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(54) Title: ANTI-SURROGATE LIGHT CHAIN ANTIBODIES

(57) **Abrégé/Abstract:**

The present invention concerns anti-surrogate light chain antibodies and their uses. In particular, the present invention concerns anti-VpreBI antibodies and their uses.



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(54) **Title:** ANTI-SURROGATE LIGHT CHAIN ANTIBODIES

(57) **Abstract:** The present invention concerns anti-surrogate light chain antibodies and their uses. In particular, the present invention concerns anti-VpreB1 antibodies and their uses.

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ANTI-SURROGATE LIGHT CHAIN ANTIBODIES

Background of the Invention

Antibody (Ig) molecules produced by B-lymphocytes are built of heavy (H) and light (L) chains. The amino acid sequences of the amino terminal domains of the H and L chains are variable (V_H and V_L), especially at the three hypervariable regions (CDR1, CDR2, CDR3) that form the antigen combining site. The assembly of the H and L chains is stabilized by a disulfide bond between the constant region of the L chain (C_L) and the first constant region of the heavy chain (C_{H1}) and by non-covalent interactions between the V_H and V_L domains.

In humans and many animals, such as mice, the genes encoding the antibody H and L chains are assembled by stepwise somatic rearrangements of gene fragments encoding parts of the V regions. Various stages of B lymphocyte development are characterized by the rearrangement status of the Ig gene loci (see, e.g. Melchers, F. & Rolink, A., *B-Lymphocyte Development and Biology*, Paul, W.E., ed., 1999, Lippincott, Philadelphia).

Precursors of B cells (pre-B cells) have been identified in the bone marrow by their production of a set of genes called VpreB(1-3) and $\lambda 5$, instead of the fully developed light chains, and coexpression of μ heavy chains.

The main isoform of human VpreB1 (CAG30495) is a 145 aa-long polypeptide (SEQ ID NO: 1). It has an Ig V domain-like structure, but lacks the last β -strand ($\beta 7$) of a typical V domain, and has a carboxyl terminal end that shows no sequence homologies to any other proteins. VpreB2 has several isoforms, including a 142-amino acid mouse VpreB2 polypeptide (P13373; SEQ ID NO: 2), and a 171 amino acids long splice variant of the mouse VpreB2 sequence (CAA019641 SEQ ID NO: 3). VpreB1 and VpreB2 sequences have been disclosed in EP 0 269 127 and U.S. Patent No. 5,182,205; Collins et al., *Genome Biol.* 5(10):R84 (2004); and Hollins et al., *Proc. Natl. Acad. Sci. USA* 86(14):5552-5556 (1989). The main isoform of human VpreB3 (SEQ ID NO: 4) is a 123 aa-long protein (CAG30496), disclosed in Collins et al., *Genome Biol.* 5(10):R84 (2004).

VpreB(1-3) are non-covalently associated with another protein, $\lambda 5$. The human $\lambda 5$ is a 209-amino acid polypeptide (CAA01962; SEQ ID NO: 7), that carries an Ig C domain-like structure with strong homologies to antibody light chains and, towards its amino terminal end, two functionally distinct regions, one of which shows strong homology to the $\beta 7$ strand of the $V\lambda$ domains. A human $\lambda 5$ -like protein has 213 amino acids (NP_064455; SEQ ID NO: 8) and shows about 84% sequence identity to the antibody λ light chain constant region.

For further details, see the following review papers: Karasuyama et al., *Adv. Immunol.* 63:1-41 (1996); Melchers et al., *Immunology Today* 14:60-68 (1993); and Melchers, *Proc. Natl. Acad. Sci. USA* 96:2571-2573 (1999).

The VpreB and $\lambda 5$ polypeptides together form a non-covalently associated, Ig light chain-like structure, which is called the surrogate light chain or pseudo light chain. On the surface of early preB cells, the surrogate light chain is disulfide-linked to membrane-bound Ig μ heavy chain in association with a signal transducer CD79a/CD79b heterodimer to form a B cell receptor-like structure, the so-called preB cell receptor (pre-BCR).

Surroboodies are based on the pre-B cell receptor (pre-BCR), which is produced during normal development of antibody repertoire. Unlike antibodies, pre-BCR is a trimer, composed of an antibody heavy chain paired with two surrogate light chain components, VpreB and $\lambda 5$. Both VpreB and $\lambda 5$ are encoded by genes that do not undergo gene rearrangement and are expressed in early pre-B cells before V(D)J recombination begins. The pre-BCR is structurally different from a mature immunoglobulin in that it is composed of a heavy chain and two non-covalently associated proteins: VpreB and $\lambda 5$, i.e., they have three components as opposed to two in antibodies. Furthermore, although VpreB is homologous to the $V\lambda$ Ig domain, and $\lambda 5$ is homologous to the $C\lambda$ domain of antibodies, each has noncanonical peptide extensions: VpreB1 has additional 21 residues on its C terminus; $\lambda 5$ has a 50 amino acid extension at its N terminus.

A κ -like B cell receptor (κ -like BCR) has been identified, utilizing a κ -like surrogate light chain (κ -like SLC) (Frances et al., *EMBO J* 13:5937-43 (1994); Thompson et al., *Immunogenetics* 48:305-11 (1998); Rangel et al., *J Biol Chem* 280:17807-14 (2005)).

Rangel et al., *J Biol Chem* 280(18):17807-17814 (2005) report the identification and molecular characterization of a V κ -like protein that is the product of an unrearranged V κ gene, which turned out to be identical to the cDNA sequence previously reported by Thompson et al., *Immunogenetics* 48:305-311 (1998). Whereas, Frances et al., *EMBO J* 13:5937-43 (1994) reported the identification and characterization of a rearranged germline J κ that has the capacity to associate with μ heavy chains at the surface of B cell precursors, thereby providing an alternative to the $\lambda 5$ pathway for B cell development.

It has been proposed that κ -like and λ -like pre-BCRs work in concert to promote light chain rearrangement and ensure the maturation of B cell progenitors. For a review, see McKeller and Martinez-Valdez *Seminars in Immunology* 18:4043 (2006).

Further details of the design and production of Surrobodyes are provided in Xu et al., *Proc. Natl. Acad. Sci. USA* 2008, 105(31):10756-61, in PCT Publication WO 2008/118970 published on October 2, 2008, in U.S. Provisional Application No.61/134,929 filed July 11, 2008, and in Xu et al., *J. Mol. Biol.* 2010, 397, 352-360, the entire disclosures of which are expressly incorporated by reference herein.

It has been described that the diversity of a filamentous phage-based combinatorial antibody library can be increased by shuffling of the heavy and light chain genes (Kang et al., *Proc. Natl. Acad. Sci. USA*, 88:11120-11123, (1991)) or by introducing random mutations into the library by error-prone polymerase chain reactions (PCR) (Gram et al., *Proc. Natl. Acad. Sci. USA*, 89:3576-3580, (1992)). The use of defined frameworks as the basis for generating antibody libraries has been described by Barbas et al., *Proc. Nat. Acad. Sci. USA* 89:4457-4461 (1992) (randomizing CD3-H3); Barbas et al., *Gene* 137:57-62 (2003) (extending randomization to V.sub..kappa. CDR3); and Hayanashi et al., *Biotechniques* 17:310 (1994) (simultaneous mutagenesis of antibody CDR regions by overlap extension and PCR). Others report combination of CDR-H3 libraries with a single V.sub.L gene (Nissim et al., *EMBO J.* 13:692-698 (1994)), a limited set of V_L genes (De Kruif et al., *J. Mol. Biol.* 248:97-105 (1995)); or a randomized repertoire of V_L genes (Griffiths et al., *EMBO J.* 13:3245-3260 (1994)).

See also U.S. Pat. Nos. 5,667,988; 6,096,551; 7,067,284 describing methods for producing antibody libraries using universal or randomized immunoglobulin light chains.

Knappik et al., *J. Mol. Biol.* 296:57-86 (2000) describe a different concept for designing and constructing human antibody libraries, designated HuCAL (Human Combinatorial Antibody Libraries). This approach is based on the finding that each of the human V.sub.H and V.sub.L subfamilies that is frequently used during an immune response is represented by one consensus framework, resulting in seven HuCAL consensus genes for heavy chains and seven HuCAL consensus genes for light chains, which yield 49 possible combinations. All genes are made by total synthesis, taking into consideration codon usage, unfavorable residues that promote protein aggregation, and unique and general restriction sites flanking all CDRs. The approach leads to the generation of modular antibody genes containing CDRs that can be converted into different antibody formats, as needed. The design and synthesis of HuCAL antibody libraries is described in U.S. Pat. Nos. 6,300,064; 6,696,248; 6,706,484; and 6,828,422.

The construction of diverse synthetic antibody libraries is described in U.S. Patent No. 8,131,480.

Summary of the Invention

The present invention concerns anti-Surrogate Light Chain (SLC) antibodies and their uses.

In one aspect, the present invention provides isolated antibodies capable of specifically binding to a surrogate light chain (SLC), or an antigen-binding fragment thereof. In one embodiment, the antibody, or antigen-binding fragment, specifically binds to the VpreB subunit of the SLC. In another embodiment, the VpreB subunit is human VpreB1 of SEQ ID NO: 1. In one other embodiment, the VpreB subunit is mouse VpreB2 of SEQ ID NO: 2 or SEQ ID NO: 3. In yet another embodiment, the VpreB subunit is human VpreB3 of SEQ ID NO: 4. In another embodiment, the antibody, or antigen-binding fragment, specifically binds to the λ 5 subunit of the SLC. In one other embodiment, the λ 5 subunit is human λ 5 of SEQ ID NO: 7. In yet another embodiment, the λ 5 subunit is human λ 5 dTail of SEQ ID NO: 9.

In one embodiment, the present invention provides an antibody, or antigen-binding fragment, comprising a light chain variable region sequence selected from the group consisting of SEQ ID NOs: 36 to 51. In another embodiment, the antibody or antigen-binding fragment comprises a heavy chain variable region sequence selected from the group consisting of SEQ ID NOs: 52 to 67. In yet another embodiment, the antibody, or antigen-binding fragment, comprising a light chain variable region sequence selected from the group consisting of SEQ ID NOs: 36 to 51 further comprises a heavy chain variable region sequence selected from the group consisting of SEQ ID NOs: 52 to 67. In one other embodiment, the antigen-binding fragment is selected from the group consisting of Fab, Fab', F(ab')₂, scFv, and (scFv)₂ fragments.

In another aspect, the present invention provides compositions that contain an antibody, or antigen-binding fragment, described herein. In some embodiments, the composition is a diagnostic composition.

In one other aspect, the present invention provides methods for the diagnosis of autoimmune disease. In one embodiment, the method is used for the diagnosis of rheumatoid arthritis in a subject. In one other embodiment, the subject is a human patient. In another embodiment, the method comprises contacting a biological sample from the subject with an antibody specifically binding to human surrogate light chain (SLC) and determining the expression level of SLC.

In yet another aspect, the present invention provide methods for the diagnosis of a leukemia. In one embodiment, the leukemia is associated with aberrant SLC expression. In another embodiment, the method comprises contacting a biological sample from said subject with an antibody specifically binding to human surrogate light chain (SLC) and determining the expression level of SLC.

Brief Description of the Drawings

FIG. 1 shows the human VpreB1 amino acid sequence of SEQ ID NO: 1 (native leader sequence underlined); the mouse VpreB2 sequences of SEQ ID NOS: 2 and 3; the human VpreB3-like sequence of SEQ ID NO: 4, and the sequence of the truncated VpreB1 sequence in the "trimer" is shown as SEQ ID NO: 5; and the human VpreB1 amino acid sequence of SEQ ID

NO:6 (murine Ig kappa leader underlined). Underlining indicates the leader sequences within the VpreB amino acid sequences.

FIG. 2 shows the human $\lambda 5$ sequence of SEQ ID NO: 7; the human $\lambda 5$ -like sequence of SEQ ID NO: 8; the sequence of the truncated $\lambda 5$ sequence in the “trimer” designated as “ $\lambda 5$ dTail” (SEQ ID NO: 9); and the human $\lambda 5$ dTail sequence of SEQ ID NO: 10 with a murine Ig κ leader sequence. Underlining indicates the leader sequences within the $\lambda 5$ amino acid sequences.

FIG. 3 shows the human VpreB1- $\lambda 5$ chimeric amino acid sequence as SEQ ID NO:35 (murine Ig κ leader sequence underlined).

FIG. 4A and 4B show (A) the human V κ -like nucleotide sequence of SEQ ID NO:11 and the amino acid sequence of the encoded protein (AJ004956; SEQ ID NO:12) (native leader sequence underlined), and (B) the predicted mature amino acid sequences of V κ -like proteins possible from all V κ families, each bearing different lengths of extensions (SEQ ID NOS: 13-24) aligned with AJ004956 V κ -like prototype sequence (SEQ ID NO:12).

FIG 5A-C shows (A) the human JC κ nucleotide sequence of SEQ ID NO:25 and the amino acid sequence of the encoded protein (SEQ ID NO:26) (unique sequence compared to predicted mature JC κ proteins is doubly underlined and potential leader cleavage sequence singly underlined), (B) the predicted JC κ -like amino acid sequences from the remaining kappa J-constant region rearrangements (J1-J5C κ) (SEQ ID NOS:27-31), and (C) the JC κ engineered secretion optimized variants, including JC κ with an appended murine Ig κ leader sequence underlined (SEQ ID NO:32), a recombined JC κ only with an appended murine Ig κ leader sequence underlined (SEQ ID NO:33), and a predicted processed JC κ with an appended murine Ig κ leader sequence underlined (SEQ ID NO:34).

FIG. 6 shows the light chain sequences of anti-human VpreB1 Fab proteins (SEQ ID NOS: 36-51).

FIG. 7 shows the heavy chain sequences (VH) of anti-human VpreB1 Fab proteins (SEQ ID NOS: 52-67).

FIG. 8 illustrates an overview of the characterization methods used for anti-human VpreB1 IgG1 (2460B04 IgG1).

FIG. 9 demonstrates that anti-VpreB1 antibody (2460B04 IgG1) detects HGF-bound 2-piece Surrobody in 50% serum.

FIG. 10 demonstrates that anti-VpreB1 antibody (2460B04 IgG1) detects HGF-bound 3-piece Surrobody in 50% serum.

FIG. 11 demonstrates that anti-VpreB1 antibody (2460B04 IgG1) captures 2-piece Surrobody in 50% serum.

FIG. 12 demonstrates that anti-VpreB1 antibody (2460B04 IgG1) captures 3-piece Surrobody in 50% serum.

FIG. 13A-D demonstrates that anti-VpreB1 mAb (2460B04 IgG1) used as a detection reagent does not bind to IgG containing human VL ORF.

FIG. 14A-C demonstrates that anti-VpreB1 mAb Is unable to capture VL-contained IgG (448C12-HC).

FIG. 15A-C demonstrates that anti-VpreB1 mAb Is unable to capture VL-contained IgG (2547C02 HC)

FIG. 16A-C demonstrates that anti-VpreB1 mAb Is unable to capture VL-contained IgG (2211A01_N56H-HC).

FIG. 17 shows the PK serum ELISA results of the pre-immune serum samples.

FIG. 18 - shows the PK serum ELISA results for SL-541_αHGF SgG over the 5 min to 96hr timepoints.

FIG. 19 shows the PK serum ELISA results for SL-541_αHGF SgG over the 168hr to 672hr timepoints.

FIG. 20 shows the PK serum ELISA results for SL-656_αHGF SgG over the 5 min to 96hr timepoints.

FIG. 21 shows the PK serum ELISA results for SL-656_αHGF SgG over the 168hr to 672hr timepoints.

FIG.22 shows the PK properties of bispecific Surrobodies.

Detailed Description of the Invention

A. Definitions

Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Singleton *et al.*, *Dictionary of Microbiology and Molecular Biology* 2nd ed., J. Wiley & Sons (New York, NY 1994), provides one skilled in the art with a general guide to many of the terms used in the present application.

One skilled in the art will recognize many methods and materials similar or equivalent to those described herein, which could be used in the practice of the present invention. Indeed, the present invention is in no way limited to the methods and materials described. For purposes of the present invention, the following terms are defined below.

Throughout this application, the use of singular includes the plural unless expressly stated otherwise.

In this application, the use of “or” includes “and/or”, unless expressly stated otherwise.

Furthermore, the terms, “include,” “including,” and “included,” are not limiting.

In the context of the present invention, the term "antibody" (Ab) is used to refer to a native antibody from a classically recombined heavy chain derived from V(D)J gene

recombination and a classically recombined light chain also derived from VJ gene recombination, or a fragment thereof.

A “native antibody” is heterotetrameric glycoprotein of about 150,000 daltons, composed of two identical light (L) chains and two identical heavy (H) chains. Each light chain is linked to a heavy chain by covalent disulfide bond(s), while the number of disulfide linkages varies between the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has, at one end, a variable domain (V_H) followed by a number of constant domains. Each light chain has a variable domain at one end (V_L) and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light chain variable domain is aligned with the variable domain of the heavy chain. Particular amino acid residues are believed to form an interface between the light- and heavy-chain variable domains, Chothia *et al.*, *J. Mol. Biol.* 186:651 (1985); Novotny and Haber, *Proc. Natl. Acad. Sci. U.S.A.* 82:4592 (1985).

The term "variable" with reference to antibody chains is used to refer to portions of the antibody chains which differ extensively in sequence among antibodies and participate in the binding and specificity of each particular antibody for its particular antigen. Such variability is concentrated in three segments called hypervariable regions both in the light chain and the heavy chain variable domains. The more highly conserved portions of variable domains are called the framework region (FR). The variable domains of native heavy and light chains each comprise four FRs (FR1, FR2, FR3 and FR4, respectively), largely adopting a β -sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β -sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat *et al.*, *Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991), pages 647-669). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody-dependent cellular toxicity.

The term "hypervariable region" when used herein refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region comprises amino acid residues from a "complementarity determining region" or "CDR" (*i.e.*, residues 30-36 (L1), 46-55 (L2) and 86-96 (L3) in the light chain variable domain and 30-35 (H1), 47-58 (H2) and 93-101 (H3) in the heavy chain variable domain; MacCallum *et al.*, *J Mol Biol.* 262(5):732-45 (1996).

The term "framework region" refers to the art recognized portions of an antibody variable region that exist between the more divergent CDR regions. Such framework regions are typically referred to as frameworks 1 through 4 (FR1, FR2, FR3, and FR4) and provide a scaffold for holding, in three-dimensional space, the three CDRs found in a heavy or light chain antibody variable region, such that the CDRs can form an antigen-binding surface.

Depending on the amino acid sequence of the constant domain of their heavy chains, antibodies can be assigned to different classes. There are five major classes of antibodies IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2. In a preferred embodiment, the immunoglobulin sequences used in the construction of the immunoadhesins of the present invention are from an IgG immunoglobulin heavy chain domain. For human immunoadhesins, the use of human IgG1 and IgG3 immunoglobulin sequences is preferred. A major advantage of using the IgG1 is that IgG1 immunoadhesins can be purified efficiently on immobilized protein A. However, other structural and functional properties should be taken into account when choosing the Ig fusion partner for a particular immunoadhesin construction. For example, the IgG3 hinge is longer and more flexible, so that it can accommodate larger "adhesin" domains that may not fold or function properly when fused to IgG1. Another consideration may be valency; IgG immunoadhesins are bivalent homodimers, whereas Ig subtypes like IgA and IgM may give rise to dimeric or pentameric structures, respectively, of the basic Ig homodimer unit. For VEGF receptor Ig-like domain/immunoglobulin chimeras designed for in vivo applications, the pharmacokinetic properties and the effector functions specified by the Fc region are important as well. Although IgG1, IgG2 and IgG4 all have in vivo half-lives of 21 days, their relative potencies at activating the complement system are different. Moreover, various immunoglobulins possess varying numbers of allotypic isotypes.

The heavy-chain constant domains that correspond to the different classes of immunoglobulins are called α , δ , ϵ , γ , and μ , respectively.

The "light chains" of antibodies from any vertebrate species can be assigned to one of two clearly distinct types, called kappa (κ) and lambda (λ), based on the amino acid sequences of their constant domains. Any reference to an antibody light chain herein includes both κ and λ light chains.

"Antibody fragments" comprise a portion of a full length antibody, generally the antigen binding or a variable domain thereof. Examples of antibody fragments include, but are not limited to, Fab, Fab', F(ab')₂, scFv, and (scFv)₂ fragments.

As used herein the term "antibody binding region" refers to one or more portions of an immunoglobulin or antibody variable region capable of binding an antigen(s). Typically, the antibody binding region is, for example, an antibody light chain (VL) (or variable region thereof), an antibody heavy chain (VH) (or variable region thereof), a heavy chain Fd region, a combined antibody light and heavy chain (or variable region thereof) such as a Fab, F(ab')₂, single domain, or single chain antibody (scFv), or a full length antibody, for example, an IgG (e.g., an IgG1, IgG2, IgG3, or IgG4 subtype), IgA1, IgA2, IgD, IgE, or IgM antibody.

The term "epitope" as used herein, refers to a sequence of at least about 3 to 5, preferably at least about 5 to 10, or at least about 5 to 15 amino acids, and typically not more than about 500, or about 1,000 amino acids, which define a sequence that by itself, or as part of a larger sequence, binds to an antibody generated in response to such sequence. An epitope is not limited to a polypeptide having a sequence identical to the portion of the parent protein from which it is derived. Indeed, viral genomes are in a state of constant change and exhibit relatively high degrees of variability between isolates. Thus the term "epitope" encompasses sequences identical to the native sequence, as well as modifications, such as deletions, substitutions and/or insertions to the native sequence. Generally, such modifications are conservative in nature but non-conservative modifications are also contemplated. The term specifically includes "mimotopes," i.e. sequences that do not identify a continuous linear native sequence or do not

necessarily occur in a native protein, but functionally mimic an epitope on a native protein. The term “epitope” specifically includes linear and conformational epitopes.

The term “surrogate light chain polypeptide” or “SLC polypeptide” is used herein to refer to a VpreB polypeptide, a $\lambda 5$ polypeptide, a V κ -like polypeptide, a J κ polypeptide, or variants thereof.

The term “non-surrogate light chain molecule” or “non-SLC molecule” is used herein to refer to a molecule that is not an SLC polypeptide. The non-SLC molecule may be a polypeptide, such as a cytokine or antibody fragment.

The term “VpreB” is used herein in the broadest sense and refers to any native sequence or variant VpreB polypeptide, specifically including, without limitation, human VpreB1 of SEQ ID NO: 1, mouse VpreB2 of SEQ ID NOS: 2 and 3, human VpreB3-like sequence of SEQ ID NO: 4, human VpreB dT of SEQ ID NO:5, human VpreB1 amino acid sequence of SEQ ID NO:6 and isoforms, including splice variants and variants formed by posttranslational modifications, other mammalian homologues thereof, as well as variants of such native sequence polypeptides. (Figure 1)

The term “ $\lambda 5$ ” is used herein in the broadest sense and refers to any native sequence or variant $\lambda 5$ polypeptide, specifically including, without limitation, human $\lambda 5$ of SEQ ID NO: 7, human $\lambda 5$ -like protein of SEQ ID NO: 8, the human $\lambda 5$ dT shown as SEQ ID NOS: 9 and 10, and their isoforms, including splice variants and variants formed by posttranslational modifications, other mammalian homologous thereof, as well as variants of such native sequence polypeptides. (Figure 2)

Specific examples of λ -like Surrobodyes include polypeptides in which a VpreB sequence, such as a VpreB1, VpreB2, or VpreB3 sequence, including fragments and variants of the native sequences, is conjugated to a $\lambda 5$ sequence, including fragments and variants of the native sequence. Representative fusions of this type are provided in PCT Publication WO 2008/118970 published on October 2, 2008, the entire disclosures of which are expressly

incorporated by reference herein. An example of a fusion with a heterogeneous leader sequence is illustrated in Figure 3 (SEQ ID NO:35).

The terms “variant VpreB polypeptide” and “a variant of a VpreB polypeptide” are used interchangeably, and are defined herein as a polypeptide differing from a native sequence VpreB polypeptide at one or more amino acid positions as a result of an amino acid modification. The “variant VpreB polypeptide,” as defined herein, will be different from a native antibody λ or κ light chain sequence, or a fragment thereof. The “variant VpreB polypeptide” will preferably retain at least about 65%, or at least about 70%, or at least about 75%, or at least about 80%, or at least about 85%, or at least about 90%, or at least about 95%, or at least about 98% sequence identity with a native sequence VpreB polypeptide. In another preferred embodiment, the “variant VpreB polypeptide” will be less than 95%, or less than 90%, or less than 85%, or less than 80%, or less than 75%, or less than 70%, or less than 65%, or less than 60% identical in its amino acid sequence to a native antibody λ or κ light chain sequence. Variant VpreB polypeptides specifically include, without limitation, VpreB polypeptides in which the non-Ig-like unique tail at the C-terminus of the VpreB sequence is partially or completely removed.

The terms “variant $\lambda 5$ polypeptide” and “a variant of a $\lambda 5$ polypeptide” are used interchangeably, and are defined herein as a polypeptide differing from a native sequence $\lambda 5$ polypeptide at one or more amino acid positions as a result of an amino acid modification. The “variant $\lambda 5$ polypeptide,” as defined herein, will be different from a native antibody λ or κ light chain sequence, or a fragment thereof. The “variant $\lambda 5$ polypeptide” will preferably retain at least about 65%, or at least about 70%, or at least about 75%, or at least about 80%, or at least about 85%, or at least about 90%, or at least about 95%, or at least about 98% sequence identity with a native sequence $\lambda 5$ polypeptide. In another preferred embodiment, the “variant $\lambda 5$ polypeptide” will be less than 95%, or less than 90%, or less than 85%, or less than 80%, or less than 75%, or less than 70%, or less than 65%, or less than 60% identical in its amino acid sequence to a native antibody λ or κ light chain sequence. Variant $\lambda 5$ polypeptides specifically include, without limitation, $\lambda 5$ polypeptides in which the unique tail at the N-terminus of the $\lambda 5$ sequence is partially or completely removed.

The terms “variant V κ -like polypeptide” and “a variant of a V κ -like polypeptide” are used interchangeably, and are defined herein as a polypeptide differing from a native sequence V κ -like polypeptide at one or more amino acid positions as a result of an amino acid modification. The “variant V κ -like polypeptide,” as defined herein, will be different from a native antibody λ or κ light chain sequence, or a fragment thereof. (Figure 4) The “variant V κ -like polypeptide” will preferably retain at least about 65%, or at least about 70%, or at least about 75%, or at least about 80%, or at least about 85%, or at least about 90%, or at least about 95%, or at least about 98% sequence identity with a native sequence V κ -like polypeptide. In another preferred embodiment, the “variant V κ -like polypeptide” will be less than 95%, or less than 90%, or less than 85%, or less than 80%, or less than 75%, or less than 70%, or less than 65%, or less than 60% identical in its amino acid sequence to a native antibody λ or κ light chain sequence. Variant V κ -like polypeptides specifically include, without limitation, V κ -like polypeptides in which the non-Ig-like unique tail at the C-terminus of the V κ -like sequence is partially or completely removed.

The terms “variant J κ polypeptide” and “a variant of a J κ polypeptide” are used interchangeably, and are defined herein as a polypeptide differing from a native sequence J κ polypeptide at one or more amino acid positions as a result of an amino acid modification. (Figure 5) The “variant J κ polypeptide,” as defined herein, will be different from a native antibody λ or κ light chain sequence, or a fragment thereof. The “variant J κ polypeptide” will preferably retain at least about 65%, or at least about 70%, or at least about 75%, or at least about 80%, or at least about 85%, or at least about 90%, or at least about 95%, or at least about 98% sequence identity with a native sequence J κ polypeptide. In another preferred embodiment, the “variant J κ polypeptide” will be less than 95%, or less than 90%, or less than 85%, or less than 80%, or less than 75%, or less than 70%, or less than 65%, or less than 60% identical in its amino acid sequence to a native antibody λ or κ light chain sequence. Variant J κ polypeptides specifically include, without limitation, J κ polypeptides in which the unique tail at the N-terminus of the J κ sequence is partially or completely removed.

Percent amino acid sequence identity may be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-

BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

The term “VpreB sequence” is used herein to refer to the sequence of “VpreB,” as hereinabove defined, or a fragment thereof.

The term “ λ 5 sequence” is used herein to refers to the sequence of “ λ 5,” as hereinabove defined, or a fragment thereof.

The term “V κ -like sequence” is used herein to refer to the sequence of “V κ -like,” as hereinabove defined, or a fragment thereof.

The term “JC κ sequence” is used herein to refer to the sequence of “JC κ ,” as hereinabove defined, or a fragment thereof.

The term “ λ -like surrogate light chain,” as used herein, refers to a dimer formed by the non-covalent association of a VpreB and a λ 5 protein.

The term “ κ -like surrogate light chain,” as used herein, refers to a dimer formed by the non-covalent association of a V κ -like and a JC κ protein.

The term “ λ -like surrogate light chain sequence,” as defined herein, means any polypeptide sequence that comprises a “VpreB sequence” and/or a “ λ 5 sequence,” as hereinabove defined. The “ λ -like surrogate light chain sequence,” as defined herein, specifically includes, without limitation, the human VpreB1 sequence of SEQ ID NO 1, the mouse VpreB2 sequences of SEQ ID NOS: 2 and 3, and the human VpreB3 sequence of SEQ ID NO: 4, the human VpreB dT shown as SEQ ID NO: 5; and the human VpreB1 amino acid sequence of SEQ ID NO:6 and their various isoforms, including splice variants and variants formed by posttranslational modifications, homologues thereof in other mammalian species, as well as

fragments and variants thereof. The term “ λ -like surrogate light chain sequence” additionally includes, without limitation, the human $\lambda 5$ sequence of SEQ ID NO: 7, the human $\lambda 5$ -like sequence of SEQ ID NO: 8, the human $\lambda 5$ dTail shown as SEQ ID NO: 9, the human $\lambda 5$ dTail sequence of SEQ ID NO: 10 and their isoforms, including splice variants and variants formed by posttranslational modifications, homologues thereof in other mammalian species, as well as fragments and variants thereof. The term “ λ -like surrogate light chain sequence” additionally includes a sequence comprising both VpreB and $\lambda 5$ sequences as hereinabove defined.

The term “ κ -like surrogate light chain sequence,” as defined herein, means any polypeptide sequence that comprises a “V κ -like sequence” and/or a “JC κ ,” as hereinabove defined. The “ κ -like surrogate light chain sequence,” as defined herein, specifically includes, without limitation, the human V κ -like sequence of any of SEQ ID NOS:12-24, and their various isoforms, including splice variants and variants formed by posttranslational modifications, homologues thereof in other mammalian species, as well as fragments and variants thereof. The term “ κ -like surrogate light chain sequence” additionally includes, without limitation, the human V κ -like sequence of any of SEQ ID NOS:12-24, the human JC κ sequence of any of SEQ ID NO:25-35, and their isoforms, including splice variants and variants formed by posttranslational modifications, homologues thereof in other mammalian species, as well as fragments and variants thereof. The term “ κ -like surrogate light chain sequence” additionally includes a sequence comprising both V κ -like and JC κ sequences as hereinabove defined.

The term, “surrogate light chain construct” is used in the broadest sense and includes any and all additional heterogeneous components, including a heterogeneous amino acid sequence, nucleic acid, and other molecules conjugated to a surrogate light chain sequence, wherein “conjugation” is defined below.

A “surrogate light chain construct” is also referred herein as a “Surrobody™,” or “Surrobody” and the two terms are used interchangeably. Certain Surrobody™ λ -like surrogate light chain constructs are disclosed in Xu et al., *Proc. Natl. Acad. Sci. USA* 2008, 105(31):10756-61 and in PCT Publication WO 2008/118970 published on October 2, 2008. Also contemplated are κ -like surrogate light chain constructs as described in U.S. Patent Publication No. 2010-

0062950, and Xu et al., *J. Mol. Biol.* 2010, 397, 352-360, the entire disclosures of which are expressly incorporated by reference herein.

In the context of the polypeptides of the present invention, the term “heterogeneous amino acid sequence,” relative to a first amino acid sequence, is used to refer to an amino acid sequence not naturally associated with the first amino acid sequence, at least not in the form it is present in the surrogate light chain constructs herein. Thus, a “heterogeneous amino acid sequence” relative to a VpreB, $\lambda 5$, V κ -like, or JC κ is any amino acid sequence not associated with native VpreB, $\lambda 5$, V κ -like, or JC κ in its native environment. These include, without limitation, i) $\lambda 5$ sequences that are different from those $\lambda 5$ sequences that, together with VpreB, form the surrogate light chain on developing B cells, such as amino acid sequence variants, e.g. truncated and/or derivatized $\lambda 5$ sequences; ii) VpreB sequences that are different from those VpreB sequences that, together with $\lambda 5$, form the surrogate light chain on developing B cells, such as amino acid sequence variants, e.g. truncated and/or derivatized VpreB sequences, iii) V κ -like sequences that are different from those V κ -like sequences that, together with JC κ , form the κ -like surrogate light chain on developing B cells, such as amino acid sequence variants, e.g. truncated and/or derivatized V κ -like sequences; and iv) JC κ sequences that are different from those JC κ sequences that, together with V κ -like, form the κ -like surrogate light chain on developing B cells, such as amino acid sequence variants, e.g. truncated and/or derivatized JC κ sequences.

A “heterogeneous amino acid sequence” relative to a VpreB or $\lambda 5$ also includes VpreB or $\lambda 5$ sequences covalently associated with, e.g. fused to, a corresponding VpreB or $\lambda 5$, including native sequence VpreB or $\lambda 5$, since in their native environment, the VpreB and $\lambda 5$ sequences are not covalently associated, e.g. fused, to each other. Similarly, a “heterogeneous amino acid sequence” relative to a V κ -like or JC κ also includes V κ -like or JC κ sequences covalently associated with, e.g. fused to, a corresponding V κ -like or JC κ , including native sequence V κ -like or JC κ , since in their native environment, the V κ -like or JC κ sequences are not covalently associated, e.g. fused, to each other. Heterogeneous amino acid sequences also include, without limitation, antibody sequences, including antibody and heavy chain sequences and fragments

thereof, such as, for example, antibody light and heavy chain variable region sequences, and antibody light and heavy chain constant region sequences.

The terms “conjugate,” “conjugated,” and “conjugation” refer to any and all forms of covalent or non-covalent linkage, and include, without limitation, direct genetic or chemical fusion, coupling through a linker or a cross-linking agent, and non-covalent association, for example through Van der Waals forces, or by using a leucine zipper.

The term “flexible linker” is used herein to refer to any linker that is not predicted, based on its chemical structure, to be fixed in three-dimensional space in its intended context and environment.

The term “fusion” is used herein to refer to the combination of amino acid sequences of different origin in one polypeptide chain by in-frame combination of their coding nucleotide sequences. The term “fusion” explicitly encompasses internal fusions, i.e., insertion of sequences of different origin within a polypeptide chain, in addition to fusion to one of its termini.

As used herein, the terms “peptide,” “polypeptide” and “protein” all refer to a primary sequence of amino acids that are joined by covalent “peptide linkages.” In general, a peptide consists of a few amino acids, typically from about 2 to about 50 amino acids, and is shorter than a protein. The term “polypeptide,” as defined herein, encompasses peptides and proteins.

The term “amino acid” or “amino acid residue” typically refers to an amino acid having its art recognized definition such as an amino acid selected from the group consisting of: alanine (Ala); arginine (Arg); asparagine (Asn); aspartic acid (Asp); cysteine (Cys); glutamine (Gln); glutamic acid (Glu); glycine (Gly); histidine (His); isoleucine (Ile); leucine (Leu); lysine (Lys); methionine (Met); phenylalanine (Phe); proline (Pro); serine (Ser); threonine (Thr); tryptophan (Trp); tyrosine (Tyr); and valine (Val) although modified, synthetic, or rare amino acids may be used as desired. Thus, modified and unusual amino acids listed in 37 CFR 1.822(b)(4) are specifically included within this definition and expressly incorporated herein by reference. Amino acids can be subdivided into various sub-groups. Thus, amino acids can be grouped as having a nonpolar side chain (*e.g.*, Ala, Cys, Ile, Leu, Met, Phe, Pro, Val); a negatively charged side chain (*e.g.*, Asp, Glu); a positively charged side chain (*e.g.*, Arg, His, Lys); or an uncharged

polar side chain (*e.g.*, Asn, Cys, Gln, Gly, His, Met, Phe, Ser, Thr, Trp, and Tyr). Amino acids can also be grouped as small amino acids (Gly, Ala), nucleophilic amino acids (Ser, His, Thr, Cys), hydrophobic amino acids (Val, Leu, Ile, Met, Pro), aromatic amino acids (Phe, Tyr, Trp, Asp, Glu), amides (Asp, Glu), and basic amino acids (Lys, Arg).

The term "polynucleotide(s)" refers to nucleic acids such as DNA molecules and RNA molecules and analogs thereof (*e.g.*, DNA or RNA generated using nucleotide analogs or using nucleic acid chemistry). As desired, the polynucleotides may be made synthetically, *e.g.*, using art-recognized nucleic acid chemistry or enzymatically using, *e.g.*, a polymerase, and, if desired, be modified. Typical modifications include methylation, biotinylation, and other art-known modifications. In addition, the nucleic acid molecule can be single-stranded or double-stranded and, where desired, linked to a detectable moiety.

The term "variant" with respect to a reference polypeptide refers to a polypeptide that possesses at least one amino acid mutation or modification (*i.e.*, alteration) as compared to a native polypeptide. Variants generated by "amino acid modifications" can be produced, for example, by substituting, deleting, inserting and/or chemically modifying at least one amino acid in the native amino acid sequence.

An "amino acid modification" refers to a change in the amino acid sequence of a predetermined amino acid sequence. Exemplary modifications include an amino acid substitution, insertion and/or deletion.

An "amino acid modification at" a specified position, refers to the substitution or deletion of the specified residue, or the insertion of at least one amino acid residue adjacent the specified residue. By insertion "adjacent" a specified residue is meant insertion within one to two residues thereof. The insertion may be N-terminal or C-terminal to the specified residue.

An "amino acid substitution" refers to the replacement of at least one existing amino acid residue in a predetermined amino acid sequence with another different "replacement" amino acid residue. The replacement residue or residues may be "naturally occurring amino acid residues" (*i.e.* encoded by the genetic code) and selected from the group consisting of: alanine (Ala); arginine (Arg); asparagine (Asn); aspartic acid (Asp); cysteine (Cys); glutamine (Gln); glutamic

acid (Glu); glycine (Gly); histidine (His); isoleucine (Ile); leucine (Leu); lysine (Lys); methionine (Met); phenylalanine (Phe); proline (Pro); serine (Ser); threonine (Thr); tryptophan (Trp); tyrosine (Tyr); and valine (Val). Substitution with one or more non-naturally occurring amino acid residues is also encompassed by the definition of an amino acid substitution herein.

A "non-naturally occurring amino acid residue" refers to a residue, other than those naturally occurring amino acid residues listed above, which is able to covalently bind adjacent amino acid residues(s) in a polypeptide chain. Examples of non-naturally occurring amino acid residues include norleucine, ornithine, norvaline, homoserine and other amino acid residue analogues such as those described in Ellman et al. Meth. Enzym. 202:301 336 (1991). To generate such non-naturally occurring amino acid residues, the procedures of Noren et al. Science 244:182 (1989) and Ellman et al., supra, can be used. Briefly, these procedures involve chemically activating a suppressor tRNA with a non-naturally occurring amino acid residue followed by in vitro transcription and translation of the RNA.

An "amino acid insertion" refers to the incorporation of at least one amino acid into a predetermined amino acid sequence. While the insertion will usually consist of the insertion of one or two amino acid residues, the present application contemplates larger "peptide insertions", e.g. insertion of about three to about five or even up to about ten amino acid residues. The inserted residue(s) may be naturally occurring or non-naturally occurring as disclosed above.

An "amino acid deletion" refers to the removal of at least one amino acid residue from a predetermined amino acid sequence.

The term "mutagenesis" refers to, unless otherwise specified, any art recognized technique for altering a polynucleotide or polypeptide sequence. Preferred types of mutagenesis include error prone PCR mutagenesis, saturation mutagenesis, or other site directed mutagenesis.

"Site-directed mutagenesis" is a technique standard in the art, and is conducted using a synthetic oligonucleotide primer complementary to a single-stranded phage DNA to be mutagenized except for limited mismatching, representing the desired mutation. Briefly, the synthetic oligonucleotide is used as a primer to direct synthesis of a strand complementary to the single-stranded phage DNA, and the resulting double-stranded DNA is transformed into a phage-

supporting host bacterium. Cultures of the transformed bacteria are plated in top agar, permitting plaque formation from single cells that harbor the phage. Theoretically, 50% of the new plaques will contain the phage having, as a single strand, the mutated form; 50% will have the original sequence. Plaques of interest are selected by hybridizing with kinased synthetic primer at a temperature that permits hybridization of an exact match, but at which the mismatches with the original strand are sufficient to prevent hybridization. Plaques that hybridize with the probe are then selected, sequenced and cultured, and the DNA is recovered.

The term “vector” is used to refer to a rDNA molecule capable of autonomous replication in a cell and to which a DNA segment, e.g., gene or polynucleotide, can be operatively linked so as to bring about replication of the attached segment. Vectors capable of directing the expression of genes encoding for one or more polypeptides are referred to herein as “expression vectors.” The term “control sequences” refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers. A vector may be a “plasmid” referring to a circular double-stranded DNA loop into which additional DNA segments may be ligated. A vector may be a phage vector or a viral vector, in which additional DNA segments may be ligated into the viral genome. Suitable vectors are capable of autonomous replication in a host cell into which they are introduced, e.g., bacterial vector with a bacterial origin of replication and episomal mammalian vectors. A vector may be integrated into the host cell genome, e.g., a non-episomal mammalian vector, upon introduction into the host cell, and replicated along with the host genome.

Nucleic acid is “operably linked” when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, “operably linked” means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is

accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

A "phage display library" is a protein expression library that expresses a collection of cloned protein sequences as fusions with a phage coat protein. Thus, the phrase "phage display library" refers herein to a collection of phage (e.g., filamentous phage) wherein the phage express an external (typically heterologous) protein. The external protein is free to interact with (bind to) other moieties with which the phage are contacted. Each phage displaying an external protein is a "member" of the phage display library.

The term "filamentous phage" refers to a viral particle capable of displaying a heterogeneous polypeptide on its surface, and includes, without limitation, f1, fd, Pf1, and M13. The filamentous phage may contain a selectable marker such as tetracycline (e.g., "fd-tet"). Various filamentous phage display systems are well known to those of skill in the art (see, e.g., Zacher et al. Gene 9: 127-140 (1980), Smith et al. Science 228: 1315-1317 (1985); and Parmley and Smith Gene 73: 305-318 (1988)).

The term "panning" is used to refer to the multiple rounds of screening process in identification and isolation of phages carrying compounds, such as antibodies, with high affinity and specificity to a target.

A "host cell" includes an individual cell or cell culture which can be or has been a recipient for transformation of nucleic acid(s) and/or vector(s) containing nucleic acids encoding the molecules described herein. In methods of the present invention, a host cell can be a eukaryotic cell, such as a Chinese Hamster Ovary (CHO) cell, or a human embryonic kidney (HEK) 293 cell. Other suitable host cells are known to those skilled in the art.

B. Detailed Description

Techniques for performing the methods of the present invention are well known in the art and described in standard laboratory textbooks, including, for example, Ausubel *et al.*, *Current Protocols of Molecular Biology*, John Wiley and Sons (1997); *Molecular Cloning: A Laboratory Manual*, Third Edition, J. Sambrook and D. W. Russell, eds., Cold Spring Harbor, New York,

USA, Cold Spring Harbor Laboratory Press, 2001; O'Brian et al., *Analytical Chemistry of Bacillus Thuringiensis*, Hickie and Fitch, eds., Am. Chem. Soc., 1990; *Bacillus thuringiensis: biology, ecology and safety*, T.R. Glare and M. O'Callaghan, eds., John Wiley, 2000; *Antibody Phage Display, Methods and Protocols*, Humana Press, 2001; and *Antibodies*, G. Subramanian, ed., Kluwer Academic, 2004. Mutagenesis can, for example, be performed using site-directed mutagenesis (Kunkel et al., *Proc. Natl. Acad. Sci USA* 82:488-492 (1985)). PCR amplification methods are described in U.S. Pat. Nos. 4,683,192, 4,683,202, 4,800,159, and 4,965,188, and in several textbooks including *PCR Technology: Principles and Applications for DNA Amplification*, H. Erlich, ed., Stockton Press, New York (1989); and *PCR Protocols: A Guide to Methods and Applications*, Innis et al., eds., Academic Press, San Diego, Calif. (1990).

The present invention concerns antibodies against the Surrogate Light Chain (SLC). The antibodies can be directed against the VpreB subunit, the $\lambda 5$ subunit, or the fusion junction as each of these antibodies will specifically bind the Surrogate Light Chain.

Anti-SLC antibodies may be used for a variety of applications. One application is detection of SLC-containing proteins in complex biological fluids in pharmacokinetic/pharmacodynamic studies, immunohistochemistry studies or for in vitro diagnostic uses.

Another application for anti-SLC antibodies is for diagnostic purposes. There are a number of conditions known in the art associated with the absence or deficiency of SLC. For example, $\lambda 5$ -deficient mice show a dramatic decrease in B-cell development, (Kitamura D, Kudo A, Schaal S, Muller W, Melchers F, Rajewsky K. A critical role of lambda 5 protein in B cell development. *Cell*. 1992;69(5):823-831) whereas mutations in the human $\lambda 5$ gene result in agammaglobulinemia, (Minegishi Y, Coustan-Smith E, Wang YH, Cooper MD, Campana D, Conley ME. Mutations in the human lambda5/14.1 gene result in B cell deficiency and agammaglobulinemia. *J Exp Med*. 1998;187(1):71-77.) In humans, self-reactive B cells have been identified which express SLC and these cells have been shown to accumulate in the joints of patients with RA (Meffre et al., (2000) *Nature Immunology* 1, 207 - 213). Thus, SLC could be a marker for poly-reactive cells and aberrant pre-BCR function. Accordingly,

anti-SLC antibodies may be a useful reagent for diagnosing certain leukemias and autoimmune diseases that are associated with aberrant SLC expression and B cell function.

In addition, purification of SLC complexes as fusion proteins, non-covalent heteromers, or as cell populations can also be considered for the use of anti-SLC antibodies. As a research reagent, anti-SLC antibodies can be used to assess the biophysical and functional characteristics of SLC-containing complexes in vitro. Quantification, affinity determination, effective or inhibitory concentration, immunoprecipitation, and immunosorbent applications for SLC-complexes are examples of important uses for the anti-SLC antibodies.

The antibodies of the present invention can, for example, be obtained by screening antibody libraries, such as diverse antibody libraries described in U.S. Patent No. 8,131,480, which, in a preferred embodiment, use of phage vectors to express the diverse antibody libraries. The method generally involves the use of a filamentous phage (phagemid) surface expression vector system for cloning and expression. See, e.g., Kang et al., *Proc. Natl. Acad. Sci., USA*, 88:4363-4366 (1991); Barbas et al., *Proc. Natl. Acad. Sci., USA*, 88:7978-7982 (1991); Zebedee et al., *Proc. Natl. Acad. Sci., USA*, 89:3175-3179 (1992); Kang et al., *Proc. Natl. Acad. Sci., USA*, 88:11120-11123 (1991); Barbas et al., *Proc. Natl. Acad. Sci., USA*, 89:4457-4461 (1992); Gram et al., *Proc. Natl. Acad. Sci., USA*, 89:3576-3580 (1992); Brinkman et al., *J. Immunol. Methods* 182:41-50 (1995); Ames et al., *J. Immunol. Methods* 184:177-186 (1995); Kettleborough et al., *Eur. J. Immunol.* 24:952-958 (1994); Persic et al., *Gene* 187 9-18 (1997); Burton et al., *Advances in Immunology* 57:191-280 (1994); and U.S. Pat. Nos. 5,698,426; 5,233,409; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,403,484; 5,571,698; 5,516,637; 5,780,225; 5,658,727; 5,733,743; 5,837,500; 5,969,108; 6,326,155; 5,885,793; 6,521,404; 6,492,160; 6,492,123; 6,489,123; 6,342,588; 6,291,650; 6,225,447; 6,180,336; 6,172,197; 6,140,471; 5,994,519; 6,969,108; 5,871,907; and 5,858,657.

The vector is used to transform a recombinant host cell, which is cultured to allow the introduced phage genes and display protein genes to be expressed, and for phage particles to be assembled and shed from the host cell. The shed phage particles are then harvested (collected) from the host cell culture media and screened for desirable antibody binding properties. Typically, the harvested particles are "panned" for binding with a preselected antigen. The

strongly binding particles are collected, and individual species of particles are clonally isolated and further screened for binding to the antigen. Phages which produce a binding site of desired antigen binding specificity are selected.

The invention is further described in the following non-limiting Examples.

EXAMPLES

Example 1 - Identification of anti-VpreB1 Fabs

Sea Lane's proprietary Fab fragment libraries were panned against human VpreB-1 for 4 rounds. Typically, after three to four rounds of panning, individual clones from enriched phage pools were analyzed by ELISA against human VpreB1, and the positive clones were sequenced to determine their heavy and light chain sequences. From these studies, Fab clonal analyses identified 16 unique human VpreB1 binders (Table 1). As further characterized in Table 2, both kappa and lambda light chains were identified with 4 different heavy chain frameworks.

Table 1 - Unique Positive Clones for Anti-human VpreB1

Unique Sequence	VL	VH
2462VpreBlam5E07	VK1_L8	VH3-321
2462VpreBlam5C04	VK1_L8	VH3-323
2462VpreBlam5B09	VK3_A27	VH1-102
2463VpreBlam5B05	VK1_L1	VH1-1e
2463VpreBlam5D07	VK1_L1	VH1-102
2460-VpreBlam5D10	VK1_L8	VH3-321
2460VpreBlam5B04	VK1_L8	VH3-321
2462VpreBlam5A07	VK1_L8	VH3-321
2460VpreBlam5E01	VK1_L8	VH1-102
2462VpreBlam5D05	VL3_2a2	VH1-1e
2462VpreBlam5A05	VL3_3m	VH1-102
2462VpreBlam5C09	VL3_2a2	VH3-323
2460-VpreBlam5F05	VL3_2a2	VH3-323
2462VpreBlam5E08	VL3_3L	VH3-323
2462VpreBlam5C05	VL3_2a2	VH3-321
2463VpreBlam5C04	VL2_2a2	VH1-102

Table 2 - Overview of light and heavy chain sequences among the anti-human VpreB1 Fab hits

	Lambda	Kappa
VH1_02	2	3
VH1-e	1	1
VH3_21	1	4
VH3_23	3	1

The amino acid sequence of the specific anti-human VpreB1 Fab clones was determined and the variable region sequences were identified and analyzed using the FASTA program. The light chain sequences (VL) of the anti-human VpreB1 Fab clones were aligned as depicted in Figure 6. Within this alignment, the variable light chain starts at residue number 3 and the point at which the variable light chain sequence transitions to the constant light chain (Cκ or Cλ) is

demarcated with arrows. The heavy chain sequences (VH) of anti-human VpreB1 Fab clones were aligned as depicted in Figure 7. Within this alignment, the variable heavy chain starts at residue number 1 and the point at which the variable heavy chain and J-chain sequence transitions to the constant heavy chain is demarcated with arrows.

Example 2 - Characterization of selected anti-VpreB1 IgG mAbs

ELISA assays were performed to characterize the SgG-binding affinity, sensitivity and serum background of individual panned phage Fab antibodies having affinity for human VpreB1. Figure 8 provides an overview of the characterization of anti-human VpreB1 IgG1 (2460B04 IgG1). SgG proteins refer to surrogate light chain (SLC) constructs, also referred herein as a “Surrobody,” and the two terms are used interchangeably. In general, the 2-piece format includes an SLC fusion and an antibody heavy chain, while the 3-piece format includes two SLC polypeptides and an antibody heavy chain.

Detection

To assess the anti-human VpreB1 IgG1 (2460B04 IgG1) as a detection antibody, HGF-specific S2gG & S3gG were detected by unlabeled, biotin-labeled & DIG-labeled anti-VpreB1 antibodies in ELISA. In the assays to detect either the 2-piece or 3- piece surrobody, wells were coated with HGF (0.1 mL of 0.001 mg/mL), 1% BSA-PBST was used as a blocking and diluent buffer, and S2gG or S3gG were serial diluted in 50% serum. HGF-bound S2gG or S3gG was detected by biotinylated anti-VpreB1 IgG & HRP-conjugated streptavidin. As demonstrated in Figure 9, the anti-VpreB1 antibody detects the HGF-bound 2-Piece Surrobody in 50% Serum. Similarly, the anti-VpreB1 antibody also detects HGF-Bound 3-Piece Surrobody in 50% Serum (Figure 10). The EC50 values for the different SLC constructs used in the detection assays are provided in Table 3 below.

Table 3 - Unlabeled vs. Labeled Anti-Human VpreB1 IgG Antibody

SgG	EC50 (nM) (ELISA)		
	Unlabeled	Biotin-labeled	DIG-labeled
S2gG	0.605	0.549	0.535
S3gG	0.482	0.48	0.432

Capture

In the assays to assess 2-piece or 3- piece surrobody capture by anti-VpreB1 IgG (2460B04 IgG1), wells were coated with anti-VpreB1 IgG (0.1 mL of 0.001 mg/mL), 1% BSA-PBST was used as a blocking and diluent buffer, and S2gG or S3gG were serial diluted in 50% serum. HGF-bound S2gG was detected by HRP-conjugated goat anti-E tag Ab. As demonstrated in Figure 11, the anti-VpreB1 antibody captures 2-Piece surrobody in 50% Serum. The anti-VpreB1 Antibody also captures the 3-Piece Surrobody in 50% Serum (Figure 12).

Affinity

The binding affinity of anti-human VpreB1 IgG mAb (2460B04 IgG1) to SgG was tested by Biolayer Interferometry on a ForteBio Octet (“octet analysis”). Kinetic binding analysis was performed and the apparent affinities are reported in Table 4. The results indicate a sub-nanomolar affinity to bind to 2-piece or 3-piece surroglobulins.

Table 4 - Binding Affinity of Anti-Human VpreB1 IgG mAb to SgG Measured by Octet

Run	SA Biosensor Immobilization	Binding Titration Format	K _D [nM]	kobsRsq
1	0.75ug/ml αHGF S2gG-biotin	100ug/ml αVpreB_IgG	0.280 – 0.100	0.979 – 0.998
2	0.75ug/ml αHGF S2gG-biotin	50ug/ml αVpreB_IgG	0.120 – 0.066	0.981 – 0.998
3	0.75ug/ml αVpreB_IgG_biotin	50ug/ml αHGF S2gG	0.048 – 0.016	0.967 – 0.988
4	0.75ug/ml αVpreB_IgG_biotin	50ug/ml αHGF S3gG	0.058 – 0.032	0.983 – 0.993

The anti-human VpreB1 IgG mAb (2460B04 IgG1) demonstrated a clean background in the presence of human, mouse or *Cynomolgus* monkey serum. This suggests that the 2460B04 IgG1 antibody would be useful in pharmacokinetic (PK) studies. Further applications suggested by these results are as a detection reagent with minimal cross reactivity in human, mouse and monkey serum (15 ng/mL), as a capture reagent with minimal cross reactivity in human, mouse and monkey serum, and as an affinity antibody to enrich libraries in VpreB1-contained library construction.

Cross Reactivity

Cross-reactivities of the anti-VpreB1 mAb (2460B04 IgG1) to Human VL were examined by ELISA. Table 5 provides an overview of the methods used to examine the cross-reactivity of the Anti-VpreB1 mAb. Table 6 identifies the protein sequence similarity of IgG Containing Human VL ORFs.

Table 5 - Characterization of Cross-Reactivity of the Anti-VpreB1 mAb

Capture Reagent	Detection Reagent	Goal
Target (hHGF)	Donkey anti-human IgG Fcγ-HRP (Jackson 709-035-098)	Target binding
	Goat anti-human λ-HRP (Southern)	
	Anti-VpreB1 hIgG1-HRP	
Anti-VpreB1 mIgG2a	Mouse αhuman λ mAb-HRP (Clone JDC-10, Southern)	Complex formation
	Goat anti-human λ-HRP (Southern)	VpreB1-captured CL
Donkey anti-human IgG Fcγ (Jackson 709-005-098)	Goat anti-human λ-HRP (Southern)	Complex formation

Table 6 - Human VL Protein Sequence Similarities

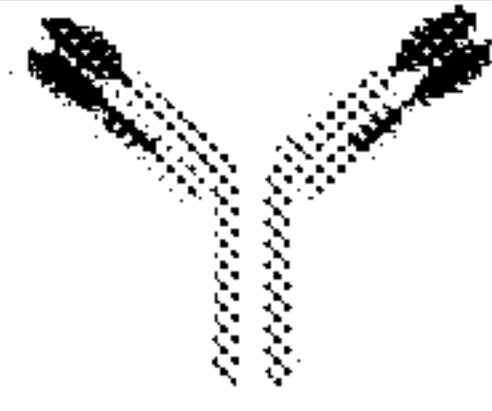
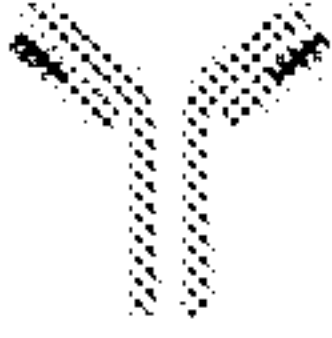
	VpredT-λ5_J (F1)	VpreBdT-λ5-B11 JL (F2)	VL5e_JL	VL1b_JL	VL1c_JL	VL2a2_JL	VL3L_JL	VL3m_JL
VpredT-λ5_J (F1)	100	98	60	41	44	44	42	42
VpreBdT-λ5-B11 JL (F2)		100	62	43	46	46	44	44
VL5e_JL			100	52	56	55	50	56
VL1b_JL				100	62	66	66	62
VL1c_JL					100	69	62	59
VL2a2_JL						100	65	64
VL3L_JL							100	75
VL3m_JL								100

When used as a detection reagent, the anti-VpreB1 mAb does not bind to IgG containing human VL ORF (Figure 13 A-D). Likewise, when used as a capture reagent, the anti-VpreB1 mAb is unable to capture VL-contained IgG (448C12-HC) (Figure 14 A-C). The anti-VpreB1 mAb is also unable to capture the VL-contained IgGs represented by 2547C02 HC (Figure 15 A-C) or 2211A01_N56H-HC (Figure 16 A-C). Thus, there appears to be no cross reactivity to traditional light chain proteins.

Example 3 - Pharmacokinetic Study of Surrobodyes in Cynomolgus Monkey

The utility of the anti-VpreB1 IgG mAbs was further demonstrated in pharmacokinetic (PK) studies of Surrobodyes in the *Cynomolgus* monkey. The PK profile of Surrobodyes in *Cynomolgus* monkeys was assessed by measurements of half life (T_{1/2}), maximum plasma/serum concentration (C_{max}), elimination rate constant, AUC_{0-t} (area under the plasma concentration-time curve to the last observed data point), and clearance. We also examined the anti-SgG response that resulted from a single-injection. The Surrobody test articles used in the *Cynomolgus* monkey PK study are identified in Table 7.

Table 7 - Surrobody Test Articles Used in *Cynomolgus* Monkey PK Study

SL No	Target	SgG Format	SgG Structure
SL-349	HGF/PIGF	SgG1_SVD (Stacked Variable Domain)	
SL-521	HGF/PIGF	SgG1_Ball/Socket	
SL-541	HGF	SgG1	
SL-542	PIGF	SgG1	
SL-656	HGF	IgG1	

Detection of Target – Specific Surrobody in PK Cynomolgus Monkey Serum

Biologically naïve *Cynomolgus* monkeys were used to evaluate five SgG test articles, as identified in Figure 17. Three monkeys were studied in each of the test article groups. Among the five groups there was a total of 15 monkeys, weighing 3.37 – 5.67 kg each and health reports were maintained for each monkey. The mean weight of each group was 4.34 – 4.87 kg. A single 10 mg/mL injection was given by i.v. Each monkey serum was collected and prepared at up to 28 days. The time points for serum collection included short intervals (0 and 5 min), intermediate intervals (1, 4, 8 and 24 hrs) and long intervals (48hr (2d), 72hr (3d), 96hr (4d), 168hr (7d), 240hr (10d), 336hr (14d), 408hr (17d), 504hr (21d), 576hr (24d) and 672hr (28d)). ELISA assays were used for detecting SgG in the *Cynomolgus* monkey serum. One PK timepoint was assayed per plate and a serial dilution of standard/sample was performed in 2 mL deep-well blocks. The 1:3 serial dilution comprised 800 uL 1% BSA-PBST + 400 uL sample. One dilution was made for each of the HGF-binding, PlGF-binding and complex ELISAs.

The pre-immune serum samples from all monkeys in each of the 5 test groups were clean for SgG proteins (Figure 17). An example of the ELISA data gathered for SL-541_αHGF SgG over the 5min – 96hr timepoints is provided in Figure 18 and the data for this SgG structure over the 168hr - 672hr timepoints is provided in Figure 19. An example of the ELISA data gathered for SL-656_αHGF IgG over the 5min – 96hr timepoints is provided in Figure 20 and the data for this SgG structure over the 168hr - 672hr timepoints is provided in Figure 21. The results indicate that the half-life of the test subject ranged from 6-10 days. These results further demonstrate the utility of the VpreB1 IgG mAb (2460B04 IgG1) for determining the PK properties of therapeutic Surrobodies. PK studies help determine the distribution, metabolism, and elimination of potential therapeutic drugs. These data will provide a basis for historical comparison between the investigational therapeutic product and a licensed therapeutic, as well as help determine the optimum dosing schedule and withdrawal period for the product. Thus, the VpreB1 IgG mAbs are useful for determining the proper dosing of Surrobodies, by establishing both a clinically efficacious amount and the clearance time to achieve the clinically relevant dose.

We also looked at the PK properties of bispecific Surrobodyes and found them to be comparable to parentals in *Cynomolgus*. (Figure 22) Naïve groups (n=3) of *Cynomolgus* monkeys were administered single IV doses of Surrobodyes (10 mg/kg) and their serum was tested over a 28 day period. The overall PK properties of the bispecific Surrobodyes were found to be very similar to the nonspecific HGF and PIGF Surrobodyes.

Although in the foregoing description the invention is illustrated with reference to certain embodiments, it is not so limited. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

All publications, patents and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, patent or patent application were specifically and individually indicated to be so incorporated by reference.

CLAIMS:

1. An isolated antibody specifically binding to a surrogate light chain (SLC), or an antigen-binding fragment thereof.
2. The antibody, or antigen-binding fragment, of claim 1, wherein the antibody specifically binds to the VpreB subunit of the SLC.
3. The antibody, or antigen-binding fragment, of claim 2, wherein the VpreB subunit is human VpreB1 of SEQ ID NO: 1.
4. The antibody, or antigen-binding fragment, of claim 2, wherein the VpreB subunit is mouse VpreB2 of SEQ ID NO: 2 or SEQ ID NO: 3.
5. The antibody, or antigen-binding fragment, of claim 2, wherein the VpreB subunit is human VpreB3 of SEQ ID NO: 4.
6. The antibody, or antigen-binding fragment, of claim 1, wherein the antibody specifically binds to the $\lambda 5$ subunit of the SLC.
7. The antibody, or antigen-binding fragment, of claim 6, wherein the $\lambda 5$ subunit is human $\lambda 5$ of SEQ ID NO: 7.
8. The antibody, or antigen-binding fragment, of claim 6, wherein the $\lambda 5$ subunit is human $\lambda 5$ dTail of SEQ ID NO: 9.
9. The antibody, or antigen-binding fragment, of claim 3, wherein said antibody comprises a light chain variable region sequence selected from the group consisting of SEQ ID NOs: 36 to 51.
10. The antibody, or antigen-binding fragment, of claim 3, wherein said antibody comprises a heavy chain variable region sequence selected from the group consisting of SEQ ID NOs: 52 to 67.

11. The antibody, or antigen-binding fragment, of claim 9, wherein said antibody comprises a heavy chain variable region sequence selected from the group consisting of SEQ ID NOs: 52 to 67.

12. The antibody of claim 2, wherein said antigen-binding fragment is selected from the group consisting of Fab, Fab', F(ab')₂, scFv, and (scFv)₂ fragments.

13. A composition comprising an antibody, or antigen-binding fragment, of any one of claims 1 to 12.

14. The composition of claim 13, which is a diagnostic composition.

15. A method for the diagnosis of rheumatoid arthritis in a human subject, comprising contacting a biological sample from said subject with an antibody specifically binding to human surrogate light chain (SLC), and determining the expression level of SLC.

16. A method for the diagnosis of a leukemia or autoimmune disease associated with aberrant SLC expression comprising contacting a biological sample from said subject with an antibody specifically binding to human surrogate light chain (SLC), and determining the expression level of SLC.

Figure 1

MSWAPVLLMLFVYCTGCGPQPVLHQPPAMSSALGTTIRLTCTLRNDHDIGVYSVYWYQ
QRPQHPPRFLRLRYFSQSDKSQGPQVPPRFSGSKDVARNRGYLSISELQPEDEAMYCAM
GARSSEKEEREREWEEMEPTAARTRVP

(SEQ ID NO:1)

MAWTSVLLMLLAHLTGCGPQPMVHQPPSASSSLGATIRLSCTLSNDHNIGIYSIYWYQQ
RPGHPPRFLRLRYFSHSDKHQGPDIPIPRFSGSKDTARNLGYSISELQPEDEAVYYCAVGL
RSHEKKRMEREWEGEKS YTDLGS

(SEQ ID NO:2)

MAWTSVLLMLLAHLTGKGT LGVQGFLAPPVALLCPSDGHASIFSGCGPQPMVHQPPSA
SSSLGATIRLSCTLSNDHNIGIYSIYWYQQRPQHPPRFLRLRYFSHSDKHQGPDIPIPRFSGSK
DTARNLGYSISELQPEDEAVYYCAVGLRSHEKKRMEREWEGEKS YTDLGS

(SEQ ID NO:3)

MACRCLSELLMGTFELSVSQT VLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQ
QRAGSAPRYLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISP VQPEDDADYYCSV
GYGFSP

(SEQ ID NO:4)

MSWAPVLLMLFVYCTGCGPQPVLHQPPAMSSALGTTIRLTCTLRNDHDIGVYSVYWYQ
QRPQHPPRFLRLRYFSQSDKSQGPQVPPRFSGSKDVARNRGYLSISELQPEDEAMYCAM
GA

(SEQ ID NO:5)

METDTLLLWVLLLWVPGSTGQPVLHQPPAMSSALGTTIRLTCTLRNDHDIGVYSVYWY
QRPQHPPRFLRLRYFSQSDKSQGPQVPPRFSGSKDVARNRGYLSISELQPEDEAMYCA
MGARSSEKEEREREWEEMEPTAARTRVP

(SEQ ID NO:6)

Figure 2

MKLRVGQTLGTIPROCEVLLLLLLLGLVDGVHHILSPSSAERSRAVGPGASVGSNRPSL
WALPORLLFQIIPRGAGPRCSPHRLPSKPQFWYVFGGGTQLTILGQPKSDPLVTLFLPSLK
NLQPTRPHVVCLVSEFYPGTLVVDWKVDGVPVTQGVETTQPSKQTNNKYMVSSYLTLI
SDQWMPHSRYSCRVTHEGNTVEKSVSPAEC

(SEQ ID NO:7)

MRPGTGQGGLEAPGEPGNLRQRWPLLLLGLAVVTHGLLRPTAASQSRAVGPGAPGGS
SRSSLRSRWGRFLLQRGSWTGPRCWPRGFQSKHNSVTHVFGSGTQLTVLSQPKATPSVT
LFPPSSEELQANKATLVCLMNDFYPGILTVTWKADGTPITQGVEMTTPSKQSNKYAAS
SYLSLTPEQWRSRRSYSCQVMHEGSTVEKTVAPAEC

(SEQ ID NO:8)

MRPGTGQGGLEAPGEPGNLRQRWPLLLLGLAVVTHGSVTHVFGSGTQLTVLSQPKAT
PSVTLFPPSSEELQANKATLVCLMNDFYPGILTVTWKADGTPITQGVEMTTPSKQSNK
YAASSYLSLTPEQWRSRRSYSCQVMHEGSTVEKTVAPAEC

(SEQ ID NO:9)

METDTLLLWVLLLWVPGSTGSVTHVFGSGTQLTVLSQPKATPSVTLFPPSSEELQANKA
TLVCLMNDFYPGILTVTWKADGTPITQGVEMTTPSKQSNKYAASSYLSLTPEQWRSRR
SYSCQVMHEGSTVEKTVAPAEC

(SEQ ID NO:10)

Figure 3

METDTLLLWVLLLWVPGSTGQPVLHQPPAMSSALGTTIRLTCTLRNDHDIGVYSVYWY
QQRPGHPPRFLLRYFSQSDKSQGPQVPPRFSGSKDVARNRGYLSISELQPEDEAMYYCA
MGARSSVTHVFGSGTQLTVLSQPKATPSVTLFPPSSEELQANKATLVCLMNDFYPGILTV
TWKADGTPITQGVEMTTPSKQSNNKYAASSYLSLTPEQWRSRRSYSCQVMHEGSTVEK
TVAPAECS

(SEQ ID NO:35)

Figure 4A

1 CAGCARGAIGGTGTT GCGACCCAGGCTCT CATTTCTCTGTGCT CTGGATCTCTGGTC CTACGGGGACATCGT
GTCGTTCTACCCACAA CGTCTGGGTCCAGAA GTAAAGAGACAAACGA GACCTAGAGACACAG GATGCCCTGTAGCA

76 M T Q S F D S L A V S L G E R A T I N C K S S Q S
GATGACCCAGTCTCC AGACTCCCTGGCTGT GTCTCTGGGCGAGAG GGCACCATCAACTG CAAGTCCAGCCAGAG
CTACTGGGTACAGAG TCTGAGGAGACCGACA CAGAGACCCGCTCT CCGGTGAGTGTGAC GTTCAGGTCCGCTC

151 V L Y S S N M K N Y L A W Y Q Q K P G Q P P K L L
TGTTTATACAGCTC CACCAATAGAACTA CTAGCTTGTACCA GCGAAGAACCAAGACA GCTCTTAAAGCTCT
ACAAATATGTGAG GTTGTATTTCTTGT GATTCGAAACCAAGGT CGTCTTGTGCTCTGT CCGAGGATTCGACGA

226 I Y W A S T R E S G V P D R F S G S G S G T D F T
CATTTACTGGGCATC TACCCGGGAATCCGG GGTCCTGACCGATT CAGTGGCAGGCGGTC TGGACAGATTTCAC
GTAAATGACCCGTAG ATGGGCCCTTAGGCC CCAGGAGCTGGCTAA GTCAACGCTGGCCAG ACCCTGTCTTAAAGTG

301 L T I S S L Q A E D V A V Y Y C Q Q Y Y S T P P T
TCACCATCATCAGAG CCTGCAGGCTGAGAA TGTGGCGTTTATTA CTGTACGCAATATTA TAGTACTCTCTCCAC
AGAGTGGTACTGTC GGAAGTCCGACTTCT ACACCTGCAATAAT GACAGTCTTATAT ATCATGAGAGAGGCTG

376 V L Q P R T Q T S S P Y A G P V G L C C S S C F L
AGTGCCTCAGCTCG AACACAAACCTCTC CCATACGCTGGGCC AGTAGGCTCTTCTG CAGCAGCTGCTTCT
TCACGAGTCCGAGC TTGTGTTTGGAGGAG CGGTATCGGACCCCG TCATCCAGAAACGAC GTCTCCAGCAAGGA

451 C T Q P P T C M L P L C V G E V T L L I Y S L E G
CTGCACACAGCCCC AACATGCTGCTTCC TCTGTGTGTGGGA GTCACTCTCTTGTAT TTATTGTTGGAGG
GACGTGTGTGGGG TTGTACGTACGAGG AGACACACACACCCCT CCAGTCAAGAGACTA AATAAGCAACCTCCC

526 L Q G P G L N *
TTTCAGGGGCCCAGG ATTAAATTAAGAGAC TTGACTTTTGTGGA TCCTTTTGTAGAA GATTATTAAGCAA
AAGCTCCCGGCTCC TAAATTAAATTTCTG AACTGAAACAGACCT AGAGAAACAAATCTT CTAATAATTTCTT

601 ATGTTGTAAGATCC CTTAGAGACATGTC AGGAGTTTGTGCTT ACAGGAACCTGCTATG TTTCACATGACACAA
TACAAATTTCTAGG GAAATCTCTGTACAG TCTCAAAACACAA TGTCTTGGACGTAC AAGTGTACCTGTGT

676 TCACATGACCGAGCC AATAGATTTATCTT TACTCT
AGTGTACTGGCTCGG TTTATCTAATAGAA ATGAGA

(SEQ ID NOS:1-12)

Figure 4B

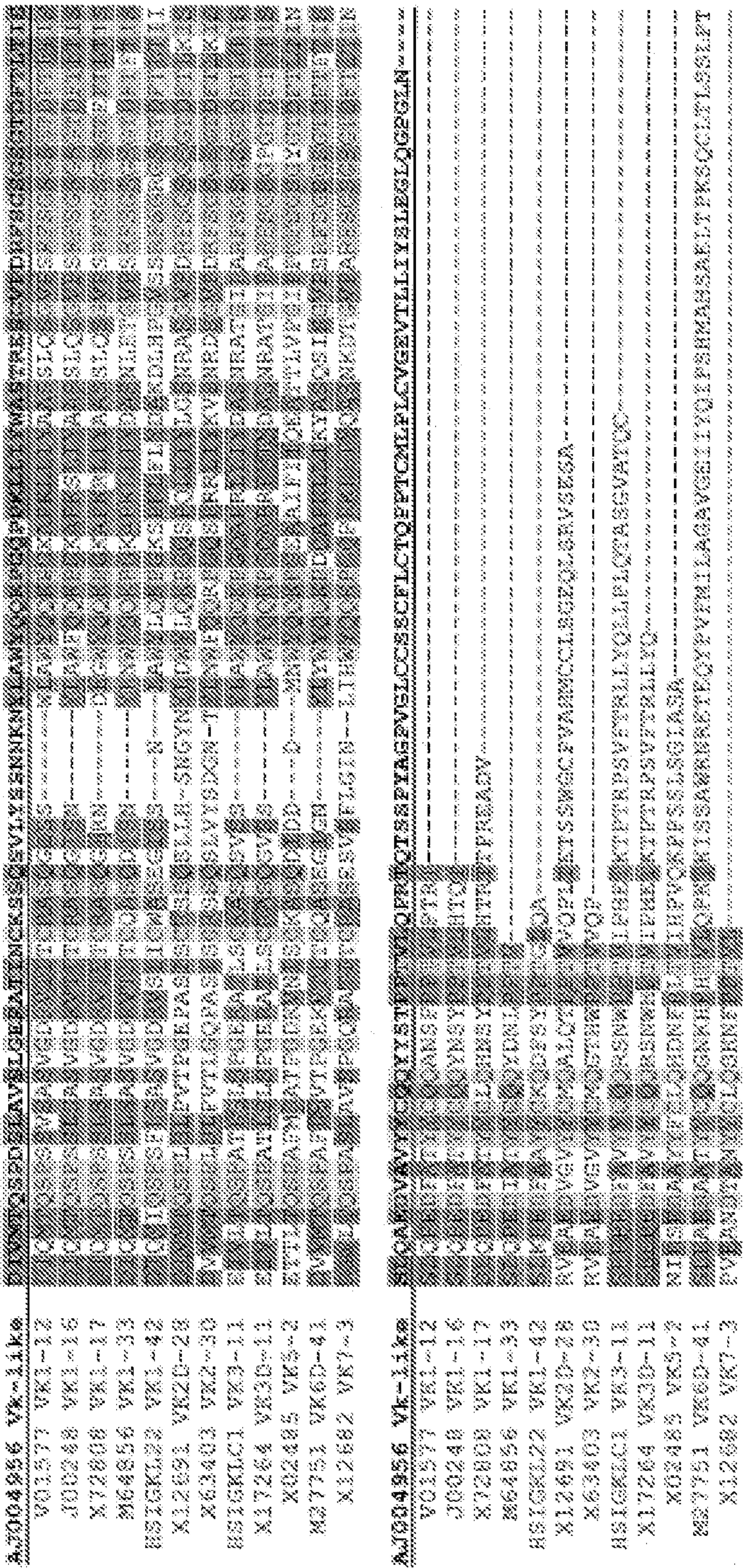
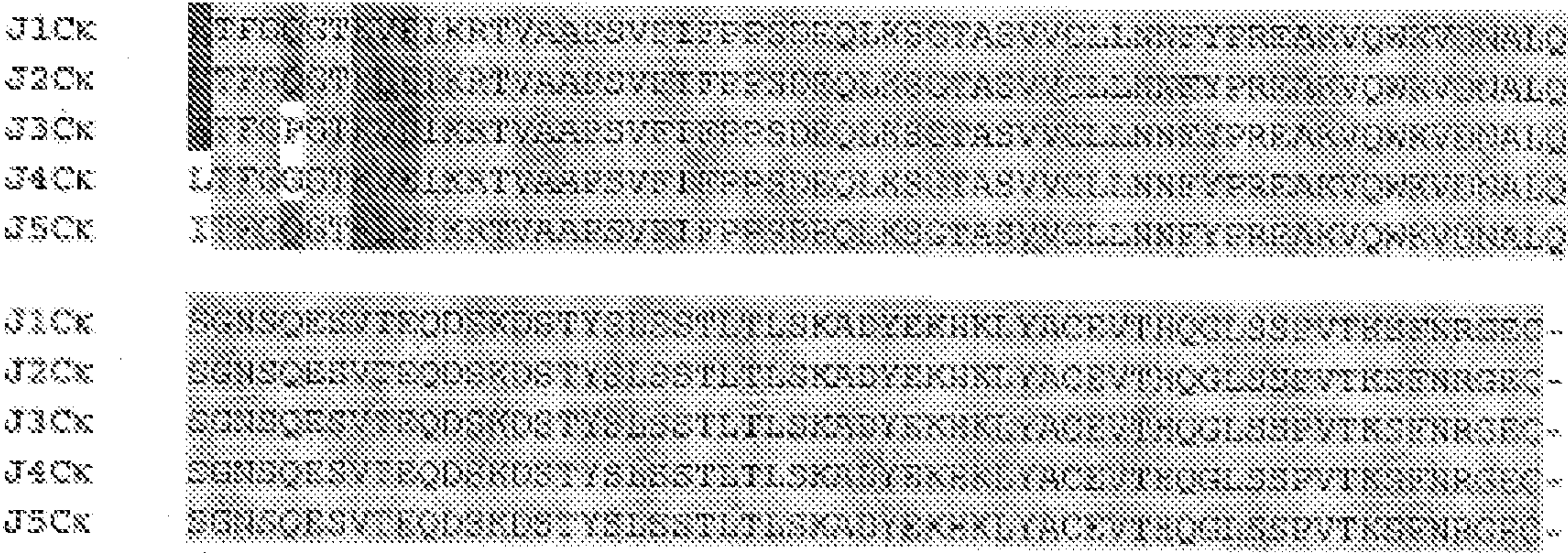


Figure 5A

V R R V F V Q Q D N G E L T L W W T F G
1 GTGAGAGGG TTTTGTTC GAGAGACAT GAGAGCTCA CACTGTGTG GAGTTCCGC
CACTCTTCCC AAAAACAGT CTTCTCTTA CTTCTCGAGT GTGACACCC CCGAAGCCG
Q G T K V E I K R T V A A P S V F I F P
61 CAAGGACCA AGGTGGAAT CAAAGCACT GTGGCTGCAC CACTGTCTT CACTTCCCG
GTTCCCTGTT TCCACCTTTA GTTGTCTTGA CACCGACGTG GTGACACGA GTAGAGCGC
P S D E Q L K S G T A S V V C L L N N F
121 CCATCTGATG AGCAGTTGA ATCTGGACT CCTCTGTG TGTCCTGCT GATTAATTC
GATAGACTAC TCGTCAACTT TAGACCTTGA CCGAGACAC ACACGGACA CTATTTGAG
Y P R E A K V Q W K V D N A L Q S G N S
181 TATCCAGAG AGCCAAAGT ACAGTGAGG GTGATTAAG CCTCCATC GGTAACTCC
ATAGGCTTC TCGGTTCA TGTCACTTC CACTATTGC GAGACCTTAC CCAATTGAG
Q E S V T E Q D S K D S T Y S L S S T L
241 CAGGAGTG TCACAGCA GACAGCAG GACAGCACT ACAGCTTCA CAGACCTTG
GTCTCTCAC AGTGCTCGT CCTGTCTTC CTGTCTGGA TTCTCGATC GTGTGGCAC
T L S K A D Y E K H K L Y A C E V T H Q
301 AGCTGAGCA AACAGACTA CAGAAACAC AACCTCTAG CTTGGAGT CACCATGAG
TCCGACTGT TTGCTGAT GCTCTTGTG TTTGAGATC GAGACCTTCA GTGGTATC
G L S S P V T K S P N R G E C *
361 CCGCTGAGCT CCGCTGCAC AAGAGCTTC AACAGGAG AGTCTTAC
CCGACTCA GCGGAGTG TTTCTGAG TTCTCCCTC TCACATC

Figure 5B



(SEQ ID NOS: 27-31)

Figure 5C

MEIDTLLLVVLLLVPGSTGVRRVFVQODNGELTLWWTFGQGTKVEIKRTVAAPSVFI
FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQGNSQESVTEQDSKDYSLSS
TLTLKADYEKHKLYACEVTHQGLSSPVTKSFNRGEC

MEIDTLLLVVLLLVPGSTGWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC
LLNNFYPREAKVQWKVDNALQGNSQESVTEQDSKDYSLSS TLTLKADYEKHKLYA
CEVTHQGLSSPVTKSFNRGEC

MEIDTLLLVVLLLVPGSTGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY
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(SEQ ID NOS:32-34)

Figure 6

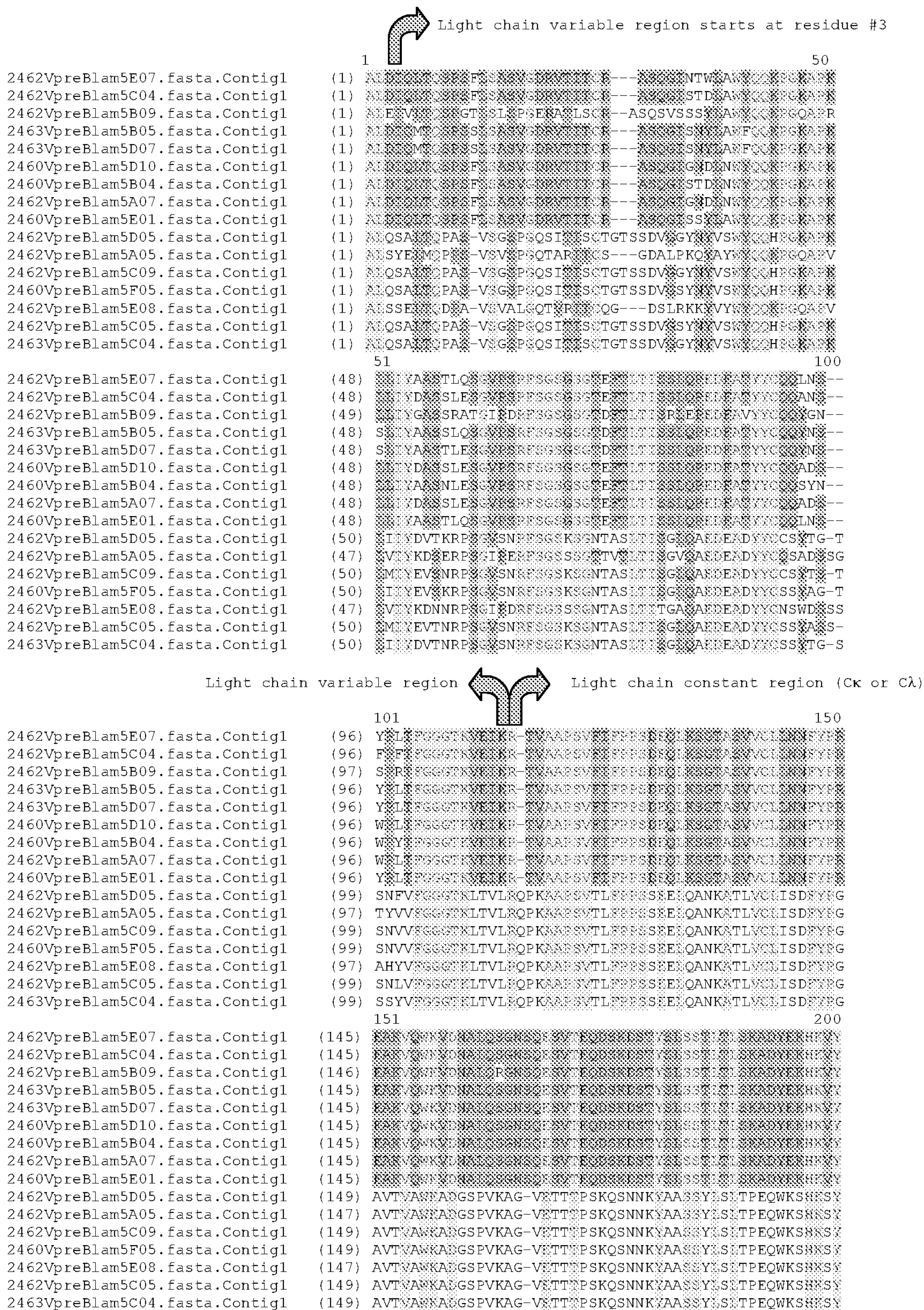


Figure 6 continued

		201		250
2462VpreBlam5E07.fasta.Contig1	(195)			
2462VpreBlam5C04.fasta.Contig1	(195)			
2462VpreBlam5B09.fasta.Contig1	(196)			
2463VpreBlam5B05.fasta.Contig1	(195)			
2463VpreBlam5D07.fasta.Contig1	(195)			
2460VpreBlam5D10.fasta.Contig1	(195)			
2460VpreBlam5B04.fasta.Contig1	(195)			
2462VpreBlam5A07.fasta.Contig1	(195)			
2460VpreBlam5E01.fasta.Contig1	(195)			
2462VpreBlam5D05.fasta.Contig1	(198)		SEQTSEGSTVEKTVAPTECS	
2462VpreBlam5A05.fasta.Contig1	(196)		SEQTSEGSTVEKTVAPTECS	
2462VpreBlam5C09.fasta.Contig1	(198)		SEQTSEGSTVEKTVAPTECS	
2460VpreBlam5F05.fasta.Contig1	(198)		SEQTSEGSTVEKTVAPTECS	
2462VpreBlam5E08.fasta.Contig1	(196)		SEQTSEGSTVEKTVAPTECS	
2462VpreBlam5C05.fasta.Contig1	(198)		SEQTSEGSTVEKTVAPTECS	
2463VpreBlam5C04.fasta.Contig1	(198)		SEQTSEGSTVEKTVAPTECS	

(SEQ ID NOS: 36-51)

Figure 7



2462VpreBlam5E07.fasta.Contigl	(51)	...NGS...YIY...A...G...P...T...S...D...M...A...N...S...Y...I...G...S...I...P...A...E...D...T...A...V...Y...C...A...G...Q...
2462VpreBlam5C04.fasta.Contigl	(51)	...SGSG...ASTY...A...G...P...T...S...D...M...A...N...S...Y...I...G...S...I...P...A...E...D...T...A...V...Y...C...A...G...Y...
2462VpreBlam5B09.fasta.Contigl	(51)	...PNS...G...G...T...N...Y...A...Q...K...F...Q...G...V...I...M...T...E...D...T...S...I...S...A...Y...M...E...L...S...R...I...R...S...D...D...T...A...V...Y...C...A...G...R...P...
2463VpreBlam5B05.fasta.Contigl	(51)	...P...V...G...F...G...A...N...Y...A...Q...K...F...Q...G...V...I...M...T...E...D...T...S...I...S...A...Y...M...E...L...S...R...I...R...S...D...D...T...A...V...Y...C...A...G...R...D...D...
2463VpreBlam5D07.fasta.Contigl	(51)	...P...I...S...I...T...A...T...Y...A...Q...K...F...Q...G...V...I...M...T...E...D...T...S...I...S...A...Y...M...E...L...S...R...I...R...S...D...D...T...A...V...Y...C...A...G...K...D...L...
2460VpreBlam5D10.fasta.Contigl	(51)	...K...Y...D...G...A...N...K...Y...A...G...S...P...P...T...S...D...M...A...N...S...Y...I...G...S...I...P...A...E...D...T...A...V...Y...C...A...G...R...A...S...
2460VpreBlam5B04.fasta.Contigl	(51)	...S...S...N...G...R...Y...I...A...G...S...P...P...T...S...D...M...A...N...S...Y...I...G...S...I...P...A...E...D...T...A...V...Y...C...A...G...R...V...V...
2462VpreBlam5A07.fasta.Contigl	(51)	...K...Y...D...G...A...N...K...Y...A...G...S...P...P...T...S...D...M...A...N...S...Y...I...G...S...I...P...A...E...D...T...A...V...Y...C...A...G...R...A...S...
2460VpreBlam5E01.fasta.Contigl	(51)	...P...I...T...I...T...A...T...Y...A...Q...K...F...Q...G...V...I...M...T...E...D...T...S...I...S...A...Y...M...E...L...S...R...I...R...S...D...D...T...A...V...Y...C...A...G...G...
2462VpreBlam5D05.fasta.Contigl	(51)	...S...P...F...S...G...G...T...N...Y...A...Q...K...F...Q...G...V...I...M...T...E...D...T...S...I...S...A...Y...M...E...L...S...R...I...R...S...D...D...T...A...V...Y...C...A...G...Q...
2462VpreBlam5A05.fasta.Contigl	(51)	...P...N...S...G...G...T...N...Y...A...Q...K...F...Q...G...V...I...M...T...E...D...T...S...I...S...A...Y...M...E...L...S...R...I...R...S...D...D...T...A...V...Y...C...A...G...P...
2462VpreBlam5C09.fasta.Contigl	(51)	...G...Y...G...G...T...N...T...Y...A...G...S...P...P...T...S...D...M...A...N...S...Y...I...G...S...I...P...A...E...D...T...A...V...Y...C...A...G...R...E...A...
2460VpreBlam5F05.fasta.Contigl	(51)	...S...G...N...S...A...D...K...Y...A...G...S...P...P...T...S...D...M...A...N...S...Y...I...G...S...I...P...A...E...D...T...A...V...Y...C...A...G...R...D...
2462VpreBlam5E08.fasta.Contigl	(51)	...Y...Y...S...G...T...S...K...Y...A...G...S...P...P...T...S...D...M...A...N...S...Y...I...G...S...I...P...A...E...D...T...A...V...Y...C...A...G...R...D...
2462VpreBlam5C05.fasta.Contigl	(51)	...S...W...N...G...G...T...T...Y...A...G...S...P...P...T...S...D...M...A...N...S...Y...I...G...S...I...P...A...E...D...T...A...V...Y...C...A...G...R...S...G...
2463VpreBlam5C04.fasta.Contigl	(51)	...M...A...N...S...G...T...S...Y...A...Q...K...F...Q...G...V...I...M...T...E...D...T...S...I...S...A...Y...M...E...L...S...R...I...R...S...D...D...T...A...V...Y...C...A...G...D...D...



2462VpreBlam5E07.fasta.Contigl	(101)	WWSG----GDFYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2462VpreBlam5C04.fasta.Contigl	(101)	RASDSDYYGWMYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2462VpreBlam5B09.fasta.Contigl	(101)	AG-----PWALFYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2463VpreBlam5B05.fasta.Contigl	(101)	Y-----WTSVYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2463VpreBlam5D07.fasta.Contigl	(101)	IGWI-SHSYNGFYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2460VpreBlam5D10.fasta.Contigl	(101)	PYG----PSFYYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2460VpreBlam5B04.fasta.Contigl	(101)	DFQDYN---GFFYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2462VpreBlam5A07.fasta.Contigl	(101)	PYGP-----SFFYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2460VpreBlam5E01.fasta.Contigl	(101)	WSN-----WGFFYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2462VpreBlam5D05.fasta.Contigl	(101)	WWYG----DAFFYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2462VpreBlam5A05.fasta.Contigl	(101)	IRSRGGK-YGGFYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2462VpreBlam5C09.fasta.Contigl	(101)	GYDR--YGYGFFYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2460VpreBlam5F05.fasta.Contigl	(101)	GLN-----YLFYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2462VpreBlam5E08.fasta.Contigl	(101)	YKS-----YTYALFYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2462VpreBlam5C05.fasta.Contigl	(101)	G---AFYLSGLEFYWGQGTTLVTVSSASTKGPVVFELAPSSKETS
2463VpreBlam5C04.fasta.Contigl	(101)	G-----GAYVYWGQGTTLVTVSSASTKGPVVFELAPSSKETS

(SEQ ID NOS: 52-67)

Figure 8

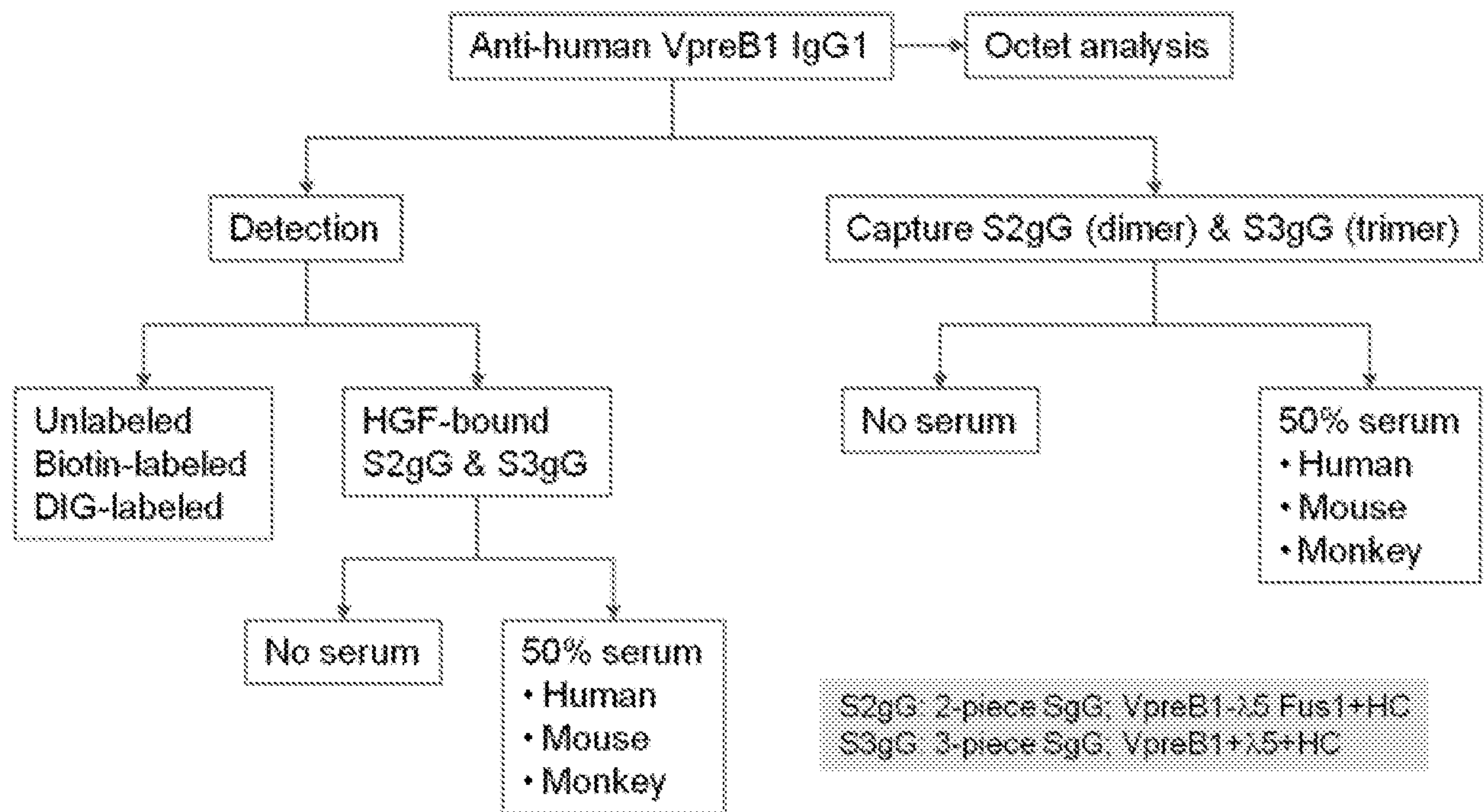


Figure 9

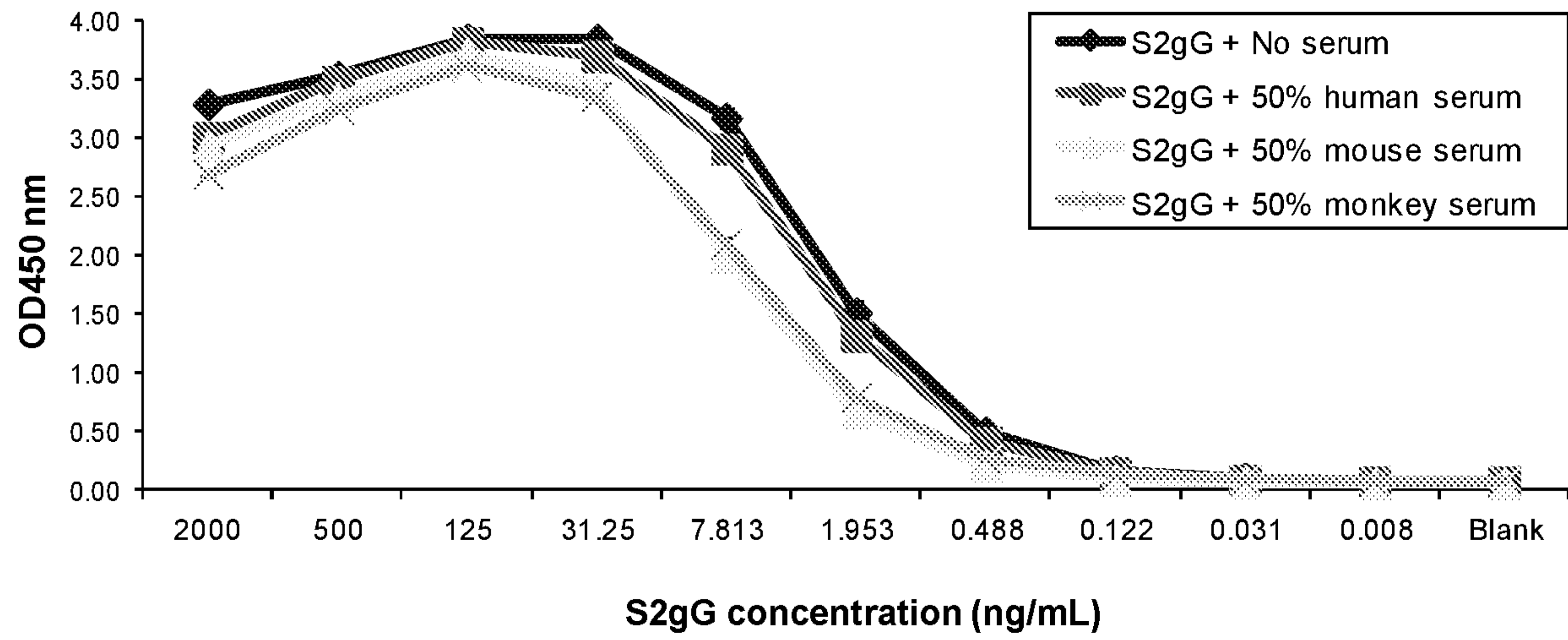


Figure 10

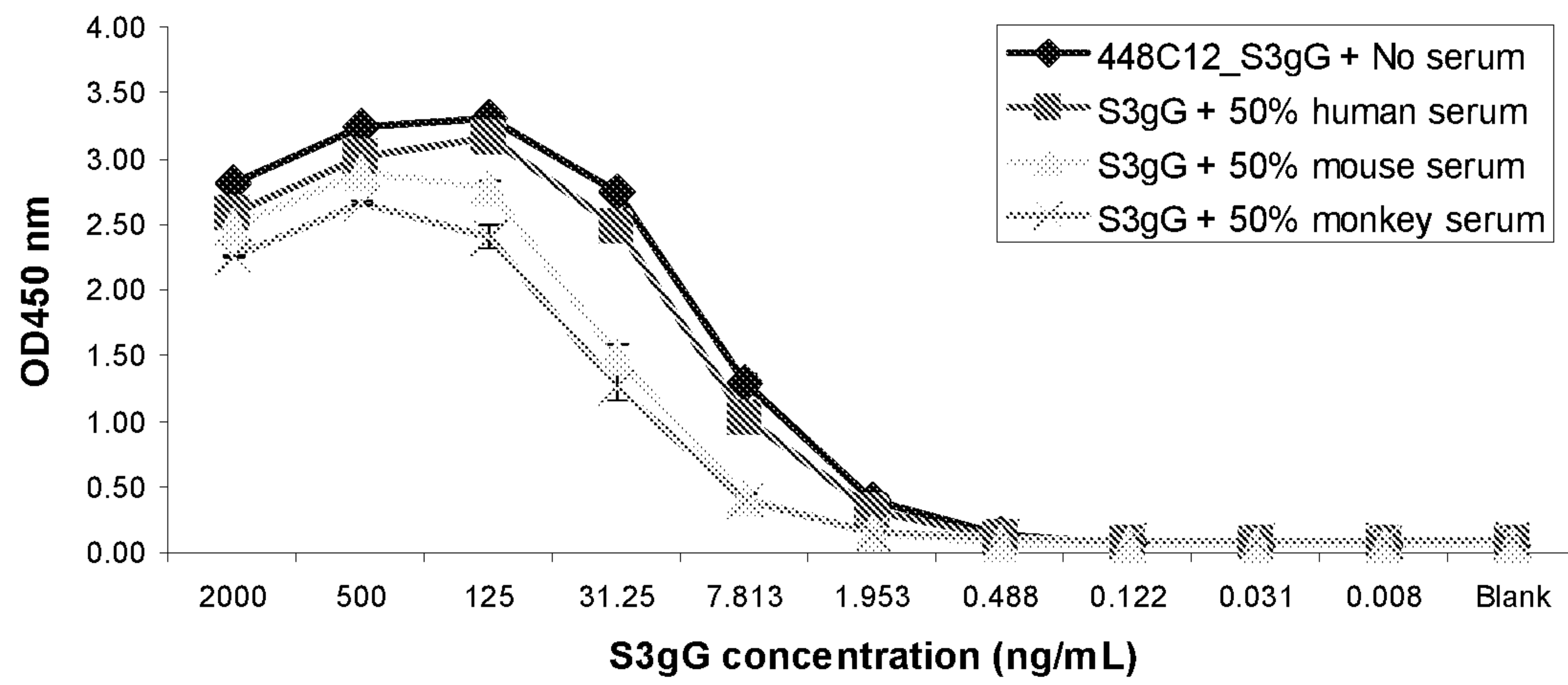


Figure 11

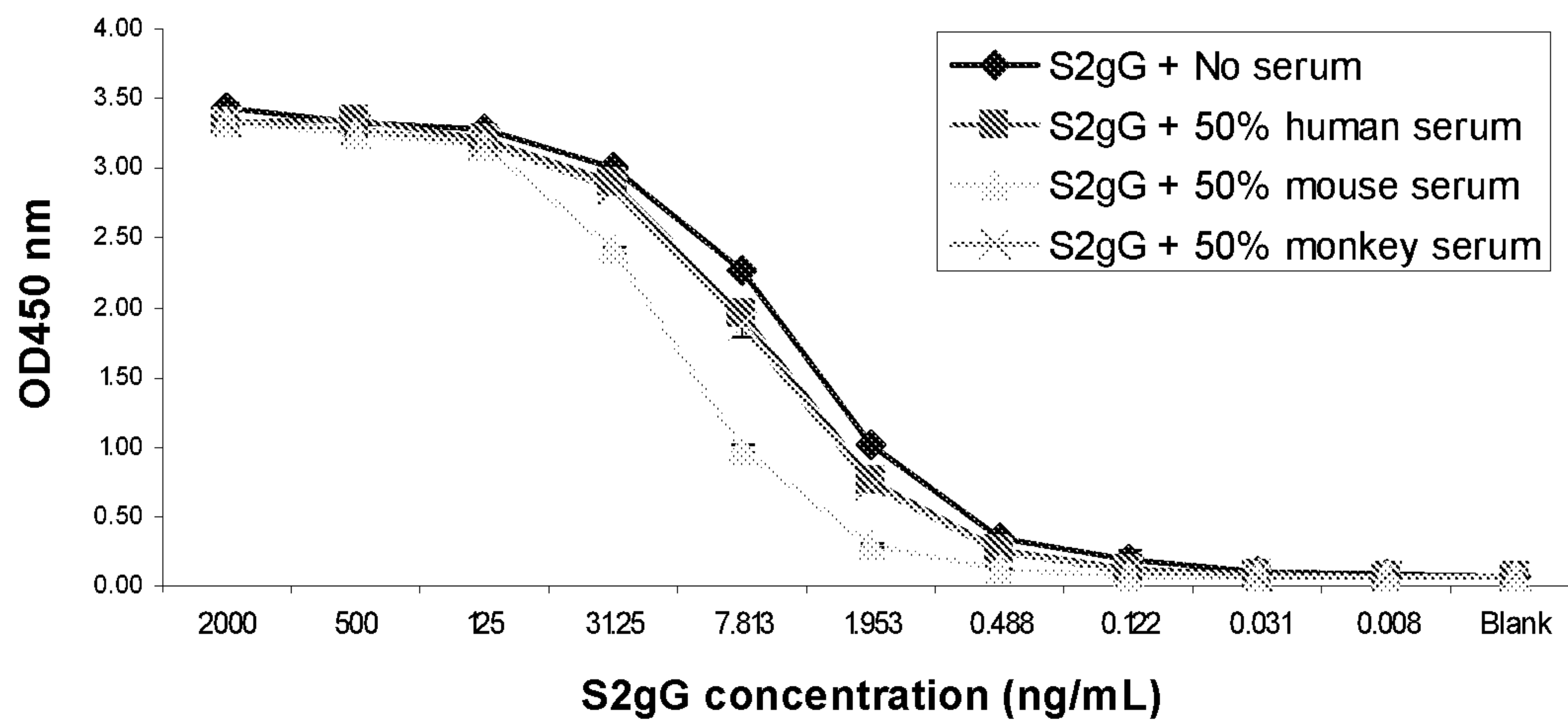


Figure 12

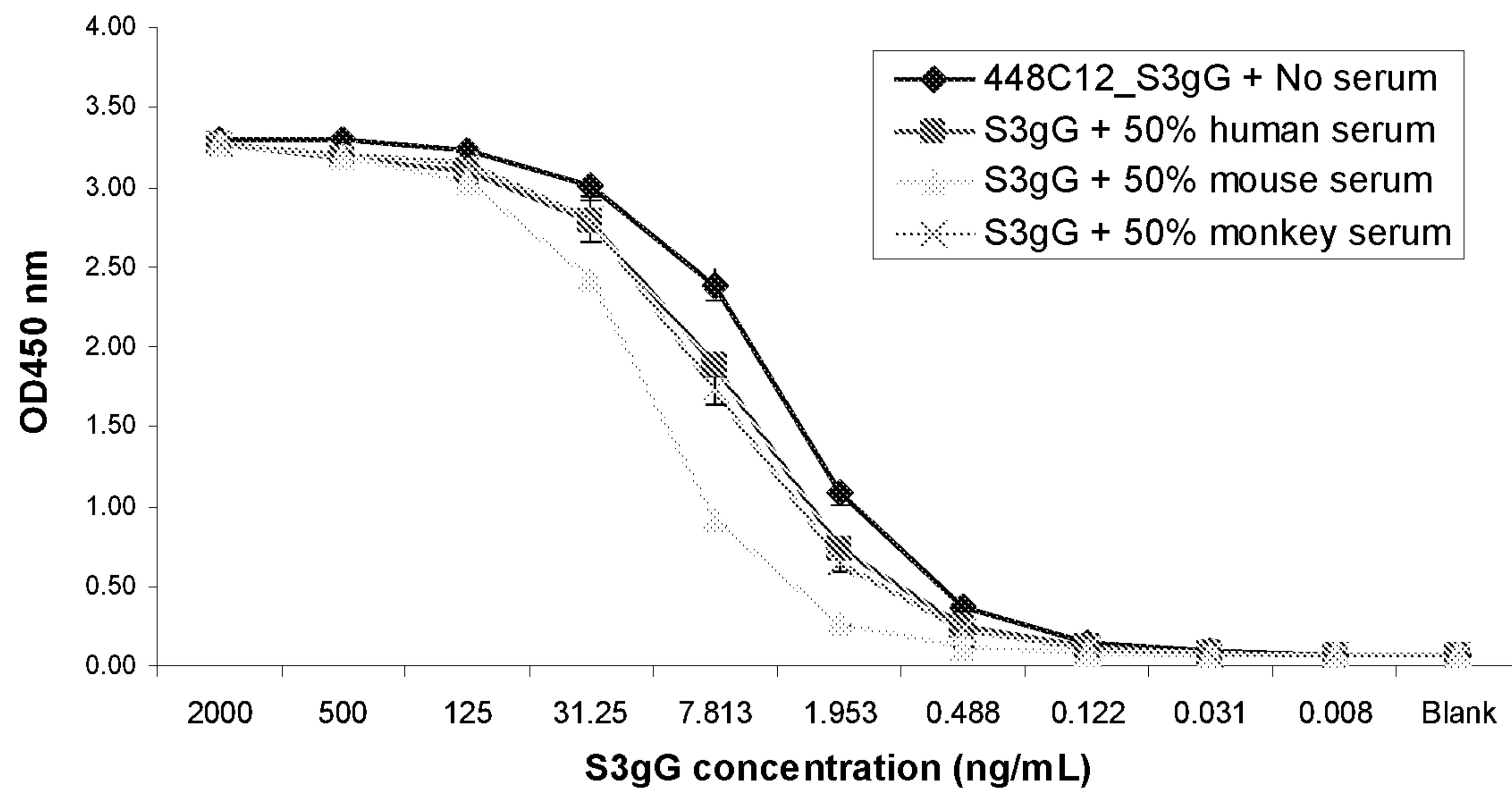


Figure 13

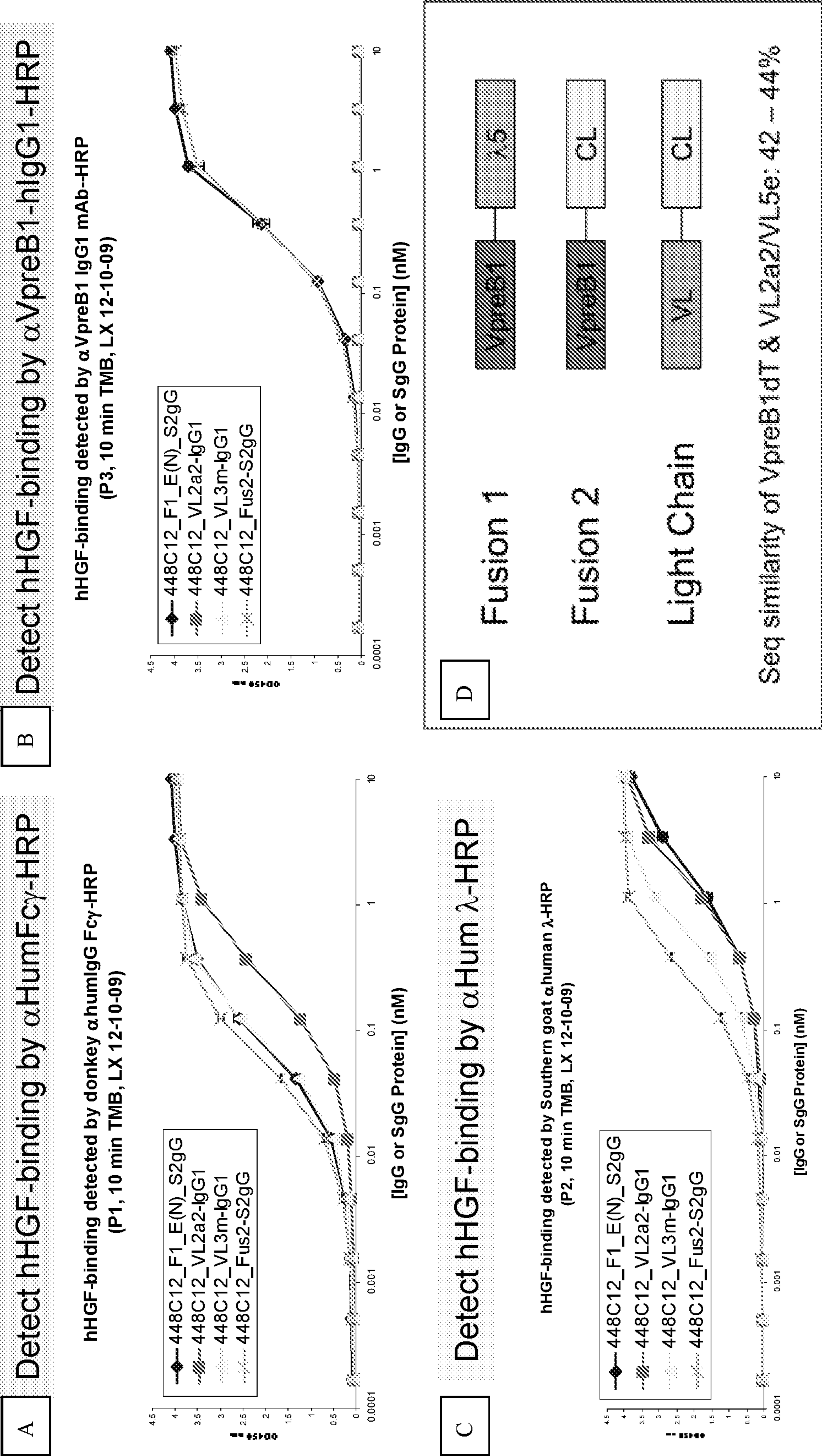


Figure 14

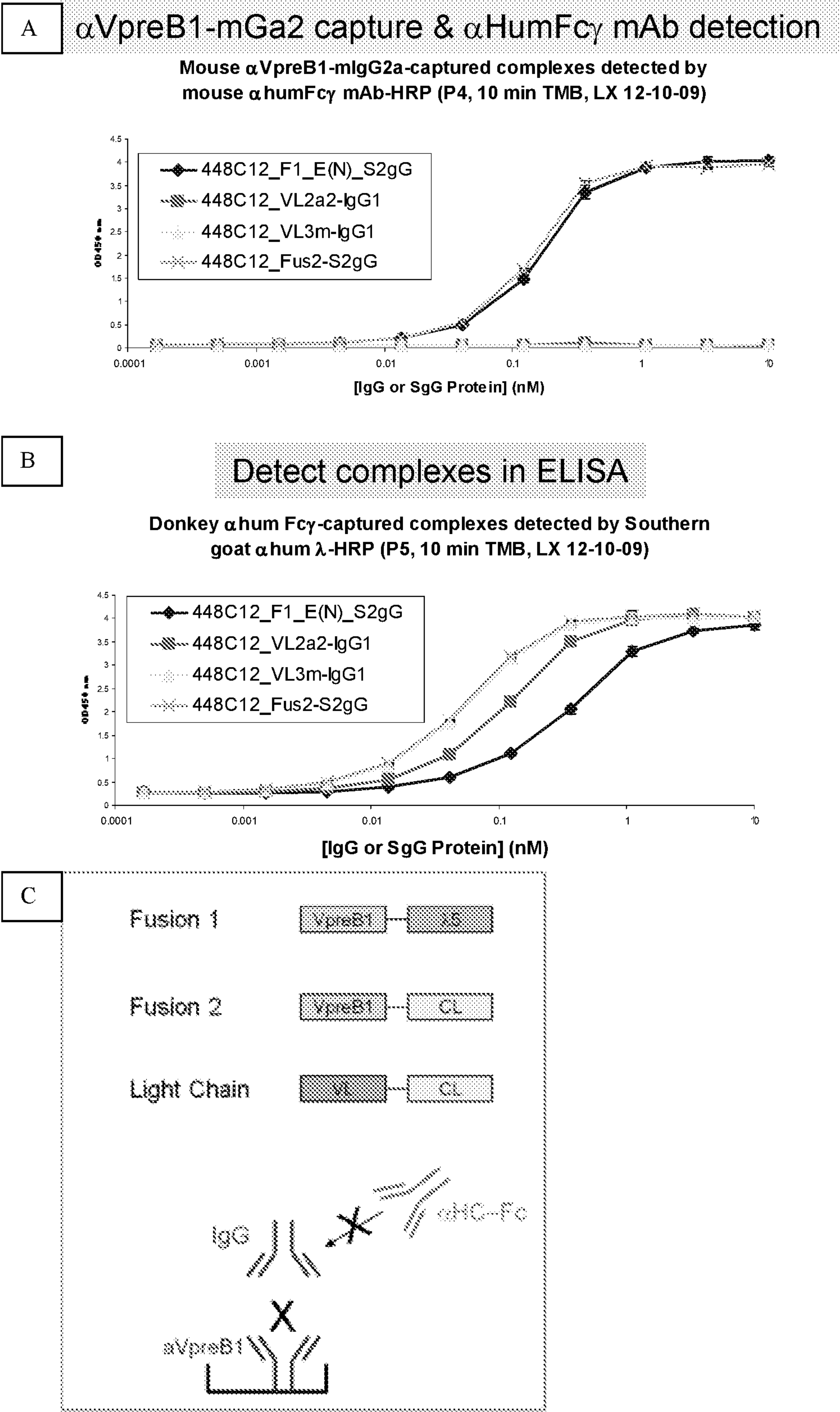
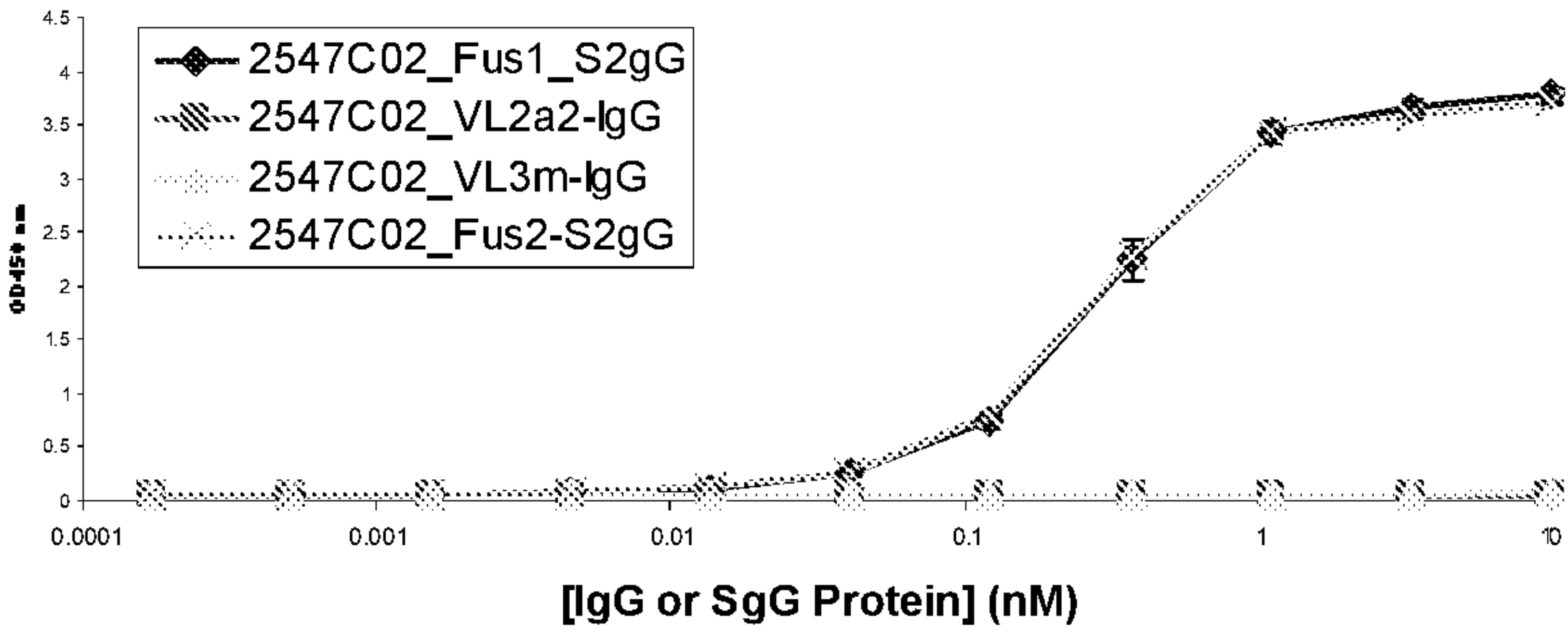


Figure 15

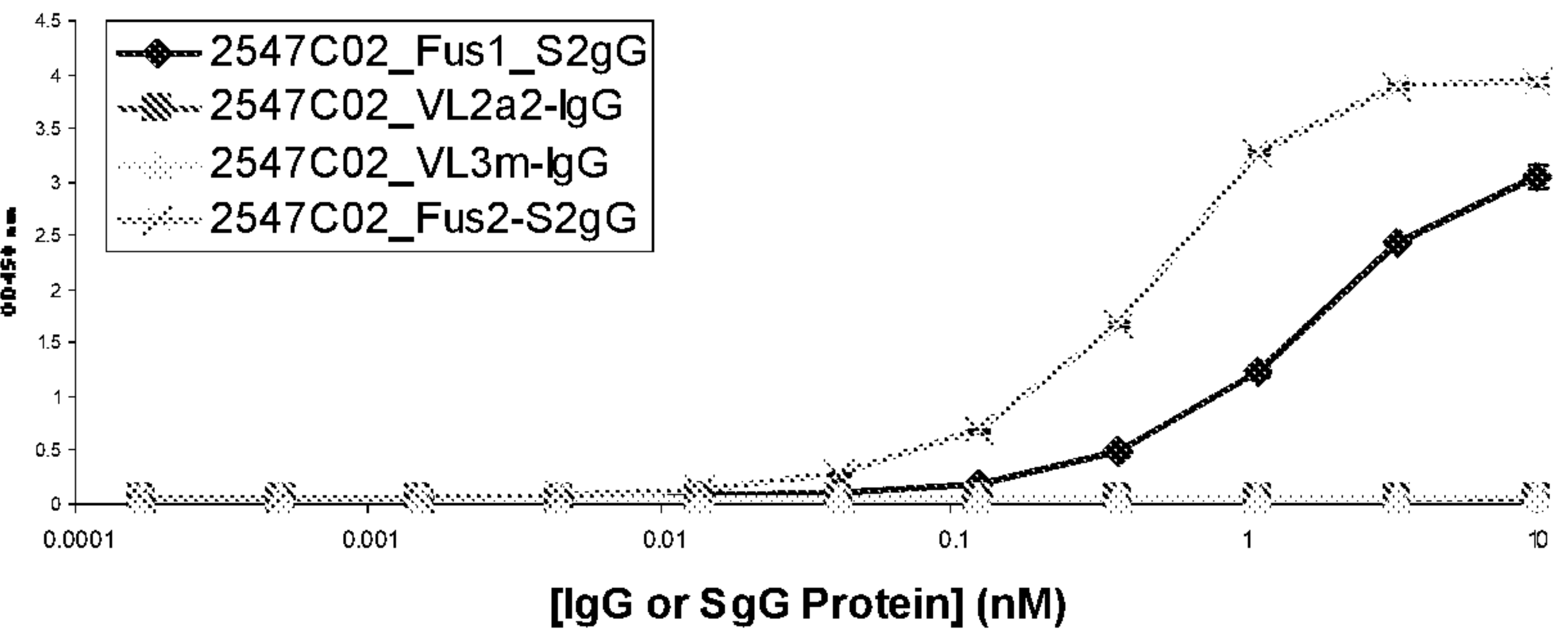
A

α VpreB1-mouse IgG2a-captured complexes detected by mouse α humIgG Fc γ mAb-HRP (P3, 10 min TMB, LX 12-11-09)



B

α VpreB1-mouse IgG2a-captured complexes detected by Southern goat α hum λ -HRP (P4, 10 min TMB, LX 12-11-09)



C

Fusion 1



Fusion 2



Light Chain

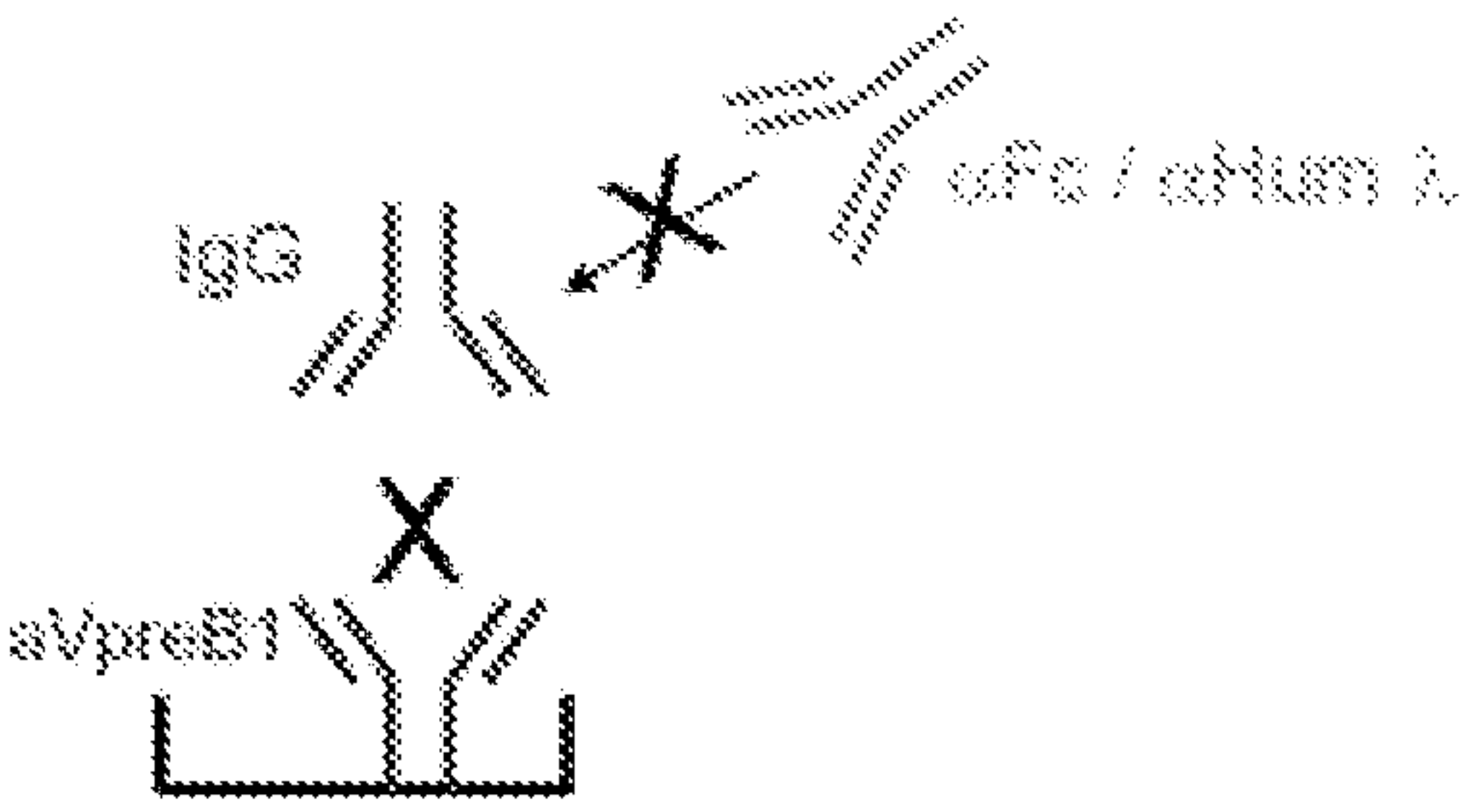


Figure 16

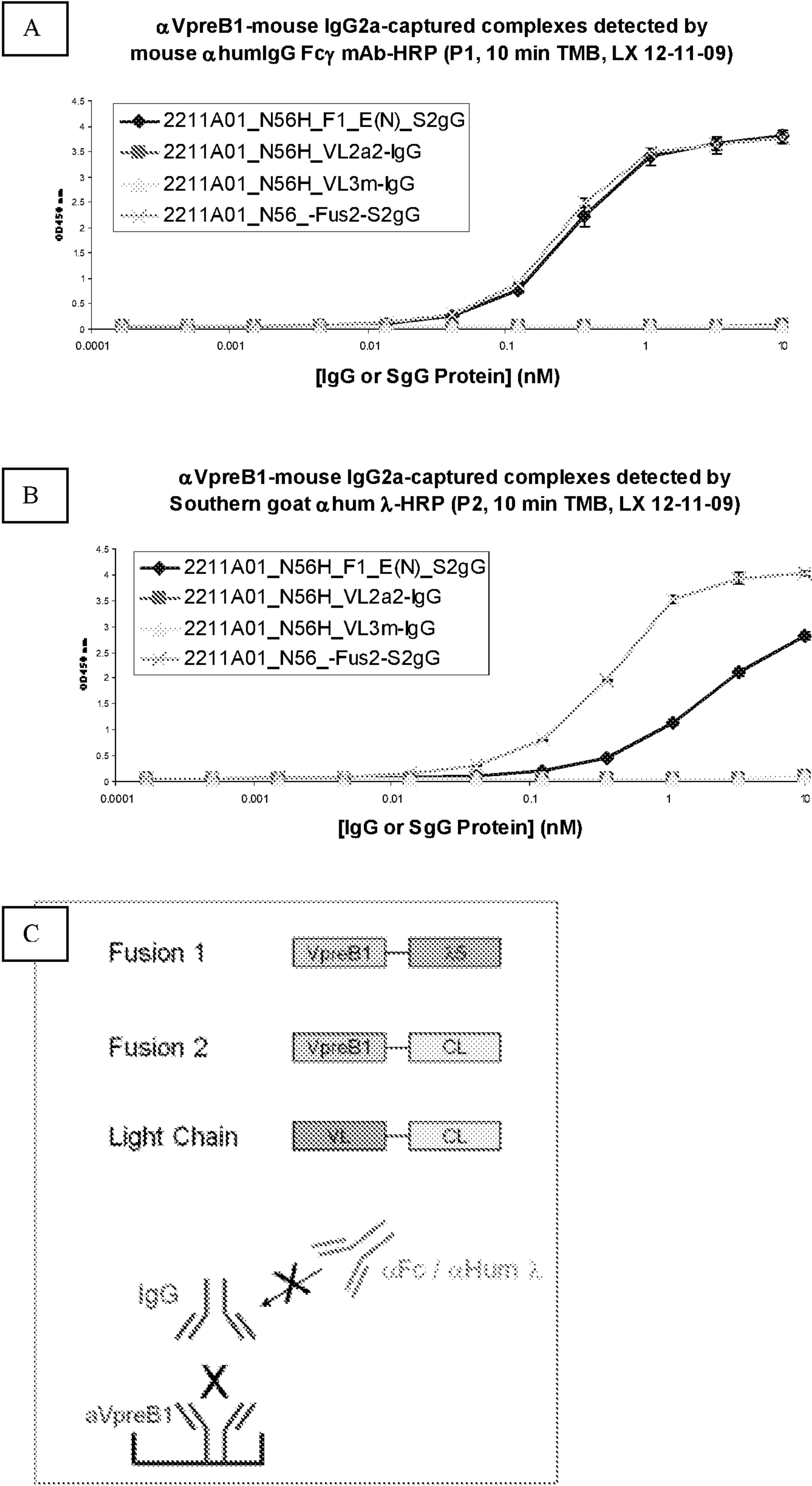


Figure 17

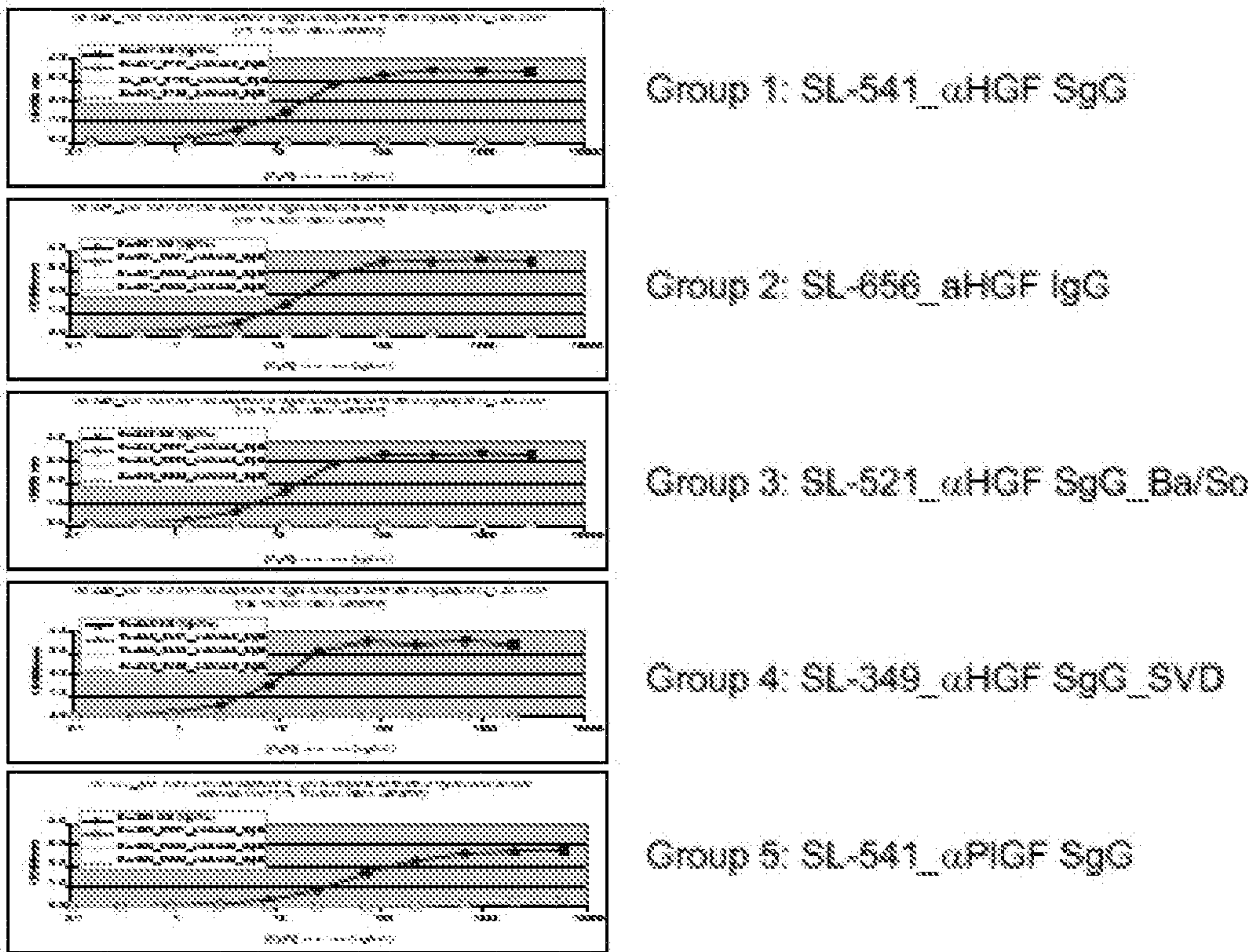


Figure 18

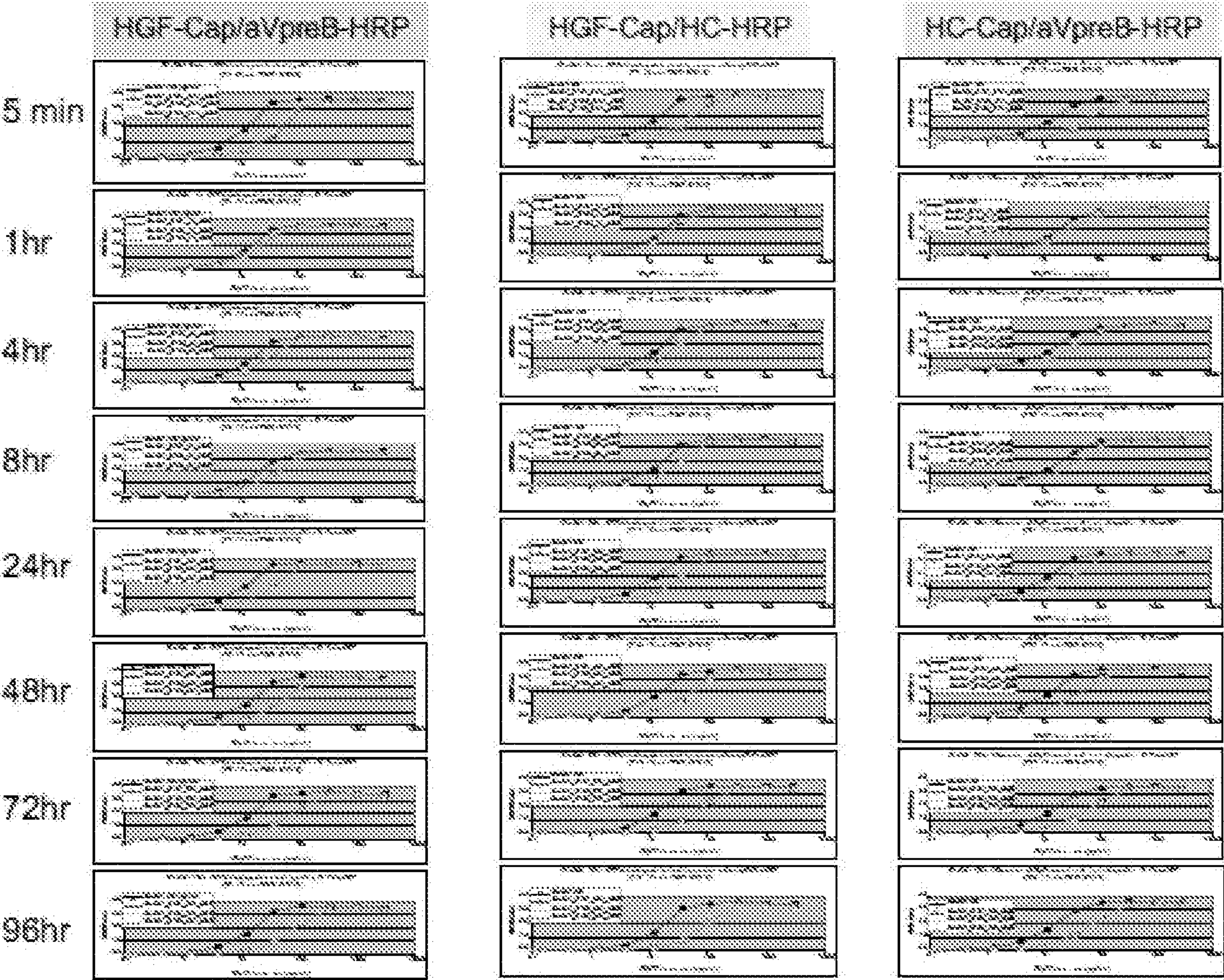


Figure 19

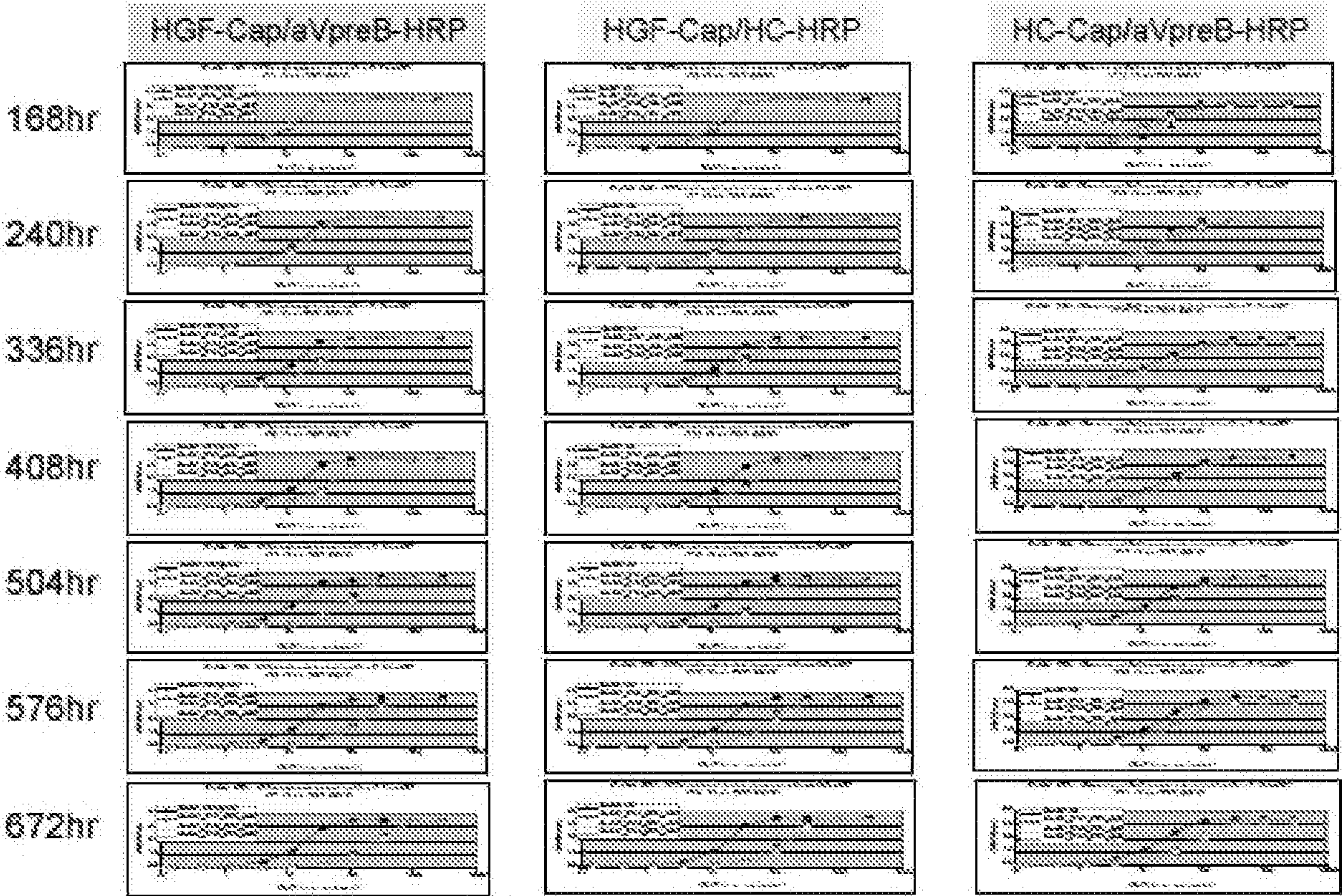


Figure 20

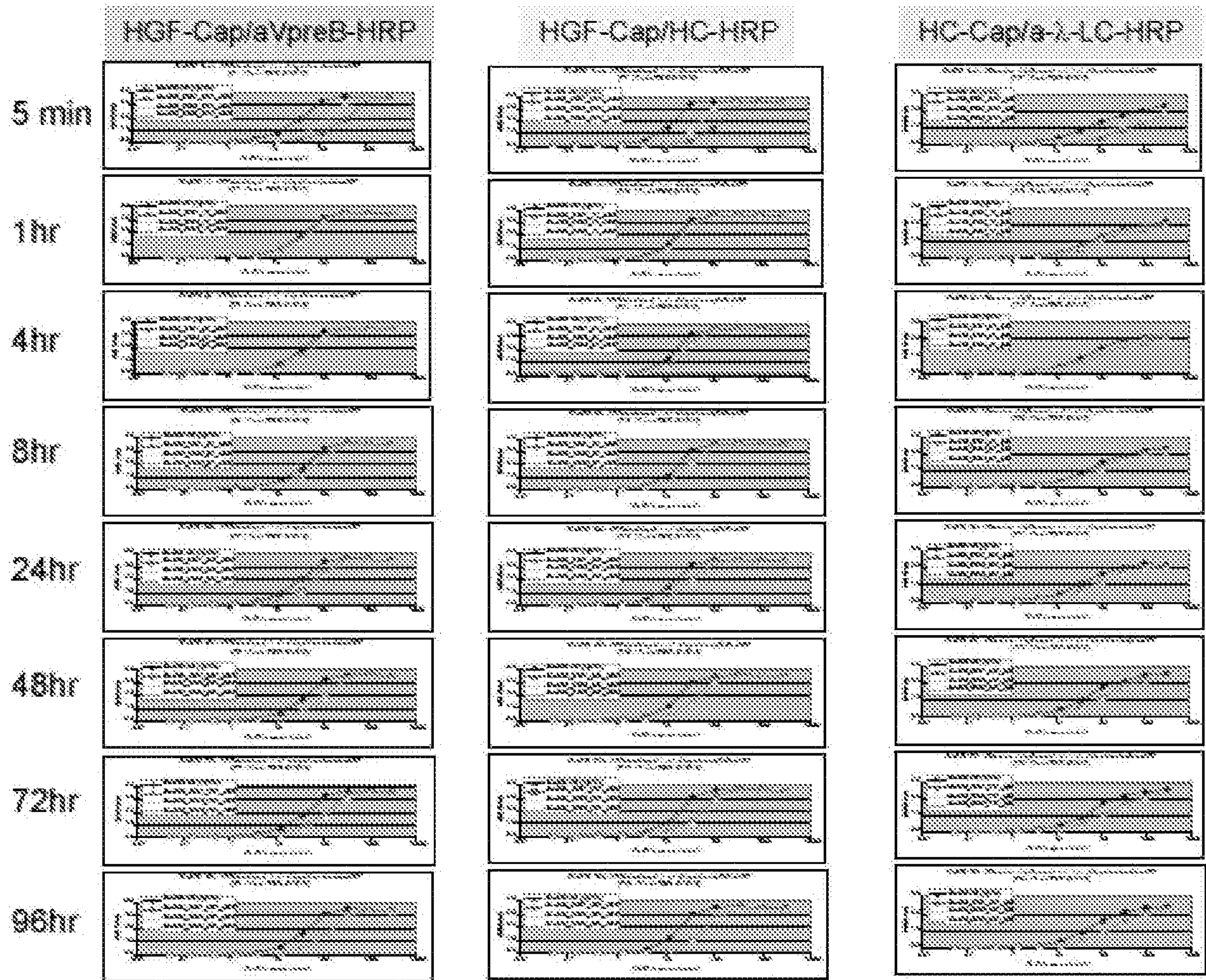


Figure 21

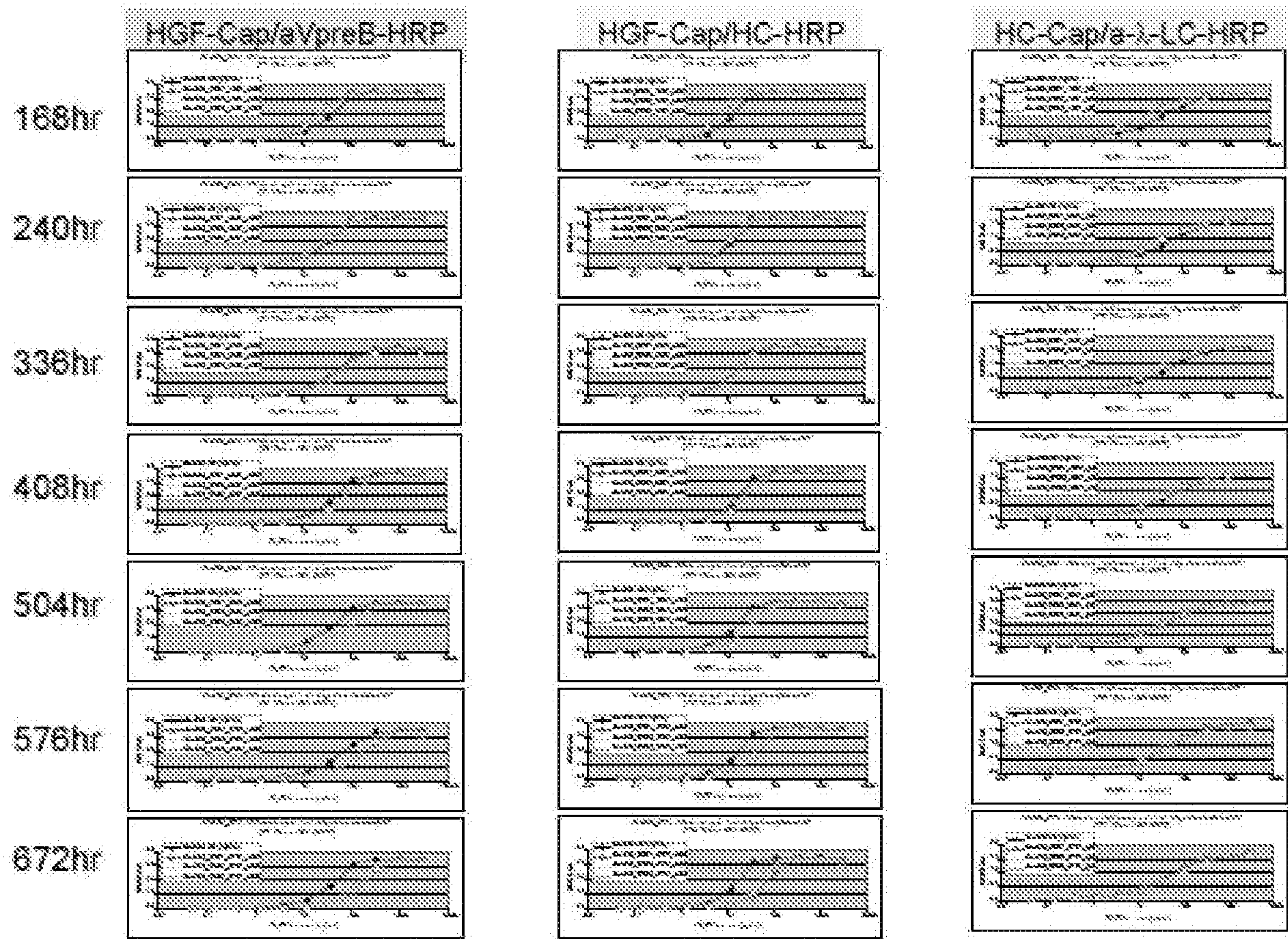
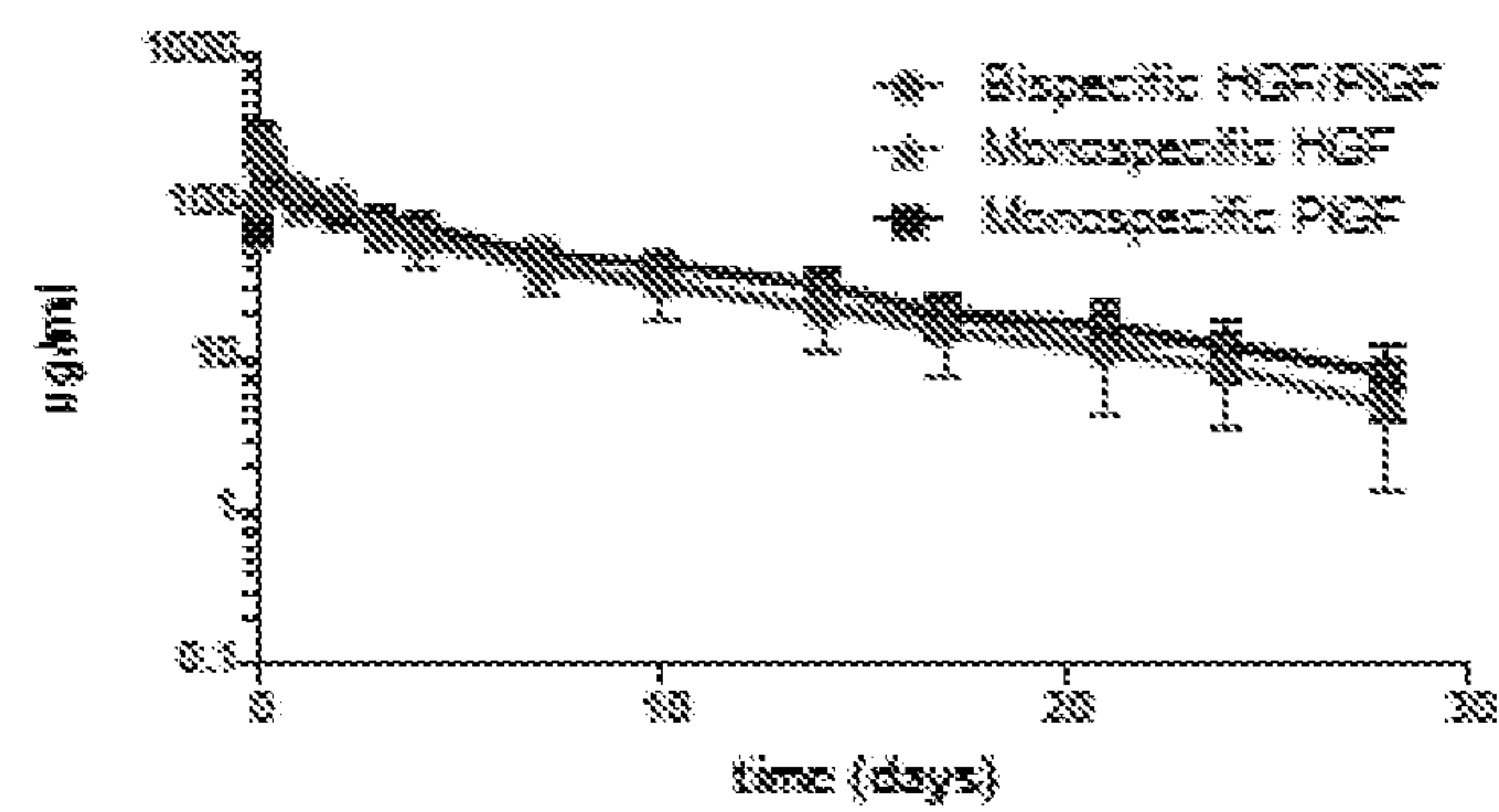


Figure 22



Agent	Half-life (days)	Clearance (mL/hr/kg)	Vss (mL/kg)
SL-521_HGF/PIGF	6.04	0.42	77.2
SL-541_HGF	6.28	0.40	110
SL-542_PIGF	6.35	0.35	78.5