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(54) Title: CANINE IMMUNOGLOBULIN VARIABLE DOMAINS, CANINIZED ANTIBODIES, AND METHODS FOR MAKING AND USING THEM

(57) **Abrégé/Abstract:**

The present invention provides canine heavy chain and light chain (both λ and κ) variable domain nucleic acids and polypeptides. The present invention also provides caninized antibodies comprised of the present disclosed canine variable domain framework sequences and CDRs specific for an antigen obtained from antibodies from other than canines (preferably mouse). The invention also provides methods of making caninized antibodies and using them. This disclosure specifically describes caninized antibodies that are useful in the treatment of canine allergy. The general process of caninization permits the development of useful therapeutics, which includes but is not limited to allergy, osteoarcoma's and lymphoma's.



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(54) Title: CANINE IMMUNOGLOBULIN VARIABLE DOMAINS, CANINIZED ANTIBODIES, AND METHODS FOR MAK-
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(57) Abstract: The present invention provides canine heavy chain and light chain (both λ and κ) variable domain nucleic acids and polypeptides. The present invention also provides caninized antibodies comprised of the present disclosed canine variable domain framework sequences and CDRs specific for an antigen obtained from antibodies from other than canines (preferably mouse). The invention also provides methods of making caninized antibodies and using them. This disclosure specifically describes caninized antibodies that are useful in the treatment of canine allergy. The general process of caninization permits the development of useful therapeutics, which includes but is not limited to allergy, osteoarcoma's and lymphomma's.



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DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS
COMPREND PLUS D'UN TOME.**

CECI EST LE TOME __1__ DE __2__

NOTE: Pour les tomes additionels, veuillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

**THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE
THAN ONE VOLUME.**

THIS IS VOLUME __1__ OF __2__

NOTE: For additional volumes please contact the Canadian Patent Office.

**CANINE IMMUNOGLOBULIN VARIABLE DOMAINS,
CANINIZED ANTIBODIES, AND METHODS FOR MAKING AND USING THEM**

BACKGROUND OF THE INVENTION

Field of the Invention

[0001] The present invention relates to the field of immunology. More specifically, the present invention relates to canine immunoglobulin light and heavy chain variable domains, caninized antibodies, and methods for making and using them.

Summary of the Related Art

[0002] The process of modifying a monoclonal antibody from an animal to render it less immunogenic for therapeutic administration to humans (humanization) has been aggressively pursued and has been described in a number of publications (e.g. *Antibody Engineering: A practical Guide*. Carl A.K. Borrebaeck ed. W.H. Freeman and Company, 1992). However, this process has not been applied for the development of therapeutic or diagnostics for canines. In fact, very little has been published with regard to canine variable domains at all.

[0003] Wasserman and Capra, *Biochem.* **16**, 3160 (1977), determined the amino acid sequence of the variable regions of both a canine IgM and a canine IgA heavy chain.

[0004] Wasserman and Capra, *Immunochem.* **15**, 303 (1978), determined the amino acid sequence of the K light chain from a canine IgA.

[0005] McCumber and Capra, *Mol. Immunol.* **16**, 565 (1979), disclose the complete amino-acid sequence of a canine mu chain.

[0006] Tang et al., *Vet. Immunology Immunopathology* **80**, 259 (2001), discloses a single canine IgG-A γ chain cDNA and four canine IgG-A γ chain protein sequences. It describes PCR amplification of a canine spleen cDNA library with a degenerate oligonucleotide primer designed from the conserved regions of human, mouse, pig, and bovine IgGs.

[0007] The paucity of information available on canine antibodies prevents their development as therapeutics for the treatment canine disease.

SUMMARY OF THE INVENTION

[0008] The present invention provides canine heavy chain and light chain (both λ and κ) domain nucleic acids and polypeptides

[0009] The present invention also provides caninized antibodies comprised of the presently disclosed canine variable and CDRs specific

for an antigen obtained from antibodies from other than canines (preferably mouse or canine).

[0010] The invention also provides methods of making caninized antibodies and using them. This disclosure specifically describes caninized antibodies that are useful in the treatment of canine allergy. The general process of caninization permits the development of useful therapeutics, which includes but is not limited to allergy, osteosarcoma and lymphoma.

BRIEF DESCRIPTION OF THE DRAWINGS

[0011] Figure 1 displays the results for screening of functional heavy and light chain variable domains by measuring secretion of IgG_H from COS cells.

[0012] Figure 2 displays light chain variable domain selected for caninization and its alignment to 15A2. Amino acid differences are indicated by vertical lines.

[0013] Figure 3 displays the H74 heavy chain variable domain selected for caninization and its alignment to 15A2. Differences are indicated with vertical lines.

[0014] Figure 4 displays CDR grafting of the 15A2 CDR's onto canine variable domains and the construction of full-length heavy and light chains.

[0015] Figure 5 displays the interpretation of the molecular modeling of 15A2: light chain followed by heavy chain.

[0016] Fig. 6 displays enhanced binding to IgE by caninized light chain variable domains carrying back mutations.

[0017] Figure 7 displays the results of combining individual light chain back mutations into a single molecule and the enhanced binding to IgE.

[0018] Figures 8A and 8B display enhanced binding to IgE by caninized heavy chain variable domains carrying back mutations.

[0019] Figure 9 displays the neutralization of IgE by fully caninized immunoglobulins.

DETAILED DESCRIPTION OF THE INVENTION

[0020] IDEXX has engaged in the development of a therapeutic monoclonal antibody for the treatment of allergy in canines. The therapeutic antibody used in canine clinical trials was a chimeric recombi-

nant molecule, consisting of canine antibody constant domains of the heavy and light chains attached to murine derived antibody variable domains of the mouse monoclonal antibody 15A2. Therapeutic administration of this antibody to dogs sensitized to rag weed alleviated the symptoms of allergy and was considered successful. However, repeated and extended administration of the chimeric molecule in canines caused the induction of a neutralizing humoral immune response to the therapeutic, rendering it ineffective. Analysis of the anti-chimeric response clearly demonstrated the response was to the murine component of the therapeutic molecule. Accordingly, we set forth to overcome this disadvantage by "caninization" of an antibody: taking a monoclonal antibody from another organism, usually a mouse, and substituting canine immunoglobulin sequences into the variable domain to render the molecule less immunogenic when administered to canines. In particular, this process focuses on the framework regions of the immunoglobulin variable domain, but could also include the complement determinant regions (CDR's) of the variable domain. The enabling steps and reduction to practice for this process are described in this disclosure.

Polypeptide Compositions of Matter

In a first aspect, the present invention comprises chimeric canine variable domain polypeptides having one or more CDR's from a non-canine antibody.

1. H58 family genus

[0021] In one embodiment, the present invention provides chimeric canine heavy chain variable domain polypeptides having one or more CDR's from a non-canine antibody. The chimeric canine heavy chain variable domain polypeptides according to the invention are compounds comprising the sequence:



wherein

Fr^1 is $\text{X}^1 \text{X}^2 \text{X}^3 \text{X}^4 \text{X}^5 \text{X}^6 \text{X}^7 \text{X}^8 \text{X}^9 \text{X}^{10} \text{X}^{11} \text{X}^{12} \text{X}^{13} \text{X}^{14} \text{X}^{15} \text{X}^{16} \text{X}^{17} \text{X}^{18} \text{X}^{19} \text{X}^{20} \text{X}^{21} \text{X}^{22} \text{X}^{23} \text{X}^{24} \text{X}^{81}$ (SEQ ID NO: 2);

Fr^2 is $\text{X}^{25} \text{X}^{26} \text{X}^{27} \text{X}^{28} \text{X}^{29} \text{X}^{30} \text{X}^{31} \text{X}^{32} \text{X}^{33} \text{X}^{34} \text{X}^{35} \text{X}^{36} \text{X}^{37} \text{X}^{38}$ (SEQ ID NO: 3);

Fr^3 is $\text{X}^{39} \text{X}^{40} \text{X}^{41} \text{X}^{42} \text{X}^{43} \text{X}^{44} \text{X}^{45} \text{X}^{46} \text{X}^{47} \text{X}^{48} \text{X}^{49} \text{X}^{50} \text{X}^{51} \text{X}^{52} \text{X}^{53} \text{X}^{54} \text{X}^{55} \text{X}^{56} \text{X}^{57} \text{X}^{58} \text{X}^{59} \text{X}^{60} \text{X}^{61} \text{X}^{62} \text{X}^{63} \text{X}^{64} \text{X}^{65} \text{X}^{66} \text{X}^{67} \text{X}^{68} \text{X}^{69} \text{X}^{70}$ (SEQ ID NO: 4);

Fr^4 is $\text{X}^{71} \text{X}^{72} \text{X}^{73} \text{X}^{74} \text{X}^{75} \text{X}^{76} \text{X}^{77} \text{X}^{78} \text{X}^{79} \text{X}^{80}$ (SEQ ID NO: 5);

X^1 is <u>E</u> ,	X^2 is <u>V</u> ,	X^3 is <u>Q</u> or H;	X^4 is <u>L</u> ,	X^5 is <u>V</u> or M;
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X ⁶ is <u>E</u> or Q;	X ⁷ is <u>S</u> ,	X ⁸ is <u>G</u> ,	X ⁹ is <u>G</u> ,	X ¹⁰ is <u>D</u> or N;
X ¹¹ is <u>L</u> ,	X ¹² is <u>V</u> ,	X ¹³ is <u>K</u> or R,	X ¹⁴ is <u>P</u> ,	X ¹⁵ is <u>G</u> , A, S, or E
X ¹⁶ is <u>G</u> ,	X ¹⁷ is <u>S</u> ,	X ¹⁸ is <u>L</u> ,	X ¹⁹ is <u>R</u> ,	X ²⁰ is <u>L</u>
X ²¹ is <u>S</u> ,	X ²² is <u>C</u> ,	X ²³ is <u>V</u> ,	X ²⁴ is <u>A</u> , T, V, or G'	X ²⁵ is <u>W</u> ,
X ²⁶ is <u>V</u> ,	X ²⁷ is <u>R</u> ,	X ²⁸ is <u>Q</u> , H, R, or E;	X ²⁹ is <u>A</u> , T, ,P, C, or S;	X ³⁰ is <u>P</u> ,
X ³¹ is <u>G</u> or E;	X ³² is <u>K</u> ,	X ³³ is <u>G</u> ,	X ³⁴ is <u>L</u> ,	X ³⁵ is <u>Q</u> , E, or K;
X ³⁶ is <u>W</u> , L, or Y;	X ³⁷ is <u>V</u> or I;	X ³⁸ is <u>A</u> , G, V, or T;	X ³⁹ is <u>R</u> ,	X ⁴⁰ is <u>F</u> ,
X ⁴¹ is <u>T</u> or I;	X ⁴² is <u>I</u> or V;	X ⁴³ is <u>S</u> ,	X ⁴⁴ is <u>R</u> ,	X ⁴⁵ is <u>D</u> ,
X ⁴⁶ is <u>N</u> , L, S, or D;	X ⁴⁷ is <u>A</u> ,	X ⁴⁸ is <u>K</u> , R, or E;	X ⁴⁹ is <u>N</u> or S;	X ⁵⁰ is <u>T</u> ,
X ⁵¹ is <u>L</u> , V, or F;	X ⁵² is <u>Y</u> , F, or S;	X ⁵³ is <u>L</u> ,	X ⁵⁴ is <u>Q</u> , H, or E;	X ⁵⁵ is <u>M</u> or L;
X ⁵⁶ is <u>N</u> , D, or E;	X ⁵⁷ is <u>S</u> or N;	X ⁵⁸ is <u>L</u>	X ⁵⁹ is <u>R</u> or T;	X ⁶⁰ is <u>A</u> , V, D, P, G, or T;
X ⁶¹ is <u>E</u> or D;	X ⁶² is <u>D</u> ,	X ⁶³ is <u>T</u> ,	X ⁶⁴ is <u>V</u> , I, T, R, M;	X ⁶⁵ is <u>A</u> ,
X ⁶⁶ is <u>Y</u> or F;	X ⁶⁷ is <u>Y</u> ,	X ⁶⁸ is <u>A</u> , G, T, G, or V	X ⁶⁹ is <u>C</u>	X ⁷⁰ is <u>R</u> , T, G, S, A, P, or K,
X ⁷¹ is <u>Y</u> , S, H, or L	X ⁷² is <u>W</u> ,	X ⁷³ is <u>G</u> ,	X ⁷⁴ is <u>Q</u> or R;	X ⁷⁵ is <u>G</u> ,
X ⁷⁶ is <u>T</u> , N, or A;	X ⁷⁷ is <u>L</u> or P;	X ⁷⁸ is <u>V</u> ,	X ⁷⁹ is <u>T</u> or --;	X ⁸⁰ is <u>V</u> or --; and
X ⁸¹ is <u>S</u> .				

provided that when X⁷⁹ is -, X⁸⁰ is - ("- means no residue or residues are present at the respective position).

2. H58 family subgenus

[0022] Preferably, the canine heavy chain variable domain according to the invention is a compound comprising the sequence:



wherein

Fr¹ is

EVQLVESGGDLVKPAGSLRLSCVTS SEQ ID NO: 6	EVQLMESGGDLVKPGGSLRLSCVAS SEQ ID NO: 7	EVQLVESGGDLVKPEGSLRLSCVVS SEQ ID NO: 8
EVQLVESGGDLVKPAGSLRLSCVAS SEQ ID NO: 9	EVQLVESGGDLVRPGGSLRLSCVAS SEQ ID NO: 10	EVQLVESGGXLVKFGGSLXLSCVAS SEQ ID NO: 11
EVHLVESGGDLVKPGGSLRLSCVAS SEQ ID NO: 12	EVQLVESGGDLVKPGGSLRLSCVAS SEQ ID NO: 13	EVQLVESGGDLVKPGGSLRLSCVGS SEQ ID NO: 14
EVQLVESGGDLVKPGGSLRLSCVTS SEQ ID NO: 15	EVQLVQSGGDLVKPSGSLRLSCVAS SEQ ID NO: 16	or EVQL- VESGGNLVKPGGSLRLSCVAS SEQ ID NO: 17;

Fr² is

WVRQAPGKGLQWVA SEQ ID NO: 18	WVRQAPGKGLQLVA SEQ ID NO: 19	WVRQSPGKGLQWVA SEQ ID NO: 20	WVRQAPEKGLQLVA SEQ ID NO: 21
WVREAPGKGLQWVA SEQ ID NO: 22	WVRRAPGKGLQWIA SEQ ID NO: 23	WVRHSPGKGLQWVA SEQ ID NO: 24	WVRQCPGKGLQWVT SEQ ID NO: 25

WVRQPPGKGLQWIV SEQ ID NO: 26	WVRQPPGKGPQWVA SEQ ID NO: 27	WVRQAPGKGLQYVA SEQ ID NO: 28	WVRQAPGKGLKWVA SEQ ID NO: 29
WVRQAPGEGLOWIG SEQ ID NO: 30	or	WVRQTPERGLELVA SEQ ID NO: 31;	

Fr³ is

RFTISRDNAKNTVYLQMNSLRAEDTAVYY- CAK SEQ ID NO: 32	RFTISRDNAKNTFYLMNSLRAEDSAMYY- CAA SEQ ID NO: 33
RFTISRDNAKNTLYLQMNSLRTEdTAVYY- CAR SEQ ID NO: 34	RFTISRDNAKNTVYLQMNSLRAEDTAMYY- CAP SEQ ID NO: 35
RFTISRDNAKNTVYLQMNSLRGEDTAMYY- CAK SEQ ID NO: 36	RFTISRDNAKNTLYLQMNSLRAEDTAVYY- CAK SEQ ID NO: 37
RFTISRDNAKNTLYLQLNSLRVEDTAVYY- CAR SEQ ID NO: 38	RFTISRDNARENTLYLQMNSLRPEDTAVYY- CAS SEQ ID NO: 39
RFTISRDNAKSTLYLEMNRLRPDXTA- MYCVT SEQ ID NO: 40	RFTISRDDANNTLYLQMNSLRAEDTAVYY- CAK SEQ ID NO: 41
RFTISRDNAKNTLYLQLNSLRAEDTAVYY- CAK SEQ ID NO: 42	RFTISRDNAKNTLSLEMNSLRDEDTAMYY- CAR SEQ ID NO: 43
RFTISRDSAKNTLYLQLNSLTAEDTARYY- CAG SEQ ID NO: 44	RFTISRDNAKNTLYLXMNSLRAED- TAVYYCGK SEQ ID NO: 45
RFTISRDNAKNTLYLQMNSLRAXDTAVYY- CAR SEQ ID NO: 46	RFTISRDNARNTVYLQMNSLRAEDTAVYY- CAK SEQ ID NO: 47
RFTISRDNAKNTLSLHMNSLRVED- TAVYFCTR SEQ ID NO: 48	RFTISRDNARNTLYLQMNSLRAED- TAVYFCAK SEQ ID NO: 49
RFTVSRDNASTLYLQMENLRAEDTAVYY- CAT SEQ ID NO: 50	RFTISRDNAKNTLFLQMHSRAEDTAIYY- CAR SEQ ID NO: 51
RFIISRDLAKSTVYLQMDNLRADDTATYY- CAR SEQ ID NO: 52	or RFTISRDNARNTVYLQLNSLRAED- TAVYYCGK SEQ ID NO: 53;

and

Fr⁴ is

HWGQGTLVTV SEQ ID NO: 54	LWGPGLTVTV SEQ ID NO: 55	YWGQGTLVTV SEQ ID NO: 56	SWGQGTLVTV SEQ ID NO: 57	YWGQGTLVT SEQ ID NO: 58
LWGQGTLVT SEQ ID NO: 59	LWGQGTLTV SEQ ID NO: 60	HWGQGTLVT SEQ ID NO: 61	YWGQGTLV SEQ ID NO: 62	YWGQGTPVTV SEQ ID NO: 63
GWGQGTLVTV SEQ ID NO:	HWGQGTLV SEQ ID NO:	YWGPGTLVTV SEQ ID NO:	YWGQGNLTVTV SEQ ID NO:	or SWGRGALVTV

64	65	66	67	SEQ ID NO: 68.
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3. H58 family species

[0023] In a more preferred embodiment, the chimeric heavy chain variable region according to the invention is a compound comprising the sequence:



wherein Fr^1 , Fr^2 , Fr^3 , and Fr^4 are selected from the following combinations:

#	Fr^1	Fr^2	Fr^3	Fr^4
H3	EVQL- VESGGDLVKPAGSLRLSCVTS SEQ ID NO: 6	WVRQAPGKGLQWVA SEQ ID NO: 18	RFTISRDNKNTVYLQMNSLRAEDTAVYY- CAK SEQ ID NO: 32	HWGQGTLLTV SEQ ID NO: 54;
H4	EVQL- MESGGDLVKPGGSLRLSCVAS SEQ ID NO: 7	WVRQAPGKGLQWVA SEQ ID NO: 18	RFTISRDNKNTFYLMNSLRAEDSAMY- CAA SEQ ID NO: 33	LWGPGLTVTV SEQ ID NO: 55;
H53	EVQL- VESGGDLVKPEGSLRLSCVVS SEQ ID NO: 8	WVRQAPGKGLQWVA SEQ ID NO: 18	RFTISRDNKNTLYLMNSLRTEDEAVYY- CAR SEQ ID NO: 34	YWGQGTLLTV SEQ ID NO: 56;
H67	EVQL- VESGGDLVKPAGSLRLSCVAS SEQ ID NO: 9	WVRQAPGKGLQLVA SEQ ID NO: 19	RFTISRDNKNTVYLQMNSLRAEDTAMY- CAP SEQ ID NO: 35	SWGQGTLLTV SEQ ID NO: 57;
H51	EVQL- VESGGDLVKPAGSLRLSCVAS SEQ ID NO: 9	WVRQAPGKGLQLVA SEQ ID NO: 19	RFTISRDNKNTVYLQMNSLRGEDTAMY- CAK SEQ ID NO: 36	YWGQGTLLTV SEQ ID NO: 58;
H7	EVQL- VESGGDLVRPGGSLRLSCVAS SEQ ID NO: 10	WVRQSPGKGLQWVA SEQ ID NO: 20	RFTISRDNKNTLYLMNSLRAEDTAVYY- CAK SEQ ID NO: 37	YWGQGTLLTV SEQ ID NO: 56;
H40 4	EVQL- VESGGXLVKFGGSLXLSCVAS SEQ ID NO: 11	WVRQAPGKGLQLVA SEQ ID NO: 21	RFTISRDNKNTLYLQNSLRVEDTAVYY- CAR SEQ ID NO: 38	LWGQGTLLTV SEQ ID NO: 59;
H44 5	EVHL- VESGGDLVKPGGSLRLSCVAS SEQ ID NO: 12	WVREAPGKGLQWVA SEQ ID NO: 22	RFTISRDNKNTLYLMNSLRPEDTAVYY- CAS SEQ ID NO: 39	LWGQGTLLTV SEQ ID NO: 60;
H42 2	EVQL- VESGGDLVKPGGSLRLSCVAS SEQ ID NO: 13	WVRRAPGKGLQWIA SEQ ID NO: 23	RFTISRDNKNTLYLMNSLRPDXTA- MYICVT SEQ ID NO: 40	HWGQGTLLTV SEQ ID NO: 54;
H44 2	EVQL- VESGGDLVKPGGSLRLSCVAS SEQ ID NO: 13	WVRRAPGKGLQWIA SEQ ID NO: 23	RFTISRDNKNTLYLMNSLRPDXTA- MYICVT SEQ ID NO: 40	HWGQGTLLTV SEQ ID NO: 61;
H2	EVQL- VESGGDLVKPGGSLRLSCVAS SEQ ID NO: 13	WVRHSPGKGLQWVA SEQ ID NO: 24	RFTISRDNKNTLYLMNSLRAEDTAVYY- CAK SEQ ID NO: 41	YWGQGTLLTV SEQ ID NO: 62;
H60 2	EVQL- VESGGDLVKPGGSLRLSCVAS SEQ ID NO: 13	WVRQCPGKGLQWVT SEQ ID NO: 42	RFTISRDNKNTLYLQNSLRAEDTAVYY- CAK SEQ ID NO: 42	YWGQGTLLTV SEQ ID NO

#	Fr ¹	Fr ²	Fr ³	Fr ⁴
		25		63:
H39 6	EVQL- VESGGDLVKPGGSLRLSCVGS SEQ ID NO: 14	WVRQPPGKGLQWIV SEQ ID NO: 26	RFTISRDNKNTLSLEMNSLRDEDTAMYY- CAR SEQ ID NO: 43	YWGQGLTVT SEQ ID NO: 58;
H5	EVQL- VESGGDLVKPGGSLRLSCVAS SEQ ID NO: 13	WVRQPPGKGPQWVA SEQ ID NO: 27	RFTISRDSKNTLYLQNLSTAEDTARYY- CAG SEQ ID NO: 44	YWGQGLTVTV SEQ ID NO: 56;
H57 4	EVQL- VESGGDLVKPGGSLRLSCVAS SEQ ID NO: 13	WVRQAPGKGLQYVA SEQ ID NO: 28	RFTISRDNKNTLYLXMNSLRAED- TAVYYCGK SEQ ID NO: 45	SWGQGLTVTV SEQ ID NO: 57;
H37 8	EVQL- VESGGDLVKPGGSLRLSCVTS SEQ ID NO: 15	WVRQAPGKGLQWVA SEQ ID NO: 18	RFTISRDNKNTLYLQMNSLRAXDTAVYY- CAR SEQ ID NO: 46	GWGQGLTVTV SEQ ID NO: 64;
H8	EVQL- VESGGDLVKPGGSLRLSCVAS SEQ ID NO: 13	WVRQAPGKGLQWVA SEQ ID NO: 18	RFTISRDNARNTVYLQMNSLRAEDTAVYY- CAK SEQ ID NO: 47	YWGQGLTVTV SEQ ID NO: 56;
H59 2	EVQL- VESGGDLVKPGGSLRLSCVGS SEQ ID NO: 14	WVRQAPGKGLQWVA SEQ ID NO: 18	RFTISRDNKNTLSLHMNSLRVED- TAVYFCTR SEQ ID NO: 48	HWGQGLTV SEQ ID NO: 65;
H9	EVQL- VESGGDLVKPGGSLRLSCVAS SEQ ID NO: 13	WVRQAPGKGLQWVA SEQ ID NO: 18	RFTISRDNARNTLYLQMNSLRAED- TAVYFCAK SEQ ID NO: 49	YWGPGTLTVTV SEQ ID NO: 66;
H55	EVQL- VESGGDLVKPGGSLRLSCVAS SEQ ID NO: 13	WVRQAPGKGLKWVA SEQ ID NO: 29	RFTVSRDNKSTLYLQMENLRAEDTAVYY- CAT SEQ ID NO: 50	YWGQGLTVTV SEQ ID NO: 56;
H58 5	EVQL- VESGGDLVKPGGSLRLSCVGS SEQ ID NO: 14	WVRQAPGEGGLQWIG SEQ ID NO: 30	RFTISRDNKNTLFLQMHSRAEDTAIYY- CAR SEQ ID NO: 51	YWGQGNLTVTV SEQ ID NO: 67;
H56	EVQLVQSGGDLVKPSGSLRLSCVA S SEQ ID NO: 16	WVRQTPERGLELVA SEQ ID NO: 31	RFIISRDLAKSTVYLQMDNLRADDTATYY- CAR SEQ ID NO: 52	SWGRGALTVTV SEQ ID NO: 68;
H58	EVQL- VESGGNLVKPGGSLRLSCVAS SEQ ID NO: 17	WVRQAPGKGLQWVA SEQ ID NO: 18	RFTISRDNARNTVYLQNLRAED- TAVYYCGK SEQ ID NO: 53	YWGQGLTVTV SEQ ID NO: 56.

4. H74 Heavy Chain Variable Domain Genus

[0024] The canine group H74 heavy chain variable domain polypeptides according to the invention are compounds comprising the sequence:

$$\text{Fr}^1\text{-CDR}^1\text{-Fr}^2\text{-CDR}^2\text{-Fr}^3\text{-CDR}^3\text{-Fr}^4$$

wherein

Fr¹ is X¹ X² X³ X⁴ X⁵ X⁶ X⁷ X⁸ X⁹ X¹⁰ X¹¹ X¹² X¹³ X¹⁴ X¹⁵ X¹⁶
X¹⁷ X¹⁸ X¹⁹ X²⁰ X²¹ X²² X²³ X²⁴ X²⁵ (SEQ ID NO: 69);

Fr² is X²⁶ X²⁷ X²⁸ X²⁹ X³⁰ X³¹ X³² X³³ X³⁴ X³⁵ X³⁶ X³⁷ X³⁸ X³⁹ X⁴⁰
(SEQ ID NO: 70)

Fr³ is X⁴¹ X⁴² X⁴³ X⁴⁴ X⁴⁵ X⁴⁶ X⁴⁷ X⁴⁸ X⁴⁹ X⁵⁰ X⁵¹ X⁵² X⁵³ X⁵⁴ X⁵⁵
X⁵⁶ X⁵⁷ X⁵⁸ X⁵⁹ X⁶⁰ X⁶¹ X⁶² X⁶³ X⁶⁴ X⁶⁵ X⁶⁶ X⁶⁷ X⁶⁸ X⁶⁹ X⁷⁰ X⁷¹
X⁷² (SEQ ID NO: 71), and
Fr⁴ is X⁷³ X⁷⁴ X⁷⁵ X⁷⁶ X⁷⁷ X⁷⁸ X⁷⁹ X⁸⁰ X⁸¹ X⁸² (SEQ ID NO: 72),
wherein

X ¹ is <u>E</u> ,	X ² is <u>V</u> ,	X ³ is <u>Q</u> ;	X ⁴ is <u>L</u> ,	X ⁵ is <u>V</u> ;
X ⁶ is <u>Q</u> ;	X ⁷ is <u>S</u> ,	X ⁸ is <u>A</u> ,	X ⁹ is <u>A</u> ,	X ¹⁰ is <u>E</u> ;
X ¹¹ is <u>V</u> ,	X ¹² is <u>K</u> ,	X ¹³ is <u>K</u> ,	X ¹⁴ is <u>P</u> ,	X ¹⁵ is <u>G</u> ,
X ¹⁶ is <u>A</u> ,	X ¹⁷ is <u>S</u> ,	X ¹⁸ is <u>V</u> ,	X ¹⁹ is <u>K</u> ,	X ²⁰ is <u>V</u>
X ²¹ is <u>S</u> ,	X ²² is <u>C</u> ,	X ²³ is <u>K</u> ,	X ²⁴ is <u>T</u> ,	X ²⁵ is <u>S</u> ,
X ²⁶ is <u>W</u> ,	X ²⁷ is <u>V</u> ,	X ²⁸ is <u>Q</u> ,	X ²⁹ is <u>Q</u> ,	X ³⁰ is <u>A</u> ,
X ³¹ is <u>P</u> ;	X ³² is <u>G</u> ,	X ³³ is <u>A</u> ,	X ³⁴ is <u>G</u> ,	X ³⁵ is <u>L</u> ,
X ³⁶ is <u>D</u> or E,	X ³⁷ is <u>W</u> ,	X ³⁸ is <u>M</u> ,	X ³⁹ is <u>G</u> ,	X ⁴⁰ is <u>W</u> ,
X ⁴¹ is <u>R</u> ,	X ⁴² is <u>V</u> ,	X ⁴³ is <u>T</u> ,	X ⁴⁴ is <u>L</u> ,	X ⁴⁵ is <u>T</u> ,
X ⁴⁶ is <u>A</u> ,	X ⁴⁷ is <u>D</u> ,	X ⁴⁸ is <u>T</u> ,	X ⁴⁹ is <u>S</u> ,	X ⁵⁰ is <u>T</u> ,
X ⁵¹ is <u>S</u> or N,	X ⁵² is <u>T</u> ,	X ⁵³ is <u>A</u> or V,	X ⁵⁴ is <u>Y</u> ,	X ⁵⁵ is <u>M</u> ,
X ⁵⁶ is <u>E</u> ,	X ⁵⁷ is <u>L</u> ,	X ⁵⁸ is <u>S</u>	X ⁵⁹ is <u>S</u> or N,	X ⁶⁰ is <u>L</u> ,
X ⁶¹ is <u>R</u> ,	X ⁶² is <u>A</u> or T,	X ⁶³ is <u>E</u> ,	X ⁶⁴ is <u>D</u> ,	X ⁶⁵ is <u>T</u> or A,
X ⁶⁶ is <u>A</u> ,	X ⁶⁷ is <u>V</u> ,	X ⁶⁸ is <u>Y</u> ,	X ⁶⁹ is <u>Y</u> ,	X ⁷⁰ is <u>C</u> ,
X ⁷¹ is <u>A</u> ,	X ⁷² is <u>R</u> or <u>S</u> ,	X ⁷³ is <u>Y</u> or L,	X ⁷⁴ is <u>W</u> ;	X ⁷⁵ is <u>G</u> ,
X ⁷⁶ is <u>Q</u> ,	X ⁷⁷ is <u>G</u> ,	X ⁷⁸ is <u>T</u> ,	X ⁷⁹ is <u>L</u> ,	X ⁸⁰ is <u>V</u> ,
X ⁸¹ is <u>T</u> , and	X ⁸² is <u>V</u> .			

5. H74 Heavy Chain Variable Domain Subgenus

[0025] Preferably, the canine heavy chain variable domain according to the invention is a compound comprising the sequence:



wherein

Fr¹ is EVQLVQSAAEVKKPGASVKVSCCKTS (SEQ ID NO: 73),

Fr² is WVQQAPGAGLDWMGW (SEQ ID NO: 74) or WVQQAPGAGLEWMGW (SEQ ID NO: 75),

Fr³ is RVTLTADTSTSTAYMELSSLRAEDTAVYYCAS (SEQ ID NO: 76),

RVTLTADTSTNTVYMELSNLRTEDTAVYYCAR (SEQ ID NO: 77), or

RVTLTADTSTSTAYMELSSLRAEDAAVYYCAS (SEQ ID NO: 78), and

Fr⁴ is YWGQGTLLTV (SEQ ID NO: 56) or LWGQGTLLTV (SEQ ID NO: 79).

6. H74 Heavy Chain Variable Domain Species

[0026] In a more preferred embodiment, the chimeric heavy chain variable region according to the invention is a compound comprising the sequence:



wherein Fr^1 , Fr^2 , Fr^3 , and Fr^4 are selected from the following combinations:

#	Fr^1	Fr^2	Fr^3	Fr^4
H39 2	EVQL- VQSAAEVKKPGASVKVSCCKTS SEQ ID NO: 73	WVQQAPGAGLDWMGW SEQ ID NO: 74	RVTLTADTSTSTAYMELSSLRAEDTAVYYCAS SEQ ID NO: 76	YWGQGTLLVT V SEQ ID NO: 56
H76	EVQL- VQSAAEVKKPGASVKVSCCKTS SEQ ID NO: 73	WVQQAPGAGLDWMGW SEQ ID NO: 74	RVTLTADTSTSTAYMELSSLRAEDTAVYYCAR SEQ ID NO: 80	YWGQGTLLVT V SEQ ID NO: 56
H64 5	EVQL- VQSAAEVKKPGASVKVSCCKTS SEQ ID NO: 73	WVQQAPGAGLEWMGW SEQ ID NO: 75	RVTLTADTSTNTVYMELSNLRTEDTAVYYCAR SEQ ID NO: 77	YWGQGTLLVT V SEQ ID NO: 56
Or				
H74	EVQL- VQSAAEVKKPGASVKVSCCKTS SEQ ID NO: 73	WVQQAPGAGLDWMGW SEQ ID NO: 74	RVTLTADTSTSTAYMELSSLRAEDAAVYYCAS SEQ ID NO: 78	LWGQGTLLVT V SEQ ID NO: 79

7. H103 Heavy Chain Variable Domain Genus

[0027] A canine heavy chain variable domain polypeptide comprising the sequence:



wherein

Fr^1 is $X^1 X^2 X^3 X^4 X^5 X^6 X^7 X^8 X^9 X^{10} X^{11} X^{12} X^{13} X^{14} X^{15} X^{16} X^{17} X^{18} X^{19} X^{20} X^{21} X^{22} X^{23} X^{24} X^{25}$ (SEQ ID NO: 81)

Fr^2 is $X^{26} X^{27} X^{28} X^{29} X^{30} X^{31} X^{32} X^{33} X^{34} X^{35} X^{36} X^{37} X^{38} X^{39}$ (SEQ ID NO: 82);

Fr^3 is $X^{40} X^{41} X^{42} X^{43} X^{44} X^{45} X^{46} X^{47} X^{48} X^{49} X^{50} X^{51} X^{52} X^{53} X^{54} X^{55} X^{56} X^{57} X^{58} X^{59} X^{60} X^{61} X^{62} X^{63} X^{64} X^{65} X^{66} X^{67} X^{68} X^{69}$ (SEQ ID NO: 83);

Fr^4 is $X^{70} X^{71} X^{72} X^{73} X^{74} X^{75} X^{76} X^{77} X^{78} X^{79}$ (SEQ ID NO: 84);

X^1 is <u>E</u> ,	X^2 is <u>V</u> or L,	X^3 is <u>I</u> or T,	X^4 is <u>L</u> ,	X^5 is <u>Q</u> ,
X^6 is <u>E</u> ,	X^7 is <u>S</u> or A,	X^8 is <u>G</u> ,	X^9 is <u>P</u> ,	X^{10} is <u>G</u> ,
X^{11} is <u>L</u> ,	X^{12} is <u>V</u> ,	X^{13} is <u>K</u> ,	X^{14} is <u>P</u> ,	X^{15} is <u>S</u> ,
X^{16} is <u>Q</u> or E,	X^{17} is <u>T</u> ,	X^{18} is <u>L</u> ,	X^{19} is <u>S</u> ,	X^{20} is <u>L</u>
X^{21} is <u>T</u> ,	X^{22} is <u>C</u> ,	X^{23} is <u>T</u> or L,	X^{24} is <u>X</u> or V,	X^{25} is <u>S</u> ,
X^{26} is <u>W</u> ,	X^{27} is <u>I</u> ,	X^{28} is <u>R</u> ,	X^{29} is <u>Q</u> or R,	X^{30} is <u>R</u> ,
X^{31} is <u>P</u> ,	X^{32} is <u>D</u> or G,	X^{33} is <u>R</u> or G,	X^{34} is <u>G</u> or E,	X^{35} is <u>L</u> ,

X ³⁶ is <u>E</u> ,	X ³⁷ is <u>W</u> ,	X ³⁸ is <u>M</u> ,	X ³⁹ is <u>G</u> ,	X ⁴⁰ is <u>S</u> ,
X ⁴¹ is <u>I</u> ,	X ⁴² is <u>T</u> ,	X ⁴³ is <u>A</u> or T,	X ⁴⁴ is <u>D</u> ,	X ⁴⁵ is <u>G</u> or T,
X ⁴⁶ is <u>T</u> or A,	X ⁴⁷ is <u>K</u> or T,	X ⁴⁸ is <u>N</u> ,	X ⁴⁹ is <u>H</u> or Q,	X ⁵⁰ is <u>L</u> or F,
X ⁵¹ is <u>S</u> or F,	X ⁵² is <u>L</u> ,	X ⁵³ is <u>Q</u> ,	X ⁵⁴ is <u>L</u> ,	X ⁵⁵ is <u>T</u> ,
X ⁵⁶ is <u>S</u> ,	X ⁵⁷ is <u>T</u> or V,	X ⁵⁸ is <u>T</u> ,	X ⁵⁹ is <u>T</u> ,	X ⁶⁰ is <u>E</u> ,
X ⁶¹ is <u>D</u> ,	X ⁶² is <u>T</u> ,	X ⁶³ is <u>A</u> ,	X ⁶⁴ is <u>V</u> ,	X ⁶⁵ is <u>Y</u> ,
X ⁶⁶ is <u>Y</u> or F,	X ⁶⁷ is <u>C</u> ,	X ⁶⁸ is <u>T</u> or I,	X ⁶⁹ is <u>R</u> ,	X ⁷⁰ is <u>V</u> or F,
X ⁷¹ is <u>W</u> ,	X ⁷² is <u>G</u> ,	X ⁷³ is <u>Q</u> ,	X ⁷⁴ is <u>G</u> ,	X ⁷⁵ is <u>T</u> ,
X ⁷⁶ is <u>L</u> ,	X ⁷⁷ is <u>V</u> ,	X ⁷⁸ is <u>T</u> , and	X ⁷⁹ is <u>V</u> ,	

8. H103 Heavy Chain Variable Domain Sub-genus

[0028] In another embodiment, the invention comprises a canine heavy chain variable domain polypeptide according to paragraph [0027] comprising the sequence:



wherein

Fr¹ is EVILQESGPGLVKPSQTLSTCTXS (SEQ ID NO: 85) or

ELTLQEAGPGLVKPSETLSLTCLVS (SEQ ID NO: 86);

Fr² is WIRQRPDRGLEWMG (SEQ ID NO: 87) or WIRRRPGGELEWMG (SEQ ID NO: 88);

Fr³ is SITADGTKNHLQLTSTTTEDTAVYYCTR (SEQ ID NO: 89) or

SITTDATNQFFLQLTSVTTEDTAVYFCIR (SEQ ID NO: 90); and

Fr⁴ is VWGQGTLLVTV (SEQ ID NO: 91) or FWGQGTLLVTV (SEQ ID NO: 92).

9. H103 Heavy Chain Variable Domain Species

[0029] In another embodiment, the invention comprises a canine heavy chain variable domain polypeptide according to paragraph [0027] comprising the sequence:



wherein

#	Fr ¹	Fr ²	Fr ³	Fr ⁴
H637	EVILQESGPGLVKPSQTLSTCTXS SEQ ID NO: 85	WIRQRPDRGLEWMG SEQ ID NO: 87	SITADGTKNHLQLTSTTTEDTAVYYCTR SEQ ID NO: 89	VWGQGTLLVTV SEQ ID NO: 91
H103	ELTLQEAGPGLVKPSETLSLTCLVS SEQ ID NO: 86	WIRRRPGGELEWMG SEQ ID NO: 88	SITTDATNQFFLQLTSVTTEDTAVYFCIR SEQ ID NO: 90	FWGQGTLLVTV SEQ ID NO: 92

10. Other Heavy Chain Variable Domains

[0030] In another embodiment, the invention comprises the sequence:



wherein Fr^1 , Fr^2 , Fr^3 , and Fr^4 are framework regions selected from the framework regions of the heavy chain variable sequences displayed in Table N_{Other H}. The framework sequences of the polypeptides in Table N_{Other H} are readily and routinely determinable by those of ordinary skill in the art as those sequences that align with corresponding framework sequences of any of the known human variable domain sequences using any of the many accepted and widely available sequence alignment programs.

11. Group 2 λ Light Chain Variable Domain Genus

[0031] The chimeric canine light chain variable domain polypeptides according to the invention are compounds comprising the sequence:



wherein

Fr^1 is $\text{Y}^1 \text{ Y}^2 \text{ Y}^3 \text{ Y}^4 \text{ Y}^5 \text{ Y}^6 \text{ Y}^7 \text{ Y}^8 \text{ Y}^9 \text{ Y}^{10} \text{ Y}^{11} \text{ Y}^{12} \text{ Y}^{13} \text{ Y}^{14} \text{ Y}^{15} \text{ Y}^{16} \text{ Y}^{17} \text{ Y}^{18} \text{ Y}^{19} \text{ Y}^{20} \text{ Y}^{21} \text{ Y}^{22} \text{ Y}^{23} \text{ Y}^{24} \text{ Y}^{25}$ (SEQ ID NO: 1136);

Fr^2 is $\text{Y}^{26} \text{ Y}^{27} \text{ Y}^{28} \text{ Y}^{29} \text{ Y}^{30} \text{ Y}^{31} \text{ Y}^{32} \text{ Y}^{33} \text{ Y}^{34} \text{ Y}^{35} \text{ Y}^{36} \text{ Y}^{37} \text{ Y}^{38} \text{ Y}^{39} \text{ Y}^{40}$ (SEQ ID NO: 1137);

Fr^3 is $\text{Y}^{41} \text{ Y}^{42} \text{ Y}^{43} \text{ Y}^{44} \text{ Y}^{45} \text{ Y}^{46} \text{ Y}^{47} \text{ Y}^{48} \text{ Y}^{49} \text{ Y}^{50} \text{ Y}^{51} \text{ Y}^{52} \text{ Y}^{53} \text{ Y}^{54} \text{ Y}^{55} \text{ Y}^{56} \text{ Y}^{57} \text{ Y}^{58} \text{ Y}^{59} \text{ Y}^{60} \text{ Y}^{61} \text{ Y}^{62} \text{ Y}^{63} \text{ Y}^{64} \text{ Y}^{65} \text{ Y}^{66} \text{ Y}^{67} \text{ Y}^{68} \text{ Y}^{69} \text{ Y}^{70} \text{ Y}^{71} \text{ Y}^{72}$ (SEQ ID NO: 1138);

Fr^4 is $\text{Y}^{73} \text{ Y}^{74} \text{ Y}^{75} \text{ Y}^{76} \text{ Y}^{77} \text{ Y}^{78} \text{ Y}^{79} \text{ Y}^{80} \text{ Y}^{81} \text{ Y}^{82} \text{ Y}^{83} \text{ Y}^{84} \text{ Y}^{85} \text{ Y}^{86}$ (SEQ ID NO: 1);

Y^1 is <u>S</u> , or --	Y^2 is <u>W</u> or --,	Y^3 is <u>A</u> or --,	Y^4 is <u>Q</u> or --,
Y^5 is <u>S</u> A, or --	Y^6 is <u>V</u> , L, A, N, C, M, or --	Y^7 is <u>L</u> , V, or --	Y^8 is <u>T</u> , N, or --
Y^9 is <u>Q</u> or --,	Y^{10} is <u>P</u> , A, S, or --	Y^{11} is <u>A</u> , P, T, S, or --	Y^{12} is <u>S</u> , A, or --
Y^{13} is <u>V</u> , M, or --	Y^{14} is <u>S</u> , T or --	Y^{15} is <u>G</u> , or --	Y^{16} is <u>S</u> , A, P, F, or --
Y^{17} is <u>L</u> , or --	Y^{18} is <u>G</u> or --,	Y^{19} is <u>Q</u> or --,	Y^{20} is <u>R</u> , K, T, S, E, or --
Y^{21} is <u>V</u> , I, or --	Y^{22} is <u>T</u> , S, or --	Y^{23} is <u>I</u> , L, V, or --	Y^{24} is <u>S</u> , or --
Y^{25} is <u>C</u> , or --,	Y^{26} is <u>W</u> ,	Y^{27} is <u>Y</u> , F, H, or C,	Y^{28} is <u>Q</u> or R,
Y^{29} is <u>Q</u> , E, N, L, or H,	Y^{30} is <u>L</u> , F, V, I, or Y,	Y^{31} is <u>P</u> ,	Y^{32} is <u>G</u> , or E,
Y^{33} is <u>T</u> , K, R, A, I, or E,	Y^{34} is <u>G</u> , S, A, or R,	Y^{35} is <u>P</u> ,	Y^{36} is <u>R</u> , K, T, or E,
Y^{37} is <u>T</u> , L, S, N, or I,	Y^{38} is <u>L</u> , V, I, or F,	Y^{39} is <u>I</u> , L, V, or M,	Y^{40} is <u>Y</u> , F, N, D, H, or S
Y^{41} is <u>G</u> , R, or E,	Y^{42} is <u>V</u> , I, or A,	Y^{43} is <u>P</u> or S,	Y^{44} is <u>D</u> , A, N, or E,
Y^{45} is <u>R</u> ,	Y^{46} is <u>F</u> ,	Y^{47} is <u>S</u> ,	Y^{48} is <u>G</u> , A, or V,
Y^{49} is <u>S</u> ,	Y^{50} is <u>R</u> , K T, N, S, I, or E,	Y^{51} is <u>S</u> ,	Y^{52} is <u>G</u> , D, or R,
Y^{53} is <u>S</u> , N, A, R, I, T, or F,	Y^{54} is <u>T</u> , S, or A,	Y^{55} is <u>A</u> , G, or S,	Y^{56} is <u>T</u> , S, A, or I,

Y ⁵⁷ is <u>L</u> ,	Y ⁵⁸ is <u>T</u> ,	Y ⁵⁹ is <u>I</u> ,	Y ⁶⁰ is <u>S</u> , T, or A,
Y ⁶¹ is <u>G</u> , V, or E,	Y ⁶² is <u>L</u> ,	Y ⁶³ is <u>Q</u> , R, or L,	Y ⁶⁴ is <u>A</u> , or P,
Y ⁶⁵ is <u>E</u> or D,	Y ⁶⁶ is <u>D</u> ,	Y ⁶⁷ is <u>E</u> ,	Y ⁶⁸ is <u>A</u> or G,
Y ⁶⁹ is <u>D</u> , E, I, or A,	Y ⁷⁰ is <u>Y</u> or --,	Y ⁷¹ is <u>Y</u> , F, or H,	Y ⁷² is <u>C</u>
Y ⁷³ is <u>F</u>	Y ⁷⁴ is <u>G</u> or --,	Y ⁷⁵ is <u>G</u> , S, P, or --,	Y ⁷⁶ is <u>G</u> or --,
Y ⁷⁷ is <u>T</u> , A, or --,	Y ⁷⁸ is <u>H</u> , Q, L, Y, R, or --,	Y ⁷⁹ is <u>L</u> or --,	Y ⁸⁰ is <u>T</u> , A, or --,
Y ⁸¹ is <u>V</u> or --,	Y ⁸² is <u>L</u> or --,	Y ⁸³ is <u>G</u> , S, or --,	Y ⁸⁴ is <u>Q</u> or --,
Y ⁸⁵ is <u>P</u> , and	Y ⁸⁶ is <u>K</u> , or R		

provided that when Y^k for k ≤ 40 is --, Y^l for l < k is --, and when Yⁿ for n ≥ 69 is --, Y^m for m > n is --.

12. Group 2 λ Light Chain Variable Domain Subgenus

[0032] Preferably, the canine λ light chain variable domain according to the invention is a compound comprising the sequence:



wherein

Fr¹ is

SWAQSLLTQPASVSGSLGQRTV LSC SEQ ID NO: 93	SWAQSVLTQPASVSGSLGQRTV ISC SEQ ID NO: 94	CLTQPASVSGSLGQRTVISC SEQ ID NO: 95
SWAQSVLTQPASVSGSLGQRI- TISC SEQ ID NO: 96	SWAQSAITQPASVTGSLGQRTV ISC SEQ ID NO: 97	SWAQSVLTQPASVSGSLGQRTV ISC SEQ ID NO: 98
SWAQSLLTQPASVSGSLGQRTV ISC SEQ ID NO: 99	SWAQSVLTQPASVSGSLGQKVT ISC SEQ ID NO: 100	SWAQSVLTQPASVTGSLGQRTV ISC SEQ ID NO: 101
SWAQAVLNQPASVSGAL- GQKVTISC SEQ ID NO: 102	SWAQSILTQPASVSGSLGQKVT ISC SEQ ID NO: 103	SWAQSVLTQPASMSGSLGQKVT ISC SEQ ID NO: 104
SWAQSAITQPASVSGSLGQRTV ISC SEQ ID NO: 105	SWAQSVLTQPASVSGFLGQRTV ISC SEQ ID NO: 106	SWAQSVLTQPASVSGSLGQRTV VSC SEQ ID NO: 107
SWAQSLLTQPASVSGSLGQKVT ISC SEQ ID NO: 108	SWAQSMILTQPASVSGSLGQRTV ISC SEQ ID NO: 109	SWAQSVLTQPASVSGSLGQRTV ISC SEQ ID NO: 110
SWAQSVLTQPASVSGPLGQKVT ISC SEQ ID NO: 111	SWAQSMILTQPASVSGSLGQKVT ISC SEQ ID NO: 112	SWAQSVXTQPASVSGSLGQRTV TSC SEQ ID NO: 113
SWAQSVLTQPASVSGSLGQRTV VSC SEQ ID NO: 114	SWAQSVLTQPASVSGSLGQSVT ISC SEQ ID NO: 115	SWAQSVLTQPASVSGPLGQRTV ISC SEQ ID NO: 116
SLGQRTVISC SEQ ID NO: 117	VTISC SEQ ID NO: 118	SWAQSELTQSAAVSGSLGQEV- TISC SEQ ID NO: 119
SWAQSIIVTQAASVSGSLGQRI- TISC SEQ ID NO: 120	SWAQSILTQPSSVSGSLGQRTV ISC SEQ ID NO: 121	or-;

Fr² is

WYQHLPGTGPRTL IY SEQ ID NO: 122	WY- QQIPGTGPRTVIY SEQ ID NO: 123	WYQQFPGAG- PRTLIIY SEQ ID NO: 124	WYQQLPGRSPKLL VY SEQ ID NO: 125
WYQQLPGRGPRTV IY SEQ ID NO: 126	WFQQVPGTGPRTV IY SEQ ID NO: 127	WYQQLPGTRPRT LIY SEQ ID NO: 128	WFQQLPKGKGPRTV IY SEQ ID NO: 129
WFQELPGTGPKIL IY SEQ ID NO: 130	WYQQLPGTGPRTL IY SEQ ID NO: 131	WFQQFPGKGPKT VIY SEQ ID NO: 132	WYQQLPGTGPKTL IY SEQ ID NO: 133
WYQQLPKGKAPKLL VD SEQ ID NO: 134	WYQQLPGIGPKTV IY SEQ ID NO: 135	WFQQFPGEGPRT VIY SEQ ID NO: 136	WYRQLPGTGPTTL IY SEQ ID NO: 137
WYQQFPGTGPRIL IY SEQ ID NO: 138	WYQQLPKGKAPKLL LN SEQ ID NO: 139	WLQQLPGTGPKT VIY SEQ ID NO: 140	WFQQLPGTGPRTV IY SEQ ID NO: 141
WHQQVPETGPRNI IY SEQ ID NO: 142	WYQQLPGRGPRTL LY SEQ ID NO: 143	WYQQLPGIGPRT VIY SEQ ID NO: 144	WYQQVPGTRPRTL IY SEQ ID NO: 145
WYQQFPGRGPRSV IY SEQ ID NO: 146	WYQQLPKGKAPKLL VY SEQ ID NO: 147	WYQNLPGKGPKT VIF SEQ ID NO: 148	WY- QQIPGTGPRTLIIY SEQ ID NO: 149
WY- QQYPGTGPKTLIIY SEQ ID NO: 150	WYQQVPGTGPRTL IH SEQ ID NO: 151	WYRQFPGKAPEL LIY SEQ ID NO: 152	WYQQLPGIGPRTV IS SEQ ID NO: 153
WFQQFPGTGPRTV IY SEQ ID NO: 154	WHQQLPGTGPRTL IY SEQ ID NO: 155	WYQQLPETGPRT LIY SEQ ID NO: 156	WYQQVPGTGPRTL IY SEQ ID NO: 157
WYQQVPGIGPRTV MY SEQ ID NO: 158	WFQHLPGTRPKSL IY SEQ ID NO: 159	WFQQLPGTGPRT VIC SEQ ID NO: 160	WYQLVPGTGPRTL IY SEQ ID NO: 161
WYQQLPGRGPRTV IH SEQ ID NO: 162	WCQQLPKGKAPKLL VD SEQ ID NO: 163	WYQQFPGTGPRT LIY SEQ ID NO: 164	or
WYRQLPGEAPKLL LY SEQ ID NO: 165;			

Fr³ is

GVPDRFSGSRSGITATLTIS- GLQAEDEADYYC SEQ ID NO: 166	GVPDRFSGPRSGITSTLTISGLRAEDEG- DYYC SEQ ID NO: 167
GVPDRFSGSTSGSTATLTISGLRAEDEAD YYC SEQ ID NO: 168	GVPDRFSGSKSDNSATLTFTGLQAEDEADY YC SEQ ID NO: 169
GVPDRFSGSKSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 170	GVPDRFSGSRSGSTATLTIS- GLQAEDEAEYYC SEQ ID NO: 171
GVPDRFSGSKSRSTATLTIX- GLQAEDEADYXC SEQ ID NO: 172	GVPDRFSGSTSGNTATLTISGLQPEDET- DYYC SEQ ID NO: 173
GVPDRFSGSTSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 174	GVPDRFSGSRSGTTATLTIS- GLQAEDEADYYC SEQ ID NO: 175
GVPDRFSGSRSGSTATLTIS- GLQPEDEADYYC SEQ ID NO: 176	GVPDRFSGSSSGNSGTLTIT- GLQAEDEADYYC SEQ ID NO: 177
GVPDRFSGSKSGNSATLTIS- GLQPEDEAEYYC SEQ ID NO: 178	GVPDRFSGSKSGSTATLTISELQAEDEADY YC SEQ ID NO: 179
GVPNRFGSRSGSTATLTISGLQAD- DEADYYC SEQ ID NO: 180	GVPDRFSGSRSGYTAALTIS- GLQAEDEADYYC SEQ ID NO: 181
GVPDRFSGSNSGASATLTIT- GLQAEDEADYYC SEQ ID NO: 182	GVPDRFSGSRSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 183
GVPDRFSGSRSGSTATLTISGLLAED- DADYYC SEQ ID NO: 184	GVPDRFSGSKSGSTATLTISVLQAEDEADY YC SEQ ID NO: 185
GVPDRFSGSRSGRTATLTIS- GLQAEDEADYYC SEQ ID NO: 186	GISDRFSGSKSGNSASLTIS- GLQAEDEADYFC SEQ ID NO: 187
GVPDRFSVSKSGSSATLTIS- GLQAEDEAEYYC SEQ ID NO: 188	GVPDRFSGSNSGNSATLTIT- GLQAEDEADYYC SEQ ID NO: 189
GVPDRFSGSRSGSSATLTIS- GLQAEDEADYYC SEQ ID NO: 190	GVPDRFSASRSGNSATLTIS- GLQAEDEADYYC SEQ ID NO: 191
GVPDRFSASASGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 192	GVPGRFSGSISGNSATLTIT- GLQAEDEADYHC SEQ ID NO: 193
GVPDRFSGSKSGSSATLTIS- GLQAEDEAEYYC SEQ ID NO: 194	GVPDRFSGSRSGSTAILTIS- GLQAEDEAEYYC SEQ ID NO: 195
GVPDRFSGSKSGSAATLTIS- GLQAEDEADYYC SEQ ID NO: 196	GVPDRFSGSRSGSTATLTISGLQAD- DEADYYC SEQ ID NO: 197
GVPDRFSGSKSGSTAALTIS- GLQAEDEADYYC	GAPDRFSGSRSGSTATLTIS- GLQAEDEAEYYC

SEQ ID NO: 198	SEQ ID NO: 199
GVPDRFSSSRSGSSATLTIA- GLQAEDEAAYYC SEQ ID NO: 200	GVPDRFSGSKSGSTATLTISGLQAEDEAI- YYC SEQ ID NO: 201
RVPDRFSGSESGNSATLTIT- GLQAEDEADYYC SEQ ID NO: 202	GVPDRFSGSRSGRTATLTIS- GLQAEDEAEYYC SEQ ID NO: 203
GVPDRFSGSRSGSTATLTIS- GLQAEDEAEYYC SEQ ID NO: 204	GVPDRFSGSKSGTTAILTISGLQAD- DEADYFC SEQ ID NO: 205
GVPDRFSGSKSGSTATLTISGLQAD- DEADYYC SEQ ID NO: 206	GIPDRFSGSRSDNSGILTIS- GLQAEDEADYHC SEQ ID NO: 207
GVPARFSGSRSGNTATLTISGLLA- EADYYC SEQ ID NO: 208	EVSDRFSGSRSGNTATLTISGLXAEDEADY YC SEQ ID NO: 209
GVPDRFSGSNSGFSATLTITGLQAD- DEADYYC SEQ ID NO: 210	or GVPDRFSGSRSGTTGTLTIS- GLQAEDEADYYC SEQ ID NO: 211;

Fr⁴ is

FGGGTHLTVLGQP K SEQ ID NO: 212	FGGGTHLAVLGQP K SEQ ID NO: 213	FGSGTQLTVLGQP K SEQ ID NO: 214	F
FGGGTHLTVLSQP K SEQ ID NO: 215	FGGGTLLTVLGQP K SEQ ID NO: 216	FGGGTQLTVLGQP KA SEQ ID NO: 217	FGGGTH SEQ ID NO: 218
FGGGTHLTVLGQP SEQ ID NO: 219	FGGGTHLTVLGQP E SEQ ID NO: 220	FGSGTQLTVLGQP SEQ ID NO: 221	FGGGTHL SEQ ID NO: 222
FGSGTQLTVLSQP KA SEQ ID NO: 223	FGGGTYLTVVGQP KA SEQ ID NO: 224	FGGGTHLTVLGQ SEQ ID NO: 225	FGGGTHLTVLGQPR A SEQ ID NO: 226
FGSGTHLTAL- GQPKA SEQ ID NO: 227	FGSGTQLTVLGQP KA SEQ ID NO: 228	FGGGTHLTVLGQP KA SEQ ID NO: 229	FGGGTHLTVLSQPK A SEQ ID NO: 230
FGGGAHLTVLGQP KA SEQ ID NO: 231	FGPGTQLTVLGQP KA SEQ ID NO: 232	FGGGTRLTVLGQP KA SEQ ID NO: 233	or FGGGTHLTVLGQPK SEQ ID NO: 212.

13. Group 2 Light Chain Variable Domain Species

[0033] Preferably, the canine λ light chain variable domain according to the invention is a compound comprising the sequence:



wherein Fr^1 , Fr^2 , Fr^3 , and Fr^4 are selected from the following combinations:

#	Fr^1	Fr^2	Fr^3	Fr^4
λ_{101}	SWAQSLLTQPASVSGSLGQR VTISC SEQ ID NO: 93	WYQHLPGTGPRTLIY SEQ ID NO: 122	GVPDRFSGSRSGITATLTISGLQAEDEADYYC SEQ ID NO: 166	FGGGTHLTVLGQPK SEQ ID NO: 212
λ_{109}	SWAQSVLTQPASVSGSLGQT VTISC SEQ ID NO: 94	WYQQIPGTGPRTVIY SEQ ID NO: 123	GVPDRFSGSRSGITSTLTISGLRAEDEGDYYC SEQ ID NO: 167	FGGGTHLTVLGQPK SEQ ID NO: 212
λ_{111}	CLTQPASVSGSLGQRVTISC SEQ ID NO: 95	WYQQFPGAGPRTLIY SEQ ID NO: 124	GVPDRFSGSTSGSTATLTISGLRAEDEADYYC SEQ ID NO: 168	FGGGTHLAVLGQPK SEQ ID NO: 213
λ_{120}	--	WYQQLPGRSPKLLVY SEQ ID NO: 125	GVPDRFSGSKSDNSATLTFTGLQAEDEADYYC SEQ ID NO: 169	FGGGTHLTVLGQPK SEQ ID NO: 212
λ_{127}	SWAQSVLTQPASVSGSLGQR ITISC SEQ ID NO: 96	WYQQLPGRGPRTVIY SEQ ID NO: 126	GVPDRFSGSKSGSTATLTISGLQAEDEADYYC SEQ ID NO: 170	FGSGTQLTVLGQPK SEQ ID NO: 214
λ_{201}	SWAQSAITQPASVTGSLGQR VTISC SEQ ID NO: 97	WFQQVPGTGPRTVIY SEQ ID NO: 127	GVPDRFSGSRSGSTATLTISGLQAEDEAEYYC SEQ ID NO: 171	FGGGTHLTVLGQPK SEQ ID NO: 212
λ_{203}	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WYQQLPGTRPRTLIY SEQ ID NO: 128	GVPDRFSGSKSGSTATLTISGLQAEDEADYYC SEQ ID NO: 170	FGGGTHLTVLGQPK SEQ ID NO: 212
λ_{204}	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WFQQLPGKGPRTVIY SEQ ID NO: 129	GVPDRFSGSKSRSTATLTIXGLQAEDEADYYC SEQ ID NO: 172	F
λ_{207}	SWAQSLLTQPASVSGSLGQR VTISC SEQ ID NO: 99	WFQELPGTGPKILIY SEQ ID NO: 130	GVPDRFSGSTSGNTATLTISGLQPEDETDYYC SEQ ID NO: 173	FGGGTHLTVLGQPK SEQ ID NO: 212
λ_{215}	SWAQSVLTQPASVSGSLGQK VTISC SEQ ID NO: 100	WYQQLPGTGPRTLIY SEQ ID NO: 131	GVPDRFSGSTSGSTATLTISGLQAEDEADYYC SEQ ID NO: 174	FGGGTHLTVLGQPK SEQ ID NO: 212
λ_{220}	SWAQSVLTQPASVTGSLGQR VTISC SEQ ID NO: 101	WFQQFPGKGPRTVIY SEQ ID NO: 132	GVPDRFSGSRSGTTATLTISGLQAEDEADYYC SEQ ID NO: 175	FGGGTHLTVLGQPK SEQ ID NO: 212
λ_{225}	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WYQQLPGTGPKTLIY SEQ ID NO: 133	GVPDRFSGSRSGSTATLTISGLQPEDEADYYC SEQ ID NO: 176	FGGGTHLTVLSQPK SEQ ID NO: 215
λ_{227}	SWAQAVLNQPASVSGAL- GQKVTISC SEQ ID NO: 102	WYQQLPGKAPKLLVD SEQ ID NO: 134	GVPDRFSGSSSGNSGTLTITGLQAEDEADYYC SEQ ID NO: 177	FGGGTHLTVLGQPK SEQ ID NO: 212
λ_{228}	SWAQSVLTQPASVSGSLGQK VTISC SEQ ID NO: 103	WYQQLPGIGPKTVIY SEQ ID NO: 135	GVPDRFSGSKSGNSATLTISGLQPEDEAEYYC SEQ ID NO: 178	FGGGTLLTVLGQPK SEQ ID NO: 216
λ_{302}	SWAQSVLTQPASMSGSLGQK VTISC SEQ ID NO: 104	WFQQFPGEGPRTVIY SEQ ID NO: 136	GVPDRFSGSKSGSTATLTISELQAEDEADYYC SEQ ID NO: 179	FGGGTH SEQ ID NO: 218
λ_{306}	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WYRQLPGTGPTTLIY SEQ ID NO: 137	GVPDRFSGSRSGSTATLTISGLQADDEADYYC SEQ ID NO: 180	FGGGTHLTVLGQP SEQ ID NO: 219
λ_{310}	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WYQQFPGTGPRILIY SEQ ID NO: 138	GVPDRFSGSRSGYTAALTISGLQAEDEADYYC SEQ ID NO: 181	FGGGTHLTVLGQPE SEQ ID NO: 220
λ_{320}	SWAQSAITQPTSVSGSLGQR VSISC SEQ ID NO: 105	WYQQLPGKAPKLLLN SEQ ID NO: 139	GVPDRFSGSNSGASATLTITGLQAEDEADYYC SEQ ID NO: 182	FGSGTQLTVLGQP SEQ ID NO: 221
λ_{325}	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WLQQLPGTGPKTVIY SEQ ID NO: 140	GVPDRFSGSRSGSTATLTISGLQAEDEADYYC SEQ ID NO: 183	FGGGTHLTVLGQPK SEQ ID NO: 212
λ_{326}	SWAQSVLTQPASVTGSLGQR VTISC SEQ ID NO: 101	WFQQLPGTGPRTVIY SEQ ID NO: 141	GVPDRFSGSRSGSTATLTISGLLAEDDADYYC SEQ ID NO: 184	FGGGTHLTVLGQ SEQ ID NO: 225
λ_{129}	SWAQSVLTQPASVSGFLGQR VTISC SEQ ID NO: 106	WHQQVPETGPRNIY SEQ ID NO: 142	GVPDRFSGSKSGSTATLTISVLQAEDEADYYC SEQ ID NO: 185	FGGGTHLTVLGQPRA SEQ ID NO: 226
λ_{130}	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 107	WYQQLPGRGPPTLLY SEQ ID NO: 143	GVPDRFSGSRSGRTATLTISGLQAEDEADYYC SEQ ID NO: 186	FGSGTHLTALGQPKA SEQ ID NO: 227
λ_{134}	SWAQSLLTQPASVSGSLGQK VTISC SEQ ID NO: 108	WYQQLPGIGPRTVIY SEQ ID NO: 144	GIDRFSGSKSGNSASLTISGLQAEDEADYFC SEQ ID NO: 187	FGSGTQLTVLGQPKA SEQ ID NO: 228
λ_{213}	SWAQSVLTQPASVSGSLGQR ITISC SEQ ID NO: 96	WYQQLPGRGPRTVIY SEQ ID NO: 126	GVPDRFSGSKSGSTATLTISGLQAEDEADYYC SEQ ID NO: 170	FGGGTHLTVLGQPKA SEQ ID NO: 229
λ_{214}	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WYQQVPGTRPRTLIY SEQ ID NO: 145	GVPDRFSGSKSGSTATLTISGLQAEDEADYYC SEQ ID NO: 170	FGGGTHLTVLSQPKA SEQ ID NO: 230
λ_{216} A	SWAQSMILTQPASVSGSLGQT VTISC SEQ ID NO: 109	WYQQFPGRGPRSVIY SEQ ID NO: 146	GVPDRFSVSKSGSSATLTISGLQAEDEAEYYC SEQ ID NO: 188	FGSGTQLTVLSQPKA SEQ ID NO: 223
λ_{204} -79	SWAQSVLTQPTSVSGSLGQR VTISC SEQ ID NO: 110	WYQQLPGKAPKLLVY SEQ ID NO: 147	GVPDRFSGSNSGNSATLTITGLQAEDEADYYC SEQ ID NO: 189	FGSGTQLTVLGQPKA SEQ ID NO: 228
λ_{205} -79	SWAQSVLTQPASVSGSLGQK VTISC SEQ ID NO: 103	WYQNLPGKGPKTIVF SEQ ID NO: 148	GVPDRFSGSRSGSSATLTISGLQAEDEADYYC SEQ ID NO: 190	FGGGTHLTVLGQ SEQ ID NO: 225

L206-79	SWAQSVLTQPASVSGPLGQK VTISC SEQ ID NO: 111	WYQQIPGTGPRTLIY SEQ ID NO: 149	GVPDRFSGSRSGSTATLTISGLQAEDEADYYC SEQ ID NO: 183	FGGGTHLTVLGQPKA SEQ ID NO: 229
L207-79	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WYQQYPGTGPKTLIY SEQ ID NO: 150	GVPDRFSASRSGNSATLTISGLQAEDEADYYC SEQ ID NO: 191	FGGGTYLTVVGQPKA SEQ ID NO: 224
L210-79	SWAQSLLTQPASVSGSLGQK VTISC SEQ ID NO: 108	WYQQVPGTGPRTLIH SEQ ID NO: 151	GVPDRFSASASGSTATLTISGLQAEDEADYYC SEQ ID NO: 192	FGGGTHLTVLGQPKA SEQ ID NO: 229
L215-79	SWAQSVLTQPTSVSGSLGQR VTISC SEQ ID NO: 110	WYRQFPGKAPELLIY SEQ ID NO: 152	GVPGRFSGSISGNSATLTITGLQAEDEADYHC SEQ ID NO: 193	FGGGTHLTVLGQPKA SEQ ID NO: 229
L216-79	SWAQSVLTQPASVSGSLGQK VTISC SEQ ID NO: 112	WYQQLPGIGPRTVIS SEQ ID NO: 153	GVPDRFSGSKSGSSATLTISGLQAEDEAEYYC SEQ ID NO: 194	FGGGTHLTVLGQP SEQ ID NO: 219
L217-79	SWAQSVLTQPASVTGSLGQR VTISC SEQ ID NO: 101	WFQQFPGTGPRTVIY SEQ ID NO: 154	GVPDRFSGSRSGSTAILTISGLQAEDEAEYYC SEQ ID NO: 195	FGGGTHLTVLGQPKA SEQ ID NO: 229
L201-90	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WYQQVPGTRPRTLIY SEQ ID NO: 145	GVPDRFSGSKSGSTATLTISGLQAEDEADYYC SEQ ID NO: 170	FGGGTHLTVLSQPKA SEQ ID NO: 230
L217-90	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WYQQVPGTRPRTLIY SEQ ID NO: 145	GVPDRFSGSKSGSTATLTISGLQAEDEADYYC SEQ ID NO: 170	FGGGTHLTVLSQPKA SEQ ID NO: 230
L242-90	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WYQQVPGTRPRTLIY SEQ ID NO: 145	GVPDRFSGSKSGSAATLTISGLQAEDEADYYC SEQ ID NO: 196	FGGGTHLTVLSQPKA SEQ ID NO: 230
L1-706	SWAQSVXTQPASVSGSLGQR VTISC SEQ ID NO: 113	WHQQLPGTGPRTLIY SEQ ID NO: 155	GVPDRFSGSRSGSTATLTISGLQPEDEADYYC SEQ ID NO: 176	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-710	SWAQSVLTQPASVSGSLGQR ITVSC SEQ ID NO: 114	WYQQLPGRGPRTVIY SEQ ID NO: 126	GVPDRFSGSRSGTTATLTISGLQAEDEADYYC SEQ ID NO: 175	FGSGTQLTVLGQPKA SEQ ID NO: 228
L1-714	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WYQQLPETGPRTLIY SEQ ID NO: 156	GVPDRFSGSRSGSTATLTISGLQADDEADYYC SEQ ID NO: 197	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-715	SWAQSVLTQPASVSGSLGQS VTISC SEQ ID NO: 115	WYQQVPGTGPRTLIY SEQ ID NO: 157	GVPDRFSGSKSGSTAALTISGLQAEDEADYYC SEQ ID NO: 198	FGGGTQLTVLGQPKA SEQ ID NO: 217
L1-720	SWAQSVLTQPASVTGSLGQR VTISC SEQ ID NO: 101	WFQQLPGTGPRTVIY SEQ ID NO: 141	GAPDRFSGSRSGSTATLTISGLQAEDEAEYYC SEQ ID NO: 199	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-721	SWAQSVLTQPASVSGSLGQK VTISC SEQ ID NO: 112	WYQQVPGIGPRTVMY SEQ ID NO: 158	GVPDRFSSSRSGSSATLTITAGLQAEDEAAYYC SEQ ID NO: 200	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-723	SWAQSVLTQPASVSGPLGQR VTISC SEQ ID NO: 116	WFQHLPGTRPKSLIY SEQ ID NO: 159	GVPDRFSGSKSGSTATLTISGLQAEDEAIYYC SEQ ID NO: 201	FGSGTQLTVLGQPKA SEQ ID NO: 228
L1-731	SLGQRVTISC SEQ ID NO: 117	WYQQLPKGAPKLLVD SEQ ID NO: 134	RVPDRFSGSESGNSATLTITGLQAEDEADYYC SEQ ID NO: 202	FGSGTQLTVLGQPKA SEQ ID NO: 228
L1-732	SWAQSVLTQPASVTGSLGQR VTISC SEQ ID NO: 101	WFQQLPGTGPRTVIY SEQ ID NO: 141	GVPDRFSGSRSGRTATLTISGLQAEDEAEYYC SEQ ID NO: 203	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-733	SWAQSVLTQPASVTGSLGQR VTISC SEQ ID NO: 101	WFQQLPGTGPRTVIC SEQ ID NO: 160	GVPDRFSGSRSGSTATLTISGLQAEDEAEYYC SEQ ID NO: 204	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-737	--	WYQQLPGRGPRTVIY SEQ ID NO: 126	GVPDRFSGSKSGSTATLTISGLQAEDEADYYC SEQ ID NO: 170	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-739	VTISC SEQ ID NO: 118	WYQLVPGTGPRTLIY SEQ ID NO: 161	GVPDRFSGSKSGTTAILTISGLQADDEADYFC SEQ ID NO: 205	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-742	SWAQSVLTQPASVSGSLGQR ITISC SEQ ID NO: 96	WYQQLPGRGPRTVIH SEQ ID NO: 162	GVPDRFSGSKSGSTATLTISGLQADDEADYYC SEQ ID NO: 206	FGGGAHLTVLGQPKA SEQ ID NO: 231
L1-747	SWAQAVLNQPASVSGAL- GQKVTISC SEQ ID NO: 102	WCQQLPKGAPKLLVD SEQ ID NO: 163	GIPDRFSGSRSDNSGILTISGLQAEDEADYHC SEQ ID NO: 207	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-749	SWAQSELTSAAVSGSLGQE VTISC SEQ ID NO: 119	WYQQFPGTGPRTLIY SEQ ID NO: 164	GVPARFSGSRSGNTATLTISGLLADEADYYC SEQ ID NO: 208	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-758	SWAQSVLTQPSSVSGSLGQR VTISC SEQ ID NO: 121	WYRQLPGEAPKLLLY SEQ ID NO: 165	GVPDRFSGSNSGFSATLTITGLQADDEADYYC SEQ ID NO: 210	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-757	-	-	GVPDRFSGSRSGSTATLTISGLQAEDEAEYYC SEQ ID NO: 171	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-760	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WYQQLPGTGPRTLIY SEQ ID NO: 131	GVPDRFSGSRSGTTGTLTISGLQAEDEADYYC SEQ ID NO: 211	FGGGTRLTVLGQPKA SEQ ID NO: 233
or				
cnsnss	SWAQSVLTQPASVSGSLGQR VTISC SEQ ID NO: 98	WYQQLPGTGPRTLIY SEQ ID NO: 131	GVPDRFSGSRSGSTATLTISGLQAEDEADYYC SEQ ID NO: 183	FGGGTHLTVLGQPK SEQ ID NO: 212

14. Group 1 Light Chain Variable Domain Genus

[0034] The chimeric canine group Group 1 light chain variable domain polypeptides according to the invention are compounds comprising the sequence:



wherein

Fr¹ is Z¹ Z² Z³ Z⁴ Z⁵ Z⁶ Z⁷ Z⁸ Z⁹ Z¹⁰ Z¹¹ Z¹² Z¹³ Z¹⁴ Z¹⁵ Z¹⁶ Z¹⁷ Z¹⁸ Z¹⁹ Z²⁰ Z²¹ Z²² Z²³ Z²⁴ Z²⁵ (SEQ ID NO: 234);

Fr² is Z²⁶ Z²⁷ Z²⁸ Z²⁹ Z³⁰ Z³¹ Z³² Z³³ Z³⁴ Z³⁵ Z³⁶ Z³⁷ Z³⁸ Z³⁹ Z⁴⁰ (SEQ ID NO: 235)

Fr³ is Z⁴¹ Z⁴² Z⁴³ Z⁴⁴ Z⁴⁵ Z⁴⁶ Z⁴⁷ Z⁴⁸ Z⁴⁹ Z⁵⁰ Z⁵¹ Z⁵² Z⁵³ Z⁵⁴ Z⁵⁵ Z⁵⁶ Z⁵⁷ Z⁵⁸ Z⁵⁹ Z⁶⁰ Z⁶¹ Z⁶² Z⁶³ Z⁶⁴ Z⁶⁵ Z⁶⁶ Z⁶⁷ Z⁶⁸ Z⁶⁹ Z⁷⁰ Z⁷¹ Z⁷² (SEQ ID NO: 236), and

Fr⁴ is Z⁷³ Z⁷⁴ Z⁷⁵ Z⁷⁶ Z⁷⁷ Z⁷⁸ Z⁷⁹ Z⁸⁰ Z⁸¹ Z⁸² Z⁸³ Z⁸⁴ Z⁸⁵ Z⁸⁶ Z⁸⁷ (SEQ ID NO: 237)

wherein

Z ¹ is <u>A</u> , T, or -,	Z ² is <u>D</u> or -,	Z ³ is <u>S</u> or -,	Z ⁴ is <u>Q</u> or -,	Z ⁵ is <u>T</u> or -,
Z ⁶ is <u>V</u> or -,	Z ⁷ is <u>V</u> or -,	Z ⁸ is <u>T</u> or -,	Z ⁹ is <u>Q</u> or -,	Z ¹⁰ is <u>E</u> or -,
Z ¹¹ is <u>P</u> , A, or -,	Z ¹² is <u>S</u> , F, or -,	Z ¹³ is <u>L</u> , V, or -,	Z ¹⁴ is <u>S</u> or -,	Z ¹⁵ is <u>V</u> or -,
Z ¹⁶ is <u>S</u> or -,	Z ¹⁷ is <u>P</u> , L, or -,	Z ¹⁸ is <u>G</u> or -,	Z ¹⁹ is <u>G</u> or -,	Z ²⁰ is <u>T</u> or -,
Z ²¹ is <u>V</u> , I, or -,	Z ²² is <u>T</u> or -,	Z ²³ is <u>L</u> or -,	Z ²⁴ is <u>T</u> or -,	Z ²⁵ is <u>C</u> or -,
Z ²⁶ is <u>W</u> ,	Z ²⁷ is <u>Y</u> or S,	Z ²⁸ is <u>Q</u> ,	Z ²⁹ is <u>Q</u> or H	Z ³⁰ is <u>T</u> ,
Z ³¹ is <u>L</u> , Q, or P,	Z ³² <u>G</u> ,	Z ³³ is <u>R</u> or Q,	Z ³⁴ is <u>A</u> ,	Z ³⁵ is <u>P</u> ,
Z ³⁶ is <u>R</u> ,	Z ³⁷ is <u>T</u> or P,	Z ³⁸ is <u>I</u> ,	Z ³⁹ is <u>I</u> or L,	Z ⁴⁰ is <u>Y</u> or S;
Z ⁴¹ is <u>G</u> ,	Z ⁴² is <u>V</u> ,	Z ⁴³ is <u>P</u> ,	Z ⁴⁴ is <u>N</u> , S, D, or R,	Z ⁴⁵ is <u>R</u> ,
Z ⁴⁶ is <u>F</u> ,	Z ⁴⁷ is <u>S</u> or T,	Z ⁴⁸ is <u>G</u> or A,	Z ⁴⁹ is <u>S</u> ,	Z ⁵⁰ is <u>I</u> or V,
Z ⁵¹ is <u>S</u> ,	Z ⁵² is <u>G</u> or D,	Z ⁵³ is <u>N</u> ,	Z ⁵⁴ is <u>K</u> or R,	Z ⁵⁵ is <u>A</u> ,
Z ⁵⁶ is <u>A</u> or <u>T</u> ,	Z ⁵⁷ is <u>L</u> ,	Z ⁵⁸ is <u>T</u> ,	Z ⁵⁹ is <u>I</u> ,	Z ⁶⁰ is <u>T</u> ,
Z ⁶¹ is <u>G</u> ,	Z ⁶² is <u>A</u> or V,	Z ⁶³ is <u>Q</u> or R,	Z ⁶⁴ is <u>P</u> ,	Z ⁶⁵ is <u>E</u> ,
Z ⁶⁶ is <u>D</u> ,	Z ⁶⁷ is <u>E</u> ,	Z ⁶⁸ is <u>A</u> , T, or G,	Z ⁶⁹ is <u>D</u> ,	Z ⁷⁰ is <u>Y</u> ,
Z ⁷¹ is <u>Y</u> or H, and	Z ⁷² is <u>C</u> ,	Z ⁷³ is <u>F</u> or V,	Z ⁷⁴ is <u>G</u> ,	Z ⁷⁵ is <u>G</u> or S,
Z ⁷⁶ is <u>G</u> ,	Z ⁷⁷ is <u>T</u> ,	Z ⁷⁸ is <u>H</u> or	Z ⁷⁹ is <u>L</u> ,	Z ⁸⁰ is <u>T</u> ,

		Q,		
Z ⁸¹ is <u>V</u> ,	Z ⁸² is <u>L</u> ,	Z ⁸³ is <u>G</u> ,	Z ⁸⁴ is <u>Q</u> ,	Z ⁸⁵ is <u>P</u> ,
Z ⁸⁶ is <u>K</u> ,	and Z ⁸⁷ is <u>A</u> .			

provided that when Y^a for a ≤ 25 is --, Y^b for b < a is --, and when Y^c for c ≥ 94 is --, Y^d for d > c is --.

15. Group 1 Light Chain Variable Domain Subgenus

[0035] The chimeric canine group Group 1 light chain variable domain polypeptides according to the invention are compounds comprising the sequence:



wherein

Fr¹ is

--	ADSQTVVTQEPSLSVSPGGTVTLT C SEQ ID NO: 238
ITLTC SEQ ID NO: 239	GTVTLTC SEQ ID NO: 240
TDSQTVVTQEPSLSVSPGGTVTL TC SEQ ID NO: 241	ADSQTVVTQEPSLSVSLGGTVTLT C SEQ ID NO: 242
ADSQTVVTQEASVSVSPGGTVTL TC SEQ ID NO: 243	or ADSQTVVIQEPFLSVSPGGTVTLT C SEQ ID NO: 244;

Fr² is

WYQQTLGRAPRTI IY SEQ ID NO: 245	WY- QQTQGRAPRTIIY SEQ ID NO: 246	WSQQTPGQAPR- TIIY SEQ ID NO: 247	WYQQTLGRPPRTI IS SEQ ID NO: 248
WYQQTLGRPPRPI IY SEQ ID NO: 249	WSQQTPGQAPRTIL Y SEQ ID NO: 250	or	WY- QHTQGRAPRTIIY SEQ ID NO: 251;

Fr³ is

GVPNRFSGSISGNKAALTIT- GAQPEDEADYYC SEQ ID NO: 252	GVPNRFSGSIS- GNKAALTIIGVQPEDEADYYC SEQ ID NO: 253
GVPNRFSGSISDNKAALTIT- GVQPEDEADYYC SEQ ID NO: 254	GVPSRFSGSISGNKATLTIT- GARPEDEADYHC SEQ ID NO: 255
GVPSRFTGSISGNRAALTIT- GARPEDEADYYC	GVPDRFSGSISGNKAALTITGAQPEDEG- DYYC

SEQ ID NO: 256	SEQ ID NO: 257
GVPNRFTGSISGNKAALTIT- GAQPEDEADYYC	GVPRRFSASVSGNKATLTIT- GAQPEDEADYYC
SEQ ID NO: 258	SEQ ID NO: 259
GVPNRFTASISGNKAALTIT- GAQPEDEADYYC	or
SEQ ID NO: 260	
GVPNRFSGSISGNKAALTITGAQPEDET- DYYC	
SEQ ID NO: 261;	

Fr⁴ is

FGGGTHLTVLGQPKA SEQ ID NO: 229	VGGGTHLTVLGQPKA SEQ ID NO: 262	FGSGTQLTVLGQPKA SEQ ID NO: 228	FGGGTHLTVLGQ P SEQ ID NO: 219
FGSGTQLTVLGQ SEQ ID NO: 263	or	FGGGTHLTVLGQ SEQ ID NO: 225.	

16. Group 1 Light Chain Variable Domain Species

[0036] Preferably, the canine Group 1 light chain variable domain according to the invention is a compound comprising the sequence:



wherein Fr¹, Fr², Fr³, and Fr⁴ are selected from the following combinations:

#	Fr ¹	Fr ²	Fr ³	Fr ⁴
L1-783	-	WYQQTILGRAPRTIY SEQ ID NO: 1135	GVPNRFSGSISGNKAALTITGAQPEDEADYYC SEQ ID NO: 252	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-776	-	WYQQTQGRAPRTIY SEQ ID NO: 246	GVPNRFSGSISGNKAALTITGAQPEDEADYYC SEQ ID NO: 252	VGGGTHLTVLGQPKA SEQ ID NO: 262
L1-785	ADSQTVVTQEPSLSVSPGGTVTLTC SEQ ID NO: 238	WYQQTILGRAPRTIY SEQ ID NO: 245	GVPNRFSGSISGNKAALTIIGVQPEDEADYYC SEQ ID NO: 253	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-789	ITLTC SEQ ID NO: 239	WYQQTILGRAPRTIY SEQ ID NO: 245	GVPNRFSGSISDNKAALTITGVQPEDEADYYC SEQ ID NO: 254	FGSGTQLTVLGQPKA SEQ ID NO: 228
λ307	GTVTLTC SEQ ID NO: 240	WYQQTQGRAPRTIY SEQ ID NO: 246	GVPNRFSGSISGNKAALTITGAQPEDEADYYC SEQ ID NO: 252	FGGGTHLTVLGQP SEQ ID NO: 219
λ322	ADSQTVVTQEPSLSVSPGGTVTLTC SEQ ID NO: 238	WYQQTQGRAPRTIY SEQ ID NO: 246	GVPNRFSGSISGNKAALTITGAQPEDEADYYC SEQ ID NO: 252	FGSGTQLTVLGQ SEQ ID NO: 263
λ305	TDSQTVVTQEPSLSVSPGGTVTLTC SEQ ID NO: 241	WYQQTQGRAPRTIY SEQ ID NO: 246	GVPNRFSGSISGNKATLTITGARPEDEADYHC SEQ ID NO: 255	FGGGTHLTVLGQ SEQ ID NO: 225
λ303	ADSQTVVTQEPSLSVSPGGTVTLTC SEQ ID NO: 238	WYQQTQGRAPRTIY SEQ ID NO: 246	GVPNRFSGSISGNKAALTITGAQPEDEADYYC SEQ ID NO: 252	FGGGTHLTVLGQPKA SEQ ID NO: 229
λ125	ADSQTVVTQEPSLSVSPGGTVTLTC SEQ ID NO: 238	WYQQTILGRAPRTIY SEQ ID NO: 245	GVPNRFSGSISGNKAALTITGAQPEDEADYYC SEQ ID NO: 252	FGSGTQLTVLGQPKA SEQ ID NO: 228
λ104	ADSQTVVTQEPSLSVSLGGTVTLTC SEQ ID NO: 242	WSQQTTPGQAPRTIY SEQ ID NO: 247	GVPNRFSGSISGNRAALTITGARPEDEADYYC SEQ ID NO: 256	FGGGTHLTVLGQPKA SEQ ID NO: 229
L220-79	ADSQTVVTQEASVSVSPGGTVTLTC SEQ ID NO: 243	WYQQTILGRPPRTIIS SEQ ID NO: 248	GVPDRFSGSISGNKAALTITGAQPEDEGDYYC SEQ ID NO: 257	FGGGTHLTVLGQ SEQ ID NO: 225
L214-79	ADSQTVVTQEPSLSVSLGGTVTLTC SEQ ID NO: 242	WSQQTTPGQAPRTIY SEQ ID NO: 247	GVPNRFSGSISGNKAALTITGAQPEDEADYYC SEQ ID NO: 258	FGSGTQLTVLGQPKA SEQ ID NO: 228
L1-705	ADSQTVVIQEPFLSVSPGGTVTLTC SEQ ID NO: 244	WYQQTILGRPPRPRIY SEQ ID NO: 249	GVPNRFSGSISGNKATLTITGAQPEDEADYYC SEQ ID NO: 259	FGGGTHLTVLGQPKA SEQ ID NO: 229

#	Fr ¹	Fr ²	Fr ³	Fr ⁴
L1-729	ADSQTVVTQEPSLSVSLGGTVTLTC SEQ ID NO: 242	WSQQTTPGQAPRTILY SEQ ID NO: 250	GVPNRFTASISGNKAALTITGAQPEDEADYYC SEQ ID NO: 260	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-743	ADSQTVVTQEPSLSVSPGGTVTLTC SEQ ID NO: 238	WYQHTQGRAPRTIY SEQ ID NO: 251	GVPNRFSGSISGNKAALTITGAQPEDEADYYC SEQ ID NO: 252	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-753	ADSQTVVTQEPSLSVSPGGTVTLTC SEQ ID NO: 238	WYQQTQGRAPRTIY SEQ ID NO: 246	GVPNRFSGSISGNKAALTITGAQPEDETDYYC SEQ ID NO: 261	FGGGTHLTVLGQPKA SEQ ID NO: 229
L1-759	ADSQTVVTQEPSLSVSPGGTVTLTC SEQ ID NO: 238	WYQQTQGRAPRTIY SEQ ID NO: 246	GVPNRFSGSISGNKAALTITGAQPEDEADYYC SEQ ID NO: 252	--
Cnsnss	ADSQTVVTQEPSLSVSPGGTVTLTC SEQ ID NO: 238	WYQQTQGRAPRTIY SEQ ID NO: 245	GVPNRFSGSISGNKAALTITGAQPEDEADYYC SEQ ID NO: 252	FGGGTHLTVLGQPKA SEQ ID NO: 229

17. Group 3 Light Chain Variable Domain Genus

[0037] The chimeric canine light chain variable domain polypeptides according to the invention are compounds comprising the sequence:



wherein

Fr¹ is Y'¹ Y'² Y'³ Y'⁴ Y'⁵ Y'⁶ Y'⁷ Y'⁸ Y'⁹ Y'¹⁰ Y'¹¹ Y'¹² Y'¹³ Y'¹⁴ Y'¹⁵ Y'¹⁶ Y'¹⁷ Y'¹⁸ Y'¹⁹ Y'²⁰ Y'²¹ Y'²² Y'²³ Y'²⁴ Y'²⁵ (SEQ ID NO: 264);

Fr² is Y'²⁶ Y'²⁷ Y'²⁸ Y'²⁹ Y'³⁰ Y'³¹ Y'³² Y'³³ Y'³⁴ Y'³⁵ Y'³⁶ Y'³⁷ Y'³⁸ Y'³⁹ Y'⁴⁰ (SEQ ID NO: 265);

Fr³ is Y'⁴¹ Y'⁴² Y'⁴³ Y'⁴⁴ Y'⁴⁵ Y'⁴⁶ Y'⁴⁷ Y'⁴⁸ Y'⁴⁹ Y'⁵⁰ Y'⁵¹ Y'⁵² Y'⁵³ Y'⁵⁴ Y'⁵⁵ Y'⁵⁶ Y'⁵⁷ Y'⁵⁸ Y'⁵⁹ Y'⁶⁰ Y'⁶¹ Y'⁶² Y'⁶³ Y'⁶⁴ Y'⁶⁵ Y'⁶⁶ Y'⁶⁷ Y'⁶⁸ Y'⁶⁹ Y'⁷⁰ Y'⁷¹ Y'⁷² (SEQ ID NO: 266);

Fr⁴ is Y'⁷³ Y'⁷⁴ Y'⁷⁵ Y'⁷⁶ Y'⁷⁷ Y'⁷⁸ Y'⁷⁹ Y'⁸⁰ Y'⁸¹ Y'⁸² Y'⁸³ Y'⁸⁴ Y'⁸⁵ Y'⁸⁶ (SEQ ID NO: 267);

Y' ¹ is <u>S</u> , P, or --	Y' ² is <u>W</u> , A, or --,	Y' ³ is <u>A</u> or - -	Y' ⁴ is <u>Q</u> or -- ,
Y' ⁵ is <u>S</u> A, T, or --	Y' ⁶ is <u>V</u> , M, or --	Y' ⁷ is <u>L</u> or - -	Y' ⁸ is <u>T</u> or --
Y' ⁹ is <u>Q</u> or --,	Y' ¹⁰ is <u>P</u> or - -	Y' ¹¹ is <u>A</u> , P, S, or --	Y' ¹² is <u>S</u> , P, or --
Y' ¹³ is <u>V</u> , M, or --	Y' ¹⁴ is <u>S</u> or - -	Y' ¹⁵ is <u>G</u> , A, T, or --	Y' ¹⁶ is <u>S</u> , A, T, or --
Y' ¹⁷ is <u>L</u> , P, or --	Y' ¹⁸ is <u>G</u> or - -	Y' ¹⁹ is <u>Q</u> or --,	Y' ²⁰ is <u>R</u> , T, or --
Y' ²¹ is <u>V</u> or --	Y' ²² is <u>T</u> or - -	Y' ²³ is <u>I</u> ,	Y' ²⁴ is <u>S</u> ,
Y' ²⁵ is <u>C</u> ,	Y' ²⁶ is <u>W</u> ,	Y' ²⁷ is <u>Y</u> or F,	Y' ²⁸ is <u>Q</u> or R,
Y' ²⁹ is <u>Q</u> or H,	Y' ³⁰ is <u>L</u> , F, or V,	Y' ³¹ is <u>P</u> or L,	Y' ³² is <u>G</u> ,
Y' ³³ is <u>T</u> or K,	Y' ³⁴ is <u>G</u> , S, or A,	Y' ³⁵ is <u>P</u> ,	Y' ³⁶ is <u>R</u> , K, or S,
Y' ³⁷ is <u>T</u> , L, or S,	Y' ³⁸ is <u>L</u> , V, I, or F,	Y' ³⁹ is <u>I</u> , or A,	Y' ⁴⁰ is <u>Y</u> , F, or H,
Y' ⁴¹ is <u>G</u> ,	Y' ⁴² is <u>V</u> or I,	Y' ⁴³ is <u>P</u> ,	Y' ⁴⁴ is <u>D</u> , A, V, or E,
Y' ⁴⁵ is <u>R</u> ,	Y' ⁴⁶ is <u>F</u> ,	Y' ⁴⁷ is <u>S</u> ,	Y' ⁴⁸ is <u>G</u> , or A,

Y' ⁴⁹ is <u>S</u> or P,	Y' ⁵⁰ is <u>R</u> , K, S, or A,	Y' ⁵¹ is <u>S</u> ,	Y' ⁵² is <u>G</u> ,
Y' ⁵³ is <u>S</u> or N,	Y' ⁵⁴ is <u>T</u> , or S,	Y' ⁵⁵ is <u>A</u> or S,	Y' ⁵⁶ is <u>T</u> , S, or A,
Y' ⁵⁷ is <u>L</u> ,	Y' ⁵⁸ is <u>T</u> ,	Y' ⁵⁹ is <u>I</u> ,	Y' ⁶⁰ is <u>S</u> , T, or A,
Y' ⁶¹ is <u>G</u> or V,	Y' ⁶² is <u>L</u> or I,	Y' ⁶³ is <u>Q</u> ,	Y' ⁶⁴ is <u>A</u> or T,
Y' ⁶⁵ is <u>E</u> ,	Y' ⁶⁶ is <u>D</u> ,	Y' ⁶⁷ is <u>E</u> ,	Y' ⁶⁸ is <u>A</u> , T, or G,
Y' ⁶⁹ is <u>D</u> , E, or N,	Y' ⁷⁰ is <u>Y</u> ,	Y' ⁷¹ is <u>Y</u> or F,	Y' ⁷² is <u>C</u> ,
Y' ⁷³ is <u>F</u>	Y' ⁷⁴ is <u>G</u> , S, or E,	Y' ⁷⁵ is <u>G</u> ,	Y' ⁷⁶ is <u>G</u> ,
Y' ⁷⁷ is <u>T</u> or Q,	Y' ⁷⁸ is <u>H</u> ,	Y' ⁷⁹ is <u>L</u> ,	Y' ⁸⁰ is <u>T</u> or -
Y' ⁸¹ is <u>V</u> , F, or --,	Y' ⁸² is <u>L</u> or -	Y' ⁸³ is <u>G</u> or --,	Y' ⁸⁴ is <u>Q</u> , H, N, or --,
Y' ⁸⁵ is <u>P</u> or E, and	Y' ⁸⁶ is <u>K</u> or -		

provided that when Y'^k for k ≤ 22 is --, Y'^l for l < k is --, and when Y'ⁿ for n ≥ 80 is --, Y'^m for m > n is -.

18. Group 3 Light Chain Variable Domain Subgenus

[0038] Preferably, the canine λ light chain variable domain according to the invention is a compound comprising the sequence:



wherein

Fr¹ is

SWAQAVLTQPPSVSAALGQRVTISC SEQ ID NO: 268	SWAQSVLTQPASVSGSLGQRVTISC SEQ ID NO: 98	SWAQSAVTQPPSSVSGTLGQTVTISC SEQ ID NO: 269
PWAQSVLTQPASVXGSXGQRVTISC SEQ ID NO: 270	SWAQSVLTQPASVXGSXGQRVTISC SEQ ID NO: 271	SWAQAVLTQPPSMSTALGQRVTITC SEQ ID NO: 272
SWAQTVLTQPASVSGSLGQTVTISC SEQ ID NO: 273	SLGQTVTISC SEQ ID NO: 274	PVSAAPGQRVTISC SEQ ID NO: 275
GSLGQTVTISC SEQ ID NO: 276	SWAQAVLTQPPASVSGSLGQRVTISC SEQ ID NO: 277	SWAQSVLTQPASVSGSXGQRVTISC SEQ ID NO: 278
ISC	RVTISC SEQ ID NO: 279	or
SWAQSMVTQPPASVSGSLGQKVTISC SEQ ID NO: 112;		

Fr² is

WYQQVPGKSPKTFI Y SEQ ID NO: 280	WYQQFPGTGPRTLII Y SEQ ID NO: 164	WYQQLPGTGPRTLII Y SEQ ID NO: 131	WYQQLPGTSPRTLII Y SEQ ID NO: 281
WFQHFPGTSPKLLI Y SEQ ID NO: 282	WYQQVPGTSPRTLII Y SEQ ID NO: 283	WYQQLPGTSPKTLII Y SEQ ID NO: 284	WYQQFPGTGPRTLII Y SEQ ID NO: 285
WYQQLPGKSPKSII F SEQ ID NO: 286	WYRQFPGTGPRTVAY Y SEQ ID NO: 287	WYQQLPGTGPKTLII Y SEQ ID NO: 133	WYQQLPGKSPKTLII Y SEQ ID NO: 288
WYQQLPGTSPRTLII H SEQ ID NO: 289	WYQQFLGTGPRTLII Y SEQ ID NO: 290	WYQQLPGKAPSLII Y SEQ ID NO: 291; or	WYQQLPGKGPRTLVI Y SEQ ID NO: 292;

Fr³ is

GVPVRFSGSKSGSTATLTITGIQAEDET- DYC SEQ ID NO: 293	GVPDRFSGSRSGSTATLTISGLQTEDEADYY C SEQ ID NO: 294
GVPDRFSGSRSGNTATLTIS- GLQAEDEADYYC SEQ ID NO: 295	GVPDRFSGSRSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 183
GIPARFSGSRSGNTASLTIS- GLQAEDEADYYC SEQ ID NO: 296	GVPDRFSGSKSGSTATLTIXSGLQAEDEADYY C SEQ ID NO: 297
GVPARFSGSKSGNTATLTIT- GIQAEDEADYYC SEQ ID NO: 298	GVPDRFSASSSGSTSTLTIAQLQAEDEG- DYC SEQ ID NO: 299
GIPDRFSGSRSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 300	GVPDRFSGSKSGSTATLTISVLQAEDEADYY C SEQ ID NO: 185
GVPDRFSGSSSGSATLTIS- GLQAEDEADYYC SEQ ID NO: 301	GVXDRFSGSRSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 302
GVPDRFSGSRSGSTAALTIS- GLQAEDEADYYC SEQ ID NO: 303	GVPDRFSGSKSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 170
GVPDRFSGSRSGSTATLTIS- GLQAEDEADYFC SEQ ID NO: 304	GVPDRFSGSKSGSSATLTIT- GLQAEDEADYYC SEQ ID NO: 305
GVPDRFSGSRSGNTATLTTSGLQAEDEADYF C SEQ ID NO: 306, or	GVPDRFSGSASGSSATLTIS- GLQAEDEADYYC SEQ ID NO: 307;

Fr⁴ is

FGSGTQLTVLGQPK SEQ ID NO: 214	FGGGTHLTVLGQPK SEQ ID NO: 212	FGSGTQLTVLGQNE SEQ ID NO: 308	FGGGTHLTVLGQP SEQ ID NO: 219
FGGGTHLTVLGQHE SEQ ID NO: 309	FGGGTHL SEQ ID NO: 222	FGGGTQLTVLGQPKA SEQ ID NO: 217	FGGGTHLTVLGQPK A SEQ ID NO: 229

FGGGTHLTVLGQ SEQ ID NO: 225	FGEGTHLTVLGQPK A SEQ ID NO: 310	FGGGTHLTVFGQPKA SEQ ID NO: 311, or	FGSGTQLTVLGQPK A SEQ ID NO: 228.
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19. Group 3 Light Chain Variable Domain Species

[0039] Preferably, the canine Group 3 light chain variable domain according to the invention is a compound comprising the sequence:



wherein Fr^1 , Fr^2 , Fr^3 , and Fr^4 are selected from the following combinations:

#	Fr^1	Fr^2	Fr^3	Fr^4
λ 124	SWAQAVLTQPPSVSAAALGQRTIS C SEQ ID NO: 268	WYQQVPGKSPKTFI Y SEQ ID NO: 280	GVPVRFSGSKSGSTATLTITGIQAEDET- DYCYC SEQ ID NO: 293	FGSGTQLTVLGQPK SEQ ID NO: 214
λ 212	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQFPGTGPRTLI Y SEQ ID NO: 164	GVPDRFSGSRSGSTATLTISGLQTEDEADY YC SEQ ID NO: 294	FGGGTHLTVLGQPK SEQ ID NO: 212
λ 216	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQFPGTGPRTLI Y SEQ ID NO: 164	GVPDRFSGSRSGSTATLTISGLQTEDEADY YC SEQ ID NO: 294	FGGGTHLTVLGQPK SEQ ID NO: 212
λ 218	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQLPGTGPRTLI Y SEQ ID NO: 131	GVPDRFSGSRSGNTATLTIS- GLQAEDEADYCYC SEQ ID NO: 295	FGGGTHLTVLGQPK SEQ ID NO: 212
λ 231	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQLPGTSPRTLI Y SEQ ID NO: 281	GVPDRFSGSRSGSTATLTIS- GLQAEDEADYCYC SEQ ID NO: 183	FGSGTQLTVLGQPK SEQ ID NO: 214
λ 301	SWAQSVLTQPSSVSGTLGQTVTIS C SEQ ID NO: 269	WFQHFPGTSPKLLI Y SEQ ID NO: 282	GIPARFSGSRSGNTASLTIS- GLQAEDEADYCYC SEQ ID NO: 296	FGSGTQLTVLGQNE SEQ ID NO: 308
λ 308	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQVPGTSPRTLI Y SEQ ID NO: 283	GVPDRFSGSRSGSTATLTIS- GLQAEDEADYCYC SEQ ID NO: 183	FGGGTHLTVLGQP SEQ ID NO: 219
λ 311	PWAQSVLTQPASVXSXGQRTIS C SEQ ID NO: 270	WYQQLPGTSPKTLI Y SEQ ID NO: 284	GVPDRFSGSRSGSTATLTIS- GLQAEDEADYCYC SEQ ID NO: 183	FGGGTHLTVLGQHE SEQ ID NO: 309
λ 316	SWAQSVLTQPASVXSXGQRTIS C SEQ ID NO: 271	WYQQFPGTGPRTII Y SEQ ID NO: 285	GVPDRFSGSKSGSTATLTXSGLQAEDEADY YC SEQ ID NO: 297	FGGGTHL SEQ ID NO: 222
λ 131	SWAQAVLTQPPSMSTALGQRTIT C SEQ ID NO: 272	WYQQLPKGSPKSII F SEQ ID NO: 286	GVPARFSGSKSGNTATLTIT- GIQAEDEADYCYC SEQ ID NO: 298	FGGGTQLTVLGQPK A SEQ ID NO: 217
L202- 79	SWAQTVLTQPASVSGSLGQTVTIS C SEQ ID NO: 273	WYRQFPGTGPRTVA Y SEQ ID NO: 287	GVPDRFSASSSGSTSTLTITAGLQAEDEG- DYCYC SEQ ID NO: 299	FGGGTHLTVLGQPK SEQ ID NO: 212
L208- 79	SLGQTVTISC SEQ ID NO: 274	WYQQLPGTGPKTLI Y SEQ ID NO: 133	GIPDRFSGSRSGSTATLTIS- GLQAEDEADYCYC SEQ ID NO: 300	FGGGTHLTVLGQPK A SEQ ID NO: 229

L211-79	PVSAAPGQRTISC SEQ ID NO: 275	WYQQLPGKSPKTII Y SEQ ID NO: 288	GVPDRFSGSKSGSTATLTISVLQAEDEADY YC SEQ ID NO: 185	FGGGTHLTVLGQPK A SEQ ID NO: 229
L212-79	GSLGQTVTISC SEQ ID NO: 276	WYQQLPGTGPKTLI Y SEQ ID NO: 133	GIPDRFSGSRSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 300	FGGGTHLTVLGQPK A SEQ ID NO: 229
L218-79	SWAQAV- LTQPASVSGSLGQRTISC SEQ ID NO: 277	WYQQLPGTGPKTLI Y SEQ ID NO: 133	GVPDRFSGSSSGSSATLTIS- GLQAEDEADYYC SEQ ID NO: 301	FGGGTHLTVLGQ SEQ ID NO: 225
L1-704	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQLPGTGPRTLI Y SEQ ID NO: 131	GVPDRFSGSRSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 183	FGGGTHLTVLGQPK A SEQ ID NO: 229
L1-711	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQLPGTSPRTLII Y SEQ ID NO: 281	GVPDRFSGSRSGSTAALTIS- GLQAEDEADYYC SEQ ID NO: 303	FGGGTHLTVLGQPK A SEQ ID NO: 229
L1-713	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQFPGTGPRTLII Y SEQ ID NO: 285	GVPDRFSGSKSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 170	FGGGTHLTVLGQPK A SEQ ID NO: 310
L1-716	ISC	WYQQLPGTGPRTLI Y SEQ ID NO: 131	GVPDRFSGSRSGSTATLTIS- GLQAEDEADYFC SEQ ID NO: 304	FGGGTHLTVFGQPK A SEQ ID NO: 311
L1-717	RVTISC SEQ ID NO: 279	WYQQLPGTSPRTLII Y SEQ ID NO: 281	GVPDRFSGSRSGNTATLTIS- GLQAEDEADYYC SEQ ID NO: 295	FGGGTHLTVLGQPK A SEQ ID NO: 229
L1-718	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQLPGTSPRTLII H SEQ ID NO: 289	GVPDRFSGSRSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 183	FGGGTHLTVLGQPK A SEQ ID NO: 229
L1-727	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQFLGTGPRTLII Y SEQ ID NO: 290	GVPDRFSGSKSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 170	FGGGTHLTVLGQPK A SEQ ID NO: 229
L1-730	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQLPGKAPSLII Y SEQ ID NO: 291	GVPERFSGSKSGSSATLTIT- GLQAEDEANYC SEQ ID NO: 305	FGSGTQLTVLGQPK A SEQ ID NO: 228
L1-741	SWAQAV- LTQPASVSGSLGQRTISC SEQ ID NO: 277	WYQQLPGTSPRTLII Y SEQ ID NO: 281	GVPDRFSGSRSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 183	FGGGTHLTVLGQPK A SEQ ID NO: 229
L1-754	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQLPGTSPRTLII Y SEQ ID NO: 281	GVPDRFSGSRSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 183	FGGGTHLTVLGQPK A SEQ ID NO: 229
L1-748	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQLPGTSPKTLII Y SEQ ID NO: 284	GVPDRFSGSRSGNTATLTTSGLQAEDEADY FC SEQ ID NO: 306	FGGGTHLTVLGQPK A SEQ ID NO: 229
L1-735	SWAQSMILTQPASVSGSLGQKVTIS C SEQ ID NO: 112	WYQQLPGKGPRTVI Y SEQ ID NO: 292	GVPDRFSGSASGSSATLTIS- GLQAEDEAEYYC SEQ ID NO: 307	FGGGTHLTVLGQPK A SEQ ID NO: 229
or				
cnsns s	SWAQSVLTQPASVSGSLGQRTIS C SEQ ID NO: 98	WYQQLPGTGPRTLII Y SEQ ID NO: 131	GVPDRFSGSRSGSTATLTIS- GLQAEDEADYYC SEQ ID NO: 183	FGGGTHLTVLGQPK A SEQ ID NO: 212,

20. Kappa Light Chain Variable Domain Genus

[0040] The invention also comprises a kappa light chain variable domain polypeptide of formula:



wherein

Fr¹ is Z¹ Z² Z³ Z⁴ Z⁵ Z⁶ Z⁷ Z⁸ Z⁹ Z¹⁰ Z¹¹ Z¹² Z¹³ Z¹⁴ Z¹⁵ Z¹⁶ Z¹⁷ Z¹⁸ Z¹⁹ Z²⁰ Z²¹ Z²² Z²³ (SEQ ID NO: 312);

Fr² is Z²⁴ Z²⁵ Z²⁶ Z²⁷ Z²⁸ Z²⁹ Z³⁰ Z³¹ Z³² Z³³ Z³⁴ Z³⁵ Z³⁶ Z³⁷ Z³⁸ (SEQ ID NO: 313)

Fr³ is Z³⁹ Z⁴⁰ Z⁴¹ Z⁴² Z⁴³ Z⁴⁴ Z⁴⁵ Z⁴⁶ Z⁴⁷ Z⁴⁸ Z⁴⁹ Z⁵⁰ Z⁵¹ Z⁵² Z⁵³ Z⁵⁴ Z⁵⁵ Z⁵⁶ Z⁵⁷ Z⁵⁸ Z⁵⁹ Z⁶⁰ Z⁶¹ Z⁶² Z⁶³ Z⁶⁴ Z⁶⁵ Z⁶⁶ Z⁶⁷ Z⁶⁸ Z⁶⁹ Z⁷⁰ (SEQ ID NO: 314), and

Fr⁴ is Z⁷¹ Z⁷² Z⁷³ Z⁷⁴ Z⁷⁵ Z⁷⁶ Z⁷⁷ Z⁷⁸ Z⁷⁹ Z⁸⁰ Z⁸¹ Z⁸² Z⁸³ Z⁸⁴ Z⁸⁵ Z⁸⁶ Z⁸⁷ Z⁸⁸ (SEQ ID NO: 315)

wherein

Z ¹ is <u>D</u> , E, A or -;	Z ² is <u>I</u> , L, V or -;	Z ³ is <u>V</u> or -;	Z ⁴ is <u>M</u> , L, or -;	Z ⁵ is <u>T</u> or -;
Z ⁶ is <u>Q</u> , E, or -;	Z ⁷ is <u>T</u> , A, or -;	Z ⁸ is <u>P</u> or -;	Z ⁹ is <u>P</u> , L, R, S, or -;	Z ¹⁰ is <u>S</u> , P, or -;
Z ¹¹ is <u>L</u> or -;	Z ¹² is <u>S</u> or -;	Z ¹³ is <u>V</u> , A, or -;	Z ¹⁴ is <u>S</u> or -;	Z ¹⁵ is <u>P</u> or -;
Z ¹⁶ is <u>G</u> , R, or -;	Z ¹⁷ is <u>E</u> or -;	Z ¹⁸ is <u>P</u> , T, S, or -;	Z ¹⁹ is <u>A</u> or -;	Z ²⁰ is <u>S</u> , F, or -;
Z ²¹ is <u>I</u> or -;	Z ²² is <u>S</u> or -;	Z ²³ is <u>C</u> , Y, or -;	Z ²⁴ is <u>W</u> or -;	Z ²⁵ is <u>F</u> , Y, S, L, or -;
Z ²⁶ is <u>R</u> , L, Q, M, or -;	Z ²⁷ is <u>Q</u> , H, or -;	Z ²⁸ is <u>K</u> , R, or -;	Z ²⁹ is <u>P</u> , S, or -;	Z ³⁰ is <u>G</u> or -;
Z ³¹ is <u>Q</u> , H, or -;	Z ³² is <u>S</u> , A, or -;	Z ³³ is <u>P</u> or -;	Z ³⁴ is <u>Q</u> , E, R, or -;	Z ³⁵ is <u>R</u> , G, D, L, T, I, A, or -;
Z ³⁶ is <u>L</u> , R, or -;	Z ³⁷ is <u>T</u> or -;	Z ³⁸ is <u>Y</u> , H, S, W, F, or -;	Z ³⁹ is <u>G</u> ;	Z ⁴⁰ is <u>V</u> ;
Z ⁴¹ is <u>S</u> or P;	Z ⁴² is <u>D</u> or E;	Z ⁴³ is <u>R</u> or G;	Z ⁴⁴ is <u>F</u> or <u>I</u> ;	Z ⁴⁵ is <u>S</u> or A;
Z ⁴⁶ is <u>G</u> ;	Z ⁴⁷ is <u>S</u> or R;	Z ⁴⁸ is <u>G</u> ;	Z ⁴⁹ is <u>S</u> ;	Z ⁵⁰ is <u>G</u> or V;
Z ⁵¹ is <u>T</u> or A;	Z ⁵² is <u>D</u> ;	Z ⁵³ is <u>F</u> or C;	Z ⁵⁴ is <u>T</u> ;	Z ⁵⁵ is <u>L</u> ;
Z ⁵⁶ is <u>R</u> , K, T or E;	Z ⁵⁷ is <u>I</u> ;	Z ⁵⁸ is <u>S</u> , T, or G;	Z ⁵⁹ is <u>R</u> or G;	Z ⁶⁰ is <u>V</u> or A;
Z ⁶¹ is <u>E</u> , V, or G;	Z ⁶² is <u>A</u> or D;	Z ⁶³ is <u>D</u> , N, A, E, or G;	Z ⁶⁴ is <u>D</u> or G;	Z ⁶⁵ is <u>A</u> , T, S, V, or G;
Z ⁶⁶ is <u>G</u> or A;	Z ⁶⁷ is <u>V</u> , L, or I;	Z ⁶⁸ is <u>Y</u> ;	Z ⁶⁹ is <u>Y</u> , H, F, or C;	Z ⁷⁰ is <u>C</u> ;
Z ⁷¹ is <u>F</u> , L, or S;	Z ⁷² is <u>S</u> or G;	Z ⁷³ is <u>Q</u> , A, K, P, or T;	Z ⁷⁴ is <u>G</u> ;	Z ⁷⁵ is <u>T</u> or A;
Z ⁷⁶ is <u>K</u> , N, or H;	Z ⁷⁷ is <u>L</u> or V;	Z ⁷⁸ is <u>E</u> , D, V, or G;	Z ⁷⁹ is <u>I</u> , M, or L;	Z ⁸⁰ is <u>K</u> or R;
Z ⁸¹ is <u>R</u> ;	Z ⁸² is <u>N</u> ;	Z ⁸³ is <u>D</u> ;	Z ⁸⁴ is <u>A</u> ;	Z ⁸⁵ is <u>Q</u> ;
Z ⁸⁶ is <u>P</u> ;	Z ⁸⁷ is <u>A</u> ;	Z ⁸⁸ is <u>V</u> ;		

provided that when Z^k for k ≤ 37 is --, Z¹ for 1 < k is --.

21. Kappa Light Chain Variable Domain Sub-genus

[0041] Preferably, the canine k light chain variable domain according to the invention is a compound comprising the sequence:



wherein

Fr¹ is

DTVLTQTTPPSLSVSPGEPA-SISC SEQ ID NO: 316	DIVMTQAPPSLSVSPGEPA-SISC SEQ ID NO: 317	DLVLTQTTPRSLSVSPGETASISC SEQ ID NO: 318
DIVMTQTPLSLSVSPGEPA-SISC SEQ ID NO: 319	DIVMTQAPPPLSVSPGEPA-SISC SEQ ID NO: 320	DIVMTQTTPPSLSVSPREPASISC SEQ ID NO: 321
ASISC SEQ ID NO: 322	SLSVSPGEPAFISC SEQ ID NO: 323	VMTQTPLSLSVSPGEPASISC SEQ ID NO: 324
IVMTQTPLSLSVSPGEPA-SISC SEQ ID NO: 325	DIVMTQAPPSXSVSPGEPA-SISC SEQ ID NO: 326	DVVMQTQAPPSLSVSPREPASISC SEQ ID NO: 327
DVVMQTQAPPSLSVSPGEPA-SISC SEQ ID NO: 328	IVMTQTPLSLSVSXXEPA-SISC SEQ ID NO: 329	DVVMQTQTTPPSLSVSPREPASISC SEQ ID NO: 330
EIVMTQTPLSLSVSPGETA-SISY SEQ ID NO: 331	DIVMTQTPLSLSASPGETA-SISC SEQ ID NO: 332	DIVMTEAPPSLSVSPGESASISC SEQ ID NO: 333
DIVMTQIPLSLSVSPGEPA-SISC SEQ ID NO: 334	DIVMTQTPLSLSVSPGETA-SISC SEQ ID NO: 335	DIVMTQTTPPSLSVSPGEPASISC SEQ ID NO: 336
IIVMTQTPLSLSASPGEA-SISC SEQ ID NO: 337	AIVMTQAPPSLSVSPGEPA-SISC SEQ ID NO: 338	DIVMTQTTPPSLSVSPGETASISC SEQ ID NO: 339
--- MTQAPPSLSVSPGEPASISC SEQ ID NO: 340	PSLSVSPREPASISC SEQ ID NO: 341	TQAPSSLSVSPGEPASISC SEQ ID NO: 342
DIVMTQTTPPSLSVSPXEPA-SISC SEQ ID NO: 343	or -;	

Fr² is

WYLQKPGQSPQLLIY SEQ ID NO: 344	WYRQKPGQSPED-LIY SEQ ID NO: 345	WFRQKPGQSPQRLIY SEQ ID NO: 346	WFRQKPGQSPEG-LIY SEQ ID NO: 347
WFQQKPGQSPEG-LIY SEQ ID NO: 348	WFRQKPGQSPEG-LIH SEQ ID NO: 349	WFRQKPGQSPQRLIS SEQ ID NO: 350	WFQQKPGQSPQRLIW SEQ ID NO: 351
WFRQKPGQSPED-LIY SEQ ID NO: 352	WFQQKPGQSPQGLIY SEQ ID NO: 353	WFRHKPGQSPQTLIY SEQ ID NO: 354	WFQQKPGHSPRGLIY SEQ ID NO: 355

WYMQKPGQSPQGRI Y SEQ ID NO: 356	WFRQRPQGQSPQRLI Y SEQ ID NO: 357	WLRQKPGQSPEG- LIY SEQ ID NO: 358	WSRQRPQGQSPEG- LIY SEQ ID NO: 359
WYLQKPGQSPQILI Y SEQ ID NO: 360	WFRQKPGQAPQR- LIY SEQ ID NO: 361	WFRQKPGQSPQRLI F SEQ ID NO: 362	WFQQKPGQSPQRLI Y SEQ ID NO: 363
WYLQKPGQSPQRLI Y SEQ ID NO: 364	WIRQKPGQSPEG- LIY SEQ ID NO: 365	WFRQRPQGQSPEALI Y SEQ ID NO: 366	WFRQKSGQSPQRLI Y SEQ ID NO: 367
or	Y;		

Fr³ is

GVSDRFSGSGSGTDFTLRISRVEPNDTGI- YYC SEQ ID NO: 368	GVSDRFSGSGSGTDFTLRISRVEADDAGI- YYC SEQ ID NO: 369
GVPDRFSGSGSGTDFTLRISRVEADDTGLY YC SEQ ID NO: 370	GVSDRFSGSGSGTDFTLTISRVEAD- DAGVYYC SEQ ID NO: 371
GVSDRFSGSGSGTDFTLRISRVEAD- DAGVYYC SEQ ID NO: 372	GVSDRFSGSGSGTDFTLRISRVEADDA- GLYYC SEQ ID NO: 373
GVSDRFSGSGSGTDFTLRISRVEADDTGVY YC SEQ ID NO: 374	GVSDRFSGSGSGTDFTLRISRVEADDTGVY YC SEQ ID NO: 374
GVPDRFSGSGSGTDFTLRIGRVEADDTGVY YC SEQ ID NO: 375	GVPDRFSGSGSGTDFTLRISRVEADDAGI- YYC SEQ ID NO: 376
GVPDRFSGSGSGTDCCTLISRVEAD- DAGVYYC SEQ ID NO: 377	GVSDRFSGSGSGTDFTLRISRVEAD- DAVYYC SEQ ID NO: 378
GVPDRFSGSGSGTDFTLRISRVEAD- DAGVYYC SEQ ID NO: 379	GVPDRFRGSGSGTDFTLRISRAEADDAGI- YYC SEQ ID NO: 380
GVSDRFSGSGSGTDFTLRISRVEAD- DAGVYHC SEQ ID NO: 381	GVPDRFSGSGSGTDFTLRISRVEANDTGVY YC SEQ ID NO: 382
GASDRFSGSGSGADFTXRISRVEAD- DAGVYYC SEQ ID NO: 383	GVPDGFSGSGSGTDFTLRISRVEAD- DAGVYYC SEQ ID NO: 384
GVSDRFSGSGSGTDFTLKISRVEADDTGVY XC SEQ ID NO: 385	GVPDRFSGSGSGTDFTLRISRVEADDSGVY YC SEQ ID NO: 386
GVPDRFSGSGSGTDFTLRISRVEADDTGVY YC SEQ ID NO: 387	GVSDRFSGRSGSGTDFTLRISRVEAG- DAGVYYC SEQ ID NO: 388
GVSDRFSGSGSGTDFTLKISRVEAD- DAGVYFC SEQ ID NO: 389	GVPDRFSGSGSGTDFTLRISRVVAD- DAGVYYC SEQ ID NO: 390
GVPDRFSGSGSGTDFTLRISRVEDEDA- GLYYC	GVSDRFSGSGSGTDFTLRISRVEADDSGVY YC

SEQ ID NO: 391	SEQ ID NO: 392
GVPDRFSGSGSGTDFTLRISRVEADDGGVY HC	GIPDRFSGSGSGTDFTLRIS- GVEAADTGVYYC
SEQ ID NO: 393	SEQ ID NO: 394
GVSDRFSGSGSGTDFTLRISRVEANDTGVY YC	GVSDRFSGSGSGTDFTLRISRVEADDXGVY YC
SEQ ID NO: 395	SEQ ID NO: 396
GVPDRFSGSGSGTDFTLRISRVEADDTGVY FC	GVPDRFAGSGSGTDFTLRISRVEADDTGI- YYC
SEQ ID NO: 397	SEQ ID NO: 398
GVPDRFSGSGSGTDCTLTISRVEAD- GAGVYYC	GVPDRFSGSGSGTDCTLTISRVEAD- DAGVYCC
SEQ ID NO: 399	SEQ ID NO: 400
GVSERFSGSGSGTDFTLEISRVEADDVG YC	GVSDRFSGSGSGTDFTLRITRVEAD- DAGVYYC
SEQ ID NO: 401	SEQ ID NO: 402
GVSERFSGSGSGTDFTLEISRVGADDVG YC	GVSDRFSGSGSGTDFTLRISRVEADDTGLY YC
SEQ ID NO: 403	SEQ ID NO: 404
GVPDRFSGSGSGTDFTLTISRVEAD- DAGVYYC	GVSDRFSGSGSVTDFTLRISRVEADDAGI- YYC
SEQ ID NO: 405	SEQ ID NO: 406
or	GVSERISGSGSGTDFTLRISRVEADDAGI- YYC
	SEQ ID NO: 407;

Fr⁴ is

FGAGTKVELK- RNDAPAVY SEQ ID NO: 408	FGKGTHLEIKRNDAPAVY SEQ ID NO: 409	FSQGTNLEMKRNDAPAVY SEQ ID NO: 410	FGTGKVELKRNDAPAVY SEQ ID NO: 411
FSQGTKLEIKRNDAPAVY SEQ ID NO: 412	FGQGTKVEIKRNDAPAVY SEQ ID NO: 413	FSQGTPLEIKRNGAPAVY SEQ ID NO: 414	FGQGTKVDIKRNDAPAVY SEQ ID NO: 415
FGQGTKLEIKRNDAPAVY SEQ ID NO: 416	FSQGTKLEIN- RNDAPAVY SEQ ID NO: 417	FGKGTHLEIKRNDAPAVY SEQ ID NO: 418	FSQGKKLEIKRA SEQ ID NO: 419
FSQGTKLEIKRND SEQ ID NO: 420	FGQGTKLEIKRNDAPAVY SEQ ID NO: 421	FGAGTKLEIKRNDAPAVY SEQ ID NO: 422	FGQGTKLEIRRNDAPAVY SEQ ID NO: 423
FSQGTKLEIKRNDAPAVY SEQ ID NO: 424	FGAGTKVELK- RNDAPAVY SEQ ID NO: 425	FGQGTKVEIKRNDAPAVY SEQ ID NO: 426	LSQGAKLDIKRNDAPAVY SEQ ID NO: 427
SSQGTKLEIKRNDAPAVY SEQ ID NO: 428	FGQGTNLEIKRNDAPAVY SEQ ID NO: 429	FGKGTHLEIKRNDAPAVY SEQ ID NO: 430	FSQGTNLEMKRNDAPAVY SEQ ID NO: 431
FSQGTRLEIKRNDAPAVY SEQ ID NO: 432	FSQGTNLEIKRNDAPAVY SEQ ID NO: 433	FGPGAKVELKRNDAPAVY SEQ ID NO: 434	FSQGTKLVIKRNDAPAVY SEQ ID NO: 435
FGQGTXLLEIKRNDAPAVY SEQ ID NO: 436	FSQGTNLGMKRNDAPAVY SEQ ID NO: 437	LSQGTKLEIERNDAPAVY SEQ ID NO: 438	or FSQGTKLEIR- RNDAPAVY. SEQ ID NO: 439

22. Kappa Light Chain Variable Domain species

[0042] Preferably, the canine kappa light chain variable domain according to the invention is a compound comprising the sequence:



wherein Fr^1 , Fr^2 , Fr^3 , and Fr^4 are selected from the following combinations:

#	Fr^1	Fr^2	Fr^3	Fr^4
KAPA129	DTVLTQTTPPSLSVSPGEPA-SISC SEQ ID NO: 316	WYLQKPGQSPQLLIY SEQ ID NO: 344	GVSDRFSGSGSGTDFTLRISRVEPNDTGIYYC SEQ ID NO: 368	FGAGTKVELKRNDAPAVY SEQ ID NO: 408
KAPA130	DIVMTQAPPSLSVSPGEPA-SISC SEQ ID NO: 317	WYRQKPGQSPEDLIY SEQ ID NO: 345	GVSDRFSGSGSGTDFTLRISRVEADDAGIYYC SEQ ID NO: 369	FGKGTHLEIKRNDAPAVY SEQ ID NO: 409
KAPA131	DLVLTQTPRSLSVSPGETA-SISC SEQ ID NO: 318	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDTGLYYC SEQ ID NO: 370	FSQGTNLEMKRNDAPAVY SEQ ID NO: 410
KAPA212	DIVMTQTPLSLSVSPGEPA-SISC SEQ ID NO: 319	WFRQKPGQSPQGLIY SEQ ID NO: 347	GVSDRFSGSGSGTDFTLRISRVEAD-DAGVYYC SEQ ID NO: 371	FGTGTKVELKRNDAPAVY SEQ ID NO: 411
KAPA214	DLVLTQTPRSLSVSPGETA-SISC SEQ ID NO: 318	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDTGLYYC SEQ ID NO: 370	FSQGTNLEMKRNDAPAVY SEQ ID NO: 410
KAPA217	DIVMTQAPPSLSVSPGEPA-SISC SEQ ID NO: 317	WFQKPGQSPQGLIY SEQ ID NO: 348	GVSDRFSGSGSGTDFTLRISRVEAD-DAGVYYC SEQ ID NO: 372	FSQGTKLEIKRNDAPAVY SEQ ID NO: 412
KAPA218	DIVMTQAPPSLSVSPGEPA-SISC SEQ ID NO: 320	WFRQKPGQSPQGLIY SEQ ID NO: 349	GVSDRFSGSGSGTDFTLRISRVEADDA-GLYYC SEQ ID NO: 373	FGQGTKVEIKRNDAPAVY SEQ ID NO: 413
K110-79	DIVMTQTTPPSLSVSPREPA-SISC SEQ ID NO: 321	WYLQKPGQSPQLLIY SEQ ID NO: 344	GVSDRFSGSGSGTDFTLRISRVEADDTGVYYC SEQ ID NO: 374	FGAGTKVELKRNDAPAVY SEQ ID NO: 408
K114-79	ASISC SEQ ID NO: 322	WFRQKPGQSPQRLIY SEQ ID NO: 350	GVPDRFSGSGSGTDFTLRISRVEADDTGVYYC SEQ ID NO: 375	FSQGTPLEIKRNDAPAVY SEQ ID NO: 414
K127-75	-	WFQKPGQSPQRLIY SEQ ID NO: 351	GVPDRFSGSGSGTDFTLRISRVEADDAGIYYC SEQ ID NO: 376	FGQGTKVDIKRNDAPAVY SEQ ID NO: 415
K203-79	DIVMTQAPPSLSVSPGEPA-SISC SEQ ID NO: 317	WFRQKPGQSPQGLIY SEQ ID NO: 347	GVSDRFSGSGSGTDFTLRISRVEAD-DAGVYYC SEQ ID NO: 372	FSQGTKLEIKRNDAPAVY SEQ ID NO: 412
K208-79	SLSVSPGEPAFISC SEQ ID NO: 323	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDCTLTISRVEAD-DAGVYYC SEQ ID NO: 377	FGQGTKLEIKRNDAPAVY SEQ ID NO: 416
K213-79	VMTQTPLSLSVSPGEPASISC SEQ ID NO: 324	WFRQKPGQSPEDLIY SEQ ID NO: 352	GVSDRFSGSGSGTDFTLRISRVEADDAGIYYC SEQ ID NO: 369	FGKGTHLEIKRNDAPAVY SEQ ID NO: 409
K217-79	IVMTQTPLSLSVSPGEPASISC SEQ ID NO: 325	WFRQKPGQSPQGLIY SEQ ID NO: 347	GVSDRFSGSGSGTDFTLRISRVEAD-DAVYYC SEQ ID NO: 378	FSQGTKLEIKRNDAPAVY SEQ ID NO: 417
K219-79	DIVMTQAPPSXSVSPGEPA-SISC SEQ ID NO: 326	WYRQKPGQSPEDLIY SEQ ID NO: 345	GVSDRFSGSGSGTDFTLRISRVEAD-DAVYYC SEQ ID NO: 378	FSQGTKLEIKRNDAPAVY SEQ ID NO: 412
K1201	-	WFQKPGQSPQGLIY SEQ ID NO: 353	GVPDRFSGSGSGTDFTLRISRVEAD-DAGVYYC SEQ ID NO: 379	FGQGTKLEIKRNDAPAVY SEQ ID NO: 416
K1202	-	WFQKPGQSPQGLIY SEQ ID NO: 353	GVPDRFRSGSGSGTDFTLRISRVEADDAGIYYC SEQ ID NO: 380	FGKGTHLEIKRNDAPAVY SEQ ID NO: 409
K1204	DVMTQAPPSLSVSPREPA-SISC SEQ ID NO: 327	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEAD-DAGVYYC SEQ ID NO: 379	FGQGTKLEIKRNDAPAVY SEQ ID NO: 416
K1206	DIVMTQTPLSLSVSPGEPA-SISC SEQ ID NO: 319	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDAGIYYC SEQ ID NO: 376	FGKGTHLEIKRNDAPAVY SEQ ID NO: 418
K1208	DVMTQAPPSLSVSPREPA-SISC SEQ ID NO: 327	WFRQKPGQSPQGLIY SEQ ID NO: 347	GVSDRFSGSGSGTDFTLRISRVEAD-DAGVYHC SEQ ID NO: 381	FSQGTKLEIKRNDAPAVY SEQ ID NO: 412
K1212	DIVMTQTPLSLSVSPGEPA-SISC SEQ ID NO: 319	WFRHKGQSPQTLIY SEQ ID NO: 354	GVPDRFSGSGSGTDFTLRISRVEANDTGVIY C SEQ ID NO: 382	FSQGTKLEIKRNDAPAVY SEQ ID NO: 412
K1213	DVMTQAPPSLSVSPGEPA-SISC SEQ ID NO: 328	WFRQKPGQSPQGLIY SEQ ID NO: 347	GVSDRFSGSGSGTDFTLRISRVEAD-DAGVYHC SEQ ID NO: 381	FSQGTKLEIKRNDAPAVY SEQ ID NO: 412
K1218	IVMTQTPLSLSVSPXEPASISC SEQ ID NO: 329	WFRQKPGQSPQRLIY SEQ ID NO: 346	GASDRFSGSGSGADFTXRISRVEAD-DAGVYYC SEQ ID NO: 383	FSQGXKLEIKRA SEQ ID NO: 419
K1219	-	WFQKPGHSPRGLIY SEQ ID NO: 355	GVPDRFSGSGSGTDFTLRISRVEAD-DAGVYYC SEQ ID NO: 379	FGQGTKLEIKRNDAPAVY SEQ ID NO: 416
K1221	DVMTQAPPSLSVSPREPA-SISC SEQ ID NO: 327	WFRQKPGQSPQGLIY SEQ ID NO: 347	GVSDRFSGSGSGTDFTLRISRVEAD-DAGVYYC SEQ ID NO: 372	FSQGTKLEIKRNDAPAVY SEQ ID NO: 412
K1223	DVMTQTTPPSLSVSPREPA-SISC SEQ ID NO: 330	WFRQKPGQSPQGLIY SEQ ID NO: 347	GVSDRFSGSGSGTDFTLRISRVEAD-DAGVYYC SEQ ID NO: 372	FSQGTKLEIKRND SEQ ID NO: 420
K1225	-	WFQKPGQSPQGLIY SEQ ID NO: 353	GVPDGFSGSGSGTDFTLRISRVEAD-DAGVYYC SEQ ID NO: 384	FGQGTKLEIKRNDAPAVY SEQ ID NO: 421
K1278	EIVMTQTPLSLSVSPGETA-SISC	WYMQKPGQSPQGLIY	GVSDRFSGSGSGTDFTLRISRVEADDTGVYX	-

#	Fr ¹	Fr ²	Fr ³	Fr ⁴
	SISY SEQ ID NO: 331	SEQ ID NO: 356	C SEQ ID NO: 385	
K1279	-	WFRQKPGQSPQRLIY SEQ ID NO: 357	GVPDRFSGSGSGTDFTLRISRVEADDSGVYY C SEQ ID NO: 386	FGAGTKLEIKRNDAPAVY SEQ ID NO: 422
K1283	DIVMTQTPLSLSASPGETA- SISC SEQ ID NO: 332	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDTGVYY C SEQ ID NO: 387	FGQGTKLEIKRNDAPAVY SEQ ID NO: 423
K1284	DIVMTQAPPSLSVSPGES- SISC SEQ ID NO: 333	WLRQKPGQSPQRLIY SEQ ID NO: 358	GVSDRFSGSGSGTDFTLRISRVEAG- DAGVYYC SEQ ID NO: 388	FSQGTKLEIKRNDAPAVY SEQ ID NO: 412
K1285	DIVMTQTPLSLSVSPGEPA- SISC SEQ ID NO: 319	WSRQKPGQSPQRLIY SEQ ID NO: 359	GVSDRFSGSGSGTDFTLRISRVEAD- DAGVYFC SEQ ID NO: 389	FSQGTKLEIKRNDAPAVY SEQ ID NO: 424
K1286	DIVMTQIPLSLSVSPGEPA- SISC SEQ ID NO: 334	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEAD- DAGVYYC SEQ ID NO: 379	FGAGTKVELKRNDAPAVY SEQ ID NO: 425
K1287	DIVMTQAPPSLSVSPGEPA- SISC SEQ ID NO: 317	WFRQKPGQSPQRLIY SEQ ID NO: 347	GVSDRFSGSGSGTDFTLRISRVEAD- DAGVYYC SEQ ID NO: 372	FGQGTKVEIKRNDAPAVY SEQ ID NO: 426
K1288	DIVMTQTPLSLSVSPGETA- SISC SEQ ID NO: 335	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEAD- DAGVYYC SEQ ID NO: 390	FGAGTKVELKRNDAPAVY SEQ ID NO: 425
K1289	DIVMTQAPPSLSVSPGEPA- SISC SEQ ID NO: 317	WFRQKPGQSPQRLIY SEQ ID NO: 347	GVSDRFSGSGSGTDFTLRISRVEAD- DAGVYYC SEQ ID NO: 372	LSQGAKLDIRNDAPAVY SEQ ID NO: 427
K1243	IIVMTQTPLSLSASPGES- SISC SEQ ID NO: 337	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEEDA- GLYYC SEQ ID NO: 391	FGQGTKLEIKRNDAPAVY SEQ ID NO: 421
K1244	-	WYLQKPGQSPQRLIY SEQ ID NO: 360	GVSDRFSGSGSGTDFTLRISRVEADDSGVYY C SEQ ID NO: 392	FGAGTKVELKRNDAPAVY SEQ ID NO: 425
K1250	DIVMTQTPLSLSVSPGEPA- SISC SEQ ID NO: 319	WFRQKPGQAPQRLIY SEQ ID NO: 361	GVPDRFSGSGSGTDFTLRISRVEADDSGVYY C SEQ ID NO: 393	FSQGTKLEIKRNDAPAVY SEQ ID NO: 424
K1251	-	WFRQKPGQSPQRLIY SEQ ID NO: 357	GVPDRFSGSGSGTDFTLRISRVEADDSGVYY C SEQ ID NO: 386	SSQGTKLEIKRNDAPAVY SEQ ID NO: 428
K1275	AIVMTQAPPSLSVSPGEPA- SISC SEQ ID NO: 338	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDSGVYY C SEQ ID NO: 386	FGAGTKVELKRNDAPAVY SEQ ID NO: 425
K1343	DIVMTQTPLSLSVSPGETA- SISC SEQ ID NO: 339	WFRQKPGQSPQRLIY SEQ ID NO: 346	GIPDRFSGSGSGTDFTLRISR- GVEAADTGVYYC SEQ ID NO: 394	FGQGTNLEIKRNDAPAVY SEQ ID NO: 429
K1348	-MTQAPPSLSVSPGEPA- SISC SEQ ID NO: 340	WYRQKPGQSPQRLIY SEQ ID NO: 345	GVSDRFSGSGSGTDFTLRISRVEADDA- GYYC SEQ ID NO: 369	FGKGTNLEIKRNDAPAVY SEQ ID NO: 430
K1349	DLVLTQTPLSLSVSPGETA- SISC SEQ ID NO: 318	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDTGLYY C SEQ ID NO: 370	FSQGTNLEIKRNDAPAVY SEQ ID NO: 431
K1350	DLVLTQTPLSLSVSPGETA- SISC SEQ ID NO: 318	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDTGLYY C SEQ ID NO: 370	FSQGTNLEIKRNDAPAVY SEQ ID NO: 431
K1353	DIVMTQTPLSLSVSPGEPA- SISC SEQ ID NO: 319	WYLQKPGQSPQRLIY SEQ ID NO: 344	GVSDRFSGSGSGTDFTLRISRVEANDTGVYY C SEQ ID NO: 395	FGQGTKLEIKRNDAPAVY SEQ ID NO: 421
K1354	-PSLSVSPREPASISC SEQ ID NO: 341	WYLQKPGQSPQRLIY SEQ ID NO: 344	GVSDRFSGSGSGTDFTLRISRVEADDXGVYY C SEQ ID NO: 396	FSQGTNLEIKRNDAPAVY SEQ ID NO: 432
K1360	DLVLTQTPLSLSVSPGETA- SISC SEQ ID NO: 318	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDTGLYY C SEQ ID NO: 370	FSQGTNLEIKRNDAPAVY SEQ ID NO: 431
K1361	DLVLTQTPLSLSVSPGETA- SISC SEQ ID NO: 318	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDTGLYY C SEQ ID NO: 370	FSQGTNLEIKRNDAPAVY SEQ ID NO: 431
K1362	DIVMTQTPLSLSVSPGEPA- SISC SEQ ID NO: 336	WYLQKPGQSPQRLIY SEQ ID NO: 344	GVSDRFSGSGSGTDFTLRISRVEANDTGVYY C SEQ ID NO: 395	FGQGTKLEIKRNDAPAVY SEQ ID NO: 421
K1363	DIVMTQTPLSLSVSPGETA- SISC SEQ ID NO: 335	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDTGVYY C SEQ ID NO: 397	FSQGTNLEIKRNDAPAVY SEQ ID NO: 433
K1366	DLVLTQTPLSLSVSPGETA- SISC SEQ ID NO: 318	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDTGLYY C SEQ ID NO: 370	FSQGTNLEIKRNDAPAVY SEQ ID NO: 431
K1370	DIVMTQTPLSLSVSPGETA- SISC SEQ ID NO: 335	WFRQKPGQSPQRLIY SEQ ID NO: 362	GVPDRFAGSGSGTDFTLRISRVEADDTGI- YYC SEQ ID NO: 398	FGPGAKVELKRNDAPAVY SEQ ID NO: 434
K1371	DIVMTQTPLSLSVSPGEPA- SISC SEQ ID NO: 319	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDTGVYY C SEQ ID NO: 387	FSQGTNLEIKRNDAPAVY SEQ ID NO: 435
K2420	DIVMTQTPLSLSVSPGEPA- SISC SEQ ID NO: 319	WFRQKPGQSPQRLIY SEQ ID NO: 363	GVPDRFSGSGSGTDFTLRISRVEAD- GAGVYYC SEQ ID NO: 399	FGQGTKLEIKRNDAPAVY SEQ ID NO: 421
K2422	DIVMTQTPLSLSVSPGEPA- SISC SEQ ID NO: 336	WYLQKPGQSPQRLIY SEQ ID NO: 364	GVPDRFSGSGSGTDFTLRISRVEADDTGLYY C SEQ ID NO: 370	FSQGTNLEIKRNDAPAVY SEQ ID NO: 431
K2423	-	WFRQKPGQSPQRLIY SEQ ID NO: 363	GVPDRFSGSGSGTDFTLRISRVEAD- DAGVYYC SEQ ID NO: 400	FGQGTNLEIKRNDAPAVY SEQ ID NO: 436
K2425	DIVMTQTPLSLSVSPGEPA- SISC SEQ ID NO: 336	WYLQKPGQSPQRLIY SEQ ID NO: 344	GVSDRFSGSGSGTDFTLRISRVEANDTGVYY C SEQ ID NO: 395	FGQGTKLEIKRNDAPAVY SEQ ID NO: 421
K2426	DLVLTQTPLSLSVSPGETA- SISC SEQ ID NO: 318	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDTGLYY C SEQ ID NO: 370	FSQGTNLEIKRNDAPAVY SEQ ID NO: 437
K2427	DIVMTQAPPSLSVSPGEPA- SISC SEQ ID NO: 317	WFRQKPGQSPQRLIY SEQ ID NO: 347	GVSDRFSGSGSGTDFTLRISRVEADDTGVYY C SEQ ID NO: 401	FSQGTKLEIKRNDAPAVY SEQ ID NO: 424
K2430	DIVMTQTPLSLSVSPGEPA- SISC SEQ ID NO: 336	WYLQKPGQSPQRLIY SEQ ID NO: 344	GVSDRFSGSGSGTDFTLRISRVEANDTGVYY C SEQ ID NO: 395	FGQGTKLEIKRNDAPAVY SEQ ID NO: 421

#	Fr ¹	Fr ²	Fr ³	Fr ⁴
K2431	-TQAPSSLSVSPGEPASISC SEQ ID NO: 342	WIRQKPGQSPEGLIY SEQ ID NO: 365	GVSDRFSGSGSGTDFTLRITRVEAD- DAGVYYC SEQ ID NO: 402	LSQGTKLEIERNDAQPAV SEQ ID NO: 438
K2432	DIVMTQTTPPSLSVSPGEPASISC SEQ ID NO: 336	WFRQKPGQSPEGLIY SEQ ID NO: 347	GVSERFSGSGSGTDFTLEISRVGADDVGYY C SEQ ID NO: 403	FSQGTKLEIKRNDAPAV SEQ ID NO: 424
K2435	DLVLTQTPRSLSVSPGETASISC SEQ ID NO: 318	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLRISRVEADDTGLYY C SEQ ID NO: 370	FSQGTNLEMKRNDAPAV SEQ ID NO: 431
K2436	DIVMTQTTPPSLSVSPXEPA- SISC SEQ ID NO: 343	WYLQKPGQSPQLLIY SEQ ID NO: 344	GVSDRFSGSGSGTDFTLRISRVEANDTGYY C SEQ ID NO: 395	FGQGTKLEIKRNDAPAV SEQ ID NO: 421
K2437	DIVMTQTTPPSLSVSPGEPASISC SEQ ID NO: 336	WYLQKPGQSPQLLIY SEQ ID NO: 344	GVSDRFSGSGSGTDFTLRISRVEADDTGLYY C SEQ ID NO: 404	FSQGTNLEMKRNDAPAV SEQ ID NO: 431
K2438	DIVMTQTTPPSLSVSPGEPASISC SEQ ID NO: 336	WYLQKPGQSPQLLIY SEQ ID NO: 344	GVSDRFSGSGSGTDFTLRISRVEANDTGYY C SEQ ID NO: 395	FGQGTKLEIKRNDAPAV SEQ ID NO: 421
K2440	DIVMTQTTPPSLSVSPGEPASISC SEQ ID NO: 336	WYLQKPGQSPQLLIY SEQ ID NO: 344	GVSDRFSGSGSGTDFTLRISRVEANDTGYY C SEQ ID NO: 395	FGQGTKLEIKRNDAPAV SEQ ID NO: 421
K2442	DLVLTQTPRSLSVSPGETASISC SEQ ID NO: 318	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVPDRFSGSGSGTDFTLTISRVEAD- DAGVYYC SEQ ID NO: 405	FSQGTKLEIRNDAPAV SEQ ID NO: 439
K2443	-	WFRQKPGQSPEALIY SEQ ID NO: 366	GVSDRFSGSGSVTDFTLRISRVEADDAGI- YYC SEQ ID NO: 406	FGKGTNLEMKRNDAPAV SEQ ID NO: 430
K2444	-	WFRQKSGQSPQRLIY SEQ ID NO: 367	GVPDRFSGSGSGTDFTLRISRVEADDTGLYY C SEQ ID NO: 370	FSQGTNLEMKRNDAPAV SEQ ID NO: 431
K2446	-	-Y	GVSERISGSGSGTDFTLRISRVEADDAGI- YYC SEQ ID NO: 407	FGQGTKLEIKRNDAPAV SEQ ID NO: 421
K2449	-	WFQKPGQSPQRLIY SEQ ID NO: 363	GVPDRFSGSGSGTDCTLTISRVEAD- DAGVYYC SEQ ID NO: 377	FGQGTKLEIKRNDAPAV SEQ ID NO: 421
and				
Cnsnss	DIVMTQTTPPSLSVSPGEPASISC SEQ ID NO: 336	WFRQKPGQSPQRLIY SEQ ID NO: 346	GVSDRFSGSGSGTDFTLRISRVEAD- DAGVYYC SEQ ID NO: 372	FSQGTKLEIKRNDAPAV SEQ ID NO: 424.

23. Other Lambda Light Chain Variable Domains

[0043] In another embodiment, the invention comprises the sequence:

$$\text{Fr}^1\text{-CDR}^1\text{-Fr}^2\text{-CDR}^2\text{-Fr}^3\text{-CDR}^3\text{-Fr}^4$$

wherein Fr¹, Fr², Fr³, and Fr⁴ are framework regions selected from the framework regions of the heavy chain variable sequences displayed in Table N₁. The framework sequences of the polypeptides in Table N₁ are readily and routinely determinable by those of ordinary skill in the art as those sequences that align with corresponding framework sequences of any of the known human variable domain sequences using any of the many accepted and widely available sequence alignment programs.

Complimentary Determining Regions

[0044] As used herein, CDR¹, CDR², and CDR³ are CDR's, which, in one embodiment are canine CDR's, and in another embodiment are non-canine CDR's from the same non-canine antibody. Preferably, two CDR's are from the same non-canine antibody and the third (preferably CDR¹) is a canine CDR. Preferred amino acids at each position are those that are bolded and underlined. The chimeric canine heavy chain variable domain polypeptides of the invention are not immunologically reactive with canine anti-serum.

[0045] In a preferred embodiment, CDR¹ for heavy chains is:

a) C¹² C¹³ C¹⁴ C¹⁵ C¹⁶ C¹⁷ C¹⁸ C¹⁹ C¹¹⁰ C¹¹¹ (SEQ ID NO: 440), wherein

C' ² is <u>G</u> ,	C' ³ is <u>F</u> or L,	C' ⁴ is <u>T</u> , S, or N,
C' ⁵ is <u>F</u> ,	C' ⁶ is <u>S</u> , G, N, or R,	C' ⁷ is <u>S</u> , D, G, N, Y, D, R, H, T, or Y,
C' ⁸ is <u>Y</u> , F, N, or C,	C' ⁹ is <u>G</u> , D, H, W, S, L, A, or V,	C' ¹⁰ is <u>M</u> ,
and C' ¹¹ is <u>S</u> , N, G, Y, I, or L;		

b) selected from the group consisting of:

GFTFSIYGMN SEQ ID NO: 441,	GFTFSDYGMN SEQ ID NO: 442,	GFTFSSYDMS SEQ ID NO: 443,	GFTFSSYSMS SEQ ID NO: 444,	GFTFSDYGMS SEQ ID NO: 445,	GFTFSSYGMS SEQ ID NO: 446,
GFNFGSYHMG SEQ ID NO: 447,	GFTFSYYLMS SEQ ID NO: 448,	GFTFRTYGMS SEQ ID NO: 449,	GFTFSGYWMS SEQ ID NO: 450,	GLSFGDFAMN SEQ ID NO: 451,	GFTFSDYYMY SEQ ID NO: 452,
GFTFSGCAMI SEQ ID NO: 453,	GFTFSNYDMS SEQ ID NO: 454,	GFTFSAYDML SEQ ID NO: 455,	GFSFSHNDMS SEQ ID NO: 456,	GFTFSRYWMS SEQ ID NO: 457,	GFTFNSYWMS SEQ ID NO: 458,
And	GFIFSSFHMS SEQ ID NO: 459;				

c) C'¹ C'² C'³ C'⁴ C'⁵ C'⁶ C'⁷ C'⁸ C'⁹ C'¹⁰ (SEQ ID NO: 460), wherein

C' ¹ is <u>G</u> ,	C' ² is <u>Y</u> ,	C' ³ is <u>T</u> or I,
C' ⁴ is <u>F</u> ,	C' ⁵ is <u>T</u> or I,	C' ⁶ is <u>D</u> ,
C' ⁷ is <u>Y</u> or Q,	C' ⁸ is <u>Y</u> ,	C' ⁹ is <u>M</u> ,
and	C' ¹⁰ is <u>H</u> ,	

d) selected from the group consisting of GYTFTDYMH (SEQ ID NO: 461)
and GYIFIDQYMH (SEQ ID NO: 462);

e) C'¹ C'² C'³ C'⁴ C'⁵ C'⁶ C'⁷ C'⁸ C'⁹ C'¹⁰ (SEQ ID NO: 463), wherein

C' ¹ is <u>G</u> ,	C' ² is <u>S</u> ,	C' ³ is <u>V</u> ,
C' ⁴ is <u>T</u> or <u>N</u> ,	C' ⁵ is <u>D</u> or <u>S</u> ,	C' ⁶ is <u>I</u> or <u>G</u> ,
C' ⁷ is <u>Y</u> or <u>H</u> ,	C' ⁸ is <u>Y</u> ,	C' ⁹ is <u>W</u> ,
and	C' ¹⁰ is <u>S</u> ,	

f) selected from the group consisting of GSVTDIHYWS (SEQ ID NO: 464)
and GSVNSGYYS (SEQ ID NO: 465), or

g) mouse 15A2 antibody CDR¹, SGYSFTDYFMN (SEQ ID NO: 466).

[0046] In a preferred embodiment, CDR² for heavy chains is:

a) C'¹ C'² C'³ C'⁴ C'⁵ C'⁶ C'⁷ C'⁸ C'⁹ C'¹⁰ C'¹¹ C'¹² C'¹³
C'¹⁴ C'¹⁵ C'¹⁶ C'¹⁷ (SEQ ID NO: 467), wherein

C'' ¹ is <u>Y</u> , G, V, Q, D, E, S, T, A, R, or W;	C'' ² is <u>I</u> ;	C'' ³ is <u>S</u> , N, H, W, or R;
C'' ⁴ is <u>S</u> , Y, T, N, D, G, R, or D;	C'' ⁵ is <u>G</u> , D, S, or A;	C'' ⁶ is <u>G</u> , E, or A;
C'' ⁷ is <u>S</u> , D, G, T, R, Y, or E;	C'' ⁸ is <u>T</u> , S, Y, N, I, or G;	C'' ⁹ is <u>T</u> , G, R, L F, Y, I, E, or R;
C'' ¹⁰ is <u>Y</u> , S, F, -, T, D, or H;	C'' ¹¹ is <u>Y</u> , F, or H;	C'' ¹² is <u>A</u> , T, or S;
C'' ¹³ is <u>D</u> or G;	C'' ¹⁴ is <u>A</u> or T;	C'' ¹⁵ is <u>V</u> ;
C'' ¹⁶ is <u>K</u> or R; and	C'' ¹⁷ is <u>G</u> ;	

b) selected from the group consisting of

VINSAGDTG-YAGAVKG SEQ ID NO: 468	YISTGGGTTSFADAVK G SEQ ID NO: 469	YISSDGRSTSYT- DAVKG SEQ ID NO: 470	GINSGGSSTYYT- DAVKG SEQ ID NO: 471
GINSGGSTTYT- DAVKG SEQ ID NO: 472	WIRYDGSSTYY- ADAVKG SEQ ID NO: 473	YIHNDGGTRTYSDTV KG SEQ ID NO: 474	EISDSGDYLDYT- DAVKG SEQ ID NO: 475
WIWYGGSTYY- ADAVKG SEQ ID NO: 476	SISSSGGTF- YADAVKG SEQ ID NO: 477	EISGSGTTTHY- EDTVRG SEQ ID NO: 478	TINRSGTTY- YADTVKG SEQ ID NO: 479
RIRGDGTNIYY- ADAVKG SEQ ID NO: 480	YINSDGSTYY- ADAVKG SEQ ID NO: 481	AISYDGSSTYYT- DAVKG SEQ ID NO: 482	YINSGGGIIFY- ADAVKG SEQ ID NO: 483
SIRYDETGTSTY- DAVKG SEQ ID NO: 484	DISDSAYSTYYT- DAVKG SEQ ID NO: 485	QISVGGEIE- YADAVKG SEQ ID NO: 486	GINGGGTTRFYS- DAVRG SEQ ID NO: 487
and	TI- SYDGSSTFHTDAVKG SEQ ID NO: 488;		

c) C''¹ C''² C''³ C''⁴ C''⁵ C''⁶ C''⁷ C''⁸ C''⁹ C''¹⁰ C''¹¹ C''¹² C''¹³
C''¹⁴ C''¹⁵ C''¹⁶ (SEQ ID NO: 489), wherein

C'' ¹ is <u>I</u> ,	C'' ² is <u>D</u> ,	C'' ³ is <u>P</u> ,
C'' ⁴ is <u>E</u> ,	C'' ⁵ is <u>D</u> ,	C'' ⁶ is <u>G</u> or D,
C'' ⁷ is <u>T</u> ,	C'' ⁸ is <u>T</u>	C'' ⁹ is <u>S</u> or G,
C'' ¹⁰ is <u>Y</u> ,	C'' ¹¹ is <u>A</u> ,	C'' ¹² is <u>Q</u> ,
C'' ¹³ is <u>K</u> ,	C'' ¹⁴ is <u>F</u> ,	C'' ¹⁵ is <u>Q</u> ,
and	C'' ¹⁶ is <u>G</u> ,	

d) selected from the group consisting of IDPEDGTTSYAQKFQG (SEQ ID NO: 490) and IDPEDDTTGYAQKFQG (SEQ ID NO: 491)

e) C''¹ C''² C''³ C''⁴ C''⁵ C''⁶ C''⁷ C''⁸ C''⁹ C''¹⁰ C''¹¹ C''¹² C''¹³
C''¹⁴ C''¹⁵ C''¹⁶ (SEQ ID NO: 492), wherein

C ¹ is <u>Y</u> ,	C ² is <u>W</u> ,	C ³ is <u>R</u> or <u>S</u> ,
C ⁴ is <u>G</u> ,	C ⁵ is <u>G</u> or <u>T</u> ,	C ⁶ is <u>T</u> ,
C ⁷ is <u>N</u> or <u>H</u> ,	C ⁸ is <u>Y</u> or <u>H</u>	C ⁹ is <u>N</u> ,
C ¹⁰ is <u>P</u> ,	C ¹¹ is <u>A</u> or <u>T</u> ,	C ¹² is <u>F</u> ,
C ¹³ is <u>Q</u> ,	C ¹⁴ is <u>E</u> or <u>G</u> ,	C ¹⁵ is <u>R</u> ,
and	C ¹⁶ is <u>I</u> ,	

f) selected from the group consisting of YWRGGTNHNPAFQERI (SEQ ID NO: 493) and YWSGTTHYNPTFQGRI (SEQ ID NO: 494); or

g) mouse 15A2 antibody CDR², RINPFNGDPFYNQKFKG (SEQ ID NO: 495).

[0047] In a preferred embodiment, CDR³ for heavy chains is:

a) C¹ C² C³ C⁴ C⁵ C⁶ C⁷ C⁸ C⁹ C¹⁰ C¹¹
C¹² C¹³ C¹⁴ C¹⁵ C¹⁶ C¹⁷ C¹⁸ C¹⁹ C²⁰ (SEQ ID NO: 496), wherein

C ¹ is <u>D</u> , L, Y, T, G, X, E, A, V, W, I, or Q,	C ² is <u>G</u> , R, I, H, T, P, S, Y, F, D, or W,
C ³ is <u>D</u> , E, Y, V, W, G, S, A, M, I, T, L, P, or R,	C ⁴ is <u>G</u> , <u>S</u> , I, A, Y, L, T, Q, D, I, N, L, R,
C ⁵ is <u>T</u> , Y, S, F, L, C, W, X, G, or E,	C ⁶ is <u>S</u> , T, V, Y, M, H, C, G, F, P, K, W, or --,
C ⁷ is <u>_</u> , V, E, W, S, T, D, L, G, Y, or K,	C ⁸ is <u>_</u> , A, G, R, Y, E, D, W, M, or S,
C ⁹ is <u>_</u> , E, P, V, D, G, Y, W, F, or K,	C ¹⁰ is <u>_</u> , L, G, W, Y, A, N, S, F, C, D, T, or P,
C ¹¹ is <u>_</u> , D, S, F, N, Y, C, A, or R,	C ¹² is <u>_</u> , Y, F, G, L, D, or P,
C ¹³ is <u>_</u> , F, D, G, N, H, R, or G,	C ¹⁴ is <u>_</u> , D, V, I, W, or F,
C ¹⁵ is <u>_</u> , V, D, or G,	C ¹⁶ is <u>_</u> , H, or F,
C ¹⁷ is <u>_</u> or D,	C ¹⁸ is <u>_</u> or Y,
C ¹⁹ is <u>_</u> or L, and	C ²⁰ is <u>_</u> or N;

b) selected from the group consisting of

DREITTVAELD SEQ ID NO: 497,	LIYGYVEGPGSYFD SEQ ID NO: 498,	YHDGSYVRVWFY SEQ ID NO: 499,
TTVATME SEQ ID NO: 500,	GGDSSHWYPYNFD SEQ ID NO: 501,	DPWSSSWYDAFG SEQ ID NO: 502,
XTYGTSSSEGNYL SEQ ID NO: 503,	LSGYCTDDSCFNVVHDYL N SEQ ID NO: 504,	GGDLFG SEQ ID NO: 505,
GGDLFG	EYSSSFD	DPATLPTGEFD

SEQ ID NO: 505, DRGQCTVDYCADHID	SEQ ID NO: 506, ASMDTKTFD	SEQ ID NO: 507, DFGDWVL
SEQ ID NO: 508, GDSSXW	SEQ ID NO: 509, VSISSSWWGRYFD	SEQ ID NO: 510, WDTNG
SEQ ID NO: 511, EYLGE	SEQ ID NO: 512, ITPLGPGDFD	SEQ ID NO: 513, DGGITSYMKTNLD
SEQ ID NO: 514, AR- ERYCKDDYCFRWGFD	SEQ ID NO: 515, and	SEQ ID NO: 516, QWRNTWYSFPDPGFD
SEQ ID NO: 517,		SEQ ID NO: 518;

- c) selected from the group consisting of GGSRPFNAFG (SEQ ID NO: 519), KWRYYGSQD (SEQ ID NO: 520), DIWDFD (SEQ ID NO: 521), and YIYGYAAYLD (SEQ ID NO: 522);
- d) selected from the group consisting of NSD and LYRSNYLLD (SEQ ID NO: 523); or
- e) mouse 15A2 antibody CDR³, FYYGRYYAMDY (SEQ ID NO: 524).

[0048] In a preferred embodiment, CDR¹ for light chains is:

- a) C'¹ C'² C'³ C'⁴ C'⁵ C'⁶ C'⁷ C'⁸ C'⁹ C'¹⁰ C'¹¹ C'¹² C'¹³ (SEQ ID NO: 525), wherein

C' ¹ is <u>G</u> or --,	C' ² is <u>L</u> or --,	C' ³ is <u>S</u> , N, P, or --,
C' ⁴ is <u>S</u> , P, or --,	C' ⁵ is <u>G</u> or --,	C' ⁶ is <u>S</u> or --,
C' ⁷ is <u>V</u> or --,	C' ⁸ is <u>S</u> T, or --,	C' ⁹ is <u>T</u> , A, G, P, or --,
C' ¹⁰ is <u>S</u> , Q, G, N, or --,	C' ¹¹ is <u>N</u> , H, D, or --,	C' ¹² is <u>Y</u> , F, or --,
C' ¹³ is <u>P</u> or --,	and	C' ¹³ is <u>G</u> , N, A, S, or --,

provided that when C'^m is -- for m>2, C'ⁿ is -- for n<m;

- b) selected from the group consisting of

--,	NYPG SEQ ID NO: 526,	GLSSGSVSTSNYP G SEQ ID NO: 527,	GLNSGSVSTSNY PA SEQ ID NO: 528,
GLSPGSVSTSNY PN SEQ ID NO: 529,	GLSSGSVSTSNY PA SEQ ID NO: 530,	GLSSGSVTASHFP G SEQ ID NO: 531,	GLSSGSVSGSNY PG SEQ ID NO: 532,
GLPSGSVSTQNF PN SEQ ID NO: 533,	GLSSGSVSTGDF PG SEQ ID NO: 534,	GLSSGSVSTSNYP N SEQ ID NO: 535,	GLSSGSVSPSHY PG SEQ ID NO: 536,
GLSSGSVSTSNY PS	and	GLSSGSVSTNNYP G	

SEQ ID NO: 537,		SEQ ID NO: 538;
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c) C¹ C² C³ C⁴ C⁵ C⁶ C⁷ C⁸ C⁹ C¹⁰ C¹¹ C¹² C¹³ (SEQ ID NO: 539), wherein

C ¹ is <u>T</u> , S, A, or -,	C ² is <u>G</u> , R, or --,
C ³ is <u>S</u> , T, R, D, A or - -,	C ⁴ is <u>S</u> , G, E, N, T, P, V, Y, M, or --,
C ⁵ is <u>S</u> , N, D, A, Y, or K,	C ⁶ is <u>N</u> , D, or Y,
C ⁷ is <u>I</u> , V, or L,	C ⁸ is <u>G</u> , D, A, or N,
C ⁹ is <u>R</u> , Y, G, I, K, S, D, or V,	C ¹⁰ is <u>G</u> , R, V, Y, A, S, F, D, or N,
C ¹¹ is <u>Y</u> , N, G, D, F, S, or H, V, or Q,	C ¹² is <u>V</u> , A, -,
or	C ¹³ is <u>G</u> , H, S, N, A, D, T, or --;

d) selected from the group consisting of

TGSGSNIGRGYV G SEQ ID NO: 540,	TGSES- NIGRGFVG SEQ ID NO: 541,	TGSSSNVGRGYV G SEQ ID NO: 542,	NIGSVGAT SEQ ID NO: 543,
TGSGSNIGGNNV G SEQ ID NO: 544,	TGSSSNIG- GYNVG SEQ ID NO: 545,	TGSSSNIGRDYV G SEQ ID NO: 546,	TGSSSNLGRYGV A SEQ ID NO: 547,
TGTTSNIGRGFV G SEQ ID NO: 548,	TGSSSNIGSGYV G SEQ ID NO: 549,	TGSSSNIG- GYNVN SEQ ID NO: 550,	TGSSSNIGGGYV G SEQ ID NO: 551,
SGSTNDI- DIFGVS SEQ ID NO: 552,	SGDSSNIGDNFV A SEQ ID NO: 553,	TGSSSNIG- KYVVG SEQ ID NO: 554,	TGSSSNIGRGYV G SEQ ID NO: 555,
TGSSSNIGRDYV A SEQ ID NO: 556,	SGSTSNIGIVGA S SEQ ID NO: 557,	TGSPSNIGGY- DVA SEQ ID NO: 558,	TGSSSNIG- GYSVA SEQ ID NO: 559,
TGSSSNIGGNYV S SEQ ID NO: 560,	TGSNSNIGRGYV D SEQ ID NO: 561,	TGSNSNIGGNDV A SEQ ID NO: 562,	TGSVSNIGIFDV G SEQ ID NO: 563,
TGSGSNIGRDSV G SEQ ID NO: 564,	TGSSSNIGGNQV G SEQ ID NO: 565,	SGSTNDIAIVGA S SEQ ID NO: 566,	TGSSSNIGGNYV G SEQ ID NO: 567,
TRSSSNIAG- GYVA SEQ ID NO: 568,	TGSSAY- IGSGYVG SEQ ID NO: 569,	SGSTKNIGIF- GAH SEQ ID NO: 570,	TGSSSNIGGSSV G SEQ ID NO: 571,

TGSSSNIGRGFV A SEQ ID NO: 572,	TGAYSNIGTNNV G SEQ ID NO: 573,	TGSGSNIGRGYV A SEQ ID NO: 574,	TGSSINYRYVG SEQ ID NO: 575,
SGRTDNIGVA- GAA SEQ ID NO: 576,	TGSGSDIGGFG SEQ ID NO: 577,	TGSSSNIGYNVG SEQ ID NO: 578,	TGSSSNVGGGFV G SEQ ID NO: 579,
AGTNSDIGTNHV A SEQ ID NO: 580,	SGSTNDIGRFGV N SEQ ID NO: 581,	TGSTANIGSGYV N SEQ ID NO: 582,	TGSSSNIGRNNV G SEQ ID NO: 583,
SGSMYNLGVVGA T SEQ ID NO: 584,	TGSNSNIGRGYV G SEQ ID NO: 585,	or	--;

e) $C'^1 C'^2 C'^3 C'^4 C'^5 C'^6 C'^7 C'^8 C'^9 C'^{10} C'^{11} C'^{12} C'^{13} C'^{14}$ (SEQ ID NO: 586), wherein

C'^1 is <u>T</u> or D,	C'^2 is <u>G</u> ,	C'^3 is <u>S</u> , T, I, N, or R-,
C'^4 is <u>S</u> , N, T, K, D, or G,	C'^5 is <u>S</u> , T, D, or N,	C'^6 is <u>N</u> or D-,
C'^7 is <u>V</u> , I, or L,	C'^8 is <u>G</u> or D,	C'^9 is <u>Y</u> , N, F, S, D, or G,
C'^{10} is <u>G</u> , D, T, or E,	C'^{11} is <u>N</u> , D, Y, or S,	C'^{12} is <u>Y</u> , D, I, S, T, or H,
C'^{13} is <u>V</u> , A, or I,	and	C'^{13} is <u>G</u> , Q, H, or A;

or

f) selected from the group consisting of

TGTNTNIGN- GYDVH SEQ ID NO: 587	TGSSSNVGYG- DYVG SEQ ID NO: 588	TGSSSNVGYANHVG SEQ ID NO: 589	TGSSSNVGYGNYV G SEQ ID NO: 590
DGINSNIDNSNYI E SEQ ID NO: 591	TGSSSDVGY- ADYVG SEQ ID NO: 592	TGSSSNVGFNYVG SEQ ID NO: 593	XGSSSNVGSSTV G SEQ ID NO: 594
TGSKTNIGSGYDV Q SEQ ID NO: 595	TGSKDNIGYGNV G SEQ ID NO: 596	TGSNTNIGSDYDVQ SEQ ID NO: 597	TGSSSNVGYG- DYAG SEQ ID NO: 598
TGSTSNVGYGNYV G SEQ ID NO: 599	TGSNSNVGYANYV G SEQ ID NO: 600	TGSSSNVGYGDXVG SEQ ID NO: 601	TGNSSNVGYGNYV G SEQ ID NO: 602
TGSSSNVGDTSV G SEQ ID NO: 603	TGSDSNVGYGNV G SEQ ID NO: 604	TGSSSNVGYGDYVA SEQ ID NO: 605	TGSTSNLGYS- SIVG SEQ ID NO: 606

TGSTNDIG- SENYVH SEQ ID NO: 607	TGSGSNVGYGNYV G SEQ ID NO: 608	TGTSSNVGFGDYVG SEQ ID NO: 609, and	TGRSSNIG- GGNYVG SEQ ID NO: 610
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[0049] In a preferred embodiment, CDR² for light chains is:

a) C^{'1} C^{'2} C^{'3} C^{'4} C^{'5} C^{'6} C^{'7} (SEQ ID NO: 611), wherein

C ^{'1} is <u>N</u> , R, G, T, S, or H,	C ^{'2} is <u>T</u> or A,	C ^{'3} is <u>N</u> , S, Y, G, or D,
C ^{'4} is <u>S</u> , R, N, or T,	C ^{'5} is <u>R</u> ,	C ^{'6} is <u>P</u> or L,
and	C ^{'7} is <u>S</u> or L;	

b) selected from the group consisting of

RTSSRPS SEQ ID NO: 612,	NTNSRPS SEQ ID NO: 613,	GANSRPS SEQ ID NO: 614,	NTGSRPS SEQ ID NO: 615,	NTYNRLS SEQ ID NO: 616,	NTNTRPL SEQ ID NO: 617,
RTNRRPS SEQ ID NO: 618,	RTDSRPS SEQ ID NO: 619,	TTSSRPS SEQ ID NO: 620,	STSSRPS SEQ ID NO: 621,	and	HTSSRPS SEQ ID NO: 622;

c) C^{'1} C^{'2} C^{'3} C^{'4} C^{'5} C^{'6} C^{'7} (SEQ ID NO: 623), wherein

C ^{'1} is <u>G</u> , D, S, R, A, T, N, or -,	C ^{'2} is <u>T</u> , D, H, N, R, I, S, F, or K,
C ^{'3} is <u>T</u> , F, H, Y, K, D, S, R, E, or V,	C ^{'4} is <u>N</u> , S, H, D, Y, K, R, F, V, or E,
C ^{'5} is <u>R</u> ,	C ^{'6} is <u>P</u> , L, or A,
and	C ^{'7} is <u>S</u> or P;

d) selected from the group consisting of:

GDINRPS SEQ ID NO: 624,	GHNHRPS SEQ ID NO: 625,	GNNNRPS SEQ ID NO: 626,	SDGHRPS SEQ ID NO: 627,	DTYSRLS SEQ ID NO: 628,	SRSNRPS SEQ ID NO: 629,
GNSNRPS SEQ ID NO: 630,	SIDNRPS SEQ ID NO: 631,	GNGNRPS SEQ ID NO: 632,	SSSNRPS SEQ ID NO: 633,	SSTDRPS SEQ ID NO: 634,	GDSNRPS SEQ ID NO: 635,
SDGDRPS SEQ ID NO: 636,	GTIYRPS SEQ ID NO: 637,	STSYRPS SEQ ID NO: 638,	DDSSRPS SEQ ID NO: 639,	DTRSRPS SEQ ID NO: 640,	SDGSRPS SEQ ID NO: 641,
SSTNRPS SEQ ID NO: 642,	SNTKRPS SEQ ID NO: 643,	ADNYRAS SEQ ID NO: 644,	GTANRPS SEQ ID NO: 645,	GKNNRPS SEQ ID NO: 646,	STNSRPS SEQ ID NO: 647,

GTTNRPS SEQ ID NO: 648,	GDNHRPS SEQ ID NO: 649,	TFGDRPS SEQ ID NO: 650,	ADDHRPS SEQ ID NO: 651,	STTVRPS SEQ ID NO: 652,	GDSSRPS SEQ ID NO: 653,
STSNRPP SEQ ID NO: 654,	NSRERPS SEQ ID NO: 655,	GNNYRPS SEQ ID NO: 656,	SISSRPS SEQ ID NO: 657,	RSERRPS SEQ ID NO: 658,	STDSRPS SEQ ID NO: 659,
DTSRRPS SEQ ID NO: 660,	DNGKRPS SEQ ID NO: 661,	GDDNRPS SEQ ID NO: 662,	GNSKRPS SEQ ID NO: 663,	NDGHRPS SEQ ID NO: 664,	GDSDRPS SEQ ID NO: 665,
STDRRPS SEQ ID NO: 666,	GNSDRPS SEQ ID NO: 667,	TTNSRPS SEQ ID NO: 668,	TSTNRPS SEQ ID NO: 669,	STYSRPS SEQ ID NO: 670,	SNGSRPS SEQ ID NO: 671,
SSNRPS SEQ ID NO: 672,	or	DTTFRPS SEQ ID NO: 673,	DTSRRPS SEQ ID NO: 660,		

e) $C^{111} C^{112} C^{113} C^{114} C^{115} C^{116} C^{117}$ (SEQ ID NO: 674), wherein

C^{111} is <u>D</u> , G, R, H, Y, A, or F,	C^{112} is <u>S</u> , T, N, D, H, or K,	C^{113} is <u>S</u> , G, N, D, R, or T,
C^{114} is <u>S</u> , R, N, D, A, F, K, Y, or V,	C^{115} is <u>R</u> ,	C^{116} is <u>P</u> , A, or E,
and	C^{117} is <u>S</u> or A;	

or

f) selected from the group consisting of

GNNNRPS SEQ ID NO: 626,	RTGNRPS SEQ ID NO: 675,	HSSDRPS SEQ ID NO: 676,	DSSSRPS SEQ ID NO: 677,	YTNNRPS SEQ ID NO: 678,	DTSKRPS SEQ ID NO: 679,
DSSRRPS SEQ ID NO: 680,	YDGSRPS SEQ ID NO: 681,	ANDARPS SEQ ID NO: 682,	GHGFRPS SEQ ID NO: 683,	DTRRRPS SEQ ID NO: 684,	AKSNRPS SEQ ID NO: 685,
GSSYRPS SEQ ID NO: 686,	XSXSXPS SEQ ID NO: 687,	YSSSRPS SEQ ID NO: 688,	FIGSRPS SEQ ID NO: 689,	RSSNRAS SEQ ID NO: 690,	YNTGRPS SEQ ID NO: 691,
HSSSRPS SEQ ID NO: 692,	YDSSRPS SEQ ID NO: 693,	GDDNRES SEQ ID NO: 694,	ATSSRPS SEQ ID NO: 695,	DTSSRPS SEQ ID NO: 696,	DHNVSPA SEQ ID NO: 697, and
GNNRRPS SEQ ID NO: 698.					

[0050] In a preferred embodiment CDR³ for light chains is:

a) $C^{1111} C^{1112} C^{1113} C^{1114} C^{1115} C^{1116} C^{1117} C^{1118} C^{1119} C^{11110} C^{11111}$
 C^{11112} (SEQ ID NO: 699)

C ¹ is <u>S</u> or A,	C ² is <u>L</u> , F, or V,	C ³ is <u>_</u> or G,
C ⁴ is <u>Y</u> , F, L, or R,	C ⁵ is <u>T</u> , S, or M,	C ⁶ is <u>G</u> , D, S, or V,
C ⁷ is <u>S</u> , G, D, Y, T, R, or I,	C ⁸ is <u>Y</u> , Q, V, H, D, P, or S,	C ⁹ is <u>_</u> , S, or N,
C ¹⁰ is <u>T</u> , S, V, I, --, or Y,	C ¹¹ is <u>A</u> , D, V, N, P, Y, --, or G, and	C ¹² is <u>V</u> , M, --, or L,

b) selected from the group consisting of

SVYMGTYTVV SEQ ID NO: 700,	SLRTGYQNTM SEQ ID NO: 701,	SLYMGSYTDM SEQ ID NO: 702,	SLYMGGYSDV SEQ ID NO: 703,	SLYTGSYTAV SEQ ID NO: 704,
SFFTDIVVNV SEQ ID NO: 705,	SVYTDDHTPV SEQ ID NO: 706,	SFYTG DYTAV SEQ ID NO: 707,	SLYMGVYTAV SEQ ID NO: 708,	ALGFSGGDYV V SEQ ID NO: 709,
SLYMGSYTGL SEQ ID NO: 710,	ALGFSSSSSY V SEQ ID NO: 711,	SLYMDIYTGV SEQ ID NO: 712,	ALGLSGIS- SIV SEQ ID NO: 713,	SLYTGRPV SEQ ID NO: 714,
SLYTGSSTDV SEQ ID NO: 715,	And	SFYTSSY SEQ ID NO: 716;		

c) C¹ C² C³ C⁴ C⁵ C⁶ C⁷ C⁸ C⁹ C¹⁰ C¹¹ C¹² (SEQ ID NO: 717), wherein

C ¹ is <u>S</u> , Q, or A,	C ² is <u>S</u> , T, A, G, or --
C ³ is <u>W</u> , S, L, Y, F, V, or --	C ⁴ is <u>D</u> , -, or Q,
C ⁵ is <u>S</u> , N, Y, P, A, D, T, E, R, H, --, or I,	C ⁶ is <u>S</u> , N, R, T, G, A, D, -- or Y,
C ⁷ is <u>L</u> , V, R, P, -, or F,	C ⁸ is <u>S</u> , R, G, K, T, I, N, Q, P, -, or A,
C ⁹ is <u>G</u> , T, S, V, A, K, D, L, I, E, -, or Y,	C ¹⁰ is <u>V</u> , Y, T, P, S, -, G, L, Q, A, D, or N,
C ¹¹ is <u>S</u> , P, -, Y, A, D, I, or T,	and C ¹² is <u>V</u> , -, I, or L;

d) selected from the group consisting of

SSWDYSLSSTL SEQ ID NO: 718	SSXDXSLSVVL SEQ ID NO: 719	SSWDASRSVTV SEQ ID NO: 720	QSLDSNLGPV SEQ ID NO: 721	STWDDSLRAYL SEQ ID NO: 722
STWDSSLKAPV SEQ ID NO: 723	STWDNSLTVPV SEQ ID NO: 724	STYDTRLGTSV SEQ ID NO: 725	SSWDNNLIKIL SEQ ID NO: 726	STYDSTLNAV SEQ ID NO: 727
SAWDNSLKLPL SEQ ID NO: 728	SSWDTGLSALV SEQ ID NO: 729	QSVDSTLGAIV SEQ ID NO: 730	SSWDDSLXGIV SEQ ID NO: 731	STYDSSLGGSV SEQ ID NO: 732

SAYDSTLTGTV SEQ ID NO: 733	STYDSSLSGPL SEQ ID NO: 734	QSFDP TPPDHY V SEQ ID NO: 735	SAWDSTLRAGV SEQ ID NO: 736	STWDSSLKALL SEQ ID NO: 737
QSFDTALGTV SEQ ID NO: 738	SSWDDGLRALV SEQ ID NO: 739	SSWDDSLKGHV SEQ ID NO: 740	STWDENLSVPV SEQ ID NO: 741	STWDNSVTVL SEQ ID NO: 742
SSWDNDFGHV SEQ ID NO: 743	QSFDTTLGAYV SEQ ID NO: 744	SSWDRSLRGQV SEQ ID NO: 745	SGYDTTVNGVV SEQ ID NO: 746	SSWDTSRLRTI SEQ ID NO: 747
SASDSSLVSV SEQ ID NO: 748	QSFDTTLGDGDV L SEQ ID NO: 749	SSWDDSLRISV SEQ ID NO: 750	SAWDSSLKEAV SEQ ID NO: 751	STWDDSVTVL SEQ ID NO: 752
SAHDNSVSGVV SEQ ID NO: 753	SAWDDSLTAYV SEQ ID NO: 754	STYDITITGGV SEQ ID NO: 755	SSYDSSFTAD SEQ ID NO: 756	STWDSSLKAIV SEQ ID NO: 757
SSWDDSLRGHV SEQ ID NO: 758	STWDNSLTIV SEQ ID NO: 759	QSFQTTLNIYV SEQ ID NO: 760	STWDASLRVGV SEQ ID NO: 761	STWDSSLKAVV SEQ ID NO: 762
STWDDSLSEPV SEQ ID NO: 763	STYDTRLNDVI SEQ ID NO: 764	SAWDDRLTEPV SEQ ID NO: 765	QSV DHTLAAV SEQ ID NO: 766	AAYDSSLSIGV SEQ ID NO: 767
STWDDYLQIYV SEQ ID NO: 768	QSLDSTRGYHIV SEQ ID NO: 769	STWDNSLNTGV SEQ ID NO: 770	SAYDTSLSNF SEQ ID NO: 771	Or SSWDSSLSGVSV SEQ ID NO: 772;

e) C¹¹¹¹ C¹¹¹² C¹¹¹³ C¹¹¹⁴ C¹¹¹⁵ C¹¹¹⁶ C¹¹¹⁷ C¹¹¹⁸ C¹¹¹⁹ C¹¹¹¹⁰ C¹¹¹¹¹
C¹¹¹¹² (SEQ ID NO: 773)

C ¹¹¹¹ is <u>S</u> , Q, or A,	C ¹¹¹² is <u>A</u> , T, or V,	C ¹¹¹³ is <u>Y</u> , F, W, or G,
C ¹¹¹⁴ is <u>D</u> , H, --, or E,	C ¹¹¹⁵ is <u>S</u> , D, N, R, Y, or T,	C ¹¹¹⁶ is <u>S</u> , T, N, or G,
C ¹¹¹⁷ is <u>L</u> , I, V, T, P, or --,	C ¹¹¹⁸ is <u>S</u> , G, R, K, D, N, A, Q, H, or --,	C ¹¹¹⁹ is <u>G</u> , T, S, H, A, V, or --,
C ¹¹¹¹⁰ is <u>G</u> , I, V, R, P, L, Y, S, or --,	C ¹¹¹¹¹ is <u>A</u> or --, and	C ¹¹¹¹² is <u>V</u> or L,

f) selected from the group consisting of

QSYDDNLDGY V SEQ ID NO: 774,	SSFDRSVSAV , SEQ ID NO: 775	SAYDTTLNAV SEQ ID NO: 776,	SSYDSSLSGG V SEQ ID NO: 777,	SAYSGTDTYV SEQ ID NO: 778,
SSYHSSPHGV V SEQ ID NO:	SSYDSEVRVV SEQ ID NO: 780,	SSWDNSQGSV SEQ ID NO: 781,	QSYDDNLAGL V SEQ ID NO:	STYDNSLSVV SEQ ID NO: 783,

779, ASYDRTIGGG AV SEQ ID NO: 784,	SVGDDSLKAP V SEQ ID NO: 785,	SSYDSSLSGI V SEQ ID NO: 786,	782, SSYDSSLDGA V SEQ ID NO: 787,	SSYESSLRGV V SEQ ID NO: 788,
SSWDNSLKTR V SEQ ID NO: 789,	SSYDSGLSHI V SEQ ID NO: 790,	SAY- DYSLSSGV SEQ ID NO: 791,	SSYDNSLSGG V SEQ ID NO: 792,	SSWDNSLKGI V SEQ ID NO: 793,
QSYDDSLNTY V SEQ ID NO: 794,	SSYDTSLSGG V SEQ ID NO: 795,	SSYDSSLSGA V SEQ ID NO: 796,	SSYDSSLSIV SEQ ID NO: 797,	SSWDDSLRGA L SEQ ID NO: 798,
And	SAYDSSLSGG AV SEQ ID NO: 799.			

[0051] The method of choice that is used for frequency tables and CDR identification is by use of the Kabat database on the web. To get frequency tables, the tabulated data can be scored off the kabat data base by going to <http://immuno.bme.nwu.edu/> using the "variability" tool under "searching and analysis tools".... select "distribution" table, (instead of variability plot, which is the default), a table of the frequency of each amino acid at a given position for each position in the domain it given. See Kabat, E.A., Wu, T.T., Perry, H.M., Gottesman, K.S., Foeller, C., 1991. Sequences of Proteins of Immunological Interests, 5th ed. US Department of Health and Human Service, National Institutes of Health, Bethesda, MD (NIH Publication No. 91-3242).

Framework Region variations and other homologous sequences

[0052] Polypeptides of the invention also include those having one of the sequences disclosed above modified by replacement of one or more amino acids in one or more of the framework regions with a corresponding amino acid (*i.e.*, at the same position) of a human sequence. Amino acids from human sequences are found in various publicly available databases. See paragraph [0051].

[0053] For caninized variable domains and antibodies, Fr¹, F², Fr³, and Fr⁴ framework sequences should be at least 60% homologous to the corresponding framework sequences of the non-canine antibody from which the two or three non-canine CDR's are obtained. More preferably, such sequences are at least 65%, 70%, 75%, 80%, 85%, 90%, 95%,

96%, 97%, 98%, or 99% homologous. The percent homology between sequences can be determined using any art recognized alignment algorithm. Specifically excluded from the scope of the invention are the canine variable domain polypeptide sequences disclosed in:

a) Wasserman and Capra, *Biochem.* **16**, 3160 (1977)

evklvesggd lvkpggslrl scvasgftfs sngmswvrqd pgeglqwvad isssgqtyya
davkgrfsis rdnakntlyl qmedlrvedt avyycategd ieipryfggg tivtvss

evqlvesggd lvkpggslrl scvasgitfs gydmqwvrqa pgkglqkvay fndalsaggy
adavkgrfti skdnakdsly lqmnsdraed tavyycapwq feywgqgtlv tvss (SEQ ID NO:

800)

b) Wasserman and Capra, *Immunochem.* **15**, 303 (1978):

divmtqtpls lsvspgepas iscrssqsnl dylnwylqka ggsprllpeq dsqrasgvpd
rfsgsgsgtd ftlrigrvea edagiyycmq rsfypytfgg gtrlevrr (SEQ ID NO: 801)

and

c) Tang et al., *Vet. Immunology Immunopathology* **80**, 259
(2001).

[0054] Homology modeling can be used to identify amino acids in the canine framework regions for back mutation to the sequence from which the non-canine CDR's are obtained, e.g., the 15A2 murine sequence. Back mutation is defined as changing an amino acid in the canine framework region "back" to the amino acid found in the non-canine framework region.

[0055] One of ordinary skill in the art can use known methods of creating a three dimensional molecular model of a non-canine antibody having one or more CDRs for use in a caninized antibody to determine appropriate back mutations. For each model, the amino acids within a 3 angstrom shell and a 6 angstrom shell surrounding the CDR's is determined. Amino acids that are found within the 3 and 6 angstrom shells have a strong likelihood of improving affinity for the target antigen. One or more amino acids of the canine antibody framework regions that corresponds to a amino acid within the 6, and preferably 3, angstrom shell are then optionally "back mutated" to the corresponding amino acid of the non-canine antibody.

[0056] For manipulation of Brookhaven Protein Data Bank (PDB) files, model building, model refinement, and prediction of specific amino acids for site directed mutagenesis, the molecular modeling/graphics program DEEP VIEW can be used (available at <http://www.expasy.ch/spdbv/mainpage.htm>). Guex, N. and Peitsch, M.C. (1997) SWISS-MODEL and the Swiss-PdbViewer: An environment for com-

parative protein modeling. *Electrophoresis* 18, 2714-2723. In one mode of determining appropriate back mutations by this method, the linear sequences of the non-canine antibody heavy and light chain are compared to existing sequences for which crystal structures exist (e.g., in the Brookhaven Protein Data Bank). Selected sequences are those with known crystal structure having high homology to the different non-canine antibody variable domains. The non-canine antibody heavy and light chains can then be modeled based on the known crystal structures using DEEP VIEW. For each model, the amino acids within a 3 angstrom shell and a 6 angstrom shell surrounding the CDR's is determined. Comparison of the known structures and of the amino acids within these two concentric shells about the CDR's enables identification of key amino acids that may be directly and/or indirectly influence the CDR's.

[0057] The canine variable domain polypeptides according to this aspect of the invention can be made by standard techniques known to those of ordinary skill in the art. E.g., Sambrook and Russell, "Molecular Cloning: A Laboratory Manual" (3rd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 2001). Briefly, the canine variable domain polypeptides can be made via expression of the corresponding nucleic acids encoding the canine variable domain polypeptides. The nucleic acids are described more fully below. The nucleic acids according to the invention can be inserted in appropriate vectors and the canine variable domain polypeptides expressed from these vectors in suitable expression systems.

[0058] The invention also comprises a caninized variable region sequence according to any one of paragraphs [0021] - [0042] with one, two, or three CDRs according to any one of paragraphs [0045] - [0050]. The invention further comprises antibodies comprising a caninized variable region sequence according to any one of paragraphs [0021] - [0042] with 0 - 3 CDRs according to any one of paragraphs [0045] - [0050].

[0059] Also encompassed are sequences in which one or more amino acids have been added or deleted from one of the sequences expressly disclosed herein. Sequences differing from one of those expressly disclosed herein by substitution, deletion, and/or addition and having at least 95%, 96%, 97%, 98%, or 99% homology to the sequences expressly disclosed herein are contemplated as encompassed within the

invention as well. In particular, the invention also comprises sequences that are or have within them (a) framework sequences that are 95, 96, 97, 98, or 99 % homologous with the corresponding framework sequences (Fr¹-Fr⁴) of the polypeptide sequences expressly disclosed herein or (b) framework sequences and CDR¹ and CDR² that are 95, 96, 97, 98, or 99 % homologous with the corresponding sequences of the polypeptide sequences expressly disclosed herein.

[0060] A sequence that is, for example, 95% homologous with a reference sequence requires that, following alignment of the candidate sequence with the reference sequence, 95% of the amino acids in the sequence are identical to the corresponding amino acids in the reference sequence. Such a homologous sequence will include those differing from a sequence expressly disclosed herein by conservative amino acid substitutions. A conservative amino acid substitution is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

[0061] More particularly, a "conservative amino acid substitution" may involve a substitution of a native amino acid residue with a non-native residue such that there is little or no effect on the polarity or charge of the amino acid residue at that position. Furthermore, any native residue in the polypeptide may also be substituted with alanine, as has been previously described for "alanine scanning mutagenesis."

[0062] Conservative amino acid substitutions also encompass non-naturally occurring amino acid residues that are typically incorporated by chemical peptide synthesis rather than by synthesis in biological systems. These include peptidomimetics, and other reversed or inverted forms of amino acid moieties.

[0063] Naturally occurring residues may be divided into classes based on common side chain properties:

- 1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;
- 2) neutral hydrophilic: Cys, Ser, Thr;

- 3) acidic: Asp, Glu;
- 4) basic: Asn, Gln, His, Lys, Arg;
- 5) residues that influence chain orientation: Gly, Pro; and
- 6) aromatic: Trp, Tyr, Phe.

For example, non-conservative substitutions may involve the exchange of a member of one of these classes for a member from another class.

[0064] In making such changes, the hydropathic index of amino acids may be considered. Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics. The hydropathic indices are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

[0065] The importance of the hydropathic amino acid index in conferring interactive biological function on a protein is generally understood in the art (Kyte et al., 1982, *J. Mol. Biol.* 157:105-31). It is known that certain amino acids may be substituted for other amino acids having a similar hydropathic index or score and still retain a similar biological activity. In making changes based upon the hydropathic index, the substitution of amino acids whose hydropathic indices are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

[0066] It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity, particularly where the biologically functionally equivalent protein or peptide thereby created is intended for use in immunological embodiments, as in the present case. The greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigenicity, i.e., with a biological property of the protein.

[0067] The following hydrophilicity values have been assigned to these amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 $\pm$ 1); glutamate (+3.0 $\pm$ 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 $\pm$ 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3);

phenylalanine (-2.5); and tryptophan (-3.4). In making changes based upon similar hydrophilicity values, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred. One may also identify epitopes from primary amino acid sequences on the basis of hydrophilicity. These regions are also referred to as "epitopic core regions."

[0068] Desired amino acid substitutions (whether conservative or non-conservative) can be determined by those skilled in the art at the time such substitutions are desired. Exemplary amino acid substitutions are set forth in Table I.

Amino Acid Substitutions

Original Residues	Exemplary Substitutions	Preferred Substitutions
Ala	Val, Leu, Ile	Val
Arg	Lys, Gln, Asn	Lys
Asn	Gln	Gln
Asp	Glu	Glu
Cys	Ser, Ala	Ser
Gln	Asn	Asn
Glu	Asp	Asp
Gly	Pro, Ala	Ala
His	Asn, Gln, Lys, Arg	Arg
Ile	Leu, Val, Met, Ala, Phe, Norleucine	Leu
Leu	Norleucine, Ile, Val, Met, Ala, Phe	Ile
Lys	Arg, 1,4 Diaminobutyric Acid, Gln, Asn	Arg
Met	Leu, Phe, Ile	Leu
Phe	Leu, Val, Ile, Ala,, Tyr	Leu
Pro	Ala	Gly
Ser	Thr, Ala, Cys	Thr
Thr	Ser	Ser
Trp	Tyr, Phe	Tyr
Tyr	Trp, Phe, Thr, Ser	Phe
Val	Ile, Met, Leu, Phe, Ala, Norleucine	Leu

[0069] In a first variable domain amino acid sequence according to the invention that differs from a second amino acid sequence according to the invention by one or more amino acid substitutions, the amino acid substitution(s) in the second sequence are preferably conservative substitutions. In identifying which amino acid to substitute into a particular position in the first variable domain sequence to

arrive at the second sequence, one preferably selects an amino acid that appears in that position in a canine variable domain or a human variable domain having at least 80% (preferably at least 85%, 90%, or 95%) homology with the first sequence. The first sequence and the second sequence according to the invention will be at least 95% homologous.

[0070] Guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie et al., *Science*, 247:1306-1310 (1990), which teaches that there are two main strategies for studying the tolerance of an amino acid sequence to change.

[0071] The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, the amino acid positions which have been conserved between species can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions in which substitutions have been tolerated by natural selection indicate positions which are not critical for protein function. Thus, positions tolerating amino acid substitution can be modified while still maintaining specific binding activity of the polypeptide.

[0072] The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site-directed mutagenesis or alanine-scanning mutagenesis (the introduction of single alanine mutations at every residue in the molecule) can be used (Cunningham et al., *Science*, 244:1081-1085 (1989)). The resulting variant molecules can then be tested for specific binding to antibodies of the invention.

[0073] According to Bowie et al., these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, the most buried or interior (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface or exterior side chains are generally conserved.

[0074] Methods of introducing a mutation into amino acids of a protein is well known to those skilled in the art. See, e.g., Ausubel (ed.), *Current Protocols in Molecular Biology*, John Wiley and Sons,

Inc. (1994); T. Maniatis, E. F. Fritsch and J. Sambrook, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor laboratory, Cold Spring Harbor, N.Y. (1989)). Mutations can also be introduced using commercially available kits such as "QuikChange™ Site-Directed Mutagenesis Kit" (Stratagene). The generation of a functionally active variant of a polypeptide by replacing an amino acid that does not influence the function of a polypeptide can be accomplished by one skilled in the art.

[0075] As used herein, percent identity or homology of two amino acid sequences (or of two nucleic acid sequences) is determined using the algorithm of Karlin and Altschul (PNAS USA 87:2264-2268, 1990), modified as in Karlin and Altschul, PNAS USA 90:5873-5877, 1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches are performed with the NBLAST program, score=100, wordlength=12. BLAST protein searches are performed with the XBLAST program, score=50, wordlength=3. To obtain gapped alignment for comparison purposes GappedBLAST is utilized as described in Altschul et al. (Nucleic Acids Res. 25:3389-3402, 1997). When utilizing BLAST and GappedBLAST programs the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used to obtain nucleotide sequences homologous to a nucleic acid molecule of the invention.

Preferred Caninized Variable Regions

[0076] The following sequences of fully caninized heavy chain variable domains with binding affinity for canine IgE are preferred:

(a) H74-1:

EVQLVQSAAEVKKPGASVKV SCKTSGYSFTDYFMNWVQQAPGAGLDWMGRINPFNGDP-
FYNQKFKGRVTLTADTSTSTAYMELSSLRAEDAAVYYCARFYYGRYYAMDYWGQGTLVTV
(SEQ ID NO: 802)

(b) H74-15:

EVQLVQSAAEVKKPGASVKV SCKTSGYSFTDYFMNWVQQAPGKGLDWMGRINPFNGDP-
FYNQKFKGRVTLTADTSTSTAYMELSSLRAEDAAVYYCARFYYGRYYAMDYWGQGTLVTV
(SEQ ID NO: 803)

(c) H74-20:

EVQLVQSAAEVKKPGASVKV SCKTSGYSFTDYFMNWVQQAPGAGLDWMGRINPFNGDP-
FYNQKFKGRVTLTVDTSTSTAYMELSSLRAEDAAVYYCARFYYGRYYAMDYWGQGTLVTV
(SEQ ID NO: 804)

(d) H74-41:

EVQLVQSAAEVKKPGASVKV SCKTSGYSFTDYFMNWVQQAPGKGLDWMGRINPFNGDP-
FYNQKFKGRVTLTVDTSTSTAYMELSSLRAEDAAVYYCARFYYGRYYAMDYWGQGTLVTV
(SEQ ID NO: 805)

(e) H74-45

EVQLVQSAAEVKKPGASVKV SCKTSGYSFTDYFMNWVQQAPGAGLDWMGRINPFNGDP-
FYNQKFKGRVTLTVDKSTSTAYMELSSLRAEDAAVYYCARFYYGRYYAMDYWGQGTLVTV
(SEQ ID NO: 806)

(f) H74-55

EVQLVQSAAEVKKPGASVKV SCKTSGYSFTDYFMNWVQQAPGKGLDWMGRINPFNGDP-
FYNQKFKGRVTLTADKSTSTAYMELSSLRSEDAAVYYCARFYYGRYYAMDYWGQGTLVTV
(SEQ ID NO: 807).

(g) H74-58

EVQLVQSAAEVKKPGASVKV SCKTSGYSFTDYFMNWVQQAPGKGLDWMGRINPFNGDP-
FYNQKFKGRVTLTVDTSTSTAYMELRSLRAEDAAVYYCARFYYGRYYAMDYWGQGTLVTV
(SEQ ID NO: 808).

[0077] The following sequence of fully caninized light chain variable region T1c with binding affinity for canine IgE is preferred:

(a) T1c:

TDSQTVATQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTQGRAPRGIIGGPNN-
RAPGVPSRFSGSISGNKATLTITGARPEDEADYFCALWYSNHWVFGGGTHLTVL
(SEQ ID NO: 809)

Nucleic Acid Compositions of Matter

[0078] In a second aspect, the invention comprises nucleic acids encoding the canine variable domains. In the tables displaying the nucleic acid sequences (N_{H58} , N_{H74} , $N_{Other\ H}$, N_{G2} , N_{G1} , N_{G3} , N_{κ} , and N_{λ}), the underlined nucleic acid sequences code for a secretory leader sequence. The nucleic acid sequences in tables N_{H58} , N_{H74} , $N_{Other\ H}$, N_{G2} , N_{G1} , N_{G3} , N_{κ} , and N_{λ} correspond to the polypeptides of the H58, H74, G2, G1, G3, and κ families in paragraphs [0021] -- [0043], respectively. The polypeptides encoded by the nucleic acids of tables N_{H58} , N_{H74} , $N_{Other\ H}$, N_{G2} , N_{G1} , N_{G3} , N_{κ} , and N_{λ} , with and without the secretory leader sequence, are also an embodiment of the invention. The nucleic acids of the invention include the sequences in tables N_{H58} , N_{H74} , $N_{Other\ H}$, N_{G2} , N_{G1} , N_{G3} , N_{κ} , and N_{λ} , with and without the sequence coding the secretory leader. Tables $N_{Other\ H}$ and N_{λ} include the polypeptides encoded by the

disclosed nucleic acid sequences. These polypeptides, with or without the secretory leader sequence, are also an embodiment of the invention.

[0079] In particular, the nucleic acids of the invention encode a caninized light or heavy chain variable domain polypeptide and comprise framework-encoding sequences from one of the nucleic acids in tables N_{H58} , N_{H74} , $N_{Other\ H}$, N_{G2} , N_{G1} , N_{G3} , N_K , and N_λ together with CDR-encoding sequences. The framework-encoding sequences of the nucleic acids in tables N_{H58} , N_{H74} , $N_{Other\ H}$, N_{G2} , N_{G1} , N_{G3} , N_K , and N_λ are readily determinable by comparing those nucleic acid sequences with the corresponding polypeptide whose framework sequences are disclosed herein or otherwise determinable. Alternatively, one of ordinary skill in the art can routinely determine the framework encoding regions of the nucleic acid sequences of tables N_{H58} , N_{H74} , $N_{Other\ H}$, N_{G2} , N_{G1} , N_{G3} , N_K , and N_λ by comparison with known and characterized human variable domain sequences by sequence alignment using any of the accepted and widely available sequence alignment programs (discussed above). The CDR-encoding sequences will encode appropriate CDRs, such as those in paragraphs [0045] -- [0050].

[0080] Also part of the invention are the nucleic acids disclosed herein having one or more conservative nucleotide substitutions. A "conservative nucleotide substitution" within a codon does not alter the amino acid encoded by the codon.

1. H58 Heavy Chain Variable Domain

[0081] In one embodiment of this aspect of the invention, the nucleic acids comprise those in the Table N_{H58} (*infra*). These sequences encode V_H polypeptides disclosed in paragraph [0023].

[0082] In the broadest embodiment, this aspect of the invention comprises any nucleic acid encoding a variable domain polypeptide disclosed in paragraph [0021] or paragraph [0022]. The sequences of the nucleic acids are routinely determinable from the polypeptides using the genetic code.

2. H74 Heavy Chain Variable Domain

[0083] In another embodiment of this aspect of the invention, the nucleic acids comprise those in the Table N_{H74} (*infra*). These sequences encode the V_H polypeptides disclosed in paragraph [0026].

[0084] In another embodiment of this aspect, the invention comprises a nucleic acid encoding a variable domain polypeptide disclosed in paragraph [0024], or, more preferably, in paragraph [0025]. In the broadest embodiment, this aspect of the invention comprises any nucleic acid encoding a variable domain polypeptide disclosed in paragraph [0024] or paragraph [0025]. The sequences of the nucleic acids are routinely determinable using the genetic code.

3. Other Heavy Chain Variable Domains

[0085] In another embodiment of this aspect of the invention, the nucleic acids comprise those in Table N_{other H} (*infra*).

4. Group 2 Light Chain Variable Domain

[0086] In another embodiment of this aspect of the invention, the nucleic acids comprise those in the Table N_{G2} (*infra*). These sequences encode the Group 2 λ light chain variable domain polypeptides disclosed in paragraph [0033].

[0087] In another embodiment of this aspect, the invention comprises a nucleic acid encoding a variable domain polypeptide disclosed in paragraph [0031], or, more preferably, in paragraph [0032]. In the broadest embodiment, this embodiment of the invention comprises any nucleic acid encoding a variable domain polypeptide disclosed in paragraph [0031] or paragraph [0032]. The sequences of the nucleic acids are routinely determinable using the genetic code.

5. Group 1 Light Chain Variable Domain

[0088] In another embodiment of this aspect of the invention, the nucleic acids comprise those in the Table N_{G1} (*infra*). These sequences encode the Group 1 light chain variable domain polypeptides disclosed in paragraph [0036].

[0089] In another embodiment of this aspect, the invention comprises a nucleic acid encoding a variable domain polypeptide disclosed in paragraph [0034], or, more preferably, in paragraph [0035]. In the broadest embodiment, this embodiment of the invention comprises any nucleic acid encoding a variable domain polypeptide disclosed in paragraph [0034] or paragraph [0035]. The sequences of the nucleic acids are routinely determinable using the genetic code.

6. Group 3 Light Chain Variable Domain

[0090] In another embodiment of this aspect of the invention, the nucleic acids comprise those in the Table N_{G2} (*infra*). These sequences encode the Group 2 light chain variable domain polypeptides disclosed in paragraph [0039].

[0091] In another embodiment of this aspect, the invention comprises a nucleic acid encoding a variable domain polypeptide disclosed in paragraph [0037], or, more preferably, in paragraph [0038]. In the broadest embodiment, this embodiment of the invention comprises any nucleic acid encoding a variable domain polypeptide disclosed in paragraph [0037] or paragraph [0038]. The sequences of the nucleic acids are routinely determinable using the genetic code.

7. Kappa Light Chain Variable Domain

[0092] In another embodiment of this aspect of the invention, the nucleic acids comprise those in the Table N_κ (*infra*). These sequences encode the kappa light chain variable domain polypeptides disclosed in paragraph [0042]. The sequences of the nucleic acids are routinely determinable using the genetic code.

[0093] In a preferred embodiment, the nucleic acids comprise a sequence from one of Tables N_{H58}, N_{H74}, N_{Other H}, N_{G2}, N_{G1}, N_{G3}, N_κ, or N_λ modified as needed to code for the appropriate polypeptide of paragraph [0023], [0026], [0033], [0036], [0039], [0042][0040], respectively. The modification comprises substituting appropriate codons into a sequence of each of these tables to yield a sequence encoding the subject polypeptide. The codon that is substituted into the sequences of tables is selected from the codons employed in any of the tables and is generally found in sequences within the same table at the same position as the position into which the codon is substituted. Thus, for example, a nucleic acid according to this aspect of the invention encoding a polypeptide that is the same as H3 (in Table N_{H58}) except for an A→G amino acid change at position 15 of H3 would comprise the H3 nucleic acid sequence of Table N_{H58} in which the GCG codon (aa's 106-108 of the H3 nucleotide sequence encoding the A at position 15 of the H3 polypeptide) is replaced with GGG, the codon encoding the amino acid G in position 15 of H4 (and which comprises amino acids 106-108 of the H4 nucleotide sequence).

[0094] In another preferred embodiment the nucleic acids of the invention are comprised of preferred codons for the host intended to express the nucleic acids. Nakamura *et al.*, *Nucl. Acids Res.* **28**, 292 (2000). Preferred codons for numerous species ranging from prokaryotes to mammals are known and documented. *E.g.*, *Id.*. For *in vitro* applications, bacterial or other preferred codons can be employed.

[0095] The nucleic acids of the invention can be made by any suitable technique, many of which are well known to those skilled in the art. *E.g.*, Sambrook and Russell, *supra*. The nucleic acids of the invention can be synthesized using automated synthesizers and PCR amplified.

Method of Making Canine Variable Domains

[0096] In another aspect, the invention comprises a method of making a canine variable domain nucleic acid by isolating it from a canine biological sample. In view of the great homology among mammalian immunoglobulins, our first attempt to isolate canine variable domain nucleic acid sequences employed degenerate primers based on human and mouse variable domain sequences. This approach was taken because no canine variable domain nucleic acid sequences were known to date. We were surprised to discover that employing 5' primers and anchoring the reactions in the canine constant domain sequences at the 3' end, all reactions for light chains failed and heavy chain amplifications were successful at a very low rate (only 1 positive reaction out of 21 possible positive reactions). The tremendous homology among mammalian immunoglobulins made this difficulty unforeseeable. Accordingly, another approach was required, which comprises the method of this aspect of the invention.

[0097] In this aspect, the invention comprises a method of making a canine variable domain nucleic acid sequence, which method comprises subjecting a canine biological sample to 5' RACE (Rapid Amplification of cDNA Ends) using a first antisense gene specific primer complementary to a canine constant region sequence and a second gene specific sequence complementary to a sequence within the canine constant region 5' to the sequence to which the first antisense gene specific primer is complementary, wherein the canine biological sample comprises poly(A)+RNA encoding at least one canine immunoglobulin. Preferably the canine biological sample comprises canine peripheral blood lympho-

cytes. The 5' RACE technique is well known to those skilled in the art and has been the subject of several reviews. *E.g.*, Frohman, M.A. (1990) "PCR Protocols: A Guide to Methods and Applications" (Innis, M.A., Gelfand, D.H., Sninsky, J.J., and White, T.J., eds.) p. 28, Academic Press, San Diego); Loh, E. (1991) *Methods* 2, 11; and Frohman, M.A., (1993) Rapid Amplification of Complementary DNA Ends for Generation of Full-Length Complementary DNAs: Thermal RACE. *Methods in Enzymology* 218:340-356.

[0098] Many canine constant domain sequences are known in the art and can be employed to generate the first and second gene specific primers: Patel et al., *Immunogenetics* 1995;41(5):282-6; Tang et al. *Vet Immunol Immunopathol* 2001 Aug 10;80(3-4):259-70; Wasserman et al., *Science* 200 (4346), 1159-1161 (1978); U.S. 5,593,861; U.S. 5,852,183; JP 1997169795-A 3 30-JUN-1997 (Hitachi Chem Co Ltd); JP 1992040894-A 1 12-FEB-1992 (Chemo Sero Therapeut Res Inst); JP 1991123489-A 1 27-May-1991 (Chemo Sero Therapeut Res Inst); JP 1991083579-A 1 09-Apr-1991 (Chemo Sero Therapeut Res Inst); Wasserman et al., *Biochemistry* 16 (14), 3160-3168 (1977); McCumber et al., *Mol. Immunol.* 16 (8), 565-570 (1979).

Caninized Antibodies and Methods of Making Them

[0099] The present invention provides novel methods for preparing caninized immunoglobulin chains having generally one or more complementarity determining regions (CDR's) from a donor immunoglobulin and a framework region from a canine immunoglobulin. Caninization is accomplished by replacing one or more CDR's of a canine immunoglobulin with a CDR from a non-canine source. According to this aspect of the invention, the non-canine CDR can be substituted for the corresponding CDR in the complete canine immunoglobulin (or binding fragment thereof) directly, or it can be substituted into an immunoglobulin fragment containing the CDR locus (*e.g.*, the variable domain) and the substituted fragment thereafter made into the entire immunoglobulin or binding fragment thereof.

[00100] The preferred method comprises first comparing the framework or variable region amino acid sequence of the donor immunoglobulin to corresponding sequences in a collection of canine immunoglobulin chains, and selecting as the canine immunoglobulin one of the more homologous sequences from the collection. The canine immunoglobulin, or

acceptor immunoglobulin, sequence is typically selected from a collection of at least 10 to 20 immunoglobulin variable region sequences, and usually will have the highest homology to the donor immunoglobulin sequence of any sequence in the collection. The canine immunoglobulin framework sequence will typically have about 60 to 70% homology or more to the donor immunoglobulin framework sequences. The donor immunoglobulin can be either a heavy chain or light chain, and the canine collection will contain the same kind of chain. A caninized light and heavy chain can be used to form a complete caninized immunoglobulin or antibody, having two light/heavy chain pairs, with or without partial or full-length canine constant regions.

[00101] To form the caninized variable region, amino acids in the canine acceptor sequence are replaced by the corresponding amino acids from the CDR of the donor sequence using methods well known to those skilled in the art (e.g., PCR amplification of the variable domain nucleic acid sequence employing primers comprising, in part, the donor CDR coding, as exemplified in Example 5.).

[00102] In another embodiment of the present invention, either in conjunction with the above comparison step or separately, additional amino acids in the acceptor immunoglobulin chain (preferably the light chain) can be replaced with amino acids from the CDR-donor immunoglobulin chain. More specifically, further optional substitutions of a canine framework amino acid of the acceptor immunoglobulin with the corresponding amino acid from a donor immunoglobulin will be made at positions wherein:

- a. the amino acid in the canine framework region of the acceptor immunoglobulin is rare for that position and the corresponding amino acid in the donor immunoglobulin is common for that position in canine immunoglobulin sequences;
- b. the amino acid is immediately adjacent to one of the CDR's;
- c. the amino acid is predicted to be within about 6 angstroms of the CDR's in a three-dimensional immunoglobulin model and capable of interacting with the antigen or with the CDR's of the donor or caninized immunoglobulin; or
- d. the amino acid in the canine framework region of the acceptor immunoglobulin differs from the corresponding amino acid of the donor immunoglobulin.

[00103] Optionally, an amino acid in the acceptor sequence can be replaced with an amino acid typical for canine sequences at that position, if the amino acid in the acceptor immunoglobulin is rare for that position and the corresponding amino acid in the donor immunoglobulin is also rare, relative to other canine sequences.

[00104] When combined into an intact antibody, the caninized light and heavy chains of the present invention will be substantially non-immunogenic in canines and retain substantially the same affinity as the donor immunoglobulin to the antigen (such as a protein or other compound containing an epitope). These affinity levels can vary from about 10^8 M⁻¹ or higher, and may be within about 4 fold, preferably within about 2 fold of the donor immunoglobulin. Ideally, the caninized antibodies exhibit affinity levels at least about 60 to 90% of the donor immunoglobulin's original affinity to the antigen.

[00105] Once designed, the immunoglobulins of the present invention (including binding fragments) can be produced readily by a variety of recombinant DNA or other techniques. Preferably, polynucleotides encoding the desired amino acid sequences are produced synthetically and by nucleic acid sequences joined, where necessary, using PCR. The polynucleotides can be amplified using PCR or, preferably, inserted into an appropriate cloning vehicle and the encoded polypeptide expressed in a suitable expression system.

[00106] Notably, the methods of the present invention maximize the likelihood of producing caninized immunoglobulins with optimum binding characteristics. The caninized immunoglobulins are particularly useful in treating canine disorders susceptible to monoclonal antibody therapy. Thus, in another aspect, the invention comprises methods of treating a canine having an IgE-mediated affliction by administering to the canine an amount of a caninized antibody of the invention (or binding fragment thereof) sufficient to alleviate or eliminate one or more symptoms associated with the affliction.

[00107] In addition to complete caninized immunoglobulins, the invention also comprises binding fragments thereof. The use and generation of fragments of antibodies is well known, e.g., Fab fragments [Tijssen, Practice and Theory of Enzyme Immunoassays (Elsevier, Amsterdam, 1985)], Fv fragments [Hochman et al., Biochemistry 12:1130 (1973)], scFv fragments (Phage Display: A Laboratory Manual. Carl F.

Barbas III, Dennis R. Burton, Jamie K. Scott and Gregg J. Silverman. Cold Spring Harbor Laboratory Press. Cold Spring Harbor, New York).

[00108] In another aspect, the invention provides a composition comprising at least one caninized antibody of the invention and a pharmaceutically acceptable carrier.

[00109] Caninized antibodies and binding fragments thereof are also useful for *in vitro* assays for detecting the presence of an antigen in a biological sample.

EXAMPLES

Example 1.

Isolation of Canine Variable Domains

[00110] Canine lambda and kappa light-chain variable domain cDNA's, as well as IgG_H variable domain cDNA's were synthesized from mRNA isolated from canine peripheral blood lymphocytes (PBL's). Variable domain cDNA's from B-cells that had undergone V-D-J recombination and coded for functional molecules were targeted.

[00111] Five to 10 mls of canine blood was collected in Vacutainer CPTTM sodium citrate collection tubes and spun 1,500 x g for 20 minutes. After aspiration of the plasma layer, the mononuclear cell layer was collected and washed with PBS. The cell pellet was resuspended into 2 ml of PBS and the polyadenylated mRNA isolated using the Micro-fast Track mRNA isolation kit (Invitrogen) as specified by the manufacturer. After isolation mRNA was stored as a precipitate in ethanol at -80°C.

[00112] Variable domains were synthesized from mRNA using a 5'RACE kit (GIBCO Life Technologies, Version 2.0). Briefly, first strand cDNA's were generated from poly(A)+RNA by SuperScript RT II enzyme (GIBCO Life Technologies) using the antisense gene specific primers (GSP1) complementary to canine constant regions of the lambda, kappa or IgG_H constant regions. For isolation of heavy chain variable domains, GSP1 primers were derived from DNA sequences that are identical in the four different canine IgG constant chains that code for subdomain 1: two are disclosed in U.S. patent 5,593,861 (DE94 and DB31), and the other two (1e5b and 3k9c) were cloned by applicants. For isolation of light chain variable domains, GSP1 primers were derived from the sequence of the constant regions of the lambda and kappa constant

domains as disclosed in the U.S. patent 5,593,861. The GSP1 primers employed are listed in the following table.

Table 1A
GSP1 Primers

GSP1 primers for lambda first strand cDNA synthesis	LG014: 5' GTCAGGCTCAGGTAGCTG (SEQ ID NO: 810)
	LG011: 5' GGCCGCGTACTTGTGTTG (SEQ ID NO: 811)
	LG010: 5' GTCGCTGATGAGGCACACC (SEQ ID NO: 812)
GSP1 primers for Kappa first strand cDNA synthesis	LG018: 5' GCTCTTGTGAGTGATCTCAC (SEQ ID NO: 813)
	LG017: 5' GTGCTGCTGAGGCTGTAGG (SEQ ID NO: 814)
	LG016: 5' CCATCCACTTTCCACTTGAC (SEQ ID NO: 815)
GSP1 primers for IgG _H first strand cDNA synthesis	RK285: 5' GGCTTGTCTACTTTAGTTTTG (SEQ ID NO: 816)
	RK321: 5' ACTTTAGTGTTGGTGGCCGGGTGG (SEQ ID NO: 817)
	RK322: 5' ACTTTAGTTTTGCTGGCCGGGTGG (SEQ ID NO: 818)
	RK323: 5' CTCGCATTCTTTGACCACTGGCTTGTC (SEQ ID NO: 819)
	RK324: 5' TCTGCATTCAATTGAACACTGGCTTGTC (SEQ ID NO: 820)

[00113] After first strand syntheses, the RNA was degraded with RNase Mix and the cDNA was purified with the Glassmax Spin Cartridge system. The cDNA was then dC-tailed using terminal deoxynucleotide transferase. PCR amplification was performed using the Gibco Abridged Anchor Primer and the appropriate nested GSP2 primer. GSP2 primers were derived for the heavy and light chains from the same sequence used for the GSP1 primers, but modified as described by the 5' RACE protocol. The GSP2 primers employed are listed in the following table.

Table 1B
GSP2 Primers

Nested GSP2 primers for the amplification of lambda variable regions	LG011: 5'GGCCGCGTACTTGTTGTTG (SEQ ID NO: 811)
	LG010: 5'GGCCGCGTACTTGTTGTTG (SEQ ID NO: 812)
	LG012: 5'GAGCTCCTCAGAGGAG (SEQ ID NO: 821)
Nested GSP2 primers for the amplification of Kappa variable regions	LG017: 5'GTGCTGCTGAGGCTGTAGG (SEQ ID NO: 814)
	LG016: 5'CCATCCACTTTCCACTTGAC (SEQ ID NO: 815)
	LG047: 5'CAGAGGCACTTCCTGTGTGTAAGTGG (SEQ ID NO: 822)
Nested GSP2 primers for the amplification of IgG _H variable regions	RK120: 5'ACCGCTGGTCAAGGAGCCG (SEQ ID NO: 823)
	RK122: 5'TGGACCACGTTGCAGGTGAAG (SEQ ID NO: 824)
	RK281: 5'TACAGGCTCGGGGAAGTAG (SEQ ID NO: 825)
	RK282: 5'GGGTCCAGTGGGAAAAC (SEQ ID NO: 826)
	RK326: 5'GTCTCGCTGGACCACCTGCTGGA (SEQ ID NO: 827)
	RK321: 5'ACTTTAGTGTTGGTGGCCGGGTGG' (SEQ ID NO: 817)
	RK322: 5'ACTTTAGTTTGTGCTGGCCGGGTGG (SEQ ID NO: 818)

[00114] The amplified cDNA's were then cloned using the pCR 2.1 TOPO TA Cloning kit (Invitrogen) and TOP 10 competent cells (Invitrogen) according the manufacturer's protocol. Plasmid DNA was isolated from single colonies grown in a 5 ml Luria's Broth culture overnight at 37°C was then isolated using the Qiaspin Mini Isolation kit (QIAGEN) according to the manufacturer's protocol. Automated sequencing of the plasmid inserts was done at the University of Virginia's sequencing facility using an ABI PRISM sequencer model 377 Version 3.3.

[00115] DNA sequences were analyzed using the Hitachi DNAsis program. Clones possessing an open reading frame characteristic of a variable domain were selected for compilation of a canine immunoglobulin DNA database. Initial criteria used to evaluate potential heavy chain variable domain clones were the presence of the primer used for 5'RACE

at the 3' end of the putative reading frame, the presence of sequences corresponding to the 4 IgG heavy chain constant domain sequences 5' to the sequence of the primer used in 5'RACE, and, after translation of the DNA sequence to the amino acid sequence, the presence the highly conserved cysteines at positions 22 and 96. Criteria used to evaluate potential lambda chain variable domain clones were the presence of the primer used for 5'RACE at the 3'end of the putative reading frame, the presence of sequences corresponding to the kappa chain constant domain 5' to the sequence of the primer used for 5'RACE, and, after translation of the DNA sequence to the amino acid sequence, the presence of the highly conserved cysteines at positions 22 and 90 for lambda chains. Criteria used to evaluate potential kappa chain variable domain clones was the presence of the primer used for 5'RACE at the 3'end of the putative reading frame, the presence of sequences corresponding to the kappa chain constant domain 5' to the sequence of the primer used for 5'RACE, and, after translation of the DNA sequence to the amino acid sequence, the presence of the highly conserved cysteines at positions 23 and 93 for kappa chains.

[00116] Sequences with the highest homology to 15A2 were chosen as templates for caninization. Variable domains were first sorted based on the type of constant domains to which they were attached: IgG heavy chains, lambda chains, or kappa chains. Then, using the Hitachi DNAsis protein alignment program, variable domain sequences were grouped into separate genera based on homology and compared to the sequence of the 15A2 heavy chain variable domain or 15A2 light chain variable domain as appropriate. The ranking of regions of homology between mouse 15A2 and the cloned canine variable domain sequences is as follows: first appropriate variable domain family (lambda with lambda, heavy chain variable with heavy chain variable) followed by homology in framework regions 1, 2 and 3, followed by homology in CDR3 of the cloned canine variable domain with the amino acid sequences in CDR3 of the 15A2 heavy or light chain as appropriate.

Example 2.

Grafting Variable Domains onto Appropriate Constant Domain

[00117] Variable domains that were considered suitable for CDR grafting were fused to the appropriate constant domain (lambda or IgG_H) us-

ing tailed PCR reactions and tested for expression in a transient COS cell expression system.

[00118] Full length clones of canine variable domains include the secretory leader sequence that is proteolytically cleaved from the immunoglobulin during protein synthesis, secretion, and folding. For heavy chain variable domains, an oligonucleotide was synthesized corresponding to the secretory leader sequence of MDWTWRVFFLALLALATGVHS (SEQ ID NO: 828) with a consensus Kozak sequence added to the 5' end (RK278: 5'-GGATCCGCCACCATGAACTTGTGGCTAAACT (SEQ ID NO: 829) for H58 and RK271: 5'-GGATCCGCCACCATGGACTGGACCTGGAGGGTC (SEQ ID NO: 830) for H74). This oligo was paired with RK276 (sequence AC-CGAGGGCGCCGTGGTGA; SEQ ID NO: 831) and the heavy chain variable domain PCR amplified using the pCR2.1 TOPO clone as a DNA template. In a separate PCR reaction, the IgG_H DE94 constant domain (U.S. patent 5,593,861) was amplified using RK275: 5'-TCCACCACGGCGCCCTCGGT (SEQ ID NO: 832) and RK186 5'-GGGTCTAGAGCCCTTTCATTTACCCGGAGAATG (SEQ ID NO: 833). The products from these reactions were verified by checking their size using agarose gel electrophoresis, followed by gel purification.

[00119] After gel purification, approximately 2 ng of each PCR product were combined, mixed with 2 µm of 5' the primer RK271 and 2 µm of the 3' primer RK186, and subjected to PCR amplification to fuse the DNA coding for the variable domain to the DNA coding for the constant domain. The RK275 and RK276 primers create an overlap of the DNA coding sequence corresponding to the variable domain/CH1 domain junction. This overlap allows the fusion of the DNA coding for the variable to the DNA coding for the constant domain during the PCR reaction. After amplification, PCR products were gel purified, phenol-chloroform extracted and EtOH ppt. After re-suspension into TE, the amplified variable domains were then cloned using the pCDNA3.1 TOPO TA Cloning kit (Invitrogen) and transformed into TOP 10 competent cells (Invitrogen) according the manufacturer's protocol. Plasmid DNA was isolated from single colonies grown in a 5ml Luria's Broth culture overnight at 37°C was then isolated using the Qiaspin Mini Isolation kit (QIAGEN) according to the manufacturer's protocol. Clones of functional heavy chains were screened for as described below.

[00120] Full length clones of canine immunoglobulins include the secretory leader sequence that is proteolytically cleaved from the ma-

ture protein chain, the variable domain, and the constant domains. For the lambda variable domain, an oligonucleotide was synthesized corresponding to the secretory leader sequence with a consensus Kozak sequence added to the 5' end (LG036: 5'-CTACGATCTCTGAGAGTCC; SEQ ID NO: 834 for Group 2). This oligo was paired with LG012: 5'-GAGCTCCTCAGAGGAG (SEQ ID NO: 821) and the light chain variable domain amplified using PCR. In a separate PCR reaction, the lambda constant domain was amplified using LG035: CCGCCCTCCTCTGAGGAG (SEQ ID NO: 835) and LG027: 5'-CTAAGAGCACTCTGCGGG (SEQ ID NO: 836). The products from these reactions were verified by checking their size using agarose gel electrophoresis, followed by gel purification.

[00121] Approximately 2 ng of each PCR product were combined, mixed with 2 μ m of LG036 and 2 μ m of LG027, and PCR amplified as described. PCR products were gel purified, phenol-chloroform extracted and EtOH ppt. After re-suspension into TE, the amplified the full length immunoglobulin chains were then cloned using the pcDNA3.1 TOPO TA Cloning kit (Invitrogen) and TOP 10 competent cells (Invitrogen) according the manufacturer's protocol. Plasmid DNA from single colonies grown in a 5 ml Luria's Broth culture overnight at 37°C was then isolated using the Qiaspin Mini Isolation kit (QIAGEN) according to the manufacturer's protocol. Clones of functional light chains were screened for as described below.

Example 3.

Screening for Functional Variable Domains

[00122] DNA clones of functional variable domains were identified using a screen that was dependant on the efficient secretion of an IgG_H chain in a transient COS cell expression system. COS cells were transfected with no DNA (mock transfection), Hx only (1 μ g of the Hx expression vector), HxLx (1 μ g each of the Hx and Lx expression vectors), or Hx1C9L (1 μ g of the Hx expression vector and 1 μ g of an expression vector coding for the 1C9 kappa light chain). DNAs and cell culture supernatants were collected at 48 and 72 hours. Tissue culture supernatants were then assayed for IgG by ELISA, as described in Example 4.

[00123] Without a functional light chain, IgG_H chains are inefficiently secreted from COS cells by T = 48 hours post transfection (see Fig. 1). Screening of potential light chain clones was accomplished

by co-transfection with an expression clone for the 15A2 chimeric heavy chain. Conversely, screening of potential heavy chain clones was accomplished by co-transfecting with an expression clone for the 15A2 chimeric light chain.

[00124] Screening full-length lambda chains involved co-transfecting 10 μ l of miniprep DNA with 1 μ g of pcDNA3.1::c15A2IgG_H. COS cells 75-95% confluent in six well COSTAR (Corning Inc.) tissue culture plates were used for transfections. DNA was diluted with 230 μ l Opti-MEM[®]I (Gibco BRL) to a final volume of 250 μ l. 10 μ l of Lipofect AMINE[™] 2000 (Gibco-BRL) was diluted with 240 μ l of Opti-MEM[®]I, mixed with the diluted DNA and allowed to incubate at room temperature for 20 minutes to allow the DNA to complex with the Lipofect AMINE[™] 2000. During incubation, cells were prepared by removal of growth medium followed by the addition of 500 μ l of Opti-MEM[®]I. The 0.5 ml DNA/LP2000 complex was added to each well and allowed to incubate 5 hours. An additional 1 ml of growth medium was added to each well (DMEM plus 20% fetal bovine serum, plus L-glu), after which cell culture supernatants were harvested at T = 48 hours.

[00125] Cell culture supernatants were clarified of cellular debris by centrifugation at 1,000 x g for 5 minutes and adjusted to a final concentration of 0.02% sodium azide to prevent bacterial growth. Cell culture supernatants were assayed immediately for IgG_H levels and IgE binding activity or frozen at -20°C to be assayed at a later time. Control tissue culture wells were prepared by receiving no DNA, pcDNA3.1::c15A2IgG_H only, or pcDNA3.1::c15A2Ig_H/ pcDNA3.1c15A2::lambda. Production of IgG_H was assayed for as described below.

[00126] Clones scoring positive in this assay were re-transformed into *E. coli* for large scale DNA isolation using the Qiagen Endotoxin Free Kit (Qiagen Corp., Valencia, CA) and sent out for DNA sequencing.

[00127] Screening for full-length heavy chain expression clones was done in an identical manner, except 10 μ l of miniprep DNA of the potential heavy-chain expression clone was co-transfected with 1 μ g of pcDNA3.1:c15A2lambda DNA.

[00128] Isolates that encoded for functional variable domains that were of the correct DNA sequence were transfected into COS cells as described above using the ratio of 1 μ g light chain to 1 μ g of heavy chain. Cell supernatants were collected and scored for IgG_H secre-

tion, IgE binding, and the ability to compete with the recombinant high affinity IgE receptor for soluble IgE.

Example 4.

ELISA Assays

[00129] To assay for IgG_H expression, ELISA assays were performed 96 well Immulon 4 plates (Thermo Lab Systems, Helsinki, Finland).

Throughout this study, four different type of ELISA assays were performed. Determination of IgG_H concentration, IgE binding, IgE mimotope binding, and the neutralization of soluble IgE assay.

[00130] To determine IgG_H concentration in cell culture supernatants, 96 well plates were coated with rabbit anti-dog Fc (Jackson Immunologicals, West Grove, PA) diluted to 2 µg/ml in sodium carbonate buffer (100 mM, pH 10), with 100 µl applied to each well of the plate. Non-specific binding to the plates was prevented by blocking the plates with 3% bovine serum albumin. A chimeric 15A2 standard was prepared by diluting baculoviral expressed protein to 100, 50, 25, 12.5, 6.25 and 3.13 ng/ml in OptiMEM. Serial dilutions of cell culture supernatants were prepared in OptiMEM and 100 µl of each dilution was applied to the plate and incubated for 1 hour at room temperature. After incubation plates were washed 5 times with TBS 0.1% Tween 20. For detection of bound antibody, 100 µl of anti-dog Fc Horse Radish Peroxidase (HRP) conjugate (Jackson Immunologicals) diluted 1:5000 in conjugate diluent (IDEXX Labs, Inc., Westbrook ME), applied to each well and allowed to incubate for 1 hour at room temperature. After 5 washes with TBS 0.1% Tween 20, the presence of bound rabbit anti-dog HRP conjugate was detected by the addition of TMB substrate (IDEXX Labs, Inc.), allowed to develop for 10 minutes followed by the addition of stop solution (100 µl/well, IDEXX Labs, Inc.). Optical density was read at 650 nm using SOFTmax Pro software to plot a standard curve and analyze data. The activity of IgG expression activity was scored by comparison to the dilution standards of recombinant c15A2, as well as the activity in the transfection controls.

[00131] To determine IgE binding activity, 96 Immulon 4 plates were coated with recombinant canine IgE diluted to 2.5 µg/ml in sodium carbonate buffer (100 mM, pH9.5), 100 µl applied to each well of the plate. Non-specific binding to the plates was prevented by blocking

the plates with 3% bovine serum albumin. Preparation of standards and detection of IgG_H is exactly as described above.

[00132] To determine IgE mimotope binding activity, plates were coated with a peptide/KLH conjugate at 2 µg per ml, diluted in sodium carbonate buffer (100 mM, pH9.5). The peptide mimics the 15A2 epitope found on IgE. Non-specific binding to the plates was prevented by blocking the plates with 3% bovine serum albumin. Preparation of standards and detection of IgG_H is exactly as described above.

[00133] The neutralization of soluble IgE assay determines the ability of anti-IgE immunoglobulin molecules to bind and prevent soluble IgE from interacting with the high affinity IgE receptor. The 15A2 immunoglobulin binds to subdomain three of IgE, preventing it from interacting with the high affinity IgE receptor. 96 well Immulon 4 plates are coated with the high affinity IgE receptor diluted to 10 µg per ml in sodium carbonate buffer, with 100 µl applied to each well of the plate. Non-specific binding to the plates was prevented by blocking the plates with 3% bovine serum albumin. IgE was diluted to 100 ng/ml in OptiMEM medium. Serial dilutions of clarified cell culture supernatants were prepared, and mixed 1:1 (final volume 200 µl) with the diluted IgE (final concentration 50 ng). After incubation for 1 hour at room temperature, this mixture was applied to high affinity IgE receptor plate. After incubation for 1 hour, plates were washed 5 times with TBS 0.1% Tween 20. For detection of bound antibody, 100 µl of an anti-IgE monoclonal antibody conjugated to HRP diluted to 2 µg/ml in conjugate diluent (IDEXX Labs, Inc.) was applied to each well and allowed to incubate for 1 hour at room temperature. After 5 washes with TBS 0.1% Tween 20, the presence of bound anti-IgE HRP conjugate was detected by the addition of TMB substrate (IDEXX Labs, Inc.), allowed to develop for 10 minutes followed by the addition of stop solution (100 µl/well, IDEXX Labs, Inc.).

Example 5.

CDR Grafting

[00134] The complimentary determinant regions (CDR's) of mouse 15A2 were identified using the Kabat numbering system for variable domains as well as homology alignments to other mouse variable domains to which the CDR's had been identified.

[00135] CDR grafting was accomplished using the PCR reaction. The protocol for PCR amplification was performed as described, except "tailed" oligos carrying mutations of interest were used to modify the coding sequence of canine variable domains. Once a suitable heavy chain was identified for CDR grafting, synthetic oligo nucleotides were synthesized and used as shown in Figure 5. The isolated canine variable domains serving as a template for the PCR reactions. The comparison of murine 15A2 to the canine variable domains chosen as graft recipients is in Figures 2 and 3. The oligonucleotides used to graft the 15A2 CDR's into the H74 heavy chain and Group 2 light chain are shown in the following tables:

Table 2*CDR Grafting Group 2*

N-terminal primer:	LG036: 5' CTACGATCTCTGAGAGTCC (SEQ ID NO: 834)
CDR1 primers:	LG029: 5' CGTCACCGCACCCGTGCTGCTGCGACATGTGAGTGTGACTGTCC (SEQ ID NO: 837)
	LG037: 5' CGCAGCAGCACGGGTGCGGTGACGACGAGCAACTACGCCAA CTGGTATCAGCAGACCCAAGG (SEQ ID NO: 838)
CDR2 primers:	LG038: 5' CGGCGCTCTGTTGTTAGGGCCGTAGATAATCGTGCGAGG (SEQ ID NO: 839)
	LG039: 5' GGCCCTAACAAACAGAGCGCCGGGCGTCCCTAGTCGCTTCTCTGG (SEQ ID NO: 840)
CDR3 primers:	LG034: 5' TGGTACAGCAACCATTTGGGTGTTCTGGCGGAGGCACCCACC (SEQ ID NO: 841)
	LG040: 5' CACCCAATGGTTGCTGTACCACAACGCACAGTGATAGTCAGCCT C ATCC (SEQ ID NO: 842)
C-terminal primer:	LG027: 5' CTAAGAGCACTCTGCGGG (SEQ ID NO: 836)

Table 3*H74 Caninization Oligonucleotides*

N-terminal primer:	RK271: 5' GGATCCGCCACCATGGACTGGACCTGGAGGGTC (SEQ ID NO: 830)
CDR1 primers:	RK292: 5' TCATTTACTGACTACTTTATGAACTGGGTAC (SEQ ID NO: 843)
	RK293: 5' AAAGTAGTCAGTAAATGAGTAACCAGA (SEQ ID NO: 844)
CDR2 primers:	RK294: 5' GGTGATCCTTTCTACAACCAGAAGTTCAAGGGCAGAGTC (SEQ ID NO: 845)
	RK295: 5' GTTGTAGAAAGGATCACCATTGAAAGGATTAATACGTCCCATCCA (SEQ ID NO: 846)

CDR3 primers:	RK308: 5'GTGTACTACTGCGCAAGATTCTAC (SEQ ID NO: 847)
	RK309: 5'GTAGAATCTTGCGCAGTAGTACAC (SEQ ID NO: 848)
C-terminal primer:	RK186: 5'GGGTCTAGAGCCCTTTCATTTACCCGGAGAATG (SEQ ID NO: 833)

[00136] The final products of these PCR reactions were cloned into pcDNA3.1 TOPO as described. Individual clones were screened for functional secretion of IgG_H chains as described above and positive isolates had their DNA sequenced as described.

[00137] Isolates that encoded for functional variable domains and were of the correct DNA sequence were transfected into COS cells as described above. Cell supernatants were collected and scored for IgG_H concentration, IgE binding, and the ability to neutralize soluble IgE and prevent it from interacting with the high affinity IgE receptor. The results manifest IgE binding by the fully caninized molecules are displayed below. Table 4 reports the OD at 650 nm of ELISA assays performed as described. COS cell supernatants are from cells transfected with the shown constructs. Table 5 displays relative concentration levels when compared to expression levels for the 15A2 chimeric antibody. Table 6 displays OD of IgE Binding over relative expression levels. Table 7 displays the ratio IgE binding/expression.

Table 4

IgE Binding - Transient COS System

	Group 2-1	Lx
H74-1	Negative	1.3
Hx	0.32	3.0

Table 5

Relative expression levels - IgG concentration assay

	Group 2-1	Lx
H74-1	2.4	0.1
Hx	2.7	1

Table 6

OD of IgE Binding over relative expression levels

	Group 2-1	Lx
H74-1	2.4/0	1.3/.1

Hx	0.32/2.7	3/1
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Table 7*Ratio IgE Binding/Expression*

	Group 2-1	Lx
H74-1	Null	13
Hx	0.12	3

[00138] The binding affinity and IgE neutralization by a recombinant molecule in *in vivo* applications is preferably higher than displayed above. Accordingly, we undertook additional modifications of the caninized immunoglobulin to improve it's binding affinity for IgE.

Example 6.*Homology Modeling and Site Directed Mutagenesis*

[00139] Homology modeling was used to identify potential amino acids from the canine framework regions for back mutations to the 15A2 murine sequence. For manipulation of Brookhaven Protein Data Bank (PDB) files, model building, model refinement, and prediction of specific amino acids for site directed mutagenesis, the molecular modeling/graphics program DEEP VIEW was used (available at <http://www.expasy.ch/spdbv/mainpage.htm>). Guex, N. and Peitsch, M.C. (1997) SWISS-MODEL and the Swiss-PdbViewer: An environment for comparative protein modeling. *Electrophoresis* 18, 2714-2723. DEEP VIEW was formerly known as Swiss-PdbViewer.

[00140] The linear sequences of murine 15A2 heavy and light chain were found to have high homology to three different variable domains for which crystal structures existed in the Brookhaven Protein Data Bank, designated 1NGQ, 1FBI, and 2VIR. The murine 15A2 heavy and light chains were modeled onto these three separate crystal structures using DEEP VIEW. For each model, the amino acids within a 3 angstrom shell and a 6 angstrom shell surrounding the CDR's was determined. Comparison of the three structures, and of the amino acids within these two concentric shells about the CDR's identified key amino acids that could be in direct and indirect contact supporting the CDR's. Amino acids that were found within the 3 and 6 angstrom shell in all three structures were scored as high for affecting CDR conformation.

[00141] Figure 5 shows the alignment of the Group 2-1 variable domain with the mouse 15A2 light chain variable domain, and H74-1 with the mouse 15A2 heavy chain variable domain. The CDRs are displayed in

large, bold, underline typeface, the amino acids that make up the 3 angstrom shell displayed in bold, and amino acids that make up the 6 angstrom shell underlined. Amino acid differences between these domains are indicated with vertical hash marks. Those amino acids which are different within the 3 angstrom and 6 angstrom shells of the CDR's were designated for back mutation. Back mutation is defined as changing an amino acid in the canine framework region "back" to the amino acid found in the mouse framework region. It is believed these amino acids support the CDR's of the antibody, and changing the shell of amino acids supporting the CDR's to sequences found in mouse have the greatest potential in improving affinity for the target antigen.

[00142] For the light chain: T5A, Y41V, PRTI49FTGC, Y54G, S65A, S72I, N74D and H92F received this designation. Individual Group 2-1 derivatives carrying each back mutation were constructed as described above and coexpressed with the chimeric heavy chain in the transient COS cell expression system as described above. For example, Y51G is the Group 2-1 light chain carrying the additional Y51G mutation, that has been co-transfected with the 15A2 chimeric heavy chain (Hx) into COS cells as described. COS cells are transiently transfected by the indicated DNA's. At T=48 hours, COS cell supernatants are collected and assayed for canine immunoglobulin concentration and IgE binding activity. Fig. 6 shows the OD at 650 nm of Elisa assays that measured canine IgG concentration (anti-dog) or IgE binding activity. In this assay, three Group 2-1 back mutations are found to enhance IgE binding activity of Group 2-1. These are Y41G, Y54G and H92F.

[00143] Three back mutations were found to individually enhance the binding of the caninized antibody to IgE. These were Y41V, Y54G and H92F (See Fig. 6). These three backmutations were combined into a single light chain, Group 2-1, and designated T1. (For example, Y54 is the Group 2-1 light chain carrying the additional Y54 mutation that was co-transfected with the 15A2 chimeric heavy chain (Hx) into COS cells as described.) COS cells were transiently transfected by the DNA's indicated in Fig. 7. At T=48 hours, COS cell supernatants were collected and assayed for canine immunoglobulin concentration and IgE binding activity. Shown in Fig. 7 is the OD at 650 nm of Elisa assays that measure canine IgG concentration (anti-dog) or IgE binding activity. The three Group 2-1 back mutations were found to enhance IgE binding synergistically when combined into a single light chain. The

enhanced IgE binding is equivalent to the chimeric 15A2, HxLx. One isolate was found to have particularly enhanced binding to IgE. In addition to the three backmutations, this isolate of the light chain was found to have a V7A mutation, and was designated T1c. When T1c co-expressed with the chimeric heavy chain a significant increase in IgE binding and IgE receptor competition was observed in comparison to Group 2-1 (see Figure 7).

[00144] Amino acids that were backmutated for the heavy chain were: V5Q, Q38M, D46E, M48I, R67K, V68A and S84R. Individual H74-1 derivatives carrying each back mutation were constructed as described above and coexpressed with the chimeric light chain using the transient COS cell expression system as described above. One of these backmutations was found to particularly enhance IgE binding and have particularly increased efficiency in neutralizing IgE in the IgE receptor competition assay, S84R (see Figs. 8A & B, which show the OD at 650 nm of Elisa assays that measure canine IgG concentration or IgE binding activity).

[00145] Given the high identity of H74-1 variable domain to the 15A2 variable domain, it was decided to extend back mutations to regions outside of the 3 angstrom and 6 angstrom shells surrounding the CDR's. This included amino acids K12V, V20I, G44S, A72V, T74K, T76S, Y80H, R87A, and A88S. Adjacent amino acids in H74-1 variable domain that differed from the 15A2 heavy chain variable domain were also mutated in pairs. This included AA8GP, AP40SH, AG43KS, RV67KA and RA87AS. When coexpressed with the 15A2 chimeric light chain in the COS cell transient expression system, enhanced IgE binding was found in the cell supernatants from five of these constructs. These were A43K, A72V, T74K, A88S and A91S (see Figs. 8A & B).

[00146] An extensive series of derivatives of H74-1 were created mixing and matching the six back mutations A43K, A72V, T74K, S84R, A88S and A91S. Up to three mutations were combined into a single H74-1 derivative. Six derivatives of H74-1 were found to bind IgE as well as or better than the chimeric antibody (see Figure 9 and paragraph [0076]).

[00147] These antibodies were tested for the ability to neutralize IgE in the competition assay. Constructs indicated in Fig. 9 were transfected as described into COS7L cells growing in serum free medium. For each construct, 30 separate transfections were performed.

At T=48 hours cell culture supernatants were harvested (2 ml/transfection), the 30 transfections for each construct pooled, and the material centrifuged to remove cellular debris and filtered through a 0.22 micron filter. Canine immunoglobulin was purified from cell culture supernatant using protein A chromatography. A 0.25 ml gravity flow column was used, with the cell culture fluid passed through the column three times. After washing with 10 column volumes of PBS, IgG was acid eluted with Pierce ImmunoPure IgG elution buffer. The pH was immediately adjusted to pH7.0 with Na_2PO_4 . For each construct, the IgG concentration was determined as described above, and diluted to a concentration of 7.5 ug/ml for comparison to the binding activity of other constructs. A serial dilution of each construct was performed, added to 2 ug/ml of canine IgE conjugated to HRP (100 ul/reaction). After a 1 hour incubation, material was applied to a Elisa plate coated with the canine high affinity IgE receptor. The receptor competition assay was completed as described above. A lower OD indicates less IgE is bound to the high affinity receptor and was thus successfully competed by the recombinant immunoglobulins.

[00148] In this assay six different caninized 15A2 derivatives successfully prevented soluble IgE from binding the high affinity receptor. These caninized derivatives bind to IgE as well or better than the parental variable domain from the 15A2 monoclonal antibody. (See Fig. 9.)

Example 7

Therapeutic administration of anti-IgE chimeric monoclonal antibody

[00149] In order to access the effect of targeting canine IgE *in vivo*, we created a chimeric anti-IgE monoclonal antibody. The chimeric antibody, c15A2, comprised constant domains from a mouse anti-IgE monoclonal antibody (15A2) and canine anti-IgE variable domains. c15A2 binds to sub-domain 3 of IgE, it inhibits binding to high affinity IgE receptor on mast cells and basophils, but does not bind to canine IgE bound by a high affinity IgE receptor. The c15A2 chimeric antibody was compared to the mouse anti-IgE monoclonal antibody 15A2 for its ability to inhibit binding of IgE to a high affinity receptor and found to be similarly effective.

[00150] We next sought to demonstrate the feasibility of an antibody based therapy for allergy in a model system of canine allergy. We

sought to determine if we could reduce or eliminate an IgE mediated sensitivity in a live animal. We used ragweed sensitized dogs as our model with the goal to eliminate ragweed sensitivity in these animals after treatment with the chimeric antibody.

[00151] We employed the following protocol. We used 8 consecutive doses at approximately 5 day intervals. We determined the pre-experimental free IgE levels 3 days before the first infusion. The first two infusions of the chimeric antibody were given at ten times this level. All of the subsequent doses were given at 5 times the pre-experimental IgE concentration. On a weekly basis serum was taken from the dogs and assays were performed to determine free and total IgE. We also determined on a weekly basis, the amount of free chimeric antibody in these animals and the level of IgE bound to the chimeric antibody as immune complexes. We used flow cytometric analysis to determine the level of high affinity IgE receptor expression on circulating basophils.

[00152] We measured free and total serum IgE levels in a control dog over a 6 month period and found the levels to fairly closely parallel each other, generally being in the range of 15-20 $\mu\text{g/ml}$, but varying as low as about 10 $\mu\text{g/ml}$ to about 35 $\mu\text{g/ml}$. In a treated dog, the free IgE levels decreased to undetectable levels about 1.5 days after the first infusion of the chimeric anti-IgE antibody, with total serum IgE (representing the IgE bound to the chimeric antibody) displaying a monotonic decrease to undetectable levels at day 15, after three infusions of chimeric antibody. We estimate the level of sensitivity in our assay to be 5 ng/ml of IgE. We did not observe detectable levels of free or total IgE antibody in treated dogs until 150 days, long after the last infusion of chimeric anti-IgE antibody (at 33 days) and long after we determined that the chimeric antibody was cleared from circulation. Even during the period of 150-180 days, the level of IgE was only in the range of 100-200 ng/ml, far below the level in untreated dogs.

[00153] An intradermal ragweed sensitivity skin test was performed. After a pre-treatment test, additional tests were conducted at days 36, 40 and 174. In each test there was a titration of ragweed allergen from 1000 protein nitrogen units to 0.1 protein nitrogen units administered and the effects observed. Whereas a control dog showed in increasing sensitivity to ragweed over the course of the experiments,

two of three treated dogs displayed no detectable sensitivity at 36 and 40 days and decreased sensitivity (relative to pre-treatment levels). The third treated dog displayed some sensitivity at each of the three post-treatment sensitivity tests, but still below pre-treatment levels. These and other tests showed that the chimeric anti-body c15A2:bound serum IgE;

- b) prevented IgE-receptor binding;
- c) prevented mast cell degranulation;
- d) reduced IgE receptor expression on basophils and mast cells;
- e) down-regulated IgE synthesis; and
- f) eliminated skin test reactivity in ragweed sensitized dogs.

[00155] Furthermore, we observed that:

- a) free and total serum IgE levels were eliminated in dogs treated with c15a2 anti-IgE antibody for approx 6 mo.;
- b) skin test sensitivity to ragweed was eliminated after c15A2 treatment;
- c) the capacity to synthesize new IgE was eliminated in treated dogs for up to 6 mo.; and
- d) IgE receptor expression was down-regulated on circulating basophils.

Example 8

In vivo use of caninized antibodies

[00156] The caninized monoclonal antibody 15A2 can be administered to dogs in a variety of formats and cause a reduction in IgE levels.

Elisa assays to detect IgE and IgE complexes circulating in serum:

[00157] "Free" IgE - Free IgE is defined as IgE in serum that can be bound by the high affinity IgE receptor. This assay uses mouse mAb15A2 on the solid phase. Serial dilutions of canine serum are prepared in conjugate diluent IDEXX #6680 and incubated on the 15A2 plate for 1 hour. After washing the plate, IgE is detected with an α canine HRP conjugate.

[00158] IgE Complexes/Total IgE - IgE complexes are defined as IgE in serum, not capable of binding to the high affinity receptor. These IgE molecules may be bound with test article, or some other molecule. This assay uses 14K2 on the solid phase. Serial dilutions of canine serum are prepared in conjugate diluent IDEXX #6680 and incubated on

the 14k2 plate for 1 hour. After washing the plate, IgE is detected with an α canine HRP conjugate.

Dose calculation:

[00159] Test article dose calculation incorporates the concentration of IgE and the estimated blood volume of the dog based on body weight. The formula is used:

$$\mu\text{g/ml IgE (Free)} \times \text{Kg} \times .06 = \text{mgs Free IgE in serum}$$

wherein:

$\mu\text{g/ml IgE (Free)}$ is determined by Elisa as described above

Kg = kilogram weight of the dog

.06 = a constant to estimate the volume of blood in a dog

[00160] For the study disclosed below, 10X of the Free IgE concentration of the caninized 15A2 monoclonal antibody was infused intravenously in a 30 ml volume over 30 minutes. Prior to administration, the caninized antibody was diluted into PBS with 5% glycerol (vehicle). Placebo dogs received vehicle only, 30 ml volume infused intravenously over 30 minutes. The caninized monoclonal antibody (variant H74-58/Tic) was produced in mammalian cell culture using the NSO expression system. The antibody was affinity purified from tissue culture supernatant using protein A affinity column, followed by adsorption of contaminants by flowing through a mono-Q column. Dogs received a total of 9 doses of the test article weekly, except for dose number 2 that was administered on day 4.

Calculation of dose:

Dog ID	Wt. (Kg)	Free IgE ($\mu\text{g/ml}$)	1X Dose (mg)	10X Dose (mg)
CSUAKV	11	1.46	1.0	9.6
CSVAIJ	9.1	14.58	8.0	79.6
CSWAKP	10.6	4.9	Placebo	Placebo
CSXARA	11.1	1.14	Placebo	Placebo

[00161] There is some variation in the Total IgE concentration in the placebo dogs during the course of the study. In the dogs that received test article, there is an initial increase in serum IgE levels that begins to drop rapidly after 48 hours. By day 25, IgE is undetectable in serum using our assay. The sensitivity of this assay is approximately 5 ng/ml serum.

Table N_{H58}H58 Family Canine V_H Nucleic Acid Sequences

H3 SEQ

ATGGAGTGGG GGCTCAACTT GATTTTCCTT GTCGCTATTT TACAAGGTGT CCAGGGTGAG GTGCAGCTGG
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG CGGGGTCCCT GAGACTGTCC TGTGTGACCT CTGGATTACAC
 CTTCAGTATC TACGGCATGA ACTGGGTCCG CCAGGCTCCT GGGGAAGGGGC TGCAGTGGGT CGCAGTTATT
 AATAGCGCTG GAGACACAGG CTACGCAGGC GCTGTGAAGG GCCGATTACAC CATCTCCAGA GACAACGCCA
 AGAACACAGT GTATCTGCAG ATGAACAGCC TGAGAGCCGA GGACACGGCC GTGTATTACT GTGCGAAGGA
 TCGGGAAATC ACTACGGTAG CTGAGCTTGA CCACTGGGGC CAGGGAACCC TGGTCACCGT C

(SEQ ID NO: 849)

H4 SEQ

ATGAAGTTGT GGTAAAGCTT GGTTTTCCTT GTCGCTTTTT TAAAAGGTGT CCAGACTGAG GTGCAACTGA
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG GGGGATCCCT GAGACTCTCC TGTGTGGCCT CTGGATTACAC
 CTTCAGTGAC TATGGCATGA ACTGGGTCCG CCAGGCTCCA GGGGAAGGGAC TTCAATGGGT CGCTTACATT
 AGCACTGGTG GAGGTACCAC ATCCTTTGCA GATGCTGTGA AGGGCCGGTT CACCATCTCC AGAGACAACG
 CCAAGAACAC GTTCTATCTT CAGATGAACA GCCTGAGAGC CGAGGACTCG GCCATGTATT ACTGTGCGGC
 CTTGATATAT GGATACGTTG AGGGCCCGGG GTCATACTTT GACCTCTGGG GCCCGGGCAC CCTGGTCACC
 GTC (SEQ ID NO: 850)

H5 SEQ

ATGAAGTTGG GGCTAAGCTG GGTTTTCCTT GTCGCTATTC TAAAAGGTGT CCAGGGTGAG GTGCAACTGG
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 CTTCCGTGAC TTTGCCATGA ACTGGGTCCG TCAGCCTCCA GGGGAAGGGGC CGCAGTGGGT CGCGACTATT
 AACAGGAGTG GAACCACATA CTACGCAGAC ACTGTGAAGG GCCGATTACAC CATCTCCAGA GACAGCGCCA
 AGAACACGCT ATATCTGCAG TTGAACAGCC TGACAGCCGA GGACACGGCC CGGTATTACT GTGCGGGGGC
 CAGTATGGAT ACTAAGACTT TTGACTACTG GGGCCAGGGA ACCCTTGTC CCGTC (SEQ ID NO: 851)

H7 SEQ

ATGAAGTTCTG GGCTAAACTG GGTTTTCCTT GTCGCTATTT TAAAAGGTGT CCAGGGTGAG GTGCAGCTGG
 TGGAGTCTGG GGGAGACCTA GTGAGGCCTG GGGGGTCCTT AAGACTCTCC TGTGTGGCCT CTGGATTACAC
 CTTCAGTAGC TATGGCATGA GTTGGGTCCG TCAGTCTCCA GGGGAAGGGGC TGCAGTGGGT CGCATGGATT
 AGGTATGATG GAAGTAGCAC ATACTACGCA GACGCTGTGA AGGGCCGATT CACCATCTCC AGAGACAATG
 CCAAGAACAC ACTGTATCTT CAGATGAACA GCCTGAGAGC CGAGGACACG GCCGTGTATT ACTGTGCGAA
 GGATCCCTGG AGTAGCAGTT GGTACGATGC TTTTGGTTAT TGGGGCCAGG GCACCCTGGT CACTGTC

(SEQ ID NO: 852)

H9 SEQ

ATGGAGTTGT GGCTAAACTG GGTTTTTCTT GTCGCTATTC TACAAGGTGT CCAGGGTGAG GTTCAACTGG
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG GGGGGTCCCT GAGACTCTCC TGTGTAGCCT CTGGATTACAG
 CTTCAGTCAC AACGACATGA GTTGGGTCCG CCAGGCTCCT GGGGAAGGGTC TGCAGTGGGT CGCATCTATT
 AGATATGATG AGACTGGCAC ATCCTACACT GACGCTGTGA AGGGCCGATT CACCATCTCC AGAGACAACG
 CCAGGAACAC ACTGTATCTG CAGATGAACA GCCTGAGAGC CGAGGACACG GCTGTATATT TCTGTGCGAA
 GGAATATTTA GGGGAGTATT GGGGCCCGGG AACCTGGTC ACCGTC (SEQ ID NO: 853)

H51 SEQ

ATGGATATCT GCAGAAATCG CCCTTGGGAA TTCATGGAGT TTGGGCTGAG CTGGCTTTCT CTGTGCGCTA
 TTTTACAAGG TGTCCAGGGT GAGGTGCAGC TGGTGGAGTC TGGGGGAGAC CTGGTGAAGC CTGCAGGGTC
 CCTGAGACTG TCCTGTGTGG CCTCTGGATT CACCTTCAGT GACTACGGCA TGAGCTGGGT CCGCCAGGCT
 CCTGGGAAGG GGCTGCAGTT GGTGCGAGGT ATTAACAGCG GTGGAAGTAC TACATACTAC ACAGACGCAG
 TGAAGGGCCG ATTCACCATT TCCAGAGACA ACGCCAAGAA CACAGTGTAT CTGCAGATGA ACAGCCTGAG
 AGGCGAAGAC ACGGCCATGT ATTACTGTGC AAAGGGGGGG GACAGTAGTC ACTGGTACCC GTACAATTTT
 GACTACTGGG GCCAGGGAAC CCTGGTCACC (SEQ ID NO: 854)

H53 SEQ

ATGGACTTCT GGCTAAGCTG GGTTTTCCTA GTCACTATTT TAAAAGGTGT CCAGTGTGAG GTGCAGCTGG
 TGGAGTCTGG GGGAGACCTT GTGAAACCTG AGGGGTCCCT GAGACTCTCC TGTGTGGTCT CTGGCTTCAC
 CTTACAGTAGC TACGACATGA GCTGGGTCCG CCAGGCTCCA GGGGAAGGGGC TGCAGTGGGT CGCATAACATT
 AGCAGTGATG GAAGGAGCAC AAGTTACACA GACGCTGTGA AGGGCCGATT CACCATCTCC AGAGACAATG
 CCAAGAATAC GCTGTATCTG CAGATGAACA GCCTGAGAAC TGAGGACACA GCCGTGTATT ACTGTGCGAG
 GTATCACGAC GGTAAGCTACG TACGTGTCTG GTTCTACTAC TGGGGCCAAG GGACCCTGGT CACTGTG

(SEQ ID NO: 855)

H55 SEQ

ATGGAGCTTG GGCTGAGCTG GCTTTCTCTT GTCGCTATTT TACAAGGTGT CCAGGGTGAG GTGCAGCTGG
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG CAGGGTCCCT GAGACTGTCC TGTGTGGCCT CTGGATTAC
 CTTACAGTAGC TACAGCATGA GCTGGGTCCG CCAGGCTCCT GGGGAAGGGGC TGCAGTTGGT CGCAGGTATT
 AACAGCGGTG GAAGTAGCAC ATACTACACA GACGCAGTGA AGGGCCGATT CACCATCTCC AGAGACAACG
 CCAAGAACAC AGTGTATCTG CAGATGAACA GCCTGAGAGC CGAGGACACG GCCATGTATT ACTGTGCAAA
 GGCCGAGCTG ACGTACTACT GTACTGATGA TTACTGTTCC CGAACCTCAA ATTTTACTA CTGGGGCCAG
 GGAACCCTGG TCACCGTC (SEQ ID NO: 856)

H56 SEQ

ATGAACTTGG GGTAAAGCTT GGTTTTCCTT GTCGCTATTT TACAAGGTGT CCAGGGTGAG GTGCAACTGG
 TGCAGTCTGG GGGAGACCTA GTAAAGCCTT CGGGGTCCCT GAGACTGTCC TGTGTGGCCT CTGGATTAC
 CTTACAGTAGC TTCCACATGA GTTGGGTCCG CCAGACCCCT GAGAGGGGAC TGGAGTTGGT CGCAGGTATT
 AATGGCGGTG GAACCACCAG ATTCTACTCA GACGCTGTGA GGGGCCGTTT CATCATTTCC AGAGACCTCG
 CCAAGAGTAC AGTCTATCTG CAGATGGACA ACCTGCGAGC CGACGACACG GCCACTTACT ACTGTGCAAG
 GGCCCGGGAG AGATACTGTA AAGATGATTA TTGTTTCAGG TGGGGTTTTG ATTCCTGGGG CCGGGGAGCC
 CTGGTCACCGTC (SEQ ID NO: 857)

H58 SEQ

ATGAACTTGT GGCTAAACTG GATTTTCCTT GTCGCTATTT TAAAAGGTGT CCAGGGTGAG GTACAACTGG
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG GGGGGTCCCT AAGACTCTCC TGTGTGGCCT CTGGATTAC
 CTTACAGTAGT TCCGGCATGA GCTGGGTCCG TCAGTCTCCA GGGGAAGGGGC TGCAGTGGGT CGCATGGATT
 AAGTCTGATG GAAGTAGTAC ATATTATGTA GACGCTGTGA AGGGCCGATT CACCATCGCC AGAGACAACG
 CCAAGAACAC CCTGTATCTG CAGATGAACA GCCTGAGAGC CGACGACACG GCCGTGTATT ATTGTGCGAA
 GCTTTGGGAC AGTTGGGGCG CGTACAATTT TGACTACTGG GGCCAGGGAA CCCTGGTCAC CGTC

(SEQ ID NO: 858)

H67 SEQ

ATGGAGTTTG GGCTGACCTG GCTTTCTCTT GTCGCTATTT TACAAGGTGT CCAGGGTGAG GTGCAGCTGG
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG CAGGGTCCCT GAGACTGTCC TGTGTGGCCT CTGGATTAC
 CTTACAGTAGC TACAGCATGA GCTGGGTCCG CCAGGCTCCT GGGGAAGGGGC TGCAGTTGGT CGCAGGTATT
 AACAGCGGTG GAAGTAGCAC ATACTACACA GACGCAGTGA AGGGCCGATT CACCATCTCC AGAGACAACG
 CCAAGAACAC AGTGTATCTG CAGATGAACA GCCTGAGAGC CGAGGACACG GCCATGTATT ACTGTGCCCC
 TACTACGGTA GCTACTATGG AGTCCTGGGG CCAGGGAACC CTGGTCACCG TC (SEQ ID NO: 859)

H378 SEQ

ATGGAGTCTG TGCTCTGCTG GGTTTTCCTT GTCGCTATTT TAAAAGGTGT CCAGGGTGAG GTGCAGCTGG
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG GGGGGTCCCT GAGACTCTCC TGTGTGACTT CTGGATTAC
 CTTACAGTGGC TGTGCCATGA TCTGGGTCCG CCAGGCTCCA GGGGAAGGGGC TGCAGTGGGT CGCATAACATT
 AACAGTGATG GAAGTACCAC ATACTACGCA GACGCTGTGA AGGGACGATT CACCATCTCC AGAGACAACG
 CCAAGAACAC GCTCTATCTG CAGATGAACA GCCTGAGAGC TGANGACACG GCCGTGTATT ACTGTGCGAG
 GGGTGATTCT AGTANTTGGG GCTGGGGCCA AGGAACCCTGGTCATCGTC (SEQ ID NO: 860)

H396 SEQ

ATGGAATCTG TGCTCGGATG GATTTTCCTT GCCACTATTT TAAAAGGTGT CCAGGGTGAG GTGCAGTTGG
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG GGGGGTCCCT AAGACTCTCC TGTGTGGGCT CTGGATTAC
 CTTACAGTGGT TACTGGATGA GTTGGGTCCG CCAACCTCCA GGGGAAGGGGC TACAGTGGAT TGTGGAGATC
 AGCGGTAGTG GAACCACCAC AACTATGAA GACACTGTGA GGGGCCGATT TACCATTTCC AGAGACAATG
 CCAAGAACAC GCTGTCTCTG GAGATGAATA GTCTGAGAGA CGAGGACACG GCCATGTATT ATTGTGCAAG
 GGATCGGGGG CAATGTACTG TTGATTACTG CGCCGATCAT ATTGACTACT GGGGCCAGGG
 AACCTGGTCATNGTC (SEQ ID NO: 861)

H404 SEQ

ATGGAGTCTG TGCTCTGCTG GGTTTTTCCTT GTCGCTATTT TAAAAGGTGT CCAGGGTGAG GTGCAGCTGG
 TGGAGTCTGG GGGANACCTG GTGAAGTTTG GGGGGTCCCT GANACTGTCC TGTGTGGCCT CTGGATTCAC
 CTTCAGTAGC TACAGCATGA GTTGGGTCCG CCAGGCTCCT GAAAAGGGGC TGCAGTTGGT CGCAGGTATT
 AACAGCGGTG GAAGTAGCAC ATACTACACA GACGCTGTGA AGGGCCGATT CACCATCTCC AGAGACAACG
 CCAAGAACAC GCTATATCTA CAGTTGAACA GCCTGAGAGT CGAAGACACG GCCGTGTATT ACTGTGCNAG
 GCANACCTAT GGTACCTCCT CTGAGGGGAA TTACTIONAGT CTNTGGGGCC AGGGCACCCCT
 GGTCACCCTGGTCACCGTN (SEQ ID NO: 862)

H442 SEQ

ATGGAATCTG TGCTCGGATG GATTTTCCTT GCCACTATTT TAAAAGGTGT CCAGGGTGAG GTGCAGTTGG
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG GGGGGTCCCT GAGACTCTCC TGTGTGGCCT CTGGATTCAC
 CTTCAGTTAC TACTTAATGA GCTGGGTCCG CCGGGCTCCA GGAAGGGGT TACAGTGGAT TGCAGAAATT
 TCCGATAGTG GAGATTATCT GGACTATACA GACGCTGTGA AGGGCCGATT CACCATCTCC AGAGACAATG
 CCAAGAGCAC GCTGTATCTG GAGATGAACA GGCTGAGGCC CGACNACACG GCCATGTATT ACTGTGTTAC
 CGGCGGGGAC CTCTTTGGTC ACTGGGGCCA AGGCACCCTGGTCACTGTC (SEQ ID NO: 863)

H445 SEQ

ATGGAGTCTG CGCTCAGCTG GGTGTTTCCTT GTCACTATTT TAAAAGGTGT CCAGGGTGAG GTGCATCTGG
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG GAGGGTCCCT GAGACTTTCC TGTGTGGCCT CTGGATTCAA
 CTTCCGGCAGC TACCACATGG GCTGGGTCCG CGAGGCTCCA GGAAGGGGC TTCAGTGGGT CGCATAATT
 CACAATGATG GAGGTACCAG GACCTATTCA GACACTGTGA AGGGCCGATT CACCATCTCC AGAGACAACG
 CCGAGAACAC GCTGTATCTT CAGATGAACA GCCTGAGGCC CGAGGACACG GCCGTGTATT ATTGTGCGAG
 CCTATCCGGG TATTATTGTA CTGATGATTC CTGTTTCAAC GTTGTACATG ATTACTTAAA CCTCTGGGGC
 CAAGGCACCC TGGCAACCGTT (SEQ ID NO: 864)

H574 SEQ

ATGGAGTCTG TGTTCCTGCTG GGTTTTTCCTT GTCGCTATTT TAAAAGGTGT CCAGGGCGAG GTGCAGCTGG
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG GGGGGTCCCT GAGACTGTCC TGTGTGGCCT CTGGATTCAC
 CTTCAGTGAC TACTACATGT ACTGGGTCCG CCAGGCTCCA GGAAGGGGC TTCAGTACGT CGCACGGATT
 AGGGGTGATG GAACTAACAT ATACTACGCA GACGCTGTGA AGGGCCGATT CACCATCTCC AGAGACAATG
 CCAAGAACAC GCTGTATCTG CANATGAACA GCCTGAGAGC CGAGGACACG GCTGTGTATT ATTGTGGAAA
 GGATTTCCGG GACTGGGTTC TATCCTGGGG CCAGGGAACC CTGGTCACCGTT (SEQ ID NO: 865)

H585 SEQ

ATGGAATCTG TGCTCGGATG GATTTTCCTT GCCACTATTT TAAAAGGTGT CCAGGGTGAG GTGCAGTTGG
 TGGAAATCTGG GGGAGACCTG GTGAAGCCTG GGGGGTCCCT GAGACTCTCC TGTGTGGGCT CTGGATTCAC
 CTTCAATAGT TACTGGATGA GCTGGGTCCG CCAGGCTCCA GGGGAGGGGC TACAATGGAT TGGACAGATA
 AGTGTGTTGGTG GTGAAATAGA GTATGCAGAC GCTGTGAAGG GCCGATTCAC CATCTCCAGA GACAATGCCA
 AGAACACGCT GTTTCCTGCAG ATGCACAGTC TGAGAGCCGA GGACACGGCC ATATATTACT GTGCAAGAGA
 CGGGGGTATT ACCTCATACA TGAAAACGAA TCTTGACTAC TGGGGCCAGG GAAACCTGGTCACCGTC
 (SEQ ID NO: 866)

H592 SEQ

ATGGAGTCTG TGCTCTGCTG GGTTTTTCCTT GTCGCTATTT TAAAAGGTGT CCAGGGTGAG GTGCAACTGG
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG GGGGGTCCCT GAGACTCTCC TGTGTGGGCT CTGGATTCAC
 CTTCAGTGCC TATGACATGC TATGGGTCCG TCAGGCTCCA GGAAGGGGC TGCAGTGGGT CGCATAATT
 AACAGCGGTG GAGGGATCAT ATTCTACGCA GACGCTGTGA AGGGCCGATT CACCATCTCC AGAGACAACG
 CCAAGAACAC ACTCTCTCTG CATATGAACA GCCTGAGAGT CGAGGACACG GCCGTGTATT TCTGTACAAG
 ATGGGATACT AACGGACACT GGGGCCAGGG CACCCTGGTC (SEQ ID NO: 867)

H602 SEQ

ATGGAGTCTG TGCTCTGCTG GGTTTTTCCTT GTCGCCATTC TAAATGGTGT CCAGGGTGAG GTGCAGCTGG
 TAGAGTCTGG GGGAGACCTG GTGAAGCCTG GGGGGTCCCT AAGACTGTCC TGTGTGGCCT CTGGATTCAC
 CTTCAGGACC TATGGCATGA GCTGGGTCCG TCAGTGTCCA GGAAGGGAC TGCAGTGGGT CACAAGTATC
 AGCAGCAGCG GAGGCACGTT CTACGCAGAC GCTGTGAAGG GCCGATTCAC CATCTCCAGA GACAACGCCA
 AGAACACGCT GTATCTGCAG TTGAACAGCC TGAGAGCCGA GGACACGGCC GTGTATTATT GTGCGAAGGA
 TCCGGCTACG CTACCTACGG GGAATTTGA CTACTGGGGC CAGGGCACCC CGGTCACCGTC
 (SEQ ID NO: 868)

Table N_{H74}

H392 SEQ						
ATGGACTGCA	GCTGGAGAAT	CTTCTTCCTG	CTGGCACTGG	CCACAGGTGT	GCACTCTGAG	GTCCAGCTGG
TGCAGTCTGC	AGCTGAGGTT	AAAAAGCCAG	GGGCATCTGT	GAAGGTCTCC	TGCAAGACAT	CTGGATACAC
CTTCACTGAC	TACTATATGC	ACTGGGTACA	ACAGGCTCCA	GGAGCAGGGC	TTGATTGGAT	GGGATGGATT
GATCCTGAAG	ATGGTACCAC	AAGTTATGCA	CAGAAGTTCC	AGGGCAGAGT	CACCCTGACG	GCAGACACAT
CCACAAGCAC	AGCCTACATG	GAGCTGAGCA	GTCTGAGAGC	TGAGGACACA	GCTGTGTACT	ACTGTGCAAG
CGGAGGGAGT	CGGCCCTTCA	ATGCTTTTGG	TTACTGGGGC	CAGGGCACCCCTGGTCACTGTT		
(SEQ ID NO: 869)						
H74 SEQ						
ATGGACTGG	ACCTGGAGGG	TCTTCTTCCT	GCTGGCACTG	GCCACAGGTG	TGCACTCTGA	GGTCCAGCTG
GTGCAGTCTG	CAGCTGAGGT	TAAGAAGCCA	GGGGCATCTG	TGAAGGTCTC	CTGCAAGACA	TCTGGATACA
CCTTCACTGA	CTACTATATG	CACTGGGTAC	AACAGGCTCC	AGGAGCAGGG	CTTGATTGGA	TGGGATGGAT
TGATCCTGAA	GATGGTACCA	CAAGTTATGC	ACAGAAGTTC	CAGGGCAGAG	TCACCCTGAC	GGCAGACACA
TCCACAAGCA	CAGCCTACAT	GGAGCTGAGC	AGTCTGAGAG	CTGAGGACGC	AGCTGTGTAC	TACTGTGCAA
GCTTATATAT	ATATGGATAC	GCTGCTTACT	TAGACCTCTG	GGGCCAGGGC	ACCCTGGTCA	CCGTC
(SEQ ID NO: 870)						
H76 SEQ						
ATGGACTGGA	CCTGGAGGAT	CCTCTTCCTG	CTGGCACTGG	CCACAGGTGT	GCACTCTGAG	GTCCAGCTGG
TACAGTCTGC	AGCTGAGGTT	AAGAAGCCAG	GGGCATCTGT	GAAGGTCTCC	TGCAAGACAT	CTGGATACAC
CTTCACTGAC	TACTATATGC	ACTGGGTACA	ACAGGCTCCA	GGAGCAGGGC	TTGATTGGAT	GGGATGGATT
GATCCTGAAG	ATGATACCAC	AGGTTATGCA	CAGAAGTTCC	AGGGCAGAGT	CACCCTGACG	GCAGACACAT
CCACAAGCAC	AGCCTACATG	GAGCTGAGCA	GTCTGAGAGC	TGAGGACACA	GCTGTGTACT	ACTGTGCAAG
AAAGTGGAGG	TACTACGGTA	GCCAAGATTA	CTGGGGCCAG	GGAACCCTGG	TCACCGTC	
(SEQ ID NO: 871)						
H645 SEQ						
ATGGACTGCA	GCTGGAGAAT	CTTCTTCCTG	CTGGCACTGG	CCACAGGTGT	GCACTCTGAG	GTCCAGCTGG
TGCAGTCTGC	AGCTGAGGTT	AAGAAGCCAG	GGGCATCTGT	GAAGGTCTCC	TGCAAGACAT	CTGGATACAT
CTTCATTGAC	CAGTATATGC	ACTGGGTACA	GCAGGCTCCA	GGAGCAGGGC	TTGAATGGAT	GGGATGGATT
GATCCTGAGG	ATGGTACCAC	AAGTTATGCA	CAGAAGTTCC	AGGGCAGAGT	CACCCTGACG	GCAGACACAT
CCACAAACAC	AGTCTATATG	GAGCTGAGCA	ATCTGAGAAC	TGAGGACACA	GCTGTGTACT	ACTGTGCAAG
GGATATATGG	GATTTTGA	ACTGGGGCCA	GGGAACCCTG	GTCACCGTC	(SEQ ID NO: 872)	

Table N_{Other H}

Other Canine Heavy Variable Domain Sequences

H6 SEQ						
ATGAAGTTGG	GGTTAAGCTG	GATTTTTCTT	GTCGCTATTT	TACAAGGTGT	CCAGGGTGAG	GTGCAGCTGG
TGGAGTCTGG	GGGAAACCTG	GTGAAGCCGG	GGGGGTCCCT	GAGACTCTCC	TGTGTAGCCT	CTGGATTCAC
CTTCAGTAAT	TACGACATGA	GTTGGGTCCG	CCAGGCTCCT	GGGAAGGGGC	TGCAGTGGGT	CGCGACTATT
AGTTATGATG	GAAGTAGTAC	ATTTTCATACT	GACGCTGTGA	AGGGCCGATT	CACCATCTCC	AGAGACAACG
CCAGGAACAC	AGTGTATCTA	CAGCTGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTTTATT	ATTGTGGGAA
GCAGTGGAGA	AACACCTGGT	ATTCTTTTCC	CGATCCCGGT	TTTGACTATT	GGGGTCAGGG	AACCCTGGTC
ACCGTC (SEQ ID NO: 873)						
MKLGLSWIFL	VAILQGVQGE	VQLVESGGNL	VKPGGSLRLS	CVASGFTFSN	YDMSWVRQAP	GKGLQWVATI
SYDGSSTFHT	DAVKGRFTIS	RDNARNTVYL	QLNSLRAEDT	AVYYCGKQWR	NTWYSFPDPG	FDYWGQGTLV TV
(SEQ ID NO: 874)						

H27 SEQ

ATGGAGTTTCG GGTTCAACTT GATTTTCCTT GKGA CTATTT TAAAAGGTGC CCAGGGTGAG GTGCAGCTKG
 TGAATCTGG GGGAGACCTG ATGAAGCCTG GGGGGTCCCT GAGACTCTCC TGTGTGGCCT CTGGATTAC
 TTTCAGTAGC CACTACATGA ACTGGGTCCG CCAGGCTCCA GGAAGGGGC TGCAGTGGGT CGGATACATT
 AACAGTGATG GACATAGCAC GAGCTACGCA GACGCTGTGA AGGGCCGATT CACCATCTCC AGAGACAATG
 CCAAGAACAC GCTGTATCTG CAGATGAACA GCCTGAGAAC CGAGGACACC GGCCGTGTAT TACTGTGTGA
 AGGGATGGCA GGTAGTACTT ATAGGTGGGG TGGTATGGAC TACTGGGGCC ATGGC (SEQ ID NO: 875)

MEFGFNLI FL XTILKGAQGE VQXVESGGDL MKPGGSLRLS CVASGFTFSS HYMNWVRQAP GKGLQWVG I
 NSDGHSTSYA DAVKGRFTIS RDNAKNTLYL QMNSLRTE DT GRVLLCEGMA GSTYRWGGMD YWGHG
 (SEQ ID NO: 876)

H52 SEQ

ATGGAGTTCT GGTTCAACTG GATTTTCCTT GTCGSTACTT TAAAAGGTGT CCAGGGTGAG GTGCAACTGG
 TGRAGTCTKG GGGAGACATG GTGAAGCCTG GGGGGTCCCT GAGACTYTYC TSTGTGGSC TGGATTAC
 CTTCAGTAGT CACTACATGT ATTGGGTCCG CCAGGCTCCA GGAAGGGGC TTCAGTGGGT CTCACACATT
 AACGCAGATG GAGGTACCAC AAGGTATGCG GACGCTGTGA AGGGCCGATT CACCATCTCC AGAGACAACG
 CAAAGAATAC GCTGTATCTC CAGATGAACA GCCTGAGAGC CGAGGACACA GCGGTATATT ACTGTACAAA
 GGA CTCCAT ACTACGGCTA GTTTT GACTA CTGGGGCCAG GGAACCCTGG TCACC (SEQ ID NO: 877)

MEFWFNWIFL VXTLKG VQGE VQLVXSXGDM VKPGGSLRXX XVXSGFTFSS HYMYWVRQAP GKGLQWVSHI
 NADGGTTRYA DAVKGRFTIS RDNAKNTLYL QMNSLRAEDT AVYYCTKDSH TTASF DYWGQ GTLVT
 (SEQ ID NO: 878)

H60 SEQ

ATGAAGTTCT GGCTCAGCTG GGT TTTTCTT GTCGCTACTT TACAAGGTGT CCAGGGTGAG GTGCAGCTGG
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG GGGGGTCCCT GAGACTCTCC TGTGTTGCCT CCGGATTCAT
 CTTCAGTAAC TACGACATGA ACTGGGTCCG CCTGGCTCCT GGAAGGGGC TGCAGTGGGT CGCAAGTATT
 AGCTATGATG GAAGTCGCAC ATACTACACT GACGCTGTGA AGGGCCGATT CACCATCTCC AGAGACAACG
 CCACGAACAC AGTGTATCTG CAGATGAATG GCCTGAGAAC CGAGGACACG GCTGTGTATT CCTGTGCGGC
 AGATATTTGG ATCCGGGGGG TGGACTACTG GGGCCAGGGA ACCCTGGTCA CC (SEQ ID NO: 879)

MKFWLSWVFL VATLQGVQGE VQLVESGGDL VKPGGSLRLS CVASGFIFSN YDMNWVRLAP GKGLQWVASI
 SYDGSRTYYT DAVKGRFTIS RDNATNTVYL QMNGLRTE DT AVYSCADIW IRGV DYWGQ TLVT
 (SEQ ID NO: 880)

H100 SEQ

ATGCAGATGC CGTGGTCCCT CCTCTGCCTG CTGGCAGCTC CCCTGGGTGT CCTGTCTGAA CTCACACTCC
 AGGAGGCAGG GCCAGGACTG GTGAAGCCCT CAGAGACCCT CTCTCTCACC TGTCTTGTGT CCGGAGGCTC
 CGTCAACAGC GGT TATTACT GGAGTTGGAT CCGTCGACGC CCTGGGGGAG AATTGGAATG GATGGGATAC
 TGGTCAGGTA CGACCCACTA CAACCCGACA TTCCAGGGAC GCATTTCCAT TACTACTGAT ACGGCCACGA
 ACCAATTCTT CCTCCAGCTG ACTTCCGTGA CCACCGAAGA CACGGCCGTT TATTTCTGTA TACGACTCTA
 TAGGTCTAAC TACTTTCTTG ACTTTTGGGG TCAGGGAACC CTGGTCACCG TC (SEQ ID NO: 881)

MQMPWSLLCL LAAPLGVLSE LTLQEAGPGL VKPSETLSLT CLVSGGSVNS GYYWSWIRRR PGGELEWMGY
 WSGTTHYNPT FQGRISITTD TATNQFFLQL TSVTTEDTAV YFCIRLYRSN YFLDFWGQGT LVTV
 (SEQ ID NO: 882)

H101 SEQ

ATGCAGATGC CGTGGTCCCT CCTCTGCCTG CTGGCAGCTC CCCTGGGTGT CCTGTCTGAA CTCACACTCC
 AGGAGGCAGG GCCAGGACTG GTGAAGCCCT CARAGACCCT CTCTCTCACC TGTCTTGTGT CCGGAGGCTC
 CGTCAACAGC GGT TATTACT GGAGTTGGAT CCGTCGACGC CCTGGGGGAG AATTGGAATG GATGGGATAC
 TGGTCAGGTA CGACCCACTA CAACCCGACA TTCCAGGGAC GCATTTCCAT TACTACTGAT ACGGCCACGA
 ACCAATTCTT CCTCCAGCTG ACTTCCGTGA CCACCGAAGA CACGGCCGTT TATTTCTGTA TACGACTCTA
 TAGGTCTAAC TACTTTCTTG ACTTTTGGGG TCAGGGAACC CTGGTCACCG TC (SEQ ID NO: 883)

MQMPWSLLCL LAAPLGVLSE LTLQEAGPGL VKPSXTLSLT CLVSGGSVNS GYYWSWIRRR PGGELEWMGY
 WSGTTHYNPT FQGRISITTD TATNQFFLQL TSVTTEDTAV YFCIRLYRSN YFLDFWGQGT LVTV
 (SEQ ID NO: 884)

H102 SEQ

ATGGAGTTGT GGTTCAACTG GATTTTCCTT GTCGCTATTT TAAAAGGTGT CCAGGGTGAG GTGCAGTTGG
 TGGAGTCTGG GGGAGACCTG GTGAAGCCTG GGGGGTCCTT AAGACTCTCC TGTGTGGCCT CTGGATTAC
 CTTCACTGAT TATGGCATGA ACTGGGTCCG TCACTCTCCA GGAAGGGGC TGCAGTGGGT CGCATGGATT
 TGGTATGGCG GGAGTAGCAC ATACTACGCA GACGCTGTGA AGGGCCGATT CACCATCTCC AGAGACGACG
 CCAACAACAC ACTATATCTA CAGATGAACA GCCTGAGAGC CGAGGACACG GCCGTCTATT ACTGTGCGAA
 GGAGTATAGT AGTAGCTTTG ACTACTGGGG CCAGGGAACC CTGGTCACCG TCT (SEQ ID NO: 885)

MELWFNWIFL VAILKGVQGE VQLVESGGDL VKPGGSLRLS CVASGFTFSD YGMNWVRHSP GKGLQVVAWI
 WYGGSSYYA DAVKGRFTIS RDDANNTLYL QMNSLRAEDT AVYYCAKEYS SSFDYWGQGT LVT
 (SEQ ID NO: 886)

H103 SEQ

ATGCAGATGC CGTGGTCCCT CCTCTGCCTG CTGGCAGCTC CCCTGGGTGT CCTGTCTGAA CTCACACTCC
 AGGAGGCAGG GCCAGGACTG GTGAAGCCCT CAGAGACCCT CTCTCTCACC TGTCTTGTGT CCGGAGGCTC
 CGTCAACAGC GGTATTACT GGAGTTGGAT CCGTCGACGC CCTGGGGGAG AATTGGAATG GATGGGATAC
 TGGTCAGGTA CGACCCACTA CAACCCGACA TTCCAGGGAC GCATTTCCAT TACTACTGAT ACGGCCACGA
 ACCAATTCTT CCTCCAGCTG ACTTCCGTGA CCACCGAAGA CACGGCCGTT TATTTCTGTA TACGACTCTA
 TAGGTCTAAC TACCTTCTTG ACTTTTGGGG TCAGGGAACC CTGGTCACCG TC (SEQ ID NO: 887)

MQMPWSLLCL LAAPLGVLSE LTLQEAGPGL VKPSETLSLT CLVSGGSVNS GYYWSWIRRR PGGELEWMGY
 WSGTTHYNPT FQGRISITD TATNQFFLQL TSVTTEDTAV YFCIRLYRSN YLLDFWGQGT LVT
 (SEQ ID NO: 888)

H109 SEQ

ATGCAGATGC CGTGGTCCCT CCTCTGCCTG CTGGCAGCTC CCCTGGGTGT CCTGTCTGAA CTCACACTCC
 AGGAGGCAGG GCCAGGACTG GTGAAGCCCT CAGAGACCCT CTCTCTCACC TGTCTTGTGT CCGGAGGCTC
 CGTCAACAGC GGTATTACT GGAGTTGGAT CCGTCGACGC CCTGGGGGAG AATTGGAATG GATGGGATAC
 TGGTCAGGTA CGACCCACTA CAACCCGACA TTCCAGGGAC GCATTTCCAT TACTACTGAT ACGGCCACGA
 ACCAATTCTT CCTCCAGCTG ACTTCCGTGA CCACCGAAGA CACGGCCGTT TATTTCTGTA TACGACTCTA
 TAGGCCTAAC TACTTTCTTG ACTTTTGGGG TCAGGGAACC CTGGTCACCG TC (SEQ ID NO: 889)

MQMPWSLLCL LAAPLGVLSE LTLQEAGPGL VKPSETLSLT CLVSGGSVNS GYYWSWIRRR PGGELEWMGY
 WSGTTHYNPT FQGRISITD TATNQFFLQL TSVTTEDTAV YFCIRLYRPN YFLDFWGQGT LVT
 (SEQ ID NO: 890)

H637 SEQ

ATGCAGATGC CGTGGTCCCT CCTCTGCCTG CTGGCAGCTC CCCTGGGTGT CCTGTCTGAA GTCATACTGC
 AGGAGTCCGG GCCAGGACTG GTGAAGCCCT CACAGACCCT CTCTCTCACC TGTACGGNGT CCGGAGGCTC
 CGTCACCGAC ATTCATACT GGAGCTGGAT CCGCCAGCGC CCTGACAGGG GACTGGAATG GATGGGATAC
 TGGAGAGGTG GCACAAATCA CAACCCGGCA TTCCAGGAAC GCATCTCCAT CACTGCTGAC GGGACCAAAA
 ACCACCTCTC CCTGCAATTG ACCTCCACGA CCACCGAGGA CACGGCCGTC TATTACTGTA CAAGAACTC
 AGACGTCTGG GGCCAGGGCA CCCTGGTCAC CGTC (SEQ ID NO: 891)

MQMPWSLLCL LAAPLGVLSE VILQESGPGL VKPSQTLSTL CTXSGGSVTD IHYWSWIRQR PDRGLEWMGY
 WRGGTNHNPA FQERISITAD GTKNHLQL TSTTTEDTAV YYCTRNDSVW GQGT LVT
 (SEQ ID NO: 892)

H674 SEQ

ATGGAAGTCA GCTGGAGAAT CTTCTTCCTG CTGGCACTGG CCACAGGTGT GCACTCTGAG GTCCAGCTGG
 TGCAGTCTGC AGCTGAGGTT AAGAAGCCAG GGGCATCTGT GAAGGTCTCC TGCAAGACAT CTGGATACAT
 CTTCAATTGAC CAGTATATGC ACTGGGTACA GCAGGCTCCA GGAGCAGGGC TTGAATGGAT GGGATGGATT
 GATCCTGAGG ATGGTACCAC AAGTTATGCA CAGAAGTTCC AGGGCAGAGT CACCCTGACG GCAGACACAT
 CCACAAACAC AGTCTATATG GAGCTGAGCA ATCTGAGAAC TGAGGACACA GCTGTGTACT ACTGTGCAAG
 GGATATATGG GATTTTGACT ACTGGGGCCA GGAACCCTG GTCACCGTC (SEQ ID NO: 893)

MDCSWRIFFL LALATGVHSE VQLVQSAAEV KKPASVKVS CKTSGYIFID QYMHVQQAP GAGLEWMGWI
 DPEDGTTSYA QKFQGRVTLT ADTSTNTVYM ELSNLRTEDT AVYYCARDIW DFDYWGQGT LVT
 (SEQ ID NO: 894)

Table N₆₂
Group 2 Nucleic Acid Sequences

λ101:						
<u>TGGTCCCCTC</u>	<u>TCCTCCTCAC</u>	<u>CATCCTCGCT</u>	<u>CACTGCACAG</u>	<u>GGTCCTGGGC</u>	<u>CCAGTCTCTA</u>	<u>CTGACTCAGC</u>
<u>CGGCCTCAGT</u>	<u>GTCCGGGTCC</u>	<u>CTGGGCCAGA</u>	<u>GGGTCACCCT</u>	<u>CTCCTGCACT</u>	<u>GGAAGCGGCT</u>	<u>CCAACATCGG</u>
<u>TAGAGGTTAT</u>	<u>GTGGGCTGGT</u>	<u>ACCAACACCT</u>	<u>CCCGGGGACA</u>	<u>GGCCCCAGAA</u>	<u>CCCTCATCTA</u>	<u>TGGTGATATT</u>
<u>AACCGACCCT</u>	<u>CAGGGGTCCC</u>	<u>CGATCGGTTC</u>	<u>TCTGGCTCCA</u>	<u>GGTCAGGCAT</u>	<u>CACAGCCACC</u>	<u>CTGACCATCT</u>
<u>CTGGGCTCCA</u>	<u>GGCTGAGGAT</u>	<u>GAGGCTGATT</u>	<u>ATTACTGTTC</u>	<u>ATCGTGGGAC</u>	<u>TACAGTCTCA</u>	<u>GTAGTACTTT</u>
<u>GTTCGGCGGA</u>	<u>GGCACCACCC</u>	<u>TGACCGTCCT</u>	<u>CGGTCAGCCC</u>	AAGGCC (SEQ ID NO: 895)		
λ109:						
<u>ATGACCTCCA</u>	<u>CCATGGGCTG</u>	<u>GTCCCCTCTC</u>	<u>CTCCTCACCA</u>	<u>TCCTCGCTCA</u>	<u>CTGCACAGGG</u>	<u>TCCTGGGCCC</u>
<u>AATCTGTTCT</u>	<u>GACTCAGCCG</u>	<u>GCCTCAGTGT</u>	<u>CCGGGTCCCT</u>	<u>GGGCCAGACG</u>	<u>GTCACCATCT</u>	<u>CCTGCACTGG</u>
<u>AAGCGAATCC</u>	<u>AACATCGGTA</u>	<u>GAGGTTTTGT</u>	<u>TGGCTGGTAC</u>	<u>CAACAGATCC</u>	<u>CGGGAACAGG</u>	<u>CCCCAGAACC</u>
<u>GTCATTTACG</u>	<u>GTCATAATCA</u>	<u>CCGACCCTCA</u>	<u>GGGGTCCCCG</u>	<u>AACGGTTCTC</u>	<u>TGGCCCCAGG</u>	<u>TCCGGCATCA</u>
<u>CCTCTACCCT</u>	<u>GACCATCTCT</u>	<u>GGACTCCGGG</u>	<u>CTGAGGATGA</u>	<u>GGGTGATTAT</u>	<u>TATTGTTTAT</u>	<u>CCNNGGACNC</u>
<u>TAGTCTCAGT</u>	<u>GTCGTTCTGT</u>	<u>TCGGCGGAGG</u>	<u>CACCCACCTG</u>	<u>ACCGTCCTCG</u>	<u>GTCAGCCCAA</u>	<u>GGCC</u>
(SEQ ID NO: 896)						
λ111:						
<u>AGTCTGTG</u>	<u>CTTGACTCAG</u>	<u>CCGGCCTCAG</u>	<u>TGTCCGGGTC</u>	<u>CCTGGGCCAG</u>	<u>AGGGTCACCA</u>	<u>TCTCCTGCAC</u>
<u>TGGAAGCAGC</u>	<u>TCCAACGTCG</u>	<u>GTAGAGGTTA</u>	<u>TGTGGGCTGG</u>	<u>TACCAACAGT</u>	<u>TCCCAGGAGC</u>	<u>GGGCCCCAGA</u>
<u>ACCCTCATCT</u>	<u>ATGGTAATAA</u>	<u>TAATCGGCCC</u>	<u>TCAGGGGTCC</u>	<u>CCGATCGGTT</u>	<u>CTCTGGCTCC</u>	<u>ACGTCAGGCA</u>
<u>GCACAGCCAC</u>	<u>TCTGACCATC</u>	<u>TCTGGCCTCC</u>	<u>GGGCTGAGGA</u>	<u>TGAGGCTGAT</u>	<u>TATTACTGCT</u>	<u>CATCGTGGGA</u>
<u>CGCCAGTCGC</u>	<u>AGTGTTACTG</u>	<u>TCTTCGGCGG</u>	<u>AGGCACCCAC</u>	<u>CTGGCCGTCC</u>	<u>TCGGTCAGCC</u>	<u>CAAGGCC</u>
(SEQ ID NO: 897)						
λ120:						
<u>CTTGGCCAGA</u>	<u>GGGTCACCAT</u>	<u>TTCCTGCTCT</u>	<u>GGAAGTACGT</u>	<u>ACAACATCGG</u>	<u>TAGTGTTGGT</u>	<u>GCGACCTGGT</u>
<u>ACCAACAGCT</u>	<u>CCCAGGGAGG</u>	<u>TCCCCTAAAC</u>	<u>TTCTCGTCTA</u>	<u>TAGTGATGGG</u>	<u>CATCGCCCGT</u>	<u>CAGGGGTTCC</u>
<u>TGACCGGTTC</u>	<u>TCCGGCTCCA</u>	<u>AGTCTGACAA</u>	<u>CTCTGCCACC</u>	<u>CTGACCTTCA</u>	<u>CTGGGCTTCA</u>	<u>GGCTGAGGAC</u>
<u>GAGGCTGATT</u>	<u>ATTATTGTCA</u>	<u>GTCTCTTGAT</u>	<u>TCCAACCTCG</u>	<u>GGCCTGTGTT</u>	<u>CGGCGGAGGC</u>	<u>ACCCACCTGA</u>
<u>CCGTCCTCGG</u>	<u>TCAGCCCAAG</u>	GCC (SEQ ID NO: 898)				
λ127:						
<u>ATGA</u>	<u>CCTCCACCAT</u>	<u>GGCCTGGTTC</u>	<u>CCTCTCCTCC</u>	<u>TGACCCTCCT</u>	<u>TGCTCACTAC</u>	<u>ACAGGGTCCT</u>
<u>GGGCCCAGTC</u>	<u>TGTGCTGACT</u>	<u>CAGCCGGCCT</u>	<u>CAGTGTCTGG</u>	<u>GTCCCTGGGC</u>	<u>CAGAGGATCA</u>	<u>CCATCTCCTG</u>
<u>CACTGGAAGC</u>	<u>GGTTCCAACA</u>	<u>TTGGAGGTAA</u>	<u>TAATGTGGGT</u>	<u>TGGTACCAGC</u>	<u>AGCTCCCAGG</u>	<u>AAGAGGCCCC</u>
<u>AGAAGTGTCA</u>	<u>TCTATGATAC</u>	<u>TTATAGTCGA</u>	<u>CTCTCGGGGG</u>	<u>TGCCCGATCG</u>	<u>ATTCTCTGGC</u>	<u>TCCAAGTCTG</u>
<u>GCAGCACAGC</u>	<u>CACCCTGACC</u>	<u>ATCTCTGGGC</u>	<u>TCCAGGCTGA</u>	<u>GGATGAGGCT</u>	<u>GATTATTACT</u>	<u>GCTCAACGTG</u>
<u>GGATGATAGT</u>	<u>CTCCGTGCTT</u>	<u>ACTTGTTTCG</u>	<u>GTCAGGAACC</u>	<u>CAACTGACCG</u>	<u>TTCTTGGTCA</u>	<u>GCCCAAGGCC</u>
(SEQ ID NO: 899)						
λ201:						
<u>ATGACCTC</u>	<u>CACCATGGGC</u>	<u>TGGTCCCCTC</u>	<u>TCCTCCTTAC</u>	<u>CCTCCTCGCT</u>	<u>CACTGCACAG</u>	<u>GTTCTGGGGC</u>
<u>CCAGTCTGCG</u>	<u>CTGACTCAGC</u>	<u>CGGCCTCAGT</u>	<u>GACTGGGTCC</u>	<u>CTGGGCCAGA</u>	<u>GGGTCACCAT</u>	<u>CTCCTGCACT</u>
<u>GGAAGCAGCT</u>	<u>CCAACATCGG</u>	<u>TGGATATAAT</u>	<u>GTTGGCTGGT</u>	<u>TCCAACAGGT</u>	<u>CCCGGGAACA</u>	<u>GGCCCCAGAA</u>
<u>CCGTCATCTA</u>	<u>TAGTCGTAGT</u>	<u>AATCGACCCT</u>	<u>CGGGGGTCCC</u>	<u>GGATCGATTG</u>	<u>TCTGGCTCCA</u>	<u>GGTCAGGCAG</u>
<u>CACAGCCACC</u>	<u>CTGACCATCT</u>	<u>CTGGCCTCCA</u>	<u>GGCAGAAGAC</u>	<u>GAGGCTGAAT</u>	<u>ATTACTGCTC</u>	<u>AACATGGGAC</u>
<u>AGCAGTCTCA</u>	<u>AAGCTCCTGT</u>	<u>GTTCGGCGGA</u>	<u>GGCACCACCC</u>	<u>TGACCGTCCT</u>	<u>CGGTCAGCCC</u>	<u>AAGGCC</u>
(SEQ ID NO: 900)						
λ203:						
<u>ATGACCTC</u>	<u>CACCATGGCC</u>	<u>TGGTCCTCTT</u>	<u>TCCTCCTCAC</u>	<u>CCTCCTCGCT</u>	<u>CACTTCACAG</u>	<u>GTTCTGGGGC</u>
<u>CCAGTCTGTG</u>	<u>CTGACTCAAC</u>	<u>CAGCCTCAGT</u>	<u>GTCCGGGTCT</u>	<u>CTGGGCCAGA</u>	<u>GGGTCACCAT</u>	<u>CTCCTGCACT</u>
<u>GGAAGCAGCT</u>	<u>CCAACATTGG</u>	<u>TAGAGATTAT</u>	<u>GTGGGCTGGT</u>	<u>ACCAACAGCT</u>	<u>CCCGGGAACA</u>	<u>CGCCCCAGAA</u>
<u>CCCTCATCTA</u>	<u>TGGTAATAGT</u>	<u>AACCGACCCT</u>	<u>CGGGGGTCCC</u>	<u>CGATCGATTG</u>	<u>TCTGGCTCCA</u>	<u>AGTCAGGCAG</u>
<u>CACAGCCACC</u>	<u>CTGACCATCT</u>	<u>CTGGGCTCCA</u>	<u>GGCTGAGGAC</u>	<u>GAGGCTGATT</u>	<u>ATTACTGCTC</u>	<u>TACATGGGAC</u>
<u>AACAGTCTCA</u>	<u>CTGTTCTCTG</u>	<u>GTTCGGCGGA</u>	<u>GGCACCACCC</u>	<u>TGACCGTCCT</u>	<u>CGGTCAGCCC</u>	<u>AAGGCC</u>
(SEQ ID NO: 901)						

λ204:

ATGACCTCCA	CCATGGGCTG	GTCCCCTCTC	CTCCTCACCC	TCCTCGCTCA	CTGCACAGGT	TCCTGGGCCC
AGTCTGTACT	GACTCAGCCG	GCCTCAGTGT	CTGGGTCCCT	GGGTCAGAGG	GTCACCATCT	CCTGCACTGG
AAGCAGCTCC	AACCTCGGTA	GATATGGTGT	TGCCTGGTTC	CAGCAGCTCC	CGGGAAAAGG	CCCCAGAACC
GTCATCTATA	GTATTGATAA	CCGACCCTCA	GGGGTCCCTG	ATCGATTCTC	TGGCTCCAAG	TCCCGCAGTA
CAGCCACCCT	GACCATCTNT	GGGCTCCAGG	CTGAGGACGA	GGCTGATTAT	TTNTGCTCAA	CATACGACAC
CAGGCTCGGT	ACTAGTGTGT	TCGT	(SEQ ID NO: 902)			

λ207:

AT	GACCTCCACC	ATGGGCTGGT	CCCCTCTCCT	CCTCACCATC	CTCGCTCACT	GCACAGGGTC
CTGGGCCCCA	TCTCTACTGA	CGCAGCCGGC	CTCAGTGTCC	GGGTCCCTGG	GCCAGAGGGT	CACCATCTCC
TGCACCGGAA	CCACCTCCAA	CATTGGTAGA	GGTTTGTGG	GCTGGTTTCA	AGAACTCCCG	GGAACAGGCC
CCAAAATTCT	CATCTATGGC	AATGGTAACC	GACCCTCAGG	GGTCCCCGAT	CGATTCTCTG	GCTCCACGTC
AGGCAACACA	GCCACCCTGA	CCATCTCTGG	GCTCCAGCCT	GAGGATGAGA	CTGATTATTA	CTGTTCATCG
TGGGACAACA	ATCTCATAAA	AATTTTGTTC	GGCGGAGGCA	CTCATCTGAC	CGTCCTCGGT	CAGCCCAAGG
CC	(SEQ ID NO: 903)					

λ215:

A	TGACCTCCAC	CATGGGCTGG	TTCCCTNTGC	TCCTCACCTC	CCTGGCTCAC	TGCACAGGTT
CCTGGGCCCCA	GTCTGTGCTG	ACTCAGCCGG	CCTCAGTGTG	TGGGTCCCTG	GGCCAGAAGG	TCACCATCTC
CTGCACTGGG	AGCAGCTCCA	ACATAGGTAG	TGGTTATGTG	GGCTGGTACC	AGCAGCTCCC	AGGAACAGGC
CCCAGAACCC	TCATCTATAG	TAGTAGTAAC	CGACCTTCGG	GGGTCCCCGA	TCGATTCTCT	GGCTCCACGT
CAGGCAGCAC	GGCAACCCTG	ACCATCTCTG	GGCTCCAGGC	TGAGGACGAG	GCTGATTATT	ACTGCTCAAC
ATATGACAGC	ACTCTCAATG	CTGTTGTGTT	CGGCGGAGGC	ACCCACCTGA	CCGTCCTCGG	TCAGCCCAAG
GCC	(SEQ ID NO: 904)					

λ220:

ATGACCTCC	ACCATGGGCT	GGTCCCCTCT	CCTCCTTACC	CTCCTCGCTC	ACTGCACAGG	TTCTGGGGCC
CAGTCTGTGC	TGACTCAGCC	GGCCTCAGTG	ACTGGGTCCC	TGGGCCAGAG	GGTCACCATC	TCCTGCACTG
GAAGCAGCTC	CAACATCGGT	GGATATAATG	TTAATTGGTT	CCAACAGTTC	CCGGGAAAAG	GCCCCAAAAC
CGTCATCTAT	AGTAGTACTG	ACCGACCCTC	GGGGGTCCCG	GATCGATTCT	CCGGGTCCAG	GTCAGGCACC
ACAGCCACCC	TGACCATCTC	TGGACTCCAG	GCTGAGGACG	AGGCTGACTA	TTATTGCTCA	GCATGGGACA
ACAGTCTCAA	ACTTCCTCTG	TTCGGCGGAG	GCACACACCT	GACCGTCCTC	GGTCAGCCCA	AGGCC
(SEQ ID NO: 905)						

λ225:

ATGGGCTGGT	CCCCTCTCCT	CCTCACCATC	CTCGCTCACT	GCACAGGGTC	CTGGGCCCAG	TCTGTGCTGA
CTCAGCCGGC	CTCAGTGTCC	GGGTCCCTGG	GCCAGAGGGT	CACCATCTCC	TGCACTGGAA	GCAGCTCCAA
CATCGGTGGA	GGTTATGTGG	GCTGGTACCA	ACAACTCCCG	GGAACAGGCC	CCAAAACCCT	CATCTATGGT
GATAGTAACC	GACCCTCAGG	GGTCCCCGAT	CGGTTCTCTG	GCTCCAGGTC	AGGCAGCACA	GCCACCCTGA
CCATCTCTGG	GCTCCAGCCT	GAGGATGAGG	CTGATTATTA	CTGCTCATCG	TGGGACACCG	GTCTCAGTGC
TCTTGTGTTT	GGCGGAGGCA	CCCACCTGAC	CGTCCTCAGT	CAGCCCAAGG	CC	(SEQ ID NO: 906)

λ227:

ATG	TCCTCCGACA	TGGCCTGGTC	CCCTCTCCTC	TTACACTCC	TCGCTCACTG	CACAGGGTCC
TGGGCCCAGG	CTGTGCTGAA	TCAGCCGGCC	TCAGTGTCTG	GGGCCCTGGG	CCAGAAGGTC	ACCATCTCCT
GCTCTGGAAG	CACAAATGAC	ATTGATATAT	TTGGTGTGAG	CTGGTACCAA	CAGCTCCCAG	GAAAGGCCCC
TAAACTCCTC	GTGGACAGTG	ATGGGGATCG	ACCCTCAGGG	GTCCCTGACA	GATTTTCTGG	CTCCAGCTCT
GGCAACTCAG	GCACCCTGAC	CATCACTGGG	CTCCAGGCTG	AGGACGAGGC	TGATTATTAC	TGTCAGTCTG
TTGATTCCAC	GCTTGGTGCT	ATTGTGTTTC	GCGGAGGCAC	CCATCTGACC	GTCCTCGGTC	AGCCCAAGGC
C	(SEQ ID NO: 907)					

λ228:

ATG	ATCTTCACCA	TGGCCTGGTC	CCCTCTCCTC	CTCGGCCTCC	TTGCTCACTG	CACAGGGTCC
TGGGCCCAGT	CTATACTGAC	TCAGCCAGCC	TCAGTGTCTG	GGTCCCTGGG	CCAGAAGGTC	ACCATCTCCT
GCTCTGGAGA	CAGTTCCAAC	ATCGGTGATA	ATTTTGTGGC	CTGGTACCAA	CAACTCCCAG	GAATAGGCCC
AAAAACCGTC	ATCTATGGTA	CTATTTACCG	ACCTTCAGGG	GTCCCCGATC	GATTTTCTGG	CTCCAAGTCA
GGCAATTTCAG	CCACCCTGAC	CATCTCTGGG	CTCCAGCCTG	AGGACGAGGC	TGAATATTAC	TGCTCATCAT
GGGATGATAG	TCTCANAGGT	ATTGTGTTTC	GCGGAGGCAC	CCTTCTGACC	GTCCTCGGTC	AGCCCAAGGC
C	(SEQ ID NO: 908)					

λ302:

<u>ATGACCTCCA</u>	<u>CCATGGGCTG</u>	<u>GTCCCCTCTC</u>	<u>CTCCTCACCC</u>	<u>TCCTCGCTCA</u>	<u>CTGCACAGGT</u>	<u>TCCTGGGCCC</u>
AGTCTGTGCT	GACTCAGCCG	GCCTCAATGT	CTGGGTCCCT	GGGCCAGAAG	GTCACCATCT	CCTGCACTGG
AAGCAGCTCC	AACATCGGTA	AATATGTTGT	CGGCTGGTTC	CAGCAGTTTC	CGGGAGAAGG	CCCCAGAACC
GTCATCTATA	GTACTAGTTA	TCGACCCTCA	GGGGTCCCTG	ATCGATTCTC	TGGCTCCAAG	TCAGGCAGCA
CAGCCACCCT	GACCATCTCT	GAACCTCCAGG	CTGAGGACGA	GGCTGATTAT	TACTGCTCAA	CATACGACAG
CAGTCTCGGT	GGTAGTGTGT	TCGGCGGAGG	CACCCATCAT	GAC (SEQ ID NO: 909)		

λ306:

<u>ATGA</u>	<u>CCTCCACCAT</u>	<u>GGGATGGTTC</u>	<u>CCTCTGCTCC</u>	<u>TCACCCTCCT</u>	<u>GGCTCACTGC</u>	<u>ACAGGTTCTT</u>
GGGCCCAGTC	TGTGCTGACT	CAGCCGGCCT	CAGTGTCTGG	GTCCCTGGGC	CAGAGGGTCA	CCATCTCCTG
CACTGGAAGC	AGCTCCAACA	TCGGTAGAGG	TTATGTGGGC	TGGTACCGGC	AGCTCCCAGG	AACAGGCCCC
ACAACCCTCA	TCTATGATGA	TAGTAGCCGA	CCCTCGGGGG	TCCCTAATCG	ATTCTCTGGC	TCCAGGTCAG
GCAGCACTGC	AACCCTGACC	ATCTCGGGCC	TCCAGGCTGA	CGACGAGGCT	GATTATTACT	GCTCAGCATA
TGACAGCACT	CTCACTGGTA	CTGTATTCTG	CGGAGGCACC	CACCTGACCG	TCCTCGGTCA	GCCC

(SEQ ID NO: 910)

λ310:

<u>A</u>	<u>TGACCTCCAC</u>	<u>CATGGGATGG</u>	<u>TTCCCTCTGC</u>	<u>TCCTCACCTC</u>	<u>CCTGGCTCAC</u>	<u>TGCACAGGTT</u>
CCTGGGCCCCA	GTCTGTGCTG	ACTCAGCCGG	CCTCAGTGTC	TGGGTCCCTG	GGCCAGAGGG	TCACCATCTC
CTGCACTGGA	AGCAGCTCCA	ACATCGGTAG	AGATTATGTG	GCCTGGTACC	AACAGTTCCC	AGGAACAGGC
CCCAGAATCC	TCATCTATGA	TACTCGTAGC	CGACCCTCGG	GGGTCCCTGA	TCGATTCTCT	GGCTCCAGGT
CAGGCTACAC	AGCTGCCCTG	ACCATCTCTG	GACTCCAGGC	TGAGGACGAG	GCTGACTATT	ACTGCTCAAC
ATATGACAGC	AGTCTCAGTG	GTCCTCTTTT	CGGCGGAGGC	ACCCACCTGA	CCGTCCTCGG	TCAGCCCCGAG

GCC (SEQ ID NO: 911)

λ320:

<u>ATGACCTC</u>	<u>CAACATGGCN</u>	<u>TGGTCCCCTT</u>	<u>TCCTCCTCAC</u>	<u>ACTCCTTGCT</u>	<u>TACTGCACAG</u>	<u>GATCCTGGGC</u>
CCAGTCTGCG	CTGACTCAGC	CGACCTCAGT	GTCGGGGTCC	CTTGGCCAGA	GGGTCTCCAT	TTCCTGCTCT
GGAAGCACGA	GCAACATCGG	TATTGTCCGT	GCGAGCTGGT	ACCAACAAC	CCCAGGAAAG	GCCCCATAAC
TCCTCCTGAA	CAGTGATGGG	AGTCGACCGT	CAGGGGTCCC	TGACCGGTTT	TCCGGCTCCA	ACTCTGGCGC
CTCAGCCACC	CTGACCATCA	CTGGGCTTCA	GGCTGAGGAC	GAGGCTGATT	ATTACTGTCA	GTCTTTTGAT
CCCACGCCTC	CTGATCATT	CGTGTTCGGC	TCAGGAACCC	AACTGACCGT	CCTTGGTCAG	CCC

(SEQ ID NO: 912)

λ325:

<u>ATGACCTC</u>	<u>CACCATGGGC</u>	<u>TGGTCCCCTC</u>	<u>TCCTCCTTAC</u>	<u>CCTCCTCGCT</u>	<u>CACTGCACAG</u>	<u>GTTCTGGGC</u>
CCAGTCTGTA	CTGACTCAGC	CGGCCTCAGT	GAGTGGGTCC	TTGGGCCAGA	GGGTCAACAT	CTCCTGCACT
GGAAGCCCCCT	CCAACATCGG	TGGATATGAT	GTTGCCTGGC	TCCAGCAGCT	CCCGGGAACA	GGCCCCAAGA
CCGTCATCTA	TAGTAGTACT	AACCGACCTT	CGGGGGTCCC	GGATCGATTG	TCCGGCTCCA	GGTCAGGCAG
CACAGCCACC	CTGACCATCT	CTGGGCTCCA	GGCTGAGGAC	GAGGCTGACT	ATTACTGTTC	CGCATGGGAC
AGCACTCTCA	GAGCTGGTGT	GTTCCGGCGG	GGCACCCACC	TGACCGTCTT	CGGTCAGCCC	AAGGC

(SEQ ID NO: 913)

λ326:

<u>AT</u>	<u>GACCTCCACC</u>	<u>ATGGGCTGGT</u>	<u>CCCCTCTCCT</u>	<u>CCTTACCCTC</u>	<u>CTCGCTCACT</u>	<u>GCACAAGTTC</u>
CTGGGCCCCAG	TCTGTGCTGA	CTCAGCCGGC	CTCAGTGACT	GGGTCCCTGG	GCCAGAGGGT	CACCATCTCC
TGCACTGGAA	GCAGCTCCAA	CATCGGTGGA	TATAGTGTTG	CCTGGTTCCA	GCAGCTCCCG	GGAACAGGCC
CCAGAACCGT	CATCTATAGT	AATACTAAGC	GACCCTCGGG	GGTCCCAGAT	CGATTCTCTG	GCTCCAGGTC
AGGCAGCACA	GCCACCCTGA	CCATCTCTGG	GCTCCTGGCT	GAGGACGACG	CTGATTATTA	TTGCTCAACA
TGGGACAGCA	GTCTCAAAGC	TCTTCTGTTC	GGCGGAGGCA	CCCATCTGAC	CGTCCTCGGT	CAG

(SEQ ID NO: 914)

λ129:

<u>TCCT</u>	<u>GGGCCCCACTC</u>	<u>TGTCCTGACT</u>	<u>CAGCCGGCCT</u>	<u>CAGTGTCTGG</u>	<u>GTTTCTGGGC</u>	<u>CAGAGGGTCA</u>
CCATCTCCTG	CACTGGAAGC	AGCTCCAACA	TTGGTGGAAG	TTATGTGAGC	TGGCACCAGC	AGGTCCCAGA
AACAGGCCCC	AGAAACATCA	TCTATGCTGA	TAACCTACCGA	GCCTCGGGGG	TCCCTGATCG	ATTTTCTGGC
TCCAAGTCAG	GCAGCACAGC	CACCCTGACC	ATCTCTGTGC	TCCAGGCTGA	GGATGAGGCT	GATTATTACT
GCCAGTCCTT	TGATACCGCT	CTTGGTACTG	TGTTCCGGCG	AGGCACCCAC	CTGACCGTCC	TCGGTCAGCC

CAGGGCC (SEQ ID NO: 915)

λ130:

ATGACC TCCACCATGG CCTGGTTCCC TCTCCTCCTG ACCCTCCTTG CTCACTACAC AGGGTCCTGG
 GCCCAGTCTG TGCTGACTCA GCCGGCCTCA GTGTCCGGGT CCCTGGGCCA GAGGGTCACC GTCTCCTGCA
 CTGGAAGCAA CTCCAACATC GGTGAGGTT ATGTGGACTG GTACCAACAA CTCCCGGGAA GAGGCCCCAC
 AACCTCTTG TATGGTACTG CTAACCGCCC CTCAGGGGTC CCCGATCGGT TCTCTGGCTC CAGGTCAGGA
 CGCACAGCCA CCCTGACCAT CTCTGGGCTC CAGGCTGAGG ATGAGGCTGA TTATTACTGC TCATCGTGGG
 ACGACGGTCT CAGGGCTCTC GTGTTCCGGCT CAGGAACCCA CCTGACCGCC CTTGGTCAGC CCAAGGCC
 (SEQ ID NO: 916)

λ134:

CTCCTCACCA TCCTCGCTCA CTGCACAGGG TCCTGGGCCC AGTCTCTACT GA CTCAGCCA GCCTCAGTGT
 CTGGGTCCCT GGGCCAGAAG GTCACCATCT CCTGCACTGG AAGCAACTCC AACATCGGTG GTAATGATGT
 GGCCTGGTAT CAACAGCTCC CAGGAATAGG CCCTAGAACC GTCATCTATG GTAAAAATAA CCGACCTTCA
 GGAATCTCCG ATCGATTCTC TGGCTCCAAG TCAGGCAATT CAGCCAGTTT GACCATATCT GGGCTCCAGG
 CTGAGGACGA GGCTGATTAT TTCTGCTCAT CATGGGATGA TAGTCTCAA GGTACAGTGT TCGGCTCAGG
 AACCCAATG ACCGTCCTTG GTCAGCCCAA GGCC (SEQ ID NO: 917)

λ213:

ATGAC CTCCACCATG GCCTGGTTCC CTCTCCTCCT GACCCTCCTT GCTCACTACA CAGGGTCCTG
 GGCCAGTCT GTGCTGACTC AGCCGGCCTC AGTGTCTGGG TCCCTGGGCC AGAGGATCAC CATCTCCTGC
 ACTGGAAGCG TCTCCAACAT TGGCATT TTTT GATGTGGGT GGTATCAACA ACTCCCAGGA AGAGGCCCA
 GAACTGTCAT CTATTCTACA AACAGTCGCC CCTCGGGGGT GCCCGATCGA TTTTCTGGCT CCAAGTCTGG
 CAGCACAGCC ACCCTGACCA TCTCTGGGCT CCAGGCTGAG GATGAGGCTG ATTATTACTG CTCAACGTGG
 GATGAGAATC TCAGTGTTC CGTGTTCCGGC GGAGGCACCC ACCTGACCGT CCTCGGTCAG CCAAGGCC
 (SEQ ID NO: 918)

λ214:

ATGACCT CCACCATGGC CTGGTCCTCT TTCTCCTCA CCCTCCTCGC TCACTTCACA GGTTCCTGGG
 CCCAGTCTGT ACTGACTCAA CCAGCCTCAG TGTCCGGGTC TCTGGGCCAG AGGGTCACCA TCTCGTGCAC
 TGGAAGCGGC TCCAACATTG GTAGAGATTC TGTGGGCTGG TACCAACAGG TCCCGGGAAC ACGCCCCAGA
 ACCCTCATCT ATGGTACTAC TAACCGACCC TCGGGGGTCC CCGATCGATT CTCTGGCTCC AAGTCAGGCA
 GCACAGCCAC CCTGACCATC TCTGGCCTCC AGGCTGAGGA CGAGGCTGAT TATTACTGCT CTACATGGGA
 CAACAGTGTC ACTGTTCTGT TCGGCGGAGG CACCCATCTG ACCGTCCTCA GTCAGCCCAA GGCC
 (SEQ ID NO: 919)

λ216a:

ATGATCTTC ACCATGGCCT GGTCCCCTCT CCTCCTCGGC CTCCTTGCTC ACTGCACAGG GTCTGGGGCC
 CAGTCTATGC TGA CTAGCC AGCCTCAGTG TCTGGGTCCC TGGGCCAGAC GGTCAACATC TCCTGCACTG
 GAAGTAGCTC CAACATCGGT GGTAAATCAAG TGGGCTGGTA CCAACAGTTC CCAGGAAGAG GCCCTAGAAG
 CGTCATCTAT GGTGATAATC ATCGACCCTC AGGGGTCCCC GATCGATTCT CTGTCTCCAA GTCAGGCAGT
 TCAGCCACCC TGACCATCTC TGGACTCCAG GCTGAGGACG AGGCTGAATA TTA CTGCTCA TCATGGGATA
 ATGATTTCGG TCACGTGTTC GGCTCAGGAA CCCAACTGAC CGTCCTTAGT CAGCCCAAGG CC
 (SEQ ID NO: 920)

L204-79:

ATGACCT CCAACATGGC CTGGTCCCCT CTCCTCCTCA CACTCCTTGC T TACTGCACA GGGTCTTGGG
 CCCAGTCTGT GCTGACTCAG CCGACCTCAG TGTCCGGGGTC CCTTGGCCAG AGGGTCACCA TCTCCTGCTC
 TGGAAGCACG AACGACATCG CTATTGTTGG TGCAGCTGG TACCAGCAGC TCCCAGGAAA GGCCCTAAA
 CTCCTCGTGT AACTTTTGG GGATCGGCCG TCAGGGGTCC CTGACCGGTT TTCCGGCTCC AACTCTGGCA
 ACTCAGCCAC CCTGACCATC ACTGGGCTTC AGGCTGAGGA CGAGGCTGAT TATTACTGCC AGTCCTTTGA
 TACCACGCTT GGTGCTTACG TCTTCGGCTC AGGAACCCAA CTGACCGTCC TTGGTCAGCC CAAGGCC
 (SEQ ID NO: 921)

L205-79:

ATGATC TTCACCATGG CCTGGTCCCC TCTCCTCCTC GGCCTCCTTG CTCACTGCAC AGGGTCCTGG
 GCCAGTCTA TCCTGACTCA GCCAGCCTCA GTGTCTGGGT CCCTGGGCCA GAAGGTCACC ATCTCCTGCA
 CTGGAAGCAG CTCCAATATC GGTGGTAATT ATGTGGGCTG GTACCAAAAT CTCCAGGAA AAGGCCCTAA
 AACCGTCATC TTTGCTGATG ATCACCAGCC TTCAGGGGTC CCCGATCGAT TCTCTGGCTC CAGGTCAGGC
 AGTTCAGCCA CCCTGACCAT TTCTGGGCTC CAGGCTGAGG ACGAGGCTGA CTATTATTGT TCATCATGGG
 ATAGGAGTCT CAGAGGTCAG GTTTTCGGCG GAGGCACCCA CCTGACCGTC CTCGGTCAGC C
 (SEQ ID NO: 922)

L206-79:

<u>A</u>	<u>TGACCTCCAC</u>	<u>CATGGGCTGG</u>	<u>TTCCCTCTGC</u>	<u>TCCTCACCT</u>	<u>CCTGGCTCAC</u>	<u>TGCACAGGTT</u>
CCTGGGCCCCA	GTCTGTGCTG	ACTCAGCCGG	CCTCAGTGTC	TGGGCCCCCTG	GGCCAGAAGG	TCACCATCTC
CTGCACTAGA	AGCAGCTCCA	ACATTGCTGG	TGGTTATGTG	GCCTGGTACC	AGCAGATCCC	AGGAACAGGC
CCCAGAACCC	TCATCTATAG	TACTACTGTC	CGACCTTCGG	GGGTCCCCGA	TCGATTCTCT	GGCTCCAGGT
CAGGCAGCAC	AGCAACCCTG	ACCATCTCTG	GGCTCCAGGC	TGAGGACGAG	GCTGATTATT	ATTGCTCAGG
ATATGACACC	ACTGTCAATG	GTGTTGTCTT	CGGCGGAGGC	ACCCATCTGA	CCGTCCTCGG	TCAGCCCCAAG

GCC (SEQ ID NO: 923)

L207-79:

<u>ATGACCTC</u>	<u>CACCATGGGC</u>	<u>TGGTCCCCTC</u>	<u>TCCTCCTCAC</u>	<u>CATCCTCGCT</u>	<u>CACTGCACAG</u>	<u>GGTCCTGGGC</u>
CCAGTCTGTG	CTGACTCAGC	CGGCCTCAGT	GTCCGGGTCC	CTGGGCCAGA	GGGTCACCAT	CTCATGCACT
GGAAGCGGGT	CCAACATCGG	GAGAGGTTAT	GTGGGCTGGT	ACCAACAGTA	CCCGGGAACA	GGCCCCAAAA
CGCTAATCTA	TGGTGATAGT	AGTCGACCCT	CAGGGGTCCC	CGATCGGTTT	TCTGCCTCCA	GGTCAGGCAA
CTCAGCCACC	CTGACCATCT	CTGGGCTCCA	GGCTGAGGAT	GAGGCGGATT	ATTACTGTTC	ATCGTGGGAC
ACCAGTCTCA	GAACATATAT	CGGCGGAGGC	ACCTATCTGA	CCGTCGTCGG	TCAGCCCCAAG	GCC

(SEQ ID NO: 924)

L210-79:

<u>ATGACC</u>	<u>TCCACCATGG</u>	<u>GCTGGTTCCC</u>	<u>TCTGCTCCTC</u>	<u>ACCCTCCTGG</u>	<u>CTCACTGCAC</u>	<u>AGGTTCTTGG</u>
GCCCAGTCTC	TGCTGACTCA	GCCGGCCTCA	GTGTCTGGGT	CCCTGGGACA	GAAGGTCACC	ATCTCCTGCA
CTGGAAGCAG	TGCCTACATT	GGTAGTGGCT	ATGTGGGCTG	GTACCAGCAG	GTCCCAGGAA	CAGGCCCCAG
AACCCTCATT	CATAGTACCA	GTAACCGACC	CCCGGGGGTC	CCCGATCGAT	TCTCTGCCTC	CGCGTCAGGC
AGCACAGCAA	CCCTGACCAT	TTCTGGGCTC	CAGGCTGAGG	ACGAGGCTGA	TTATTACTGC	TCAGCCTCTG
ACAGCAGTCT	CAGTGTGTTG	TTCGGCGGAG	GCACCCACCT	GACCGTCCTC	GGTCAGCCCCA	AGGCC

(SEQ ID NO: 925)

L215-79:

<u>ATGGC</u>	<u>CTGGTCCCCT</u>	<u>CTCCTCCTCA</u>	<u>CACTCCTTGC</u>	<u>GTA CTGCACA</u>	<u>GGGTCCTGGG</u>	<u>CCCAGTCTGT</u>
ACTGACTCAG	CCGACCTCAG	TGTCGGGGTC	CCTTGCCAG	AGGGTCACCA	TTTCCTGCTC	TGGAAGCAGC
AAGAACATCG	GAATTTTGG	TGCGCACTGG	TACCGACAAT	TCCCGGGAAA	GGCCCCTGAA	CTCCTCATTT
ATAATAGTAG	AGAACGACCG	TCAGGGGTCC	CTGGCCGGTT	TTCCGGCTCC	ATCTCTGGCA	ACTCAGCCAC
CCTGACCATC	ACTGGGCTTC	AGGCTGAGGA	CGAGGCTGAT	TATCACTGCC	AGTCTTTTGA	TACCACGCTT
GGTGATGGTG	ATGTTTTGTT	CGGCGGCGGC	ACCCACCTGA	CCGTCCTCGG	TCAGCCCCAAG	GCC

(SEQ ID NO: 926)

L216-79:

<u>AGGATCAGTG</u>	<u>ATGATCTTCA</u>	<u>CCATGGCCTG</u>	<u>GTCCCTCTC</u>	<u>CTCCTCGGCC</u>	<u>TCCTTGCTCA</u>	<u>CTGCACAGGG</u>
TCCTGGGCCC	AGTCTATGCT	GACTCAGCCA	GCCTCAGTGT	CTGGGTCCCT	GGGCCAGAAG	GTCACCATCT
CCTGCACTGG	AAGCAGCTCC	AACATCGGTG	GTAATTATGT	GGGCTGGTAC	CAACAGCTCC	CAGGAATAGG
CCCTAGAACC	GTCATCTCTG	GTAATAATTA	CCGACCTTCA	GGGGTCCCCG	ATCGATTCTC	TGGCTCCAAG
TCAGGCAGTT	CAGCCACCCT	GACCATCTCT	GGGCTCCAGG	CTGAGGACGA	GGCTGAGTAT	TACTGCTCAT
CATGGGATGA	TAGTCTCAGA	ATTTCTGTGT	TTGGCGGAGG	CACCCACCTG	ACCGTCCTCG	GTCAGCCCCA

(SEQ ID NO: 927)

L217-79:

<u>ATGACCTC</u>	<u>CACCATGGGC</u>	<u>TGGTCCCCTC</u>	<u>TCCTCCTTAC</u>	<u>CCTCCTCGCT</u>	<u>CACTGCACAG</u>	<u>GTTCTTGGGC</u>
CCAGTCTGTG	CTGACTCAGC	CGGCCTCAGT	GACTGGGTCC	CTGGGCCAGA	GGGTCACCAT	CTCCTGCACT
GGAAGCAGCT	CCAACATCGG	TGGATCTAGT	GTTGGTTGGT	TCCAGCAGTT	CCCGGGAACA	GGCCCCAGAA
CCGTCATCTA	TAGTATTAGT	AGCCGACCCT	CGGGGGTCCC	GGATCGATTG	TCTGGCTCCA	GGTCAGGCAG
CACAGCCATC	CTGACCATCT	CTGGGCTCCA	GGCTGAGGAC	GAGGCTGAGT	ATTACTGCTC	AGCATGGGAC
AGCAGTCTCA	AAGAAGCTGT	GTTCCGGCGGA	GGCACCCACC	TGACCGTCCT	CGGTCAGCCC	AAGGCC

(SEQ ID NO: 928)

L201-90:

<u>ATGACCT</u>	<u>CCACCATGGC</u>	<u>CTGGTCCTCT</u>	<u>TTCCTCCTCA</u>	<u>CCCTCCTCGC</u>	<u>TCACTTCACA</u>	<u>GGTTCCTGGG</u>
CCCAGTCTGT	ACTGACTCAA	CCAGCCTCAG	TGTCCGGGTC	TCTGGGCCAG	AGGGTCACCA	TCTCGTGAC
TGGAAGCGGC	TCCAACATTG	GTAAGATTC	TGTGGGCTGG	TACCAACAGG	TCCCGGGAAC	ACGCCCCAGA
ACCCTCATCT	ATGGTACTAC	TAACCGACCC	TCGGGGGTCC	CCGATCGATT	CTCTGGCTCC	AAGTCAGGCA
GCACAGCCAC	CCTGACCATC	TCTGGCCTCC	AGGCTGAGGA	CGAGGCTGAT	TATTACTGCT	CTACATGGGA
CAACAGTGTC	ACTGTTCTGT	TCGGCGGAGG	CACCCATCTG	ACCGTCCTCA	GTCAGCCCCA	GGCC

(SEQ ID NO: 929)

L217-90:

<u>ATG</u>	<u>ACCTCCACCA</u>	<u>TGGCCTGGTC</u>	<u>CTCTTTCCTC</u>	<u>CTCACCTCC</u>	<u>TCGCTCACTT</u>	<u>CACAGGTTCC</u>
TGGGCCCAGT	CTGTACTGAC	TCAACCAGCC	TCAGTGTCCG	GGTCTCTGGG	CCAGAGGGTC	ACCATCTCGT
GCACTGGAAG	CGGCTCCAAC	ATTGGTAGAG	ATTCTGTGGG	CTGGTACCAA	CAGGTCCCGG	GAACACGCCC
CAGAACCCTC	ATCTATGGTA	CTACTAACCG	ACCCTCGGGG	GTCCCCGATC	GATTCTCTGG	CTCCAAGTCA
GGCAGCACAG	CCACCCTGAC	CATCTCTGGC	CTCCAGGCTG	AGGACGAGGC	TGATTATTAC	TGCTCTACAT
GGGACGACAG	TGTCACTGTT	CTGTTCCGGC	GAGGCACCCA	TCTGACCGTC	CTCAGTCAGC	CCAAGGCC

(SEQ ID NO: 930)

L242-90:

<u>ATGACCTCCA</u>	<u>CCATGGCTGG</u>	<u>TCCTCTTTCC</u>	<u>TCCTCACCTC</u>	<u>CCTCGCTCAC</u>	<u>TTCACAGGTT</u>	<u>CCTGGGCCCA</u>
GTCTGTACTG	ACTCAACCAG	CCTCAGTGTG	CGGGTCTCTG	GGCCAGAGGG	TCACCATCTC	GTGCACTGGA
AGCGGCTCCA	ACATTGGTAG	AGATTCTGTG	GGCTGGTACC	AACAGGTCCC	GGGAACACGC	CCCAGAACCC
TCATCTATGG	TACTACTAAC	CGACCCTCGG	GGGTCCCCGA	TCGATTCTCT	GGCTCCAAGT	CAGGCAGCGC
AGCCACCCTG	ACCATCTCTG	GCCTCCAGGC	TGAGGACGAG	GCTGATTATT	ACTGCTCTAC	ATGGGACAAC
AGTGTCACTG	TTCTGTTTCGG	CGGAGGCACC	CATCTGACCG	TCCTCAGTCA	GCCCAAGGCC	

SEQ ID NO: 931)

L1-706:

<u>ATGACCTC</u>	<u>CACCATGGGA</u>	<u>TGGTTCNTN</u>	<u>TGCTCCTCAC</u>	<u>CCTCCTGGCT</u>	<u>CACTGCACAG</u>	<u>GTTCNTGGGC</u>
CCAGTCTGTG	NTGACTCAGC	CGGCCTCAGT	GTCTGGGTCC	CTGGGCCAGA	GGGTCAACCAC	CTCCTGCACT
GGAAGCAGCT	CCAACATCGG	TAGAGGTTTT	GTGGCCTGGC	ACCAGCAACT	CCCAGGAACA	GGCCCCAGAA
CACTCATATA	TCGTTCTGAG	AGGCGGCCCT	CGGGGGTCCC	TGATCGATTG	TCCGGCTCCA	GGTCAGGCAG
CACAGCAACC	CTGACCATCT	CTGGGCTCCA	GCCTGAGGAC	GAGGCTGATT	ATTACTGTTC	AGCACATGAC
AACAGTGTCA	GTGGTGTGTT	GTTTCGGCGGA	GGCACCCATC	TGACCGTCCT	CGGTCAGCCC	AAGGCC

(SEQ ID NO: 932)

L1-710:

<u>ATG</u>	<u>ACCTCCACCA</u>	<u>TGGCCTGGTT</u>	<u>CCCTCTCCTC</u>	<u>CTGACCCTCC</u>	<u>TTGCTCACTA</u>	<u>CACAGGGTCC</u>
TGGGCCCAGT	CTGTGCTGAC	TCAGCCGGCC	TCAGTGTCTG	GGTCCCTGGG	CCAGAGGATC	ACCGTCTCCT
GCACTGGCGC	CTACTCCAAC	ATTGGAACCTA	ATAATGTGGG	TTGGTACCAA	CAACTCCCAG	GAAGAGGCCC
CAGAACTGTC	ATCTATAGTA	CAGATAGTCG	ACCCTCGGGG	GTGCCCCGATC	GATTCTCTGG	CTCCAGGTCT
GGCACCCTG	CCACCCTGAC	CATCTCTGGG	CTCCAGGCTG	AGGATGAGGC	TGATTATTAC	TGCTCAGCAT
GGGATGATAG	TCTCACTGCT	TACGTGTTTCG	GCTCAGGGAC	CCAAGTGACC	GTCCTTGGTC	AGCCCAAGGC

C (SEQ ID NO: 933)

L1-714:

<u>ATG</u>	<u>ACCTCCACCA</u>	<u>TGGGATGGTT</u>	<u>CCCTCTGCTC</u>	<u>CTCACCTCC</u>	<u>TGGCTCACTG</u>	<u>CACAGGTTCC</u>
TGGGCCCAGT	CTGTGCTGAC	TCAGCCGGCC	TCAGTGTCTG	GGTCCCTGGG	CCAGAGGGTC	ACCATCTCCT
GCACTGGAAG	CGGCTCCAAC	ATCGGTTCGAG	GTTATGTGGC	CTGGTACCAA	CAGCTCCCAG	AAACAGGCCC
CAGAACCCTC	ATCTATGATA	CTAGTCGTCG	ACCCTCGGGG	GTCCCTGATC	GATTCTCTGG	CTCCAGGTCA
GGCAGCACAG	CGACCCTGAC	CATCTCTGGA	CTCCAGGCAG	ACGACGAGGC	TGATTATTAC	TGTTCAACAT
ATGACATCAC	TATCACTGGT	GGTGTGTTTCG	GCGGGGGCAC	CCACCTGACC	GTCCTCGGTC	AGCCCAAGGC

C (SEQ ID NO: 934)

L1-715:

<u>ATGA</u>	<u>CCTTCACCGT</u>	<u>GGGATGGTCC</u>	<u>CCTCTCCTCC</u>	<u>TCACCTTCCT</u>	<u>TGCTCACTGC</u>	<u>ACAGGGTCTT</u>
GGGCCCAGTC	TGTCCTGACT	CAGCCGGCCT	CAGTGTCCGG	GTCTCTGGGC	CAGAGCGTCA	CCATCTCCTG
CACTGGCTCC	AGCATCAATT	ATAGATACGT	TGGCTGGTAC	CAGCAGGTCC	CGGGAACAGG	CCCCAGAACC
CTCATCTATG	ATAATGGCAA	ACGACCCTCG	GGGGTTCCCG	AGCGATTCTC	TGGCTCCAAG	TCAGGCAGCA
CAGCCGCCCT	AACCATCTCT	GGGCTCCAGG	CTGAGGACGA	GGCTGATTAT	TATTGCTCTT	CATATGACAG
CAGTTTCACT	GCTGACTTCG	GCGGAGGCAC	CCAGTTGACC	GTCCTCGGTC	AGCCCAAGGC	C

(SEQ ID NO: 935)

L1-720:

<u>ATGGG</u>	<u>NTGGTCCCCT</u>	<u>CTCCTCCTTA</u>	<u>CCCTCCTCGC</u>	<u>TCAGTGCACA</u>	<u>GGTTCCTGGG</u>	<u>CCCAGTCTGT</u>
GCTGACTCAG	CCGGCCTCAG	TGACTGGGTC	CCTGGGCCAG	AGGGTCACCA	TCTCCTGCAC	TGGAAGCAGC
TCCAACATCG	GTGGATATAA	TGTTGGCTGG	TTCCAGCAGC	TCCCGGGAAC	AGGCCCCAGA	ACCGTCATCT
ATAGTAGTAG	TAACCGACCC	TCGGGGGCC	CGGATCGATT	CTCTGGCTCC	AGGTCAGGCA	GCACAGCCAC
CCTGACCATC	TCTGGGCTCC	AGGCTGAGGA	CGAGGCTGAG	TATTACTGCT	CAACATGGGA	CAGCAGTCTC
AAAGCTATTG	TGTTCCGGCG	AGGCACCCAT	CTGACCGTCC	TCGGTCAGCC	CAAGGCC	

(SEQ ID NO: 936)

L1-721:

AT	GATCTTCACC	ATGGCTTGGT	CCCCTCTCCT	CCTCGGCCTC	CCTGCTCACT	GCACAGGGTC
CTGGGCCCAG	TCTATGCTGA	CTCAGCCAGC	CTCAGTGTCT	GGGTCCCTGG	GCCAGAAGGT	CACCATCTCC
TGCACTGGAA	GCAGTTCCAA	CATCGGTGGT	AATTATGTGG	GCTGGTACCA	ACAGGTCCCA	GGAATAGGCC
CTAGAACCGT	CATGTATGGT	GATAATAACC	GACCTTCAGG	GGTCCCCGAT	CGATTCTCTA	GCTCCAGGTC
AGGCAGTTCA	GCCACCCTGA	CCATCGCTGG	CCTCCAGGCG	GAGGACGAGG	CTGCGTATTA	CTGTTCTGTC
TGGGATGATA	GTCTCAGAGG	TCATGTGTTC	GGCGGAGGCA	CCCATCTGAC	CGTCCTCGGT	CAGCCCAAGG

CC (SEQ ID NO: 937)

L1-723:

ATGGCNTGGT	CCTCTTTCCT	CCTCACCCCTC	CTCGCTCACT	TCACAGGTTC	CTGGGCCCAG	TCTGTGCTGA
CTCAACCAGC	CTCAGTGTCC	GGGCCTCTGG	GCCAGAGGGT	CACCATCTCC	TGCACTGGAA	GCAGCTCCAA
CATTGGTAGA	GATTATGTGG	GCTGGTTCCA	ACACCTCCCG	GGAACACGCC	CCAAAAGCCT	CATCTATGGT
AATAGTAAGC	GACCCTCGGG	GGTCCCCGAT	CGATTCTCTG	GCTCCAAGTC	AGGCAGCACA	GCCACCCTGA
CCATCTCTGG	GCTCCAGGCT	GAGGACGAGG	CTATTTATTA	CTGCTCTACA	TGGGACAACA	GTCTCACTTA
CGTGTTTCGGC	TCAGGAACCC	AACTGACCGT	CCTTGGTTCAG	CCCAAGGCC	(SEQ ID NO: 938)	

L1-731:

GGGTCACCAT	CTCGTGCTCT	GGACGTACGG	ACAACATCGG	TGTCGCTGGT	GCGGCTTGGT	ACCAACAACCT
CCCAGGAAAG	GCCCCATAAC	TCCTCGTGGA	CAATGATGGC	CATCGACCGT	CAAGGGTCCC	TGACCGGTTT
TCCGGCTCCG	AGTCTGGCAA	CTCAGCCACT	CTGACCATCA	CTGGGCTTCA	GGCTGAGGAC	GAGGCTGATT
ACTACTGCCA	GTCCTTTCAA	ACCACGCTTA	ATATTTACGT	GTTTCGGCTCA	GGGACCCAAC	TGACCGTCCT

TGGTCAGCCC AAGGCC (SEQ ID NO: 939)

L1-732:

ATGACCT	CCACCATGGG	CTGGTCCCCT	CTCCTCCTTA	CCCTCCTCGC	TCACTGCACA	GGTTCCTGGG
CCCAGTCTGT	GCTGACTCAG	CCGGCCTCAG	TGACTGGGTC	CCTGGGCCAG	AGGGTCACCA	TCTCCTGCAC
TGGAAGCGGC	TCCGACATCG	GTGGATTGG	CTGGTTCCAG	CAGCTCCCGG	GAACAGGCC	CAGAACCGTC
ATCTATGGTG	ATAGTGACCG	ACCCTCGGGG	GTCCCGGATC	GATTCTCTGG	CTCCAGGTCA	GGCAGGACAG
CCACCCTGAC	CATCTCTGGG	CTCCAGGCTG	AGGACGAGGC	TGAGTATTAC	TGCTCAACAT	GGGACGCCAG
TCTCCGGGTT	GGTGTGTTCG	GCGGAGGCAC	CCACCTGACC	GTCCTCGGTC	AGCCCAAGGC	C (SEQ ID NO: 940)

L1-733:

AT	GACCTCCACC	ATGGGCTGGT	CCCCTCTCCT	CCTTACCCTC	CTCGCTCACT	GCACAGGTTC
CTGGGCCCAG	TCTGTGCTGA	CTCAGCCGGC	CTCAGTGAAT	GGGTCCCTGG	GCCAGAGGGT	CACCATCTCC
TGCACTGGAA	GCAGCTCCAA	CATCGGTGGA	TATAATGTTG	GCTGGTTCCA	GCAGCTCCCG	GGAACAGGCC
CCAGAACCGT	CATCTGTAGT	AGTAGTAACC	GACCCTCGGG	GGTCCCGGAA	CGATTCTCTG	GCTCCAGGTC
AGGCAGCACA	GCCACCCTGA	CCATCTCTGG	GCTCCAGGCT	GAAGACGAGG	CTGAGTATTA	CTGCTCAACA
TGGGACAGCA	GTCTCAAAGC	TGTTGTGTTC	GGCGGAGGCA	CCCACCTGAC	CGTCCTCGGT	CAGCCCAAGG

CC (SEQ ID NO: 941)

L1-737:

AGCAGCTCCC	AGGAAGAGGC	CCCAGAACTG	TCATCTATAG	TACAGATAGG	CGACCCTCGG	GGGTGCCCCGA
TCGATTCTCT	GGCTCCAAGT	CTGGCAGCAC	AGCCACCCTG	ACCATCTCTG	GGCTCCAGGC	TGAGGATGAG
GCTGATTATT	ACTGCTCAAC	GTGGGATGAC	AGTCTCAGTG	AACCTGTGTT	CGGCGGAGGC	ACCCACCTGA

CCGTCCTCGG TCAGCCCAAG GCC (SEQ ID NO: 942)

L1-739:

CCTGCACTGG	AAGCAGCTCC	AACGTCGGTG	GAGGTTTTGT	GGGCTGGTAC	CAACTGGTCC	CAGGGACAGG
TCCCAGAACA	CTCATCTATG	GTAATTCTGA	CCGACCCTCG	GGGGTCCCTG	ATCGGTTCTC	TGGCTCCAAG
TCAGGCACCA	CAGCCATTCT	GACCATCTCT	GGACTCCAGG	CTGACGACGA	GGCTGATTAT	TTTTGCTCGA
CATACGACAC	CAGACTCAAT	GATGTTATTT	TCGGCGGCGG	CACCCACCTG	ACCGTCCTCG	GTCAGCCCAA

GGCC (SEQ ID NO: 943)

L1-742:

AT	GACCTCCACC	ATGGCCTGGT	TCCCTCTCCT	CCTGACCCTC	CTTGCTCACT	ACACAGGGTC
CTGGGCCCAG	TCTGTGCTGA	CTCAGCCGGC	CTCAGTGTCT	GGGTCCCTGG	GCCAGAGGAT	CACCATCTCT
TGCGCTGGAA	CCAACCTCCG	CATTGGAACT	AATCATGTGG	CTTGGTACCA	GCAGCTCCCA	GGGAGAGGCC
CCAGAAGTGT	CATCCATACT	ACAAATAGTC	GGCCCTCGGG	GGTGCCCGAT	CGATTCTCTG	GTTCCAAGTC
TGGCAGCACA	GCCACCCTGA	CCATCTCTGG	GCTCCAGGCT	GACGATGAGG	CTGATTATTA	CTGTTTCAGCG
TGGGATGATC	GTCTCACTGA	GCCTGTATTC	GGCGGAGGCG	CCCACCTGAC	CGTCCTCGGT	CAGCCCAAGG

CC (SEQ ID NO: 944)

L1-747:

ATGTCCT CCGACATGGC CTGGTCCCCT CTCCTCTTCA CACTCCTCGC TCACTGCACA GGGTCCTGGG
 CCCAGGCTGT ACTGAATCAG CCGGCCTCAG TGTCTGGGGC CCTGGGCCAG AAGGTCACCA TCTCCTGCTC
 TGGTAGCACA AATGACATAG GTAGATTTGG TGTCAACTGG TGCCAACAAC TCCCAGGAAA GGCCCTAAG
 CTCCTCGTGG ACAGTGATGG GGACCGACCC TCAGGGATCC CTGACAGATT TTCAGGCTCC CGCTCTGACA
 ACTCAGGCAT CCTGACCATC AGTGGCCTCC AGGCTGAGGA CGAGGCTGAT TATCACTGTC AGTCTGTTGA
 TCACACGCTT GCCGCTGCTG TGTTCGGCGG GGGCACCCAC CTGACCGTCC TCGGTCAGCC CAAGGCC
 (SEQ ID NO: 945)

L1-749:

ATGA CCTCCACCAT GGGCTGGTTC CCTCTGCTCC TCACCCTCCT GGCTCACTGC ACAGGTTTCCT
 GGGCCCAGTC TGAAGTACT CAGTCGGCCG CCGTATCTGG GTCCCTGGGC CAGGAAGTCA CCATCTCCTG
 CACTGGAAGC ACCGCCAACA TTGGAAGTGG TTATGTGAAT TGGTACCAAC AATTCCCAGG GACAGGTCCC
 AGAACCTCA TCTATACTTC TACTAACCAG CCTTCGGGGG TCCCCGCTCG ATTTTCTGGG TCCAGGTCAG
 GCAACACAGC GACCCTGACC ATCTCTGGGC TCCTGGCTGA GGACGAGGCT GATTATTATT GCGCTGCATA
 TGACAGTAGT CTCAGTATTG GTGTGTTTCG CGGAGGCACC CACCTGACCG TCCTCGGTCA GCCCAAGGCC
 (SEQ ID NO: 946)

L1-757:

CAGAACCGTC ATCTATATGA GTAGTAACCG ACCCTCGGGG GTCCCGGATC GATTCTCTGG CTCCAGGTCA
 GGCAGCACAG CCACCCTGAC CATCTCTGGG CTCCAGGCTG AGGACGAGGC TGAGTATTAT TGCTCAACAT
 GGGACAACAG TCTCAATACT GGTGTGTTTCG GCGGGGGCAC CCACCTGACC GTCCTCGGTC AGCCCAAGGC
 C (SEQ ID NO: 947)

L1-758:

ATG ACCTCCAACA TGGCNTGGTC CCCTCTCCTC CTCCCCTCC TTGCTTACTG CACAGGGTCC
 TGGGCCAGT CTATACTGAC TCAGCCGTCC TCAGTGTCTG GGTCCCTTGG CCAGAGGGTC ACCATCTCCT
 GTTCTGGAAG CATGTACAAC CTCGGTGTG TTGGTGCGAC CTGGTACCGA CAACTCCCAG GGGAGGCCCC
 TAACTCCTC CTATACAGTA ATGGGAGTCG ACCGTCAGGG GTCCCTGACC GGTTTTCCGG CTCCAACCTC
 GGCTTCTCTG CCACCCTGAC CATCACTGGG CTTGAGGCTG ACGACGAGGC TGATTATTAC TGCCAGTCCC
 TTGATTCCAC GCGTGTTTAT CATATTGTAT TCGGCGGAGG CACCCACCTG ACCGTCCTCG GTCAGCCCAA
 GGCC (SEQ ID NO: 948)

L1-760:

ATGA CCTCCACCAT GGGATGGTTC CCTCTGCTCC TCACCCTCCT GGCTCACTGC ACAGGTTTCCT
 GGGCCCAGTC TGTGCTGACT CAGCCGGCCT CAGTGTCTGG GTCCCTGGGC CAGAGGGTCA CCATCTCCTG
 CACTGGAAGC AACTCCAACA TCGGTAGAGG TTATGTGGGC TGGTACCAGC AGCTCCCAGG AACAGGCCCC
 AGAACCTCA TCTATGATAC TACTTTCCGA CCCTCGGGGG TCCCTGATCG ATTCTCTGGC TCCCGGTCAG
 GCACCACAGG AACCTGACC ATCTCTGGGC TCCAGGCTGA GGACGAGGCT GATTATTACT GCTCAGCATA
 TGACACCACT CTCAGTAGTA ATTTCTTCGG CGGAGGCACC CGCCTGACCG TCCTCGGTCA GCCCAAGGCC
 (SEQ ID NO: 949)

Table N₆₁

Group 1 Light Chain Variable Domain Nucleic Acid Sequences

L1-783:

TGGTACCAGC AGACCCTAGG CCGGGCTCCT CGCACGATTA TCTACAGAAC AAGCAGCCGC CCCTCTGGGG
 TCCCTAATCG CTTCTCCGGA TCCATCTCTG GGAACAAAGC CGCCCTCACC ATCACAGGAG CCCAGCCTGA
 GGACGAGGCT GACTATTACT GTTCCGTGTA TATGGGTACT TACACTGTTG TGTTCGGCGG AGGCACCCAC
 CTGACCGTCC TCGGTCAGCC CAAGGCC (SEQ ID NO: 950)

L1-776:

TAATTACCCT GGNTGGTACC AGCAGACCCA AGGCCGGGCT CCTCGCACGA TTATCTACAA CACAAACAGC
 CGGCCCTCTG GGGTCCCTAA TCGCTTCTCT GGATCCATCT CTGGAAACAA AGCCGCCCTC ACCATCACAG
 GAGCCCAGCC CGAGGATGAG GCTGACTATT ATTGTTCTT GCGCACGGGT TATCAAATA CTATGGTCGG
 CGGAGGCACC CACCTGACCG TCCTCGGTCA GCCCAAGGCC (SEQ ID NO: 951)

L1-785:

GCTTGGAACG TTGCTTCTTC TTTGTGCTCC TTGCCTATGG CTCAGGAGCA GATTCTCAGA CTGTGGTAAC
 CCAGGAGCCA TCACTNTCAG TGTCTCCAGG AGGGACAGTC ACACTCACAT GTGGCCTCAG CTCTGGGTCA
 GTCTCCACAA GTAATTACCC TGGCTGGTAC CAGCAGACCC TAGGCCGGGC TCCTCGCACG ATTATCTACA
 GAACAAGCAG CCGCCCCCTCT GGGGTCCCTA ATCGCTTCTC TGGATCCATC TCTGGGAACA AAGCCGCCCT
 CACCATCATA GGAGTCCAGC CTGAGGACGA GGCTGACTAT TACTGTTCTT TATATATGGG TAGTTACACT
 GATATGTTTCG GCGGAGGCAC CCACCTGACC GTCCTCGGTC AGCCCAAGGC C (SEQ ID NO: 952)

L1-789:

GGATCACACT CACATGTGGC CTCAACTCTG GGTCAGTCTC TACAAGTAAT TACCCTGCCT GGTACCAGCA
 GACCCTAGGC CGGGCTCCTC GCACGATTAT CTATGGAGCA AACAGCCGCC CCTCTGGGGT CCCTAATCGC
 TTCTCTGGAT CCATCTCTGA CAACAAAGCC GCCCTCACCA TCACAGGAGT CCAGCCTGAG GACGAGGCTG
 ACTATTACTG TTCCTTGTAT ATGGGTGGTT ATAGTGACGT GTTCGGCTCA GGAACCCAAC TGACCGTCCT
 TGGTCAGCCC AAGGCC (SEQ ID NO: 953)

λ104:

ATGGCCTGGA CACTGATTCT CCTTGGA CTTGCTTATG GCTCAGGAGC AGATTCTCAG ACTGTGGTGA
 CCCAGGAGCC ATCACTCTCA GTGTCTCTGG GAGGGACAGT CACCCTCACA TGTGGCCTCC CCTCCGGGTC
 AGTCTCTACA CAAACTTCC CCAACTGGTC CCAGCAGACC CCAGGGCAGG CTCCTCGCAC GATTATTTAC
 AACACAAACA CCGCCCCCTT AGGGGTCCCT AGTCGCTTCA CGGGATCCAT CTCTGGGAAC AGGGCCGCCC
 TCACCATCAC AGGAGCCCGG CCTGAGGACG AGGCTGACTA CTATTGTGCT CTGGGCTTCA GTGGTGGTGA
 TTATGTCTGT TTCGGCGGAG GCACCCACCT GACCGTCCTC GGTCAGCCCA AGGCC (SEQ ID NO: 954)

L1-753:

ATGGCT TGGACGGTGC TTCTTCTTGT GCTCCTTGCC TATGGCTCAG GAGCAGATTC TCAGACTGTG
 GTAACCCAGG AGCCATCACT CTCAGTGTCT CCAGGAGGGA CAGTCACACT CACATGTGGC CTCAGCTCTG
 GGTCACTCTC TACAAATAAT TACCCTGGCT GGTACCAGCA GACCCAAGGC CGGGCTCCTC GCACGATTAT
 CTACAGCACA AGCAGCCGCC CCTCTGGGGT CCCTAATCGC TTCTCTGGAT CCATCTCTGG AAACAAAGCC
 GCCCTCACCA TCACAGGAGC CCAGCCCGAG GATGAAACTG ACTATTACTG TTCCTTATAT ACGGGTAGTT
 CCACTGATGT GTTCGGCGGA GGCACCCATC TGACCGTCCT CGGTCAGCCC AAGGCC (SEQ ID NO: 955)

λ303:

ATGGCTTG GACGGTGCTT CTCTTGTGTC TCCTTGCCCTA TGGCTCAGGA GCAGATTCTC AGACTGTGGT
 AACCCAGGAG CCATCCCTCT CAGTGTCTCC AGGAGGGACA GTCACACTCA CATGTGGCCT CAGCTCTGGG
 TCAGTCTCTA CAAGTAATTA CCCTGGCTGG TACCAGCAGA CCAAGGCCG GGCTCCTCGC ACGATTATCT
 ACAACACAAA CAGCCGCCCC TCTGGGGTCC CTAATCGCTT CTCTGGATCC ATCTCTGGAA ACAAAGCCGC
 CCTCACCATC ACAGGAGCCC AGCCCGAGGA TGAGGCTGAC TATTACTGTT CCTTCTATAC GGGTGATTAC
 ACTGCTGTGT TCGGCGGAGG CACCCACCTG ACCGTCCTCG GTCAGCCCAA GGCC (SEQ ID NO: 956)

λ305:

ATGGCTTG ACGGTGCTTC TTCTTGTGCT CCTTGCCCTAT GGCTCAGGAA CAGATTCTCA GACTGTGGTC
 ACCCAGGAG CATCACTCTC AGTGTCTCCA GGAGGGACGG TCACACTCAC ATGTGGCCTC AGCTCTGGGT
 CAGTTACTGC GAGTCATTTT CCTGGCTGGT ACCAGCAGAC CCAAGGCCGG GCTCCTCGCA CGATTATCTA
 CAACACATAC AACCGCCTTT CTGGGGTCCC TAGTCGCTTC TCTGGATCCA TCTCTGGAAA CAAAGCCACC
 CTCACCATCA CAGGGGCCCC GCCCCAGGAT GAGGCTGACT ATCACTGTTT TGTATATACG GATGATCACA
 CTCCTGTATT CGGCGGAGGC ACCCACCTGA CCGTCCTCGG TCAGCACGAG GCC (SEQ ID NO: 957)

λ307:

GGGACGGTCA CACTCACATG TGGCCTCAGC CCTGGGTGAG TCTCTACGAG TAATTACCCT AATTGGTACC
 AGCAGACCCA AGGCCGGGCT CCCCACACGA TTATCTACAA CACAGGTAGC CGCCCCTCTG GGGTCCCTAA
 TCGCTTCTCT GGATCCATCT CTGGAAACAA AGCCGCCCTC ACCATCACAG GAGCCCAGCC CGAGGATGAG
 GCTGACTATT ACTGTTCTTT ATATACGGGT AGTTATACTG CTGTGTTTCGG CGGAGGCACC CACCTGACCG
 TCCTCGGTCA GCCC (SEQ ID NO: 958)

λ322:

AT GGCTTGGACG GTGCTTCTTC TTGTGCTCCT TGCCTATGGC TCAGGAGCAG ATTCTCAGAC
 TGTGGTAACC CAGGAGCCAT CACTCTCAGT GTCTCCAGGA GGGACAGTCA CACTCACATG TGGCCTCAGC
 TCTGGGTCGG TCTCTACGAG TAATTATCCT GCCTGGTACC AGCAGACCCA AGGCCGGGCT CCTCGCACGA
 TTATCTACAA CACAAACAGC CGCCCCTCTG GGGTCCCTAA TCGCTTCTCT GGATCCATCT CTGGAAACAA
 AGCCGCCCTC ACCATCACAG GAGCCCAGCC CGAGGATGAG GCTGACTATT ATTGTTCCCTT TTTTACAGAT
 ATTGTCGTTA ACGTGTTTCGG CTCAGGAACT CAATTGACCG TCCTTGGTCA GCC (SEQ ID NO: 959)

λ125:

ATGGC TTGGACGTTG CTTCTTCTTG TGCTCCTTGC CTATGGCTCA GGAGCAGATT CTCAGACTGT
 GGTAACCCAG GAGCCATCAC TCTCAGTGTC TCCAGGAGGG ACAGTCACAC TCACATGTGG CCTCAGCTCT
 GGGTCGGTCT CTGGAAGTAA TTACCCTGGC TGGTACCAGC AGACCCTAGG CCGGGCTCCT CGCACGATTA
 TCTACAGAAC AAGCAGCCGC CCCTCTGGGG TCCCTAATCG CTTCTCTGGA TCCATCTCTG GAAACAAAGC
 CGCCCTCACC ATCACAGGAG CCCAGCCTGA GGACGAGGCT GACTATTACT GTTCCTTGTA TATGGTCGGT
 TACACTGCCG TGTTCGGCTC AGGGACCCAA CTGACCGTCC TTGGTCAGCC CAAGGCC (SEQ ID NO: 960)

L214-79:

ATGG CCTGGACACT GATTCTCCTT GGGCTTCTTG CTTATGGCTC AGGAGCAGAT TCTCAGACTG
 TGGTGACCCA GGAGCCATCA CTCTCAGTGT CTCTGGGAGG GACAGTCACC CTCACATGTG GCCTCAGCTC
 CGGGTCAGTC TCTACAAGTA ACTACCCCAA CTGGTCCCAG CAGACCCAG GGCAGGCTCC TCGCACGATT
 ATCTACAACA CAAACAGCCG CCCCTCTGGG GTCCCTAATC GCTTCACTGG ATCCATCTCT GGAACAAAG
 CCGCCCTCAC CATCACAGGA GCCCAGCCTG AGGACGAGGC TGACTIONTAC TGTGCTCTGG GATTTAGTAG
 TAGTAGTAGT TACGTGTTTCG GCTCAGGAAC CCAACTGACC GTCCTTGGTC AGCCCAAGGC C
 (SEQ ID NO: 961)

L220-79:

AT GGCTTGGACG TTGCTTCTTC TTGTGCTCCT TGCCTATGGC TCAGGAGCAG ATTCTCAGAC
 TGTGGTGACC CAGGAGGCAT CAGTCTCGGT GTCTCCAGGA GGGACAGTCA CACTCACATG TGGTCTCAGC
 TCTGGGTCAG TCTCTACAGG TGATTTCCTT GGCTGGTACC AGCAGACCCCT AGGCCGGCCT CCTCGCACGA
 TTATATCCAG AACGAATAGA CGCCCCTCTG GGGTCCCTGA TCGCTTCTCT GGATCCATCT CTGGGAACAA
 AGCCGCCCTC ACCATCACAG GAGCCCAGCC TGAGGACGAG GGTGACTATT ATTGTTCCCTT ATATATGGGT
 TCTTACACTG GTTTGTTCGG CGGAGGCACC CACCTGACCG TCCTCGGTCA GCC (SEQ ID NO: 962)

L1-705:

TTGCTTCCTC TTGTGCTCCT TGCCTATGGC TCAGGAGCCG ATTCTCAGAC TGTGGTCATC CAGGAGCCAT
 TCCTCTCAGT GTCTCCAGGA GGGACGGTCA CACTCACATG TGGCCTCAGC TCTGGGTCAG TCTCTCCAAG
 TCATTACCTT GGCTGGTACC AGCAGACCCCT AGGCCGGCCT CCTCGCCCGA TCATCTACAG AACAGACAGC
 CGCCCCTCTG GGGTCCCTCG TCGCTTCTCT GCATCCGTCT CTGGGAACAA AGCCACCCTC ACCATTACAG
 GAGCCCAGCC TGAGGACGAG GCTGACTATT ACTGTTCCCTT ATATATGGAC ATTTACACTG GTGTGTTTCGG
 CGGAGGCACC CACCTGACCG TCCTCGGTCA GCCCAAGGCC (SEQ ID NO: 963)

L1-729:

ATG GCTTGGACAC TGATTCTCCT TGGGCTTCTT GCTTATGGCT CAGGAGCAGA TTCTCAGACT
 GTGGTGACCC AGGAGCCATC ACTCTCAGTG TCTCTGGGAG GGACAGTCAC CCTCACATGT GGCCTCAGCT
 CCGGGTCAGT CTCTACAAGT AACTACCCCA GCTGGTCCCA GCAGACCCCA GGGCAGGCTC CTCGCACGAT
 TCTCTACAAC ACAACAGCC GCCCCTCTGG GGTCCCTAAT CGCTTCACTG CATCCATCTC TGGGAACAAA
 GCCGCCCTCA CCATCACAGG AGCCAGCCT GAGGACGAGG CTGACTACTA CTGTGCTCTG GGATTAAGTG
 GGATTAGCAG TATTGTGTTT GCGGAGGCA CCCACCTGAC CGTCCTCGGT CAGCCCAAGG CC
 (SEQ ID NO: 964)

L1-743:

GACGGTGT TCTTCTTGTG CTCCTTGCCT ATGGCTCAGG AGCAGATTCT CAGACTGTGG TAACCCAGGA
 GCCATCACTC TCAGTGTCTC CAGGAGGGAC AGTCACACTC ACATGTGGCC TCAGCTCTGG GTCAGTCTCT
 ACAAGTAATT ACCCTGGCTG GTACCAGCAC ACCCAAGGCC GGGCTCCTCG CACGATTATC TACACCACAA
 GCAGCCGCCC CTCTGGGGTC CCTAATCGCT TCTCTGGATC CATCTCTGGA AACAAAGCCG CCCTCACCAT
 CACAGGAGCC CAGCCCAGAG ATGAGGCTGA CTATTACTGT TCCTTGTATA CGGGTAGGCC TGTGTTTCGG
 GGAGGCACCC ACCTGACCGT CCTCGGTCTAG CCCAAGGCC (SEQ ID NO: 965)

L1-759:

ATGGC TTGGATGGTG CTTCTTCTTG TGCTCCTTGC CTATGGCTCA GGAGCAGATT CTCAGACTGT
 GGTAACCCAG GAGCCATCAC TCTCAGTGTC TCCAGGAGGG ACAGTCACAC TCACATGTGG CCTCAGCTCT
 GGGTCAGTCT CTACAAGTAA TTACCCTGGC TGGTACCAGC AGACCCAAGG CCGGGCTCCT CGCACGATTA
 TCTACCACAC AAGCAGCCGC CCCTCTGGGG TCCCTAATCG CTTCTCTGGA TCCATCTCTG GAAACAAAGC
 CGCCCTCACC ATCACAGGAG CCCAGCCCCG GGATGAGGCT GACTATTACT GTTCCTTTTA TACGAGTAGT
 TACATTGCTG CCTGGTCACG CACGAGGGGA GCACCTGACC GTCCTCGGTC AGCCCAAGGC C
 (SEQ ID NO: 966)

Table N₃

Group 3 Light Chain Variable Domain Nucleic Acid Sequences

 λ 212:

ATGACCTCC ACCATGGGCT GGTCCCCTCT CGTCCTCACC CTCTTCGCTC ACTGCGCAGG GTCCTGGGCC
 CAGTCTGTGC TGA CTGAGCC GGCCTCAGTG TCCGGGTCCC TGGGCCAGAG GGTCACCATC TCCTGCACTG
 GAAGCAGTTC CAATGTTGGT TATGGCGATT ATGTGGGCTG GTACCAGCAG TTCCAGGAA CAGGCCCCAG
 AACCTCATC TATCGTACTG GTAATCGACC CTCGGGGGTC CCTGATCGAT TCTCTGGCTC CAGGTCGGGC
 AGCACAGCAA CCCTGACCAT CTCTGGGCTC CAGACTGAGG ATGAAGCCGA TTATTACTGC TCATCCTTTG
 ACAGAAAGTGT CAGTGCTGTG TTCGGCGGAG GCACCCACCT GACCGTCCTC GGTCAGCCCA AGGCC
 (SEQ ID NO: 967)

 λ 216:

AT GACCTCCACC ATGGGCTGGT CCCCTCTCGT CTCACCCTC TTCGCTCACT GCGCAGGGTC
 CTGGGCCCAG TCTGTGCTGA CTCAGCCGGC CTCAGTGTCC GGGTCCCTGG GCCAGAGGGT CACCATCTCC
 TGCACTGGAA GCAGTTCCAA TGTGTTTAT GGCATTATG TGGGCTGGTA CCAGCAGTTC CCAGGAACAG
 GCCCCAGAAC CCTCATCTAT CGTACTGGTA ATCGACCCTC GGGGGTCCCT GATCGATTCT CTGGCTCCAG
 GTCGGGCAGC ACAGCAACCC TGACCATCTC TGGGCTCCAG ACTGAGGATG AAGCCGATTA TTACTGCTCA
 TCCTTTGACA GAAGTGTGAG TGCTGTGTTT GCGGAGGCA CCCACCTGAC CGTCCTCGGT CAGCCCAAGG
 CC (SEQ ID NO: 968)

 λ 218:

ATGGG CTGGTCCCCT CTCATCCTCA CCCTCTTCGC TCACTGCGCA GGGTCCTGGG CCCAGTCTGT
 GCTGACTCAG CCGGCCTCAG TGTCTGGGTC CCTGGGCCAG AGGGTCACCA TCTCCTGCAC TGAAGCAGC
 TCCAATGTTG GTTATGCCAA TCATGTGGGC TGGTACCAGC AGCTCCCAGG AACAGGCCCC AGAACCTCA
 TCTATCATAG TAGTGACCGA CCTTCGGGGG TCCCCGATCG ATTCTCTGGC TCCAGGTCAG GCAACACAGC
 AACCTGACC ATCTCTGGCC TCCAGGCTGA GGACGAGGCT GATTATTACT GCTCAGCGTA TGACACCACT
 CTCAATGCTG TGTTCGGCGG AGGCACACAC CTGACCGTCC TCGGTCAGCC CAAGGCC
 (SEQ ID NO: 969)

 λ 231:

ATGAT GACCTCCACC ATGGGCTGGT TCCCTCTCAT CTCACCCTC CTCGCTCACT GCGCAGGGTC
 CTGGGCCCAG TCTGTGCTGA CTCAGCCGGC CTCAGTGTCT GGGTCCCTGG GCCAGAGGGT CACCATCTCC
 TGCACTGGAA GCAGCTCCAA TGTGTTTAT GGCAATTATG TGGGCTGGTA CCAGCAGCTC CCAGGAACAA
 GCCCCAGAAC CCTCATCTAT GATAGTAGTA GCCGACCCTC GGGGGTCCCT GATCGATTCT CTGGCTCCAG
 GTCAGGCAGC ACAGCAACCC TGACCATCTC TGGGCTCCAG GCTGAGGATG AAGCCGATTA TTACTGCTCA
 TCCTATGACA GCAGTCTCAG TGGTGGCGTG TTCGGCTCAG GAACCCAACT GACCGTCCTC GGTCAGCCCA
 AGGCC (SEQ ID NO: 970)

 λ 301:

A TGGCCTGGAC TCTGGTCCTC CTCACCTTTC TCTCTCAGGG CACAGGGTCC TGGGCCCAGT
 CTGCCCTGAC TCAACCTTCC TCGGTGTCTG GGACTTTGGG CCAGACTGTC ACCATCTCCT GTGATGGAAT
 CAACAGTAAC ATTGACAATA GTAATTATAT CGAATGGTTC CAACATTTCC CAGGCACCTC CCCCAACTC
 CTGATTTACT ATACCAATAA TCGGCCATCA GGAATCCCTG CTCGCTTCTC TGGCTCCAGG TCTGGGAACA
 CGGCCTCCTT GACCATCTCT GGGCTCCAGG CTGAAGATGA GGCAGATTAT TACTGTAGCG CATATAGTGG
 CACTGATACT TACGTGTTTC GCTCAGGAAC CCAACTGACC GTCCTTGGTC AGAACGAGGC C
 (SEQ ID NO: 971)

λ308:

ATGATGAC CTCCACCATG GGCTGGTTCC CTCTCATCCT CACCCTCCTC GCTCACTGCG CAGGGTCCTG
 GGCCAGTCT GTGCTGACTC AGCCGGCCTC AGTGTCTGGG TCCCTGGGCC AGAGGGTCAC CATCTCCTGC
 ACTGGAAGCA GCTCCGATGT TGGTTATGCC GATTATGTGG GCTGGTACCA GCAGGTCCCA GGAACAAGCC
 CCAGAACCCT AATCTATGAT ACTAGTAAGC GACCCTCGGG GGTCCCTGAT CGATTCTCTG GGTCCAGGTC
 AGGCAGCACA GCAACCCTGA CCATCTCTGG GCTCCAGGCT GAGGATGAAG CCGATTATTA CTGTTTCATCC
 TATCACAGCA GTCCTCATGG TGTGTCTTC GGCGGAGGCA CCCACCTGAC CGTCCTCGGT CAGCC
 (SEQ ID NO: 972)

λ311:

ATGATGACC TCCACCATGG GCTGGTTCCC TCTCATCCTC ACCCTCCTCG CTCACTGCGC AGGGCCCTGG
 GCCCAGTCTG TGCTGACTCA GCCGGCCTCA GTGTNTGGGT CCNTGGGCCA GAGGGTCACC ATCTCCTGCA
 CTGGAAGCAG CTCCAATGTT GGTTTTGGCA ATTATGTGGG NTGGTACCAG CAGCTCCCAG GAACAAGCCC
 CAAAACCCTT ATCTATGATA GTAGTAGACG ACCCTCGGGG GTCCCTGATC GATTCTCTGG CTCCAGGTCA
 GGCAGCACAG CAACCCTGAC CATCTCTGGG CTCCAGGCTG AGGATGAAGC CGATTATTAC TGCTCATCGT
 ATGACAGCGA GGTGAGGGTT GTGTTCTGGC GAGGCACCCA CCTGACCGTC CTCGGTCAGC ACGAGGC
 (SEQ ID NO: 973)

λ316:

AT GACCTCCACC ATGGCCTGGT CCCCTCTCCT ACTCACCTC CTTGCTCATT TCACAGGGTC
 CTGGGCCCAG TCTGTGCTGA CTCAGCCAGC CTCCGTGTNT GGGTCCCTGG GCCAGAGGGT CACCATTTCN
 TGCANTGGGA GCAGCTCCAA CGTTGGTTCT GGCAGTACTG TGGGCTGGTA CCAGCAGTTC CCAGGAACAG
 GCCCCAGAAC CATCATCTAT TATGATGGTA GCCGACCCTC GGGGGTCCCC GATCGATTCT CTGGCTCCAA
 GTCTGGCAGC ACAGCCACCC TGACCNCTC TGGGCTCCAG GCTGAGGATG AGGCTGATTA TTAGTGTCTCA
 TCTTGGGACA ACAGTCAAGG TAGTGTGTTT GGCGGAGGCA CCCATCTTGA CCGTCCTCGG GTCAGCCCAA
 GGCC (SEQ ID NO: 974)

λ131:

ATGA CCTCCACCAT GGCNTGGTCC CCTCTCCTCC TCACCCTCCT CGCTCATTGC ACAGTGTCTCCT
 GGGCCCAGGC TGTGCTGACT CAGCCACCCT CTATGTCTAC AGCCCTGGGG CAGAGGGTCA CCATAACCTG
 CACTGGAAGT AAGACCAACA TCGGCAGTGG TTATGATGTA CAATGGTACC AGCAGCTCCC AGGAAAGTCC
 CCTAAAAGTA TCATCTTCGC TAATGACGCT CGACCCTCGG GGGTCCCGGC TCGATTCTCT GGCTCCAAGT
 CAGGCAACAC AGCCACCCTG ACCATCACTG GGATCCAGGC TGAGGATGAG GCTGATTATT ACTGCCAGTC
 CTATGATGAC AACCTCGCTG GTCTTGTGTT CGGCGGAGGC ACCCAGTTGA CCGTCCTCGG TCAGCCCAAG
 GCC (SEQ ID NO: 975)

L202-79:

AT GACCTCCACC ATGGGCTGGT TCCCTCTCCT CCTCACCTTC CTGGCTCACT GCACAGGGTC
 CTGGGCCCAG ACTGTATTGA CTCAGCCGGC CTCAGTGTCT GGGTCTCTGG GCCAGACGGT CACCATCTCC
 TGCAGTGGAA GCAAGGACAA TATTGGTTAT GGCAATTATG TGGGCTGGTA TCGACAATTC CCAGGAACAG
 GCCCCAGAAC CGTCGCCTAT GGTCATGGAT TTCGACCCTC GGGGGTTCCT GACCGATTCT CTGCCTCCAG
 TTCAGGCAGC ACATCCACAC TGACCATCGC CGGGCTCCAG GCTGAAGATG AAGGTGATTA TTAGTGTCTCA
 ACCTATGACA ACAGTCTCTC TGTGTGTTC GGCGGAGGCA CCCACCTGAC CGTCCTCGGT CAGCCCAAG
 (SEQ ID NO: 976)

L208-79:

CAGACGGTCA CCATCTCCTG CACTGGAAGC AGCTCCAATG TTGGTTATGG CGATTATGTG GGCTGGTACC
 AACAACTCCC AGGGACAGGT CCCAAAACCC TCATCTATGA TACTCGTAGG CGACCCTCGG GGATTCCTGA
 TCGATTCTCT GGGTCCAGGT CAGGCAGCAC AGCGACCCTG ACCATCTCTG GACTCCAGGC TGAGGATGAG
 GCCGATTATT ACTGTGCATC CTATGACCGT ACTATCGGTG GTGGTGCTGT GTTCGGCGGA GGCACCCACC
 TGACCGTCCT CGGTCAGCCC AAGGCC (SEQ ID NO: 977)

L211-79:

CCGGGGCAGA GGGTCACCAT CTCCTGCACT GGAAGTAACA CCAACATCGG CAGTGATTAT GATGTTCAAT
 GGTACCAGCA ACTCCCAGGA AAGTCCCCTA AAATATCAT TTACGCTAAG AGCAATCGAC CCTCGGGGGT
 CCCTGATCGA TTCTCTGGCT CCAAGTCAGG CAGCACAGCC ACCCTGACCA TCTCTGTGCT CCAGGCTGAG
 GATGAGGCTG ATTATTACTG CTCAGTGGGG GATGATAGTC TCAAAGCACC TGTGTTCTGGC GGAGGCACCC
 ACCTGACCGT CCTCGGTCAG CCCAAGGCC (SEQ ID NO: 978)

L212-79:

TCCCTGGGCC AGACGGTCAC CATCTCCTGC ACTGGAAGCA GCTCCAATGT TGGTTATGGC GATTATGCGG
 GCTGGTACCA ACAACTCCCA GGGACAGGTC CCAAAACCCT CATCTATGAT ACTCGTAGGC GACCCTCGGG
 GATTCCTGAT CGATTCTCTG GGTCCAGGTC AGGCAGCACA GCGACCCTGA CCATCTCTGG ACTCCAGGCT
 GAGGATGAGG CCGATTATTA CTGTGCATCC TATGACCGTA CTATCGGTGG TGGTGCTGTG TTCGGCGGAG
 GCACCCACCT GACCGTCCTC GGTCAGCCCA AGGCC (SEQ ID NO: 979)

L218-79:

ATGACCTC CACCATGGGC TGGTTCCTC TCCTCCTCAC CTTCCTGGCT CACTGCACAG GGTCCTGGGC
 CCAGGCTGTG CTGACTCAGC CGGCCTCAGT GTCTGGGTCC CTGGGCCAGA GGGTCACCAT CTCCTGCACT
 GGAAGCACCT CCAATGTTGG TTATGGCAAT TATGTGGGCT GGTACCAGCA GCTCCCAGGA ACAGGCCCA
 AAACCCTCAT CTATGGTAGT AGTTACCGAC CCTCGGGGT CCCTGATCGA TTCTCTGGCT CCAGTTCAGG
 CAGCTCAGCC AACTGACCA TCTCTGGGCT CCAGGCTGAG GATGAAGCTG ATTATTACTG CTCATCCTAT
 GACAGCAGTC TCAGTGGGAT TGTGTTCCGC GGAGGCACCC ATCTGACCGT CCTCGGTCAG C
 (SEQ ID NO: 980)

L1-704:

A TGACCTCCAC CATGGGCTGG TCCCCTATCA TCCTCACCT CCTCGCTCAC TGCGCAGGGT
 CCTGGGCCCA GTCTGTGCTG ACTCAGCCGG CCTCAGTGTC TGGGTCCCTG GGCCAGAGGG TCACCATCTC
 CTGCACTGGA AGCAACTCCA ATGTTGGTTA TGCCAATTAT GTGGGCTGGT ACCAGCAGCT CCCAGGAACA
 GGCCCCAGAA CCCTCATCTA TGATAGTAGT AGCCGACCCT CGGGGGTCCC TGATCGATTG TCTGGCTCCA
 GGTCAGGCAG CACAGCAACC CTGACCATCT CTGGGCTCCA GGCTGAGGAT GAAGCCGATT ATTACTGCTC
 ATCCTATGAC AGCAGTCTCG ATGGTGCTGT GTTCGGCGGA GGCACCCACC TGACCGTCCT CGGTCAGCCC
 AAGGCC (SEQ ID NO: 981)

L1-711:

ATGACCTCC ACCATGGGCT GGTTCCTCT CATCCTCACC CTCTTCGCTC ACTGCGCAGG GTCTTGGGCC
 CAGTCTGTGC TGA CTGAGCC GGCCTCAGTG TCTGGGTCCC TGGGCCAGAG GGTACCATC TCCTGCACTG
 GAAACAGCTC CAATGTTGGT TATGGCAATT ATGTGGGCTG GTACCAGCAG CTCCCAGGAA CAAGCCCCAG
 AACCTCATC TATTATAGTA GTAGCCGACC CTCGGGAGTC CCCGATCGAT TCTCTGGCTC CAGGTCAGGC
 AGCACAGCTG CCCTAACCAT CTCTGGGCTC CAGGCTGAGG ATGAAGCCGA TTATTACTGC TCATCCTATG
 ACAGCAGTCT CAGTGGTGGT GTATTCTGGC GAGGCACCCA TCTGACCGTC CTCGGTCAGC CCAAGGCC
 (SEQ ID NO: 982)

L1-713:

ATGA CCTCCACCAT GGCCTGGTCC CCTCTCCTAC TCACCCTCCT TGCTCATTTT ACAGGGTCCT
 GGGCCAGTC TGTGCTGACT CAGCCAGCCT CCGTGTCTGG GTCCCTGGGC CAGAGGGTCA CCATTTCTCTG
 CACTGGAAGC AGCTCCAACG TTGGTGACAC AAGTAGTGTG GGCTGGTACC AACAGTTCCC AGGAACAGGC
 CCCAGAACCA TCATCTATTT TATTGGTAGC CGACCCTCGG GGGTCCCCGA TCGCTTCTCT GGCTCCAAGT
 CTGGCAGCAC AGCCACCCTG ACCATCTCTG GGCTCCAGGC TGAGGATGAG GCTGATTATT ACTGCTCATC
 TTGGGACAAC AGTCTCAAAA CTCGGGTGTT CGGCGAAGGC ACCCATCTGA CCGTCCTCGG TCAGCCCAAG
 GCC (SEQ ID NO: 983)

L1-716:

CATCTCCTG CACTGGAAGC AGCTCCAATG TTGGTTATGG CAATTATGTG GGCTGGTACC AACAGCTCCC
 AGGAACAGGC CCCAGAACCC TCATCTATCG TAGTAGTAAC CGAGCCTCGG GGGTCCCTGA TCGATTCTCT
 GGCTCCAGGT CAGGCAGCAC AGCAACCCTG ACCATCTCTG GGCTCCAGGC TGAGGATGAG GCCGATTATT
 TCTGCTCATC CTATGACAGC GGTCTCAGTC ATATTGTGTT CGGCGGAGGC ACCCACCTGA CCGTCTTCGG
 TCAGCCCAAG GCC (SEQ ID NO: 984)

L1-717:

AGGGTCACCA TCTCCTGCA CTGGAAGCGA CTCCAATGTT GGTATGGCA ATTATGTGGG CTGGTACCAG
 CAGCTCCAG GAACAAGCCC CAGAACCCTC ATTTATTATA ATACTGGGCG ACCCTCGGGA GTCCCCGATC
 GCTTTTCTGG CTCCAGGTCA GGCAATACAG CAACCCTGAC CATCTCTGGG CTCCAGGCTG AGGATGAAGC
 CGATTATTAC TGTTCAAGCT ATGACTACAG TCTCAGTTCT GCGTCTTCG GCGGAGGCAC CCACCTGACC
 GTCCTCGGTC AGCCCAAGGC (SEQ ID NO: 985)

L1-718:

ATGACCTCC ACCATGGGCT GGTTCCCTCT CATCCTCACC CTTTTCGCTC ACTGCGCAGG GTCCTGGGCC
CAGTCTGTGC TGACTCAGCC GGCCTCAGTG TCTGGGTCCC TGGGCCAGAG GGTCACCATC TCCTGCACTG
GAAGCAGTTC CAATGTTGGT TATGGCGATT ATGTGGCCTG GTACCAGCAG CTCCCAGGAA CAAGCCCCAG
AACCCTCATC CATCATAGTA GTAGCCGACC CTCGGGAGTC CCCGATCGAT TCTCTGGCTC CAGGTCAGGC
AGCACAGCAA CCCTGACCAT CTCTGGGCTC CAGGCTGAGG ATGAAGCCGA TTATTACTGC TCATCCTATG
ACAACAGTCT CAGTGGTGGC GTGTTGCGCG GAGGCACCCA CCTGACCGTC CTCGGTCAGC CCAAGGCC
 (SEQ ID NO: 986)

L1-727:

ATGA CCTCCACCAT GGCCTGGTCC CCTCTCCTAC TCACCCTCCT TGCTCATTTT ACAGGGTCCT
GGGCCCAGTC TGTGCTGACT CAGCCAGCCT CCGTGTCTGG GTCCCTGGGC CAGAGGGTCA CCATTTCTTG
CACTGGAAGC ACCTCCAACC TTGGTTATAG CAGTATTGTG GGCTGGTACC AGCAGTTCCT AGGAACAGGC
CCCAGAACCA TCATCTATTA TGATAGTAGC CGACCCTCGG GGGTCCCCGA TCGATTCTCT GGCTCCAAGT
CTGGCAGCAC AGCCACCCTG ACCATCTCTG GGCTCCAGGC TGAGGATGAG GCTGATTATT ATTGTTTCATC
TTGGGACAAC AGTCTCAAAG GTATTGTGTT CGGCGGAGGC ACCCATCTGA CCGTCTCTCG TCAGCCCCAAG
 GCC (SEQ ID NO: 987)

L1-730:

ATGACCTCT ACCATGGCCT GGTTCCCTCT CCTCCTCACC CTCCTCGCTC ACTGCACAGG GTCCTGGGCC
CAGTCTGTGC TGACTCAGCC AGCCTCAGTG TCTGGATCCC TGGGCCAAAG GGTCACCATC TCCTGCACTG
GAAGCACAAA CGACATCGGT AGTGAGAATT ATGTGCACTG GTACCAACAG CTCCCAGGAA AGGCACCCAG
TCTCCTCATC TATGGTGATG ATAACAGAGA ATCTGGGGTC CCTGAACGAT TCTCTGGCTC CAAGTCAGGC
AGCTCAGCCA CTCTGACCAT CACTGGGCTC CAGGCTGAGG ACGAGGCTAA TTATTATTGC CAGTCCTATG
ATGACAGTCT CAATACTTAC GTGTTGCGCT CAGGAACCCA ACTGACCGTC CTTGGTCAGC CCAAGGCC
 (SEQ ID NO: 988)

L1-735:

ATGATC TTCACCATGG CCTGGTCCCC TCTCCTCCTC GGCCTCCTTG CTCACTGCAC AGGGTCCTGG
GCCCAGTCTA TGCTGACTCA GCCAGCCTCA GTGTCTGGGT CCCTGGGCCA GAAGGTCACC ATCTCCTGCA
CTGGAAGAAG CTCCAACATC GGTGGTAATT ATGTGGGCTG GTACCAACAG CTCCCAGGAA AAGGCCCTAG
AACCGTCATC TATGGTAATA ATCGTCGACC TTCAGGGGTC CCCGATCGAT TCTCTGGCTC CGCGTCAGGC
AGTTCAGCCA CCCTGACCAT CTCTGGGCTC CAGGCTGAGG ACGAGGCTGA GTATTACTGC TCATCATGGG
ATGATAGTCT CAGAGGTGCT TTGTTGCGCG GAGGCACCCA CCTGACCGTC CTCGGTCAGC CCAAGGCC
 (SEQ ID NO: 989)

L1-741:

ATGAT GACCTCCACC ATGGGNTGGT TCCCTCTCAT CCTCACCCCTC CTCGCTCACT GCGCAGGGTC
CTGGGCCCAG GCTGTGCTGA CTCAGCCGGC CTCAGTGTCT GGGTCCCTGG GCCAGAGGGT CACCATCTCC
TGCACTGGAA GCGGCTCCAA TGTTGGTTAT GGCAATTATG TGGGCTGGTA CCAGCAGCTC CCAGGAACAA
GCCCCAGAAC CCTCATCTAT GCTACTAGTA GCCGACCCTC GGGGGTCCCT GATCGATTCT CTGGCTCCAG
GTCAGGCAGC ACAGCAACCC TGACCATCTC TGGGCTCCAG GCTGAGGATG AAGCCGATTA TTACTGCTCA
TCCTATGACA CCAGTCTCAG TGGTGGCGTG TTCGGCGGAG GCACCCACCT GACCGTCCTC GGTCAGCCCA
 AGGCC (SEQ ID NO: 990)

L1-748:

ATGACCTC CACCATGGGC TGGTTCCTC TCATCCTCAC CCTCTTCGCT CACTGCGCAG GGTCCTGGGC
CCAGTCTGTG CTGACTCAGC CGGCCTCAGT GTCTGGGTCC CTGGGCCAGA GGGTCACCAT CTCCTGCACT
GGAACCAGTT CCAATGTTGG TTTTGGCGAT TATGTGGGCT GGTACCAGCA GCTCCCAGGA ACGAGCCCCA
AAACCCTCAT CTATGATCAT AATGTCCGAC CCGCGGGGGT CCCCGATCGA TTCTCTGGCT CCAGGTCAGG
CAACACAGCA ACCCTGACCA CCTCTGGGCT CCAGGCTGAG GATGAAGCCG ACTATTTCTG TTATCCTAT
GACAGTAGTC TCAGTATTGT GTTCGGCGGA GGCACCCATC TGACCGTCCT CGGTCAGCCC AAGGCC
 (SEQ ID NO: 991)

L1-754:

ATGATGAC CTCCACCATG GGCTGGTTCC CTNTCATCCT CACCCCTCCTC GCTCACTGCG CAGGGTCCTG
GGCCCAGTCT GTGCTGACTC AGCCGGCCTC AGTGTCTGGG TCCCTGGGCC AGAGGGTCAC CATCTCCTGC
ACTGGAAGCA GCTCCAATGT TGGTTATGGC AATTATGTGG GCTGGTACCA GCAGCTCCCA GGAACAAGCC
CCAGAACCCT CATCTATGAT ACTAGTAGCC GACCCTCGGG GGTCCCTGAT CGATTCTCTG GCTCCAGGTC
AGGCAGCACA GCAACCCTGA CCATCTCTGG GCTCCAGGCT GAGGATGAAG CCGATTATTA CTGCTCATCC
TATGACAGCA GTCTCAGTGG TGCTGTGTTT GGCGGAGGCA CCCACCTGAC CGTCCTCGGT CAGCCCCAAG
 CC (SEQ ID NO: 992)

Table N_k

K Light Chain Variable Domain Amino Acid Sequences

Kapa 129:						
ATGA	GGTTCCCTTC	TCAGCTCCTG	GGGCTGCTGA	TGCTCTGGAT	CCCAGGATCC	GGTGGGGATA
CTGTCCTGAC	ACAGACCCCA	CCGTCCCTGT	CTGTCAGCCC	TGGAGAGCCG	GCCTCCATCT	CCTGCAAGGC
CAGTCAGAGC	CTCCTGCACA	GTAATGGAAA	CACCAATTTA	TATTGGTACC	TGCAAAAGCC	AGGCCAGTCT
CCACAACTTC	TGATCTACTT	GGTTTCCAAC	CGCTTCACTG	GCGTGTGAGA	CAGGTTTCAGT	GGCAGCGGGT
CAGGGACAGA	TTTCACCCTC	AGAATCAGCA	GGGTGGAGCC	TAACGATACT	GGAATTTATT	ACTGCGGGCA
ACAGTCACAA	CTTCCTCCGA	CGTTCGGAGC	AGGAACCAAG	GTGGAGCTCA	AACGGAATGA	TGCCCAGCCA
GCCGTCTAT (SEQ ID NO: 993)						
Kapa130:						
CTGGGGCTG	CTGATGCTCT	GGATCCCAGG	ATCCAGTGGG	GATATTGTCA	TGACACAGGC	CCCACCGTCT
CTGTCCGTCA	GCCCTGGAGA	GCCGGCCTCC	ATCTCCTGCA	CGGCCAGTCA	GAGCCTCCTG	CACAGTAATG
GGAACGCCTA	TTTAACCTGG	TACCGACAGA	AGCCAGGCCA	GTCTCCAGAG	GACCTGATCT	ATGAGGTGTC
CAACCGCTTC	TCTGGCGTGT	CAGACAGGTT	CAGTGGCAGC	GGGTCAGGGA	CAGATTTTAC	CCTGAGAATC
AGCAGAGTGG	AGGCTGACGA	TGCTGGAATT	TATTACTGCG	GGCAGAATCT	ACAGTTTCCG	ATCACCTTTG
GCAAAGGGAC	ACATCTGGAG	ATTAAACGGA	ATGATGCCCA	GCCAGCCGTC	TAT	(SEQ ID NO: 994)
Kapa 131:						
GAGGTTT	CCATCTCAGC	TCCTGGGGCT	GCTGATGCTC	TGGATCCCAG	GATCCAGTGA	GGATCTTGTC
TTGACACAGA	CCCCACGGTC	CCTGTCTGTC	AGCCCTGGAG	AGACTGCCTC	CATCTCCTGC	AAGGCCAGTC
AGAGCCTCCT	GTCTCCTGAT	GGAAACACAT	ACTTGAATTG	GTTCCGACAG	AAGCCAGGCC	AGTCTCCTCA
GCGTTTGATC	TATAAGGTCT	CCAATAGAGA	CATTGGGGTC	CCAGACAGGT	TCAGTGGCAG	CGGGTCAGGG
ACAGATTTCA	CCCTGAGAA	CAGCAGAGTG	GAGGCTGACG	ATACTGGACT	TTATTACTGT	GGGCAAGTCA
CATATCTTCC	CATTACTTTC	AGCCAGGGAA	CCAACCTGGA	GATGAAACGG	AATGATGCCC	AGCCAGCCGT
CTAT (SEQ ID NO: 995)						
Kapa212:						
CTCCTGGG	GCTGCTGATG	CTCTGGATCC	CAGGATCCAG	TGGGGATATC	GTCATGACAC	AGACCCCACT
GTCCCTGTCC	GTCTCCCCTG	GAGAGCCGGC	CTCCATCTCC	TGCAAGGCCA	GTCAGAGTCT	CCTGCACAGT
AATGGGAACA	CCTATTTGTC	TTGGTTCCGA	CAGAAGCCAG	GCCAGTCTCC	AGAGGGCCTG	ATCTATGAGG
TGTCCAAGCG	CTTCACTGGC	GTGTCAGACA	GGTTCAGTGG	CAGCGGGTCA	GGGACAGATT	TCACCCTGAC
AATCAGTAGA	GTGGAGGCTG	ACGATGCTGG	AGTTTATTAC	TGCGGGCAGG	GTCTACAATA	TCCTCGGACG
TTCGGAACAG	GAACCAAGGT	GGAGCTCAAG	CGGAATGATG	CCCAGCCAGC	CGTCTAT	(SEQ ID NO: 996)
Kapa214:						
TTCCCATCTC	AGCTCCTGGG	GCTGCTGATG	CTCTGGATCC	CAGGATCCAG	TGAGGATCTT	GTCTTGACAC
AGACCCACAG	GTCCCTGTCT	GTCAGCCCTG	GAGAGACTGC	CTCCATCTCC	TGCAAGGCCA	GTCAGAGCCT
CCTGTCTCCT	GATGGAAACA	CATACTTGAA	TTGGTTCCGA	CAGAAGCCAG	GCCAGTCTCC	TCAGCGTTTG
ATCTATAAGG	TCTCCAATAG	AGACATTGGG	GTCCCAGACA	GGTTCAGTGG	CAGCGGGTCA	GGGACAGATT
TCACCCTGAG	AATCAGCAGA	GTGGAGGCTG	ACGATACTGG	ACTTTATTAC	TGTGGGCAAG	TCACATATCT
TCCCATTA	TTAGCCAGG	GAACCAACCT	GGAGATGAAA	CGGAATGATG	CCCAGCCAGC	CGTCTAT
(SEQ ID NO: 997)						
Kapa216:						
ATGAGGT	TCCCATCTCA	GCTCCTGGGG	CTGCTGATGC	TCTGGATCCC	AGGATCCAGT	GAGGATCTTG
TCTTGACACA	GACCCACGG	TCCCTGTCTG	TCAGCCCTGG	AGAGACTGCC	TCCATCTCCT	GCAAGGCCAG
TCAGAGCCTC	CTGTCTCCTG	ATGGAAACAC	ATACTTGAAT	TGGTTCCGAC	AGAAGCCAGG	CCAGTCTCCT
CAGCGTTTGA	TCTATAAGGT	CTCCAATAGA	GACATTGGGG	TCCCAGACAG	GTTTCAGTGGC	AGCGGGTCAG
GGACAGATTT	CACCCTGAGA	ATCAGCAGAG	TGGAGGCTGA	CGATACTGGA	CTTTATTACT	GTGGGCAAGT
CACATATCTT	CCCATTACTT	TCAGCCAGGG	AACCAACCTG	GAGATGAAAC	GGAATGATGC	CCAGCCAGCC
GTCTAT (SEQ ID NO: 998)						

Kapa217:

ATGAGGTT CCCTTCTCAG CTCCTGGGGC TGCTGATGCT CTGGATCCCA GGATCCAGTG GGGATATTGT
 CATGACACAG GCCCCACCGT CTCTGTCCGT CAGCCCTGGA GAGCCGGCCT CCATCTCCTG CAAGGCCAGT
 CAGAGCCTCC TGCACAGTAA TGGGGACACC TATTTCTCTT GGTTCACACA GAAGCCAGGC CAGTCTCCAG
 AGGGCCTGAT CTATAAGGTG TCCAATCGCT ACACTGGCGT GTCAGACAGG TTCAGTGGCA GCGGGTCAGG
 GACAGATTTT ACCCTGAGAA TCAGCAGAGT GGAGGCTGAC GATGCTGGAG TTTATTACTG CGGGCAGATT
 TCACAGTTTC CTTATACTTT CAGCCAGGGA ACCAAGCTGG AGATAAAACG GAATGATGCC CAGCCAGCCG
 TCTAT (SEQ ID NO: 999)

Kapa218:

ATGAGGTTTC CCTTCTCAGC TCCTGGGGCT GCTGATGCTC TGGATCCCAG GATCCAGTGG GGATATTGTC
 ATGACACAGG CCCCACCGCC TCTGTCCGTC AGTCCTGGAG AGCCGGCCTC CATCTCCTGC AAGGCCAGTC
 AGACCCTCCT ACACAGTAAT GGGAAACACCT ATTTGTATTG GTTCCGACAG AAGCCAGGCC AGTCTCCAGA
 GGGCCTGATC CATAAGGTGT CCAACCGCTT CACTGGCGTG TCAGACAGGT TCAGTGGCAG CGGGTGAGGG
 ACAGATTTCA CCCTGAGAAT CAGCAGAGTG GAGGCTGACG ATGCTGGACT TTATTACTGC GGGCAAAATT
 TACAGTGGCC TCTTACGTTT GGCCAAGGGA CCAAGGTGGA GATCAAACGG AATGATGCCC AGCCAGCCGT
 CTAT (SEQ ID NO: 1000)

Kapa110-79:

ATGAGG TTCCCTTCTC AGCTCCTGGG GCTGCTGATG CTCTGGATCC CAGGATCCGG TGGGGATATT
 GTCATGACAC AGACGCCACC GTCCCTGTCT GTCAGCCCTA GAGAGCCGGC CTCCATCTCC TGCAGGGCCA
 GTCAGAGCCT CCTGCACAGT AACGGGAACA CCTATTTGAG TTGGTACCTG CAAAAGCCAG GCCAGTCTCC
 ACAGCTTCTG ATCTACTTGG TTTCCAACCG CTTCACTGGC GTGTCAGACA GGTTCAAGTG CAGCGGGTCA
 GGGACAGATT TCACCCTGAG AATCAGCAGA GTGGAGGCTG ACGATACTGG AGTTTATTAC TGCAGGCAAG
 GTACACAGTT TCCTCCGACG TTCGGAGCAG GAACCAAGGT GGAGCTCAAA CGGAATGATG CCCAGCCAGC
 CGTCTAT (SEQ ID NO: 1001)

Kapa114-79:

ACTGCCTCCA TCTCCTGCAA GGCCAGTCAG AGTCTCCTGC ACAGTGATGG CTACACGTAT TTGAGTTGGT
 TCCGACAGAA GCCAGGCCAG TCTCCACAGC GTTTGATCTC TAAGGTCTCC AACAGAGACA CTGGGGTCCC
 AGACAGGTTT AGTGGCAGCG GGTGAGGGAC AGATTTTACC CTGAGAATCG GCAGAGTGGG GGCTGACGAT
 ACTGGAGTTT ATTACTGTGG GCAAGTTATA CAAGATCCTT ATACTTTTCA CCAGGGAACC CCGCTGGAGA
 TAAAACGGAA TGGTGCCAG CCAGCCGTCT AT (SEQ ID NO: 1002)

Kapa127-79:

TGCAAGGCCC AGTCAGAGTC TCTTGCACAG TAATGGGAAC ACCTATTTGT GTTGGTTCCA ACAGAAGCCA
 GGCCAGTCTC CACAGCGTTT GATCTGGCGG GTCTCCAACA GAGACCCTGG GGTCCCAGAC AGGTTCAGTG
 GCAGCGGGTC AGGGACAGAT TTTACCCTGA GAATCAGCAG AGTGGAGGCT GATGATGCTG GAATTTATTA
 CTGCGGACAA GGTACACAAT ATCCTTTTAC GTTCGGCCAA GGGACCAAGG TGGACATTAA ACGGAATGAT
 GCCAGCCAG CCGTCTAT (SEQ ID NO: 1003)

Kapa203-79:

ATGAG GTTCCCTTCT CAGCTCCTGG GGCTGCTGAT GCTCTGGATC CCAGGATCCA GTGGGGATAT
 TGTCATGACA CAGGCCCCAC CGTCTCTGTC CGTCAGCCCT GGAGAGCCGG CCTCCATCTC CTGCAAGGCC
 AGTCAGAGCT TCCTGCACAG TGATGGGAAC ACCTATTTGT ATTGGTTCCG ACAGAAGCCA GGCCAGTCTC
 CAGAGGGCCT GATCTATAAG GTGTCCAACC GCTTCACTGG CGTGTGACAG AGGTTCAGTG GCAGCGGGTC
 AGGGACAGAT TTCACCCTGA GAATCAGCAG AGTGGAGGCT GACGATGCTG GAGTTTATTA CTGCGGGCAG
 AATTTACATT TTCCTTATAC TTTGAGCCAG GGAACCAAGC TGGAGATAAA ACGGAATGAT GCCAGCCAG
 CCGTCTAT (SEQ ID NO: 1004)

Kapa208-79:

TCCGTCAGCC CTGGAGAGCC GGCCTTCATC TCCTGCAAGG CCAGTCAGAG CCTCCTGCAC AGTAATGGGT
 ACAGCTTGTT GTATTGGTTC CGACAGAAGC CAGGCCAGTC TCCTCAGCGT TTGATCTATA AGGTCTCCAA
 TAGAGACATT GGGGTCCCAG ACAGGTTTCA TGGCAGCGGG TCAGGGACAG ATTGCACCCT GACAATTAGC
 AGAGTGGAGG CTGATGATGC TGGAGTTTAT TACTGCGGGC AAGGTATACA AGATCCGTTT ACTTTTGGCC
 AAGGGACCAA ACTGGAGATC AAACGGAATG ATGCCAGCC AGCCGTCTAT (SEQ ID NO: 1005)

Kapa213-79:

ATGACACA GACCCCACTG TCCCTGTCCG TCAGCCCTGG AGAGCCGGCC TCCATCTCCT GCAAGGCCAG
 TCAGAGCCTC CTGCACAGTA ATGGGTACAG CTTGTTGTAT TGGTTCCGAC AGAAGCCAGG CCAGTCTCCA
 GAGGACCTGA TCTATGAGGT GTCCAACCGC TTCTCTGGCG TGTGACAGAG GTTCAGTGGC AGCGGGTCAG
 GGACAGATTT CACCCTGAGA ATCAGCAGAG TGGAGGCTGA CGATGCTGGA ATTTATTACT GCGGGCAGAA
 TCTACAGTTT CCGATCACCT TTGGCAAAGG GACACATCTG GAGATTAAAC GGAATGATGC CCAGCCAGCC
 GTCTAT (SEQ ID NO: 1006)

Kapa217-79:

GTCATGACA CAGACCCAC TGTCCCTGTC CGTCAGCCCT GGAGAGCCGG CCTCCATCTC CTGCAAGGCC
 AGTCAGAGCC TCCTGCACAG TAATGGGAAC ACCTATTTTA ATTGGTTCCG ACAGAAGCCA GGCCAGTCTC
 CAGAGGGCCT GATCTATCAG GTGTCCAACC GCTTCACTGG CGTGTGACAG AGGTTCACTG GCAGCGGGTC
 AGGGACAGAT TTCACCCTGA GAATCAGCAG AGTGGAGGCT GACGATGCTG CAGTTTATTA CTGCGGGCAA
 GATACACACT TTCCTTATAC TTTCAGCCAG GGAACCAAGC TGGAGATAAA TCGGAATGAT GCCCAGCCAG
 CCGTCTAT (SEQ ID NO: 1007)

Kapa219-79:

GATATTGTCATGACACAGGCCCCACCGTCTN TGTCCGTCAG CCCTGGAGAG CCGGCCTCCA TCTCCTGCAC
 GGCCGGTCAG AGCCTCCTGC ACAGTAATGG GAACACCTAT TTAACNTGGT ACCGACAGAA GCCAGGCCAG
 TCTCCAGAGG ACCTGATCTA TGAGGTGTCC AACCCTTCT CTGGNGTGTG AGACAGGTTT AGTGGCAGCG
 GGTGAGGGAC AGATTTTACC CTGAGAATCA GCAGAGTGGG GGCTGACGAT GCTGCAGTTT ATTACTGCGG
 GCAAGATACA CACTTTTCTT ATACTTTTCTG CCAGGGAACC AAGCTGGAAA TAAAACGGAA TGATGCCCAG
 CCAGCCGTCT AT (SEQ ID NO: 1008)

Kapa1201:

CTCCATCTCC TGCACAGTAC CGGGAACACC TATTTGAATT GGTTCACACA GAAGCCAGGC CAGTCTCCAC
 AGGGCCTGAT CTATAAGGTC TCCAACAGAG ACCCTGGGGT CCCAGACAGG TTCAGTGGCA GCGGGTCAGG
 GACAGATTTT ACCCTGAGAA TCAGCAGAGT GGAGGCTGAC GATGCTGGAG TTTATTACTG CATGCAAGGT
 GTACAAACTC CGTTCACTTT TGGCCAAGGG ACCAACTGG AGATCAAACG GAATGATGCC CAGCCAGCCG
 TCTAT (SEQ ID NO: 1009)

Kapa1202:

CTCCATCT CCTGCACAGT ACCGGGAACA CCTATTTGAA TTGGTTCCAA CAGAAGCCAG GCCAGTCTCC
 ACAGGGCCTG ATCTATAAGG TCTCCAACAG AGACCCTGGG GTCCCAGACA GGTTCAAGAG CAGCGGGTCA
 GGGACAGATT TCACCCTGAG AATCAGCAGA GCGGAGGCTG ATGATGCTGG AATTTATTAC TGCGGGCAAG
 GTACACAAGA TCCTCCCACC TTTGGCAAAG GGACACATCT GGAGATTAAA CGGAATGATG CCCAGCCAGC
 CGTCTAT (SEQ ID NO: 1010)

Kapa1204:

AT GAGGTTCCCT TCTCAGCTCC TGGGGCTGCT GATGCTCTGG ATCCCAGGAT CCAGTGGGGA
 TGTGTCATG ACACAGGCC CACCGTCTCT GTCCGTCAGC CCTAGAGAGC CGGCCTCCAT CTCCTGCAAG
 GCCAGTCAGA GCCTCCTGTA TAGTAATGGG AACACCTATT TGTATTGGTT CCGCCAGAAG CCAGGCCAGT
 CTCCACAGCG TTTGATCTAT AAGGTCTCCA ATAGAGACCC TGGGGTCCCA GACAGGTTCA GTGGCAGCGG
 GTCAGGGACA GATTTACCCC TGAGAATCAG CAGAGTGGAG GCTGACGATG CTGGAGTTTA TTACTGCATG
 CAAGGTGTAC AACTCCGTT CACTTTTGGC CAGGGAACCA AGCTGGAGAT AAAACGGAAT GATGCCCAGC
 CAGCCGTCTA T (SEQ ID NO: 1011)

Kapa1206:

ATGAGGTTT CCTTCTCAGC TCCTGGGGCT GCTGATGCTC TGGATCCCAG GATCCAGTGG GGATATTGTC
 ATGACACAGA CCCCACTGTC CCTGTCCGTC AGCCCTGGAG AGCCGGCCTC CATCTCCTGC AAGGCCAGTC
 AGAGCCTCCT GTATAGTAAT GGGAACACCT ATTTGTATTG GTTCCGCCAG AAGCCAGGCC AGTCTCCACA
 GCGTTTGATC TATAAGGTCT CCAATAGAGA CCCTGGGGTC CCAGACAGGT TCAGTGGCAG CGGGTGAGGG
 ACAGATTTCA CCCTGAGAAT CAGCAGAGTG GAGGCTGATG ATGCTGGAAT TTATTACTGC GGGCAAGGTA
 CACAAGATCC TCCCACCTTT GGCAAAGGGA CACATCTGGA GATTAAACGG AATGATGCCC AGCCAGCCG
 (SEQ ID NO: 1012)

Kapa1207:

ATGAGGT TCCCTTCTCA GCTCCTGGGG CTGCTGATGC TCTGGATCCC AGGATCCAGT GGGGATGTTG
 TCATGACACA GACCCACCG TCTCTGTCCG TCAGCCCTAG AGAGCCGGCC TCCATCTCCT GCAAGGCCAG
 TCAGAGCCTC CTGAACAGTA ATGGGCACAC CTATTTGTAT TGGTTCCGAC AGAAACCCGG CCAGTCTCCA
 GAGGGCCTGA TCTATAAGGT GTCCAACCGC TTCACTGGCG TGTGACAGAG ATTCAGTGGC AGCGGGTCAG
 GGACAGATTT CACCCTGAGA ATCAGCAGAG TGGAGGCTGA CGATGCTGGA GTTTATTACT GCGGGCAAGG
 TATACAGGTT CCTTATACTT TCAGCCAGGG AACCAAGCTG GAGATAAAAC GGAATGATGC CCAGCCAGCC
 GTCTAT (SEQ ID NO: 1013)

Kapal208:

ATGAGGT TCCCTTCTCA GCTCCTGGGG CTGCTGATGC TCTGGATCCC AGGATCCAGT GGGGATGTTG
 TCATGACACA GGCCCCACCG TCTCTGTCCG TCAGCCCTAG AGAGCCGGCC TCCATCTCCT GCAAGGCCAG
 TCAGAGCCTC CTGAACAGTA ATGGGCACAC CTATTTGTAT TGGTTCCGAC AGAAACCCGG CCAGTCTCCA
 GAGGGCCTGA TCTATAAGGT GTCCAACCGC TTCCTGGCG TGTGACAGAG ATTCAGTGGC AGCGGGTCAG
 GGACAGATTT CACCCTGAGA ATCAGCAGAG TGGAGGCTGA CGATGCTGGA GTTTATCACT GCGGGCAAGG
 TATACAGGTT CCTTATACTT TCAGCCAGGG AACCAAGCTG GAGATAAAAC GGAATGATGC CCAGCCAGCC
 GTCTAT (SEQ ID NO: 1014)

Kapal212:

ATGAGG TTCCCTTCTC AGCTCCTGGG GCTGCTGATG CTCTGGATCC CAGGATCCAG TGGGGATATA
 GTCATGACAC AGACCCCACT GTCCCTGTCC GTCAGCCCTG GAGAGCCGGC CTCCATCTCC TGCAAGGCCA
 GTCAGAGTCT CCTGCGCAGT AACGGGAACA CCTATTTGTT TTGGTTTCGA CACAAGCCAG GCCAGTCTCC
 ACAGACTTTG ATCTATGAGG TCTCCAACAG AGACCCTGGG GTCCCAGACA GGTTCACTGG CAGCGGGTCA
 GGGACAGACT TCACTCTGAG AATCAGCAGA GTGGAGGCTA ACGATACTGG AGTTTATTAC TGCGGACAAG
 GTACACAGTT TCCTTATACT TTCAGCCAGG GAACCAAGCT GGAGATAAAA CGGAATGATG CCCAGCCAGC
 CGTCTAT (SEQ ID NO: 1015)

Kapal213:

ATGAGGTTCC CTTCTCAGCT CCTGGGGCTG CTGATGCTCT GGATCCCAGG ATCCAGTGGG GATGTTGTCA
 TGACACAGGC CCCACCGTCT CTGTCCGTCA GCCCTGGAGA GCCGGCCTCC ATCTCCTGCA AGGCCAGTCA
 GAGCCTCCTG AACAGTAATG GGCACACCTA TTTGTATTGG TTCCGACAGA AACCCGGCCA GTCTCCAGAG
 GGCCTGATCT ATAAGGTGTC CAACCGCTTC ACTGGCGTGT CAGACAGATT CAGTGGCAGC GGGTCAGGGA
 CAGATTTTAC CCTGAGAATC AGCAGAGTGG AGGCTGACGA TGCTGGAGTT TATCACTGCG GGCAAGGTAT
 ACAGGTTTCT TATACTTTCA GCCAGGGAAC CAAGCTGGAG ATAAAACGGA ATGATGCCCA GCCAGCCGTC
 TAT (SEQ ID NO: 1016)

Kapal217:

A TGAGGTTCCC TTCTCAGCTC CTGGGGCTGC TGATGCTCTG GATCCCAGGA TCCAGTGGGG
 ATGTTGTCAT GACACAGGCC CCACCGTCTC TGTCCGTCAG CCCTAGAGAG CCGGCCTCCA TCTCCTGCAA
 GGCCAGTCAG AGCCTCCTGA ACAGTAATGG GCACACCTAT TTGTATTGGT TCCGACAGAA ACCCGGCCAG
 TCTCCAGAGG GCCTGATCTA TAAGGTGTCC AACCGCTTCA CTGGCGTGTG AGACAGATTC AGTGGCAGCG
 GGTGAGGGAC AGATTTTACC CTGAGGATCA GCAGAGTGGG GGCTGACGAT GCTGGAGTTT ATTACTGCGG
 GCAAGGTATA CAGGTTTCTT ATACTTTTCA CCAGGGAACC AAGCTGGAGA TAAAACGGAA TGATGCCCA
 (SEQ ID NO: 1017)

Kapal218:

ATGAGG TTCCNTTCTC AGCTCCTGGG GCTGCTGATG CTCTGGATCC CAGGATCCAN TNNGNATATT
 GTCATGACAC AGACCCCACT GTCCCTGTCC GTCAGCCNTG NAGAGCCGGC CTCCATCTCC TGCAAGGCCA
 GTCAGAGCCT CCTGTATAGT AATGGGAACA CCTATTTGTA TTGGTTCCGC CAGAAGCCAG GCCAGTCTCC
 TCAGCGTTTG ATCTATAAGG TGTCCAACCG CTTCACAGGC GCGTCAGACA GATTCAGTGG CAGCGGGTCA
 GGGGCAGATT TCACCNTGAG AATCAGCAGA GTGGAGGCTG ACGATGCTGG AGTTTATTAC TGCGGGCAAG
 GTATACAGGT TCCTTATACT TTCAGCCAGG GA (SEQ ID NO: 1018)

Kapal219:

ATGAGGTTCC CTTCTCAGTT CCTGGGGCTG CTGATGCTNT GGATCCCAGG ATCCAGTGGG GATATTGTCA
 TGACACAGAC CCCACTGTCC CTGTCCGTCA GCCCTGGAGA GACGGCCTCC ATCTCCTGCA CAGAACCGGG
 AACACCTATT TGAATTGGTT CCAACAGAAG CCAGGCCACT CTCCACGGGG CCTGATCTAT AAGGTCTCCA
 ACAGAGACCC TGGGGTCCCA GACAGGTTCA GTGGCAGCGG GTCAGGGACA GATTTACCC TGAGAATCAG
 CAGAGTGGAG GCTGACGATG CTGGAGTTTA TTAATGTCAT CAAGGTGTAC AAATCCGTT CACTTTTGGC
 CAAGGGACCA AACTGGAGAT CAAACGGAAT GATGCCCAGC CAGCCGTCTA T (SEQ ID NO: 1019)

Kapal220:

ATG AGGTTCCCTT CTCAGCTCCT GGGGCTGCTG ATGCTCTGGA TCCCAGGATC CAGTGGGGAT
 GTTGTGTCAT CACAGGCCCC ACCGTCTCTG TCCGTCAGCC CTAGAGAGCC GGCCTCCATC TCCTGCAAGG
 CCAGTCAGAG CCTCCTGAAC AGTAATGGGC ACACCTATTT GTATTGGTTC CGACAGAAAC CCGGCCAGTC
 TCCAGAGGGC CTGATCTATA AGGTGTCCAA CCGCTTCACT GCGGTGTCAG ACAGATTCAG TGGCAGCGGG
 TCAGGGACAG ATTTACCCCT GAGAATCAGC AGAGTGGAGG CTGACGATGC TGGAGTTTAT TACTGCGGGC
 AAGGTATACA GGTTCCTTAT ACTTTCAGCC AGGGAACCAA GCTGGAGATA AAACGGAATG ATGCCCAGCC
 AGCCGTCTAT (SEQ ID NO: 1020)

Kapa1221:

ATGAGGTT CCCTTCTCAG CCCCTGGGGC TGCTGATGCT CTGGATCCCA GGATCCAGTG GGGATGTTGT
 CATGACACAG GCCCCACCGT CTCTGTCCGT CAGCCCTAGA GAGCCGGCCT CCATCTCCTG CAAGGCCAGT
 CAGAGCCTCC TGAACAGTAA TGGGCACACC TATTTGTATT GGTTCGACA GAAACCCGGC CAGTCTCCAG
 AGGGCCTGAT CTATAAGGTG TCCAACCGCT TCACTGGCGT GTCAGACAGA TTCAGTGGCA GCGGGTCAGG
 GACAGATTTT ACCCTGAGAA TCAGCAGAGT GGAGGCTGAC GATGCTGGAG TTTATTACTG CGGGCAAGGT
 ATACAGGTTT CTTATACTTT CAGCCAGGGA ACCAAGCTGG AGATAAAACG GAATGATGCC CAGCCAGCCG
 TCTAT (SEQ ID NO: 1021)

Kapa1223:

AT GAGGTTCCCT TCTCAGCTCC TGGGGCTGCT GATGCTCTGG ATCCCAGGAT CCAGTGGGGA
 TGTGTGTCATG ACACAGACCC CACCGTCTCT GTCCGTCAGC CCTAGAGAGC CGGCCTCCAT CTCCTGCAAG
 GCCAGTCAGA GCCTCCTGAA CAGTAATGGG CACACCTATT TGTATTGGTT CCGACAGAAA CCCGGCCAGT
 CTCCAGAGGG CCTGATCTAT AAGGTGTCCA ACCGCTTCAC TGGCGTGTCA GACAGATTCA GTGGCAGCGG
 GTCAGGGACA GATTTCACCC TGAGAATCAG CAGAGTGGAG GCTGACGATG CTGGAGTTTA TTA CTGCGGG
 CAAGGTATAC AGGTTCTTA TACTTTCAGC CAGGGAACCA AGCTGGAGAT AAAACGGAAT GATGCCCAGC
 CAGCCGTC (SEQ ID NO: 1022)

Kapa1225:

ATGAG GTTCCCTTCT CAGTTCCTGG GGCTGCTGAT GCTCTGGATC CCAGGATCCA GTGGGGATAT
 TGTGTCATGACA CAGACCCAC TGTCCCTGTC CGTCAGCCCT GGAGAGACGG CCTCCATCTC CTGCACAGTA
 CCGGGAACAC CTATTTGAAT TGGTTCCAAC AGAAGCCAGG CCAGTCTCCA CAGGGCCTGA TCTATAAGGT
 CTCCAACAGA GACCCTGGGG TCCCAGACGG GTTCAGTGGC AGCGGGTCAG GGACAGATTT CACCCTGAGA
 ATCAGCAGAG TGGAGGCTGA CGATGCTGGA GTTTATTACT GCATGCAAGG TGTACAACT CCGTTCACTT
 TTGGCCAAGG GACCAAACCTG GAGATCAAAC GGAATGATGC CCAGCCAGCC GTCTA (SEQ ID NO:
 1023)

Kapa1278:

ATGA GGTTCCCTTC TCAGCTCCTG GGGCTGCTGA TGCTCTGGAT CCCAGGGTCC AGTGGGGAGA
 TCGTCATGAC ACAGACCCCA CTGTCCCTGT CCGTCAGTCC TGGAGAGACG GCCTCCATCT CCTACAGGGC
 CAAGCAGAGC CTCCTGTATA GTGATGGGAA CACCTATTTG GATTGGTACA TGCAGAAGCC AGGCCAGTCT
 CCCCAGGGCC GGATCTATTT GGTGTCCAAT CACTTCACAG GCGTGTGACA CAGGTTTCAGT GGCAGCGGGT
 CAGGGACAGA TTTCACCCTG AAGATCAGCA GAGTGGAGGC TGACGATACT GGAGTTTATT NCTGCGGGCA
 AGGTACACAC TCTCCTCCAC TTTCAGCCAG GGAACCAAGC TGGAGATA (SEQ ID NO: 1024)

Kapa1279:

GCCAGTCAGA GCCTCCTCCA CAGTAACGGG ATCACCTATT TGTTTTGGTT TCGACAGAGG CCAGGCCAGT
 CTCCACAGCG TCTGATCTAT AAGGCCTCCA ACAGAGACCC TGGGGTCCCA GACAGGTTCA GTGGCAGCGG
 GTCAGGGACA GACTTCACCC TGAGAATCAG CAGAGTGGAG GCTGACGATA GTGGAGTTTA TTA CTGCGGG
 CAAGGTCTAC AGGTTCCGTG GACGTTCCGA GCAGGAACCA AGCTGGAGAT AAAACGGAAT GATGCCCAGC
 CAGCCGTCTA T (SEQ ID NO: 1025)

Kapa1283:

ATGA GGTTCCCATC TCAGCTCCTG GGGCTGCTGA TGCTCTGGAT CCCAGGATCC AGTGGGGATA
 TTGTCATGAC ACAGACCCCA CTGTCCCTGT CTGCCAGCCC TGGAGAGACT GCCTCCATCT CCTGCAAGGC
 CAGACAGAGC CTCCTGCACA GTTATGGAAA CACGTATTTG AATTGGTTCC GACAGAAGCC AGGTCACTCT
 CCACAGCGTT TGATCTATAA GGTCTCCAAC AGAGACACTG GGGTCCCGGA CAGGTTTCAGT GGCAGCGGGT
 CAGGGACAGA TTTCACCCTG AGAATCAGCA GAGTGGAGGC TGACGATACT GGGGTTTATT ACTGCGGGCA
 AGGTATACAG TTTCCTCGCA CTTTTGGCCA AGGGACCAAA CTGGAGATCA GACGGAATGA TGCCAGCCA
 GCCGTCTAT (SEQ ID NO: 1026)

Kapa1284:

ATG AGGTTCCCTT CTCAGCTCCT GGGGCTGCTG ATGCTCTGGA TCCCAGGATC CAGCGGAGAT
 ATTGTCATGA CAGAGGCCCC ACCGTCTCTG TCCGTCAGCC CTGGAGAGTC GGCCTCCATC TCCTGCAAGG
 CCAGTCAGAG CCTCCTGCAC AGTAATGGGA ACACCTATTT GTTCTGGCTC CGACAGAAGC CAGGCCAGTC
 TCCAGAGGGC CTGATCTATA AGGTGTCCAA CCGCTTCACT GCGTGTGTCAG ACAGGTTTCAG TGGCAGAGGG
 TCAGGGACAG ATTTACCCCT GCGAATCAGC AGAGTGGAGG CTGGCGATGC TGGAGTTTAT TACTGCGGGC
 AAAATTTACA GTTTCCTTAT ACTTTCAGCC AGGGAACCAA GCTGGAGATA AAACGGAATG ATGCCCAGCC
 AGCCGTCTAT (SEQ ID NO: 1027)

Kapa1285:

ATGA GGTTCCTTC TCAGCTCCTG GGGCTGCTGA TGCTCTGGAT CCCAGGATCC AGTGGGGATA
 TCGTCATGAC ACAGACCCCA CTGTCCCTGT CCGTCAGCCC TGGAGAGCCG GCCTCCATTT CCTGCAAGGC
 CAGTCAGAGC CTCCTGCACA GTAACGGGAA CACCTATTTG TATTGGTCTC GACAGAGGCC AGGCCAGTCT
 CCGGAGGGCC TGATCTATAA GGTGTCCAAC CGCTTCATTG GCGTGTGAGA CAGGTTTCAGT GGCAGCGGGT
 CAGGGACAGA TTTCACCCTG AAAATCAGCA GAGTGGAGGC TGACGATGCT GGAGTTTATT TCTGCGGGCA
 AAATTTACAG TTTCCTTTTA CTTTCAGCCA GGGAACCAAG CTGGAGATAA AACGGAATGA TGCCCAGCCA
 GCCGTCT (SEQ ID NO: 1028)

Kapa1286:

ATGAGGTTCC CTTCTCAGCT CCTGGGGCTG CTGATGCTCT GGATCCCAGG ATCCAGTGGG GATATCGTCA
 TGACACAGAT CCCACTGTCC CTGTCCGTCA GTCCTGGAGA GCCGGCCTCC ATCTCCTGCA AGGCCAGTCA
 GAGCCTCCTG CACAGTAACG GTGTCACCTA TTTGTTTTGG TTTTCGACAGA AGCCAGGCCA GTCTCCACAG
 CGTTTGATCT ATAGGGTCTC CAGGAGAGAC CCTGGGGTCC CAGACAGGTT CAGTGGCAGC GGGTCAGGGA
 CAGATTTTAC CCTGAGAATC AGCAGAGTGG AGGCTGATGA TGCTGGAGTT TATTACTGCG GGCAAGCTTT
 ACAAACTCGT CGGACGTTTC GAGCAGGAAC CAAGGTGGAG CTCAAACGGA ATGATGCCCA GCCAGCCGTC
 TA (SEQ ID NO: 1029)

Kapa1287:

ATGAGG TTCCCTTCTC AGCTCCTGGG GCTGCTGATG CTCTGGATCC AGGATCCAGT GGGGATATTG
 TCATGACACA GGCCCCACCG TCTCTGTCCG TCAGCCCTGG AGAGCCGGCC TCCATCTCCT GCAGGGCCAG
 TCAGAGCCTC CCGCACAGTG ATGGGAACAC CTATTTGTAC TGGTTCCGCC AGAAGCCAGG CCAGTCTCCA
 GAGGGCCTGA TCTATAAGGT GTCCAACCGC TTCCTGCGC TGTCAGACAG GTTCAGTGGC AGCGGGTCAG
 GGACAGATTT CACCCTGAGA ATCAGCAGAG TGGAGGCTGA CGATGCTGGA GTTTATTACT GCGGGCAAAA
 TTTACAGTTT CCTCTTACGT TCGGCCAAGG GACCAAGGTG GAGATCAAAC GGAATGATGC CCAGCCAGCC
 GTCT (SEQ ID NO: 1030)

Kapa1288:

ATGAGGT TCCCTTCTCA GCTCCTGGGG CTGCTGATGC TCTGGATCCC AGGATCCAGT GGGGATATTG
 TCATGACACA GACTCCACTG TCCCTGTCTG TCAGCCCTGG AGAGACTGCC TCCATCTCCT GTAAGGCCAG
 TCAGAGCCTC CTGTACAGTG ATGGAACTC GATTTTGAAT TGGTTCCGAC AGAAGCCAGG CCAGTCTCCA
 CAGCGTTTGA TCTATAAGGT CTCCAACAGA GACCCTGGGG TCCCAGACAG GTTCAGTGGC AGCGGGTCAG
 GGACAGATTT CACCCTGAGA ATCAGTAGAG TGGTGGCTGA TGATGCTGGA GTTTATTACT GCGGGCAAGC
 TATACAAGAT CCGTGGACGT TCGGAGCAGG AACCAAGGTG GAGCTCAAAC GGAATGACGC CCAGCCAGCC
 GTCTA (SEQ ID NO: 1031)

Kapa1289:

ATGAGG TTCCCTTCTC AGCTCCTGGG GCTGCTGATG CTCTGGATCC CAGGATCCAG TGGGGATATT
 GTCATGACAC AGGCCCCACC GTCTCTGTCC GTCAGCCCTG GAGAGCCGGC CTCCATCTCC TGCAAGGCCA
 GTCAGAGCCT CCTGTACAGT AATGGGAATA CCTATTTGTA TTGGTTCCGA CAGAAGCCAG GCCAGTCTCC
 AGAGGGCCTG ATCTATAAGG TGTCCAACCG CTTCCTGCGC GTGTCAGACA GGTTCAGTGG CAGCGGGTCA
 GGGACAGATT TCACCCTGAG AATCAGCAGA GTGGAGGCTG ACGATGCTGG AGTTTATTAC TGCGGGCAAG
 GTATACAGTT TCCTATTACT CTCAGCCAGG GAGCCAAGCT GGACATAAAA CGGAATGATG CCCAGCCAGC
 CGTCTAT (SEQ ID NO: 1139)

Kapa1243:

A TGAGGTTCCC ATCTCAGCTC CTGGGGCTGC TGATGCTCTG GATCCCAGGA TCCAGTGGGA
 TTATTGTCAT GACACAGACC CCACTGTCCC TGTCTGCCAG CCCTGGAGAG TCTGCCTCCA TCTCCTGCAA
 GGCCAGTCAG AGCCTCCTGC ACAGTACTGG AAACACGTAT TTGAATTGGT TCCGACAGAA GCCAGGCCAG
 TCTCCACAGC GTTTGATCTA TAGGGTCTCC AACAGAGACA CGGGGGTCCC AGACAGGTTT AGTGGCAGCG
 GGTGAGGGAC AGATTTTACC CTGAGAATCA GCAGAGTGGG GGATGAGGAT GCTGGACTTT ATTACTGCGG
 GCAAGGTATA CAATATCCGT TCACTTTTGG CCAAGGGACC AAAGTGGAGA TCAAACGGAA TGATGCCAG
 CCAGCCGTCT AT (SEQ ID NO: 1032)

Kapa1244:

CAGAGCCTCC TGCACAGTAA CGGAAACACC TATTTGAATT GGTACCTGCA AAAGCCAGGC CAGTCTCCTC
 AGATTCTGAT CTACTTGGCT TCCCACCGCA GCAATGGCGT GTCAGACAGG TTCAGTGGCA GCGGGTCAGG
 GACAGACTTC ACCCTGAGAA TCAGCAGAGT GGAGGCTGAC GATAGTGGAG TTTATTACTG CGGGCAAGGT
 CTACAGGTTT CGTGGACGTT CGGAGCAGGA ACCAAGGTGG AGCTCAAACG GAATGATGCC CAGCCAGCCG
 TCTAT (SEQ ID NO: 1033)

Kapal249:

CAAGATCCTC ATACTTTCAG CCAGGGAACC AAGCTGGGGA TAAAACGGAA TGATGCCAG CCAGCCGTCT
 ATTTGTTCCA ACCATCTCCA GACCAGTTAC ACACAGGAAG TGCCTCTGTT GTGTGTTTGC TGAATAGCT
 (SEQ ID NO: 1034)

Kapal250:

CTGCTGAT GCTCTGGATC CCAGGATCCA GTGGGGATAT TGTCTGACA CAGACCCAC TGTCCCTGTC
 CGTCAGCCCT GGAGAGCCGG CCTCCATCTC CTGCAAGGCC AGTCAGAGCC TCCTGCACAG TGACGGGAAC
 ACCTACTTGT ATTGGTTCCG ACAGAAGCCA GGCCAGGCTC CACAGCGCCT GATCTACGTG GGTATCAAGA
 GAGACGCTGG GGTCCCAGAC AGGTTCAGTG GCAGCGGGTC AGGGACAGAC TTCACCCTGA GAATCAGCAG
 AGTGGAGGCT GATGATGGTG GAGTTTATCA CTGCGGGCAA GGTACACAGC TTCCTTATAC TTTCAGCCAG
 GGAACCAAGC TGGAGATAAA ACGGAATGAT GCCCAGCCAG CCGTCTAT (SEQ ID NO: 1035)

Kapal251:

CAGAGCCTCC TCCACAGTAA CGGGATCACC TATTTGTTTT GGTTCGACA GAGGCCAGGC CAGTCTCCAC
 AGCGTCTGAT CTATAAGGCC TCCAACAGAG ACCCTGGGGT CCCAGACAGG TTCAGTGGCA GCGGGTCAGG
 GACAGACTTC ACCCTGAGAA TCAGCAGAGT GGAGGCTGAC GATAGTGGAG TTTATTACTG CGGGCAAAAC
 ATAGGGTTTC CTAATACTTC CAGCCAGGGA ACCAAGCTGG AGATAAAACG GAATGATGCC CAGCCAGCCG
 TCTAT (SEQ ID NO: 1036)

Kapal275:

ATGAGGTTTC CCTTCTCAGC TCCTGGGGCT GCTGATGCTC TGGATCCCAG GATCCAGTGG GGCCATTGTC
 ATGACACAGG CCCACCGTC TCTGTCCGTC AGCCCTGGAG AGCCGGCCTC CATCTCCTGC AAGGCCAGTC
 AGAGCCTCCT GCACGGTGAT GGGACCACCT ATTTGTTTTG GTTCCGACAG AAGCCAGGCC AGTCTCCACA
 GCGTTTGATC TATAAGGCCT CCAACAGAGA CCCTGGGGTC CCAGACAGGT TCAGTGGCAG CGGGTCAGGG
 ACAGACTTCA CCCTGAGAAT CAGCAGAGTG GAGGCTGACG ATAGTGGAGT TTATTACTGC GGGCAAGGTC
 TACAGGTTCC GCGGACGTTT GGAGCAGGAA CCAAGGTGGA GCTCAAACGG AATGATGCCC AGCCAGCCGT
 CTAT (SEQ ID NO: 1037)

Kapal343:

GGGCTGCTG ATGCTCTGGA TCCCAGGATC CAGTGGGGAT ATTGTCATGA CACAGACGCC ACCGTCCCTG
 TCTGTCAGCC CTGGGGAGAC TGCCTCCATC TCCTGCAAGG CCAGTCAGAG CCTCCTGTTT AGTAACGGGA
 AAACCTATTT GTTTTGGTTT CGACAGAAGC CAGGCCAGTC TCCACAACGT TTGATCTATC AGGTCTCCAA
 TAGAGACCTT GGTATCCCAG ACAGGTTTCTG TGGCAGCGGG TCAGGGACAG ATTTACCCCT GAGAATCAGC
 GGAGTGGAGG CTGCCGATAC TGGAGTTTAT TACTGCGTGC AAGGTATACA GTTTCCTTAT ACTTTCGGCC
 AGGGAACCAA CCTGGAGATA AAACGGAATG ATGCCAGCC AGCCGTCTAT (SEQ ID NO: 1038)

Kapal346:

ATGGA AGCCCCAGCT CGCCTTCTCT GCCTTCTGTT ACTCTGGCTC CCAGATATCA CCGGAGAAAT
 CCTACTGACA CAGTCTCCAG ACTCCCTCTC CTTGTCTCAG GAGACAGAAG TCACCATCAC CTGCCGGGCC
 AGTCAGTATG TTAGCAGGGA CTTAGCCTGG TATCAACAAA AACCTGGGCA GGCCCCCAA CTCCTCATCT
 ATGGTGCCTC CAATAAGGCC ACTGGTGTCC CATCCCGTTT CAGTCGCAGT GGGTCTGGGA CAGACTTTAG
 CCTCACAATC AGCAGCCTGG AGCCCGAAGA TGTTCAGTTT TATTTCTGTC AACAGTATCA TACGGGTCCG
 CTAACGTTTC GCCAAGGGAC CAAGGTGGAG ATCCAGCGGA ATGATGCCCA GCCAGCCGTC TAT
 (SEQ ID NO: 1039)

Kapal347:

ATGGA AGCCCCAGCT CGCCTTCTCT GCCTTCTGTT ACTCTGGCTC CCAGATATCA CCGGAGAAAT
 CCTACTGACA CAGTCTCCAG ACTCCCTCTC CTTGTCTCAG GAGACAGAAG TCACCATCAC CTGCCGGGCC
 AGTCAGTATG TTAGCAGGGA CTTAGCCTGG TATCAACAAA AACCTGGGCA GGCCCCCAA CTCCTCATCT
 ATGGTGCCTC CAATAAGGCC ACTGGTGTCC CATCCCGTTT CAGTCGCAGT GGGTCTGGGA CAGACTTTAG
 CCTCATAATC AGCAGCCTGG AGCCCGAAGA TGTTCAGTTT TATTTCTGTC AACAGTATCA TACGGGTCCG
 CTAACGTTTC GCCAAGGGAC CAAGGTGGAG ATCCAGCGGA ATGATGCCCA GCCAGCCGTC TAT
 (SEQ ID NO: 1040)

Kapal348:

CCTGGGGCTG CTGATGTCTG GATCCCAGGA TCCAGTGGGG ATATTGTCAT GACACAGGCC CCACCGTCTC
 TGTCCGTCAG CCCTGGAGAG CCGGCCTCCA TCTCCTGCAC GGCCAGTCAG AGCCTCCTGC ACAGTAATGG
 GAACACCTAT TTAACCTGGT ACCGACAGAA GCCAGGCCAG TCTCCAGAGG ACCTGATCTA TGAGGTGTCC
 AACCGCTTCT CTGGCGTGTC AGACAGGTTT AGTGGCAGCG GGTACAGGAC AGATTTACC CTGAGAATCA
 GCAGAGTGGG GGCTGACGAT GCTGGAATTT ATTACTGCGG GCAGAATCTA CAGTTTCCGA TCACCTTTGG
 CAAAGGGACA CATCTGGAGA TTAAACGGAA TGATGCCAG CCAGCCGTCT AT (SEQ ID NO: 1041)

Kapa1349:

GGATCCCAG GATCCAAGTG AGGATCTTGT CTTGACACAG ACCCCACGGT CCCTGTCTGT CAGCCCTGGA
 GAGACTGCCT CCATCTCCTG CAAGGCCAGT CAGAGCCTCC TGTCTCCTGA TGGAAACACA TACTTGAATT
 GGTTCGACA GAAGCCAGGC CAGTCTCCTC AGCGTTTGAT CTATAAGGTC TCCAATAGAG ACATTGGGGT
 CCCAGACAGG TTCAGTGGCA GCGGGTCAGG GACAGATTTT ACCCTGAGAA TCAGCAGAGT GGAGGCTGAC
 GATACTGGAC TTTATTACTG TGGGCAAGTC ACACATCTTC CCATTACTTT CAGCCAGGGA ACCAACCTGG
 AGATGAAACG GAATGATGCC CAGCCAGCNG TCTAT (SEQ ID NO: 1042)

Kapa1350:

ATGAGGTT CCCTTCTCAG CTCCTGGGGC TGCTGATGCT CTGGATCCCA GGATCCAGTG AGGATCTTGT
 CTTGACACAG ACCCCACGGT CCCTGTCTGT CAGCCCTGGA GAGACTGCCT CCATCTCCTG CAAGGCCAGT
 CAGAGCCTCC TGCACAGTAA CGGGAACACC TATTTGTTTT GGTTCGACA GAAGCCAGGC CAGTCTCCAC
 AGCGTTTGAT CTATAAGGTC TCCAATAGAG ACATTGGGGT CCCAGACAGG TTCAGTGGCA GCGGGTCAGG
 GACAGATTTT ACCCTGAGAA TCAGCAGAGT GGAGGCTGAC GATACTGGAC TTTATTACTG TGGGCAAGTC
 ACATATCTTC CCATTACTTT CAGCCAAGGA ACCAACCTGG AGATGAAACG GAATGATGCC CAGCCAGCCG
 TCTAT (SEQ ID NO: 1043)

Kapa1353:

ATG AGGTTCCCTT CTCAGCTCCT GGGGCTGCTG ATGCTCTGGA TCCCAGGATC CAGTGGGGAT
 ATCGTCATGA CACAGACCCC ACTGTCCCTG TCCGTCAGCC CTGGAGAGCC GGCCTCCATC TCCTGCAAGG
 CCAGTCAGAG CCTCCTGCAC AGTAATGGAA ACACCAATTT ATATTGGTAC CTGCAAAAGC CAGGCCAGTC
 TCCACAACTT CTGATCTACT TGGTTTCCAA CCGCTTCACT GCGGTGTGAG ACAGGTTTAT TGGCAGCGGG
 TCAGGGACAG ATTTACCCCT GAGAATCAGC AGAGTGGAGG CTAACGATAC TGGAGTTTAT TACTGCGGAC
 AAGGTATATA TTTTCCGTTT GCTTTTGGCC AAGGGACCAA ACTGGAGATC AAACGGAATG ATGCCAGCC
 AGCCGTCTAT (SEQ ID NO: 1044)

Kapa1354:

CCACCGTCC CTGTCTGTCA GCCCTAGAGA GCCGGCCTCC ATCTCCTGCA GGGCCAGTCA GAGCCTCCTG
 CACAGTAACG GGAACACCTA TTTGAATTGG TACCTGCAAA AGCCAGGCCA GTCTCCACAG CTTCTGATCT
 ACTTGTTTTT CAACCGCTTC ACTGGCGTGT CAGACAGGTT CAGTGGCAGC GGGTCAGGGA CAGATTTTAC
 CCTGAGAATC AGCAGAGTGG AGGCTGACGA TANTGGAGTC TATTACTGCG GGCAAGGTAC ACAGGTTTCT
 TATACTTTCA GCCAGGGAAC CAGGCTGGAG ATAAAAAGGA ATGATGCCCA GCCAGCCGTC TAT
 (SEQ ID NO: 1045)

Kapa1356:

ATGAGGT TCCCATCTCA GCTCCTGGGG CTGCTGATGC TCTGGATCCC AGGATCCAGT GAGGATCTTG
 TCTTGACACA GACCCACGGT TCCCTGTCTG TCAGCCCTGG AGAGACTGCC TCCATCTCCT GCAAGGCCAG
 TCAGAGCCTC CTGTCTCCTG ATGGAAACAC ATACTTGAAT TGGTTCCGAC AGAAGCCAGG CCAGTCTCCT
 CAGCGTTTGA TCTATAAGGT CTCCAATAGA GACATTGGGG TCCCAGACAG GTTCAGTGGC AGCGGGTCAG
 GGACAGATTT CACCCTGAGA ATCAGCAGAG TGGAGGCTGA CGATACTGGA CTTTATTACT GTGGGCAAGT
 CACATATCTT CCCATTACTT TCAGCCAGGG AACCAACCTG GAGATGAAAC GGAATGATGC CCAGCCAGCC
 GTCTAT (SEQ ID NO: 1046)

Kapa1360:

ATGAGGTTC CCATCTCAGC TCCTGGGGCT GNTGATGCTC TGGATCCCAG GATCCAGTGA GGATCTTGTC
 TTGACACAGA CCCACGGTC CCTGTCTGTC AGCCCTGGAG AGACTGCCTC CATCTCCTGC AAGGCCAGTC
 AGAGCCTCCT GTCTCCTGAT GGAAACACAT ACTTGAATTG GTTCCGACAG AAGCCAGGCC AGTCTCCTCA
 GCGTTTGATC TATAAGGTCT CCAATAGAGA CATTGGGGTC CCAGACAGGT TCAGTGGCAG CGGGTCAGGG
 ACAGATTTCA CCCTGAGAAT CAGCAGAGTG GAGGCTGACG ATACTGGACT TTATTACTGT GGGCAAGTCA
 CACATCTTCC CATTACTTTC AGCCAGGGAA CCAACCTGGA GATGAAACGG AATGATGCCC AGCCAGCCGT
 CTAT (SEQ ID NO: 1047)

Kapa1361:

TGGATCCCAG GATCCAGTGA GGATCTTGTC TTGACACAGA CCCACGGTC CCTGTCTGTC AGCCCTGGAG
 AGACTGCCTC CATCTCCTGC AAGGCCAGTC AGAGCCTCCT GTCTCCTGAT GGAAACACAT ACTTGAATTG
 GTTCCGACAG AAGCCAGGCC AGTCTCCTCA GCGTTTGATC TATAAGGTCT CCAATAGAGA CATTGGGGTC
 CCAGACAGGT TCAGTGGCAG CGGGTCAGGG ACAGATTTCA CCCTGAGAAT CAGCAGAGTG GAGGCTGACG
 ATACTGGACT TTATTACTGT GGGCAAGTCA CATATCTTCC CATTACTTTC AGCCAGGGAA CCAACCTGGA
 GATGAAACGG AATGATGCCC AGCCAGCCGT CTAT (SEQ ID NO: 1048)

Kapa1362:

ATGAGG TTCCCTTCTC AGCTCCTGGG GCTGCTGATG CTCTGGATCC CAGGATCCAG TGGGGATATT
 GTCATGACAC AGACCCCACC GTCCCTGTCT GTCAGCCCTG GAGAGCCGGC CTCCATCTCC TGCAAGGCCA
 GTCAGAGCCT CCTGTACCCT AATGGAAATA CCTATTTGTA TTGGTATTTG CAAAAGCCAG GCCAGTCTCC
 ACAGCTTCTG ATCTACTTGG TTTCCAATCG CTTCACTGGC GTGTCAGACA GGTTCACTGG CAGCGGGTCA
 GGGACAGATT TCACCCTGCG AATTAGCAGA GTGGAGGCTA ACGATACTGG AGTTTATTAC TCGGACAAG
 GTACATATTT TCCGTTGCT TTTGGCCAAG GGACCAAACCT GGAGATCAAA CGGAATGATG CCCAGCCAGC
 CGTCTAT (SEQ ID NO: 1049)

Kapa1363:

TCTCAGCTC CTGGGGCTGC TGATGCTCTG GATCCCAGGA TCCAGTGGGG ATATTGTCAT GACACAGACC
 CCACTGTCCC TGTCTGTCAG CCCTGGAGAG ACTGCCTCCA TCTCCTGCAA GGCCAGTCAG AGCCTCCTCT
 ACAGTAATGG AAACACGTAT TTGAGTTGGT TCCGACAGAA GCCAGGCCAG TCTCCACAGC GTTTGATCTA
 TAAGGTCTCC AACAGAGACC CTGGGGTCCC AGACAGATTC AGTGGCAGCG GGTCAGGGAC AGACTTCACC
 CTGAGAATCA GCAGAGTGGA GGCTGACGAT ACTGGAGTTT ATTTTTCGG CCAAGGTATA CAGTCTCCTT
 TTAATTTTTCAG CCAGGGAACC AACCTGGAGA TAAAACGGAA TGATGCCAG CCAGCCGTCT AT
 (SEQ ID NO: 1050)

Kapa1366:

A TGAGGTTCCC ATCTCAGCTC CTGGGGCTGC TGATGCTCTG GATCCCAGGA TCCAGTGAGG
 ATCTTGTCTT GACACAGACC CCACGGTCCC TGTCTGTCAG CCCTGGAGAG ACTGCCTCCA TCTCCTGCAA
 GGCCAGTCAG AGCCTCCTGT CTCCTGATGG AAACACATAC TTGAATTGGT TCCGACAGAA GCCAGGCCAG
 TCTCCTCAGC GTTTGATCTA TAAGGTCTCC AATAGAGACA TTGGGGTCCC AGACAGGTTC AGTGGCAGCG
 GGTCAGGGAC AGATTTTACC CTGAGAATCA GCAGAGTGGA GGCTGACGAT ACTGGACTTT ATTACTGTGG
 GCAAGTCACA TATCTTCCCA TTAATTTTTCAG CCAGGGAACC AACCTGGAGA TGAAACGGAA TGATGCCAG
 CCAGCCGTCT AT (SEQ ID NO: 1051)

Kapa1370:

ATGAGGT TCCCTTCTCA GCTCCTGGGG CTGCTGATGC TCTGGATCCC AGGATCCAGT GGGGATATCG
 TCATGACACA GACCCCACTG TCCCTGTCTG TCAGCCCTGG AGAGACTGCC TCCATCTCCT GCAAGGCCGG
 TCAGAGCCTC CTCTACAGTA ATGGAAACAC GTATTTGAGT TGGTTCCGAC AGAAGCCAGG CCAGTCTCCA
 CAGCGTTTGA TCTTTGAGGT CTCCAACAGA GACACTGGGG TCCCGGACAG GTTCGCTGGC AGCGGGTCAG
 GGACAGATTT CACCCTGAGA ATCAGCAGAG TGGAGGCTGA CGATACTGGA ATTTATTACT GCGGGCAAGG
 TATACAGTTT CCTCGGACGT TCGGACCAGG AGCCAAGGTG GAACTCAAAC GGAATGATGC CCAGCCAGCC
 GTCTAT (SEQ ID NO: 1052)

Kapa1371:

CTCAGCTCCT GGGGGCTGCT TGATGTCTGG ATCCCAGGAT CCAGTGGGGA TATCGTCATG ACACAGACCC
 CACTGTCCCT GTCCGTCAGC CCTGGAGAGC CGGCCTCCAT CTCCTGCAAG GCCAGTCAGA GCCTCCTGCA
 CAGTAACGGG AACACCTATT TGTTTGGTT TCGACAGAAG CCAGGCCAGT CTCCACAGCG TTTGATCTAT
 AAGGTCTCCA ACAGAGACCC TGGGGTCCCA GACAGGTTCA GTGGCAGCGG GTCAGGGACA GATTTTACCC
 TGAGAATCAG CAGAGTGAGG GCTGACGATA CTGGAGTTTA CTACTGCGGG CAAGGTATAC AGTTTCTCA
 TACTTTTTCAG CAGGGAACCA AGCTGGTGAT AAAACGGAAT GATGCCAGC CAGCCGTCTA T
 (SEQ ID NO: 1053)

Kapa2420:

TTCCCTGGA TCCAGTGGGG ATATCGTCAT GACGCAGACC CCACTGTCCC TGTCTGTCAG CCCTGGAGAG
 CCGGCCTCCA TCTCCTGCAAG GGCCAGTCAG AGCCTCCTGC ACAGTAATGG GAACACCTAT TTCGCTTGGT
 TCCAACAGAA GCCAGGCCAG TCTCCACAGC GTTTGATCTA TCACGTCTCC AAGAGAGACC CTGGGGTTCC
 AGACAGGTTC AGTGGCAGCG GGTCAGGGAC AGATTGCACC CTGACAATTA GCAGAGTGGA GGCTGATGGT
 GCTGGAGTTT ATTACTGCGG GCAAGGTATA CAAGATCCGT TCACTTTTGG CCAAGGGACC AAACCTGGAGA
 TCAAACGGAA TGATGCCAG CCAGCCGTCT AT (SEQ ID NO: 1054)

Kapa2422:

ATGA GGTTCCTTC TCAGCTCCTG GGGCTGCTGA TGCTCTGGAT CCCAGGATCC GGTGGGGATA
 TTGTCATGAC ACAGACCCCA CCGTCCCTGT CTGTCAGCCC TGGAGAGCCG GCCTCCATCT CCTGCAAGGC
 CAGTCAGAGC CTCCTGTACC CTAATGGAAA TACCTATTTG TATTGGTATT TGCAAAAGCC AGGCCAGTCT
 CCTCAGCGTT TGATCTATAA GGTCTCCAAT AGAGACATTG GGGTCCCAGA CAGGTTTCACT GGCAGCGGGT
 CAGGGACAGA TTTACCCCTG AGAATCAGCA GAGTGGAGGC TGACGATACT GGAATTTATT ACTGTGGGCA
 AGTCACATAT CTTCCCATTA CTTTCAGCCA GGAACCAAC CTGGAGATGA AACGGAATGA TGCCAGCCA
 GCCGTCTAT (SEQ ID NO: 1055)

Kapa2423:

GCTCCTGGGG CTGCTGATGC TCTGGATCCC AGGATCCGGT GGGGATATTG TCATGACACA GACCCACCG
 TCCCTGTCTG TCAGCCCTGG AGAGCCGGCC TCCATCTCCT GCAAGCCAGT CAGAGCCTCC TGCACAGTAA
 TGGGAACACC TATTTCGCTT GGTTCACAACA GAAGCCAGGC CAGTCTCCAC AGCGTTTGAT CTATCACGTC
 TCCAAGAGAC ACCCTGGGGT TCCAGACAGG TTCAGTGGCA GCGGGTCAGG GACAGATTGC ACCCTGACAA
 TTAGCAGAGT GGAGGCTGAT GATGCTGGAG TTTATTGCTG CGGGCAAGGT ATACAAGATC CGTTCACTTT
 TGGCCAAGGG ACCNAACTGG AGATCAAACG GAATGATGCC CAGCCAGCCG TCTAT (SEQ ID NO:
 1056)

Kapa2425:

ATGAGG TTCCCTTCTC AGCTCCTGGG GCTGCTGATG CTCTGGATCC CAGGATCCGG TGGGGATATT
 GTCATGACAC AGACCCACAC GTCCCTGTCT GTCAGCCCTG GAGAGCCGGC CTCCATCTCC TGCAAGGCCA
 GTCAGAGCCT CCTGTACCTT AATGGAAATA CCTATTTGTA TTGGTATTTG CAAAAGCCAG GCCAGTCTCC
 ACAGCTTCTG ATCTACTTGG TTTCCAATCG CTTCACTGGC GTGTCAGACA GGTTCACTGG CAGCGGGTCA
 GGGACAGATT TCACCCTGCG AATTAGCAGA GTGGAGGCTA ACGATACTGG AGTTTATTAC TGCGGACAAG
 GTTCATATTT TCCGTTCGCT TTTGGCCAAG GGACCAAACCT GGAGATCAAA CGGAATGATG CCCAGCTAGC
 CGTCTAT (SEQ ID NO: 1057)

Kapa2426:

ATGAGG TTCCCATCTC AGCTCCTGGG GCTGCTGATG CTCTGGATCC CAGGATCCAG TGAGGATCTT
 GTCTTGACAC AGACCCACAG GTCCCTGTCT GTCAGCCCTG GAGAGACTGC CTCCATCTCC TGCAAGGCCA
 GTCAGAGCCT CCTGTCTCCT GATGGAAACA CATACTTGAA TTGGTTCCGA CAGAAGCCAG GCCAGTCTCC
 TCAGCGTTTG ATCTATAAGG TCTCCAATAG AGACATTGGG GTCCCAGACA GGTTCACTGG CAGCGGGTCA
 GGGACAGATT TCACCCTGAG AATCAGCAGA GTGGAGGCTG ACGATACTGG ACTTTATTAC TGTGGGCAAG
 TCACATATCT TCCCATTACT TTCAGCCAGG GAACCAACCT GGGGATGAAA CGGAATGATG CCCAGCCAGC
 CGTCTAT (SEQ ID NO: 1058)

Kapa2427:

ATGAG GTTCCCTTCT CAGCTCCTGG GGCTGCTGAT GCTCTGGATC CCAGGATCCA GTGGGGATAT
 TGTCATGACA CAGGCCCCAC CGTCTCTGTC CGTCAGCCCT GGAGAGCCGG CCTCCATCTC CTGCAAGGCC
 AGTCAGAGCC TCCTGTACAG TAATGGGAAC ACGCATTTGT ATTGGTTCCG ACAGAAGCCA GGCCAGTCTC
 CAGAGGGCCT GATCTATAGG GTGTCCAAGC GCTTCACTGG CGTGTCAAGC AGGTTCACTG GCAGCGGGTC
 AGGGACAGAT TTCACCCTGG AAATCAGCAG AGTGGAGGCT GACGATGTTG GAGTTTATTA CTGCGGGCAA
 AATTTACAGC CTCCTTATAC TTTTCAAGCAG GGAACCAAGC TGGAAATAAA ACGGAATGAT GCCCAGCCAG
 CCGTCTAT (SEQ ID NO: 1059)

Kapa2430:

ATGAG GTTCCCTTCT CAGCTCCTGG GGCTGCTGAT GCTCTGGATC CCAGGATCCG GTGGGGATAT
 TGTCATGACA CAGACCCAC CGTCCCTGTC TGTCAGCCCT GGAGAGCCGG CCTCCATCTC CTGCAAGGCC
 AGTCAGAGCC TCCTGTACCC TAATGGAAAT ACCTATTTGT ATTGGTATTT GCAAAAGCCA GGCCAGTCTC
 CACAGCTTCT GATCTACTTG GTTTCCAATC GCTTCACTGG CGTGTCAAGC AGGTTCACTG GCAGCGGGTC
 AGGGACAGAT TTCACCCTGC GAATTAGCAG AGTGGAGGCT AACGATACTG GAGTTTATTA CTGCGGACAA
 GGTACATATT TTCCGTTCGC TTTTGGCCAA GGGACCAAAC TGGAGATCAA ACGGAATGAT GCCCAGCCAG
 CCGTCTAT (SEQ ID NO: 1060)

Kapa2431:

TCGTCTCTG TCCGTCAGTC CTGGAGAGCC GGCCTCCATC TCCTGTAAGG CCAGTCAGAG CCTCCTGTCT
 AGTAATGGGA ACACCTATTT ATATTGGATC CGACAGAAGC CAGGCCAGTC TCCAGAGGGC CTGATCTACA
 AGGTGTCCAA CCGCTTCACT GCGGTGTCAG ACAGGTTTCA TGGCAGCGGA TCAGGAACAG ATTTACCCCT
 GAGAATCACC AGAGTGGAGG CTGACGATGC TGGAGTTTAT TACTGCGGGC AGAATTTCCG GTTTCCTTAT
 ACTCTCAGCC AGGGAACCAA ACTGGAGATA GAACGGAATG ATGCCAGCC AGCCGTCTAT
 (SEQ ID NO: 1061)

Kapa2432:

ATG AGGTTCCCTT CTCAGCTCCT GGGGCTGCTG ATGCTCTGGA TCCCAGGATC CCGTGGGGAT
 ATTGTCATGA CACAGACCCC ACCGTCCCTG TCTGTCAGCC CTGGAGAGCC GGCCTCCATC TCCTGCAAGG
 CCAGTCAGAG CCTCCTGTAC AGTAATGGGA ACACGCATTT GTATTGGTTC CGACAGAAGC CAGGCCAGTC
 TCCAGAGGGC CTGATCTATA GGGTGTCCAA GCGCTTCACT GCGGTGTCAG AAAGGTTTCA TGGCAGCGGG
 TCAGGGACAG ATTTACCCCT GGAAATCAGC AGAGTGGGGG CTGACGATGT TGGAGTTTAT TACTGCGGGC
 AAAATTTACA GCCTCCTTAT ACTTTCAGCC AGGGAACCAA GCTGGAAATA AAACGGAATG ATGCCAGCC
 AGCCGTCTAT (SEQ ID NO: 1062)

Kapa2435:

ATGAGGT TCCCATCTCA GCTCCTGGGG CTGCTGATGC TCTGGATCCC AGGATCCAGT GAGGATCTTG
TCTTGACACA GACCCACCGG TCCCTGTCTG TCAGCCCTGG AGAGACTGCC TCCATCTCCT GCAAGGCCAG
TCAGAGCCTC CTGTCTCCTG ATGGAAACAC ATACTTGAAT TGGTTCCGAC AGAAGCCAGG CCAGTCTCCT
CAGCGTTTGA TCTATAAGGT CTCCAATAGA GACATTGGGG TCCCAGACAG GTTCAGTGGC AGCGGGTCAG
GGACAGATTT CACCCTGAGA ATCAGCAGAG TGGAGGCTGA CGATACTGGA CTTTATTACT GTGGGCAAGT
CACATATCTT CCCATTACTT TCAGCCAGGG AACCAACCTG GAGATGAAAC GGAATGATGC CCAGCCAGCC
GTCTAT (SEQ ID NO: 1063)

Kapa2436:

AT GAGGTTCCCT TCTCAGCTCC TGGGGCTGCT GATGCTCTGG ATCCCAGGAT CCGGTGGGGA
TATTGTCATG ACACAGACCC CACCGTCCCT GTCTGTCAGC CCTGNAGAGC CGGCCTCCAT CTCCTGCAAG
GCCAGTCAGA GCCCCCTGTA CCCTAATGGA AATACCTATT TGTATTGGTA TTTGCAAAAG CCAGGCCAGT
CTCCACAGCT TCTGATCTAC TTGGTTTCCA ATCGCTTCAC TGGCGTGTCA GACAGGTTCA GTGGCAGCGG
GTCAGGGACA GATTTCACCC TGCGAATTAG CAGAGTGGAG GCTAACGATA CTGGAGTTTA TTA CTGCGGA
CAAGGTACAT ATTTTCCGTT CGCTTTTGGC CAAGGGACCA AACTGGAGAT CAAACGGAAT GATGCCCAGC
CAGCCGTCTA T (SEQ ID NO: 1064)

Kapa2437:

ATGAGG TTCCCTTCTC AGCTCCTGGG GCTGCTGATG CTCTGGATCC CAGGATCCGG TGGGGATATT
GTCATGACAC AGACCCACCC GTCCCTGTCT GTCAGCCCTG GAGAGCCGGC CTCCATCTCC TGCAAGGCCA
GTCAGAGCCT CCTGTACCCT AATGGAAATA CCTATTTGTA TTGGTATTTG CAAAAGCCAG GCCAGTCTCC
ACAGCTTCTG ATCTACTTGG TTTCCAATCG CTTCACTGGC GTGTCAGACA GGTTCAGTGG CAGCGGGTCA
GGGACAGATT TCACCCTGAG AATCAGCAGA GTGGAGGCTG ACGATACTGG ACTTTATTAC TGTGGGCAAG
TCACATATCT TCCCATTACT TTCAGCCAGG GAACCAACCT GGAGATGAAA CGGAATGATG CCCAGCCAGC
CGTCTAT (SEQ ID NO: 1065)

Kapa2438:

ATGAG GTTCCCTTCT CAGCTCCTGG GGCTGCTGAT GCTCTGGATC CCAGGATCCG GTGGGGATAT
TGTCATGACA CAGACCCAC CGTCCCTGTC TGTCAGCCCT GGAGAGCCGG CCTCCATCTC CTGCAAGGCC
AGTCAGAGCC TCCTGTACCC TAATGGAAAT ACCTATTTGT ATTGGTATTT GCAAAAGCCA GGCCAGTCTC
CACAGCTTCT GATCTACTTG GTTTCCAATC GCTTCACTGG CGTGTGAGAC AGGTTCAGTG GCAGCGGGTC
AGGGACAGAT TTCACCCTGC GAATTAGCAG AGTGGAGGCT AACGATACTG GAGTTTATTA CTGCGGGCAA
GGTATACAAG ATCCGTTTAC TTTTGGCCAA GGGACCAAAC TGGAGATCAA ACGGAATGAT GCCCAGCCAG
CCGTCTAT (SEQ ID NO: 1066)

Kapa2440:

ATGA GGTTCCCTTC TCAGCTCCTG GGGCTGCTGA TGCTCTGGAT CCCAGGATCC GGTGGGGATA
TTGTCATGAC ACAGACCCCA CCGTCCCTGT CTGTCAGCCC TGGAGAGCCG GCCTCCATCT CCTGCAAGGC
CAGTCAGAGC CTCCTGTACC CTAATGGAAA TACCTATTTG TATTGGTATT TGCAAAAGCC AGGCCAGTCT
CCACAGCTTC TGATCTACTT GGTTCCTAAT CGCTTCACTG GCGTGTGAGA CAGGTTTCACT GGCAGCGGGT
CAGGGACAGA TTTCACCCTG CGAATTAGCA GAGTGGAGGC TAACGATACT GGAGTTTATT ACTGCGGACA
AGGTACATAT TTTCCGTTTC CTTTGGCCAA AGGGACCAA CTGGAGATCA AACGGAATGA TGCCAGCCA
GCCGTCTAT (SEQ ID NO: 1067)

Kapa2442:

ATGAGG TTCCCATCTC AGCTCCTGGG GCTGCTGATG CTCTGGATCC CAGGATCCAG TGAGGATCTT
GTCTTGACAC AGACCCACG GTCCCTGTCT GTCAGCCCTG GAGAGACTGC CTCCATCTCC TGCAAGGCCA
GTCAGAGCCT CCTGTCTCCT GATGGAAACA CATACTTGAA TTGGTTCCGA CAGAAGCCAG GCCAGTCTCC
TCAGCGTTTG ATCTATAAGG TCTCCAATAG AGACATTGGG GTCCAGACA GGTTCAGTGG CAGCGGGTCA
GGGACAGATT TCACCCTGAC AATCAGCAGA GTGGAGGCTG ACGATGCTGG AGTTTATTAC TGTGGCCAAG
TTCTACAGGA TCCTTATACT TTCAGCCAGG GAACCAAGCT GGAGATAAGA CGGAATGATG CCCAGCCAGC
CGTCTAT (SEQ ID NO: 1068)

Kapa2443:

GGGAACAC CTATTTGTAT TGGTTCCGAC AGAGGCCAGG CCAGTCTCCG GAGGCCCTGA TCTATAGGGT
GTCCAGCCGC TTCCCTGGCG TGTCAGACAG GTTCAGTGGC AGCGGGTCAG TGACAGATTT CACCCTGAGA
ATCAGCAGAG TGGAGGCTGA CGATGCTGGA ATTTATTACT GCGGGCAGAA TCTACAGTTT CCGATCACCT
TTGGCAAAGG GACACATCTG GAGATTAAAC GGAATGATGC CCAGCCAGCC GTCTAT (SEQ ID NO:
1069)

Kapa2444:

AGCCTCCT GCACAGTAAC GGAACACCT ATTTGTCTTG GTTTCGACAG AAGTCAGGCC AGTCTCCACA
 ACGTTTGATC TATAGGGTCT CCAACAGAGA CCCTGGGGTC CCAGACAGGT TCAGTGGCAG CGGGTCAGGG
 ACAGATTTCA CCCTGAGAAT CAGCAGAGTG GAGGCTGACG ATACTGGACT TTATTACTGT GGGCAAGTCA
 CATATCTTCC CATTACTTTC AGCCAGGGAA CCAACCTGGA GATGAAACGG AATGATGCC AGCCAGCCGT
 CTAT (SEQ ID NO: 1070)

Kapa2446:

AAGGTGTCC AACCGCTTCA GTGGCGTGTC AGAAAGGATC AGTGGCAGCG GGTCAGGGAC AGATTTACCC
 CTGAGAATCA GCAGAGTGGA GGCTGACGAT GCTGGGATTT ATTACTGCGG GCAAACCTACA CACTTTCCTT
 ATACTTTCGG CCAGGGAACC AAGCTGGAAA TAAACCGGAA TGATGCCAG CCAGCCGTCT AT
 (SEQ ID NO: 1071)

Kapa2449:

AGCCTCCTGC ACAGTAATGG GAACACCTAT TTCGCTTGGT TCCAACAGAA GCCAGGCCAG TCTCCACAGC
 GTTTGATCTA TCACGTCTCC AAGAGAGACC CTGGGGTTCC AGACAGGTTT AGTGGCAGCG GGTCAGGAAC
 AGATTGCACC CTGACAATTA GCAGAGTGGA GGCTGATGAT GCTGGAGTTT ATTACTGCGG GCAAGGTATA
 CAAGATCCGT TACTTTTGG CCAAGGGACC AACTGGAGA TCAAACGGAA TGATGCCAG CCAGCCGTCT
 AT (SEQ ID NO: 1072)

Table N₁

Other Canine Lambda Variable Sequences

 λ 103:

ATGACCT CCAACATGGC CTGGTCCCCT CTCCTCCTCA CACTCCTTCC TTACTACACA GGGTCCTGGG
 CCCAGTCTGT GCTGACTCAG CCGACCTCAG TGTCGGGGTC CCCTGGCCAG AGGGTCACCA TCTCCTGCTC
 TGAAGCACG GACAACATCG GTCTTGTTGG TGCGAGTTGG TACCAACAAC TCCCAGGAAG GGCCCTAAA
 CTCCTCCTGT ATAGTGATGG GGATCGACCG TCAGGGGTCC CTGACCGGTT TTCCGGCTCC AGGTCTGGCA
 ACTCAGCCAC CCTGGCCATC ACTGGGCTTC AGGCTGAGGA CGAGGCTGAC TATTACTGCC AGTCCTTTGA
 TTCCACGCTT GATGGTTTCG TGTTCCGCTC AGGAACCCAA CTGACCGTCC TTGGTCAGCC CAAGGCG (SEQ
 ID NO: 1073)

MTSNMAWSPL LLTLLPYTG SWAQSFLTQP TSVSGSPGQR VTISCSGSTD NIGLVGASWY QQLPGRAPKL
 LLYSDGDRPS GVPDRFSGSR SGNSATLAI GLQAEDEADY YCQSFSTLD GFVFGSGTQL TVLGQPKA
 (SEQ ID NO: 1074)

 λ 112:

ATGGACTGG GTCCCCTTTT ACCTCCTGCC CTTCATTTTC TCTACAGGTT TCTGTGCTCC TCCTGTGCTG
 ACCCAGCCTC CAAGTGCATC TGCCTCCCTG GAAGCCTCGG TCAAGCTCAC CTGCACTCTG AGCAGTGAGC
 ACAGCAGTTA CTTTATTTAC TGGTATCAAC AACAAACAAC AGAGAAGGCC CCTCGGTATC TGATGAGGGT
 TAACAGTGAT GGAAGCCACA GCAGAGGGGA CGGGATCCCC AGTCGCTTCT CAGGCTCCAG CTCTGGGGCT
 GACCGCTATT TAACCATCTC CAACATCCAG TCTGAGGATG AGGCAGATTA TTACTGTTTT ACACCTGATG
 ATAGCAATAG TGTGTTCCGC GGAGGCACCC ATCTGACCGT CCTCGGTCAG CCAAGGCC (SEQ ID NO:
 1075)

MDWVPFYLLP FIFSTGFCAP PVLTPPPSAS ASLEASVKLT CTLSEHSSY FIYWYQQQPP EKAPRYLMRV
 NSDGSLSRGD GIPSRFSGSS SGADRYLTIS NIQSEDEADY YCFTPDSSNS VFGGTHLTV LGQPKA
 (SEQ ID NO: 1076)

 λ 121:

ATGACCTCC ACCATGGCCT GGTCCCCTCT CCTCCTCACC CTCCTCGCTC ATTGCACAGT GTCCTGGGCC
 CAGGCTGTGC TGAATCAGCC ACCCTCTGTG TCTGCAGCCC TGGGGCAGAG GGTCACCATC TCCTGCACTG
 GAACTAACAC CAACATCGGC AATGGTTATG ATGTACATTG GTACCAGCAG GTCCCAGGAA AGTCCCCTAA
 AACCTTCATC TATGGTAATA ACAATCGACC CTCGGGGGTC CCGGTTTCGAT TCTCTGGCTC CAAGTCAGGC
 AGCACAGCCA CCCTGACCAT CACTGGGATC CAGGCTGAGG ATGAGACTGA TTATTACTGC CAGTCCTATG
 ATGACAACCT CGATGGTTAC GTGTTCCGCT CGGGAACCCA ACTGACCGTC CTTGGTCAGC CCAAGGCC
 (SEQ ID NO: 1077)

MTSTMAWSPL LLTLLAHCTV SWAQAFLTQP PSVSAALGQR VTISCTGTNT NIGNGYDVHW YQQVPGKSPK
 TFIYGNNNRP SGVPVRFSGS KSGSTATLTI TGIQAEDETD YYCQSYDDNL DGYVFGSGTQ LTVLGQPKA
 (SEQ ID NO: 1078)

λ202:

ATG GACTGGGTCC CCTTTTACCT CCTGCCCTTC ATTTTCTCTA CAGGTTTCTG TGCTCCTCCT
 GTGCTGACCC AGACTCCAAG TGCATCTGCC TCCCTGGAAG ACTCGGTCAA GCTCACCTGC ACTTTGAGCA
 GGGAGCACAG CACTTACTAT ATTACCTGGT ATCAACAACA ACAACCAGGG AAGGCCCTC GGTATCTGAT
 GAAGGTTAAC AGTGATGGAA GCCACAGCAG GGGAGACGGG ATCCCCAGTC GCTTCTCAGG CTCCAGCTCT
 GGGGCTGACC GCTATTTAAC CATCTCCAAC ATCCAGTCTG AGGATGAGGC AGATTATTAC TGTTTTACAC
 CCGCTAATAG CAATAGTGTG TTCGGCGGAG GCACCCATCT GACCGTCCTC GGTCAGCCCA AGGCC
 (SEQ ID NO: 1079)

MDWVPFYLLP FIFSTGFCAP PVLQTQPSAS ASLEDSVKLT CTLSREHSTY YITWYQQQQP GKAPRYLMKV
 NSDGSHSRGD GIPSRFSGSS SGADRYLTIS NIQSEDEADY YCFTPANSNS VFGGGTHLTV LGQPKA
 (SEQ ID NO: 1080)

λ323:

TCCTGGGCCC AGTCTGTGCT GACTCAGCCG GCCTCTGTGT CTGGGTCCCT GGGCCAGAGG GTCGCCATCT
 CCTGCACTGG AAGCAGCTCC AATGTTGGTT TTGGCCCTTA TTTGGGCTGG TACCAACAGG TCCCAGGAGC
 AGGCCCCAGA ACCCTCATGT ATCGTATTAG TCGCCGCCCC TCGGGGGTCC CTGATCGATT CTCTGGCTCC
 AGGTCAGGCA ACACAGCAAC CCTGACCATC TCTGGCCTCC AGCCTGATGA TGAGGGCGAT TATTACTGCT
 CATCCTATGA CACCAGTCTC AGTGCATTG TGTTCGGCGG AGGCACCCAC CTGACCGTTG TC
 (SEQ ID NO: 1081)

SWAQSULTQP ASVSGSLGQR VAISCTGSSS NVGFGPYLGW YQVPGAGPR TLMYRISRRP SGVPDRFSGS
 RSGNTATLTI SGLQPDDEGD YYCSSYDTSL SAIVFGGGTH LTVV (SEQ ID NO: 1082)

λ115:

ATGACCTCCA CCATGGGCTG GTTCCCTCTC CTCCTCACCA TCCTCGCTCA CTGCACAGGG TCCTGGGCCC
 AGTCTGTGCT GAGTCAGCCG GCCTCAGTGT CCGGGTCCCT GGGCCAGAGG GTCACCATCT CCTGCACTGG
 AAGCAGCTCC AACATCGGTA GAGGTTATGT GGGCTGGTAC CAACAGCTCC CGGGAACAGG CCCANAACC
 CTCATCTTTG GTCCTAATAA GCGACCCTCA GGGGTCCCCG ATCGCTTCTC TGGCTCCAGG TCGGACAGCA
 CAGGCACCCCT GACCATCTCT GGGCTCCAGG CTGAGGATGA GGGTGATTAT TACTGCTCAT CGTGGGACAC
 CACTCTCAGT GCTTACGTGT TCGGCTCAGG GACCCAACTG ACCGTTCTTG GTCAGCCCAA GGCC
 (SEQ ID NO: 1083)

MTSTMGWFP LLLILAHCTG SWAQSULSQP ASVSGSLGQR VTISCTGSSS NIGRGYVGWY QQLPGTGPXT
 LIFGPNKRPS GVPDRFSGSR SDSTGTLTIS GLQAEDEGDY YCSSWDTTLS AYVFGSGTQL TVLGQPKA
 (SEQ ID NO: 1084)

λ116:

ACCATCCTCG CTCACTGCAC AGGGTCCTGG GCCAGTNTC TACTGACTCA GCCGGCCTCA GTGTCCGGGT
 CCCTGGGCCA GAGGGTCACC CTNTCCTGCA CTGGAAGCGG CTCCAACATC GGTAGAGGTT ATGTGGGCTG
 GTACCAACAC CTCCCGGGGA CAGGCCCCAG AACCTCATC TATGGTGATA TTAACCGACC CTCAGGGGTC
 CCCGATCGGT TCTCTGGCTC CAGGTCAGGC ATCACAGCCA CCCTGACCAT CTCTGGGCTC CAGGCTGAGG
 ATGAGGCTGA TTATTACTGN TCATCGTGGG ACTACAGTCT CAGTANTACT TTGTTCCGGC GAGGCACCCA
 CCTGACCGTN CTCGGTCAGC CCAAGGCC (SEQ ID NO: 1085)

TILAHCTGSW AQXLLTQPAS VSGSLGQRTV LSCTGSGSNI GRGYVGWYQH LPGTGPRTL I YGDINRPSGV
 PDRFSGSRSG ITATLTISGL QAEDEADYYX SSWDYSLSXT LFGGGTHLTV LGQPKA (SEQ ID NO:
 1086)

λ205:

GCTGATTAT TACTGTTTCTG CATATGACAG CAATCTCAGT GGTGTCCTGT TCGGCTCAGG AACCCAACTG
 ACCGTCCTTG GTCAGCCCAA GGCC (SEQ ID NO: 1087)

ADYYCSAYDS NLSGVLFSGS TQLTVLGQPK A (SEQ ID NO: 1088)

λ222:

AT GGCCTGGTCC CCTCTCCTCC TCACACTCCT TCCTTACTGC ACAGGGTCCT GGGGNGAGTC
 TATACTGACT CAGCCGACCT CACTGTCCGG GTCCCCCTGGC CAAAGGGTCA CCATTTCCCTG CTCTGGAGGC
 ACGAGCAACG TCGTCATTGT CCGTGCGAGT TGGTACCAAC AGGTCCCAGG AAAGGCCCTT AACTTCTCG
 TTTACAGTAA TGGGGATCGA CCGTCAGGGG TCCCTGACCG GTTTTCCGGC TCCAAGTCTG GCAACTCAGC
 CACCCTGACC ATCACTGGAC TTCAGGCTGA GGACGAGGCT GATTATTACT GCCAGTCCTT TGATACCACG
 CTTTCATGTTT ATCTGTTCGG CGGAGGCACC TATCTGACCG TCCTCGGTCA GCCCAAGGCC
 (SEQ ID NO: 1089)

MAWSPLLLTL LPYCTGSWGX SILTQPTSLS GSPGQRTVIS CSGGTSNVVI VGASWYQQVP GKAPKLLVYS
 NGDRPSGVPD RFSGSKSGNS ATLTITGLQA EDEADYYCQS FDTTLHVHLF GGGTYLTVLG QPKA
 (SEQ ID NO: 1090)

λ232:

ATGACCTCCA CCATGGGCTG GTCCCCCTCTC CTCCTTACCC TCCTCGCTCA CTGCACAGGN TCCTGGGCCC
 AGTCTGTGCT GACTCAGCCG GCCTCAGTGA CTGGGTCCCT GGGCCAGAGG GTCACCATCT CCTGCACTGG
 AAGCAGCTCC AACATCGGTG GATATAATGT TGGCTGGTTC CAGCAGCTCC CGGGAATAGG CCCCAGAACC
 GTCATCTATA GTAGTAGTAA GCGACCCTCG GGGGTCCCGG ATCGATTCTC TGGCTCCAGG TCAGGCAGCA
 CAGCCACCCT GACCATCTCT GGGCTCCAGG CTGAGGACGA GGCTGAGTAT TACTGCTCAA CATGGGACAC
 CAGTCTCAA GGTATTGTGT TCGGCGGAGG CACCCATCTG ACCGTCCTCG GTCAAGCCCA
 (SEQ ID NO: 1091)

MTSTMGWSPL LLTLLAHCTG SWAQSVLTQP ASVTGSLGQR VTISCTGSSS NIGGYNVGWF QQLPGIGPRT
 VIYSSSKRPS GVPDRFSGSR SGSTATLTIS GLQAEDEAEY YCSTWDTSLK GIVFGGGTHL TVLGQA
 (SEQ ID NO: 1092)

λ312:

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 GACTCAACCT TCCTCGGTGT CTGGGACTTT GGGCCANACT GTCACCATCT CCTGTGATGG GAACAACAAT
 AACATTGGCA ATAGTGATTA TATCGAATGG TACCAGCAGT TCCCAGGCAC CTCCCCCAA CTCCTGATTT
 ACTATGTCAA TAGGCGGCCA TCAGGGATCC CTACTCGCTT CTCTGCCTCC AAGTCTGGGA ACACGGCCTC
 CTTGACCATC TCTGGGCTCC AGGCTGAAGA TGAGGCTGAT TATTACTGCA ACTCTTATAT TGGCGATGAG
 GCTATGTTTCG GCGGAGGCAC TCACCTGACC GTCCTCGGTC AGCCCAAGGC C (SEQ ID NO: 1093)

MAWTLVLLTF LSQGTGSWAQ SALTQPSVS GTLGXTVTIS CDGNNNNIGN SDYIEWYQQF PGTSPKLLIY
 YVNRPSGIP TRFSASKSGN TASLTISGLQ AEDEADYYCN SYIGDEAMFG GGTHLTVLGQ PKA
 (SEQ ID NO: 1094)

λ217:

ATGACCT CCACCATGGC CTGGTCCCCT CTCCTCCTCA CCCTCCTCGC TCATTGCACA GTGTCTTGGG
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 TGAAGTGAC ACCAACATCG GCGGTTATGA TGTACAATGG TACCAGCAGG TCCCAGGAGA GTCCCCTAAA
 ACTATCATCC GTGCTAATAC CAATCGACCC TCGGGGGTCC CGGTTGATT CTCTGGCTCC AGGTCAGGCA
 CCACAGCCAC CCTGACCATC ACTGGTATCC AGGCTGAGGA TGAGGCTGAT TATTACTGTC AGTCCTATGA
 TGACAAGTCC GATGCTCTTG TGTTCGGCGG AGGCACCCAT CTGACCGTCC TCGGTCAGCC CAAGGCC GG
 (SEQ ID NO: 1095)

MTSTMAWSPL LLTLLAHCTV SWQAVLTQS PSVSAALGQR VSISCTGSDT NIGGYDVQWY QQVPGESPKT
 IIRANTNRPS GVPVRFSGSR SGTATLTIT GIQAEDEADY YCQSYDDKSD ALVFGGGTHL TVLGQPKA
 (SEQ ID NO: 1096)

L201-79:

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 GTCGTGATCC AGGACCCATC AGTCTCGGTG TCTCCAGGAG GGACAGTCAC ACTCACATGT GGCCTCAACT
 GTGGGTCACT CTCTACAAAT AATTTCCCTG GCTGGTACCA GCAGACCCTA GGCCGGGCTC CTCGCACGAT
 TATCTTCAA ACAAATAGCC GCCCTCTGG GGTCCCTGAT CGCTTCTNTG GAGCCTTNTC TGACAACAAA
 GCTGTCCTTA CCATCACAGG AGTCCAGCCT GAGGACGAGG NTGACTATCA CTGTTCTTTC NATTTGGGTA
 GTTATACTAT ATTCGGCGGA GGCACCCACT TGACCGTCCT C (SEQ ID NO: 1097)

MAXTLLLLVL LAYGSGADSQ TVVIQDPSVS VSPGGTVTLT CGLNCGSLST NNFPGWYQQT LGRAPRTIIF
 KTNSRPSGVP DRFXGAXSDN KAVLTITGVQ PEDEXDYHCS FXLGSYTIFG GGTHLTVL (SEQ ID NO: 1098)

L213-79:

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 CCAACAACCTC CCAGGGACAG GTCCCAAAAC CCTCATCTAT GATACTCGTA GGCGACCCTC GGGGATTCCCT
 GATCGATTCT CTGGGTCCAG GTCAGGCAGC ACAGCGACCC TGACCATCTC TGGACTCCAG GCTGAGGATG
 AGGCCGATTA TTACTGTGCA TCCTATGACC GTACTATCGG TGGTGGTGCT GTGTTCGGCG GAGGCACCCA
 CCTGACCGTC CTCGGTCAGC CCAAGGCC (SEQ ID NO: 1099)

QTVTISCTGS SSNVGYGDYA GWYQQLPGTG PKTLIYDTRR RPSGIPDRFS GSRSGSTATL TISGLQAEDE
 ADYYCASYDR TIGGGAVFVG GTHLTVLGQP KA (SEQ ID NO: 1100)

L1-708:

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 GGGGAGACAG CATTGGAAGT AAAAGTGCTC AATGGTACCA GCAGAAGCCG GGCCAGCCCC CCGTGCTCAT
 TATCTATGGT GATAGCAGCA GGCCGTCAGG GATCCCTGAG CGATTCTCTG GCGCCAACCTC GGGGAACACG
 GCCACCCTGA CCATCAGCGG GGCCCTGGCC GAGGACGAGG CTGACTATTA CTGCCAGGTG TGGGACCGCA
 GTGCTTACGT GTTCGGCTCA GGAACCCAAC TGACCGTCCT TGGTCAGCCC AAGGCC (SEQ ID NO:
 1101)

ASYVLSQPPS ATVTLRQTAR LTCGGDSIGS KSAQWYQKP GQPPVLIYD DSSRPSGIPE RFSGANSNT
 ATLTISGALA EDEADYYCQV WDRSAYVFGS GTQLTVLGQP KA (SEQ ID NO: 1102)

L1-712:

TGGTACCAG CAGTTCACAG GAACAGGCCC CAGAACCCTC ATCTATGATA CTAGTAGCCG ACCCTCGGGG
 GTCCCTGATC GAATCTCTGG CTCCAGGTCA GGCAGCACAG CAACACTGAC CATTTCTGGG CTCCAGGCTG
 AGGACGAGGC TGATTATTAC TGCTCAGCAT ATGACAACAG TCTCATTGCT GGTATGTTTCG GCGGAGGCAC
 CCACCTGACC GTCCTCGGTC AGCCCAAGGC C (SEQ ID NO: 1103)

WYQQFTGTGP RTLIYDTSSR PSGVPDRISG SRSGSTATLT ISGLQAEDEA DYYCSAYDNS LIAGMFGGGT
 HLTVLGQPKA (SEQ ID NO: 1104)

L1-719:

GCGGTTTC TCAGACTGTG CTAACCCAGG AGCCATCACT CTCAGTGTCT CCAGGAGGGA CAGTCACACT
 CACATGTGGC CTCAGTCTG GGTCACTCTC TACAAGTAAT TACCCTGGCT GGTACCAGCA GACCCTGGGC
 CGGGCTCCTC GCACGATTAT CTACAGAACA AGCAGCCGCC CCTCTGGGGT CCCTGATCGC TTCTCTGGAT
 CCATCTCTGG GAACACAGCC GCCCTACCA TCACAGGAGC CCAGCCTGAG GACGAGGCTG ACTATTACTG
 TTCCTTCTAT ATGGGTGATT ACACTACTCT GTTCGGCGGA GGCACCCACC TGACCGTCCT CGGTCAGCCC
 AAGGCC (SEQ ID NO: 1105)

AVSQTVLTQE PSLSVSPGGT VTLTCGLSSG SVSTSNYPGW YQOTLGRAPR TIIYRTSSRP SGVPDRFSGS
 ISGNTAALTI TGAQPEDEAD YYCSFYMGDY TTLFGGGTHL TVLGQPKA (SEQ ID NO: 1106)

L1-722:

A TGGCCTGGAC CCATCTCCTG CTCCCCGTGC TCACTCTCTG CACAGGCTCC GTGGCCTCCA
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 GAGTCTGAGT AAATATTATG CACAATGGTT CCAGCAGAAG GCAGGCCAAG CCCCTGTGTT GGTACATATAT
 AAGGACACTG AGCGGCCCTC TGGGATCCCT GACCGATTCT CTGGCTCCAG TTCAGGGAAC ACACACACCC
 TGACCATCAG CGGGGCTCGG GCCGAGGACG AGGCTGACTA TTACTGCGAG TCAGCAGTCA GTACTGATAC
 TGCTGTGTTT GCGGAGGCA CCCACCTGAC CGTCCTCGGT CAGCCCAAGG CC (SEQ ID NO: 1107)

MAWTHLLLPV LTLCTGSVAS SVVTQPPSVS VSLGQTATIS CSGESLSKYY AQWFQKAGQ APVLVIYKDT
 ERPSGIPDRF SGSSSGNTHT LTISGARAED EADYYCESAV STDTAVFGGG THLTVLGQPK A
 (SEQ ID NO: 1108)

L1-724:

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 TATCAACAAC AACACCCAGG GAGGGCCCCCT CGATATCTGA TGAAGATTAA CTTTGATGGG GAGCACACCA
 GGGGAGACGG GATCCCTAGT CGCTTCTCAG GCTCCAGCTC TGGGTCTGAC CGCTATTTAA CCATCTCCAA
 CATCCAGTCT GAGGATGAGG CAGATTATTT CTGTTTTACA CCCGCTAGTA CCAACAGTGT TTTCGGCGGA
 GGCACCCATC TGACCGTCCT CGGTCAGCCC AAGGCC (SEQ ID NO: 1109)

LPAASVNLTC TLSSEHISYF IIWYQQQHPG RAPRYLMKIN FDGEHTRGDG IPSRFSGSSS GSDRYLTISN
 IQSEDEADYF CFTPASTNSV FGGGTHLTVL GQPKA (SEQ ID NO: 1110)

L1-725:

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 CTCAGCCTCC CTCGGTATCA GTGTCTCTGG GACAGACAGC AACCATCTCC TGCTCTGGAG AGAGTCTGAG
 TAAATATTAT GCACAATGGT TCCAGCAGAA GGCAGGCCAA GCCCCTGTGT TGGTCATATA TAAGGACACT
 GAGCGGCCCT CTGGGATCCC TGACCGATTG TCCGGCTCCA GTTCAGGGAA CACACACACC CTGACCATCA
 GCGGGGCTCG GGCCGAGGAC GAGGCTGACT ATTACTGCGA GTCAGCAGTC AGTACTGATA CTGTTGTGTT
 CGGCGGAGGC ACCCACCTGA CCGTCCTCGG TCAGCCCAAG GCC (SEQ ID NO: 1111)

MAWTHLLLPV LTLCTGSVAS SVLTQPPSVS VSLGQTATIS CSGESLSKYY AQWFQOKAGQ APVLVIYKDT
 ERPSGIPDRF SGSSSGNTHT LTISGARAED EADYYCESAV STDTVVFGGG THLTVLGQPK A
 (SEQ ID NO: 1112)

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TCTC TACAGGTTTC TGTGCTCCTC CTGTTCTGAC CCAGACTCCA AGTGCTTCTG CCTCCCTGGA
 AGCCTCGGTC AAGCTCACCT GCACTTTGAG CGGTGATCAC AGCAGTCACT ATATTTCTTG GTATCAACAA
 CATCAACCAG GGAAGGCCCC TCGGTATCTG ATGAAGGTTA ACAGTGATGG AAGCCACAGC AGGGGAGACG
 GGATCCCTAG TCGCTTCTCA GGCTCCAGCT CTGGGGCTGA CCGCTATTTA AGCATCTCCA ACATCCAGTC
 TGACGATGAG GCAGATTATT ATTGTTTTAT AGCCACTGGT GACAATAGTG TATTCGGCGG AGGCACCCAT
 CTGACCGTCC TCGGTCAGCC CAAGGCC (SEQ ID NO: 1113)

STGFCAPPVL TQTPSASASL EASVKLTCTL SGDHSSHYS WYQQHQPGKA PRYLMKVNSD GSHSRGDGIP
 SRFSGSSSGA DRYLSISNIQ SDDEADYYCF IATGDNVFG GTHLTVLGQ PKA (SEQ ID NO: 1114)

L1-744:

A TGGACTGGGT CCCCTTTTAC CTCCTGCCCT TCATTTTCTC TACAGGTTTC TGTGCTCCTC
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 CAGTGAGCAC AGCAGTTACT ATATTACCTG GTATCAACAA CAACAACCAG GGAAGGCCCC TCGGTATCTG
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 CTGGGGCTGA CCGCTATTTA ACCATCTCCA ACATCCAGTC TGAGGATGAG GCAGATTATT ACTGTTTTAC
 ACCCGCTACT GGCATTAGTG TCTTCGGCGG AGGCACCCAT CTGACCGTCC TCGGTCAGCC CAAGGCC
 (SEQ ID NO: 1115)

MDWVPFYLLP FIFSTGFCAP PVLTOPTAS ASLEASVKLT CTLSSSEHSS YITWYQQQPG GKAPRYLMKV
 NSDGSHSRGD GIPSRFSGSS SGADRYLTIS NIQSEDEADY YCFTPATGIS VFGGGTHLTV LGQPKA
 (SEQ ID NO: 1116)

L1-745:

AGCAACTCC AACATCGGTA GAGGTTATGT GGGCTGGTAC CAACAGCTCC CGGGAACAGG CCCAGGACC
 CTCTTCTATG GAACTGGGAA CCGACCCTCA GGGGTCCCCG ATCGGTTCTC TGGCTCCAGG TCAGGCAGCA
 CAGCCACCCT GACCATCTCT GGGCTCCAGG CTGAGGATGA GGCTGATTAT TACTGCTCAT CGTGGGACAC
 CAGTCTCAGT ATTTACGTGT TCGCCTCAGG AACCCAACTG ACCGTCCTTG GTCAGCCCAA GGCC
 (SEQ ID NO: 1117)

SNSNIGRGYV GWYQQLPGTG PRTLFGYGTGN RPSGVPDRFS GSRSGSTATL TISGLQAEDE ADYYCSSWDT
 SLSIYVFASG TQLTVLGQPK A (SEQ ID NO: 1118)

L1-750:

ATGGACTG GGTTCCTTTT TACATCCTGC CCTTCATTTT CTCTACAGGT CTCTGTGCAT TGCCCGTGCT
 GACCCAGCCT ACAAGTGAT CTGCCCCCTT GGAAGAGTCG GTCAAGCTGA CCTGCACTTT GAGCAGTGAG
 CACAGCAATT ACATTGTTCA TTGGTATCAA CAACAACCAG GGAAGGCCCC TCGGTATCTG ATGTATGTCA
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 ACAATCAGTG GCCAATATGG TAACGTGTTT GGCTCAGGAA CCCGACTGAC CGTCCTTGGT CAGCCCAAGG
 CC (SEQ ID NO: 1119)

MDWVPFYILP FIFSTGLCAL PVLTOPTSAS APLEESVKLT CTLSSSEHSNY IVHWYQQQPG KAPRYLMYVR
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 (SEQ ID NO: 1120)

L1-751:

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AGTATAAGTG TGTTTCGGCGG AGGCACCCAT CTGACCGTCC TCGGTCAGCC CAAGGCC
 (SEQ ID NO: 1121)

MDWVPFYLLP FIFSTGFCAP PVLTQTPSAS ASLEASVKLT CTLSSSEHSSY YITWYQQQQP GKAPRYLMRV
NSDGSHSRGD GIPSRFSGSS SGADRYLTIS NIQSEDEADY YCFTPSSISV FGGGTHLTVL GQPKA
 (SEQ ID NO: 1122)

L1-755:

TGTGGGTTGG TACCAACAAC TCCCAGAAGA GGCCCCAGAA CTGTCATCTA TAGTACAAGT AGTCGACCCT
CGGGGGTGCC CGATCGATTG TCTGGCTCCA AGTCTGGCAG CACAGCCACC CTGACCATCT CTGGGCTCCA
GGCTGAGGAT GAGGCTGATT ATTACTGCTC GACGTGGGAT GATAGTCTCA GTGGTTACGT TTTCGGCTCA
GGAACCCAAT TGCAATTGAC CGTCCTTGGT CAGCCCAAGG CC (SEQ ID NO: 1123)

CGLVPTTPRR GPRTVIYSTS SRPSGVPDRF SGSKSGSTAT LTISGLQAE EADYYCSTWD DSLSGYVFGS
GTQLQLTVLG QPKA (SEQ ID NO: 1124)

L1-761:

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GAACACAGCA GTTACTATAT TACCTGGTAT CAACAACAAC AACCAGGGAA GGCCCCCTCG TATCTGATGA
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 (SEQ ID NO: 1125)

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NSDGSHSRGD GIPSRFSGSS SGADRYLTIS NIQSEDEADY YCFAPANNAV FGGGTHLTVL GQPKA
 (SEQ ID NO: 1126)

λ108:

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GTCCGGGTCC CTGGGCCAGA GGGTCAACCT CTCCTGCACT GGAAGCGGCT CCAACATCGG TAGAGGTTAT
GTGGGCTGGT ACCAACACCT CCCGGGGACA GGCCCCAGAA CCCTCATCTA TGGTGATATT AACCGACCCT
CAGGGGTCCC CGATCGGTTT TCTGGCTCCA GGTCAGGCAT CACAGCCACC CTGACCATCT CTGGGCTCCA
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GGCACCCACC TGACCGTCCT CGGTCAGCCC AAGGCC (SEQ ID NO: 1127)

LLTILAHCTG SWAQSLLTQP ASVSGSLGQR VTLSCTGSGS NIGRGYVGWY QHLPGTGPR LIYGDINRPS
GVPDRFSGSR SGITATLTIS GLQAEDEADY YCSSWDYSL STLFGGGTHL TVLGQPKA (SEQ ID NO: 1128)

λ118:

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GAAGCGGTTT CAACATTGGA GGTAATAATG TGGGTTGGTA CCAGCAGCTC CCAGGAAGAG GCCCCAGAAC
TGTCATCTAT GATACTTATA GTCGACTCTC GGGGGTGCC GATCGATTCT CTGGCTCCAA GTCTGGCAGC
ACAGCCACCC TGACCATCTC TGGGCTCCAG GCTGAGGATG AGGCTGATTA TTACTGCTCA ACGTGGGATG
ATAGTCTCCG TGCTTACTTG TTCGGGTCAG GAACCCAACT GACCGTTCTT GGTCAGCCCA AGGCC
 (SEQ ID NO: 1129)

MTSTMAWFPL LLTLLAHYTG SWAQSVLTQP ASVSGSLGQR ITISCTGSGS NIGGNNVGWY QQLPGRGPRT
VIYDTSYRLS GVPDRFSGSK SGSTATLTIS GLQAEDEADY YCSTWDDSLR AYLFGSGTQL TVLGQPKA
 (SEQ ID NO: 1130)

λ119:

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MTSTMAWFPL LLTLLAHYTG SWAQSULTQP ASVSGSLGQR ITISCTGSGS NIGGNNVGWY QQLPGRGPRT
 VIYDTYSRLS GVPDRFSGSK SGSTATLTIS GLQAEDEADY YCSTWDDSLR AYLFGSGTQL TVLGQPKA
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λ317:

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 CTCCTCCTGA ACAGTGATGG GAGTCGACCG TCAGGGGTCC CTGACCGGTT TTCCGGCTCC AACTCTGGCG
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 TCCCACGCCT CCTGATCATT ACGTGTTCGG CTCAGGAACC CAACTGACCG (SEQ ID NO: 1133)

MTSNMAWSPL LLTLLAYCTG SWAQSALTQP TSVSGSLGQR VSISCSGSTS NIGIVGASWY QQLPGKAPKL
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<120> Canine Immunoglobulin Variable Domains, Caninized Antibodies, and Methods for Making and Using Them

<130> 325-464

<140> CA 2,469,833

<141> 2002-12-20

<150> US 60/344,874

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 <222> (4)..(4)
 <223> X is Q or R

<220>
 <221> UNSURE
 <222> (6)..(6)
 <223> X is T, N, or A

<220>
 <221> UNSURE
 <222> (7)..(7)
 <223> X is L or P

<220>
 <221> UNSURE
 <222> (9)..(9)
 <223> X is T or absent

<220>
 <221> UNSURE
 <222> (10)..(10)
 <223> X is V or absent

<400> 5

Xaa Trp Gly Xaa Gly Xaa Xaa Val Xaa Xaa
 1 5 10

<210> 6
 <211> 25
 <212> PRT
 <213> canis familiaris;

<400> 6

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Ala Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Thr Ser
 20 25

<210> 7

<211> 25
 <212> PRT
 <213> canis familiaris;

<400> 7

Glu Val Gln Leu Met Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly

1				5					10						15
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser							
			20					25							
<210>	8														
<211>	25														
<212>	PRT														
<213>	canis familiaris;														
<400>	8														
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Asp	Leu	Val	Lys	Pro	Glu	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Val	Val	Ser							
			20					25							
<210>	9														
<211>	25														
<212>	PRT														
<213>	canis familiaris;														
<400>	9														
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Asp	Leu	Val	Lys	Pro	Ala	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser							
			20					25							
<210>	10														
<211>	25														
<212>	PRT														
<213>	canis familiaris;														
<400>	10														
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Asp	Leu	Val	Arg	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser							
			20					25							

<210> 11

<211> 25

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (10)..(10)

<223> X is D, X, or N

<220>

<221> UNSURE

<222> (19)..(19)

<223> X is any amino acid

<400> 11

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Xaa	Leu	Val	Lys	Phe	Gly	Gly
1				5					10					15	

Ser	Leu	Xaa	Leu	Ser	Cys	Val	Ala	Ser
			20					25

<210> 12

<211> 25

<212> PRT

<213> canis familiaris;

<400> 12

Glu	Val	His	Leu	Val	Glu	Ser	Gly	Gly	Asp	Leu	Val	Lys	Pro	Gly	Gly
1				5					10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser
			20					25

<210> 13

<211> 25

<212> PRT

<213> canis familiaris;

<400> 13

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser
20 25

<210> 14

<211> 25

<212> PRT

<213> canis familiaris;

<400> 14

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Gly Ser
20 25

<210> 15

<211> 25

<212> PRT

<213> canis familiaris;

<400> 15

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Thr Ser
20 25

<210> 16

<211> 25

<212> PRT

<213> canis familiaris;

<400> 16

Glu Val Gln Leu Val Gln Ser Gly Gly Asp Leu Val Lys Pro Ser Gly

10

<400> 20

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Gln Trp Val Ala
1 5 10

<210> 21

<211> 14

<212> PRT

<213> canis familiaris;

<400> 21

Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Gln Leu Val Ala
1 5 10

<210> 22

<211> 14

<212> PRT

<213> canis familiaris;

<400> 22

Trp Val Arg Glu Ala Pro Gly Lys Gly Leu Gln Trp Val Ala
1 5 10

<210> 23

<211> 14

<212> PRT

<213> canis familiaris;

<400> 23

Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Gln Trp Ile Ala
1 5 10

<210> 24

<211> 14

<212> PRT

<213> canis familiaris;

<400> 24

Trp Val Arg His Ser Pro Gly Lys Gly Leu Gln Trp Val Ala

1 5 10

<210> 25

<211> 14

<212> PRT

<213> canis familiaris;

<400> 25

Trp Val Arg Gln Cys Pro Gly Lys Gly Leu Gln Trp Val Thr
1 5 10

<210> 26

<211> 14

<212> PRT

<213> canis familiaris;

<400> 26

Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Gln Trp Ile Val
1 5 10

<210> 27

<211> 14

<212> PRT

<213> canis familiaris;

<400> 27

Trp Val Arg Gln Pro Pro Gly Lys Gly Pro Gln Trp Val Ala
1 5 10

<210> 28

<211> 14

<212> PRT

<213> canis familiaris;

<400> 28

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Gln Tyr Val Ala
 1 5 10

<210> 29

<211> 14

<212> PRT

<213> canis familiaris;

<400> 29

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Lys Trp Val Ala
 1 5 10

<210> 30

<211> 14

<212> PRT

<213> canis familiaris;

<400> 30

Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Gln Trp Ile Gly
 1 5 10

<210> 31

<211> 14

<213> canis familiaris;

<400> 31

Trp Val Arg Gln Thr Pro Glu Arg Gly Leu Glu Leu Val Ala
 1 5 10

<210> 32

<211> 32

<212> PRT

<213> canis familiaris;

<400> 32

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln
 1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
 20 25 30

<210> 33

<211> 32

<212> PRT

<213> canis familiaris;

<400> 33

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Phe Tyr Leu Gln
 1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Ser Ala Met Tyr Tyr Cys Ala Ala
 20 25 30

<210> 34

<211> 32

<212> PRT

<213> canis familiaris;

<400> 34

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
 1 5 10 15

Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 20 25 30

<210> 35

<211> 32

<212> PRT

<213> canis familiaris;

<400> 35

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln
 1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Met Tyr Tyr Cys Ala Pro

20 25 30

<210> 36

<211> 32

<212> PRT

<213> canis familiaris;

<400> 36

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Gly Glu Asp Thr Ala Met Tyr Tyr Cys Ala Lys
20 25 30

<210> 37

<211> 32

<212> PRT

<213> canis familiaris;

<400> 37

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
20 25 30

<210> 38

<211> 32

<212> PRT

<213> canis familiaris;

<400> 38

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Leu Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 39

<211> 32

<212> PRT

<213> canis familiaris;

<400> 39

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Glu	Asn	Thr	Leu	Tyr	Leu	Gln
1				5					10					15	

Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ser
			20					25					30		

<210> 40

<211> 32

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (24)..(24)

<223> X is D

<400> 40

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Ser	Thr	Leu	Tyr	Leu	Glu
1				5					10					15	

Met	Asn	Arg	Leu	Arg	Pro	Asp	Xaa	Thr	Ala	Met	Tyr	Tyr	Cys	Val	Thr
			20					25					30		

<210> 41

<211> 32

<212> PRT

<213> canis familiaris;

<400> 41

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ala	Asn	Asn	Thr	Leu	Tyr	Leu	Gln
1				5					10					15	

Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys
			20					25					30		

<210> 42

<211> 32

<212> PRT

<213> canis familiaris;

<400> 42

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
1				5					10					15	

Leu	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys
			20					25					30		

<210> 43

<211> 32

<212> PRT

<213> canis familiaris;

<400> 43

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Ser	Leu	Glu
1				5					10					15	

Met	Asn	Ser	Leu	Arg	Asp	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Ala	Arg
			20					25					30		

<210> 44

<211> 32

<212> PRT

<213> canis familiaris;

<400> 44

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Ser	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
1				5					10					15	

Leu	Asn	Ser	Leu	Thr	Ala	Glu	Asp	Thr	Ala	Arg	Tyr	Tyr	Cys	Ala	Gly
			20					25					30		

<210> 45

<211> 32

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (16)..(16)

<223> X is Q, H, or E

<400> 45

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Xaa
1				5					10					15	

Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Gly	Lys
			20					25					30		

<210> 46

<211> 32

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (23)..(23)

<223> X is E or D

<400> 46

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
1				5					10					15	

Met	Asn	Ser	Leu	Arg	Ala	Xaa	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg
			20					25					30		

<210> 47

<211> 32

<212> PRT

<213> canis familiaris;

<400> 47

Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Thr Val Tyr Leu Gln
 1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
 20 25 30

<210> 48

<211> 32

<212> PRT

<213> canis familiaris;

<400> 48

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Ser Leu His
 1 5 10 15

Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Phe Cys Thr Arg
 20 25 30

<210> 49

<211> 32

<212> PRT

<213> canis familiaris;

<400> 49

Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Thr Leu Tyr Leu Gln
 1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys Ala Lys
 20 25 30

<210> 50

<211> 32

<212> PRT

<213> canis familiaris;

<400> 50

Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Ser Thr Leu Tyr Leu Gln
 1 5 10 15

Met Glu Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Thr
 20 25 30

<210> 51

<211> 32

<212> PRT

<213> canis familiaris;

<400> 51

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln
 1 5 10 15

Met His Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg
 20 25 30

<210> 52

<211> 32

<212> PRT

<213> canis familiaris;

<400> 52

Arg Phe Ile Ile Ser Arg Asp Leu Ala Lys Ser Thr Val Tyr Leu Gln
 1 5 10 15

Met Asp Asn Leu Arg Ala Asp Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
 20 25 30

<210> 53

<211> 32

<212> PRT

<213> canis familiaris;

<400> 53

Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Thr Val Tyr Leu Gln
 1 5 10 15

Leu Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Gly Lys
 20 25 30

<210> 54

<211> 10

<212> PRT

<213> canis familiaris;

<400> 54

His	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
1				5					10

<210> 55

<211> 10

<212> PRT

<213> canis familiaris;

<400> 55

Leu	Trp	Gly	Pro	Gly	Thr	Leu	Val	Thr	Val
1				5					10

<210> 56

<211> 10

<212> PRT

<213> canis familiaris;

<400> 56

Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
1				5					10

<210> 57

<211> 10

<212> PRT

<213> canis familiaris;

<400> 57

Ser	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
1				5					10

<210> 58

<211> 9

<212> PRT

<213> canis familiaris;

<400> 58

Tyr Trp Gly Gln Gly Thr Leu Val Thr
1 5

<210> 59

<211> 9

<212> PRT

<213> canis familiaris;

<400> 59

Leu Trp Gly Gln Gly Thr Leu Val Thr
1 5

<210> 60

<211> 9

<212> PRT

<213> canis familiaris;

<400> 60

Leu Trp Gly Gln Gly Thr Leu Thr Val
1 5

<210> 61

<211> 9

<212> PRT

<213> canis familiaris;

<400> 61

His Trp Gly Gln Gly Thr Leu Val Thr
1 5

<210> 62

<211> 8

<212> PRT

<213> canis familiaris;

<400> 62

Tyr Trp Gly Gln Gly Thr Leu Val
1 5

<210> 63

<211> 10

<212> PRT

<213> canis familiaris;

<400> 63

Tyr Trp Gly Gln Gly Thr Pro Val Thr Val
1 5 10

<210> 64

<211> 10

<212> PRT

<213> canis familiaris;

<400> 64

Gly Trp Gly Gln Gly Thr Leu Val Thr Val
1 5 10

<210> 65

<211> 8

<212> PRT

<213> canis familiaris;

<400> 65

His Trp Gly Gln Gly Thr Leu Val
1 5

<210> 66

<211> 10

<212> PRT

<213> canis familiaris;

<400> 66

Tyr Trp Gly Pro Gly Thr Leu Val Thr Val
1 5 10

<210> 67

<211> 10

<212> PRT

<213> canis familiaris;

<400> 67

Tyr Trp Gly Gln Gly Asn Leu Val Thr Val
1 5 10

<210> 68

<211> 10

<212> PRT

<213> canis familiaris;

<400> 68

Ser Trp Gly Arg Gly Ala Leu Val Thr Val
1 5 10

<210> 69

<211> 25

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (3)..(3)

<223> X is Q or H

<400> 69

Glu	Val	Xaa	Leu	Val	Gln	Ser	Ala	Ala	Trp	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	

Ser	Val	Lys	Val	Ser	Cys	Lys	Thr	Ser
			20					25

<210> 70

<211> 15

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (11)..(11)

<223> X is D or E

<400> 70

Trp	Val	Gln	Gln	Ala	Pro	Gly	Ala	Gly	Leu	Xaa	Trp	Met	Gly	Trp
1				5					10					15

<210> 71

<211> 32

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (11)..(11)

<223> X is S or N

<220>

<221> unsure

<222> (22) .. (22)

<223> X is A or T

<220>

<221> unsure

<222> (19) .. (19)

<223> X is S or N

<220>

<221> unsure

<222> (24) .. (24)

<223> X is T or A

<220>

<221> unsure

<222> (32) .. (32)

<223> X is R or S

<400> 71

Arg	Val	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Thr	Xaa	Val	Thr	Tyr	Met	Glu
1				5					10					15	

Leu	Ser	Xaa	Leu	Arg	Xaa	Glu	Asp	Xaa	Ala	Val	Tyr	Tyr	Cys	Ala	Xaa
			20					25					30		

<210> 72

<211> 10

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (1)..(1)

<223> X is Y or L

<400> 72

Xaa	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
1				5					10

<210> 73

<211> 25

<212> PRT

<213> canis familiaris;

<400> 73

Glu	Val	Gln	Leu	Val	Gln	Ser	Ala	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	

Ser	Val	Lys	Val	Ser	Cys	Lys	Thr	Ser
			20					25

<210> 74

<211> 15

<212> PRT

<213> canis familiaris;

<400> 74

Trp	Val	Gln	Gln	Ala	Pro	Gly	Ala	Gly	Leu	Asp	Trp	Met	Gly	Trp
1				5					10					15

<210> 75

<211> 15

<212> PRT

<213> canis familiaris;

<400> 75

Trp Val Gln Gln Ala Pro Gly Ala Gly Leu Glu Trp Met Gly Trp
 1 5 10 15

<210> 76

<211> 32

<212> PRT

<213> canis familiaris;

<400> 76

1 5 10 15
 Leu Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ser
 20 25 30

<210> 77

<211> 32

<212> PRT

<213> canis familiaris;

<400> 77

Arg Val Thr Leu Thr Ala Asp Thr Ser Thr Asn Thr Val Tyr Met Glu
 1 5 10 15
 Leu Ser Asn Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 20 25 30

<210> 78

<211> 32

<212> PRT

<213> canis familiaris;

<400> 78

Arg Val Thr Leu Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
 1 5 10 15
 Leu Ser Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys Ala Ser
 20 25 30

<210> 79

<211> 10

<212> PRT

<213> canis familiaris;

<400> 79

Leu	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
1				5					10

<210> 80

<211> 32

<212> PRT

<213> canis familiaris;

<400> 80

Arg	Val	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu
1				5					10					15	

Leu	Ser	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg
			20					25					30		

<210> 81

<211> 25

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (2) .. (2)

<223> X is V or L

<220>

<221> unsure

<222> (3) .. (3)

<223> X is I or T

<220>

<221> unsure

<222> (7) .. (7)

<223> X is S or A

<220>

<221> unsure

<222> (16) .. (16)

<223> X is Q or E

<220>

<221> unsure

<222> (23) .. (23)

<223> X is T or L

<220>

<221> unsure

<222> (24) .. (24)

<223> X is X or V

<400> 81

Glu	Xaa	Xaa	Leu	Gln	Glu	Xaa	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Xaa
1				5					10					15	

Thr	Leu	Ser	Leu	Thr	Cys	Xaa	Xaa	Ser
			20					25

<210> 82

<211> 14

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (4) .. (4)

<223> X is Q or R

<220>

<221> unsure

<222> (7) .. (7)

<223> X is D or G

<220>

<221> unsure

<222> (8) .. (8)

<223> X is R or G

<220>

<221> unsure

<222> (9) .. (9)

<223> X is G or E

<400> 82

Trp	Ile	Arg	Xaa	Arg	Pro	Xaa	Xaa	Xaa	Leu	Glu	Trp	Met	Gly
1				5					10				

<210> 83

<211> 30

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (4) .. (4)

<223> X is A or T

<220>

<221> unsure

<222> (6) .. (6)

<223> X is G or T

<220>

<221> unsure

<222> (7) .. (7)

<223> X is T or A

<220>

<221> unsure

<222> (8) .. (8)

<223> X is K or T

<220>

<221> unsure

<222> (10) .. (10)

<223> X is H or Q

<220>

<221> unsure

<222> (11) .. (11)

<223> X is S or F

<220>

<221> unsure

<222> (12) .. (12)

<223> X is S or F

<220>

<221> unsure

<222> (18) .. (18)

<223> X is T or V

<220>

<221> unsure

<222> (27) .. (27)

<223> X is Y or F

<220>

<221> unsure

<222> (29) .. (29)

<223> X is T or I

<400> 83

Ser	Ile	Thr	Xaa	Asp	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Leu	Gln	Leu	Thr
1				5					10					15	

Ser	Xaa	Thr	Thr	Glu	Asp	Thr	Ala	Val	Tyr	Xaa	Cys	Xaa	Arg
			20					25					30

<210> 84

<211> 10

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (1)..(1)

<223> X is V or F

<400> 84

Xaa	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
1				5					10

<210> 85

<211> 25

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (24)..(24)

<223> X is X or V

<400> 85

Glu	Val	Ile	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gln
1				5					10					15	

Thr	Leu	Ser	Leu	Thr	Cys	Thr	Xaa	Ser
			20					25

<210> 86

<211> 25

<212> PRT

<213> canis familiaris;

<400> 86

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

<210> 87

<211> 14

<212> PRT

<213> canis familiaris;

<400> 87

Trp	Ile	Arg	Gln	Arg	Pro	Asp	Arg	Gly	Leu	Glu	Trp	Met	Gly
1				5					10				

<210> 88

<211> 14

<212> PRT

<213> canis familiaris;

<400> 88

Trp	Ile	Arg	Arg	Arg	Pro	Gly	Gly	Glu	Leu	Glu	Trp	Met	Gly
1				5					10				

<210> 89

<211> 29

<212> PRT

<213> canis familiaris;

<400> 89

Ile	Thr	Ala	Asp	Gly	Thr	Lys	Asn	His	Leu	Ser	Leu	Gln	Leu	Thr	Ser
1				5					10					15	

Thr	Thr	Thr	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Thr	Arg
			20					25				

<210> 90

<211> 30

<212> PRT

<213> canis familiaris;

<400> 90

Ser	Ile	Thr	Thr	Asp	Thr	Ala	Thr	Asn	Gln	Phe	Phe	Leu	Gln	Leu	Thr
1				5					10					15	

Ser	Val	Thr	Thr	Glu	Asp	Thr	Ala	Val	Tyr	Phe	Cys	Ile	Arg
			20					25					30

<210> 91

<211> 10

<212> PRT

<213> canis familiaris;

<400> 91

Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
1				5					10

<210> 92

<211> 10

<212> PRT

<213> canis familiaris;

<400> 92

Phe	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
1				5					10

<210> 93

<211> 25

<212> PRT

<213> canis familiaris;

<400> 93

Ser	Trp	Ala	Gln	Ser	Leu	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Arg	Val	Thr	Leu	Ser	Cys
			20					25

<210> 94

<211> 25

<212> PRT

<213> canis familiaris;

<400> 94

Ser	Trp	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Thr	Val	Thr	Ile	Ser	Cys
			20					25

<210> 95

<211> 20

<212> PRT

<213> canis familiaris;

<400> 95

Cys	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Leu	Gly	Gln	Arg	Val
1				5					10					15	

Thr	Ile	Ser	Cys
			20

<210> 96

<211> 25

<212> PRT

<400> 96

Ser	Trp	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Arg	Ile	Thr	Ile	Ser	Cys
			20					25

<210> 97

<211> 25

<212> PRT

<213> canis familiaris;

<400> 97

Ser	Trp	Ala	Gln	Ser	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Thr	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys
			20					25

<210> 98

<211> 25

<212> PRT

<213> canis familiaris;

<400> 98

Ser	Trp	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys
			20					25

<210> 99

<211> 25

<212> PRT

<213> canis familiaris;

<400> 99

Ser	Trp	Ala	Gln	Ser	Leu	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys
			20					25

<210> 100

<211> 25

<212> PRT

<213> canis familiaris;

<400> 100

Ser Trp Ala Gln Ser Val Leu Thr Gln Pro Ala Ser Val Ser Gly Ser
1 5 10 15

Leu Gly Gln Lys Val Thr Ile Ser Cys
20 25

<210> 101

<211> 25

<212> PRT

<213> canis familiaris;

<400> 101

Ser Trp Ala Gln Ser Val Leu Thr Gln Pro Ala Ser Val Thr Gly Ser
1 5 10 15

Leu Gly Gln Arg Val Thr Ile Ser Cys
20 25

<210> 102

<211> 25

<212> PRT

<213> canis familiaris;

<400> 102

Ser Trp Ala Gln Ala Val Leu Asn Gln Pro Ala Ser Val Ser Gly Ala
1 5 10 15

Leu Gly Gln Lys Val Thr Ile Ser Cys
20 25

<210> 103

<211> 25

<212> PRT

<213> canis familiaris;

<400> 103

Ser Trp Ala Gln Ser Ile Leu Thr Gln Pro Ala Ser Val Ser Gly Ser
1 5 10 15

Leu Gly Gln Lys Val Thr Ile Ser Cys
 20 25

<210> 104

<211> 25

<212> PRT

<213> canis familiaris;

<400> 104

Ser Trp Ala Gln Ser Val Leu Thr Gln Pro Ala Ser Met Ser Gly Ser
 1 5 10 15

Leu Gly Gln Lys Val Thr Ile Ser Cys
 20 25

<210> 105

<211> 25

<212> PRT

<213> canis familiaris;

<400> 105

Ser Trp Ala Gln Ser Ala Leu Thr Gln Pro Thr Ser Val Ser Gly Ser
 1 5 10 15

Leu Gly Gln Arg Val Ser Ile Ser Cys
 20 25

<210> 106

<211> 25

<212> PRT

<213> canis familiaris;

<400> 106

Ser Trp Ala Gln Ser Val Leu Thr Gln Pro Ala Ser Val Ser Gly Phe
 1 5 10 15

Leu Gly Gln Arg Val Thr Ile Ser Cys
 20 25

<210> 107

<211> 25

<212> PRT

<213> canis familiaris;

<400> 107

Ser	Trp	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Arg	Val	Thr	Val	Ser	Cys
			20					25

<210> 108

<211> 25

<212> PRT

<213> canis familiaris;

<400> 108

Ser	Trp	Ala	Gln	Ser	Leu	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Lys	Val	Thr	Ile	Ser	Cys
			20					25

<210> 109

<211> 25

<212> PRT

<213> canis familiaris;

<400> 109

Ser	Trp	Ala	Gln	Ser	Met	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Thr	Val	Thr	Ile	Ser	Cys
			20					25

<210> 110

<211> 25

<212> PRT

<213> canis familiaris;

<400> 110

Ser	Trp	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Thr	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys
			20					25

<210> 111

<211> 25

<212> PRT

<213> canis familiaris;

<400> 111

Ser	Trp	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Pro
1				5					10					15	

Leu	Gly	Gln	Lys	Val	Thr	Ile	Ser	Cys
			20					25

<210> 112

<211> 25

<212> PRT

<213> canis familiaris;

<400> 112

Ser	Trp	Ala	Gln	Ser	Met	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Lys	Val	Thr	Ile	Ser	Cys
			20					25

<210> 113

<211> 25

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (7) .. (7)

<223> X is L, V, or absent

<400> 113

Ser	Trp	Ala	Gln	Ser	Val	Xaa	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Arg	Val	Thr	Thr	Ser	Cys
		20						25

<210> 114

<211> 25

<212> PRT

<213> canis familiaris;

<400> 114

Ser	Trp	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Arg	Ile	Thr	Val	Ser	Cys
		20						25

<210> 115

<211> 25

<212> PRT

<213> canis familiaris;

<400> 115

Ser	Trp	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Ser	Val	Thr	Ile	Ser	Cys
		20						25

<210> 116

<211> 25

<212> PRT

<213> canis familiaris;

<400> 116

Ser	Trp	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Pro
1				5					10					15	

Leu	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys
			20					25

<210> 117

<211> 10

<212> PRT

<213> canis familiaris;

<400> 117

Ser	Leu	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys
1				5					10

<210> 118

<211> 5

<212> PRT

<213> canis familiaris;

<400> 118

Val	Thr	Ile	Ser	Cys
1			5	

<210> 119

<211> 25

<212> PRT

<213> canis familiaris;

<400> 119

Ser	Trp	Ala	Gln	Ser	Glu	Leu	Thr	Gln	Ser	Ala	Ala	Val	Ser	Gly	Ser
1				5					10					15	

Leu Gly Gln Glu Val Thr Ile Ser Cys
 20 25

<210> 120

<211> 25

<212> PRT

<213> canis familiaris;

<400> 120

Ser Trp Ala Gln Ser Ile Val Thr Gln Ala Ala Ser Val Ser Gly Ser
 1 5 10 15

Leu Gly Gln Arg Ile Thr Ile Ser Cys
 20 25

<210> 121

<211> 25

<212> PRT

<213> canis familiaris;

<400> 121

Ser Trp Ala Gln Ser Ile Leu Thr Gln Pro Ser Ser Val Ser Gly Ser
 1 5 10 15

Leu Gly Gln Arg Val Thr Ile Ser Cys
 20 25

<210> 122

<211> 15

<212> PRT

<213> canis familiaris;

<400> 122

Trp Tyr Gln His Leu Pro Gly Thr Gly Pro Arg Thr Leu Ile Tyr
 1 5 10 15

<210> 123

<211> 15

<212> PRT

<213> canis familiaris;

<400> 123

Trp	Tyr	Gln	Gln	Ile	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Val	Ile	Tyr
1				5					10					15

<210> 124

<211> 15

<212> PRT

<213> canis familiaris;

<400> 124

Trp	Tyr	Gln	Gln	Phe	Pro	Gly	Ala	Gly	Pro	Arg	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 125

<211> 15

<212> PRT

<213> canis familiaris;

<400> 125

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Arg	Ser	Pro	Lys	Leu	Leu	Val	Tyr
1				5					10					15

<210> 126

<211> 15

<212> PRT

<213> canis familiaris;

<400> 126

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Arg	Gly	Pro	Arg	Thr	Val	Ile	Tyr
1				5					10					15

<210> 127

<211> 15

<212> PRT

<213> canis familiaris;

<400> 127

Trp	Phe	Gln	Gln	Val	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Val	Ile	Tyr
1				5					10					15

<210> 128

<211> 15

<212> PRT

<213> canis familiaris;

<400> 128

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Arg	Pro	Arg	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 129

<211> 15

<212> PRT

<213> canis familiaris;

<400> 129

Trp	Phe	Gln	Gln	Leu	Pro	Gly	Lys	Gly	Pro	Arg	Thr	Val	Ile	Tyr
1				5					10					15

<210> 130

<211> 15

<212> PRT

<213> canis familiaris;

<400> 130

Trp	Phe	Gln	Glu	Leu	Pro	Gly	Thr	Gly	Pro	Lys	Ile	Leu	Ile	Tyr
1				5					10					15

<210> 131

<211> 15

<212> PRT

<213> canis familiaris;

<400> 131

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 132

<211> 15

<212> PRT

<213> canis familiaris;

<400> 132

Trp	Phe	Gln	Gln	Phe	Pro	Gly	Lys	Gly	Pro	Lys	Thr	Val	Ile	Tyr
1				5					10					15

<210> 133

<211> 15

<212> PRT

<213> canis familiaris;

<400> 133

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Gly	Pro	Lys	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 134

<211> 15

<212> PRT

<213> canis familiaris;

<400> 134

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Val	Asp
1				5					10					15

<210> 135

<211> 15

<212> PRT

<213> canis familiaris;

<400> 135

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Ile	Gly	Pro	Lys	Thr	Val	Ile	Tyr
1				5					10					15

<210> 136

<211> 15

<212> PRT

<213> canis familiaris;

<400> 136

Trp	Phe	Gln	Gln	Phe	Pro	Gly	Glu	Gly	Pro	Arg	Thr	Val	Ile	Tyr
1				5					10					15

<210> 137

<211> 15

<212> PRT

<213> canis familiaris;

<400> 137

Trp	Tyr	Arg	Gln	Leu	Pro	Gly	Thr	Gly	Pro	Thr	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 138

<211> 15

<212> PRT

<213> canis familiaris;

<400> 138

Trp	Tyr	Gln	Gln	Phe	Pro	Gly	Thr	Gly	Pro	Arg	Ile	Leu	Ile	Tyr
1				5					10					15

<210> 139

<211> 15

<212> PRT

<213> canis familiaris;

<400> 139

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Leu	Asn
1				5					10					15

<210> 140

<211> 15

<212> PRT

<213> canis familiaris;

<400> 140

Trp	Leu	Gln	Gln	Leu	Pro	Gly	Thr	Gly	Pro	Lys	Thr	Val	Ile	Tyr
1				5					10					15

<210> 141

<211> 15

<212> PRT

<213> canis familiaris;

<400> 141

Trp	Phe	Gln	Gln	Leu	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Val	Ile	Tyr
1				5					10					15

<210> 142

<211> 15

<212> PRT

<213> canis familiaris;

<400> 142

Trp	His	Gln	Gln	Val	Pro	Glu	Thr	Gly	Pro	Arg	Asn	Ile	Ile	Tyr
1				5					10					15

<210> 143

<211> 15

<212> PRT

<213> canis familiaris;

<400> 143

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Arg	Gly	Pro	Thr	Thr	Leu	Leu	Tyr
1				5					10					15

<210> 144

<211> 15

<212> PRT

<213> canis familiaris;

<400> 144

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Ile	Gly	Pro	Arg	Thr	Val	Ile	Tyr
1				5					10					15

<210> 145

<211> 15

<212> PRT

<213> canis familiaris;

<400> 145

Trp	Tyr	Gln	Gln	Val	Pro	Gly	Thr	Arg	Pro	Arg	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 146

<211> 15

<212> PRT

<213> canis familiaris;

<400> 146

Trp	Tyr	Gln	Gln	Phe	Pro	Gly	Arg	Gly	Pro	Arg	Ser	Val	Ile	Tyr
1				5					10					15

<210> 147

<211> 15

<212> PRT

<213> canis familiaris;

<400> 147

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Val	Tyr
1				5					10					15

<210> 148

<211> 15

<212> PRT

<213> canis familiaris;

<400> 148

Trp	Tyr	Gln	Asn	Leu	Pro	Gly	Lys	Gly	Pro	Lys	Thr	Val	Ile	Phe
1				5					10					15

<210> 149

<211> 15

<212> PRT

<213> canis familiaris;

<400> 149

Trp	Tyr	Gln	Gln	Ile	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 150

<211> 15

<212> PRT

<213> canis familiaris;

<400> 150

Trp	Tyr	Gln	Gln	Tyr	Pro	Gly	Thr	Gly	Pro	Lys	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 151

<211> 15

<212> PRT

<213> canis familiaris;

<400> 151

Trp	Tyr	Gln	Gln	Val	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Leu	Ile	His
1				5					10					15

<210> 152

<211> 15

<212> PRT

<213> canis familiaris;

<400> 152

Trp	Tyr	Arg	Gln	Phe	Pro	Gly	Lys	Ala	Pro	Glu	Leu	Leu	Ile	Tyr
1				5					10					15

<210> 153

<211> 15

<212> PRT

<213> canis familiaris;

<400> 153

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Ile	Gly	Pro	Arg	Thr	Val	Ile	Ser
1				5					10					15

<210> 154

<211> 15

<212> PRT

<213> canis familiaris;

<400> 154

Trp	Phe	Gln	Gln	Phe	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Val	Ile	Tyr
1				5					10					15

<210> 155

<211> 15

<212> PRT

<213> canis familiaris;

<400> 155

Trp	His	Gln	Gln	Leu	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 156

<211> 15

<212> PRT

<213> canis familiaris;

<400> 156

Trp	Tyr	Gln	Gln	Leu	Pro	Glu	Thr	Gly	Pro	Arg	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 157

<211> 15

<212> PRT

<213> canis familiaris;

<400> 157

Trp	Tyr	Gln	Gln	Val	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 158

<211> 15

<212> PRT

<213> canis familiaris;

<400> 158

Trp	Tyr	Gln	Gln	Val	Pro	Gly	Ile	Gly	Pro	Arg	Thr	Val	Met	Tyr
1				5					10					15

<210> 159

<211> 15

<212> PRT

<213> canis familiaris;

<400> 159

Trp	Phe	Gln	His	Leu	Pro	Gly	Thr	Arg	Pro	Lys	Ser	Leu	Ile	Tyr
1				5					10					15

<210> 160

<211> 15

<212> PRT

<213> canis familiaris;

<400> 160

Trp	Phe	Gln	Gln	Leu	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Val	Ile	Cys
1				5					10					15

<210> 161

<211> 15

<212> PRT

<213> canis familiaris;

<400> 161

Trp	Tyr	Gln	Leu	Val	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 162

<211> 15

<212> PRT

<213> canis familiaris;

<400> 162

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Arg	Gly	Pro	Arg	Thr	Val	Ile	His
1				5					10					15

<210> 163

<211> 15

<212> PRT

<213> canis familiaris;

<400> 163

Trp	Cys	Gln	Gln	Leu	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Val	Asp
1				5					10					15

<210> 164

<211> 15

<212> PRT

<213> canis familiaris;

<400> 164

Trp	Tyr	Gln	Gln	Phe	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 165

<211> 15

<212> PRT

<213> canis familiaris;

<400> 165

Trp	Tyr	Arg	Gln	Leu	Pro	Gly	Glu	Ala	Pro	Lys	Leu	Leu	Leu	Tyr
1				5					10					15

<210> 166

<211> 32

<212> PRT

<213> canis familiaris;

<400> 166

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ile	Thr	Ala	Thr
1				5					10					15	

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 167

<211> 32

<212> PRT

<213> canis familiaris;

<400> 167

Gly Val Pro Glu Arg Phe Ser Gly Pro Arg Ser Gly Ile Thr Ser Thr
 1 5 10 15

Leu Thr Ile Ser Gly Leu Arg Ala Glu Asp Glu Gly Asp Tyr Tyr Cys
 20 25 30

<210> 168

<211> 32

<212> PRT

<213> canis familiaris;

<400> 168

Gly Val Pro Asp Arg Phe Ser Gly Ser Thr Ser Gly Ser Thr Ala Thr
 1 5 10 15

Leu Thr Ile Ser Gly Leu Arg Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 169

<211> 32

<212> PRT

<213> canis familiaris;

<400> 169

Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Asp Asn Ser Ala Thr
 1 5 10 15

Leu Thr Phe Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 170

<211> 32

<212> PRT

<213> canis familiaris;

<400> 170

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Ser	Thr	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 171

<211> 32

<212> PRT

<213> canis familiaris;

<400> 171

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Thr	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Glu	Tyr	Tyr	Cys
			20					25					30		

<210> 172

<211> 32

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (20) .. (20)

<223> X is S, T, or A

<220>

<221> UNSURE

<222> (31)..(31)

<223> X is Y, F, or H

<400> 172

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

<210> 173

<211> 32

<212> PRT

<213> canis familiaris;

<400> 173

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

<210> 174

<211> 32

<212> PRT

<213> canis familiaris;

<400> 174

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

<210> 175

<211> 32

<212> PRT

<213> canis familiaris;

<400> 175

Gly Val Pro Asp Arg Phe Ser Gly Ser Arg Ser Gly Thr Thr Ala Thr
 1 5 10 15

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 176

<211> 32

<212> PRT

<213> canis familiaris;

<400> 176

Gly Val Pro Asp Arg Phe Ser Gly Ser Arg Ser Gly Ser Thr Ala Thr
 1 5 10 15

Leu Thr Ile Ser Gly Leu Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 177

<211> 32

<212> PRT

<213> canis familiaris;

<400> 177

Gly Val Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Ser Gly Thr
 1 5 10 15

Leu Thr Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 178

<211> 32

<212> PRT

<213> canis familiaris;

<400> 178

Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Ser Ala Thr
 1 5 10 15

Leu Thr Ile Ser Gly Leu Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
 20 25 30

<210> 179

<211> 32

<212> PRT

<213> canis familiaris;

<400> 179

Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Ser Thr Ala Thr
 1 5 10 15

Leu Thr Ile Ser Glu Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 180

<211> 32

<212> PRT

<213> canis familiaris;

<400> 180

Gly Val Pro Asn Arg Phe Ser Gly Ser Arg Ser Gly Ser Thr Ala Thr
 1 5 10 15

Leu Thr Ile Ser Gly Leu Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 181

<211> 32

<212> PRT

<213> canis familiaris;

<400> 181

Gly Val Pro Asp Arg Phe Ser Gly Ser Arg Ser Gly Tyr Thr Ala Ala
 1 5 10 15

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 182

<211> 32

<212> PRT

<213> canis familiaris;

<400> 182

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

<210> 183

<211> 32

<212> PRT

<213> canis familiaris;

<400> 183

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

<210> 184

<211> 32

<212> PRT

<213> canis familiaris;

<400> 184

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

<210> 185

<211> 32

<212> PRT

<213> canis familiaris;

<400> 185

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Ser	Thr	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Val	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 186

<211> 32

<212> PRT

<213> canis familiaris;

<400> 186

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Arg	Thr	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 187

<211> 32

<212> PRT

<213> canis familiaris;

<400> 187

Gly	Ile	Ser	Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Asn	Ser	Ala	Ser
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Phe	Cys
			20					25					30		

<210> 188

<211> 32

<212> PRT

<213> canis familiaris;

<400> 188

Gly	Val	Pro	Asp	Arg	Phe	Ser	Val	Ser	Lys	Ser	Gly	Ser	Ser	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Glu	Tyr	Tyr	Cys
			20					25					30		

<210> 189

<211> 32

<212> PRT

<213> canis familiaris;

<400> 189

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Asn	Ser	Gly	Asn	Ser	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Thr	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 190

<211> 32

<212> PRT

<213> canis familiaris;

<400> 190

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Ser	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 191

<211> 32

<212> PRT

<213> canis familiaris;

<400> 191

Gly	Val	Pro	Asp	Arg	Phe	Ser	Ala	Ser	Arg	Ser	Gly	Asn	Ser	Ala	Thr
1				5					10					15	

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 192

<211> 32

<212> PRT

<213> canis familiaris;

<400> 192

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

<210> 193

<211> 32

<212> PRT

<213> canis familiaris;

<400> 193

Gly Val Pro Gly Arg Phe Ser Gly Ser Ile Ser Gly Asn Ser Ala Thr
 1 5 10 15
 Leu Thr Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr His Cys
 20 25 30

<210> 194

<211> 32

<212> PRT

<213> canis familiaris;

<400> 194

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

<210> 195

<211> 32

<212> PRT

<213> canis familiaris;

<400> 195

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Thr	Ala	Ile
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Glu	Tyr	Tyr	Cys
			20					25					30		

<210> 196

<211> 32

<212> PRT

<213> canis familiaris;

<400> 196

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Ser	Ala	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 197

<211> 32

<212> PRT

<213> canis familiaris;

<400> 197

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Thr	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Asp	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 198

<211> 32

<212> PRT

<213> canis familiaris;

<400> 198

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

<210> 199

<211> 32

<212> PRT

<213> canis familiaris;

<400> 199

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

<210> 200

<211> 32

<212> PRT

<213> canis familiaris;

<400> 200

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

<210> 201

<211> 32

<212> PRT

<213> canis familiaris;

<400> 201

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Ser	Thr	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Ile	Tyr	Tyr	Cys
			20					25					30		

<210> 202

<211> 32

<212> PRT

<213> canis familiaris;

<400> 202

Arg	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Glu	Ser	Gly	Asn	Ser	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Thr	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 203

<211> 32

<212> PRT

<213> canis familiaris;

<400> 203

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Arg	Thr	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Glu	Tyr	Tyr	Cys
			20					25					30		

<210> 204

<211> 32

<212> PRT

<213> canis familiaris;

<400> 204

Gly	Val	Pro	Glu	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Thr	Ala	Thr
1				5					10					15	

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Glu Tyr Tyr Cys
 20 25 30

<210> 205

<211> 32

<212> PRT

<213> canis familiaris;

<400> 205

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

<210> 206

<211> 32

<212> PRT

<213> canis familiaris;

<400> 206

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

<210> 207

<211> 32

<212> PRT

<213> canis familiaris;

<400> 207

Gly Ile Pro Asp Arg Phe Ser Gly Ser Arg Ser Asp Asn Ser Gly Ile
 1 5 10 15
 Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr His Cys
 20 25 30

<210> 208

<211> 32

<212> PRT

<213> canis familiaris;

<400> 208

Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Asn	Thr	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Leu	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 209

<211> 32

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (23) .. (23)

<223> X is Q, R, or L

<400> 209

Glu	Val	Ser	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Asn	Thr	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Xaa	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 210

<211> 32

<212> PRT

<213> canis familiaris;

<400> 210

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Asn	Ser	Gly	Phe	Ser	Ala	Thr
1				5					10					15	

Leu Thr Ile Thr Gly Leu Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 211

<211> 32

<212> PRT

<213> canis familiaris;

<400> 211

Gly Val Pro Asp Arg Phe Ser Gly Ser Arg Ser Gly Thr Thr Gly Thr
 1 5 10 15

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 212

<211> 14

<212> PRT

<213> canis familiaris;

<400> 212

Phe Gly Gly Gly Thr His Leu Thr Val Leu Gly Gln Pro Lys
 1 5 10

<210> 213

<211> 14

<212> PRT

<213> canis familiaris;

<400> 213

Phe Gly Gly Gly Thr His Leu Ala Val Leu Gly Gln Pro Lys
 1 5 10

<210> 214

<211> 14

<212> PRT

<213> canis familiaris;

<400> 214

Phe	Gly	Ser	Gly	Thr	Gln	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys
1				5					10				

<210> 215

<211> 14

<212> PRT

<213> canis familiaris;

<400> 215

Phe	Gly	Gly	Gly	Thr	His	Leu	Thr	Val	Leu	Ser	Gln	Pro	Lys
1				5					10				

<210> 216

<211> 14

<212> PRT

<213> canis familiaris;

<400> 216

Phe	Gly	Gly	Gly	Thr	Leu	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys
1				5					10				

<210> 217

<211> 15

<212> PRT

<213> canis familiaris;

<400> 217

Phe	Gly	Gly	Gly	Thr	Gln	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala
1				5					10					15

<210> 218

<211> 6

<212> PRT

<213> canis familiaris;

<400> 218

Phe Gly Gly Gly Thr His
1 5

<210> 219

<211> 13

<212> PRT

<213> canis familiaris;

<400> 219

Phe Gly Gly Gly Thr His Leu Thr Val Leu Gly Gln Pro
1 5 10

<210> 220

<211> 14

<212> PRT

<213> canis familiaris;

<400> 220

Phe Gly Gly Gly Thr His Leu Thr Val Leu Gly Gln Pro Glu
1 5 10

<210> 221

<211> 13

<212> PRT

<213> canis familiaris;

<400> 221

Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Gly Gln Pro
1 5 10

<210> 222

<211> 7

<212> PRT

<213> canis familiaris;

<400> 222

Phe Gly Gly Gly Thr His Leu
1 5

<210> 223

<211> 15

<212> PRT

<213> canis familiaris;

<400> 223

Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Ser Gln Pro Lys Ala
1 5 10 15

<210> 224

<211> 15

<212> PRT

<213> canis familiaris;

<400> 224

Phe Gly Gly Gly Thr Tyr Leu Thr Val Val Gly Gln Pro Lys Ala
1 5 10 15

<210> 225

<211> 12

<212> PRT

<213> canis familiaris;

<400> 225

Phe Gly Gly Gly Thr His Leu Thr Val Leu Gly Gln
1 5 10

<210> 226

<211> 15

<212> PRT

<213> canis familiaris;

<400> 226

Phe	Gly	Gly	Gly	Thr	His	Leu	Thr	Val	Leu	Gly	Gln	Pro	Arg	Ala
1				5					10					15

<210> 227

<211> 15

<212> PRT

<213> canis familiaris;

<400> 227

Phe	Gly	Ser	Gly	Thr	His	Leu	Thr	Ala	Leu	Gly	Gln	Pro	Lys	Ala
1				5					10					15

<210> 228

<211> 15

<212> PRT

<213> canis familiaris;

<400> 228

Phe	Gly	Ser	Gly	Thr	Gln	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala
1				5					10					15

<210> 229

<211> 15

<212> PRT

<213> canis familiaris;

<400> 229

Phe	Gly	Gly	Gly	Thr	His	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala
1				5					10					15

<210> 230

<211> 15

<212> PRT

<213> canis familiaris;

<400> 230

Phe	Gly	Gly	Gly	Thr	His	Leu	Thr	Val	Leu	Ser	Gln	Pro	Lys	Ala
1				5					10					15

<210> 231

<211> 15

<212> PRT

<213> canis familiaris;

<400> 231

Phe	Gly	Gly	Gly	Ala	His	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala
1				5					10					15

<210> 232

<211> 15

<212> PRT

<213> canis familiaris;

<400> 232

Phe	Gly	Pro	Gly	Thr	Gln	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala
1				5					10					15

<210> 233

<211> 15

<212> PRT

<213> canis familiaris;

<400> 233

Phe	Gly	Gly	Gly	Thr	Arg	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala
1				5					10					15

<210> 234

<211> 25

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (1) .. (1)

<223> X is A, T, or absent

<220>

<221> UNSURE

<222> (2) .. (2)

<223> X is D or absent

<220>

<221> UNSURE

<222> (3) .. (3)

<223> X is S or absent

<220>

<221> UNSURE

<222> (4) .. (4)

<223> X is Q or absent

<220>

<221> UNSURE

<222> (5) .. (5)

<223> X is T or absent

<220>

<221> UNSURE

<222> (6) .. (6)

<223> X is V or absent

<220>

<221> UNSURE

<222> (7) .. (7)

<223> X is V or absent

<220>

<221> UNSURE

<222> (8) .. (8)

<223> X is T or absent

<220>

<221> UNSURE

<222> (9) .. (9)

<223> X is Q or absent

<220>

<221> UNSURE

<222> (10) .. (10)

<223> X is E or absent

<220>

<221> UNSURE

<222> (11) .. (11)

<223> X is P, A, or absent

<220>

<221> UNSURE

<222> (12) .. (12)

<223> X is S, F, or absent

<220>

<221> UNSURE

<222> (13) .. (13)

<223> X is L, V, or absent

<220>

<221> UNSURE

<222> (14) .. (14)

<223> X is S or absent

<220>

<221> UNSURE

<222> (15) .. (15)

<223> X is V or absent

<220>

<221> UNSURE

<222> (16) .. (16)

<223> X is S or absent

<220>

<221> UNSURE

<222> (17) .. (17)

<223> X is P, L, or absent

<220>

<221> UNSURE

<222> (18) .. (18)

<223> X is G or absent

<220>

<221> UNSURE

<222> (19)..(19)

<223> X is G or absent

<220>

<221> UNSURE

<222> (20)..(20)

<223> X is T or absent

<220>

<221> UNSURE

<222> (21)..(21)

<223> X is V, I, or absent

<220>

<221> UNSURE

<222> (22)..(22)

<223> X is T or absent

<220>

<221> UNSURE

<222> (23)..(23)

<223> X is L or absent

<220>

<221> UNSURE

<222> (24)..(24)

<223> X is T or absent

<220>

<221> UNSURE

<222> (25)..(25)

<223> X is C or absent

<400> 234

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10						15	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25

<210> 235

<211> 15

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (2) .. (2)

<223> X is Y or S

<220>

<221> UNSURE

<222> (4) .. (4)

<223> X is Q or H

<220>

<221> UNSURE

<222> (6) .. (6)

<223> X is L, Q, or P

<220>

<221> UNSURE

<222> (8) .. (8)

<223> X is R or Q

<220>

<221> UNSURE

<222> (12) .. (12)

<223> X is T or P

<220>

<221> UNSURE

<222> (14) .. (14)

<223> X is I or L

<220>

<221> UNSURE

<222> (15) .. (15)

<223> X is Y or S

<400> 235

Trp	Xaa	Gln	Xaa	Thr	Xaa	Gly	Xaa	Ala	Pro	Arg	Xaa	Ile	Xaa	Xaa
1				5					10					15

<210> 236

<211> 32

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (4) .. (4)

<223> X is N, S, D, or R

<220>

<221> UNSURE

<222> (7) .. (7)

<223> X is S or T

<220>

<221> UNSURE

<222> (8) .. (8)

<223> X is G or A

<220>

<221> UNSURE

<222> (10) .. (10)

<223> X is I or V

<220>

<221> UNSURE

<222> (12) .. (12)

<223> X is G or D

<220>

<221> UNSURE

<222> (14) .. (14)

<223> X is K or R

<220>

<221> UNSURE

<222> (16) .. (16)

<223> X is A or T

<220>

<221> UNSURE

<222> (22) .. (22)

<223> X is A or V

<220>

<221> UNSURE

<222> (23) .. (23)

<223> X is Q or R

<220>

<221> UNSURE

<222> (28) .. (28)

<223> X is A, T, or G

<220>

<221> UNSURE

<222> (31) .. (31)

<223> X is Y or H

<400> 236

Gly	Val	Pro	Xaa	Arg	Phe	Xaa	Xaa	Ser	Xaa	Ser	Xaa	Asn	Xaa	Ala	Xaa
1				5				10						15	

Leu	Thr	Ile	Thr	Gly	Xaa	Xaa	Pro	Glu	Asp	Glu	Xaa	Asp	Tyr	Xaa	Cys
			20				25						30		

<210> 237

<211> 14

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (1) .. (1)

<223> X is F or V

<220>

<221> UNSURE

<222> (3) .. (3)

<223> X is G or S

<220>

<221> UNSURE

<222> (6)..(6)

<223> X is H or Q

<400> 237

Xaa	Gly	Xaa	Gly	Thr	Xaa	Leu	Thr	Leu	Gly	Gln	Pro	Lys	Ala
1				5					10				

<210> 238

<211> 25

<212> PRT

<213> canis familiaris;

<400> 238

Ala	Asp	Ser	Gln	Thr	Val	Val	Thr	Gln	Glu	Pro	Ser	Leu	Ser	Val	Ser
1				5					10					15	

Pro	Gly	Gly	Thr	Val	Thr	Leu	Thr	Cys
			20					25

<210> 239

<211> 5

<212> PRT

<213> canis familiaris;

<400> 239

Ile	Thr	Leu	Thr	Cys
1			5	

<210> 240

<211> 7

<212> PRT

<213> canis familiaris;

<400> 240

Gly	Thr	Val	Thr	Leu	Thr	Cys
1				5		

<210> 241

<211> 25

<212> PRT

<213> canis familiaris;

<400> 241

Thr	Asp	Ser	Gln	Thr	Val	Val	Thr	Gln	Glu	Pro	Ser	Leu	Ser	Val	Ser
1				5					10					15	

Pro	Gly	Gly	Thr	Val	Thr	Leu	Thr	Cys
			20					25

<210> 242

<211> 25

<212> PRT

<213> canis familiaris;

<400> 242

Ala	Asp	Ser	Gln	Thr	Val	Val	Thr	Gln	Glu	Pro	Ser	Leu	Ser	Val	Ser
1				5					10					15	

Leu	Gly	Gly	Thr	Val	Thr	Leu	Thr	Cys
			20					25

<210> 243

<211> 25

<212> PRT

<213> canis familiaris;

<400> 243

Ala	Asp	Ser	Gln	Thr	Val	Val	Thr	Gln	Glu	Ala	Ser	Val	Ser	Val	Ser
1				5					10					15	

Pro	Gly	Gly	Thr	Val	Thr	Leu	Thr	Cys
			20					25

<210> 244

<211> 25

<212> PRT

<213> canis familiaris;

<400> 244

Ala	Asp	Ser	Gln	Thr	Val	Val	Ile	Gln	Glu	Pro	Phe	Leu	Ser	Val	Ser
1				5					10					15	

Pro	Gly	Gly	Thr	Val	Thr	Leu	Thr	Cys
			20					25

<210> 245

<211> 15

<212> PRT

<213> canis familiaris;

<400> 245

Trp	Tyr	Gln	Gln	Thr	Leu	Gly	Arg	Ala	Pro	Arg	Thr	Ile	Ile	Tyr
1				5					10					15

<210> 246

<211> 15

<212> PRT

<213> canis familiaris;

<400> 246

Trp	Tyr	Gln	Gln	Thr	Gln	Gly	Arg	Ala	Pro	Arg	Thr	Ile	Ile	Tyr
1				5					10					15

<210> 247

<211> 15

<212> PRT

<213> canis familiaris;

<400> 247

Trp	Ser	Gln	Gln	Thr	Pro	Gly	Gln	Ala	Pro	Arg	Thr	Ile	Ile	Tyr
1				5					10					15

<210> 248

<211> 15

<212> PRT

<213> canis familiaris;

<400> 248

Trp	Tyr	Gln	Gln	Thr	Leu	Gly	Arg	Pro	Pro	Arg	Thr	Ile	Ile	Ser
1				5					10					15

<210> 249

<211> 15

<212> PRT

<213> canis familiaris;

<400> 249

Trp	Tyr	Gln	Gln	Thr	Leu	Gly	Arg	Pro	Pro	Arg	Pro	Ile	Ile	Tyr
1				5					10					15

<210> 250

<211> 15

<212> PRT

<213> canis familiaris;

<400> 250

Trp	Ser	Gln	Gln	Thr	Pro	Gly	Gln	Ala	Pro	Arg	Thr	Ile	Leu	Tyr
1				5					10					15

<210> 251

<211> 15

<212> PRT

<213> canis familiaris;

<400> 251

Trp	Tyr	Gln	His	Thr	Gln	Gly	Arg	Ala	Pro	Arg	Thr	Ile	Ile	Tyr
1				5					10					15

<210> 252

<211> 32

<212> PRT

<213> canis familiaris;

<400> 252

Gly	Val	Pro	Asn	Arg	Phe	Ser	Gly	Ser	Ile	Ser	Gly	Asn	Lys	Ala	Ala
1				5					10					15	

Leu	Thr	Ile	Thr	Gly	Ala	Gln	Pro	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 253

<211> 32

<212> PRT

<213> canis familiaris;

<400> 253

Gly	Val	Pro	Asn	Arg	Phe	Ser	Gly	Ser	Ile	Ser	Gly	Asn	Lys	Ala	Ala
1				5					10					15	

Leu	Thr	Ile	Ile	Gly	Val	Gln	Pro	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 254

<211> 32

<212> PRT

<213> canis familiaris;

<400> 254

Gly	Val	Pro	Asn	Arg	Phe	Ser	Gly	Ser	Ile	Ser	Asp	Asn	Lys	Ala	Ala
1				5					10					15	

Leu	Thr	Ile	Thr	Gly	Val	Gln	Pro	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 255

<211> 32

<212> PRT

<213> canis familiaris;

<400> 255

Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Ile	Ser	Gly	Asn	Lys	Ala	Thr
1				5					10					15	
Leu	Thr	Ile	Thr	Gly	Ala	Arg	Pro	Glu	Asp	Glu	Ala	Asp	Tyr	His	Cys
			20					25					30		

<210> 256

<211> 32

<212> PRT

<213> canis familiaris;

<400> 256

Gly	Val	Pro	Ser	Arg	Phe	Thr	Gly	Ser	Ile	Ser	Gly	Asn	Arg	Ala	Ala
1				5					10					15	
Leu	Thr	Ile	Thr	Gly	Ala	Arg	Pro	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 257

<211> 32

<212> PRT

<213> canis familiaris;

<400> 257

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

<210> 258

<211> 32

<212> PRT

<213> canis familiaris;

<400> 258

Gly	Val	Pro	Asn	Arg	Phe	Thr	Gly	Ser	Ile	Ser	Gly	Asn	Lys	Ala	Ala
1				5					10					15	

Leu	Thr	Ile	Thr	Gly	Ala	Gln	Pro	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 259

<211> 32

<212> PRT

<213> canis familiaris;

<400> 259

Gly	Val	Pro	Arg	Arg	Phe	Ser	Ala	Ser	Val	Ser	Gly	Asn	Lys	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Thr	Gly	Ala	Gln	Pro	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 260

<211> 32

<212> PRT

<213> canis familiaris;

<400> 260

Gly	Val	Pro	Asn	Arg	Phe	Thr	Ala	Ser	Ile	Ser	Gly	Asn	Lys	Ala	Ala
1				5					10					15	

Leu	Thr	Ile	Thr	Gly	Ala	Gln	Pro	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 261

<211> 32

<212> PRT

<213> canis familiaris;

<400> 261

Gly	Val	Pro	Asn	Arg	Phe	Ser	Gly	Ser	Ile	Ser	Gly	Asn	Lys	Ala	Ala
1				5					10					15	

Leu Thr Ile Thr Gly Ala Gln Pro Glu Asp Glu Thr Asp Tyr Tyr Cys
 20 25 30

<210> 262

<211> 15

<212> PRT

<213> canis familiaris;

<400> 262

Val Gly Gly Gly Thr His Leu Thr Val Leu Gly Gln Pro Lys Ala
 1 5 10 15

<210> 263

<211> 12

<212> PRT

<213> canis familiaris;

<400> 263

Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Gly Gln
 1 5 10

<210> 264

<211> 25

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (1) .. (1)

<223> X is S, P, or absent

<220>

<221> unsure

<222> (2) .. (2)

<223> X is W, A, or absent

<220>

<221> unsure

<222> (3) .. (3)

<223> X is A or absent

<220>

<221> unsure

<222> (4) .. (4)

<223> X is Q or absent

<220>

<221> unsure

<222> (5) .. (5)

<223> X is A, S, T, or absent

<220>

<221> unsure

<222> (6) .. (6)

<223> X is V, M, or absent

<220>

<221> unsure

<222> (7) .. (7)

<223> X is L or absent

<220>

<221> unsure

<222> (8) .. (8)

<223> X is T or absent

<220>

<221> unsure

<222> (9) .. (9)

<223> X is Q or absent

<220>

<221> unsure

<222> (10) .. (10)

<223> X is P or absent

<221> unsure

<222> (11) .. (11)

<223> X is A, P, S, or absent

<220>

<221> unsure

<222> (12) .. (12)

<223> X is P, S, or absent

<220>

<221> unsure

<222> (13) .. (13)

<223> X is V, M, or absent

<220>

<221> unsure

<222> (14) .. (14)

<223> X is S or absent

<220>

<221> unsure

<222> (15)..(15)

<223> X is G, A, T, or absent

<220>

<221> unsure

<222> (16)..(16)

<223> X is S, A, T, or absent

<220>

<221> unsure

<222> (17)..(17)

<223> X is L, P, or absent

<220>

<221> unsure

<222> (18)..(18)

<223> X is G or absent

<220>

<221> unsure

<222> (19)..(19)

<223> X is Q or absent

<220>

<221> unsure

<222> (20)..(20)

<223> X is R, T, or absent

<220>

<221> unsure

<222> (21) .. (21)

<223> X is V or absent

<220>

<221> unsure

<223> X is T or absent

<400> 264

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ile	Ser	Cys
			20					25

<210> 265

<211> 17

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (2) .. (2)

<223> X is Y or F

<220>

<221> unsure

<222> (3) .. (3)

<223> X is Q or R

<220>

<221> unsure

<222> (4) .. (4)

<223> X is Q or H

<220>

<221> unsure

<222> (5) .. (5)

<223> X is L, F, or V

<220>

<221> unsure

<222> (6) .. (6)

<223> X is P or L

<220>

<221> unsure

<222> (9) .. (9)

<223> X is T or K

<220>

<221> unsure

<222> (10) .. (10)

<223> X is G, S, or A

<220>

<221> unsure

<222> (13) .. (13)

<223> X is R, K, or S

<220>

<221> unsure

<222> (14) .. (14)

<223> X is T, L, or S

<220>

<221> unsure

<222> (15)..(15)

<223> X is L, V, I, or F

<220>

<221> unsure

<222> (16)..(16)

<223> X is I or A

<220>

<221> unsure

<222> (17)..(17)

<223> X is Y, F, or H

<400> 265

Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Gly	Xaa	Xaa	Tyr	Pro	Xaa	Xaa	Xaa	Xaa
1				5					10					15	

Xaa

<210> 266

<211> 32

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (2)..(2)

<223> X is V or I

<220>

<221> unsure

<222> (4) .. (4)

<223> X is D, A, V, or E

<220>

<221> unsure

<222> (8) .. (8)

<223> X is G or A

<220>

<221> unsure

<222> (9) .. (9)

<223> X is S or P

<220>

<221> unsure

<222> (10) .. (10)

<223> X is R, K, S, or A

<220>

<221> unsure

<222> (13) .. (13)

<223> X is S or N

<220>

<221> unsure

<222> (14) .. (14)

<223> X is T or S

<220>

<221> unsure

<222> (15) .. (15)

<223> X is S or A

<220>

<221> unsure

<222> (16) .. (16)

<223> X is S, T, or A

<220>

<221> unsure

<222> (20) .. (20)

<223> X is S, T, or A

<220>

<221> unsure

<222> (21) .. (21)

<223> X is G or V

<220>

<221> unsure

<222> (22) .. (22)

<223> X is L or I

<220>

<221> unsure

<222> (24) .. (24)

<223> X is A or T

<220>

<221> unsure

<222> (28) .. (28)

<223> X is A, T, or G

<220>

<221> unsure

<222> (29) .. (29)

<223> X is D, E, or N

<220>

<221> unsure

<222> (31) .. (31)

<223> X is Y or F

<400> 266

Gly	Xaa	Pro	Xaa	Arg	Phe	Ser	Xaa	Xaa	Xaa	Ser	Gly	Xaa	Xaa	Xaa	Xaa
1				5					10					15	

Leu	Thr	Ile	Xaa	Xaa	Xaa	Gln	Xaa	Glu	Asp	Glu	Xaa	Xaa	Tyr	Xaa	Cys
			20					25					30		

<210> 267

<211> 14

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (2) .. (2)

<223> X is G, S, or E

<220>

<221> unsure

<222> (5) .. (5)

<223> X is T or Q

<220>

<221> unsure

<222> (8) .. (8)

<223> X is T or absent

<220>

<221> unsure

<222> (9) .. (9)

<223> X is V, F, or absent

<220>

<221> unsure

<222> (10) .. (10)

<223> X is L or absent

<220>

<221> unsure

<222> (11) .. (11)

<223> X is G or absent

<220>

<221> unsure

<222> (12) .. (12)

<223> X is Q, H, N, or absent

<220>

<221> unsure

<222> (13) .. (13)

<223> X is P or E

<220>

<221> unsure

<222> (14) .. (14)

<223> X is K or absent

<400> 267

Phe	Xaa	Gly	Gly	Xaa	His	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10				

<210> 268

<211> 25

<212> PRT

<213> canis familiaris;

<400> 268

Ser	Trp	Ala	Gln	Ala	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Ala	Ala
1				5					10					15	

Leu	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys
			20					25

<210> 269

<211> 25

<212> PRT

<213> canis familiaris;

<400> 269

Ser Trp Ala Gln Ser Ala Leu Thr Gln Pro Ser Ser Val Ser Gly Thr
 1 5 10 15

Leu Gly Gln Thr Val Thr Ile Ser Cys
 20 25

<210> 270

<211> 25

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (14)..(14)

<223> X is S or absent

<220>

<221> UNSURE

<222> (17)..(17)

<223> X is L, P, or absent

<400> 270

Pro Trp Ala Gln Ser Val Leu Thr Gln Pro Ala Ser Val Xaa Gly Ser
 1 5 10 15

Xaa Gly Gln Arg Val Thr Ile Ser Cys
 20 25

<210> 271

<211> 25

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (14)..(14)

<223> X is S or absent

<400> 271

Ser	Trp	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Xaa	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys
			20					25

<210> 272

<211> 25

<212> PRT

<213> canis familiaris;

<400> 272

Ser	Trp	Ala	Gln	Ala	Val	Leu	Thr	Gln	Pro	Pro	Ser	Met	Ser	Thr	Ala
1				5					10					15	

Leu	Gly	Gln	Arg	Val	Thr	Ile	Thr	Cys
			20					25

<210> 273

<211> 25

<212> PRT

<213> canis familiaris;

<400> 273

Ser	Trp	Ala	Gln	Thr	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Leu	Gly	Gln	Thr	Val	Thr	Ile	Ser	Cys
			20					25

<210> 274

<211> 10

<212> PRT

<213> canis familiaris;

<400> 274

Ser Leu Gly Gln Thr Val Thr Ile Ser Cys

1 5 10

<210> 275

<211> 14

<212> PRT

<213> canis familiaris;

<400> 275

Pro Val Ser Ala Ala Pro Gly Gln Arg Val Thr Ile Ser Cys
1 5 10

<210> 276

<211> 11

<212> PRT

<213> canis familiaris;

<400> 276

Gly Ser Leu Gly Gln Thr Val Thr Ile Ser Cys
1 5 10

<210> 277

<211> 25

<212> PRT

<213> canis familiaris;

<400> 277

Ser Trp Ala Gln Ala Val Leu Thr Gln Pro Ala Ser Val Ser Gly Ser
1 5 10 15

Leu Gly Gln Arg Val Thr Ile Ser Cys
20 25

<210> 278

<211> 25

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (17)..(17)

<223> X is L, P, or absent

<400> 278

Ser	Trp	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser
1				5					10					15	

Xaa	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys
			20					25

<210> 279

<211> 6

<212> PRT

<213> canis familiaris;

<400> 279

Arg	Val	Thr	Ile	Ser	Cys
1				5	

<210> 280

<211> 15

<212> PRT

<213> canis familiaris;

<400> 280

Trp	Tyr	Gln	Gln	Val	Pro	Gly	Lys	Ser	Pro	Lys	Thr	Phe	Ile	Tyr
1				5					10					15

<210> 281

<211> 15

<212> PRT

<213> canis familiaris;

<400> 281

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ser	Pro	Arg	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 282

<211> 15

<212> PRT

<213> canis familiaris;

<400> 282

Trp	Phe	Gln	His	Phe	Pro	Gly	Thr	Ser	Pro	Lys	Leu	Leu	Ile	Tyr
1				5					10					15

<210> 283

<211> 15

<212> PRT

<213> canis familiaris;

<400> 283

Trp	Tyr	Gln	Gln	Val	Pro	Gly	Thr	Ser	Pro	Arg	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 284

<211> 15

<212> PRT

<213> canis familiaris;

<400> 284

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ser	Pro	Lys	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 285

<211> 15

<212> PRT

<213> canis familiaris;

<400> 285

Trp	Tyr	Gln	Gln	Phe	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Ile	Ile	Tyr
1				5					10					15

<210> 286

<211> 15

<212> PRT

<213> canis familiaris;

<400> 286

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Lys	Ser	Pro	Lys	Ser	Ile	Ile	Phe
1				5					10					15

<210> 287

<211> 15

<212> PRT

<213> canis familiaris;

<400> 287

Trp	Tyr	Arg	Gln	Phe	Pro	Gly	Thr	Gly	Pro	Arg	Thr	Val	Ala	Tyr
1				5					10					15

<210> 288

<211> 15

<212> PRT

<213> canis familiaris;

<400> 288

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Lys	Ser	Pro	Lys	Thr	Ile	Ile	Tyr
1				5					10					15

<210> 289

<211> 15

<212> PRT

<213> canis familiaris;

<400> 289

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ser	Pro	Arg	Thr	Leu	Ile	His
1				5					10					15

<210> 290

<211> 15

<212> PRT

<213> canis familiaris;

<400> 290

Trp	Tyr	Gln	Gln	Phe	Leu	Gly	Thr	Gly	Pro	Arg	Thr	Ile	Ile	Tyr
1				5					10					15

<210> 291

<211> 15

<212> PRT

<213> canis familiaris;

<400> 291

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Lys	Ala	Pro	Ser	Leu	Leu	Ile	Tyr
1				5					10					15

<210> 292

<211> 15

<212> PRT

<213> canis familiaris;

<400> 292

Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Lys	Gly	Pro	Arg	Thr	Val	Ile	Tyr
1				5					10					15

<210> 293

<211> 32

<212> PRT

<213> canis familiaris;

<400> 293

Gly	Val	Pro	Val	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Ser	Thr	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Thr	Gly	Ile	Gln	Ala	Glu	Asp	Glu	Thr	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 294

<211> 32

<212> PRT

<213> canis familiaris;

<400> 294

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Thr	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Thr	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 295

<211> 32

<212> PRT

<213> canis familiaris;

<400> 295

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Asn	Thr	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 296

<211> 32

<212> PRT

<213> canis familiaris;

<400> 296

Gly Ile Pro Ala Arg Phe Ser Gly Ser Arg Ser Gly Asn Thr Ala Ser
 1 5 10 15

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 297

<211> 32

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (19) .. (19)

<223> X is I

<400> 297

Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Ser Thr Ala Thr
 1 5 10 15

Leu Thr Xaa Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 298

<211> 32

<212> PRT

<213> canis familiaris;

<400> 298

Gly Val Pro Ala Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr
 1 5 10 15

Leu Thr Ile Thr Gly Ile Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
 20 25 30

<210> 299

<211> 32

<212> PRT

<213> canis familiaris;

<400> 299

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

<210> 300

<211> 32

<212> PRT

<213> canis familiaris;

<400> 300

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

<210> 301

<211> 32

<212> PRT

<213> canis familiaris;

<400> 301

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

<210> 302

<211> 32

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (3)..(3)

<223> X is P

<400> 302

Gly	Val	Xaa	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Thr	Ala	Thr
1				5					10					15	
Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			20					25					30		

<210> 303

<211> 32

<212> PRT

<213> canis familiaris;

<400> 303

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

<210> 304

<211> 32

<212> PRT

<213> canis familiaris;

<400> 304

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

<210> 305

<211> 32

<212> PRT

<213> canis familiaris;

<400> 305

Gly	Val	Pro	Glu	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Ser	Ser	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Thr	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asn	Tyr	Tyr	Cys
			20					25					30		

<210> 306

<211> 32

<212> PRT

<213> canis familiaris;

<400> 306

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Asn	Thr	Ala	Thr
1				5					10					15	

Leu	Thr	Thr	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Phe	Cys
			20					25					30		

<210> 307

<211> 32

<212> PRT

<213> canis familiaris;

<400> 307

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ala	Ser	Gly	Ser	Ser	Ala	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Glu	Tyr	Tyr	Cys
			20					25					30		

<210> 308

<211> 14

<212> PRT

<213> canis familiaris;

<400> 308

Phe	Gly	Ser	Gly	Thr	Gln	Leu	Thr	Val	Leu	Gly	Gln	Asn	Glu
1				5					10				

<210> 309

<211> 14

<212> PRT

<213> canis familiaris;

<400> 309

Phe	Gly	Gly	Gly	Thr	His	Leu	Thr	Val	Leu	Gly	Gln	His	Glu
1				5					10				

<210> 310

<211> 15

<212> PRT

<213> canis familiaris;

<400> 310

Phe	Gly	Glu	Gly	Thr	His	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala
1				5					10					15

<210> 311

<211> 15

<212> PRT

<213> canis familiaris;

<400> 311

Phe	Gly	Gly	Gly	Thr	His	Leu	Thr	Val	Phe	Gly	Gln	Pro	Lys	Ala
1				5					10					15

<210> 312

<211> 23

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (1) .. (1)

<223> X is D, E, A, or absent

<220>

<221> unsure

<222> (2) .. (2)

<223> X is I, L, V, or absent

<220>

<221> unsure

<222> (3) .. (3)

<223> X is V or absent

<220>

<221> unsure

<222> (4) .. (4)

<223> X is M, L, or absent

<220>

<221> unsure

<222> (5) .. (5)

<223> X is T or absent

<220>

<221> unsure

<222> (6) .. (6)

<223> X is Q, E, or absent

<220>

<221> unsure

<222> (7) .. (7)

<223> X is T, A, or absent

<220>

<221> unsure

<222> (8) .. (8)

<223> X is P or absent

<220>

<221> unsure

<222> (9) .. (9)

<223> X is P, L, R, S, or absent

<220>

<221> unsure

<222> (10) .. (10)

<223> X is P, S, or absent

<220>

<221> unsure

<222> (11) .. (11)

<223> X is L or absent

<220>

<221> unsure

<222> (12) .. (12)

<223> X is S or absent

<220>

<221> unsure

<222> (13) .. (13)

<223> X is V, A, or absent

<220>

<221> unsure

<222> (14) .. (14)

<223> X is S or absent

<220>

<221> unsure

<222> (15) .. (15)

<223> X is P or absent

<220>

<221> unsure

<222> (16) .. (16)

<223> X is G, R, or absent

<220>

<221> unsure

<222> (17) .. (17)

<223> X is E or absent

<220>

<221> unsure

<222> (18) .. (18)

<223> X is P, T, S, or absent

<220>

<221> unsure

<222> (19) .. (19)

<223> X is A or absent

<220>

<221> unsure

<222> (20) .. (20)

<223> X is S, F, or absent

<220>

<221> unsure

<222> (21) .. (21)

<223> X is I or absent

<220>

<221> unsure

<222> (22) .. (22)

<223> X is S or absent

<220>

<221> unsure

<222> (23) .. (23)

<223> X is C, Y, or absent

<400> 312

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15	

Xaa Xaa Xaa Xaa Xaa Xaa Xaa

20

<210> 313

<211> 15

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (1) .. (1)

<223> X is W or absent

<220>

<221> unsure

<222> (2) .. (2)

<223> X is F, Y, S, L, or absent

<220>

<221> unsure

<222> (3) .. (3)

<223> X is R, L, Q, M, or absent

<220>

<221> unsure

<222> (4) .. (4)

<223> X is Q, H, or absent

<220>

<221> unsure

<222> (5) .. (5)

<223> X is K, R, or absent

<220>

<221> unsure

<222> (6) .. (6)

<223> X is P, S, or absent

<220>

<221> unsure

<222> (7) .. (7)

<223> X is G or absent

<220>

<221> unsure

<222> (8) .. (8)

<223> X is Q, H, or absent

<220>

<221> unsure

<222> (9) .. (9)

<223> X is S, A, or absent

<220>

<221> unsure

<222> (10) .. (10)

<223> X is P or absent

<220>

<221> unsure

<222> (11) .. (11)

<223> X is Q, E, R, or absent

<220>

<221> unsure

<222> (12) .. (12)

<223> X is R, G, D, L, T, I, A, or absent

<220>

<221> unsure

<222> (13) .. (13)

<223> X is R, L, or absent

<220>

<221> unsure

<222> (14) .. (14)

<223> X is T or absent

<220>

<221> unsure

<222> (15) .. (15)

<223> X is Y, H, S, W, F, or absent

<400> 313

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15

<210> 314

<211> 32

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (3) .. (3)

<223> X is S or P

<220>

<221> unsure

<222> (4) .. (4)

<223> X is D or E

<220>

<221> unsure

<222> (5) .. (5)

<223> X is R or G

<220>

<221> unsure

<222> (6) .. (6)

<223> X is F or I

<220>

<221> unsure

<222> (7) .. (7)

<223> X is S or A

<220>

<221> unsure

<222> (9) .. (9)

<223> X is S or R

<220>

<221> unsure

<222> (12) .. (12)

<223> X is G or V

<220>

<221> unsure

<222> (13) .. (13)

<223> X is T or A

<220>

<221> unsure

<222> (15) .. (15)

<223> X is F or C

<220>

<221> unsure

<222> (18) .. (18)

<223> X is R, K, T, or E

<220>

<221> unsure

<222> (20) .. (20)

<223> X is S, T, or G

<220>

<221> unsure

<222> (21) .. (21)

<223> X is R or G

<220>

<221> unsure

<222> (22) .. (22)

<223> X is V or A

<220>

<221> unsure

<222> (23) .. (23)

<223> X is E, V, or G

<220>

<221> unsure

<222> (24) .. (24)

<223> X is A or D

<220>

<221> unsure

<222> (25) .. (25)

<223> X is D, N, A, E, or G

<220>

<221> unsure

<222> (26) .. (26)

<223> X is D or G

<220>

<221> unsure

<222> (27) .. (27)

<223> X is A, T, S, V, or G

<220>

<221> unsure

<222> (28) .. (28)

<223> X is A or G

<220>

<221> unsure

<222> (29) .. (29)

<223> X is V, L, or I

<220>

<221> unsure

<222> (31) .. (31)

<223> X is Y, H, F, or C

<400> 314

Gly	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Gly	Ser	Xaa	Xaa	Asp	Xaa	Thr
1			5						10					15	

Leu	Xaa	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Xaa	Cys
			20					25					30		

<210> 315

<211> 18

<212> PRT

<213> canis familiaris;

<220>

<221> unsure

<222> (1) .. (1)

<223> X is F, L, or S

<220>

<221> unsure

<222> (2) .. (2)

<223> X is S or G

<220>

<221> unsure

<222> (3) .. (3)

<223> X is Q, A, K, P, or T

<220>

<221> unsure

<222> (5) .. (5)

<223> X is T or A

<220>

<221> unsure

<222> (6) .. (6)

<223> X is K, N, or H

<220>

<221> unsure

<222> (7) .. (7)

<223> X is L or V

<220>

<221> unsure

<222> (8) .. (8)

<223> X is E, D, V, or G

<220>

<221> unsure

<222> (9) .. (9)

<223> X is I, M, or L

<220>

<221> unsure

<222> (10) .. (10)

<223> X is K or R

<400> 315

Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Asn	Asp	Ala	Gln	Pro
1				5					10					15	

Ala Val

<210> 316

<211> 23

<212> PRT

<213> canis familiaris;

<400> 316

Asp	Thr	Val	Leu	Thr	Gln	Thr	Pro	Pro	Ser	Leu	Ser	Val	Ser	Pro	Gly
1				5					10					15	

Glu	Pro	Ala	Ser	Ile	Ser	Cys
			20			

<210> 317

<211> 23

<212> PRT

<213> canis familiaris;

<400> 317

Asp	Ile	Val	Met	Thr	Gln	Ala	Pro	Pro	Ser	Leu	Ser	Val	Ser	Pro	Gly
1				5					10					15	

Glu	Pro	Ala	Ser	Ile	Ser	Cys
			20			

<210> 318

<211> 23

<212> PRT

<213> canis familiaris;

<400> 318

Asp	Leu	Val	Leu	Thr	Gln	Thr	Pro	Arg	Ser	Leu	Ser	Val	Ser	Pro	Gly
1				5					10					15	

Glu	Thr	Ala	Ser	Ile	Ser	Cys
			20			

<210> 319

<211> 23

<212> PRT

<213> canis familiaris;

<400> 319

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Ser	Val	Ser	Pro	Gly
1				5					10					15	

Glu	Pro	Ala	Ser	Ile	Ser	Cys
			20			

<210> 320

<211> 23

<212> PRT

<213> canis familiaris;

<400> 320

Asp	Ile	Val	Met	Thr	Gln	Ala	Pro	Pro	Pro	Leu	Ser	Val	Ser	Pro	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

11. $\frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$

<213> canis familiaris;

<400> 324

Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Ser	Val	Ser	Pro	Gly	Glu	Pro
1				5					10					15	

Ala	Ser	Ile	Ser	Cys
			20	

<210> 325

<211> 22

<212> PRT

<213> canis familiaris;

<400> 325

Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Ser	Val	Ser	Pro	Gly	Glu
1				5					10					15	

Pro	Ala	Ser	Ile	Ser	Cys
			20		

<210> 326

<211> 23

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (11)..(11)

<223> X is L or absent

<400> 326

Asp	Ile	Val	Met	Thr	Gln	Ala	Pro	Pro	Ser	Xaa	Ser	Val	Ser	Pro	Gly
1				5					10					15	

Glu	Pro	Ala	Ser	Ile	Ser	Cys
			20			

<210> 327

<211> 23

<212> PRT

<213> canis familiaris;

<400> 327

Asp	Val	Val	Met	Thr	Gln	Ala	Pro	Pro	Ser	Leu	Ser	Val	Ser	Pro	Arg
1				5					10					15	

Glu	Pro	Ala	Ser	Ile	Ser	Cys
				20		

<210> 328

<211> 23

<212> PRT

<213> canis familiaris;

<400> 328

Asp	Val	Val	Met	Thr	Gln	Ala	Pro	Pro	Ser	Leu	Ser	Val	Ser	Pro	Gly
1				5					10					15	

Glu	Pro	Ala	Ser	Ile	Ser	Cys
				20		

<210> 329

<211> 22

<212> PRT

<213> canis familiaris;

<220>

<221> UNSURE

<222> (14) .. (14)

<223> X is S or absent

<220>

<221> UNSURE

<222> (15)..(15)

<223> X is P or absent

<400> 329

Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Ser	Val	Ser	Xaa	Xaa	Glu
1				5					10					15	

Pro	Ala	Ser	Ile	Ser	Cys
			20		

<210> 330

<211> 23

<212> PRT

<213> canis familiaris;

<400> 330

Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Pro	Ser	Leu	Ser	Val	Ser	Pro	Arg
1				5					10					15	

Glu	Pro	Ala	Ser	Ile	Ser	Cys
			20			

<210> 331

<211> 23

<212> PRT

<213> canis familiaris;

<400> 331

Glu	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Ser	Val	Ser	Pro	Gly
1				5					10					15	

Glu	Thr	Ala	Ser	Ile	Ser	Tyr
			20			

<210> 332

<211> 23

<212> PRT

DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS
COMPREND PLUS D'UN TOME.**

CECI EST LE TOME __1__ DE __2__

NOTE: Pour les tomes additionels, veuillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

**THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE
THAN ONE VOLUME.**

THIS IS VOLUME __1__ OF __2__

NOTE: For additional volumes please contact the Canadian Patent Office.

THE EMBODIMENTS OF THE INVENTION FOR WHICH AN EXCLUSIVE PROPERTY OR PRIVILEGE IS CLAIMED ARE DEFINED AS FOLLOWS:

1. A canine heavy chain variable domain polypeptide comprising the sequence:



wherein

Fr^1 is $\text{X}'^1 \text{X}'^2 \text{X}'^3 \text{X}'^4 \text{X}'^5 \text{X}'^6 \text{X}'^7 \text{X}'^8 \text{X}'^9 \text{X}'^{10} \text{X}'^{11} \text{X}'^{12} \text{X}'^{13} \text{X}'^{14} \text{X}'^{15}$
 $\text{X}'^{16} \text{X}'^{17} \text{X}'^{18} \text{X}'^{19} \text{X}'^{20} \text{X}'^{21} \text{X}'^{22} \text{X}'^{23} \text{X}'^{24} \text{X}'^{25}$;

Fr^2 is $\text{X}'^{26} \text{X}'^{27} \text{X}'^{28} \text{X}'^{29} \text{X}'^{30} \text{X}'^{31} \text{X}'^{32} \text{X}'^{33} \text{X}'^{34} \text{X}'^{35} \text{X}'^{36} \text{X}'^{37} \text{X}'^{38} \text{X}'^{39}$
 X'^{40}

Fr^3 is $\text{X}'^{41} \text{X}'^{42} \text{X}'^{43} \text{X}'^{44} \text{X}'^{45} \text{X}'^{46} \text{X}'^{47} \text{X}'^{48} \text{X}'^{49} \text{X}'^{50} \text{X}'^{51} \text{X}'^{52} \text{X}'^{53} \text{X}'^{54}$
 $\text{X}'^{55} \text{X}'^{56} \text{X}'^{57} \text{X}'^{58} \text{X}'^{59} \text{X}'^{60} \text{X}'^{61} \text{X}'^{62} \text{X}'^{63} \text{X}'^{64} \text{X}'^{65} \text{X}'^{66} \text{X}'^{67} \text{X}'^{68} \text{X}'^{69}$
 $\text{X}'^{70} \text{X}'^{71} \text{X}'^{72}$, and

Fr^4 is $\text{X}'^{73} \text{X}'^{74} \text{X}'^{75} \text{X}'^{76} \text{X}'^{77} \text{X}'^{78} \text{X}'^{79} \text{X}'^{80} \text{X}'^{81} \text{X}'^{82}$,

X'^1 is <u>E</u> ,	X'^2 is <u>V</u> ,	X'^3 is <u>Q</u> ;	X'^4 is <u>L</u> ,	X'^5 is <u>V</u> ;
X'^6 is <u>Q</u> ;	X'^7 is <u>S</u> ,	X'^8 is <u>A</u> ,	X'^9 is <u>A</u> ,	X'^{10} is <u>E</u> ;
X'^{11} is <u>V</u> ,	X'^{12} is <u>K</u> ,	X'^{13} is <u>K</u> ,	X'^{14} is <u>P</u> ,	X'^{15} is <u>G</u> ,
X'^{16} is <u>A</u> ,	X'^{17} is <u>S</u> ,	X'^{18} is <u>V</u> ,	X'^{19} is <u>K</u> ,	X'^{20} is <u>V</u>
X'^{21} is <u>S</u> ,	X'^{22} is <u>C</u> ,	X'^{23} is <u>K</u> ,	X'^{24} is <u>T</u> ,	X'^{25} is <u>S</u> ,
X'^{26} is <u>W</u> ,	X'^{27} is <u>V</u> ,	X'^{28} is <u>Q</u> ,	X'^{29} is <u>Q</u> ,	X'^{30} is <u>A</u> ,
X'^{31} is <u>P</u> ;	X'^{32} is <u>G</u> ,	X'^{33} is <u>A</u> ,	X'^{34} is <u>G</u> ,	X'^{35} is <u>L</u> ,
X'^{36} is <u>D</u> or E,	X'^{37} is <u>W</u> ,	X'^{38} is <u>M</u> ,	X'^{39} is <u>G</u> ,	X'^{40} is <u>W</u> ,
X'^{41} is <u>R</u> ,	X'^{42} is <u>V</u> ,	X'^{43} is <u>T</u> ,	X'^{44} is <u>L</u> ,	X'^{45} is <u>T</u> ,
X'^{46} is <u>A</u> ,	X'^{47} is <u>D</u> ,	X'^{48} is <u>T</u> ,	X'^{49} is <u>S</u> ,	X'^{50} is <u>T</u> ,
X'^{51} is <u>S</u> or N,	X'^{52} is <u>T</u> ,	X'^{53} is <u>A</u> or V,	X'^{54} is <u>Y</u> ,	X'^{55} is <u>M</u> ,
X'^{56} is <u>E</u> ,	X'^{57} is <u>L</u> ,	X'^{58} is <u>S</u>	X'^{59} is <u>S</u> or N,	X'^{60} is <u>L</u> ,
X'^{61} is <u>R</u> ,	X'^{62} is <u>A</u> or T,	X'^{63} is <u>E</u> ,	X'^{64} is <u>D</u> ,	X'^{65} is <u>T</u> or A,
X'^{66} is <u>A</u> ,	X'^{67} is <u>V</u> ,	X'^{68} is <u>Y</u> ,	X'^{69} is <u>Y</u> ,	X'^{70} is <u>C</u> ,
X'^{71} is <u>A</u> ,	X'^{72} is <u>R</u> or <u>S</u> ,	X'^{73} is <u>Y</u> or L,	X'^{74} is <u>W</u> ;	X'^{75} is <u>G</u> ,
X'^{76} is <u>Q</u> ,	X'^{77} is <u>G</u> ,	X'^{78} is <u>T</u> ,	X'^{79} is <u>L</u> ,	X'^{80} is <u>V</u> ,
X'^{81} is <u>T</u> , and	X'^{82} is <u>V</u> .			

2. The canine heavy chain variable domain polypeptide according to claim 1 comprising the sequence:



wherein

Fr¹ is EVQLVQSAAEVKKPGASVKVTSCKTS,

Fr² is WVQQAPGAGLDWMGW or WVQQAPGAGLEWMGW,

Fr³ is RVTLTADTSTSTAYMELSSLRAEDTAVYYCAS,

RVTLTADTSTNTVYMELSNLRTEDTAVYYCAR, or

RVTLTADTSTSTAYMELSSLRAEDAAVYYCAS, and

Fr⁴ is YWGQGTLVTV or LWGQGTLVTV.

3. The canine heavy chain variable domain polypeptide according to claim 1 comprising the sequence:



wherein

#	Fr ¹	Fr ²	Fr ³	Fr ⁴
H39 2	EVQLVQSAAEVKKPGASVKVTSCK TS	WVQQAPGAGL DWMGW	RVTLTADTSTSTAYM ELSSLRAEDTAVYYC AS	YWGQGTLVT V
H76	EVQLVQSAAEVKKPGASVKVTSCK TS	WVQQAPGAGL DWMGW	RVTLTADTSTSTAYM ELSSLRAEDTAVYYC AR	YWGQGTLVT V
H64 5	EVQLVQSAAEVKKPGASVKVTSCK TS	WVQQAPGAGL EWMGW	RVTLTADTSTNTVYM ELSNLRTEDTAVYYC AR	YWGQGTLVT V
Or				
H74	EVQLVQSAAEVKKPGASVKVTSCK TS	WVQQAPGAGL DWMGW	RVTLTADTSTSTAYM ELSSLRAEDAAVYYC AS	LWGQGTLVT V

4. The canine heavy chain variable domain polypeptide according to any one of claims 1 - 3, wherein the CDR's are all from a canine antibody.
5. The canine heavy chain variable domain polypeptide according to any one of claims 1 - 3, wherein the CDR's are all from the same non-canine antibody.

6. The canine heavy chain variable domain polypeptide according to any one of claims 1 - 3, wherein two CDR's are from the same non-canine antibody and the third is a canine CDR.
7. The canine heavy chain variable domain polypeptide according to claim 6, wherein the canine CDR is CDR¹.
8. The canine heavy chain variable domain polypeptide according to any one of claims 1 - 3, wherein CDR¹ is

a) C¹₂ C¹₃ C¹₄ C¹₅ C¹₆ C¹₇ C¹₈ C¹₉ C¹₁₀ C¹₁₁, wherein

C ¹ ₂ is <u>G</u> ,	C ¹ ₃ is <u>F</u> or L,	C ¹ ₄ is <u>T</u> , S, or N,
C ¹ ₅ is <u>F</u> ,	C ¹ ₆ is <u>S</u> , G, N, or R,	C ¹ ₇ is <u>S</u> , D, G, N, Y, D, R, H, T, or Y,
C ¹ ₈ is <u>Y</u> , F, N, or C,	C ¹ ₉ is <u>G</u> , D, H, W, S, L, A, or V,	C ¹ ₁₀ is <u>M</u> ,
and C ¹ ₁₁ is <u>S</u> , N, G, Y, I, or L;		

b) selected from the group consisting of:

GFTFSIYGMN	GFTFSDYGMN	GFTFSSYDM	GFTFSSYSMS	GFTFSDYGMS	GFTFSSYGMS
,	,	S,	,	,	,
GFNFGSYHMG	GFTFSYYLMS	GFTFRTYGM	GFTFSGYWMS	GLSFGDFAMN	GFTFSDYYMY
,	,	S,	,	,	,
GFTFSGCAMI	GFTFSNYDMS	GFTFSAYDM	GFSFSHNDMS	GFTFSRYWMS	GFTFNSYWMS
,	,	L,	,	,	,
and	GFIFSSFHMS				
	;				

c) C¹₁ C¹₂ C¹₃ C¹₄ C¹₅ C¹₆ C¹₇ C¹₈ C¹₉ C¹₁₀, wherein

C ¹ ₁ is <u>G</u> ,	C ¹ ₂ is <u>Y</u> ,	C ¹ ₃ is <u>T</u> or I,
C ¹ ₄ is <u>F</u> ,	C ¹ ₅ is <u>T</u> or I,	C ¹ ₆ is <u>D</u> ,
C ¹ ₇ is <u>Y</u> or Q,	C ¹ ₈ is <u>Y</u> ,	C ¹ ₉ is <u>M</u> ,
and	C ¹ ₁₀ is <u>H</u> ,	

d) selected from the group consisting of GYTFTDYMH and GYIFIDQYMH;

e) C¹₁ C¹₂ C¹₃ C¹₄ C¹₅ C¹₆ C¹₇ C¹₈ C¹₉ C¹₁₀, wherein

C ¹ is <u>G</u> ,	C ² is <u>S</u> ,	C ³ is <u>V</u> ,
C ⁴ is <u>T</u> or <u>N</u> ,	C ⁵ is <u>D</u> or <u>S</u> ,	C ⁶ is <u>I</u> or <u>G</u> ,
C ⁷ is <u>Y</u> or <u>H</u> ,	C ⁸ is <u>Y</u> ,	C ⁹ is <u>W</u> ,
and	C ¹⁰ is <u>S</u> ,	

f) selected from the group consisting of GSVTDIHYWS and GSVNSGGYYWS, or

g) mouse 15A2 antibody CDR¹, SGYSFTDYFMN.

9. The canine heavy chain variable domain polypeptide according to any one of claims 1 - 3, wherein CDR² is

a) C¹¹ C¹² C¹³ C¹⁴ C¹⁵ C¹⁶ C¹⁷ C¹⁸ C¹⁹ C²⁰ C²¹ C²² C²³ C²⁴ C²⁵ C²⁶ C²⁷, wherein

C ¹¹ is <u>Y</u> , G, V, Q, D, E, S, T, A, R, or W;	C ¹² is <u>I</u> ;	C ¹³ is <u>S</u> , N, H, W, or R;
C ¹⁴ is <u>S</u> , Y, T, N, D, G, R, or D;	C ¹⁵ is <u>G</u> , D, S, or A;	C ¹⁶ is <u>G</u> , E, or A;
C ¹⁷ is <u>S</u> , D, G, T, R, Y, or E;	C ¹⁸ is <u>T</u> , S, Y, N, I, or G;	C ¹⁹ is <u>T</u> , G, R, L F, Y, I, E, or R;
C ²⁰ is <u>Y</u> , S, F, -, T, D, or H;	C ²¹ is <u>Y</u> , F, or H;	C ²² is <u>A</u> , T, or S;
C ²³ is <u>D</u> or G;	C ²⁴ is <u>A</u> or T;	C ²⁵ is <u>V</u> ;
C ²⁶ is <u>K</u> or R; and	C ²⁷ is <u>G</u> ;	

b) selected from the group consisting of

VINSAGDTG-YAGAVKG	YISTGGGTTSFADAVKG	YISSDGRSTSYTDAVKG	GINSGGSSTYYTDAVKG
GINSGGSTYYTDAVKG	WIRYDGSSTYYADAVKG	YIHNDGGTRTYSDTVKG	EISDSGDYLDYTDAVKG
WIWYGGSTYYADAVKG	SISSSGGTF-YADAVKG	EISGSGTTTHYEDTVRG	TINRSGTTY-YADTVKG
RIRGDGTNIYYADAVKG	YINSDGSTYYADAVKG	AI SYDGSSTYYTDAVKG	YINSGGGIIFYADAVKG
SIRYDETGTSYTDAVKG	DISDSAYSTYYTDAVKG	QISVGGEIE-YADAVKG	GINGGGTTRFYSDAVRG
and	TISYDGSSTFHTDAVKG;		

c) C¹¹ C¹² C¹³ C¹⁴ C¹⁵ C¹⁶ C¹⁷ C¹⁸ C¹⁹ C²⁰ C²¹ C²² C²³ C²⁴ C²⁵ C²⁶, wherein

C ¹¹ is <u>I</u> ,	C ¹² is <u>D</u> ,	C ¹³ is <u>P</u> ,
C ¹⁴ is <u>E</u> ,	C ¹⁵ is <u>D</u> ,	C ¹⁶ is <u>G</u> or D,
C ¹⁷ is <u>T</u> ,	C ¹⁸ is <u>T</u> ,	C ¹⁹ is <u>S</u> or G,
C ¹¹⁰ is <u>Y</u> ,	C ¹¹¹ is <u>A</u> ,	C ¹¹² is <u>Q</u> ,
C ¹¹³ is <u>K</u> ,	C ¹¹⁴ is <u>F</u> ,	C ¹¹⁵ is <u>Q</u> ,
and	C ¹¹⁶ is <u>G</u> ,	

d) selected from the group consisting of IDPEDGTTSYAQKFQG and IDPEDDTTGYAQKFQG

e) C¹¹ C¹² C¹³ C¹⁴ C¹⁵ C¹⁶ C¹⁷ C¹⁸ C¹⁹ C¹¹⁰ C¹¹¹ C¹¹² C¹¹³ C¹¹⁴ C¹¹⁵ C¹¹⁶, wherein

C ¹¹ is <u>Y</u> ,	C ¹² is <u>W</u> ,	C ¹³ is <u>R</u> or <u>S</u> ,
C ¹⁴ is <u>G</u> ,	C ¹⁵ is <u>G</u> or <u>T</u> ,	C ¹⁶ is <u>T</u> ,
C ¹⁷ is <u>N</u> or <u>H</u> ,	C ¹⁸ is <u>Y</u> or <u>H</u> ,	C ¹⁹ is <u>N</u> ,
C ¹¹⁰ is <u>P</u> ,	C ¹¹¹ is <u>A</u> or <u>T</u> ,	C ¹¹² is <u>F</u> ,
C ¹¹³ is <u>Q</u> ,	C ¹¹⁴ is <u>E</u> or <u>G</u> ,	C ¹¹⁵ is <u>R</u> ,
and	C ¹¹⁶ is <u>I</u> ,	

f) selected from the group consisting of YWRGGTNHNPFAQERI and YWSGTTHYNPTFQGRI; or

g) mouse 15A2 antibody CDR², RINPFNGDPFYNQKFKG.

10. The canine heavy chain variable domain polypeptide according to any one of claims 1 - 3, wherein CDR³ is

a) C¹¹¹ C¹¹² C¹¹³ C¹¹⁴ C¹¹⁵ C¹¹⁶ C¹¹⁷ C¹¹⁸ C¹¹⁹ C¹¹¹⁰ C¹¹¹¹ C¹¹¹² C¹¹¹³ C¹¹¹⁴ C¹¹¹⁵ C¹¹¹⁶ C¹¹¹⁷ C¹¹¹⁸ C¹¹¹⁹ C¹¹²⁰, wherein

C ¹¹¹ is <u>D</u> , L, Y, T, G, X, E, A, V, W, I, or Q,	C ¹¹² is <u>G</u> , R, I, H, T, P, S, Y, F, D, or W,
C ¹¹³ is <u>D</u> , E, Y, V, W, G, S, A, M, I, T, L, P, or R,	C ¹¹⁴ is <u>G</u> , <u>S</u> , I, A, Y, L, T, Q, D, I, N, L, R,

C' ' ' ' ' ⁵ is <u>T</u> , Y, S, F, L, C, W, X, G, or E,	C' ' ' ' ' ⁶ is <u>S</u> , T, V, Y, M, H, C, G, F, P, K, W, or --,
C' ' ' ' ' ⁷ is <u>_</u> , V, E, W, S, T, D, L, G, Y, or K,	C' ' ' ' ' ⁸ is <u>_</u> , A, G, R, Y, E, D, W, M, or S,
C' ' ' ' ' ⁹ is <u>_</u> , E, P, V, D, G, Y, W, F, or K,	C' ' ' ' ' ¹⁰ is <u>_</u> , L, G, W, Y, A, N, S, F, C, D, T, or P,
C' ' ' ' ' ¹¹ is <u>_</u> , D, S, F, N, Y, C, A, or R,	C' ' ' ' ' ¹² is <u>_</u> , Y, F, G, L, D, or P,
C' ' ' ' ' ¹³ is <u>_</u> , F, D, G, N, H, R, or G,	C' ' ' ' ' ¹⁴ is <u>_</u> , D, V, I, W, or F,
C' ' ' ' ' ¹⁵ is <u>_</u> , V, D, or G,	C' ' ' ' ' ¹⁶ is <u>_</u> , H, or F,
C' ' ' ' ' ¹⁷ is <u>_</u> or D,	C' ' ' ' ' ¹⁸ is <u>_</u> or Y,
C' ' ' ' ' ¹⁹ is <u>_</u> or L, and	C' ' ' ' ' ²⁰ is <u>_</u> or N;

b) selected from the group consisting of

DREITTVAELD,	LIYGYVEGPGSYFD,	YHDGSYVRVWFY,
TTVATME,	GGDSSHWPYNFD,	DPWSSSWYDAFG,
XTYGTSSEGNYLG,	LSGYCTDDSCFNVVHDYL N,	GGDLFG,
GGDLFG,	EYSSSFD,	DPATLPTGEFD,
DRGQCTVDYCADHID,	ASMDTKTFD,	DFGDWVL,
GDSSXW,	VSISSSWWGRYFD,	WDNG,
EYLGE,	ITPLGPGDFD,	DGGITSYMKTNLD,
ARERYCKDDYCFRWGFD ,	and	QWRNTWYSFPDPGFD ;

- c) selected from the group consisting of GGSRPFNAFG, KWRYYGSQD, DIWDFD, and YIYGAAAYLD;
- d) selected from the group consisting of NSD and LYRSNYLLD; or
- e) mouse 15A2 antibody CDR³, FYYGRYYAMDY.

11. The canine heavy chain variable domain polypeptide according to any one of claims 1 - 3, wherein

CDR¹ is mouse 15A2 antibody CDR¹, SGYSFTDYFMN; and/or

CDR² is mouse 15A2 antibody CDR², RINPFNGDPFYNQKFKG; and/or

CDR³ is mouse 15A2 antibody CDR³, FYYGRYYAMDY.

12. A canine heavy chain variable domain polypeptide that is:

EVQLVQSAAEVKKPGASVKVCKTSGYSFTDYFMNWVQQAPGKGLDWMGRINPFNGDPFYNQ
KFKGRVTLTADTSTSTAYMELSSLRAEDAAVYYCARFYYGRYYAMDYWGQGTLLVTV.

13. A nucleic acid encoding the canine heavy chain variable domain polypeptide according to any one of claims 1 - 12, wherein each codon is any codon of the genetic code that codes for the corresponding amino acid of the polypeptide.
14. A nucleic acid encoding a canine heavy chain variable domain, the nucleic acid comprising framework-encoding sequences selected from
- (a) the framework-encoding nucleic acid sequences of one of the nucleic acids selected from the group consisting of:
- (i) ATGGACTGCA GCTGGAGAAT CTTCTTCCTG CTGGCACTGG CCACAGGTGT
GCACTCT[GAG GTCCAGCTGG TGCAGTCTGC AGCTGAGGTT
AAAAAGCCAG GGGCATCTGT GAAGGTCTCC TGCAAGACAT
CT]GGATACAC CTTCACTGAC TACTATATGC AC[TGGGTACA
ACAGGCTCCA GGAGCAGGGC TTGATTGGAT GGGATGG]ATT
GATCCTGAAG ATGGTACCAC AAGTTATGCA CAGAAGTTCC
AGGGC[AGAGT CACCCTGACG GCAGACACAT CCACAAGCAC
AGCCTACATG GAGCTGAGCA GTCTGAGAGC TGAGGACACA GCTGTGTACT
ACTGTGCAAG C]GGAGGGAGT CGGCCCTTCA ATGCTTTTGG
T[TACTGGGGC CAGGGCACCTGGTCACTGTT];
- (ii) ATGGACTGG ACCTGGAGGG TCTTCTTCCT GCTGGCACTG GCCACAGGTG
TGCACTCT[GA GGTCCAGCTG GTGCAGTCTG CAGCTGAGGT
TAAGAAGCCA GGGGCATCTG TGAAGGTCTC CTGCAAGACA
TCT]GGATACA CCTTCACTGA CTACTATATG CAC[TGGGTAC
AACAGGCTCC AGGAGCAGGG CTTGATTGGA TGGGATGG]AT
TGATCCTGAA GATGGTACCA CAAGTTATGC ACAGAAGTTC
CAGGGC[AGAG TCACCCTGAC GGCAGACACA TCCACAAGCA
CAGCCTACAT GGAGCTGAGC AGTCTGAGAG CTGAGGACGC AGCTGTGTAC
TACTGTGCAA GC]TTATATAT ATATGGATAC GCTGCTTACT
TAGAC[CTCTG GGGCCAGGGC ACCCTGGTCA CCGTC];
- (iii) ATGGACTGGA CCTGGAGGAT CCTCTTCCTG CTGGCACTGG CCACAGGTGT
GCACTCT[GAG GTCCAGCTGG TACAGTCTGC AGCTGAGGTT
AAGAAGCCAG GGGCATCTGT GAAGGTCTCC TGCAAGACAT
CT]GGATACAC CTTCACTGAC TACTATATGC AC[TGGGTACA
ACAGGCTCCA GGAGCAGGGC TTGATTGGAT GGGATGG]ATT
GATCCTGAAG ATGATACCAC AGGTTATGCA CAGAAGTTCC
AGGGC[AGAGT CACCCTGACG GCAGACACAT CCACAAGCAC
AGCCTACATG GAGCTGAGCA GTCTGAGAGC TGAGGACACA GCTGTGTACT
ACTGTGCAAG A]AAGTGGAGG TACTACGGTA GCCAAGAT[TA
CTGGGGCCAG GGAACCCTGG TCACCGTC]; and

(iv) ATGGACTGCA GCTGGAGAAT CTTCTTCCTG CTGGCACTGG CCACAGGTGT
 GCACTCT[GAG GTCCAGCTGG TGCAGTCTGC AGCTGAGGTT
 AAGAAGCCAG GGGCATCTGT GAAGGTCTCC TGCAAGACAT
 CT]GGATACAT CTTCAATTGAC CAGTATATGC AC[TGGGTACA
 GCAGGCTCCA GGAGCAGGGC TTGAATGGAT GGGATGG]ATT
 GATCCTGAGG ATGGTACCAC AAGTTATGCA CAGAAGTTCC
 AGGGC[AGAGT CACCCTGACG GCAGACACAT CCACAAACAC
 AGTCTATATG GAGCTGAGCA ATCTGAGAAC TGAGGACACA GCTGTGTACT
 ACTGTGCAAG G]GATATATGG GATTTTGAC[T ACTGGGGCCA
 GGGAACCCTG GTCACCGTC]

wherein the framework-encoding sequences are denoted by being enclosed within brackets

and

(b) the framework-encoding nucleic acid sequences of one of the nucleic acids of (i) - (iv) with one or more conservative nucleotide substitutions, wherein the framework-encoding nucleic acid sequence with said one or more conservative nucleotide substitutions encodes the same amino acid sequence as any one of the nucleic acids of (i) - (iv).

15. The nucleic acid according to claim 13 or 14 that encodes the canine heavy chain variable domain

EVQLVQSAAEVKKPGASVKVSCKTSGYSFTDYFMNWWQQAPGKGLDWMGRINPFNGDPFY
 NQKFKGRVTLTADTSTSTAYMELSSLRAEDAAVYYCARFYYGRYYAMDYWGQGTLLTV.

16. An antibody comprising a heavy chain variable domain and a light chain variable domain, wherein the heavy chain variable domain comprises the canine heavy chain variable domain polypeptide according to any one of claims 1-12.

17. The antibody according to claim 16 further comprising a light chain variable domain having the sequence:

TDSQTVATQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWWQQTQGRAPRTIIGGPNNRAPGVPS
 RFSGSISGNKATLTITGARPEDEADYFCALWYSNHWVFGGGTHLTVL.

18. A fragment of the antibody according to claim 16 or 17 comprising Fr¹, Fr², Fr³ and Fr⁴, wherein the fragment specifically binds to an antigen to which the antibody specifically binds.
19. A method of making a caninized immunoglobulin, wherein the method comprises:
- a) comparing a donor immunoglobulin framework or variable region amino acid sequence to corresponding sequences in a collection of canine immunoglobulins,
 - b) selecting an acceptor immunoglobulin, wherein the acceptor immunoglobulin is a canine immunoglobulin from the collection that has at least 60% identity to the donor immunoglobulin sequence; and
 - c) replacing one, two, or three CDR's of the acceptor immunoglobulin with the corresponding CDR(s) of the donor immunoglobulin thereby making said caninized immunoglobulin;
- wherein the acceptor immunoglobulin is the antibody according to claim 16 or 17 or the fragment of claim 18.
20. A method of making a caninized immunoglobulin, wherein the method comprises substituting at least one framework amino acid of an acceptor canine immunoglobulin with the corresponding amino acid from a donor canine immunoglobulin wherein:
- a) the amino acid of the acceptor immunoglobulin is rare for its position and the corresponding amino acid is common or rare for its position in canine immunoglobulin sequences;
 - b) the amino acid of the acceptor immunoglobulin is immediately adjacent to a CDR;
 - c) the amino acid of the acceptor immunoglobulin or the corresponding amino acid of the donor immunoglobulin is predicted to be within about 6 Å of a CDR in a three-dimensional immunoglobulin model and interacts with an antigen to which the immunoglobulin binds or with a CDR of the corresponding donor or acceptor immunoglobulin, or

d) the amino acid in the canine framework region of the acceptor immunoglobulin differs from the corresponding amino acid of the donor immunoglobulin, thereby making said caninized immunoglobulin;

wherein the donor and acceptor immunoglobulin are more than 60% identical to each other and bind to at least one common antigen, and wherein the acceptor canine immunoglobulin is the antibody according to claim 16 or 17 or the fragment of claim 18.

21. The method according to claim 20 wherein the acceptor canine immunoglobulin comprises the light chain variable domain having the sequence:

TDSQTVATQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTQGRAPRTIIGGPNNRAPGVPS
RFSGSISGNKATLTITGARPEDEADYFCALWYSNHWVFGGGTHLTVL.

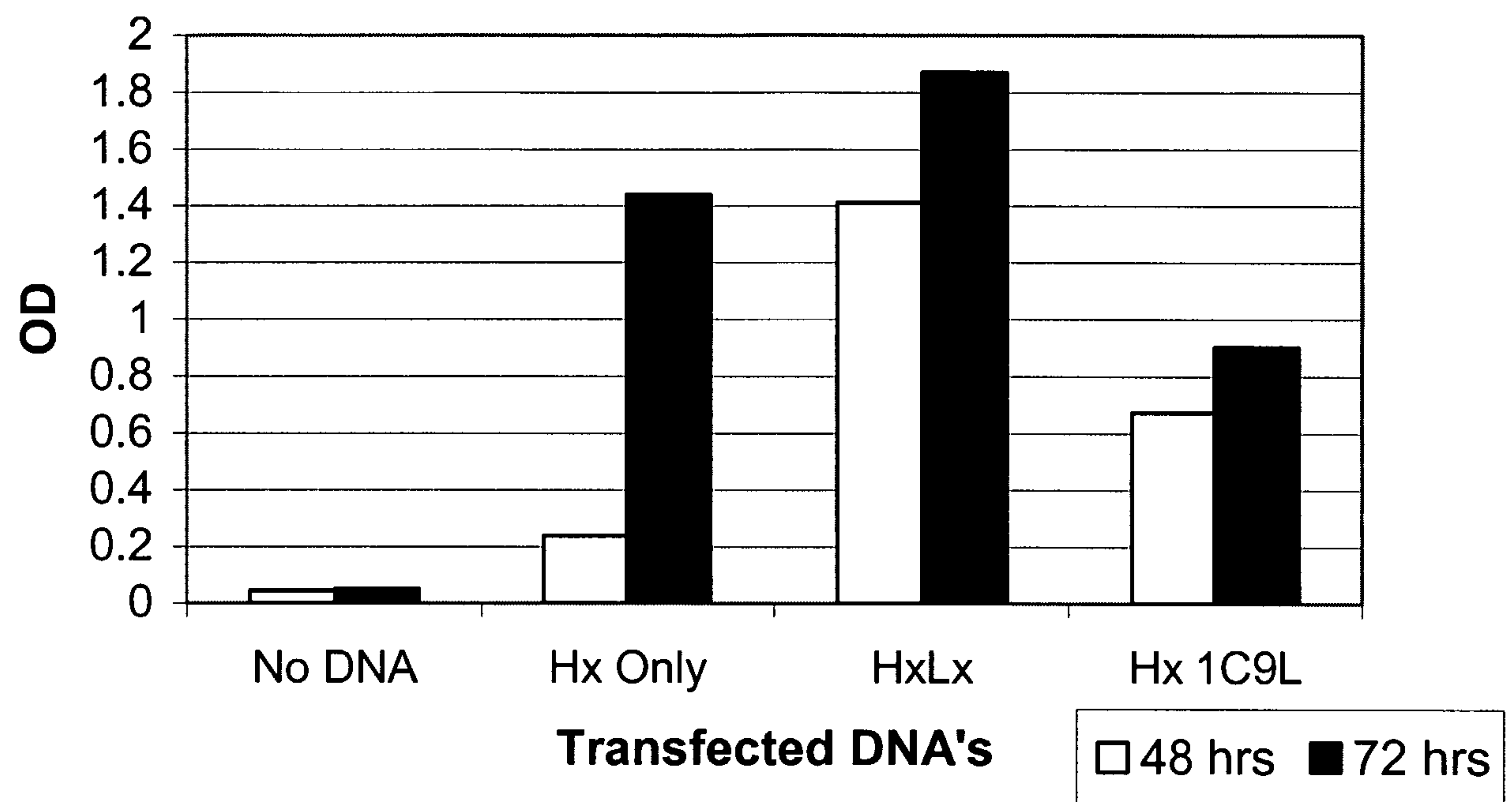
22. A caninized immunoglobulin produced according to the method of claim 20 or 21.

23. The antibody or binding fragment thereof according to any one of claims 16 - 18, wherein said antibody or binding fragment thereof specifically binds IgE.

24. Use of a therapeutically effective amount of the antibody or binding fragment thereof according to claim 23 for treatment of a canine having an IgE-mediated affliction, wherein said amount is sufficient to alleviate or eliminate one or more symptoms associated with the affliction.

25. Use of the antibody or binding fragment thereof according to claim 23 in the preparation of a medicament for treatment of a canine having an IgE-mediated affliction.

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**Fig. 1**

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		10	20	30	40	50
LAMB305	1	TDSQTVVVTQE	PSLSVSPGGT	VT LTCGLSSG	SVTASHFPGW	YQQTQGRAPR
15A2	1	AISQAVVTQE	SALTTSPGET	VT LTCRSSTG	AVTTSNYANW	VQEKPDHLFT
		60	70	80	90	
100						
LAMB305	51	TIIYNTYNRL	SGVPSRFSGS	ISGNKATLTI	TGARPEDEAD	YHCSVYTDDH
15A2	51	GLIGGPNNRA	PGVPARFSGS	LIGDKAALTI	TGAQTEDEAI	YFCALWYSNH
		110				
LAMB305	101	TPVFGGGTHL	TVLGQ			
15A2	101	W-VFGGGTKL	TVLGQ			

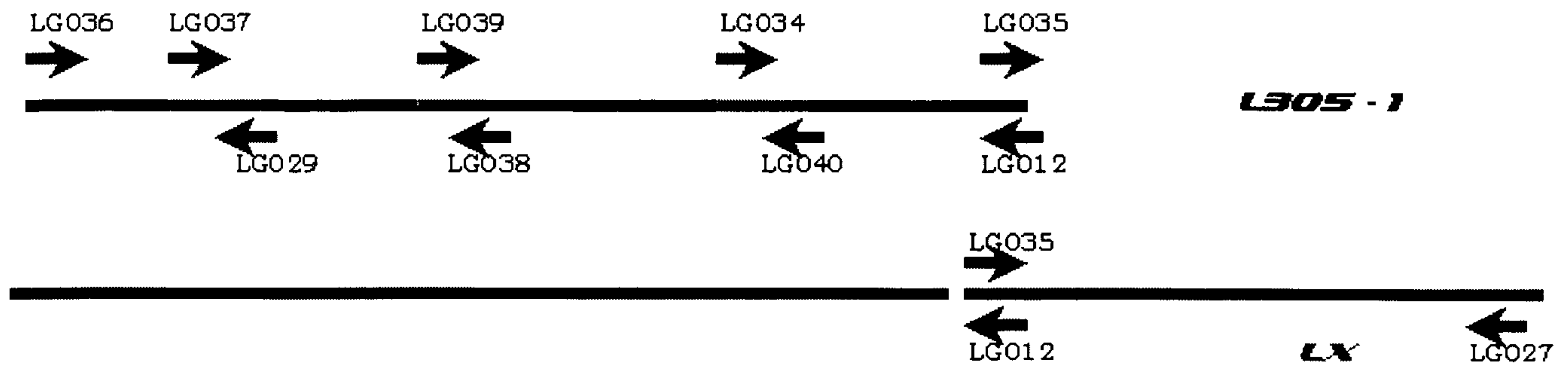
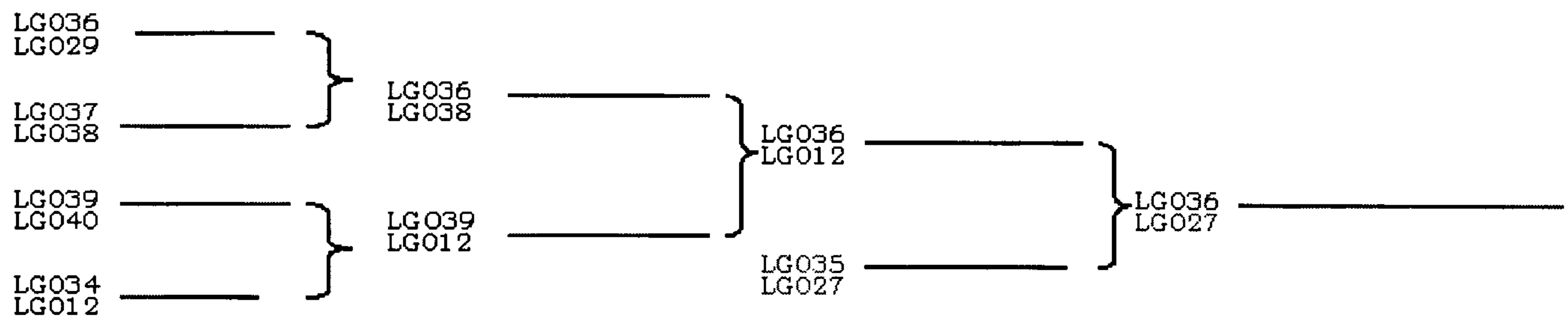
Fig. 2

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	10	20	30	40	50
15A2	EVQLQQSGPE	LVKPGASVKI	SCKASGYSFT	DYFMNWVMQS	HGKSLEWIGR
H74	EVQLVQSAAE	VKKPGASVKV	SCKTSGYTFT	DYYMHWVQQA	PGAGLDWMGW
	60	70	80	90	100
15A2	INPFNGDPFY	NQKFKGKATL	TVDKSSSTAH	MELRSLASED	SAVYYCARFY
H74	IDPEDGTTSY	AQKFQGRVTL	TADTSTSTAY	MELSSLRAED	AAVYYCASLY
	110				
15A2	YGRYYAM-DY	WGQ			
H74	IYGYAAYLDL	WGQ			

Fig. 3

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SCHEMATIC DIAGRAM (A)**SCHEMATIC DIAGRAM (B)****Fig. 4**

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Light Chain

15A2/1NGQ	QAVVTQESALTTSPGETVTLTC	<u>RSSTGAVTTSNYAN</u>	WVQEKPDHLFTGLI
15A2/1FBI	SQAVVTQESALTTSPGETVTLTC	<u>RSSTGAVTTSNYAN</u>	WVQEKPDHLFTGLI
15A2/2VIR	QAVVTQESALTTSPGETVTLTC	<u>RSSTGAVTTSNYAN</u>	WVQEKPDHLFTGLI
LAMB305-1	QTVVTQEPSLSVSPGGTVTLTC	<u>RSSTGAVTTSNYAN</u>	WYQQTQGRAPRTII
15A2/1NGQ	<u>G</u> GPNNRAP	<u>G</u> VPARFSGSLIGDKAALTITGAQTEDEAIYFC	<u>ALWYSNHWV</u> F
15A2/1FBI	<u>G</u> GPNNRAP	<u>G</u> VPARFSGSLIGDKAALTITGAQTEDEAIYFC	<u>ALWYSNHWV</u> F
15A2/2VIR	<u>G</u> GPNNRAP	<u>G</u> VPARFSGSLIGDKAALTITGAQTEDEAIYFC	<u>ALWYSNHWV</u> F
LAMB305-1	Y <u>G</u> GPNNRAP	GVPSRFSGSISGNKATLTITGARPEDEADYHC	<u>ALWYSNHWV</u> F
15A2/1NGQ	GGGTKLTVL		
15A2/1FBI	GGGTKLTVL		
15A2/2VIR	GGGTKLTVL		
LAMB305-1	GGGTHLTVL		

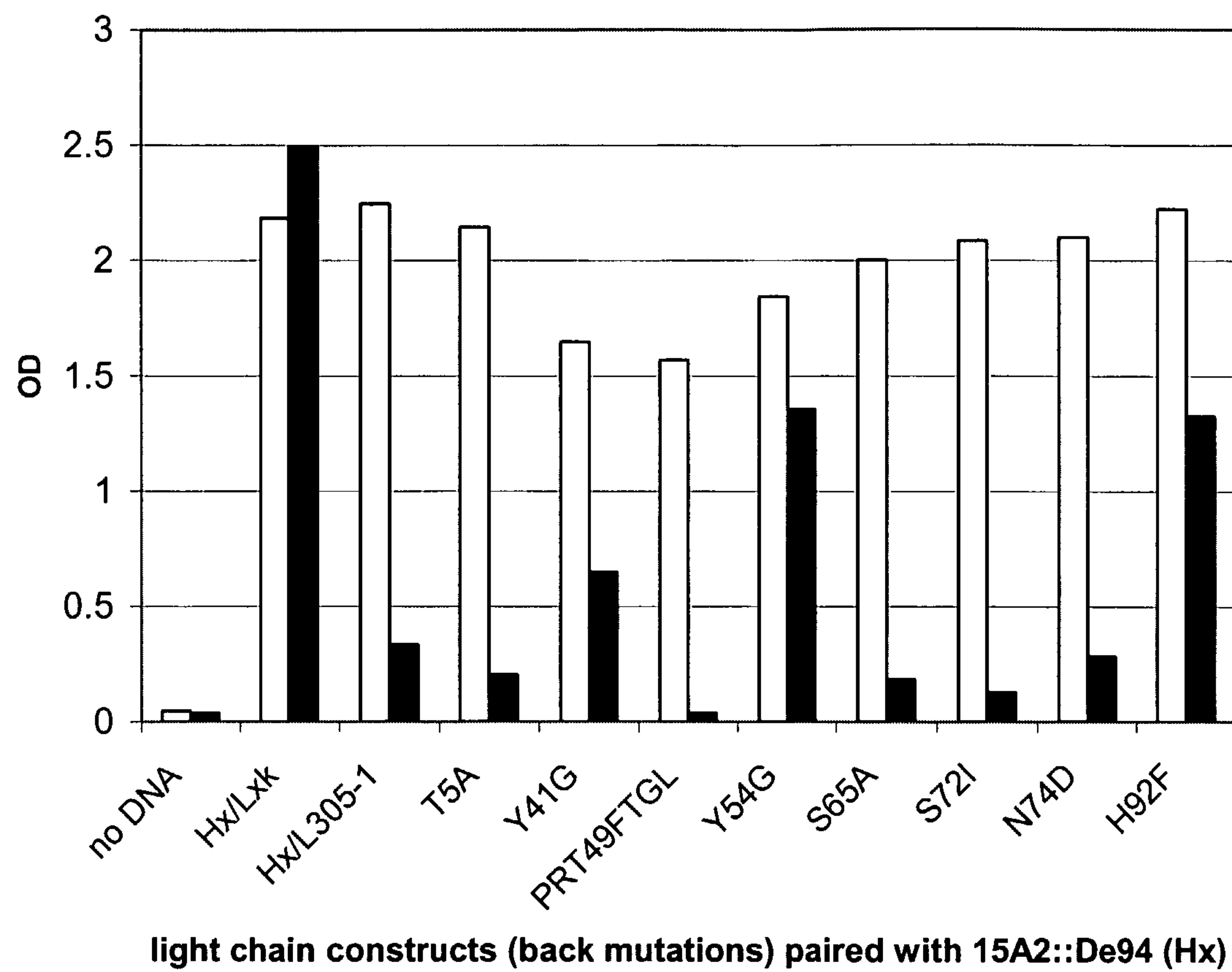
Heavy Chain

15A2/1NGQ		EVQLQQSGPELVKPGASVKISCKA	<u>SGYSFTDYFMN</u>	WVMQSHGKSLEWIG
15A2/1FBI		EVQLQQSGPELVKPGASVKISCKA	<u>SGYSFTDYFMN</u>	WVMQSHGKSLEWIG
15A2/2VIR		EVQLQQSGPELVKPGASVKISCKA	<u>SGYSFTDYFMN</u>	WVMQSHGKSLEWIG
H74-1		EVQLVQSAAEVKKPGASVKVSCKT	<u>SGYSFTDYFMN</u>	WVQQAPGAGLDWMG
15A2/1NGQ	153	<u>RINPFNGDPFYNQKF</u>	<u>KGKATLTVDKSSSTAHMELRSLASEDSAVYYCAR</u>	
15A2/1FBI	152	<u>RINPFNGDPFYNQKF</u>	<u>KGKATLTVDKSSSTAHMELRSLASEDSAVYYCAR</u>	
15A2/2VIR	153	<u>RINPFNGDPFYNQKF</u>	<u>KGKATLTVDKSSSTAHMELRSLASEDSAVYYCAR</u>	
H74-1		<u>RINPFNGDPFYNQKF</u>	KGKATLTVDKSSSTAHMELRSLASEDSAVYYCAR	
15A2/1NGQ	203	<u>FYYGRYYAM</u>	DYWGQGTSVTVSS	
15A2/1FBI	202	<u>FYYGRYYAM</u>	DYWGQGTSVTVSS	
15A2/2VIR	203	<u>FYYGRYYAM</u>	DYWGQGTSVTVSS	
H74-1		<u>FYYGRYYAM</u>	DYWGQ	

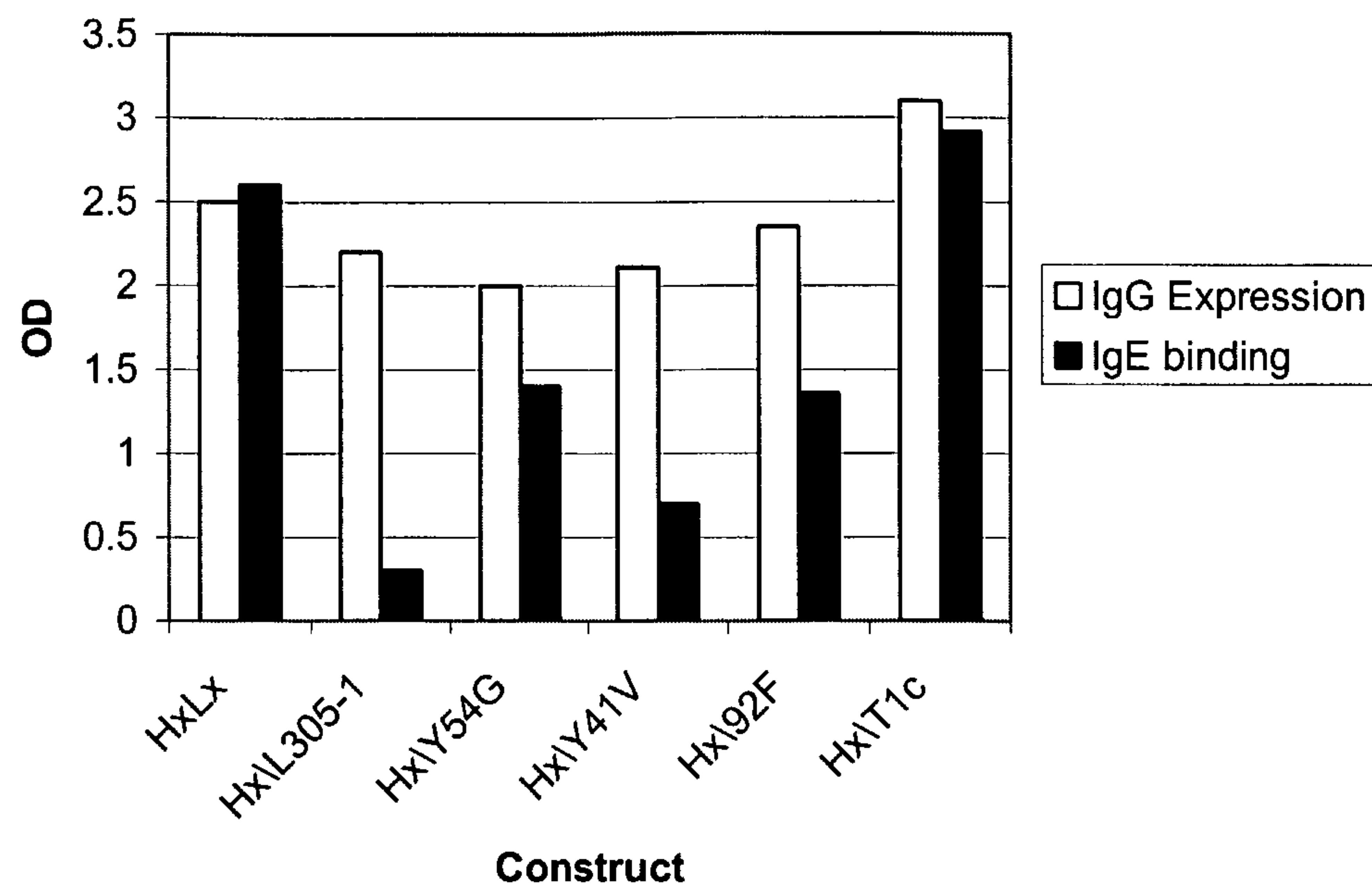
Fig. 5

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□ IgG Concentration
■ IgE binding

Screening transfections - L305.4 #2**Fig. 6**

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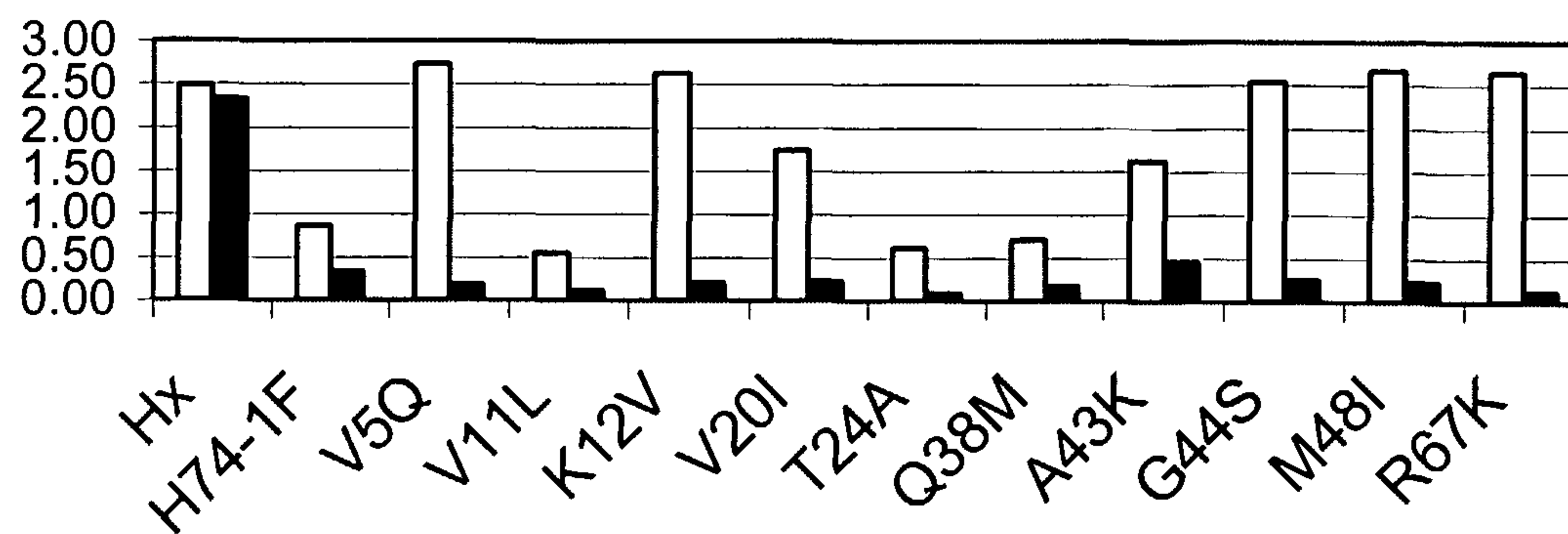
**Fig. 7**

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□ IgG expression

Heavy Chain Back Mutations

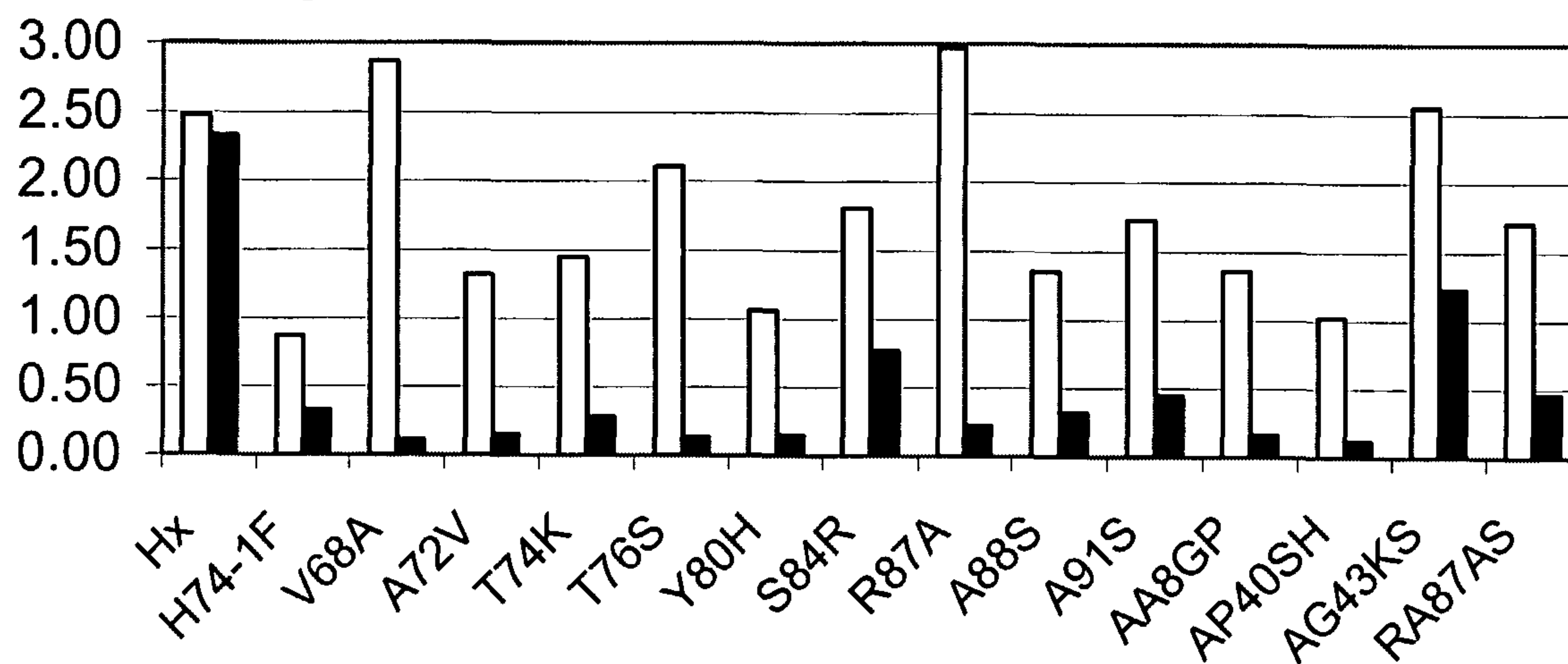
■ IgE binding

**Fig. 8A**

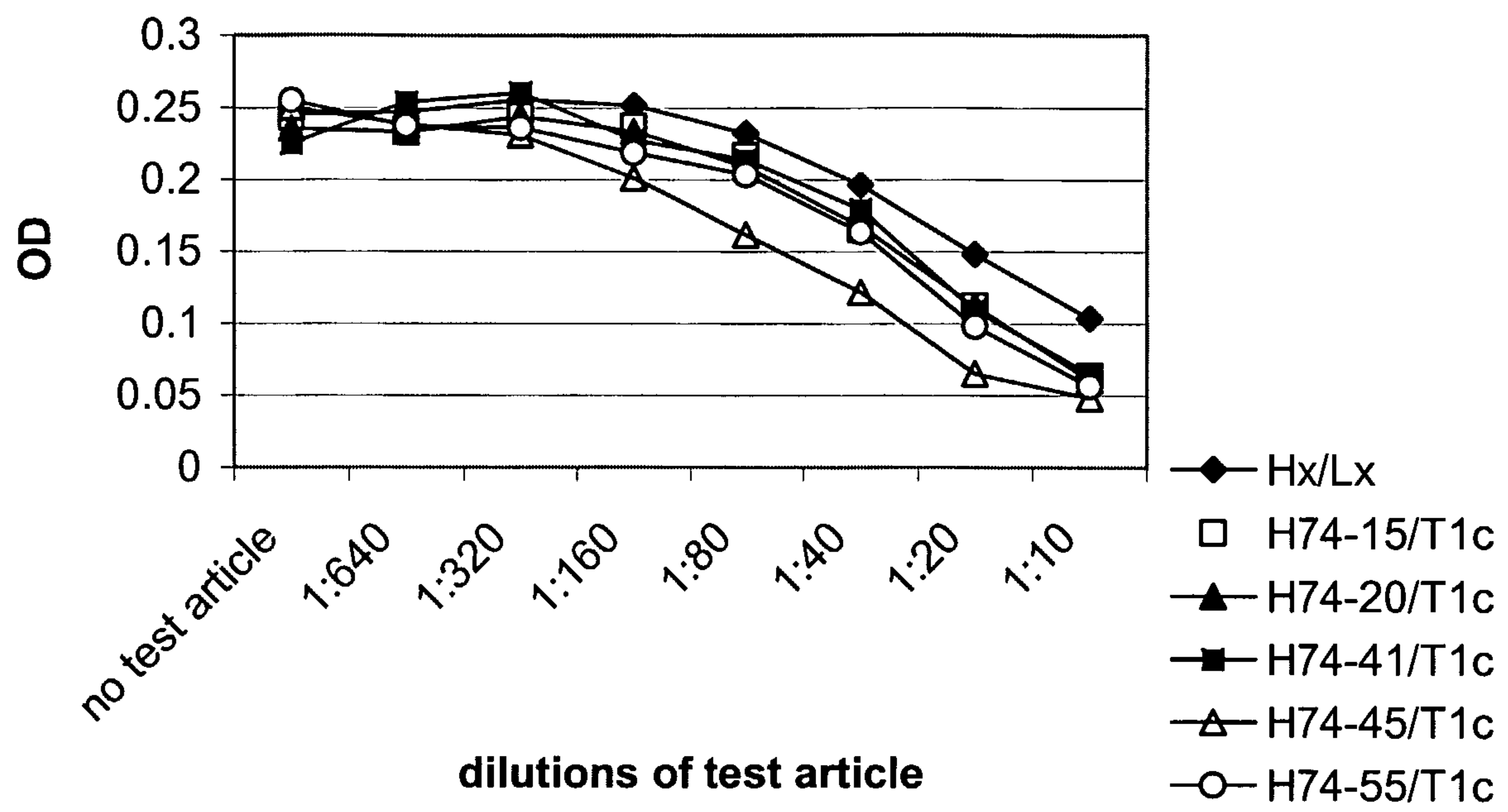
□ IgG expression

Heavy Chain Back Mutations

■ IgE binding

**Fig. 8B**

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IgE-Receptor Competition - normalized for expression**Fig. 9**