2012192300 A1	26-07-2012	GEEN	
US 2012021409 A1	26-01-2012	AU 2012249953 A1 CA 2846806 A1 CN 103596424 A EP 2701499 A2 KR 20140024909 A SG 194466 A1 US 2012021409 A1 WO 2012148873 A2	02-05-2013 01-11-2012 19-02-2014 05-03-2014 03-03-2014 30-12-2013 26-01-2012 01-11-2012
US 2011195454 A1	11-08-2011	AU 2011213585 A1 CA 2789154 A1 CN 102791866 A EP 2501817 A1 EP 2505654 A1 JP 2013518597 A KR 20130010110 A NZ 601679 A RU 2012138431 A SG 183149 A1 US 2011195454 A1 US 2013302836 A1 WO 2011097603 A1	30-08-2012 11-08-2011 21-11-2012 26-09-2012 03-10-2012 23-05-2013 25-01-2013 31-01-2014 20-03-2014 27-09-2012 11-08-2011 14-11-2013 11-08-2011
WO 2013134263 A1	12-09-2013	AU 2013204140 A1 WO 2013134263 A1	26-09-2013 12-09-2013
WO 2013184761 A1	12-12-2013	GEEN	
WO 2004009618 A2	29-01-2004	AT 514717 T AU 2003250074 A1 AU 2010249150 A1 CA 2492377 A1 CN 1668636 A CN 101537180 A DK 1523496 T3 DK 2314629 T3 EP 1523496 A2 EP 2314629 A1 ES 2368733 T3 ES 2442615 T3 HK 1070902 A1 JP 4836451 B2	15-07-2011 09-02-2004 23-12-2010 29-01-2004 14-09-2005 23-09-2009 17-10-2011 20-01-2014 20-04-2005 27-04-2011 21-11-2011 12-02-2014 07-10-2011 14-12-2011

**AANHANGSEL BEHORENDE BIJ HET RAPPORT BETREFFENDE
HET ONDERZOEK NAAR DE STAND VAN DE TECHNIEK,
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11-07-2014

In het rapport genoemd octrooigeschrift	Datum van publicatie	Overeenkomend(e) geschrift(en)	Datum van publicatie
		JP 2006515503 A	01-06-2006
		JP 2011177193 A	15-09-2011
		NZ 537277 A	30-04-2008
		PT 1523496 E	29-09-2011
		PT 2314629 E	22-01-2014
		SI 1523496 T1	30-11-2011
		US 2005170398 A1	04-08-2005
		US 2007054362 A1	08-03-2007
		US 2007077624 A1	05-04-2007
		US 2009263864 A1	22-10-2009
		US 2011177073 A1	21-07-2011
		US 2013243773 A1	19-09-2013
		WO 2004009618 A2	29-01-2004

SCHRIFTELIJKE OPINIE

DOSSIER NUMMER NO138927	INDIENINGSDATUM 13.03.2014	VOORRANGSDATUM 13.03.2013	AANVRAAGNUMMER NL2012424
CLASSIFICATIE INV. C07K16/00 C07K16/46 A01K67/027 C12N15/85			
AANVRAGER Regeneron Pharmaceuticals, Inc.			

Deze schriftelijke opinie bevat een toelichting op de volgende onderdelen:

- ☒ Onderdeel I Basis van de schriftelijke opinie
- ☐ Onderdeel II Voorrang
- ☐ Onderdeel III Vaststelling nieuwheid, inventiviteit en industriële toepasbaarheid niet mogelijk
- ☐ Onderdeel IV De aanvraag heeft betrekking op meer dan één uitvinding
- ☒ Onderdeel V Gemotiveerde verklaring ten aanzien van nieuwheid, inventiviteit en industriële toepasbaarheid
- ☒ Onderdeel VI Andere geciteerde documenten
- ☐ Onderdeel VII Overige gebreken
- ☒ Onderdeel VIII Overige opmerkingen

	DE BEVOEGDE AMBTENAAR van Heusden, Miranda
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SCHRIFTELIJKE OPINIE

Aanvraag nr.:

NL2012424

Onderdeel I Basis van de Schriftelijke Opinie

1. Deze schriftelijke opinie is opgesteld op basis van de meest recente conclusies ingediend voor aanvang van het onderzoek.
2. Met betrekking tot **nucleotide en/of aminozuur sequenties** die genoemd worden in de aanvraag en relevant zijn voor de uitvinding zoals beschreven in de conclusies, is dit onderzoek gedaan op basis van:
 - a. type materiaal:
 - ☒ sequentie opsomming
 - ☐ tabel met betrekking tot de sequentie lijst
 - b. vorm van het materiaal:
 - ☐ op papier
 - ☒ in elektronische vorm
 - c. moment van indiening/aanlevering:
 - ☒ opgenomen in de aanvraag zoals ingediend
 - ☐ samen met de aanvraag elektronisch ingediend
 - ☐ later aangeleverd voor het onderzoek
3. ☐ In geval er meer dan één versie of kopie van een sequentie opsomming of tabel met betrekking op een sequentie is ingediend of aangeleverd, zijn de benodigde verklaringen ingediend dat de informatie in de latere of additionele kopieën identiek is aan de aanvraag zoals ingediend of niet meer informatie bevatten dan de aanvraag zoals oorspronkelijk werd ingediend.
4. Overige opmerkingen:

SCHRIFTELIJKE OPINIE

Aanvraag nr.:

NL2012424

Onderdeel V Gemotiveerde verklaring ten aanzien van nieuwheid, inventiviteit en industriële toepasbaarheid

1. Verklaring

Nieuwheid	Ja: Conclusies 11, 25, 38, 43-51 Nee: Conclusies 1-10, 12-24, 26-37, 39-42, 52
Inventiviteit	Ja: Conclusies Nee: Conclusies 1-52
Industriële toepasbaarheid	Ja: Conclusies 1-52 Nee: Conclusies

2. Citaties en toelichting:

Zie aparte bladzijde

Onderdeel VI Andere geciteerde documenten

☒ Andere geciteerde openbaarmakingen

Zie aparte bladzijde

☐ Niet schriftelijke openbaarmakingen

Onderdeel VIII Overige opmerkingen

De volgende opmerkingen met betrekking tot de duidelijkheid van de conclusies, beschrijving, en figuren, of met betrekking tot de vraag of de conclusies nawerkbaar zijn, worden gemaakt:

Zie aparte bladzijde

Re Item V

Reasoned statement with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

- 1 The quoted documents are numbered as in the International Search Report (ISR), i.e. D1 corresponds to the first document of the ISR etc.
- 2 Document D1 discloses (in [088], [103]) a method of making a human bispecific antibody (using the Velocimmune mouse) by expressing a fully human V_H sequence (identified in a Velocimmune mouse) with a human V_L sequence and a second human V_H sequence, binding to the same light chain. The light chain may be V_k1-39/J_k5 or V_k3-20/J_k1 (in [220]).
As indicated below under item VIII, the transgenic mouse in which the human V_H "is found" is not a limiting feature of claims 1-42.
Furthermore the antibodies according to claims 15, 42 and 52 (defined as product-by-process, see below under section VIII) cannot be discriminated from those obtained by the method as disclosed in D1. Even for claim 52, where the mouse used in the method of claim 43 comprises more V_H gene segments than the mouse used in D1, the antibodies produced by said mouse still encompass also those produced by the mice used in D1-D4.

Therefore D1 anticipates the subject matter of claims 1-10, 12-24, 26-37, 39-42 and 52.
- 3 The same objection is raised in view of D2-D4, which all disclose the production of a bispecific antibody by identifying a (or two) human V_H in a Velocimmune mouse and expressing these with a single human V_k light chain. In addition documents D1-D3 disclose (in Table 5 of D1 and D2 or in paragraph [29] of D3) a mouse which comprises a B cell which comprises rearranged immunoglobulin heavy chain variable region gene sequences comprising a $VH/DH/JH$ region as listed in Table 25, e.g. 3-23/2-8/4, which falls within the scope of claim 10.
- 4 The only difference between the present application and D1-D4 seems to be the transgenic mouse that is used for the identification of human V_H regions that pair with a single human V_k gene segment. Since claims 1-42 and 52 are not limited to using the mouse as defined, these claims cannot be distinguished over said prior art. In claim 43, however, the method includes the step of exposing the modified mice (as defined under i) and ii)) to a first and a second antigen and identifying in said mice the human heavy chain

variable regions (that both pair with the same human light chain Vk1-39/J or Vk3-20/J). The modified mouse as defined in claim 43 is not disclosed in any of the cited prior art and therefore claims 43-51 are novel.

- 5 Claims 43-51 relate to a method of making a bispecific antigen-binding protein, wherein the step of using the genetically modified mouse as defined under i) and ii) is a limiting feature of the claim. This method differs from the method as disclosed in any of D1-D4 in that the modified mouse comprises a larger selection of human V_H gene segments. It is obvious for the skilled person to optimize the method as disclosed in any of D1-D4 by increasing the number of V_H gene segments in the transgenic mouse, as has already been done when comparing D1 and D2 compared to D3 or D4. The human V_H gene segments (and D_H and J_H gene segments) which are functional are known from D5. Therefore it seems that no inventive step is required to increase the number of human V_H gene segments by introducing further (known) functional human V_H gene segments into the modified mouse.
- 6 With regard to claims 11, 25, 38 and 50, relating to a selection of 4 alternative V_H gene segments, it seems that said 4 segments amount to a selection from the known functional human V_H segments (see D5), which selection is arbitrary because it is not characterized by a unexpected technical effect.

Re Item VI

Certain documents

- 7 Documents D6 and D7, also relating to the production of a human bispecific antibody starting from a transgenic mouse comprising a common human light chain and multiple human V_H gene segments, could become relevant depending on the validity of the claimed priority date.

Re Item VIII

Certain observations on the international application, clarity

- 8 Claim 1 relates to a method of making a fully human bispecific antibody. The method comprises the step of expressing a first human heavy chain comprising a first human variable region, followed by the step of pairing said first human heavy chain with a human light chain and a second human heavy chain binding the same light chain. Whereas the first human heavy chain should be present in ("is found in") B cells of a genetically engineered mouse as defined under i) and ii), this feature merely amounts to defining a possible origin of the first heavy chain. It does not limit the claim to a method including a step of identifying/isolating said first human heavy chain from said

transgenic mouse. Thus any method of expressing a human heavy chain based on any of the listed V_H gene segments and pairing it with a second one which binds to the same light chain falls under the scope of claim 1.

Furthermore, it is noted that the claim reads "*wherein the rearranged human V_H gene segments include...*". Thus strictly speaking the human V_H gene segments may also include other segments and the listed segments are not even limiting on the scope of the claim. The same is true for the further independent method claims 16 and 29.

- 9 Claims 15, 42 and 52 relate to bispecific antibodies defined as product-by-process, which is considered to lack clarity. An antibody should be defined by technical features (structure, sequence). The claims encompass any bispecific antibody comprising a human heavy chain based on one of the listed V_H gene segments and a second human heavy chain, both pairing with the same (any) human (kappa, e.g. V_k1-39/J_k or V_k3-20/J_k) light chain, irrespective of the method by which the antibody is produced.
- 10 Claim 16 relates to a method of identifying a human heavy chain variable region as expressed in B cells of a genetically engineered mouse (the mouse being as defined under i) and ii)). The claim lacks any details on how the heavy chain variable region is identified (how a specific one is identified or selected). The wording "as expressed in" is considered to lack clarity in that it is not clear whether the identification is performed using a B cell of a mouse as defined, or whether the region only has to be expressed in a B cell of a mouse as defined but the identification can be done from any other source. The same objection applies to the wording "as expressed in" in claim 29.
- 11 It is not quite clear what the difference is between claims 12 and 13 (as well as claims 26 and 27, and claims 39 and 40).